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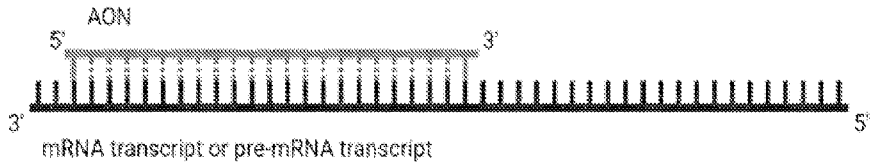

FIGURE 1

(57) Abstract: Disclosed herein are antisense oligonucleotides, such as gapmer antisense oligonucleotides with a modified backbone chemistry (e.g., with one or more spacers). Such gapmer antisense oligonucleotides with modified backbone chemistries may be useful for treating various diseases, such as neurological diseases.

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GAPMER ANTISENSE OLIGONUCLEOTIDES WITH MODIFIED BACKBONE CHEMISTRIES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 63/285,705, filed on December 3, 2021, U.S. Provisional Application No. 63/285,888, filed on December 3, 2021, U.S. Provisional Application No. 63/285,692, filed on December 3, 2021, U.S. Provisional Application No. 63/285,696, filed on December 3, 2021, and U.S. Provisional Application No. 63/285,665, filed on December 3, 2021, each of which is hereby incorporated herein by reference in their entireties for all purposes.

REFERENCE TO A SEQUENCE LISTING XML

[0002] This application contains a sequence listing which has been submitted electronically in XML format. The Sequence Listing XML is incorporated herein by reference. Said XML file, created on November 17, 2022, is named QRL-011WO_SL.xml and is 418,206,230 in size.

BACKGROUND

[0003] Antisense oligonucleotides are nucleic acid-based compounds that can be used to inhibit expression of certain genes that are linked to diseases. Although antisense oligonucleotides can be generally designed to hybridize with target genes, conventional antisense oligonucleotides often exhibit poor efficacy. Thus, there is a need to develop modified antisense oligonucleotides that exhibit improved performance and efficacy for preventing, ameliorating, and treating diseases, examples of which include neurological diseases.

SUMMARY

[0004] Disclosed herein is a compound comprising a gapmer oligonucleotide, and wherein the gapmer oligonucleotide comprises a spacer. Additionally disclosed herein is a gapmer oligonucleotide, wherein the gapmer oligonucleotide comprises a spacer. In various embodiments, the gapmer oligonucleotide comprises a second spacer that is non-adjacent to the spacer.

[0005] In various embodiments, the gapmer oligonucleotide comprises a sequence that is between 85 and 98% complementary to an equal length portion of a transcript whose presence leads to a neurological disease. In various embodiments, the gapmer oligonucleotide comprises a sequence that is between 85 and 98% complementary to an equal length portion of a PPM1A

mRNA or pre-mRNA transcript, an ATXN2 mRNA or pre-mRNA transcript, a SOD1 mRNA or pre-mRNA transcript, or a MAPT mRNA or pre-mRNA transcript. In various embodiments, the gapmer oligonucleotide comprises a sequence that is between 85 and 98% complementary to an equal length portion of any one of SEQ ID NOs: 1909-1913, 149355-149361, 167802-167804, or 301567-301589, a sequence having 90% identity thereof, or to a 15 to 50 contiguous nucleobase portion thereof.

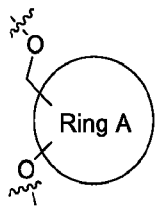
[0006] In various embodiments, the gapmer oligonucleotide comprises a sequence that shares at least 85% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566,SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In various embodiments, the gapmer oligonucleotide comprises a sequence that shares at least 90% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In various embodiments, the gapmer oligonucleotide comprises a sequence that shares at least 95% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In various embodiments, the gapmer oligonucleotide comprises a sequence that shares at least 100% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[0007] In various embodiments, the gapmer oligonucleotide comprises a segment with at most 11 linked nucleosides, and wherein the gapmer oligonucleotide comprises a sequence that shares at least 85% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In various embodiments, the gapmer oligonucleotide comprises a segment with at most 10, 9, 8, 7, 6, 5, 4, 3, or 2 linked nucleosides, and wherein the gapmer oligonucleotide comprises a sequence that shares at least 85% identity with an equal length portion of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In various embodiments, the gapmer oligonucleotide comprises a segment with at most 11 linked nucleosides, and wherein the gapmer oligonucleotide comprises a sequence that shares at least 90% identity with an equal length portion of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In various embodiments, the gapmer oligonucleotide comprises a segment with at most 10, 9, 8, 7, 6, 5, 4, 3, or 2 linked nucleosides, and wherein the gapmer oligonucleotide comprises a sequence that shares at least 90% identity with an equal length portion of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[0008] In various embodiments, the gapmer oligonucleotide is at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, or at least 25 oligonucleotide units in length. In various embodiments, at least one (*i.e.*, one or more) nucleoside linkage of the gapmer oligonucleotide is a non-natural linkage, In various embodiments, the gapmer oligonucleotide is at least 19 oligonucleotide units in length.

[0009] In various embodiments, the spacer is a nucleoside-replacement group comprising a non-sugar substitute that is incapable of linking to a nucleotide base. In various embodiments, the spacer is located between positions 5 and 11 of the gapmer oligonucleotide. In various embodiments, the spacer is located between positions 7 and 11 of the gapmer oligonucleotide. In various embodiments, the gapmer oligonucleotide further comprises a second spacer, and wherein the spacer and the second spacer are non-adjacent to one another. In various embodiments, the gapmer oligonucleotide further comprises a second spacer, wherein the second spacer is located between positions 15 and 19 of the gapmer oligonucleotide. In various embodiments, the spacer and the second spacer are separated by at least 5 nucleobases, at least 6 nucleobases, or at least 7 nucleobases in the gapmer oligonucleotide. In various embodiments, the spacer is located between positions 5 and 11 of the gapmer oligonucleotide, and wherein the second spacer is located between positions 15 and 19 of the gapmer oligonucleotide. In various embodiments, the spacer is located at position 8 of the gapmer oligonucleotide, and wherein the second spacer is located at position 16 of the gapmer oligonucleotide. In various embodiments, the spacer is located at position 5 of the gapmer oligonucleotide, and wherein the second spacer is located at position 17 of the gapmer oligonucleotide. In various embodiments, the spacer is located at position 7 of the gapmer oligonucleotide, and wherein the second spacer is located at position 15 of the gapmer oligonucleotide. In various embodiments, the spacer is located at position 11 of the gapmer oligonucleotide, and wherein the second spacer is located at position 19 of the gapmer oligonucleotide.

[0010] In various embodiments, each of the spacer or second spacer is a nucleoside-replacement group comprising a non-sugar substitute wherein the non-sugar substitute does not contain a ketone, aldehyde, ketal, hemiketal, acetal, hemiacetal, aminal or hemiaminal moiety and is incapable of forming a covalent bond with a nucleotide base. In various embodiments, each of the spacer or second spacer is independently represented by Formula (X), wherein:

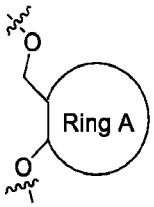


Formula (X)

Ring A is an optionally substituted 4-8 member monocyclic cycloalkyl group or a 4-8 member monocyclic heterocyclyl group, wherein the heterocyclyl group contains 1 or 2 heteroatoms selected from O, S and N, provided that A is not capable of forming a covalent bond to a nucleobase; and

the  symbol represents the point of connection to an internucleoside linkage.

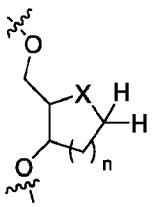
[0011] In various embodiments, each of the spacer or second spacer is independently represented by Formula (Xa), wherein:



Formula (Xa).

[0012] In various embodiments, ring A is an optionally substituted 4-8 member monocyclic cycloalkyl group selected from cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and cyclooctyl; or a 4-8 member monocyclic heterocyclyl group, selected from oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, 1,4-dioxanyl, pyrrolidinyl, piperidinyl, piperazinyl, morpholinyl and azepanyl. In various embodiments, ring A is tetrahydrofuranyl. In various embodiments, ring A is tetrahydropyranyl.

[0013] In various embodiments, each of the spacer and second spacer is independently represented by Formula I, wherein:

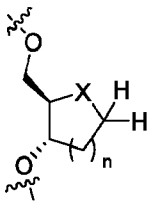


Formula (I)

X is selected from $-CH_2-$ and -O-; and

n is 0, 1, 2 or 3.

[0014] In various embodiments, each of the spacer and second spacer is independently represented by Formula I', wherein:

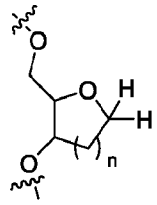


Formula (I')

X is selected from -CH_2- and -O-; and

n is 0, 1, 2 or 3.

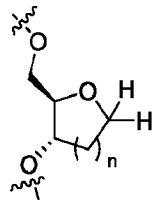
[0015] In various embodiments, each of the spacer and second spacer is independently represented by Formula (Ia), wherein:



Formula (Ia); and

n is 0, 1, 2 or 3.

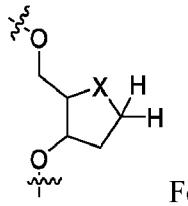
[0016] In various embodiments, each of the spacer and second spacer is independently represented by Formula (Ia'), wherein:



Formula (Ia'); and

n is 0, 1, 2 or 3.

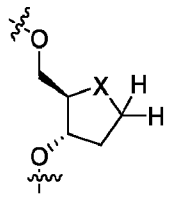
[0017] In various embodiments, each of the spacer and second spacer is independently represented by Formula II, wherein:



Formula (II); and

X is selected from -CH_2- and -O-.

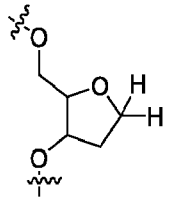
[0018] In various embodiments, each of the spacer and second spacer is independently represented by Formula II', wherein:



Formula (II'); and

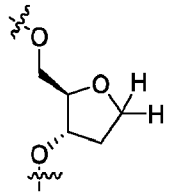
X is selected from -CH_2- and -O-.

[0019] In various embodiments, each of the spacer and second spacer is independently represented by Formula (Iia), wherein:



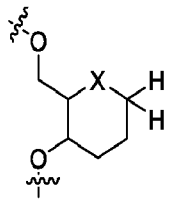
Formula (Iia).

[0020] In various embodiments, each of the spacer and second spacer is independently represented by Formula (Iia'), wherein:



Formula (Iia').

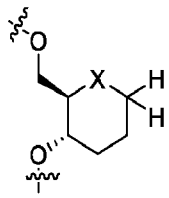
[0021] In various embodiments, each of the spacer and second spacer is independently is independently represented by Formula III, wherein:



Formula (III); and

X is selected from -CH_2- and -O-.

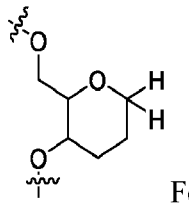
[0022] In various embodiments, each of the spacer and second spacer is independently represented by Formula III', wherein:



Formula (III'); and

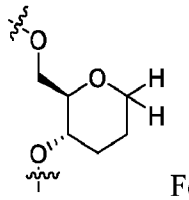
X is selected from -CH_2- and -O-.

[0023] In various embodiments, each of the spacer and second spacer is independently represented by Formula (IIIa), wherein:



Formula (IIIa).

[0024] In various embodiments, each of the spacer and second spacer is independently represented by Formula (IIIa'), wherein:



Formula (IIIa').

[0025] In various embodiments, the gapmer oligonucleotide comprising the spacer has a GC content of at least 10%. In various embodiments, the gapmer oligonucleotide comprising the spacer has a GC content of at least 20%. In various embodiments, the gapmer oligonucleotide comprising the spacer has a GC content of at least 25%. In various embodiments, the gapmer oligonucleotide comprising the spacer has a GC content of at least 30%. In various embodiments, the gapmer oligonucleotide comprising the spacer has a GC content of at least 40%. In various embodiments, the gapmer oligonucleotide comprising the spacer has a GC content of at least 50%. In various embodiments, at least one (*i.e.*, one or more) nucleoside linkage of the gapmer oligonucleotide is independently selected from the group consisting of a phosphodiester linkage, a phosphorothioate linkage, an alkyl phosphate linkage, a phosphorodithioate linkage, a phosphotriester linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a thiophosphorodiamidate linkage, a phosphorodiamidate linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage. In various embodiments, at least one internucleoside linkage of the nucleotide sequence is a phosphorothioate linkage. In various embodiments, the phosphorothioate internucleoside linkage is in one of a *R*p configuration or a *S*p configuration.

[0026] In various embodiments, the gapmer oligonucleotide comprises one or more chiral centers and/or double bonds. In various embodiments, the gapmer oligonucleotide exists as stereoisomers selected from geometric isomers, enantiomers, and diastereomers. In various embodiments, all internucleoside linkages of the nucleotide sequence are phosphorothioate

linkages. In various embodiments, the gapmer oligonucleotide comprises at least one modified nucleobase. In various embodiments, the at least one modified nucleobase is 5-methylcytosine, pseudouridine, or 5-methoxyuridine. In various embodiments, the gapmer oligonucleotide comprises at least one nucleoside with a modified sugar moiety. In various embodiments, the modified sugar moiety is one of a 2'-OMe modified sugar moiety, bicyclic sugar moiety, 2'-*O*-(2-methoxyethyl) (2'-MOE), 2'-O-(N-methylacetamide), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt), *S*-cEt, hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA).

[0027] In various embodiments, the gapmer oligonucleotide comprises two, three, four, five, six, seven, eight, nine, or ten nucleosides with modified sugar moieties. In various embodiments, the modified sugar moieties are independently any one of a 2'-OMe modified sugar moiety, bicyclic sugar moiety, 2'-*O*-(2-methoxyethyl) (2'-MOE), 2'-O-(N-methylacetamide), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt), *S*-cEt, hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA). In various embodiments, the gapmer oligonucleotide comprises ten 2'-*O*-(2-methoxyethyl) (2'-MOE) nucleosides. In various embodiments, five of the 2'-*O*-(2-methoxyethyl) (2'-MOE) nucleosides are located at the 3' end of the gapmer oligonucleotide, and wherein five of the 2'-*O*-(2-methoxyethyl) (2'-MOE) nucleosides are located at the 5' end of the gapmer oligonucleotide. In various embodiments, the at least one nucleoside with the modified sugar moiety or the nucleosides with modified sugar moieties are ribonucleosides. In various embodiments, the gapmer oligonucleotide comprises at least one deoxyribonucleoside. In various embodiments, the gapmer oligonucleotide comprises two, three, four, five, six, seven, eight, nine, or ten deoxyribonucleosides.

[0028] In various embodiments, the gapmer oligonucleotide comprises: a gap segment comprising one or more of linked deoxyribonucleosides, 2'-Fluoro Arabino Nucleic Acids (FANA), and Fluoro Cyclohexenyl nucleic acid (F-CeNA); a 5' wing region comprising linked nucleosides; and a 3' wing region comprising linked nucleosides; wherein the central region comprises a region of at least 8 oligonucleotide units comprising at least 4 contiguous nucleobases, the region having at least 80% identity to an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566 , SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C positioned between the 5' wing segment and the 3' wing segment; wherein the 5' wing region and the 3' wing region each comprises at least two linked nucleosides; and wherein at least one nucleoside of each wing region comprises a modified sugar.

[0029] In various embodiments, the at least two linked nucleosides of the 5' wing region are linked through a phosphorothioate internucleoside linkage and/or wherein the at least two linked nucleosides of the 3' wing region are independently linked through a phosphorothioate internucleoside linkage. In various embodiments, every internucleoside linkage of the 5' wing region and/or every internucleoside linkage of the 3' wing region, independently are phosphorothioate internucleoside linkages. In various embodiments, the 5' wing region further comprises at least one phosphodiester internucleoside linkage. In various embodiments, the 3' wing region further comprises at least one phosphodiester internucleoside linkage. In various embodiments, the at least two linked nucleosides of the 5' wing region are linked through a phosphodiester internucleoside linkage and/or wherein the at least two linked nucleosides of the 3' wing region are independently linked through a phosphodiester internucleoside linkage. In various embodiments, at least one of the internucleoside linkages of the central region is a phosphodiester linkage. In various embodiments, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, or at least nine of the internucleoside linkages of the central region are phosphodiester linkages. In various embodiments, at least one of the internucleoside linkages of the central region is a phosphorothioate internucleoside linkage. In various embodiments, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, or at least nine of the internucleoside linkages of the central region are phosphorothioate internucleoside linkages. In various embodiments, all internucleoside linkages of the gapmer oligonucleotide are phosphorothioate internucleoside linkages. In various embodiments, any one or all of the phosphorothioate internucleoside linkages are in a *R*p configuration, a *S*p configuration, or in any combination of *R*p and *S*p configuration.

[0030] In various embodiments, the gapmer oligonucleotide comprises at least one modified sugar moiety. In various embodiments, the 5' wing region or the 3' wing region comprises the at least one modified sugar moiety. In various embodiments, the central region comprises the at least one modified sugar moiety. In various embodiments, the at least one modified sugar moiety is any one of a 2'-OMe modified sugar moiety, bicyclic sugar moiety, 2'-O-(2-methoxyethyl) (2'-MOE), 2'-O-(N-methylacetamide), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt), *S*-cEt, tcDNA, hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA). In various embodiments, the gapmer oligonucleotide comprises one or more 2'-MOE nucleosides. In various embodiments, the 5' wing region or the 3' wing region comprise one or more 2'-MOE nucleosides. In various embodiments, the 5' wing region or the 3' wing region comprise two, three, four, five, or six 2'-MOE nucleosides. In various embodiments, every nucleoside of the 5' wing region or the 3' wing

region is a 2'-MOE nucleoside. In various embodiments, the central region comprises one or more 2'-MOE nucleosides. In various embodiments, the central region comprises two, three, four, five, six, seven, eight, nine, or ten 2'-MOE nucleosides. In various embodiments, every nucleoside of the central region is a 2'- MOE nucleoside. In various embodiments, the one or more 2'-MOE nucleosides are linked through phosphorothioate internucleoside linkages.

[0031] In various embodiments, the gapmer oligonucleotide comprises sugar modifications in any of the following patterns: eeeee-d10-eeeee, eeeee-d8-eeeee, eeeeee-d11-eeeeee, eee-d8-eee, eee-d10-eee, eeee-d10-eeee, and eeee-d8-eeee, wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside, and wherein at least one "e" or at least one "d" is replaced with a spacer. In various embodiments, the gapmer oligonucleotide comprises internucleoside linkages in any of the following patterns: sssssooooooooosssss; ooooosssssssssooooo; ooooooooooooooosssss; soosssssssssssssss; sososssssssssssosos; sssssssssssssssoos; sssssooooooooooooo; sssssssssssssssssss; sssssssssssssssssssss; sssoooooooosss; ooosssssssooo; sssssssssssss; sossssssssssos; sossssssssssss; sssssssssssos; sssssssssssooo; ooosssssssssss; sssooooooooosss; ooosssssssssooo; sssssssssssssss; sssssssssssssooo; ooosssssssssssss; sossssssssssssos; sossssssssssssss; sssssssssssssos; sssooooooooooosssss; ooooosssssssssooooo; sssssssssssssssss; sssssssssssssooooo; soosssssssssssoos; soosssssssssssssss; sssssssssssssssoos; ooooosssssssssssss; sssssooooooosssss; ooooosssssssooooo; sssssssssssssooooo; ooooosssssssssss; soossssssssssoos; soossssssssssss; sssssssssssssoos; soooosssssssssssoooos; soooosssssssssssooss; sossssssssssssoss; sossssssssssssssosss; or sssssssssssssss; wherein s= a phosphorothioate linkage, and o= a phosphodiester linkage.

[0032] In various embodiments, the gapmer oligonucleotide comprises sugar modification and internucleoside linkage combinations, respectively, in any of the following patterns:

a) eeeee-d10-eeeee and sssssooooooooosssss;

b) eeeee-d10-eeeee and ooooosssssssssooooo;

c) eeeee-d10-eeeee and sssssssssssssssssss;

d) eee-d8-eee and sssooooooosss;

e) eee-d8-eee and ooosssssssooo

f) eee-d8-eee and sssssssssssss;

g) eee-d10-eee and sssooooooooosss;

h) eee-d10-eee and ooosssssssssooo;

i) eee-d10-eee and sssssssssssssss;

j) eeee-d10-eeee and ssssoooooooossss;

k) eeee-d10-eeee and oooossssssssoooo;

l) eeee-d10-eeee and sssssssssssssss;

m) eeee-d8-eeee and ssssooooooossss,

n) eeee-d8-eeee and oooossssssoooo,

o) eeee-d8-eeee and sssssssssssss,

p) eeeeee-d11-eeeeee and sssssssssssssssssssss;

q) eeeee-d10-eeeee and sosossssssssssosos;

r) eeeee-d10-eeeee and soooossssssssssooos;

s) eeeee-d10-eeeee and soooossssssssssooss;

t) eeeee-d8-eeeee and sossssssssssssoss;

u) eeeee-d10-eeeee and sossssssssssssosss;

v) eeeeee-d10-eeee and sssssssssssssssss;

wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside, and wherein s= a phosphorothioate linkage, and o= a phosphodiester linkage, and wherein at least one "e" or at least one "d" of the gapmer oligonucleotide is replaced with a spacer.

[0033] In various embodiments, the gapmer oligonucleotide comprises at least one modified nucleobase. In various embodiments, the 5' wing region or the 3' wing region comprises the at least one modified nucleobase. In various embodiments, the central region comprises the at least one modified nucleobase. In various embodiments, the at least one modified nucleobase is 5-methylcytosine, pseudouridine, or 5-methoxyuridine. In various embodiments, every cytosine in the 5' wing region or the 3' wing region is a 5-methylcytosine. In various embodiments, every cytosine in the central region is a 5-methylcytosine. In various embodiments, the gapmer oligonucleotide comprises sugar modification and internucleoside linkage combination of: eeeee-d10-eeeee and sssssssssssssssss, wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside, wherein s= a phosphorothioate linkage, wherein at least one "e" or at least one "d" of the gapmer oligonucleotide is replaced with a spacer, and wherein each cytosine of the 2'-MOE nucleosides is a 5-methylcytosine.

[0034] In various embodiments, the gapmer oligonucleotide further comprises a conjugate moiety. In various embodiments, the conjugate moiety is a cholesterol conjugate located on the 3' end of the gapmer oligonucleotide.

[0035] Additionally disclosed herein is a pharmaceutical composition comprising a gapmer oligonucleotide disclosed herein, or a pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable excipient.

[0036] Additionally disclosed herein is a method of treating a neurological disease in a patient in need thereof, the method comprising administering to the patient a gapmer oligonucleotide disclosed herein or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition disclosed herein. In various embodiments, the neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Limbic-predominant age-related TDP-43 encephalopathy (LATE)), Cerebral Age-Related TDP-43 With Sclerosis (CARTS), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and synaptic diseases like autism.

[0037] In various embodiments, the gapmer oligonucleotide is administered topically, parenterally, intrathecally, orally, pulmonarily, intratracheally, intranasally, transdermally, buccally, intrathalamically, intracerebroventricularly, intraocularly, sublingually, rectally, vaginally, or intraduodenally. In various embodiments, the gapmer oligonucleotide is administered intrathecally. In various embodiments, a therapeutically effective amount of the gapmer oligonucleotide is administered. In various embodiments, the patient is a human. In various embodiments, the pharmaceutical composition is suitable for topical, parenteral,

intrathecal, oral, pulmonary, intratracheal, intranasal, transdermal, buccal, intrathalamical, intracerebroventricular, intraocular, sublingual, rectal, vaginal, or intraduodenal.

[0038] Additionally disclosed herein is use of a gapmer oligonucleotide in the manufacture of a medicament for the treatment of neurological disease. In various embodiments, the neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Limbic-predominant age-related TDP-43 encephalopathy (LATE)), Cerebral Age-Related TDP-43 With Sclerosis (CARTS), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and synaptic diseases like autism. In various embodiments, the gapmer oligonucleotide is a gapmer oligonucleotide disclosed herein.

[0039] Additionally disclosed herein is a method of treating a neurological disease in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a pharmaceutical composition comprising a gapmer oligonucleotide, and a pharmaceutically acceptable excipient. In various embodiments, the neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia

(SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Limbic-predominant age-related TDP-43 encephalopathy (LATE)), Cerebral Age-Related TDP-43 With Sclerosis (CARTS), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and synaptic diseases like autism. In various embodiments, the gapmer oligonucleotide is the gapmer oligonucleotide disclosed herein, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition disclosed herein. In various embodiments, the pharmaceutical composition is administered topically, parenterally, orally, pulmonarily, rectally, buccally, sublingually, vaginally, intratracheally, intranasally, intrathecally, intracisternally, transdermally, or intraduodenally. In various embodiments, the pharmaceutical composition is administered intrathecally. In various embodiments, the patient is human.

[0040] Additionally disclosed herein is a gapmer oligonucleotide, or a pharmaceutically acceptable salt thereof, for use as a medicament. Additionally disclosed herein is a gapmer oligonucleotide, or a pharmaceutically acceptable salt thereof, for use in the treatment of a neurological disease. In various embodiments, said neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism.

[0041] Additionally disclosed herein is a gapmer oligonucleotide comprising the sequence of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, or a pharmaceutically acceptable salt thereof; wherein the gapmer oligonucleotide further comprises: a

gap segment comprising one or more of linked deoxyribonucleosides, 2'-Fluoro Arabino Nucleic Acids (FANA), and Fluoro Cyclohexenyl nucleic acid (F-CeNA); a 5' wing region comprising linked nucleosides; and a 3' wing region comprising linked nucleosides; wherein the gapmer oligonucleotide comprises sugar modifications of eeeee-d10-eeeee, wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside, wherein at least one "e" or at least one "d" is replaced with a spacer, and wherein each cytosine of the 2'MOE nucleosides is a 5-methylcytosine.

[0042] In various embodiments, at least one internucleoside linkage of the gapmer oligonucleotide is a phosphorothioate linkage. In various embodiments, the phosphorothioate internucleoside linkage is in one of a *R*p configuration or a *S*p configuration. In various embodiments, all internucleoside linkages of the gapmer oligonucleotide are phosphorothioate linkages. In various embodiments, the gapmer oligonucleotide comprises sugar modification and internucleoside linkage combinations, respectively, in any of the following patterns:

a) eeeee-d10-eeeee and sssssoooooooossssss;

b) eeeee-d10-eeeee and ooooosssssssssooooo;

c) eeeee-d10-eeeee and sssssssssssssssssss;

d) eee-d8-eee and sssooooooosss;

e) eee-d8-eee and ooosssssssooo

f) eee-d8-eee and sssssssssssss;

g) eee-d10-eee and sssooooooooosss;

h) eee-d10-eee and ooosssssssssooo;

i) eee-d10-eee and sssssssssssssss;

j) eeee-d10-eeee and ssssooooooooossss;

k) eeee-d10-eeee and ooooosssssssssooooo;

l) eeee-d10-eeee and sssssssssssssssss;

m) eeee-d8-eeee and ssssooooooossss,

n) eeee-d8-eeee and ooooosssssssoooo,

o) eeee-d8-eeee and sssssssssssssss,

p) eeeeee-d11-eeeeee and sssssssssssssssssssss;

q) eeeee-d10-eeeee and sosossssssssssosos;

r) eeeee-d10-eeeee and soooosssssssssooos;

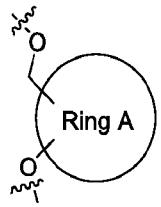
s) eeeee-d10-eeeee and soooossssssssssooss;

t) eeeee-d8-eeeee and sosssssssssssoss;

u) eeeee-d10-eeeee and sosssssssssssssosss,

wherein at least one "e" or at least one "d" of the gapmer oligonucleotide is replaced with a spacer.

[0043] Additionally disclosed herein is a pharmaceutical composition comprising an antisense gapmer oligonucleotide disclosed herein, or a pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable excipient. In various embodiments, the spacer is a nucleoside-replacement group comprising a non-sugar substitute wherein the non-sugar substitute does not contain a ketone, aldehyde, ketal, hemiketal, acetal, hemiacetal, aminal or hemiaminal moiety and is incapable of forming a covalent bond with a nucleotide base. In various embodiments, the spacer is represented by Formula (X), wherein:

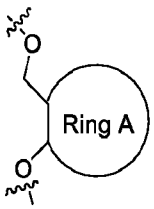


Formula (X)

Ring A is is an optionally substituted 4-8 member monocyclic cycloalkyl group or a 4-8 member monocyclic heterocyclyl group, wherein the heterocyclyl group contains 1 or 2 heteroatoms selected from O, S and N, provided that A is not capable of forming a covalent bond to a nucleobase; and

the  symbol represents the point of connection to an internucleoside linkage.

[0044] In various embodiments, the spacer is represented by Formula (Xa), wherein:

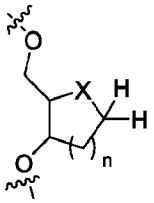


Formula (Xa).

[0045] In various embodiments, ring A is an optionally substituted 4-8 member monocyclic cycloalkyl group selected from cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and cyclooctyl; or a 4-8 member monocyclic heterocyclyl group, selected from oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, 1,4-dioxanyl, pyrolidinyl, piperidinyl, piperazinyl, morpholinyl and azepanyl.

In various embodiments, ring A is tetrahydrofuranyl. In various embodiments, ring A is tetrahydropyranyl.

[0046] In various embodiments, the spacer is represented by Formula (I), wherein:

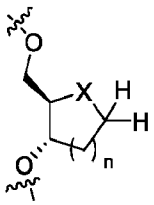


Formula (I)

X is selected from -CH_2- and -O-; and

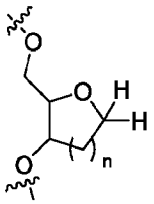
n is 0, 1, 2 or 3.

[0047] In various embodiments, the spacer is represented by Formula (I'), wherein:



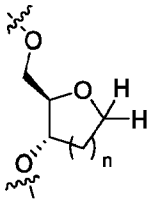
Formula (I').

[0048] In various embodiments, the spacer is represented by Formula (Ia), wherein:



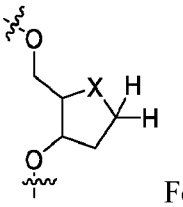
Formula (Ia).

[0049] In various embodiments, the spacer is represented by Formula (Ia'), wherein:



Formula (Ia').

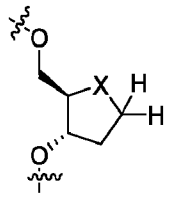
[0050] In various embodiments, the spacer is represented by Formula II, wherein:



Formula (II); and

X is selected from -CH_2- and -O-.

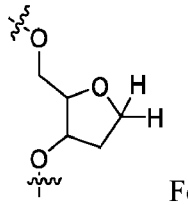
[0051] In various embodiments, the spacer is represented by Formula II', wherein:



Formula (II'); and

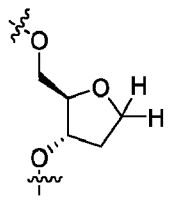
X is selected from -CH_2- and -O-.

[0052] In various embodiments, the spacer is represented by Formula (Iia), wherein:



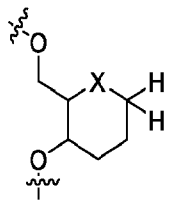
Formula (Iia).

[0053] In various embodiments, the spacer is represented by Formula (Iia'), wherein:



Formula (Iia').

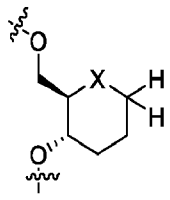
[0054] In various embodiments, the spacer is represented by Formula III, wherein:



Formula (III); and

X is selected from -CH_2- and -O-.

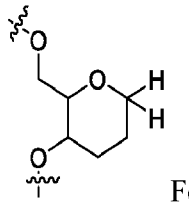
[0055] In various embodiments, the spacer is represented by Formula III', wherein:



Formula (III'); and

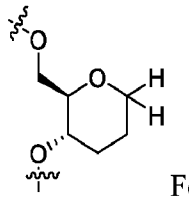
X is selected from -CH_2- and -O-.

[0056] In various embodiments, the spacer is represented by Formula (IIIa), wherein:



Formula (IIIa).

[0057] In various embodiments, the spacer is represented by Formula (IIIa'), wherein:



Formula (IIIa').

[0058] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising Riluzole (Rilutek), troriluzole, Edaravone (Radicava), rivastigmine, donepezil, QRL-101, QRL-201, galantamine, selective serotonin reuptake inhibitor, antipsychotic agents, cholinesterase inhibitors, memantine, benzodiazepine antianxiety drugs, AMX0035 (ELYBRIO®), ZILUCOPLAN (RA101495), dual AON intrathecal administration (*e.g.*, BIIB067, BIIB078), BIIB100, levodopa/carbidopa, dopaminergic agents (*e.g.*, ropinirole, pramipexole, rotigotine), medroxyprogesterone, KCNQ2/KCNQ3 openers, Pridopidine, PrimeC (combination of ciprofloxacin and Celebrex), olanzapine (Zyprexa), quetiapine (Seroquel), SSRIs, divalproex sodium (Depakote), carbamazepine (Tegretol), medroxyprogestrone, lithium, anticonvulsants and psychostimulant agents, breathing care, physical therapy, occupational therapy, speech therapy, nutritional support, or any combination thereof. In various embodiments, the neurological disease is any one of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), or ALS with FTD.

[0059] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising Memantine, Rivastigmine, Galantamine, Donepezil, QRL-101, QRL-201, Aricept®, Exelon® (Rivastigmine), Razadyne®, Aducanumab, BAN2401, BIIB091 (gosuranemab), BIIB076, BIIB080 (IONIS-MAPTRx), Elayta (CT1812),

MK1942, allogenic hMSC, nilotinib, ABT-957, acitretin, ABT-354, GV1001, Riluzole, CAD106, CNP520, AD-35, Rilapladib, DHP1401, T-817 MA, TC-5619, TPI-287, RVT-101, LY450139, JNJ-54861911, Dapagliflozin, GSK239512, PF-04360365, ASP0777, SB-742457 (a 5-HT6 receptor antagonist), PF-03654746 (an H_3 receptor antagonist), GSK933776 (an Fc-inactivated anti-β amyloid (Aβ) monoclonal antibody (mAb)), Posiphen ((+)-phenserine tartrate), AMX0035 (ELYBRIO®), coenzyme Q10, aducanamab (ADUHLEM), memantine (NAMENDA), Namzeric, Suvorexant (belsomra), lecanemab, or any combination thereof. In various embodiments, the neurological disease is Alzheimer's Disease.

[0060] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising Levodopa, Carbidopa-levidopa, pramipexole (MIRAPEX), ropinirole (REQUIP), rotigotine (NEUPRO), apomorphine (APOKYN, KYNMOBI), selegiline (EDLEPRYL, ZELAPAR), rasagiline, entacapone (COMTAN), tolcapone (TASMAR), amantadine (GOCOVRI, SYMMETREL, OSMOLEX), trihexyphenidyl (ARTANE), BIIB054 (cinepanemab), BIIB094, BIIB118, ABBV-0805, zonisamide, deep brain stimulation, brain-derived neurotrophic factor, stem-cell transplant, Niacin, brain stem stimulation, nicotine, nabilone, PF-06649751, DNL201, LRRK2 inhibitors, CK1 inhibitors, isradipine, CLR4001, IRX4204, Yohimbine, coenzyme Q10, OXB-102, duloxetine, pioglitazone, preladenant, istradefylline (NOURIANZ), safinamide (XADAGO), benztropine (COGENTIN), opicapone (ongentys), exenatide, lingzhi, Caffeine, sarizotan, embryonic dopamine cell implantation, or any combination thereof. In various embodiments, the neurological disease is Parkinson's Disease.

[0061] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising UCB0107, ABBV-8E12, F-18 AV1451, BIIB092, C2N-8E12, tideglusib, deep transcranial magnetic stimulation, lipoic acid, tolfenamica acid, lithium, AZP2006, Glial Clell Line-Derived Neurotrophic Factor, NBMI, suvorxant, zolpidem, TPI 287, davunetide, pimavanserin, Levodopa, Carbidopa-levidopa, pramipexole, ropinirole, rotigotine, apomorphine, selegiline, rasagiline, entacapone, tolcapone, amantadine, trihexyphenidyl, BIIB054 (cinepanemab), BIIB094, BIIB118, ABBV-0805, zonisamide, deep

brain stimulation, brain-derived neurotrophic factor, stem-cell transplant, Niacin, brain stem stimulation, nicotine, nabilone, PF-06649751, DNL201, LRRK2 inhibitors, CK1 inhibitors, isradipine, CLR4001, IRX4204, Yohimbine, coenzyme Q10, OXB-102, duloxetine, pioglitazone, preladenant, or any combination thereof. In various embodiments, the neurological disease is progressive supranuclear palsy (PSP).

[0062] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising Tetrabenazine, deutetrabenazine, physical therapy, risperidone, haloperidol, chlorpromazine, clonazepam, diazepam, benzodiazepines, selective serotonin reuptake inhibitors. quetiapine, carbatrol, valproate, lamotrigine, pridopidine, delta-9-tetrahydrocannabinol, cannabidiol, stem-cell therapy, ISIS-443139, nilotinib, resveratrol, neflamapimod, fenofibrate, creatine, RO7234292, SAGE-718, WVE-120102, WVE-120101, dimebon, minocycline, deep brain stimulation, ursodiol, coenzyme Q10, OMS643762, VX15/2503, PF-02545920, BN82451B, SEN0014196, olanzapine, tiapridal (tiapride), or any combination thereof. In various embodiments, the neurological disease is Huntington's Disease.

[0063] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising anticoagulants, antidepressants, muscle relaxants, stimulants, anticonvulsants, anti-anxiety medication, erythropoietin, hyperbaric treatment, rehabilitation therapies (*e.g.*, physical, occupational, speech, psychological, or vocational counseling), or any combination thereof. In various embodiments, the neurological disease is brain trauma.

[0064] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising AXER-204, glyburide, 5-hydroxytryptophan (5-HTP), L-3,4-dihydroxyphenylalanine (L-DOPA), or rehabilitation therapies (*e.g.*, physical therapy, occupational therapy, recreational therapy, use of assistive devices, improved strategies

for exercise and healthy diets), or any combination thereof. In various embodiments, the neurological disease is spinal cord injury.

[0065] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising TPI-287, lithium, occupational, physical, and speech therapy, or any combination thereof can be selected as an additional therapy. In various embodiments, the neurological disease is corticobasal degeneration.

[0066] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising gabapentin, pregabalin, lamotrigine, carbamazepine, duloxetine, gabapentinoids, tricyclic antidepressants, serotonin-norepinephrine reuptake inhibitors, opioids, neurotoxin, dextromethorphan, nicotinamide riboside, auto-antibodies targeting neuronal antigens (TS-HDS and FGFR3), or any combination thereof. In various embodiments, the neuropathy is a chemotherapy induced neuropathy.

[0067] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising amantadine, armodafinil, baclofen, buspirone, carbamazepine, citalopram, clonazepam, desvenlafaxine, diazepam, duloxetine, escitalopram, flunarizine, fluoxetine, fluvoxamine, gabapentin, isoniazid, levetiracetam, levodopa, memantine, modafinil, ondansetron, paroxetine, pramipexole, primidone, riluzole, ropinirole, sertraline, tizanidine, topiramate, trihexyphenidyl, valproic acid, venlafaxine, BHV-4157, or a combination thereof. In various embodiments, the neurological disease is spinocerebellar ataxia.

[0068] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising Brivaracetam (briviact), cannabidiol (epidiolex), carbamazepine (carbatrol, Tegretol), cenobamate (xcopri), diazepam (valium),

lorazepam (Ativan), clonazepam (klonopin), eslicarbazepine (aptiom), ethosuximide (zarontin), felbamate (felbatol), fenfluramine (fintepla), lacosamide (VIMPAT), lamotrigine (Lamictal), levetiracetam (Keppra), oxcarbazepine (oxtellar xr, Trileptal), perampanel (fycompa), phenobarbital, phenytoin (dilantin), pregabalin (lyrica), tiagabine (gabitril), topiramate (topamax), valproate (depakene, depakote), zonisamide (zonegran), or any combination thereof. In various embodiments, the neurological disease is epilepsy.

[0069] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising nusinersen (SPINRAZA), onasemnogene abeparvovec-xioi (ZOLGENSMA), risdiplam (EVRYSDI), or any combination thereof. In various embodiments, the neurological disease is spinal muscular atrophy.

[0070] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising anti-seizure medications, speech therapy, physical therapy, occupational therapy, Adrabetadex, Arimoclomol, N-Acetyl-L-Leucine, or any combination thereof. In various embodiments, the neurological disease is Niemann-Pick disease type C.

[0071] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising physical and occupational therapies, orthopedic surgery, orthopedic devices, PXT3003, or any combination thereof. In various embodiments, the neurological disease is Charcot-Marie-Tooth Disease (CMT).

[0072] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising enzyme replacement therapy: idursulfase (Elaprase), surgical intervention (tonsillectomy and/or adenoidectomy), RGX-121 gene therapy,

adalimumab, MT2013-31, or any combination thereof. In various embodiments, the neurological disease is Mucopolysaccharidosis type II (MPSIIA).

[0073] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising physical, occupational, and speech therapies, contact lenses and artificial tears, genetic counseling, or any combination thereof. In various embodiments, the neurological disease is Mucolipidosis IV.

[0074] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising anticonvulsants, physical and occupational therapies, galactosidase, gene delivery of galactosidase, LYS-GM101 gene therapy, or any combination thereof. In various embodiments, the neurological disease is GM1 gangliosidosis.

[0075] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising physical and occupational therapies, use of devices such as braces, walkers, wheelchairs, immunosuppressants, BYM338, or any combination thereof. In various embodiments, the neurological disease is Sporadic inclusion body myositis (sIBM).

[0076] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second therapeutic agent selected from a group comprising corticosteroids, colchicine, dapsone, azathioprine, or any combination thereof. In various embodiments, the neurological disease is Henoch-Schonlein purpura (HSP).

[0077] Additionally disclosed herein is a method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide, or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition, in combination with a second

therapeutic agent selected from a group comprising enzyme replacement therapy, substrate reduction therapy, N-acetylcysteine, GZ/SAR402671, cerezyme, or any combination thereof. In various embodiments, the neurological disease is Gaucher's disease.

BRIEF DESCRIPTION OF THE DRAWINGS

[0078] Figure 1 shows an example antisense oligonucleotide (AON), a portion of which is complementary to a mRNA transcript or pre-mRNA transcript. Dashed lines indicate positions of the AON which may or may not be complementary to corresponding positions of the transcript.

DETAILED DESCRIPTION

[0079] The features and other details of the disclosure will now be more particularly described. Before further description of the present invention, certain terms employed in the specification, examples and appended claims are collected here. These definitions should be read in light of the remainder of the disclosure and understood as by a person of skill in the art. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by a person of ordinary skill in the art.

Definitions

[0080] The terms "treat," "treatment," "treating," and the like are used herein to generally mean obtaining a desired pharmacological and/or physiological effect. The effect may be therapeutic in terms of partially or completely curing a disease and/or adverse effect attributed to the disease. The term "treatment" as used herein covers any treatment of a disease in a mammal, particularly a human, and includes: (a) inhibiting the disease, *i.e.*, preventing the disease from increasing in severity or scope; (b) relieving the disease, *i.e.*, causing partial or complete amelioration of the disease; or (c) preventing relapse of the disease, *i.e.*, preventing the disease from returning to an active state following previous successful treatment of symptoms of the disease or treatment of the disease.

[0081] "Preventing" includes delaying the onset of clinical symptoms, complications, or biochemical indicia of the state, disorder, disease, or condition developing in a subject that may be afflicted with or predisposed to the state, disorder, disease, or condition but does not yet experience or display clinical or subclinical symptoms of the state, disorder, disease, or condition. "Preventing" includes prophylactically treating a state, disorder, disease, or condition in or developing in a subject, including prophylactically treating clinical symptoms, complications, or biochemical indicia of the state, disorder, disease, or condition in or developing in a subject.

[0082] The term "pharmaceutically acceptable carrier" or "pharmaceutically acceptable excipient" as used herein interchangeably refers to any and all solvents, dispersion media, coatings, isotonic and absorption delaying agents, and the like, that are compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. The compositions may also contain other active compounds providing supplemental, additional, or enhanced therapeutic functions.

[0083] The term "pharmaceutical composition" as used herein refers to a composition comprising at least one biologically active compound, for example, an antisense oligonucleotide (AON), as disclosed herein formulated together with one or more pharmaceutically acceptable excipients.

[0084] "Individual," "patient," or "subject" are used interchangeably and include any animal, including mammals, preferably mice, rats, other rodents, rabbits, dogs, cats, swine, cattle, sheep, horses, or non-human primates, and most preferably humans. The compounds of the invention can be administered to a mammal, such as a human, but can also be other mammals such as an animal in need of veterinary treatment, *e.g.*, domestic animals (*e.g.*, dogs, cats, and the like), farm animals (*e.g.*, cows, sheep, pigs, horses, and the like) and laboratory animals (*e.g.*, rats, mice, guinea pigs, non-human primates, and the like). In some embodiments, the mammal treated in the methods of the invention is desirably a mammal in whom modulation of a target expression and/or activity is desired.

[0085] As used herein, "PPM1A" (also known as Protein Phosphatase, Mg^{2+}/Mn^{2+} Dependent 1A, Protein Phosphatase 1A (Formerly 2C), Magnesium-Dependent, Alpha Isoform, Protein Phosphatase 1A, EC 3.1.3.16, Protein Phosphatase 2C Isoform Alpha, Protein Phosphatase IA, Phosphatase 2C Alpha, PP2C-Alpha, PPPM1A, and PP2CA) refers to the gene or gene products (*e.g.*, protein or mRNA transcript (including pre-mRNA) encoded by the gene) identified by Entrez Gene ID No. 5494 and allelic variants thereof, as well as orthologs found in non-human species (*e.g.*, non-human primates or mice).

[0086] As used herein, "ATXN2" (also known as Ataxin 2, ATX2, TNRC13, SCA2, Trinucleotide Repeat-Containing Gene 13 Protein, Spinocerebellar Ataxia Type 2 Protein, Ataxin-2, Spincocerebellar Ataxia 2 (Olivopontocerebellar Ataxia 2, Autosomal Dominant, Ataxin 2), and Trinucleotide Repeat Containing 13) refers to the gene or gene products (*e.g.*, protein or mRNA transcript (including pre-mRNA) encoded by the gene) identified by Entrez Gene ID No. 6311 and allelic variants thereof, as well as orthologs found in non-human species (*e.g.*, non-human primates or mice).

[0087] As used herein, "SOD1" (also known as Superoxide Dismutase 1, IPOA, Superoxide Dismutase 1, Soluble, Superoxide Dismutase [Cu-Zn], EC 1.15.1.1, HSod1, ALS1, ALS, Amyotrophic Lateral Sclerosis 1 (Adult), Epididymis Secretory Protein Li 44, Superoxide Dismutase, Cystolic, Cu/Zn Superoxide Dismutase, Indophenoloxidase A, SOD, Soluble, Homodimer, HEL-S-44, STAHP, and SOD) refers to the gene or gene products (*e.g.*, protein or mRNA transcript (including pre-mRNA) encoded by the gene) identified by Entrez Gene ID No. 6647 and allelic variants thereof, as well as orthologs found in non-human species (*e.g.*, non-human primates or mice).

[0088] As used herein, "MAPT" (also known as Microtubule Associated Protein Tau, MTBT1, PPP1R103, FTDP-17, MTBT2, MAPTL, PPND, MSTD, TAU, G Protein Beta1/Gamma2, Subunit-Interacting Factor, Protein Phosphatase 1, Regulatory Subunit 103, Microtubule-Associated Protein Tau, Neurofibrillary Tangle Protein, Paired Helical Filament-Tau, MGC138549, FLJ31424 , PHF-Tau, Tau-40, DDPAC, Tau, and Microtubule-Associated Protein Tau, Isoform 4) refers to the gene or gene products (*e.g.*, protein or mRNA transcript (including pre-mRNA) encoded by the gene) identified by Entrez Gene ID No. 4137 and allelic variants thereof, as well as orthologs found in non-human species (*e.g.*, non-human primates or mice).

[0089] In the present specification, the term "therapeutically effective amount" means the amount of the subject AON that will elicit the biological or medical response of a tissue, system, animal or human that is being sought by the researcher, veterinarian, medical doctor, or other clinician. The AONs of the invention are administered in therapeutically effective amounts to treat and/or prevent a disease, condition, disorder, or state, for example, ALS, FTD, ALS with FTD, or another motor neuron disease or neurological disease or condition. Alternatively, a therapeutically effective amount of an AON is the quantity required to achieve a desired therapeutic and/or prophylactic effect, such as an amount which results in the prevention of or a decrease in the symptoms associated with a disease disclosed herein.

[0090] As used herein, the term "antisense oligonucleotide" or "AON" encompasses antisense oligonucleotides that target genes or gene products of any of PPM1A, ATXN2, SOD1, or MAPT. "Antisense oligonucleotide" or "AON" encompass any of a parent oligonucleotide, an oligonucleotide variant, an oligonucleotide with one or more spacers, an oligonucleotide variant with one or more spacers, a gapmer antisense oligonucleotide (AON), and a gapmer AON with one or more spacers. Examples of antisense oligonucleotides include oligonucleotides comprising a sequence of any one of antisense oligonucleotide comprising any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354,

149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[0091] The terms "parent oligonucleotide," "parent antisense oligonucleotide," or "parent AON" refer to an antisense oligonucleotide that is complementary to a portion of a target gene product, such as any one of a PPM1A, ATXN2, SOD1, or MAPT mRNA or pre-mRNA transcript. Parent oligonucleotides do not include a spacer. In particular embodiments, parent oligonucleotides include 20 linked nucleosides. In such embodiments, parent oligonucleotides are 20mers. Examples of parent oligonucleotides are AONs with a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. As described hereafter, oligonucleotide with spacers, oligonucleotide variants, and gapmer AONs are described in relation to a corresponding parent oligonucleotide.

[0092] The term "oligonucleotide variant" refers to an antisense oligonucleotide that represents a modified version of a corresponding parent oligonucleotide. For example, an oligonucleotide variant represents a shortened version of a parent oligonucleotide. In various embodiments, an oligonucleotide variant is any one of a 15mer, 16mer, 17mer, 18mer 19mer, 20mer, 21mer, 22mer or 23mer. For example, an AON variant may be a shorter or longer version of a corresponding parent oligonucleotide that comprises a nucleobase sequence selected from any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566). Examples of oligonucleotide variants include oligonucleotides comprising a sequence of any one of SEQ ID NOs: 301590-301594. In various embodiments, oligonucleotide variants comprise one or more spacers.

[0093] The term "oligonucleotide with one or more spacers" or "oligonucleotide comprising a spacer" refers to an oligonucleotide with at least one spacer. An oligonucleotide with one or more spacers can, in various embodiments, include one spacer, two spacers, three spacers, four spacer, five spacers, six spacers, seven spacers, eight spacers, nine spacers, or ten spacers. In various embodiments, an oligonucleotide comprising one or more spacers includes at least one segment with at most 10 linked nucleosides. For example, as described in a 5' to 3' direction, an oligonucleotide comprising a spacer can include a segment with 10 linked nucleosides followed by a spacer, followed by a second segment of 9 linked nucleosides. In various embodiments, an oligonucleotide comprising one or more spacers includes at least one segment with at most 7 linked nucleosides. For example, as described in a 5' to 3' direction, an oligonucleotide comprising a spacer can include a segment with 7 linked nucleosides, followed by a spacer, a second segment with 9 linked nucleosides, followed by a second spacer, and a third segment with 7 linked nucleosides. Here, the first segment of 7 linked nucleosides and the third segment of 7 linked nucleosides each represents segments with 7 linked nucleosides. In various embodiments,

an oligonucleotide comprising one or more spacers includes at least one segment with at most 6 linked nucleosides. For example, as described in a 5' to 3' direction, an oligonucleotide comprising a spacer can include a segment with 6 linked nucleosides, followed by a spacer, a second segment with 6 linked nucleosides, followed by a second spacer, and a third segment with 6 linked nucleosides. Here, the first segment of 6 linked nucleosides, the second segement of 6 linked nucleosides, and the third segment of 6 linked nucleosides each represents segments with 6 linked nucleosides. Here, every segment of an oligonucleotide with one or more spacers has at most 6 linked nucleosides In various embodiments, the gapmer oligonucleotide comprises a segment with at most 10, 9, 8, 7, 6, 5, 4, 3, or 2 linked nucleosides.

[0094] As another example, an oligonucleotide comprising a spacer can include a segment with 10 linked nucleosides, followed by a spacer, a second segment with 10 linked nucleosides, followed by a second spacer, and a third segment with 3 linked nucleosides. Here, the third segment of 3 linked nucleosides represents the segment with at most 6 or at most 7 linked nucleosides. In various embodiments, an oligonucleotide with one or more spacers includes multiple segments with at most 6 or at most 7 linked nucleosides. In various embodiments, every segment of an oligonucleotide with one or more spacers has at most 6 or at most 7 linked nucleosides. For example, the oligonucleotide may be a 20mer and include two spacers that divide the 20mer into three separate segments of 6 linked nucleosides each. Therefore, each segment of the oligonucleotide has at most 6 linked nucleosides. For example, the oligonucleotide may be a 23mer and include two spacers that divide the 23mer into three separate segments of 7 linked nucleosides each. Therefore, each segment of the oligonucleotide has at most 7 linked nucleosides. Generally, oligonucleotides comprising one or more spacers are described in reference to a corresponding parent oligonucleotide or a corresponding oligonucleotide variant. Example oligonucleotides comprising one or spacers include any of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[0095] In various embodiments, one or more spacers may be located at one or more positions of an oligonucleotide. A spacer may be located between a first position and a second position of the oligonucleotide. As used herein, a spacer located between a first position and second position encompasses the spacer being located at the first position, located at the second position, or located at any position of the oligonucleotide sandwiched by the first position and the second position.

[0096] The term "gapmer antisense oligonucleotide," "gapmer AON," or "gapmer AON variant" refers to an AON with at least three distinct structural regions including a 5′-wing region, a central region, and a 3′-wing region, in '5→3' orientation. The central region comprises a

stretch of nucleosides that enable recruitment and activation of RNAseH. For example, the central region comprises linked DNA nucleosides, 2'-Fluoro Arabino Nucleic Acids (FANA), and Fluoro Cyclohexenyl nucleic acid (F-CeNA). Example gapmer AONs or gapmer oligonucleoide variants include any of SEQ ID NOs: 301595-301607. In various embodiments, gapmer AONs comprise a sequence that shares at least 85%, at least 90%, at least 95%, at least 98%, or 100% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. In various embodiments, a gapmer AON may include one or more spacers. Example gapmer AONs comprising one or spacers comprise a sequence that shares at least 85%, at least 90%, at least 95%, at least 98% identity, or 100% identity with an equal length portion of any one of SEQ ID NOs: SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[0097] The term "pharmaceutically acceptable salt(s)" as used herein refers to salts of acidic or basic groups that may be present in antisense oligonucleotides used in the present compositions. Antisense oligonucleotides included in the present compositions that are basic in nature are capable of forming a wide variety of salts with various inorganic and organic acids. The acids that may be used to prepare pharmaceutically acceptable acid addition salts of such basic compounds are those that form non-toxic acid addition salts, *e.g.*, salts containing pharmacologically acceptable anions, including but not limited to malate, oxalate, chloride, bromide, iodide, nitrate, sulfate, bisulfate, phosphate, acid phosphate, isonicotinate, acetate, lactate, salicylate, citrate, tartrate, oleate, tannate, pantothenate, bitartrate, ascorbate, succinate, maleate, gentisinate, fumarate, gluconate, glucuronate, saccharate, formate, benzoate, glutamate, methanesulfonate, ethanesulfonate, benzenesulfonate, *p*-toluenesulfonate and pamoate (*e.g.*, 1,1'-methylene-bis-(2-hydroxy-3-naphthoate)) salts. Antisense oligonucleotides included in the present compositions that include an amino moiety may form pharmaceutically acceptable salts with various amino acids, in addition to the acids mentioned above. Compounds included in the present compositions that are acidic in nature are capable of forming base salts with various pharmacologically acceptable cations. Examples of such salts include alkali metal or alkaline earth metal salts and, particularly, calcium, magnesium, sodium, lithium, zinc, potassium, and iron salts. Pharmaceutically acceptable salts of the disclosure include, for example, pharmaceutically acceptable salts of AONs that include a nucleotide sequence of any of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[0098] Antisense oligonucleotides of the disclosure may contain one or more chiral centers, groups, linkages, and/or double bonds and, therefore, exist as stereoisomers, such as geometric

isomers, enantiomers or diastereomers. The term "stereoisomers" when used herein consist of all geometric isomers, enantiomers or diastereomers. These compounds may be designated by the symbols "*R*" or "*S*" (or "*R*p" or "*S*p") depending on the configuration of substituents around the stereogenic atom, for example, a stereogenic carbon, phosphorus, or sulfur atom. In some embodiments, one or more linkages of the compound may have a *R*p or *S*p configuration (*e.g.*, one or more phosphorothioate linkages have either a *R*p or *S*p configuration). The configuration of each phosphorothioate linkage may be independent of another phosphorothioate linkage (*e.g.*, one phosphorothioate linkage has a *R*p configuration and a second phosphorothioate linkage has a *S*p configuration). The present invention encompasses various stereoisomers of these compounds and mixtures thereof. Stereoisomers include enantiomers and diastereomers. Mixtures of enantiomers or diastereomers may be designated "(±)" in nomenclature, but the skilled artisan will recognize that a structure may denote a chiral center implicitly. Individual stereoisomers of antisense oligonucleotides of the present invention can be prepared synthetically from commercially available starting materials that contain asymmetric or stereogenic centers, or by preparation of racemic mixtures followed by resolution methods well known to those of ordinary skill in the art. These methods of resolution are exemplified by (1) attachment of a mixture of enantiomers to a chiral auxiliary, separation of the resulting mixture of diastereomers by recrystallization or chromatography and liberation of the optically pure product from the auxiliary, (2) salt formation employing an optically active resolving agent, or (3) direct separation of the mixture of optical enantiomers on chiral chromatographic columns. Stereoisomeric mixtures can also be resolved into their component stereoisomers by well-known methods, such as chiral-phase gas chromatography, chiral-phase super critical fluid chromatography, chiral-phase simulated moving bed chromatography, chiral-phase high performance liquid chromatography, crystallizing the compound as a chiral salt complex, or crystallizing the compound in a chiral solvent. Stereoisomers can also be obtained from stereomerically-pure intermediates, reagents, and catalysts by well-known asymmetric synthetic methods.

[0099] Individual stereoisomers antisense oligonucleotides of the present invention can be prepared synthetically from commercially available starting materials that contain asymmetric or stereogenic centers, or by preparation of racemic mixtures followed by resolution methods well known to those of ordinary skill in the art. These methods of resolution are exemplified by (1) attachment of a mixture of enantiomers to a chiral auxiliary, separation of the resulting mixture of diastereomers by recrystallization or chromatography and liberation of the optically pure product from the auxiliary, (2) salt formation employing an optically active resolving agent, or (3) direct separation of the mixture of optical enantiomers on chiral chromatographic columns.

Stereoisomeric mixtures can also be resolved into their component stereoisomers by well-known methods, such as chiral-phase super critical fluid chromatography, chiral-phase simulated moving bed chromatography, chiral-phase gas chromatography, chiral-phase high performance liquid chromatography, crystallizing the compound as a chiral salt complex, or crystallizing the compound in a chiral solvent. Stereoisomers can also be obtained from stereomerically-pure intermediates, reagents, and catalysts by well-known asymmetric synthetic methods.

[00100] The antisense oligonucleotides disclosed herein can exist in solvated as well as unsolvated forms with pharmaceutically acceptable solvents such as water, ethanol, and the like, and it is intended that the invention embrace both solvated and unsolvated forms.

[00101] The invention also embraces isotopically labeled compounds of the invention (*e.g.*, isotopically labeled antisense oligonucleotides) which are identical to those recited herein, except that one or more atoms are replaced by an atom having an atomic mass or mass number different from the atomic mass or mass number most abundantly found in nature. Examples of isotopes that can be incorporated into compounds of the invention include isotopes of hydrogen, carbon, nitrogen, oxygen, phosphorus, fluorine and chlorine, such as ^{2}H, ^{3}H, ^{11}C, ^{13}C, ^{14}C, ^{15}N, ^{18}O, ^{17}O, ^{31}P, ^{32}P, ^{35}S, ^{18}F, and ^{36}Cl, respectively.

[00102] Certain isotopically labeled disclosed compounds (*e.g.*, those labeled with ^{3}H and ^{14}C) are useful in compound and/or substrate tissue distribution assays. Tritiated (*i.e.*, ^{3}H), carbon-14 (*i.e.*, ^{14}C), or ^{35}S phosphorothioate isotopes are particularly preferred for their ease of preparation and detectability. Further, substitution with heavier isotopes such as deuterium (*i.e.*, ^{2}H) may afford certain therapeutic advantages resulting from greater metabolic stability (*e.g.*, increased *in vivo* half-life or reduced dosage requirements) and hence may be preferred in some circumstances.

[00103] As used herein, "2'-*O*-(2-methoxyethyl)" (also 2'-MOE and 2'-$O(CH_2)_2OCH_3$ and MOE) refers to an *O*-methoxyethyl modification of the 2' position of a furanose ring. A 2'-O-(2-methoxyethyl) is used interchangeably as "2'-*O*-methoxyethyl" in the present disclosure. A sugar moiety in a nucleoside modified with 2'-MOE is a modified sugar.

[00104] As used herein, "2'-MOE nucleoside" (also 2'-*O*-(2-methoxyethyl) nucleoside) means a nucleoside comprising a 2'-MOE modified sugar moiety.

[00105] As used herein, "2'-substituted nucleoside" means a nucleoside comprising a substituent at the 2'-position of the furanose ring other than H or OH. In certain embodiments, 2' substituted nucleosides include nucleosides with bicyclic sugar modifications.

[00106] As used herein, "5-methyl cytosine" (5-MeC) means a cytosine modified with a methyl group attached to the 5 position. A 5-methyl cytosine (5-MeC) is a modified nucleobase.

[00107] As used herein, "bicyclic sugar" means a furanose ring modified by the bridging of two atoms. A bicyclic sugar is a modified sugar.

[00108] As used herein, "bicyclic nucleoside" (also BNA) means a nucleoside having a sugar moiety comprising a bridge connecting two carbon atoms of the sugar ring, thereby forming a bicyclic ring system. In certain embodiments, the bridge connects the 4'-carbon and the 2'-carbon of the sugar ring.

[00109] As used herein, "cEt" or "constrained ethyl" means a bicyclic nucleoside having a sugar moiety comprising a bridge connecting the 4'-carbon and the 2'-carbon, wherein the bridge has the formula: 4'-$CH(CH_3)$—*O*-2'.

[00110] As used herein, "constrained ethyl nucleoside" (also cEt nucleoside) means a nucleoside comprising a bicyclic sugar moiety comprising a 4'-$CH(CH_3)$—*O*-2' bridge. In some embodiments, cEt can be modified. In some embodiments, the cEt can be *S*-cEt (in an *S*-constrained ethyl 2'-4'-bridged nucleic acid). In some other embodiments, the cEt can be *R*-cEt.

[00111] As used herein, "internucleoside linkage" refers to the atom or group that links the 3' and 5' position of the sugar or corresponding positions of a sugar mimetic. In some embodiments, as used herein, "non-natural linkage" refers to a "modified internucleoside linkage."

[00112] As used herein, "contiguous" in the context of an oligonucleotide refers to nucleosides, nucleobases, sugar moieties, or internucleoside linkages that are immediately adjacent to each other. For example, "contiguous nucleobases" means nucleobases that are immediately adjacent to each other in a sequence. As an example to the contrary, two nucleosides separated by a spacer are not contiguous.

[00113] As used herein, "modified nucleobase" means any nucleobase other than adenine, cytosine, guanine, thymine, or uracil. Examples of a modified nucleobase include 5-methyl cytosine, pseudouridine, or 5-methoxyuridine. An "unmodified nucleobase" means the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C), and uracil (U).

[00114] As used herein, a "spacer" refers to a nucleoside-replacement group (*e.g.*, a non-nucleoside group that replaces a nucleoside present in a parent oligonucleotide). The spacer is characterized by the lack of a nucleotide base and by the replacement of the nucleoside sugar moiety with a non-sugar substitute. The non-sugar substitute group of a spacer lacks an aldehyde, ketone, acetal, ketal, hemiacetal or hemiketal group. The non-sugar substitute group of a spacer is thus capable of connecting to the 3' and 5' positions of the nucleosides adjacent to the spacer through an internucleoside linker as described herein, but not capable of forming a covalent bond with a nucleotide base (*i.e.*, not capable of linking a nucleobase to another group, such as an

internucleoside linkage, conjugate group, or terminal group in an oligonucleotide). Generally, an antisense oligonucleotide with a spacer is described in relation to a parent antisense oligonucleotide, wherein the spacer replaces a nucleoside of the parent antisense oligonucleotide. In all embodiments of the present disclosure, a spacer cannot hybridize to a nucleoside comprising a nucleobase at the corresponding position of a transcript (e.g., pre-mRNA or mRNA transcript), within the numerical order of the length of the AON (*i.e.*, if the spacer is positioned after nucleoside 4 of an AON (*i.e.*, at position 5 from the 5'-end), the spacer is not complementary to the nucleoside (A, C, G, or U) at the same corresponding position of the target transcript)).

[00115] As used herein, a "modified nucleoside" means a nucleoside having, independently, a modified sugar moiety and/or modified nucleobase. A universal base is a modified nucleobase that can pair with any one of the five unmodified nucleobases. Modified nucleosides include abasic nucleosides, which lack a nucleobase. However, modified nucleosides do not include spacers or other groups that are incapable of linking a nucleobase.

[00116] As used herein, "linked nucleosides" are nucleosides that are connected in a contiguous sequence (*i.e.*, no additional nucleosides are presented between those that are linked). In various embodiments, an oligonucleotide may have different segments of linked nucleosides connected through a spacer. Here, the spacer (*i.e.*, nucleoside replacement) is not considered a nucleoside and therefore, divides up the oligonucleotide into two segments of linked nucleosides. The oligonucleotide may have a first segment of Y linked nucleosides (*e.g.*, Y nucleosides that are connected in a contiguous sequence), followed by a spacer, and then a second segment of Z linked nucleosides. Here, the Y and Z linked nucleosides is described in either the 5' to 3' direction or the 3' to 5' direction. In various embodiments, the first segment consists of 7 or fewer linked nucleosides (e.g., Y = 7 or fewer) whereas the second segment comprises 8 or more linked nucleosides (*e.g.*, Z = 8 or more).

[00117] As used herein, "locked nucleic acid" or "LNA" or "LNA nucleosides" means nucleic acid monomers having a bridge (*e.g.*, methylene, ethylene, aminooxy, or oxyimino bridge) connecting two carbon atoms between the 4' and 2' position of the nucleoside sugar unit, thereby forming a bicyclic sugar. Examples of such bicyclic sugar include, but are not limited to (A) α-L-Methyleneoxy (4'-CH_2—O-2') LNA, (B) β-D-Methyleneoxy (4'-CH_2—O-2') LNA, (C) Ethyleneoxy (4'-$(CH_2)_2$—O-2') LNA, (D) Aminooxy (4'-CH_2—O—N(R)-2') LNA and (E) Oxyamino (4'-CH_2—N(R)—O-2') LNA; wherein R is H, C_1-C_{12} alkyl, or a protecting group (see U.S. Pat. No. 7,427,672, issued on Sep. 23, 2008).

[00118] As used herein, LNA compounds include, but are not limited to, compounds having at least one bridge between the 4' and the 2' position of the sugar wherein each of the bridges

independently comprises 1 or from 2 to 4 linked groups independently selected from —$[C(R_1)(R_2)]_n$ —, —$C(R_1)=C(R_2)$—, —$C(R_1)=N$—, —$C(=NR_1)$—, —C(=O)—, —C(=S)—, —O—, —$Si(R_1)_2$—, —$S(=O)_x$— and —$N(R_1)$ —; wherein: x is 0, 1, or 2; n is 1, 2, 3, or 4; each R_1 and R_2 is, independently, H, a protecting group, hydroxyl, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, a heterocycle radical, a substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5-C_7 alicyclic radical, substituted C_5-C_7 alicyclic radical, halogen, OJ_1, NJ_1J_2, SJ_1, N_3, $COOJ_1$, acyl (C(=O) —H), substituted acyl, CN, sulfonyl ($S(=O)_2$-J_1), or sulfoxyl (S(=O)- J_1); and each J_1 and J_2 is, independently, H, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, acyl (C(=O) —H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C_1-C_{12} aminoalkyl, substituted C_1-C_{12} aminoalkyl or a protecting group.

[00119] Examples of 4'-2' bridging groups encompassed within the definition of LNA include, but are not limited to one of formulae: —$[C(R_1)(R_2)]_n$ —, — $[C(R_1)(R_2)]_n$—O—, — $C(R_1R_2)$—N(R_1)—O— or —$C(R_1R_2)$—O—N(R_1)—. Furthermore, other bridging groups encompassed with the definition of LNA are 4'-CH_2-2', 4'-$(CH_2)_2$-2', 4'-$(CH_2)_3$-2', 4'-CH_2—O-2', 4'-$(CH_2)_2$—O-2', 4'- CH_2—O—N(R_1)-2' and 4'- CH_2—N(R_1)—O-2'- bridges, wherein each R_1 and R_2 is, independently, H, a protecting group or C_1-C_{12} alkyl.

[00120] Also included within the definition of LNA according to the invention are LNAs in which the 2'-hydroxyl group of the ribosyl sugar ring is connected to the 4' carbon atom of the sugar ring, thereby forming a bridge to form the bicyclic sugar moiety. The bridge can be a methylene (—CH_2—) group connecting the 2' oxygen atom and the 4' carbon atom, for which the term methyleneoxy (4'-CH_2—O-2') LNA is used. Furthermore, in the case of the bicyclic sugar moiety having an ethylene bridging group in this position, the term ethyleneoxy (4'-CH_2CH_2—O-2') LNA is used. A-L-methyleneoxy (4'-CH_2-O-2'), an isomer of methyleneoxy (4'-CH_2—O-2') LNA is also encompassed within the definition of LNA, as used herein.

[00121] As used herein, "hybridization" means the pairing or annealing of complementary oligonucleotides and/or nucleic acids. While not limited to a particular mechanism, the most common mechanism of hybridization involves hydrogen bonding, which may be Watson-Crick, Hoosteen or reversed Hoosteen hydrogen bonding between complementary nucleobases.

[00122] As used herein, "increasing the amount of activity" refers to more transcriptional expression, more accurate splicing resulting in full length mature mRNA and/or protein expression, and/or more activity relative to the transcriptional expression or activity in an untreated or control sample.

[00123] As used herein, "mismatch" or "non-complementary nucleobase" refers to the case when a group (e.g., nucleobase) of a first nucleic acid is not capable of pairing with the corresponding group (e.g., nucleobase) of a second or target nucleic acid.

[00124] As used herein, "modified internucleoside linkage" refers to a substitution or any change from a naturally occurring internucleoside linkage (*e.g.*, a phosphodiester internucleoside bond). "Phosphorothioate linkage" is a modified internucleoside linkage in which one of the non-bridging oxygen atoms of a phosphodiester internucleoside linkage is replaced with a sulfur atom.

[00125] As used herein, "modified oligonucleotide" means an oligonucleotide comprising at least one (*i.e.*, one or more) modified internucleoside linkage, modified sugar, and/or modified nucleobase.

[00126] As used herein, "modified sugar" or "modified sugar moiety" means a modified furanosyl sugar moiety or a modified sugar moiety having other than a furanosyl moiety that can link a nucleobase to another group, such as an internucleoside linkage, conjugate group, or terminal group in an oligonucleotide.

[00127] As used herein, "monomer" means a single unit of an oligomer. Monomers include, but are not limited to, nucleosides and nucleotides, whether naturally occurring or modified.

[00128] As used herein, "motif" means the pattern of unmodified and modified nucleosides in an antisense compound.

[00129] As used herein, "natural sugar moiety" means a sugar moiety found in DNA (2'-H) or RNA (2'-OH).

[00130] As used herein, "naturally occurring internucleoside linkage" means a 3' to 5' phosphodiester linkage.

[00131] As used herein, "nucleobase" means a heterocyclic moiety capable of pairing with a base of another nucleic acid.

[00132] As used herein, "nucleobase complementarity" refers to a nucleobase that is capable of base pairing with another nucleobase. For example, in DNA, adenine (A) is complementary to thymine (T). For example, in RNA, adenine (A) is complementary to uracil (U). In certain embodiments, complementary nucleobase refers to a nucleobase of an antisense compound that is capable of base pairing with a nucleobase of its target nucleic acid. For example, if a nucleobase at a certain position of an antisense compound is capable of hydrogen bonding with a nucleobase at a certain position of a target nucleic acid, then the position of hydrogen bonding between the oligonucleotide and the target nucleic acid is considered to be complementary at that nucleobase pair.

[00133] As used herein, "non-complementary nucleobases" refers to a pair of nucleobases that do not form hydrogen bonds with one another or otherwise support hybridization.

[00134] As used herein, "nucleic acid" refers to molecules composed of monomeric nucleotides. A nucleic acid includes, but is not limited to, ribonucleic acids (RNA), deoxyribonucleic acids (DNA), single-stranded nucleic acids, double-stranded nucleic acids, non-coding RNA, small interfering ribonucleic acids (siRNA), short-hairpin RNA (shRNA), circular RNA, circular DNA, and microRNAs (miRNA).

[00135] As used herein, "nucleobase sequence" means the order of nucleobases independent of any sugar, linkage, and/or nucleobase modification.

[00136] As used herein, "nucleoside" refers to a nucleobase linked to a sugar. The term "nucleoside" also includes a "modified nucleoside" which has independently, a modified sugar moiety and/or modified nucleobase.

[00137] As used herein, "oligonucleotide unit" refers to either a nucleoside (e.g., a nucleoside which includes a sugar and/or a nucleobase) or a nucleoside-replacement group (e.g., a spacer) of the oligonucleotide. An oligonucleotide unit encompasses nucleosides, modified nucleosides, and spacers. For example, an oligonucleotide may have 20 oligonucleotide units, wherein one of the oligonucleotide units is a spacer and the other 19 oligonucleotide units are nucleosides or modified nucleosides. As another example, an oligonucleotide may have 20 oligonucleotide units, wherein two of the oligonucleotide units are spacers, and the other 18 oligonucleotide units are nucleosides or modified nucleosides.

[00138] As used herein, "nucleoside mimetic" includes those structures used to replace the sugar or the sugar and the base and not necessarily the linkage at one or more positions of an oligomeric compound such as for example nucleoside mimetics having morpholino, cyclohexenyl, cyclohexyl, tetrahydropyranyl, bicyclo, or tricyclo sugar mimetics, *e.g.*, non-furanose sugar units. Nucleotide mimetic includes those structures used to replace the nucleoside and the linkage at one or more positions of an oligomeric compound such as for example peptide nucleic acids or morpholinos (morpholinos linked by a phosphorodiamidate or other non-phosphodiester linkage). Sugar surrogate overlaps with the slightly broader term nucleoside mimetic but is intended to indicate replacement of the sugar unit (furanose ring) only. The tetrahydropyranyl rings provided herein are illustrative of an example of a sugar surrogate wherein the furanose sugar group has been replaced with a tetrahydropyranyl ring system. "Mimetic" refers to groups that are substituted for a sugar, a nucleobase, and/or internucleoside linkage. Generally, a mimetic is used in place of the sugar or sugar-internucleoside linkage combination, and the nucleobase is maintained for hybridization to a selected target.

[00139] As used herein, "nucleotide" means a nucleoside having a phosphate group covalently linked to the sugar portion of the nucleoside.

[00140] As used herein, "oligomeric compound" or "oligomer" means a polymer of linked monomeric subunits which is capable of hybridizing to at least a region of a nucleic acid molecule.

[00141] As used herein, "oligonucleotide" means a polymer of one or more segments of linked nucleosides each of which can be modified or unmodified, independent one from another.

[00142] The disclosure provides methods for treating, ameliorating, or preventing a disease such as, but not limited to, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism, in a patient, comprising administering to a patient a composition comprising a therapeutically effective amount of an antisense oligonucleotide, and a pharmaceutically acceptable excipient.

[00143] Also provided herein are methods for treating, ameliorating, or preventing a disease, the method comprising administering to a patient a composition comprising a therapeutically effective amount of an antisense oligonucleotide and a pharmaceutically acceptable excipient. For example, in some embodiments, methods for treating, ameliorating, or preventing a disease comprise administering a pharmaceutically acceptable composition, for example, a pharmaceutically acceptable formulation, that includes one or more antisense oligonucleotides, to a patient. Antisense oligonucleotides disclosed herein can target transcripts (e.g., mRNA or pre-mRNA transcripts) of any one of PPM1A, ATXN2, SOD1, or MAPT. Antisense oligonucleotides can modulate expression of transcripts for treating a disease disclosed herein.

[00144] The present disclosure also provides pharmaceutical compositions comprising antisense oligonucleotides as disclosed herein formulated together with one or more pharmaceutically or cosmetically acceptable excipients. These formulations include those suitable for oral, sublingual, intratracheal, intranasal, vaginal, rectal, topical, transdermal, pulmonary, intrathecal, intracisternal, intrathecal, intrathalamic, intracerebroventricular, intraocular, buccal, and parenteral (*e.g.*, subcutaneous, intramuscular, intradermal, intraduodenal, or intravenous) administration, or for topical use, *e.g.*, as part of a composition suitable for applying topically to skin and/or mucous membrane, for example, a composition in the form of a gel, a paste, a wax, a cream, a spray, a liquid, a foam, a lotion, an ointment, a topical solution, a transdermal patch, a powder, a vapor, or a tincture. Although the most suitable form of administration in any given case will depend on the degree and severity of the condition being treated and on the nature of the particular antisense oligonucleotide being used.

[00145] The present invention also provides a pharmaceutical composition comprising an antisense oligonucleotide, or a pharmaceutically acceptable salt thereof. The present disclosure also provides methods that include the use of pharmaceutical compositions comprising antisense oligonucleotides as disclosed herein (*e.g.*, an AON comprising any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C) formulated together with one or more pharmaceutically acceptable excipients. Exemplary compositions provided herein include compositions comprising an antisense oligonucleotide, as described above, and one or more pharmaceutically acceptable excipients. Formulations include those suitable for oral, sublingual, intratracheal, intranasal, rectal, vaginal, topical, transdermal, pulmonary, intrathecal, intracisternal, intrathecal, intrathalamic, intracerebroventricular, intraocular, buccal, and parenteral (*e.g.*, subcutaneous, intramuscular, intradermal, intraduodenal, or intravenous) administration, or for topical use. The most suitable form of administration in any given case will depend on the clinical symptoms, complications, or biochemical indicia of the state, disorder, disease, or condition that one is trying to prevent in a subject; the state, disorder, disease, or condition one is trying to prevent in a subject; and/or on the nature of the particular compound and/or the composition being used.

Antisense Therapeutics

[00146] Antisense therapeutics are a class of nucleic acid-based compounds that can be used to inhibit gene expression. Antisense therapeutics may be single- or double-stranded deoxyribonucleic acid (DNA)-based, ribonucleic acid (RNA)-based, or DNA/RNA chemical

analogue compounds. In general, antisense therapeutics are designed to include a nucleotide sequence that is complementary or nearly complementary to an mRNA or pre-mRNA sequence of a given gene in order to promote binding between the antisense therapeutic and the pre-mRNA or mRNA. Examples of given genes disclosed herein include, but are not limited to PPM1A, ATXN2, SOD1, or MAPT.

[00147] Without being bound by theory, it is believed that in most instances antisense therapeutics act by binding to an mRNA or pre-mRNA, thereby inhibiting protein translation, altering pre-mRNA splicing into mature mRNA, and/or causing destruction of mRNA. In most instances, the antisense therapeutic nucleotide sequence is complementary to a portion of a targeted gene's, mRNA's, or pre-mRNA's sense sequence. Antisense therapeutics described herein are oligonucleotide-based compounds that include an oligonucleotide sequence complementary to a gene sense, pre-mRNA sense, and/or mRNA sense sequence, or a portion thereof. Antisense therapeutics described herein can also be nucleotide chemical analog-based compounds capable of binding to a gene sense, pre-mRNA sense, and/or mRNA sense sequence, or a portion thereof. Antisense therapeutics include antisense oligonucleotides, shRNAs, siRNAs, PNAs, LNAs, and morpholino oligomers.

[00148] Antisense oligonucleotides (AONs) are short oligonucleotide-based sequences that include an oligonucleotide sequence complementary to a target RNA sequence. AONs are typically between 8 to 50 nucleotides in length, for example, 18 nucleotides in length, 20 nucleotides in length, or 23 nucleotides in length. AONs may include chemically modified nucleosides (for example, 2'-O-methylated nucleosides or 2'-O-(2-methoxyethyl) nucleosides) as well as modified internucleoside linkages (for example, phosphorothioate linkages). AONs described herein include oligonucleotide sequences that are complementary to RNA sequences, such as mRNA or pre-mRNA transcripts. AONs described herein can include chemically modified nucleosides and modified internucleoside linkages (for example, phosphorothioate linkages).

[00149] Peptide nucleic acids (PNAs) are short, artificially synthesized polymers with a structure that mimics DNA or RNA. PNAs include a backbone composed of repeating N-(2-aminoethyl)-glycine units linked by peptide bonds. PNAs described herein can be used as antisense therapeutics that bind to mRNA or pre-mRNA sequences with high specificity and inhibit target gene expression.

[00150] Locked nucleic acids (LNAs) are oligonucleotide sequences that include one or more modified RNA nucleotides in which the ribose moiety is modified with an extra bridge connecting the 2' oxygen and 4' carbon. LNAs are believed to have higher Tm's than analogous

oligonucleotide sequences. LNAs described herein can be used as antisense therapeutics that bind to RNA sequences with high specificity and inhibit target gene expression.

[00151] Morpholino oligomers are oligonucleotide compounds that include DNA bases attached to a backbone of methylenemorpholine rings linked through phosphorodiamidate groups. Morpholino oligomers of the present invention can be designed to bind to specific RNA sequences of interest (for example, mRNA or pre-mRNA sequences of interest), thereby preventing gene expression. Morpholino oligomers described herein can be used as antisense therapeutics that bind to mRNA sequences with high specificity and inhibit gene expression. Morpholino oligomers described herein can also be used to bind pre-mRNA sequences, altering pre-mRNA splicing and gene expression.

[00152] Small hairpin RNAs (shRNAs) are generally RNA molecules with a hairpin-like structure that can be used to silence gene expression. shRNAs are generally expressed from plasmids encoding the shRNA sequence, and can be expressed from viral vectors to allow lentiviral, adenoviral, or adeno-associated viral expression. Without being bound by theory, it is believed that shRNA inhibits gene expression by taking advantage of RNA interference (RNAi) processes. In brief, the shRNA transcript is processed by Drosha and Dicer, and then loaded onto the RNA-induced silencing complex (RISC), allowing targeting of specific mRNA, and either mRNA degradation or repression of protein translation. shRNAs described herein can inhibit target gene expression.

[00153] Small interfering RNAs (siRNAs) are double-stranded RNA molecules of approximately 20-25 base pairs in length that take advantage of RNAi machinery (*e.g.*, Drosha and RISC) to bind and target mRNA for degradation. siRNAs are not dependent upon plasmids or vectors for expression, and can generally be delivered directly to a target cell, for instance, by transfection. siRNAs are double-stranded RNA sequences that include an RNA sequence complementary to a mRNA sequence, and which prevent protein translation.

[00154] The number of nucleotides included in an antisense therapeutic, for example, an antisense oligonucleotide described herein may vary. For example, in some embodiments, the antisense oligonucleotide is from 12 to 15 oligonucleotide units in length. In some embodiments, the antisense oligonucleotide is from 15 to 20 oligonucleotide units in length. In some embodiments, the antisense oligonucleotide is from 20 to 40 oligonucleotide units in length. In some embodiments, the antisense oligonucleotide is from 20 to 22 oligonucleotide units in length. In some embodiments, the antisense oligonucleotide is from 22 to 40 oligonucleotide units in length. In some embodiments, the antisense oligonucleotide is from 20 to 30, 25 to 35, or 30 to 40 oligonucleotide units in length. In particular embodiments, the antisense oligonucleotide is 18

oligonucleotide units in length. In particular embodiments, the antisense oligonucleotide is 20 oligonucleotide units in length. In particular embodiments, the antisense oligonucleotide is 23 oligonucleotide units in length.

Antisense Oligonucleotides

[00155] Antisense oligonucleotides (AONs) described herein are short synthetic oligonucleotide sequence complementary to a portion of a gene product, such as any of a PPM1A, ATXN2, SOD1, or MAPT transcript (for example, a PPM1A, ATXN2, SOD1, or MAPT mRNA transcript, or a PPM1A, ATXN2, SOD1, or MAPT pre-mRNA transcript).

[00156] In various embodiments, AONs include linked nucleosides with a nucleobase sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or that is 100% complementary to a portion of a target gene product, such as a mRNA or pre-mRNA sequence. In some embodiments, an AON can include a non-duplexed oligonucleotide. In some embodiments, an AON can include a duplex of two oligonucleotides where the first oligonucleotide includes a nucleotide sequence that is completely or almost completely complementary to a target mRNA sequence and the second oligonucleotide includes a nucleotide sequence that is complementary to the nucleotide sequence of the first oligonucleotide. AON binding specificity can be assessed via measurement of parameters such as dissociation constant, melting temperature (Tm), or other criteria such as changes in protein or RNA expression levels or other assays that measure target activity or expression.

[00157] An AON, such as disclosed herein, may be an oligonucleotide sequence of 5 to 100 oligonucleotide units in length, for example, 10 to 40 oligonucleotide units in length, for example, 14 to 40 oligonucleotide units in length, 10 to 30 oligonucleotide units in length, for example, 14 to 30 oligonucleotide units in length, for example, 14 to 25 oligonucleotide units in length, 15 to 22 oligonucleotide units in length, 18 to 21 oligonucleotide units in length, or 18, 19, 20, 21, 22, 23, 24, or 25 oligonucleotide units in length. In particular embodiments, an AON is 18 oligonucleotide units in length. In particular embodiments, an AON is 20 oligonucleotide units in length. In particular embodiments, an AON is 23 oligonucleotide units in length. In particular embodiments, an AON includes 20 linked nucleosides. As used herein, "parent oligonucleotides" refer to AONs including 20 linked nucleosides.

[00158] AONs described herein also include antisense oligonucleotides comprising the oligonucleotide sequences listed in Tables 1A-1D. Specifically, Table 1A shows example PPM1A AONs. In various embodiments, PPM1A AONs comprise a sequence of any one of SEQ ID NOs: 1-954. Table 1B shows example ATXN2 AONs. In various embodiments, ATXN2

AONs comprise a sequence of any one of SEQ ID NOs: 1914-149354. Table 1C shows example SOD1 AONs. In various embodiments, SOD1 AONs comprise a sequence of any one of SEQ ID NOs: 149362-158581. Table 1D shows example MAPT AONs. In various embodiments, MAPT AONs comprise a sequence of any one of SEQ ID NOs: 167805-301566.

[00159] In various embodiments, the AONs shown in Tables 1A-1D comprise at least one nucleoside linkage selected from a phosphorothioate linkage, an alkyl phosphate linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a phosphorodithioate linkage, a phosphotriester linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose) linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage.

[00160] In particular embodiments, disclosed herein are gapmer oligonucleotides comprising a sequence that shares at least 85% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In particular embodiments, disclosed herein are gapmer oligonucleotides comprising a sequence that shares at least 90% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In particular embodiments, disclosed herein are gapmer oligonucleotides comprising a sequence that shares at least 95% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In particular embodiments, disclosed herein are gapmer oligonucleotides comprising a sequence that shares at least 98% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C. In particular embodiments, disclosed herein are gapmer oligonucleotides comprising a sequence that shares 100% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

Oligonucleotide Variants

[00161] In various embodiments, AONs include different variants (e.g., AONs of different lengths), hereafter referred to as AON variants. An AON variant may be an oligonucleotide sequence of 5 to 100 nucleobases in length, for example, 10 to 40 nucleobases in length, for example, 14 to 40 nucleobases in length, 10 to 30 nucleobases in length, for example, 14 to 30 nucleobases in length, for example, 16 to 28 nucleobases in length, for example, 19 to 23 nucleobases in length, for example, 18 to 21 nucleobases in length, for example, or 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleobases in length. An AON variant may be an oligonucleotide sequence complementary to a portion of a target mRNA sequence or a target pre-mRNA sequence.

[00162] In various embodiments, an AON variant represents a modified version of a corresponding parent oligonucleotide that includes a nucleobase sequence selected from any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. In some embodiments, an AON variant includes a nucleobase sequence that represents a shortened version of a nucleobase sequence of an AON selected from any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. As one example, if a parent oligonucleotide includes a 20mer (*e.g.*, 20 nucleotide bases in length), a variant (*e.g.*, an AON variant) may include a shorter version (*e.g.*, 15mer, 16mer, 17mer, 18mer, or 19mer) of the 20mer parent oligonucleotide or a longer version (e.g., 21mer, 22mer, 23mer, 24mer, 25mer, 26mer, 27mer, 28mer, 29mer, or 30mer) of the 20mer parent oligonucleotide. In one embodiment, a nucleobase sequence of an AON variant differs from a corresponding nucleobase sequence of a parent oligonucleotide in that 1, 2, 3, 4, 5, or 6 nucleotide bases are removed from or added to one or both of the 3' and 5' ends of the nucleobase sequence of the parent oligonucleotide.

[00163] In one embodiment, the corresponding AON variant may include a 18mer where one nucleotide base was removed from each of the 3' and 5' end of a 20mer included in the parent oligonucleotide. For example, a 18mer AON variant may comprise a sequence in which one nucleotide base is removed from each of the 3' and 5' end of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566.

[00164] In one embodiment, the corresponding AON variant may include a 18mer where two nucleotide bases were removed from the 3' end of a 20mer included in the parent oligonucleotide. For example, a 18mer AON variant may comprise a sequence in which two nucleotide bases are removed from the 3' end of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. In one embodiment, the corresponding AON variant may include a 18mer where two nucleotide bases were removed from the 5' end of a 20mer included in the parent oligonucleotide. For example, a 18mer AON variant may comprise a sequence in which two

nucleotide bases are removed from the 5' end of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566.

[00165] In one embodiment, the corresponding AON variant may include a 19mer where one nucleotide base was removed from either the 3' or 5' end of a 20mer included in the parent oligonucleotide. For example, a 19mer AON variant may comprise a sequence in which one nucleotide base is removed from the 3' end of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. For example, a 19mer AON variant may comprise a sequence in which one nucleotide base is removed from the 5' end of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566.

[00166] In one embodiment, the corresponding AON variant may include a 23mer where three nucleotide bases are added to either the 3' or 5' end of the 20mer included in the parent oligonucleotide. For example, a 19mer AON variant may comprise a sequence in which three nucleotide bases are added to either the 3' end or the 5' end of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566.

[00167] Example sequences of AON variants are shown below in Tables 2A-2B.

Table 2A. Example MAPT AON Variant Sequences.

SEQ ID NO:	Length	MAPT AON Sequence (5'-3')*
301590	18 oligonucleotide units	CCGTTTTCTTACCACCCT

Table 2B. Example PPM1A AON Variant Sequences

SEQ ID NO:	Length	PPM1A AON Sequence (5'-3')*
301591	23 oligonucleotide units	TCCACTTGGCAAACCGATCACAG
301592	23 oligonucleotide units	GTCCACTTGGCAAACCGATCACA
301593	23 oligonucleotide units	CCACTTGGCAAACCGATCACAGC
301594	23 oligonucleotide units	AGTCCACTTGGCAAACCGATCAC

In Tables 2A and 2B, "*" indicates that at least one nucleoside linkage of the nucleobase sequence is selected from a phosphorothioate linkage, an alkyl phosphate linkage, a phosphorodithioate linkage, a phosphotriester linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate

linkage, a thiophosphorodiamidate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose) linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage.

Gapmer AONs

[00168] In particular embodiments, AONs disclosed herein have a gapmer design or structure also referred to herein as "gapmer" or "gapmer AONs." In a gapmer structure the AON comprises at least three distinct structural regions including a 5′-wing region, a central region, and a 3′-wing region, in '5→3' orientation.

[00169] In various embodiments, the 5' wing region includes one, two, three, four, five, six, seven, eight, nine, or ten oligonucleotide units. In various embodiments, at least one of the oligonucleotide units of the 5' wing region includes a spacer. In various embodiments, the 5' wing region includes one, two, three, four, five, six, seven, eight, nine, or ten linked nucleosides. In various embodiments, the 3' wing region includes one, two, three, four, five, six, seven, eight, nine, or ten oligonucleotide units. In various embodiments, at least one of the oligonucleotide units of the 3' wing region includes a spacer. In various embodiments, the 3' wing region includes one, two, three, four, five, six, seven, eight, nine, or ten linked nucleosides. The 5' and 3' wing regions (also termed flanking regions) comprise at least one oligonucleotide unit that is adjacent to the central region, which, in some embodiments, comprises a stretch of contiguous nucleosides. The 5' and 3' wing regions may be symmetrical or asymmetrical with respect to the number of oligonucleotide units or linked nucleosides they include.

[00170] In various embodiments, the 5' wing region comprises one or more RNA nucleosides (e.g, ribonucleosides). In various embodiments, the 5' wing region comprises one or more DNA nucleosides (e.g, deoxyribonucleosides). In various embodiments, the 5' wing region comprises both RNA nucleosides and DNA nucleosides. In various embodiments, the 3' wing region comprises one or more RNA nucleosides. In various embodiments, the 3' wing region comprises one or more DNA nucleosides. In various embodiments, the 3' wing region comprises both RNA nucleosides and DNA nucleosides.

[00171] In various embodiments, the central region includes one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty oligonucleotide units. In various embodiments, the central region includes one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen,

sixteen, seventeen, eighteen, nineteen, or twenty linked nucleosides. In some embodiments, the central region comprises a stretch of nucleosides that enable recruitment and activation of RNAseH. In some embodiments, the central region comprises one or more of linked DNA nucleosides, 2'-Fluoro Arabino Nucleic Acids (FANA), and Fluoro Cyclohexenyl nucleic acid (F-CeNA). In some embodiments, all nucleosides of the central region are DNA nucleosides. In some embodiments, the central region comprises a contiguous stretch of 5-16 DNA nucleosides. In some embodiments, the central region comprises a contiguous stretch of 6-15, 7-14, 8-13, or 9-11 DNA nucleosides. In various embodiments, the central region comprises a mix of DNA nucleosides and RNA nucleosides. In various embodiments, at least one oligonucleotide unit of the central region is a spacer. In some embodiments, one oligonucleotide unit of the central region is a spacer. In some embodiments, two oligonucleotide units of the central region are spacers.

[00172] In some embodiments, all of the nucleosides of the central region are DNA nucleosides. In further embodiments the central region may consist of a mixture of DNA nucleosides and other nucleosides (2'-Fluoro Arabino Nucleic Acids (FANA), and Fluoro Cyclohexenyl nucleic acid (F-CeNA)) capable of mediating RNase H cleavage. In some embodiments, at least 50% of the nucleosides of the central region are DNA nucleosides, such as at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% DNA nucleosides.

[00173] In particular embodiments, the AON includes a 5' wing region of 5 linked nucleosides, a central region of 10 linked nucleosides, and a 3' wing region of 5 linked nucleosides, also referred to as a 5-10-5 gapmer. In particular embodiments, the AON includes a 5' wing region of 3 linked nucleosides, a central region of 8 linked nucleosides, and a 3' wing region of 3 linked nucleosides, also referred to as a 3-8-3 gapmer. In particular embodiments, the AON includes a 5' wing region of 3 linked nucleosides, a central region of 10 linked nucleosides, and a 3' wing region of 3 linked nucleosides, also referred to as a 3-10-3 gapmer. In particular embodiments, the AON includes a 5' wing region of 4 linked nucleosides, a central region of 10 linked nucleosides, and a 3' wing region of 4 linked nucleosides, also referred to as a 4-10-4 gapmer. In particular embodiments, the AON includes a 5' wing region of 4 linked nucleosides, a central region of 8 linked nucleosides, and a 3' wing region of 4 linked nucleosides, also referred to as a 4-8-4 gapmer. In various embodiments, at least one of the nucleosides in any of the 3' wing region, 5' wing region, or central is replaced with a spacer. Embodiments of gapmer AONs with one or more spacers is described in further detail herein.

[00174] In particular embodiments, gapmer AONs discloed herein comprise a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, wherein the gapmer AON includes a 5' wing region comprising one or more RNA nucleosides, a central region comprising one or more DNA nucleosides, and a 3' wing region comprising one or more RNA nucleosides. In particular embodiments, gapmer AONs discloed herein comprise a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 are 5-10-5 gapmers (e.g., 5' wing region of 5 linked nucleosides, a central region of 10 linked nucleosides, and a 3' wing region of 5 linked nucleosides). In particular embodiments, gapmer AONs discloed herein comprise a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 are 6-11-6 gapmers (e.g., 5' wing region of 6 linked nucleosides, a central region of 11 linked nucleosides, and a 3' wing region of 6 linked nucleosides). In particular embodiments, gapmer AONs disclosed herein comprise a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 are 5-8-5 gapmers (e.g., 5' wing region of 5 linked nucleosides, a central region of 8 linked nucleosides, and a 3' wing region of 5 linked nucleosides).

[00175] Further example Gapmer AONs described herein can include those identified below in Tables 3A-3D. Specifically, Table 3A shows example PPM1A gapmer AONs, Table 3B shows example ATXN2 gapmer AONs, Table 3C shows example SOD1 gapmer AONs, and Table 3D shows example MAPT gapmer AONs. In various embodiments, all cytosines of gapmer AONs shown in Tables 3A-3D are 5 methylcytosines (5-MeC).

Table 3A: Example PPM1A Gapmer AONs and Gapmer variant AONs. In the gapmer structure, "e" refers to a ribonucleoside, such as a 2'-MOE modified ribonucleoside, and "d10" or "d11" denotes 10 or 11 DNA deoxyribonucleosides, respectively

SEQ ID NO:	PPM1A AON Sequence (5'-3')	Gapmer structure
301595	TCCACTTGGCAAACCGATCACAG	eeeeee-d11-eeeeee
301596	GTCCACTTGGCAAACCGATCACA	eeeeee-d11-eeeeee
301597	CCACTTGGCAAACCGATCACAGC	eeeeee-d11-eeeeee
301598	AGTCCACTTGGCAAACCGATCAC	eeeeee-d11-eeeeee
301599	CCACTTGGCAAACCGATCAC	eeeee-d10-eeeee
301600	GCCCATCATACACAGCAAAG	eeeee-d10-eeeee

Table 3B: Example ATXN2 Gapmer AONs. In the gapmer structure, "e" refers to a ribonucleoside, such as a 2'-MOE modified ribonucleoside, and "d10" denotes 10 deoxyribonucleosides.

SEQ ID NO:	ATXN2 AON Sequence (5'-3')	Gapmer structure
301601	GCTAACTGGTTTGCCCTTGC	eeeee-d10-eeeee
301602	GTGGGATACAAATTCTAGGC	eeeee-d10-eeeee
301603	GGAGCTGGAGAACCATGAGC	eeeee-d10-eeeee
301604	TGTACTTCACATTTGGAGCC	eeeee-d10-eeeee

Table 3C: Example SOD1 Gapmer AON. In the gapmer structure, "e" refers to a ribonucleoside, such as a 2'-MOE modified ribonucleoside, and "d10" denotes 10 deoxyribonucleosides.

SEQ ID NO:	SOD1 AON Sequence (5'-3')	Gapmer structure
301605	CAGGATACATTTCTACAGCT	eeeee-d10-eeeee

Table 3D: Example MAPT Gapmer AONs and Gapmer variant AONs. In the gapmer structure, "e" refers to a ribonucleoside, such as a 2'-MOE modified ribonucleoside, and "d8" or "d10" denotes 8 or 10 deoxyribonucleosides, respectively.

SEQ ID NO:	MAPT AON Sequence (5'-3')	Gapmer structure
301606	CCGTTTTCTTACCACCCT	eeeee-d8-eeeee
301607	CCGTTTTCTTACCACCCTAA	eeeee-d10-eeeee

[00176] In various embodiments, gapmer AONs, such as gapmer AONs comprising a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or any of the gapmer AON sequences shown in Tables 3A-3D (e.g., SEQ ID NOs: 301595-301607), include a mixture of ribonucleosides and deoxyribonucleosides (including modified ribonucleosides and/or modified deoxyribonucleosides) in the 5' wing region and/or the 3' wing region.

[00177] In particular embodiments, gapmer AONs, such as gapmer AONs comprising a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or any of the gapmer AON sequences shown in Tables 3A-3D (e.g., SEQ ID NOs: 301595-301607), include modified ribonucleosides in the 5' wing region and/or the 3' wing region. In particular embodiments, each nucleoside in the 5' wing region and the 3' wing region is a modified nucleoside e.g., a 2'-O-(2-methoxyethyl) (2'-MOE) nucleoside. For example, each guanonsine in the 5' wing region or 3' wing region may be a modified 2'-O-(2-methoxyethyl)guanosine. For example, each adenosine in the 5' wing region or 3' wing region may be a modified 2'-O-(2-methoxyethyl)adenosine. For example, each cytosine in the 5' wing region and 3' wing region may be a 2'-O-(2-methoxyethyl)-5-methylcytosine. For example, each thymidine in the 5' wing region and the 3' wing region may be a 2'-O-(2-methoxyethyl)thymidine.

[00178] In various embodiments, examplary gapmer AONs have one or more modified internucleoside linkages, such as any of a phosphorothioate linkage, an alkyl phosphate linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a phosphorodithioate linkage, a phosphotriester linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose) linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage.

Antisense Oligonucleotides with One or more Spacers

[00179] Embodiments disclosed herein include antisense oligonucleotides (AONs) comprising one or more spacers. In particular embodiments, an AON includes one spacer. In particular embodiments, an AON includes two spacers. In particular embodiments, an AON includes three spacers. Generally, a spacer refers to a nucleoside-replacement group lacking a nucleobase and wherein the nucleoside sugar moiety is replaced by a non-sugar substitute group. The non-sugar substitute group is not capable of linking to a nucleobase, but is capable of linking with the 3' and 5' positions of nucleosides adjacent to the spacer through an internucleoside linking group.

[00180] In various embodiments, AONs with one or more spacers include parent AONs (e.g., antisense oligonucleotides that are complementary to a portion of a target gene product, such as any one of a PPM1A, ATXN2, SOD1, or MAPT mRNA transcript) in which one or more of the nucleosides of the parent oligonucleotides (e.g., any of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566) are replaced with a spacer.

[00181] In various embodiments, AONs with one or more spacers include oligonucleotide variants (e.g., an antisense oligonucleotide that represents a modified version (e.g., shorter or longer) of a corresponding parent oligonucleotide) in which one or more of the nucleosides of the oligonucleotide variants (e.g., a shorter or longer version of a corresponding parent oligonucleotide that includes a nucleobase sequence selected from any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566) are replaced with a spacer.

[00182] In various embodiments, AONs with one or more spacers include gapmer AONs which include at least three distinct structural regions (e.g., a 5′-wing region, a central region, and a 3′-wing region, in '5→3' orientation), in which one or more of the nucleosides of the gapmer AONs (e.g., gapmer AONs comprising a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or any of the gapmer AON sequences shown in Tables 3A-3D (e.g., SEQ ID NOs: 301595-301607)) are replaced with a spacer. In particular embodiments, for a gapmer AON with one or more spacers, a nucleoside in the 5'-wing region is replaced with a spacer. In particular embodiments, for a gapmer AON with one or more spacers, a nucleoside in the 3'-wing region is replaced with a spacer. In particular embodiments, for a gapmer AON with one or more spacers, a nucleoside in the central region is replaced with a spacer. In particular embodiments, for a gapmer AON with one or more spacers, a nucleoside in the 5'-wing region is replaced with a spacer and a nucleoside in the central region is replaced with a spacer. In particular embodiments, for a gapmer AON with one or more spacers, a nucleoside in the 5'-wing region is replaced with a spacer and a nucleoside in the 3'-wing region is replaced with a spacer. In particular embodiments, for a gapmer AON with one or more spacers, a nucleoside in the central region is replaced with a spacer and a nucleoside in the 3'-wing region is replaced with a spacer.

[00183] In particular embodiments, the gapmer oligonucleotide comprises sugar modifications in any of the following patterns: eeeee-d10-eeeee, eeeee-d8-eeeee, eeeeee-d11-eeeeee, eee-d8-eee, eee-d10-eee, eeee-d10-eeee, and eeee-d8-eeee, wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside. In such embodiments, a spacer may replace at least one "e" (e.g., a 2'-MOE nucleoside) or may replace at least one "d" (e.g., a deoxyribonucleoside) in the gapmer oligonucleotide.

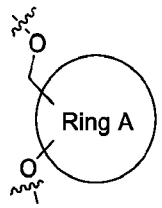
[00184] As used herein, an "AON with one or more spacers" refers to any of a parent AON (e.g., any of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566) with one or more spacers, an AON variant (e.g., a shorter or longer version of a corresponding parent oligonucleotide that comprises a nucleobase sequence selected from any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566) with one or more spacers, or a gapmer

AON (e.g., a gapmer AON comprising a sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or any of the gapmer AON sequences shown in Tables 3A-3D (e.g., SEQ ID NOs: 301595-301607)) with one or more spacers. In certain embodiments, an AON with one or more spacers may be an oligonucleotide with 5 to 100 oligonucleotide units in length, for example, 10 to 60 oligonucleotide units in length, for example, 12 to 50 oligonucleotide units in length, 14 to 40 oligonucleotide units in length, 10 to 30 oligonucleotide units in length, for example, 14 to 30 oligonucleotide units in length, for example, 14 to 25 or 15 to 22 oligonucleotide units in length, or 18, 19, 20, 21, 22, 23, 24, or 25 oligonucleotide units in length. As used herein, an "oligonucleotide unit" refers to either a nucleoside (e.g., a nucleoside which includes a sugar and/or a nucleobase) or a nucleoside-replacement group (e.g., a spacer) of the oligonucleotide.

[00185] In particular embodiments, AONs with one or more spacers are 25 oligonucleotide units in length. In particular embodiments, AONs with one or more spacers are 23 oligonucleotide units in length. In particular embodiments, AONs with one or more spacers are 21 oligonucleotide units in length. In particular embodiments, AONs with one or more spacers are 20 oligonucleotide units in length. In particular embodiments, AONs with one or more spacers are 19 oligonucleotide units in length. In particular embodiments, AONs with one or more spacers are 18 oligonucleotide units in length. In various embodiments, AONs with one or more spacers are at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, or at least 25 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 15 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 16 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 17 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 18 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 19 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 20 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 21 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 22 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 23 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 24 oligonucleotide units in length. In various embodiments, the AONs with one or more spacers are at least 25 oligonucleotide units in length.

[00186] In various embodiments, an AON with one or more spacers comprises a sequence that shares at least 80% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. In various embodiments, an AON with one or more spacers comprises a sequence that shares at least 85% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. In various embodiments, an AON with one or more spacers comprises a sequence that shares at least 90% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. In various embodiments, an AON with one or more spacers comprises a sequence that shares at least 95% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566. In various embodiments, an AON comprises a sequence that shares 98% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566.

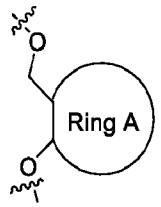
[00187] In some embodiments, the spacer is of Formula (X):



Formula (X)

wherein ring A is as defined herein.

[00188] In some embodiments, the spacer is of Formula (Xa):

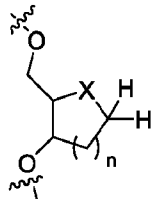


Formula (Xa)

wherein ring A is as defined herein and the -CH_2-O- group is on a ring A atom adjacent to the -O- group.

[00189] As generally defined herein, ring A of formulae (X) and (Xa), is an optionally substituted 4-8 member monocyclic cycloalkyl group (*e.g.* ring A is cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl, cyclooctyl) or a 4-8 member monocyclic heterocyclyl group, wherein the heterocyclyl group contains 1 or 2 heteroatoms selected from O, S and N (*e.g.* ring A is oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, 1,4-dioxanyl, pyrrolidinyl, piperidinyl, piperazinyl, morpholinyl, azepanyl). In some embodiments, ring A is tetrahydrofuranyl. In some embodiments, ring A is tetrahydropyranyl. In some embodiments, ring A is pyrrolidinyl. In some embodiments, ring A is cyclopentyl. In some embodiments, the monocyclic cycloalkyl or monocyclic heterocyclyl is not further substituted. In some embodiments, the cycloalkyl or

heterocyclyl is further substituted with 0, 1, 2 or 3 substituents selected from halo (*e.g.*, -F, -Cl), -OMe, -OEt -O(CH_2)OMe, -O(CH_2)$_2$OMe and CN. In some embodiments, the spacer is represented by Formula (I), wherein:

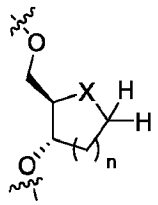


Formula (I)

X is selected from -CH_2- and -O-; and

n is 0, 1, 2 or 3.

[00190] In some embodiments, the spacer is represented by Formula (I'), wherein:

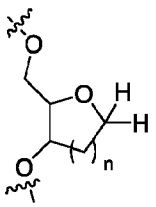


Formula (I')

X is selected from -CH_2-and -O-; and

n is 0, 1, 2 or 3.

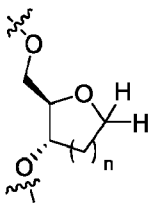
[00191] In some embodiments, the spacer is represented by Formula (Ia), wherein:



Formula (Ia)

and n is 0, 1, 2 or 3.

[00192] In some embodiments, the spacer is represented by Formula (Ia'), wherein:



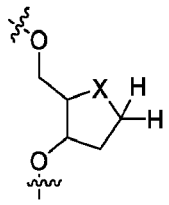
Formula (Ia')

and n is 0, 1, 2 or 3.

[00193] As generally defined herein, X is selected from -CH_2- and -O-. In some embodiments, X is -CH_2-. In other embodiments, X is -O-.

[00194] As generally defined herein, n is 0, 1, 2 or 3. In some embodiments, n is 0. In some embodiments, n is 1 or 2. In some embodiments, n is 1. In other embodiments, n is 2. In certain embodiments, n is 3.

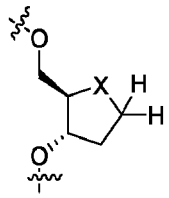
[00195] In some embodiments, the spacer is represented by Formula (II), wherein:



Formula (II)

X is selected from -CH_2- and -O-.

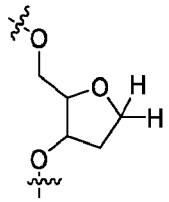
[00196] In some embodiments, the spacer is represented by Formula (II'), wherein:



Formula (II')

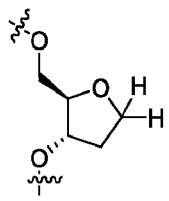
X is selected from -CH_2-and -O.

[00197] In some embodiments, the spacer is represented by Formula (Iia), wherein:



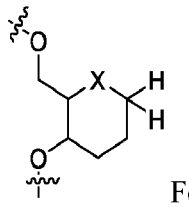
Formula (Iia).

[00198] In some embodiments, the spacer is represented by Formula (Iia'), wherein:



Formula (Iia').

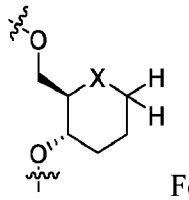
[00199] In some embodiments, the spacer is represented by Formula (III), wherein:



Formula (III)

X is selected from -CH_2- and -O-.

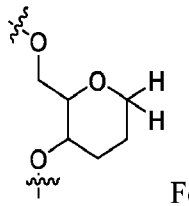
[00200] In some embodiments, the spacer is represented by Formula (III'), wherein:



Formula (III')

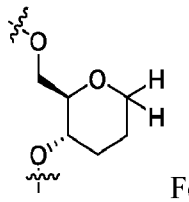
X is selected from -CH_2-and -O.

[00201] In some embodiments, the spacer is represented by Formula (IIIa), wherein:



Formula (IIIa).

[00202] In some embodiments, the spacer is represented by Formula (IIIa'), wherein:



Formula (IIIa').

[00203] In some embodiments, the open positions of Formulae (I), (I'), (Ia), (Ia'), (II), (II'), (Iia), (Iia'), (III), (III'), (IIIa) and (IIIa') (*i.e.*, the positions not specifically depicted as bearing exclusively hydrogen atoms, including the -CH_2- group of X) are further substituted with 0-3 substituents selected from halo (*e.g.*, -F, -Cl), -OMe, -OEt -O(CH_2)OMe, -O(CH_2)$_2$OMe and CN. In some embodiments, Formulae (I), (I'), (Ia), (Ia'), (II), (II'), (Iia), (Iia'), (III), (III'), (IIIa) and (IIIa') are not further substituted.

[00204] As described further below, an AON with one or more spacers is described in reference to a corresponding parent oligonucleotide, to a corresponding oligonucleotide variant, or to a corresponding gapmer oligonucleotide. In various embodiments, an oligonucleotide with one or

more spacers differs from a parent oligonucleotide, an oligonucleotide variant, or a gapmer oligonucleotide in that each of the one or more spacers replaces a nucleoside in parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. As used hereafter, the "position" of the oligonucleotide refers to a particular location as counted from the 5' end of the oligonucleotide. In various embodiments, the spacer replaces a nucleoside at any one of positions 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 of the parent oligonucleotide, of the oligonucleotide variant, or of the gapmer oligonucleotide. In particular embodiments, a spacer replaces a nucleoside at position 7 of the parent oligonucleotide, of the oligonucleotide variant, or of the gapmer oligonucleotide. In particular embodiments, a spacer replaces a nucleoside at position 8 of the parent oligonucleotide, of the oligonucleotide variant, or of the gapmer oligonucleotide. In particular embodiments, a spacer replaces a nucleoside at position 11 of the parent oligonucleotide, of the oligonucleotide variant, or of the gapmer oligonucleotide. In particular embodiments, a spacer replaces a nucleoside at position 14 of the parent oligonucleotide, of the oligonucleotide variant, or of the gapmer oligonucleotide. In particular embodiments, a spacer replaces a nucleoside at position 16 of the parent oligonucleotide, of the oligonucleotide variant, or of the gapmer oligonucleotide. In particular embodiments, a spacer replaces a nucleoside at position 19 of the parent oligonucleotide, of the oligonucleotide variant, or of the gapmer oligonucleotide. In particular embodiments, a spacer replaces a nucleoside at position 22 of the oligonucleotide variant or of the gapmer oligonucleotide.

[00205] In various embodiments, an oligonucleotide includes one spacer that replaces a nucleoside in the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide (e.g., one spacer replaces one nucleoside of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide). Example oligonucleotides with one spacer are shown below in Table 4A. In particular embodiments, the spacer replaces a nucleoside between positions 9 and 15 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the spacer replaces a nucleoside between positions 9 and 12 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the spacer replaces a nucleoside at position 9 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the spacer replaces a nucleoside at position 10 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the spacer replaces a nucleoside at position 11 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the spacer replaces a nucleoside at position 12 of the parent oligonucleotide, oligonucleotide

variant, or gapmer oligonucleotide. In particular embodiments, the spacer replaces a nucleoside between positions 12 and 16 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the spacer replaces a nucleoside at position 15 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide.

[00206] In various embodiments, an oligonucleotide including one spacer has 2 segments, where at least one of the 2 segments has at most 11 linked nucleosides. For example, the oligonucleotide may be 23 oligonucleotide units in length, and the spacer can be located at position 12. Therefore, the oligonucleotide has 2 segments divided by the spacer, where both of the 2 segments are 11 nucleosides in length. In various embodiments, an oligonucleotide including one spacer has 2 segments, where at least one of the 2 segments has at most 10 linked nucleosides. For example, the oligonucleotide may be 21 oligonucleotide units in length, and the spacer can be located at position 11. Therefore, the oligonucleotide has 2 segments divided by the spacer, where both of the 2 segments are 10 nucleosides in length. As another example, the oligonucleotide may be 25 oligonucleotide units in length, and the spacer can be located at position 15. Therefore, the oligonucleotide has 2 segments divided by the spacer, where one of the 2 segments is 14 nucleobases in length and the second of the 2 segments is 10 nucleobases in length. As another example, the oligonucleotide may be 20 oligonucleotide units in length, and the spacer can be located at position 11. Therefore, the oligonucleotide has 2 segments divided by the spacer, where one of the 2 segments is 10 nucleobases in length and the second of the 2 segments is 9 nucleobases in length. As another example, the oligonucleotide may be 18 oligonucleotide units in length, and the spacer can be located at position 11. Therefore, the oligonucleotide has 2 segments divided by the spacer, where one of the 2 segments is 10 nucleobases in length and the second of the 2 segments is 7 nucleobases in length. As another example, the oligonucleotide may be 18 oligonucleotide units in length, and the spacer can be located at position 9. Therefore, the oligonucleotide has 2 segments divided by the spacer, where one of the 2 segments is 8 nucleobases in length and the second of the 2 segments is 9 nucleobases in length.

[00207] In various embodiments, an oligonucleotide includes two spacers that each replace a nucleoside in the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide (e.g., two spacers replace two separate nucleosides of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide). Example oligonucleotides with two spacers are shown below in Table 4B and Table 4C. In various embodiments, a first spacer and a second spacer are separated by at least 5 nucleobases, at least 6 nucleobases, at least 7 nucleobases, at least 8 nucleobases, at least 9 nucleobases, or at least 10 nucleobases in the oligonucleotide. In particular

embodiments, a first spacer and a second spacer are separated by at least 5 nucleobases, at least 6 nucleobases, or at least 7 nucleobases. In particular embodiments, the first spacer and the second spacer are not adjacent to one another in the oligonucleotide.

[00208] In particular embodiments, the first spacer replaces a nucleoside between positions 7 and 11 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In various embodiments, the first spacer replaces a nucleoside between positions 8 and 11, positions 9 and 11, positions 10 and 11, positions 7 and 10, positions 7 and 9, positions 7 and 8, positions 8 and 10, positions 8 and 9, or positions 9 and 10 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the second spacer replaces a nucleoside between positions 14 and 22 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In various embodiments, the second spacer replaces a nucleoside between positions 15 and 22, positions 16 and 22, positions 17 and 22, position 18 and 22, position 19 and 22, positions 20 and 22, positions 21 and 22, positions 15 and 21, position 16 and 21, positions 17 and 21, positions 18 and 21, positions 19 and 21, positions 20 and 21, positions 15 and 20, positions 16 and 20, positions 17 and 20, positions 18 and 20, positions 19 and 20, positions 15 and 19, positions 16 and 19, positions 17 and 19, positions 18 and 19, positions 15 and 18, position 16 and 18, position 17 and 18, positions 15 and 17, positions 16 and 17, or positions 15 and 16 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide.

[00209] In preferred embodiments, the first spacer replaces a nucleoside at position 7 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide and the second spacer replaces a nucleoside at position 14 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In preferred embodiments, the first spacer replaces a nucleoside at position 7 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide and the second spacer replaces a nucleoside at position 15 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In preferred embodiments, the first spacer replaces a nucleoside at position 7 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide and the second spacer replaces a nucleoside at position 19 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In preferred embodiments, the first spacer replaces a nucleoside at position 8 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide and the second spacer replaces a nucleoside at position 16 of the K parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In preferred embodiments, the first spacer replaces a nucleoside at position 11 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide and the second spacer replaces a nucleoside at position 19 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In

preferred embodiments, the first spacer replaces a nucleoside at position 11 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide and the second spacer replaces a nucleoside at position 22 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In preferred embodiments, the first spacer replaces a nucleoside at position 9 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide and the second spacer replaces a nucleoside at position 19 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In preferred embodiments, the first spacer replaces a nucleoside at position 5 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide and the second spacer replaces a nucleoside at position 17 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide.

[00210] In various embodiments, an oligonucleotide includes three spacers that each replace a nucleoside in the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide (e.g., three spacers replace three separate nucleosides of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide). In particular embodiments, the first spacer replaces a nucleoside between positions 7 and 11 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the second spacer replaces a nucleoside between positions 14 and 22 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the third spacer replaces a nucleoside between positions 21 and 24 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In some embodiments, the first spacer replaces a nucleoside between positions 2 and 5 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the second spacer replaces a nucleoside between positions 8 and 12 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. In particular embodiments, the third spacer replaces a nucleoside between positions 18 and 22 of the parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide.

[00211] In various embodiments, the three spacers in an oligonucleotide are positioned such that each of the four segments of the oligonucleotide are at most 7 linked nucleosides in length. For example, an oligonucleotide may have a first segment with 7 linked nucleosides connected to a first spacer, then a second segment with 7 linked nucleosides connected on one end to the first spacer and connected on another end to a second spacer, then a third segment with 6 linked nucleosides connected on one end to the second spacer and connected on another end to a third spacer, then a fourth segment with 6 linked nucleosides connected to the third spacer.

[00212] In various embodiments, the one or more spacers are positioned in the oligonucleotide to replace one or more adenosine or thymine nucleosides (as opposed to guanine or cytosine

nucleosides). For example, the one or more spacers can replace one, two, three, four, five, six, seven, eight, or nine adenosine or thymine nucleosides in the oligonucleotide. In various embodiments, the one or more spacers are positioned in the oligonucleotide to replace one or more guanine or cytosine nucleosides (as opposed to adenosine or thymine nucleosides). For example, the one or more spacers can replace one, two, three, four, five, six, seven, eight, or nine guanine or cytosine nucleosides in the oligonucleotide. In various embodiments, the spacers are positioned in the oligonucleotide to replace an equal number of adenosine/thymine nucleosides and guanine/cytosine nucleosides. For example, a first spacer in the oligonucleotide may replace an adenosine/thymine nucleoside and a second spacer in the oligonucleotide may replace a guanine/cytosine nucleoside.

[00213] In various embodiments, the one or more spacers are positioned in the oligonucleotide to control the sequence content in the oligonucleotide. For example, the one or more spacers are positioned such that at least one of the spacers is located adjacent to a guanine group. In various embodiments, an oligonucleotide with spacers can include one spacer adjacent to a guanine group, two spacers adjacent to guanine groups, three spacers adjacent to guanine groups, four spacers adjacent to guanine groups, or five spacers adjacent to guanine groups. In one embodiment, if counting from the 5' end of the oligonucleotide, a spacer immediately precedes a guanine group in the sequence. Thus, in various embodiments, an oligonucleotide with spacers can include one spacer that immediately precedes a guanine group, two spacers that each immediately precede a guanine group, three spacers that each immediately precede a guanine group, four spacers that each immediately precede a guanine group, or five spacers that each immediately precede a guanine group. In one embodiment, if counting from the 5' end of the oligonucleotide, a guanine group is immediately succeeded by a spacer. Thus, in various embodiments, an oligonucleotide with spacers can include one spacer that immediately succeeds a guanine group, two spacers that each immediately succeed a guanine group, three spacers that each immediately succeed a guanine group, four spacers that each immediately succeed a guanine group, or five spacers that each immediately succeed a guanine group. In various embodiments, the spacers in the oligonucleotide can be positioned to maximize the number of spacers adjacent to guanine groups.

[00214] In various embodiments, the one or more spacers are positioned in the oligonucleotide to replace one or more adenosine or thymine nucleosides such that the one or more spacers are located adjacent guanine groups. For example, two spacers can replace adenosine or thymine nucleosides in the oligonucleotide, each of the two spacers being located adjacent to a guanine group.

[00215] In various embodiments, the oligonucleotide with one or more spacers has a particular GC content. As used herein, GC content (or guanine-cytosine content) is the percentage of nitrogenous bases in the oligonucleotide that are either guanine (G) or cytosine (C). In various embodiments, the oligonucleotide with one or more spacers has at least 10% GC content, at least 20% GC content, at least 25% GC content, at least 30% GC content, at least 35% GC content, at least 40% GC content, at least 45% GC content, at least 50% GC content, at least 55% GC content, at least 60% GC content, at least 65% GC content, at least 75% GC content, at least 80% GC content, at least 85% GC content, at least 90% GC content, or at least 95% GC content. In particular embodiments, the oligonucleotide with one or more spacers has at least 30% GC content. In particular embodiments, the oligonucleotide with one or more spacers has at least 40% GC content. In various embodiments, the one or more spacers are positioned in the oligonucleotide to maximize GC content. For example, instead of selecting a guanine or cytosine for replacement by a spacer in the oligonucleotide, a thymine or adenine can be selected for replacement by a spacer.

[00216] In various embodiments, an oligonucleotide with spacers is designed such that 1) each segment of the oligonucleotide has at most 7 linked nucleosides and 2) at least two, three, or four spacers are positioned adjacent to a guanine group. In some embodiments, an oligonucleotide with spacers is designed such that 1) each segment of the oligonucleotide has at most 7 linked nucleosides and 2) each of two spacers precede a guanine group.

[00217] In various embodiments, the inclusion of one or more spacers in the oligonucleotide does not decrease the effectiveness of the oligonucleotide with the spacers in reducing the frequency of target mRNA or pre-mRNA transcripts in comparison to the effect of a corresponding parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide. Example mRNA or pre-mRNa transcripts include gene products of any of PPM1A, ATXN2, SOD1, or MAPT. In various embodiments, the inclusion of one or more spacers in the oligonucleotide increases the effectiveness of the oligonucleotide with the spacers in reducing the frequency of target mRNA or pre-mRNA transcripts in comparison to the effect of a corresponding parent oligonucleotide, oligonucleotide variant, or gapmer oligonucleotide.

[00218] Tables 4A, 4B, and 4C document example AONs with one or more spacers and their relation to corresponding parent oligonucleotides, corresponding oligonucleotide variants, and/or corresponding gapmer oligonucleotides. Each oligonucleotide is assigned a sequence name. As used hereafter, the nomenclature of the sequence name is expressed as "X_spA" (for an AON with one spacer), "X_spA_spB" (for an AON with two spacers), or "X_spA_spB_spC" (for an AON with three spacers). Here, "X" refers to the length of the AON, "A" refers to the position in

the AON where the first spacer is located, "B" refers to the position in the AON where the second spacer is located, and if present, "C" refers to the position in the AON where the third spacer is located.

[00219] Example AONs with one spacer are documented below in Table 4A.

Table 4A: Identification of AONs with one spacer. Here, each AON has 2 segments.

Sequence name	**Relation to gapmer oligonucleotide or gapmer oligonucleotide variant**	**Sequence* (where *X* indicates a nucleoside of the gapmer oligonucleotide or oligonucleotide gapmer variant and S_y indicates presence of a Spacer where *y* denotes the position)** (5' → 3')
Gapmer oligonucleotide (e.g., 5-10-5 gapmer)	N/A	XXXXXXXXXXXXXXXXXXXX (20mer)
Gapmer oligonucleotide (20mer) with Spacer at position 1 (AON 20_sp1)	Nucleoside at position 1 of 20mer is substituted with a spacer	$\mathbf{S_1}$XXXXXXXXXXXXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 2 (AON 20_sp2)	Nucleoside at position 2 of 20mer is substituted with a spacer	X$\mathbf{S_2}$XXXXXXXXXXXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 3 (AON 20_sp3)	Nucleoside at position 3 of 20mer is substituted with a spacer	XX$\mathbf{S_3}$XXXXXXXXXXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 4 (AON 20_sp4)	Nucleoside at position 4 of 20mer is substituted with a spacer	XXX$\mathbf{S_4}$XXXXXXXXXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 5 (AON 20_sp5)	Nucleoside at position 5 of 20mer is substituted with a spacer	XXXX$\mathbf{S_5}$XXXXXXXXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 6 (AON 20_sp7)	Nucleoside at position 6 of 20mer is substituted with a spacer	XXXXX$\mathbf{S_6}$XXXXXXXXXXXXX
Gapmer oligonucleotide	Nucleoside at position 7 of	XXXXXX$\mathbf{S_7}$XXXXXXXXXXXX

(20mer) with Spacer at position 7 (AON 20_sp7)	20mer is substituted with a spacer	
Gapmer oligonucleotide (20mer) with Spacer at position 8 (AON 20_sp8)	Nucleoside at position 8 of 20mer is substituted with a spacer	XXXXXXX$\mathbf{S}_8$XXXXXXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 9 (AON 20_sp9)	Nucleoside at position 9 of 20mer is substituted with a spacer	XXXXXXXX$\mathbf{S}_9$XXXXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 10 (AON 20_sp10)	Nucleoside at position 10 of 20mer is substituted with a spacer	XXXXXXXXX$\mathbf{S}_{10}$XXXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 11 (AON 20_sp11)	Nucleoside at position 11 of 20mer is substituted with a spacer	XXXXXXXXXX$\mathbf{S}_{11}$XXXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 12 (AON 20_sp12)	Nucleoside at position 12 of 20mer is substituted with a spacer	XXXXXXXXXXX$\mathbf{S}_{12}$XXXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 13 (AON 20_sp13)	Nucleoside at position 13 of 20mer is substituted with a spacer	XXXXXXXXXXXX$\mathbf{S}_{13}$XXXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 14 (AON 20_sp14)	Nucleoside at position 14 of 20mer is substituted with a spacer	XXXXXXXXXXXXX$\mathbf{S}_{14}$XXXXX
Gapmer oligonucleotide (20mer) with Spacer at position 15 (AON 20_sp15)	Nucleoside at position 15 of 20mer is substituted with a spacer	XXXXXXXXXXXXXX$\mathbf{S}_{15}$XXXX
Gapmer oligonucleotide (20mer) with Spacer at position 16 (AON 20_sp16)	Nucleoside at position 16 of 20mer is substituted with a spacer	XXXXXXXXXXXXXXX$\mathbf{S}_{16}$XXX
Gapmer oligonucleotide	Nucleoside at position 17 of	XXXXXXXXXXXXXXXX$\mathbf{S}_{17}$XX

(20mer) with Spacer at position 17 (AON 20_sp17)	20mer is substituted with a spacer	
Gapmer oligonucleotide (20mer) with Spacer at position 18 (AON 20_sp18)	Nucleoside at position 18 of 20mer is substituted with a spacer	XXXXXXXXXXXXXXXXX$\mathbf{S}_{18}$XX
Gapmer oligonucleotide (20mer) with Spacer at position 18 (AON 20_sp19)	Nucleoside at position 19 of 20mer is substituted with a spacer	XXXXXXXXXXXXXXXXXX$\mathbf{S}_{19}$X
Gapmer oligonucleotide (20mer) with Spacer at position 20 (AON 20_sp18)	Nucleoside at position 20 of 20mer is substituted with a spacer	XXXXXXXXXXXXXXXXXX$\mathbf{S}_{20}$
Gapmer oligonucleotide variant (23mer) (e.g., 6-11-6 gapmer)	N/A	XXXXXXXXXXXXXXXXXXXXXXX (23mer)
Gapmer oligonucleotide (23mer) with Spacer at position 12 (AON 23_sp12)	Nucleoside at position 12 of 23mer is substituted with a spacer	XXXXXXXXXXX$\mathbf{S}_{12}$XXXXXXXXXXX
Gapmer oligonucleotide variant (21mer)	N/A	XXXXXXXXXXXXXXXXXXXXX (21mer)
Gapmer oligonucleotide (21mer) with Spacer at position 11 (AON 21_sp11)	Nucleoside at position 11 of 21mer is substituted with a spacer	XXXXXXXXXX$\mathbf{S}_{11}$XXXXXXXXXX
Gapmer oligonucleotide variant (19mer)	N/A	XXXXXXXXXXXXXXXXXXX (19mer)
Gapmer oligonucleotide (19mer) with Spacer at position 10 (AON 19_sp10)	Nucleoside at position 10 of 19mer is substituted with a spacer	XXXXXXXXX$\mathbf{S}_{10}$XXXXXXXXX
Gapmer oligonucleotide variant (18mer) (e.g., 4-10-4 gapmer)	N/A	XXXXXXXXXXXXXXXXXX (18mer)
Gapmer oligonucleotide	Nucleoside at position 9 of 18mer is	XXXXXXXX$\mathbf{S}_{9}$XXXXXXXXX

(18mer) with Spacer at position 9 (AON 18_sp9)	substituted with a spacer	
Gapmer oligonucleotide (18mer) with Spacer at position 10 (AON 18_sp10)	Nucleoside at position 10 of 18mer is substituted with a spacer	XXXXXXXXX$\mathbf{S_{10}}$XXXXXXXX
Gapmer oligonucleotide (18mer) with Spacer at position 11 (AON 18_sp11)	Nucleoside at position 11 of 18mer is substituted with a spacer	XXXXXXXXXX$\mathbf{S_{11}}$XXXXXXX

* At least one nucleoside linkage of the nucleobase sequence is selected from a phosphorothioate linkage, an alkyl phosphate linkage, a phosphorodithioate linkage, a phosphotriester linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose) linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage.

[00220] In various embodiments, oligonucleotides disclosed herein include two spacers. In various embodiments, the inclusion of two spacers divide up the oligonucleotide into three separate segments, where at least one of the segments is at most 7 linked nucleosides in length.

[00221] In particular embodiments, a first spacer is located between positions 5 and 11 of the oligonucleotide. In various embodiments, the first spacer is located between positions 7 and 11 of the oligonucleotide. In various embodiments, the second spacer is located between positions 15 and 19 of the oligonucleotide. In various embodiments, the first spacer and the second spacer are separated by at least 5 nucleobases, at least 6 nucleobases, or at least 7 nucleobases in the oligonucleotide.

[00222] In various embodiments, the first spacer is located between positions 5 and 11 of the oligonucleotide, and the second spacer is located between positions 15 and 19 of the oligonucleotide. In various embodiments, the first spacer is located at position 8 of the oligonucleotide, and wherein the second spacer is located at position 16 of the oligonucleotide. In various embodiments, the first spacer is located at position 5 of the oligonucleotide, and wherein the second spacer is located at position 17 of the oligonucleotide. In various embodiments, the first spacer is located at position 7 of the oligonucleotide, and wherein the second spacer is

located at position 14 of the oligonucleotide. In various embodiments, the first spacer is located at position 7 of the oligonucleotide, and wherein the second spacer is located at position 15 of the oligonucleotide. In various embodiments, the first spacer is located at position 11 of the oligonucleotide, and wherein the second spacer is located at position 19 of the oligonucleotide.

Example AONs with two spacers are documented below in Table 4B.

Table 4B: Identification of AONs with two spacers. Here, each AON has 3 segments.

Sequence name	**Relation to gapmer oligonucleotide**	**Sequence* (where *X* indicates a nucleoside of the gapmer oligonucleotide and S_y indicates presence of a Spacer where *y* denotes the position)** (5' → 3')
20mer Gapmer oligonucleotide (e.g., 5-10-5 gapmer)	N/A	XXXXXXXXXXXXXXXXXXXX
Gapmer oligonucleotide with Spacers at positions 5 and 15 (AON 20_sp5sp15)	Nucleosides at positions 5 and 15 are each substituted with a spacer	XXXX$\mathbf{S_5}$XXXXXXXXX$\mathbf{S_{15}}$XXXXX
Gapmer oligonucleotide with Spacers at positions 5 and 16 (AON 20_sp5sp16)	Nucleosides at positions 5 and 16 are each substituted with a spacer	XXXX$\mathbf{S_5}$XXXXXXXXXX$\mathbf{S_{16}}$XXXX
Gapmer oligonucleotide with Spacers at positions 5 and 17 (AON 20_sp5sp17)	Nucleosides at positions 5 and 17 are each substituted with a spacer	XXXX$\mathbf{S_5}$XXXXXXXXXXX$\mathbf{S_{17}}$XXX
Gapmer oligonucleotide with Spacers at positions 5 and 18 (AON 20_sp5sp18)	Nucleosides at positions 5 and 18 are each substituted with a spacer	XXXX$\mathbf{S_5}$XXXXXXXXXXXX$\mathbf{S_{18}}$XX
Gapmer oligonucleotide with Spacers at positions 5 and 19 (AON 20_sp5sp19)	Nucleosides at positions 5 and 19 are each substituted with a spacer	XXXX$\mathbf{S_5}$XXXXXXXXXXXXX$\mathbf{S_{19}}$X
Gapmer oligonucleotide with Spacers at positions 6 and 15 (AON 20_sp6sp15)	Nucleosides at positions 6 and 15 are each substituted with a spacer	XXXXX$\mathbf{S_6}$XXXXXXXX$\mathbf{S_{15}}$XXXXX

Gapmer oligonucleotide with Spacers at positions 6 and 16 (AON 20_sp6sp16)	Nucleosides at positions 6 and 16 are each substituted with a spacer	XXXXX$\mathbf{S_6}$XXXXXXXXX$\mathbf{S_{16}}$XXXX
Gapmer oligonucleotide with Spacers at positions 6 and 17 (AON 20_sp6sp17)	Nucleosides at positions 6 and 17 are each substituted with a spacer	XXXXX$\mathbf{S_6}$XXXXXXXXXX$\mathbf{S_{17}}$XXX
Gapmer oligonucleotide with Spacers at positions 6 and 18 (AON 20_sp6sp18)	Nucleosides at positions 6 and 18 are each substituted with a spacer	XXXXX$\mathbf{S_6}$XXXXXXXXXXX$\mathbf{S_{18}}$XX
Gapmer oligonucleotide with Spacers at positions 6 and 19 (AON 20_sp6sp19)	Nucleosides at positions 6 and 19 are each substituted with a spacer	XXXXX$\mathbf{S_6}$XXXXXXXXXXXX$\mathbf{S_{19}}$X
Gapmer oligonucleotide with Spacers at positions 7 and 14 (AON 20_sp7sp14)	Nucleosides at positions 7 and 14 are each substituted with a spacer	XXXXXX$\mathbf{S_7}$XXXXXX$\mathbf{S_{14}}$XXXXXX
Gapmer oligonucleotide with Spacers at positions 7 and 15 (AON 20_sp7sp15)	Nucleosides at positions 7 and 15 are each substituted with a spacer	XXXXXX$\mathbf{S_7}$XXXXXXX$\mathbf{S_{15}}$XXXXX
Gapmer oligonucleotide with Spacers at positions 7 and 16 (AON 20_sp7sp16)	Nucleosides at positions 7 and 16 are each substituted with a spacer	XXXXXX$\mathbf{S_7}$XXXXXXXX$\mathbf{S_{16}}$XXXX
Gapmer oligonucleotide with Spacers at positions 7 and 17 (AON 20_sp7sp17)	Nucleosides at positions 7 and 17 are each substituted with a spacer	XXXXXX$\mathbf{S_7}$XXXXXXXXX$\mathbf{S_{17}}$XXX
Gapmer oligonucleotide with Spacers at positions 7 and 18 (AON 20_sp7sp18)	Nucleosides at positions 7 and 18 are each substituted with a spacer	XXXXXX$\mathbf{S_7}$XXXXXXXXXX$\mathbf{S_{18}}$XX
Gapmer oligonucleotide with Spacers at positions 7 and 19 (AON 20_sp7sp19)	Nucleosides at positions 7 and 19 are each substituted with a spacer	XXXXXX$\mathbf{S_7}$XXXXXXXXXXX$\mathbf{S_{19}}$X

Gapmer oligonucleotide with Spacers at positions 8 and 15 (AON 20_sp8sp15)	Nucleosides at positions 8 and 15 are each substituted with a spacer	XXXXXXX$\mathbf{S_8}$XXXXXX$\mathbf{S_{15}}$XXXXX
Gapmer oligonucleotide with Spacers at positions 8 and 16 (AON 20_sp8sp16)	Nucleosides at positions 8 and 16 are each substituted with a spacer	XXXXXXX$\mathbf{S_8}$XXXXXXX$\mathbf{S_{16}}$XXXX
Gapmer oligonucleotide with Spacers at positions 8 and 17 (AON 20_sp8sp17)	Nucleosides at positions 8 and 17 are each substituted with a spacer	XXXXXXX$\mathbf{S_8}$XXXXXXXX$\mathbf{S_{17}}$XXX
Gapmer oligonucleotide with Spacers at positions 8 and 18 (AON 20_sp8sp18)	Nucleosides at positions 8 and 18 are each substituted with a spacer	XXXXXXX$\mathbf{S_8}$XXXXXXXXX$\mathbf{S_{18}}$XX
Gapmer oligonucleotide with Spacers at positions 8 and 19 (AON 20_sp8sp19)	Nucleosides at positions 8 and 19 are each substituted with a spacer	XXXXXXX$\mathbf{S_8}$XXXXXXXXXX$\mathbf{S_{19}}$X
Gapmer oligonucleotide with Spacers at positions 9 and 15 (AON 20_sp9sp15)	Nucleosides at positions 9 and 15 are each substituted with a spacer	XXXXXXXX$\mathbf{S_9}$XXXXX$\mathbf{S_{15}}$XXXXX
Gapmer oligonucleotide with Spacers at positions 9 and 16 (AON 20_sp9sp16)	Nucleosides at positions 9 and 16 are each substituted with a spacer	XXXXXXXX$\mathbf{S_9}$XXXXXX$\mathbf{S_{16}}$XXXX
Gapmer oligonucleotide with Spacers at positions 9 and 17 (AON 20_sp9sp17)	Nucleosides at positions 9 and 17 are each substituted with a spacer	XXXXXXXX$\mathbf{S_9}$XXXXXXX$\mathbf{S_{17}}$XXX
Gapmer oligonucleotide with Spacers at positions 9 and 18 (AON 20_sp9sp18)	Nucleosides at positions 9 and 18 are each substituted with a spacer	XXXXXXXX$\mathbf{S_9}$XXXXXXXX$\mathbf{S_{18}}$XX
Gapmer oligonucleotide with Spacers at positions 9 and 19 (AON 20_sp9sp19)	Nucleosides at positions 9 and 19 are each substituted with a spacer	XXXXXXXX$\mathbf{S_9}$XXXXXXXXX$\mathbf{S_{19}}$X

Gapmer oligonucleotide with Spacers at positions 10 and 15 (AON 20_sp10sp15)	Nucleosides at positions 10 and 15 are each substituted with a spacer	XXXXXXXXX$\mathbf{S_{10}}$XXXX$\mathbf{S_{15}}$XXXXX
Gapmer oligonucleotide with Spacers at positions 10 and 16 (AON 20_sp10sp16)	Nucleosides at positions 10 and 16 are each substituted with a spacer	XXXXXXXXX$\mathbf{S_{10}}$XXXXX$\mathbf{S_{16}}$XXXX
Gapmer oligonucleotide with Spacers at positions 10 and 17 (AON 20_sp10sp17)	Nucleosides at positions 10 and 17 are each substituted with a spacer	XXXXXXXXX$\mathbf{S_{10}}$XXXXXX$\mathbf{S_{17}}$XXX
Gapmer oligonucleotide with Spacers at positions 10 and 18 (AON 20_sp10sp18)	Nucleosides at positions 10 and 18 are each substituted with a spacer	XXXXXXXXX$\mathbf{S_{10}}$XXXXXXX$\mathbf{S_{18}}$XX
Gapmer oligonucleotide with Spacers at positions 10 and 19 (AON 20_sp10sp19)	Nucleosides at positions 10 and 19 are each substituted with a spacer	XXXXXXXXX$\mathbf{S_{10}}$XXXXXXXX$\mathbf{S_{19}}$X
Gapmer oligonucleotide with Spacers at positions 11 and 15 (AON 20_sp11sp15)	Nucleosides at positions 11 and 15 are each substituted with a spacer	XXXXXXXXXX$\mathbf{S_{11}}$XXX$\mathbf{S_{15}}$XXXXX
Gapmer oligonucleotide with Spacers at positions 11 and 16 (AON 20_sp11sp16)	Nucleosides at positions 11 and 16 are each substituted with a spacer	XXXXXXXXXX$\mathbf{S_{11}}$XXXX$\mathbf{S_{16}}$XXXX
Gapmer oligonucleotide with Spacers at positions 11 and 17 (AON 20_sp11sp17)	Nucleosides at positions 11 and 17 are each substituted with a spacer	XXXXXXXXXX$\mathbf{S_{11}}$XXXXX$\mathbf{S_{17}}$XXX
Gapmer oligonucleotide	Nucleosides at positions 11 and	XXXXXXXXXX$\mathbf{S_{11}}$XXXXXX$\mathbf{S_{18}}$XX

with Spacers at positions 11 and 18 (AON 20_sp11sp18)	18 are each substituted with a spacer	
Gapmer oligonucleotide with Spacers at positions 11 and 19 (AON 20_sp11sp19)	Nucleosides at positions 11 and 19 are each substituted with a spacer	XXXXXXXXXX$\mathbf{S_{11}}$XXXXXXX$\mathbf{S_{19}}$X

* At least one nucleoside linkage of the nucleobase sequence is selected from a phosphorothioate linkage, an alkyl phosphate linkage, a phosphorodithioate linkage, a phosphotriester linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose) linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage.

[00223] In various embodiments, AONs with one or more spacers are reduced in length or increased in length in comparison to the AONs described above in Tables 4A and 4B. For example, such AONs may be oligonucleotide variants with one or more spacers. In various embodiments, the oligonucleotide variants with one or more spacers are 23mers, 21mers, 19mers, or 18mers. In various embodiments, oligonucleotide variants include two spacers such that the oligonucleotide variant includes three segments that are divided up by the two spacers. In various embodiments, at least one of the three segments has at most 7 linked nucleosides. In various embodiments, each of the three segments has at most 7 linked nueclosides. Example oligonucleotide variants with one or more spacers are shown below in Table 4C.

Table 4C: AON variants with two spacers. Here, each AON variant has 3 segments.

Sequence name	**Relation to oligonucleotide variant**	**Sequence* (where *X* indicates a nucleoside of the oligonucleotide variant and S_y indicates presence of a Spacer where *y* denotes the position)** (5' → 3')
Gapmer oligonucleotide variant (23mer) (e.g., 6-11-6 gapmer)	N/A	XXXXXXXXXXXXXXXXXXXXXXX (23mer)

Gapmer oligonucleotide variant (23mer) with Spacers at positions 8 and 16 (AON variant 23_sp8sp16)	Nucleosides at positions 8 and 16 are substituted with spacers	XXXXXXX$\mathbf{S_8}$XXXXXXX$\mathbf{S_{16}}$XXXXXXX
Gapmer oligonucleotide variant (21mer)	N/A	XXXXXXXXXXXXXXXXXXXXX (21mer)
Gapmer oligonucleotide variant (21mer) with Spacers at positions 5 and 12 (AON variant 21_sp5sp12)	Nucleosides at positions 5 and 12 are substituted with spacers	XXXX$\mathbf{S_5}$XXXXXX$\mathbf{S_{12}}$XXXXXXXXX
Gapmer oligonucleotide variant (21mer) with Spacers at positions 8 and 16 (AON variant 21_sp8sp16)	Nucleosides at positions 8 and 16 are substituted with spacers	XXXXXXX$\mathbf{S_8}$XXXXXXX$\mathbf{S_{16}}$XXXXX
Gapmer oligonucleotide variant (21mer) with Spacers at positions 6 and 14 (AON variant 21_sp6sp14)	Nucleosides at positions 6 and 14 are substituted with spacers	XXXXX$\mathbf{S_6}$XXXXXXX$\mathbf{S_{14}}$XXXXXXX
Gapmer oligonucleotide variant (21mer) with Spacers at positions 8 and 14 (AON variant 21_sp8sp14)	Nucleosides at positions 8 and 14 are substituted with spacers	XXXXXXX$\mathbf{S_8}$XXXXX$\mathbf{S_{14}}$XXXXXXX
Gapmer oligonucleotide variant (21mer) with Spacers at positions 8 and 14 (AON	Nucleosides at positions 6 and 20 are substituted with spacers	XXXXX$\mathbf{S_6}$XXXXXXXXXXXXX$\mathbf{S_{20}}$X

variant 21_sp8sp14)		
Gapmer oligonucleotide variant (19mer)	N/A	XXXXXXXXXXXXXXXXXXX (19mer)
Gapmer oligonucleotide variant (19mer) with Spacers at positions 5 and 12 (AON variant 19_sp5sp12)	Nucleosides at positions 5 and 12 are substituted with spacers	XXXX$\mathbf{S_5}$XXXXXX$\mathbf{S_{12}}$XXXXXXX
Gapmer oligonucleotide variant (19mer) with Spacers at positions 8 and 15 (AON variant 19_sp8sp15)	Nucleosides at positions 8 and 15 are substituted with spacers	XXXXXXX$\mathbf{S_8}$XXXXXX$\mathbf{S_{15}}$XXXX
Gapmer oligonucleotide variant (18mer) (e.g., 5-8-5 gapmer)	N/A	XXXXXXXXXXXXXXXXXX (18mer)
Gapmer oligonucleotide variant (18mer) with Spacers at positions 5 and 12 (AON variant 18_sp5sp12)	Nucleosides at positions 5 and 12 are substituted with spacers	XXXX$\mathbf{S_5}$XXXXXX$\mathbf{S_{12}}$XXXXXX
Gapmer oligonucleotide variant (18mer) with Spacers at positions 8 and 15 (AON variant 18_sp8sp15)	Nucleosides at positions 8 and 15 are substituted with spacers	XXXXXXX$\mathbf{S_8}$XXXXXX$\mathbf{S_{15}}$XXX

* At least one nucleoside linkage of the nucleobase sequence is selected from a phosphorothioate linkage, an alkyl phosphate linkage, a phosphorodithioate linkage, a phosphotriester linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose)

linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage.

[00224] In various embodiments, antisense oligonucleotides disclosed herein (e.g.,PPM1A AONs, ATXN2 AONs, SOD1 AONs, or MAPT AONs) comprise one or more locked nucleic acids (LNAs). In particular embodiments, an antisense oligonucleotide includes one LNA. In particular embodiments, an antisense oligonucleotide includes two LNAs. In particular embodiments, an antisense oligonucleotide includes three LNAs. Generally, a LNA refers to nucleic acid monomers having a bridge (*e.g.*, methylene, ethylene, aminooxy, or oxyimino bridge) connecting two carbon atoms between the 4' and 2' position of the nucleoside sugar unit, thereby forming a bicyclic sugar.

[00225] In some embodiments, antisense oligonucleotides disclosed herein (e.g.,PPM1A AONs, ATXN2 AONs, SOD1 AONs, or MAPT AONs) comprise one or more spacers as well as one or more locked nucleic acids (LNAs). In some embodiments, antisense oligonucleotides disclosed herein (e.g.,PPM1A AONs, ATXN2 AONs, SOD1 AONs, or MAPT AONs) comprise two spacers and two LNAs. In some embodiments, an antisense oligonucleotide disclosed herein comprises two spacers and three LNAs.

[00226] In various embodiments, a spacer and a LNA are located adjacent to one another in an antisense oligonucleotide. For example, a spacer can be located at position M of the antisense oligonucleotide. Additionally, a LNA can be located at a position $M + 1$ or position $M - 1$ of the antisense oligonucleotide. In various embodiments, a first spacer is located adjacent to a first LNA and a second spacer is located adjacent to a second LNA in an antisense oligonucleotide. For example, a first spacer can be located at position M of the antisense oligonucleotide and a second spacer can be located at position N of the antisense oligonucleotide. A first LNA can be located at a position $M + 1$ or position $M - 1$ of the antisense oligonucleotide and a second LNA can be located at a position $N + 1$ or position $N - 1$ of the antisense oligonucleotide. In other embodiments, one or more spacers and one or more LNAs are not located adjacent to one another in an antisense oligonucleotide. For example, there may be one, two, three, four, five, six, seven, eight, nine, or ten oligonucleotide units between a spacer and a LNA in an antisense oligonucleotide.

Chemical Modifications to AONs

[00227] As described herein, AONs, such as AONs with a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, may include one or more chemical modifications to one or more nucleosides and/or to one or more internucleoside linkages. A nucleoside is a base-sugar combination. The nucleobase (also known as base) portion of the nucleoside is normally a heterocyclic base moiety. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to the 2', 3' or 5' hydroxyl moiety of the sugar. Oligonucleotides are formed through the covalent linkage of adjacent nucleosides to one another, to form a linear polymeric oligonucleotide. Within the oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside linkages of the oligonucleotide.

[00228] Modifications to AONs encompass substitutions or changes to internucleoside linkages and/or nucleosides (*e.g.*, sugar moieties or nucleobases of nucleosides). Modified AONs can be preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for nucleic acid target, increased stability in the presence of nucleases, or increased inhibitory activity. Chemically modified nucleosides, nucleobases, and internucleoside linkages are described in Agrawal and Gait, *History and Development of Nucleotide Analogues in Nucleic Acids Drugs*, in Drug Discovery Series No. 68, Advances in Nucleic Acid Therapeutics, 1-21 (Agrawal and Gait eds., 2019), the contents of which are incorporated by reference herein.

Modified Internucleoside Linkages

[00229] In various embodiments, AONs, such as AONs comprising a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C), include one or more modified internucleoside linkages. The naturally occurring internucleoside linkage of RNA and DNA is a 3' to 5' phosphodiester linkage. AONs having one or more modified, *i.e.*, non-naturally occurring, internucleoside linkages can be selected over antisense compounds having naturally occurring internucleoside linkages because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for target nucleic acids, and increased stability in the presence of nucleases.

[00230] Modified internucleoside linkages include internucleoside linkages that retain a phosphorus atom as well as internucleoside linkages that do not have a phosphorus atom. Representative phosphorus containing internucleoside linkages include, but are not limited to, phosphodiesters, phosphotriesters, methylphosphonates, phosphoramidate, and phosphorothioates. Methods of preparation of phosphorous-containing and non-phosphorous-containing linkages are well known. Examples of modified internucleoside linkages include any one of a phosphorothioate linkage, an alkyl phosphate linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a phosphorodithioate linkage, a phosphotriester linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose) linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage.

[00231] In various embodiments, AONs include one or more modified internucleoside linkages that link the oligonucleotide units. In various embodiments, AONs include one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, or nineteen modified internucleoside linkages that link the oligonucleotide units.

[00232] In various embodiments, each modified internucleoside linkage of the AON can be designed independent of other modified internucleoside linkages of the AON. In other words, the modified internucleoside linkages of an AON need not all be the same type of modified internucleoside linkage. In various embodiments, the modified internucleoside linkages are interspersed throughout the antisense compound.

[00233] In various embodiments, AONs include at least one phosphorothioate linkage. In various embodiments, AONs include at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, or at least nineteen phosphorothioate linkages. In particular embodiments, AONs include thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, twenty, twenty one, or twenty two phosphorothioate linkages. In particular embodiments, AONs include 17 phosphorothioate linkages. In particular embodiments, AONs include 19 phosphorothioate linkages. In particular embodiments, AONs include 22 phosphorothioate linkages. In particular embodiments, all internucleoside linkages of the AON are phosphorothioate linkages.

[00234] In various embodiments, an AON includes a mixture of modified internucleoside linkages and naturally occurring phosphodiester linkages. For example, an AON includes at least one phosphodiester linkage and at least one phosphorothioate linkage. In various embodiments, an AON includes between 6 and 10, between 6 and 9, between 6 and 8, between 7 and 10, between 7 and 9, or 6, 7, or 8 phosphorothioate linkages. In some embodiments, an AON includes 6, 7, 8, 9, or 10 phosphorothioate linkages. In some embodiments, an AON includes between 6 and 10, between 6 and 9, between 6 and 8, between 7 and 10, between 7 and 9, or 6, 7, or 8 phosphodiester linkages. In some embodiments, an AON includes 6, 7, 8, 9, or 10 phosphodiester linkages.

[00235] In particular embodiments, an AON includes 10 phosphorothioate linkages and 9 phosphodiester linkages. In particular embodiments, an AON includes 6 phosphorothioate linkages and 7 phosphodiester linkages. In particular embodiments, an AON includes 6 phosphorothioate linkages and 9 phosphodiester linkages. In particular embodiments, an AON includes 8 phosphorothioate linkages and 9 phosphodiester linkages. In particular embodiments, an AON includes 8 phosphorothioate linkages and 7 phosphodiester linkages. In particular embodiments, an AON includes 12 phosphorothioate linkages and 7 phosphodiester linkages. In particular embodiments, an AON includes 15 phosphorothioate linkages and 4 phosphodiester linkages. In particular embodiments, an AON includes 15 phosphorothioate linkages and 2 phosphodiester linkages. In particular embodiments, an AON includes 17 phosphorothioate linkages and 2 phosphodiester linkages.

[00236] In some embodiments, AONs include internucleoside linkages that are designed according to the gapmer design of the AON. In some embodiments, the 5' wing region includes at least one modified internucleoside linkage (*e.g.*, modified from the naturally occurring internucleoside linkage of a 3' to 5' phosphodiester linkage). In some embodiments, the 5' wing region includes at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or at least ten modified internucleoside linkages. In some embodiments, the 3' wing region includes at least one modified internucleoside linkage. In some embodiments, the 3' wing region includes at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or at least ten modified internucleoside linkages. In some embodiments, the central region includes at least one modified internucleoside linkage. In some embodiments, the central region includes at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or at least ten modified internucleoside linkages.

[00237] In particular embodiments all internucleoside linkages of the 5' wing region are modified internucleoside linkages, such as phosphorothioate linkages. In particular embodiments all internucleoside linkages of the 3' wing region are modified internucleoside linkages, such as phosphorothioate linkages. In particular embodiments all internucleoside linkages of the central region are modified internucleoside linkages, such as phosphorothioate linkages. In particular embodiments all internucleoside linkages of each of the 5' wing region, 3' wing region, and the central region are modified internucleoside linkages, such as phosphorothioate linkages.

[00238] In various embodiments, two internucleoside linkages of the 5' wing region are phosphorothioate linkages. In various embodiments, two internucleoside linkages of the 5' wing region are phosphodiester linkages. In various embodiments, two internucleoside linkages of the 5' wing region are phosphorothioate linkages and another two internucleoside linkages of the 5' wing region are phosphodiester linkages. In various embodiments, two internucleoside linkages of the 3' wing region are phosphorothioate linkages. In various embodiments, two internucleoside linkages of the 3' wing region are phosphodiester linkages. In various embodiments, two internucleoside linkages of the 3' wing region are phosphorothioate linkages and another two internucleoside linkages of the 3' wing region are phosphodiester linkages.

[00239] In various embodiments, four internucleoside linkages of the 5' wing region are phosphorothioate linkages. In various embodiments, four internucleoside linkages of the 5' wing region are phosphorothioate linkages and two internucleoside linkages of the 3' wing region are phosphorothioate linkages. In various embodiments, one internucleoside linkage of the 5' wing region is a phosphorothioate linkage. In various embodiments, one internucleoside linkage of the 3' wing region is a phosphorothioate linkage. In various embodiments, one internucleoside linkage of the 5' wing region is a phosphorothioate linkage and one internucleoside linkage of the 3' wing region is a phosphorothioate linkage.

[00240] In some embodiments, the one or more modified internucleoside linkages in the 5' wing region, 3' wing region, or the central region are phosphorothioate internucleoside linkages. In some embodiments, the phosphorothioate linkages are stereochemically pure phosphorothioate linkages. In some embodiments the phosphorothioate linkages are *S*p phosphorothioate linkages. In other embodiments, the phosphorothioate linkages are *R*p phosphorothioate linkages.

[00241] In some embodiments, the one or more modified internucleoside linkages in the 5' wing region, 3' wing region, or the central region can be any of an alkyl phosphate linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a phosphorodithioate linkage, a phosphotriester linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a

phosphoramidothioate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose) linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage. In various embodiments, each modified internucleoside linkage of the 5' wing region, 3' wing region, or the central region can be designed independent of other modified internucleoside linkages. In other words, the modified internucleoside linkages of 5' wing region, 3' wing region, and the central region need not all be the same type of modified internucleoside linkage. In various embodiments, modified internucleoside linkages are interspersed throughout the antisense compound.

[00242] In various embodiments, one or more internucleoside linkages of the 5' wing region, the 3' wing region, or the central region are naturally occurring linkages (*e.g.*, phosphodiester bonds). In various embodiments, all internucleoside linkages of the central region are unmodified internucleoside linkages (*e.g.*, phosphodiester linkages).

[00243] In various embodiments, the internucleoside linkages of the one region (*e.g.*, 5' wing region, 3' wing region, or the central region) may differ from the internucleoside linkages of another region. In particular embodiments, the 5' wing region includes at least one modified internucleoside linkage, the 3' wing region includes at least one modified internucleoside linkage, and all internucleoside linkages of the central region are unmodified internucleoside linkages (*e.g.*, phosphodiester linkages). In some embodiments, the central region of the oligonucleotide comprises phosphodiester bonds and the 5' wing region and 3' wing region each comprises one or more phosphorothioate linkages. In particular embodiments, all internucleoside linkages of the 5' wing region are modified internucleoside linkages, all internucleoside linkages of the 3' wing region are modified internucleoside linkages, and all internucleoside linkages of the central region are unmodified internucleoside linkages (*e.g.*, phosphodiester linkages).

[00244] In particular embodiments, the gapmer AON is a 5-10-5 gapmer and the internucleoside linkages of the gapmer AON are denoted as: sssssssssssssssss (where "s" refers to a phosphorothioate bond). In particular embodiments, the gapmer AON is a 5-10-5 gapmer and the internucleoside linkages of the gapmer AON are denoted as any of: sssssssssssssssss, sossssssssssssssoss, sssssoooooooooosssss, sosossssssssssosos, soooossssssssssoooos, soooossssssssssooss, ooooossssssssssooooo, ooooooooooooooosssss, soossssssssssssoos, soossssssssssssssss, sssssssssssssssoos, and sssssoooooooooooooo (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In particular embodiments, the

gapmer AON is a 3-8-3 gapmer and the internucleoside linkages of the gapmer AON are denoted as: sssssssssssss (where "s" refers to a phosphorothioate bond).

[00245] In particular embodiments, the gapmer AON is a 3-8-3 gapmer and the internucleoside linkages of the gapmer AON are denoted as any of: sssooooooosss, ooosssssssooo, sssssssssooo, sossssssssos, sossssssssss, sssssssssssos, and ooossssssssss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In particular embodiments, the gapmer AON is a 3-10-3 gapmer and the internucleoside linkages of the gapmer AON are denoted as: sssssssssssssss (where "s" refers to a phosphorothioate bond).

[00246] In particular embodiments, the gapmer AON is a 3-10-3 gapmer and the internucleoside linkages of the gapmer AON are denoted as any of: sssooooooooosss, ooosssssssssooo, sssssssssssooo, sossssssssssos, sossssssssssss, sssssssssssssos, and ooossssssssssss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In particular embodiments, the gapmer AON is a 4-10-4 gapmer and the internucleoside linkages of the gapmer AON are denoted as: ssssssssssssssss (where "s" refers to a phosphorothioate bond).

[00247] In particular embodiments, the gapmer AON is a 4-10-4 gapmer and the internucleoside linkages of the gapmer AON are denoted as any of: ssssooooooooosssss, oooosssssssssoooo, sssssssssssssoooo, soossssssssssoos, soossssssssssss, sssssssssssssoos, and oooossssssssssss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In particular embodiments, the gapmer AON is a 4-8-4 gapmer and the internucleoside linkages of the gapmer AON are denoted as: ssssssssssssss (where "s" refers to a phosphorothioate bond).

[00248] In particular embodiments, the gapmer AON is a 4-8-4 gapmer and the internucleoside linkages of the gapmer AON are denoted as any of: ssssooooooosssss, oooosssssssoooo, sssssssssssoooo, soossssssssssoos, soossssssssssss, sssssssssssssoos, and oooossssssssssss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond).

[00249] In particular embodiments, the gapmer AON is a 5-8-5 gapmer and the internucleoside linkages of the gapmer AON are denoted as any of: sssssssssssssssss or sossssssssssssoss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond).

Modified Sugar Moieties

[00250] AONs, such as AONs with a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C), can contain one or more nucleosides wherein the sugar group has been modified. Such sugar

modified nucleosides may impart enhanced nuclease stability, increased binding affinity, or some other beneficial biological property to the antisense compounds.

[00251] In various embodiments, nucleosides with a modified sugar moiety include a ribose in which the 2′-OH group may be replaced by any one selected from the group consisting of OR, R, R′OR, SH, SR, NH_2, NR_2, N_3, CN, F, Cl, Br, and I (wherein R is an alkyl or aryl and R′ is an alkylene), a 2'-O-methyl (2'-OMe) nucleoside, 2'-O-(2-methoxyethyl) (2'-MOE) nucleoside, peptide nucleic acid (PNA), bicyclic nucleic acid (BNA), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt), *S*-cEt, morpholino oligomer, tcDNA, 2′-O, 4′-C-ethylene linked nucleic acid (ENA), hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA).

[00252] In certain embodiments, nucleosides comprise chemically modified ribofuranose ring moieties. Examples of chemically modified ribofuranose rings include without limitation, addition of substituent groups (including 5' and 2' substituent groups, bridging of non-geminal ring atoms to form bicyclic nucleic acids (BNA), replacement of the ribosyl ring oxygen atom with S, N(R), or $C(R_1)(R_2)$ (R, R_1 and R_2 are each independently H, C_1-C_{12} alkyl or a protecting group) and combinations thereof. Examples of chemically modified sugars include 2'-F-5'-methyl substituted nucleoside (*see* PCT International Application WO 2008/101157 Published on Aug. 21, 2008 for other disclosed 5',2'-bis substituted nucleosides) or replacement of the ribosyl ring oxygen atom with S or CF_2 with further substitution at the 2'-position (*see* published U.S. Patent Application US2005-0130923, published on Jun. 16, 2005) or alternatively 5'-substitution of a BNA (*see* PCT International Application WO 2007/134181 Published on Nov. 22, 2007 wherein LNA is substituted with for example a 5'-methyl or a 5'-vinyl group).

[00253] Examples of nucleosides having modified sugar moieties include without limitation nucleosides comprising 5'-vinyl, 5'-methyl (R or 5), 4'-S, 2'-F, 2'-OCH_3, 2'-OCH_2CH_3, 2'-O CH_2 CH_2F and 2'-$O(CH_2)_2OCH_3$ substituent groups. The substituent at the 2' position can also be selected from allyl, amino, azido, thio, O-allyl, O—C_1-C_{10} alkyl, OCF_3, OCH_2F, $O(CH_2)_2S$ CH_3, $O(CH_2)_2$—O—$N(R_m)(R_n)$, O—CH_2—C(=O)—$N(R_m)(R_n)$, and O—CH_2—C(=O)—$N(R_1)$—($CH_2)_2$—$N(R_m)(R_n)$- , where each R_l, R_m and R_n is, independently, H or substituted or unsubstituted C_1-C_{10} alkyl.

[00254] Additional examples of modified sugar moieties include a 2'-OMe modified sugar moiety, bicyclic sugar moiety, 2'-O-(2-methoxyethyl) (2'-MOE), 2'-O-(N-methylacetamide), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt) (4'-$CH(CH_3)$-O-2'), *S*-constrained ethyl (*S*-cEt) 2'-4'-bridged nucleic acid, 4' -CH_2-O-CH_2-2', 4' -CH_2-N(R)-2', 4'-$CH(CH_2OCH_3)$-O-2'

("constrained MOE" or "cMOE"), hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA).

[00255] In some embodiments, AONs comprise a 2'-O-methyl nucleoside (2'OMe) (*e.g.*, an AON comprising one or more 2'OMe modified sugar), 2'-O-(2-methoxyethyl) (2'-MOE) (*e.g.*, an AON comprising one or more 2'-MOE modified sugar (*e.g.*, 2'-MOE)), peptide nucleic acid (PNA) (*e.g.*, an AON comprising one or more *N*-(2-aminoethyl)-glycine units linked by amide bonds or carbonyl methylene linkage as repeating units in place of a sugar-phosphate backbone), locked nucleic acid (LNA) (*e.g.*, an AON comprising one or more locked ribose, and can be a mixture of 2'-deoxy nucleotides or 2'OMe nucleotides), constrained ethyl 2'-4'-bridged nucleic acid (c-ET) (*e.g.*, an AON comprising one or more cET sugar), cMOE (*e.g.*, an AON comprising one or more cMOE sugar), morpholino oligomer (*e.g.*, an AON comprising a backbone comprising one or more PMO), deoxy-2'-fluoro nucleoside (*e.g.*, an AON comprising one or more 2'-fluoro-β-D-arabinonucleoside), 2′-O,4′-C-ethylene linked nucleic acid (ENA) (*e.g.*, an AON comprising one or more ENA modified sugar), hexitol nucleic acid (HNA) (*e.g.*, an AON comprising one or more HNA modified sugar), or tricyclic analog (tcDNA) (*e.g.*, an AON comprising one or more tcDNA modified sugar).

[00256] As used herein, "bicyclic nucleosides" refer to modified nucleosides comprising a bicyclic sugar moiety. Examples of bicyclic nucleosides include without limitation nucleosides comprising a bridge between the 4' and the 2' ribosyl ring atoms. In certain embodiments, antisense compounds provided herein include one or more bicyclic nucleosides comprising a 4' to 2' bridge. Examples of such 4' to 2' bridged bicyclic nucleosides, include but are not limited to one of the formulae: 4'-(CH_2)—O-2' (LNA); 4'-(CH_2)—S-2'; 4'-(CH_2)$_2$—O-2' (ENA); 4'-CH(CH_3)—O-2' and 4'-CH(CH_2OCH_3)—O-2' (and analogs thereof (*see* U.S. Pat. No. 7,399,845, issued on Jul. 15, 2008)); 4'-C(CH_3)(CH_3)—O-2' (and analogs thereof (*see* published International Application WO/2009/006478, published Jan. 8, 2009)); 4'-CH_2—N(OCH_3)-2' (and analogs thereof (*see* published International Application WO/2008/150729, published Dec. 11, 2008)); 4'-CH_2—O—N(CH_3)-2' (*see* published U.S. Patent Application US2004-0171570, published Sep. 2, 2004); 4'- CH_2—N(R)—O-2', wherein R is H, C_1-C_{12} alkyl, or a protecting group (*see* U.S. Pat. No. 7,427,672, issued on Sep. 23, 2008); 4'-CH_2—C(H)(CH_3)-2' (see Chattopadhyaya et al., J. Org. Chem., 2009, 74, 118-134); and 4'-CH_2—C—(=CH_2)-2' (and analogs thereof (*see* published International Application WO 2008/154401, published on Dec. 8, 2008)).

[00257] Further reports related to bicyclic nucleosides can also be found in published literature (*see* for example: Singh et al., Chem. Commun., 1998, 4, 455-456; Koshkin et al., Tetrahedron, 1998, 54, 3607-3630; Wahlestedt et al., Proc. Natl. Acad. Sci. U.S.A., 2000, 97, 5633-5638;

Kumar et al., Bioorg. Med. Chem. Lett., 1998, 8, 2219-2222; Singh et al., J. Org. Chem., 1998, 63, 10035-10039; Srivastava et al., J. Am. Chem. Soc., 2007, 129(26) 8362-8379; Elayadi et al., Curr. Opinion Invest. Drugs, 2001, 2, 558-561; Braasch et al., Chem. Biol., 2001, 8, 1-7; and Orum et al., Curr. Opinion Mol. Ther., 2001, 3, 239-243; U.S. Pat. Nos. 6,268,490; 6,525,191; 6,670,461; 6,770,748; 6,794,499; 7,034,133; 7,053,207; 7,399,845; 7,547,684; and 7,696,345; U.S. Patent Publication No. US2008-0039618; US2009-0012281; U.S. Patent Ser. No. 60/989,574; 61/026,995; 61/026,998; 61/056,564; 61/086,231; 61/097,787; and 61/099,844; Published PCT International applications WO 1994/014226; WO 2004/106356; WO 2005/021570; WO 2007/134181; WO 2008/150729; WO 2008/154401; and WO 2009/006478. Each of the foregoing bicyclic nucleosides can be prepared having one or more stereochemical sugar configurations including for example α-L-ribofuranose and β-D-ribofuranose (see PCT international application PCT/DK98/00393, published on Mar. 25, 1999 as WO 99/14226).

[00258] In certain embodiments, bicyclic sugar moieties of BNA nucleosides include, but are not limited to, compounds having at least one bridge between the 4' and the 2' position of the pentofuranosyl sugar moiety wherein such bridges independently comprises 1 or from 2 to 4 linked groups independently selected from $—[C(R_a)(R_b)]_n—$, $—C(R_a)=C(R_b)—$, $—C(R_a)=N—$, $—C(=O)—$, $—C(=NR_a)—$, $—C(=S)—$, $—O—$, $—Si(R_a)_2—$, $—S(=O)_x—$, and $—N(R_a)—$; wherein:

x is 0, 1, or 2;

n is 1, 2, 3, or 4;

each R_a and R_b is, independently, H, a protecting group, hydroxyl, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5-C_7 alicyclic radical, substituted C_5-C_7 alicyclic radical, halogen, OJ_1, NJ_1J_2, SJ_1, N_3, $COOJ_1$, acyl (C(=O)—H), substituted acyl, CN, sulfonyl ($S(=O)_2$-J_1), or sulfoxyl (S(=O)-J_1); and

each J_1 and J_2 is, independently, H, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, acyl (C(=O)—H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C_1-C_{12} aminoalkyl, substituted C_1-C_{12} aminoalkyl or a protecting group.

[00259] In certain embodiments, the bridge of a bicyclic sugar moiety is $—[C(R_a)(R_b)]_n—$, $—[—[C(R_a)(R_b)]_n—O—$, $—C(R_aR_b)—N(R)—O—$ or $—C(R_aR_b)—O—N(R)—$. In certain embodiments, the bridge is 4'-CH_2-2', 4'-$(CH_2)_2$-2', 4'-$(CH_2)_3$-2', 4'-CH_2—O-2', 4'-$(CH_2)_2$—O-2', 4'-CH_2—O—N(R)-2' and 4'-CH_2—N(R)—O-2'- wherein each R is, independently, H, a protecting

group or C_1-C_{12} alkyl, each R_a and R_b is, independently, H, a protecting group, hydroxyl, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5-C_7 alicyclic radical, substituted C_5-C_7 alicyclic radical, halogen, OJ_1, NJ_1J_2, SJ_1, N_3, $COOJ_1$, acyl (C(=O)--H), substituted acyl, CN, sulfonyl ($S(=O)_2$-J_1), or sulfoxyl (S(=O)-J_1).

[00260] In certain embodiments, bicyclic nucleosides are further defined by isomeric configuration. For example, a nucleoside comprising a 4'-2' methylene-oxy bridge, may be in the α-L configuration or in the β-D configuration. Previously, α-L-methyleneoxy (4'-CH_2—O-2') BNA's have been incorporated into antisense oligonucleotides that showed antisense activity (Frieden et al., Nucleic Acids Research, 2003, 21, 6365-6372).

[00261] In certain embodiments, bicyclic nucleosides include, but are not limited to, α-L-methyleneoxy (4'-CH_2—O-2') BNA, β-D-methyleneoxy (4'-CH_2—O-2') BNA, ethyleneoxy (4'-$(CH_2)_2$—O-2) BNA, aminooxy (4'-CH_2—O—N(R)-2') BNA, oxyamino (4'-CH_2—N(R)—O-2') BNA, methyl(methyleneoxy) (4'-$CH(CH_3)$—O-2') BNA, methylene-thio (4'-CH_2—S-2') BNA, methylene-amino (4'-CH_2—N(R)-2') BNA, methyl carbocyclic (4'-CH_2—$CH(CH_3)$-2') BNA, and propylene carbocyclic (4'-$(CH_2)_3$-2') BNA.

[00262] As used herein, "locked nucleic acid" or "LNA" or "LNA nucleosides" refer to modified nucleosides having a bridge (*e.g.*, methylene, ethylene, aminooxy, or oxyimino bridge) connecting two carbon atoms between the 4' and 2' position of the nucleoside sugar unit, thereby forming a bicyclic sugar. Examples of such bicyclic sugar include, but are not limited to (A) α-L-Methyleneoxy (4'-CH_2—O-2') LNA, (B) β-D-Methyleneoxy (4'-CH_2—O-2') LNA, (C) Ethyleneoxy (4'-$(CH_2)_2$—O-2') LNA, (D) Aminooxy (4'-CH_2—O—N(R)-2') LNA and (E) Oxyamino (4'-CH_2—N(R)—O-2') LNA; wherein R is H, C_1-C_{12} alkyl, or a protecting group (*see* U.S. Pat. No. 7,427,672, issued on Sep. 23, 2008).

[00263] As used herein, LNA nucleosides include, but are not limited to, nucleosides having at least one bridge between the 4' and the 2' position of the sugar wherein each of the bridges independently comprises 1 or from 2 to 4 linked groups independently selected from —$[C(R_1)(R_2)]_n$ —, —$C(R_1)$=$C(R_2)$—, —$C(R_1)$=N—, —C(=NR_1)—, —C(=O)—, —C(=S)—, —O—, —$Si(R_1)_2$—, —$S(=O)_x$— and —$N(R_1)$ —; wherein: x is 0, 1, or 2; n is 1, 2, 3, or 4; each R_1 and R_2 is, independently, H, a protecting group, hydroxyl, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, a heterocycle radical, a substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5-C_7 alicyclic radical, substituted C_5-C_7 alicyclic radical, halogen, OJ_1,

NJ_1J_2, SJ_1, N_3, $COOJ_1$, acyl (C(=O) —H), substituted acyl, CN, sulfonyl ($S(=O)_2$-J_1), or sulfoxyl (S(=O)- J_1); and each J_1 and J_2 is, independently, H, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, acyl (C(=O) —H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C_1-C_{12} aminoalkyl, substituted C_1-C_{12} aminoalkyl or a protecting group.

[00264] Examples of 4'-2' bridging groups encompassed within the definition of LNA include, but are not limited to one of formulae: —$[C(R_1)(R_2)]_n$ —, — $[C(R_1)(R_2)]_n$—O—, — $C(R_1R_2)$—$N(R_1)$—O— or —$C(R_1R_2)$—O—$N(R_1)$—. Furthermore, other bridging groups encompassed with the definition of LNA are 4'-CH_2-2', 4'-$(CH_2)_2$-2', 4'-$(CH_2)_3$-2', 4'-CH_2—O-2', 4'-$(CH_2)_2$—O-2', 4'-CH_2—O—$N(R_1)$-2' and 4'- CH_2—$N(R_1)$—O-2'- bridges, wherein each R_1 and R_2 is, independently, H, a protecting group or C_1-C_{12} alkyl.

[00265] Also included within the definition of LNA according to the invention are LNAs in which the 2'-hydroxyl group of the ribosyl sugar ring is connected to the 4' carbon atom of the sugar ring, thereby forming a bridge to form the bicyclic sugar moiety. The bridge can be a methylene (—CH_2—) group connecting the 2' oxygen atom and the 4' carbon atom, for which the term methyleneoxy (4'-CH_2—O-2') LNA is used. Furthermore, in the case of the bicyclic sugar moiety having an ethylene bridging group in this position, the term ethyleneoxy (4'-CH_2CH_2—O-2') LNA is used. α-L-methyleneoxy (4'-CH_2-O-2'), an isomer of methyleneoxy (4'-CH_2—O-2') LNA is also encompassed within the definition of LNA, as used herein.

[00266] In various embodiments, AONs disclosed herein include one or more 2'-O-(2-methoxyethyl) (2'-MOE) nucleosides. In various embodiments, AONs disclosed herein include two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventee, eighteen, nineteen, twenty, twenty one, twenty two, twenty three, twenty four, or twenty five 2'-*O*-(2-methoxyethyl) (2'-MOE) nucleosides. In various embodimens, AONs disclosed herein include more than twenty five 2'-*O*-(2-methoxyethyl) (2'-MOE) nucleosides.

[00267] In some embodiments, AONs include modified sugar moieties that are designed according to the gapmer design of the gapmer AON. In various embodiments, gapmer AONs include one or more modified sugar moieties. In various embodiments, the 5' wing region includes at least one modified sugar moiety. In various embodiments, the 3' wing region includes at least one modified sugar moiety. In various embodiments, the 5' wing region includes at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or at least ten modified sugar moieties. In various embodiments, the 3' wing region includes at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or at least ten modified sugar moieties. In some embodiments, each of the 5' wing region

and/or the 3' wing region includes from 1 to 7 modified sugar moieties, such as from two to six modified sugar moieties, from two to five modified sugar moieties, from two to four modified sugar moieties, or from one to three modified sugar moieties. In particular embodiments, the 5' wing region includes 3 modified sugar moieties and the 3' wing region includes 3 modified sugar moieties. In particular embodiments, the 5' wing region includes 4 modified sugar moieties and the 3' wing region includes 4 modified sugar moieties. In particular embodiments, the 5' wing region includes 5 modified sugar moieties and the 3' wing region includes 5 modified sugar moieties.

[00268] In various embodiments, the nucleosides with a modified sugar moiety in the 5' and 3' wing regions are any one of a ribose in which the 2′-OH group may be replaced by any one selected from the group consisting of OR, R, R′OR, SH, SR, NH_2, NR_2, N_3, CN, F, Cl, Br, and I (wherein R is an alkyl or aryl and R′ is an alkylene), a 2'-O-methyl (2'-OMe) nucleoside, 2'-O-(2-methoxyethyl) (2'-MOE) nucleoside, peptide nucleic acid (PNA), bicyclic nucleic acid (BNA), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt), *S*-cEt, morpholino oligomer, tcDNA, 2′-O,4′-C-ethylene linked nucleic acid (ENA), hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA).

[00269] In some embodiments, the 5' wing region and/or 3′ wing region comprises at least one 2'-MOE nucleoside. In some embodiments both the 5′ and 3′ wing regions comprise at least one 2'-MOE nucleoside. In some embodiments, each of the 5′ wing region and the 3′ wing region comprises two, three, four, five, six, seven, eight, nine, or ten 2'-MOE nucleosides. In particular embodiments, each of the 5′ wing region and the 3′ wing region comprises four 2'-MOE nucleosides. In particular embodiments, each of the 5′ wing region and the 3′ wing region comprises five 2'-MOE nucleosides. In some embodiments, all the nucleosides in each of the 5' wing region and the 3' wing region are 2'-MOE nucleosides.

[00270] In other embodiments, the wing regions may comprise both 2'-MOE nucleosides and other nucleosides (mixed wings), such as DNA nucleosides and/or non-MOE modified nucleosides, such as bicyclic nucleosides (BNAs) (*e.g.*, locked nucleic acid (LNA) nucleosides or constrained ethyl 2'-4'-bridged nucleic acid (cEt) nucleosides), 2'-O-methyl nucleosides, tricycloDNA, *S*-cEt, morpholinos, or other 2' substituted nucleosides.

[00271] In some embodiments, the 5' wing region or the 3′ wing region comprises at least one BNA (*e.g.*, at least one LNA nucleoside or cET nucleoside). In some embodiments each of the 5′ and 3′ wing regions comprises a BNA. In some embodiments all the nucleosides in the 5' and 3' wing regions are BNAs. In a further embodiment, the BNAs in the 5' and/or 3' wing regions are

independently selected from the group comprising oxy-LNA, thio-LNA, amino-LNA, cET, and/or ENA, in either the beta-D or alpha-L configurations or combinations thereof.

[00272] In some embodiments, the 5' and/ or 3′ wing comprises at least one 2'-O-methyl nucleoside. In some embodiments, the 5′ wing comprises at least one 2'-O-methyl nucleoside. In some embodiments both the 5′ and 3′ wing regions comprise a 2'-O-methyl nucleoside. In some embodiments all the nucleosides in the wing regions are 2'-O-methyl nucleosides.

Modified Nucleobase

[00273] AONs, such as AONs with a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C), include one or more modified nucleobases. Examples of modified nucleobases, including a 5-methylpyrimidine, for example, 5-methylcytosine or 5-methoxyuridine, a 5-methylpurine, for example, 5-methylguanine, or pseudouridine.

[00274] In various embodiments, an AON includes at least one modified nucleobase. In various embodiments, an AON includes two, three, four, five, six, seven, eight, nine, or ten modified nucleobases. In various embodiments, an AON includes at least one 5-methylcytosine nucleobase. In various embodiments, an AON includes two, three, four, five, six, seven, eight, nine, or ten 5-methylcytosine nucleobases.

[00275] In various embodiments, an AON includes both modified and unmodified nucleobases. For example, an AON may include both cytosines and 5-methyl cytosines. In some embodiments, an AON may include one, two three, four, five, six, seven, eight, nine, or ten cytosines and further include one, two, three, four, five, six seven, eight, nine, or ten 5-methylcytosines.

[00276] In various embodiments, each of a particular type of nucleobase in the AON is replaced with a corresponding modified nucleobase. For example, every guanine of the AON is replaced with a 5-methyl guanine. As another example, every cytosine of the AON is replaced with a 5-methylcytosine.

[00277] In some embodiments, an AON includes modified nucleobases that are designed according to the gapmer design of the gapmer AON. In various embodiments, the linked nucleosides of the 5' wing region, the linked nucleosides of the 3' wing region, or the linked nucleosides of the central region comprise one or more modified nucleobases. In some embodiments, the 5' wing region and/or the 3' wing region includes one to ten modified nucleobases, such as from two to eight modified nucleobases, from three to six modified

nucleobases, or from four to five modified nucleobases. In some embodiments, the 5' wing region and/or the 3' wing region includes one, two, three, four, five, six, seven, eight, nine, or ten modified nucleobases. In some embodiments, the central region includes one to ten modified nucleobases, such as from two to eight modified nucleobases, from three to six modified nucleobases, or from four to five modified nucleobases. In some embodiments, the central region includes one, two, three, four, five, six, seven, eight, nine, or ten modified nucleobases. Examples of modified nucleobases include a 5-methylpyrimidine, for example, pseudouridine, 5-methylcytosine or 5-methoxyuridine, a 5-methylpurine, for example, 5-methylguanine.

[00278] In various embodiments, at least one cytosine in the 5' wing region and/or the 3' wing region of the AON is replaced with a modified nucleobase, such as a 5-methylcytosine. In various embodiments, at least one cytosine in the 5' wing region is replaced with a modified nucleobase, such as a 5-methylcytosine. In various embodiments, at least one cytosine in the 3' wing region is replaced with a modified nucleobase, such as a 5-methylcytosine. In various embodiments, at least one cytosine in the central region is replaced with a modified nucleobase, such as a 5-methylcytosine. In various embodiments, all cytosines in the 5' wing region are replaced with modified nucleobases, such as 5-methylcytosines. In various embodiments, all cytosines in the 3' wing region are replaced with modified nucleobases, such as 5-methylcytosines. In various embodiments, all cytosines in the central region are replaced with modified nucleobases, such as 5-methylcytosines.

[00279] In particular embodiments, all cytosines in the 5' wing region, all cytosines in the 3' wing region, and all cytosines in the central region are replaced with modified nucleobases, such as 5-methylcytosines. In particular embodiments, all cytosines in the 5' wing region, all cytosines in the 3' wing region are replaced with modified nucleobases, such as 5-methylcytosines; however, all cytosines in the central region are unmodified nucleobases.

Modified Oligonucleotides

[00280] Described herein are additional embodiments of modified oligonucleotides, which can include any of the modified internucleoside linkages and/or modified nucleosides (*e.g.*, modified sugar moieties, and/or modified nucleobases) described above.

[00281] In some embodiments, an AON, or a pharmaceutically acceptable salt thereof, comprises the sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C), where at least one nucleoside of the sequence is substituted with a 2'-O-(2-methoxyethyl) nucleoside, a 2'-O-methyl

nucleoside, a 2'-O-(N-methylacetamide) nucleoside, a 2'-deoxy-2'-fluoro nucleoside, a 2'-fluoro-β-D-arabinonucleoside, a bicylic nucleic acid, a bridged nucleic acid, a locked nucleic acid (LNA), a constrained ethyl (cET) nucleic acid, a tricyclo-DNA (tcDNA), a 2′-O,4′-C-ethylene linked nucleic acid (ENA), or a peptide nucleic acid (PNA). In particular embodiments, at least one internucleoside linkage of the AON is a phosphorothioate linkage. In some embodiments, all internucleoside linkages of the AON are phosphorothioate linkages. Also described herein are pharmaceutical compositions that include any of the foregoing antisense oligonucleotides, or a pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable excipient.

[00282] AONs described herein, can include chemically modified nucleosides, including modified ribonucleosides and/or modified deoxyribonucleosides. Chemically modified nucleosides include 2'-substituted nucleosides in which the 2' position of the sugar ring includes a moiety other than -H or -OH (for example, -F or an O-alkyl group). For example, chemically modified nucleosides include, but are not limited to 2'-O-(2-methoxyethyl) modifications, for example, 2'-O-(2-methoxyethyl)guanosine, 2'-O-(2-methoxyethyl)adenosine, 2'-O-(2-methoxyethyl)cytosine, 2'-O-(2-methoxyethyl)thymidine, and 2'-O-(2-methoxyethyl)-5-methylcytosine.

[00283] In some embodiments, AONs can include chemically modified nucleosides, for example, 2' O-methyl ribonucleosides, for example, 2' O-methyl cytidine, 2' O-methyl guanosine, 2' O-methyl uridine, and/or 2' O-methyl adenosine. AONs described herein, can also include one or more chemically modified bases, including a 5-methyl pyrimidine, for example, 5-methylcytosine, and/or a 5-methyl purine, for example, 5-methyl guanine. AONs described herein, can also include any of the following chemically modified nucleosides: 5-methyl-2'-O-methylcytidine, 5-methyl-2'-O-methylthymidine, 5-methylcytidine, 5-methyluridine, and/or 5-methyl 2'-deoxycytidine.

[00284] It is contemplated that in some embodiments, a disclosed AON may optionally have at least one modified nucleobase, *e.g.*, 5-methylcytosine, and/or at least one methylphosphonate nucleotide, which is placed, for example, either at only one of the 5′ or 3′ ends or at both 5′ and 3′ ends or along the oligonucleotide sequence.

[00285] In certain embodiments, the disclosure provides mixed modalities of AONs with combinations of modified nucleosides, *e.g.*, a combination of a peptide nucleic acid (PNA) and a locked nucleic acid (LNA). Chemically modified nucleosides also include, but are not limited to, locked nucleic acids (LNAs), 2'-O-methyl, 2'-fluoro, and 2'-fluoro-β-D-arabinonucleotide (FANA) modifications. Chemically modified nucleosides that can be included in AONs described herein are described in Johannes and Lucchino, (2018) "Current Challenges in Delivery

and Cytosolic Translocation of Therapeutic RNAs" *Nucleic Acid Ther.* 28(3): 178–93; Rettig and Behlke, (2012) "Progress toward in vivo use of siRNAs-II" *Mol Ther* 20:483–512; and Khvorova and Watts, (2017) "The chemical evolution of oligonucleotide therapies of clinical utility" *Nat Biotechnol.*, 35(3):238-48, the contents of each of which are incorporated by reference herein.

[00286] AONs described herein can include chemical modifications that promote stabilization of an oligonucleotide's terminal 5'-phosphate and phosphatase-resistant analogs of 5′-phosphate. Chemical modifications that promote oligonucleotide terminal 5'-phosphate stabilization or which are phosphatase-resistant analogs of 5′-phosphate include, but are not limited to, 5′-methyl phosphonate, 5′-methylenephosphonate, 5′-methylenephosphonate analogs, 5′-*E*-vinyl phosphonate (5′-*E*-VP), 5′-phosphorothioate, and 5′-*C*-methyl analogs. Chemical modifications that promote AON terminal 5'-phosphate stabilization and phosphatase-resistant analogues of 5′-phosphate are described in Khvorova and Watts, (2017) "The chemical evolution of oligonucleotide therapies of clinical utility" *Nat Biotechnol.*, 35(3):238-48, the contents of which are incorporated by reference herein.

[00287] In some embodiments described herein, an AON, or a pharmaceutically acceptable salt thereof, is a modified oligonucleotide which includes the sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C), and at least one nucleoside linkage of the nucleotide sequence is a a phosphorothioate linkage, an alkyl phosphate linkage, an alkylphosphonate linkage, a 3-methoxypropyl phosphonate linkage, a phosphorodithioate linkage, a phosphotriester linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a phosphorodiamidate (*e.g.*, comprising a phosphorodiamidate morpholino (PMO), 3' amino ribose, or 5' amino ribose) linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage. In particular embodiments, at least one internucleoside linkage of the nucleotide sequence is a phosphorothioate linkage. In some embodiments of AONs described herein, one, two, three, or more internucleoside linkages of the nucleotide sequence is a phosphorothioate linkage. In various embodiments of AONs described herein, all internucleoside linkages of the nucleotide sequence are phosphorothioate linkages. Thus, in some embodiments, all of the nucleotide linkages of an AON sequence of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with

one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, are phosphorothioate linkages.

[00288] Contemplated AONs may optionally include at least one modified sugar. For example, the sugar moiety of at least one nucleotide constituting the oligonucleotide is a ribose in which the 2′-OH group may be replaced by any one selected from the group consisting of OR, R, R′OR, SH, SR, NH_2, NR_2, N_3, CN, F, Cl, Br, and I (wherein R is an alkyl or aryl and R′ is an alkylene).

[00289] In particular embodiments, an AON has a structure of eeeee-d10-eeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes five 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes five 2'-MOE modified nucleosides. In various embodiments, the internucleoside linkages of the 5-10-5 gapmer AON can have the sequence of sssssooooooooosssss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond) where all the phosphorothioate bonds are in the 5' wing region or the 3' wing region and all the phosphodiester bonds are in the central region of the AON. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00290] In particular embodiments, an AON has a structure of eeeee-d10-eeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes five 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes five 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of ooooossssssssssooooo (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00291] In particular embodiments, an AON has a structure of eeeee-d10-eeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes five 2'-MOE modified

nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes five 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of sssssssssssssssss (where "s" refers to a phosphorothioate bond) where all internucleoside linkages of the AON are phosphorothioate bonds. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00292] In particular embodiments, an AON has a structure of eee-d8-eee (where "e" denotes a 2'-MOE modified nucleoside and where "d8" denotes a contiguous 8 DNA nucleobase sequence). In this embodiment, the 5' wing region includes three 2'-MOE modified nucleosides, the gap region includes 8 oligonucloetide units comprising at least 4 contiguous nucleobases, and the 3' wing region includes three 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of sssooooooosss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond) where all the phosphorothioate bonds are in the 5' wing region or the 3' wing region and all the phosphodiester bonds are in the central region of the AON. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00293] In particular embodiments, an AON has a structure of eee-d8-eee (where "e" denotes a 2'-MOE modified nucleoside and where "d8" denotes a contiguous 8 DNA nucleobase sequence). In this embodiment, the 5' wing region includes three 2'-MOE modified nucleosides, the gap region includes 8 oligonucleotide units comprising 4 contiguous DNA nucleobases, and the 3' wing region includes three 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of ooosssssssooo (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond) where all the phosphodiester bonds are in the 5' wing region or the 3' wing region and all the phosphorothioate bonds are in the central region of the AON. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00294] In particular embodiments, an AON has a structure of eee-d8-eee (where "e" denotes a 2'-MOE modified nucleoside and where "d8" denotes a contiguous 8 DNA nucleobase sequence). In this embodiment, the 5' wing region includes three 2'-MOE modified nucleosides, the gap region includes 8 oligonucleotide units comprising 4 contiguous DNA nucleobases, and the 3' wing region includes three 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of sssssssssssss (where "s" refers to a phosphorothioate bond) where all internucleoside linkages of the AON are phosphorothioate bonds. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00295] In particular embodiments, an AON has a structure of eee-d10-eee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes three 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes three 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of sssooooooooosss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond) where all the phosphorothioate bonds are in the 5' wing region or the 3' wing region and all the phosphodiester bonds are in the central region of the AON. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00296] In particular embodiments, an AON has a structure of eee-d10-eee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes three 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes three 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of ooosssssssssooo (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine).

[00297] In particular embodiments, an AON has a structure of eee-d10-eee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes three 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes three 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of sssssssssssss (where "s" refers to a phosphorothioate bond) where all internucleoside linkages of the AON are phosphorothioate bonds. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00298] In particular embodiments, an AON has a structure of eeee-d10-eeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes four 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes four 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of ssssoooooooossss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond) where all the phosphorothioate bonds are in the 5' wing region or the 3' wing region and all the phosphodiester bonds are in the central region of the AON. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00299] In particular embodiments, an AON has a structure of eeee-d10-eeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes four 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes four 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of oooossssssssoooo (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00300] In particular embodiments, an AON has a structure of eeee-d10-eeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes four 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes four 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of sssssssssssssss (where "s" refers to a phosphorothioate bond) where all internucleoside linkages of the AON are phosphorothioate bonds. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00301] In particular embodiments, an AON has a structure of eeee-d8-eeee (where "e" denotes a 2'-MOE modified nucleoside and where "d8" denotes a contiguous 8 DNA nucleobase sequence). In this embodiment, the 5' wing region includes four 2'-MOE modified nucleosides, the gap region includes 8 oligonucleotide units comprising 4 contiguous DNA nucleobases, and the 3' wing region includes four 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of ssssooooooossss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond) where all the phosphorothioate bonds are in the 5' wing region or the 3' wing region and all the phosphodiester bonds are in the central region of the AON. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00302] In particular embodiments, an AON has a structure of eeee-d8-eeee (where "e" denotes a 2'-MOE modified nucleoside and where "d8" denotes a contiguous 8 DNA nucleobase sequence). In this embodiment, the 5' wing region includes four 2'-MOE modified nucleosides, the gap region includes 8 oligonucleotide units comprising 4 contiguous DNA nucleobases, and the 3' wing region includes four 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of oooossssssssoooo (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing

region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00303] In particular embodiments, an AON has a structure of eeee-d8-eeee (where "e" denotes a 2'-MOE modified nucleoside and where "d8" denotes a contiguous 8 DNA nucleobase sequence). In this embodiment, the 5' wing region includes four 2'-MOE modified nucleosides, the gap region includes 8 oligonucleotide units comprising 4 contiguous DNA nucleobases, and the 3' wing region includes four 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of sssssssssssssss (where "s" refers to a phosphorothioate bond) where all internucleoside linkages of the AON are phosphorothioate bonds. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine).

[00304] In particular embodiments, an AON has a structure of eeeeee-d11-eeeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d11" denotes a contiguous 11 DNA nucleobase sequence). In this embodiment, the 5' wing region includes six 2'-MOE modified nucleosides, the gap region includes 11 contiguous DNA nucleobases, and the 3' wing region includes six 2'-MOE modified nucleosides. In various embodiments, the internucleoside linkages of the 6-11-6 gapmer AON can have the sequence of sssssssssssssssssssss (where "s" refers to a phosphorothioate bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00305] In particular embodiments, an AON has a structure of eeeee-d10-eeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes five 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes five 2'-MOE modified nucleosides. In various embodiments, the internucleoside linkages of the 5-10-5 gapmer AON can have the sequence of sosossssssssssosos (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00306] In particular embodiments, an AON has a structure of eeeee-d10-eeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes five 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes five 2'-MOE modified nucleosides. In various embodiments, the internucleoside linkages of the 5-10-5 gapmer AON can have the sequence of soooossssssssssooos (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00307] In particular embodiments, an AON has a structure of eeeee-d10-eeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes five 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes five 2'-MOE modified nucleosides. In various embodiments, the internucleoside linkages of the 5-10-5 gapmer AON can have the sequence of soooossssssssssooss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00308] In particular embodiments, an AON has a structure of eeeee-d8-eeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d8" denotes a contiguous 8 DNA nucleobase sequence). In this embodiment, the 5' wing region includes five 2'-MOE modified nucleosides, the gap region includes 8 oligonucleotide units comprising 4 contiguous DNA nucleobases, and the 3' wing region includes five 2'-MOE modified nucleosides. In various embodiments, the internucleoside linkages of the 5-8-5 gapmer AON can have the sequence of sosssssssssssoss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00309] In particular embodiments, an AON has a structure of eeeee-d10-eeeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes five 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes five 2'-MOE modified nucleosides. In various embodiments, the internucleoside linkages of the 5-10-5 gapmer AON can have the sequence of sosssssssssssssosss (where "s" refers to a phosphorothioate bond and "o" refers to a phosphodiester bond). In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

[00310] In particular embodiments, an AON has a structure of eeeeee-d10-eeee (where "e" denotes a 2'-MOE modified nucleoside and where "d10" denotes a contiguous 10 DNA nucleobase sequence). In this embodiment, the 5' wing region includes six 2'-MOE modified nucleosides, the gap region includes 10 contiguous DNA nucleobases, and the 3' wing region includes four 2'-MOE modified nucleosides. The internucleoside linkages of the AON can have the sequence of sssssssssssssss (where "s" refers to a phosphorothioate bond) where all internucleoside linkages of the AON are phosphorothioate bonds. In various embodiments, the AON includes unmodified cytosines. In various embodiments, the AON includes modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the 5' wing region and the 3' wing region are modified cytosines (*e.g.*, 5-methylcytosine). In various embodiments, all cytosines of the central region are modified cytosines (*e.g.*, 5-methylcytosine).

Target Gene Product

[00311] Generally, an AON disclosed herein includes linked nucleosides with a nucleobase sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or that is 100% complementary to a portion of a target gene product. Example target gene products include any of PPM1A, ATXN2, SOD1, or MAPT gene products. In particular embodiments, an AON disclosed herein includes linked nucleosides with a nucleobase sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or that is 100% complementary to a portion of a gene product. In particular embodiments, an AON disclosed herein includes linked nucleosides with a nucleobase sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or that is 100% complementary to a portion of an ATXN2 gene product.

In particular embodiments, an AON disclosed herein includes linked nucleosides with a nucleobase sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or that is 100% complementary to a portion of a SOD1 gene product. In particular embodiments, an AON disclosed herein includes linked nucleosides with a nucleobase sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or that is 100% complementary to a portion of a MAPT gene product.

[00312] In embodiments of the invention described herein, an AON can target gene products of genes of one or more species. For example, an AON can target a gene product of a mammalian gene, for example, a human (*i.e.*, *Homo sapiens*) gene, a rodent gene (for example, a mouse (*Mus musculus*) gene), and/or a primate gene (for example, a *Macaca fascicularis* gene or a *Macaca mulatta* gene). In particular embodiments, the AON targets a human gene product.

[00313] A gene product can be, for example, an RNA gene product, for example, an mRNA gene product, or a protein product of a target gene. In some embodiments, the AON includes a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or that is 100% complementary to a sequence of a gene or a RNA, for example a mRNA or a pre-mRNA, or a portion thereof. In some embodiments the AON includes a nucleobase sequence that is complementary to a portion of a sequence that is shared between genes or RNAs (for example, mRNAs) of multiple species. For example, in some embodiments, the AON is an antisense therapeutic, for example, an AON that is complementary to a sequence shared by a human, mouse, and/or primate genes or mRNAs.

PPM1A

[00314] In some embodiments of the disclosure, the PPM1A gene product is a PPM1A mRNA or PPM1A pre-mRNA comprising sequences from nucleotide 41,932 to nucleotide 42,787 and from nucleotide 44,874 to nucleotide 44,990 of a PPM1A gene sequence (for example the PPM1A gene sequence of NCBI Reference Sequence NG_029698.1 (SEQ ID NO: 1909) or a PPM1A coding sequence), or a portion thereof. In some embodiments of the disclosure, the PPM1A gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a PPM1A mRNA or PPM1A pre-mRNA comprising sequences from nucleotide 41,932 to nucleotide 42,787 and from nucleotide 44,874 to nucleotide 44,990 of a PPM1A gene sequence (for example the PPM1A gene sequence of NCBI Reference Sequence NG_029698.1 (SEQ ID NO: 1909) or a PPM1A coding sequence), or a portion thereof.

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[00315] In some embodiments of the disclosure, the PPM1A gene product is a PPM1A mRNA or PPM1A pre-mRNA comprising sequences from one or more of nucleotides 8470-8926, 41933-42787, 44874-45990, 49055-49164, 50647-50704, and 51703-58336 of a PPM1A gene sequence (for example the PPM1A gene sequence of NCBI Reference Sequence NG_029698.1 (SEQ ID NO: 1909). In some embodiments of the disclosure, the PPM1A gene product is a PPM1A mRNA or PPM1A pre-mRNA comprising sequences from the coding region of a PPM1A gene sequence, such as a coding region including nucleotides 8470-8926, 41933-42787, 44874-45990, 49055-49164, 50647-50704, and 51703-58336 of a PPM1A gene sequence (for example the PPM1A gene sequence of NCBI Reference Sequence NG_029698.1 (SEQ ID NO: 1909). In various embodiments, the PPM1A mRNA is PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (SEQ ID NO: 1910).

[00316] In some embodiments of the disclosure, the PPM1A gene product is a PPM1A mRNA or PPM1A pre-mRNA comprising sequences from one or more of nucleotides 8470-8926, 9629-9730, 41933-42787, and 44874-47804 of a PPM1A gene sequence (for example the PPM1A gene sequence of NCBI Reference Sequence NG_029698.1 (SEQ ID NO: 1909). In some embodiments of the disclosure, the PPM1A gene product is a PPM1A mRNA or PPM1A pre-mRNA comprising sequences from the coding region of a PPM1A gene sequence, such as a coding region including one or more of nucleotides 8470-8926, 9629-9730, 41933-42787, and 44874-47804 of a PPM1A gene sequence (for example the PPM1A gene sequence of NCBI Reference Sequence NG_029698.1 (SEQ ID NO: 1909). In various embodiments, the PPM1A mRNA is PPM1A mRNA transcript variant 2, corresponding to NCBI Reference Sequence NM_177951.3 (SEQ ID NO: 1911).

[00317] In some embodiments of the disclosure, the PPM1A gene product is a PPM1A mRNA or PPM1A pre-mRNA comprising sequences from one or more of nucleotides 4999-5295, 41933-42787, 44874-44990, 49055-49164, 50647-50704, 51703-58336 of a PPM1A gene sequence (for example the PPM1A gene sequence of NCBI Reference Sequence NG_029698.1 (SEQ ID NO: 1909). In some embodiments of the disclosure, the PPM1A gene product is a PPM1A mRNA or PPM1A pre-mRNA comprising sequences from one or more coding regions of a PPM1A gene sequence, such as a coding region including nucleotides 4999-5295, 41933-42787, 44874-44990, 49055-49164, 50647-50704, 51703-58336 of a PPM1A gene sequence (for example the PPM1A gene sequence of NCBI Reference Sequence NG_029698.1 (SEQ ID NO: 1909). In various embodiments, the PPM1A mRNA is PPM1A mRNA transcript variant 3, corresponding to NCBI Reference Sequence NM_177952.3 (SEQ ID NO: 1912).

[00318] In some embodiments of the disclosure, the PPM1A gene product comprises a sequence including nucleotides 457-1429 of PPM1A mRNA transcript variant 1 (*i.e.*, nucleotides 457-1429 of, for example, PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (SEQ ID NO: 1910)), or a portion thereof. In some embodiments of the disclosure, the PPM1A gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with nucleotides 457-1429 of PPM1A mRNA transcript variant 1 (*i.e.*, nucleotides 457-1429 of, for example, PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (SEQ ID NO: 1910)), or a portion thereof.

[00319] In some embodiments described herein, a PPM1A gene product is a PPM1A mRNA isoform transcript (for example, PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (SEQ ID NO: 1910)), or a portion thereof. In some embodiments described herein, a PPM1A gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a PPM1A mRNA isoform transcript (for example, PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (SEQ ID NO: 1910)), or a portion thereof.

PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (SEQ ID NO: 1910)

1 agaggcggcg gcggcggcgg tggcggcgct agggacggga gcgcgcgcgg gagctagaga
61 gcagtggtct cggcgctcgt ccggcccgca gcttcgggtc ctcaggcggc tgttgctccg
121 gaacgggtgg ttggggaggg gggggtgggg ggactctaga cagctgaggc gcgaaagcga
181 tgagtcctcg gctcttcctc ctccttctcc gggacccgct ctctgcctcc ctctccaacg
241 cccggatgat ctgagccgcg agggcgccga cagccggggg cccggacgca gcccggctcc
301 tcccctcctc cgccccttcc ccagcctgac ctggcccgcc gctgcagcgg tgacccctcc
361 cccggctgcc gccgtcgccg ccgcggtgac cccctccccg gctgccgccg ccgccgcctc
421 ggccgaccag ggacctgccc gcctgcggct gctccggacc tagaggatca agacataatg
481 ggagcatttt tagacaagcc aaagatggaa aagcataatg cccaggggca gggtaatggg
541 ttgcgatatg ggctaagcag catgcaaggc tggcgtgttg aaatggagga tgcacatacg
601 gctgtgatcg gtttgccaag tggacttgaa tcgtggtcat tctttgctgt gtatgatggg
661 catgctggtt ctcaggttgc caaatactgc tgtgagcatt tgttagatca catcaccaat
721 aaccaggatt ttaaagggtc tgcaggagca ccttctgtgg aaaatgtaaa gaatggaatc
781 agaacaggtt ttctggagat tgatgaacac atgagagtta tgtcagagaa gaaacatggt
841 gcagatagaa gtgggtcaac agctgtaggt gtcttaattt ctccccaaca tacttatttc
901 attaactgtg gagactcaag aggtttactt tgtaggaaca ggaaagttca tttcttcaca
961 caagatcaca aaccaagtaa tccgctggag aaagaacgaa ttcagaatgc aggtggctct
1021 gtaatgattc agcgtgtgaa tggctctctg gctgtatcga gggcccttgg ggattttgat
1081 tacaaatgtg tccatggaaa aggtcctact gagcagcttg tctcaccaga gcctgaagtc
1141 catgatattg aaagatctga agaagatgat cagttcatta tccttgcatg tgatggtatc
1201 tgggatgtta tgggaaatga agagctctgt gattttgtaa gatccagact tgaagtcact
1261 gatgaccttg agaaagtttg caatgaagta gtcgacacct gtttgtataa gggaagtcga
1321 gacaacatga gtgtgatttt gatctgtttt ccaaatgcac ccaaagtatc gccagaagca
1381 gtgaagaagg aggcagagtt ggacaagtac ctggaatgca gagtagaaga aatcataaag
1441 aagcaggggg aaggcgtccc cgacttagtc catgtgatgc gcacattagc gagtgagaac
1501 atccccagcc tcccaccagg gggtgaattg gcaagcaaga ggaatgttat tgaagccgtt
1561 tacaatagac tgaatcctta caaaaatgac gacactgact ctacatcaac agatgatatg
1621 tggtaaaact gctcatctag ccatggagtt taccttcacc tccaaaggag agtacagctc
1681 aactttgttg aaacttttaa catccatcct caactttaag gaaggggata tgacatgggt
1741 gagaatgatt acatcagaga acttcagcag tacaacagct agcccagaac tgatttttt
1801 ttttttttt gtaaatttga gacttatgta agcgtgattt caaaccataa ttcgtgttgt
1861 aaatcagact ccagcaattt ttgttgtatg attttgtttt tttgtaaagt gtaattgtcc
1921 ttgtacaaaa tgctcatatt taattatgaa ctgctttaaa tcactatcaa agttacaaga
1981 aatgtttggc ttattgtgtg atgcaacaga tatatagccc tttcaagtca tgttgtgttt

2041 ggacttgggg ttggaacagg gagagcagca gccatgtcag ctacacgctc aaatgtgcag
2101 atgattatgg aaaataacct caaaatctta caaagctgaa catccaagga gttattgaaa
2161 actatcttaa atgttcttgg taggggagtt ggcattgttg ataaagccag tcccttcatt
2221 taactgtctt tcaggatgtt ccttcgttgt ttccatgagt attgcaggta ataatacagt
2281 gtattcataa gaatctcaat cttggggcta aatgccttgt ttctttgcac ctcttttcaa
2341 gtccttacat ttaattacta attgataagc agcagcttcc tacatatagt aggaaactgc
2401 cacatttttg ctatcatgat tggctgggcc tgctgctgtt cctagtaaga tattctgaat
2461 tccattttat caataaagct tgatttaaca aacaagaaac ttaatcatgt atgtgtaatt
2521 cctcttttac cctggccttt taaaacactg tgccgttgta atgagacgtt tctcataggg
2581 aaagatgtta gtctctttta attggacaac actgtcactc aaggcataga tgaaactttc
2641 cttccattag aaagactaaa agatttaatt cttggttgta ccttaatcta ttttttaaat
2701 aggtttcttt caggctgctt atttttcatt aagatgtgta tcagcttgga tttgcctact
2761 gtttaattaa aatatttatt gtcaaagttt gacaatctaa cactctatgg taggggtgtg
2821 tgtgtgtgtg tttgtgagtg tgtgtttgcc tgtgattttt aattggccca tgtctttaga
2881 atccaagtgg ttaagatgta tttgtgattt gaaatatagc atgttgataa tatttagctg
2941 ttggccttta caaataactt tcaaagctta aggaattgta gatataaaaa taacctaatt
3001 taatttaggc ttaaattcct ctgattaagc atgtgaaagt aagttttaaa atctgtcgca
3061 ttgaaaagat tactgttccg tgcccttctg tatttttgtc tctttaggtt gaatattgta
3121 tttatcacca tgtaatcatt cagtaggcag attcccacta gaaaactgtt gaaatgtaag
3181 actaaaatac aacattgaat acaaaatcaa aattttgtgt ataaaaacca gtatagtcca
3241 ttttgttata tttgtttttt ccctaacttg gaaatataca tatttgtata tatagcctta
3301 aaattaatgt aaagttaggg gagtagtggg gaaagtaatg tgaaatgtct cagatttaag
3361 tagttaaata ccagcaaaat cttttcatta tccctcttat tttgtgaggt gattaaatgt
3421 aacttaattg tatttaattt atatcttatt ccagcatgaa tgaggaaaaa ctgaagtact
3481 atttatattt agaaattcat atcagttgaa attacagaac caattccata cttacaataa
3541 atacttaatg tctaaatctg tggtagagtg cgaagtatga taatgttcta agttatggct
3601 ttgcaagcat ctaaatgtgc atttaatgaa taccagtgct tctagtatag actaattacc
3661 agacatactg gtactgaaag ctaaatccct attataacaa accagttcct taatatttta
3721 agtagactga caactttagt tccagaaatt gcaaaacttt gaactggact gtgtaatctt
3781 ttgagatgca aaacttaagt cacaagtaga gtatgtgatg gaaagctgta tttcaaacca
3841 taacagcata tttagagcct tttttttttg agtctttaaa caagagaaaa ttaaaatatt
3901 cctgtcaaaa ttattagtat tgaaattagg cttggacacg agagagaacc gtatttgagt
3961 gatgtgagaa gactaaatct tttccacatg agtcagcact gccatactaa taatttttt
4021 actataaaaa tacaggaagg aagtatacat tataacagca gactgtgtgt gttcctgatt

4081 cctggaggta atagtggggg gaaaccaacc atacttttta aaggcacttt tgcacctcta
4141 ttgtgcactt cattcttgta ccacttaaat tcttcacccc catccccttt ttttgtgcta
4201 attagcatct cagggcaatg cctcaaaaat gtttgatgtg ttctgttctt tggagggaaa
4261 aagttcttat gtgatgataa tatagtactc aaaatatact tttatcattt aaatgtctta
4321 tttgctgcta tgaataggaa ataacatttt gtatagcagg ctctgtttta ccctaacatt
4381 aaaaaatttc actgatcttt ctttcattaa cagggtagaa tctcctaatt tccactttct
4441 tgggaatata cttttataga caatagaagc agttctcaat attagcatat actttaaaaa
4501 atcaaagtga taacttaatt cagctttgga agtatctcaa acatattttt actttatagt
4561 gcattaactt gcttctagag tacttaatgc aactgctcta gccacttaat tttttatact
4621 aatctcaaca ttaagaaatt tggattaagt aataaattag ttatgtaatt caagtaatct
4681 gaattacagc agtactttta gtgatcattc ataggactat atattaaccc agctaataac
4741 tcagtttttt tacaaaatgt ttcgagtatt attggtaaaa cactgttcta ggctaagcac
4801 attgggactg taaagaaatg agtagatcct tggcttcaag tttacatctg gacaatttat
4861 aatctagtgt atgttagtat tataactgga tcactcatca aaaaatatat atatatatct
4921 attgcccacc tgctatctac caggtactta gctgatcaag gcaggcccct gccctaaaga
4981 ccttgtttat acttccttta ctcacctgaa aactgttctc cagtttattt tcttctctct
5041 aaagttaaag agtaattcag aagaaaattt tgcttagcat aagaataaaa ttggactgaa
5101 gaggcttaag cccattcagt atccttgatt gcatttatcc aacggccttt attcttcctg
5161 ctgacagcag taactcagag gaataggtag tagatttctg aaaattatcc agccatggaa
5221 atgtaggtgg ggtttgagtt taaggcattt aaaaatgtaa atatctctag ctaaatttat
5281 cttaagtaga actctgtgtt tttgtaacac actgccagtg ttaatatcaa attttagcca
5341 aattattact atgtgtttta atattttaaa ataatttcac tgcccatctt tactggacaa
5401 actcatttgg agttcaactt gtgatttctg aaagaactga tgaaattggg tactgctttt
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5641 tacttttgct cacagaaact gctggtgaga ttaccatttt ttgagtatct agtcttctag
5701 tttttctttt aggcattagg aagccttctt tagagttcaa aattttagaa gcctaatttg
5761 ctcttacttc cttcaattat gtgccatgtg ttttggtttg tatatgtttt aaattgtata
5821 tttccttgga atatgcttga aatatttaag aatacatttt caaaatgtat aatactgtat
5881 tgttttgttg atcagaataa taagtctcag ttaaatgttt gttattactg atagtcaaaa
5941 tgctcaatag aaatgatgag aggcattggt tccaattcat tgtcaaatga acgttttcta
6001 attttgttca cagattcttt ccctttcgat tgttctgtat gttaagatag tggcttctgc
6061 tctcactgtt ttcctattta tattactagc aggtaggagt gctaattaga aaaacttaga

6121 tggtattgaa attacagttg acaacttata tttttatgag atggagaaaa aagattaagt
6181 tgatataaca acaaagtgga ctttttttct tccttatcct gcacgaaata ttgcccttgt
6241 ttcctctact ttcctcttgg tgttttctct ttttttcaaa cagaaacagg ccaattccat
6301 tttcttgagc aagaaagctt agtgtgttac ttcatcaagg ccagctaata ctgtgttaaa
6361 ccgggctgaa aatgagaaaa cttgggagat ggaggaatgg ggaaatggca gtgggatagg
6421 tagggaagga ttactcttaa ttgttttaaa agccatagga aagtcttcct tgtacgtggc
6481 tgtaaattta taagaactat tgtgtcacat aaaccaacaa gaatgaacct ttgctgcttc
6541 agataatttg atttttccag caaggaaatt aataagttac tgattcttca gcatagaaac
6601 aactgagaag aattaatgca atgtttcttc actagaaaac ccaacccttc atttcttttc
6661 attgctccaa aacccagttt tcaactaatg gttttctcat taaactaaat gtttagaaaa
6721 gttgtttaga gtttttcttt ttcttttaca tagtcctcct gatccagtat aagactattt
6781 agtaacgtgc atttgtatgg tactatctaa agtaagttag attgatgtaa gagatcgggt
6841 agctgcggaa caaaattagt tatatcctaa ttaggtacag tgaatgacac aaaatcattt
6901 tagcaatgct tcttaacctt ttggggtcac aggcgttttg agactgatga atcctaggga
6961 cttatttacc caggaaaatg cgtatataac atacatatct ccctaaagtt tacaatattg
7021 tagtggttca tgggcccccc ggttaagagc ccattctaaa gtacaatagg gcatcatccc
7081 ttttcctgca aagcccaaaa gtatatttct agggcatgaa aataacttga gtctatttta
7141 aggaattgtt tcactctaga ggtagatagg ggacctggct agaatctgac attaaaatat
7201 acttttaaa aaatattata tttggggtgg ggaaagtgat taaaaggtga aaaaaaaaca
7261 tagtattcag aagttttgga ggttaatgtc tttctctaag atttgccact ttagaaattc
7321 aacagaaaag aggtaaaaca gaaatggaat gtatctggaa catttttggc ctccatagtg
7381 cagatatact atattaacaa gtaatacatt tatttacctg tcagatctcc aggttttaag
7441 attttgagct ttctagtatt aggattcatt aaatgttcaa ttcatttcat attctaagga
7501 attaggttat ttacttacta attcaggatg ttaaaataac atccaagtcg gacaaccacc
7561 accaatgcac acagttaatg agatttctaa aatataataa gtacaatgta acaaacgtat
7621 agaattttgc atttgttgcc aaaattagat gtttaatgac agcttattta attcccattt
7681 gtgggacttc tggaacatag aaaccattat cttacctggt tatcccttga ctaaatagca
7741 tatctgcagg aaaatatctt gtttgtagtg atatgcccca atagtgattg atttcactct
7801 tgaaatgagt tatatcactt aatttgtata aatgttatga gtggagagac atgtacatgt
7861 taaaagcatg ttgcattata tattcatttt ttaaactcta taaatgttaa gaataatata
7921 attgcagaaa tatttttctt aaatacaatg tgtaacaaaa ttctccgtag caactcaccc
7981 actttgcagt ttatgtgatc cacactttta aagaaattcc ataaatgtat attttgtatt
8041 atgtattatt tcctggtcca aagaaaatat gtgaattcag ttctaacttt aagaatgtac
8101 tgtttgtttt caagttcatt gaaaaattgc attcagcctg cgaatggttg cagattgtat

8161 gttagatgaa aagtagaaat aatttctagt ttggaaaact ggtgccacta ataaaacagg

8221 caattacata a ((SEQ ID NO: 1910)

[00320] In some embodiments described herein, a PPM1A gene product is a PPM1A mRNA isoform transcript (for example, PPM1A mRNA transcript variant 2, corresponding to NCBI Reference Sequence NM_177951.3 (SEQ ID NO: 1911)), or a portion thereof. In some embodiments described herein, a PPM1A gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a PPM1A mRNA isoform transcript (for example, PPM1A mRNA transcript variant 2, corresponding to NCBI Reference Sequence NM_177951.3 (SEQ ID NO: 1911)), or a portion thereof.

[00321] In some embodiments described herein, a PPM1A gene product is a PPM1A mRNA isoform transcript (for example, PPM1A mRNA transcript variant 3, corresponding to NCBI Reference Sequence NM_177952.3 (SEQ ID NO: 1912)), or a portion thereof. In some embodiments described herein, a PPM1A gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a PPM1A mRNA isoform transcript (for example, PPM1A mRNA transcript variant 3, corresponding to NCBI Reference Sequence NM_177952.3 (SEQ ID NO: 1912)), or a portion thereof.

[00322] In some embodiments described herein, a PPM1A gene product is a *Mus musculus* PPM1A mRNA isoform transcript (for example, *Mus musculus* PPM1A mRNA alpha isoform transcript, corresponding to NCBI Reference Sequence NM_008910.3 (SEQ ID NO: 1913)), or a portion thereof. In some embodiments described herein, a PPM1A gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identity, or 100% identity with a PPM1A mRNA isoform transcript (for example, *Mus musculus* PPM1A mRNA alpha isoform transcript, corresponding to NCBI Reference Sequence NM_008910.3 (SEQ ID NO: 1913)), or a portion thereof.

[00323] In some embodiments of the disclosure, the PPM1A gene product is a PPM1A mRNA transcript variant other than the PPM1A transcripts described above (*e.g.*, PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (SEQ ID NO: 1910), PPM1A mRNA transcript variant 2, corresponding to NCBI Reference Sequence

NM_177951.3 (SEQ ID NO: 1911), PPM1A mRNA transcript variant 3, corresponding to NCBI Reference Sequence NM_177952.3 (SEQ ID NO: 1912), or *Mus musculus* PPM1A mRNA alpha isoform transcript, corresponding to NCBI Reference Sequence NM_008910.3 (SEQ ID NO: 1913)). In some embodiments, the PPM1A gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identity, or 100% identity with a sequence homologous to a sequence of PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (SEQ ID NO: 1910), PPM1A mRNA transcript variant 2, corresponding to NCBI Reference Sequence NM_177951.3 (SEQ ID NO: 1911), PPM1A mRNA transcript variant 3, corresponding to NCBI Reference Sequence NM_177952.3 (SEQ ID NO: 1912), or *Mus musculus* PPM1A mRNA alpha isoform transcript, corresponding to NCBI Reference Sequence NM_008910.3 (SEQ ID NO: 1913). In some embodiments, the PPM1A gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a sequence homologous to nucleotides 457-1429 of PPM1A mRNA transcript variant 1, corresponding to NCBI Reference Sequence NM_021003.5 (*i.e.*, nucleotides 457-1429 of SEQ ID NO: 1910), or a portion thereof.

ATXN2

[00324] In some embodiments of the disclosure, the ATXN2 gene product is an ATNX2 mRNA or ATNX2 pre-mRNA comprising sequences from an ATXN2 gene sequence (for example the ATXN2 gene sequence of NCBI Reference Sequence NG_011572.3 (SEQ ID NO: 149355), the ATXN2 gene sequence of NCBI Reference Sequence NC_000012.12 (Reference GRCh38.p13 Primary Assembly), or an ATXN2 coding sequence), or a portion thereof. In some embodiments of the disclosure, the ATXN2 gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with an ATXN2 mRNA or ATXN2 pre-mRNA sequence (for example the ATXN2 gene sequence of NCBI Reference Sequence NG_011572.3 (SEQ ID NO: 149355), the ATXN2 gene sequence of NCBI Reference Sequence NC_000012.12 (Reference GRCh38.p13 Primary Assembly), or an ATXN2 coding sequence), or a portion thereof.

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1 ccagcacttt gggaggccaa ggcaggcaga tcacttgagg tgaggagttc tggccaacac
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  61 gaaaaaatgt cgtctctact aaaaatacaa aaattagctg gacatggtgg tgagtgccta
 121 taatcccagc tacatggaag gctgagcggg gaggatcact tgaacccagg aggtggaggt
 181 tacagtgaac tgagattgtg ccactgcatt ccagcctggg caagacagca agactctgcc
 241 taaaaacaaa caaacaaatc ccccaaaact aacaaaaatt agctgggtgt ggtggtgcac
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NCBI Reference NG_011572.3 (SEQ ID NO: 149355)

[00325] In various embodiments, the ATXN2 gene product is an ATXN2 mRNA isoform, comprising NCBI Reference Sequence NM_001310121.1 (SEQ ID NO: 149357). In various embodiments, the ATXN2 gene product comprises a sequence that shares at least 80%, at least

81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with an ATXN2 mRNA isoform, comprising NCBI Reference Sequence NM_001310121.1 (SEQ ID NO: 149357).

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3901 aagggaaaaa cttttacttt gtagataata taaaataaaa acttaaaaaa aatttaaaaa
3961 ataaaaaaag ttttaaaaac tgaaaaaaaa aaa
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NCBI Reference NM_001310121.1 (SEQ ID NO: 149357)

[00326] In various embodiments, the ATXN2 gene product is an ATXN2 mRNA isoform comprising NCBI Reference Sequence NM_001310123.1 (SEQ ID NO: 149358). In various embodiments, the ATXN2 gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with an ATXN2 mRNA isoform, comprising NCBI Reference Sequence NM_001310123.1 (SEQ ID NO: 149358).

[00327] In various embodiments, the ATXN2 gene product is an ATXN2 mRNA isoform comprising NCBI Reference Sequence NM_001372574.1 (SEQ ID NO: 149359). In various embodiments, the ATXN2 gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with an ATXN2 mRNA isoform, comprising NCBI Reference Sequence NM_001372574.1 (SEQ ID NO: 149359).

[00328] In various embodiments, the ATXN2 gene product is an ATXN2 mRNA isoform comprising NCBI Reference Sequence NM_002973.4 (SEQ ID NO: 149360). In various embodiments, the ATXN2 gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with an ATXN2 mRNA isoform, comprising NCBI Reference Sequence NM_002973.4 (SEQ ID NO: 149360).

[00329] In various embodiments, the ATXN2 gene product is an ATXN2 mRNA transcript variant comprising NCBI Reference Sequence NR_132311.2 (SEQ ID NO: 149361). In various embodiments, the ATXN2 gene product comprises a sequence that shares at least 80%, at least

81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with an ATXN2 mRNA transcript variant, comprising NCBI Reference Sequence NR_132311.2 (SEQ ID NO: 149361).

SOD1

[00330] In some embodiments of the disclosure, the SOD1 gene product is a SOD1 mRNA or SOD1 pre-mRNA comprising sequences from a SOD1 gene sequence (for example the SOD1 gene sequence of NCBI Reference Sequence NG_008689.1 (SEQ ID NO: 167802), the SOD1 gene sequence of NCBI Reference Sequence NC_000021.9 (Reference GRCh38.p13 Primary Assembly) (SEQ ID NO: 167803), or a SOD1 coding sequence), or a portion thereof. In some embodiments of the disclosure, the SOD1 gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a SOD1 mRNA or SOD1 pre-mRNA sequence (for example the SOD1 gene sequence of NCBI Reference Sequence NG_008689.1 (SEQ ID NO: 167802), the SOD1 gene sequence of NCBI Reference Sequence NC_000021.9 (Reference GRCh38.p13 Primary Assembly) (SEQ ID NO: 167803), or a SOD1 coding sequence), or a portion thereof.

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16261 acatatgaaa gtgagaataa ctacataaaa tgtctatttt catcaaataa

NCBI Reference Sequence NG_008689.1 (SEQ ID NO: 167802)

[00331] In various embodiments, the SOD1 gene product is a SOD1 mRNA sequence comprising NCBI Reference Sequence NM_000454.5 (SEQ ID NO: 167804). In various embodiments, the SOD1 gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a SOD1 mRNA sequence comprising NCBI Reference Sequence NM_000454.5 (SEQ ID NO: 167804).

```
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NM_000454.5 (SEQ ID NO: 167804)

MAPT

[00332] In some embodiments of the disclosure, the MAPT gene product is a MAPT mRNA or MAPT pre-mRNA comprising sequences from a MAPT gene sequence (for example the MAPT gene sequence of NCBI Reference Sequence NG_007398.2 (SEQ ID NO: 301567), the MAPT gene sequence of NCBI Reference Sequence NC_000017.11 (Reference GRCh38.p13 Primary Assembly) (SEQ ID NO: 301568), or a MAPT coding sequence), or a portion thereof. In some embodiments of the disclosure, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA or MAPT pre-mRNA sequence (for example the MAPT gene sequence of NCBI Reference Sequence NG_007398.2 (SEQ ID NO: 301567), the MAPT gene sequence of NCBI Reference Sequence NC_000017.11 (Reference GRCh38.p13 Primary Assembly) (SEQ ID NO: 301568), or a MAPT coding sequence), or a portion thereof.

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1 gggattacag gcgtgagcca ccacacccag cccagaatgt ttattagaat gcacaattaa
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140701 ctaaaagggt tattcagaat tttcaacctt ataaatagaa gaagcacttt atgcataggg
140761 atatggtgca ttattgtatt tttttttaaa gaaacaatga caaaccctit aacttgcaaa
140821 cagaaaaaaa aatcactaat gttgaaaatt gtgaaaaaac cccaaccatt aa
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NG_007398.2 (SEQ ID NO: 301567)

[00333] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001123066.4 (SEQ ID NO: 301569). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least

81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001123066.4 (SEQ ID NO: 301569).

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NCBI Reference Sequence NM_001123066.4 (SEQ ID NO: 301569).

[00334] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001123067.4 (SEQ ID NO: 301570). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001123067.4 (SEQ ID NO: 301570).

[00335] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001203251.2 (SEQ ID NO: 301571). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001203251.2 (SEQ ID NO: 301571).

[00336] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001203252.2 (SEQ ID NO: 301572). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001203252.2 (SEQ ID NO: 301572).

[00337] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001377265.1 (SEQ ID NO: 301573). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001377265.1 (SEQ ID NO: 301573).

[00338] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001377266.1 (SEQ ID NO: 301574). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at

least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001377266.1 (SEQ ID NO: 301574).

[00339] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001377267.1 (SEQ ID NO: 301575). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001377267.1 (SEQ ID NO: 301575).

[00340] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001377268.1 (SEQ ID NO: 301576). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_001377268.1 (SEQ ID NO: 301576).

[00341] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_005910.6 (SEQ ID NO: 301577). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_005910.6 (SEQ ID NO: 301577).

[00342] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_016834.5 (SEQ ID NO: 301578). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_016834.5 (SEQ ID NO: 301578).

[00343] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_016835.5 (SEQ ID NO: 301579). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%,

at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_016835.5 (SEQ ID NO: 301579).

[00344] In various embodiments, the MAPT gene product is a MAPT mRNA sequence comprising NCBI Reference Sequence NM_016841.5 (SEQ ID NO: 301580). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA sequence comprising NCBI Reference Sequence NM_016841.5 (SEQ ID NO: 301580).

[00345] In various embodiments, the MAPT gene product is a MAPT RNA sequence comprising NCBI Reference Sequence NR_165166.1 (SEQ ID NO: 301581). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT RNA sequence comprising NCBI Reference Sequence NR_165166.1 (SEQ ID NO: 301581).

[00346] In various embodiments, the MAPT gene product is a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257370.4 (SEQ ID NO: 301582). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257370.4 (SEQ ID NO: 301582).

[00347] In various embodiments, the MAPT gene product is a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257366.3 (SEQ ID NO: 301583). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257366.3 (SEQ ID NO: 301583).

[00348] In various embodiments, the MAPT gene product is a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257362.4 (SEQ ID NO: 301584). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257362.4 (SEQ ID NO: 301584).

[00349] In various embodiments, the MAPT gene product is a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257365.4 (SEQ ID NO: 301585). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257365.4 (SEQ ID NO: 301585).

[00350] In various embodiments, the MAPT gene product is a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257367.4 (SEQ ID NO: 301586). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257367.4 (SEQ ID NO: 301586).

[00351] In various embodiments, the MAPT gene product is a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257368.4 (SEQ ID NO: 301587). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257368.4 (SEQ ID NO: 301587).

[00352] In various embodiments, the MAPT gene product is a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257369.4 (SEQ ID NO: 301588). In various

embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257369.4 (SEQ ID NO: 301588).

[00353] In various embodiments, the MAPT gene product is a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257371.4 (SEQ ID NO: 301589). In various embodiments, the MAPT gene product comprises a sequence that shares at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity with a MAPT mRNA transcript variant comprising NCBI Reference Sequence XM_005257371.4 (SEQ ID NO: 301589).

AONs Targeting Gene Product

PPM1A AONs

[00354] In various embodiments, a PPM1A AON disclosed herein, such as PPM1A AONs comprising a sequence of any one of SEQ ID NOs: 1-954, or a sequence of any one SEQ ID NOs: 1-954 in which one or more nucleosides are replaced with the one or more spacers, such as a sequence of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, target specific portions of a PPM1A gene product, such as a PPM1A mRNA or pre-mRNA transcript (*e.g.*, any one of SEQ ID NO: 1909-1913). In some embodiments, a PPM1A AON may be an oligonucleotide sequence at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% complementary to a portion of a PPM1A gene product or to PPM1A gene sequence (*e.g.*, any one of SEQ ID NOs: 1909-1913). In particular embodiments, a PPM1A AON may be an oligonucleotide sequence at least 85% complementary to a portion of a PPM1A gene product or to PPM1A gene sequence (*e.g.*, any one of SEQ ID NOs: 1909-1913). In particular embodiments, a PPM1A AON may be an oligonucleotide sequence at least 90% complementary to a portion of a PPM1A gene product or to PPM1A gene sequence (*e.g.*, any one of SEQ ID NOs: 1909-1913). In particular embodiments, a PPM1A AON may be an oligonucleotide sequence at least 95% complementary to a portion of a PPM1A gene product or to PPM1A gene sequence (*e.g.*, any one of SEQ ID NOs: 1909-1913). In particular

embodiments, a PPM1A AON may be an oligonucleotide sequence at least 98% complementary to a portion of a PPM1A gene product or to PPM1A gene sequence (*e.g.*, any one of SEQ ID NOs: 1909-1913). In particular embodiments, a PPM1A AON may be an oligonucleotide sequence at least 99% complementary to a portion of a PPM1A gene product or to PPM1A gene sequence (*e.g.*, any one of SEQ ID NOs: 1909-1913). In particular embodiments, a PPM1A AON may be an oligonucleotide sequence that is 100% complementary to a portion of a PPM1A gene product or to PPM1A gene sequence (*e.g.*, any one of SEQ ID NOs: 1909-1913).

[00355] In some embodiments described herein, a PPM1A AON targets a specific portion of a PPM1A gene product, such as a PPM1A mRNA transcript or a PPM1A pre-mRNA transcript. For example, as described herein, a PPM1A AON comprises a sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% complementary to a specific portion of a PPM1A gene product, for example, a PPM1A mRNA transcript or a PPM1A pre-mRNA transcript (*e.g.*, any one of SEQ ID NOs: 1909-1913).

[00356] In some embodiments, a PPM1A AON comprises a sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% complementary to a sequence of an untranslated region (UTR) of a PPM1A mRNA sequence, for example a 5' UTR or a 3' UTR of a PPM1A mRNA sequence. In some embodiments, a PPM1A AON comprises a sequence that is 100% complementary to a nucleotide sequence of an untranslated region (UTR) of a PPM1A mRNA sequence, for example a 5' UTR or a 3' UTR of a PPM1A mRNA sequence.

ATXN2 AONs

[00357] In various embodiments, a ATXN2 AON disclosed herein, such as ATXN2 AONs with a sequence of any one of SEQ ID NOs: 1914-149354 or a sequence of any one SEQ ID NOs: 1914-149354 in which one or more nucleosides are replaced with the one or more spacers, such as a sequence of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C), target specific portions of a ATXN2 gene product, such as a ATXN2 mRNA transcript (*e.g.*, any one of SEQ ID NOs: 149355-149361). In some embodiments, a ATXN2 AON may be an oligonucleotide sequence at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% complementary to a portion of an ATXN2 gene

product or to ATXN2 gene sequence (*e.g.*, any one of SEQ ID NOs: 149355-149361). In particular embodiments, an ATXN2 AON may be an oligonucleotide sequence at least 85% complementary to a portion of an ATXN2 gene product or to ATXN2 gene sequence (*e.g.*, any one of SEQ ID NOs: 149355-149361). In particular embodiments, an ATXN2 AON may be an oligonucleotide sequence at least 90% complementary to a portion of an ATXN2 gene product or to ATXN2 gene sequence (*e.g.*, any one of SEQ ID NOs: 149355-149361). In particular embodiments, an ATXN2 AON may be an oligonucleotide sequence at least 95% complementary to a portion of an ATXN2 gene product or to ATXN2 gene sequence (*e.g.*, any one of SEQ ID NOs: 149355-149361). In particular embodiments, an ATXN2 AON may be an oligonucleotide sequence at least 98% complementary to a portion of an ATXN2 gene product or to ATXN2 gene sequence (*e.g.*, any one of SEQ ID NOs: 149355-149361). In particular embodiments, an ATXN2 AON may be an oligonucleotide sequence at least 99% complementary to a portion of an ATXN2 gene product or to ATXN2 gene sequence (*e.g.*, any one of SEQ ID NOs: 149355-149361). In particular embodiments, an ATXN2 AON may be an oligonucleotide sequence that is 100% complementary to a portion of an ATXN2 gene product or to ATXN2 gene sequence (*e.g.*, any one of SEQ ID NOs: 149355-149361).

[00358] In some embodiments described herein, an ATXN2 AON targets a specific portion of an ATXN2 gene product, such as an ATXN2 mRNA transcript or an ATXN2 pre-mRNA transcript. For example, as described herein, an ATXN2 AON comprises a sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% complementary to a specific portion of an ATXN2 gene product, for example, an ATXN2 mRNA transcript or an ATXN2 pre-mRNA transcript (*e.g.*, any one of SEQ ID NOs: 149355-149361).

SOD1 AONs

[00359] In various embodiments, a SOD1 AON disclosed herein, such as SOD1 AONs with a sequence of any one of 149362-158581, or SOD1 AONs with one or more spacers (e.g., a SOD1 AON with a sequence of any one SEQ ID NOs: 149362-158581 in which one or more nucleosides are replaced with the one or more spacers), such as a sequence of any one of SEQ ID NOs: 301610-301741), target specific portions of a SOD1 gene product, such as a SOD1 mRNA transcript (*e.g.*, any one of SEQ ID NOs: 167802-167804). In some embodiments, a SOD1 AON may be an oligonucleotide sequence at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least

96%, at least 97%, at least 98%, at least 99%, or 100% complementary to a portion of a SOD1 gene product or to SOD1 gene sequence (*e.g.*, any one of SEQ ID NOs: 167802-167804). In particular embodiments, a SOD1 AON may be an oligonucleotide sequence at least 85% complementary to a portion of a SOD1 gene product or to SOD1 gene sequence (*e.g.*, any one of SEQ ID NOs: 167802-167804). In particular embodiments, a SOD1 AON may be an oligonucleotide sequence at least 90% complementary to a portion of a SOD1 gene product or to SOD1 gene sequence (*e.g.*, any one of SEQ ID NOs: 167802-167804). In particular embodiments, a SOD1 AON may be an oligonucleotide sequence at least 95% complementary to a portion of a SOD1 gene product or to SOD1 gene sequence (*e.g.*, any one of SEQ ID NOs: 167802-167804). In particular embodiments, a SOD1 AON may be an oligonucleotide sequence at least 98% complementary to a portion of a SOD1 gene product or to SOD1 gene sequence (*e.g.*, any one of SEQ ID NOs: 167802-167804). In particular embodiments, a SOD1 AON may be an oligonucleotide sequence at least 99% complementary to a portion of a SOD1 gene product or to SOD1 gene sequence (*e.g.*, any one of SEQ ID NOs: 167802-167804). In particular embodiments, a SOD1 AON may be an oligonucleotide sequence that is 100% complementary to a portion of a SOD1 gene product or to SOD1 gene sequence (*e.g.*, any one of SEQ ID NOs: 167802-167804).

[00360] In some embodiments described herein, a SOD1 AON targets a specific portion of a SOD1 gene product, such as a SOD1 mRNA transcript or a SOD1 pre-mRNA transcript. For example, as described herein, a SOD1 AON comprises a sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% complementary to a specific portion of a SOD1 gene product, for example, a SOD1 mRNA transcript or a SOD1 pre-mRNA transcript (*e.g.*, any one of SEQ ID NOs: 167802-167804).

MAPT AONs

[00361] In various embodiments, a MAPT AON disclosed herein, such as MAPT AONs with a sequence of any one of SEQ ID NOs: 167805-301566, or MAPT AONs with one or more spacers (e.g., a MAPT AON with a sequence of any one SEQ ID NOs: 167805-301566 in which one or more nucleosides are replaced with the one or more spacers), such as a sequence of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C), target specific portions of a MAPT gene product, such as a MAPT mRNA or pre-mRNA transcript (*e.g.*, any one of SEQ ID NOs: 301567-301589). In some embodiments, a MAPT AON may be an oligonucleotide sequence at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least

91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% complementary to a portion of a MAPT gene product or to MAPT gene sequence (*e.g.*, any one of SEQ ID NOs: 301567-301589). In particular embodiments, a MAPT AON may be an oligonucleotide sequence at least 85% complementary to a portion of a MAPT gene product or to MAPT gene sequence (*e.g.*, any one of SEQ ID NOs: 301567-301589). In particular embodiments, a MAPT AON may be an oligonucleotide sequence at least 90% complementary to a portion of a MAPT gene product or to MAPT gene sequence (*e.g.*, any one of SEQ ID NOs: 301567-301589). In particular embodiments, a MAPT AON may be an oligonucleotide sequence at least 95% complementary to a portion of a MAPT gene product or to MAPT gene sequence (*e.g.*, any one of SEQ ID NOs: 301567-301589). In particular embodiments, a MAPT AON may be an oligonucleotide sequence at least 98% complementary to a portion of a MAPT gene product or to MAPT gene sequence (*e.g.*, any one of SEQ ID NOs: 301567-301589). In particular embodiments, a MAPT AON may be an oligonucleotide sequence at least 99% complementary to a portion of a MAPT gene product or to MAPT gene sequence (*e.g.*, any one of S SEQ ID NOs: 301567-301589). In particular embodiments, a MAPT AON may be an oligonucleotide sequence that is 100% complementary to a portion of a MAPT gene product or to MAPT gene sequence (*e.g.*, any one of SEQ ID NOs: 301567-301589).

[00362] In some embodiments described herein, a MAPT AON targets a specific portion of a MAPT gene product, such as a MAPT mRNA transcript or a MAPT pre-mRNA transcript. For example, as described herein, a MAPT AON comprises a sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% complementary to a specific portion of a MAPT gene product, for example, a MAPT mRNA transcript or a MAPT pre-mRNA transcript (*e.g.*, any one of SEQ ID NOs: 301567-301589).

Nuclease-Mediated Inhibition

[00363] In one aspect, the present disclosure provides a nuclease to reduce expression of target gene products (e.g., gene products of any one of PPM1A, ATXN2, SOD1, or MAPT). In some embodiments, the nuclease can be a RNAse (e.g., RNAseH), Zinc Finger nuclease (ZFN), a meganuclease, a transcription activator-like effector nuclease (TALEN), or a clustered regularly interspaced short palindromic repeats (CRISPR) associated protein.

[00364] In certain embodiments, target gene products are inhibited, eliminated, or reduced in quantity using zinc finger nucleases (ZFNs). Synthetic ZFNs are composed of a zinc finger binding domain fused with, *e.g.*, a FokI DNA cleavage domain. ZFNs can be

designed/engineered for editing the genome of a cell, including, but not limited to, knock-out or knock-in gene expression, in a wide range of organisms. A meganuclease, a TALEN, or a CRISPR associated protein can be used for genome engineering in cells of a patient suffering from or at risk of a neurological disease, including neurons, for example, motor neurons, and other cells of the nervous system. The described reagents can be used to target promoters, protein-encoding regions (exons), introns, 5′ and 3′ UTRs, and more.

[00365] CRISPR genome editing typically comprises two distinct components: (1) a guide RNA and (2) an endonuclease, specifically a CRISPR associated (Cas) nuclease (*e.g.*, Cas9). The guide RNA is a combination of the endogenous bacterial crRNA and tracrRNA into a single chimeric guide RNA (gRNA) transcript. Without being bound by theory, it is believed that when gRNA and the Cas are expressed in the cell, the genomic target sequence can be modified or permanently disrupted.

[00366] A gRNA/Cas complex can be recruited to a target sequence, for example, the target gene (e.g., any one of PPM1A, ATXN2, SOD1, or MAPT) by base-pairing between the gRNA sequence and the complement to the target DNA sequence in the target gene. An appropriate genomic target sequence contains a Protospacer Adjacent Motif (PAM) sequence immediately following the target sequence. The binding of the gRNA/Cas complex localizes the Cas to the target sequence, allowing wild-type Cas to cut both strands of DNA, causing a double strand break. The double strand break is repaired through one of two general repair pathways: (1) the non-homologous end joining DNA repair pathway or (2) the homology directed repair pathway. The non-homologous repair pathway can result in insertions/deletions at the double strand break that can lead to frameshifts and/or premature stop codons, effectively disrupting the open reading frame of the target gene. The homology directed repair pathway requires the presence of a repair template, which is used to fix the double strand break.

[00367] In certain embodiments, target gene expression is reduced using CRISPR genome editing. In some embodiments, a gRNA pair is used to target a target gene to reduce and/or eliminate expression of the target gene. In certain embodiments, one gRNA pair is used to reduce expression of the target gene. In certain other embodiments, multiple gRNA pairs are used to reduce expression of the target gene. gRNA pairs can be designed using known techniques and based on the gene sequence. In certain embodiments, gRNA sequences may include modifications such as 2' O-methyl analogs and 3' phosphorothioate internucleotide linkages in the terminal three nucleotides on both 5' and 3' ends of the gRNA.

Neurological Diseases

[00368] Methods described herein may be used to treat neurological diseases including, but not limited to, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism.

[00369] Motor neuron diseases are a group of diseases characterized by loss of function of motor neurons that coordinate voluntary movement of muscles by the brain. Motor neuron diseases may affect upper and/or lower motor neurons, and may have sporadic or familial origins. Motor neuron diseases include amyotrophic lateral sclerosis (ALS or Lou Gehrig's disease), progressive bulbar palsy, pseudobulbar palsy, progressive muscular atrophy, primary lateral sclerosis, spinal muscular atrophy, post-polio syndrome, and ALS with frontotemporal dementia.

[00370] Symptoms of motor neuron diseases include muscle decay or weakening, muscle pain, spasms, slurred speech, difficulty swallowing, loss of muscle control, joint pain, stiff limbs, difficulty breathing, drooling, and complete loss of muscle control, including over basic functions such as breathing, swallowing, eating, speaking, and limb movement. These symptoms are also sometimes accompanied by depression, loss of memory, difficulty with planning, language deficits, altered behavior, and difficulty assessing spatial relationships and/or changes in personality.

[00371] Motor neuron diseases can be assessed and diagnosed by a clinician of skill, for example, a neurologist, using various tools and tests. For example, the presence or risk of developing a motor neuron disease can be assessed or diagnosed using blood and urine tests (for example, tests that assay for the presence of creatinine kinase), magnetic resonance imaging (MRI), electromyography (EMG), nerve conduction study (NCS), spinal tap, lumbar puncture, and/or muscle biopsy. Motor neuron diseases can be diagnosed with the aid of a physical exam

and/or a neurological exam to assess motor and sensory skills, nerve function, hearing and speech, vision, coordination and balance, mental status, and changes in mood or behavior.

[00372] A patient suffering from ALS, FTD, ALS with FTD, or another neurological or motor neuron disease can be a patient that is diagnosed with the disease or that displays symptoms of the disease. A patient suffering from ALS, FTD, ALS with FTD, or another neurological or motor neuron disease can be a patient that previously suffered from the disease and, after recovering or experiencing complete or partial amelioration of the disease and/or disease symptoms, experiences a complete or partial relapse of the disease or disease symptoms. A patient suffering from ALS, FTD, ALS with FTD, or another neurological or motor neuron disease or condition can be a patient that harbors a genetic mutation associated with manifestation of the disease or condition. For example, a patient suffering from ALS can be a patient that harbors a genetic mutation in any of SOD1, C9orf72, Ataxin 2 (ATXN2), Charged Multivesicular Body Protein 2B (CHMP2B), Dynactin 1 (DCTN1), Human Epidermal Growth Factor Receptor 4 (ERBB4), FIG4 phosphoinositide 5-phosphatase (FIG4), NIMA related kinase 1 (NEK1), Heterogeneous nuclear ribonucleoprotein A1 (HNRNPA1), Neurofilament Heavy (NEFH), Peripherin (PRPH), TAR DNA binding protein 43 (TDP43 or TARDP), Fused in Sarcoma (FUS), Ubiquilin-2 (UBQLN2), Kinesin Family Member 5A (KIF5A), Valosin-Containing Protein (VCP), Alsin (ALS2), Senataxin (SETX), Sigma Non-Opioid Intracellular Receptor 1 (SIGMAR1), Survival of Motor Neuron 1 (SMN1), Spastic Paraplegia 11 (SPG11), Autosomal Recessive, Transient Receptor Potential Cation Channel Subfamily M Member 7 (TRPM7), Vesicle-Associated Membrane Protein-Associated Protein B/C (VAPB), Angiogenin (ANG), Profilin-1 (PFN1), Matrin-3 (MATR3), Coiled-coil-helix-coiled-coil-helix domain Containing 10 (CHCHD10), Tubulin, Alpha 4A (TUBA4A), TBK1, C21orf2, Sequestosome-1 (SQSTM1, also known as Ubiquitin-binding protein p62), and/or optineurin (OPTN), in particular, where the mutation is associated with ALS or a high risk of developing ALS.

[00373] A patient at risk of ALS, FTD, ALS with FTD, or another neurological or motor neuron disease can include those patients with a familial history of the disease or a genetic predisposition to the disease (*e.g.*, a patient that harbors a genetic mutation associated with high disease risk, for example), or patients exposed to environmental factors that increase disease risk. For example, a patient may be at risk of ALS if the patient harbors a mutation in any of SOD1, C9orf72, ATXN2, CHMP2B, DCTN1, ERBB4, FIG4, HNRNPA1, NEFH, PRPH, NEK1, TDP43, FUS, UBQLN2, KIF5A, VCP, ALS2, SETX, SIGMAR1, SMN1, SPG11, TRPM7, VAPB, ANG, PFN1, MATR3, CHCHD10, TUBA4A, TBK1, SQSTM1, C21orf2, and/or OPTN, in particular, where the mutation is associated with ALS or high risk of developing ALS. A patient at risk may also

include those patients diagnosed with a disease or condition that has a high comorbidity with ALS, FTD, ALS with FTD, or another neurological or motor neuron disease (for example, a patient suffering from dementia, which is significantly associated with higher odds of a family history of ALS, FTD, and of bulbar onset ALS (*see* Trojsi, F., *et al.* (2017) "Comorbidity of dementia with amyotrophic lateral sclerosis (ALS): insights from a large multicenter Italian cohort" *J Neurol* 264: 2224-31)).

Amyotrophic Lateral Sclerosis

[00374] ALS is a progressive motor neuron disease that disrupts signals to all voluntary muscles. ALS results in atrophy of both upper and lower motor neurons. Symptoms of ALS include weakening and wasting of the bulbar muscles, general and bilateral loss of strength, spasticity, muscle spasms, muscle cramps, fasciculations, slurred speech, and difficulty breathing or loss of ability to breathe. Some individuals with ALS also suffer from cognitive decline. At the molecular level, ALS is characterized by protein and RNA aggregates in the cytoplasm of motor neurons, including aggregates of the RNA-binding protein TDP43.

[00375] ALS is most common in males above 40 years of age, although it can also occur in women and children. Risk of ALS is also heightened in individuals who smoke, are exposed to chemicals such as lead, or who have served in the military. Most instances of ALS are sporadic, while only about 10% of cases are familial. Causes of ALS include sporadic or inherited genetic mutations, high levels of glutamate, protein mishandling. Genetic mutations associated with ALS include mutations in the genes SOD1, C9orf72, TARDP, FUS, ANG, ATXN2, CHCHD10, CHMP2B, DCTN1, ERBB4, FIG4, HNRPA1, MATR3, NEFH, OPTN, PFN1, PRPH, SETX, SIGMAR1, SMN1, SPG11, SQSTM1, TBK1, TRPM7, TUBA4A, UBQLN2, VAPB, and VCP.

Frontotemporal Dementia

[00376] Frontotemporal dementia (FTD) is a form of dementia that affects the frontal and temporal lobes of the brain. It has an earlier average age of onset than Alzheimer's disease – 40 years of age. Symptoms of FTD include extreme changes in behavior and personality, speech and language problems, and movement-related symptoms such as tremor, rigidity, muscle spasm, weakness, and difficulty swallowing. Subtypes of FTD include behavior variant frontotemporal dementia (bvFTD), characterized by changes in personality and behavior and primary progressive aphasia (PPA), which affects language skills, speaking, writing and comprehension. FTD is associated with tau protein accumulation (Pick bodies) and function of altered TDP43 function. About 30% of cases of FTD are familial, and no other risk factors other than family history of the

disease are known. Genetic mutations associated with FTD include mutations in the genes C9orf72, Progranulin (GRN), microtubule-associated protein tau (MAPT), UBQLN2, VPC, CHMP2B, TARDP, FUS, ITM2B, CHCHD10, SQSTM1, PSEN1, PSEN2, CTSF, CYP27A1, TBK1 and TBP.

[00377] Amyotrophic lateral sclerosis with frontotemporal dementia (ALS with FTD) is a clinical syndrome in which FTD and ALS occur in the same individual. Interestingly, mutations in C9orf72 are the most common cause of familial forms of ALS and FTD. Additionally, mutations in TBK1, VCP, SQSTMI, UBQLN2 and CHMP2B are also associated with ALS with FTD. Symptoms of ALS with FTD include dramatic changes in personality, as well as muscle weakness, muscle atrophy, fasciculations, spasticity, dysarthria, dysphagia, and degeneration of the spinal cord, motor neurons, and frontal and temporal lobes of the brain. At the molecular level, ALS with FTD is characterized by the accumulation of TDP-43 and/or FUS proteins. TBK1 mutations are associated with ALS, FTD, and ALS with FTD.

TBK1 and RIPK1 Function

[00378] In one aspect, methods described herein include exposing a cell to a PPM1A AON to modify the activity, function, or other characteristics of a gene or a gene product, for example, an mRNA or protein. For example, methods described herein include a method of increasing or decreasing or inhibiting the activity, function, or other characteristics of a gene or a gene product. For example, described herein is a method of increasing phosphorylation of a residue of TANK-binding kinase 1 (also known as Serine/threonine-protein kinase TBK1; "TBK1"). For example, described herein is a method of increasing TBK1 serine residue 172 (ser172) phosphorylation in a cell, where the method includes exposing the cell to a PPM1A AON. In some embodiments, TBK1 ser172 phosphorylation is increased in a cell of a patient suffering from ALS, FTD, or ALS with FTD. In some embodiments, the method of increasing TBK1 ser172 phosphorylation includes exposing a cell to a PPM1A antisense oligonucleotide of any one of SEQ ID NOs: 1-954, or a sequence of any one SEQ ID NOs: 1-954 in which one or more nucleosides are replaced with the one or more spacers, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[00379] Also described herein is a method of increasing TBK1 function in a cell, where the method includes exposing the cell to a PPM1A AON. For example, described herein is a method of increasing TBK1 function in a cell, where the method includes exposing the cell to a PPM1A AON. In some embodiments, TBK1 function is increased in a cell of a patient suffering from ALS, FTD, or ALS with FTD. In some embodiments, the method of increasing TBK1 function includes exposing a cell to a PPM1A antisense oligonucleotide of any one of SEQ ID NOs: 1-954,

or a sequence of any one SEQ ID NOs: 1-954 in which one or more nucleosides are replaced with the one or more spacers, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[00380] Tank-binding kinase 1 (TBK1) is an IKK family of kinases that induces type-1 interferon activity and plays a major role in the phosphorylation of autophagy adaptors. Mutations in TBK1 are thought to result in impaired autophagy and contribute to the accumulation of protein aggregates and ALS pathology. At least 92 mutations in TBK1 have been identified in patients with ALS, FTD, or ALS with FTD (*see* Oakes *et al.*, (2017) "TBK1: a new player in ALS linking autophagy and neuroinflammation" *Molecular Brain* 10:5, pg. 1-10). Furthermore, along with mutations in C9orf72, OPTN, SQSTM1/p62, UBQLN2, and TDP43, mutations in TBK1 account for approximately 15% of ALS and FTD patients. Furthermore, TBK1 haploinsufficiency associated with loss of function mutations has been identified as a major driver of familial ALS (*see* Freischmidt *et al.*, (2015) "Haploinsufficiency of TBK1 causes familial ALS and fronto-temporal dementia" *Nature Neuroscience*, 18(5):631-6).

[00381] Autophagy is a process by which proteins and damaged organelles are degraded and recycled. Abnormal protein aggregates are a hallmark of ALS pathology, and mutations in several genes involved in regulating autophagy are associated with ALS (for example, SQSTM1, SOD1, OPTN, VCP, UBQLN2, and TBK1). Thus, disruption of autophagy appears to contribute to ALS pathology.

[00382] Phosphorylation of residue Ser172 of TBK1 results in conformational changes in TBK1, that allow substrate binding by the protein's kinase domain. TBK1 phosphorylates a number of autophagy adaptors, and several TBK1 mutations identified in ALS patients inhibit the ability of TBK1 to phosphorylate these adaptors. Other TBK1 mutations result in decreased mRNA and protein levels. Additionally, individuals carrying mutations in TBK1 also display TDP43-positive aggregates in various brain regions. Thus, TBK1 mutations may result in decreased autophagy and accumulation of protein aggregates in motor neurons.

[00383] PPM1A is a member of the PP2C family of Ser/Thr protein phosphatases. PP2C family members are negative regulators of cellular stress-response pathways and are involved in regulating the cell-cycle and NF-κB pathways. PPM1A also dephosphorylates and inactivates TBK1. In particular, PPM1A dephosphorylates Ser172 of TBK1. Activated TBK1 can phosphorylate RIPK1 in such a manner that RIPK1 is deactivated. Thus PPM1A activity indirectly activates RIPK1, and therefore, reducing PPM1A expression indirectly inactivates RIPK1.

[00384] The present disclosure is based in part on the finding that increasing TBK1 activity, for example, increasing TBK1 activity in an individual or the cell of an individual who is suffering from TBK1 haploinsufficiency, can be used as a mechanism to treat neurological diseases, for example, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism.

[00385] The disclosure is also based in part on the finding that increasing TBK1 activity, for example, increasing residual TBK1 activity in an individual and/or a cell of an individual suffering from TBK1 haploinsufficiency, can be achieved by increasing the amount of phosphorylated TBK1, for example, by increasing the amount of phosphorylated Ser172 TBK1, for example, an individual and/or a cell of an individual suffering from TBK1 haploinsufficiency. The disclosure is also based in part on the finding that increasing TBK1 activity, for example, increasing residual TBK1 activity in an individual and/or a cell of an individual suffering from TBK1 haploinsufficiency, can be achieved by increasing the ratio of phosphorylated TBK1 to total TBK1, for example, increasing the ratio of phosphorylated Ser172 TBK1 to unphosphorylated Ser172 TBK1, for example, in an individual and/or a cell of an individual suffering from TBK1 haploinsufficiency.

[00386] The disclosure is further based in part on the finding that increasing TBK1 activity (for example, increasing residual TBK1 activity in an individual and/or a cell of an individual suffering from TBK1 haploinsufficiency), increasing the amount of phosphorylated TBK1 (for example, increasing the amount of phosphorylated Ser172 TBK1, for example, in an individual and/or a cell of an individual suffering from TBK1 haploinsufficiency), and/or increasing the ratio of phosphorylated TBK1 to unphosphorylated TBK1 (for example, increasing the ratio of

phosphorylated Ser172 TBK1 to unphosphorylated Ser172 TBK1, for example, in an individual and/or a cell of an individual suffering from TBK1 haploinsufficiency) can be achieved by inhibiting PPM1A activity and/or decreasing PPM1A protein levels, for example, in an individual and/or a cell of an individual suffering from a TBK1 haploinsufficiency. Without being bound by theory, it is believed that inhibiting PPM1A activity and/or decreasing PPM1A protein levels can be achieved by administering to a patient or a cell of a patient, a PPM1A AON, for example, a PPM1A AON described herein. In particular embodiments, the disclosure provides methods of inhibiting PPM1A activity and/or decreasing PPM1A protein amounts by administering to a patient or a cell of a patient (for example, a patient suffering from a neurological disease or a cell of a patient suffering from a neurological disease, for example, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism) a PPM1A AON, for example, a PPM1A AON comprising the nucleotide sequence of any one of SEQ ID NOs: 1-954, or a sequence of any one SEQ ID NOs: 1-954 in which one or more nucleosides are replaced with the one or more spacers, such as a sequence of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[00387] Additionally disclosed herein is a method of modulating activity of Receptor Interacting Serine/Threonine Kinase 1 (also known as "RIPK1"). For example, described herein is a method of modulating RIPK1 activity in a cell, where the method includes exposing the cell to a PPM1A AON. In various embodiments, modulating activity of RIPK1 can be useful for treating various diseases, including acute neuronal injury, multiple sclerosis, ALS, Alzheimer's Disease, Lysosomal Storage Diseases, Parkinson's Disease, and other human central nervous system

diseases. In some embodiments, RIPK1 activity is modulated in a cell of a patient suffering from ALS, FTD, or ALS with FTD. In some embodiments, the method of modulating RIPK1 activity includes exposing a cell to a PPM1A antisense oligonucleotide of any one of SEQ ID NOs: 1-954, or a sequence of any one SEQ ID NOs: 1-954 in which one or more nucleosides are replaced with the one or more spacers, such as a sequence of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[00388] TBK1 regulates RIPK1 through direct phosphorylation on multiple sites including Thr189 to suppress RIPK1 kinase activity by blocking the interaction with its substrates. Degterev, A. et al. Targeting RIPK1 for the Treatment of Human Diseases, PNAS (2019), 116(20) 9714-9722. Therefore, increasing TBK1 function by increasing phosphorylation of a residue of TANK-binding kinase 1 can result in suppression of RIPK1 activity.

Methods of Treatment

[00389] The disclosure contemplates, in part, treating neurological diseases (for example, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism) in a patient in need thereof comprising administering a disclosed AON. In some embodiments, provided herein are methods for treatment of a neurological disease in a patient in need thereof, comprising administering a disclosed AON. In some embodiments of the disclosure, an effective amount of a disclosed AON may be administered to a patient in need thereof to treat a neurological disease, for example, to restore autophagy in cells of a patient suffering from a neurological disease, and/or to reduce or inhibit a target gene product. In some embodiments of the disclosure, an effective amount of a disclosed AON may be administered to a patient in need thereof to increase TBK1

phosphorylation (for example TBK1 ser172 phosphorylation) in a cell and/or to increase TBK1 function (for example, TBK1 kinase function) in a cell.

[00390] In some embodiments, methods of treating a neurological disease associated with impaired autophagy and/or protein aggregation (for example, TDP-43 protein aggregation, for example, in motor neurons) in a patient in need thereof are provided comprising administering a disclosed compound. In some embodiments, treating a neurological disease comprises at least ameliorating or reducing one symptom associated with the neurological disease (for example, reducing muscle weakness in a patient with ALS). Methods of treating a neurological disease (for example, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism) in a patient suffering therefrom are provided, that include administering a disclosed AON. In some embodiments, methods of slowing the progression of a neurological disease, for example, a motor neuron disease, are provided.

[00391] Provided herein are methods of treating, reducing the risk of developing, or delaying the onset of a neurological disease in a subject in need thereof comprising administering a disclosed AON. The methods include for example, treating a subject at risk of developing a neurological disease; *e.g.*, administering to the subject an effective amount of a disclosed AON. Neurological diseases that can be treated in this manner include amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease,

tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism.

[00392] Methods of preventing or treating neurological diseases (for example, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism) form part of this disclosure. Such methods may comprise administering to a patient in need thereof or a patient at risk, a pharmaceutical preparation comprising an AON disclosed herein. For example, a method of preventing or treating a neurological disease is provided comprising administering to a patient in need thereof an AON disclosed herein.

[00393] Patients treated using an above method may experience a reduction of at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or even 95% in the amount of a target gene product in a target cell (for example, a motor neuron) after administering an AON disclosed herein, after *e.g.* 1 day, 2 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 1 month, 2 months, 3, months, 4 months, 5, months, or 6 months or more. Administering

such an AON may be on, *e.g.*, at least a daily basis. The AON may be administered orally. In some embodiments, the AON is administered intrathecally or intracisternally. For example, in an embodiment described herein, an AON is administered intrathecally or intracisternally about every 3 months. The delay or worsening of clinical manifestation of a neurological disease in a patient as a consequence of administering an AON disclosed here may be at least *e.g.*, 6 months, 1 year, 18 months or even 2 years or more as compared to a patient who is not administered an AON such as one disclosed herein.

[00394] In another aspect, the disclosure provides methods of preventing, ameliorating, and/or treating a neurological disease, for example, a motor neuron disease. For example described herein are methods of preventing, ameliorating, and/or treating ALS, FTD, and ALS with FTD. In some embodiments, the disclosure provides a method of treating a neurological disease in a patient, for example, a patient in need of treatment of a neurological disease, where the method comprises administering to the patient an AON. In some embodiments, the neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Limbic-predominant age-related TDP-43 encephalopathy (LATE)), Cerebral Age-Related TDP-43 With Sclerosis (CARTS), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and synaptic diseases like autism.

[00395] In some embodiments, the patient is a mammal, for example, a human, a primate, a dog, a cat, a horse, a cow, a goat, a sheep, a mouse, or a rat. In particular embodiments, the patient is a human patient, for example, a human patient in need of treatment of a neurological disease, for example, ALS, FTD, or ALS with FTD. In some embodiments, the patient is a patient at risk of developing a neurological disease, for example, ALS, FTD, or ALS with FTD. In some

embodiments, the patient is a patient suffering from a neurological disease, for example, ALS, FTD, or ALS with FTD. In some embodiments, the patient is a patient exhibiting symptoms associated with a neurological disease, for example, ALS, FTD, or ALS with FTD.

[00396] In another aspect, described herein are methods of modifying or restoring cellular function or activity, for example, cellular function or activity of a motor neuron. For example, described herein is a method of modifying or restoring cellular function or activity of a motor neuron of a patient at risk of or suffering from a neurological disease, for example, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism. In some embodiments, the method includes exposing a cell to an AON. In some embodiments, the method includes exposing the cell to an AON *in vivo* or *ex vivo*.

[00397] In an embodiment described herein, the disclosure provides a method of increasing or restoring autophagy in a cell, where the method includes exposing the cell to an AON or contacting the cell with an AON. In some embodiments, the cell is a cell of a patient in need of treatment of a neurological disease. In some embodiments, the neurological disease is any one of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy,

amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism. In some embodiments, the exposing or contacting is performed *in vivo* or *ex vivo*. For example, in an embodiment described herein, a cell of a patient suffering from ALS, FTD, or ALS with FTD is exposed to or contacted with an AON, for example, an antisense oligonucleotide comprising any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[00398] The AONs of the invention can be used alone or in combination with each other where by at least two AONs of the invention are used together in a single composition or as part of a treatment regimen. The AONs of the invention may also be used in combination with other drugs for treating neurological diseases or conditions.

[00399] In various embodiments, methods of treating a neurological disease comprises selecting a patient for treatment using an AON disclosed herein. Selecting a patient for treatment can include measuring the presence or level of expression of certain markers of neurological disease. Examples of markers include neurofilament light (NEFL), neurofilament heavy (NEFH), phosphorylated neurofilament heavy chain (pNFH), TDP-43, or $p75^{ECD}$. Such markers can be measured from the plasma, the spinal cord fluid, the cerebrospinal fluid, the extracellular vesicles (for example, CSF exosomes), the blood, the urine, the lymphatic fluid, fecal matter, or a tissue of the patient.

[00400] In particular embodiments, the patient for treatment is selected by measuring phosphorylated neurofilament heavy chain (pNFH) in cerebrospinal fluid (CSF). In particular embodiments, the the pNFH in the CSF of the patient is used to predict disease status and survival in C9ORF72-associated amyotrophic lateral sclerosis (c9ALS) patients after initial administration and/or during on-going treatment.

[00401] In some embodiments, selecting a patient for treatment can include determining whether the patient expresses a mutation of a disease-associated gene. For example, a disease-associated gene can be an ALS-associated gene selected from any of TBK1, TARDBP, SQSTM1, VCP,

C9orf72, FUS, and CHCHD10. For example, the patient can be identified as a candidate patient for treatment according to the determination that the patient includes one or more mutations in the disease-associated genes.

[00402] In various embodiments, a patient selected for treatment can be administered an AON disclosed herein and/or or a pharmaceutical composition thereof.

Treatment and Evaluation

[00403] In another aspect, the methods described herein include exposing a cell to an AON to inhibit or decrease activity or function of a gene or gene product, for example, an mRNA or protein. For example, described herein is a method of inhibiting expression, activity, and/or function of any of PPM1A, ATXN2, SOD1, or MAPT in a cell. In some embodiments, expression, activity, and/or function of a target is is inhibited in a cell of a patient suffering from ALS, FTD, or ALS with FTD. In some embodiments, the method of inhibiting a target includes exposing a cell to an AON of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[00404] In methods described herein, exposing a cell to an AON can include administering the AON, or a pharmaceutical composition that includes the AON, to a patient, for example, a patient suffering from or at risk of developing a neurological disease such as amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism. Thus, embodiments described herein can include

administering an AON, or a pharmaceutical composition that includes an AON, to a patient in need of treatment, for example, a patient suffering from or at risk of developing a neurological disease such as amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism. Methods described herein embrace methods of administering an AON that allow administration of a therapeutically effective amount of the AON to a patient, for example, to a cell of a patient and/or to a site for treatment of a patient. For example, methods described herein include, but are not limited to, methods where an AON, or a pharmaceutical composition that includes an AON, is administered topically, parenterally, orally, buccally, sublingually, pulmonarily, intrathecally, intracisternally, intratracheally, intrathalamically, intracerebroventricularly, intraocularly, intranasally, transdermally, rectally, vaginally, or intraduodenally. In particular embodiments, the AON is administered orally. In some embodiments, the AON is administered intrathecally or intracisternally. In embodiments described herein, the methods include administering a therapeutically effective amount of an AON, for example, a therapeutically effective amount of an AON.

[00405] The methods described herein include methods of administering to a patient and/or exposing a cell to an AON, for example, an AON of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, or a pharmaceutically acceptable salt thereof.

[00406] In a further aspect, described herein is a use of an AON in the manufacture of a medicament for the treatment of neurological disease. For example, described herein is a use of an AON in the manufacture of a medicament for the treatment of ALS, FTD, or ALS with FTD. In some embodiments, the AON for use in the manufacture of a medicament for treatment is an AON of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, or a pharmaceutically acceptable salt thereof.

[00407] In a further aspect, described herein is a method of treating a neurological disease in a patient in need thereof, where the method includes administering to the patient in need thereof a pharmaceutical composition comprising a therapeutically effective amount of an AON, and a pharmaceutically acceptable excipient. In some embodiments, the neurological disease is amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism. In some embodiments, the AON includes any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, or a pharmaceutically acceptable salt thereof.

[00408] In embodiments described herein, the pharmaceutical composition comprising a therapeutically effective amount of an AON, and a pharmaceutically acceptable excipient can be

administered in any number of ways to achieve therapeutic delivery to a cell of a patient and/or to a site for treatment of a patient in need thereof. For example, in embodiments described herein, a pharmaceutical composition comprising a therapeutically effective amount of an AON, and a pharmaceutically acceptable excipient can be administered topically, parenterally, intrathecally, orally, pulmonarily, intratracheally, intranasally, transdermally, buccally, intrathalamically, intracerebroventricularly, intraocularly, sublingually, rectally, vaginally, or intraduodenally. In particular embodiments, the pharmaceutical composition is administered orally. In some embodiments, the pharmaceutical composition is administered intrathecally or intracisternally. In embodiments described herein, the patient is a mammal, for example, a human patient.

[00409] In some embodiments, an AON described herein is for use as a medicament. For example, described herein is AON of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, or a pharmaceutically acceptable salt thereof, for use as a medicament.

[00410] In some embodiments, an AON disclosed herein, is for use in the treatment of a neurological disease. For example, described herein is an AON, or a pharmaceutically acceptable salt thereof, for use in the treatment of a neurological disease. In some embodiments, the neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Limbic-predominant age-related TDP-43 encephalopathy (LATE)), Cerebral Age-Related TDP-43 With Sclerosis (CARTS), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and synaptic diseases like autism.

[00411] A patient, as described herein, refers to any animal at risk for, suffering from or diagnosed with a neurological disease, including, but not limited to, mammals, primates, and humans. In certain embodiments, the patient may be a non-human mammal such as, for example, a cat, a dog, or a horse. A patient may be an individual diagnosed with a high risk of developing a neurological disease, someone who has been diagnosed with a neurological disease, someone who previously suffered from a neurological disease, or an individual evaluated for symptoms or indications of a neurological disease, or any of the signs or symptoms associated with neurological diseases such as amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism.

[00412] "A patient in need," as used herein, refers to a patient suffering from any of the symptoms or manifestations of a neurological disease, a patient who may suffer from any of the symptoms or manifestations of a neurological disease, or any patient who might benefit from a method of the disclosure for treating a neurological disease. A patient in need may include a patient who is diagnosed with a risk of developing a neurological disease, a patient who has suffered from a neurological disease in the past, or a patient who has previously been treated for a neurological disease.

[00413] "Effective amount," as used herein, refers to the amount of an agent that is sufficient to at least partially treat a condition when administered to a patient. The therapeutically effective amount will vary depending on the severity of the condition, the route of administration of the component, and the age, weight, etc. of the patient being treated. Accordingly, an effective amount of a disclosed AON is the amount of the AON necessary to treat a neurological disease in a patient such that administration of the agent prevents a neurological disease from occurring in a

subject, prevents neurological disease progression (*e.g.*, prevents the onset or increased severity of symptoms of the neurological disease such as muscle weakening, spasms, or fasciculation), or relieves or completely ameliorates all associated symptoms of a neurological disease, *e.g.*, causes regression of the disease.

[00414] Efficacy of treatment may be evaluated by means of evaluation of gross symptoms associated with a neurological disease, analysis of tissue histology, biochemical assay, imaging methods such as, for example, magnetic resonance imaging, or other known methods. For instance, efficacy of treatment may be evaluated by analyzing gross symptoms of the disease such as changes in muscle strength and control or other aspects of gross pathology associated with a neurological disease following administration of a disclosed AON to a patient suffering from a neurological disease.

[00415] Efficacy of treatment may also be evaluated at the tissue or cellular level, for example, by means of obtaining a tissue biopsy (*e.g.*, a brain, spinal, muscle, or motor neuron tissue biopsy) and evaluating gross tissue or cell morphology or staining properties, or by obtaining a biofluid (e.g., cerebrospinal fluid, exosomes, plasma, or urine) and examining target expression in the fluid using a biochemical assay that examines protein or RNA expression. Such biochemical assays can include ddPCR, qRT-PCR, western blot, ELISA, and/or SIMOA. For instance, one may evaluate levels of a protein (*e.g.*, e.g., protein levels of any of PPM1A, ATXN2, SOD1, or MAPT) indicative of a disease or a neurological disease, in dissociated cells or non-dissociated tissue via immunocytochemical, immunohistochemical, Western blotting, or Northern blotting methods, or methods useful for evaluating RNA levels such as quantitative or semi-quantitative polymerase chain (*e.g.*, digital PCR (DigitalPCR, dPCR, or ddPCR), qPCR etc.) reaction. One may also evaluate the presence or level of expression of useful biomarkers (*e.g.*, neurofilament light (NEFL), neurofilament heavy (NEFH), SOD1/SOD1 transcripts, TDP-43 or p75 extracellular domain ($p75^{ECD}$)) found in spinal cord fluid, cerebrospinal fluid, plasma, extracellular vesicles (for example, exosome-like cerebrospinal fluid extracellular vesicles ("CSF exosomes"), such as those described in Welton *et al.*, (2017) "Cerebrospinal fluid extracellular vesicle enrichment for protein biomarker discovery in neurological disease; multiple sclerosis" *J Extracell Vesicles.*, 6(1):1-10; and Street *et al.*, (2012) "Identification and proteomic profiling of exosomes in human cerebrospinal fluid" *J Transl. Med.*, 10:5), urine, fecal matter, lymphatic fluid, blood, plasma, or serum to evaluate disease state and efficacy of treatment. Additional measurements of efficacy may include strength duration time constant (SDTC), short interval cortical inhibition (SICI), dynamometry, accurate test of limb isometric strength (ATLIS), compound muscle action potential (CMAP), and ALSFRS-R. In certain embodiments, urinary

neurotrophin receptor p75 extracellular domain ($p75^{ECD}$) is a disease progression and prognostic biomarker in amyotrophic lateral sclerosis (ALS). Phosphorylated neurofilament heavy chain (pNFH) in cerebrospinal fluid (CSF) predict disease status and survival in amyotrophic lateral sclerosis (ALS) patients. CSF pNFH can serve as a prognostic biomarker for clinical trials, which will increase the likelihood of successfully developing a treatment for ALS. In various embodiments, efficacy may be determined via any of MRI, fMRI, PET, EEG, or EMG.

[00416] In some embodiments, in evaluating the efficacy of a treatment against Alzheimer's disease, mental performance can be used for measuring efficacy such as with the Mini-Mental State Examination (MMSE). For measuring efficacy, the Functional Assessment Staging Test (FAST), the Motor Screening Task, Paired Associates Learning, Spatial Working Memory, Reaction time, Rapid Visual Information Processing, Delayed Matching to Sample, Pattern Recognition Memory can be used.

[00417] In some embodiments, in evaluating the efficacy of a treatment against Parkinson's disease, the Unified Parkinson's Disease Rating Scale (UPDRS) can be implemented as the performance measure. Other measures for quantifying aspects of functional performance not measured by the UPDRS can include the Berg Balance Scale (BBS), Forward Functional Reach Test (FFR), Backward Functional Reach Test (BFR), Timed "Up & Go" Test (TUG), and gait speed.

[00418] In evaluating efficacy of treatment, suitable controls may be chosen to ensure a valid assessment. For instance, one can compare symptoms evaluated in a patient with a neurological disease following administration of a disclosed AON to those symptoms in the same patient prior to treatment or at an earlier point in the course of treatment or in another patient not diagnosed with the neurological disease. Alternatively, one may compare the results of biochemical or histological analysis of tissue following administration of a disclosed AON with those of tissue from the same patient or from an individual not diagnosed with the neurological disease or from the same patient prior to administration of the AON. Additionally, one may compare blood, plasma, serum, cell, urine, lymphatic fluid, spinal cord fluid, cerebrospinal fluid, or fecal samples following administration of the AON with comparable samples from an individual not diagnosed with the neurological disease or from the same patient prior to administration of the AON. In some embodiments one may compare extracellular vesicles (for example CSF exosomes), following administration of the AON with extracellular vesicles from an individual not diagnosed with the neurological disease or from the same patient prior to administration of the AON.

[00419] Validation of target inhibition may be determined by direct or indirect assessment of target expression levels or activity. For instance, biochemical assays that measure any of PPM1A,

ATXN2, SOD1, or MAPT protein or RNA expression may be used to evaluate overall inhibition. For instance, one may measure target protein levels in cells or tissue by Western blot to evaluate overall levels. One may also measure target mRNA levels by means of Northern blot or quantitative polymerase chain reaction to determine overall target inhibition. One may also evaluate target protein levels or levels of another protein indicative of the target signaling activity in dissociated cells, non-dissociated tissue, extracellular vesicles (for example, CSF exosomes), blood, serum, or fecal matter via immunocytochemical or immunohistochemical methods.

[00420] Methods of treatment disclosed herein include methods of increasing or restoring autophagy in a cell. "Autophagy" refers to the natural, regulated mechanism of the cell that disassembles unnecessary or dysfunctional components, allowing orderly degradation and recycling of cellular components. Autophagy is generally responsible for degrading relatively long-lived, cytoplasmic proteins, soluble and insoluble misfolded proteins, and also entire organelles. Failure in autophagy machinery is thought to contribute to the formation of toxic protein aggregates in motor neurons (*See* Ramesh and Pandley, (2017) "Autophagy Dysregulation in ALS: When Protein Aggregates Get Out of Hand" *Front Mol Neurosci*. 10 (Article 263)). Dysregulation of autophagy and protein aggregation and mislocalization is implicated in neurological diseases, including ALS. Methods of increasing or restoring autophagy include methods that reduce expression levels of targets in a patient suffering from a neurological disease. Methods of increasing or restoring autophagy also include methods that increase TBK1 activity or expression or TBK1 phosphorylation (for example, TBK1 ser172 phosphorylation) in cells of a patient suffering from a neurological disease.

[00421] The disclosure also provides methods of inhibiting target gene products (e.g., PPM1A, ATXN2, SOD1, or MAPT) in cells of a patient suffering from a neurological disease. Target gene products may be inhibited in any cell in which the target expression or activity occurs, including cells of the nervous system (including the central nervous system, the peripheral nervous system, motor neurons, the brain, the brain stem, the frontal lobes, the temporal lobes, the spinal cord), the musculoskeletal system, spinal fluid, and cerebrospinal fluid. Cells of the musculoskeletal system include skeletal muscle cells (*e.g.*, myocytes). Motor neurons include upper motor neurons and lower motor neurons.

Pharmaceutical Compositions and Routes of Administration

[00422] The present disclosure also provides methods for treating a neurological disease via administration of a pharmaceutical composition comprising a disclosed AON. In another aspect, the disclosure provides a pharmaceutical composition for use in treating a neurological disease. The pharmaceutical composition may be comprised of a disclosed antisense oligonucleotide and a

pharmaceutically acceptable carrier. As used herein the term "pharmaceutical composition" means, for example, a mixture containing a specified amount of a therapeutic compound, *e.g.*, a therapeutically effective amount, of a therapeutic compound in a pharmaceutically acceptable carrier to be administered to a mammal, *e.g.*, a human, in order to treat a neurological disease. In some embodiments, contemplated herein are pharmaceutical compositions comprising a disclosed AON and a pharmaceutically acceptable carrier. In another aspect, the disclosure provides use of a disclosed AON in the manufacture of a medicament for treating a neurological disease. "Medicament," as used herein, has essentially the same meaning as the term "pharmaceutical composition."

[00423] As used herein, "pharmaceutically acceptable carrier" means buffers, carriers, and excipients suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio. The carrier(s) should be "acceptable" in the sense of being compatible with the other ingredients of the formulations and not deleterious to the recipient. Pharmaceutically acceptable carriers include buffers, solvents, dispersion media, coatings, isotonic and absorption delaying agents, and the like, that are compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is known in the art. In one embodiment the pharmaceutical composition is administered orally and includes an enteric coating suitable for regulating the site of absorption of the encapsulated substances within the digestive system or gut. For example, an enteric coating can include an ethylacrylate-methacrylic acid copolymer.

[00424] In some embodiments, an AON of the disclosure, is in the form of a pharmaceutically acceptable salt. AONs described herein that are acidic in nature are capable of forming base salts with various pharmacologically acceptable cations. Examples of such salts include alkali metal or alkaline earth metal salts and, particularly, calcium, magnesium, sodium, lithium, zinc, potassium, and iron salts. Pharmaceutically acceptable salts of the disclosure include, for example, pharmaceutically acceptable salts of an AON of any of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

[00425] Also described herein are pharmaceutical compositions comprising an AON and a pharmaceutically acceptable excipient. For example, a pharmaceutical composition described herein can include an AON, for example, an AON of any one of SEQ ID NOs: 1-954, 1914-

149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, and a pharmaceutically acceptable excipient.

[00426] In some embodiments, an AON can be encapsulated in a nanoparticle coating. It is believed that nanoparticle encapsulation prevents AON degradation and enhances cellular uptake. For example, in some embodiments an AON is encapsulated in a coating of a cationic polymer, for example, a synthetic polymer (*e.g.*, poly-L-lysine, polyamidoamine, a poly(β-amino ester), and polyethyleneimine) or a naturally occurring polymer (*e.g.*, chitosan and a protamine). In some embodiments, an AON is encapsulated in a lipid or lipid-like material, for example, a cationic lipid, a cationic lipid-like material, or an ionizable lipid that is positively charged only at an acidic pH. For example, in some embodiments, an AON is encapsulated in a lipid nanoparticle that includes hydrophobic moieties, *e.g.*, cholesterol and/or a polyethylene glycol (PEG) lipid.

[00427] In some embodiments, an AON is conjugated to a bioactive ligand. For example, in some embodiments described herein, an AON is conjugated to a peptide, a lipid, N-acetylgalactosamine (GalNAc), cholesterol, vitamin E, an antibody, or a cell-penetrating peptide (for example, transactivator of transcription (TAT) and penetratine).

[00428] Pharmaceutical compositions containing a disclosed AON, such as those disclosed herein, can be presented in a dosage unit form and can be prepared by any suitable method. A pharmaceutical composition should be formulated to be compatible with its intended route of administration. Useful formulations can be prepared by methods well known in the pharmaceutical art. For example, see *Remington's Pharmaceutical Sciences*, 18th ed. (Mack Publishing Company, 1990).

[00429] Pharmaceutical formulations, for example, are sterile. Sterilization can be accomplished, for example, by filtration through sterile filtration membranes. Where the composition is lyophilized, filter sterilization can be conducted prior to or following lyophilization and reconstitution.

[00430] In one embodiment, a disclosed AON and any pharmaceutical composition thereof may be administered by one or several routes, including topically, parenterally, intrathecally, orally, pulmonarily, intratracheally, intranasally, transdermally, buccally, intrathalamically, intracerebroventricularly, intraocularly, sublingually, rectally, vaginally, or intraduodenally. The term parenteral as used herein includes subcutaneous injections, intrapancreatic administration, intravenous, intracisternal, intrathecal, intramuscular, intraperitoneal, intrasternal injection or infusion techniques. For example, a disclosed AON may be administered subcutaneously to a

subject. In another example, a disclosed AON may be administered orally to a subject. In another example, a disclosed AON may be administered directly to the nervous system, or specific regions or cells of the nervous system (*e.g.*, the brain, brain stem, lower motor neurons, spinal cord, upper motor neurons) via parenteral administration, for example, a disclosed AON may be administered intrathecally or intracisternally.

[00431] It will be appreciated that the AON administered to the patient having or at risk of a neurological disease in methods described herein, can be administered by various administration routes. In various embodiments, the AON can be administered by one or several routes, including orally (*e.g.*, by inhalation spray), topically, vaginally, rectally, intrathecally, intratracheally, intracisternally, intranasally, transdermally, intrathalamically, intracerebroventricularly, intraocularly, intraduodenally, buccally, sublingually, parenterally, *e.g.*, by subcutaneous injection. The term parenteral as used herein includes subcutaneous injections, intrapancreatic administration, and intravenous, intrathecal, intracisternal, intramuscular, intraperitoneal, and intrasternal injection or infusion techniques.

Parenteral Administration

[00432] The pharmaceutical compositions of the disclosure can be formulated for parenteral administration, *e.g.*, formulated for injection via the intravenous, intracisternal, intramuscular, subcutaneous, intrathecal, intralesional, or intraperitoneal routes. The preparation of an aqueous composition, such as an aqueous pharmaceutical composition containing a disclosed AON, will be known to those of skill in the art in light of the present disclosure. Typically, such compositions can be prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for using to prepare solutions or suspensions upon the addition of a liquid prior to injection can also be prepared; and the preparations can also be emulsified.

[00433] The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions; formulations including sesame oil, peanut oil or aqueous propylene glycol; and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi.

[00434] Solutions of active compounds as free base or pharmacologically acceptable salts can be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. In addition, sterile, fixed oils may be employed as a solvent or suspending medium. For this purpose any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty

acids such as oleic acid can be used in the preparation of injectables. The sterile injectable preparation may also be a sterile injectable solution, suspension, or emulsion in a nontoxic parenterally acceptable diluent or solvent, for example, as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, U.S.P., and isotonic sodium chloride solution. In one embodiment, a disclosed AON may be suspended in a carrier fluid comprising 1% (w/v) sodium carboxymethylcellulose and 0.1% (v/v) TWEEN™ 80. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

[00435] Injectable preparations, for example, sterile injectable aqueous or oleaginous suspensions may be formulated according to the known art using suitable dispersing or wetting agents and suspending agents. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. Sterile injectable solutions of the disclosure may be prepared by incorporating a disclosed AON in the required amount of the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The injectable formulations can be sterilized, for example, by filtration through a bacteria-retaining filter.

[00436] The preparation of more, or highly concentrated solutions for intramuscular injection is also contemplated. In this regard, the use of DMSO as solvent is preferred as this will result in extremely rapid penetration, delivering high concentrations of the disclosed AON to a small area.

[00437] Suitable preservatives for use in such a solution include benzalkonium chloride, benzethonium chloride, chlorobutanol, thimerosal and the like. Suitable buffers include boric acid, sodium and potassium bicarbonate, sodium and potassium borates, sodium and potassium carbonate, sodium acetate, sodium biphosphate and the like, in amounts sufficient to maintain the pH at between about pH 6 and pH 8, and for example, between about pH 7 and pH 7.5. Suitable tonicity agents are dextran 40, dextran 70, dextrose, glycerin, potassium chloride, propylene glycol, sodium chloride, and the like, such that the sodium chloride equivalent of the solution is in the range 0.9 plus or minus 0.2%. Suitable antioxidants and stabilizers include sodium bisulfite, sodium metabisulfite, sodium thiosulfite, thiourea and the like. Suitable wetting and clarifying agents include polysorbate 80, polysorbate 20, poloxamer 282 and tyloxapol. Suitable viscosity-increasing agents include dextran 40, dextran 70, gelatin, glycerin, hydroxyethylcellulose,

hydroxymethylpropylcellulose, lanolin, methylcellulose, petrolatum, polyethylene glycol, polyvinyl alcohol, polyvinylpyrrolidone, carboxymethylcellulose and the like.

Intrathecal Administration

[00438] In some embodiments, an AON, or a pharmaceutical composition of the disclosure that includes an AON, is delivered to the CNS through intrathecal administration, thereby ensuring delivery into the cerebrospinal fluid (CSF) of a patient in need of treatment. In various embodiments, intrathecal administration (also referred to as intrathecal injection) refers to an injection into the spinal canal (intrathecal space surrounding the spinal cord). Various techniques may be used including, without limitation, lateral cerebroventricular injection through a burrhole or cisternal or lumbar puncture or the like. In some embodiments, "intrathecal administration" or "intrathecal delivery" according to the present invention refers to IT administration or delivery via the lumbar area or region, *e.g.*, lumbar IT administration or delivery. As used herein, the term "lumbar region" or "lumbar area" refers to the area between the third and fourth lumbar (lower back) vertebrae and, more inclusively, the L2-S1 region of the spine.

[00439] In various embodiments, compositions comprising a disclosed AON can be suitable for intrathecal delivery. For example, a composition suitable for intrathecal delivery can comprise the AON and any of cerebrospinal fluid, artificial cerebrospinal fluid, phosphate buffered saline (PBS), salt buffer, Ringer's solution, and Lactated Ringer's solution.

Oral Administration

[00440] In some embodiments, contemplated herein are compositions suitable for oral delivery of a disclosed AON, *e.g.*, tablets that include an enteric coating, *e.g.*, a gastro-resistant coating, such that the compositions may deliver an AON to, *e.g.*, the gastrointestinal tract of a patient.

[00441] For example, a tablet for oral administration is provided that comprises granules (*e.g.*, is at least partially formed from granules) that include a disclosed AON , *e.g.*, an AON of any of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, and pharmaceutically acceptable excipients. Such a tablet may be coated with an enteric coating. Contemplated tablets may include pharmaceutically acceptable excipients such as fillers, binders, disintegrants, and/or lubricants, as well as coloring agents, release agents, coating agents, sweetening, flavoring such as wintergreen, orange, xylitol, sorbitol, fructose, and maltodextrin, and perfuming agents, preservatives and/or antioxidants.

[00442] In some embodiments, contemplated pharmaceutical formulations include an intra-granular phase that includes a disclosed AON, *e.g.* an AON of any of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566 or an AON with one or more spacers that replace one or more nucleosides of a sequence of any one SEQ ID NOs: 1-954, 1914-149354, 149362-158581, or 167805-301566, such as any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, and a pharmaceutically acceptable salt (*e.g.*, a pharmaceutically acceptable filler). For example, a disclosed AON and a filler may be blended together, optionally, with other excipients, and formed into granules. In some embodiments, the intragranular phase may be formed using wet granulation, *e.g.* a liquid (*e.g.*, water) is added to the blended AON compound and filler, and then the combination is dried, milled and/or sieved to produce granules. One of skill in the art would understand that other processes may be used to achieve an intragranular phase.

[00443] In some embodiments, contemplated formulations include an extra-granular phase, which may include one or more pharmaceutically acceptable excipients, and which may be blended with the intragranular phase to form a disclosed formulation.

[00444] A disclosed formulation may include an intragranular phase that includes a filler. Exemplary fillers include, but are not limited to, cellulose, gelatin, calcium phosphate, lactose, sucrose, glucose, mannitol, sorbitol, microcrystalline cellulose, pectin, polyacrylates, dextrose, cellulose acetate, hydroxypropylmethyl cellulose, partially pre-gelatinized starch, calcium carbonate, and others including combinations thereof.

[00445] In some embodiments, a disclosed formulation may include an intragranular phase and/or an extragranular phase that includes a binder, which may generally function to hold the ingredients of the pharmaceutical formulation together. Exemplary binders of the disclosure may include, but are not limited to, the following: starches, sugars, cellulose or modified cellulose such as hydroxypropyl cellulose, lactose, pre-gelatinized maize starch, polyvinyl pyrrolidone, hydroxypropyl cellulose, hydroxypropylmethyl cellulose, low substituted hydroxypropyl cellulose, sodium carboxymethyl cellulose, methyl cellulose, ethyl cellulose, sugar alcohols and others including combinations thereof.

[00446] Contemplated formulations, *e.g.*, that include an intragranular phase and/or an extragranular phase, may include a disintegrant such as but are not limited to, starch, cellulose, crosslinked polyvinyl pyrrolidone, sodium starch glycolate, sodium carboxymethyl cellulose, alginates, corn starch, crosmellose sodium, crosslinked carboxymethyl cellulose, low substituted hydroxypropyl cellulose, acacia, and others including combinations thereof. For example, an intragranular phase and/or an extragranular phase may include a disintegrant.

[00447] In some embodiments, a contemplated formulation includes an intra-granular phase comprising a disclosed AON and excipients chosen from: mannitol, microcrystalline cellulose, hydroxypropylmethyl cellulose, and sodium starch glycolate or combinations thereof, and an extra-granular phase comprising one or more of: microcrystalline cellulose, sodium starch glycolate, and magnesium stearate or mixtures thereof.

[00448] In some embodiments, a contemplated formulation may include a lubricant, *e.g.* an extra-granular phase may contain a lubricant. Lubricants include but are not limited to talc, silica, fats, stearin, magnesium stearate, calcium phosphate, silicone dioxide, calcium silicate, calcium phosphate, colloidal silicon dioxide, metallic stearates, hydrogenated vegetable oil, corn starch, sodium benzoate, polyethylene glycols, sodium acetate, calcium stearate, sodium lauryl sulfate, sodium chloride, magnesium lauryl sulfate, talc, and stearic acid.

[00449] In some embodiments, the pharmaceutical formulation comprises an enteric coating. Generally, enteric coatings create a barrier for the oral medication that controls the location at which the drug is absorbed along the digestive track. Enteric coatings may include a polymer that disintegrates at different rates according to pH. Enteric coatings may include for example, cellulose acetate phthalate, methyl acrylate-methacrylic acid copolymers, cellulose acetate succinate, hydroxylpropylmethyl cellulose phthalate, methyl methacrylate-methacrylic acid copolymers, ethylacrylate-methacrylic acid copolymers, methacrylic acid copolymer type C, polyvinyl acetate-phthalate, and cellulose acetate phthalate.

[00450] Exemplary enteric coatings include Opadry® AMB, Acryl-EZE®, Eudragit® grades. In some embodiments, an enteric coating may comprise about 5% to about 10%, about 5% to about 20%, 8 to about 15%, about 8% to about 20%, about 10% to about 20%, or about 12 to about 20%, or about 18% of a contemplated tablet by weight. For example, enteric coatings may include an ethylacrylate-methacrylic acid copolymer.

[00451] For example, in a contemplated embodiment, a tablet is provided that comprises or consists essentially of about 0.5% to about 70%, *e.g.* about 0.5% to about 10%, or about 1% to about 20%, by weight of a disclosed AON or a pharmaceutically acceptable salt thereof. Such a tablet may include for example, about 0.5% to about 60% by weight of mannitol, *e.g.* about 30% to about 50% by weight mannitol, *e.g.* about 40% by weight mannitol; and/or about 20% to about 40% by weight of microcrystalline cellulose, or about 10% to about 30% by weight of microcrystalline cellulose. For example, a disclosed tablet may comprise an intragranular phase that includes about 30% to about 60%, *e.g.* about 45% to about 65% by weight, or alternatively, about 5 to about 10% by weight of a disclosed AON, about 30% to about 50%, or alternatively, about 5% to about 15% by weight mannitol, about 5% to about 15% microcrystalline cellulose,

about 0% to about 4%, or about 1% to about 7% hydroxypropylmethylcellulose, and about 0% to about 4%, *e.g.* about 2% to about 4% sodium starch glycolate by weight.

[00452] In another contemplated embodiment, a pharmaceutical tablet formulation for oral administration of a disclosed AON comprises an intra-granular phase, wherein the intra-granular phase includes a disclosed AON or a pharmaceutically acceptable salt thereof (such as a sodium salt), and a pharmaceutically acceptable filler, and which may also include an extra-granular phase, that may include a pharmaceutically acceptable excipient such as a disintegrant. The extra-granular phase may include components chosen from microcrystalline cellulose, magnesium stearate, and mixtures thereof. The pharmaceutical composition may also include an enteric coating of about 12% to 20% by weight of the tablet. For example, a pharmaceutically acceptable tablet for oral use may comprise about 0.5% to 10% by weight of a disclosed AON, *e.g.*, a disclosed AON or a pharmaceutically acceptable salt thereof, about 30% to 50% by weight mannitol, about 10% to 30% by weight microcrystalline cellulose, and an enteric coating comprising an ethylacrylate-methacrylic acid copolymer.

[00453] In another example, a pharmaceutically acceptable tablet for oral use may comprise an intra-granular phase, comprising about 5 to about 10% by weight of a disclosed AON, *e.g.*, a disclosed AON or a pharmaceutically acceptable salt thereof, about 40% by weight mannitol, about 8% by weight microcrystalline cellulose, about 5% by weight hydroxypropylmethyl cellulose, and about 2% by weight sodium starch glycolate; an extra-granular phase comprising about 17% by weight microcrystalline cellulose, about 2% by weight sodium starch glycolate, about 0.4% by weight magnesium stearate; and an enteric coating over the tablet comprising an ethylacrylate-methacrylic acid copolymer.

[00454] In some embodiments the pharmaceutical composition may contain an enteric coating comprising about 13% or about 15%, 16%, 17% or 18% by weight, *e.g.*, AcyrlEZE® (see, *e.g.*, PCT Publication No. WO 2010/054826, which is hereby incorporated by reference in its entirety).

[00455] The rate at which the coating dissolves and the active ingredient is released is its dissolution rate. In an embodiment, a contemplated tablet may have a dissolution profile, *e.g.* when tested in a USP/EP Type 2 apparatus (paddle) at 100 rpm and 37 °C in a phosphate buffer with a pH of 7.2, of about 50% to about 100% of the AON releasing after about 120 minutes to about 240 minutes, for example after 180 minutes. In another embodiment, a contemplated tablet may have a dissolution profile, *e.g.* when tested in a USP/EP Type 2 apparatus (paddle) at 100 rpm and 37°C in diluted HCl with a pH of 1.0, where substantially none of the AON is released after 120 minutes. A contemplated tablet, in another embodiment, may have a dissolution profile, *e.g.* when tested in USP/EP Type 2 apparatus (paddle) at 100 rpm and 37 °C in a phosphate buffer

with a pH of 6.6, of about 10% to about 30%, or not more than about 50%, of the AON releasing after 30 minutes.

[00456] In some embodiments, methods provided herein may further include administering at least one other agent that is directed to treatment of diseases and disorders disclosed herein. In one embodiment, contemplated other agents may be co-administered (*e.g.*, sequentially or simultaneously).

Dosage and Frequency of Administration

[00457] Exemplary formulations include dosage forms that include or consist essentially of about 35 mg to about 500 mg of a disclosed AON, such as any of a PPM1A AON, ATXN2 AON, SOD1 AON, or MAPT AON. For example, formulations that include about 35 mg, 40 mg, 50 mg, 60 mg, 70 mg, 80 mg, 90 mg, 100 mg, 110 mg, 120 mg, 130 mg, 140 mg, 150 mg, 160 mg, 170 mg, 180 mg, 190 mg, 200 mg, 250 mg, 300 mg, 350 mg, 400 mg, 450 mg, 500 mg, 600 mg, 700 mg, 800 mg, 900 mg, 1 g, 1.5 g, 2.0 g, 2.5 g, 3.0 g, 3.5 g, 4.0 g, 4.5 g, or 5.0 g of a disclosed AON are contemplated herein. In one embodiment, a formulation may include about 40 mg, 80 mg, or 160 mg of a disclosed AON. In some embodiments, a formulation may include at least 100 µg of a disclosed AON. For example, formulations may include about 0.1 mg, 0.2 mg, 0.3 mg, 0.4 mg, 0.5 mg, 1 mg, 5 mg, 10 mg, 15 mg, 20 mg, 25 mg, or 30 mg of a disclosed AON.

[00458] In some embodiments, methods described herein include administering at least 1 µg, at least 5 µg, at least 10 µg, at least 20 µg, at least 30 µg, at least 40 µg, at least 50 µg, at least 60 µg, at least 70 µg, at least 80 µg, at least 90 µg, or at least 100 µg of an AON. In some embodiments, methods of the invention include administering from 35 mg to 500 mg, from 1 mg to 10 mg, from 10 mg to 20 mg, from 20 mg to 30 mg, from 30 mg to 40 mg, from 40 mg to 50 mg, from 50 mg to 60 mg, from 60 mg to 70 mg, from 70 mg to 80 mg, from 80 mg to 90 mg, from 90 mg to 100 mg, from 100 mg to 150 mg, from 150 mg to 200 mg, from 200 mg to 250 mg, from 250 mg to 300 mg, from 300 mg to 350 mg, from 350 mg to 400 mg, from 400 mg to 450 mg, from 450 mg to 500 mg, from 500 mg to 600 mg, from 600 mg to 700 mg, from 700 mg to 800 mg, from 800 mg to 900 mg, from 900 mg to 1 g, from 1 mg to 50 mg, from 20 mg to 40 mg, or from 1 mg to 500 mg of a AON.

[00459] The amount administered will depend on variables such as the type and extent of disease or indication to be treated, the overall health and size of the patient, the *in vivo* potency of the AON, the pharmaceutical formulation, and the route of administration. The initial dosage can be increased beyond the upper level in order to rapidly achieve the desired blood-level or tissue level. Alternatively, the initial dosage can be smaller than the optimum, and the dosage may be progressively increased during the course of treatment. Human dosage can be optimized, *e.g.*, in

a conventional Phase I dose escalation study. Dosing frequency can vary, depending on factors such as route of administration, dosage amount and the disease being treated. Exemplary dosing frequencies are once per day, once per week and once every two weeks. In some embodiments, dosing is once per day for 7 days. In some embodiments, dosing is once per month. In some embodiments, dosing is once every 3 months.

Combination Therapies

[00460] In various embodiments, an AON as disclosed herein can be administered in combination with one or more additional therapies. The combination therapy of the disclosed oligonucleotide and the one or more additional therapies can, in some embodiments, be synergistic in treating any of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism.

[00461] Example additional therapies for treating amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), or ALS with FTD include any of Riluzole (Rilutek), troriluzole, Edaravone (Radicava), rivastigmine, donepezil, QRL-101, QRL-201, galantamine, selective serotonin reuptake inhibitor, antipsychotic agents, cholinesterase inhibitors, memantine, benzodiazepine antianxiety drugs, AMX0035 (ELYBRIO®), ZILUCOPLAN (RA101495), dual AON intrathecal administration (*e.g.*, BIIB067, BIIB078), BIIB100, levodopa/carbidopa, dopaminergic agents (*e.g.*, ropinirole, pramipexole, rotigotine), medroxyprogesterone, KCNQ2/KCNQ3 openers, Pridopidine, PrimeC (combination of ciprofloxacin and Celebrex), olanzapine (Zyprexa), quetiapine (Seroquel), SSRIs, divalproex sodium (Depakote), carbamazepine (Tegretol), medroxyprogestrone, lithium, anticonvulsants and psychostimulant agents. Additional therapies can further include breathing care, physical therapy, occupational

therapy, speech therapy, and nutritional support. In various embodiments, an additional therapy can be a second antisense oligonucleotide. As an example, the second antisense oligonucleotide may be a second AON that targets a transcript.

[00462] A combination therapy (*e.g.*, in combination with an AON) may be selected according to the disease that is to be treated. For example, for treating Alzheimer's Disease, any Memantine, Rivastigmine, Galantamine, Donepezil, Aricept®, Exelon® (Rivastigmine), Razadyne®, Aducanumab, BAN2401, BIIB091 (gosuranemab), BIIB076, BIIB080 (IONIS-MAPTRx), Elayta (CT1812), MK1942, allogenic hMSC, nilotinib, ABT-957, acitretin, ABT-354, GV1001, Riluzole, CAD106, CNP520, AD-35, Rilapladib, DHP1401, T-817 MA, TC-5619, TPI-287, RVT-101, LY450139, JNJ-54861911, Dapagliflozin, GSK239512, PF-04360365, ASP0777, SB-742457 (a 5-HT6 receptor antagonist), PF-03654746 (an H_3 receptor antagonist), GSK933776 (an Fc-inactivated anti-β amyloid (Aβ) monoclonal antibody (mAb)), Posiphen ((+)-phenserine tartrate), AMX0035 (ELYBRIO®), coenzyme Q10, aducanamab (ADUHLEM), memantine (NAMENDA), Namzeric, Suvorexant (belsomra), lecanemab, or any combination thereof can be selected as an additional therapy.

[00463] For example for treating Parkinson's Disease, any of Levodopa, Carbidopa-levidopa, pramipexole (MIRAPEX), ropinirole (REQUIP), rotigotine (NEUPRO), apomorphine (APOKYN, KYNMOBI), selegiline (EDLEPRYL, ZELAPAR), rasagiline, entacapone (COMTAN), tolcapone (TASMAR), amantadine (GOCOVRI, SYMMETREL, OSMOLEX), trihexyphenidyl (ARTANE), BIIB054 (cinepanemab), BIIB094, BIIB118, ABBV-0805, zonisamide, deep brain stimulation, brain-derived neurotrophic factor, stem-cell transplant, Niacin, brain stem stimulation, nicotine, nabilone, PF-06649751, DNL201, LRRK2 inhibitors, CK1 inhibitors, isradipine, CLR4001, IRX4204, Yohimbine, coenzyme Q10, OXB-102, duloxetine, pioglitazone, preladenant, istradefylline (NOURIANZ), safinamide (XADAGO), benztropine (COGENTIN), opicapone (ongentys), exenatide, lingzhi, Caffeine, sarizotan, embryonic dopamine cell implantation, or any combination thereof can be selected as an additional therapy.

[00464] For example, for treating progressive supranuclear palsy (PSP), any of UCB0107, ABBV-8E12, F-18 AV1451, BIIB092, C2N-8E12, tideglusib, deep transcranial magnetic stimulation, lipoic acid, tolfenamica acid, lithium, AZP2006, Glial Clell Line-Derived Neurotrophic Factor, NBMI, suvorxant, zolpidem, TPI 287, davunetide, pimavanserin, Levodopa, Carbidopa-levidopa, pramipexole, ropinirole, rotigotine, apomorphine, selegiline, rasagiline, entacapone, tolcapone, amantadine, trihexyphenidyl, BIIB054 (cinepanemab), BIIB094, BIIB118, ABBV-0805, zonisamide, deep brain stimulation, brain-derived neurotrophic factor, stem-cell

transplant, Niacin, brain stem stimulation, nicotine, nabilone, PF-06649751, DNL201, LRRK2 inhibitors, CK1 inhibitors, isradipine, CLR4001, IRX4204, Yohimbine, coenzyme Q10, OXB-102, duloxetine, pioglitazone, preladenant, or any combination thereof can be selected as an additional therapy.

[00465] For example, for treating epilepsy, any of Brivaracetam (briviact), cannabidiol (epidiolex), carbamazepine (carbatrol, Tegretol), cenobamate (xcopri), diazepam (valium), lorazepam (Ativan), clonazepam (klonopin), eslicarbazepine (aptiom), ethosuximide (zarontin), felbamate (felbatol), fenfluramine (fintepla), lacosamide (VIMPAT), lamotrigine (Lamictal), levetiracetam (Keppra), oxcarbazepine (oxtellar xr, Trileptal), perampanel (fycompa), phenobarbital, phenytoin (dilantin), pregabalin (lyrica), tiagabine (gabitril), topiramate (topamax), valproate (depakene, depakote), zonisamide (zonegran), or any combination thereof can be selected an additional therapy.

[00466] For example for treating Huntington's Disease, any of Tetrabenazine, deutetrabenazine, physical therapy, risperidone, haloperidol, chlorpromazine, clonazepam, diazepam, benzodiazepines, selective serotonin reuptake inhibitors. quetiapine, carbatrol, valproate, lamotrigine, pridopidine, delta-9-tetrahydrocannabinol, cannabidiol, stem-cell therapy, ISIS-443139, nilotinib, resveratrol, neflamapimod, fenofibrate, creatine, RO7234292, SAGE-718, WVE-120102, WVE-120101, dimebon, minocycline, deep brain stimulation, ursodiol, coenzyme Q10, OMS643762, VX15/2503, PF-02545920, BN82451B, SEN0014196, olanzapine, tiapridal (tiapride), or any combination thereof, can be selected as an additional therapy.

[00467] For example, for treating brain trauma, any of anticoagulants, antidepressants, muscle relaxants, stimulants, anticonvulsants, anti-anxiety medication, erythropoietin, hyperbaric treatment, rehabilitation therapies (*e.g.*, physical, occupational, speech, psychological, or vocational counseling), or any combination thereof can be selected as an additional therapy.

[00468] For example, for treating spinal cord injury, any of AXER-204, glyburide, 5-hydroxytryptophan (5-HTP), L-3,4-dihydroxyphenylalanine (L-DOPA), or rehabilitation therapies (*e.g.*, physical therapy, occupational therapy, recreational therapy, use of assistive devices, improved strategies for exercise and healthy diets), or any combination thereof can be selected as an additional therapy.

[00469] For example, for treating corticobasal degeneration, any of TPI-287, lithium, occupational, physical, and speech therapy, or any combination thereof can be selected as an additional therapy.

[00470] For example, for treating neuropathies, such as a chemotherapy induced neuropathy, any of gabapentin, pregabalin, lamotrigine, carbamazepine, duloxetine, gabapentinoids, tricyclic

antidepressants, serotonin-norepinephrine reuptake inhibitors, opioids, neurotoxin, dextromethorphan, nicotinamide riboside, auto-antibodies targeting neuronal antigens (TS-HDS and FGFR3), or any combination thereof can be selected as an additional therapy.

[00471] For example, for treating spinal muscular atrophy, any of nusinersen (SPINRAZA), onasemnogene abeparvovec-xioi (ZOLGENSMA), risdiplam (EVRYSDI), or a combination thereof can be selectd as an additional therapy.

[00472] For example, for treating spinocerebellar ataxia, any of amantadine, armodafinil, baclofen, buspirone, carbamazepine, citalopram, clonazepam, desvenlafaxine, diazepam, duloxetine, escitalopram, flunarizine, fluoxetine, fluvoxamine, gabapentin, isoniazid, levetiracetam, levodopa, memantine, modafinil, ondansetron, paroxetine, pramipexole, primidone, riluzole, ropinirole, sertraline, tizanidine, topiramate, trihexyphenidyl, valproic acid, venlafaxine, BHV-4157, or a combination thereof can be selected as an additional therapy.

[00473] For example, for treating Niemann-Pick disease type C, any of anti-seizure medications, speech therapy, physical therapy, occupational therapy, Adrabetadex, Arimoclomol, N-Acetyl-L-Leucine, or any combination thereof can be selected as an additional therapy.

[00474] For example, for treating Charcot-Marie-Tooth Disease (CMT), any of physical and occupational therapies, orthopedic surgery, orthopedic devices, PXT3003, or any combination thereof can be selected as an additional therapy.

[00475] For example, for treating Mucopolysaccharidosis type II (MPSIIA), any of enzyme replacement therapy: idursulfase (Elaprase), surgical intervention (tonsillectomy and/or adenoidectomy), RGX-121 gene therapy, adalimumab, MT2013-31, or any combination thereof can be selected as an additional therapy.

[00476] For example, for treating Mucolipidosis IV, any of physical, occupational, and speech therapies, contact lenses and artificial tears, genetic counseling, or any combination thereof can be selected as an additional therapy.

[00477] For example, for treating GM1 gangliosidosis, any of anticonvulsants, physical and occupational therapies, galactosidase, gene delivery of galactosidase, LYS-GM101 gene therapy, or any combination thereof can be selected as an additional therapy.

[00478] For example, for treating Sporadic inclusion body myositis (sIBM), any of physical and occupational therapies, use of devices such as braces, walkers, wheelchairs, immunosuppressants, BYM338, or any combination thereof can be selected as an additional therapy.

[00479] For example, for treating Henoch-Schonlein purpura (HSP), any of corticosteroids, colchicine, dapsone, azathioprine, or any combination thereof can be selected as an additional therapy.

[00480] For example, for treating Gaucher's disease, any of enzyme replacement therapy, substrate reduction therapy, N-acetylcysteine, GZ/SAR402671, cerezyme, or any combination thereof can be selected as an additional therapy.

[00481] In various embodiments, the disclosed oligonucleotide and the one or more additional therapies can be conjugated to one another and provided in a conjugated form. Further description regarding conjugates involving the disclosed oligonucleotide is described below. When administering a combination therapy to a patient in need of such administration, the therapeutic agents in the combination, or a pharmaceutical composition or compositions comprising the therapeutic agents, may be administered in any order such as, for example, sequentially, concurrently, together, simultaneously and the like. In various embodiments, the disclosed oligonucleotide and one or more additional therapies are provided concurrently. In various embodiments, the disclosed oligonucleotide and one or more additional therapies are provided simultaneously. In various embodiments, the disclosed oligonucleotide and one or more additional therapies are provided sequentially.

Conjugates

[00482] In certain embodiments, provided herein are oligomeric compounds, which comprise an oligonucleotide (*e.g.*, AON) and optionally one or more conjugate groups and/or terminal groups. Conjugate groups include one or more conjugate moiety and a conjugate linker which links the conjugate moiety to the oligonucleotide. Conjugate groups may be attached to either or both ends of an oligonucleotide and/or at any internal position. In certain embodiments, conjugate groups are attached to the 2'-position of a nucleoside of a modified oligonucleotide. In certain embodiments, conjugate groups that are attached to either or both ends of an oligonucleotide are terminal groups. In certain such embodiments, conjugate groups or terminal groups are attached at the 3' and/or 5'-end of oligonucleotides. In certain such embodiments, conjugate groups (or terminal groups) are attached at the 3'-end of oligonucleotides. In certain embodiments, conjugate groups are attached near the 3'-end of oligonucleotides. In certain embodiments, conjugate groups (or terminal groups) are attached at the 5'-end of oligonucleotides. In certain embodiments, conjugate groups are attached near the 5'-end of oligonucleotides.

[00483] Examples of terminal groups include but are not limited to conjugate groups, capping groups, phosphate moieties, protecting groups, modified or unmodified nucleosides, and two or more nucleosides that are independently modified or unmodified.

Conjugate Groups

[00484] In certain embodiments, an AON is covalently attached to one or more conjugate groups. In certain embodiments, conjugate groups modify one or more properties of the attached oligonucleotide, including but not limited to pharmacodynamics, pharmacokinetics, stability, binding, absorption, tissue distribution, cellular distribution, cellular uptake, charge, and clearance. In particular embodiments, conjugate groups modify the circulation time (*e.g.*, increase) of the oligonucleotides in the bloodstream such that increased concentrations of the oligonucleotides are delivered to the brain. In particular embodiments, conjugate groups modify the residence time (*e.g.*, increase residence time) of the oligonucleotides in a target organ (*e.g.*, brain) such that increased residence time of the oligonucleotides improves their performance (*e.g.*, efficacy). In particular embodiments, conjugate groups increase the delivery of the oligonucleotide to the brain through the blood brain barrier and/or brain parenchyma (*e.g.*, through receptor mediated transcytosis). In particular embodiments, conjugate groups enable the oligonucleotide to target a specific organ (*e.g.*, the brain). In certain embodiments, conjugate groups impart a new property on the attached oligonucleotide, e.g., fluorophores or reporter groups that enable detection of the oligonucleotide. Certain conjugate groups and conjugate moieties have been described previously, for example: cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86, 6553-6556), cholic acid (Manoharan et al., Bioorg. Med. Chem. Lett., 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., Ann. NY. Acad. Sci., 1992, 660, 306-309; Manoharan et al., Bioorg. Med. Chem. Lett., 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., Nucl. Acids Res., 1992, 20, 533-538), an aliphatic chain, e.g., do-decan-diol or undecyl residues (Saison-Behmoaras et al., EMBO J, 1991, 10, 1111-1118; Kabanov et al., FEBS Lett., 1990, 259, 327-330; Svinarchuk et al., Biochimie, 1993, 75, 49-54), a phospholipid, *e.g.*, di-hexadecyl-rac -glycerol or triethyl -ammonium l,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654; Shea et al., Nucl. Acids Res., 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., Nucleosides & Nucleotides, 1995, 14, 969-973), or adamantane acetic acid a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264, 229-237), an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., J. Pharmacol. Exp. Ther., 1996, 277, 923-937), a tocopherol group (Nishina *et al.*, Molecular Therapy Nucleic Acids, 2015, 4, e220; and Nishina *et al.*, Molecular Therapy, 2008, 16, 734-740), or a GalNAc cluster (*e.g.*, WO2014/179620).

Conjugate Moieties

[00485] Conjugate moieties include, without limitation, intercalators, reporter molecules, polyamines, polyamides, peptides, carbohydrates, vitamin moieties, polyethylene glycols,

thioethers, polyethers, cholesterols, thiocholesterols, cholic acid moieties, folate, lipids, phospholipids, biotin, phenazine, phenanthridine, anthraquinone, adamantane, acridine, fluoresceins, rhodamines, coumarins, bile acids, phenylbutyrate, fluorophores, and dyes. In particular embodiments, conjugate moieties are selected from a peptide, a lipid, N-acetylgalactosamine (GalNAc), cholesterol, vitamin E, lipoic acid, panthothenic acid, polyethylene glycol, an antibody (*e.g.*, an antibody for crossing the blood brain barrier such as anti-transferrin receptor antibody), or a cell-penetrating peptide (*e.g.*, transactivator of transcription (TAT) and penetratine).

[00486] In certain embodiments, a conjugate moiety comprises an active drug substance, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fen-bufen, ketoprofen, (*S*)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, fingolimod, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethacin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic.

Conjugate Linkers

[00487] Conjugate moieties are attached to an AON through conjugate linkers. In certain oligomeric compounds, the conjugate linker is a single chemical bond (*e.g.*, the conjugate moiety is attached directly to an oligonucleotide through a single bond). In certain embodiments, the conjugate linker comprises a chain structure, an oligomer of repeating units such as ethylene glycol, nucleosides, or amino acid units.

[00488] In certain embodiments, a conjugate linker comprises one or more groups selected from alkyl, amino, oxo, amide, disulfide, polyethylene glycol, ether, thioether, and hydroxylamino. In certain such embodiments, the conjugate linker comprises groups selected from alkyl, amino, oxo, amide and ether groups. In certain embodiments, the conjugate linker comprises groups selected from alkyl and amide groups. In certain embodiments, the conjugate linker comprises groups selected from alkyl and ether groups. In certain embodiments, the conjugate linker comprises at least one phosphorus moiety. In certain embodiments, the conjugate linker comprises at least one phosphate group. In certain embodiments, the conjugate linker includes at least one neutral linking group.

[00489] In certain embodiments, conjugate linkers, including the conjugate linkers described above, are bifunctional linking moieties, *e.g.*, those known in the art to be useful for attaching conjugate groups to parent compounds, such as the oligonucleotides provided herein. In general, a bifunctional linking moiety comprises at least two functional groups. One of the functional groups is selected to bind to a particular site on a parent compound and the other is selected to bind to a conjugate group. Examples of functional groups used in a bifunctional linking moiety include but

are not limited to electrophiles for reacting with nucleophilic groups and nucleophiles for reacting with electrophilic groups. In certain embodiments, bifunctional linking moieties comprise one or more groups selected from amino, hydroxyl, carboxylic acid, thiol, alkyl, alkenyl, and alkynyl.

[00490] Examples of conjugate linkers include but are not limited to pyrrolidine, 8-amino-3,6-dioxaoctanoic acid (ADO), succinimidyl 4-(N-maleimidomethyl) cyclohexane- l-carboxylate (SMCC) and 6-aminohexanoic acid (AHEX or AHA). Other conjugate linkers include but are not limited to substituted or unsubstituted C_1-C_{10} alkyl, substituted or unsubstituted C_2-C_{10} alkenyl or substituted or unsubstituted C_2-C_{10} alkynyl, wherein a nonlimiting list of preferred substituent groups includes hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro, thiol, thioalkoxy, halogen, alkyl, aryl, alkenyl and alkynyl.

[00491] In certain embodiments, conjugate linkers comprise 1-10 linker-nucleosides. In certain embodiments, conjugate linkers comprise 2-5 linker-nucleosides. In certain embodiments, conjugate linkers comprise 3 linker-nucleosides.

[00492] In certain embodiments, such linker-nucleosides are modified nucleosides. In certain embodiments such linker-nucleosides comprise a modified sugar moiety. In certain embodiments, linker-nucleosides are unmodified. In certain embodiments, linker-nucleosides comprise an optionally protected heterocyclic base selected from a purine, substituted purine, pyrimidine or substituted pyrimidine. In certain embodiments, a cleavable moiety is a nucleoside selected from uracil, thymine, cytosine, 4-N-benzoylcytosine, 5-methylcytosine, 4-N -benzoyl-5 -methyl cytosine, adenine, 6-N-benzoyladenine, guanine and 2-N-isobutyrylguanine. It is typically desirable for linker-nucleosides to be cleaved from the oligomeric compound after it reaches a target tissue. Accordingly, linker-nucleosides are typically linked to one another and to the remainder of the oligomeric compound through cleavable bonds. In certain embodiments, such cleavable bonds are phosphodiester bonds.

[00493] Herein, linker-nucleosides are not considered to be part of the oligonucleotide. Accordingly, in embodiments in which an oligomeric compound comprises an oligonucleotide consisting of a specified number or range of linked nucleosides and/or a specified percent complementarity to a reference nucleic acid and the oligomeric compound also comprises a conjugate group comprising a conjugate linker comprising linker-nucleosides, those linker-nucleosides are not counted toward the length of the oligonucleotide and are not used in determining the percent complementarity of the oligonucleotide for the reference nucleic acid.

[00494] In certain embodiments, it is desirable for a conjugate group to be cleaved from the AON. For example, in certain circumstances oligomeric compounds comprising a particular conjugate moiety are better taken up by a particular cell type, but once the oligomeric compound

has been taken up, it is desirable that the conjugate group be cleaved to release the unconjugated or parent oligonucleotide. Thus, certain conjugate linkers may comprise one or more cleavable moieties. In certain embodiments, a cleavable moiety is a cleavable bond. In certain embodiments, a cleavable moiety is a group of atoms comprising at least one cleavable bond. In certain embodiments, a cleavable moiety comprises a group of atoms having one, two, three, four, or more than four cleavable bonds. In certain embodiments, a cleavable moiety is selectively cleaved inside a cell or subcellular compartment, such as a lysosome. In certain embodiments, a cleavable moiety is selectively cleaved by endogenous enzymes, such as nucleases.

[00495] In certain embodiments, a cleavable bond is selected from among: an amide, an ester, an ether, one or both esters of a phosphodiester, a phosphate ester, a carbamate, or a disulfide. In certain embodiments, a cleavable bond is one or both of the esters of a phosphodiester. In certain embodiments, a cleavable moiety comprises a phosphate or phosphodiester. In certain embodiments, the cleavable moiety is a phosphate linkage between an oligonucleotide and a conjugate moiety or conjugate group.

[00496] In certain embodiments, a cleavable moiety comprises or consists of one or more linker-nucleosides. In certain such embodiments, the one or more linker-nucleosides are linked to one another and/or to the remainder of the oligomeric compound through cleavable bonds. In certain embodiments, such cleavable bonds are unmodified phosphodiester bonds. In certain embodiments, a cleavable moiety is 2'-deoxy nucleoside that is attached to either the 3' or 5'-terminal nucleoside of an oligonucleotide by a phosphate internucleoside linkage and covalently attached to the remainder of the conjugate linker or conjugate moiety by a phosphate or phosphorothioate linkage. In certain such embodiments, the cleavable moiety is 2'-deoxy adenosine.

Terminal Groups

[00497] In certain embodiments, oligomeric compounds comprise one or more terminal groups. In certain such embodiments, oligomeric compounds comprise a stabilized 5'-phosphate. Stabilized 5'-phosphates include, but are not limited to 5'-phosphonates, including, but not limited to 5'-vinylphosphonates. In certain embodiments, terminal groups comprise one or more abasic nucleosides and/or inverted nucleosides. In certain embodiments, terminal groups comprise one or more 2'-linked nucleosides. In certain such embodiments, the 2'-linked nucleoside is an abasic nucleoside.

Diagnostic Methods

[00498] The disclosure also provides a method of diagnosing a patient with a neurological disease that relies upon detecting levels of target expression signal in one or more biological samples of a patient. As used herein, the term "target expression signal" can refer to any indication of target gene expression, or gene or gene product activity (e.g., target gene expression, or gene or gene product activity for any one of PPM1A, ATXN2, SOD1, or MAPT). Gene products include RNA (*e.g.*, mRNA), peptides, and proteins. Indices of gene expression that can be assessed include, but are not limited to, gene or chromatin state, gene interaction with cellular components that regulate gene expression, gene product expression levels (*e.g.*, RNA expression levels, protein expression levels), or interaction of RNA or protein with transcriptional, translational, or post-translational processing machinery. Indices of gene product activity include, but are not limited to, assessment of signaling activity (*e.g.*, assessment of protein signaling activation or phosphorylation).

[00499] Detection of target expression signal may be accomplished through *in vivo*, *in vitro*, or *ex vivo* methods. In a preferred embodiment, methods of the disclosure may be carried out *in vitro*. Methods of detecting may involve detection in blood, serum, fecal matter, tissue, cerebrospinal fluid, spinal fluid, extracellular vesicles (for example, CSF exosomes), or cells of a patient. Detection may be achieved by measuring target expression signal in whole tissue, tissue explants, cell cultures, dissociated cells, cell extract, extracellular vesicles (for example, CSF exosomes), or body fluids, including blood, spinal fluid, cerebrospinal fluid, urine, lymphatic fluid, or serum. Biochemical assays that examine protein or RNA expression may also be used for detection. For instance, one may evaluate levels of a protein indicative of a neurological disease, in dissociated cells or non-dissociated tissue via immunocytochemical, immunohistochemical, Western blotting, or Northern blotting methods, or methods useful for evaluating RNA levels such as quantitative or semi-quantitative polymerase chain (*e.g.*, digital PCR (DigitalPCR, dPCR, or ddPCR), qPCR etc.) reaction.

[00500] One may also evaluate the presence or level of expression of useful biomarkers (*e.g.*, neurofilament light (NEFL), neurofilament heavy (NEFH), SOD1/SOD1 transcripts, TDP-43 or p75 extracellular domain ($p75^{ECD}$)) found in spinal cord fluid, cerebrospinal fluid, plasma, extracellular vesicles (for example, exosome-like cerebrospinal fluid extracellular vesicles ("CSF exosomes"), such as those described in Welton *et al.*, (2017) "Cerebrospinal fluid extracellular vesicle enrichment for protein biomarker discovery in neurological disease; multiple sclerosis" *J Extracell Vesicles.*, 6(1):1-10; and Street *et al.*, (2012) "Identification and proteomic profiling of exosomes in human cerebrospinal fluid" *J Transl. Med.*, 10:5), urine, fecal matter, lymphatic fluid, blood, plasma, or serum to evaluate disease state. Additional measurements may include

strength duration time constant (SDTC), short interval cortical inhibition (SICI), dynamometry, accurate test of limb isometric strength (ATLIS), compound muscle action potential (CMAP), and ALSFRS-R. In certain embodiments, urinary neurotrophin receptor p75 extracellular domain ($p75^{ECD}$) is a disease progression and prognostic biomarker in amyotrophic lateral sclerosis (ALS). Phosphorylated neurofilament heavy chain (pNFH) in cerebrospinal fluid (CSF) predict disease status and survival in amyotrophic lateral sclerosis (ALS) patients. CSF pNFH can serve as a prognostic biomarker for clinical trials, which will increase the likelihood of successfully developing a treatment for ALS.

[00501] In some embodiments, diagnosing a patient with a neurological disease such as Alzheimer's disease can involve evaluating mental performance of the patient. Evaluation of mental performance can involve a Mini-Mental State Examination (MMSE). Additional examples for measuring mental performance include the Functional Assessment Staging Test (FAST), the Motor Screening Task, Paired Associates Learning, Spatial Working Memory, Reaction time, Rapid Visual Information Processing, Delayed Matching to Sample, and Pattern Recognition Memory In some embodiments, diagnosing a patient with a neurological disease such as Parkinson's disease involves implementing the Unified Parkinson's Disease Rating Scale (UPDRS) as the performance measure. Other measures for quantifying aspects of functional performance not measured by the UPDRS can include the Berg Balance Scale (BBS), Forward Functional Reach Test (FFR), Backward Functional Reach Test (BFR), Timed "Up & Go" Test (TUG), and gait speed.

Modifications in General

[00502] While certain compounds, compositions and methods described herein have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds described herein and are not intended to limit the same. Each of the references, GenBank accession numbers, and the like recited in the present application is incorporated herein by reference in its entirety.

[00503] Although the sequence listing accompanying this filing identifies each sequence as either "RNA" or "DNA" as required, in reality, those sequences may be modified with any combination of chemical modifications. Accordingly, nucleic acid sequences provided herein, including, but not limited to those in the sequence listing, are intended to encompass nucleic acids containing any combination of natural or modified RNA and/or DNA, including, but not limited to such nucleic acids having modified nucleobases. By way of further example and without limitation, an oligomeric compound having the nucleobase sequence "ATCGATCG" encompasses any

oligomeric compounds having such nucleobase sequence, whether modified or unmodified, including, but not limited to, oligomeric compounds having other modified nucleobases, such as "AT^{m}CGAUCG," wherein ^{m}C indicates a cytosine base comprising a methyl group at the 5-position.

[00504] Certain compounds described herein (*e.g.*, modified oligonucleotides) have one or more asymmetric center and thus give rise to enantiomers, diastereomers, and other stereoisomeric configurations that may be defined, in terms of absolute stereochemistry, as (R) or (S), as α or β such as for sugar anomers, or as (D) or (L), such as for amino acids, etc. Compounds provided herein that are drawn or described as having certain stereoisomeric configurations include only the indicated compounds. Compounds provided herein that are drawn or described with undefined stereochemistry included all such possible isomers, including their stereorandom and optically pure forms, unless specified otherwise. Likewise, all tautomeric forms of the compounds herein are also included unless otherwise indicated. Unless otherwise indicated, compounds described herein are intended to include corresponding salt forms.

[00505] The compounds described herein include variations in which one or more atoms are replaced with a non-radioactive isotope or radioactive isotope of the indicated element. For example, compounds herein that comprise hydrogen atoms encompass all possible deuterium substitutions for each of the ^{1}H hydrogen atoms. Isotopic substitutions encompassed by the compounds herein include but are not limited to: ^{2}H or ^{3}H in place of ^{1}H, ^{13}C or ^{14}C in place of ^{12}C, ^{15}N in place of ^{14}N, ^{17}O or ^{18}O in place of ^{16}O, and ^{33}S, ^{34}S, ^{35}S, or ^{36}S in place of ^{32}S. In certain embodiments, non-radioactive isotopic substitutions may impart new properties on the oligomeric compound that are beneficial for use as a therapeutic or research tool.

EXAMPLES

[00506] The disclosure is further illustrated by the following examples. The examples are provided for illustrative purposes only, and are not to be construed as limiting the scope or content of the disclosure in any way.

Example 1: Design and Selection of PPM1A Gapmer Antisense Oligonucleotides

[00507] PPM1A antisense oligonucleotides were evaluated in iPSC derived human motor neurons (hMN) purchased from FujiFilm Cellular Dynamics (Catalog #: C1050). The cells were seeded in 96-well plates at a density of 10,000 cells/ well. Antisense oligonucleotide (AON) to PPM1A were transfected with Endoporter (Gene Tools, Philomath, OR, USA) to decrease

expression of *PPM1A* transcript. Vehicle control consisted of motor neuron treatment with Endoporter alone.

[00508] To evaluate PPM1A AON ability to knock down PPM1A mRNA transcripts, antisense oligonucleotides to PPM1A were incubated with Endoporter in media before addition to the cells. After 72 hours, cells lysate was prepared and collected from the 96-well plates for RT-qPCR. From the cell lysates, cDNA was generated, and multiplexed RT-qPCR assay performed with Taqman probes for PPM1A and reference GAPDH quantification.

[00509] Using the Applied Biosystems® PCR Thermal Cycler (SimpliAmp), cDNA was prepared directly from the cell lysates by performing one cycle of reverse transcription at 37°C for 30 minutes, followed by heat inactivation of the RT enzyme at 95°C for 5 minutes.

[00510] Transcript levels were detected by RT-qPCR using Taqman. Specifically, RT-qPCR was performed for detecting GAPDH using Thermofisher TaqMan Gene Expression Assay Hs_03929097_g1. RT-qPCR was performed for detecting PPM1A using Thermofisher TaqMan Gene Expression Assay Hs06637123_g1.

[00511] RT-qPCR was performed on Applied Biosystems® QuantStudio 6 Flex Real-Time PCR System. One cycle of uracil-N-glycosylase (UNG) incubation was performed at a temperature of 50°C for 2 min. One cycle of polymerase activation/initial denaturation was performed at a temperature of 95°C for 20 seconds. Forty cycles of amplification were performed at a temperature of 95°C for 1 second followed by 60°C for 20 seconds.

[00512] PPM1A signal cycle threshold (Ct) was normalized to GAPDH (ΔCt). To visualize the quantitative changes (*e.g.*, ratio of PPM1A transcript decrease), the normalized PPM1A signal was further normalized to the mean vehicle signal (treated with Endoporter alone, ΔΔCt). Relative quantity (RQ) of transcript level was calculated using the equation $RQ=2^{-\Delta\Delta Ct}$ and is used to describe the treatment condition comparison to normal, healthy levels.

[00513] PPM1A AON knock-down of PPM1A transcripts were presented as mean relative quantity (RQ_{mean}) of the technical triplicates, compared to mean endogenous PPM1A expression ($RQ_{mean}=1$).

Table 5A: PPM1A AON sequences (including PPM1A gapmer sequences and PPM1A gapmer sequences with one or two spacers)

SEQ ID NO:	AON sequence 5'-3'*	Spacer Position	Internucleoside Linkage Pattern ("s" indicates phosphorothioate, "o" indicates phosphodiester)	Gapmer structure	500 nM Dose Relative Quantity	200 nM Dose Relative Quantity
148	CCACTTGGCAAACCGATCAC	N/A	sssssssssssssssss	eeeee-d10-eeeee	0.171	0.287
148	CCACTTGGCAAACCGATCAC	N/A	sosossssssssssosos	eeeee-d10-eeeee	0.119	0.269
301692	CCSCTTGGCAAACCGATCAC	3	sssssssssssssssss	eeeee-d10-eeeee	0.367	0.751
301693	CCACSTGGCAAACCGATCAC	5	sssssssssssssssss	eeeee-d10-eeeee	0.380	0.580
301694	CCACTTGGCAAACCGSTCAC	16	sssssssssssssssss	eeeee-d10-eeeee	0.246	0.375
301695	CCACTTGSCAAACCGATCAC	8	sssssssssssssssss	eeeee-d10-eeeee	0.409	0.635
301696	CCACTTGGCAAASCGATCAC	13	sssssssssssssssss	eeeee-d10-eeeee	0.342	0.515
301697	CCACTTGGCASACCGATCAC	11	sssssssssssssssss	eeeee-d10-eeeee	0.319	0.474
301698	CCACTTGGCAAACCGATCSC	19	sssssssssssssssss	eeeee-d10-eeeee	0.167	0.245
301699	CCACTTGGCASACCGATCSC	11 and 19	sssssssssssssssss	eeeee-d10-eeeee	0.211	0.441
301700	CCACTTSGCAAACCGATCAC	7	sssssssssssssssss	eeeee-d10-eeeee	0.164	0.292
301701	SCACTTGGCAAACCGATCAC	1	sssssssssssssssss	eeeee-d10-eeeee	0.215	0.444
301702	CSACTTGGCAAACCGATCAC	2	sssssssssssssssss	eeeee-d10-eeeee	0.160	0.384
301703	CCASTTGGCAAACCGATCAC	4	sssssssssssssssss	eeeee-d10-eeeee	0.189	0.365
301704	CCACTSGGCAAACCGATCAC	6	sssssssssssssssss	eeeee-d10-eeeee	0.101	0.254
301705	CCACTTGGSAAACCGATCAC	9	sssssssssssssssss	eeeee-d10-eeeee	0.244	0.433
301706	CCACTTGGCSAACCGATCAC	10	sssssssssssssssss	eeeee-d10-eeeee	0.262	0.377
301707	CCACTTGGCAASCCGATCAC	12	sssssssssssssssss	eeeee-d10-eeeee	0.143	0.288
301708	CCACTTGGCAAACSGATCAC	14	sssssssssssssssss	eeeee-d10-eeeee	0.091	0.228
301709	CCACTTGGCAAACCSATCAC	15	sssssssssssssssss	eeeee-d10-eeeee	0.126	0.275
301710	CCACTTGGCAAACCGASCAC	17	sssssssssssssssss	eeeee-d10-eeeee	0.063	0.185
301711	CCACTTGGCAAACCGATSAC	18	sssssssssssssssss	eeeee-d10-eeeee	0.110	0.187

301712	CCACTTGGCAAACCGATCAS	20	sssssssssssssssss	eeeee-d10-eeeee	0.041	0.117
186	GCCCATCATACACAGCAAAG	N/A	sssssssssssssssss	eeeee-d10-eeeee	0.024	0.054
301713	GCSCATCATACACAGCAAAG	3	sssssssssssssssss	eeeee-d10-eeeee	0.350	0.491
301714	GCCCSTCATACACAGCAAAG	5	sssssssssssssssss	eeeee-d10-eeeee	N/A	N/A
301715	GCCCATCATACACAGSAAAG	16	sssssssssssssssss	eeeee-d10-eeeee	0.101	0.195
301716	GCCCATCSTACACAGCAAAG	8	sssssssssssssssss	eeeee-d10-eeeee	0.190	0.472
301717	GCCCATCATACASAGCAAAG	13	sssssssssssssssss	eeeee-d10-eeeee	0.381	0.486
301718	GCCCATCATASACAGCAAAG	11	sssssssssssssssss	eeeee-d10-eeeee	0.223	0.461
301719	GCCCATCATACACAGCAASG	19	sssssssssssssssss	eeeee-d10-eeeee	0.091	0.168
301720	GCCCATCSTACACAGSAAAG	8 and 16	sssssssssssssssss	eeeee-d10-eeeee	0.720	0.999
301721	GCCCATCATASACAGCAASG	11 and 19	sssssssssssssssss	eeeee-d10-eeeee	0.330	0.565
301722	GCCCATSATACACAGCAAAG	7	sssssssssssssssss	eeeee-d10-eeeee	0.083	0.214
301598	AGTCCACTTGGCAAACCGATCAC	N/A	sssssssssssssssssssss	eeeeee-d11-eeeeee	0.077	0.219
301595	TCCACTTGGCAAACCGATCACAG	N/A	sssssssssssssssssssss	eeeeee-d11-eeeeee	0.045	0.114
301723	GTCCACTTGGCAAACCGATCACA	N/A	sssssssssssssssssssss	eeeeee-d11-eeeeee	0.066	0.158
301724	CCACTTGGCAAACCGATCACAGC	N/A	sssssssssssssssssssss	eeeeee-d11-eeeeee	0.030	0.101
301725	AGTCCACSTGGCAAASCGATCAC	8 and 16	sssssssssssssssssssss	eeeeee-d11-eeeeee	0.418	0.555
301726	TCCACTTSGCAAACCSATCACAG	8 and 16	sssssssssssssssssssss	eeeeee-d11-eeeeee	0.486	0.651
301727	GTCCACTSGGCAAACSGATCACA	8 and 16	sssssssssssssssssssss	eeeeee-d11-eeeeee	0.138	0.298
301728	CCACTTGSCAAACCGSTCACAGC	8 and 16	sssssssssssssssssssss	eeeeee-d11-eeeeee	0.563	0.700

* Unless otherwise noted, for the sequences described in Table 5, the gapmer structure is denoted by "e" = a ribonucleoside and "d" = a deoxyribonucleoside. Every ribonucleoside is a 2'-MOE modified ribonucleoside. Each "C" cytosine that is a ribonucleoside is a 5-methylcytosine (5-MeC) (and therefore is a 5-MeC, 2'-MOE modified ribonucleoside). Spacer, as indicated by S, is not a nucleoside. S is a spacer represented by Formula (Iia').

Table 5B: PPM1A AON sequences (including PPM1A gapmer sequences and PPM1A gapmer sequences with one or two spacers)

SEQ ID NO:	AON sequence 5'-3'*	Spacer Position	Internucleoside Linkage Pattern	Gapmer structure	500 nM Dose	200 nM Dose	50 nM Dose	20 nM Dose	5 nM Dose

			("s" indicates phosphorothioate, "o" indicates phosphodiester)		Relative Quantity	Relative Quantity	Relative Quantity	Relative Quantity	Relative Quantity
301692	CCSCTTGGCAAACCGATCAC	3	sosossssssssssosos	eeeee-d10-eeeee	0.364	0.444	0.688	0.764	1.070
301704	CCACTSGGCAAACCGATCAC	6	sosossssssssssosos	eeeee-d10-eeeee	0.095	0.249	0.633	1.168	N/A
301694	CCACTTGGCAAACCGSTCAC	16	sosossssssssssosos	eeeee-d10-eeeee	0.193	0.176	0.356	0.546	0.940
301695	CCACTTGSCAAACCGATCAC	8	sosossssssssssosos	eeeee-d10-eeeee	0.292	0.561	0.672	1.063	1.010
301696	CCACTTGGCAAASCGATCAC	13	sosossssssssssosos	eeeee-d10-eeeee	0.355	0.352	0.754	0.852	0.917
301697	CCACTTGGCASACCGATCAC	11	sosossssssssssosos	eeeee-d10-eeeee	0.153	0.325	0.517	0.736	0.745
301698	CCACTTGGCAAACCGATCSC	19	sosossssssssssosos	eeeee-d10-eeeee	0.612	0.933	0.950	0.852	0.746
301742	CCACTTGSCAAACCGSTCAC	8 and 16	sssssssssssssssss	eeeee-d10-eeeee	0.835	0.911	1.108	1.132	1.116

* Unless otherwise noted, for the sequences described in Table 5, the gapmer structure is denoted by "e" = a ribonucleoside and "d" = a deoxyribonucleoside. Every ribonucleoside is a 2'-MOE modified ribonucleoside. Each "C" cytosine that is a ribonucleoside is a 5-methylcytosine (5-MeC) (and therefore is a 5-MeC, 2'-MOE modified ribonucleoside). Spacer, as indicated by S, is not a nucleoside. S is a spacer represented by Formula (Iia').

Example 2: Design and Selection of ATXN2 Antisense Oligonucleotides

[00514] ATXN2 antisense oligonucleotides were evaluated in iPSC derived human motor neurons (hMN) purchased from FujiFilm Cellular Dynamics (Catalog #: C1050). The cells were seeded in 96-well plates at a density of 10,000 cells/ well. Antisense oligonucleotide (AON) to ATXN2 were transfected with Endoporter (Gene Tools, Philomath, OR, USA) to decrease expression of *ATXN2* transcript. Vehicle control consisted of motor neuron treatment with Endoporter alone.

[00515] To evaluate ATXN2 AON ability to knock down ATXN2 mRNA transcripts, antisense oligonucleotides to ATXN2 were incubated with Endoporter in media before addition to the cells. After 72 hours, cells lysate was prepared and collected from the 96-well plates for RT-qPCR. From the cell lysates, cDNA was generated, and multiplexed RT-qPCR assay performed with Taqman probes for ATXN2 and reference GAPDH quantification.

[00516] Using the Applied Biosystems® PCR Thermal Cycler (SimpliAmp), cDNA was prepared directly from the cell lysates by performing one cycle of reverse transcription at 37°C for 30 minutes, followed by heat inactivation of the RT enzyme at 95°C for 5 minutes.

[00517] Transcript levels were detected by RT-qPCR using Taqman. Specifically, RT-qPCR was performed for detecting GAPDH using Thermofisher TaqMan Gene Expression Assay Hs_03929097_g1. RT-qPCR was performed for detecting ATXN2 using Thermofisher TaqMan Gene Expression Assay Hs00268077_m1.

[00518] RT-qPCR was performed on Applied Biosystems® QuantStudio 6 Flex Real-Time PCR System. One cycle of UNG incubation was performed at a temperature of 50°C for 2 min. One cycle of polymerase activation/initial denaturation was performed at a temperature of 95°C for 20 seconds. Forty cycles of amplification were performed at a temperature of 95°C for 1 second followed by 60°C for 20 seconds.

[00519] ATXN2 signal cycle threshold (Ct) was normalized to GAPDH (ΔCt). To visualize the quantitative changes (*e.g.*, ratio of ATXN2 transcript decrease), the normalized ATXN2 signal was further normalized to the mean vehicle signal (treated with Endoporter alone, ΔΔCt). Relative quantity (RQ) of transcript level was calculated using the equation $RQ=2^{-\Delta\Delta Ct}$ and is used to describe the treatment condition comparison to normal, healthy levels.

[00520] ATXN2 AON knock-down of ATXN2 transcripts were presented as mean relative quantity (RQ_{mean}) of the technical triplicates, compared to mean endogenous ATXN2 expression ($RQ_{mean}=1$).

Table 6: ATXN2 AON sequences (including ATXN2 gapmer sequences and ATXN2 gapmer sequences with one or two spacers)

SEQ ID NO:	AON sequence 5'-3'*	Spacer Position	Internucleoside Linkage Pattern ("s" indicates phosphorothioate, "o" indicates phosphodiester)	Gapmer structure	500 nM Dose Relative Quantity	200 nM Dose Relative Quantity
301601	GCTAACTGGTTTGCCCTTGC	N/A	soooosssssssssooss	eeeee-d10-eeeee	0.258	0.440
301602	GTGGGATACAAATTCTAGGC	N/A	soooosssssssssooss	eeeee-d10-eeeee	0.066	0.240
301603	GGAGCTGGAGAACCATGAGC	N/A	sssssssssssssssss	eeeee-d10-eeeee	0.754	0.693
301604	TGTACTTCACATTTGGAGCC	N/A	sssssssssssssssss	eeeeee-d10-eeee	0.416	0.642
301729	GCTAACTGGTSTGCCCTTGC	11	soooosssssssssooss	eeeee-d10-eeeee	0.455	0.693
301730	GTGGGATACASATTCTAGGC	11	soooosssssssssooss	eeeee-d10-eeeee	0.170	0.473
301731	GGAGCTGGAGSACCATGAGC	11	sssssssssssssssss	eeeee-d10-eeeee	0.654	0.773
301732	TGTACTTCACSTTTGGAGCC	11	sssssssssssssssss	eeeeee-d10-eeee	0.911	1.280

* Unless otherwise noted, for the sequences described in Table 6, the gapmer structure is denoted by "e" = a ribonucleoside and "d" = a deoxyribonucleoside. Every ribonucleoside is a 2'-MOE modified ribonucleoside. Each "C" cytosine is a 5-methylcytosine (5-MeC). Spacer, as indicated by S, is not a nucleoside. S is a spacer represented by Formula (Iia').

Example 3: Design and Selection of SOD1 Antisense Oligonucleotides

[00521] SOD1 antisense oligonucleotides were evaluated in iPSC derived human motor neurons (hMN). The cells were seeded in 96-well plates at a density of 20,000 cells/ well. Antisense oligonucleotide (AON) to SOD1 were transfected with Endoporter (Gene Tools, Philomath, OR, USA) to decrease expression of SOD1 transcript. Vehicle control consisted of motor neuron treatment with Endoporter alone.

[00522] To evaluate SOD1 AON ability to knock down SOD1 mRNA transcripts, antisense oligonucleotides to SOD1 were incubated with Endoporter in media before addition to the cells. After 72 hours, cells lysate was prepared and collected from the 96-well plates for RT-qPCR. From the cell lysates, cDNA was generated, and multiplexed RT-qPCR assay performed with Taqman probes for SOD1 and reference GAPDH quantification.

[00523] Transcript levels were detected by RT-qPCR using Taqman. Specifically, RT-qPCR was performed for detecting GAPDH using Thermofisher TaqMan Gene Expression Assay Hs_03929097_g1. RT-qPCR was performed for detecting SOD1 using Thermofisher TaqMan Gene Expression Assay Hs00533490_m1.

[00524] RT-qPCR was performed on Applied Biosystems ® 7500 Real-time PCR systems. One cycle of reverse transcription was performed at a temperature of 50oC for 5 min. One cycle of RT inactivation/initial denaturation was performed at a temperature of 95oC for 20 seconds. Forty five cycles of amplification were performed at a temperature of 95oC for 1 second followed by 60oC for 20 seconds.

[00525] SOD1 signal cycle threshold (Ct) was normalized to GAPDH (ΔCt). To visualize the quantitative changes (e.g., ratio of SOD1 transcript decrease), the normalized SOD1 signal was further normalized to the mean vehicle signal (treated with Endoporter alone, ΔΔCt). Relative quantity (RQ) of transcript level was calculated using the equation $RQ=2^{-\Delta\Delta Ct}$ and is used to describe the treatment condition comparison to normal, healthy levels.

[00526] SOD1 AON knock-down of SOD1 transcripts were presented as mean relative quantity (RQ_{mean}) of the technical triplicates, compared to mean endogenous SOD1 expression ($RQ_{mean}=1$).

Table 7: SOD1 AON sequences (including SOD1 gapmer sequences and SOD1 gapmer sequences with one or two spacers)

SEQ ID NO:	AON sequence 5'-3' S indicates presence of spacer	Spacer Position	Internucleoside Linkage Pattern ("s" indicates phosphorothioate, "o" indicates phosphodiester)	Gapmer structure	500 nM Dose Relative Quantity	200 nM Dose Relative Quantity
301605	CAGGATACATTTCTACAGCT	N/A	sosossssssssssosos	eeeee-d10-eeeee	0.019	0.024
301733	CAGGSTACATTTCTACAGCT	5	sosossssssssssosos	eeeee-d10-eeeee	0.124	0.159
301734	CAGGATACATTTCTACSGCT	17	sosossssssssssosos	eeeee-d10-eeeee	0.117	0.179
301735	CAGGATACATSTCTACAGCT	11	sosossssssssssosos	eeeee-d10-eeeee	0.021	0.051
301736	CAGGATSCATTTCTSCAGCT	7 and 15	sosossssssssssosos	eeeee-d10-eeeee	0.393	0.582
301737	CAGGSTACATTTCTACSGCT	5 and 17	sosossssssssssosos	eeeee-d10-eeeee	1.150	1.070

* Unless otherwise noted, for the sequences described in Table 7, the gapmer structure is denoted by "e" = a ribonucleoside and "d" = a deoxyribonucleoside. Every ribonucleoside is a 2'-MOE modified ribonucleoside. Each "C" cytosine is a 5-methylcytosine (5-MeC). Spacer, as indicated by S, is not a nucleoside. S is a spacer represented by Formula (Iia').

Example 4: Design and Selection of MAPT Antisense Oligonucleotides

[00527] MAPT antisense oligonucleotides were evaluated in iPSC derived human motor neurons (hMN) purchased from FujiFilm Cellular Dynamics (Catalog #: C1050). The cells were seeded in 96-well plates at a density of 10,000 cells/ well. Antisense oligonucleotide (AON) to MAPT were transfected with Endoporter (Gene Tools, Philomath, OR, USA) to decrease expression of MAPT transcript. Vehicle control consisted of motor neuron treatment with Endoporter alone.

[00528] To evaluate MAPT AON ability to knock down MAPT mRNA transcripts, antisense oligonucleotides to MAPT were incubated with Endoporter in media before addition to the cells. After 72 hours, cells lysate was prepared and collected from the 96-well plates for RT-qPCR. From the cell lysates, cDNA was generated, and multiplexed RT-qPCR assay performed with Taqman probes for MAPT and reference GAPDH quantification.

[00529] Using the Applied Biosystems® QuantStudio 6 Flex Real-Time PCR System, cDNA was prepared directly from the cell lysates by performing one cycle of reverse transcription at 37°C for 30 minutes, followed by heat inactivation of the RT enzyme at 95°C for 5 minutes.

[00530] Transcript levels were detected by RT-qPCR using Taqman. Specifically, RT-qPCR was performed for detecting GAPDH using Thermofisher TaqMan Gene Expression Assay Hs_03929097_g1. RT-qPCR was performed for detecting MAPT using Thermofisher TaqMan Gene Expression Assay Hs00902194_m1.

[00531] RT-qPCR was performed on Applied Biosystems® QuantStudio 6 Flex Real-Time PCR System. One cycle of UNG incubation was performed at a temperature of 50°C for 2 min. One cycle of polymerase activation/initial denaturation was performed at a temperature of 95°C for 20 seconds. Forty cycles of amplification were performed at a temperature of 95°C for 1 second followed by 60°C for 20 seconds.

[00532] MAPT signal cycle threshold (Ct) was normalized to GAPDH (ΔCt). To visualize the quantitative changes (e.g., ratio of MAPT transcript decrease), the normalized MAPT signal was further normalized to the mean vehicle signal (treated with Endoporter alone, ΔΔCt). Relative quantity (RQ) of transcript level was calculated using the equation $RQ=2^{-\Delta\Delta Ct}$ and is used to describe the treatment condition comparison to normal, healthy levels.

[00533] MAPT AON knock-down of MAPT transcripts were presented as mean relative quantity (RQ_{mean}) of the technical triplicates, compared to mean endogenous MAPT expression ($RQ_{mean}=1$).

Table 8: MAPT AON sequences (including MAPT gapmer sequences and MAPT gapmer sequences with one or two spacers)

SEQ ID NO:	AON sequence 5'-3' S indicates presence of spacer	Spacer Position	Internucleoside Linkage Pattern ("s" indicates phosphorothioate, "o" indicates phosphodiester)	Gapmer structure	500 nM Dose Relative Quantity	200 nM Dose Relative Quantity
301606	CCGTTTTCTTACCACCCT	N/A	sosssssssssssoss	eeeee-d8-eeeee	0.230	0.407
301607	CCGTTTTCTTACCACCCTAA	N/A	sosssssssssssssosss	eeeee-d10-eeeee	0.138	0.270
301738	CCGTTTTCTTSCCACCCT	11	sosssssssssssoss	eeeee-d8-eeeee	1.037	1.283
301739	CCGTTTTCSTACCACCCT	9	sosssssssssssoss	eeeee-d8-eeeee	0.841	1.117
301740	CCGTTTTCTSACCACCCT	10	sosssssssssssoss	eeeee-d8-eeeee	1.007	1.215
301741	CCGTTTTCTTSCCACCCTAA	11	sosssssssssssssosss	eeeee-d10-eeeee	0.141	0.420

* Unless otherwise noted, for the sequences described in Table 8, the gapmer structure is denoted by "e" = a ribonucleoside and "d" = a deoxyribonucleoside. Every ribonucleoside is a 2'-MOE modified ribonucleoside. Each "C" cytosine is a 5-methylcytosine (5-MeC). Spacer, as indicated by S, is not a nucleoside. S is a spacer represented by Formula (Iia').

INCORPORATION BY REFERENCE

[00534] The entire disclosure of each of the patent documents and scientific articles cited herein is incorporated by reference for all purposes.

EQUIVALENTS

[00535] The disclosure can be embodied in other specific forms with departing from the essential characteristics thereof. The foregoing embodiments therefore are to be considered illustrative rather than limiting on the disclosure described herein. The scope of the disclosure is indicated by the appended claims rather than by the foregoing description, and all changes that come within the meaning and range of equivalency of the claims are intended to be embraced therein.

Table 1A: Example PPM1A AON sequences and Corresponding Target Sequences

SEQ ID NO:	Start Position	PPM1A AON sequence (5'→3')*	SEQ ID NO:	Target Sequence (5'→3')
1	457	ATGTCTTGATCCTCTAGGTC	955	GACCTAGAGGATCAAGACAT
2	458	TATGTCTTGATCCTCTAGGT	956	ACCTAGAGGATCAAGACATA
3	459	TTATGTCTTGATCCTCTAGG	957	CCTAGAGGATCAAGACATAA
4	460	ATTATGTCTTGATCCTCTAG	958	CTAGAGGATCAAGACATAAT
5	461	CATTATGTCTTGATCCTCTA	959	TAGAGGATCAAGACATAATG
6	462	CCATTATGTCTTGATCCTCT	960	AGAGGATCAAGACATAATGG
7	463	CCCATTATGTCTTGATCCTC	961	GAGGATCAAGACATAATGGG
8	464	TCCCATTATGTCTTGATCCT	962	AGGATCAAGACATAATGGGA
9	465	CTCCCATTATGTCTTGATCC	963	GGATCAAGACATAATGGGAG
10	466	GCTCCCATTATGTCTTGATC	964	GATCAAGACATAATGGGAGC
11	467	TGCTCCCATTATGTCTTGAT	965	ATCAAGACATAATGGGAGCA
12	468	ATGCTCCCATTATGTCTTGA	966	TCAAGACATAATGGGAGCAT
13	469	AATGCTCCCATTATGTCTTG	967	CAAGACATAATGGGAGCATT
14	470	AAATGCTCCCATTATGTCTT	968	AAGACATAATGGGAGCATTT
15	471	AAAATGCTCCCATTATGTCT	969	AGACATAATGGGAGCATTTT
16	472	AAAAATGCTCCCATTATGTC	970	GACATAATGGGAGCATTTTT
17	473	TAAAAATGCTCCCATTATGT	971	ACATAATGGGAGCATTTTTA
18	474	CTAAAAATGCTCCCATTATG	972	CATAATGGGAGCATTTTTAG
19	475	TCTAAAAATGCTCCCATTAT	973	ATAATGGGAGCATTTTTAGA
20	476	GTCTAAAAATGCTCCCATTA	974	TAATGGGAGCATTTTTAGAC
21	477	TGTCTAAAAATGCTCCCATT	975	AATGGGAGCATTTTTAGACA
22	478	TTGTCTAAAAATGCTCCCAT	976	ATGGGAGCATTTTTAGACAA
23	479	CTTGTCTAAAAATGCTCCCA	977	TGGGAGCATTTTTAGACAAG
24	480	GCTTGTCTAAAAATGCTCCC	978	GGGAGCATTTTTAGACAAGC
25	481	GGCTTGTCTAAAAATGCTCC	979	GGAGCATTTTTAGACAAGCC
26	482	TGGCTTGTCTAAAAATGCTC	980	GAGCATTTTTAGACAAGCCA
27	483	TTGGCTTGTCTAAAAATGCT	981	AGCATTTTTAGACAAGCCAA
28	484	TTTGGCTTGTCTAAAAATGC	982	GCATTTTTAGACAAGCCAAA
29	485	CTTTGGCTTGTCTAAAAATG	983	CATTTTTAGACAAGCCAAAG
30	486	TCTTTGGCTTGTCTAAAAAT	984	ATTTTTAGACAAGCCAAAGA
31	487	ATCTTTGGCTTGTCTAAAAA	985	TTTTTAGACAAGCCAAAGAT
32	488	CATCTTTGGCTTGTCTAAAA	986	TTTTAGACAAGCCAAAGATG
33	489	CCATCTTTGGCTTGTCTAAA	987	TTTAGACAAGCCAAAGATGG
34	490	TCCATCTTTGGCTTGTCTAA	988	TTAGACAAGCCAAAGATGGA
35	491	TTCCATCTTTGGCTTGTCTA	989	TAGACAAGCCAAAGATGGAA
36	492	TTTCCATCTTTGGCTTGTCT	990	AGACAAGCCAAAGATGGAAA
37	493	TTTTCCATCTTTGGCTTGTC	991	GACAAGCCAAAGATGGAAAA
38	494	CTTTTCCATCTTTGGCTTGT	992	ACAAGCCAAAGATGGAAAAG
39	495	GCTTTTCCATCTTTGGCTTG	993	CAAGCCAAAGATGGAAAAGC
40	496	TGCTTTTCCATCTTTGGCTT	994	AAGCCAAAGATGGAAAAGCA
41	497	ATGCTTTTCCATCTTTGGCT	995	AGCCAAAGATGGAAAAGCAT
42	498	TATGCTTTTCCATCTTTGGC	996	GCCAAAGATGGAAAAGCATA
43	499	TTATGCTTTTCCATCTTTGG	997	CCAAAGATGGAAAAGCATAA
44	500	ATTATGCTTTTCCATCTTTG	998	CAAAGATGGAAAAGCATAAT
45	501	CATTATGCTTTTCCATCTTT	999	AAAGATGGAAAAGCATAATG
46	502	GCATTATGCTTTTCCATCTT	1000	AAGATGGAAAAGCATAATGC
47	503	GGCATTATGCTTTTCCATCT	1001	AGATGGAAAAGCATAATGCC
48	504	GGGCATTATGCTTTTCCATC	1002	GATGGAAAAGCATAATGCCC
49	505	TGGGCATTATGCTTTTCCAT	1003	ATGGAAAAGCATAATGCCCA
50	506	CTGGGCATTATGCTTTTCCA	1004	TGGAAAAGCATAATGCCCAG
51	507	CCTGGGCATTATGCTTTTCC	1005	GGAAAAGCATAATGCCCAGG
52	508	CCCTGGGCATTATGCTTTTC	1006	GAAAAGCATAATGCCCAGGG
53	509	CCCCTGGGCATTATGCTTTT	1007	AAAAGCATAATGCCCAGGGG
54	510	GCCCCTGGGCATTATGCTTT	1008	AAAGCATAATGCCCAGGGGC
55	511	TGCCCCTGGGCATTATGCTT	1009	AAGCATAATGCCCAGGGGCA
56	512	CTGCCCCTGGGCATTATGCT	1010	AGCATAATGCCCAGGGGCAG
57	513	CCTGCCCCTGGGCATTATGC	1011	GCATAATGCCCAGGGGCAGG
58	514	CCCTGCCCCTGGGCATTATG	1012	CATAATGCCCAGGGGCAGGG
59	515	ACCCTGCCCCTGGGCATTAT	1013	ATAATGCCCAGGGGCAGGGT
60	516	TACCCTGCCCCTGGGCATTA	1014	TAATGCCCAGGGGCAGGGTA
61	517	TTACCCTGCCCCTGGGCATT	1015	AATGCCCAGGGGCAGGGTAA
62	518	ATTACCCTGCCCCTGGGCAT	1016	ATGCCCAGGGGCAGGGTAAT
63	519	CATTACCCTGCCCCTGGGCA	1017	TGCCCAGGGGCAGGGTAATG
64	520	CCATTACCCTGCCCCTGGGC	1018	GCCCAGGGGCAGGGTAATGG
65	521	CCCATTACCCTGCCCCTGGG	1019	CCCAGGGGCAGGGTAATGGG
66	522	ACCCATTACCCTGCCCCTGG	1020	CCAGGGGCAGGGTAATGGGT
67	523	AACCCATTACCCTGCCCCTG	1021	CAGGGGCAGGGTAATGGGTT
68	524	CAACCCATTACCCTGCCCCT	1022	AGGGGCAGGGTAATGGGTTG
69	525	GCAACCCATTACCCTGCCCC	1023	GGGGCAGGGTAATGGGTTGC

70	526	CGCAACCCATTACCCTGCCC	1024	GGGCAGGGTAATGGGTTGCG
71	527	TCGCAACCCATTACCCTGCC	1025	GGCAGGGTAATGGGTTGCGA
72	528	ATCGCAACCCATTACCCTGC	1026	GCAGGGTAATGGGTTGCGAT
73	529	TATCGCAACCCATTACCCTG	1027	CAGGGTAATGGGTTGCGATA
74	530	ATATCGCAACCCATTACCCT	1028	AGGGTAATGGGTTGCGATAT
75	531	CATATCGCAACCCATTACCC	1029	GGGTAATGGGTTGCGATATG
76	532	CCATATCGCAACCCATTACC	1030	GGTAATGGGTTGCGATATGG
77	533	CCCATATCGCAACCCATTAC	1031	GTAATGGGTTGCGATATGGG
78	534	GCCCATATCGCAACCCATTA	1032	TAATGGGTTGCGATATGGGC
79	535	AGCCCATATCGCAACCCATT	1033	AATGGGTTGCGATATGGGCT
80	536	TAGCCCATATCGCAACCCAT	1034	ATGGGTTGCGATATGGGCTA
81	537	TTAGCCCATATCGCAACCCA	1035	TGGGTTGCGATATGGGCTAA
82	538	CTTAGCCCATATCGCAACCC	1036	GGGTTGCGATATGGGCTAAG
83	539	GCTTAGCCCATATCGCAACC	1037	GGTTGCGATATGGGCTAAGC
84	540	TGCTTAGCCCATATCGCAAC	1038	GTTGCGATATGGGCTAAGCA
85	541	CTGCTTAGCCCATATCGCAA	1039	TTGCGATATGGGCTAAGCAG
86	542	GCTGCTTAGCCCATATCGCA	1040	TGCGATATGGGCTAAGCAGC
87	543	TGCTGCTTAGCCCATATCGC	1041	GCGATATGGGCTAAGCAGCA
88	544	ATGCTGCTTAGCCCATATCG	1042	CGATATGGGCTAAGCAGCAT
89	545	CATGCTGCTTAGCCCATATC	1043	GATATGGGCTAAGCAGCATG
90	546	GCATGCTGCTTAGCCCATAT	1044	ATATGGGCTAAGCAGCATGC
91	547	TGCATGCTGCTTAGCCCATA	1045	TATGGGCTAAGCAGCATGCA
92	548	TTGCATGCTGCTTAGCCCAT	1046	ATGGGCTAAGCAGCATGCAA
93	549	CTTGCATGCTGCTTAGCCCA	1047	TGGGCTAAGCAGCATGCAAG
94	550	CCTTGCATGCTGCTTAGCCC	1048	GGGCTAAGCAGCATGCAAGG
95	551	GCCTTGCATGCTGCTTAGCC	1049	GGCTAAGCAGCATGCAAGGC
96	552	AGCCTTGCATGCTGCTTAGC	1050	GCTAAGCAGCATGCAAGGCT
97	553	CAGCCTTGCATGCTGCTTAG	1051	CTAAGCAGCATGCAAGGCTG
98	554	CCAGCCTTGCATGCTGCTTA	1052	TAAGCAGCATGCAAGGCTGG
99	555	GCCAGCCTTGCATGCTGCTT	1053	AAGCAGCATGCAAGGCTGGC
100	556	CGCCAGCCTTGCATGCTGCT	1054	AGCAGCATGCAAGGCTGGCG
101	557	ACGCCAGCCTTGCATGCTGC	1055	GCAGCATGCAAGGCTGGCGT
102	558	CACGCCAGCCTTGCATGCTG	1056	CAGCATGCAAGGCTGGCGTG
103	559	ACACGCCAGCCTTGCATGCT	1057	AGCATGCAAGGCTGGCGTGT
104	560	AACACGCCAGCCTTGCATGC	1058	GCATGCAAGGCTGGCGTGTT
105	561	CAACACGCCAGCCTTGCATG	1059	CATGCAAGGCTGGCGTGTTG
106	562	TCAACACGCCAGCCTTGCAT	1060	ATGCAAGGCTGGCGTGTTGA
107	563	TTCAACACGCCAGCCTTGCA	1061	TGCAAGGCTGGCGTGTTGAA
108	564	TTTCAACACGCCAGCCTTGC	1062	GCAAGGCTGGCGTGTTGAAA
109	565	ATTTCAACACGCCAGCCTTG	1063	CAAGGCTGGCGTGTTGAAAT
110	566	CATTTCAACACGCCAGCCTT	1064	AAGGCTGGCGTGTTGAAATG
111	567	CCATTTCAACACGCCAGCCT	1065	AGGCTGGCGTGTTGAAATGG
112	568	TCCATTTCAACACGCCAGCC	1066	GGCTGGCGTGTTGAAATGGA
113	569	CTCCATTTCAACACGCCAGC	1067	GCTGGCGTGTTGAAATGGAG
114	570	CCTCCATTTCAACACGCCAG	1068	CTGGCGTGTTGAAATGGAGG
115	571	TCCTCCATTTCAACACGCCA	1069	TGGCGTGTTGAAATGGAGGA
116	572	ATCCTCCATTTCAACACGCC	1070	GGCGTGTTGAAATGGAGGAT
117	573	CATCCTCCATTTCAACACGC	1071	GCGTGTTGAAATGGAGGATG
118	574	GCATCCTCCATTTCAACACG	1072	CGTGTTGAAATGGAGGATGC
119	575	TGCATCCTCCATTTCAACAC	1073	GTGTTGAAATGGAGGATGCA
120	576	GTGCATCCTCCATTTCAACA	1074	TGTTGAAATGGAGGATGCAC
121	577	TGTGCATCCTCCATTTCAAC	1075	GTTGAAATGGAGGATGCACA
122	578	ATGTGCATCCTCCATTTCAA	1076	TTGAAATGGAGGATGCACAT
123	579	TATGTGCATCCTCCATTTCA	1077	TGAAATGGAGGATGCACATA
124	580	GTATGTGCATCCTCCATTTC	1078	GAAATGGAGGATGCACATAC
125	581	CGTATGTGCATCCTCCATTT	1079	AAATGGAGGATGCACATACG
126	582	CCGTATGTGCATCCTCCATT	1080	AATGGAGGATGCACATACGG
127	583	GCCGTATGTGCATCCTCCAT	1081	ATGGAGGATGCACATACGGC
128	584	AGCCGTATGTGCATCCTCCA	1082	TGGAGGATGCACATACGGCT
129	585	CAGCCGTATGTGCATCCTCC	1083	GGAGGATGCACATACGGCTG
130	586	ACAGCCGTATGTGCATCCTC	1084	GAGGATGCACATACGGCTGT
131	587	CACAGCCGTATGTGCATCCT	1085	AGGATGCACATACGGCTGTG
132	588	TCACAGCCGTATGTGCATCC	1086	GGATGCACATACGGCTGTGA
133	589	ATCACAGCCGTATGTGCATC	1087	GATGCACATACGGCTGTGAT
134	590	GATCACAGCCGTATGTGCAT	1088	ATGCACATACGGCTGTGATC
135	591	CGATCACAGCCGTATGTGCA	1089	TGCACATACGGCTGTGATCG
136	592	CCGATCACAGCCGTATGTGC	1090	GCACATACGGCTGTGATCGG
137	593	ACCGATCACAGCCGTATGTG	1091	CACATACGGCTGTGATCGGT
138	594	AACCGATCACAGCCGTATGT	1092	ACATACGGCTGTGATCGGTT
139	595	AAACCGATCACAGCCGTATG	1093	CATACGGCTGTGATCGGTTT
140	596	CAAACCGATCACAGCCGTAT	1094	ATACGGCTGTGATCGGTTTG

141	597	GCAAACCGATCACAGCCGTA	1095	TACGGCTGTGATCGGTTTGC
142	598	GGCAAACCGATCACAGCCGT	1096	ACGGCTGTGATCGGTTTGCC
143	599	TGGCAAACCGATCACAGCCG	1097	CGGCTGTGATCGGTTTGCCA
144	600	TTGGCAAACCGATCACAGCC	1098	GGCTGTGATCGGTTTGCCAA
145	601	CTTGGCAAACCGATCACAGC	1099	GCTGTGATCGGTTTGCCAAG
146	602	ACTTGGCAAACCGATCACAG	1100	CTGTGATCGGTTTGCCAAGT
147	603	CACTTGGCAAACCGATCACA	1101	TGTGATCGGTTTGCCAAGTG
148	604	CCACTTGGCAAACCGATCAC	1102	GTGATCGGTTTGCCAAGTGG
149	605	TCCACTTGGCAAACCGATCA	1103	TGATCGGTTTGCCAAGTGGA
150	606	GTCCACTTGGCAAACCGATC	1104	GATCGGTTTGCCAAGTGGAC
151	607	AGTCCACTTGGCAAACCGAT	1105	ATCGGTTTGCCAAGTGGACT
152	608	AAGTCCACTTGGCAAACCGA	1106	TCGGTTTGCCAAGTGGACTT
153	609	CAAGTCCACTTGGCAAACCG	1107	CGGTTTGCCAAGTGGACTTG
154	610	TCAAGTCCACTTGGCAAACC	1108	GGTTTGCCAAGTGGACTTGA
155	611	TTCAAGTCCACTTGGCAAAC	1109	GTTTGCCAAGTGGACTTGAA
156	612	ATTCAAGTCCACTTGGCAAA	1110	TTTGCCAAGTGGACTTGAAT
157	613	GATTCAAGTCCACTTGGCAA	1111	TTGCCAAGTGGACTTGAATC
158	614	CGATTCAAGTCCACTTGGCA	1112	TGCCAAGTGGACTTGAATCG
159	615	ACGATTCAAGTCCACTTGGC	1113	GCCAAGTGGACTTGAATCGT
160	616	CACGATTCAAGTCCACTTGG	1114	CCAAGTGGACTTGAATCGTG
161	617	CCACGATTCAAGTCCACTTG	1115	CAAGTGGACTTGAATCGTGG
162	618	ACCACGATTCAAGTCCACTT	1116	AAGTGGACTTGAATCGTGGT
163	619	GACCACGATTCAAGTCCACT	1117	AGTGGACTTGAATCGTGGTC
164	620	TGACCACGATTCAAGTCCAC	1118	GTGGACTTGAATCGTGGTCA
165	621	ATGACCACGATTCAAGTCCA	1119	TGGACTTGAATCGTGGTCAT
166	622	AATGACCACGATTCAAGTCC	1120	GGACTTGAATCGTGGTCATT
167	623	GAATGACCACGATTCAAGTC	1121	GACTTGAATCGTGGTCATTC
168	624	AGAATGACCACGATTCAAGT	1122	ACTTGAATCGTGGTCATTCT
169	625	AAGAATGACCACGATTCAAG	1123	CTTGAATCGTGGTCATTCTT
170	626	AAAGAATGACCACGATTCAA	1124	TTGAATCGTGGTCATTCTTT
171	627	CAAAGAATGACCACGATTCA	1125	TGAATCGTGGTCATTCTTTG
172	628	GCAAAGAATGACCACGATTC	1126	GAATCGTGGTCATTCTTTGC
173	629	AGCAAAGAATGACCACGATT	1127	AATCGTGGTCATTCTTTGCT
174	630	CAGCAAAGAATGACCACGAT	1128	ATCGTGGTCATTCTTTGCTG
175	631	ACAGCAAAGAATGACCACGA	1129	TCGTGGTCATTCTTTGCTGT
176	632	CACAGCAAAGAATGACCACG	1130	CGTGGTCATTCTTTGCTGTG
177	633	ACACAGCAAAGAATGACCAC	1131	GTGGTCATTCTTTGCTGTGT
178	634	TACACAGCAAAGAATGACCA	1132	TGGTCATTCTTTGCTGTGTA
179	635	ATACACAGCAAAGAATGACC	1133	GGTCATTCTTTGCTGTGTAT
180	636	CATACACAGCAAAGAATGAC	1134	GTCATTCTTTGCTGTGTATG
181	637	TCATACACAGCAAAGAATGA	1135	TCATTCTTTGCTGTGTATGA
182	638	ATCATACACAGCAAAGAATG	1136	CATTCTTTGCTGTGTATGAT
183	639	CATCATACACAGCAAAGAAT	1137	ATTCTTTGCTGTGTATGATG
184	640	CCATCATACACAGCAAAGAA	1138	TTCTTTGCTGTGTATGATGG
185	641	CCCATCATACACAGCAAAGA	1139	TCTTTGCTGTGTATGATGGG
186	642	GCCCATCATACACAGCAAAG	1140	CTTTGCTGTGTATGATGGGC
187	643	TGCCCATCATACACAGCAAA	1141	TTTGCTGTGTATGATGGGCA
188	644	ATGCCCATCATACACAGCAA	1142	TTGCTGTGTATGATGGGCAT
189	645	CATGCCCATCATACACAGCA	1143	TGCTGTGTATGATGGGCATG
190	646	GCATGCCCATCATACACAGC	1144	GCTGTGTATGATGGGCATGC
191	647	AGCATGCCCATCATACACAG	1145	CTGTGTATGATGGGCATGCT
192	648	CAGCATGCCCATCATACACA	1146	TGTGTATGATGGGCATGCTG
193	649	CCAGCATGCCCATCATACAC	1147	GTGTATGATGGGCATGCTGG
194	650	ACCAGCATGCCCATCATACA	1148	TGTATGATGGGCATGCTGGT
195	651	AACCAGCATGCCCATCATAC	1149	GTATGATGGGCATGCTGGTT
196	652	GAACCAGCATGCCCATCATA	1150	TATGATGGGCATGCTGGTTC
197	653	AGAACCAGCATGCCCATCAT	1151	ATGATGGGCATGCTGGTTCT
198	654	GAGAACCAGCATGCCCATCA	1152	TGATGGGCATGCTGGTTCTC
199	655	TGAGAACCAGCATGCCCATC	1153	GATGGGCATGCTGGTTCTCA
200	656	CTGAGAACCAGCATGCCCAT	1154	ATGGGCATGCTGGTTCTCAG
201	657	CCTGAGAACCAGCATGCCCA	1155	TGGGCATGCTGGTTCTCAGG
202	658	ACCTGAGAACCAGCATGCCC	1156	GGGCATGCTGGTTCTCAGGT
203	659	AACCTGAGAACCAGCATGCC	1157	GGCATGCTGGTTCTCAGGTT
204	660	CAACCTGAGAACCAGCATGC	1158	GCATGCTGGTTCTCAGGTTG
205	661	GCAACCTGAGAACCAGCATG	1159	CATGCTGGTTCTCAGGTTGC
206	662	GGCAACCTGAGAACCAGCAT	1160	ATGCTGGTTCTCAGGTTGCC
207	663	TGGCAACCTGAGAACCAGCA	1161	TGCTGGTTCTCAGGTTGCCA
208	664	TTGGCAACCTGAGAACCAGC	1162	GCTGGTTCTCAGGTTGCCAA
209	665	TTTGGCAACCTGAGAACCAG	1163	CTGGTTCTCAGGTTGCCAAA
210	666	ATTTGGCAACCTGAGAACCA	1164	TGGTTCTCAGGTTGCCAAAT
211	667	TATTTGGCAACCTGAGAACC	1165	GGTTCTCAGGTTGCCAAATA

212	668	GTATTTGGCAACCTGAGAAC	1166	GTTCTCAGGTTGCCAAATAC
213	669	AGTATTTGGCAACCTGAGAA	1167	TTCTCAGGTTGCCAAATACT
214	670	CAGTATTTGGCAACCTGAGA	1168	TCTCAGGTTGCCAAATACTG
215	671	GCAGTATTTGGCAACCTGAG	1169	CTCAGGTTGCCAAATACTGC
216	672	AGCAGTATTTGGCAACCTGA	1170	TCAGGTTGCCAAATACTGCT
217	673	CAGCAGTATTTGGCAACCTG	1171	CAGGTTGCCAAATACTGCTG
218	674	ACAGCAGTATTTGGCAACCT	1172	AGGTTGCCAAATACTGCTGT
219	675	CACAGCAGTATTTGGCAACC	1173	GGTTGCCAAATACTGCTGTG
220	676	TCACAGCAGTATTTGGCAAC	1174	GTTGCCAAATACTGCTGTGA
221	677	CTCACAGCAGTATTTGGCAA	1175	TTGCCAAATACTGCTGTGAG
222	678	GCTCACAGCAGTATTTGGCA	1176	TGCCAAATACTGCTGTGAGC
223	679	TGCTCACAGCAGTATTTGGC	1177	GCCAAATACTGCTGTGAGCA
224	680	ATGCTCACAGCAGTATTTGG	1178	CCAAATACTGCTGTGAGCAT
225	681	AATGCTCACAGCAGTATTTG	1179	CAAATACTGCTGTGAGCATT
226	682	AAATGCTCACAGCAGTATTT	1180	AAATACTGCTGTGAGCATTT
227	683	CAAATGCTCACAGCAGTATT	1181	AATACTGCTGTGAGCATTTG
228	684	ACAAATGCTCACAGCAGTAT	1182	ATACTGCTGTGAGCATTTGT
229	685	AACAAATGCTCACAGCAGTA	1183	TACTGCTGTGAGCATTTGTT
230	686	TAACAAATGCTCACAGCAGT	1184	ACTGCTGTGAGCATTTGTTA
231	687	CTAACAAATGCTCACAGCAG	1185	CTGCTGTGAGCATTTGTTAG
232	688	TCTAACAAATGCTCACAGCA	1186	TGCTGTGAGCATTTGTTAGA
233	689	ATCTAACAAATGCTCACAGC	1187	GCTGTGAGCATTTGTTAGAT
234	690	GATCTAACAAATGCTCACAG	1188	CTGTGAGCATTTGTTAGATC
235	691	TGATCTAACAAATGCTCACA	1189	TGTGAGCATTTGTTAGATCA
236	692	GTGATCTAACAAATGCTCAC	1190	GTGAGCATTTGTTAGATCAC
237	693	TGTGATCTAACAAATGCTCA	1191	TGAGCATTTGTTAGATCACA
238	694	ATGTGATCTAACAAATGCTC	1192	GAGCATTTGTTAGATCACAT
239	695	GATGTGATCTAACAAATGCT	1193	AGCATTTGTTAGATCACATC
240	696	TGATGTGATCTAACAAATGC	1194	GCATTTGTTAGATCACATCA
241	697	GTGATGTGATCTAACAAATG	1195	CATTTGTTAGATCACATCAC
242	698	GGTGATGTGATCTAACAAAT	1196	ATTTGTTAGATCACATCACC
243	699	TGGTGATGTGATCTAACAAA	1197	TTTGTTAGATCACATCACCA
244	700	TTGGTGATGTGATCTAACAA	1198	TTGTTAGATCACATCACCAA
245	701	ATTGGTGATGTGATCTAACA	1199	TGTTAGATCACATCACCAAT
246	702	TATTGGTGATGTGATCTAAC	1200	GTTAGATCACATCACCAATA
247	703	TTATTGGTGATGTGATCTAA	1201	TTAGATCACATCACCAATAA
248	704	GTTATTGGTGATGTGATCTA	1202	TAGATCACATCACCAATAAC
249	705	GGTTATTGGTGATGTGATCT	1203	AGATCACATCACCAATAACC
250	706	TGGTTATTGGTGATGTGATC	1204	GATCACATCACCAATAACCA
251	707	CTGGTTATTGGTGATGTGAT	1205	ATCACATCACCAATAACCAG
252	708	CCTGGTTATTGGTGATGTGA	1206	TCACATCACCAATAACCAGG
253	709	TCCTGGTTATTGGTGATGTG	1207	CACATCACCAATAACCAGGA
254	710	ATCCTGGTTATTGGTGATGT	1208	ACATCACCAATAACCAGGAT
255	711	AATCCTGGTTATTGGTGATG	1209	CATCACCAATAACCAGGATT
256	712	AAATCCTGGTTATTGGTGAT	1210	ATCACCAATAACCAGGATTT
257	713	AAAATCCTGGTTATTGGTGA	1211	TCACCAATAACCAGGATTTT
258	714	TAAAATCCTGGTTATTGGTG	1212	CACCAATAACCAGGATTTTA
259	715	TTAAAATCCTGGTTATTGGT	1213	ACCAATAACCAGGATTTTAA
260	716	TTTAAAATCCTGGTTATTGG	1214	CCAATAACCAGGATTTTAAA
261	717	CTTTAAAATCCTGGTTATTG	1215	CAATAACCAGGATTTTAAAG
262	718	CCTTTAAAATCCTGGTTATT	1216	AATAACCAGGATTTTAAAGG
263	719	CCCTTTAAAATCCTGGTTAT	1217	ATAACCAGGATTTTAAAGGG
264	720	ACCCTTTAAAATCCTGGTTA	1218	TAACCAGGATTTTAAAGGGT
265	721	GACCCTTTAAAATCCTGGTT	1219	AACCAGGATTTTAAAGGGTC
266	722	AGACCCTTTAAAATCCTGGT	1220	ACCAGGATTTTAAAGGGTCT
267	723	CAGACCCTTTAAAATCCTGG	1221	CCAGGATTTTAAAGGGTCTG
268	724	GCAGACCCTTTAAAATCCTG	1222	CAGGATTTTAAAGGGTCTGC
269	725	TGCAGACCCTTTAAAATCCT	1223	AGGATTTTAAAGGGTCTGCA
270	726	CTGCAGACCCTTTAAAATCC	1224	GGATTTTAAAGGGTCTGCAG
271	727	CCTGCAGACCCTTTAAAATC	1225	GATTTTAAAGGGTCTGCAGG
272	728	TCCTGCAGACCCTTTAAAAT	1226	ATTTTAAAGGGTCTGCAGGA
273	729	CTCCTGCAGACCCTTTAAAA	1227	TTTTAAAGGGTCTGCAGGAG
274	730	GCTCCTGCAGACCCTTTAAA	1228	TTTAAAGGGTCTGCAGGAGC
275	731	TGCTCCTGCAGACCCTTTAA	1229	TTAAAGGGTCTGCAGGAGCA
276	732	GTGCTCCTGCAGACCCTTTA	1230	TAAAGGGTCTGCAGGAGCAC
277	733	GGTGCTCCTGCAGACCCTTT	1231	AAAGGGTCTGCAGGAGCACC
278	734	AGGTGCTCCTGCAGACCCTT	1232	AAGGGTCTGCAGGAGCACCT
279	735	AAGGTGCTCCTGCAGACCCT	1233	AGGGTCTGCAGGAGCACCTT
280	736	GAAGGTGCTCCTGCAGACCC	1234	GGGTCTGCAGGAGCACCTTC
281	737	AGAAGGTGCTCCTGCAGACC	1235	GGTCTGCAGGAGCACCTTCT
282	738	CAGAAGGTGCTCCTGCAGAC	1236	GTCTGCAGGAGCACCTTCTG

283	739	ACAGAAGGTGCTCCTGCAGA	1237	TCTGCAGGAGCACCTTCTGT
284	740	CACAGAAGGTGCTCCTGCAG	1238	CTGCAGGAGCACCTTCTGTG
285	741	CCACAGAAGGTGCTCCTGCA	1239	TGCAGGAGCACCTTCTGTGG
286	742	TCCACAGAAGGTGCTCCTGC	1240	GCAGGAGCACCTTCTGTGGA
287	743	TTCCACAGAAGGTGCTCCTG	1241	CAGGAGCACCTTCTGTGGAA
288	744	TTTCCACAGAAGGTGCTCCT	1242	AGGAGCACCTTCTGTGGAAA
289	745	TTTTCCACAGAAGGTGCTCC	1243	GGAGCACCTTCTGTGGAAAA
290	746	ATTTTCCACAGAAGGTGCTC	1244	GAGCACCTTCTGTGGAAAAT
291	747	CATTTTCCACAGAAGGTGCT	1245	AGCACCTTCTGTGGAAAATG
292	748	ACATTTTCCACAGAAGGTGC	1246	GCACCTTCTGTGGAAAATGT
293	749	TACATTTTCCACAGAAGGTG	1247	CACCTTCTGTGGAAAATGTA
294	750	TTACATTTTCCACAGAAGGT	1248	ACCTTCTGTGGAAAATGTAA
295	751	TTTACATTTTCCACAGAAGG	1249	CCTTCTGTGGAAAATGTAAA
296	752	CTTTACATTTTCCACAGAAG	1250	CTTCTGTGGAAAATGTAAAG
297	753	TCTTTACATTTTCCACAGAA	1251	TTCTGTGGAAAATGTAAAGA
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299	755	ATTCTTTACATTTTCCACAG	1253	CTGTGGAAAATGTAAAGAAT
300	756	CATTCTTTACATTTTCCACA	1254	TGTGGAAAATGTAAAGAATG
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304	760	ATTCCATTCTTTACATTTTC	1258	GAAAATGTAAAGAATGGAAT
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306	762	TGATTCCATTCTTTACATTT	1260	AAATGTAAAGAATGGAATCA
307	763	CTGATTCCATTCTTTACATT	1261	AATGTAAAGAATGGAATCAG
308	764	TCTGATTCCATTCTTTACAT	1262	ATGTAAAGAATGGAATCAGA
309	765	TTCTGATTCCATTCTTTACA	1263	TGTAAAGAATGGAATCAGAA
310	766	GTTCTGATTCCATTCTTTAC	1264	GTAAAGAATGGAATCAGAAC
311	767	TGTTCTGATTCCATTCTTTA	1265	TAAAGAATGGAATCAGAACA
312	768	CTGTTCTGATTCCATTCTTT	1266	AAAGAATGGAATCAGAACAG
313	769	CCTGTTCTGATTCCATTCTT	1267	AAGAATGGAATCAGAACAGG
314	770	ACCTGTTCTGATTCCATTCT	1268	AGAATGGAATCAGAACAGGT
315	771	AACCTGTTCTGATTCCATTC	1269	GAATGGAATCAGAACAGGTT
316	772	AAACCTGTTCTGATTCCATT	1270	AATGGAATCAGAACAGGTTT
317	773	AAAACCTGTTCTGATTCCAT	1271	ATGGAATCAGAACAGGTTTT
318	774	GAAAACCTGTTCTGATTCCA	1272	TGGAATCAGAACAGGTTTTC
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320	776	CAGAAAACCTGTTCTGATTC	1274	GAATCAGAACAGGTTTTCTG
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322	778	TCCAGAAAACCTGTTCTGAT	1276	ATCAGAACAGGTTTTCTGGA
323	779	CTCCAGAAAACCTGTTCTGA	1277	TCAGAACAGGTTTTCTGGAG
324	780	TCTCCAGAAAACCTGTTCTG	1278	CAGAACAGGTTTTCTGGAGA
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326	782	AATCTCCAGAAAACCTGTTC	1280	GAACAGGTTTTCTGGAGATT
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328	784	TCAATCTCCAGAAAACCTGT	1282	ACAGGTTTTCTGGAGATTGA
329	785	ATCAATCTCCAGAAAACCTG	1283	CAGGTTTTCTGGAGATTGAT
330	786	CATCAATCTCCAGAAAACCT	1284	AGGTTTTCTGGAGATTGATG
331	787	TCATCAATCTCCAGAAAACC	1285	GGTTTTCTGGAGATTGATGA
332	788	TTCATCAATCTCCAGAAAAC	1286	GTTTTCTGGAGATTGATGAA
333	789	GTTCATCAATCTCCAGAAAA	1287	TTTTCTGGAGATTGATGAAC
334	790	TGTTCATCAATCTCCAGAAA	1288	TTTCTGGAGATTGATGAACA
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336	792	TGTGTTCATCAATCTCCAGA	1290	TCTGGAGATTGATGAACACA
337	793	ATGTGTTCATCAATCTCCAG	1291	CTGGAGATTGATGAACACAT
338	794	CATGTGTTCATCAATCTCCA	1292	TGGAGATTGATGAACACATG
339	795	TCATGTGTTCATCAATCTCC	1293	GGAGATTGATGAACACATGA
340	796	CTCATGTGTTCATCAATCTC	1294	GAGATTGATGAACACATGAG
341	797	TCTCATGTGTTCATCAATCT	1295	AGATTGATGAACACATGAGA
342	798	CTCTCATGTGTTCATCAATC	1296	GATTGATGAACACATGAGAG
343	799	ACTCTCATGTGTTCATCAAT	1297	ATTGATGAACACATGAGAGT
344	800	AACTCTCATGTGTTCATCAA	1298	TTGATGAACACATGAGAGTT
345	801	TAACTCTCATGTGTTCATCA	1299	TGATGAACACATGAGAGTTA
346	802	ATAACTCTCATGTGTTCATC	1300	GATGAACACATGAGAGTTAT
347	803	CATAACTCTCATGTGTTCAT	1301	ATGAACACATGAGAGTTATG
348	804	ACATAACTCTCATGTGTTCA	1302	TGAACACATGAGAGTTATGT
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352	808	TCTGACATAACTCTCATGTG	1306	CACATGAGAGTTATGTCAGA
353	809	CTCTGACATAACTCTCATGT	1307	ACATGAGAGTTATGTCAGAG

354	810	TCTCTGACATAACTCTCATG	1308	CATGAGAGTTATGTCAGAGA
355	811	TTCTCTGACATAACTCTCAT	1309	ATGAGAGTTATGTCAGAGAA
356	812	CTTCTCTGACATAACTCTCA	1310	TGAGAGTTATGTCAGAGAAG
357	813	TCTTCTCTGACATAACTCTC	1311	GAGAGTTATGTCAGAGAAGA
358	814	TTCTTCTCTGACATAACTCT	1312	AGAGTTATGTCAGAGAAGAA
359	815	TTTCTTCTCTGACATAACTC	1313	GAGTTATGTCAGAGAAGAAA
360	816	GTTTCTTCTCTGACATAACT	1314	AGTTATGTCAGAGAAGAAAC
361	817	TGTTTCTTCTCTGACATAAC	1315	GTTATGTCAGAGAAGAAACA
362	818	ATGTTTCTTCTCTGACATAA	1316	TTATGTCAGAGAAGAAACAT
363	819	CATGTTTCTTCTCTGACATA	1317	TATGTCAGAGAAGAAACATG
364	820	CCATGTTTCTTCTCTGACAT	1318	ATGTCAGAGAAGAAACATGG
365	821	ACCATGTTTCTTCTCTGACA	1319	TGTCAGAGAAGAAACATGGT
366	822	CACCATGTTTCTTCTCTGAC	1320	GTCAGAGAAGAAACATGGTG
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368	824	TGCACCATGTTTCTTCTCTG	1322	CAGAGAAGAAACATGGTGCA
369	825	CTGCACCATGTTTCTTCTCT	1323	AGAGAAGAAACATGGTGCAG
370	826	TCTGCACCATGTTTCTTCTC	1324	GAGAAGAAACATGGTGCAGA
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372	828	TATCTGCACCATGTTTCTTC	1326	GAAGAAACATGGTGCAGATA
373	829	CTATCTGCACCATGTTTCTT	1327	AAGAAACATGGTGCAGATAG
374	830	TCTATCTGCACCATGTTTCT	1328	AGAAACATGGTGCAGATAGA
375	831	TTCTATCTGCACCATGTTTC	1329	GAAACATGGTGCAGATAGAA
376	832	CTTCTATCTGCACCATGTTT	1330	AAACATGGTGCAGATAGAAG
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381	837	ACCCACTTCTATCTGCACCA	1335	TGGTGCAGATAGAAGTGGGT
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383	839	TGACCCACTTCTATCTGCAC	1337	GTGCAGATAGAAGTGGGTCA
384	840	TTGACCCACTTCTATCTGCA	1338	TGCAGATAGAAGTGGGTCAA
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410	866	GGGAGAAATTAAGACACCTA	1364	TAGGTGTCTTAATTTCTCCC
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413	869	TTGGGGAGAAATTAAGACAC	1367	GTGTCTTAATTTCTCCCCAA
414	870	GTTGGGGAGAAATTAAGACA	1368	TGTCTTAATTTCTCCCCAAC
415	871	TGTTGGGGAGAAATTAAGAC	1369	GTCTTAATTTCTCCCCAACA
416	872	ATGTTGGGGAGAAATTAAGA	1370	TCTTAATTTCTCCCCAACAT
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418	874	GTATGTTGGGGAGAAATTAA	1372	TTAATTTCTCCCCAACATAC
419	875	AGTATGTTGGGGAGAAATTA	1373	TAATTTCTCCCCAACATACT
420	876	AAGTATGTTGGGGAGAAATT	1374	AATTTCTCCCCAACATACTT
421	877	TAAGTATGTTGGGGAGAAAT	1375	ATTTCTCCCCAACATACTTA
422	878	ATAAGTATGTTGGGGAGAAA	1376	TTTCTCCCCAACATACTTAT
423	879	AATAAGTATGTTGGGGAGAA	1377	TTCTCCCCAACATACTTATT
424	880	AAATAAGTATGTTGGGGAGA	1378	TCTCCCCAACATACTTATTT

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426	882	TGAAATAAGTATGTTGGGGA	1380	TCCCCAACATACTTATTTCA
427	883	ATGAAATAAGTATGTTGGGG	1381	CCCCAACATACTTATTTCAT
428	884	AATGAAATAAGTATGTTGGG	1382	CCCAACATACTTATTTCATT
429	885	TAATGAAATAAGTATGTTGG	1383	CCAACATACTTATTTCATTA
430	886	TTAATGAAATAAGTATGTTG	1384	CAACATACTTATTTCATTAA
431	887	GTTAATGAAATAAGTATGTT	1385	AACATACTTATTTCATTAAC
432	888	AGTTAATGAAATAAGTATGT	1386	ACATACTTATTTCATTAACT
433	889	CAGTTAATGAAATAAGTATG	1387	CATACTTATTTCATTAACTG
434	890	ACAGTTAATGAAATAAGTAT	1388	ATACTTATTTCATTAACTGT
435	891	CACAGTTAATGAAATAAGTA	1389	TACTTATTTCATTAACTGTG
436	892	CCACAGTTAATGAAATAAGT	1390	ACTTATTTCATTAACTGTGG
437	893	TCCACAGTTAATGAAATAAG	1391	CTTATTTCATTAACTGTGGA
438	894	CTCCACAGTTAATGAAATAA	1392	TTATTTCATTAACTGTGGAG
439	895	TCTCCACAGTTAATGAAATA	1393	TATTTCATTAACTGTGGAGA
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441	897	AGTCTCCACAGTTAATGAAA	1395	TTTCATTAACTGTGGAGACT
442	898	GAGTCTCCACAGTTAATGAA	1396	TTCATTAACTGTGGAGACTC
443	899	TGAGTCTCCACAGTTAATGA	1397	TCATTAACTGTGGAGACTCA
444	900	TTGAGTCTCCACAGTTAATG	1398	CATTAACTGTGGAGACTCAA
445	901	CTTGAGTCTCCACAGTTAAT	1399	ATTAACTGTGGAGACTCAAG
446	902	TCTTGAGTCTCCACAGTTAA	1400	TTAACTGTGGAGACTCAAGA
447	903	CTCTTGAGTCTCCACAGTTA	1401	TAACTGTGGAGACTCAAGAG
448	904	CCTCTTGAGTCTCCACAGTT	1402	AACTGTGGAGACTCAAGAGG
449	905	ACCTCTTGAGTCTCCACAGT	1403	ACTGTGGAGACTCAAGAGGT
450	906	AACCTCTTGAGTCTCCACAG	1404	CTGTGGAGACTCAAGAGGTT
451	907	AAACCTCTTGAGTCTCCACA	1405	TGTGGAGACTCAAGAGGTTT
452	908	TAAACCTCTTGAGTCTCCAC	1406	GTGGAGACTCAAGAGGTTTA
453	909	GTAAACCTCTTGAGTCTCCA	1407	TGGAGACTCAAGAGGTTTAC
454	910	AGTAAACCTCTTGAGTCTCC	1408	GGAGACTCAAGAGGTTTACT
455	911	AAGTAAACCTCTTGAGTCTC	1409	GAGACTCAAGAGGTTTACTT
456	912	AAAGTAAACCTCTTGAGTCT	1410	AGACTCAAGAGGTTTACTTT
457	913	CAAAGTAAACCTCTTGAGTC	1411	GACTCAAGAGGTTTACTTTG
458	914	ACAAAGTAAACCTCTTGAGT	1412	ACTCAAGAGGTTTACTTTGT
459	915	TACAAAGTAAACCTCTTGAG	1413	CTCAAGAGGTTTACTTTGTA
460	916	CTACAAAGTAAACCTCTTGA	1414	TCAAGAGGTTTACTTTGTAG
461	917	CCTACAAAGTAAACCTCTTG	1415	CAAGAGGTTTACTTTGTAGG
462	918	TCCTACAAAGTAAACCTCTT	1416	AAGAGGTTTACTTTGTAGGA
463	919	TTCCTACAAAGTAAACCTCT	1417	AGAGGTTTACTTTGTAGGAA
464	920	GTTCCTACAAAGTAAACCTC	1418	GAGGTTTACTTTGTAGGAAC
465	921	TGTTCCTACAAAGTAAACCT	1419	AGGTTTACTTTGTAGGAACA
466	922	CTGTTCCTACAAAGTAAACC	1420	GGTTTACTTTGTAGGAACAG
467	923	CCTGTTCCTACAAAGTAAAC	1421	GTTTACTTTGTAGGAACAGG
468	924	TCCTGTTCCTACAAAGTAAA	1422	TTTACTTTGTAGGAACAGGA
469	925	TTCCTGTTCCTACAAAGTAA	1423	TTACTTTGTAGGAACAGGAA
470	926	TTTCCTGTTCCTACAAAGTA	1424	TACTTTGTAGGAACAGGAAA
471	927	CTTTCCTGTTCCTACAAAGT	1425	ACTTTGTAGGAACAGGAAAG
472	928	ACTTTCCTGTTCCTACAAAG	1426	CTTTGTAGGAACAGGAAAGT
473	929	AACTTTCCTGTTCCTACAAA	1427	TTTGTAGGAACAGGAAAGTT
474	930	GAACTTTCCTGTTCCTACAA	1428	TTGTAGGAACAGGAAAGTTC
475	931	TGAACTTTCCTGTTCCTACA	1429	TGTAGGAACAGGAAAGTTCA
476	932	ATGAACTTTCCTGTTCCTAC	1430	GTAGGAACAGGAAAGTTCAT
477	933	AATGAACTTTCCTGTTCCTA	1431	TAGGAACAGGAAAGTTCATT
478	934	AAATGAACTTTCCTGTTCCT	1432	AGGAACAGGAAAGTTCATTT
479	935	GAAATGAACTTTCCTGTTCC	1433	GGAACAGGAAAGTTCATTTC
480	936	AGAAATGAACTTTCCTGTTC	1434	GAACAGGAAAGTTCATTTCT
481	937	AAGAAATGAACTTTCCTGTT	1435	AACAGGAAAGTTCATTTCTT
482	938	GAAGAAATGAACTTTCCTGT	1436	ACAGGAAAGTTCATTTCTTC
483	939	TGAAGAAATGAACTTTCCTG	1437	CAGGAAAGTTCATTTCTTCA
484	940	GTGAAGAAATGAACTTTCCT	1438	AGGAAAGTTCATTTCTTCAC
485	941	TGTGAAGAAATGAACTTTCC	1439	GGAAAGTTCATTTCTTCACA
486	942	GTGTGAAGAAATGAACTTTC	1440	GAAAGTTCATTTCTTCACAC
487	943	TGTGTGAAGAAATGAACTTT	1441	AAAGTTCATTTCTTCACACA
488	944	TTGTGTGAAGAAATGAACTT	1442	AAGTTCATTTCTTCACACAA
489	945	CTTGTGTGAAGAAATGAACT	1443	AGTTCATTTCTTCACACAAG
490	946	TCTTGTGTGAAGAAATGAAC	1444	GTTCATTTCTTCACACAAGA
491	947	ATCTTGTGTGAAGAAATGAA	1445	TTCATTTCTTCACACAAGAT
492	948	GATCTTGTGTGAAGAAATGA	1446	TCATTTCTTCACACAAGATC
493	949	TGATCTTGTGTGAAGAAATG	1447	CATTTCTTCACACAAGATCA
494	950	GTGATCTTGTGTGAAGAAAT	1448	ATTTCTTCACACAAGATCAC
495	951	TGTGATCTTGTGTGAAGAAA	1449	TTTCTTCACACAAGATCACA

496	952	TTGTGATCTTGTGTGAAGAA	1450	TTCTTCACACAAGATCACAA
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498	954	GTTTGTGATCTTGTGTGAAG	1452	CTTCACACAAGATCACAAAC
499	955	GGTTTGTGATCTTGTGTGAA	1453	TTCACACAAGATCACAAACC
500	956	TGGTTTGTGATCTTGTGTGA	1454	TCACACAAGATCACAAACCA
501	957	TTGGTTTGTGATCTTGTGTG	1455	CACACAAGATCACAAACCAA
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503	959	ACTTGGTTTGTGATCTTGTG	1457	CACAAGATCACAAACCAAGT
504	960	TACTTGGTTTGTGATCTTGT	1458	ACAAGATCACAAACCAAGTA
505	961	TTACTTGGTTTGTGATCTTG	1459	CAAGATCACAAACCAAGTAA
506	962	ATTACTTGGTTTGTGATCTT	1460	AAGATCACAAACCAAGTAAT
507	963	GATTACTTGGTTTGTGATCT	1461	AGATCACAAACCAAGTAATC
508	964	GGATTACTTGGTTTGTGATC	1462	GATCACAAACCAAGTAATCC
509	965	CGGATTACTTGGTTTGTGAT	1463	ATCACAAACCAAGTAATCCG
510	966	GCGGATTACTTGGTTTGTGA	1464	TCACAAACCAAGTAATCCGC
511	967	AGCGGATTACTTGGTTTGTG	1465	CACAAACCAAGTAATCCGCT
512	968	CAGCGGATTACTTGGTTTGT	1466	ACAAACCAAGTAATCCGCTG
513	969	CCAGCGGATTACTTGGTTTG	1467	CAAACCAAGTAATCCGCTGG
514	970	TCCAGCGGATTACTTGGTTT	1468	AAACCAAGTAATCCGCTGGA
515	971	CTCCAGCGGATTACTTGGTT	1469	AACCAAGTAATCCGCTGGAG
516	972	TCTCCAGCGGATTACTTGGT	1470	ACCAAGTAATCCGCTGGAGA
517	973	TTCTCCAGCGGATTACTTGG	1471	CCAAGTAATCCGCTGGAGAA
518	974	TTTCTCCAGCGGATTACTTG	1472	CAAGTAATCCGCTGGAGAAA
519	975	CTTTCTCCAGCGGATTACTT	1473	AAGTAATCCGCTGGAGAAAG
520	976	TCTTTCTCCAGCGGATTACT	1474	AGTAATCCGCTGGAGAAAGA
521	977	TTCTTTCTCCAGCGGATTAC	1475	GTAATCCGCTGGAGAAAGAA
522	978	GTTCTTTCTCCAGCGGATTA	1476	TAATCCGCTGGAGAAAGAAC
523	979	CGTTCTTTCTCCAGCGGATT	1477	AATCCGCTGGAGAAAGAACG
524	980	TCGTTCTTTCTCCAGCGGAT	1478	ATCCGCTGGAGAAAGAACGA
525	981	TTCGTTCTTTCTCCAGCGGA	1479	TCCGCTGGAGAAAGAACGAA
526	982	ATTCGTTCTTTCTCCAGCGG	1480	CCGCTGGAGAAAGAACGAAT
527	983	AATTCGTTCTTTCTCCAGCG	1481	CGCTGGAGAAAGAACGAATT
528	984	GAATTCGTTCTTTCTCCAGC	1482	GCTGGAGAAAGAACGAATTC
529	985	TGAATTCGTTCTTTCTCCAG	1483	CTGGAGAAAGAACGAATTCA
530	986	CTGAATTCGTTCTTTCTCCA	1484	TGGAGAAAGAACGAATTCAG
531	987	TCTGAATTCGTTCTTTCTCC	1485	GGAGAAAGAACGAATTCAGA
532	988	TTCTGAATTCGTTCTTTCTC	1486	GAGAAAGAACGAATTCAGAA
533	989	ATTCTGAATTCGTTCTTTCT	1487	AGAAAGAACGAATTCAGAAT
534	990	CATTCTGAATTCGTTCTTTC	1488	GAAAGAACGAATTCAGAATG
535	991	GCATTCTGAATTCGTTCTTT	1489	AAAGAACGAATTCAGAATGC
536	992	TGCATTCTGAATTCGTTCTT	1490	AAGAACGAATTCAGAATGCA
537	993	CTGCATTCTGAATTCGTTCT	1491	AGAACGAATTCAGAATGCAG
538	994	CCTGCATTCTGAATTCGTTC	1492	GAACGAATTCAGAATGCAGG
539	995	ACCTGCATTCTGAATTCGTT	1493	AACGAATTCAGAATGCAGGT
540	996	CACCTGCATTCTGAATTCGT	1494	ACGAATTCAGAATGCAGGTG
541	997	CCACCTGCATTCTGAATTCG	1495	CGAATTCAGAATGCAGGTGG
542	998	GCCACCTGCATTCTGAATTC	1496	GAATTCAGAATGCAGGTGGC
543	999	AGCCACCTGCATTCTGAATT	1497	AATTCAGAATGCAGGTGGCT
544	1000	GAGCCACCTGCATTCTGAAT	1498	ATTCAGAATGCAGGTGGCTC
545	1001	AGAGCCACCTGCATTCTGAA	1499	TTCAGAATGCAGGTGGCTCT
546	1002	CAGAGCCACCTGCATTCTGA	1500	TCAGAATGCAGGTGGCTCTG
547	1003	ACAGAGCCACCTGCATTCTG	1501	CAGAATGCAGGTGGCTCTGT
548	1004	TACAGAGCCACCTGCATTCT	1502	AGAATGCAGGTGGCTCTGTA
549	1005	TTACAGAGCCACCTGCATTC	1503	GAATGCAGGTGGCTCTGTAA
550	1006	ATTACAGAGCCACCTGCATT	1504	AATGCAGGTGGCTCTGTAAT
551	1007	CATTACAGAGCCACCTGCAT	1505	ATGCAGGTGGCTCTGTAATG
552	1008	TCATTACAGAGCCACCTGCA	1506	TGCAGGTGGCTCTGTAATGA
553	1009	ATCATTACAGAGCCACCTGC	1507	GCAGGTGGCTCTGTAATGAT
554	1010	AATCATTACAGAGCCACCTG	1508	CAGGTGGCTCTGTAATGATT
555	1011	GAATCATTACAGAGCCACCT	1509	AGGTGGCTCTGTAATGATTC
556	1012	TGAATCATTACAGAGCCACC	1510	GGTGGCTCTGTAATGATTCA
557	1013	CTGAATCATTACAGAGCCAC	1511	GTGGCTCTGTAATGATTCAG
558	1014	GCTGAATCATTACAGAGCCA	1512	TGGCTCTGTAATGATTCAGC
559	1015	CGCTGAATCATTACAGAGCC	1513	GGCTCTGTAATGATTCAGCG
560	1016	ACGCTGAATCATTACAGAGC	1514	GCTCTGTAATGATTCAGCGT
561	1017	CACGCTGAATCATTACAGAG	1515	CTCTGTAATGATTCAGCGTG
562	1018	ACACGCTGAATCATTACAGA	1516	TCTGTAATGATTCAGCGTGT
563	1019	CACACGCTGAATCATTACAG	1517	CTGTAATGATTCAGCGTGTG
564	1020	TCACACGCTGAATCATTACA	1518	TGTAATGATTCAGCGTGTGA
565	1021	TTCACACGCTGAATCATTAC	1519	GTAATGATTCAGCGTGTGAA
566	1022	ATTCACACGCTGAATCATTA	1520	TAATGATTCAGCGTGTGAAT

567	1023	CATTCACACGCTGAATCATT	1521	AATGATTCAGCGTGTGAATG
568	1024	CCATTCACACGCTGAATCAT	1522	ATGATTCAGCGTGTGAATGG
569	1025	GCCATTCACACGCTGAATCA	1523	TGATTCAGCGTGTGAATGGC
570	1026	AGCCATTCACACGCTGAATC	1524	GATTCAGCGTGTGAATGGCT
571	1027	GAGCCATTCACACGCTGAAT	1525	ATTCAGCGTGTGAATGGCTC
572	1028	AGAGCCATTCACACGCTGAA	1526	TTCAGCGTGTGAATGGCTCT
573	1029	GAGAGCCATTCACACGCTGA	1527	TCAGCGTGTGAATGGCTCTC
574	1030	AGAGAGCCATTCACACGCTG	1528	CAGCGTGTGAATGGCTCTCT
575	1031	CAGAGAGCCATTCACACGCT	1529	AGCGTGTGAATGGCTCTCTG
576	1032	CCAGAGAGCCATTCACACGC	1530	GCGTGTGAATGGCTCTCTGG
577	1033	GCCAGAGAGCCATTCACACG	1531	CGTGTGAATGGCTCTCTGGC
578	1034	AGCCAGAGAGCCATTCACAC	1532	GTGTGAATGGCTCTCTGGCT
579	1035	CAGCCAGAGAGCCATTCACA	1533	TGTGAATGGCTCTCTGGCTG
580	1036	ACAGCCAGAGAGCCATTCAC	1534	GTGAATGGCTCTCTGGCTGT
581	1037	TACAGCCAGAGAGCCATTCA	1535	TGAATGGCTCTCTGGCTGTA
582	1038	ATACAGCCAGAGAGCCATTC	1536	GAATGGCTCTCTGGCTGTAT
583	1039	GATACAGCCAGAGAGCCATT	1537	AATGGCTCTCTGGCTGTATC
584	1040	CGATACAGCCAGAGAGCCAT	1538	ATGGCTCTCTGGCTGTATCG
585	1041	TCGATACAGCCAGAGAGCCA	1539	TGGCTCTCTGGCTGTATCGA
586	1042	CTCGATACAGCCAGAGAGCC	1540	GGCTCTCTGGCTGTATCGAG
587	1043	CCTCGATACAGCCAGAGAGC	1541	GCTCTCTGGCTGTATCGAGG
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589	1045	GCCCTCGATACAGCCAGAGA	1543	TCTCTGGCTGTATCGAGGGC
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591	1047	GGGCCCTCGATACAGCCAGA	1545	TCTGGCTGTATCGAGGGCCC
592	1048	AGGGCCCTCGATACAGCCAG	1546	CTGGCTGTATCGAGGGCCCT
593	1049	AAGGGCCCTCGATACAGCCA	1547	TGGCTGTATCGAGGGCCCTT
594	1050	CAAGGGCCCTCGATACAGCC	1548	GGCTGTATCGAGGGCCCTTG
595	1051	CCAAGGGCCCTCGATACAGC	1549	GCTGTATCGAGGGCCCTTGG
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605	1061	ATCAAAATCCCCAAGGGCCC	1559	GGGCCCTTGGGGATTTTGAT
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608	1064	GTAATCAAAATCCCCAAGGG	1562	CCCTTGGGGATTTTGATTAC
609	1065	TGTAATCAAAATCCCCAAGG	1563	CCTTGGGGATTTTGATTACA
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611	1067	TTTGTAATCAAAATCCCCAA	1565	TTGGGGATTTTGATTACAAA
612	1068	ATTTGTAATCAAAATCCCCA	1566	TGGGGATTTTGATTACAAAT
613	1069	CATTTGTAATCAAAATCCCC	1567	GGGGATTTTGATTACAAATG
614	1070	ACATTTGTAATCAAAATCCC	1568	GGGATTTTGATTACAAATGT
615	1071	CACATTTGTAATCAAAATCC	1569	GGATTTTGATTACAAATGTG
616	1072	ACACATTTGTAATCAAAATC	1570	GATTTTGATTACAAATGTGT
617	1073	GACACATTTGTAATCAAAAT	1571	ATTTTGATTACAAATGTGTC
618	1074	GGACACATTTGTAATCAAAA	1572	TTTTGATTACAAATGTGTCC
619	1075	TGGACACATTTGTAATCAAA	1573	TTTGATTACAAATGTGTCCA
620	1076	ATGGACACATTTGTAATCAA	1574	TTGATTACAAATGTGTCCAT
621	1077	CATGGACACATTTGTAATCA	1575	TGATTACAAATGTGTCCATG
622	1078	CCATGGACACATTTGTAATC	1576	GATTACAAATGTGTCCATGG
623	1079	TCCATGGACACATTTGTAAT	1577	ATTACAAATGTGTCCATGGA
624	1080	TTCCATGGACACATTTGTAA	1578	TTACAAATGTGTCCATGGAA
625	1081	TTTCCATGGACACATTTGTA	1579	TACAAATGTGTCCATGGAAA
626	1082	TTTTCCATGGACACATTTGT	1580	ACAAATGTGTCCATGGAAAA
627	1083	CTTTTCCATGGACACATTTG	1581	CAAATGTGTCCATGGAAAAG
628	1084	CCTTTTCCATGGACACATTT	1582	AAATGTGTCCATGGAAAAGG
629	1085	ACCTTTTCCATGGACACATT	1583	AATGTGTCCATGGAAAAGGT
630	1086	GACCTTTTCCATGGACACAT	1584	ATGTGTCCATGGAAAAGGTC
631	1087	GGACCTTTTCCATGGACACA	1585	TGTGTCCATGGAAAAGGTCC
632	1088	AGGACCTTTTCCATGGACAC	1586	GTGTCCATGGAAAAGGTCCT
633	1089	TAGGACCTTTTCCATGGACA	1587	TGTCCATGGAAAAGGTCCTA
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635	1091	AGTAGGACCTTTTCCATGGA	1589	TCCATGGAAAAGGTCCTACT
636	1092	CAGTAGGACCTTTTCCATGG	1590	CCATGGAAAAGGTCCTACTG
637	1093	TCAGTAGGACCTTTTCCATG	1591	CATGGAAAAGGTCCTACTGA

638	1094	CTCAGTAGGACCTTTTCCAT	1592	ATGGAAAAGGTCCTACTGAG
639	1095	GCTCAGTAGGACCTTTTCCA	1593	TGGAAAAGGTCCTACTGAGC
640	1096	TGCTCAGTAGGACCTTTTCC	1594	GGAAAAGGTCCTACTGAGCA
641	1097	CTGCTCAGTAGGACCTTTTC	1595	GAAAAGGTCCTACTGAGCAG
642	1098	GCTGCTCAGTAGGACCTTTT	1596	AAAAGGTCCTACTGAGCAGC
643	1099	AGCTGCTCAGTAGGACCTTT	1597	AAAGGTCCTACTGAGCAGCT
644	1100	AAGCTGCTCAGTAGGACCTT	1598	AAGGTCCTACTGAGCAGCTT
645	1101	CAAGCTGCTCAGTAGGACCT	1599	AGGTCCTACTGAGCAGCTTG
646	1102	ACAAGCTGCTCAGTAGGACC	1600	GGTCCTACTGAGCAGCTTGT
647	1103	GACAAGCTGCTCAGTAGGAC	1601	GTCCTACTGAGCAGCTTGTC
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667	1123	TGGACTTCAGGCTCTGGTGA	1621	TCACCAGAGCCTGAAGTCCA
668	1124	ATGGACTTCAGGCTCTGGTG	1622	CACCAGAGCCTGAAGTCCAT
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683	1139	AGATCTTTCAATATCATGGA	1637	TCCATGATATTGAAAGATCT
684	1140	CAGATCTTTCAATATCATGG	1638	CCATGATATTGAAAGATCTG
685	1141	TCAGATCTTTCAATATCATG	1639	CATGATATTGAAAGATCTGA
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688	1144	TCTTCAGATCTTTCAATATC	1642	GATATTGAAAGATCTGAAGA
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691	1147	TCTTCTTCAGATCTTTCAAT	1645	ATTGAAAGATCTGAAGAAGA
692	1148	ATCTTCTTCAGATCTTTCAA	1646	TTGAAAGATCTGAAGAAGAT
693	1149	CATCTTCTTCAGATCTTTCA	1647	TGAAAGATCTGAAGAAGATG
694	1150	TCATCTTCTTCAGATCTTTC	1648	GAAAGATCTGAAGAAGATGA
695	1151	ATCATCTTCTTCAGATCTTT	1649	AAAGATCTGAAGAAGATGAT
696	1152	GATCATCTTCTTCAGATCTT	1650	AAGATCTGAAGAAGATGATC
697	1153	TGATCATCTTCTTCAGATCT	1651	AGATCTGAAGAAGATGATCA
698	1154	CTGATCATCTTCTTCAGATC	1652	GATCTGAAGAAGATGATCAG
699	1155	ACTGATCATCTTCTTCAGAT	1653	ATCTGAAGAAGATGATCAGT
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703	1159	ATGAACTGATCATCTTCTTC	1657	GAAGAAGATGATCAGTTCAT
704	1160	AATGAACTGATCATCTTCTT	1658	AAGAAGATGATCAGTTCATT
705	1161	TAATGAACTGATCATCTTCT	1659	AGAAGATGATCAGTTCATTA
706	1162	ATAATGAACTGATCATCTTC	1660	GAAGATGATCAGTTCATTAT
707	1163	GATAATGAACTGATCATCTT	1661	AAGATGATCAGTTCATTATC
708	1164	GGATAATGAACTGATCATCT	1662	AGATGATCAGTTCATTATCC

709	1165	AGGATAATGAACTGATCATC	1663	GATGATCAGTTCATTATCCT
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711	1167	CAAGGATAATGAACTGATCA	1665	TGATCAGTTCATTATCCTTG
712	1168	GCAAGGATAATGAACTGATC	1666	GATCAGTTCATTATCCTTGC
713	1169	TGCAAGGATAATGAACTGAT	1667	ATCAGTTCATTATCCTTGCA
714	1170	ATGCAAGGATAATGAACTGA	1668	TCAGTTCATTATCCTTGCAT
715	1171	CATGCAAGGATAATGAACTG	1669	CAGTTCATTATCCTTGCATG
716	1172	ACATGCAAGGATAATGAACT	1670	AGTTCATTATCCTTGCATGT
717	1173	CACATGCAAGGATAATGAAC	1671	GTTCATTATCCTTGCATGTG
718	1174	TCACATGCAAGGATAATGAA	1672	TTCATTATCCTTGCATGTGA
719	1175	ATCACATGCAAGGATAATGA	1673	TCATTATCCTTGCATGTGAT
720	1176	CATCACATGCAAGGATAATG	1674	CATTATCCTTGCATGTGATG
721	1177	CCATCACATGCAAGGATAAT	1675	ATTATCCTTGCATGTGATGG
722	1178	ACCATCACATGCAAGGATAA	1676	TTATCCTTGCATGTGATGGT
723	1179	TACCATCACATGCAAGGATA	1677	TATCCTTGCATGTGATGGTA
724	1180	ATACCATCACATGCAAGGAT	1678	ATCCTTGCATGTGATGGTAT
725	1181	GATACCATCACATGCAAGGA	1679	TCCTTGCATGTGATGGTATC
726	1182	AGATACCATCACATGCAAGG	1680	CCTTGCATGTGATGGTATCT
727	1183	CAGATACCATCACATGCAAG	1681	CTTGCATGTGATGGTATCTG
728	1184	CCAGATACCATCACATGCAA	1682	TTGCATGTGATGGTATCTGG
729	1185	CCCAGATACCATCACATGCA	1683	TGCATGTGATGGTATCTGGG
730	1186	TCCCAGATACCATCACATGC	1684	GCATGTGATGGTATCTGGGA
731	1187	ATCCCAGATACCATCACATG	1685	CATGTGATGGTATCTGGGAT
732	1188	CATCCCAGATACCATCACAT	1686	ATGTGATGGTATCTGGGATG
733	1189	ACATCCCAGATACCATCACA	1687	TGTGATGGTATCTGGGATGT
734	1190	AACATCCCAGATACCATCAC	1688	GTGATGGTATCTGGGATGTT
735	1191	TAACATCCCAGATACCATCA	1689	TGATGGTATCTGGGATGTTA
736	1192	ATAACATCCCAGATACCATC	1690	GATGGTATCTGGGATGTTAT
737	1193	CATAACATCCCAGATACCAT	1691	ATGGTATCTGGGATGTTATG
738	1194	CCATAACATCCCAGATACCA	1692	TGGTATCTGGGATGTTATGG
739	1195	CCCATAACATCCCAGATACC	1693	GGTATCTGGGATGTTATGGG
740	1196	TCCCATAACATCCCAGATAC	1694	GTATCTGGGATGTTATGGGA
741	1197	TTCCCATAACATCCCAGATA	1695	TATCTGGGATGTTATGGGAA
742	1198	TTTCCCATAACATCCCAGAT	1696	ATCTGGGATGTTATGGGAAA
743	1199	ATTTCCCATAACATCCCAGA	1697	TCTGGGATGTTATGGGAAAT
744	1200	CATTTCCCATAACATCCCAG	1698	CTGGGATGTTATGGGAAATG
745	1201	TCATTTCCCATAACATCCCA	1699	TGGGATGTTATGGGAAATGA
746	1202	TTCATTTCCCATAACATCCC	1700	GGGATGTTATGGGAAATGAA
747	1203	CTTCATTTCCCATAACATCC	1701	GGATGTTATGGGAAATGAAG
748	1204	TCTTCATTTCCCATAACATC	1702	GATGTTATGGGAAATGAAGA
749	1205	CTCTTCATTTCCCATAACAT	1703	ATGTTATGGGAAATGAAGAG
750	1206	GCTCTTCATTTCCCATAACA	1704	TGTTATGGGAAATGAAGAGC
751	1207	AGCTCTTCATTTCCCATAAC	1705	GTTATGGGAAATGAAGAGCT
752	1208	GAGCTCTTCATTTCCCATAA	1706	TTATGGGAAATGAAGAGCTC
753	1209	AGAGCTCTTCATTTCCCATA	1707	TATGGGAAATGAAGAGCTCT
754	1210	CAGAGCTCTTCATTTCCCAT	1708	ATGGGAAATGAAGAGCTCTG
755	1211	ACAGAGCTCTTCATTTCCCA	1709	TGGGAAATGAAGAGCTCTGT
756	1212	CACAGAGCTCTTCATTTCCC	1710	GGGAAATGAAGAGCTCTGTG
757	1213	TCACAGAGCTCTTCATTTCC	1711	GGAAATGAAGAGCTCTGTGA
758	1214	ATCACAGAGCTCTTCATTTC	1712	GAAATGAAGAGCTCTGTGAT
759	1215	AATCACAGAGCTCTTCATTT	1713	AAATGAAGAGCTCTGTGATT
760	1216	AAATCACAGAGCTCTTCATT	1714	AATGAAGAGCTCTGTGATTT
761	1217	AAAATCACAGAGCTCTTCAT	1715	ATGAAGAGCTCTGTGATTTT
762	1218	CAAAATCACAGAGCTCTTCA	1716	TGAAGAGCTCTGTGATTTTG
763	1219	ACAAAATCACAGAGCTCTTC	1717	GAAGAGCTCTGTGATTTTGT
764	1220	TACAAAATCACAGAGCTCTT	1718	AAGAGCTCTGTGATTTTGTA
765	1221	TTACAAAATCACAGAGCTCT	1719	AGAGCTCTGTGATTTTGTAA
766	1222	CTTACAAAATCACAGAGCTC	1720	GAGCTCTGTGATTTTGTAAG
767	1223	TCTTACAAAATCACAGAGCT	1721	AGCTCTGTGATTTTGTAAGA
768	1224	ATCTTACAAAATCACAGAGC	1722	GCTCTGTGATTTTGTAAGAT
769	1225	GATCTTACAAAATCACAGAG	1723	CTCTGTGATTTTGTAAGATC
770	1226	GGATCTTACAAAATCACAGA	1724	TCTGTGATTTTGTAAGATCC
771	1227	TGGATCTTACAAAATCACAG	1725	CTGTGATTTTGTAAGATCCA
772	1228	CTGGATCTTACAAAATCACA	1726	TGTGATTTTGTAAGATCCAG
773	1229	TCTGGATCTTACAAAATCAC	1727	GTGATTTTGTAAGATCCAGA
774	1230	GTCTGGATCTTACAAAATCA	1728	TGATTTTGTAAGATCCAGAC
775	1231	AGTCTGGATCTTACAAAATC	1729	GATTTTGTAAGATCCAGACT
776	1232	AAGTCTGGATCTTACAAAAT	1730	ATTTTGTAAGATCCAGACTT
777	1233	CAAGTCTGGATCTTACAAAA	1731	TTTTGTAAGATCCAGACTTG
778	1234	TCAAGTCTGGATCTTACAAA	1732	TTTGTAAGATCCAGACTTGA
779	1235	TTCAAGTCTGGATCTTACAA	1733	TTGTAAGATCCAGACTTGAA

780	1236	CTTCAAGTCTGGATCTTACA	1734	TGTAAGATCCAGACTTGAAG
781	1237	ACTTCAAGTCTGGATCTTAC	1735	GTAAGATCCAGACTTGAAGT
782	1238	GACTTCAAGTCTGGATCTTA	1736	TAAGATCCAGACTTGAAGTC
783	1239	TGACTTCAAGTCTGGATCTT	1737	AAGATCCAGACTTGAAGTCA
784	1240	GTGACTTCAAGTCTGGATCT	1738	AGATCCAGACTTGAAGTCAC
785	1241	AGTGACTTCAAGTCTGGATC	1739	GATCCAGACTTGAAGTCACT
786	1242	CAGTGACTTCAAGTCTGGAT	1740	ATCCAGACTTGAAGTCACTG
787	1243	TCAGTGACTTCAAGTCTGGA	1741	TCCAGACTTGAAGTCACTGA
788	1244	ATCAGTGACTTCAAGTCTGG	1742	CCAGACTTGAAGTCACTGAT
789	1245	CATCAGTGACTTCAAGTCTG	1743	CAGACTTGAAGTCACTGATG
790	1246	TCATCAGTGACTTCAAGTCT	1744	AGACTTGAAGTCACTGATGA
791	1247	GTCATCAGTGACTTCAAGTC	1745	GACTTGAAGTCACTGATGAC
792	1248	GGTCATCAGTGACTTCAAGT	1746	ACTTGAAGTCACTGATGACC
793	1249	AGGTCATCAGTGACTTCAAG	1747	CTTGAAGTCACTGATGACCT
794	1250	AAGGTCATCAGTGACTTCAA	1748	TTGAAGTCACTGATGACCTT
795	1251	CAAGGTCATCAGTGACTTCA	1749	TGAAGTCACTGATGACCTTG
796	1252	TCAAGGTCATCAGTGACTTC	1750	GAAGTCACTGATGACCTTGA
797	1253	CTCAAGGTCATCAGTGACTT	1751	AAGTCACTGATGACCTTGAG
798	1254	TCTCAAGGTCATCAGTGACT	1752	AGTCACTGATGACCTTGAGA
799	1255	TTCTCAAGGTCATCAGTGAC	1753	GTCACTGATGACCTTGAGAA
800	1256	TTTCTCAAGGTCATCAGTGA	1754	TCACTGATGACCTTGAGAAA
801	1257	CTTTCTCAAGGTCATCAGTG	1755	CACTGATGACCTTGAGAAAG
802	1258	ACTTTCTCAAGGTCATCAGT	1756	ACTGATGACCTTGAGAAAGT
803	1259	AACTTTCTCAAGGTCATCAG	1757	CTGATGACCTTGAGAAAGTT
804	1260	AAACTTTCTCAAGGTCATCA	1758	TGATGACCTTGAGAAAGTTT
805	1261	CAAACTTTCTCAAGGTCATC	1759	GATGACCTTGAGAAAGTTTG
806	1262	GCAAACTTTCTCAAGGTCAT	1760	ATGACCTTGAGAAAGTTTGC
807	1263	TGCAAACTTTCTCAAGGTCA	1761	TGACCTTGAGAAAGTTTGCA
808	1264	TTGCAAACTTTCTCAAGGTC	1762	GACCTTGAGAAAGTTTGCAA
809	1265	ATTGCAAACTTTCTCAAGGT	1763	ACCTTGAGAAAGTTTGCAAT
810	1266	CATTGCAAACTTTCTCAAGG	1764	CCTTGAGAAAGTTTGCAATG
811	1267	TCATTGCAAACTTTCTCAAG	1765	CTTGAGAAAGTTTGCAATGA
812	1268	TTCATTGCAAACTTTCTCAA	1766	TTGAGAAAGTTTGCAATGAA
813	1269	CTTCATTGCAAACTTTCTCA	1767	TGAGAAAGTTTGCAATGAAG
814	1270	ACTTCATTGCAAACTTTCTC	1768	GAGAAAGTTTGCAATGAAGT
815	1271	TACTTCATTGCAAACTTTCT	1769	AGAAAGTTTGCAATGAAGTA
816	1272	CTACTTCATTGCAAACTTTC	1770	GAAAGTTTGCAATGAAGTAG
817	1273	ACTACTTCATTGCAAACTTT	1771	AAAGTTTGCAATGAAGTAGT
818	1274	GACTACTTCATTGCAAACTT	1772	AAGTTTGCAATGAAGTAGTC
819	1275	CGACTACTTCATTGCAAACT	1773	AGTTTGCAATGAAGTAGTCG
820	1276	TCGACTACTTCATTGCAAAC	1774	GTTTGCAATGAAGTAGTCGA
821	1277	GTCGACTACTTCATTGCAAA	1775	TTTGCAATGAAGTAGTCGAC
822	1278	TGTCGACTACTTCATTGCAA	1776	TTGCAATGAAGTAGTCGACA
823	1279	GTGTCGACTACTTCATTGCA	1777	TGCAATGAAGTAGTCGACAC
824	1280	GGTGTCGACTACTTCATTGC	1778	GCAATGAAGTAGTCGACACC
825	1281	AGGTGTCGACTACTTCATTG	1779	CAATGAAGTAGTCGACACCT
826	1282	CAGGTGTCGACTACTTCATT	1780	AATGAAGTAGTCGACACCTG
827	1283	ACAGGTGTCGACTACTTCAT	1781	ATGAAGTAGTCGACACCTGT
828	1284	AACAGGTGTCGACTACTTCA	1782	TGAAGTAGTCGACACCTGTT
829	1285	AAACAGGTGTCGACTACTTC	1783	GAAGTAGTCGACACCTGTTT
830	1286	CAAACAGGTGTCGACTACTT	1784	AAGTAGTCGACACCTGTTTG
831	1287	ACAAACAGGTGTCGACTACT	1785	AGTAGTCGACACCTGTTTGT
832	1288	TACAAACAGGTGTCGACTAC	1786	GTAGTCGACACCTGTTTGTA
833	1289	ATACAAACAGGTGTCGACTA	1787	TAGTCGACACCTGTTTGTAT
834	1290	TATACAAACAGGTGTCGACT	1788	AGTCGACACCTGTTTGTATA
835	1291	TTATACAAACAGGTGTCGAC	1789	GTCGACACCTGTTTGTATAA
836	1292	CTTATACAAACAGGTGTCGA	1790	TCGACACCTGTTTGTATAAG
837	1293	CCTTATACAAACAGGTGTCG	1791	CGACACCTGTTTGTATAAGG
838	1294	CCCTTATACAAACAGGTGTC	1792	GACACCTGTTTGTATAAGGG
839	1295	TCCCTTATACAAACAGGTGT	1793	ACACCTGTTTGTATAAGGGA
840	1296	TTCCCTTATACAAACAGGTG	1794	CACCTGTTTGTATAAGGGAA
841	1297	CTTCCCTTATACAAACAGGT	1795	ACCTGTTTGTATAAGGGAAG
842	1298	ACTTCCCTTATACAAACAGG	1796	CCTGTTTGTATAAGGGAAGT
843	1299	GACTTCCCTTATACAAACAG	1797	CTGTTTGTATAAGGGAAGTC
844	1300	CGACTTCCCTTATACAAACA	1798	TGTTTGTATAAGGGAAGTCG
845	1301	TCGACTTCCCTTATACAAAC	1799	GTTTGTATAAGGGAAGTCGA
846	1302	CTCGACTTCCCTTATACAAA	1800	TTTGTATAAGGGAAGTCGAG
847	1303	TCTCGACTTCCCTTATACAA	1801	TTGTATAAGGGAAGTCGAGA
848	1304	GTCTCGACTTCCCTTATACA	1802	TGTATAAGGGAAGTCGAGAC
849	1305	TGTCTCGACTTCCCTTATAC	1803	GTATAAGGGAAGTCGAGACA
850	1306	TTGTCTCGACTTCCCTTATA	1804	TATAAGGGAAGTCGAGACAA

851	1307	GTTGTCTCGACTTCCCTTAT	1805	ATAAGGGAAGTCGAGACAAC
852	1308	TGTTGTCTCGACTTCCCTTA	1806	TAAGGGAAGTCGAGACAACA
853	1309	ATGTTGTCTCGACTTCCCTT	1807	AAGGGAAGTCGAGACAACAT
854	1310	CATGTTGTCTCGACTTCCCT	1808	AGGGAAGTCGAGACAACATG
855	1311	TCATGTTGTCTCGACTTCCC	1809	GGGAAGTCGAGACAACATGA
856	1312	CTCATGTTGTCTCGACTTCC	1810	GGAAGTCGAGACAACATGAG
857	1313	ACTCATGTTGTCTCGACTTC	1811	GAAGTCGAGACAACATGAGT
858	1314	CACTCATGTTGTCTCGACTT	1812	AAGTCGAGACAACATGAGTG
859	1315	ACACTCATGTTGTCTCGACT	1813	AGTCGAGACAACATGAGTGT
860	1316	CACACTCATGTTGTCTCGAC	1814	GTCGAGACAACATGAGTGTG
861	1317	TCACACTCATGTTGTCTCGA	1815	TCGAGACAACATGAGTGTGA
862	1318	ATCACACTCATGTTGTCTCG	1816	CGAGACAACATGAGTGTGAT
863	1319	AATCACACTCATGTTGTCTC	1817	GAGACAACATGAGTGTGATT
864	1320	AAATCACACTCATGTTGTCT	1818	AGACAACATGAGTGTGATTT
865	1321	AAAATCACACTCATGTTGTC	1819	GACAACATGAGTGTGATTTT
866	1322	CAAAATCACACTCATGTTGT	1820	ACAACATGAGTGTGATTTTG
867	1323	TCAAAATCACACTCATGTTG	1821	CAACATGAGTGTGATTTTGA
868	1324	ATCAAAATCACACTCATGTT	1822	AACATGAGTGTGATTTTGAT
869	1325	GATCAAAATCACACTCATGT	1823	ACATGAGTGTGATTTTGATC
870	1326	AGATCAAAATCACACTCATG	1824	CATGAGTGTGATTTTGATCT
871	1327	CAGATCAAAATCACACTCAT	1825	ATGAGTGTGATTTTGATCTG
872	1328	ACAGATCAAAATCACACTCA	1826	TGAGTGTGATTTTGATCTGT
873	1329	AACAGATCAAAATCACACTC	1827	GAGTGTGATTTTGATCTGTT
874	1330	AAACAGATCAAAATCACACT	1828	AGTGTGATTTTGATCTGTTT
875	1331	AAAACAGATCAAAATCACAC	1829	GTGTGATTTTGATCTGTTTT
876	1332	GAAAACAGATCAAAATCACA	1830	TGTGATTTTGATCTGTTTTC
877	1333	GGAAAACAGATCAAAATCAC	1831	GTGATTTTGATCTGTTTTCC
878	1334	TGGAAAACAGATCAAAATCA	1832	TGATTTTGATCTGTTTTCCA
879	1335	TTGGAAAACAGATCAAAATC	1833	GATTTTGATCTGTTTTCCAA
880	1336	TTTGGAAAACAGATCAAAAT	1834	ATTTTGATCTGTTTTCCAAA
881	1337	ATTTGGAAAACAGATCAAAA	1835	TTTTGATCTGTTTTCCAAAT
882	1338	CATTTGGAAAACAGATCAAA	1836	TTTGATCTGTTTTCCAAATG
883	1339	GCATTTGGAAAACAGATCAA	1837	TTGATCTGTTTTCCAAATGC
884	1340	TGCATTTGGAAAACAGATCA	1838	TGATCTGTTTTCCAAATGCA
885	1341	GTGCATTTGGAAAACAGATC	1839	GATCTGTTTTCCAAATGCAC
886	1342	GGTGCATTTGGAAAACAGAT	1840	ATCTGTTTTCCAAATGCACC
887	1343	GGGTGCATTTGGAAAACAGA	1841	TCTGTTTTCCAAATGCACCC
888	1344	TGGGTGCATTTGGAAAACAG	1842	CTGTTTTCCAAATGCACCCA
889	1345	TTGGGTGCATTTGGAAAACA	1843	TGTTTTCCAAATGCACCCAA
890	1346	TTTGGGTGCATTTGGAAAAC	1844	GTTTTCCAAATGCACCCAAA
891	1347	CTTTGGGTGCATTTGGAAAA	1845	TTTTCCAAATGCACCCAAAG
892	1348	ACTTTGGGTGCATTTGGAAA	1846	TTTCCAAATGCACCCAAAGT
893	1349	TACTTTGGGTGCATTTGGAA	1847	TTCCAAATGCACCCAAAGTA
894	1350	ATACTTTGGGTGCATTTGGA	1848	TCCAAATGCACCCAAAGTAT
895	1351	GATACTTTGGGTGCATTTGG	1849	CCAAATGCACCCAAAGTATC
896	1352	CGATACTTTGGGTGCATTTG	1850	CAAATGCACCCAAAGTATCG
897	1353	GCGATACTTTGGGTGCATTT	1851	AAATGCACCCAAAGTATCGC
898	1354	GGCGATACTTTGGGTGCATT	1852	AATGCACCCAAAGTATCGCC
899	1355	TGGCGATACTTTGGGTGCAT	1853	ATGCACCCAAAGTATCGCCA
900	1356	CTGGCGATACTTTGGGTGCA	1854	TGCACCCAAAGTATCGCCAG
901	1357	TCTGGCGATACTTTGGGTGC	1855	GCACCCAAAGTATCGCCAGA
902	1358	TTCTGGCGATACTTTGGGTG	1856	CACCCAAAGTATCGCCAGAA
903	1359	CTTCTGGCGATACTTTGGGT	1857	ACCCAAAGTATCGCCAGAAG
904	1360	GCTTCTGGCGATACTTTGGG	1858	CCCAAAGTATCGCCAGAAGC
905	1361	TGCTTCTGGCGATACTTTGG	1859	CCAAAGTATCGCCAGAAGCA
906	1362	CTGCTTCTGGCGATACTTTG	1860	CAAAGTATCGCCAGAAGCAG
907	1363	ACTGCTTCTGGCGATACTTT	1861	AAAGTATCGCCAGAAGCAGT
908	1364	CACTGCTTCTGGCGATACTT	1862	AAGTATCGCCAGAAGCAGTG
909	1365	TCACTGCTTCTGGCGATACT	1863	AGTATCGCCAGAAGCAGTGA
910	1366	TTCACTGCTTCTGGCGATAC	1864	GTATCGCCAGAAGCAGTGAA
911	1367	CTTCACTGCTTCTGGCGATA	1865	TATCGCCAGAAGCAGTGAAG
912	1368	TCTTCACTGCTTCTGGCGAT	1866	ATCGCCAGAAGCAGTGAAGA
913	1369	TTCTTCACTGCTTCTGGCGA	1867	TCGCCAGAAGCAGTGAAGAA
914	1370	CTTCTTCACTGCTTCTGGCG	1868	CGCCAGAAGCAGTGAAGAAG
915	1371	CCTTCTTCACTGCTTCTGGC	1869	GCCAGAAGCAGTGAAGAAGG
916	1372	TCCTTCTTCACTGCTTCTGG	1870	CCAGAAGCAGTGAAGAAGGA
917	1373	CTCCTTCTTCACTGCTTCTG	1871	CAGAAGCAGTGAAGAAGGAG
918	1374	CCTCCTTCTTCACTGCTTCT	1872	AGAAGCAGTGAAGAAGGAGG
919	1375	GCCTCCTTCTTCACTGCTTC	1873	GAAGCAGTGAAGAAGGAGGC
920	1376	TGCCTCCTTCTTCACTGCTT	1874	AAGCAGTGAAGAAGGAGGCA
921	1377	CTGCCTCCTTCTTCACTGCT	1875	AGCAGTGAAGAAGGAGGCAG

922	1378	TCTGCCTCCTTCTTCACTGC	1876	GCAGTGAAGAAGGAGGCAGA
923	1379	CTCTGCCTCCTTCTTCACTG	1877	CAGTGAAGAAGGAGGCAGAG
924	1380	ACTCTGCCTCCTTCTTCACT	1878	AGTGAAGAAGGAGGCAGAGT
925	1381	AACTCTGCCTCCTTCTTCAC	1879	GTGAAGAAGGAGGCAGAGTT
926	1382	CAACTCTGCCTCCTTCTTCA	1880	TGAAGAAGGAGGCAGAGTTG
927	1383	CCAACTCTGCCTCCTTCTTC	1881	GAAGAAGGAGGCAGAGTTGG
928	1384	TCCAACTCTGCCTCCTTCTT	1882	AAGAAGGAGGCAGAGTTGGA
929	1385	GTCCAACTCTGCCTCCTTCT	1883	AGAAGGAGGCAGAGTTGGAC
930	1386	TGTCCAACTCTGCCTCCTTC	1884	GAAGGAGGCAGAGTTGGACA
931	1387	TTGTCCAACTCTGCCTCCTT	1885	AAGGAGGCAGAGTTGGACAA
932	1388	CTTGTCCAACTCTGCCTCCT	1886	AGGAGGCAGAGTTGGACAAG
933	1389	ACTTGTCCAACTCTGCCTCC	1887	GGAGGCAGAGTTGGACAAGT
934	1390	TACTTGTCCAACTCTGCCTC	1888	GAGGCAGAGTTGGACAAGTA
935	1391	GTACTTGTCCAACTCTGCCT	1889	AGGCAGAGTTGGACAAGTAC
936	1392	GGTACTTGTCCAACTCTGCC	1890	GGCAGAGTTGGACAAGTACC
937	1393	AGGTACTTGTCCAACTCTGC	1891	GCAGAGTTGGACAAGTACCT
938	1394	CAGGTACTTGTCCAACTCTG	1892	CAGAGTTGGACAAGTACCTG
939	1395	CCAGGTACTTGTCCAACTCT	1893	AGAGTTGGACAAGTACCTGG
940	1396	TCCAGGTACTTGTCCAACTC	1894	GAGTTGGACAAGTACCTGGA
941	1397	TTCCAGGTACTTGTCCAACT	1895	AGTTGGACAAGTACCTGGAA
942	1398	ATTCCAGGTACTTGTCCAAC	1896	GTTGGACAAGTACCTGGAAT
943	1399	CATTCCAGGTACTTGTCCAA	1897	TTGGACAAGTACCTGGAATG
944	1400	GCATTCCAGGTACTTGTCCA	1898	TGGACAAGTACCTGGAATGC
945	1401	TGCATTCCAGGTACTTGTCC	1899	GGACAAGTACCTGGAATGCA
946	1402	CTGCATTCCAGGTACTTGTC	1900	GACAAGTACCTGGAATGCAG
947	1403	TCTGCATTCCAGGTACTTGT	1901	ACAAGTACCTGGAATGCAGA
948	1404	CTCTGCATTCCAGGTACTTG	1902	CAAGTACCTGGAATGCAGAG
949	1405	ACTCTGCATTCCAGGTACTT	1903	AAGTACCTGGAATGCAGAGT
950	1406	TACTCTGCATTCCAGGTACT	1904	AGTACCTGGAATGCAGAGTA
951	1407	CTACTCTGCATTCCAGGTAC	1905	GTACCTGGAATGCAGAGTAG
952	1408	TCTACTCTGCATTCCAGGTA	1906	TACCTGGAATGCAGAGTAGA
953	1409	TTCTACTCTGCATTCCAGGT	1907	ACCTGGAATGCAGAGTAGAA
954	1410	CTTCTACTCTGCATTCCAGG	1908	CCTGGAATGCAGAGTAGAAG

Table 1B: Example ATXN2 AON sequences

SEQ ID	Oligo	AON Sequence 5' to 3'	SEQ ID	Oligo	AON Sequence 5' to 3'	SEQ ID	Oligo	AON Sequence 5' to 3'
1914	1	CGCTGGGTTGCTTTCTCGGG	51061	49148	AATTCAACTAAAATTTTATC	100208	98295	AAGCAACAAAAACAGAACCT
1915	2	GCGCTGGGTTGCTTTCTCGG	51062	49149	AAATTCAACTAAAATTTTAT	100209	98296	CAAGCAACAAAAACAGAACC
1916	3	CGCGCTGGGTTGCTTTCTCG	51063	49150	TAAATTCAACTAAAATTTTA	100210	98297	ACAAGCAACAAAAACAGAAC
1917	4	GCGCGCTGGGTTGCTTTCTC	51064	49151	TTAAATTCAACTAAAATTTT	100211	98298	TACAAGCAACAAAAACAGAA
1918	5	GGCGCGCTGGGTTGCTTTCT	51065	49152	ATTAAATTCAACTAAAATTT	100212	98299	GTACAAGCAACAAAAACAGA
1919	6	CGGCGCGCTGGGTTGCTTTC	51066	49153	TATTAAATTCAACTAAAATT	100213	98300	AGTACAAGCAACAAAAACAG
1920	7	GCGGCGCGCTGGGTTGCTTT	51067	49154	GTATTAAATTCAACTAAAAT	100214	98301	AAGTACAAGCAACAAAAACA
1921	8	GGCGGCGCGCTGGGTTGCTT	51068	49155	TGTATTAAATTCAACTAAAA	100215	98302	CAAGTACAAGCAACAAAAAC
1922	9	GGGCGGCGCGCTGGGTTGCT	51069	49156	ATGTATTAAATTCAACTAAA	100216	98303	GCAAGTACAAGCAACAAAAA
1923	10	CGGGCGGCGCGCTGGGTTGC	51070	49157	TATGTATTAAATTCAACTAA	100217	98304	AGCAAGTACAAGCAACAAAA
1924	11	GCGGGCGGCGCGCTGGGTTG	51071	49158	CTATGTATTAAATTCAACTA	100218	98305	GAGCAAGTACAAGCAACAAA
1925	12	AGCGGGCGGCGCGCTGGGTT	51072	49159	GCTATGTATTAAATTCAACT	100219	98306	GGAGCAAGTACAAGCAACAA
1926	13	GAGCGGGCGGCGCGCTGGGT	51073	49160	TGCTATGTATTAAATTCAAC	100220	98307	GGGAGCAAGTACAAGCAACA
1927	14	GGAGCGGGCGGCGCGCTGGG	51074	49161	GTGCTATGTATTAAATTCAA	100221	98308	GGGGAGCAAGTACAAGCAAC
1928	15	AGGAGCGGGCGGCGCGCTGG	51075	49162	AGTGCTATGTATTAAATTCA	100222	98309	GGGGGAGCAAGTACAAGCAA
1929	16	GAGGAGCGGGCGGCGCGCTG	51076	49163	GAGTGCTATGTATTAAATTC	100223	98310	AGGGGGAGCAAGTACAAGCA
1930	17	TGAGGAGCGGGCGGCGCGCT	51077	49164	AGAGTGCTATGTATTAAATT	100224	98311	AAGGGGGAGCAAGTACAAGC
1931	18	GTGAGGAGCGGGCGGCGCGC	51078	49165	CAGAGTGCTATGTATTAAAT	100225	98312	AAAGGGGGAGCAAGTACAAG
1932	19	CGTGAGGAGCGGGCGGCGCG	51079	49166	CCAGAGTGCTATGTATTAAA	100226	98313	AAAAGGGGGAGCAAGTACAA
1933	20	ACGTGAGGAGCGGGCGGCGC	51080	49167	TCCAGAGTGCTATGTATTAA	100227	98314	AAAAAGGGGGAGCAAGTACA
1934	21	CACGTGAGGAGCGGGCGGCG	51081	49168	TTCCAGAGTGCTATGTATTA	100228	98315	AAAAAAGGGGGAGCAAGTAC
1935	22	ACACGTGAGGAGCGGGCGGC	51082	49169	TTTCCAGAGTGCTATGTATT	100229	98316	GAAAAAAGGGGGAGCAAGTA
1936	23	GACACGTGAGGAGCGGGCGG	51083	49170	CTTTCCAGAGTGCTATGTAT	100230	98317	TGAAAAAAGGGGGAGCAAGT
1937	24	GGACACGTGAGGAGCGGGCG	51084	49171	TCTTTCCAGAGTGCTATGTA	100231	98318	CTGAAAAAAGGGGGAGCAAG
1938	25	GGGACACGTGAGGAGCGGGC	51085	49172	CTCTTTCCAGAGTGCTATGT	100232	98319	GCTGAAAAAAGGGGGAGCAA
1939	26	AGGGACACGTGAGGAGCGGG	51086	49173	ACTCTTTCCAGAGTGCTATG	100233	98320	GGCTGAAAAAAGGGGGAGCA
1940	27	GAGGGACACGTGAGGAGCGG	51087	49174	TACTCTTTCCAGAGTGCTAT	100234	98321	TGGCTGAAAAAAGGGGGAGC
1941	28	GGAGGGACACGTGAGGAGCG	51088	49175	ATACTCTTTCCAGAGTGCTA	100235	98322	ATGGCTGAAAAAAGGGGGAG
1942	29	GGGAGGGACACGTGAGGAGC	51089	49176	AATACTCTTTCCAGAGTGCT	100236	98323	AATGGCTGAAAAAAGGGGGA
1943	30	CGGGAGGGACACGTGAGGAG	51090	49177	CAATACTCTTTCCAGAGTGC	100237	98324	GAATGGCTGAAAAAAGGGGG
1944	31	CCGGGAGGGACACGTGAGGA	51091	49178	CCAATACTCTTTCCAGAGTG	100238	98325	GGAATGGCTGAAAAAAGGGG
1945	32	GCCGGGAGGGACACGTGAGG	51092	49179	GCCAATACTCTTTCCAGAGT	100239	98326	AGGAATGGCTGAAAAAAGGG
1946	33	GGCCGGGAGGGACACGTGAG	51093	49180	GGCCAATACTCTTTCCAGAG	100240	98327	CAGGAATGGCTGAAAAAAGG
1947	34	GGGCCGGGAGGGACACGTGA	51094	49181	TGGCCAATACTCTTTCCAGA	100241	98328	ACAGGAATGGCTGAAAAAAG
1948	35	GGGGCCGGGAGGGACACGTG	51095	49182	GTGGCCAATACTCTTTCCAG	100242	98329	AACAGGAATGGCTGAAAAAA
1949	36	CGGGGCCGGGAGGGACACGT	51096	49183	TGTGGCCAATACTCTTTCCA	100243	98330	AAACAGGAATGGCTGAAAAA
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1951	38	CCCGGGGCCGGGAGGGACAC	51098	49185	GTTGTGGCCAATACTCTTTC	100245	98332	GAAAACAGGAATGGCTGAAA
1952	39	CCCCGGGGCCGGGAGGGACA	51099	49186	TGTTGTGGCCAATACTCTTT	100246	98333	AGAAAACAGGAATGGCTGAA
1953	40	GCCCCGGGGCCGGGAGGGAC	51100	49187	TTGTTGTGGCCAATACTCTT	100247	98334	AAGAAAACAGGAATGGCTGA
1954	41	GGCCCCGGGGCCGGGAGGGA	51101	49188	TTTGTTGTGGCCAATACTCT	100248	98335	AAAGAAAACAGGAATGGCTG
1955	42	TGGCCCCGGGGCCGGGAGGG	51102	49189	TTTTGTTGTGGCCAATACTC	100249	98336	GAAAGAAAACAGGAATGGCT
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1957	44	GGTGGCCCCGGGGCCGGGAG	51104	49191	TTTTTTGTTGTGGCCAATAC	100251	98338	AAGAAAGAAAACAGGAATGG
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1959	46	GAGGTGGCCCCGGGGCCGGG	51106	49193	TTTTTTTTGTTGTGGCCAAT	100253	98340	AAAAGAAAGAAAACAGGAAT
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1969	56	AGCAGAACGTGAGGTGGCCC	51116	49203	TAGGGAACCTTTTTTTTTGT	100263	98350	CATCCTCTACAAAAGAAAGA
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51265	49352	TAATTTTGAAGAGGAGCAAG
51266	49353	TTAATTTTGAAGAGGAGCAA
51267	49354	ATTAATTTTGAAGAGGAGCA
51268	49355	CATTAATTTTGAAGAGGAGC
51269	49356	ACATTAATTTTGAAGAGGAG
51270	49357	GACATTAATTTTGAAGAGGA

100347	98434	TTAGCAAAATAAGTGATGAG
100348	98435	ATTAGCAAAATAAGTGATGA
100349	98436	TATTAGCAAAATAAGTGATG
100350	98437	ATATTAGCAAAATAAGTGAT
100351	98438	GATATTAGCAAAATAAGTGA
100352	98439	AGATATTAGCAAAATAAGTG
100353	98440	AAGATATTAGCAAAATAAGT
100354	98441	AAAGATATTAGCAAAATAAG
100355	98442	CAAAGATATTAGCAAAATAA
100356	98443	ACAAAGATATTAGCAAAATA
100357	98444	GACAAAGATATTAGCAAAAT
100358	98445	AGACAAAGATATTAGCAAAA
100359	98446	AAGACAAAGATATTAGCAAA
100360	98447	GAAGACAAAGATATTAGCAA
100361	98448	AGAAGACAAAGATATTAGCA
100362	98449	CAGAAGACAAAGATATTAGC
100363	98450	ACAGAAGACAAAGATATTAG
100364	98451	AACAGAAGACAAAGATATTA
100365	98452	GAACAGAAGACAAAGATATT
100366	98453	AGAACAGAAGACAAAGATAT
100367	98454	AAGAACAGAAGACAAAGATA
100368	98455	AAAGAACAGAAGACAAAGAT
100369	98456	AAAAGAACAGAAGACAAAGA
100370	98457	AAAAAGAACAGAAGACAAAG
100371	98458	CAAAAAGAACAGAAGACAAA
100372	98459	TCAAAAAGAACAGAAGACAA
100373	98460	ATCAAAAAGAACAGAAGACA
100374	98461	CATCAAAAAGAACAGAAGAC
100375	98462	CCATCAAAAAGAACAGAAGA
100376	98463	ACCATCAAAAAGAACAGAAG
100377	98464	GACCATCAAAAAGAACAGAA
100378	98465	GGACCATCAAAAAGAACAGA
100379	98466	AGGACCATCAAAAAGAACAG
100380	98467	AAGGACCATCAAAAAGAACA
100381	98468	CAAGGACCATCAAAAAGAAC
100382	98469	CCAAGGACCATCAAAAAGAA
100383	98470	ACCAAGGACCATCAAAAAGA
100384	98471	AACCAAGGACCATCAAAAAG
100385	98472	AAACCAAGGACCATCAAAAA
100386	98473	AAAACCAAGGACCATCAAAA
100387	98474	CAAAACCAAGGACCATCAAA
100388	98475	GCAAAACCAAGGACCATCAA
100389	98476	TGCAAAACCAAGGACCATCA
100390	98477	CTGCAAAACCAAGGACCATC
100391	98478	ACTGCAAAACCAAGGACCAT
100392	98479	GACTGCAAAACCAAGGACCA
100393	98480	AGACTGCAAAACCAAGGACC
100394	98481	TAGACTGCAAAACCAAGGAC
100395	98482	GTAGACTGCAAAACCAAGGA
100396	98483	AGTAGACTGCAAAACCAAGG
100397	98484	AAGTAGACTGCAAAACCAAG
100398	98485	AAAGTAGACTGCAAAACCAA
100399	98486	TAAAGTAGACTGCAAAACCA
100400	98487	TTAAAGTAGACTGCAAAACC
100401	98488	TTTAAAGTAGACTGCAAAAC
100402	98489	CTTTAAAGTAGACTGCAAAA
100403	98490	CCTTTAAAGTAGACTGCAAA
100404	98491	ACCTTTAAAGTAGACTGCAA
100405	98492	AACCTTTAAAGTAGACTGCA
100406	98493	AAACCTTTAAAGTAGACTGC
100407	98494	AAAACCTTTAAAGTAGACTG
100408	98495	AAAAACCTTTAAAGTAGACT
100409	98496	TAAAAACCTTTAAAGTAGAC
100410	98497	ATAAAAACCTTTAAAGTAGA
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100412	98499	AAATAAAAACCTTTAAAGTA
100413	98500	AAAATAAAAACCTTTAAAGT
100414	98501	AAAAATAAAAACCTTTAAAG
100415	98502	AAAAAATAAAAACCTTTAAA
100416	98503	AAAAAAATAAAAACCTTTAA
100417	98504	TAAAAAAATAAAAACCTTTA

2124	211	CTGGCTGCGGCGAAGCGGCG
2125	212	CCTGGCTGCGGCGAAGCGGC
2126	213	ACCTGGCTGCGGCGAAGCGG
2127	214	CACCTGGCTGCGGCGAAGCG
2128	215	CCACCTGGCTGCGGCGAAGC
2129	216	GCCACCTGGCTGCGGCGAAG
2130	217	GGCCACCTGGCTGCGGCGAA
2131	218	GGGCCACCTGGCTGCGGCGA
2132	219	CGGGCCACCTGGCTGCGGCG
2133	220	CCGGGCCACCTGGCTGCGGC
2134	221	CCCGGGCCACCTGGCTGCGG
2135	222	ACCCGGGCCACCTGGCTGCG
2136	223	CACCCGGGCCACCTGGCTGC
2137	224	CCACCCGGGCCACCTGGCTG
2138	225	GCCACCCGGGCCACCTGGCT
2139	226	CGCCACCCGGGCCACCTGGC
2140	227	GCGCCACCCGGGCCACCTGG
2141	228	AGCGCCACCCGGGCCACCTG
2142	229	GAGCGCCACCCGGGCCACCT
2143	230	CGAGCGCCACCCGGGCCACC
2144	231	GCGAGCGCCACCCGGGCCAC
2145	232	AGCGAGCGCCACCCGGGCCA
2146	233	GAGCGAGCGCCACCCGGGCC
2147	234	GGAGCGAGCGCCACCCGGGC
2148	235	TGGAGCGAGCGCCACCCGGG
2149	236	CTGGAGCGAGCGCCACCCGG
2150	237	GCTGGAGCGAGCGCCACCCG
2151	238	CGCTGGAGCGAGCGCCACCC
2152	239	CCGCTGGAGCGAGCGCCACC
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2154	241	GGCCGCTGGAGCGAGCGCCA
2155	242	CGGCCGCTGGAGCGAGCGCC
2156	243	CCGGCCGCTGGAGCGAGCGC
2157	244	GCCGGCCGCTGGAGCGAGCG
2158	245	CGCCGGCCGCTGGAGCGAGC
2159	246	GCGCCGGCCGCTGGAGCGAG
2160	247	CGCGCCGGCCGCTGGAGCGA
2161	248	CCGCGCCGGCCGCTGGAGCG
2162	249	GCCGCGCCGGCCGCTGGAGC
2163	250	CGCCGCGCCGGCCGCTGGAG
2164	251	CCGCCGCGCCGGCCGCTGGA
2165	252	TCCGCCGCGCCGGCCGCTGG
2166	253	CTCCGCCGCGCCGGCCGCTG
2167	254	GCTCCGCCGCGCCGGCCGCT
2168	255	CGCTCCGCCGCGCCGGCCGC
2169	256	CCGCTCCGCCGCGCCGGCCG
2170	257	CCCGCTCCGCCGCGCCGGCC
2171	258	GCCCGCTCCGCCGCGCCGGC
2172	259	CGCCCGCTCCGCCGCGCCGG
2173	260	CCGCCCGCTCCGCCGCGCCG
2174	261	CCCGCCCGCTCCGCCGCGCC
2175	262	CCCCGCCCGCTCCGCCGCGC
2176	263	GCCCCGCCCGCTCCGCCGCG
2177	264	CGCCCCGCCCGCTCCGCCGC
2178	265	CCGCCCCGCCCGCTCCGCCG
2179	266	GCCGCCCCGCCCGCTCCGCC
2180	267	CGCCGCCCCGCCCGCTCCGC
2181	268	CCGCCGCCCCGCCCGCTCCG
2182	269	ACCGCCGCCCCGCCCGCTCC
2183	270	CACCGCCGCCCCGCCCGCTC
2184	271	CCACCGCCGCCCCGCCCGCT
2185	272	GCCACCGCCGCCCCGCCCGC
2186	273	CGCCACCGCCGCCCCGCCCG
2187	274	GCGCCACCGCCGCCCCGCCC
2188	275	CGCGCCACCGCCGCCCCGCC
2189	276	CCGCGCCACCGCCGCCCCGC
2190	277	GCCGCGCCACCGCCGCCCCG
2191	278	GGCCGCGCCACCGCCGCCCC
2192	279	GGGCCGCGCCACCGCCGCCC
2193	280	GGGGCCGCGCCACCGCCGCC
2194	281	CGGGGCCGCGCCACCGCCGC

51271	49358	TGACATTAATTTTGAAGAGG
51272	49359	ATGACATTAATTTTGAAGAG
51273	49360	AATGACATTAATTTTGAAGA
51274	49361	TAATGACATTAATTTTGAAG
51275	49362	TTAATGACATTAATTTTGAA
51276	49363	TTTAATGACATTAATTTTGA
51277	49364	ATTTAATGACATTAATTTTG
51278	49365	AATTTAATGACATTAATTTT
51279	49366	AAATTTAATGACATTAATTT
51280	49367	AAAATTTAATGACATTAATT
51281	49368	AAAAATTTAATGACATTAAT
51282	49369	TAAAAATTTAATGACATTAA
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51288	49375	AAGTAATAAAAATTTAATGA
51289	49376	AAAGTAATAAAAATTTAATG
51290	49377	TAAAGTAATAAAAATTTAAT
51291	49378	ATAAAGTAATAAAAATTTAA
51292	49379	AATAAAGTAATAAAAATTTA
51293	49380	TAATAAAGTAATAAAAATTT
51294	49381	CTAATAAAGTAATAAAAATT
51295	49382	TCTAATAAAGTAATAAAAAT
51296	49383	ATCTAATAAAGTAATAAAAA
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51302	49389	ATGAAGATCTAATAAAGTAA
51303	49390	AATGAAGATCTAATAAAGTA
51304	49391	AAATGAAGATCTAATAAAGT
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51306	49393	AGAAATGAAGATCTAATAAA
51307	49394	GAGAAATGAAGATCTAATAA
51308	49395	TGAGAAATGAAGATCTAATA
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51315	49402	AATTATCTGAGAAATGAAGA
51316	49403	AAATTATCTGAGAAATGAAG
51317	49404	AAAATTATCTGAGAAATGAA
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51319	49406	CTAAAATTATCTGAGAAATG
51320	49407	ACTAAAATTATCTGAGAAAT
51321	49408	AACTAAAATTATCTGAGAAA
51322	49409	GAACTAAAATTATCTGAGAA
51323	49410	TGAACTAAAATTATCTGAGA
51324	49411	ATGAACTAAAATTATCTGAG
51325	49412	AATGAACTAAAATTATCTGA
51326	49413	TAATGAACTAAAATTATCTG
51327	49414	ATAATGAACTAAAATTATCT
51328	49415	TATAATGAACTAAAATTATC
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51331	49418	TTCTATAATGAACTAAAATT
51332	49419	TTTCTATAATGAACTAAAAT
51333	49420	CTTTCTATAATGAACTAAAA
51334	49421	CCTTTCTATAATGAACTAAA
51335	49422	GCCTTTCTATAATGAACTAA
51336	49423	TGCCTTTCTATAATGAACTA
51337	49424	TTGCCTTTCTATAATGAACT
51338	49425	CTTGCCTTTCTATAATGAAC
51339	49426	TCTTGCCTTTCTATAATGAA
51340	49427	TTCTTGCCTTTCTATAATGA
51341	49428	TTTCTTGCCTTTCTATAATG

100418	98505	ATAAAAAAATAAAAACCTTT
100419	98506	CATAAAAAAATAAAAACCTT
100420	98507	CCATAAAAAAATAAAAACCT
100421	98508	CCCATAAAAAAATAAAAACC
100422	98509	ACCCATAAAAAAATAAAAAC
100423	98510	TACCCATAAAAAAATAAAAA
100424	98511	GTACCCATAAAAAAATAAAA
100425	98512	TGTACCCATAAAAAAATAAA
100426	98513	ATGTACCCATAAAAAAATAA
100427	98514	TATGTACCCATAAAAAAATA
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100430	98517	TACTATGTACCCATAAAAAA
100431	98518	CTACTATGTACCCATAAAAA
100432	98519	TCTACTATGTACCCATAAAA
100433	98520	GTCTACTATGTACCCATAAA
100434	98521	CGTCTACTATGTACCCATAA
100435	98522	ACGTCTACTATGTACCCATA
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100437	98524	ATACGTCTACTATGTACCCA
100438	98525	AATACGTCTACTATGTACCC
100439	98526	TAATACGTCTACTATGTACC
100440	98527	ATAATACGTCTACTATGTAC
100441	98528	AATAATACGTCTACTATGTA
100442	98529	GAATAATACGTCTACTATGT
100443	98530	TGAATAATACGTCTACTATG
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100446	98533	CTATGAATAATACGTCTACT
100447	98534	CCTATGAATAATACGTCTAC
100448	98535	CCCTATGAATAATACGTCTA
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100453	98540	ACAGACCCTATGAATAATAC
100454	98541	CACAGACCCTATGAATAATA
100455	98542	TCACAGACCCTATGAATAAT
100456	98543	CTCACAGACCCTATGAATAA
100457	98544	TCTCACAGACCCTATGAATA
100458	98545	ATCTCACAGACCCTATGAAT
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100461	98548	AATATCTCACAGACCCTATG
100462	98549	AAATATCTCACAGACCCTAT
100463	98550	TAAATATCTCACAGACCCTA
100464	98551	CTAAATATCTCACAGACCCT
100465	98552	TCTAAATATCTCACAGACCC
100466	98553	ATCTAAATATCTCACAGACC
100467	98554	TATCTAAATATCTCACAGAC
100468	98555	TTATCTAAATATCTCACAGA
100469	98556	TTTATCTAAATATCTCACAG
100470	98557	CTTTATCTAAATATCTCACA
100471	98558	CCTTTATCTAAATATCTCAC
100472	98559	GCCTTTATCTAAATATCTCA
100473	98560	TGCCTTTATCTAAATATCTC
100474	98561	ATGCCTTTATCTAAATATCT
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100476	98563	ATATGCCTTTATCTAAATAT
100477	98564	TATATGCCTTTATCTAAATA
100478	98565	TTATATGCCTTTATCTAAAT
100479	98566	ATTATATGCCTTTATCTAAA
100480	98567	CATTATATGCCTTTATCTAA
100481	98568	ACATTATATGCCTTTATCTA
100482	98569	CACATTATATGCCTTTATCT
100483	98570	ACACATTATATGCCTTTATC
100484	98571	TACACATTATATGCCTTTAT
100485	98572	TTACACATTATATGCCTTTA
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100487	98574	TATTACACATTATATGCCTT
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2195	282	CCGGGGCCGCGCCACCGCCG
2196	283	CCCGGGGCCGCGCCACCGCC
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2198	285	GTCCCGGGGCCGCGCCACCG
2199	286	GGTCCCGGGGCCGCGCCACC
2200	287	CGGTCCCGGGGCCGCGCCAC
2201	288	ACGGTCCCGGGGCCGCGCCA
2202	289	TACGGTCCCGGGGCCGCGCC
2203	290	ATACGGTCCCGGGGCCGCGC
2204	291	GATACGGTCCCGGGGCCGCG
2205	292	GGATACGGTCCCGGGGCCGC
2206	293	GGGATACGGTCCCGGGGCCG
2207	294	AGGGATACGGTCCCGGGGCC
2208	295	GAGGGATACGGTCCCGGGGC
2209	296	GGAGGGATACGGTCCCGGGG
2210	297	CGGAGGGATACGGTCCCGGG
2211	298	GCGGAGGGATACGGTCCCGG
2212	299	GGCGGAGGGATACGGTCCCG
2213	300	CGGCGGAGGGATACGGTCCC
2214	301	GCGGCGGAGGGATACGGTCC
2215	302	GGCGGCGGAGGGATACGGTC
2216	303	GGGCGGCGGAGGGATACGGT
2217	304	GGGGCGGCGGAGGGATACGG
2218	305	AGGGGCGGCGGAGGGATACG
2219	306	GAGGGGCGGCGGAGGGATAC
2220	307	GGAGGGGCGGCGGAGGGATA
2221	308	GGGAGGGGCGGCGGAGGGAT
2222	309	GGGGAGGGGCGGCGGAGGGA
2223	310	GGGGGAGGGGCGGCGGAGGG
2224	311	CGGGGGAGGGGCGGCGGAGG
2225	312	GCGGGGGAGGGGCGGCGGAG
2226	313	GGCGGGGGAGGGGCGGCGGA
2227	314	GGGCGGGGGAGGGGCGGCGG
2228	315	CGGGCGGGGGAGGGGCGGCG
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2230	317	GCCGGGCGGGGGAGGGGCGG
2231	318	GGCCGGGCGGGGGAGGGGCG
2232	319	GGGCCGGGCGGGGGAGGGGC
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2234	321	CGGGGCCGGGCGGGGGAGGG
2235	322	CCGGGGCCGGGCGGGGGAGG
2236	323	GCCGGGGCCGGGCGGGGGAG
2237	324	GGCCGGGGCCGGGCGGGGGA
2238	325	GGGCCGGGGCCGGGCGGGGG
2239	326	GGGGCCGGGGCCGGGCGGGG
2240	327	GGGGGCCGGGGCCGGGCGGG
2241	328	GGGGGGCCGGGGCCGGGCGG
2242	329	AGGGGGGCCGGGGCCGGGCG
2243	330	GAGGGGGGCCGGGGCCGGGC
2244	331	GGAGGGGGGCCGGGGCCGGG
2245	332	GGGAGGGGGGCCGGGGCCGG
2246	333	AGGGAGGGGGGCCGGGGCCG
2247	334	GAGGGAGGGGGGCCGGGGCC
2248	335	GGAGGGAGGGGGGCCGGGGC
2249	336	GGGAGGGAGGGGGGCCGGGG
2250	337	CGGGAGGGAGGGGGGCCGGG
2251	338	CCGGGAGGGAGGGGGGCCGG
2252	339	GCCGGGAGGGAGGGGGGCCG
2253	340	TGCCGGGAGGGAGGGGGGCC
2254	341	CTGCCGGGAGGGAGGGGGGC
2255	342	TCTGCCGGGAGGGAGGGGGG
2256	343	CTCTGCCGGGAGGGAGGGGG
2257	344	GCTCTGCCGGGAGGGAGGGG
2258	345	AGCTCTGCCGGGAGGGAGGG
2259	346	GAGCTCTGCCGGGAGGGAGG
2260	347	CGAGCTCTGCCGGGAGGGAG
2261	348	GCGAGCTCTGCCGGGAGGGA
2262	349	GGCGAGCTCTGCCGGGAGGG
2263	350	AGGCGAGCTCTGCCGGGAGG
2264	351	GAGGCGAGCTCTGCCGGGAG
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51342	49429	TTTTCTTGCCTTTCTATAAT
51343	49430	ATTTTCTTGCCTTTCTATAA
51344	49431	TATTTTCTTGCCTTTCTATA
51345	49432	GTATTTTCTTGCCTTTCTAT
51346	49433	TGTATTTTCTTGCCTTTCTA
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51348	49435	TCTGTATTTTCTTGCCTTTC
51349	49436	ATCTGTATTTTCTTGCCTTT
51350	49437	GATCTGTATTTTCTTGCCTT
51351	49438	TGATCTGTATTTTCTTGCCT
51352	49439	CTGATCTGTATTTTCTTGCC
51353	49440	TCTGATCTGTATTTTCTTGC
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51355	49442	ACTCTGATCTGTATTTTCTT
51356	49443	CACTCTGATCTGTATTTTCT
51357	49444	TCACTCTGATCTGTATTTTC
51358	49445	GTCACTCTGATCTGTATTTT
51359	49446	TGTCACTCTGATCTGTATTT
51360	49447	TTGTCACTCTGATCTGTATT
51361	49448	GTTGTCACTCTGATCTGTAT
51362	49449	AGTTGTCACTCTGATCTGTA
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51365	49452	CAAAGTTGTCACTCTGATCT
51366	49453	TCAAAGTTGTCACTCTGATC
51367	49454	TTCAAAGTTGTCACTCTGAT
51368	49455	TTTCAAAGTTGTCACTCTGA
51369	49456	TTTTCAAAGTTGTCACTCTG
51370	49457	ATTTTCAAAGTTGTCACTCT
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51372	49459	AGATTTTCAAAGTTGTCACT
51373	49460	GAGATTTTCAAAGTTGTCAC
51374	49461	TGAGATTTTCAAAGTTGTCA
51375	49462	GTGAGATTTTCAAAGTTGTC
51376	49463	AGTGAGATTTTCAAAGTTGT
51377	49464	GAGTGAGATTTTCAAAGTTG
51378	49465	AGAGTGAGATTTTCAAAGTT
51379	49466	TAGAGTGAGATTTTCAAAGT
51380	49467	GTAGAGTGAGATTTTCAAAG
51381	49468	AGTAGAGTGAGATTTTCAAA
51382	49469	GAGTAGAGTGAGATTTTCAA
51383	49470	TGAGTAGAGTGAGATTTTCA
51384	49471	ATGAGTAGAGTGAGATTTTC
51385	49472	TATGAGTAGAGTGAGATTTT
51386	49473	TTATGAGTAGAGTGAGATTT
51387	49474	CTTATGAGTAGAGTGAGATT
51388	49475	CCTTATGAGTAGAGTGAGAT
51389	49476	CCCTTATGAGTAGAGTGAGA
51390	49477	CCCCTTATGAGTAGAGTGAG
51391	49478	TCCCCTTATGAGTAGAGTGA
51392	49479	ATCCCCTTATGAGTAGAGTG
51393	49480	CATCCCCTTATGAGTAGAGT
51394	49481	CCATCCCCTTATGAGTAGAG
51395	49482	CCCATCCCCTTATGAGTAGA
51396	49483	ACCCATCCCCTTATGAGTAG
51397	49484	CACCCATCCCCTTATGAGTA
51398	49485	ACACCCATCCCCTTATGAGT
51399	49486	TACACCCATCCCCTTATGAG
51400	49487	ATACACCCATCCCCTTATGA
51401	49488	AATACACCCATCCCCTTATG
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51403	49490	AAAATACACCCATCCCCTTA
51404	49491	CAAAATACACCCATCCCCTT
51405	49492	GCAAAATACACCCATCCCCT
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51407	49494	TAGCAAAATACACCCATCCC
51408	49495	ATAGCAAAATACACCCATCC
51409	49496	TATAGCAAAATACACCCATC
51410	49497	ATATAGCAAAATACACCCAT
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100489	98576	ATTATTACACATTATATGCC
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100492	98579	GTGATTATTACACATTATAT
100493	98580	TGTGATTATTACACATTATA
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100498	98585	CCTAATGTGATTATTACACA
100499	98586	CCCTAATGTGATTATTACAC
100500	98587	ACCCTAATGTGATTATTACA
100501	98588	TACCCTAATGTGATTATTAC
100502	98589	TTACCCTAATGTGATTATTA
100503	98590	TTTACCCTAATGTGATTATT
100504	98591	ATTTACCCTAATGTGATTAT
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100510	98597	TACCCCATTTACCCTAATGT
100511	98598	ATACCCCATTTACCCTAATG
100512	98599	GATACCCCATTTACCCTAAT
100513	98600	GGATACCCCATTTACCCTAA
100514	98601	TGGATACCCCATTTACCCTA
100515	98602	ATGGATACCCCATTTACCCT
100516	98603	GATGGATACCCCATTTACCC
100517	98604	TGATGGATACCCCATTTACC
100518	98605	GTGATGGATACCCCATTTAC
100519	98606	GGTGATGGATACCCCATTTA
100520	98607	TGGTGATGGATACCCCATTT
100521	98608	ATGGTGATGGATACCCCATT
100522	98609	GATGGTGATGGATACCCCAT
100523	98610	TGATGGTGATGGATACCCCA
100524	98611	ATGATGGTGATGGATACCCC
100525	98612	GATGATGGTGATGGATACCC
100526	98613	TGATGATGGTGATGGATACC
100527	98614	ATGATGATGGTGATGGATAC
100528	98615	AATGATGATGGTGATGGATA
100529	98616	GAATGATGATGGTGATGGAT
100530	98617	TGAATGATGATGGTGATGGA
100531	98618	ATGAATGATGATGGTGATGG
100532	98619	GATGAATGATGATGGTGATG
100533	98620	TGATGAATGATGATGGTGAT
100534	98621	ATGATGAATGATGATGGTGA
100535	98622	AATGATGAATGATGATGGTG
100536	98623	AAATGATGAATGATGATGGT
100537	98624	GAAATGATGAATGATGATGG
100538	98625	AGAAATGATGAATGATGATG
100539	98626	AAGAAATGATGAATGATGAT
100540	98627	AAAGAAATGATGAATGATGA
100541	98628	CAAAGAAATGATGAATGATG
100542	98629	ACAAAGAAATGATGAATGAT
100543	98630	CACAAAGAAATGATGAATGA
100544	98631	ACACAAAGAAATGATGAATG
100545	98632	TACACAAAGAAATGATGAAT
100546	98633	TTACACAAAGAAATGATGAA
100547	98634	ATTACACAAAGAAATGATGA
100548	98635	CATTACACAAAGAAATGATG
100549	98636	TCATTACACAAAGAAATGAT
100550	98637	TTCATTACACAAAGAAATGA
100551	98638	GTTCATTACACAAAGAAATG
100552	98639	CGTTCATTACACAAAGAAAT
100553	98640	ACGTTCATTACACAAAGAAA
100554	98641	AACGTTCATTACACAAAGAA
100555	98642	CAACGTTCATTACACAAAGA
100556	98643	GCAACGTTCATTACACAAAG
100557	98644	TGCAACGTTCATTACACAAA
100558	98645	TTGCAACGTTCATTACACAA
100559	98646	ATTGCAACGTTCATTACACA

2266	353	GGGAGGCGAGCTCTGCCGGG
2267	354	AGGGAGGCGAGCTCTGCCGG
2268	355	GAGGGAGGCGAGCTCTGCCG
2269	356	GGAGGGAGGCGAGCTCTGCC
2270	357	CGGAGGGAGGCGAGCTCTGC
2271	358	GCGGAGGGAGGCGAGCTCTG
2272	359	GGCGGAGGGAGGCGAGCTCT
2273	360	AGGCGGAGGGAGGCGAGCTC
2274	361	GAGGCGGAGGGAGGCGAGCT
2275	362	TGAGGCGGAGGGAGGCGAGC
2276	363	CTGAGGCGGAGGGAGGCGAG
2277	364	TCTGAGGCGGAGGGAGGCGA
2278	365	GTCTGAGGCGGAGGGAGGCG
2279	366	AGTCTGAGGCGGAGGGAGGC
2280	367	CAGTCTGAGGCGGAGGGAGG
2281	368	ACAGTCTGAGGCGGAGGGAG
2282	369	AACAGTCTGAGGCGGAGGGA
2283	370	AAACAGTCTGAGGCGGAGGG
2284	371	AAAACAGTCTGAGGCGGAGG
2285	372	CAAAACAGTCTGAGGCGGAG
2286	373	CCAAAACAGTCTGAGGCGGA
2287	374	ACCAAAACAGTCTGAGGCGG
2288	375	TACCAAAACAGTCTGAGGCG
2289	376	CTACCAAAACAGTCTGAGGC
2290	377	GCTACCAAAACAGTCTGAGG
2291	378	TGCTACCAAAACAGTCTGAG
2292	379	TTGCTACCAAAACAGTCTGA
2293	380	GTTGCTACCAAAACAGTCTG
2294	381	CGTTGCTACCAAAACAGTCT
2295	382	CCGTTGCTACCAAAACAGTC
2296	383	GCCGTTGCTACCAAAACAGT
2297	384	TGCCGTTGCTACCAAAACAG
2298	385	TTGCCGTTGCTACCAAAACA
2299	386	GTTGCCGTTGCTACCAAAAC
2300	387	CGTTGCCGTTGCTACCAAAA
2301	388	CCGTTGCCGTTGCTACCAAA
2302	389	GCCGTTGCCGTTGCTACCAA
2303	390	CGCCGTTGCCGTTGCTACCA
2304	391	CCGCCGTTGCCGTTGCTACC
2305	392	GCCGCCGTTGCCGTTGCTAC
2306	393	CGCCGCCGTTGCCGTTGCTA
2307	394	CCGCCGCCGTTGCCGTTGCT
2308	395	GCCGCCGCCGTTGCCGTTGC
2309	396	CGCCGCCGCCGTTGCCGTTG
2310	397	GCGCCGCCGCCGTTGCCGTT
2311	398	CGCGCCGCCGCCGTTGCCGT
2312	399	ACGCGCCGCCGCCGTTGCCG
2313	400	AACGCGCCGCCGCCGTTGCC
2314	401	AAACGCGCCGCCGCCGTTGC
2315	402	GAAACGCGCCGCCGCCGTTG
2316	403	CGAAACGCGCCGCCGCCGTT
2317	404	CCGAAACGCGCCGCCGCCGT
2318	405	GCCGAAACGCGCCGCCGCCG
2319	406	GGCCGAAACGCGCCGCCGCC
2320	407	GGGCCGAAACGCGCCGCCGC
2321	408	CGGGCCGAAACGCGCCGCCG
2322	409	CCGGGCCGAAACGCGCCGCC
2323	410	GCCGGGCCGAAACGCGCCGC
2324	411	AGCCGGGCCGAAACGCGCCG
2325	412	GAGCCGGGCCGAAACGCGCC
2326	413	GGAGCCGGGCCGAAACGCGC
2327	414	GGGAGCCGGGCCGAAACGCG
2328	415	CGGGAGCCGGGCCGAAACGC
2329	416	CCGGGAGCCGGGCCGAAACG
2330	417	GCCGGGAGCCGGGCCGAAAC
2331	418	CGCCGGGAGCCGGGCCGAAA
2332	419	CCGCCGGGAGCCGGGCCGAA
2333	420	GCCGCCGGGAGCCGGGCCGA
2334	421	AGCCGCCGGGAGCCGGGCCG
2335	422	GAGCCGCCGGGAGCCGGGCC
2336	423	GGAGCCGCCGGGAGCCGGGC

51413	49500	AATATATAGCAAAATACACC
51414	49501	TAATATATAGCAAAATACAC
51415	49502	GTAATATATAGCAAAATACA
51416	49503	TGTAATATATAGCAAAATAC
51417	49504	TTGTAATATATAGCAAAATA
51418	49505	TTTGTAATATATAGCAAAAT
51419	49506	TTTTGTAATATATAGCAAAA
51420	49507	ATTTTGTAATATATAGCAAA
51421	49508	AATTTTGTAATATATAGCAA
51422	49509	TAATTTTGTAATATATAGCA
51423	49510	CTAATTTTGTAATATATAGC
51424	49511	ACTAATTTTGTAATATATAG
51425	49512	AACTAATTTTGTAATATATA
51426	49513	AAACTAATTTTGTAATATAT
51427	49514	AAAACTAATTTTGTAATATA
51428	49515	GAAAACTAATTTTGTAATAT
51429	49516	AGAAAACTAATTTTGTAATA
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51433	49520	ATCAAGAAAACTAATTTTGT
51434	49521	CATCAAGAAAACTAATTTTG
51435	49522	TCATCAAGAAAACTAATTTT
51436	49523	CTCATCAAGAAAACTAATTT
51437	49524	CCTCATCAAGAAAACTAATT
51438	49525	TCCTCATCAAGAAAACTAAT
51439	49526	GTCCTCATCAAGAAAACTAA
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51441	49528	ATGTCCTCATCAAGAAAACT
51442	49529	GATGTCCTCATCAAGAAAAC
51443	49530	GGATGTCCTCATCAAGAAAA
51444	49531	TGGATGTCCTCATCAAGAAA
51445	49532	GTGGATGTCCTCATCAAGAA
51446	49533	AGTGGATGTCCTCATCAAGA
51447	49534	TAGTGGATGTCCTCATCAAG
51448	49535	ATAGTGGATGTCCTCATCAA
51449	49536	AATAGTGGATGTCCTCATCA
51450	49537	CAATAGTGGATGTCCTCATC
51451	49538	CCAATAGTGGATGTCCTCAT
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51453	49540	CTCCAATAGTGGATGTCCTC
51454	49541	ACTCCAATAGTGGATGTCCT
51455	49542	TACTCCAATAGTGGATGTCC
51456	49543	TTACTCCAATAGTGGATGTC
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51458	49545	AATTACTCCAATAGTGGATG
51459	49546	AAATTACTCCAATAGTGGAT
51460	49547	GAAATTACTCCAATAGTGGA
51461	49548	TGAAATTACTCCAATAGTGG
51462	49549	CTGAAATTACTCCAATAGTG
51463	49550	CCTGAAATTACTCCAATAGT
51464	49551	ACCTGAAATTACTCCAATAG
51465	49552	TACCTGAAATTACTCCAATA
51466	49553	ATACCTGAAATTACTCCAAT
51467	49554	GATACCTGAAATTACTCCAA
51468	49555	AGATACCTGAAATTACTCCA
51469	49556	AAGATACCTGAAATTACTCC
51470	49557	TAAGATACCTGAAATTACTC
51471	49558	ATAAGATACCTGAAATTACT
51472	49559	AATAAGATACCTGAAATTAC
51473	49560	AAATAAGATACCTGAAATTA
51474	49561	AAAATAAGATACCTGAAATT
51475	49562	AAAAATAAGATACCTGAAAT
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51479	49566	AAGAAAAAATAAGATACCTG
51480	49567	AAAGAAAAAATAAGATACCT
51481	49568	AAAAGAAAAAATAAGATACC
51482	49569	GAAAAGAAAAAATAAGATAC
51483	49570	AGAAAAGAAAAAATAAGATA

100560	98647	AATTGCAACGTTCATTACAC
100561	98648	CAATTGCAACGTTCATTACA
100562	98649	ACAATTGCAACGTTCATTAC
100563	98650	TACAATTGCAACGTTCATTA
100564	98651	GTACAATTGCAACGTTCATT
100565	98652	AGTACAATTGCAACGTTCAT
100566	98653	GAGTACAATTGCAACGTTCA
100567	98654	GGAGTACAATTGCAACGTTC
100568	98655	GGGAGTACAATTGCAACGTT
100569	98656	AGGGAGTACAATTGCAACGT
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100571	98658	TGAGGGAGTACAATTGCAAC
100572	98659	CTGAGGGAGTACAATTGCAA
100573	98660	ACTGAGGGAGTACAATTGCA
100574	98661	AACTGAGGGAGTACAATTGC
100575	98662	TAACTGAGGGAGTACAATTG
100576	98663	ATAACTGAGGGAGTACAATT
100577	98664	AATAACTGAGGGAGTACAAT
100578	98665	GAATAACTGAGGGAGTACAA
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100580	98667	TAGAATAACTGAGGGAGTAC
100581	98668	TTAGAATAACTGAGGGAGTA
100582	98669	TTTAGAATAACTGAGGGAGT
100583	98670	TTTTAGAATAACTGAGGGAG
100584	98671	TTTTTAGAATAACTGAGGGA
100585	98672	CTTTTTAGAATAACTGAGGG
100586	98673	ACTTTTTAGAATAACTGAGG
100587	98674	TACTTTTTAGAATAACTGAG
100588	98675	GTACTTTTTAGAATAACTGA
100589	98676	TGTACTTTTTAGAATAACTG
100590	98677	TTGTACTTTTTAGAATAACT
100591	98678	GTTGTACTTTTTAGAATAAC
100592	98679	TGTTGTACTTTTTAGAATAA
100593	98680	TTGTTGTACTTTTTAGAATA
100594	98681	TTTGTTGTACTTTTTAGAAT
100595	98682	ATTTGTTGTACTTTTTAGAA
100596	98683	AATTTGTTGTACTTTTTAGA
100597	98684	TAATTTGTTGTACTTTTTAG
100598	98685	TTAATTTGTTGTACTTTTTA
100599	98686	ATTAATTTGTTGTACTTTTT
100600	98687	CATTAATTTGTTGTACTTTT
100601	98688	GCATTAATTTGTTGTACTTT
100602	98689	AGCATTAATTTGTTGTACTT
100603	98690	CAGCATTAATTTGTTGTACT
100604	98691	TCAGCATTAATTTGTTGTAC
100605	98692	GTCAGCATTAATTTGTTGTA
100606	98693	AGTCAGCATTAATTTGTTGT
100607	98694	CAGTCAGCATTAATTTGTTG
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100611	98698	ACTACAGTCAGCATTAATTT
100612	98699	GACTACAGTCAGCATTAATT
100613	98700	TGACTACAGTCAGCATTAAT
100614	98701	GTGACTACAGTCAGCATTAA
100615	98702	GGTGACTACAGTCAGCATTA
100616	98703	GGGTGACTACAGTCAGCATT
100617	98704	AGGGTGACTACAGTCAGCAT
100618	98705	CAGGGTGACTACAGTCAGCA
100619	98706	GCAGGGTGACTACAGTCAGC
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100621	98708	AAGCAGGGTGACTACAGTCA
100622	98709	AAAGCAGGGTGACTACAGTC
100623	98710	CAAAGCAGGGTGACTACAGT
100624	98711	ACAAAGCAGGGTGACTACAG
100625	98712	AACAAAGCAGGGTGACTACA
100626	98713	CAACAAAGCAGGGTGACTAC
100627	98714	ACAACAAAGCAGGGTGACTA
100628	98715	GACAACAAAGCAGGGTGACT
100629	98716	TGACAACAAAGCAGGGTGAC
100630	98717	TTGACAACAAAGCAGGGTGA

2337	424	AGGAGCCGCCGGGAGCCGGG
2338	425	AAGGAGCCGCCGGGAGCCGG
2339	426	CAAGGAGCCGCCGGGAGCCG
2340	427	CCAAGGAGCCGCCGGGAGCC
2341	428	ACCAAGGAGCCGCCGGGAGC
2342	429	GACCAAGGAGCCGCCGGGAG
2343	430	AGACCAAGGAGCCGCCGGGA
2344	431	GAGACCAAGGAGCCGCCGGG
2345	432	CGAGACCAAGGAGCCGCCGG
2346	433	CCGAGACCAAGGAGCCGCCG
2347	434	GCCGAGACCAAGGAGCCGCC
2348	435	CGCCGAGACCAAGGAGCCGC
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2350	437	CCCGCCGAGACCAAGGAGCC
2351	438	GCCCGCCGAGACCAAGGAGC
2352	439	GGCCCGCCGAGACCAAGGAG
2353	440	AGGCCCGCCGAGACCAAGGA
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2355	442	GGAGGCCCGCCGAGACCAAG
2356	443	GGGAGGCCCGCCGAGACCAA
2357	444	GGGGAGGCCCGCCGAGACCA
2358	445	CGGGGAGGCCCGCCGAGACC
2359	446	GCGGGGAGGCCCGCCGAGAC
2360	447	GGCGGGGAGGCCCGCCGAGA
2361	448	GGGCGGGGAGGCCCGCCGAG
2362	449	GGGGCGGGGAGGCCCGCCGA
2363	450	AGGGGCGGGGAGGCCCGCCG
2364	451	AAGGGGCGGGGAGGCCCGCC
2365	452	GAAGGGGCGGGGAGGCCCGC
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2367	454	ACGAAGGGGCGGGGAGGCCC
2368	455	GACGAAGGGGCGGGGAGGCC
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2370	457	ACGACGAAGGGGCGGGGAGG
2371	458	GACGACGAAGGGGCGGGGAG
2372	459	GGACGACGAAGGGGCGGGGA
2373	460	AGGACGACGAAGGGGCGGGG
2374	461	GAGGACGACGAAGGGGCGGG
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2376	463	AGGAGGACGACGAAGGGGCG
2377	464	AAGGAGGACGACGAAGGGGC
2378	465	GAAGGAGGACGACGAAGGGG
2379	466	AGAAGGAGGACGACGAAGGG
2380	467	GAGAAGGAGGACGACGAAGG
2381	468	GGAGAAGGAGGACGACGAAG
2382	469	GGGAGAAGGAGGACGACGAA
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2384	471	GGGGGAGAAGGAGGACGACG
2385	472	AGGGGGAGAAGGAGGACGAC
2386	473	GAGGGGGAGAAGGAGGACGA
2387	474	CGAGGGGGAGAAGGAGGACG
2388	475	GCGAGGGGGAGAAGGAGGAC
2389	476	GGCGAGGGGGAGAAGGAGGA
2390	477	TGGCGAGGGGGAGAAGGAGG
2391	478	CTGGCGAGGGGGAGAAGGAG
2392	479	GCTGGCGAGGGGGAGAAGGA
2393	480	GGCTGGCGAGGGGGAGAAGG
2394	481	GGGCTGGCGAGGGGGAGAAG
2395	482	CGGGCTGGCGAGGGGGAGAA
2396	483	CCGGGCTGGCGAGGGGGAGA
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2398	485	GCCCGGGCTGGCGAGGGGGA
2399	486	CGCCCGGGCTGGCGAGGGGG
2400	487	GCGCCCGGGCTGGCGAGGGG
2401	488	GGCGCCCGGGCTGGCGAGGG
2402	489	GGGCGCCCGGGCTGGCGAGG
2403	490	GGGGCGCCCGGGCTGGCGAG
2404	491	AGGGGCGCCCGGGCTGGCGA
2405	492	GAGGGGCGCCCGGGCTGGCG
2406	493	GGAGGGGCGCCCGGGCTGGC
2407	494	CGGAGGGGCGCCCGGGCTGG

51484	49571	GAGAAAAGAAAAAATAAGAT
51485	49572	AGAGAAAAGAAAAAATAAGA
51486	49573	GAGAGAAAAGAAAAAATAAG
51487	49574	AGAGAGAAAAGAAAAAATAA
51488	49575	GAGAGAGAAAAGAAAAAATA
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51491	49578	AAAGAGAGAGAAAAGAAAAA
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51495	49582	AAAAAAAGAGAGAGAAAAGA
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51512	49599	CGTCTCCAAAAAAAAAAAAA
51513	49600	CCGTCTCCAAAAAAAAAAAA
51514	49601	TCCGTCTCCAAAAAAAAAAA
51515	49602	CTCCGTCTCCAAAAAAAAAA
51516	49603	ACTCCGTCTCCAAAAAAAAA
51517	49604	AACTCCGTCTCCAAAAAAAA
51518	49605	AAACTCCGTCTCCAAAAAAA
51519	49606	GAAACTCCGTCTCCAAAAAA
51520	49607	CGAAACTCCGTCTCCAAAAA
51521	49608	GCGAAACTCCGTCTCCAAAA
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51523	49610	GAGCGAAACTCCGTCTCCAA
51524	49611	AGAGCGAAACTCCGTCTCCA
51525	49612	CAGAGCGAAACTCCGTCTCC
51526	49613	ACAGAGCGAAACTCCGTCTC
51527	49614	AACAGAGCGAAACTCCGTCT
51528	49615	CAACAGAGCGAAACTCCGTC
51529	49616	GCAACAGAGCGAAACTCCGT
51530	49617	GGCAACAGAGCGAAACTCCG
51531	49618	GGGCAACAGAGCGAAACTCC
51532	49619	TGGGCAACAGAGCGAAACTC
51533	49620	CTGGGCAACAGAGCGAAACT
51534	49621	CCTGGGCAACAGAGCGAAAC
51535	49622	GCCTGGGCAACAGAGCGAAA
51536	49623	AGCCTGGGCAACAGAGCGAA
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51539	49626	TCCAGCCTGGGCAACAGAGC
51540	49627	CTCCAGCCTGGGCAACAGAG
51541	49628	ACTCCAGCCTGGGCAACAGA
51542	49629	CACTCCAGCCTGGGCAACAG
51543	49630	GCACTCCAGCCTGGGCAACA
51544	49631	TGCACTCCAGCCTGGGCAAC
51545	49632	CTGCACTCCAGCCTGGGCAA
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51551	49638	AGGCCACTGCACTCCAGCCT
51552	49639	CAGGCCACTGCACTCCAGCC
51553	49640	TCAGGCCACTGCACTCCAGC
51554	49641	ATCAGGCCACTGCACTCCAG

100631	98718	TTTGACAACAAAGCAGGGTG
100632	98719	ATTTGACAACAAAGCAGGGT
100633	98720	TATTTGACAACAAAGCAGGG
100634	98721	GTATTTGACAACAAAGCAGG
100635	98722	AGTATTTGACAACAAAGCAG
100636	98723	TAGTATTTGACAACAAAGCA
100637	98724	CTAGTATTTGACAACAAAGC
100638	98725	TCTAGTATTTGACAACAAAG
100639	98726	ATCTAGTATTTGACAACAAA
100640	98727	GATCTAGTATTTGACAACAA
100641	98728	AGATCTAGTATTTGACAACA
100642	98729	AAGATCTAGTATTTGACAAC
100643	98730	TAAGATCTAGTATTTGACAA
100644	98731	ATAAGATCTAGTATTTGACA
100645	98732	AATAAGATCTAGTATTTGAC
100646	98733	GAATAAGATCTAGTATTTGA
100647	98734	TGAATAAGATCTAGTATTTG
100648	98735	ATGAATAAGATCTAGTATTT
100649	98736	AATGAATAAGATCTAGTATT
100650	98737	GAATGAATAAGATCTAGTAT
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100652	98739	AAGAATGAATAAGATCTAGT
100653	98740	AAAGAATGAATAAGATCTAG
100654	98741	TAAAGAATGAATAAGATCTA
100655	98742	ATAAAGAATGAATAAGATCT
100656	98743	AATAAAGAATGAATAAGATC
100657	98744	AAATAAAGAATGAATAAGAT
100658	98745	TAAATAAAGAATGAATAAGA
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100661	98748	AGTTAAATAAAGAATGAATA
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100663	98750	AAAGTTAAATAAAGAATGAA
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100665	98752	AAAAAGTTAAATAAAGAATG
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100674	98761	TTAAAATTTAAAAAGTTAAA
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100678	98765	AAGTTTAAAATTTAAAAAGT
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100680	98767	ATAAGTTTAAAATTTAAAAA
100681	98768	AATAAGTTTAAAATTTAAAA
100682	98769	AAATAAGTTTAAAATTTAAA
100683	98770	AAAATAAGTTTAAAATTTAA
100684	98771	TAAAATAAGTTTAAAATTTA
100685	98772	ATAAAATAAGTTTAAAATTT
100686	98773	AATAAAATAAGTTTAAAATT
100687	98774	AAATAAAATAAGTTTAAAAT
100688	98775	TAAATAAAATAAGTTTAAAA
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100697	98784	AAAAATAAATAAATAAAATA
100698	98785	TAAAAATAAATAAATAAAAT
100699	98786	CTAAAAATAAATAAATAAAA
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2408	495	CCGGAGGGGCGCCCGGGCTG
2409	496	GCCGGAGGGGCGCCCGGGCT
2410	497	GGCCGGAGGGGCGCCCGGGC
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2416	503	TGGCGCGGCCGGAGGGGCGC
2417	504	TTGGCGCGGCCGGAGGGGCG
2418	505	GTTGGCGCGGCCGGAGGGGC
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2421	508	CGGGTTGGCGCGGCCGGAGG
2422	509	GCGGGTTGGCGCGGCCGGAG
2423	510	CGCGGGTTGGCGCGGCCGGA
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2425	512	GGCGCGGGTTGGCGCGGCCG
2426	513	AGGCGCGGGTTGGCGCGGCC
2427	514	GAGGCGCGGGTTGGCGCGGC
2428	515	GGAGGCGCGGGTTGGCGCGG
2429	516	GGGAGGCGCGGGTTGGCGCG
2430	517	GGGGAGGCGCGGGTTGGCGC
2431	518	CGGGGAGGCGCGGGTTGGCG
2432	519	GCGGGGAGGCGCGGGTTGGC
2433	520	AGCGGGGAGGCGCGGGTTGG
2434	521	GAGCGGGGAGGCGCGGGTTG
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2437	524	GCCGAGCGGGGAGGCGCGGG
2438	525	CGCCGAGCGGGGAGGCGCGG
2439	526	GCGCCGAGCGGGGAGGCGCG
2440	527	GGCGCCGAGCGGGGAGGCGC
2441	528	GGGCGCCGAGCGGGGAGGCG
2442	529	CGGGCGCCGAGCGGGGAGGC
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2444	531	CGCGGGCGCCGAGCGGGGAG
2445	532	GCGCGGGCGCCGAGCGGGGA
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2447	534	ACGCGCGGGCGCCGAGCGGG
2448	535	GACGCGCGGGCGCCGAGCGG
2449	536	GGACGCGCGGGCGCCGAGCG
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2452	539	CGGGGACGCGCGGGCGCCGA
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2454	541	GGCGGGGACGCGCGGGCGCC
2455	542	CGGCGGGGACGCGCGGGCGC
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2463	550	CCGGAACGCGGCGGGGACGC
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2465	552	CGCCGGAACGCGGCGGGGAC
2466	553	ACGCCGGAACGCGGCGGGGA
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2471	558	AGGAGACGCCGGAACGCGGC
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2476	563	CGCCAAGGAGACGCCGGAAC
2477	564	GCGCCAAGGAGACGCCGGAA
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51557	49644	GAGATCAGGCCACTGCACTC
51558	49645	CGAGATCAGGCCACTGCACT
51559	49646	CCGAGATCAGGCCACTGCAC
51560	49647	GCCGAGATCAGGCCACTGCA
51561	49648	AGCCGAGATCAGGCCACTGC
51562	49649	GAGCCGAGATCAGGCCACTG
51563	49650	TGAGCCGAGATCAGGCCACT
51564	49651	GTGAGCCGAGATCAGGCCAC
51565	49652	GGTGAGCCGAGATCAGGCCA
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51567	49654	GCGGTGAGCCGAGATCAGGC
51568	49655	TGCGGTGAGCCGAGATCAGG
51569	49656	TTGCGGTGAGCCGAGATCAG
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51571	49658	GGTTGCGGTGAGCCGAGATC
51572	49659	AGGTTGCGGTGAGCCGAGAT
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51584	49671	CCCAGGAGGCAGAGGTTGCG
51585	49672	ACCCAGGAGGCAGAGGTTGC
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51612	49699	GGAGGCTGAGGCAAGAGAAT
51613	49700	GGGAGGCTGAGGCAAGAGAA
51614	49701	CGGGAGGCTGAGGCAAGAGA
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51618	49705	TACTCGGGAGGCTGAGGCAA
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51623	49710	CCAGCTACTCGGGAGGCTGA
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100704	98791	TCCGTCTAAAAATAAATAAA
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100711	98798	GTGAGACTCCGTCTAAAAAT
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100717	98804	GACAGAGTGAGACTCCGTCT
100718	98805	CGACAGAGTGAGACTCCGTC
100719	98806	GCGACAGAGTGAGACTCCGT
100720	98807	GGCGACAGAGTGAGACTCCG
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100722	98809	CTGGCGACAGAGTGAGACTC
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100725	98812	AGCCTGGCGACAGAGTGAGA
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100727	98814	CCAGCCTGGCGACAGAGTGA
100728	98815	TCCAGCCTGGCGACAGAGTG
100729	98816	CTCCAGCCTGGCGACAGAGT
100730	98817	ACTCCAGCCTGGCGACAGAG
100731	98818	CACTCCAGCCTGGCGACAGA
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100733	98820	CGCACTCCAGCCTGGCGACA
100734	98821	CCGCACTCCAGCCTGGCGAC
100735	98822	ACCGCACTCCAGCCTGGCGA
100736	98823	CACCGCACTCCAGCCTGGCG
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100738	98825	GCCACCGCACTCCAGCCTGG
100739	98826	CGCCACCGCACTCCAGCCTG
100740	98827	GCGCCACCGCACTCCAGCCT
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100742	98829	CTGCGCCACCGCACTCCAGC
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100744	98831	GACTGCGCCACCGCACTCCA
100745	98832	AGACTGCGCCACCGCACTCC
100746	98833	GAGACTGCGCCACCGCACTC
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100748	98835	TTGAGACTGCGCCACCGCAC
100749	98836	GTTGAGACTGCGCCACCGCA
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100752	98839	TGAGTTGAGACTGCGCCACC
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100767	98854	AGGCGGAGGTTGCAGTGAGT
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100769	98856	GGAGGCGGAGGTTGCAGTGA
100770	98857	TGGAGGCGGAGGTTGCAGTG
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100827	98914	CACGTGCCTGTAGTTCCAGC
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51701	49788	GCCTGGCCAACATAGTGAAA
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51710	49797	TCAAGACCAGCCTGGCCAAC
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51714	49801	GAGTTCAAGACCAGCCTGGC
51715	49802	GGAGTTCAAGACCAGCCTGG
51716	49803	AGGAGTTCAAGACCAGCCTG
51717	49804	CAGGAGTTCAAGACCAGCCT
51718	49805	TCAGGAGTTCAAGACCAGCC
51719	49806	GTCAGGAGTTCAAGACCAGC
51720	49807	GGTCAGGAGTTCAAGACCAG
51721	49808	AGGTCAGGAGTTCAAGACCA
51722	49809	AAGGTCAGGAGTTCAAGACC
51723	49810	CAAGGTCAGGAGTTCAAGAC
51724	49811	ACAAGGTCAGGAGTTCAAGA
51725	49812	CACAAGGTCAGGAGTTCAAG
51726	49813	TCACAAGGTCAGGAGTTCAA
51727	49814	ATCACAAGGTCAGGAGTTCA
51728	49815	GATCACAAGGTCAGGAGTTC
51729	49816	GGATCACAAGGTCAGGAGTT
51730	49817	AGGATCACAAGGTCAGGAGT
51731	49818	GAGGATCACAAGGTCAGGAG
51732	49819	GGAGGATCACAAGGTCAGGA
51733	49820	AGGAGGATCACAAGGTCAGG
51734	49821	CAGGAGGATCACAAGGTCAG
51735	49822	GCAGGAGGATCACAAGGTCA
51736	49823	GGCAGGAGGATCACAAGGTC
51737	49824	AGGCAGGAGGATCACAAGGT
51738	49825	AAGGCAGGAGGATCACAAGG
51739	49826	CAAGGCAGGAGGATCACAAG
51740	49827	CCAAGGCAGGAGGATCACAA
51741	49828	GCCAAGGCAGGAGGATCACA
51742	49829	GGCCAAGGCAGGAGGATCAC
51743	49830	AGGCCAAGGCAGGAGGATCA
51744	49831	GAGGCCAAGGCAGGAGGATC
51745	49832	GGAGGCCAAGGCAGGAGGAT
51746	49833	GGGAGGCCAAGGCAGGAGGA
51747	49834	TGGGAGGCCAAGGCAGGAGG
51748	49835	CTGGGAGGCCAAGGCAGGAG
51749	49836	TCTGGGAGGCCAAGGCAGGA
51750	49837	CTCTGGGAGGCCAAGGCAGG
51751	49838	ACTCTGGGAGGCCAAGGCAG
51752	49839	CACTCTGGGAGGCCAAGGCA
51753	49840	GCACTCTGGGAGGCCAAGGC
51754	49841	AGCACTCTGGGAGGCCAAGG
51755	49842	CAGCACTCTGGGAGGCCAAG
51756	49843	CCAGCACTCTGGGAGGCCAA
51757	49844	CCCAGCACTCTGGGAGGCCA
51758	49845	TCCCAGCACTCTGGGAGGCC
51759	49846	ATCCCAGCACTCTGGGAGGC
51760	49847	AATCCCAGCACTCTGGGAGG
51761	49848	TAATCCCAGCACTCTGGGAG
51762	49849	ATAATCCCAGCACTCTGGGA
51763	49850	TATAATCCCAGCACTCTGGG
51764	49851	CTATAATCCCAGCACTCTGG
51765	49852	CCTATAATCCCAGCACTCTG
51766	49853	GCCTATAATCCCAGCACTCT
51767	49854	CGCCTATAATCCCAGCACTC

100844	98931	TTAGCTGGGCGTGGTGGCAC
100845	98932	ATTAGCTGGGCGTGGTGGCA
100846	98933	AATTAGCTGGGCGTGGTGGC
100847	98934	AAATTAGCTGGGCGTGGTGG
100848	98935	AAAATTAGCTGGGCGTGGTG
100849	98936	AAAAATTAGCTGGGCGTGGT
100850	98937	CAAAAATTAGCTGGGCGTGG
100851	98938	ACAAAAATTAGCTGGGCGTG
100852	98939	TACAAAAATTAGCTGGGCGT
100853	98940	ATACAAAAATTAGCTGGGCG
100854	98941	AATACAAAAATTAGCTGGGC
100855	98942	AAATACAAAAATTAGCTGGG
100856	98943	AAAATACAAAAATTAGCTGG
100857	98944	AAAAATACAAAAATTAGCTG
100858	98945	TAAAAATACAAAAATTAGCT
100859	98946	CTAAAAATACAAAAATTAGC
100860	98947	ACTAAAAATACAAAAATTAG
100861	98948	TACTAAAAATACAAAAATTA
100862	98949	CTACTAAAAATACAAAAATT
100863	98950	TCTACTAAAAATACAAAAAT
100864	98951	CTCTACTAAAAATACAAAAA
100865	98952	TCTCTACTAAAAATACAAAA
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100867	98954	CGTCTCTACTAAAAATACAA
100868	98955	CCGTCTCTACTAAAAATACA
100869	98956	CCCGTCTCTACTAAAAATAC
100870	98957	CCCCGTCTCTACTAAAAATA
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100872	98959	AACCCCGTCTCTACTAAAAA
100873	98960	AAACCCCGTCTCTACTAAAA
100874	98961	GAAACCCCGTCTCTACTAAA
100875	98962	TGAAACCCCGTCTCTACTAA
100876	98963	GTGAAACCCCGTCTCTACTA
100877	98964	AGTGAAACCCCGTCTCTACT
100878	98965	TAGTGAAACCCCGTCTCTAC
100879	98966	ATAGTGAAACCCCGTCTCTA
100880	98967	CATAGTGAAACCCCGTCTCT
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100882	98969	AACATAGTGAAACCCCGTCT
100883	98970	CAACATAGTGAAACCCCGTC
100884	98971	CCAACATAGTGAAACCCCGT
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100886	98973	AGCCAACATAGTGAAACCCC
100887	98974	CAGCCAACATAGTGAAACCC
100888	98975	CCAGCCAACATAGTGAAACC
100889	98976	CCCAGCCAACATAGTGAAAC
100890	98977	TCCCAGCCAACATAGTGAAA
100891	98978	ATCCCAGCCAACATAGTGAA
100892	98979	CATCCCAGCCAACATAGTGA
100893	98980	CCATCCCAGCCAACATAGTG
100894	98981	ACCATCCCAGCCAACATAGT
100895	98982	GACCATCCCAGCCAACATAG
100896	98983	AGACCATCCCAGCCAACATA
100897	98984	AAGACCATCCCAGCCAACAT
100898	98985	CAAGACCATCCCAGCCAACA
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100904	98991	AGAGATCAAGACCATCCCAG
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100908	98995	GTCAAGAGATCAAGACCATC
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100910	98997	AGGTCAAGAGATCAAGACCA
100911	98998	AAGGTCAAGAGATCAAGACC
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100913	99000	ACAAGGTCAAGAGATCAAGA
100914	99001	CACAAGGTCAAGAGATCAAG

2621	708	GCGGCTGCTGCTGCTGCTGC
2622	709	GGCGGCTGCTGCTGCTGCTG
2623	710	CGGCGGCTGCTGCTGCTGCT
2624	711	GCGGCGGCTGCTGCTGCTGC
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2626	713	GGGCGGCGGCTGCTGCTGCT
2627	714	CGGGCGGCGGCTGCTGCTGC
2628	715	GCGGGCGGCGGCTGCTGCTG
2629	716	CGCGGGCGGCGGCTGCTGCT
2630	717	CCGCGGGCGGCGGCTGCTGC
2631	718	GCCGCGGGCGGCGGCTGCTG
2632	719	AGCCGCGGGCGGCGGCTGCT
2633	720	CAGCCGCGGGCGGCGGCTGC
2634	721	GCAGCCGCGGGCGGCGGCTG
2635	722	GGCAGCCGCGGGCGGCGGCT
2636	723	TGGCAGCCGCGGGCGGCGGC
2637	724	TTGGCAGCCGCGGGCGGCGG
2638	725	ATTGGCAGCCGCGGGCGGCG
2639	726	CATTGGCAGCCGCGGGCGGC
2640	727	ACATTGGCAGCCGCGGGCGG
2641	728	GACATTGGCAGCCGCGGGCG
2642	729	GGACATTGGCAGCCGCGGGC
2643	730	CGGACATTGGCAGCCGCGGG
2644	731	GCGGACATTGGCAGCCGCGG
2645	732	TGCGGACATTGGCAGCCGCG
2646	733	TTGCGGACATTGGCAGCCGC
2647	734	CTTGCGGACATTGGCAGCCG
2648	735	GCTTGCGGACATTGGCAGCC
2649	736	GGCTTGCGGACATTGGCAGC
2650	737	GGGCTTGCGGACATTGGCAG
2651	738	CGGGCTTGCGGACATTGGCA
2652	739	CCGGGCTTGCGGACATTGGC
2653	740	GCCGGGCTTGCGGACATTGG
2654	741	CGCCGGGCTTGCGGACATTG
2655	742	CCGCCGGGCTTGCGGACATT
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2657	744	TGCCGCCGGGCTTGCGGACA
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2659	746	GCTGCCGCCGGGCTTGCGGA
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2661	748	CCGCTGCCGCCGGGCTTGCG
2662	749	GCCGCTGCCGCCGGGCTTGC
2663	750	GGCCGCTGCCGCCGGGCTTG
2664	751	AGGCCGCTGCCGCCGGGCTT
2665	752	AAGGCCGCTGCCGCCGGGCT
2666	753	GAAGGCCGCTGCCGCCGGGC
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2668	755	TAGAAGGCCGCTGCCGCCGG
2669	756	CTAGAAGGCCGCTGCCGCCG
2670	757	GCTAGAAGGCCGCTGCCGCC
2671	758	CGCTAGAAGGCCGCTGCCGC
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2674	761	CGACGCTAGAAGGCCGCTGC
2675	762	GCGACGCTAGAAGGCCGCTG
2676	763	GGCGACGCTAGAAGGCCGCT
2677	764	GGGCGACGCTAGAAGGCCGC
2678	765	CGGGCGACGCTAGAAGGCCG
2679	766	GCGGGCGACGCTAGAAGGCC
2680	767	GGCGGGCGACGCTAGAAGGC
2681	768	CGGCGGGCGACGCTAGAAGG
2682	769	GCGGCGGGCGACGCTAGAAG
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2686	773	CGCGGCGGCGGGCGACGCTA
2687	774	GCGCGGCGGCGGGCGACGCT
2688	775	GGCGCGGCGGCGGGCGACGC
2689	776	AGGCGCGGCGGCGGGCGACG
2690	777	AAGGCGCGGCGGCGGGCGAC
2691	778	GAAGGCGCGGCGGCGGGCGA

51768	49855	ACGCCTATAATCCCAGCACT
51769	49856	CACGCCTATAATCCCAGCAC
51770	49857	TCACGCCTATAATCCCAGCA
51771	49858	CTCACGCCTATAATCCCAGC
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51773	49860	GGCTCACGCCTATAATCCCA
51774	49861	TGGCTCACGCCTATAATCCC
51775	49862	GTGGCTCACGCCTATAATCC
51776	49863	GGTGGCTCACGCCTATAATC
51777	49864	TGGTGGCTCACGCCTATAAT
51778	49865	GTGGTGGCTCACGCCTATAA
51779	49866	CGTGGTGGCTCACGCCTATA
51780	49867	GCGTGGTGGCTCACGCCTAT
51781	49868	GGCGTGGTGGCTCACGCCTA
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51784	49871	CCAGGCGTGGTGGCTCACGC
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51786	49873	GCCCAGGCGTGGTGGCTCAC
51787	49874	TGCCCAGGCGTGGTGGCTCA
51788	49875	CTGCCCAGGCGTGGTGGCTC
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51793	49880	GATACCTGCCCAGGCGTGGT
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51796	49883	TAAGATACCTGCCCAGGCGT
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51819	49906	CTAAACCACTGTAAGTTTTG
51820	49907	ACTAAACCACTGTAAGTTTT
51821	49908	CACTAAACCACTGTAAGTTT
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51824	49911	ATTCACTAAACCACTGTAAG
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51826	49913	TAATTCACTAAACCACTGTA
51827	49914	ATAATTCACTAAACCACTGT
51828	49915	TATAATTCACTAAACCACTG
51829	49916	GTATAATTCACTAAACCACT
51830	49917	TGTATAATTCACTAAACCAC
51831	49918	TTGTATAATTCACTAAACCA
51832	49919	ATTGTATAATTCACTAAACC
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51834	49921	CAATTGTATAATTCACTAAA
51835	49922	GCAATTGTATAATTCACTAA
51836	49923	CGCAATTGTATAATTCACTA
51837	49924	ACGCAATTGTATAATTCACT
51838	49925	GACGCAATTGTATAATTCAC

100915	99002	TCACAAGGTCAAGAGATCAA
100916	99003	ATCACAAGGTCAAGAGATCA
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100918	99005	GGATCACAAGGTCAAGAGAT
100919	99006	CGGATCACAAGGTCAAGAGA
100920	99007	CCGGATCACAAGGTCAAGAG
100921	99008	GCCGGATCACAAGGTCAAGA
100922	99009	AGCCGGATCACAAGGTCAAG
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100924	99011	GCAGCCGGATCACAAGGTCA
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100926	99013	TGGCAGCCGGATCACAAGGT
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100930	99017	GCTGTGGCAGCCGGATCACA
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100933	99020	GAGGCTGTGGCAGCCGGATC
100934	99021	GGAGGCTGTGGCAGCCGGAT
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100936	99023	TGGGAGGCTGTGGCAGCCGG
100937	99024	TTGGGAGGCTGTGGCAGCCG
100938	99025	TTTGGGAGGCTGTGGCAGCC
100939	99026	CTTTGGGAGGCTGTGGCAGC
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100941	99028	CACTTTGGGAGGCTGTGGCA
100942	99029	GCACTTTGGGAGGCTGTGGC
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100944	99031	CAGCACTTTGGGAGGCTGTG
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100946	99033	CCCAGCACTTTGGGAGGCTG
100947	99034	CCCCAGCACTTTGGGAGGCT
100948	99035	ACCCCAGCACTTTGGGAGGC
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100961	99048	GCTCACGCCTGCAACCCCAG
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100965	99052	GGTGGCTCACGCCTGCAACC
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100968	99055	CACGGTGGCTCACGCCTGCA
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100981	99068	TTTAAAGGCCGGGCACGGTG
100982	99069	TTTTAAAGGCCGGGCACGGT
100983	99070	ATTTTAAAGGCCGGGCACGG
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2692	779	CGAAGGCGCGGCGGCGGGCG
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2695	782	CGGCGAAGGCGCGGCGGCGG
2696	783	ACGGCGAAGGCGCGGCGGCG
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2701	788	CGAGGACGGCGAAGGCGCGG
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2703	790	GACGAGGACGGCGAAGGCGC
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2706	793	GAGGACGAGGACGGCGAAGG
2707	794	CGAGGACGAGGACGGCGAAG
2708	795	CCGAGGACGAGGACGGCGAA
2709	796	ACCGAGGACGAGGACGGCGA
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2713	800	GGAGACCGAGGACGAGGACG
2714	801	AGGAGACCGAGGACGAGGAC
2715	802	GAGGAGACCGAGGACGAGGA
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2724	811	GCCGAGGACGAGGAGACCGA
2725	812	GGCCGAGGACGAGGAGACCG
2726	813	TGGCCGAGGACGAGGAGACC
2727	814	GTGGCCGAGGACGAGGAGAC
2728	815	CGTGGCCGAGGACGAGGAGA
2729	816	CCGTGGCCGAGGACGAGGAG
2730	817	GCCGTGGCCGAGGACGAGGA
2731	818	AGCCGTGGCCGAGGACGAGG
2732	819	GAGCCGTGGCCGAGGACGAG
2733	820	GGAGCCGTGGCCGAGGACGA
2734	821	GGGAGCCGTGGCCGAGGACG
2735	822	AGGGAGCCGTGGCCGAGGAC
2736	823	GAGGGAGCCGTGGCCGAGGA
2737	824	GGAGGGAGCCGTGGCCGAGG
2738	825	AGGAGGGAGCCGTGGCCGAG
2739	826	GAGGAGGGAGCCGTGGCCGA
2740	827	CGAGGAGGGAGCCGTGGCCG
2741	828	CCGAGGAGGGAGCCGTGGCC
2742	829	ACCGAGGAGGGAGCCGTGGC
2743	830	CACCGAGGAGGGAGCCGTGG
2744	831	CCACCGAGGAGGGAGCCGTG
2745	832	ACCACCGAGGAGGGAGCCGT
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2747	834	CGACCACCGAGGAGGGAGCC
2748	835	GCGACCACCGAGGAGGGAGC
2749	836	CGCGACCACCGAGGAGGGAG
2750	837	CCGCGACCACCGAGGAGGGA
2751	838	GCCGCGACCACCGAGGAGGG
2752	839	CGCCGCGACCACCGAGGAGG
2753	840	TCGCCGCGACCACCGAGGAG
2754	841	GTCGCCGCGACCACCGAGGA
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2756	843	AGGTCGCCGCGACCACCGAG
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2759	846	CGGAGGTCGCCGCGACCACC
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2761	848	GCCGGAGGTCGCCGCGACCA
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51839	49926	GGACGCAATTGTATAATTCA
51840	49927	TGGACGCAATTGTATAATTC
51841	49928	CTGGACGCAATTGTATAATT
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51846	49933	ACGCACTGGACGCAATTGTA
51847	49934	TACGCACTGGACGCAATTGT
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51859	49946	TTTTCAGGATACTACGCACT
51860	49947	ATTTTCAGGATACTACGCAC
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51865	49952	ATACTATTTTCAGGATACTA
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51867	49954	TAATACTATTTTCAGGATAC
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51870	49957	ACTTAATACTATTTTCAGGA
51871	49958	GACTTAATACTATTTTCAGG
51872	49959	TGACTTAATACTATTTTCAG
51873	49960	ATGACTTAATACTATTTTCA
51874	49961	CATGACTTAATACTATTTTC
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51878	49965	AACACATGACTTAATACTAT
51879	49966	AAACACATGACTTAATACTA
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51882	49969	CCTAAACACATGACTTAATA
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51884	49971	GTCCTAAACACATGACTTAA
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51886	49973	ATGTCCTAAACACATGACTT
51887	49974	GATGTCCTAAACACATGACT
51888	49975	TGATGTCCTAAACACATGAC
51889	49976	CTGATGTCCTAAACACATGA
51890	49977	CCTGATGTCCTAAACACATG
51891	49978	ACCTGATGTCCTAAACACAT
51892	49979	GACCTGATGTCCTAAACACA
51893	49980	AGACCTGATGTCCTAAACAC
51894	49981	GAGACCTGATGTCCTAAACA
51895	49982	AGAGACCTGATGTCCTAAAC
51896	49983	AAGAGACCTGATGTCCTAAA
51897	49984	TAAGAGACCTGATGTCCTAA
51898	49985	TTAAGAGACCTGATGTCCTA
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51901	49988	AGCTTAAGAGACCTGATGTC
51902	49989	TAGCTTAAGAGACCTGATGT
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51904	49991	CTTAGCTTAAGAGACCTGAT
51905	49992	TCTTAGCTTAAGAGACCTGA
51906	49993	GTCTTAGCTTAAGAGACCTG
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51908	49995	TAGTCTTAGCTTAAGAGACC
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100986	99073	ATAATTTTAAAGGCCGGGCA
100987	99074	AATAATTTTAAAGGCCGGGC
100988	99075	AAATAATTTTAAAGGCCGGG
100989	99076	AAAATAATTTTAAAGGCCGG
100990	99077	TAAAATAATTTTAAAGGCCG
100991	99078	TTAAAATAATTTTAAAGGCC
100992	99079	TTTAAAATAATTTTAAAGGC
100993	99080	ATTTAAAATAATTTTAAAGG
100994	99081	GATTTAAAATAATTTTAAAG
100995	99082	TGATTTAAAATAATTTTAAA
100996	99083	ATGATTTAAAATAATTTTAA
100997	99084	AATGATTTAAAATAATTTTA
100998	99085	AAATGATTTAAAATAATTTT
100999	99086	AAAATGATTTAAAATAATTT
101000	99087	TAAAATGATTTAAAATAATT
101001	99088	TTAAAATGATTTAAAATAAT
101002	99089	ATTAAAATGATTTAAAATAA
101003	99090	TATTAAAATGATTTAAAATA
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101005	99092	GATATTAAAATGATTTAAAA
101006	99093	AGATATTAAAATGATTTAAA
101007	99094	AAGATATTAAAATGATTTAA
101008	99095	AAAGATATTAAAATGATTTA
101009	99096	AAAAGATATTAAAATGATTT
101010	99097	AAAAAGATATTAAAATGATT
101011	99098	GAAAAAGATATTAAAATGAT
101012	99099	TGAAAAAGATATTAAAATGA
101013	99100	ATGAAAAAGATATTAAAATG
101014	99101	AATGAAAAAGATATTAAAAT
101015	99102	AAATGAAAAAGATATTAAAA
101016	99103	GAAATGAAAAAGATATTAAA
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101019	99106	GCAGAAATGAAAAAGATATT
101020	99107	GGCAGAAATGAAAAAGATAT
101021	99108	AGGCAGAAATGAAAAAGATA
101022	99109	GAGGCAGAAATGAAAAAGAT
101023	99110	GGAGGCAGAAATGAAAAAGA
101024	99111	CGGAGGCAGAAATGAAAAAG
101025	99112	CCGGAGGCAGAAATGAAAAA
101026	99113	ACCGGAGGCAGAAATGAAAA
101027	99114	GACCGGAGGCAGAAATGAAA
101028	99115	GGACCGGAGGCAGAAATGAA
101029	99116	AGGACCGGAGGCAGAAATGA
101030	99117	CAGGACCGGAGGCAGAAATG
101031	99118	GCAGGACCGGAGGCAGAAAT
101032	99119	TGCAGGACCGGAGGCAGAAA
101033	99120	CTGCAGGACCGGAGGCAGAA
101034	99121	TCTGCAGGACCGGAGGCAGA
101035	99122	CTCTGCAGGACCGGAGGCAG
101036	99123	ACTCTGCAGGACCGGAGGCA
101037	99124	AACTCTGCAGGACCGGAGGC
101038	99125	GAACTCTGCAGGACCGGAGG
101039	99126	AGAACTCTGCAGGACCGGAG
101040	99127	AAGAACTCTGCAGGACCGGA
101041	99128	TAAGAACTCTGCAGGACCGG
101042	99129	ATAAGAACTCTGCAGGACCG
101043	99130	AATAAGAACTCTGCAGGACC
101044	99131	GAATAAGAACTCTGCAGGAC
101045	99132	CGAATAAGAACTCTGCAGGA
101046	99133	ACGAATAAGAACTCTGCAGG
101047	99134	AACGAATAAGAACTCTGCAG
101048	99135	GAACGAATAAGAACTCTGCA
101049	99136	AGAACGAATAAGAACTCTGC
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101051	99138	AAAGAACGAATAAGAACTCT
101052	99139	GAAAGAACGAATAAGAACTC
101053	99140	AGAAAGAACGAATAAGAACT
101054	99141	TAGAAAGAACGAATAAGAAC
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101056	99143	TTTAGAAAGAACGAATAAGA

2763	850	CCGCCGGAGGTCGCCGCGAC
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2765	852	CGCCGCCGGAGGTCGCCGCG
2766	853	CCGCCGCCGGAGGTCGCCGC
2767	854	CCCGCCGCCGGAGGTCGCCG
2768	855	TCCCGCCGCCGGAGGTCGCC
2769	856	CTCCCGCCGCCGGAGGTCGC
2770	857	CCTCCCGCCGCCGGAGGTCG
2771	858	GCCTCCCGCCGCCGGAGGTC
2772	859	GGCCTCCCGCCGCCGGAGGT
2773	860	GGGCCTCCCGCCGCCGGAGG
2774	861	CGGGCCTCCCGCCGCCGGAG
2775	862	CCGGGCCTCCCGCCGCCGGA
2776	863	GCCGGGCCTCCCGCCGCCGG
2777	864	GGCCGGGCCTCCCGCCGCCG
2778	865	AGGCCGGGCCTCCCGCCGCC
2779	866	CAGGCCGGGCCTCCCGCCGC
2780	867	CCAGGCCGGGCCTCCCGCCG
2781	868	CCCAGGCCGGGCCTCCCGCC
2782	869	GCCCAGGCCGGGCCTCCCGC
2783	870	TGCCCAGGCCGGGCCTCCCG
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2787	874	CACCTGCCCAGGCCGGGCCT
2788	875	CCACCTGCCCAGGCCGGGCC
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2796	883	GCCGACACCCACCTGCCCAG
2797	884	TGCCGACACCCACCTGCCCA
2798	885	GTGCCGACACCCACCTGCCC
2799	886	GGTGCCGACACCCACCTGCC
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2801	888	GGGGTGCCGACACCCACCTG
2802	889	TGGGGTGCCGACACCCACCT
2803	890	CTGGGGTGCCGACACCCACC
2804	891	GCTGGGGTGCCGACACCCAC
2805	892	GGCTGGGGTGCCGACACCCA
2806	893	GGGCTGGGGTGCCGACACCC
2807	894	GGGGCTGGGGTGCCGACACC
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2809	896	AGGGGGCTGGGGTGCCGACA
2810	897	GAGGGGGCTGGGGTGCCGAC
2811	898	GGAGGGGGCTGGGGTGCCGA
2812	899	CGGAGGGGGCTGGGGTGCCG
2813	900	GCGGAGGGGGCTGGGGTGCC
2814	901	AGCGGAGGGGGCTGGGGTGC
2815	902	GAGCGGAGGGGGCTGGGGTG
2816	903	GGAGCGGAGGGGGCTGGGGT
2817	904	CGGAGCGGAGGGGGCTGGGG
2818	905	CCGGAGCGGAGGGGGCTGGG
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2820	907	GCCCGGAGCGGAGGGGGCTG
2821	908	GGCCCGGAGCGGAGGGGGCT
2822	909	GGGCCCGGAGCGGAGGGGGC
2823	910	CGGGCCCGGAGCGGAGGGGG
2824	911	CCGGGCCCGGAGCGGAGGGG
2825	912	GCCGGGCCCGGAGCGGAGGG
2826	913	CGCCGGGCCCGGAGCGGAGG
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2828	915	GACGCCGGGCCCGGAGCGGA
2829	916	GGACGCCGGGCCCGGAGCGG
2830	917	GGGACGCCGGGCCCGGAGCG
2831	918	GGGGACGCCGGGCCCGGAGC
2832	919	AGGGGACGCCGGGCCCGGAG
2833	920	GAGGGGACGCCGGGCCCGGA

51910	49997	GATAGTCTTAGCTTAAGAGA
51911	49998	GGATAGTCTTAGCTTAAGAG
51912	49999	TGGATAGTCTTAGCTTAAGA
51913	50000	CTGGATAGTCTTAGCTTAAG
51914	50001	CCTGGATAGTCTTAGCTTAA
51915	50002	GCCTGGATAGTCTTAGCTTA
51916	50003	TGCCTGGATAGTCTTAGCTT
51917	50004	CTGCCTGGATAGTCTTAGCT
51918	50005	TCTGCCTGGATAGTCTTAGC
51919	50006	TTCTGCCTGGATAGTCTTAG
51920	50007	TTTCTGCCTGGATAGTCTTA
51921	50008	ATTTCTGCCTGGATAGTCTT
51922	50009	AATTTCTGCCTGGATAGTCT
51923	50010	CAATTTCTGCCTGGATAGTC
51924	50011	GCAATTTCTGCCTGGATAGT
51925	50012	GGCAATTTCTGCCTGGATAG
51926	50013	GGGCAATTTCTGCCTGGATA
51927	50014	AGGGCAATTTCTGCCTGGAT
51928	50015	GAGGGCAATTTCTGCCTGGA
51929	50016	AGAGGGCAATTTCTGCCTGG
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51931	50018	GAAGAGGGCAATTTCTGCCT
51932	50019	AGAAGAGGGCAATTTCTGCC
51933	50020	TAGAAGAGGGCAATTTCTGC
51934	50021	ATAGAAGAGGGCAATTTCTG
51935	50022	TATAGAAGAGGGCAATTTCT
51936	50023	TTATAGAAGAGGGCAATTTC
51937	50024	TTTATAGAAGAGGGCAATTT
51938	50025	TTTTATAGAAGAGGGCAATT
51939	50026	CTTTTATAGAAGAGGGCAAT
51940	50027	TCTTTTATAGAAGAGGGCAA
51941	50028	TTCTTTTATAGAAGAGGGCA
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51945	50032	TTTCTTCTTTTATAGAAGAG
51946	50033	TTTTCTTCTTTTATAGAAGA
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51948	50035	ACTTTTCTTCTTTTATAGAA
51949	50036	TACTTTTCTTCTTTTATAGA
51950	50037	ATACTTTTCTTCTTTTATAG
51951	50038	AATACTTTTCTTCTTTTATA
51952	50039	TAATACTTTTCTTCTTTTAT
51953	50040	TTAATACTTTTCTTCTTTTA
51954	50041	ATTAATACTTTTCTTCTTTT
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51956	50043	TAATTAATACTTTTCTTCTT
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51959	50046	TCCTAATTAATACTTTTCTT
51960	50047	TTCCTAATTAATACTTTTCT
51961	50048	CTTCCTAATTAATACTTTTC
51962	50049	ACTTCCTAATTAATACTTTT
51963	50050	TACTTCCTAATTAATACTTT
51964	50051	GTACTTCCTAATTAATACTT
51965	50052	AGTACTTCCTAATTAATACT
51966	50053	TAGTACTTCCTAATTAATAC
51967	50054	ATAGTACTTCCTAATTAATA
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51974	50061	CATACTGATAGTACTTCCTA
51975	50062	CCATACTGATAGTACTTCCT
51976	50063	TCCATACTGATAGTACTTCC
51977	50064	CTCCATACTGATAGTACTTC
51978	50065	TCTCCATACTGATAGTACTT
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51980	50067	TTTCTCCATACTGATAGTAC

101057	99144	ATTTAGAAAGAACGAATAAG
101058	99145	AATTTAGAAAGAACGAATAA
101059	99146	AAATTTAGAAAGAACGAATA
101060	99147	AAAATTTAGAAAGAACGAAT
101061	99148	GAAAATTTAGAAAGAACGAA
101062	99149	AGAAAATTTAGAAAGAACGA
101063	99150	AAGAAAATTTAGAAAGAACG
101064	99151	AAAGAAAATTTAGAAAGAAC
101065	99152	CAAAGAAAATTTAGAAAGAA
101066	99153	GCAAAGAAAATTTAGAAAGA
101067	99154	TGCAAAGAAAATTTAGAAAG
101068	99155	GTGCAAAGAAAATTTAGAAA
101069	99156	GGTGCAAAGAAAATTTAGAA
101070	99157	GGGTGCAAAGAAAATTTAGA
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101073	99160	AGTGGGTGCAAAGAAAATTT
101074	99161	TAGTGGGTGCAAAGAAAATT
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101079	99166	GTGATTAGTGGGTGCAAAGA
101080	99167	GGTGATTAGTGGGTGCAAAG
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101083	99170	TGAGGTGATTAGTGGGTGCA
101084	99171	ATGAGGTGATTAGTGGGTGC
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101087	99174	GAAATGAGGTGATTAGTGGG
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101093	99180	AGAAGGGAAATGAGGTGATT
101094	99181	AAGAAGGGAAATGAGGTGAT
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101096	99183	AGAAGAAGGGAAATGAGGTG
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101099	99186	GGGAGAAGAAGGGAAATGAG
101100	99187	GGGGAGAAGAAGGGAAATGA
101101	99188	TGGGGAGAAGAAGGGAAATG
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101105	99192	GTAATGGGGAGAAGAAGGGA
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101113	99200	TGGGAAGGGTAATGGGGAGA
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101121	99208	CCAGAAGTTGGGAAGGGTAA
101122	99209	ACCAGAAGTTGGGAAGGGTA
101123	99210	TACCAGAAGTTGGGAAGGGT
101124	99211	TTACCAGAAGTTGGGAAGGG
101125	99212	GTTACCAGAAGTTGGGAAGG
101126	99213	GGTTACCAGAAGTTGGGAAG
101127	99214	TGGTTACCAGAAGTTGGGAA

2834	921	GGAGGGGACGCCGGGCCCGG
2835	922	GGGAGGGGACGCCGGGCCCG
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2837	924	GGGGGAGGGGACGCCGGGCC
2838	925	CGGGGGAGGGGACGCCGGGC
2839	926	GCGGGGGAGGGGACGCCGGG
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2841	928	CCGCGGGGGAGGGGACGCCG
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2843	930	GGCCGCGGGGGAGGGGACGC
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2877	964	GCCCGGCGGGTCACGGGGCG
2878	965	AGCCCGGCGGGTCACGGGGC
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2880	967	GTAGCCCGGCGGGTCACGGG
2881	968	GGTAGCCCGGCGGGTCACGG
2882	969	GGGTAGCCCGGCGGGTCACG
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2889	976	CCACCCCGGGTAGCCCGGCG
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2892	979	AGCCCACCCCGGGTAGCCCG
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2901	988	CCGGCCCCCAGCCCACCCCG
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51981	50068	TTTTCTCCATACTGATAGTA
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52045	50132	GAGACTCCATCTCGAAATAA
52046	50133	TGAGACTCCATCTCGAAATA
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101128	99215	ATGGTTACCAGAAGTTGGGA
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101138	99225	AGATAGCAGAATGGTTACCA
101139	99226	GAGATAGCAGAATGGTTACC
101140	99227	GGAGATAGCAGAATGGTTAC
101141	99228	TGGAGATAGCAGAATGGTTA
101142	99229	ATGGAGATAGCAGAATGGTT
101143	99230	CATGGAGATAGCAGAATGGT
101144	99231	ACATGGAGATAGCAGAATGG
101145	99232	CACATGGAGATAGCAGAATG
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101147	99234	AACACATGGAGATAGCAGAA
101148	99235	GAACACATGGAGATAGCAGA
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101152	99239	AATTGAACACATGGAGATAG
101153	99240	CAATTGAACACATGGAGATA
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101155	99242	AACAATTGAACACATGGAGA
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101159	99246	TAAAAACAATTGAACACATG
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101176	99263	TTTGCAGGCACTAAAAATAA
101177	99264	GTTTGCAGGCACTAAAAATA
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101179	99266	TCGTTTGCAGGCACTAAAAA
101180	99267	CTCGTTTGCAGGCACTAAAA
101181	99268	ACTCGTTTGCAGGCACTAAA
101182	99269	TACTCGTTTGCAGGCACTAA
101183	99270	TTACTCGTTTGCAGGCACTA
101184	99271	CTTACTCGTTTGCAGGCACT
101185	99272	TCTTACTCGTTTGCAGGCAC
101186	99273	TTCTTACTCGTTTGCAGGCA
101187	99274	ATTCTTACTCGTTTGCAGGC
101188	99275	TATTCTTACTCGTTTGCAGG
101189	99276	ATATTCTTACTCGTTTGCAG
101190	99277	CATATTCTTACTCGTTTGCA
101191	99278	GCATATTCTTACTCGTTTGC
101192	99279	TGCATATTCTTACTCGTTTG
101193	99280	TTGCATATTCTTACTCGTTT
101194	99281	TTTGCATATTCTTACTCGTT
101195	99282	CTTTGCATATTCTTACTCGT
101196	99283	ACTTTGCATATTCTTACTCG
101197	99284	AACTTTGCATATTCTTACTC
101198	99285	AAACTTTGCATATTCTTACT

2905	992	GCTGCCGGCCCCCAGCCCAC
2906	993	CGCTGCCGGCCCCCAGCCCA
2907	994	GCGCTGCCGGCCCCCAGCCC
2908	995	CGCGCTGCCGGCCCCCAGCC
2909	996	CCGCGCTGCCGGCCCCCAGC
2910	997	CCCGCGCTGCCGGCCCCCAG
2911	998	CCCCGCGCTGCCGGCCCCCA
2912	999	CCCCCGCGCTGCCGGCCCCC
2913	1000	TCCCCCGCGCTGCCGGCCCC
2914	1001	CTCCCCCGCGCTGCCGGCCC
2915	1002	TCTCCCCCGCGCTGCCGGCC
2916	1003	GTCTCCCCCGCGCTGCCGGC
2917	1004	AGTCTCCCCCGCGCTGCCGG
2918	1005	GAGTCTCCCCCGCGCTGCCG
2919	1006	CGAGTCTCCCCCGCGCTGCC
2920	1007	GCGAGTCTCCCCCGCGCTGC
2921	1008	AGCGAGTCTCCCCCGCGCTG
2922	1009	GAGCGAGTCTCCCCCGCGCT
2923	1010	CGAGCGAGTCTCCCCCGCGC
2924	1011	CCGAGCGAGTCTCCCCCGCG
2925	1012	CCCGAGCGAGTCTCCCCCGC
2926	1013	GCCCGAGCGAGTCTCCCCCG
2927	1014	GGCCCGAGCGAGTCTCCCCC
2928	1015	AGGCCCGAGCGAGTCTCCCC
2929	1016	CAGGCCCGAGCGAGTCTCCC
2930	1017	TCAGGCCCGAGCGAGTCTCC
2931	1018	CTCAGGCCCGAGCGAGTCTC
2932	1019	GCTCAGGCCCGAGCGAGTCT
2933	1020	GGCTCAGGCCCGAGCGAGTC
2934	1021	GGGCTCAGGCCCGAGCGAGT
2935	1022	GGGGCTCAGGCCCGAGCGAG
2936	1023	CGGGGCTCAGGCCCGAGCGA
2937	1024	TCGGGGCTCAGGCCCGAGCG
2938	1025	CTCGGGGCTCAGGCCCGAGC
2939	1026	CCTCGGGGCTCAGGCCCGAG
2940	1027	GCCTCGGGGCTCAGGCCCGA
2941	1028	AGCCTCGGGGCTCAGGCCCG
2942	1029	GAGCCTCGGGGCTCAGGCCC
2943	1030	CGAGCCTCGGGGCTCAGGCC
2944	1031	CCGAGCCTCGGGGCTCAGGC
2945	1032	GCCGAGCCTCGGGGCTCAGG
2946	1033	GGCCGAGCCTCGGGGCTCAG
2947	1034	CGGCCGAGCCTCGGGGCTCA
2948	1035	CCGGCCGAGCCTCGGGGCTC
2949	1036	ACCGGCCGAGCCTCGGGGCT
2950	1037	CACCGGCCGAGCCTCGGGGC
2951	1038	CCACCGGCCGAGCCTCGGGG
2952	1039	CCCACCGGCCGAGCCTCGGG
2953	1040	GCCCACCGGCCGAGCCTCGG
2954	1041	CGCCCACCGGCCGAGCCTCG
2955	1042	GCGCCCACCGGCCGAGCCTC
2956	1043	TGCGCCCACCGGCCGAGCCT
2957	1044	CTGCGCCCACCGGCCGAGCC
2958	1045	GCTGCGCCCACCGGCCGAGC
2959	1046	GGCTGCGCCCACCGGCCGAG
2960	1047	CGGCTGCGCCCACCGGCCGA
2961	1048	CCGGCTGCGCCCACCGGCCG
2962	1049	CCCGGCTGCGCCCACCGGCC
2963	1050	CCCCGGCTGCGCCCACCGGC
2964	1051	ACCCCGGCTGCGCCCACCGG
2965	1052	GACCCCGGCTGCGCCCACCG
2966	1053	GGACCCCGGCTGCGCCCACC
2967	1054	AGGACCCCGGCTGCGCCCAC
2968	1055	GAGGACCCCGGCTGCGCCCA
2969	1056	AGAGGACCCCGGCTGCGCCC
2970	1057	CAGAGGACCCCGGCTGCGCC
2971	1058	CCAGAGGACCCCGGCTGCGC
2972	1059	CCCAGAGGACCCCGGCTGCG
2973	1060	TCCCAGAGGACCCCGGCTGC
2974	1061	ATCCCAGAGGACCCCGGCTG
2975	1062	AATCCCAGAGGACCCCGGCT

52052	50139	ATAGAGTGAGACTCCATCTC
52053	50140	AATAGAGTGAGACTCCATCT
52054	50141	AAATAGAGTGAGACTCCATC
52055	50142	GAAATAGAGTGAGACTCCAT
52056	50143	GGAAATAGAGTGAGACTCCA
52057	50144	GGGAAATAGAGTGAGACTCC
52058	50145	TGGGAAATAGAGTGAGACTC
52059	50146	CTGGGAAATAGAGTGAGACT
52060	50147	CCTGGGAAATAGAGTGAGAC
52061	50148	GCCTGGGAAATAGAGTGAGA
52062	50149	AGCCTGGGAAATAGAGTGAG
52063	50150	CAGCCTGGGAAATAGAGTGA
52064	50151	CCAGCCTGGGAAATAGAGTG
52065	50152	TCCAGCCTGGGAAATAGAGT
52066	50153	CTCCAGCCTGGGAAATAGAG
52067	50154	ACTCCAGCCTGGGAAATAGA
52068	50155	CACTCCAGCCTGGGAAATAG
52069	50156	GCACTCCAGCCTGGGAAATA
52070	50157	TGCACTCCAGCCTGGGAAAT
52071	50158	CTGCACTCCAGCCTGGGAAA
52072	50159	ACTGCACTCCAGCCTGGGAA
52073	50160	CACTGCACTCCAGCCTGGGA
52074	50161	CCACTGCACTCCAGCCTGGG
52075	50162	ACCACTGCACTCCAGCCTGG
52076	50163	CACCACTGCACTCCAGCCTG
52077	50164	GCACCACTGCACTCCAGCCT
52078	50165	CGCACCACTGCACTCCAGCC
52079	50166	TCGCACCACTGCACTCCAGC
52080	50167	ATCGCACCACTGCACTCCAG
52081	50168	GATCGCACCACTGCACTCCA
52082	50169	AGATCGCACCACTGCACTCC
52083	50170	GAGATCGCACCACTGCACTC
52084	50171	CGAGATCGCACCACTGCACT
52085	50172	CCGAGATCGCACCACTGCAC
52086	50173	GCCGAGATCGCACCACTGCA
52087	50174	AGCCGAGATCGCACCACTGC
52088	50175	GAGCCGAGATCGCACCACTG
52089	50176	TGAGCCGAGATCGCACCACT
52090	50177	GTGAGCCGAGATCGCACCAC
52091	50178	AGTGAGCCGAGATCGCACCA
52092	50179	CAGTGAGCCGAGATCGCACC
52093	50180	GCAGTGAGCCGAGATCGCAC
52094	50181	TGCAGTGAGCCGAGATCGCA
52095	50182	TTGCAGTGAGCCGAGATCGC
52096	50183	GTTGCAGTGAGCCGAGATCG
52097	50184	GGTTGCAGTGAGCCGAGATC
52098	50185	AGGTTGCAGTGAGCCGAGAT
52099	50186	GAGGTTGCAGTGAGCCGAGA
52100	50187	AGAGGTTGCAGTGAGCCGAG
52101	50188	CAGAGGTTGCAGTGAGCCGA
52102	50189	GCAGAGGTTGCAGTGAGCCG
52103	50190	GGCAGAGGTTGCAGTGAGCC
52104	50191	AGGCAGAGGTTGCAGTGAGC
52105	50192	GAGGCAGAGGTTGCAGTGAG
52106	50193	GGAGGCAGAGGTTGCAGTGA
52107	50194	AGGAGGCAGAGGTTGCAGTG
52108	50195	CAGGAGGCAGAGGTTGCAGT
52109	50196	CCAGGAGGCAGAGGTTGCAG
52110	50197	CCCAGGAGGCAGAGGTTGCA
52111	50198	ACCCAGGAGGCAGAGGTTGC
52112	50199	AACCCAGGAGGCAGAGGTTG
52113	50200	AAACCCAGGAGGCAGAGGTT
52114	50201	TAAACCCAGGAGGCAGAGGT
52115	50202	TTAAACCCAGGAGGCAGAGG
52116	50203	CTTAAACCCAGGAGGCAGAG
52117	50204	GCTTAAACCCAGGAGGCAGA
52118	50205	CGCTTAAACCCAGGAGGCAG
52119	50206	TCGCTTAAACCCAGGAGGCA
52120	50207	ATCGCTTAAACCCAGGAGGC
52121	50208	AATCGCTTAAACCCAGGAGG
52122	50209	GAATCGCTTAAACCCAGGAG

101199	99286	TAAACTTTGCATATTCTTAC
101200	99287	ATAAACTTTGCATATTCTTA
101201	99288	GATAAACTTTGCATATTCTT
101202	99289	AGATAAACTTTGCATATTCT
101203	99290	AAGATAAACTTTGCATATTC
101204	99291	AAAGATAAACTTTGCATATT
101205	99292	GAAAGATAAACTTTGCATAT
101206	99293	AGAAAGATAAACTTTGCATA
101207	99294	CAGAAAGATAAACTTTGCAT
101208	99295	ACAGAAAGATAAACTTTGCA
101209	99296	GACAGAAAGATAAACTTTGC
101210	99297	GGACAGAAAGATAAACTTTG
101211	99298	GGGACAGAAAGATAAACTTT
101212	99299	AGGGACAGAAAGATAAACTT
101213	99300	CAGGGACAGAAAGATAAACT
101214	99301	CCAGGGACAGAAAGATAAAC
101215	99302	GCCAGGGACAGAAAGATAAA
101216	99303	AGCCAGGGACAGAAAGATAA
101217	99304	AAGCCAGGGACAGAAAGATA
101218	99305	TAAGCCAGGGACAGAAAGAT
101219	99306	ATAAGCCAGGGACAGAAAGA
101220	99307	AATAAGCCAGGGACAGAAAG
101221	99308	AAATAAGCCAGGGACAGAAA
101222	99309	AAAATAAGCCAGGGACAGAA
101223	99310	TAAAATAAGCCAGGGACAGA
101224	99311	GTAAAATAAGCCAGGGACAG
101225	99312	AGTAAAATAAGCCAGGGACA
101226	99313	AAGTAAAATAAGCCAGGGAC
101227	99314	TAAGTAAAATAAGCCAGGGA
101228	99315	TTAAGTAAAATAAGCCAGGG
101229	99316	GTTAAGTAAAATAAGCCAGG
101230	99317	TGTTAAGTAAAATAAGCCAG
101231	99318	ATGTTAAGTAAAATAAGCCA
101232	99319	TATGTTAAGTAAAATAAGCC
101233	99320	TTATGTTAAGTAAAATAAGC
101234	99321	ATTATGTTAAGTAAAATAAG
101235	99322	CATTATGTTAAGTAAAATAA
101236	99323	ACATTATGTTAAGTAAAATA
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101238	99325	GGACATTATGTTAAGTAAAA
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101240	99327	GAGGACATTATGTTAAGTAA
101241	99328	GGAGGACATTATGTTAAGTA
101242	99329	TGGAGGACATTATGTTAAGT
101243	99330	CTGGAGGACATTATGTTAAG
101244	99331	ACTGGAGGACATTATGTTAA
101245	99332	CACTGGAGGACATTATGTTA
101246	99333	GCACTGGAGGACATTATGTT
101247	99334	GGCACTGGAGGACATTATGT
101248	99335	TGGCACTGGAGGACATTATG
101249	99336	ATGGCACTGGAGGACATTAT
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101252	99339	TAGATGGCACTGGAGGACAT
101253	99340	GTAGATGGCACTGGAGGACA
101254	99341	TGTAGATGGCACTGGAGGAC
101255	99342	ATGTAGATGGCACTGGAGGA
101256	99343	AATGTAGATGGCACTGGAGG
101257	99344	CAATGTAGATGGCACTGGAG
101258	99345	GCAATGTAGATGGCACTGGA
101259	99346	AGCAATGTAGATGGCACTGG
101260	99347	CAGCAATGTAGATGGCACTG
101261	99348	GCAGCAATGTAGATGGCACT
101262	99349	TGCAGCAATGTAGATGGCAC
101263	99350	TTGCAGCAATGTAGATGGCA
101264	99351	TTTGCAGCAATGTAGATGGC
101265	99352	ATTTGCAGCAATGTAGATGG
101266	99353	CATTTGCAGCAATGTAGATG
101267	99354	TCATTTGCAGCAATGTAGAT
101268	99355	GTCATTTGCAGCAATGTAGA
101269	99356	TGTCATTTGCAGCAATGTAG

2976	1063	CAATCCCAGAGGACCCCGGC
2977	1064	ACAATCCCAGAGGACCCCGG
2978	1065	GACAATCCCAGAGGACCCCG
2979	1066	TGACAATCCCAGAGGACCCC
2980	1067	CTGACAATCCCAGAGGACCC
2981	1068	CCTGACAATCCCAGAGGACC
2982	1069	GCCTGACAATCCCAGAGGAC
2983	1070	GGCCTGACAATCCCAGAGGA
2984	1071	AGGCCTGACAATCCCAGAGG
2985	1072	CAGGCCTGACAATCCCAGAG
2986	1073	ACAGGCCTGACAATCCCAGA
2987	1074	GACAGGCCTGACAATCCCAG
2988	1075	GGACAGGCCTGACAATCCCA
2989	1076	TGGACAGGCCTGACAATCCC
2990	1077	CTGGACAGGCCTGACAATCC
2991	1078	GCTGGACAGGCCTGACAATC
2992	1079	GGCTGGACAGGCCTGACAAT
2993	1080	AGGCTGGACAGGCCTGACAA
2994	1081	GAGGCTGGACAGGCCTGACA
2995	1082	GGAGGCTGGACAGGCCTGAC
2996	1083	GGGAGGCTGGACAGGCCTGA
2997	1084	CGGGAGGCTGGACAGGCCTG
2998	1085	GCGGGAGGCTGGACAGGCCT
2999	1086	TGCGGGAGGCTGGACAGGCC
3000	1087	CTGCGGGAGGCTGGACAGGC
3001	1088	GCTGCGGGAGGCTGGACAGG
3002	1089	TGCTGCGGGAGGCTGGACAG
3003	1090	ATGCTGCGGGAGGCTGGACA
3004	1091	GATGCTGCGGGAGGCTGGAC
3005	1092	GGATGCTGCGGGAGGCTGGA
3006	1093	GGGATGCTGCGGGAGGCTGG
3007	1094	GGGGATGCTGCGGGAGGCTG
3008	1095	CGGGGATGCTGCGGGAGGCT
3009	1096	GCGGGGATGCTGCGGGAGGC
3010	1097	GGCGGGGATGCTGCGGGAGG
3011	1098	GGGCGGGGATGCTGCGGGAG
3012	1099	GGGGCGGGGATGCTGCGGGA
3013	1100	GGGGGCGGGGATGCTGCGGG
3014	1101	AGGGGGCGGGGATGCTGCGG
3015	1102	GAGGGGGCGGGGATGCTGCG
3016	1103	GGAGGGGGCGGGGATGCTGC
3017	1104	GGGAGGGGGCGGGGATGCTG
3018	1105	GGGGAGGGGGCGGGGATGCT
3019	1106	GGGGGAGGGGGCGGGGATGC
3020	1107	CGGGGGAGGGGGCGGGGATG
3021	1108	CCGGGGGAGGGGGCGGGGAT
3022	1109	GCCGGGGGAGGGGGCGGGGA
3023	1110	CGCCGGGGGAGGGGGCGGGG
3024	1111	CCGCCGGGGGAGGGGGCGGG
3025	1112	ACCGCCGGGGGAGGGGGCGG
3026	1113	GACCGCCGGGGGAGGGGGCG
3027	1114	TGACCGCCGGGGGAGGGGGC
3028	1115	TTGACCGCCGGGGGAGGGGG
3029	1116	CTTGACCGCCGGGGGAGGGG
3030	1117	TCTTGACCGCCGGGGGAGGG
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3032	1119	CATCTTGACCGCCGGGGGAG
3033	1120	CCATCTTGACCGCCGGGGGA
3034	1121	TCCATCTTGACCGCCGGGGG
3035	1122	CTCCATCTTGACCGCCGGGG
3036	1123	CCTCCATCTTGACCGCCGGG
3037	1124	CCCTCCATCTTGACCGCCGG
3038	1125	TCCCTCCATCTTGACCGCCG
3039	1126	CTCCCTCCATCTTGACCGCC
3040	1127	GCTCCCTCCATCTTGACCGC
3041	1128	CGCTCCCTCCATCTTGACCG
3042	1129	CCGCTCCCTCCATCTTGACC
3043	1130	CCCGCTCCCTCCATCTTGAC
3044	1131	GCCCGCTCCCTCCATCTTGA
3045	1132	CGCCCGCTCCCTCCATCTTG
3046	1133	CCGCCCGCTCCCTCCATCTT

52123	50210	AGAATCGCTTAAACCCAGGA
52124	50211	GAGAATCGCTTAAACCCAGG
52125	50212	GGAGAATCGCTTAAACCCAG
52126	50213	AGGAGAATCGCTTAAACCCA
52127	50214	CAGGAGAATCGCTTAAACCC
52128	50215	GCAGGAGAATCGCTTAAACC
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52130	50217	AGGCAGGAGAATCGCTTAAA
52131	50218	GAGGCAGGAGAATCGCTTAA
52132	50219	TGAGGCAGGAGAATCGCTTA
52133	50220	CTGAGGCAGGAGAATCGCTT
52134	50221	GCTGAGGCAGGAGAATCGCT
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52136	50223	AGGCTGAGGCAGGAGAATCG
52137	50224	GAGGCTGAGGCAGGAGAATC
52138	50225	GGAGGCTGAGGCAGGAGAAT
52139	50226	GGGAGGCTGAGGCAGGAGAA
52140	50227	CGGGAGGCTGAGGCAGGAGA
52141	50228	TCGGGAGGCTGAGGCAGGAG
52142	50229	CTCGGGAGGCTGAGGCAGGA
52143	50230	ACTCGGGAGGCTGAGGCAGG
52144	50231	TACTCGGGAGGCTGAGGCAG
52145	50232	CTACTCGGGAGGCTGAGGCA
52146	50233	GCTACTCGGGAGGCTGAGGC
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52148	50235	CAGCTACTCGGGAGGCTGAG
52149	50236	CCAGCTACTCGGGAGGCTGA
52150	50237	CCCAGCTACTCGGGAGGCTG
52151	50238	TCCCAGCTACTCGGGAGGCT
52152	50239	ATCCCAGCTACTCGGGAGGC
52153	50240	AATCCCAGCTACTCGGGAGG
52154	50241	TAATCCCAGCTACTCGGGAG
52155	50242	ATAATCCCAGCTACTCGGGA
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52157	50244	CTATAATCCCAGCTACTCGG
52158	50245	CCTATAATCCCAGCTACTCG
52159	50246	GCCTATAATCCCAGCTACTC
52160	50247	TGCCTATAATCCCAGCTACT
52161	50248	GTGCCTATAATCCCAGCTAC
52162	50249	TGTGCCTATAATCCCAGCTA
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52164	50251	TATGTGCCTATAATCCCAGC
52165	50252	GTATGTGCCTATAATCCCAG
52166	50253	GGTATGTGCCTATAATCCCA
52167	50254	TGGTATGTGCCTATAATCCC
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52169	50256	GGTGGTATGTGCCTATAATC
52170	50257	TGGTGGTATGTGCCTATAAT
52171	50258	ATGGTGGTATGTGCCTATAA
52172	50259	CATGGTGGTATGTGCCTATA
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52174	50261	GGCATGGTGGTATGTGCCTA
52175	50262	GGGCATGGTGGTATGTGCCT
52176	50263	AGGGCATGGTGGTATGTGCC
52177	50264	CAGGGCATGGTGGTATGTGC
52178	50265	GCAGGGCATGGTGGTATGTG
52179	50266	AGCAGGGCATGGTGGTATGT
52180	50267	TAGCAGGGCATGGTGGTATG
52181	50268	TTAGCAGGGCATGGTGGTAT
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52186	50273	AAAAATTAGCAGGGCATGGT
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52188	50275	AAAAAAATTAGCAGGGCATG
52189	50276	AAAAAAAATTAGCAGGGCAT
52190	50277	AAAAAAAAATTAGCAGGGCA
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52192	50279	AAAAAAAAAAATTAGCAGGG
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101270	99357	CTGTCATTTGCAGCAATGTA
101271	99358	CCTGTCATTTGCAGCAATGT
101272	99359	TCCTGTCATTTGCAGCAATG
101273	99360	ATCCTGTCATTTGCAGCAAT
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101275	99362	AGATCCTGTCATTTGCAGCA
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101277	99364	TGAGATCCTGTCATTTGCAG
101278	99365	ATGAGATCCTGTCATTTGCA
101279	99366	AATGAGATCCTGTCATTTGC
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101281	99368	AGAATGAGATCCTGTCATTT
101282	99369	AAGAATGAGATCCTGTCATT
101283	99370	AAAGAATGAGATCCTGTCAT
101284	99371	AAAAGAATGAGATCCTGTCA
101285	99372	AAAAAGAATGAGATCCTGTC
101286	99373	AAAAAAGAATGAGATCCTGT
101287	99374	TAAAAAAGAATGAGATCCTG
101288	99375	ATAAAAAAGAATGAGATCCT
101289	99376	CATAAAAAAGAATGAGATCC
101290	99377	CCATAAAAAAGAATGAGATC
101291	99378	GCCATAAAAAAGAATGAGAT
101292	99379	AGCCATAAAAAAGAATGAGA
101293	99380	CAGCCATAAAAAAGAATGAG
101294	99381	TCAGCCATAAAAAAGAATGA
101295	99382	TTCAGCCATAAAAAAGAATG
101296	99383	ATTCAGCCATAAAAAAGAAT
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101298	99385	CCATTCAGCCATAAAAAAGA
101299	99386	ACCATTCAGCCATAAAAAAG
101300	99387	TACCATTCAGCCATAAAAAA
101301	99388	TTACCATTCAGCCATAAAAA
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101303	99390	GATTACCATTCAGCCATAAA
101304	99391	AGATTACCATTCAGCCATAA
101305	99392	TAGATTACCATTCAGCCATA
101306	99393	ATAGATTACCATTCAGCCAT
101307	99394	AATAGATTACCATTCAGCCA
101308	99395	CAATAGATTACCATTCAGCC
101309	99396	ACAATAGATTACCATTCAGC
101310	99397	CACAATAGATTACCATTCAG
101311	99398	ACACAATAGATTACCATTCA
101312	99399	TACACAATAGATTACCATTC
101313	99400	ATACACAATAGATTACCATT
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101315	99402	ATATACACAATAGATTACCA
101316	99403	TATATACACAATAGATTACC
101317	99404	ATATATACACAATAGATTAC
101318	99405	TATATATACACAATAGATTA
101319	99406	GTATATATACACAATAGATT
101320	99407	GGTATATATACACAATAGAT
101321	99408	TGGTATATATACACAATAGA
101322	99409	GTGGTATATATACACAATAG
101323	99410	TGTGGTATATATACACAATA
101324	99411	ATGTGGTATATATACACAAT
101325	99412	AATGTGGTATATATACACAA
101326	99413	AAATGTGGTATATATACACA
101327	99414	AAAATGTGGTATATATACAC
101328	99415	GAAAATGTGGTATATATACA
101329	99416	AGAAAATGTGGTATATATAC
101330	99417	AAGAAAATGTGGTATATATA
101331	99418	AAAGAAAATGTGGTATATAT
101332	99419	GAAAGAAAATGTGGTATATA
101333	99420	AGAAAGAAAATGTGGTATAT
101334	99421	GAGAAAGAAAATGTGGTATA
101335	99422	GGAGAAAGAAAATGTGGTAT
101336	99423	TGGAGAAAGAAAATGTGGTA
101337	99424	ATGGAGAAAGAAAATGTGGT
101338	99425	AATGGAGAAAGAAAATGTGG
101339	99426	AAATGGAGAAAGAAAATGTG
101340	99427	CAAATGGAGAAAGAAAATGT

3047	1134	GCCGCCCGCTCCCTCCATCT
3048	1135	GGCCGCCCGCTCCCTCCATC
3049	1136	AGGCCGCCCGCTCCCTCCAT
3050	1137	GAGGCCGCCCGCTCCCTCCA
3051	1138	GGAGGCCGCCCGCTCCCTCC
3052	1139	GGGAGGCCGCCCGCTCCCTC
3053	1140	GGGGAGGCCGCCCGCTCCCT
3054	1141	AGGGGAGGCCGCCCGCTCCC
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3056	1143	GGAGGGGAGGCCGCCCGCTC
3057	1144	GGGAGGGGAGGCCGCCCGCT
3058	1145	GGGGAGGGGAGGCCGCCCGC
3059	1146	TGGGGAGGGGAGGCCGCCCG
3060	1147	GTGGGGAGGGGAGGCCGCCC
3061	1148	CGTGGGGAGGGGAGGCCGCC
3062	1149	GCGTGGGGAGGGGAGGCCGC
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3066	1153	ACACGCGTGGGGAGGGGAGG
3067	1154	AACACGCGTGGGGAGGGGAG
3068	1155	CAACACGCGTGGGGAGGGGA
3069	1156	CCAACACGCGTGGGGAGGGG
3070	1157	CCCAACACGCGTGGGGAGGG
3071	1158	TCCCAACACGCGTGGGGAGG
3072	1159	CTCCCAACACGCGTGGGGAG
3073	1160	CCTCCCAACACGCGTGGGGA
3074	1161	CCCTCCCAACACGCGTGGGG
3075	1162	CCCCTCCCAACACGCGTGGG
3076	1163	ACCCCTCCCAACACGCGTGG
3077	1164	AACCCCTCCCAACACGCGTG
3078	1165	GAACCCCTCCCAACACGCGT
3079	1166	AGAACCCCTCCCAACACGCG
3080	1167	GAGAACCCCTCCCAACACGC
3081	1168	CGAGAACCCCTCCCAACACG
3082	1169	CCGAGAACCCCTCCCAACAC
3083	1170	CCCGAGAACCCCTCCCAACA
3084	1171	ACCCGAGAACCCCTCCCAAC
3085	1172	TACCCGAGAACCCCTCCCAA
3086	1173	CTACCCGAGAACCCCTCCCA
3087	1174	GCTACCCGAGAACCCCTCCC
3088	1175	CGCTACCCGAGAACCCCTCC
3089	1176	CCGCTACCCGAGAACCCCTC
3090	1177	GCCGCTACCCGAGAACCCCT
3091	1178	CGCCGCTACCCGAGAACCCC
3092	1179	TCGCCGCTACCCGAGAACCC
3093	1180	ATCGCCGCTACCCGAGAACC
3094	1181	CATCGCCGCTACCCGAGAAC
3095	1182	CCATCGCCGCTACCCGAGAA
3096	1183	ACCATCGCCGCTACCCGAGA
3097	1184	GACCATCGCCGCTACCCGAG
3098	1185	TGACCATCGCCGCTACCCGA
3099	1186	CTGACCATCGCCGCTACCCG
3100	1187	GCTGACCATCGCCGCTACCC
3101	1188	GGCTGACCATCGCCGCTACC
3102	1189	GGGCTGACCATCGCCGCTAC
3103	1190	GGGGCTGACCATCGCCGCTA
3104	1191	CGGGGCTGACCATCGCCGCT
3105	1192	CCGGGGCTGACCATCGCCGC
3106	1193	GCCGGGGCTGACCATCGCCG
3107	1194	AGCCGGGGCTGACCATCGCC
3108	1195	GAGCCGGGGCTGACCATCGC
3109	1196	GGAGCCGGGGCTGACCATCG
3110	1197	GGGAGCCGGGGCTGACCATC
3111	1198	GGGGAGCCGGGGCTGACCAT
3112	1199	GGGGGAGCCGGGGCTGACCA
3113	1200	AGGGGGAGCCGGGGCTGACC
3114	1201	AAGGGGGAGCCGGGGCTGAC
3115	1202	GAAGGGGGAGCCGGGGCTGA
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3117	1204	CGGAAGGGGGAGCCGGGGCT

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52196	50283	AAACAAAAAAAAAAATTAGC
52197	50284	CAAACAAAAAAAAAAATTAG
52198	50285	ACAAACAAAAAAAAAAATTA
52199	50286	TACAAACAAAAAAAAAAATT
52200	50287	ATACAAACAAAAAAAAAAAT
52201	50288	AATACAAACAAAAAAAAAAA
52202	50289	GAATACAAACAAAAAAAAAA
52203	50290	AGAATACAAACAAAAAAAAA
52204	50291	AAGAATACAAACAAAAAAAA
52205	50292	TAAGAATACAAACAAAAAAA
52206	50293	CTAAGAATACAAACAAAAAA
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52211	50298	CTGTACTAAGAATACAAACA
52212	50299	TCTGTACTAAGAATACAAAC
52213	50300	GTCTGTACTAAGAATACAAA
52214	50301	AGTCTGTACTAAGAATACAA
52215	50302	CAGTCTGTACTAAGAATACA
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52217	50304	CCCAGTCTGTACTAAGAATA
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52219	50306	AACCCAGTCTGTACTAAGAA
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52222	50309	TGAAACCCAGTCTGTACTAA
52223	50310	GTGAAACCCAGTCTGTACTA
52224	50311	GGTGAAACCCAGTCTGTACT
52225	50312	TGGTGAAACCCAGTCTGTAC
52226	50313	ATGGTGAAACCCAGTCTGTA
52227	50314	CATGGTGAAACCCAGTCTGT
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52230	50317	CAACATGGTGAAACCCAGTC
52231	50318	CCAACATGGTGAAACCCAGT
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52234	50321	TGGCCAACATGGTGAAACCC
52235	50322	CTGGCCAACATGGTGAAACC
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52237	50324	GCCTGGCCAACATGGTGAAA
52238	50325	GGCCTGGCCAACATGGTGAA
52239	50326	CGGCCTGGCCAACATGGTGA
52240	50327	GCGGCCTGGCCAACATGGTG
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52243	50330	CATGCGGCCTGGCCAACATG
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52262	50349	TTTTGTTATTAAGGAAAACC
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52264	50351	AATTTTGTTATTAAGGAAAA

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101342	99429	GACAAATGGAGAAAGAAAAT
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101344	99431	CAGACAAATGGAGAAAGAAA
101345	99432	ACAGACAAATGGAGAAAGAA
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101348	99435	CTGACAGACAAATGGAGAAA
101349	99436	ACTGACAGACAAATGGAGAA
101350	99437	CACTGACAGACAAATGGAGA
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101354	99441	TGTCCACTGACAGACAAATG
101355	99442	GTGTCCACTGACAGACAAAT
101356	99443	CGTGTCCACTGACAGACAAA
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101358	99445	TACGTGTCCACTGACAGACA
101359	99446	CTACGTGTCCACTGACAGAC
101360	99447	CCTACGTGTCCACTGACAGA
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101362	99449	AACCTACGTGTCCACTGACA
101363	99450	CAACCTACGTGTCCACTGAC
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101366	99453	AATCAACCTACGTGTCCACT
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101374	99461	AGATTTGGAATCAACCTACG
101375	99462	AAGATTTGGAATCAACCTAC
101376	99463	CAAGATTTGGAATCAACCTA
101377	99464	CCAAGATTTGGAATCAACCT
101378	99465	GCCAAGATTTGGAATCAACC
101379	99466	AGCCAAGATTTGGAATCAAC
101380	99467	CAGCCAAGATTTGGAATCAA
101381	99468	ACAGCCAAGATTTGGAATCA
101382	99469	AACAGCCAAGATTTGGAATC
101383	99470	CAACAGCCAAGATTTGGAAT
101384	99471	ACAACAGCCAAGATTTGGAA
101385	99472	CACAACAGCCAAGATTTGGA
101386	99473	ACACAACAGCCAAGATTTGG
101387	99474	TACACAACAGCCAAGATTTG
101388	99475	ATACACAACAGCCAAGATTT
101389	99476	TATACACAACAGCCAAGATT
101390	99477	ATATACACAACAGCCAAGAT
101391	99478	TATATACACAACAGCCAAGA
101392	99479	CTATATACACAACAGCCAAG
101393	99480	ACTATATACACAACAGCCAA
101394	99481	CACTATATACACAACAGCCA
101395	99482	GCACTATATACACAACAGCC
101396	99483	GGCACTATATACACAACAGC
101397	99484	CGGCACTATATACACAACAG
101398	99485	ACGGCACTATATACACAACA
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101408	99495	CATGTTTACTACGGCACTAT
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3122	1209	TCGTGCGGAAGGGGGAGCCG
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3129	1216	CGGAGGATCGTGCGGAAGGG
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3135	1222	TGCGGGCGGAGGATCGTGCG
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3137	1224	GCTGCGGGCGGAGGATCGTG
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3139	1226	ACGCTGCGGGCGGAGGATCG
3140	1227	CACGCTGCGGGCGGAGGATC
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3142	1229	CCCACGCTGCGGGCGGAGGA
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3163	1250	TGGAGGAGCTGCCCGAGCAT
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3174	1261	TAAACCGGGAGTGGAGGAGC
3175	1262	CTAAACCGGGAGTGGAGGAG
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3177	1264	ACCTAAACCGGGAGTGGAGG
3178	1265	CACCTAAACCGGGAGTGGAG
3179	1266	ACACCTAAACCGGGAGTGGA
3180	1267	CACACCTAAACCGGGAGTGG
3181	1268	TCACACCTAAACCGGGAGTG
3182	1269	TTCACACCTAAACCGGGAGT
3183	1270	GTTCACACCTAAACCGGGAG
3184	1271	CGTTCACACCTAAACCGGGA
3185	1272	ACGTTCACACCTAAACCGGG
3186	1273	AACGTTCACACCTAAACCGG
3187	1274	CAACGTTCACACCTAAACCG
3188	1275	CCAACGTTCACACCTAAACC

52265	50352	TAATTTTGTTATTAAGGAAA
52266	50353	TTAATTTTGTTATTAAGGAA
52267	50354	CTTAATTTTGTTATTAAGGA
52268	50355	CCTTAATTTTGTTATTAAGG
52269	50356	GCCTTAATTTTGTTATTAAG
52270	50357	TGCCTTAATTTTGTTATTAA
52271	50358	ATGCCTTAATTTTGTTATTA
52272	50359	AATGCCTTAATTTTGTTATT
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52276	50363	AATAAATGCCTTAATTTTGT
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52278	50365	GTAATAAATGCCTTAATTTT
52279	50366	AGTAATAAATGCCTTAATTT
52280	50367	CAGTAATAAATGCCTTAATT
52281	50368	GCAGTAATAAATGCCTTAAT
52282	50369	TGCAGTAATAAATGCCTTAA
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52294	50381	AAAAAATCTAGATGCAGTAA
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52311	50398	TCTCTAATAAAAAATAAAAA
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52320	50407	CTGAGTAAGTCTCTAATAAA
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52322	50409	ATCTGAGTAAGTCTCTAATA
52323	50410	AATCTGAGTAAGTCTCTAAT
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52325	50412	GTAATCTGAGTAAGTCTCTA
52326	50413	AGTAATCTGAGTAAGTCTCT
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52329	50416	GGGAGTAATCTGAGTAAGTC
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52331	50418	TTGGGAGTAATCTGAGTAAG
52332	50419	TTTGGGAGTAATCTGAGTAA
52333	50420	CTTTGGGAGTAATCTGAGTA
52334	50421	ACTTTGGGAGTAATCTGAGT
52335	50422	TACTTTGGGAGTAATCTGAG

101412	99499	CTCCCATGTTTACTACGGCA
101413	99500	ACTCCCATGTTTACTACGGC
101414	99501	CACTCCCATGTTTACTACGG
101415	99502	GCACTCCCATGTTTACTACG
101416	99503	TGCACTCCCATGTTTACTAC
101417	99504	CTGCACTCCCATGTTTACTA
101418	99505	TCTGCACTCCCATGTTTACT
101419	99506	ATCTGCACTCCCATGTTTAC
101420	99507	TATCTGCACTCCCATGTTTA
101421	99508	ATATCTGCACTCCCATGTTT
101422	99509	AATATCTGCACTCCCATGTT
101423	99510	GAATATCTGCACTCCCATGT
101424	99511	GGAATATCTGCACTCCCATG
101425	99512	AGGAATATCTGCACTCCCAT
101426	99513	AAGGAATATCTGCACTCCCA
101427	99514	GAAGGAATATCTGCACTCCC
101428	99515	TGAAGGAATATCTGCACTCC
101429	99516	TTGAAGGAATATCTGCACTC
101430	99517	ATTGAAGGAATATCTGCACT
101431	99518	TATTGAAGGAATATCTGCAC
101432	99519	TTATTGAAGGAATATCTGCA
101433	99520	TTTATTGAAGGAATATCTGC
101434	99521	GTTTATTGAAGGAATATCTG
101435	99522	AGTTTATTGAAGGAATATCT
101436	99523	CAGTTTATTGAAGGAATATC
101437	99524	TCAGTTTATTGAAGGAATAT
101438	99525	ATCAGTTTATTGAAGGAATA
101439	99526	AATCAGTTTATTGAAGGAAT
101440	99527	AAATCAGTTTATTGAAGGAA
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101444	99531	AAGGAAATCAGTTTATTGAA
101445	99532	AAAGGAAATCAGTTTATTGA
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101447	99534	AGAAAGGAAATCAGTTTATT
101448	99535	CAGAAAGGAAATCAGTTTAT
101449	99536	TCAGAAAGGAAATCAGTTTA
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101454	99541	TATACTCAGAAAGGAAATCA
101455	99542	ATATACTCAGAAAGGAAATC
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101460	99547	TAGGTATATACTCAGAAAGG
101461	99548	CTAGGTATATACTCAGAAAG
101462	99549	GCTAGGTATATACTCAGAAA
101463	99550	TGCTAGGTATATACTCAGAA
101464	99551	CTGCTAGGTATATACTCAGA
101465	99552	ACTGCTAGGTATATACTCAG
101466	99553	CACTGCTAGGTATATACTCA
101467	99554	GCACTGCTAGGTATATACTC
101468	99555	TGCACTGCTAGGTATATACT
101469	99556	TTGCACTGCTAGGTATATAC
101470	99557	ATTGCACTGCTAGGTATATA
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101477	99564	TCCAGCAATTGCACTGCTAG
101478	99565	ATCCAGCAATTGCACTGCTA
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101480	99567	TGATCCAGCAATTGCACTGC
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3189	1276	TCCAACGTTCACACCTAAAC
3190	1277	CTCCAACGTTCACACCTAAA
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3192	1279	CCCTCCAACGTTCACACCTA
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3194	1281	ACCCCTCCAACGTTCACACC
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3198	1285	CCAGACCCCTCCAACGTTCA
3199	1286	TCCAGACCCCTCCAACGTTC
3200	1287	CTCCAGACCCCTCCAACGTT
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3202	1289	GCCTCCAGACCCCTCCAACG
3203	1290	AGCCTCCAGACCCCTCCAAC
3204	1291	CAGCCTCCAGACCCCTCCAA
3205	1292	ACAGCCTCCAGACCCCTCCA
3206	1293	CACAGCCTCCAGACCCCTCC
3207	1294	CCACAGCCTCCAGACCCCTC
3208	1295	ACCACAGCCTCCAGACCCCT
3209	1296	CACCACAGCCTCCAGACCCC
3210	1297	CCACCACAGCCTCCAGACCC
3211	1298	GCCACCACAGCCTCCAGACC
3212	1299	CGCCACCACAGCCTCCAGAC
3213	1300	ACGCCACCACAGCCTCCAGA
3214	1301	AACGCCACCACAGCCTCCAG
3215	1302	AAACGCCACCACAGCCTCCA
3216	1303	AAAACGCCACCACAGCCTCC
3217	1304	GAAAACGCCACCACAGCCTC
3218	1305	GGAAAACGCCACCACAGCCT
3219	1306	CGGAAAACGCCACCACAGCC
3220	1307	CCGGAAAACGCCACCACAGC
3221	1308	TCCGGAAAACGCCACCACAG
3222	1309	TTCCGGAAAACGCCACCACA
3223	1310	GTTCCGGAAAACGCCACCAC
3224	1311	TGTTCCGGAAAACGCCACCA
3225	1312	ATGTTCCGGAAAACGCCACC
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3227	1314	ACATGTTCCGGAAAACGCCA
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3229	1316	GGACATGTTCCGGAAAACGC
3230	1317	GGGACATGTTCCGGAAAACG
3231	1318	GGGGACATGTTCCGGAAAAC
3232	1319	GGGGGACATGTTCCGGAAAA
3233	1320	AGGGGGACATGTTCCGGAAA
3234	1321	GAGGGGGACATGTTCCGGAA
3235	1322	GGAGGGGGACATGTTCCGGA
3236	1323	TGGAGGGGGACATGTTCCGG
3237	1324	ATGGAGGGGGACATGTTCCG
3238	1325	CATGGAGGGGGACATGTTCC
3239	1326	CCATGGAGGGGGACATGTTC
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3244	1331	GTCCCCCATGGAGGGGGACA
3245	1332	TGTCCCCCATGGAGGGGGAC
3246	1333	ATGTCCCCCATGGAGGGGGA
3247	1334	GATGTCCCCCATGGAGGGGG
3248	1335	AGATGTCCCCCATGGAGGGG
3249	1336	GAGATGTCCCCCATGGAGGG
3250	1337	AGAGATGTCCCCCATGGAGG
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3252	1339	CCAGAGATGTCCCCCATGGA
3253	1340	TCCAGAGATGTCCCCCATGG
3254	1341	CTCCAGAGATGTCCCCCATG
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52336	50423	TTACTTTGGGAGTAATCTGA
52337	50424	TTTACTTTGGGAGTAATCTG
52338	50425	CTTTACTTTGGGAGTAATCT
52339	50426	CCTTTACTTTGGGAGTAATC
52340	50427	TCCTTTACTTTGGGAGTAAT
52341	50428	TTCCTTTACTTTGGGAGTAA
52342	50429	CTTCCTTTACTTTGGGAGTA
52343	50430	CCTTCCTTTACTTTGGGAGT
52344	50431	ACCTTCCTTTACTTTGGGAG
52345	50432	TACCTTCCTTTACTTTGGGA
52346	50433	ATACCTTCCTTTACTTTGGG
52347	50434	CATACCTTCCTTTACTTTGG
52348	50435	CCATACCTTCCTTTACTTTG
52349	50436	ACCATACCTTCCTTTACTTT
52350	50437	AACCATACCTTCCTTTACTT
52351	50438	AAACCATACCTTCCTTTACT
52352	50439	TAAACCATACCTTCCTTTAC
52353	50440	TTAAACCATACCTTCCTTTA
52354	50441	ATTAAACCATACCTTCCTTT
52355	50442	GATTAAACCATACCTTCCTT
52356	50443	TGATTAAACCATACCTTCCT
52357	50444	TTGATTAAACCATACCTTCC
52358	50445	ATTGATTAAACCATACCTTC
52359	50446	CATTGATTAAACCATACCTT
52360	50447	GCATTGATTAAACCATACCT
52361	50448	AGCATTGATTAAACCATACC
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52365	50452	AAGAAGCATTGATTAAACCA
52366	50453	TAAGAAGCATTGATTAAACC
52367	50454	TTAAGAAGCATTGATTAAAC
52368	50455	ATTAAGAAGCATTGATTAAA
52369	50456	CATTAAGAAGCATTGATTAA
52370	50457	GCATTAAGAAGCATTGATTA
52371	50458	AGCATTAAGAAGCATTGATT
52372	50459	CAGCATTAAGAAGCATTGAT
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52374	50461	CCCAGCATTAAGAAGCATTG
52375	50462	ACCCAGCATTAAGAAGCATT
52376	50463	AACCCAGCATTAAGAAGCAT
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52378	50465	TGAACCCAGCATTAAGAAGC
52379	50466	GTGAACCCAGCATTAAGAAG
52380	50467	CGTGAACCCAGCATTAAGAA
52381	50468	ACGTGAACCCAGCATTAAGA
52382	50469	AACGTGAACCCAGCATTAAG
52383	50470	AAACGTGAACCCAGCATTAA
52384	50471	TAAACGTGAACCCAGCATTA
52385	50472	CTAAACGTGAACCCAGCATT
52386	50473	ACTAAACGTGAACCCAGCAT
52387	50474	GACTAAACGTGAACCCAGCA
52388	50475	TGACTAAACGTGAACCCAGC
52389	50476	GTGACTAAACGTGAACCCAG
52390	50477	GGTGACTAAACGTGAACCCA
52391	50478	AGGTGACTAAACGTGAACCC
52392	50479	CAGGTGACTAAACGTGAACC
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52394	50481	CCCAGGTGACTAAACGTGAA
52395	50482	CCCCAGGTGACTAAACGTGA
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52398	50485	ACTCCCCAGGTGACTAAACG
52399	50486	AACTCCCCAGGTGACTAAAC
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101484	99571	CATATGATCCAGCAATTGCA
101485	99572	CCATATGATCCAGCAATTGC
101486	99573	ACCATATGATCCAGCAATTG
101487	99574	TACCATATGATCCAGCAATT
101488	99575	CTACCATATGATCCAGCAAT
101489	99576	GCTACCATATGATCCAGCAA
101490	99577	AGCTACCATATGATCCAGCA
101491	99578	GAGCTACCATATGATCCAGC
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101493	99580	TAGAGCTACCATATGATCCA
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101495	99582	AATAGAGCTACCATATGATC
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101497	99584	AAAATAGAGCTACCATATGA
101498	99585	AAAAATAGAGCTACCATATG
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101500	99587	CTAAAAATAGAGCTACCATA
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101502	99589	AACTAAAAATAGAGCTACCA
101503	99590	AAACTAAAAATAGAGCTACC
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101531	99618	ATGGAGAACAGTATGGAAAT
101532	99619	TATGGAGAACAGTATGGAAA
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101541	99628	TAAAACCACTATGGAGAACA
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101550	99637	GTAAATTGGTAAAACCACTA
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101552	99639	ATGTAAATTGGTAAAACCAC
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3260	1347	TCTCCCCTCCAGAGATGTCC
3261	1348	TTCTCCCCTCCAGAGATGTC
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3263	1350	ACTTCTCCCCTCCAGAGATG
3264	1351	AACTTCTCCCCTCCAGAGAT
3265	1352	TAACTTCTCCCCTCCAGAGA
3266	1353	CTAACTTCTCCCCTCCAGAG
3267	1354	CCTAACTTCTCCCCTCCAGA
3268	1355	CCCTAACTTCTCCCCTCCAG
3269	1356	GCCCTAACTTCTCCCCTCCA
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3272	1359	GCGGCCCTAACTTCTCCCCT
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3274	1361	ACGCGGCCCTAACTTCTCCC
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3276	1363	GGACGCGGCCCTAACTTCTC
3277	1364	GGGACGCGGCCCTAACTTCT
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3279	1366	GGGGGACGCGGCCCTAACTT
3280	1367	CGGGGGACGCGGCCCTAACT
3281	1368	ACGGGGGACGCGGCCCTAAC
3282	1369	CACGGGGGACGCGGCCCTAA
3283	1370	GCACGGGGGACGCGGCCCTA
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3285	1372	CGGCACGGGGGACGCGGCCC
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3287	1374	ACCGGCACGGGGGACGCGGC
3288	1375	AACCGGCACGGGGGACGCGG
3289	1376	TAACCGGCACGGGGGACGCG
3290	1377	TTAACCGGCACGGGGGACGC
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3294	1381	CCCTTTAACCGGCACGGGGG
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3304	1391	CGGTGCCTACCCCTTTAACC
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3306	1393	CCCGGTGCCTACCCCTTTAA
3307	1394	GCCCGGTGCCTACCCCTTTA
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3311	1398	AGGAGCCCGGTGCCTACCCC
3312	1399	GAGGAGCCCGGTGCCTACCC
3313	1400	GGAGGAGCCCGGTGCCTACC
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3315	1402	CCGGAGGAGCCCGGTGCCTA
3316	1403	TCCGGAGGAGCCCGGTGCCT
3317	1404	TTCCGGAGGAGCCCGGTGCC
3318	1405	ATTCCGGAGGAGCCCGGTGC
3319	1406	GATTCCGGAGGAGCCCGGTG
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3326	1413	CCCTGATGATTCCGGAGGAG
3327	1414	ACCCTGATGATTCCGGAGGA
3328	1415	GACCCTGATGATTCCGGAGG
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3330	1417	CAGACCCTGATGATTCCGGA

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52415	50502	TGAGAACATTTTTAAAAACT
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52426	50513	ATCCCTAGAAGTGAGAACAT
52427	50514	GATCCCTAGAAGTGAGAACA
52428	50515	GGATCCCTAGAAGTGAGAAC
52429	50516	AGGATCCCTAGAAGTGAGAA
52430	50517	CAGGATCCCTAGAAGTGAGA
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52432	50519	ACCAGGATCCCTAGAAGTGA
52433	50520	AACCAGGATCCCTAGAAGTG
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52449	50536	AGGCTAATTATAATTAAACC
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52451	50538	CCAGGCTAATTATAATTAAA
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52454	50541	CACCCAGGCTAATTATAATT
52455	50542	TCACCCAGGCTAATTATAAT
52456	50543	CTCACCCAGGCTAATTATAA
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52459	50546	AGCCTCACCCAGGCTAATTA
52460	50547	GAGCCTCACCCAGGCTAATT
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52470	50557	TGACTGTCCAGAGCCTCACC
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101554	99641	ACATGTAAATTGGTAAAACC
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101571	99658	TCACACACTGTTGGTGGACA
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101574	99661	CCTTCACACACTGTTGGTGG
101575	99662	ACCTTCACACACTGTTGGTG
101576	99663	AACCTTCACACACTGTTGGT
101577	99664	GAACCTTCACACACTGTTGG
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101582	99669	AAGGGGAACCTTCACACACT
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101605	99692	AAATGCTGGTAACGATGTGG
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101611	99698	AATAACAAATGCTGGTAACG
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101613	99700	GCAATAACAAATGCTGGTAA
101614	99701	GGCAATAACAAATGCTGGTA
101615	99702	AGGCAATAACAAATGCTGGT
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101619	99706	AGACAGGCAATAACAAATGC
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3331	1418	ACAGACCCTGATGATTCCGG
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3334	1421	CCGACAGACCCTGATGATTC
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3344	1431	GGAGAGAGCCCCGACAGACC
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3346	1433	GGGGAGAGAGCCCCGACAGA
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3349	1436	GGCGGGGAGAGAGCCCCGAC
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3362	1449	AGGACTCGGAGGGGGCGGGG
3363	1450	CAGGACTCGGAGGGGGCGGG
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3365	1452	CCCAGGACTCGGAGGGGGCG
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3373	1460	CGATCTTTCCCAGGACTCGG
3374	1461	CCGATCTTTCCCAGGACTCG
3375	1462	TCCGATCTTTCCCAGGACTC
3376	1463	CTCCGATCTTTCCCAGGACT
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3382	1469	CCCGTCCTCCGATCTTTCCC
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3384	1471	ACCCCGTCCTCCGATCTTTC
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3386	1473	CCACCCCGTCCTCCGATCTT
3387	1474	TCCACCCCGTCCTCCGATCT
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3392	1479	TTGTCTCCACCCCGTCCTCC
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52478	50565	TCACACCCTGACTGTCCAGA
52479	50566	CTCACACCCTGACTGTCCAG
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52481	50568	AGCTCACACCCTGACTGTCC
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52484	50571	CATAGCTCACACCCTGACTG
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52488	50575	AACCCATAGCTCACACCCTG
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52490	50577	GAAACCCATAGCTCACACCC
52491	50578	TGAAACCCATAGCTCACACC
52492	50579	ATGAAACCCATAGCTCACAC
52493	50580	CATGAAACCCATAGCTCACA
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52502	50589	ATCTCATCACATGAAACCCA
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52511	50598	ACTCCTGGGATCTCATCACA
52512	50599	CACTCCTGGGATCTCATCAC
52513	50600	CCACTCCTGGGATCTCATCA
52514	50601	GCCACTCCTGGGATCTCATC
52515	50602	AGCCACTCCTGGGATCTCAT
52516	50603	GAGCCACTCCTGGGATCTCA
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52518	50605	CAGAGCCACTCCTGGGATCT
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52521	50608	GAACAGAGCCACTCCTGGGA
52522	50609	AGAACAGAGCCACTCCTGGG
52523	50610	CAGAACAGAGCCACTCCTGG
52524	50611	ACAGAACAGAGCCACTCCTG
52525	50612	CACAGAACAGAGCCACTCCT
52526	50613	CCACAGAACAGAGCCACTCC
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52528	50615	GGCCACAGAACAGAGCCACT
52529	50616	AGGCCACAGAACAGAGCCAC
52530	50617	AAGGCCACAGAACAGAGCCA
52531	50618	CAAGGCCACAGAACAGAGCC
52532	50619	TCAAGGCCACAGAACAGAGC
52533	50620	CTCAAGGCCACAGAACAGAG
52534	50621	TCTCAAGGCCACAGAACAGA
52535	50622	TTCTCAAGGCCACAGAACAG
52536	50623	ATTCTCAAGGCCACAGAACA
52537	50624	AATTCTCAAGGCCACAGAAC
52538	50625	AAATTCTCAAGGCCACAGAA
52539	50626	CAAATTCTCAAGGCCACAGA
52540	50627	ACAAATTCTCAAGGCCACAG
52541	50628	CACAAATTCTCAAGGCCACA
52542	50629	GCACAAATTCTCAAGGCCAC
52543	50630	AGCACAAATTCTCAAGGCCA
52544	50631	AAGCACAAATTCTCAAGGCC
52545	50632	AAAGCACAAATTCTCAAGGC
52546	50633	GAAAGCACAAATTCTCAAGG
52547	50634	AGAAAGCACAAATTCTCAAG
52548	50635	TAGAAAGCACAAATTCTCAA

101625	99712	TCCAAAAGACAGGCAATAAC
101626	99713	ATCCAAAAGACAGGCAATAA
101627	99714	TATCCAAAAGACAGGCAATA
101628	99715	TTATCCAAAAGACAGGCAAT
101629	99716	TTTATCCAAAAGACAGGCAA
101630	99717	TTTTATCCAAAAGACAGGCA
101631	99718	CTTTTATCCAAAAGACAGGC
101632	99719	GCTTTTATCCAAAAGACAGG
101633	99720	GGCTTTTATCCAAAAGACAG
101634	99721	TGGCTTTTATCCAAAAGACA
101635	99722	ATGGCTTTTATCCAAAAGAC
101636	99723	AATGGCTTTTATCCAAAAGA
101637	99724	AAATGGCTTTTATCCAAAAG
101638	99725	AAAATGGCTTTTATCCAAAA
101639	99726	TAAAATGGCTTTTATCCAAA
101640	99727	TTAAAATGGCTTTTATCCAA
101641	99728	GTTAAAATGGCTTTTATCCA
101642	99729	AGTTAAAATGGCTTTTATCC
101643	99730	CAGTTAAAATGGCTTTTATC
101644	99731	CCAGTTAAAATGGCTTTTAT
101645	99732	CCCAGTTAAAATGGCTTTTA
101646	99733	CCCCAGTTAAAATGGCTTTT
101647	99734	ACCCCAGTTAAAATGGCTTT
101648	99735	CACCCCAGTTAAAATGGCTT
101649	99736	TCACCCCAGTTAAAATGGCT
101650	99737	CTCACCCCAGTTAAAATGGC
101651	99738	TCTCACCCCAGTTAAAATGG
101652	99739	ATCTCACCCCAGTTAAAATG
101653	99740	CATCTCACCCCAGTTAAAAT
101654	99741	TCATCTCACCCCAGTTAAAA
101655	99742	ATCATCTCACCCCAGTTAAA
101656	99743	TATCATCTCACCCCAGTTAA
101657	99744	ATATCATCTCACCCCAGTTA
101658	99745	GATATCATCTCACCCCAGTT
101659	99746	AGATATCATCTCACCCCAGT
101660	99747	AAGATATCATCTCACCCCAG
101661	99748	CAAGATATCATCTCACCCCA
101662	99749	ACAAGATATCATCTCACCCC
101663	99750	AACAAGATATCATCTCACCC
101664	99751	CAACAAGATATCATCTCACC
101665	99752	ACAACAAGATATCATCTCAC
101666	99753	TACAACAAGATATCATCTCA
101667	99754	CTACAACAAGATATCATCTC
101668	99755	ACTACAACAAGATATCATCT
101669	99756	AACTACAACAAGATATCATC
101670	99757	AAACTACAACAAGATATCAT
101671	99758	AAAACTACAACAAGATATCA
101672	99759	TAAAACTACAACAAGATATC
101673	99760	TTAAAACTACAACAAGATAT
101674	99761	ATTAAAACTACAACAAGATA
101675	99762	AATTAAAACTACAACAAGAT
101676	99763	AAATTAAAACTACAACAAGA
101677	99764	GAAATTAAAACTACAACAAG
101678	99765	GGAAATTAAAACTACAACAA
101679	99766	TGGAAATTAAAACTACAACA
101680	99767	ATGGAAATTAAAACTACAAC
101681	99768	AATGGAAATTAAAACTACAA
101682	99769	AAATGGAAATTAAAACTACA
101683	99770	AAAATGGAAATTAAAACTAC
101684	99771	AAAAATGGAAATTAAAACTA
101685	99772	GAAAAATGGAAATTAAAACT
101686	99773	AGAAAAATGGAAATTAAAAC
101687	99774	CAGAAAAATGGAAATTAAAA
101688	99775	CCAGAAAAATGGAAATTAAA
101689	99776	ACCAGAAAAATGGAAATTAA
101690	99777	CACCAGAAAAATGGAAATTA
101691	99778	TCACCAGAAAAATGGAAATT
101692	99779	ATCACCAGAAAAATGGAAAT
101693	99780	GATCACCAGAAAAATGGAAA
101694	99781	TGATCACCAGAAAAATGGAA
101695	99782	CTGATCACCAGAAAAATGGA

3402	1489	CAAGGCCCACTTGTCTCCAC
3403	1490	CCAAGGCCCACTTGTCTCCA
3404	1491	GCCAAGGCCCACTTGTCTCC
3405	1492	GGCCAAGGCCCACTTGTCTC
3406	1493	GGGCCAAGGCCCACTTGTCT
3407	1494	GGGGCCAAGGCCCACTTGTC
3408	1495	GGGGGCCAAGGCCCACTTGT
3409	1496	CGGGGGCCAAGGCCCACTTG
3410	1497	GCGGGGGCCAAGGCCCACTT
3411	1498	TGCGGGGGCCAAGGCCCACT
3412	1499	GTGCGGGGGCCAAGGCCCAC
3413	1500	GGTGCGGGGGCCAAGGCCCA
3414	1501	GGGTGCGGGGGCCAAGGCCC
3415	1502	GGGGTGCGGGGGCCAAGGCC
3416	1503	AGGGGTGCGGGGGCCAAGGC
3417	1504	GAGGGGTGCGGGGGCCAAGG
3418	1505	AGAGGGGTGCGGGGGCCAAG
3419	1506	CAGAGGGGTGCGGGGGCCAA
3420	1507	GCAGAGGGGTGCGGGGGCCA
3421	1508	CGCAGAGGGGTGCGGGGGCC
3422	1509	ACGCAGAGGGGTGCGGGGGC
3423	1510	AACGCAGAGGGGTGCGGGGG
3424	1511	GAACGCAGAGGGGTGCGGGG
3425	1512	CGAACGCAGAGGGGTGCGGG
3426	1513	ACGAACGCAGAGGGGTGCGG
3427	1514	CACGAACGCAGAGGGGTGCG
3428	1515	ACACGAACGCAGAGGGGTGC
3429	1516	GACACGAACGCAGAGGGGTG
3430	1517	GGACACGAACGCAGAGGGGT
3431	1518	CGGACACGAACGCAGAGGGG
3432	1519	TCGGACACGAACGCAGAGGG
3433	1520	CTCGGACACGAACGCAGAGG
3434	1521	CCTCGGACACGAACGCAGAG
3435	1522	GCCTCGGACACGAACGCAGA
3436	1523	CGCCTCGGACACGAACGCAG
3437	1524	CCGCCTCGGACACGAACGCA
3438	1525	GCCGCCTCGGACACGAACGC
3439	1526	CGCCGCCTCGGACACGAACG
3440	1527	CCGCCGCCTCGGACACGAAC
3441	1528	GCCGCCGCCTCGGACACGAA
3442	1529	CGCCGCCGCCTCGGACACGA
3443	1530	CCGCCGCCGCCTCGGACACG
3444	1531	CCCGCCGCCGCCTCGGACAC
3445	1532	CCCCGCCGCCGCCTCGGACA
3446	1533	CCCCCGCCGCCGCCTCGGAC
3447	1534	GCCCCCGCCGCCGCCTCGGA
3448	1535	AGCCCCCGCCGCCGCCTCGG
3449	1536	GAGCCCCCGCCGCCGCCTCG
3450	1537	GGAGCCCCCGCCGCCGCCTC
3451	1538	GGGAGCCCCCGCCGCCGCCT
3452	1539	CGGGAGCCCCCGCCGCCGCC
3453	1540	TCGGGAGCCCCCGCCGCCGC
3454	1541	TTCGGGAGCCCCCGCCGCCG
3455	1542	GTTCGGGAGCCCCCGCCGCC
3456	1543	AGTTCGGGAGCCCCCGCCGC
3457	1544	GAGTTCGGGAGCCCCCGCCG
3458	1545	GGAGTTCGGGAGCCCCCGCC
3459	1546	GGGAGTTCGGGAGCCCCCGC
3460	1547	GGGGAGTTCGGGAGCCCCCG
3461	1548	AGGGGAGTTCGGGAGCCCCC
3462	1549	CAGGGGAGTTCGGGAGCCCC
3463	1550	TCAGGGGAGTTCGGGAGCCC
3464	1551	TTCAGGGGAGTTCGGGAGCC
3465	1552	TTTCAGGGGAGTTCGGGAGC
3466	1553	ATTTCAGGGGAGTTCGGGAG
3467	1554	GATTTCAGGGGAGTTCGGGA
3468	1555	CGATTTCAGGGGAGTTCGGG
3469	1556	ACGATTTCAGGGGAGTTCGG
3470	1557	CACGATTTCAGGGGAGTTCG
3471	1558	CCACGATTTCAGGGGAGTTC
3472	1559	CCCACGATTTCAGGGGAGTT

52549	50636	CTAGAAAGCACAAATTCTCA
52550	50637	CCTAGAAAGCACAAATTCTC
52551	50638	GCCTAGAAAGCACAAATTCT
52552	50639	GGCCTAGAAAGCACAAATTC
52553	50640	TGGCCTAGAAAGCACAAATT
52554	50641	CTGGCCTAGAAAGCACAAAT
52555	50642	CCTGGCCTAGAAAGCACAAA
52556	50643	ACCTGGCCTAGAAAGCACAA
52557	50644	CACCTGGCCTAGAAAGCACA
52558	50645	GCACCTGGCCTAGAAAGCAC
52559	50646	CGCACCTGGCCTAGAAAGCA
52560	50647	CCGCACCTGGCCTAGAAAGC
52561	50648	ACCGCACCTGGCCTAGAAAG
52562	50649	CACCGCACCTGGCCTAGAAA
52563	50650	CCACCGCACCTGGCCTAGAA
52564	50651	GCCACCGCACCTGGCCTAGA
52565	50652	AGCCACCGCACCTGGCCTAG
52566	50653	GAGCCACCGCACCTGGCCTA
52567	50654	TGAGCCACCGCACCTGGCCT
52568	50655	GTGAGCCACCGCACCTGGCC
52569	50656	AGTGAGCCACCGCACCTGGC
52570	50657	GAGTGAGCCACCGCACCTGG
52571	50658	GGAGTGAGCCACCGCACCTG
52572	50659	AGGAGTGAGCCACCGCACCT
52573	50660	CAGGAGTGAGCCACCGCACC
52574	50661	ACAGGAGTGAGCCACCGCAC
52575	50662	TACAGGAGTGAGCCACCGCA
52576	50663	TTACAGGAGTGAGCCACCGC
52577	50664	ATTACAGGAGTGAGCCACCG
52578	50665	GATTACAGGAGTGAGCCACC
52579	50666	AGATTACAGGAGTGAGCCAC
52580	50667	GAGATTACAGGAGTGAGCCA
52581	50668	TGAGATTACAGGAGTGAGCC
52582	50669	GTGAGATTACAGGAGTGAGC
52583	50670	AGTGAGATTACAGGAGTGAG
52584	50671	AAGTGAGATTACAGGAGTGA
52585	50672	AAAGTGAGATTACAGGAGTG
52586	50673	CAAAGTGAGATTACAGGAGT
52587	50674	CCAAAGTGAGATTACAGGAG
52588	50675	CCCAAAGTGAGATTACAGGA
52589	50676	TCCCAAAGTGAGATTACAGG
52590	50677	CTCCCAAAGTGAGATTACAG
52591	50678	TCTCCCAAAGTGAGATTACA
52592	50679	GTCTCCCAAAGTGAGATTAC
52593	50680	GGTCTCCCAAAGTGAGATTA
52594	50681	TGGTCTCCCAAAGTGAGATT
52595	50682	TTGGTCTCCCAAAGTGAGAT
52596	50683	CTTGGTCTCCCAAAGTGAGA
52597	50684	CCTTGGTCTCCCAAAGTGAG
52598	50685	ACCTTGGTCTCCCAAAGTGA
52599	50686	CACCTTGGTCTCCCAAAGTG
52600	50687	CCACCTTGGTCTCCCAAAGT
52601	50688	CCCACCTTGGTCTCCCAAAG
52602	50689	GCCCACCTTGGTCTCCCAAA
52603	50690	TGCCCACCTTGGTCTCCCAA
52604	50691	CTGCCCACCTTGGTCTCCCA
52605	50692	TCTGCCCACCTTGGTCTCCC
52606	50693	ATCTGCCCACCTTGGTCTCC
52607	50694	GATCTGCCCACCTTGGTCTC
52608	50695	TGATCTGCCCACCTTGGTCT
52609	50696	ATGATCTGCCCACCTTGGTC
52610	50697	AATGATCTGCCCACCTTGGT
52611	50698	AAATGATCTGCCCACCTTGG
52612	50699	CAAATGATCTGCCCACCTTG
52613	50700	TCAAATGATCTGCCCACCTT
52614	50701	CTCAAATGATCTGCCCACCT
52615	50702	CCTCAAATGATCTGCCCACC
52616	50703	ACCTCAAATGATCTGCCCAC
52617	50704	GACCTCAAATGATCTGCCCA
52618	50705	TGACCTCAAATGATCTGCCC
52619	50706	CTGACCTCAAATGATCTGCC

101696	99783	ACTGATCACCAGAAAAATGG
101697	99784	TACTGATCACCAGAAAAATG
101698	99785	CTACTGATCACCAGAAAAAT
101699	99786	ACTACTGATCACCAGAAAAA
101700	99787	TACTACTGATCACCAGAAAA
101701	99788	ATACTACTGATCACCAGAAA
101702	99789	AATACTACTGATCACCAGAA
101703	99790	CAATACTACTGATCACCAGA
101704	99791	TCAATACTACTGATCACCAG
101705	99792	TTCAATACTACTGATCACCA
101706	99793	ATTCAATACTACTGATCACC
101707	99794	TATTCAATACTACTGATCAC
101708	99795	GTATTCAATACTACTGATCA
101709	99796	GGTATTCAATACTACTGATC
101710	99797	AGGTATTCAATACTACTGAT
101711	99798	AAGGTATTCAATACTACTGA
101712	99799	AAAGGTATTCAATACTACTG
101713	99800	GAAAGGTATTCAATACTACT
101714	99801	TGAAAGGTATTCAATACTAC
101715	99802	ATGAAAGGTATTCAATACTA
101716	99803	TATGAAAGGTATTCAATACT
101717	99804	ATATGAAAGGTATTCAATAC
101718	99805	TATATGAAAGGTATTCAATA
101719	99806	GTATATGAAAGGTATTCAAT
101720	99807	GGTATATGAAAGGTATTCAA
101721	99808	AGGTATATGAAAGGTATTCA
101722	99809	CAGGTATATGAAAGGTATTC
101723	99810	ACAGGTATATGAAAGGTATT
101724	99811	AACAGGTATATGAAAGGTAT
101725	99812	AAACAGGTATATGAAAGGTA
101726	99813	CAAACAGGTATATGAAAGGT
101727	99814	GCAAACAGGTATATGAAAGG
101728	99815	GGCAAACAGGTATATGAAAG
101729	99816	TGGCAAACAGGTATATGAAA
101730	99817	ATGGCAAACAGGTATATGAA
101731	99818	AATGGCAAACAGGTATATGA
101732	99819	GAATGGCAAACAGGTATATG
101733	99820	TGAATGGCAAACAGGTATAT
101734	99821	ATGAATGGCAAACAGGTATA
101735	99822	TATGAATGGCAAACAGGTAT
101736	99823	TTATGAATGGCAAACAGGTA
101737	99824	TTTATGAATGGCAAACAGGT
101738	99825	ATTTATGAATGGCAAACAGG
101739	99826	TATTTATGAATGGCAAACAG
101740	99827	TTATTTATGAATGGCAAACA
101741	99828	GTTATTTATGAATGGCAAAC
101742	99829	CGTTATTTATGAATGGCAAA
101743	99830	TCGTTATTTATGAATGGCAA
101744	99831	ATCGTTATTTATGAATGGCA
101745	99832	CATCGTTATTTATGAATGGC
101746	99833	TCATCGTTATTTATGAATGG
101747	99834	CTCATCGTTATTTATGAATG
101748	99835	CCTCATCGTTATTTATGAAT
101749	99836	ACCTCATCGTTATTTATGAA
101750	99837	GACCTCATCGTTATTTATGA
101751	99838	AGACCTCATCGTTATTTATG
101752	99839	AAGACCTCATCGTTATTTAT
101753	99840	CAAGACCTCATCGTTATTTA
101754	99841	GCAAGACCTCATCGTTATTT
101755	99842	AGCAAGACCTCATCGTTATT
101756	99843	CAGCAAGACCTCATCGTTAT
101757	99844	ACAGCAAGACCTCATCGTTA
101758	99845	AACAGCAAGACCTCATCGTT
101759	99846	AAACAGCAAGACCTCATCGT
101760	99847	CAAACAGCAAGACCTCATCG
101761	99848	CCAAACAGCAAGACCTCATC
101762	99849	GCCAAACAGCAAGACCTCAT
101763	99850	GGCCAAACAGCAAGACCTCA
101764	99851	GGGCCAAACAGCAAGACCTC
101765	99852	TGGGCCAAACAGCAAGACCT
101766	99853	CTGGGCCAAACAGCAAGACC

3473	1560	CCCCACGATTTCAGGGGAGT
3474	1561	GCCCCACGATTTCAGGGGAG
3475	1562	AGCCCCACGATTTCAGGGGA
3476	1563	GAGCCCCACGATTTCAGGGG
3477	1564	GGAGCCCCACGATTTCAGGG
3478	1565	TGGAGCCCCACGATTTCAGG
3479	1566	ATGGAGCCCCACGATTTCAG
3480	1567	CATGGAGCCCCACGATTTCA
3481	1568	ACATGGAGCCCCACGATTTC
3482	1569	CACATGGAGCCCCACGATTT
3483	1570	CCACATGGAGCCCCACGATT
3484	1571	GCCACATGGAGCCCCACGAT
3485	1572	GGCCACATGGAGCCCCACGA
3486	1573	AGGCCACATGGAGCCCCACG
3487	1574	GAGGCCACATGGAGCCCCAC
3488	1575	GGAGGCCACATGGAGCCCCA
3489	1576	CGGAGGCCACATGGAGCCCC
3490	1577	CCGGAGGCCACATGGAGCCC
3491	1578	GCCGGAGGCCACATGGAGCC
3492	1579	TGCCGGAGGCCACATGGAGC
3493	1580	CTGCCGGAGGCCACATGGAG
3494	1581	GCTGCCGGAGGCCACATGGA
3495	1582	CGCTGCCGGAGGCCACATGG
3496	1583	ACGCTGCCGGAGGCCACATG
3497	1584	AACGCTGCCGGAGGCCACAT
3498	1585	GAACGCTGCCGGAGGCCACA
3499	1586	GGAACGCTGCCGGAGGCCAC
3500	1587	TGGAACGCTGCCGGAGGCCA
3501	1588	GTGGAACGCTGCCGGAGGCC
3502	1589	GGTGGAACGCTGCCGGAGGC
3503	1590	GGGTGGAACGCTGCCGGAGG
3504	1591	AGGGTGGAACGCTGCCGGAG
3505	1592	GAGGGTGGAACGCTGCCGGA
3506	1593	GGAGGGTGGAACGCTGCCGG
3507	1594	GGGAGGGTGGAACGCTGCCG
3508	1595	GGGGAGGGTGGAACGCTGCC
3509	1596	GGGGGAGGGTGGAACGCTGC
3510	1597	TGGGGGAGGGTGGAACGCTG
3511	1598	GTGGGGGAGGGTGGAACGCT
3512	1599	GGTGGGGGAGGGTGGAACGC
3513	1600	AGGTGGGGGAGGGTGGAACG
3514	1601	CAGGTGGGGGAGGGTGGAAC
3515	1602	CCAGGTGGGGGAGGGTGGAA
3516	1603	CCCAGGTGGGGGAGGGTGGA
3517	1604	CCCCAGGTGGGGGAGGGTGG
3518	1605	TCCCCAGGTGGGGGAGGGTG
3519	1606	TTCCCCAGGTGGGGGAGGGT
3520	1607	CTTCCCCAGGTGGGGGAGGG
3521	1608	CCTTCCCCAGGTGGGGGAGG
3522	1609	CCCTTCCCCAGGTGGGGGAG
3523	1610	TCCCTTCCCCAGGTGGGGGA
3524	1611	TTCCCTTCCCCAGGTGGGGG
3525	1612	CTTCCCTTCCCCAGGTGGGG
3526	1613	CCTTCCCTTCCCCAGGTGGG
3527	1614	CCCTTCCCTTCCCCAGGTGG
3528	1615	CCCCTTCCCTTCCCCAGGTG
3529	1616	ACCCCTTCCCTTCCCCAGGT
3530	1617	CACCCCTTCCCTTCCCCAGG
3531	1618	CCACCCCTTCCCTTCCCCAG
3532	1619	CCCACCCCTTCCCTTCCCCA
3533	1620	CCCCACCCCTTCCCTTCCCC
3534	1621	TCCCCACCCCTTCCCTTCCC
3535	1622	CTCCCCACCCCTTCCCTTCC
3536	1623	ACTCCCCACCCCTTCCCTTC
3537	1624	CACTCCCCACCCCTTCCCTT
3538	1625	GCACTCCCCACCCCTTCCCT
3539	1626	GGCACTCCCCACCCCTTCCC
3540	1627	GGGCACTCCCCACCCCTTCC
3541	1628	CGGGCACTCCCCACCCCTTC
3542	1629	CCGGGCACTCCCCACCCCTT
3543	1630	GCCGGGCACTCCCCACCCCT

52620	50707	CCTGACCTCAAATGATCTGC
52621	50708	TCCTGACCTCAAATGATCTG
52622	50709	CTCCTGACCTCAAATGATCT
52623	50710	ACTCCTGACCTCAAATGATC
52624	50711	AACTCCTGACCTCAAATGAT
52625	50712	GAACTCCTGACCTCAAATGA
52626	50713	CGAACTCCTGACCTCAAATG
52627	50714	TCGAACTCCTGACCTCAAAT
52628	50715	CTCGAACTCCTGACCTCAAA
52629	50716	TCTCGAACTCCTGACCTCAA
52630	50717	GTCTCGAACTCCTGACCTCA
52631	50718	GGTCTCGAACTCCTGACCTC
52632	50719	TGGTCTCGAACTCCTGACCT
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52640	50727	GGCCAGGCTGGTCTCGAACT
52641	50728	TGGCCAGGCTGGTCTCGAAC
52642	50729	TTGGCCAGGCTGGTCTCGAA
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52644	50731	TGTTGGCCAGGCTGGTCTCG
52645	50732	ATGTTGGCCAGGCTGGTCTC
52646	50733	CATGTTGGCCAGGCTGGTCT
52647	50734	ACATGTTGGCCAGGCTGGTC
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52650	50737	TCAACATGTTGGCCAGGCTG
52651	50738	TTCAACATGTTGGCCAGGCT
52652	50739	TTTCAACATGTTGGCCAGGC
52653	50740	GTTTCAACATGTTGGCCAGG
52654	50741	GGTTTCAACATGTTGGCCAG
52655	50742	GGGTTTCAACATGTTGGCCA
52656	50743	GGGGTTTCAACATGTTGGCC
52657	50744	CGGGGTTTCAACATGTTGGC
52658	50745	ACGGGGTTTCAACATGTTGG
52659	50746	GACGGGGTTTCAACATGTTG
52660	50747	AGACGGGGTTTCAACATGTT
52661	50748	AAGACGGGGTTTCAACATGT
52662	50749	AAAGACGGGGTTTCAACATG
52663	50750	TAAAGACGGGGTTTCAACAT
52664	50751	GTAAAGACGGGGTTTCAACA
52665	50752	AGTAAAGACGGGGTTTCAAC
52666	50753	TAGTAAAGACGGGGTTTCAA
52667	50754	TTAGTAAAGACGGGGTTTCA
52668	50755	TTTAGTAAAGACGGGGTTTC
52669	50756	TTTTAGTAAAGACGGGGTTT
52670	50757	TTTTTAGTAAAGACGGGGTT
52671	50758	TTTTTTAGTAAAGACGGGGT
52672	50759	CTTTTTTAGTAAAGACGGGG
52673	50760	ACTTTTTTAGTAAAGACGGG
52674	50761	TACTTTTTTAGTAAAGACGG
52675	50762	TTACTTTTTTAGTAAAGACG
52676	50763	TTTACTTTTTTAGTAAAGAC
52677	50764	TTTTACTTTTTTAGTAAAGA
52678	50765	TTTTTACTTTTTTAGTAAAG
52679	50766	TTTTTTACTTTTTTAGTAAA
52680	50767	ATTTTTTTACTTTTTTAGTAA
52681	50768	AATTTTTTACTTTTTTAGTA
52682	50769	TAATTTTTTACTTTTTTAGT
52683	50770	CTAATTTTTTACTTTTTTAG
52684	50771	GCTAATTTTTTACTTTTTTA
52685	50772	CGCTAATTTTTTACTTTTTT
52686	50773	CCGCTAATTTTTTACTTTTT
52687	50774	CCCGCTAATTTTTTACTTTT
52688	50775	TCCCGCTAATTTTTTACTTT
52689	50776	GTCCCGCTAATTTTTTACTT
52690	50777	CGTCCCGCTAATTTTTTACT

101767	99854	CCTGGGCCAAACAGCAAGAC
101768	99855	GCCTGGGCCAAACAGCAAGA
101769	99856	AGCCTGGGCCAAACAGCAAG
101770	99857	CAGCCTGGGCCAAACAGCAA
101771	99858	CCAGCCTGGGCCAAACAGCA
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101773	99860	GACCAGCCTGGGCCAAACAG
101774	99861	AGACCAGCCTGGGCCAAACA
101775	99862	GAGACCAGCCTGGGCCAAAC
101776	99863	CGAGACCAGCCTGGGCCAAA
101777	99864	TCGAGACCAGCCTGGGCCAA
101778	99865	TTCGAGACCAGCCTGGGCCA
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101780	99867	AGTTCGAGACCAGCCTGGGC
101781	99868	GAGTTCGAGACCAGCCTGGG
101782	99869	GGAGTTCGAGACCAGCCTGG
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101789	99876	GAGCCCAGGAGTTCGAGACC
101790	99877	TGAGCCCAGGAGTTCGAGAC
101791	99878	TTGAGCCCAGGAGTTCGAGA
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101793	99880	GCTTGAGCCCAGGAGTTCGA
101794	99881	TGCTTGAGCCCAGGAGTTCG
101795	99882	TTGCTTGAGCCCAGGAGTTC
101796	99883	ATTGCTTGAGCCCAGGAGTT
101797	99884	GATTGCTTGAGCCCAGGAGT
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101799	99886	AGGATTGCTTGAGCCCAGGA
101800	99887	GAGGATTGCTTGAGCCCAGG
101801	99888	GGAGGATTGCTTGAGCCCAG
101802	99889	GGGAGGATTGCTTGAGCCCA
101803	99890	TGGGAGGATTGCTTGAGCCC
101804	99891	GTGGGAGGATTGCTTGAGCC
101805	99892	GGTGGGAGGATTGCTTGAGC
101806	99893	AGGTGGGAGGATTGCTTGAG
101807	99894	AAGGTGGGAGGATTGCTTGA
101808	99895	CAAGGTGGGAGGATTGCTTG
101809	99896	CCAAGGTGGGAGGATTGCTT
101810	99897	GCCAAGGTGGGAGGATTGCT
101811	99898	AGCCAAGGTGGGAGGATTGC
101812	99899	AAGCCAAGGTGGGAGGATTG
101813	99900	GAAGCCAAGGTGGGAGGATT
101814	99901	GGAAGCCAAGGTGGGAGGAT
101815	99902	GGGAAGCCAAGGTGGGAGGA
101816	99903	TGGGAAGCCAAGGTGGGAGG
101817	99904	TTGGGAAGCCAAGGTGGGAG
101818	99905	TTTGGGAAGCCAAGGTGGGA
101819	99906	TTTTGGGAAGCCAAGGTGGG
101820	99907	ATTTTGGGAAGCCAAGGTGG
101821	99908	CATTTTGGGAAGCCAAGGTG
101822	99909	GCATTTTGGGAAGCCAAGGT
101823	99910	AGCATTTTGGGAAGCCAAGG
101824	99911	CAGCATTTTGGGAAGCCAAG
101825	99912	TCAGCATTTTGGGAAGCCAA
101826	99913	TTCAGCATTTTGGGAAGCCA
101827	99914	TTTCAGCATTTTGGGAAGCC
101828	99915	ATTTCAGCATTTTGGGAAGC
101829	99916	AATTTCAGCATTTTGGGAAG
101830	99917	TAATTTCAGCATTTTGGGAA
101831	99918	ATAATTTCAGCATTTTGGGA
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101834	99921	ACTATAATTTCAGCATTTTG
101835	99922	AACTATAATTTCAGCATTTT
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101837	99924	ACAACTATAATTTCAGCATT

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3545	1632	GGGCCGGGCACTCCCCACCC
3546	1633	GGGGCCGGGCACTCCCCACC
3547	1634	CGGGGCCGGGCACTCCCCAC
3548	1635	ACGGGGCCGGGCACTCCCCA
3549	1636	GACGGGGCCGGGCACTCCCC
3550	1637	GGACGGGGCCGGGCACTCCC
3551	1638	GGGACGGGGCCGGGCACTCC
3552	1639	CGGGACGGGGCCGGGCACTC
3553	1640	CCGGGACGGGGCCGGGCACT
3554	1641	GCCGGGACGGGGCCGGGCAC
3555	1642	GGCCGGGACGGGGCCGGGCA
3556	1643	AGGCCGGGACGGGGCCGGGC
3557	1644	AAGGCCGGGACGGGGCCGGG
3558	1645	GAAGGCCGGGACGGGGCCGG
3559	1646	GGAAGGCCGGGACGGGGCCG
3560	1647	AGGAAGGCCGGGACGGGGCC
3561	1648	GAGGAAGGCCGGGACGGGGC
3562	1649	GGAGGAAGGCCGGGACGGGG
3563	1650	AGGAGGAAGGCCGGGACGGG
3564	1651	AAGGAGGAAGGCCGGGACGG
3565	1652	GAAGGAGGAAGGCCGGGACG
3566	1653	GGAAGGAGGAAGGCCGGGAC
3567	1654	GGGAAGGAGGAAGGCCGGGA
3568	1655	GGGGAAGGAGGAAGGCCGGG
3569	1656	GGGGGAAGGAGGAAGGCCGG
3570	1657	CGGGGGAAGGAGGAAGGCCG
3571	1658	GCGGGGGAAGGAGGAAGGCC
3572	1659	GGCGGGGGAAGGAGGAAGGC
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3574	1661	CTGGCGGGGGAAGGAGGAAG
3575	1662	TCTGGCGGGGGAAGGAGGAA
3576	1663	GTCTGGCGGGGGAAGGAGGA
3577	1664	GGTCTGGCGGGGGAAGGAGG
3578	1665	AGGTCTGGCGGGGGAAGGAG
3579	1666	GAGGTCTGGCGGGGGAAGGA
3580	1667	AGAGGTCTGGCGGGGGAAGG
3581	1668	GAGAGGTCTGGCGGGGGAAG
3582	1669	GGAGAGGTCTGGCGGGGGAA
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3585	1672	GCCGGAGAGGTCTGGCGGGG
3586	1673	CGCCGGAGAGGTCTGGCGGG
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3588	1675	CGCGCCGGAGAGGTCTGGCG
3589	1676	GCGCGCCGGAGAGGTCTGGC
3590	1677	CGCGCGCCGGAGAGGTCTGG
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3592	1679	CCCGCGCGCCGGAGAGGTCT
3593	1680	ACCCGCGCGCCGGAGAGGTC
3594	1681	CACCCGCGCGCCGGAGAGGT
3595	1682	CCACCCGCGCGCCGGAGAGG
3596	1683	ACCACCCGCGCGCCGGAGAG
3597	1684	CACCACCCGCGCGCCGGAGA
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3599	1686	GCCACCACCCGCGCGCCGGA
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3601	1688	CGGCCACCACCCGCGCGCCG
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3605	1692	GGATCGGCCACCACCCGCGC
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3607	1694	GCGGATCGGCCACCACCCGC
3608	1695	TGCGGATCGGCCACCACCCG
3609	1696	ATGCGGATCGGCCACCACCC
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3611	1698	CAATGCGGATCGGCCACCAC
3612	1699	GCAATGCGGATCGGCCACCA
3613	1700	AGCAATGCGGATCGGCCACC
3614	1701	CAGCAATGCGGATCGGCCAC

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52695	50782	CATCACGTCCCGCTAATTTT
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52697	50784	GCCATCACGTCCCGCTAATT
52698	50785	TGCCATCACGTCCCGCTAAT
52699	50786	GTGCCATCACGTCCCGCTAA
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52702	50789	CATGTGCCATCACGTCCCGC
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52704	50791	GACATGTGCCATCACGTCCC
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52706	50793	TAGACATGTGCCATCACGTC
52707	50794	ATAGACATGTGCCATCACGT
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52720	50807	AGTAGCTGGGATTATAGACA
52721	50808	AAGTAGCTGGGATTATAGAC
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52726	50813	TCCCCAAGTAGCTGGGATTA
52727	50814	CTCCCCAAGTAGCTGGGATT
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52739	50826	CTGCCTCAGCCTCTCCCCAA
52740	50827	TCTGCCTCAGCCTCTCCCCA
52741	50828	TTCTGCCTCAGCCTCTCCCC
52742	50829	CTTCTGCCTCAGCCTCTCCC
52743	50830	TCTTCTGCCTCAGCCTCTCC
52744	50831	TTCTTCTGCCTCAGCCTCTC
52745	50832	ATTCTTCTGCCTCAGCCTCT
52746	50833	GATTCTTCTGCCTCAGCCTC
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52760	50847	TCCCGGGTTCAAGCGATTCT
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101839	99926	TCACAACTATAATTTCAGCA
101840	99927	CTCACAACTATAATTTCAGC
101841	99928	GCTCACAACTATAATTTCAG
101842	99929	GGCTCACAACTATAATTTCA
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101845	99932	AGTGGCTCACAACTATAATT
101846	99933	CAGTGGCTCACAACTATAAT
101847	99934	GCAGTGGCTCACAACTATAA
101848	99935	TGCAGTGGCTCACAACTATA
101849	99936	GTGCAGTGGCTCACAACTAT
101850	99937	GGTGCAGTGGCTCACAACTA
101851	99938	AGGTGCAGTGGCTCACAACT
101852	99939	CAGGTGCAGTGGCTCACAAC
101853	99940	CCAGGTGCAGTGGCTCACAA
101854	99941	GCCAGGTGCAGTGGCTCACA
101855	99942	GGCCAGGTGCAGTGGCTCAC
101856	99943	AGGCCAGGTGCAGTGGCTCA
101857	99944	AAGGCCAGGTGCAGTGGCTC
101858	99945	CAAGGCCAGGTGCAGTGGCT
101859	99946	ACAAGGCCAGGTGCAGTGGC
101860	99947	TACAAGGCCAGGTGCAGTGG
101861	99948	ATACAAGGCCAGGTGCAGTG
101862	99949	CATACAAGGCCAGGTGCAGT
101863	99950	ACATACAAGGCCAGGTGCAG
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101869	99956	AGGAAGACATACAAGGCCAG
101870	99957	AAGGAAGACATACAAGGCCA
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101872	99959	AAAAGGAAGACATACAAGGC
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101876	99963	AAAAAAAAGGAAGACATACA
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101881	99968	AACAAAAAAAAAAGGAAGAC
101882	99969	AAACAAAAAAAAAGGAAGA
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101886	99973	AACAAAACAAAAAAAAAGG
101887	99974	AAACAAAACAAAAAAAAAG
101888	99975	AAAACAAAACAAAAAAAAA
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101890	99977	ACAAAACAAAACAAAAAAA
101891	99978	AACAAAACAAAACAAAAAA
101892	99979	AAACAAAACAAAACAAAAA
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101895	99982	CAAAAACAAAACAAAACAA
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101901	99988	CTGTCTCAAAAACAAAACA
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101904	99991	ACTCTGTCTCAAAAACAAA
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101906	99993	AGACTCTGTCTCAAAAACA
101907	99994	GAGACTCTGTCTCAAAAAC
101908	99995	TGAGACTCTGTCTCAAAAA

3615	1702	ACAGCAATGCGGATCGGCCA
3616	1703	AACAGCAATGCGGATCGGCC
3617	1704	GAACAGCAATGCGGATCGGC
3618	1705	CGAACAGCAATGCGGATCGG
3619	1706	TCGAACAGCAATGCGGATCG
3620	1707	CTCGAACAGCAATGCGGATC
3621	1708	CCTCGAACAGCAATGCGGAT
3622	1709	GCCTCGAACAGCAATGCGGA
3623	1710	GGCCTCGAACAGCAATGCGG
3624	1711	CGGCCTCGAACAGCAATGCG
3625	1712	GCGGCCTCGAACAGCAATGC
3626	1713	TGCGGCCTCGAACAGCAATG
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3628	1715	ACTGCGGCCTCGAACAGCAA
3629	1716	CACTGCGGCCTCGAACAGCA
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3632	1719	CTCCACTGCGGCCTCGAACA
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3634	1721	TTCTCCACTGCGGCCTCGAA
3635	1722	CTTCTCCACTGCGGCCTCGA
3636	1723	CCTTCTCCACTGCGGCCTCG
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3638	1725	CGCCTTCTCCACTGCGGCCT
3639	1726	GCGCCTTCTCCACTGCGGCC
3640	1727	GGCGCCTTCTCCACTGCGGC
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3642	1729	CAGGCGCCTTCTCCACTGCG
3643	1730	ACAGGCGCCTTCTCCACTGC
3644	1731	CACAGGCGCCTTCTCCACTG
3645	1732	CCACAGGCGCCTTCTCCACT
3646	1733	TCCACAGGCGCCTTCTCCAC
3647	1734	TTCCACAGGCGCCTTCTCCA
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3649	1736	TGTTCCACAGGCGCCTTCTC
3650	1737	ATGTTCCACAGGCGCCTTCT
3651	1738	GATGTTCCACAGGCGCCTTC
3652	1739	CGATGTTCCACAGGCGCCTT
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3654	1741	ACCGATGTTCCACAGGCGCC
3655	1742	CACCGATGTTCCACAGGCGC
3656	1743	CCACCGATGTTCCACAGGCG
3657	1744	CCCACCGATGTTCCACAGGC
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3659	1746	CACCCACCGATGTTCCACAG
3660	1747	TCACCCACCGATGTTCCACA
3661	1748	CTCACCCACCGATGTTCCAC
3662	1749	CCTCACCCACCGATGTTCCA
3663	1750	CCCTCACCCACCGATGTTCC
3664	1751	GCCCTCACCCACCGATGTTC
3665	1752	AGCCCTCACCCACCGATGTT
3666	1753	CAGCCCTCACCCACCGATGT
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3671	1758	GGGTCCAGCCCTCACCCACC
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3673	1760	CTGGGTCCAGCCCTCACCCA
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3675	1762	GCCTGGGTCCAGCCCTCACC
3676	1763	AGCCTGGGTCCAGCCCTCAC
3677	1764	CAGCCTGGGTCCAGCCCTCA
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3682	1769	GGGTCCAGCCTGGGTCCAGC
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52762	50849	CCTCCCGGGTTCAAGCGATT
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52776	50863	TCTCGCAATCTCTGCCTCCC
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52829	50916	AAGCACAAATTCTTTTTTTA
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101913	100000	CAAAGTGAGACTCTGTCTCA
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101919	100006	GGGCAACAAAGTGAGACTCT
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101921	100008	CTGGGCAACAAAGTGAGACT
101922	100009	CCTGGGCAACAAAGTGAGAC
101923	100010	GCCTGGGCAACAAAGTGAGA
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101927	100014	TCCAGCCTGGGCAACAAAGT
101928	100015	CTCCAGCCTGGGCAACAAAG
101929	100016	GCTCCAGCCTGGGCAACAAA
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101931	100018	ACGCTCCAGCCTGGGCAACA
101932	100019	TACGCTCCAGCCTGGGCAAC
101933	100020	CTACGCTCCAGCCTGGGCAA
101934	100021	ACTACGCTCCAGCCTGGGCA
101935	100022	CACTACGCTCCAGCCTGGGC
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101937	100024	ACCACTACGCTCCAGCCTGG
101938	100025	CACCACTACGCTCCAGCCTG
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101941	100028	TCACACCACTACGCTCCAGC
101942	100029	ATCACACCACTACGCTCCAG
101943	100030	GATCACACCACTACGCTCCA
101944	100031	AGATCACACCACTACGCTCC
101945	100032	AAGATCACACCACTACGCTC
101946	100033	CAAGATCACACCACTACGCT
101947	100034	CCAAGATCACACCACTACGC
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101949	100036	AGCCAAGATCACACCACTAC
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101960	100047	AGGGCGCAGTGAGCCAAGAT
101961	100048	TAGGGCGCAGTGAGCCAAGA
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101963	100050	TGTAGGGCGCAGTGAGCCAA
101964	100051	GTGTAGGGCGCAGTGAGCCA
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101973	100060	ATCCGGGAGGTGTAGGGCGC
101974	100061	AATCCGGGAGGTGTAGGGCG
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3686	1773	TCCAGGGTCCAGCCTGGGTC
3687	1774	CTCCAGGGTCCAGCCTGGGT
3688	1775	TCTCCAGGGTCCAGCCTGGG
3689	1776	ATCTCCAGGGTCCAGCCTGG
3690	1777	GATCTCCAGGGTCCAGCCTG
3691	1778	GGATCTCCAGGGTCCAGCCT
3692	1779	CGGATCTCCAGGGTCCAGCC
3693	1780	CCGGATCTCCAGGGTCCAGC
3694	1781	CCCGGATCTCCAGGGTCCAG
3695	1782	CCCCGGATCTCCAGGGTCCA
3696	1783	ACCCCGGATCTCCAGGGTCC
3697	1784	CACCCCGGATCTCCAGGGTC
3698	1785	CCACCCCGGATCTCCAGGGT
3699	1786	GCCACCCCGGATCTCCAGGG
3700	1787	CGCCACCCCGGATCTCCAGG
3701	1788	CCGCCACCCCGGATCTCCAG
3702	1789	ACCGCCACCCCGGATCTCCA
3703	1790	CACCGCCACCCCGGATCTCC
3704	1791	GCACCGCCACCCCGGATCTC
3705	1792	AGCACCGCCACCCCGGATCT
3706	1793	CAGCACCGCCACCCCGGATC
3707	1794	CCAGCACCGCCACCCCGGAT
3708	1795	ACCAGCACCGCCACCCCGGA
3709	1796	CACCAGCACCGCCACCCCGG
3710	1797	CCACCAGCACCGCCACCCCG
3711	1798	GCCACCAGCACCGCCACCCC
3712	1799	TGCCACCAGCACCGCCACCC
3713	1800	CTGCCACCAGCACCGCCACC
3714	1801	CCTGCCACCAGCACCGCCAC
3715	1802	CCCTGCCACCAGCACCGCCA
3716	1803	CCCCTGCCACCAGCACCGCC
3717	1804	CCCCCTGCCACCAGCACCGC
3718	1805	GCCCCCTGCCACCAGCACCG
3719	1806	CGCCCCCTGCCACCAGCACC
3720	1807	CCGCCCCCTGCCACCAGCAC
3721	1808	CCCGCCCCCTGCCACCAGCA
3722	1809	GCCCGCCCCCTGCCACCAGC
3723	1810	TGCCCGCCCCCTGCCACCAG
3724	1811	GTGCCCGCCCCCTGCCACCA
3725	1812	GGTGCCCGCCCCCTGCCACC
3726	1813	GGGTGCCCGCCCCCTGCCAC
3727	1814	AGGGTGCCCGCCCCCTGCCA
3728	1815	CAGGGTGCCCGCCCCCTGCC
3729	1816	GCAGGGTGCCCGCCCCCTGC
3730	1817	CGCAGGGTGCCCGCCCCCTG
3731	1818	GCGCAGGGTGCCCGCCCCCT
3732	1819	TGCGCAGGGTGCCCGCCCCC
3733	1820	GTGCGCAGGGTGCCCGCCCC
3734	1821	AGTGCGCAGGGTGCCCGCCC
3735	1822	AAGTGCGCAGGGTGCCCGCC
3736	1823	TAAGTGCGCAGGGTGCCCGC
3737	1824	ATAAGTGCGCAGGGTGCCCG
3738	1825	GATAAGTGCGCAGGGTGCCC
3739	1826	GGATAAGTGCGCAGGGTGCC
3740	1827	GGGATAAGTGCGCAGGGTGC
3741	1828	TGGGATAAGTGCGCAGGGTG
3742	1829	TTGGGATAAGTGCGCAGGGT
3743	1830	GTTGGGATAAGTGCGCAGGG
3744	1831	GGTTGGGATAAGTGCGCAGG
3745	1832	GGGTTGGGATAAGTGCGCAG
3746	1833	GGGGTTGGGATAAGTGCGCA
3747	1834	GGGGGTTGGGATAAGTGCGC
3748	1835	CGGGGGTTGGGATAAGTGCG
3749	1836	GCGGGGGTTGGGATAAGTGC
3750	1837	GGCGGGGGTTGGGATAAGTG
3751	1838	GGGCGGGGGTTGGGATAAGT
3752	1839	GGGGCGGGGGTTGGGATAAG
3753	1840	TGGGGCGGGGGTTGGGATAA
3754	1841	TTGGGGCGGGGGTTGGGATA
3755	1842	ATTGGGGCGGGGGTTGGGAT
3756	1843	AATTGGGGCGGGGGTTGGGA

52833	50920	AATAAAGCACAAATTCTTTT
52834	50921	AAATAAAGCACAAATTCTTT
52835	50922	AAAATAAAGCACAAATTCTT
52836	50923	GAAAATAAAGCACAAATTCT
52837	50924	AGAAAATAAAGCACAAATTC
52838	50925	AAGAAAATAAAGCACAAATT
52839	50926	CAAGAAAATAAAGCACAAAT
52840	50927	GCAAGAAAATAAAGCACAAA
52841	50928	GGCAAGAAAATAAAGCACAA
52842	50929	AGGCAAGAAAATAAAGCACA
52843	50930	GAGGCAAGAAAATAAAGCAC
52844	50931	TGAGGCAAGAAAATAAAGCA
52845	50932	GTGAGGCAAGAAAATAAAGC
52846	50933	TGTGAGGCAAGAAAATAAAG
52847	50934	CTGTGAGGCAAGAAAATAAA
52848	50935	ACTGTGAGGCAAGAAAATAA
52849	50936	GACTGTGAGGCAAGAAAATA
52850	50937	GGACTGTGAGGCAAGAAAAT
52851	50938	GGGACTGTGAGGCAAGAAAA
52852	50939	GGGGACTGTGAGGCAAGAAA
52853	50940	AGGGGACTGTGAGGCAAGAA
52854	50941	AAGGGGACTGTGAGGCAAGA
52855	50942	AAAGGGGACTGTGAGGCAAG
52856	50943	GAAAGGGGACTGTGAGGCAA
52857	50944	AGAAAGGGGACTGTGAGGCA
52858	50945	CAGAAAGGGGACTGTGAGGC
52859	50946	ACAGAAAGGGGACTGTGAGG
52860	50947	GACAGAAAGGGGACTGTGAG
52861	50948	AGACAGAAAGGGGACTGTGA
52862	50949	GAGACAGAAAGGGGACTGTG
52863	50950	TGAGACAGAAAGGGGACTGT
52864	50951	CTGAGACAGAAAGGGGACTG
52865	50952	TCTGAGACAGAAAGGGGACT
52866	50953	TTCTGAGACAGAAAGGGGAC
52867	50954	ATTCTGAGACAGAAAGGGGA
52868	50955	AATTCTGAGACAGAAAGGGG
52869	50956	CAATTCTGAGACAGAAAGGG
52870	50957	CCAATTCTGAGACAGAAAGG
52871	50958	GCCAATTCTGAGACAGAAAG
52872	50959	TGCCAATTCTGAGACAGAAA
52873	50960	TTGCCAATTCTGAGACAGAA
52874	50961	GTTGCCAATTCTGAGACAGA
52875	50962	AGTTGCCAATTCTGAGACAG
52876	50963	CAGTTGCCAATTCTGAGACA
52877	50964	GCAGTTGCCAATTCTGAGAC
52878	50965	GGCAGTTGCCAATTCTGAGA
52879	50966	AGGCAGTTGCCAATTCTGAG
52880	50967	CAGGCAGTTGCCAATTCTGA
52881	50968	TCAGGCAGTTGCCAATTCTG
52882	50969	TTCAGGCAGTTGCCAATTCT
52883	50970	TTTCAGGCAGTTGCCAATTC
52884	50971	ATTTCAGGCAGTTGCCAATT
52885	50972	TATTTCAGGCAGTTGCCAAT
52886	50973	CTATTTCAGGCAGTTGCCAA
52887	50974	ACTATTTCAGGCAGTTGCCA
52888	50975	GACTATTTCAGGCAGTTGCC
52889	50976	AGACTATTTCAGGCAGTTGC
52890	50977	GAGACTATTTCAGGCAGTTG
52891	50978	AGAGACTATTTCAGGCAGTT
52892	50979	CAGAGACTATTTCAGGCAGT
52893	50980	GCAGAGACTATTTCAGGCAG
52894	50981	AGCAGAGACTATTTCAGGCA
52895	50982	CAGCAGAGACTATTTCAGGC
52896	50983	ACAGCAGAGACTATTTCAGG
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52898	50985	TAACAGCAGAGACTATTTCA
52899	50986	ATAACAGCAGAGACTATTTC
52900	50987	GATAACAGCAGAGACTATTT
52901	50988	TGATAACAGCAGAGACTATT
52902	50989	ATGATAACAGCAGAGACTAT
52903	50990	AATGATAACAGCAGAGACTA

101980	100067	TGCTTGAATCCGGGAGGTGT
101981	100068	TTGCTTGAATCCGGGAGGTG
101982	100069	ATTGCTTGAATCCGGGAGGT
101983	100070	AATTGCTTGAATCCGGGAGG
101984	100071	GAATTGCTTGAATCCGGGAG
101985	100072	AGAATTGCTTGAATCCGGGA
101986	100073	GAGAATTGCTTGAATCCGGG
101987	100074	GGAGAATTGCTTGAATCCGG
101988	100075	AGGAGAATTGCTTGAATCCG
101989	100076	CAGGAGAATTGCTTGAATCC
101990	100077	GCAGGAGAATTGCTTGAATC
101991	100078	GGCAGGAGAATTGCTTGAAT
101992	100079	AGGCAGGAGAATTGCTTGAA
101993	100080	GAGGCAGGAGAATTGCTTGA
101994	100081	GGAGGCAGGAGAATTGCTTG
101995	100082	AGGAGGCAGGAGAATTGCTT
101996	100083	CAGGAGGCAGGAGAATTGCT
101997	100084	GCAGGAGGCAGGAGAATTGC
101998	100085	GGCAGGAGGCAGGAGAATTG
101999	100086	TGGCAGGAGGCAGGAGAATT
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102001	100088	GGTGGCAGGAGGCAGGAGAA
102002	100089	TGGTGGCAGGAGGCAGGAGA
102003	100090	ATGGTGGCAGGAGGCAGGAG
102004	100091	CATGGTGGCAGGAGGCAGGA
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102006	100093	GACATGGTGGCAGGAGGCAG
102007	100094	AGACATGGTGGCAGGAGGCA
102008	100095	CAGACATGGTGGCAGGAGGC
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102014	100101	ATTAGGCAGACATGGTGGCA
102015	100102	AATTAGGCAGACATGGTGGC
102016	100103	AAATTAGGCAGACATGGTGG
102017	100104	AAAATTAGGCAGACATGGTG
102018	100105	AAAAATTAGGCAGACATGGT
102019	100106	CAAAAATTAGGCAGACATGG
102020	100107	ACAAAAATTAGGCAGACATG
102021	100108	TACAAAAATTAGGCAGACAT
102022	100109	ATACAAAAATTAGGCAGACA
102023	100110	AATACAAAAATTAGGCAGAC
102024	100111	AAATACAAAAATTAGGCAGA
102025	100112	AAAATACAAAAATTAGGCAG
102026	100113	AAAAATACAAAAATTAGGCA
102027	100114	TAAAAATACAAAAATTAGGC
102028	100115	CTAAAAATACAAAAATTAGG
102029	100116	ACTAAAAATACAAAAATTAG
102030	100117	TACTAAAAATACAAAAATTA
102031	100118	CTACTAAAAATACAAAAATT
102032	100119	TCTACTAAAAATACAAAAAT
102033	100120	CTCTACTAAAAATACAAAAA
102034	100121	TCTCTACTAAAAATACAAAA
102035	100122	GTCTCTACTAAAAATACAAA
102036	100123	CGTCTCTACTAAAAATACAA
102037	100124	CCGTCTCTACTAAAAATACA
102038	100125	CCCGTCTCTACTAAAAATAC
102039	100126	TCCCGTCTCTACTAAAAATA
102040	100127	ATCCCGTCTCTACTAAAAAT
102041	100128	AATCCCGTCTCTACTAAAAA
102042	100129	AAATCCCGTCTCTACTAAAA
102043	100130	GAAATCCCGTCTCTACTAAA
102044	100131	AGAAATCCCGTCTCTACTAA
102045	100132	GAGAAATCCCGTCTCTACTA
102046	100133	GGAGAAATCCCGTCTCTACT
102047	100134	AGGAGAAATCCCGTCTCTAC
102048	100135	AAGGAGAAATCCCGTCTCTA
102049	100136	CAAGGAGAAATCCCGTCTCT
102050	100137	ACAAGGAGAAATCCCGTCTC

3757	1844	AAATTGGGGCGGGGGTTGGG
3758	1845	GAAATTGGGGCGGGGGTTGG
3759	1846	CGAAATTGGGGCGGGGGTTG
3760	1847	CCGAAATTGGGGCGGGGGTT
3761	1848	TCCGAAATTGGGGCGGGGGT
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3765	1852	CATTTCCGAAATTGGGGCGG
3766	1853	GCATTTCCGAAATTGGGGCG
3767	1854	AGCATTTCCGAAATTGGGGC
3768	1855	TAGCATTTCCGAAATTGGGG
3769	1856	CTAGCATTTCCGAAATTGGG
3770	1857	CCTAGCATTTCCGAAATTGG
3771	1858	TCCTAGCATTTCCGAAATTG
3772	1859	CTCCTAGCATTTCCGAAATT
3773	1860	TCTCCTAGCATTTCCGAAAT
3774	1861	CTCTCCTAGCATTTCCGAAA
3775	1862	TCTCTCCTAGCATTTCCGAA
3776	1863	CTCTCTCCTAGCATTTCCGA
3777	1864	TCTCTCTCCTAGCATTTCCG
3778	1865	CTCTCTCTCCTAGCATTTCC
3779	1866	TCTCTCTCTCCTAGCATTTC
3780	1867	ATCTCTCTCTCCTAGCATTT
3781	1868	AATCTCTCTCTCCTAGCATT
3782	1869	CAATCTCTCTCTCCTAGCAT
3783	1870	GCAATCTCTCTCTCCTAGCA
3784	1871	TGCAATCTCTCTCTCCTAGC
3785	1872	CTGCAATCTCTCTCTCCTAG
3786	1873	GCTGCAATCTCTCTCTCCTA
3787	1874	TGCTGCAATCTCTCTCTCCT
3788	1875	CTGCTGCAATCTCTCTCTCC
3789	1876	CCTGCTGCAATCTCTCTCTC
3790	1877	CCCTGCTGCAATCTCTCTCT
3791	1878	CCCCTGCTGCAATCTCTCTC
3792	1879	TCCCCTGCTGCAATCTCTCT
3793	1880	GTCCCCTGCTGCAATCTCTC
3794	1881	CGTCCCCTGCTGCAATCTCT
3795	1882	ACGTCCCCTGCTGCAATCTC
3796	1883	CACGTCCCCTGCTGCAATCT
3797	1884	CCACGTCCCCTGCTGCAATC
3798	1885	ACCACGTCCCCTGCTGCAAT
3799	1886	GACCACGTCCCCTGCTGCAA
3800	1887	CGACCACGTCCCCTGCTGCA
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3802	1889	CCCGACCACGTCCCCTGCTG
3803	1890	ACCCGACCACGTCCCCTGCT
3804	1891	AACCCGACCACGTCCCCTGC
3805	1892	GAACCCGACCACGTCCCCTG
3806	1893	GGAACCCGACCACGTCCCCT
3807	1894	AGGAACCCGACCACGTCCCC
3808	1895	CAGGAACCCGACCACGTCCC
3809	1896	TCAGGAACCCGACCACGTCC
3810	1897	TTCAGGAACCCGACCACGTC
3811	1898	CTTCAGGAACCCGACCACGT
3812	1899	CCTTCAGGAACCCGACCACG
3813	1900	GCCTTCAGGAACCCGACCAC
3814	1901	TGCCTTCAGGAACCCGACCA
3815	1902	CTGCCTTCAGGAACCCGACC
3816	1903	TCTGCCTTCAGGAACCCGAC
3817	1904	TTCTGCCTTCAGGAACCCGA
3818	1905	TTTCTGCCTTCAGGAACCCG
3819	1906	CTTTCTGCCTTCAGGAACCC
3820	1907	CCTTTCTGCCTTCAGGAACC
3821	1908	GCCTTTCTGCCTTCAGGAAC
3822	1909	CGCCTTTCTGCCTTCAGGAA
3823	1910	CCGCCTTTCTGCCTTCAGGA
3824	1911	CCCGCCTTTCTGCCTTCAGG
3825	1912	ACCCGCCTTTCTGCCTTCAG
3826	1913	CACCCGCCTTTCTGCCTTCA
3827	1914	ACACCCGCCTTTCTGCCTTC

52904	50991	AAATGATAACAGCAGAGACT
52905	50992	CAAATGATAACAGCAGAGAC
52906	50993	TCAAATGATAACAGCAGAGA
52907	50994	ATCAAATGATAACAGCAGAG
52908	50995	TATCAAATGATAACAGCAGA
52909	50996	CTATCAAATGATAACAGCAG
52910	50997	ACTATCAAATGATAACAGCA
52911	50998	TACTATCAAATGATAACAGC
52912	50999	GTACTATCAAATGATAACAG
52913	51000	AGTACTATCAAATGATAACA
52914	51001	AAGTACTATCAAATGATAAC
52915	51002	AAAGTACTATCAAATGATAA
52916	51003	AAAAGTACTATCAAATGATA
52917	51004	GAAAAGTACTATCAAATGAT
52918	51005	GGAAAAGTACTATCAAATGA
52919	51006	TGGAAAAGTACTATCAAATG
52920	51007	GTGGAAAAGTACTATCAAAT
52921	51008	TGTGGAAAAGTACTATCAAA
52922	51009	ATGTGGAAAAGTACTATCAA
52923	51010	GATGTGGAAAAGTACTATCA
52924	51011	AGATGTGGAAAAGTACTATC
52925	51012	AAGATGTGGAAAAGTACTAT
52926	51013	CAAGATGTGGAAAAGTACTA
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52928	51015	TTCAAGATGTGGAAAAGTAC
52929	51016	ATTCAAGATGTGGAAAAGTA
52930	51017	CATTCAAGATGTGGAAAAGT
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52932	51019	TCCATTCAAGATGTGGAAAA
52933	51020	ATCCATTCAAGATGTGGAAA
52934	51021	TATCCATTCAAGATGTGGAA
52935	51022	CTATCCATTCAAGATGTGGA
52936	51023	TCTATCCATTCAAGATGTGG
52937	51024	ATCTATCCATTCAAGATGTG
52938	51025	TATCTATCCATTCAAGATGT
52939	51026	CTATCTATCCATTCAAGATG
52940	51027	TCTATCTATCCATTCAAGAT
52941	51028	CTCTATCTATCCATTCAAGA
52942	51029	ACTCTATCTATCCATTCAAG
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52944	51031	ACACTCTATCTATCCATTCA
52945	51032	AACACTCTATCTATCCATTC
52946	51033	AAACACTCTATCTATCCATT
52947	51034	AAAACACTCTATCTATCCAT
52948	51035	AAAAACACTCTATCTATCCA
52949	51036	AAAAAACACTCTATCTATCC
52950	51037	TAAAAAACACTCTATCTATC
52951	51038	ATAAAAAACACTCTATCTAT
52952	51039	TATAAAAAACACTCTATCTA
52953	51040	TTATAAAAAACACTCTATCT
52954	51041	ATTATAAAAAACACTCTATC
52955	51042	TATTATAAAAAACACTCTAT
52956	51043	CTATTATAAAAAACACTCTA
52957	51044	TCTATTATAAAAAACACTCT
52958	51045	TTCTATTATAAAAAACACTC
52959	51046	CTTCTATTATAAAAAACACT
52960	51047	ACTTCTATTATAAAAAACAC
52961	51048	CACTTCTATTATAAAAAACA
52962	51049	CCACTTCTATTATAAAAAAC
52963	51050	TCCACTTCTATTATAAAAAA
52964	51051	ATCCACTTCTATTATAAAAA
52965	51052	CATCCACTTCTATTATAAAA
52966	51053	TCATCCACTTCTATTATAAA
52967	51054	TTCATCCACTTCTATTATAA
52968	51055	ATTCATCCACTTCTATTATA
52969	51056	CATTCATCCACTTCTATTAT
52970	51057	TCATTCATCCACTTCTATTA
52971	51058	ATCATTCATCCACTTCTATT
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52974	51061	CTAATCATTCATCCACTTCT

102051	100138	AACAAGGAGAAATCCCGTCT
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102053	100140	GCAACAAGGAGAAATCCCGT
102054	100141	GGCAACAAGGAGAAATCCCG
102055	100142	GGGCAACAAGGAGAAATCCC
102056	100143	TGGGCAACAAGGAGAAATCC
102057	100144	CTGGGCAACAAGGAGAAATC
102058	100145	CCTGGGCAACAAGGAGAAAT
102059	100146	GCCTGGGCAACAAGGAGAAA
102060	100147	AGCCTGGGCAACAAGGAGAA
102061	100148	CAGCCTGGGCAACAAGGAGA
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102063	100150	ACCAGCCTGGGCAACAAGGA
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102065	100152	AGACCAGCCTGGGCAACAAG
102066	100153	AAGACCAGCCTGGGCAACAA
102067	100154	CAAGACCAGCCTGGGCAACA
102068	100155	TCAAGACCAGCCTGGGCAAC
102069	100156	TTCAAGACCAGCCTGGGCAA
102070	100157	GTTCAAGACCAGCCTGGGCA
102071	100158	AGTTCAAGACCAGCCTGGGC
102072	100159	GAGTTCAAGACCAGCCTGGG
102073	100160	GGAGTTCAAGACCAGCCTGG
102074	100161	AGGAGTTCAAGACCAGCCTG
102075	100162	TAGGAGTTCAAGACCAGCCT
102076	100163	TTAGGAGTTCAAGACCAGCC
102077	100164	GTTAGGAGTTCAAGACCAGC
102078	100165	GGTTAGGAGTTCAAGACCAG
102079	100166	AGGTTAGGAGTTCAAGACCA
102080	100167	GAGGTTAGGAGTTCAAGACC
102081	100168	TGAGGTTAGGAGTTCAAGAC
102082	100169	CTGAGGTTAGGAGTTCAAGA
102083	100170	CCTGAGGTTAGGAGTTCAAG
102084	100171	ACCTGAGGTTAGGAGTTCAA
102085	100172	CACCTGAGGTTAGGAGTTCA
102086	100173	TCACCTGAGGTTAGGAGTTC
102087	100174	ATCACCTGAGGTTAGGAGTT
102088	100175	AATCACCTGAGGTTAGGAGT
102089	100176	AAATCACCTGAGGTTAGGAG
102090	100177	TAAATCACCTGAGGTTAGGA
102091	100178	GTAAATCACCTGAGGTTAGG
102092	100179	GGTAAATCACCTGAGGTTAG
102093	100180	AGGTAAATCACCTGAGGTTA
102094	100181	CAGGTAAATCACCTGAGGTT
102095	100182	GCAGGTAAATCACCTGAGGT
102096	100183	GGCAGGTAAATCACCTGAGG
102097	100184	AGGCAGGTAAATCACCTGAG
102098	100185	GAGGCAGGTAAATCACCTGA
102099	100186	TGAGGCAGGTAAATCACCTG
102100	100187	CTGAGGCAGGTAAATCACCT
102101	100188	GCTGAGGCAGGTAAATCACC
102102	100189	GGCTGAGGCAGGTAAATCAC
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102104	100191	GAGGCTGAGGCAGGTAAATC
102105	100192	GGAGGCTGAGGCAGGTAAAT
102106	100193	GGGAGGCTGAGGCAGGTAAA
102107	100194	TGGGAGGCTGAGGCAGGTAA
102108	100195	TTGGGAGGCTGAGGCAGGTA
102109	100196	TTTGGGAGGCTGAGGCAGGT
102110	100197	CTTTGGGAGGCTGAGGCAGG
102111	100198	ACTTTGGGAGGCTGAGGCAG
102112	100199	CACTTTGGGAGGCTGAGGCA
102113	100200	GCACTTTGGGAGGCTGAGGC
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102115	100202	TAGCACTTTGGGAGGCTGAG
102116	100203	CTAGCACTTTGGGAGGCTGA
102117	100204	CCTAGCACTTTGGGAGGCTG
102118	100205	TCCTAGCACTTTGGGAGGCT
102119	100206	ATCCTAGCACTTTGGGAGGC
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3828	1915	AACACCCGCCTTTCTGCCTT
3829	1916	AAACACCCGCCTTTCTGCCT
3830	1917	TAAACACCCGCCTTTCTGCC
3831	1918	GTAAACACCCGCCTTTCTGC
3832	1919	AGTAAACACCCGCCTTTCTG
3833	1920	TAGTAAACACCCGCCTTTCT
3834	1921	CTAGTAAACACCCGCCTTTC
3835	1922	GCTAGTAAACACCCGCCTTT
3836	1923	CGCTAGTAAACACCCGCCTT
3837	1924	ACGCTAGTAAACACCCGCCT
3838	1925	GACGCTAGTAAACACCCGCC
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3840	1927	AAGACGCTAGTAAACACCCG
3841	1928	AAAGACGCTAGTAAACACCC
3842	1929	AAAAGACGCTAGTAAACACC
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3844	1931	GAAAAAGACGCTAGTAAACA
3845	1932	GGAAAAAGACGCTAGTAAAC
3846	1933	GGGAAAAAGACGCTAGTAAA
3847	1934	AGGGAAAAAGACGCTAGTAA
3848	1935	GAGGGAAAAAGACGCTAGTA
3849	1936	GGAGGGAAAAAGACGCTAGT
3850	1937	AGGAGGGAAAAAGACGCTAG
3851	1938	TAGGAGGGAAAAAGACGCTA
3852	1939	TTAGGAGGGAAAAAGACGCT
3853	1940	CTTAGGAGGGAAAAAGACGC
3854	1941	GCTTAGGAGGGAAAAAGACG
3855	1942	GGCTTAGGAGGGAAAAAGAC
3856	1943	CGGCTTAGGAGGGAAAAAGA
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3858	1945	CCCGGCTTAGGAGGGAAAAA
3859	1946	CCCCGGCTTAGGAGGGAAAA
3860	1947	ACCCCGGCTTAGGAGGGAAA
3861	1948	AACCCCGGCTTAGGAGGGAA
3862	1949	CAACCCCGGCTTAGGAGGGA
3863	1950	ACAACCCCGGCTTAGGAGGG
3864	1951	TACAACCCCGGCTTAGGAGG
3865	1952	CTACAACCCCGGCTTAGGAG
3866	1953	ACTACAACCCCGGCTTAGGA
3867	1954	TACTACAACCCCGGCTTAGG
3868	1955	CTACTACAACCCCGGCTTAG
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3870	1957	CCCTACTACAACCCCGGCTT
3871	1958	CCCCTACTACAACCCCGGCT
3872	1959	GCCCCTACTACAACCCCGGC
3873	1960	AGCCCCTACTACAACCCCGG
3874	1961	CAGCCCCTACTACAACCCCG
3875	1962	CCAGCCCCTACTACAACCCC
3876	1963	CCCAGCCCCTACTACAACCC
3877	1964	CCCCAGCCCCTACTACAACC
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3879	1966	GCCCCCAGCCCCTACTACAA
3880	1967	AGCCCCCAGCCCCTACTACA
3881	1968	GAGCCCCCAGCCCCTACTAC
3882	1969	TGAGCCCCCAGCCCCTACTA
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3884	1971	ACTGAGCCCCCAGCCCCTAC
3885	1972	CACTGAGCCCCCAGCCCCTA
3886	1973	ACACTGAGCCCCCAGCCCCT
3887	1974	AACACTGAGCCCCCAGCCCC
3888	1975	CAACACTGAGCCCCCAGCCC
3889	1976	ACAACACTGAGCCCCCAGCC
3890	1977	GACAACACTGAGCCCCCAGC
3891	1978	GGACAACACTGAGCCCCCAG
3892	1979	GGGACAACACTGAGCCCCCA
3893	1980	CGGGACAACACTGAGCCCCC
3894	1981	CCGGGACAACACTGAGCCCC
3895	1982	GCCGGGACAACACTGAGCCC
3896	1983	AGCCGGGACAACACTGAGCC
3897	1984	TAGCCGGGACAACACTGAGC
3898	1985	TTAGCCGGGACAACACTGAG

52975	51062	TCTAATCATTCATCCACTTC
52976	51063	CTCTAATCATTCATCCACTT
52977	51064	ACTCTAATCATTCATCCACT
52978	51065	TACTCTAATCATTCATCCAC
52979	51066	ATACTCTAATCATTCATCCA
52980	51067	TATACTCTAATCATTCATCC
52981	51068	GTATACTCTAATCATTCATC
52982	51069	AGTATACTCTAATCATTCAT
52983	51070	TAGTATACTCTAATCATTCA
52984	51071	TTAGTATACTCTAATCATTC
52985	51072	ATTAGTATACTCTAATCATT
52986	51073	TATTAGTATACTCTAATCAT
52987	51074	ATATTAGTATACTCTAATCA
52988	51075	CATATTAGTATACTCTAATC
52989	51076	TCATATTAGTATACTCTAAT
52990	51077	GTCATATTAGTATACTCTAA
52991	51078	TGTCATATTAGTATACTCTA
52992	51079	ATGTCATATTAGTATACTCT
52993	51080	AATGTCATATTAGTATACTC
52994	51081	CAATGTCATATTAGTATACT
52995	51082	ACAATGTCATATTAGTATAC
52996	51083	TACAATGTCATATTAGTATA
52997	51084	ATACAATGTCATATTAGTAT
52998	51085	AATACAATGTCATATTAGTA
52999	51086	AAATACAATGTCATATTAGT
53000	51087	AAAATACAATGTCATATTAG
53001	51088	GAAAATACAATGTCATATTA
53002	51089	GGAAAATACAATGTCATATT
53003	51090	AGGAAAATACAATGTCATAT
53004	51091	TAGGAAAATACAATGTCATA
53005	51092	TTAGGAAAATACAATGTCAT
53006	51093	TTTAGGAAAATACAATGTCA
53007	51094	TTTTAGGAAAATACAATGTC
53008	51095	CTTTTAGGAAAATACAATGT
53009	51096	TCTTTTAGGAAAATACAATG
53010	51097	ATCTTTTAGGAAAATACAAT
53011	51098	TATCTTTTAGGAAAATACAA
53012	51099	ATATCTTTTAGGAAAATACA
53013	51100	CATATCTTTTAGGAAAATAC
53014	51101	TCATATCTTTTAGGAAAATA
53015	51102	TTCATATCTTTTAGGAAAAT
53016	51103	ATTCATATCTTTTAGGAAAA
53017	51104	AATTCATATCTTTTAGGAAA
53018	51105	CAATTCATATCTTTTAGGAA
53019	51106	TCAATTCATATCTTTTAGGA
53020	51107	ATCAATTCATATCTTTTAGG
53021	51108	AATCAATTCATATCTTTTAG
53022	51109	AAATCAATTCATATCTTTTA
53023	51110	GAAATCAATTCATATCTTTT
53024	51111	TGAAATCAATTCATATCTTT
53025	51112	ATGAAATCAATTCATATCTT
53026	51113	AATGAAATCAATTCATATCT
53027	51114	AAATGAAATCAATTCATATC
53028	51115	GAAATGAAATCAATTCATAT
53029	51116	AGAAATGAAATCAATTCATA
53030	51117	CAGAAATGAAATCAATTCAT
53031	51118	TCAGAAATGAAATCAATTCA
53032	51119	CTCAGAAATGAAATCAATTC
53033	51120	GCTCAGAAATGAAATCAATT
53034	51121	AGCTCAGAAATGAAATCAAT
53035	51122	AAGCTCAGAAATGAAATCAA
53036	51123	AAAGCTCAGAAATGAAATCA
53037	51124	AAAAGCTCAGAAATGAAATC
53038	51125	TAAAAGCTCAGAAATGAAAT
53039	51126	ATAAAAGCTCAGAAATGAAA
53040	51127	TATAAAAGCTCAGAAATGAA
53041	51128	TTATAAAAGCTCAGAAATGA
53042	51129	ATTATAAAAGCTCAGAAATG
53043	51130	AATTATAAAAGCTCAGAAAT
53044	51131	GAATTATAAAAGCTCAGAAA
53045	51132	AGAATTATAAAAGCTCAGAA

102122	100209	GTAATCCTAGCACTTTGGGA
102123	100210	TGTAATCCTAGCACTTTGGG
102124	100211	CTGTAATCCTAGCACTTTGG
102125	100212	CCTGTAATCCTAGCACTTTG
102126	100213	GCCTGTAATCCTAGCACTTT
102127	100214	CGCCTGTAATCCTAGCACTT
102128	100215	ACGCCTGTAATCCTAGCACT
102129	100216	CACGCCTGTAATCCTAGCAC
102130	100217	TCACGCCTGTAATCCTAGCA
102131	100218	CTCACGCCTGTAATCCTAGC
102132	100219	GCTCACGCCTGTAATCCTAG
102133	100220	AGCTCACGCCTGTAATCCTA
102134	100221	CAGCTCACGCCTGTAATCCT
102135	100222	GCAGCTCACGCCTGTAATCC
102136	100223	AGCAGCTCACGCCTGTAATC
102137	100224	CAGCAGCTCACGCCTGTAAT
102138	100225	GCAGCAGCTCACGCCTGTAA
102139	100226	CGCAGCAGCTCACGCCTGTA
102140	100227	GCGCAGCAGCTCACGCCTGT
102141	100228	GGCGCAGCAGCTCACGCCTG
102142	100229	GGGCGCAGCAGCTCACGCCT
102143	100230	TGGGCGCAGCAGCTCACGCC
102144	100231	CTGGGCGCAGCAGCTCACGC
102145	100232	GCTGGGCGCAGCAGCTCACG
102146	100233	GGCTGGGCGCAGCAGCTCAC
102147	100234	AGGCTGGGCGCAGCAGCTCA
102148	100235	CAGGCTGGGCGCAGCAGCTC
102149	100236	ACAGGCTGGGCGCAGCAGCT
102150	100237	TACAGGCTGGGCGCAGCAGC
102151	100238	ATACAGGCTGGGCGCAGCAG
102152	100239	CATACAGGCTGGGCGCAGCA
102153	100240	ACATACAGGCTGGGCGCAGC
102154	100241	GACATACAGGCTGGGCGCAG
102155	100242	CGACATACAGGCTGGGCGCA
102156	100243	ACGACATACAGGCTGGGCGC
102157	100244	GACGACATACAGGCTGGGCG
102158	100245	AGACGACATACAGGCTGGGC
102159	100246	AAGACGACATACAGGCTGGG
102160	100247	AAAGACGACATACAGGCTGG
102161	100248	AAAAGACGACATACAGGCTG
102162	100249	CAAAAGACGACATACAGGCT
102163	100250	TCAAAAGACGACATACAGGC
102164	100251	CTCAAAAGACGACATACAGG
102165	100252	TCTCAAAAGACGACATACAG
102166	100253	TTCTCAAAAGACGACATACA
102167	100254	TTTCTCAAAAGACGACATAC
102168	100255	ATTTCTCAAAAGACGACATA
102169	100256	CATTTCTCAAAAGACGACAT
102170	100257	ACATTTCTCAAAAGACGACA
102171	100258	GACATTTCTCAAAAGACGAC
102172	100259	AGACATTTCTCAAAAGACGA
102173	100260	TAGACATTTCTCAAAAGACG
102174	100261	ATAGACATTTCTCAAAAGAC
102175	100262	AATAGACATTTCTCAAAAGA
102176	100263	GAATAGACATTTCTCAAAAG
102177	100264	TGAATAGACATTTCTCAAAA
102178	100265	CTGAATAGACATTTCTCAAA
102179	100266	TCTGAATAGACATTTCTCAA
102180	100267	ATCTGAATAGACATTTCTCA
102181	100268	GATCTGAATAGACATTTCTC
102182	100269	AGATCTGAATAGACATTTCT
102183	100270	AAGATCTGAATAGACATTTC
102184	100271	AAAGATCTGAATAGACATTT
102185	100272	AAAAGATCTGAATAGACATT
102186	100273	CAAAAGATCTGAATAGACAT
102187	100274	GCAAAAGATCTGAATAGACA
102188	100275	GGCAAAAGATCTGAATAGAC
102189	100276	GGGCAAAAGATCTGAATAGA
102190	100277	TGGGCAAAAGATCTGAATAG
102191	100278	ATGGGCAAAAGATCTGAATA
102192	100279	AATGGGCAAAAGATCTGAAT

3899	1986	GTTAGCCGGGACAACACTGA
3900	1987	AGTTAGCCGGGACAACACTG
3901	1988	CAGTTAGCCGGGACAACACT
3902	1989	CCAGTTAGCCGGGACAACAC
3903	1990	CCCAGTTAGCCGGGACAACA
3904	1991	ACCCAGTTAGCCGGGACAAC
3905	1992	AACCCAGTTAGCCGGGACAA
3906	1993	AAACCCAGTTAGCCGGGACA
3907	1994	CAAACCCAGTTAGCCGGGAC
3908	1995	TCAAACCCAGTTAGCCGGGA
3909	1996	GTCAAACCCAGTTAGCCGGG
3910	1997	AGTCAAACCCAGTTAGCCGG
3911	1998	GAGTCAAACCCAGTTAGCCG
3912	1999	CGAGTCAAACCCAGTTAGCC
3913	2000	TCGAGTCAAACCCAGTTAGC
3914	2001	CTCGAGTCAAACCCAGTTAG
3915	2002	CCTCGAGTCAAACCCAGTTA
3916	2003	CCCTCGAGTCAAACCCAGTT
3917	2004	ACCCTCGAGTCAAACCCAGT
3918	2005	CACCCTCGAGTCAAACCCAG
3919	2006	ACACCCTCGAGTCAAACCCA
3920	2007	CACACCCTCGAGTCAAACCC
3921	2008	ACACACCCTCGAGTCAAACC
3922	2009	AACACACCCTCGAGTCAAAC
3923	2010	AAACACACCCTCGAGTCAAA
3924	2011	CAAACACACCCTCGAGTCAA
3925	2012	ACAAACACACCCTCGAGTCA
3926	2013	CACAAACACACCCTCGAGTC
3927	2014	GCACAAACACACCCTCGAGT
3928	2015	TGCACAAACACACCCTCGAG
3929	2016	CTGCACAAACACACCCTCGA
3930	2017	CCTGCACAAACACACCCTCG
3931	2018	TCCTGCACAAACACACCCTC
3932	2019	CTCCTGCACAAACACACCCT
3933	2020	CCTCCTGCACAAACACACCC
3934	2021	CCCTCCTGCACAAACACACC
3935	2022	GCCCTCCTGCACAAACACAC
3936	2023	GGCCCTCCTGCACAAACACA
3937	2024	AGGCCCTCCTGCACAAACAC
3938	2025	CAGGCCCTCCTGCACAAACA
3939	2026	ACAGGCCCTCCTGCACAAAC
3940	2027	AACAGGCCCTCCTGCACAAA
3941	2028	CAACAGGCCCTCCTGCACAA
3942	2029	CCAACAGGCCCTCCTGCACA
3943	2030	CCCAACAGGCCCTCCTGCAC
3944	2031	CCCCAACAGGCCCTCCTGCA
3945	2032	CCCCCAACAGGCCCTCCTGC
3946	2033	ACCCCCAACAGGCCCTCCTG
3947	2034	CACCCCCAACAGGCCCTCCT
3948	2035	CCACCCCCAACAGGCCCTCC
3949	2036	GCCACCCCCAACAGGCCCTC
3950	2037	CGCCACCCCCAACAGGCCCT
3951	2038	CCGCCACCCCCAACAGGCCC
3952	2039	CCCGCCACCCCCAACAGGCC
3953	2040	GCCCGCCACCCCCAACAGGC
3954	2041	CGCCCGCCACCCCCAACAGG
3955	2042	CCGCCCGCCACCCCCAACAG
3956	2043	ACCGCCCGCCACCCCCAACA
3957	2044	AACCGCCCGCCACCCCCAAC
3958	2045	CAACCGCCCGCCACCCCCAA
3959	2046	ACAACCGCCCGCCACCCCCA
3960	2047	GACAACCGCCCGCCACCCCC
3961	2048	TGACAACCGCCCGCCACCCC
3962	2049	CTGACAACCGCCCGCCACCC
3963	2050	ACTGACAACCGCCCGCCACC
3964	2051	AACTGACAACCGCCCGCCAC
3965	2052	GAACTGACAACCGCCCGCCA
3966	2053	CGAACTGACAACCGCCCGCC
3967	2054	ACGAACTGACAACCGCCCGC
3968	2055	TACGAACTGACAACCGCCCG
3969	2056	ATACGAACTGACAACCGCCC

53046	51133	GAGAATTATAAAAGCTCAGA
53047	51134	AGAGAATTATAAAAGCTCAG
53048	51135	AAGAGAATTATAAAAGCTCA
53049	51136	GAAGAGAATTATAAAAGCTC
53050	51137	AGAAGAGAATTATAAAAGCT
53051	51138	CAGAAGAGAATTATAAAAGC
53052	51139	ACAGAAGAGAATTATAAAAG
53053	51140	TACAGAAGAGAATTATAAAA
53054	51141	TTACAGAAGAGAATTATAAA
53055	51142	ATTACAGAAGAGAATTATAA
53056	51143	TATTACAGAAGAGAATTATA
53057	51144	CTATTACAGAAGAGAATTAT
53058	51145	ACTATTACAGAAGAGAATTA
53059	51146	GACTATTACAGAAGAGAATT
53060	51147	AGACTATTACAGAAGAGAAT
53061	51148	CAGACTATTACAGAAGAGAA
53062	51149	ACAGACTATTACAGAAGAGA
53063	51150	GACAGACTATTACAGAAGAG
53064	51151	TGACAGACTATTACAGAAGA
53065	51152	TTGACAGACTATTACAGAAG
53066	51153	TTTGACAGACTATTACAGAA
53067	51154	ATTTGACAGACTATTACAGA
53068	51155	AATTTGACAGACTATTACAG
53069	51156	TAATTTGACAGACTATTACA
53070	51157	ATAATTTGACAGACTATTAC
53071	51158	AATAATTTGACAGACTATTA
53072	51159	TAATAATTTGACAGACTATT
53073	51160	TTAATAATTTGACAGACTAT
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53075	51162	CCTTAATAATTTGACAGACT
53076	51163	ACCTTAATAATTTGACAGAC
53077	51164	AACCTTAATAATTTGACAGA
53078	51165	CAACCTTAATAATTTGACAG
53079	51166	TCAACCTTAATAATTTGACA
53080	51167	ATCAACCTTAATAATTTGAC
53081	51168	TATCAACCTTAATAATTTGA
53082	51169	TTATCAACCTTAATAATTTG
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53084	51171	TATTATCAACCTTAATAATT
53085	51172	ATATTATCAACCTTAATAAT
53086	51173	AATATTATCAACCTTAATAA
53087	51174	TAATATTATCAACCTTAATA
53088	51175	TTAATATTATCAACCTTAAT
53089	51176	GTTAATATTATCAACCTTAA
53090	51177	AGTTAATATTATCAACCTTA
53091	51178	TAGTTAATATTATCAACCTT
53092	51179	TTAGTTAATATTATCAACCT
53093	51180	TTTAGTTAATATTATCAACC
53094	51181	TTTTAGTTAATATTATCAAC
53095	51182	ATTTTAGTTAATATTATCAA
53096	51183	AATTTTAGTTAATATTATCA
53097	51184	AAATTTTAGTTAATATTATC
53098	51185	CAAATTTTAGTTAATATTAT
53099	51186	TCAAATTTTAGTTAATATTA
53100	51187	CTCAAATTTTAGTTAATATT
53101	51188	ACTCAAATTTTAGTTAATAT
53102	51189	CACTCAAATTTTAGTTAATA
53103	51190	GCACTCAAATTTTAGTTAAT
53104	51191	TGCACTCAAATTTTAGTTAA
53105	51192	ATGCACTCAAATTTTAGTTA
53106	51193	TATGCACTCAAATTTTAGTT
53107	51194	ATATGCACTCAAATTTTAGT
53108	51195	AATATGCACTCAAATTTTAG
53109	51196	GAATATGCACTCAAATTTTA
53110	51197	AGAATATGCACTCAAATTTT
53111	51198	TAGAATATGCACTCAAATTT
53112	51199	ATAGAATATGCACTCAAATT
53113	51200	CATAGAATATGCACTCAAAT
53114	51201	ACATAGAATATGCACTCAAA
53115	51202	CACATAGAATATGCACTCAA
53116	51203	GCACATAGAATATGCACTCA

102193	100280	AAATGGGCAAAAGATCTGAA
102194	100281	AAAATGGGCAAAAGATCTGA
102195	100282	AAAAATGGGCAAAAGATCTG
102196	100283	TAAAAATGGGCAAAAGATCT
102197	100284	TTAAAAATGGGCAAAAGATC
102198	100285	ATTAAAAATGGGCAAAAGAT
102199	100286	AATTAAAAATGGGCAAAAGA
102200	100287	CAATTAAAAATGGGCAAAAG
102201	100288	TCAATTAAAAATGGGCAAAA
102202	100289	CTCAATTAAAAATGGGCAAA
102203	100290	ACTCAATTAAAAATGGGCAA
102204	100291	AACTCAATTAAAAATGGGCA
102205	100292	TAACTCAATTAAAAATGGGC
102206	100293	GTAACTCAATTAAAAATGGG
102207	100294	AGTAACTCAATTAAAAATGG
102208	100295	TAGTAACTCAATTAAAAATG
102209	100296	TTAGTAACTCAATTAAAAAT
102210	100297	TTTAGTAACTCAATTAAAAA
102211	100298	TTTTAGTAACTCAATTAAAA
102212	100299	ATTTTAGTAACTCAATTAAA
102213	100300	AATTTTAGTAACTCAATTAA
102214	100301	AAATTTTAGTAACTCAATTA
102215	100302	AAAATTTTAGTAACTCAATT
102216	100303	GAAAATTTTAGTAACTCAAT
102217	100304	GGAAAATTTTAGTAACTCAA
102218	100305	GGGAAAATTTTAGTAACTCA
102219	100306	AGGGAAAATTTTAGTAACTC
102220	100307	TAGGGAAAATTTTAGTAACT
102221	100308	ATAGGGAAAATTTTAGTAAC
102222	100309	CATAGGGAAAATTTTAGTAA
102223	100310	CCATAGGGAAAATTTTAGTA
102224	100311	TCCATAGGGAAAATTTTAGT
102225	100312	CTCCATAGGGAAAATTTTAG
102226	100313	ACTCCATAGGGAAAATTTTA
102227	100314	AACTCCATAGGGAAAATTTT
102228	100315	CAACTCCATAGGGAAAATTT
102229	100316	GCAACTCCATAGGGAAAATT
102230	100317	AGCAACTCCATAGGGAAAAT
102231	100318	AAGCAACTCCATAGGGAAAA
102232	100319	CAAGCAACTCCATAGGGAAA
102233	100320	TCAAGCAACTCCATAGGGAA
102234	100321	CTCAAGCAACTCCATAGGGA
102235	100322	ACTCAAGCAACTCCATAGGG
102236	100323	CACTCAAGCAACTCCATAGG
102237	100324	GCACTCAAGCAACTCCATAG
102238	100325	GGCACTCAAGCAACTCCATA
102239	100326	AGGCACTCAAGCAACTCCAT
102240	100327	AAGGCACTCAAGCAACTCCA
102241	100328	AAAGGCACTCAAGCAACTCC
102242	100329	AAAAGGCACTCAAGCAACTC
102243	100330	TAAAAGGCACTCAAGCAACT
102244	100331	ATAAAAGGCACTCAAGCAAC
102245	100332	TATAAAAGGCACTCAAGCAA
102246	100333	ATATAAAAGGCACTCAAGCA
102247	100334	AATATAAAAGGCACTCAAGC
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102250	100337	CAGAATATAAAAGGCACTCA
102251	100338	CCAGAATATAAAAGGCACTC
102252	100339	ACCAGAATATAAAAGGCACT
102253	100340	AACCAGAATATAAAAGGCAC
102254	100341	TAACCAGAATATAAAAGGCA
102255	100342	ATAACCAGAATATAAAAGGC
102256	100343	AATAACCAGAATATAAAAGG
102257	100344	CAATAACCAGAATATAAAAG
102258	100345	TCAATAACCAGAATATAAAA
102259	100346	ATCAATAACCAGAATATAAA
102260	100347	GATCAATAACCAGAATATAA
102261	100348	GGATCAATAACCAGAATATA
102262	100349	GGGATCAATAACCAGAATAT
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3970	2057	AATACGAACTGACAACCGCC
3971	2058	AAATACGAACTGACAACCGC
3972	2059	GAAATACGAACTGACAACCG
3973	2060	TGAAATACGAACTGACAACC
3974	2061	GTGAAATACGAACTGACAAC
3975	2062	CGTGAAATACGAACTGACAA
3976	2063	TCGTGAAATACGAACTGACA
3977	2064	TTCGTGAAATACGAACTGAC
3978	2065	GTTCGTGAAATACGAACTGA
3979	2066	AGTTCGTGAAATACGAACTG
3980	2067	TAGTTCGTGAAATACGAACT
3981	2068	TTAGTTCGTGAAATACGAAC
3982	2069	CTTAGTTCGTGAAATACGAA
3983	2070	TCTTAGTTCGTGAAATACGA
3984	2071	TTCTTAGTTCGTGAAATACG
3985	2072	TTTCTTAGTTCGTGAAATAC
3986	2073	TTTTCTTAGTTCGTGAAATA
3987	2074	ATTTTCTTAGTTCGTGAAAT
3988	2075	CATTTTCTTAGTTCGTGAAA
3989	2076	GCATTTTCTTAGTTCGTGAA
3990	2077	AGCATTTTCTTAGTTCGTGA
3991	2078	AAGCATTTTCTTAGTTCGTG
3992	2079	TAAGCATTTTCTTAGTTCGT
3993	2080	CTAAGCATTTTCTTAGTTCG
3994	2081	ACTAAGCATTTTCTTAGTTC
3995	2082	CACTAAGCATTTTCTTAGTT
3996	2083	ACACTAAGCATTTTCTTAGT
3997	2084	AACACTAAGCATTTTCTTAG
3998	2085	GAACACTAAGCATTTTCTTA
3999	2086	TGAACACTAAGCATTTTCTT
4000	2087	TTGAACACTAAGCATTTTCT
4001	2088	TTTGAACACTAAGCATTTTC
4002	2089	CTTTGAACACTAAGCATTTT
4003	2090	CCTTTGAACACTAAGCATTT
4004	2091	CCCTTTGAACACTAAGCATT
4005	2092	TCCCTTTGAACACTAAGCAT
4006	2093	CTCCCTTTGAACACTAAGCA
4007	2094	TCTCCCTTTGAACACTAAGC
4008	2095	TTCTCCCTTTGAACACTAAG
4009	2096	CTTCTCCCTTTGAACACTAA
4010	2097	CCTTCTCCCTTTGAACACTA
4011	2098	TCCTTCTCCCTTTGAACACT
4012	2099	TTCCTTCTCCCTTTGAACAC
4013	2100	TTTCCTTCTCCCTTTGAACA
4014	2101	GTTTCCTTCTCCCTTTGAAC
4015	2102	CGTTTCCTTCTCCCTTTGAA
4016	2103	ACGTTTCCTTCTCCCTTTGA
4017	2104	GACGTTTCCTTCTCCCTTTG
4018	2105	TGACGTTTCCTTCTCCCTTT
4019	2106	TTGACGTTTCCTTCTCCCTT
4020	2107	ATTGACGTTTCCTTCTCCCT
4021	2108	TATTGACGTTTCCTTCTCCC
4022	2109	CTATTGACGTTTCCTTCTCC
4023	2110	TCTATTGACGTTTCCTTCTC
4024	2111	GTCTATTGACGTTTCCTTCT
4025	2112	AGTCTATTGACGTTTCCTTC
4026	2113	GAGTCTATTGACGTTTCCTT
4027	2114	GGAGTCTATTGACGTTTCCT
4028	2115	TGGAGTCTATTGACGTTTCC
4029	2116	ATGGAGTCTATTGACGTTTC
4030	2117	AATGGAGTCTATTGACGTTT
4031	2118	GAATGGAGTCTATTGACGTT
4032	2119	GGAATGGAGTCTATTGACGT
4033	2120	TGGAATGGAGTCTATTGACG
4034	2121	ATGGAATGGAGTCTATTGAC
4035	2122	AATGGAATGGAGTCTATTGA
4036	2123	CAATGGAATGGAGTCTATTG
4037	2124	ACAATGGAATGGAGTCTATT
4038	2125	CACAATGGAATGGAGTCTAT
4039	2126	CCACAATGGAATGGAGTCTA
4040	2127	GCCACAATGGAATGGAGTCT

53117	51204	GGCACATAGAATATGCACTC
53118	51205	TGGCACATAGAATATGCACT
53119	51206	CTGGCACATAGAATATGCAC
53120	51207	TCTGGCACATAGAATATGCA
53121	51208	GTCTGGCACATAGAATATGC
53122	51209	AGTCTGGCACATAGAATATG
53123	51210	GAGTCTGGCACATAGAATAT
53124	51211	AGAGTCTGGCACATAGAATA
53125	51212	CAGAGTCTGGCACATAGAAT
53126	51213	ACAGAGTCTGGCACATAGAA
53127	51214	CACAGAGTCTGGCACATAGA
53128	51215	GCACAGAGTCTGGCACATAG
53129	51216	AGCACAGAGTCTGGCACATA
53130	51217	TAGCACAGAGTCTGGCACAT
53131	51218	TTAGCACAGAGTCTGGCACA
53132	51219	GTTAGCACAGAGTCTGGCAC
53133	51220	TGTTAGCACAGAGTCTGGCA
53134	51221	CTGTTAGCACAGAGTCTGGC
53135	51222	TCTGTTAGCACAGAGTCTGG
53136	51223	ATCTGTTAGCACAGAGTCTG
53137	51224	AATCTGTTAGCACAGAGTCT
53138	51225	AAATCTGTTAGCACAGAGTC
53139	51226	TAAATCTGTTAGCACAGAGT
53140	51227	GTAAATCTGTTAGCACAGAG
53141	51228	GGTAAATCTGTTAGCACAGA
53142	51229	AGGTAAATCTGTTAGCACAG
53143	51230	TAGGTAAATCTGTTAGCACA
53144	51231	GTAGGTAAATCTGTTAGCAC
53145	51232	TGTAGGTAAATCTGTTAGCA
53146	51233	ATGTAGGTAAATCTGTTAGC
53147	51234	AATGTAGGTAAATCTGTTAG
53148	51235	AAATGTAGGTAAATCTGTTA
53149	51236	CAAATGTAGGTAAATCTGTT
53150	51237	ACAAATGTAGGTAAATCTGT
53151	51238	AACAAATGTAGGTAAATCTG
53152	51239	GAACAAATGTAGGTAAATCT
53153	51240	TGAACAAATGTAGGTAAATC
53154	51241	GTGAACAAATGTAGGTAAAT
53155	51242	TGTGAACAAATGTAGGTAAA
53156	51243	ATGTGAACAAATGTAGGTAA
53157	51244	TATGTGAACAAATGTAGGTA
53158	51245	TTATGTGAACAAATGTAGGT
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53160	51247	GATTATGTGAACAAATGTAG
53161	51248	TGATTATGTGAACAAATGTA
53162	51249	ATGATTATGTGAACAAATGT
53163	51250	GATGATTATGTGAACAAATG
53164	51251	TGATGATTATGTGAACAAAT
53165	51252	GTGATGATTATGTGAACAAA
53166	51253	TGTGATGATTATGTGAACAA
53167	51254	TTGTGATGATTATGTGAACA
53168	51255	CTTGTGATGATTATGTGAAC
53169	51256	ACTTGTGATGATTATGTGAA
53170	51257	AACTTGTGATGATTATGTGA
53171	51258	CAACTTGTGATGATTATGTG
53172	51259	ACAACTTGTGATGATTATGT
53173	51260	AACAACTTGTGATGATTATG
53174	51261	AAACAACTTGTGATGATTAT
53175	51262	GAAACAACTTGTGATGATTA
53176	51263	AGAAACAACTTGTGATGATT
53177	51264	CAGAAACAACTTGTGATGAT
53178	51265	ACAGAAACAACTTGTGATGA
53179	51266	TACAGAAACAACTTGTGATG
53180	51267	CTACAGAAACAACTTGTGAT
53181	51268	ACTACAGAAACAACTTGTGA
53182	51269	TACTACAGAAACAACTTGTG
53183	51270	CTACTACAGAAACAACTTGT
53184	51271	TCTACTACAGAAACAACTTG
53185	51272	ATCTACTACAGAAACAACTT
53186	51273	TATCTACTACAGAAACAACT
53187	51274	GTATCTACTACAGAAACAAC

102264	100351	AAGGGATCAATAACCAGAAT
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102266	100353	ACAAGGGATCAATAACCAGA
102267	100354	GACAAGGGATCAATAACCAG
102268	100355	TGACAAGGGATCAATAACCA
102269	100356	CTGACAAGGGATCAATAACC
102270	100357	TCTGACAAGGGATCAATAAC
102271	100358	ATCTGACAAGGGATCAATAA
102272	100359	CATCTGACAAGGGATCAATA
102273	100360	TCATCTGACAAGGGATCAAT
102274	100361	CTCATCTGACAAGGGATCAA
102275	100362	ACTCATCTGACAAGGGATCA
102276	100363	TACTCATCTGACAAGGGATC
102277	100364	CTACTCATCTGACAAGGGAT
102278	100365	ACTACTCATCTGACAAGGGA
102279	100366	AACTACTCATCTGACAAGGG
102280	100367	AAACTACTCATCTGACAAGG
102281	100368	CAAACTACTCATCTGACAAG
102282	100369	GCAAACTACTCATCTGACAA
102283	100370	TGCAAACTACTCATCTGACA
102284	100371	TTGCAAACTACTCATCTGAC
102285	100372	TTTGCAAACTACTCATCTGA
102286	100373	ATTTGCAAACTACTCATCTG
102287	100374	TATTTGCAAACTACTCATCT
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102292	100379	GAAAATATTTGCAAACTACT
102293	100380	AGAAAATATTTGCAAACTAC
102294	100381	GAGAAAATATTTGCAAACTA
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102296	100383	GGGAGAAAATATTTGCAAAC
102297	100384	TGGGAGAAAATATTTGCAAA
102298	100385	ATGGGAGAAAATATTTGCAA
102299	100386	AATGGGAGAAAATATTTGCA
102300	100387	GAATGGGAGAAAATATTTGC
102301	100388	AGAATGGGAGAAAATATTTG
102302	100389	CAGAATGGGAGAAAATATTT
102303	100390	ACAGAATGGGAGAAAATATT
102304	100391	CACAGAATGGGAGAAAATAT
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102306	100393	CCCACAGAATGGGAGAAAAT
102307	100394	GCCCACAGAATGGGAGAAAA
102308	100395	AGCCCACAGAATGGGAGAAA
102309	100396	CAGCCCACAGAATGGGAGAA
102310	100397	ACAGCCCACAGAATGGGAGA
102311	100398	GACAGCCCACAGAATGGGAG
102312	100399	AGACAGCCCACAGAATGGGA
102313	100400	GAGACAGCCCACAGAATGGG
102314	100401	AGAGACAGCCCACAGAATGG
102315	100402	AAGAGACAGCCCACAGAATG
102316	100403	GAAGAGACAGCCCACAGAAT
102317	100404	TGAAGAGACAGCCCACAGAA
102318	100405	GTGAAGAGACAGCCCACAGA
102319	100406	AGTGAAGAGACAGCCCACAG
102320	100407	AAGTGAAGAGACAGCCCACA
102321	100408	AAAGTGAAGAGACAGCCCAC
102322	100409	CAAAGTGAAGAGACAGCCCA
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102325	100412	CAACAAAGTGAAGAGACAGC
102326	100413	TCAACAAAGTGAAGAGACAG
102327	100414	ATCAACAAAGTGAAGAGACA
102328	100415	CATCAACAAAGTGAAGAGAC
102329	100416	CCATCAACAAAGTGAAGAGA
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102331	100418	AACCATCAACAAAGTGAAGA
102332	100419	AAACCATCAACAAAGTGAAG
102333	100420	GAAACCATCAACAAAGTGAA
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4043	2130	CCGGCCACAATGGAATGGAG
4044	2131	ACCGGCCACAATGGAATGGA
4045	2132	CACCGGCCACAATGGAATGG
4046	2133	ACACCGGCCACAATGGAATG
4047	2134	GACACCGGCCACAATGGAAT
4048	2135	GGACACCGGCCACAATGGAA
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4056	2143	GAAGTTAAGGACACCGGCCA
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4058	2145	CCGAAGTTAAGGACACCGGC
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4063	2150	CACTCCCGAAGTTAAGGACA
4064	2151	GCACTCCCGAAGTTAAGGAC
4065	2152	GGCACTCCCGAAGTTAAGGA
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4067	2154	GCGGCACTCCCGAAGTTAAG
4068	2155	GGCGGCACTCCCGAAGTTAA
4069	2156	TGGCGGCACTCCCGAAGTTA
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4074	2161	AGCTCTGGCGGCACTCCCGA
4075	2162	AAGCTCTGGCGGCACTCCCG
4076	2163	TAAGCTCTGGCGGCACTCCC
4077	2164	GTAAGCTCTGGCGGCACTCC
4078	2165	GGTAAGCTCTGGCGGCACTC
4079	2166	TGGTAAGCTCTGGCGGCACT
4080	2167	TTGGTAAGCTCTGGCGGCAC
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4082	2169	CCTTGGTAAGCTCTGGCGGC
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4084	2171	GCCCTTGGTAAGCTCTGGCG
4085	2172	TGCCCTTGGTAAGCTCTGGC
4086	2173	GTGCCCTTGGTAAGCTCTGG
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4095	2182	TGGACTTGCGTGCCCTTGGT
4096	2183	ATGGACTTGCGTGCCCTTGG
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4106	2193	CACAAGGGAAATGGACTTGC
4107	2194	GCACAAGGGAAATGGACTTG
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4109	2196	AGGCACAAGGGAAATGGACT
4110	2197	GAGGCACAAGGGAAATGGAC
4111	2198	TGAGGCACAAGGGAAATGGA

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53189	51276	CTGTATCTACTACAGAAACA
53190	51277	GCTGTATCTACTACAGAAAC
53191	51278	AGCTGTATCTACTACAGAAA
53192	51279	TAGCTGTATCTACTACAGAA
53193	51280	ATAGCTGTATCTACTACAGA
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53195	51282	TAATAGCTGTATCTACTACA
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53250	51337	GTCCTCACTTTAGCAAGTTT
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53252	51339	GTGTCCTCACTTTAGCAAGT
53253	51340	TGTGTCCTCACTTTAGCAAG
53254	51341	TTGTGTCCTCACTTTAGCAA
53255	51342	TTTGTGTCCTCACTTTAGCA
53256	51343	ATTTGTGTCCTCACTTTAGC
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102365	100452	ACATCAAGTTAAAAAGCTTC
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102372	100459	TGGGATCACATCAAGTTAAA
102373	100460	ATGGGATCACATCAAGTTAA
102374	100461	AATGGGATCACATCAAGTTA
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102376	100463	CAAATGGGATCACATCAAGT
102377	100464	ACAAATGGGATCACATCAAG
102378	100465	GACAAATGGGATCACATCAA
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102385	100472	AAAGATGGACAAATGGGATC
102386	100473	CAAAGATGGACAAATGGGAT
102387	100474	GCAAAGATGGACAAATGGGA
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102390	100477	AAAGCAAAGATGGACAAATG
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102402	100489	GTACAGGCAACCAAAGCAAA
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102404	100491	AAGTACAGGCAACCAAAGCA
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4124	2211	ACACGGATGGACTTGAGGCA
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4131	2218	GCCTACAACACGGATGGACT
4132	2219	TGCCTACAACACGGATGGAC
4133	2220	GTGCCTACAACACGGATGGA
4134	2221	AGTGCCTACAACACGGATGG
4135	2222	TAGTGCCTACAACACGGATG
4136	2223	GTAGTGCCTACAACACGGAT
4137	2224	AGTAGTGCCTACAACACGGA
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4139	2226	ACAGTAGTGCCTACAACACG
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4158	2245	GCCTAGGCCTAAAGAAGGCA
4159	2246	GGCCTAGGCCTAAAGAAGGC
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4163	2250	CGGCGGCCTAGGCCTAAAGA
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4165	2252	GCCGGCGGCCTAGGCCTAAA
4166	2253	AGCCGGCGGCCTAGGCCTAA
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53282	51369	AACATGAGTTAGAGTAGAAA
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53284	51371	AGAACATGAGTTAGAGTAGA
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53314	51401	CATAATTTATGTCACTGCAG
53315	51402	ACATAATTTATGTCACTGCA
53316	51403	CACATAATTTATGTCACTGC
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53318	51405	ACCACATAATTTATGTCACT
53319	51406	AACCACATAATTTATGTCAC
53320	51407	AAACCACATAATTTATGTCA
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102410	100497	CCCCAAAAGTACAGGCAACC
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102412	100499	TACCCCAAAAGTACAGGCAA
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102419	100506	TGAGTAATACCCCAAAAGTA
102420	100507	TTGAGTAATACCCCAAAAGT
102421	100508	CTTGAGTAATACCCCAAAAG
102422	100509	TCTTGAGTAATACCCCAAAA
102423	100510	TTCTTGAGTAATACCCCAAA
102424	100511	TTTCTTGAGTAATACCCCAA
102425	100512	ATTTCTTGAGTAATACCCCA
102426	100513	GATTTCTTGAGTAATACCCC
102427	100514	AGATTTCTTGAGTAATACCC
102428	100515	AAGATTTCTTGAGTAATACC
102429	100516	AAAGATTTCTTGAGTAATAC
102430	100517	CAAAGATTTCTTGAGTAATA
102431	100518	GCAAAGATTTCTTGAGTAAT
102432	100519	GGCAAAGATTTCTTGAGTAA
102433	100520	GGGCAAAGATTTCTTGAGTA
102434	100521	TGGGCAAAGATTTCTTGAGT
102435	100522	CTGGGCAAAGATTTCTTGAG
102436	100523	TCTGGGCAAAGATTTCTTGA
102437	100524	CTCTGGGCAAAGATTTCTTG
102438	100525	ACTCTGGGCAAAGATTTCTT
102439	100526	TACTCTGGGCAAAGATTTCT
102440	100527	TTACTCTGGGCAAAGATTTC
102441	100528	ATTACTCTGGGCAAAGATTT
102442	100529	CATTACTCTGGGCAAAGATT
102443	100530	ACATTACTCTGGGCAAAGAT
102444	100531	GACATTACTCTGGGCAAAGA
102445	100532	GGACATTACTCTGGGCAAAG
102446	100533	GGGACATTACTCTGGGCAAA
102447	100534	AGGGACATTACTCTGGGCAA
102448	100535	CAGGGACATTACTCTGGGCA
102449	100536	CCAGGGACATTACTCTGGGC
102450	100537	CCCAGGGACATTACTCTGGG
102451	100538	TCCCAGGGACATTACTCTGG
102452	100539	CTCCCAGGGACATTACTCTG
102453	100540	ACTCCCAGGGACATTACTCT
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102455	100542	AAACTCCCAGGGACATTACT
102456	100543	TAAACTCCCAGGGACATTAC
102457	100544	TTAAACTCCCAGGGACATTA
102458	100545	ATTAAACTCCCAGGGACATT
102459	100546	CATTAAACTCCCAGGGACAT
102460	100547	ACATTAAACTCCCAGGGACA
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4185	2272	CGCCGGTCACCCGCCGTCAA
4186	2273	ACGCCGGTCACCCGCCGTCA
4187	2274	GACGCCGGTCACCCGCCGTC
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4189	2276	AGGACGCCGGTCACCCGCCG
4190	2277	GAGGACGCCGGTCACCCGCC
4191	2278	GGAGGACGCCGGTCACCCGC
4192	2279	AGGAGGACGCCGGTCACCCG
4193	2280	AAGGAGGACGCCGGTCACCC
4194	2281	TAAGGAGGACGCCGGTCACC
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4196	2283	TTTAAGGAGGACGCCGGTCA
4197	2284	ATTTAAGGAGGACGCCGGTC
4198	2285	TATTTAAGGAGGACGCCGGT
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4200	2287	CCTATTTAAGGAGGACGCCG
4201	2288	GCCTATTTAAGGAGGACGCC
4202	2289	TGCCTATTTAAGGAGGACGC
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4205	2292	AGATGCCTATTTAAGGAGGA
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4208	2295	CCAAGATGCCTATTTAAGGA
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4211	2298	AGCCCAAGATGCCTATTTAA
4212	2299	AAGCCCAAGATGCCTATTTA
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4214	2301	CAAAGCCCAAGATGCCTATT
4215	2302	CCAAAGCCCAAGATGCCTAT
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4225	2312	ATTCCACCTTCCAAAGCCCA
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4228	2315	CTTATTCCACCTTCCAAAGC
4229	2316	TCTTATTCCACCTTCCAAAG
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4231	2318	CCTCTTATTCCACCTTCCAA
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4233	2320	ATCCTCTTATTCCACCTTCC
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4236	2323	AAAATCCTCTTATTCCACCT
4237	2324	AAAAATCCTCTTATTCCACC
4238	2325	GAAAAATCCTCTTATTCCAC
4239	2326	TGAAAAATCCTCTTATTCCA
4240	2327	ATGAAAAATCCTCTTATTCC
4241	2328	AATGAAAAATCCTCTTATTC
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4250	2337	ACTCGGGTGAATGAAAAATC
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53335	51422	GATAAACAACAAACCAAACC
53336	51423	AGATAAACAACAAACCAAAC
53337	51424	GAGATAAACAACAAACCAAA
53338	51425	TGAGATAAACAACAAACCAA
53339	51426	CTGAGATAAACAACAAACCA
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53343	51430	ACAACTGAGATAAACAACAA
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53347	51434	TATGACAACTGAGATAAACA
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53363	51450	AAACATTAATTCGACTTATG
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102481	100568	CTATGAAACTACTAAAAGAA
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102501	100588	TTTAAATCTAAGACCTCAAA
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102504	100591	AGATTTAAATCTAAGACCTC
102505	100592	AAGATTTAAATCTAAGACCT
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102508	100595	CTAAAGATTTAAATCTAAGA
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102513	100600	ATGGACTAAAGATTTAAATC
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102519	100606	ATCAAAATGGACTAAAGATT
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102544	100631	TCCCACCATATTAAAAAAAA
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102547	100634	GTGTCCCACCATATTAAAAA

4254	2341	GAAAACTCGGGTGAATGAAA
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4321	2408	GATGGGGAATTTCTGCTGTA
4322	2409	TGATGGGGAATTTCTGCTGT
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102562	100649	TGAAACCAGACCCCTGTGTC
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102605	100692	AATAAATGGTGCTGGGAAAA
102606	100693	CAATAAATGGTGCTGGGAAA
102607	100694	TCAATAAATGGTGCTGGGAA
102608	100695	TTCAATAAATGGTGCTGGGA
102609	100696	CTTCAATAAATGGTGCTGGG
102610	100697	TCTTCAATAAATGGTGCTGG
102611	100698	CTCTTCAATAAATGGTGCTG
102612	100699	TCTCTTCAATAAATGGTGCT
102613	100700	GTCTCTTCAATAAATGGTGC
102614	100701	AGTCTCTTCAATAAATGGTG
102615	100702	CAGTCTCTTCAATAAATGGT
102616	100703	ACAGTCTCTTCAATAAATGG
102617	100704	GACAGTCTCTTCAATAAATG
102618	100705	GGACAGTCTCTTCAATAAAT

4325	2412	TCTTGATGGGGAATTTCTGC
4326	2413	CTCTTGATGGGGAATTTCTG
4327	2414	CCTCTTGATGGGGAATTTCT
4328	2415	TCCTCTTGATGGGGAATTTC
4329	2416	TTCCTCTTGATGGGGAATTT
4330	2417	ATTCCTCTTGATGGGGAATT
4331	2418	GATTCCTCTTGATGGGGAAT
4332	2419	TGATTCCTCTTGATGGGGAA
4333	2420	CTGATTCCTCTTGATGGGGA
4334	2421	GCTGATTCCTCTTGATGGGG
4335	2422	AGCTGATTCCTCTTGATGGG
4336	2423	CAGCTGATTCCTCTTGATGG
4337	2424	CCAGCTGATTCCTCTTGATG
4338	2425	ACCAGCTGATTCCTCTTGAT
4339	2426	AACCAGCTGATTCCTCTTGA
4340	2427	AAACCAGCTGATTCCTCTTG
4341	2428	AAAACCAGCTGATTCCTCTT
4342	2429	AAAAACCAGCTGATTCCTCT
4343	2430	TAAAAACCAGCTGATTCCTC
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4346	2433	CCTTAAAAACCAGCTGATTC
4347	2434	TCCTTAAAAACCAGCTGATT
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4350	2437	AATTCCTTAAAAACCAGCTG
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4355	2442	AGCAGAATTCCTTAAAAACC
4356	2443	CAGCAGAATTCCTTAAAAAC
4357	2444	GCAGCAGAATTCCTTAAAAA
4358	2445	GGCAGCAGAATTCCTTAAAA
4359	2446	AGGCAGCAGAATTCCTTAAA
4360	2447	AAGGCAGCAGAATTCCTTAA
4361	2448	GAAGGCAGCAGAATTCCTTA
4362	2449	TGAAGGCAGCAGAATTCCTT
4363	2450	TTGAAGGCAGCAGAATTCCT
4364	2451	TTTGAAGGCAGCAGAATTCC
4365	2452	CTTTGAAGGCAGCAGAATTC
4366	2453	CCTTTGAAGGCAGCAGAATT
4367	2454	CCCTTTGAAGGCAGCAGAAT
4368	2455	CCCCTTTGAAGGCAGCAGAA
4369	2456	CCCCCTTTGAAGGCAGCAGA
4370	2457	GCCCCCTTTGAAGGCAGCAG
4371	2458	CGCCCCCTTTGAAGGCAGCA
4372	2459	CCGCCCCCTTTGAAGGCAGC
4373	2460	TCCGCCCCCTTTGAAGGCAG
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4376	2463	GTTTCCGCCCCCTTTGAAGG
4377	2464	TGTTTCCGCCCCCTTTGAAG
4378	2465	CTGTTTCCGCCCCCTTTGAA
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4380	2467	GACTGTTTCCGCCCCCTTTG
4381	2468	CGACTGTTTCCGCCCCCTTT
4382	2469	CCGACTGTTTCCGCCCCCTT
4383	2470	ACCGACTGTTTCCGCCCCCT
4384	2471	AACCGACTGTTTCCGCCCCC
4385	2472	TAACCGACTGTTTCCGCCCC
4386	2473	ATAACCGACTGTTTCCGCCC
4387	2474	AATAACCGACTGTTTCCGCC
4388	2475	AAATAACCGACTGTTTCCGC
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4392	2479	AGTCAAATAACCGACTGTTT
4393	2480	AAGTCAAATAACCGACTGTT
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4395	2482	TAAAGTCAAATAACCGACTG

53472	51559	AGCAAGATAACTGCTTGAAC
53473	51560	AAGCAAGATAACTGCTTGAA
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53475	51562	TGAAGCAAGATAACTGCTTG
53476	51563	CTGAAGCAAGATAACTGCTT
53477	51564	GCTGAAGCAAGATAACTGCT
53478	51565	GGCTGAAGCAAGATAACTGC
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53494	51581	TCCCAGTTATTAGGGAGGCT
53495	51582	ATCCCAGTTATTAGGGAGGC
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53512	51599	GGTGGTACGTGCCTGTAATC
53513	51600	TGGTGGTACGTGCCTGTAAT
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53515	51602	TGTGGTGGTACGTGCCTGTA
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53518	51605	GGGTGTGGTGGTACGTGCCT
53519	51606	CGGGTGTGGTGGTACGTGCC
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53522	51609	ACCCGGGTGTGGTGGTACGT
53523	51610	TACCCGGGTGTGGTGGTACG
53524	51611	TTACCCGGGTGTGGTGGTAC
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53527	51614	AAATTACCCGGGTGTGGTGG
53528	51615	AAAATTACCCGGGTGTGGTG
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53538	51625	TAAAAATACAAAAATTACCC
53539	51626	CTAAAAATACAAAAATTACC
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102621	100708	AAAGGACAGTCTCTTCAATA
102622	100709	GAAAGGACAGTCTCTTCAAT
102623	100710	GGAAAGGACAGTCTCTTCAA
102624	100711	GGGAAAGGACAGTCTCTTCA
102625	100712	GGGGAAAGGACAGTCTCTTC
102626	100713	TGGGGAAAGGACAGTCTCTT
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102630	100717	ACACTGGGGAAAGGACAGTC
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102633	100720	CATACACTGGGGAAAGGACA
102634	100721	ACATACACTGGGGAAAGGAC
102635	100722	AACATACACTGGGGAAAGGA
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102637	100724	TGAACATACACTGGGGAAAG
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102642	100729	AGCCATGAACATACACTGGG
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102645	100732	AGAAGCCATGAACATACACT
102646	100733	AAGAAGCCATGAACATACAC
102647	100734	AAAGAAGCCATGAACATACA
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102667	100754	TAAGTGAACTCATTTTCCAC
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102669	100756	TCTAAGTGAACTCATTTTCC
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102674	100761	ATACGTCTAAGTGAACTCAT
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102683	100770	AATGAATCCATACGTCTAAG
102684	100771	AAATGAATCCATACGTCTAA
102685	100772	GAAATGAATCCATACGTCTA
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102687	100774	CAGAAATGAATCCATACGTC
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4396	2483	GTAAAGTCAAATAACCGACT
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4398	2485	GTGTAAAGTCAAATAACCGA
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4400	2487	GCGTGTAAAGTCAAATAACC
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4418	2505	AGGGGAAGGGGGGGCGGGGC
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4437	2524	GATGCTTCAGACTCAGAGAA
4438	2525	GGATGCTTCAGACTCAGAGA
4439	2526	GGGATGCTTCAGACTCAGAG
4440	2527	TGGGATGCTTCAGACTCAGA
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4443	2530	GTTTGGGATGCTTCAGACTC
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4446	2533	AGTGTTTGGGATGCTTCAGA
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4463	2550	AACTAGTTTGGCTAAGTAGT
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53559	51646	ATGGTAAAACCCCATCTCTA
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53577	51664	GAAATCAGCCTGGCCAACAT
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53581	51668	GCTTGAAATCAGCCTGGCCA
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53583	51670	GAGCTTGAAATCAGCCTGGC
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53585	51672	AGGAGCTTGAAATCAGCCTG
53586	51673	CAGGAGCTTGAAATCAGCCT
53587	51674	TCAGGAGCTTGAAATCAGCC
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53589	51676	GGTCAGGAGCTTGAAATCAG
53590	51677	AGGTCAGGAGCTTGAAATCA
53591	51678	AAGGTCAGGAGCTTGAAATC
53592	51679	TAAGGTCAGGAGCTTGAAAT
53593	51680	CTAAGGTCAGGAGCTTGAAA
53594	51681	CCTAAGGTCAGGAGCTTGAA
53595	51682	ACCTAAGGTCAGGAGCTTGA
53596	51683	CACCTAAGGTCAGGAGCTTG
53597	51684	TCACCTAAGGTCAGGAGCTT
53598	51685	ATCACCTAAGGTCAGGAGCT
53599	51686	GATCACCTAAGGTCAGGAGC
53600	51687	GGATCACCTAAGGTCAGGAG
53601	51688	TGGATCACCTAAGGTCAGGA
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102690	100777	ACTCAGAAATGAATCCATAC
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102693	100780	AGAACTCAGAAATGAATCCA
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102697	100784	ACAGAGAACTCAGAAATGAA
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102705	100792	GAAACAGAACAGAGAACTCA
102706	100793	TGAAACAGAACAGAGAACTC
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102714	100801	TAGATCAATGAAACAGAACA
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102716	100803	TATAGATCAATGAAACAGAA
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102719	100806	AGATATAGATCAATGAAACA
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102746	100833	AAAATGGCATGGTACTGGCA
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4467	2554	TCTGAACTAGTTTGGCTAAG
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4481	2568	AAACGATCACTTCATCTGAA
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4485	2572	GGGGAAACGATCACTTCATC
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4487	2574	TTGGGGAAACGATCACTTCA
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4491	2578	CTACTTGGGGAAACGATCAC
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4494	2581	ACCCTACTTGGGGAAACGAT
4495	2582	TACCCTACTTGGGGAAACGA
4496	2583	TTACCCTACTTGGGGAAACG
4497	2584	GTTACCCTACTTGGGGAAAC
4498	2585	AGTTACCCTACTTGGGGAAA
4499	2586	AAGTTACCCTACTTGGGGAA
4500	2587	GAAGTTACCCTACTTGGGGA
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4502	2589	CTGAAGTTACCCTACTTGGG
4503	2590	ACTGAAGTTACCCTACTTGG
4504	2591	AACTGAAGTTACCCTACTTG
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4507	2594	GGAAACTGAAGTTACCCTAC
4508	2595	GGGAAACTGAAGTTACCCTA
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4510	2597	AAGGGAAACTGAAGTTACCC
4511	2598	AAAGGGAAACTGAAGTTACC
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4527	2614	GCTAGATGCCAACGAAAAAG
4528	2615	CGCTAGATGCCAACGAAAAA
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4531	2618	TTTCGCTAGATGCCAACGAA
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4533	2620	TTTTTCGCTAGATGCCAACG
4534	2621	ATTTTTCGCTAGATGCCAAC
4535	2622	CATTTTTCGCTAGATGCCAA
4536	2623	TCATTTTTCGCTAGATGCCA
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53615	51702	GAGGCCCAGGTGGGTGGATC
53616	51703	GGAGGCCCAGGTGGGTGGAT
53617	51704	GGGAGGCCCAGGTGGGTGGA
53618	51705	TGGGAGGCCCAGGTGGGTGG
53619	51706	TTGGGAGGCCCAGGTGGGTG
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53681	51768	CCTTTAACAACCATGGAACT
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102779	100866	GGAATCATTATCTGACTTCA
102780	100867	AGGAATCATTATCTGACTTC
102781	100868	GAGGAATCATTATCTGACTT
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102783	100870	GGGAGGAATCATTATCTGAC
102784	100871	CGGGAGGAATCATTATCTGA
102785	100872	ACGGGAGGAATCATTATCTG
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4545	2632	TAAATTTTTTCATTTTTCGC
4546	2633	TTAAATTTTTTCATTTTTCG
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53748	51835	CTTATATTGCTTGAGAATT
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4669	2756	TGCAACTTAATAACCTTAGT
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4671	2758	AATGCAACTTAATAACCTTA
4672	2759	CAATGCAACTTAATAACCTT
4673	2760	TCAATGCAACTTAATAACCT
4674	2761	GTCAATGCAACTTAATAACC
4675	2762	AGTCAATGCAACTTAATAAC
4676	2763	TAGTCAATGCAACTTAATAA
4677	2764	GTAGTCAATGCAACTTAATA
4678	2765	AGTAGTCAATGCAACTTAAT
4679	2766	TAGTAGTCAATGCAACTTAA

53756	51843	GTCTGCATCTTATATTGCTT
53757	51844	AGTCTGCATCTTATATTGCT
53758	51845	TAGTCTGCATCTTATATTGC
53759	51846	ATAGTCTGCATCTTATATTG
53760	51847	AATAGTCTGCATCTTATATT
53761	51848	TAATAGTCTGCATCTTATAT
53762	51849	ATAATAGTCTGCATCTTATA
53763	51850	CATAATAGTCTGCATCTTAT
53764	51851	ACATAATAGTCTGCATCTTA
53765	51852	AACATAATAGTCTGCATCTT
53766	51853	CAACATAATAGTCTGCATCT
53767	51854	ACAACATAATAGTCTGCATC
53768	51855	AACAACATAATAGTCTGCAT
53769	51856	GAACAACATAATAGTCTGCA
53770	51857	TGAACAACATAATAGTCTGC
53771	51858	TTGAACAACATAATAGTCTG
53772	51859	CTTGAACAACATAATAGTCT
53773	51860	ACTTGAACAACATAATAGTC
53774	51861	AACTTGAACAACATAATAGT
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53776	51863	AAAACTTGAACAACATAATA
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53778	51865	AAAAAACTTGAACAACATAA
53779	51866	AAAAAAACTTGAACAACATA
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53781	51868	AAAAAAAAACTTGAACAACA
53782	51869	AAAAAAAAAACTTGAACAAC
53783	51870	AAAAAAAAAAACTTGAACAA
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53785	51872	AAAAAAAAAAAAACTTGAAC
53786	51873	AAAAAAAAAAAAAACTTGAA
53787	51874	AAAAAAAAAAAAAAACTTGA
53788	51875	AAAAAAAAAAAAAAAACTTG
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53790	51877	AAAAAAAAAAAAAAAAAACT
53791	51878	TAAAAAAAAAAAAAAAAAAC
53792	51879	TTAAAAAAAAAAAAAAAAAA
53793	51880	ATTAAAAAAAAAAAAAAAAA
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53796	51883	AAGATTAAAAAAAAAAAAAA
53797	51884	AAAGATTAAAAAAAAAAAAA
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53801	51888	AGCCAAAGATTAAAAAAAAA
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53805	51892	ATAAAGCCAAAGATTAAAAA
53806	51893	AATAAAGCCAAAGATTAAAA
53807	51894	AAATAAAGCCAAAGATTAAA
53808	51895	AAAATAAAGCCAAAGATTAA
53809	51896	AAAAATAAAGCCAAAGATTA
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53812	51899	CCCAAAAATAAAGCCAAAGA
53813	51900	CCCCAAAAATAAAGCCAAAG
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53821	51908	AAAGGTTTCCCCAAAAATAA
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53824	51911	AAAAAAGGTTTCCCCAAAAA
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102906	100993	GCAATCCCTATCAAAATACC
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102908	100995	GTGCAATCCCTATCAAAATA
102909	100996	AGTGCAATCCCTATCAAAAT
102910	100997	CAGTGCAATCCCTATCAAAA
102911	100998	TCAGTGCAATCCCTATCAAA
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102920	101007	TCTACAGATTCAGTGCAATC
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102922	101009	AATCTACAGATTCAGTGCAA
102923	101010	CAATCTACAGATTCAGTGCA
102924	101011	GCAATCTACAGATTCAGTGC
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102926	101013	AAGCAATCTACAGATTCAGT
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102929	101016	TCAAAGCAATCTACAGATTC
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4683	2770	AGCCTAGTAGTCAATGCAAC
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4725	2812	TCAAACTACTCAGGAGCAAA
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4807	2894	ATTAACCTTAAATTGTTGTA
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53922	52009	ACCCAGAAGGCGGAGGTTGC
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53931	52018	ATCGCTTGAACCCAGAAGGC
53932	52019	AATCGCTTGAACCCAGAAGG
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53934	52021	AGAATCGCTTGAACCCAGAA
53935	52022	GAGAATCGCTTGAACCCAGA
53936	52023	GGAGAATCGCTTGAACCCAG
53937	52024	AGGAGAATCGCTTGAACCCA
53938	52025	TAGGAGAATCGCTTGAACCC
53939	52026	ATAGGAGAATCGCTTGAACC
53940	52027	GATAGGAGAATCGCTTGAAC
53941	52028	AGATAGGAGAATCGCTTGAA
53942	52029	GAGATAGGAGAATCGCTTGA
53943	52030	TGAGATAGGAGAATCGCTTG
53944	52031	CTGAGATAGGAGAATCGCTT
53945	52032	GCTGAGATAGGAGAATCGCT
53946	52033	GGCTGAGATAGGAGAATCGC
53947	52034	AGGCTGAGATAGGAGAATCG
53948	52035	GAGGCTGAGATAGGAGAATC
53949	52036	GGAGGCTGAGATAGGAGAAT
53950	52037	GGGAGGCTGAGATAGGAGAA
53951	52038	CGGGAGGCTGAGATAGGAGA
53952	52039	TCGGGAGGCTGAGATAGGAG
53953	52040	CTCGGGAGGCTGAGATAGGA
53954	52041	ACTCGGGAGGCTGAGATAGG
53955	52042	TACTCGGGAGGCTGAGATAG
53956	52043	CTACTCGGGAGGCTGAGATA
53957	52044	GCTACTCGGGAGGCTGAGAT
53958	52045	AGCTACTCGGGAGGCTGAGA
53959	52046	CAGCTACTCGGGAGGCTGAG
53960	52047	CCAGCTACTCGGGAGGCTGA
53961	52048	CCCAGCTACTCGGGAGGCTG
53962	52049	TCCCAGCTACTCGGGAGGCT
53963	52050	ATCCCAGCTACTCGGGAGGC
53964	52051	AATCCCAGCTACTCGGGAGG
53965	52052	TAATCCCAGCTACTCGGGAG
53966	52053	GTAATCCCAGCTACTCGGGA
53967	52054	TGTAATCCCAGCTACTCGGG
53968	52055	CTGTAATCCCAGCTACTCGG

103045	101132	AAGATTTCTATAATGACAAC
103046	101133	AAAGATTTCTATAATGACAA
103047	101134	AAAAGATTTCTATAATGACA
103048	101135	TAAAAGATTTCTATAATGAC
103049	101136	GTAAAAGATTTCTATAATGA
103050	101137	AGTAAAAGATTTCTATAATG
103051	101138	GAGTAAAAGATTTCTATAAT
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103053	101140	ATGAGTAAAAGATTTCTATA
103054	101141	AATGAGTAAAAGATTTCTAT
103055	101142	AAATGAGTAAAAGATTTCTA
103056	101143	CAAATGAGTAAAAGATTTCT
103057	101144	CCAAATGAGTAAAAGATTTC
103058	101145	ACCAAATGAGTAAAAGATTT
103059	101146	AACCAAATGAGTAAAAGATT
103060	101147	TAACCAAATGAGTAAAAGAT
103061	101148	TTAACCAAATGAGTAAAAGA
103062	101149	CTTAACCAAATGAGTAAAAG
103063	101150	ACTTAACCAAATGAGTAAAA
103064	101151	AACTTAACCAAATGAGTAAA
103065	101152	AAACTTAACCAAATGAGTAA
103066	101153	TAAACTTAACCAAATGAGTA
103067	101154	ATAAACTTAACCAAATGAGT
103068	101155	AATAAACTTAACCAAATGAG
103069	101156	GAATAAACTTAACCAAATGA
103070	101157	GGAATAAACTTAACCAAATG
103071	101158	AGGAATAAACTTAACCAAAT
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103075	101162	ACTTAGGAATAAACTTAACC
103076	101163	TACTTAGGAATAAACTTAAC
103077	101164	ATACTTAGGAATAAACTTAA
103078	101165	AATACTTAGGAATAAACTTA
103079	101166	AAATACTTAGGAATAAACTT
103080	101167	AAAATACTTAGGAATAAACT
103081	101168	TAAAATACTTAGGAATAAAC
103082	101169	ATAAAATACTTAGGAATAAA
103083	101170	AATAAAATACTTAGGAATAA
103084	101171	TAATAAAATACTTAGGAATA
103085	101172	ATAATAAAATACTTAGGAAT
103086	101173	TATAATAAAATACTTAGGAA
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103088	101175	AATATAATAAAATACTTAGG
103089	101176	AAATATAATAAAATACTTAG
103090	101177	CAAATATAATAAAATACTTA
103091	101178	ACAAATATAATAAAATACTT
103092	101179	TACAAATATAATAAAATACT
103093	101180	CTACAAATATAATAAAATAC
103094	101181	GCTACAAATATAATAAAATA
103095	101182	AGCTACAAATATAATAAAAT
103096	101183	TAGCTACAAATATAATAAAA
103097	101184	ATAGCTACAAATATAATAAA
103098	101185	AATAGCTACAAATATAATAA
103099	101186	CAATAGCTACAAATATAATA
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103102	101189	TTACAATAGCTACAAATATA
103103	101190	TTTACAATAGCTACAAATAT
103104	101191	ATTTACAATAGCTACAAATA
103105	101192	CATTTACAATAGCTACAAAT
103106	101193	CCATTTACAATAGCTACAAA
103107	101194	CCCATTTACAATAGCTACAA
103108	101195	TCCCATTTACAATAGCTACA
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103113	101200	CGCAATCCCATTTACAATAG
103114	101201	ACGCAATCCCATTTACAATA
103115	101202	AACGCAATCCCATTTACAAT

4822	2909	CAAGGAAAAATCTAAATTAA
4823	2910	GCAAGGAAAAATCTAAATTA
4824	2911	AGCAAGGAAAAATCTAAATT
4825	2912	AAGCAAGGAAAAATCTAAAT
4826	2913	AAAGCAAGGAAAAATCTAAA
4827	2914	TAAAGCAAGGAAAAATCTAA
4828	2915	TTAAAGCAAGGAAAAATCTA
4829	2916	CTTAAAGCAAGGAAAAATCT
4830	2917	ACTTAAAGCAAGGAAAAATC
4831	2918	AACTTAAAGCAAGGAAAAAT
4832	2919	GAACTTAAAGCAAGGAAAAA
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4840	2927	AAGTAAAAGAACTTAAAGCA
4841	2928	CAAGTAAAAGAACTTAAAGC
4842	2929	TCAAGTAAAAGAACTTAAAG
4843	2930	CTCAAGTAAAAGAACTTAAA
4844	2931	TCTCAAGTAAAAGAACTTAA
4845	2932	GTCTCAAGTAAAAGAACTTA
4846	2933	GGTCTCAAGTAAAAGAACTT
4847	2934	AGGTCTCAAGTAAAAGAACT
4848	2935	TAGGTCTCAAGTAAAAGAAC
4849	2936	TTAGGTCTCAAGTAAAAGAA
4850	2937	TTTAGGTCTCAAGTAAAAGA
4851	2938	ATTTAGGTCTCAAGTAAAAG
4852	2939	CATTTAGGTCTCAAGTAAAA
4853	2940	CCATTTAGGTCTCAAGTAAA
4854	2941	GCCATTTAGGTCTCAAGTAA
4855	2942	TGCCATTTAGGTCTCAAGTA
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4858	2945	GGCTGCCATTTAGGTCTCAA
4859	2946	GGGCTGCCATTTAGGTCTCA
4860	2947	AGGGCTGCCATTTAGGTCTC
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4864	2951	AATAAGGGCTGCCATTTAGG
4865	2952	GAATAAGGGCTGCCATTTAG
4866	2953	AGAATAAGGGCTGCCATTTA
4867	2954	AAGAATAAGGGCTGCCATTT
4868	2955	AAAGAATAAGGGCTGCCATT
4869	2956	GAAAGAATAAGGGCTGCCAT
4870	2957	AGAAAGAATAAGGGCTGCCA
4871	2958	CAGAAAGAATAAGGGCTGCC
4872	2959	TCAGAAAGAATAAGGGCTGC
4873	2960	ATCAGAAAGAATAAGGGCTG
4874	2961	CATCAGAAAGAATAAGGGCT
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4881	2968	ACCTATTCATCAGAAAGAAT
4882	2969	CACCTATTCATCAGAAAGAA
4883	2970	TCACCTATTCATCAGAAAGA
4884	2971	TTCACCTATTCATCAGAAAG
4885	2972	TTTCACCTATTCATCAGAAA
4886	2973	ATTTCACCTATTCATCAGAA
4887	2974	AATTTCACCTATTCATCAGA
4888	2975	AAATTTCACCTATTCATCAG
4889	2976	AAAATTTCACCTATTCATCA
4890	2977	CAAAATTTCACCTATTCATC
4891	2978	ACAAAATTTCACCTATTCAT
4892	2979	AACAAAATTTCACCTATTCA

53969	52056	CCTGTAATCCCAGCTACTCG
53970	52057	GCCTGTAATCCCAGCTACTC
53971	52058	TGCCTGTAATCCCAGCTACT
53972	52059	ATGCCTGTAATCCCAGCTAC
53973	52060	CATGCCTGTAATCCCAGCTA
53974	52061	ACATGCCTGTAATCCCAGCT
53975	52062	CACATGCCTGTAATCCCAGC
53976	52063	GCACATGCCTGTAATCCCAG
53977	52064	GGCACATGCCTGTAATCCCA
53978	52065	TGGCACATGCCTGTAATCCC
53979	52066	GTGGCACATGCCTGTAATCC
53980	52067	GGTGGCACATGCCTGTAATC
53981	52068	TGGTGGCACATGCCTGTAAT
53982	52069	ATGGTGGCACATGCCTGTAA
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53989	52076	GCCGGGCATGGTGGCACATG
53990	52077	AGCCGGGCATGGTGGCACAT
53991	52078	TAGCCGGGCATGGTGGCACA
53992	52079	TTAGCCGGGCATGGTGGCAC
53993	52080	GTTAGCCGGGCATGGTGGCA
53994	52081	AGTTAGCCGGGCATGGTGGC
53995	52082	AAGTTAGCCGGGCATGGTGG
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54001	52088	AATACAAAGTTAGCCGGGCA
54002	52089	AAATACAAAGTTAGCCGGGC
54003	52090	AAAATACAAAGTTAGCCGGG
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54005	52092	TAAAAATACAAAGTTAGCCG
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54011	52098	CTCTACTAAAAATACAAAGT
54012	52099	TCTCTACTAAAAATACAAAG
54013	52100	GTCTCTACTAAAAATACAAA
54014	52101	AGTCTCTACTAAAAATACAA
54015	52102	CAGTCTCTACTAAAAATACA
54016	52103	CCAGTCTCTACTAAAAATAC
54017	52104	CCCAGTCTCTACTAAAAATA
54018	52105	ACCCAGTCTCTACTAAAAAT
54019	52106	AACCCAGTCTCTACTAAAAA
54020	52107	AAACCCAGTCTCTACTAAAA
54021	52108	GAAACCCAGTCTCTACTAAA
54022	52109	AGAAACCCAGTCTCTACTAA
54023	52110	GAGAAACCCAGTCTCTACTA
54024	52111	GGAGAAACCCAGTCTCTACT
54025	52112	TGGAGAAACCCAGTCTCTAC
54026	52113	GTGGAGAAACCCAGTCTCTA
54027	52114	CGTGGAGAAACCCAGTCTCT
54028	52115	ACGTGGAGAAACCCAGTCTC
54029	52116	AACGTGGAGAAACCCAGTCT
54030	52117	CAACGTGGAGAAACCCAGTC
54031	52118	CCAACGTGGAGAAACCCAGT
54032	52119	ACCAACGTGGAGAAACCCAG
54033	52120	GACCAACGTGGAGAAACCCA
54034	52121	TGACCAACGTGGAGAAACCC
54035	52122	CTGACCAACGTGGAGAAACC
54036	52123	CCTGACCAACGTGGAGAAAC
54037	52124	GCCTGACCAACGTGGAGAAA
54038	52125	AGCCTGACCAACGTGGAGAA
54039	52126	CAGCCTGACCAACGTGGAGA

103116	101203	AAACGCAATCCCATTTACAA
103117	101204	TAAACGCAATCCCATTTACA
103118	101205	TTAAACGCAATCCCATTTAC
103119	101206	TTTAAACGCAATCCCATTTA
103120	101207	TTTTAAACGCAATCCCATTT
103121	101208	TTTTTAAACGCAATCCCATT
103122	101209	TTTTTTAAACGCAATCCCAT
103123	101210	ATTTTTTAAACGCAATCCCA
103124	101211	AATTTTTTAAACGCAATCCC
103125	101212	AAATTTTTTAAACGCAATCC
103126	101213	AAAATTTTTTAAACGCAATC
103127	101214	AAAAATTTTTTAAACGCAAT
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103131	101218	TCTGAAAAATTTTTTAAACG
103132	101219	ATCTGAAAAATTTTTTAAAC
103133	101220	AATCTGAAAAATTTTTTAAA
103134	101221	CAATCTGAAAAATTTTTTAA
103135	101222	ACAATCTGAAAAATTTTTTA
103136	101223	AACAATCTGAAAAATTTTTT
103137	101224	AAACAATCTGAAAAATTTTT
103138	101225	CAAACAATCTGAAAAATTTT
103139	101226	GCAAACAATCTGAAAAATTT
103140	101227	AGCAAACAATCTGAAAAATT
103141	101228	CAGCAAACAATCTGAAAAAT
103142	101229	ACAGCAAACAATCTGAAAAA
103143	101230	AACAGCAAACAATCTGAAAA
103144	101231	TAACAGCAAACAATCTGAAA
103145	101232	TTAACAGCAAACAATCTGAA
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103147	101234	ATTTAACAGCAAACAATCTG
103148	101235	TATTTAACAGCAAACAATCT
103149	101236	ATATTTAACAGCAAACAATC
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103152	101239	TTTATATTTAACAGCAAACA
103153	101240	TTTTATATTTAACAGCAAAC
103154	101241	TTTTTATATTTAACAGCAAA
103155	101242	ATTTTTATATTTAACAGCAA
103156	101243	CATTTTTATATTTAACAGCA
103157	101244	GCATTTTTATATTTAACAGC
103158	101245	AGCATTTTTATATTTAACAG
103159	101246	GAGCATTTTTATATTTAACA
103160	101247	GGAGCATTTTTATATTTAAC
103161	101248	AGGAGCATTTTTATATTTAA
103162	101249	CAGGAGCATTTTTATATTTA
103163	101250	TCAGGAGCATTTTTATATTT
103164	101251	ATCAGGAGCATTTTTATATT
103165	101252	AATCAGGAGCATTTTTATAT
103166	101253	AAATCAGGAGCATTTTTATA
103167	101254	AAAATCAGGAGCATTTTTAT
103168	101255	AAAAATCAGGAGCATTTTTA
103169	101256	CAAAAATCAGGAGCATTTTT
103170	101257	ACAAAAATCAGGAGCATTTT
103171	101258	CACAAAAATCAGGAGCATTT
103172	101259	ACACAAAAATCAGGAGCATT
103173	101260	CACACAAAAATCAGGAGCAT
103174	101261	ACACACAAAAATCAGGAGCA
103175	101262	AACACACAAAAATCAGGAGC
103176	101263	CAACACACAAAAATCAGGAG
103177	101264	TCAACACACAAAAATCAGGA
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103180	101267	AAATCAACACACAAAAATCA
103181	101268	AAAATCAACACACAAAAATC
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103183	101270	CAAAAATCAACACACAAAAA
103184	101271	ACAAAAATCAACACACAAAA
103185	101272	TACAAAAATCAACACACAAA
103186	101273	ATACAAAAATCAACACACAA

4893	2980	AAACAAAATTTCACCTATTC
4894	2981	TAAACAAAATTTCACCTATT
4895	2982	GTAAACAAAATTTCACCTAT
4896	2983	AGTAAACAAAATTTCACCTA
4897	2984	CAGTAAACAAAATTTCACCT
4898	2985	ACAGTAAACAAAATTTCACC
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4900	2987	ACACAGTAAACAAAATTTCA
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4902	2989	CAACACAGTAAACAAAATTT
4903	2990	CCAACACAGTAAACAAAATT
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4906	2993	AATCCAACACAGTAAACAAA
4907	2994	AAATCCAACACAGTAAACAA
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4911	2998	ACACAAATCCAACACAGTAA
4912	2999	TACACAAATCCAACACAGTA
4913	3000	TTACACAAATCCAACACAGT
4914	3001	ATTACACAAATCCAACACAG
4915	3002	CATTACACAAATCCAACACA
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4917	3004	CACATTACACAAATCCAACA
4918	3005	TCACATTACACAAATCCAAC
4919	3006	TTCACATTACACAAATCCAA
4920	3007	CTTCACATTACACAAATCCA
4921	3008	ACTTCACATTACACAAATCC
4922	3009	AACTTCACATTACACAAATC
4923	3010	AAACTTCACATTACACAAAT
4924	3011	AAAACTTCACATTACACAAA
4925	3012	TAAAACTTCACATTACACAA
4926	3013	ATAAAACTTCACATTACACA
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4932	3019	TCAAGAATAAAACTTCACAT
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4935	3022	TGTTCAAGAATAAAACTTCA
4936	3023	CTGTTCAAGAATAAAACTTC
4937	3024	TCTGTTCAAGAATAAAACTT
4938	3025	ATCTGTTCAAGAATAAAACT
4939	3026	GATCTGTTCAAGAATAAAAC
4940	3027	CGATCTGTTCAAGAATAAAA
4941	3028	ACGATCTGTTCAAGAATAAA
4942	3029	AACGATCTGTTCAAGAATAA
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4953	3040	ACAAGTACATTAACGATCTG
4954	3041	TACAAGTACATTAACGATCT
4955	3042	CTACAAGTACATTAACGATC
4956	3043	TCTACAAGTACATTAACGAT
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4958	3045	ATTCTACAAGTACATTAACG
4959	3046	AATTCTACAAGTACATTAAC
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4961	3048	GTAATTCTACAAGTACATTA
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54040	52127	CCAGCCTGACCAACGTGGAG
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54054	52141	TCAGGAGTTCAAGACCAGCC
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54056	52143	GGTCAGGAGTTCAAGACCAG
54057	52144	AGGTCAGGAGTTCAAGACCA
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54059	52146	TGAGGTCAGGAGTTCAAGAC
54060	52147	CTGAGGTCAGGAGTTCAAGA
54061	52148	CCTGAGGTCAGGAGTTCAAG
54062	52149	ACCTGAGGTCAGGAGTTCAA
54063	52150	CACCTGAGGTCAGGAGTTCA
54064	52151	TCACCTGAGGTCAGGAGTTC
54065	52152	ATCACCTGAGGTCAGGAGTT
54066	52153	GATCACCTGAGGTCAGGAGT
54067	52154	GGATCACCTGAGGTCAGGAG
54068	52155	TGGATCACCTGAGGTCAGGA
54069	52156	GTGGATCACCTGAGGTCAGG
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54074	52161	GGCAGGTGGATCACCTGAGG
54075	52162	AGGCAGGTGGATCACCTGAG
54076	52163	TAGGCAGGTGGATCACCTGA
54077	52164	CTAGGCAGGTGGATCACCTG
54078	52165	CCTAGGCAGGTGGATCACCT
54079	52166	GCCTAGGCAGGTGGATCACC
54080	52167	GGCCTAGGCAGGTGGATCAC
54081	52168	AGGCCTAGGCAGGTGGATCA
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54083	52170	GGAGGCCTAGGCAGGTGGAT
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54085	52172	TGGGAGGCCTAGGCAGGTGG
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54090	52177	CACTTTGGGAGGCCTAGGCA
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54093	52180	CAGCACTTTGGGAGGCCTAG
54094	52181	CCAGCACTTTGGGAGGCCTA
54095	52182	CCCAGCACTTTGGGAGGCCT
54096	52183	TCCCAGCACTTTGGGAGGCC
54097	52184	ATCCCAGCACTTTGGGAGGC
54098	52185	GATCCCAGCACTTTGGGAGG
54099	52186	TGATCCCAGCACTTTGGGAG
54100	52187	GTGATCCCAGCACTTTGGGA
54101	52188	TGTGATCCCAGCACTTTGGG
54102	52189	TTGTGATCCCAGCACTTTGG
54103	52190	CTTGTGATCCCAGCACTTTG
54104	52191	GCTTGTGATCCCAGCACTTT
54105	52192	CGCTTGTGATCCCAGCACTT
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54107	52194	CACGCTTGTGATCCCAGCAC
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103187	101274	GATACAAAAATCAACACACA
103188	101275	GGATACAAAAATCAACACAC
103189	101276	AGGATACAAAAATCAACACA
103190	101277	CAGGATACAAAAATCAACAC
103191	101278	GCAGGATACAAAAATCAACA
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103194	101281	ATTGCAGGATACAAAAATCA
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103197	101284	AAAATTGCAGGATACAAAAA
103198	101285	TAAAATTGCAGGATACAAAA
103199	101286	GTAAAATTGCAGGATACAAA
103200	101287	AGTAAAATTGCAGGATACAA
103201	101288	CAGTAAAATTGCAGGATACA
103202	101289	TCAGTAAAATTGCAGGATAC
103203	101290	TTCAGTAAAATTGCAGGATA
103204	101291	ATTCAGTAAAATTGCAGGAT
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103206	101293	AAATTCAGTAAAATTGCAGG
103207	101294	CAAATTCAGTAAAATTGCAG
103208	101295	ACAAATTCAGTAAAATTGCA
103209	101296	AACAAATTCAGTAAAATTGC
103210	101297	AAACAAATTCAGTAAAATTG
103211	101298	CAAACAAATTCAGTAAAATT
103212	101299	ACAAACAAATTCAGTAAAAT
103213	101300	GACAAACAAATTCAGTAAAA
103214	101301	TGACAAACAAATTCAGTAAA
103215	101302	CTGACAAACAAATTCAGTAA
103216	101303	ACTGACAAACAAATTCAGTA
103217	101304	AACTGACAAACAAATTCAGT
103218	101305	GAACTGACAAACAAATTCAG
103219	101306	AGAACTGACAAACAAATTCA
103220	101307	TAGAACTGACAAACAAATTC
103221	101308	TTAGAACTGACAAACAAATT
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103225	101312	CCTATTAGAACTGACAAACA
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103227	101314	AACCTATTAGAACTGACAAA
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103229	101316	AAAACCTATTAGAACTGACA
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103254	101341	GGAAAAACCTAGACTCCAAA
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4967	3054	TTCAAAGTAATTCTACAAGT
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4970	3057	AAATTCAAAGTAATTCTACA
4971	3058	CAAATTCAAAGTAATTCTAC
4972	3059	TCAAATTCAAAGTAATTCTA
4973	3060	TTCAAATTCAAAGTAATTCT
4974	3061	ATTCAAATTCAAAGTAATTC
4975	3062	GATTCAAATTCAAAGTAATT
4976	3063	TGATTCAAATTCAAAGTAAT
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4979	3066	AAGTGATTCAAATTCAAAGT
4980	3067	AAAGTGATTCAAATTCAAAG
4981	3068	GAAAGTGATTCAAATTCAAA
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4983	3070	AGGAAAGTGATTCAAATTCA
4984	3071	CAGGAAAGTGATTCAAATTC
4985	3072	GCAGGAAAGTGATTCAAATT
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5005	3092	GAAACTTATTTACAAGGAAT
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5015	3102	TCTAGAAGCTGAAACTTATT
5016	3103	TTCTAGAAGCTGAAACTTAT
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5031	3118	ACCTAAGTGAGGAGATTCTA
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54115	52202	CGGTGGCTCACGCTTGTGAT
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54119	52206	GGCGCGGTGGCTCACGCTTG
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54123	52210	GCTGGGCGCGGTGGCTCACG
54124	52211	GGCTGGGCGCGGTGGCTCAC
54125	52212	TGGCTGGGCGCGGTGGCTCA
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54144	52231	CTCAAAATAAAGGTTTCCCT
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54147	52234	CGCCTCAAAATAAAGGTTTC
54148	52235	CCGCCTCAAAATAAAGGTTT
54149	52236	TCCGCCTCAAAATAAAGGTT
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54151	52238	ACTCCGCCTCAAAATAAAGG
54152	52239	GACTCCGCCTCAAAATAAAG
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103286	101373	TCCTTGTTTGCAGATAATAT
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103305	101392	AATGGAAGAAGTCAAATTAT
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103346	101433	GCAATCAGACAACAGAAAGA
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103354	101441	TAATTGGAGCAATCAGACAA
103355	101442	CTAATTGGAGCAATCAGACA
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103386	101473	CCATTGTTATTCAACATAAT
103387	101474	ACCATTGTTATTCAACATAA
103388	101475	CACCATTGTTATTCAACATA
103389	101476	TCACCATTGTTATTCAACAT
103390	101477	TTCACCATTGTTATTCAACA
103391	101478	TTTCACCATTGTTATTCAAC
103392	101479	CTTTCACCATTGTTATTCAA
103393	101480	ACTTTCACCATTGTTATTCA
103394	101481	CACTTTCACCATTGTTATTC
103395	101482	CCACTTTCACCATTGTTATT
103396	101483	CCCACTTTCACCATTGTTAT
103397	101484	GCCCACTTTCACCATTGTTA
103398	101485	TGCCCACTTTCACCATTGTT
103399	101486	ATGCCCACTTTCACCATTGT

5106	3193	AACTTGTCAAACCGAATGCT
5107	3194	AAACTTGTCAAACCGAATGC
5108	3195	GAAACTTGTCAAACCGAATG
5109	3196	CGAAACTTGTCAAACCGAAT
5110	3197	TCGAAACTTGTCAAACCGAA
5111	3198	CTCGAAACTTGTCAAACCGA
5112	3199	TCTCGAAACTTGTCAAACCG
5113	3200	ATCTCGAAACTTGTCAAACC
5114	3201	TATCTCGAAACTTGTCAAAC
5115	3202	CTATCTCGAAACTTGTCAAA
5116	3203	GCTATCTCGAAACTTGTCAA
5117	3204	TGCTATCTCGAAACTTGTCA
5118	3205	TTGCTATCTCGAAACTTGTC
5119	3206	TTTGCTATCTCGAAACTTGT
5120	3207	TTTTGCTATCTCGAAACTTG
5121	3208	ATTTTGCTATCTCGAAACTT
5122	3209	TATTTTGCTATCTCGAAACT
5123	3210	ATATTTTGCTATCTCGAAAC
5124	3211	CATATTTTGCTATCTCGAAA
5125	3212	GCATATTTTGCTATCTCGAA
5126	3213	AGCATATTTTGCTATCTCGA
5127	3214	AAGCATATTTTGCTATCTCG
5128	3215	CAAGCATATTTTGCTATCTC
5129	3216	TCAAGCATATTTTGCTATCT
5130	3217	TTCAAGCATATTTTGCTATC
5131	3218	TTTCAAGCATATTTTGCTAT
5132	3219	CTTTCAAGCATATTTTGCTA
5133	3220	ACTTTCAAGCATATTTTGCT
5134	3221	GACTTTCAAGCATATTTTGC
5135	3222	AGACTTTCAAGCATATTTTG
5136	3223	CAGACTTTCAAGCATATTTT
5137	3224	CCAGACTTTCAAGCATATTT
5138	3225	TCCAGACTTTCAAGCATATT
5139	3226	TTCCAGACTTTCAAGCATAT
5140	3227	TTTCCAGACTTTCAAGCATA
5141	3228	ATTTCCAGACTTTCAAGCAT
5142	3229	AATTTCCAGACTTTCAAGCA
5143	3230	GAATTTCCAGACTTTCAAGC
5144	3231	TGAATTTCCAGACTTTCAAG
5145	3232	GTGAATTTCCAGACTTTCAA
5146	3233	TGTGAATTTCCAGACTTTCA
5147	3234	ATGTGAATTTCCAGACTTTC
5148	3235	GATGTGAATTTCCAGACTTT
5149	3236	AGATGTGAATTTCCAGACTT
5150	3237	CAGATGTGAATTTCCAGACT
5151	3238	GCAGATGTGAATTTCCAGAC
5152	3239	AGCAGATGTGAATTTCCAGA
5153	3240	AAGCAGATGTGAATTTCCAG
5154	3241	AAAGCAGATGTGAATTTCCA
5155	3242	TAAAGCAGATGTGAATTTCC
5156	3243	TTAAAGCAGATGTGAATTTC
5157	3244	CTTAAAGCAGATGTGAATTT
5158	3245	TCTTAAAGCAGATGTGAATT
5159	3246	TTCTTAAAGCAGATGTGAAT
5160	3247	TTTCTTAAAGCAGATGTGAA
5161	3248	GTTTCTTAAAGCAGATGTGA
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5163	3250	ATGTTTCTTAAAGCAGATGT
5164	3251	AATGTTTCTTAAAGCAGATG
5165	3252	AAATGTTTCTTAAAGCAGAT
5166	3253	GAAATGTTTCTTAAAGCAGA
5167	3254	TGAAATGTTTCTTAAAGCAG
5168	3255	ATGAAATGTTTCTTAAAGCA
5169	3256	TATGAAATGTTTCTTAAAGC
5170	3257	TTATGAAATGTTTCTTAAAG
5171	3258	ATTATGAAATGTTTCTTAAA
5172	3259	AATTATGAAATGTTTCTTAA
5173	3260	AAATTATGAAATGTTTCTTA
5174	3261	CAAATTATGAAATGTTTCTT
5175	3262	TCAAATTATGAAATGTTTCT
5176	3263	GTCAAATTATGAAATGTTTC

54253	52340	TCCTCGGGAGGCTTAGGCAG
54254	52341	CTCCTCGGGAGGCTTAGGCA
54255	52342	GCTCCTCGGGAGGCTTAGGC
54256	52343	AGCTCCTCGGGAGGCTTAGG
54257	52344	CAGCTCCTCGGGAGGCTTAG
54258	52345	CCAGCTCCTCGGGAGGCTTA
54259	52346	CCCAGCTCCTCGGGAGGCTT
54260	52347	TCCCAGCTCCTCGGGAGGCT
54261	52348	ATCCCAGCTCCTCGGGAGGC
54262	52349	AATCCCAGCTCCTCGGGAGG
54263	52350	TAATCCCAGCTCCTCGGGAG
54264	52351	ATAATCCCAGCTCCTCGGGA
54265	52352	TATAATCCCAGCTCCTCGGG
54266	52353	CTATAATCCCAGCTCCTCGG
54267	52354	CCTATAATCCCAGCTCCTCG
54268	52355	GCCTATAATCCCAGCTCCTC
54269	52356	CGCCTATAATCCCAGCTCCT
54270	52357	ACGCCTATAATCCCAGCTCC
54271	52358	GACGCCTATAATCCCAGCTC
54272	52359	AGACGCCTATAATCCCAGCT
54273	52360	CAGACGCCTATAATCCCAGC
54274	52361	GCAGACGCCTATAATCCCAG
54275	52362	GGCAGACGCCTATAATCCCA
54276	52363	TGGCAGACGCCTATAATCCC
54277	52364	GTGGCAGACGCCTATAATCC
54278	52365	GGTGGCAGACGCCTATAATC
54279	52366	TGGTGGCAGACGCCTATAAT
54280	52367	ATGGTGGCAGACGCCTATAA
54281	52368	CATGGTGGCAGACGCCTATA
54282	52369	GCATGGTGGCAGACGCCTAT
54283	52370	GGCATGGTGGCAGACGCCTA
54284	52371	GGGCATGGTGGCAGACGCCT
54285	52372	TGGGCATGGTGGCAGACGCC
54286	52373	CTGGGCATGGTGGCAGACGC
54287	52374	GCTGGGCATGGTGGCAGACG
54288	52375	AGCTGGGCATGGTGGCAGAC
54289	52376	TAGCTGGGCATGGTGGCAGA
54290	52377	TTAGCTGGGCATGGTGGCAG
54291	52378	ATTAGCTGGGCATGGTGGCA
54292	52379	AATTAGCTGGGCATGGTGGC
54293	52380	AAATTAGCTGGGCATGGTGG
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54298	52385	TATAAAAATTAGCTGGGCAT
54299	52386	ATATAAAAATTAGCTGGGCA
54300	52387	AATATAAAAATTAGCTGGGC
54301	52388	AAATATAAAAATTAGCTGGG
54302	52389	AAAATATAAAAATTAGCTGG
54303	52390	AAAAATATAAAAATTAGCTG
54304	52391	TAAAAATATAAAAATTAGCT
54305	52392	CTAAAAATATAAAAATTAGC
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54313	52400	CGTCTCTACTAAAAATATAA
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54315	52402	CCCGTCTCTACTAAAAATAT
54316	52403	CCCCGTCTCTACTAAAAATA
54317	52404	ACCCCGTCTCTACTAAAAAT
54318	52405	AACCCCGTCTCTACTAAAAA
54319	52406	AAACCCCGTCTCTACTAAAA
54320	52407	GAAACCCCGTCTCTACTAAA
54321	52408	TGAAACCCCGTCTCTACTAA
54322	52409	GTGAAACCCCGTCTCTACTA
54323	52410	GGTGAAACCCCGTCTCTACT

103400	101487	GATGCCCACTTTCACCATTG
103401	101488	GGATGCCCACTTTCACCATT
103402	101489	AGGATGCCCACTTTCACCAT
103403	101490	AAGGATGCCCACTTTCACCA
103404	101491	CAAGGATGCCCACTTTCACC
103405	101492	ACAAGGATGCCCACTTTCAC
103406	101493	GACAAGGATGCCCACTTTCA
103407	101494	AGACAAGGATGCCCACTTTC
103408	101495	AAGACAAGGATGCCCACTTT
103409	101496	CAAGACAAGGATGCCCACTT
103410	101497	ACAAGACAAGGATGCCCACT
103411	101498	AACAAGACAAGGATGCCCAC
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103413	101500	GGAACAAGACAAGGATGCCC
103414	101501	TGGAACAAGACAAGGATGCC
103415	101502	CTGGAACAAGACAAGGATGC
103416	101503	TCTGGAACAAGACAAGGATG
103417	101504	ATCTGGAACAAGACAAGGAT
103418	101505	GATCTGGAACAAGACAAGGA
103419	101506	AGATCTGGAACAAGACAAGG
103420	101507	AAGATCTGGAACAAGACAAG
103421	101508	TAAGATCTGGAACAAGACAA
103422	101509	CTAAGATCTGGAACAAGACA
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103427	101514	TTCCTCTAAGATCTGGAACA
103428	101515	TTTCCTCTAAGATCTGGAAC
103429	101516	CTTTCCTCTAAGATCTGGAA
103430	101517	GCTTTCCTCTAAGATCTGGA
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103440	101527	AAACTGAAAGGCTTTCCTCT
103441	101528	AAAACTGAAAGGCTTTCCTC
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103453	101540	ACTGAAAAGGGAAAAACTGA
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103455	101542	ATACTGAAAAGGGAAAAACT
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103464	101551	ACTAGTACCATACTGAAAAG
103465	101552	AACTAGTACCATACTGAAAA
103466	101553	TAACTAGTACCATACTGAAA
103467	101554	ATAACTAGTACCATACTGAA
103468	101555	CATAACTAGTACCATACTGA
103469	101556	CCATAACTAGTACCATACTG
103470	101557	CCCATAACTAGTACCATACT

5177	3264	AGTCAAATTATGAAATGTTT
5178	3265	AAGTCAAATTATGAAATGTT
5179	3266	AAAGTCAAATTATGAAATGT
5180	3267	CAAAGTCAAATTATGAAATG
5181	3268	ACAAAGTCAAATTATGAAAT
5182	3269	CACAAAGTCAAATTATGAAA
5183	3270	ACACAAAGTCAAATTATGAA
5184	3271	CACACAAAGTCAAATTATGA
5185	3272	ACACACAAAGTCAAATTATG
5186	3273	CACACACAAAGTCAAATTAT
5187	3274	ACACACACAAAGTCAAATTA
5188	3275	CACACACACAAAGTCAAATT
5189	3276	ACACACACACAAAGTCAAAT
5190	3277	CACACACACACAAAGTCAAA
5191	3278	ACACACACACACAAAGTCAA
5192	3279	CACACACACACACAAAGTCA
5193	3280	ACACACACACACACAAAGTC
5194	3281	CACACACACACACACAAAGT
5195	3282	TCACACACACACACACAAAG
5196	3283	TTCACACACACACACACAAA
5197	3284	ATTCACACACACACACACAA
5198	3285	TATTCACACACACACACACA
5199	3286	CTATTCACACACACACACAC
5200	3287	ACTATTCACACACACACACA
5201	3288	AACTATTCACACACACACAC
5202	3289	AAACTATTCACACACACACA
5203	3290	AAAACTATTCACACACACAC
5204	3291	AAAAACTATTCACACACACA
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5206	3293	TGAAAAACTATTCACACACA
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5220	3307	ACTTCTGAAAGTCATGAAAA
5221	3308	CACTTCTGAAAGTCATGAAA
5222	3309	TCACTTCTGAAAGTCATGAA
5223	3310	ATCACTTCTGAAAGTCATGA
5224	3311	AATCACTTCTGAAAGTCATG
5225	3312	AAATCACTTCTGAAAGTCAT
5226	3313	TAAATCACTTCTGAAAGTCA
5227	3314	ATAAATCACTTCTGAAAGTC
5228	3315	AATAAATCACTTCTGAAAGT
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5230	3317	AAAATAAATCACTTCTGAAA
5231	3318	CAAAATAAATCACTTCTGAA
5232	3319	ACAAAATAAATCACTTCTGA
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5237	3324	AAAGAACAAAATAAATCACT
5238	3325	CAAAGAACAAAATAAATCAC
5239	3326	ACAAAGAACAAAATAAATCA
5240	3327	AACAAAGAACAAAATAAATC
5241	3328	TAACAAAGAACAAAATAAAT
5242	3329	ATAACAAAGAACAAAATAAA
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5244	3331	ATATAACAAAGAACAAAATA
5245	3332	TATATAACAAAGAACAAAAT
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54324	52411	TGGTGAAACCCCGTCTCTAC
54325	52412	ATGGTGAAACCCCGTCTCTA
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54328	52415	AATATGGTGAAACCCCGTCT
54329	52416	CAATATGGTGAAACCCCGTC
54330	52417	CCAATATGGTGAAACCCCGT
54331	52418	GCCAATATGGTGAAACCCCG
54332	52419	GGCCAATATGGTGAAACCCC
54333	52420	TGGCCAATATGGTGAAACCC
54334	52421	CTGGCCAATATGGTGAAACC
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54338	52425	GAGCCTGGCCAATATGGTGA
54339	52426	AGAGCCTGGCCAATATGGTG
54340	52427	AAGAGCCTGGCCAATATGGT
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54342	52429	AGAAGAGCCTGGCCAATATG
54343	52430	GAGAAGAGCCTGGCCAATAT
54344	52431	TGAGAAGAGCCTGGCCAATA
54345	52432	TTGAGAAGAGCCTGGCCAAT
54346	52433	TTTGAGAAGAGCCTGGCCAA
54347	52434	ATTTGAGAAGAGCCTGGCCA
54348	52435	AATTTGAGAAGAGCCTGGCC
54349	52436	GAATTTGAGAAGAGCCTGGC
54350	52437	GGAATTTGAGAAGAGCCTGG
54351	52438	AGGAATTTGAGAAGAGCCTG
54352	52439	CAGGAATTTGAGAAGAGCCT
54353	52440	TCAGGAATTTGAGAAGAGCC
54354	52441	GTCAGGAATTTGAGAAGAGC
54355	52442	GGTCAGGAATTTGAGAAGAG
54356	52443	AGGTCAGGAATTTGAGAAGA
54357	52444	GAGGTCAGGAATTTGAGAAG
54358	52445	TGAGGTCAGGAATTTGAGAA
54359	52446	ATGAGGTCAGGAATTTGAGA
54360	52447	CATGAGGTCAGGAATTTGAG
54361	52448	TCATGAGGTCAGGAATTTGA
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54363	52450	GATCATGAGGTCAGGAATTT
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54369	52456	TGGGTGGATCATGAGGTCAG
54370	52457	GTGGGTGGATCATGAGGTCA
54371	52458	GGTGGGTGGATCATGAGGTC
54372	52459	AGGTGGGTGGATCATGAGGT
54373	52460	AAGGTGGGTGGATCATGAGG
54374	52461	CAAGGTGGGTGGATCATGAG
54375	52462	CCAAGGTGGGTGGATCATGA
54376	52463	GCCAAGGTGGGTGGATCATG
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54378	52465	AGGCCAAGGTGGGTGGATCA
54379	52466	GAGGCCAAGGTGGGTGGATC
54380	52467	GGAGGCCAAGGTGGGTGGAT
54381	52468	GGGAGGCCAAGGTGGGTGGA
54382	52469	TGGGAGGCCAAGGTGGGTGG
54383	52470	TTGGGAGGCCAAGGTGGGTG
54384	52471	TTTGGGAGGCCAAGGTGGGT
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54390	52477	TAGCACTTTGGGAGGCCAAG
54391	52478	CTAGCACTTTGGGAGGCCAA
54392	52479	CCTAGCACTTTGGGAGGCCA
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103471	101558	ACCCATAACTAGTACCATAC
103472	101559	GACCCATAACTAGTACCATA
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103474	101561	CAGACCCATAACTAGTACCA
103475	101562	ACAGACCCATAACTAGTACC
103476	101563	GACAGACCCATAACTAGTAC
103477	101564	TGACAGACCCATAACTAGTA
103478	101565	ATGACAGACCCATAACTAGT
103479	101566	TATGACAGACCCATAACTAG
103480	101567	ATATGACAGACCCATAACTA
103481	101568	TATATGACAGACCCATAACT
103482	101569	ATATATGACAGACCCATAAC
103483	101570	CATATATGACAGACCCATAA
103484	101571	CCATATATGACAGACCCATA
103485	101572	GCCATATATGACAGACCCAT
103486	101573	AGCCATATATGACAGACCCA
103487	101574	AAGCCATATATGACAGACCC
103488	101575	GAAGCCATATATGACAGACC
103489	101576	AGAAGCCATATATGACAGAC
103490	101577	CAGAAGCCATATATGACAGA
103491	101578	ACAGAAGCCATATATGACAG
103492	101579	AACAGAAGCCATATATGACA
103493	101580	AAACAGAAGCCATATATGAC
103494	101581	AAAACAGAAGCCATATATGA
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103496	101583	ACAAAACAGAAGCCATATAT
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103501	101588	CCTCAACAAAACAGAAGCCA
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103503	101590	TACCTCAACAAAACAGAAGC
103504	101591	ATACCTCAACAAAACAGAAG
103505	101592	TATACCTCAACAAAACAGAA
103506	101593	ATATACCTCAACAAAACAGA
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103508	101595	GAATATACCTCAACAAAACA
103509	101596	GGAATATACCTCAACAAAAC
103510	101597	AGGAATATACCTCAACAAAA
103511	101598	AAGGAATATACCTCAACAAA
103512	101599	GAAGGAATATACCTCAACAA
103513	101600	AGAAGGAATATACCTCAACA
103514	101601	TAGAAGGAATATACCTCAAC
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103516	101603	TATAGAAGGAATATACCTCA
103517	101604	GTATAGAAGGAATATACCTC
103518	101605	GGTATAGAAGGAATATACCT
103519	101606	GGGTATAGAAGGAATATACC
103520	101607	TGGGTATAGAAGGAATATAC
103521	101608	CTGGGTATAGAAGGAATATA
103522	101609	ACTGGGTATAGAAGGAATAT
103523	101610	AACTGGGTATAGAAGGAATA
103524	101611	GAACTGGGTATAGAAGGAAT
103525	101612	AGAACTGGGTATAGAAGGAA
103526	101613	AAGAACTGGGTATAGAAGGA
103527	101614	AAAGAACTGGGTATAGAAGG
103528	101615	CAAAGAACTGGGTATAGAAG
103529	101616	CCAAAGAACTGGGTATAGAA
103530	101617	CCCAAAGAACTGGGTATAGA
103531	101618	CCCCAAAGAACTGGGTATAG
103532	101619	ACCCCAAAGAACTGGGTATA
103533	101620	AACCCCAAAGAACTGGGTAT
103534	101621	AAACCCCAAAGAACTGGGTA
103535	101622	AAAACCCCAAAGAACTGGGT
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103538	101625	AAAAAAACCCCAAAGAACTG
103539	101626	CAAAAAAACCCCAAAGAACT
103540	101627	ACAAAAAAACCCCAAAGAAC
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5248	3335	ATATATATAACAAAGAACAA
5249	3336	AATATATATAACAAAGAACA
5250	3337	AAATATATATAACAAAGAAC
5251	3338	AAAATATATATAACAAAGAA
5252	3339	AAAAATATATATAACAAAGA
5253	3340	CAAAAATATATATAACAAAG
5254	3341	TCAAAAATATATATAACAAA
5255	3342	TTCAAAAATATATATAACAA
5256	3343	CTTCAAAAATATATATAACA
5257	3344	CCTTCAAAAATATATATAAC
5258	3345	ACCTTCAAAAATATATATAA
5259	3346	CACCTTCAAAAATATATATA
5260	3347	CCACCTTCAAAAATATATAT
5261	3348	GCCACCTTCAAAAATATATA
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5268	3355	TAAAACAGCCACCTTCAAAA
5269	3356	CTAAAACAGCCACCTTCAAA
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5271	3358	TCCTAAAACAGCCACCTTCA
5272	3359	TTCCTAAAACAGCCACCTTC
5273	3360	TTTCCTAAAACAGCCACCTT
5274	3361	CTTTCCTAAAACAGCCACCT
5275	3362	TCTTTCCTAAAACAGCCACC
5276	3363	ATCTTTCCTAAAACAGCCAC
5277	3364	TATCTTTCCTAAAACAGCCA
5278	3365	TTATCTTTCCTAAAACAGCC
5279	3366	ATTATCTTTCCTAAAACAGC
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5281	3368	ACATTATCTTTCCTAAAACA
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5283	3370	TTACATTATCTTTCCTAAAA
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5286	3373	TGATTACATTATCTTTCCTA
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5288	3375	TGTGATTACATTATCTTTCC
5289	3376	TTGTGATTACATTATCTTTC
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5291	3378	TATTGTGATTACATTATCTT
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5293	3380	AATATTGTGATTACATTATC
5294	3381	TAATATTGTGATTACATTAT
5295	3382	CTAATATTGTGATTACATTA
5296	3383	TCTAATATTGTGATTACATT
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5299	3386	TGTTCTAATATTGTGATTAC
5300	3387	ATGTTCTAATATTGTGATTA
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5303	3390	ATTATGTTCTAATATTGTGA
5304	3391	AATTATGTTCTAATATTGTG
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5307	3394	TAAAATTATGTTCTAATATT
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5309	3396	AGTAAAATTATGTTCTAATA
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5311	3398	ACAGTAAAATTATGTTCTAA
5312	3399	TACAGTAAAATTATGTTCTA
5313	3400	TTACAGTAAAATTATGTTCT
5314	3401	ATTACAGTAAAATTATGTTC
5315	3402	GATTACAGTAAAATTATGTT
5316	3403	AGATTACAGTAAAATTATGT
5317	3404	TAGATTACAGTAAAATTATG
5318	3405	TTAGATTACAGTAAAATTAT

54395	52482	AATCCTAGCACTTTGGGAGG
54396	52483	TAATCCTAGCACTTTGGGAG
54397	52484	GTAATCCTAGCACTTTGGGA
54398	52485	TGTAATCCTAGCACTTTGGG
54399	52486	CTGTAATCCTAGCACTTTGG
54400	52487	CCTGTAATCCTAGCACTTTG
54401	52488	GCCTGTAATCCTAGCACTTT
54402	52489	CGCCTGTAATCCTAGCACTT
54403	52490	ACGCCTGTAATCCTAGCACT
54404	52491	CACGCCTGTAATCCTAGCAC
54405	52492	TCACGCCTGTAATCCTAGCA
54406	52493	CTCACGCCTGTAATCCTAGC
54407	52494	GCTCACGCCTGTAATCCTAG
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54410	52497	GTGGCTCACGCCTGTAATCC
54411	52498	GGTGGCTCACGCCTGTAATC
54412	52499	TGGTGGCTCACGCCTGTAAT
54413	52500	GTGGTGGCTCACGCCTGTAA
54414	52501	TGTGGTGGCTCACGCCTGTA
54415	52502	GTGTGGTGGCTCACGCCTGT
54416	52503	AGTGTGGTGGCTCACGCCTG
54417	52504	GAGTGTGGTGGCTCACGCCT
54418	52505	CGAGTGTGGTGGCTCACGCC
54419	52506	CCGAGTGTGGTGGCTCACGC
54420	52507	GCCGAGTGTGGTGGCTCACG
54421	52508	AGCCGAGTGTGGTGGCTCAC
54422	52509	CAGCCGAGTGTGGTGGCTCA
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54425	52512	CAGCAGCCGAGTGTGGTGGC
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54427	52514	CCCAGCAGCCGAGTGTGGTG
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54430	52517	TTCCCCAGCAGCCGAGTGTG
54431	52518	TTTCCCCAGCAGCCGAGTGT
54432	52519	GTTTCCCCAGCAGCCGAGTG
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54434	52521	AGGTTTCCCCAGCAGCCGAG
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54436	52523	AAAGGTTTCCCCAGCAGCCG
54437	52524	AAAAGGTTTCCCCAGCAGCC
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54439	52526	TTAAAAGGTTTCCCCAGCAG
54440	52527	GTTAAAAGGTTTCCCCAGCA
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54442	52529	ATGTTAAAAGGTTTCCCCAG
54443	52530	CATGTTAAAAGGTTTCCCCA
54444	52531	TCATGTTAAAAGGTTTCCCC
54445	52532	CTCATGTTAAAAGGTTTCCC
54446	52533	ACTCATGTTAAAAGGTTTCC
54447	52534	TACTCATGTTAAAAGGTTTC
54448	52535	TTACTCATGTTAAAAGGTTT
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54450	52537	CCTTACTCATGTTAAAAGGT
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54452	52539	GACCTTACTCATGTTAAAAG
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54456	52543	CACTGACCTTACTCATGTTA
54457	52544	ACACTGACCTTACTCATGTT
54458	52545	CACACTGACCTTACTCATGT
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54461	52548	AGTCACACTGACCTTACTCA
54462	52549	AAGTCACACTGACCTTACTC
54463	52550	AAAGTCACACTGACCTTACT
54464	52551	AAAAGTCACACTGACCTTAC
54465	52552	TAAAAGTCACACTGACCTTA

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103546	101633	AAACAAACAAAAAAACCCCA
103547	101634	CAAACAAACAAAAAAACCCC
103548	101635	ACAAACAAACAAAAAAACCC
103549	101636	AACAAACAAACAAAAAAACC
103550	101637	AAACAAACAAACAAAAAAAC
103551	101638	AAAACAAACAAACAAAAAAA
103552	101639	AAAAACAAACAAACAAAAAA
103553	101640	CAAAAACAAACAAACAAAAA
103554	101641	TCAAAAACAAACAAACAAAA
103555	101642	CTCAAAAACAAACAAACAAA
103556	101643	TCTCAAAAACAAACAAACAA
103557	101644	ATCTCAAAAACAAACAAACA
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103559	101646	CCATCTCAAAAACAAACAAA
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103563	101650	GACTCCATCTCAAAAACAAA
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103565	101652	GAGACTCCATCTCAAAAACA
103566	101653	TGAGACTCCATCTCAAAAAC
103567	101654	GTGAGACTCCATCTCAAAAA
103568	101655	AGTGAGACTCCATCTCAAAA
103569	101656	GAGTGAGACTCCATCTCAAA
103570	101657	AGAGTGAGACTCCATCTCAA
103571	101658	CAGAGTGAGACTCCATCTCA
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103574	101661	TGACAGAGTGAGACTCCATC
103575	101662	GTGACAGAGTGAGACTCCAT
103576	101663	GGTGACAGAGTGAGACTCCA
103577	101664	GGGTGACAGAGTGAGACTCC
103578	101665	TGGGTGACAGAGTGAGACTC
103579	101666	CTGGGTGACAGAGTGAGACT
103580	101667	CCTGGGTGACAGAGTGAGAC
103581	101668	GCCTGGGTGACAGAGTGAGA
103582	101669	AGCCTGGGTGACAGAGTGAG
103583	101670	CAGCCTGGGTGACAGAGTGA
103584	101671	CCAGCCTGGGTGACAGAGTG
103585	101672	TCCAGCCTGGGTGACAGAGT
103586	101673	CTCCAGCCTGGGTGACAGAG
103587	101674	ACTCCAGCCTGGGTGACAGA
103588	101675	CACTCCAGCCTGGGTGACAG
103589	101676	GCACTCCAGCCTGGGTGACA
103590	101677	TGCACTCCAGCCTGGGTGAC
103591	101678	CTGCACTCCAGCCTGGGTGA
103592	101679	ACTGCACTCCAGCCTGGGTG
103593	101680	CACTGCACTCCAGCCTGGGT
103594	101681	CCACTGCACTCCAGCCTGGG
103595	101682	GCCACTGCACTCCAGCCTGG
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5319	3406	ATTAGATTACAGTAAAATTA
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5328	3415	ACACACAAAATTAGATTACA
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5341	3428	CACACACACACACACACACA
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5345	3432	CACACACACACACACACACA
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5364	3451	AAACACACACACACACACAC
5365	3452	AAAACACACACACACACACA
5366	3453	CAAAACACACACACACACAC
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5368	3455	TCCAAAACACACACACACAC
5369	3456	ATCCAAAACACACACACACA
5370	3457	CATCCAAAACACACACACAC
5371	3458	CCATCCAAAACACACACACA
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5373	3460	TTCCATCCAAAACACACACA
5374	3461	ATTCCATCCAAAACACACAC
5375	3462	GATTCCATCCAAAACACACA
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5381	3468	GAGTGAGATTCCATCCAAAA
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5383	3470	CAGAGTGAGATTCCATCCAA
5384	3471	ACAGAGTGAGATTCCATCCA
5385	3472	GACAGAGTGAGATTCCATCC
5386	3473	CGACAGAGTGAGATTCCATC
5387	3474	GCGACAGAGTGAGATTCCAT
5388	3475	GGCGACAGAGTGAGATTCCA
5389	3476	GGGCGACAGAGTGAGATTCC

54466	52553	TTAAAAGTCACACTGACCTT
54467	52554	CTTAAAAGTCACACTGACCT
54468	52555	ACTTAAAAGTCACACTGACC
54469	52556	AACTTAAAAGTCACACTGAC
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54471	52558	AGAACTTAAAAGTCACACTG
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54478	52565	AGCATCAAGAACTTAAAAGT
54479	52566	TAGCATCAAGAACTTAAAAG
54480	52567	TTAGCATCAAGAACTTAAAA
54481	52568	GTTAGCATCAAGAACTTAAA
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54483	52570	ATGTTAGCATCAAGAACTTA
54484	52571	GATGTTAGCATCAAGAACTT
54485	52572	TGATGTTAGCATCAAGAACT
54486	52573	ATGATGTTAGCATCAAGAAC
54487	52574	AATGATGTTAGCATCAAGAA
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54489	52576	TCAATGATGTTAGCATCAAG
54490	52577	ATCAATGATGTTAGCATCAA
54491	52578	AATCAATGATGTTAGCATCA
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54495	52582	TTGAAATCAATGATGTTAGC
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54497	52584	TATTGAAATCAATGATGTTA
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54511	52598	TAACTTTTAAACTTTATTGA
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54514	52601	ATATAACTTTTAAACTTTAT
54515	52602	AATATAACTTTTAAACTTTA
54516	52603	GAATATAACTTTTAAACTTT
54517	52604	TGAATATAACTTTTAAACTT
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54519	52606	CATGAATATAACTTTTAAAC
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54523	52610	TATGCATGAATATAACTTTT
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54525	52612	TATATGCATGAATATAACTT
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54527	52614	CATATATGCATGAATATAAC
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54529	52616	TGCATATATGCATGAATATA
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54532	52619	ATTTGCATATATGCATGAAT
54533	52620	CATTTGCATATATGCATGAA
54534	52621	TCATTTGCATATATGCATGA
54535	52622	TTCATTTGCATATATGCATG
54536	52623	ATTCATTTGCATATATGCAT

103613	101700	GCAGTGAGCCAACATTGCGC
103614	101701	TGCAGTGAGCCAACATTGCG
103615	101702	TTGCAGTGAGCCAACATTGC
103616	101703	CTTGCAGTGAGCCAACATTG
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103619	101706	GAGCTTGCAGTGAGCCAACA
103620	101707	GGAGCTTGCAGTGAGCCAAC
103621	101708	TGGAGCTTGCAGTGAGCCAA
103622	101709	GTGGAGCTTGCAGTGAGCCA
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103624	101711	AGGTGGAGCTTGCAGTGAGC
103625	101712	GAGGTGGAGCTTGCAGTGAG
103626	101713	GGAGGTGGAGCTTGCAGTGA
103627	101714	AGGAGGTGGAGCTTGCAGTG
103628	101715	CAGGAGGTGGAGCTTGCAGT
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103630	101717	CCCAGGAGGTGGAGCTTGCA
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103633	101720	GAACCCAGGAGGTGGAGCTT
103634	101721	TGAACCCAGGAGGTGGAGCT
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103636	101723	CATGAACCCAGGAGGTGGAG
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103639	101726	CGGCATGAACCCAGGAGGTG
103640	101727	ACGGCATGAACCCAGGAGGT
103641	101728	AACGGCATGAACCCAGGAGG
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103643	101730	AGAACGGCATGAACCCAGGA
103644	101731	GAGAACGGCATGAACCCAGG
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103646	101733	AGGAGAACGGCATGAACCCA
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103648	101735	GCAGGAGAACGGCATGAACC
103649	101736	GGCAGGAGAACGGCATGAAC
103650	101737	AGGCAGGAGAACGGCATGAA
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103652	101739	TGAGGCAGGAGAACGGCATG
103653	101740	CTGAGGCAGGAGAACGGCAT
103654	101741	GCTGAGGCAGGAGAACGGCA
103655	101742	GGCTGAGGCAGGAGAACGGC
103656	101743	AGGCTGAGGCAGGAGAACGG
103657	101744	GAGGCTGAGGCAGGAGAACG
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103665	101752	CTACTCGGGAGGCTGAGGCA
103666	101753	GCTACTCGGGAGGCTGAGGC
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103668	101755	CAGCTACTCGGGAGGCTGAG
103669	101756	CCAGCTACTCGGGAGGCTGA
103670	101757	CCCAGCTACTCGGGAGGCTG
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103672	101759	GTCCCAGCTACTCGGGAGGC
103673	101760	AGTCCCAGCTACTCGGGAGG
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103680	101767	CACCTGTAGTCCCAGCTACT
103681	101768	ACACCTGTAGTCCCAGCTAC
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5390	3477	TGGGCGACAGAGTGAGATTC
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5399	3486	ACTCCAGCCTGGGCGACAGA
5400	3487	CACTCCAGCCTGGGCGACAG
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5407	3494	GCCACTGCACTCCAGCCTGG
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5411	3498	TCAGGCCACTGCACTCCAGC
5412	3499	ATCAGGCCACTGCACTCCAG
5413	3500	GATCAGGCCACTGCACTCCA
5414	3501	AGATCAGGCCACTGCACTCC
5415	3502	GAGATCAGGCCACTGCACTC
5416	3503	TGAGATCAGGCCACTGCACT
5417	3504	CTGAGATCAGGCCACTGCAC
5418	3505	GCTGAGATCAGGCCACTGCA
5419	3506	AGCTGAGATCAGGCCACTGC
5420	3507	AAGCTGAGATCAGGCCACTG
5421	3508	TAAGCTGAGATCAGGCCACT
5422	3509	GTAAGCTGAGATCAGGCCAC
5423	3510	AGTAAGCTGAGATCAGGCCA
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5426	3513	TGCAGTAAGCTGAGATCAGG
5427	3514	CTGCAGTAAGCTGAGATCAG
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5430	3517	AGACTGCAGTAAGCTGAGAT
5431	3518	GAGACTGCAGTAAGCTGAGA
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5433	3520	CAGAGACTGCAGTAAGCTGA
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5435	3522	GACAGAGACTGCAGTAAGCT
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5438	3525	GGAGACAGAGACTGCAGTAA
5439	3526	AGGAGACAGAGACTGCAGTA
5440	3527	CAGGAGACAGAGACTGCAGT
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5445	3532	GAACCCAGGAGACAGAGACT
5446	3533	TGAACCCAGGAGACAGAGAC
5447	3534	ATGAACCCAGGAGACAGAGA
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5449	3536	AAATGAACCCAGGAGACAGA
5450	3537	TAAATGAACCCAGGAGACAG
5451	3538	TTAAATGAACCCAGGAGACA
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5453	3540	ACTTAAATGAACCCAGGAGA
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5456	3543	ATCACTTAAATGAACCCAGG
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54537	52624	TATTCATTTGCATATATGCA
54538	52625	TTATTCATTTGCATATATGC
54539	52626	TTTATTCATTTGCATATATG
54540	52627	TTTTATTCATTTGCATATAT
54541	52628	CTTTTATTCATTTGCATATA
54542	52629	CCTTTTATTCATTTGCATAT
54543	52630	GCCTTTTATTCATTTGCATA
54544	52631	AGCCTTTTATTCATTTGCAT
54545	52632	AAGCCTTTTATTCATTTGCA
54546	52633	AAAGCCTTTTATTCATTTGC
54547	52634	CAAAGCCTTTTATTCATTTG
54548	52635	TCAAAGCCTTTTATTCATTT
54549	52636	TTCAAAGCCTTTTATTCATT
54550	52637	TTTCAAAGCCTTTTATTCAT
54551	52638	ATTTCAAAGCCTTTTATTCA
54552	52639	TATTTCAAAGCCTTTTATTC
54553	52640	CTATTTCAAAGCCTTTTATT
54554	52641	ACTATTTCAAAGCCTTTTAT
54555	52642	CACTATTTCAAAGCCTTTTA
54556	52643	TCACTATTTCAAAGCCTTTT
54557	52644	GTCACTATTTCAAAGCCTTT
54558	52645	AGTCACTATTTCAAAGCCTT
54559	52646	AAGTCACTATTTCAAAGCCT
54560	52647	GAAGTCACTATTTCAAAGCC
54561	52648	AGAAGTCACTATTTCAAAGC
54562	52649	AAGAAGTCACTATTTCAAAG
54563	52650	TAAGAAGTCACTATTTCAAA
54564	52651	GTAAGAAGTCACTATTTCAA
54565	52652	CGTAAGAAGTCACTATTTCA
54566	52653	CCGTAAGAAGTCACTATTTC
54567	52654	ACCGTAAGAAGTCACTATTT
54568	52655	TACCGTAAGAAGTCACTATT
54569	52656	GTACCGTAAGAAGTCACTAT
54570	52657	TGTACCGTAAGAAGTCACTA
54571	52658	CTGTACCGTAAGAAGTCACT
54572	52659	ACTGTACCGTAAGAAGTCAC
54573	52660	CACTGTACCGTAAGAAGTCA
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54575	52662	TTCACTGTACCGTAAGAAGT
54576	52663	ATTCACTGTACCGTAAGAAG
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54579	52666	CTTATTCACTGTACCGTAAG
54580	52667	ACTTATTCACTGTACCGTAA
54581	52668	AACTTATTCACTGTACCGTA
54582	52669	AAACTTATTCACTGTACCGT
54583	52670	GAAACTTATTCACTGTACCG
54584	52671	GGAAACTTATTCACTGTACC
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54586	52673	AAGGAAACTTATTCACTGTA
54587	52674	AAAGGAAACTTATTCACTGT
54588	52675	CAAAGGAAACTTATTCACTG
54589	52676	CCAAAGGAAACTTATTCACT
54590	52677	ACCAAAGGAAACTTATTCAC
54591	52678	GACCAAAGGAAACTTATTCA
54592	52679	AGACCAAAGGAAACTTATTC
54593	52680	GAGACCAAAGGAAACTTATT
54594	52681	AGAGACCAAAGGAAACTTAT
54595	52682	AAGAGACCAAAGGAAACTTA
54596	52683	CAAGAGACCAAAGGAAACTT
54597	52684	TCAAGAGACCAAAGGAAACT
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54600	52687	CATTCAAGAGACCAAAGGAA
54601	52688	ACATTCAAGAGACCAAAGGA
54602	52689	AACATTCAAGAGACCAAAGG
54603	52690	TAACATTCAAGAGACCAAAG
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54607	52694	TGTATAACATTCAAGAGACC

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103686	101773	AGCGGACACCTGTAGTCCCA
103687	101774	TAGCGGACACCTGTAGTCCC
103688	101775	TTAGCGGACACCTGTAGTCC
103689	101776	GTTAGCGGACACCTGTAGTC
103690	101777	TGTTAGCGGACACCTGTAGT
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103692	101779	CGTGTTAGCGGACACCTGTA
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103694	101781	GGCGTGTTAGCGGACACCTG
103695	101782	GGGCGTGTTAGCGGACACCT
103696	101783	CGGGCGTGTTAGCGGACACC
103697	101784	CCGGGCGTGTTAGCGGACAC
103698	101785	GCCGGGCGTGTTAGCGGACA
103699	101786	AGCCGGGCGTGTTAGCGGAC
103700	101787	TAGCCGGGCGTGTTAGCGGA
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103702	101789	ATTAGCCGGGCGTGTTAGCG
103703	101790	AATTAGCCGGGCGTGTTAGC
103704	101791	AAATTAGCCGGGCGTGTTAG
103705	101792	AAAATTAGCCGGGCGTGTTA
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103707	101794	AAAAAATTAGCCGGGCGTGT
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103729	101816	ACCCCGTCTCTACTAAAAAT
103730	101817	AACCCCGTCTCTACTAAAAA
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103732	101819	GAAACCCCGTCTCTACTAAA
103733	101820	TGAAACCCCGTCTCTACTAA
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103736	101823	CGGTGAAACCCCGTCTCTAC
103737	101824	ACGGTGAAACCCCGTCTCTA
103738	101825	CACGGTGAAACCCCGTCTCT
103739	101826	ACACGGTGAAACCCCGTCTC
103740	101827	AACACGGTGAAACCCCGTCT
103741	101828	TAACACGGTGAAACCCCGTC
103742	101829	CTAACACGGTGAAACCCCGT
103743	101830	GCTAACACGGTGAAACCCCG
103744	101831	GGCTAACACGGTGAAACCCC
103745	101832	TGGCTAACACGGTGAAACCC
103746	101833	CTGGCTAACACGGTGAAACC
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103750	101837	CATCCTGGCTAACACGGTGA
103751	101838	CCATCCTGGCTAACACGGTG
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5465	3552	GGCTGGAGAATCACTTAAAT
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5473	3560	GAGGCTGAGGCTGGAGAATC
5474	3561	GGAGGCTGAGGCTGGAGAAT
5475	3562	GGGAGGCTGAGGCTGGAGAA
5476	3563	GGGGAGGCTGAGGCTGGAGA
5477	3564	TGGGGAGGCTGAGGCTGGAG
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5480	3567	TACTGGGGAGGCTGAGGCTG
5481	3568	CTACTGGGGAGGCTGAGGCT
5482	3569	GCTACTGGGGAGGCTGAGGC
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5484	3571	CAGCTACTGGGGAGGCTGAG
5485	3572	CCAGCTACTGGGGAGGCTGA
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5529	3616	AATACAAAAAAATTAGCCAG
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54635	52722	CAGTTTCTCAGTAAATCAAA
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54637	52724	TTCAGTTTCTCAGTAAATCA
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54676	52763	TGCCAAGGTGACTCACAGCT
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103755	101842	GAGACCATCCTGGCTAACAC
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103778	101865	GCAGATCATGAGGTCAGGAG
103779	101866	GGCAGATCATGAGGTCAGGA
103780	101867	GGGCAGATCATGAGGTCAGG
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103782	101869	ACGGGCAGATCATGAGGTCA
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54679	52766	ATGTGCCAAGGTGACTCACA
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54705	52792	AATCTGATGGTCTCTTCTAA
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54717	52804	TTTTCCAATGATAATCTGAT
54718	52805	ATTTTCCAATGATAATCTGA
54719	52806	GATTTTCCAATGATAATCTG
54720	52807	TGATTTTCCAATGATAATCT
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103835	101922	TTGGCCGGGCGTGGTGGCTC
103836	101923	CTTGGCCGGGCGTGGTGGCT
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103988	102075	ATAAACATGGTACATCTTAA
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104166	102253	AACCAAAGGACACATCAAAA
104167	102254	AAACCAAAGGACACATCAAA
104168	102255	AAAACCAAAGGACACATCAA
104169	102256	CAAAACCAAAGGACACATCA
104170	102257	ACAAAACCAAAGGACACATC
104171	102258	TACAAAACCAAAGGACACAT
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104173	102260	TATACAAAACCAAAGGACAC
104174	102261	CTATACAAAACCAAAGGACA
104175	102262	CCTATACAAAACCAAAGGAC
104176	102263	CCCTATACAAAACCAAAGGA
104177	102264	ACCCTATACAAAACCAAAGG
104178	102265	TACCCTATACAAAACCAAAG
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104180	102267	ATTACCCTATACAAAACCAA

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5890	3977	TTCAGGGGAAAAAAGCTAAC
5891	3978	GTTCAGGGGAAAAAAGCTAA
5892	3979	CGTTCAGGGGAAAAAAGCTA
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5894	3981	AACGTTCAGGGGAAAAAAGC
5895	3982	CAACGTTCAGGGGAAAAAAG
5896	3983	ACAACGTTCAGGGGAAAAAA
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5903	3990	TTACAATACAACGTTCAGGG
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5912	3999	AATTTACATTTACAATACAA
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5915	4002	AAAAATTTACATTTACAATA
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5917	4004	AAAAAAATTTACATTTACAA
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5937	4024	ACTCTGTCTCAAAAAAAAAA
5938	4025	GACTCTGTCTCAAAAAAAAA
5939	4026	AGACTCTGTCTCAAAAAAAA
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5945	4032	ACACCGAGACTCTGTCTCAA
5946	4033	AACACCGAGACTCTGTCTCA
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5948	4035	CAAACACCGAGACTCTGTCT
5949	4036	GCAAACACCGAGACTCTGTC
5950	4037	GGCAAACACCGAGACTCTGT
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55040	53127	ATGAAGCAGTAGGAAAAAGT
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55045	53132	AGAAAATGAAGCAGTAGGAA
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55048	53135	CAAAGAAAATGAAGCAGTAG
55049	53136	GCAAAGAAAATGAAGCAGTA
55050	53137	TGCAAAGAAAATGAAGCAGT
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55052	53139	ACTGCAAAGAAAATGAAGCA
55053	53140	TACTGCAAAGAAAATGAAGC
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55055	53142	AATACTGCAAAGAAAATGAA
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55057	53144	AGAATACTGCAAAGAAAATG
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55059	53146	TGAGAATACTGCAAAGAAAA
55060	53147	CTGAGAATACTGCAAAGAAA
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55065	53152	CTAGGCTGAGAATACTGCAA
55066	53153	TCTAGGCTGAGAATACTGCA
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55071	53158	TATCATCTAGGCTGAGAATA
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55073	53160	CCTATCATCTAGGCTGAGAA
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55076	53163	ACCCCTATCATCTAGGCTGA
55077	53164	GACCCCTATCATCTAGGCTG
55078	53165	TGACCCCTATCATCTAGGCT
55079	53166	CTGACCCCTATCATCTAGGC
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55081	53168	TGCTGACCCCTATCATCTAG
55082	53169	TTGCTGACCCCTATCATCTA
55083	53170	TTTGCTGACCCCTATCATCT
55084	53171	ATTTGCTGACCCCTATCATC
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55100	53187	ATTTACTGATGAGCAGATTT
55101	53188	TATTTACTGATGAGCAGATT
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55103	53190	TTTATTTACTGATGAGCAGA
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104184	102271	CACTATTACCCTATACAAAA
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104187	102274	GGCCACTATTACCCTATACA
104188	102275	AGGCCACTATTACCCTATAC
104189	102276	AAGGCCACTATTACCCTATA
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104192	102279	TACAAGGCCACTATTACCCT
104193	102280	CTACAAGGCCACTATTACCC
104194	102281	TCTACAAGGCCACTATTACC
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104201	102288	AACTCATTCTACAAGGCCAC
104202	102289	AAACTCATTCTACAAGGCCA
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104204	102291	CTAAACTCATTCTACAAGGC
104205	102292	TCTAAACTCATTCTACAAGG
104206	102293	TTCTAAACTCATTCTACAAG
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104208	102295	ACTTCTAAACTCATTCTACA
104209	102296	TACTTCTAAACTCATTCTAC
104210	102297	ATACTTCTAAACTCATTCTA
104211	102298	AATACTTCTAAACTCATTCT
104212	102299	GAATACTTCTAAACTCATTC
104213	102300	GGAATACTTCTAAACTCATT
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104218	102305	AAGAGGGAATACTTCTAAAC
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104221	102308	AGGAAGAGGGAATACTTCTA
104222	102309	CAGGAAGAGGGAATACTTCT
104223	102310	ACAGGAAGAGGGAATACTTC
104224	102311	TACAGGAAGAGGGAATACTT
104225	102312	ATACAGGAAGAGGGAATACT
104226	102313	AATACAGGAAGAGGGAATAC
104227	102314	CAATACAGGAAGAGGGAATA
104228	102315	ACAATACAGGAAGAGGGAAT
104229	102316	CACAATACAGGAAGAGGGAA
104230	102317	ACACAATACAGGAAGAGGGA
104231	102318	AACACAATACAGGAAGAGGG
104232	102319	CAACACAATACAGGAAGAGG
104233	102320	CCAACACAATACAGGAAGAG
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104235	102322	TTCCAACACAATACAGGAAG
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104245	102332	ACTCAAACTATTCCAACACA
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5959	4046	TTCAGACTGGGCAAACACCG
5960	4047	CTTCAGACTGGGCAAACACC
5961	4048	ACTTCAGACTGGGCAAACAC
5962	4049	CACTTCAGACTGGGCAAACA
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5971	4058	GTACCACTGCACTTCAGACT
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5973	4060	TCGTACCACTGCACTTCAGA
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5976	4063	AGATCGTACCACTGCACTTC
5977	4064	GAGATCGTACCACTGCACTT
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5979	4066	CTGAGATCGTACCACTGCAC
5980	4067	GCTGAGATCGTACCACTGCA
5981	4068	AGCTGAGATCGTACCACTGC
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5983	4070	TGAGCTGAGATCGTACCACT
5984	4071	GTGAGCTGAGATCGTACCAC
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6014	4101	ATCGCTTGAACCCAGGAGTC
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55105	53192	AATTTATTTACTGATGAGCA
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55126	53213	GGCATAGCTATGCTACAATA
55127	53214	GGGCATAGCTATGCTACAAT
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55142	53229	AATGCACAAACGCATGGGCA
55143	53230	CAATGCACAAACGCATGGGC
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55149	53236	CATAGACAATGCACAAACGC
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55161	53248	CATCAAAACAGCCATAGACA
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104256	102343	ATACCAATCCTACTCAAACT
104257	102344	AATACCAATCCTACTCAAAC
104258	102345	TAATACCAATCCTACTCAAA
104259	102346	CTAATACCAATCCTACTCAA
104260	102347	ACTAATACCAATCCTACTCA
104261	102348	AACTAATACCAATCCTACTC
104262	102349	GAACTAATACCAATCCTACT
104263	102350	AGAACTAATACCAATCCTAC
104264	102351	AAGAACTAATACCAATCCTA
104265	102352	GAAGAACTAATACCAATCCT
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104276	102363	AAACCTTTAAAGAAGAACTA
104277	102364	TAAACCTTTAAAGAAGAACT
104278	102365	CTAAACCTTTAAAGAAGAAC
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104281	102368	CTACTAAACCTTTAAAGAAG
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104283	102370	TTCTACTAAACCTTTAAAGA
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104298	102385	GGCTTCACTGCTGAATTCTA
104299	102386	TGGCTTCACTGCTGAATTCT
104300	102387	ATGGCTTCACTGCTGAATTC
104301	102388	GATGGCTTCACTGCTGAATT
104302	102389	TGATGGCTTCACTGCTGAAT
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104305	102392	ACCTGATGGCTTCACTGCTG
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104307	102394	GGACCTGATGGCTTCACTGC
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104310	102397	CATGGACCTGATGGCTTCAC
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104319	102406	AAGAAAAGCCATGGACCTGA
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104321	102408	CAAAGAAAAGCCATGGACCT
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6029	4116	GGCTGAGGTGGGAGAATCGC
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6049	4136	GTAGCCCCAGCTACTCAAGA
6050	4137	TGTAGCCCCAGCTACTCAAG
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6056	4143	CATTCCTGTAGCCCCAGCTA
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6058	4145	AACATTCCTGTAGCCCCAGC
6059	4146	GAACATTCCTGTAGCCCCAG
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6062	4149	GTGGAACATTCCTGTAGCCC
6063	4150	GGTGGAACATTCCTGTAGCC
6064	4151	TGGTGGAACATTCCTGTAGC
6065	4152	GTGGTGGAACATTCCTGTAG
6066	4153	CGTGGTGGAACATTCCTGTA
6067	4154	GCGTGGTGGAACATTCCTGT
6068	4155	AGCGTGGTGGAACATTCCTG
6069	4156	AAGCGTGGTGGAACATTCCT
6070	4157	CAAGCGTGGTGGAACATTCC
6071	4158	CCAAGCGTGGTGGAACATTC
6072	4159	GCCAAGCGTGGTGGAACATT
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6076	4163	ATTAGCCAAGCGTGGTGGAA
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6079	4166	AAAATTAGCCAAGCGTGGTG
6080	4167	AAAAATTAGCCAAGCGTGGT
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6095	4182	CTCTACCAAAAATACAAAAA
6096	4183	TCTCTACCAAAAATACAAAA
6097	4184	GTCTCTACCAAAAATACAAA
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55176	53263	CTCTATGGCTACAGCCATCA
55177	53264	ACTCTATGGCTACAGCCATC
55178	53265	AACTCTATGGCTACAGCCAT
55179	53266	CAACTCTATGGCTACAGCCA
55180	53267	TCAACTCTATGGCTACAGCC
55181	53268	CTCAACTCTATGGCTACAGC
55182	53269	ACTCAACTCTATGGCTACAG
55183	53270	TACTCAACTCTATGGCTACA
55184	53271	CTACTCAACTCTATGGCTAC
55185	53272	ACTACTCAACTCTATGGCTA
55186	53273	AACTACTCAACTCTATGGCT
55187	53274	CAACTACTCAACTCTATGGC
55188	53275	ACAACTACTCAACTCTATGG
55189	53276	TACAACTACTCAACTCTATG
55190	53277	CTACAACTACTCAACTCTAT
55191	53278	GCTACAACTACTCAACTCTA
55192	53279	AGCTACAACTACTCAACTCT
55193	53280	CAGCTACAACTACTCAACTC
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55207	53294	GCAAGTCCTACAGTCAGCTA
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55219	53306	TTTTCTGGCTTTGCAAGTCC
55220	53307	ATTTTCTGGCTTTGCAAGTC
55221	53308	AATTTTCTGGCTTTGCAAGT
55222	53309	AAATTTTCTGGCTTTGCAAG
55223	53310	CAAATTTTCTGGCTTTGCAA
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55227	53314	CAGTCAAATTTTCTGGCTTT
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55229	53316	GACAGTCAAATTTTCTGGCT
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55235	53322	TAAAGAGACAGTCAAATTTT
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55237	53324	TGTAAAGAGACAGTCAAATT
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55239	53326	TCTGTAAAGAGACAGTCAAA
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104327	102414	TCCCAGCAAAGAAAAGCCAT
104328	102415	CTCCCAGCAAAGAAAAGCCA
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104345	102432	AAGCTATAAGAAATAGTCTC
104346	102433	AAAGCTATAAGAAATAGTCT
104347	102434	CAAAGCTATAAGAAATAGTC
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104351	102438	AGATCAAAGCTATAAGAAAT
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104355	102442	AACGAGATCAAAGCTATAAG
104356	102443	TAACGAGATCAAAGCTATAA
104357	102444	GTAACGAGATCAAAGCTATA
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104366	102453	CAATAACAAGTAACGAGATC
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104370	102457	AGACCAATAACAAGTAACGA
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104373	102460	ACGAGACCAATAACAAGTAA
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104375	102462	TAACGAGACCAATAACAAGT
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104385	102472	CAATAACAAGTAACGAGACC
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104387	102474	TACAATAACAAGTAACGAGA
104388	102475	ATACAATAACAAGTAACGAG
104389	102476	AATACAATAACAAGTAACGA
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6104	4191	AAACCTTGTCTCTACCAAAA
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6108	4195	GGTGAAACCTTGTCTCTACC
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6143	4230	TGAGGTCGGTAGTACGAGAC
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6152	4239	CGCATCACCTGAGGTCGGTA
6153	4240	GCGCATCACCTGAGGTCGGT
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6156	4243	CGGGCGCATCACCTGAGGTC
6157	4244	GCGGGCGCATCACCTGAGGT
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6167	4254	GGAGGCCGAGGCGGGCGCAT
6168	4255	GGGAGGCCGAGGCGGGCGCA
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55247	53334	CAAACTTTTCTGTAAAGAGA
55248	53335	GCAAACTTTTCTGTAAAGAG
55249	53336	GGCAAACTTTTCTGTAAAGA
55250	53337	TGGCAAACTTTTCTGTAAAG
55251	53338	CTGGCAAACTTTTCTGTAAA
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55253	53340	AGCTGGCAAACTTTTCTGTA
55254	53341	GAGCTGGCAAACTTTTCTGT
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55274	53361	GAAAATATGATTTAGGCCAA
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104398	102485	CAAAACCCAAATACAATAAC
104399	102486	CCAAAACCCAAATACAATAA
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104403	102490	AAATCCAAAACCCAAATACA
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104415	102502	TGAACCACAAAGAAATCCAA
104416	102503	CTGAACCACAAAGAAATCCA
104417	102504	ACTGAACCACAAAGAAATCC
104418	102505	GACTGAACCACAAAGAAATC
104419	102506	AGACTGAACCACAAAGAAAT
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104421	102508	CAAGACTGAACCACAAAGAA
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104425	102512	CTACCAAGACTGAACCACAA
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104433	102520	CATACAACCTACCAAGACTG
104434	102521	ACATACAACCTACCAAGACT
104435	102522	CACATACAACCTACCAAGAC
104436	102523	ACACATACAACCTACCAAGA
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104438	102525	AGACACATACAACCTACCAA
104439	102526	TAGACACATACAACCTACCA
104440	102527	CTAGACACATACAACCTACC
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104442	102529	TCCTAGACACATACAACCTA
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104444	102531	ATTCCTAGACACATACAACC
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6171	4258	TTTGGGAGGCCGAGGCGGGC
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6173	4260	ACTTTGGGAGGCCGAGGCGG
6174	4261	CACTTTGGGAGGCCGAGGCG
6175	4262	GCACTTTGGGAGGCCGAGGC
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6194	4281	GCTCACGCCTGCAATCCCAG
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6239	4326	CAACAATAGAATGGTTAAGT
6240	4327	CCAACAATAGAATGGTTAAG
6241	4328	CCCAACAATAGAATGGTTAA

55318	53405	TAGCATGTATTTTTGATCAG
55319	53406	ATAGCATGTATTTTTGATCA
55320	53407	TATAGCATGTATTTTTGATC
55321	53408	GTATAGCATGTATTTTTGAT
55322	53409	AGTATAGCATGTATTTTTGA
55323	53410	CAGTATAGCATGTATTTTTG
55324	53411	CCAGTATAGCATGTATTTTT
55325	53412	GCCAGTATAGCATGTATTTT
55326	53413	AGCCAGTATAGCATGTATTT
55327	53414	AAGCCAGTATAGCATGTATT
55328	53415	AAAGCCAGTATAGCATGTAT
55329	53416	CAAAGCCAGTATAGCATGTA
55330	53417	CCAAAGCCAGTATAGCATGT
55331	53418	ACCAAAGCCAGTATAGCATG
55332	53419	CACCAAAGCCAGTATAGCAT
55333	53420	TCACCAAAGCCAGTATAGCA
55334	53421	TTCACCAAAGCCAGTATAGC
55335	53422	CTTCACCAAAGCCAGTATAG
55336	53423	ACTTCACCAAAGCCAGTATA
55337	53424	TACTTCACCAAAGCCAGTAT
55338	53425	TTACTTCACCAAAGCCAGTA
55339	53426	GTTACTTCACCAAAGCCAGT
55340	53427	TGTTACTTCACCAAAGCCAG
55341	53428	CTGTTACTTCACCAAAGCCA
55342	53429	TCTGTTACTTCACCAAAGCC
55343	53430	TTCTGTTACTTCACCAAAGC
55344	53431	ATTCTGTTACTTCACCAAAG
55345	53432	CATTCTGTTACTTCACCAAA
55346	53433	ACATTCTGTTACTTCACCAA
55347	53434	CACATTCTGTTACTTCACCA
55348	53435	GCACATTCTGTTACTTCACC
55349	53436	AGCACATTCTGTTACTTCAC
55350	53437	GAGCACATTCTGTTACTTCA
55351	53438	AGAGCACATTCTGTTACTTC
55352	53439	CAGAGCACATTCTGTTACTT
55353	53440	ACAGAGCACATTCTGTTACT
55354	53441	GACAGAGCACATTCTGTTAC
55355	53442	GGACAGAGCACATTCTGTTA
55356	53443	AGGACAGAGCACATTCTGTT
55357	53444	AAGGACAGAGCACATTCTGT
55358	53445	AAAGGACAGAGCACATTCTG
55359	53446	TAAAGGACAGAGCACATTCT
55360	53447	TTAAAGGACAGAGCACATTC
55361	53448	TTTAAAGGACAGAGCACATT
55362	53449	GTTTAAAGGACAGAGCACAT
55363	53450	AGTTTAAAGGACAGAGCACA
55364	53451	AAGTTTAAAGGACAGAGCAC
55365	53452	TAAGTTTAAAGGACAGAGCA
55366	53453	GTAAGTTTAAAGGACAGAGC
55367	53454	TGTAAGTTTAAAGGACAGAG
55368	53455	TTGTAAGTTTAAAGGACAGA
55369	53456	GTTGTAAGTTTAAAGGACAG
55370	53457	AGTTGTAAGTTTAAAGGACA
55371	53458	TAGTTGTAAGTTTAAAGGAC
55372	53459	TTAGTTGTAAGTTTAAAGGA
55373	53460	ATTAGTTGTAAGTTTAAAGG
55374	53461	AATTAGTTGTAAGTTTAAAG
55375	53462	CAATTAGTTGTAAGTTTAAA
55376	53463	GCAATTAGTTGTAAGTTTAA
55377	53464	TGCAATTAGTTGTAAGTTTA
55378	53465	ATGCAATTAGTTGTAAGTTT
55379	53466	CATGCAATTAGTTGTAAGTT
55380	53467	GCATGCAATTAGTTGTAAGT
55381	53468	AGCATGCAATTAGTTGTAAG
55382	53469	AAGCATGCAATTAGTTGTAA
55383	53470	AAAGCATGCAATTAGTTGTA
55384	53471	CAAAGCATGCAATTAGTTGT
55385	53472	TCAAAGCATGCAATTAGTTG
55386	53473	ATCAAAGCATGCAATTAGTT
55387	53474	AATCAAAGCATGCAATTAGT
55388	53475	GAATCAAAGCATGCAATTAG

104465	102552	AAACCTTGAAGAAATGGATA
104466	102553	AAAACCTTGAAGAAATGGAT
104467	102554	GAAAACCTTGAAGAAATGGA
104468	102555	GGAAAACCTTGAAGAAATGG
104469	102556	TGGAAAACCTTGAAGAAATG
104470	102557	TTGGAAAACCTTGAAGAAAT
104471	102558	ATTGGAAAACCTTGAAGAAA
104472	102559	CATTGGAAAACCTTGAAGAA
104473	102560	ACATTGGAAAACCTTGAAGA
104474	102561	TACATTGGAAAACCTTGAAG
104475	102562	ATACATTGGAAAACCTTGAA
104476	102563	GATACATTGGAAAACCTTGA
104477	102564	TGATACATTGGAAAACCTTG
104478	102565	CTGATACATTGGAAAACCTT
104479	102566	GCTGATACATTGGAAAACCT
104480	102567	TGCTGATACATTGGAAAACC
104481	102568	ATGCTGATACATTGGAAAAC
104482	102569	TATGCTGATACATTGGAAAA
104483	102570	ATATGCTGATACATTGGAAA
104484	102571	TATATGCTGATACATTGGAA
104485	102572	CTATATGCTGATACATTGGA
104486	102573	TCTATATGCTGATACATTGG
104487	102574	ATCTATATGCTGATACATTG
104488	102575	CATCTATATGCTGATACATT
104489	102576	GCATCTATATGCTGATACAT
104490	102577	AGCATCTATATGCTGATACA
104491	102578	GAGCATCTATATGCTGATAC
104492	102579	TGAGCATCTATATGCTGATA
104493	102580	ATGAGCATCTATATGCTGAT
104494	102581	TATGAGCATCTATATGCTGA
104495	102582	CTATGAGCATCTATATGCTG
104496	102583	ACTATGAGCATCTATATGCT
104497	102584	TACTATGAGCATCTATATGC
104498	102585	CTACTATGAGCATCTATATG
104499	102586	ACTACTATGAGCATCTATAT
104500	102587	GACTACTATGAGCATCTATA
104501	102588	AGACTACTATGAGCATCTAT
104502	102589	GAGACTACTATGAGCATCTA
104503	102590	AGAGACTACTATGAGCATCT
104504	102591	TAGAGACTACTATGAGCATC
104505	102592	TTAGAGACTACTATGAGCAT
104506	102593	ATTAGAGACTACTATGAGCA
104507	102594	CATTAGAGACTACTATGAGC
104508	102595	TCATTAGAGACTACTATGAG
104509	102596	ATCATTAGAGACTACTATGA
104510	102597	GATCATTAGAGACTACTATG
104511	102598	GGATCATTAGAGACTACTAT
104512	102599	AGGATCATTAGAGACTACTA
104513	102600	AAGGATCATTAGAGACTACT
104514	102601	AAAGGATCATTAGAGACTAC
104515	102602	CAAAGGATCATTAGAGACTA
104516	102603	TCAAAGGATCATTAGAGACT
104517	102604	TTCAAAGGATCATTAGAGAC
104518	102605	ATTCAAAGGATCATTAGAGA
104519	102606	AATTCAAAGGATCATTAGAG
104520	102607	AAATTCAAAGGATCATTAGA
104521	102608	GAAATTCAAAGGATCATTAG
104522	102609	CGAAATTCAAAGGATCATTA
104523	102610	CCGAAATTCAAAGGATCATT
104524	102611	ACCGAAATTCAAAGGATCAT
104525	102612	CACCGAAATTCAAAGGATCA
104526	102613	CCACCGAAATTCAAAGGATC
104527	102614	ACCACCGAAATTCAAAGGAT
104528	102615	TACCACCGAAATTCAAAGGA
104529	102616	TTACCACCGAAATTCAAAGG
104530	102617	GTTACCACCGAAATTCAAAG
104531	102618	TGTTACCACCGAAATTCAAA
104532	102619	TTGTTACCACCGAAATTCAA
104533	102620	ATTGTTACCACCGAAATTCA
104534	102621	AATTGTTACCACCGAAATTC
104535	102622	TAATTGTTACCACCGAAATT

6242	4329	TCCCAACAATAGAATGGTTA
6243	4330	TTCCCAACAATAGAATGGTT
6244	4331	ATTCCCAACAATAGAATGGT
6245	4332	AATTCCCAACAATAGAATGG
6246	4333	CAATTCCCAACAATAGAATG
6247	4334	CCAATTCCCAACAATAGAAT
6248	4335	CCCAATTCCCAACAATAGAA
6249	4336	ACCCAATTCCCAACAATAGA
6250	4337	AACCCAATTCCCAACAATAG
6251	4338	AAACCCAATTCCCAACAATA
6252	4339	GAAACCCAATTCCCAACAAT
6253	4340	GGAAACCCAATTCCCAACAA
6254	4341	TGGAAACCCAATTCCCAACA
6255	4342	GTGGAAACCCAATTCCCAAC
6256	4343	AGTGGAAACCCAATTCCCAA
6257	4344	AAGTGGAAACCCAATTCCCA
6258	4345	AAAGTGGAAACCCAATTCCC
6259	4346	AAAAGTGGAAACCCAATTCC
6260	4347	AAAAAGTGGAAACCCAATTC
6261	4348	AAAAAAGTGGAAACCCAATT
6262	4349	CAAAAAAGTGGAAACCCAAT
6263	4350	ACAAAAAAGTGGAAACCCAA
6264	4351	AACAAAAAAGTGGAAACCCA
6265	4352	TAACAAAAAAGTGGAAACCC
6266	4353	ATAACAAAAAAGTGGAAACC
6267	4354	TATAACAAAAAAGTGGAAAC
6268	4355	CTATAACAAAAAAGTGGAAA
6269	4356	TCTATAACAAAAAAGTGGAA
6270	4357	ATCTATAACAAAAAAGTGGA
6271	4358	TATCTATAACAAAAAAGTGG
6272	4359	CTATCTATAACAAAAAAGTG
6273	4360	ACTATCTATAACAAAAAAGT
6274	4361	CACTATCTATAACAAAAAAG
6275	4362	CCACTATCTATAACAAAAAA
6276	4363	ACCACTATCTATAACAAAAA
6277	4364	CACCACTATCTATAACAAAA
6278	4365	GCACCACTATCTATAACAAA
6279	4366	TGCACCACTATCTATAACAA
6280	4367	CTGCACCACTATCTATAACA
6281	4368	ACTGCACCACTATCTATAAC
6282	4369	CACTGCACCACTATCTATAA
6283	4370	TCACTGCACCACTATCTATA
6284	4371	TTCACTGCACCACTATCTAT
6285	4372	GTTCACTGCACCACTATCTA
6286	4373	TGTTCACTGCACCACTATCT
6287	4374	ATGTTCACTGCACCACTATC
6288	4375	AATGTTCACTGCACCACTAT
6289	4376	AAATGTTCACTGCACCACTA
6290	4377	AAAATGTTCACTGCACCACT
6291	4378	AAAAATGTTCACTGCACCAC
6292	4379	TAAAAATGTTCACTGCACCA
6293	4380	TTAAAAATGTTCACTGCACC
6294	4381	TTTAAAAATGTTCACTGCAC
6295	4382	ATTTAAAAATGTTCACTGCA
6296	4383	TATTTAAAAATGTTCACTGC
6297	4384	CTATTTAAAAATGTTCACTG
6298	4385	GCTATTTAAAAATGTTCACT
6299	4386	AGCTATTTAAAAATGTTCAC
6300	4387	AAGCTATTTAAAAATGTTCA
6301	4388	AAAGCTATTTAAAAATGTTC
6302	4389	AAAAGCTATTTAAAAATGTT
6303	4390	AAAAAGCTATTTAAAAATGT
6304	4391	CAAAAAGCTATTTAAAAATG
6305	4392	GCAAAAAGCTATTTAAAAAT
6306	4393	AGCAAAAAGCTATTTAAAAA
6307	4394	AAGCAAAAAGCTATTTAAAA
6308	4395	GAAGCAAAAAGCTATTTAAA
6309	4396	TGAAGCAAAAAGCTATTTAA
6310	4397	CTGAAGCAAAAAGCTATTTA
6311	4398	ACTGAAGCAAAAAGCTATTT
6312	4399	CACTGAAGCAAAAAGCTATT

55389	53476	AGAATCAAAGCATGCAATTA
55390	53477	TAGAATCAAAGCATGCAATT
55391	53478	TTAGAATCAAAGCATGCAAT
55392	53479	ATTAGAATCAAAGCATGCAA
55393	53480	TATTAGAATCAAAGCATGCA
55394	53481	GTATTAGAATCAAAGCATGC
55395	53482	AGTATTAGAATCAAAGCATG
55396	53483	CAGTATTAGAATCAAAGCAT
55397	53484	ACAGTATTAGAATCAAAGCA
55398	53485	TACAGTATTAGAATCAAAGC
55399	53486	ATACAGTATTAGAATCAAAG
55400	53487	TATACAGTATTAGAATCAAA
55401	53488	TTATACAGTATTAGAATCAA
55402	53489	ATTATACAGTATTAGAATCA
55403	53490	TATTATACAGTATTAGAATC
55404	53491	ATATTATACAGTATTAGAAT
55405	53492	GATATTATACAGTATTAGAA
55406	53493	GGATATTATACAGTATTAGA
55407	53494	AGGATATTATACAGTATTAG
55408	53495	CAGGATATTATACAGTATTA
55409	53496	GCAGGATATTATACAGTATT
55410	53497	CGCAGGATATTATACAGTAT
55411	53498	TCGCAGGATATTATACAGTA
55412	53499	ATCGCAGGATATTATACAGT
55413	53500	AATCGCAGGATATTATACAG
55414	53501	GAATCGCAGGATATTATACA
55415	53502	AGAATCGCAGGATATTATAC
55416	53503	AAGAATCGCAGGATATTATA
55417	53504	TAAGAATCGCAGGATATTAT
55418	53505	ATAAGAATCGCAGGATATTA
55419	53506	AATAAGAATCGCAGGATATT
55420	53507	GAATAAGAATCGCAGGATAT
55421	53508	TGAATAAGAATCGCAGGATA
55422	53509	ATGAATAAGAATCGCAGGAT
55423	53510	CATGAATAAGAATCGCAGGA
55424	53511	TCATGAATAAGAATCGCAGG
55425	53512	GTCATGAATAAGAATCGCAG
55426	53513	GGTCATGAATAAGAATCGCA
55427	53514	TGGTCATGAATAAGAATCGC
55428	53515	ATGGTCATGAATAAGAATCG
55429	53516	AATGGTCATGAATAAGAATC
55430	53517	GAATGGTCATGAATAAGAAT
55431	53518	AGAATGGTCATGAATAAGAA
55432	53519	TAGAATGGTCATGAATAAGA
55433	53520	TTAGAATGGTCATGAATAAG
55434	53521	ATTAGAATGGTCATGAATAA
55435	53522	AATTAGAATGGTCATGAATA
55436	53523	CAATTAGAATGGTCATGAAT
55437	53524	CCAATTAGAATGGTCATGAA
55438	53525	TCCAATTAGAATGGTCATGA
55439	53526	ATCCAATTAGAATGGTCATG
55440	53527	AATCCAATTAGAATGGTCAT
55441	53528	AATCCAATTAGAATGGTCA
55442	53529	TAATCCAATTAGAATGGTC
55443	53530	CTAAATCCAATTAGAATGGT
55444	53531	ACTAAATCCAATTAGAATGG
55445	53532	GACTAAATCCAATTAGAATG
55446	53533	AGACTAAATCCAATTAGAAT
55447	53534	CAGACTAAATCCAATTAGAA
55448	53535	TCAGACTAAATCCAATTAGA
55449	53536	TTCAGACTAAATCCAATTAG
55450	53537	CTTCAGACTAAATCCAATTA
55451	53538	TCTTCAGACTAAATCCAATT
55452	53539	TTCTTCAGACTAAATCCAAT
55453	53540	ATTCTTCAGACTAAATCCAA
55454	53541	AATTCTTCAGACTAAATCCA
55455	53542	TAATTCTTCAGACTAAATCC
55456	53543	GTAATTCTTCAGACTAAATC
55457	53544	AGTAATTCTTCAGACTAAAT
55458	53545	AAGTAATTCTTCAGACTAAA
55459	53546	AAAGTAATTCTTCAGACTAA

104536	102623	ATAATTGTTACCACCGAAAT
104537	102624	TATAATTGTTACCACCGAAA
104538	102625	TTATAATTGTTACCACCGAA
104539	102626	ATTATAATTGTTACCACCGA
104540	102627	CATTATAATTGTTACCACCG
104541	102628	ACATTATAATTGTTACCACC
104542	102629	GACATTATAATTGTTACCAC
104543	102630	AGACATTATAATTGTTACCA
104544	102631	GAGACATTATAATTGTTACC
104545	102632	GGAGACATTATAATTGTTAC
104546	102633	AGGAGACATTATAATTGTTA
104547	102634	AAGGAGACATTATAATTGTT
104548	102635	AAAGGAGACATTATAATTGT
104549	102636	AAAAGGAGACATTATAATTG
104550	102637	AAAAAGGAGACATTATAATT
104551	102638	GAAAAAGGAGACATTATAAT
104552	102639	TGAAAAAGGAGACATTATAA
104553	102640	ATGAAAAAGGAGACATTATA
104554	102641	GATGAAAAAGGAGACATTAT
104555	102642	AGATGAAAAAGGAGACATTA
104556	102643	GAGATGAAAAAGGAGACATT
104557	102644	AGAGATGAAAAAGGAGACAT
104558	102645	GAGAGATGAAAAAGGAGACA
104559	102646	TGAGAGATGAAAAAGGAGAC
104560	102647	ATGAGAGATGAAAAAGGAGA
104561	102648	AATGAGAGATGAAAAAGGAG
104562	102649	AAATGAGAGATGAAAAAGGA
104563	102650	AAAATGAGAGATGAAAAAGG
104564	102651	TAAAATGAGAGATGAAAAAG
104565	102652	ATAAAATGAGAGATGAAAAA
104566	102653	AATAAAATGAGAGATGAAAA
104567	102654	TAATAAAATGAGAGATGAAA
104568	102655	ATAATAAAATGAGAGATGAA
104569	102656	AATAATAAAATGAGAGATGA
104570	102657	AAATAATAAAATGAGAGATG
104571	102658	CAAATAATAAAATGAGAGAT
104572	102659	CCAAATAATAAAATGAGAGA
104573	102660	CCCAAATAATAAAATGAGAG
104574	102661	ACCCAAATAATAAAATGAGA
104575	102662	AACCCAAATAATAAAATGAG
104576	102663	AAACCCAAATAATAAAATGA
104577	102664	AAAACCCAAATAATAAAATG
104578	102665	GAAAACCCAAATAATAAAAT
104579	102666	AGAAAACCCAAATAATAAAA
104580	102667	GAGAAAACCCAAATAATAAA
104581	102668	AGAGAAAACCCAAATAATAA
104582	102669	AAGAGAAAACCCAAATAATA
104583	102670	AAAGAGAAAACCCAAATAAT
104584	102671	AAAAGAGAAAACCCAAATAA
104585	102672	AAAAAGAGAAAACCCAAATA
104586	102673	AAAAAAGAGAAAACCCAAAT
104587	102674	AAAAAAAGAGAAAACCCAAA
104588	102675	AAAAAAAAGAGAAAACCCAA
104589	102676	GAAAAAAAAGAGAAAACCCA
104590	102677	AGAAAAAAAAGAGAAAACCC
104591	102678	CAGAAAAAAAAGAGAAAACC
104592	102679	TCAGAAAAAAAAGAGAAAAC
104593	102680	CTCAGAAAAAAAAGAGAAAA
104594	102681	ACTCAGAAAAAAAAGAGAAA
104595	102682	GACTCAGAAAAAAAAGAGAA
104596	102683	AGACTCAGAAAAAAAAGAGA
104597	102684	CAGACTCAGAAAAAAAAGAG
104598	102685	CCAGACTCAGAAAAAAAAGA
104599	102686	GCCAGACTCAGAAAAAAAAG
104600	102687	AGCCAGACTCAGAAAAAAAA
104601	102688	TAGCCAGACTCAGAAAAAAA
104602	102689	TTAGCCAGACTCAGAAAAAA
104603	102690	TTTAGCCAGACTCAGAAAAA
104604	102691	CTTTAGCCAGACTCAGAAAA
104605	102692	CCTTTAGCCAGACTCAGAAA
104606	102693	ACCTTTAGCCAGACTCAGAA

6313	4400	ACACTGAAGCAAAAAGCTAT
6314	4401	TACACTGAAGCAAAAAGCTA
6315	4402	TTACACTGAAGCAAAAAGCT
6316	4403	ATTACACTGAAGCAAAAAGC
6317	4404	AATTACACTGAAGCAAAAAG
6318	4405	TAATTACACTGAAGCAAAAA
6319	4406	ATAATTACACTGAAGCAAAA
6320	4407	AATAATTACACTGAAGCAAA
6321	4408	AAATAATTACACTGAAGCAA
6322	4409	GAAATAATTACACTGAAGCA
6323	4410	GGAAATAATTACACTGAAGC
6324	4411	AGGAAATAATTACACTGAAG
6325	4412	AAGGAAATAATTACACTGAA
6326	4413	TAAGGAAATAATTACACTGA
6327	4414	CTAAGGAAATAATTACACTG
6328	4415	TCTAAGGAAATAATTACACT
6329	4416	CTCTAAGGAAATAATTACAC
6330	4417	TCTCTAAGGAAATAATTACA
6331	4418	TTCTCTAAGGAAATAATTAC
6332	4419	TTTCTCTAAGGAAATAATTA
6333	4420	CTTTCTCTAAGGAAATAATT
6334	4421	ACTTTCTCTAAGGAAATAAT
6335	4422	AACTTTCTCTAAGGAAATAA
6336	4423	TAACTTTCTCTAAGGAAATA
6337	4424	GTAACTTTCTCTAAGGAAAT
6338	4425	GGTAACTTTCTCTAAGGAAA
6339	4426	TGGTAACTTTCTCTAAGGAA
6340	4427	TTGGTAACTTTCTCTAAGGA
6341	4428	CTTGGTAACTTTCTCTAAGG
6342	4429	TCTTGGTAACTTTCTCTAAG
6343	4430	CTCTTGGTAACTTTCTCTAA
6344	4431	ACTCTTGGTAACTTTCTCTA
6345	4432	CACTCTTGGTAACTTTCTCT
6346	4433	CCACTCTTGGTAACTTTCTC
6347	4434	ACCACTCTTGGTAACTTTCT
6348	4435	AACCACTCTTGGTAACTTTC
6349	4436	AAACCACTCTTGGTAACTTT
6350	4437	AAAACCACTCTTGGTAACTT
6351	4438	TAAAACCACTCTTGGTAACT
6352	4439	GTAAAACCACTCTTGGTAAC
6353	4440	AGTAAAACCACTCTTGGTAA
6354	4441	TAGTAAAACCACTCTTGGTA
6355	4442	CTAGTAAAACCACTCTTGGT
6356	4443	ACTAGTAAAACCACTCTTGG
6357	4444	AACTAGTAAAACCACTCTTG
6358	4445	GAACTAGTAAAACCACTCTT
6359	4446	TGAACTAGTAAAACCACTCT
6360	4447	CTGAACTAGTAAAACCACTC
6361	4448	TCTGAACTAGTAAAACCACT
6362	4449	CTCTGAACTAGTAAAACCAC
6363	4450	CCTCTGAACTAGTAAAACCA
6364	4451	CCCTCTGAACTAGTAAAACC
6365	4452	GCCCTCTGAACTAGTAAAAC
6366	4453	AGCCCTCTGAACTAGTAAAA
6367	4454	AAGCCCTCTGAACTAGTAAA
6368	4455	GAAGCCCTCTGAACTAGTAA
6369	4456	TGAAGCCCTCTGAACTAGTA
6370	4457	CTGAAGCCCTCTGAACTAGT
6371	4458	CCTGAAGCCCTCTGAACTAG
6372	4459	TCCTGAAGCCCTCTGAACTA
6373	4460	ATCCTGAAGCCCTCTGAACT
6374	4461	AATCCTGAAGCCCTCTGAAC
6375	4462	AAATCCTGAAGCCCTCTGAA
6376	4463	AAAATCCTGAAGCCCTCTGA
6377	4464	AAAAATCCTGAAGCCCTCTG
6378	4465	TAAAAATCCTGAAGCCCTCT
6379	4466	ATAAAAATCCTGAAGCCCTC
6380	4467	CATAAAAATCCTGAAGCCCT
6381	4468	CCATAAAAATCCTGAAGCCC
6382	4469	GCCATAAAAATCCTGAAGCC
6383	4470	AGCCATAAAAATCCTGAAGC

55460	53547	AAAAGTAATTCTTCAGACTA
55461	53548	CAAAAGTAATTCTTCAGACT
55462	53549	GCAAAAGTAATTCTTCAGAC
55463	53550	AGCAAAAGTAATTCTTCAGA
55464	53551	AAGCAAAAGTAATTCTTCAG
55465	53552	TAAGCAAAAGTAATTCTTCA
55466	53553	TTAAGCAAAAGTAATTCTTC
55467	53554	GTTAAGCAAAAGTAATTCTT
55468	53555	TGTTAAGCAAAAGTAATTCT
55469	53556	CTGTTAAGCAAAAGTAATTC
55470	53557	TCTGTTAAGCAAAAGTAATT
55471	53558	ATCTGTTAAGCAAAAGTAAT
55472	53559	AATCTGTTAAGCAAAAGTAA
55473	53560	GAATCTGTTAAGCAAAAGTA
55474	53561	AGAATCTGTTAAGCAAAAGT
55475	53562	AAGAATCTGTTAAGCAAAAG
55476	53563	AAAGAATCTGTTAAGCAAAA
55477	53564	CAAAGAATCTGTTAAGCAAA
55478	53565	ACAAAGAATCTGTTAAGCAA
55479	53566	GACAAAGAATCTGTTAAGCA
55480	53567	TGACAAAGAATCTGTTAAGC
55481	53568	GTGACAAAGAATCTGTTAAG
55482	53569	TGTGACAAAGAATCTGTTAA
55483	53570	ATGTGACAAAGAATCTGTTA
55484	53571	AATGTGACAAAGAATCTGTT
55485	53572	AAATGTGACAAAGAATCTGT
55486	53573	TAAATGTGACAAAGAATCTG
55487	53574	CTAAATGTGACAAAGAATCT
55488	53575	ACTAAATGTGACAAAGAATC
55489	53576	CACTAAATGTGACAAAGAAT
55490	53577	TCACTAAATGTGACAAAGAA
55491	53578	TTCACTAAATGTGACAAAGA
55492	53579	TTTCACTAAATGTGACAAAG
55493	53580	TTTTCACTAAATGTGACAAA
55494	53581	TTTTTCACTAAATGTGACAA
55495	53582	ATTTTTCACTAAATGTGACA
55496	53583	GATTTTTCACTAAATGTGAC
55497	53584	TGATTTTTCACTAAATGTGA
55498	53585	ATGATTTTTCACTAAATGTG
55499	53586	TATGATTTTTCACTAAATGT
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104760	102847	TACATCCTAAAGAACTAGAA
104761	102848	ATACATCCTAAAGAACTAGA
104762	102849	AATACATCCTAAAGAACTAG
104763	102850	CAATACATCCTAAAGAACTA
104764	102851	CCAATACATCCTAAAGAACT
104765	102852	GCCAATACATCCTAAAGAAC
104766	102853	TGCCAATACATCCTAAAGAA
104767	102854	CTGCCAATACATCCTAAAGA
104768	102855	TCTGCCAATACATCCTAAAG
104769	102856	ATCTGCCAATACATCCTAAA
104770	102857	CATCTGCCAATACATCCTAA
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104772	102859	TTCATCTGCCAATACATCCT
104773	102860	CTTCATCTGCCAATACATCC
104774	102861	ACTTCATCTGCCAATACATC
104775	102862	AACTTCATCTGCCAATACAT
104776	102863	AAACTTCATCTGCCAATACA
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104807	102894	AGCAGTAAGTGCCTACATCA
104808	102895	CAGCAGTAAGTGCCTACATC
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104810	102897	TACAGCAGTAAGTGCCTACA
104811	102898	TTACAGCAGTAAGTGCCTAC
104812	102899	TTTACAGCAGTAAGTGCCTA
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104815	102902	ATGTTTACAGCAGTAAGTGC
104816	102903	AATGTTTACAGCAGTAAGTG
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104819	102906	AGGAATGTTTACAGCAGTAA

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6527	4614	TTGACAGTAAAAATGCAATT
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6529	4616	ACTTGACAGTAAAAATGCAA
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6531	4618	GCACTTGACAGTAAAAATGC
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6570	4657	CAATAATCCAGTAACTAACA
6571	4658	TCAATAATCCAGTAACTAAC
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6576	4663	AAATATCAATAATCCAGTAA
6577	4664	CAAATATCAATAATCCAGTA
6578	4665	TCAAATATCAATAATCCAGT
6579	4666	CTCAAATATCAATAATCCAG
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6581	4668	AACTCAAATATCAATAATCC
6582	4669	AAACTCAAATATCAATAATC
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6593	4680	GGAACCAAATTAAACTCAAA
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55676	53763	GAAGTCGAGGCTGCAGTGAG
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55680	53767	CTGGGAAGTCGAGGCTGCAG
55681	53768	CCTGGGAAGTCGAGGCTGCA
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55685	53772	TGAGCCTGGGAAGTCGAGGC
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55688	53775	ACCTGAGCCTGGGAAGTCGA
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55690	53777	TCACCTGAGCCTGGGAAGTC
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55697	53784	GAGAGGATCACCTGAGCCTG
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55740	53827	AGTGATGTGCACATACAGTC
55741	53828	TAGTGATGTGCACATACAGT
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104862	102949	CAGCTTATCAAAACCTATAG
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104867	102954	AAACACAGCTTATCAAAACC
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55744	53831	GCATAGTGATGTGCACATAC
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104938	103025	CTGAATGACCAGTGGGTCCA
104939	103026	CCTGAATGACCAGTGGGTCC
104940	103027	TCCTGAATGACCAGTGGGTC
104941	103028	CTCCTGAATGACCAGTGGGT
104942	103029	GCTCCTGAATGACCAGTGGG
104943	103030	TGCTCCTGAATGACCAGTGG
104944	103031	ATGCTCCTGAATGACCAGTG
104945	103032	TATGCTCCTGAATGACCAGT
104946	103033	ATATGCTCCTGAATGACCAG
104947	103034	AATATGCTCCTGAATGACCA
104948	103035	CAATATGCTCCTGAATGACC
104949	103036	GCAATATGCTCCTGAATGAC
104950	103037	AGCAATATGCTCCTGAATGA
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104959	103046	TGAAAATTAAGCAATATGCT
104960	103047	ATGAAAATTAAGCAATATGC
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6670	4757	ACCAAGTACCCTCATTAATA
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6673	4760	TAAACCAAGTACCCTCATTA
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6677	4764	CAGATAAACCAAGTACCCTC
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6679	4766	GACAGATAAACCAAGTACCC
6680	4767	CGACAGATAAACCAAGTACC
6681	4768	ACGACAGATAAACCAAGTAC
6682	4769	CACGACAGATAAACCAAGTA
6683	4770	GCACGACAGATAAACCAAGT
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6687	4774	ATCAGCACGACAGATAAACC
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6691	4778	TACTATCAGCACGACAGATA
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6693	4780	AGTACTATCAGCACGACAGA
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6695	4782	TCAGTACTATCAGCACGACA
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6708	4795	TCCTGCACTTTACTCAGTAC
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6718	4805	GGAATTTCATTCCTGCACTT
6719	4806	AGGAATTTCATTCCTGCACT
6720	4807	CAGGAATTTCATTCCTGCAC
6721	4808	TCAGGAATTTCATTCCTGCA
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55825	53912	GGCCCAGCAGTTTGAGACCA
55826	53913	AGGCCCAGCAGTTTGAGACC
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55835	53922	AAGACTCTTAGGCCCAGCAG
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55839	53926	TGGGAAGACTCTTAGGCCCA
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55868	53955	TGTAATCCCAGGACTTTGGG
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55882	53969	GGTGCGGTGACTCATGTAAT
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104965	103052	AATACATGAAAATTAAGCAA
104966	103053	AAATACATGAAAATTAAGCA
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104969	103056	TACAAATACATGAAAATTAA
104970	103057	ATACAAATACATGAAAATTA
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104975	103062	AAAGTATACAAATACATGAA
104976	103063	GAAAGTATACAAATACATGA
104977	103064	GGAAAGTATACAAATACATG
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104983	103070	AACTTTGGAAAGTATACAAA
104984	103071	GAACTTTGGAAAGTATACAA
104985	103072	GGAACTTTGGAAAGTATACA
104986	103073	AGGAACTTTGGAAAGTATAC
104987	103074	GAGGAACTTTGGAAAGTATA
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104989	103076	AAGAGGAACTTTGGAAAGTA
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105005	103092	AATAACACTAGATAACAAGA
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105008	103095	TAAAATAACACTAGATAACA
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6745	4832	ACAACAAAGCTTTAGAACAG
6746	4833	AACAACAAAGCTTTAGAACA
6747	4834	CAACAACAAAGCTTTAGAAC
6748	4835	ACAACAACAAAGCTTTAGAA
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6765	4852	AAAAAGAAAGGTTAACAACA
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6781	4868	AAAACACTTTCAGATGAAAA
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55939	54026	GAAGTTGGCTTAAAAATCCT
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55945	54032	ATGATTGAAGTTGGCTTAAA
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55950	54037	AGGGCATGATTGAAGTTGGC
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105055	103142	GTGACAGAGCGAGACTCCAT
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6834	4921	AAATTACAAAAAAGTTACCA
6835	4922	GAAATTACAAAAAAGTTACC
6836	4923	TGAAATTACAAAAAAGTTAC
6837	4924	ATGAAATTACAAAAAAGTTA
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6839	4926	CCATGAAATTACAAAAAAGT
6840	4927	GCCATGAAATTACAAAAAAG
6841	4928	TGCCATGAAATTACAAAAAA
6842	4929	GTGCCATGAAATTACAAAAA
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6844	4931	TAGTGCCATGAAATTACAAA
6845	4932	ATAGTGCCATGAAATTACAA
6846	4933	AATAGTGCCATGAAATTACA
6847	4934	CAATAGTGCCATGAAATTAC
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6849	4936	CCCAATAGTGCCATGAAATT
6850	4937	TCCCAATAGTGCCATGAAAT
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6852	4939	ATTCCCAATAGTGCCATGAA
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6854	4941	AAATTCCCAATAGTGCCATG
6855	4942	AAAATTCCCAATAGTGCCAT
6856	4943	GAAAATTCCCAATAGTGCCA
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6858	4945	GCGAAAATTCCCAATAGTGC
6859	4946	AGCGAAAATTCCCAATAGTG
6860	4947	CAGCGAAAATTCCCAATAGT
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6862	4949	ACCAGCGAAAATTCCCAATA
6863	4950	AACCAGCGAAAATTCCCAAT
6864	4951	CAACCAGCGAAAATTCCCAA
6865	4952	TCAACCAGCGAAAATTCCCA
6866	4953	GTCAACCAGCGAAAATTCCC
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6868	4955	GAGTCAACCAGCGAAAATTC
6869	4956	AGAGTCAACCAGCGAAAATT
6870	4957	AAGAGTCAACCAGCGAAAAT
6871	4958	GAAGAGTCAACCAGCGAAAA
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6873	4960	AAGAAGAGTCAACCAGCGAA
6874	4961	GAAGAAGAGTCAACCAGCGA
6875	4962	AGAAGAAGAGTCAACCAGCG
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6877	4964	GAAGAAGAAGAGTCAACCAG
6878	4965	AGAAGAAGAAGAGTCAACCA
6879	4966	TAGAAGAAGAAGAGTCAACC
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55959	54046	AGAGAGTCAAGGGCATGATT
55960	54047	GAGAGAGTCAAGGGCATGAT
55961	54048	GGAGAGAGTCAAGGGCATGA
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55963	54050	AGGGAGAGAGTCAAGGGCAT
55964	54051	AAGGGAGAGAGTCAAGGGCA
55965	54052	GAAGGGAGAGAGTCAAGGGC
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55967	54054	TAGAAGGGAGAGAGTCAAGG
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55969	54056	AGTAGAAGGGAGAGAGTCAA
55970	54057	AAGTAGAAGGGAGAGAGTCA
55971	54058	TAAGTAGAAGGGAGAGAGTC
55972	54059	GTAAGTAGAAGGGAGAGAGT
55973	54060	GGTAAGTAGAAGGGAGAGAG
55974	54061	AGGTAAGTAGAAGGGAGAGA
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55976	54063	GGAGGTAAGTAGAAGGGAGA
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55981	54068	AACAAGGAGGTAAGTAGAAG
55982	54069	GAACAAGGAGGTAAGTAGAA
55983	54070	AGAACAAGGAGGTAAGTAGA
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55985	54072	AGAGAACAAGGAGGTAAGTA
55986	54073	AAGAGAACAAGGAGGTAAGT
55987	54074	AAAGAGAACAAGGAGGTAAG
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55993	54080	AAAGAAAAAGAGAACAAGGA
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55995	54082	AAAAAGAAAAAGAGAACAAG
55996	54083	GAAAAAGAAAAAGAGAACAA
55997	54084	AGAAAAAGAAAAAGAGAACA
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105106	103193	GGAGGCAGAGGTTGCAGTAA
105107	103194	GGGAGGCAGAGGTTGCAGTA
105108	103195	GGGGAGGCAGAGGTTGCAGT
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105110	103197	CTGGGGAGGCAGAGGTTGCA
105111	103198	ACTGGGGAGGCAGAGGTTGC
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105116	103203	CTTGAACTGGGGAGGCAGAG
105117	103204	ACTTGAACTGGGGAGGCAGA
105118	103205	CACTTGAACTGGGGAGGCAG
105119	103206	TCACTTGAACTGGGGAGGCA
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105145	103232	CTACTCAGGAGGCTGAGGCA
105146	103233	GCTACTCAGGAGGCTGAGGC
105147	103234	AGCTACTCAGGAGGCTGAGG
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105149	103236	CCAGCTACTCAGGAGGCTGA
105150	103237	CCCAGCTACTCAGGAGGCTG
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105152	103239	ATCCCAGCTACTCAGGAGGC
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105159	103246	GCCTGTAATCCCAGCTACTC
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105171	103258	GTGGTGGTACATGCCTGTAA
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105173	103260	GAGTGGTGGTACATGCCTGT
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6884	4971	GAATGTAGAAGAAGAAGAGT
6885	4972	GGAATGTAGAAGAAGAAGAG
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6903	4990	TTATTTTTAATGGGGAAGGG
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6906	4993	TTTTTATTTTTAATGGGGAA
6907	4994	ATTTTTATTTTTAATGGGGA
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6909	4996	ATATTTTTATTTTTAATGGG
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6923	5010	ACAATTGTAAATCCATATTT
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6928	5015	GAGTAACAATTGTAAATCCA
6929	5016	AGAGTAACAATTGTAAATCC
6930	5017	TAGAGTAACAATTGTAAATC
6931	5018	ATAGAGTAACAATTGTAAAT
6932	5019	AATAGAGTAACAATTGTAAA
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6934	5021	GGAATAGAGTAACAATTGTA
6935	5022	AGGAATAGAGTAACAATTGT
6936	5023	TAGGAATAGAGTAACAATTG
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6948	5035	ATTATTTAGGTTTAGGAATA
6949	5036	TATTATTTAGGTTTAGGAAT
6950	5037	ATATTATTTAGGTTTAGGAA
6951	5038	CATATTATTTAGGTTTAGGA

56028	54115	GGTGACAGACCGAGACTCCA
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56047	54134	GCCACTGCACTTCAGCCTGG
56048	54135	CGCCACTGCACTTCAGCCTG
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56052	54139	ATCACGCCACTGCACTTCAG
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56069	54156	GGCTGCAGTGAGCTGAAATC
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56076	54163	AGGCTGAGGCTGCAGTGAGC
56077	54164	GAGGCTGAGGCTGCAGTGAG
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56095	54182	ATAGCCCCAGCTACTCAGGA
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105175	103262	AGGAGTGGTGGTACATGCCT
105176	103263	CAGGAGTGGTGGTACATGCC
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105178	103265	GCCAGGAGTGGTGGTACATG
105179	103266	AGCCAGGAGTGGTGGTACAT
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105219	103306	TGGTGAAACCCCCTCTCTAC
105220	103307	ATGGTGAAACCCCCTCTCTA
105221	103308	CATGGTGAAACCCCCTCTCT
105222	103309	ACATGGTGAAACCCCCTCTC
105223	103310	AACATGGTGAAACCCCCTCT
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105227	103314	GACCAACATGGTGAAACCCC
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105229	103316	TTGACCAACATGGTGAAACC
105230	103317	CTTGACCAACATGGTGAAAC
105231	103318	GCTTGACCAACATGGTGAAA
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105233	103320	CAGCTTGACCAACATGGTGA
105234	103321	TCAGCTTGACCAACATGGTG
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105237	103324	AGATCAGCTTGACCAACATG
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6952	5039	TCATATTATTTAGGTTTAGG
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6959	5046	TCTAATGTCATATTATTTAG
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7015	5102	GAAAATCACTAAAAGAAAAA
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56099	54186	ACCTATAGCCCCAGCTACTC
56100	54187	CACCTATAGCCCCAGCTACT
56101	54188	GCACCTATAGCCCCAGCTAC
56102	54189	GGCACCTATAGCCCCAGCTA
56103	54190	AGGCACCTATAGCCCCAGCT
56104	54191	CAGGCACCTATAGCCCCAGC
56105	54192	GCAGGCACCTATAGCCCCAG
56106	54193	GGCAGGCACCTATAGCCCCA
56107	54194	TGGCAGGCACCTATAGCCCC
56108	54195	GTGGCAGGCACCTATAGCCC
56109	54196	GGTGGCAGGCACCTATAGCC
56110	54197	TGGTGGCAGGCACCTATAGC
56111	54198	GTGGTGGCAGGCACCTATAG
56112	54199	CGTGGTGGCAGGCACCTATA
56113	54200	GCGTGGTGGCAGGCACCTAT
56114	54201	GGCGTGGTGGCAGGCACCTA
56115	54202	GGGCGTGGTGGCAGGCACCT
56116	54203	CGGGCGTGGTGGCAGGCACC
56117	54204	CCGGGCGTGGTGGCAGGCAC
56118	54205	GCCGGGCGTGGTGGCAGGCA
56119	54206	AGCCGGGCGTGGTGGCAGGC
56120	54207	TAGCCGGGCGTGGTGGCAGG
56121	54208	TTAGCCGGGCGTGGTGGCAG
56122	54209	ATTAGCCGGGCGTGGTGGCA
56123	54210	AATTAGCCGGGCGTGGTGGC
56124	54211	AAATTAGCCGGGCGTGGTGG
56125	54212	AAAATTAGCCGGGCGTGGTG
56126	54213	AAAAATTAGCCGGGCGTGGT
56127	54214	CAAAAATTAGCCGGGCGTGG
56128	54215	ACAAAAATTAGCCGGGCGTG
56129	54216	TACAAAAATTAGCCGGGCGT
56130	54217	ATACAAAAATTAGCCGGGCG
56131	54218	AATACAAAAATTAGCCGGGC
56132	54219	AAATACAAAAATTAGCCGGG
56133	54220	AAAATACAAAAATTAGCCGG
56134	54221	AAAAATACAAAAATTAGCCG
56135	54222	TAAAAATACAAAAATTAGCC
56136	54223	CTAAAAATACAAAAATTAGC
56137	54224	ACTAAAAATACAAAAATTAG
56138	54225	TACTAAAAATACAAAAATTA
56139	54226	CTACTAAAAATACAAAAATT
56140	54227	TCTACTAAAAATACAAAAAT
56141	54228	CTCTACTAAAAATACAAAAA
56142	54229	TCTCTACTAAAAATACAAAA
56143	54230	ATCTCTACTAAAAATACAAA
56144	54231	CATCTCTACTAAAAATACAA
56145	54232	CCATCTCTACTAAAAATACA
56146	54233	CCCATCTCTACTAAAAATAC
56147	54234	CCCCATCTCTACTAAAAATA
56148	54235	ACCCCATCTCTACTAAAAAT
56149	54236	AACCCCATCTCTACTAAAAA
56150	54237	AAACCCCATCTCTACTAAAA
56151	54238	GAAACCCCATCTCTACTAAA
56152	54239	TGAAACCCCATCTCTACTAA
56153	54240	GTGAAACCCCATCTCTACTA
56154	54241	GGTGAAACCCCATCTCTACT
56155	54242	TGGTGAAACCCCATCTCTAC
56156	54243	ATGGTGAAACCCCATCTCTA
56157	54244	CATGGTGAAACCCCATCTCT
56158	54245	ACATGGTGAAACCCCATCTC
56159	54246	AACATGGTGAAACCCCATCT
56160	54247	CAACATGGTGAAACCCCATC
56161	54248	CCAACATGGTGAAACCCCAT
56162	54249	GCCAACATGGTGAAACCCCA
56163	54250	GGCCAACATGGTGAAACCCC
56164	54251	TGGCCAACATGGTGAAACCC
56165	54252	CTGGCCAACATGGTGAAACC
56166	54253	CCTGGCCAACATGGTGAAAC
56167	54254	GCCTGGCCAACATGGTGAAA
56168	54255	AGCCTGGCCAACATGGTGAA
56169	54256	CAGCCTGGCCAACATGGTGA

105246	103333	AGGAGTTCGAGATCAGCTTG
105247	103334	CAGGAGTTCGAGATCAGCTT
105248	103335	TCAGGAGTTCGAGATCAGCT
105249	103336	GTCAGGAGTTCGAGATCAGC
105250	103337	GGTCAGGAGTTCGAGATCAG
105251	103338	AGGTCAGGAGTTCGAGATCA
105252	103339	GAGGTCAGGAGTTCGAGATC
105253	103340	TGAGGTCAGGAGTTCGAGAT
105254	103341	CTGAGGTCAGGAGTTCGAGA
105255	103342	TCTGAGGTCAGGAGTTCGAG
105256	103343	ATCTGAGGTCAGGAGTTCGA
105257	103344	CATCTGAGGTCAGGAGTTCG
105258	103345	TCATCTGAGGTCAGGAGTTC
105259	103346	ATCATCTGAGGTCAGGAGTT
105260	103347	GATCATCTGAGGTCAGGAGT
105261	103348	GGATCATCTGAGGTCAGGAG
105262	103349	TGGATCATCTGAGGTCAGGA
105263	103350	GTGGATCATCTGAGGTCAGG
105264	103351	GGTGGATCATCTGAGGTCAG
105265	103352	GGGTGGATCATCTGAGGTCA
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105267	103354	GTGGGTGGATCATCTGAGGT
105268	103355	GGTGGGTGGATCATCTGAGG
105269	103356	AGGTGGGTGGATCATCTGAG
105270	103357	AAGGTGGGTGGATCATCTGA
105271	103358	CAAGGTGGGTGGATCATCTG
105272	103359	CCAAGGTGGGTGGATCATCT
105273	103360	GCCAAGGTGGGTGGATCATC
105274	103361	GGCCAAGGTGGGTGGATCAT
105275	103362	AGGCCAAGGTGGGTGGATCA
105276	103363	GAGGCCAAGGTGGGTGGATC
105277	103364	GGAGGCCAAGGTGGGTGGAT
105278	103365	AGGAGGCCAAGGTGGGTGGA
105279	103366	TAGGAGGCCAAGGTGGGTGG
105280	103367	TTAGGAGGCCAAGGTGGGTG
105281	103368	TTTAGGAGGCCAAGGTGGGT
105282	103369	CTTTAGGAGGCCAAGGTGGG
105283	103370	ACTTTAGGAGGCCAAGGTGG
105284	103371	CACTTTAGGAGGCCAAGGTG
105285	103372	GCACTTTAGGAGGCCAAGGT
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105287	103374	CAGCACTTTAGGAGGCCAAG
105288	103375	CCAGCACTTTAGGAGGCCAA
105289	103376	TCCAGCACTTTAGGAGGCCA
105290	103377	TTCCAGCACTTTAGGAGGCC
105291	103378	ATTCCAGCACTTTAGGAGGC
105292	103379	AATTCCAGCACTTTAGGAGG
105293	103380	TAATTCCAGCACTTTAGGAG
105294	103381	GTAATTCCAGCACTTTAGGA
105295	103382	TGTAATTCCAGCACTTTAGG
105296	103383	CTGTAATTCCAGCACTTTAG
105297	103384	CCTGTAATTCCAGCACTTTA
105298	103385	GCCTGTAATTCCAGCACTTT
105299	103386	TGCCTGTAATTCCAGCACTT
105300	103387	ATGCCTGTAATTCCAGCACT
105301	103388	CATGCCTGTAATTCCAGCAC
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105303	103390	CTCATGCCTGTAATTCCAGC
105304	103391	GCTCATGCCTGTAATTCCAG
105305	103392	GGCTCATGCCTGTAATTCCA
105306	103393	TGGCTCATGCCTGTAATTCC
105307	103394	GTGGCTCATGCCTGTAATTC
105308	103395	GGTGGCTCATGCCTGTAATT
105309	103396	CGGTGGCTCATGCCTGTAAT
105310	103397	ACGGTGGCTCATGCCTGTAA
105311	103398	CACGGTGGCTCATGCCTGTA
105312	103399	GCACGGTGGCTCATGCCTGT
105313	103400	GGCACGGTGGCTCATGCCTG
105314	103401	GGGCACGGTGGCTCATGCCT
105315	103402	CGGGCACGGTGGCTCATGCC
105316	103403	CCGGGCACGGTGGCTCATGC

7023	5110	ACTAAGCTGAAAATCACTAA
7024	5111	TACTAAGCTGAAAATCACTA
7025	5112	ATACTAAGCTGAAAATCACT
7026	5113	AATACTAAGCTGAAAATCAC
7027	5114	AAATACTAAGCTGAAAATCA
7028	5115	AAAATACTAAGCTGAAAATC
7029	5116	AAAAATACTAAGCTGAAAAT
7030	5117	TAAAAATACTAAGCTGAAAA
7031	5118	GTAAAAATACTAAGCTGAAA
7032	5119	AGTAAAAATACTAAGCTGAA
7033	5120	CAGTAAAAATACTAAGCTGA
7034	5121	GCAGTAAAAATACTAAGCTG
7035	5122	AGCAGTAAAAATACTAAGCT
7036	5123	AAGCAGTAAAAATACTAAGC
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7041	5128	GAAAGAAGCAGTAAAAATAC
7042	5129	AGAAAGAAGCAGTAAAAATA
7043	5130	GAGAAAGAAGCAGTAAAAAT
7044	5131	AGAGAAAGAAGCAGTAAAAA
7045	5132	AAGAGAAAGAAGCAGTAAAA
7046	5133	CAAGAGAAAGAAGCAGTAAA
7047	5134	TCAAGAGAAAGAAGCAGTAA
7048	5135	CTCAAGAGAAAGAAGCAGTA
7049	5136	CCTCAAGAGAAAGAAGCAGT
7050	5137	GCCTCAAGAGAAAGAAGCAG
7051	5138	TGCCTCAAGAGAAAGAAGCA
7052	5139	ATGCCTCAAGAGAAAGAAGC
7053	5140	AATGCCTCAAGAGAAAGAAG
7054	5141	CAATGCCTCAAGAGAAAGAA
7055	5142	GCAATGCCTCAAGAGAAAGA
7056	5143	TGCAATGCCTCAAGAGAAAG
7057	5144	TTGCAATGCCTCAAGAGAAA
7058	5145	GTTGCAATGCCTCAAGAGAA
7059	5146	AGTTGCAATGCCTCAAGAGA
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7064	5151	TTTTAAGTTGCAATGCCTCA
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7066	5153	ATTTTTAAGTTGCAATGCCT
7067	5154	AATTTTTAAGTTGCAATGCC
7068	5155	CAATTTTTAAGTTGCAATGC
7069	5156	ACAATTTTTAAGTTGCAATG
7070	5157	CACAATTTTTAAGTTGCAAT
7071	5158	GCACAATTTTTAAGTTGCAA
7072	5159	AGCACAATTTTTAAGTTGCA
7073	5160	CAGCACAATTTTTAAGTTGC
7074	5161	ACAGCACAATTTTTAAGTTG
7075	5162	AACAGCACAATTTTTAAGTT
7076	5163	AAACAGCACAATTTTTAAGT
7077	5164	TAAACAGCACAATTTTTAAG
7078	5165	CTAAACAGCACAATTTTTAA
7079	5166	GCTAAACAGCACAATTTTTA
7080	5167	GGCTAAACAGCACAATTTTT
7081	5168	TGGCTAAACAGCACAATTTT
7082	5169	CTGGCTAAACAGCACAATTT
7083	5170	CCTGGCTAAACAGCACAATT
7084	5171	GCCTGGCTAAACAGCACAAT
7085	5172	CGCCTGGCTAAACAGCACAA
7086	5173	GCGCCTGGCTAAACAGCACA
7087	5174	GGCGCCTGGCTAAACAGCAC
7088	5175	AGGCGCCTGGCTAAACAGCA
7089	5176	CAGGCGCCTGGCTAAACAGC
7090	5177	ACAGGCGCCTGGCTAAACAG
7091	5178	TACAGGCGCCTGGCTAAACA
7092	5179	TTACAGGCGCCTGGCTAAAC
7093	5180	ATTACAGGCGCCTGGCTAAA

56170	54257	CCAGCCTGGCCAACATGGTG
56171	54258	ACCAGCCTGGCCAACATGGT
56172	54259	GACCAGCCTGGCCAACATGG
56173	54260	AGACCAGCCTGGCCAACATG
56174	54261	GAGACCAGCCTGGCCAACAT
56175	54262	CGAGACCAGCCTGGCCAACA
56176	54263	TCGAGACCAGCCTGGCCAAC
56177	54264	TTCGAGACCAGCCTGGCCAA
56178	54265	GTTCGAGACCAGCCTGGCCA
56179	54266	AGTTCGAGACCAGCCTGGCC
56180	54267	GAGTTCGAGACCAGCCTGGC
56181	54268	GGAGTTCGAGACCAGCCTGG
56182	54269	AGGAGTTCGAGACCAGCCTG
56183	54270	CAGGAGTTCGAGACCAGCCT
56184	54271	TCAGGAGTTCGAGACCAGCC
56185	54272	GTCAGGAGTTCGAGACCAGC
56186	54273	GGTCAGGAGTTCGAGACCAG
56187	54274	AGGTCAGGAGTTCGAGACCA
56188	54275	GAGGTCAGGAGTTCGAGACC
56189	54276	TGAGGTCAGGAGTTCGAGAC
56190	54277	TTGAGGTCAGGAGTTCGAGA
56191	54278	CTTGAGGTCAGGAGTTCGAG
56192	54279	ACTTGAGGTCAGGAGTTCGA
56193	54280	CACTTGAGGTCAGGAGTTCG
56194	54281	TCACTTGAGGTCAGGAGTTC
56195	54282	ATCACTTGAGGTCAGGAGTT
56196	54283	GATCACTTGAGGTCAGGAGT
56197	54284	TGATCACTTGAGGTCAGGAG
56198	54285	GTGATCACTTGAGGTCAGGA
56199	54286	GGTGATCACTTGAGGTCAGG
56200	54287	AGGTGATCACTTGAGGTCAG
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56210	54297	AGGCTGAGGCAGGTGATCAC
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56212	54299	GGAGGCTGAGGCAGGTGATC
56213	54300	GGGAGGCTGAGGCAGGTGAT
56214	54301	TGGGAGGCTGAGGCAGGTGA
56215	54302	TTGGGAGGCTGAGGCAGGTG
56216	54303	TTTGGGAGGCTGAGGCAGGT
56217	54304	CTTTGGGAGGCTGAGGCAGG
56218	54305	ACTTTGGGAGGCTGAGGCAG
56219	54306	CACTTTGGGAGGCTGAGGCA
56220	54307	GCACTTTGGGAGGCTGAGGC
56221	54308	AGCACTTTGGGAGGCTGAGG
56222	54309	CAGCACTTTGGGAGGCTGAG
56223	54310	CCAGCACTTTGGGAGGCTGA
56224	54311	CCCAGCACTTTGGGAGGCTG
56225	54312	TCCCAGCACTTTGGGAGGCT
56226	54313	ATCCCAGCACTTTGGGAGGC
56227	54314	AATCCCAGCACTTTGGGAGG
56228	54315	TAATCCCAGCACTTTGGGAG
56229	54316	GTAATCCCAGCACTTTGGGA
56230	54317	TGTAATCCCAGCACTTTGGG
56231	54318	CTGTAATCCCAGCACTTTGG
56232	54319	CCTGTAATCCCAGCACTTTG
56233	54320	GCCTGTAATCCCAGCACTTT
56234	54321	CGCCTGTAATCCCAGCACTT
56235	54322	ACGCCTGTAATCCCAGCACT
56236	54323	CACGCCTGTAATCCCAGCAC
56237	54324	TCACGCCTGTAATCCCAGCA
56238	54325	CTCACGCCTGTAATCCCAGC
56239	54326	GCTCACGCCTGTAATCCCAG
56240	54327	GGCTCACGCCTGTAATCCCA

105317	103404	GCCGGGCACGGTGGCTCATG
105318	103405	GGCCGGGCACGGTGGCTCAT
105319	103406	AGGCCGGGCACGGTGGCTCA
105320	103407	GAGGCCGGGCACGGTGGCTC
105321	103408	AGAGGCCGGGCACGGTGGCT
105322	103409	TAGAGGCCGGGCACGGTGGC
105323	103410	CTAGAGGCCGGGCACGGTGG
105324	103411	ACTAGAGGCCGGGCACGGTG
105325	103412	CACTAGAGGCCGGGCACGGT
105326	103413	ACACTAGAGGCCGGGCACGG
105327	103414	AACACTAGAGGCCGGGCACG
105328	103415	TAACACTAGAGGCCGGGCAC
105329	103416	ATAACACTAGAGGCCGGGCA
105330	103417	GATAACACTAGAGGCCGGGC
105331	103418	AGATAACACTAGAGGCCGGG
105332	103419	AAGATAACACTAGAGGCCGG
105333	103420	TAAGATAACACTAGAGGCCG
105334	103421	ATAAGATAACACTAGAGGCC
105335	103422	AATAAGATAACACTAGAGGC
105336	103423	CAATAAGATAACACTAGAGG
105337	103424	ACAATAAGATAACACTAGAG
105338	103425	CACAATAAGATAACACTAGA
105339	103426	TCACAATAAGATAACACTAG
105340	103427	ATCACAATAAGATAACACTA
105341	103428	GATCACAATAAGATAACACT
105342	103429	TGATCACAATAAGATAACAC
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105344	103431	TCTGATCACAATAAGATAAC
105345	103432	CTCTGATCACAATAAGATAA
105346	103433	TCTCTGATCACAATAAGATA
105347	103434	TTCTCTGATCACAATAAGAT
105348	103435	CTTCTCTGATCACAATAAGA
105349	103436	TCTTCTCTGATCACAATAAG
105350	103437	ATCTTCTCTGATCACAATAA
105351	103438	TATCTTCTCTGATCACAATA
105352	103439	CTATCTTCTCTGATCACAAT
105353	103440	ACTATCTTCTCTGATCACAA
105354	103441	AACTATCTTCTCTGATCACA
105355	103442	CAACTATCTTCTCTGATCAC
105356	103443	TCAACTATCTTCTCTGATCA
105357	103444	ATCAACTATCTTCTCTGATC
105358	103445	TATCAACTATCTTCTCTGAT
105359	103446	ATATCAACTATCTTCTCTGA
105360	103447	CATATCAACTATCTTCTCTG
105361	103448	TCATATCAACTATCTTCTCT
105362	103449	ATCATATCAACTATCTTCTC
105363	103450	AATCATATCAACTATCTTCT
105364	103451	AAATCATATCAACTATCTTC
105365	103452	AAAATCATATCAACTATCTT
105366	103453	TAAAATCATATCAACTATCT
105367	103454	TTAAAATCATATCAACTATC
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105373	103460	AAAAAGTTAAAATCATATCA
105374	103461	AAAAAAGTTAAAATCATATC
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105387	103474	TAAATAAAAATTCAAAAAAG

7094	5181	GATTACAGGCGCCTGGCTAA
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7097	5184	TGGGATTACAGGCGCCTGGC
7098	5185	CTGGGATTACAGGCGCCTGG
7099	5186	GCTGGGATTACAGGCGCCTG
7100	5187	AGCTGGGATTACAGGCGCCT
7101	5188	TAGCTGGGATTACAGGCGCC
7102	5189	GTAGCTGGGATTACAGGCGC
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7104	5191	AAGTAGCTGGGATTACAGGC
7105	5192	CAAGTAGCTGGGATTACAGG
7106	5193	CCAAGTAGCTGGGATTACAG
7107	5194	CCCAAGTAGCTGGGATTACA
7108	5195	TCCCAAGTAGCTGGGATTAC
7109	5196	CTCCCAAGTAGCTGGGATTA
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7111	5198	GCCTCCCAAGTAGCTGGGAT
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7114	5201	TCAGCCTCCCAAGTAGCTGG
7115	5202	CTCAGCCTCCCAAGTAGCTG
7116	5203	CCTCAGCCTCCCAAGTAGCT
7117	5204	GCCTCAGCCTCCCAAGTAGC
7118	5205	TGCCTCAGCCTCCCAAGTAG
7119	5206	CTGCCTCAGCCTCCCAAGTA
7120	5207	CCTGCCTCAGCCTCCCAAGT
7121	5208	TCCTGCCTCAGCCTCCCAAG
7122	5209	CTCCTGCCTCAGCCTCCCAA
7123	5210	GCTCCTGCCTCAGCCTCCCA
7124	5211	TGCTCCTGCCTCAGCCTCCC
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7126	5213	GATGCTCCTGCCTCAGCCTC
7127	5214	TGATGCTCCTGCCTCAGCCT
7128	5215	GTGATGCTCCTGCCTCAGCC
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7132	5219	TCAAGTGATGCTCCTGCCTC
7133	5220	CTCAAGTGATGCTCCTGCCT
7134	5221	GCTCAAGTGATGCTCCTGCC
7135	5222	GGCTCAAGTGATGCTCCTGC
7136	5223	GGGCTCAAGTGATGCTCCTG
7137	5224	TGGGCTCAAGTGATGCTCCT
7138	5225	CTGGGCTCAAGTGATGCTCC
7139	5226	CCTGGGCTCAAGTGATGCTC
7140	5227	TCCTGGGCTCAAGTGATGCT
7141	5228	CTCCTGGGCTCAAGTGATGC
7142	5229	CCTCCTGGGCTCAAGTGATG
7143	5230	GCCTCCTGGGCTCAAGTGAT
7144	5231	CGCCTCCTGGGCTCAAGTGA
7145	5232	CCGCCTCCTGGGCTCAAGTG
7146	5233	TCCGCCTCCTGGGCTCAAGT
7147	5234	CTCCGCCTCCTGGGCTCAAG
7148	5235	CCTCCGCCTCCTGGGCTCAA
7149	5236	ACCTCCGCCTCCTGGGCTCA
7150	5237	AACCTCCGCCTCCTGGGCTC
7151	5238	CAACCTCCGCCTCCTGGGCT
7152	5239	GCAACCTCCGCCTCCTGGGC
7153	5240	TGCAACCTCCGCCTCCTGGG
7154	5241	CTGCAACCTCCGCCTCCTGG
7155	5242	ACTGCAACCTCCGCCTCCTG
7156	5243	GACTGCAACCTCCGCCTCCT
7157	5244	TGACTGCAACCTCCGCCTCC
7158	5245	CTGACTGCAACCTCCGCCTC
7159	5246	GCTGACTGCAACCTCCGCCT
7160	5247	AGCTGACTGCAACCTCCGCC
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7163	5250	CTCAGCTGACTGCAACCTCC
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56241	54328	TGGCTCACGCCTGTAATCCC
56242	54329	GTGGCTCACGCCTGTAATCC
56243	54330	GGTGGCTCACGCCTGTAATC
56244	54331	TGGTGGCTCACGCCTGTAAT
56245	54332	GTGGTGGCTCACGCCTGTAA
56246	54333	CGTGGTGGCTCACGCCTGTA
56247	54334	GCGTGGTGGCTCACGCCTGT
56248	54335	GGCGTGGTGGCTCACGCCTG
56249	54336	AGGCGTGGTGGCTCACGCCT
56250	54337	CAGGCGTGGTGGCTCACGCC
56251	54338	CCAGGCGTGGTGGCTCACGC
56252	54339	GCCAGGCGTGGTGGCTCACG
56253	54340	GGCCAGGCGTGGTGGCTCAC
56254	54341	TGGCCAGGCGTGGTGGCTCA
56255	54342	ATGGCCAGGCGTGGTGGCTC
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56267	54354	AGAAAAAAAAAGATGGCCAG
56268	54355	GAGAAAAAAAAAGATGGCCA
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56270	54357	AGGAGAAAAAAAAAGATGGC
56271	54358	AAGGAGAAAAAAAAAGATGG
56272	54359	CAAGGAGAAAAAAAAAGATG
56273	54360	GCAAGGAGAAAAAAAAAGAT
56274	54361	AGCAAGGAGAAAAAAAAAGA
56275	54362	GAGCAAGGAGAAAAAAAAAG
56276	54363	AGAGCAAGGAGAAAAAAAAA
56277	54364	AAGAGCAAGGAGAAAAAAAA
56278	54365	AAAGAGCAAGGAGAAAAAAA
56279	54366	AAAAGAGCAAGGAGAAAAAA
56280	54367	TAAAAGAGCAAGGAGAAAAA
56281	54368	ATAAAAGAGCAAGGAGAAAA
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56283	54370	GTATAAAAGAGCAAGGAGAA
56284	54371	GGTATAAAAGAGCAAGGAGA
56285	54372	TGGTATAAAAGAGCAAGGAG
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56287	54374	AGTGGTATAAAAGAGCAAGG
56288	54375	AAGTGGTATAAAAGAGCAAG
56289	54376	GAAGTGGTATAAAAGAGCAA
56290	54377	AGAAGTGGTATAAAAGAGCA
56291	54378	GAGAAGTGGTATAAAAGAGC
56292	54379	AGAGAAGTGGTATAAAAGAG
56293	54380	CAGAGAAGTGGTATAAAAGA
56294	54381	ACAGAGAAGTGGTATAAAAG
56295	54382	AACAGAGAAGTGGTATAAAA
56296	54383	AAACAGAGAAGTGGTATAAA
56297	54384	GAAACAGAGAAGTGGTATAA
56298	54385	AGAAACAGAGAAGTGGTATA
56299	54386	CAGAAACAGAGAAGTGGTAT
56300	54387	CCAGAAACAGAGAAGTGGTA
56301	54388	CCCAGAAACAGAGAAGTGGT
56302	54389	GCCCAGAAACAGAGAAGTGG
56303	54390	AGCCCAGAAACAGAGAAGTG
56304	54391	GAGCCCAGAAACAGAGAAGT
56305	54392	AGAGCCCAGAAACAGAGAAG
56306	54393	AAGAGCCCAGAAACAGAGAA
56307	54394	GAAGAGCCCAGAAACAGAGA
56308	54395	TGAAGAGCCCAGAAACAGAG
56309	54396	TTGAAGAGCCCAGAAACAGA
56310	54397	GTTGAAGAGCCCAGAAACAG
56311	54398	TGTTGAAGAGCCCAGAAACA

105388	103475	ATAAATAAAAATTCAAAAAA
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105391	103478	TAAATAAATAAAAATTCAAA
105392	103479	ATAAATAAATAAAAATTCAA
105393	103480	AATAAATAAATAAAAATTCA
105394	103481	AAATAAATAAATAAAAATTC
105395	103482	CAAATAAATAAATAAAAATT
105396	103483	ACAAATAAATAAATAAAAAT
105397	103484	AACAAATAAATAAATAAAAA
105398	103485	AAACAAATAAATAAATAAAA
105399	103486	CAAACAAATAAATAAATAAA
105400	103487	ACAAACAAATAAATAAATAA
105401	103488	AACAAACAAATAAATAAATA
105402	103489	AAACAAACAAATAAATAAAT
105403	103490	CAAACAAACAAATAAATAAA
105404	103491	ACAAACAAACAAATAAATAA
105405	103492	AACAAACAAACAAATAAATA
105406	103493	AAACAAACAAACAAATAAAT
105407	103494	CAAACAAACAAACAAATAAA
105408	103495	ACAAACAAACAAACAAATAA
105409	103496	AACAAACAAACAAACAAATA
105410	103497	AAACAAACAAACAAACAAAT
105411	103498	CAAACAAACAAACAAACAAA
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105414	103501	AAACAAACAAACAAACAAAC
105415	103502	CAAACAAACAAACAAACAAA
105416	103503	ACAAACAAACAAACAAACAA
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105418	103505	TTACAAACAAACAAACAAAC
105419	103506	GTTACAAACAAACAAACAAA
105420	103507	TGTTACAAACAAACAAACAA
105421	103508	CTGTTACAAACAAACAAACA
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105423	103510	CTCTGTTACAAACAAACAAA
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105425	103512	GACTCTGTTACAAACAAACA
105426	103513	AGACTCTGTTACAAACAAAC
105427	103514	GAGACTCTGTTACAAACAAA
105428	103515	TGAGACTCTGTTACAAACAA
105429	103516	GTGAGACTCTGTTACAAACA
105430	103517	AGTGAGACTCTGTTACAAAC
105431	103518	GAGTGAGACTCTGTTACAAA
105432	103519	AGAGTGAGACTCTGTTACAA
105433	103520	CAGAGTGAGACTCTGTTACA
105434	103521	ACAGAGTGAGACTCTGTTAC
105435	103522	AACAGAGTGAGACTCTGTTA
105436	103523	TAACAGAGTGAGACTCTGTT
105437	103524	GTAACAGAGTGAGACTCTGT
105438	103525	GGTAACAGAGTGAGACTCTG
105439	103526	GGGTAACAGAGTGAGACTCT
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105442	103529	CCTGGGTAACAGAGTGAGAC
105443	103530	GCCTGGGTAACAGAGTGAGA
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105446	103533	CCAGCCTGGGTAACAGAGTG
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105451	103538	GTACTCCAGCCTGGGTAACA
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105458	103545	ATGACATGTACTCCAGCCTG

7165	5252	ATCTCAGCTGACTGCAACCT
7166	5253	AATCTCAGCTGACTGCAACC
7167	5254	CAATCTCAGCTGACTGCAAC
7168	5255	ACAATCTCAGCTGACTGCAA
7169	5256	CACAATCTCAGCTGACTGCA
7170	5257	GCACAATCTCAGCTGACTGC
7171	5258	GGCACAATCTCAGCTGACTG
7172	5259	TGGCACAATCTCAGCTGACT
7173	5260	GTGGCACAATCTCAGCTGAC
7174	5261	AGTGGCACAATCTCAGCTGA
7175	5262	CAGTGGCACAATCTCAGCTG
7176	5263	GCAGTGGCACAATCTCAGCT
7177	5264	TGCAGTGGCACAATCTCAGC
7178	5265	GTGCAGTGGCACAATCTCAG
7179	5266	AGTGCAGTGGCACAATCTCA
7180	5267	GAGTGCAGTGGCACAATCTC
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7182	5269	TGGAGTGCAGTGGCACAATC
7183	5270	CTGGAGTGCAGTGGCACAAT
7184	5271	GCTGGAGTGCAGTGGCACAA
7185	5272	GGCTGGAGTGCAGTGGCACA
7186	5273	AGGCTGGAGTGCAGTGGCAC
7187	5274	CAGGCTGGAGTGCAGTGGCA
7188	5275	CCAGGCTGGAGTGCAGTGGC
7189	5276	CCCAGGCTGGAGTGCAGTGG
7190	5277	TCCCAGGCTGGAGTGCAGTG
7191	5278	CTCCCAGGCTGGAGTGCAGT
7192	5279	TCTCCCAGGCTGGAGTGCAG
7193	5280	GTCTCCCAGGCTGGAGTGCA
7194	5281	TGTCTCCCAGGCTGGAGTGC
7195	5282	CTGTCTCCCAGGCTGGAGTG
7196	5283	TCTGTCTCCCAGGCTGGAGT
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7198	5285	ACTCTGTCTCCCAGGCTGGA
7199	5286	CACTCTGTCTCCCAGGCTGG
7200	5287	TCACTCTGTCTCCCAGGCTG
7201	5288	CTCACTCTGTCTCCCAGGCT
7202	5289	TCTCACTCTGTCTCCCAGGC
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7204	5291	AGTCTCACTCTGTCTCCCAG
7205	5292	GAGTCTCACTCTGTCTCCCA
7206	5293	AGAGTCTCACTCTGTCTCCC
7207	5294	TAGAGTCTCACTCTGTCTCC
7208	5295	ATAGAGTCTCACTCTGTCTC
7209	5296	GATAGAGTCTCACTCTGTCT
7210	5297	AGATAGAGTCTCACTCTGTC
7211	5298	GAGATAGAGTCTCACTCTGT
7212	5299	TGAGATAGAGTCTCACTCTG
7213	5300	TTGAGATAGAGTCTCACTCT
7214	5301	TTTGAGATAGAGTCTCACTC
7215	5302	TTTTGAGATAGAGTCTCACT
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7220	5307	TTTTTTTTTGAGATAGAGTC
7221	5308	TTTTTTTTTTGAGATAGAGT
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7223	5310	TTTTTTTTTTTTGAGATAGA
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7231	5318	AGCACATTTTTTTTTTTTTT
7232	5319	CAGCACATTTTTTTTTTTTT
7233	5320	ACAGCACATTTTTTTTTTTT
7234	5321	CACAGCACATTTTTTTTTTT
7235	5322	TCACAGCACATTTTTTTTTT

56312	54399	ATGTTGAAGAGCCCAGAAAC
56313	54400	GATGTTGAAGAGCCCAGAAA
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56315	54402	CAGATGTTGAAGAGCCCAGA
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56318	54405	AGGCAGATGTTGAAGAGCCC
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56322	54409	AGAAAGGCAGATGTTGAAGA
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56331	54418	AGATTAACTAGAAAGGCAGA
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56333	54420	AAAGATTAACTAGAAAGGCA
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56339	54426	AAAGGGAAAGATTAACTAGA
56340	54427	TAAAGGGAAAGATTAACTAG
56341	54428	CTAAAGGGAAAGATTAACTA
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56344	54431	ATGCTAAAGGGAAAGATTAA
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56359	54446	AGTGAATAGGTTTTCATGCT
56360	54447	AAGTGAATAGGTTTTCATGC
56361	54448	GAAGTGAATAGGTTTTCATG
56362	54449	GGAAGTGAATAGGTTTTCAT
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56370	54457	GATGAGCAGGAAGTGAATAG
56371	54458	GGATGAGCAGGAAGTGAATA
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56373	54460	TAGGATGAGCAGGAAGTGAA
56374	54461	TTAGGATGAGCAGGAAGTGA
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56378	54465	CTTTTTAGGATGAGCAGGAA
56379	54466	CCTTTTTAGGATGAGCAGGA
56380	54467	TCCTTTTTAGGATGAGCAGG
56381	54468	ATCCTTTTTAGGATGAGCAG
56382	54469	AATCCTTTTTAGGATGAGCA

105459	103546	CATGACATGTACTCCAGCCT
105460	103547	TCATGACATGTACTCCAGCC
105461	103548	ATCATGACATGTACTCCAGC
105462	103549	GATCATGACATGTACTCCAG
105463	103550	AGATCATGACATGTACTCCA
105464	103551	AAGATCATGACATGTACTCC
105465	103552	CAAGATCATGACATGTACTC
105466	103553	CCAAGATCATGACATGTACT
105467	103554	GCCAAGATCATGACATGTAC
105468	103555	AGCCAAGATCATGACATGTA
105469	103556	GAGCCAAGATCATGACATGT
105470	103557	TGAGCCAAGATCATGACATG
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105474	103561	CAGGTGAGCCAAGATCATGA
105475	103562	GCAGGTGAGCCAAGATCATG
105476	103563	TGCAGGTGAGCCAAGATCAT
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105478	103565	GTTGCAGGTGAGCCAAGATC
105479	103566	GGTTGCAGGTGAGCCAAGAT
105480	103567	AGGTTGCAGGTGAGCCAAGA
105481	103568	GAGGTTGCAGGTGAGCCAAG
105482	103569	GGAGGTTGCAGGTGAGCCAA
105483	103570	CGGAGGTTGCAGGTGAGCCA
105484	103571	GCGGAGGTTGCAGGTGAGCC
105485	103572	GGCGGAGGTTGCAGGTGAGC
105486	103573	AGGCGGAGGTTGCAGGTGAG
105487	103574	AAGGCGGAGGTTGCAGGTGA
105488	103575	GAAGGCGGAGGTTGCAGGTG
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105526	103613	TACTTGGAAGGCTAAGGTGG
105527	103614	CTACTTGGAAGGCTAAGGTG
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105529	103616	AGCTACTTGGAAGGCTAAGG

7236	5323	ATCACAGCACATTTTTTTTT
7237	5324	AATCACAGCACATTTTTTTT
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7239	5326	TAAATCACAGCACATTTTTT
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7244	5331	TACATTAAATCACAGCACAT
7245	5332	CTACATTAAATCACAGCACA
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7250	5337	AACAACTACATTAAATCACA
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7252	5339	TGAACAACTACATTAAATCA
7253	5340	ATGAACAACTACATTAAATC
7254	5341	GATGAACAACTACATTAAAT
7255	5342	TGATGAACAACTACATTAAA
7256	5343	ATGATGAACAACTACATTAA
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7258	5345	GCATGATGAACAACTACATT
7259	5346	AGCATGATGAACAACTACAT
7260	5347	AAGCATGATGAACAACTACA
7261	5348	GAAGCATGATGAACAACTAC
7262	5349	GGAAGCATGATGAACAACTA
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7265	5352	AATGGAAGCATGATGAACAA
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7267	5354	TAAATGGAAGCATGATGAAC
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7276	5363	ACTGAAATTTAAATGGAAGC
7277	5364	CACTGAAATTTAAATGGAAG
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7281	5368	GTCTCACTGAAATTTAAATG
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7290	5377	AGATGAACAGTCTCACTGAA
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56383	54470	GAATCCTTTTTAGGATGAGC
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56431	54518	CAAGAGCGAGACTCTGTCTC
56432	54519	GCAAGAGCGAGACTCTGTCT
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56438	54525	GCCTGGGCAAGAGCGAGACT
56439	54526	AGCCTGGGCAAGAGCGAGAC
56440	54527	CAGCCTGGGCAAGAGCGAGA
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56442	54529	TCCAGCCTGGGCAAGAGCGA
56443	54530	CTCCAGCCTGGGCAAGAGCG
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56449	54536	ACTGCACTCCAGCCTGGGCA
56450	54537	CACTGCACTCCAGCCTGGGC
56451	54538	CCACTGCACTCCAGCCTGGG
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56453	54540	TGCCACTGCACTCCAGCCTG

105530	103617	CAGCTACTTGGAAGGCTAAG
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105536	103623	TAGTCCCAGCTACTTGGAAG
105537	103624	GTAGTCCCAGCTACTTGGAA
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105539	103626	CTGTAGTCCCAGCTACTTGG
105540	103627	CCTGTAGTCCCAGCTACTTG
105541	103628	GCCTGTAGTCCCAGCTACTT
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105543	103630	GTGCCTGTAGTCCCAGCTAC
105544	103631	TGTGCCTGTAGTCCCAGCTA
105545	103632	ATGTGCCTGTAGTCCCAGCT
105546	103633	CATGTGCCTGTAGTCCCAGC
105547	103634	GCATGTGCCTGTAGTCCCAG
105548	103635	GGCATGTGCCTGTAGTCCCA
105549	103636	CGGCATGTGCCTGTAGTCCC
105550	103637	ACGGCATGTGCCTGTAGTCC
105551	103638	GACGGCATGTGCCTGTAGTC
105552	103639	TGACGGCATGTGCCTGTAGT
105553	103640	GTGACGGCATGTGCCTGTAG
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105562	103649	CAGCCATATGTGACGGCATG
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105564	103651	ATCAGCCATATGTGACGGCA
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105623	103710	ACAACCCTGGGACACATCGC
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105625	103712	AAACAACCCTGGGACACATC
105626	103713	GAAACAACCCTGGGACACAT
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105668	103755	TTGGGAGGCCGAAATAGGTG
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105721	103808	CAAGTCTAAAGATTTGACGT
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105723	103810	AACAAGTCTAAAGATTTGAC
105724	103811	AAACAAGTCTAAAGATTTGA
105725	103812	AAAACAAGTCTAAAGATTTG
105726	103813	CAAAACAAGTCTAAAGATTT
105727	103814	ACAAAACAAGTCTAAAGATT
105728	103815	CACAAAACAAGTCTAAAGAT
105729	103816	CCACAAAACAAGTCTAAAGA
105730	103817	GCCACAAAACAAGTCTAAAG
105731	103818	AGCCACAAAACAAGTCTAAA
105732	103819	AAGCCACAAAACAAGTCTAA
105733	103820	TAAGCCACAAAACAAGTCTA
105734	103821	TTAAGCCACAAAACAAGTCT
105735	103822	GTTAAGCCACAAAACAAGTC
105736	103823	TGTTAAGCCACAAAACAAGT
105737	103824	ATGTTAAGCCACAAAACAAG
105738	103825	TATGTTAAGCCACAAAACAA
105739	103826	CTATGTTAAGCCACAAAACA
105740	103827	CCTATGTTAAGCCACAAAAC
105741	103828	CCCTATGTTAAGCCACAAAA
105742	103829	ACCCTATGTTAAGCCACAAA

7449	5536	CATTGTCTGCCTAGTCACAT
7450	5537	TCATTGTCTGCCTAGTCACA
7451	5538	CTCATTGTCTGCCTAGTCAC
7452	5539	TCTCATTGTCTGCCTAGTCA
7453	5540	GTCTCATTGTCTGCCTAGTC
7454	5541	TGTCTCATTGTCTGCCTAGT
7455	5542	ATGTCTCATTGTCTGCCTAG
7456	5543	AATGTCTCATTGTCTGCCTA
7457	5544	TAATGTCTCATTGTCTGCCT
7458	5545	TTAATGTCTCATTGTCTGCC
7459	5546	TTTAATGTCTCATTGTCTGC
7460	5547	ATTTAATGTCTCATTGTCTG
7461	5548	AATTTAATGTCTCATTGTCT
7462	5549	TAATTTAATGTCTCATTGTC
7463	5550	GTAATTTAATGTCTCATTGT
7464	5551	GGTAATTTAATGTCTCATTG
7465	5552	TGGTAATTTAATGTCTCATT
7466	5553	CTGGTAATTTAATGTCTCAT
7467	5554	GCTGGTAATTTAATGTCTCA
7468	5555	GGCTGGTAATTTAATGTCTC
7469	5556	AGGCTGGTAATTTAATGTCT
7470	5557	TAGGCTGGTAATTTAATGTC
7471	5558	ATAGGCTGGTAATTTAATGT
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7473	5560	ACATAGGCTGGTAATTTAAT
7474	5561	TACATAGGCTGGTAATTTAA
7475	5562	ATACATAGGCTGGTAATTTA
7476	5563	TATACATAGGCTGGTAATTT
7477	5564	TTATACATAGGCTGGTAATT
7478	5565	ATTATACATAGGCTGGTAAT
7479	5566	TATTATACATAGGCTGGTAA
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7481	5568	ACTATTATACATAGGCTGGT
7482	5569	CACTATTATACATAGGCTGG
7483	5570	ACACTATTATACATAGGCTG
7484	5571	TACACTATTATACATAGGCT
7485	5572	ATACACTATTATACATAGGC
7486	5573	TATACACTATTATACATAGG
7487	5574	TTATACACTATTATACATAG
7488	5575	CTTATACACTATTATACATA
7489	5576	TCTTATACACTATTATACAT
7490	5577	CTCTTATACACTATTATACA
7491	5578	GCTCTTATACACTATTATAC
7492	5579	AGCTCTTATACACTATTATA
7493	5580	TAGCTCTTATACACTATTAT
7494	5581	ATAGCTCTTATACACTATTA
7495	5582	CATAGCTCTTATACACTATT
7496	5583	CCATAGCTCTTATACACTAT
7497	5584	TCCATAGCTCTTATACACTA
7498	5585	TTCCATAGCTCTTATACACT
7499	5586	ATTCCATAGCTCTTATACAC
7500	5587	AATTCCATAGCTCTTATACA
7501	5588	TAATTCCATAGCTCTTATAC
7502	5589	CTAATTCCATAGCTCTTATA
7503	5590	TCTAATTCCATAGCTCTTAT
7504	5591	TTCTAATTCCATAGCTCTTA
7505	5592	CTTCTAATTCCATAGCTCTT
7506	5593	TCTTCTAATTCCATAGCTCT
7507	5594	TTCTTCTAATTCCATAGCTC
7508	5595	TTTCTTCTAATTCCATAGCT
7509	5596	CTTTCTTCTAATTCCATAGC
7510	5597	GCTTTCTTCTAATTCCATAG
7511	5598	TGCTTTCTTCTAATTCCATA
7512	5599	CTGCTTTCTTCTAATTCCAT
7513	5600	TCTGCTTTCTTCTAATTCCA
7514	5601	ATCTGCTTTCTTCTAATTCC
7515	5602	AATCTGCTTTCTTCTAATTC
7516	5603	TAATCTGCTTTCTTCTAATT
7517	5604	TTAATCTGCTTTCTTCTAAT
7518	5605	TTTAATCTGCTTTCTTCTAA
7519	5606	CTTTAATCTGCTTTCTTCTA

56596	54683	ACACGGTGAAACCCCATCTC
56597	54684	AACACGGTGAAACCCCATCT
56598	54685	TAACACGGTGAAACCCCATC
56599	54686	CTAACACGGTGAAACCCCAT
56600	54687	GCTAACACGGTGAAACCCCA
56601	54688	AGCTAACACGGTGAAACCCC
56602	54689	TAGCTAACACGGTGAAACCC
56603	54690	CTAGCTAACACGGTGAAACC
56604	54691	CCTAGCTAACACGGTGAAAC
56605	54692	TCCTAGCTAACACGGTGAAA
56606	54693	ATCCTAGCTAACACGGTGAA
56607	54694	CATCCTAGCTAACACGGTGA
56608	54695	CCATCCTAGCTAACACGGTG
56609	54696	ACCATCCTAGCTAACACGGT
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56611	54698	AGACCATCCTAGCTAACACG
56612	54699	GAGACCATCCTAGCTAACAC
56613	54700	CGAGACCATCCTAGCTAACA
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56615	54702	ATCGAGACCATCCTAGCTAA
56616	54703	GATCGAGACCATCCTAGCTA
56617	54704	AGATCGAGACCATCCTAGCT
56618	54705	GAGATCGAGACCATCCTAGC
56619	54706	GGAGATCGAGACCATCCTAG
56620	54707	AGGAGATCGAGACCATCCTA
56621	54708	CAGGAGATCGAGACCATCCT
56622	54709	TCAGGAGATCGAGACCATCC
56623	54710	GTCAGGAGATCGAGACCATC
56624	54711	GGTCAGGAGATCGAGACCAT
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56626	54713	AAGGTCAGGAGATCGAGACC
56627	54714	CAAGGTCAGGAGATCGAGAC
56628	54715	ACAAGGTCAGGAGATCGAGA
56629	54716	CACAAGGTCAGGAGATCGAG
56630	54717	TCACAAGGTCAGGAGATCGA
56631	54718	ATCACAAGGTCAGGAGATCG
56632	54719	GATCACAAGGTCAGGAGATC
56633	54720	GGATCACAAGGTCAGGAGAT
56634	54721	TGGATCACAAGGTCAGGAGA
56635	54722	ATGGATCACAAGGTCAGGAG
56636	54723	GATGGATCACAAGGTCAGGA
56637	54724	AGATGGATCACAAGGTCAGG
56638	54725	CAGATGGATCACAAGGTCAG
56639	54726	GCAGATGGATCACAAGGTCA
56640	54727	GGCAGATGGATCACAAGGTC
56641	54728	AGGCAGATGGATCACAAGGT
56642	54729	GAGGCAGATGGATCACAAGG
56643	54730	CGAGGCAGATGGATCACAAG
56644	54731	CCGAGGCAGATGGATCACAA
56645	54732	GCCGAGGCAGATGGATCACA
56646	54733	GGCCGAGGCAGATGGATCAC
56647	54734	AGGCCGAGGCAGATGGATCA
56648	54735	GAGGCCGAGGCAGATGGATC
56649	54736	GGAGGCCGAGGCAGATGGAT
56650	54737	GGGAGGCCGAGGCAGATGGA
56651	54738	TGGGAGGCCGAGGCAGATGG
56652	54739	TTGGGAGGCCGAGGCAGATG
56653	54740	TTTGGGAGGCCGAGGCAGAT
56654	54741	CTTTGGGAGGCCGAGGCAGA
56655	54742	ACTTTGGGAGGCCGAGGCAG
56656	54743	CACTTTGGGAGGCCGAGGCA
56657	54744	GCACTTTGGGAGGCCGAGGC
56658	54745	AGCACTTTGGGAGGCCGAGG
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56662	54749	TCCCAGCACTTTGGGAGGCC
56663	54750	ATCCCAGCACTTTGGGAGGC
56664	54751	AATCCCAGCACTTTGGGAGG
56665	54752	TAATCCCAGCACTTTGGGAG
56666	54753	GTAATCCCAGCACTTTGGGA

105743	103830	GACCCTATGTTAAGCCACAA
105744	103831	AGACCCTATGTTAAGCCACA
105745	103832	TAGACCCTATGTTAAGCCAC
105746	103833	ATAGACCCTATGTTAAGCCA
105747	103834	GATAGACCCTATGTTAAGCC
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105749	103836	AAGATAGACCCTATGTTAAG
105750	103837	AAAGATAGACCCTATGTTAA
105751	103838	CAAAGATAGACCCTATGTTA
105752	103839	TCAAAGATAGACCCTATGTT
105753	103840	CTCAAAGATAGACCCTATGT
105754	103841	TCTCAAAGATAGACCCTATG
105755	103842	CTCTCAAAGATAGACCCTAT
105756	103843	GCTCTCAAAGATAGACCCTA
105757	103844	TGCTCTCAAAGATAGACCCT
105758	103845	TTGCTCTCAAAGATAGACCC
105759	103846	ATTGCTCTCAAAGATAGACC
105760	103847	GATTGCTCTCAAAGATAGAC
105761	103848	GGATTGCTCTCAAAGATAGA
105762	103849	TGGATTGCTCTCAAAGATAG
105763	103850	ATGGATTGCTCTCAAAGATA
105764	103851	TATGGATTGCTCTCAAAGAT
105765	103852	ATATGGATTGCTCTCAAAGA
105766	103853	CATATGGATTGCTCTCAAAG
105767	103854	ACATATGGATTGCTCTCAAA
105768	103855	AACATATGGATTGCTCTCAA
105769	103856	CAACATATGGATTGCTCTCA
105770	103857	TCAACATATGGATTGCTCTC
105771	103858	CTCAACATATGGATTGCTCT
105772	103859	CCTCAACATATGGATTGCTC
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105774	103861	CTCCTCAACATATGGATTGC
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105777	103864	CTTCTCCTCAACATATGGAT
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105779	103866	TTCTTCTCCTCAACATATGG
105780	103867	ATTCTTCTCCTCAACATATG
105781	103868	CATTCTTCTCCTCAACATAT
105782	103869	ACATTCTTCTCCTCAACATA
105783	103870	CACATTCTTCTCCTCAACAT
105784	103871	ACACATTCTTCTCCTCAACA
105785	103872	TACACATTCTTCTCCTCAAC
105786	103873	ATACACATTCTTCTCCTCAA
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105790	103877	TAGAATACACATTCTTCTCC
105791	103878	ATAGAATACACATTCTTCTC
105792	103879	TATAGAATACACATTCTTCT
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105794	103881	GCTATAGAATACACATTCTT
105795	103882	AGCTATAGAATACACATTCT
105796	103883	CAGCTATAGAATACACATTC
105797	103884	ACAGCTATAGAATACACATT
105798	103885	AACAGCTATAGAATACACAT
105799	103886	CAACAGCTATAGAATACACA
105800	103887	CCAACAGCTATAGAATACAC
105801	103888	TCCAACAGCTATAGAATACA
105802	103889	GTCCAACAGCTATAGAATAC
105803	103890	TGTCCAACAGCTATAGAATA
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105806	103893	TTGTGTCCAACAGCTATAGA
105807	103894	ATTGTGTCCAACAGCTATAG
105808	103895	CATTGTGTCCAACAGCTATA
105809	103896	ACATTGTGTCCAACAGCTAT
105810	103897	AACATTGTGTCCAACAGCTA
105811	103898	GAACATTGTGTCCAACAGCT
105812	103899	AGAACATTGTGTCCAACAGC
105813	103900	CAGAACATTGTGTCCAACAG

7520	5607	CCTTTAATCTGCTTTCTTCT
7521	5608	ACCTTTAATCTGCTTTCTTC
7522	5609	TACCTTTAATCTGCTTTCTT
7523	5610	ATACCTTTAATCTGCTTTCT
7524	5611	TATACCTTTAATCTGCTTTC
7525	5612	CTATACCTTTAATCTGCTTT
7526	5613	CCTATACCTTTAATCTGCTT
7527	5614	CCCTATACCTTTAATCTGCT
7528	5615	TCCCTATACCTTTAATCTGC
7529	5616	CTCCCTATACCTTTAATCTG
7530	5617	ACTCCCTATACCTTTAATCT
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7532	5619	ACACTCCCTATACCTTTAAT
7533	5620	CACACTCCCTATACCTTTAA
7534	5621	CCACACTCCCTATACCTTTA
7535	5622	CCCACACTCCCTATACCTTT
7536	5623	CCCCACACTCCCTATACCTT
7537	5624	TCCCCACACTCCCTATACCT
7538	5625	CTCCCCACACTCCCTATACC
7539	5626	CCTCCCCACACTCCCTATAC
7540	5627	CCCTCCCCACACTCCCTATA
7541	5628	CCCCTCCCCACACTCCCTAT
7542	5629	TCCCCTCCCCACACTCCCTA
7543	5630	TTCCCCTCCCCACACTCCCT
7544	5631	ATTCCCCTCCCCACACTCCC
7545	5632	CATTCCCCTCCCCACACTCC
7546	5633	TCATTCCCCTCCCCACACTC
7547	5634	CTCATTCCCCTCCCCACACT
7548	5635	ACTCATTCCCCTCCCCACAC
7549	5636	AACTCATTCCCCTCCCCACA
7550	5637	TAACTCATTCCCCTCCCCAC
7551	5638	GTAACTCATTCCCCTCCCCA
7552	5639	TGTAACTCATTCCCCTCCCC
7553	5640	TTGTAACTCATTCCCCTCCC
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7558	5645	TAAAATTGTAACTCATTCCC
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7560	5647	TTTAAAATTGTAACTCATTC
7561	5648	ATTTAAAATTGTAACTCATT
7562	5649	CATTTAAAATTGTAACTCAT
7563	5650	CCATTTAAAATTGTAACTCA
7564	5651	TCCATTTAAAATTGTAACTC
7565	5652	ATCCATTTAAAATTGTAACT
7566	5653	AATCCATTTAAAATTGTAAC
7567	5654	CAATCCATTTAAAATTGTAA
7568	5655	CCAATCCATTTAAAATTGTA
7569	5656	CCCAATCCATTTAAAATTGT
7570	5657	CCCCAATCCATTTAAAATTG
7571	5658	CCCCCAATCCATTTAAAATT
7572	5659	TCCCCCAATCCATTTAAAAT
7573	5660	TTCCCCCAATCCATTTAAAA
7574	5661	GTTCCCCCAATCCATTTAAA
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7576	5663	AAGTTCCCCCAATCCATTTA
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7579	5666	ATTAAGTTCCCCCAATCCAT
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7581	5668	CAATTAAGTTCCCCCAATCC
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7586	5673	CTCCTCAATTAAGTTCCCCC
7587	5674	GCTCCTCAATTAAGTTCCCC
7588	5675	AGCTCCTCAATTAAGTTCCC
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7590	5677	TTAGCTCCTCAATTAAGTTC

56667	54754	TGTAATCCCAGCACTTTGGG
56668	54755	CTGTAATCCCAGCACTTTGG
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56670	54757	GCCTGTAATCCCAGCACTTT
56671	54758	TGCCTGTAATCCCAGCACTT
56672	54759	ATGCCTGTAATCCCAGCACT
56673	54760	CATGCCTGTAATCCCAGCAC
56674	54761	TCATGCCTGTAATCCCAGCA
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56676	54763	GCTCATGCCTGTAATCCCAG
56677	54764	GGCTCATGCCTGTAATCCCA
56678	54765	TGGCTCATGCCTGTAATCCC
56679	54766	GTGGCTCATGCCTGTAATCC
56680	54767	GGTGGCTCATGCCTGTAATC
56681	54768	CGGTGGCTCATGCCTGTAAT
56682	54769	GCGGTGGCTCATGCCTGTAA
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56684	54771	GTGCGGTGGCTCATGCCTGT
56685	54772	AGTGCGGTGGCTCATGCCTG
56686	54773	CAGTGCGGTGGCTCATGCCT
56687	54774	CCAGTGCGGTGGCTCATGCC
56688	54775	CCCAGTGCGGTGGCTCATGC
56689	54776	GCCCAGTGCGGTGGCTCATG
56690	54777	GGCCCAGTGCGGTGGCTCAT
56691	54778	GGGCCCAGTGCGGTGGCTCA
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56701	54788	GAATCCTTTTGGGCCCAGTG
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56703	54790	AAGAATCCTTTTGGGCCCAG
56704	54791	AAAGAATCCTTTTGGGCCCA
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56710	54797	GATTAAAAAGAATCCTTTTG
56711	54798	GGATTAAAAAGAATCCTTTT
56712	54799	AGGATTAAAAAGAATCCTTT
56713	54800	CAGGATTAAAAAGAATCCTT
56714	54801	TCAGGATTAAAAAGAATCCT
56715	54802	TTCAGGATTAAAAAGAATCC
56716	54803	ATTCAGGATTAAAAAGAATC
56717	54804	AATTCAGGATTAAAAAGAAT
56718	54805	GAATTCAGGATTAAAAAGAA
56719	54806	AGAATTCAGGATTAAAAAGA
56720	54807	AAGAATTCAGGATTAAAAAG
56721	54808	GAAGAATTCAGGATTAAAAA
56722	54809	AGAAGAATTCAGGATTAAAA
56723	54810	TAGAAGAATTCAGGATTAAA
56724	54811	CTAGAAGAATTCAGGATTAA
56725	54812	GCTAGAAGAATTCAGGATTA
56726	54813	GGCTAGAAGAATTCAGGATT
56727	54814	TGGCTAGAAGAATTCAGGAT
56728	54815	ATGGCTAGAAGAATTCAGGA
56729	54816	AATGGCTAGAAGAATTCAGG
56730	54817	TAATGGCTAGAAGAATTCAG
56731	54818	ATAATGGCTAGAAGAATTCA
56732	54819	GATAATGGCTAGAAGAATTC
56733	54820	GGATAATGGCTAGAAGAATT
56734	54821	AGGATAATGGCTAGAAGAAT
56735	54822	CAGGATAATGGCTAGAAGAA
56736	54823	GCAGGATAATGGCTAGAAGA
56737	54824	GGCAGGATAATGGCTAGAAG

105814	103901	ACAGAACATTGTGTCCAACA
105815	103902	TACAGAACATTGTGTCCAAC
105816	103903	TTACAGAACATTGTGTCCAA
105817	103904	TTTACAGAACATTGTGTCCA
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105823	103910	TACATATTTACAGAACATTG
105824	103911	ATACATATTTACAGAACATT
105825	103912	AATACATATTTACAGAACAT
105826	103913	CAATACATATTTACAGAACA
105827	103914	CCAATACATATTTACAGAAC
105828	103915	CCCAATACATATTTACAGAA
105829	103916	GCCCAATACATATTTACAGA
105830	103917	GGCCCAATACATATTTACAG
105831	103918	AGGCCCAATACATATTTACA
105832	103919	TAGGCCCAATACATATTTAC
105833	103920	ATAGGCCCAATACATATTTA
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105835	103922	AAATAGGCCCAATACATATT
105836	103923	CAAATAGGCCCAATACATAT
105837	103924	CCAAATAGGCCCAATACATA
105838	103925	ACCAAATAGGCCCAATACAT
105839	103926	GACCAAATAGGCCCAATACA
105840	103927	AGACCAAATAGGCCCAATAC
105841	103928	TAGACCAAATAGGCCCAATA
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105843	103930	TATAGACCAAATAGGCCCAA
105844	103931	CTATAGACCAAATAGGCCCA
105845	103932	TCTATAGACCAAATAGGCCC
105846	103933	CTCTATAGACCAAATAGGCC
105847	103934	GCTCTATAGACCAAATAGGC
105848	103935	TGCTCTATAGACCAAATAGG
105849	103936	TTGCTCTATAGACCAAATAG
105850	103937	TTTGCTCTATAGACCAAATA
105851	103938	ATTTGCTCTATAGACCAAAT
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105853	103940	TAATTTGCTCTATAGACCAA
105854	103941	CTAATTTGCTCTATAGACCA
105855	103942	CCTAATTTGCTCTATAGACC
105856	103943	ACCTAATTTGCTCTATAGAC
105857	103944	GACCTAATTTGCTCTATAGA
105858	103945	AGACCTAATTTGCTCTATAG
105859	103946	TAGACCTAATTTGCTCTATA
105860	103947	TTAGACCTAATTTGCTCTAT
105861	103948	ATTAGACCTAATTTGCTCTA
105862	103949	CATTAGACCTAATTTGCTCT
105863	103950	ACATTAGACCTAATTTGCTC
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105866	103953	GAAACATTAGACCTAATTTG
105867	103954	AGAAACATTAGACCTAATTT
105868	103955	AAGAAACATTAGACCTAATT
105869	103956	AAAGAAACATTAGACCTAAT
105870	103957	CAAAGAAACATTAGACCTAA
105871	103958	ACAAAGAAACATTAGACCTA
105872	103959	AACAAAGAAACATTAGACCT
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105875	103962	ATCAACAAAGAAACATTAGA
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105877	103964	AAATCAACAAAGAAACATTA
105878	103965	AAAATCAACAAAGAAACATT
105879	103966	GAAAATCAACAAAGAAACAT
105880	103967	AGAAAATCAACAAAGAAACA
105881	103968	CAGAAAATCAACAAAGAAAC
105882	103969	ACAGAAAATCAACAAAGAAA
105883	103970	GACAGAAAATCAACAAAGAA
105884	103971	AGACAGAAAATCAACAAAGA

7591	5678	GTTAGCTCCTCAATTAAGTT
7592	5679	TGTTAGCTCCTCAATTAAGT
7593	5680	ATGTTAGCTCCTCAATTAAG
7594	5681	AATGTTAGCTCCTCAATTAA
7595	5682	AAATGTTAGCTCCTCAATTA
7596	5683	CAAATGTTAGCTCCTCAATT
7597	5684	TCAAATGTTAGCTCCTCAAT
7598	5685	CTCAAATGTTAGCTCCTCAA
7599	5686	GCTCAAATGTTAGCTCCTCA
7600	5687	TGCTCAAATGTTAGCTCCTC
7601	5688	TTGCTCAAATGTTAGCTCCT
7602	5689	TTTGCTCAAATGTTAGCTCC
7603	5690	CTTTGCTCAAATGTTAGCTC
7604	5691	TCTTTGCTCAAATGTTAGCT
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7607	5694	AAATCTTTGCTCAAATGTTA
7608	5695	CAAATCTTTGCTCAAATGTT
7609	5696	TCAAATCTTTGCTCAAATGT
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7611	5698	CTTCAAATCTTTGCTCAAAT
7612	5699	CCTTCAAATCTTTGCTCAAA
7613	5700	ACCTTCAAATCTTTGCTCAA
7614	5701	AACCTTCAAATCTTTGCTCA
7615	5702	CAACCTTCAAATCTTTGCTC
7616	5703	CCAACCTTCAAATCTTTGCT
7617	5704	CCCAACCTTCAAATCTTTGC
7618	5705	ACCCAACCTTCAAATCTTTG
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7656	5743	ATGACTAATTAACCTAGATA
7657	5744	CATGACTAATTAACCTAGAT
7658	5745	ACATGACTAATTAACCTAGA
7659	5746	CACATGACTAATTAACCTAG
7660	5747	CCACATGACTAATTAACCTA
7661	5748	GCCACATGACTAATTAACCT

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7779	5866	AATGACCCTCAATGTCAATT
7780	5867	TAATGACCCTCAATGTCAAT
7781	5868	CTAATGACCCTCAATGTCAA
7782	5869	TCTAATGACCCTCAATGTCA
7783	5870	CTCTAATGACCCTCAATGTC
7784	5871	CCTCTAATGACCCTCAATGT
7785	5872	ACCTCTAATGACCCTCAATG
7786	5873	TACCTCTAATGACCCTCAAT
7787	5874	TTACCTCTAATGACCCTCAA
7788	5875	TTTACCTCTAATGACCCTCA
7789	5876	ATTTACCTCTAATGACCCTC
7790	5877	AATTTACCTCTAATGACCCT
7791	5878	CAATTTACCTCTAATGACCC
7792	5879	ACAATTTACCTCTAATGACC
7793	5880	TACAATTTACCTCTAATGAC
7794	5881	CTACAATTTACCTCTAATGA
7795	5882	TCTACAATTTACCTCTAATG
7796	5883	ATCTACAATTTACCTCTAAT
7797	5884	CATCTACAATTTACCTCTAA
7798	5885	CCATCTACAATTTACCTCTA
7799	5886	GCCATCTACAATTTACCTCT
7800	5887	AGCCATCTACAATTTACCTC
7801	5888	TAGCCATCTACAATTTACCT
7802	5889	ATAGCCATCTACAATTTACC
7803	5890	AATAGCCATCTACAATTTAC

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56882	54969	ATGAGGCAGGGAAGGAATGA
56883	54970	AATGAGGCAGGGAAGGAATG
56884	54971	GAATGAGGCAGGGAAGGAAT
56885	54972	GGAATGAGGCAGGGAAGGAA
56886	54973	AGGAATGAGGCAGGGAAGGA
56887	54974	CAGGAATGAGGCAGGGAAGG
56888	54975	CCAGGAATGAGGCAGGGAAG
56889	54976	CCCAGGAATGAGGCAGGGAA
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56891	54978	AGCCCAGGAATGAGGCAGGG
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56893	54980	GAAGCCCAGGAATGAGGCAG
56894	54981	AGAAGCCCAGGAATGAGGCA
56895	54982	AAGAAGCCCAGGAATGAGGC
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56922	55009	CACACATCTAAGGGGTGTGT
56923	55010	ACACACATCTAAGGGGTGTG
56924	55011	GACACACATCTAAGGGGTGT
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56927	55014	GGGGACACACATCTAAGGGG
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56931	55018	CACTGGGGACACACATCTAA
56932	55019	ACACTGGGGACACACATCTA
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56934	55021	AAACACTGGGGACACACATC
56935	55022	CAAACACTGGGGACACACAT
56936	55023	ACAAACACTGGGGACACACA
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56938	55025	AAACAAACACTGGGGACACA
56939	55026	GAAACAAACACTGGGGACAC
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106036	104123	GCAAGAGGTTATAACAAGTA
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57031	55118	CATGGTATAAGGGCAATGAT
57032	55119	ACATGGTATAAGGGCAATGA
57033	55120	AACATGGTATAAGGGCAATG
57034	55121	CAACATGGTATAAGGGCAAT
57035	55122	ACAACATGGTATAAGGGCAA
57036	55123	TACAACATGGTATAAGGGCA
57037	55124	ATACAACATGGTATAAGGGC
57038	55125	AATACAACATGGTATAAGGG
57039	55126	TAATACAACATGGTATAAGG
57040	55127	TTAATACAACATGGTATAAG
57041	55128	TTTAATACAACATGGTATAA
57042	55129	TTTTAATACAACATGGTATA
57043	55130	ATTTTAATACAACATGGTAT
57044	55131	AATTTTAATACAACATGGTA
57045	55132	TAATTTTAATACAACATGGT
57046	55133	ATAATTTTAATACAACATGG
57047	55134	TATAATTTTAATACAACATG
57048	55135	ATATAATTTTAATACAACAT
57049	55136	CATATAATTTTAATACAACA
57050	55137	GCATATAATTTTAATACAAC
57051	55138	AGCATATAATTTTAATACAA
57052	55139	AAGCATATAATTTTAATACA
57053	55140	CAAGCATATAATTTTAATAC
57054	55141	ACAAGCATATAATTTTAATA
57055	55142	GACAAGCATATAATTTTAAT
57056	55143	AGACAAGCATATAATTTTAA
57057	55144	GAGACAAGCATATAATTTTA
57058	55145	GGAGACAAGCATATAATTTT
57059	55146	GGGAGACAAGCATATAATTT
57060	55147	GGGGAGACAAGCATATAATT
57061	55148	AGGGGAGACAAGCATATAAT
57062	55149	CAGGGGAGACAAGCATATAA
57063	55150	ACAGGGGAGACAAGCATATA
57064	55151	AACAGGGGAGACAAGCATAT
57065	55152	TAACAGGGGAGACAAGCATA
57066	55153	GTAACAGGGGAGACAAGCAT
57067	55154	TGTAACAGGGGAGACAAGCA
57068	55155	CTGTAACAGGGGAGACAAGC
57069	55156	ACTGTAACAGGGGAGACAAG
57070	55157	AACTGTAACAGGGGAGACAA
57071	55158	AAACTGTAACAGGGGAGACA
57072	55159	CAAACTGTAACAGGGGAGAC
57073	55160	TCAAACTGTAACAGGGGAGA
57074	55161	CTCAAACTGTAACAGGGGAG
57075	55162	GCTCAAACTGTAACAGGGGA
57076	55163	AGCTCAAACTGTAACAGGGG
57077	55164	GAGCTCAAACTGTAACAGGG
57078	55165	AGAGCTCAAACTGTAACAGG
57079	55166	AAGAGCTCAAACTGTAACAG
57080	55167	AAAGAGCTCAAACTGTAACA
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57084	55171	GCACAAAGAGCTCAAACTGT
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57088	55175	TGGAGCACAAAGAGCTCAAA
57089	55176	TTGGAGCACAAAGAGCTCAA
57090	55177	CTTGGAGCACAAAGAGCTCA
57091	55178	ACTTGGAGCACAAAGAGCTC
57092	55179	TACTTGGAGCACAAAGAGCT

106169	104256	GAAAACAATATTCCATGCAA
106170	104257	GGAAAACAATATTCCATGCA
106171	104258	TGGAAAACAATATTCCATGC
106172	104259	CTGGAAAACAATATTCCATG
106173	104260	GCTGGAAAACAATATTCCAT
106174	104261	AGCTGGAAAACAATATTCCA
106175	104262	GAGCTGGAAAACAATATTCC
106176	104263	AGAGCTGGAAAACAATATTC
106177	104264	AAGAGCTGGAAAACAATATT
106178	104265	GAAGAGCTGGAAAACAATAT
106179	104266	TGAAGAGCTGGAAAACAATA
106180	104267	TTGAAGAGCTGGAAAACAAT
106181	104268	ATTGAAGAGCTGGAAAACAA
106182	104269	AATTGAAGAGCTGGAAAACA
106183	104270	AAATTGAAGAGCTGGAAAAC
106184	104271	AAAATTGAAGAGCTGGAAAA
106185	104272	TAAAATTGAAGAGCTGGAAA
106186	104273	CTAAAATTGAAGAGCTGGAA
106187	104274	ACTAAAATTGAAGAGCTGGA
106188	104275	GACTAAAATTGAAGAGCTGG
106189	104276	AGACTAAAATTGAAGAGCTG
106190	104277	TAGACTAAAATTGAAGAGCT
106191	104278	ATAGACTAAAATTGAAGAGC
106192	104279	CATAGACTAAAATTGAAGAG
106193	104280	ACATAGACTAAAATTGAAGA
106194	104281	CACATAGACTAAAATTGAAG
106195	104282	ACACATAGACTAAAATTGAA
106196	104283	CACACATAGACTAAAATTGA
106197	104284	TCACACATAGACTAAAATTG
106198	104285	ATCACACATAGACTAAAATT
106199	104286	AATCACACATAGACTAAAAT
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106201	104288	AAAATCACACATAGACTAAA
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106203	104290	ATAAAATCACACATAGACTA
106204	104291	TATAAAATCACACATAGACT
106205	104292	CTATAAAATCACACATAGAC
106206	104293	CCTATAAAATCACACATAGA
106207	104294	ACCTATAAAATCACACATAG
106208	104295	TACCTATAAAATCACACATA
106209	104296	TTACCTATAAAATCACACAT
106210	104297	TTTACCTATAAAATCACACA
106211	104298	CTTTACCTATAAAATCACAC
106212	104299	ACTTTACCTATAAAATCACA
106213	104300	CACTTTACCTATAAAATCAC
106214	104301	ACACTTTACCTATAAAATCA
106215	104302	CACACTTTACCTATAAAATC
106216	104303	ACACACTTTACCTATAAAAT
106217	104304	AACACACTTTACCTATAAAA
106218	104305	AAACACACTTTACCTATAAA
106219	104306	GAAACACACTTTACCTATAA
106220	104307	AGAAACACACTTTACCTATA
106221	104308	AAGAAACACACTTTACCTAT
106222	104309	CAAGAAACACACTTTACCTA
106223	104310	ACAAGAAACACACTTTACCT
106224	104311	TACAAGAAACACACTTTACC
106225	104312	CTACAAGAAACACACTTTAC
106226	104313	CCTACAAGAAACACACTTTA
106227	104314	GCCTACAAGAAACACACTTT
106228	104315	TGCCTACAAGAAACACACTT
106229	104316	TTGCCTACAAGAAACACACT
106230	104317	ATTGCCTACAAGAAACACAC
106231	104318	CATTGCCTACAAGAAACACA
106232	104319	CCATTGCCTACAAGAAACAC
106233	104320	TCCATTGCCTACAAGAAACA
106234	104321	ATCCATTGCCTACAAGAAAC
106235	104322	GATCCATTGCCTACAAGAAA
106236	104323	AGATCCATTGCCTACAAGAA
106237	104324	AAGATCCATTGCCTACAAGA
106238	104325	AAAGATCCATTGCCTACAAG
106239	104326	CAAAGATCCATTGCCTACAA

7946	6033	AAGAAAAAGAAAAAGAAAAC
7947	6034	AAAGAAAAAGAAAAAGAAAA
7948	6035	AAAAGAAAAAGAAAAAGAAA
7949	6036	AAAAAGAAAAAGAAAAAGAA
7950	6037	AAAAAAGAAAAAGAAAAAGA
7951	6038	AAAAAAAGAAAAAGAAAAAG
7952	6039	AAAAAAAAGAAAAAGAAAAA
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7971	6058	TACATTTTTCTCTTAAAAAA
7972	6059	TTACATTTTTCTCTTAAAAA
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7974	6061	GCTTACATTTTTCTCTTAAA
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7976	6063	AGGCTTACATTTTTCTCTTA
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7979	6066	TACAGGCTTACATTTTTCTC
7980	6067	CTACAGGCTTACATTTTTCT
7981	6068	ACTACAGGCTTACATTTTTC
7982	6069	AACTACAGGCTTACATTTTT
7983	6070	CAACTACAGGCTTACATTTT
7984	6071	GCAACTACAGGCTTACATTT
7985	6072	AGCAACTACAGGCTTACATT
7986	6073	AAGCAACTACAGGCTTACAT
7987	6074	TAAGCAACTACAGGCTTACA
7988	6075	TTAAGCAACTACAGGCTTAC
7989	6076	TTTAAGCAACTACAGGCTTA
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7992	6079	ATCTTTAAGCAACTACAGGC
7993	6080	AATCTTTAAGCAACTACAGG
7994	6081	GAATCTTTAAGCAACTACAG
7995	6082	GGAATCTTTAAGCAACTACA
7996	6083	TGGAATCTTTAAGCAACTAC
7997	6084	GTGGAATCTTTAAGCAACTA
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8001	6088	GAATGTGGAATCTTTAAGCA
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8004	6091	TCAGAATGTGGAATCTTTAA
8005	6092	TTCAGAATGTGGAATCTTTA
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8007	6094	GTTTCAGAATGTGGAATCTT
8008	6095	TGTTTCAGAATGTGGAATCT
8009	6096	CTGTTTCAGAATGTGGAATC
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8014	6101	TTTCACTGTTTCAGAATGTG
8015	6102	TTTTCACTGTTTCAGAATGT
8016	6103	GTTTTCACTGTTTCAGAATG

57093	55180	TTACTTGGAGCACAAAGAGC
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57095	55182	CTTTACTTGGAGCACAAAGA
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57104	55191	TATCACTGTCTTTACTTGGA
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57106	55193	AGTATCACTGTCTTTACTTG
57107	55194	CAGTATCACTGTCTTTACTT
57108	55195	ACAGTATCACTGTCTTTACT
57109	55196	GACAGTATCACTGTCTTTAC
57110	55197	AGACAGTATCACTGTCTTTA
57111	55198	AAGACAGTATCACTGTCTTT
57112	55199	AAAGACAGTATCACTGTCTT
57113	55200	TAAAGACAGTATCACTGTCT
57114	55201	ATAAAGACAGTATCACTGTC
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57120	55207	TAAATAATAAAGACAGTATC
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57130	55217	ACCATGAGAATAAATAATAA
57131	55218	GACCATGAGAATAAATAATA
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57140	55227	ACTATACTAGACCATGAGAA
57141	55228	CACTATACTAGACCATGAGA
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57147	55234	CCAAAGCACTATACTAGACC
57148	55235	GCCAAAGCACTATACTAGAC
57149	55236	TGCCAAAGCACTATACTAGA
57150	55237	GTGCCAAAGCACTATACTAG
57151	55238	TGTGCCAAAGCACTATACTA
57152	55239	ATGTGCCAAAGCACTATACT
57153	55240	TATGTGCCAAAGCACTATAC
57154	55241	CTATGTGCCAAAGCACTATA
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57156	55243	TACTATGTGCCAAAGCACTA
57157	55244	GTACTATGTGCCAAAGCACT
57158	55245	TGTACTATGTGCCAAAGCAC
57159	55246	CTGTACTATGTGCCAAAGCA
57160	55247	CCTGTACTATGTGCCAAAGC
57161	55248	GCCTGTACTATGTGCCAAAG
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106240	104327	CCAAAGATCCATTGCCTACA
106241	104328	ACCAAAGATCCATTGCCTAC
106242	104329	AACCAAAGATCCATTGCCTA
106243	104330	AAACCAAAGATCCATTGCCT
106244	104331	AAAACCAAAGATCCATTGCC
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106249	104336	AAAAAAAAACCAAAGATCCA
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106252	104339	AAAAAAAAAAAACCAAAGAT
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106254	104341	AAAAAAAAAAAAAACCAAAG
106255	104342	AAAAAAAAAAAAAAACCAAA
106256	104343	AAAAAAAAAAAAAAAACCAA
106257	104344	AAAAAAAAAAAAAAAAACCA
106258	104345	AAAAAAAAAAAAAAAAAACC
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106260	104347	CAAAAAAAAAAAAAAAAAAA
106261	104348	TCAAAAAAAAAAAAAAAAAA
106262	104349	CTCAAAAAAAAAAAAAAAAA
106263	104350	TCTCAAAAAAAAAAAAAAAA
106264	104351	GTCTCAAAAAAAAAAAAAAA
106265	104352	TGTCTCAAAAAAAAAAAAAA
106266	104353	CTGTCTCAAAAAAAAAAAAA
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106269	104356	ACTCTGTCTCAAAAAAAAAA
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106273	104360	CAAAACTCTGTCTCAAAAAA
106274	104361	GCAAAACTCTGTCTCAAAAA
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106278	104365	AATAGCAAAACTCTGTCTCA
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106287	104374	CTGGGCAACAATAGCAAAAC
106288	104375	CCTGGGCAACAATAGCAAAA
106289	104376	GCCTGGGCAACAATAGCAAA
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106291	104378	CAGCCTGGGCAACAATAGCA
106292	104379	CCAGCCTGGGCAACAATAGC
106293	104380	TCCAGCCTGGGCAACAATAG
106294	104381	CTCCAGCCTGGGCAACAATA
106295	104382	CCTCCAGCCTGGGCAACAAT
106296	104383	CCCTCCAGCCTGGGCAACAA
106297	104384	GCCCTCCAGCCTGGGCAACA
106298	104385	TGCCCTCCAGCCTGGGCAAC
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106300	104387	ATTGCCCTCCAGCCTGGGCA
106301	104388	CATTGCCCTCCAGCCTGGGC
106302	104389	CCATTGCCCTCCAGCCTGGG
106303	104390	GCCATTGCCCTCCAGCCTGG
106304	104391	CGCCATTGCCCTCCAGCCTG
106305	104392	GCGCCATTGCCCTCCAGCCT
106306	104393	AGCGCCATTGCCCTCCAGCC
106307	104394	TAGCGCCATTGCCCTCCAGC
106308	104395	ATAGCGCCATTGCCCTCCAG
106309	104396	GATAGCGCCATTGCCCTCCA
106310	104397	AGATAGCGCCATTGCCCTCC

8017	6104	TGTTTTCACTGTTTCAGAAT
8018	6105	ATGTTTTCACTGTTTCAGAA
8019	6106	CATGTTTTCACTGTTTCAGA
8020	6107	CCATGTTTTCACTGTTTCAG
8021	6108	CCCATGTTTTCACTGTTTCA
8022	6109	TCCCATGTTTTCACTGTTTC
8023	6110	ATCCCATGTTTTCACTGTTT
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8025	6112	TGATCCCATGTTTTCACTGT
8026	6113	CTGATCCCATGTTTTCACTG
8027	6114	ACTGATCCCATGTTTTCACT
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8030	6117	ATGACTGATCCCATGTTTTC
8031	6118	CATGACTGATCCCATGTTTT
8032	6119	CCATGACTGATCCCATGTTT
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8034	6121	CACCATGACTGATCCCATGT
8035	6122	ACACCATGACTGATCCCATG
8036	6123	AACACCATGACTGATCCCAT
8037	6124	GAACACCATGACTGATCCCA
8038	6125	GGAACACCATGACTGATCCC
8039	6126	AGGAACACCATGACTGATCC
8040	6127	AAGGAACACCATGACTGATC
8041	6128	AAAGGAACACCATGACTGAT
8042	6129	AAAAGGAACACCATGACTGA
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8056	6143	TACATTTAACCAAAAAAAGG
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8059	6146	GTTTACATTTAACCAAAAAA
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8062	6149	CAAGTTTACATTTAACCAAA
8063	6150	ACAAGTTTACATTTAACCAA
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8070	6157	TGAAAATACAAGTTTACATT
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8083	6170	ATTAGAGTAACACTGAAAAT
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8085	6172	TAATTAGAGTAACACTGAAA
8086	6173	CTAATTAGAGTAACACTGAA
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57164	55251	TGAGCCTGTACTATGTGCCA
57165	55252	TTGAGCCTGTACTATGTGCC
57166	55253	ATTGAGCCTGTACTATGTGC
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57177	55264	AACACATTTATATTGAGCCT
57178	55265	AAACACATTTATATTGAGCC
57179	55266	CAAACACATTTATATTGAGC
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57181	55268	TTCAAACACATTTATATTGA
57182	55269	ATTCAAACACATTTATATTG
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57189	55276	TTCATTTATTCAAACACATT
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57194	55281	TGAATTTCATTTATTCAAAC
57195	55282	CTGAATTTCATTTATTCAAA
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57197	55284	CACTGAATTTCATTTATTCA
57198	55285	GCACTGAATTTCATTTATTC
57199	55286	GGCACTGAATTTCATTTATT
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57202	55289	TAAGGCACTGAATTTCATTT
57203	55290	TTAAGGCACTGAATTTCATT
57204	55291	ATTAAGGCACTGAATTTCAT
57205	55292	TATTAAGGCACTGAATTTCA
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57218	55305	TTCTACAAAAGTGTATTAAG
57219	55306	CTTCTACAAAAGTGTATTAA
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57225	55312	ATAATGCTTCTACAAAAGTG
57226	55313	AATAATGCTTCTACAAAAGT
57227	55314	AAATAATGCTTCTACAAAAG
57228	55315	AAAATAATGCTTCTACAAAA
57229	55316	TAAAATAATGCTTCTACAAA
57230	55317	ATAAAATAATGCTTCTACAA
57231	55318	CATAAAATAATGCTTCTACA
57232	55319	CCATAAAATAATGCTTCTAC
57233	55320	TCCATAAAATAATGCTTCTA
57234	55321	TTCCATAAAATAATGCTTCT

106311	104398	GAGATAGCGCCATTGCCCTC
106312	104399	TGAGATAGCGCCATTGCCCT
106313	104400	CTGAGATAGCGCCATTGCCC
106314	104401	GCTGAGATAGCGCCATTGCC
106315	104402	AGCTGAGATAGCGCCATTGC
106316	104403	GAGCTGAGATAGCGCCATTG
106317	104404	TGAGCTGAGATAGCGCCATT
106318	104405	GTGAGCTGAGATAGCGCCAT
106319	104406	AGTGAGCTGAGATAGCGCCA
106320	104407	CAGTGAGCTGAGATAGCGCC
106321	104408	GCAGTGAGCTGAGATAGCGC
106322	104409	TGCAGTGAGCTGAGATAGCG
106323	104410	TTGCAGTGAGCTGAGATAGC
106324	104411	GTTGCAGTGAGCTGAGATAG
106325	104412	GGTTGCAGTGAGCTGAGATA
106326	104413	AGGTTGCAGTGAGCTGAGAT
106327	104414	GAGGTTGCAGTGAGCTGAGA
106328	104415	GGAGGTTGCAGTGAGCTGAG
106329	104416	CGGAGGTTGCAGTGAGCTGA
106330	104417	GCGGAGGTTGCAGTGAGCTG
106331	104418	GGCGGAGGTTGCAGTGAGCT
106332	104419	AGGCGGAGGTTGCAGTGAGC
106333	104420	GAGGCGGAGGTTGCAGTGAG
106334	104421	GGAGGCGGAGGTTGCAGTGA
106335	104422	AGGAGGCGGAGGTTGCAGTG
106336	104423	CAGGAGGCGGAGGTTGCAGT
106337	104424	TCAGGAGGCGGAGGTTGCAG
106338	104425	CTCAGGAGGCGGAGGTTGCA
106339	104426	ACTCAGGAGGCGGAGGTTGC
106340	104427	AACTCAGGAGGCGGAGGTTG
106341	104428	GAACTCAGGAGGCGGAGGTT
106342	104429	TGAACTCAGGAGGCGGAGGT
106343	104430	TTGAACTCAGGAGGCGGAGG
106344	104431	CTTGAACTCAGGAGGCGGAG
106345	104432	GCTTGAACTCAGGAGGCGGA
106346	104433	CGCTTGAACTCAGGAGGCGG
106347	104434	TCGCTTGAACTCAGGAGGCG
106348	104435	ATCGCTTGAACTCAGGAGGC
106349	104436	AATCGCTTGAACTCAGGAGG
106350	104437	GAATCGCTTGAACTCAGGAG
106351	104438	AGAATCGCTTGAACTCAGGA
106352	104439	GAGAATCGCTTGAACTCAGG
106353	104440	GGAGAATCGCTTGAACTCAG
106354	104441	AGGAGAATCGCTTGAACTCA
106355	104442	CAGGAGAATCGCTTGAACTC
106356	104443	GCAGGAGAATCGCTTGAACT
106357	104444	GGCAGGAGAATCGCTTGAAC
106358	104445	AGGCAGGAGAATCGCTTGAA
106359	104446	GAGGCAGGAGAATCGCTTGA
106360	104447	TGAGGCAGGAGAATCGCTTG
106361	104448	CTGAGGCAGGAGAATCGCTT
106362	104449	GCTGAGGCAGGAGAATCGCT
106363	104450	GGCTGAGGCAGGAGAATCGC
106364	104451	AGGCTGAGGCAGGAGAATCG
106365	104452	GAGGCTGAGGCAGGAGAATC
106366	104453	GGAGGCTGAGGCAGGAGAAT
106367	104454	GGGAGGCTGAGGCAGGAGAA
106368	104455	TGGGAGGCTGAGGCAGGAGA
106369	104456	TTGGGAGGCTGAGGCAGGAG
106370	104457	CTTGGGAGGCTGAGGCAGGA
106371	104458	ACTTGGGAGGCTGAGGCAGG
106372	104459	TACTTGGGAGGCTGAGGCAG
106373	104460	CTACTTGGGAGGCTGAGGCA
106374	104461	GCTACTTGGGAGGCTGAGGC
106375	104462	AGCTACTTGGGAGGCTGAGG
106376	104463	CAGCTACTTGGGAGGCTGAG
106377	104464	CCAGCTACTTGGGAGGCTGA
106378	104465	CCCAGCTACTTGGGAGGCTG
106379	104466	TCCCAGCTACTTGGGAGGCT
106380	104467	ATCCCAGCTACTTGGGAGGC
106381	104468	AATCCCAGCTACTTGGGAGG

8088	6175	TGCTAATTAGAGTAACACTG
8089	6176	TTGCTAATTAGAGTAACACT
8090	6177	ATTGCTAATTAGAGTAACAC
8091	6178	CATTGCTAATTAGAGTAACA
8092	6179	CCATTGCTAATTAGAGTAAC
8093	6180	ACCATTGCTAATTAGAGTAA
8094	6181	AACCATTGCTAATTAGAGTA
8095	6182	AAACCATTGCTAATTAGAGT
8096	6183	TAAACCATTGCTAATTAGAG
8097	6184	ATAAACCATTGCTAATTAGA
8098	6185	TATAAACCATTGCTAATTAG
8099	6186	GTATAAACCATTGCTAATTA
8100	6187	AGTATAAACCATTGCTAATT
8101	6188	AAGTATAAACCATTGCTAAT
8102	6189	GAAGTATAAACCATTGCTAA
8103	6190	AGAAGTATAAACCATTGCTA
8104	6191	TAGAAGTATAAACCATTGCT
8105	6192	GTAGAAGTATAAACCATTGC
8106	6193	TGTAGAAGTATAAACCATTG
8107	6194	ATGTAGAAGTATAAACCATT
8108	6195	TATGTAGAAGTATAAACCAT
8109	6196	TTATGTAGAAGTATAAACCA
8110	6197	CTTATGTAGAAGTATAAACC
8111	6198	CCTTATGTAGAAGTATAAAC
8112	6199	CCCTTATGTAGAAGTATAAA
8113	6200	TCCCTTATGTAGAAGTATAA
8114	6201	ATCCCTTATGTAGAAGTATA
8115	6202	CATCCCTTATGTAGAAGTAT
8116	6203	ACATCCCTTATGTAGAAGTA
8117	6204	AACATCCCTTATGTAGAAGT
8118	6205	TAACATCCCTTATGTAGAAG
8119	6206	TTAACATCCCTTATGTAGAA
8120	6207	GTTAACATCCCTTATGTAGA
8121	6208	AGTTAACATCCCTTATGTAG
8122	6209	GAGTTAACATCCCTTATGTA
8123	6210	TGAGTTAACATCCCTTATGT
8124	6211	ATGAGTTAACATCCCTTATG
8125	6212	TATGAGTTAACATCCCTTAT
8126	6213	ATATGAGTTAACATCCCTTA
8127	6214	AATATGAGTTAACATCCCTT
8128	6215	CAATATGAGTTAACATCCCT
8129	6216	ACAATATGAGTTAACATCCC
8130	6217	TACAATATGAGTTAACATCC
8131	6218	CTACAATATGAGTTAACATC
8132	6219	GCTACAATATGAGTTAACAT
8133	6220	AGCTACAATATGAGTTAACA
8134	6221	TAGCTACAATATGAGTTAAC
8135	6222	ATAGCTACAATATGAGTTAA
8136	6223	AATAGCTACAATATGAGTTA
8137	6224	AAATAGCTACAATATGAGTT
8138	6225	TAAATAGCTACAATATGAGT
8139	6226	TTAAATAGCTACAATATGAG
8140	6227	ATTAAATAGCTACAATATGA
8141	6228	TATTAAATAGCTACAATATG
8142	6229	CTATTAAATAGCTACAATAT
8143	6230	GCTATTAAATAGCTACAATA
8144	6231	GGCTATTAAATAGCTACAAT
8145	6232	TGGCTATTAAATAGCTACAA
8146	6233	ATGGCTATTAAATAGCTACA
8147	6234	TATGGCTATTAAATAGCTAC
8148	6235	ATATGGCTATTAAATAGCTA
8149	6236	TATATGGCTATTAAATAGCT
8150	6237	ATATATGGCTATTAAATAGC
8151	6238	AATATATGGCTATTAAATAG
8152	6239	AAATATATGGCTATTAAATA
8153	6240	AAAATATATGGCTATTAAAT
8154	6241	CAAAATATATGGCTATTAAA
8155	6242	TCAAAATATATGGCTATTAA
8156	6243	GTCAAAATATATGGCTATTA
8157	6244	AGTCAAAATATATGGCTATT
8158	6245	AAGTCAAAATATATGGCTAT

57235	55322	TTTCCATAAAATAATGCTTC
57236	55323	CTTTCCATAAAATAATGCTT
57237	55324	TCTTTCCATAAAATAATGCT
57238	55325	TTCTTTCCATAAAATAATGC
57239	55326	ATTCTTTCCATAAAATAATG
57240	55327	CATTCTTTCCATAAAATAAT
57241	55328	TCATTCTTTCCATAAAATAA
57242	55329	TTCATTCTTTCCATAAAATA
57243	55330	TTTCATTCTTTCCATAAAAT
57244	55331	TTTTCATTCTTTCCATAAAA
57245	55332	TTTTTCATTCTTTCCATAAA
57246	55333	CTTTTTCATTCTTTCCATAA
57247	55334	GCTTTTTCATTCTTTCCATA
57248	55335	AGCTTTTTCATTCTTTCCAT
57249	55336	CAGCTTTTTCATTCTTTCCA
57250	55337	ACAGCTTTTTCATTCTTTCC
57251	55338	TACAGCTTTTTCATTCTTTC
57252	55339	TTACAGCTTTTTCATTCTTT
57253	55340	CTTACAGCTTTTTCATTCTT
57254	55341	ACTTACAGCTTTTTCATTCT
57255	55342	CACTTACAGCTTTTTCATTC
57256	55343	CCACTTACAGCTTTTTCATT
57257	55344	ACCACTTACAGCTTTTTCAT
57258	55345	GACCACTTACAGCTTTTTCA
57259	55346	AGACCACTTACAGCTTTTTC
57260	55347	AAGACCACTTACAGCTTTTT
57261	55348	TAAGACCACTTACAGCTTTT
57262	55349	GTAAGACCACTTACAGCTTT
57263	55350	TGTAAGACCACTTACAGCTT
57264	55351	ATGTAAGACCACTTACAGCT
57265	55352	TATGTAAGACCACTTACAGC
57266	55353	ATATGTAAGACCACTTACAG
57267	55354	TATATGTAAGACCACTTACA
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57269	55356	TATATATGTAAGACCACTTA
57270	55357	CTATATATGTAAGACCACTT
57271	55358	ACTATATATGTAAGACCACT
57272	55359	GACTATATATGTAAGACCAC
57273	55360	TGACTATATATGTAAGACCA
57274	55361	ATGACTATATATGTAAGACC
57275	55362	GATGACTATATATGTAAGAC
57276	55363	GGATGACTATATATGTAAGA
57277	55364	TGGATGACTATATATGTAAG
57278	55365	CTGGATGACTATATATGTAA
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57289	55376	CTAAGTATCTGCTGGATGAC
57290	55377	TCTAAGTATCTGCTGGATGA
57291	55378	CTCTAAGTATCTGCTGGATG
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57293	55380	CTCTCTAAGTATCTGCTGGA
57294	55381	GCTCTCTAAGTATCTGCTGG
57295	55382	AGCTCTCTAAGTATCTGCTG
57296	55383	GAGCTCTCTAAGTATCTGCT
57297	55384	AGAGCTCTCTAAGTATCTGC
57298	55385	CAGAGCTCTCTAAGTATCTG
57299	55386	CCAGAGCTCTCTAAGTATCT
57300	55387	CCCAGAGCTCTCTAAGTATC
57301	55388	TCCCAGAGCTCTCTAAGTAT
57302	55389	ATCCCAGAGCTCTCTAAGTA
57303	55390	CATCCCAGAGCTCTCTAAGT
57304	55391	ACATCCCAGAGCTCTCTAAG
57305	55392	CACATCCCAGAGCTCTCTAA

106382	104469	TAATCCCAGCTACTTGGGAG
106383	104470	GTAATCCCAGCTACTTGGGA
106384	104471	TGTAATCCCAGCTACTTGGG
106385	104472	CTGTAATCCCAGCTACTTGG
106386	104473	CCTGTAATCCCAGCTACTTG
106387	104474	GCCTGTAATCCCAGCTACTT
106388	104475	CGCCTGTAATCCCAGCTACT
106389	104476	GCGCCTGTAATCCCAGCTAC
106390	104477	GGCGCCTGTAATCCCAGCTA
106391	104478	AGGCGCCTGTAATCCCAGCT
106392	104479	CAGGCGCCTGTAATCCCAGC
106393	104480	GCAGGCGCCTGTAATCCCAG
106394	104481	GGCAGGCGCCTGTAATCCCA
106395	104482	TGGCAGGCGCCTGTAATCCC
106396	104483	GTGGCAGGCGCCTGTAATCC
106397	104484	GGTGGCAGGCGCCTGTAATC
106398	104485	TGGTGGCAGGCGCCTGTAAT
106399	104486	TTGGTGGCAGGCGCCTGTAA
106400	104487	CTTGGTGGCAGGCGCCTGTA
106401	104488	GCTTGGTGGCAGGCGCCTGT
106402	104489	GGCTTGGTGGCAGGCGCCTG
106403	104490	GGGCTTGGTGGCAGGCGCCT
106404	104491	TGGGCTTGGTGGCAGGCGCC
106405	104492	CTGGGCTTGGTGGCAGGCGC
106406	104493	GCTGGGCTTGGTGGCAGGCG
106407	104494	AGCTGGGCTTGGTGGCAGGC
106408	104495	TAGCTGGGCTTGGTGGCAGG
106409	104496	TTAGCTGGGCTTGGTGGCAG
106410	104497	TTTAGCTGGGCTTGGTGGCA
106411	104498	ATTTAGCTGGGCTTGGTGGC
106412	104499	AATTTAGCTGGGCTTGGTGG
106413	104500	AAATTTAGCTGGGCTTGGTG
106414	104501	AAAATTTAGCTGGGCTTGGT
106415	104502	AAAAATTTAGCTGGGCTTGG
106416	104503	AAAAAATTTAGCTGGGCTTG
106417	104504	CAAAAAATTTAGCTGGGCTT
106418	104505	ACAAAAAATTTAGCTGGGCT
106419	104506	TACAAAAAATTTAGCTGGGC
106420	104507	ATACAAAAAATTTAGCTGGG
106421	104508	AATACAAAAAATTTAGCTGG
106422	104509	AAATACAAAAAATTTAGCTG
106423	104510	AAAATACAAAAAATTTAGCT
106424	104511	GAAAATACAAAAAATTTAGC
106425	104512	TGAAAATACAAAAAATTTAG
106426	104513	CTGAAAATACAAAAAATTTA
106427	104514	ACTGAAAATACAAAAAATTT
106428	104515	TACTGAAAATACAAAAAATT
106429	104516	CTACTGAAAATACAAAAAAT
106430	104517	TCTACTGAAAATACAAAAAA
106431	104518	CTCTACTGAAAATACAAAAA
106432	104519	TCTCTACTGAAAATACAAAA
106433	104520	ATCTCTACTGAAAATACAAA
106434	104521	CATCTCTACTGAAAATACAA
106435	104522	CCATCTCTACTGAAAATACA
106436	104523	CCCATCTCTACTGAAAATAC
106437	104524	CCCCATCTCTACTGAAAATA
106438	104525	ACCCCATCTCTACTGAAAAT
106439	104526	AACCCCATCTCTACTGAAAA
106440	104527	AAACCCCATCTCTACTGAAA
106441	104528	GAAACCCCATCTCTACTGAA
106442	104529	TGAAACCCCATCTCTACTGA
106443	104530	CTGAAACCCCATCTCTACTG
106444	104531	ACTGAAACCCCATCTCTACT
106445	104532	TACTGAAACCCCATCTCTAC
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106447	104534	CATACTGAAACCCCATCTCT
106448	104535	ACATACTGAAACCCCATCTC
106449	104536	AACATACTGAAACCCCATCT
106450	104537	GAACATACTGAAACCCCATC
106451	104538	CGAACATACTGAAACCCCAT
106452	104539	ACGAACATACTGAAACCCCA

8159	6246	TAAGTCAAAATATATGGCTA
8160	6247	TTAAGTCAAAATATATGGCT
8161	6248	TTTAAGTCAAAATATATGGC
8162	6249	CTTTAAGTCAAAATATATGG
8163	6250	CCTTTAAGTCAAAATATATG
8164	6251	TCCTTTAAGTCAAAATATAT
8165	6252	CTCCTTTAAGTCAAAATATA
8166	6253	CCTCCTTTAAGTCAAAATAT
8167	6254	TCCTCCTTTAAGTCAAAATA
8168	6255	ATCCTCCTTTAAGTCAAAAT
8169	6256	GATCCTCCTTTAAGTCAAAA
8170	6257	AGATCCTCCTTTAAGTCAAA
8171	6258	GAGATCCTCCTTTAAGTCAA
8172	6259	TGAGATCCTCCTTTAAGTCA
8173	6260	TTGAGATCCTCCTTTAAGTC
8174	6261	CTTGAGATCCTCCTTTAAGT
8175	6262	CCTTGAGATCCTCCTTTAAG
8176	6263	GCCTTGAGATCCTCCTTTAA
8177	6264	GGCCTTGAGATCCTCCTTTA
8178	6265	TGGCCTTGAGATCCTCCTTT
8179	6266	CTGGCCTTGAGATCCTCCTT
8180	6267	CCTGGCCTTGAGATCCTCCT
8181	6268	GCCTGGCCTTGAGATCCTCC
8182	6269	CGCCTGGCCTTGAGATCCTC
8183	6270	GCGCCTGGCCTTGAGATCCT
8184	6271	CGCGCCTGGCCTTGAGATCC
8185	6272	CCGCGCCTGGCCTTGAGATC
8186	6273	ACCGCGCCTGGCCTTGAGAT
8187	6274	CACCGCGCCTGGCCTTGAGA
8188	6275	CCACCGCGCCTGGCCTTGAG
8189	6276	GCCACCGCGCCTGGCCTTGA
8190	6277	AGCCACCGCGCCTGGCCTTG
8191	6278	GAGCCACCGCGCCTGGCCTT
8192	6279	TGAGCCACCGCGCCTGGCCT
8193	6280	ATGAGCCACCGCGCCTGGCC
8194	6281	TATGAGCCACCGCGCCTGGC
8195	6282	GTATGAGCCACCGCGCCTGG
8196	6283	GGTATGAGCCACCGCGCCTG
8197	6284	AGGTATGAGCCACCGCGCCT
8198	6285	CAGGTATGAGCCACCGCGCC
8199	6286	ACAGGTATGAGCCACCGCGC
8200	6287	TACAGGTATGAGCCACCGCG
8201	6288	TTACAGGTATGAGCCACCGC
8202	6289	ATTACAGGTATGAGCCACCG
8203	6290	GATTACAGGTATGAGCCACC
8204	6291	GGATTACAGGTATGAGCCAC
8205	6292	GGGATTACAGGTATGAGCCA
8206	6293	TGGGATTACAGGTATGAGCC
8207	6294	CTGGGATTACAGGTATGAGC
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8209	6296	TGCTGGGATTACAGGTATGA
8210	6297	GTGCTGGGATTACAGGTATG
8211	6298	AGTGCTGGGATTACAGGTAT
8212	6299	AAGTGCTGGGATTACAGGTA
8213	6300	AAAGTGCTGGGATTACAGGT
8214	6301	TAAAGTGCTGGGATTACAGG
8215	6302	CTAAAGTGCTGGGATTACAG
8216	6303	CCTAAAGTGCTGGGATTACA
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8218	6305	CTCCTAAAGTGCTGGGATTA
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8220	6307	GCCTCCTAAAGTGCTGGGAT
8221	6308	AGCCTCCTAAAGTGCTGGGA
8222	6309	CAGCCTCCTAAAGTGCTGGG
8223	6310	TCAGCCTCCTAAAGTGCTGG
8224	6311	CTCAGCCTCCTAAAGTGCTG
8225	6312	CCTCAGCCTCCTAAAGTGCT
8226	6313	GCCTCAGCCTCCTAAAGTGC
8227	6314	CGCCTCAGCCTCCTAAAGTG
8228	6315	CCGCCTCAGCCTCCTAAAGT
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57306	55393	ACACATCCCAGAGCTCTCTA
57307	55394	AACACATCCCAGAGCTCTCT
57308	55395	GAACACATCCCAGAGCTCTC
57309	55396	GGAACACATCCCAGAGCTCT
57310	55397	AGGAACACATCCCAGAGCTC
57311	55398	AAGGAACACATCCCAGAGCT
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57315	55402	CAGCAAGGAACACATCCCAG
57316	55403	ACAGCAAGGAACACATCCCA
57317	55404	CACAGCAAGGAACACATCCC
57318	55405	GCACAGCAAGGAACACATCC
57319	55406	AGCACAGCAAGGAACACATC
57320	55407	AAGCACAGCAAGGAACACAT
57321	55408	CAAGCACAGCAAGGAACACA
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57323	55410	AACAAGCACAGCAAGGAACA
57324	55411	CAACAAGCACAGCAAGGAAC
57325	55412	GCAACAAGCACAGCAAGGAA
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57327	55414	TAGCAACAAGCACAGCAAGG
57328	55415	ATAGCAACAAGCACAGCAAG
57329	55416	CATAGCAACAAGCACAGCAA
57330	55417	CCATAGCAACAAGCACAGCA
57331	55418	TCCATAGCAACAAGCACAGC
57332	55419	GTCCATAGCAACAAGCACAG
57333	55420	TGTCCATAGCAACAAGCACA
57334	55421	CTGTCCATAGCAACAAGCAC
57335	55422	ACTGTCCATAGCAACAAGCA
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57337	55424	GTACTGTCCATAGCAACAAG
57338	55425	CGTACTGTCCATAGCAACAA
57339	55426	CCGTACTGTCCATAGCAACA
57340	55427	TCCGTACTGTCCATAGCAAC
57341	55428	CTCCGTACTGTCCATAGCAA
57342	55429	TCTCCGTACTGTCCATAGCA
57343	55430	TTCTCCGTACTGTCCATAGC
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57348	55435	TGTATTTCTCCGTACTGTCC
57349	55436	TTGTATTTCTCCGTACTGTC
57350	55437	CTTGTATTTCTCCGTACTGT
57351	55438	TCTTGTATTTCTCCGTACTG
57352	55439	TTCTTGTATTTCTCCGTACT
57353	55440	ATTCTTGTATTTCTCCGTAC
57354	55441	GATTCTTGTATTTCTCCGTA
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57358	55445	AATAGATTCTTGTATTTCTC
57359	55446	AAATAGATTCTTGTATTTCT
57360	55447	AAAATAGATTCTTGTATTTC
57361	55448	CAAAATAGATTCTTGTATTT
57362	55449	CCAAAATAGATTCTTGTATT
57363	55450	CCCAAAATAGATTCTTGTAT
57364	55451	ACCCAAAATAGATTCTTGTA
57365	55452	GACCCAAAATAGATTCTTGT
57366	55453	GGACCCAAAATAGATTCTTG
57367	55454	GGGACCCAAAATAGATTCTT
57368	55455	AGGGACCCAAAATAGATTCT
57369	55456	AAGGGACCCAAAATAGATTC
57370	55457	AAAGGGACCCAAAATAGATT
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57372	55459	CAAAAGGGACCCAAAATAGA
57373	55460	TCAAAAGGGACCCAAAATAG
57374	55461	CTCAAAAGGGACCCAAAATA
57375	55462	TCTCAAAAGGGACCCAAAAT
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106453	104540	GACGAACATACTGAAACCCC
106454	104541	TGACGAACATACTGAAACCC
106455	104542	CTGACGAACATACTGAAACC
106456	104543	CCTGACGAACATACTGAAAC
106457	104544	GCCTGACGAACATACTGAAA
106458	104545	AGCCTGACGAACATACTGAA
106459	104546	CAGCCTGACGAACATACTGA
106460	104547	ACAGCCTGACGAACATACTG
106461	104548	AACAGCCTGACGAACATACT
106462	104549	GAACAGCCTGACGAACATAC
106463	104550	AGAACAGCCTGACGAACATA
106464	104551	AAGAACAGCCTGACGAACAT
106465	104552	CAAGAACAGCCTGACGAACA
106466	104553	TCAAGAACAGCCTGACGAAC
106467	104554	TTCAAGAACAGCCTGACGAA
106468	104555	GTTCAAGAACAGCCTGACGA
106469	104556	AGTTCAAGAACAGCCTGACG
106470	104557	GAGTTCAAGAACAGCCTGAC
106471	104558	GGAGTTCAAGAACAGCCTGA
106472	104559	AGGAGTTCAAGAACAGCCTG
106473	104560	TAGGAGTTCAAGAACAGCCT
106474	104561	TTAGGAGTTCAAGAACAGCC
106475	104562	GTTAGGAGTTCAAGAACAGC
106476	104563	GGTTAGGAGTTCAAGAACAG
106477	104564	AGGTTAGGAGTTCAAGAACA
106478	104565	GAGGTTAGGAGTTCAAGAAC
106479	104566	TGAGGTTAGGAGTTCAAGAA
106480	104567	CTGAGGTTAGGAGTTCAAGA
106481	104568	CCTGAGGTTAGGAGTTCAAG
106482	104569	ACCTGAGGTTAGGAGTTCAA
106483	104570	CACCTGAGGTTAGGAGTTCA
106484	104571	TCACCTGAGGTTAGGAGTTC
106485	104572	ATCACCTGAGGTTAGGAGTT
106486	104573	AATCACCTGAGGTTAGGAGT
106487	104574	AAATCACCTGAGGTTAGGAG
106488	104575	CAAATCACCTGAGGTTAGGA
106489	104576	GCAAATCACCTGAGGTTAGG
106490	104577	GGCAAATCACCTGAGGTTAG
106491	104578	AGGCAAATCACCTGAGGTTA
106492	104579	CAGGCAAATCACCTGAGGTT
106493	104580	GCAGGCAAATCACCTGAGGT
106494	104581	GGCAGGCAAATCACCTGAGG
106495	104582	AGGCAGGCAAATCACCTGAG
106496	104583	AAGGCAGGCAAATCACCTGA
106497	104584	CAAGGCAGGCAAATCACCTG
106498	104585	CCAAGGCAGGCAAATCACCT
106499	104586	GCCAAGGCAGGCAAATCACC
106500	104587	GGCCAAGGCAGGCAAATCAC
106501	104588	AGGCCAAGGCAGGCAAATCA
106502	104589	GAGGCCAAGGCAGGCAAATC
106503	104590	GGAGGCCAAGGCAGGCAAAT
106504	104591	GGGAGGCCAAGGCAGGCAAA
106505	104592	TGGGAGGCCAAGGCAGGCAA
106506	104593	TTGGGAGGCCAAGGCAGGCA
106507	104594	TTTGGGAGGCCAAGGCAGGC
106508	104595	CTTTGGGAGGCCAAGGCAGG
106509	104596	ACTTTGGGAGGCCAAGGCAG
106510	104597	GACTTTGGGAGGCCAAGGCA
106511	104598	GGACTTTGGGAGGCCAAGGC
106512	104599	AGGACTTTGGGAGGCCAAGG
106513	104600	CAGGACTTTGGGAGGCCAAG
106514	104601	CCAGGACTTTGGGAGGCCAA
106515	104602	CCCAGGACTTTGGGAGGCCA
106516	104603	TCCCAGGACTTTGGGAGGCC
106517	104604	ATCCCAGGACTTTGGGAGGC
106518	104605	AATCCCAGGACTTTGGGAGG
106519	104606	TAATCCCAGGACTTTGGGAG
106520	104607	GTAATCCCAGGACTTTGGGA
106521	104608	TGTAATCCCAGGACTTTGGG
106522	104609	CTGTAATCCCAGGACTTTGG
106523	104610	CCTGTAATCCCAGGACTTTG

8230	6317	ACCCGCCTCAGCCTCCTAAA
8231	6318	CACCCGCCTCAGCCTCCTAA
8232	6319	CCACCCGCCTCAGCCTCCTA
8233	6320	TCCACCCGCCTCAGCCTCCT
8234	6321	ATCCACCCGCCTCAGCCTCC
8235	6322	GATCCACCCGCCTCAGCCTC
8236	6323	TGATCCACCCGCCTCAGCCT
8237	6324	GTGATCCACCCGCCTCAGCC
8238	6325	GGTGATCCACCCGCCTCAGC
8239	6326	AGGTGATCCACCCGCCTCAG
8240	6327	CAGGTGATCCACCCGCCTCA
8241	6328	CCAGGTGATCCACCCGCCTC
8242	6329	CCCAGGTGATCCACCCGCCT
8243	6330	CCCCAGGTGATCCACCCGCC
8244	6331	ACCCCAGGTGATCCACCCGC
8245	6332	GACCCCAGGTGATCCACCCG
8246	6333	TGACCCCAGGTGATCCACCC
8247	6334	CTGACCCCAGGTGATCCACC
8248	6335	CCTGACCCCAGGTGATCCAC
8249	6336	TCCTGACCCCAGGTGATCCA
8250	6337	CTCCTGACCCCAGGTGATCC
8251	6338	ACTCCTGACCCCAGGTGATC
8252	6339	AACTCCTGACCCCAGGTGAT
8253	6340	AAACTCCTGACCCCAGGTGA
8254	6341	CAAACTCCTGACCCCAGGTG
8255	6342	TCAAACTCCTGACCCCAGGT
SEQ ID	**Oligo**	**AON Sequence 5' to 3'**
1914	1	CGCTGGGTTGCTTTCTCGGG
1915	2	GCGCTGGGTTGCTTTCTCGG
1916	3	CGCGCTGGGTTGCTTTCTCG
1917	4	GCGCGCTGGGTTGCTTTCTC
1918	5	GGCGCGCTGGGTTGCTTTCT
1919	6	CGGCGCGCTGGGTTGCTTTC
1920	7	GCGGCGCGCTGGGTTGCTTT
1921	8	GGCGGCGCGCTGGGTTGCTT
1922	9	GGGCGGCGCGCTGGGTTGCT
1923	10	CGGGCGGCGCGCTGGGTTGC
1924	11	GCGGGCGGCGCGCTGGGTTG
1925	12	AGCGGGCGGCGCGCTGGGTT
1926	13	GAGCGGGCGGCGCGCTGGGT
1927	14	GGAGCGGGCGGCGCGCTGGG
1928	15	AGGAGCGGGCGGCGCGCTGG
1929	16	GAGGAGCGGGCGGCGCGCTG
1930	17	TGAGGAGCGGGCGGCGCGCT
1931	18	GTGAGGAGCGGGCGGCGCGC
1932	19	CGTGAGGAGCGGGCGGCGCG
1933	20	ACGTGAGGAGCGGGCGGCGC
1934	21	CACGTGAGGAGCGGGCGGCG
1935	22	ACACGTGAGGAGCGGGCGGC
1936	23	GACACGTGAGGAGCGGGCGG
1937	24	GGACACGTGAGGAGCGGGCG
1938	25	GGGACACGTGAGGAGCGGGC
1939	26	AGGGACACGTGAGGAGCGGG
1940	27	GAGGGACACGTGAGGAGCGG
1941	28	GGAGGGACACGTGAGGAGCG
1942	29	GGGAGGGACACGTGAGGAGC
1943	30	CGGGAGGGACACGTGAGGAG
1944	31	CCGGGAGGGACACGTGAGGA
1945	32	GCCGGGAGGGACACGTGAGG
1946	33	GGCCGGGAGGGACACGTGAG
1947	34	GGGCCGGGAGGGACACGTGA
1948	35	GGGGCCGGGAGGGACACGTG
1949	36	CGGGGCCGGGAGGGACACGT
1950	37	CCGGGGCCGGGAGGGACACG
1951	38	CCCGGGGCCGGGAGGGACAC
1952	39	CCCCGGGGCCGGGAGGGACA
1953	40	GCCCCGGGGCCGGGAGGGAC
1954	41	GGCCCCGGGGCCGGGAGGGA
1955	42	TGGCCCCGGGGCCGGGAGGG
1956	43	GTGGCCCCGGGGCCGGGAGG
1957	44	GGTGGCCCCGGGGCCGGGAG

57377	55464	GTTCTCAAAAGGGACCCAAA
57378	55465	GGTTCTCAAAAGGGACCCAA
57379	55466	AGGTTCTCAAAAGGGACCCA
57380	55467	TAGGTTCTCAAAAGGGACCC
57381	55468	CTAGGTTCTCAAAAGGGACC
57382	55469	ACTAGGTTCTCAAAAGGGAC
57383	55470	CACTAGGTTCTCAAAAGGGA
57384	55471	TCACTAGGTTCTCAAAAGGG
57385	55472	TTCACTAGGTTCTCAAAAGG
57386	55473	TTTCACTAGGTTCTCAAAAG
57387	55474	GTTTCACTAGGTTCTCAAAA
57388	55475	AGTTTCACTAGGTTCTCAAA
57389	55476	CAGTTTCACTAGGTTCTCAA
57390	55477	ACAGTTTCACTAGGTTCTCA
57391	55478	CACAGTTTCACTAGGTTCTC
57392	55479	ACACAGTTTCACTAGGTTCT
57393	55480	TACACAGTTTCACTAGGTTC
57394	55481	GTACACAGTTTCACTAGGTT
57395	55482	GGTACACAGTTTCACTAGGT
57396	55483	AGGTACACAGTTTCACTAGG
57397	55484	TAGGTACACAGTTTCACTAG
57398	55485	CTAGGTACACAGTTTCACTA
57399	55486	ACTAGGTACACAGTTTCACT
57400	55487	CACTAGGTACACAGTTTCAC
57401	55488	TCACTAGGTACACAGTTTCA
57402	55489	TTCACTAGGTACACAGTTTC
SEQ ID	**Oligo**	**AON Sequence 5' to 3'**
51061	49148	AATTCAACTAAAATTTTATC
51062	49149	AAATTCAACTAAAATTTTAT
51063	49150	TAAATTCAACTAAAATTTTA
51064	49151	TTAAATTCAACTAAAATTTT
51065	49152	ATTAAATTCAACTAAAATTT
51066	49153	TATTAAATTCAACTAAAATT
51067	49154	GTATTAAATTCAACTAAAAT
51068	49155	TGTATTAAATTCAACTAAAA
51069	49156	ATGTATTAAATTCAACTAAA
51070	49157	TATGTATTAAATTCAACTAA
51071	49158	CTATGTATTAAATTCAACTA
51072	49159	GCTATGTATTAAATTCAACT
51073	49160	TGCTATGTATTAAATTCAAC
51074	49161	GTGCTATGTATTAAATTCAA
51075	49162	AGTGCTATGTATTAAATTCA
51076	49163	GAGTGCTATGTATTAAATTC
51077	49164	AGAGTGCTATGTATTAAATT
51078	49165	CAGAGTGCTATGTATTAAAT
51079	49166	CCAGAGTGCTATGTATTAAA
51080	49167	TCCAGAGTGCTATGTATTAA
51081	49168	TTCCAGAGTGCTATGTATTA
51082	49169	TTTCCAGAGTGCTATGTATT
51083	49170	CTTTCCAGAGTGCTATGTAT
51084	49171	TCTTTCCAGAGTGCTATGTA
51085	49172	CTCTTTCCAGAGTGCTATGT
51086	49173	ACTCTTTCCAGAGTGCTATG
51087	49174	TACTCTTTCCAGAGTGCTAT
51088	49175	ATACTCTTTCCAGAGTGCTA
51089	49176	AATACTCTTTCCAGAGTGCT
51090	49177	CAATACTCTTTCCAGAGTGC
51091	49178	CCAATACTCTTTCCAGAGTG
51092	49179	GCCAATACTCTTTCCAGAGT
51093	49180	GGCCAATACTCTTTCCAGAG
51094	49181	TGGCCAATACTCTTTCCAGA
51095	49182	GTGGCCAATACTCTTTCCAG
51096	49183	TGTGGCCAATACTCTTTCCA
51097	49184	TTGTGGCCAATACTCTTTCC
51098	49185	GTTGTGGCCAATACTCTTTC
51099	49186	TGTTGTGGCCAATACTCTTT
51100	49187	TTGTTGTGGCCAATACTCTT
51101	49188	TTTGTTGTGGCCAATACTCT
51102	49189	TTTTGTTGTGGCCAATACTC
51103	49190	TTTTTGTTGTGGCCAATACT
51104	49191	TTTTTTGTTGTGGCCAATAC

106524	104611	GCCTGTAATCCCAGGACTTT
106525	104612	CGCCTGTAATCCCAGGACTT
106526	104613	ACGCCTGTAATCCCAGGACT
106527	104614	CACGCCTGTAATCCCAGGAC
106528	104615	TCACGCCTGTAATCCCAGGA
106529	104616	CTCACGCCTGTAATCCCAGG
106530	104617	GCTCACGCCTGTAATCCCAG
106531	104618	GGCTCACGCCTGTAATCCCA
106532	104619	TGGCTCACGCCTGTAATCCC
106533	104620	GTGGCTCACGCCTGTAATCC
106534	104621	GGTGGCTCACGCCTGTAATC
106535	104622	CGGTGGCTCACGCCTGTAAT
106536	104623	GCGGTGGCTCACGCCTGTAA
106537	104624	TGCGGTGGCTCACGCCTGTA
106538	104625	GTGCGGTGGCTCACGCCTGT
106539	104626	GGTGCGGTGGCTCACGCCTG
106540	104627	GGGTGCGGTGGCTCACGCCT
106541	104628	TGGGTGCGGTGGCTCACGCC
106542	104629	CTGGGTGCGGTGGCTCACGC
106543	104630	GCTGGGTGCGGTGGCTCACG
106544	104631	GGCTGGGTGCGGTGGCTCAC
106545	104632	AGGCTGGGTGCGGTGGCTCA
106546	104633	AAGGCTGGGTGCGGTGGCTC
106547	104634	AAAGGCTGGGTGCGGTGGCT
106548	104635	AAAAGGCTGGGTGCGGTGGC
106549	104636	AAAAAGGCTGGGTGCGGTGG
SEQ ID	**Oligo**	**AON Sequence 5' to 3'**
100208	98295	AAGCAACAAAAACAGAACCT
100209	98296	CAAGCAACAAAAACAGAACC
100210	98297	ACAAGCAACAAAAACAGAAC
100211	98298	TACAAGCAACAAAAACAGAA
100212	98299	GTACAAGCAACAAAAACAGA
100213	98300	AGTACAAGCAACAAAAACAG
100214	98301	AAGTACAAGCAACAAAAACA
100215	98302	CAAGTACAAGCAACAAAAAC
100216	98303	GCAAGTACAAGCAACAAAAA
100217	98304	AGCAAGTACAAGCAACAAAA
100218	98305	GAGCAAGTACAAGCAACAAA
100219	98306	GGAGCAAGTACAAGCAACAA
100220	98307	GGGAGCAAGTACAAGCAACA
100221	98308	GGGGAGCAAGTACAAGCAAC
100222	98309	GGGGGAGCAAGTACAAGCAA
100223	98310	AGGGGGAGCAAGTACAAGCA
100224	98311	AAGGGGGAGCAAGTACAAGC
100225	98312	AAAGGGGGAGCAAGTACAAG
100226	98313	AAAAGGGGGAGCAAGTACAA
100227	98314	AAAAAGGGGGAGCAAGTACA
100228	98315	AAAAAAGGGGGAGCAAGTAC
100229	98316	GAAAAAAGGGGGAGCAAGTA
100230	98317	TGAAAAAAGGGGGAGCAAGT
100231	98318	CTGAAAAAAGGGGGAGCAAG
100232	98319	GCTGAAAAAAGGGGGAGCAA
100233	98320	GGCTGAAAAAAGGGGGAGCA
100234	98321	TGGCTGAAAAAAGGGGGAGC
100235	98322	ATGGCTGAAAAAAGGGGGAG
100236	98323	AATGGCTGAAAAAAGGGGGA
100237	98324	GAATGGCTGAAAAAAGGGGG
100238	98325	GGAATGGCTGAAAAAAGGGG
100239	98326	AGGAATGGCTGAAAAAAGGG
100240	98327	CAGGAATGGCTGAAAAAAGG
100241	98328	ACAGGAATGGCTGAAAAAAG
100242	98329	AACAGGAATGGCTGAAAAAA
100243	98330	AAACAGGAATGGCTGAAAAA
100244	98331	AAAACAGGAATGGCTGAAAA
100245	98332	GAAAACAGGAATGGCTGAAA
100246	98333	AGAAAACAGGAATGGCTGAA
100247	98334	AAGAAAACAGGAATGGCTGA
100248	98335	AAAGAAAACAGGAATGGCTG
100249	98336	GAAAGAAAACAGGAATGGCT
100250	98337	AGAAAGAAAACAGGAATGGC
100251	98338	AAGAAAGAAAACAGGAATGG

8301	6388	TATTTTTAGTAGAGATGGGG
8302	6389	GTATTTTTAGTAGAGATGGG
8303	6390	TGTATTTTTAGTAGAGATGG
8304	6391	TTGTATTTTTAGTAGAGATG
8305	6392	TTTGTATTTTTAGTAGAGAT
8306	6393	TTTTGTATTTTTAGTAGAGA
8307	6394	TTTTTGTATTTTTAGTAGAG
8308	6395	ATTTTTGTATTTTTAGTAGA
8309	6396	AATTTTTGTATTTTTAGTAG
8310	6397	TAATTTTTGTATTTTTAGTA
8311	6398	CTAATTTTTGTATTTTTAGT
8312	6399	GCTAATTTTTGTATTTTTAG
8313	6400	GGCTAATTTTTGTATTTTTA
8314	6401	CGGCTAATTTTTGTATTTTT
8315	6402	CCGGCTAATTTTTGTATTTT
8316	6403	CCCGGCTAATTTTTGTATTT
8317	6404	GCCCGGCTAATTTTTGTATT
8318	6405	TGCCCGGCTAATTTTTGTAT
8319	6406	ATGCCCGGCTAATTTTTGTA
8320	6407	CATGCCCGGCTAATTTTTGT
8321	6408	CCATGCCCGGCTAATTTTTG
8322	6409	ACCATGCCCGGCTAATTTTT
8323	6410	CACCATGCCCGGCTAATTTT
8324	6411	CCACCATGCCCGGCTAATTT
8325	6412	ACCACCATGCCCGGCTAATT
8326	6413	CACCACCATGCCCGGCTAAT
8327	6414	CCACCACCATGCCCGGCTAA
8328	6415	CCCACCACCATGCCCGGCTA
8329	6416	GCCCACCACCATGCCCGGCT
8330	6417	CGCCCACCACCATGCCCGGC
8331	6418	GCGCCCACCACCATGCCCGG
8332	6419	GGCGCCCACCACCATGCCCG
8333	6420	AGGCGCCCACCACCATGCCC
8334	6421	CAGGCGCCCACCACCATGCC
8335	6422	ACAGGCGCCCACCACCATGC
8336	6423	TACAGGCGCCCACCACCATG
8337	6424	TTACAGGCGCCCACCACCAT
8338	6425	ATTACAGGCGCCCACCACCA
8339	6426	GATTACAGGCGCCCACCACC
8340	6427	GGATTACAGGCGCCCACCAC
8341	6428	GGGATTACAGGCGCCCACCA
8342	6429	TGGGATTACAGGCGCCCACC
8343	6430	CTGGGATTACAGGCGCCCAC
8344	6431	GCTGGGATTACAGGCGCCCA
8345	6432	AGCTGGGATTACAGGCGCCC
8346	6433	AAGCTGGGATTACAGGCGCC
8347	6434	GAAGCTGGGATTACAGGCGC
8348	6435	AGAAGCTGGGATTACAGGCG
8349	6436	AAGAAGCTGGGATTACAGGC
8350	6437	CAAGAAGCTGGGATTACAGG
8351	6438	CCAAGAAGCTGGGATTACAG
8352	6439	CCCAAGAAGCTGGGATTACA
8353	6440	TCCCAAGAAGCTGGGATTAC
8354	6441	CTCCCAAGAAGCTGGGATTA
8355	6442	CCTCCCAAGAAGCTGGGATT
8356	6443	GCCTCCCAAGAAGCTGGGAT
8357	6444	AGCCTCCCAAGAAGCTGGGA
8358	6445	CAGCCTCCCAAGAAGCTGGG
8359	6446	TCAGCCTCCCAAGAAGCTGG
8360	6447	CTCAGCCTCCCAAGAAGCTG
8361	6448	CCTCAGCCTCCCAAGAAGCT
8362	6449	CCCTCAGCCTCCCAAGAAGC
8363	6450	TCCCTCAGCCTCCCAAGAAG
8364	6451	TTCCCTCAGCCTCCCAAGAA
8365	6452	CTTCCCTCAGCCTCCCAAGA
8366	6453	TCTTCCCTCAGCCTCCCAAG
8367	6454	CTCTTCCCTCAGCCTCCCAA
8368	6455	TCTCTTCCCTCAGCCTCCCA
8369	6456	TTCTCTTCCCTCAGCCTCCC
8370	6457	ATTCTCTTCCCTCAGCCTCC
8371	6458	AATTCTCTTCCCTCAGCCTC

57448	55535	TAAAATCTACATGTGTGTAA
57449	55536	GTAAAATCTACATGTGTGTA
57450	55537	TGTAAAATCTACATGTGTGT
57451	55538	ATGTAAAATCTACATGTGTG
57452	55539	CATGTAAAATCTACATGTGT
57453	55540	ACATGTAAAATCTACATGTG
57454	55541	TACATGTAAAATCTACATGT
57455	55542	TTACATGTAAAATCTACATG
57456	55543	ATTACATGTAAAATCTACAT
57457	55544	AATTACATGTAAAATCTACA
57458	55545	GAATTACATGTAAAATCTAC
57459	55546	AGAATTACATGTAAAATCTA
57460	55547	AAGAATTACATGTAAAATCT
57461	55548	AAAGAATTACATGTAAAATC
57462	55549	AAAAGAATTACATGTAAAAT
57463	55550	TAAAAGAATTACATGTAAAA
57464	55551	TTAAAAGAATTACATGTAAA
57465	55552	TTTAAAAGAATTACATGTAA
57466	55553	TTTTAAAAGAATTACATGTA
57467	55554	TTTTTAAAAGAATTACATGT
57468	55555	ATTTTTAAAAGAATTACATG
57469	55556	AATTTTTAAAAGAATTACAT
57470	55557	TAATTTTTAAAAGAATTACA
57471	55558	TTAATTTTTAAAAGAATTAC
57472	55559	ATTAATTTTTAAAAGAATTA
57473	55560	AATTAATTTTTAAAAGAATT
57474	55561	AAATTAATTTTTAAAAGAAT
57475	55562	AAAATTAATTTTTAAAAGAA
57476	55563	AAAAATTAATTTTTAAAAGA
57477	55564	AAAAAATTAATTTTTAAAAG
57478	55565	AAAAAAATTAATTTTTAAAA
57479	55566	AAAAAAAATTAATTTTTAAA
57480	55567	GAAAAAAAATTAATTTTTAA
57481	55568	AGAAAAAAAATTAATTTTTA
57482	55569	AAGAAAAAAAATTAATTTTT
57483	55570	AAAGAAAAAAAATTAATTTT
57484	55571	AAAAGAAAAAAAATTAATTT
57485	55572	AAAAAGAAAAAAAATTAATT
57486	55573	AAAAAAGAAAAAAAATTAAT
57487	55574	AAAAAAAGAAAAAAAATTAA
57488	55575	AAAAAAAAGAAAAAAAATTA
57489	55576	TAAAAAAAAGAAAAAAAATT
57490	55577	TTAAAAAAAAGAAAAAAAAT
57491	55578	TTTAAAAAAAAGAAAAAAAA
57492	55579	CTTTAAAAAAAAGAAAAAAA
57493	55580	TCTTTAAAAAAAAGAAAAAA
57494	55581	TTCTTTAAAAAAAAGAAAAA
57495	55582	TTTCTTTAAAAAAAAGAAAA
57496	55583	GTTTCTTTAAAAAAAAGAAA
57497	55584	TGTTTCTTTAAAAAAAAGAA
57498	55585	CTGTTTCTTTAAAAAAAAGA
57499	55586	CCTGTTTCTTTAAAAAAAAG
57500	55587	CCCTGTTTCTTTAAAAAAAA
57501	55588	ACCCTGTTTCTTTAAAAAAA
57502	55589	GACCCTGTTTCTTTAAAAAA
57503	55590	TGACCCTGTTTCTTTAAAAA
57504	55591	ATGACCCTGTTTCTTTAAAA
57505	55592	CATGACCCTGTTTCTTTAAA
57506	55593	GCATGACCCTGTTTCTTTAA
57507	55594	AGCATGACCCTGTTTCTTTA
57508	55595	GAGCATGACCCTGTTTCTTT
57509	55596	AGAGCATGACCCTGTTTCTT
57510	55597	CAGAGCATGACCCTGTTTCT
57511	55598	ACAGAGCATGACCCTGTTTC
57512	55599	GACAGAGCATGACCCTGTTT
57513	55600	TGACAGAGCATGACCCTGTT
57514	55601	GTGACAGAGCATGACCCTGT
57515	55602	AGTGACAGAGCATGACCCTG
57516	55603	GAGTGACAGAGCATGACCCT
57517	55604	TGAGTGACAGAGCATGACCC
57518	55605	CTGAGTGACAGAGCATGACC

106595	104682	CTAAACTCTCCAATCAAAAG
106596	104683	ACTAAACTCTCCAATCAAAA
106597	104684	GACTAAACTCTCCAATCAAA
106598	104685	CGACTAAACTCTCCAATCAA
106599	104686	TCGACTAAACTCTCCAATCA
106600	104687	ATCGACTAAACTCTCCAATC
106601	104688	AATCGACTAAACTCTCCAAT
106602	104689	AAATCGACTAAACTCTCCAA
106603	104690	TAAATCGACTAAACTCTCCA
106604	104691	GTAAATCGACTAAACTCTCC
106605	104692	TGTAAATCGACTAAACTCTC
106606	104693	ATGTAAATCGACTAAACTCT
106607	104694	AATGTAAATCGACTAAACTC
106608	104695	GAATGTAAATCGACTAAACT
106609	104696	TGAATGTAAATCGACTAAAC
106610	104697	CTGAATGTAAATCGACTAAA
106611	104698	ACTGAATGTAAATCGACTAA
106612	104699	CACTGAATGTAAATCGACTA
106613	104700	ACACTGAATGTAAATCGACT
106614	104701	AACACTGAATGTAAATCGAC
106615	104702	CAACACTGAATGTAAATCGA
106616	104703	ACAACACTGAATGTAAATCG
106617	104704	AACAACACTGAATGTAAATC
106618	104705	TAACAACACTGAATGTAAAT
106619	104706	GTAACAACACTGAATGTAAA
106620	104707	AGTAACAACACTGAATGTAA
106621	104708	CAGTAACAACACTGAATGTA
106622	104709	TCAGTAACAACACTGAATGT
106623	104710	ATCAGTAACAACACTGAATG
106624	104711	AATCAGTAACAACACTGAAT
106625	104712	TAATCAGTAACAACACTGAA
106626	104713	CTAATCAGTAACAACACTGA
106627	104714	ACTAATCAGTAACAACACTG
106628	104715	CACTAATCAGTAACAACACT
106629	104716	TCACTAATCAGTAACAACAC
106630	104717	CTCACTAATCAGTAACAACA
106631	104718	CCTCACTAATCAGTAACAAC
106632	104719	TCCTCACTAATCAGTAACAA
106633	104720	GTCCTCACTAATCAGTAACA
106634	104721	AGTCCTCACTAATCAGTAAC
106635	104722	AAGTCCTCACTAATCAGTAA
106636	104723	TAAGTCCTCACTAATCAGTA
106637	104724	TTAAGTCCTCACTAATCAGT
106638	104725	GTTAAGTCCTCACTAATCAG
106639	104726	AGTTAAGTCCTCACTAATCA
106640	104727	TAGTTAAGTCCTCACTAATC
106641	104728	GTAGTTAAGTCCTCACTAAT
106642	104729	AGTAGTTAAGTCCTCACTAA
106643	104730	TAGTAGTTAAGTCCTCACTA
106644	104731	GTAGTAGTTAAGTCCTCACT
106645	104732	GGTAGTAGTTAAGTCCTCAC
106646	104733	TGGTAGTAGTTAAGTCCTCA
106647	104734	ATGGTAGTAGTTAAGTCCTC
106648	104735	AATGGTAGTAGTTAAGTCCT
106649	104736	AAATGGTAGTAGTTAAGTCC
106650	104737	AAAATGGTAGTAGTTAAGTC
106651	104738	CAAAATGGTAGTAGTTAAGT
106652	104739	ACAAAATGGTAGTAGTTAAG
106653	104740	AACAAAATGGTAGTAGTTAA
106654	104741	TAACAAAATGGTAGTAGTTA
106655	104742	GTAACAAAATGGTAGTAGTT
106656	104743	AGTAACAAAATGGTAGTAGT
106657	104744	AAGTAACAAAATGGTAGTAG
106658	104745	TAAGTAACAAAATGGTAGTA
106659	104746	ATAAGTAACAAAATGGTAGT
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106661	104748	TAATAAGTAACAAAATGGTA
106662	104749	ATAATAAGTAACAAAATGGT
106663	104750	GATAATAAGTAACAAAATGG
106664	104751	AGATAATAAGTAACAAAATG
106665	104752	CAGATAATAAGTAACAAAAT

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8373	6460	GCAATTCTCTTCCCTCAGCC
8374	6461	AGCAATTCTCTTCCCTCAGC
8375	6462	AAGCAATTCTCTTCCCTCAG
8376	6463	CAAGCAATTCTCTTCCCTCA
8377	6464	TCAAGCAATTCTCTTCCCTC
8378	6465	ATCAAGCAATTCTCTTCCCT
8379	6466	GATCAAGCAATTCTCTTCCC
8380	6467	GGATCAAGCAATTCTCTTCC
8381	6468	GGGATCAAGCAATTCTCTTC
8382	6469	CGGGATCAAGCAATTCTCTT
8383	6470	CCGGGATCAAGCAATTCTCT
8384	6471	TCCGGGATCAAGCAATTCTC
8385	6472	CTCCGGGATCAAGCAATTCT
8386	6473	CCTCCGGGATCAAGCAATTC
8387	6474	ACCTCCGGGATCAAGCAATT
8388	6475	AACCTCCGGGATCAAGCAAT
8389	6476	CAACCTCCGGGATCAAGCAA
8390	6477	GCAACCTCCGGGATCAAGCA
8391	6478	TGCAACCTCCGGGATCAAGC
8392	6479	TTGCAACCTCCGGGATCAAG
8393	6480	ATTGCAACCTCCGGGATCAA
8394	6481	CATTGCAACCTCCGGGATCA
8395	6482	TCATTGCAACCTCCGGGATC
8396	6483	CTCATTGCAACCTCCGGGAT
8397	6484	ACTCATTGCAACCTCCGGGA
8398	6485	CACTCATTGCAACCTCCGGG
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8403	6490	CTCCGCACTCATTGCAACCT
8404	6491	CCTCCGCACTCATTGCAACC
8405	6492	ACCTCCGCACTCATTGCAAC
8406	6493	AACCTCCGCACTCATTGCAA
8407	6494	CAACCTCCGCACTCATTGCA
8408	6495	GCAACCTCCGCACTCATTGC
8409	6496	TGCAACCTCCGCACTCATTG
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8411	6498	ACTGCAACCTCCGCACTCAT
8412	6499	CACTGCAACCTCCGCACTCA
8413	6500	TCACTGCAACCTCCGCACTC
8414	6501	CTCACTGCAACCTCCGCACT
8415	6502	GCTCACTGCAACCTCCGCAC
8416	6503	AGCTCACTGCAACCTCCGCA
8417	6504	CAGCTCACTGCAACCTCCGC
8418	6505	TCAGCTCACTGCAACCTCCG
8419	6506	CTCAGCTCACTGCAACCTCC
8420	6507	TCTCAGCTCACTGCAACCTC
8421	6508	ATCTCAGCTCACTGCAACCT
8422	6509	GATCTCAGCTCACTGCAACC
8423	6510	TGATCTCAGCTCACTGCAAC
8424	6511	ATGATCTCAGCTCACTGCAA
8425	6512	CATGATCTCAGCTCACTGCA
8426	6513	GCATGATCTCAGCTCACTGC
8427	6514	GGCATGATCTCAGCTCACTG
8428	6515	TGGCATGATCTCAGCTCACT
8429	6516	ATGGCATGATCTCAGCTCAC
8430	6517	AATGGCATGATCTCAGCTCA
8431	6518	TAATGGCATGATCTCAGCTC
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8439	6526	CTGGAGTGTAATGGCATGAT
8440	6527	GCTGGAGTGTAATGGCATGA
8441	6528	GGCTGGAGTGTAATGGCATG
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57522	55609	CAGCCTGAGTGACAGAGCAT
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57526	55613	ATTCCAGCCTGAGTGACAGA
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57534	55621	ACCACTGCATTCCAGCCTGA
57535	55622	CACCACTGCATTCCAGCCTG
57536	55623	ACACCACTGCATTCCAGCCT
57537	55624	CACACCACTGCATTCCAGCC
57538	55625	TCACACCACTGCATTCCAGC
57539	55626	ATCACACCACTGCATTCCAG
57540	55627	GATCACACCACTGCATTCCA
57541	55628	TGATCACACCACTGCATTCC
57542	55629	ATGATCACACCACTGCATTC
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57546	55633	AGCCATGATCACACCACTGC
57547	55634	AAGCCATGATCACACCACTG
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57550	55637	AGTAAGCCATGATCACACCA
57551	55638	CAGTAAGCCATGATCACACC
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57561	55648	GTCGAGGCTACAGTAAGCCA
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57565	55652	GGAGGTCGAGGCTACAGTAA
57566	55653	AGGAGGTCGAGGCTACAGTA
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57569	55656	GCCAGGAGGTCGAGGCTACA
57570	55657	AGCCAGGAGGTCGAGGCTAC
57571	55658	GAGCCAGGAGGTCGAGGCTA
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57575	55662	GCTTGAGCCAGGAGGTCGAG
57576	55663	CGCTTGAGCCAGGAGGTCGA
57577	55664	TCGCTTGAGCCAGGAGGTCG
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57581	55668	AGAGTCGCTTGAGCCAGGAG
57582	55669	GAGAGTCGCTTGAGCCAGGA
57583	55670	GGAGAGTCGCTTGAGCCAGG
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57587	55674	GGTGGGAGAGTCGCTTGAGC
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106667	104754	ACCAGATAATAAGTAACAAA
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106669	104756	CAACCAGATAATAAGTAACA
106670	104757	ACAACCAGATAATAAGTAAC
106671	104758	AACAACCAGATAATAAGTAA
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106673	104760	AAAACAACCAGATAATAAGT
106674	104761	CAAAACAACCAGATAATAAG
106675	104762	ACAAAACAACCAGATAATAA
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106682	104769	TAGGACTACAAAACAACCAG
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106686	104773	GGAGTAGGACTACAAAACAA
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106688	104775	AGGGAGTAGGACTACAAAAC
106689	104776	GAGGGAGTAGGACTACAAAA
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106692	104779	AGGGAGGGAGTAGGACTACA
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106701	104788	GAAGGGGGAAGGGAGGGAGT
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8443	6530	CAGGCTGGAGTGTAATGGCA
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8445	6532	CCCAGGCTGGAGTGTAATGG
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57598	55685	TGGGAGGCTGAGGTGGGAGA
57599	55686	TTGGGAGGCTGAGGTGGGAG
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57618	55705	CACCTGTAGCCCCAGCTACT
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106741	104828	AGGGAGGGAGGGAAAAAAGG
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106743	104830	GAAGGGAGGGAGGGAAAAAA
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106747	104834	CAAGGAAGGGAGGGAGGGAA
106748	104835	ACAAGGAAGGGAGGGAGGGA
106749	104836	AACAAGGAAGGGAGGGAGGG
106750	104837	AAACAAGGAAGGGAGGGAGG
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106755	104842	TTTCAAAACAAGGAAGGGAG
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106759	104846	TCACTTTCAAAACAAGGAAG
106760	104847	ATCACTTTCAAAACAAGGAA
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106771	104858	CACCAGAGAAAATCACTTTC
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106775	104862	ATACCACCAGAGAAAATCAC
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106778	104865	AACATACCACCAGAGAAAAT
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106782	104869	TTAAAACATACCACCAGAGA
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8516	6603	TTAGGACAAAAAAATGAGAT
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8537	6624	TTCTAACACGGCTGTAGCTA
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8539	6626	AGTTCTAACACGGCTGTAGC
8540	6627	CAGTTCTAACACGGCTGTAG
8541	6628	ACAGTTCTAACACGGCTGTA
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8543	6630	TGACAGTTCTAACACGGCTG
8544	6631	GTGACAGTTCTAACACGGCT
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8581	6668	AATTCGTTTCAAAGTAAAAA
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8583	6670	AAAATTCGTTTCAAAGTAAA
8584	6671	TAAAATTCGTTTCAAAGTAA

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57809	55896	CCCTGAAGAAACTGTGAACA
57810	55897	TCCCTGAAGAAACTGTGAAC
57811	55898	CTCCCTGAAGAAACTGTGAA
57812	55899	ACTCCCTGAAGAAACTGTGA
57813	55900	AACTCCCTGAAGAAACTGTG
57814	55901	GAACTCCCTGAAGAAACTGT
57815	55902	TGAACTCCCTGAAGAAACTG
57816	55903	ATGAACTCCCTGAAGAAACT
57817	55904	TATGAACTCCCTGAAGAAAC
57818	55905	ATATGAACTCCCTGAAGAAA
57819	55906	TATATGAACTCCCTGAAGAA
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57821	55908	CGTATATGAACTCCCTGAAG
57822	55909	GCGTATATGAACTCCCTGAA
57823	55910	GGCGTATATGAACTCCCTGA
57824	55911	TGGCGTATATGAACTCCCTG
57825	55912	ATGGCGTATATGAACTCCCT
57826	55913	CATGGCGTATATGAACTCCC
57827	55914	ACATGGCGTATATGAACTCC
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57829	55916	GTACATGGCGTATATGAACT
57830	55917	AGTACATGGCGTATATGAAC
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57835	55922	AATAGAGTACATGGCGTATA
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57838	55925	TAGAATAGAGTACATGGCGT
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57844	55931	AATGCTTAGAATAGAGTACA
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57846	55933	AAAATGCTTAGAATAGAGTA
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57851	55938	CTCTAAAAATGCTTAGAATA
57852	55939	ACTCTAAAAATGCTTAGAAT
57853	55940	AACTCTAAAAATGCTTAGAA
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57870	55957	CGTGCTTTGCTATCTCTAAC
57871	55958	ACGTGCTTTGCTATCTCTAA
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106951	105038	GGTTTCACCATGTTAGCCAG
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106955	105042	ATGGGGTTTCACCATGTTAG
106956	105043	GATGGGGTTTCACCATGTTA
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106958	105045	GAGATGGGGTTTCACCATGT
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106960	105047	TAGAGATGGGGTTTCACCAT
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106965	105052	TTTAGTAGAGATGGGGTTTC
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106968	105055	ATTTTTAGTAGAGATGGGGT
106969	105056	TATTTTTAGTAGAGATGGGG
106970	105057	GTATTTTTAGTAGAGATGGG
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106972	105059	TTGTATTTTTAGTAGAGATG
106973	105060	TTTGTATTTTTAGTAGAGAT
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106986	105073	CGCCTGGCTAAGTTTTGTAT
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106988	105075	CACGCCTGGCTAAGTTTTGT
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107001	105088	AGGCACGTGCCTCCACGCCT
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107016	105103	AGTATCTGAGATTACAGGCA
107017	105104	GAGTATCTGAGATTACAGGC
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8736	6823	GTTTACATCTCCGTTGAAGT
8737	6824	TGTTTACATCTCCGTTGAAG
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8740	6827	AACTGTTTACATCTCCGTTG
8741	6828	AAACTGTTTACATCTCCGTT
8742	6829	TAAACTGTTTACATCTCCGT
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57927	56014	TCCATTTGATATTCAATGTC
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107047	105134	GTTCAAGCAATTCTCCTGCC
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107071	105158	CTCACTGCAACCTCTGCCTC
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57947	56034	CAATTATTTGCATCGCTGAC
57948	56035	ACAATTATTTGCATCGCTGA
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57984	56071	CCAGCACACCAGGCTAATTT
57985	56072	ACCAGCACACCAGGCTAATT
57986	56073	CACCAGCACACCAGGCTAAT
57987	56074	ACACCAGCACACCAGGCTAA
57988	56075	CACACCAGCACACCAGGCTA
57989	56076	GCACACCAGCACACCAGGCT
57990	56077	CGCACACCAGCACACCAGGC
57991	56078	GCGCACACCAGCACACCAGG
57992	56079	GGCGCACACCAGCACACCAG
57993	56080	AGGCGCACACCAGCACACCA
57994	56081	GAGGCGCACACCAGCACACC
57995	56082	AGAGGCGCACACCAGCACAC
57996	56083	TAGAGGCGCACACCAGCACA
57997	56084	TTAGAGGCGCACACCAGCAC
57998	56085	ATTAGAGGCGCACACCAGCA
57999	56086	GATTAGAGGCGCACACCAGC
58000	56087	GGATTAGAGGCGCACACCAG
58001	56088	GGGATTAGAGGCGCACACCA
58002	56089	TGGGATTAGAGGCGCACACC
58003	56090	CTGGGATTAGAGGCGCACAC
58004	56091	GCTGGGATTAGAGGCGCACA
58005	56092	AGCTGGGATTAGAGGCGCAC
58006	56093	TAGCTGGGATTAGAGGCGCA
58007	56094	GTAGCTGGGATTAGAGGCGC
58008	56095	AGTAGCTGGGATTAGAGGCG
58009	56096	GAGTAGCTGGGATTAGAGGC
58010	56097	CGAGTAGCTGGGATTAGAGG
58011	56098	CCGAGTAGCTGGGATTAGAG
58012	56099	CCCGAGTAGCTGGGATTAGA
58013	56100	TCCCGAGTAGCTGGGATTAG
58014	56101	CTCCCGAGTAGCTGGGATTA
58015	56102	CCTCCCGAGTAGCTGGGATT

107092	105179	GGTGCAGTGGCACAATATTG
107093	105180	GGGTGCAGTGGCACAATATT
107094	105181	GGGGTGCAGTGGCACAATAT
107095	105182	TGGGGTGCAGTGGCACAATA
107096	105183	CTGGGGTGCAGTGGCACAAT
107097	105184	GCTGGGGTGCAGTGGCACAA
107098	105185	GGCTGGGGTGCAGTGGCACA
107099	105186	AGGCTGGGGTGCAGTGGCAC
107100	105187	CAGGCTGGGGTGCAGTGGCA
107101	105188	CCAGGCTGGGGTGCAGTGGC
107102	105189	CCCAGGCTGGGGTGCAGTGG
107103	105190	GCCCAGGCTGGGGTGCAGTG
107104	105191	CGCCCAGGCTGGGGTGCAGT
107105	105192	TCGCCCAGGCTGGGGTGCAG
107106	105193	GTCGCCCAGGCTGGGGTGCA
107107	105194	TGTCGCCCAGGCTGGGGTGC
107108	105195	CTGTCGCCCAGGCTGGGGTG
107109	105196	TCTGTCGCCCAGGCTGGGGT
107110	105197	CTCTGTCGCCCAGGCTGGGG
107111	105198	ACTCTGTCGCCCAGGCTGGG
107112	105199	CACTCTGTCGCCCAGGCTGG
107113	105200	TCACTCTGTCGCCCAGGCTG
107114	105201	CTCACTCTGTCGCCCAGGCT
107115	105202	TCTCACTCTGTCGCCCAGGC
107116	105203	GTCTCACTCTGTCGCCCAGG
107117	105204	AGTCTCACTCTGTCGCCCAG
107118	105205	GAGTCTCACTCTGTCGCCCA
107119	105206	GGAGTCTCACTCTGTCGCCC
107120	105207	CGGAGTCTCACTCTGTCGCC
107121	105208	ACGGAGTCTCACTCTGTCGC
107122	105209	GACGGAGTCTCACTCTGTCG
107123	105210	AGACGGAGTCTCACTCTGTC
107124	105211	GAGACGGAGTCTCACTCTGT
107125	105212	TGAGACGGAGTCTCACTCTG
107126	105213	TTGAGACGGAGTCTCACTCT
107127	105214	TTTGAGACGGAGTCTCACTC
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107132	105219	TTTTTTTTGAGACGGAGTCT
107133	105220	TTTTTTTTTGAGACGGAGTC
107134	105221	TTTTTTTTTTGAGACGGAGT
107135	105222	TTTTTTTTTTTGAGACGGAG
107136	105223	TTTTTTTTTTTTGAGACGGA
107137	105224	TTTTTTTTTTTTTGAGACGG
107138	105225	TTTTTTTTTTTTTTGAGACG
107139	105226	TTTTTTTTTTTTTTTGAGAC
107140	105227	TTTTTTTTTTTTTTTTGAGA
107141	105228	TTTTTTTTTTTTTTTTTGAG
107142	105229	TTTTTTTTTTTTTTTTTTGA
107143	105230	CTTTTTTTTTTTTTTTTTTG
107144	105231	TCTTTTTTTTTTTTTTTTTT
107145	105232	CTCTTTTTTTTTTTTTTTTT
107146	105233	TCTCTTTTTTTTTTTTTTTT
107147	105234	ATCTCTTTTTTTTTTTTTTT
107148	105235	GATCTCTTTTTTTTTTTTTT
107149	105236	TGATCTCTTTTTTTTTTTTT
107150	105237	GTGATCTCTTTTTTTTTTTT
107151	105238	TGTGATCTCTTTTTTTTTTT
107152	105239	ATGTGATCTCTTTTTTTTTT
107153	105240	TATGTGATCTCTTTTTTTTT
107154	105241	TTATGTGATCTCTTTTTTTT
107155	105242	CTTATGTGATCTCTTTTTTT
107156	105243	CCTTATGTGATCTCTTTTTT
107157	105244	CCCTTATGTGATCTCTTTTT
107158	105245	ACCCTTATGTGATCTCTTTT
107159	105246	AACCCTTATGTGATCTCTTT
107160	105247	CAACCCTTATGTGATCTCTT
107161	105248	GCAACCCTTATGTGATCTCT
107162	105249	TGCAACCCTTATGTGATCTC

8869	6956	CTTGAACCCGGGAGGCAAAG
8870	6957	ACTTGAACCCGGGAGGCAAA
8871	6958	CACTTGAACCCGGGAGGCAA
8872	6959	TCACTTGAACCCGGGAGGCA
8873	6960	ATCACTTGAACCCGGGAGGC
8874	6961	AATCACTTGAACCCGGGAGG
8875	6962	GAATCACTTGAACCCGGGAG
8876	6963	AGAATCACTTGAACCCGGGA
8877	6964	GAGAATCACTTGAACCCGGG
8878	6965	GGAGAATCACTTGAACCCGG
8879	6966	AGGAGAATCACTTGAACCCG
8880	6967	CAGGAGAATCACTTGAACCC
8881	6968	GCAGGAGAATCACTTGAACC
8882	6969	GGCAGGAGAATCACTTGAAC
8883	6970	AGGCAGGAGAATCACTTGAA
8884	6971	GAGGCAGGAGAATCACTTGA
8885	6972	TGAGGCAGGAGAATCACTTG
8886	6973	CTGAGGCAGGAGAATCACTT
8887	6974	GCTGAGGCAGGAGAATCACT
8888	6975	GGCTGAGGCAGGAGAATCAC
8889	6976	AGGCTGAGGCAGGAGAATCA
8890	6977	GAGGCTGAGGCAGGAGAATC
8891	6978	GGAGGCTGAGGCAGGAGAAT
8892	6979	AGGAGGCTGAGGCAGGAGAA
8893	6980	CAGGAGGCTGAGGCAGGAGA
8894	6981	TCAGGAGGCTGAGGCAGGAG
8895	6982	CTCAGGAGGCTGAGGCAGGA
8896	6983	ACTCAGGAGGCTGAGGCAGG
8897	6984	TACTCAGGAGGCTGAGGCAG
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8901	6988	CAGCTACTCAGGAGGCTGAG
8902	6989	CCAGCTACTCAGGAGGCTGA
8903	6990	CCCAGCTACTCAGGAGGCTG
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8905	6992	GACCCAGCTACTCAGGAGGC
8906	6993	AGACCCAGCTACTCAGGAGG
8907	6994	TAGACCCAGCTACTCAGGAG
8908	6995	GTAGACCCAGCTACTCAGGA
8909	6996	TGTAGACCCAGCTACTCAGG
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8913	7000	CGCATGTAGACCCAGCTACT
8914	7001	GCGCATGTAGACCCAGCTAC
8915	7002	TGCGCATGTAGACCCAGCTA
8916	7003	GTGCGCATGTAGACCCAGCT
8917	7004	TGTGCGCATGTAGACCCAGC
8918	7005	GTGTGCGCATGTAGACCCAG
8919	7006	GGTGTGCGCATGTAGACCCA
8920	7007	TGGTGTGCGCATGTAGACCC
8921	7008	GTGGTGTGCGCATGTAGACC
8922	7009	GGTGGTGTGCGCATGTAGAC
8923	7010	TGGTGGTGTGCGCATGTAGA
8924	7011	GTGGTGGTGTGCGCATGTAG
8925	7012	CGTGGTGGTGTGCGCATGTA
8926	7013	GCGTGGTGGTGTGCGCATGT
8927	7014	GGCGTGGTGGTGTGCGCATG
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8936	7023	AATTAGCCAGGCGTGGTGGT
8937	7024	AAATTAGCCAGGCGTGGTGG
8938	7025	AAAATTAGCCAGGCGTGGTG
8939	7026	AAAAATTAGCCAGGCGTGGT

58016	56103	GCCTCCCGAGTAGCTGGGAT
58017	56104	AGCCTCCCGAGTAGCTGGGA
58018	56105	CAGCCTCCCGAGTAGCTGGG
58019	56106	TCAGCCTCCCGAGTAGCTGG
58020	56107	CTCAGCCTCCCGAGTAGCTG
58021	56108	TCTCAGCCTCCCGAGTAGCT
58022	56109	GTCTCAGCCTCCCGAGTAGC
58023	56110	TGTCTCAGCCTCCCGAGTAG
58024	56111	CTGTCTCAGCCTCCCGAGTA
58025	56112	CCTGTCTCAGCCTCCCGAGT
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58027	56114	CTCCTGTCTCAGCCTCCCGA
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58032	56119	TGATTCTCCTGTCTCAGCCT
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58036	56123	CAAATGATTCTCCTGTCTCA
58037	56124	TCAAATGATTCTCCTGTCTC
58038	56125	TTCAAATGATTCTCCTGTCT
58039	56126	GTTCAAATGATTCTCCTGTC
58040	56127	GGTTCAAATGATTCTCCTGT
58041	56128	GGGTTCAAATGATTCTCCTG
58042	56129	TGGGTTCAAATGATTCTCCT
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58051	56138	TCCACCTTCTGGGTTCAAAT
58052	56139	CTCCACCTTCTGGGTTCAAA
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58054	56141	ACCTCCACCTTCTGGGTTCA
58055	56142	AACCTCCACCTTCTGGGTTC
58056	56143	CAACCTCCACCTTCTGGGTT
58057	56144	GCAACCTCCACCTTCTGGGT
58058	56145	TGCAACCTCCACCTTCTGGG
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58060	56147	ATTGCAACCTCCACCTTCTG
58061	56148	CATTGCAACCTCCACCTTCT
58062	56149	TCATTGCAACCTCCACCTTC
58063	56150	CTCATTGCAACCTCCACCTT
58064	56151	GCTCATTGCAACCTCCACCT
58065	56152	AGCTCATTGCAACCTCCACC
58066	56153	CAGCTCATTGCAACCTCCAC
58067	56154	TCAGCTCATTGCAACCTCCA
58068	56155	CTCAGCTCATTGCAACCTCC
58069	56156	TCTCAGCTCATTGCAACCTC
58070	56157	ATCTCAGCTCATTGCAACCT
58071	56158	GATCTCAGCTCATTGCAACC
58072	56159	CGATCTCAGCTCATTGCAAC
58073	56160	ACGATCTCAGCTCATTGCAA
58074	56161	TACGATCTCAGCTCATTGCA
58075	56162	GTACGATCTCAGCTCATTGC
58076	56163	GGTACGATCTCAGCTCATTG
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58078	56165	GTGGTACGATCTCAGCTCAT
58079	56166	AGTGGTACGATCTCAGCTCA
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58081	56168	GCAGTGGTACGATCTCAGCT
58082	56169	TGCAGTGGTACGATCTCAGC
58083	56170	GTGCAGTGGTACGATCTCAG
58084	56171	AGTGCAGTGGTACGATCTCA
58085	56172	GAGTGCAGTGGTACGATCTC
58086	56173	GGAGTGCAGTGGTACGATCT

107163	105250	TTGCAACCCTTATGTGATCT
107164	105251	TTTGCAACCCTTATGTGATC
107165	105252	ATTTGCAACCCTTATGTGAT
107166	105253	TATTTGCAACCCTTATGTGA
107167	105254	TTATTTGCAACCCTTATGTG
107168	105255	GTTATTTGCAACCCTTATGT
107169	105256	TGTTATTTGCAACCCTTATG
107170	105257	ATGTTATTTGCAACCCTTAT
107171	105258	AATGTTATTTGCAACCCTTA
107172	105259	AAATGTTATTTGCAACCCTT
107173	105260	AAAATGTTATTTGCAACCCT
107174	105261	TAAAATGTTATTTGCAACCC
107175	105262	ATAAAATGTTATTTGCAACC
107176	105263	TATAAAATGTTATTTGCAAC
107177	105264	TTATAAAATGTTATTTGCAA
107178	105265	GTTATAAAATGTTATTTGCA
107179	105266	GGTTATAAAATGTTATTTGC
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107181	105268	TGGGTTATAAAATGTTATTT
107182	105269	ATGGGTTATAAAATGTTATT
107183	105270	AATGGGTTATAAAATGTTAT
107184	105271	TAATGGGTTATAAAATGTTA
107185	105272	ATAATGGGTTATAAAATGTT
107186	105273	AATAATGGGTTATAAAATGT
107187	105274	AAATAATGGGTTATAAAATG
107188	105275	AAAATAATGGGTTATAAAAT
107189	105276	TAAAATAATGGGTTATAAAA
107190	105277	TTAAAATAATGGGTTATAAA
107191	105278	TTTAAAATAATGGGTTATAA
107192	105279	GTTTAAAATAATGGGTTATA
107193	105280	GGTTTAAAATAATGGGTTAT
107194	105281	TGGTTTAAAATAATGGGTTA
107195	105282	TTGGTTTAAAATAATGGGTT
107196	105283	ATTGGTTTAAAATAATGGGT
107197	105284	CATTGGTTTAAAATAATGGG
107198	105285	TCATTGGTTTAAAATAATGG
107199	105286	GTCATTGGTTTAAAATAATG
107200	105287	TGTCATTGGTTTAAAATAAT
107201	105288	TTGTCATTGGTTTAAAATAA
107202	105289	GTTGTCATTGGTTTAAAATA
107203	105290	AGTTGTCATTGGTTTAAAAT
107204	105291	AAGTTGTCATTGGTTTAAAA
107205	105292	CAAGTTGTCATTGGTTTAAA
107206	105293	TCAAGTTGTCATTGGTTTAA
107207	105294	TTCAAGTTGTCATTGGTTTA
107208	105295	TTTCAAGTTGTCATTGGTTT
107209	105296	GTTTCAAGTTGTCATTGGTT
107210	105297	AGTTTCAAGTTGTCATTGGT
107211	105298	AAGTTTCAAGTTGTCATTGG
107212	105299	AAAGTTTCAAGTTGTCATTG
107213	105300	CAAAGTTTCAAGTTGTCATT
107214	105301	TCAAAGTTTCAAGTTGTCAT
107215	105302	ATCAAAGTTTCAAGTTGTCA
107216	105303	AATCAAAGTTTCAAGTTGTC
107217	105304	CAATCAAAGTTTCAAGTTGT
107218	105305	GCAATCAAAGTTTCAAGTTG
107219	105306	TGCAATCAAAGTTTCAAGTT
107220	105307	TTGCAATCAAAGTTTCAAGT
107221	105308	TTTGCAATCAAAGTTTCAAG
107222	105309	TTTTGCAATCAAAGTTTCAA
107223	105310	TTTTTGCAATCAAAGTTTCA
107224	105311	GTTTTTGCAATCAAAGTTTC
107225	105312	TGTTTTTGCAATCAAAGTTT
107226	105313	TTGTTTTTGCAATCAAAGTT
107227	105314	CTTGTTTTTGCAATCAAAGT
107228	105315	GCTTGTTTTTGCAATCAAAG
107229	105316	TGCTTGTTTTTGCAATCAAA
107230	105317	TTGCTTGTTTTTGCAATCAA
107231	105318	CTTGCTTGTTTTTGCAATCA
107232	105319	GCTTGCTTGTTTTTGCAATC
107233	105320	TGCTTGCTTGTTTTTGCAAT

8940	7027	CAAAAATTAGCCAGGCGTGG
8941	7028	ACAAAAATTAGCCAGGCGTG
8942	7029	TACAAAAATTAGCCAGGCGT
8943	7030	ATACAAAAATTAGCCAGGCG
8944	7031	AATACAAAAATTAGCCAGGC
8945	7032	AAATACAAAAATTAGCCAGG
8946	7033	AAAATACAAAAATTAGCCAG
8947	7034	AAAAATACAAAAATTAGCCA
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8949	7036	CTAAAAATACAAAAATTAGC
8950	7037	ACTAAAAATACAAAAATTAG
8951	7038	TACTAAAAATACAAAAATTA
8952	7039	CTACTAAAAATACAAAAATT
8953	7040	TCTACTAAAAATACAAAAAT
8954	7041	CTCTACTAAAAATACAAAAA
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8956	7043	GTCTCTACTAAAAATACAAA
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8958	7045	CTGTCTCTACTAAAAATACA
8959	7046	CCTGTCTCTACTAAAAATAC
8960	7047	CCCTGTCTCTACTAAAAATA
8961	7048	ACCCTGTCTCTACTAAAAAT
8962	7049	AACCCTGTCTCTACTAAAAA
8963	7050	AAACCCTGTCTCTACTAAAA
8964	7051	GAAACCCTGTCTCTACTAAA
8965	7052	TGAAACCCTGTCTCTACTAA
8966	7053	GTGAAACCCTGTCTCTACTA
8967	7054	GGTGAAACCCTGTCTCTACT
8968	7055	TGGTGAAACCCTGTCTCTAC
8969	7056	ATGGTGAAACCCTGTCTCTA
8970	7057	CATGGTGAAACCCTGTCTCT
8971	7058	ACATGGTGAAACCCTGTCTC
8972	7059	AACATGGTGAAACCCTGTCT
8973	7060	CAACATGGTGAAACCCTGTC
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8975	7062	GCCAACATGGTGAAACCCTG
8976	7063	AGCCAACATGGTGAAACCCT
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8978	7065	CTAGCCAACATGGTGAAACC
8979	7066	TCTAGCCAACATGGTGAAAC
8980	7067	TTCTAGCCAACATGGTGAAA
8981	7068	ATTCTAGCCAACATGGTGAA
8982	7069	CATTCTAGCCAACATGGTGA
8983	7070	CCATTCTAGCCAACATGGTG
8984	7071	ACCATTCTAGCCAACATGGT
8985	7072	GACCATTCTAGCCAACATGG
8986	7073	AGACCATTCTAGCCAACATG
8987	7074	GAGACCATTCTAGCCAACAT
8988	7075	TGAGACCATTCTAGCCAACA
8989	7076	TTGAGACCATTCTAGCCAAC
8990	7077	TTTGAGACCATTCTAGCCAA
8991	7078	GTTTGAGACCATTCTAGCCA
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8993	7080	GAGTTTGAGACCATTCTAGC
8994	7081	GGAGTTTGAGACCATTCTAG
8995	7082	AGGAGTTTGAGACCATTCTA
8996	7083	CAGGAGTTTGAGACCATTCT
8997	7084	TCAGGAGTTTGAGACCATTC
8998	7085	GTCAGGAGTTTGAGACCATT
8999	7086	GGTCAGGAGTTTGAGACCAT
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9001	7088	GAGGTCAGGAGTTTGAGACC
9002	7089	TGAGGTCAGGAGTTTGAGAC
9003	7090	CTGAGGTCAGGAGTTTGAGA
9004	7091	CCTGAGGTCAGGAGTTTGAG
9005	7092	ACCTGAGGTCAGGAGTTTGA
9006	7093	CACCTGAGGTCAGGAGTTTG
9007	7094	TCACCTGAGGTCAGGAGTTT
9008	7095	ATCACCTGAGGTCAGGAGTT
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58087	56174	TGGAGTGCAGTGGTACGATC
58088	56175	CTGGAGTGCAGTGGTACGAT
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58099	56186	TGTCACTCAGGCTGGAGTGC
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58105	56192	TCGCTCTGTCACTCAGGCTG
58106	56193	CTCGCTCTGTCACTCAGGCT
58107	56194	TCTCGCTCTGTCACTCAGGC
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58109	56196	AGTCTCGCTCTGTCACTCAG
58110	56197	GAGTCTCGCTCTGTCACTCA
58111	56198	GGAGTCTCGCTCTGTCACTC
58112	56199	TGGAGTCTCGCTCTGTCACT
58113	56200	ATGGAGTCTCGCTCTGTCAC
58114	56201	GATGGAGTCTCGCTCTGTCA
58115	56202	AGATGGAGTCTCGCTCTGTC
58116	56203	GAGATGGAGTCTCGCTCTGT
58117	56204	TGAGATGGAGTCTCGCTCTG
58118	56205	TTGAGATGGAGTCTCGCTCT
58119	56206	TTTGAGATGGAGTCTCGCTC
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58125	56212	TTTATTTTTGAGATGGAGTC
58126	56213	TTTTATTTTTGAGATGGAGT
58127	56214	TTTTTATTTTTGAGATGGAG
58128	56215	TTTTTTATTTTTGAGATGGA
58129	56216	ATTTTTTATTTTTGAGATGG
58130	56217	TATTTTTTATTTTTGAGATG
58131	56218	TTATTTTTTATTTTTGAGAT
58132	56219	TTTATTTTTTATTTTTGAGA
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58140	56227	ACAATTCTTTTATTTTTTAT
58141	56228	CACAATTCTTTTATTTTTTA
58142	56229	ACACAATTCTTTTATTTTTT
58143	56230	TACACAATTCTTTTATTTTT
58144	56231	CTACACAATTCTTTTATTTT
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58146	56233	ATCTACACAATTCTTTTATT
58147	56234	AATCTACACAATTCTTTTAT
58148	56235	AAATCTACACAATTCTTTTA
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107234	105321	TTGCTTGCTTGTTTTTGCAA
107235	105322	TTTGCTTGCTTGTTTTTGCA
107236	105323	CTTTGCTTGCTTGTTTTTGC
107237	105324	TCTTTGCTTGCTTGTTTTTG
107238	105325	CTCTTTGCTTGCTTGTTTTT
107239	105326	TCTCTTTGCTTGCTTGTTTT
107240	105327	TTCTCTTTGCTTGCTTGTTT
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107242	105329	TTTTCTCTTTGCTTGCTTGT
107243	105330	GTTTTCTCTTTGCTTGCTTG
107244	105331	AGTTTTCTCTTTGCTTGCTT
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107248	105335	TATTAGTTTTCTCTTTGCTT
107249	105336	TTATTAGTTTTCTCTTTGCT
107250	105337	TTTATTAGTTTTCTCTTTGC
107251	105338	TTTTATTAGTTTTCTCTTTG
107252	105339	TTTTTATTAGTTTTCTCTTT
107253	105340	GTTTTTATTAGTTTTCTCTT
107254	105341	AGTTTTTATTAGTTTTCTCT
107255	105342	GAGTTTTTATTAGTTTTCTC
107256	105343	AGAGTTTTTATTAGTTTTCT
107257	105344	TAGAGTTTTTATTAGTTTTC
107258	105345	GTAGAGTTTTTATTAGTTTT
107259	105346	TGTAGAGTTTTTATTAGTTT
107260	105347	GTGTAGAGTTTTTATTAGTT
107261	105348	AGTGTAGAGTTTTTATTAGT
107262	105349	AAGTGTAGAGTTTTTATTAG
107263	105350	GAAGTGTAGAGTTTTTATTA
107264	105351	TGAAGTGTAGAGTTTTTATT
107265	105352	ATGAAGTGTAGAGTTTTTAT
107266	105353	GATGAAGTGTAGAGTTTTTA
107267	105354	AGATGAAGTGTAGAGTTTTT
107268	105355	CAGATGAAGTGTAGAGTTTT
107269	105356	GCAGATGAAGTGTAGAGTTT
107270	105357	GGCAGATGAAGTGTAGAGTT
107271	105358	GGGCAGATGAAGTGTAGAGT
107272	105359	CGGGCAGATGAAGTGTAGAG
107273	105360	GCGGGCAGATGAAGTGTAGA
107274	105361	AGCGGGCAGATGAAGTGTAG
107275	105362	AAGCGGGCAGATGAAGTGTA
107276	105363	AAAGCGGGCAGATGAAGTGT
107277	105364	AAAAGCGGGCAGATGAAGTG
107278	105365	AAAAAGCGGGCAGATGAAGT
107279	105366	TAAAAAGCGGGCAGATGAAG
107280	105367	TTAAAAAGCGGGCAGATGAA
107281	105368	GTTAAAAAGCGGGCAGATGA
107282	105369	AGTTAAAAAGCGGGCAGATG
107283	105370	AAGTTAAAAAGCGGGCAGAT
107284	105371	AAAGTTAAAAAGCGGGCAGA
107285	105372	AAAAGTTAAAAAGCGGGCAG
107286	105373	CAAAAGTTAAAAAGCGGGCA
107287	105374	ACAAAAGTTAAAAAGCGGGC
107288	105375	AACAAAAGTTAAAAAGCGGG
107289	105376	CAACAAAAGTTAAAAAGCGG
107290	105377	ACAACAAAAGTTAAAAAGCG
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107292	105379	AAACAACAAAAGTTAAAAAG
107293	105380	AAAACAACAAAAGTTAAAAA
107294	105381	AAAAACAACAAAAGTTAAAA
107295	105382	TAAAAACAACAAAAGTTAAA
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107297	105384	AATAAAAACAACAAAAGTTA
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107300	105387	ATAAATAAAAACAACAAAAG
107301	105388	TATAAATAAAAACAACAAAA
107302	105389	ATATAAATAAAAACAACAAA
107303	105390	GATATAAATAAAAACAACAA
107304	105391	AGATATAAATAAAAACAACA

9011	7098	TGGATCACCTGAGGTCAGGA
9012	7099	GTGGATCACCTGAGGTCAGG
9013	7100	GGTGGATCACCTGAGGTCAG
9014	7101	AGGTGGATCACCTGAGGTCA
9015	7102	CAGGTGGATCACCTGAGGTC
9016	7103	GCAGGTGGATCACCTGAGGT
9017	7104	GGCAGGTGGATCACCTGAGG
9018	7105	AGGCAGGTGGATCACCTGAG
9019	7106	GAGGCAGGTGGATCACCTGA
9020	7107	TGAGGCAGGTGGATCACCTG
9021	7108	CTGAGGCAGGTGGATCACCT
9022	7109	GCTGAGGCAGGTGGATCACC
9023	7110	GGCTGAGGCAGGTGGATCAC
9024	7111	AGGCTGAGGCAGGTGGATCA
9025	7112	GAGGCTGAGGCAGGTGGATC
9026	7113	GGAGGCTGAGGCAGGTGGAT
9027	7114	GGGAGGCTGAGGCAGGTGGA
9028	7115	TGGGAGGCTGAGGCAGGTGG
9029	7116	TTGGGAGGCTGAGGCAGGTG
9030	7117	TTTGGGAGGCTGAGGCAGGT
9031	7118	CTTTGGGAGGCTGAGGCAGG
9032	7119	ACTTTGGGAGGCTGAGGCAG
9033	7120	AACTTTGGGAGGCTGAGGCA
9034	7121	GAACTTTGGGAGGCTGAGGC
9035	7122	AGAACTTTGGGAGGCTGAGG
9036	7123	CAGAACTTTGGGAGGCTGAG
9037	7124	CCAGAACTTTGGGAGGCTGA
9038	7125	CCCAGAACTTTGGGAGGCTG
9039	7126	TCCCAGAACTTTGGGAGGCT
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9042	7129	TAATCCCAGAACTTTGGGAG
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9044	7131	TGTAATCCCAGAACTTTGGG
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9046	7133	CCTGTAATCCCAGAACTTTG
9047	7134	GCCTGTAATCCCAGAACTTT
9048	7135	TGCCTGTAATCCCAGAACTT
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9050	7137	CATGCCTGTAATCCCAGAAC
9051	7138	TCATGCCTGTAATCCCAGAA
9052	7139	CTCATGCCTGTAATCCCAGA
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9054	7141	GGCTCATGCCTGTAATCCCA
9055	7142	TGGCTCATGCCTGTAATCCC
9056	7143	GTGGCTCATGCCTGTAATCC
9057	7144	GGTGGCTCATGCCTGTAATC
9058	7145	CGGTGGCTCATGCCTGTAAT
9059	7146	ACGGTGGCTCATGCCTGTAA
9060	7147	CACGGTGGCTCATGCCTGTA
9061	7148	GCACGGTGGCTCATGCCTGT
9062	7149	AGCACGGTGGCTCATGCCTG
9063	7150	AAGCACGGTGGCTCATGCCT
9064	7151	CAAGCACGGTGGCTCATGCC
9065	7152	CCAAGCACGGTGGCTCATGC
9066	7153	GCCAAGCACGGTGGCTCATG
9067	7154	GGCCAAGCACGGTGGCTCAT
9068	7155	CGGCCAAGCACGGTGGCTCA
9069	7156	GCGGCCAAGCACGGTGGCTC
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9074	7161	CGGCAGCGGCCAAGCACGGT
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9077	7164	ATACGGCAGCGGCCAAGCAC
9078	7165	GATACGGCAGCGGCCAAGCA
9079	7166	AGATACGGCAGCGGCCAAGC
9080	7167	AAGATACGGCAGCGGCCAAG
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58161	56248	CTTCCAACTACTAAAATCTA
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58168	56255	CCAACTTCTTCCAACTACTA
58169	56256	TCCAACTTCTTCCAACTACT
58170	56257	CTCCAACTTCTTCCAACTAC
58171	56258	ACTCCAACTTCTTCCAACTA
58172	56259	CACTCCAACTTCTTCCAACT
58173	56260	ACACTCCAACTTCTTCCAAC
58174	56261	AACACTCCAACTTCTTCCAA
58175	56262	TAACACTCCAACTTCTTCCA
58176	56263	TTAACACTCCAACTTCTTCC
58177	56264	ATTAACACTCCAACTTCTTC
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58182	56269	TACACATTAACACTCCAACT
58183	56270	TTACACATTAACACTCCAAC
58184	56271	ATTACACATTAACACTCCAA
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58219	56306	ACAATCTGTAGAATTTTATT
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58224	56311	ATAAAACAATCTGTAGAATT
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107305	105392	AAGATATAAATAAAAACAAC
107306	105393	AAAGATATAAATAAAAACAA
107307	105394	TAAAGATATAAATAAAAACA
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107309	105396	AATAAAGATATAAATAAAAA
107310	105397	TAATAAAGATATAAATAAAA
107311	105398	ATAATAAAGATATAAATAAA
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107313	105400	GTATAATAAAGATATAAATA
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107319	105406	GACATAGTATAATAAAGATA
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107321	105408	AAGACATAGTATAATAAAGA
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107323	105410	TTAAGACATAGTATAATAAA
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107337	105424	ATAACTACAGTTTTTTAAGA
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107339	105426	TTATAACTACAGTTTTTTAA
107340	105427	CTTATAACTACAGTTTTTTA
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107342	105429	GGCTTATAACTACAGTTTTT
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107345	105432	CCTGGCTTATAACTACAGTT
107346	105433	GCCTGGCTTATAACTACAGT
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107348	105435	GCGCCTGGCTTATAACTACA
107349	105436	TGCGCCTGGCTTATAACTAC
107350	105437	CTGCGCCTGGCTTATAACTA
107351	105438	ACTGCGCCTGGCTTATAACT
107352	105439	CACTGCGCCTGGCTTATAAC
107353	105440	CCACTGCGCCTGGCTTATAA
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107357	105444	TGAACCACTGCGCCTGGCTT
107358	105445	GTGAACCACTGCGCCTGGCT
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107361	105448	CACGTGAACCACTGCGCCTG
107362	105449	ACACGTGAACCACTGCGCCT
107363	105450	CACACGTGAACCACTGCGCC
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107365	105452	TACACACGTGAACCACTGCG
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107369	105456	GGATTACACACGTGAACCAC
107370	105457	GGGATTACACACGTGAACCA
107371	105458	TGGGATTACACACGTGAACC
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107373	105460	GCTGGGATTACACACGTGAA
107374	105461	TGCTGGGATTACACACGTGA
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9083	7170	AAAAAGATACGGCAGCGGCC
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9093	7180	ACTTTCATTTAAAAAGATAC
9094	7181	TACTTTCATTTAAAAAGATA
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9096	7183	AGTACTTTCATTTAAAAAGA
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9098	7185	CAAGTACTTTCATTTAAAAA
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9100	7187	CACAAGTACTTTCATTTAAA
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9104	7191	AAAACACAAGTACTTTCATT
9105	7192	AAAAACACAAGTACTTTCAT
9106	7193	AAAAAACACAAGTACTTTCA
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9137	7224	GATGACCCAGATATCCTTTG
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9139	7226	TAGATGACCCAGATATCCTT
9140	7227	ATAGATGACCCAGATATCCT
9141	7228	CATAGATGACCCAGATATCC
9142	7229	TCATAGATGACCCAGATATC
9143	7230	ATCATAGATGACCCAGATAT
9144	7231	CATCATAGATGACCCAGATA
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9146	7233	AACATCATAGATGACCCAGA
9147	7234	TAACATCATAGATGACCCAG
9148	7235	GTAACATCATAGATGACCCA
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9150	7237	CAGTAACATCATAGATGACC
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58229	56316	CCAGAATAAAACAATCTGTA
58230	56317	ACCAGAATAAAACAATCTGT
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107376	105463	AGTGCTGGGATTACACACGT
107377	105464	AAGTGCTGGGATTACACACG
107378	105465	AAAGTGCTGGGATTACACAC
107379	105466	CAAAGTGCTGGGATTACACA
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107386	105473	AGCCTCCCAAAGTGCTGGGA
107387	105474	CAGCCTCCCAAAGTGCTGGG
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107392	105479	CACCTCAGCCTCCCAAAGTG
107393	105480	CCACCTCAGCCTCCCAAAGT
107394	105481	CCCACCTCAGCCTCCCAAAG
107395	105482	GCCCACCTCAGCCTCCCAAA
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107397	105484	CCGCCCACCTCAGCCTCCCA
107398	105485	TCCGCCCACCTCAGCCTCCC
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107400	105487	GATCCGCCCACCTCAGCCTC
107401	105488	TGATCCGCCCACCTCAGCCT
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107405	105492	TAGGTGATCCGCCCACCTCA
107406	105493	TTAGGTGATCCGCCCACCTC
107407	105494	CTTAGGTGATCCGCCCACCT
107408	105495	CCTTAGGTGATCCGCCCACC
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107420	105507	TCGAACTCCTGACCTTAGGT
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107423	105510	GTCTCGAACTCCTGACCTTA
107424	105511	GGTCTCGAACTCCTGACCTT
107425	105512	TGGTCTCGAACTCCTGACCT
107426	105513	CTGGTCTCGAACTCCTGACC
107427	105514	GCTGGTCTCGAACTCCTGAC
107428	105515	GGCTGGTCTCGAACTCCTGA
107429	105516	AGGCTGGTCTCGAACTCCTG
107430	105517	TAGGCTGGTCTCGAACTCCT
107431	105518	CTAGGCTGGTCTCGAACTCC
107432	105519	GCTAGGCTGGTCTCGAACTC
107433	105520	GGCTAGGCTGGTCTCGAACT
107434	105521	TGGCTAGGCTGGTCTCGAAC
107435	105522	TTGGCTAGGCTGGTCTCGAA
107436	105523	ATTGGCTAGGCTGGTCTCGA
107437	105524	TATTGGCTAGGCTGGTCTCG
107438	105525	ATATTGGCTAGGCTGGTCTC
107439	105526	CATATTGGCTAGGCTGGTCT
107440	105527	CCATATTGGCTAGGCTGGTC
107441	105528	GCCATATTGGCTAGGCTGGT
107442	105529	TGCCATATTGGCTAGGCTGG
107443	105530	TTGCCATATTGGCTAGGCTG
107444	105531	TTTGCCATATTGGCTAGGCT
107445	105532	TTTTGCCATATTGGCTAGGC
107446	105533	GTTTTGCCATATTGGCTAGG

9153	7240	TAACAGTAACATCATAGATG
9154	7241	GTAACAGTAACATCATAGAT
9155	7242	GGTAACAGTAACATCATAGA
9156	7243	TGGTAACAGTAACATCATAG
9157	7244	ATGGTAACAGTAACATCATA
9158	7245	GATGGTAACAGTAACATCAT
9159	7246	AGATGGTAACAGTAACATCA
9160	7247	TAGATGGTAACAGTAACATC
9161	7248	TTAGATGGTAACAGTAACAT
9162	7249	CTTAGATGGTAACAGTAACA
9163	7250	CCTTAGATGGTAACAGTAAC
9164	7251	CCCTTAGATGGTAACAGTAA
9165	7252	ACCCTTAGATGGTAACAGTA
9166	7253	AACCCTTAGATGGTAACAGT
9167	7254	AAACCCTTAGATGGTAACAG
9168	7255	AAAACCCTTAGATGGTAACA
9169	7256	AAAAACCCTTAGATGGTAAC
9170	7257	AAAAAACCCTTAGATGGTAA
9171	7258	AAAAAAACCCTTAGATGGTA
9172	7259	CAAAAAAACCCTTAGATGGT
9173	7260	ACAAAAAAACCCTTAGATGG
9174	7261	AACAAAAAAACCCTTAGATG
9175	7262	AAACAAAAAAACCCTTAGAT
9176	7263	CAAACAAAAAAACCCTTAGA
9177	7264	ACAAACAAAAAAACCCTTAG
9178	7265	AACAAACAAAAAAACCCTTA
9179	7266	AAACAAACAAAAAAACCCTT
9180	7267	AAAACAAACAAAAAAACCCT
9181	7268	AAAAACAAACAAAAAAACCC
9182	7269	CAAAAACAAACAAAAAAACC
9183	7270	TCAAAAACAAACAAAAAAAC
9184	7271	CTCAAAAACAAACAAAAAAA
9185	7272	TCTCAAAAACAAACAAAAAA
9186	7273	GTCTCAAAAACAAACAAAAA
9187	7274	TGTCTCAAAAACAAACAAAA
9188	7275	CTGTCTCAAAAACAAACAAA
9189	7276	TCTGTCTCAAAAACAAACAA
9190	7277	CTCTGTCTCAAAAACAAACA
9191	7278	ACTCTGTCTCAAAAACAAAC
9192	7279	GACTCTGTCTCAAAAACAAA
9193	7280	AGACTCTGTCTCAAAAACAA
9194	7281	GAGACTCTGTCTCAAAAACA
9195	7282	AGAGACTCTGTCTCAAAAAC
9196	7283	CAGAGACTCTGTCTCAAAAA
9197	7284	ACAGAGACTCTGTCTCAAAA
9198	7285	GACAGAGACTCTGTCTCAAA
9199	7286	CGACAGAGACTCTGTCTCAA
9200	7287	GCGACAGAGACTCTGTCTCA
9201	7288	GGCGACAGAGACTCTGTCTC
9202	7289	GGGCGACAGAGACTCTGTCT
9203	7290	TGGGCGACAGAGACTCTGTC
9204	7291	CTGGGCGACAGAGACTCTGT
9205	7292	CCTGGGCGACAGAGACTCTG
9206	7293	GCCTGGGCGACAGAGACTCT
9207	7294	AGCCTGGGCGACAGAGACTC
9208	7295	CAGCCTGGGCGACAGAGACT
9209	7296	CCAGCCTGGGCGACAGAGAC
9210	7297	TCCAGCCTGGGCGACAGAGA
9211	7298	CTCCAGCCTGGGCGACAGAG
9212	7299	ACTCCAGCCTGGGCGACAGA
9213	7300	CACTCCAGCCTGGGCGACAG
9214	7301	GCACTCCAGCCTGGGCGACA
9215	7302	TGCACTCCAGCCTGGGCGAC
9216	7303	CTGCACTCCAGCCTGGGCGA
9217	7304	ACTGCACTCCAGCCTGGGCG
9218	7305	CACTGCACTCCAGCCTGGGC
9219	7306	CCACTGCACTCCAGCCTGGG
9220	7307	GCCACTGCACTCCAGCCTGG
9221	7308	CGCCACTGCACTCCAGCCTG
9222	7309	ACGCCACTGCACTCCAGCCT
9223	7310	CACGCCACTGCACTCCAGCC

58300	56387	TGTTACTCGTACTCTGTTAC
58301	56388	TTGTTACTCGTACTCTGTTA
58302	56389	TTTGTTACTCGTACTCTGTT
58303	56390	GTTTGTTACTCGTACTCTGT
58304	56391	TGTTTGTTACTCGTACTCTG
58305	56392	CTGTTTGTTACTCGTACTCT
58306	56393	CCTGTTTGTTACTCGTACTC
58307	56394	CCCTGTTTGTTACTCGTACT
58308	56395	TCCCTGTTTGTTACTCGTAC
58309	56396	ATCCCTGTTTGTTACTCGTA
58310	56397	GATCCCTGTTTGTTACTCGT
58311	56398	AGATCCCTGTTTGTTACTCG
58312	56399	GAGATCCCTGTTTGTTACTC
58313	56400	AGAGATCCCTGTTTGTTACT
58314	56401	AAGAGATCCCTGTTTGTTAC
58315	56402	GAAGAGATCCCTGTTTGTTA
58316	56403	AGAAGAGATCCCTGTTTGTT
58317	56404	CAGAAGAGATCCCTGTTTGT
58318	56405	TCAGAAGAGATCCCTGTTTG
58319	56406	TTCAGAAGAGATCCCTGTTT
58320	56407	GTTCAGAAGAGATCCCTGTT
58321	56408	CGTTCAGAAGAGATCCCTGT
58322	56409	CCGTTCAGAAGAGATCCCTG
58323	56410	GCCGTTCAGAAGAGATCCCT
58324	56411	CGCCGTTCAGAAGAGATCCC
58325	56412	ACGCCGTTCAGAAGAGATCC
58326	56413	CACGCCGTTCAGAAGAGATC
58327	56414	TCACGCCGTTCAGAAGAGAT
58328	56415	GTCACGCCGTTCAGAAGAGA
58329	56416	TGTCACGCCGTTCAGAAGAG
58330	56417	ATGTCACGCCGTTCAGAAGA
58331	56418	AATGTCACGCCGTTCAGAAG
58332	56419	TAATGTCACGCCGTTCAGAA
58333	56420	CTAATGTCACGCCGTTCAGA
58334	56421	TCTAATGTCACGCCGTTCAG
58335	56422	TTCTAATGTCACGCCGTTCA
58336	56423	TTTCTAATGTCACGCCGTTC
58337	56424	TTTTCTAATGTCACGCCGTT
58338	56425	CTTTTCTAATGTCACGCCGT
58339	56426	GCTTTTCTAATGTCACGCCG
58340	56427	AGCTTTTCTAATGTCACGCC
58341	56428	CAGCTTTTCTAATGTCACGC
58342	56429	ACAGCTTTTCTAATGTCACG
58343	56430	AACAGCTTTTCTAATGTCAC
58344	56431	AAACAGCTTTTCTAATGTCA
58345	56432	TAAACAGCTTTTCTAATGTC
58346	56433	GTAAACAGCTTTTCTAATGT
58347	56434	CGTAAACAGCTTTTCTAATG
58348	56435	CCGTAAACAGCTTTTCTAAT
58349	56436	GCCGTAAACAGCTTTTCTAA
58350	56437	GGCCGTAAACAGCTTTTCTA
58351	56438	AGGCCGTAAACAGCTTTTCT
58352	56439	GAGGCCGTAAACAGCTTTTC
58353	56440	TGAGGCCGTAAACAGCTTTT
58354	56441	TTGAGGCCGTAAACAGCTTT
58355	56442	GTTGAGGCCGTAAACAGCTT
58356	56443	AGTTGAGGCCGTAAACAGCT
58357	56444	AAGTTGAGGCCGTAAACAGC
58358	56445	AAAGTTGAGGCCGTAAACAG
58359	56446	CAAAGTTGAGGCCGTAAACA
58360	56447	GCAAAGTTGAGGCCGTAAAC
58361	56448	AGCAAAGTTGAGGCCGTAAA
58362	56449	CAGCAAAGTTGAGGCCGTAA
58363	56450	ACAGCAAAGTTGAGGCCGTA
58364	56451	CACAGCAAAGTTGAGGCCGT
58365	56452	CCACAGCAAAGTTGAGGCCG
58366	56453	ACCACAGCAAAGTTGAGGCC
58367	56454	AACCACAGCAAAGTTGAGGC
58368	56455	AAACCACAGCAAAGTTGAGG
58369	56456	TAAACCACAGCAAAGTTGAG
58370	56457	ATAAACCACAGCAAAGTTGA

107447	105534	GGTTTTGCCATATTGGCTAG
107448	105535	GGGTTTTGCCATATTGGCTA
107449	105536	GGGGTTTTGCCATATTGGCT
107450	105537	GGGGGTTTTGCCATATTGGC
107451	105538	AGGGGGTTTTGCCATATTGG
107452	105539	GAGGGGGTTTTGCCATATTG
107453	105540	AGAGGGGGTTTTGCCATATT
107454	105541	GAGAGGGGGTTTTGCCATAT
107455	105542	AGAGAGGGGGTTTTGCCATA
107456	105543	TAGAGAGGGGGTTTTGCCAT
107457	105544	GTAGAGAGGGGGTTTTGCCA
107458	105545	AGTAGAGAGGGGGTTTTGCC
107459	105546	TAGTAGAGAGGGGGTTTTGC
107460	105547	TTAGTAGAGAGGGGGTTTTG
107461	105548	TTTAGTAGAGAGGGGGTTTT
107462	105549	TTTTAGTAGAGAGGGGGTTT
107463	105550	TTTTTAGTAGAGAGGGGGTT
107464	105551	ATTTTTAGTAGAGAGGGGGT
107465	105552	TATTTTTAGTAGAGAGGGGG
107466	105553	CTATTTTTAGTAGAGAGGGG
107467	105554	TCTATTTTTAGTAGAGAGGG
107468	105555	TTCTATTTTTAGTAGAGAGG
107469	105556	TTTCTATTTTTAGTAGAGAG
107470	105557	TTTTCTATTTTTAGTAGAGA
107471	105558	TTTTTCTATTTTTAGTAGAG
107472	105559	ATTTTTCTATTTTTAGTAGA
107473	105560	AATTTTTCTATTTTTAGTAG
107474	105561	TAATTTTTCTATTTTTAGTA
107475	105562	CTAATTTTTCTATTTTTAGT
107476	105563	GCTAATTTTTCTATTTTTAG
107477	105564	GGCTAATTTTTCTATTTTTA
107478	105565	CGGCTAATTTTTCTATTTTT
107479	105566	CCGGCTAATTTTTCTATTTT
107480	105567	TCCGGCTAATTTTTCTATTT
107481	105568	GTCCGGCTAATTTTTCTATT
107482	105569	TGTCCGGCTAATTTTTCTAT
107483	105570	ATGTCCGGCTAATTTTTCTA
107484	105571	CATGTCCGGCTAATTTTTCT
107485	105572	CCATGTCCGGCTAATTTTTC
107486	105573	ACCATGTCCGGCTAATTTTT
107487	105574	CACCATGTCCGGCTAATTTT
107488	105575	CCACCATGTCCGGCTAATTT
107489	105576	GCCACCATGTCCGGCTAATT
107490	105577	CGCCACCATGTCCGGCTAAT
107491	105578	CCGCCACCATGTCCGGCTAA
107492	105579	CCCGCCACCATGTCCGGCTA
107493	105580	ACCCGCCACCATGTCCGGCT
107494	105581	CACCCGCCACCATGTCCGGC
107495	105582	GCACCCGCCACCATGTCCGG
107496	105583	GGCACCCGCCACCATGTCCG
107497	105584	AGGCACCCGCCACCATGTCC
107498	105585	CAGGCACCCGCCACCATGTC
107499	105586	ACAGGCACCCGCCACCATGT
107500	105587	TACAGGCACCCGCCACCATG
107501	105588	TTACAGGCACCCGCCACCAT
107502	105589	ATTACAGGCACCCGCCACCA
107503	105590	GATTACAGGCACCCGCCACC
107504	105591	GGATTACAGGCACCCGCCAC
107505	105592	GGGATTACAGGCACCCGCCA
107506	105593	TGGGATTACAGGCACCCGCC
107507	105594	CTGGGATTACAGGCACCCGC
107508	105595	GCTGGGATTACAGGCACCCG
107509	105596	AGCTGGGATTACAGGCACCC
107510	105597	TAGCTGGGATTACAGGCACC
107511	105598	GTAGCTGGGATTACAGGCAC
107512	105599	AGTAGCTGGGATTACAGGCA
107513	105600	GAGTAGCTGGGATTACAGGC
107514	105601	CGAGTAGCTGGGATTACAGG
107515	105602	CCGAGTAGCTGGGATTACAG
107516	105603	TCCGAGTAGCTGGGATTACA
107517	105604	CTCCGAGTAGCTGGGATTAC

9224	7311	TCACGCCACTGCACTCCAGC
9225	7312	ATCACGCCACTGCACTCCAG
9226	7313	GATCACGCCACTGCACTCCA
9227	7314	AGATCACGCCACTGCACTCC
9228	7315	AAGATCACGCCACTGCACTC
9229	7316	CAAGATCACGCCACTGCACT
9230	7317	CCAAGATCACGCCACTGCAC
9231	7318	GCCAAGATCACGCCACTGCA
9232	7319	AGCCAAGATCACGCCACTGC
9233	7320	GAGCCAAGATCACGCCACTG
9234	7321	TGAGCCAAGATCACGCCACT
9235	7322	GTGAGCCAAGATCACGCCAC
9236	7323	AGTGAGCCAAGATCACGCCA
9237	7324	CAGTGAGCCAAGATCACGCC
9238	7325	GCAGTGAGCCAAGATCACGC
9239	7326	TGCAGTGAGCCAAGATCACG
9240	7327	TTGCAGTGAGCCAAGATCAC
9241	7328	GTTGCAGTGAGCCAAGATCA
9242	7329	GGTTGCAGTGAGCCAAGATC
9243	7330	AGGTTGCAGTGAGCCAAGAT
9244	7331	GAGGTTGCAGTGAGCCAAGA
9245	7332	GGAGGTTGCAGTGAGCCAAG
9246	7333	CGGAGGTTGCAGTGAGCCAA
9247	7334	GCGGAGGTTGCAGTGAGCCA
9248	7335	GGCGGAGGTTGCAGTGAGCC
9249	7336	AGGCGGAGGTTGCAGTGAGC
9250	7337	GAGGCGGAGGTTGCAGTGAG
9251	7338	GGAGGCGGAGGTTGCAGTGA
9252	7339	GGGAGGCGGAGGTTGCAGTG
9253	7340	TGGGAGGCGGAGGTTGCAGT
9254	7341	CTGGGAGGCGGAGGTTGCAG
9255	7342	CCTGGGAGGCGGAGGTTGCA
9256	7343	ACCTGGGAGGCGGAGGTTGC
9257	7344	AACCTGGGAGGCGGAGGTTG
9258	7345	GAACCTGGGAGGCGGAGGTT
9259	7346	TGAACCTGGGAGGCGGAGGT
9260	7347	TTGAACCTGGGAGGCGGAGG
9261	7348	CTTGAACCTGGGAGGCGGAG
9262	7349	GCTTGAACCTGGGAGGCGGA
9263	7350	TGCTTGAACCTGGGAGGCGG
9264	7351	TTGCTTGAACCTGGGAGGCG
9265	7352	ATTGCTTGAACCTGGGAGGC
9266	7353	AATTGCTTGAACCTGGGAGG
9267	7354	GAATTGCTTGAACCTGGGAG
9268	7355	AGAATTGCTTGAACCTGGGA
9269	7356	GAGAATTGCTTGAACCTGGG
9270	7357	GGAGAATTGCTTGAACCTGG
9271	7358	AGGAGAATTGCTTGAACCTG
9272	7359	CAGGAGAATTGCTTGAACCT
9273	7360	GCAGGAGAATTGCTTGAACC
9274	7361	GGCAGGAGAATTGCTTGAAC
9275	7362	AGGCAGGAGAATTGCTTGAA
9276	7363	AAGGCAGGAGAATTGCTTGA
9277	7364	TAAGGCAGGAGAATTGCTTG
9278	7365	CTAAGGCAGGAGAATTGCTT
9279	7366	GCTAAGGCAGGAGAATTGCT
9280	7367	GGCTAAGGCAGGAGAATTGC
9281	7368	GGGCTAAGGCAGGAGAATTG
9282	7369	AGGGCTAAGGCAGGAGAATT
9283	7370	GAGGGCTAAGGCAGGAGAAT
9284	7371	GGAGGGCTAAGGCAGGAGAA
9285	7372	GGGAGGGCTAAGGCAGGAGA
9286	7373	CGGGAGGGCTAAGGCAGGAG
9287	7374	TCGGGAGGGCTAAGGCAGGA
9288	7375	TTCGGGAGGGCTAAGGCAGG
9289	7376	ATTCGGGAGGGCTAAGGCAG
9290	7377	TATTCGGGAGGGCTAAGGCA
9291	7378	CTATTCGGGAGGGCTAAGGC
9292	7379	GCTATTCGGGAGGGCTAAGG
9293	7380	AGCTATTCGGGAGGGCTAAG
9294	7381	CAGCTATTCGGGAGGGCTAA

58371	56458	AATAAACCACAGCAAAGTTG
58372	56459	TAATAAACCACAGCAAAGTT
58373	56460	TTAATAAACCACAGCAAAGT
58374	56461	CTTAATAAACCACAGCAAAG
58375	56462	TCTTAATAAACCACAGCAAA
58376	56463	GTCTTAATAAACCACAGCAA
58377	56464	TGTCTTAATAAACCACAGCA
58378	56465	GTGTCTTAATAAACCACAGC
58379	56466	TGTGTCTTAATAAACCACAG
58380	56467	CTGTGTCTTAATAAACCACA
58381	56468	TCTGTGTCTTAATAAACCAC
58382	56469	ATCTGTGTCTTAATAAACCA
58383	56470	TATCTGTGTCTTAATAAACC
58384	56471	ATATCTGTGTCTTAATAAAC
58385	56472	CATATCTGTGTCTTAATAAA
58386	56473	ACATATCTGTGTCTTAATAA
58387	56474	CACATATCTGTGTCTTAATA
58388	56475	ACACATATCTGTGTCTTAAT
58389	56476	AACACATATCTGTGTCTTAA
58390	56477	GAACACATATCTGTGTCTTA
58391	56478	TGAACACATATCTGTGTCTT
58392	56479	ATGAACACATATCTGTGTCT
58393	56480	AATGAACACATATCTGTGTC
58394	56481	GAATGAACACATATCTGTGT
58395	56482	AGAATGAACACATATCTGTG
58396	56483	CAGAATGAACACATATCTGT
58397	56484	CCAGAATGAACACATATCTG
58398	56485	CCCAGAATGAACACATATCT
58399	56486	CCCCAGAATGAACACATATC
58400	56487	GCCCCAGAATGAACACATAT
58401	56488	GGCCCCAGAATGAACACATA
58402	56489	TGGCCCCAGAATGAACACAT
58403	56490	TTGGCCCCAGAATGAACACA
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58405	56492	GCTTGGCCCCAGAATGAACA
58406	56493	TGCTTGGCCCCAGAATGAAC
58407	56494	CTGCTTGGCCCCAGAATGAA
58408	56495	ACTGCTTGGCCCCAGAATGA
58409	56496	TACTGCTTGGCCCCAGAATG
58410	56497	TTACTGCTTGGCCCCAGAAT
58411	56498	GTTACTGCTTGGCCCCAGAA
58412	56499	AGTTACTGCTTGGCCCCAGA
58413	56500	CAGTTACTGCTTGGCCCCAG
58414	56501	CCAGTTACTGCTTGGCCCCA
58415	56502	TCCAGTTACTGCTTGGCCCC
58416	56503	CTCCAGTTACTGCTTGGCCC
58417	56504	TCTCCAGTTACTGCTTGGCC
58418	56505	CTCTCCAGTTACTGCTTGGC
58419	56506	ACTCTCCAGTTACTGCTTGG
58420	56507	CACTCTCCAGTTACTGCTTG
58421	56508	CCACTCTCCAGTTACTGCTT
58422	56509	GCCACTCTCCAGTTACTGCT
58423	56510	TGCCACTCTCCAGTTACTGC
58424	56511	GTGCCACTCTCCAGTTACTG
58425	56512	AGTGCCACTCTCCAGTTACT
58426	56513	AAGTGCCACTCTCCAGTTAC
58427	56514	TAAGTGCCACTCTCCAGTTA
58428	56515	ATAAGTGCCACTCTCCAGTT
58429	56516	AATAAGTGCCACTCTCCAGT
58430	56517	CAATAAGTGCCACTCTCCAG
58431	56518	TCAATAAGTGCCACTCTCCA
58432	56519	CTCAATAAGTGCCACTCTCC
58433	56520	CCTCAATAAGTGCCACTCTC
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58435	56522	GGCCTCAATAAGTGCCACTC
58436	56523	TGGCCTCAATAAGTGCCACT
58437	56524	CTGGCCTCAATAAGTGCCAC
58438	56525	ACTGGCCTCAATAAGTGCCA
58439	56526	TACTGGCCTCAATAAGTGCC
58440	56527	ATACTGGCCTCAATAAGTGC
58441	56528	CATACTGGCCTCAATAAGTG

107518	105605	CCTCCGAGTAGCTGGGATTA
107519	105606	GCCTCCGAGTAGCTGGGATT
107520	105607	AGCCTCCGAGTAGCTGGGAT
107521	105608	CAGCCTCCGAGTAGCTGGGA
107522	105609	TCAGCCTCCGAGTAGCTGGG
107523	105610	CTCAGCCTCCGAGTAGCTGG
107524	105611	CCTCAGCCTCCGAGTAGCTG
107525	105612	GCCTCAGCCTCCGAGTAGCT
107526	105613	TGCCTCAGCCTCCGAGTAGC
107527	105614	CTGCCTCAGCCTCCGAGTAG
107528	105615	CCTGCCTCAGCCTCCGAGTA
107529	105616	TCCTGCCTCAGCCTCCGAGT
107530	105617	CTCCTGCCTCAGCCTCCGAG
107531	105618	TCTCCTGCCTCAGCCTCCGA
107532	105619	TTCTCCTGCCTCAGCCTCCG
107533	105620	ATTCTCCTGCCTCAGCCTCC
107534	105621	GATTCTCCTGCCTCAGCCTC
107535	105622	TGATTCTCCTGCCTCAGCCT
107536	105623	GTGATTCTCCTGCCTCAGCC
107537	105624	AGTGATTCTCCTGCCTCAGC
107538	105625	AAGTGATTCTCCTGCCTCAG
107539	105626	CAAGTGATTCTCCTGCCTCA
107540	105627	TCAAGTGATTCTCCTGCCTC
107541	105628	TTCAAGTGATTCTCCTGCCT
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107548	105635	TCCTGGGTTCAAGTGATTCT
107549	105636	CTCCTGGGTTCAAGTGATTC
107550	105637	CCTCCTGGGTTCAAGTGATT
107551	105638	GCCTCCTGGGTTCAAGTGAT
107552	105639	GGCCTCCTGGGTTCAAGTGA
107553	105640	GGGCCTCCTGGGTTCAAGTG
107554	105641	TGGGCCTCCTGGGTTCAAGT
107555	105642	CTGGGCCTCCTGGGTTCAAG
107556	105643	CCTGGGCCTCCTGGGTTCAA
107557	105644	ACCTGGGCCTCCTGGGTTCA
107558	105645	AACCTGGGCCTCCTGGGTTC
107559	105646	CAACCTGGGCCTCCTGGGTT
107560	105647	GCAACCTGGGCCTCCTGGGT
107561	105648	TGCAACCTGGGCCTCCTGGG
107562	105649	CTGCAACCTGGGCCTCCTGG
107563	105650	ACTGCAACCTGGGCCTCCTG
107564	105651	CACTGCAACCTGGGCCTCCT
107565	105652	TCACTGCAACCTGGGCCTCC
107566	105653	CTCACTGCAACCTGGGCCTC
107567	105654	GCTCACTGCAACCTGGGCCT
107568	105655	GGCTCACTGCAACCTGGGCC
107569	105656	CGGCTCACTGCAACCTGGGC
107570	105657	TCGGCTCACTGCAACCTGGG
107571	105658	CTCGGCTCACTGCAACCTGG
107572	105659	TCTCGGCTCACTGCAACCTG
107573	105660	CTCTCGGCTCACTGCAACCT
107574	105661	ACTCTCGGCTCACTGCAACC
107575	105662	CACTCTCGGCTCACTGCAAC
107576	105663	GCACTCTCGGCTCACTGCAA
107577	105664	CGCACTCTCGGCTCACTGCA
107578	105665	GCGCACTCTCGGCTCACTGC
107579	105666	GGCGCACTCTCGGCTCACTG
107580	105667	TGGCGCACTCTCGGCTCACT
107581	105668	GTGGCGCACTCTCGGCTCAC
107582	105669	AGTGGCGCACTCTCGGCTCA
107583	105670	CAGTGGCGCACTCTCGGCTC
107584	105671	GCAGTGGCGCACTCTCGGCT
107585	105672	TGCAGTGGCGCACTCTCGGC
107586	105673	GTGCAGTGGCGCACTCTCGG
107587	105674	AGTGCAGTGGCGCACTCTCG
107588	105675	GAGTGCAGTGGCGCACTCTC

9295	7382	CCAGCTATTCGGGAGGGCTA
9296	7383	CCCAGCTATTCGGGAGGGCT
9297	7384	TCCCAGCTATTCGGGAGGGC
9298	7385	ATCCCAGCTATTCGGGAGGG
9299	7386	AATCCCAGCTATTCGGGAGG
9300	7387	TAATCCCAGCTATTCGGGAG
9301	7388	GTAATCCCAGCTATTCGGGA
9302	7389	TGTAATCCCAGCTATTCGGG
9303	7390	CTGTAATCCCAGCTATTCGG
9304	7391	CCTGTAATCCCAGCTATTCG
9305	7392	GCCTGTAATCCCAGCTATTC
9306	7393	TGCCTGTAATCCCAGCTATT
9307	7394	GTGCCTGTAATCCCAGCTAT
9308	7395	GGTGCCTGTAATCCCAGCTA
9309	7396	GGGTGCCTGTAATCCCAGCT
9310	7397	CGGGTGCCTGTAATCCCAGC
9311	7398	GCGGGTGCCTGTAATCCCAG
9312	7399	GGCGGGTGCCTGTAATCCCA
9313	7400	TGGCGGGTGCCTGTAATCCC
9314	7401	GTGGCGGGTGCCTGTAATCC
9315	7402	GGTGGCGGGTGCCTGTAATC
9316	7403	TGGTGGCGGGTGCCTGTAAT
9317	7404	ATGGTGGCGGGTGCCTGTAA
9318	7405	CATGGTGGCGGGTGCCTGTA
9319	7406	GCATGGTGGCGGGTGCCTGT
9320	7407	GGCATGGTGGCGGGTGCCTG
9321	7408	AGGCATGGTGGCGGGTGCCT
9322	7409	CAGGCATGGTGGCGGGTGCC
9323	7410	CCAGGCATGGTGGCGGGTGC
9324	7411	GCCAGGCATGGTGGCGGGTG
9325	7412	AGCCAGGCATGGTGGCGGGT
9326	7413	TAGCCAGGCATGGTGGCGGG
9327	7414	TTAGCCAGGCATGGTGGCGG
9328	7415	CTTAGCCAGGCATGGTGGCG
9329	7416	ACTTAGCCAGGCATGGTGGC
9330	7417	AACTTAGCCAGGCATGGTGG
9331	7418	AAACTTAGCCAGGCATGGTG
9332	7419	AAAACTTAGCCAGGCATGGT
9333	7420	CAAAACTTAGCCAGGCATGG
9334	7421	GCAAAACTTAGCCAGGCATG
9335	7422	TGCAAAACTTAGCCAGGCAT
9336	7423	ATGCAAAACTTAGCCAGGCA
9337	7424	AATGCAAAACTTAGCCAGGC
9338	7425	AAATGCAAAACTTAGCCAGG
9339	7426	AAAATGCAAAACTTAGCCAG
9340	7427	AAAAATGCAAAACTTAGCCA
9341	7428	TAAAAATGCAAAACTTAGCC
9342	7429	CTAAAAATGCAAAACTTAGC
9343	7430	ACTAAAAATGCAAAACTTAG
9344	7431	TACTAAAAATGCAAAACTTA
9345	7432	CTACTAAAAATGCAAAACTT
9346	7433	TCTACTAAAAATGCAAAACT
9347	7434	ATCTACTAAAAATGCAAAAC
9348	7435	TATCTACTAAAAATGCAAAA
9349	7436	ATATCTACTAAAAATGCAAA
9350	7437	CATATCTACTAAAAATGCAA
9351	7438	CCATATCTACTAAAAATGCA
9352	7439	TCCATATCTACTAAAAATGC
9353	7440	CTCCATATCTACTAAAAATG
9354	7441	ACTCCATATCTACTAAAAAT
9355	7442	AACTCCATATCTACTAAAAA
9356	7443	AAACTCCATATCTACTAAAA
9357	7444	GAAACTCCATATCTACTAAA
9358	7445	TGAAACTCCATATCTACTAA
9359	7446	GTGAAACTCCATATCTACTA
9360	7447	GGTGAAACTCCATATCTACT
9361	7448	TGGTGAAACTCCATATCTAC
9362	7449	ATGGTGAAACTCCATATCTA
9363	7450	CATGGTGAAACTCCATATCT
9364	7451	ACATGGTGAAACTCCATATC
9365	7452	AACATGGTGAAACTCCATAT

58442	56529	CCATACTGGCCTCAATAAGT
58443	56530	TCCATACTGGCCTCAATAAG
58444	56531	CTCCATACTGGCCTCAATAA
58445	56532	CCTCCATACTGGCCTCAATA
58446	56533	GCCTCCATACTGGCCTCAAT
58447	56534	TGCCTCCATACTGGCCTCAA
58448	56535	CTGCCTCCATACTGGCCTCA
58449	56536	ACTGCCTCCATACTGGCCTC
58450	56537	TACTGCCTCCATACTGGCCT
58451	56538	GTACTGCCTCCATACTGGCC
58452	56539	TGTACTGCCTCCATACTGGC
58453	56540	CTGTACTGCCTCCATACTGG
58454	56541	TCTGTACTGCCTCCATACTG
58455	56542	CTCTGTACTGCCTCCATACT
58456	56543	TCTCTGTACTGCCTCCATAC
58457	56544	ATCTCTGTACTGCCTCCATA
58458	56545	AATCTCTGTACTGCCTCCAT
58459	56546	TAATCTCTGTACTGCCTCCA
58460	56547	ATAATCTCTGTACTGCCTCC
58461	56548	AATAATCTCTGTACTGCCTC
58462	56549	CAATAATCTCTGTACTGCCT
58463	56550	TCAATAATCTCTGTACTGCC
58464	56551	CTCAATAATCTCTGTACTGC
58465	56552	TCTCAATAATCTCTGTACTG
58466	56553	ATCTCAATAATCTCTGTACT
58467	56554	AATCTCAATAATCTCTGTAC
58468	56555	TAATCTCAATAATCTCTGTA
58469	56556	TTAATCTCAATAATCTCTGT
58470	56557	TTTAATCTCAATAATCTCTG
58471	56558	TTTTAATCTCAATAATCTCT
58472	56559	CTTTTAATCTCAATAATCTC
58473	56560	TCTTTTAATCTCAATAATCT
58474	56561	TTCTTTTAATCTCAATAATC
58475	56562	TTTCTTTTAATCTCAATAAT
58476	56563	CTTTCTTTTAATCTCAATAA
58477	56564	TCTTTCTTTTAATCTCAATA
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58482	56569	CTGTTTCTTTCTTTTAATCT
58483	56570	CCTGTTTCTTTCTTTTAATC
58484	56571	ACCTGTTTCTTTCTTTTAAT
58485	56572	CACCTGTTTCTTTCTTTTAA
58486	56573	CCACCTGTTTCTTTCTTTTA
58487	56574	TCCACCTGTTTCTTTCTTTT
58488	56575	TTCCACCTGTTTCTTTCTTT
58489	56576	GTTCCACCTGTTTCTTTCTT
58490	56577	CGTTCCACCTGTTTCTTTCT
58491	56578	CCGTTCCACCTGTTTCTTTC
58492	56579	TCCGTTCCACCTGTTTCTTT
58493	56580	ATCCGTTCCACCTGTTTCTT
58494	56581	GATCCGTTCCACCTGTTTCT
58495	56582	AGATCCGTTCCACCTGTTTC
58496	56583	TAGATCCGTTCCACCTGTTT
58497	56584	ATAGATCCGTTCCACCTGTT
58498	56585	CATAGATCCGTTCCACCTGT
58499	56586	ACATAGATCCGTTCCACCTG
58500	56587	TACATAGATCCGTTCCACCT
58501	56588	TTACATAGATCCGTTCCACC
58502	56589	ATTACATAGATCCGTTCCAC
58503	56590	CATTACATAGATCCGTTCCA
58504	56591	CCATTACATAGATCCGTTCC
58505	56592	TCCATTACATAGATCCGTTC
58506	56593	TTCCATTACATAGATCCGTT
58507	56594	TTTCCATTACATAGATCCGT
58508	56595	CTTTCCATTACATAGATCCG
58509	56596	GCTTTCCATTACATAGATCC
58510	56597	AGCTTTCCATTACATAGATC
58511	56598	TAGCTTTCCATTACATAGAT
58512	56599	TTAGCTTTCCATTACATAGA

107589	105676	GGAGTGCAGTGGCGCACTCT
107590	105677	TGGAGTGCAGTGGCGCACTC
107591	105678	CTGGAGTGCAGTGGCGCACT
107592	105679	ACTGGAGTGCAGTGGCGCAC
107593	105680	GACTGGAGTGCAGTGGCGCA
107594	105681	AGACTGGAGTGCAGTGGCGC
107595	105682	CAGACTGGAGTGCAGTGGCG
107596	105683	CCAGACTGGAGTGCAGTGGC
107597	105684	CCCAGACTGGAGTGCAGTGG
107598	105685	GCCCAGACTGGAGTGCAGTG
107599	105686	TGCCCAGACTGGAGTGCAGT
107600	105687	TTGCCCAGACTGGAGTGCAG
107601	105688	GTTGCCCAGACTGGAGTGCA
107602	105689	TGTTGCCCAGACTGGAGTGC
107603	105690	CTGTTGCCCAGACTGGAGTG
107604	105691	TCTGTTGCCCAGACTGGAGT
107605	105692	CTCTGTTGCCCAGACTGGAG
107606	105693	ACTCTGTTGCCCAGACTGGA
107607	105694	TACTCTGTTGCCCAGACTGG
107608	105695	TTACTCTGTTGCCCAGACTG
107609	105696	CTTACTCTGTTGCCCAGACT
107610	105697	TCTTACTCTGTTGCCCAGAC
107611	105698	GTCTTACTCTGTTGCCCAGA
107612	105699	AGTCTTACTCTGTTGCCCAG
107613	105700	CAGTCTTACTCTGTTGCCCA
107614	105701	ACAGTCTTACTCTGTTGCCC
107615	105702	GACAGTCTTACTCTGTTGCC
107616	105703	AGACAGTCTTACTCTGTTGC
107617	105704	GAGACAGTCTTACTCTGTTG
107618	105705	TGAGACAGTCTTACTCTGTT
107619	105706	TTGAGACAGTCTTACTCTGT
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107624	105711	GTTTTTTGAGACAGTCTTAC
107625	105712	TGTTTTTTGAGACAGTCTTA
107626	105713	TTGTTTTTTGAGACAGTCTT
107627	105714	ATTGTTTTTTGAGACAGTCT
107628	105715	TATTGTTTTTTGAGACAGTC
107629	105716	GTATTGTTTTTTGAGACAGT
107630	105717	TGTATTGTTTTTTGAGACAG
107631	105718	TTGTATTGTTTTTTGAGACA
107632	105719	TTTGTATTGTTTTTTGAGAC
107633	105720	TTTTGTATTGTTTTTTGAGA
107634	105721	GTTTTGTATTGTTTTTTGAG
107635	105722	TGTTTTGTATTGTTTTTTGA
107636	105723	TTGTTTTGTATTGTTTTTTG
107637	105724	TTTGTTTTGTATTGTTTTTT
107638	105725	TTTTGTTTTGTATTGTTTTT
107639	105726	GTTTTGTTTTGTATTGTTTT
107640	105727	TGTTTTGTTTTGTATTGTTT
107641	105728	TTGTTTTGTTTTGTATTGTT
107642	105729	TTTGTTTTGTTTTGTATTGT
107643	105730	TTTTGTTTTGTTTTGTATTG
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107648	105735	CAGGGTTTTGTTTTGTTTTG
107649	105736	CCAGGGTTTTGTTTTGTTTT
107650	105737	GCCAGGGTTTTGTTTTGTTT
107651	105738	GGCCAGGGTTTTGTTTTGTT
107652	105739	AGGCCAGGGTTTTGTTTTGT
107653	105740	TAGGCCAGGGTTTTGTTTTG
107654	105741	CTAGGCCAGGGTTTTGTTTT
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107657	105744	CCACTAGGCCAGGGTTTTGT
107658	105745	GCCACTAGGCCAGGGTTTTG
107659	105746	AGCCACTAGGCCAGGGTTTT

9366	7453	CAACATGGTGAAACTCCATA
9367	7454	CCAACATGGTGAAACTCCAT
9368	7455	GCCAACATGGTGAAACTCCA
9369	7456	GGCCAACATGGTGAAACTCC
9370	7457	TGGCCAACATGGTGAAACTC
9371	7458	CTGGCCAACATGGTGAAACT
9372	7459	CCTGGCCAACATGGTGAAAC
9373	7460	GCCTGGCCAACATGGTGAAA
9374	7461	AGCCTGGCCAACATGGTGAA
9375	7462	CAGCCTGGCCAACATGGTGA
9376	7463	GCAGCCTGGCCAACATGGTG
9377	7464	AGCAGCCTGGCCAACATGGT
9378	7465	GAGCAGCCTGGCCAACATGG
9379	7466	AGAGCAGCCTGGCCAACATG
9380	7467	AAGAGCAGCCTGGCCAACAT
9381	7468	CAAGAGCAGCCTGGCCAACA
9382	7469	TCAAGAGCAGCCTGGCCAAC
9383	7470	TTCAAGAGCAGCCTGGCCAA
9384	7471	GTTCAAGAGCAGCCTGGCCA
9385	7472	AGTTCAAGAGCAGCCTGGCC
9386	7473	GAGTTCAAGAGCAGCCTGGC
9387	7474	GGAGTTCAAGAGCAGCCTGG
9388	7475	AGGAGTTCAAGAGCAGCCTG
9389	7476	CAGGAGTTCAAGAGCAGCCT
9390	7477	TCAGGAGTTCAAGAGCAGCC
9391	7478	GTCAGGAGTTCAAGAGCAGC
9392	7479	GGTCAGGAGTTCAAGAGCAG
9393	7480	AGGTCAGGAGTTCAAGAGCA
9394	7481	GAGGTCAGGAGTTCAAGAGC
9395	7482	TGAGGTCAGGAGTTCAAGAG
9396	7483	CTGAGGTCAGGAGTTCAAGA
9397	7484	CCTGAGGTCAGGAGTTCAAG
9398	7485	ACCTGAGGTCAGGAGTTCAA
9399	7486	CACCTGAGGTCAGGAGTTCA
9400	7487	TCACCTGAGGTCAGGAGTTC
9401	7488	ATCACCTGAGGTCAGGAGTT
9402	7489	AATCACCTGAGGTCAGGAGT
9403	7490	GAATCACCTGAGGTCAGGAG
9404	7491	CGAATCACCTGAGGTCAGGA
9405	7492	GCGAATCACCTGAGGTCAGG
9406	7493	AGCGAATCACCTGAGGTCAG
9407	7494	AAGCGAATCACCTGAGGTCA
9408	7495	CAAGCGAATCACCTGAGGTC
9409	7496	GCAAGCGAATCACCTGAGGT
9410	7497	GGCAAGCGAATCACCTGAGG
9411	7498	AGGCAAGCGAATCACCTGAG
9412	7499	GAGGCAAGCGAATCACCTGA
9413	7500	CGAGGCAAGCGAATCACCTG
9414	7501	CCGAGGCAAGCGAATCACCT
9415	7502	GCCGAGGCAAGCGAATCACC
9416	7503	GGCCGAGGCAAGCGAATCAC
9417	7504	AGGCCGAGGCAAGCGAATCA
9418	7505	GAGGCCGAGGCAAGCGAATC
9419	7506	GGAGGCCGAGGCAAGCGAAT
9420	7507	GGGAGGCCGAGGCAAGCGAA
9421	7508	TGGGAGGCCGAGGCAAGCGA
9422	7509	TTGGGAGGCCGAGGCAAGCG
9423	7510	TTTGGGAGGCCGAGGCAAGC
9424	7511	CTTTGGGAGGCCGAGGCAAG
9425	7512	ACTTTGGGAGGCCGAGGCAA
9426	7513	CACTTTGGGAGGCCGAGGCA
9427	7514	GCACTTTGGGAGGCCGAGGC
9428	7515	AGCACTTTGGGAGGCCGAGG
9429	7516	CAGCACTTTGGGAGGCCGAG
9430	7517	CCAGCACTTTGGGAGGCCGA
9431	7518	CCCAGCACTTTGGGAGGCCG
9432	7519	TCCCAGCACTTTGGGAGGCC
9433	7520	ATCCCAGCACTTTGGGAGGC
9434	7521	AATCCCAGCACTTTGGGAGG
9435	7522	TAATCCCAGCACTTTGGGAG
9436	7523	GTAATCCCAGCACTTTGGGA

58513	56600	TTTAGCTTTCCATTACATAG
58514	56601	GTTTAGCTTTCCATTACATA
58515	56602	TGTTTAGCTTTCCATTACAT
58516	56603	CTGTTTAGCTTTCCATTACA
58517	56604	TCTGTTTAGCTTTCCATTAC
58518	56605	TTCTGTTTAGCTTTCCATTA
58519	56606	ATTCTGTTTAGCTTTCCATT
58520	56607	TATTCTGTTTAGCTTTCCAT
58521	56608	CTATTCTGTTTAGCTTTCCA
58522	56609	ACTATTCTGTTTAGCTTTCC
58523	56610	AACTATTCTGTTTAGCTTTC
58524	56611	GAACTATTCTGTTTAGCTTT
58525	56612	CGAACTATTCTGTTTAGCTT
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58528	56615	CCACGAACTATTCTGTTTAG
58529	56616	ACCACGAACTATTCTGTTTA
58530	56617	TACCACGAACTATTCTGTTT
58531	56618	GTACCACGAACTATTCTGTT
58532	56619	TGTACCACGAACTATTCTGT
58533	56620	GTGTACCACGAACTATTCTG
58534	56621	TGTGTACCACGAACTATTCT
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58536	56623	ACTGTGTACCACGAACTATT
58537	56624	TACTGTGTACCACGAACTAT
58538	56625	CTACTGTGTACCACGAACTA
58539	56626	TCTACTGTGTACCACGAACT
58540	56627	TTCTACTGTGTACCACGAAC
58541	56628	TTTCTACTGTGTACCACGAA
58542	56629	TTTTCTACTGTGTACCACGA
58543	56630	CTTTTCTACTGTGTACCACG
58544	56631	GCTTTTCTACTGTGTACCAC
58545	56632	TGCTTTTCTACTGTGTACCA
58546	56633	ATGCTTTTCTACTGTGTACC
58547	56634	AATGCTTTTCTACTGTGTAC
58548	56635	TAATGCTTTTCTACTGTGTA
58549	56636	GTAATGCTTTTCTACTGTGT
58550	56637	TGTAATGCTTTTCTACTGTG
58551	56638	ATGTAATGCTTTTCTACTGT
58552	56639	CATGTAATGCTTTTCTACTG
58553	56640	ACATGTAATGCTTTTCTACT
58554	56641	AACATGTAATGCTTTTCTAC
58555	56642	AAACATGTAATGCTTTTCTA
58556	56643	TAAACATGTAATGCTTTTCT
58557	56644	ATAAACATGTAATGCTTTTC
58558	56645	AATAAACATGTAATGCTTTT
58559	56646	TAATAAACATGTAATGCTTT
58560	56647	TTAATAAACATGTAATGCTT
58561	56648	CTTAATAAACATGTAATGCT
58562	56649	TCTTAATAAACATGTAATGC
58563	56650	ATCTTAATAAACATGTAATG
58564	56651	TATCTTAATAAACATGTAAT
58565	56652	ATATCTTAATAAACATGTAA
58566	56653	CATATCTTAATAAACATGTA
58567	56654	CCATATCTTAATAAACATGT
58568	56655	ACCATATCTTAATAAACATG
58569	56656	GACCATATCTTAATAAACAT
58570	56657	TGACCATATCTTAATAAACA
58571	56658	ATGACCATATCTTAATAAAC
58572	56659	GATGACCATATCTTAATAAA
58573	56660	AGATGACCATATCTTAATAA
58574	56661	AAGATGACCATATCTTAATA
58575	56662	GAAGATGACCATATCTTAAT
58576	56663	GGAAGATGACCATATCTTAA
58577	56664	TGGAAGATGACCATATCTTA
58578	56665	ATGGAAGATGACCATATCTT
58579	56666	AATGGAAGATGACCATATCT
58580	56667	AAATGGAAGATGACCATATC
58581	56668	TAAATGGAAGATGACCATAT
58582	56669	ATAAATGGAAGATGACCATA
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107660	105747	GAGCCACTAGGCCAGGGTTT
107661	105748	TGAGCCACTAGGCCAGGGTT
107662	105749	GTGAGCCACTAGGCCAGGGT
107663	105750	CGTGAGCCACTAGGCCAGGG
107664	105751	GCGTGAGCCACTAGGCCAGG
107665	105752	GGCGTGAGCCACTAGGCCAG
107666	105753	AGGCGTGAGCCACTAGGCCA
107667	105754	TAGGCGTGAGCCACTAGGCC
107668	105755	TTAGGCGTGAGCCACTAGGC
107669	105756	ATTAGGCGTGAGCCACTAGG
107670	105757	GATTAGGCGTGAGCCACTAG
107671	105758	GGATTAGGCGTGAGCCACTA
107672	105759	GGGATTAGGCGTGAGCCACT
107673	105760	TGGGATTAGGCGTGAGCCAC
107674	105761	CTGGGATTAGGCGTGAGCCA
107675	105762	GCTGGGATTAGGCGTGAGCC
107676	105763	TGCTGGGATTAGGCGTGAGC
107677	105764	GTGCTGGGATTAGGCGTGAG
107678	105765	AGTGCTGGGATTAGGCGTGA
107679	105766	AAGTGCTGGGATTAGGCGTG
107680	105767	AAAGTGCTGGGATTAGGCGT
107681	105768	CAAAGTGCTGGGATTAGGCG
107682	105769	CCAAAGTGCTGGGATTAGGC
107683	105770	TCCAAAGTGCTGGGATTAGG
107684	105771	TTCCAAAGTGCTGGGATTAG
107685	105772	CTTCCAAAGTGCTGGGATTA
107686	105773	CCTTCCAAAGTGCTGGGATT
107687	105774	GCCTTCCAAAGTGCTGGGAT
107688	105775	TGCCTTCCAAAGTGCTGGGA
107689	105776	TTGCCTTCCAAAGTGCTGGG
107690	105777	TTTGCCTTCCAAAGTGCTGG
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107697	105784	CCCCACCTTTGCCTTCCAAA
107698	105785	GCCCCACCTTTGCCTTCCAA
107699	105786	CGCCCCACCTTTGCCTTCCA
107700	105787	TCGCCCCACCTTTGCCTTCC
107701	105788	TTCGCCCCACCTTTGCCTTC
107702	105789	ATTCGCCCCACCTTTGCCTT
107703	105790	GATTCGCCCCACCTTTGCCT
107704	105791	TGATTCGCCCCACCTTTGCC
107705	105792	GTGATTCGCCCCACCTTTGC
107706	105793	TGTGATTCGCCCCACCTTTG
107707	105794	TTGTGATTCGCCCCACCTTT
107708	105795	CTTGTGATTCGCCCCACCTT
107709	105796	CCTTGTGATTCGCCCCACCT
107710	105797	ACCTTGTGATTCGCCCCACC
107711	105798	AACCTTGTGATTCGCCCCAC
107712	105799	TAACCTTGTGATTCGCCCCA
107713	105800	CTAACCTTGTGATTCGCCCC
107714	105801	CCTAACCTTGTGATTCGCCC
107715	105802	TCCTAACCTTGTGATTCGCC
107716	105803	CTCCTAACCTTGTGATTCGC
107717	105804	ACTCCTAACCTTGTGATTCG
107718	105805	AACTCCTAACCTTGTGATTC
107719	105806	GAACTCCTAACCTTGTGATT
107720	105807	CGAACTCCTAACCTTGTGAT
107721	105808	TCGAACTCCTAACCTTGTGA
107722	105809	CTCGAACTCCTAACCTTGTG
107723	105810	TCTCGAACTCCTAACCTTGT
107724	105811	GTCTCGAACTCCTAACCTTG
107725	105812	GGTCTCGAACTCCTAACCTT
107726	105813	TGGTCTCGAACTCCTAACCT
107727	105814	CTGGTCTCGAACTCCTAACC
107728	105815	GCTGGTCTCGAACTCCTAAC
107729	105816	GGCTGGTCTCGAACTCCTAA
107730	105817	AGGCTGGTCTCGAACTCCTA

9437	7524	TGTAATCCCAGCACTTTGGG
9438	7525	CTGTAATCCCAGCACTTTGG
9439	7526	CCTGTAATCCCAGCACTTTG
9440	7527	GCCTGTAATCCCAGCACTTT
9441	7528	CGCCTGTAATCCCAGCACTT
9442	7529	ACGCCTGTAATCCCAGCACT
9443	7530	CACGCCTGTAATCCCAGCAC
9444	7531	TCACGCCTGTAATCCCAGCA
9445	7532	CTCACGCCTGTAATCCCAGC
9446	7533	GCTCACGCCTGTAATCCCAG
9447	7534	GGCTCACGCCTGTAATCCCA
9448	7535	TGGCTCACGCCTGTAATCCC
9449	7536	GTGGCTCACGCCTGTAATCC
9450	7537	GGTGGCTCACGCCTGTAATC
9451	7538	GGGTGGCTCACGCCTGTAAT
9452	7539	GGGGTGGCTCACGCCTGTAA
9453	7540	GGGGGTGGCTCACGCCTGTA
9454	7541	CGGGGGTGGCTCACGCCTGT
9455	7542	GCGGGGGTGGCTCACGCCTG
9456	7543	GGCGGGGGTGGCTCACGCCT
9457	7544	GGGCGGGGGTGGCTCACGCC
9458	7545	TGGGCGGGGGTGGCTCACGC
9459	7546	CTGGGCGGGGGTGGCTCACG
9460	7547	GCTGGGCGGGGGTGGCTCAC
9461	7548	GGCTGGGCGGGGGTGGCTCA
9462	7549	AGGCTGGGCGGGGGTGGCTC
9463	7550	GAGGCTGGGCGGGGGTGGCT
9464	7551	TGAGGCTGGGCGGGGGTGGC
9465	7552	ATGAGGCTGGGCGGGGGTGG
9466	7553	CATGAGGCTGGGCGGGGGTG
9467	7554	TCATGAGGCTGGGCGGGGGT
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9469	7556	GCTCATGAGGCTGGGCGGGG
9470	7557	AGCTCATGAGGCTGGGCGGG
9471	7558	TAGCTCATGAGGCTGGGCGG
9472	7559	TTAGCTCATGAGGCTGGGCG
9473	7560	CTTAGCTCATGAGGCTGGGC
9474	7561	CCTTAGCTCATGAGGCTGGG
9475	7562	ACCTTAGCTCATGAGGCTGG
9476	7563	CACCTTAGCTCATGAGGCTG
9477	7564	ACACCTTAGCTCATGAGGCT
9478	7565	AACACCTTAGCTCATGAGGC
9479	7566	AAACACCTTAGCTCATGAGG
9480	7567	AAAACACCTTAGCTCATGAG
9481	7568	AAAAACACCTTAGCTCATGA
9482	7569	AAAAAACACCTTAGCTCATG
9483	7570	AAAAAAACACCTTAGCTCAT
9484	7571	AAAAAAAACACCTTAGCTCA
9485	7572	AAAAAAAAACACCTTAGCTC
9486	7573	AAAAAAAAAACACCTTAGCT
9487	7574	AAAAAAAAAAACACCTTAGC
9488	7575	AAAAAAAAAAAACACCTTAG
9489	7576	AAAAAAAAAAAAACACCTTA
9490	7577	AAAAAAAAAAAAAACACCTT
9491	7578	CAAAAAAAAAAAAAACACCT
9492	7579	TCAAAAAAAAAAAAAACACC
9493	7580	CTCAAAAAAAAAAAAAACAC
9494	7581	TCTCAAAAAAAAAAAAAACA
9495	7582	GTCTCAAAAAAAAAAAAAAC
9496	7583	TGTCTCAAAAAAAAAAAAAA
9497	7584	CTGTCTCAAAAAAAAAAAAA
9498	7585	ACTGTCTCAAAAAAAAAAAA
9499	7586	AACTGTCTCAAAAAAAAAAA
9500	7587	AAACTGTCTCAAAAAAAAAA
9501	7588	AAAACTGTCTCAAAAAAAAA
9502	7589	CAAAACTGTCTCAAAAAAAA
9503	7590	GCAAAACTGTCTCAAAAAAA
9504	7591	AGCAAAACTGTCTCAAAAAA
9505	7592	GAGCAAAACTGTCTCAAAAA
9506	7593	AGAGCAAAACTGTCTCAAAA
9507	7594	AAGAGCAAAACTGTCTCAAA

58584	56671	TAATAAATGGAAGATGACCA
58585	56672	TTAATAAATGGAAGATGACC
58586	56673	TTTAATAAATGGAAGATGAC
58587	56674	CTTTAATAAATGGAAGATGA
58588	56675	ACTTTAATAAATGGAAGATG
58589	56676	AACTTTAATAAATGGAAGAT
58590	56677	TAACTTTAATAAATGGAAGA
58591	56678	GTAACTTTAATAAATGGAAG
58592	56679	TGTAACTTTAATAAATGGAA
58593	56680	ATGTAACTTTAATAAATGGA
58594	56681	CATGTAACTTTAATAAATGG
58595	56682	ACATGTAACTTTAATAAATG
58596	56683	AACATGTAACTTTAATAAAT
58597	56684	AAACATGTAACTTTAATAAA
58598	56685	AAAACATGTAACTTTAATAA
58599	56686	TAAAACATGTAACTTTAATA
58600	56687	ATAAAACATGTAACTTTAAT
58601	56688	TATAAAACATGTAACTTTAA
58602	56689	TTATAAAACATGTAACTTTA
58603	56690	ATTATAAAACATGTAACTTT
58604	56691	AATTATAAAACATGTAACTT
58605	56692	AAATTATAAAACATGTAACT
58606	56693	AAAATTATAAAACATGTAAC
58607	56694	AAAAATTATAAAACATGTAA
58608	56695	TAAAAATTATAAAACATGTA
58609	56696	CTAAAAATTATAAAACATGT
58610	56697	TCTAAAAATTATAAAACATG
58611	56698	CTCTAAAAATTATAAAACAT
58612	56699	ACTCTAAAAATTATAAAACA
58613	56700	TACTCTAAAAATTATAAAAC
58614	56701	ATACTCTAAAAATTATAAAA
58615	56702	TATACTCTAAAAATTATAAA
58616	56703	ATATACTCTAAAAATTATAA
58617	56704	TATATACTCTAAAAATTATA
58618	56705	CTATATACTCTAAAAATTAT
58619	56706	TCTATATACTCTAAAAATTA
58620	56707	TTCTATATACTCTAAAAATT
58621	56708	TTTCTATATACTCTAAAAAT
58622	56709	ATTTCTATATACTCTAAAAA
58623	56710	AATTTCTATATACTCTAAAA
58624	56711	GAATTTCTATATACTCTAAA
58625	56712	AGAATTTCTATATACTCTAA
58626	56713	GAGAATTTCTATATACTCTA
58627	56714	AGAGAATTTCTATATACTCT
58628	56715	TAGAGAATTTCTATATACTC
58629	56716	GTAGAGAATTTCTATATACT
58630	56717	GGTAGAGAATTTCTATATAC
58631	56718	GGGTAGAGAATTTCTATATA
58632	56719	AGGGTAGAGAATTTCTATAT
58633	56720	TAGGGTAGAGAATTTCTATA
58634	56721	ATAGGGTAGAGAATTTCTAT
58635	56722	GATAGGGTAGAGAATTTCTA
58636	56723	TGATAGGGTAGAGAATTTCT
58637	56724	ATGATAGGGTAGAGAATTTC
58638	56725	CATGATAGGGTAGAGAATTT
58639	56726	ACATGATAGGGTAGAGAATT
58640	56727	AACATGATAGGGTAGAGAAT
58641	56728	AAACATGATAGGGTAGAGAA
58642	56729	CAAACATGATAGGGTAGAGA
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58644	56731	GGCAAACATGATAGGGTAGA
58645	56732	TGGCAAACATGATAGGGTAG
58646	56733	TTGGCAAACATGATAGGGTA
58647	56734	TTTGGCAAACATGATAGGGT
58648	56735	CTTTGGCAAACATGATAGGG
58649	56736	ACTTTGGCAAACATGATAGG
58650	56737	GACTTTGGCAAACATGATAG
58651	56738	TGACTTTGGCAAACATGATA
58652	56739	CTGACTTTGGCAAACATGAT
58653	56740	TCTGACTTTGGCAAACATGA
58654	56741	TTCTGACTTTGGCAAACATG

107731	105818	CAGGCTGGTCTCGAACTCCT
107732	105819	TCAGGCTGGTCTCGAACTCC
107733	105820	GTCAGGCTGGTCTCGAACTC
107734	105821	GGTCAGGCTGGTCTCGAACT
107735	105822	TGGTCAGGCTGGTCTCGAAC
107736	105823	TTGGTCAGGCTGGTCTCGAA
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107738	105825	CGTTGGTCAGGCTGGTCTCG
107739	105826	ACGTTGGTCAGGCTGGTCTC
107740	105827	CACGTTGGTCAGGCTGGTCT
107741	105828	CCACGTTGGTCAGGCTGGTC
107742	105829	ACCACGTTGGTCAGGCTGGT
107743	105830	CACCACGTTGGTCAGGCTGG
107744	105831	TCACCACGTTGGTCAGGCTG
107745	105832	TTCACCACGTTGGTCAGGCT
107746	105833	TTTCACCACGTTGGTCAGGC
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107749	105836	GAGTTTCACCACGTTGGTCA
107750	105837	AGAGTTTCACCACGTTGGTC
107751	105838	CAGAGTTTCACCACGTTGGT
107752	105839	ACAGAGTTTCACCACGTTGG
107753	105840	GACAGAGTTTCACCACGTTG
107754	105841	AGACAGAGTTTCACCACGTT
107755	105842	GAGACAGAGTTTCACCACGT
107756	105843	AGAGACAGAGTTTCACCACG
107757	105844	TAGAGACAGAGTTTCACCAC
107758	105845	GTAGAGACAGAGTTTCACCA
107759	105846	AGTAGAGACAGAGTTTCACC
107760	105847	TAGTAGAGACAGAGTTTCAC
107761	105848	TTAGTAGAGACAGAGTTTCA
107762	105849	TTTAGTAGAGACAGAGTTTC
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107765	105852	ATTTTTAGTAGAGACAGAGT
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107767	105854	GTATTTTTAGTAGAGACAGA
107768	105855	TGTATTTTTAGTAGAGACAG
107769	105856	TTGTATTTTTAGTAGAGACA
107770	105857	TTTGTATTTTTAGTAGAGAC
107771	105858	TTTTGTATTTTTAGTAGAGA
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107773	105860	ATTTTTGTATTTTTAGTAGA
107774	105861	AATTTTTGTATTTTTAGTAG
107775	105862	TAATTTTTGTATTTTTAGTA
107776	105863	CTAATTTTTGTATTTTTAGT
107777	105864	GCTAATTTTTGTATTTTTAG
107778	105865	GGCTAATTTTTGTATTTTTA
107779	105866	TGGCTAATTTTTGTATTTTT
107780	105867	CTGGCTAATTTTTGTATTTT
107781	105868	CCTGGCTAATTTTTGTATTT
107782	105869	GCCTGGCTAATTTTTGTATT
107783	105870	CGCCTGGCTAATTTTTGTAT
107784	105871	ACGCCTGGCTAATTTTTGTA
107785	105872	CACGCCTGGCTAATTTTTGT
107786	105873	CCACGCCTGGCTAATTTTTG
107787	105874	ACCACGCCTGGCTAATTTTT
107788	105875	CACCACGCCTGGCTAATTTT
107789	105876	CCACCACGCCTGGCTAATTT
107790	105877	GCCACCACGCCTGGCTAATT
107791	105878	TGCCACCACGCCTGGCTAAT
107792	105879	GTGCCACCACGCCTGGCTAA
107793	105880	CGTGCCACCACGCCTGGCTA
107794	105881	GCGTGCCACCACGCCTGGCT
107795	105882	TGCGTGCCACCACGCCTGGC
107796	105883	GTGCGTGCCACCACGCCTGG
107797	105884	GGTGCGTGCCACCACGCCTG
107798	105885	AGGTGCGTGCCACCACGCCT
107799	105886	CAGGTGCGTGCCACCACGCC
107800	105887	ACAGGTGCGTGCCACCACGC
107801	105888	TACAGGTGCGTGCCACCACG

9508	7595	AAAGAGCAAAACTGTCTCAA
9509	7596	GAAAGAGCAAAACTGTCTCA
9510	7597	GGAAAGAGCAAAACTGTCTC
9511	7598	GGGAAAGAGCAAAACTGTCT
9512	7599	TGGGAAAGAGCAAAACTGTC
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9515	7602	GCCTGGGAAAGAGCAAAACT
9516	7603	AGCCTGGGAAAGAGCAAAAC
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9519	7606	TCCAGCCTGGGAAAGAGCAA
9520	7607	CTCCAGCCTGGGAAAGAGCA
9521	7608	ACTCCAGCCTGGGAAAGAGC
9522	7609	CACTCCAGCCTGGGAAAGAG
9523	7610	GCACTCCAGCCTGGGAAAGA
9524	7611	TGCACTCCAGCCTGGGAAAG
9525	7612	CTGCACTCCAGCCTGGGAAA
9526	7613	ACTGCACTCCAGCCTGGGAA
9527	7614	CACTGCACTCCAGCCTGGGA
9528	7615	CCACTGCACTCCAGCCTGGG
9529	7616	ACCACTGCACTCCAGCCTGG
9530	7617	CACCACTGCACTCCAGCCTG
9531	7618	GCACCACTGCACTCCAGCCT
9532	7619	TGCACCACTGCACTCCAGCC
9533	7620	TTGCACCACTGCACTCCAGC
9534	7621	ATTGCACCACTGCACTCCAG
9535	7622	GATTGCACCACTGCACTCCA
9536	7623	AGATTGCACCACTGCACTCC
9537	7624	GAGATTGCACCACTGCACTC
9538	7625	TGAGATTGCACCACTGCACT
9539	7626	CTGAGATTGCACCACTGCAC
9540	7627	GCTGAGATTGCACCACTGCA
9541	7628	AGCTGAGATTGCACCACTGC
9542	7629	GAGCTGAGATTGCACCACTG
9543	7630	TGAGCTGAGATTGCACCACT
9544	7631	GTGAGCTGAGATTGCACCAC
9545	7632	AGTGAGCTGAGATTGCACCA
9546	7633	CAGTGAGCTGAGATTGCACC
9547	7634	GCAGTGAGCTGAGATTGCAC
9548	7635	TGCAGTGAGCTGAGATTGCA
9549	7636	TTGCAGTGAGCTGAGATTGC
9550	7637	GTTGCAGTGAGCTGAGATTG
9551	7638	GGTTGCAGTGAGCTGAGATT
9552	7639	AGGTTGCAGTGAGCTGAGAT
9553	7640	GAGGTTGCAGTGAGCTGAGA
9554	7641	AGAGGTTGCAGTGAGCTGAG
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9556	7643	ACAGAGGTTGCAGTGAGCTG
9557	7644	AACAGAGGTTGCAGTGAGCT
9558	7645	AAACAGAGGTTGCAGTGAGC
9559	7646	GAAACAGAGGTTGCAGTGAG
9560	7647	GGAAACAGAGGTTGCAGTGA
9561	7648	GGGAAACAGAGGTTGCAGTG
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9564	7651	CCCGGGAAACAGAGGTTGCA
9565	7652	ACCCGGGAAACAGAGGTTGC
9566	7653	AACCCGGGAAACAGAGGTTG
9567	7654	GAACCCGGGAAACAGAGGTT
9568	7655	TGAACCCGGGAAACAGAGGT
9569	7656	TTGAACCCGGGAAACAGAGG
9570	7657	CTTGAACCCGGGAAACAGAG
9571	7658	GCTTGAACCCGGGAAACAGA
9572	7659	CGCTTGAACCCGGGAAACAG
9573	7660	TCGCTTGAACCCGGGAAACA
9574	7661	ATCGCTTGAACCCGGGAAAC
9575	7662	AATCGCTTGAACCCGGGAAA
9576	7663	GAATCGCTTGAACCCGGGAA
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9578	7665	GAGAATCGCTTGAACCCGGG

58655	56742	GTTCTGACTTTGGCAAACAT
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58659	56746	TATTGTTCTGACTTTGGCAA
58660	56747	TTATTGTTCTGACTTTGGCA
58661	56748	GTTATTGTTCTGACTTTGGC
58662	56749	AGTTATTGTTCTGACTTTGG
58663	56750	AAGTTATTGTTCTGACTTTG
58664	56751	GAAGTTATTGTTCTGACTTT
58665	56752	TGAAGTTATTGTTCTGACTT
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58669	56756	TAAATGAAGTTATTGTTCTG
58670	56757	ATAAATGAAGTTATTGTTCT
58671	56758	AATAAATGAAGTTATTGTTC
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58673	56760	TTAATAAATGAAGTTATTGT
58674	56761	TTTAATAAATGAAGTTATTG
58675	56762	ATTTAATAAATGAAGTTATT
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58678	56765	TATATTTAATAAATGAAGTT
58679	56766	TTATATTTAATAAATGAAGT
58680	56767	TTTATATTTAATAAATGAAG
58681	56768	TTTTATATTTAATAAATGAA
58682	56769	TTTTTATATTTAATAAATGA
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58684	56771	TTTTTTTATATTTAATAAAT
58685	56772	TTTTTTTTATATTTAATAAA
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58692	56779	GTTTTTATTTTTTTTATATT
58693	56780	GGTTTTTATTTTTTTTATAT
58694	56781	AGGTTTTTATTTTTTTTATA
58695	56782	GAGGTTTTTATTTTTTTTAT
58696	56783	AGAGGTTTTTATTTTTTTTA
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58700	56787	TGCTAGAGGTTTTTATTTTT
58701	56788	ATGCTAGAGGTTTTTATTTT
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58708	56795	CTATTTTATGCTAGAGGTTT
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58713	56800	AAATTCTATTTTATGCTAGA
58714	56801	AAAATTCTATTTTATGCTAG
58715	56802	TAAAATTCTATTTTATGCTA
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58717	56804	AATAAAATTCTATTTTATGC
58718	56805	AAATAAAATTCTATTTTATG
58719	56806	CAAATAAAATTCTATTTTAT
58720	56807	CCAAATAAAATTCTATTTTA
58721	56808	TCCAAATAAAATTCTATTTT
58722	56809	GTCCAAATAAAATTCTATTT
58723	56810	TGTCCAAATAAAATTCTATT
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107802	105889	TTACAGGTGCGTGCCACCAC
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107806	105893	AGGATTACAGGTGCGTGCCA
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107808	105895	CTAGGATTACAGGTGCGTGC
107809	105896	GCTAGGATTACAGGTGCGTG
107810	105897	AGCTAGGATTACAGGTGCGT
107811	105898	TAGCTAGGATTACAGGTGCG
107812	105899	GTAGCTAGGATTACAGGTGC
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107814	105901	GAGTAGCTAGGATTACAGGT
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107823	105910	CAGCCTCCTGAGTAGCTAGG
107824	105911	TCAGCCTCCTGAGTAGCTAG
107825	105912	CTCAGCCTCCTGAGTAGCTA
107826	105913	CCTCAGCCTCCTGAGTAGCT
107827	105914	GCCTCAGCCTCCTGAGTAGC
107828	105915	TGCCTCAGCCTCCTGAGTAG
107829	105916	CTGCCTCAGCCTCCTGAGTA
107830	105917	CCTGCCTCAGCCTCCTGAGT
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107832	105919	CTCCTGCCTCAGCCTCCTGA
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107842	105929	TCAAGCGATTCTCCTGCCTC
107843	105930	TTCAAGCGATTCTCCTGCCT
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107845	105932	GGTTCAAGCGATTCTCCTGC
107846	105933	AGGTTCAAGCGATTCTCCTG
107847	105934	CAGGTTCAAGCGATTCTCCT
107848	105935	CCAGGTTCAAGCGATTCTCC
107849	105936	CCCAGGTTCAAGCGATTCTC
107850	105937	TCCCAGGTTCAAGCGATTCT
107851	105938	CTCCCAGGTTCAAGCGATTC
107852	105939	CCTCCCAGGTTCAAGCGATT
107853	105940	GCCTCCCAGGTTCAAGCGAT
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107855	105942	CCGCCTCCCAGGTTCAAGCG
107856	105943	TCCGCCTCCCAGGTTCAAGC
107857	105944	CTCCGCCTCCCAGGTTCAAG
107858	105945	CCTCCGCCTCCCAGGTTCAA
107859	105946	ACCTCCGCCTCCCAGGTTCA
107860	105947	AACCTCCGCCTCCCAGGTTC
107861	105948	CAACCTCCGCCTCCCAGGTT
107862	105949	GCAACCTCCGCCTCCCAGGT
107863	105950	TGCAACCTCCGCCTCCCAGG
107864	105951	CTGCAACCTCCGCCTCCCAG
107865	105952	ACTGCAACCTCCGCCTCCCA
107866	105953	AACTGCAACCTCCGCCTCCC
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107868	105955	CTAACTGCAACCTCCGCCTC
107869	105956	GCTAACTGCAACCTCCGCCT
107870	105957	GGCTAACTGCAACCTCCGCC
107871	105958	CGGCTAACTGCAACCTCCGC
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9579	7666	GGAGAATCGCTTGAACCCGG
9580	7667	AGGAGAATCGCTTGAACCCG
9581	7668	CAGGAGAATCGCTTGAACCC
9582	7669	GCAGGAGAATCGCTTGAACC
9583	7670	GGCAGGAGAATCGCTTGAAC
9584	7671	AGGCAGGAGAATCGCTTGAA
9585	7672	GAGGCAGGAGAATCGCTTGA
9586	7673	TGAGGCAGGAGAATCGCTTG
9587	7674	CTGAGGCAGGAGAATCGCTT
9588	7675	GCTGAGGCAGGAGAATCGCT
9589	7676	GGCTGAGGCAGGAGAATCGC
9590	7677	AGGCTGAGGCAGGAGAATCG
9591	7678	AAGGCTGAGGCAGGAGAATC
9592	7679	GAAGGCTGAGGCAGGAGAAT
9593	7680	AGAAGGCTGAGGCAGGAGAA
9594	7681	CAGAAGGCTGAGGCAGGAGA
9595	7682	TCAGAAGGCTGAGGCAGGAG
9596	7683	CTCAGAAGGCTGAGGCAGGA
9597	7684	ACTCAGAAGGCTGAGGCAGG
9598	7685	TACTCAGAAGGCTGAGGCAG
9599	7686	CTACTCAGAAGGCTGAGGCA
9600	7687	GCTACTCAGAAGGCTGAGGC
9601	7688	AGCTACTCAGAAGGCTGAGG
9602	7689	CAGCTACTCAGAAGGCTGAG
9603	7690	TCAGCTACTCAGAAGGCTGA
9604	7691	CTCAGCTACTCAGAAGGCTG
9605	7692	TCTCAGCTACTCAGAAGGCT
9606	7693	ATCTCAGCTACTCAGAAGGC
9607	7694	AATCTCAGCTACTCAGAAGG
9608	7695	TAATCTCAGCTACTCAGAAG
9609	7696	GTAATCTCAGCTACTCAGAA
9610	7697	TGTAATCTCAGCTACTCAGA
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9612	7699	CCTGTAATCTCAGCTACTCA
9613	7700	ACCTGTAATCTCAGCTACTC
9614	7701	CACCTGTAATCTCAGCTACT
9615	7702	GCACCTGTAATCTCAGCTAC
9616	7703	GGCACCTGTAATCTCAGCTA
9617	7704	AGGCACCTGTAATCTCAGCT
9618	7705	CAGGCACCTGTAATCTCAGC
9619	7706	GCAGGCACCTGTAATCTCAG
9620	7707	AGCAGGCACCTGTAATCTCA
9621	7708	TAGCAGGCACCTGTAATCTC
9622	7709	GTAGCAGGCACCTGTAATCT
9623	7710	GGTAGCAGGCACCTGTAATC
9624	7711	GGGTAGCAGGCACCTGTAAT
9625	7712	GGGGTAGCAGGCACCTGTAA
9626	7713	TGGGGTAGCAGGCACCTGTA
9627	7714	GTGGGGTAGCAGGCACCTGT
9628	7715	AGTGGGGTAGCAGGCACCTG
9629	7716	GAGTGGGGTAGCAGGCACCT
9630	7717	TGAGTGGGGTAGCAGGCACC
9631	7718	CTGAGTGGGGTAGCAGGCAC
9632	7719	GCTGAGTGGGGTAGCAGGCA
9633	7720	AGCTGAGTGGGGTAGCAGGC
9634	7721	TAGCTGAGTGGGGTAGCAGG
9635	7722	TTAGCTGAGTGGGGTAGCAG
9636	7723	ATTAGCTGAGTGGGGTAGCA
9637	7724	AATTAGCTGAGTGGGGTAGC
9638	7725	AAATTAGCTGAGTGGGGTAG
9639	7726	AAAATTAGCTGAGTGGGGTA
9640	7727	AAAAATTAGCTGAGTGGGGT
9641	7728	CAAAAATTAGCTGAGTGGGG
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9644	7731	ATACAAAAATTAGCTGAGTG
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9646	7733	AAATACAAAAATTAGCTGAG
9647	7734	AAAATACAAAAATTAGCTGA
9648	7735	AAAAATACAAAAATTAGCTG
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58726	56813	GTTTGTCCAAATAAAATTCT
58727	56814	CGTTTGTCCAAATAAAATTC
58728	56815	TCGTTTGTCCAAATAAAATT
58729	56816	ATCGTTTGTCCAAATAAAAT
58730	56817	TATCGTTTGTCCAAATAAAA
58731	56818	TTATCGTTTGTCCAAATAAA
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58733	56820	TTTTATCGTTTGTCCAAATA
58734	56821	TTTTTATCGTTTGTCCAAAT
58735	56822	TTTTTTATCGTTTGTCCAAA
58736	56823	TTTTTTTATCGTTTGTCCAA
58737	56824	ATTTTTTTATCGTTTGTCCA
58738	56825	TATTTTTTTATCGTTTGTCC
58739	56826	GTATTTTTTTATCGTTTGTC
58740	56827	AGTATTTTTTTATCGTTTGT
58741	56828	CAGTATTTTTTTATCGTTTG
58742	56829	ACAGTATTTTTTTATCGTTT
58743	56830	CACAGTATTTTTTTATCGTT
58744	56831	ACACAGTATTTTTTTATCGT
58745	56832	CACACAGTATTTTTTTATCG
58746	56833	CCACACAGTATTTTTTTATC
58747	56834	ACCACACAGTATTTTTTTAT
58748	56835	TACCACACAGTATTTTTTTA
58749	56836	GTACCACACAGTATTTTTTT
58750	56837	AGTACCACACAGTATTTTTT
58751	56838	TAGTACCACACAGTATTTTT
58752	56839	CTAGTACCACACAGTATTTT
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58754	56841	TACTAGTACCACACAGTATT
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58757	56844	TCTTACTAGTACCACACAGT
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58759	56846	ACTCTTACTAGTACCACACA
58760	56847	TACTCTTACTAGTACCACAC
58761	56848	TTACTCTTACTAGTACCACA
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58763	56850	CCTTACTCTTACTAGTACCA
58764	56851	ACCTTACTCTTACTAGTACC
58765	56852	AACCTTACTCTTACTAGTAC
58766	56853	CAACCTTACTCTTACTAGTA
58767	56854	TCAACCTTACTCTTACTAGT
58768	56855	ATCAACCTTACTCTTACTAG
58769	56856	AATCAACCTTACTCTTACTA
58770	56857	GAATCAACCTTACTCTTACT
58771	56858	TGAATCAACCTTACTCTTAC
58772	56859	TTGAATCAACCTTACTCTTA
58773	56860	CTTGAATCAACCTTACTCTT
58774	56861	TCTTGAATCAACCTTACTCT
58775	56862	ATCTTGAATCAACCTTACTC
58776	56863	TATCTTGAATCAACCTTACT
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58778	56865	TGTATCTTGAATCAACCTTA
58779	56866	ATGTATCTTGAATCAACCTT
58780	56867	CATGTATCTTGAATCAACCT
58781	56868	CCATGTATCTTGAATCAACC
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58783	56870	TCCCATGTATCTTGAATCAA
58784	56871	CTCCCATGTATCTTGAATCA
58785	56872	GCTCCCATGTATCTTGAATC
58786	56873	TGCTCCCATGTATCTTGAAT
58787	56874	CTGCTCCCATGTATCTTGAA
58788	56875	TCTGCTCCCATGTATCTTGA
58789	56876	TTCTGCTCCCATGTATCTTG
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58792	56879	GGATTCTGCTCCCATGTATC
58793	56880	TGGATTCTGCTCCCATGTAT
58794	56881	TTGGATTCTGCTCCCATGTA
58795	56882	TTTGGATTCTGCTCCCATGT
58796	56883	CTTTGGATTCTGCTCCCATG

107873	105960	CTCGGCTAACTGCAACCTCC
107874	105961	TCTCGGCTAACTGCAACCTC
107875	105962	ATCTCGGCTAACTGCAACCT
107876	105963	GATCTCGGCTAACTGCAACC
107877	105964	CGATCTCGGCTAACTGCAAC
107878	105965	GCGATCTCGGCTAACTGCAA
107879	105966	CGCGATCTCGGCTAACTGCA
107880	105967	GCGCGATCTCGGCTAACTGC
107881	105968	GGCGCGATCTCGGCTAACTG
107882	105969	TGGCGCGATCTCGGCTAACT
107883	105970	GTGGCGCGATCTCGGCTAAC
107884	105971	AGTGGCGCGATCTCGGCTAA
107885	105972	CAGTGGCGCGATCTCGGCTA
107886	105973	GCAGTGGCGCGATCTCGGCT
107887	105974	GGCAGTGGCGCGATCTCGGC
107888	105975	CGGCAGTGGCGCGATCTCGG
107889	105976	ACGGCAGTGGCGCGATCTCG
107890	105977	GACGGCAGTGGCGCGATCTC
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107893	105980	CTGGACGGCAGTGGCGCGAT
107894	105981	GCTGGACGGCAGTGGCGCGA
107895	105982	GGCTGGACGGCAGTGGCGCG
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107898	105985	CCAGGCTGGACGGCAGTGGC
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107919	106006	GACAGAGTCTTGCTCTGCTG
107920	106007	AGACAGAGTCTTGCTCTGCT
107921	106008	GAGACAGAGTCTTGCTCTGC
107922	106009	TGAGACAGAGTCTTGCTCTG
107923	106010	GTGAGACAGAGTCTTGCTCT
107924	106011	TGTGAGACAGAGTCTTGCTC
107925	106012	TTGTGAGACAGAGTCTTGCT
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107927	106014	TTTTGTGAGACAGAGTCTTG
107928	106015	TTTTTGTGAGACAGAGTCTT
107929	106016	TTTTTTGTGAGACAGAGTCT
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107931	106018	TTTTTTTTGTGAGACAGAGT
107932	106019	TTTTTTTTTGTGAGACAGAG
107933	106020	TTTTTTTTTTGTGAGACAGA
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107935	106022	TTTTTTTTTTTTGTGAGACA
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107939	106026	AATTTTTTTTTTTTTTTGTGA
107940	106027	CAATTTTTTTTTTTTTTTGTG
107941	106028	ACAATTTTTTTTTTTTTTTGT
107942	106029	TACAATTTTTTTTTTTTTTTG
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9650	7737	CTAAAAATACAAAAATTAGC
9651	7738	GCTAAAAATACAAAAATTAG
9652	7739	TGCTAAAAATACAAAAATTA
9653	7740	CTGCTAAAAATACAAAAATT
9654	7741	TCTGCTAAAAATACAAAAAT
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9656	7743	TCTCTGCTAAAAATACAAAA
9657	7744	GTCTCTGCTAAAAATACAAA
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9659	7746	CTGTCTCTGCTAAAAATACA
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9661	7748	CCCTGTCTCTGCTAAAAATA
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9663	7750	AACCCTGTCTCTGCTAAAAA
9664	7751	AAACCCTGTCTCTGCTAAAA
9665	7752	GAAACCCTGTCTCTGCTAAA
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9670	7757	ATGGTGAAACCCTGTCTCTG
9671	7758	CATGGTGAAACCCTGTCTCT
9672	7759	ACATGGTGAAACCCTGTCTC
9673	7760	AACATGGTGAAACCCTGTCT
9674	7761	CAACATGGTGAAACCCTGTC
9675	7762	CCAACATGGTGAAACCCTGT
9676	7763	ACCAACATGGTGAAACCCTG
9677	7764	AACCAACATGGTGAAACCCT
9678	7765	TAACCAACATGGTGAAACCC
9679	7766	CTAACCAACATGGTGAAACC
9680	7767	CCTAACCAACATGGTGAAAC
9681	7768	GCCTAACCAACATGGTGAAA
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9683	7770	GAGCCTAACCAACATGGTGA
9684	7771	TGAGCCTAACCAACATGGTG
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9692	7779	GTTCGAGATGAGCCTAACCA
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9720	7807	AAGGCAGGTGGATCGCTTAA

58797	56884	ACTTTGGATTCTGCTCCCAT
58798	56885	CACTTTGGATTCTGCTCCCA
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58800	56887	TACACTTTGGATTCTGCTCC
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58820	56907	CACTGCACCTGGCCTATTTC
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58824	56911	GAGCCACTGCACCTGGCCTA
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107944	106031	ACTACAATTTTTTTTTTTTT
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107947	106034	AGAACTACAATTTTTTTTTT
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107949	106036	TAAGAACTACAATTTTTTTT
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107963	106050	GAACCTTTCAAAAATAAGAA
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107982	106069	AGCAGGAAGAATAAAAAATG
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9721	7808	CAAGGCAGGTGGATCGCTTA
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9723	7810	GCCAAGGCAGGTGGATCGCT
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9735	7822	GCACTTTGGGAGGCCAAGGC
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9738	7825	CCAGCACTTTGGGAGGCCAA
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9741	7828	ATCCCAGCACTTTGGGAGGC
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9746	7833	CTATAATCCCAGCACTTTGG
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9759	7846	CGGTGGCTCATGCCTATAAT
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9765	7852	TGCGCACGGTGGCTCATGCC
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9768	7855	GGCTGCGCACGGTGGCTCAT
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58868	56955	CATCCTCCCGCCTCAGCCTC
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58872	56959	AACTCATCCTCCCGCCTCAG
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58882	56969	TGAACTCCTGAACTCATCCT
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58900	56987	AGTTGCCAAGGCGAGTCTTG
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58921	57008	TGTAGAGATGGGGTTTTGCC
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58923	57010	TTTGTAGAGATGGGGTTTTG
58924	57011	TTTTGTAGAGATGGGGTTTT
58925	57012	TTTTTGTAGAGATGGGGTTT
58926	57013	CTTTTTGTAGAGATGGGGTT
58927	57014	ACTTTTTGTAGAGATGGGGT
58928	57015	TACTTTTTGTAGAGATGGGG
58929	57016	GTACTTTTTGTAGAGATGGG
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58933	57020	TTTTGTACTTTTTGTAGAGA
58934	57021	TTTTTGTACTTTTTGTAGAG
58935	57022	ATTTTTGTACTTTTTGTAGA
58936	57023	AATTTTTGTACTTTTTGTAG
58937	57024	TAATTTTTGTACTTTTTGTA
58938	57025	CTAATTTTTGTACTTTTTGT

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108016	106103	TAATTGTGGTGTATAAACTA
108017	106104	GTAATTGTGGTGTATAAACT
108018	106105	TGTAATTGTGGTGTATAAAC
108019	106106	CTGTAATTGTGGTGTATAAA
108020	106107	ACTGTAATTGTGGTGTATAA
108021	106108	CACTGTAATTGTGGTGTATA
108022	106109	ACACTGTAATTGTGGTGTAT
108023	106110	AACACTGTAATTGTGGTGTA
108024	106111	TAACACTGTAATTGTGGTGT
108025	106112	GTAACACTGTAATTGTGGTG
108026	106113	TGTAACACTGTAATTGTGGT
108027	106114	TTGTAACACTGTAATTGTGG
108028	106115	ATTGTAACACTGTAATTGTG
108029	106116	TATTGTAACACTGTAATTGT
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108032	106119	GAATATTGTAACACTGTAAT
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108034	106121	CAGAATATTGTAACACTGTA
108035	106122	ACAGAATATTGTAACACTGT
108036	106123	TACAGAATATTGTAACACTG
108037	106124	ATACAGAATATTGTAACACT
108038	106125	AATACAGAATATTGTAACAC
108039	106126	AAATACAGAATATTGTAACA
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108041	106128	AAAAATACAGAATATTGTAA
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108043	106130	AGAAAAATACAGAATATTGT
108044	106131	CAGAAAAATACAGAATATTG
108045	106132	ACAGAAAAATACAGAATATT
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108047	106134	ACACAGAAAAATACAGAATA
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108052	106139	CAAGTACACAGAAAAATACA
108053	106140	ACAAGTACACAGAAAAATAC
108054	106141	AACAAGTACACAGAAAAATA
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108060	106147	ACTGGTAACAAGTACACAGA
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108064	106151	ACTCACTGGTAACAAGTACA
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108082	106169	TCACCTGAAGGTGCAAAAAC
108083	106170	ATCACCTGAAGGTGCAAAAA
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108085	106172	AAATCACCTGAAGGTGCAAA

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9793	7880	TTACTGTTTTTTAAGAGACA
9794	7881	GTTACTGTTTTTTAAGAGAC
9795	7882	TGTTACTGTTTTTTAAGAGA
9796	7883	TTGTTACTGTTTTTTAAGAG
9797	7884	GTTGTTACTGTTTTTTAAGA
9798	7885	TGTTGTTACTGTTTTTTAAG
9799	7886	TTGTTGTTACTGTTTTTTAA
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9807	7894	TGTTGTTGTTGTTGTTACTG
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9813	7900	TTTTGTTGTTGTTGTTGTTG
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9815	7902	TTTTTTGTTGTTGTTGTTGT
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9827	7914	TAAGATTTAGGATTTTTTGT
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9835	7922	TCCATTTTTAAGATTTAGGA
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9847	7934	GAGTTTTTGCCTTCCATTTT
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9849	7936	TAGAGTTTTTGCCTTCCATT
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9857	7944	TCAAAGCTTAGAGTTTTTGC
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58944	57031	ACCCGGCTAATTTTTGTACT
58945	57032	CACCCGGCTAATTTTTGTAC
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58979	57066	ACCAAGTAGCTGGGTTTACA
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58985	57072	CAGCCCACCAAGTAGCTGGG
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108086	106173	TAAATCACCTGAAGGTGCAA
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108088	106175	AATAAATCACCTGAAGGTGC
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108092	106179	CAATAATAAATCACCTGAAG
108093	106180	ACAATAATAAATCACCTGAA
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108095	106182	AAACAATAATAAATCACCTG
108096	106183	CAAACAATAATAAATCACCT
108097	106184	ACAAACAATAATAAATCACC
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108099	106186	TAACAAACAATAATAAATCA
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108106	106193	AGGATGTTAACAAACAATAA
108107	106194	AAGGATGTTAACAAACAATA
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9865	7952	CTAATCTCTCAAAGCTTAGA
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9874	7961	GCAAGTCCCCTAATCTCTCA
9875	7962	GGCAAGTCCCCTAATCTCTC
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9877	7964	TGGGCAAGTCCCCTAATCTC
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59017	57104	TGACTTACTGGCTGCAAGTG
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59019	57106	CTTGACTTACTGGCTGCAAG
59020	57107	CCTTGACTTACTGGCTGCAA
59021	57108	GCCTTGACTTACTGGCTGCA
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108190	106277	CCACTGCACTCCAGGCTGGT
108191	106278	ACCACTGCACTCCAGGCTGG
108192	106279	CACCACTGCACTCCAGGCTG
108193	106280	GCACCACTGCACTCCAGGCT
108194	106281	GGCACCACTGCACTCCAGGC
108195	106282	TGGCACCACTGCACTCCAGG
108196	106283	ATGGCACCACTGCACTCCAG
108197	106284	GATGGCACCACTGCACTCCA
108198	106285	AGATGGCACCACTGCACTCC
108199	106286	AAGATGGCACCACTGCACTC
108200	106287	CAAGATGGCACCACTGCACT
108201	106288	CCAAGATGGCACCACTGCAC
108202	106289	GCCAAGATGGCACCACTGCA
108203	106290	AGCCAAGATGGCACCACTGC
108204	106291	GAGCCAAGATGGCACCACTG
108205	106292	TGAGCCAAGATGGCACCACT
108206	106293	GTGAGCCAAGATGGCACCAC
108207	106294	AGTGAGCCAAGATGGCACCA
108208	106295	TAGTGAGCCAAGATGGCACC
108209	106296	GTAGTGAGCCAAGATGGCAC
108210	106297	TGTAGTGAGCCAAGATGGCA
108211	106298	TTGTAGTGAGCCAAGATGGC
108212	106299	GTTGTAGTGAGCCAAGATGG
108213	106300	GGTTGTAGTGAGCCAAGATG
108214	106301	AGGTTGTAGTGAGCCAAGAT
108215	106302	GAGGTTGTAGTGAGCCAAGA
108216	106303	GGAGGTTGTAGTGAGCCAAG
108217	106304	TGGAGGTTGTAGTGAGCCAA
108218	106305	TTGGAGGTTGTAGTGAGCCA
108219	106306	GTTGGAGGTTGTAGTGAGCC
108220	106307	AGTTGGAGGTTGTAGTGAGC
108221	106308	GAGTTGGAGGTTGTAGTGAG
108222	106309	GGAGTTGGAGGTTGTAGTGA
108223	106310	GGGAGTTGGAGGTTGTAGTG
108224	106311	TGGGAGTTGGAGGTTGTAGT
108225	106312	CTGGGAGTTGGAGGTTGTAG
108226	106313	CCTGGGAGTTGGAGGTTGTA
108227	106314	ACCTGGGAGTTGGAGGTTGT

9934	8021	TGACTCTAAAAAAATAAATA
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9936	8023	CTTGACTCTAAAAAAATAAA
9937	8024	CCTTGACTCTAAAAAAATAA
9938	8025	ACCTTGACTCTAAAAAAATA
9939	8026	GACCTTGACTCTAAAAAAAT
9940	8027	AGACCTTGACTCTAAAAAAA
9941	8028	GAGACCTTGACTCTAAAAAA
9942	8029	GGAGACCTTGACTCTAAAAA
9943	8030	GGGAGACCTTGACTCTAAAA
9944	8031	AGGGAGACCTTGACTCTAAA
9945	8032	GAGGGAGACCTTGACTCTAA
9946	8033	AGAGGGAGACCTTGACTCTA
9947	8034	CAGAGGGAGACCTTGACTCT
9948	8035	ACAGAGGGAGACCTTGACTC
9949	8036	GACAGAGGGAGACCTTGACT
9950	8037	TGACAGAGGGAGACCTTGAC
9951	8038	GTGACAGAGGGAGACCTTGA
9952	8039	GGTGACAGAGGGAGACCTTG
9953	8040	GGGTGACAGAGGGAGACCTT
9954	8041	TGGGTGACAGAGGGAGACCT
9955	8042	CTGGGTGACAGAGGGAGACC
9956	8043	CCTGGGTGACAGAGGGAGAC
9957	8044	GCCTGGGTGACAGAGGGAGA
9958	8045	AGCCTGGGTGACAGAGGGAG
9959	8046	CAGCCTGGGTGACAGAGGGA
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9961	8048	TCCAGCCTGGGTGACAGAGG
9962	8049	CTCCAGCCTGGGTGACAGAG
9963	8050	ACTCCAGCCTGGGTGACAGA
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9965	8052	GCACTCCAGCCTGGGTGACA
9966	8053	TGCACTCCAGCCTGGGTGAC
9967	8054	CTGCACTCCAGCCTGGGTGA
9968	8055	GCTGCACTCCAGCCTGGGTG
9969	8056	GGCTGCACTCCAGCCTGGGT
9970	8057	AGGCTGCACTCCAGCCTGGG
9971	8058	GAGGCTGCACTCCAGCCTGG
9972	8059	TGAGGCTGCACTCCAGCCTG
9973	8060	TTGAGGCTGCACTCCAGCCT
9974	8061	ATTGAGGCTGCACTCCAGCC
9975	8062	GATTGAGGCTGCACTCCAGC
9976	8063	AGATTGAGGCTGCACTCCAG
9977	8064	TAGATTGAGGCTGCACTCCA
9978	8065	ATAGATTGAGGCTGCACTCC
9979	8066	CATAGATTGAGGCTGCACTC
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9981	8068	CCCATAGATTGAGGCTGCAC
9982	8069	CCCCATAGATTGAGGCTGCA
9983	8070	GCCCCATAGATTGAGGCTGC
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9985	8072	TGGCCCCATAGATTGAGGCT
9986	8073	TTGGCCCCATAGATTGAGGC
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9988	8075	GCTTGGCCCCATAGATTGAG
9989	8076	TGCTTGGCCCCATAGATTGA
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9993	8080	GAAATGCTTGGCCCCATAGA
9994	8081	AGAAATGCTTGGCCCCATAG
9995	8082	GAGAAATGCTTGGCCCCATA
9996	8083	GGAGAAATGCTTGGCCCCAT
9997	8084	AGGAGAAATGCTTGGCCCCA
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9999	8086	ACAGGAGAAATGCTTGGCCC
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10001	8088	AGACAGGAGAAATGCTTGGC
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59081	57168	GAGACAAGGTCTTGCTTGTC
59082	57169	TGAGACAAGGTCTTGCTTGT
59083	57170	TTGAGACAAGGTCTTGCTTG
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59086	57173	TTTTTGAGACAAGGTCTTGC
59087	57174	GTTTTTGAGACAAGGTCTTG
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59089	57176	TTGTTTTTGAGACAAGGTCT
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59095	57182	GCTGGTTTGTTTTTGAGACA
59096	57183	GGCTGGTTTGTTTTTGAGAC
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59098	57185	CTGGCTGGTTTGTTTTTGAG
59099	57186	CCTGGCTGGTTTGTTTTTGA
59100	57187	GCCTGGCTGGTTTGTTTTTG
59101	57188	CGCCTGGCTGGTTTGTTTTT
59102	57189	ACGCCTGGCTGGTTTGTTTT
59103	57190	CACGCCTGGCTGGTTTGTTT
59104	57191	CCACGCCTGGCTGGTTTGTT
59105	57192	GCCACGCCTGGCTGGTTTGT
59106	57193	CGCCACGCCTGGCTGGTTTG
59107	57194	CCGCCACGCCTGGCTGGTTT
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59109	57196	ATCCGCCACGCCTGGCTGGT
59110	57197	GATCCGCCACGCCTGGCTGG
59111	57198	TGATCCGCCACGCCTGGCTG
59112	57199	GTGATCCGCCACGCCTGGCT
59113	57200	GGTGATCCGCCACGCCTGGC
59114	57201	AGGTGATCCGCCACGCCTGG
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59121	57208	TTACCTCAGGTGATCCGCCA
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59128	57215	CAACTCCTTACCTCAGGTGA
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59130	57217	TCCAACTCCTTACCTCAGGT
59131	57218	CTCCAACTCCTTACCTCAGG
59132	57219	TCTCCAACTCCTTACCTCAG
59133	57220	GTCTCCAACTCCTTACCTCA
59134	57221	GGTCTCCAACTCCTTACCTC
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59137	57224	GCTGGTCTCCAACTCCTTAC
59138	57225	GGCTGGTCTCCAACTCCTTA
59139	57226	AGGCTGGTCTCCAACTCCTT
59140	57227	CAGGCTGGTCTCCAACTCCT
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59148	57235	ATGTCGGCCAGGCTGGTCTC
59149	57236	CATGTCGGCCAGGCTGGTCT
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59151	57238	GCCATGTCGGCCAGGCTGGT

108228	106315	AACCTGGGAGTTGGAGGTTG
108229	106316	GAACCTGGGAGTTGGAGGTT
108230	106317	TGAACCTGGGAGTTGGAGGT
108231	106318	TTGAACCTGGGAGTTGGAGG
108232	106319	CTTGAACCTGGGAGTTGGAG
108233	106320	GCTTGAACCTGGGAGTTGGA
108234	106321	CGCTTGAACCTGGGAGTTGG
108235	106322	TCGCTTGAACCTGGGAGTTG
108236	106323	ATCGCTTGAACCTGGGAGTT
108237	106324	AATCGCTTGAACCTGGGAGT
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108239	106326	AGAATCGCTTGAACCTGGGA
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108251	106338	GGCTGAGGCAGAAGAATCGC
108252	106339	AGGCTGAGGCAGAAGAATCG
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108263	106350	AGCTACTTGGGAGGCTGAGG
108264	106351	CAGCTACTTGGGAGGCTGAG
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108270	106357	TAATCCCAGCTACTTGGGAG
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108278	106365	CATGCTTGTAATCCCAGCTA
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108280	106367	CACATGCTTGTAATCCCAGC
108281	106368	GCACATGCTTGTAATCCCAG
108282	106369	GGCACATGCTTGTAATCCCA
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108285	106372	GGTGGCACATGCTTGTAATC
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108294	106381	GCTGGGCGTGGTGGCACATG
108295	106382	AGCTGGGCGTGGTGGCACAT
108296	106383	TAGCTGGGCGTGGTGGCACA
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10008	8095	GAGGCTAAGACAGGAGAAAT
10009	8096	GGAGGCTAAGACAGGAGAAA
10010	8097	AGGAGGCTAAGACAGGAGAA
10011	8098	CAGGAGGCTAAGACAGGAGA
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10013	8100	CTCAGGAGGCTAAGACAGGA
10014	8101	ACTCAGGAGGCTAAGACAGG
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10021	8108	TCCAGCTACTCAGGAGGCTA
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10026	8113	GTAGTTCCAGCTACTCAGGA
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10029	8116	CCTGTAGTTCCAGCTACTCA
10030	8117	ACCTGTAGTTCCAGCTACTC
10031	8118	CACCTGTAGTTCCAGCTACT
10032	8119	ACACCTGTAGTTCCAGCTAC
10033	8120	TACACCTGTAGTTCCAGCTA
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10035	8122	TGTACACCTGTAGTTCCAGC
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10044	8131	GCCAGCTGGTGTACACCTGT
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10049	8136	TGTTAGCCAGCTGGTGTACA
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10051	8138	AATGTTAGCCAGCTGGTGTA
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59152	57239	AGCCATGTCGGCCAGGCTGG
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59156	57243	GTAGAGCCATGTCGGCCAGG
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108299	106386	AAGTAGCTGGGCGTGGTGGC
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108306	106393	ATACAAAAAGTAGCTGGGCG
108307	106394	AATACAAAAAGTAGCTGGGC
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108319	106406	GTCTTTACTAAAAATACAAA
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108326	106413	AAACCCCGTCTTTACTAAAA
108327	106414	AAAACCCCGTCTTTACTAAA
108328	106415	CAAAACCCCGTCTTTACTAA
108329	106416	GCAAAACCCCGTCTTTACTA
108330	106417	GGCAAAACCCCGTCTTTACT
108331	106418	TGGCAAAACCCCGTCTTTAC
108332	106419	ATGGCAAAACCCCGTCTTTA
108333	106420	TATGGCAAAACCCCGTCTTT
108334	106421	ATATGGCAAAACCCCGTCTT
108335	106422	AATATGGCAAAACCCCGTCT
108336	106423	AAATATGGCAAAACCCCGTC
108337	106424	CAAATATGGCAAAACCCCGT
108338	106425	GCAAATATGGCAAAACCCCG
108339	106426	GGCAAATATGGCAAAACCCC
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108341	106428	CTGGCAAATATGGCAAAACC
108342	106429	CCTGGCAAATATGGCAAAAC
108343	106430	GCCTGGCAAATATGGCAAAA
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108345	106432	CAGCCTGGCAAATATGGCAA
108346	106433	CCAGCCTGGCAAATATGGCA
108347	106434	ACCAGCCTGGCAAATATGGC
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108351	106438	CAAGACCAGCCTGGCAAATA
108352	106439	TCAAGACCAGCCTGGCAAAT
108353	106440	CTCAAGACCAGCCTGGCAAA
108354	106441	GCTCAAGACCAGCCTGGCAA
108355	106442	AGCTCAAGACCAGCCTGGCA
108356	106443	GAGCTCAAGACCAGCCTGGC
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108358	106445	AGGAGCTCAAGACCAGCCTG
108359	106446	CAGGAGCTCAAGACCAGCCT
108360	106447	TCAGGAGCTCAAGACCAGCC
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108364	106451	GAGGTCAGGAGCTCAAGACC
108365	106452	TGAGGTCAGGAGCTCAAGAC
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108368	106455	CCCTGAGGTCAGGAGCTCAA
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10076	8163	GGACCCTGTCTCTACAAAAA
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10078	8165	CAGGACCCTGTCTCTACAAA
10079	8166	GCAGGACCCTGTCTCTACAA
10080	8167	GGCAGGACCCTGTCTCTACA
10081	8168	TGGCAGGACCCTGTCTCTAC
10082	8169	ATGGCAGGACCCTGTCTCTA
10083	8170	CATGGCAGGACCCTGTCTCT
10084	8171	ACATGGCAGGACCCTGTCTC
10085	8172	AACATGGCAGGACCCTGTCT
10086	8173	CAACATGGCAGGACCCTGTC
10087	8174	GCAACATGGCAGGACCCTGT
10088	8175	GGCAACATGGCAGGACCCTG
10089	8176	GGGCAACATGGCAGGACCCT
10090	8177	TGGGCAACATGGCAGGACCC
10091	8178	CTGGGCAACATGGCAGGACC
10092	8179	TCTGGGCAACATGGCAGGAC
10093	8180	ATCTGGGCAACATGGCAGGA
10094	8181	AATCTGGGCAACATGGCAGG
10095	8182	CAATCTGGGCAACATGGCAG
10096	8183	CCAATCTGGGCAACATGGCA
10097	8184	ACCAATCTGGGCAACATGGC
10098	8185	GACCAATCTGGGCAACATGG
10099	8186	AGACCAATCTGGGCAACATG
10100	8187	GAGACCAATCTGGGCAACAT
10101	8188	TGAGACCAATCTGGGCAACA
10102	8189	TTGAGACCAATCTGGGCAAC
10103	8190	TTTGAGACCAATCTGGGCAA
10104	8191	GTTTGAGACCAATCTGGGCA
10105	8192	AGTTTGAGACCAATCTGGGC
10106	8193	GAGTTTGAGACCAATCTGGG
10107	8194	GGAGTTTGAGACCAATCTGG
10108	8195	AGGAGTTTGAGACCAATCTG
10109	8196	CAGGAGTTTGAGACCAATCT
10110	8197	CCAGGAGTTTGAGACCAATC
10111	8198	CCCAGGAGTTTGAGACCAAT
10112	8199	GCCCAGGAGTTTGAGACCAA
10113	8200	AGCCCAGGAGTTTGAGACCA
10114	8201	GAGCCCAGGAGTTTGAGACC
10115	8202	TGAGCCCAGGAGTTTGAGAC
10116	8203	TTGAGCCCAGGAGTTTGAGA
10117	8204	CTTGAGCCCAGGAGTTTGAG
10118	8205	ACTTGAGCCCAGGAGTTTGA
10119	8206	CACTTGAGCCCAGGAGTTTG
10120	8207	TCACTTGAGCCCAGGAGTTT
10121	8208	ATCACTTGAGCCCAGGAGTT
10122	8209	GATCACTTGAGCCCAGGAGT
10123	8210	GGATCACTTGAGCCCAGGAG
10124	8211	AGGATCACTTGAGCCCAGGA
10125	8212	GAGGATCACTTGAGCCCAGG
10126	8213	GGAGGATCACTTGAGCCCAG
10127	8214	AGGAGGATCACTTGAGCCCA
10128	8215	CAGGAGGATCACTTGAGCCC
10129	8216	GCAGGAGGATCACTTGAGCC
10130	8217	GGCAGGAGGATCACTTGAGC
10131	8218	AGGCAGGAGGATCACTTGAG
10132	8219	GAGGCAGGAGGATCACTTGA
10133	8220	TGAGGCAGGAGGATCACTTG
10134	8221	CTGAGGCAGGAGGATCACTT
10135	8222	GCTGAGGCAGGAGGATCACT
10136	8223	AGCTGAGGCAGGAGGATCAC
10137	8224	AAGCTGAGGCAGGAGGATCA
10138	8225	GAAGCTGAGGCAGGAGGATC
10139	8226	GGAAGCTGAGGCAGGAGGAT
10140	8227	GGGAAGCTGAGGCAGGAGGA
10141	8228	TGGGAAGCTGAGGCAGGAGG
10142	8229	TTGGGAAGCTGAGGCAGGAG
10143	8230	TTTGGGAAGCTGAGGCAGGA
10144	8231	CTTTGGGAAGCTGAGGCAGG
10145	8232	ACTTTGGGAAGCTGAGGCAG
10146	8233	CACTTTGGGAAGCTGAGGCA

59223	57310	CTCAGCCTCCCAAGTAGCTG
59224	57311	CCTCAGCCTCCCAAGTAGCT
59225	57312	GCCTCAGCCTCCCAAGTAGC
59226	57313	TGCCTCAGCCTCCCAAGTAG
59227	57314	CTGCCTCAGCCTCCCAAGTA
59228	57315	CCTGCCTCAGCCTCCCAAGT
59229	57316	TCCTGCCTCAGCCTCCCAAG
59230	57317	CTCCTGCCTCAGCCTCCCAA
59231	57318	TCTCCTGCCTCAGCCTCCCA
59232	57319	TTCTCCTGCCTCAGCCTCCC
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59234	57321	GATTCTCCTGCCTCAGCCTC
59235	57322	CGATTCTCCTGCCTCAGCCT
59236	57323	GCGATTCTCCTGCCTCAGCC
59237	57324	AGCGATTCTCCTGCCTCAGC
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59246	57333	CTGGATTCAAGCGATTCTCC
59247	57334	CCTGGATTCAAGCGATTCTC
59248	57335	TCCTGGATTCAAGCGATTCT
59249	57336	CTCCTGGATTCAAGCGATTC
59250	57337	TCTCCTGGATTCAAGCGATT
59251	57338	GTCTCCTGGATTCAAGCGAT
59252	57339	CGTCTCCTGGATTCAAGCGA
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59254	57341	TCCGTCTCCTGGATTCAAGC
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59256	57343	ACTCCGTCTCCTGGATTCAA
59257	57344	AACTCCGTCTCCTGGATTCA
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59259	57346	CAAACTCCGTCTCCTGGATT
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59261	57348	TGCAAACTCCGTCTCCTGGA
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59264	57351	CATTGCAAACTCCGTCTCCT
59265	57352	TCATTGCAAACTCCGTCTCC
59266	57353	CTCATTGCAAACTCCGTCTC
59267	57354	GCTCATTGCAAACTCCGTCT
59268	57355	GGCTCATTGCAAACTCCGTC
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59270	57357	TCGGCTCATTGCAAACTCCG
59271	57358	CTCGGCTCATTGCAAACTCC
59272	57359	TCTCGGCTCATTGCAAACTC
59273	57360	ATCTCGGCTCATTGCAAACT
59274	57361	CATCTCGGCTCATTGCAAAC
59275	57362	CCATCTCGGCTCATTGCAAA
59276	57363	ACCATCTCGGCTCATTGCAA
59277	57364	CACCATCTCGGCTCATTGCA
59278	57365	CCACCATCTCGGCTCATTGC
59279	57366	ACCACCATCTCGGCTCATTG
59280	57367	CACCACCATCTCGGCTCATT
59281	57368	GCACCACCATCTCGGCTCAT
59282	57369	AGCACCACCATCTCGGCTCA
59283	57370	CAGCACCACCATCTCGGCTC
59284	57371	GCAGCACCACCATCTCGGCT
59285	57372	TGCAGCACCACCATCTCGGC
59286	57373	GTGCAGCACCACCATCTCGG
59287	57374	AGTGCAGCACCACCATCTCG
59288	57375	GAGTGCAGCACCACCATCTC
59289	57376	GGAGTGCAGCACCACCATCT
59290	57377	TGGAGTGCAGCACCACCATC
59291	57378	CTGGAGTGCAGCACCACCAT
59292	57379	GCTGGAGTGCAGCACCACCA
59293	57380	GGCTGGAGTGCAGCACCACC

108370	106457	CACCCTGAGGTCAGGAGCTC
108371	106458	TCACCCTGAGGTCAGGAGCT
108372	106459	ATCACCCTGAGGTCAGGAGC
108373	106460	GATCACCCTGAGGTCAGGAG
108374	106461	GGATCACCCTGAGGTCAGGA
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108377	106464	GGCGGATCACCCTGAGGTCA
108378	106465	GGGCGGATCACCCTGAGGTC
108379	106466	CGGGCGGATCACCCTGAGGT
108380	106467	GCGGGCGGATCACCCTGAGG
108381	106468	GGCGGGCGGATCACCCTGAG
108382	106469	AGGCGGGCGGATCACCCTGA
108383	106470	AAGGCGGGCGGATCACCCTG
108384	106471	CAAGGCGGGCGGATCACCCT
108385	106472	CCAAGGCGGGCGGATCACCC
108386	106473	GCCAAGGCGGGCGGATCACC
108387	106474	TGCCAAGGCGGGCGGATCAC
108388	106475	ATGCCAAGGCGGGCGGATCA
108389	106476	GATGCCAAGGCGGGCGGATC
108390	106477	GGATGCCAAGGCGGGCGGAT
108391	106478	AGGATGCCAAGGCGGGCGGA
108392	106479	TAGGATGCCAAGGCGGGCGG
108393	106480	TTAGGATGCCAAGGCGGGCG
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108396	106483	ACTTTAGGATGCCAAGGCGG
108397	106484	CACTTTAGGATGCCAAGGCG
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108399	106486	AGCACTTTAGGATGCCAAGG
108400	106487	TAGCACTTTAGGATGCCAAG
108401	106488	CTAGCACTTTAGGATGCCAA
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108406	106493	TAATCCTAGCACTTTAGGAT
108407	106494	ATAATCCTAGCACTTTAGGA
108408	106495	TATAATCCTAGCACTTTAGG
108409	106496	TTATAATCCTAGCACTTTAG
108410	106497	CTTATAATCCTAGCACTTTA
108411	106498	GCTTATAATCCTAGCACTTT
108412	106499	CGCTTATAATCCTAGCACTT
108413	106500	ACGCTTATAATCCTAGCACT
108414	106501	CACGCTTATAATCCTAGCAC
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108416	106503	CTCACGCTTATAATCCTAGC
108417	106504	ACTCACGCTTATAATCCTAG
108418	106505	GACTCACGCTTATAATCCTA
108419	106506	TGACTCACGCTTATAATCCT
108420	106507	ATGACTCACGCTTATAATCC
108421	106508	GATGACTCACGCTTATAATC
108422	106509	CGATGACTCACGCTTATAAT
108423	106510	ACGATGACTCACGCTTATAA
108424	106511	CACGATGACTCACGCTTATA
108425	106512	GCACGATGACTCACGCTTAT
108426	106513	GGCACGATGACTCACGCTTA
108427	106514	GGGCACGATGACTCACGCTT
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108429	106516	TTGGGCACGATGACTCACGC
108430	106517	GTTGGGCACGATGACTCACG
108431	106518	AGTTGGGCACGATGACTCAC
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108437	106524	CAACCAAGTTGGGCACGATG
108438	106525	ACAACCAAGTTGGGCACGAT
108439	106526	AACAACCAAGTTGGGCACGA
108440	106527	AAACAACCAAGTTGGGCACG

10147	8234	GCACTTTGGGAAGCTGAGGC
10148	8235	AGCACTTTGGGAAGCTGAGG
10149	8236	CAGCACTTTGGGAAGCTGAG
10150	8237	TCAGCACTTTGGGAAGCTGA
10151	8238	CTCAGCACTTTGGGAAGCTG
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10153	8240	ATCTCAGCACTTTGGGAAGC
10154	8241	AATCTCAGCACTTTGGGAAG
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10157	8244	TGTAATCTCAGCACTTTGGG
10158	8245	CTGTAATCTCAGCACTTTGG
10159	8246	CCTGTAATCTCAGCACTTTG
10160	8247	ACCTGTAATCTCAGCACTTT
10161	8248	CACCTGTAATCTCAGCACTT
10162	8249	ACACCTGTAATCTCAGCACT
10163	8250	CACACCTGTAATCTCAGCAC
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10177	8264	TCGGTGCAGTGGCTCACACC
10178	8265	CTCGGTGCAGTGGCTCACAC
10179	8266	GCTCGGTGCAGTGGCTCACA
10180	8267	GGCTCGGTGCAGTGGCTCAC
10181	8268	GGGCTCGGTGCAGTGGCTCA
10182	8269	GGGGCTCGGTGCAGTGGCTC
10183	8270	GGGGGCTCGGTGCAGTGGCT
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10186	8273	GGAGGGGGCTCGGTGCAGTG
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10189	8276	AAGGGAGGGGGCTCGGTGCA
10190	8277	AAAGGGAGGGGGCTCGGTGC
10191	8278	TAAAGGGAGGGGGCTCGGTG
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10195	8282	AAAATAAAGGGAGGGGGCTC
10196	8283	AAAAATAAAGGGAGGGGGCT
10197	8284	TAAAAATAAAGGGAGGGGGC
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10199	8286	AATAAAAATAAAGGGAGGGG
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10207	8294	AATTTAAAAATAAAAATAAA
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10211	8298	TTAAAATTTAAAAATAAAAA
10212	8299	CTTAAAATTTAAAAATAAAA
10213	8300	ACTTAAAATTTAAAAATAAA
10214	8301	AACTTAAAATTTAAAAATAA
10215	8302	GAACTTAAAATTTAAAAATA
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10217	8304	CAGAACTTAAAATTTAAAAA

59294	57381	AGGCTGGAGTGCAGCACCAC
59295	57382	CAGGCTGGAGTGCAGCACCA
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59298	57385	ACCCAGGCTGGAGTGCAGCA
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59300	57387	TCACCCAGGCTGGAGTGCAG
59301	57388	GTCACCCAGGCTGGAGTGCA
59302	57389	TGTCACCCAGGCTGGAGTGC
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59304	57391	TCTGTCACCCAGGCTGGAGT
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59306	57393	GCTCTGTCACCCAGGCTGGA
59307	57394	GGCTCTGTCACCCAGGCTGG
59308	57395	TGGCTCTGTCACCCAGGCTG
59309	57396	CTGGCTCTGTCACCCAGGCT
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59313	57400	GAGTCTGGCTCTGTCACCCA
59314	57401	AGAGTCTGGCTCTGTCACCC
59315	57402	CAGAGTCTGGCTCTGTCACC
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59319	57406	GAGACAGAGTCTGGCTCTGT
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59335	57422	GCTTATTTTTGTTTTTGAGA
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59337	57424	ATGCTTATTTTTGTTTTTGA
59338	57425	TATGCTTATTTTTGTTTTTG
59339	57426	CTATGCTTATTTTTGTTTTT
59340	57427	CCTATGCTTATTTTTGTTTT
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59344	57431	ATGTCCTATGCTTATTTTTG
59345	57432	CATGTCCTATGCTTATTTTT
59346	57433	CCATGTCCTATGCTTATTTT
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59352	57439	TTATCCCCATGTCCTATGCT
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59355	57442	AATTTATCCCCATGTCCTAT
59356	57443	CAATTTATCCCCATGTCCTA
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108441	106528	TAAACAACCAAGTTGGGCAC
108442	106529	ATAAACAACCAAGTTGGGCA
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108450	106537	ATTTGAAAATAAACAACCAA
108451	106538	TATTTGAAAATAAACAACCA
108452	106539	CTATTTGAAAATAAACAACC
108453	106540	GCTATTTGAAAATAAACAAC
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108458	106545	TTCAGGCTATTTGAAAATAA
108459	106546	ATTCAGGCTATTTGAAAATA
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108461	106548	GAATTCAGGCTATTTGAAAA
108462	106549	TGAATTCAGGCTATTTGAAA
108463	106550	TTGAATTCAGGCTATTTGAA
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108465	106552	GCTTGAATTCAGGCTATTTG
108466	106553	AGCTTGAATTCAGGCTATTT
108467	106554	GAGCTTGAATTCAGGCTATT
108468	106555	TGAGCTTGAATTCAGGCTAT
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108470	106557	AGTGAGCTTGAATTCAGGCT
108471	106558	TAGTGAGCTTGAATTCAGGC
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108474	106561	CATTAGTGAGCTTGAATTCA
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108478	106565	AAAACATTAGTGAGCTTGAA
108479	106566	GAAAACATTAGTGAGCTTGA
108480	106567	AGAAAACATTAGTGAGCTTG
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108486	106573	AGCAGCAGAAAACATTAGTG
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108488	106575	CAAGCAGCAGAAAACATTAG
108489	106576	TCAAGCAGCAGAAAACATTA
108490	106577	ATCAAGCAGCAGAAAACATT
108491	106578	TATCAAGCAGCAGAAAACAT
108492	106579	GTATCAAGCAGCAGAAAACA
108493	106580	TGTATCAAGCAGCAGAAAAC
108494	106581	ATGTATCAAGCAGCAGAAAA
108495	106582	AATGTATCAAGCAGCAGAAA
108496	106583	AAATGTATCAAGCAGCAGAA
108497	106584	GAAATGTATCAAGCAGCAGA
108498	106585	AGAAATGTATCAAGCAGCAG
108499	106586	CAGAAATGTATCAAGCAGCA
108500	106587	GCAGAAATGTATCAAGCAGC
108501	106588	AGCAGAAATGTATCAAGCAG
108502	106589	TAGCAGAAATGTATCAAGCA
108503	106590	ATAGCAGAAATGTATCAAGC
108504	106591	AATAGCAGAAATGTATCAAG
108505	106592	CAATAGCAGAAATGTATCAA
108506	106593	TCAATAGCAGAAATGTATCA
108507	106594	CTCAATAGCAGAAATGTATC
108508	106595	TCTCAATAGCAGAAATGTAT
108509	106596	CTCTCAATAGCAGAAATGTA
108510	106597	TCTCTCAATAGCAGAAATGT
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10218	8305	CCAGAACTTAAAATTTAAAA
10219	8306	CCCAGAACTTAAAATTTAAA
10220	8307	CCCCAGAACTTAAAATTTAA
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10222	8309	GGCCCCAGAACTTAAAATTT
10223	8310	GGGCCCCAGAACTTAAAATT
10224	8311	GGGGCCCCAGAACTTAAAAT
10225	8312	AGGGGCCCCAGAACTTAAAA
10226	8313	GAGGGGCCCCAGAACTTAAA
10227	8314	GGAGGGGCCCCAGAACTTAA
10228	8315	GGGAGGGGCCCCAGAACTTA
10229	8316	AGGGAGGGGCCCCAGAACTT
10230	8317	AAGGGAGGGGCCCCAGAACT
10231	8318	CAAGGGAGGGGCCCCAGAAC
10232	8319	TCAAGGGAGGGGCCCCAGAA
10233	8320	TTCAAGGGAGGGGCCCCAGA
10234	8321	TTTCAAGGGAGGGGCCCCAG
10235	8322	ATTTCAAGGGAGGGGCCCCA
10236	8323	TATTTCAAGGGAGGGGCCCC
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10239	8326	ATTTATTTCAAGGGAGGGGC
10240	8327	TATTTATTTCAAGGGAGGGG
10241	8328	CTATTTATTTCAAGGGAGGG
10242	8329	TCTATTTATTTCAAGGGAGG
10243	8330	TTCTATTTATTTCAAGGGAG
10244	8331	TTTCTATTTATTTCAAGGGA
10245	8332	GTTTCTATTTATTTCAAGGG
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10252	8339	ATATTACGTTTCTATTTATT
10253	8340	TATATTACGTTTCTATTTAT
10254	8341	ATATATTACGTTTCTATTTA
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10256	8343	GTATATATTACGTTTCTATT
10257	8344	TGTATATATTACGTTTCTAT
10258	8345	GTGTATATATTACGTTTCTA
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10262	8349	TCTTGTGTATATATTACGTT
10263	8350	ATCTTGTGTATATATTACGT
10264	8351	GATCTTGTGTATATATTACG
10265	8352	TGATCTTGTGTATATATTAC
10266	8353	ATGATCTTGTGTATATATTA
10267	8354	CATGATCTTGTGTATATATT
10268	8355	GCATGATCTTGTGTATATAT
10269	8356	AGCATGATCTTGTGTATATA
10270	8357	CAGCATGATCTTGTGTATAT
10271	8358	ACAGCATGATCTTGTGTATA
10272	8359	CACAGCATGATCTTGTGTAT
10273	8360	ACACAGCATGATCTTGTGTA
10274	8361	TACACAGCATGATCTTGTGT
10275	8362	ATACACAGCATGATCTTGTG
10276	8363	AATACACAGCATGATCTTGT
10277	8364	AAATACACAGCATGATCTTG
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10279	8366	TAAAATACACAGCATGATCT
10280	8367	TTAAAATACACAGCATGATC
10281	8368	CTTAAAATACACAGCATGAT
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10284	8371	TGCCTTAAAATACACAGCAT
10285	8372	TTGCCTTAAAATACACAGCA
10286	8373	ATTGCCTTAAAATACACAGC
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59365	57452	ATAAATCTTCAATTTATCCC
59366	57453	CATAAATCTTCAATTTATCC
59367	57454	TCATAAATCTTCAATTTATC
59368	57455	TTCATAAATCTTCAATTTAT
59369	57456	CTTCATAAATCTTCAATTTA
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59371	57458	GTCTTCATAAATCTTCAATT
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59374	57461	TGTGTCTTCATAAATCTTCA
59375	57462	CTGTGTCTTCATAAATCTTC
59376	57463	GCTGTGTCTTCATAAATCTT
59377	57464	AGCTGTGTCTTCATAAATCT
59378	57465	CAGCTGTGTCTTCATAAATC
59379	57466	TCAGCTGTGTCTTCATAAAT
59380	57467	TTCAGCTGTGTCTTCATAAA
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59384	57471	CTCCTTCAGCTGTGTCTTCA
59385	57472	TCTCCTTCAGCTGTGTCTTC
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59387	57474	TGTCTCCTTCAGCTGTGTCT
59388	57475	ATGTCTCCTTCAGCTGTGTC
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59391	57478	TTTATGTCTCCTTCAGCTGT
59392	57479	TTTTATGTCTCCTTCAGCTG
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59406	57493	TTAGCCAAATCTACTTTTAT
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59408	57495	ATTTAGCCAAATCTACTTTT
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59415	57502	TGTTTCCATTTAGCCAAATC
59416	57503	ATGTTTCCATTTAGCCAAAT
59417	57504	CATGTTTCCATTTAGCCAAA
59418	57505	GCATGTTTCCATTTAGCCAA
59419	57506	GGCATGTTTCCATTTAGCCA
59420	57507	TGGCATGTTTCCATTTAGCC
59421	57508	ATGGCATGTTTCCATTTAGC
59422	57509	TATGGCATGTTTCCATTTAG
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59424	57511	AGTATGGCATGTTTCCATTT
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59427	57514	CAAAGTATGGCATGTTTCCA
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59432	57519	CCATTCAAAGTATGGCATGT
59433	57520	TCCATTCAAAGTATGGCATG
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108512	106599	AGTCTCTCAATAGCAGAAAT
108513	106600	CAGTCTCTCAATAGCAGAAA
108514	106601	TCAGTCTCTCAATAGCAGAA
108515	106602	ATCAGTCTCTCAATAGCAGA
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108519	106606	ATGCATCAGTCTCTCAATAG
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108522	106609	AAAATGCATCAGTCTCTCAA
108523	106610	AAAAATGCATCAGTCTCTCA
108524	106611	GAAAAATGCATCAGTCTCTC
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108527	106614	ACTGAAAAATGCATCAGTCT
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108531	106618	ACAAACTGAAAAATGCATCA
108532	106619	GACAAACTGAAAAATGCATC
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108535	106622	ATTGACAAACTGAAAAATGC
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108549	106636	AGTGGAAAAATTCAATTGAC
108550	106637	AAGTGGAAAAATTCAATTGA
108551	106638	AAAGTGGAAAAATTCAATTG
108552	106639	CAAAGTGGAAAAATTCAATT
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108566	106653	TCAAGCAGAAATCCCAAAGT
108567	106654	ATCAAGCAGAAATCCCAAAG
108568	106655	AATCAAGCAGAAATCCCAAA
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108570	106657	AGAATCAAGCAGAAATCCCA
108571	106658	AAGAATCAAGCAGAAATCCC
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108573	106660	AAAAGAATCAAGCAGAAATC
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108580	106667	ATTAGTAAAAAGAATCAAGC
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10289	8376	ACCATTGCCTTAAAATACAC
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59436	57523	AATTCCATTCAAAGTATGGC
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59445	57532	GTATTAAATAATTCCATTCA
59446	57533	AGTATTAAATAATTCCATTC
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59478	57565	GAGATTTATTTGAGGAAAAT
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108583	106670	ATTATTAGTAAAAAGAATCA
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108593	106680	GACTGCAATAATTATTAGTA
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108610	106697	TATAAATTTAAAAAAGAGAC
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108614	106701	ATCCTATAAATTTAAAAAAG
108615	106702	AATCCTATAAATTTAAAAAA
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108622	106709	AATTCAGAATCCTATAAATT
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108624	106711	CAAATTCAGAATCCTATAAA
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108626	106713	AACAAATTCAGAATCCTATA
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108629	106716	GAGAACAAATTCAGAATCCT
108630	106717	AGAGAACAAATTCAGAATCC
108631	106718	CAGAGAACAAATTCAGAATC
108632	106719	ACAGAGAACAAATTCAGAAT
108633	106720	TACAGAGAACAAATTCAGAA
108634	106721	ATACAGAGAACAAATTCAGA
108635	106722	AATACAGAGAACAAATTCAG
108636	106723	TAATACAGAGAACAAATTCA
108637	106724	ATAATACAGAGAACAAATTC
108638	106725	GATAATACAGAGAACAAATT
108639	106726	AGATAATACAGAGAACAAAT
108640	106727	AAGATAATACAGAGAACAAA
108641	106728	CAAGATAATACAGAGAACAA
108642	106729	CCAAGATAATACAGAGAACA
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108644	106731	ATCCAAGATAATACAGAGAA
108645	106732	AATCCAAGATAATACAGAGA
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10360	8447	AAAATCATCCCCTGCCCCTA
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10364	8451	TCTCAAAATCATCCCCTGCC
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10373	8460	ACAGTTTCATCTCAAAATCA
10374	8461	AACAGTTTCATCTCAAAATC
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10390	8477	CGTGCCCGGCCGGTGGAACA
10391	8478	CCGTGCCCGGCCGGTGGAAC
10392	8479	ACCGTGCCCGGCCGGTGGAA
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10397	8484	GAGCCACCGTGCCCGGCCGG
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10419	8506	AAAGTGCTGGGATTACAGGC
10420	8507	CAAAGTGCTGGGATTACAGG
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10424	8511	CTCCCAAAGTGCTGGGATTA
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59507	57594	CCCGGCCAAAACTGAATATA
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59512	57599	ACGTGCCCGGCCAAAACTGA
59513	57600	AACGTGCCCGGCCAAAACTG
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59515	57602	CCAACGTGCCCGGCCAAAAC
59516	57603	GCCAACGTGCCCGGCCAAAA
59517	57604	AGCCAACGTGCCCGGCCAAA
59518	57605	GAGCCAACGTGCCCGGCCAA
59519	57606	TGAGCCAACGTGCCCGGCCA
59520	57607	GTGAGCCAACGTGCCCGGCC
59521	57608	CGTGAGCCAACGTGCCCGGC
59522	57609	GCGTGAGCCAACGTGCCCGG
59523	57610	GGCGTGAGCCAACGTGCCCG
59524	57611	AGGCGTGAGCCAACGTGCCC
59525	57612	CAGGCGTGAGCCAACGTGCC
59526	57613	ACAGGCGTGAGCCAACGTGC
59527	57614	TACAGGCGTGAGCCAACGTG
59528	57615	TTACAGGCGTGAGCCAACGT
59529	57616	ATTACAGGCGTGAGCCAACG
59530	57617	GATTACAGGCGTGAGCCAAC
59531	57618	GGATTACAGGCGTGAGCCAA
59532	57619	GGGATTACAGGCGTGAGCCA
59533	57620	TGGGATTACAGGCGTGAGCC
59534	57621	CTGGGATTACAGGCGTGAGC
59535	57622	GCTGGGATTACAGGCGTGAG
59536	57623	TGCTGGGATTACAGGCGTGA
59537	57624	GTGCTGGGATTACAGGCGTG
59538	57625	AGTGCTGGGATTACAGGCGT
59539	57626	AAGTGCTGGGATTACAGGCG
59540	57627	AAAGTGCTGGGATTACAGGC
59541	57628	CAAAGTGCTGGGATTACAGG
59542	57629	CCAAAGTGCTGGGATTACAG
59543	57630	TCCAAAGTGCTGGGATTACA
59544	57631	TTCCAAAGTGCTGGGATTAC
59545	57632	CTTCCAAAGTGCTGGGATTA
59546	57633	CCTTCCAAAGTGCTGGGATT
59547	57634	GCCTTCCAAAGTGCTGGGAT
59548	57635	AGCCTTCCAAAGTGCTGGGA
59549	57636	CAGCCTTCCAAAGTGCTGGG
59550	57637	TCAGCCTTCCAAAGTGCTGG
59551	57638	CTCAGCCTTCCAAAGTGCTG
59552	57639	CCTCAGCCTTCCAAAGTGCT
59553	57640	ACCTCAGCCTTCCAAAGTGC
59554	57641	CACCTCAGCCTTCCAAAGTG
59555	57642	CCACCTCAGCCTTCCAAAGT
59556	57643	CCCACCTCAGCCTTCCAAAG
59557	57644	GCCCACCTCAGCCTTCCAAA
59558	57645	GGCCCACCTCAGCCTTCCAA
59559	57646	CGGCCCACCTCAGCCTTCCA
59560	57647	TCGGCCCACCTCAGCCTTCC
59561	57648	ATCGGCCCACCTCAGCCTTC
59562	57649	GATCGGCCCACCTCAGCCTT
59563	57650	TGATCGGCCCACCTCAGCCT
59564	57651	GTGATCGGCCCACCTCAGCC
59565	57652	AGTGATCGGCCCACCTCAGC
59566	57653	AAGTGATCGGCCCACCTCAG
59567	57654	CAAGTGATCGGCCCACCTCA
59568	57655	TCAAGTGATCGGCCCACCTC
59569	57656	CTCAAGTGATCGGCCCACCT
59570	57657	CCTCAAGTGATCGGCCCACC
59571	57658	TCCTCAAGTGATCGGCCCAC
59572	57659	GTCCTCAAGTGATCGGCCCA
59573	57660	CGTCCTCAAGTGATCGGCCC
59574	57661	CCGTCCTCAAGTGATCGGCC
59575	57662	CCCGTCCTCAAGTGATCGGC
59576	57663	TCCCGTCCTCAAGTGATCGG
59577	57664	CTCCCGTCCTCAAGTGATCG

108654	106741	GTTCAACGAAATCCAAGATA
108655	106742	AGTTCAACGAAATCCAAGAT
108656	106743	AAGTTCAACGAAATCCAAGA
108657	106744	AAAGTTCAACGAAATCCAAG
108658	106745	GAAAGTTCAACGAAATCCAA
108659	106746	AGAAAGTTCAACGAAATCCA
108660	106747	GAGAAAGTTCAACGAAATCC
108661	106748	TGAGAAAGTTCAACGAAATC
108662	106749	TTGAGAAAGTTCAACGAAAT
108663	106750	TTTGAGAAAGTTCAACGAAA
108664	106751	CTTTGAGAAAGTTCAACGAA
108665	106752	GCTTTGAGAAAGTTCAACGA
108666	106753	TGCTTTGAGAAAGTTCAACG
108667	106754	ATGCTTTGAGAAAGTTCAAC
108668	106755	AATGCTTTGAGAAAGTTCAA
108669	106756	GAATGCTTTGAGAAAGTTCA
108670	106757	TGAATGCTTTGAGAAAGTTC
108671	106758	CTGAATGCTTTGAGAAAGTT
108672	106759	GCTGAATGCTTTGAGAAAGT
108673	106760	AGCTGAATGCTTTGAGAAAG
108674	106761	AAGCTGAATGCTTTGAGAAA
108675	106762	CAAGCTGAATGCTTTGAGAA
108676	106763	TCAAGCTGAATGCTTTGAGA
108677	106764	TTCAAGCTGAATGCTTTGAG
108678	106765	ATTCAAGCTGAATGCTTTGA
108679	106766	AATTCAAGCTGAATGCTTTG
108680	106767	GAATTCAAGCTGAATGCTTT
108681	106768	AGAATTCAAGCTGAATGCTT
108682	106769	CAGAATTCAAGCTGAATGCT
108683	106770	ACAGAATTCAAGCTGAATGC
108684	106771	GACAGAATTCAAGCTGAATG
108685	106772	AGACAGAATTCAAGCTGAAT
108686	106773	CAGACAGAATTCAAGCTGAA
108687	106774	TCAGACAGAATTCAAGCTGA
108688	106775	TTCAGACAGAATTCAAGCTG
108689	106776	TTTCAGACAGAATTCAAGCT
108690	106777	CTTTCAGACAGAATTCAAGC
108691	106778	ACTTTCAGACAGAATTCAAG
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108693	106780	GAACTTTCAGACAGAATTCA
108694	106781	TGAACTTTCAGACAGAATTC
108695	106782	GTGAACTTTCAGACAGAATT
108696	106783	TGTGAACTTTCAGACAGAAT
108697	106784	ATGTGAACTTTCAGACAGAA
108698	106785	TATGTGAACTTTCAGACAGA
108699	106786	ATATGTGAACTTTCAGACAG
108700	106787	GATATGTGAACTTTCAGACA
108701	106788	AGATATGTGAACTTTCAGAC
108702	106789	GAGATATGTGAACTTTCAGA
108703	106790	AGAGATATGTGAACTTTCAG
108704	106791	AAGAGATATGTGAACTTTCA
108705	106792	TAAGAGATATGTGAACTTTC
108706	106793	ATAAGAGATATGTGAACTTT
108707	106794	GATAAGAGATATGTGAACTT
108708	106795	TGATAAGAGATATGTGAACT
108709	106796	GTGATAAGAGATATGTGAAC
108710	106797	AGTGATAAGAGATATGTGAA
108711	106798	AAGTGATAAGAGATATGTGA
108712	106799	CAAGTGATAAGAGATATGTG
108713	106800	CCAAGTGATAAGAGATATGT
108714	106801	CCCAAGTGATAAGAGATATG
108715	106802	TCCCAAGTGATAAGAGATAT
108716	106803	TTCCCAAGTGATAAGAGATA
108717	106804	ATTCCCAAGTGATAAGAGAT
108718	106805	AATTCCCAAGTGATAAGAGA
108719	106806	CAATTCCCAAGTGATAAGAG
108720	106807	CCAATTCCCAAGTGATAAGA
108721	106808	ACCAATTCCCAAGTGATAAG
108722	106809	GACCAATTCCCAAGTGATAA
108723	106810	TGACCAATTCCCAAGTGATA
108724	106811	GTGACCAATTCCCAAGTGAT

10431	8518	CCTCGGCCTCCCAAAGTGCT
10432	8519	GCCTCGGCCTCCCAAAGTGC
10433	8520	CGCCTCGGCCTCCCAAAGTG
10434	8521	CCGCCTCGGCCTCCCAAAGT
10435	8522	CCCGCCTCGGCCTCCCAAAG
10436	8523	GCCCGCCTCGGCCTCCCAAA
10437	8524	TGCCCGCCTCGGCCTCCCAA
10438	8525	CTGCCCGCCTCGGCCTCCCA
10439	8526	TCTGCCCGCCTCGGCCTCCC
10440	8527	ATCTGCCCGCCTCGGCCTCC
10441	8528	GATCTGCCCGCCTCGGCCTC
10442	8529	TGATCTGCCCGCCTCGGCCT
10443	8530	GTGATCTGCCCGCCTCGGCC
10444	8531	CGTGATCTGCCCGCCTCGGC
10445	8532	TCGTGATCTGCCCGCCTCGG
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10447	8534	CCTCGTGATCTGCCCGCCTC
10448	8535	ACCTCGTGATCTGCCCGCCT
10449	8536	GACCTCGTGATCTGCCCGCC
10450	8537	TGACCTCGTGATCTGCCCGC
10451	8538	CTGACCTCGTGATCTGCCCG
10452	8539	CCTGACCTCGTGATCTGCCC
10453	8540	TCCTGACCTCGTGATCTGCC
10454	8541	CTCCTGACCTCGTGATCTGC
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10456	8543	ATCTCCTGACCTCGTGATCT
10457	8544	GATCTCCTGACCTCGTGATC
10458	8545	CGATCTCCTGACCTCGTGAT
10459	8546	TCGATCTCCTGACCTCGTGA
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10462	8549	GTCTCGATCTCCTGACCTCG
10463	8550	GGTCTCGATCTCCTGACCTC
10464	8551	TGGTCTCGATCTCCTGACCT
10465	8552	ATGGTCTCGATCTCCTGACC
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10467	8554	GGATGGTCTCGATCTCCTGA
10468	8555	AGGATGGTCTCGATCTCCTG
10469	8556	CAGGATGGTCTCGATCTCCT
10470	8557	CCAGGATGGTCTCGATCTCC
10471	8558	GCCAGGATGGTCTCGATCTC
10472	8559	AGCCAGGATGGTCTCGATCT
10473	8560	TAGCCAGGATGGTCTCGATC
10474	8561	TTAGCCAGGATGGTCTCGAT
10475	8562	GTTAGCCAGGATGGTCTCGA
10476	8563	TGTTAGCCAGGATGGTCTCG
10477	8564	ATGTTAGCCAGGATGGTCTC
10478	8565	CATGTTAGCCAGGATGGTCT
10479	8566	CCATGTTAGCCAGGATGGTC
10480	8567	ACCATGTTAGCCAGGATGGT
10481	8568	CACCATGTTAGCCAGGATGG
10482	8569	TCACCATGTTAGCCAGGATG
10483	8570	TTCACCATGTTAGCCAGGAT
10484	8571	TTTCACCATGTTAGCCAGGA
10485	8572	GTTTCACCATGTTAGCCAGG
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10487	8574	GGGTTTCACCATGTTAGCCA
10488	8575	GGGGTTTCACCATGTTAGCC
10489	8576	GGGGGTTTCACCATGTTAGC
10490	8577	GGGGGGTTTCACCATGTTAG
10491	8578	AGGGGGGTTTCACCATGTTA
10492	8579	GAGGGGGGTTTCACCATGTT
10493	8580	AGAGGGGGGTTTCACCATGT
10494	8581	TAGAGGGGGGTTTCACCATG
10495	8582	GTAGAGGGGGGTTTCACCAT
10496	8583	AGTAGAGGGGGGTTTCACCA
10497	8584	TAGTAGAGGGGGGTTTCACC
10498	8585	TTAGTAGAGGGGGGTTTCAC
10499	8586	TTTAGTAGAGGGGGGTTTCA
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10501	8588	TTTTTAGTAGAGGGGGGTTT

59578	57665	ACTCCCGTCCTCAAGTGATC
59579	57666	AACTCCCGTCCTCAAGTGAT
59580	57667	AAACTCCCGTCCTCAAGTGA
59581	57668	CAAACTCCCGTCCTCAAGTG
59582	57669	TCAAACTCCCGTCCTCAAGT
59583	57670	CTCAAACTCCCGTCCTCAAG
59584	57671	TCTCAAACTCCCGTCCTCAA
59585	57672	GTCTCAAACTCCCGTCCTCA
59586	57673	GGTCTCAAACTCCCGTCCTC
59587	57674	TGGTCTCAAACTCCCGTCCT
59588	57675	CTGGTCTCAAACTCCCGTCC
59589	57676	GCTGGTCTCAAACTCCCGTC
59590	57677	GGCTGGTCTCAAACTCCCGT
59591	57678	AGGCTGGTCTCAAACTCCCG
59592	57679	CAGGCTGGTCTCAAACTCCC
59593	57680	CCAGGCTGGTCTCAAACTCC
59594	57681	GCCAGGCTGGTCTCAAACTC
59595	57682	GGCCAGGCTGGTCTCAAACT
59596	57683	TGGCCAGGCTGGTCTCAAAC
59597	57684	TTGGCCAGGCTGGTCTCAAA
59598	57685	GTTGGCCAGGCTGGTCTCAA
59599	57686	TGTTGGCCAGGCTGGTCTCA
59600	57687	ATGTTGGCCAGGCTGGTCTC
59601	57688	CATGTTGGCCAGGCTGGTCT
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59603	57690	ACCATGTTGGCCAGGCTGGT
59604	57691	CACCATGTTGGCCAGGCTGG
59605	57692	TCACCATGTTGGCCAGGCTG
59606	57693	TTCACCATGTTGGCCAGGCT
59607	57694	TTTCACCATGTTGGCCAGGC
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59609	57696	GGTTTCACCATGTTGGCCAG
59610	57697	GGGTTTCACCATGTTGGCCA
59611	57698	AGGGTTTCACCATGTTGGCC
59612	57699	CAGGGTTTCACCATGTTGGC
59613	57700	ACAGGGTTTCACCATGTTGG
59614	57701	GACAGGGTTTCACCATGTTG
59615	57702	AGACAGGGTTTCACCATGTT
59616	57703	GAGACAGGGTTTCACCATGT
59617	57704	AGAGACAGGGTTTCACCATG
59618	57705	TAGAGACAGGGTTTCACCAT
59619	57706	GTAGAGACAGGGTTTCACCA
59620	57707	AGTAGAGACAGGGTTTCACC
59621	57708	TAGTAGAGACAGGGTTTCAC
59622	57709	TTAGTAGAGACAGGGTTTCA
59623	57710	TTTAGTAGAGACAGGGTTTC
59624	57711	TTTTAGTAGAGACAGGGTTT
59625	57712	TTTTTAGTAGAGACAGGGTT
59626	57713	ATTTTTAGTAGAGACAGGGT
59627	57714	TATTTTTAGTAGAGACAGGG
59628	57715	GTATTTTTAGTAGAGACAGG
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59630	57717	TTGTATTTTTAGTAGAGACA
59631	57718	TTTGTATTTTTAGTAGAGAC
59632	57719	TTTTGTATTTTTAGTAGAGA
59633	57720	TTTTTGTATTTTTAGTAGAG
59634	57721	ATTTTTGTATTTTTAGTAGA
59635	57722	GATTTTTGTATTTTTAGTAG
59636	57723	TGATTTTTGTATTTTTAGTA
59637	57724	ATGATTTTTGTATTTTTAGT
59638	57725	GATGATTTTTGTATTTTTAG
59639	57726	AGATGATTTTTGTATTTTTA
59640	57727	CAGATGATTTTTGTATTTTT
59641	57728	CCAGATGATTTTTGTATTTT
59642	57729	TCCAGATGATTTTTGTATTT
59643	57730	GTCCAGATGATTTTTGTATT
59644	57731	TGTCCAGATGATTTTTGTAT
59645	57732	ATGTCCAGATGATTTTTGTA
59646	57733	CATGTCCAGATGATTTTTGT
59647	57734	CCATGTCCAGATGATTTTTG
59648	57735	ACCATGTCCAGATGATTTTT

108725	106812	AGTGACCAATTCCCAAGTGA
108726	106813	CAGTGACCAATTCCCAAGTG
108727	106814	CCAGTGACCAATTCCCAAGT
108728	106815	ACCAGTGACCAATTCCCAAG
108729	106816	CACCAGTGACCAATTCCCAA
108730	106817	ACACCAGTGACCAATTCCCA
108731	106818	GACACCAGTGACCAATTCCC
108732	106819	GGACACCAGTGACCAATTCC
108733	106820	AGGACACCAGTGACCAATTC
108734	106821	AAGGACACCAGTGACCAATT
108735	106822	AAAGGACACCAGTGACCAAT
108736	106823	TAAAGGACACCAGTGACCAA
108737	106824	ATAAAGGACACCAGTGACCA
108738	106825	AATAAAGGACACCAGTGACC
108739	106826	AAATAAAGGACACCAGTGAC
108740	106827	AAAATAAAGGACACCAGTGA
108741	106828	AAAAATAAAGGACACCAGTG
108742	106829	TAAAAATAAAGGACACCAGT
108743	106830	CTAAAAATAAAGGACACCAG
108744	106831	ACTAAAAATAAAGGACACCA
108745	106832	AACTAAAAATAAAGGACACC
108746	106833	GAACTAAAAATAAAGGACAC
108747	106834	TGAACTAAAAATAAAGGACA
108748	106835	ATGAACTAAAAATAAAGGAC
108749	106836	AATGAACTAAAAATAAAGGA
108750	106837	AAATGAACTAAAAATAAAGG
108751	106838	CAAATGAACTAAAAATAAAG
108752	106839	CCAAATGAACTAAAAATAAA
108753	106840	ACCAAATGAACTAAAAATAA
108754	106841	CACCAAATGAACTAAAAATA
108755	106842	TCACCAAATGAACTAAAAAT
108756	106843	CTCACCAAATGAACTAAAAA
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108758	106845	ACCTCACCAAATGAACTAAA
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108760	106847	TGACCTCACCAAATGAACTA
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108762	106849	CATGACCTCACCAAATGAAC
108763	106850	ACATGACCTCACCAAATGAA
108764	106851	AACATGACCTCACCAAATGA
108765	106852	AAACATGACCTCACCAAATG
108766	106853	AAAACATGACCTCACCAAAT
108767	106854	GAAAACATGACCTCACCAAA
108768	106855	AGAAAACATGACCTCACCAA
108769	106856	GAGAAAACATGACCTCACCA
108770	106857	TGAGAAAACATGACCTCACC
108771	106858	CTGAGAAAACATGACCTCAC
108772	106859	TCTGAGAAAACATGACCTCA
108773	106860	ATCTGAGAAAACATGACCTC
108774	106861	CATCTGAGAAAACATGACCT
108775	106862	CCATCTGAGAAAACATGACC
108776	106863	GCCATCTGAGAAAACATGAC
108777	106864	GGCCATCTGAGAAAACATGA
108778	106865	AGGCCATCTGAGAAAACATG
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108781	106868	TCAAGGCCATCTGAGAAAAC
108782	106869	ATCAAGGCCATCTGAGAAAA
108783	106870	CATCAAGGCCATCTGAGAAA
108784	106871	GCATCAAGGCCATCTGAGAA
108785	106872	AGCATCAAGGCCATCTGAGA
108786	106873	AAGCATCAAGGCCATCTGAG
108787	106874	CAAGCATCAAGGCCATCTGA
108788	106875	ACAAGCATCAAGGCCATCTG
108789	106876	CACAAGCATCAAGGCCATCT
108790	106877	CCACAAGCATCAAGGCCATC
108791	106878	TCCACAAGCATCAAGGCCAT
108792	106879	ATCCACAAGCATCAAGGCCA
108793	106880	CATCCACAAGCATCAAGGCC
108794	106881	ACATCCACAAGCATCAAGGC
108795	106882	AACATCCACAAGCATCAAGG

10502	8589	ATTTTTAGTAGAGGGGGGTT
10503	8590	TATTTTTAGTAGAGGGGGGT
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10505	8592	TGTATTTTTAGTAGAGGGGG
10506	8593	TTGTATTTTTAGTAGAGGGG
10507	8594	TTTGTATTTTTAGTAGAGGG
10508	8595	TTTTGTATTTTTAGTAGAGG
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10510	8597	TTTTTTGTATTTTTAGTAGA
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10512	8599	ATTTTTTTGTATTTTTAGTA
10513	8600	AATTTTTTTGTATTTTTAGT
10514	8601	TAATTTTTTTGTATTTTTAG
10515	8602	CTAATTTTTTTGTATTTTTA
10516	8603	GCTAATTTTTTTGTATTTTT
10517	8604	AGCTAATTTTTTTGTATTTT
10518	8605	CAGCTAATTTTTTTGTATTT
10519	8606	CCAGCTAATTTTTTTGTATT
10520	8607	CCCAGCTAATTTTTTTGTAT
10521	8608	GCCCAGCTAATTTTTTTGTA
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10523	8610	GCGCCCAGCTAATTTTTTTG
10524	8611	CGCGCCCAGCTAATTTTTTT
10525	8612	CCGCGCCCAGCTAATTTTTT
10526	8613	ACCGCGCCCAGCTAATTTTT
10527	8614	CACCGCGCCCAGCTAATTTT
10528	8615	CCACCGCGCCCAGCTAATTT
10529	8616	TCCACCGCGCCCAGCTAATT
10530	8617	CTCCACCGCGCCCAGCTAAT
10531	8618	CCTCCACCGCGCCCAGCTAA
10532	8619	CCCTCCACCGCGCCCAGCTA
10533	8620	GCCCTCCACCGCGCCCAGCT
10534	8621	CGCCCTCCACCGCGCCCAGC
10535	8622	GCGCCCTCCACCGCGCCCAG
10536	8623	GGCGCCCTCCACCGCGCCCA
10537	8624	AGGCGCCCTCCACCGCGCCC
10538	8625	CAGGCGCCCTCCACCGCGCC
10539	8626	ACAGGCGCCCTCCACCGCGC
10540	8627	TACAGGCGCCCTCCACCGCG
10541	8628	CTACAGGCGCCCTCCACCGC
10542	8629	ACTACAGGCGCCCTCCACCG
10543	8630	GACTACAGGCGCCCTCCACC
10544	8631	TGACTACAGGCGCCCTCCAC
10545	8632	GTGACTACAGGCGCCCTCCA
10546	8633	TGTGACTACAGGCGCCCTCC
10547	8634	CTGTGACTACAGGCGCCCTC
10548	8635	GCTGTGACTACAGGCGCCCT
10549	8636	AGCTGTGACTACAGGCGCCC
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10551	8638	GTAGCTGTGACTACAGGCGC
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10554	8641	GGAGTAGCTGTGACTACAGG
10555	8642	CGGAGTAGCTGTGACTACAG
10556	8643	CCGGAGTAGCTGTGACTACA
10557	8644	TCCGGAGTAGCTGTGACTAC
10558	8645	CTCCGGAGTAGCTGTGACTA
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10560	8647	GCCTCCGGAGTAGCTGTGAC
10561	8648	GGCCTCCGGAGTAGCTGTGA
10562	8649	CGGCCTCCGGAGTAGCTGTG
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10564	8651	CTCGGCCTCCGGAGTAGCTG
10565	8652	CCTCGGCCTCCGGAGTAGCT
10566	8653	GCCTCGGCCTCCGGAGTAGC
10567	8654	TGCCTCGGCCTCCGGAGTAG
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10569	8656	CTTGCCTCGGCCTCCGGAGT
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10571	8658	CTCTTGCCTCGGCCTCCGGA
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59649	57736	CACCATGTCCAGATGATTTT
59650	57737	CCACCATGTCCAGATGATTT
59651	57738	GCCACCATGTCCAGATGATT
59652	57739	TGCCACCATGTCCAGATGAT
59653	57740	CTGCCACCATGTCCAGATGA
59654	57741	CCTGCCACCATGTCCAGATG
59655	57742	ACCTGCCACCATGTCCAGAT
59656	57743	TACCTGCCACCATGTCCAGA
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59658	57745	GGTACCTGCCACCATGTCCA
59659	57746	TGGTACCTGCCACCATGTCC
59660	57747	CTGGTACCTGCCACCATGTC
59661	57748	GCTGGTACCTGCCACCATGT
59662	57749	AGCTGGTACCTGCCACCATG
59663	57750	TAGCTGGTACCTGCCACCAT
59664	57751	GTAGCTGGTACCTGCCACCA
59665	57752	AGTAGCTGGTACCTGCCACC
59666	57753	AAGTAGCTGGTACCTGCCAC
59667	57754	CAAGTAGCTGGTACCTGCCA
59668	57755	CCAAGTAGCTGGTACCTGCC
59669	57756	CCCAAGTAGCTGGTACCTGC
59670	57757	TCCCAAGTAGCTGGTACCTG
59671	57758	TTCCCAAGTAGCTGGTACCT
59672	57759	CTTCCCAAGTAGCTGGTACC
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59674	57761	AGCTTCCCAAGTAGCTGGTA
59675	57762	CAGCTTCCCAAGTAGCTGGT
59676	57763	TCAGCTTCCCAAGTAGCTGG
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59678	57765	CCTCAGCTTCCCAAGTAGCT
59679	57766	GCCTCAGCTTCCCAAGTAGC
59680	57767	TGCCTCAGCTTCCCAAGTAG
59681	57768	CTGCCTCAGCTTCCCAAGTA
59682	57769	CCTGCCTCAGCTTCCCAAGT
59683	57770	TCCTGCCTCAGCTTCCCAAG
59684	57771	CTCCTGCCTCAGCTTCCCAA
59685	57772	TCTCCTGCCTCAGCTTCCCA
59686	57773	TTCTCCTGCCTCAGCTTCCC
59687	57774	ATTCTCCTGCCTCAGCTTCC
59688	57775	AATTCTCCTGCCTCAGCTTC
59689	57776	TAATTCTCCTGCCTCAGCTT
59690	57777	GTAATTCTCCTGCCTCAGCT
59691	57778	AGTAATTCTCCTGCCTCAGC
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59694	57781	TCGAGTAATTCTCCTGCCTC
59695	57782	TTCGAGTAATTCTCCTGCCT
59696	57783	GTTCGAGTAATTCTCCTGCC
59697	57784	GGTTCGAGTAATTCTCCTGC
59698	57785	GGGTTCGAGTAATTCTCCTG
59699	57786	GGGGTTCGAGTAATTCTCCT
59700	57787	CGGGGTTCGAGTAATTCTCC
59701	57788	ACGGGGTTCGAGTAATTCTC
59702	57789	TACGGGGTTCGAGTAATTCT
59703	57790	CTACGGGGTTCGAGTAATTC
59704	57791	CCTACGGGGTTCGAGTAATT
59705	57792	ACCTACGGGGTTCGAGTAAT
59706	57793	CACCTACGGGGTTCGAGTAA
59707	57794	CCACCTACGGGGTTCGAGTA
59708	57795	TCCACCTACGGGGTTCGAGT
59709	57796	CTCCACCTACGGGGTTCGAG
59710	57797	CCTCCACCTACGGGGTTCGA
59711	57798	ACCTCCACCTACGGGGTTCG
59712	57799	AACCTCCACCTACGGGGTTC
59713	57800	CAACCTCCACCTACGGGGTT
59714	57801	GCAACCTCCACCTACGGGGT
59715	57802	TGCAACCTCCACCTACGGGG
59716	57803	CTGCAACCTCCACCTACGGG
59717	57804	ACTGCAACCTCCACCTACGG
59718	57805	CACTGCAACCTCCACCTACG
59719	57806	TCACTGCAACCTCCACCTAC

108796	106883	GAACATCCACAAGCATCAAG
108797	106884	TGAACATCCACAAGCATCAA
108798	106885	ATGAACATCCACAAGCATCA
108799	106886	GATGAACATCCACAAGCATC
108800	106887	TGATGAACATCCACAAGCAT
108801	106888	CTGATGAACATCCACAAGCA
108802	106889	ACTGATGAACATCCACAAGC
108803	106890	CACTGATGAACATCCACAAG
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108805	106892	GACACTGATGAACATCCACA
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108807	106894	CAGACACTGATGAACATCCA
108808	106895	CCAGACACTGATGAACATCC
108809	106896	CCCAGACACTGATGAACATC
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108820	106907	ACTCTTCAATGCCCAGACAC
108821	106908	AACTCTTCAATGCCCAGACA
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108823	106910	CCAACTCTTCAATGCCCAGA
108824	106911	CCCAACTCTTCAATGCCCAG
108825	106912	ACCCAACTCTTCAATGCCCA
108826	106913	TACCCAACTCTTCAATGCCC
108827	106914	ATACCCAACTCTTCAATGCC
108828	106915	AATACCCAACTCTTCAATGC
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108830	106917	AGAATACCCAACTCTTCAAT
108831	106918	CAGAATACCCAACTCTTCAA
108832	106919	ACAGAATACCCAACTCTTCA
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108834	106921	GAACAGAATACCCAACTCTT
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108837	106924	AAAGAACAGAATACCCAACT
108838	106925	CAAAGAACAGAATACCCAAC
108839	106926	ACAAAGAACAGAATACCCAA
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10579	8666	ATGCCATTCTCTTGCCTCGG
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10582	8669	TTCATGCCATTCTCTTGCCT
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10588	8675	CCGGGTTTCATGCCATTCTC
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10595	8682	CTGCCTCCCGGGTTTCATGC
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10598	8685	GCTCTGCCTCCCGGGTTTCA
10599	8686	AGCTCTGCCTCCCGGGTTTC
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10636	8723	AGGCTGAAGTACAGTGGTGC
10637	8724	CAGGCTGAAGTACAGTGGTG
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59720	57807	CTCACTGCAACCTCCACCTA
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59731	57818	TGCAATCTCAGCTCACTGCA
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59736	57823	TGGAGTGCAATCTCAGCTCA
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108870	106957	AAAAAAGAATGCGTACAAAC
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59839	57926	ATAATCTAATAAGCTTTAGA
59840	57927	CATAATCTAATAAGCTTTAG
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59848	57935	TTAATACACATAATCTAATA
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108945	107032	GGTGAGCAAAGACTGTGCCA
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108947	107034	GCGGTGAGCAAAGACTGTGC
108948	107035	TGCGGTGAGCAAAGACTGTG
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108950	107037	GTTGCGGTGAGCAAAGACTG
108951	107038	GGTTGCGGTGAGCAAAGACT
108952	107039	AGGTTGCGGTGAGCAAAGAC
108953	107040	GAGGTTGCGGTGAGCAAAGA
108954	107041	GGAGGTTGCGGTGAGCAAAG
108955	107042	CGGAGGTTGCGGTGAGCAAA
108956	107043	ACGGAGGTTGCGGTGAGCAA
108957	107044	GACGGAGGTTGCGGTGAGCA
108958	107045	AGACGGAGGTTGCGGTGAGC
108959	107046	GAGACGGAGGTTGCGGTGAG
108960	107047	GGAGACGGAGGTTGCGGTGA
108961	107048	GGGAGACGGAGGTTGCGGTG
108962	107049	CGGGAGACGGAGGTTGCGGT
108963	107050	CCGGGAGACGGAGGTTGCGG
108964	107051	TCCGGGAGACGGAGGTTGCG
108965	107052	ATCCGGGAGACGGAGGTTGC
108966	107053	AATCCGGGAGACGGAGGTTG
108967	107054	GAATCCGGGAGACGGAGGTT
108968	107055	TGAATCCGGGAGACGGAGGT
108969	107056	TTGAATCCGGGAGACGGAGG
108970	107057	CTTGAATCCGGGAGACGGAG
108971	107058	GCTTGAATCCGGGAGACGGA
108972	107059	TGCTTGAATCCGGGAGACGG
108973	107060	TTGCTTGAATCCGGGAGACG
108974	107061	ATTGCTTGAATCCGGGAGAC
108975	107062	AATTGCTTGAATCCGGGAGA
108976	107063	GAATTGCTTGAATCCGGGAG
108977	107064	AGAATTGCTTGAATCCGGGA
108978	107065	GAGAATTGCTTGAATCCGGG
108979	107066	GGAGAATTGCTTGAATCCGG
108980	107067	AGGAGAATTGCTTGAATCCG
108981	107068	CAGGAGAATTGCTTGAATCC
108982	107069	GCAGGAGAATTGCTTGAATC
108983	107070	GGCAGGAGAATTGCTTGAAT
108984	107071	AGGCAGGAGAATTGCTTGAA
108985	107072	GAGGCAGGAGAATTGCTTGA
108986	107073	TGAGGCAGGAGAATTGCTTG
108987	107074	CTGAGGCAGGAGAATTGCTT
108988	107075	GCTGAGGCAGGAGAATTGCT
108989	107076	GGCTGAGGCAGGAGAATTGC
108990	107077	AGGCTGAGGCAGGAGAATTG
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108992	107079	GGAGGCTGAGGCAGGAGAAT
108993	107080	AGGAGGCTGAGGCAGGAGAA
108994	107081	CAGGAGGCTGAGGCAGGAGA
108995	107082	TCAGGAGGCTGAGGCAGGAG
108996	107083	CTCAGGAGGCTGAGGCAGGA
108997	107084	ACTCAGGAGGCTGAGGCAGG
108998	107085	TACTCAGGAGGCTGAGGCAG
108999	107086	CTACTCAGGAGGCTGAGGCA
109000	107087	GCTACTCAGGAGGCTGAGGC
109001	107088	AGCTACTCAGGAGGCTGAGG
109002	107089	CAGCTACTCAGGAGGCTGAG
109003	107090	CCAGCTACTCAGGAGGCTGA
109004	107091	CCCAGCTACTCAGGAGGCTG
109005	107092	TCCCAGCTACTCAGGAGGCT
109006	107093	ATCCCAGCTACTCAGGAGGC
109007	107094	AATCCCAGCTACTCAGGAGG
109008	107095	TAATCCCAGCTACTCAGGAG

10715	8802	TATGAGAATCTAACAAATGC
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10717	8804	TTTATGAGAATCTAACAAAT
10718	8805	CTTTATGAGAATCTAACAAA
10719	8806	TCTTTATGAGAATCTAACAA
10720	8807	CTCTTTATGAGAATCTAACA
10721	8808	GCTCTTTATGAGAATCTAAC
10722	8809	TGCTCTTTATGAGAATCTAA
10723	8810	ATGCTCTTTATGAGAATCTA
10724	8811	TATGCTCTTTATGAGAATCT
10725	8812	GTATGCTCTTTATGAGAATC
10726	8813	TGTATGCTCTTTATGAGAAT
10727	8814	TTGTATGCTCTTTATGAGAA
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10731	8818	TAGGTTGTATGCTCTTTATG
10732	8819	GTAGGTTGTATGCTCTTTAT
10733	8820	TGTAGGTTGTATGCTCTTTA
10734	8821	ATGTAGGTTGTATGCTCTTT
10735	8822	GATGTAGGTTGTATGCTCTT
10736	8823	AGATGTAGGTTGTATGCTCT
10737	8824	GAGATGTAGGTTGTATGCTC
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10739	8826	AAGAGATGTAGGTTGTATGC
10740	8827	CAAGAGATGTAGGTTGTATG
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10747	8834	CATATAGCAAGAGATGTAGG
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10756	8843	TGGGAACTGCATATAGCAAG
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10758	8845	ACTGGGAACTGCATATAGCA
10759	8846	TACTGGGAACTGCATATAGC
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10763	8850	ACCCTACTGGGAACTGCATA
10764	8851	AACCCTACTGGGAACTGCAT
10765	8852	AAACCCTACTGGGAACTGCA
10766	8853	CAAACCCTACTGGGAACTGC
10767	8854	ACAAACCCTACTGGGAACTG
10768	8855	CACAAACCCTACTGGGAACT
10769	8856	GCACAAACCCTACTGGGAAC
10770	8857	AGCACAAACCCTACTGGGAA
10771	8858	AAGCACAAACCCTACTGGGA
10772	8859	GAAGCACAAACCCTACTGGG
10773	8860	AGAAGCACAAACCCTACTGG
10774	8861	TAGAAGCACAAACCCTACTG
10775	8862	ATAGAAGCACAAACCCTACT
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59866	57953	ATTTCCAAAGTTCTTCTGTT
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59869	57956	AAAATTTCCAAAGTTCTTCT
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59871	57958	AAAAAATTTCCAAAGTTCTT
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59873	57960	GAAAAAAATTTCCAAAGTTC
59874	57961	GGAAAAAAATTTCCAAAGTT
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59877	57964	TGTGGAAAAAAATTTCCAAA
59878	57965	TTGTGGAAAAAAATTTCCAA
59879	57966	CTTGTGGAAAAAAATTTCCA
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59885	57972	ATGACTCTTGTGGAAAAAAA
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59905	57992	TGTAGGGCAAGTCCTCCTTT
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59907	57994	TTTGTAGGGCAAGTCCTCCT
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59928	58015	TATGTTTTAATTCTGACATA
59929	58016	TTATGTTTTAATTCTGACAT
59930	58017	GTTATGTTTTAATTCTGACA
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109009	107096	GTAATCCCAGCTACTCAGGA
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109012	107099	CCTGTAATCCCAGCTACTCA
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109014	107101	CACCTGTAATCCCAGCTACT
109015	107102	GCACCTGTAATCCCAGCTAC
109016	107103	CGCACCTGTAATCCCAGCTA
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109019	107106	GCACGCACCTGTAATCCCAG
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109021	107108	TGGCACGCACCTGTAATCCC
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109023	107110	GGTGGCACGCACCTGTAATC
109024	107111	TGGTGGCACGCACCTGTAAT
109025	107112	GTGGTGGCACGCACCTGTAA
109026	107113	CGTGGTGGCACGCACCTGTA
109027	107114	GCGTGGTGGCACGCACCTGT
109028	107115	GGCGTGGTGGCACGCACCTG
109029	107116	AGGCGTGGTGGCACGCACCT
109030	107117	CAGGCGTGGTGGCACGCACC
109031	107118	CCAGGCGTGGTGGCACGCAC
109032	107119	GCCAGGCGTGGTGGCACGCA
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109036	107123	ATTAGCCAGGCGTGGTGGCA
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109072	107159	ACATGGTGAAACACCATATT
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109076	107163	ACCAACATGGTGAAACACCA
109077	107164	GACCAACATGGTGAAACACC
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10786	8873	ATTAGGTTCTTATAGAAGCA
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10789	8876	AGCATTAGGTTCTTATAGAA
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10827	8914	AGCATTAGCACCTGAGCCCC
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10832	8919	GTGTGAGCATTAGCACCTGA
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10837	8924	GAGCTGTGTGAGCATTAGCA
10838	8925	GGAGCTGTGTGAGCATTAGC
10839	8926	AGGAGCTGTGTGAGCATTAG
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10844	8931	ACAACAGGAGCTGTGTGAGC
10845	8932	CACAACAGGAGCTGTGTGAG
10846	8933	GCACAACAGGAGCTGTGTGA
10847	8934	TGCACAACAGGAGCTGTGTG
10848	8935	CTGCACAACAGGAGCTGTGT
10849	8936	ACTGCACAACAGGAGCTGTG
10850	8937	GACTGCACAACAGGAGCTGT
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59940	58027	CAGCTGACAAGTTATGTTTT
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59944	58031	CACCCAGCTGACAAGTTATG
59945	58032	GCACCCAGCTGACAAGTTAT
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59954	58041	TGAGCCACCGCACCCAGCTG
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59958	58045	GGCGTGAGCCACCGCACCCA
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59962	58049	TATAGGCGTGAGCCACCGCA
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59995	58082	TCTGCCTGCCTCAGCCTCCC
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109091	107178	TTCGAGACCAGCCTGACCAA
109092	107179	GTTCGAGACCAGCCTGACCA
109093	107180	AGTTCGAGACCAGCCTGACC
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109095	107182	GGAGTTCGAGACCAGCCTGA
109096	107183	AGGAGTTCGAGACCAGCCTG
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109098	107185	TTAGGAGTTCGAGACCAGCC
109099	107186	GTTAGGAGTTCGAGACCAGC
109100	107187	GGTTAGGAGTTCGAGACCAG
109101	107188	AGGTTAGGAGTTCGAGACCA
109102	107189	GAGGTTAGGAGTTCGAGACC
109103	107190	CGAGGTTAGGAGTTCGAGAC
109104	107191	ACGAGGTTAGGAGTTCGAGA
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109106	107193	TCACGAGGTTAGGAGTTCGA
109107	107194	ATCACGAGGTTAGGAGTTCG
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109110	107197	CAGATCACGAGGTTAGGAGT
109111	107198	ACAGATCACGAGGTTAGGAG
109112	107199	GACAGATCACGAGGTTAGGA
109113	107200	GGACAGATCACGAGGTTAGG
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109117	107204	AGGCGGACAGATCACGAGGT
109118	107205	AAGGCGGACAGATCACGAGG
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109120	107207	CCAAGGCGGACAGATCACGA
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109122	107209	GGCCAAGGCGGACAGATCAC
109123	107210	AGGCCAAGGCGGACAGATCA
109124	107211	GAGGCCAAGGCGGACAGATC
109125	107212	AGAGGCCAAGGCGGACAGAT
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109130	107217	CTCTGAGAGGCCAAGGCGGA
109131	107218	ACTCTGAGAGGCCAAGGCGG
109132	107219	CACTCTGAGAGGCCAAGGCG
109133	107220	ACACTCTGAGAGGCCAAGGC
109134	107221	AACACTCTGAGAGGCCAAGG
109135	107222	CAACACTCTGAGAGGCCAAG
109136	107223	CCAACACTCTGAGAGGCCAA
109137	107224	CCCAACACTCTGAGAGGCCA
109138	107225	TCCCAACACTCTGAGAGGCC
109139	107226	ATCCCAACACTCTGAGAGGC
109140	107227	AATCCCAACACTCTGAGAGG
109141	107228	TAATCCCAACACTCTGAGAG
109142	107229	GTAATCCCAACACTCTGAGA
109143	107230	TGTAATCCCAACACTCTGAG
109144	107231	CTGTAATCCCAACACTCTGA
109145	107232	CCTGTAATCCCAACACTCTG
109146	107233	GCCTGTAATCCCAACACTCT
109147	107234	CGCCTGTAATCCCAACACTC
109148	107235	ACGCCTGTAATCCCAACACT
109149	107236	AACGCCTGTAATCCCAACAC
109150	107237	TAACGCCTGTAATCCCAACA

10857	8944	GGAACCAGACTGCACAACAG
10858	8945	AGGAACCAGACTGCACAACA
10859	8946	TAGGAACCAGACTGCACAAC
10860	8947	TTAGGAACCAGACTGCACAA
10861	8948	GTTAGGAACCAGACTGCACA
10862	8949	TGTTAGGAACCAGACTGCAC
10863	8950	CTGTTAGGAACCAGACTGCA
10864	8951	CCTGTTAGGAACCAGACTGC
10865	8952	GCCTGTTAGGAACCAGACTG
10866	8953	GGCCTGTTAGGAACCAGACT
10867	8954	AGGCCTGTTAGGAACCAGAC
10868	8955	CAGGCCTGTTAGGAACCAGA
10869	8956	ACAGGCCTGTTAGGAACCAG
10870	8957	AACAGGCCTGTTAGGAACCA
10871	8958	AAACAGGCCTGTTAGGAACC
10872	8959	AAAACAGGCCTGTTAGGAAC
10873	8960	AAAAACAGGCCTGTTAGGAA
10874	8961	AAAAAACAGGCCTGTTAGGA
10875	8962	AAAAAAACAGGCCTGTTAGG
10876	8963	AAAAAAAACAGGCCTGTTAG
10877	8964	AAAAAAAAACAGGCCTGTTA
10878	8965	AAAAAAAAAACAGGCCTGTT
10879	8966	AAAAAAAAAAACAGGCCTGT
10880	8967	AAAAAAAAAAAACAGGCCTG
10881	8968	AAAAAAAAAAAAACAGGCCT
10882	8969	TAAAAAAAAAAAAACAGGCC
10883	8970	TTAAAAAAAAAAAAACAGGC
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10885	8972	AATTAAAAAAAAAAAAACAG
10886	8973	TAATTAAAAAAAAAAAAACA
10887	8974	CTAATTAAAAAAAAAAAAAC
10888	8975	TCTAATTAAAAAAAAAAAAA
10889	8976	ATCTAATTAAAAAAAAAAAA
10890	8977	CATCTAATTAAAAAAAAAAA
10891	8978	CCATCTAATTAAAAAAAAAA
10892	8979	TCCATCTAATTAAAAAAAAA
10893	8980	CTCCATCTAATTAAAAAAAA
10894	8981	ACTCCATCTAATTAAAAAAA
10895	8982	GACTCCATCTAATTAAAAAA
10896	8983	AGACTCCATCTAATTAAAAA
10897	8984	GAGACTCCATCTAATTAAAA
10898	8985	CGAGACTCCATCTAATTAAA
10899	8986	GCGAGACTCCATCTAATTAA
10900	8987	AGCGAGACTCCATCTAATTA
10901	8988	GAGCGAGACTCCATCTAATT
10902	8989	AGAGCGAGACTCCATCTAAT
10903	8990	CAGAGCGAGACTCCATCTAA
10904	8991	ACAGAGCGAGACTCCATCTA
10905	8992	GACAGAGCGAGACTCCATCT
10906	8993	TGACAGAGCGAGACTCCATC
10907	8994	GTGACAGAGCGAGACTCCAT
10908	8995	GGTGACAGAGCGAGACTCCA
10909	8996	TGGTGACAGAGCGAGACTCC
10910	8997	CTGGTGACAGAGCGAGACTC
10911	8998	CCTGGTGACAGAGCGAGACT
10912	8999	GCCTGGTGACAGAGCGAGAC
10913	9000	AGCCTGGTGACAGAGCGAGA
10914	9001	CAGCCTGGTGACAGAGCGAG
10915	9002	CCAGCCTGGTGACAGAGCGA
10916	9003	TCCAGCCTGGTGACAGAGCG
10917	9004	CTCCAGCCTGGTGACAGAGC
10918	9005	ACTCCAGCCTGGTGACAGAG
10919	9006	CACTCCAGCCTGGTGACAGA
10920	9007	GCACTCCAGCCTGGTGACAG
10921	9008	TGCACTCCAGCCTGGTGACA
10922	9009	CTGCACTCCAGCCTGGTGAC
10923	9010	ACTGCACTCCAGCCTGGTGA
10924	9011	CACTGCACTCCAGCCTGGTG
10925	9012	CCACTGCACTCCAGCCTGGT
10926	9013	GCCACTGCACTCCAGCCTGG
10927	9014	TGCCACTGCACTCCAGCCTG

60004	58091	TGGTCATGATCTGCCTGCCT
60005	58092	CTGGTCATGATCTGCCTGCC
60006	58093	GCTGGTCATGATCTGCCTGC
60007	58094	GGCTGGTCATGATCTGCCTG
60008	58095	AGGCTGGTCATGATCTGCCT
60009	58096	CAGGCTGGTCATGATCTGCC
60010	58097	TCAGGCTGGTCATGATCTGC
60011	58098	GTCAGGCTGGTCATGATCTG
60012	58099	GGTCAGGCTGGTCATGATCT
60013	58100	TGGTCAGGCTGGTCATGATC
60014	58101	TTGGTCAGGCTGGTCATGAT
60015	58102	GTTGGTCAGGCTGGTCATGA
60016	58103	TGTTGGTCAGGCTGGTCATG
60017	58104	ATGTTGGTCAGGCTGGTCAT
60018	58105	CATGTTGGTCAGGCTGGTCA
60019	58106	CCATGTTGGTCAGGCTGGTC
60020	58107	TCCATGTTGGTCAGGCTGGT
60021	58108	CTCCATGTTGGTCAGGCTGG
60022	58109	TCTCCATGTTGGTCAGGCTG
60023	58110	TTCTCCATGTTGGTCAGGCT
60024	58111	TTTCTCCATGTTGGTCAGGC
60025	58112	GTTTCTCCATGTTGGTCAGG
60026	58113	GGTTTCTCCATGTTGGTCAG
60027	58114	GGGTTTCTCCATGTTGGTCA
60028	58115	GGGGTTTCTCCATGTTGGTC
60029	58116	CGGGGTTTCTCCATGTTGGT
60030	58117	ACGGGGTTTCTCCATGTTGG
60031	58118	GACGGGGTTTCTCCATGTTG
60032	58119	AGACGGGGTTTCTCCATGTT
60033	58120	GAGACGGGGTTTCTCCATGT
60034	58121	AGAGACGGGGTTTCTCCATG
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60036	58123	GTAGAGACGGGGTTTCTCCA
60037	58124	AGTAGAGACGGGGTTTCTCC
60038	58125	TAGTAGAGACGGGGTTTCTC
60039	58126	TTAGTAGAGACGGGGTTTCT
60040	58127	TTTAGTAGAGACGGGGTTTC
60041	58128	TTTTAGTAGAGACGGGGTTT
60042	58129	TTTTTAGTAGAGACGGGGTT
60043	58130	ATTTTTAGTAGAGACGGGGT
60044	58131	TATTTTTAGTAGAGACGGGG
60045	58132	GTATTTTTAGTAGAGACGGG
60046	58133	TGTATTTTTAGTAGAGACGG
60047	58134	TTGTATTTTTAGTAGAGACG
60048	58135	TTTGTATTTTTAGTAGAGAC
60049	58136	TTTTGTATTTTTAGTAGAGA
60050	58137	ATTTTGTATTTTTAGTAGAG
60051	58138	AATTTTGTATTTTTAGTAGA
60052	58139	TAATTTTGTATTTTTAGTAG
60053	58140	CTAATTTTGTATTTTTAGTA
60054	58141	GCTAATTTTGTATTTTTAGT
60055	58142	GGCTAATTTTGTATTTTTAG
60056	58143	CGGCTAATTTTGTATTTTTA
60057	58144	CCGGCTAATTTTGTATTTTT
60058	58145	ACCGGCTAATTTTGTATTTT
60059	58146	GACCGGCTAATTTTGTATTT
60060	58147	TGACCGGCTAATTTTGTATT
60061	58148	ATGACCGGCTAATTTTGTAT
60062	58149	CATGACCGGCTAATTTTGTA
60063	58150	CCATGACCGGCTAATTTTGT
60064	58151	ACCATGACCGGCTAATTTTG
60065	58152	CACCATGACCGGCTAATTTT
60066	58153	CCACCATGACCGGCTAATTT
60067	58154	GCCACCATGACCGGCTAATT
60068	58155	CGCCACCATGACCGGCTAAT
60069	58156	GCGCCACCATGACCGGCTAA
60070	58157	TGCGCCACCATGACCGGCTA
60071	58158	ATGCGCCACCATGACCGGCT
60072	58159	TATGCGCCACCATGACCGGC
60073	58160	GTATGCGCCACCATGACCGG
60074	58161	GGTATGCGCCACCATGACCG

109151	107238	CTAACGCCTGTAATCCCAAC
109152	107239	GCTAACGCCTGTAATCCCAA
109153	107240	GGCTAACGCCTGTAATCCCA
109154	107241	TGGCTAACGCCTGTAATCCC
109155	107242	GTGGCTAACGCCTGTAATCC
109156	107243	AGTGGCTAACGCCTGTAATC
109157	107244	CAGTGGCTAACGCCTGTAAT
109158	107245	GCAGTGGCTAACGCCTGTAA
109159	107246	TGCAGTGGCTAACGCCTGTA
109160	107247	ATGCAGTGGCTAACGCCTGT
109161	107248	GATGCAGTGGCTAACGCCTG
109162	107249	GGATGCAGTGGCTAACGCCT
109163	107250	CGGATGCAGTGGCTAACGCC
109164	107251	CCGGATGCAGTGGCTAACGC
109165	107252	GCCGGATGCAGTGGCTAACG
109166	107253	AGCCGGATGCAGTGGCTAAC
109167	107254	GAGCCGGATGCAGTGGCTAA
109168	107255	GGAGCCGGATGCAGTGGCTA
109169	107256	GGGAGCCGGATGCAGTGGCT
109170	107257	TGGGAGCCGGATGCAGTGGC
109171	107258	ATGGGAGCCGGATGCAGTGG
109172	107259	AATGGGAGCCGGATGCAGTG
109173	107260	GAATGGGAGCCGGATGCAGT
109174	107261	AGAATGGGAGCCGGATGCAG
109175	107262	AAGAATGGGAGCCGGATGCA
109176	107263	GAAGAATGGGAGCCGGATGC
109177	107264	AGAAGAATGGGAGCCGGATG
109178	107265	AAGAAGAATGGGAGCCGGAT
109179	107266	CAAGAAGAATGGGAGCCGGA
109180	107267	TCAAGAAGAATGGGAGCCGG
109181	107268	CTCAAGAAGAATGGGAGCCG
109182	107269	TCTCAAGAAGAATGGGAGCC
109183	107270	TTCTCAAGAAGAATGGGAGC
109184	107271	CTTCTCAAGAAGAATGGGAG
109185	107272	CCTTCTCAAGAAGAATGGGA
109186	107273	ACCTTCTCAAGAAGAATGGG
109187	107274	AACCTTCTCAAGAAGAATGG
109188	107275	AAACCTTCTCAAGAAGAATG
109189	107276	AAAACCTTCTCAAGAAGAAT
109190	107277	AAAAACCTTCTCAAGAAGAA
109191	107278	GAAAAACCTTCTCAAGAAGA
109192	107279	TGAAAAACCTTCTCAAGAAG
109193	107280	TTGAAAAACCTTCTCAAGAA
109194	107281	CTTGAAAAACCTTCTCAAGA
109195	107282	ACTTGAAAAACCTTCTCAAG
109196	107283	TACTTGAAAAACCTTCTCAA
109197	107284	ATACTTGAAAAACCTTCTCA
109198	107285	AATACTTGAAAAACCTTCTC
109199	107286	GAATACTTGAAAAACCTTCT
109200	107287	TGAATACTTGAAAAACCTTC
109201	107288	TTGAATACTTGAAAAACCTT
109202	107289	TTTGAATACTTGAAAAACCT
109203	107290	CTTTGAATACTTGAAAAACC
109204	107291	CCTTTGAATACTTGAAAAAC
109205	107292	CCCTTTGAATACTTGAAAAA
109206	107293	TCCCTTTGAATACTTGAAAA
109207	107294	TTCCCTTTGAATACTTGAAA
109208	107295	ATTCCCTTTGAATACTTGAA
109209	107296	AATTCCCTTTGAATACTTGA
109210	107297	TAATTCCCTTTGAATACTTG
109211	107298	TTAATTCCCTTTGAATACTT
109212	107299	CTTAATTCCCTTTGAATACT
109213	107300	ACTTAATTCCCTTTGAATAC
109214	107301	CACTTAATTCCCTTTGAATA
109215	107302	ACACTTAATTCCCTTTGAAT
109216	107303	AACACTTAATTCCCTTTGAA
109217	107304	CAACACTTAATTCCCTTTGA
109218	107305	ACAACACTTAATTCCCTTTG
109219	107306	GACAACACTTAATTCCCTTT
109220	107307	TGACAACACTTAATTCCCTT
109221	107308	ATGACAACACTTAATTCCCT

10928	9015	GTGCCACTGCACTCCAGCCT
10929	9016	CGTGCCACTGCACTCCAGCC
10930	9017	TCGTGCCACTGCACTCCAGC
10931	9018	ATCGTGCCACTGCACTCCAG
10932	9019	GATCGTGCCACTGCACTCCA
10933	9020	AGATCGTGCCACTGCACTCC
10934	9021	GAGATCGTGCCACTGCACTC
10935	9022	TGAGATCGTGCCACTGCACT
10936	9023	CTGAGATCGTGCCACTGCAC
10937	9024	GCTGAGATCGTGCCACTGCA
10938	9025	AGCTGAGATCGTGCCACTGC
10939	9026	GAGCTGAGATCGTGCCACTG
10940	9027	TGAGCTGAGATCGTGCCACT
10941	9028	GTGAGCTGAGATCGTGCCAC
10942	9029	AGTGAGCTGAGATCGTGCCA
10943	9030	CAGTGAGCTGAGATCGTGCC
10944	9031	GCAGTGAGCTGAGATCGTGC
10945	9032	TGCAGTGAGCTGAGATCGTG
10946	9033	TTGCAGTGAGCTGAGATCGT
10947	9034	GTTGCAGTGAGCTGAGATCG
10948	9035	GGTTGCAGTGAGCTGAGATC
10949	9036	AGGTTGCAGTGAGCTGAGAT
10950	9037	GAGGTTGCAGTGAGCTGAGA
10951	9038	AGAGGTTGCAGTGAGCTGAG
10952	9039	CAGAGGTTGCAGTGAGCTGA
10953	9040	GCAGAGGTTGCAGTGAGCTG
10954	9041	GGCAGAGGTTGCAGTGAGCT
10955	9042	AGGCAGAGGTTGCAGTGAGC
10956	9043	GAGGCAGAGGTTGCAGTGAG
10957	9044	GGAGGCAGAGGTTGCAGTGA
10958	9045	GGGAGGCAGAGGTTGCAGTG
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10960	9047	CCGGGAGGCAGAGGTTGCAG
10961	9048	CCCGGGAGGCAGAGGTTGCA
10962	9049	ACCCGGGAGGCAGAGGTTGC
10963	9050	AACCCGGGAGGCAGAGGTTG
10964	9051	GAACCCGGGAGGCAGAGGTT
10965	9052	TGAACCCGGGAGGCAGAGGT
10966	9053	TTGAACCCGGGAGGCAGAGG
10967	9054	CTTGAACCCGGGAGGCAGAG
10968	9055	GCTTGAACCCGGGAGGCAGA
10969	9056	CGCTTGAACCCGGGAGGCAG
10970	9057	TCGCTTGAACCCGGGAGGCA
10971	9058	ATCGCTTGAACCCGGGAGGC
10972	9059	AATCGCTTGAACCCGGGAGG
10973	9060	GAATCGCTTGAACCCGGGAG
10974	9061	AGAATCGCTTGAACCCGGGA
10975	9062	GAGAATCGCTTGAACCCGGG
10976	9063	GGAGAATCGCTTGAACCCGG
10977	9064	AGGAGAATCGCTTGAACCCG
10978	9065	CAGGAGAATCGCTTGAACCC
10979	9066	GCAGGAGAATCGCTTGAACC
10980	9067	GGCAGGAGAATCGCTTGAAC
10981	9068	AGGCAGGAGAATCGCTTGAA
10982	9069	AAGGCAGGAGAATCGCTTGA
10983	9070	TAAGGCAGGAGAATCGCTTG
10984	9071	CTAAGGCAGGAGAATCGCTT
10985	9072	GCTAAGGCAGGAGAATCGCT
10986	9073	GGCTAAGGCAGGAGAATCGC
10987	9074	AGGCTAAGGCAGGAGAATCG
10988	9075	GAGGCTAAGGCAGGAGAATC
10989	9076	GGAGGCTAAGGCAGGAGAAT
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10991	9078	TGGGAGGCTAAGGCAGGAGA
10992	9079	ATGGGAGGCTAAGGCAGGAG
10993	9080	CATGGGAGGCTAAGGCAGGA
10994	9081	ACATGGGAGGCTAAGGCAGG
10995	9082	TACATGGGAGGCTAAGGCAG
10996	9083	CTACATGGGAGGCTAAGGCA
10997	9084	ACTACATGGGAGGCTAAGGC
10998	9085	AACTACATGGGAGGCTAAGG

60075	58162	AGGTATGCGCCACCATGACC
60076	58163	CAGGTATGCGCCACCATGAC
60077	58164	ACAGGTATGCGCCACCATGA
60078	58165	TACAGGTATGCGCCACCATG
60079	58166	CTACAGGTATGCGCCACCAT
60080	58167	ACTACAGGTATGCGCCACCA
60081	58168	GACTACAGGTATGCGCCACC
60082	58169	GGACTACAGGTATGCGCCAC
60083	58170	GGGACTACAGGTATGCGCCA
60084	58171	TGGGACTACAGGTATGCGCC
60085	58172	CTGGGACTACAGGTATGCGC
60086	58173	GCTGGGACTACAGGTATGCG
60087	58174	AGCTGGGACTACAGGTATGC
60088	58175	TAGCTGGGACTACAGGTATG
60089	58176	GTAGCTGGGACTACAGGTAT
60090	58177	AGTAGCTGGGACTACAGGTA
60091	58178	GAGTAGCTGGGACTACAGGT
60092	58179	CGAGTAGCTGGGACTACAGG
60093	58180	CCGAGTAGCTGGGACTACAG
60094	58181	CCCGAGTAGCTGGGACTACA
60095	58182	TCCCGAGTAGCTGGGACTAC
60096	58183	CTCCCGAGTAGCTGGGACTA
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60098	58185	GCCTCCCGAGTAGCTGGGAC
60099	58186	AGCCTCCCGAGTAGCTGGGA
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60102	58189	CTCAGCCTCCCGAGTAGCTG
60103	58190	CCTCAGCCTCCCGAGTAGCT
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60105	58192	TGCCTCAGCCTCCCGAGTAG
60106	58193	CTGCCTCAGCCTCCCGAGTA
60107	58194	CCTGCCTCAGCCTCCCGAGT
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60109	58196	CTCCTGCCTCAGCCTCCCGA
60110	58197	TCTCCTGCCTCAGCCTCCCG
60111	58198	TTCTCCTGCCTCAGCCTCCC
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60113	58200	GATTCTCCTGCCTCAGCCTC
60114	58201	CGATTCTCCTGCCTCAGCCT
60115	58202	GCGATTCTCCTGCCTCAGCC
60116	58203	AGCGATTCTCCTGCCTCAGC
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60121	58208	GTTCAAGCGATTCTCCTGCC
60122	58209	AGTTCAAGCGATTCTCCTGC
60123	58210	GAGTTCAAGCGATTCTCCTG
60124	58211	CGAGTTCAAGCGATTCTCCT
60125	58212	CCGAGTTCAAGCGATTCTCC
60126	58213	CCCGAGTTCAAGCGATTCTC
60127	58214	TCCCGAGTTCAAGCGATTCT
60128	58215	CTCCCGAGTTCAAGCGATTC
60129	58216	CCTCCCGAGTTCAAGCGATT
60130	58217	ACCTCCCGAGTTCAAGCGAT
60131	58218	CACCTCCCGAGTTCAAGCGA
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60134	58221	CTCCACCTCCCGAGTTCAAG
60135	58222	CCTCCACCTCCCGAGTTCAA
60136	58223	ACCTCCACCTCCCGAGTTCA
60137	58224	AACCTCCACCTCCCGAGTTC
60138	58225	CAACCTCCACCTCCCGAGTT
60139	58226	GCAACCTCCACCTCCCGAGT
60140	58227	TGCAACCTCCACCTCCCGAG
60141	58228	CTGCAACCTCCACCTCCCGA
60142	58229	ACTGCAACCTCCACCTCCCG
60143	58230	CACTGCAACCTCCACCTCCC
60144	58231	TCACTGCAACCTCCACCTCC
60145	58232	CTCACTGCAACCTCCACCTC

109222	107309	GATGACAACACTTAATTCCC
109223	107310	AGATGACAACACTTAATTCC
109224	107311	TAGATGACAACACTTAATTC
109225	107312	TTAGATGACAACACTTAATT
109226	107313	CTTAGATGACAACACTTAAT
109227	107314	ACTTAGATGACAACACTTAA
109228	107315	GACTTAGATGACAACACTTA
109229	107316	AGACTTAGATGACAACACTT
109230	107317	AAGACTTAGATGACAACACT
109231	107318	GAAGACTTAGATGACAACAC
109232	107319	CGAAGACTTAGATGACAACA
109233	107320	GCGAAGACTTAGATGACAAC
109234	107321	AGCGAAGACTTAGATGACAA
109235	107322	GAGCGAAGACTTAGATGACA
109236	107323	TGAGCGAAGACTTAGATGAC
109237	107324	GTGAGCGAAGACTTAGATGA
109238	107325	AGTGAGCGAAGACTTAGATG
109239	107326	CAGTGAGCGAAGACTTAGAT
109240	107327	GCAGTGAGCGAAGACTTAGA
109241	107328	TGCAGTGAGCGAAGACTTAG
109242	107329	CTGCAGTGAGCGAAGACTTA
109243	107330	GCTGCAGTGAGCGAAGACTT
109244	107331	GGCTGCAGTGAGCGAAGACT
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109249	107336	TGTATGGCTGCAGTGAGCGA
109250	107337	ATGTATGGCTGCAGTGAGCG
109251	107338	CATGTATGGCTGCAGTGAGC
109252	107339	GCATGTATGGCTGCAGTGAG
109253	107340	TGCATGTATGGCTGCAGTGA
109254	107341	ATGCATGTATGGCTGCAGTG
109255	107342	AATGCATGTATGGCTGCAGT
109256	107343	TAATGCATGTATGGCTGCAG
109257	107344	CTAATGCATGTATGGCTGCA
109258	107345	TCTAATGCATGTATGGCTGC
109259	107346	CTCTAATGCATGTATGGCTG
109260	107347	CCTCTAATGCATGTATGGCT
109261	107348	CCCTCTAATGCATGTATGGC
109262	107349	GCCCTCTAATGCATGTATGG
109263	107350	TGCCCTCTAATGCATGTATG
109264	107351	GTGCCCTCTAATGCATGTAT
109265	107352	GGTGCCCTCTAATGCATGTA
109266	107353	GGGTGCCCTCTAATGCATGT
109267	107354	GGGGTGCCCTCTAATGCATG
109268	107355	TGGGGTGCCCTCTAATGCAT
109269	107356	TTGGGGTGCCCTCTAATGCA
109270	107357	CTTGGGGTGCCCTCTAATGC
109271	107358	TCTTGGGGTGCCCTCTAATG
109272	107359	GTCTTGGGGTGCCCTCTAAT
109273	107360	AGTCTTGGGGTGCCCTCTAA
109274	107361	TAGTCTTGGGGTGCCCTCTA
109275	107362	CTAGTCTTGGGGTGCCCTCT
109276	107363	ACTAGTCTTGGGGTGCCCTC
109277	107364	TACTAGTCTTGGGGTGCCCT
109278	107365	TTACTAGTCTTGGGGTGCCC
109279	107366	ATTACTAGTCTTGGGGTGCC
109280	107367	CATTACTAGTCTTGGGGTGC
109281	107368	ACATTACTAGTCTTGGGGTG
109282	107369	AACATTACTAGTCTTGGGGT
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109288	107375	AGTCACAACATTACTAGTCT
109289	107376	GAGTCACAACATTACTAGTC
109290	107377	AGAGTCACAACATTACTAGT
109291	107378	CAGAGTCACAACATTACTAG
109292	107379	ACAGAGTCACAACATTACTA

10999	9086	CAACTACATGGGAGGCTAAG
11000	9087	CCAACTACATGGGAGGCTAA
11001	9088	ACCAACTACATGGGAGGCTA
11002	9089	TACCAACTACATGGGAGGCT
11003	9090	GTACCAACTACATGGGAGGC
11004	9091	AGTACCAACTACATGGGAGG
11005	9092	TAGTACCAACTACATGGGAG
11006	9093	GTAGTACCAACTACATGGGA
11007	9094	TGTAGTACCAACTACATGGG
11008	9095	CTGTAGTACCAACTACATGG
11009	9096	CCTGTAGTACCAACTACATG
11010	9097	GCCTGTAGTACCAACTACAT
11011	9098	CGCCTGTAGTACCAACTACA
11012	9099	GCGCCTGTAGTACCAACTAC
11013	9100	TGCGCCTGTAGTACCAACTA
11014	9101	GTGCGCCTGTAGTACCAACT
11015	9102	TGTGCGCCTGTAGTACCAAC
11016	9103	GTGTGCGCCTGTAGTACCAA
11017	9104	AGTGTGCGCCTGTAGTACCA
11018	9105	CAGTGTGCGCCTGTAGTACC
11019	9106	ACAGTGTGCGCCTGTAGTAC
11020	9107	CACAGTGTGCGCCTGTAGTA
11021	9108	TCACAGTGTGCGCCTGTAGT
11022	9109	ATCACAGTGTGCGCCTGTAG
11023	9110	CATCACAGTGTGCGCCTGTA
11024	9111	GCATCACAGTGTGCGCCTGT
11025	9112	GGCATCACAGTGTGCGCCTG
11026	9113	GGGCATCACAGTGTGCGCCT
11027	9114	TGGGCATCACAGTGTGCGCC
11028	9115	CTGGGCATCACAGTGTGCGC
11029	9116	GCTGGGCATCACAGTGTGCG
11030	9117	AGCTGGGCATCACAGTGTGC
11031	9118	TAGCTGGGCATCACAGTGTG
11032	9119	TTAGCTGGGCATCACAGTGT
11033	9120	ATTAGCTGGGCATCACAGTG
11034	9121	AATTAGCTGGGCATCACAGT
11035	9122	AAATTAGCTGGGCATCACAG
11036	9123	AAAATTAGCTGGGCATCACA
11037	9124	AAAAATTAGCTGGGCATCAC
11038	9125	CAAAAATTAGCTGGGCATCA
11039	9126	ACAAAAATTAGCTGGGCATC
11040	9127	TACAAAAATTAGCTGGGCAT
11041	9128	ATACAAAAATTAGCTGGGCA
11042	9129	AATACAAAAATTAGCTGGGC
11043	9130	AAATACAAAAATTAGCTGGG
11044	9131	AAAATACAAAAATTAGCTGG
11045	9132	AAAAATACAAAAATTAGCTG
11046	9133	TAAAAATACAAAAATTAGCT
11047	9134	CTAAAAATACAAAAATTAGC
11048	9135	ACTAAAAATACAAAAATTAG
11049	9136	TACTAAAAATACAAAAATTA
11050	9137	CTACTAAAAATACAAAAATT
11051	9138	TCTACTAAAAATACAAAAAT
11052	9139	CTCTACTAAAAATACAAAAA
11053	9140	TCTCTACTAAAAATACAAAA
11054	9141	GTCTCTACTAAAAATACAAA
11055	9142	CGTCTCTACTAAAAATACAA
11056	9143	CCGTCTCTACTAAAAATACA
11057	9144	CCCGTCTCTACTAAAAATAC
11058	9145	CCCCGTCTCTACTAAAAATA
11059	9146	ACCCCGTCTCTACTAAAAAT
11060	9147	AACCCCGTCTCTACTAAAAA
11061	9148	AAACCCCGTCTCTACTAAAA
11062	9149	GAAACCCCGTCTCTACTAAA
11063	9150	TGAAACCCCGTCTCTACTAA
11064	9151	GTGAAACCCCGTCTCTACTA
11065	9152	GGTGAAACCCCGTCTCTACT
11066	9153	TGGTGAAACCCCGTCTCTAC
11067	9154	ATGGTGAAACCCCGTCTCTA
11068	9155	CATGGTGAAACCCCGTCTCT
11069	9156	ACATGGTGAAACCCCGTCTC

60146	58233	GCTCACTGCAACCTCCACCT
60147	58234	GGCTCACTGCAACCTCCACC
60148	58235	CGGCTCACTGCAACCTCCAC
60149	58236	TCGGCTCACTGCAACCTCCA
60150	58237	CTCGGCTCACTGCAACCTCC
60151	58238	TCTCGGCTCACTGCAACCTC
60152	58239	ATCTCGGCTCACTGCAACCT
60153	58240	GATCTCGGCTCACTGCAACC
60154	58241	CGATCTCGGCTCACTGCAAC
60155	58242	GCGATCTCGGCTCACTGCAA
60156	58243	CGCGATCTCGGCTCACTGCA
60157	58244	GCGCGATCTCGGCTCACTGC
60158	58245	GGCGCGATCTCGGCTCACTG
60159	58246	TGGCGCGATCTCGGCTCACT
60160	58247	ATGGCGCGATCTCGGCTCAC
60161	58248	AATGGCGCGATCTCGGCTCA
60162	58249	CAATGGCGCGATCTCGGCTC
60163	58250	GCAATGGCGCGATCTCGGCT
60164	58251	TGCAATGGCGCGATCTCGGC
60165	58252	GTGCAATGGCGCGATCTCGG
60166	58253	AGTGCAATGGCGCGATCTCG
60167	58254	GAGTGCAATGGCGCGATCTC
60168	58255	GGAGTGCAATGGCGCGATCT
60169	58256	TGGAGTGCAATGGCGCGATC
60170	58257	CTGGAGTGCAATGGCGCGAT
60171	58258	GCTGGAGTGCAATGGCGCGA
60172	58259	GGCTGGAGTGCAATGGCGCG
60173	58260	AGGCTGGAGTGCAATGGCGC
60174	58261	CAGGCTGGAGTGCAATGGCG
60175	58262	CCAGGCTGGAGTGCAATGGC
60176	58263	CCCAGGCTGGAGTGCAATGG
60177	58264	GCCCAGGCTGGAGTGCAATG
60178	58265	TGCCCAGGCTGGAGTGCAAT
60179	58266	TTGCCCAGGCTGGAGTGCAA
60180	58267	GTTGCCCAGGCTGGAGTGCA
60181	58268	TGTTGCCCAGGCTGGAGTGC
60182	58269	TTGTTGCCCAGGCTGGAGTG
60183	58270	CTTGTTGCCCAGGCTGGAGT
60184	58271	TCTTGTTGCCCAGGCTGGAG
60185	58272	CTCTTGTTGCCCAGGCTGGA
60186	58273	ACTCTTGTTGCCCAGGCTGG
60187	58274	TACTCTTGTTGCCCAGGCTG
60188	58275	TTACTCTTGTTGCCCAGGCT
60189	58276	TTTACTCTTGTTGCCCAGGC
60190	58277	TTTTACTCTTGTTGCCCAGG
60191	58278	GTTTTACTCTTGTTGCCCAG
60192	58279	AGTTTTACTCTTGTTGCCCA
60193	58280	GAGTTTTACTCTTGTTGCCC
60194	58281	AGAGTTTTACTCTTGTTGCC
60195	58282	CAGAGTTTTACTCTTGTTGC
60196	58283	ACAGAGTTTTACTCTTGTTG
60197	58284	AACAGAGTTTTACTCTTGTT
60198	58285	AAACAGAGTTTTACTCTTGT
60199	58286	GAAACAGAGTTTTACTCTTG
60200	58287	TGAAACAGAGTTTTACTCTT
60201	58288	TTGAAACAGAGTTTTACTCT
60202	58289	TTTGAAACAGAGTTTTACTC
60203	58290	TTTTGAAACAGAGTTTTACT
60204	58291	TTTTTGAAACAGAGTTTTAC
60205	58292	TTTTTTGAAACAGAGTTTTA
60206	58293	TTTTTTTGAAACAGAGTTTT
60207	58294	TTTTTTTTGAAACAGAGTTT
60208	58295	TTTTTTTTTGAAACAGAGTT
60209	58296	TTTTTTTTTTGAAACAGAGT
60210	58297	TTTTTTTTTTTGAAACAGAG
60211	58298	TTTTTTTTTTTTGAAACAGA
60212	58299	TTTTTTTTTTTTTGAAACAG
60213	58300	TTTTTTTTTTTTTTGAAACA
60214	58301	TTTTTTTTTTTTTTTGAAAC
60215	58302	TTTTTTTTTTTTTTTTGAAA
60216	58303	TTTTTTTTTTTTTTTTTGAA

109293	107380	TACAGAGTCACAACATTACT
109294	107381	CTACAGAGTCACAACATTAC
109295	107382	TCTACAGAGTCACAACATTA
109296	107383	CTCTACAGAGTCACAACATT
109297	107384	CCTCTACAGAGTCACAACAT
109298	107385	ACCTCTACAGAGTCACAACA
109299	107386	TACCTCTACAGAGTCACAAC
109300	107387	ATACCTCTACAGAGTCACAA
109301	107388	GATACCTCTACAGAGTCACA
109302	107389	TGATACCTCTACAGAGTCAC
109303	107390	GTGATACCTCTACAGAGTCA
109304	107391	GGTGATACCTCTACAGAGTC
109305	107392	AGGTGATACCTCTACAGAGT
109306	107393	AAGGTGATACCTCTACAGAG
109307	107394	CAAGGTGATACCTCTACAGA
109308	107395	CCAAGGTGATACCTCTACAG
109309	107396	ACCAAGGTGATACCTCTACA
109310	107397	TACCAAGGTGATACCTCTAC
109311	107398	CTACCAAGGTGATACCTCTA
109312	107399	ACTACCAAGGTGATACCTCT
109313	107400	GACTACCAAGGTGATACCTC
109314	107401	AGACTACCAAGGTGATACCT
109315	107402	AAGACTACCAAGGTGATACC
109316	107403	CAAGACTACCAAGGTGATAC
109317	107404	CCAAGACTACCAAGGTGATA
109318	107405	CCCAAGACTACCAAGGTGAT
109319	107406	CCCCAAGACTACCAAGGTGA
109320	107407	TCCCCAAGACTACCAAGGTG
109321	107408	TTCCCCAAGACTACCAAGGT
109322	107409	CTTCCCCAAGACTACCAAGG
109323	107410	TCTTCCCCAAGACTACCAAG
109324	107411	ATCTTCCCCAAGACTACCAA
109325	107412	GATCTTCCCCAAGACTACCA
109326	107413	AGATCTTCCCCAAGACTACC
109327	107414	CAGATCTTCCCCAAGACTAC
109328	107415	CCAGATCTTCCCCAAGACTA
109329	107416	CCCAGATCTTCCCCAAGACT
109330	107417	TCCCAGATCTTCCCCAAGAC
109331	107418	CTCCCAGATCTTCCCCAAGA
109332	107419	TCTCCCAGATCTTCCCCAAG
109333	107420	TTCTCCCAGATCTTCCCCAA
109334	107421	ATTCTCCCAGATCTTCCCCA
109335	107422	AATTCTCCCAGATCTTCCCC
109336	107423	GAATTCTCCCAGATCTTCCC
109337	107424	GGAATTCTCCCAGATCTTCC
109338	107425	GGGAATTCTCCCAGATCTTC
109339	107426	AGGGAATTCTCCCAGATCTT
109340	107427	CAGGGAATTCTCCCAGATCT
109341	107428	ACAGGGAATTCTCCCAGATC
109342	107429	TACAGGGAATTCTCCCAGAT
109343	107430	ATACAGGGAATTCTCCCAGA
109344	107431	AATACAGGGAATTCTCCCAG
109345	107432	TAATACAGGGAATTCTCCCA
109346	107433	GTAATACAGGGAATTCTCCC
109347	107434	GGTAATACAGGGAATTCTCC
109348	107435	TGGTAATACAGGGAATTCTC
109349	107436	CTGGTAATACAGGGAATTCT
109350	107437	CCTGGTAATACAGGGAATTC
109351	107438	GCCTGGTAATACAGGGAATT
109352	107439	TGCCTGGTAATACAGGGAAT
109353	107440	CTGCCTGGTAATACAGGGAA
109354	107441	ACTGCCTGGTAATACAGGGA
109355	107442	GACTGCCTGGTAATACAGGG
109356	107443	AGACTGCCTGGTAATACAGG
109357	107444	GAGACTGCCTGGTAATACAG
109358	107445	AGAGACTGCCTGGTAATACA
109359	107446	AAGAGACTGCCTGGTAATAC
109360	107447	CAAGAGACTGCCTGGTAATA
109361	107448	ACAAGAGACTGCCTGGTAAT
109362	107449	GACAAGAGACTGCCTGGTAA
109363	107450	GGACAAGAGACTGCCTGGTA

11070	9157	AACATGGTGAAACCCCGTCT
11071	9158	CAACATGGTGAAACCCCGTC
11072	9159	CCAACATGGTGAAACCCCGT
11073	9160	GCCAACATGGTGAAACCCCG
11074	9161	GGCCAACATGGTGAAACCCC
11075	9162	TGGCCAACATGGTGAAACCC
11076	9163	CTGGCCAACATGGTGAAACC
11077	9164	CCTGGCCAACATGGTGAAAC
11078	9165	TCCTGGCCAACATGGTGAAA
11079	9166	ATCCTGGCCAACATGGTGAA
11080	9167	CATCCTGGCCAACATGGTGA
11081	9168	CCATCCTGGCCAACATGGTG
11082	9169	ACCATCCTGGCCAACATGGT
11083	9170	CACCATCCTGGCCAACATGG
11084	9171	ACACCATCCTGGCCAACATG
11085	9172	GACACCATCCTGGCCAACAT
11086	9173	CGACACCATCCTGGCCAACA
11087	9174	TCGACACCATCCTGGCCAAC
11088	9175	ATCGACACCATCCTGGCCAA
11089	9176	GATCGACACCATCCTGGCCA
11090	9177	AGATCGACACCATCCTGGCC
11091	9178	GAGATCGACACCATCCTGGC
11092	9179	GGAGATCGACACCATCCTGG
11093	9180	AGGAGATCGACACCATCCTG
11094	9181	CAGGAGATCGACACCATCCT
11095	9182	TCAGGAGATCGACACCATCC
11096	9183	GTCAGGAGATCGACACCATC
11097	9184	GGTCAGGAGATCGACACCAT
11098	9185	AGGTCAGGAGATCGACACCA
11099	9186	AAGGTCAGGAGATCGACACC
11100	9187	CAAGGTCAGGAGATCGACAC
11101	9188	ACAAGGTCAGGAGATCGACA
11102	9189	CACAAGGTCAGGAGATCGAC
11103	9190	TCACAAGGTCAGGAGATCGA
11104	9191	ATCACAAGGTCAGGAGATCG
11105	9192	GATCACAAGGTCAGGAGATC
11106	9193	GGATCACAAGGTCAGGAGAT
11107	9194	CGGATCACAAGGTCAGGAGA
11108	9195	GCGGATCACAAGGTCAGGAG
11109	9196	GGCGGATCACAAGGTCAGGA
11110	9197	GGGCGGATCACAAGGTCAGG
11111	9198	TGGGCGGATCACAAGGTCAG
11112	9199	TTGGGCGGATCACAAGGTCA
11113	9200	GTTGGGCGGATCACAAGGTC
11114	9201	TGTTGGGCGGATCACAAGGT
11115	9202	CTGTTGGGCGGATCACAAGG
11116	9203	GCTGTTGGGCGGATCACAAG
11117	9204	GGCTGTTGGGCGGATCACAA
11118	9205	AGGCTGTTGGGCGGATCACA
11119	9206	GAGGCTGTTGGGCGGATCAC
11120	9207	GGAGGCTGTTGGGCGGATCA
11121	9208	GGGAGGCTGTTGGGCGGATC
11122	9209	TGGGAGGCTGTTGGGCGGAT
11123	9210	TTGGGAGGCTGTTGGGCGGA
11124	9211	TTTGGGAGGCTGTTGGGCGG
11125	9212	CTTTGGGAGGCTGTTGGGCG
11126	9213	ACTTTGGGAGGCTGTTGGGC
11127	9214	CACTTTGGGAGGCTGTTGGG
11128	9215	GCACTTTGGGAGGCTGTTGG
11129	9216	AGCACTTTGGGAGGCTGTTG
11130	9217	CAGCACTTTGGGAGGCTGTT
11131	9218	CCAGCACTTTGGGAGGCTGT
11132	9219	TCCAGCACTTTGGGAGGCTG
11133	9220	TTCCAGCACTTTGGGAGGCT
11134	9221	ATTCCAGCACTTTGGGAGGC
11135	9222	AATTCCAGCACTTTGGGAGG
11136	9223	TAATTCCAGCACTTTGGGAG
11137	9224	GTAATTCCAGCACTTTGGGA
11138	9225	TGTAATTCCAGCACTTTGGG
11139	9226	CTGTAATTCCAGCACTTTGG
11140	9227	CCTGTAATTCCAGCACTTTG

60217	58304	TTTTTTTTTTTTTTTTTGA
60218	58305	TTTTTTTTTTTTTTTTTG
60219	58306	TTTTTTTTTTTTTTTTTT
60220	58307	TTTTTTTTTTTTTTTTTT
60221	58308	TTTTTTTTTTTTTTTTTT
60222	58309	CTTTTTTTTTTTTTTTTT
60223	58310	TCTTTTTTTTTTTTTTTT
60224	58311	TTCTTTTTTTTTTTTTTT
60225	58312	ATTCTTTTTTTTTTTTTT
60226	58313	AATTCTTTTTTTTTTTTT
60227	58314	TAATTCTTTTTTTTTTTT
60228	58315	ATAATTCTTTTTTTTTTT
60229	58316	TATAATTCTTTTTTTTTT
60230	58317	TTATAATTCTTTTTTTTT
60231	58318	GTTATAATTCTTTTTTTT
60232	58319	AGTTATAATTCTTTTTTT
60233	58320	CAGTTATAATTCTTTTTT
60234	58321	ACAGTTATAATTCTTTTT
60235	58322	GACAGTTATAATTCTTTT
60236	58323	TGACAGTTATAATTCTTT
60237	58324	GTGACAGTTATAATTCTT
60238	58325	TGTGACAGTTATAATTCT
60239	58326	CTGTGACAGTTATAATTC
60240	58327	ACTGTGACAGTTATAATT
60241	58328	CACTGTGACAGTTATAATC
60242	58329	CCACTGTGACAGTTATAAT
60243	58330	GCCACTGTGACAGTTATAA
60244	58331	AGCCACTGTGACAGTTATA
60245	58332	TAGCCACTGTGACAGTTAT
60246	58333	GTAGCCACTGTGACAGTTA
60247	58334	CGTAGCCACTGTGACAGTT
60248	58335	ACGTAGCCACTGTGACAGT
60249	58336	TACGTAGCCACTGTGACAG
60250	58337	ATACGTAGCCACTGTGACAG
60251	58338	CATACGTAGCCACTGTGACA
60252	58339	CCATACGTAGCCACTGTGAC
60253	58340	TCCATACGTAGCCACTGTGA
60254	58341	CTCCATACGTAGCCACTGTG
60255	58342	GCTCCATACGTAGCCACTGT
60256	58343	TGCTCCATACGTAGCCACTG
60257	58344	ATGCTCCATACGTAGCCACT
60258	58345	GATGCTCCATACGTAGCCAC
60259	58346	GGATGCTCCATACGTAGCCA
60260	58347	TGGATGCTCCATACGTAGCC
60261	58348	TTGGATGCTCCATACGTAGC
60262	58349	TTTGGATGCTCCATACGTAG
60263	58350	TTTTGGATGCTCCATACGTA
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60265	58352	AGTTTTGGATGCTCCATACG
60266	58353	CAGTTTTGGATGCTCCATAC
60267	58354	TCAGTTTTGGATGCTCCATA
60268	58355	TTCAGTTTTGGATGCTCCAT
60269	58356	ATTCAGTTTTGGATGCTCCA
60270	58357	AATTCAGTTTTGGATGCTCC
60271	58358	AAATTCAGTTTTGGATGCTC
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60275	58362	ACATAAATTCAGTTTTGGAT
60276	58363	CACATAAATTCAGTTTTGGA
60277	58364	CCACATAAATTCAGTTTTGG
60278	58365	CCCACATAAATTCAGTTTTG
60279	58366	ACCCACATAAATTCAGTTTT
60280	58367	TACCCACATAAATTCAGTTT
60281	58368	ATACCCACATAAATTCAGTT
60282	58369	AATACCCACATAAATTCAGT
60283	58370	AAATACCCACATAAATTCAG
60284	58371	AAAATACCCACATAAATTCA
60285	58372	TAAAATACCCACATAAATTC
60286	58373	ATAAAATACCCACATAAATT
60287	58374	AATAAAATACCCACATAAAT

109364	107451	AGGACAAGAGACTGCCTGGT
109365	107452	GAGGACAAGAGACTGCCTGG
109366	107453	AGAGGACAAGAGACTGCCTG
109367	107454	AAGAGGACAAGAGACTGCCT
109368	107455	TAAGAGGACAAGAGACTGCC
109369	107456	GTAAGAGGACAAGAGACTGC
109370	107457	TGTAAGAGGACAAGAGACTG
109371	107458	ATGTAAGAGGACAAGAGACT
109372	107459	AATGTAAGAGGACAAGAGAC
109373	107460	AAATGTAAGAGGACAAGAGA
109374	107461	GAAATGTAAGAGGACAAGAG
109375	107462	AGAAATGTAAGAGGACAAGA
109376	107463	GAGAAATGTAAGAGGACAAG
109377	107464	GGAGAAATGTAAGAGGACAA
109378	107465	TGGAGAAATGTAAGAGGACA
109379	107466	TTGGAGAAATGTAAGAGGAC
109380	107467	TTTGGAGAAATGTAAGAGGA
109381	107468	GTTTGGAGAAATGTAAGAGG
109382	107469	TGTTTGGAGAAATGTAAGAG
109383	107470	TTGTTTGGAGAAATGTAAGA
109384	107471	TTTGTTTGGAGAAATGTAAG
109385	107472	ATTTGTTTGGAGAAATGTAA
109386	107473	CATTTGTTTGGAGAAATGTA
109387	107474	CCATTTGTTTGGAGAAATGT
109388	107475	TCCATTTGTTTGGAGAAATG
109389	107476	CTCCATTTGTTTGGAGAAAT
109390	107477	ACTCCATTTGTTTGGAGAAA
109391	107478	GACTCCATTTGTTTGGAGAA
109392	107479	AGACTCCATTTGTTTGGAGA
109393	107480	GAGACTCCATTTGTTTGGAG
109394	107481	AGAGACTCCATTTGTTTGGA
109395	107482	GAGAGACTCCATTTGTTTGG
109396	107483	AGAGAGACTCCATTTGTTTG
109397	107484	AAGAGAGACTCCATTTGTTT
109398	107485	AAAGAGAGACTCCATTTGTT
109399	107486	CAAAGAGAGACTCCATTTGT
109400	107487	ACAAAGAGAGACTCCATTTG
109401	107488	CACAAAGAGAGACTCCATTT
109402	107489	GCACAAAGAGAGACTCCATT
109403	107490	AGCACAAAGAGAGACTCCAT
109404	107491	CAGCACAAAGAGAGACTCCA
109405	107492	TCAGCACAAAGAGAGACTCC
109406	107493	CTCAGCACAAAGAGAGACTC
109407	107494	GCTCAGCACAAAGAGAGACT
109408	107495	AGCTCAGCACAAAGAGAGAC
109409	107496	CAGCTCAGCACAAAGAGAGA
109410	107497	GCAGCTCAGCACAAAGAGAG
109411	107498	AGCAGCTCAGCACAAAGAGA
109412	107499	AAGCAGCTCAGCACAAAGAG
109413	107500	CAAGCAGCTCAGCACAAAGA
109414	107501	CCAAGCAGCTCAGCACAAAG
109415	107502	TCCAAGCAGCTCAGCACAAA
109416	107503	CTCCAAGCAGCTCAGCACAA
109417	107504	ACTCCAAGCAGCTCAGCACA
109418	107505	AACTCCAAGCAGCTCAGCAC
109419	107506	AAACTCCAAGCAGCTCAGCA
109420	107507	CAAACTCCAAGCAGCTCAGC
109421	107508	CCAAACTCCAAGCAGCTCAG
109422	107509	CCCAAACTCCAAGCAGCTCA
109423	107510	CCCCAAACTCCAAGCAGCTC
109424	107511	TCCCCAAACTCCAAGCAGCT
109425	107512	TTCCCCAAACTCCAAGCAGC
109426	107513	CTTCCCCAAACTCCAAGCAG
109427	107514	CCTTCCCCAAACTCCAAGCA
109428	107515	CCCTTCCCCAAACTCCAAGC
109429	107516	ACCCTTCCCCAAACTCCAAG
109430	107517	CACCCTTCCCCAAACTCCAA
109431	107518	TCACCCTTCCCCAAACTCCA
109432	107519	GTCACCCTTCCCCAAACTCC
109433	107520	TGTCACCCTTCCCCAAACTC
109434	107521	GTGTCACCCTTCCCCAAACT

11141	9228	GCCTGTAATTCCAGCACTTT
11142	9229	CGCCTGTAATTCCAGCACTT
11143	9230	ACGCCTGTAATTCCAGCACT
11144	9231	CACGCCTGTAATTCCAGCAC
11145	9232	TCACGCCTGTAATTCCAGCA
11146	9233	CTCACGCCTGTAATTCCAGC
11147	9234	GCTCACGCCTGTAATTCCAG
11148	9235	AGCTCACGCCTGTAATTCCA
11149	9236	CAGCTCACGCCTGTAATTCC
11150	9237	GCAGCTCACGCCTGTAATTC
11151	9238	AGCAGCTCACGCCTGTAATT
11152	9239	CAGCAGCTCACGCCTGTAAT
11153	9240	GCAGCAGCTCACGCCTGTAA
11154	9241	CGCAGCAGCTCACGCCTGTA
11155	9242	ACGCAGCAGCTCACGCCTGT
11156	9243	GACGCAGCAGCTCACGCCTG
11157	9244	GGACGCAGCAGCTCACGCCT
11158	9245	CGGACGCAGCAGCTCACGCC
11159	9246	CCGGACGCAGCAGCTCACGC
11160	9247	GCCGGACGCAGCAGCTCACG
11161	9248	GGCCGGACGCAGCAGCTCAC
11162	9249	GGGCCGGACGCAGCAGCTCA
11163	9250	GGGGCCGGACGCAGCAGCTC
11164	9251	GGGGGCCGGACGCAGCAGCT
11165	9252	AGGGGGCCGGACGCAGCAGC
11166	9253	TAGGGGGCCGGACGCAGCAG
11167	9254	TTAGGGGGCCGGACGCAGCA
11168	9255	GTTAGGGGGCCGGACGCAGC
11169	9256	TGTTAGGGGGCCGGACGCAG
11170	9257	CTGTTAGGGGGCCGGACGCA
11171	9258	CCTGTTAGGGGGCCGGACGC
11172	9259	GCCTGTTAGGGGGCCGGACG
11173	9260	AGCCTGTTAGGGGGCCGGAC
11174	9261	AAGCCTGTTAGGGGGCCGGA
11175	9262	CAAGCCTGTTAGGGGGCCGG
11176	9263	ACAAGCCTGTTAGGGGGCCG
11177	9264	AACAAGCCTGTTAGGGGGCC
11178	9265	AAACAAGCCTGTTAGGGGGC
11179	9266	AAAACAAGCCTGTTAGGGGG
11180	9267	TAAAACAAGCCTGTTAGGGG
11181	9268	ATAAAACAAGCCTGTTAGGG
11182	9269	CATAAAACAAGCCTGTTAGG
11183	9270	CCATAAAACAAGCCTGTTAG
11184	9271	TCCATAAAACAAGCCTGTTA
11185	9272	TTCCATAAAACAAGCCTGTT
11186	9273	ATTCCATAAAACAAGCCTGT
11187	9274	TATTCCATAAAACAAGCCTG
11188	9275	GTATTCCATAAAACAAGCCT
11189	9276	TGTATTCCATAAAACAAGCC
11190	9277	CTGTATTCCATAAAACAAGC
11191	9278	ACTGTATTCCATAAAACAAG
11192	9279	GACTGTATTCCATAAAACAA
11193	9280	TGACTGTATTCCATAAAACA
11194	9281	GTGACTGTATTCCATAAAAC
11195	9282	CGTGACTGTATTCCATAAAA
11196	9283	CCGTGACTGTATTCCATAAA
11197	9284	TCCGTGACTGTATTCCATAA
11198	9285	GTCCGTGACTGTATTCCATA
11199	9286	TGTCCGTGACTGTATTCCAT
11200	9287	CTGTCCGTGACTGTATTCCA
11201	9288	ACTGTCCGTGACTGTATTCC
11202	9289	TACTGTCCGTGACTGTATTC
11203	9290	GTACTGTCCGTGACTGTATT
11204	9291	AGTACTGTCCGTGACTGTAT
11205	9292	AAGTACTGTCCGTGACTGTA
11206	9293	CAAGTACTGTCCGTGACTGT
11207	9294	GCAAGTACTGTCCGTGACTG
11208	9295	GGCAAGTACTGTCCGTGACT
11209	9296	GGGCAAGTACTGTCCGTGAC
11210	9297	AGGGCAAGTACTGTCCGTGA
11211	9298	AAGGGCAAGTACTGTCCGTG

60288	58375	TAATAAAATACCCACATAAA
60289	58376	TTAATAAAATACCCACATAA
60290	58377	ATTAATAAAATACCCACATA
60291	58378	TATTAATAAAATACCCACAT
60292	58379	ATATTAATAAAATACCCACA
60293	58380	CATATTAATAAAATACCCAC
60294	58381	GCATATTAATAAAATACCCA
60295	58382	TGCATATTAATAAAATACCC
60296	58383	TTGCATATTAATAAAATACC
60297	58384	ATTGCATATTAATAAAATAC
60298	58385	TATTGCATATTAATAAAATA
60299	58386	ATATTGCATATTAATAAAAT
60300	58387	TATATTGCATATTAATAAAA
60301	58388	CTATATTGCATATTAATAAA
60302	58389	GCTATATTGCATATTAATAA
60303	58390	TGCTATATTGCATATTAATA
60304	58391	GTGCTATATTGCATATTAAT
60305	58392	AGTGCTATATTGCATATTAA
60306	58393	AAGTGCTATATTGCATATTA
60307	58394	AAAGTGCTATATTGCATATT
60308	58395	TAAAGTGCTATATTGCATAT
60309	58396	TTAAAGTGCTATATTGCATA
60310	58397	ATTAAAGTGCTATATTGCAT
60311	58398	AATTAAAGTGCTATATTGCA
60312	58399	GAATTAAAGTGCTATATTGC
60313	58400	AGAATTAAAGTGCTATATTG
60314	58401	CAGAATTAAAGTGCTATATT
60315	58402	CCAGAATTAAAGTGCTATAT
60316	58403	TCCAGAATTAAAGTGCTATA
60317	58404	CTCCAGAATTAAAGTGCTAT
60318	58405	CCTCCAGAATTAAAGTGCTA
60319	58406	TCCTCCAGAATTAAAGTGCT
60320	58407	TTCCTCCAGAATTAAAGTGC
60321	58408	TTTCCTCCAGAATTAAAGTG
60322	58409	CTTTCCTCCAGAATTAAAGT
60323	58410	CCTTTCCTCCAGAATTAAAG
60324	58411	ACCTTTCCTCCAGAATTAAA
60325	58412	CACCTTTCCTCCAGAATTAA
60326	58413	CCACCTTTCCTCCAGAATTA
60327	58414	TCCACCTTTCCTCCAGAATT
60328	58415	ATCCACCTTTCCTCCAGAAT
60329	58416	AATCCACCTTTCCTCCAGAA
60330	58417	TAATCCACCTTTCCTCCAGA
60331	58418	ATAATCCACCTTTCCTCCAG
60332	58419	AATAATCCACCTTTCCTCCA
60333	58420	GAATAATCCACCTTTCCTCC
60334	58421	TGAATAATCCACCTTTCCTC
60335	58422	CTGAATAATCCACCTTTCCT
60336	58423	ACTGAATAATCCACCTTTCC
60337	58424	TACTGAATAATCCACCTTTC
60338	58425	TTACTGAATAATCCACCTTT
60339	58426	TTTACTGAATAATCCACCTT
60340	58427	ATTTACTGAATAATCCACCT
60341	58428	CATTTACTGAATAATCCACC
60342	58429	TCATTTACTGAATAATCCAC
60343	58430	ATCATTTACTGAATAATCCA
60344	58431	AATCATTTACTGAATAATCC
60345	58432	GAATCATTTACTGAATAATC
60346	58433	AGAATCATTTACTGAATAAT
60347	58434	CAGAATCATTTACTGAATAA
60348	58435	CCAGAATCATTTACTGAATA
60349	58436	CCCAGAATCATTTACTGAAT
60350	58437	TCCCAGAATCATTTACTGAA
60351	58438	GTCCCAGAATCATTTACTGA
60352	58439	TGTCCCAGAATCATTTACTG
60353	58440	ATGTCCCAGAATCATTTACT
60354	58441	AATGTCCCAGAATCATTTAC
60355	58442	CAATGTCCCAGAATCATTTA
60356	58443	CCAATGTCCCAGAATCATTT
60357	58444	CCCAATGTCCCAGAATCATT
60358	58445	CCCCAATGTCCCAGAATCAT

109435	107522	TGTGTCACCCTTCCCCAAAC
109436	107523	TTGTGTCACCCTTCCCCAAA
109437	107524	CTTGTGTCACCCTTCCCCAA
109438	107525	GCTTGTGTCACCCTTCCCCA
109439	107526	TGCTTGTGTCACCCTTCCCC
109440	107527	GTGCTTGTGTCACCCTTCCC
109441	107528	AGTGCTTGTGTCACCCTTCC
109442	107529	CAGTGCTTGTGTCACCCTTC
109443	107530	GCAGTGCTTGTGTCACCCTT
109444	107531	GGCAGTGCTTGTGTCACCCT
109445	107532	TGGCAGTGCTTGTGTCACCC
109446	107533	ATGGCAGTGCTTGTGTCACC
109447	107534	CATGGCAGTGCTTGTGTCAC
109448	107535	CCATGGCAGTGCTTGTGTCA
109449	107536	GCCATGGCAGTGCTTGTGTC
109450	107537	GGCCATGGCAGTGCTTGTGT
109451	107538	TGGCCATGGCAGTGCTTGTG
109452	107539	GTGGCCATGGCAGTGCTTGT
109453	107540	GGTGGCCATGGCAGTGCTTG
109454	107541	CGGTGGCCATGGCAGTGCTT
109455	107542	ACGGTGGCCATGGCAGTGCT
109456	107543	GACGGTGGCCATGGCAGTGC
109457	107544	TGACGGTGGCCATGGCAGTG
109458	107545	GTGACGGTGGCCATGGCAGT
109459	107546	AGTGACGGTGGCCATGGCAG
109460	107547	CAGTGACGGTGGCCATGGCA
109461	107548	CCAGTGACGGTGGCCATGGC
109462	107549	TCCAGTGACGGTGGCCATGG
109463	107550	TTCCAGTGACGGTGGCCATG
109464	107551	GTTCCAGTGACGGTGGCCAT
109465	107552	AGTTCCAGTGACGGTGGCCA
109466	107553	CAGTTCCAGTGACGGTGGCC
109467	107554	ACAGTTCCAGTGACGGTGGC
109468	107555	TACAGTTCCAGTGACGGTGG
109469	107556	GTACAGTTCCAGTGACGGTG
109470	107557	AGTACAGTTCCAGTGACGGT
109471	107558	AAGTACAGTTCCAGTGACGG
109472	107559	CAAGTACAGTTCCAGTGACG
109473	107560	CCAAGTACAGTTCCAGTGAC
109474	107561	ACCAAGTACAGTTCCAGTGA
109475	107562	GACCAAGTACAGTTCCAGTG
109476	107563	AGACCAAGTACAGTTCCAGT
109477	107564	GAGACCAAGTACAGTTCCAG
109478	107565	TGAGACCAAGTACAGTTCCA
109479	107566	GTGAGACCAAGTACAGTTCC
109480	107567	GGTGAGACCAAGTACAGTTC
109481	107568	GGGTGAGACCAAGTACAGTT
109482	107569	TGGGTGAGACCAAGTACAGT
109483	107570	TTGGGTGAGACCAAGTACAG
109484	107571	CTTGGGTGAGACCAAGTACA
109485	107572	CCTTGGGTGAGACCAAGTAC
109486	107573	GCCTTGGGTGAGACCAAGTA
109487	107574	GGCCTTGGGTGAGACCAAGT
109488	107575	AGGCCTTGGGTGAGACCAAG
109489	107576	CAGGCCTTGGGTGAGACCAA
109490	107577	ACAGGCCTTGGGTGAGACCA
109491	107578	CACAGGCCTTGGGTGAGACC
109492	107579	CCACAGGCCTTGGGTGAGAC
109493	107580	GCCACAGGCCTTGGGTGAGA
109494	107581	TGCCACAGGCCTTGGGTGAG
109495	107582	CTGCCACAGGCCTTGGGTGA
109496	107583	GCTGCCACAGGCCTTGGGTG
109497	107584	AGCTGCCACAGGCCTTGGGT
109498	107585	TAGCTGCCACAGGCCTTGGG
109499	107586	ATAGCTGCCACAGGCCTTGG
109500	107587	AATAGCTGCCACAGGCCTTG
109501	107588	AAATAGCTGCCACAGGCCTT
109502	107589	AAAATAGCTGCCACAGGCCT
109503	107590	GAAAATAGCTGCCACAGGCC
109504	107591	AGAAAATAGCTGCCACAGGC
109505	107592	CAGAAAATAGCTGCCACAGG

11212	9299	GAAGGGCAAGTACTGTCCGT
11213	9300	TGAAGGGCAAGTACTGTCCG
11214	9301	CTGAAGGGCAAGTACTGTCC
11215	9302	CCTGAAGGGCAAGTACTGTC
11216	9303	TCCTGAAGGGCAAGTACTGT
11217	9304	ATCCTGAAGGGCAAGTACTG
11218	9305	TATCCTGAAGGGCAAGTACT
11219	9306	ATATCCTGAAGGGCAAGTAC
11220	9307	GATATCCTGAAGGGCAAGTA
11221	9308	AGATATCCTGAAGGGCAAGT
11222	9309	AAGATATCCTGAAGGGCAAG
11223	9310	AAAGATATCCTGAAGGGCAA
11224	9311	AAAAGATATCCTGAAGGGCA
11225	9312	AAAAAGATATCCTGAAGGGC
11226	9313	CAAAAAGATATCCTGAAGGG
11227	9314	ACAAAAAGATATCCTGAAGG
11228	9315	TACAAAAAGATATCCTGAAG
11229	9316	TTACAAAAAGATATCCTGAA
11230	9317	GTTACAAAAAGATATCCTGA
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11232	9319	AGGTTACAAAAAGATATCCT
11233	9320	AAGGTTACAAAAAGATATCC
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11236	9323	ATCAAGGTTACAAAAAGATA
11237	9324	AATCAAGGTTACAAAAAGAT
11238	9325	AAATCAAGGTTACAAAAAGA
11239	9326	AAAATCAAGGTTACAAAAAG
11240	9327	CAAAATCAAGGTTACAAAAA
11241	9328	CCAAAATCAAGGTTACAAAA
11242	9329	GCCAAAATCAAGGTTACAAA
11243	9330	AGCCAAAATCAAGGTTACAA
11244	9331	AAGCCAAAATCAAGGTTACA
11245	9332	CAAGCCAAAATCAAGGTTAC
11246	9333	GCAAGCCAAAATCAAGGTTA
11247	9334	AGCAAGCCAAAATCAAGGTT
11248	9335	TAGCAAGCCAAAATCAAGGT
11249	9336	TTAGCAAGCCAAAATCAAGG
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11258	9345	CCTCCTATTTTAGCAAGCCA
11259	9346	ACCTCCTATTTTAGCAAGCC
11260	9347	GACCTCCTATTTTAGCAAGC
11261	9348	AGACCTCCTATTTTAGCAAG
11262	9349	TAGACCTCCTATTTTAGCAA
11263	9350	ATAGACCTCCTATTTTAGCA
11264	9351	AATAGACCTCCTATTTTAGC
11265	9352	AAATAGACCTCCTATTTTAG
11266	9353	AAAATAGACCTCCTATTTTA
11267	9354	GAAAATAGACCTCCTATTTT
11268	9355	AGAAAATAGACCTCCTATTT
11269	9356	AAGAAAATAGACCTCCTATT
11270	9357	AAAGAAAATAGACCTCCTAT
11271	9358	AAAAGAAAATAGACCTCCTA
11272	9359	GAAAAGAAAATAGACCTCCT
11273	9360	AGAAAAGAAAATAGACCTCC
11274	9361	AAGAAAAGAAAATAGACCTC
11275	9362	AAAGAAAAGAAAATAGACCT
11276	9363	CAAAGAAAAGAAAATAGACC
11277	9364	ACAAAGAAAAGAAAATAGAC
11278	9365	AACAAAGAAAAGAAAATAGA
11279	9366	AAACAAAGAAAAGAAAATAG
11280	9367	AAAACAAAGAAAAGAAAATA
11281	9368	AAAAACAAAGAAAAGAAAAT
11282	9369	TAAAAACAAAGAAAAGAAAA

60359	58446	TCCCCAATGTCCCAGAATCA
60360	58447	GTCCCCAATGTCCCAGAATC
60361	58448	TGTCCCCAATGTCCCAGAAT
60362	58449	TTGTCCCCAATGTCCCAGAA
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60364	58451	ATTTGTCCCCAATGTCCCAG
60365	58452	AATTTGTCCCCAATGTCCCA
60366	58453	TAATTTGTCCCCAATGTCCC
60367	58454	CTAATTTGTCCCCAATGTCC
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60370	58457	TATCTAATTTGTCCCCAATG
60371	58458	GTATCTAATTTGTCCCCAAT
60372	58459	GGTATCTAATTTGTCCCCAA
60373	58460	AGGTATCTAATTTGTCCCCA
60374	58461	TAGGTATCTAATTTGTCCCC
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60377	58464	AAGTAGGTATCTAATTTGTC
60378	58465	GAAGTAGGTATCTAATTTGT
60379	58466	TGAAGTAGGTATCTAATTTG
60380	58467	GTGAAGTAGGTATCTAATTT
60381	58468	TGTGAAGTAGGTATCTAATT
60382	58469	GTGTGAAGTAGGTATCTAAT
60383	58470	AGTGTGAAGTAGGTATCTAA
60384	58471	CAGTGTGAAGTAGGTATCTA
60385	58472	TCAGTGTGAAGTAGGTATCT
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60387	58474	TATCAGTGTGAAGTAGGTAT
60388	58475	TTATCAGTGTGAAGTAGGTA
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60401	58488	TATTTGGTTTTATTTATCAG
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60403	58490	TCTATTTGGTTTTATTTATC
60404	58491	ATCTATTTGGTTTTATTTAT
60405	58492	AATCTATTTGGTTTTATTTA
60406	58493	TAATCTATTTGGTTTTATTT
60407	58494	TTAATCTATTTGGTTTTATT
60408	58495	ATTAATCTATTTGGTTTTAT
60409	58496	CATTAATCTATTTGGTTTTA
60410	58497	TCATTAATCTATTTGGTTTT
60411	58498	CTCATTAATCTATTTGGTTT
60412	58499	TCTCATTAATCTATTTGGTT
60413	58500	TTCTCATTAATCTATTTGGT
60414	58501	TTTCTCATTAATCTATTTGG
60415	58502	TTTTCTCATTAATCTATTTG
60416	58503	GTTTTCTCATTAATCTATTT
60417	58504	AGTTTTCTCATTAATCTATT
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60419	58506	ACAGTTTTCTCATTAATCTA
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60424	58511	TAATCACAGTTTTCTCATTA
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60426	58513	TTTAATCACAGTTTTCTCAT
60427	58514	GTTTAATCACAGTTTTCTCA
60428	58515	TGTTTAATCACAGTTTTCTC
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109506	107593	CCAGAAAATAGCTGCCACAG
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109508	107595	GGCCAGAAAATAGCTGCCAC
109509	107596	TGGCCAGAAAATAGCTGCCA
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109511	107598	GGTGGCCAGAAAATAGCTGC
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109513	107600	GTGGTGGCCAGAAAATAGCT
109514	107601	AGTGGTGGCCAGAAAATAGC
109515	107602	CAGTGGTGGCCAGAAAATAG
109516	107603	TCAGTGGTGGCCAGAAAATA
109517	107604	ATCAGTGGTGGCCAGAAAAT
109518	107605	CATCAGTGGTGGCCAGAAAA
109519	107606	ACATCAGTGGTGGCCAGAAA
109520	107607	AACATCAGTGGTGGCCAGAA
109521	107608	TAACATCAGTGGTGGCCAGA
109522	107609	TTAACATCAGTGGTGGCCAG
109523	107610	ATTAACATCAGTGGTGGCCA
109524	107611	AATTAACATCAGTGGTGGCC
109525	107612	AAATTAACATCAGTGGTGGC
109526	107613	TAAATTAACATCAGTGGTGG
109527	107614	TTAAATTAACATCAGTGGTG
109528	107615	CTTAAATTAACATCAGTGGT
109529	107616	CCTTAAATTAACATCAGTGG
109530	107617	GCCTTAAATTAACATCAGTG
109531	107618	GGCCTTAAATTAACATCAGT
109532	107619	GGGCCTTAAATTAACATCAG
109533	107620	TGGGCCTTAAATTAACATCA
109534	107621	TTGGGCCTTAAATTAACATC
109535	107622	CTTGGGCCTTAAATTAACAT
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109540	107627	GCACCCTTGGGCCTTAAATT
109541	107628	AGCACCCTTGGGCCTTAAAT
109542	107629	AAGCACCCTTGGGCCTTAAA
109543	107630	AAAGCACCCTTGGGCCTTAA
109544	107631	TAAAGCACCCTTGGGCCTTA
109545	107632	CTAAAGCACCCTTGGGCCTT
109546	107633	ACTAAAGCACCCTTGGGCCT
109547	107634	GACTAAAGCACCCTTGGGCC
109548	107635	TGACTAAAGCACCCTTGGGC
109549	107636	CTGACTAAAGCACCCTTGGG
109550	107637	ACTGACTAAAGCACCCTTGG
109551	107638	TACTGACTAAAGCACCCTTG
109552	107639	CTACTGACTAAAGCACCCTT
109553	107640	CCTACTGACTAAAGCACCCT
109554	107641	ACCTACTGACTAAAGCACCC
109555	107642	CACCTACTGACTAAAGCACC
109556	107643	TCACCTACTGACTAAAGCAC
109557	107644	TTCACCTACTGACTAAAGCA
109558	107645	CTTCACCTACTGACTAAAGC
109559	107646	TCTTCACCTACTGACTAAAG
109560	107647	TTCTTCACCTACTGACTAAA
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109562	107649	GATTCTTCACCTACTGACTA
109563	107650	GGATTCTTCACCTACTGACT
109564	107651	AGGATTCTTCACCTACTGAC
109565	107652	CAGGATTCTTCACCTACTGA
109566	107653	GCAGGATTCTTCACCTACTG
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109568	107655	TTGCAGGATTCTTCACCTAC
109569	107656	CTTGCAGGATTCTTCACCTA
109570	107657	TCTTGCAGGATTCTTCACCT
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109572	107659	GTTCTTGCAGGATTCTTCAC
109573	107660	AGTTCTTGCAGGATTCTTCA
109574	107661	CAGTTCTTGCAGGATTCTTC
109575	107662	CCAGTTCTTGCAGGATTCTT
109576	107663	CCCAGTTCTTGCAGGATTCT

11283	9370	TTAAAAACAAAGAAAAGAAA
11284	9371	ATTAAAAACAAAGAAAAGAA
11285	9372	CATTAAAAACAAAGAAAAGA
11286	9373	ACATTAAAAACAAAGAAAAG
11287	9374	TACATTAAAAACAAAGAAAA
11288	9375	ATACATTAAAAACAAAGAAA
11289	9376	CATACATTAAAAACAAAGAA
11290	9377	ACATACATTAAAAACAAAGA
11291	9378	CACATACATTAAAAACAAAG
11292	9379	CCACATACATTAAAAACAAA
11293	9380	ACCACATACATTAAAAACAA
11294	9381	AACCACATACATTAAAAACA
11295	9382	GAACCACATACATTAAAAAC
11296	9383	AGAACCACATACATTAAAAA
11297	9384	CAGAACCACATACATTAAAA
11298	9385	ACAGAACCACATACATTAAA
11299	9386	TACAGAACCACATACATTAA
11300	9387	GTACAGAACCACATACATTA
11301	9388	AGTACAGAACCACATACATT
11302	9389	AAGTACAGAACCACATACAT
11303	9390	TAAGTACAGAACCACATACA
11304	9391	GTAAGTACAGAACCACATAC
11305	9392	CGTAAGTACAGAACCACATA
11306	9393	ACGTAAGTACAGAACCACAT
11307	9394	CACGTAAGTACAGAACCACA
11308	9395	CCACGTAAGTACAGAACCAC
11309	9396	ACCACGTAAGTACAGAACCA
11310	9397	CACCACGTAAGTACAGAACC
11311	9398	ACACCACGTAAGTACAGAAC
11312	9399	CACACCACGTAAGTACAGAA
11313	9400	TCACACCACGTAAGTACAGA
11314	9401	TTCACACCACGTAAGTACAG
11315	9402	TTTCACACCACGTAAGTACA
11316	9403	ATTTCACACCACGTAAGTAC
11317	9404	GATTTCACACCACGTAAGTA
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11319	9406	TAGATTTCACACCACGTAAG
11320	9407	GTAGATTTCACACCACGTAA
11321	9408	TGTAGATTTCACACCACGTA
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11323	9410	TATGTAGATTTCACACCACG
11324	9411	TTATGTAGATTTCACACCAC
11325	9412	TTTATGTAGATTTCACACCA
11326	9413	ATTTATGTAGATTTCACACC
11327	9414	CATTTATGTAGATTTCACAC
11328	9415	ACATTTATGTAGATTTCACA
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11330	9417	TAACATTTATGTAGATTTCA
11331	9418	TTAACATTTATGTAGATTTC
11332	9419	TTTAACATTTATGTAGATTT
11333	9420	ATTTAACATTTATGTAGATT
11334	9421	GATTTAACATTTATGTAGAT
11335	9422	GGATTTAACATTTATGTAGA
11336	9423	AGGATTTAACATTTATGTAG
11337	9424	AAGGATTTAACATTTATGTA
11338	9425	CAAGGATTTAACATTTATGT
11339	9426	CCAAGGATTTAACATTTATG
11340	9427	ACCAAGGATTTAACATTTAT
11341	9428	AACCAAGGATTTAACATTTA
11342	9429	TAACCAAGGATTTAACATTT
11343	9430	ATAACCAAGGATTTAACATT
11344	9431	AATAACCAAGGATTTAACAT
11345	9432	AAATAACCAAGGATTTAACA
11346	9433	TAAATAACCAAGGATTTAAC
11347	9434	ATAAATAACCAAGGATTTAA
11348	9435	AATAAATAACCAAGGATTTA
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11350	9437	TAAATAAATAACCAAGGATT
11351	9438	ATAAATAAATAACCAAGGAT
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60430	58517	TTTGTTTAATCACAGTTTTC
60431	58518	TTTTGTTTAATCACAGTTTT
60432	58519	GTTTTGTTTAATCACAGTTT
60433	58520	TGTTTTGTTTAATCACAGTT
60434	58521	TTGTTTTGTTTAATCACAGT
60435	58522	GTTGTTTTGTTTAATCACAG
60436	58523	TGTTGTTTTGTTTAATCACA
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60446	58533	GTAGTCTGGGTGTTGTTTTG
60447	58534	TGTAGTCTGGGTGTTGTTTT
60448	58535	GTGTAGTCTGGGTGTTGTTT
60449	58536	AGTGTAGTCTGGGTGTTGTT
60450	58537	CAGTGTAGTCTGGGTGTTGT
60451	58538	CCAGTGTAGTCTGGGTGTTG
60452	58539	TCCAGTGTAGTCTGGGTGTT
60453	58540	CTCCAGTGTAGTCTGGGTGT
60454	58541	GCTCCAGTGTAGTCTGGGTG
60455	58542	TGCTCCAGTGTAGTCTGGGT
60456	58543	TTGCTCCAGTGTAGTCTGGG
60457	58544	TTTGCTCCAGTGTAGTCTGG
60458	58545	ATTTGCTCCAGTGTAGTCTG
60459	58546	GATTTGCTCCAGTGTAGTCT
60460	58547	AGATTTGCTCCAGTGTAGTC
60461	58548	CAGATTTGCTCCAGTGTAGT
60462	58549	ACAGATTTGCTCCAGTGTAG
60463	58550	CACAGATTTGCTCCAGTGTA
60464	58551	TCACAGATTTGCTCCAGTGT
60465	58552	TTCACAGATTTGCTCCAGTG
60466	58553	ATTCACAGATTTGCTCCAGT
60467	58554	AATTCACAGATTTGCTCCAG
60468	58555	AAATTCACAGATTTGCTCCA
60469	58556	CAAATTCACAGATTTGCTCC
60470	58557	ACAAATTCACAGATTTGCTC
60471	58558	AACAAATTCACAGATTTGCT
60472	58559	AAACAAATTCACAGATTTGC
60473	58560	TAAACAAATTCACAGATTTG
60474	58561	TTAAACAAATTCACAGATTT
60475	58562	ATTAAACAAATTCACAGATT
60476	58563	AATTAAACAAATTCACAGAT
60477	58564	AAATTAAACAAATTCACAGA
60478	58565	AAAATTAAACAAATTCACAG
60479	58566	CAAAATTAAACAAATTCACA
60480	58567	TCAAAATTAAACAAATTCAC
60481	58568	CTCAAAATTAAACAAATTCA
60482	58569	ACTCAAAATTAAACAAATTC
60483	58570	CACTCAAAATTAAACAAATT
60484	58571	CCACTCAAAATTAAACAAAT
60485	58572	TCCACTCAAAATTAAACAAA
60486	58573	CTCCACTCAAAATTAAACAA
60487	58574	TCTCCACTCAAAATTAAACA
60488	58575	TTCTCCACTCAAAATTAAAC
60489	58576	CTTCTCCACTCAAAATTAAA
60490	58577	CCTTCTCCACTCAAAATTAA
60491	58578	TCCTTCTCCACTCAAAATTA
60492	58579	GTCCTTCTCCACTCAAAATT
60493	58580	AGTCCTTCTCCACTCAAAAT
60494	58581	AAGTCCTTCTCCACTCAAAA
60495	58582	AAAGTCCTTCTCCACTCAAA
60496	58583	TAAAGTCCTTCTCCACTCAA
60497	58584	ATAAAGTCCTTCTCCACTCA
60498	58585	TATAAAGTCCTTCTCCACTC
60499	58586	TTATAAAGTCCTTCTCCACT
60500	58587	CTTATAAAGTCCTTCTCCAC

109577	107664	ACCCAGTTCTTGCAGGATTC
109578	107665	GACCCAGTTCTTGCAGGATT
109579	107666	AGACCCAGTTCTTGCAGGAT
109580	107667	AAGACCCAGTTCTTGCAGGA
109581	107668	AAAGACCCAGTTCTTGCAGG
109582	107669	TAAAGACCCAGTTCTTGCAG
109583	107670	GTAAAGACCCAGTTCTTGCA
109584	107671	AGTAAAGACCCAGTTCTTGC
109585	107672	AAGTAAAGACCCAGTTCTTG
109586	107673	AAAGTAAAGACCCAGTTCTT
109587	107674	GAAAGTAAAGACCCAGTTCT
109588	107675	TGAAAGTAAAGACCCAGTTC
109589	107676	CTGAAAGTAAAGACCCAGTT
109590	107677	ACTGAAAGTAAAGACCCAGT
109591	107678	CACTGAAAGTAAAGACCCAG
109592	107679	GCACTGAAAGTAAAGACCCA
109593	107680	TGCACTGAAAGTAAAGACCC
109594	107681	CTGCACTGAAAGTAAAGACC
109595	107682	GCTGCACTGAAAGTAAAGAC
109596	107683	TGCTGCACTGAAAGTAAAGA
109597	107684	CTGCTGCACTGAAAGTAAAG
109598	107685	CCTGCTGCACTGAAAGTAAA
109599	107686	ACCTGCTGCACTGAAAGTAA
109600	107687	AACCTGCTGCACTGAAAGTA
109601	107688	GAACCTGCTGCACTGAAAGT
109602	107689	GGAACCTGCTGCACTGAAAG
109603	107690	GGGAACCTGCTGCACTGAAA
109604	107691	AGGGAACCTGCTGCACTGAA
109605	107692	AAGGGAACCTGCTGCACTGA
109606	107693	GAAGGGAACCTGCTGCACTG
109607	107694	AGAAGGGAACCTGCTGCACT
109608	107695	CAGAAGGGAACCTGCTGCAC
109609	107696	CCAGAAGGGAACCTGCTGCA
109610	107697	GCCAGAAGGGAACCTGCTGC
109611	107698	GGCCAGAAGGGAACCTGCTG
109612	107699	GGGCCAGAAGGGAACCTGCT
109613	107700	TGGGCCAGAAGGGAACCTGC
109614	107701	CTGGGCCAGAAGGGAACCTG
109615	107702	CCTGGGCCAGAAGGGAACCT
109616	107703	CCCTGGGCCAGAAGGGAACC
109617	107704	ACCCTGGGCCAGAAGGGAAC
109618	107705	CACCCTGGGCCAGAAGGGAA
109619	107706	ACACCCTGGGCCAGAAGGGA
109620	107707	CACACCCTGGGCCAGAAGGG
109621	107708	ACACACCCTGGGCCAGAAGG
109622	107709	GACACACCCTGGGCCAGAAG
109623	107710	AGACACACCCTGGGCCAGAA
109624	107711	TAGACACACCCTGGGCCAGA
109625	107712	CTAGACACACCCTGGGCCAG
109626	107713	TCTAGACACACCCTGGGCCA
109627	107714	TTCTAGACACACCCTGGGCC
109628	107715	TTTCTAGACACACCCTGGGC
109629	107716	ATTTCTAGACACACCCTGGG
109630	107717	CATTTCTAGACACACCCTGG
109631	107718	GCATTTCTAGACACACCCTG
109632	107719	AGCATTTCTAGACACACCCT
109633	107720	CAGCATTTCTAGACACACCC
109634	107721	GCAGCATTTCTAGACACACC
109635	107722	GGCAGCATTTCTAGACACAC
109636	107723	GGGCAGCATTTCTAGACACA
109637	107724	TGGGCAGCATTTCTAGACAC
109638	107725	CTGGGCAGCATTTCTAGACA
109639	107726	CCTGGGCAGCATTTCTAGAC
109640	107727	TCCTGGGCAGCATTTCTAGA
109641	107728	CTCCTGGGCAGCATTTCTAG
109642	107729	GCTCCTGGGCAGCATTTCTA
109643	107730	GGCTCCTGGGCAGCATTTCT
109644	107731	TGGCTCCTGGGCAGCATTTC
109645	107732	CTGGCTCCTGGGCAGCATTT
109646	107733	CCTGGCTCCTGGGCAGCATT
109647	107734	CCCTGGCTCCTGGGCAGCAT

11354	9441	AAAATAAATAAATAACCAAG
11355	9442	CAAAATAAATAAATAACCAA
11356	9443	TCAAAATAAATAAATAACCA
11357	9444	CTCAAAATAAATAAATAACC
11358	9445	TCTCAAAATAAATAAATAAC
11359	9446	GTCTCAAAATAAATAAATAA
11360	9447	TGTCTCAAAATAAATAAATA
11361	9448	CTGTCTCAAAATAAATAAAT
11362	9449	TCTGTCTCAAAATAAATAAA
11363	9450	CTCTGTCTCAAAATAAATAA
11364	9451	ACTCTGTCTCAAAATAAATA
11365	9452	GACTCTGTCTCAAAATAAAT
11366	9453	AGACTCTGTCTCAAAATAAA
11367	9454	GAGACTCTGTCTCAAAATAA
11368	9455	TGAGACTCTGTCTCAAAATA
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11370	9457	AGTGAGACTCTGTCTCAAAA
11371	9458	GAGTGAGACTCTGTCTCAAA
11372	9459	AGAGTGAGACTCTGTCTCAA
11373	9460	CAGAGTGAGACTCTGTCTCA
11374	9461	ACAGAGTGAGACTCTGTCTC
11375	9462	GACAGAGTGAGACTCTGTCT
11376	9463	TGACAGAGTGAGACTCTGTC
11377	9464	GTGACAGAGTGAGACTCTGT
11378	9465	GGTGACAGAGTGAGACTCTG
11379	9466	GGGTGACAGAGTGAGACTCT
11380	9467	TGGGTGACAGAGTGAGACTC
11381	9468	CTGGGTGACAGAGTGAGACT
11382	9469	ACTGGGTGACAGAGTGAGAC
11383	9470	GACTGGGTGACAGAGTGAGA
11384	9471	AGACTGGGTGACAGAGTGAG
11385	9472	CAGACTGGGTGACAGAGTGA
11386	9473	CCAGACTGGGTGACAGAGTG
11387	9474	TCCAGACTGGGTGACAGAGT
11388	9475	TTCCAGACTGGGTGACAGAG
11389	9476	TTTCCAGACTGGGTGACAGA
11390	9477	CTTTCCAGACTGGGTGACAG
11391	9478	GCTTTCCAGACTGGGTGACA
11392	9479	TGCTTTCCAGACTGGGTGAC
11393	9480	CTGCTTTCCAGACTGGGTGA
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11396	9483	CCACTGCTTTCCAGACTGGG
11397	9484	GCCACTGCTTTCCAGACTGG
11398	9485	TGCCACTGCTTTCCAGACTG
11399	9486	ATGCCACTGCTTTCCAGACT
11400	9487	TATGCCACTGCTTTCCAGAC
11401	9488	TTATGCCACTGCTTTCCAGA
11402	9489	ATTATGCCACTGCTTTCCAG
11403	9490	GATTATGCCACTGCTTTCCA
11404	9491	AGATTATGCCACTGCTTTCC
11405	9492	GAGATTATGCCACTGCTTTC
11406	9493	CGAGATTATGCCACTGCTTT
11407	9494	CCGAGATTATGCCACTGCTT
11408	9495	GCCGAGATTATGCCACTGCT
11409	9496	AGCCGAGATTATGCCACTGC
11410	9497	GAGCCGAGATTATGCCACTG
11411	9498	TGAGCCGAGATTATGCCACT
11412	9499	GTGAGCCGAGATTATGCCAC
11413	9500	AGTGAGCCGAGATTATGCCA
11414	9501	CAGTGAGCCGAGATTATGCC
11415	9502	ACAGTGAGCCGAGATTATGC
11416	9503	TACAGTGAGCCGAGATTATG
11417	9504	TTACAGTGAGCCGAGATTAT
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11419	9506	GGTTACAGTGAGCCGAGATT
11420	9507	AGGTTACAGTGAGCCGAGAT
11421	9508	GAGGTTACAGTGAGCCGAGA
11422	9509	GGAGGTTACAGTGAGCCGAG
11423	9510	TGGAGGTTACAGTGAGCCGA
11424	9511	GTGGAGGTTACAGTGAGCCG

60501	58588	GCTTATAAAGTCCTTCTCCA
60502	58589	TGCTTATAAAGTCCTTCTCC
60503	58590	ATGCTTATAAAGTCCTTCTC
60504	58591	CATGCTTATAAAGTCCTTCT
60505	58592	TCATGCTTATAAAGTCCTTC
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60508	58595	TAGTCATGCTTATAAAGTCC
60509	58596	GTAGTCATGCTTATAAAGTC
60510	58597	GGTAGTCATGCTTATAAAGT
60511	58598	TGGTAGTCATGCTTATAAAG
60512	58599	CTGGTAGTCATGCTTATAAA
60513	58600	TCTGGTAGTCATGCTTATAA
60514	58601	CTCTGGTAGTCATGCTTATA
60515	58602	GCTCTGGTAGTCATGCTTAT
60516	58603	TGCTCTGGTAGTCATGCTTA
60517	58604	TTGCTCTGGTAGTCATGCTT
60518	58605	TTTGCTCTGGTAGTCATGCT
60519	58606	TTTTGCTCTGGTAGTCATGC
60520	58607	TTTTTGCTCTGGTAGTCATG
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60524	58611	GATTTTTTTGCTCTGGTAGT
60525	58612	TGATTTTTTTGCTCTGGTAG
60526	58613	ATGATTTTTTTGCTCTGGTA
60527	58614	CATGATTTTTTTGCTCTGGT
60528	58615	TCATGATTTTTTTGCTCTGG
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60534	58621	TTTACTTCATGATTTTTTTG
60535	58622	TTTTACTTCATGATTTTTTT
60536	58623	CTTTTACTTCATGATTTTTT
60537	58624	TCTTTTACTTCATGATTTTT
60538	58625	ATCTTTTACTTCATGATTTT
60539	58626	GATCTTTTACTTCATGATTT
60540	58627	CGATCTTTTACTTCATGATT
60541	58628	TCGATCTTTTACTTCATGAT
60542	58629	ATCGATCTTTTACTTCATGA
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60546	58633	AGGTATCGATCTTTTACTTC
60547	58634	AAGGTATCGATCTTTTACTT
60548	58635	AAAGGTATCGATCTTTTACT
60549	58636	CAAAGGTATCGATCTTTTAC
60550	58637	TCAAAGGTATCGATCTTTTA
60551	58638	ATCAAAGGTATCGATCTTTT
60552	58639	AATCAAAGGTATCGATCTTT
60553	58640	TAATCAAAGGTATCGATCTT
60554	58641	ATAATCAAAGGTATCGATCT
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60558	58645	CTTTATAATCAAAGGTATCG
60559	58646	TCTTTATAATCAAAGGTATC
60560	58647	CTCTTTATAATCAAAGGTAT
60561	58648	TCTCTTTATAATCAAAGGTA
60562	58649	ATCTCTTTATAATCAAAGGT
60563	58650	AATCTCTTTATAATCAAAGG
60564	58651	TAATCTCTTTATAATCAAAG
60565	58652	TTAATCTCTTTATAATCAAA
60566	58653	TTTAATCTCTTTATAATCAA
60567	58654	CTTTAATCTCTTTATAATCA
60568	58655	TCTTTAATCTCTTTATAATC
60569	58656	ATCTTTAATCTCTTTATAAT
60570	58657	AATCTTTAATCTCTTTATAA
60571	58658	AAATCTTTAATCTCTTTATA

109648	107735	GCCCTGGCTCCTGGGCAGCA
109649	107736	GGCCCTGGCTCCTGGGCAGC
109650	107737	AGGCCCTGGCTCCTGGGCAG
109651	107738	CAGGCCCTGGCTCCTGGGCA
109652	107739	CCAGGCCCTGGCTCCTGGGC
109653	107740	CCCAGGCCCTGGCTCCTGGG
109654	107741	TCCCAGGCCCTGGCTCCTGG
109655	107742	ATCCCAGGCCCTGGCTCCTG
109656	107743	GATCCCAGGCCCTGGCTCCT
109657	107744	CGATCCCAGGCCCTGGCTCC
109658	107745	CCGATCCCAGGCCCTGGCTC
109659	107746	CCCGATCCCAGGCCCTGGCT
109660	107747	TCCCGATCCCAGGCCCTGGC
109661	107748	CTCCCGATCCCAGGCCCTGG
109662	107749	GCTCCCGATCCCAGGCCCTG
109663	107750	AGCTCCCGATCCCAGGCCCT
109664	107751	AAGCTCCCGATCCCAGGCCC
109665	107752	AAAGCTCCCGATCCCAGGCC
109666	107753	TAAAGCTCCCGATCCCAGGC
109667	107754	CTAAAGCTCCCGATCCCAGG
109668	107755	CCTAAAGCTCCCGATCCCAG
109669	107756	TCCTAAAGCTCCCGATCCCA
109670	107757	TTCCTAAAGCTCCCGATCCC
109671	107758	ATTCCTAAAGCTCCCGATCC
109672	107759	GATTCCTAAAGCTCCCGATC
109673	107760	AGATTCCTAAAGCTCCCGAT
109674	107761	CAGATTCCTAAAGCTCCCGA
109675	107762	GCAGATTCCTAAAGCTCCCG
109676	107763	AGCAGATTCCTAAAGCTCCC
109677	107764	AAGCAGATTCCTAAAGCTCC
109678	107765	AAAGCAGATTCCTAAAGCTC
109679	107766	TAAAGCAGATTCCTAAAGCT
109680	107767	ATAAAGCAGATTCCTAAAGC
109681	107768	AATAAAGCAGATTCCTAAAG
109682	107769	CAATAAAGCAGATTCCTAAA
109683	107770	ACAATAAAGCAGATTCCTAA
109684	107771	TACAATAAAGCAGATTCCTA
109685	107772	GTACAATAAAGCAGATTCCT
109686	107773	AGTACAATAAAGCAGATTCC
109687	107774	CAGTACAATAAAGCAGATTC
109688	107775	CCAGTACAATAAAGCAGATT
109689	107776	CCCAGTACAATAAAGCAGAT
109690	107777	CCCCAGTACAATAAAGCAGA
109691	107778	GCCCCAGTACAATAAAGCAG
109692	107779	AGCCCCAGTACAATAAAGCA
109693	107780	CAGCCCCAGTACAATAAAGC
109694	107781	TCAGCCCCAGTACAATAAAG
109695	107782	CTCAGCCCCAGTACAATAAA
109696	107783	GCTCAGCCCCAGTACAATAA
109697	107784	AGCTCAGCCCCAGTACAATA
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109699	107786	CCAGCTCAGCCCCAGTACAA
109700	107787	GCCAGCTCAGCCCCAGTACA
109701	107788	TGCCAGCTCAGCCCCAGTAC
109702	107789	GTGCCAGCTCAGCCCCAGTA
109703	107790	GGTGCCAGCTCAGCCCCAGT
109704	107791	GGGTGCCAGCTCAGCCCCAG
109705	107792	TGGGTGCCAGCTCAGCCCCA
109706	107793	GTGGGTGCCAGCTCAGCCCC
109707	107794	AGTGGGTGCCAGCTCAGCCC
109708	107795	AAGTGGGTGCCAGCTCAGCC
109709	107796	CAAGTGGGTGCCAGCTCAGC
109710	107797	GCAAGTGGGTGCCAGCTCAG
109711	107798	TGCAAGTGGGTGCCAGCTCA
109712	107799	TTGCAAGTGGGTGCCAGCTC
109713	107800	CTTGCAAGTGGGTGCCAGCT
109714	107801	TCTTGCAAGTGGGTGCCAGC
109715	107802	ATCTTGCAAGTGGGTGCCAG
109716	107803	TATCTTGCAAGTGGGTGCCA
109717	107804	TTATCTTGCAAGTGGGTGCC
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11425	9512	AGTGGAGGTTACAGTGAGCC
11426	9513	AAGTGGAGGTTACAGTGAGC
11427	9514	GAAGTGGAGGTTACAGTGAG
11428	9515	GGAAGTGGAGGTTACAGTGA
11429	9516	GGGAAGTGGAGGTTACAGTG
11430	9517	TGGGAAGTGGAGGTTACAGT
11431	9518	CTGGGAAGTGGAGGTTACAG
11432	9519	CCTGGGAAGTGGAGGTTACA
11433	9520	ACCTGGGAAGTGGAGGTTAC
11434	9521	AACCTGGGAAGTGGAGGTTA
11435	9522	GAACCTGGGAAGTGGAGGTT
11436	9523	GGAACCTGGGAAGTGGAGGT
11437	9524	TGGAACCTGGGAAGTGGAGG
11438	9525	CTGGAACCTGGGAAGTGGAG
11439	9526	ACTGGAACCTGGGAAGTGGA
11440	9527	CACTGGAACCTGGGAAGTGG
11441	9528	TCACTGGAACCTGGGAAGTG
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11444	9531	GAATCACTGGAACCTGGGAA
11445	9532	AGAATCACTGGAACCTGGGA
11446	9533	GAGAATCACTGGAACCTGGG
11447	9534	GGAGAATCACTGGAACCTGG
11448	9535	AGGAGAATCACTGGAACCTG
11449	9536	CAGGAGAATCACTGGAACCT
11450	9537	GCAGGAGAATCACTGGAACC
11451	9538	GGCAGGAGAATCACTGGAAC
11452	9539	AGGCAGGAGAATCACTGGAA
11453	9540	GAGGCAGGAGAATCACTGGA
11454	9541	TGAGGCAGGAGAATCACTGG
11455	9542	CTGAGGCAGGAGAATCACTG
11456	9543	GCTGAGGCAGGAGAATCACT
11457	9544	GGCTGAGGCAGGAGAATCAC
11458	9545	AGGCTGAGGCAGGAGAATCA
11459	9546	GAGGCTGAGGCAGGAGAATC
11460	9547	GGAGGCTGAGGCAGGAGAAT
11461	9548	AGGAGGCTGAGGCAGGAGAA
11462	9549	CAGGAGGCTGAGGCAGGAGA
11463	9550	TCAGGAGGCTGAGGCAGGAG
11464	9551	CTCAGGAGGCTGAGGCAGGA
11465	9552	ACTCAGGAGGCTGAGGCAGG
11466	9553	TACTCAGGAGGCTGAGGCAG
11467	9554	CTACTCAGGAGGCTGAGGCA
11468	9555	GCTACTCAGGAGGCTGAGGC
11469	9556	AGCTACTCAGGAGGCTGAGG
11470	9557	CAGCTACTCAGGAGGCTGAG
11471	9558	CCAGCTACTCAGGAGGCTGA
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11473	9560	TCCCAGCTACTCAGGAGGCT
11474	9561	ATCCCAGCTACTCAGGAGGC
11475	9562	AATCCCAGCTACTCAGGAGG
11476	9563	TAATCCCAGCTACTCAGGAG
11477	9564	GTAATCCCAGCTACTCAGGA
11478	9565	TGTAATCCCAGCTACTCAGG
11479	9566	CTGTAATCCCAGCTACTCAG
11480	9567	CCTGTAATCCCAGCTACTCA
11481	9568	GCCTGTAATCCCAGCTACTC
11482	9569	TGCCTGTAATCCCAGCTACT
11483	9570	ATGCCTGTAATCCCAGCTAC
11484	9571	CATGCCTGTAATCCCAGCTA
11485	9572	GCATGCCTGTAATCCCAGCT
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11487	9574	GTGCATGCCTGTAATCCCAG
11488	9575	GGTGCATGCCTGTAATCCCA
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11490	9577	GTGGTGCATGCCTGTAATCC
11491	9578	AGTGGTGCATGCCTGTAATC
11492	9579	TAGTGGTGCATGCCTGTAAT
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11494	9581	TGTAGTGGTGCATGCCTGTA
11495	9582	GTGTAGTGGTGCATGCCTGT

60572	58659	TAAATCTTTAATCTCTTTAT
60573	58660	CTAAATCTTTAATCTCTTTA
60574	58661	CCTAAATCTTTAATCTCTTT
60575	58662	GCCTAAATCTTTAATCTCTT
60576	58663	GGCCTAAATCTTTAATCTCT
60577	58664	CGGCCTAAATCTTTAATCTC
60578	58665	CCGGCCTAAATCTTTAATCT
60579	58666	CCCGGCCTAAATCTTTAATC
60580	58667	ACCCGGCCTAAATCTTTAAT
60581	58668	CACCCGGCCTAAATCTTTAA
60582	58669	ACACCCGGCCTAAATCTTTA
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60584	58671	CCACACCCGGCCTAAATCTT
60585	58672	ACCACACCCGGCCTAAATCT
60586	58673	CACCACACCCGGCCTAAATC
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60588	58675	AGCACCACACCCGGCCTAAA
60589	58676	GAGCACCACACCCGGCCTAA
60590	58677	TGAGCACCACACCCGGCCTA
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60592	58679	CGTGAGCACCACACCCGGCC
60593	58680	GCGTGAGCACCACACCCGGC
60594	58681	AGCGTGAGCACCACACCCGG
60595	58682	AAGCGTGAGCACCACACCCG
60596	58683	CAAGCGTGAGCACCACACCC
60597	58684	ACAAGCGTGAGCACCACACC
60598	58685	TACAAGCGTGAGCACCACAC
60599	58686	TTACAAGCGTGAGCACCACA
60600	58687	ATTACAAGCGTGAGCACCAC
60601	58688	GATTACAAGCGTGAGCACCA
60602	58689	GGATTACAAGCGTGAGCACC
60603	58690	GGGATTACAAGCGTGAGCAC
60604	58691	TGGGATTACAAGCGTGAGCA
60605	58692	CTGGGATTACAAGCGTGAGC
60606	58693	GCTGGGATTACAAGCGTGAG
60607	58694	TGCTGGGATTACAAGCGTGA
60608	58695	GTGCTGGGATTACAAGCGTG
60609	58696	AGTGCTGGGATTACAAGCGT
60610	58697	AAGTGCTGGGATTACAAGCG
60611	58698	AAAGTGCTGGGATTACAAGC
60612	58699	CAAAGTGCTGGGATTACAAG
60613	58700	CCAAAGTGCTGGGATTACAA
60614	58701	CCCAAAGTGCTGGGATTACA
60615	58702	TCCCAAAGTGCTGGGATTAC
60616	58703	CTCCCAAAGTGCTGGGATTA
60617	58704	CCTCCCAAAGTGCTGGGATT
60618	58705	GCCTCCCAAAGTGCTGGGAT
60619	58706	GGCCTCCCAAAGTGCTGGGA
60620	58707	TGGCCTCCCAAAGTGCTGGG
60621	58708	TTGGCCTCCCAAAGTGCTGG
60622	58709	TTTGGCCTCCCAAAGTGCTG
60623	58710	CTTTGGCCTCCCAAAGTGCT
60624	58711	GCTTTGGCCTCCCAAAGTGC
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60626	58713	CCGCTTTGGCCTCCCAAAGT
60627	58714	CCCGCTTTGGCCTCCCAAAG
60628	58715	ACCCGCTTTGGCCTCCCAAA
60629	58716	CACCCGCTTTGGCCTCCCAA
60630	58717	CCACCCGCTTTGGCCTCCCA
60631	58718	TCCACCCGCTTTGGCCTCCC
60632	58719	ATCCACCCGCTTTGGCCTCC
60633	58720	GATCCACCCGCTTTGGCCTC
60634	58721	TGATCCACCCGCTTTGGCCT
60635	58722	GTGATCCACCCGCTTTGGCC
60636	58723	AGTGATCCACCCGCTTTGGC
60637	58724	AAGTGATCCACCCGCTTTGG
60638	58725	CAAGTGATCCACCCGCTTTG
60639	58726	TCAAGTGATCCACCCGCTTT
60640	58727	CTCAAGTGATCCACCCGCTT
60641	58728	CCTCAAGTGATCCACCCGCT
60642	58729	ACCTCAAGTGATCCACCCGC

109719	107806	CTTTATCTTGCAAGTGGGTG
109720	107807	ACTTTATCTTGCAAGTGGGT
109721	107808	GACTTTATCTTGCAAGTGGG
109722	107809	GGACTTTATCTTGCAAGTGG
109723	107810	AGGACTTTATCTTGCAAGTG
109724	107811	AAGGACTTTATCTTGCAAGT
109725	107812	AAAGGACTTTATCTTGCAAG
109726	107813	AAAAGGACTTTATCTTGCAA
109727	107814	AAAAAGGACTTTATCTTGCA
109728	107815	TAAAAAGGACTTTATCTTGC
109729	107816	GTAAAAAGGACTTTATCTTG
109730	107817	AGTAAAAAGGACTTTATCTT
109731	107818	GAGTAAAAAGGACTTTATCT
109732	107819	AGAGTAAAAAGGACTTTATC
109733	107820	AAGAGTAAAAAGGACTTTAT
109734	107821	GAAGAGTAAAAAGGACTTTA
109735	107822	AGAAGAGTAAAAAGGACTTT
109736	107823	GAGAAGAGTAAAAAGGACTT
109737	107824	AGAGAAGAGTAAAAAGGACT
109738	107825	GAGAGAAGAGTAAAAAGGAC
109739	107826	TGAGAGAAGAGTAAAAAGGA
109740	107827	GTGAGAGAAGAGTAAAAAGG
109741	107828	GGTGAGAGAAGAGTAAAAAG
109742	107829	AGGTGAGAGAAGAGTAAAAA
109743	107830	GAGGTGAGAGAAGAGTAAAA
109744	107831	TGAGGTGAGAGAAGAGTAAA
109745	107832	TTGAGGTGAGAGAAGAGTAA
109746	107833	CTTGAGGTGAGAGAAGAGTA
109747	107834	GCTTGAGGTGAGAGAAGAGT
109748	107835	TGCTTGAGGTGAGAGAAGAG
109749	107836	CTGCTTGAGGTGAGAGAAGA
109750	107837	CCTGCTTGAGGTGAGAGAAG
109751	107838	ACCTGCTTGAGGTGAGAGAA
109752	107839	CACCTGCTTGAGGTGAGAGA
109753	107840	CCACCTGCTTGAGGTGAGAG
109754	107841	CCCACCTGCTTGAGGTGAGA
109755	107842	ACCCACCTGCTTGAGGTGAG
109756	107843	GACCCACCTGCTTGAGGTGA
109757	107844	AGACCCACCTGCTTGAGGTG
109758	107845	GAGACCCACCTGCTTGAGGT
109759	107846	GGAGACCCACCTGCTTGAGG
109760	107847	GGGAGACCCACCTGCTTGAG
109761	107848	GGGGAGACCCACCTGCTTGA
109762	107849	TGGGGAGACCCACCTGCTTG
109763	107850	ATGGGGAGACCCACCTGCTT
109764	107851	CATGGGGAGACCCACCTGCT
109765	107852	CCATGGGGAGACCCACCTGC
109766	107853	TCCATGGGGAGACCCACCTG
109767	107854	GTCCATGGGGAGACCCACCT
109768	107855	TGTCCATGGGGAGACCCACC
109769	107856	GTGTCCATGGGGAGACCCAC
109770	107857	GGTGTCCATGGGGAGACCCA
109771	107858	TGGTGTCCATGGGGAGACCC
109772	107859	GTGGTGTCCATGGGGAGACC
109773	107860	TGTGGTGTCCATGGGGAGAC
109774	107861	CTGTGGTGTCCATGGGGAGA
109775	107862	GCTGTGGTGTCCATGGGGAG
109776	107863	AGCTGTGGTGTCCATGGGGA
109777	107864	CAGCTGTGGTGTCCATGGGG
109778	107865	ACAGCTGTGGTGTCCATGGG
109779	107866	CACAGCTGTGGTGTCCATGG
109780	107867	TCACAGCTGTGGTGTCCATG
109781	107868	TTCACAGCTGTGGTGTCCAT
109782	107869	ATTCACAGCTGTGGTGTCCA
109783	107870	CATTCACAGCTGTGGTGTCC
109784	107871	ACATTCACAGCTGTGGTGTC
109785	107872	CACATTCACAGCTGTGGTGT
109786	107873	GCACATTCACAGCTGTGGTG
109787	107874	CGCACATTCACAGCTGTGGT
109788	107875	CCGCACATTCACAGCTGTGG
109789	107876	CCCGCACATTCACAGCTGTG

11496	9583	GGTGTAGTGGTGCATGCCTG
11497	9584	AGGTGTAGTGGTGCATGCCT
11498	9585	CAGGTGTAGTGGTGCATGCC
11499	9586	CCAGGTGTAGTGGTGCATGC
11500	9587	GCCAGGTGTAGTGGTGCATG
11501	9588	TGCCAGGTGTAGTGGTGCAT
11502	9589	TTGCCAGGTGTAGTGGTGCA
11503	9590	TTTGCCAGGTGTAGTGGTGC
11504	9591	ATTTGCCAGGTGTAGTGGTG
11505	9592	AATTTGCCAGGTGTAGTGGT
11506	9593	AAATTTGCCAGGTGTAGTGG
11507	9594	AAAATTTGCCAGGTGTAGTG
11508	9595	AAAAATTTGCCAGGTGTAGT
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11510	9597	ACAAAAATTTGCCAGGTGTA
11511	9598	TACAAAAATTTGCCAGGTGT
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11514	9601	AAATACAAAAATTTGCCAGG
11515	9602	AAAATACAAAAATTTGCCAG
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11531	9618	CCATCTCTACTAAAAAAAAA
11532	9619	CCCATCTCTACTAAAAAAAA
11533	9620	CCCCATCTCTACTAAAAAAA
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11536	9623	AAACCCCATCTCTACTAAAA
11537	9624	GAAACCCCATCTCTACTAAA
11538	9625	TGAAACCCCATCTCTACTAA
11539	9626	GTGAAACCCCATCTCTACTA
11540	9627	GGTGAAACCCCATCTCTACT
11541	9628	TGGTGAAACCCCATCTCTAC
11542	9629	ATGGTGAAACCCCATCTCTA
11543	9630	CATGGTGAAACCCCATCTCT
11544	9631	ACATGGTGAAACCCCATCTC
11545	9632	AACATGGTGAAACCCCATCT
11546	9633	CAACATGGTGAAACCCCATC
11547	9634	CCAACATGGTGAAACCCCAT
11548	9635	GCCAACATGGTGAAACCCCA
11549	9636	GGCCAACATGGTGAAACCCC
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11552	9639	CCTGGCCAACATGGTGAAAC
11553	9640	GCCTGGCCAACATGGTGAAA
11554	9641	AGCCTGGCCAACATGGTGAA
11555	9642	GAGCCTGGCCAACATGGTGA
11556	9643	CGAGCCTGGCCAACATGGTG
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11560	9647	AAGACGAGCCTGGCCAACAT
11561	9648	CAAGACGAGCCTGGCCAACA
11562	9649	TCAAGACGAGCCTGGCCAAC
11563	9650	TTCAAGACGAGCCTGGCCAA
11564	9651	GTTCAAGACGAGCCTGGCCA
11565	9652	AGTTCAAGACGAGCCTGGCC
11566	9653	GAGTTCAAGACGAGCCTGGC

60643	58730	GACCTCAAGTGATCCACCCG
60644	58731	TGACCTCAAGTGATCCACCC
60645	58732	CTGACCTCAAGTGATCCACC
60646	58733	CCTGACCTCAAGTGATCCAC
60647	58734	TCCTGACCTCAAGTGATCCA
60648	58735	CTCCTGACCTCAAGTGATCC
60649	58736	ACTCCTGACCTCAAGTGATC
60650	58737	AACTCCTGACCTCAAGTGAT
60651	58738	AAACTCCTGACCTCAAGTGA
60652	58739	CAAACTCCTGACCTCAAGTG
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60662	58749	AGGTTGGTCTCAAACTCCTG
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60665	58752	ACCAGGTTGGTCTCAAACTC
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60670	58757	GGTTGACCAGGTTGGTCTCA
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60680	58767	GGTTTCACCAGGTTGACCAG
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60684	58771	ATGGGGTTTCACCAGGTTGA
60685	58772	GATGGGGTTTCACCAGGTTG
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60688	58775	AGAGATGGGGTTTCACCAGG
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60699	58786	GTATTTTTAGTAGAGATGGG
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60701	58788	TTGTATTTTTAGTAGAGATG
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60705	58792	TTTTTTGTATTTTTAGTAGA
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60707	58794	ATTTTTTTGTATTTTTAGTA
60708	58795	AATTTTTTTGTATTTTTAGT
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60710	58797	CTAATTTTTTTGTATTTTTA
60711	58798	ACTAATTTTTTTGTATTTTT
60712	58799	GACTAATTTTTTTGTATTTT
60713	58800	TGACTAATTTTTTTGTATTT

109790	107877	CCCCGCACATTCACAGCTGT
109791	107878	ACCCCGCACATTCACAGCTG
109792	107879	GACCCCGCACATTCACAGCT
109793	107880	TGACCCCGCACATTCACAGC
109794	107881	ATGACCCCGCACATTCACAG
109795	107882	TATGACCCCGCACATTCACA
109796	107883	ATATGACCCCGCACATTCAC
109797	107884	GATATGACCCCGCACATTCA
109798	107885	AGATATGACCCCGCACATTC
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109800	107887	TCAGATATGACCCCGCACAT
109801	107888	TTCAGATATGACCCCGCACA
109802	107889	CTTCAGATATGACCCCGCAC
109803	107890	GCTTCAGATATGACCCCGCA
109804	107891	AGCTTCAGATATGACCCCGC
109805	107892	CAGCTTCAGATATGACCCCG
109806	107893	CCAGCTTCAGATATGACCCC
109807	107894	GCCAGCTTCAGATATGACCC
109808	107895	TGCCAGCTTCAGATATGACC
109809	107896	GTGCCAGCTTCAGATATGAC
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109812	107899	ATTGTGCCAGCTTCAGATAT
109813	107900	TATTGTGCCAGCTTCAGATA
109814	107901	GTATTGTGCCAGCTTCAGAT
109815	107902	CGTATTGTGCCAGCTTCAGA
109816	107903	TCGTATTGTGCCAGCTTCAG
109817	107904	GTCGTATTGTGCCAGCTTCA
109818	107905	TGTCGTATTGTGCCAGCTTC
109819	107906	ATGTCGTATTGTGCCAGCTT
109820	107907	CATGTCGTATTGTGCCAGCT
109821	107908	CCATGTCGTATTGTGCCAGC
109822	107909	GCCATGTCGTATTGTGCCAG
109823	107910	TGCCATGTCGTATTGTGCCA
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109826	107913	AGGTGCCATGTCGTATTGTG
109827	107914	AAGGTGCCATGTCGTATTGT
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109829	107916	ACAAGGTGCCATGTCGTATT
109830	107917	AACAAGGTGCCATGTCGTAT
109831	107918	AAACAAGGTGCCATGTCGTA
109832	107919	AAAACAAGGTGCCATGTCGT
109833	107920	AAAAACAAGGTGCCATGTCG
109834	107921	AAAAAACAAGGTGCCATGTC
109835	107922	TAAAAAACAAGGTGCCATGT
109836	107923	ATAAAAAACAAGGTGCCATG
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109845	107932	GTGCCTTGAATAAAAAACAA
109846	107933	TGTGCCTTGAATAAAAAACA
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109849	107936	CCTTGTGCCTTGAATAAAAA
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109851	107938	GCCCTTGTGCCTTGAATAAA
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109859	107946	ACTAAAGAGCCCTTGTGCCT
109860	107947	GACTAAAGAGCCCTTGTGCC

11567	9654	GGAGTTCAAGACGAGCCTGG
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11569	9656	CAGGAGTTCAAGACGAGCCT
11570	9657	TCAGGAGTTCAAGACGAGCC
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11579	9666	CACCTAAGGTCAGGAGTTCA
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11583	9670	AGATCACCTAAGGTCAGGAG
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11587	9674	AGGCAGATCACCTAAGGTCA
11588	9675	CAGGCAGATCACCTAAGGTC
11589	9676	ACAGGCAGATCACCTAAGGT
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11591	9678	AGACAGGCAGATCACCTAAG
11592	9679	AAGACAGGCAGATCACCTAA
11593	9680	CAAGACAGGCAGATCACCTA
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11595	9682	GCCAAGACAGGCAGATCACC
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11597	9684	AGGCCAAGACAGGCAGATCA
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11617	9704	TGTAATCCCAAAACTTTGGG
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11619	9706	GCTGTAATCCCAAAACTTTG
11620	9707	TGCTGTAATCCCAAAACTTT
11621	9708	ATGCTGTAATCCCAAAACTT
11622	9709	CATGCTGTAATCCCAAAACT
11623	9710	TCATGCTGTAATCCCAAAAC
11624	9711	CTCATGCTGTAATCCCAAAA
11625	9712	GCTCATGCTGTAATCCCAAA
11626	9713	GGCTCATGCTGTAATCCCAA
11627	9714	TGGCTCATGCTGTAATCCCA
11628	9715	GTGGCTCATGCTGTAATCCC
11629	9716	AGTGGCTCATGCTGTAATCC
11630	9717	CAGTGGCTCATGCTGTAATC
11631	9718	GCAGTGGCTCATGCTGTAAT
11632	9719	CGCAGTGGCTCATGCTGTAA
11633	9720	GCGCAGTGGCTCATGCTGTA
11634	9721	GGCGCAGTGGCTCATGCTGT
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11636	9723	GAGGCGCAGTGGCTCATGCT
11637	9724	CGAGGCGCAGTGGCTCATGC

60714	58801	CTGACTAATTTTTTTGTATT
60715	58802	CCTGACTAATTTTTTTGTAT
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60717	58804	TGCCTGACTAATTTTTTTGT
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60719	58806	CATGCCTGACTAATTTTTTT
60720	58807	CCATGCCTGACTAATTTTTT
60721	58808	ACCATGCCTGACTAATTTTT
60722	58809	TACCATGCCTGACTAATTTT
60723	58810	CTACCATGCCTGACTAATTT
60724	58811	GCTACCATGCCTGACTAATT
60725	58812	TGCTACCATGCCTGACTAAT
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60727	58814	TGTGCTACCATGCCTGACTA
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60731	58818	GGCATGTGCTACCATGCCTG
60732	58819	AGGCATGTGCTACCATGCCT
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60736	58823	TTACAGGCATGTGCTACCAT
60737	58824	ATTACAGGCATGTGCTACCA
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60740	58827	GGGATTACAGGCATGTGCTA
60741	58828	TGGGATTACAGGCATGTGCT
60742	58829	CTGGGATTACAGGCATGTGC
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60747	58834	AGTAGCTGGGATTACAGGCA
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60773	58860	AGCAATTCTCCTGCCTTAGC
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60776	58863	TCAAGCAATTCTCCTGCCTT
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60778	58865	ATTCAAGCAATTCTCCTGCC
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60781	58868	CAAATTCAAGCAATTCTCCT
60782	58869	CCAAATTCAAGCAATTCTCC
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109861	107948	TGACTAAAGAGCCCTTGTGC
109862	107949	CTGACTAAAGAGCCCTTGTG
109863	107950	GCTGACTAAAGAGCCCTTGT
109864	107951	AGCTGACTAAAGAGCCCTTG
109865	107952	CAGCTGACTAAAGAGCCCTT
109866	107953	CCAGCTGACTAAAGAGCCCT
109867	107954	ACCAGCTGACTAAAGAGCCC
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109871	107958	CACCACCAGCTGACTAAAGA
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109873	107960	TTCACCACCAGCTGACTAAA
109874	107961	ATTCACCACCAGCTGACTAA
109875	107962	GATTCACCACCAGCTGACTA
109876	107963	GGATTCACCACCAGCTGACT
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109879	107966	GTAGGATTCACCACCAGCTG
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109883	107970	CCTAGTAGGATTCACCACCA
109884	107971	TCCTAGTAGGATTCACCACC
109885	107972	GTCCTAGTAGGATTCACCAC
109886	107973	AGTCCTAGTAGGATTCACCA
109887	107974	TAGTCCTAGTAGGATTCACC
109888	107975	CTAGTCCTAGTAGGATTCAC
109889	107976	CCTAGTCCTAGTAGGATTCA
109890	107977	ACCTAGTCCTAGTAGGATTC
109891	107978	TACCTAGTCCTAGTAGGATT
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109894	107981	AAATACCTAGTCCTAGTAGG
109895	107982	GAAATACCTAGTCCTAGTAG
109896	107983	GGAAATACCTAGTCCTAGTA
109897	107984	GGGAAATACCTAGTCCTAGT
109898	107985	AGGGAAATACCTAGTCCTAG
109899	107986	AAGGGAAATACCTAGTCCTA
109900	107987	GAAGGGAAATACCTAGTCCT
109901	107988	TGAAGGGAAATACCTAGTCC
109902	107989	TTGAAGGGAAATACCTAGTC
109903	107990	CTTGAAGGGAAATACCTAGT
109904	107991	CCTTGAAGGGAAATACCTAG
109905	107992	GCCTTGAAGGGAAATACCTA
109906	107993	TGCCTTGAAGGGAAATACCT
109907	107994	TTGCCTTGAAGGGAAATACC
109908	107995	ATTGCCTTGAAGGGAAATAC
109909	107996	CATTGCCTTGAAGGGAAATA
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109914	108001	GAACCCATTGCCTTGAAGGG
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109927	108014	CTGGACCAGAAGGGAACCCA
109928	108015	TCTGGACCAGAAGGGAACCC
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11646	9733	AAAATAAGGCGAGGCGCAGT
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110070	108157	GCTCTGGGAGGAGAGGGAAG
110071	108158	AGCTCTGGGAGGAGAGGGAA
110072	108159	CAGCTCTGGGAGGAGAGGGA
110073	108160	ACAGCTCTGGGAGGAGAGGG

11780	9867	GCATGCCTGTGGTCCCAGCT
11781	9868	CGCATGCCTGTGGTCCCAGC
11782	9869	GCGCATGCCTGTGGTCCCAG
11783	9870	GGCGCATGCCTGTGGTCCCA
11784	9871	TGGCGCATGCCTGTGGTCCC
11785	9872	GTGGCGCATGCCTGTGGTCC
11786	9873	AGTGGCGCATGCCTGTGGTC
11787	9874	TAGTGGCGCATGCCTGTGGT
11788	9875	ATAGTGGCGCATGCCTGTGG
11789	9876	CATAGTGGCGCATGCCTGTG
11790	9877	GCATAGTGGCGCATGCCTGT
11791	9878	GGCATAGTGGCGCATGCCTG
11792	9879	GGGCATAGTGGCGCATGCCT
11793	9880	TGGGCATAGTGGCGCATGCC
11794	9881	CTGGGCATAGTGGCGCATGC
11795	9882	GCTGGGCATAGTGGCGCATG
11796	9883	TGCTGGGCATAGTGGCGCAT
11797	9884	TTGCTGGGCATAGTGGCGCA
11798	9885	TTTGCTGGGCATAGTGGCGC
11799	9886	TTTTGCTGGGCATAGTGGCG
11800	9887	ATTTTGCTGGGCATAGTGGC
11801	9888	AATTTTGCTGGGCATAGTGG
11802	9889	AAATTTTGCTGGGCATAGTG
11803	9890	AAAATTTTGCTGGGCATAGT
11804	9891	AAAAATTTTGCTGGGCATAG
11805	9892	CAAAAATTTTGCTGGGCATA
11806	9893	ACAAAAATTTTGCTGGGCAT
11807	9894	AACAAAAATTTTGCTGGGCA
11808	9895	AAACAAAAATTTTGCTGGGC
11809	9896	GAAACAAAAATTTTGCTGGG
11810	9897	TGAAACAAAAATTTTGCTGG
11811	9898	GTGAAACAAAAATTTTGCTG
11812	9899	AGTGAAACAAAAATTTTGCT
11813	9900	GAGTGAAACAAAAATTTTGC
11814	9901	AGAGTGAAACAAAAATTTTG
11815	9902	CAGAGTGAAACAAAAATTTT
11816	9903	ACAGAGTGAAACAAAAATTT
11817	9904	AACAGAGTGAAACAAAAATT
11818	9905	CAACAGAGTGAAACAAAAAT
11819	9906	GCAACAGAGTGAAACAAAAA
11820	9907	GGCAACAGAGTGAAACAAAA
11821	9908	AGGCAACAGAGTGAAACAAA
11822	9909	TAGGCAACAGAGTGAAACAA
11823	9910	CTAGGCAACAGAGTGAAACA
11824	9911	CCTAGGCAACAGAGTGAAAC
11825	9912	CCCTAGGCAACAGAGTGAAA
11826	9913	ACCCTAGGCAACAGAGTGAA
11827	9914	CACCCTAGGCAACAGAGTGA
11828	9915	CCACCCTAGGCAACAGAGTG
11829	9916	CCCACCCTAGGCAACAGAGT
11830	9917	CCCCACCCTAGGCAACAGAG
11831	9918	ACCCCACCCTAGGCAACAGA
11832	9919	CACCCCACCCTAGGCAACAG
11833	9920	GCACCCCACCCTAGGCAACA
11834	9921	TGCACCCCACCCTAGGCAAC
11835	9922	CTGCACCCCACCCTAGGCAA
11836	9923	ACTGCACCCCACCCTAGGCA
11837	9924	CACTGCACCCCACCCTAGGC
11838	9925	CCACTGCACCCCACCCTAGG
11839	9926	GCCACTGCACCCCACCCTAG
11840	9927	TGCCACTGCACCCCACCCTA
11841	9928	CTGCCACTGCACCCCACCCT
11842	9929	CCTGCCACTGCACCCCACCC
11843	9930	TCCTGCCACTGCACCCCACC
11844	9931	ATCCTGCCACTGCACCCCAC
11845	9932	TATCCTGCCACTGCACCCCA
11846	9933	ATATCCTGCCACTGCACCCC
11847	9934	GATATCCTGCCACTGCACCC
11848	9935	CGATATCCTGCCACTGCACC
11849	9936	CCGATATCCTGCCACTGCAC
11850	9937	GCCGATATCCTGCCACTGCA

60927	59014	TCCCAGTTTGTGGCATGTCT
60928	59015	TTCCCAGTTTGTGGCATGTC
60929	59016	TTTCCCAGTTTGTGGCATGT
60930	59017	TTTTCCCAGTTTGTGGCATG
60931	59018	CTTTTCCCAGTTTGTGGCAT
60932	59019	ACTTTTCCCAGTTTGTGGCA
60933	59020	TACTTTTCCCAGTTTGTGGC
60934	59021	CTACTTTTCCCAGTTTGTGG
60935	59022	TCTACTTTTCCCAGTTTGTG
60936	59023	TTCTACTTTTCCCAGTTTGT
60937	59024	TTTCTACTTTTCCCAGTTTG
60938	59025	TTTTCTACTTTTCCCAGTTT
60939	59026	TTTTTCTACTTTTCCCAGTT
60940	59027	ATTTTTCTACTTTTCCCAGT
60941	59028	TATTTTTCTACTTTTCCCAG
60942	59029	CTATTTTTCTACTTTTCCCA
60943	59030	ACTATTTTTCTACTTTTCCC
60944	59031	AACTATTTTTCTACTTTTCC
60945	59032	AAACTATTTTTCTACTTTTC
60946	59033	AAAACTATTTTTCTACTTTT
60947	59034	TAAAACTATTTTTCTACTTT
60948	59035	TTAAAACTATTTTTCTACTT
60949	59036	TTTAAAACTATTTTTCTACT
60950	59037	TTTTAAAACTATTTTTCTAC
60951	59038	TTTTTAAAACTATTTTTCTA
60952	59039	ATTTTTAAAACTATTTTTCT
60953	59040	CATTTTTAAAACTATTTTTC
60954	59041	TCATTTTTAAAACTATTTTT
60955	59042	GTCATTTTTAAAACTATTTT
60956	59043	GGTCATTTTTAAAACTATTT
60957	59044	TGGTCATTTTTAAAACTATT
60958	59045	CTGGTCATTTTTAAAACTAT
60959	59046	ACTGGTCATTTTTAAAACTA
60960	59047	CACTGGTCATTTTTAAAACT
60961	59048	TCACTGGTCATTTTTAAAAC
60962	59049	TTCACTGGTCATTTTTAAAA
60963	59050	ATTCACTGGTCATTTTTAAA
60964	59051	CATTCACTGGTCATTTTTAA
60965	59052	ACATTCACTGGTCATTTTTA
60966	59053	TACATTCACTGGTCATTTTT
60967	59054	ATACATTCACTGGTCATTTT
60968	59055	CATACATTCACTGGTCATTT
60969	59056	TCATACATTCACTGGTCATT
60970	59057	TTCATACATTCACTGGTCAT
60971	59058	TTTCATACATTCACTGGTCA
60972	59059	TTTTCATACATTCACTGGTC
60973	59060	CTTTTCATACATTCACTGGT
60974	59061	CCTTTTCATACATTCACTGG
60975	59062	ACCTTTTCATACATTCACTG
60976	59063	CACCTTTTCATACATTCACT
60977	59064	CCACCTTTTCATACATTCAC
60978	59065	GCCACCTTTTCATACATTCA
60979	59066	GGCCACCTTTTCATACATTC
60980	59067	GGGCCACCTTTTCATACATT
60981	59068	AGGGCCACCTTTTCATACAT
60982	59069	GAGGGCCACCTTTTCATACA
60983	59070	GGAGGGCCACCTTTTCATAC
60984	59071	AGGAGGGCCACCTTTTCATA
60985	59072	GAGGAGGGCCACCTTTTCAT
60986	59073	TGAGGAGGGCCACCTTTTCA
60987	59074	GTGAGGAGGGCCACCTTTTC
60988	59075	AGTGAGGAGGGCCACCTTTT
60989	59076	AAGTGAGGAGGGCCACCTTT
60990	59077	CAAGTGAGGAGGGCCACCTT
60991	59078	ACAAGTGAGGAGGGCCACCT
60992	59079	TACAAGTGAGGAGGGCCACC
60993	59080	TTACAAGTGAGGAGGGCCAC
60994	59081	ATTACAAGTGAGGAGGGCCA
60995	59082	CATTACAAGTGAGGAGGGCC
60996	59083	TCATTACAAGTGAGGAGGGC
60997	59084	ATCATTACAAGTGAGGAGGG

110074	108161	CACAGCTCTGGGAGGAGAGG
110075	108162	TCACAGCTCTGGGAGGAGAG
110076	108163	CTCACAGCTCTGGGAGGAGA
110077	108164	GCTCACAGCTCTGGGAGGAG
110078	108165	AGCTCACAGCTCTGGGAGGA
110079	108166	CAGCTCACAGCTCTGGGAGG
110080	108167	ACAGCTCACAGCTCTGGGAG
110081	108168	CACAGCTCACAGCTCTGGGA
110082	108169	CCACAGCTCACAGCTCTGGG
110083	108170	ACCACAGCTCACAGCTCTGG
110084	108171	TACCACAGCTCACAGCTCTG
110085	108172	GTACCACAGCTCACAGCTCT
110086	108173	GGTACCACAGCTCACAGCTC
110087	108174	AGGTACCACAGCTCACAGCT
110088	108175	CAGGTACCACAGCTCACAGC
110089	108176	CCAGGTACCACAGCTCACAG
110090	108177	TCCAGGTACCACAGCTCACA
110091	108178	CTCCAGGTACCACAGCTCAC
110092	108179	ACTCCAGGTACCACAGCTCA
110093	108180	AACTCCAGGTACCACAGCTC
110094	108181	CAACTCCAGGTACCACAGCT
110095	108182	CCAACTCCAGGTACCACAGC
110096	108183	CCCAACTCCAGGTACCACAG
110097	108184	CCCCAACTCCAGGTACCACA
110098	108185	CCCCCAACTCCAGGTACCAC
110099	108186	TCCCCCAACTCCAGGTACCA
110100	108187	TTCCCCCAACTCCAGGTACC
110101	108188	CTTCCCCCAACTCCAGGTAC
110102	108189	CCTTCCCCCAACTCCAGGTA
110103	108190	GCCTTCCCCCAACTCCAGGT
110104	108191	AGCCTTCCCCCAACTCCAGG
110105	108192	CAGCCTTCCCCCAACTCCAG
110106	108193	CCAGCCTTCCCCCAACTCCA
110107	108194	GCCAGCCTTCCCCCAACTCC
110108	108195	TGCCAGCCTTCCCCCAACTC
110109	108196	GTGCCAGCCTTCCCCCAACT
110110	108197	TGTGCCAGCCTTCCCCCAAC
110111	108198	TTGTGCCAGCCTTCCCCCAA
110112	108199	CTTGTGCCAGCCTTCCCCCA
110113	108200	GCTTGTGCCAGCCTTCCCCC
110114	108201	TGCTTGTGCCAGCCTTCCCC
110115	108202	GTGCTTGTGCCAGCCTTCCC
110116	108203	AGTGCTTGTGCCAGCCTTCC
110117	108204	GAGTGCTTGTGCCAGCCTTC
110118	108205	GGAGTGCTTGTGCCAGCCTT
110119	108206	GGGAGTGCTTGTGCCAGCCT
110120	108207	AGGGAGTGCTTGTGCCAGCC
110121	108208	AAGGGAGTGCTTGTGCCAGC
110122	108209	CAAGGGAGTGCTTGTGCCAG
110123	108210	CCAAGGGAGTGCTTGTGCCA
110124	108211	GCCAAGGGAGTGCTTGTGCC
110125	108212	GGCCAAGGGAGTGCTTGTGC
110126	108213	TGGCCAAGGGAGTGCTTGTG
110127	108214	GTGGCCAAGGGAGTGCTTGT
110128	108215	GGTGGCCAAGGGAGTGCTTG
110129	108216	GGGTGGCCAAGGGAGTGCTT
110130	108217	AGGGTGGCCAAGGGAGTGCT
110131	108218	TAGGGTGGCCAAGGGAGTGC
110132	108219	CTAGGGTGGCCAAGGGAGTG
110133	108220	GCTAGGGTGGCCAAGGGAGT
110134	108221	AGCTAGGGTGGCCAAGGGAG
110135	108222	CAGCTAGGGTGGCCAAGGGA
110136	108223	CCAGCTAGGGTGGCCAAGGG
110137	108224	ACCAGCTAGGGTGGCCAAGG
110138	108225	CACCAGCTAGGGTGGCCAAG
110139	108226	ACACCAGCTAGGGTGGCCAA
110140	108227	GACACCAGCTAGGGTGGCCA
110141	108228	AGACACCAGCTAGGGTGGCC
110142	108229	GAGACACCAGCTAGGGTGGC
110143	108230	TGAGACACCAGCTAGGGTGG
110144	108231	CTGAGACACCAGCTAGGGTG

11851	9938	AGCCGATATCCTGCCACTGC
11852	9939	GAGCCGATATCCTGCCACTG
11853	9940	TGAGCCGATATCCTGCCACT
11854	9941	CTGAGCCGATATCCTGCCAC
11855	9942	ACTGAGCCGATATCCTGCCA
11856	9943	CACTGAGCCGATATCCTGCC
11857	9944	GCACTGAGCCGATATCCTGC
11858	9945	TGCACTGAGCCGATATCCTG
11859	9946	TTGCACTGAGCCGATATCCT
11860	9947	GTTGCACTGAGCCGATATCC
11861	9948	GGTTGCACTGAGCCGATATC
11862	9949	AGGTTGCACTGAGCCGATAT
11863	9950	GAGGTTGCACTGAGCCGATA
11864	9951	AGAGGTTGCACTGAGCCGAT
11865	9952	CAGAGGTTGCACTGAGCCGA
11866	9953	GCAGAGGTTGCACTGAGCCG
11867	9954	GGCAGAGGTTGCACTGAGCC
11868	9955	AGGCAGAGGTTGCACTGAGC
11869	9956	GAGGCAGAGGTTGCACTGAG
11870	9957	AGAGGCAGAGGTTGCACTGA
11871	9958	AAGAGGCAGAGGTTGCACTG
11872	9959	CAAGAGGCAGAGGTTGCACT
11873	9960	GCAAGAGGCAGAGGTTGCAC
11874	9961	CGCAAGAGGCAGAGGTTGCA
11875	9962	ACGCAAGAGGCAGAGGTTGC
11876	9963	AACGCAAGAGGCAGAGGTTG
11877	9964	GAACGCAAGAGGCAGAGGTT
11878	9965	TGAACGCAAGAGGCAGAGGT
11879	9966	TTGAACGCAAGAGGCAGAGG
11880	9967	TTTGAACGCAAGAGGCAGAG
11881	9968	ATTTGAACGCAAGAGGCAGA
11882	9969	CATTTGAACGCAAGAGGCAG
11883	9970	TCATTTGAACGCAAGAGGCA
11884	9971	ATCATTTGAACGCAAGAGGC
11885	9972	AATCATTTGAACGCAAGAGG
11886	9973	GAATCATTTGAACGCAAGAG
11887	9974	AGAATCATTTGAACGCAAGA
11888	9975	GAGAATCATTTGAACGCAAG
11889	9976	TGAGAATCATTTGAACGCAA
11890	9977	ATGAGAATCATTTGAACGCA
11891	9978	CATGAGAATCATTTGAACGC
11892	9979	GCATGAGAATCATTTGAACG
11893	9980	GGCATGAGAATCATTTGAAC
11894	9981	AGGCATGAGAATCATTTGAA
11895	9982	GAGGCATGAGAATCATTTGA
11896	9983	TGAGGCATGAGAATCATTTG
11897	9984	CTGAGGCATGAGAATCATTT
11898	9985	GCTGAGGCATGAGAATCATT
11899	9986	GGCTGAGGCATGAGAATCAT
11900	9987	AGGCTGAGGCATGAGAATCA
11901	9988	GAGGCTGAGGCATGAGAATC
11902	9989	GGAGGCTGAGGCATGAGAAT
11903	9990	GGGAGGCTGAGGCATGAGAA
11904	9991	CGGGAGGCTGAGGCATGAGA
11905	9992	TCGGGAGGCTGAGGCATGAG
11906	9993	CTCGGGAGGCTGAGGCATGA
11907	9994	ACTCGGGAGGCTGAGGCATG
11908	9995	TACTCGGGAGGCTGAGGCAT
11909	9996	CTACTCGGGAGGCTGAGGCA
11910	9997	GCTACTCGGGAGGCTGAGGC
11911	9998	AGCTACTCGGGAGGCTGAGG
11912	9999	CAGCTACTCGGGAGGCTGAG
11913	10000	CCAGCTACTCGGGAGGCTGA
11914	10001	CCCAGCTACTCGGGAGGCTG
11915	10002	TCCCAGCTACTCGGGAGGCT
11916	10003	ATCCCAGCTACTCGGGAGGC
11917	10004	AATCCCAGCTACTCGGGAGG
11918	10005	TAATCCCAGCTACTCGGGAG
11919	10006	ATAATCCCAGCTACTCGGGA
11920	10007	TATAATCCCAGCTACTCGGG
11921	10008	CTATAATCCCAGCTACTCGG

60998	59085	AATCATTACAAGTGAGGAGG
60999	59086	AAATCATTACAAGTGAGGAG
61000	59087	TAAATCATTACAAGTGAGGA
61001	59088	TTAAATCATTACAAGTGAGG
61002	59089	CTTAAATCATTACAAGTGAG
61003	59090	TCTTAAATCATTACAAGTGA
61004	59091	TTCTTAAATCATTACAAGTG
61005	59092	TTTCTTAAATCATTACAAGT
61006	59093	ATTTCTTAAATCATTACAAG
61007	59094	CATTTCTTAAATCATTACAA
61008	59095	GCATTTCTTAAATCATTACA
61009	59096	TGCATTTCTTAAATCATTAC
61010	59097	CTGCATTTCTTAAATCATTA
61011	59098	ACTGCATTTCTTAAATCATT
61012	59099	AACTGCATTTCTTAAATCAT
61013	59100	AAACTGCATTTCTTAAATCA
61014	59101	TAAACTGCATTTCTTAAATC
61015	59102	ATAAACTGCATTTCTTAAAT
61016	59103	AATAAACTGCATTTCTTAAA
61017	59104	AAATAAACTGCATTTCTTAA
61018	59105	AAAATAAACTGCATTTCTTA
61019	59106	AAAAATAAACTGCATTTCTT
61020	59107	TAAAAATAAACTGCATTTCT
61021	59108	ATAAAAATAAACTGCATTTC
61022	59109	AATAAAAATAAACTGCATTT
61023	59110	AAATAAAAATAAACTGCATT
61024	59111	AAAATAAAAATAAACTGCAT
61025	59112	TAAAATAAAAATAAACTGCA
61026	59113	ATAAAATAAAAATAAACTGC
61027	59114	AATAAAATAAAAATAAACTG
61028	59115	CAATAAAATAAAAATAAACT
61029	59116	ACAATAAAATAAAAATAAAC
61030	59117	TACAATAAAATAAAAATAAA
61031	59118	ATACAATAAAATAAAAATAA
61032	59119	AATACAATAAAATAAAAATA
61033	59120	AAATACAATAAAATAAAAAT
61034	59121	AAAATACAATAAAATAAAAA
61035	59122	AAAAATACAATAAAATAAAA
61036	59123	TAAAAATACAATAAAATAAA
61037	59124	TTAAAAATACAATAAAATAA
61038	59125	TTTAAAAATACAATAAAATA
61039	59126	CTTTAAAAATACAATAAAAT
61040	59127	TCTTTAAAAATACAATAAAA
61041	59128	TTCTTTAAAAATACAATAAA
61042	59129	TTTCTTTAAAAATACAATAA
61043	59130	ATTTCTTTAAAAATACAATA
61044	59131	AATTTCTTTAAAAATACAAT
61045	59132	GAATTTCTTTAAAAATACAA
61046	59133	TGAATTTCTTTAAAAATACA
61047	59134	CTGAATTTCTTTAAAAATAC
61048	59135	ACTGAATTTCTTTAAAAATA
61049	59136	AACTGAATTTCTTTAAAAAT
61050	59137	AAACTGAATTTCTTTAAAAA
61051	59138	AAAACTGAATTTCTTTAAAA
61052	59139	TAAAACTGAATTTCTTTAAA
61053	59140	TTAAAACTGAATTTCTTTAA
61054	59141	TTTAAAACTGAATTTCTTTA
61055	59142	CTTTAAAACTGAATTTCTTT
61056	59143	GCTTTAAAACTGAATTTCTT
61057	59144	TGCTTTAAAACTGAATTTCT
61058	59145	CTGCTTTAAAACTGAATTTC
61059	59146	ACTGCTTTAAAACTGAATTT
61060	59147	CACTGCTTTAAAACTGAATT
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61062	59149	TCCACTGCTTTAAAACTGAA
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61064	59151	ATTCCACTGCTTTAAAACTG
61065	59152	TATTCCACTGCTTTAAAACT
61066	59153	ATATTCCACTGCTTTAAAAC
61067	59154	CATATTCCACTGCTTTAAAA
61068	59155	TCATATTCCACTGCTTTAAA

110145	108232	ACTGAGACACCAGCTAGGGT
110146	108233	CACTGAGACACCAGCTAGGG
110147	108234	CCACTGAGACACCAGCTAGG
110148	108235	CCCACTGAGACACCAGCTAG
110149	108236	ACCCACTGAGACACCAGCTA
110150	108237	GACCCACTGAGACACCAGCT
110151	108238	TGACCCACTGAGACACCAGC
110152	108239	GTGACCCACTGAGACACCAG
110153	108240	TGTGACCCACTGAGACACCA
110154	108241	ATGTGACCCACTGAGACACC
110155	108242	CATGTGACCCACTGAGACAC
110156	108243	ACATGTGACCCACTGAGACA
110157	108244	TACATGTGACCCACTGAGAC
110158	108245	GTACATGTGACCCACTGAGA
110159	108246	GGTACATGTGACCCACTGAG
110160	108247	GGGTACATGTGACCCACTGA
110161	108248	GGGGTACATGTGACCCACTG
110162	108249	TGGGGTACATGTGACCCACT
110163	108250	TTGGGGTACATGTGACCCAC
110164	108251	CTTGGGGTACATGTGACCCA
110165	108252	ACTTGGGGTACATGTGACCC
110166	108253	GACTTGGGGTACATGTGACC
110167	108254	GGACTTGGGGTACATGTGAC
110168	108255	TGGACTTGGGGTACATGTGA
110169	108256	GTGGACTTGGGGTACATGTG
110170	108257	AGTGGACTTGGGGTACATGT
110171	108258	CAGTGGACTTGGGGTACATG
110172	108259	TCAGTGGACTTGGGGTACAT
110173	108260	GTCAGTGGACTTGGGGTACA
110174	108261	AGTCAGTGGACTTGGGGTAC
110175	108262	TAGTCAGTGGACTTGGGGTA
110176	108263	ATAGTCAGTGGACTTGGGGT
110177	108264	CATAGTCAGTGGACTTGGGG
110178	108265	TCATAGTCAGTGGACTTGGG
110179	108266	CTCATAGTCAGTGGACTTGG
110180	108267	GCTCATAGTCAGTGGACTTG
110181	108268	GGCTCATAGTCAGTGGACTT
110182	108269	GGGCTCATAGTCAGTGGACT
110183	108270	TGGGCTCATAGTCAGTGGAC
110184	108271	CTGGGCTCATAGTCAGTGGA
110185	108272	GCTGGGCTCATAGTCAGTGG
110186	108273	TGCTGGGCTCATAGTCAGTG
110187	108274	GTGCTGGGCTCATAGTCAGT
110188	108275	TGTGCTGGGCTCATAGTCAG
110189	108276	CTGTGCTGGGCTCATAGTCA
110190	108277	ACTGTGCTGGGCTCATAGTC
110191	108278	TACTGTGCTGGGCTCATAGT
110192	108279	GTACTGTGCTGGGCTCATAG
110193	108280	GGTACTGTGCTGGGCTCATA
110194	108281	TGGTACTGTGCTGGGCTCAT
110195	108282	ATGGTACTGTGCTGGGCTCA
110196	108283	CATGGTACTGTGCTGGGCTC
110197	108284	TCATGGTACTGTGCTGGGCT
110198	108285	GTCATGGTACTGTGCTGGGC
110199	108286	AGTCATGGTACTGTGCTGGG
110200	108287	AAGTCATGGTACTGTGCTGG
110201	108288	CAAGTCATGGTACTGTGCTG
110202	108289	ACAAGTCATGGTACTGTGCT
110203	108290	GACAAGTCATGGTACTGTGC
110204	108291	GGACAAGTCATGGTACTGTG
110205	108292	TGGACAAGTCATGGTACTGT
110206	108293	CTGGACAAGTCATGGTACTG
110207	108294	CCTGGACAAGTCATGGTACT
110208	108295	TCCTGGACAAGTCATGGTAC
110209	108296	TTCCTGGACAAGTCATGGTA
110210	108297	ATTCCTGGACAAGTCATGGT
110211	108298	AATTCCTGGACAAGTCATGG
110212	108299	CAATTCCTGGACAAGTCATG
110213	108300	GCAATTCCTGGACAAGTCAT
110214	108301	TGCAATTCCTGGACAAGTCA
110215	108302	CTGCAATTCCTGGACAAGTC

11922	10009	CCTATAATCCCAGCTACTCG
11923	10010	GCCTATAATCCCAGCTACTC
11924	10011	TGCCTATAATCCCAGCTACT
11925	10012	ATGCCTATAATCCCAGCTAC
11926	10013	CATGCCTATAATCCCAGCTA
11927	10014	GCATGCCTATAATCCCAGCT
11928	10015	CGCATGCCTATAATCCCAGC
11929	10016	GCGCATGCCTATAATCCCAG
11930	10017	GGCGCATGCCTATAATCCCA
11931	10018	TGGCGCATGCCTATAATCCC
11932	10019	GTGGCGCATGCCTATAATCC
11933	10020	AGTGGCGCATGCCTATAATC
11934	10021	TAGTGGCGCATGCCTATAAT
11935	10022	GTAGTGGCGCATGCCTATAA
11936	10023	TGTAGTGGCGCATGCCTATA
11937	10024	GTGTAGTGGCGCATGCCTAT
11938	10025	GGTGTAGTGGCGCATGCCTA
11939	10026	AGGTGTAGTGGCGCATGCCT
11940	10027	CAGGTGTAGTGGCGCATGCC
11941	10028	CCAGGTGTAGTGGCGCATGC
11942	10029	GCCAGGTGTAGTGGCGCATG
11943	10030	AGCCAGGTGTAGTGGCGCAT
11944	10031	TAGCCAGGTGTAGTGGCGCA
11945	10032	TTAGCCAGGTGTAGTGGCGC
11946	10033	ATTAGCCAGGTGTAGTGGCG
11947	10034	AATTAGCCAGGTGTAGTGGC
11948	10035	AAATTAGCCAGGTGTAGTGG
11949	10036	AAAATTAGCCAGGTGTAGTG
11950	10037	AAAAATTAGCCAGGTGTAGT
11951	10038	CAAAAATTAGCCAGGTGTAG
11952	10039	ACAAAAATTAGCCAGGTGTA
11953	10040	TACAAAAATTAGCCAGGTGT
11954	10041	ATACAAAAATTAGCCAGGTG
11955	10042	AATACAAAAATTAGCCAGGT
11956	10043	TAATACAAAAATTAGCCAGG
11957	10044	ATAATACAAAAATTAGCCAG
11958	10045	AATAATACAAAAATTAGCCA
11959	10046	CAATAATACAAAAATTAGCC
11960	10047	CCAATAATACAAAAATTAGC
11961	10048	ACCAATAATACAAAAATTAG
11962	10049	TACCAATAATACAAAAATTA
11963	10050	CTACCAATAATACAAAAATT
11964	10051	TCTACCAATAATACAAAAAT
11965	10052	CTCTACCAATAATACAAAAA
11966	10053	TCTCTACCAATAATACAAAA
11967	10054	ATCTCTACCAATAATACAAA
11968	10055	CATCTCTACCAATAATACAA
11969	10056	CCATCTCTACCAATAATACA
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11971	10058	CCCCATCTCTACCAATAATA
11972	10059	ACCCCATCTCTACCAATAAT
11973	10060	AACCCCATCTCTACCAATAA
11974	10061	AAACCCCATCTCTACCAATA
11975	10062	AAAACCCCATCTCTACCAAT
11976	10063	TAAAACCCCATCTCTACCAA
11977	10064	ATAAAACCCCATCTCTACCA
11978	10065	GATAAAACCCCATCTCTACC
11979	10066	TGATAAAACCCCATCTCTAC
11980	10067	ATGATAAAACCCCATCTCTA
11981	10068	CATGATAAAACCCCATCTCT
11982	10069	ACATGATAAAACCCCATCTC
11983	10070	AACATGATAAAACCCCATCT
11984	10071	CAACATGATAAAACCCCATC
11985	10072	CCAACATGATAAAACCCCAT
11986	10073	GCCAACATGATAAAACCCCA
11987	10074	GGCCAACATGATAAAACCCC
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11989	10076	CTGGCCAACATGATAAAACC
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11991	10078	GCCTGGCCAACATGATAAAA
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61069	59156	ATCATATTCCACTGCTTTAA
61070	59157	AATCATATTCCACTGCTTTA
61071	59158	CAATCATATTCCACTGCTTT
61072	59159	ACAATCATATTCCACTGCTT
61073	59160	GACAATCATATTCCACTGCT
61074	59161	AGACAATCATATTCCACTGC
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61076	59163	ATAGACAATCATATTCCACT
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61078	59165	TGATAGACAATCATATTCCA
61079	59166	CTGATAGACAATCATATTCC
61080	59167	GCTGATAGACAATCATATTC
61081	59168	AGCTGATAGACAATCATATT
61082	59169	AAGCTGATAGACAATCATAT
61083	59170	CAAGCTGATAGACAATCATA
61084	59171	GCAAGCTGATAGACAATCAT
61085	59172	CGCAAGCTGATAGACAATCA
61086	59173	GCGCAAGCTGATAGACAATC
61087	59174	AGCGCAAGCTGATAGACAAT
61088	59175	CAGCGCAAGCTGATAGACAA
61089	59176	TCAGCGCAAGCTGATAGACA
61090	59177	TTCAGCGCAAGCTGATAGAC
61091	59178	ATTCAGCGCAAGCTGATAGA
61092	59179	CATTCAGCGCAAGCTGATAG
61093	59180	CCATTCAGCGCAAGCTGATA
61094	59181	ACCATTCAGCGCAAGCTGAT
61095	59182	TACCATTCAGCGCAAGCTGA
61096	59183	TTACCATTCAGCGCAAGCTG
61097	59184	TTTACCATTCAGCGCAAGCT
61098	59185	ATTTACCATTCAGCGCAAGC
61099	59186	CATTTACCATTCAGCGCAAG
61100	59187	ACATTTACCATTCAGCGCAA
61101	59188	CACATTTACCATTCAGCGCA
61102	59189	TCACATTTACCATTCAGCGC
61103	59190	CTCACATTTACCATTCAGCG
61104	59191	TCTCACATTTACCATTCAGC
61105	59192	TTCTCACATTTACCATTCAG
61106	59193	TTTCTCACATTTACCATTCA
61107	59194	CTTTCTCACATTTACCATTC
61108	59195	TCTTTCTCACATTTACCATT
61109	59196	ATCTTTCTCACATTTACCAT
61110	59197	AATCTTTCTCACATTTACCA
61111	59198	TAATCTTTCTCACATTTACC
61112	59199	GTAATCTTTCTCACATTTAC
61113	59200	AGTAATCTTTCTCACATTTA
61114	59201	TAGTAATCTTTCTCACATTT
61115	59202	GTAGTAATCTTTCTCACATT
61116	59203	AGTAGTAATCTTTCTCACAT
61117	59204	TAGTAGTAATCTTTCTCACA
61118	59205	GTAGTAGTAATCTTTCTCAC
61119	59206	AGTAGTAGTAATCTTTCTCA
61120	59207	AAGTAGTAGTAATCTTTCTC
61121	59208	TAAGTAGTAGTAATCTTTCT
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61123	59210	ACTAAGTAGTAGTAATCTTT
61124	59211	CACTAAGTAGTAGTAATCTT
61125	59212	CCACTAAGTAGTAGTAATCT
61126	59213	ACCACTAAGTAGTAGTAATC
61127	59214	TACCACTAAGTAGTAGTAAT
61128	59215	GTACCACTAAGTAGTAGTAA
61129	59216	AGTACCACTAAGTAGTAGTA
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61131	59218	TCAGTACCACTAAGTAGTAG
61132	59219	CTCAGTACCACTAAGTAGTA
61133	59220	CCTCAGTACCACTAAGTAGT
61134	59221	CCCTCAGTACCACTAAGTAG
61135	59222	TCCCTCAGTACCACTAAGTA
61136	59223	CTCCCTCAGTACCACTAAGT
61137	59224	ACTCCCTCAGTACCACTAAG
61138	59225	AACTCCCTCAGTACCACTAA
61139	59226	CAACTCCCTCAGTACCACTA

110216	108303	ACTGCAATTCCTGGACAAGT
110217	108304	GACTGCAATTCCTGGACAAG
110218	108305	GGACTGCAATTCCTGGACAA
110219	108306	AGGACTGCAATTCCTGGACA
110220	108307	AAGGACTGCAATTCCTGGAC
110221	108308	GAAGGACTGCAATTCCTGGA
110222	108309	AGAAGGACTGCAATTCCTGG
110223	108310	CAGAAGGACTGCAATTCCTG
110224	108311	CCAGAAGGACTGCAATTCCT
110225	108312	ACCAGAAGGACTGCAATTCC
110226	108313	GACCAGAAGGACTGCAATTC
110227	108314	AGACCAGAAGGACTGCAATT
110228	108315	TAGACCAGAAGGACTGCAAT
110229	108316	CTAGACCAGAAGGACTGCAA
110230	108317	TCTAGACCAGAAGGACTGCA
110231	108318	GTCTAGACCAGAAGGACTGC
110232	108319	AGTCTAGACCAGAAGGACTG
110233	108320	CAGTCTAGACCAGAAGGACT
110234	108321	GCAGTCTAGACCAGAAGGAC
110235	108322	GGCAGTCTAGACCAGAAGGA
110236	108323	AGGCAGTCTAGACCAGAAGG
110237	108324	AAGGCAGTCTAGACCAGAAG
110238	108325	AAAGGCAGTCTAGACCAGAA
110239	108326	GAAAGGCAGTCTAGACCAGA
110240	108327	TGAAAGGCAGTCTAGACCAG
110241	108328	TTGAAAGGCAGTCTAGACCA
110242	108329	CTTGAAAGGCAGTCTAGACC
110243	108330	ACTTGAAAGGCAGTCTAGAC
110244	108331	AACTTGAAAGGCAGTCTAGA
110245	108332	AAACTTGAAAGGCAGTCTAG
110246	108333	TAAACTTGAAAGGCAGTCTA
110247	108334	ATAAACTTGAAAGGCAGTCT
110248	108335	AATAAACTTGAAAGGCAGTC
110249	108336	AAATAAACTTGAAAGGCAGT
110250	108337	TAAATAAACTTGAAAGGCAG
110251	108338	CTAAATAAACTTGAAAGGCA
110252	108339	CCTAAATAAACTTGAAAGGC
110253	108340	TCCTAAATAAACTTGAAAGG
110254	108341	GTCCTAAATAAACTTGAAAG
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110257	108344	GGGGTCCTAAATAAACTTGA
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110260	108347	TCTGGGGTCCTAAATAAACT
110261	108348	CTCTGGGGTCCTAAATAAAC
110262	108349	CCTCTGGGGTCCTAAATAAA
110263	108350	TCCTCTGGGGTCCTAAATAA
110264	108351	GTCCTCTGGGGTCCTAAATA
110265	108352	AGTCCTCTGGGGTCCTAAAT
110266	108353	AAGTCCTCTGGGGTCCTAAA
110267	108354	AAAGTCCTCTGGGGTCCTAA
110268	108355	TAAAGTCCTCTGGGGTCCTA
110269	108356	GTAAAGTCCTCTGGGGTCCT
110270	108357	GGTAAAGTCCTCTGGGGTCC
110271	108358	GGGTAAAGTCCTCTGGGGTC
110272	108359	TGGGTAAAGTCCTCTGGGGT
110273	108360	GTGGGTAAAGTCCTCTGGGG
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110275	108362	CCGTGGGTAAAGTCCTCTGG
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110281	108368	CCACCACCGTGGGTAAAGTC
110282	108369	CCCACCACCGTGGGTAAAGT
110283	108370	CCCCACCACCGTGGGTAAAG
110284	108371	GCCCCACCACCGTGGGTAAA
110285	108372	AGCCCCACCACCGTGGGTAA
110286	108373	AAGCCCCACCACCGTGGGTA

11993	10080	CAGCCTGGCCAACATGATAA
11994	10081	CCAGCCTGGCCAACATGATA
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11996	10083	GACCAGCCTGGCCAACATGA
11997	10084	AGACCAGCCTGGCCAACATG
11998	10085	GAGACCAGCCTGGCCAACAT
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12001	10088	TTCGAGACCAGCCTGGCCAA
12002	10089	GTTCGAGACCAGCCTGGCCA
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12010	10097	GGTCGGGAGTTCGAGACCAG
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12014	10101	CTGAGGTCGGGAGTTCGAGA
12015	10102	CCTGAGGTCGGGAGTTCGAG
12016	10103	ACCTGAGGTCGGGAGTTCGA
12017	10104	CACCTGAGGTCGGGAGTTCG
12018	10105	TCACCTGAGGTCGGGAGTTC
12019	10106	ATCACCTGAGGTCGGGAGTT
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12023	10110	ATGGATCACCTGAGGTCGGG
12024	10111	TATGGATCACCTGAGGTCGG
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12045	10132	GCACTTCAGGAGGCCAAGGT
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12052	10139	AATTCCAGCACTTCAGGAGG
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12057	10144	CCTGTAATTCCAGCACTTCA
12058	10145	GCCTGTAATTCCAGCACTTC
12059	10146	TGCCTGTAATTCCAGCACTT
12060	10147	ATGCCTGTAATTCCAGCACT
12061	10148	TATGCCTGTAATTCCAGCAC
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61140	59227	GCAACTCCCTCAGTACCACT
61141	59228	TGCAACTCCCTCAGTACCAC
61142	59229	TTGCAACTCCCTCAGTACCA
61143	59230	TTTGCAACTCCCTCAGTACC
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61145	59232	GTTTTGCAACTCCCTCAGTA
61146	59233	TGTTTTGCAACTCCCTCAGT
61147	59234	GTGTTTTGCAACTCCCTCAG
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61149	59236	AAGTGTTTTGCAACTCCCTC
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61159	59246	TAGCAGTGTTAAGTGTTTTG
61160	59247	CTAGCAGTGTTAAGTGTTTT
61161	59248	ACTAGCAGTGTTAAGTGTTT
61162	59249	CACTAGCAGTGTTAAGTGTT
61163	59250	CCACTAGCAGTGTTAAGTGT
61164	59251	CCCACTAGCAGTGTTAAGTG
61165	59252	TCCCACTAGCAGTGTTAAGT
61166	59253	ATCCCACTAGCAGTGTTAAG
61167	59254	CATCCCACTAGCAGTGTTAA
61168	59255	CCATCCCACTAGCAGTGTTA
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61170	59257	AACCATCCCACTAGCAGTGT
61171	59258	AAACCATCCCACTAGCAGTG
61172	59259	TAAACCATCCCACTAGCAGT
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61181	59268	TGTTTTACTTAAACCATCCC
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61184	59271	ACTTGTTTTACTTAAACCAT
61185	59272	TACTTGTTTTACTTAAACCA
61186	59273	CTACTTGTTTTACTTAAACC
61187	59274	GCTACTTGTTTTACTTAAAC
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61190	59277	AATGCTACTTGTTTTACTTA
61191	59278	GAATGCTACTTGTTTTACTT
61192	59279	AGAATGCTACTTGTTTTACT
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61196	59283	TTTAAGAATGCTACTTGTTT
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61198	59285	AGTTTAAGAATGCTACTTGT
61199	59286	GAGTTTAAGAATGCTACTTG
61200	59287	AGAGTTTAAGAATGCTACTT
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61202	59289	AGAGAGTTTAAGAATGCTAC
61203	59290	TAGAGAGTTTAAGAATGCTA
61204	59291	ATAGAGAGTTTAAGAATGCT
61205	59292	AATAGAGAGTTTAAGAATGC
61206	59293	TAATAGAGAGTTTAAGAATG
61207	59294	CTAATAGAGAGTTTAAGAAT
61208	59295	CCTAATAGAGAGTTTAAGAA
61209	59296	ACCTAATAGAGAGTTTAAGA
61210	59297	TACCTAATAGAGAGTTTAAG

110287	108374	TAAGCCCCACCACCGTGGGT
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110290	108377	TGGTAAGCCCCACCACCGTG
110291	108378	TTGGTAAGCCCCACCACCGT
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110293	108380	TTTTGGTAAGCCCCACCACC
110294	108381	ATTTTGGTAAGCCCCACCAC
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110296	108383	TAATTTTGGTAAGCCCCACC
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110307	108394	CAAAAGAATCTTAATTTTGG
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110311	108398	AAACCAAAAGAATCTTAATT
110312	108399	AAAACCAAAAGAATCTTAAT
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110332	108419	AGAGCGAAACTCTGCCAAAA
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110341	108428	TGGGCAATAAGAGCGAAACT
110342	108429	CTGGGCAATAAGAGCGAAAC
110343	108430	CCTGGGCAATAAGAGCGAAA
110344	108431	GCCTGGGCAATAAGAGCGAA
110345	108432	AGCCTGGGCAATAAGAGCGA
110346	108433	CAGCCTGGGCAATAAGAGCG
110347	108434	CCAGCCTGGGCAATAAGAGC
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110350	108437	ACTCCAGCCTGGGCAATAAG
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110353	108440	TATACTCCAGCCTGGGCAAT
110354	108441	CTATACTCCAGCCTGGGCAA
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110356	108443	CACTATACTCCAGCCTGGGC
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12064	10151	GCTTATGCCTGTAATTCCAG
12065	10152	GGCTTATGCCTGTAATTCCA
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12067	10154	GTGGCTTATGCCTGTAATTC
12068	10155	AGTGGCTTATGCCTGTAATT
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12070	10157	GCAGTGGCTTATGCCTGTAA
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12072	10159	GCGCAGTGGCTTATGCCTGT
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12074	10161	AGGCGCAGTGGCTTATGCCT
12075	10162	TAGGCGCAGTGGCTTATGCC
12076	10163	CTAGGCGCAGTGGCTTATGC
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12078	10165	AGCTAGGCGCAGTGGCTTAT
12079	10166	AAGCTAGGCGCAGTGGCTTA
12080	10167	AAAGCTAGGCGCAGTGGCTT
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12083	10170	AAAAAAGCTAGGCGCAGTGG
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12085	10172	ACAAAAAAGCTAGGCGCAGT
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12087	10174	AAACAAAAAAGCTAGGCGCA
12088	10175	CAAACAAAAAAGCTAGGCGC
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12091	10178	AAACAAACAAAAAAGCTAGG
12092	10179	AAAACAAACAAAAAAGCTAG
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12095	10182	ATAAAAACAAACAAAAAAGC
12096	10183	AATAAAAACAAACAAAAAAG
12097	10184	AAATAAAAACAAACAAAAAA
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12108	10195	CTGTCCCTACAAAATAAAAA
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12110	10197	CTCTGTCCCTACAAAATAAA
12111	10198	TCTCTGTCCCTACAAAATAA
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12117	10204	GTAAAATCTCTGTCCCTACA
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12120	10207	CAGGTAAAATCTCTGTCCCT
12121	10208	ACAGGTAAAATCTCTGTCCC
12122	10209	AACAGGTAAAATCTCTGTCC
12123	10210	CAACAGGTAAAATCTCTGTC
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12125	10212	GGCAACAGGTAAAATCTCTG
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12127	10214	TGGGCAACAGGTAAAATCTC
12128	10215	CTGGGCAACAGGTAAAATCT
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12131	10218	ATCCTGGGCAACAGGTAAAA
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61211	59298	TTACCTAATAGAGAGTTTAA
61212	59299	TTTACCTAATAGAGAGTTTA
61213	59300	CTTTACCTAATAGAGAGTTT
61214	59301	TCTTTACCTAATAGAGAGTT
61215	59302	TTCTTTACCTAATAGAGAGT
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61217	59304	TATTCTTTACCTAATAGAGA
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61219	59306	CCTATTCTTTACCTAATAGA
61220	59307	ACCTATTCTTTACCTAATAG
61221	59308	TACCTATTCTTTACCTAATA
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61223	59310	CTTACCTATTCTTTACCTAA
61224	59311	ACTTACCTATTCTTTACCTA
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61231	59318	ATGCATTACTTACCTATTCT
61232	59319	TATGCATTACTTACCTATTC
61233	59320	ATATGCATTACTTACCTATT
61234	59321	CATATGCATTACTTACCTAT
61235	59322	ACATATGCATTACTTACCTA
61236	59323	AACATATGCATTACTTACCT
61237	59324	AAACATATGCATTACTTACC
61238	59325	GAAACATATGCATTACTTAC
61239	59326	GGAAACATATGCATTACTTA
61240	59327	TGGAAACATATGCATTACTT
61241	59328	CTGGAAACATATGCATTACT
61242	59329	CCTGGAAACATATGCATTAC
61243	59330	TCCTGGAAACATATGCATTA
61244	59331	GTCCTGGAAACATATGCATT
61245	59332	TGTCCTGGAAACATATGCAT
61246	59333	ATGTCCTGGAAACATATGCA
61247	59334	AATGTCCTGGAAACATATGC
61248	59335	AAATGTCCTGGAAACATATG
61249	59336	AAAATGTCCTGGAAACATAT
61250	59337	GAAAATGTCCTGGAAACATA
61251	59338	TGAAAATGTCCTGGAAACAT
61252	59339	CTGAAAATGTCCTGGAAACA
61253	59340	ACTGAAAATGTCCTGGAAAC
61254	59341	TACTGAAAATGTCCTGGAAA
61255	59342	TTACTGAAAATGTCCTGGAA
61256	59343	CTTACTGAAAATGTCCTGGA
61257	59344	TCTTACTGAAAATGTCCTGG
61258	59345	GTCTTACTGAAAATGTCCTG
61259	59346	AGTCTTACTGAAAATGTCCT
61260	59347	CAGTCTTACTGAAAATGTCC
61261	59348	ACAGTCTTACTGAAAATGTC
61262	59349	AACAGTCTTACTGAAAATGT
61263	59350	AAACAGTCTTACTGAAAATG
61264	59351	TAAACAGTCTTACTGAAAAT
61265	59352	GTAAACAGTCTTACTGAAAA
61266	59353	AGTAAACAGTCTTACTGAAA
61267	59354	CAGTAAACAGTCTTACTGAA
61268	59355	TCAGTAAACAGTCTTACTGA
61269	59356	ATCAGTAAACAGTCTTACTG
61270	59357	TATCAGTAAACAGTCTTACT
61271	59358	CTATCAGTAAACAGTCTTAC
61272	59359	CCTATCAGTAAACAGTCTTA
61273	59360	CCCTATCAGTAAACAGTCTT
61274	59361	ACCCTATCAGTAAACAGTCT
61275	59362	AACCCTATCAGTAAACAGTC
61276	59363	CAACCCTATCAGTAAACAGT
61277	59364	ACAACCCTATCAGTAAACAG
61278	59365	CACAACCCTATCAGTAAACA
61279	59366	ACACAACCCTATCAGTAAAC
61280	59367	TACACAACCCTATCAGTAAA
61281	59368	TTACACAACCCTATCAGTAA

110358	108445	GTCACTATACTCCAGCCTGG
110359	108446	CGTCACTATACTCCAGCCTG
110360	108447	GCGTCACTATACTCCAGCCT
110361	108448	TGCGTCACTATACTCCAGCC
110362	108449	TTGCGTCACTATACTCCAGC
110363	108450	ATTGCGTCACTATACTCCAG
110364	108451	GATTGCGTCACTATACTCCA
110365	108452	AGATTGCGTCACTATACTCC
110366	108453	GAGATTGCGTCACTATACTC
110367	108454	TGAGATTGCGTCACTATACT
110368	108455	CTGAGATTGCGTCACTATAC
110369	108456	GCTGAGATTGCGTCACTATA
110370	108457	AGCTGAGATTGCGTCACTAT
110371	108458	GAGCTGAGATTGCGTCACTA
110372	108459	TGAGCTGAGATTGCGTCACT
110373	108460	GTGAGCTGAGATTGCGTCAC
110374	108461	GGTGAGCTGAGATTGCGTCA
110375	108462	TGGTGAGCTGAGATTGCGTC
110376	108463	GTGGTGAGCTGAGATTGCGT
110377	108464	TGTGGTGAGCTGAGATTGCG
110378	108465	TTGTGGTGAGCTGAGATTGC
110379	108466	GTTGTGGTGAGCTGAGATTG
110380	108467	GGTTGTGGTGAGCTGAGATT
110381	108468	AGGTTGTGGTGAGCTGAGAT
110382	108469	GAGGTTGTGGTGAGCTGAGA
110383	108470	GGAGGTTGTGGTGAGCTGAG
110384	108471	CGGAGGTTGTGGTGAGCTGA
110385	108472	GCGGAGGTTGTGGTGAGCTG
110386	108473	GGCGGAGGTTGTGGTGAGCT
110387	108474	AGGCGGAGGTTGTGGTGAGC
110388	108475	GAGGCGGAGGTTGTGGTGAG
110389	108476	GGAGGCGGAGGTTGTGGTGA
110390	108477	GGGAGGCGGAGGTTGTGGTG
110391	108478	CGGGAGGCGGAGGTTGTGGT
110392	108479	CCGGGAGGCGGAGGTTGTGG
110393	108480	CCCGGGAGGCGGAGGTTGTG
110394	108481	ACCCGGGAGGCGGAGGTTGT
110395	108482	AACCCGGGAGGCGGAGGTTG
110396	108483	GAACCCGGGAGGCGGAGGTT
110397	108484	TGAACCCGGGAGGCGGAGGT
110398	108485	TTGAACCCGGGAGGCGGAGG
110399	108486	TTTGAACCCGGGAGGCGGAG
110400	108487	ATTTGAACCCGGGAGGCGGA
110401	108488	TATTTGAACCCGGGAGGCGG
110402	108489	TTATTTGAACCCGGGAGGCG
110403	108490	ATTATTTGAACCCGGGAGGC
110404	108491	AATTATTTGAACCCGGGAGG
110405	108492	GAATTATTTGAACCCGGGAG
110406	108493	AGAATTATTTGAACCCGGGA
110407	108494	GAGAATTATTTGAACCCGGG
110408	108495	GGAGAATTATTTGAACCCGG
110409	108496	AGGAGAATTATTTGAACCCG
110410	108497	TAGGAGAATTATTTGAACCC
110411	108498	GTAGGAGAATTATTTGAACC
110412	108499	GGTAGGAGAATTATTTGAAC
110413	108500	AGGTAGGAGAATTATTTGAA
110414	108501	GAGGTAGGAGAATTATTTGA
110415	108502	TGAGGTAGGAGAATTATTTG
110416	108503	CTGAGGTAGGAGAATTATTT
110417	108504	GCTGAGGTAGGAGAATTATT
110418	108505	GGCTGAGGTAGGAGAATTAT
110419	108506	AGGCTGAGGTAGGAGAATTA
110420	108507	GAGGCTGAGGTAGGAGAATT
110421	108508	GGAGGCTGAGGTAGGAGAAT
110422	108509	AGGAGGCTGAGGTAGGAGAA
110423	108510	CAGGAGGCTGAGGTAGGAGA
110424	108511	TCAGGAGGCTGAGGTAGGAG
110425	108512	CTCAGGAGGCTGAGGTAGGA
110426	108513	ACTCAGGAGGCTGAGGTAGG
110427	108514	TACTCAGGAGGCTGAGGTAG
110428	108515	CTACTCAGGAGGCTGAGGTA

12135	10222	GGCCATCCTGGGCAACAGGT
12136	10223	AGGCCATCCTGGGCAACAGG
12137	10224	AAGGCCATCCTGGGCAACAG
12138	10225	CAAGGCCATCCTGGGCAACA
12139	10226	TCAAGGCCATCCTGGGCAAC
12140	10227	TTCAAGGCCATCCTGGGCAA
12141	10228	ATTCAAGGCCATCCTGGGCA
12142	10229	AATTCAAGGCCATCCTGGGC
12143	10230	GAATTCAAGGCCATCCTGGG
12144	10231	GGAATTCAAGGCCATCCTGG
12145	10232	AGGAATTCAAGGCCATCCTG
12146	10233	CAGGAATTCAAGGCCATCCT
12147	10234	TCAGGAATTCAAGGCCATCC
12148	10235	GTCAGGAATTCAAGGCCATC
12149	10236	GGTCAGGAATTCAAGGCCAT
12150	10237	AGGTCAGGAATTCAAGGCCA
12151	10238	GAGGTCAGGAATTCAAGGCC
12152	10239	TGAGGTCAGGAATTCAAGGC
12153	10240	TTGAGGTCAGGAATTCAAGG
12154	10241	TTTGAGGTCAGGAATTCAAG
12155	10242	GTTTGAGGTCAGGAATTCAA
12156	10243	TGTTTGAGGTCAGGAATTCA
12157	10244	TTGTTTGAGGTCAGGAATTC
12158	10245	ATTGTTTGAGGTCAGGAATT
12159	10246	AATTGTTTGAGGTCAGGAAT
12160	10247	AAATTGTTTGAGGTCAGGAA
12161	10248	CAAATTGTTTGAGGTCAGGA
12162	10249	GCAAATTGTTTGAGGTCAGG
12163	10250	GGCAAATTGTTTGAGGTCAG
12164	10251	GGGCAAATTGTTTGAGGTCA
12165	10252	AGGGCAAATTGTTTGAGGTC
12166	10253	GAGGGCAAATTGTTTGAGGT
12167	10254	GGAGGGCAAATTGTTTGAGG
12168	10255	AGGAGGGCAAATTGTTTGAG
12169	10256	AAGGAGGGCAAATTGTTTGA
12170	10257	CAAGGAGGGCAAATTGTTTG
12171	10258	CCAAGGAGGGCAAATTGTTT
12172	10259	GCCAAGGAGGGCAAATTGTT
12173	10260	GGCCAAGGAGGGCAAATTGT
12174	10261	AGGCCAAGGAGGGCAAATTG
12175	10262	GAGGCCAAGGAGGGCAAATT
12176	10263	GGAGGCCAAGGAGGGCAAAT
12177	10264	GGGAGGCCAAGGAGGGCAAA
12178	10265	TGGGAGGCCAAGGAGGGCAA
12179	10266	TTGGGAGGCCAAGGAGGGCA
12180	10267	CTTGGGAGGCCAAGGAGGGC
12181	10268	CCTTGGGAGGCCAAGGAGGG
12182	10269	ACCTTGGGAGGCCAAGGAGG
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12184	10271	GCACCTTGGGAGGCCAAGGA
12185	10272	AGCACCTTGGGAGGCCAAGG
12186	10273	CAGCACCTTGGGAGGCCAAG
12187	10274	CCAGCACCTTGGGAGGCCAA
12188	10275	CCCAGCACCTTGGGAGGCCA
12189	10276	TCCCAGCACCTTGGGAGGCC
12190	10277	ATCCCAGCACCTTGGGAGGC
12191	10278	AATCCCAGCACCTTGGGAGG
12192	10279	TAATCCCAGCACCTTGGGAG
12193	10280	GTAATCCCAGCACCTTGGGA
12194	10281	TGTAATCCCAGCACCTTGGG
12195	10282	CTGTAATCCCAGCACCTTGG
12196	10283	CCTGTAATCCCAGCACCTTG
12197	10284	ACCTGTAATCCCAGCACCTT
12198	10285	CACCTGTAATCCCAGCACCT
12199	10286	ACACCTGTAATCCCAGCACC
12200	10287	CACACCTGTAATCCCAGCAC
12201	10288	TCACACCTGTAATCCCAGCA
12202	10289	CTCACACCTGTAATCCCAGC
12203	10290	GCTCACACCTGTAATCCCAG
12204	10291	GGCTCACACCTGTAATCCCA
12205	10292	TGGCTCACACCTGTAATCCC

61282	59369	ATTACACAACCCTATCAGTA
61283	59370	CATTACACAACCCTATCAGT
61284	59371	GCATTACACAACCCTATCAG
61285	59372	AGCATTACACAACCCTATCA
61286	59373	TAGCATTACACAACCCTATC
61287	59374	TTAGCATTACACAACCCTAT
61288	59375	ATTAGCATTACACAACCCTA
61289	59376	TATTAGCATTACACAACCCT
61290	59377	ATATTAGCATTACACAACCC
61291	59378	TATATTAGCATTACACAACC
61292	59379	GTATATTAGCATTACACAAC
61293	59380	AGTATATTAGCATTACACAA
61294	59381	AAGTATATTAGCATTACACA
61295	59382	TAAGTATATTAGCATTACAC
61296	59383	GTAAGTATATTAGCATTACA
61297	59384	AGTAAGTATATTAGCATTAC
61298	59385	TAGTAAGTATATTAGCATTA
61299	59386	ATAGTAAGTATATTAGCATT
61300	59387	GATAGTAAGTATATTAGCAT
61301	59388	AGATAGTAAGTATATTAGCA
61302	59389	TAGATAGTAAGTATATTAGC
61303	59390	CTAGATAGTAAGTATATTAG
61304	59391	ACTAGATAGTAAGTATATTA
61305	59392	AACTAGATAGTAAGTATATT
61306	59393	AAACTAGATAGTAAGTATAT
61307	59394	AAAACTAGATAGTAAGTATA
61308	59395	TAAAACTAGATAGTAAGTAT
61309	59396	CTAAAACTAGATAGTAAGTA
61310	59397	ACTAAAACTAGATAGTAAGT
61311	59398	TACTAAAACTAGATAGTAAG
61312	59399	ATACTAAAACTAGATAGTAA
61313	59400	AATACTAAAACTAGATAGTA
61314	59401	TAATACTAAAACTAGATAGT
61315	59402	ATAATACTAAAACTAGATAG
61316	59403	AATAATACTAAAACTAGATA
61317	59404	AAATAATACTAAAACTAGAT
61318	59405	AAAATAATACTAAAACTAGA
61319	59406	AAAAATAATACTAAAACTAG
61320	59407	AAAAAATAATACTAAAACTA
61321	59408	AAAAAAATAATACTAAAACT
61322	59409	GAAAAAAATAATACTAAAAC
61323	59410	AGAAAAAAATAATACTAAAA
61324	59411	GAGAAAAAAATAATACTAAA
61325	59412	AGAGAAAAAAATAATACTAA
61326	59413	AAGAGAAAAAAATAATACTA
61327	59414	CAAGAGAAAAAAATAATACT
61328	59415	ACAAGAGAAAAAAATAATAC
61329	59416	GACAAGAGAAAAAAATAATA
61330	59417	AGACAAGAGAAAAAAATAAT
61331	59418	AAGACAAGAGAAAAAAATAA
61332	59419	CAAGACAAGAGAAAAAAATA
61333	59420	CCAAGACAAGAGAAAAAAAT
61334	59421	TCCAAGACAAGAGAAAAAAA
61335	59422	ATCCAAGACAAGAGAAAAAA
61336	59423	CATCCAAGACAAGAGAAAAA
61337	59424	CCATCCAAGACAAGAGAAAA
61338	59425	ACCATCCAAGACAAGAGAAA
61339	59426	AACCATCCAAGACAAGAGAA
61340	59427	AAACCATCCAAGACAAGAGA
61341	59428	GAAACCATCCAAGACAAGAG
61342	59429	TGAAACCATCCAAGACAAGA
61343	59430	TTGAAACCATCCAAGACAAG
61344	59431	ATTGAAACCATCCAAGACAA
61345	59432	CATTGAAACCATCCAAGACA
61346	59433	CCATTGAAACCATCCAAGAC
61347	59434	TCCATTGAAACCATCCAAGA
61348	59435	CTCCATTGAAACCATCCAAG
61349	59436	ACTCCATTGAAACCATCCAA
61350	59437	GACTCCATTGAAACCATCCA
61351	59438	AGACTCCATTGAAACCATCC
61352	59439	AAGACTCCATTGAAACCATC

110429	108516	GCTACTCAGGAGGCTGAGGT
110430	108517	AGCTACTCAGGAGGCTGAGG
110431	108518	CAGCTACTCAGGAGGCTGAG
110432	108519	CCAGCTACTCAGGAGGCTGA
110433	108520	CCCAGCTACTCAGGAGGCTG
110434	108521	TCCCAGCTACTCAGGAGGCT
110435	108522	ATCCCAGCTACTCAGGAGGC
110436	108523	AATCCCAGCTACTCAGGAGG
110437	108524	TAATCCCAGCTACTCAGGAG
110438	108525	GTAATCCCAGCTACTCAGGA
110439	108526	GGTAATCCCAGCTACTCAGG
110440	108527	CGGTAATCCCAGCTACTCAG
110441	108528	CCGGTAATCCCAGCTACTCA
110442	108529	GCCGGTAATCCCAGCTACTC
110443	108530	TGCCGGTAATCCCAGCTACT
110444	108531	ATGCCGGTAATCCCAGCTAC
110445	108532	CATGCCGGTAATCCCAGCTA
110446	108533	GCATGCCGGTAATCCCAGCT
110447	108534	CGCATGCCGGTAATCCCAGC
110448	108535	GCGCATGCCGGTAATCCCAG
110449	108536	AGCGCATGCCGGTAATCCCA
110450	108537	TAGCGCATGCCGGTAATCCC
110451	108538	GTAGCGCATGCCGGTAATCC
110452	108539	GGTAGCGCATGCCGGTAATC
110453	108540	TGGTAGCGCATGCCGGTAAT
110454	108541	GTGGTAGCGCATGCCGGTAA
110455	108542	GGTGGTAGCGCATGCCGGTA
110456	108543	AGGTGGTAGCGCATGCCGGT
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110458	108545	AGAGGTGGTAGCGCATGCCG
110459	108546	CAGAGGTGGTAGCGCATGCC
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110461	108548	GCCAGAGGTGGTAGCGCATG
110462	108549	AGCCAGAGGTGGTAGCGCAT
110463	108550	TAGCCAGAGGTGGTAGCGCA
110464	108551	TTAGCCAGAGGTGGTAGCGC
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110466	108553	AATTAGCCAGAGGTGGTAGC
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110468	108555	AAAATTAGCCAGAGGTGGTA
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110475	108562	AAACAAAAAAATTAGCCAGA
110476	108563	AAAACAAAAAAATTAGCCAG
110477	108564	AAAAACAAAAAAATTAGCCA
110478	108565	AAAAAACAAAAAAATTAGCC
110479	108566	TAAAAAACAAAAAAATTAGC
110480	108567	CTAAAAAACAAAAAAATTAG
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110482	108569	TACTAAAAAACAAAAAAATT
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110486	108573	TCTCTACTAAAAAACAAAAA
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110495	108582	GAAACCTCATCTCTACTAAA
110496	108583	AGAAACCTCATCTCTACTAA
110497	108584	GAGAAACCTCATCTCTACTA
110498	108585	GGAGAAACCTCATCTCTACT
110499	108586	TGGAGAAACCTCATCTCTAC

12206	10293	GTGGCTCACACCTGTAATCC
12207	10294	AGTGGCTCACACCTGTAATC
12208	10295	TAGTGGCTCACACCTGTAAT
12209	10296	ATAGTGGCTCACACCTGTAA
12210	10297	CATAGTGGCTCACACCTGTA
12211	10298	GCATAGTGGCTCACACCTGT
12212	10299	GGCATAGTGGCTCACACCTG
12213	10300	AGGCATAGTGGCTCACACCT
12214	10301	CAGGCATAGTGGCTCACACC
12215	10302	CCAGGCATAGTGGCTCACAC
12216	10303	GCCAGGCATAGTGGCTCACA
12217	10304	AGCCAGGCATAGTGGCTCAC
12218	10305	CAGCCAGGCATAGTGGCTCA
12219	10306	CCAGCCAGGCATAGTGGCTC
12220	10307	ACCAGCCAGGCATAGTGGCT
12221	10308	AACCAGCCAGGCATAGTGGC
12222	10309	AAACCAGCCAGGCATAGTGG
12223	10310	AAAACCAGCCAGGCATAGTG
12224	10311	AAAAACCAGCCAGGCATAGT
12225	10312	AAAAAACCAGCCAGGCATAG
12226	10313	TAAAAAACCAGCCAGGCATA
12227	10314	TTAAAAAACCAGCCAGGCAT
12228	10315	TTTAAAAAACCAGCCAGGCA
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12230	10317	AATTTAAAAAACCAGCCAGG
12231	10318	TAATTTAAAAAACCAGCCAG
12232	10319	ATAATTTAAAAAACCAGCCA
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12236	10323	AATAATAATTTAAAAAACCA
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12239	10326	AATAATAATAATTTAAAAAA
12240	10327	CAATAATAATAATTTAAAAA
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12244	10331	CAAACAATAATAATAATTTA
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12246	10333	CACAAACAATAATAATAATT
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12251	10338	ACACACACAAACAATAATAA
12252	10339	CACACACACAAACAATAATA
12253	10340	ACACACACACAAACAATAAT
12254	10341	CACACACACACAAACAATAA
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12256	10343	AACACACACACACAAACAAT
12257	10344	CAACACACACACACAAACAA
12258	10345	GCAACACACACACACAAACA
12259	10346	TGCAACACACACACACAAAC
12260	10347	CTGCAACACACACACACAAA
12261	10348	CCTGCAACACACACACACAA
12262	10349	TCCTGCAACACACACACACA
12263	10350	ATCCTGCAACACACACACAC
12264	10351	GATCCTGCAACACACACACA
12265	10352	AGATCCTGCAACACACACAC
12266	10353	AAGATCCTGCAACACACACA
12267	10354	TAAGATCCTGCAACACACAC
12268	10355	GTAAGATCCTGCAACACACA
12269	10356	GGTAAGATCCTGCAACACAC
12270	10357	GGGTAAGATCCTGCAACACA
12271	10358	AGGGTAAGATCCTGCAACAC
12272	10359	CAGGGTAAGATCCTGCAACA
12273	10360	ACAGGGTAAGATCCTGCAAC
12274	10361	GACAGGGTAAGATCCTGCAA
12275	10362	TGACAGGGTAAGATCCTGCA
12276	10363	GTGACAGGGTAAGATCCTGC

61353	59440	TAAGACTCCATTGAAACCAT
61354	59441	ATAAGACTCCATTGAAACCA
61355	59442	CATAAGACTCCATTGAAACC
61356	59443	GCATAAGACTCCATTGAAAC
61357	59444	TGCATAAGACTCCATTGAAA
61358	59445	ATGCATAAGACTCCATTGAA
61359	59446	CATGCATAAGACTCCATTGA
61360	59447	GCATGCATAAGACTCCATTG
61361	59448	TGCATGCATAAGACTCCATT
61362	59449	CTGCATGCATAAGACTCCAT
61363	59450	TCTGCATGCATAAGACTCCA
61364	59451	ATCTGCATGCATAAGACTCC
61365	59452	TATCTGCATGCATAAGACTC
61366	59453	ATATCTGCATGCATAAGACT
61367	59454	TATATCTGCATGCATAAGAC
61368	59455	ATATATCTGCATGCATAAGA
61369	59456	AATATATCTGCATGCATAAG
61370	59457	TAATATATCTGCATGCATAA
61371	59458	TTAATATATCTGCATGCATA
61372	59459	TTTAATATATCTGCATGCAT
61373	59460	TTTTAATATATCTGCATGCA
61374	59461	GTTTTAATATATCTGCATGC
61375	59462	AGTTTTAATATATCTGCATG
61376	59463	TAGTTTTAATATATCTGCAT
61377	59464	CTAGTTTTAATATATCTGCA
61378	59465	ACTAGTTTTAATATATCTGC
61379	59466	TACTAGTTTTAATATATCTG
61380	59467	TTACTAGTTTTAATATATCT
61381	59468	ATTACTAGTTTTAATATATC
61382	59469	TATTACTAGTTTTAATATAT
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61386	59473	GCTTTATTACTAGTTTTAAT
61387	59474	TGCTTTATTACTAGTTTTAA
61388	59475	TTGCTTTATTACTAGTTTTA
61389	59476	CTTGCTTTATTACTAGTTTT
61390	59477	TCTTGCTTTATTACTAGTTT
61391	59478	CTCTTGCTTTATTACTAGTT
61392	59479	TCTCTTGCTTTATTACTAGT
61393	59480	TTCTCTTGCTTTATTACTAG
61394	59481	CTTCTCTTGCTTTATTACTA
61395	59482	CCTTCTCTTGCTTTATTACT
61396	59483	TCCTTCTCTTGCTTTATTAC
61397	59484	TTCCTTCTCTTGCTTTATTA
61398	59485	ATTCCTTCTCTTGCTTTATT
61399	59486	CATTCCTTCTCTTGCTTTAT
61400	59487	ACATTCCTTCTCTTGCTTTA
61401	59488	CACATTCCTTCTCTTGCTTT
61402	59489	CCACATTCCTTCTCTTGCTT
61403	59490	TCCACATTCCTTCTCTTGCT
61404	59491	ATCCACATTCCTTCTCTTGC
61405	59492	TATCCACATTCCTTCTCTTG
61406	59493	TTATCCACATTCCTTCTCTT
61407	59494	TTTATCCACATTCCTTCTCT
61408	59495	ATTTATCCACATTCCTTCTC
61409	59496	AATTTATCCACATTCCTTCT
61410	59497	TAATTTATCCACATTCCTTC
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61412	59499	GATAATTTATCCACATTCCT
61413	59500	AGATAATTTATCCACATTCC
61414	59501	GAGATAATTTATCCACATTC
61415	59502	AGAGATAATTTATCCACATT
61416	59503	TAGAGATAATTTATCCACAT
61417	59504	TTAGAGATAATTTATCCACA
61418	59505	ATTAGAGATAATTTATCCAC
61419	59506	AATTAGAGATAATTTATCCA
61420	59507	AAATTAGAGATAATTTATCC
61421	59508	GAAATTAGAGATAATTTATC
61422	59509	AGAAATTAGAGATAATTTAT
61423	59510	TAGAAATTAGAGATAATTTA

110500	108587	ATGGAGAAACCTCATCTCTA
110501	108588	CATGGAGAAACCTCATCTCT
110502	108589	ACATGGAGAAACCTCATCTC
110503	108590	AACATGGAGAAACCTCATCT
110504	108591	CAACATGGAGAAACCTCATC
110505	108592	CCAACATGGAGAAACCTCAT
110506	108593	ACCAACATGGAGAAACCTCA
110507	108594	GACCAACATGGAGAAACCTC
110508	108595	TGACCAACATGGAGAAACCT
110509	108596	CTGACCAACATGGAGAAACC
110510	108597	CCTGACCAACATGGAGAAAC
110511	108598	GCCTGACCAACATGGAGAAA
110512	108599	AGCCTGACCAACATGGAGAA
110513	108600	CAGCCTGACCAACATGGAGA
110514	108601	CCAGCCTGACCAACATGGAG
110515	108602	ACCAGCCTGACCAACATGGA
110516	108603	GACCAGCCTGACCAACATGG
110517	108604	AGACCAGCCTGACCAACATG
110518	108605	AAGACCAGCCTGACCAACAT
110519	108606	CAAGACCAGCCTGACCAACA
110520	108607	TCAAGACCAGCCTGACCAAC
110521	108608	TTCAAGACCAGCCTGACCAA
110522	108609	GTTCAAGACCAGCCTGACCA
110523	108610	AGTTCAAGACCAGCCTGACC
110524	108611	GAGTTCAAGACCAGCCTGAC
110525	108612	GGAGTTCAAGACCAGCCTGA
110526	108613	GGGAGTTCAAGACCAGCCTG
110527	108614	CGGGAGTTCAAGACCAGCCT
110528	108615	TCGGGAGTTCAAGACCAGCC
110529	108616	GTCGGGAGTTCAAGACCAGC
110530	108617	GGTCGGGAGTTCAAGACCAG
110531	108618	AGGTCGGGAGTTCAAGACCA
110532	108619	GAGGTCGGGAGTTCAAGACC
110533	108620	TGAGGTCGGGAGTTCAAGAC
110534	108621	CTGAGGTCGGGAGTTCAAGA
110535	108622	CCTGAGGTCGGGAGTTCAAG
110536	108623	ACCTGAGGTCGGGAGTTCAA
110537	108624	AACCTGAGGTCGGGAGTTCA
110538	108625	TAACCTGAGGTCGGGAGTTC
110539	108626	ATAACCTGAGGTCGGGAGTT
110540	108627	GATAACCTGAGGTCGGGAGT
110541	108628	GGATAACCTGAGGTCGGGAG
110542	108629	CGGATAACCTGAGGTCGGGA
110543	108630	ACGGATAACCTGAGGTCGGG
110544	108631	GACGGATAACCTGAGGTCGG
110545	108632	GGACGGATAACCTGAGGTCG
110546	108633	CGGACGGATAACCTGAGGTC
110547	108634	GCGGACGGATAACCTGAGGT
110548	108635	GGCGGACGGATAACCTGAGG
110549	108636	AGGCGGACGGATAACCTGAG
110550	108637	GAGGCGGACGGATAACCTGA
110551	108638	CGAGGCGGACGGATAACCTG
110552	108639	CCGAGGCGGACGGATAACCT
110553	108640	GCCGAGGCGGACGGATAACC
110554	108641	GGCCGAGGCGGACGGATAAC
110555	108642	AGGCCGAGGCGGACGGATAA
110556	108643	GAGGCCGAGGCGGACGGATA
110557	108644	GGAGGCCGAGGCGGACGGAT
110558	108645	GGGAGGCCGAGGCGGACGGA
110559	108646	TGGGAGGCCGAGGCGGACGG
110560	108647	TTGGGAGGCCGAGGCGGACG
110561	108648	TTTGGGAGGCCGAGGCGGAC
110562	108649	CTTTGGGAGGCCGAGGCGGA
110563	108650	ACTTTGGGAGGCCGAGGCGG
110564	108651	CACTTTGGGAGGCCGAGGCG
110565	108652	GCACTTTGGGAGGCCGAGGC
110566	108653	AGCACTTTGGGAGGCCGAGG
110567	108654	CAGCACTTTGGGAGGCCGAG
110568	108655	CCAGCACTTTGGGAGGCCGA
110569	108656	CCCAGCACTTTGGGAGGCCG
110570	108657	TCCCAGCACTTTGGGAGGCC

12277	10364	GGTGACAGGGTAAGATCCTG
12278	10365	GGGTGACAGGGTAAGATCCT
12279	10366	TGGGTGACAGGGTAAGATCC
12280	10367	CTGGGTGACAGGGTAAGATC
12281	10368	CCTGGGTGACAGGGTAAGAT
12282	10369	GCCTGGGTGACAGGGTAAGA
12283	10370	AGCCTGGGTGACAGGGTAAG
12284	10371	CAGCCTGGGTGACAGGGTAA
12285	10372	CCAGCCTGGGTGACAGGGTA
12286	10373	TCCAGCCTGGGTGACAGGGT
12287	10374	TTCCAGCCTGGGTGACAGGG
12288	10375	ATTCCAGCCTGGGTGACAGG
12289	10376	CATTCCAGCCTGGGTGACAG
12290	10377	GCATTCCAGCCTGGGTGACA
12291	10378	TGCATTCCAGCCTGGGTGAC
12292	10379	CTGCATTCCAGCCTGGGTGA
12293	10380	ACTGCATTCCAGCCTGGGTG
12294	10381	CACTGCATTCCAGCCTGGGT
12295	10382	TCACTGCATTCCAGCCTGGG
12296	10383	ATCACTGCATTCCAGCCTGG
12297	10384	CATCACTGCATTCCAGCCTG
12298	10385	ACATCACTGCATTCCAGCCT
12299	10386	CACATCACTGCATTCCAGCC
12300	10387	TCACATCACTGCATTCCAGC
12301	10388	ATCACATCACTGCATTCCAG
12302	10389	GATCACATCACTGCATTCCA
12303	10390	AGATCACATCACTGCATTCC
12304	10391	GAGATCACATCACTGCATTC
12305	10392	CGAGATCACATCACTGCATT
12306	10393	CCGAGATCACATCACTGCAT
12307	10394	GCCGAGATCACATCACTGCA
12308	10395	AGCCGAGATCACATCACTGC
12309	10396	AAGCCGAGATCACATCACTG
12310	10397	TAAGCCGAGATCACATCACT
12311	10398	GTAAGCCGAGATCACATCAC
12312	10399	AGTAAGCCGAGATCACATCA
12313	10400	CAGTAAGCCGAGATCACATC
12314	10401	GCAGTAAGCCGAGATCACAT
12315	10402	TGCAGTAAGCCGAGATCACA
12316	10403	TTGCAGTAAGCCGAGATCAC
12317	10404	GTTGCAGTAAGCCGAGATCA
12318	10405	GGTTGCAGTAAGCCGAGATC
12319	10406	AGGTTGCAGTAAGCCGAGAT
12320	10407	GAGGTTGCAGTAAGCCGAGA
12321	10408	GGAGGTTGCAGTAAGCCGAG
12322	10409	CGGAGGTTGCAGTAAGCCGA
12323	10410	GCGGAGGTTGCAGTAAGCCG
12324	10411	GGCGGAGGTTGCAGTAAGCC
12325	10412	AGGCGGAGGTTGCAGTAAGC
12326	10413	GAGGCGGAGGTTGCAGTAAG
12327	10414	GGAGGCGGAGGTTGCAGTAA
12328	10415	AGGAGGCGGAGGTTGCAGTA
12329	10416	TAGGAGGCGGAGGTTGCAGT
12330	10417	CTAGGAGGCGGAGGTTGCAG
12331	10418	CCTAGGAGGCGGAGGTTGCA
12332	10419	ACCTAGGAGGCGGAGGTTGC
12333	10420	AACCTAGGAGGCGGAGGTTG
12334	10421	GAACCTAGGAGGCGGAGGTT
12335	10422	TGAACCTAGGAGGCGGAGGT
12336	10423	TTGAACCTAGGAGGCGGAGG
12337	10424	CTTGAACCTAGGAGGCGGAG
12338	10425	ACTTGAACCTAGGAGGCGGA
12339	10426	CACTTGAACCTAGGAGGCGG
12340	10427	TCACTTGAACCTAGGAGGCG
12341	10428	ATCACTTGAACCTAGGAGGC
12342	10429	AATCACTTGAACCTAGGAGG
12343	10430	CAATCACTTGAACCTAGGAG
12344	10431	ACAATCACTTGAACCTAGGA
12345	10432	GACAATCACTTGAACCTAGG
12346	10433	GGACAATCACTTGAACCTAG
12347	10434	AGGACAATCACTTGAACCTA

61424	59511	ATAGAAATTAGAGATAATTT
61425	59512	AATAGAAATTAGAGATAATT
61426	59513	AAATAGAAATTAGAGATAAT
61427	59514	AAAATAGAAATTAGAGATAA
61428	59515	CAAAATAGAAATTAGAGATA
61429	59516	ACAAAATAGAAATTAGAGAT
61430	59517	AACAAAATAGAAATTAGAGA
61431	59518	GAACAAAATAGAAATTAGAG
61432	59519	AGAACAAAATAGAAATTAGA
61433	59520	TAGAACAAAATAGAAATTAG
61434	59521	ATAGAACAAAATAGAAATTA
61435	59522	AATAGAACAAAATAGAAATT
61436	59523	AAATAGAACAAAATAGAAAT
61437	59524	GAAATAGAACAAAATAGAAA
61438	59525	AGAAATAGAACAAAATAGAA
61439	59526	TAGAAATAGAACAAAATAGA
61440	59527	ATAGAAATAGAACAAAATAG
61441	59528	AATAGAAATAGAACAAAATA
61442	59529	AAATAGAAATAGAACAAAAT
61443	59530	GAAATAGAAATAGAACAAAA
61444	59531	TGAAATAGAAATAGAACAAA
61445	59532	ATGAAATAGAAATAGAACAA
61446	59533	TATGAAATAGAAATAGAACA
61447	59534	GTATGAAATAGAAATAGAAC
61448	59535	AGTATGAAATAGAAATAGAA
61449	59536	GAGTATGAAATAGAAATAGA
61450	59537	GGAGTATGAAATAGAAATAG
61451	59538	AGGAGTATGAAATAGAAATA
61452	59539	CAGGAGTATGAAATAGAAAT
61453	59540	CCAGGAGTATGAAATAGAAA
61454	59541	CCCAGGAGTATGAAATAGAA
61455	59542	TCCCAGGAGTATGAAATAGA
61456	59543	TTCCCAGGAGTATGAAATAG
61457	59544	TTTCCCAGGAGTATGAAATA
61458	59545	CTTTCCCAGGAGTATGAAAT
61459	59546	TCTTTCCCAGGAGTATGAAA
61460	59547	TTCTTTCCCAGGAGTATGAA
61461	59548	ATTCTTTCCCAGGAGTATGA
61462	59549	TATTCTTTCCCAGGAGTATG
61463	59550	ATATTCTTTCCCAGGAGTAT
61464	59551	AATATTCTTTCCCAGGAGTA
61465	59552	TAATATTCTTTCCCAGGAGT
61466	59553	TTAATATTCTTTCCCAGGAG
61467	59554	CTTAATATTCTTTCCCAGGA
61468	59555	ACTTAATATTCTTTCCCAGG
61469	59556	CACTTAATATTCTTTCCCAG
61470	59557	CCACTTAATATTCTTTCCCA
61471	59558	CCCACTTAATATTCTTTCCC
61472	59559	GCCCACTTAATATTCTTTCC
61473	59560	TGCCCACTTAATATTCTTTC
61474	59561	ATGCCCACTTAATATTCTTT
61475	59562	CATGCCCACTTAATATTCTT
61476	59563	ACATGCCCACTTAATATTCT
61477	59564	CACATGCCCACTTAATATTC
61478	59565	ACACATGCCCACTTAATATT
61479	59566	TACACATGCCCACTTAATAT
61480	59567	GTACACATGCCCACTTAATA
61481	59568	AGTACACATGCCCACTTAAT
61482	59569	AAGTACACATGCCCACTTAA
61483	59570	CAAGTACACATGCCCACTTA
61484	59571	TCAAGTACACATGCCCACTT
61485	59572	TTCAAGTACACATGCCCACT
61486	59573	GTTCAAGTACACATGCCCAC
61487	59574	TGTTCAAGTACACATGCCCA
61488	59575	CTGTTCAAGTACACATGCCC
61489	59576	ACTGTTCAAGTACACATGCC
61490	59577	AACTGTTCAAGTACACATGC
61491	59578	CAACTGTTCAAGTACACATG
61492	59579	ACAACTGTTCAAGTACACAT
61493	59580	AACAACTGTTCAAGTACACA
61494	59581	GAACAACTGTTCAAGTACAC

110571	108658	ATCCCAGCACTTTGGGAGGC
110572	108659	AATCCCAGCACTTTGGGAGG
110573	108660	TAATCCCAGCACTTTGGGAG
110574	108661	GTAATCCCAGCACTTTGGGA
110575	108662	TGTAATCCCAGCACTTTGGG
110576	108663	CTGTAATCCCAGCACTTTGG
110577	108664	TCTGTAATCCCAGCACTTTG
110578	108665	GTCTGTAATCCCAGCACTTT
110579	108666	GGTCTGTAATCCCAGCACTT
110580	108667	TGGTCTGTAATCCCAGCACT
110581	108668	ATGGTCTGTAATCCCAGCAC
110582	108669	TATGGTCTGTAATCCCAGCA
110583	108670	CTATGGTCTGTAATCCCAGC
110584	108671	ACTATGGTCTGTAATCCCAG
110585	108672	CACTATGGTCTGTAATCCCA
110586	108673	GCACTATGGTCTGTAATCCC
110587	108674	GGCACTATGGTCTGTAATCC
110588	108675	GGGCACTATGGTCTGTAATC
110589	108676	TGGGCACTATGGTCTGTAAT
110590	108677	CTGGGCACTATGGTCTGTAA
110591	108678	GCTGGGCACTATGGTCTGTA
110592	108679	GGCTGGGCACTATGGTCTGT
110593	108680	GGGCTGGGCACTATGGTCTG
110594	108681	CGGGCTGGGCACTATGGTCT
110595	108682	TCGGGCTGGGCACTATGGTC
110596	108683	TTCGGGCTGGGCACTATGGT
110597	108684	TTTCGGGCTGGGCACTATGG
110598	108685	ATTTCGGGCTGGGCACTATG
110599	108686	AATTTCGGGCTGGGCACTAT
110600	108687	GAATTTCGGGCTGGGCACTA
110601	108688	TGAATTTCGGGCTGGGCACT
110602	108689	CTGAATTTCGGGCTGGGCAC
110603	108690	TCTGAATTTCGGGCTGGGCA
110604	108691	ATCTGAATTTCGGGCTGGGC
110605	108692	AATCTGAATTTCGGGCTGGG
110606	108693	GAATCTGAATTTCGGGCTGG
110607	108694	AGAATCTGAATTTCGGGCTG
110608	108695	TAGAATCTGAATTTCGGGCT
110609	108696	TTAGAATCTGAATTTCGGGC
110610	108697	ATTAGAATCTGAATTTCGGG
110611	108698	GATTAGAATCTGAATTTCGG
110612	108699	TGATTAGAATCTGAATTTCG
110613	108700	GTGATTAGAATCTGAATTTC
110614	108701	AGTGATTAGAATCTGAATTT
110615	108702	CAGTGATTAGAATCTGAATT
110616	108703	CCAGTGATTAGAATCTGAAT
110617	108704	CCCAGTGATTAGAATCTGAA
110618	108705	TCCCAGTGATTAGAATCTGA
110619	108706	ATCCCAGTGATTAGAATCTG
110620	108707	CATCCCAGTGATTAGAATCT
110621	108708	CCATCCCAGTGATTAGAATC
110622	108709	TCCATCCCAGTGATTAGAAT
110623	108710	GTCCATCCCAGTGATTAGAA
110624	108711	TGTCCATCCCAGTGATTAGA
110625	108712	TTGTCCATCCCAGTGATTAG
110626	108713	ATTGTCCATCCCAGTGATTA
110627	108714	AATTGTCCATCCCAGTGATT
110628	108715	GAATTGTCCATCCCAGTGAT
110629	108716	GGAATTGTCCATCCCAGTGA
110630	108717	GGGAATTGTCCATCCCAGTG
110631	108718	GGGGAATTGTCCATCCCAGT
110632	108719	AGGGGAATTGTCCATCCCAG
110633	108720	GAGGGGAATTGTCCATCCCA
110634	108721	AGAGGGGAATTGTCCATCCC
110635	108722	CAGAGGGGAATTGTCCATCC
110636	108723	TCAGAGGGGAATTGTCCATC
110637	108724	GTCAGAGGGGAATTGTCCAT
110638	108725	AGTCAGAGGGGAATTGTCCA
110639	108726	TAGTCAGAGGGGAATTGTCC
110640	108727	CTAGTCAGAGGGGAATTGTC
110641	108728	CCTAGTCAGAGGGGAATTGT

12348	10435	CAGGACAATCACTTGAACCT
12349	10436	GCAGGACAATCACTTGAACC
12350	10437	GGCAGGACAATCACTTGAAC
12351	10438	AGGCAGGACAATCACTTGAA
12352	10439	GAGGCAGGACAATCACTTGA
12353	10440	TGAGGCAGGACAATCACTTG
12354	10441	CTGAGGCAGGACAATCACTT
12355	10442	GCTGAGGCAGGACAATCACT
12356	10443	GGCTGAGGCAGGACAATCAC
12357	10444	AGGCTGAGGCAGGACAATCA
12358	10445	GAGGCTGAGGCAGGACAATC
12359	10446	GGAGGCTGAGGCAGGACAAT
12360	10447	AGGAGGCTGAGGCAGGACAA
12361	10448	CAGGAGGCTGAGGCAGGACA
12362	10449	TCAGGAGGCTGAGGCAGGAC
12363	10450	CTCAGGAGGCTGAGGCAGGA
12364	10451	ACTCAGGAGGCTGAGGCAGG
12365	10452	TACTCAGGAGGCTGAGGCAG
12366	10453	CTACTCAGGAGGCTGAGGCA
12367	10454	GCTACTCAGGAGGCTGAGGC
12368	10455	AGCTACTCAGGAGGCTGAGG
12369	10456	CAGCTACTCAGGAGGCTGAG
12370	10457	CCAGCTACTCAGGAGGCTGA
12371	10458	CCCAGCTACTCAGGAGGCTG
12372	10459	TCCCAGCTACTCAGGAGGCT
12373	10460	ATCCCAGCTACTCAGGAGGC
12374	10461	TATCCCAGCTACTCAGGAGG
12375	10462	TTATCCCAGCTACTCAGGAG
12376	10463	GTTATCCCAGCTACTCAGGA
12377	10464	TGTTATCCCAGCTACTCAGG
12378	10465	CTGTTATCCCAGCTACTCAG
12379	10466	GCTGTTATCCCAGCTACTCA
12380	10467	AGCTGTTATCCCAGCTACTC
12381	10468	CAGCTGTTATCCCAGCTACT
12382	10469	ACAGCTGTTATCCCAGCTAC
12383	10470	CACAGCTGTTATCCCAGCTA
12384	10471	ACACAGCTGTTATCCCAGCT
12385	10472	CACACAGCTGTTATCCCAGC
12386	10473	GCACACAGCTGTTATCCCAG
12387	10474	GGCACACAGCTGTTATCCCA
12388	10475	TGGCACACAGCTGTTATCCC
12389	10476	GTGGCACACAGCTGTTATCC
12390	10477	GGTGGCACACAGCTGTTATC
12391	10478	TGGTGGCACACAGCTGTTAT
12392	10479	ATGGTGGCACACAGCTGTTA
12393	10480	CATGGTGGCACACAGCTGTT
12394	10481	GCATGGTGGCACACAGCTGT
12395	10482	GGCATGGTGGCACACAGCTG
12396	10483	AGGCATGGTGGCACACAGCT
12397	10484	CAGGCATGGTGGCACACAGC
12398	10485	CCAGGCATGGTGGCACACAG
12399	10486	GCCAGGCATGGTGGCACACA
12400	10487	AGCCAGGCATGGTGGCACAC
12401	10488	TAGCCAGGCATGGTGGCACA
12402	10489	TTAGCCAGGCATGGTGGCAC
12403	10490	ATTAGCCAGGCATGGTGGCA
12404	10491	AATTAGCCAGGCATGGTGGC
12405	10492	AAATTAGCCAGGCATGGTGG
12406	10493	AAAATTAGCCAGGCATGGTG
12407	10494	AAAAATTAGCCAGGCATGGT
12408	10495	CAAAAATTAGCCAGGCATGG
12409	10496	ACAAAAATTAGCCAGGCATG
12410	10497	TACAAAAATTAGCCAGGCAT
12411	10498	ATACAAAAATTAGCCAGGCA
12412	10499	AATACAAAAATTAGCCAGGC
12413	10500	AAATACAAAAATTAGCCAGG
12414	10501	AAAATACAAAAATTAGCCAG
12415	10502	AAAAATACAAAAATTAGCCA
12416	10503	TAAAAATACAAAAATTAGCC
12417	10504	CTAAAAATACAAAAATTAGC
12418	10505	ACTAAAAATACAAAAATTAG

61495	59582	AGAACAACTGTTCAAGTACA
61496	59583	CAGAACAACTGTTCAAGTAC
61497	59584	ACAGAACAACTGTTCAAGTA
61498	59585	AACAGAACAACTGTTCAAGT
61499	59586	AAACAGAACAACTGTTCAAG
61500	59587	AAAACAGAACAACTGTTCAA
61501	59588	AAAAACAGAACAACTGTTCA
61502	59589	AAAAAACAGAACAACTGTTC
61503	59590	TAAAAAACAGAACAACTGTT
61504	59591	ATAAAAAACAGAACAACTGT
61505	59592	AATAAAAAACAGAACAACTG
61506	59593	TAATAAAAAACAGAACAACT
61507	59594	CTAATAAAAAACAGAACAAC
61508	59595	TCTAATAAAAAACAGAACAA
61509	59596	TTCTAATAAAAAACAGAACA
61510	59597	TTTCTAATAAAAAACAGAAC
61511	59598	TTTTCTAATAAAAAACAGAA
61512	59599	CTTTTCTAATAAAAAACAGA
61513	59600	TCTTTTCTAATAAAAAACAG
61514	59601	TTCTTTTCTAATAAAAAACA
61515	59602	ATTCTTTTCTAATAAAAAAC
61516	59603	GATTCTTTTCTAATAAAAAA
61517	59604	GGATTCTTTTCTAATAAAAA
61518	59605	CGGATTCTTTTCTAATAAAA
61519	59606	TCGGATTCTTTTCTAATAAA
61520	59607	TTCGGATTCTTTTCTAATAA
61521	59608	ATTCGGATTCTTTTCTAATA
61522	59609	GATTCGGATTCTTTTCTAAT
61523	59610	AGATTCGGATTCTTTTCTAA
61524	59611	TAGATTCGGATTCTTTTCTA
61525	59612	ATAGATTCGGATTCTTTTCT
61526	59613	TATAGATTCGGATTCTTTTC
61527	59614	TTATAGATTCGGATTCTTTT
61528	59615	TTTATAGATTCGGATTCTTT
61529	59616	TTTTATAGATTCGGATTCTT
61530	59617	ATTTTATAGATTCGGATTCT
61531	59618	CATTTTATAGATTCGGATTC
61532	59619	ACATTTTATAGATTCGGATT
61533	59620	AACATTTTATAGATTCGGAT
61534	59621	AAACATTTTATAGATTCGGA
61535	59622	AAAACATTTTATAGATTCGG
61536	59623	TAAAACATTTTATAGATTCG
61537	59624	GTAAAACATTTTATAGATTC
61538	59625	TGTAAAACATTTTATAGATT
61539	59626	ATGTAAAACATTTTATAGAT
61540	59627	TATGTAAAACATTTTATAGA
61541	59628	ATATGTAAAACATTTTATAG
61542	59629	AATATGTAAAACATTTTATA
61543	59630	AAATATGTAAAACATTTTAT
61544	59631	CAAATATGTAAAACATTTTA
61545	59632	GCAAATATGTAAAACATTTT
61546	59633	GGCAAATATGTAAAACATTT
61547	59634	TGGCAAATATGTAAAACATT
61548	59635	CTGGCAAATATGTAAAACAT
61549	59636	CCTGGCAAATATGTAAAACA
61550	59637	CCCTGGCAAATATGTAAAAC
61551	59638	TCCCTGGCAAATATGTAAAA
61552	59639	TTCCCTGGCAAATATGTAAA
61553	59640	TTTCCCTGGCAAATATGTAA
61554	59641	GTTTCCCTGGCAAATATGTA
61555	59642	TGTTTCCCTGGCAAATATGT
61556	59643	CTGTTTCCCTGGCAAATATG
61557	59644	TCTGTTTCCCTGGCAAATAT
61558	59645	TTCTGTTTCCCTGGCAAATA
61559	59646	TTTCTGTTTCCCTGGCAAAT
61560	59647	TTTTCTGTTTCCCTGGCAAA
61561	59648	CTTTTCTGTTTCCCTGGCAA
61562	59649	TCTTTTCTGTTTCCCTGGCA
61563	59650	ATCTTTTCTGTTTCCCTGGC
61564	59651	TATCTTTTCTGTTTCCCTGG
61565	59652	ATATCTTTTCTGTTTCCCTG

110642	108729	CCCTAGTCAGAGGGGAATTG
110643	108730	GCCCTAGTCAGAGGGGAATT
110644	108731	AGCCCTAGTCAGAGGGGAAT
110645	108732	TAGCCCTAGTCAGAGGGGAA
110646	108733	CTAGCCCTAGTCAGAGGGGA
110647	108734	ACTAGCCCTAGTCAGAGGGG
110648	108735	GACTAGCCCTAGTCAGAGGG
110649	108736	AGACTAGCCCTAGTCAGAGG
110650	108737	TAGACTAGCCCTAGTCAGAG
110651	108738	TTAGACTAGCCCTAGTCAGA
110652	108739	TTTAGACTAGCCCTAGTCAG
110653	108740	ATTTAGACTAGCCCTAGTCA
110654	108741	TATTTAGACTAGCCCTAGTC
110655	108742	GTATTTAGACTAGCCCTAGT
110656	108743	AGTATTTAGACTAGCCCTAG
110657	108744	GAGTATTTAGACTAGCCCTA
110658	108745	GGAGTATTTAGACTAGCCCT
110659	108746	GGGAGTATTTAGACTAGCCC
110660	108747	AGGGAGTATTTAGACTAGCC
110661	108748	GAGGGAGTATTTAGACTAGC
110662	108749	AGAGGGAGTATTTAGACTAG
110663	108750	CAGAGGGAGTATTTAGACTA
110664	108751	ACAGAGGGAGTATTTAGACT
110665	108752	CACAGAGGGAGTATTTAGAC
110666	108753	CCACAGAGGGAGTATTTAGA
110667	108754	CCCACAGAGGGAGTATTTAG
110668	108755	ACCCACAGAGGGAGTATTTA
110669	108756	CACCCACAGAGGGAGTATTT
110670	108757	GCACCCACAGAGGGAGTATT
110671	108758	AGCACCCACAGAGGGAGTAT
110672	108759	CAGCACCCACAGAGGGAGTA
110673	108760	CCAGCACCCACAGAGGGAGT
110674	108761	GCCAGCACCCACAGAGGGAG
110675	108762	AGCCAGCACCCACAGAGGGA
110676	108763	CAGCCAGCACCCACAGAGGG
110677	108764	TCAGCCAGCACCCACAGAGG
110678	108765	TTCAGCCAGCACCCACAGAG
110679	108766	ATTCAGCCAGCACCCACAGA
110680	108767	AATTCAGCCAGCACCCACAG
110681	108768	GAATTCAGCCAGCACCCACA
110682	108769	AGAATTCAGCCAGCACCCAC
110683	108770	CAGAATTCAGCCAGCACCCA
110684	108771	ACAGAATTCAGCCAGCACCC
110685	108772	GACAGAATTCAGCCAGCACC
110686	108773	GGACAGAATTCAGCCAGCAC
110687	108774	AGGACAGAATTCAGCCAGCA
110688	108775	TAGGACAGAATTCAGCCAGC
110689	108776	ATAGGACAGAATTCAGCCAG
110690	108777	CATAGGACAGAATTCAGCCA
110691	108778	GCATAGGACAGAATTCAGCC
110692	108779	AGCATAGGACAGAATTCAGC
110693	108780	CAGCATAGGACAGAATTCAG
110694	108781	GCAGCATAGGACAGAATTCA
110695	108782	AGCAGCATAGGACAGAATTC
110696	108783	AAGCAGCATAGGACAGAATT
110697	108784	AAAGCAGCATAGGACAGAAT
110698	108785	GAAAGCAGCATAGGACAGAA
110699	108786	GGAAAGCAGCATAGGACAGA
110700	108787	TGGAAAGCAGCATAGGACAG
110701	108788	GTGGAAAGCAGCATAGGACA
110702	108789	AGTGGAAAGCAGCATAGGAC
110703	108790	CAGTGGAAAGCAGCATAGGA
110704	108791	ACAGTGGAAAGCAGCATAGG
110705	108792	CACAGTGGAAAGCAGCATAG
110706	108793	TCACAGTGGAAAGCAGCATA
110707	108794	GTCACAGTGGAAAGCAGCAT
110708	108795	TGTCACAGTGGAAAGCAGCA
110709	108796	CTGTCACAGTGGAAAGCAGC
110710	108797	CCTGTCACAGTGGAAAGCAG
110711	108798	CCCTGTCACAGTGGAAAGCA
110712	108799	GCCCTGTCACAGTGGAAAGC

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12421	10508	TCTACTAAAAATACAAAAAT
12422	10509	CTCTACTAAAAATACAAAAA
12423	10510	TCTCTACTAAAAATACAAAA
12424	10511	ATCTCTACTAAAAATACAAA
12425	10512	CATCTCTACTAAAAATACAA
12426	10513	CCATCTCTACTAAAAATACA
12427	10514	CCCATCTCTACTAAAAATAC
12428	10515	CCCCATCTCTACTAAAAATA
12429	10516	ACCCCATCTCTACTAAAAAT
12430	10517	AACCCCATCTCTACTAAAAA
12431	10518	AAACCCCATCTCTACTAAAA
12432	10519	GAAACCCCATCTCTACTAAA
12433	10520	TGAAACCCCATCTCTACTAA
12434	10521	ATGAAACCCCATCTCTACTA
12435	10522	GATGAAACCCCATCTCTACT
12436	10523	TGATGAAACCCCATCTCTAC
12437	10524	ATGATGAAACCCCATCTCTA
12438	10525	CATGATGAAACCCCATCTCT
12439	10526	ACATGATGAAACCCCATCTC
12440	10527	AACATGATGAAACCCCATCT
12441	10528	CAACATGATGAAACCCCATC
12442	10529	CCAACATGATGAAACCCCAT
12443	10530	GCCAACATGATGAAACCCCA
12444	10531	GGCCAACATGATGAAACCCC
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12446	10533	CTGGCCAACATGATGAAACC
12447	10534	CCTGGCCAACATGATGAAAC
12448	10535	GCCTGGCCAACATGATGAAA
12449	10536	AGCCTGGCCAACATGATGAA
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12451	10538	CCAGCCTGGCCAACATGATG
12452	10539	ACCAGCCTGGCCAACATGAT
12453	10540	GACCAGCCTGGCCAACATGA
12454	10541	AGACCAGCCTGGCCAACATG
12455	10542	GAGACCAGCCTGGCCAACAT
12456	10543	CGAGACCAGCCTGGCCAACA
12457	10544	TCGAGACCAGCCTGGCCAAC
12458	10545	TTCGAGACCAGCCTGGCCAA
12459	10546	GTTCGAGACCAGCCTGGCCA
12460	10547	AGTTCGAGACCAGCCTGGCC
12461	10548	GAGTTCGAGACCAGCCTGGC
12462	10549	GGAGTTCGAGACCAGCCTGG
12463	10550	AGGAGTTCGAGACCAGCCTG
12464	10551	CAGGAGTTCGAGACCAGCCT
12465	10552	TCAGGAGTTCGAGACCAGCC
12466	10553	GTCAGGAGTTCGAGACCAGC
12467	10554	GGTCAGGAGTTCGAGACCAG
12468	10555	AGGTCAGGAGTTCGAGACCA
12469	10556	AAGGTCAGGAGTTCGAGACC
12470	10557	TAAGGTCAGGAGTTCGAGAC
12471	10558	CTAAGGTCAGGAGTTCGAGA
12472	10559	TCTAAGGTCAGGAGTTCGAG
12473	10560	ATCTAAGGTCAGGAGTTCGA
12474	10561	CATCTAAGGTCAGGAGTTCG
12475	10562	TCATCTAAGGTCAGGAGTTC
12476	10563	ATCATCTAAGGTCAGGAGTT
12477	10564	GATCATCTAAGGTCAGGAGT
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12479	10566	TGGATCATCTAAGGTCAGGA
12480	10567	GTGGATCATCTAAGGTCAGG
12481	10568	GGTGGATCATCTAAGGTCAG
12482	10569	GGGTGGATCATCTAAGGTCA
12483	10570	CGGGTGGATCATCTAAGGTC
12484	10571	GCGGGTGGATCATCTAAGGT
12485	10572	GGCGGGTGGATCATCTAAGG
12486	10573	AGGCGGGTGGATCATCTAAG
12487	10574	GAGGCGGGTGGATCATCTAA
12488	10575	CGAGGCGGGTGGATCATCTA
12489	10576	ACGAGGCGGGTGGATCATCT

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61568	59655	CAAATATCTTTTCTGTTTCC
61569	59656	ACAAATATCTTTTCTGTTTC
61570	59657	TACAAATATCTTTTCTGTTT
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61572	59659	TGTACAAATATCTTTTCTGT
61573	59660	CTGTACAAATATCTTTTCTG
61574	59661	GCTGTACAAATATCTTTTCT
61575	59662	AGCTGTACAAATATCTTTTC
61576	59663	CAGCTGTACAAATATCTTTT
61577	59664	ACAGCTGTACAAATATCTTT
61578	59665	TACAGCTGTACAAATATCTT
61579	59666	TTACAGCTGTACAAATATCT
61580	59667	CTTACAGCTGTACAAATATC
61581	59668	TCTTACAGCTGTACAAATAT
61582	59669	TTCTTACAGCTGTACAAATA
61583	59670	ATTCTTACAGCTGTACAAAT
61584	59671	AATTCTTACAGCTGTACAAA
61585	59672	CAATTCTTACAGCTGTACAA
61586	59673	CCAATTCTTACAGCTGTACA
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61588	59675	TTCCAATTCTTACAGCTGTA
61589	59676	ATTCCAATTCTTACAGCTGT
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61598	59685	ATGAAATTAATTCCAATTCT
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61603	59690	GTAAAATGAAATTAATTCCA
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61605	59692	CAGTAAAATGAAATTAATTC
61606	59693	TCAGTAAAATGAAATTAATT
61607	59694	GTCAGTAAAATGAAATTAAT
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61609	59696	AAGTCAGTAAAATGAAATTA
61610	59697	AAAGTCAGTAAAATGAAATT
61611	59698	AAAAGTCAGTAAAATGAAAT
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61613	59700	GGAAAAGTCAGTAAAATGAA
61614	59701	AGGAAAAGTCAGTAAAATGA
61615	59702	AAGGAAAAGTCAGTAAAATG
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61618	59705	GTTAAGGAAAAGTCAGTAAA
61619	59706	GGTTAAGGAAAAGTCAGTAA
61620	59707	AGGTTAAGGAAAAGTCAGTA
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61623	59710	ATTAGGTTAAGGAAAAGTCA
61624	59711	AATTAGGTTAAGGAAAAGTC
61625	59712	GAATTAGGTTAAGGAAAAGT
61626	59713	AGAATTAGGTTAAGGAAAAG
61627	59714	CAGAATTAGGTTAAGGAAAA
61628	59715	TCAGAATTAGGTTAAGGAAA
61629	59716	TTCAGAATTAGGTTAAGGAA
61630	59717	GTTCAGAATTAGGTTAAGGA
61631	59718	TGTTCAGAATTAGGTTAAGG
61632	59719	GTGTTCAGAATTAGGTTAAG
61633	59720	AGTGTTCAGAATTAGGTTAA
61634	59721	AAGTGTTCAGAATTAGGTTA
61635	59722	AAAGTGTTCAGAATTAGGTT
61636	59723	AAAAGTGTTCAGAATTAGGT

110713	108800	TGCCCTGTCACAGTGGAAAG
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110718	108805	AGTGCTGCCCTGTCACAGTG
110719	108806	CAGTGCTGCCCTGTCACAGT
110720	108807	TCAGTGCTGCCCTGTCACAG
110721	108808	CTCAGTGCTGCCCTGTCACA
110722	108809	ACTCAGTGCTGCCCTGTCAC
110723	108810	AACTCAGTGCTGCCCTGTCA
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110730	108817	GCATTGAAACTCAGTGCTGC
110731	108818	TGCATTGAAACTCAGTGCTG
110732	108819	TTGCATTGAAACTCAGTGCT
110733	108820	TTTGCATTGAAACTCAGTGC
110734	108821	TTTTGCATTGAAACTCAGTG
110735	108822	ATTTTGCATTGAAACTCAGT
110736	108823	GATTTTGCATTGAAACTCAG
110737	108824	GGATTTTGCATTGAAACTCA
110738	108825	GGGATTTTGCATTGAAACTC
110739	108826	TGGGATTTTGCATTGAAACT
110740	108827	GTGGGATTTTGCATTGAAAC
110741	108828	TGTGGGATTTTGCATTGAAA
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110743	108830	ACTGTGGGATTTTGCATTGA
110744	108831	GACTGTGGGATTTTGCATTG
110745	108832	TGACTGTGGGATTTTGCATT
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110747	108834	AATGACTGTGGGATTTTGCA
110748	108835	AAATGACTGTGGGATTTTGC
110749	108836	GAAATGACTGTGGGATTTTG
110750	108837	AGAAATGACTGTGGGATTTT
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110752	108839	AGAGAAATGACTGTGGGATT
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110754	108841	AGAGAGAAATGACTGTGGGA
110755	108842	GAGAGAGAAATGACTGTGGG
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110759	108846	GAGAGAGAGAGAAATGACTG
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110761	108848	GGGAGAGAGAGAGAAATGAC
110762	108849	GGGGAGAGAGAGAGAAATGA
110763	108850	GGGGGAGAGAGAGAGAAATG
110764	108851	CGGGGGAGAGAGAGAGAAAT
110765	108852	TCGGGGGAGAGAGAGAGAAA
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110767	108854	GCTCGGGGGAGAGAGAGAGA
110768	108855	TGCTCGGGGGAGAGAGAGAG
110769	108856	GTGCTCGGGGGAGAGAGAGA
110770	108857	TGTGCTCGGGGGAGAGAGAG
110771	108858	GTGTGCTCGGGGGAGAGAGA
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110773	108860	CTGTGTGCTCGGGGGAGAGA
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110780	108867	AAAGAATCTGTGTGCTCGGG
110781	108868	GAAAGAATCTGTGTGCTCGG
110782	108869	AGAAAGAATCTGTGTGCTCG
110783	108870	GAGAAAGAATCTGTGTGCTC

12490	10577	GACGAGGCGGGTGGATCATC
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12492	10579	AGGACGAGGCGGGTGGATCA
12493	10580	GAGGACGAGGCGGGTGGATC
12494	10581	GGAGGACGAGGCGGGTGGAT
12495	10582	GGGAGGACGAGGCGGGTGGA
12496	10583	TGGGAGGACGAGGCGGGTGG
12497	10584	TTGGGAGGACGAGGCGGGTG
12498	10585	TTTGGGAGGACGAGGCGGGT
12499	10586	CTTTGGGAGGACGAGGCGGG
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12510	10597	TAATCCCAGCACTTTGGGAG
12511	10598	GTAATCCCAGCACTTTGGGA
12512	10599	TGTAATCCCAGCACTTTGGG
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12514	10601	CCTGTAATCCCAGCACTTTG
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12516	10603	CACCTGTAATCCCAGCACTT
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61645	59732	ACCTATGGCAAAAGTGTTCA
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61682	59769	GAAGAATAGTAGTCATTTTA
61683	59770	TGAAGAATAGTAGTCATTTT
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61688	59775	ATTAGTGAAGAATAGTAGTC
61689	59776	TATTAGTGAAGAATAGTAGT
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61692	59779	TACTATTAGTGAAGAATAGT
61693	59780	ATACTATTAGTGAAGAATAG
61694	59781	AATACTATTAGTGAAGAATA
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61696	59783	CCAATACTATTAGTGAAGAA
61697	59784	GCCAATACTATTAGTGAAGA
61698	59785	TGCCAATACTATTAGTGAAG
61699	59786	ATGCCAATACTATTAGTGAA
61700	59787	AATGCCAATACTATTAGTGA
61701	59788	AAATGCCAATACTATTAGTG
61702	59789	GAAATGCCAATACTATTAGT
61703	59790	TGAAATGCCAATACTATTAG
61704	59791	TTGAAATGCCAATACTATTA
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110784	108871	GGAGAAAGAATCTGTGTGCT
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110794	108881	AGTGTGGGGTGGAGAAAGAA
110795	108882	CAGTGTGGGGTGGAGAAAGA
110796	108883	GCAGTGTGGGGTGGAGAAAG
110797	108884	TGCAGTGTGGGGTGGAGAAA
110798	108885	ATGCAGTGTGGGGTGGAGAA
110799	108886	AATGCAGTGTGGGGTGGAGA
110800	108887	CAATGCAGTGTGGGGTGGAG
110801	108888	ACAATGCAGTGTGGGGTGGA
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110814	108901	CTGACATTCCCCCACAATGC
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110816	108903	CCCTGACATTCCCCCACAAT
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110821	108908	AACACCCCTGACATTCCCCC
110822	108909	CAACACCCCTGACATTCCCC
110823	108910	CCAACACCCCTGACATTCCC
110824	108911	TCCAACACCCCTGACATTCC
110825	108912	CTCCAACACCCCTGACATTC
110826	108913	CCTCCAACACCCCTGACATT
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110829	108916	GCCCCTCCAACACCCCTGAC
110830	108917	TGCCCCTCCAACACCCCTGA
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110832	108919	ACTGCCCCTCCAACACCCCT
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110835	108922	TGAACTGCCCCTCCAACACC
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110837	108924	CTTGAACTGCCCCTCCAACA
110838	108925	TCTTGAACTGCCCCTCCAAC
110839	108926	GTCTTGAACTGCCCCTCCAA
110840	108927	AGTCTTGAACTGCCCCTCCA
110841	108928	TAGTCTTGAACTGCCCCTCC
110842	108929	ATAGTCTTGAACTGCCCCTC
110843	108930	GATAGTCTTGAACTGCCCCT
110844	108931	AGATAGTCTTGAACTGCCCC
110845	108932	AAGATAGTCTTGAACTGCCC
110846	108933	GAAGATAGTCTTGAACTGCC
110847	108934	GGAAGATAGTCTTGAACTGC
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110850	108937	TAAGGAAGATAGTCTTGAAC
110851	108938	ATAAGGAAGATAGTCTTGAA
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12561	10648	AAAAAAAAAAAAAAAAACT
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12564	10651	AAAAAAAAAAAAAAAAAAA
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12581	10668	TTCTCAAAAAAAAAAAAAA
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12587	10674	CGAGATTTCTCAAAAAAAA
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12595	10682	CGACAGAGCGAGATTTCTCA
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12613	10700	ACCGCACTCTAGCCTGGGCG
12614	10701	CACCGCACTCTAGCCTGGGC
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12616	10703	GTCACCGCACTCTAGCCTGG
12617	10704	TGTCACCGCACTCTAGCCTG
12618	10705	GTGTCACCGCACTCTAGCCT
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12622	10709	GATTGTGTCACCGCACTCTA
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12624	10711	GAGATTGTGTCACCGCACTC
12625	10712	TGAGATTGTGTCACCGCACT
12626	10713	CTGAGATTGTGTCACCGCAC
12627	10714	GCTGAGATTGTGTCACCGCA
12628	10715	AGCTGAGATTGTGTCACCGC
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12630	10717	TGAGCTGAGATTGTGTCACC
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61710	59797	TAGGAATTGAAATGCCAATA
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61712	59799	TTTAGGAATTGAAATGCCAA
61713	59800	ATTTAGGAATTGAAATGCCA
61714	59801	AATTTAGGAATTGAAATGCC
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61839	59926	ACAGAGCAAGACTCTGTCTC
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110939	109026	GAAAGCACCTTCATAAGAAC
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110943	109030	ACAAGAAAGCACCTTCATAA
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12768	10855	GCTAACACAGTGAAACCCCA
12769	10856	GGCTAACACAGTGAAACCCC
12770	10857	TGGCTAACACAGTGAAACCC
12771	10858	CTGGCTAACACAGTGAAACC
12772	10859	CCTGGCTAACACAGTGAAAC
12773	10860	TCCTGGCTAACACAGTGAAA

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61851	59938	CCAGCCTGGGCAACAGAGCA
61852	59939	TCCAGCCTGGGCAACAGAGC
61853	59940	CTCCAGCCTGGGCAACAGAG
61854	59941	ACTCCAGCCTGGGCAACAGA
61855	59942	CACTCCAGCCTGGGCAACAG
61856	59943	GCACTCCAGCCTGGGCAACA
61857	59944	TGCACTCCAGCCTGGGCAAC
61858	59945	CTGCACTCCAGCCTGGGCAA
61859	59946	ACTGCACTCCAGCCTGGGCA
61860	59947	TACTGCACTCCAGCCTGGGC
61861	59948	CTACTGCACTCCAGCCTGGG
61862	59949	GCTACTGCACTCCAGCCTGG
61863	59950	CGCTACTGCACTCCAGCCTG
61864	59951	GCGCTACTGCACTCCAGCCT
61865	59952	CGCGCTACTGCACTCCAGCC
61866	59953	TCGCGCTACTGCACTCCAGC
61867	59954	ATCGCGCTACTGCACTCCAG
61868	59955	GATCGCGCTACTGCACTCCA
61869	59956	AGATCGCGCTACTGCACTCC
61870	59957	GAGATCGCGCTACTGCACTC
61871	59958	CGAGATCGCGCTACTGCACT
61872	59959	CCGAGATCGCGCTACTGCAC
61873	59960	GCCGAGATCGCGCTACTGCA
61874	59961	AGCCGAGATCGCGCTACTGC
61875	59962	GAGCCGAGATCGCGCTACTG
61876	59963	TGAGCCGAGATCGCGCTACT
61877	59964	GTGAGCCGAGATCGCGCTAC
61878	59965	AGTGAGCCGAGATCGCGCTA
61879	59966	CAGTGAGCCGAGATCGCGCT
61880	59967	GCAGTGAGCCGAGATCGCGC
61881	59968	TGCAGTGAGCCGAGATCGCG
61882	59969	TTGCAGTGAGCCGAGATCGC
61883	59970	CTTGCAGTGAGCCGAGATCG
61884	59971	GCTTGCAGTGAGCCGAGATC
61885	59972	AGCTTGCAGTGAGCCGAGAT
61886	59973	GAGCTTGCAGTGAGCCGAGA
61887	59974	GGAGCTTGCAGTGAGCCGAG
61888	59975	CGGAGCTTGCAGTGAGCCGA
61889	59976	GCGGAGCTTGCAGTGAGCCG
61890	59977	GGCGGAGCTTGCAGTGAGCC
61891	59978	AGGCGGAGCTTGCAGTGAGC
61892	59979	GAGGCGGAGCTTGCAGTGAG
61893	59980	GGAGGCGGAGCTTGCAGTGA
61894	59981	GGGAGGCGGAGCTTGCAGTG
61895	59982	CGGGAGGCGGAGCTTGCAGT
61896	59983	CCGGGAGGCGGAGCTTGCAG
61897	59984	CCCGGGAGGCGGAGCTTGCA
61898	59985	ACCCGGGAGGCGGAGCTTGC
61899	59986	AACCCGGGAGGCGGAGCTTG
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61901	59988	TGAACCCGGGAGGCGGAGCT
61902	59989	ATGAACCCGGGAGGCGGAGC
61903	59990	CATGAACCCGGGAGGCGGAG
61904	59991	GCATGAACCCGGGAGGCGGA
61905	59992	GGCATGAACCCGGGAGGCGG
61906	59993	TGGCATGAACCCGGGAGGCG
61907	59994	ATGGCATGAACCCGGGAGGC
61908	59995	AATGGCATGAACCCGGGAGG
61909	59996	AAATGGCATGAACCCGGGAG
61910	59997	AAAATGGCATGAACCCGGGA
61911	59998	GAAAATGGCATGAACCCGGG
61912	59999	AGAAAATGGCATGAACCCGG
61913	60000	GAGAAAATGGCATGAACCCG
61914	60001	GGAGAAAATGGCATGAACCC
61915	60002	AGGAGAAAATGGCATGAACC
61916	60003	CAGGAGAAAATGGCATGAAC
61917	60004	GCAGGAGAAAATGGCATGAA
61918	60005	GGCAGGAGAAAATGGCATGA
61919	60006	AGGCAGGAGAAAATGGCATG
61920	60007	GAGGCAGGAGAAAATGGCAT

110997	109084	GAACCTTCCAGTGATCATCC
110998	109085	AGAACCTTCCAGTGATCATC
110999	109086	CAGAACCTTCCAGTGATCAT
111000	109087	ACAGAACCTTCCAGTGATCA
111001	109088	AACAGAACCTTCCAGTGATC
111002	109089	AAACAGAACCTTCCAGTGAT
111003	109090	CAAACAGAACCTTCCAGTGA
111004	109091	CCAAACAGAACCTTCCAGTG
111005	109092	GCCAAACAGAACCTTCCAGT
111006	109093	GGCCAAACAGAACCTTCCAG
111007	109094	TGGCCAAACAGAACCTTCCA
111008	109095	GTGGCCAAACAGAACCTTCC
111009	109096	GGTGGCCAAACAGAACCTTC
111010	109097	TGGTGGCCAAACAGAACCTT
111011	109098	ATGGTGGCCAAACAGAACCT
111012	109099	CATGGTGGCCAAACAGAACC
111013	109100	GCATGGTGGCCAAACAGAAC
111014	109101	AGCATGGTGGCCAAACAGAA
111015	109102	GAGCATGGTGGCCAAACAGA
111016	109103	AGAGCATGGTGGCCAAACAG
111017	109104	CAGAGCATGGTGGCCAAACA
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111019	109106	GACAGAGCATGGTGGCCAAA
111020	109107	AGACAGAGCATGGTGGCCAA
111021	109108	GAGACAGAGCATGGTGGCCA
111022	109109	AGAGACAGAGCATGGTGGCC
111023	109110	AAGAGACAGAGCATGGTGGC
111024	109111	GAAGAGACAGAGCATGGTGG
111025	109112	AGAAGAGACAGAGCATGGTG
111026	109113	GAGAAGAGACAGAGCATGGT
111027	109114	GGAGAAGAGACAGAGCATGG
111028	109115	GGGAGAAGAGACAGAGCATG
111029	109116	GGGGAGAAGAGACAGAGCAT
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111031	109118	CAGGGGAGAAGAGACAGAGC
111032	109119	GCAGGGGAGAAGAGACAGAG
111033	109120	GGCAGGGGAGAAGAGACAGA
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111035	109122	ATGGCAGGGGAGAAGAGACA
111036	109123	GATGGCAGGGGAGAAGAGAC
111037	109124	AGATGGCAGGGGAGAAGAGA
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111039	109126	GGAGATGGCAGGGGAGAAGA
111040	109127	AGGAGATGGCAGGGGAGAAG
111041	109128	AAGGAGATGGCAGGGGAGAA
111042	109129	AAAGGAGATGGCAGGGGAGA
111043	109130	AAAAGGAGATGGCAGGGGAG
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111045	109132	AAAAAAGGAGATGGCAGGGG
111046	109133	AAAAAAAGGAGATGGCAGGG
111047	109134	TAAAAAAAGGAGATGGCAGG
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111049	109136	AGTAAAAAAAGGAGATGGCA
111050	109137	AAGTAAAAAAAGGAGATGGC
111051	109138	TAAGTAAAAAAAGGAGATGG
111052	109139	CTAAGTAAAAAAAGGAGATG
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111055	109142	CCCCTAAGTAAAAAAAGGAG
111056	109143	ACCCCTAAGTAAAAAAAGGA
111057	109144	AACCCCTAAGTAAAAAAAGG
111058	109145	AAACCCCTAAGTAAAAAAAG
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111063	109150	ATTCTAAACCCCTAAGTAAA
111064	109151	CATTCTAAACCCCTAAGTAA
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111066	109153	GACATTCTAAACCCCTAAGT
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12774	10861	ATCCTGGCTAACACAGTGAA
12775	10862	AATCCTGGCTAACACAGTGA
12776	10863	CAATCCTGGCTAACACAGTG
12777	10864	ACAATCCTGGCTAACACAGT
12778	10865	GACAATCCTGGCTAACACAG
12779	10866	AGACAATCCTGGCTAACACA
12780	10867	GAGACAATCCTGGCTAACAC
12781	10868	TGAGACAATCCTGGCTAACA
12782	10869	TTGAGACAATCCTGGCTAAC
12783	10870	ATTGAGACAATCCTGGCTAA
12784	10871	GATTGAGACAATCCTGGCTA
12785	10872	AGATTGAGACAATCCTGGCT
12786	10873	GAGATTGAGACAATCCTGGC
12787	10874	GGAGATTGAGACAATCCTGG
12788	10875	GGGAGATTGAGACAATCCTG
12789	10876	CGGGAGATTGAGACAATCCT
12790	10877	TCGGGAGATTGAGACAATCC
12791	10878	GTCGGGAGATTGAGACAATC
12792	10879	GGTCGGGAGATTGAGACAAT
12793	10880	AGGTCGGGAGATTGAGACAA
12794	10881	GAGGTCGGGAGATTGAGACA
12795	10882	AGAGGTCGGGAGATTGAGAC
12796	10883	AAGAGGTCGGGAGATTGAGA
12797	10884	CAAGAGGTCGGGAGATTGAG
12798	10885	TCAAGAGGTCGGGAGATTGA
12799	10886	ATCAAGAGGTCGGGAGATTG
12800	10887	GATCAAGAGGTCGGGAGATT
12801	10888	AGATCAAGAGGTCGGGAGAT
12802	10889	CAGATCAAGAGGTCGGGAGA
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12805	10892	GGGCAGATCAAGAGGTCGGG
12806	10893	CGGGCAGATCAAGAGGTCGG
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12811	10898	CGAGGCGGGCAGATCAAGAG
12812	10899	CCGAGGCGGGCAGATCAAGA
12813	10900	GCCGAGGCGGGCAGATCAAG
12814	10901	AGCCGAGGCGGGCAGATCAA
12815	10902	AAGCCGAGGCGGGCAGATCA
12816	10903	GAAGCCGAGGCGGGCAGATC
12817	10904	GGAAGCCGAGGCGGGCAGAT
12818	10905	GGGAAGCCGAGGCGGGCAGA
12819	10906	TGGGAAGCCGAGGCGGGCAG
12820	10907	TTGGGAAGCCGAGGCGGGCA
12821	10908	TTTGGGAAGCCGAGGCGGGC
12822	10909	CTTTGGGAAGCCGAGGCGGG
12823	10910	ACTTTGGGAAGCCGAGGCGG
12824	10911	CACTTTGGGAAGCCGAGGCG
12825	10912	GCACTTTGGGAAGCCGAGGC
12826	10913	AGCACTTTGGGAAGCCGAGG
12827	10914	CAGCACTTTGGGAAGCCGAG
12828	10915	CCAGCACTTTGGGAAGCCGA
12829	10916	CCCAGCACTTTGGGAAGCCG
12830	10917	TCCCAGCACTTTGGGAAGCC
12831	10918	ATCCCAGCACTTTGGGAAGC
12832	10919	AATCCCAGCACTTTGGGAAG
12833	10920	TAATCCCAGCACTTTGGGAA
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12835	10922	TATAATCCCAGCACTTTGGG
12836	10923	CTATAATCCCAGCACTTTGG
12837	10924	CCTATAATCCCAGCACTTTG
12838	10925	GCCTATAATCCCAGCACTTT
12839	10926	TGCCTATAATCCCAGCACTT
12840	10927	ATGCCTATAATCCCAGCACT
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12842	10929	TCATGCCTATAATCCCAGCA
12843	10930	CTCATGCCTATAATCCCAGC
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61921	60008	TGAGGCAGGAGAAAATGGCA
61922	60009	CTGAGGCAGGAGAAAATGGC
61923	60010	GCTGAGGCAGGAGAAAATGG
61924	60011	GGCTGAGGCAGGAGAAAATG
61925	60012	AGGCTGAGGCAGGAGAAAAT
61926	60013	GAGGCTGAGGCAGGAGAAAA
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61928	60015	GGGAGGCTGAGGCAGGAGAA
61929	60016	CGGGAGGCTGAGGCAGGAGA
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61931	60018	CCCGGGAGGCTGAGGCAGGA
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61940	60027	TCCCAGCTACCCGGGAGGCT
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61943	60030	TAGTCCCAGCTACCCGGGAG
61944	60031	CTAGTCCCAGCTACCCGGGA
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61946	60033	CTCTAGTCCCAGCTACCCGG
61947	60034	CCTCTAGTCCCAGCTACCCG
61948	60035	ACCTCTAGTCCCAGCTACCC
61949	60036	TACCTCTAGTCCCAGCTACC
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111069	109156	TTAGACATTCTAAACCCCTA
111070	109157	GTTAGACATTCTAAACCCCT
111071	109158	AGTTAGACATTCTAAACCCC
111072	109159	CAGTTAGACATTCTAAACCC
111073	109160	TCAGTTAGACATTCTAAACC
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111075	109162	GGTCAGTTAGACATTCTAAA
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111088	109175	GACTGTACATATTGGTCAGT
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111102	109189	TCAGAATGAGACCTGACTGT
111103	109190	TTCAGAATGAGACCTGACTG
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111105	109192	AATTCAGAATGAGACCTGAC
111106	109193	GAATTCAGAATGAGACCTGA
111107	109194	TGAATTCAGAATGAGACCTG
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12845	10932	GGCTCATGCCTATAATCCCA
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12847	10934	GTGGCTCATGCCTATAATCC
12848	10935	GGTGGCTCATGCCTATAATC
12849	10936	CGGTGGCTCATGCCTATAAT
12850	10937	GCGGTGGCTCATGCCTATAA
12851	10938	CGCGGTGGCTCATGCCTATA
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12899	10986	TTTCATAAACAACCCAGACT
12900	10987	TTTTCATAAACAACCCAGAC
12901	10988	GTTTTCATAAACAACCCAGA
12902	10989	AGTTTTCATAAACAACCCAG
12903	10990	AAGTTTTCATAAACAACCCA
12904	10991	CAAGTTTTCATAAACAACCC
12905	10992	ACAAGTTTTCATAAACAACC
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12907	10994	TGACAAGTTTTCATAAACAA
12908	10995	GTGACAAGTTTTCATAAACA
12909	10996	TGTGACAAGTTTTCATAAAC
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62019	60106	CACCTTGGCTAACACGGTGA
62020	60107	CCACCTTGGCTAACACGGTG
62021	60108	ACCACCTTGGCTAACACGGT
62022	60109	GACCACCTTGGCTAACACGG
62023	60110	AGACCACCTTGGCTAACACG
62024	60111	GAGACCACCTTGGCTAACAC
62025	60112	TGAGACCACCTTGGCTAACA
62026	60113	TTGAGACCACCTTGGCTAAC
62027	60114	ATTGAGACCACCTTGGCTAA
62028	60115	GATTGAGACCACCTTGGCTA
62029	60116	AGATTGAGACCACCTTGGCT
62030	60117	GAGATTGAGACCACCTTGGC
62031	60118	GGAGATTGAGACCACCTTGG
62032	60119	AGGAGATTGAGACCACCTTG
62033	60120	CAGGAGATTGAGACCACCTT
62034	60121	TCAGGAGATTGAGACCACCT
62035	60122	GTCAGGAGATTGAGACCACC
62036	60123	GGTCAGGAGATTGAGACCAC
62037	60124	AGGTCAGGAGATTGAGACCA
62038	60125	GAGGTCAGGAGATTGAGACC
62039	60126	CGAGGTCAGGAGATTGAGAC
62040	60127	ACGAGGTCAGGAGATTGAGA
62041	60128	CACGAGGTCAGGAGATTGAG
62042	60129	TCACGAGGTCAGGAGATTGA
62043	60130	ATCACGAGGTCAGGAGATTG
62044	60131	GATCACGAGGTCAGGAGATT
62045	60132	GGATCACGAGGTCAGGAGAT
62046	60133	TGGATCACGAGGTCAGGAGA
62047	60134	ATGGATCACGAGGTCAGGAG
62048	60135	GATGGATCACGAGGTCAGGA
62049	60136	GGATGGATCACGAGGTCAGG
62050	60137	CGGATGGATCACGAGGTCAG
62051	60138	GCGGATGGATCACGAGGTCA
62052	60139	GGCGGATGGATCACGAGGTC
62053	60140	AGGCGGATGGATCACGAGGT
62054	60141	GAGGCGGATGGATCACGAGG
62055	60142	CGAGGCGGATGGATCACGAG
62056	60143	CCGAGGCGGATGGATCACGA
62057	60144	GCCGAGGCGGATGGATCACG
62058	60145	GGCCGAGGCGGATGGATCAC
62059	60146	AGGCCGAGGCGGATGGATCA
62060	60147	GAGGCCGAGGCGGATGGATC
62061	60148	GGAGGCCGAGGCGGATGGAT
62062	60149	GGGAGGCCGAGGCGGATGGA

111139	109226	GGCCTAGTCAGCTTGGAAGG
111140	109227	GGGCCTAGTCAGCTTGGAAG
111141	109228	TGGGCCTAGTCAGCTTGGAA
111142	109229	CTGGGCCTAGTCAGCTTGGA
111143	109230	GCTGGGCCTAGTCAGCTTGG
111144	109231	CGCTGGGCCTAGTCAGCTTG
111145	109232	GCGCTGGGCCTAGTCAGCTT
111146	109233	AGCGCTGGGCCTAGTCAGCT
111147	109234	AAGCGCTGGGCCTAGTCAGC
111148	109235	TAAGCGCTGGGCCTAGTCAG
111149	109236	CTAAGCGCTGGGCCTAGTCA
111150	109237	ACTAAGCGCTGGGCCTAGTC
111151	109238	GACTAAGCGCTGGGCCTAGT
111152	109239	GGACTAAGCGCTGGGCCTAG
111153	109240	TGGACTAAGCGCTGGGCCTA
111154	109241	CTGGACTAAGCGCTGGGCCT
111155	109242	GCTGGACTAAGCGCTGGGCC
111156	109243	GGCTGGACTAAGCGCTGGGC
111157	109244	AGGCTGGACTAAGCGCTGGG
111158	109245	GAGGCTGGACTAAGCGCTGG
111159	109246	GGAGGCTGGACTAAGCGCTG
111160	109247	TGGAGGCTGGACTAAGCGCT
111161	109248	ATGGAGGCTGGACTAAGCGC
111162	109249	CATGGAGGCTGGACTAAGCG
111163	109250	TCATGGAGGCTGGACTAAGC
111164	109251	GTCATGGAGGCTGGACTAAG
111165	109252	CGTCATGGAGGCTGGACTAA
111166	109253	CCGTCATGGAGGCTGGACTA
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111168	109255	GACCGTCATGGAGGCTGGAC
111169	109256	GGACCGTCATGGAGGCTGGA
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111171	109258	AGGGACCGTCATGGAGGCTG
111172	109259	GAGGGACCGTCATGGAGGCT
111173	109260	GGAGGGACCGTCATGGAGGC
111174	109261	TGGAGGGACCGTCATGGAGG
111175	109262	GTGGAGGGACCGTCATGGAG
111176	109263	TGTGGAGGGACCGTCATGGA
111177	109264	ATGTGGAGGGACCGTCATGG
111178	109265	GATGTGGAGGGACCGTCATG
111179	109266	GGATGTGGAGGGACCGTCAT
111180	109267	AGGATGTGGAGGGACCGTCA
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111186	109273	CTAATTAGGATGTGGAGGGA
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111188	109275	GGCTAATTAGGATGTGGAGG
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111193	109280	AGGGAGGCTAATTAGGATGT
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111196	109283	TGGAGGGAGGCTAATTAGGA
111197	109284	CTGGAGGGAGGCTAATTAGG
111198	109285	ACTGGAGGGAGGCTAATTAG
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111201	109288	TGAACTGGAGGGAGGCTAAT
111202	109289	ATGAACTGGAGGGAGGCTAA
111203	109290	AATGAACTGGAGGGAGGCTA
111204	109291	AAATGAACTGGAGGGAGGCT
111205	109292	GAAATGAACTGGAGGGAGGC
111206	109293	TGAAATGAACTGGAGGGAGG
111207	109294	GTGAAATGAACTGGAGGGAG
111208	109295	TGTGAAATGAACTGGAGGGA
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12916	11003	TAACAGCTGTGACAAGTTTT
12917	11004	TTAACAGCTGTGACAAGTTT
12918	11005	GTTAACAGCTGTGACAAGTT
12919	11006	GGTTAACAGCTGTGACAAGT
12920	11007	AGGTTAACAGCTGTGACAAG
12921	11008	AAGGTTAACAGCTGTGACAA
12922	11009	TAAGGTTAACAGCTGTGACA
12923	11010	TTAAGGTTAACAGCTGTGAC
12924	11011	GTTAAGGTTAACAGCTGTGA
12925	11012	AGTTAAGGTTAACAGCTGTG
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12927	11014	AAAGTTAAGGTTAACAGCTG
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12938	11025	AAGAAAAAAAAAAAGTTAAG
12939	11026	AAAGAAAAAAAAAAAGTTAA
12940	11027	AAAAGAAAAAAAAAAAGTTA
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12959	11046	GAGACTCCGTCTCGGAAAAA
12960	11047	CGAGACTCCGTCTCGGAAAA
12961	11048	GCGAGACTCCGTCTCGGAAA
12962	11049	AGCGAGACTCCGTCTCGGAA
12963	11050	GAGCGAGACTCCGTCTCGGA
12964	11051	AGAGCGAGACTCCGTCTCGG
12965	11052	CAGAGCGAGACTCCGTCTCG
12966	11053	ACAGAGCGAGACTCCGTCTC
12967	11054	GACAGAGCGAGACTCCGTCT
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12969	11056	GTGACAGAGCGAGACTCCGT
12970	11057	GGTGACAGAGCGAGACTCCG
12971	11058	AGGTGACAGAGCGAGACTCC
12972	11059	TAGGTGACAGAGCGAGACTC
12973	11060	CTAGGTGACAGAGCGAGACT
12974	11061	CCTAGGTGACAGAGCGAGAC
12975	11062	GCCTAGGTGACAGAGCGAGA
12976	11063	AGCCTAGGTGACAGAGCGAG
12977	11064	CAGCCTAGGTGACAGAGCGA
12978	11065	CCAGCCTAGGTGACAGAGCG
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12980	11067	CTCCAGCCTAGGTGACAGAG
12981	11068	ACTCCAGCCTAGGTGACAGA
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12983	11070	GCACTCCAGCCTAGGTGACA
12984	11071	TGCACTCCAGCCTAGGTGAC
12985	11072	CTGCACTCCAGCCTAGGTGA
12986	11073	ACTGCACTCCAGCCTAGGTG

62063	60150	TGGGAGGCCGAGGCGGATGG
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62065	60152	TTTGGGAGGCCGAGGCGGAT
62066	60153	CTTTGGGAGGCCGAGGCGGA
62067	60154	ACTTTGGGAGGCCGAGGCGG
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62079	60166	TGTAATCCCAGCACTTTGGG
62080	60167	CTGTAATCCCAGCACTTTGG
62081	60168	CCTGTAATCCCAGCACTTTG
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62083	60170	TGCCTGTAATCCCAGCACTT
62084	60171	ATGCCTGTAATCCCAGCACT
62085	60172	CATGCCTGTAATCCCAGCAC
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62088	60175	GCTCATGCCTGTAATCCCAG
62089	60176	GGCTCATGCCTGTAATCCCA
62090	60177	TGGCTCATGCCTGTAATCCC
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62092	60179	GATGGCTCATGCCTGTAATC
62093	60180	CGATGGCTCATGCCTGTAAT
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62095	60182	TGCGATGGCTCATGCCTGTA
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62099	60186	CGGGTGCGATGGCTCATGCC
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62113	60200	GAAAAAAAGAAGGCCGGGTG
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62123	60210	TAAAGAGAAAGAAAAAAAGA
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62125	60212	GTTAAAGAGAAAGAAAAAAA
62126	60213	AGTTAAAGAGAAAGAAAAAA
62127	60214	AAGTTAAAGAGAAAGAAAAA
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62129	60216	AGAAGTTAAAGAGAAAGAAA
62130	60217	CAGAAGTTAAAGAGAAAGAA
62131	60218	TCAGAAGTTAAAGAGAAAGA
62132	60219	CTCAGAAGTTAAAGAGAAAG
62133	60220	GCTCAGAAGTTAAAGAGAAA

111210	109297	TGTGTGAAATGAACTGGAGG
111211	109298	TTGTGTGAAATGAACTGGAG
111212	109299	TTTGTGTGAAATGAACTGGA
111213	109300	CTTTGTGTGAAATGAACTGG
111214	109301	GCTTTGTGTGAAATGAACTG
111215	109302	AGCTTTGTGTGAAATGAACT
111216	109303	CAGCTTTGTGTGAAATGAAC
111217	109304	GCAGCTTTGTGTGAAATGAA
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111219	109306	CAGCAGCTTTGTGTGAAATG
111220	109307	ACAGCAGCTTTGTGTGAAAT
111221	109308	CACAGCAGCTTTGTGTGAAA
111222	109309	ACACAGCAGCTTTGTGTGAA
111223	109310	AACACAGCAGCTTTGTGTGA
111224	109311	GAACACAGCAGCTTTGTGTG
111225	109312	TGAACACAGCAGCTTTGTGT
111226	109313	GTGAACACAGCAGCTTTGTG
111227	109314	GGTGAACACAGCAGCTTTGT
111228	109315	AGGTGAACACAGCAGCTTTG
111229	109316	AAGGTGAACACAGCAGCTTT
111230	109317	AAAGGTGAACACAGCAGCTT
111231	109318	GAAAGGTGAACACAGCAGCT
111232	109319	AGAAAGGTGAACACAGCAGC
111233	109320	CAGAAAGGTGAACACAGCAG
111234	109321	TCAGAAAGGTGAACACAGCA
111235	109322	TTCAGAAAGGTGAACACAGC
111236	109323	GTTCAGAAAGGTGAACACAG
111237	109324	AGTTCAGAAAGGTGAACACA
111238	109325	TAGTTCAGAAAGGTGAACAC
111239	109326	ATAGTTCAGAAAGGTGAACA
111240	109327	TATAGTTCAGAAAGGTGAAC
111241	109328	TTATAGTTCAGAAAGGTGAA
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111243	109330	ATTTATAGTTCAGAAAGGTG
111244	109331	GATTTATAGTTCAGAAAGGT
111245	109332	AGATTTATAGTTCAGAAAGG
111246	109333	CAGATTTATAGTTCAGAAAG
111247	109334	GCAGATTTATAGTTCAGAAA
111248	109335	GGCAGATTTATAGTTCAGAA
111249	109336	GGGCAGATTTATAGTTCAGA
111250	109337	TGGGCAGATTTATAGTTCAG
111251	109338	CTGGGCAGATTTATAGTTCA
111252	109339	ACTGGGCAGATTTATAGTTC
111253	109340	TACTGGGCAGATTTATAGTT
111254	109341	GTACTGGGCAGATTTATAGT
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111256	109343	GAGTACTGGGCAGATTTATA
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111258	109345	TAGAGTACTGGGCAGATTTA
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111260	109347	GGTAGAGTACTGGGCAGATT
111261	109348	GGGTAGAGTACTGGGCAGAT
111262	109349	AGGGTAGAGTACTGGGCAGA
111263	109350	TAGGGTAGAGTACTGGGCAG
111264	109351	GTAGGGTAGAGTACTGGGCA
111265	109352	AGTAGGGTAGAGTACTGGGC
111266	109353	AAGTAGGGTAGAGTACTGGG
111267	109354	TAAGTAGGGTAGAGTACTGG
111268	109355	TTAAGTAGGGTAGAGTACTG
111269	109356	TTTAAGTAGGGTAGAGTACT
111270	109357	TTTTAAGTAGGGTAGAGTAC
111271	109358	ATTTTAAGTAGGGTAGAGTA
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111273	109360	GAATTTTAAGTAGGGTAGAG
111274	109361	GGAATTTTAAGTAGGGTAGA
111275	109362	CGGAATTTTAAGTAGGGTAG
111276	109363	ACGGAATTTTAAGTAGGGTA
111277	109364	TACGGAATTTTAAGTAGGGT
111278	109365	ATACGGAATTTTAAGTAGGG
111279	109366	TATACGGAATTTTAAGTAGG
111280	109367	CTATACGGAATTTTAAGTAG

12987	11074	CACTGCACTCCAGCCTAGGT
12988	11075	CCACTGCACTCCAGCCTAGG
12989	11076	ACCACTGCACTCCAGCCTAG
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12992	11079	CGCACCACTGCACTCCAGCC
12993	11080	TCGCACCACTGCACTCCAGC
12994	11081	ATCGCACCACTGCACTCCAG
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12996	11083	AGATCGCACCACTGCACTCC
12997	11084	GAGATCGCACCACTGCACTC
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12999	11086	CCGAGATCGCACCACTGCAC
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13003	11090	TGAGCCGAGATCGCACCACT
13004	11091	ATGAGCCGAGATCGCACCAC
13005	11092	AATGAGCCGAGATCGCACCA
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13008	11095	TGCAATGAGCCGAGATCGCA
13009	11096	TTGCAATGAGCCGAGATCGC
13010	11097	GTTGCAATGAGCCGAGATCG
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13012	11099	AGGTTGCAATGAGCCGAGAT
13013	11100	GAGGTTGCAATGAGCCGAGA
13014	11101	AGAGGTTGCAATGAGCCGAG
13015	11102	CAGAGGTTGCAATGAGCCGA
13016	11103	GCAGAGGTTGCAATGAGCCG
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13018	11105	AGGCAGAGGTTGCAATGAGC
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13024	11111	CCTGGGAGGCAGAGGTTGCA
13025	11112	ACCTGGGAGGCAGAGGTTGC
13026	11113	AACCTGGGAGGCAGAGGTTG
13027	11114	TAACCTGGGAGGCAGAGGTT
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13029	11116	TTTAACCTGGGAGGCAGAGG
13030	11117	CTTTAACCTGGGAGGCAGAG
13031	11118	GCTTTAACCTGGGAGGCAGA
13032	11119	CGCTTTAACCTGGGAGGCAG
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13034	11121	ATCGCTTTAACCTGGGAGGC
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13036	11123	AAATCGCTTTAACCTGGGAG
13037	11124	AAAATCGCTTTAACCTGGGA
13038	11125	AAAAATCGCTTTAACCTGGG
13039	11126	GAAAAATCGCTTTAACCTGG
13040	11127	AGAAAAATCGCTTTAACCTG
13041	11128	CAGAAAAATCGCTTTAACCT
13042	11129	GCAGAAAAATCGCTTTAACC
13043	11130	GGCAGAAAAATCGCTTTAAC
13044	11131	AGGCAGAAAAATCGCTTTAA
13045	11132	GAGGCAGAAAAATCGCTTTA
13046	11133	TGAGGCAGAAAAATCGCTTT
13047	11134	CTGAGGCAGAAAAATCGCTT
13048	11135	GCTGAGGCAGAAAAATCGCT
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13055	11142	TCAGGAGGCTGAGGCAGAAA
13056	11143	CTCAGGAGGCTGAGGCAGAA
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62134	60221	AGCTCAGAAGTTAAAGAGAA
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62138	60225	TTTCAGCTCAGAAGTTAAAG
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62143	60230	ACTATTTTCAGCTCAGAAGT
62144	60231	TACTATTTTCAGCTCAGAAG
62145	60232	GTACTATTTTCAGCTCAGAA
62146	60233	GGTACTATTTTCAGCTCAGA
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62148	60235	AAGGTACTATTTTCAGCTCA
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62174	60261	ATCATCGTTTGAGCACTTCT
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62176	60263	CAATCATCGTTTGAGCACTT
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62178	60265	TCCAATCATCGTTTGAGCAC
62179	60266	GTCCAATCATCGTTTGAGCA
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62184	60271	AATCAGTCCAATCATCGTTT
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62186	60273	GAAATCAGTCCAATCATCGT
62187	60274	AGAAATCAGTCCAATCATCG
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62190	60277	AGGAGAAATCAGTCCAATCA
62191	60278	AAGGAGAAATCAGTCCAATC
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111283	109370	AGTCTATACGGAATTTTAAG
111284	109371	CAGTCTATACGGAATTTTAA
111285	109372	GCAGTCTATACGGAATTTTA
111286	109373	GGCAGTCTATACGGAATTTT
111287	109374	GGGCAGTCTATACGGAATTT
111288	109375	TGGGCAGTCTATACGGAATT
111289	109376	ATGGGCAGTCTATACGGAAT
111290	109377	AATGGGCAGTCTATACGGAA
111291	109378	AAATGGGCAGTCTATACGGA
111292	109379	CAAATGGGCAGTCTATACGG
111293	109380	GCAAATGGGCAGTCTATACG
111294	109381	GGCAAATGGGCAGTCTATAC
111295	109382	GGGCAAATGGGCAGTCTATA
111296	109383	AGGGCAAATGGGCAGTCTAT
111297	109384	CAGGGCAAATGGGCAGTCTA
111298	109385	TCAGGGCAAATGGGCAGTCT
111299	109386	CTCAGGGCAAATGGGCAGTC
111300	109387	TCTCAGGGCAAATGGGCAGT
111301	109388	TTCTCAGGGCAAATGGGCAG
111302	109389	ATTCTCAGGGCAAATGGGCA
111303	109390	AATTCTCAGGGCAAATGGGC
111304	109391	TAATTCTCAGGGCAAATGGG
111305	109392	TTAATTCTCAGGGCAAATGG
111306	109393	TTTAATTCTCAGGGCAAATG
111307	109394	TTTTAATTCTCAGGGCAAAT
111308	109395	CTTTTAATTCTCAGGGCAAA
111309	109396	GCTTTTAATTCTCAGGGCAA
111310	109397	GGCTTTTAATTCTCAGGGCA
111311	109398	TGGCTTTTAATTCTCAGGGC
111312	109399	TTGGCTTTTAATTCTCAGGG
111313	109400	TTTGGCTTTTAATTCTCAGG
111314	109401	CTTTGGCTTTTAATTCTCAG
111315	109402	ACTTTGGCTTTTAATTCTCA
111316	109403	GACTTTGGCTTTTAATTCTC
111317	109404	GGACTTTGGCTTTTAATTCT
111318	109405	AGGACTTTGGCTTTTAATTC
111319	109406	TAGGACTTTGGCTTTTAATT
111320	109407	TTAGGACTTTGGCTTTTAAT
111321	109408	TTTAGGACTTTGGCTTTTAA
111322	109409	GTTTAGGACTTTGGCTTTTA
111323	109410	CGTTTAGGACTTTGGCTTTT
111324	109411	ACGTTTAGGACTTTGGCTTT
111325	109412	TACGTTTAGGACTTTGGCTT
111326	109413	CTACGTTTAGGACTTTGGCT
111327	109414	GCTACGTTTAGGACTTTGGC
111328	109415	AGCTACGTTTAGGACTTTGG
111329	109416	AAGCTACGTTTAGGACTTTG
111330	109417	AAAGCTACGTTTAGGACTTT
111331	109418	AAAAGCTACGTTTAGGACTT
111332	109419	AAAAAGCTACGTTTAGGACT
111333	109420	TAAAAAGCTACGTTTAGGAC
111334	109421	TTAAAAAGCTACGTTTAGGA
111335	109422	TTTAAAAAGCTACGTTTAGG
111336	109423	TTTTAAAAAGCTACGTTTAG
111337	109424	GTTTTAAAAAGCTACGTTTA
111338	109425	AGTTTTAAAAAGCTACGTTT
111339	109426	AAGTTTTAAAAAGCTACGTT
111340	109427	AAAGTTTTAAAAAGCTACGT
111341	109428	AAAAGTTTTAAAAAGCTACG
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111343	109430	AAAAAAGTTTTAAAAAGCTA
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111345	109432	AAAAAAAAGTTTTAAAAAGC
111346	109433	AAAAAAAAAGTTTTAAAAAG
111347	109434	AAAAAAAAAAGTTTTAAAAA
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111349	109436	AAAAAAAAAAAAGTTTTAAA
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111351	109438	AAAAAAAAAAAAAAGTTTTA

13058	11145	TACTCAGGAGGCTGAGGCAG
13059	11146	CTACTCAGGAGGCTGAGGCA
13060	11147	GCTACTCAGGAGGCTGAGGC
13061	11148	AGCTACTCAGGAGGCTGAGG
13062	11149	CAGCTACTCAGGAGGCTGAG
13063	11150	CCAGCTACTCAGGAGGCTGA
13064	11151	CCCAGCTACTCAGGAGGCTG
13065	11152	TCCCAGCTACTCAGGAGGCT
13066	11153	GTCCCAGCTACTCAGGAGGC
13067	11154	AGTCCCAGCTACTCAGGAGG
13068	11155	CAGTCCCAGCTACTCAGGAG
13069	11156	GCAGTCCCAGCTACTCAGGA
13070	11157	TGCAGTCCCAGCTACTCAGG
13071	11158	CTGCAGTCCCAGCTACTCAG
13072	11159	CCTGCAGTCCCAGCTACTCA
13073	11160	GCCTGCAGTCCCAGCTACTC
13074	11161	TGCCTGCAGTCCCAGCTACT
13075	11162	GTGCCTGCAGTCCCAGCTAC
13076	11163	CGTGCCTGCAGTCCCAGCTA
13077	11164	GCGTGCCTGCAGTCCCAGCT
13078	11165	TGCGTGCCTGCAGTCCCAGC
13079	11166	GTGCGTGCCTGCAGTCCCAG
13080	11167	GGTGCGTGCCTGCAGTCCCA
13081	11168	TGGTGCGTGCCTGCAGTCCC
13082	11169	ATGGTGCGTGCCTGCAGTCC
13083	11170	GATGGTGCGTGCCTGCAGTC
13084	11171	AGATGGTGCGTGCCTGCAGT
13085	11172	GAGATGGTGCGTGCCTGCAG
13086	11173	CGAGATGGTGCGTGCCTGCA
13087	11174	GCGAGATGGTGCGTGCCTGC
13088	11175	GGCGAGATGGTGCGTGCCTG
13089	11176	AGGCGAGATGGTGCGTGCCT
13090	11177	CAGGCGAGATGGTGCGTGCC
13091	11178	CCAGGCGAGATGGTGCGTGC
13092	11179	GCCAGGCGAGATGGTGCGTG
13093	11180	AGCCAGGCGAGATGGTGCGT
13094	11181	TAGCCAGGCGAGATGGTGCG
13095	11182	TTAGCCAGGCGAGATGGTGC
13096	11183	ATTAGCCAGGCGAGATGGTG
13097	11184	AATTAGCCAGGCGAGATGGT
13098	11185	AAATTAGCCAGGCGAGATGG
13099	11186	AAAATTAGCCAGGCGAGATG
13100	11187	AAAAATTAGCCAGGCGAGAT
13101	11188	CAAAAATTAGCCAGGCGAGA
13102	11189	ACAAAAATTAGCCAGGCGAG
13103	11190	TACAAAAATTAGCCAGGCGA
13104	11191	ATACAAAAATTAGCCAGGCG
13105	11192	AATACAAAAATTAGCCAGGC
13106	11193	AAATACAAAAATTAGCCAGG
13107	11194	AAAATACAAAAATTAGCCAG
13108	11195	TAAAATACAAAAATTAGCCA
13109	11196	CTAAAATACAAAAATTAGCC
13110	11197	ACTAAAATACAAAAATTAGC
13111	11198	TACTAAAATACAAAAATTAG
13112	11199	CTACTAAAATACAAAAATTA
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13114	11201	CTCTACTAAAATACAAAAAT
13115	11202	TCTCTACTAAAATACAAAAA
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13117	11204	CATCTCTACTAAAATACAAA
13118	11205	CCATCTCTACTAAAATACAA
13119	11206	CCCATCTCTACTAAAATACA
13120	11207	CCCCATCTCTACTAAAATAC
13121	11208	ACCCCATCTCTACTAAAATA
13122	11209	AACCCCATCTCTACTAAAAT
13123	11210	AAACCCCATCTCTACTAAAA
13124	11211	GAAACCCCATCTCTACTAAA
13125	11212	TGAAACCCCATCTCTACTAA
13126	11213	GTGAAACCCCATCTCTACTA
13127	11214	GGTGAAACCCCATCTCTACT
13128	11215	TGGTGAAACCCCATCTCTAC

62205	60292	AGAAAGAGAGAAATAAGGAG
62206	60293	GAGAAAGAGAGAAATAAGGA
62207	60294	AGAGAAAGAGAGAAATAAGG
62208	60295	GAGAGAAAGAGAGAAATAAG
62209	60296	AGAGAGAAAGAGAGAAATAA
62210	60297	CAGAGAGAAAGAGAGAAATA
62211	60298	ACAGAGAGAAAGAGAGAAAT
62212	60299	GACAGAGAGAAAGAGAGAAA
62213	60300	AGACAGAGAGAAAGAGAGAA
62214	60301	GAGACAGAGAGAAAGAGAGA
62215	60302	AGAGACAGAGAGAAAGAGAG
62216	60303	AAGAGACAGAGAGAAAGAGA
62217	60304	AAAGAGACAGAGAGAAAGAG
62218	60305	GAAAGAGACAGAGAGAAAGA
62219	60306	TGAAAGAGACAGAGAGAAAG
62220	60307	GTGAAAGAGACAGAGAGAAA
62221	60308	AGTGAAAGAGACAGAGAGAA
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62224	60311	GAGAGTGAAAGAGACAGAGA
62225	60312	AGAGAGTGAAAGAGACAGAG
62226	60313	AAGAGAGTGAAAGAGACAGA
62227	60314	AAAGAGAGTGAAAGAGACAG
62228	60315	AAAAGAGAGTGAAAGAGACA
62229	60316	AAAAAGAGAGTGAAAGAGAC
62230	60317	TAAAAAGAGAGTGAAAGAGA
62231	60318	CTAAAAAGAGAGTGAAAGAG
62232	60319	TCTAAAAAGAGAGTGAAAGA
62233	60320	TTCTAAAAAGAGAGTGAAAG
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62236	60323	AAATTCTAAAAAGAGAGTGA
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62240	60327	AGAAAAATTCTAAAAAGAGA
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62244	60331	AAAAAGAAAAATTCTAAAAA
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62246	60333	TAAAAAAGAAAAATTCTAAA
62247	60334	TTAAAAAAGAAAAATTCTAA
62248	60335	CTTAAAAAAGAAAAATTCTA
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62250	60337	TACTTAAAAAAGAAAAATTC
62251	60338	CTACTTAAAAAAGAAAAATT
62252	60339	TCTACTTAAAAAAGAAAAAT
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62258	60345	CTCGTCTCTACTTAAAAAAG
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62260	60347	ACCTCGTCTCTACTTAAAAA
62261	60348	GACCTCGTCTCTACTTAAAA
62262	60349	GGACCTCGTCTCTACTTAAA
62263	60350	GGGACCTCGTCTCTACTTAA
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62267	60354	TAGTGGGACCTCGTCTCTAC
62268	60355	ATAGTGGGACCTCGTCTCTA
62269	60356	CATAGTGGGACCTCGTCTCT
62270	60357	ACATAGTGGGACCTCGTCTC
62271	60358	AACATAGTGGGACCTCGTCT
62272	60359	CAACATAGTGGGACCTCGTC
62273	60360	GCAACATAGTGGGACCTCGT
62274	60361	GGCAACATAGTGGGACCTCG
62275	60362	GGGCAACATAGTGGGACCTC

111352	109439	AAAAAAAAAAAAAAAGTTTT
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111370	109457	CTCCATCTAAAAATTAAAA
111371	109458	ACTCCATCTAAAAATTAAA
111372	109459	GACTCCATCTAAAAATTAA
111373	109460	AGACTCCATCTAAAAATTAA
111374	109461	AAGACTCCATCTAAAAATTA
111375	109462	CAAGACTCCATCTAAAAATT
111376	109463	GCAAGACTCCATCTAAAAAT
111377	109464	AGCAAGACTCCATCTAAAAA
111378	109465	GAGCAAGACTCCATCTAAAA
111379	109466	AGAGCAAGACTCCATCTAAA
111380	109467	CAGAGCAAGACTCCATCTAA
111381	109468	ACAGAGCAAGACTCCATCTA
111382	109469	GACAGAGCAAGACTCCATCT
111383	109470	TGACAGAGCAAGACTCCATC
111384	109471	GTGACAGAGCAAGACTCCAT
111385	109472	GGTGACAGAGCAAGACTCCA
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111387	109474	TGGGTGACAGAGCAAGACTC
111388	109475	CTGGGTGACAGAGCAAGACT
111389	109476	CCTGGGTGACAGAGCAAGAC
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111391	109478	AGCCTGGGTGACAGAGCAAG
111392	109479	CAGCCTGGGTGACAGAGCAA
111393	109480	CCAGCCTGGGTGACAGAGCA
111394	109481	TCCAGCCTGGGTGACAGAGC
111395	109482	CTCCAGCCTGGGTGACAGAG
111396	109483	ACTCCAGCCTGGGTGACAGA
111397	109484	CACTCCAGCCTGGGTGACAG
111398	109485	GCACTCCAGCCTGGGTGACA
111399	109486	TGCACTCCAGCCTGGGTGAC
111400	109487	CTGCACTCCAGCCTGGGTGA
111401	109488	ACTGCACTCCAGCCTGGGTG
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111403	109490	CCACTGCACTCCAGCCTGGG
111404	109491	ACCACTGCACTCCAGCCTGG
111405	109492	CACCACTGCACTCCAGCCTG
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111407	109494	CACACCACTGCACTCCAGCC
111408	109495	TCACACCACTGCACTCCAGC
111409	109496	ATCACACCACTGCACTCCAG
111410	109497	GATCACACCACTGCACTCCA
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111412	109499	AAGATCACACCACTGCACTC
111413	109500	CAAGATCACACCACTGCACT
111414	109501	CCAAGATCACACCACTGCAC
111415	109502	GCCAAGATCACACCACTGCA
111416	109503	AGCCAAGATCACACCACTGC
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111418	109505	TGAGCCAAGATCACACCACT
111419	109506	GTGAGCCAAGATCACACCAC
111420	109507	AGTGAGCCAAGATCACACCA
111421	109508	CAGTGAGCCAAGATCACACC
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13129	11216	ATGGTGAAACCCCATCTCTA
13130	11217	TATGGTGAAACCCCATCTCT
13131	11218	ATATGGTGAAACCCCATCTC
13132	11219	AATATGGTGAAACCCCATCT
13133	11220	CAATATGGTGAAACCCCATC
13134	11221	CCAATATGGTGAAACCCCAT
13135	11222	GCCAATATGGTGAAACCCCA
13136	11223	GGCCAATATGGTGAAACCCC
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13138	11225	CTGGCCAATATGGTGAAACC
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13140	11227	GCCTGGCCAATATGGTGAAA
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13142	11229	CAGCCTGGCCAATATGGTGA
13143	11230	CCAGCCTGGCCAATATGGTG
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13146	11233	AGACCAGCCTGGCCAATATG
13147	11234	CAGACCAGCCTGGCCAATAT
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13149	11236	TCCAGACCAGCCTGGCCAAT
13150	11237	TTCCAGACCAGCCTGGCCAA
13151	11238	GTTCCAGACCAGCCTGGCCA
13152	11239	AGTTCCAGACCAGCCTGGCC
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13157	11244	CCAGAAGTTCCAGACCAGCC
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13161	11248	GAGGCCAGAAGTTCCAGACC
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13163	11250	TTGAGGCCAGAAGTTCCAGA
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13167	11254	TCACTTGAGGCCAGAAGTTC
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13170	11257	GGATCACTTGAGGCCAGAAG
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13172	11259	GTGGATCACTTGAGGCCAGA
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13174	11261	AGGTGGATCACTTGAGGCCA
13175	11262	CAGGTGGATCACTTGAGGCC
13176	11263	GCAGGTGGATCACTTGAGGC
13177	11264	GGCAGGTGGATCACTTGAGG
13178	11265	AGGCAGGTGGATCACTTGAG
13179	11266	AAGGCAGGTGGATCACTTGA
13180	11267	CAAGGCAGGTGGATCACTTG
13181	11268	CCAAGGCAGGTGGATCACTT
13182	11269	GCCAAGGCAGGTGGATCACT
13183	11270	GGCCAAGGCAGGTGGATCAC
13184	11271	AGGCCAAGGCAGGTGGATCA
13185	11272	GAGGCCAAGGCAGGTGGATC
13186	11273	GGAGGCCAAGGCAGGTGGAT
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13189	11276	ATGGGAGGCCAAGGCAGGTG
13190	11277	CATGGGAGGCCAAGGCAGGT
13191	11278	GCATGGGAGGCCAAGGCAGG
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13194	11281	CAGGCATGGGAGGCCAAGGC
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13196	11283	GCCAGGCATGGGAGGCCAAG
13197	11284	TGCCAGGCATGGGAGGCCAA
13198	11285	TTGCCAGGCATGGGAGGCCA
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62276	60363	TGGGCAACATAGTGGGACCT
62277	60364	CTGGGCAACATAGTGGGACC
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62279	60366	GCCTGGGCAACATAGTGGGA
62280	60367	AGCCTGGGCAACATAGTGGG
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62285	60372	AAGACAGCCTGGGCAACATA
62286	60373	CAAGACAGCCTGGGCAACAT
62287	60374	TCAAGACAGCCTGGGCAACA
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62289	60376	GTTCAAGACAGCCTGGGCAA
62290	60377	AGTTCAAGACAGCCTGGGCA
62291	60378	GAGTTCAAGACAGCCTGGGC
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62293	60380	AGGAGTTCAAGACAGCCTGG
62294	60381	CAGGAGTTCAAGACAGCCTG
62295	60382	TCAGGAGTTCAAGACAGCCT
62296	60383	CTCAGGAGTTCAAGACAGCC
62297	60384	GCTCAGGAGTTCAAGACAGC
62298	60385	GGCTCAGGAGTTCAAGACAG
62299	60386	GGGCTCAGGAGTTCAAGACA
62300	60387	TGGGCTCAGGAGTTCAAGAC
62301	60388	TTGGGCTCAGGAGTTCAAGA
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62308	60395	GGATTGCTTGGGCTCAGGAG
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62313	60400	AAAGAGGATTGCTTGGGCTC
62314	60401	CAAAGAGGATTGCTTGGGCT
62315	60402	GCAAAGAGGATTGCTTGGGC
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62317	60404	AGGCAAAGAGGATTGCTTGG
62318	60405	GAGGCAAAGAGGATTGCTTG
62319	60406	TGAGGCAAAGAGGATTGCTT
62320	60407	CTGAGGCAAAGAGGATTGCT
62321	60408	GCTGAGGCAAAGAGGATTGC
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62323	60410	AGGCTGAGGCAAAGAGGATT
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62326	60413	GGGAGGCTGAGGCAAAGAGG
62327	60414	TGGGAGGCTGAGGCAAAGAG
62328	60415	TTGGGAGGCTGAGGCAAAGA
62329	60416	TTTGGGAGGCTGAGGCAAAG
62330	60417	CTTTGGGAGGCTGAGGCAAA
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62332	60419	CACTTTGGGAGGCTGAGGCA
62333	60420	GCACTTTGGGAGGCTGAGGC
62334	60421	AGCACTTTGGGAGGCTGAGG
62335	60422	GAGCACTTTGGGAGGCTGAG
62336	60423	CGAGCACTTTGGGAGGCTGA
62337	60424	CCGAGCACTTTGGGAGGCTG
62338	60425	TCCGAGCACTTTGGGAGGCT
62339	60426	ATCCGAGCACTTTGGGAGGC
62340	60427	AATCCGAGCACTTTGGGAGG
62341	60428	TAATCCGAGCACTTTGGGAG
62342	60429	GTAATCCGAGCACTTTGGGA
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111423	109510	TGCAGTGAGCCAAGATCACA
111424	109511	TTGCAGTGAGCCAAGATCAC
111425	109512	GTTGCAGTGAGCCAAGATCA
111426	109513	GGTTGCAGTGAGCCAAGATC
111427	109514	AGGTTGCAGTGAGCCAAGAT
111428	109515	GAGGTTGCAGTGAGCCAAGA
111429	109516	GGAGGTTGCAGTGAGCCAAG
111430	109517	CGGAGGTTGCAGTGAGCCAA
111431	109518	GCGGAGGTTGCAGTGAGCCA
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111433	109520	AGGCGGAGGTTGCAGTGAGC
111434	109521	GAGGCGGAGGTTGCAGTGAG
111435	109522	GGAGGCGGAGGTTGCAGTGA
111436	109523	AGGAGGCGGAGGTTGCAGTG
111437	109524	CAGGAGGCGGAGGTTGCAGT
111438	109525	CCAGGAGGCGGAGGTTGCAG
111439	109526	CCCAGGAGGCGGAGGTTGCA
111440	109527	ACCCAGGAGGCGGAGGTTGC
111441	109528	AACCCAGGAGGCGGAGGTTG
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111443	109530	TGAACCCAGGAGGCGGAGGT
111444	109531	TTGAACCCAGGAGGCGGAGG
111445	109532	CTTGAACCCAGGAGGCGGAG
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111447	109534	TGCTTGAACCCAGGAGGCGG
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111449	109536	ATTGCTTGAACCCAGGAGGC
111450	109537	AATTGCTTGAACCCAGGAGG
111451	109538	GAATTGCTTGAACCCAGGAG
111452	109539	AGAATTGCTTGAACCCAGGA
111453	109540	GAGAATTGCTTGAACCCAGG
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111456	109543	TATGAGAATTGCTTGAACCC
111457	109544	ATATGAGAATTGCTTGAACC
111458	109545	CATATGAGAATTGCTTGAAC
111459	109546	ACATATGAGAATTGCTTGAA
111460	109547	GACATATGAGAATTGCTTGA
111461	109548	TGACATATGAGAATTGCTTG
111462	109549	CTGACATATGAGAATTGCTT
111463	109550	GCTGACATATGAGAATTGCT
111464	109551	GGCTGACATATGAGAATTGC
111465	109552	AGGCTGACATATGAGAATTG
111466	109553	GAGGCTGACATATGAGAATT
111467	109554	GGAGGCTGACATATGAGAAT
111468	109555	GGGAGGCTGACATATGAGAA
111469	109556	TGGGAGGCTGACATATGAGA
111470	109557	TTGGGAGGCTGACATATGAG
111471	109558	CTTGGGAGGCTGACATATGA
111472	109559	ACTTGGGAGGCTGACATATG
111473	109560	TACTTGGGAGGCTGACATAT
111474	109561	CTACTTGGGAGGCTGACATA
111475	109562	GCTACTTGGGAGGCTGACAT
111476	109563	AGCTACTTGGGAGGCTGACA
111477	109564	CAGCTACTTGGGAGGCTGAC
111478	109565	CCAGCTACTTGGGAGGCTGA
111479	109566	CCCAGCTACTTGGGAGGCTG
111480	109567	TCCCAGCTACTTGGGAGGCT
111481	109568	ATCCCAGCTACTTGGGAGGC
111482	109569	AATCCCAGCTACTTGGGAGG
111483	109570	AAATCCCAGCTACTTGGGAG
111484	109571	TAAATCCCAGCTACTTGGGA
111485	109572	GTAAATCCCAGCTACTTGGG
111486	109573	TGTAAATCCCAGCTACTTGG
111487	109574	GTGTAAATCCCAGCTACTTG
111488	109575	CGTGTAAATCCCAGCTACTT
111489	109576	ACGTGTAAATCCCAGCTACT
111490	109577	CACGTGTAAATCCCAGCTAC
111491	109578	ACACGTGTAAATCCCAGCTA
111492	109579	CACACGTGTAAATCCCAGCT
111493	109580	GCACACGTGTAAATCCCAGC

13200	11287	GGTTGCCAGGCATGGGAGGC
13201	11288	AGGTTGCCAGGCATGGGAGG
13202	11289	AAGGTTGCCAGGCATGGGAG
13203	11290	TAAGGTTGCCAGGCATGGGA
13204	11291	TTAAGGTTGCCAGGCATGGG
13205	11292	GTTAAGGTTGCCAGGCATGG
13206	11293	AGTTAAGGTTGCCAGGCATG
13207	11294	AAGTTAAGGTTGCCAGGCAT
13208	11295	AAAGTTAAGGTTGCCAGGCA
13209	11296	AAAAGTTAAGGTTGCCAGGC
13210	11297	AAAAAGTTAAGGTTGCCAGG
13211	11298	TAAAAAGTTAAGGTTGCCAG
13212	11299	ATAAAAAGTTAAGGTTGCCA
13213	11300	AATAAAAAGTTAAGGTTGCC
13214	11301	AAATAAAAAGTTAAGGTTGC
13215	11302	CAAATAAAAAGTTAAGGTTG
13216	11303	GCAAATAAAAAGTTAAGGTT
13217	11304	AGCAAATAAAAAGTTAAGGT
13218	11305	CAGCAAATAAAAAGTTAAGG
13219	11306	CCAGCAAATAAAAAGTTAAG
13220	11307	ACCAGCAAATAAAAAGTTAA
13221	11308	TACCAGCAAATAAAAAGTTA
13222	11309	TTACCAGCAAATAAAAAGTT
13223	11310	ATTACCAGCAAATAAAAAGT
13224	11311	AATTACCAGCAAATAAAAAG
13225	11312	TAATTACCAGCAAATAAAAA
13226	11313	ATAATTACCAGCAAATAAAA
13227	11314	AATAATTACCAGCAAATAAA
13228	11315	AAATAATTACCAGCAAATAA
13229	11316	CAAATAATTACCAGCAAATA
13230	11317	ACAAATAATTACCAGCAAAT
13231	11318	CACAAATAATTACCAGCAAA
13232	11319	ACACAAATAATTACCAGCAA
13233	11320	AACACAAATAATTACCAGCA
13234	11321	AAACACAAATAATTACCAGC
13235	11322	CAAACACAAATAATTACCAG
13236	11323	GCAAACACAAATAATTACCA
13237	11324	TGCAAACACAAATAATTACC
13238	11325	ATGCAAACACAAATAATTAC
13239	11326	AATGCAAACACAAATAATTA
13240	11327	GAATGCAAACACAAATAATT
13241	11328	TGAATGCAAACACAAATAAT
13242	11329	ATGAATGCAAACACAAATAA
13243	11330	CATGAATGCAAACACAAATA
13244	11331	ACATGAATGCAAACACAAAT
13245	11332	CACATGAATGCAAACACAAA
13246	11333	TCACATGAATGCAAACACAA
13247	11334	TTCACATGAATGCAAACACA
13248	11335	TTTCACATGAATGCAAACAC
13249	11336	TTTTCACATGAATGCAAACA
13250	11337	ATTTTCACATGAATGCAAAC
13251	11338	AATTTTCACATGAATGCAAA
13252	11339	AAATTTTCACATGAATGCAA
13253	11340	CAAATTTTCACATGAATGCA
13254	11341	TCAAATTTTCACATGAATGC
13255	11342	TTCAAATTTTCACATGAATG
13256	11343	TTTCAAATTTTCACATGAAT
13257	11344	ATTTCAAATTTTCACATGAA
13258	11345	AATTTCAAATTTTCACATGA
13259	11346	GAATTTCAAATTTTCACATG
13260	11347	AGAATTTCAAATTTTCACAT
13261	11348	GAGAATTTCAAATTTTCACA
13262	11349	TGAGAATTTCAAATTTTCAC
13263	11350	ATGAGAATTTCAAATTTTCA
13264	11351	AATGAGAATTTCAAATTTTC
13265	11352	TAATGAGAATTTCAAATTTT
13266	11353	TTAATGAGAATTTCAAATTT
13267	11354	GTTAATGAGAATTTCAAATT
13268	11355	TGTTAATGAGAATTTCAAAT
13269	11356	ATGTTAATGAGAATTTCAAA
13270	11357	AATGTTAATGAGAATTTCAA

62347	60434	AGCCTGTAATCCGAGCACTT
62348	60435	AAGCCTGTAATCCGAGCACT
62349	60436	TAAGCCTGTAATCCGAGCAC
62350	60437	TTAAGCCTGTAATCCGAGCA
62351	60438	CTTAAGCCTGTAATCCGAGC
62352	60439	GCTTAAGCCTGTAATCCGAG
62353	60440	AGCTTAAGCCTGTAATCCGA
62354	60441	TAGCTTAAGCCTGTAATCCG
62355	60442	ATAGCTTAAGCCTGTAATCC
62356	60443	GATAGCTTAAGCCTGTAATC
62357	60444	TGATAGCTTAAGCCTGTAAT
62358	60445	GTGATAGCTTAAGCCTGTAA
62359	60446	TGTGATAGCTTAAGCCTGTA
62360	60447	GTGTGATAGCTTAAGCCTGT
62361	60448	GGTGTGATAGCTTAAGCCTG
62362	60449	TGGTGTGATAGCTTAAGCCT
62363	60450	CTGGTGTGATAGCTTAAGCC
62364	60451	CCTGGTGTGATAGCTTAAGC
62365	60452	GCCTGGTGTGATAGCTTAAG
62366	60453	GGCCTGGTGTGATAGCTTAA
62367	60454	AGGCCTGGTGTGATAGCTTA
62368	60455	TAGGCCTGGTGTGATAGCTT
62369	60456	CTAGGCCTGGTGTGATAGCT
62370	60457	CCTAGGCCTGGTGTGATAGC
62371	60458	GCCTAGGCCTGGTGTGATAG
62372	60459	AGCCTAGGCCTGGTGTGATA
62373	60460	TAGCCTAGGCCTGGTGTGAT
62374	60461	TTAGCCTAGGCCTGGTGTGA
62375	60462	ATTAGCCTAGGCCTGGTGTG
62376	60463	AATTAGCCTAGGCCTGGTGT
62377	60464	AAATTAGCCTAGGCCTGGTG
62378	60465	GAAATTAGCCTAGGCCTGGT
62379	60466	TGAAATTAGCCTAGGCCTGG
62380	60467	ATGAAATTAGCCTAGGCCTG
62381	60468	TATGAAATTAGCCTAGGCCT
62382	60469	ATATGAAATTAGCCTAGGCC
62383	60470	AATATGAAATTAGCCTAGGC
62384	60471	AAATATGAAATTAGCCTAGG
62385	60472	AAAATATGAAATTAGCCTAG
62386	60473	CAAAATATGAAATTAGCCTA
62387	60474	TCAAAATATGAAATTAGCCT
62388	60475	CTCAAAATATGAAATTAGCC
62389	60476	TCTCAAAATATGAAATTAGC
62390	60477	ATCTCAAAATATGAAATTAG
62391	60478	CATCTCAAAATATGAAATTA
62392	60479	CCATCTCAAAATATGAAATT
62393	60480	GCCATCTCAAAATATGAAAT
62394	60481	TGCCATCTCAAAATATGAAA
62395	60482	GTGCCATCTCAAAATATGAA
62396	60483	TGTGCCATCTCAAAATATGA
62397	60484	TTGTGCCATCTCAAAATATG
62398	60485	TTTGTGCCATCTCAAAATAT
62399	60486	ATTTGTGCCATCTCAAAATA
62400	60487	AATTTGTGCCATCTCAAAAT
62401	60488	AAATTTGTGCCATCTCAAAA
62402	60489	GAAATTTGTGCCATCTCAAA
62403	60490	AGAAATTTGTGCCATCTCAA
62404	60491	AAGAAATTTGTGCCATCTCA
62405	60492	AAAGAAATTTGTGCCATCTC
62406	60493	GAAAGAAATTTGTGCCATCT
62407	60494	TGAAAGAAATTTGTGCCATC
62408	60495	CTGAAAGAAATTTGTGCCAT
62409	60496	CCTGAAAGAAATTTGTGCCA
62410	60497	ACCTGAAAGAAATTTGTGCC
62411	60498	TACCTGAAAGAAATTTGTGC
62412	60499	CTACCTGAAAGAAATTTGTG
62413	60500	GCTACCTGAAAGAAATTTGT
62414	60501	AGCTACCTGAAAGAAATTTG
62415	60502	TAGCTACCTGAAAGAAATTT
62416	60503	CTAGCTACCTGAAAGAAATT
62417	60504	GCTAGCTACCTGAAAGAAAT

111494	109581	GGCACACGTGTAAATCCCAG
111495	109582	TGGCACACGTGTAAATCCCA
111496	109583	ATGGCACACGTGTAAATCCC
111497	109584	GATGGCACACGTGTAAATCC
111498	109585	TGATGGCACACGTGTAAATC
111499	109586	GTGATGGCACACGTGTAAAT
111500	109587	CGTGATGGCACACGTGTAAA
111501	109588	GCGTGATGGCACACGTGTAA
111502	109589	GGCGTGATGGCACACGTGTA
111503	109590	AGGCGTGATGGCACACGTGT
111504	109591	CAGGCGTGATGGCACACGTG
111505	109592	CCAGGCGTGATGGCACACGT
111506	109593	GCCAGGCGTGATGGCACACG
111507	109594	AGCCAGGCGTGATGGCACAC
111508	109595	TAGCCAGGCGTGATGGCACA
111509	109596	TTAGCCAGGCGTGATGGCAC
111510	109597	ATTAGCCAGGCGTGATGGCA
111511	109598	AATTAGCCAGGCGTGATGGC
111512	109599	AAATTAGCCAGGCGTGATGG
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111514	109601	AAAAATTAGCCAGGCGTGAT
111515	109602	AAAAAATTAGCCAGGCGTGA
111516	109603	AAAAAAATTAGCCAGGCGTG
111517	109604	AAAAAAAATTAGCCAGGCGT
111518	109605	AAAAAAAAATTAGCCAGGCG
111519	109606	AAAAAAAAAATTAGCCAGGC
111520	109607	AAAAAAAAAAATTAGCCAGG
111521	109608	AAAAAAAAAAAATTAGCCAG
111522	109609	TAAAAAAAAAAAATTAGCCA
111523	109610	ATAAAAAAAAAAAATTAGCC
111524	109611	GATAAAAAAAAAAAATTAGC
111525	109612	AGATAAAAAAAAAAAATTAG
111526	109613	AAGATAAAAAAAAAAAATTA
111527	109614	AAAGATAAAAAAAAAAAATT
111528	109615	TAAAGATAAAAAAAAAAAAT
111529	109616	CTAAAGATAAAAAAAAAAAA
111530	109617	ACTAAAGATAAAAAAAAAAA
111531	109618	TACTAAAGATAAAAAAAAAA
111532	109619	CTACTAAAGATAAAAAAAAA
111533	109620	TCTACTAAAGATAAAAAAAA
111534	109621	CTCTACTAAAGATAAAAAAA
111535	109622	TCTCTACTAAAGATAAAAAA
111536	109623	GTCTCTACTAAAGATAAAAA
111537	109624	CGTCTCTACTAAAGATAAAA
111538	109625	CCGTCTCTACTAAAGATAAA
111539	109626	TCCGTCTCTACTAAAGATAA
111540	109627	CTCCGTCTCTACTAAAGATA
111541	109628	ACTCCGTCTCTACTAAAGAT
111542	109629	AACTCCGTCTCTACTAAAGA
111543	109630	AAACTCCGTCTCTACTAAAG
111544	109631	GAAACTCCGTCTCTACTAAA
111545	109632	TGAAACTCCGTCTCTACTAA
111546	109633	GTGAAACTCCGTCTCTACTA
111547	109634	GGTGAAACTCCGTCTCTACT
111548	109635	TGGTGAAACTCCGTCTCTAC
111549	109636	ATGGTGAAACTCCGTCTCTA
111550	109637	CATGGTGAAACTCCGTCTCT
111551	109638	ACATGGTGAAACTCCGTCTC
111552	109639	AACATGGTGAAACTCCGTCT
111553	109640	CAACATGGTGAAACTCCGTC
111554	109641	CCAACATGGTGAAACTCCGT
111555	109642	GCCAACATGGTGAAACTCCG
111556	109643	GGCCAACATGGTGAAACTCC
111557	109644	TGGCCAACATGGTGAAACTC
111558	109645	CTGGCCAACATGGTGAAACT
111559	109646	ACTGGCCAACATGGTGAAAC
111560	109647	GACTGGCCAACATGGTGAAA
111561	109648	AGACTGGCCAACATGGTGAA
111562	109649	CAGACTGGCCAACATGGTGA
111563	109650	CCAGACTGGCCAACATGGTG
111564	109651	ACCAGACTGGCCAACATGGT

13271	11358	AAATGTTAATGAGAATTTCA
13272	11359	TAAATGTTAATGAGAATTTC
13273	11360	TTAAATGTTAATGAGAATTT
13274	11361	TTTAAATGTTAATGAGAATT
13275	11362	CTTTAAATGTTAATGAGAAT
13276	11363	TCTTTAAATGTTAATGAGAA
13277	11364	ATCTTTAAATGTTAATGAGA
13278	11365	AATCTTTAAATGTTAATGAG
13279	11366	GAATCTTTAAATGTTAATGA
13280	11367	AGAATCTTTAAATGTTAATG
13281	11368	AAGAATCTTTAAATGTTAAT
13282	11369	TAAGAATCTTTAAATGTTAA
13283	11370	GTAAGAATCTTTAAATGTTA
13284	11371	TGTAAGAATCTTTAAATGTT
13285	11372	ATGTAAGAATCTTTAAATGT
13286	11373	TATGTAAGAATCTTTAAATG
13287	11374	CTATGTAAGAATCTTTAAAT
13288	11375	TCTATGTAAGAATCTTTAAA
13289	11376	ATCTATGTAAGAATCTTTAA
13290	11377	AATCTATGTAAGAATCTTTA
13291	11378	CAATCTATGTAAGAATCTTT
13292	11379	GCAATCTATGTAAGAATCTT
13293	11380	AGCAATCTATGTAAGAATCT
13294	11381	AAGCAATCTATGTAAGAATC
13295	11382	CAAGCAATCTATGTAAGAAT
13296	11383	ACAAGCAATCTATGTAAGAA
13297	11384	TACAAGCAATCTATGTAAGA
13298	11385	TTACAAGCAATCTATGTAAG
13299	11386	ATTACAAGCAATCTATGTAA
13300	11387	AATTACAAGCAATCTATGTA
13301	11388	AAATTACAAGCAATCTATGT
13302	11389	AAAATTACAAGCAATCTATG
13303	11390	TAAAATTACAAGCAATCTAT
13304	11391	TTAAAATTACAAGCAATCTA
13305	11392	GTTAAAATTACAAGCAATCT
13306	11393	GGTTAAAATTACAAGCAATC
13307	11394	GGGTTAAAATTACAAGCAAT
13308	11395	AGGGTTAAAATTACAAGCAA
13309	11396	CAGGGTTAAAATTACAAGCA
13310	11397	TCAGGGTTAAAATTACAAGC
13311	11398	TTCAGGGTTAAAATTACAAG
13312	11399	CTTCAGGGTTAAAATTACAA
13313	11400	ACTTCAGGGTTAAAATTACA
13314	11401	AACTTCAGGGTTAAAATTAC
13315	11402	CAACTTCAGGGTTAAAATTA
13316	11403	ACAACTTCAGGGTTAAAATT
13317	11404	CACAACTTCAGGGTTAAAAT
13318	11405	ACACAACTTCAGGGTTAAAA
13319	11406	GACACAACTTCAGGGTTAAA
13320	11407	TGACACAACTTCAGGGTTAA
13321	11408	TTGACACAACTTCAGGGTTA
13322	11409	CTTGACACAACTTCAGGGTT
13323	11410	ACTTGACACAACTTCAGGGT
13324	11411	CACTTGACACAACTTCAGGG
13325	11412	TCACTTGACACAACTTCAGG
13326	11413	GTCACTTGACACAACTTCAG
13327	11414	AGTCACTTGACACAACTTCA
13328	11415	AAGTCACTTGACACAACTTC
13329	11416	AAAGTCACTTGACACAACTT
13330	11417	TAAAGTCACTTGACACAACT
13331	11418	GTAAAGTCACTTGACACAAC
13332	11419	TGTAAAGTCACTTGACACAA
13333	11420	TTGTAAAGTCACTTGACACA
13334	11421	ATTGTAAAGTCACTTGACAC
13335	11422	CATTGTAAAGTCACTTGACA
13336	11423	ACATTGTAAAGTCACTTGAC
13337	11424	GACATTGTAAAGTCACTTGA
13338	11425	TGACATTGTAAAGTCACTTG
13339	11426	TTGACATTGTAAAGTCACTT
13340	11427	ATTGACATTGTAAAGTCACT
13341	11428	AATTGACATTGTAAAGTCAC

62418	60505	AGCTAGCTACCTGAAAGAAA
62419	60506	AAGCTAGCTACCTGAAAGAA
62420	60507	AAAGCTAGCTACCTGAAAGA
62421	60508	AAAAGCTAGCTACCTGAAAG
62422	60509	GAAAAGCTAGCTACCTGAAA
62423	60510	GGAAAAGCTAGCTACCTGAA
62424	60511	AGGAAAAGCTAGCTACCTGA
62425	60512	GAGGAAAAGCTAGCTACCTG
62426	60513	GGAGGAAAAGCTAGCTACCT
62427	60514	AGGAGGAAAAGCTAGCTACC
62428	60515	GAGGAGGAAAAGCTAGCTAC
62429	60516	GGAGGAGGAAAAGCTAGCTA
62430	60517	AGGAGGAGGAAAAGCTAGCT
62431	60518	GAGGAGGAGGAAAAGCTAGC
62432	60519	GGAGGAGGAGGAAAAGCTAG
62433	60520	GGGAGGAGGAGGAAAAGCTA
62434	60521	GGGGAGGAGGAGGAAAAGCT
62435	60522	TGGGGAGGAGGAGGAAAAGC
62436	60523	GTGGGGAGGAGGAGGAAAAG
62437	60524	AGTGGGGAGGAGGAGGAAAA
62438	60525	AAGTGGGGAGGAGGAGGAAA
62439	60526	TAAGTGGGGAGGAGGAGGAA
62440	60527	TTAAGTGGGGAGGAGGAGGA
62441	60528	TTTAAGTGGGGAGGAGGAGG
62442	60529	TTTTAAGTGGGGAGGAGGAG
62443	60530	ATTTTAAGTGGGGAGGAGGA
62444	60531	TATTTTAAGTGGGGAGGAGG
62445	60532	CTATTTTAAGTGGGGAGGAG
62446	60533	TCTATTTTAAGTGGGGAGGA
62447	60534	ATCTATTTTAAGTGGGGAGG
62448	60535	GATCTATTTTAAGTGGGGAG
62449	60536	GGATCTATTTTAAGTGGGGA
62450	60537	AGGATCTATTTTAAGTGGGG
62451	60538	CAGGATCTATTTTAAGTGGG
62452	60539	TCAGGATCTATTTTAAGTGG
62453	60540	ATCAGGATCTATTTTAAGTG
62454	60541	GATCAGGATCTATTTTAAGT
62455	60542	GGATCAGGATCTATTTTAAG
62456	60543	TGGATCAGGATCTATTTTAA
62457	60544	CTGGATCAGGATCTATTTTA
62458	60545	TCTGGATCAGGATCTATTTT
62459	60546	TTCTGGATCAGGATCTATTT
62460	60547	CTTCTGGATCAGGATCTATT
62461	60548	GCTTCTGGATCAGGATCTAT
62462	60549	GGCTTCTGGATCAGGATCTA
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62475	60562	ATTTTCTCCATTAGGCTTCT
62476	60563	CATTTTCTCCATTAGGCTTC
62477	60564	TCATTTTCTCCATTAGGCTT
62478	60565	TTCATTTTCTCCATTAGGCT
62479	60566	TTTCATTTTCTCCATTAGGC
62480	60567	TTTTCATTTTCTCCATTAGG
62481	60568	GTTTTCATTTTCTCCATTAG
62482	60569	TGTTTTCATTTTCTCCATTA
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62485	60572	TTCTGTTTTCATTTTCTCCA
62486	60573	ATTCTGTTTTCATTTTCTCC
62487	60574	CATTCTGTTTTCATTTTCTC
62488	60575	ACATTCTGTTTTCATTTTCT

111565	109652	GACCAGACTGGCCAACATGG
111566	109653	AGACCAGACTGGCCAACATG
111567	109654	AAGACCAGACTGGCCAACAT
111568	109655	TAAGACCAGACTGGCCAACA
111569	109656	TTAAGACCAGACTGGCCAAC
111570	109657	TTTAAGACCAGACTGGCCAA
111571	109658	GTTTAAGACCAGACTGGCCA
111572	109659	AGTTTAAGACCAGACTGGCC
111573	109660	GAGTTTAAGACCAGACTGGC
111574	109661	GGAGTTTAAGACCAGACTGG
111575	109662	AGGAGTTTAAGACCAGACTG
111576	109663	CAGGAGTTTAAGACCAGACT
111577	109664	TCAGGAGTTTAAGACCAGAC
111578	109665	GTCAGGAGTTTAAGACCAGA
111579	109666	GGTCAGGAGTTTAAGACCAG
111580	109667	AGGTCAGGAGTTTAAGACCA
111581	109668	GAGGTCAGGAGTTTAAGACC
111582	109669	TGAGGTCAGGAGTTTAAGAC
111583	109670	TTGAGGTCAGGAGTTTAAGA
111584	109671	CTTGAGGTCAGGAGTTTAAG
111585	109672	ACTTGAGGTCAGGAGTTTAA
111586	109673	CACTTGAGGTCAGGAGTTTA
111587	109674	TCACTTGAGGTCAGGAGTTT
111588	109675	ATCACTTGAGGTCAGGAGTT
111589	109676	GATCACTTGAGGTCAGGAGT
111590	109677	GGATCACTTGAGGTCAGGAG
111591	109678	TGGATCACTTGAGGTCAGGA
111592	109679	GTGGATCACTTGAGGTCAGG
111593	109680	GGTGGATCACTTGAGGTCAG
111594	109681	AGGTGGATCACTTGAGGTCA
111595	109682	CAGGTGGATCACTTGAGGTC
111596	109683	GCAGGTGGATCACTTGAGGT
111597	109684	GGCAGGTGGATCACTTGAGG
111598	109685	AGGCAGGTGGATCACTTGAG
111599	109686	AAGGCAGGTGGATCACTTGA
111600	109687	CAAGGCAGGTGGATCACTTG
111601	109688	CCAAGGCAGGTGGATCACTT
111602	109689	GCCAAGGCAGGTGGATCACT
111603	109690	AGCCAAGGCAGGTGGATCAC
111604	109691	AAGCCAAGGCAGGTGGATCA
111605	109692	GAAGCCAAGGCAGGTGGATC
111606	109693	GGAAGCCAAGGCAGGTGGAT
111607	109694	GGGAAGCCAAGGCAGGTGGA
111608	109695	TGGGAAGCCAAGGCAGGTGG
111609	109696	TTGGGAAGCCAAGGCAGGTG
111610	109697	TTTGGGAAGCCAAGGCAGGT
111611	109698	CTTTGGGAAGCCAAGGCAGG
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111616	109703	TAGCACTTTGGGAAGCCAAG
111617	109704	CTAGCACTTTGGGAAGCCAA
111618	109705	CCTAGCACTTTGGGAAGCCA
111619	109706	TCCTAGCACTTTGGGAAGCC
111620	109707	ATCCTAGCACTTTGGGAAGC
111621	109708	CATCCTAGCACTTTGGGAAG
111622	109709	TCATCCTAGCACTTTGGGAA
111623	109710	ATCATCCTAGCACTTTGGGA
111624	109711	TATCATCCTAGCACTTTGGG
111625	109712	CTATCATCCTAGCACTTTGG
111626	109713	CCTATCATCCTAGCACTTTG
111627	109714	ACCTATCATCCTAGCACTTT
111628	109715	CACCTATCATCCTAGCACTT
111629	109716	ACACCTATCATCCTAGCACT
111630	109717	AACACCTATCATCCTAGCAC
111631	109718	TAACACCTATCATCCTAGCA
111632	109719	CTAACACCTATCATCCTAGC
111633	109720	GCTAACACCTATCATCCTAG
111634	109721	GGCTAACACCTATCATCCTA
111635	109722	TGGCTAACACCTATCATCCT

13342	11429	AAATTGACATTGTAAAGTCA
13343	11430	CAAATTGACATTGTAAAGTC
13344	11431	ACAAATTGACATTGTAAAGT
13345	11432	AACAAATTGACATTGTAAAG
13346	11433	AAACAAATTGACATTGTAAA
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13348	11435	TAAAACAAATTGACATTGTA
13349	11436	ATAAAACAAATTGACATTGT
13350	11437	AATAAAACAAATTGACATTG
13351	11438	AAATAAAACAAATTGACATT
13352	11439	TAAATAAAACAAATTGACAT
13353	11440	ATAAATAAAACAAATTGACA
13354	11441	AATAAATAAAACAAATTGAC
13355	11442	AAATAAATAAAACAAATTGA
13356	11443	TAAATAAATAAAACAAATTG
13357	11444	ATAAATAAATAAAACAAATT
13358	11445	AATAAATAAATAAAACAAAT
13359	11446	AAATAAATAAATAAAACAAA
13360	11447	TAAATAAATAAATAAAACAA
13361	11448	ATAAATAAATAAATAAAACA
13362	11449	AATAAATAAATAAATAAAAC
13363	11450	AAATAAATAAATAAATAAAA
13364	11451	TAAATAAATAAATAAATAAA
13365	11452	ATAAATAAATAAATAAATAA
13366	11453	AATAAATAAATAAATAAATA
13367	11454	AAATAAATAAATAAATAAAT
13368	11455	TAAATAAATAAATAAATAAA
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13370	11457	AATAAATAAATAAATAAATA
13371	11458	AAATAAATAAATAAATAAAT
13372	11459	TAAATAAATAAATAAATAAA
13373	11460	ATAAATAAATAAATAAATAA
13374	11461	AATAAATAAATAAATAAATA
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13376	11463	TAAATAAATAAATAAATAAA
13377	11464	ATAAATAAATAAATAAATAA
13378	11465	AATAAATAAATAAATAAATA
13379	11466	AAATAAATAAATAAATAAAT
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13381	11468	AAAAATAAATAAATAAATAA
13382	11469	CAAAAATAAATAAATAAATA
13383	11470	ACAAAAATAAATAAATAAAT
13384	11471	CACAAAAATAAATAAATAAA
13385	11472	TCACAAAAATAAATAAATAA
13386	11473	ATCACAAAAATAAATAAATA
13387	11474	TATCACAAAAATAAATAAAT
13388	11475	CTATCACAAAAATAAATAAA
13389	11476	CCTATCACAAAAATAAATAA
13390	11477	TCCTATCACAAAAATAAATA
13391	11478	ATCCTATCACAAAAATAAAT
13392	11479	GATCCTATCACAAAAATAAA
13393	11480	AGATCCTATCACAAAAATAA
13394	11481	CAGATCCTATCACAAAAATA
13395	11482	CCAGATCCTATCACAAAAAT
13396	11483	GCCAGATCCTATCACAAAAA
13397	11484	AGCCAGATCCTATCACAAAA
13398	11485	GAGCCAGATCCTATCACAAA
13399	11486	AGAGCCAGATCCTATCACAA
13400	11487	CAGAGCCAGATCCTATCACA
13401	11488	ACAGAGCCAGATCCTATCAC
13402	11489	AACAGAGCCAGATCCTATCA
13403	11490	CAACAGAGCCAGATCCTATC
13404	11491	GCAACAGAGCCAGATCCTAT
13405	11492	AGCAACAGAGCCAGATCCTA
13406	11493	TAGCAACAGAGCCAGATCCT
13407	11494	TTAGCAACAGAGCCAGATCC
13408	11495	CTTAGCAACAGAGCCAGATC
13409	11496	CCTTAGCAACAGAGCCAGAT
13410	11497	GCCTTAGCAACAGAGCCAGA
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13412	11499	CAGCCTTAGCAACAGAGCCA

62489	60576	AACATTCTGTTTTCATTTTC
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62491	60578	TGAACATTCTGTTTTCATTT
62492	60579	GTGAACATTCTGTTTTCATT
62493	60580	GGTGAACATTCTGTTTTCAT
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62495	60582	TGGGTGAACATTCTGTTTTC
62496	60583	ATGGGTGAACATTCTGTTTT
62497	60584	TATGGGTGAACATTCTGTTT
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62499	60586	TTTATGGGTGAACATTCTGT
62500	60587	GTTTATGGGTGAACATTCTG
62501	60588	TGTTTATGGGTGAACATTCT
62502	60589	CTGTTTATGGGTGAACATTC
62503	60590	ACTGTTTATGGGTGAACATT
62504	60591	TACTGTTTATGGGTGAACAT
62505	60592	ATACTGTTTATGGGTGAACA
62506	60593	GATACTGTTTATGGGTGAAC
62507	60594	AGATACTGTTTATGGGTGAA
62508	60595	AAGATACTGTTTATGGGTGA
62509	60596	AAAGATACTGTTTATGGGTG
62510	60597	CAAAGATACTGTTTATGGGT
62511	60598	ACAAAGATACTGTTTATGGG
62512	60599	TACAAAGATACTGTTTATGG
62513	60600	ATACAAAGATACTGTTTATG
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62520	60607	GATTCCAATACAAAGATACT
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62524	60611	AAAAGATTCCAATACAAAGA
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62533	60620	AAGTTTTAGAAAAGATTCCA
62534	60621	GAAGTTTTAGAAAAGATTCC
62535	60622	AGAAGTTTTAGAAAAGATTC
62536	60623	AAGAAGTTTTAGAAAAGATT
62537	60624	AAAGAAGTTTTAGAAAAGAT
62538	60625	AAAAGAAGTTTTAGAAAAGA
62539	60626	CAAAAGAAGTTTTAGAAAAG
62540	60627	TCAAAAGAAGTTTTAGAAAA
62541	60628	ATCAAAAGAAGTTTTAGAAA
62542	60629	GATCAAAAGAAGTTTTAGAA
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62554	60641	ATCTCCTAAAAAGATCAAAA
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62556	60643	CTATCTCCTAAAAAGATCAA
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62558	60645	CACTATCTCCTAAAAAGATC
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111637	109724	AGTGGCTAACACCTATCATC
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111639	109726	GCAGTGGCTAACACCTATCA
111640	109727	TGCAGTGGCTAACACCTATC
111641	109728	GTGCAGTGGCTAACACCTAT
111642	109729	CGTGCAGTGGCTAACACCTA
111643	109730	GCGTGCAGTGGCTAACACCT
111644	109731	TGCGTGCAGTGGCTAACACC
111645	109732	CTGCGTGCAGTGGCTAACAC
111646	109733	GCTGCGTGCAGTGGCTAACA
111647	109734	GGCTGCGTGCAGTGGCTAAC
111648	109735	GGGCTGCGTGCAGTGGCTAA
111649	109736	AGGGCTGCGTGCAGTGGCTA
111650	109737	CAGGGCTGCGTGCAGTGGCT
111651	109738	TCAGGGCTGCGTGCAGTGGC
111652	109739	TTCAGGGCTGCGTGCAGTGG
111653	109740	GTTCAGGGCTGCGTGCAGTG
111654	109741	TGTTCAGGGCTGCGTGCAGT
111655	109742	ATGTTCAGGGCTGCGTGCAG
111656	109743	TATGTTCAGGGCTGCGTGCA
111657	109744	CTATGTTCAGGGCTGCGTGC
111658	109745	GCTATGTTCAGGGCTGCGTG
111659	109746	AGCTATGTTCAGGGCTGCGT
111660	109747	AAGCTATGTTCAGGGCTGCG
111661	109748	AAAGCTATGTTCAGGGCTGC
111662	109749	AAAAGCTATGTTCAGGGCTG
111663	109750	TAAAAGCTATGTTCAGGGCT
111664	109751	TTAAAAGCTATGTTCAGGGC
111665	109752	CTTAAAAGCTATGTTCAGGG
111666	109753	ACTTAAAAGCTATGTTCAGG
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111673	109760	TAAAGGAACTTAAAAGCTAT
111674	109761	ATAAAGGAACTTAAAAGCTA
111675	109762	AATAAAGGAACTTAAAAGCT
111676	109763	CAATAAAGGAACTTAAAAGC
111677	109764	ACAATAAAGGAACTTAAAAG
111678	109765	GACAATAAAGGAACTTAAAA
111679	109766	TGACAATAAAGGAACTTAAA
111680	109767	ATGACAATAAAGGAACTTAA
111681	109768	TATGACAATAAAGGAACTTA
111682	109769	ATATGACAATAAAGGAACTT
111683	109770	AATATGACAATAAAGGAACT
111684	109771	GAATATGACAATAAAGGAAC
111685	109772	GGAATATGACAATAAAGGAA
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111687	109774	AAGGAATATGACAATAAAGG
111688	109775	AAAGGAATATGACAATAAAG
111689	109776	AAAAGGAATATGACAATAAA
111690	109777	CAAAAGGAATATGACAATAA
111691	109778	TCAAAAGGAATATGACAATA
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111693	109780	CGTCAAAAGGAATATGACAA
111694	109781	TCGTCAAAAGGAATATGACA
111695	109782	CTCGTCAAAAGGAATATGAC
111696	109783	ACTCGTCAAAAGGAATATGA
111697	109784	GACTCGTCAAAAGGAATATG
111698	109785	AGACTCGTCAAAAGGAATAT
111699	109786	TAGACTCGTCAAAAGGAATA
111700	109787	ATAGACTCGTCAAAAGGAAT
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111702	109789	TGATAGACTCGTCAAAAGGA
111703	109790	ATGATAGACTCGTCAAAAGG
111704	109791	AATGATAGACTCGTCAAAAG
111705	109792	AAATGATAGACTCGTCAAAA
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13413	11500	CCAGCCTTAGCAACAGAGCC
13414	11501	TCCAGCCTTAGCAACAGAGC
13415	11502	CTCCAGCCTTAGCAACAGAG
13416	11503	ACTCCAGCCTTAGCAACAGA
13417	11504	CACTCCAGCCTTAGCAACAG
13418	11505	GCACTCCAGCCTTAGCAACA
13419	11506	TGCACTCCAGCCTTAGCAAC
13420	11507	CTGCACTCCAGCCTTAGCAA
13421	11508	ACTGCACTCCAGCCTTAGCA
13422	11509	CACTGCACTCCAGCCTTAGC
13423	11510	ACACTGCACTCCAGCCTTAG
13424	11511	AACACTGCACTCCAGCCTTA
13425	11512	CAACACTGCACTCCAGCCTT
13426	11513	GCAACACTGCACTCCAGCCT
13427	11514	TGCAACACTGCACTCCAGCC
13428	11515	TTGCAACACTGCACTCCAGC
13429	11516	TTTGCAACACTGCACTCCAG
13430	11517	ATTTGCAACACTGCACTCCA
13431	11518	TATTTGCAACACTGCACTCC
13432	11519	GTATTTGCAACACTGCACTC
13433	11520	CGTATTTGCAACACTGCACT
13434	11521	CCGTATTTGCAACACTGCAC
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13438	11525	TGAGCCGTATTTGCAACACT
13439	11526	GTGAGCCGTATTTGCAACAC
13440	11527	AGTGAGCCGTATTTGCAACA
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13442	11529	GCAGTGAGCCGTATTTGCAA
13443	11530	TGCAGTGAGCCGTATTTGCA
13444	11531	TTGCAGTGAGCCGTATTTGC
13445	11532	GTTGCAGTGAGCCGTATTTG
13446	11533	GGTTGCAGTGAGCCGTATTT
13447	11534	AGGTTGCAGTGAGCCGTATT
13448	11535	GAGGTTGCAGTGAGCCGTAT
13449	11536	AGAGGTTGCAGTGAGCCGTA
13450	11537	CAGAGGTTGCAGTGAGCCGT
13451	11538	ACAGAGGTTGCAGTGAGCCG
13452	11539	GACAGAGGTTGCAGTGAGCC
13453	11540	AGACAGAGGTTGCAGTGAGC
13454	11541	GAGACAGAGGTTGCAGTGAG
13455	11542	GGAGACAGAGGTTGCAGTGA
13456	11543	GGGAGACAGAGGTTGCAGTG
13457	11544	CGGGAGACAGAGGTTGCAGT
13458	11545	CCGGGAGACAGAGGTTGCAG
13459	11546	CCCGGGAGACAGAGGTTGCA
13460	11547	ACCCGGGAGACAGAGGTTGC
13461	11548	AACCCGGGAGACAGAGGTTG
13462	11549	GAACCCGGGAGACAGAGGTT
13463	11550	TGAACCCGGGAGACAGAGGT
13464	11551	TTGAACCCGGGAGACAGAGG
13465	11552	CTTGAACCCGGGAGACAGAG
13466	11553	GCTTGAACCCGGGAGACAGA
13467	11554	GGCTTGAACCCGGGAGACAG
13468	11555	TGGCTTGAACCCGGGAGACA
13469	11556	ATGGCTTGAACCCGGGAGAC
13470	11557	GATGGCTTGAACCCGGGAGA
13471	11558	GGATGGCTTGAACCCGGGAG
13472	11559	AGGATGGCTTGAACCCGGGA
13473	11560	GAGGATGGCTTGAACCCGGG
13474	11561	GGAGGATGGCTTGAACCCGG
13475	11562	GGGAGGATGGCTTGAACCCG
13476	11563	TGGGAGGATGGCTTGAACCC
13477	11564	GTGGGAGGATGGCTTGAACC
13478	11565	GGTGGGAGGATGGCTTGAAC
13479	11566	AGGTGGGAGGATGGCTTGAA
13480	11567	GAGGTGGGAGGATGGCTTGA
13481	11568	TGAGGTGGGAGGATGGCTTG
13482	11569	CTGAGGTGGGAGGATGGCTT
13483	11570	GCTGAGGTGGGAGGATGGCT

62560	60647	CACACTATCTCCTAAAAAGA
62561	60648	CCACACTATCTCCTAAAAAG
62562	60649	CCCACACTATCTCCTAAAAA
62563	60650	TCCCACACTATCTCCTAAAA
62564	60651	TTCCCACACTATCTCCTAAA
62565	60652	ATTCCCACACTATCTCCTAA
62566	60653	GATTCCCACACTATCTCCTA
62567	60654	TGATTCCCACACTATCTCCT
62568	60655	CTGATTCCCACACTATCTCC
62569	60656	GCTGATTCCCACACTATCTC
62570	60657	TGCTGATTCCCACACTATCT
62571	60658	TTGCTGATTCCCACACTATC
62572	60659	ATTGCTGATTCCCACACTAT
62573	60660	GATTGCTGATTCCCACACTA
62574	60661	AGATTGCTGATTCCCACACT
62575	60662	TAGATTGCTGATTCCCACAC
62576	60663	CTAGATTGCTGATTCCCACA
62577	60664	ACTAGATTGCTGATTCCCAC
62578	60665	TACTAGATTGCTGATTCCCA
62579	60666	ATACTAGATTGCTGATTCCC
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62581	60668	TAATACTAGATTGCTGATTC
62582	60669	GTAATACTAGATTGCTGATT
62583	60670	CGTAATACTAGATTGCTGAT
62584	60671	ACGTAATACTAGATTGCTGA
62585	60672	TACGTAATACTAGATTGCTG
62586	60673	GTACGTAATACTAGATTGCT
62587	60674	CGTACGTAATACTAGATTGC
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62589	60676	CACGTACGTAATACTAGATT
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62593	60680	ATTCCACGTACGTAATACTA
62594	60681	GATTCCACGTACGTAATACT
62595	60682	AGATTCCACGTACGTAATAC
62596	60683	CAGATTCCACGTACGTAATA
62597	60684	ACAGATTCCACGTACGTAAT
62598	60685	GACAGATTCCACGTACGTAA
62599	60686	TGACAGATTCCACGTACGTA
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62601	60688	GGTGACAGATTCCACGTACG
62602	60689	AGGTGACAGATTCCACGTAC
62603	60690	AAGGTGACAGATTCCACGTA
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62606	60693	AACAAGGTGACAGATTCCAC
62607	60694	AAACAAGGTGACAGATTCCA
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62609	60696	AAAAACAAGGTGACAGATTC
62610	60697	AAAAAACAAGGTGACAGATT
62611	60698	AAAAAAACAAGGTGACAGAT
62612	60699	TAAAAAAACAAGGTGACAGA
62613	60700	TTAAAAAAACAAGGTGACAG
62614	60701	TTTAAAAAAACAAGGTGACA
62615	60702	ATTTAAAAAAACAAGGTGAC
62616	60703	TATTTAAAAAAACAAGGTGA
62617	60704	GTATTTAAAAAAACAAGGTG
62618	60705	TGTATTTAAAAAAACAAGGT
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62626	60713	AGGTTTGCTGTATTTAAAAA
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111707	109794	GAAAATGATAGACTCGTCAA
111708	109795	AGAAAATGATAGACTCGTCA
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111710	109797	TCAGAAAATGATAGACTCGT
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111714	109801	TGAGTCAGAAAATGATAGAC
111715	109802	GTGAGTCAGAAAATGATAGA
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111717	109804	AAGTGAGTCAGAAAATGATA
111718	109805	CAAGTGAGTCAGAAAATGAT
111719	109806	ACAAGTGAGTCAGAAAATGA
111720	109807	TACAAGTGAGTCAGAAAATG
111721	109808	GTACAAGTGAGTCAGAAAAT
111722	109809	TGTACAAGTGAGTCAGAAAA
111723	109810	ATGTACAAGTGAGTCAGAAA
111724	109811	CATGTACAAGTGAGTCAGAA
111725	109812	ACATGTACAAGTGAGTCAGA
111726	109813	CACATGTACAAGTGAGTCAG
111727	109814	ACACATGTACAAGTGAGTCA
111728	109815	CACACATGTACAAGTGAGTC
111729	109816	ACACACATGTACAAGTGAGT
111730	109817	GACACACATGTACAAGTGAG
111731	109818	AGACACACATGTACAAGTGA
111732	109819	GAGACACACATGTACAAGTG
111733	109820	TGAGACACACATGTACAAGT
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111735	109822	GGTGAGACACACATGTACAA
111736	109823	GGGTGAGACACACATGTACA
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111738	109825	AAGGGTGAGACACACATGTA
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111741	109828	ACCAAGGGTGAGACACACAT
111742	109829	GACCAAGGGTGAGACACACA
111743	109830	GGACCAAGGGTGAGACACAC
111744	109831	TGGACCAAGGGTGAGACACA
111745	109832	CTGGACCAAGGGTGAGACAC
111746	109833	GCTGGACCAAGGGTGAGACA
111747	109834	GGCTGGACCAAGGGTGAGAC
111748	109835	TGGCTGGACCAAGGGTGAGA
111749	109836	ATGGCTGGACCAAGGGTGAG
111750	109837	AATGGCTGGACCAAGGGTGA
111751	109838	CAATGGCTGGACCAAGGGTG
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111754	109841	CACCAATGGCTGGACCAAGG
111755	109842	GCACCAATGGCTGGACCAAG
111756	109843	AGCACCAATGGCTGGACCAA
111757	109844	AAGCACCAATGGCTGGACCA
111758	109845	AAAGCACCAATGGCTGGACC
111759	109846	AAAAGCACCAATGGCTGGAC
111760	109847	GAAAAGCACCAATGGCTGGA
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111762	109849	AAGAAAAGCACCAATGGCTG
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111764	109851	TAAAGAAAAGCACCAATGGC
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111770	109857	AAGAAGTAAAGAAAAGCACC
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111773	109860	ATAAAGAAGTAAAGAAAAGC
111774	109861	AATAAAGAAGTAAAGAAAAG
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13484	11571	GGCTGAGGTGGGAGGATGGC
13485	11572	AGGCTGAGGTGGGAGGATGG
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13487	11574	GGAGGCTGAGGTGGGAGGAT
13488	11575	GGGAGGCTGAGGTGGGAGGA
13489	11576	TGGGAGGCTGAGGTGGGAGG
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13491	11578	CTTGGGAGGCTGAGGTGGGA
13492	11579	ACTTGGGAGGCTGAGGTGGG
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13500	11587	TTCCAACTACTTGGGAGGCT
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13511	11598	CGCACCAGTAGTTCCAACTA
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13513	11600	GGCGCACCAGTAGTTCCAAC
13514	11601	GGGCGCACCAGTAGTTCCAA
13515	11602	GGGGCGCACCAGTAGTTCCA
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13517	11604	GTGGGGCGCACCAGTAGTTC
13518	11605	TGTGGGGCGCACCAGTAGTT
13519	11606	CTGTGGGGCGCACCAGTAGT
13520	11607	ACTGTGGGGCGCACCAGTAG
13521	11608	CACTGTGGGGCGCACCAGTA
13522	11609	GCACTGTGGGGCGCACCAGT
13523	11610	GGCACTGTGGGGCGCACCAG
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13525	11612	CAGGCACTGTGGGGCGCACC
13526	11613	GCAGGCACTGTGGGGCGCAC
13527	11614	GGCAGGCACTGTGGGGCGCA
13528	11615	AGGCAGGCACTGTGGGGCGC
13529	11616	TAGGCAGGCACTGTGGGGCG
13530	11617	CTAGGCAGGCACTGTGGGGC
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13532	11619	AACTAGGCAGGCACTGTGGG
13533	11620	AAACTAGGCAGGCACTGTGG
13534	11621	AAAACTAGGCAGGCACTGTG
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13537	11624	AAAAAAACTAGGCAGGCACT
13538	11625	CAAAAAAACTAGGCAGGCAC
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13549	11636	TACTGAAAATACAAAAAAAC
13550	11637	CTACTGAAAATACAAAAAAA
13551	11638	TCTACTGAAAATACAAAAAA
13552	11639	ATCTACTGAAAATACAAAAA
13553	11640	CATCTACTGAAAATACAAAA
13554	11641	ACATCTACTGAAAATACAAA

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62632	60719	TTCATGAGGTTTGCTGTATT
62633	60720	CTTCATGAGGTTTGCTGTAT
62634	60721	ACTTCATGAGGTTTGCTGTA
62635	60722	CACTTCATGAGGTTTGCTGT
62636	60723	TCACTTCATGAGGTTTGCTG
62637	60724	TTCACTTCATGAGGTTTGCT
62638	60725	ATTCACTTCATGAGGTTTGC
62639	60726	AATTCACTTCATGAGGTTTG
62640	60727	AAATTCACTTCATGAGGTTT
62641	60728	GAAATTCACTTCATGAGGTT
62642	60729	GGAAATTCACTTCATGAGGT
62643	60730	TGGAAATTCACTTCATGAGG
62644	60731	ATGGAAATTCACTTCATGAG
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62648	60735	AAATATGGAAATTCACTTCA
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62654	60741	AAGAAAAAATATGGAAATTC
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62679	60766	TGAGTGGTGCAAAACTAACA
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62681	60768	CCTGAGTGGTGCAAAACTAA
62682	60769	GCCTGAGTGGTGCAAAACTA
62683	60770	AGCCTGAGTGGTGCAAAACT
62684	60771	AAGCCTGAGTGGTGCAAAAC
62685	60772	AAAGCCTGAGTGGTGCAAAA
62686	60773	CAAAGCCTGAGTGGTGCAAA
62687	60774	GCAAAGCCTGAGTGGTGCAA
62688	60775	AGCAAAGCCTGAGTGGTGCA
62689	60776	CAGCAAAGCCTGAGTGGTGC
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62692	60779	CTACAGCAAAGCCTGAGTGG
62693	60780	TCTACAGCAAAGCCTGAGTG
62694	60781	TTCTACAGCAAAGCCTGAGT
62695	60782	ATTCTACAGCAAAGCCTGAG
62696	60783	AATTCTACAGCAAAGCCTGA
62697	60784	AAATTCTACAGCAAAGCCTG
62698	60785	CAAATTCTACAGCAAAGCCT
62699	60786	TCAAATTCTACAGCAAAGCC
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62701	60788	CATCAAATTCTACAGCAAAG

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111794	109881	AAATAAAATAAAATAACAAA
111795	109882	AAAATAAAATAAAATAACAA
111796	109883	TAAAATAAAATAAAATAACA
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111798	109885	AATAAAATAAAATAAAATAA
111799	109886	TAATAAAATAAAATAAAATA
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111801	109888	AATAATAAAATAAAATAAAA
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111807	109894	AAAAATAATAATAAAATAAA
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111823	109910	TACCCTGTCTCATTTAAAAA
111824	109911	ATACCCTGTCTCATTTAAAA
111825	109912	GATACCCTGTCTCATTTAAA
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111827	109914	GTGATACCCTGTCTCATTTA
111828	109915	AGTGATACCCTGTCTCATTT
111829	109916	TAGTGATACCCTGTCTCATT
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111831	109918	CATAGTGATACCCTGTCTCA
111832	109919	ACATAGTGATACCCTGTCTC
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111835	109922	GCAACATAGTGATACCCTGT
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111837	109924	GGGCAACATAGTGATACCCT
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111839	109926	CTGGGCAACATAGTGATACC
111840	109927	CCTGGGCAACATAGTGATAC
111841	109928	GCCTGGGCAACATAGTGATA
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111844	109931	CCAGCCTGGGCAACATAGTG
111845	109932	ACCAGCCTGGGCAACATAGT
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13555	11642	CACATCTACTGAAAATACAA
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13618	11705	TAGGAGGCCTAAGTGGGGTG
13619	11706	TTAGGAGGCCTAAGTGGGGT
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62712	60799	AATCAAATATACATCAAATT
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62724	60811	CATGCTCTACAGAATCAAAT
62725	60812	CCATGCTCTACAGAATCAAA
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62738	60825	GAAGATCAATAGCCCATGCT
62739	60826	TGAAGATCAATAGCCCATGC
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62741	60828	AGTGAAGATCAATAGCCCAT
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62750	60837	TGAAAGCTGAGTGAAGATCA
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62757	60844	ATTCCTCTGAAAGCTGAGTG
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111856	109943	AGGAGTTCAAGACCAGCCTG
111857	109944	CAGGAGTTCAAGACCAGCCT
111858	109945	TCAGGAGTTCAAGACCAGCC
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111860	109947	GCTCAGGAGTTCAAGACCAG
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111917	110004	GTAGCTCATCACTGTAATTC
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13626	11713	CAGCATGTTAGGAGGCCTAA
13627	11714	CCAGCATGTTAGGAGGCCTA
13628	11715	ACCAGCATGTTAGGAGGCCT
13629	11716	CACCAGCATGTTAGGAGGCC
13630	11717	ACACCAGCATGTTAGGAGGC
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13632	11719	TAACACCAGCATGTTAGGAG
13633	11720	GTAACACCAGCATGTTAGGA
13634	11721	TGTAACACCAGCATGTTAGG
13635	11722	CTGTAACACCAGCATGTTAG
13636	11723	CCTGTAACACCAGCATGTTA
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13638	11725	CACCTGTAACACCAGCATGT
13639	11726	ACACCTGTAACACCAGCATG
13640	11727	CACACCTGTAACACCAGCAT
13641	11728	TCACACCTGTAACACCAGCA
13642	11729	CTCACACCTGTAACACCAGC
13643	11730	GCTCACACCTGTAACACCAG
13644	11731	GGCTCACACCTGTAACACCA
13645	11732	TGGCTCACACCTGTAACACC
13646	11733	GTGGCTCACACCTGTAACAC
13647	11734	AGTGGCTCACACCTGTAACA
13648	11735	CAGTGGCTCACACCTGTAAC
13649	11736	ACAGTGGCTCACACCTGTAA
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13654	11741	TGGACACAGTGGCTCACACC
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13656	11743	GCTGGACACAGTGGCTCACA
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13670	11757	ACTGACATTTTCGGGCTGGA
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13673	11760	GAAACTGACATTTTCGGGCT
13674	11761	CGAAACTGACATTTTCGGGC
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13678	11765	GGCACGAAACTGACATTTTC
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13684	11771	AATCATGGCACGAAACTGAC
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13688	11775	TATTAATCATGGCACGAAAC
13689	11776	CTATTAATCATGGCACGAAA
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62773	60860	CAAACTTACTAATCAGATTC
62774	60861	TCAAACTTACTAATCAGATT
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62776	60863	ACTCAAACTTACTAATCAGA
62777	60864	AACTCAAACTTACTAATCAG
62778	60865	AAACTCAAACTTACTAATCA
62779	60866	AAAACTCAAACTTACTAATC
62780	60867	AAAAACTCAAACTTACTAAT
62781	60868	AAAAAACTCAAACTTACTAA
62782	60869	TAAAAAACTCAAACTTACTA
62783	60870	ATAAAAAACTCAAACTTACT
62784	60871	AATAAAAAACTCAAACTTAC
62785	60872	TAATAAAAAACTCAAACTTA
62786	60873	ATAATAAAAAACTCAAACTT
62787	60874	AATAATAAAAAACTCAAACT
62788	60875	AAATAATAAAAAACTCAAAC
62789	60876	AAAATAATAAAAAACTCAAA
62790	60877	AAAAATAATAAAAAACTCAA
62791	60878	AAAAAATAATAAAAAACTCA
62792	60879	TAAAAAATAATAAAAAACTC
62793	60880	CTAAAAAATAATAAAAAACT
62794	60881	ACTAAAAAATAATAAAAAAC
62795	60882	AACTAAAAAATAATAAAAAA
62796	60883	CAACTAAAAAATAATAAAAA
62797	60884	TCAACTAAAAAATAATAAAA
62798	60885	ATCAACTAAAAAATAATAAA
62799	60886	AATCAACTAAAAAATAATAA
62800	60887	AAATCAACTAAAAAATAATA
62801	60888	AAAATCAACTAAAAAATAAT
62802	60889	CAAAATCAACTAAAAAATAA
62803	60890	TCAAAATCAACTAAAAAATA
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62805	60892	CTTCAAAATCAACTAAAAAA
62806	60893	ACTTCAAAATCAACTAAAAA
62807	60894	TACTTCAAAATCAACTAAAA
62808	60895	TTACTTCAAAATCAACTAAA
62809	60896	TTTACTTCAAAATCAACTAA
62810	60897	TTTTACTTCAAAATCAACTA
62811	60898	ATTTTACTTCAAAATCAACT
62812	60899	TATTTTACTTCAAAATCAAC
62813	60900	GTATTTTACTTCAAAATCAA
62814	60901	TGTATTTTACTTCAAAATCA
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62816	60903	GCTGTATTTTACTTCAAAAT
62817	60904	TGCTGTATTTTACTTCAAAA
62818	60905	GTGCTGTATTTTACTTCAAA
62819	60906	GGTGCTGTATTTTACTTCAA
62820	60907	TGGTGCTGTATTTTACTTCA
62821	60908	ATGGTGCTGTATTTTACTTC
62822	60909	AATGGTGCTGTATTTTACTT
62823	60910	AAATGGTGCTGTATTTTACT
62824	60911	AAAATGGTGCTGTATTTTAC
62825	60912	TAAAATGGTGCTGTATTTTA
62826	60913	TTAAAATGGTGCTGTATTTT
62827	60914	GTTAAAATGGTGCTGTATTT
62828	60915	AGTTAAAATGGTGCTGTATT
62829	60916	CAGTTAAAATGGTGCTGTAT
62830	60917	TCAGTTAAAATGGTGCTGTA
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62833	60920	GTATCAGTTAAAATGGTGCT
62834	60921	GGTATCAGTTAAAATGGTGC
62835	60922	TGGTATCAGTTAAAATGGTG
62836	60923	ATGGTATCAGTTAAAATGGT
62837	60924	AATGGTATCAGTTAAAATGG
62838	60925	AAATGGTATCAGTTAAAATG
62839	60926	GAAATGGTATCAGTTAAAAT
62840	60927	AGAAATGGTATCAGTTAAAA
62841	60928	TAGAAATGGTATCAGTTAAA
62842	60929	TTAGAAATGGTATCAGTTAA
62843	60930	TTTAGAAATGGTATCAGTTA

111920	110007	ACAGTAGCTCATCACTGTAA
111921	110008	CACAGTAGCTCATCACTGTA
111922	110009	GCACAGTAGCTCATCACTGT
111923	110010	GGCACAGTAGCTCATCACTG
111924	110011	GGGCACAGTAGCTCATCACT
111925	110012	TGGGCACAGTAGCTCATCAC
111926	110013	CTGGGCACAGTAGCTCATCA
111927	110014	GCTGGGCACAGTAGCTCATC
111928	110015	AGCTGGGCACAGTAGCTCAT
111929	110016	GAGCTGGGCACAGTAGCTCA
111930	110017	TGAGCTGGGCACAGTAGCTC
111931	110018	ATGAGCTGGGCACAGTAGCT
111932	110019	AATGAGCTGGGCACAGTAGC
111933	110020	CAATGAGCTGGGCACAGTAG
111934	110021	CCAATGAGCTGGGCACAGTA
111935	110022	ACCAATGAGCTGGGCACAGT
111936	110023	CACCAATGAGCTGGGCACAG
111937	110024	GCACCAATGAGCTGGGCACA
111938	110025	AGCACCAATGAGCTGGGCAC
111939	110026	TAGCACCAATGAGCTGGGCA
111940	110027	ATAGCACCAATGAGCTGGGC
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111942	110029	AGATAGCACCAATGAGCTGG
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111944	110031	AAAGATAGCACCAATGAGCT
111945	110032	AAAAGATAGCACCAATGAGC
111946	110033	AAAAAGATAGCACCAATGAG
111947	110034	AAAAAAGATAGCACCAATGA
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111949	110036	AAAAAAAAGATAGCACCAAT
111950	110037	AAAAAAAAAGATAGCACCAA
111951	110038	AAAAAAAAAAGATAGCACCA
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111955	110042	AAAAAAAAAAAAAAGATAGC
111956	110043	AAAAAAAAAAAAAAAGATAG
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111969	110056	GAGACTCCGTCTCAAAAAAA
111970	110057	CGAGACTCCGTCTCAAAAAA
111971	110058	GCGAGACTCCGTCTCAAAAA
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111973	110060	GAGCGAGACTCCGTCTCAAA
111974	110061	AGAGCGAGACTCCGTCTCAA
111975	110062	CAGAGCGAGACTCCGTCTCA
111976	110063	ACAGAGCGAGACTCCGTCTC
111977	110064	GACAGAGCGAGACTCCGTCT
111978	110065	TGACAGAGCGAGACTCCGTC
111979	110066	GTGACAGAGCGAGACTCCGT
111980	110067	GGTGACAGAGCGAGACTCCG
111981	110068	GGGTGACAGAGCGAGACTCC
111982	110069	TGGGTGACAGAGCGAGACTC
111983	110070	CTGGGTGACAGAGCGAGACT
111984	110071	CCTGGGTGACAGAGCGAGAC
111985	110072	GCCTGGGTGACAGAGCGAGA
111986	110073	AGCCTGGGTGACAGAGCGAG
111987	110074	CAGCCTGGGTGACAGAGCGA
111988	110075	CCAGCCTGGGTGACAGAGCG
111989	110076	TCCAGCCTGGGTGACAGAGC
111990	110077	CTCCAGCCTGGGTGACAGAG

13697	11784	GTAGTTAGCTATTAATCATG
13698	11785	TGTAGTTAGCTATTAATCAT
13699	11786	ATGTAGTTAGCTATTAATCA
13700	11787	AATGTAGTTAGCTATTAATC
13701	11788	AAATGTAGTTAGCTATTAAT
13702	11789	AAAATGTAGTTAGCTATTAA
13703	11790	CAAAATGTAGTTAGCTATTA
13704	11791	CCAAAATGTAGTTAGCTATT
13705	11792	CCCAAAATGTAGTTAGCTAT
13706	11793	TCCCAAAATGTAGTTAGCTA
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13708	11795	ATTCCCAAAATGTAGTTAGC
13709	11796	CATTCCCAAAATGTAGTTAG
13710	11797	ACATTCCCAAAATGTAGTTA
13711	11798	TACATTCCCAAAATGTAGTT
13712	11799	TTACATTCCCAAAATGTAGT
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13715	11802	TTATTACATTCCCAAAATGT
13716	11803	TTTATTACATTCCCAAAATG
13717	11804	TTTTATTACATTCCCAAAAT
13718	11805	ATTTTATTACATTCCCAAAA
13719	11806	AATTTTATTACATTCCCAAA
13720	11807	AAATTTTATTACATTCCCAA
13721	11808	GAAATTTTATTACATTCCCA
13722	11809	TGAAATTTTATTACATTCCC
13723	11810	ATGAAATTTTATTACATTCC
13724	11811	AATGAAATTTTATTACATTC
13725	11812	GAATGAAATTTTATTACATT
13726	11813	AGAATGAAATTTTATTACAT
13727	11814	TAGAATGAAATTTTATTACA
13728	11815	ATAGAATGAAATTTTATTAC
13729	11816	TATAGAATGAAATTTTATTA
13730	11817	TTATAGAATGAAATTTTATT
13731	11818	ATTATAGAATGAAATTTTAT
13732	11819	CATTATAGAATGAAATTTTA
13733	11820	TCATTATAGAATGAAATTTT
13734	11821	TTCATTATAGAATGAAATTT
13735	11822	CTTCATTATAGAATGAAATT
13736	11823	ACTTCATTATAGAATGAAAT
13737	11824	GACTTCATTATAGAATGAAA
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13741	11828	CAAAGACTTCATTATAGAAT
13742	11829	ACAAAGACTTCATTATAGAA
13743	11830	TACAAAGACTTCATTATAGA
13744	11831	TTACAAAGACTTCATTATAG
13745	11832	TTTACAAAGACTTCATTATA
13746	11833	TTTTACAAAGACTTCATTAT
13747	11834	GTTTTACAAAGACTTCATTA
13748	11835	AGTTTTACAAAGACTTCATT
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13750	11837	TGAGTTTTACAAAGACTTCA
13751	11838	ATGAGTTTTACAAAGACTTC
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13754	11841	CTAATGAGTTTTACAAAGAC
13755	11842	ACTAATGAGTTTTACAAAGA
13756	11843	AACTAATGAGTTTTACAAAG
13757	11844	CAACTAATGAGTTTTACAAA
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13759	11846	CACAACTAATGAGTTTTACA
13760	11847	CCACAACTAATGAGTTTTAC
13761	11848	ACCACAACTAATGAGTTTTA
13762	11849	TACCACAACTAATGAGTTTT
13763	11850	ATACCACAACTAATGAGTTT
13764	11851	CATACCACAACTAATGAGTT
13765	11852	TCATACCACAACTAATGAGT
13766	11853	CTCATACCACAACTAATGAG
13767	11854	CCTCATACCACAACTAATGA

62844	60931	GTTTAGAAATGGTATCAGTT
62845	60932	TGTTTAGAAATGGTATCAGT
62846	60933	TTGTTTAGAAATGGTATCAG
62847	60934	ATTGTTTAGAAATGGTATCA
62848	60935	AATTGTTTAGAAATGGTATC
62849	60936	AAATTGTTTAGAAATGGTAT
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62858	60945	TTGAACTGAAAATTGTTTAG
62859	60946	TTTGAACTGAAAATTGTTTA
62860	60947	ATTTGAACTGAAAATTGTTT
62861	60948	AATTTGAACTGAAAATTGTT
62862	60949	AAATTTGAACTGAAAATTGT
62863	60950	AAAATTTGAACTGAAAATTG
62864	60951	TAAAATTTGAACTGAAAATT
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62868	60955	AACTTAAAATTTGAACTGAA
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62871	60958	GCTAACTTAAAATTTGAACT
62872	60959	AGCTAACTTAAAATTTGAAC
62873	60960	TAGCTAACTTAAAATTTGAA
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62875	60962	ATTAGCTAACTTAAAATTTG
62876	60963	AATTAGCTAACTTAAAATTT
62877	60964	AAATTAGCTAACTTAAAATT
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62884	60971	AAGCTCTAAATTAGCTAACT
62885	60972	TAAGCTCTAAATTAGCTAAC
62886	60973	TTAAGCTCTAAATTAGCTAA
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62889	60976	TTCTTAAGCTCTAAATTAGC
62890	60977	TTTCTTAAGCTCTAAATTAG
62891	60978	TTTTCTTAAGCTCTAAATTA
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62894	60981	CAATTTTCTTAAGCTCTAAA
62895	60982	GCAATTTTCTTAAGCTCTAA
62896	60983	AGCAATTTTCTTAAGCTCTA
62897	60984	AAGCAATTTTCTTAAGCTCT
62898	60985	AAAGCAATTTTCTTAAGCTC
62899	60986	TAAAGCAATTTTCTTAAGCT
62900	60987	TTAAAGCAATTTTCTTAAGC
62901	60988	TTTAAAGCAATTTTCTTAAG
62902	60989	TTTTAAAGCAATTTTCTTAA
62903	60990	TTTTTAAAGCAATTTTCTTA
62904	60991	GTTTTTAAAGCAATTTTCTT
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62906	60993	ATGTTTTTAAAGCAATTTTC
62907	60994	TATGTTTTTAAAGCAATTTT
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62909	60996	TTTATGTTTTTAAAGCAATT
62910	60997	TTTTATGTTTTTAAAGCAAT
62911	60998	ATTTTATGTTTTTAAAGCAA
62912	60999	AATTTTATGTTTTTAAAGCA
62913	61000	TAATTTTATGTTTTTAAAGC
62914	61001	GTAATTTTATGTTTTTAAAG

111991	110078	ACTCCAGCCTGGGTGACAGA
111992	110079	CACTCCAGCCTGGGTGACAG
111993	110080	GCACTCCAGCCTGGGTGACA
111994	110081	TGCACTCCAGCCTGGGTGAC
111995	110082	CTGCACTCCAGCCTGGGTGA
111996	110083	ACTGCACTCCAGCCTGGGTG
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111998	110085	CCACTGCACTCCAGCCTGGG
111999	110086	GCCACTGCACTCCAGCCTGG
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112001	110088	ACGCCACTGCACTCCAGCCT
112002	110089	CACGCCACTGCACTCCAGCC
112003	110090	TCACGCCACTGCACTCCAGC
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112005	110092	GATCACGCCACTGCACTCCA
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112007	110094	AAGATCACGCCACTGCACTC
112008	110095	CAAGATCACGCCACTGCACT
112009	110096	CCAAGATCACGCCACTGCAC
112010	110097	GCCAAGATCACGCCACTGCA
112011	110098	AGCCAAGATCACGCCACTGC
112012	110099	GAGCCAAGATCACGCCACTG
112013	110100	TGAGCCAAGATCACGCCACT
112014	110101	GTGAGCCAAGATCACGCCAC
112015	110102	AGTGAGCCAAGATCACGCCA
112016	110103	CAGTGAGCCAAGATCACGCC
112017	110104	GCAGTGAGCCAAGATCACGC
112018	110105	TGCAGTGAGCCAAGATCACG
112019	110106	CTGCAGTGAGCCAAGATCAC
112020	110107	GCTGCAGTGAGCCAAGATCA
112021	110108	AGCTGCAGTGAGCCAAGATC
112022	110109	GAGCTGCAGTGAGCCAAGAT
112023	110110	GGAGCTGCAGTGAGCCAAGA
112024	110111	TGGAGCTGCAGTGAGCCAAG
112025	110112	GTGGAGCTGCAGTGAGCCAA
112026	110113	AGTGGAGCTGCAGTGAGCCA
112027	110114	AAGTGGAGCTGCAGTGAGCC
112028	110115	GAAGTGGAGCTGCAGTGAGC
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112030	110117	GGGAAGTGGAGCTGCAGTGA
112031	110118	TGGGAAGTGGAGCTGCAGTG
112032	110119	CTGGGAAGTGGAGCTGCAGT
112033	110120	CCTGGGAAGTGGAGCTGCAG
112034	110121	ACCTGGGAAGTGGAGCTGCA
112035	110122	AACCTGGGAAGTGGAGCTGC
112036	110123	GAACCTGGGAAGTGGAGCTG
112037	110124	TGAACCTGGGAAGTGGAGCT
112038	110125	GTGAACCTGGGAAGTGGAGC
112039	110126	TGTGAACCTGGGAAGTGGAG
112040	110127	GTGTGAACCTGGGAAGTGGA
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112043	110130	ATGGTGTGAACCTGGGAAGT
112044	110131	AATGGTGTGAACCTGGGAAG
112045	110132	GAATGGTGTGAACCTGGGAA
112046	110133	AGAATGGTGTGAACCTGGGA
112047	110134	GAGAATGGTGTGAACCTGGG
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112050	110137	TAGGAGAATGGTGTGAACCT
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112055	110142	TGAGGTAGGAGAATGGTGTG
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13768	11855	GCCTCATACCACAACTAATG
13769	11856	AGCCTCATACCACAACTAAT
13770	11857	AAGCCTCATACCACAACTAA
13771	11858	CAAGCCTCATACCACAACTA
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13774	11861	CGACAAGCCTCATACCACAA
13775	11862	CCGACAAGCCTCATACCACA
13776	11863	GCCGACAAGCCTCATACCAC
13777	11864	TGCCGACAAGCCTCATACCA
13778	11865	TTGCCGACAAGCCTCATACC
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13780	11867	TATTGCCGACAAGCCTCATA
13781	11868	ATATTGCCGACAAGCCTCAT
13782	11869	TATATTGCCGACAAGCCTCA
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13784	11871	CTTATATTGCCGACAAGCCT
13785	11872	ACTTATATTGCCGACAAGCC
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13789	11876	GTTCACTTATATTGCCGACA
13790	11877	CGTTCACTTATATTGCCGAC
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13792	11879	CACGTTCACTTATATTGCCG
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13794	11881	ACCACGTTCACTTATATTGC
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13797	11884	TAAACCACGTTCACTTATAT
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13811	11898	ACAGTTAATAAAAATAAACC
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13813	11900	ATACAGTTAATAAAAATAAA
13814	11901	GATACAGTTAATAAAAATAA
13815	11902	TGATACAGTTAATAAAAATA
13816	11903	CTGATACAGTTAATAAAAAT
13817	11904	TCTGATACAGTTAATAAAAA
13818	11905	TTCTGATACAGTTAATAAAA
13819	11906	GTTCTGATACAGTTAATAAA
13820	11907	AGTTCTGATACAGTTAATAA
13821	11908	AAGTTCTGATACAGTTAATA
13822	11909	AAAGTTCTGATACAGTTAAT
13823	11910	TAAAGTTCTGATACAGTTAA
13824	11911	CTAAAGTTCTGATACAGTTA
13825	11912	TCTAAAGTTCTGATACAGTT
13826	11913	TTCTAAAGTTCTGATACAGT
13827	11914	ATTCTAAAGTTCTGATACAG
13828	11915	CATTCTAAAGTTCTGATACA
13829	11916	ACATTCTAAAGTTCTGATAC
13830	11917	AACATTCTAAAGTTCTGATA
13831	11918	CAACATTCTAAAGTTCTGAT
13832	11919	CCAACATTCTAAAGTTCTGA
13833	11920	ACCAACATTCTAAAGTTCTG
13834	11921	GACCAACATTCTAAAGTTCT
13835	11922	AGACCAACATTCTAAAGTTC
13836	11923	GAGACCAACATTCTAAAGTT
13837	11924	GGAGACCAACATTCTAAAGT
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62915	61002	AGTAATTTTATGTTTTTAAA
62916	61003	CAGTAATTTTATGTTTTTAA
62917	61004	CCAGTAATTTTATGTTTTTA
62918	61005	GCCAGTAATTTTATGTTTTT
62919	61006	AGCCAGTAATTTTATGTTTT
62920	61007	CAGCCAGTAATTTTATGTTT
62921	61008	CCAGCCAGTAATTTTATGTT
62922	61009	CCCAGCCAGTAATTTTATGT
62923	61010	ACCCAGCCAGTAATTTTATG
62924	61011	TACCCAGCCAGTAATTTTAT
62925	61012	GTACCCAGCCAGTAATTTTA
62926	61013	TGTACCCAGCCAGTAATTTT
62927	61014	CTGTACCCAGCCAGTAATTT
62928	61015	ACTGTACCCAGCCAGTAATT
62929	61016	CACTGTACCCAGCCAGTAAT
62930	61017	CCACTGTACCCAGCCAGTAA
62931	61018	GCCACTGTACCCAGCCAGTA
62932	61019	AGCCACTGTACCCAGCCAGT
62933	61020	GAGCCACTGTACCCAGCCAG
62934	61021	TGAGCCACTGTACCCAGCCA
62935	61022	ATGAGCCACTGTACCCAGCC
62936	61023	AATGAGCCACTGTACCCAGC
62937	61024	GAATGAGCCACTGTACCCAG
62938	61025	GGAATGAGCCACTGTACCCA
62939	61026	AGGAATGAGCCACTGTACCC
62940	61027	CAGGAATGAGCCACTGTACC
62941	61028	ACAGGAATGAGCCACTGTAC
62942	61029	TACAGGAATGAGCCACTGTA
62943	61030	TTACAGGAATGAGCCACTGT
62944	61031	ATTACAGGAATGAGCCACTG
62945	61032	GATTACAGGAATGAGCCACT
62946	61033	AGATTACAGGAATGAGCCAC
62947	61034	GAGATTACAGGAATGAGCCA
62948	61035	TGAGATTACAGGAATGAGCC
62949	61036	CTGAGATTACAGGAATGAGC
62950	61037	GCTGAGATTACAGGAATGAG
62951	61038	TGCTGAGATTACAGGAATGA
62952	61039	GTGCTGAGATTACAGGAATG
62953	61040	AGTGCTGAGATTACAGGAAT
62954	61041	AAGTGCTGAGATTACAGGAA
62955	61042	AAAGTGCTGAGATTACAGGA
62956	61043	CAAAGTGCTGAGATTACAGG
62957	61044	CCAAAGTGCTGAGATTACAG
62958	61045	CCCAAAGTGCTGAGATTACA
62959	61046	TCCCAAAGTGCTGAGATTAC
62960	61047	CTCCCAAAGTGCTGAGATTA
62961	61048	CCTCCCAAAGTGCTGAGATT
62962	61049	GCCTCCCAAAGTGCTGAGAT
62963	61050	GGCCTCCCAAAGTGCTGAGA
62964	61051	TGGCCTCCCAAAGTGCTGAG
62965	61052	TTGGCCTCCCAAAGTGCTGA
62966	61053	CTTGGCCTCCCAAAGTGCTG
62967	61054	CCTTGGCCTCCCAAAGTGCT
62968	61055	GCCTTGGCCTCCCAAAGTGC
62969	61056	TGCCTTGGCCTCCCAAAGTG
62970	61057	CTGCCTTGGCCTCCCAAAGT
62971	61058	TCTGCCTTGGCCTCCCAAAG
62972	61059	ATCTGCCTTGGCCTCCCAAA
62973	61060	CATCTGCCTTGGCCTCCCAA
62974	61061	TCATCTGCCTTGGCCTCCCA
62975	61062	TTCATCTGCCTTGGCCTCCC
62976	61063	ATTCATCTGCCTTGGCCTCC
62977	61064	AATTCATCTGCCTTGGCCTC
62978	61065	CAATTCATCTGCCTTGGCCT
62979	61066	GCAATTCATCTGCCTTGGCC
62980	61067	AGCAATTCATCTGCCTTGGC
62981	61068	AAGCAATTCATCTGCCTTGG
62982	61069	CAAGCAATTCATCTGCCTTG
62983	61070	TCAAGCAATTCATCTGCCTT
62984	61071	CTCAAGCAATTCATCTGCCT
62985	61072	GCTCAAGCAATTCATCTGCC

112062	110149	GGGAGGCTGAGGTAGGAGAA
112063	110150	CGGGAGGCTGAGGTAGGAGA
112064	110151	TCGGGAGGCTGAGGTAGGAG
112065	110152	CTCGGGAGGCTGAGGTAGGA
112066	110153	ACTCGGGAGGCTGAGGTAGG
112067	110154	TACTCGGGAGGCTGAGGTAG
112068	110155	CTACTCGGGAGGCTGAGGTA
112069	110156	GCTACTCGGGAGGCTGAGGT
112070	110157	TGCTACTCGGGAGGCTGAGG
112071	110158	CTGCTACTCGGGAGGCTGAG
112072	110159	CCTGCTACTCGGGAGGCTGA
112073	110160	CCCTGCTACTCGGGAGGCTG
112074	110161	TCCCTGCTACTCGGGAGGCT
112075	110162	GTCCCTGCTACTCGGGAGGC
112076	110163	AGTCCCTGCTACTCGGGAGG
112077	110164	TAGTCCCTGCTACTCGGGAG
112078	110165	ATAGTCCCTGCTACTCGGGA
112079	110166	TATAGTCCCTGCTACTCGGG
112080	110167	CTATAGTCCCTGCTACTCGG
112081	110168	CCTATAGTCCCTGCTACTCG
112082	110169	GCCTATAGTCCCTGCTACTC
112083	110170	CGCCTATAGTCCCTGCTACT
112084	110171	GCGCCTATAGTCCCTGCTAC
112085	110172	GGCGCCTATAGTCCCTGCTA
112086	110173	AGGCGCCTATAGTCCCTGCT
112087	110174	CAGGCGCCTATAGTCCCTGC
112088	110175	GCAGGCGCCTATAGTCCCTG
112089	110176	GGCAGGCGCCTATAGTCCCT
112090	110177	TGGCAGGCGCCTATAGTCCC
112091	110178	GTGGCAGGCGCCTATAGTCC
112092	110179	GGTGGCAGGCGCCTATAGTC
112093	110180	TGGTGGCAGGCGCCTATAGT
112094	110181	ATGGTGGCAGGCGCCTATAG
112095	110182	CATGGTGGCAGGCGCCTATA
112096	110183	GCATGGTGGCAGGCGCCTAT
112097	110184	GGCATGGTGGCAGGCGCCTA
112098	110185	AGGCATGGTGGCAGGCGCCT
112099	110186	CAGGCATGGTGGCAGGCGCC
112100	110187	CCAGGCATGGTGGCAGGCGC
112101	110188	GCCAGGCATGGTGGCAGGCG
112102	110189	AGCCAGGCATGGTGGCAGGC
112103	110190	TAGCCAGGCATGGTGGCAGG
112104	110191	TTAGCCAGGCATGGTGGCAG
112105	110192	ATTAGCCAGGCATGGTGGCA
112106	110193	AATTAGCCAGGCATGGTGGC
112107	110194	AAATTAGCCAGGCATGGTGG
112108	110195	AAAATTAGCCAGGCATGGTG
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112111	110198	ACAAAAATTAGCCAGGCATG
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112113	110200	ATACAAAAATTAGCCAGGCA
112114	110201	AATACAAAAATTAGCCAGGC
112115	110202	AAATACAAAAATTAGCCAGG
112116	110203	AAAATACAAAAATTAGCCAG
112117	110204	AAAAATACAAAAATTAGCCA
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112119	110206	CTAAAAATACAAAAATTAGC
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112123	110210	TCTACTAAAAATACAAAAAT
112124	110211	CTCTACTAAAAATACAAAAA
112125	110212	TCTCTACTAAAAATACAAAA
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112129	110216	CCCATCTCTACTAAAAATAC
112130	110217	CCCCATCTCTACTAAAAATA
112131	110218	ACCCCATCTCTACTAAAAAT
112132	110219	AACCCCATCTCTACTAAAAA

13839	11926	CAGGAGACCAACATTCTAAA
13840	11927	TCAGGAGACCAACATTCTAA
13841	11928	TTCAGGAGACCAACATTCTA
13842	11929	TTTCAGGAGACCAACATTCT
13843	11930	GTTTCAGGAGACCAACATTC
13844	11931	GGTTTCAGGAGACCAACATT
13845	11932	TGGTTTCAGGAGACCAACAT
13846	11933	ATGGTTTCAGGAGACCAACA
13847	11934	AATGGTTTCAGGAGACCAAC
13848	11935	CAATGGTTTCAGGAGACCAA
13849	11936	GCAATGGTTTCAGGAGACCA
13850	11937	GGCAATGGTTTCAGGAGACC
13851	11938	AGGCAATGGTTTCAGGAGAC
13852	11939	AAGGCAATGGTTTCAGGAGA
13853	11940	CAAGGCAATGGTTTCAGGAG
13854	11941	TCAAGGCAATGGTTTCAGGA
13855	11942	CTCAAGGCAATGGTTTCAGG
13856	11943	TCTCAAGGCAATGGTTTCAG
13857	11944	CTCTCAAGGCAATGGTTTCA
13858	11945	CCTCTCAAGGCAATGGTTTC
13859	11946	GCCTCTCAAGGCAATGGTTT
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13861	11948	AAGCCTCTCAAGGCAATGGT
13862	11949	AAAGCCTCTCAAGGCAATGG
13863	11950	TAAAGCCTCTCAAGGCAATG
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13866	11953	CAATAAAGCCTCTCAAGGCA
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13871	11958	CTGTTCAATAAAGCCTCTCA
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13879	11966	TGGCAACACTGTTCAATAAA
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13881	11968	ATTGGCAACACTGTTCAATA
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13883	11970	TCATTGGCAACACTGTTCAA
13884	11971	ATCATTGGCAACACTGTTCA
13885	11972	GATCATTGGCAACACTGTTC
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13889	11976	AACTGATCATTGGCAACACT
13890	11977	AAACTGATCATTGGCAACAC
13891	11978	AAAACTGATCATTGGCAACA
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13893	11980	AAAAAACTGATCATTGGCAA
13894	11981	AAAAAAACTGATCATTGGCA
13895	11982	AAAAAAAACTGATCATTGGC
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13905	11992	AGGAAATTTAAAAAAAAACT
13906	11993	AAGGAAATTTAAAAAAAAAC
13907	11994	AAAGGAAATTTAAAAAAAAA
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13909	11996	AAAAAGGAAATTTAAAAAAA

62986	61073	GGCTCAAGCAATTCATCTGC
62987	61074	GGGCTCAAGCAATTCATCTG
62988	61075	TGGGCTCAAGCAATTCATCT
62989	61076	CTGGGCTCAAGCAATTCATC
62990	61077	ACTGGGCTCAAGCAATTCAT
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62992	61079	CTACTGGGCTCAAGCAATTC
62993	61080	ACTACTGGGCTCAAGCAATT
62994	61081	AACTACTGGGCTCAAGCAAT
62995	61082	GAACTACTGGGCTCAAGCAA
62996	61083	TGAACTACTGGGCTCAAGCA
62997	61084	TTGAACTACTGGGCTCAAGC
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62999	61086	TCTTGAACTACTGGGCTCAA
63000	61087	GTCTTGAACTACTGGGCTCA
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63002	61089	TGGTCTTGAACTACTGGGCT
63003	61090	CTGGTCTTGAACTACTGGGC
63004	61091	GCTGGTCTTGAACTACTGGG
63005	61092	GGCTGGTCTTGAACTACTGG
63006	61093	AGGCTGGTCTTGAACTACTG
63007	61094	CAGGCTGGTCTTGAACTACT
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63009	61096	CCCAGGCTGGTCTTGAACTA
63010	61097	GCCCAGGCTGGTCTTGAACT
63011	61098	TGCCCAGGCTGGTCTTGAAC
63012	61099	TTGCCCAGGCTGGTCTTGAA
63013	61100	ATTGCCCAGGCTGGTCTTGA
63014	61101	TATTGCCCAGGCTGGTCTTG
63015	61102	ATATTGCCCAGGCTGGTCTT
63016	61103	CATATTGCCCAGGCTGGTCT
63017	61104	CCATATTGCCCAGGCTGGTC
63018	61105	ACCATATTGCCCAGGCTGGT
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63021	61108	TCCACCATATTGCCCAGGCT
63022	61109	TTCCACCATATTGCCCAGGC
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63024	61111	GGTTCCACCATATTGCCCAG
63025	61112	GGGTTCCACCATATTGCCCA
63026	61113	GGGGTTCCACCATATTGCCC
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63028	61115	ACGGGGTTCCACCATATTGC
63029	61116	AACGGGGTTCCACCATATTG
63030	61117	AAACGGGGTTCCACCATATT
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63033	61120	TAGAAACGGGGTTCCACCAT
63034	61121	GTAGAAACGGGGTTCCACCA
63035	61122	TGTAGAAACGGGGTTCCACC
63036	61123	TTGTAGAAACGGGGTTCCAC
63037	61124	TTTGTAGAAACGGGGTTCCA
63038	61125	TTTTGTAGAAACGGGGTTCC
63039	61126	TTTTTGTAGAAACGGGGTTC
63040	61127	TTTTTTGTAGAAACGGGGTT
63041	61128	TTTTTTTGTAGAAACGGGGT
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63043	61130	ATTTTTTTTGTAGAAACGGG
63044	61131	TATTTTTTTTGTAGAAACGG
63045	61132	GTATTTTTTTTGTAGAAACG
63046	61133	TGTATTTTTTTTGTAGAAAC
63047	61134	TTGTATTTTTTTTGTAGAAA
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63049	61136	TTTTGTATTTTTTTTGTAGA
63050	61137	TTTTTGTATTTTTTTTGTAG
63051	61138	CTTTTTGTATTTTTTTTGTA
63052	61139	ACTTTTTGTATTTTTTTTGT
63053	61140	TACTTTTTGTATTTTTTTTG
63054	61141	CTACTTTTTGTATTTTTTTT
63055	61142	GCTACTTTTTGTATTTTTTT
63056	61143	GGCTACTTTTTGTATTTTTT

112133	110220	AAACCCCATCTCTACTAAAA
112134	110221	GAAACCCCATCTCTACTAAA
112135	110222	TGAAACCCCATCTCTACTAA
112136	110223	CTGAAACCCCATCTCTACTA
112137	110224	GCTGAAACCCCATCTCTACT
112138	110225	CGCTGAAACCCCATCTCTAC
112139	110226	ACGCTGAAACCCCATCTCTA
112140	110227	CACGCTGAAACCCCATCTCT
112141	110228	ACACGCTGAAACCCCATCTC
112142	110229	CACACGCTGAAACCCCATCT
112143	110230	TCACACGCTGAAACCCCATC
112144	110231	CTCACACGCTGAAACCCCAT
112145	110232	GCTCACACGCTGAAACCCCA
112146	110233	GGCTCACACGCTGAAACCCC
112147	110234	TGGCTCACACGCTGAAACCC
112148	110235	TTGGCTCACACGCTGAAACC
112149	110236	CTTGGCTCACACGCTGAAAC
112150	110237	TCTTGGCTCACACGCTGAAA
112151	110238	ATCTTGGCTCACACGCTGAA
112152	110239	CATCTTGGCTCACACGCTGA
112153	110240	CCATCTTGGCTCACACGCTG
112154	110241	ACCATCTTGGCTCACACGCT
112155	110242	GACCATCTTGGCTCACACGC
112156	110243	AGACCATCTTGGCTCACACG
112157	110244	GAGACCATCTTGGCTCACAC
112158	110245	CGAGACCATCTTGGCTCACA
112159	110246	TCGAGACCATCTTGGCTCAC
112160	110247	ATCGAGACCATCTTGGCTCA
112161	110248	GATCGAGACCATCTTGGCTC
112162	110249	AGATCGAGACCATCTTGGCT
112163	110250	GAGATCGAGACCATCTTGGC
112164	110251	GGAGATCGAGACCATCTTGG
112165	110252	AGGAGATCGAGACCATCTTG
112166	110253	CAGGAGATCGAGACCATCTT
112167	110254	TCAGGAGATCGAGACCATCT
112168	110255	GTCAGGAGATCGAGACCATC
112169	110256	GGTCAGGAGATCGAGACCAT
112170	110257	AGGTCAGGAGATCGAGACCA
112171	110258	GAGGTCAGGAGATCGAGACC
112172	110259	CGAGGTCAGGAGATCGAGAC
112173	110260	ACGAGGTCAGGAGATCGAGA
112174	110261	CACGAGGTCAGGAGATCGAG
112175	110262	TCACGAGGTCAGGAGATCGA
112176	110263	ATCACGAGGTCAGGAGATCG
112177	110264	GATCACGAGGTCAGGAGATC
112178	110265	GGATCACGAGGTCAGGAGAT
112179	110266	CGGATCACGAGGTCAGGAGA
112180	110267	GCGGATCACGAGGTCAGGAG
112181	110268	GGCGGATCACGAGGTCAGGA
112182	110269	AGGCGGATCACGAGGTCAGG
112183	110270	CAGGCGGATCACGAGGTCAG
112184	110271	GCAGGCGGATCACGAGGTCA
112185	110272	GGCAGGCGGATCACGAGGTC
112186	110273	AGGCAGGCGGATCACGAGGT
112187	110274	AAGGCAGGCGGATCACGAGG
112188	110275	CAAGGCAGGCGGATCACGAG
112189	110276	CCAAGGCAGGCGGATCACGA
112190	110277	GCCAAGGCAGGCGGATCACG
112191	110278	GGCCAAGGCAGGCGGATCAC
112192	110279	AGGCCAAGGCAGGCGGATCA
112193	110280	GAGGCCAAGGCAGGCGGATC
112194	110281	GGAGGCCAAGGCAGGCGGAT
112195	110282	GGGAGGCCAAGGCAGGCGGA
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112197	110284	TTGGGAGGCCAAGGCAGGCG
112198	110285	TTTGGGAGGCCAAGGCAGGC
112199	110286	CTTTGGGAGGCCAAGGCAGG
112200	110287	ACTTTGGGAGGCCAAGGCAG
112201	110288	CACTTTGGGAGGCCAAGGCA
112202	110289	GCACTTTGGGAGGCCAAGGC
112203	110290	AGCACTTTGGGAGGCCAAGG

13910	11997	AAAAAAGGAAATTTAAAAAA
13911	11998	AAAAAAAGGAAATTTAAAAA
13912	11999	AAAAAAAAGGAAATTTAAAA
13913	12000	CAAAAAAAAGGAAATTTAAA
13914	12001	TCAAAAAAAAGGAAATTTAA
13915	12002	CTCAAAAAAAAGGAAATTTA
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13917	12004	GTCTCAAAAAAAAGGAAATT
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13919	12006	CAGTCTCAAAAAAAAGGAAA
13920	12007	TCAGTCTCAAAAAAAAGGAA
13921	12008	CTCAGTCTCAAAAAAAAGGA
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13923	12010	GACTCAGTCTCAAAAAAAAG
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13925	12012	AAGACTCAGTCTCAAAAAAA
13926	12013	TAAGACTCAGTCTCAAAAAA
13927	12014	GTAAGACTCAGTCTCAAAAA
13928	12015	GGTAAGACTCAGTCTCAAAA
13929	12016	GGGTAAGACTCAGTCTCAAA
13930	12017	AGGGTAAGACTCAGTCTCAA
13931	12018	CAGGGTAAGACTCAGTCTCA
13932	12019	ACAGGGTAAGACTCAGTCTC
13933	12020	AACAGGGTAAGACTCAGTCT
13934	12021	CAACAGGGTAAGACTCAGTC
13935	12022	CCAACAGGGTAAGACTCAGT
13936	12023	GCCAACAGGGTAAGACTCAG
13937	12024	GGCCAACAGGGTAAGACTCA
13938	12025	TGGCCAACAGGGTAAGACTC
13939	12026	CTGGCCAACAGGGTAAGACT
13940	12027	CCTGGCCAACAGGGTAAGAC
13941	12028	ACCTGGCCAACAGGGTAAGA
13942	12029	AACCTGGCCAACAGGGTAAG
13943	12030	CAACCTGGCCAACAGGGTAA
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13945	12032	TCCAACCTGGCCAACAGGGT
13946	12033	CTCCAACCTGGCCAACAGGG
13947	12034	ACTCCAACCTGGCCAACAGG
13948	12035	TACTCCAACCTGGCCAACAG
13949	12036	ATACTCCAACCTGGCCAACA
13950	12037	TATACTCCAACCTGGCCAAC
13951	12038	CTATACTCCAACCTGGCCAA
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13953	12040	CACTATACTCCAACCTGGCC
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13956	12043	TACCACTATACTCCAACCTG
13957	12044	ATACCACTATACTCCAACCT
13958	12045	CATACCACTATACTCCAACC
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13960	12047	ACCATACCACTATACTCCAA
13961	12048	GACCATACCACTATACTCCA
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13963	12050	ATGACCATACCACTATACTC
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13971	12058	AGTGAGCCATGACCATACCA
13972	12059	CAGTGAGCCATGACCATACC
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13974	12061	TGCAGTGAGCCATGACCATA
13975	12062	CTGCAGTGAGCCATGACCAT
13976	12063	GCTGCAGTGAGCCATGACCA
13977	12064	GGCTGCAGTGAGCCATGACC
13978	12065	AGGCTGCAGTGAGCCATGAC
13979	12066	GAGGCTGCAGTGAGCCATGA
13980	12067	TGAGGCTGCAGTGAGCCATG

63057	61144	TGGCTACTTTTTGTATTTTT
63058	61145	CTGGCTACTTTTTGTATTTT
63059	61146	TCTGGCTACTTTTTGTATTT
63060	61147	GTCTGGCTACTTTTTGTATT
63061	61148	TGTCTGGCTACTTTTTGTAT
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63069	61156	TACCACCGTGTCTGGCTACT
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63071	61158	CATACCACCGTGTCTGGCTA
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63073	61160	TACATACCACCGTGTCTGGC
63074	61161	GTACATACCACCGTGTCTGG
63075	61162	GGTACATACCACCGTGTCTG
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63083	61170	GGACTACAGGTACATACCAC
63084	61171	GGGACTACAGGTACATACCA
63085	61172	TGGGACTACAGGTACATACC
63086	61173	CTGGGACTACAGGTACATAC
63087	61174	GCTGGGACTACAGGTACATA
63088	61175	AGCTGGGACTACAGGTACAT
63089	61176	TAGCTGGGACTACAGGTACA
63090	61177	ATAGCTGGGACTACAGGTAC
63091	61178	AATAGCTGGGACTACAGGTA
63092	61179	GAATAGCTGGGACTACAGGT
63093	61180	CGAATAGCTGGGACTACAGG
63094	61181	CCGAATAGCTGGGACTACAG
63095	61182	CCCGAATAGCTGGGACTACA
63096	61183	ACCCGAATAGCTGGGACTAC
63097	61184	CACCCGAATAGCTGGGACTA
63098	61185	CCACCCGAATAGCTGGGACT
63099	61186	GCCACCCGAATAGCTGGGAC
63100	61187	TGCCACCCGAATAGCTGGGA
63101	61188	CTGCCACCCGAATAGCTGGG
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63103	61190	CTCTGCCACCCGAATAGCTG
63104	61191	CCTCTGCCACCCGAATAGCT
63105	61192	ACCTCTGCCACCCGAATAGC
63106	61193	CACCTCTGCCACCCGAATAG
63107	61194	TCACCTCTGCCACCCGAATA
63108	61195	CTCACCTCTGCCACCCGAAT
63109	61196	TCTCACCTCTGCCACCCGAA
63110	61197	CTCTCACCTCTGCCACCCGA
63111	61198	CCTCTCACCTCTGCCACCCG
63112	61199	TCCTCTCACCTCTGCCACCC
63113	61200	ATCCTCTCACCTCTGCCACC
63114	61201	GATCCTCTCACCTCTGCCAC
63115	61202	TGATCCTCTCACCTCTGCCA
63116	61203	ATGATCCTCTCACCTCTGCC
63117	61204	GATGATCCTCTCACCTCTGC
63118	61205	AGATGATCCTCTCACCTCTG
63119	61206	CAGATGATCCTCTCACCTCT
63120	61207	TCAGATGATCCTCTCACCTC
63121	61208	CTCAGATGATCCTCTCACCT
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63123	61210	CGCTCAGATGATCCTCTCAC
63124	61211	GCGCTCAGATGATCCTCTCA
63125	61212	TGCGCTCAGATGATCCTCTC
63126	61213	CTGCGCTCAGATGATCCTCT
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112204	110291	CAGCACTTTGGGAGGCCAAG
112205	110292	CCAGCACTTTGGGAGGCCAA
112206	110293	CCCAGCACTTTGGGAGGCCA
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112208	110295	ATCCCAGCACTTTGGGAGGC
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112214	110301	CCTGTAATCCCAGCACTTTG
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112216	110303	CGCCTGTAATCCCAGCACTT
112217	110304	ACGCCTGTAATCCCAGCACT
112218	110305	CACGCCTGTAATCCCAGCAC
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112221	110308	GCTCACGCCTGTAATCCCAG
112222	110309	GGCTCACGCCTGTAATCCCA
112223	110310	TGGCTCACGCCTGTAATCCC
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112226	110313	CGGTGGCTCACGCCTGTAAT
112227	110314	ACGGTGGCTCACGCCTGTAA
112228	110315	CACGGTGGCTCACGCCTGTA
112229	110316	GCACGGTGGCTCACGCCTGT
112230	110317	GGCACGGTGGCTCACGCCTG
112231	110318	GGGCACGGTGGCTCACGCCT
112232	110319	CGGGCACGGTGGCTCACGCC
112233	110320	CCGGGCACGGTGGCTCACGC
112234	110321	GCCGGGCACGGTGGCTCACG
112235	110322	GGCCGGGCACGGTGGCTCAC
112236	110323	GGGCCGGGCACGGTGGCTCA
112237	110324	GGGGCCGGGCACGGTGGCTC
112238	110325	GGGGGCCGGGCACGGTGGCT
112239	110326	TGGGGGCCGGGCACGGTGGC
112240	110327	ATGGGGGCCGGGCACGGTGG
112241	110328	AATGGGGGCCGGGCACGGTG
112242	110329	CAATGGGGGCCGGGCACGGT
112243	110330	CCAATGGGGGCCGGGCACGG
112244	110331	ACCAATGGGGGCCGGGCACG
112245	110332	CACCAATGGGGGCCGGGCAC
112246	110333	GCACCAATGGGGGCCGGGCA
112247	110334	AGCACCAATGGGGGCCGGGC
112248	110335	TAGCACCAATGGGGGCCGGG
112249	110336	ATAGCACCAATGGGGGCCGG
112250	110337	AATAGCACCAATGGGGGCCG
112251	110338	CAATAGCACCAATGGGGGCC
112252	110339	ACAATAGCACCAATGGGGGC
112253	110340	AACAATAGCACCAATGGGGG
112254	110341	AAACAATAGCACCAATGGGG
112255	110342	AAAACAATAGCACCAATGGG
112256	110343	TAAAACAATAGCACCAATGG
112257	110344	ATAAAACAATAGCACCAATG
112258	110345	CATAAAACAATAGCACCAAT
112259	110346	ACATAAAACAATAGCACCAA
112260	110347	CACATAAAACAATAGCACCA
112261	110348	TCACATAAAACAATAGCACC
112262	110349	ATCACATAAAACAATAGCAC
112263	110350	TATCACATAAAACAATAGCA
112264	110351	CTATCACATAAAACAATAGC
112265	110352	TCTATCACATAAAACAATAG
112266	110353	CTCTATCACATAAAACAATA
112267	110354	GCTCTATCACATAAAACAAT
112268	110355	GGCTCTATCACATAAAACAA
112269	110356	TGGCTCTATCACATAAAACA
112270	110357	CTGGCTCTATCACATAAAAC
112271	110358	GCTGGCTCTATCACATAAAA
112272	110359	AGCTGGCTCTATCACATAAA
112273	110360	AAGCTGGCTCTATCACATAA
112274	110361	GAAGCTGGCTCTATCACATA

13981	12068	TTGAGGCTGCAGTGAGCCAT
13982	12069	GTTGAGGCTGCAGTGAGCCA
13983	12070	TGTTGAGGCTGCAGTGAGCC
13984	12071	ATGTTGAGGCTGCAGTGAGC
13985	12072	GATGTTGAGGCTGCAGTGAG
13986	12073	GGATGTTGAGGCTGCAGTGA
13987	12074	AGGATGTTGAGGCTGCAGTG
13988	12075	CAGGATGTTGAGGCTGCAGT
13989	12076	CCAGGATGTTGAGGCTGCAG
13990	12077	CCCAGGATGTTGAGGCTGCA
13991	12078	GCCCAGGATGTTGAGGCTGC
13992	12079	AGCCCAGGATGTTGAGGCTG
13993	12080	GAGCCCAGGATGTTGAGGCT
13994	12081	TGAGCCCAGGATGTTGAGGC
13995	12082	TTGAGCCCAGGATGTTGAGG
13996	12083	CTTGAGCCCAGGATGTTGAG
13997	12084	GCTTGAGCCCAGGATGTTGA
13998	12085	TGCTTGAGCCCAGGATGTTG
13999	12086	CTGCTTGAGCCCAGGATGTT
14000	12087	ACTGCTTGAGCCCAGGATGT
14001	12088	GACTGCTTGAGCCCAGGATG
14002	12089	GGACTGCTTGAGCCCAGGAT
14003	12090	AGGACTGCTTGAGCCCAGGA
14004	12091	GAGGACTGCTTGAGCCCAGG
14005	12092	GGAGGACTGCTTGAGCCCAG
14006	12093	AGGAGGACTGCTTGAGCCCA
14007	12094	TAGGAGGACTGCTTGAGCCC
14008	12095	GTAGGAGGACTGCTTGAGCC
14009	12096	GGTAGGAGGACTGCTTGAGC
14010	12097	AGGTAGGAGGACTGCTTGAG
14011	12098	GAGGTAGGAGGACTGCTTGA
14012	12099	TGAGGTAGGAGGACTGCTTG
14013	12100	CTGAGGTAGGAGGACTGCTT
14014	12101	ACTGAGGTAGGAGGACTGCT
14015	12102	GACTGAGGTAGGAGGACTGC
14016	12103	AGACTGAGGTAGGAGGACTG
14017	12104	GAGACTGAGGTAGGAGGACT
14018	12105	GGAGACTGAGGTAGGAGGAC
14019	12106	GGGAGACTGAGGTAGGAGGA
14020	12107	CGGGAGACTGAGGTAGGAGG
14021	12108	TCGGGAGACTGAGGTAGGAG
14022	12109	CTCGGGAGACTGAGGTAGGA
14023	12110	ACTCGGGAGACTGAGGTAGG
14024	12111	TACTCGGGAGACTGAGGTAG
14025	12112	CTACTCGGGAGACTGAGGTA
14026	12113	GCTACTCGGGAGACTGAGGT
14027	12114	AGCTACTCGGGAGACTGAGG
14028	12115	CAGCTACTCGGGAGACTGAG
14029	12116	CCAGCTACTCGGGAGACTGA
14030	12117	TCCAGCTACTCGGGAGACTG
14031	12118	TTCCAGCTACTCGGGAGACT
14032	12119	GTTCCAGCTACTCGGGAGAC
14033	12120	AGTTCCAGCTACTCGGGAGA
14034	12121	TAGTTCCAGCTACTCGGGAG
14035	12122	GTAGTTCCAGCTACTCGGGA
14036	12123	TGTAGTTCCAGCTACTCGGG
14037	12124	CTGTAGTTCCAGCTACTCGG
14038	12125	CCTGTAGTTCCAGCTACTCG
14039	12126	ACCTGTAGTTCCAGCTACTC
14040	12127	CACCTGTAGTTCCAGCTACT
14041	12128	ACACCTGTAGTTCCAGCTAC
14042	12129	TACACCTGTAGTTCCAGCTA
14043	12130	ATACACCTGTAGTTCCAGCT
14044	12131	CATACACCTGTAGTTCCAGC
14045	12132	GCATACACCTGTAGTTCCAG
14046	12133	GGCATACACCTGTAGTTCCA
14047	12134	TGGCATACACCTGTAGTTCC
14048	12135	GTGGCATACACCTGTAGTTC
14049	12136	GGTGGCATACACCTGTAGTT
14050	12137	TGGTGGCATACACCTGTAGT
14051	12138	ATGGTGGCATACACCTGTAG

63128	61215	CCCTGCGCTCAGATGATCCT
63129	61216	TCCCTGCGCTCAGATGATCC
63130	61217	CTCCCTGCGCTCAGATGATC
63131	61218	TCTCCCTGCGCTCAGATGAT
63132	61219	ATCTCCCTGCGCTCAGATGA
63133	61220	AATCTCCCTGCGCTCAGATG
63134	61221	CAATCTCCCTGCGCTCAGAT
63135	61222	TCAATCTCCCTGCGCTCAGA
63136	61223	CTCAATCTCCCTGCGCTCAG
63137	61224	CCTCAATCTCCCTGCGCTCA
63138	61225	GCCTCAATCTCCCTGCGCTC
63139	61226	AGCCTCAATCTCCCTGCGCT
63140	61227	CAGCCTCAATCTCCCTGCGC
63141	61228	GCAGCCTCAATCTCCCTGCG
63142	61229	TGCAGCCTCAATCTCCCTGC
63143	61230	CTGCAGCCTCAATCTCCCTG
63144	61231	ACTGCAGCCTCAATCTCCCT
63145	61232	CACTGCAGCCTCAATCTCCC
63146	61233	TCACTGCAGCCTCAATCTCC
63147	61234	CTCACTGCAGCCTCAATCTC
63148	61235	GCTCACTGCAGCCTCAATCT
63149	61236	GGCTCACTGCAGCCTCAATC
63150	61237	TGGCTCACTGCAGCCTCAAT
63151	61238	TTGGCTCACTGCAGCCTCAA
63152	61239	CTTGGCTCACTGCAGCCTCA
63153	61240	ACTTGGCTCACTGCAGCCTC
63154	61241	CACTTGGCTCACTGCAGCCT
63155	61242	TCACTTGGCTCACTGCAGCC
63156	61243	CTCACTTGGCTCACTGCAGC
63157	61244	TCTCACTTGGCTCACTGCAG
63158	61245	GTCTCACTTGGCTCACTGCA
63159	61246	GGTCTCACTTGGCTCACTGC
63160	61247	GGGTCTCACTTGGCTCACTG
63161	61248	AGGGTCTCACTTGGCTCACT
63162	61249	CAGGGTCTCACTTGGCTCAC
63163	61250	CCAGGGTCTCACTTGGCTCA
63164	61251	ACCAGGGTCTCACTTGGCTC
63165	61252	AACCAGGGTCTCACTTGGCT
63166	61253	AAACCAGGGTCTCACTTGGC
63167	61254	GAAACCAGGGTCTCACTTGG
63168	61255	TGAAACCAGGGTCTCACTTG
63169	61256	TTGAAACCAGGGTCTCACTT
63170	61257	TTTGAAACCAGGGTCTCACT
63171	61258	TTTTGAAACCAGGGTCTCAC
63172	61259	TTTTTGAAACCAGGGTCTCA
63173	61260	TTTTTTGAAACCAGGGTCTC
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63175	61262	TTTTTTTTGAAACCAGGGTC
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63179	61266	CTTTTTTTTTTTGAAACCAG
63180	61267	CCTTTTTTTTTTTGAAACCA
63181	61268	ACCTTTTTTTTTTTTGAAACC
63182	61269	AACCTTTTTTTTTTTTGAAAC
63183	61270	TAACCTTTTTTTTTTTTGAAA
63184	61271	GTAACCTTTTTTTTTTTTGAA
63185	61272	AGTAACCTTTTTTTTTTTTGA
63186	61273	TAGTAACCTTTTTTTTTTTTG
63187	61274	TTAGTAACCTTTTTTTTTTT
63188	61275	ATTAGTAACCTTTTTTTTTT
63189	61276	AATTAGTAACCTTTTTTTTT
63190	61277	CAATTAGTAACCTTTTTTTT
63191	61278	GCAATTAGTAACCTTTTTTT
63192	61279	TGCAATTAGTAACCTTTTTT
63193	61280	CTGCAATTAGTAACCTTTTT
63194	61281	ACTGCAATTAGTAACCTTTT
63195	61282	CACTGCAATTAGTAACCTTT
63196	61283	GCACTGCAATTAGTAACCTT
63197	61284	GGCACTGCAATTAGTAACCT
63198	61285	AGGCACTGCAATTAGTAACC

112275	110362	AGAAGCTGGCTCTATCACAT
112276	110363	GAGAAGCTGGCTCTATCACA
112277	110364	GGAGAAGCTGGCTCTATCAC
112278	110365	GGGAGAAGCTGGCTCTATCA
112279	110366	AGGGAGAAGCTGGCTCTATC
112280	110367	AAGGGAGAAGCTGGCTCTAT
112281	110368	AAAGGGAGAAGCTGGCTCTA
112282	110369	AAAAGGGAGAAGCTGGCTCT
112283	110370	GAAAAGGGAGAAGCTGGCTC
112284	110371	AGAAAAGGGAGAAGCTGGCT
112285	110372	AAGAAAAGGGAGAAGCTGGC
112286	110373	AAAGAAAAGGGAGAAGCTGG
112287	110374	CAAAGAAAAGGGAGAAGCTG
112288	110375	CCAAAGAAAAGGGAGAAGCT
112289	110376	TCCAAAGAAAAGGGAGAAGC
112290	110377	ATCCAAAGAAAAGGGAGAAG
112291	110378	AATCCAAAGAAAAGGGAGAA
112292	110379	AAATCCAAAGAAAAGGGAGA
112293	110380	AAAATCCAAAGAAAAGGGAG
112294	110381	AAAAATCCAAAGAAAAGGGA
112295	110382	TAAAAATCCAAAGAAAAGGG
112296	110383	TTAAAAATCCAAAGAAAAGG
112297	110384	TTTAAAAATCCAAAGAAAAG
112298	110385	GTTTAAAAATCCAAAGAAAA
112299	110386	TGTTTAAAAATCCAAAGAAA
112300	110387	ATGTTTAAAAATCCAAAGAA
112301	110388	TATGTTTAAAAATCCAAAGA
112302	110389	GTATGTTTAAAAATCCAAAG
112303	110390	AGTATGTTTAAAAATCCAAA
112304	110391	GAGTATGTTTAAAAATCCAA
112305	110392	AGAGTATGTTTAAAAATCCA
112306	110393	AAGAGTATGTTTAAAAATCC
112307	110394	GAAGAGTATGTTTAAAAATC
112308	110395	GGAAGAGTATGTTTAAAAAT
112309	110396	AGGAAGAGTATGTTTAAAAA
112310	110397	AAGGAAGAGTATGTTTAAAA
112311	110398	AAAGGAAGAGTATGTTTAAA
112312	110399	AAAAGGAAGAGTATGTTTAA
112313	110400	TAAAAGGAAGAGTATGTTTA
112314	110401	GTAAAAGGAAGAGTATGTTT
112315	110402	AGTAAAAGGAAGAGTATGTT
112316	110403	AAGTAAAAGGAAGAGTATGT
112317	110404	TAAGTAAAAGGAAGAGTATG
112318	110405	CTAAGTAAAAGGAAGAGTAT
112319	110406	TCTAAGTAAAAGGAAGAGTA
112320	110407	GTCTAAGTAAAAGGAAGAGT
112321	110408	AGTCTAAGTAAAAGGAAGAG
112322	110409	TAGTCTAAGTAAAAGGAAGA
112323	110410	ATAGTCTAAGTAAAAGGAAG
112324	110411	AATAGTCTAAGTAAAAGGAA
112325	110412	GAATAGTCTAAGTAAAAGGA
112326	110413	AGAATAGTCTAAGTAAAAGG
112327	110414	GAGAATAGTCTAAGTAAAAG
112328	110415	GGAGAATAGTCTAAGTAAAA
112329	110416	TGGAGAATAGTCTAAGTAAA
112330	110417	ATGGAGAATAGTCTAAGTAA
112331	110418	GATGGAGAATAGTCTAAGTA
112332	110419	GGATGGAGAATAGTCTAAGT
112333	110420	GGGATGGAGAATAGTCTAAG
112334	110421	TGGGATGGAGAATAGTCTAA
112335	110422	TTGGGATGGAGAATAGTCTA
112336	110423	GTTGGGATGGAGAATAGTCT
112337	110424	TGTTGGGATGGAGAATAGTC
112338	110425	GTGTTGGGATGGAGAATAGT
112339	110426	GGTGTTGGGATGGAGAATAG
112340	110427	AGGTGTTGGGATGGAGAATA
112341	110428	AAGGTGTTGGGATGGAGAAT
112342	110429	AAAGGTGTTGGGATGGAGAA
112343	110430	GAAAGGTGTTGGGATGGAGA
112344	110431	GGAAAGGTGTTGGGATGGAG
112345	110432	AGGAAAGGTGTTGGGATGGA

14052	12139	CATGGTGGCATACACCTGTA
14053	12140	GCATGGTGGCATACACCTGT
14054	12141	GGCATGGTGGCATACACCTG
14055	12142	AGGCATGGTGGCATACACCT
14056	12143	CAGGCATGGTGGCATACACC
14057	12144	CCAGGCATGGTGGCATACAC
14058	12145	GCCAGGCATGGTGGCATACA
14059	12146	AGCCAGGCATGGTGGCATAC
14060	12147	AAGCCAGGCATGGTGGCATA
14061	12148	AAAGCCAGGCATGGTGGCAT
14062	12149	AAAAGCCAGGCATGGTGGCA
14063	12150	CAAAAGCCAGGCATGGTGGC
14064	12151	ACAAAAGCCAGGCATGGTGG
14065	12152	TACAAAAGCCAGGCATGGTG
14066	12153	ATACAAAAGCCAGGCATGGT
14067	12154	TATACAAAAGCCAGGCATGG
14068	12155	ATATACAAAAGCCAGGCATG
14069	12156	AATATACAAAAGCCAGGCAT
14070	12157	AAATATACAAAAGCCAGGCA
14071	12158	AAAATATACAAAAGCCAGGC
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14073	12160	ACAAAATATACAAAAGCCAG
14074	12161	TACAAAATATACAAAAGCCA
14075	12162	CTACAAAATATACAAAAGCC
14076	12163	TCTACAAAATATACAAAAGC
14077	12164	CTCTACAAAATATACAAAAG
14078	12165	TCTCTACAAAATATACAAAA
14079	12166	GTCTCTACAAAATATACAAA
14080	12167	TGTCTCTACAAAATATACAA
14081	12168	CTGTCTCTACAAAATATACA
14082	12169	CCTGTCTCTACAAAATATAC
14083	12170	CCCTGTCTCTACAAAATATA
14084	12171	ACCCTGTCTCTACAAAATAT
14085	12172	AACCCTGTCTCTACAAAATA
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14087	12174	TAAACCCTGTCTCTACAAAA
14088	12175	CTAAACCCTGTCTCTACAAA
14089	12176	GCTAAACCCTGTCTCTACAA
14090	12177	GGCTAAACCCTGTCTCTACA
14091	12178	TGGCTAAACCCTGTCTCTAC
14092	12179	ATGGCTAAACCCTGTCTCTA
14093	12180	CATGGCTAAACCCTGTCTCT
14094	12181	ACATGGCTAAACCCTGTCTC
14095	12182	AACATGGCTAAACCCTGTCT
14096	12183	CAACATGGCTAAACCCTGTC
14097	12184	GCAACATGGCTAAACCCTGT
14098	12185	GGCAACATGGCTAAACCCTG
14099	12186	GGGCAACATGGCTAAACCCT
14100	12187	TGGGCAACATGGCTAAACCC
14101	12188	CTGGGCAACATGGCTAAACC
14102	12189	CCTGGGCAACATGGCTAAAC
14103	12190	GCCTGGGCAACATGGCTAAA
14104	12191	AGCCTGGGCAACATGGCTAA
14105	12192	CAGCCTGGGCAACATGGCTA
14106	12193	CCAGCCTGGGCAACATGGCT
14107	12194	ACCAGCCTGGGCAACATGGC
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14109	12196	AGACCAGCCTGGGCAACATG
14110	12197	GAGACCAGCCTGGGCAACAT
14111	12198	TGAGACCAGCCTGGGCAACA
14112	12199	TTGAGACCAGCCTGGGCAAC
14113	12200	TTTGAGACCAGCCTGGGCAA
14114	12201	GTTTGAGACCAGCCTGGGCA
14115	12202	AGTTTGAGACCAGCCTGGGC
14116	12203	GAGTTTGAGACCAGCCTGGG
14117	12204	AGAGTTTGAGACCAGCCTGG
14118	12205	AAGAGTTTGAGACCAGCCTG
14119	12206	TAAGAGTTTGAGACCAGCCT
14120	12207	TTAAGAGTTTGAGACCAGCC
14121	12208	TTTAAGAGTTTGAGACCAGC
14122	12209	ATTTAAGAGTTTGAGACCAG

63199	61286	AAGGCACTGCAATTAGTAAC
63200	61287	AAAGGCACTGCAATTAGTAA
63201	61288	AAAAGGCACTGCAATTAGTA
63202	61289	TAAAAGGCACTGCAATTAGT
63203	61290	ATAAAAGGCACTGCAATTAG
63204	61291	GATAAAAGGCACTGCAATTA
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63215	61302	CCATTAAATAAGATAAAAGG
63216	61303	CCCATTAAATAAGATAAAAG
63217	61304	GCCCATTAAATAAGATAAAA
63218	61305	AGCCCATTAAATAAGATAAA
63219	61306	AAGCCCATTAAATAAGATAA
63220	61307	TAAGCCCATTAAATAAGATA
63221	61308	CTAAGCCCATTAAATAAGAT
63222	61309	ACTAAGCCCATTAAATAAGA
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63225	61312	TTGACTAAGCCCATTAAATA
63226	61313	TTTGACTAAGCCCATTAAAT
63227	61314	GTTTGACTAAGCCCATTAAA
63228	61315	AGTTTGACTAAGCCCATTAA
63229	61316	TAGTTTGACTAAGCCCATTA
63230	61317	TTAGTTTGACTAAGCCCATT
63231	61318	CTTAGTTTGACTAAGCCCAT
63232	61319	TCTTAGTTTGACTAAGCCCA
63233	61320	ATCTTAGTTTGACTAAGCCC
63234	61321	CATCTTAGTTTGACTAAGCC
63235	61322	TCATCTTAGTTTGACTAAGC
63236	61323	ATCATCTTAGTTTGACTAAG
63237	61324	CATCATCTTAGTTTGACTAA
63238	61325	ACATCATCTTAGTTTGACTA
63239	61326	TACATCATCTTAGTTTGACT
63240	61327	ATACATCATCTTAGTTTGAC
63241	61328	AATACATCATCTTAGTTTGA
63242	61329	AAATACATCATCTTAGTTTG
63243	61330	AAAATACATCATCTTAGTTT
63244	61331	TAAAATACATCATCTTAGTT
63245	61332	ATAAAATACATCATCTTAGT
63246	61333	GATAAAATACATCATCTTAG
63247	61334	AGATAAAATACATCATCTTA
63248	61335	AAGATAAAATACATCATCTT
63249	61336	TAAGATAAAATACATCATCT
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63255	61342	CATTTATAAGATAAAATACA
63256	61343	ACATTTATAAGATAAAATAC
63257	61344	AACATTTATAAGATAAAATA
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63259	61346	AAAACATTTATAAGATAAAA
63260	61347	GAAAACATTTATAAGATAAA
63261	61348	GGAAAACATTTATAAGATAA
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63265	61352	CAAGGGAAAACATTTATAAG
63266	61353	TCAAGGGAAAACATTTATAA
63267	61354	TTCAAGGGAAAACATTTATA
63268	61355	ATTCAAGGGAAAACATTTAT
63269	61356	AATTCAAGGGAAAACATTTA

112346	110433	TAGGAAAGGTGTTGGGATGG
112347	110434	TTAGGAAAGGTGTTGGGATG
112348	110435	TTTAGGAAAGGTGTTGGGAT
112349	110436	GTTTAGGAAAGGTGTTGGGA
112350	110437	AGTTTAGGAAAGGTGTTGGG
112351	110438	AAGTTTAGGAAAGGTGTTGG
112352	110439	GAAGTTTAGGAAAGGTGTTG
112353	110440	AGAAGTTTAGGAAAGGTGTT
112354	110441	AAGAAGTTTAGGAAAGGTGT
112355	110442	AAAGAAGTTTAGGAAAGGTG
112356	110443	GAAAGAAGTTTAGGAAAGGT
112357	110444	TGAAAGAAGTTTAGGAAAGG
112358	110445	GTGAAAGAAGTTTAGGAAAG
112359	110446	TGTGAAAGAAGTTTAGGAAA
112360	110447	GTGTGAAAGAAGTTTAGGAA
112361	110448	GGTGTGAAAGAAGTTTAGGA
112362	110449	AGGTGTGAAAGAAGTTTAGG
112363	110450	AAGGTGTGAAAGAAGTTTAG
112364	110451	TAAGGTGTGAAAGAAGTTTA
112365	110452	CTAAGGTGTGAAAGAAGTTT
112366	110453	TCTAAGGTGTGAAAGAAGTT
112367	110454	GTCTAAGGTGTGAAAGAAGT
112368	110455	AGTCTAAGGTGTGAAAGAAG
112369	110456	TAGTCTAAGGTGTGAAAGAA
112370	110457	CTAGTCTAAGGTGTGAAAGA
112371	110458	GCTAGTCTAAGGTGTGAAAG
112372	110459	AGCTAGTCTAAGGTGTGAAA
112373	110460	CAGCTAGTCTAAGGTGTGAA
112374	110461	TCAGCTAGTCTAAGGTGTGA
112375	110462	GTCAGCTAGTCTAAGGTGTG
112376	110463	TGTCAGCTAGTCTAAGGTGT
112377	110464	GTGTCAGCTAGTCTAAGGTG
112378	110465	AGTGTCAGCTAGTCTAAGGT
112379	110466	AAGTGTCAGCTAGTCTAAGG
112380	110467	AAAGTGTCAGCTAGTCTAAG
112381	110468	TAAAGTGTCAGCTAGTCTAA
112382	110469	GTAAAGTGTCAGCTAGTCTA
112383	110470	AGTAAAGTGTCAGCTAGTCT
112384	110471	CAGTAAAGTGTCAGCTAGTC
112385	110472	TCAGTAAAGTGTCAGCTAGT
112386	110473	CTCAGTAAAGTGTCAGCTAG
112387	110474	TCTCAGTAAAGTGTCAGCTA
112388	110475	TTCTCAGTAAAGTGTCAGCT
112389	110476	TTTCTCAGTAAAGTGTCAGC
112390	110477	GTTTCTCAGTAAAGTGTCAG
112391	110478	GGTTTCTCAGTAAAGTGTCA
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112393	110480	AAGGTTTCTCAGTAAAGTGT
112394	110481	AAAGGTTTCTCAGTAAAGTG
112395	110482	GAAAGGTTTCTCAGTAAAGT
112396	110483	AGAAAGGTTTCTCAGTAAAG
112397	110484	AAGAAAGGTTTCTCAGTAAA
112398	110485	AAAGAAAGGTTTCTCAGTAA
112399	110486	AAAAGAAAGGTTTCTCAGTA
112400	110487	AAAAAGAAAGGTTTCTCAGT
112401	110488	AAAAAAGAAAGGTTTCTCAG
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112403	110490	ATAAAAAAGAAAGGTTTCTC
112404	110491	TATAAAAAAGAAAGGTTTCT
112405	110492	CTATAAAAAAGAAAGGTTTC
112406	110493	CCTATAAAAAAGAAAGGTTT
112407	110494	ACCTATAAAAAAGAAAGGTT
112408	110495	AACCTATAAAAAAGAAAGGT
112409	110496	CAACCTATAAAAAAGAAAGG
112410	110497	GCAACCTATAAAAAAGAAAG
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112413	110500	AAAGCAACCTATAAAAAAGA
112414	110501	AAAAGCAACCTATAAAAAAG
112415	110502	AAAAAGCAACCTATAAAAAA
112416	110503	GAAAAAGCAACCTATAAAAA

14123	12210	AATTTAAGAGTTTGAGACCA
14124	12211	GAATTTAAGAGTTTGAGACC
14125	12212	TGAATTTAAGAGTTTGAGAC
14126	12213	TTGAATTTAAGAGTTTGAGA
14127	12214	TTTGAATTTAAGAGTTTGAG
14128	12215	ATTTGAATTTAAGAGTTTGA
14129	12216	CATTTGAATTTAAGAGTTTG
14130	12217	TCATTTGAATTTAAGAGTTT
14131	12218	ATCATTTGAATTTAAGAGTT
14132	12219	GATCATTTGAATTTAAGAGT
14133	12220	GGATCATTTGAATTTAAGAG
14134	12221	TGGATCATTTGAATTTAAGA
14135	12222	GTGGATCATTTGAATTTAAG
14136	12223	GGTGGATCATTTGAATTTAA
14137	12224	GGGTGGATCATTTGAATTTA
14138	12225	TGGGTGGATCATTTGAATTT
14139	12226	GTGGGTGGATCATTTGAATT
14140	12227	GGTGGGTGGATCATTTGAAT
14141	12228	AGGTGGGTGGATCATTTGAA
14142	12229	TAGGTGGGTGGATCATTTGA
14143	12230	CTAGGTGGGTGGATCATTTG
14144	12231	ACTAGGTGGGTGGATCATTT
14145	12232	AACTAGGTGGGTGGATCATT
14146	12233	AAACTAGGTGGGTGGATCAT
14147	12234	AAAACTAGGTGGGTGGATCA
14148	12235	GAAAACTAGGTGGGTGGATC
14149	12236	GGAAAACTAGGTGGGTGGAT
14150	12237	GGGAAAACTAGGTGGGTGGA
14151	12238	TGGGAAAACTAGGTGGGTGG
14152	12239	TTGGGAAAACTAGGTGGGTG
14153	12240	TTTGGGAAAACTAGGTGGGT
14154	12241	CTTTGGGAAAACTAGGTGGG
14155	12242	ACTTTGGGAAAACTAGGTGG
14156	12243	CACTTTGGGAAAACTAGGTG
14157	12244	GCACTTTGGGAAAACTAGGT
14158	12245	AGCACTTTGGGAAAACTAGG
14159	12246	AAGCACTTTGGGAAAACTAG
14160	12247	AAAGCACTTTGGGAAAACTA
14161	12248	TAAAGCACTTTGGGAAAACT
14162	12249	TTAAAGCACTTTGGGAAAAC
14163	12250	ATTAAAGCACTTTGGGAAAA
14164	12251	AATTAAAGCACTTTGGGAAA
14165	12252	TAATTAAAGCACTTTGGGAA
14166	12253	GTAATTAAAGCACTTTGGGA
14167	12254	TGTAATTAAAGCACTTTGGG
14168	12255	ATGTAATTAAAGCACTTTGG
14169	12256	CATGTAATTAAAGCACTTTG
14170	12257	ACATGTAATTAAAGCACTTT
14171	12258	CACATGTAATTAAAGCACTT
14172	12259	ACACATGTAATTAAAGCACT
14173	12260	CACACATGTAATTAAAGCAC
14174	12261	TCACACATGTAATTAAAGCA
14175	12262	CTCACACATGTAATTAAAGC
14176	12263	CCTCACACATGTAATTAAAG
14177	12264	GCCTCACACATGTAATTAAA
14178	12265	TGCCTCACACATGTAATTAA
14179	12266	GTGCCTCACACATGTAATTA
14180	12267	GGTGCCTCACACATGTAATT
14181	12268	CGGTGCCTCACACATGTAAT
14182	12269	ACGGTGCCTCACACATGTAA
14183	12270	CACGGTGCCTCACACATGTA
14184	12271	CCACGGTGCCTCACACATGT
14185	12272	GCCACGGTGCCTCACACATG
14186	12273	AGCCACGGTGCCTCACACAT
14187	12274	CAGCCACGGTGCCTCACACA
14188	12275	CCAGCCACGGTGCCTCACAC
14189	12276	GCCAGCCACGGTGCCTCACA
14190	12277	GGCCAGCCACGGTGCCTCAC
14191	12278	TGGCCAGCCACGGTGCCTCA
14192	12279	CTGGCCAGCCACGGTGCCTC
14193	12280	CCTGGCCAGCCACGGTGCCT

63270	61357	AAATTCAAGGGAAAACATTT
63271	61358	AAAATTCAAGGGAAAACATT
63272	61359	TAAAATTCAAGGGAAAACAT
63273	61360	TTAAAATTCAAGGGAAAACA
63274	61361	GTTAAAATTCAAGGGAAAAC
63275	61362	AGTTAAAATTCAAGGGAAAA
63276	61363	CAGTTAAAATTCAAGGGAAA
63277	61364	TCAGTTAAAATTCAAGGGAA
63278	61365	TTCAGTTAAAATTCAAGGGA
63279	61366	CTTCAGTTAAAATTCAAGGG
63280	61367	TCTTCAGTTAAAATTCAAGG
63281	61368	TTCTTCAGTTAAAATTCAAG
63282	61369	ATTCTTCAGTTAAAATTCAA
63283	61370	GATTCTTCAGTTAAAATTCA
63284	61371	GGATTCTTCAGTTAAAATTC
63285	61372	TGGATTCTTCAGTTAAAATT
63286	61373	TTGGATTCTTCAGTTAAAAT
63287	61374	ATTGGATTCTTCAGTTAAAA
63288	61375	AATTGGATTCTTCAGTTAAA
63289	61376	AAATTGGATTCTTCAGTTAA
63290	61377	CAAATTGGATTCTTCAGTTA
63291	61378	ACAAATTGGATTCTTCAGTT
63292	61379	TACAAATTGGATTCTTCAGT
63293	61380	GTACAAATTGGATTCTTCAG
63294	61381	GGTACAAATTGGATTCTTCA
63295	61382	AGGTACAAATTGGATTCTTC
63296	61383	GAGGTACAAATTGGATTCTT
63297	61384	AGAGGTACAAATTGGATTCT
63298	61385	GAGAGGTACAAATTGGATTC
63299	61386	TGAGAGGTACAAATTGGATT
63300	61387	GTGAGAGGTACAAATTGGAT
63301	61388	TGTGAGAGGTACAAATTGGA
63302	61389	TTGTGAGAGGTACAAATTGG
63303	61390	TTTGTGAGAGGTACAAATTG
63304	61391	GTTTGTGAGAGGTACAAATT
63305	61392	TGTTTGTGAGAGGTACAAAT
63306	61393	CTGTTTGTGAGAGGTACAAA
63307	61394	TCTGTTTGTGAGAGGTACAA
63308	61395	TTCTGTTTGTGAGAGGTACA
63309	61396	ATTCTGTTTGTGAGAGGTAC
63310	61397	CATTCTGTTTGTGAGAGGTA
63311	61398	ACATTCTGTTTGTGAGAGGT
63312	61399	TACATTCTGTTTGTGAGAGG
63313	61400	ATACATTCTGTTTGTGAGAG
63314	61401	AATACATTCTGTTTGTGAGA
63315	61402	TAATACATTCTGTTTGTGAG
63316	61403	CTAATACATTCTGTTTGTGA
63317	61404	ACTAATACATTCTGTTTGTG
63318	61405	TACTAATACATTCTGTTTGT
63319	61406	TTACTAATACATTCTGTTTG
63320	61407	CTTACTAATACATTCTGTTT
63321	61408	CCTTACTAATACATTCTGTT
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63324	61411	TTTCCTTACTAATACATTCT
63325	61412	TTTTCCTTACTAATACATTC
63326	61413	ATTTTCCTTACTAATACATT
63327	61414	TATTTTCCTTACTAATACAT
63328	61415	TTATTTTCCTTACTAATACA
63329	61416	TTTATTTTCCTTACTAATAC
63330	61417	ATTTATTTTCCTTACTAATA
63331	61418	TATTTATTTTCCTTACTAAT
63332	61419	GTATTTATTTTCCTTACTAA
63333	61420	AGTATTTATTTTCCTTACTA
63334	61421	CAGTATTTATTTTCCTTACT
63335	61422	GCAGTATTTATTTTCCTTAC
63336	61423	AGCAGTATTTATTTTCCTTA
63337	61424	AAGCAGTATTTATTTTCCTT
63338	61425	AAAGCAGTATTTATTTTCCT
63339	61426	AAAAGCAGTATTTATTTTCC
63340	61427	AAAAAGCAGTATTTATTTTC

112417	110504	AGAAAAAGCAACCTATAAAA
112418	110505	TAGAAAAAGCAACCTATAAA
112419	110506	ATAGAAAAAGCAACCTATAA
112420	110507	TATAGAAAAAGCAACCTATA
112421	110508	CTATAGAAAAAGCAACCTAT
112422	110509	TCTATAGAAAAAGCAACCTA
112423	110510	GTCTATAGAAAAAGCAACCT
112424	110511	AGTCTATAGAAAAAGCAACC
112425	110512	GAGTCTATAGAAAAAGCAAC
112426	110513	AGAGTCTATAGAAAAAGCAA
112427	110514	GAGAGTCTATAGAAAAAGCA
112428	110515	AGAGAGTCTATAGAAAAAGC
112429	110516	AAGAGAGTCTATAGAAAAAG
112430	110517	TAAGAGAGTCTATAGAAAAA
112431	110518	CTAAGAGAGTCTATAGAAAA
112432	110519	GCTAAGAGAGTCTATAGAAA
112433	110520	TGCTAAGAGAGTCTATAGAA
112434	110521	ATGCTAAGAGAGTCTATAGA
112435	110522	AATGCTAAGAGAGTCTATAG
112436	110523	AAATGCTAAGAGAGTCTATA
112437	110524	TAAATGCTAAGAGAGTCTAT
112438	110525	GTAAATGCTAAGAGAGTCTA
112439	110526	AGTAAATGCTAAGAGAGTCT
112440	110527	GAGTAAATGCTAAGAGAGTC
112441	110528	TGAGTAAATGCTAAGAGAGT
112442	110529	ATGAGTAAATGCTAAGAGAG
112443	110530	AATGAGTAAATGCTAAGAGA
112444	110531	AAATGAGTAAATGCTAAGAG
112445	110532	AAAATGAGTAAATGCTAAGA
112446	110533	TAAAATGAGTAAATGCTAAG
112447	110534	ATAAAATGAGTAAATGCTAA
112448	110535	AATAAAATGAGTAAATGCTA
112449	110536	CAATAAAATGAGTAAATGCT
112450	110537	ACAATAAAATGAGTAAATGC
112451	110538	CACAATAAAATGAGTAAATG
112452	110539	TCACAATAAAATGAGTAAAT
112453	110540	TTCACAATAAAATGAGTAAA
112454	110541	CTTCACAATAAAATGAGTAA
112455	110542	ACTTCACAATAAAATGAGTA
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112458	110545	GACACTTCACAATAAAATGA
112459	110546	AGACACTTCACAATAAAATG
112460	110547	CAGACACTTCACAATAAAAT
112461	110548	TCAGACACTTCACAATAAAA
112462	110549	ATCAGACACTTCACAATAAA
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112464	110551	AGATCAGACACTTCACAATA
112465	110552	AAGATCAGACACTTCACAAT
112466	110553	TAAGATCAGACACTTCACAA
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112474	110561	CATTTAAATAAGATCAGACA
112475	110562	TCATTTAAATAAGATCAGAC
112476	110563	GTCATTTAAATAAGATCAGA
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112478	110565	TTGTCATTTAAATAAGATCA
112479	110566	CTTGTCATTTAAATAAGATC
112480	110567	ACTTGTCATTTAAATAAGAT
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112484	110571	TTATACTTGTCATTTAAATA
112485	110572	CTTATACTTGTCATTTAAAT
112486	110573	TCTTATACTTGTCATTTAAA
112487	110574	CTCTTATACTTGTCATTTAA

14194	12281	ACCTGGCCAGCCACGGTGCC
14195	12282	GACCTGGCCAGCCACGGTGC
14196	12283	TGACCTGGCCAGCCACGGTG
14197	12284	TTGACCTGGCCAGCCACGGT
14198	12285	TTTGACCTGGCCAGCCACGG
14199	12286	ATTTGACCTGGCCAGCCACG
14200	12287	TATTTGACCTGGCCAGCCAC
14201	12288	ATATTTGACCTGGCCAGCCA
14202	12289	AATATTTGACCTGGCCAGCC
14203	12290	AAATATTTGACCTGGCCAGC
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14205	12292	AAAAATATTTGACCTGGCCA
14206	12293	GAAAAATATTTGACCTGGCC
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14212	12299	GTCAATGAAAAATATTTGAC
14213	12300	CGTCAATGAAAAATATTTGA
14214	12301	ACGTCAATGAAAAATATTTG
14215	12302	AACGTCAATGAAAAATATTT
14216	12303	AAACGTCAATGAAAAATATT
14217	12304	AAAACGTCAATGAAAAATAT
14218	12305	AAAAACGTCAATGAAAAATA
14219	12306	GAAAAACGTCAATGAAAAAT
14220	12307	TGAAAAACGTCAATGAAAAA
14221	12308	ATGAAAAACGTCAATGAAAA
14222	12309	TATGAAAAACGTCAATGAAA
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14238	12325	TGACTTTAAAAAGCAATATG
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14241	12328	ACATGACTTTAAAAAGCAAT
14242	12329	AACATGACTTTAAAAAGCAA
14243	12330	TAACATGACTTTAAAAAGCA
14244	12331	TTAACATGACTTTAAAAAGC
14245	12332	TTTAACATGACTTTAAAAAG
14246	12333	TTTTAACATGACTTTAAAAA
14247	12334	ATTTTAACATGACTTTAAAA
14248	12335	TATTTTAACATGACTTTAAA
14249	12336	ATATTTTAACATGACTTTAA
14250	12337	AATATTTTAACATGACTTTA
14251	12338	GAATATTTTAACATGACTTT
14252	12339	AGAATATTTTAACATGACTT
14253	12340	AAGAATATTTTAACATGACT
14254	12341	TAAGAATATTTTAACATGAC
14255	12342	TTAAGAATATTTTAACATGA
14256	12343	ATTAAGAATATTTTAACATG
14257	12344	TATTAAGAATATTTTAACAT
14258	12345	TTATTAAGAATATTTTAACA
14259	12346	ATTATTAAGAATATTTTAAC
14260	12347	AATTATTAAGAATATTTTAA
14261	12348	AAATTATTAAGAATATTTTA
14262	12349	AAAATTATTAAGAATATTTT
14263	12350	AAAAATTATTAAGAATATTT
14264	12351	GAAAAATTATTAAGAATATT

63341	61428	TAAAAAGCAGTATTTATTTT
63342	61429	ATAAAAAGCAGTATTTATTT
63343	61430	AATAAAAAGCAGTATTTATT
63344	61431	TAATAAAAAGCAGTATTTAT
63345	61432	GTAATAAAAAGCAGTATTTA
63346	61433	AGTAATAAAAAGCAGTATTT
63347	61434	AAGTAATAAAAAGCAGTATT
63348	61435	TAAGTAATAAAAAGCAGTAT
63349	61436	TTAAGTAATAAAAAGCAGTA
63350	61437	TTTAAGTAATAAAAAGCAGT
63351	61438	ATTTAAGTAATAAAAAGCAG
63352	61439	TATTTAAGTAATAAAAAGCA
63353	61440	CTATTTAAGTAATAAAAAGC
63354	61441	CCTATTTAAGTAATAAAAAG
63355	61442	TCCTATTTAAGTAATAAAAA
63356	61443	ATCCTATTTAAGTAATAAAA
63357	61444	TATCCTATTTAAGTAATAAA
63358	61445	ATATCCTATTTAAGTAATAA
63359	61446	TATATCCTATTTAAGTAATA
63360	61447	ATATATCCTATTTAAGTAAT
63361	61448	AATATATCCTATTTAAGTAA
63362	61449	AAATATATCCTATTTAAGTA
63363	61450	AAAATATATCCTATTTAAGT
63364	61451	AAAAATATATCCTATTTAAG
63365	61452	GAAAAATATATCCTATTTAA
63366	61453	AGAAAAATATATCCTATTTA
63367	61454	GAGAAAAATATATCCTATTT
63368	61455	AGAGAAAAATATATCCTATT
63369	61456	AAGAGAAAAATATATCCTAT
63370	61457	TAAGAGAAAAATATATCCTA
63371	61458	CTAAGAGAAAAATATATCCT
63372	61459	CCTAAGAGAAAAATATATCC
63373	61460	CCCTAAGAGAAAAATATATC
63374	61461	TCCCTAAGAGAAAAATATAT
63375	61462	ATCCCTAAGAGAAAAATATA
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63379	61466	AAAAATCCCTAAGAGAAAAA
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63382	61469	AAAAAAAATCCCTAAGAGAA
63383	61470	GAAAAAAAATCCCTAAGAGA
63384	61471	AGAAAAAAAATCCCTAAGAG
63385	61472	TAGAAAAAAAATCCCTAAGA
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63387	61474	AATAGAAAAAAAAATCCCTAA
63388	61475	AAATAGAAAAAAAAATCCCTA
63389	61476	AAAATAGAAAAAAAAATCCCT
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63392	61479	GATAAAATAGAAAAAAAATC
63393	61480	AGATAAAATAGAAAAAAAAT
63394	61481	GAGATAAAATAGAAAAAAAA
63395	61482	TGAGATAAAATAGAAAAAAA
63396	61483	GTGAGATAAAATAGAAAAAA
63397	61484	AGTGAGATAAAATAGAAAAA
63398	61485	AAGTGAGATAAAATAGAAAA
63399	61486	AAAGTGAGATAAAATAGAAA
63400	61487	TAAAGTGAGATAAAATAGAA
63401	61488	ATAAAGTGAGATAAAATAGA
63402	61489	GATAAAGTGAGATAAAATAG
63403	61490	CGATAAAGTGAGATAAAATA
63404	61491	ACGATAAAGTGAGATAAAAT
63405	61492	TACGATAAAGTGAGATAAAA
63406	61493	CTACGATAAAGTGAGATAAA
63407	61494	ACTACGATAAAGTGAGATAA
63408	61495	CACTACGATAAAGTGAGATA
63409	61496	GCACTACGATAAAGTGAGAT
63410	61497	AGCACTACGATAAAGTGAGA
63411	61498	TAGCACTACGATAAAGTGAG

112488	110575	CCTCTTATACTTGTCATTTA
112489	110576	TCCTCTTATACTTGTCATTT
112490	110577	ATCCTCTTATACTTGTCATT
112491	110578	TATCCTCTTATACTTGTCAT
112492	110579	CTATCCTCTTATACTTGTCA
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112497	110584	AGTTTCTATCCTCTTATACT
112498	110585	TAGTTTCTATCCTCTTATAC
112499	110586	ATAGTTTCTATCCTCTTATA
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112501	110588	AAATAGTTTCTATCCTCTTA
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112503	110590	TGAAATAGTTTCTATCCTCT
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112510	110597	AAAAATATGAAATAGTTTCT
112511	110598	GAAAAATATGAAATAGTTTC
112512	110599	AGAAAAATATGAAATAGTTT
112513	110600	GAGAAAAATATGAAATAGTT
112514	110601	TGAGAAAAATATGAAATAGT
112515	110602	GTGAGAAAAATATGAAATAG
112516	110603	GGTGAGAAAAATATGAAATA
112517	110604	GGGTGAGAAAAATATGAAAT
112518	110605	TGGGTGAGAAAAATATGAAA
112519	110606	CTGGGTGAGAAAAATATGAA
112520	110607	GCTGGGTGAGAAAAATATGA
112521	110608	TGCTGGGTGAGAAAAATATG
112522	110609	CTGCTGGGTGAGAAAAATAT
112523	110610	CCTGCTGGGTGAGAAAAATA
112524	110611	GCCTGCTGGGTGAGAAAAAT
112525	110612	TGCCTGCTGGGTGAGAAAAA
112526	110613	GTGCCTGCTGGGTGAGAAAA
112527	110614	TGTGCCTGCTGGGTGAGAAA
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112530	110617	AATTGTGCCTGCTGGGTGAG
112531	110618	AAATTGTGCCTGCTGGGTGA
112532	110619	GAAATTGTGCCTGCTGGGTG
112533	110620	AGAAATTGTGCCTGCTGGGT
112534	110621	CAGAAATTGTGCCTGCTGGG
112535	110622	TCAGAAATTGTGCCTGCTGG
112536	110623	GTCAGAAATTGTGCCTGCTG
112537	110624	TGTCAGAAATTGTGCCTGCT
112538	110625	ATGTCAGAAATTGTGCCTGC
112539	110626	CATGTCAGAAATTGTGCCTG
112540	110627	ACATGTCAGAAATTGTGCCT
112541	110628	CACATGTCAGAAATTGTGCC
112542	110629	CCACATGTCAGAAATTGTGC
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112546	110633	CTTACCACATGTCAGAAATT
112547	110634	GCTTACCACATGTCAGAAAT
112548	110635	TGCTTACCACATGTCAGAAA
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112550	110637	AGTGCTTACCACATGTCAGA
112551	110638	GAGTGCTTACCACATGTCAG
112552	110639	TGAGTGCTTACCACATGTCA
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112555	110642	TACTGAGTGCTTACCACATG
112556	110643	TTACTGAGTGCTTACCACAT
112557	110644	TTTACTGAGTGCTTACCACA
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14265	12352	AGAAAAATTATTAAGAATAT
14266	12353	TAGAAAAATTATTAAGAATA
14267	12354	TTAGAAAAATTATTAAGAAT
14268	12355	CTTAGAAAAATTATTAAGAA
14269	12356	ACTTAGAAAAATTATTAAGA
14270	12357	CACTTAGAAAAATTATTAAG
14271	12358	CCACTTAGAAAAATTATTAA
14272	12359	TCCACTTAGAAAAATTATTA
14273	12360	TTCCACTTAGAAAAATTATT
14274	12361	ATTCCACTTAGAAAAATTAT
14275	12362	AATTCCACTTAGAAAAATTA
14276	12363	TAATTCCACTTAGAAAAATT
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14279	12366	GATTAATTCCACTTAGAAAA
14280	12367	AGATTAATTCCACTTAGAAA
14281	12368	AAGATTAATTCCACTTAGAA
14282	12369	CAAGATTAATTCCACTTAGA
14283	12370	TCAAGATTAATTCCACTTAG
14284	12371	ATCAAGATTAATTCCACTTA
14285	12372	AATCAAGATTAATTCCACTT
14286	12373	TAATCAAGATTAATTCCACT
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14289	12376	TTATAATCAAGATTAATTCC
14290	12377	ATTATAATCAAGATTAATTC
14291	12378	AATTATAATCAAGATTAATT
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14293	12380	AAAATTATAATCAAGATTAA
14294	12381	TAAAATTATAATCAAGATTA
14295	12382	CTAAAATTATAATCAAGATT
14296	12383	ACTAAAATTATAATCAAGAT
14297	12384	AACTAAAATTATAATCAAGA
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14301	12388	AAAAAACTAAAATTATAATC
14302	12389	TAAAAAACTAAAATTATAAT
14303	12390	ATAAAAAACTAAAATTATAA
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14306	12393	TTTATAAAAAACTAAAATTA
14307	12394	CTTTATAAAAAACTAAAATT
14308	12395	CCTTTATAAAAAACTAAAAT
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14310	12397	GCCCTTTATAAAAAACTAAA
14311	12398	CGCCCTTTATAAAAAACTAA
14312	12399	CCGCCCTTTATAAAAAACTA
14313	12400	CCCGCCCTTTATAAAAAACT
14314	12401	ACCCGCCCTTTATAAAAAAC
14315	12402	AACCCGCCCTTTATAAAAAA
14316	12403	AAACCCGCCCTTTATAAAAA
14317	12404	AAAACCCGCCCTTTATAAAA
14318	12405	CAAAACCCGCCCTTTATAAA
14319	12406	TCAAAACCCGCCCTTTATAA
14320	12407	TTCAAAACCCGCCCTTTATA
14321	12408	TTTCAAAACCCGCCCTTTAT
14322	12409	GTTTCAAAACCCGCCCTTTA
14323	12410	TGTTTCAAAACCCGCCCTTT
14324	12411	TTGTTTCAAAACCCGCCCTT
14325	12412	CTTGTTTCAAAACCCGCCCT
14326	12413	ACTTGTTTCAAAACCCGCCC
14327	12414	TACTTGTTTCAAAACCCGCC
14328	12415	GTACTTGTTTCAAAACCCGC
14329	12416	AGTACTTGTTTCAAAACCCG
14330	12417	CAGTACTTGTTTCAAAACCC
14331	12418	GCAGTACTTGTTTCAAAACC
14332	12419	TGCAGTACTTGTTTCAAAAC
14333	12420	ATGCAGTACTTGTTTCAAAA
14334	12421	AATGCAGTACTTGTTTCAAA
14335	12422	AAATGCAGTACTTGTTTCAA

63412	61499	CTAGCACTACGATAAAGTGA
63413	61500	TCTAGCACTACGATAAAGTG
63414	61501	TTCTAGCACTACGATAAAGT
63415	61502	TTTCTAGCACTACGATAAAG
63416	61503	TTTTCTAGCACTACGATAAA
63417	61504	ATTTTCTAGCACTACGATAA
63418	61505	AATTTTCTAGCACTACGATA
63419	61506	AAATTTTCTAGCACTACGAT
63420	61507	TAAATTTTCTAGCACTACGA
63421	61508	TTAAATTTTCTAGCACTACG
63422	61509	ATTAAATTTTCTAGCACTAC
63423	61510	GATTAAATTTTCTAGCACTA
63424	61511	TGATTAAATTTTCTAGCACT
63425	61512	ATGATTAAATTTTCTAGCAC
63426	61513	AATGATTAAATTTTCTAGCA
63427	61514	GAATGATTAAATTTTCTAGC
63428	61515	TGAATGATTAAATTTTCTAG
63429	61516	ATGAATGATTAAATTTTCTA
63430	61517	AATGAATGATTAAATTTTCT
63431	61518	AAATGAATGATTAAATTTTC
63432	61519	CAAATGAATGATTAAATTTT
63433	61520	TCAAATGAATGATTAAATTT
63434	61521	CTCAAATGAATGATTAAATT
63435	61522	TCTCAAATGAATGATTAAAT
63436	61523	ATCTCAAATGAATGATTAAA
63437	61524	TATCTCAAATGAATGATTAA
63438	61525	CTATCTCAAATGAATGATTA
63439	61526	CCTATCTCAAATGAATGATT
63440	61527	CCCTATCTCAAATGAATGAT
63441	61528	TCCCTATCTCAAATGAATGA
63442	61529	CTCCCTATCTCAAATGAATG
63443	61530	TCTCCCTATCTCAAATGAAT
63444	61531	TTCTCCCTATCTCAAATGAA
63445	61532	TTTCTCCCTATCTCAAATGA
63446	61533	TTTTCTCCCTATCTCAAATG
63447	61534	ATTTTCTCCCTATCTCAAAT
63448	61535	AATTTTCTCCCTATCTCAAA
63449	61536	TAATTTTCTCCCTATCTCAA
63450	61537	CTAATTTTCTCCCTATCTCA
63451	61538	CCTAATTTTCTCCCTATCTC
63452	61539	ACCTAATTTTCTCCCTATCT
63453	61540	AACCTAATTTTCTCCCTATC
63454	61541	AAACCTAATTTTCTCCCTAT
63455	61542	AAAACCTAATTTTCTCCCTA
63456	61543	AAAAACCTAATTTTCTCCCT
63457	61544	AAAAAACCTAATTTTCTCCC
63458	61545	AAAAAAACCTAATTTTCTCC
63459	61546	AAAAAAAACCTAATTTTCTC
63460	61547	AAAAAAAAACCTAATTTTCT
63461	61548	AAAAAAAAAACCTAATTTTC
63462	61549	AAAAAAAAAAACCTAATTTT
63463	61550	GAAAAAAAAAAACCTAATTT
63464	61551	AGAAAAAAAAAAACCTAATT
63465	61552	AAGAAAAAAAAAAACCTAAT
63466	61553	GAAGAAAAAAAAAAACCTAA
63467	61554	AGAAGAAAAAAAAAAACCTA
63468	61555	TAGAAGAAAAAAAAAAACCT
63469	61556	ATAGAAGAAAAAAAAAAACC
63470	61557	AATAGAAGAAAAAAAAAAAC
63471	61558	AAATAGAAGAAAAAAAAAAA
63472	61559	AAAATAGAAGAAAAAAAAAA
63473	61560	CAAAATAGAAGAAAAAAAAA
63474	61561	TCAAAATAGAAGAAAAAAAA
63475	61562	CTCAAAATAGAAGAAAAAAA
63476	61563	TCTCAAAATAGAAGAAAAAA
63477	61564	GTCTCAAAATAGAAGAAAAA
63478	61565	TGTCTCAAAATAGAAGAAAA
63479	61566	CTGTCTCAAAATAGAAGAAA
63480	61567	CCTGTCTCAAAATAGAAGAA
63481	61568	CCCTGTCTCAAAATAGAAGA
63482	61569	ACCCTGTCTCAAAATAGAAG

112559	110646	TATTTACTGAGTGCTTACCA
112560	110647	ATATTTACTGAGTGCTTACC
112561	110648	AATATTTACTGAGTGCTTAC
112562	110649	CAATATTTACTGAGTGCTTA
112563	110650	TCAATATTTACTGAGTGCTT
112564	110651	TTCAATATTTACTGAGTGCT
112565	110652	GTTCAATATTTACTGAGTGC
112566	110653	AGTTCAATATTTACTGAGTG
112567	110654	AAGTTCAATATTTACTGAGT
112568	110655	AAAGTTCAATATTTACTGAG
112569	110656	TAAAGTTCAATATTTACTGA
112570	110657	CTAAAGTTCAATATTTACTG
112571	110658	TCTAAAGTTCAATATTTACT
112572	110659	CTCTAAAGTTCAATATTTAC
112573	110660	CCTCTAAAGTTCAATATTTA
112574	110661	GCCTCTAAAGTTCAATATTT
112575	110662	AGCCTCTAAAGTTCAATATT
112576	110663	TAGCCTCTAAAGTTCAATAT
112577	110664	CTAGCCTCTAAAGTTCAATA
112578	110665	CCTAGCCTCTAAAGTTCAAT
112579	110666	TCCTAGCCTCTAAAGTTCAA
112580	110667	GTCCTAGCCTCTAAAGTTCA
112581	110668	TGTCCTAGCCTCTAAAGTTC
112582	110669	ATGTCCTAGCCTCTAAAGTT
112583	110670	AATGTCCTAGCCTCTAAAGT
112584	110671	AAATGTCCTAGCCTCTAAAG
112585	110672	CAAATGTCCTAGCCTCTAAA
112586	110673	TCAAATGTCCTAGCCTCTAA
112587	110674	CTCAAATGTCCTAGCCTCTA
112588	110675	ACTCAAATGTCCTAGCCTCT
112589	110676	CACTCAAATGTCCTAGCCTC
112590	110677	GCACTCAAATGTCCTAGCCT
112591	110678	AGCACTCAAATGTCCTAGCC
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112596	110683	ACCAAAGCACTCAAATGTCC
112597	110684	CACCAAAGCACTCAAATGTC
112598	110685	TCACCAAAGCACTCAAATGT
112599	110686	GTCACCAAAGCACTCAAATG
112600	110687	AGTCACCAAAGCACTCAAAT
112601	110688	CAGTCACCAAAGCACTCAAA
112602	110689	ACAGTCACCAAAGCACTCAA
112603	110690	CACAGTCACCAAAGCACTCA
112604	110691	CCACAGTCACCAAAGCACTC
112605	110692	ACCACAGTCACCAAAGCACT
112606	110693	AACCACAGTCACCAAAGCAC
112607	110694	CAACCACAGTCACCAAAGCA
112608	110695	ACAACCACAGTCACCAAAGC
112609	110696	CACAACCACAGTCACCAAAG
112610	110697	GCACAACCACAGTCACCAAA
112611	110698	AGCACAACCACAGTCACCAA
112612	110699	TAGCACAACCACAGTCACCA
112613	110700	ATAGCACAACCACAGTCACC
112614	110701	TATAGCACAACCACAGTCAC
112615	110702	ATATAGCACAACCACAGTCA
112616	110703	TATATAGCACAACCACAGTC
112617	110704	CTATATAGCACAACCACAGT
112618	110705	CCTATATAGCACAACCACAG
112619	110706	ACCTATATAGCACAACCACA
112620	110707	TACCTATATAGCACAACCAC
112621	110708	GTACCTATATAGCACAACCA
112622	110709	AGTACCTATATAGCACAACC
112623	110710	GAGTACCTATATAGCACAAC
112624	110711	AGAGTACCTATATAGCACAA
112625	110712	CAGAGTACCTATATAGCACA
112626	110713	ACAGAGTACCTATATAGCAC
112627	110714	AACAGAGTACCTATATAGCA
112628	110715	TAACAGAGTACCTATATAGC
112629	110716	ATAACAGAGTACCTATATAG

14336	12423	AAAATGCAGTACTTGTTTCA
14337	12424	AAAAATGCAGTACTTGTTTC
14338	12425	GAAAAATGCAGTACTTGTTT
14339	12426	AGAAAAATGCAGTACTTGTT
14340	12427	AAGAAAAATGCAGTACTTGT
14341	12428	AAAGAAAAATGCAGTACTTG
14342	12429	AAAAGAAAAATGCAGTACTT
14343	12430	GAAAAGAAAAATGCAGTACT
14344	12431	CGAAAAGAAAAATGCAGTAC
14345	12432	CCGAAAAGAAAAATGCAGTA
14346	12433	CCCGAAAAGAAAAATGCAGT
14347	12434	ACCCGAAAAGAAAAATGCAG
14348	12435	AACCCGAAAAGAAAAATGCA
14349	12436	AAACCCGAAAAGAAAAATGC
14350	12437	TAAACCCGAAAAGAAAAATG
14351	12438	ATAAACCCGAAAAGAAAAAT
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14356	12443	TGTTTATAAACCCGAAAAGA
14357	12444	ATGTTTATAAACCCGAAAAG
14358	12445	AATGTTTATAAACCCGAAAA
14359	12446	AAATGTTTATAAACCCGAAA
14360	12447	CAAATGTTTATAAACCCGAA
14361	12448	GCAAATGTTTATAAACCCGA
14362	12449	AGCAAATGTTTATAAACCCG
14363	12450	CAGCAAATGTTTATAAACCC
14364	12451	ACAGCAAATGTTTATAAACC
14365	12452	CACAGCAAATGTTTATAAAC
14366	12453	CCACAGCAAATGTTTATAAA
14367	12454	TCCACAGCAAATGTTTATAA
14368	12455	GTCCACAGCAAATGTTTATA
14369	12456	AGTCCACAGCAAATGTTTAT
14370	12457	AAGTCCACAGCAAATGTTTA
14371	12458	AAAGTCCACAGCAAATGTTT
14372	12459	CAAAGTCCACAGCAAATGTT
14373	12460	ACAAAGTCCACAGCAAATGT
14374	12461	CACAAAGTCCACAGCAAATG
14375	12462	GCACAAAGTCCACAGCAAAT
14376	12463	TGCACAAAGTCCACAGCAAA
14377	12464	CTGCACAAAGTCCACAGCAA
14378	12465	ACTGCACAAAGTCCACAGCA
14379	12466	AACTGCACAAAGTCCACAGC
14380	12467	TAACTGCACAAAGTCCACAG
14381	12468	TTAACTGCACAAAGTCCACA
14382	12469	GTTAACTGCACAAAGTCCAC
14383	12470	AGTTAACTGCACAAAGTCCA
14384	12471	TAGTTAACTGCACAAAGTCC
14385	12472	ATAGTTAACTGCACAAAGTC
14386	12473	AATAGTTAACTGCACAAAGT
14387	12474	AAATAGTTAACTGCACAAAG
14388	12475	AAAATAGTTAACTGCACAAA
14389	12476	GAAAATAGTTAACTGCACAA
14390	12477	TGAAAATAGTTAACTGCACA
14391	12478	ATGAAAATAGTTAACTGCAC
14392	12479	AATGAAAATAGTTAACTGCA
14393	12480	GAATGAAAATAGTTAACTGC
14394	12481	GGAATGAAAATAGTTAACTG
14395	12482	AGGAATGAAAATAGTTAACT
14396	12483	CAGGAATGAAAATAGTTAAC
14397	12484	TCAGGAATGAAAATAGTTAA
14398	12485	TTCAGGAATGAAAATAGTTA
14399	12486	TTTCAGGAATGAAAATAGTT
14400	12487	GTTTCAGGAATGAAAATAGT
14401	12488	TGTTTCAGGAATGAAAATAG
14402	12489	GTGTTTCAGGAATGAAAATA
14403	12490	TGTGTTTCAGGAATGAAAAT
14404	12491	ATGTGTTTCAGGAATGAAAA
14405	12492	AATGTGTTTCAGGAATGAAA
14406	12493	AAATGTGTTTCAGGAATGAA

63483	61570	GACCCTGTCTCAAAATAGAA
63484	61571	AGACCCTGTCTCAAAATAGA
63485	61572	GAGACCCTGTCTCAAAATAG
63486	61573	TGAGACCCTGTCTCAAAATA
63487	61574	ATGAGACCCTGTCTCAAAAT
63488	61575	AATGAGACCCTGTCTCAAAA
63489	61576	AAATGAGACCCTGTCTCAAA
63490	61577	AAAATGAGACCCTGTCTCAA
63491	61578	CAAAATGAGACCCTGTCTCA
63492	61579	ACAAAATGAGACCCTGTCTC
63493	61580	AACAAAATGAGACCCTGTCT
63494	61581	CAACAAAATGAGACCCTGTC
63495	61582	ACAACAAAATGAGACCCTGT
63496	61583	GACAACAAAATGAGACCCTG
63497	61584	GGACAACAAAATGAGACCCT
63498	61585	TGGACAACAAAATGAGACCC
63499	61586	CTGGACAACAAAATGAGACC
63500	61587	CCTGGACAACAAAATGAGAC
63501	61588	GCCTGGACAACAAAATGAGA
63502	61589	AGCCTGGACAACAAAATGAG
63503	61590	CAGCCTGGACAACAAAATGA
63504	61591	CCAGCCTGGACAACAAAATG
63505	61592	TCCAGCCTGGACAACAAAAT
63506	61593	CTCCAGCCTGGACAACAAAA
63507	61594	ACTCCAGCCTGGACAACAAA
63508	61595	CACTCCAGCCTGGACAACAA
63509	61596	GCACTCCAGCCTGGACAACA
63510	61597	TGCACTCCAGCCTGGACAAC
63511	61598	CTGCACTCCAGCCTGGACAA
63512	61599	ACTGCACTCCAGCCTGGACA
63513	61600	CACTGCACTCCAGCCTGGAC
63514	61601	CCACTGCACTCCAGCCTGGA
63515	61602	GCCACTGCACTCCAGCCTGG
63516	61603	CGCCACTGCACTCCAGCCTG
63517	61604	GCGCCACTGCACTCCAGCCT
63518	61605	GGCGCCACTGCACTCCAGCC
63519	61606	TGGCGCCACTGCACTCCAGC
63520	61607	ATGGCGCCACTGCACTCCAG
63521	61608	GATGGCGCCACTGCACTCCA
63522	61609	CGATGGCGCCACTGCACTCC
63523	61610	ACGATGGCGCCACTGCACTC
63524	61611	TACGATGGCGCCACTGCACT
63525	61612	CTACGATGGCGCCACTGCAC
63526	61613	GCTACGATGGCGCCACTGCA
63527	61614	AGCTACGATGGCGCCACTGC
63528	61615	GAGCTACGATGGCGCCACTG
63529	61616	TGAGCTACGATGGCGCCACT
63530	61617	GTGAGCTACGATGGCGCCAC
63531	61618	GGTGAGCTACGATGGCGCCA
63532	61619	TGGTGAGCTACGATGGCGCC
63533	61620	ATGGTGAGCTACGATGGCGC
63534	61621	TATGGTGAGCTACGATGGCG
63535	61622	TTATGGTGAGCTACGATGGC
63536	61623	GTTATGGTGAGCTACGATGG
63537	61624	GGTTATGGTGAGCTACGATG
63538	61625	AGGTTATGGTGAGCTACGAT
63539	61626	GAGGTTATGGTGAGCTACGA
63540	61627	TGAGGTTATGGTGAGCTACG
63541	61628	TTGAGGTTATGGTGAGCTAC
63542	61629	TTTGAGGTTATGGTGAGCTA
63543	61630	GTTTGAGGTTATGGTGAGCT
63544	61631	AGTTTGAGGTTATGGTGAGC
63545	61632	GAGTTTGAGGTTATGGTGAG
63546	61633	TGAGTTTGAGGTTATGGTGA
63547	61634	ATGAGTTTGAGGTTATGGTG
63548	61635	CATGAGTTTGAGGTTATGGT
63549	61636	CCATGAGTTTGAGGTTATGG
63550	61637	CCCATGAGTTTGAGGTTATG
63551	61638	ACCCATGAGTTTGAGGTTAT
63552	61639	AACCCATGAGTTTGAGGTTA
63553	61640	GAACCCATGAGTTTGAGGTT

112630	110717	AATAACAGAGTACCTATATA
112631	110718	CAATAACAGAGTACCTATAT
112632	110719	ACAATAACAGAGTACCTATA
112633	110720	AACAATAACAGAGTACCTAT
112634	110721	TAACAATAACAGAGTACCTA
112635	110722	CTAACAATAACAGAGTACCT
112636	110723	ACTAACAATAACAGAGTACC
112637	110724	AACTAACAATAACAGAGTAC
112638	110725	AAACTAACAATAACAGAGTA
112639	110726	TAAACTAACAATAACAGAGT
112640	110727	ATAAACTAACAATAACAGAG
112641	110728	TATAAACTAACAATAACAGA
112642	110729	CTATAAACTAACAATAACAG
112643	110730	ACTATAAACTAACAATAACA
112644	110731	TACTATAAACTAACAATAAC
112645	110732	TTACTATAAACTAACAATAA
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112653	110740	TAATGCTTTTACTATAAACT
112654	110741	GTAATGCTTTTACTATAAAC
112655	110742	AGTAATGCTTTTACTATAAA
112656	110743	GAGTAATGCTTTTACTATAA
112657	110744	AGAGTAATGCTTTTACTATA
112658	110745	AAGAGTAATGCTTTTACTAT
112659	110746	TAAGAGTAATGCTTTTACTA
112660	110747	TTAAGAGTAATGCTTTTACT
112661	110748	TTTAAGAGTAATGCTTTTAC
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112663	110750	ACTTTAAGAGTAATGCTTTT
112664	110751	TACTTTAAGAGTAATGCTTT
112665	110752	ATACTTTAAGAGTAATGCTT
112666	110753	CATACTTTAAGAGTAATGCT
112667	110754	TCATACTTTAAGAGTAATGC
112668	110755	TTCATACTTTAAGAGTAATG
112669	110756	TTTCATACTTTAAGAGTAAT
112670	110757	TTTTCATACTTTAAGAGTAA
112671	110758	TTTTTCATACTTTAAGAGTA
112672	110759	TTTTTTCATACTTTAAGAGT
112673	110760	CTTTTTTCATACTTTAAGAG
112674	110761	GCTTTTTTCATACTTTAAGA
112675	110762	GGCTTTTTTCATACTTTAAG
112676	110763	AGGCTTTTTTCATACTTTAA
112677	110764	AAGGCTTTTTTCATACTTTA
112678	110765	TAAGGCTTTTTTCATACTTT
112679	110766	ATAAGGCTTTTTTCATACTT
112680	110767	AATAAGGCTTTTTTCATACT
112681	110768	GAATAAGGCTTTTTTCATAC
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112684	110771	TCTGAATAAGGCTTTTTTCA
112685	110772	TTCTGAATAAGGCTTTTTTC
112686	110773	GTTCTGAATAAGGCTTTTTT
112687	110774	TGTTCTGAATAAGGCTTTTT
112688	110775	ATGTTCTGAATAAGGCTTTT
112689	110776	AATGTTCTGAATAAGGCTTT
112690	110777	AAATGTTCTGAATAAGGCTT
112691	110778	GAAATGTTCTGAATAAGGCT
112692	110779	TGAAATGTTCTGAATAAGGC
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112696	110783	CGCATGAAATGTTCTGAATA
112697	110784	ACGCATGAAATGTTCTGAAT
112698	110785	TACGCATGAAATGTTCTGAA
112699	110786	ATACGCATGAAATGTTCTGA
112700	110787	TATACGCATGAAATGTTCTG

14407	12494	GAAATGTGTTTCAGGAATGA
14408	12495	CGAAATGTGTTTCAGGAATG
14409	12496	TCGAAATGTGTTTCAGGAAT
14410	12497	TTCGAAATGTGTTTCAGGAA
14411	12498	TTTCGAAATGTGTTTCAGGA
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14414	12501	TGATTTCGAAATGTGTTTCA
14415	12502	CTGATTTCGAAATGTGTTTC
14416	12503	CCTGATTTCGAAATGTGTTT
14417	12504	TCCTGATTTCGAAATGTGTT
14418	12505	TTCCTGATTTCGAAATGTGT
14419	12506	ATTCCTGATTTCGAAATGTG
14420	12507	AATTCCTGATTTCGAAATGT
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14429	12516	TTAGTCTTCAATTCCTGATT
14430	12517	TTTAGTCTTCAATTCCTGAT
14431	12518	ATTTAGTCTTCAATTCCTGA
14432	12519	CATTTAGTCTTCAATTCCTG
14433	12520	ACATTTAGTCTTCAATTCCT
14434	12521	GACATTTAGTCTTCAATTCC
14435	12522	AGACATTTAGTCTTCAATTC
14436	12523	AAGACATTTAGTCTTCAATT
14437	12524	AAAGACATTTAGTCTTCAAT
14438	12525	AAAAGACATTTAGTCTTCAA
14439	12526	GAAAAGACATTTAGTCTTCA
14440	12527	TGAAAAGACATTTAGTCTTC
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14443	12530	CAGTGAAAAGACATTTAGTC
14444	12531	TCAGTGAAAAGACATTTAGT
14445	12532	TTCAGTGAAAAGACATTTAG
14446	12533	CTTCAGTGAAAAGACATTTA
14447	12534	GCTTCAGTGAAAAGACATTT
14448	12535	AGCTTCAGTGAAAAGACATT
14449	12536	AAGCTTCAGTGAAAAGACAT
14450	12537	CAAGCTTCAGTGAAAAGACA
14451	12538	TCAAGCTTCAGTGAAAAGAC
14452	12539	CTCAAGCTTCAGTGAAAAGA
14453	12540	GCTCAAGCTTCAGTGAAAAG
14454	12541	TGCTCAAGCTTCAGTGAAAA
14455	12542	CTGCTCAAGCTTCAGTGAAA
14456	12543	TCTGCTCAAGCTTCAGTGAA
14457	12544	ATCTGCTCAAGCTTCAGTGA
14458	12545	AATCTGCTCAAGCTTCAGTG
14459	12546	AAATCTGCTCAAGCTTCAGT
14460	12547	AAAATCTGCTCAAGCTTCAG
14461	12548	TAAAATCTGCTCAAGCTTCA
14462	12549	CTAAAATCTGCTCAAGCTTC
14463	12550	TCTAAAATCTGCTCAAGCTT
14464	12551	TTCTAAAATCTGCTCAAGCT
14465	12552	TTTCTAAAATCTGCTCAAGC
14466	12553	CTTTCTAAAATCTGCTCAAG
14467	12554	CCTTTCTAAAATCTGCTCAA
14468	12555	CCCTTTCTAAAATCTGCTCA
14469	12556	CCCCTTTCTAAAATCTGCTC
14470	12557	TCCCCTTTCTAAAATCTGCT
14471	12558	CTCCCCTTTCTAAAATCTGC
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14473	12560	AACTCCCCTTTCTAAAATCT
14474	12561	GAACTCCCCTTTCTAAAATC
14475	12562	AGAACTCCCCTTTCTAAAAT
14476	12563	AAGAACTCCCCTTTCTAAAA
14477	12564	AAAGAACTCCCCTTTCTAAA

63554	61641	TGAACCCATGAGTTTGAGGT
63555	61642	CTGAACCCATGAGTTTGAGG
63556	61643	CCTGAACCCATGAGTTTGAG
63557	61644	ACCTGAACCCATGAGTTTGA
63558	61645	CACCTGAACCCATGAGTTTG
63559	61646	TCACCTGAACCCATGAGTTT
63560	61647	ATCACCTGAACCCATGAGTT
63561	61648	AATCACCTGAACCCATGAGT
63562	61649	GAATCACCTGAACCCATGAG
63563	61650	TGAATCACCTGAACCCATGA
63564	61651	GTGAATCACCTGAACCCATG
63565	61652	GGTGAATCACCTGAACCCAT
63566	61653	AGGTGAATCACCTGAACCCA
63567	61654	AAGGTGAATCACCTGAACCC
63568	61655	TAAGGTGAATCACCTGAACC
63569	61656	CTAAGGTGAATCACCTGAAC
63570	61657	GCTAAGGTGAATCACCTGAA
63571	61658	GGCTAAGGTGAATCACCTGA
63572	61659	AGGCTAAGGTGAATCACCTG
63573	61660	GAGGCTAAGGTGAATCACCT
63574	61661	GGAGGCTAAGGTGAATCACC
63575	61662	AGGAGGCTAAGGTGAATCAC
63576	61663	CAGGAGGCTAAGGTGAATCA
63577	61664	TCAGGAGGCTAAGGTGAATC
63578	61665	ATCAGGAGGCTAAGGTGAAT
63579	61666	AATCAGGAGGCTAAGGTGAA
63580	61667	TAATCAGGAGGCTAAGGTGA
63581	61668	TTAATCAGGAGGCTAAGGTG
63582	61669	CTTAATCAGGAGGCTAAGGT
63583	61670	GCTTAATCAGGAGGCTAAGG
63584	61671	AGCTTAATCAGGAGGCTAAG
63585	61672	CAGCTTAATCAGGAGGCTAA
63586	61673	CCAGCTTAATCAGGAGGCTA
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63588	61675	TCCCAGCTTAATCAGGAGGC
63589	61676	GTCCCAGCTTAATCAGGAGG
63590	61677	AGTCCCAGCTTAATCAGGAG
63591	61678	CAGTCCCAGCTTAATCAGGA
63592	61679	GCAGTCCCAGCTTAATCAGG
63593	61680	TGCAGTCCCAGCTTAATCAG
63594	61681	CTGCAGTCCCAGCTTAATCA
63595	61682	TCTGCAGTCCCAGCTTAATC
63596	61683	ATCTGCAGTCCCAGCTTAAT
63597	61684	CATCTGCAGTCCCAGCTTAA
63598	61685	ACATCTGCAGTCCCAGCTTA
63599	61686	CACATCTGCAGTCCCAGCTT
63600	61687	ACACATCTGCAGTCCCAGCT
63601	61688	TACACATCTGCAGTCCCAGC
63602	61689	ATACACATCTGCAGTCCCAG
63603	61690	GATACACATCTGCAGTCCCA
63604	61691	TGATACACATCTGCAGTCCC
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63606	61693	GGTGATACACATCTGCAGTC
63607	61694	TGGTGATACACATCTGCAGT
63608	61695	GTGGTGATACACATCTGCAG
63609	61696	AGTGGTGATACACATCTGCA
63610	61697	GAGTGGTGATACACATCTGC
63611	61698	GGAGTGGTGATACACATCTG
63612	61699	AGGAGTGGTGATACACATCT
63613	61700	CAGGAGTGGTGATACACATC
63614	61701	CCAGGAGTGGTGATACACAT
63615	61702	GCCAGGAGTGGTGATACACA
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63617	61704	TAGCCAGGAGTGGTGATACA
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63619	61706	ATTAGCCAGGAGTGGTGATA
63620	61707	AATTAGCCAGGAGTGGTGAT
63621	61708	AAATTAGCCAGGAGTGGTGA
63622	61709	AAAATTAGCCAGGAGTGGTG
63623	61710	AAAAATTAGCCAGGAGTGGT
63624	61711	CAAAAATTAGCCAGGAGTGG

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112702	110789	ACTATACGCATGAAATGTTC
112703	110790	AACTATACGCATGAAATGTT
112704	110791	TAACTATACGCATGAAATGT
112705	110792	TTAACTATACGCATGAAATG
112706	110793	ATTAACTATACGCATGAAAT
112707	110794	TATTAACTATACGCATGAAA
112708	110795	ATATTAACTATACGCATGAA
112709	110796	AATATTAACTATACGCATGA
112710	110797	TAATATTAACTATACGCATG
112711	110798	GTAATATTAACTATACGCAT
112712	110799	CGTAATATTAACTATACGCA
112713	110800	ACGTAATATTAACTATACGC
112714	110801	TACGTAATATTAACTATACG
112715	110802	CTACGTAATATTAACTATAC
112716	110803	GCTACGTAATATTAACTATA
112717	110804	AGCTACGTAATATTAACTAT
112718	110805	AAGCTACGTAATATTAACTA
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112720	110807	ACAAGCTACGTAATATTAAC
112721	110808	CACAAGCTACGTAATATTAA
112722	110809	GCACAAGCTACGTAATATTA
112723	110810	AGCACAAGCTACGTAATATT
112724	110811	GAGCACAAGCTACGTAATAT
112725	110812	TGAGCACAAGCTACGTAATA
112726	110813	ATGAGCACAAGCTACGTAAT
112727	110814	CATGAGCACAAGCTACGTAA
112728	110815	CCATGAGCACAAGCTACGTA
112729	110816	GCCATGAGCACAAGCTACGT
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112731	110818	TTGCCATGAGCACAAGCTAC
112732	110819	TTTGCCATGAGCACAAGCTA
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112734	110821	TTTTTGCCATGAGCACAAGC
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112736	110823	CATTTTTGCCATGAGCACAA
112737	110824	ACATTTTTGCCATGAGCACA
112738	110825	TACATTTTTGCCATGAGCAC
112739	110826	ATACATTTTTGCCATGAGCA
112740	110827	AATACATTTTTGCCATGAGC
112741	110828	TAATACATTTTTGCCATGAG
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112747	110834	CTTTAGTAATACATTTTTGC
112748	110835	ACTTTAGTAATACATTTTTG
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112750	110837	TAACTTTAGTAATACATTTT
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112758	110845	ATCTTAAATAACTTTAGTAA
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112761	110848	AATATCTTAAATAACTTTAG
112762	110849	AAATATCTTAAATAACTTTA
112763	110850	TAAATATCTTAAATAACTTT
112764	110851	TTAAATATCTTAAATAACTT
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112766	110853	ACTTAAATATCTTAAATAAC
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14481	12568	AAAAAAAGAACTCCCCTTTC
14482	12569	AAAAAAAAGAACTCCCCTTT
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14485	12572	AAAAAAAAAAAGAACTCCCC
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14514	12601	ACAAGACCCCCATTTCTACC
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14516	12603	TAACAAGACCCCCATTTCTA
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14519	12606	ACATAACAAGACCCCCATTT
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14521	12608	CAACATAACAAGACCCCCAT
14522	12609	GCAACATAACAAGACCCCCA
14523	12610	GGCAACATAACAAGACCCCC
14524	12611	GGGCAACATAACAAGACCCC
14525	12612	TGGGCAACATAACAAGACCC
14526	12613	CTGGGCAACATAACAAGACC
14527	12614	CCTGGGCAACATAACAAGAC
14528	12615	GCCTGGGCAACATAACAAGA
14529	12616	AGCCTGGGCAACATAACAAG
14530	12617	CAGCCTGGGCAACATAACAA
14531	12618	CCAGCCTGGGCAACATAACA
14532	12619	GCCAGCCTGGGCAACATAAC
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14544	12631	CAGAAGTTGGAGGCCAGCCT
14545	12632	CCAGAAGTTGGAGGCCAGCC
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14547	12634	GCCCAGAAGTTGGAGGCCAG
14548	12635	AGCCCAGAAGTTGGAGGCCA

63625	61712	ACAAAAATTAGCCAGGAGTG
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63630	61717	TAACAACAAAAATTAGCCAG
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63635	61722	AAAAATAACAACAAAAATTA
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63651	61738	GAGACCTCATCAAACAAAAA
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63661	61748	GCAACATAATGAGACCTCAT
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63671	61758	ACCAGCCTGGGCAACATAAT
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63675	61762	TGAGACCAGCCTGGGCAACA
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63685	61772	GCCCAGAGTTTGAGACCAGC
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63692	61779	ATTTGAGGCCCAGAGTTTGA
63693	61780	CATTTGAGGCCCAGAGTTTG
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112772	110859	AATTATACTTAAATATCTTA
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112775	110862	AACAATTATACTTAAATATC
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112796	110883	TGGCTGTAACTAAATAAAGG
112797	110884	TTGGCTGTAACTAAATAAAG
112798	110885	CTTGGCTGTAACTAAATAAA
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112800	110887	AACTTGGCTGTAACTAAATA
112801	110888	GAACTTGGCTGTAACTAAAT
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112821	110908	GATCCATAGATTCAGAAGTA
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14568	12655	TAAAGCAGGAGGACAGTTTA
14569	12656	CTAAAGCAGGAGGACAGTTT
14570	12657	GCTAAAGCAGGAGGACAGTT
14571	12658	GGCTAAAGCAGGAGGACAGT
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14600	12687	AGAGGCCATAAAGAACTCTC
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63697	61784	GGATCATTTGAGGCCCAGAG
63698	61785	AGGATCATTTGAGGCCCAGA
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63720	61807	CACTTTGGGAGGCTGGGGCA
63721	61808	GCACTTTGGGAGGCTGGGGC
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63733	61820	CCTGTAATCCCAGCACTTTG
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63735	61822	TGCCTGTAATCCCAGCACTT
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63740	61827	GTTCATGCCTGTAATCCCAG
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63743	61830	GAGGTTCATGCCTGTAATCC
63744	61831	AGAGGTTCATGCCTGTAATC
63745	61832	CAGAGGTTCATGCCTGTAAT
63746	61833	GCAGAGGTTCATGCCTGTAA
63747	61834	AGCAGAGGTTCATGCCTGTA
63748	61835	GAGCAGAGGTTCATGCCTGT
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63750	61837	GGGAGCAGAGGTTCATGCCT
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112856	110943	TGATTTTTCTCCCTCTCTAT
112857	110944	TTGATTTTTCTCCCTCTCTA
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112859	110946	TCTTGATTTTTCTCCCTCTC
112860	110947	CTCTTGATTTTTCTCCCTCT
112861	110948	TCTCTTGATTTTTCTCCCTC
112862	110949	ATCTCTTGATTTTTCTCCCT
112863	110950	AATCTCTTGATTTTTCTCCC
112864	110951	AAATCTCTTGATTTTTCTCC
112865	110952	CAAATCTCTTGATTTTTCTC
112866	110953	TCAAATCTCTTGATTTTTCT
112867	110954	ATCAAATCTCTTGATTTTTC
112868	110955	GATCAAATCTCTTGATTTTT
112869	110956	TGATCAAATCTCTTGATTTT
112870	110957	TTGATCAAATCTCTTGATTT
112871	110958	TTTGATCAAATCTCTTGATT
112872	110959	CTTTGATCAAATCTCTTGAT
112873	110960	TCTTTGATCAAATCTCTTGA
112874	110961	GTCTTTGATCAAATCTCTTG
112875	110962	TGTCTTTGATCAAATCTCTT
112876	110963	TTGTCTTTGATCAAATCTCT
112877	110964	TTTGTCTTTGATCAAATCTC
112878	110965	TTTTGTCTTTGATCAAATCT
112879	110966	ATTTTGTCTTTGATCAAATC
112880	110967	AATTTTGTCTTTGATCAAAT
112881	110968	CAATTTTGTCTTTGATCAAA
112882	110969	TCAATTTTGTCTTTGATCAA
112883	110970	TTCAATTTTGTCTTTGATCA
112884	110971	GTTCAATTTTGTCTTTGATC
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112886	110973	TGGTTCAATTTTGTCTTTGA
112887	110974	TTGGTTCAATTTTGTCTTTG
112888	110975	CTTGGTTCAATTTTGTCTTT
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112890	110977	CACTTGGTTCAATTTTGTCT
112891	110978	GCACTTGGTTCAATTTTGTC
112892	110979	AGCACTTGGTTCAATTTTGT
112893	110980	TAGCACTTGGTTCAATTTTG
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112895	110982	CTTAGCACTTGGTTCAATTT
112896	110983	CCTTAGCACTTGGTTCAATT
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112898	110985	ATCCTTAGCACTTGGTTCAA
112899	110986	AATCCTTAGCACTTGGTTCA
112900	110987	GAATCCTTAGCACTTGGTTC
112901	110988	AGAATCCTTAGCACTTGGTT
112902	110989	AAGAATCCTTAGCACTTGGT
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112904	110991	GAAAGAATCCTTAGCACTTG
112905	110992	TGAAAGAATCCTTAGCACTT
112906	110993	ATGAAAGAATCCTTAGCACT
112907	110994	AATGAAAGAATCCTTAGCAC
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112910	110997	TTCAATGAAAGAATCCTTAG
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14626	12713	ATCATGTGTAAAGTAAAAGT
14627	12714	AATCATGTGTAAAGTAAAAG
14628	12715	GAATCATGTGTAAAGTAAAA
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14630	12717	TAGAATCATGTGTAAAGTAA
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14636	12723	GCTAGATAGAATCATGTGTA
14637	12724	AGCTAGATAGAATCATGTGT
14638	12725	AAGCTAGATAGAATCATGTG
14639	12726	AAAGCTAGATAGAATCATGT
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14663	12750	CTGCCAATATGTACATCAGA
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14671	12758	TCTACTTGCTGCCAATATGT
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14673	12760	TTTCTACTTGCTGCCAATAT
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14686	12773	TGAAAACATTGCTTTTCTAC
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63767	61854	ATTTTAAAAAATGGGCTGGG
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63769	61856	ATATTTTAAAAAATGGGCTG
63770	61857	TATATTTTAAAAAATGGGCT
63771	61858	ATATATTTTAAAAAATGGGC
63772	61859	AATATATTTTAAAAAATGGG
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63774	61861	TGAATATATTTTAAAAAATG
63775	61862	GTGAATATATTTTAAAAAAT
63776	61863	TGTGAATATATTTTAAAAAA
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63780	61867	ATGCTGTGAATATATTTTAA
63781	61868	AATGCTGTGAATATATTTTA
63782	61869	CAATGCTGTGAATATATTTT
63783	61870	ACAATGCTGTGAATATATTT
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63785	61872	GCACAATGCTGTGAATATAT
63786	61873	TGCACAATGCTGTGAATATA
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63814	61901	GAAAATGTAAATTGATTGTA
63815	61902	TGAAAATGTAAATTGATTGT
63816	61903	ATGAAAATGTAAATTGATTG
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63821	61908	GGGTGATGAAAATGTAAATT
63822	61909	AGGGTGATGAAAATGTAAAT
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63825	61912	TTCAGGGTGATGAAAATGTA
63826	61913	TTTCAGGGTGATGAAAATGT
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63831	61918	TTTCTTTTCAGGGTGATGAA
63832	61919	GTTTCTTTTCAGGGTGATGA
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63834	61921	GAGTTTCTTTTCAGGGTGAT
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63836	61923	CAGAGTTTCTTTTCAGGGTG
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112914	111001	TATTTTCAATGAAAGAATCC
112915	111002	CTATTTTCAATGAAAGAATC
112916	111003	GCTATTTTCAATGAAAGAAT
112917	111004	TGCTATTTTCAATGAAAGAA
112918	111005	CTGCTATTTTCAATGAAAGA
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112923	111010	TGCTGCTGCTATTTTCAATG
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112927	111014	CAGTTGCTGCTGCTATTTTC
112928	111015	ACAGTTGCTGCTGCTATTTT
112929	111016	TACAGTTGCTGCTGCTATTT
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112932	111019	TGGTACAGTTGCTGCTGCTA
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112943	111030	GCTGCTGCCACTGGTACAGT
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112981	111068	CTAAGTATTGAAGGGGAAAT
112982	111069	ACTAAGTATTGAAGGGGAAA
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14691	12778	GCCTCTGAAAACATTGCTTT
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14694	12781	TCTGCCTCTGAAAACATTGC
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14697	12784	ATATCTGCCTCTGAAAACAT
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14702	12789	TTAATATATCTGCCTCTGAA
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63847	61934	GCTAAGGGGTTCAGAGTTTC
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112985	111072	GTTACTAAGTATTGAAGGGG
112986	111073	TGTTACTAAGTATTGAAGGG
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112989	111076	CCGTGTTACTAAGTATTGAA
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112994	111081	GTGCTCCGTGTTACTAAGTA
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113016	111103	AAGTGACCTCAGGTCCCCTC
113017	111104	GAAGTGACCTCAGGTCCCCT
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113023	111110	CCTTGGGAAGTGACCTCAGG
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113025	111112	CCCCTTGGGAAGTGACCTCA
113026	111113	ACCCCTTGGGAAGTGACCTC
113027	111114	AACCCCTTGGGAAGTGACCT
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113031	111118	TCTGAACCCCTTGGGAAGTG
113032	111119	GTCTGAACCCCTTGGGAAGT
113033	111120	AGTCTGAACCCCTTGGGAAG
113034	111121	AAGTCTGAACCCCTTGGGAA
113035	111122	GAAGTCTGAACCCCTTGGGA
113036	111123	GGAAGTCTGAACCCCTTGGG
113037	111124	TGGAAGTCTGAACCCCTTGG
113038	111125	CTGGAAGTCTGAACCCCTTG
113039	111126	GCTGGAAGTCTGAACCCCTT
113040	111127	GGCTGGAAGTCTGAACCCCT
113041	111128	GGGCTGGAAGTCTGAACCCC
113042	111129	TGGGCTGGAAGTCTGAACCC
113043	111130	CTGGGCTGGAAGTCTGAACC
113044	111131	GCTGGGCTGGAAGTCTGAAC
113045	111132	TGCTGGGCTGGAAGTCTGAA
113046	111133	ATGCTGGGCTGGAAGTCTGA
113047	111134	CATGCTGGGCTGGAAGTCTG
113048	111135	ACATGCTGGGCTGGAAGTCT
113049	111136	TACATGCTGGGCTGGAAGTC
113050	111137	TTACATGCTGGGCTGGAAGT
113051	111138	TTTACATGCTGGGCTGGAAG
113052	111139	GTTTACATGCTGGGCTGGAA
113053	111140	TGTTTACATGCTGGGCTGGA
113054	111141	TTGTTTACATGCTGGGCTGG
113055	111142	CTTGTTTACATGCTGGGCTG

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14763	12850	GCCACCGCACCCAGCTAAGT
14764	12851	AGCCACCGCACCCAGCTAAG
14765	12852	GAGCCACCGCACCCAGCTAA
14766	12853	TGAGCCACCGCACCCAGCTA
14767	12854	GTGAGCCACCGCACCCAGCT
14768	12855	CGTGAGCCACCGCACCCAGC
14769	12856	GCGTGAGCCACCGCACCCAG
14770	12857	AGCGTGAGCCACCGCACCCA
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14772	12859	CAAGCGTGAGCCACCGCACC
14773	12860	ACAAGCGTGAGCCACCGCAC
14774	12861	TACAAGCGTGAGCCACCGCA
14775	12862	TTACAAGCGTGAGCCACCGC
14776	12863	ATTACAAGCGTGAGCCACCG
14777	12864	GATTACAAGCGTGAGCCACC
14778	12865	GGATTACAAGCGTGAGCCAC
14779	12866	GGGATTACAAGCGTGAGCCA
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14786	12873	AAGTGCTGGGATTACAAGCG
14787	12874	AAAGTGCTGGGATTACAAGC
14788	12875	CAAAGTGCTGGGATTACAAG
14789	12876	CCAAAGTGCTGGGATTACAA
14790	12877	CCCAAAGTGCTGGGATTACA
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14796	12883	TGGCCTCCCAAAGTGCTGGG
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14798	12885	CTTGGCCTCCCAAAGTGCTG
14799	12886	CCTTGGCCTCCCAAAGTGCT
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14806	12893	CCACCCTCCTTGGCCTCCCA
14807	12894	TCCACCCTCCTTGGCCTCCC
14808	12895	ATCCACCCTCCTTGGCCTCC
14809	12896	GATCCACCCTCCTTGGCCTC
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14811	12898	GTGATCCACCCTCCTTGGCC
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14814	12901	CAAGTGATCCACCCTCCTTG
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14821	12908	CTGACCTCAAGTGATCCACC
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63911	61998	TATGAAGACAATAAATCAAT
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63915	62002	AACCTATGAAGACAATAAAT
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63918	62005	GCAAACCTATGAAGACAATA
63919	62006	GGCAAACCTATGAAGACAAT
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63923	62010	AATGGGCAAACCTATGAAGA
63924	62011	GAATGGGCAAACCTATGAAG
63925	62012	AGAATGGGCAAACCTATGAA
63926	62013	CAGAATGGGCAAACCTATGA
63927	62014	CCAGAATGGGCAAACCTATG
63928	62015	TCCAGAATGGGCAAACCTAT
63929	62016	GTCCAGAATGGGCAAACCTA
63930	62017	TGTCCAGAATGGGCAAACCT
63931	62018	ATGTCCAGAATGGGCAAACC
63932	62019	AATGTCCAGAATGGGCAAAC
63933	62020	CAATGTCCAGAATGGGCAAA
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63935	62022	CGCAATGTCCAGAATGGGCA
63936	62023	ACGCAATGTCCAGAATGGGC
63937	62024	TACGCAATGTCCAGAATGGG
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63939	62026	AATACGCAATGTCCAGAATG
63940	62027	TAATACGCAATGTCCAGAAT
63941	62028	TTAATACGCAATGTCCAGAA
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63945	62032	TCCATTAATACGCAATGTCC
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63954	62041	TTATATGATTCCATTAATAC
63955	62042	ATTATATGATTCCATTAATA
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63957	62044	ATATTATATGATTCCATTAA
63958	62045	TATATTATATGATTCCATTA
63959	62046	ATATATTATATGATTCCATT
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63963	62050	GGCTATATATTATATGATTC
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113060	111147	TTTCTCTTGTTTACATGCTG
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113065	111152	TCGTCTTTCTCTTGTTTACA
113066	111153	ATCGTCTTTCTCTTGTTTAC
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113077	111164	TTCTCTTCCTTATCGTCTTT
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113123	111210	ACAGGATGGTCTAAGTTCCA
113124	111211	AACAGGATGGTCTAAGTTCC
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14875	12962	TGTTTTTCAGTAGAGACAGG
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14899	12986	AGCCACCACGCCCGGCCCTT
14900	12987	GAGCCACCACGCCCGGCCCT
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113172	111259	CAGTTGGAAGGACCTAAATG
113173	111260	ACAGTTGGAAGGACCTAAAT
113174	111261	CACAGTTGGAAGGACCTAAA
113175	111262	TCACAGTTGGAAGGACCTAA
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113178	111265	TCTTCACAGTTGGAAGGACC
113179	111266	TTCTTCACAGTTGGAAGGAC
113180	111267	ATTCTTCACAGTTGGAAGGA
113181	111268	GATTCTTCACAGTTGGAAGG
113182	111269	GGATTCTTCACAGTTGGAAG
113183	111270	TGGATTCTTCACAGTTGGAA
113184	111271	ATGGATTCTTCACAGTTGGA
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113187	111274	CAGATGGATTCTTCACAGTT
113188	111275	CCAGATGGATTCTTCACAGT
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14904	12991	GGGTGAGCCACCACGCCCGG
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14914	13001	GGGATTACAGGGGTGAGCCA
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14916	13003	CTGGGATTACAGGGGTGAGC
14917	13004	GCTGGGATTACAGGGGTGAG
14918	13005	TGCTGGGATTACAGGGGTGA
14919	13006	GTGCTGGGATTACAGGGGTG
14920	13007	AGTGCTGGGATTACAGGGGT
14921	13008	AAGTGCTGGGATTACAGGGG
14922	13009	AAAGTGCTGGGATTACAGGG
14923	13010	CAAAGTGCTGGGATTACAGG
14924	13011	CCAAAGTGCTGGGATTACAG
14925	13012	CCCAAAGTGCTGGGATTACA
14926	13013	TCCCAAAGTGCTGGGATTAC
14927	13014	CTCCCAAAGTGCTGGGATTA
14928	13015	CCTCCCAAAGTGCTGGGATT
14929	13016	ACCTCCCAAAGTGCTGGGAT
14930	13017	AACCTCCCAAAGTGCTGGGA
14931	13018	CAACCTCCCAAAGTGCTGGG
14932	13019	TCAACCTCCCAAAGTGCTGG
14933	13020	CTCAACCTCCCAAAGTGCTG
14934	13021	CCTCAACCTCCCAAAGTGCT
14935	13022	TCCTCAACCTCCCAAAGTGC
14936	13023	CTCCTCAACCTCCCAAAGTG
14937	13024	CCTCCTCAACCTCCCAAAGT
14938	13025	CCCTCCTCAACCTCCCAAAG
14939	13026	GCCCTCCTCAACCTCCCAAA
14940	13027	CGCCCTCCTCAACCTCCCAA
14941	13028	CCGCCCTCCTCAACCTCCCA
14942	13029	TCCGCCCTCCTCAACCTCCC
14943	13030	ATCCGCCCTCCTCAACCTCC
14944	13031	AATCCGCCCTCCTCAACCTC
14945	13032	TAATCCGCCCTCCTCAACCT
14946	13033	GTAATCCGCCCTCCTCAACC
14947	13034	TGTAATCCGCCCTCCTCAAC
14948	13035	TTGTAATCCGCCCTCCTCAA
14949	13036	CTTGTAATCCGCCCTCCTCA
14950	13037	CCTTGTAATCCGCCCTCCTC
14951	13038	ACCTTGTAATCCGCCCTCCT
14952	13039	GACCTTGTAATCCGCCCTCC
14953	13040	TGACCTTGTAATCCGCCCTC
14954	13041	TTGACCTTGTAATCCGCCCT
14955	13042	CTTGACCTTGTAATCCGCCC
14956	13043	TCTTGACCTTGTAATCCGCC
14957	13044	CTCTTGACCTTGTAATCCGC
14958	13045	TCTCTTGACCTTGTAATCCG
14959	13046	ATCTCTTGACCTTGTAATCC
14960	13047	AATCTCTTGACCTTGTAATC
14961	13048	CAATCTCTTGACCTTGTAAT
14962	13049	TCAATCTCTTGACCTTGTAA
14963	13050	CTCAATCTCTTGACCTTGTA
14964	13051	TCTCAATCTCTTGACCTTGT
14965	13052	GTCTCAATCTCTTGACCTTG
14966	13053	GGTCTCAATCTCTTGACCTT
14967	13054	TGGTCTCAATCTCTTGACCT
14968	13055	ATGGTCTCAATCTCTTGACC
14969	13056	AATGGTCTCAATCTCTTGAC
14970	13057	GAATGGTCTCAATCTCTTGA
14971	13058	AGAATGGTCTCAATCTCTTG
14972	13059	CAGAATGGTCTCAATCTCTT
14973	13060	CCAGAATGGTCTCAATCTCT
14974	13061	GCCAGAATGGTCTCAATCTC

64051	62138	AGGATGCAGTGAGCTGCAAT
64052	62139	GAGGATGCAGTGAGCTGCAA
64053	62140	AGAGGATGCAGTGAGCTGCA
64054	62141	CAGAGGATGCAGTGAGCTGC
64055	62142	GCAGAGGATGCAGTGAGCTG
64056	62143	GGCAGAGGATGCAGTGAGCT
64057	62144	AGGCAGAGGATGCAGTGAGC
64058	62145	GAGGCAGAGGATGCAGTGAG
64059	62146	GGAGGCAGAGGATGCAGTGA
64060	62147	GGGAGGCAGAGGATGCAGTG
64061	62148	TGGGAGGCAGAGGATGCAGT
64062	62149	CTGGGAGGCAGAGGATGCAG
64063	62150	CCTGGGAGGCAGAGGATGCA
64064	62151	ACCTGGGAGGCAGAGGATGC
64065	62152	AACCTGGGAGGCAGAGGATG
64066	62153	CAACCTGGGAGGCAGAGGAT
64067	62154	TCAACCTGGGAGGCAGAGGA
64068	62155	TTCAACCTGGGAGGCAGAGG
64069	62156	CTTCAACCTGGGAGGCAGAG
64070	62157	GCTTCAACCTGGGAGGCAGA
64071	62158	CGCTTCAACCTGGGAGGCAG
64072	62159	TCGCTTCAACCTGGGAGGCA
64073	62160	ATCGCTTCAACCTGGGAGGC
64074	62161	AATCGCTTCAACCTGGGAGG
64075	62162	GAATCGCTTCAACCTGGGAG
64076	62163	AGAATCGCTTCAACCTGGGA
64077	62164	GAGAATCGCTTCAACCTGGG
64078	62165	GGAGAATCGCTTCAACCTGG
64079	62166	AGGAGAATCGCTTCAACCTG
64080	62167	CAGGAGAATCGCTTCAACCT
64081	62168	GCAGGAGAATCGCTTCAACC
64082	62169	GGCAGGAGAATCGCTTCAAC
64083	62170	AGGCAGGAGAATCGCTTCAA
64084	62171	GAGGCAGGAGAATCGCTTCA
64085	62172	TGAGGCAGGAGAATCGCTTC
64086	62173	CTGAGGCAGGAGAATCGCTT
64087	62174	GCTGAGGCAGGAGAATCGCT
64088	62175	GGCTGAGGCAGGAGAATCGC
64089	62176	AGGCTGAGGCAGGAGAATCG
64090	62177	GAGGCTGAGGCAGGAGAATC
64091	62178	AGAGGCTGAGGCAGGAGAAT
64092	62179	AAGAGGCTGAGGCAGGAGAA
64093	62180	CAAGAGGCTGAGGCAGGAGA
64094	62181	TCAAGAGGCTGAGGCAGGAG
64095	62182	CTCAAGAGGCTGAGGCAGGA
64096	62183	ACTCAAGAGGCTGAGGCAGG
64097	62184	TACTCAAGAGGCTGAGGCAG
64098	62185	CTACTCAAGAGGCTGAGGCA
64099	62186	GCTACTCAAGAGGCTGAGGC
64100	62187	AGCTACTCAAGAGGCTGAGG
64101	62188	CAGCTACTCAAGAGGCTGAG
64102	62189	CCAGCTACTCAAGAGGCTGA
64103	62190	CCCAGCTACTCAAGAGGCTG
64104	62191	TCCCAGCTACTCAAGAGGCT
64105	62192	GTCCCAGCTACTCAAGAGGC
64106	62193	AGTCCCAGCTACTCAAGAGG
64107	62194	TAGTCCCAGCTACTCAAGAG
64108	62195	ATAGTCCCAGCTACTCAAGA
64109	62196	TATAGTCCCAGCTACTCAAG
64110	62197	CTATAGTCCCAGCTACTCAA
64111	62198	CCTATAGTCCCAGCTACTCA
64112	62199	GCCTATAGTCCCAGCTACTC
64113	62200	CGCCTATAGTCCCAGCTACT
64114	62201	GCGCCTATAGTCCCAGCTAC
64115	62202	GGCGCCTATAGTCCCAGCTA
64116	62203	AGGCGCCTATAGTCCCAGCT
64117	62204	CAGGCGCCTATAGTCCCAGC
64118	62205	GCAGGCGCCTATAGTCCCAG
64119	62206	GGCAGGCGCCTATAGTCCCA
64120	62207	TGGCAGGCGCCTATAGTCCC
64121	62208	GTGGCAGGCGCCTATAGTCC

113198	111285	GTCTAAAAGTCCAGATGGAT
113199	111286	AGTCTAAAAGTCCAGATGGA
113200	111287	TAGTCTAAAAGTCCAGATGG
113201	111288	GTAGTCTAAAAGTCCAGATG
113202	111289	AGTAGTCTAAAAGTCCAGAT
113203	111290	AAGTAGTCTAAAAGTCCAGA
113204	111291	AAAGTAGTCTAAAAGTCCAG
113205	111292	TAAAGTAGTCTAAAAGTCCA
113206	111293	ATAAAGTAGTCTAAAAGTCC
113207	111294	TATAAAGTAGTCTAAAAGTC
113208	111295	GTATAAAGTAGTCTAAAAGT
113209	111296	TGTATAAAGTAGTCTAAAAG
113210	111297	ATGTATAAAGTAGTCTAAAA
113211	111298	AATGTATAAAGTAGTCTAAA
113212	111299	CAATGTATAAAGTAGTCTAA
113213	111300	GCAATGTATAAAGTAGTCTA
113214	111301	GGCAATGTATAAAGTAGTCT
113215	111302	GGGCAATGTATAAAGTAGTC
113216	111303	AGGGCAATGTATAAAGTAGT
113217	111304	AAGGGCAATGTATAAAGTAG
113218	111305	TAAGGGCAATGTATAAAGTA
113219	111306	CTAAGGGCAATGTATAAAGT
113220	111307	ACTAAGGGCAATGTATAAAG
113221	111308	AACTAAGGGCAATGTATAAA
113222	111309	AAACTAAGGGCAATGTATAA
113223	111310	TAAACTAAGGGCAATGTATA
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113226	111313	TTGTAAACTAAGGGCAATGT
113227	111314	TTTGTAAACTAAGGGCAATG
113228	111315	GTTTGTAAACTAAGGGCAAT
113229	111316	TGTTTGTAAACTAAGGGCAA
113230	111317	CTGTTTGTAAACTAAGGGCA
113231	111318	GCTGTTTGTAAACTAAGGGC
113232	111319	AGCTGTTTGTAAACTAAGGG
113233	111320	TAGCTGTTTGTAAACTAAGG
113234	111321	CTAGCTGTTTGTAAACTAAG
113235	111322	ACTAGCTGTTTGTAAACTAA
113236	111323	GACTAGCTGTTTGTAAACTA
113237	111324	GGACTAGCTGTTTGTAAACT
113238	111325	TGGACTAGCTGTTTGTAAAC
113239	111326	TTGGACTAGCTGTTTGTAAA
113240	111327	TTTGGACTAGCTGTTTGTAA
113241	111328	GTTTGGACTAGCTGTTTGTA
113242	111329	TGTTTGGACTAGCTGTTTGT
113243	111330	TTGTTTGGACTAGCTGTTTG
113244	111331	TTTGTTTGGACTAGCTGTTT
113245	111332	ATTTGTTTGGACTAGCTGTT
113246	111333	CATTTGTTTGGACTAGCTGT
113247	111334	TCATTTGTTTGGACTAGCTG
113248	111335	GTCATTTGTTTGGACTAGCT
113249	111336	TGTCATTTGTTTGGACTAGC
113250	111337	ATGTCATTTGTTTGGACTAG
113251	111338	GATGTCATTTGTTTGGACTA
113252	111339	AGATGTCATTTGTTTGGACT
113253	111340	AAGATGTCATTTGTTTGGAC
113254	111341	TAAGATGTCATTTGTTTGGA
113255	111342	TTAAGATGTCATTTGTTTGG
113256	111343	CTTAAGATGTCATTTGTTTG
113257	111344	ACTTAAGATGTCATTTGTTT
113258	111345	TACTTAAGATGTCATTTGTT
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113262	111349	CATTTACTTAAGATGTCATT
113263	111350	TCATTTACTTAAGATGTCAT
113264	111351	CTCATTTACTTAAGATGTCA
113265	111352	CCTCATTTACTTAAGATGTC
113266	111353	ACCTCATTTACTTAAGATGT
113267	111354	AACCTCATTTACTTAAGATG
113268	111355	TAACCTCATTTACTTAAGAT

14975	13062	GGCCAGAATGGTCTCAATCT
14976	13063	TGGCCAGAATGGTCTCAATC
14977	13064	TTGGCCAGAATGGTCTCAAT
14978	13065	GTTGGCCAGAATGGTCTCAA
14979	13066	TGTTGGCCAGAATGGTCTCA
14980	13067	CTGTTGGCCAGAATGGTCTC
14981	13068	CCTGTTGGCCAGAATGGTCT
14982	13069	CCCTGTTGGCCAGAATGGTC
14983	13070	ACCCTGTTGGCCAGAATGGT
14984	13071	CACCCTGTTGGCCAGAATGG
14985	13072	TCACCCTGTTGGCCAGAATG
14986	13073	TTCACCCTGTTGGCCAGAAT
14987	13074	TTTCACCCTGTTGGCCAGAA
14988	13075	GTTTCACCCTGTTGGCCAGA
14989	13076	GGTTTCACCCTGTTGGCCAG
14990	13077	GGGTTTCACCCTGTTGGCCA
14991	13078	GGGGTTTCACCCTGTTGGCC
14992	13079	TGGGGTTTCACCCTGTTGGC
14993	13080	ATGGGGTTTCACCCTGTTGG
14994	13081	GATGGGGTTTCACCCTGTTG
14995	13082	AGATGGGGTTTCACCCTGTT
14996	13083	GAGATGGGGTTTCACCCTGT
14997	13084	AGAGATGGGGTTTCACCCTG
14998	13085	TAGAGATGGGGTTTCACCCT
14999	13086	GTAGAGATGGGGTTTCACCC
15000	13087	AGTAGAGATGGGGTTTCACC
15001	13088	TAGTAGAGATGGGGTTTCAC
15002	13089	TTAGTAGAGATGGGGTTTCA
15003	13090	TTTAGTAGAGATGGGGTTTC
15004	13091	TTTTAGTAGAGATGGGGTTT
15005	13092	TTTTTAGTAGAGATGGGGTT
15006	13093	ATTTTTAGTAGAGATGGGGT
15007	13094	TATTTTTAGTAGAGATGGGG
15008	13095	GTATTTTTAGTAGAGATGGG
15009	13096	TGTATTTTTAGTAGAGATGG
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15011	13098	TTTGTATTTTTAGTAGAGAT
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15015	13102	TTTTTTTGTATTTTTAGTAG
15016	13103	ATTTTTTTGTATTTTTAGTA
15017	13104	AATTTTTTTGTATTTTTAGT
15018	13105	TAATTTTTTTGTATTTTTAG
15019	13106	TTAATTTTTTTGTATTTTTA
15020	13107	TTTAATTTTTTTGTATTTTT
15021	13108	ATTTAATTTTTTTGTATTTT
15022	13109	CATTTAATTTTTTTGTATTT
15023	13110	CCATTTAATTTTTTTGTATT
15024	13111	CCCATTTAATTTTTTTGTAT
15025	13112	GCCCATTTAATTTTTTTGTA
15026	13113	CGCCCATTTAATTTTTTTGT
15027	13114	ACGCCCATTTAATTTTTTTG
15028	13115	CACGCCCATTTAATTTTTTT
15029	13116	CCACGCCCATTTAATTTTTT
15030	13117	ACCACGCCCATTTAATTTTT
15031	13118	CACCACGCCCATTTAATTTT
15032	13119	TCACCACGCCCATTTAATTT
15033	13120	ATCACCACGCCCATTTAATT
15034	13121	CATCACCACGCCCATTTAAT
15035	13122	ACATCACCACGCCCATTTAA
15036	13123	CACATCACCACGCCCATTTA
15037	13124	ACACATCACCACGCCCATTT
15038	13125	CACACATCACCACGCCCATT
15039	13126	GCACACATCACCACGCCCAT
15040	13127	GGCACACATCACCACGCCCA
15041	13128	AGGCACACATCACCACGCCC
15042	13129	CAGGCACACATCACCACGCC
15043	13130	ACAGGCACACATCACCACGC
15044	13131	TACAGGCACACATCACCACG
15045	13132	CTACAGGCACACATCACCAC

64122	62209	GGTGGCAGGCGCCTATAGTC
64123	62210	TGGTGGCAGGCGCCTATAGT
64124	62211	GTGGTGGCAGGCGCCTATAG
64125	62212	TGTGGTGGCAGGCGCCTATA
64126	62213	GTGTGGTGGCAGGCGCCTAT
64127	62214	GGTGTGGTGGCAGGCGCCTA
64128	62215	AGGTGTGGTGGCAGGCGCCT
64129	62216	TAGGTGTGGTGGCAGGCGCC
64130	62217	GTAGGTGTGGTGGCAGGCGC
64131	62218	AGTAGGTGTGGTGGCAGGCG
64132	62219	TAGTAGGTGTGGTGGCAGGC
64133	62220	TTAGTAGGTGTGGTGGCAGG
64134	62221	ATTAGTAGGTGTGGTGGCAG
64135	62222	AATTAGTAGGTGTGGTGGCA
64136	62223	AAATTAGTAGGTGTGGTGGC
64137	62224	AAAATTAGTAGGTGTGGTGG
64138	62225	TAAAATTAGTAGGTGTGGTG
64139	62226	ATAAAATTAGTAGGTGTGGT
64140	62227	TATAAAATTAGTAGGTGTGG
64141	62228	ATATAAAATTAGTAGGTGTG
64142	62229	AATATAAAATTAGTAGGTGT
64143	62230	AAATATAAAATTAGTAGGTG
64144	62231	AAAATATAAAATTAGTAGGT
64145	62232	AAAAATATAAAATTAGTAGG
64146	62233	TAAAAATATAAAATTAGTAG
64147	62234	CTAAAAATATAAAATTAGTA
64148	62235	ACTAAAAATATAAAATTAGT
64149	62236	TACTAAAAATATAAAATTAG
64150	62237	TTACTAAAAATATAAAATTA
64151	62238	TTTACTAAAAATATAAAATT
64152	62239	CTTTACTAAAAATATAAAAT
64153	62240	TCTTTACTAAAAATATAAAA
64154	62241	GTCTTTACTAAAAATATAAA
64155	62242	CGTCTTTACTAAAAATATAA
64156	62243	CCGTCTTTACTAAAAATATA
64157	62244	CCCGTCTTTACTAAAAATAT
64158	62245	CCCCGTCTTTACTAAAAATA
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64160	62247	AACCCCGTCTTTACTAAAAA
64161	62248	CAACCCCGTCTTTACTAAAA
64162	62249	GCAACCCCGTCTTTACTAAA
64163	62250	TGCAACCCCGTCTTTACTAA
64164	62251	GTGCAACCCCGTCTTTACTA
64165	62252	GGTGCAACCCCGTCTTTACT
64166	62253	TGGTGCAACCCCGTCTTTAC
64167	62254	ATGGTGCAACCCCGTCTTTA
64168	62255	CATGGTGCAACCCCGTCTTT
64169	62256	ACATGGTGCAACCCCGTCTT
64170	62257	AACATGGTGCAACCCCGTCT
64171	62258	CAACATGGTGCAACCCCGTC
64172	62259	CCAACATGGTGCAACCCCGT
64173	62260	GCCAACATGGTGCAACCCCG
64174	62261	GGCCAACATGGTGCAACCCC
64175	62262	TGGCCAACATGGTGCAACCC
64176	62263	CTGGCCAACATGGTGCAACC
64177	62264	CCTGGCCAACATGGTGCAAC
64178	62265	GCCTGGCCAACATGGTGCAA
64179	62266	AGCCTGGCCAACATGGTGCA
64180	62267	CAGCCTGGCCAACATGGTGC
64181	62268	CCAGCCTGGCCAACATGGTG
64182	62269	ACCAGCCTGGCCAACATGGT
64183	62270	GACCAGCCTGGCCAACATGG
64184	62271	AGACCAGCCTGGCCAACATG
64185	62272	GAGACCAGCCTGGCCAACAT
64186	62273	CGAGACCAGCCTGGCCAACA
64187	62274	TCGAGACCAGCCTGGCCAAC
64188	62275	TTCGAGACCAGCCTGGCCAA
64189	62276	ATTCGAGACCAGCCTGGCCA
64190	62277	AATTCGAGACCAGCCTGGCC
64191	62278	GAATTCGAGACCAGCCTGGC
64192	62279	GGAATTCGAGACCAGCCTGG

113269	111356	ATAACCTCATTTACTTAAGA
113270	111357	AATAACCTCATTTACTTAAG
113271	111358	CAATAACCTCATTTACTTAA
113272	111359	GCAATAACCTCATTTACTTA
113273	111360	TGCAATAACCTCATTTACTT
113274	111361	GTGCAATAACCTCATTTACT
113275	111362	GGTGCAATAACCTCATTTAC
113276	111363	GGGTGCAATAACCTCATTTA
113277	111364	AGGGTGCAATAACCTCATTT
113278	111365	CAGGGTGCAATAACCTCATT
113279	111366	ACAGGGTGCAATAACCTCAT
113280	111367	CACAGGGTGCAATAACCTCA
113281	111368	GCACAGGGTGCAATAACCTC
113282	111369	AGCACAGGGTGCAATAACCT
113283	111370	TAGCACAGGGTGCAATAACC
113284	111371	GTAGCACAGGGTGCAATAAC
113285	111372	AGTAGCACAGGGTGCAATAA
113286	111373	GAGTAGCACAGGGTGCAATA
113287	111374	AGAGTAGCACAGGGTGCAAT
113288	111375	AAGAGTAGCACAGGGTGCAA
113289	111376	GAAGAGTAGCACAGGGTGCA
113290	111377	AGAAGAGTAGCACAGGGTGC
113291	111378	CAGAAGAGTAGCACAGGGTG
113292	111379	ACAGAAGAGTAGCACAGGGT
113293	111380	AACAGAAGAGTAGCACAGGG
113294	111381	GAACAGAAGAGTAGCACAGG
113295	111382	AGAACAGAAGAGTAGCACAG
113296	111383	AAGAACAGAAGAGTAGCACA
113297	111384	GAAGAACAGAAGAGTAGCAC
113298	111385	GGAAGAACAGAAGAGTAGCA
113299	111386	GGGAAGAACAGAAGAGTAGC
113300	111387	GGGGAAGAACAGAAGAGTAG
113301	111388	AGGGGAAGAACAGAAGAGTA
113302	111389	AAGGGGAAGAACAGAAGAGT
113303	111390	AAAGGGGAAGAACAGAAGAG
113304	111391	AAAAGGGGAAGAACAGAAGA
113305	111392	AAAAAGGGGAAGAACAGAAG
113306	111393	AAAAAAGGGGAAGAACAGAA
113307	111394	CAAAAAAGGGGAAGAACAGA
113308	111395	ACAAAAAAGGGGAAGAACAG
113309	111396	TACAAAAAAGGGGAAGAACA
113310	111397	GTACAAAAAAGGGGAAGAAC
113311	111398	GGTACAAAAAAGGGGAAGAA
113312	111399	GGGTACAAAAAAGGGGAAGA
113313	111400	GGGGTACAAAAAAGGGGAAG
113314	111401	TGGGGTACAAAAAAGGGGAA
113315	111402	CTGGGGTACAAAAAAGGGGA
113316	111403	CCTGGGGTACAAAAAAGGGG
113317	111404	CCCTGGGGTACAAAAAAGGG
113318	111405	GCCCTGGGGTACAAAAAAGG
113319	111406	AGCCCTGGGGTACAAAAAAG
113320	111407	TAGCCCTGGGGTACAAAAAA
113321	111408	CTAGCCCTGGGGTACAAAAA
113322	111409	TCTAGCCCTGGGGTACAAAA
113323	111410	TTCTAGCCCTGGGGTACAAA
113324	111411	TTTCTAGCCCTGGGGTACAA
113325	111412	TTTTCTAGCCCTGGGGTACA
113326	111413	TTTTTCTAGCCCTGGGGTAC
113327	111414	GTTTTTCTAGCCCTGGGGTA
113328	111415	TGTTTTTCTAGCCCTGGGGT
113329	111416	TTGTTTTTCTAGCCCTGGGG
113330	111417	CTTGTTTTTCTAGCCCTGGG
113331	111418	CCTTGTTTTTCTAGCCCTGG
113332	111419	GCCTTGTTTTTCTAGCCCTG
113333	111420	TGCCTTGTTTTTCTAGCCCT
113334	111421	ATGCCTTGTTTTTCTAGCCC
113335	111422	TATGCCTTGTTTTTCTAGCC
113336	111423	TTATGCCTTGTTTTTCTAGC
113337	111424	TTTATGCCTTGTTTTTCTAG
113338	111425	ATTTATGCCTTGTTTTTCTA
113339	111426	AATTTATGCCTTGTTTTTCT

15046	13133	ACTACAGGCACACATCACCA
15047	13134	GACTACAGGCACACATCACC
15048	13135	GGACTACAGGCACACATCAC
15049	13136	GGGACTACAGGCACACATCA
15050	13137	TGGGACTACAGGCACACATC
15051	13138	CTGGGACTACAGGCACACAT
15052	13139	GCTGGGACTACAGGCACACA
15053	13140	AGCTGGGACTACAGGCACAC
15054	13141	TAGCTGGGACTACAGGCACA
15055	13142	GTAGCTGGGACTACAGGCAC
15056	13143	AGTAGCTGGGACTACAGGCA
15057	13144	GAGTAGCTGGGACTACAGGC
15058	13145	CGAGTAGCTGGGACTACAGG
15059	13146	CCGAGTAGCTGGGACTACAG
15060	13147	CCCGAGTAGCTGGGACTACA
15061	13148	TCCCGAGTAGCTGGGACTAC
15062	13149	CTCCCGAGTAGCTGGGACTA
15063	13150	CCTCCCGAGTAGCTGGGACT
15064	13151	GCCTCCCGAGTAGCTGGGAC
15065	13152	AGCCTCCCGAGTAGCTGGGA
15066	13153	CAGCCTCCCGAGTAGCTGGG
15067	13154	TCAGCCTCCCGAGTAGCTGG
15068	13155	CTCAGCCTCCCGAGTAGCTG
15069	13156	CCTCAGCCTCCCGAGTAGCT
15070	13157	GCCTCAGCCTCCCGAGTAGC
15071	13158	TGCCTCAGCCTCCCGAGTAG
15072	13159	CTGCCTCAGCCTCCCGAGTA
15073	13160	CCTGCCTCAGCCTCCCGAGT
15074	13161	TCCTGCCTCAGCCTCCCGAG
15075	13162	CTCCTGCCTCAGCCTCCCGA
15076	13163	TCTCCTGCCTCAGCCTCCCG
15077	13164	TTCTCCTGCCTCAGCCTCCC
15078	13165	ATTCTCCTGCCTCAGCCTCC
15079	13166	AATTCTCCTGCCTCAGCCTC
15080	13167	CAATTCTCCTGCCTCAGCCT
15081	13168	GCAATTCTCCTGCCTCAGCC
15082	13169	AGCAATTCTCCTGCCTCAGC
15083	13170	AAGCAATTCTCCTGCCTCAG
15084	13171	CAAGCAATTCTCCTGCCTCA
15085	13172	TCAAGCAATTCTCCTGCCTC
15086	13173	TTCAAGCAATTCTCCTGCCT
15087	13174	GTTCAAGCAATTCTCCTGCC
15088	13175	GGTTCAAGCAATTCTCCTGC
15089	13176	GGGTTCAAGCAATTCTCCTG
15090	13177	CGGGTTCAAGCAATTCTCCT
15091	13178	CCGGGTTCAAGCAATTCTCC
15092	13179	CCCGGGTTCAAGCAATTCTC
15093	13180	TCCCGGGTTCAAGCAATTCT
15094	13181	CTCCCGGGTTCAAGCAATTC
15095	13182	CCTCCCGGGTTCAAGCAATT
15096	13183	GCCTCCCGGGTTCAAGCAAT
15097	13184	TGCCTCCCGGGTTCAAGCAA
15098	13185	CTGCCTCCCGGGTTCAAGCA
15099	13186	TCTGCCTCCCGGGTTCAAGC
15100	13187	CTCTGCCTCCCGGGTTCAAG
15101	13188	CCTCTGCCTCCCGGGTTCAA
15102	13189	ACCTCTGCCTCCCGGGTTCA
15103	13190	AACCTCTGCCTCCCGGGTTC
15104	13191	CAACCTCTGCCTCCCGGGTT
15105	13192	GCAACCTCTGCCTCCCGGGT
15106	13193	TGCAACCTCTGCCTCCCGGG
15107	13194	CTGCAACCTCTGCCTCCCGG
15108	13195	ACTGCAACCTCTGCCTCCCG
15109	13196	CACTGCAACCTCTGCCTCCC
15110	13197	TCACTGCAACCTCTGCCTCC
15111	13198	CTCACTGCAACCTCTGCCTC
15112	13199	GCTCACTGCAACCTCTGCCT
15113	13200	GGCTCACTGCAACCTCTGCC
15114	13201	CGGCTCACTGCAACCTCTGC
15115	13202	TCGGCTCACTGCAACCTCTG
15116	13203	CTCGGCTCACTGCAACCTCT

64193	62280	AGGAATTCGAGACCAGCCTG
64194	62281	CAGGAATTCGAGACCAGCCT
64195	62282	TCAGGAATTCGAGACCAGCC
64196	62283	GTCAGGAATTCGAGACCAGC
64197	62284	GGTCAGGAATTCGAGACCAG
64198	62285	AGGTCAGGAATTCGAGACCA
64199	62286	GAGGTCAGGAATTCGAGACC
64200	62287	TGAGGTCAGGAATTCGAGAC
64201	62288	TTGAGGTCAGGAATTCGAGA
64202	62289	CTTGAGGTCAGGAATTCGAG
64203	62290	ACTTGAGGTCAGGAATTCGA
64204	62291	CACTTGAGGTCAGGAATTCG
64205	62292	TCACTTGAGGTCAGGAATTC
64206	62293	ATCACTTGAGGTCAGGAATT
64207	62294	GATCACTTGAGGTCAGGAAT
64208	62295	AGATCACTTGAGGTCAGGAA
64209	62296	CAGATCACTTGAGGTCAGGA
64210	62297	GCAGATCACTTGAGGTCAGG
64211	62298	GGCAGATCACTTGAGGTCAG
64212	62299	GGGCAGATCACTTGAGGTCA
64213	62300	TGGGCAGATCACTTGAGGTC
64214	62301	GTGGGCAGATCACTTGAGGT
64215	62302	GGTGGGCAGATCACTTGAGG
64216	62303	AGGTGGGCAGATCACTTGAG
64217	62304	GAGGTGGGCAGATCACTTGA
64218	62305	CGAGGTGGGCAGATCACTTG
64219	62306	CCGAGGTGGGCAGATCACTT
64220	62307	TCCGAGGTGGGCAGATCACT
64221	62308	GTCCGAGGTGGGCAGATCAC
64222	62309	AGTCCGAGGTGGGCAGATCA
64223	62310	GAGTCCGAGGTGGGCAGATC
64224	62311	GGAGTCCGAGGTGGGCAGAT
64225	62312	GGGAGTCCGAGGTGGGCAGA
64226	62313	TGGGAGTCCGAGGTGGGCAG
64227	62314	TTGGGAGTCCGAGGTGGGCA
64228	62315	TTTGGGAGTCCGAGGTGGGC
64229	62316	CTTTGGGAGTCCGAGGTGGG
64230	62317	ACTTTGGGAGTCCGAGGTGG
64231	62318	CACTTTGGGAGTCCGAGGTG
64232	62319	GCACTTTGGGAGTCCGAGGT
64233	62320	AGCACTTTGGGAGTCCGAGG
64234	62321	CAGCACTTTGGGAGTCCGAG
64235	62322	CCAGCACTTTGGGAGTCCGA
64236	62323	CCCAGCACTTTGGGAGTCCG
64237	62324	TCCCAGCACTTTGGGAGTCC
64238	62325	ATCCCAGCACTTTGGGAGTC
64239	62326	AATCCCAGCACTTTGGGAGT
64240	62327	CAATCCCAGCACTTTGGGAG
64241	62328	GCAATCCCAGCACTTTGGGA
64242	62329	TGCAATCCCAGCACTTTGGG
64243	62330	CTGCAATCCCAGCACTTTGG
64244	62331	GCTGCAATCCCAGCACTTTG
64245	62332	GGCTGCAATCCCAGCACTTT
64246	62333	TGGCTGCAATCCCAGCACTT
64247	62334	ATGGCTGCAATCCCAGCACT
64248	62335	CATGGCTGCAATCCCAGCAC
64249	62336	TCATGGCTGCAATCCCAGCA
64250	62337	CTCATGGCTGCAATCCCAGC
64251	62338	GCTCATGGCTGCAATCCCAG
64252	62339	GGCTCATGGCTGCAATCCCA
64253	62340	TGGCTCATGGCTGCAATCCC
64254	62341	GTGGCTCATGGCTGCAATCC
64255	62342	GGTGGCTCATGGCTGCAATC
64256	62343	CGGTGGCTCATGGCTGCAAT
64257	62344	GCGGTGGCTCATGGCTGCAA
64258	62345	TGCGGTGGCTCATGGCTGCA
64259	62346	ATGCGGTGGCTCATGGCTGC
64260	62347	GATGCGGTGGCTCATGGCTG
64261	62348	AGATGCGGTGGCTCATGGCT
64262	62349	CAGATGCGGTGGCTCATGGC
64263	62350	CCAGATGCGGTGGCTCATGG

113340	111427	TAATTTATGCCTTGTTTTTC
113341	111428	TTAATTTATGCCTTGTTTTT
113342	111429	CTTAATTTATGCCTTGTTTT
113343	111430	TCTTAATTTATGCCTTGTTT
113344	111431	TTCTTAATTTATGCCTTGTT
113345	111432	TTTCTTAATTTATGCCTTGT
113346	111433	TTTTCTTAATTTATGCCTTG
113347	111434	CTTTTCTTAATTTATGCCTT
113348	111435	ACTTTTCTTAATTTATGCCT
113349	111436	AACTTTTCTTAATTTATGCC
113350	111437	AAACTTTTCTTAATTTATGC
113351	111438	AAAACTTTTCTTAATTTATG
113352	111439	AAAAACTTTTCTTAATTTAT
113353	111440	GAAAAACTTTTCTTAATTTA
113354	111441	AGAAAAACTTTTCTTAATTT
113355	111442	CAGAAAAACTTTTCTTAATT
113356	111443	ACAGAAAAACTTTTCTTAAT
113357	111444	TACAGAAAAACTTTTCTTAA
113358	111445	TTACAGAAAAACTTTTCTTA
113359	111446	TTTACAGAAAAACTTTTCTT
113360	111447	ATTTACAGAAAAACTTTTCT
113361	111448	CATTTACAGAAAAACTTTTC
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113363	111450	TTCATTTACAGAAAAACTTT
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113365	111452	TGTTCATTTACAGAAAAACT
113366	111453	CTGTTCATTTACAGAAAAAC
113367	111454	CCTGTTCATTTACAGAAAAA
113368	111455	TCCTGTTCATTTACAGAAAA
113369	111456	CTCCTGTTCATTTACAGAAA
113370	111457	ACTCCTGTTCATTTACAGAA
113371	111458	AACTCCTGTTCATTTACAGA
113372	111459	CAACTCCTGTTCATTTACAG
113373	111460	TCAACTCCTGTTCATTTACA
113374	111461	TTCAACTCCTGTTCATTTAC
113375	111462	TTTCAACTCCTGTTCATTTA
113376	111463	TTTTCAACTCCTGTTCATTT
113377	111464	TTTTTCAACTCCTGTTCATT
113378	111465	ATTTTTCAACTCCTGTTCAT
113379	111466	AATTTTTCAACTCCTGTTCA
113380	111467	TAATTTTTCAACTCCTGTTC
113381	111468	ATAATTTTTCAACTCCTGTT
113382	111469	GATAATTTTTCAACTCCTGT
113383	111470	TGATAATTTTTCAACTCCTG
113384	111471	TTGATAATTTTTCAACTCCT
113385	111472	ATTGATAATTTTTCAACTCC
113386	111473	AATTGATAATTTTTCAACTC
113387	111474	GAATTGATAATTTTTCAACT
113388	111475	TGAATTGATAATTTTTCAAC
113389	111476	CTGAATTGATAATTTTTCAA
113390	111477	CCTGAATTGATAATTTTTCA
113391	111478	CCCTGAATTGATAATTTTTC
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113393	111480	TCCCCTGAATTGATAATTTT
113394	111481	GTCCCCTGAATTGATAATTT
113395	111482	GGTCCCCTGAATTGATAATT
113396	111483	AGGTCCCCTGAATTGATAAT
113397	111484	TAGGTCCCCTGAATTGATAA
113398	111485	ATAGGTCCCCTGAATTGATA
113399	111486	GATAGGTCCCCTGAATTGAT
113400	111487	AGATAGGTCCCCTGAATTGA
113401	111488	AAGATAGGTCCCCTGAATTG
113402	111489	AAAGATAGGTCCCCTGAATT
113403	111490	TAAAGATAGGTCCCCTGAAT
113404	111491	GTAAAGATAGGTCCCCTGAA
113405	111492	AGTAAAGATAGGTCCCCTGA
113406	111493	CAGTAAAGATAGGTCCCCTG
113407	111494	CCAGTAAAGATAGGTCCCCT
113408	111495	TCCAGTAAAGATAGGTCCCC
113409	111496	ATCCAGTAAAGATAGGTCCC
113410	111497	AATCCAGTAAAGATAGGTCC

15117	13204	TCTCGGCTCACTGCAACCTC
15118	13205	ATCTCGGCTCACTGCAACCT
15119	13206	GATCTCGGCTCACTGCAACC
15120	13207	CGATCTCGGCTCACTGCAAC
15121	13208	CCGATCTCGGCTCACTGCAA
15122	13209	CCCGATCTCGGCTCACTGCA
15123	13210	GCCCGATCTCGGCTCACTGC
15124	13211	GGCCCGATCTCGGCTCACTG
15125	13212	TGGCCCGATCTCGGCTCACT
15126	13213	GTGGCCCGATCTCGGCTCAC
15127	13214	AGTGGCCCGATCTCGGCTCA
15128	13215	CAGTGGCCCGATCTCGGCTC
15129	13216	GCAGTGGCCCGATCTCGGCT
15130	13217	TGCAGTGGCCCGATCTCGGC
15131	13218	GTGCAGTGGCCCGATCTCGG
15132	13219	AGTGCAGTGGCCCGATCTCG
15133	13220	CAGTGCAGTGGCCCGATCTC
15134	13221	TCAGTGCAGTGGCCCGATCT
15135	13222	GTCAGTGCAGTGGCCCGATC
15136	13223	CGTCAGTGCAGTGGCCCGAT
15137	13224	TCGTCAGTGCAGTGGCCCGA
15138	13225	GTCGTCAGTGCAGTGGCCCG
15139	13226	TGTCGTCAGTGCAGTGGCCC
15140	13227	CTGTCGTCAGTGCAGTGGCC
15141	13228	TCTGTCGTCAGTGCAGTGGC
15142	13229	CTCTGTCGTCAGTGCAGTGG
15143	13230	CCTCTGTCGTCAGTGCAGTG
15144	13231	CCCTCTGTCGTCAGTGCAGT
15145	13232	TCCCTCTGTCGTCAGTGCAG
15146	13233	CTCCCTCTGTCGTCAGTGCA
15147	13234	TCTCCCTCTGTCGTCAGTGC
15148	13235	GTCTCCCTCTGTCGTCAGTG
15149	13236	AGTCTCCCTCTGTCGTCAGT
15150	13237	GAGTCTCCCTCTGTCGTCAG
15151	13238	GGAGTCTCCCTCTGTCGTCA
15152	13239	CGGAGTCTCCCTCTGTCGTC
15153	13240	ACGGAGTCTCCCTCTGTCGT
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15155	13242	AGACGGAGTCTCCCTCTGTC
15156	13243	TAGACGGAGTCTCCCTCTGT
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15158	13245	TTTAGACGGAGTCTCCCTCT
15159	13246	TTTTAGACGGAGTCTCCCTC
15160	13247	TTTTTAGACGGAGTCTCCCT
15161	13248	TTTTTTAGACGGAGTCTCCC
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15163	13250	TTTTTTTTAGACGGAGTCTC
15164	13251	TTTTTTTTTAGACGGAGTCT
15165	13252	TTTTTTTTTTAGACGGAGTC
15166	13253	TTTTTTTTTTTAGACGGAGT
15167	13254	TTTTTTTTTTTTAGACGGAG
15168	13255	TTTTTTTTTTTTTAGACGGA
15169	13256	TTTTTTTTTTTTTTAGACGG
15170	13257	TTTTTTTTTTTTTTTAGACG
15171	13258	TTTTTTTTTTTTTTTTAGAC
15172	13259	TTTTTTTTTTTTTTTTTAGA
15173	13260	TTTTTTTTTTTTTTTTTTAG
15174	13261	TTTTTTTTTTTTTTTTTTTA
15175	13262	TTTTTTTTTTTTTTTTTTTT
15176	13263	TTTTTTTTTTTTTTTTTTTT
15177	13264	TTTTTTTTTTTTTTTTTTTT
15178	13265	TTTTTTTTTTTTTTTTTTTT
15179	13266	TTTTTTTTTTTTTTTTTTTT
15180	13267	GTTTTTTTTTTTTTTTTTTT
15181	13268	GGTTTTTTTTTTTTTTTTTT
15182	13269	TGGTTTTTTTTTTTTTTTTT
15183	13270	CTGGTTTTTTTTTTTTTTTT
15184	13271	TCTGGTTTTTTTTTTTTTTT
15185	13272	GTCTGGTTTTTTTTTTTTTT
15186	13273	AGTCTGGTTTTTTTTTTTTT
15187	13274	AAGTCTGGTTTTTTTTTTTT

64264	62351	GCCAGATGCGGTGGCTCATG
64265	62352	GGCCAGATGCGGTGGCTCAT
64266	62353	TGGCCAGATGCGGTGGCTCA
64267	62354	ATGGCCAGATGCGGTGGCTC
64268	62355	TATGGCCAGATGCGGTGGCT
64269	62356	ATATGGCCAGATGCGGTGGC
64270	62357	TATATGGCCAGATGCGGTGG
64271	62358	ATATATGGCCAGATGCGGTG
64272	62359	TATATATGGCCAGATGCGGT
64273	62360	ATATATATGGCCAGATGCGG
64274	62361	AATATATATGGCCAGATGCG
64275	62362	TAATATATATGGCCAGATGC
64276	62363	ATAATATATATGGCCAGATG
64277	62364	CATAATATATATGGCCAGAT
64278	62365	TCATAATATATATGGCCAGA
64279	62366	ATCATAATATATATGGCCAG
64280	62367	TATCATAATATATATGGCCA
64281	62368	CTATCATAATATATATGGCC
64282	62369	CCTATCATAATATATATGGC
64283	62370	GCCTATCATAATATATATGG
64284	62371	AGCCTATCATAATATATATG
64285	62372	AAGCCTATCATAATATATAT
64286	62373	CAAGCCTATCATAATATATA
64287	62374	ACAAGCCTATCATAATATAT
64288	62375	AACAAGCCTATCATAATATA
64289	62376	AAACAAGCCTATCATAATAT
64290	62377	GAAACAAGCCTATCATAATA
64291	62378	TGAAACAAGCCTATCATAAT
64292	62379	GTGAAACAAGCCTATCATAA
64293	62380	AGTGAAACAAGCCTATCATA
64294	62381	AAGTGAAACAAGCCTATCAT
64295	62382	TAAGTGAAACAAGCCTATCA
64296	62383	CTAAGTGAAACAAGCCTATC
64297	62384	ACTAAGTGAAACAAGCCTAT
64298	62385	TACTAAGTGAAACAAGCCTA
64299	62386	ATACTAAGTGAAACAAGCCT
64300	62387	CATACTAAGTGAAACAAGCC
64301	62388	ACATACTAAGTGAAACAAGC
64302	62389	AACATACTAAGTGAAACAAG
64303	62390	AAACATACTAAGTGAAACAA
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64305	62392	AGAAACATACTAAGTGAAAC
64306	62393	AAGAAACATACTAAGTGAAA
64307	62394	GAAGAAACATACTAAGTGAA
64308	62395	GGAAGAAACATACTAAGTGA
64309	62396	TGGAAGAAACATACTAAGTG
64310	62397	ATGGAAGAAACATACTAAGT
64311	62398	CATGGAAGAAACATACTAAG
64312	62399	GCATGGAAGAAACATACTAA
64313	62400	AGCATGGAAGAAACATACTA
64314	62401	CAGCATGGAAGAAACATACT
64315	62402	ACAGCATGGAAGAAACATAC
64316	62403	TACAGCATGGAAGAAACATA
64317	62404	CTACAGCATGGAAGAAACAT
64318	62405	GCTACAGCATGGAAGAAACA
64319	62406	TGCTACAGCATGGAAGAAAC
64320	62407	ATGCTACAGCATGGAAGAAA
64321	62408	CATGCTACAGCATGGAAGAA
64322	62409	ACATGCTACAGCATGGAAGA
64323	62410	TACATGCTACAGCATGGAAG
64324	62411	ATACATGCTACAGCATGGAA
64325	62412	AATACATGCTACAGCATGGA
64326	62413	TAATACATGCTACAGCATGG
64327	62414	CTAATACATGCTACAGCATG
64328	62415	ACTAATACATGCTACAGCAT
64329	62416	TACTAATACATGCTACAGCA
64330	62417	GTACTAATACATGCTACAGC
64331	62418	AGTACTAATACATGCTACAG
64332	62419	AAGTACTAATACATGCTACA
64333	62420	GAAGTACTAATACATGCTAC
64334	62421	AGAAGTACTAATACATGCTA

113411	111498	GAATCCAGTAAAGATAGGTC
113412	111499	GGAATCCAGTAAAGATAGGT
113413	111500	TGGAATCCAGTAAAGATAGG
113414	111501	GTGGAATCCAGTAAAGATAG
113415	111502	AGTGGAATCCAGTAAAGATA
113416	111503	GAGTGGAATCCAGTAAAGAT
113417	111504	TGAGTGGAATCCAGTAAAGA
113418	111505	ATGAGTGGAATCCAGTAAAG
113419	111506	AATGAGTGGAATCCAGTAAA
113420	111507	TAATGAGTGGAATCCAGTAA
113421	111508	CTAATGAGTGGAATCCAGTA
113422	111509	ACTAATGAGTGGAATCCAGT
113423	111510	GACTAATGAGTGGAATCCAG
113424	111511	TGACTAATGAGTGGAATCCA
113425	111512	GTGACTAATGAGTGGAATCC
113426	111513	GGTGACTAATGAGTGGAATC
113427	111514	GGGTGACTAATGAGTGGAAT
113428	111515	AGGGTGACTAATGAGTGGAA
113429	111516	GAGGGTGACTAATGAGTGGA
113430	111517	TGAGGGTGACTAATGAGTGG
113431	111518	GTGAGGGTGACTAATGAGTG
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113433	111520	CAGTGAGGGTGACTAATGAG
113434	111521	ACAGTGAGGGTGACTAATGA
113435	111522	CACAGTGAGGGTGACTAATG
113436	111523	GCACAGTGAGGGTGACTAAT
113437	111524	AGCACAGTGAGGGTGACTAA
113438	111525	CAGCACAGTGAGGGTGACTA
113439	111526	GCAGCACAGTGAGGGTGACT
113440	111527	AGCAGCACAGTGAGGGTGAC
113441	111528	TAGCAGCACAGTGAGGGTGA
113442	111529	CTAGCAGCACAGTGAGGGTG
113443	111530	CCTAGCAGCACAGTGAGGGT
113444	111531	ACCTAGCAGCACAGTGAGGG
113445	111532	AACCTAGCAGCACAGTGAGG
113446	111533	CAACCTAGCAGCACAGTGAG
113447	111534	TCAACCTAGCAGCACAGTGA
113448	111535	TTCAACCTAGCAGCACAGTG
113449	111536	TTTCAACCTAGCAGCACAGT
113450	111537	TTTTCAACCTAGCAGCACAG
113451	111538	TTTTTCAACCTAGCAGCACA
113452	111539	GTTTTTCAACCTAGCAGCAC
113453	111540	AGTTTTTCAACCTAGCAGCA
113454	111541	CAGTTTTTCAACCTAGCAGC
113455	111542	GCAGTTTTTCAACCTAGCAG
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113457	111544	TGGCAGTTTTTCAACCTAGC
113458	111545	GTGGCAGTTTTTCAACCTAG
113459	111546	AGTGGCAGTTTTTCAACCTA
113460	111547	CAGTGGCAGTTTTTCAACCT
113461	111548	ACAGTGGCAGTTTTTCAACC
113462	111549	GACAGTGGCAGTTTTTCAAC
113463	111550	TGACAGTGGCAGTTTTTCAA
113464	111551	TTGACAGTGGCAGTTTTTCA
113465	111552	CTTGACAGTGGCAGTTTTTC
113466	111553	CCTTGACAGTGGCAGTTTTT
113467	111554	TCCTTGACAGTGGCAGTTTT
113468	111555	CTCCTTGACAGTGGCAGTTT
113469	111556	TCTCCTTGACAGTGGCAGTT
113470	111557	CTCTCCTTGACAGTGGCAGT
113471	111558	TCTCTCCTTGACAGTGGCAG
113472	111559	TTCTCTCCTTGACAGTGGCA
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113476	111563	ATGCTTCTCTCCTTGACAGT
113477	111564	CATGCTTCTCTCCTTGACAG
113478	111565	GCATGCTTCTCTCCTTGACA
113479	111566	CGCATGCTTCTCTCCTTGAC
113480	111567	CCGCATGCTTCTCTCCTTGA
113481	111568	ACCGCATGCTTCTCTCCTTG

15188	13275	CAAGTCTGGTTTTTTTTTT
15189	13276	CCAAGTCTGGTTTTTTTTT
15190	13277	CCCAAGTCTGGTTTTTTTT
15191	13278	CCCCAAGTCTGGTTTTTTT
15192	13279	GCCCCAAGTCTGGTTTTTT
15193	13280	AGCCCCAAGTCTGGTTTTT
15194	13281	CAGCCCCAAGTCTGGTTTT
15195	13282	CCAGCCCCAAGTCTGGTTT
15196	13283	CCCAGCCCCAAGTCTGGTT
15197	13284	GCCCAGCCCCAAGTCTGGTT
15198	13285	CGCCCAGCCCCAAGTCTGGT
15199	13286	CCGCCCAGCCCCAAGTCTGG
15200	13287	CCCGCCCAGCCCCAAGTCTG
15201	13288	GCCCGCCCAGCCCCAAGTCT
15202	13289	CGCCCGCCCAGCCCCAAGTC
15203	13290	GCGCCCGCCCAGCCCCAAGT
15204	13291	GGCGCCCGCCCAGCCCCAAG
15205	13292	AGGCGCCCGCCCAGCCCCAA
15206	13293	CAGGCGCCCGCCCAGCCCCA
15207	13294	ACAGGCGCCCGCCCAGCCCC
15208	13295	TACAGGCGCCCGCCCAGCCC
15209	13296	TTACAGGCGCCCGCCCAGCC
15210	13297	ATTACAGGCGCCCGCCCAGC
15211	13298	GATTACAGGCGCCCGCCCAG
15212	13299	GGATTACAGGCGCCCGCCCA
15213	13300	GGGATTACAGGCGCCCGCCC
15214	13301	TGGGATTACAGGCGCCCGCC
15215	13302	CTGGGATTACAGGCGCCCGC
15216	13303	GCTGGGATTACAGGCGCCCG
15217	13304	AGCTGGGATTACAGGCGCCC
15218	13305	TAGCTGGGATTACAGGCGCC
15219	13306	GTAGCTGGGATTACAGGCGC
15220	13307	AGTAGCTGGGATTACAGGCG
15221	13308	AAGTAGCTGGGATTACAGGC
15222	13309	CAAGTAGCTGGGATTACAGG
15223	13310	CCAAGTAGCTGGGATTACAG
15224	13311	CCCAAGTAGCTGGGATTACA
15225	13312	TCCCAAGTAGCTGGGATTAC
15226	13313	CTCCCAAGTAGCTGGGATTA
15227	13314	CCTCCCAAGTAGCTGGGATT
15228	13315	GCCTCCCAAGTAGCTGGGAT
15229	13316	AGCCTCCCAAGTAGCTGGGA
15230	13317	CAGCCTCCCAAGTAGCTGGG
15231	13318	TCAGCCTCCCAAGTAGCTGG
15232	13319	CTCAGCCTCCCAAGTAGCTG
15233	13320	CCTCAGCCTCCCAAGTAGCT
15234	13321	GCCTCAGCCTCCCAAGTAGC
15235	13322	TGCCTCAGCCTCCCAAGTAG
15236	13323	CTGCCTCAGCCTCCCAAGTA
15237	13324	CCTGCCTCAGCCTCCCAAGT
15238	13325	TCCTGCCTCAGCCTCCCAAG
15239	13326	CTCCTGCCTCAGCCTCCCAA
15240	13327	TCTCCTGCCTCAGCCTCCCA
15241	13328	TTCTCCTGCCTCAGCCTCCC
15242	13329	ATTCTCCTGCCTCAGCCTCC
15243	13330	GATTCTCCTGCCTCAGCCTC
15244	13331	CGATTCTCCTGCCTCAGCCT
15245	13332	GCGATTCTCCTGCCTCAGCC
15246	13333	AGCGATTCTCCTGCCTCAGC
15247	13334	AAGCGATTCTCCTGCCTCAG
15248	13335	CAAGCGATTCTCCTGCCTCA
15249	13336	TCAAGCGATTCTCCTGCCTC
15250	13337	TTCAAGCGATTCTCCTGCCT
15251	13338	GTTCAAGCGATTCTCCTGCC
15252	13339	GGTTCAAGCGATTCTCCTGC
15253	13340	GGGTTCAAGCGATTCTCCTG
15254	13341	CGGGTTCAAGCGATTCTCCT
15255	13342	CCGGGTTCAAGCGATTCTCC
15256	13343	CCCGGGTTCAAGCGATTCTC
15257	13344	TCCCGGGTTCAAGCGATTCT
15258	13345	CTCCCGGGTTCAAGCGATTC

64335	62422	AAGAAGTACTAATACATGCT
64336	62423	AAAGAAGTACTAATACATGC
64337	62424	GAAAGAAGTACTAATACATG
64338	62425	AGAAAGAAGTACTAATACAT
64339	62426	AAGAAAGAAGTACTAATACA
64340	62427	AAAGAAAGAAGTACTAATAC
64341	62428	AAAAGAAAGAAGTACTAATA
64342	62429	AAAAAGAAAGAAGTACTAAT
64343	62430	GAAAAAGAAAGAAGTACTAA
64344	62431	TGAAAAAGAAAGAAGTACTA
64345	62432	ATGAAAAAGAAAGAAGTACT
64346	62433	CATGAAAAAGAAAGAAGTAC
64347	62434	CCATGAAAAAGAAAGAAGTA
64348	62435	GCCATGAAAAAGAAAGAAGT
64349	62436	GGCCATGAAAAAGAAAGAAG
64350	62437	TGGCCATGAAAAAGAAAGAA
64351	62438	TTGGCCATGAAAAAGAAAGA
64352	62439	TTTGGCCATGAAAAAGAAAG
64353	62440	ATTTGGCCATGAAAAAGAAA
64354	62441	TATTTGGCCATGAAAAAGAA
64355	62442	ATATTTGGCCATGAAAAAGA
64356	62443	AATATTTGGCCATGAAAAAG
64357	62444	GAATATTTGGCCATGAAAAA
64358	62445	GGAATATTTGGCCATGAAAA
64359	62446	TGGAATATTTGGCCATGAAA
64360	62447	ATGGAATATTTGGCCATGAA
64361	62448	AATGGAATATTTGGCCATGA
64362	62449	TAATGGAATATTTGGCCATG
64363	62450	ATAATGGAATATTTGGCCAT
64364	62451	TATAATGGAATATTTGGCCA
64365	62452	GTATAATGGAATATTTGGCC
64366	62453	TGTATAATGGAATATTTGGC
64367	62454	CTGTATAATGGAATATTTGG
64368	62455	ACTGTATAATGGAATATTTG
64369	62456	AACTGTATAATGGAATATTT
64370	62457	TAACTGTATAATGGAATATT
64371	62458	GTAACTGTATAATGGAATAT
64372	62459	TGTAACTGTATAATGGAATA
64373	62460	GTGTAACTGTATAATGGAAT
64374	62461	TGTGTAACTGTATAATGGAA
64375	62462	CTGTGTAACTGTATAATGGA
64376	62463	CCTGTGTAACTGTATAATGG
64377	62464	ACCTGTGTAACTGTATAATG
64378	62465	TACCTGTGTAACTGTATAAT
64379	62466	GTACCTGTGTAACTGTATAA
64380	62467	TGTACCTGTGTAACTGTATA
64381	62468	GTGTACCTGTGTAACTGTAT
64382	62469	AGTGTACCTGTGTAACTGTA
64383	62470	TAGTGTACCTGTGTAACTGT
64384	62471	GTAGTGTACCTGTGTAACTG
64385	62472	TGTAGTGTACCTGTGTAACT
64386	62473	ATGTAGTGTACCTGTGTAAC
64387	62474	AATGTAGTGTACCTGTGTAA
64388	62475	AAATGTAGTGTACCTGTGTA
64389	62476	AAAATGTAGTGTACCTGTGT
64390	62477	CAAAATGTAGTGTACCTGTG
64391	62478	ACAAAATGTAGTGTACCTGT
64392	62479	AACAAAATGTAGTGTACCTG
64393	62480	AAACAAAATGTAGTGTACCT
64394	62481	TAAACAAAATGTAGTGTACC
64395	62482	ATAAACAAAATGTAGTGTAC
64396	62483	AATAAACAAAATGTAGTGTA
64397	62484	GAATAAACAAAATGTAGTGT
64398	62485	TGAATAAACAAAATGTAGTG
64399	62486	ATGAATAAACAAAATGTAGT
64400	62487	GATGAATAAACAAAATGTAG
64401	62488	TGATGAATAAACAAAATGTA
64402	62489	CTGATGAATAAACAAAATGT
64403	62490	ACTGATGAATAAACAAAATG
64404	62491	AACTGATGAATAAACAAAAT
64405	62492	CAACTGATGAATAAACAAAA

113482	111569	CACCGCATGCTTCTCTCCTT
113483	111570	GCACCGCATGCTTCTCTCCT
113484	111571	AGCACCGCATGCTTCTCTCC
113485	111572	AAGCACCGCATGCTTCTCTC
113486	111573	GAAGCACCGCATGCTTCTCT
113487	111574	AGAAGCACCGCATGCTTCTC
113488	111575	TAGAAGCACCGCATGCTTCT
113489	111576	GTAGAAGCACCGCATGCTTC
113490	111577	AGTAGAAGCACCGCATGCTT
113491	111578	AAGTAGAAGCACCGCATGCT
113492	111579	CAAGTAGAAGCACCGCATGC
113493	111580	CCAAGTAGAAGCACCGCATG
113494	111581	TCCAAGTAGAAGCACCGCAT
113495	111582	TTCCAAGTAGAAGCACCGCA
113496	111583	ATTCCAAGTAGAAGCACCGC
113497	111584	AATTCCAAGTAGAAGCACCG
113498	111585	GAATTCCAAGTAGAAGCACC
113499	111586	TGAATTCCAAGTAGAAGCAC
113500	111587	TTGAATTCCAAGTAGAAGCA
113501	111588	TTTGAATTCCAAGTAGAAGC
113502	111589	TTTTGAATTCCAAGTAGAAG
113503	111590	ATTTTGAATTCCAAGTAGAA
113504	111591	TATTTTGAATTCCAAGTAGA
113505	111592	ATATTTTGAATTCCAAGTAG
113506	111593	AATATTTTGAATTCCAAGTA
113507	111594	AAATATTTTGAATTCCAAGT
113508	111595	AAAATATTTTGAATTCCAAG
113509	111596	AAAAATATTTTGAATTCCAA
113510	111597	GAAAAATATTTTGAATTCCA
113511	111598	TGAAAAATATTTTGAATTCC
113512	111599	ATGAAAAATATTTTGAATTC
113513	111600	GATGAAAAATATTTTGAATT
113514	111601	TGATGAAAAATATTTTGAAT
113515	111602	CTGATGAAAAATATTTTGAA
113516	111603	TCTGATGAAAAATATTTTGA
113517	111604	TTCTGATGAAAAATATTTTG
113518	111605	TTTCTGATGAAAAATATTTT
113519	111606	GTTTCTGATGAAAAATATTT
113520	111607	AGTTTCTGATGAAAAATATT
113521	111608	CAGTTTCTGATGAAAAATAT
113522	111609	ACAGTTTCTGATGAAAAATA
113523	111610	CACAGTTTCTGATGAAAAAT
113524	111611	ACACAGTTTCTGATGAAAAA
113525	111612	AACACAGTTTCTGATGAAAA
113526	111613	AAACACAGTTTCTGATGAAA
113527	111614	AAAACACAGTTTCTGATGAA
113528	111615	TAAAACACAGTTTCTGATGA
113529	111616	CTAAAACACAGTTTCTGATG
113530	111617	ACTAAAACACAGTTTCTGAT
113531	111618	AACTAAAACACAGTTTCTGA
113532	111619	TAACTAAAACACAGTTTCTG
113533	111620	TTAACTAAAACACAGTTTCT
113534	111621	ATTAACTAAAACACAGTTTC
113535	111622	CATTAACTAAAACACAGTTT
113536	111623	ACATTAACTAAAACACAGTT
113537	111624	AACATTAACTAAAACACAGT
113538	111625	AAACATTAACTAAAACACAG
113539	111626	TAAACATTAACTAAAACACA
113540	111627	CTAAACATTAACTAAAACAC
113541	111628	TCTAAACATTAACTAAAACA
113542	111629	ATCTAAACATTAACTAAAAC
113543	111630	AATCTAAACATTAACTAAAA
113544	111631	AAATCTAAACATTAACTAAA
113545	111632	CAAATCTAAACATTAACTAA
113546	111633	ACAAATCTAAACATTAACTA
113547	111634	AACAAATCTAAACATTAACT
113548	111635	TAACAAATCTAAACATTAAC
113549	111636	TTAACAAATCTAAACATTAA
113550	111637	CTTAACAAATCTAAACATTA
113551	111638	TCTTAACAAATCTAAACATT
113552	111639	ATCTTAACAAATCTAAACAT

15259	13346	CCTCCCGGGTTCAAGCGATT
15260	13347	ACCTCCCGGGTTCAAGCGAT
15261	13348	CACCTCCCGGGTTCAAGCGA
15262	13349	TCACCTCCCGGGTTCAAGCG
15263	13350	TTCACCTCCCGGGTTCAAGC
15264	13351	CTTCACCTCCCGGGTTCAAG
15265	13352	CCTTCACCTCCCGGGTTCAA
15266	13353	ACCTTCACCTCCCGGGTTCA
15267	13354	AACCTTCACCTCCCGGGTTC
15268	13355	CAACCTTCACCTCCCGGGTT
15269	13356	GCAACCTTCACCTCCCGGGT
15270	13357	TGCAACCTTCACCTCCCGGG
15271	13358	CTGCAACCTTCACCTCCCGG
15272	13359	ACTGCAACCTTCACCTCCCG
15273	13360	CACTGCAACCTTCACCTCCC
15274	13361	TCACTGCAACCTTCACCTCC
15275	13362	CTCACTGCAACCTTCACCTC
15276	13363	GCTCACTGCAACCTTCACCT
15277	13364	AGCTCACTGCAACCTTCACC
15278	13365	GAGCTCACTGCAACCTTCAC
15279	13366	TGAGCTCACTGCAACCTTCA
15280	13367	CTGAGCTCACTGCAACCTTC
15281	13368	TCTGAGCTCACTGCAACCTT
15282	13369	ATCTGAGCTCACTGCAACCT
15283	13370	AATCTGAGCTCACTGCAACC
15284	13371	CAATCTGAGCTCACTGCAAC
15285	13372	ACAATCTGAGCTCACTGCAA
15286	13373	CACAATCTGAGCTCACTGCA
15287	13374	GCACAATCTGAGCTCACTGC
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15291	13378	AGTGGCACAATCTGAGCTCA
15292	13379	CAGTGGCACAATCTGAGCTC
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15294	13381	CACAGTGGCACAATCTGAGC
15295	13382	GCACAGTGGCACAATCTGAG
15296	13383	GGCACAGTGGCACAATCTGA
15297	13384	GGGCACAGTGGCACAATCTG
15298	13385	GGGGCACAGTGGCACAATCT
15299	13386	TGGGGCACAGTGGCACAATC
15300	13387	CTGGGGCACAGTGGCACAAT
15301	13388	GCTGGGGCACAGTGGCACAA
15302	13389	GGCTGGGGCACAGTGGCACA
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15304	13391	CAGGCTGGGGCACAGTGGCA
15305	13392	CCAGGCTGGGGCACAGTGGC
15306	13393	CCCAGGCTGGGGCACAGTGG
15307	13394	GCCCAGGCTGGGGCACAGTG
15308	13395	GGCCCAGGCTGGGGCACAGT
15309	13396	TGGCCCAGGCTGGGGCACAG
15310	13397	GTGGCCCAGGCTGGGGCACA
15311	13398	TGTGGCCCAGGCTGGGGCAC
15312	13399	CTGTGGCCCAGGCTGGGGCA
15313	13400	TCTGTGGCCCAGGCTGGGGC
15314	13401	CTCTGTGGCCCAGGCTGGGG
15315	13402	GCTCTGTGGCCCAGGCTGGG
15316	13403	TGCTCTGTGGCCCAGGCTGG
15317	13404	CTGCTCTGTGGCCCAGGCTG
15318	13405	TCTGCTCTGTGGCCCAGGCT
15319	13406	CTCTGCTCTGTGGCCCAGGC
15320	13407	ACTCTGCTCTGTGGCCCAGG
15321	13408	CACTCTGCTCTGTGGCCCAG
15322	13409	TCACTCTGCTCTGTGGCCCA
15323	13410	CTCACTCTGCTCTGTGGCCC
15324	13411	TCTCACTCTGCTCTGTGGCC
15325	13412	GTCTCACTCTGCTCTGTGGC
15326	13413	AGTCTCACTCTGCTCTGTGG
15327	13414	GAGTCTCACTCTGCTCTGTG
15328	13415	AGAGTCTCACTCTGCTCTGT
15329	13416	CAGAGTCTCACTCTGCTCTG

64406	62493	CCAACTGATGAATAAACAAA
64407	62494	ACCAACTGATGAATAAACAA
64408	62495	CACCAACTGATGAATAAACA
64409	62496	CCACCAACTGATGAATAAAC
64410	62497	TCCACCAACTGATGAATAAA
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64420	62507	AATGAAAATGTCCACCAACT
64421	62508	CAATGAAAATGTCCACCAAC
64422	62509	ACAATGAAAATGTCCACCAA
64423	62510	AACAATGAAAATGTCCACCA
64424	62511	AAACAATGAAAATGTCCACC
64425	62512	GAAACAATGAAAATGTCCAC
64426	62513	GGAAACAATGAAAATGTCCA
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64439	62526	TAAATCAAAAGGTGGAAACA
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64458	62545	TTCGCAGCAGGATTATGTAT
64459	62546	GTTCGCAGCAGGATTATGTA
64460	62547	TGTTCGCAGCAGGATTATGT
64461	62548	CTGTTCGCAGCAGGATTATG
64462	62549	ACTGTTCGCAGCAGGATTAT
64463	62550	CACTGTTCGCAGCAGGATTA
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64473	62560	CTTTAAAAGTCACTGTTCGC
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64475	62562	AACTTTAAAAGTCACTGTTC
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113553	111640	TATCTTAACAAATCTAAACA
113554	111641	CTATCTTAACAAATCTAAAC
113555	111642	TCTATCTTAACAAATCTAAA
113556	111643	GTCTATCTTAACAAATCTAA
113557	111644	AGTCTATCTTAACAAATCTA
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113559	111646	TAAGTCTATCTTAACAAATC
113560	111647	TTAAGTCTATCTTAACAAAT
113561	111648	ATTAAGTCTATCTTAACAAA
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113563	111650	GAATTAAGTCTATCTTAACA
113564	111651	AGAATTAAGTCTATCTTAAC
113565	111652	CAGAATTAAGTCTATCTTAA
113566	111653	GCAGAATTAAGTCTATCTTA
113567	111654	TGCAGAATTAAGTCTATCTT
113568	111655	GTGCAGAATTAAGTCTATCT
113569	111656	TGTGCAGAATTAAGTCTATC
113570	111657	ATGTGCAGAATTAAGTCTAT
113571	111658	AATGTGCAGAATTAAGTCTA
113572	111659	GAATGTGCAGAATTAAGTCT
113573	111660	TGAATGTGCAGAATTAAGTC
113574	111661	CTGAATGTGCAGAATTAAGT
113575	111662	ACTGAATGTGCAGAATTAAG
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113579	111666	ATATACTGAATGTGCAGAAT
113580	111667	AATATACTGAATGTGCAGAA
113581	111668	TAATATACTGAATGTGCAGA
113582	111669	TTAATATACTGAATGTGCAG
113583	111670	ATTAATATACTGAATGTGCA
113584	111671	AATTAATATACTGAATGTGC
113585	111672	TAATTAATATACTGAATGTG
113586	111673	TTAATTAATATACTGAATGT
113587	111674	TTTAATTAATATACTGAATG
113588	111675	ATTTAATTAATATACTGAAT
113589	111676	CATTTAATTAATATACTGAA
113590	111677	CCATTTAATTAATATACTGA
113591	111678	TCCATTTAATTAATATACTG
113592	111679	GTCCATTTAATTAATATACT
113593	111680	AGTCCATTTAATTAATATAC
113594	111681	AAGTCCATTTAATTAATATA
113595	111682	AAAGTCCATTTAATTAATAT
113596	111683	AAAAGTCCATTTAATTAATA
113597	111684	TAAAAGTCCATTTAATTAAT
113598	111685	CTAAAAGTCCATTTAATTAA
113599	111686	CCTAAAAGTCCATTTAATTA
113600	111687	CCCTAAAAGTCCATTTAATT
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113602	111689	GCCCCTAAAAGTCCATTTAA
113603	111690	AGCCCCTAAAAGTCCATTTA
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113605	111692	TTAGCCCCTAAAAGTCCATT
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113607	111694	GGTTAGCCCCTAAAAGTCCA
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113611	111698	CTGAGGTTAGCCCCTAAAAG
113612	111699	TCTGAGGTTAGCCCCTAAAA
113613	111700	TTCTGAGGTTAGCCCCTAAA
113614	111701	GTTCTGAGGTTAGCCCCTAA
113615	111702	AGTTCTGAGGTTAGCCCCTA
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113617	111704	TAAGTTCTGAGGTTAGCCCC
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113620	111707	AGTTAAGTTCTGAGGTTAGC
113621	111708	TAGTTAAGTTCTGAGGTTAG
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113623	111710	GGTAGTTAAGTTCTGAGGTT

15330	13417	ACAGAGTCTCACTCTGCTCT
15331	13418	GACAGAGTCTCACTCTGCTC
15332	13419	AGACAGAGTCTCACTCTGCT
15333	13420	GAGACAGAGTCTCACTCTGC
15334	13421	TGAGACAGAGTCTCACTCTG
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15343	13430	TTTTTTTTTTGAGACAGAGT
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15345	13432	TTTTTTTTTTTTGAGACAGA
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15347	13434	TTTTTTTTTTTTTGAGACA
15348	13435	TTTTTTTTTTTTTTGAGAC
15349	13436	CTTTTTTTTTTTTTTGAGA
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15351	13438	AACTTTTTTTTTTTTTTTGA
15352	13439	AAACTTTTTTTTTTTTTTTG
15353	13440	CAAACTTTTTTTTTTTTTTT
15354	13441	CCAAACTTTTTTTTTTTTTT
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15358	13445	TCTTCCAAACTTTTTTTTTT
15359	13446	GTCTTCCAAACTTTTTTTTT
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15361	13448	CAGTCTTCCAAACTTTTTTT
15362	13449	CCAGTCTTCCAAACTTTTTT
15363	13450	ACCAGTCTTCCAAACTTTTT
15364	13451	CACCAGTCTTCCAAACTTTT
15365	13452	CCACCAGTCTTCCAAACTTT
15366	13453	GCCACCAGTCTTCCAAACTT
15367	13454	AGCCACCAGTCTTCCAAACT
15368	13455	CAGCCACCAGTCTTCCAAAC
15369	13456	CCAGCCACCAGTCTTCCAAA
15370	13457	CCCAGCCACCAGTCTTCCAA
15371	13458	GCCCAGCCACCAGTCTTCCA
15372	13459	TGCCCAGCCACCAGTCTTCC
15373	13460	ATGCCCAGCCACCAGTCTTC
15374	13461	CATGCCCAGCCACCAGTCTT
15375	13462	CCATGCCCAGCCACCAGTCT
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15377	13464	CACCATGCCCAGCCACCAGT
15378	13465	CCACCATGCCCAGCCACCAG
15379	13466	GCCACCATGCCCAGCCACCA
15380	13467	AGCCACCATGCCCAGCCACC
15381	13468	GAGCCACCATGCCCAGCCAC
15382	13469	TGAGCCACCATGCCCAGCCA
15383	13470	GTGAGCCACCATGCCCAGCC
15384	13471	TGTGAGCCACCATGCCCAGC
15385	13472	GTGTGAGCCACCATGCCCAG
15386	13473	GGTGTGAGCCACCATGCCCA
15387	13474	AGGTGTGAGCCACCATGCCC
15388	13475	CAGGTGTGAGCCACCATGCC
15389	13476	ACAGGTGTGAGCCACCATGC
15390	13477	TACAGGTGTGAGCCACCATG
15391	13478	TTACAGGTGTGAGCCACCAT
15392	13479	ATTACAGGTGTGAGCCACCA
15393	13480	GATTACAGGTGTGAGCCACC
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15395	13482	GGGATTACAGGTGTGAGCCA
15396	13483	TGGGATTACAGGTGTGAGCC
15397	13484	TTGGGATTACAGGTGTGAGC
15398	13485	GTTGGGATTACAGGTGTGAG
15399	13486	TGTTGGGATTACAGGTGTGA
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64477	62564	AAAACTTTAAAAGTCACTGT
64478	62565	AAAAACTTTAAAAGTCACTG
64479	62566	CAAAAACTTTAAAAGTCACT
64480	62567	ACAAAAACTTTAAAAGTCAC
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64482	62569	ACACAAAAACTTTAAAAGTC
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64484	62571	CCACACAAAAACTTTAAAAG
64485	62572	CCCACACAAAAACTTTAAAA
64486	62573	GCCCACACAAAAACTTTAAA
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64488	62575	CGGCCCACACAAAAACTTTA
64489	62576	CCGGCCCACACAAAAACTTT
64490	62577	CCCGGCCCACACAAAAACTT
64491	62578	ACCCGGCCCACACAAAAACT
64492	62579	CACCCGGCCCACACAAAAAC
64493	62580	ACACCCGGCCCACACAAAAA
64494	62581	CACACCCGGCCCACACAAAA
64495	62582	CCACACCCGGCCCACACAAA
64496	62583	ACCACACCCGGCCCACACAA
64497	62584	CACCACACCCGGCCCACACA
64498	62585	CCACCACACCCGGCCCACAC
64499	62586	GCCACCACACCCGGCCCACA
64500	62587	AGCCACCACACCCGGCCCAC
64501	62588	GAGCCACCACACCCGGCCCA
64502	62589	TGAGCCACCACACCCGGCCC
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64504	62591	CATGAGCCACCACACCCGGC
64505	62592	GCATGAGCCACCACACCCGG
64506	62593	GGCATGAGCCACCACACCCG
64507	62594	AGGCATGAGCCACCACACCC
64508	62595	GAGGCATGAGCCACCACACC
64509	62596	AGAGGCATGAGCCACCACAC
64510	62597	CAGAGGCATGAGCCACCACA
64511	62598	ACAGAGGCATGAGCCACCAC
64512	62599	TACAGAGGCATGAGCCACCA
64513	62600	TTACAGAGGCATGAGCCACC
64514	62601	ATTACAGAGGCATGAGCCAC
64515	62602	GATTACAGAGGCATGAGCCA
64516	62603	GGATTACAGAGGCATGAGCC
64517	62604	GGGATTACAGAGGCATGAGC
64518	62605	TGGGATTACAGAGGCATGAG
64519	62606	CTGGGATTACAGAGGCATGA
64520	62607	GCTGGGATTACAGAGGCATG
64521	62608	TGCTGGGATTACAGAGGCAT
64522	62609	GTGCTGGGATTACAGAGGCA
64523	62610	AGTGCTGGGATTACAGAGGC
64524	62611	AAGTGCTGGGATTACAGAGG
64525	62612	AAAGTGCTGGGATTACAGAG
64526	62613	CAAAGTGCTGGGATTACAGA
64527	62614	CCAAAGTGCTGGGATTACAG
64528	62615	CCCAAAGTGCTGGGATTACA
64529	62616	TCCCAAAGTGCTGGGATTAC
64530	62617	CTCCCAAAGTGCTGGGATTA
64531	62618	CCTCCCAAAGTGCTGGGATT
64532	62619	GCCTCCCAAAGTGCTGGGAT
64533	62620	AGCCTCCCAAAGTGCTGGGA
64534	62621	CAGCCTCCCAAAGTGCTGGG
64535	62622	CCAGCCTCCCAAAGTGCTGG
64536	62623	CCCAGCCTCCCAAAGTGCTG
64537	62624	CCCCAGCCTCCCAAAGTGCT
64538	62625	GCCCCAGCCTCCCAAAGTGC
64539	62626	AGCCCCAGCCTCCCAAAGTG
64540	62627	CAGCCCCAGCCTCCCAAAGT
64541	62628	CCAGCCCCAGCCTCCCAAAG
64542	62629	GCCAGCCCCAGCCTCCCAAA
64543	62630	TGCCAGCCCCAGCCTCCCAA
64544	62631	CTGCCAGCCCCAGCCTCCCA
64545	62632	TCTGCCAGCCCCAGCCTCCC
64546	62633	ATCTGCCAGCCCCAGCCTCC
64547	62634	GATCTGCCAGCCCCAGCCTC

113624	111711	TGGTAGTTAAGTTCTGAGGT
113625	111712	ATGGTAGTTAAGTTCTGAGG
113626	111713	AATGGTAGTTAAGTTCTGAG
113627	111714	CAATGGTAGTTAAGTTCTGA
113628	111715	TCAATGGTAGTTAAGTTCTG
113629	111716	GTCAATGGTAGTTAAGTTCT
113630	111717	AGTCAATGGTAGTTAAGTTC
113631	111718	AAGTCAATGGTAGTTAAGTT
113632	111719	TAAGTCAATGGTAGTTAAGT
113633	111720	CTAAGTCAATGGTAGTTAAG
113634	111721	CCTAAGTCAATGGTAGTTAA
113635	111722	ACCTAAGTCAATGGTAGTTA
113636	111723	CACCTAAGTCAATGGTAGTT
113637	111724	ACACCTAAGTCAATGGTAGT
113638	111725	AACACCTAAGTCAATGGTAG
113639	111726	AAACACCTAAGTCAATGGTA
113640	111727	CAAACACCTAAGTCAATGGT
113641	111728	CCAAACACCTAAGTCAATGG
113642	111729	CCCAAACACCTAAGTCAATG
113643	111730	ACCCAAACACCTAAGTCAAT
113644	111731	TACCCAAACACCTAAGTCAA
113645	111732	GTACCCAAACACCTAAGTCA
113646	111733	GGTACCCAAACACCTAAGTC
113647	111734	TGGTACCCAAACACCTAAGT
113648	111735	TTGGTACCCAAACACCTAAG
113649	111736	TTTGGTACCCAAACACCTAA
113650	111737	GTTTGGTACCCAAACACCTA
113651	111738	TGTTTGGTACCCAAACACCT
113652	111739	TTGTTTGGTACCCAAACACC
113653	111740	ATTGTTTGGTACCCAAACAC
113654	111741	GATTGTTTGGTACCCAAACA
113655	111742	GGATTGTTTGGTACCCAAAC
113656	111743	TGGATTGTTTGGTACCCAAA
113657	111744	CTGGATTGTTTGGTACCCAA
113658	111745	ACTGGATTGTTTGGTACCCA
113659	111746	AACTGGATTGTTTGGTACCC
113660	111747	TAACTGGATTGTTTGGTACC
113661	111748	TTAACTGGATTGTTTGGTAC
113662	111749	TTTAACTGGATTGTTTGGTA
113663	111750	CTTTAACTGGATTGTTTGGT
113664	111751	GCTTTAACTGGATTGTTTGG
113665	111752	AGCTTTAACTGGATTGTTTG
113666	111753	CAGCTTTAACTGGATTGTTT
113667	111754	TCAGCTTTAACTGGATTGTT
113668	111755	TTCAGCTTTAACTGGATTGT
113669	111756	CTTCAGCTTTAACTGGATTG
113670	111757	ACTTCAGCTTTAACTGGATT
113671	111758	AACTTCAGCTTTAACTGGAT
113672	111759	AAACTTCAGCTTTAACTGGA
113673	111760	AAAACTTCAGCTTTAACTGG
113674	111761	CAAAACTTCAGCTTTAACTG
113675	111762	CCAAAACTTCAGCTTTAACT
113676	111763	TCCAAAACTTCAGCTTTAAC
113677	111764	TTCCAAAACTTCAGCTTTAA
113678	111765	ATTCCAAAACTTCAGCTTTA
113679	111766	CATTCCAAAACTTCAGCTTT
113680	111767	GCATTCCAAAACTTCAGCTT
113681	111768	TGCATTCCAAAACTTCAGCT
113682	111769	CTGCATTCCAAAACTTCAGC
113683	111770	GCTGCATTCCAAAACTTCAG
113684	111771	AGCTGCATTCCAAAACTTCA
113685	111772	AAGCTGCATTCCAAAACTTC
113686	111773	TAAGCTGCATTCCAAAACTT
113687	111774	ATAAGCTGCATTCCAAAACT
113688	111775	AATAAGCTGCATTCCAAAAC
113689	111776	CAATAAGCTGCATTCCAAAA
113690	111777	TCAATAAGCTGCATTCCAAA
113691	111778	ATCAATAAGCTGCATTCCAA
113692	111779	TATCAATAAGCTGCATTCCA
113693	111780	TTATCAATAAGCTGCATTCC
113694	111781	TTTATCAATAAGCTGCATTC

15401	13488	AGTGTTGGGATTACAGGTGT
15402	13489	AAGTGTTGGGATTACAGGTG
15403	13490	AAAGTGTTGGGATTACAGGT
15404	13491	CAAAGTGTTGGGATTACAGG
15405	13492	CCAAAGTGTTGGGATTACAG
15406	13493	CCCAAAGTGTTGGGATTACA
15407	13494	TCCCAAAGTGTTGGGATTAC
15408	13495	CTCCCAAAGTGTTGGGATTA
15409	13496	CCTCCCAAAGTGTTGGGATT
15410	13497	GCCTCCCAAAGTGTTGGGAT
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15412	13499	CAGCCTCCCAAAGTGTTGGG
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15414	13501	TTCAGCCTCCCAAAGTGTTG
15415	13502	CTTCAGCCTCCCAAAGTGTT
15416	13503	GCTTCAGCCTCCCAAAGTGT
15417	13504	TGCTTCAGCCTCCCAAAGTG
15418	13505	CTGCTTCAGCCTCCCAAAGT
15419	13506	CCTGCTTCAGCCTCCCAAAG
15420	13507	GCCTGCTTCAGCCTCCCAAA
15421	13508	TGCCTGCTTCAGCCTCCCAA
15422	13509	CTGCCTGCTTCAGCCTCCCA
15423	13510	TCTGCCTGCTTCAGCCTCCC
15424	13511	ATCTGCCTGCTTCAGCCTCC
15425	13512	AATCTGCCTGCTTCAGCCTC
15426	13513	TAATCTGCCTGCTTCAGCCT
15427	13514	GTAATCTGCCTGCTTCAGCC
15428	13515	GGTAATCTGCCTGCTTCAGC
15429	13516	AGGTAATCTGCCTGCTTCAG
15430	13517	CAGGTAATCTGCCTGCTTCA
15431	13518	TCAGGTAATCTGCCTGCTTC
15432	13519	CTCAGGTAATCTGCCTGCTT
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15434	13521	GGCTCAGGTAATCTGCCTGC
15435	13522	GGGCTCAGGTAATCTGCCTG
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15443	13530	GAACTCCTGGGCTCAGGTAA
15444	13531	TGAACTCCTGGGCTCAGGTA
15445	13532	TTGAACTCCTGGGCTCAGGT
15446	13533	CTTGAACTCCTGGGCTCAGG
15447	13534	ACTTGAACTCCTGGGCTCAG
15448	13535	GACTTGAACTCCTGGGCTCA
15449	13536	GGACTTGAACTCCTGGGCTC
15450	13537	TGGACTTGAACTCCTGGGCT
15451	13538	CTGGACTTGAACTCCTGGGC
15452	13539	GCTGGACTTGAACTCCTGGG
15453	13540	GGCTGGACTTGAACTCCTGG
15454	13541	AGGCTGGACTTGAACTCCTG
15455	13542	CAGGCTGGACTTGAACTCCT
15456	13543	CCAGGCTGGACTTGAACTCC
15457	13544	CCCAGGCTGGACTTGAACTC
15458	13545	GCCCAGGCTGGACTTGAACT
15459	13546	TGCCCAGGCTGGACTTGAAC
15460	13547	TTGCCCAGGCTGGACTTGAA
15461	13548	GTTGCCCAGGCTGGACTTGA
15462	13549	TGTTGCCCAGGCTGGACTTG
15463	13550	GTGTTGCCCAGGCTGGACTT
15464	13551	TGTGTTGCCCAGGCTGGACT
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15466	13553	CCTGTGTTGCCCAGGCTGGA
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15468	13555	TCCCTGTGTTGCCCAGGCTG
15469	13556	TTCCCTGTGTTGCCCAGGCT
15470	13557	TTTCCCTGTGTTGCCCAGGC
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64548	62635	TGATCTGCCAGCCCCAGCCT
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64550	62637	AATGATCTGCCAGCCCCAGC
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64552	62639	CAAATGATCTGCCAGCCCCA
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64557	62644	GGCCTCAAATGATCTGCCAG
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64570	62657	GTCTCGAACTCCCGGCCTCA
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64573	62660	CTGGTCTCGAACTCCCGGCC
64574	62661	GCTGGTCTCGAACTCCCGGC
64575	62662	GGCTGGTCTCGAACTCCCGG
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64577	62664	CAGGCTGGTCTCGAACTCCC
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64579	62666	GGCAGGCTGGTCTCGAACTC
64580	62667	GGGCAGGCTGGTCTCGAACT
64581	62668	TGGGCAGGCTGGTCTCGAAC
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64595	62682	GGGTTTCACCATGTTGGGCA
64596	62683	AGGGTTTCACCATGTTGGGC
64597	62684	CAGGGTTTCACCATGTTGGG
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64599	62686	GACAGGGTTTCACCATGTTG
64600	62687	AGACAGGGTTTCACCATGTT
64601	62688	GAGACAGGGTTTCACCATGT
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64603	62690	TAGAGACAGGGTTTCACCAT
64604	62691	GTAGAGACAGGGTTTCACCA
64605	62692	AGTAGAGACAGGGTTTCACC
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64607	62694	TTAGTAGAGACAGGGTTTCA
64608	62695	TTTAGTAGAGACAGGGTTTC
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64611	62698	ATTTTTAGTAGAGACAGGGT
64612	62699	TATTTTTAGTAGAGACAGGG
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64615	62702	TTGTATTTTTAGTAGAGACA
64616	62703	TTTGTATTTTTAGTAGAGAC
64617	62704	TTTTGTATTTTTAGTAGAGA
64618	62705	TTTTTGTATTTTTAGTAGAG

113695	111782	ATTTATCAATAAGCTGCATT
113696	111783	AATTTATCAATAAGCTGCAT
113697	111784	CAATTTATCAATAAGCTGCA
113698	111785	CCAATTTATCAATAAGCTGC
113699	111786	CCCAATTTATCAATAAGCTG
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113702	111789	GTCCCCAATTTATCAATAAG
113703	111790	AGTCCCCAATTTATCAATAA
113704	111791	CAGTCCCCAATTTATCAATA
113705	111792	GCAGTCCCCAATTTATCAAT
113706	111793	AGCAGTCCCCAATTTATCAA
113707	111794	AAGCAGTCCCCAATTTATCA
113708	111795	TAAGCAGTCCCCAATTTATC
113709	111796	ATAAGCAGTCCCCAATTTAT
113710	111797	AATAAGCAGTCCCCAATTTA
113711	111798	GAATAAGCAGTCCCCAATTT
113712	111799	AGAATAAGCAGTCCCCAATT
113713	111800	AAGAATAAGCAGTCCCCAAT
113714	111801	CAAGAATAAGCAGTCCCCAA
113715	111802	TCAAGAATAAGCAGTCCCCA
113716	111803	ATCAAGAATAAGCAGTCCCC
113717	111804	AATCAAGAATAAGCAGTCCC
113718	111805	AAATCAAGAATAAGCAGTCC
113719	111806	CAAATCAAGAATAAGCAGTC
113720	111807	TCAAATCAAGAATAAGCAGT
113721	111808	CTCAAATCAAGAATAAGCAG
113722	111809	CCTCAAATCAAGAATAAGCA
113723	111810	GCCTCAAATCAAGAATAAGC
113724	111811	TGCCTCAAATCAAGAATAAG
113725	111812	TTGCCTCAAATCAAGAATAA
113726	111813	ATTGCCTCAAATCAAGAATA
113727	111814	AATTGCCTCAAATCAAGAAT
113728	111815	AAATTGCCTCAAATCAAGAA
113729	111816	AAAATTGCCTCAAATCAAGA
113730	111817	AAAAATTGCCTCAAATCAAG
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113732	111819	AAAAAAATTGCCTCAAATCA
113733	111820	AAAAAAAATTGCCTCAAATC
113734	111821	AAAAAAAAATTGCCTCAAAT
113735	111822	TAAAAAAAAATTGCCTCAAA
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113737	111824	TGTAAAAAAAAATTGCCTCA
113738	111825	CTGTAAAAAAAAATTGCCTC
113739	111826	GCTGTAAAAAAAAATTGCCT
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113743	111830	CATGGCTGTAAAAAAAAATT
113744	111831	TCATGGCTGTAAAAAAAAAT
113745	111832	GTCATGGCTGTAAAAAAAAA
113746	111833	AGTCATGGCTGTAAAAAAAA
113747	111834	AAGTCATGGCTGTAAAAAAA
113748	111835	AAAGTCATGGCTGTAAAAAA
113749	111836	AAAAGTCATGGCTGTAAAAA
113750	111837	AAAAAGTCATGGCTGTAAAA
113751	111838	GAAAAAGTCATGGCTGTAAA
113752	111839	GGAAAAAGTCATGGCTGTAA
113753	111840	TGGAAAAAGTCATGGCTGTA
113754	111841	CTGGAAAAAGTCATGGCTGT
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113756	111843	ACCTGGAAAAAGTCATGGCT
113757	111844	TACCTGGAAAAAGTCATGGC
113758	111845	ATACCTGGAAAAAGTCATGG
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113760	111847	ACATACCTGGAAAAAGTCAT
113761	111848	GACATACCTGGAAAAAGTCA
113762	111849	TGACATACCTGGAAAAAGTC
113763	111850	ATGACATACCTGGAAAAAGT
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15472	13559	GGTTTCCCTGTGTTGCCCAG
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15474	13561	GGGGTTTCCCTGTGTTGCCC
15475	13562	TGGGGTTTCCCTGTGTTGCC
15476	13563	ATGGGGTTTCCCTGTGTTGC
15477	13564	GATGGGGTTTCCCTGTGTTG
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15482	13569	GTTGAGATGGGGTTTCCCTG
15483	13570	TGTTGAGATGGGGTTTCCCT
15484	13571	TTGTTGAGATGGGGTTTCCC
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15500	13587	TTTGTATTAATATTTTTTGT
15501	13588	TTTTGTATTAATATTTTTTG
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15503	13590	TTTTTTGTATTAATATTTTT
15504	13591	ATTTTTTGTATTAATATTTT
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15506	13593	AAATTTTTTGTATTAATATT
15507	13594	TAAATTTTTTGTATTAATAT
15508	13595	CTAAATTTTTTGTATTAATA
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15515	13602	TGACTGGCTAAATTTTTTGT
15516	13603	ATGACTGGCTAAATTTTTTG
15517	13604	CATGACTGGCTAAATTTTTT
15518	13605	CCATGACTGGCTAAATTTTT
15519	13606	ACCATGACTGGCTAAATTTT
15520	13607	GACCATGACTGGCTAAATTT
15521	13608	CGACCATGACTGGCTAAATT
15522	13609	ACGACCATGACTGGCTAAAT
15523	13610	CACGACCATGACTGGCTAAA
15524	13611	GCACGACCATGACTGGCTAA
15525	13612	TGCACGACCATGACTGGCTA
15526	13613	GTGCACGACCATGACTGGCT
15527	13614	AGTGCACGACCATGACTGGC
15528	13615	AAGTGCACGACCATGACTGG
15529	13616	GAAGTGCACGACCATGACTG
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15531	13618	CAGAAGTGCACGACCATGAC
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15533	13620	TACAGAAGTGCACGACCATG
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15536	13623	GACTACAGAAGTGCACGACC
15537	13624	AGACTACAGAAGTGCACGAC
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15539	13626	TGAGACTACAGAAGTGCACG
15540	13627	CTGAGACTACAGAAGTGCAC
15541	13628	GCTGAGACTACAGAAGTGCA
15542	13629	AGCTGAGACTACAGAAGTGC

64619	62706	ATTTTTGTATTTTTAGTAGA
64620	62707	CATTTTTGTATTTTTAGTAG
64621	62708	TCATTTTTGTATTTTTAGTA
64622	62709	CTCATTTTTGTATTTTTAGT
64623	62710	GCTCATTTTTGTATTTTTAG
64624	62711	AGCTCATTTTTGTATTTTTA
64625	62712	CAGCTCATTTTTGTATTTTT
64626	62713	CCAGCTCATTTTTGTATTTT
64627	62714	CCCAGCTCATTTTTGTATTT
64628	62715	ACCCAGCTCATTTTTGTATT
64629	62716	CACCCAGCTCATTTTTGTAT
64630	62717	ACACCCAGCTCATTTTTGTA
64631	62718	CACACCCAGCTCATTTTTGT
64632	62719	CCACACCCAGCTCATTTTTG
64633	62720	ACCACACCCAGCTCATTTTT
64634	62721	CACCACACCCAGCTCATTTT
64635	62722	CCACCACACCCAGCTCATTT
64636	62723	GCCACCACACCCAGCTCATT
64637	62724	CGCCACCACACCCAGCTCAT
64638	62725	ACGCCACCACACCCAGCTCA
64639	62726	CACGCCACCACACCCAGCTC
64640	62727	GCACGCCACCACACCCAGCT
64641	62728	TGCACGCCACCACACCCAGC
64642	62729	GTGCACGCCACCACACCCAG
64643	62730	GGTGCACGCCACCACACCCA
64644	62731	AGGTGCACGCCACCACACCC
64645	62732	CAGGTGCACGCCACCACACC
64646	62733	ACAGGTGCACGCCACCACAC
64647	62734	TACAGGTGCACGCCACCACA
64648	62735	TTACAGGTGCACGCCACCAC
64649	62736	ATTACAGGTGCACGCCACCA
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64654	62741	CTGAGATTACAGGTGCACGC
64655	62742	GCTGAGATTACAGGTGCACG
64656	62743	AGCTGAGATTACAGGTGCAC
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64661	62748	CTAGTAGCTGAGATTACAGG
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64663	62750	CCCTAGTAGCTGAGATTACA
64664	62751	TCCCTAGTAGCTGAGATTAC
64665	62752	CTCCCTAGTAGCTGAGATTA
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64667	62754	GCCTCCCTAGTAGCTGAGAT
64668	62755	AGCCTCCCTAGTAGCTGAGA
64669	62756	CAGCCTCCCTAGTAGCTGAG
64670	62757	TCAGCCTCCCTAGTAGCTGA
64671	62758	CTCAGCCTCCCTAGTAGCTG
64672	62759	CCTCAGCCTCCCTAGTAGCT
64673	62760	GCCTCAGCCTCCCTAGTAGC
64674	62761	TGCCTCAGCCTCCCTAGTAG
64675	62762	CTGCCTCAGCCTCCCTAGTA
64676	62763	TCTGCCTCAGCCTCCCTAGT
64677	62764	CTCTGCCTCAGCCTCCCTAG
64678	62765	TCTCTGCCTCAGCCTCCCTA
64679	62766	TTCTCTGCCTCAGCCTCCCT
64680	62767	ATTCTCTGCCTCAGCCTCCC
64681	62768	GATTCTCTGCCTCAGCCTCC
64682	62769	TGATTCTCTGCCTCAGCCTC
64683	62770	GTGATTCTCTGCCTCAGCCT
64684	62771	AGTGATTCTCTGCCTCAGCC
64685	62772	AAGTGATTCTCTGCCTCAGC
64686	62773	CAAGTGATTCTCTGCCTCAG
64687	62774	TCAAGTGATTCTCTGCCTCA
64688	62775	TTCAAGTGATTCTCTGCCTC
64689	62776	CTTCAAGTGATTCTCTGCCT

113766	111853	TACATGACATACCTGGAAAA
113767	111854	TTACATGACATACCTGGAAA
113768	111855	TTTACATGACATACCTGGAA
113769	111856	TTTTACATGACATACCTGGA
113770	111857	ATTTTACATGACATACCTGG
113771	111858	TATTTTACATGACATACCTG
113772	111859	ATATTTTACATGACATACCT
113773	111860	GATATTTTACATGACATACC
113774	111861	AGATATTTTACATGACATAC
113775	111862	AAGATATTTTACATGACATA
113776	111863	GAAGATATTTTACATGACAT
113777	111864	AGAAGATATTTTACATGACA
113778	111865	GAGAAGATATTTTACATGAC
113779	111866	TGAGAAGATATTTTACATGA
113780	111867	GTGAGAAGATATTTTACATG
113781	111868	TGTGAGAAGATATTTTACAT
113782	111869	ATGTGAGAAGATATTTTACA
113783	111870	TATGTGAGAAGATATTTTAC
113784	111871	TTATGTGAGAAGATATTTTA
113785	111872	CTTATGTGAGAAGATATTTT
113786	111873	TCTTATGTGAGAAGATATTT
113787	111874	TTCTTATGTGAGAAGATATT
113788	111875	ATTCTTATGTGAGAAGATAT
113789	111876	AATTCTTATGTGAGAAGATA
113790	111877	TAATTCTTATGTGAGAAGAT
113791	111878	GTAATTCTTATGTGAGAAGA
113792	111879	AGTAATTCTTATGTGAGAAG
113793	111880	CAGTAATTCTTATGTGAGAA
113794	111881	GCAGTAATTCTTATGTGAGA
113795	111882	TGCAGTAATTCTTATGTGAG
113796	111883	ATGCAGTAATTCTTATGTGA
113797	111884	CATGCAGTAATTCTTATGTG
113798	111885	GCATGCAGTAATTCTTATGT
113799	111886	AGCATGCAGTAATTCTTATG
113800	111887	TAGCATGCAGTAATTCTTAT
113801	111888	CTAGCATGCAGTAATTCTTA
113802	111889	TCTAGCATGCAGTAATTCTT
113803	111890	TTCTAGCATGCAGTAATTCT
113804	111891	ATTCTAGCATGCAGTAATTC
113805	111892	TATTCTAGCATGCAGTAATT
113806	111893	ATATTCTAGCATGCAGTAAT
113807	111894	AATATTCTAGCATGCAGTAA
113808	111895	CAATATTCTAGCATGCAGTA
113809	111896	CCAATATTCTAGCATGCAGT
113810	111897	ACCAATATTCTAGCATGCAG
113811	111898	TACCAATATTCTAGCATGCA
113812	111899	ATACCAATATTCTAGCATGC
113813	111900	CATACCAATATTCTAGCATG
113814	111901	ACATACCAATATTCTAGCAT
113815	111902	AACATACCAATATTCTAGCA
113816	111903	CAACATACCAATATTCTAGC
113817	111904	TCAACATACCAATATTCTAG
113818	111905	GTCAACATACCAATATTCTA
113819	111906	AGTCAACATACCAATATTCT
113820	111907	CAGTCAACATACCAATATTC
113821	111908	CCAGTCAACATACCAATATT
113822	111909	ACCAGTCAACATACCAATAT
113823	111910	TACCAGTCAACATACCAATA
113824	111911	CTACCAGTCAACATACCAAT
113825	111912	GCTACCAGTCAACATACCAA
113826	111913	AGCTACCAGTCAACATACCA
113827	111914	GAGCTACCAGTCAACATACC
113828	111915	TGAGCTACCAGTCAACATAC
113829	111916	ATGAGCTACCAGTCAACATA
113830	111917	TATGAGCTACCAGTCAACAT
113831	111918	GTATGAGCTACCAGTCAACA
113832	111919	GGTATGAGCTACCAGTCAAC
113833	111920	AGGTATGAGCTACCAGTCAA
113834	111921	TAGGTATGAGCTACCAGTCA
113835	111922	ATAGGTATGAGCTACCAGTC
113836	111923	TATAGGTATGAGCTACCAGT

15543	13630	TAGCTGAGACTACAGAAGTG
15544	13631	GTAGCTGAGACTACAGAAGT
15545	13632	AGTAGCTGAGACTACAGAAG
15546	13633	AAGTAGCTGAGACTACAGAA
15547	13634	CAAGTAGCTGAGACTACAGA
15548	13635	CCAAGTAGCTGAGACTACAG
15549	13636	CCCAAGTAGCTGAGACTACA
15550	13637	TCCCAAGTAGCTGAGACTAC
15551	13638	CTCCCAAGTAGCTGAGACTA
15552	13639	CCTCCCAAGTAGCTGAGACT
15553	13640	GCCTCCCAAGTAGCTGAGAC
15554	13641	AGCCTCCCAAGTAGCTGAGA
15555	13642	CAGCCTCCCAAGTAGCTGAG
15556	13643	TCAGCCTCCCAAGTAGCTGA
15557	13644	CTCAGCCTCCCAAGTAGCTG
15558	13645	CCTCAGCCTCCCAAGTAGCT
15559	13646	GCCTCAGCCTCCCAAGTAGC
15560	13647	TGCCTCAGCCTCCCAAGTAG
15561	13648	CTGCCTCAGCCTCCCAAGTA
15562	13649	CCTGCCTCAGCCTCCCAAGT
15563	13650	ACCTGCCTCAGCCTCCCAAG
15564	13651	CACCTGCCTCAGCCTCCCAA
15565	13652	CCACCTGCCTCAGCCTCCCA
15566	13653	ACCACCTGCCTCAGCCTCCC
15567	13654	AACCACCTGCCTCAGCCTCC
15568	13655	GAACCACCTGCCTCAGCCTC
15569	13656	TGAACCACCTGCCTCAGCCT
15570	13657	GTGAACCACCTGCCTCAGCC
15571	13658	AGTGAACCACCTGCCTCAGC
15572	13659	AAGTGAACCACCTGCCTCAG
15573	13660	TAAGTGAACCACCTGCCTCA
15574	13661	TTAAGTGAACCACCTGCCTC
15575	13662	CTTAAGTGAACCACCTGCCT
15576	13663	ACTTAAGTGAACCACCTGCC
15577	13664	GACTTAAGTGAACCACCTGC
15578	13665	AGACTTAAGTGAACCACCTG
15579	13666	CAGACTTAAGTGAACCACCT
15580	13667	CCAGACTTAAGTGAACCACC
15581	13668	TCCAGACTTAAGTGAACCAC
15582	13669	ATCCAGACTTAAGTGAACCA
15583	13670	CATCCAGACTTAAGTGAACC
15584	13671	ACATCCAGACTTAAGTGAAC
15585	13672	GACATCCAGACTTAAGTGAA
15586	13673	CGACATCCAGACTTAAGTGA
15587	13674	TCGACATCCAGACTTAAGTG
15588	13675	CTCGACATCCAGACTTAAGT
15589	13676	CCTCGACATCCAGACTTAAG
15590	13677	ACCTCGACATCCAGACTTAA
15591	13678	CACCTCGACATCCAGACTTA
15592	13679	TCACCTCGACATCCAGACTT
15593	13680	CTCACCTCGACATCCAGACT
15594	13681	GCTCACCTCGACATCCAGAC
15595	13682	GGCTCACCTCGACATCCAGA
15596	13683	TGGCTCACCTCGACATCCAG
15597	13684	ATGGCTCACCTCGACATCCA
15598	13685	CATGGCTCACCTCGACATCC
15599	13686	TCATGGCTCACCTCGACATC
15600	13687	ATCATGGCTCACCTCGACAT
15601	13688	AATCATGGCTCACCTCGACA
15602	13689	CAATCATGGCTCACCTCGAC
15603	13690	GCAATCATGGCTCACCTCGA
15604	13691	TGCAATCATGGCTCACCTCG
15605	13692	GTGCAATCATGGCTCACCTC
15606	13693	GGTGCAATCATGGCTCACCT
15607	13694	TGGTGCAATCATGGCTCACC
15608	13695	GTGGTGCAATCATGGCTCAC
15609	13696	AGTGGTGCAATCATGGCTCA
15610	13697	CAGTGGTGCAATCATGGCTC
15611	13698	GCAGTGGTGCAATCATGGCT
15612	13699	TGCAGTGGTGCAATCATGGC
15613	13700	GTGCAGTGGTGCAATCATGG

64690	62777	GCTTCAAGTGATTCTCTGCC
64691	62778	AGCTTCAAGTGATTCTCTGC
64692	62779	CAGCTTCAAGTGATTCTCTG
64693	62780	CCAGCTTCAAGTGATTCTCT
64694	62781	CCCAGCTTCAAGTGATTCTC
64695	62782	TCCCAGCTTCAAGTGATTCT
64696	62783	TTCCCAGCTTCAAGTGATTC
64697	62784	CTTCCCAGCTTCAAGTGATT
64698	62785	GCTTCCCAGCTTCAAGTGAT
64699	62786	GGCTTCCCAGCTTCAAGTGA
64700	62787	CGGCTTCCCAGCTTCAAGTG
64701	62788	TCGGCTTCCCAGCTTCAAGT
64702	62789	CTCGGCTTCCCAGCTTCAAG
64703	62790	CCTCGGCTTCCCAGCTTCAA
64704	62791	GCCTCGGCTTCCCAGCTTCA
64705	62792	AGCCTCGGCTTCCCAGCTTC
64706	62793	TAGCCTCGGCTTCCCAGCTT
64707	62794	GTAGCCTCGGCTTCCCAGCT
64708	62795	TGTAGCCTCGGCTTCCCAGC
64709	62796	CTGTAGCCTCGGCTTCCCAG
64710	62797	ACTGTAGCCTCGGCTTCCCA
64711	62798	CACTGTAGCCTCGGCTTCCC
64712	62799	TCACTGTAGCCTCGGCTTCC
64713	62800	CTCACTGTAGCCTCGGCTTC
64714	62801	GCTCACTGTAGCCTCGGCTT
64715	62802	GGCTCACTGTAGCCTCGGCT
64716	62803	CGGCTCACTGTAGCCTCGGC
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64720	62807	ATCTCGGCTCACTGTAGCCT
64721	62808	GATCTCGGCTCACTGTAGCC
64722	62809	TGATCTCGGCTCACTGTAGC
64723	62810	GTGATCTCGGCTCACTGTAG
64724	62811	CGTGATCTCGGCTCACTGTA
64725	62812	GCGTGATCTCGGCTCACTGT
64726	62813	GGCGTGATCTCGGCTCACTG
64727	62814	TGGCGTGATCTCGGCTCACT
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64730	62817	CAGTGGCGTGATCTCGGCTC
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64733	62820	GTGCAGTGGCGTGATCTCGG
64734	62821	AGTGCAGTGGCGTGATCTCG
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64736	62823	GGAGTGCAGTGGCGTGATCT
64737	62824	TGGAGTGCAGTGGCGTGATC
64738	62825	CTGGAGTGCAGTGGCGTGAT
64739	62826	GCTGGAGTGCAGTGGCGTGA
64740	62827	GGCTGGAGTGCAGTGGCGTG
64741	62828	AGGCTGGAGTGCAGTGGCGT
64742	62829	CAGGCTGGAGTGCAGTGGCG
64743	62830	CCAGGCTGGAGTGCAGTGGC
64744	62831	CCCAGGCTGGAGTGCAGTGG
64745	62832	ACCCAGGCTGGAGTGCAGTG
64746	62833	CACCCAGGCTGGAGTGCAGT
64747	62834	TCACCCAGGCTGGAGTGCAG
64748	62835	GTCACCCAGGCTGGAGTGCA
64749	62836	TGTCACCCAGGCTGGAGTGC
64750	62837	CTGTCACCCAGGCTGGAGTG
64751	62838	TCTGTCACCCAGGCTGGAGT
64752	62839	CTCTGTCACCCAGGCTGGAG
64753	62840	ACTCTGTCACCCAGGCTGGA
64754	62841	CACTCTGTCACCCAGGCTGG
64755	62842	TCACTCTGTCACCCAGGCTG
64756	62843	TTCACTCTGTCACCCAGGCT
64757	62844	TTTCACTCTGTCACCCAGGC
64758	62845	GTTTCACTCTGTCACCCAGG
64759	62846	AGTTTCACTCTGTCACCCAG
64760	62847	AAGTTTCACTCTGTCACCCA

113837	111924	TTATAGGTATGAGCTACCAG
113838	111925	ATTATAGGTATGAGCTACCA
113839	111926	GATTATAGGTATGAGCTACC
113840	111927	GGATTATAGGTATGAGCTAC
113841	111928	GGGATTATAGGTATGAGCTA
113842	111929	TGGGATTATAGGTATGAGCT
113843	111930	CTGGGATTATAGGTATGAGC
113844	111931	GCTGGGATTATAGGTATGAG
113845	111932	TGCTGGGATTATAGGTATGA
113846	111933	GTGCTGGGATTATAGGTATG
113847	111934	AGTGCTGGGATTATAGGTAT
113848	111935	GAGTGCTGGGATTATAGGTA
113849	111936	AGAGTGCTGGGATTATAGGT
113850	111937	CAGAGTGCTGGGATTATAGG
113851	111938	CCAGAGTGCTGGGATTATAG
113852	111939	CCCAGAGTGCTGGGATTATA
113853	111940	TCCCAGAGTGCTGGGATTAT
113854	111941	CTCCCAGAGTGCTGGGATTA
113855	111942	CCTCCCAGAGTGCTGGGATT
113856	111943	ACCTCCCAGAGTGCTGGGAT
113857	111944	GACCTCCCAGAGTGCTGGGA
113858	111945	GGACCTCCCAGAGTGCTGGG
113859	111946	TGGACCTCCCAGAGTGCTGG
113860	111947	TTGGACCTCCCAGAGTGCTG
113861	111948	CTTGGACCTCCCAGAGTGCT
113862	111949	GCTTGGACCTCCCAGAGTGC
113863	111950	TGCTTGGACCTCCCAGAGTG
113864	111951	CTGCTTGGACCTCCCAGAGT
113865	111952	CCTGCTTGGACCTCCCAGAG
113866	111953	ACCTGCTTGGACCTCCCAGA
113867	111954	TACCTGCTTGGACCTCCCAG
113868	111955	CTACCTGCTTGGACCTCCCA
113869	111956	TCTACCTGCTTGGACCTCCC
113870	111957	ATCTACCTGCTTGGACCTCC
113871	111958	AATCTACCTGCTTGGACCTC
113872	111959	TAATCTACCTGCTTGGACCT
113873	111960	GTAATCTACCTGCTTGGACC
113874	111961	AGTAATCTACCTGCTTGGAC
113875	111962	AAGTAATCTACCTGCTTGGA
113876	111963	CAAGTAATCTACCTGCTTGG
113877	111964	TCAAGTAATCTACCTGCTTG
113878	111965	CTCAAGTAATCTACCTGCTT
113879	111966	CCTCAAGTAATCTACCTGCT
113880	111967	ACCTCAAGTAATCTACCTGC
113881	111968	AACCTCAAGTAATCTACCTG
113882	111969	TAACCTCAAGTAATCTACCT
113883	111970	CTAACCTCAAGTAATCTACC
113884	111971	CCTAACCTCAAGTAATCTAC
113885	111972	TCCTAACCTCAAGTAATCTA
113886	111973	CTCCTAACCTCAAGTAATCT
113887	111974	ACTCCTAACCTCAAGTAATC
113888	111975	AACTCCTAACCTCAAGTAAT
113889	111976	CAACTCCTAACCTCAAGTAA
113890	111977	TCAACTCCTAACCTCAAGTA
113891	111978	TTCAACTCCTAACCTCAAGT
113892	111979	CTTCAACTCCTAACCTCAAG
113893	111980	TCTTCAACTCCTAACCTCAA
113894	111981	GTCTTCAACTCCTAACCTCA
113895	111982	GGTCTTCAACTCCTAACCTC
113896	111983	TGGTCTTCAACTCCTAACCT
113897	111984	CTGGTCTTCAACTCCTAACC
113898	111985	GCTGGTCTTCAACTCCTAAC
113899	111986	GGCTGGTCTTCAACTCCTAA
113900	111987	AGGCTGGTCTTCAACTCCTA
113901	111988	CAGGCTGGTCTTCAACTCCT
113902	111989	CCAGGCTGGTCTTCAACTCC
113903	111990	GCCAGGCTGGTCTTCAACTC
113904	111991	GGCCAGGCTGGTCTTCAACT
113905	111992	TGGCCAGGCTGGTCTTCAAC
113906	111993	TTGGCCAGGCTGGTCTTCAA
113907	111994	GTTGGCCAGGCTGGTCTTCA

15614	13701	AGTGCAGTGGTGCAATCATG
15615	13702	GAGTGCAGTGGTGCAATCAT
15616	13703	GGAGTGCAGTGGTGCAATCA
15617	13704	TGGAGTGCAGTGGTGCAATC
15618	13705	CTGGAGTGCAGTGGTGCAAT
15619	13706	GCTGGAGTGCAGTGGTGCAA
15620	13707	GGCTGGAGTGCAGTGGTGCA
15621	13708	AGGCTGGAGTGCAGTGGTGC
15622	13709	CAGGCTGGAGTGCAGTGGTG
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15624	13711	CCCAGGCTGGAGTGCAGTGG
15625	13712	GCCCAGGCTGGAGTGCAGTG
15626	13713	CGCCCAGGCTGGAGTGCAGT
15627	13714	ACGCCCAGGCTGGAGTGCAG
15628	13715	AACGCCCAGGCTGGAGTGCA
15629	13716	TAACGCCCAGGCTGGAGTGC
15630	13717	TTAACGCCCAGGCTGGAGTG
15631	13718	TTTAACGCCCAGGCTGGAGT
15632	13719	TTTTAACGCCCAGGCTGGAG
15633	13720	ATTTTAACGCCCAGGCTGGA
15634	13721	CATTTTAACGCCCAGGCTGG
15635	13722	TCATTTTAACGCCCAGGCTG
15636	13723	CTCATTTTAACGCCCAGGCT
15637	13724	TCTCATTTTAACGCCCAGGC
15638	13725	GTCTCATTTTAACGCCCAGG
15639	13726	GGTCTCATTTTAACGCCCAG
15640	13727	AGGTCTCATTTTAACGCCCA
15641	13728	AAGGTCTCATTTTAACGCCC
15642	13729	TAAGGTCTCATTTTAACGCC
15643	13730	ATAAGGTCTCATTTTAACGC
15644	13731	GATAAGGTCTCATTTTAACG
15645	13732	AGATAAGGTCTCATTTTAAC
15646	13733	GAGATAAGGTCTCATTTTAA
15647	13734	TGAGATAAGGTCTCATTTTA
15648	13735	TTGAGATAAGGTCTCATTTT
15649	13736	TTTGAGATAAGGTCTCATTT
15650	13737	TTTTGAGATAAGGTCTCATT
15651	13738	TTTTTGAGATAAGGTCTCAT
15652	13739	TTTTTTGAGATAAGGTCTCA
15653	13740	TTTTTTTGAGATAAGGTCTC
15654	13741	GTTTTTTTGAGATAAGGTCT
15655	13742	TGTTTTTTTGAGATAAGGTC
15656	13743	TTGTTTTTTTGAGATAAGGT
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15659	13746	GCTTTGTTTTTTTGAGATAA
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15661	13748	TTGCTTTGTTTTTTTGAGAT
15662	13749	TTTGCTTTGTTTTTTTGAGA
15663	13750	CTTTGCTTTGTTTTTTTGAG
15664	13751	TCTTTGCTTTGTTTTTTTGA
15665	13752	CTCTTTGCTTTGTTTTTTTG
15666	13753	GCTCTTTGCTTTGTTTTTTT
15667	13754	GGCTCTTTGCTTTGTTTTTT
15668	13755	AGGCTCTTTGCTTTGTTTTT
15669	13756	CAGGCTCTTTGCTTTGTTTT
15670	13757	CCAGGCTCTTTGCTTTGTTT
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15673	13760	TTCCCAGGCTCTTTGCTTTG
15674	13761	GTTCCCAGGCTCTTTGCTTT
15675	13762	AGTTCCCAGGCTCTTTGCTT
15676	13763	TAGTTCCCAGGCTCTTTGCT
15677	13764	GTAGTTCCCAGGCTCTTTGC
15678	13765	AGTAGTTCCCAGGCTCTTTG
15679	13766	TAGTAGTTCCCAGGCTCTTT
15680	13767	TTAGTAGTTCCCAGGCTCTT
15681	13768	TTTAGTAGTTCCCAGGCTCT
15682	13769	TTTTAGTAGTTCCCAGGCTC
15683	13770	ATTTTAGTAGTTCCCAGGCT
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64761	62848	GAAGTTTCACTCTGTCACCC
64762	62849	TGAAGTTTCACTCTGTCACC
64763	62850	ATGAAGTTTCACTCTGTCAC
64764	62851	GATGAAGTTTCACTCTGTCA
64765	62852	AGATGAAGTTTCACTCTGTC
64766	62853	GAGATGAAGTTTCACTCTGT
64767	62854	TGAGATGAAGTTTCACTCTG
64768	62855	TTGAGATGAAGTTTCACTCT
64769	62856	TTTGAGATGAAGTTTCACTC
64770	62857	TTTTGAGATGAAGTTTCACT
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64793	62880	CAGTTTTTTTTTTTTTTTT
64794	62881	GCAGTTTTTTTTTTTTTTT
64795	62882	CGCAGTTTTTTTTTTTTTT
64796	62883	ACGCAGTTTTTTTTTTTTT
64797	62884	CACGCAGTTTTTTTTTTTT
64798	62885	ACACGCAGTTTTTTTTTTT
64799	62886	CACACGCAGTTTTTTTTTT
64800	62887	CCACACGCAGTTTTTTTTT
64801	62888	TCCACACGCAGTTTTTTTT
64802	62889	GTCCACACGCAGTTTTTTT
64803	62890	TGTCCACACGCAGTTTTTT
64804	62891	ATGTCCACACGCAGTTTTT
64805	62892	TATGTCCACACGCAGTTTT
64806	62893	CTATGTCCACACGCAGTTT
64807	62894	CCTATGTCCACACGCAGTT
64808	62895	ACCTATGTCCACACGCAGTT
64809	62896	AACCTATGTCCACACGCAGT
64810	62897	AAACCTATGTCCACACGCAG
64811	62898	AAAACCTATGTCCACACGCA
64812	62899	GAAAACCTATGTCCACACGC
64813	62900	TGAAAACCTATGTCCACACG
64814	62901	TTGAAAACCTATGTCCACAC
64815	62902	ATTGAAAACCTATGTCCACA
64816	62903	AATTGAAAACCTATGTCCAC
64817	62904	GAATTGAAAACCTATGTCCA
64818	62905	AGAATTGAAAACCTATGTCC
64819	62906	GAGAATTGAAAACCTATGTC
64820	62907	TGAGAATTGAAAACCTATGT
64821	62908	ATGAGAATTGAAAACCTATG
64822	62909	CATGAGAATTGAAAACCTAT
64823	62910	CCATGAGAATTGAAAACCTA
64824	62911	CCCATGAGAATTGAAAACCT
64825	62912	CCCCATGAGAATTGAAAACC
64826	62913	CCCCCATGAGAATTGAAAAC
64827	62914	ACCCCCATGAGAATTGAAAA
64828	62915	CACCCCCATGAGAATTGAAA
64829	62916	ACACCCCCATGAGAATTGAA
64830	62917	CACACCCCCATGAGAATTGA
64831	62918	ACACACCCCCATGAGAATTG

113908	111995	TGTTGGCCAGGCTGGTCTTC
113909	111996	ATGTTGGCCAGGCTGGTCTT
113910	111997	CATGTTGGCCAGGCTGGTCT
113911	111998	ACATGTTGGCCAGGCTGGTC
113912	111999	CACATGTTGGCCAGGCTGGT
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113914	112001	TTCACATGTTGGCCAGGCTG
113915	112002	TTTCACATGTTGGCCAGGCT
113916	112003	GTTTCACATGTTGGCCAGGC
113917	112004	GGTTTCACATGTTGGCCAGG
113918	112005	GGGTTTCACATGTTGGCCAG
113919	112006	AGGGTTTCACATGTTGGCCA
113920	112007	CAGGGTTTCACATGTTGGCC
113921	112008	ACAGGGTTTCACATGTTGGC
113922	112009	GACAGGGTTTCACATGTTGG
113923	112010	AGACAGGGTTTCACATGTTG
113924	112011	CAGACAGGGTTTCACATGTT
113925	112012	ACAGACAGGGTTTCACATGT
113926	112013	TACAGACAGGGTTTCACATG
113927	112014	GTACAGACAGGGTTTCACAT
113928	112015	AGTACAGACAGGGTTTCACA
113929	112016	TAGTACAGACAGGGTTTCAC
113930	112017	TTAGTACAGACAGGGTTTCA
113931	112018	TTTAGTACAGACAGGGTTTC
113932	112019	TTTTAGTACAGACAGGGTTT
113933	112020	TTTTTAGTACAGACAGGGTT
113934	112021	ATTTTTAGTACAGACAGGGT
113935	112022	TATTTTTAGTACAGACAGGG
113936	112023	GTATTTTTAGTACAGACAGG
113937	112024	TGTATTTTTAGTACAGACAG
113938	112025	TTGTATTTTTAGTACAGACA
113939	112026	TTTGTATTTTTAGTACAGAC
113940	112027	TTTTGTATTTTTAGTACAGA
113941	112028	TTTTTGTATTTTTAGTACAG
113942	112029	ATTTTTGTATTTTTAGTACA
113943	112030	AATTTTTGTATTTTTAGTAC
113944	112031	TAATTTTTGTATTTTTAGTA
113945	112032	CTAATTTTTGTATTTTTAGT
113946	112033	GCTAATTTTTGTATTTTTAG
113947	112034	GGCTAATTTTTGTATTTTTA
113948	112035	TGGCTAATTTTTGTATTTTT
113949	112036	CTGGCTAATTTTTGTATTTT
113950	112037	CCTGGCTAATTTTTGTATTT
113951	112038	GCCTGGCTAATTTTTGTATT
113952	112039	TGCCTGGCTAATTTTTGTAT
113953	112040	ATGCCTGGCTAATTTTTGTA
113954	112041	CATGCCTGGCTAATTTTTGT
113955	112042	CCATGCCTGGCTAATTTTTG
113956	112043	ACCATGCCTGGCTAATTTTT
113957	112044	CACCATGCCTGGCTAATTTT
113958	112045	CCACCATGCCTGGCTAATTT
113959	112046	ACCACCATGCCTGGCTAATT
113960	112047	TACCACCATGCCTGGCTAAT
113961	112048	CTACCACCATGCCTGGCTAA
113962	112049	CCTACCACCATGCCTGGCTA
113963	112050	ACCTACCACCATGCCTGGCT
113964	112051	CACCTACCACCATGCCTGGC
113965	112052	GCACCTACCACCATGCCTGG
113966	112053	GGCACCTACCACCATGCCTG
113967	112054	AGGCACCTACCACCATGCCT
113968	112055	CAGGCACCTACCACCATGCC
113969	112056	ACAGGCACCTACCACCATGC
113970	112057	TACAGGCACCTACCACCATG
113971	112058	ATACAGGCACCTACCACCAT
113972	112059	GATACAGGCACCTACCACCA
113973	112060	GGATACAGGCACCTACCACC
113974	112061	GGGATACAGGCACCTACCAC
113975	112062	TGGGATACAGGCACCTACCA
113976	112063	CTGGGATACAGGCACCTACC
113977	112064	GCTGGGATACAGGCACCTAC
113978	112065	AGCTGGGATACAGGCACCTA

15685	13772	CCATTTTAGTAGTTCCCAGG
15686	13773	CCCATTTTAGTAGTTCCCAG
15687	13774	TCCCATTTTAGTAGTTCCCA
15688	13775	TTCCCATTTTAGTAGTTCCC
15689	13776	GTTCCCATTTTAGTAGTTCC
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15691	13778	TAGTTCCCATTTTAGTAGTT
15692	13779	GTAGTTCCCATTTTAGTAGT
15693	13780	AGTAGTTCCCATTTTAGTAG
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15698	13785	TTTTTAGTAGTTCCCATTTT
15699	13786	TTTTTTAGTAGTTCCCATTT
15700	13787	GTTTTTTAGTAGTTCCCATT
15701	13788	TGTTTTTTAGTAGTTCCCAT
15702	13789	CTGTTTTTTAGTAGTTCCCA
15703	13790	TCTGTTTTTTAGTAGTTCCC
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15714	13801	GAGCTCTTGTGTCTGTTTTT
15715	13802	TGAGCTCTTGTGTCTGTTTT
15716	13803	TTGAGCTCTTGTGTCTGTTT
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15718	13805	TGTTGAGCTCTTGTGTCTGT
15719	13806	TTGTTGAGCTCTTGTGTCTG
15720	13807	CTTGTTGAGCTCTTGTGTCT
15721	13808	ACTTGTTGAGCTCTTGTGTC
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15723	13810	ATACTTGTTGAGCTCTTGTG
15724	13811	TATACTTGTTGAGCTCTTGT
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15732	13819	CAGAATGGTATACTTGTTGA
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15735	13822	TCCCAGAATGGTATACTTGT
15736	13823	CTCCCAGAATGGTATACTTG
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15738	13825	ACCTCCCAGAATGGTATACT
15739	13826	AACCTCCCAGAATGGTATAC
15740	13827	AAACCTCCCAGAATGGTATA
15741	13828	AAAACCTCCCAGAATGGTAT
15742	13829	AAAAACCTCCCAGAATGGTA
15743	13830	AAAAAACCTCCCAGAATGGT
15744	13831	AAAAAAACCTCCCAGAATGG
15745	13832	AAAAAAAACCTCCCAGAATG
15746	13833	AAAAAAAAACCTCCCAGAAT
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64834	62921	CACACACACCCCCATGAGAA
64835	62922	ACACACACACCCCCATGAGA
64836	62923	TACACACACACCCCCATGAG
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64838	62925	CATACACACACACCCCCATG
64839	62926	GCATACACACACACCCCCAT
64840	62927	TGCATACACACACACCCCCA
64841	62928	ATGCATACACACACACCCCC
64842	62929	TATGCATACACACACACCCC
64843	62930	GTATGCATACACACACACCC
64844	62931	AGTATGCATACACACACACC
64845	62932	GAGTATGCATACACACACAC
64846	62933	TGAGTATGCATACACACACA
64847	62934	ATGAGTATGCATACACACAC
64848	62935	TATGAGTATGCATACACACA
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64853	62940	GTATGTATGAGTATGCATAC
64854	62941	TGTATGTATGAGTATGCATA
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64856	62943	TATGTATGTATGAGTATGCA
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64884	62971	GAGCCAGCAATTATCTTGCA
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64897	62984	AGATTTAGCATACGAGCCAG
64898	62985	TAGATTTAGCATACGAGCCA
64899	62986	ATAGATTTAGCATACGAGCC
64900	62987	CATAGATTTAGCATACGAGC
64901	62988	ACATAGATTTAGCATACGAG
64902	62989	AACATAGATTTAGCATACGA

113979	112066	TAGCTGGGATACAGGCACCT
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113982	112069	GAGTAGCTGGGATACAGGCA
113983	112070	CGAGTAGCTGGGATACAGGC
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113985	112072	CCCGAGTAGCTGGGATACAG
113986	112073	TCCCGAGTAGCTGGGATACA
113987	112074	CTCCCGAGTAGCTGGGATAC
113988	112075	CCTCCCGAGTAGCTGGGATA
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113990	112077	AGCCTCCCGAGTAGCTGGGA
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113992	112079	TCAGCCTCCCGAGTAGCTGG
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113995	112082	GCCTCAGCCTCCCGAGTAGC
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114001	112088	TCTCCTGCCTCAGCCTCCCG
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114005	112092	CAATTCTCCTGCCTCAGCCT
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114007	112094	AGCAATTCTCCTGCCTCAGC
114008	112095	AAGCAATTCTCCTGCCTCAG
114009	112096	CAAGCAATTCTCCTGCCTCA
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114018	112105	TTCTGGGTTCAAGCAATTCT
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114020	112107	CCTTCTGGGTTCAAGCAATT
114021	112108	ACCTTCTGGGTTCAAGCAAT
114022	112109	CACCTTCTGGGTTCAAGCAA
114023	112110	CCACCTTCTGGGTTCAAGCA
114024	112111	TCCACCTTCTGGGTTCAAGC
114025	112112	CTCCACCTTCTGGGTTCAAG
114026	112113	CCTCCACCTTCTGGGTTCAA
114027	112114	GCCTCCACCTTCTGGGTTCA
114028	112115	AGCCTCCACCTTCTGGGTTC
114029	112116	CAGCCTCCACCTTCTGGGTT
114030	112117	GCAGCCTCCACCTTCTGGGT
114031	112118	TGCAGCCTCCACCTTCTGGG
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114033	112120	ACTGCAGCCTCCACCTTCTG
114034	112121	CACTGCAGCCTCCACCTTCT
114035	112122	TCACTGCAGCCTCCACCTTC
114036	112123	CTCACTGCAGCCTCCACCTT
114037	112124	GCTCACTGCAGCCTCCACCT
114038	112125	GGCTCACTGCAGCCTCCACC
114039	112126	CGGCTCACTGCAGCCTCCAC
114040	112127	TCGGCTCACTGCAGCCTCCA
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114044	112131	GATCTCGGCTCACTGCAGCC
114045	112132	TGATCTCGGCTCACTGCAGC
114046	112133	ATGATCTCGGCTCACTGCAG
114047	112134	CATGATCTCGGCTCACTGCA
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15773	13860	CCATCTCAAAAAAAAAAAA
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15777	13864	AACTCCATCTCAAAAAAAA
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15781	13868	GCAAAACTCCATCTCAAAA
15782	13869	AGCAAAACTCCATCTCAAA
15783	13870	GAGCAAAACTCCATCTCAA
15784	13871	AGAGCAAAACTCCATCTCAA
15785	13872	AAGAGCAAAACTCCATCTCA
15786	13873	CAAGAGCAAAACTCCATCTC
15787	13874	ACAAGAGCAAAACTCCATCT
15788	13875	GACAAGAGCAAAACTCCATC
15789	13876	TGACAAGAGCAAAACTCCAT
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15794	13881	CTGGGTGACAAGAGCAAAAC
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15806	13893	TTGCACTCCAGCCTGGGTGA
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15808	13895	CATTGCACTCCAGCCTGGGT
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15821	13908	GCAGAGATGGCGCCATTGCA
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15823	13910	GAGCAGAGATGGCGCCATTG
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64904	62991	TCAACATAGATTTAGCATAC
64905	62992	TTCAACATAGATTTAGCATA
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64941	63028	AAAGAAAACAAAACAGCCCA
64942	63029	AAAAGAAAACAAAACAGCCC
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64945	63032	ATAAAAAGAAAACAAAACAG
64946	63033	AATAAAAAGAAAACAAAACA
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114053	112140	CAGTGGCATGATCTCGGCTC
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114082	112169	AGTCTCGCTCTGTCACCCAG
114083	112170	GAGTCTCGCTCTGTCACCCA
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114085	112172	CAGAGTCTCGCTCTGTCACC
114086	112173	ACAGAGTCTCGCTCTGTCAC
114087	112174	GACAGAGTCTCGCTCTGTCA
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114090	112177	TGAGACAGAGTCTCGCTCTG
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114116	112203	CTTTTATTTATTTATTTATT
114117	112204	CCTTTTATTTATTTATTTAT
114118	112205	TCCTTTTATTTATTTATTTA
114119	112206	ATCCTTTTATTTATTTATTT
114120	112207	TATCCTTTTATTTATTTATT

15827	13914	CAGTGAGCAGAGATGGCGCC
15828	13915	ACAGTGAGCAGAGATGGCGC
15829	13916	TACAGTGAGCAGAGATGGCG
15830	13917	CTACAGTGAGCAGAGATGGC
15831	13918	ACTACAGTGAGCAGAGATGG
15832	13919	AACTACAGTGAGCAGAGATG
15833	13920	GAACTACAGTGAGCAGAGAT
15834	13921	GGAACTACAGTGAGCAGAGA
15835	13922	CGGAACTACAGTGAGCAGAG
15836	13923	GCGGAACTACAGTGAGCAGA
15837	13924	GGCGGAACTACAGTGAGCAG
15838	13925	AGGCGGAACTACAGTGAGCA
15839	13926	GAGGCGGAACTACAGTGAGC
15840	13927	GGAGGCGGAACTACAGTGAG
15841	13928	GGGAGGCGGAACTACAGTGA
15842	13929	TGGGAGGCGGAACTACAGTG
15843	13930	CTGGGAGGCGGAACTACAGT
15844	13931	CCTGGGAGGCGGAACTACAG
15845	13932	ACCTGGGAGGCGGAACTACA
15846	13933	AACCTGGGAGGCGGAACTAC
15847	13934	GAACCTGGGAGGCGGAACTA
15848	13935	TGAACCTGGGAGGCGGAACT
15849	13936	TTGAACCTGGGAGGCGGAAC
15850	13937	CTTGAACCTGGGAGGCGGAA
15851	13938	GCTTGAACCTGGGAGGCGGA
15852	13939	TGCTTGAACCTGGGAGGCGG
15853	13940	CTGCTTGAACCTGGGAGGCG
15854	13941	ACTGCTTGAACCTGGGAGGC
15855	13942	AACTGCTTGAACCTGGGAGG
15856	13943	GAACTGCTTGAACCTGGGAG
15857	13944	AGAACTGCTTGAACCTGGGA
15858	13945	GAGAACTGCTTGAACCTGGG
15859	13946	GGAGAACTGCTTGAACCTGG
15860	13947	AGGAGAACTGCTTGAACCTG
15861	13948	CAGGAGAACTGCTTGAACCT
15862	13949	GCAGGAGAACTGCTTGAACC
15863	13950	GGCAGGAGAACTGCTTGAAC
15864	13951	AGGCAGGAGAACTGCTTGAA
15865	13952	CAGGCAGGAGAACTGCTTGA
15866	13953	TCAGGCAGGAGAACTGCTTG
15867	13954	GTCAGGCAGGAGAACTGCTT
15868	13955	AGTCAGGCAGGAGAACTGCT
15869	13956	GAGTCAGGCAGGAGAACTGC
15870	13957	GGAGTCAGGCAGGAGAACTG
15871	13958	AGGAGTCAGGCAGGAGAACT
15872	13959	CAGGAGTCAGGCAGGAGAAC
15873	13960	TCAGGAGTCAGGCAGGAGAA
15874	13961	CTCAGGAGTCAGGCAGGAGA
15875	13962	ACTCAGGAGTCAGGCAGGAG
15876	13963	TACTCAGGAGTCAGGCAGGA
15877	13964	CTACTCAGGAGTCAGGCAGG
15878	13965	GCTACTCAGGAGTCAGGCAG
15879	13966	AGCTACTCAGGAGTCAGGCA
15880	13967	CAGCTACTCAGGAGTCAGGC
15881	13968	CCAGCTACTCAGGAGTCAGG
15882	13969	CCCAGCTACTCAGGAGTCAG
15883	13970	TCCCAGCTACTCAGGAGTCA
15884	13971	CTCCCAGCTACTCAGGAGTC
15885	13972	ACTCCCAGCTACTCAGGAGT
15886	13973	TACTCCCAGCTACTCAGGAG
15887	13974	GTACTCCCAGCTACTCAGGA
15888	13975	TGTACTCCCAGCTACTCAGG
15889	13976	CTGTACTCCCAGCTACTCAG
15890	13977	TCTGTACTCCCAGCTACTCA
15891	13978	ATCTGTACTCCCAGCTACTC
15892	13979	TATCTGTACTCCCAGCTACT
15893	13980	ATATCTGTACTCCCAGCTAC
15894	13981	AATATCTGTACTCCCAGCTA
15895	13982	CAATATCTGTACTCCCAGCT
15896	13983	CCAATATCTGTACTCCCAGC
15897	13984	ACCAATATCTGTACTCCCAG

64974	63061	TGAGACCCCAACTCTATTTT
64975	63062	GTGAGACCCCAACTCTATTT
64976	63063	AGTGAGACCCCAACTCTATT
64977	63064	CAGTGAGACCCCAACTCTAT
64978	63065	ACAGTGAGACCCCAACTCTA
64979	63066	AACAGTGAGACCCCAACTCT
64980	63067	CAACAGTGAGACCCCAACTC
64981	63068	GCAACAGTGAGACCCCAACT
64982	63069	TGCAACAGTGAGACCCCAAC
64983	63070	GTGCAACAGTGAGACCCCAA
64984	63071	TGTGCAACAGTGAGACCCCA
64985	63072	CTGTGCAACAGTGAGACCCC
64986	63073	CCTGTGCAACAGTGAGACCC
64987	63074	GCCTGTGCAACAGTGAGACC
64988	63075	AGCCTGTGCAACAGTGAGAC
64989	63076	CAGCCTGTGCAACAGTGAGA
64990	63077	TCAGCCTGTGCAACAGTGAG
64991	63078	ATCAGCCTGTGCAACAGTGA
64992	63079	AATCAGCCTGTGCAACAGTG
64993	63080	AAATCAGCCTGTGCAACAGT
64994	63081	GAAATCAGCCTGTGCAACAG
64995	63082	GGAAATCAGCCTGTGCAACA
64996	63083	AGGAAATCAGCCTGTGCAAC
64997	63084	CAGGAAATCAGCCTGTGCAA
64998	63085	CCAGGAAATCAGCCTGTGCA
64999	63086	CCCAGGAAATCAGCCTGTGC
65000	63087	GCCCAGGAAATCAGCCTGTG
65001	63088	TGCCCAGGAAATCAGCCTGT
65002	63089	ATGCCCAGGAAATCAGCCTG
65003	63090	TATGCCCAGGAAATCAGCCT
65004	63091	CTATGCCCAGGAAATCAGCC
65005	63092	ACTATGCCCAGGAAATCAGC
65006	63093	CACTATGCCCAGGAAATCAG
65007	63094	CCACTATGCCCAGGAAATCA
65008	63095	GCCACTATGCCCAGGAAATC
65009	63096	AGCCACTATGCCCAGGAAAT
65010	63097	CAGCCACTATGCCCAGGAAA
65011	63098	ACAGCCACTATGCCCAGGAA
65012	63099	TACAGCCACTATGCCCAGGA
65013	63100	ATACAGCCACTATGCCCAGG
65014	63101	GATACAGCCACTATGCCCAG
65015	63102	TGATACAGCCACTATGCCCA
65016	63103	ATGATACAGCCACTATGCCC
65017	63104	AATGATACAGCCACTATGCC
65018	63105	AAATGATACAGCCACTATGC
65019	63106	AAAATGATACAGCCACTATG
65020	63107	TAAAATGATACAGCCACTAT
65021	63108	GTAAAATGATACAGCCACTA
65022	63109	TGTAAAATGATACAGCCACT
65023	63110	TTGTAAAATGATACAGCCAC
65024	63111	ATTGTAAAATGATACAGCCA
65025	63112	GATTGTAAAATGATACAGCC
65026	63113	GGATTGTAAAATGATACAGC
65027	63114	AGGATTGTAAAATGATACAG
65028	63115	TAGGATTGTAAAATGATACA
65029	63116	GTAGGATTGTAAAATGATAC
65030	63117	TGTAGGATTGTAAAATGATA
65031	63118	ATGTAGGATTGTAAAATGAT
65032	63119	TATGTAGGATTGTAAAATGA
65033	63120	CTATGTAGGATTGTAAAATG
65034	63121	GCTATGTAGGATTGTAAAAT
65035	63122	AGCTATGTAGGATTGTAAAA
65036	63123	CAGCTATGTAGGATTGTAAA
65037	63124	ACAGCTATGTAGGATTGTAA
65038	63125	AACAGCTATGTAGGATTGTA
65039	63126	AAACAGCTATGTAGGATTGT
65040	63127	GAAACAGCTATGTAGGATTG
65041	63128	GGAAACAGCTATGTAGGATT
65042	63129	TGGAAACAGCTATGTAGGAT
65043	63130	TTGGAAACAGCTATGTAGGA
65044	63131	GTTGGAAACAGCTATGTAGG

114121	112208	GTATCCTTTTATTTATTTAT
114122	112209	AGTATCCTTTTATTTATTTA
114123	112210	CAGTATCCTTTTATTTATTT
114124	112211	ACAGTATCCTTTTATTTATT
114125	112212	AACAGTATCCTTTTATTTAT
114126	112213	TAACAGTATCCTTTTATTTA
114127	112214	ATAACAGTATCCTTTTATTT
114128	112215	CATAACAGTATCCTTTTATT
114129	112216	ACATAACAGTATCCTTTTAT
114130	112217	AACATAACAGTATCCTTTTA
114131	112218	TAACATAACAGTATCCTTTT
114132	112219	TTAACATAACAGTATCCTTT
114133	112220	CTTAACATAACAGTATCCTT
114134	112221	TCTTAACATAACAGTATCCT
114135	112222	TTCTTAACATAACAGTATCC
114136	112223	ATTCTTAACATAACAGTATC
114137	112224	AATTCTTAACATAACAGTAT
114138	112225	CAATTCTTAACATAACAGTA
114139	112226	GCAATTCTTAACATAACAGT
114140	112227	AGCAATTCTTAACATAACAG
114141	112228	AAGCAATTCTTAACATAACA
114142	112229	AAAGCAATTCTTAACATAAC
114143	112230	AAAAGCAATTCTTAACATAA
114144	112231	TAAAAGCAATTCTTAACATA
114145	112232	TTAAAAGCAATTCTTAACAT
114146	112233	CTTAAAAGCAATTCTTAACA
114147	112234	CCTTAAAAGCAATTCTTAAC
114148	112235	TCCTTAAAAGCAATTCTTAA
114149	112236	ATCCTTAAAAGCAATTCTTA
114150	112237	TATCCTTAAAAGCAATTCTT
114151	112238	ATATCCTTAAAAGCAATTCT
114152	112239	AATATCCTTAAAAGCAATTC
114153	112240	AAATATCCTTAAAAGCAATT
114154	112241	GAAATATCCTTAAAAGCAAT
114155	112242	TGAAATATCCTTAAAAGCAA
114156	112243	ATGAAATATCCTTAAAAGCA
114157	112244	TATGAAATATCCTTAAAAGC
114158	112245	TTATGAAATATCCTTAAAAG
114159	112246	CTTATGAAATATCCTTAAAA
114160	112247	ACTTATGAAATATCCTTAAA
114161	112248	TACTTATGAAATATCCTTAA
114162	112249	CTACTTATGAAATATCCTTA
114163	112250	GCTACTTATGAAATATCCTT
114164	112251	AGCTACTTATGAAATATCCT
114165	112252	TAGCTACTTATGAAATATCC
114166	112253	GTAGCTACTTATGAAATATC
114167	112254	AGTAGCTACTTATGAAATAT
114168	112255	CAGTAGCTACTTATGAAATA
114169	112256	ACAGTAGCTACTTATGAAAT
114170	112257	GACAGTAGCTACTTATGAAA
114171	112258	AGACAGTAGCTACTTATGAA
114172	112259	AAGACAGTAGCTACTTATGA
114173	112260	AAAGACAGTAGCTACTTATG
114174	112261	AAAAGACAGTAGCTACTTAT
114175	112262	GAAAAGACAGTAGCTACTTA
114176	112263	TGAAAAGACAGTAGCTACTT
114177	112264	CTGAAAAGACAGTAGCTACT
114178	112265	GCTGAAAAGACAGTAGCTAC
114179	112266	AGCTGAAAAGACAGTAGCTA
114180	112267	GAGCTGAAAAGACAGTAGCT
114181	112268	TGAGCTGAAAAGACAGTAGC
114182	112269	TTGAGCTGAAAAGACAGTAG
114183	112270	CTTGAGCTGAAAAGACAGTA
114184	112271	ACTTGAGCTGAAAAGACAGT
114185	112272	CACTTGAGCTGAAAAGACAG
114186	112273	ACACTTGAGCTGAAAAGACA
114187	112274	AACACTTGAGCTGAAAAGAC
114188	112275	AAACACTTGAGCTGAAAAGA
114189	112276	CAAACACTTGAGCTGAAAAG
114190	112277	ACAAACACTTGAGCTGAAAA
114191	112278	AACAAACACTTGAGCTGAAA

15898	13985	GACCAATATCTGTACTCCCA
15899	13986	TGACCAATATCTGTACTCCC
15900	13987	GTGACCAATATCTGTACTCC
15901	13988	TGTGACCAATATCTGTACTC
15902	13989	GTGTGACCAATATCTGTACT
15903	13990	TGTGTGACCAATATCTGTAC
15904	13991	GTGTGTGACCAATATCTGTA
15905	13992	GGTGTGTGACCAATATCTGT
15906	13993	CGGTGTGTGACCAATATCTG
15907	13994	CCGGTGTGTGACCAATATCT
15908	13995	CCCGGTGTGTGACCAATATC
15909	13996	ACCCGGTGTGTGACCAATAT
15910	13997	AACCCGGTGTGTGACCAATA
15911	13998	TAACCCGGTGTGTGACCAAT
15912	13999	TTAACCCGGTGTGTGACCAA
15913	14000	ATTAACCCGGTGTGTGACCA
15914	14001	AATTAACCCGGTGTGTGACC
15915	14002	AAATTAACCCGGTGTGTGAC
15916	14003	AAAATTAACCCGGTGTGTGA
15917	14004	AAAAATTAACCCGGTGTGTG
15918	14005	CAAAAATTAACCCGGTGTGT
15919	14006	ACAAAAATTAACCCGGTGTG
15920	14007	TACAAAAATTAACCCGGTGT
15921	14008	ATACAAAAATTAACCCGGTG
15922	14009	AATACAAAAATTAACCCGGT
15923	14010	AAATACAAAAATTAACCCGG
15924	14011	AAAATACAAAAATTAACCCG
15925	14012	AAAAATACAAAAATTAACCC
15926	14013	TAAAAATACAAAAATTAACC
15927	14014	CTAAAAATACAAAAATTAAC
15928	14015	ACTAAAAATACAAAAATTAA
15929	14016	TACTAAAAATACAAAAATTA
15930	14017	CTACTAAAAATACAAAAATT
15931	14018	TCTACTAAAAATACAAAAAT
15932	14019	CTCTACTAAAAATACAAAAA
15933	14020	TCTCTACTAAAAATACAAAA
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15935	14022	CGTCTCTACTAAAAATACAA
15936	14023	CCGTCTCTACTAAAAATACA
15937	14024	CCCGTCTCTACTAAAAATAC
15938	14025	CCCCGTCTCTACTAAAAATA
15939	14026	ACCCCGTCTCTACTAAAAAT
15940	14027	AACCCCGTCTCTACTAAAAA
15941	14028	AAACCCCGTCTCTACTAAAA
15942	14029	GAAACCCCGTCTCTACTAAA
15943	14030	GGAAACCCCGTCTCTACTAA
15944	14031	GGGAAACCCCGTCTCTACTA
15945	14032	GGGGAAACCCCGTCTCTACT
15946	14033	TGGGGAAACCCCGTCTCTAC
15947	14034	ATGGGGAAACCCCGTCTCTA
15948	14035	AATGGGGAAACCCCGTCTCT
15949	14036	AAATGGGGAAACCCCGTCTC
15950	14037	AAAATGGGGAAACCCCGTCT
15951	14038	CAAAATGGGGAAACCCCGTC
15952	14039	CCAAAATGGGGAAACCCCGT
15953	14040	GCCAAAATGGGGAAACCCCG
15954	14041	GGCCAAAATGGGGAAACCCC
15955	14042	TGGCCAAAATGGGGAAACCC
15956	14043	CTGGCCAAAATGGGGAAACC
15957	14044	CCTGGCCAAAATGGGGAAAC
15958	14045	GCCTGGCCAAAATGGGGAAA
15959	14046	AGCCTGGCCAAAATGGGGAA
15960	14047	CAGCCTGGCCAAAATGGGGA
15961	14048	CCAGCCTGGCCAAAATGGGG
15962	14049	ACCAGCCTGGCCAAAATGGG
15963	14050	GACCAGCCTGGCCAAAATGG
15964	14051	AGACCAGCCTGGCCAAAATG
15965	14052	GAGACCAGCCTGGCCAAAAT
15966	14053	CGAGACCAGCCTGGCCAAAA
15967	14054	TCGAGACCAGCCTGGCCAAA
15968	14055	TTCGAGACCAGCCTGGCCAA

65045	63132	CGTTGGAAACAGCTATGTAG
65046	63133	ACGTTGGAAACAGCTATGTA
65047	63134	TACGTTGGAAACAGCTATGT
65048	63135	CTACGTTGGAAACAGCTATG
65049	63136	GCTACGTTGGAAACAGCTAT
65050	63137	AGCTACGTTGGAAACAGCTA
65051	63138	CAGCTACGTTGGAAACAGCT
65052	63139	ACAGCTACGTTGGAAACAGC
65053	63140	TACAGCTACGTTGGAAACAG
65054	63141	ATACAGCTACGTTGGAAACA
65055	63142	GATACAGCTACGTTGGAAAC
65056	63143	TGATACAGCTACGTTGGAAA
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65058	63145	AATGATACAGCTACGTTGGA
65059	63146	AAATGATACAGCTACGTTGG
65060	63147	AAAATGATACAGCTACGTTG
65061	63148	TAAAATGATACAGCTACGTT
65062	63149	GTAAAATGATACAGCTACGT
65063	63150	TGTAAAATGATACAGCTACG
65064	63151	TTGTAAAATGATACAGCTAC
65065	63152	ATTGTAAAATGATACAGCTA
65066	63153	GATTGTAAAATGATACAGCT
65067	63154	GGATTGTAAAATGATACAGC
65068	63155	AGGATTGTAAAATGATACAG
65069	63156	TAGGATTGTAAAATGATACA
65070	63157	GTAGGATTGTAAAATGATAC
65071	63158	AGTAGGATTGTAAAATGATA
65072	63159	TAGTAGGATTGTAAAATGAT
65073	63160	CTAGTAGGATTGTAAAATGA
65074	63161	GCTAGTAGGATTGTAAAATG
65075	63162	TGCTAGTAGGATTGTAAAAT
65076	63163	CTGCTAGTAGGATTGTAAAA
65077	63164	ACTGCTAGTAGGATTGTAAA
65078	63165	CACTGCTAGTAGGATTGTAA
65079	63166	ACACTGCTAGTAGGATTGTA
65080	63167	GACACTGCTAGTAGGATTGT
65081	63168	AGACACTGCTAGTAGGATTG
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65085	63172	CCTCAGACACTGCTAGTAGG
65086	63173	ACCTCAGACACTGCTAGTAG
65087	63174	AACCTCAGACACTGCTAGTA
65088	63175	AAACCTCAGACACTGCTAGT
65089	63176	GAAACCTCAGACACTGCTAG
65090	63177	AGAAACCTCAGACACTGCTA
65091	63178	AAGAAACCTCAGACACTGCT
65092	63179	TAAGAAACCTCAGACACTGC
65093	63180	ATAAGAAACCTCAGACACTG
65094	63181	CATAAGAAACCTCAGACACT
65095	63182	ACATAAGAAACCTCAGACAC
65096	63183	AACATAAGAAACCTCAGACA
65097	63184	AAACATAAGAAACCTCAGAC
65098	63185	AAAACATAAGAAACCTCAGA
65099	63186	AAAAACATAAGAAACCTCAG
65100	63187	GAAAAACATAAGAAACCTCA
65101	63188	TGAAAAACATAAGAAACCTC
65102	63189	GTGAAAAACATAAGAAACCT
65103	63190	TGTGAAAAACATAAGAAACC
65104	63191	ATGTGAAAAACATAAGAAAC
65105	63192	GATGTGAAAAACATAAGAAA
65106	63193	GGATGTGAAAAACATAAGAA
65107	63194	AGGATGTGAAAAACATAAGA
65108	63195	GAGGATGTGAAAAACATAAG
65109	63196	TGAGGATGTGAAAAACATAA
65110	63197	GTGAGGATGTGAAAAACATA
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65112	63199	TGGTGAGGATGTGAAAAACA
65113	63200	CTGGTGAGGATGTGAAAAAC
65114	63201	GCTGGTGAGGATGTGAAAAA
65115	63202	TGCTGGTGAGGATGTGAAAA

114192	112279	CAACAAACACTTGAGCTGAA
114193	112280	TCAACAAACACTTGAGCTGA
114194	112281	ATCAACAAACACTTGAGCTG
114195	112282	AATCAACAAACACTTGAGCT
114196	112283	CAATCAACAAACACTTGAGC
114197	112284	CCAATCAACAAACACTTGAG
114198	112285	GCCAATCAACAAACACTTGA
114199	112286	GGCCAATCAACAAACACTTG
114200	112287	TGGCCAATCAACAAACACTT
114201	112288	CTGGCCAATCAACAAACACT
114202	112289	CCTGGCCAATCAACAAACAC
114203	112290	GCCTGGCCAATCAACAAACA
114204	112291	CGCCTGGCCAATCAACAAAC
114205	112292	ACGCCTGGCCAATCAACAAA
114206	112293	CACGCCTGGCCAATCAACAA
114207	112294	CCACGCCTGGCCAATCAACA
114208	112295	ACCACGCCTGGCCAATCAAC
114209	112296	TACCACGCCTGGCCAATCAA
114210	112297	CTACCACGCCTGGCCAATCA
114211	112298	GCTACCACGCCTGGCCAATC
114212	112299	AGCTACCACGCCTGGCCAAT
114213	112300	GAGCTACCACGCCTGGCCAA
114214	112301	TGAGCTACCACGCCTGGCCA
114215	112302	ATGAGCTACCACGCCTGGCC
114216	112303	TATGAGCTACCACGCCTGGC
114217	112304	GTATGAGCTACCACGCCTGG
114218	112305	GGTATGAGCTACCACGCCTG
114219	112306	AGGTATGAGCTACCACGCCT
114220	112307	CAGGTATGAGCTACCACGCC
114221	112308	ACAGGTATGAGCTACCACGC
114222	112309	TACAGGTATGAGCTACCACG
114223	112310	TTACAGGTATGAGCTACCAC
114224	112311	ATTACAGGTATGAGCTACCA
114225	112312	GATTACAGGTATGAGCTACC
114226	112313	GGATTACAGGTATGAGCTAC
114227	112314	GGGATTACAGGTATGAGCTA
114228	112315	TGGGATTACAGGTATGAGCT
114229	112316	CTGGGATTACAGGTATGAGC
114230	112317	GCTGGGATTACAGGTATGAG
114231	112318	TGCTGGGATTACAGGTATGA
114232	112319	GTGCTGGGATTACAGGTATG
114233	112320	AGTGCTGGGATTACAGGTAT
114234	112321	AAGTGCTGGGATTACAGGTA
114235	112322	AAAGTGCTGGGATTACAGGT
114236	112323	CAAAGTGCTGGGATTACAGG
114237	112324	CCAAAGTGCTGGGATTACAG
114238	112325	CCCAAAGTGCTGGGATTACA
114239	112326	TCCCAAAGTGCTGGGATTAC
114240	112327	CTCCCAAAGTGCTGGGATTA
114241	112328	CCTCCCAAAGTGCTGGGATT
114242	112329	GCCTCCCAAAGTGCTGGGAT
114243	112330	AGCCTCCCAAAGTGCTGGGA
114244	112331	CAGCCTCCCAAAGTGCTGGG
114245	112332	TCAGCCTCCCAAAGTGCTGG
114246	112333	CTCAGCCTCCCAAAGTGCTG
114247	112334	ACTCAGCCTCCCAAAGTGCT
114248	112335	GACTCAGCCTCCCAAAGTGC
114249	112336	TGACTCAGCCTCCCAAAGTG
114250	112337	CTGACTCAGCCTCCCAAAGT
114251	112338	CCTGACTCAGCCTCCCAAAG
114252	112339	GCCTGACTCAGCCTCCCAAA
114253	112340	TGCCTGACTCAGCCTCCCAA
114254	112341	CTGCCTGACTCAGCCTCCCA
114255	112342	TCTGCCTGACTCAGCCTCCC
114256	112343	ATCTGCCTGACTCAGCCTCC
114257	112344	GATCTGCCTGACTCAGCCTC
114258	112345	TGATCTGCCTGACTCAGCCT
114259	112346	GTGATCTGCCTGACTCAGCC
114260	112347	AGTGATCTGCCTGACTCAGC
114261	112348	AAGTGATCTGCCTGACTCAG
114262	112349	TAAGTGATCTGCCTGACTCA

15969	14056	GTTCGAGACCAGCCTGGCCA
15970	14057	AGTTCGAGACCAGCCTGGCC
15971	14058	GAGTTCGAGACCAGCCTGGC
15972	14059	GGAGTTCGAGACCAGCCTGG
15973	14060	AGGAGTTCGAGACCAGCCTG
15974	14061	CAGGAGTTCGAGACCAGCCT
15975	14062	TCAGGAGTTCGAGACCAGCC
15976	14063	GTCAGGAGTTCGAGACCAGC
15977	14064	GGTCAGGAGTTCGAGACCAG
15978	14065	AGGTCAGGAGTTCGAGACCA
15979	14066	GAGGTCAGGAGTTCGAGACC
15980	14067	TGAGGTCAGGAGTTCGAGAC
15981	14068	CTGAGGTCAGGAGTTCGAGA
15982	14069	CCTGAGGTCAGGAGTTCGAG
15983	14070	ACCTGAGGTCAGGAGTTCGA
15984	14071	CACCTGAGGTCAGGAGTTCG
15985	14072	TCACCTGAGGTCAGGAGTTC
15986	14073	ATCACCTGAGGTCAGGAGTT
15987	14074	GATCACCTGAGGTCAGGAGT
15988	14075	GGATCACCTGAGGTCAGGAG
15989	14076	CGGATCACCTGAGGTCAGGA
15990	14077	GCGGATCACCTGAGGTCAGG
15991	14078	GGCGGATCACCTGAGGTCAG
15992	14079	AGGCGGATCACCTGAGGTCA
15993	14080	CAGGCGGATCACCTGAGGTC
15994	14081	GCAGGCGGATCACCTGAGGT
15995	14082	AGCAGGCGGATCACCTGAGG
15996	14083	AAGCAGGCGGATCACCTGAG
15997	14084	GAAGCAGGCGGATCACCTGA
15998	14085	TGAAGCAGGCGGATCACCTG
15999	14086	CTGAAGCAGGCGGATCACCT
16000	14087	GCTGAAGCAGGCGGATCACC
16001	14088	GGCTGAAGCAGGCGGATCAC
16002	14089	AGGCTGAAGCAGGCGGATCA
16003	14090	GAGGCTGAAGCAGGCGGATC
16004	14091	GGAGGCTGAAGCAGGCGGAT
16005	14092	GGGAGGCTGAAGCAGGCGGA
16006	14093	TGGGAGGCTGAAGCAGGCGG
16007	14094	TTGGGAGGCTGAAGCAGGCG
16008	14095	TTTGGGAGGCTGAAGCAGGC
16009	14096	CTTTGGGAGGCTGAAGCAGG
16010	14097	ACTTTGGGAGGCTGAAGCAG
16011	14098	CACTTTGGGAGGCTGAAGCA
16012	14099	GCACTTTGGGAGGCTGAAGC
16013	14100	GGCACTTTGGGAGGCTGAAG
16014	14101	CGGCACTTTGGGAGGCTGAA
16015	14102	CCGGCACTTTGGGAGGCTGA
16016	14103	CCCGGCACTTTGGGAGGCTG
16017	14104	TCCCGGCACTTTGGGAGGCT
16018	14105	GTCCCGGCACTTTGGGAGGC
16019	14106	GGTCCCGGCACTTTGGGAGG
16020	14107	TGGTCCCGGCACTTTGGGAG
16021	14108	GTGGTCCCGGCACTTTGGGA
16022	14109	TGTGGTCCCGGCACTTTGGG
16023	14110	CTGTGGTCCCGGCACTTTGG
16024	14111	CCTGTGGTCCCGGCACTTTG
16025	14112	GCCTGTGGTCCCGGCACTTT
16026	14113	CGCCTGTGGTCCCGGCACTT
16027	14114	ACGCCTGTGGTCCCGGCACT
16028	14115	CACGCCTGTGGTCCCGGCAC
16029	14116	TCACGCCTGTGGTCCCGGCA
16030	14117	CTCACGCCTGTGGTCCCGGC
16031	14118	GCTCACGCCTGTGGTCCCGG
16032	14119	GGCTCACGCCTGTGGTCCCG
16033	14120	TGGCTCACGCCTGTGGTCCC
16034	14121	GTGGCTCACGCCTGTGGTCC
16035	14122	GGTGGCTCACGCCTGTGGTC
16036	14123	CGGTGGCTCACGCCTGTGGT
16037	14124	GCGGTGGCTCACGCCTGTGG
16038	14125	TGCGGTGGCTCACGCCTGTG
16039	14126	GTGCGGTGGCTCACGCCTGT

65116	63203	ATGCTGGTGAGGATGTGAAA
65117	63204	AATGCTGGTGAGGATGTGAA
65118	63205	AAATGCTGGTGAGGATGTGA
65119	63206	CAAATGCTGGTGAGGATGTG
65120	63207	ACAAATGCTGGTGAGGATGT
65121	63208	AACAAATGCTGGTGAGGATG
65122	63209	TAACAAATGCTGGTGAGGAT
65123	63210	ATAACAAATGCTGGTGAGGA
65124	63211	AATAACAAATGCTGGTGAGG
65125	63212	CAATAACAAATGCTGGTGAG
65126	63213	ACAATAACAAATGCTGGTGA
65127	63214	GACAATAACAAATGCTGGTG
65128	63215	AGACAATAACAAATGCTGGT
65129	63216	CAGACAATAACAAATGCTGG
65130	63217	ACAGACAATAACAAATGCTG
65131	63218	GACAGACAATAACAAATGCT
65132	63219	AGACAGACAATAACAAATGC
65133	63220	GAGACAGACAATAACAAATG
65134	63221	AGAGACAGACAATAACAAAT
65135	63222	AAGAGACAGACAATAACAAA
65136	63223	AAAGAGACAGACAATAACAA
65137	63224	CAAAGAGACAGACAATAACA
65138	63225	TCAAAGAGACAGACAATAAC
65139	63226	ATCAAAGAGACAGACAATAA
65140	63227	AATCAAAGAGACAGACAATA
65141	63228	TAATCAAAGAGACAGACAAT
65142	63229	ATAATCAAAGAGACAGACAA
65143	63230	TATAATCAAAGAGACAGACA
65144	63231	GTATAATCAAAGAGACAGAC
65145	63232	GGTATAATCAAAGAGACAGA
65146	63233	GGGTATAATCAAAGAGACAG
65147	63234	TGGGTATAATCAAAGAGACA
65148	63235	ATGGGTATAATCAAAGAGAC
65149	63236	GATGGGTATAATCAAAGAGA
65150	63237	GGATGGGTATAATCAAAGAG
65151	63238	AGGATGGGTATAATCAAAGA
65152	63239	TAGGATGGGTATAATCAAAG
65153	63240	CTAGGATGGGTATAATCAAA
65154	63241	ACTAGGATGGGTATAATCAA
65155	63242	CACTAGGATGGGTATAATCA
65156	63243	CCACTAGGATGGGTATAATC
65157	63244	CCCACTAGGATGGGTATAAT
65158	63245	TCCCACTAGGATGGGTATAA
65159	63246	CTCCCACTAGGATGGGTATA
65160	63247	TCTCCCACTAGGATGGGTAT
65161	63248	CTCTCCCACTAGGATGGGTA
65162	63249	ACTCTCCCACTAGGATGGGT
65163	63250	TACTCTCCCACTAGGATGGG
65164	63251	TTACTCTCCCACTAGGATGG
65165	63252	CTTACTCTCCCACTAGGATG
65166	63253	TCTTACTCTCCCACTAGGAT
65167	63254	TTCTTACTCTCCCACTAGGA
65168	63255	CTTCTTACTCTCCCACTAGG
65169	63256	ACTTCTTACTCTCCCACTAG
65170	63257	TACTTCTTACTCTCCCACTA
65171	63258	CTACTTCTTACTCTCCCACT
65172	63259	ACTACTTCTTACTCTCCCAC
65173	63260	TACTACTTCTTACTCTCCCA
65174	63261	ATACTACTTCTTACTCTCCC
65175	63262	GATACTACTTCTTACTCTCC
65176	63263	AGATACTACTTCTTACTCTC
65177	63264	GAGATACTACTTCTTACTCT
65178	63265	TGAGATACTACTTCTTACTC
65179	63266	GTGAGATACTACTTCTTACT
65180	63267	AGTGAGATACTACTTCTTAC
65181	63268	CAGTGAGATACTACTTCTTA
65182	63269	ACAGTGAGATACTACTTCTT
65183	63270	TACAGTGAGATACTACTTCT
65184	63271	CTACAGTGAGATACTACTTC
65185	63272	TCTACAGTGAGATACTACTT
65186	63273	ATCTACAGTGAGATACTACT

114263	112350	TTAAGTGATCTGCCTGACTC
114264	112351	CTTAAGTGATCTGCCTGACT
114265	112352	CCTTAAGTGATCTGCCTGAC
114266	112353	ACCTTAAGTGATCTGCCTGA
114267	112354	GACCTTAAGTGATCTGCCTG
114268	112355	TGACCTTAAGTGATCTGCCT
114269	112356	CTGACCTTAAGTGATCTGCC
114270	112357	GCTGACCTTAAGTGATCTGC
114271	112358	CGCTGACCTTAAGTGATCTG
114272	112359	ACGCTGACCTTAAGTGATCT
114273	112360	CACGCTGACCTTAAGTGATC
114274	112361	CCACGCTGACCTTAAGTGAT
114275	112362	GCCACGCTGACCTTAAGTGA
114276	112363	GGCCACGCTGACCTTAAGTG
114277	112364	TGGCCACGCTGACCTTAAGT
114278	112365	TTGGCCACGCTGACCTTAAG
114279	112366	TTTGGCCACGCTGACCTTAA
114280	112367	TTTTGGCCACGCTGACCTTA
114281	112368	ATTTTGGCCACGCTGACCTT
114282	112369	CATTTTGGCCACGCTGACCT
114283	112370	CCATTTTGGCCACGCTGACC
114284	112371	ACCATTTTGGCCACGCTGAC
114285	112372	CACCATTTTGGCCACGCTGA
114286	112373	TCACCATTTTGGCCACGCTG
114287	112374	TTCACCATTTTGGCCACGCT
114288	112375	TTTCACCATTTTGGCCACGC
114289	112376	GTTTCACCATTTTGGCCACG
114290	112377	GGTTTCACCATTTTGGCCAC
114291	112378	GGGTTTCACCATTTTGGCCA
114292	112379	GGGGTTTCACCATTTTGGCC
114293	112380	TGGGGTTTCACCATTTTGGC
114294	112381	ATGGGGTTTCACCATTTTGG
114295	112382	GATGGGGTTTCACCATTTTG
114296	112383	AGATGGGGTTTCACCATTTT
114297	112384	AAGATGGGGTTTCACCATTT
114298	112385	AAAGATGGGGTTTCACCATT
114299	112386	TAAAGATGGGGTTTCACCAT
114300	112387	GTAAAGATGGGGTTTCACCA
114301	112388	AGTAAAGATGGGGTTTCACC
114302	112389	TAGTAAAGATGGGGTTTCAC
114303	112390	TTAGTAAAGATGGGGTTTCA
114304	112391	TTTAGTAAAGATGGGGTTTC
114305	112392	TTTTAGTAAAGATGGGGTTT
114306	112393	TTTTTAGTAAAGATGGGGTT
114307	112394	ATTTTTAGTAAAGATGGGGT
114308	112395	TATTTTTAGTAAAGATGGGG
114309	112396	TTATTTTTAGTAAAGATGGG
114310	112397	TTTATTTTTAGTAAAGATGG
114311	112398	ATTTATTTTTAGTAAAGATG
114312	112399	TATTTATTTTTAGTAAAGAT
114313	112400	ATATTTATTTTTAGTAAAGA
114314	112401	AATATTTATTTTTAGTAAAG
114315	112402	TAATATTTATTTTTAGTAAA
114316	112403	TTAATATTTATTTTTAGTAA
114317	112404	TTTAATATTTATTTTTAGTA
114318	112405	TTTTAATATTTATTTTTAGT
114319	112406	TTTTTAATATTTATTTTTAG
114320	112407	TTTTTTAATATTTATTTTTA
114321	112408	TTTTTTTAATATTTATTTTT
114322	112409	TTTTTTTTAATATTTATTTT
114323	112410	ATTTTTTTTAATATTTATTT
114324	112411	AATTTTTTTTAATATTTATT
114325	112412	TAATTTTTTTTAATATTTAT
114326	112413	CTAATTTTTTTTAATATTTA
114327	112414	GCTAATTTTTTTTAATATTT
114328	112415	AGCTAATTTTTTTTAATATT
114329	112416	CAGCTAATTTTTTTTAATAT
114330	112417	CCAGCTAATTTTTTTTAATA
114331	112418	CCCAGCTAATTTTTTTTAAT
114332	112419	GCCCAGCTAATTTTTTTTAA
114333	112420	CGCCCAGCTAATTTTTTTTA

16040	14127	GGTGCGGTGGCTCACGCCTG
16041	14128	AGGTGCGGTGGCTCACGCCT
16042	14129	CAGGTGCGGTGGCTCACGCC
16043	14130	CCAGGTGCGGTGGCTCACGC
16044	14131	GCCAGGTGCGGTGGCTCACG
16045	14132	AGCCAGGTGCGGTGGCTCAC
16046	14133	AAGCCAGGTGCGGTGGCTCA
16047	14134	AAAGCCAGGTGCGGTGGCTC
16048	14135	AAAAGCCAGGTGCGGTGGCT
16049	14136	AAAAAGCCAGGTGCGGTGGC
16050	14137	AAAAAAGCCAGGTGCGGTGG
16051	14138	AAAAAAAGCCAGGTGCGGTG
16052	14139	AAAAAAAAGCCAGGTGCGGT
16053	14140	AAAAAAAAAGCCAGGTGCGG
16054	14141	AAAAAAAAAAGCCAGGTGCG
16055	14142	AAAAAAAAAAAGCCAGGTGC
16056	14143	CAAAAAAAAAAAGCCAGGTG
16057	14144	TCAAAAAAAAAAAGCCAGGT
16058	14145	GTCAAAAAAAAAAAGCCAGG
16059	14146	TGTCAAAAAAAAAAAGCCAG
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16061	14148	TATGTCAAAAAAAAAAAGCC
16062	14149	CTATGTCAAAAAAAAAAAGC
16063	14150	TCTATGTCAAAAAAAAAAAG
16064	14151	TTCTATGTCAAAAAAAAAA
16065	14152	ATTCTATGTCAAAAAAAAA
16066	14153	GATTCTATGTCAAAAAAAA
16067	14154	AGATTCTATGTCAAAAAAA
16068	14155	AAGATTCTATGTCAAAAAA
16069	14156	CAAGATTCTATGTCAAAAA
16070	14157	ACAAGATTCTATGTCAAAA
16071	14158	AACAAGATTCTATGTCAAA
16072	14159	GAACAAGATTCTATGTCAAA
16073	14160	AGAACAAGATTCTATGTCAA
16074	14161	CAGAACAAGATTCTATGTCA
16075	14162	ACAGAACAAGATTCTATGTC
16076	14163	AACAGAACAAGATTCTATGT
16077	14164	CAACAGAACAAGATTCTATG
16078	14165	GCAACAGAACAAGATTCTAT
16079	14166	GGCAACAGAACAAGATTCTA
16080	14167	GGGCAACAGAACAAGATTCT
16081	14168	TGGGCAACAGAACAAGATTC
16082	14169	CTGGGCAACAGAACAAGATT
16083	14170	CCTGGGCAACAGAACAAGAT
16084	14171	GCCTGGGCAACAGAACAAGA
16085	14172	AGCCTGGGCAACAGAACAAG
16086	14173	CAGCCTGGGCAACAGAACAA
16087	14174	CCAGCCTGGGCAACAGAACA
16088	14175	TCCAGCCTGGGCAACAGAAC
16089	14176	CTCCAGCCTGGGCAACAGAA
16090	14177	ACTCCAGCCTGGGCAACAGA
16091	14178	CACTCCAGCCTGGGCAACAG
16092	14179	GCACTCCAGCCTGGGCAACA
16093	14180	TGCACTCCAGCCTGGGCAAC
16094	14181	TTGCACTCCAGCCTGGGCAA
16095	14182	ATTGCACTCCAGCCTGGGCA
16096	14183	CATTGCACTCCAGCCTGGGC
16097	14184	CCATTGCACTCCAGCCTGGG
16098	14185	ACCATTGCACTCCAGCCTGG
16099	14186	TACCATTGCACTCCAGCCTG
16100	14187	GTACCATTGCACTCCAGCCT
16101	14188	TGTACCATTGCACTCCAGCC
16102	14189	TTGTACCATTGCACTCCAGC
16103	14190	ATTGTACCATTGCACTCCAG
16104	14191	GATTGTACCATTGCACTCCA
16105	14192	AGATTGTACCATTGCACTCC
16106	14193	AAGATTGTACCATTGCACTC
16107	14194	CAAGATTGTACCATTGCACT
16108	14195	CCAAGATTGTACCATTGCAC
16109	14196	GCCAAGATTGTACCATTGCA
16110	14197	GGCCAAGATTGTACCATTGC

65187	63274	AATCTACAGTGAGATACTAC
65188	63275	AAATCTACAGTGAGATACTA
65189	63276	AAAATCTACAGTGAGATACT
65190	63277	AAAAATCTACAGTGAGATAC
65191	63278	AAAAAATCTACAGTGAGATA
65192	63279	AAAAAAATCTACAGTGAGAT
65193	63280	AAAAAAAATCTACAGTGAGA
65194	63281	AAAAAAAAATCTACAGTGAG
65195	63282	AAAAAAAAAATCTACAGTGA
65196	63283	GAAAAAAAAAATCTACAGTG
65197	63284	AGAAAAAAAAAATCTACAGT
65198	63285	CAGAAAAAAAAAATCTACAG
65199	63286	ACAGAAAAAAAAAATCTACA
65200	63287	AACAGAAAAAAAAAATCTAC
65201	63288	AAACAGAAAAAAAAAATCTA
65202	63289	TAAACAGAAAAAAAAAATCT
65203	63290	GTAAACAGAAAAAAAAAATC
65204	63291	TGTAAACAGAAAAAAAAAAT
65205	63292	TTGTAAACAGAAAAAAAAAA
65206	63293	GTTGTAAACAGAAAAAAAAA
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65211	63298	GTAAAGTTGTAAACAGAAAA
65212	63299	AGTAAAGTTGTAAACAGAAA
65213	63300	AAGTAAAGTTGTAAACAGAA
65214	63301	AAAGTAAAGTTGTAAACAGA
65215	63302	TAAAGTAAAGTTGTAAACAG
65216	63303	TTAAAGTAAAGTTGTAAACA
65217	63304	TTTAAAGTAAAGTTGTAAAC
65218	63305	TTTTAAAGTAAAGTTGTAAA
65219	63306	TTTTTAAAGTAAAGTTGTAA
65220	63307	ATTTTTAAAGTAAAGTTGTA
65221	63308	AATTTTTAAAGTAAAGTTGT
65222	63309	TAATTTTTAAAGTAAAGTTG
65223	63310	ATAATTTTTAAAGTAAAGTT
65224	63311	TATAATTTTTAAAGTAAAGT
65225	63312	ATATAATTTTTAAAGTAAAG
65226	63313	TATATAATTTTTAAAGTAAA
65227	63314	ATATATAATTTTTAAAGTAA
65228	63315	CATATATAATTTTTAAAGTA
65229	63316	GCATATATAATTTTTAAAGT
65230	63317	TGCATATATAATTTTTAAAG
65231	63318	GTGCATATATAATTTTTAAA
65232	63319	TGTGCATATATAATTTTTAA
65233	63320	GTGTGCATATATAATTTTTA
65234	63321	TGTGTGCATATATAATTTTT
65235	63322	ATGTGTGCATATATAATTTT
65236	63323	CATGTGTGCATATATAATTT
65237	63324	CCATGTGTGCATATATAATT
65238	63325	ACCATGTGTGCATATATAAT
65239	63326	TACCATGTGTGCATATATAA
65240	63327	TTACCATGTGTGCATATATA
65241	63328	TTTACCATGTGTGCATATAT
65242	63329	TTTTACCATGTGTGCATATA
65243	63330	TTTTTACCATGTGTGCATAT
65244	63331	CTTTTTACCATGTGTGCATA
65245	63332	ACTTTTTACCATGTGTGCAT
65246	63333	AACTTTTTACCATGTGTGCA
65247	63334	GAACTTTTTACCATGTGTGC
65248	63335	TGAACTTTTTACCATGTGTG
65249	63336	TTGAACTTTTTACCATGTGT
65250	63337	TTTGAACTTTTTACCATGTG
65251	63338	TTTTGAACTTTTTACCATGT
65252	63339	GTTTTGAACTTTTTACCATG
65253	63340	CGTTTTGAACTTTTTACCAT
65254	63341	ACGTTTTGAACTTTTTACCA
65255	63342	CACGTTTTGAACTTTTTACC
65256	63343	ACACGTTTTGAACTTTTTAC
65257	63344	CACACGTTTTGAACTTTTTA

114334	112421	ACGCCCAGCTAATTTTTTTT
114335	112422	CACGCCCAGCTAATTTTTTT
114336	112423	CCACGCCCAGCTAATTTTTT
114337	112424	ACCACGCCCAGCTAATTTTT
114338	112425	CACCACGCCCAGCTAATTTT
114339	112426	CCACCACGCCCAGCTAATTT
114340	112427	GCCACCACGCCCAGCTAATT
114341	112428	TGCCACCACGCCCAGCTAAT
114342	112429	CTGCCACCACGCCCAGCTAA
114343	112430	ACTGCCACCACGCCCAGCTA
114344	112431	GACTGCCACCACGCCCAGCT
114345	112432	AGACTGCCACCACGCCCAGC
114346	112433	GAGACTGCCACCACGCCCAG
114347	112434	GGAGACTGCCACCACGCCCA
114348	112435	AGGAGACTGCCACCACGCCC
114349	112436	CAGGAGACTGCCACCACGCC
114350	112437	ACAGGAGACTGCCACCACGC
114351	112438	TACAGGAGACTGCCACCACG
114352	112439	TTACAGGAGACTGCCACCAC
114353	112440	ATTACAGGAGACTGCCACCA
114354	112441	GATTACAGGAGACTGCCACC
114355	112442	GGATTACAGGAGACTGCCAC
114356	112443	GGGATTACAGGAGACTGCCA
114357	112444	TGGGATTACAGGAGACTGCC
114358	112445	CTGGGATTACAGGAGACTGC
114359	112446	GCTGGGATTACAGGAGACTG
114360	112447	AGCTGGGATTACAGGAGACT
114361	112448	TAGCTGGGATTACAGGAGAC
114362	112449	TTAGCTGGGATTACAGGAGA
114363	112450	ATTAGCTGGGATTACAGGAG
114364	112451	GATTAGCTGGGATTACAGGA
114365	112452	TGATTAGCTGGGATTACAGG
114366	112453	CTGATTAGCTGGGATTACAG
114367	112454	CCTGATTAGCTGGGATTACA
114368	112455	TCCTGATTAGCTGGGATTAC
114369	112456	CTCCTGATTAGCTGGGATTA
114370	112457	CCTCCTGATTAGCTGGGATT
114371	112458	GCCTCCTGATTAGCTGGGAT
114372	112459	AGCCTCCTGATTAGCTGGGA
114373	112460	TAGCCTCCTGATTAGCTGGG
114374	112461	TTAGCCTCCTGATTAGCTGG
114375	112462	CTTAGCCTCCTGATTAGCTG
114376	112463	CCTTAGCCTCCTGATTAGCT
114377	112464	GCCTTAGCCTCCTGATTAGC
114378	112465	TGCCTTAGCCTCCTGATTAG
114379	112466	TTGCCTTAGCCTCCTGATTA
114380	112467	CTTGCCTTAGCCTCCTGATT
114381	112468	TCTTGCCTTAGCCTCCTGAT
114382	112469	CTCTTGCCTTAGCCTCCTGA
114383	112470	TCTCTTGCCTTAGCCTCCTG
114384	112471	TTCTCTTGCCTTAGCCTCCT
114385	112472	ATTCTCTTGCCTTAGCCTCC
114386	112473	CATTCTCTTGCCTTAGCCTC
114387	112474	CCATTCTCTTGCCTTAGCCT
114388	112475	GCCATTCTCTTGCCTTAGCC
114389	112476	AGCCATTCTCTTGCCTTAGC
114390	112477	AAGCCATTCTCTTGCCTTAG
114391	112478	TAAGCCATTCTCTTGCCTTA
114392	112479	TTAAGCCATTCTCTTGCCTT
114393	112480	TTTAAGCCATTCTCTTGCCT
114394	112481	GTTTAAGCCATTCTCTTGCC
114395	112482	AGTTTAAGCCATTCTCTTGC
114396	112483	GAGTTTAAGCCATTCTCTTG
114397	112484	CGAGTTTAAGCCATTCTCTT
114398	112485	CCGAGTTTAAGCCATTCTCT
114399	112486	CCCGAGTTTAAGCCATTCTC
114400	112487	TCCCGAGTTTAAGCCATTCT
114401	112488	CTCCCGAGTTTAAGCCATTC
114402	112489	CCTCCCGAGTTTAAGCCATT
114403	112490	GCCTCCCGAGTTTAAGCCAT
114404	112491	TGCCTCCCGAGTTTAAGCCA

16111	14198	GGGCCAAGATTGTACCATTG
16112	14199	TGGGCCAAGATTGTACCATT
16113	14200	GTGGGCCAAGATTGTACCAT
16114	14201	AGTGGGCCAAGATTGTACCA
16115	14202	CAGTGGGCCAAGATTGTACC
16116	14203	GCAGTGGGCCAAGATTGTAC
16117	14204	TGCAGTGGGCCAAGATTGTA
16118	14205	TTGCAGTGGGCCAAGATTGT
16119	14206	GTTGCAGTGGGCCAAGATTG
16120	14207	GGTTGCAGTGGGCCAAGATT
16121	14208	AGGTTGCAGTGGGCCAAGAT
16122	14209	GAGGTTGCAGTGGGCCAAGA
16123	14210	AGAGGTTGCAGTGGGCCAAG
16124	14211	CAGAGGTTGCAGTGGGCCAA
16125	14212	GCAGAGGTTGCAGTGGGCCA
16126	14213	GGCAGAGGTTGCAGTGGGCC
16127	14214	AGGCAGAGGTTGCAGTGGGC
16128	14215	GAGGCAGAGGTTGCAGTGGG
16129	14216	GGAGGCAGAGGTTGCAGTGG
16130	14217	GGGAGGCAGAGGTTGCAGTG
16131	14218	TGGGAGGCAGAGGTTGCAGT
16132	14219	CTGGGAGGCAGAGGTTGCAG
16133	14220	GCTGGGAGGCAGAGGTTGCA
16134	14221	AGCTGGGAGGCAGAGGTTGC
16135	14222	AAGCTGGGAGGCAGAGGTTG
16136	14223	GAAGCTGGGAGGCAGAGGTT
16137	14224	AGAAGCTGGGAGGCAGAGGT
16138	14225	TAGAAGCTGGGAGGCAGAGG
16139	14226	CTAGAAGCTGGGAGGCAGAG
16140	14227	GCTAGAAGCTGGGAGGCAGA
16141	14228	CGCTAGAAGCTGGGAGGCAG
16142	14229	TCGCTAGAAGCTGGGAGGCA
16143	14230	ATCGCTAGAAGCTGGGAGGC
16144	14231	AATCGCTAGAAGCTGGGAGG
16145	14232	AAATCGCTAGAAGCTGGGAG
16146	14233	AAAATCGCTAGAAGCTGGGA
16147	14234	GAAAATCGCTAGAAGCTGGG
16148	14235	GGAAAATCGCTAGAAGCTGG
16149	14236	AGGAAAATCGCTAGAAGCTG
16150	14237	CAGGAAAATCGCTAGAAGCT
16151	14238	GCAGGAAAATCGCTAGAAGC
16152	14239	GGCAGGAAAATCGCTAGAAG
16153	14240	AGGCAGGAAAATCGCTAGAA
16154	14241	GAGGCAGGAAAATCGCTAGA
16155	14242	AGAGGCAGGAAAATCGCTAG
16156	14243	CAGAGGCAGGAAAATCGCTA
16157	14244	TCAGAGGCAGGAAAATCGCT
16158	14245	GTCAGAGGCAGGAAAATCGC
16159	14246	AGTCAGAGGCAGGAAAATCG
16160	14247	GAGTCAGAGGCAGGAAAATC
16161	14248	GGAGTCAGAGGCAGGAAAAT
16162	14249	AGGAGTCAGAGGCAGGAAAA
16163	14250	CAGGAGTCAGAGGCAGGAAA
16164	14251	TCAGGAGTCAGAGGCAGGAA
16165	14252	CTCAGGAGTCAGAGGCAGGA
16166	14253	ACTCAGGAGTCAGAGGCAGG
16167	14254	TACTCAGGAGTCAGAGGCAG
16168	14255	CTACTCAGGAGTCAGAGGCA
16169	14256	GCTACTCAGGAGTCAGAGGC
16170	14257	AGCTACTCAGGAGTCAGAGG
16171	14258	CAGCTACTCAGGAGTCAGAG
16172	14259	CCAGCTACTCAGGAGTCAGA
16173	14260	CCCAGCTACTCAGGAGTCAG
16174	14261	TCCCAGCTACTCAGGAGTCA
16175	14262	ATCCCAGCTACTCAGGAGTC
16176	14263	AATCCCAGCTACTCAGGAGT
16177	14264	TAATCCCAGCTACTCAGGAG
16178	14265	GTAATCCCAGCTACTCAGGA
16179	14266	CGTAATCCCAGCTACTCAGG
16180	14267	CCGTAATCCCAGCTACTCAG
16181	14268	CCCGTAATCCCAGCTACTCA

65258	63345	ACACACGTTTTGAACTTTTT
65259	63346	TACACACGTTTTGAACTTTT
65260	63347	GTACACACGTTTTGAACTTT
65261	63348	GGTACACACGTTTTGAACTT
65262	63349	TGGTACACACGTTTTGAACT
65263	63350	TTGGTACACACGTTTTGAAC
65264	63351	TTTGGTACACACGTTTTGAA
65265	63352	TTTTGGTACACACGTTTTGA
65266	63353	CTTTTGGTACACACGTTTTG
65267	63354	TCTTTTGGTACACACGTTTT
65268	63355	ATCTTTTGGTACACACGTTT
65269	63356	AATCTTTTGGTACACACGTT
65270	63357	AAATCTTTTGGTACACACGT
65271	63358	TAAATCTTTTGGTACACACG
65272	63359	TTAAATCTTTTGGTACACAC
65273	63360	GTTAAATCTTTTGGTACACA
65274	63361	TGTTAAATCTTTTGGTACAC
65275	63362	CTGTTAAATCTTTTGGTACA
65276	63363	ACTGTTAAATCTTTTGGTAC
65277	63364	CACTGTTAAATCTTTTGGTA
65278	63365	TCACTGTTAAATCTTTTGGT
65279	63366	TTCACTGTTAAATCTTTTGG
65280	63367	TTTCACTGTTAAATCTTTTG
65281	63368	TTTTCACTGTTAAATCTTTT
65282	63369	ATTTTCACTGTTAAATCTTT
65283	63370	TATTTTCACTGTTAAATCTT
65284	63371	CTATTTTCACTGTTAAATCT
65285	63372	TCTATTTTCACTGTTAAATC
65286	63373	TTCTATTTTCACTGTTAAAT
65287	63374	TTTCTATTTTCACTGTTAAA
65288	63375	TTTTCTATTTTCACTGTTAA
65289	63376	ATTTTCTATTTTCACTGTTA
65290	63377	TATTTTCTATTTTCACTGTT
65291	63378	TTATTTTCTATTTTCACTGT
65292	63379	CTTATTTTCTATTTTCACTG
65293	63380	ACTTATTTTCTATTTTCACT
65294	63381	CACTTATTTTCTATTTTCAC
65295	63382	ACACTTATTTTCTATTTTCA
65296	63383	CACACTTATTTTCTATTTTC
65297	63384	CCACACTTATTTTCTATTTT
65298	63385	ACCACACTTATTTTCTATTT
65299	63386	GACCACACTTATTTTCTATT
65300	63387	GGACCACACTTATTTTCTAT
65301	63388	AGGACCACACTTATTTTCTA
65302	63389	AAGGACCACACTTATTTTCT
65303	63390	CAAGGACCACACTTATTTTC
65304	63391	ACAAGGACCACACTTATTTT
65305	63392	AACAAGGACCACACTTATTT
65306	63393	AAACAAGGACCACACTTATT
65307	63394	AAAACAAGGACCACACTTAT
65308	63395	GAAAACAAGGACCACACTTA
65309	63396	AGAAAACAAGGACCACACTT
65310	63397	AAGAAAACAAGGACCACACT
65311	63398	GAAGAAAACAAGGACCACAC
65312	63399	GGAAGAAAACAAGGACCACA
65313	63400	TGGAAGAAAACAAGGACCAC
65314	63401	GTGGAAGAAAACAAGGACCA
65315	63402	GGTGGAAGAAAACAAGGACC
65316	63403	TGGTGGAAGAAAACAAGGAC
65317	63404	TTGGTGGAAGAAAACAAGGA
65318	63405	CTTGGTGGAAGAAAACAAGG
65319	63406	CCTTGGTGGAAGAAAACAAG
65320	63407	GCCTTGGTGGAAGAAAACAA
65321	63408	TGCCTTGGTGGAAGAAAACA
65322	63409	TTGCCTTGGTGGAAGAAAAC
65323	63410	TTTGCCTTGGTGGAAGAAAA
65324	63411	ATTTGCCTTGGTGGAAGAAA
65325	63412	TATTTGCCTTGGTGGAAGAA
65326	63413	ATATTTGCCTTGGTGGAAGA
65327	63414	AATATTTGCCTTGGTGGAAG
65328	63415	CAATATTTGCCTTGGTGGAA

114405	112492	CTGCCTCCCGAGTTTAAGCC
114406	112493	TCTGCCTCCCGAGTTTAAGC
114407	112494	CTCTGCCTCCCGAGTTTAAG
114408	112495	CCTCTGCCTCCCGAGTTTAA
114409	112496	ACCTCTGCCTCCCGAGTTTA
114410	112497	AACCTCTGCCTCCCGAGTTT
114411	112498	CAACCTCTGCCTCCCGAGTT
114412	112499	GCAACCTCTGCCTCCCGAGT
114413	112500	TGCAACCTCTGCCTCCCGAG
114414	112501	CTGCAACCTCTGCCTCCCGA
114415	112502	ACTGCAACCTCTGCCTCCCG
114416	112503	CACTGCAACCTCTGCCTCCC
114417	112504	TCACTGCAACCTCTGCCTCC
114418	112505	CTCACTGCAACCTCTGCCTC
114419	112506	GCTCACTGCAACCTCTGCCT
114420	112507	GGCTCACTGCAACCTCTGCC
114421	112508	TGGCTCACTGCAACCTCTGC
114422	112509	TTGGCTCACTGCAACCTCTG
114423	112510	CTTGGCTCACTGCAACCTCT
114424	112511	TCTTGGCTCACTGCAACCTC
114425	112512	ATCTTGGCTCACTGCAACCT
114426	112513	AATCTTGGCTCACTGCAACC
114427	112514	CAATCTTGGCTCACTGCAAC
114428	112515	GCAATCTTGGCTCACTGCAA
114429	112516	TGCAATCTTGGCTCACTGCA
114430	112517	GTGCAATCTTGGCTCACTGC
114431	112518	AGTGCAATCTTGGCTCACTG
114432	112519	CAGTGCAATCTTGGCTCACT
114433	112520	GCAGTGCAATCTTGGCTCAC
114434	112521	AGCAGTGCAATCTTGGCTCA
114435	112522	CAGCAGTGCAATCTTGGCTC
114436	112523	GCAGCAGTGCAATCTTGGCT
114437	112524	TGCAGCAGTGCAATCTTGGC
114438	112525	GTGCAGCAGTGCAATCTTGG
114439	112526	AGTGCAGCAGTGCAATCTTG
114440	112527	GAGTGCAGCAGTGCAATCTT
114441	112528	GGAGTGCAGCAGTGCAATCT
114442	112529	TGGAGTGCAGCAGTGCAATC
114443	112530	TTGGAGTGCAGCAGTGCAAT
114444	112531	GTTGGAGTGCAGCAGTGCAA
114445	112532	GGTTGGAGTGCAGCAGTGCA
114446	112533	AGGTTGGAGTGCAGCAGTGC
114447	112534	CAGGTTGGAGTGCAGCAGTG
114448	112535	TCAGGTTGGAGTGCAGCAGT
114449	112536	CTCAGGTTGGAGTGCAGCAG
114450	112537	GCTCAGGTTGGAGTGCAGCA
114451	112538	TGCTCAGGTTGGAGTGCAGC
114452	112539	TTGCTCAGGTTGGAGTGCAG
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114454	112541	TGTTGCTCAGGTTGGAGTGC
114455	112542	CTGTTGCTCAGGTTGGAGTG
114456	112543	TCTGTTGCTCAGGTTGGAGT
114457	112544	CTCTGTTGCTCAGGTTGGAG
114458	112545	ACTCTGTTGCTCAGGTTGGA
114459	112546	CACTCTGTTGCTCAGGTTGG
114460	112547	CCACTCTGTTGCTCAGGTTG
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114466	112553	AGAGTCCCACTCTGTTGCTC
114467	112554	CAGAGTCCCACTCTGTTGCT
114468	112555	ACAGAGTCCCACTCTGTTGC
114469	112556	CACAGAGTCCCACTCTGTTG
114470	112557	TCACAGAGTCCCACTCTGTT
114471	112558	TTCACAGAGTCCCACTCTGT
114472	112559	CTTCACAGAGTCCCACTCTG
114473	112560	CCTTCACAGAGTCCCACTCT
114474	112561	TCCTTCACAGAGTCCCACTC
114475	112562	TTCCTTCACAGAGTCCCACT

16182	14269	ACCCGTAATCCCAGCTACTC
16183	14270	CACCCGTAATCCCAGCTACT
16184	14271	GCACCCGTAATCCCAGCTAC
16185	14272	GGCACCCGTAATCCCAGCTA
16186	14273	GGGCACCCGTAATCCCAGCT
16187	14274	CGGGCACCCGTAATCCCAGC
16188	14275	GCGGGCACCCGTAATCCCAG
16189	14276	GGCGGGCACCCGTAATCCCA
16190	14277	TGGCGGGCACCCGTAATCCC
16191	14278	GTGGCGGGCACCCGTAATCC
16192	14279	GGTGGCGGGCACCCGTAATC
16193	14280	TGGTGGCGGGCACCCGTAAT
16194	14281	GTGGTGGCGGGCACCCGTAA
16195	14282	TGTGGTGGCGGGCACCCGTA
16196	14283	GTGTGGTGGCGGGCACCCGT
16197	14284	GGTGTGGTGGCGGGCACCCG
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16199	14286	CGGGTGTGGTGGCGGGCACC
16200	14287	CCGGGTGTGGTGGCGGGCAC
16201	14288	TCCGGGTGTGGTGGCGGGCA
16202	14289	ATCCGGGTGTGGTGGCGGGC
16203	14290	TATCCGGGTGTGGTGGCGGG
16204	14291	TTATCCGGGTGTGGTGGCGG
16205	14292	ATTATCCGGGTGTGGTGGCG
16206	14293	AATTATCCGGGTGTGGTGGC
16207	14294	AAATTATCCGGGTGTGGTGG
16208	14295	AAAATTATCCGGGTGTGGTG
16209	14296	AAAAATTATCCGGGTGTGGT
16210	14297	CAAAAATTATCCGGGTGTGG
16211	14298	ACAAAAATTATCCGGGTGTG
16212	14299	TACAAAAATTATCCGGGTGT
16213	14300	ATACAAAAATTATCCGGGTG
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16215	14302	AAATACAAAAATTATCCGGG
16216	14303	AAAATACAAAAATTATCCGG
16217	14304	AAAAATACAAAAATTATCCG
16218	14305	TAAAAATACAAAAATTATCC
16219	14306	CTAAAAATACAAAAATTATC
16220	14307	ACTAAAAATACAAAAATTAT
16221	14308	TACTAAAAATACAAAAATTA
16222	14309	CTACTAAAAATACAAAAATT
16223	14310	TCTACTAAAAATACAAAAAT
16224	14311	CTCTACTAAAAATACAAAAA
16225	14312	TCTCTACTAAAAATACAAAA
16226	14313	ATCTCTACTAAAAATACAAA
16227	14314	CATCTCTACTAAAAATACAA
16228	14315	CCATCTCTACTAAAAATACA
16229	14316	CCCATCTCTACTAAAAATAC
16230	14317	CCCCATCTCTACTAAAAATA
16231	14318	ACCCCATCTCTACTAAAAAT
16232	14319	AACCCCATCTCTACTAAAAA
16233	14320	AAACCCCATCTCTACTAAAA
16234	14321	AAAACCCCATCTCTACTAAA
16235	14322	CAAAACCCCATCTCTACTAA
16236	14323	GCAAAACCCCATCTCTACTA
16237	14324	GGCAAAACCCCATCTCTACT
16238	14325	TGGCAAAACCCCATCTCTAC
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16240	14327	TATGGCAAAACCCCATCTCT
16241	14328	ATATGGCAAAACCCCATCTC
16242	14329	AATATGGCAAAACCCCATCT
16243	14330	CAATATGGCAAAACCCCATC
16244	14331	CCAATATGGCAAAACCCCAT
16245	14332	GCCAATATGGCAAAACCCCA
16246	14333	GGCCAATATGGCAAAACCCC
16247	14334	TGGCCAATATGGCAAAACCC
16248	14335	CTGGCCAATATGGCAAAACC
16249	14336	CCTGGCCAATATGGCAAAAC
16250	14337	GCCTGGCCAATATGGCAAAA
16251	14338	GGCCTGGCCAATATGGCAAA
16252	14339	CGGCCTGGCCAATATGGCAA

65329	63416	ACAATATTTGCCTTGGTGGA
65330	63417	AACAATATTTGCCTTGGTGG
65331	63418	TAACAATATTTGCCTTGGTG
65332	63419	ATAACAATATTTGCCTTGGT
65333	63420	TATAACAATATTTGCCTTGG
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65335	63422	ATTATAACAATATTTGCCTT
65336	63423	GATTATAACAATATTTGCCT
65337	63424	AGATTATAACAATATTTGCC
65338	63425	GAGATTATAACAATATTTGC
65339	63426	GGAGATTATAACAATATTTG
65340	63427	AGGAGATTATAACAATATTT
65341	63428	TAGGAGATTATAACAATATT
65342	63429	TTAGGAGATTATAACAATAT
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65346	63433	TTGTTTAGGAGATTATAACA
65347	63434	GTTGTTTAGGAGATTATAAC
65348	63435	AGTTGTTTAGGAGATTATAA
65349	63436	AAGTTGTTTAGGAGATTATA
65350	63437	CAAGTTGTTTAGGAGATTAT
65351	63438	ACAAGTTGTTTAGGAGATTA
65352	63439	GACAAGTTGTTTAGGAGATT
65353	63440	AGACAAGTTGTTTAGGAGAT
65354	63441	AAGACAAGTTGTTTAGGAGA
65355	63442	GAAGACAAGTTGTTTAGGAG
65356	63443	GGAAGACAAGTTGTTTAGGA
65357	63444	TGGAAGACAAGTTGTTTAGG
65358	63445	CTGGAAGACAAGTTGTTTAG
65359	63446	TCTGGAAGACAAGTTGTTTA
65360	63447	ATCTGGAAGACAAGTTGTTT
65361	63448	AATCTGGAAGACAAGTTGTT
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65366	63453	TGAGAAATCTGGAAGACAAG
65367	63454	ATGAGAAATCTGGAAGACAA
65368	63455	AATGAGAAATCTGGAAGACA
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65371	63458	GAAAATGAGAAATCTGGAAG
65372	63459	TGAAAATGAGAAATCTGGAA
65373	63460	CTGAAAATGAGAAATCTGGA
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65375	63462	GACTGAAAATGAGAAATCTG
65376	63463	TGACTGAAAATGAGAAATCT
65377	63464	TTGACTGAAAATGAGAAATC
65378	63465	ATTGACTGAAAATGAGAAAT
65379	63466	GATTGACTGAAAATGAGAAA
65380	63467	AGATTGACTGAAAATGAGAA
65381	63468	AAGATTGACTGAAAATGAGA
65382	63469	CAAGATTGACTGAAAATGAG
65383	63470	CCAAGATTGACTGAAAATGA
65384	63471	CCCAAGATTGACTGAAAATG
65385	63472	GCCCAAGATTGACTGAAAAT
65386	63473	TGCCCAAGATTGACTGAAAA
65387	63474	ATGCCCAAGATTGACTGAAA
65388	63475	AATGCCCAAGATTGACTGAA
65389	63476	CAATGCCCAAGATTGACTGA
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65396	63483	TTTATGTCAATGCCCAAGAT
65397	63484	CTTTATGTCAATGCCCAAGA
65398	63485	TCTTTATGTCAATGCCCAAG
65399	63486	TTCTTTATGTCAATGCCCAA

114476	112563	TTTCCTTCACAGAGTCCCAC
114477	112564	TTTTCCTTCACAGAGTCCCA
114478	112565	TTTTTCCTTCACAGAGTCCC
114479	112566	TTTTTTCCTTCACAGAGTCC
114480	112567	TTTTTTTCCTTCACAGAGTC
114481	112568	TTTTTTTTCCTTCACAGAGT
114482	112569	TTTTTTTTTCCTTCACAGAG
114483	112570	TTTTTTTTTTCCTTCACAGA
114484	112571	TTTTTTTTTTTCCTTCACAG
114485	112572	CTTTTTTTTTTTCCTTCACA
114486	112573	ACTTTTTTTTTTTCCTTCAC
114487	112574	TACTTTTTTTTTTTCCTTCA
114488	112575	ATACTTTTTTTTTTTCCTTC
114489	112576	AATACTTTTTTTTTTTCCTT
114490	112577	AAATACTTTTTTTTTTTCCT
114491	112578	AAAATACTTTTTTTTTTTCC
114492	112579	AAAAATACTTTTTTTTTTTC
114493	112580	AAAAAATACTTTTTTTTTTT
114494	112581	CAAAAAATACTTTTTTTTTT
114495	112582	TCAAAAAATACTTTTTTTTT
114496	112583	ATCAAAAAATACTTTTTTTT
114497	112584	AATCAAAAAATACTTTTTTT
114498	112585	CAATCAAAAAATACTTTTTT
114499	112586	GCAATCAAAAAATACTTTTT
114500	112587	GGCAATCAAAAAATACTTTT
114501	112588	AGGCAATCAAAAAATACTTT
114502	112589	AAGGCAATCAAAAAATACTT
114503	112590	AAAGGCAATCAAAAAATACT
114504	112591	CAAAGGCAATCAAAAAATAC
114505	112592	TCAAAGGCAATCAAAAAATA
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114507	112594	TCTCAAAGGCAATCAAAAAA
114508	112595	CTCTCAAAGGCAATCAAAAA
114509	112596	CCTCTCAAAGGCAATCAAAA
114510	112597	TCCTCTCAAAGGCAATCAAA
114511	112598	TTCCTCTCAAAGGCAATCAA
114512	112599	GTTCCTCTCAAAGGCAATCA
114513	112600	CGTTCCTCTCAAAGGCAATC
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114515	112602	ACCGTTCCTCTCAAAGGCAA
114516	112603	AACCGTTCCTCTCAAAGGCA
114517	112604	CAACCGTTCCTCTCAAAGGC
114518	112605	ACAACCGTTCCTCTCAAAGG
114519	112606	TACAACCGTTCCTCTCAAAG
114520	112607	ATACAACCGTTCCTCTCAAA
114521	112608	TATACAACCGTTCCTCTCAA
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114526	112613	AGTAATATACAACCGTTCCT
114527	112614	GAGTAATATACAACCGTTCC
114528	112615	TGAGTAATATACAACCGTTC
114529	112616	CTGAGTAATATACAACCGTT
114530	112617	TCTGAGTAATATACAACCGT
114531	112618	ATCTGAGTAATATACAACCG
114532	112619	AATCTGAGTAATATACAACC
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114535	112622	AAAAATCTGAGTAATATACA
114536	112623	TAAAAATCTGAGTAATATAC
114537	112624	TTAAAAATCTGAGTAATATA
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114539	112626	TTTTAAAAATCTGAGTAATA
114540	112627	TTTTTAAAAATCTGAGTAAT
114541	112628	TTTTTTAAAAATCTGAGTAA
114542	112629	ATTTTTTAAAAATCTGAGTA
114543	112630	AATTTTTTAAAAATCTGAGT
114544	112631	CAATTTTTTAAAAATCTGAG
114545	112632	ACAATTTTTTAAAAATCTGA
114546	112633	AACAATTTTTTAAAAATCTG

16253	14340	CCGGCCTGGCCAATATGGCA
16254	14341	ACCGGCCTGGCCAATATGGC
16255	14342	GACCGGCCTGGCCAATATGG
16256	14343	AGACCGGCCTGGCCAATATG
16257	14344	AAGACCGGCCTGGCCAATAT
16258	14345	CAAGACCGGCCTGGCCAATA
16259	14346	TCAAGACCGGCCTGGCCAAT
16260	14347	TTCAAGACCGGCCTGGCCAA
16261	14348	GTTCAAGACCGGCCTGGCCA
16262	14349	AGTTCAAGACCGGCCTGGCC
16263	14350	GAGTTCAAGACCGGCCTGGC
16264	14351	GGAGTTCAAGACCGGCCTGG
16265	14352	AGGAGTTCAAGACCGGCCTG
16266	14353	CAGGAGTTCAAGACCGGCCT
16267	14354	TCAGGAGTTCAAGACCGGCC
16268	14355	GTCAGGAGTTCAAGACCGGC
16269	14356	GGTCAGGAGTTCAAGACCGG
16270	14357	AGGTCAGGAGTTCAAGACCG
16271	14358	GAGGTCAGGAGTTCAAGACC
16272	14359	TGAGGTCAGGAGTTCAAGAC
16273	14360	CTGAGGTCAGGAGTTCAAGA
16274	14361	TCTGAGGTCAGGAGTTCAAG
16275	14362	ATCTGAGGTCAGGAGTTCAA
16276	14363	CATCTGAGGTCAGGAGTTCA
16277	14364	TCATCTGAGGTCAGGAGTTC
16278	14365	ATCATCTGAGGTCAGGAGTT
16279	14366	GATCATCTGAGGTCAGGAGT
16280	14367	GGATCATCTGAGGTCAGGAG
16281	14368	TGGATCATCTGAGGTCAGGA
16282	14369	GTGGATCATCTGAGGTCAGG
16283	14370	GGTGGATCATCTGAGGTCAG
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16288	14375	AGGCAGGTGGATCATCTGAG
16289	14376	TAGGCAGGTGGATCATCTGA
16290	14377	CTAGGCAGGTGGATCATCTG
16291	14378	CCTAGGCAGGTGGATCATCT
16292	14379	GCCTAGGCAGGTGGATCATC
16293	14380	GGCCTAGGCAGGTGGATCAT
16294	14381	AGGCCTAGGCAGGTGGATCA
16295	14382	GAGGCCTAGGCAGGTGGATC
16296	14383	GGAGGCCTAGGCAGGTGGAT
16297	14384	GGGAGGCCTAGGCAGGTGGA
16298	14385	TGGGAGGCCTAGGCAGGTGG
16299	14386	TTGGGAGGCCTAGGCAGGTG
16300	14387	TTTGGGAGGCCTAGGCAGGT
16301	14388	CTTTGGGAGGCCTAGGCAGG
16302	14389	ACTTTGGGAGGCCTAGGCAG
16303	14390	CACTTTGGGAGGCCTAGGCA
16304	14391	GCACTTTGGGAGGCCTAGGC
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16306	14393	CGGCACTTTGGGAGGCCTAG
16307	14394	CCGGCACTTTGGGAGGCCTA
16308	14395	CCCGGCACTTTGGGAGGCCT
16309	14396	TCCCGGCACTTTGGGAGGCC
16310	14397	ATCCCGGCACTTTGGGAGGC
16311	14398	AATCCCGGCACTTTGGGAGG
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16319	14406	ACGCCTGTAATCCCGGCACT
16320	14407	CACGCCTGTAATCCCGGCAC
16321	14408	TCACGCCTGTAATCCCGGCA
16322	14409	CTCACGCCTGTAATCCCGGC
16323	14410	GCTCACGCCTGTAATCCCGG

65400	63487	TTTCTTTATGTCAATGCCCA
65401	63488	ATTTCTTTATGTCAATGCCC
65402	63489	AATTTCTTTATGTCAATGCC
65403	63490	GAATTTCTTTATGTCAATGC
65404	63491	AGAATTTCTTTATGTCAATG
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65406	63493	TAAGAATTTCTTTATGTCAA
65407	63494	CTAAGAATTTCTTTATGTCA
65408	63495	TCTAAGAATTTCTTTATGTC
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65410	63497	TGTCTAAGAATTTCTTTATG
65411	63498	ATGTCTAAGAATTTCTTTAT
65412	63499	AATGTCTAAGAATTTCTTTA
65413	63500	CAATGTCTAAGAATTTCTTT
65414	63501	GCAATGTCTAAGAATTTCTT
65415	63502	AGCAATGTCTAAGAATTTCT
65416	63503	AAGCAATGTCTAAGAATTTC
65417	63504	AAAGCAATGTCTAAGAATTT
65418	63505	AAAAGCAATGTCTAAGAATT
65419	63506	TAAAAGCAATGTCTAAGAAT
65420	63507	ATAAAAGCAATGTCTAAGAA
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65422	63509	TAATAAAAGCAATGTCTAAG
65423	63510	CTAATAAAAGCAATGTCTAA
65424	63511	TCTAATAAAAGCAATGTCTA
65425	63512	ATCTAATAAAAGCAATGTCT
65426	63513	GATCTAATAAAAGCAATGTC
65427	63514	TGATCTAATAAAAGCAATGT
65428	63515	ATGATCTAATAAAAGCAATG
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65432	63519	TGAGATGATCTAATAAAAGC
65433	63520	ATGAGATGATCTAATAAAAG
65434	63521	GATGAGATGATCTAATAAAA
65435	63522	GGATGAGATGATCTAATAAA
65436	63523	GGGATGAGATGATCTAATAA
65437	63524	AGGGATGAGATGATCTAATA
65438	63525	AAGGGATGAGATGATCTAAT
65439	63526	CAAGGGATGAGATGATCTAA
65440	63527	GCAAGGGATGAGATGATCTA
65441	63528	AGCAAGGGATGAGATGATCT
65442	63529	GAGCAAGGGATGAGATGATC
65443	63530	TGAGCAAGGGATGAGATGAT
65444	63531	TTGAGCAAGGGATGAGATGA
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65448	63535	GATTTTGAGCAAGGGATGAG
65449	63536	AGATTTTGAGCAAGGGATGA
65450	63537	AAGATTTTGAGCAAGGGATG
65451	63538	GAAGATTTTGAGCAAGGGAT
65452	63539	TGAAGATTTTGAGCAAGGGA
65453	63540	CTGAAGATTTTGAGCAAGGG
65454	63541	ACTGAAGATTTTGAGCAAGG
65455	63542	CACTGAAGATTTTGAGCAAG
65456	63543	CCACTGAAGATTTTGAGCAA
65457	63544	GCCACTGAAGATTTTGAGCA
65458	63545	GGCCACTGAAGATTTTGAGC
65459	63546	TGGCCACTGAAGATTTTGAG
65460	63547	GTGGCCACTGAAGATTTTGA
65461	63548	AGTGGCCACTGAAGATTTTG
65462	63549	CAGTGGCCACTGAAGATTTT
65463	63550	ACAGTGGCCACTGAAGATTT
65464	63551	AACAGTGGCCACTGAAGATT
65465	63552	CAACAGTGGCCACTGAAGAT
65466	63553	ACAACAGTGGCCACTGAAGA
65467	63554	AACAACAGTGGCCACTGAAG
65468	63555	AAACAACAGTGGCCACTGAA
65469	63556	TAAACAACAGTGGCCACTGA
65470	63557	GTAAACAACAGTGGCCACTG

114547	112634	GAACAATTTTTTAAAAATCT
114548	112635	AGAACAATTTTTTAAAAATC
114549	112636	AAGAACAATTTTTTAAAAAT
114550	112637	AAAGAACAATTTTTTAAAAA
114551	112638	AAAAGAACAATTTTTTAAAA
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114553	112640	ATAAAAGAACAATTTTTTAA
114554	112641	CATAAAAGAACAATTTTTTA
114555	112642	CCATAAAAGAACAATTTTTT
114556	112643	GCCATAAAAGAACAATTTTT
114557	112644	AGCCATAAAAGAACAATTTT
114558	112645	CAGCCATAAAAGAACAATTT
114559	112646	ACAGCCATAAAAGAACAATT
114560	112647	TACAGCCATAAAAGAACAAT
114561	112648	ATACAGCCATAAAAGAACAA
114562	112649	AATACAGCCATAAAAGAACA
114563	112650	GAATACAGCCATAAAAGAAC
114564	112651	AGAATACAGCCATAAAAGAA
114565	112652	AAGAATACAGCCATAAAAGA
114566	112653	AAAGAATACAGCCATAAAAG
114567	112654	TAAAGAATACAGCCATAAAA
114568	112655	TTAAAGAATACAGCCATAAA
114569	112656	CTTAAAGAATACAGCCATAA
114570	112657	CCTTAAAGAATACAGCCATA
114571	112658	CCCTTAAAGAATACAGCCAT
114572	112659	TCCCTTAAAGAATACAGCCA
114573	112660	ATCCCTTAAAGAATACAGCC
114574	112661	AATCCCTTAAAGAATACAGC
114575	112662	TAATCCCTTAAAGAATACAG
114576	112663	TTAATCCCTTAAAGAATACA
114577	112664	CTTAATCCCTTAAAGAATAC
114578	112665	CCTTAATCCCTTAAAGAATA
114579	112666	TCCTTAATCCCTTAAAGAAT
114580	112667	TTCCTTAATCCCTTAAAGAA
114581	112668	ATTCCTTAATCCCTTAAAGA
114582	112669	CATTCCTTAATCCCTTAAAG
114583	112670	CCATTCCTTAATCCCTTAAA
114584	112671	CCCATTCCTTAATCCCTTAA
114585	112672	GCCCATTCCTTAATCCCTTA
114586	112673	TGCCCATTCCTTAATCCCTT
114587	112674	TTGCCCATTCCTTAATCCCT
114588	112675	ATTGCCCATTCCTTAATCCC
114589	112676	TATTGCCCATTCCTTAATCC
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114591	112678	TATATTGCCCATTCCTTAAT
114592	112679	TTATATTGCCCATTCCTTAA
114593	112680	CTTATATTGCCCATTCCTTA
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114595	112682	CACTTATATTGCCCATTCCT
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114597	112684	TACACTTATATTGCCCATTC
114598	112685	ATACACTTATATTGCCCATT
114599	112686	TATACACTTATATTGCCCAT
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114601	112688	CATATACACTTATATTGCCC
114602	112689	ACATATACACTTATATTGCC
114603	112690	AACATATACACTTATATTGC
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114605	112692	GAAACATATACACTTATATT
114606	112693	TGAAACATATACACTTATAT
114607	112694	TTGAAACATATACACTTATA
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114611	112698	TTTATTGAAACATATACACT
114612	112699	TTTTATTGAAACATATACAC
114613	112700	TTTTTATTGAAACATATACA
114614	112701	GTTTTTATTGAAACATATAC
114615	112702	CGTTTTTATTGAAACATATA
114616	112703	TCGTTTTTATTGAAACATAT
114617	112704	ATCGTTTTTATTGAAACATA

16324	14411	GGCTCACGCCTGTAATCCCG
16325	14412	TGGCTCACGCCTGTAATCCC
16326	14413	GTGGCTCACGCCTGTAATCC
16327	14414	GGTGGCTCACGCCTGTAATC
16328	14415	TGGTGGCTCACGCCTGTAAT
16329	14416	GTGGTGGCTCACGCCTGTAA
16330	14417	AGTGGTGGCTCACGCCTGTA
16331	14418	GAGTGGTGGCTCACGCCTGT
16332	14419	GGAGTGGTGGCTCACGCCTG
16333	14420	GGGAGTGGTGGCTCACGCCT
16334	14421	CGGGAGTGGTGGCTCACGCC
16335	14422	CCGGGAGTGGTGGCTCACGC
16336	14423	GCCGGGAGTGGTGGCTCACG
16337	14424	GGCCGGGAGTGGTGGCTCAC
16338	14425	AGGCCGGGAGTGGTGGCTCA
16339	14426	CAGGCCGGGAGTGGTGGCTC
16340	14427	CCAGGCCGGGAGTGGTGGCT
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16343	14430	CTCCCAGGCCGGGAGTGGTG
16344	14431	ACTCCCAGGCCGGGAGTGGT
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16347	14434	AAAACTCCCAGGCCGGGAGT
16348	14435	CAAAACTCCCAGGCCGGGAG
16349	14436	TCAAAACTCCCAGGCCGGGA
16350	14437	GTCAAAACTCCCAGGCCGGG
16351	14438	AGTCAAAACTCCCAGGCCGG
16352	14439	CAGTCAAAACTCCCAGGCCG
16353	14440	ACAGTCAAAACTCCCAGGCC
16354	14441	TACAGTCAAAACTCCCAGGC
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16356	14443	CTTACAGTCAAAACTCCCAG
16357	14444	ACTTACAGTCAAAACTCCCA
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16362	14449	TATAAACTTACAGTCAAAAC
16363	14450	CTATAAACTTACAGTCAAAA
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16366	14453	CAGCTATAAACTTACAGTCA
16367	14454	ACAGCTATAAACTTACAGTC
16368	14455	TACAGCTATAAACTTACAGT
16369	14456	ATACAGCTATAAACTTACAG
16370	14457	TATACAGCTATAAACTTACA
16371	14458	ATATACAGCTATAAACTTAC
16372	14459	GATATACAGCTATAAACTTA
16373	14460	AGATATACAGCTATAAACTT
16374	14461	AAGATATACAGCTATAAACT
16375	14462	TAAGATATACAGCTATAAAC
16376	14463	CTAAGATATACAGCTATAAA
16377	14464	CCTAAGATATACAGCTATAA
16378	14465	GCCTAAGATATACAGCTATA
16379	14466	GGCCTAAGATATACAGCTAT
16380	14467	GGGCCTAAGATATACAGCTA
16381	14468	AGGGCCTAAGATATACAGCT
16382	14469	TAGGGCCTAAGATATACAGC
16383	14470	TTAGGGCCTAAGATATACAG
16384	14471	CTTAGGGCCTAAGATATACA
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16386	14473	CCCTTAGGGCCTAAGATATA
16387	14474	GCCCTTAGGGCCTAAGATAT
16388	14475	TGCCCTTAGGGCCTAAGATA
16389	14476	ATGCCCTTAGGGCCTAAGAT
16390	14477	AATGCCCTTAGGGCCTAAGA
16391	14478	TAATGCCCTTAGGGCCTAAG
16392	14479	GTAATGCCCTTAGGGCCTAA
16393	14480	AGTAATGCCCTTAGGGCCTA
16394	14481	CAGTAATGCCCTTAGGGCCT

65471	63558	TGTAAACAACAGTGGCCACT
65472	63559	CTGTAAACAACAGTGGCCAC
65473	63560	TCTGTAAACAACAGTGGCCA
65474	63561	TTCTGTAAACAACAGTGGCC
65475	63562	ATTCTGTAAACAACAGTGGC
65476	63563	TATTCTGTAAACAACAGTGG
65477	63564	TTATTCTGTAAACAACAGTG
65478	63565	TTTATTCTGTAAACAACAGT
65479	63566	CTTTATTCTGTAAACAACAG
65480	63567	ACTTTATTCTGTAAACAACA
65481	63568	AACTTTATTCTGTAAACAAC
65482	63569	CAACTTTATTCTGTAAACAA
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65484	63571	CCCAACTTTATTCTGTAAAC
65485	63572	TCCCAACTTTATTCTGTAAA
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65487	63574	CATCCCAACTTTATTCTGTA
65488	63575	GCATCCCAACTTTATTCTGT
65489	63576	AGCATCCCAACTTTATTCTG
65490	63577	TAGCATCCCAACTTTATTCT
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65492	63579	TATAGCATCCCAACTTTATT
65493	63580	GTATAGCATCCCAACTTTAT
65494	63581	TGTATAGCATCCCAACTTTA
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65499	63586	GGCCCTGTATAGCATCCCAA
65500	63587	GGGCCCTGTATAGCATCCCA
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65507	63594	CTGGGAAGGGCCCTGTATAG
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65514	63601	AGTTCCACTGGGAAGGGCCC
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65519	63606	AGAGAAGTTCCACTGGGAAG
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65524	63611	GAAAAAGAGAAGTTCCACTG
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65527	63614	GTTGAAAAAGAGAAGTTCCA
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65529	63616	AGGTTGAAAAAGAGAAGTTC
65530	63617	AAGGTTGAAAAAGAGAAGTT
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65537	63624	GAGAGATAAGGTTGAAAAAG
65538	63625	TGAGAGATAAGGTTGAAAAA
65539	63626	ATGAGAGATAAGGTTGAAAA
65540	63627	AATGAGAGATAAGGTTGAAA
65541	63628	TAATGAGAGATAAGGTTGAA

114618	112705	AATCGTTTTTATTGAAACAT
114619	112706	TAATCGTTTTTATTGAAACA
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114621	112708	ACTAATCGTTTTTATTGAAA
114622	112709	CACTAATCGTTTTTATTGAA
114623	112710	TCACTAATCGTTTTTATTGA
114624	112711	ATCACTAATCGTTTTTATTG
114625	112712	GATCACTAATCGTTTTTATT
114626	112713	AGATCACTAATCGTTTTTAT
114627	112714	AAGATCACTAATCGTTTTTA
114628	112715	GAAGATCACTAATCGTTTTT
114629	112716	AGAAGATCACTAATCGTTTT
114630	112717	TAGAAGATCACTAATCGTTT
114631	112718	CTAGAAGATCACTAATCGTT
114632	112719	ACTAGAAGATCACTAATCGT
114633	112720	CACTAGAAGATCACTAATCG
114634	112721	TCACTAGAAGATCACTAATC
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114646	112733	TTTAAACTGTTCTCACTAGA
114647	112734	ATTTAAACTGTTCTCACTAG
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114650	112737	TAGATTTAAACTGTTCTCAC
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114656	112743	TAAATATAGATTTAAACTGT
114657	112744	CTAAATATAGATTTAAACTG
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114659	112746	TGCTAAATATAGATTTAAAC
114660	112747	TTGCTAAATATAGATTTAAA
114661	112748	ATTGCTAAATATAGATTTAA
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114665	112752	AAAAATTGCTAAATATAGAT
114666	112753	AAAAAATTGCTAAATATAGA
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114668	112755	AAAAAAAATTGCTAAATATA
114669	112756	TAAAAAAAATTGCTAAATAT
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114675	112762	ACAATTTAAAAAAAATTGCT
114676	112763	GACAATTTAAAAAAAATTGC
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114683	112770	CATACCTGACAATTTAAAAA
114684	112771	CCATACCTGACAATTTAAAA
114685	112772	TCCATACCTGACAATTTAAA
114686	112773	TTCCATACCTGACAATTTAA
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16395	14482	ACAGTAATGCCCTTAGGGCC
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16407	14494	CTGTGCTATAAAACAGTAAT
16408	14495	ACTGTGCTATAAAACAGTAA
16409	14496	CACTGTGCTATAAAACAGTA
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16412	14499	CTACACTGTGCTATAAAACA
16413	14500	ACTACACTGTGCTATAAAAC
16414	14501	AACTACACTGTGCTATAAAA
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16417	14504	ACTAACTACACTGTGCTATA
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16419	14506	TAACTAACTACACTGTGCTA
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16427	14514	GAGCACATTAACTAACTACA
16428	14515	TGAGCACATTAACTAACTAC
16429	14516	ATGAGCACATTAACTAACTA
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16431	14518	TTATGAGCACATTAACTAAC
16432	14519	ATTATGAGCACATTAACTAA
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16435	14522	ACCATTATGAGCACATTAAC
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16445	14532	GTTATGAGTCACCATTATGA
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16449	14536	TGGTGTTATGAGTCACCATT
16450	14537	CTGGTGTTATGAGTCACCAT
16451	14538	CCTGGTGTTATGAGTCACCA
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16454	14541	TAACCTGGTGTTATGAGTCA
16455	14542	TTAACCTGGTGTTATGAGTC
16456	14543	TTTAACCTGGTGTTATGAGT
16457	14544	ATTTAACCTGGTGTTATGAG
16458	14545	CATTTAACCTGGTGTTATGA
16459	14546	TCATTTAACCTGGTGTTATG
16460	14547	ATCATTTAACCTGGTGTTAT
16461	14548	AATCATTTAACCTGGTGTTA
16462	14549	AAATCATTTAACCTGGTGTT
16463	14550	AAAATCATTTAACCTGGTGT
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65542	63629	ATAATGAGAGATAAGGTTGA
65543	63630	AATAATGAGAGATAAGGTTG
65544	63631	AAATAATGAGAGATAAGGTT
65545	63632	GAAATAATGAGAGATAAGGT
65546	63633	GGAAATAATGAGAGATAAGG
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65549	63636	TTGGGAAATAATGAGAGATA
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65587	63674	CAGAGCGAGACTCCGTCTCA
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65589	63676	GACAGAGCGAGACTCCGTCT
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65595	63682	CTGGGCGACAGAGCGAGACT
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65600	63687	CCAGCCTGGGCGACAGAGCG
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65604	63691	CACTCCAGCCTGGGCGACAG
65605	63692	GCACTCCAGCCTGGGCGACA
65606	63693	TGCACTCCAGCCTGGGCGAC
65607	63694	CTGCACTCCAGCCTGGGCGA
65608	63695	ACTGCACTCCAGCCTGGGCG
65609	63696	CACTGCACTCCAGCCTGGGC
65610	63697	CCACTGCACTCCAGCCTGGG
65611	63698	GCCACTGCACTCCAGCCTGG
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114689	112776	ATCTTCCATACCTGACAATT
114690	112777	AATCTTCCATACCTGACAAT
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114697	112784	GCTCTAAAATCTTCCATACC
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114699	112786	TTGCTCTAAAATCTTCCATA
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114706	112793	CTTTACGTTGCTCTAAAATC
114707	112794	ACTTTACGTTGCTCTAAAAT
114708	112795	GACTTTACGTTGCTCTAAAA
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114710	112797	TGGACTTTACGTTGCTCTAA
114711	112798	ATGGACTTTACGTTGCTCTA
114712	112799	CATGGACTTTACGTTGCTCT
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114716	112803	TCTACATGGACTTTACGTTG
114717	112804	ATCTACATGGACTTTACGTT
114718	112805	AATCTACATGGACTTTACGT
114719	112806	AAATCTACATGGACTTTACG
114720	112807	GAAATCTACATGGACTTTAC
114721	112808	TGAAATCTACATGGACTTTA
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114723	112810	AGTGAAATCTACATGGACTT
114724	112811	CAGTGAAATCTACATGGACT
114725	112812	CCAGTGAAATCTACATGGAC
114726	112813	GCCAGTGAAATCTACATGGA
114727	112814	GGCCAGTGAAATCTACATGG
114728	112815	AGGCCAGTGAAATCTACATG
114729	112816	AAGGCCAGTGAAATCTACAT
114730	112817	AAAGGCCAGTGAAATCTACA
114731	112818	TAAAGGCCAGTGAAATCTAC
114732	112819	ATAAAGGCCAGTGAAATCTA
114733	112820	TATAAAGGCCAGTGAAATCT
114734	112821	ATATAAAGGCCAGTGAAATC
114735	112822	AATATAAAGGCCAGTGAAAT
114736	112823	AAATATAAAGGCCAGTGAAA
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114738	112825	AAAAATATAAAGGCCAGTGA
114739	112826	AAAAAATATAAAGGCCAGTG
114740	112827	AAAAAAATATAAAGGCCAGT
114741	112828	AAAAAAAATATAAAGGCCAG
114742	112829	TAAAAAAAATATAAAGGCCA
114743	112830	CTAAAAAAAATATAAAGGCC
114744	112831	CCTAAAAAAAATATAAAGGC
114745	112832	GCCTAAAAAAAATATAAAGG
114746	112833	TGCCTAAAAAAAATATAAAG
114747	112834	TTGCCTAAAAAAAATATAAA
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114749	112836	ACTTGCCTAAAAAAAATATA
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114756	112843	TTTCCTAACTTGCCTAAAAA
114757	112844	ATTTCCTAACTTGCCTAAAA
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114759	112846	TGATTTCCTAACTTGCCTAA

16466	14553	TAAAAAATCATTTAACCTGG
16467	14554	ATAAAAAATCATTTAACCTG
16468	14555	TATAAAAAATCATTTAACCT
16469	14556	ATATAAAAAATCATTTAACC
16470	14557	GATATAAAAAATCATTTAAC
16471	14558	AGATATAAAAAATCATTTAA
16472	14559	GAGATATAAAAAATCATTTA
16473	14560	GGAGATATAAAAAATCATTT
16474	14561	GGGAGATATAAAAAATCATT
16475	14562	TGGGAGATATAAAAAATCAT
16476	14563	TTGGGAGATATAAAAAATCA
16477	14564	TTTGGGAGATATAAAAAATC
16478	14565	CTTTGGGAGATATAAAAAAT
16479	14566	TCTTTGGGAGATATAAAAAA
16480	14567	TTCTTTGGGAGATATAAAAA
16481	14568	CTTCTTTGGGAGATATAAAA
16482	14569	ACTTCTTTGGGAGATATAAA
16483	14570	TACTTCTTTGGGAGATATAA
16484	14571	ATACTTCTTTGGGAGATATA
16485	14572	AATACTTCTTTGGGAGATAT
16486	14573	AAATACTTCTTTGGGAGATA
16487	14574	AAAATACTTCTTTGGGAGAT
16488	14575	AAAAATACTTCTTTGGGAGA
16489	14576	GAAAAATACTTCTTTGGGAG
16490	14577	TGAAAAATACTTCTTTGGGA
16491	14578	TTGAAAAATACTTCTTTGGG
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16493	14580	GATTGAAAAATACTTCTTTG
16494	14581	AGATTGAAAAATACTTCTTT
16495	14582	CAGATTGAAAAATACTTCTT
16496	14583	GCAGATTGAAAAATACTTCT
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16499	14586	TCTGCAGATTGAAAAATACT
16500	14587	ATCTGCAGATTGAAAAATAC
16501	14588	GATCTGCAGATTGAAAAATA
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16503	14590	ATGATCTGCAGATTGAAAAA
16504	14591	CATGATCTGCAGATTGAAAA
16505	14592	TCATGATCTGCAGATTGAAA
16506	14593	GTCATGATCTGCAGATTGAA
16507	14594	GGTCATGATCTGCAGATTGA
16508	14595	GGGTCATGATCTGCAGATTG
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16511	14598	AAGGGGTCATGATCTGCAGA
16512	14599	TAAGGGGTCATGATCTGCAG
16513	14600	CTAAGGGGTCATGATCTGCA
16514	14601	ACTAAGGGGTCATGATCTGC
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16516	14603	CTACTAAGGGGTCATGATCT
16517	14604	TCTACTAAGGGGTCATGATC
16518	14605	ATCTACTAAGGGGTCATGAT
16519	14606	AATCTACTAAGGGGTCATGA
16520	14607	CAATCTACTAAGGGGTCATG
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16522	14609	CACAATCTACTAAGGGGTCA
16523	14610	TCACAATCTACTAAGGGGTC
16524	14611	TTCACAATCTACTAAGGGGT
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16533	14620	CTAATGTGTTTCACAATCTA
16534	14621	ACTAATGTGTTTCACAATCT
16535	14622	CACTAATGTGTTTCACAATC
16536	14623	CCACTAATGTGTTTCACAAT

65613	63700	CCGCCACTGCACTCCAGCCT
65614	63701	CCCGCCACTGCACTCCAGCC
65615	63702	TCCCGCCACTGCACTCCAGC
65616	63703	ATCCCGCCACTGCACTCCAG
65617	63704	GATCCCGCCACTGCACTCCA
65618	63705	AGATCCCGCCACTGCACTCC
65619	63706	GAGATCCCGCCACTGCACTC
65620	63707	CGAGATCCCGCCACTGCACT
65621	63708	CCGAGATCCCGCCACTGCAC
65622	63709	GCCGAGATCCCGCCACTGCA
65623	63710	AGCCGAGATCCCGCCACTGC
65624	63711	GAGCCGAGATCCCGCCACTG
65625	63712	TGAGCCGAGATCCCGCCACT
65626	63713	GTGAGCCGAGATCCCGCCAC
65627	63714	AGTGAGCCGAGATCCCGCCA
65628	63715	CAGTGAGCCGAGATCCCGCC
65629	63716	GCAGTGAGCCGAGATCCCGC
65630	63717	TGCAGTGAGCCGAGATCCCG
65631	63718	TTGCAGTGAGCCGAGATCCC
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65633	63720	GCTTGCAGTGAGCCGAGATC
65634	63721	AGCTTGCAGTGAGCCGAGAT
65635	63722	GAGCTTGCAGTGAGCCGAGA
65636	63723	GGAGCTTGCAGTGAGCCGAG
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65638	63725	GCGGAGCTTGCAGTGAGCCG
65639	63726	GGCGGAGCTTGCAGTGAGCC
65640	63727	AGGCGGAGCTTGCAGTGAGC
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65643	63730	AGGAGGCGGAGCTTGCAGTG
65644	63731	CAGGAGGCGGAGCTTGCAGT
65645	63732	CCAGGAGGCGGAGCTTGCAG
65646	63733	CCCAGGAGGCGGAGCTTGCA
65647	63734	ACCCAGGAGGCGGAGCTTGC
65648	63735	AACCCAGGAGGCGGAGCTTG
65649	63736	GAACCCAGGAGGCGGAGCTT
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65651	63738	GTGAACCCAGGAGGCGGAGC
65652	63739	CGTGAACCCAGGAGGCGGAG
65653	63740	GCGTGAACCCAGGAGGCGGA
65654	63741	GGCGTGAACCCAGGAGGCGG
65655	63742	TGGCGTGAACCCAGGAGGCG
65656	63743	ATGGCGTGAACCCAGGAGGC
65657	63744	AATGGCGTGAACCCAGGAGG
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65659	63746	AGAATGGCGTGAACCCAGGA
65660	63747	GAGAATGGCGTGAACCCAGG
65661	63748	GGAGAATGGCGTGAACCCAG
65662	63749	AGGAGAATGGCGTGAACCCA
65663	63750	CAGGAGAATGGCGTGAACCC
65664	63751	GCAGGAGAATGGCGTGAACC
65665	63752	GGCAGGAGAATGGCGTGAAC
65666	63753	AGGCAGGAGAATGGCGTGAA
65667	63754	GAGGCAGGAGAATGGCGTGA
65668	63755	TGAGGCAGGAGAATGGCGTG
65669	63756	CTGAGGCAGGAGAATGGCGT
65670	63757	GCTGAGGCAGGAGAATGGCG
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65674	63761	GGAGGCTGAGGCAGGAGAAT
65675	63762	GGGAGGCTGAGGCAGGAGAA
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65679	63766	ACTTGGGAGGCTGAGGCAGG
65680	63767	TACTTGGGAGGCTGAGGCAG
65681	63768	CTACTTGGGAGGCTGAGGCA
65682	63769	GCTACTTGGGAGGCTGAGGC
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114760	112847	TTGATTTCCTAACTTGCCTA
114761	112848	GTTGATTTCCTAACTTGCCT
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114767	112854	TTCAATGTTGATTTCCTAAC
114768	112855	ATTCAATGTTGATTTCCTAA
114769	112856	GATTCAATGTTGATTTCCTA
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114777	112864	TGCATTGGGATTCAATGTTG
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114781	112868	CCTTTGCATTGGGATTCAAT
114782	112869	TCCTTTGCATTGGGATTCAA
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114792	112879	TGGGTTGAACTCCTTTGCAT
114793	112880	GTGGGTTGAACTCCTTTGCA
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114797	112884	GAACGTGGGTTGAACTCCTT
114798	112885	GGAACGTGGGTTGAACTCCT
114799	112886	AGGAACGTGGGTTGAACTCC
114800	112887	AAGGAACGTGGGTTGAACTC
114801	112888	GAAGGAACGTGGGTTGAACT
114802	112889	AGAAGGAACGTGGGTTGAAC
114803	112890	GAGAAGGAACGTGGGTTGAA
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114805	112892	GAGAGAAGGAACGTGGGTTG
114806	112893	TGAGAGAAGGAACGTGGGTT
114807	112894	CTGAGAGAAGGAACGTGGGT
114808	112895	CCTGAGAGAAGGAACGTGGG
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114810	112897	TACCTGAGAGAAGGAACGTG
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114812	112899	CCTACCTGAGAGAAGGAACG
114813	112900	ACCTACCTGAGAGAAGGAAC
114814	112901	AACCTACCTGAGAGAAGGAA
114815	112902	AAACCTACCTGAGAGAAGGA
114816	112903	TAAACCTACCTGAGAGAAGG
114817	112904	ATAAACCTACCTGAGAGAAG
114818	112905	AATAAACCTACCTGAGAGAA
114819	112906	TAATAAACCTACCTGAGAGA
114820	112907	GTAATAAACCTACCTGAGAG
114821	112908	AGTAATAAACCTACCTGAGA
114822	112909	AAGTAATAAACCTACCTGAG
114823	112910	AAAGTAATAAACCTACCTGA
114824	112911	GAAAGTAATAAACCTACCTG
114825	112912	AGAAAGTAATAAACCTACCT
114826	112913	AAGAAAGTAATAAACCTACC
114827	112914	AAAGAAAGTAATAAACCTAC
114828	112915	CAAAGAAAGTAATAAACCTA
114829	112916	TCAAAGAAAGTAATAAACCT
114830	112917	CTCAAAGAAAGTAATAAACC

16537	14624	TCCACTAATGTGTTTCACAA
16538	14625	ATCCACTAATGTGTTTCACA
16539	14626	AATCCACTAATGTGTTTCAC
16540	14627	TAATCCACTAATGTGTTTCA
16541	14628	ATAATCCACTAATGTGTTTC
16542	14629	CATAATCCACTAATGTGTTT
16543	14630	TCATAATCCACTAATGTGTT
16544	14631	GTCATAATCCACTAATGTGT
16545	14632	TGTCATAATCCACTAATGTG
16546	14633	TTGTCATAATCCACTAATGT
16547	14634	CTTGTCATAATCCACTAATG
16548	14635	GCTTGTCATAATCCACTAAT
16549	14636	TGCTTGTCATAATCCACTAA
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16565	14652	TTCATTTTTCTAAAAATGCT
16566	14653	TTTCATTTTTCTAAAAATGC
16567	14654	TTTTCATTTTTCTAAAAATG
16568	14655	TTTTTCATTTTTCTAAAAAT
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16570	14657	TCTTTTTCATTTTTCTAAAA
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16577	14664	TTCTTATTCTTTTTCATTTT
16578	14665	CTTCTTATTCTTTTTCATTT
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16582	14669	AACACTTCTTATTCTTTTTC
16583	14670	TAACACTTCTTATTCTTTTT
16584	14671	CTAACACTTCTTATTCTTTT
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16593	14680	CAATGCATCCTAACACTTCT
16594	14681	GCAATGCATCCTAACACTTC
16595	14682	TGCAATGCATCCTAACACTT
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16601	14688	CAATAATGCAATGCATCCTA
16602	14689	TCAATAATGCAATGCATCCT
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65684	63771	CAGCTACTTGGGAGGCTGAG
65685	63772	CCAGCTACTTGGGAGGCTGA
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65687	63774	TCCCAGCTACTTGGGAGGCT
65688	63775	GTCCCAGCTACTTGGGAGGC
65689	63776	AGTCCCAGCTACTTGGGAGG
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65691	63778	GTAGTCCCAGCTACTTGGGA
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65695	63782	GCCTGTAGTCCCAGCTACTT
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65697	63784	GCGCCTGTAGTCCCAGCTAC
65698	63785	GGCGCCTGTAGTCCCAGCTA
65699	63786	GGGCGCCTGTAGTCCCAGCT
65700	63787	CGGGCGCCTGTAGTCCCAGC
65701	63788	GCGGGCGCCTGTAGTCCCAG
65702	63789	GGCGGGCGCCTGTAGTCCCA
65703	63790	TGGCGGGCGCCTGTAGTCCC
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65705	63792	AGTGGCGGGCGCCTGTAGTC
65706	63793	TAGTGGCGGGCGCCTGTAGT
65707	63794	GTAGTGGCGGGCGCCTGTAG
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65709	63796	GCGTAGTGGCGGGCGCCTGT
65710	63797	GGCGTAGTGGCGGGCGCCTG
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65730	63817	AAAATACAAAAAATTAGCCG
65731	63818	AAAAATACAAAAAATTAGCC
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65735	63822	TACTAAAAATACAAAAAATT
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65737	63824	TCTACTAAAAATACAAAAAA
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65741	63828	CGTCTCTACTAAAAATACAA
65742	63829	CCGTCTCTACTAAAAATACA
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65746	63833	AACCCCGTCTCTACTAAAAA
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114831	112918	CCTCAAAGAAAGTAATAAAC
114832	112919	ACCTCAAAGAAAGTAATAAA
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114834	112921	TAACCTCAAAGAAAGTAATA
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114836	112923	GATAACCTCAAAGAAAGTAA
114837	112924	AGATAACCTCAAAGAAAGTA
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114839	112926	CTAGATAACCTCAAAGAAAG
114840	112927	ACTAGATAACCTCAAAGAAA
114841	112928	GACTAGATAACCTCAAAGAA
114842	112929	GGACTAGATAACCTCAAAGA
114843	112930	GGGACTAGATAACCTCAAAG
114844	112931	TGGGACTAGATAACCTCAAA
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114871	112958	GACTATTACTAATAATTTTT
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114874	112961	AAGGACTATTACTAATAATT
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114883	112970	GTATGGAAGAAGGACTATTA
114884	112971	GGTATGGAAGAAGGACTATT
114885	112972	AGGTATGGAAGAAGGACTAT
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114897	112984	AATTCAGATGGCAGGTATGG
114898	112985	AAATTCAGATGGCAGGTATG
114899	112986	AAAATTCAGATGGCAGGTAT
114900	112987	CAAAATTCAGATGGCAGGTA
114901	112988	ACAAAATTCAGATGGCAGGT

16608	14695	ATTATTTCAATAATGCAATG
16609	14696	AATTATTTCAATAATGCAAT
16610	14697	CAATTATTTCAATAATGCAA
16611	14698	ACAATTATTTCAATAATGCA
16612	14699	AACAATTATTTCAATAATGC
16613	14700	AAACAATTATTTCAATAATG
16614	14701	AAAACAATTATTTCAATAAT
16615	14702	AAAAACAATTATTTCAATAA
16616	14703	CAAAAACAATTATTTCAATA
16617	14704	TCAAAAACAATTATTTCAAT
16618	14705	CTCAAAAACAATTATTTCAA
16619	14706	TCTCAAAAACAATTATTTCA
16620	14707	ATCTCAAAAACAATTATTTC
16621	14708	CATCTCAAAAACAATTATTT
16622	14709	CCATCTCAAAAACAATTATT
16623	14710	TCCATCTCAAAAACAATTAT
16624	14711	CTCCATCTCAAAAACAATTA
16625	14712	ACTCCATCTCAAAAACAATT
16626	14713	AACTCCATCTCAAAAACAAT
16627	14714	AAACTCCATCTCAAAAACAA
16628	14715	GAAACTCCATCTCAAAAACA
16629	14716	CGAAACTCCATCTCAAAAAC
16630	14717	GCGAAACTCCATCTCAAAAA
16631	14718	AGCGAAACTCCATCTCAAAA
16632	14719	GAGCGAAACTCCATCTCAAA
16633	14720	AGAGCGAAACTCCATCTCAA
16634	14721	AAGAGCGAAACTCCATCTCA
16635	14722	TAAGAGCGAAACTCCATCTC
16636	14723	CTAAGAGCGAAACTCCATCT
16637	14724	ACTAAGAGCGAAACTCCATC
16638	14725	AACTAAGAGCGAAACTCCAT
16639	14726	CAACTAAGAGCGAAACTCCA
16640	14727	GCAACTAAGAGCGAAACTCC
16641	14728	GGCAACTAAGAGCGAAACTC
16642	14729	CGGCAACTAAGAGCGAAACT
16643	14730	TCGGCAACTAAGAGCGAAAC
16644	14731	CTCGGCAACTAAGAGCGAAA
16645	14732	CCTCGGCAACTAAGAGCGAA
16646	14733	GCCTCGGCAACTAAGAGCGA
16647	14734	AGCCTCGGCAACTAAGAGCG
16648	14735	CAGCCTCGGCAACTAAGAGC
16649	14736	CCAGCCTCGGCAACTAAGAG
16650	14737	TCCAGCCTCGGCAACTAAGA
16651	14738	CTCCAGCCTCGGCAACTAAG
16652	14739	ACTCCAGCCTCGGCAACTAA
16653	14740	CACTCCAGCCTCGGCAACTA
16654	14741	GCACTCCAGCCTCGGCAACT
16655	14742	TGCACTCCAGCCTCGGCAAC
16656	14743	TTGCACTCCAGCCTCGGCAA
16657	14744	ATTGCACTCCAGCCTCGGCA
16658	14745	CATTGCACTCCAGCCTCGGC
16659	14746	CCATTGCACTCCAGCCTCGG
16660	14747	GCCATTGCACTCCAGCCTCG
16661	14748	GGCCATTGCACTCCAGCCTC
16662	14749	GGGCCATTGCACTCCAGCCT
16663	14750	CGGGCCATTGCACTCCAGCC
16664	14751	TCGGGCCATTGCACTCCAGC
16665	14752	ATCGGGCCATTGCACTCCAG
16666	14753	GATCGGGCCATTGCACTCCA
16667	14754	AGATCGGGCCATTGCACTCC
16668	14755	CAGATCGGGCCATTGCACTC
16669	14756	GCAGATCGGGCCATTGCACT
16670	14757	GGCAGATCGGGCCATTGCAC
16671	14758	AGGCAGATCGGGCCATTGCA
16672	14759	GAGGCAGATCGGGCCATTGC
16673	14760	GGAGGCAGATCGGGCCATTG
16674	14761	GGGAGGCAGATCGGGCCATT
16675	14762	CGGGAGGCAGATCGGGCCAT
16676	14763	CCGGGAGGCAGATCGGGCCA
16677	14764	CCCGGGAGGCAGATCGGGCC
16678	14765	ACCCGGGAGGCAGATCGGGC

65755	63842	AAACGGTGAAACCCCGTCTC
65756	63843	AAAACGGTGAAACCCCGTCT
65757	63844	TAAAACGGTGAAACCCCGTC
65758	63845	CTAAAACGGTGAAACCCCGT
65759	63846	GCTAAAACGGTGAAACCCCG
65760	63847	GGCTAAAACGGTGAAACCCC
65761	63848	CGGCTAAAACGGTGAAACCC
65762	63849	CCGGCTAAAACGGTGAAACC
65763	63850	CCCGGCTAAAACGGTGAAAC
65764	63851	TCCCGGCTAAAACGGTGAAA
65765	63852	ATCCCGGCTAAAACGGTGAA
65766	63853	CATCCCGGCTAAAACGGTGA
65767	63854	CCATCCCGGCTAAAACGGTG
65768	63855	ACCATCCCGGCTAAAACGGT
65769	63856	GACCATCCCGGCTAAAACGG
65770	63857	AGACCATCCCGGCTAAAACG
65771	63858	GAGACCATCCCGGCTAAAAC
65772	63859	CGAGACCATCCCGGCTAAAA
65773	63860	TCGAGACCATCCCGGCTAAA
65774	63861	ATCGAGACCATCCCGGCTAA
65775	63862	GATCGAGACCATCCCGGCTA
65776	63863	AGATCGAGACCATCCCGGCT
65777	63864	GAGATCGAGACCATCCCGGC
65778	63865	GGAGATCGAGACCATCCCGG
65779	63866	AGGAGATCGAGACCATCCCG
65780	63867	CAGGAGATCGAGACCATCCC
65781	63868	TCAGGAGATCGAGACCATCC
65782	63869	GTCAGGAGATCGAGACCATC
65783	63870	GGTCAGGAGATCGAGACCAT
65784	63871	AGGTCAGGAGATCGAGACCA
65785	63872	GAGGTCAGGAGATCGAGACC
65786	63873	CGAGGTCAGGAGATCGAGAC
65787	63874	ACGAGGTCAGGAGATCGAGA
65788	63875	CACGAGGTCAGGAGATCGAG
65789	63876	TCACGAGGTCAGGAGATCGA
65790	63877	ATCACGAGGTCAGGAGATCG
65791	63878	GATCACGAGGTCAGGAGATC
65792	63879	GGATCACGAGGTCAGGAGAT
65793	63880	CGGATCACGAGGTCAGGAGA
65794	63881	GCGGATCACGAGGTCAGGAG
65795	63882	GGCGGATCACGAGGTCAGGA
65796	63883	GGGCGGATCACGAGGTCAGG
65797	63884	TGGGCGGATCACGAGGTCAG
65798	63885	GTGGGCGGATCACGAGGTCA
65799	63886	GGTGGGCGGATCACGAGGTC
65800	63887	AGGTGGGCGGATCACGAGGT
65801	63888	GAGGTGGGCGGATCACGAGG
65802	63889	CGAGGTGGGCGGATCACGAG
65803	63890	CCGAGGTGGGCGGATCACGA
65804	63891	GCCGAGGTGGGCGGATCACG
65805	63892	GGCCGAGGTGGGCGGATCAC
65806	63893	AGGCCGAGGTGGGCGGATCA
65807	63894	GAGGCCGAGGTGGGCGGATC
65808	63895	GGAGGCCGAGGTGGGCGGAT
65809	63896	GGGAGGCCGAGGTGGGCGGA
65810	63897	TGGGAGGCCGAGGTGGGCGG
65811	63898	TTGGGAGGCCGAGGTGGGCG
65812	63899	TTTGGGAGGCCGAGGTGGGC
65813	63900	CTTTGGGAGGCCGAGGTGGG
65814	63901	ACTTTGGGAGGCCGAGGTGG
65815	63902	CACTTTGGGAGGCCGAGGTG
65816	63903	GCACTTTGGGAGGCCGAGGT
65817	63904	AGCACTTTGGGAGGCCGAGG
65818	63905	CAGCACTTTGGGAGGCCGAG
65819	63906	CCAGCACTTTGGGAGGCCGA
65820	63907	CCCAGCACTTTGGGAGGCCG
65821	63908	TCCCAGCACTTTGGGAGGCC
65822	63909	ATCCCAGCACTTTGGGAGGC
65823	63910	AATCCCAGCACTTTGGGAGG
65824	63911	TAATCCCAGCACTTTGGGAG
65825	63912	GTAATCCCAGCACTTTGGGA

114902	112989	AACAAAATTCAGATGGCAGG
114903	112990	AAACAAAATTCAGATGGCAG
114904	112991	AAAACAAAATTCAGATGGCA
114905	112992	TAAAACAAAATTCAGATGGC
114906	112993	CTAAAACAAAATTCAGATGG
114907	112994	ACTAAAACAAAATTCAGATG
114908	112995	CACTAAAACAAAATTCAGAT
114909	112996	ACACTAAAACAAAATTCAGA
114910	112997	CACACTAAAACAAAATTCAG
114911	112998	GCACACTAAAACAAAATTCA
114912	112999	AGCACACTAAAACAAAATTC
114913	113000	CAGCACACTAAAACAAAATT
114914	113001	TCAGCACACTAAAACAAAAT
114915	113002	TTCAGCACACTAAAACAAAA
114916	113003	GTTCAGCACACTAAAACAAA
114917	113004	GGTTCAGCACACTAAAACAA
114918	113005	TGGTTCAGCACACTAAAACA
114919	113006	TTGGTTCAGCACACTAAAAC
114920	113007	GTTGGTTCAGCACACTAAAA
114921	113008	GGTTGGTTCAGCACACTAAA
114922	113009	AGGTTGGTTCAGCACACTAA
114923	113010	AAGGTTGGTTCAGCACACTA
114924	113011	GAAGGTTGGTTCAGCACACT
114925	113012	AGAAGGTTGGTTCAGCACAC
114926	113013	AAGAAGGTTGGTTCAGCACA
114927	113014	AAAGAAGGTTGGTTCAGCAC
114928	113015	GAAAGAAGGTTGGTTCAGCA
114929	113016	AGAAAGAAGGTTGGTTCAGC
114930	113017	AAGAAAGAAGGTTGGTTCAG
114931	113018	AAAGAAAGAAGGTTGGTTCA
114932	113019	AAAAGAAAGAAGGTTGGTTC
114933	113020	AAAAAGAAAGAAGGTTGGTT
114934	113021	AAAAAAGAAAGAAGGTTGGT
114935	113022	AAAAAAAGAAAGAAGGTTGG
114936	113023	AAAAAAAAGAAAGAAGGTTG
114937	113024	TAAAAAAAAGAAAGAAGGTT
114938	113025	GTAAAAAAAAGAAAGAAGGT
114939	113026	TGTAAAAAAAAGAAAGAAGG
114940	113027	ATGTAAAAAAAAGAAAGAAG
114941	113028	CATGTAAAAAAAAGAAAGAA
114942	113029	CCATGTAAAAAAAAGAAAGA
114943	113030	GCCATGTAAAAAAAAGAAAG
114944	113031	GGCCATGTAAAAAAAAGAAA
114945	113032	TGGCCATGTAAAAAAAAGAA
114946	113033	ATGGCCATGTAAAAAAAAGA
114947	113034	AATGGCCATGTAAAAAAAAG
114948	113035	TAATGGCCATGTAAAAAAAA
114949	113036	TTAATGGCCATGTAAAAAAA
114950	113037	ATTAATGGCCATGTAAAAAA
114951	113038	CATTAATGGCCATGTAAAAA
114952	113039	TCATTAATGGCCATGTAAAA
114953	113040	TTCATTAATGGCCATGTAAA
114954	113041	ATTCATTAATGGCCATGTAA
114955	113042	TATTCATTAATGGCCATGTA
114956	113043	GTATTCATTAATGGCCATGT
114957	113044	AGTATTCATTAATGGCCATG
114958	113045	AAGTATTCATTAATGGCCAT
114959	113046	AAAGTATTCATTAATGGCCA
114960	113047	AAAAGTATTCATTAATGGCC
114961	113048	AAAAAGTATTCATTAATGGC
114962	113049	TAAAAAGTATTCATTAATGG
114963	113050	TTAAAAAGTATTCATTAATG
114964	113051	TTTAAAAAGTATTCATTAAT
114965	113052	GTTTAAAAAGTATTCATTAA
114966	113053	TGTTTAAAAAGTATTCATTA
114967	113054	ATGTTTAAAAAGTATTCATT
114968	113055	AATGTTTAAAAAGTATTCAT
114969	113056	TAATGTTTAAAAAGTATTCA
114970	113057	TTAATGTTTAAAAAGTATTC
114971	113058	TTTAATGTTTAAAAAGTATT
114972	113059	TTTTAATGTTTAAAAAGTAT

16679	14766	AACCCGGGAGGCAGATCGGG
16680	14767	GAACCCGGGAGGCAGATCGG
16681	14768	TGAACCCGGGAGGCAGATCG
16682	14769	TTGAACCCGGGAGGCAGATC
16683	14770	CTTGAACCCGGGAGGCAGAT
16684	14771	ACTTGAACCCGGGAGGCAGA
16685	14772	CACTTGAACCCGGGAGGCAG
16686	14773	TCACTTGAACCCGGGAGGCA
16687	14774	ATCACTTGAACCCGGGAGGC
16688	14775	AATCACTTGAACCCGGGAGG
16689	14776	GAATCACTTGAACCCGGGAG
16690	14777	AGAATCACTTGAACCCGGGA
16691	14778	GAGAATCACTTGAACCCGGG
16692	14779	GGAGAATCACTTGAACCCGG
16693	14780	AGGAGAATCACTTGAACCCG
16694	14781	TAGGAGAATCACTTGAACCC
16695	14782	GTAGGAGAATCACTTGAACC
16696	14783	GGTAGGAGAATCACTTGAAC
16697	14784	AGGTAGGAGAATCACTTGAA
16698	14785	GAGGTAGGAGAATCACTTGA
16699	14786	TGAGGTAGGAGAATCACTTG
16700	14787	CTGAGGTAGGAGAATCACTT
16701	14788	GCTGAGGTAGGAGAATCACT
16702	14789	GGCTGAGGTAGGAGAATCAC
16703	14790	AGGCTGAGGTAGGAGAATCA
16704	14791	GAGGCTGAGGTAGGAGAATC
16705	14792	GGAGGCTGAGGTAGGAGAAT
16706	14793	AGGAGGCTGAGGTAGGAGAA
16707	14794	CAGGAGGCTGAGGTAGGAGA
16708	14795	TCAGGAGGCTGAGGTAGGAG
16709	14796	CTCAGGAGGCTGAGGTAGGA
16710	14797	ACTCAGGAGGCTGAGGTAGG
16711	14798	TACTCAGGAGGCTGAGGTAG
16712	14799	CTACTCAGGAGGCTGAGGTA
16713	14800	GCTACTCAGGAGGCTGAGGT
16714	14801	AGCTACTCAGGAGGCTGAGG
16715	14802	CAGCTACTCAGGAGGCTGAG
16716	14803	CCAGCTACTCAGGAGGCTGA
16717	14804	CCCAGCTACTCAGGAGGCTG
16718	14805	TCCCAGCTACTCAGGAGGCT
16719	14806	ATCCCAGCTACTCAGGAGGC
16720	14807	AATCCCAGCTACTCAGGAGG
16721	14808	TAATCCCAGCTACTCAGGAG
16722	14809	GTAATCCCAGCTACTCAGGA
16723	14810	TGTAATCCCAGCTACTCAGG
16724	14811	CTGTAATCCCAGCTACTCAG
16725	14812	TCTGTAATCCCAGCTACTCA
16726	14813	GTCTGTAATCCCAGCTACTC
16727	14814	TGTCTGTAATCCCAGCTACT
16728	14815	ATGTCTGTAATCCCAGCTAC
16729	14816	CATGTCTGTAATCCCAGCTA
16730	14817	GCATGTCTGTAATCCCAGCT
16731	14818	AGCATGTCTGTAATCCCAGC
16732	14819	GAGCATGTCTGTAATCCCAG
16733	14820	GGAGCATGTCTGTAATCCCA
16734	14821	TGGAGCATGTCTGTAATCCC
16735	14822	GTGGAGCATGTCTGTAATCC
16736	14823	GGTGGAGCATGTCTGTAATC
16737	14824	TGGTGGAGCATGTCTGTAAT
16738	14825	ATGGTGGAGCATGTCTGTAA
16739	14826	CATGGTGGAGCATGTCTGTA
16740	14827	GCATGGTGGAGCATGTCTGT
16741	14828	GGCATGGTGGAGCATGTCTG
16742	14829	AGGCATGGTGGAGCATGTCT
16743	14830	CAGGCATGGTGGAGCATGTC
16744	14831	CCAGGCATGGTGGAGCATGT
16745	14832	GCCAGGCATGGTGGAGCATG
16746	14833	AGCCAGGCATGGTGGAGCAT
16747	14834	TAGCCAGGCATGGTGGAGCA
16748	14835	TTAGCCAGGCATGGTGGAGC
16749	14836	ATTAGCCAGGCATGGTGGAG

65826	63913	TGTAATCCCAGCACTTTGGG
65827	63914	CTGTAATCCCAGCACTTTGG
65828	63915	CCTGTAATCCCAGCACTTTG
65829	63916	GCCTGTAATCCCAGCACTTT
65830	63917	CGCCTGTAATCCCAGCACTT
65831	63918	ACGCCTGTAATCCCAGCACT
65832	63919	CACGCCTGTAATCCCAGCAC
65833	63920	TCACGCCTGTAATCCCAGCA
65834	63921	CTCACGCCTGTAATCCCAGC
65835	63922	GCTCACGCCTGTAATCCCAG
65836	63923	GGCTCACGCCTGTAATCCCA
65837	63924	TGGCTCACGCCTGTAATCCC
65838	63925	GTGGCTCACGCCTGTAATCC
65839	63926	GGTGGCTCACGCCTGTAATC
65840	63927	CGGTGGCTCACGCCTGTAAT
65841	63928	GCGGTGGCTCACGCCTGTAA
65842	63929	CGCGGTGGCTCACGCCTGTA
65843	63930	GCGCGGTGGCTCACGCCTGT
65844	63931	GGCGCGGTGGCTCACGCCTG
65845	63932	GGGCGCGGTGGCTCACGCCT
65846	63933	CGGGCGCGGTGGCTCACGCC
65847	63934	CCGGGCGCGGTGGCTCACGC
65848	63935	GCCGGGCGCGGTGGCTCACG
65849	63936	GGCCGGGCGCGGTGGCTCAC
65850	63937	AGGCCGGGCGCGGTGGCTCA
65851	63938	TAGGCCGGGCGCGGTGGCTC
65852	63939	ATAGGCCGGGCGCGGTGGCT
65853	63940	AATAGGCCGGGCGCGGTGGC
65854	63941	AAATAGGCCGGGCGCGGTGG
65855	63942	GAAATAGGCCGGGCGCGGTG
65856	63943	GGAAATAGGCCGGGCGCGGT
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65858	63945	TGGGAAATAGGCCGGGCGCG
65859	63946	TTGGGAAATAGGCCGGGCGC
65860	63947	ATTGGGAAATAGGCCGGGCG
65861	63948	CATTGGGAAATAGGCCGGGC
65862	63949	ACATTGGGAAATAGGCCGGG
65863	63950	AACATTGGGAAATAGGCCGG
65864	63951	TAACATTGGGAAATAGGCCG
65865	63952	TTAACATTGGGAAATAGGCC
65866	63953	ATTAACATTGGGAAATAGGC
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65868	63955	AGATTAACATTGGGAAATAG
65869	63956	TAGATTAACATTGGGAAATA
65870	63957	GTAGATTAACATTGGGAAAT
65871	63958	AGTAGATTAACATTGGGAAA
65872	63959	AAGTAGATTAACATTGGGAA
65873	63960	TAAGTAGATTAACATTGGGA
65874	63961	ATAAGTAGATTAACATTGGG
65875	63962	AATAAGTAGATTAACATTGG
65876	63963	CAATAAGTAGATTAACATTG
65877	63964	TCAATAAGTAGATTAACATT
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65883	63970	AGTAGGTCAATAAGTAGATT
65884	63971	TAGTAGGTCAATAAGTAGAT
65885	63972	TTAGTAGGTCAATAAGTAGA
65886	63973	CTTAGTAGGTCAATAAGTAG
65887	63974	GCTTAGTAGGTCAATAAGTA
65888	63975	AGCTTAGTAGGTCAATAAGT
65889	63976	CAGCTTAGTAGGTCAATAAG
65890	63977	CCAGCTTAGTAGGTCAATAA
65891	63978	GCCAGCTTAGTAGGTCAATA
65892	63979	TGCCAGCTTAGTAGGTCAAT
65893	63980	ATGCCAGCTTAGTAGGTCAA
65894	63981	CATGCCAGCTTAGTAGGTCA
65895	63982	ACATGCCAGCTTAGTAGGTC
65896	63983	AACATGCCAGCTTAGTAGGT

114973	113060	TTTTTAATGTTTAAAAAGTA
114974	113061	TTTTTTAATGTTTAAAAAGT
114975	113062	TTTTTTTAATGTTTAAAAAG
114976	113063	CTTTTTTTAATGTTTAAAAA
114977	113064	CCTTTTTTTAATGTTTAAAA
114978	113065	ACCTTTTTTTAATGTTTAAA
114979	113066	GACCTTTTTTTAATGTTTAA
114980	113067	AGACCTTTTTTTAATGTTTA
114981	113068	AAGACCTTTTTTTAATGTTT
114982	113069	AAAGACCTTTTTTTAATGTT
114983	113070	CAAAGACCTTTTTTTAATGT
114984	113071	ACAAAGACCTTTTTTTAATG
114985	113072	AACAAAGACCTTTTTTTAAT
114986	113073	AAACAAAGACCTTTTTTTAA
114987	113074	AAAACAAAGACCTTTTTTTA
114988	113075	CAAAACAAAGACCTTTTTTT
114989	113076	ACAAAACAAAGACCTTTTTT
114990	113077	GACAAAACAAAGACCTTTTT
114991	113078	TGACAAAACAAAGACCTTTT
114992	113079	ATGACAAAACAAAGACCTTT
114993	113080	GATGACAAAACAAAGACCTT
114994	113081	TGATGACAAAACAAAGACCT
114995	113082	TTGATGACAAAACAAAGACC
114996	113083	ATTGATGACAAAACAAAGAC
114997	113084	AATTGATGACAAAACAAAGA
114998	113085	TAATTGATGACAAAACAAAG
114999	113086	CTAATTGATGACAAAACAAA
115000	113087	TCTAATTGATGACAAAACAA
115001	113088	ATCTAATTGATGACAAAACA
115002	113089	CATCTAATTGATGACAAAAC
115003	113090	ACATCTAATTGATGACAAAA
115004	113091	CACATCTAATTGATGACAAA
115005	113092	TCACATCTAATTGATGACAA
115006	113093	ATCACATCTAATTGATGACA
115007	113094	GATCACATCTAATTGATGAC
115008	113095	AGATCACATCTAATTGATGA
115009	113096	AAGATCACATCTAATTGATG
115010	113097	CAAGATCACATCTAATTGAT
115011	113098	CCAAGATCACATCTAATTGA
115012	113099	CCCAAGATCACATCTAATTG
115013	113100	GCCCAAGATCACATCTAATT
115014	113101	TGCCCAAGATCACATCTAAT
115015	113102	TTGCCCAAGATCACATCTAA
115016	113103	TTTGCCCAAGATCACATCTA
115017	113104	ATTTGCCCAAGATCACATCT
115018	113105	GATTTGCCCAAGATCACATC
115019	113106	AGATTTGCCCAAGATCACAT
115020	113107	AAGATTTGCCCAAGATCACA
115021	113108	AAAGATTTGCCCAAGATCAC
115022	113109	CAAAGATTTGCCCAAGATCA
115023	113110	TCAAAGATTTGCCCAAGATC
115024	113111	TTCAAAGATTTGCCCAAGAT
115025	113112	ATTCAAAGATTTGCCCAAGA
115026	113113	AATTCAAAGATTTGCCCAAG
115027	113114	AAATTCAAAGATTTGCCCAA
115028	113115	GAAATTCAAAGATTTGCCCA
115029	113116	AGAAATTCAAAGATTTGCCC
115030	113117	GAGAAATTCAAAGATTTGCC
115031	113118	AGAGAAATTCAAAGATTTGC
115032	113119	CAGAGAAATTCAAAGATTTG
115033	113120	TCAGAGAAATTCAAAGATTT
115034	113121	GTCAGAGAAATTCAAAGATT
115035	113122	GGTCAGAGAAATTCAAAGAT
115036	113123	GGGTCAGAGAAATTCAAAGA
115037	113124	TGGGTCAGAGAAATTCAAAG
115038	113125	CTGGGTCAGAGAAATTCAAA
115039	113126	TCTGGGTCAGAGAAATTCAA
115040	113127	TTCTGGGTCAGAGAAATTCA
115041	113128	ATTCTGGGTCAGAGAAATTC
115042	113129	AATTCTGGGTCAGAGAAATT
115043	113130	AAATTCTGGGTCAGAGAAAT

16750	14837	AATTAGCCAGGCATGGTGGA
16751	14838	AAATTAGCCAGGCATGGTGG
16752	14839	AAAATTAGCCAGGCATGGTG
16753	14840	CAAAATTAGCCAGGCATGGT
16754	14841	ACAAAATTAGCCAGGCATGG
16755	14842	TACAAAATTAGCCAGGCATG
16756	14843	ATACAAAATTAGCCAGGCAT
16757	14844	AATACAAAATTAGCCAGGCA
16758	14845	AAATACAAAATTAGCCAGGC
16759	14846	TAAATACAAAATTAGCCAGG
16760	14847	CTAAATACAAAATTAGCCAG
16761	14848	ACTAAATACAAAATTAGCCA
16762	14849	AACTAAATACAAAATTAGCC
16763	14850	AAACTAAATACAAAATTAGC
16764	14851	AAAACTAAATACAAAATTAG
16765	14852	TAAAACTAAATACAAAATTA
16766	14853	CTAAAACTAAATACAAAATT
16767	14854	ACTAAAACTAAATACAAAAT
16768	14855	TACTAAAACTAAATACAAAA
16769	14856	CTACTAAAACTAAATACAAA
16770	14857	TCTACTAAAACTAAATACAA
16771	14858	CTCTACTAAAACTAAATACA
16772	14859	TCTCTACTAAAACTAAATAC
16773	14860	ATCTCTACTAAAACTAAATA
16774	14861	CATCTCTACTAAAACTAAAT
16775	14862	CCATCTCTACTAAAACTAAA
16776	14863	CCCATCTCTACTAAAACTAA
16777	14864	CCCCATCTCTACTAAAACTA
16778	14865	ACCCCATCTCTACTAAAACT
16779	14866	AACCCCATCTCTACTAAAAC
16780	14867	AAACCCCATCTCTACTAAAA
16781	14868	GAAACCCCATCTCTACTAAA
16782	14869	AGAAACCCCATCTCTACTAA
16783	14870	GAGAAACCCCATCTCTACTA
16784	14871	GGAGAAACCCCATCTCTACT
16785	14872	TGGAGAAACCCCATCTCTAC
16786	14873	ATGGAGAAACCCCATCTCTA
16787	14874	CATGGAGAAACCCCATCTCT
16788	14875	ACATGGAGAAACCCCATCTC
16789	14876	AACATGGAGAAACCCCATCT
16790	14877	CAACATGGAGAAACCCCATC
16791	14878	CCAACATGGAGAAACCCCAT
16792	14879	ACCAACATGGAGAAACCCCA
16793	14880	GACCAACATGGAGAAACCCC
16794	14881	TGACCAACATGGAGAAACCC
16795	14882	CTGACCAACATGGAGAAACC
16796	14883	CCTGACCAACATGGAGAAAC
16797	14884	GCCTGACCAACATGGAGAAA
16798	14885	AGCCTGACCAACATGGAGAA
16799	14886	CAGCCTGACCAACATGGAGA
16800	14887	CCAGCCTGACCAACATGGAG
16801	14888	ACCAGCCTGACCAACATGGA
16802	14889	GACCAGCCTGACCAACATGG
16803	14890	AGACCAGCCTGACCAACATG
16804	14891	AAGACCAGCCTGACCAACAT
16805	14892	CAAGACCAGCCTGACCAACA
16806	14893	TCAAGACCAGCCTGACCAAC
16807	14894	TTCAAGACCAGCCTGACCAA
16808	14895	GTTCAAGACCAGCCTGACCA
16809	14896	AGTTCAAGACCAGCCTGACC
16810	14897	GAGTTCAAGACCAGCCTGAC
16811	14898	GGAGTTCAAGACCAGCCTGA
16812	14899	AGGAGTTCAAGACCAGCCTG
16813	14900	CAGGAGTTCAAGACCAGCCT
16814	14901	TCAGGAGTTCAAGACCAGCC
16815	14902	GTCAGGAGTTCAAGACCAGC
16816	14903	GGTCAGGAGTTCAAGACCAG
16817	14904	AGGTCAGGAGTTCAAGACCA
16818	14905	GAGGTCAGGAGTTCAAGACC
16819	14906	TGAGGTCAGGAGTTCAAGAC
16820	14907	CTGAGGTCAGGAGTTCAAGA

65897	63984	GAACATGCCAGCTTAGTAGG
65898	63985	AGAACATGCCAGCTTAGTAG
65899	63986	CAGAACATGCCAGCTTAGTA
65900	63987	ACAGAACATGCCAGCTTAGT
65901	63988	CACAGAACATGCCAGCTTAG
65902	63989	ACACAGAACATGCCAGCTTA
65903	63990	CACACAGAACATGCCAGCTT
65904	63991	ACACACAGAACATGCCAGCT
65905	63992	AACACACAGAACATGCCAGC
65906	63993	TAACACACAGAACATGCCAG
65907	63994	CTAACACACAGAACATGCCA
65908	63995	TCTAACACACAGAACATGCC
65909	63996	GTCTAACACACAGAACATGC
65910	63997	TGTCTAACACACAGAACATG
65911	63998	ATGTCTAACACACAGAACAT
65912	63999	GATGTCTAACACACAGAACA
65913	64000	TGATGTCTAACACACAGAAC
65914	64001	GTGATGTCTAACACACAGAA
65915	64002	GGTGATGTCTAACACACAGA
65916	64003	TGGTGATGTCTAACACACAG
65917	64004	TTGGTGATGTCTAACACACA
65918	64005	GTTGGTGATGTCTAACACAC
65919	64006	AGTTGGTGATGTCTAACACA
65920	64007	AAGTTGGTGATGTCTAACAC
65921	64008	AAAGTTGGTGATGTCTAACA
65922	64009	CAAAGTTGGTGATGTCTAAC
65923	64010	ACAAAGTTGGTGATGTCTAA
65924	64011	CACAAAGTTGGTGATGTCTA
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65926	64013	GGCACAAAGTTGGTGATGTC
65927	64014	AGGCACAAAGTTGGTGATGT
65928	64015	AAGGCACAAAGTTGGTGATG
65929	64016	GAAGGCACAAAGTTGGTGAT
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65931	64018	AAGAAGGCACAAAGTTGGTG
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65933	64020	AAAAGAAGGCACAAAGTTGG
65934	64021	AAAAAGAAGGCACAAAGTTG
65935	64022	AAAAAAGAAGGCACAAAGTT
65936	64023	AAAAAAAGAAGGCACAAAGT
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65938	64025	ACAAAAAAAGAAGGCACAAA
65939	64026	AACAAAAAAAGAAGGCACAA
65940	64027	AAACAAAAAAAGAAGGCACA
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65942	64029	ACAAACAAAAAAAGAAGGCA
65943	64030	AACAAACAAAAAAAGAAGGC
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65945	64032	AAAACAAACAAAAAAAGAAG
65946	64033	AAAAACAAACAAAAAAAGAA
65947	64034	CAAAAACAAACAAAAAAAGA
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65950	64037	ACTCAAAAACAAACAAAAAA
65951	64038	AACTCAAAAACAAACAAAAA
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65955	64042	CTCCAACTCAAAAACAAACA
65956	64043	ACTCCAACTCAAAAACAAAC
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65959	64046	GAGACTCCAACTCAAAAACA
65960	64047	TGAGACTCCAACTCAAAAAC
65961	64048	GTGAGACTCCAACTCAAAAA
65962	64049	AGTGAGACTCCAACTCAAAA
65963	64050	GAGTGAGACTCCAACTCAAA
65964	64051	AGAGTGAGACTCCAACTCAA
65965	64052	CAGAGTGAGACTCCAACTCA
65966	64053	ACAGAGTGAGACTCCAACTC
65967	64054	AACAGAGTGAGACTCCAACT

115044	113131	CAAATTCTGGGTCAGAGAAA
115045	113132	TCAAATTCTGGGTCAGAGAA
115046	113133	GTCAAATTCTGGGTCAGAGA
115047	113134	CGTCAAATTCTGGGTCAGAG
115048	113135	TCGTCAAATTCTGGGTCAGA
115049	113136	ATCGTCAAATTCTGGGTCAG
115050	113137	CATCGTCAAATTCTGGGTCA
115051	113138	CCATCGTCAAATTCTGGGTC
115052	113139	ACCATCGTCAAATTCTGGGT
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115054	113141	CAACCATCGTCAAATTCTGG
115055	113142	CCAACCATCGTCAAATTCTG
115056	113143	GCCAACCATCGTCAAATTCT
115057	113144	AGCCAACCATCGTCAAATTC
115058	113145	TAGCCAACCATCGTCAAATT
115059	113146	CTAGCCAACCATCGTCAAAT
115060	113147	GCTAGCCAACCATCGTCAAA
115061	113148	AGCTAGCCAACCATCGTCAA
115062	113149	TAGCTAGCCAACCATCGTCA
115063	113150	CTAGCTAGCCAACCATCGTC
115064	113151	CCTAGCTAGCCAACCATCGT
115065	113152	GCCTAGCTAGCCAACCATCG
115066	113153	AGCCTAGCTAGCCAACCATC
115067	113154	CAGCCTAGCTAGCCAACCAT
115068	113155	ACAGCCTAGCTAGCCAACCA
115069	113156	GACAGCCTAGCTAGCCAACC
115070	113157	TGACAGCCTAGCTAGCCAAC
115071	113158	CTGACAGCCTAGCTAGCCAA
115072	113159	CCTGACAGCCTAGCTAGCCA
115073	113160	ACCTGACAGCCTAGCTAGCC
115074	113161	AACCTGACAGCCTAGCTAGC
115075	113162	AAACCTGACAGCCTAGCTAG
115076	113163	TAAACCTGACAGCCTAGCTA
115077	113164	ATAAACCTGACAGCCTAGCT
115078	113165	TATAAACCTGACAGCCTAGC
115079	113166	CTATAAACCTGACAGCCTAG
115080	113167	TCTATAAACCTGACAGCCTA
115081	113168	ATCTATAAACCTGACAGCCT
115082	113169	TATCTATAAACCTGACAGCC
115083	113170	GTATCTATAAACCTGACAGC
115084	113171	CGTATCTATAAACCTGACAG
115085	113172	ACGTATCTATAAACCTGACA
115086	113173	GACGTATCTATAAACCTGAC
115087	113174	GGACGTATCTATAAACCTGA
115088	113175	AGGACGTATCTATAAACCTG
115089	113176	GAGGACGTATCTATAAACCT
115090	113177	AGAGGACGTATCTATAAACC
115091	113178	CAGAGGACGTATCTATAAAC
115092	113179	GCAGAGGACGTATCTATAAA
115093	113180	TGCAGAGGACGTATCTATAA
115094	113181	GTGCAGAGGACGTATCTATA
115095	113182	GGTGCAGAGGACGTATCTAT
115096	113183	AGGTGCAGAGGACGTATCTA
115097	113184	CAGGTGCAGAGGACGTATCT
115098	113185	TCAGGTGCAGAGGACGTATC
115099	113186	CTCAGGTGCAGAGGACGTAT
115100	113187	CCTCAGGTGCAGAGGACGTA
115101	113188	CCCTCAGGTGCAGAGGACGT
115102	113189	ACCCTCAGGTGCAGAGGACG
115103	113190	AACCCTCAGGTGCAGAGGAC
115104	113191	AAACCCTCAGGTGCAGAGGA
115105	113192	AAAACCCTCAGGTGCAGAGG
115106	113193	CAAAACCCTCAGGTGCAGAG
115107	113194	GCAAAACCCTCAGGTGCAGA
115108	113195	TGCAAAACCCTCAGGTGCAG
115109	113196	ATGCAAAACCCTCAGGTGCA
115110	113197	GATGCAAAACCCTCAGGTGC
115111	113198	TGATGCAAAACCCTCAGGTG
115112	113199	GTGATGCAAAACCCTCAGGT
115113	113200	AGTGATGCAAAACCCTCAGG
115114	113201	CAGTGATGCAAAACCCTCAG

16821	14908	CCTGAGGTCAGGAGTTCAAG
16822	14909	ACCTGAGGTCAGGAGTTCAA
16823	14910	CACCTGAGGTCAGGAGTTCA
16824	14911	TCACCTGAGGTCAGGAGTTC
16825	14912	ATCACCTGAGGTCAGGAGTT
16826	14913	GATCACCTGAGGTCAGGAGT
16827	14914	GGATCACCTGAGGTCAGGAG
16828	14915	TGGATCACCTGAGGTCAGGA
16829	14916	GTGGATCACCTGAGGTCAGG
16830	14917	AGTGGATCACCTGAGGTCAG
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16835	14922	AGGCAAGTGGATCACCTGAG
16836	14923	GAGGCAAGTGGATCACCTGA
16837	14924	CGAGGCAAGTGGATCACCTG
16838	14925	CCGAGGCAAGTGGATCACCT
16839	14926	GCCGAGGCAAGTGGATCACC
16840	14927	GGCCGAGGCAAGTGGATCAC
16841	14928	AGGCCGAGGCAAGTGGATCA
16842	14929	GAGGCCGAGGCAAGTGGATC
16843	14930	GGAGGCCGAGGCAAGTGGAT
16844	14931	GGGAGGCCGAGGCAAGTGGA
16845	14932	TGGGAGGCCGAGGCAAGTGG
16846	14933	TTGGGAGGCCGAGGCAAGTG
16847	14934	TTTGGGAGGCCGAGGCAAGT
16848	14935	CTTTGGGAGGCCGAGGCAAG
16849	14936	ACTTTGGGAGGCCGAGGCAA
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16854	14941	CCAGCACTTTGGGAGGCCGA
16855	14942	CCCAGCACTTTGGGAGGCCG
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16863	14950	CCTGTATCCCCAGCACTTTG
16864	14951	GCCTGTATCCCCAGCACTTT
16865	14952	TGCCTGTATCCCCAGCACTT
16866	14953	ATGCCTGTATCCCCAGCACT
16867	14954	CATGCCTGTATCCCCAGCAC
16868	14955	TCATGCCTGTATCCCCAGCA
16869	14956	TTCATGCCTGTATCCCCAGC
16870	14957	GTTCATGCCTGTATCCCCAG
16871	14958	GGTTCATGCCTGTATCCCCA
16872	14959	GGGTTCATGCCTGTATCCCC
16873	14960	GGGGTTCATGCCTGTATCCC
16874	14961	AGGGGTTCATGCCTGTATCC
16875	14962	CAGGGGTTCATGCCTGTATC
16876	14963	ACAGGGGTTCATGCCTGTAT
16877	14964	CACAGGGGTTCATGCCTGTA
16878	14965	GCACAGGGGTTCATGCCTGT
16879	14966	GGCACAGGGGTTCATGCCTG
16880	14967	GGGCACAGGGGTTCATGCCT
16881	14968	CGGGCACAGGGGTTCATGCC
16882	14969	CCGGGCACAGGGGTTCATGC
16883	14970	GCCGGGCACAGGGGTTCATG
16884	14971	GGCCGGGCACAGGGGTTCAT
16885	14972	AGGCCGGGCACAGGGGTTCA
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16888	14975	ATTAGGCCGGGCACAGGGGT
16889	14976	AATTAGGCCGGGCACAGGGG
16890	14977	AAATTAGGCCGGGCACAGGG
16891	14978	AAAATTAGGCCGGGCACAGG

65968	64055	CAACAGAGTGAGACTCCAAC
65969	64056	GCAACAGAGTGAGACTCCAA
65970	64057	GGCAACAGAGTGAGACTCCA
65971	64058	GGGCAACAGAGTGAGACTCC
65972	64059	TGGGCAACAGAGTGAGACTC
65973	64060	CTGGGCAACAGAGTGAGACT
65974	64061	CCTGGGCAACAGAGTGAGAC
65975	64062	ACCTGGGCAACAGAGTGAGA
65976	64063	AACCTGGGCAACAGAGTGAG
65977	64064	CAACCTGGGCAACAGAGTGA
65978	64065	CCAACCTGGGCAACAGAGTG
65979	64066	TCCAACCTGGGCAACAGAGT
65980	64067	CTCCAACCTGGGCAACAGAG
65981	64068	ACTCCAACCTGGGCAACAGA
65982	64069	CACTCCAACCTGGGCAACAG
65983	64070	GCACTCCAACCTGGGCAACA
65984	64071	TGCACTCCAACCTGGGCAAC
65985	64072	CTGCACTCCAACCTGGGCAA
65986	64073	ACTGCACTCCAACCTGGGCA
65987	64074	CACTGCACTCCAACCTGGGC
65988	64075	CCACTGCACTCCAACCTGGG
65989	64076	GCCACTGCACTCCAACCTGG
65990	64077	CGCCACTGCACTCCAACCTG
65991	64078	GCGCCACTGCACTCCAACCT
65992	64079	CGCGCCACTGCACTCCAACC
65993	64080	TCGCGCCACTGCACTCCAAC
65994	64081	ATCGCGCCACTGCACTCCAA
65995	64082	GATCGCGCCACTGCACTCCA
65996	64083	AGATCGCGCCACTGCACTCC
65997	64084	AAGATCGCGCCACTGCACTC
65998	64085	CAAGATCGCGCCACTGCACT
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66003	64090	TGAGCCAAGATCGCGCCACT
66004	64091	GTGAGCCAAGATCGCGCCAC
66005	64092	GGTGAGCCAAGATCGCGCCA
66006	64093	TGGTGAGCCAAGATCGCGCC
66007	64094	GTGGTGAGCCAAGATCGCGC
66008	64095	TGTGGTGAGCCAAGATCGCG
66009	64096	TTGTGGTGAGCCAAGATCGC
66010	64097	GTTGTGGTGAGCCAAGATCG
66011	64098	GGTTGTGGTGAGCCAAGATC
66012	64099	AGGTTGTGGTGAGCCAAGAT
66013	64100	GAGGTTGTGGTGAGCCAAGA
66014	64101	AGAGGTTGTGGTGAGCCAAG
66015	64102	CAGAGGTTGTGGTGAGCCAA
66016	64103	GCAGAGGTTGTGGTGAGCCA
66017	64104	GGCAGAGGTTGTGGTGAGCC
66018	64105	AGGCAGAGGTTGTGGTGAGC
66019	64106	GAGGCAGAGGTTGTGGTGAG
66020	64107	GGAGGCAGAGGTTGTGGTGA
66021	64108	GGGAGGCAGAGGTTGTGGTG
66022	64109	CGGGAGGCAGAGGTTGTGGT
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66027	64114	GAACCCGGGAGGCAGAGGTT
66028	64115	GGAACCCGGGAGGCAGAGGT
66029	64116	TGGAACCCGGGAGGCAGAGG
66030	64117	CTGGAACCCGGGAGGCAGAG
66031	64118	ACTGGAACCCGGGAGGCAGA
66032	64119	CACTGGAACCCGGGAGGCAG
66033	64120	TCACTGGAACCCGGGAGGCA
66034	64121	ATCACTGGAACCCGGGAGGC
66035	64122	AATCACTGGAACCCGGGAGG
66036	64123	GAATCACTGGAACCCGGGAG
66037	64124	AGAATCACTGGAACCCGGGA
66038	64125	GAGAATCACTGGAACCCGGG

115115	113202	CCAGTGATGCAAAACCCTCA
115116	113203	TCCAGTGATGCAAAACCCTC
115117	113204	ATCCAGTGATGCAAAACCCT
115118	113205	AATCCAGTGATGCAAAACCC
115119	113206	GAATCCAGTGATGCAAAACC
115120	113207	TGAATCCAGTGATGCAAAAC
115121	113208	TTGAATCCAGTGATGCAAAA
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115123	113210	GGTTGAATCCAGTGATGCAA
115124	113211	TGGTTGAATCCAGTGATGCA
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115130	113217	CATGGTTGGTTGAATCCAGT
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115132	113219	TCCATGGTTGGTTGAATCCA
115133	113220	ATCCATGGTTGGTTGAATCC
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115135	113222	TGATCCATGGTTGGTTGAAT
115136	113223	TTGATCCATGGTTGGTTGAA
115137	113224	TTTGATCCATGGTTGGTTGA
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115139	113226	TTTTTGATCCATGGTTGGTT
115140	113227	GTTTTTGATCCATGGTTGGT
115141	113228	TGTTTTTGATCCATGGTTGG
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115144	113231	CTATGTTTTTGATCCATGGT
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115146	113233	AACTATGTTTTTGATCCATG
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115153	113240	TTATCCTAACTATGTTTTTG
115154	113241	ATTATCCTAACTATGTTTTT
115155	113242	GATTATCCTAACTATGTTTT
115156	113243	AGATTATCCTAACTATGTTT
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115159	113246	TATAGATTATCCTAACTATG
115160	113247	GTATAGATTATCCTAACTAT
115161	113248	AGTATAGATTATCCTAACTA
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115163	113250	TCAGTATAGATTATCCTAAC
115164	113251	TTCAGTATAGATTATCCTAA
115165	113252	GTTCAGTATAGATTATCCTA
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115167	113254	GTGTTCAGTATAGATTATCC
115168	113255	TGTGTTCAGTATAGATTATC
115169	113256	ATGTGTTCAGTATAGATTAT
115170	113257	CATGTGTTCAGTATAGATTA
115171	113258	GCATGTGTTCAGTATAGATT
115172	113259	TGCATGTGTTCAGTATAGAT
115173	113260	CTGCATGTGTTCAGTATAGA
115174	113261	TCTGCATGTGTTCAGTATAG
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115176	113263	CGTCTGCATGTGTTCAGTAT
115177	113264	ACGTCTGCATGTGTTCAGTA
115178	113265	AACGTCTGCATGTGTTCAGT
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115180	113267	GAAACGTCTGCATGTGTTCA
115181	113268	GGAAACGTCTGCATGTGTTC
115182	113269	AGGAAACGTCTGCATGTGTT
115183	113270	AAGGAAACGTCTGCATGTGT
115184	113271	CAAGGAAACGTCTGCATGTG
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16892	14979	AAAAATTAGGCCGGGCACAG
16893	14980	CAAAAATTAGGCCGGGCACA
16894	14981	ACAAAAATTAGGCCGGGCAC
16895	14982	TACAAAAATTAGGCCGGGCA
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16899	14986	AAAATACAAAAATTAGGCCG
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16905	14992	CTACTAAAAATACAAAAATT
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16907	14994	CTCTACTAAAAATACAAAAA
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16910	14997	CATCTCTACTAAAAATACAA
16911	14998	CCATCTCTACTAAAAATACA
16912	14999	CCCATCTCTACTAAAAATAC
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16915	15002	AACCCCATCTCTACTAAAAA
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16917	15004	GAAACCCCATCTCTACTAAA
16918	15005	TGAAACCCCATCTCTACTAA
16919	15006	GTGAAACCCCATCTCTACTA
16920	15007	GGTGAAACCCCATCTCTACT
16921	15008	TGGTGAAACCCCATCTCTAC
16922	15009	ATGGTGAAACCCCATCTCTA
16923	15010	CATGGTGAAACCCCATCTCT
16924	15011	ACATGGTGAAACCCCATCTC
16925	15012	AACATGGTGAAACCCCATCT
16926	15013	CAACATGGTGAAACCCCATC
16927	15014	CCAACATGGTGAAACCCCAT
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16929	15016	GGCCAACATGGTGAAACCCC
16930	15017	TGGCCAACATGGTGAAACCC
16931	15018	CTGGCCAACATGGTGAAACC
16932	15019	CCTGGCCAACATGGTGAAAC
16933	15020	TCCTGGCCAACATGGTGAAA
16934	15021	ATCCTGGCCAACATGGTGAA
16935	15022	TATCCTGGCCAACATGGTGA
16936	15023	CTATCCTGGCCAACATGGTG
16937	15024	ACTATCCTGGCCAACATGGT
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16939	15026	AGACTATCCTGGCCAACATG
16940	15027	AAGACTATCCTGGCCAACAT
16941	15028	CAAGACTATCCTGGCCAACA
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16946	15033	GAGATCAAGACTATCCTGGC
16947	15034	AGAGATCAAGACTATCCTGG
16948	15035	AAGAGATCAAGACTATCCTG
16949	15036	CAAGAGATCAAGACTATCCT
16950	15037	TCAAGAGATCAAGACTATCC
16951	15038	GTCAAGAGATCAAGACTATC
16952	15039	GGTCAAGAGATCAAGACTAT
16953	15040	AGGTCAAGAGATCAAGACTA
16954	15041	GAGGTCAAGAGATCAAGACT
16955	15042	CGAGGTCAAGAGATCAAGAC
16956	15043	ACGAGGTCAAGAGATCAAGA
16957	15044	TACGAGGTCAAGAGATCAAG
16958	15045	TTACGAGGTCAAGAGATCAA
16959	15046	ATTACGAGGTCAAGAGATCA
16960	15047	GATTACGAGGTCAAGAGATC
16961	15048	AGATTACGAGGTCAAGAGAT
16962	15049	CAGATTACGAGGTCAAGAGA

66039	64126	GGAGAATCACTGGAACCCGG
66040	64127	AGGAGAATCACTGGAACCCG
66041	64128	CAGGAGAATCACTGGAACCC
66042	64129	GCAGGAGAATCACTGGAACC
66043	64130	GGCAGGAGAATCACTGGAAC
66044	64131	AGGCAGGAGAATCACTGGAA
66045	64132	CAGGCAGGAGAATCACTGGA
66046	64133	TCAGGCAGGAGAATCACTGG
66047	64134	CTCAGGCAGGAGAATCACTG
66048	64135	GCTCAGGCAGGAGAATCACT
66049	64136	GGCTCAGGCAGGAGAATCAC
66050	64137	AGGCTCAGGCAGGAGAATCA
66051	64138	GAGGCTCAGGCAGGAGAATC
66052	64139	GGAGGCTCAGGCAGGAGAAT
66053	64140	GGGAGGCTCAGGCAGGAGAA
66054	64141	CGGGAGGCTCAGGCAGGAGA
66055	64142	TCGGGAGGCTCAGGCAGGAG
66056	64143	CTCGGGAGGCTCAGGCAGGA
66057	64144	TCTCGGGAGGCTCAGGCAGG
66058	64145	TTCTCGGGAGGCTCAGGCAG
66059	64146	CTTCTCGGGAGGCTCAGGCA
66060	64147	GCTTCTCGGGAGGCTCAGGC
66061	64148	AGCTTCTCGGGAGGCTCAGG
66062	64149	CAGCTTCTCGGGAGGCTCAG
66063	64150	TCAGCTTCTCGGGAGGCTCA
66064	64151	CTCAGCTTCTCGGGAGGCTC
66065	64152	TCTCAGCTTCTCGGGAGGCT
66066	64153	GTCTCAGCTTCTCGGGAGGC
66067	64154	CGTCTCAGCTTCTCGGGAGG
66068	64155	TCGTCTCAGCTTCTCGGGAG
66069	64156	GTCGTCTCAGCTTCTCGGGA
66070	64157	TGTCGTCTCAGCTTCTCGGG
66071	64158	CTGTCGTCTCAGCTTCTCGG
66072	64159	CCTGTCGTCTCAGCTTCTCG
66073	64160	GCCTGTCGTCTCAGCTTCTC
66074	64161	CGCCTGTCGTCTCAGCTTCT
66075	64162	GCGCCTGTCGTCTCAGCTTC
66076	64163	CGCGCCTGTCGTCTCAGCTT
66077	64164	GCGCGCCTGTCGTCTCAGCT
66078	64165	CGCGCGCCTGTCGTCTCAGC
66079	64166	GCGCGCGCCTGTCGTCTCAG
66080	64167	GGCGCGCGCCTGTCGTCTCA
66081	64168	TGGCGCGCGCCTGTCGTCTC
66082	64169	GTGGCGCGCGCCTGTCGTCT
66083	64170	GGTGGCGCGCGCCTGTCGTC
66084	64171	TGGTGGCGCGCGCCTGTCGT
66085	64172	ATGGTGGCGCGCGCCTGTCG
66086	64173	CATGGTGGCGCGCGCCTGTC
66087	64174	GCATGGTGGCGCGCGCCTGT
66088	64175	GGCATGGTGGCGCGCGCCTG
66089	64176	GGGCATGGTGGCGCGCGCCT
66090	64177	AGGGCATGGTGGCGCGCGCC
66091	64178	CAGGGCATGGTGGCGCGCGC
66092	64179	GCAGGGCATGGTGGCGCGCG
66093	64180	AGCAGGGCATGGTGGCGCGC
66094	64181	TAGCAGGGCATGGTGGCGCG
66095	64182	TTAGCAGGGCATGGTGGCGC
66096	64183	GTTAGCAGGGCATGGTGGCG
66097	64184	AGTTAGCAGGGCATGGTGGC
66098	64185	AAGTTAGCAGGGCATGGTGG
66099	64186	AAAGTTAGCAGGGCATGGTG
66100	64187	AAAAGTTAGCAGGGCATGGT
66101	64188	CAAAAGTTAGCAGGGCATGG
66102	64189	ACAAAAGTTAGCAGGGCATG
66103	64190	TACAAAAGTTAGCAGGGCAT
66104	64191	ATACAAAAGTTAGCAGGGCA
66105	64192	AATACAAAAGTTAGCAGGGC
66106	64193	AAATACAAAAGTTAGCAGGG
66107	64194	AAAATACAAAAGTTAGCAGG
66108	64195	AAAAATACAAAAGTTAGCAG
66109	64196	TAAAAATACAAAAGTTAGCA

115186	113273	GACAAGGAAACGTCTGCATG
115187	113274	TGACAAGGAAACGTCTGCAT
115188	113275	ATGACAAGGAAACGTCTGCA
115189	113276	AATGACAAGGAAACGTCTGC
115190	113277	TAATGACAAGGAAACGTCTG
115191	113278	ATAATGACAAGGAAACGTCT
115192	113279	AATAATGACAAGGAAACGTC
115193	113280	GAATAATGACAAGGAAACGT
115194	113281	GGAATAATGACAAGGAAACG
115195	113282	TGGAATAATGACAAGGAAAC
115196	113283	TTGGAATAATGACAAGGAAA
115197	113284	TTTGGAATAATGACAAGGAA
115198	113285	TTTTGGAATAATGACAAGGA
115199	113286	GTTTTGGAATAATGACAAGG
115200	113287	TGTTTTGGAATAATGACAAG
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115213	113300	TGCTTTACTGTATTGTTTTG
115214	113301	ATGCTTTACTGTATTGTTTT
115215	113302	AATGCTTTACTGTATTGTTT
115216	113303	AAATGCTTTACTGTATTGTT
115217	113304	TAAATGCTTTACTGTATTGT
115218	113305	GTAAATGCTTTACTGTATTG
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115220	113307	AGGTAAATGCTTTACTGTAT
115221	113308	AAGGTAAATGCTTTACTGTA
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115224	113311	AACAAGGTAAATGCTTTACT
115225	113312	AAACAAGGTAAATGCTTTAC
115226	113313	AAAACAAGGTAAATGCTTTA
115227	113314	TAAAACAAGGTAAATGCTTT
115228	113315	CTAAAACAAGGTAAATGCTT
115229	113316	CCTAAAACAAGGTAAATGCT
115230	113317	ACCTAAAACAAGGTAAATGC
115231	113318	TACCTAAAACAAGGTAAATG
115232	113319	ATACCTAAAACAAGGTAAAT
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115235	113322	ATAATACCTAAAACAAGGTA
115236	113323	TATAATACCTAAAACAAGGT
115237	113324	TTATAATACCTAAAACAAGG
115238	113325	TTTATAATACCTAAAACAAG
115239	113326	ATTTATAATACCTAAAACAA
115240	113327	TATTTATAATACCTAAAACA
115241	113328	TTATTTATAATACCTAAAAC
115242	113329	ATTATTTATAATACCTAAAA
115243	113330	GATTATTTATAATACCTAAA
115244	113331	AGATTATTTATAATACCTAA
115245	113332	TAGATTATTTATAATACCTA
115246	113333	CTAGATTATTTATAATACCT
115247	113334	TCTAGATTATTTATAATACC
115248	113335	CTCTAGATTATTTATAATAC
115249	113336	TCTCTAGATTATTTATAATA
115250	113337	ATCTCTAGATTATTTATAAT
115251	113338	CATCTCTAGATTATTTATAA
115252	113339	TCATCTCTAGATTATTTATA
115253	113340	ATCATCTCTAGATTATTTAT
115254	113341	CATCATCTCTAGATTATTTA
115255	113342	ACATCATCTCTAGATTATTT
115256	113343	TACATCATCTCTAGATTATT

16963	15050	GCAGATTACGAGGTCAAGAG
16964	15051	GGCAGATTACGAGGTCAAGA
16965	15052	GGGCAGATTACGAGGTCAAG
16966	15053	TGGGCAGATTACGAGGTCAA
16967	15054	GTGGGCAGATTACGAGGTCA
16968	15055	GGTGGGCAGATTACGAGGTC
16969	15056	AGGTGGGCAGATTACGAGGT
16970	15057	GAGGTGGGCAGATTACGAGG
16971	15058	CGAGGTGGGCAGATTACGAG
16972	15059	TCGAGGTGGGCAGATTACGA
16973	15060	GTCGAGGTGGGCAGATTACG
16974	15061	AGTCGAGGTGGGCAGATTAC
16975	15062	GAGTCGAGGTGGGCAGATTA
16976	15063	GGAGTCGAGGTGGGCAGATT
16977	15064	GGGAGTCGAGGTGGGCAGAT
16978	15065	TGGGAGTCGAGGTGGGCAGA
16979	15066	TTGGGAGTCGAGGTGGGCAG
16980	15067	TTTGGGAGTCGAGGTGGGCA
16981	15068	CTTTGGGAGTCGAGGTGGGC
16982	15069	ACTTTGGGAGTCGAGGTGGG
16983	15070	CACTTTGGGAGTCGAGGTGG
16984	15071	GCACTTTGGGAGTCGAGGTG
16985	15072	AGCACTTTGGGAGTCGAGGT
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16993	15080	GTAATCCCAGCACTTTGGGA
16994	15081	TGTAATCCCAGCACTTTGGG
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16996	15083	CCTGTAATCCCAGCACTTTG
16997	15084	ACCTGTAATCCCAGCACTTT
16998	15085	CACCTGTAATCCCAGCACTT
16999	15086	ACACCTGTAATCCCAGCACT
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17001	15088	TCACACCTGTAATCCCAGCA
17002	15089	CTCACACCTGTAATCCCAGC
17003	15090	GCTCACACCTGTAATCCCAG
17004	15091	GGCTCACACCTGTAATCCCA
17005	15092	TGGCTCACACCTGTAATCCC
17006	15093	GTGGCTCACACCTGTAATCC
17007	15094	AGTGGCTCACACCTGTAATC
17008	15095	CAGTGGCTCACACCTGTAAT
17009	15096	GCAGTGGCTCACACCTGTAA
17010	15097	TGCAGTGGCTCACACCTGTA
17011	15098	GTGCAGTGGCTCACACCTGT
17012	15099	GGTGCAGTGGCTCACACCTG
17013	15100	GGGTGCAGTGGCTCACACCT
17014	15101	TGGGTGCAGTGGCTCACACC
17015	15102	CTGGGTGCAGTGGCTCACAC
17016	15103	GCTGGGTGCAGTGGCTCACA
17017	15104	AGCTGGGTGCAGTGGCTCAC
17018	15105	CAGCTGGGTGCAGTGGCTCA
17019	15106	GCAGCTGGGTGCAGTGGCTC
17020	15107	GGCAGCTGGGTGCAGTGGCT
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17022	15109	TTGGCAGCTGGGTGCAGTGG
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17025	15112	TTCTTGGCAGCTGGGTGCAG
17026	15113	ATTCTTGGCAGCTGGGTGCA
17027	15114	AATTCTTGGCAGCTGGGTGC
17028	15115	CAATTCTTGGCAGCTGGGTG
17029	15116	ACAATTCTTGGCAGCTGGGT
17030	15117	AACAATTCTTGGCAGCTGGG
17031	15118	AAACAATTCTTGGCAGCTGG
17032	15119	AAAACAATTCTTGGCAGCTG
17033	15120	TAAAACAATTCTTGGCAGCT

66110	64197	CTAAAAATACAAAAGTTAGC
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66112	64199	TACTAAAAATACAAAAGTTA
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66114	64201	TCTACTAAAAATACAAAAGT
66115	64202	CTCTACTAAAAATACAAAAG
66116	64203	TCTCTACTAAAAATACAAAA
66117	64204	ATCTCTACTAAAAATACAAA
66118	64205	CATCTCTACTAAAAATACAA
66119	64206	CCATCTCTACTAAAAATACA
66120	64207	CCCATCTCTACTAAAAATAC
66121	64208	ACCCATCTCTACTAAAAATA
66122	64209	AACCCATCTCTACTAAAAAT
66123	64210	AAACCCATCTCTACTAAAAA
66124	64211	GAAACCCATCTCTACTAAAA
66125	64212	TGAAACCCATCTCTACTAAA
66126	64213	GTGAAACCCATCTCTACTAA
66127	64214	AGTGAAACCCATCTCTACTA
66128	64215	CAGTGAAACCCATCTCTACT
66129	64216	ACAGTGAAACCCATCTCTAC
66130	64217	CACAGTGAAACCCATCTCTA
66131	64218	ACACAGTGAAACCCATCTCT
66132	64219	AACACAGTGAAACCCATCTC
66133	64220	AAACACAGTGAAACCCATCT
66134	64221	GAAACACAGTGAAACCCATC
66135	64222	GGAAACACAGTGAAACCCAT
66136	64223	GGGAAACACAGTGAAACCCA
66137	64224	TGGGAAACACAGTGAAACCC
66138	64225	CTGGGAAACACAGTGAAACC
66139	64226	CCTGGGAAACACAGTGAAAC
66140	64227	GCCTGGGAAACACAGTGAAA
66141	64228	AGCCTGGGAAACACAGTGAA
66142	64229	CAGCCTGGGAAACACAGTGA
66143	64230	CCAGCCTGGGAAACACAGTG
66144	64231	ACCAGCCTGGGAAACACAGT
66145	64232	GACCAGCCTGGGAAACACAG
66146	64233	AGACCAGCCTGGGAAACACA
66147	64234	GAGACCAGCCTGGGAAACAC
66148	64235	CGAGACCAGCCTGGGAAACA
66149	64236	TCGAGACCAGCCTGGGAAAC
66150	64237	TTCGAGACCAGCCTGGGAAA
66151	64238	GTTCGAGACCAGCCTGGGAA
66152	64239	AGTTCGAGACCAGCCTGGGA
66153	64240	GAGTTCGAGACCAGCCTGGG
66154	64241	GGAGTTCGAGACCAGCCTGG
66155	64242	AGGAGTTCGAGACCAGCCTG
66156	64243	CAGGAGTTCGAGACCAGCCT
66157	64244	TCAGGAGTTCGAGACCAGCC
66158	64245	GTCAGGAGTTCGAGACCAGC
66159	64246	GGTCAGGAGTTCGAGACCAG
66160	64247	AGGTCAGGAGTTCGAGACCA
66161	64248	AAGGTCAGGAGTTCGAGACC
66162	64249	CAAGGTCAGGAGTTCGAGAC
66163	64250	ACAAGGTCAGGAGTTCGAGA
66164	64251	CACAAGGTCAGGAGTTCGAG
66165	64252	TCACAAGGTCAGGAGTTCGA
66166	64253	ATCACAAGGTCAGGAGTTCG
66167	64254	GATCACAAGGTCAGGAGTTC
66168	64255	GGATCACAAGGTCAGGAGTT
66169	64256	TGGATCACAAGGTCAGGAGT
66170	64257	GTGGATCACAAGGTCAGGAG
66171	64258	GGTGGATCACAAGGTCAGGA
66172	64259	AGGTGGATCACAAGGTCAGG
66173	64260	CAGGTGGATCACAAGGTCAG
66174	64261	GCAGGTGGATCACAAGGTCA
66175	64262	GGCAGGTGGATCACAAGGTC
66176	64263	AGGCAGGTGGATCACAAGGT
66177	64264	AAGGCAGGTGGATCACAAGG
66178	64265	CAAGGCAGGTGGATCACAAG
66179	64266	CCAAGGCAGGTGGATCACAA
66180	64267	CCCAAGGCAGGTGGATCACA

115257	113344	TTACATCATCTCTAGATTAT
115258	113345	TTTACATCATCTCTAGATTA
115259	113346	CTTTACATCATCTCTAGATT
115260	113347	ACTTTACATCATCTCTAGAT
115261	113348	TACTTTACATCATCTCTAGA
115262	113349	ATACTTTACATCATCTCTAG
115263	113350	TATACTTTACATCATCTCTA
115264	113351	ATATACTTTACATCATCTCT
115265	113352	TATATACTTTACATCATCTC
115266	113353	CTATATACTTTACATCATCT
115267	113354	CCTATATACTTTACATCATC
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115272	113359	ATCCTCCTATATACTTTACA
115273	113360	TATCCTCCTATATACTTTAC
115274	113361	ATATCCTCCTATATACTTTA
115275	113362	CATATCCTCCTATATACTTT
115276	113363	GCATATCCTCCTATATACTT
115277	113364	TGCATATCCTCCTATATACT
115278	113365	ATGCATATCCTCCTATATAC
115279	113366	TATGCATATCCTCCTATATA
115280	113367	CTATGCATATCCTCCTATAT
115281	113368	CCTATGCATATCCTCCTATA
115282	113369	ACCTATGCATATCCTCCTAT
115283	113370	AACCTATGCATATCCTCCTA
115284	113371	CAACCTATGCATATCCTCCT
115285	113372	ACAACCTATGCATATCCTCC
115286	113373	TACAACCTATGCATATCCTC
115287	113374	ATACAACCTATGCATATCCT
115288	113375	CATACAACCTATGCATATCC
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115291	113378	TCGCATACAACCTATGCATA
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115294	113381	TATTCGCATACAACCTATGC
115295	113382	GTATTCGCATACAACCTATG
115296	113383	AGTATTCGCATACAACCTAT
115297	113384	TAGTATTCGCATACAACCTA
115298	113385	GTAGTATTCGCATACAACCT
115299	113386	TGTAGTATTCGCATACAACC
115300	113387	ATGTAGTATTCGCATACAAC
115301	113388	CATGTAGTATTCGCATACAA
115302	113389	TCATGTAGTATTCGCATACA
115303	113390	ATCATGTAGTATTCGCATAC
115304	113391	AATCATGTAGTATTCGCATA
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115306	113393	AAAATCATGTAGTATTCGCA
115307	113394	TAAAATCATGTAGTATTCGC
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115310	113397	ACATAAAATCATGTAGTATT
115311	113398	TACATAAAATCATGTAGTAT
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115313	113400	CTTACATAAAATCATGTAGT
115314	113401	CCTTACATAAAATCATGTAG
115315	113402	CCCTTACATAAAATCATGTA
115316	113403	TCCCTTACATAAAATCATGT
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115318	113405	AGTCCCTTACATAAAATCAT
115319	113406	AAGTCCCTTACATAAAATCA
115320	113407	CAAGTCCCTTACATAAAATC
115321	113408	TCAAGTCCCTTACATAAAAT
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115323	113410	GCTCAAGTCCCTTACATAAA
115324	113411	TGCTCAAGTCCCTTACATAA
115325	113412	ATGCTCAAGTCCCTTACATA
115326	113413	AATGCTCAAGTCCCTTACAT
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17034	15121	TTAAAACAATTCTTGGCAGC
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17036	15123	GCTTAAAACAATTCTTGGCA
17037	15124	AGCTTAAAACAATTCTTGGC
17038	15125	AAGCTTAAAACAATTCTTGG
17039	15126	AAAGCTTAAAACAATTCTTG
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17041	15128	CCAAAGCTTAAAACAATTCT
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17046	15133	TCAAACCAAAGCTTAAAACA
17047	15134	CTCAAACCAAAGCTTAAAAC
17048	15135	ACTCAAACCAAAGCTTAAAA
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17052	15139	ATTAACTCAAACCAAAGCTT
17053	15140	CATTAACTCAAACCAAAGCT
17054	15141	ACATTAACTCAAACCAAAGC
17055	15142	TACATTAACTCAAACCAAAG
17056	15143	ATACATTAACTCAAACCAAA
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17058	15145	ATATACATTAACTCAAACCA
17059	15146	TATATACATTAACTCAAACC
17060	15147	ATATATACATTAACTCAAAC
17061	15148	TATATATACATTAACTCAAA
17062	15149	GTATATATACATTAACTCAA
17063	15150	GGTATATATACATTAACTCA
17064	15151	CGGTATATATACATTAACTC
17065	15152	GCGGTATATATACATTAACT
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17069	15156	CAATGCGGTATATATACATT
17070	15157	ACAATGCGGTATATATACAT
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17073	15160	ATTACAATGCGGTATATATA
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17075	15162	GAATTACAATGCGGTATATA
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17077	15164	TTGAATTACAATGCGGTATA
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17085	15172	ATTACATTTTGAATTACAAT
17086	15173	AATTACATTTTGAATTACAA
17087	15174	AAATTACATTTTGAATTACA
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17089	15176	AAAAATTACATTTTGAATTA
17090	15177	CAAAAATTACATTTTGAATT
17091	15178	CCAAAAATTACATTTTGAAT
17092	15179	GCCAAAAATTACATTTTGAA
17093	15180	GGCCAAAAATTACATTTTGA
17094	15181	TGGCCAAAAATTACATTTTG
17095	15182	TTGGCCAAAAATTACATTTT
17096	15183	GTTGGCCAAAAATTACATTT
17097	15184	AGTTGGCCAAAAATTACATT
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17099	15186	AGAGTTGGCCAAAAATTACA
17100	15187	CAGAGTTGGCCAAAAATTAC
17101	15188	CCAGAGTTGGCCAAAAATTA
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17103	15190	GCCCAGAGTTGGCCAAAAAT
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66181	64268	GCCCAAGGCAGGTGGATCAC
66182	64269	AGCCCAAGGCAGGTGGATCA
66183	64270	GAGCCCAAGGCAGGTGGATC
66184	64271	GGAGCCCAAGGCAGGTGGAT
66185	64272	GGGAGCCCAAGGCAGGTGGA
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66187	64274	TTGGGAGCCCAAGGCAGGTG
66188	64275	TTTGGGAGCCCAAGGCAGGT
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66190	64277	AATTTGGGAGCCCAAGGCAG
66191	64278	CAATTTGGGAGCCCAAGGCA
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66195	64282	CCAGCAATTTGGGAGCCCAA
66196	64283	CCCAGCAATTTGGGAGCCCA
66197	64284	TCCCAGCAATTTGGGAGCCC
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66199	64286	AATCCCAGCAATTTGGGAGC
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66206	64293	CGCCTGTAATCCCAGCAATT
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66208	64295	CACGCCTGTAATCCCAGCAA
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66212	64299	GGCTCACGCCTGTAATCCCA
66213	64300	TGGCTCACGCCTGTAATCCC
66214	64301	GTGGCTCACGCCTGTAATCC
66215	64302	GGTGGCTCACGCCTGTAATC
66216	64303	CGGTGGCTCACGCCTGTAAT
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66219	64306	CCGCGGTGGCTCACGCCTGT
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66221	64308	GGCCGCGGTGGCTCACGCCT
66222	64309	GGGCCGCGGTGGCTCACGCC
66223	64310	GGGGCCGCGGTGGCTCACGC
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66225	64312	AGGGGGCCGCGGTGGCTCAC
66226	64313	CAGGGGGCCGCGGTGGCTCA
66227	64314	ACAGGGGGCCGCGGTGGCTC
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66234	64321	AGAAGGCACAGGGGGCCGCG
66235	64322	AAGAAGGCACAGGGGGCCGC
66236	64323	GAAGAAGGCACAGGGGGCCG
66237	64324	AGAAGAAGGCACAGGGGGCC
66238	64325	AAGAAGAAGGCACAGGGGGC
66239	64326	AAAGAAGAAGGCACAGGGGG
66240	64327	AAAAGAAGAAGGCACAGGGG
66241	64328	TAAAAGAAGAAGGCACAGGG
66242	64329	GTAAAAGAAGAAGGCACAGG
66243	64330	AGTAAAAGAAGAAGGCACAG
66244	64331	GAGTAAAAGAAGAAGGCACA
66245	64332	GGAGTAAAAGAAGAAGGCAC
66246	64333	AGGAGTAAAAGAAGAAGGCA
66247	64334	CAGGAGTAAAAGAAGAAGGC
66248	64335	CCAGGAGTAAAAGAAGAAGG
66249	64336	TCCAGGAGTAAAAGAAGAAG
66250	64337	ATCCAGGAGTAAAAGAAGAA
66251	64338	AATCCAGGAGTAAAAGAAGA

115328	113415	GGAATGCTCAAGTCCCTTAC
115329	113416	TGGAATGCTCAAGTCCCTTA
115330	113417	TTGGAATGCTCAAGTCCCTT
115331	113418	CTTGGAATGCTCAAGTCCCT
115332	113419	TCTTGGAATGCTCAAGTCCC
115333	113420	GTCTTGGAATGCTCAAGTCC
115334	113421	AGTCTTGGAATGCTCAAGTC
115335	113422	AAGTCTTGGAATGCTCAAGT
115336	113423	AAAGTCTTGGAATGCTCAAG
115337	113424	CAAAGTCTTGGAATGCTCAA
115338	113425	CCAAAGTCTTGGAATGCTCA
115339	113426	ACCAAAGTCTTGGAATGCTC
115340	113427	TACCAAAGTCTTGGAATGCT
115341	113428	ATACCAAAGTCTTGGAATGC
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115343	113430	AGATACCAAAGTCTTGGAAT
115344	113431	AAGATACCAAAGTCTTGGAA
115345	113432	GAAGATACCAAAGTCTTGGA
115346	113433	TGAAGATACCAAAGTCTTGG
115347	113434	GTGAAGATACCAAAGTCTTG
115348	113435	TGTGAAGATACCAAAGTCTT
115349	113436	CTGTGAAGATACCAAAGTCT
115350	113437	CCTGTGAAGATACCAAAGTC
115351	113438	CCCTGTGAAGATACCAAAGT
115352	113439	ACCCTGTGAAGATACCAAAG
115353	113440	TACCCTGTGAAGATACCAAA
115354	113441	GTACCCTGTGAAGATACCAA
115355	113442	AGTACCCTGTGAAGATACCA
115356	113443	CAGTACCCTGTGAAGATACC
115357	113444	ACAGTACCCTGTGAAGATAC
115358	113445	TACAGTACCCTGTGAAGATA
115359	113446	TTACAGTACCCTGTGAAGAT
115360	113447	GTTACAGTACCCTGTGAAGA
115361	113448	GGTTACAGTACCCTGTGAAG
115362	113449	TGGTTACAGTACCCTGTGAA
115363	113450	TTGGTTACAGTACCCTGTGA
115364	113451	ATTGGTTACAGTACCCTGTG
115365	113452	GATTGGTTACAGTACCCTGT
115366	113453	GGATTGGTTACAGTACCCTG
115367	113454	GGGATTGGTTACAGTACCCT
115368	113455	GGGGATTGGTTACAGTACCC
115369	113456	GGGGGATTGGTTACAGTACC
115370	113457	TGGGGGATTGGTTACAGTAC
115371	113458	GTGGGGGATTGGTTACAGTA
115372	113459	TGTGGGGGATTGGTTACAGT
115373	113460	CTGTGGGGGATTGGTTACAG
115374	113461	TCTGTGGGGGATTGGTTACA
115375	113462	ATCTGTGGGGGATTGGTTAC
115376	113463	TATCTGTGGGGGATTGGTTA
115377	113464	GTATCTGTGGGGGATTGGTT
115378	113465	AGTATCTGTGGGGGATTGGT
115379	113466	TAGTATCTGTGGGGGATTGG
115380	113467	TTAGTATCTGTGGGGGATTG
115381	113468	CTTAGTATCTGTGGGGGATT
115382	113469	TCTTAGTATCTGTGGGGGAT
115383	113470	CTCTTAGTATCTGTGGGGGA
115384	113471	TCTCTTAGTATCTGTGGGGG
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115386	113473	CATCTCTTAGTATCTGTGGG
115387	113474	TCATCTCTTAGTATCTGTGG
115388	113475	GTCATCTCTTAGTATCTGTG
115389	113476	AGTCATCTCTTAGTATCTGT
115390	113477	CAGTCATCTCTTAGTATCTG
115391	113478	ACAGTCATCTCTTAGTATCT
115392	113479	TACAGTCATCTCTTAGTATC
115393	113480	GTACAGTCATCTCTTAGTAT
115394	113481	AGTACAGTCATCTCTTAGTA
115395	113482	TAGTACAGTCATCTCTTAGT
115396	113483	ATAGTACAGTCATCTCTTAG
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115398	113485	CAATAGTACAGTCATCTCTT

17105	15192	GTGCCCAGAGTTGGCCAAAA
17106	15193	TGTGCCCAGAGTTGGCCAAA
17107	15194	ATGTGCCCAGAGTTGGCCAA
17108	15195	AATGTGCCCAGAGTTGGCCA
17109	15196	CAATGTGCCCAGAGTTGGCC
17110	15197	GCAATGTGCCCAGAGTTGGC
17111	15198	GGCAATGTGCCCAGAGTTGG
17112	15199	AGGCAATGTGCCCAGAGTTG
17113	15200	TAGGCAATGTGCCCAGAGTT
17114	15201	ATAGGCAATGTGCCCAGAGT
17115	15202	CATAGGCAATGTGCCCAGAG
17116	15203	CCATAGGCAATGTGCCCAGA
17117	15204	TCCATAGGCAATGTGCCCAG
17118	15205	GTCCATAGGCAATGTGCCCA
17119	15206	AGTCCATAGGCAATGTGCCC
17120	15207	TAGTCCATAGGCAATGTGCC
17121	15208	CTAGTCCATAGGCAATGTGC
17122	15209	ACTAGTCCATAGGCAATGTG
17123	15210	GACTAGTCCATAGGCAATGT
17124	15211	GGACTAGTCCATAGGCAATG
17125	15212	AGGACTAGTCCATAGGCAAT
17126	15213	CAGGACTAGTCCATAGGCAA
17127	15214	GCAGGACTAGTCCATAGGCA
17128	15215	AGCAGGACTAGTCCATAGGC
17129	15216	GAGCAGGACTAGTCCATAGG
17130	15217	AGAGCAGGACTAGTCCATAG
17131	15218	CAGAGCAGGACTAGTCCATA
17132	15219	GCAGAGCAGGACTAGTCCAT
17133	15220	GGCAGAGCAGGACTAGTCCA
17134	15221	TGGCAGAGCAGGACTAGTCC
17135	15222	GTGGCAGAGCAGGACTAGTC
17136	15223	CGTGGCAGAGCAGGACTAGT
17137	15224	TCGTGGCAGAGCAGGACTAG
17138	15225	CTCGTGGCAGAGCAGGACTA
17139	15226	GCTCGTGGCAGAGCAGGACT
17140	15227	TGCTCGTGGCAGAGCAGGAC
17141	15228	CTGCTCGTGGCAGAGCAGGA
17142	15229	GCTGCTCGTGGCAGAGCAGG
17143	15230	TGCTGCTCGTGGCAGAGCAG
17144	15231	TTGCTGCTCGTGGCAGAGCA
17145	15232	GTTGCTGCTCGTGGCAGAGC
17146	15233	TGTTGCTGCTCGTGGCAGAG
17147	15234	CTGTTGCTGCTCGTGGCAGA
17148	15235	ACTGTTGCTGCTCGTGGCAG
17149	15236	AACTGTTGCTGCTCGTGGCA
17150	15237	GAACTGTTGCTGCTCGTGGC
17151	15238	TGAACTGTTGCTGCTCGTGG
17152	15239	TTGAACTGTTGCTGCTCGTG
17153	15240	ATTGAACTGTTGCTGCTCGT
17154	15241	CATTGAACTGTTGCTGCTCG
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17156	15243	TTCATTGAACTGTTGCTGCT
17157	15244	ATTCATTGAACTGTTGCTGC
17158	15245	AATTCATTGAACTGTTGCTG
17159	15246	AAATTCATTGAACTGTTGCT
17160	15247	AAAATTCATTGAACTGTTGC
17161	15248	AAAAATTCATTGAACTGTTG
17162	15249	AAAAAATTCATTGAACTGTT
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17170	15257	AAAAAAAAAAAAAATTCATT
17171	15258	AAAAAAAAAAAAAAATTCAT
17172	15259	AAAAAAAAAAAAAAAATTCA
17173	15260	AAAAAAAAAAAAAAAAATTC
17174	15261	AAAAAAAAAAAAAAAAAATT
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66252	64339	AAATCCAGGAGTAAAAGAAG
66253	64340	TAAATCCAGGAGTAAAAGAA
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66255	64342	ATTAAATCCAGGAGTAAAAG
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66259	64346	TGGGATTAAATCCAGGAGTA
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66261	64348	GTTGGGATTAAATCCAGGAG
66262	64349	CGTTGGGATTAAATCCAGGA
66263	64350	ACGTTGGGATTAAATCCAGG
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66265	64352	TCACGTTGGGATTAAATCCA
66266	64353	TTCACGTTGGGATTAAATCC
66267	64354	CTTCACGTTGGGATTAAATC
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66274	64361	GTAGATTCTTCACGTTGGGA
66275	64362	GGTAGATTCTTCACGTTGGG
66276	64363	AGGTAGATTCTTCACGTTGG
66277	64364	AAGGTAGATTCTTCACGTTG
66278	64365	TAAGGTAGATTCTTCACGTT
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66281	64368	TAGTAAGGTAGATTCTTCAC
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66299	64386	AGTATCTAAAACTCTAGTTA
66300	64387	AAGTATCTAAAACTCTAGTT
66301	64388	AAAGTATCTAAAACTCTAGT
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66320	64407	ATGTGGGCTTGGTTTTGAAA
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66322	64409	AGATGTGGGCTTGGTTTTGA

115399	113486	ACAATAGTACAGTCATCTCT
115400	113487	AACAATAGTACAGTCATCTC
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115403	113490	AATAACAATAGTACAGTCAT
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115410	113497	GTCGAATAATAACAATAGTA
115411	113498	AGTCGAATAATAACAATAGT
115412	113499	CAGTCGAATAATAACAATAG
115413	113500	TCAGTCGAATAATAACAATA
115414	113501	CTCAGTCGAATAATAACAAT
115415	113502	TCTCAGTCGAATAATAACAA
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115420	113507	TATGATCTCAGTCGAATAAT
115421	113508	TTATGATCTCAGTCGAATAA
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115428	113515	TATCTTCTTATGATCTCAGT
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115431	113518	ATATATCTTCTTATGATCTC
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115435	113522	ATAAATATATCTTCTTATGA
115436	113523	AATAAATATATCTTCTTATG
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115438	113525	AAAATAAATATATCTTCTTA
115439	113526	AAAAATAAATATATCTTCTT
115440	113527	TAAAAATAAATATATCTTCT
115441	113528	TTAAAAATAAATATATCTTC
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115445	113532	AAAATTAAAAATAAATATAT
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115456	113543	AAGTGTTTTTAAAAATTAAA
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115458	113545	GGAAGTGTTTTTAAAAATTA
115459	113546	TGGAAGTGTTTTTAAAAATT
115460	113547	ATGGAAGTGTTTTTAAAAAT
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115464	113551	ACTGATGGAAGTGTTTTTAA
115465	113552	AACTGATGGAAGTGTTTTTA
115466	113553	AAACTGATGGAAGTGTTTTT
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17176	15263	AAAAAAAAAAAAAAAAAAA
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17201	15288	GACCCTGTCTCAAAAAAAA
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17207	15294	GACAGAGACCCTGTCTCAA
17208	15295	TGACAGAGACCCTGTCTCA
17209	15296	GTGACAGAGACCCTGTCTC
17210	15297	GGTGACAGAGACCCTGTCT
17211	15298	TGGTGACAGAGACCCTGTC
17212	15299	TTGGTGACAGAGACCCTGT
17213	15300	CTTGGTGACAGAGACCCTG
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17216	15303	AGCCTTGGTGACAGAGACC
17217	15304	TAGCCTTGGTGACAGAGAC
17218	15305	CTAGCCTTGGTGACAGAGA
17219	15306	TCTAGCCTTGGTGACAGAG
17220	15307	TTCTAGCCTTGGTGACAGA
17221	15308	ATTCTAGCCTTGGTGACAG
17222	15309	CATTCTAGCCTTGGTGACA
17223	15310	ACATTCTAGCCTTGGTGAC
17224	15311	TACATTCTAGCCTTGGTGA
17225	15312	CTACATTCTAGCCTTGGTG
17226	15313	ACTACATTCTAGCCTTGGT
17227	15314	CACTACATTCTAGCCTTGG
17228	15315	CCACTACATTCTAGCCTTG
17229	15316	ACCACTACATTCTAGCCTT
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17232	15319	TGCACCACTACATTCTAGC
17233	15320	CTGCACCACTACATTCTAG
17234	15321	ACTGCACCACTACATTCTA
17235	15322	GACTGCACCACTACATTCT
17236	15323	AGACTGCACCACTACATTC
17237	15324	GAGACTGCACCACTACATT
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17243	15330	TGAGCCGAGACTGCACCAC
17244	15331	GTGAGCCGAGACTGCACCA
17245	15332	AGTGAGCCGAGACTGCACC
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66323	64410	CAGATGTGGGCTTGGTTTTG
66324	64411	ACAGATGTGGGCTTGGTTTT
66325	64412	GACAGATGTGGGCTTGGTTT
66326	64413	GGACAGATGTGGGCTTGGTT
66327	64414	AGGACAGATGTGGGCTTGGT
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66331	64418	AAAAAGGACAGATGTGGGCT
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66344	64431	CAGAGAAGACTCTAAAAAGG
66345	64432	TCAGAGAAGACTCTAAAAAG
66346	64433	GTCAGAGAAGACTCTAAAAA
66347	64434	GGTCAGAGAAGACTCTAAAA
66348	64435	AGGTCAGAGAAGACTCTAAA
66349	64436	AAGGTCAGAGAAGACTCTAA
66350	64437	GAAGGTCAGAGAAGACTCTA
66351	64438	GGAAGGTCAGAGAAGACTCT
66352	64439	GGGAAGGTCAGAGAAGACTC
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66368	64455	CAAACCACAATGAGCAGGGA
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66391	64478	GCCATTGTTACAGGCAATAA
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115506	113593	CAATTAAAAAATATTAAAAA
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115512	113599	CTTTGTCAATTAAAAAATAT
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115514	113601	AACTTTGTCAATTAAAAAAT
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115516	113603	AAAACTTTGTCAATTAAAAA
115517	113604	TAAAACTTTGTCAATTAAAA
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115521	113608	AACTTAAAACTTTGTCAATT
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115524	113611	AGGAACTTAAAACTTTGTCA
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115528	113615	CAGTAGGAACTTAAAACTTT
115529	113616	TCAGTAGGAACTTAAAACTT
115530	113617	TTCAGTAGGAACTTAAAACT
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115535	113622	AATGTTTCAGTAGGAACTTA
115536	113623	AAATGTTTCAGTAGGAACTT
115537	113624	AAAATGTTTCAGTAGGAACT
115538	113625	AAAAATGTTTCAGTAGGAAC
115539	113626	AAAAAATGTTTCAGTAGGAA
115540	113627	GAAAAAATGTTTCAGTAGGA

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17249	15336	TTGCAGTGAGCCGAGACTGC
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17251	15338	GGTTGCAGTGAGCCGAGACT
17252	15339	AGGTTGCAGTGAGCCGAGAC
17253	15340	GAGGTTGCAGTGAGCCGAGA
17254	15341	AGAGGTTGCAGTGAGCCGAG
17255	15342	CAGAGGTTGCAGTGAGCCGA
17256	15343	ACAGAGGTTGCAGTGAGCCG
17257	15344	AACAGAGGTTGCAGTGAGCC
17258	15345	AAACAGAGGTTGCAGTGAGC
17259	15346	GAAACAGAGGTTGCAGTGAG
17260	15347	GGAAACAGAGGTTGCAGTGA
17261	15348	AGGAAACAGAGGTTGCAGTG
17262	15349	CAGGAAACAGAGGTTGCAGT
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17264	15351	CCCAGGAAACAGAGGTTGCA
17265	15352	GCCCAGGAAACAGAGGTTGC
17266	15353	AGCCCAGGAAACAGAGGTTG
17267	15354	GAGCCCAGGAAACAGAGGTT
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17269	15356	TTGAGCCCAGGAAACAGAGG
17270	15357	CTTGAGCCCAGGAAACAGAG
17271	15358	GCTTGAGCCCAGGAAACAGA
17272	15359	CGCTTGAGCCCAGGAAACAG
17273	15360	TCGCTTGAGCCCAGGAAACA
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66416	64503	TTAATTTAAAATGTAAAGTT
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66448	64535	TTTCTCAACAAATAAATACA
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66461	64548	CAGAGAGAGACCCTTTCTCA
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115578	113665	CAAAAACACAGCACATAAAT
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115618	113705	CTAATTTTACTTGCTTTAAC
115619	113706	TCTAATTTTACTTGCTTTAA
115620	113707	TTCTAATTTTACTTGCTTTA
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115622	113709	CTTTCTAATTTTACTTGCTT
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115676	113763	ATCTCAAGGTAACAGATGAA
115677	113764	TATCTCAAGGTAACAGATGA
115678	113765	TTATCTCAAGGTAACAGATG
115679	113766	ATTATCTCAAGGTAACAGAT
115680	113767	AATTATCTCAAGGTAACAGA
115681	113768	CAATTATCTCAAGGTAACAG
115682	113769	TCAATTATCTCAAGGTAACA

17389	15476	CAAGACTAGCCTGAACAACA
17390	15477	TCAAGACTAGCCTGAACAAC
17391	15478	TTCAAGACTAGCCTGAACAA
17392	15479	GTTCAAGACTAGCCTGAACA
17393	15480	AGTTCAAGACTAGCCTGAAC
17394	15481	GAGTTCAAGACTAGCCTGAA
17395	15482	AGAGTTCAAGACTAGCCTGA
17396	15483	CAGAGTTCAAGACTAGCCTG
17397	15484	CCAGAGTTCAAGACTAGCCT
17398	15485	TCCAGAGTTCAAGACTAGCC
17399	15486	CTCCAGAGTTCAAGACTAGC
17400	15487	GCTCCAGAGTTCAAGACTAG
17401	15488	AGCTCCAGAGTTCAAGACTA
17402	15489	GAGCTCCAGAGTTCAAGACT
17403	15490	TGAGCTCCAGAGTTCAAGAC
17404	15491	CTGAGCTCCAGAGTTCAAGA
17405	15492	TCTGAGCTCCAGAGTTCAAG
17406	15493	ATCTGAGCTCCAGAGTTCAA
17407	15494	CATCTGAGCTCCAGAGTTCA
17408	15495	TCATCTGAGCTCCAGAGTTC
17409	15496	ATCATCTGAGCTCCAGAGTT
17410	15497	GATCATCTGAGCTCCAGAGT
17411	15498	GGATCATCTGAGCTCCAGAG
17412	15499	TGGATCATCTGAGCTCCAGA
17413	15500	GTGGATCATCTGAGCTCCAG
17414	15501	GGTGGATCATCTGAGCTCCA
17415	15502	GGGTGGATCATCTGAGCTCC
17416	15503	TGGGTGGATCATCTGAGCTC
17417	15504	GTGGGTGGATCATCTGAGCT
17418	15505	GGTGGGTGGATCATCTGAGC
17419	15506	AGGTGGGTGGATCATCTGAG
17420	15507	AAGGTGGGTGGATCATCTGA
17421	15508	CAAGGTGGGTGGATCATCTG
17422	15509	CCAAGGTGGGTGGATCATCT
17423	15510	ACCAAGGTGGGTGGATCATC
17424	15511	CACCAAGGTGGGTGGATCAT
17425	15512	ACACCAAGGTGGGTGGATCA
17426	15513	GACACCAAGGTGGGTGGATC
17427	15514	GGACACCAAGGTGGGTGGAT
17428	15515	TGGACACCAAGGTGGGTGGA
17429	15516	CTGGACACCAAGGTGGGTGG
17430	15517	TCTGGACACCAAGGTGGGTG
17431	15518	TTCTGGACACCAAGGTGGGT
17432	15519	TTTCTGGACACCAAGGTGGG
17433	15520	ATTTCTGGACACCAAGGTGG
17434	15521	CATTTCTGGACACCAAGGTG
17435	15522	GCATTTCTGGACACCAAGGT
17436	15523	AGCATTTCTGGACACCAAGG
17437	15524	CAGCATTTCTGGACACCAAG
17438	15525	CCAGCATTTCTGGACACCAA
17439	15526	CCCAGCATTTCTGGACACCA
17440	15527	TCCCAGCATTTCTGGACACC
17441	15528	ATCCCAGCATTTCTGGACAC
17442	15529	AATCCCAGCATTTCTGGACA
17443	15530	TAATCCCAGCATTTCTGGAC
17444	15531	GTAATCCCAGCATTTCTGGA
17445	15532	TGTAATCCCAGCATTTCTGG
17446	15533	CTGTAATCCCAGCATTTCTG
17447	15534	CCTGTAATCCCAGCATTTCT
17448	15535	CCCTGTAATCCCAGCATTTC
17449	15536	TCCCTGTAATCCCAGCATTT
17450	15537	ATCCCTGTAATCCCAGCATT
17451	15538	CATCCCTGTAATCCCAGCAT
17452	15539	TCATCCCTGTAATCCCAGCA
17453	15540	CTCATCCCTGTAATCCCAGC
17454	15541	GCTCATCCCTGTAATCCCAG
17455	15542	GGCTCATCCCTGTAATCCCA
17456	15543	TGGCTCATCCCTGTAATCCC
17457	15544	GTGGCTCATCCCTGTAATCC
17458	15545	GGTGGCTCATCCCTGTAATC
17459	15546	CGGTGGCTCATCCCTGTAAT

66536	64623	GGCTGAAATGGGAGAACAGC
66537	64624	AGGCTGAAATGGGAGAACAG
66538	64625	GAGGCTGAAATGGGAGAACA
66539	64626	GGAGGCTGAAATGGGAGAAC
66540	64627	GGGAGGCTGAAATGGGAGAA
66541	64628	GGGGAGGCTGAAATGGGAGA
66542	64629	TGGGGAGGCTGAAATGGGAG
66543	64630	ATGGGGAGGCTGAAATGGGA
66544	64631	CATGGGGAGGCTGAAATGGG
66545	64632	GCATGGGGAGGCTGAAATGG
66546	64633	TGCATGGGGAGGCTGAAATG
66547	64634	GTGCATGGGGAGGCTGAAAT
66548	64635	GGTGCATGGGGAGGCTGAAA
66549	64636	TGGTGCATGGGGAGGCTGAA
66550	64637	GTGGTGCATGGGGAGGCTGA
66551	64638	GGTGGTGCATGGGGAGGCTG
66552	64639	GGGTGGTGCATGGGGAGGCT
66553	64640	AGGGTGGTGCATGGGGAGGC
66554	64641	TAGGGTGGTGCATGGGGAGG
66555	64642	GTAGGGTGGTGCATGGGGAG
66556	64643	GGTAGGGTGGTGCATGGGGA
66557	64644	AGGTAGGGTGGTGCATGGGG
66558	64645	CAGGTAGGGTGGTGCATGGG
66559	64646	CCAGGTAGGGTGGTGCATGG
66560	64647	GCCAGGTAGGGTGGTGCATG
66561	64648	AGCCAGGTAGGGTGGTGCAT
66562	64649	TAGCCAGGTAGGGTGGTGCA
66563	64650	TTAGCCAGGTAGGGTGGTGC
66564	64651	ATTAGCCAGGTAGGGTGGTG
66565	64652	AATTAGCCAGGTAGGGTGGT
66566	64653	AAATTAGCCAGGTAGGGTGG
66567	64654	AAAATTAGCCAGGTAGGGTG
66568	64655	AAAAATTAGCCAGGTAGGGT
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66570	64657	AAAAAAATTAGCCAGGTAGG
66571	64658	CAAAAAAATTAGCCAGGTAG
66572	64659	ACAAAAAAATTAGCCAGGTA
66573	64660	AACAAAAAAATTAGCCAGGT
66574	64661	AAACAAAAAAATTAGCCAGG
66575	64662	CAAACAAAAAAATTAGCCAG
66576	64663	ACAAACAAAAAAATTAGCCA
66577	64664	AACAAACAAAAAAATTAGCC
66578	64665	AAACAAACAAAAAAATTAGC
66579	64666	AAAACAAACAAAAAAATTAG
66580	64667	AAAAACAAACAAAAAAATTA
66581	64668	AAAAAACAAACAAAAAAATT
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66583	64670	AAAAAAAACAAACAAAAAAA
66584	64671	TAAAAAAAACAAACAAAAAA
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66588	64675	AAACTAAAAAAAACAAACAA
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66590	64677	CTAAACTAAAAAAAACAAAC
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66592	64679	AACTAAACTAAAAAAAACAA
66593	64680	AAACTAAACTAAAAAAAACA
66594	64681	AAAACTAAACTAAAAAAAAC
66595	64682	AAAAACTAAACTAAAAAAAA
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66598	64685	TACAAAAACTAAACTAAAAA
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66603	64690	GTCTCTACAAAAACTAAACT
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115683	113770	TTCAATTATCTCAAGGTAAC
115684	113771	ATTCAATTATCTCAAGGTAA
115685	113772	AATTCAATTATCTCAAGGTA
115686	113773	AAATTCAATTATCTCAAGGT
115687	113774	TAAATTCAATTATCTCAAGG
115688	113775	ATAAATTCAATTATCTCAAG
115689	113776	AATAAATTCAATTATCTCAA
115690	113777	CAATAAATTCAATTATCTCA
115691	113778	ACAATAAATTCAATTATCTC
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115697	113784	AAAACAACAATAAATTCAAT
115698	113785	AAAAACAACAATAAATTCAA
115699	113786	CAAAAACAACAATAAATTCA
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115701	113788	TACAAAAACAACAATAAATT
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115703	113790	GCTACAAAAACAACAATAAA
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115705	113792	TGGCTACAAAAACAACAATA
115706	113793	TTGGCTACAAAAACAACAAT
115707	113794	TTTGGCTACAAAAACAACAA
115708	113795	CTTTGGCTACAAAAACAACA
115709	113796	GCTTTGGCTACAAAAACAAC
115710	113797	GGCTTTGGCTACAAAAACAA
115711	113798	AGGCTTTGGCTACAAAAACA
115712	113799	AAGGCTTTGGCTACAAAAAC
115713	113800	GAAGGCTTTGGCTACAAAAA
115714	113801	AGAAGGCTTTGGCTACAAAA
115715	113802	TAGAAGGCTTTGGCTACAAA
115716	113803	GTAGAAGGCTTTGGCTACAA
115717	113804	AGTAGAAGGCTTTGGCTACA
115718	113805	TAGTAGAAGGCTTTGGCTAC
115719	113806	GTAGTAGAAGGCTTTGGCTA
115720	113807	GGTAGTAGAAGGCTTTGGCT
115721	113808	GGGTAGTAGAAGGCTTTGGC
115722	113809	GGGGTAGTAGAAGGCTTTGG
115723	113810	TGGGGTAGTAGAAGGCTTTG
115724	113811	TTGGGGTAGTAGAAGGCTTT
115725	113812	GTTGGGGTAGTAGAAGGCTT
115726	113813	AGTTGGGGTAGTAGAAGGCT
115727	113814	AAGTTGGGGTAGTAGAAGGC
115728	113815	GAAGTTGGGGTAGTAGAAGG
115729	113816	TGAAGTTGGGGTAGTAGAAG
115730	113817	GTGAAGTTGGGGTAGTAGAA
115731	113818	GGTGAAGTTGGGGTAGTAGA
115732	113819	AGGTGAAGTTGGGGTAGTAG
115733	113820	GAGGTGAAGTTGGGGTAGTA
115734	113821	CGAGGTGAAGTTGGGGTAGT
115735	113822	CCGAGGTGAAGTTGGGGTAG
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115743	113830	GCTTGAGGCCGAGGTGAAGT
115744	113831	TGCTTGAGGCCGAGGTGAAG
115745	113832	GTGCTTGAGGCCGAGGTGAA
115746	113833	TGTGCTTGAGGCCGAGGTGA
115747	113834	TTGTGCTTGAGGCCGAGGTG
115748	113835	GTTGTGCTTGAGGCCGAGGT
115749	113836	GGTTGTGCTTGAGGCCGAGG
115750	113837	AGGTTGTGCTTGAGGCCGAG
115751	113838	TAGGTTGTGCTTGAGGCCGA
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17460	15547	ACGGTGGCTCATCCCTGTAA
17461	15548	CACGGTGGCTCATCCCTGTA
17462	15549	GCACGGTGGCTCATCCCTGT
17463	15550	GGCACGGTGGCTCATCCCTG
17464	15551	AGGCACGGTGGCTCATCCCT
17465	15552	TAGGCACGGTGGCTCATCCC
17466	15553	CTAGGCACGGTGGCTCATCC
17467	15554	GCTAGGCACGGTGGCTCATC
17468	15555	GGCTAGGCACGGTGGCTCAT
17469	15556	TGGCTAGGCACGGTGGCTCA
17470	15557	TTGGCTAGGCACGGTGGCTC
17471	15558	TTTGGCTAGGCACGGTGGCT
17472	15559	TTTTGGCTAGGCACGGTGGC
17473	15560	TTTTTGGCTAGGCACGGTGG
17474	15561	ATTTTTGGCTAGGCACGGTG
17475	15562	AATTTTTGGCTAGGCACGGT
17476	15563	AAATTTTTGGCTAGGCACGG
17477	15564	AAAATTTTTGGCTAGGCACG
17478	15565	AAAAATTTTTGGCTAGGCAC
17479	15566	AAAAAATTTTTGGCTAGGCA
17480	15567	AAAAAAATTTTTGGCTAGGC
17481	15568	AAAAAAAATTTTTGGCTAGG
17482	15569	AAAAAAAAATTTTTGGCTAG
17483	15570	TAAAAAAAAATTTTTGGCTA
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17485	15572	CTTAAAAAAAAATTTTTGGC
17486	15573	ACTTAAAAAAAAATTTTTGG
17487	15574	TACTTAAAAAAAAATTTTTG
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17506	15593	GACTATATCAATAAAAAATT
17507	15594	TGACTATATCAATAAAAAAT
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17515	15602	AACTTTTTTGACTATATCAA
17516	15603	TAACTTTTTTGACTATATCA
17517	15604	GTAACTTTTTTGACTATATC
17518	15605	AGTAACTTTTTTGACTATAT
17519	15606	CAGTAACTTTTTTGACTATA
17520	15607	GCAGTAACTTTTTTGACTAT
17521	15608	AGCAGTAACTTTTTTGACTA
17522	15609	AAGCAGTAACTTTTTTGACT
17523	15610	AAAGCAGTAACTTTTTTGAC
17524	15611	TAAAGCAGTAACTTTTTTGA
17525	15612	CTAAAGCAGTAACTTTTTTG
17526	15613	TCTAAAGCAGTAACTTTTTT
17527	15614	CTCTAAAGCAGTAACTTTTT
17528	15615	GCTCTAAAGCAGTAACTTTT
17529	15616	GGCTCTAAAGCAGTAACTTT
17530	15617	TGGCTCTAAAGCAGTAACTT

66607	64694	ATCTGTCTCTACAAAAACTA
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66610	64697	GACATCTGTCTCTACAAAAA
66611	64698	AGACATCTGTCTCTACAAAA
66612	64699	GAGACATCTGTCTCTACAAA
66613	64700	TGAGACATCTGTCTCTACAA
66614	64701	GTGAGACATCTGTCTCTACA
66615	64702	AGTGAGACATCTGTCTCTAC
66616	64703	CAGTGAGACATCTGTCTCTA
66617	64704	ACAGTGAGACATCTGTCTCT
66618	64705	CACAGTGAGACATCTGTCTC
66619	64706	ACACAGTGAGACATCTGTCT
66620	64707	AACACAGTGAGACATCTGTC
66621	64708	CAACACAGTGAGACATCTGT
66622	64709	GCAACACAGTGAGACATCTG
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66624	64711	GTGCAACACAGTGAGACATC
66625	64712	TGTGCAACACAGTGAGACAT
66626	64713	CTGTGCAACACAGTGAGACA
66627	64714	CCTGTGCAACACAGTGAGAC
66628	64715	GCCTGTGCAACACAGTGAGA
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66648	64735	AGCCCAGGAGTTCAAGATCA
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66650	64737	TGAGCCCAGGAGTTCAAGAT
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66652	64739	AGTGAGCCCAGGAGTTCAAG
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66674	64761	GGAGGCTGAGATGGGAGGAT
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115754	113841	GGCTAGGTTGTGCTTGAGGC
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115768	113855	ACCCACCATAGATGGGCTAG
115769	113856	GACCCACCATAGATGGGCTA
115770	113857	TGACCCACCATAGATGGGCT
115771	113858	ATGACCCACCATAGATGGGC
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115774	113861	TTGATGACCCACCATAGATG
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115778	113865	GCTGTTGATGACCCACCATA
115779	113866	GGCTGTTGATGACCCACCAT
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115783	113870	AGTTGGCTGTTGATGACCCA
115784	113871	GAGTTGGCTGTTGATGACCC
115785	113872	GGAGTTGGCTGTTGATGACC
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115787	113874	CTGGAGTTGGCTGTTGATGA
115788	113875	ACTGGAGTTGGCTGTTGATG
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115796	113883	GAGTATAAACTGGAGTTGGC
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115798	113885	CTGAGTATAAACTGGAGTTG
115799	113886	GCTGAGTATAAACTGGAGTT
115800	113887	GGCTGAGTATAAACTGGAGT
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115802	113889	CAGGCTGAGTATAAACTGGA
115803	113890	ACAGGCTGAGTATAAACTGG
115804	113891	AACAGGCTGAGTATAAACTG
115805	113892	AAACAGGCTGAGTATAAACT
115806	113893	CAAACAGGCTGAGTATAAAC
115807	113894	ACAAACAGGCTGAGTATAAA
115808	113895	AACAAACAGGCTGAGTATAA
115809	113896	AAACAAACAGGCTGAGTATA
115810	113897	AAAACAAACAGGCTGAGTAT
115811	113898	CAAAACAAACAGGCTGAGTA
115812	113899	GCAAAACAAACAGGCTGAGT
115813	113900	TGCAAAACAAACAGGCTGAG
115814	113901	GTGCAAAACAAACAGGCTGA
115815	113902	GGTGCAAAACAAACAGGCTG
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115817	113904	TTGGTGCAAAACAAACAGGC
115818	113905	TTTGGTGCAAAACAAACAGG
115819	113906	ATTTGGTGCAAAACAAACAG
115820	113907	TATTTGGTGCAAAACAAACA
115821	113908	ATATTTGGTGCAAAACAAAC
115822	113909	CATATTTGGTGCAAAACAAA
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17531	15618	CTGGCTCTAAAGCAGTAACT
17532	15619	TCTGGCTCTAAAGCAGTAAC
17533	15620	CTCTGGCTCTAAAGCAGTAA
17534	15621	TCTCTGGCTCTAAAGCAGTA
17535	15622	TTCTCTGGCTCTAAAGCAGT
17536	15623	TTTCTCTGGCTCTAAAGCAG
17537	15624	GTTTCTCTGGCTCTAAAGCA
17538	15625	CGTTTCTCTGGCTCTAAAGC
17539	15626	GCGTTTCTCTGGCTCTAAAG
17540	15627	TGCGTTTCTCTGGCTCTAAA
17541	15628	CTGCGTTTCTCTGGCTCTAA
17542	15629	ACTGCGTTTCTCTGGCTCTA
17543	15630	TACTGCGTTTCTCTGGCTCT
17544	15631	TTACTGCGTTTCTCTGGCTC
17545	15632	TTTACTGCGTTTCTCTGGCT
17546	15633	TTTTACTGCGTTTCTCTGGC
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17551	15638	AATCCTTTTACTGCGTTTCT
17552	15639	CAATCCTTTTACTGCGTTTC
17553	15640	TCAATCCTTTTACTGCGTTT
17554	15641	CTCAATCCTTTTACTGCGTT
17555	15642	TCTCAATCCTTTTACTGCGT
17556	15643	TTCTCAATCCTTTTACTGCG
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17560	15647	CTCTTTCTCAATCCTTTTAC
17561	15648	ACTCTTTCTCAATCCTTTTA
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17563	15650	AAACTCTTTCTCAATCCTTT
17564	15651	AAAACTCTTTCTCAATCCTT
17565	15652	CAAAACTCTTTCTCAATCCT
17566	15653	TCAAAACTCTTTCTCAATCC
17567	15654	CTCAAAACTCTTTCTCAATC
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17569	15656	ACCTCAAAACTCTTTCTCAA
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17574	15661	ATATAACCTCAAAACTCTTT
17575	15662	GATATAACCTCAAAACTCTT
17576	15663	AGATATAACCTCAAAACTCT
17577	15664	TAGATATAACCTCAAAACTC
17578	15665	TTAGATATAACCTCAAAACT
17579	15666	CTTAGATATAACCTCAAAAC
17580	15667	GCTTAGATATAACCTCAAAA
17581	15668	AGCTTAGATATAACCTCAAA
17582	15669	TAGCTTAGATATAACCTCAA
17583	15670	CTAGCTTAGATATAACCTCA
17584	15671	CCTAGCTTAGATATAACCTC
17585	15672	CCCTAGCTTAGATATAACCT
17586	15673	ACCCTAGCTTAGATATAACC
17587	15674	AACCCTAGCTTAGATATAAC
17588	15675	CAACCCTAGCTTAGATATAA
17589	15676	ACAACCCTAGCTTAGATATA
17590	15677	GACAACCCTAGCTTAGATAT
17591	15678	TGACAACCCTAGCTTAGATA
17592	15679	CTGACAACCCTAGCTTAGAT
17593	15680	TCTGACAACCCTAGCTTAGA
17594	15681	ATCTGACAACCCTAGCTTAG
17595	15682	AATCTGACAACCCTAGCTTA
17596	15683	AAATCTGACAACCCTAGCTT
17597	15684	CAAATCTGACAACCCTAGCT
17598	15685	CCAAATCTGACAACCCTAGC
17599	15686	GCCAAATCTGACAACCCTAG
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66678	64765	TTGGGGAGGCTGAGATGGGA
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66680	64767	ACTTGGGGAGGCTGAGATGG
66681	64768	CACTTGGGGAGGCTGAGATG
66682	64769	GCACTTGGGGAGGCTGAGAT
66683	64770	AGCACTTGGGGAGGCTGAGA
66684	64771	CAGCACTTGGGGAGGCTGAG
66685	64772	CCAGCACTTGGGGAGGCTGA
66686	64773	CCCAGCACTTGGGGAGGCTG
66687	64774	TCCCAGCACTTGGGGAGGCT
66688	64775	ATCCCAGCACTTGGGGAGGC
66689	64776	AATCCCAGCACTTGGGGAGG
66690	64777	TAATCCCAGCACTTGGGGAG
66691	64778	GTAATCCCAGCACTTGGGGA
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66693	64780	CTGTAATCCCAGCACTTGGG
66694	64781	CCTGTAATCCCAGCACTTGG
66695	64782	ACCTGTAATCCCAGCACTTG
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66700	64787	CTCACACCTGTAATCCCAGC
66701	64788	ACTCACACCTGTAATCCCAG
66702	64789	GACTCACACCTGTAATCCCA
66703	64790	TGACTCACACCTGTAATCCC
66704	64791	GTGACTCACACCTGTAATCC
66705	64792	GGTGACTCACACCTGTAATC
66706	64793	TGGTGACTCACACCTGTAAT
66707	64794	ATGGTGACTCACACCTGTAA
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66710	64797	GGCATGGTGACTCACACCTG
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66712	64799	TGGGCATGGTGACTCACACC
66713	64800	CTGGGCATGGTGACTCACAC
66714	64801	TCTGGGCATGGTGACTCACA
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66716	64803	AGTCTGGGCATGGTGACTCA
66717	64804	AAGTCTGGGCATGGTGACTC
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66719	64806	TAAAGTCTGGGCATGGTGAC
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66722	64809	TGTTAAAGTCTGGGCATGGT
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66730	64817	AAAGAAAATGTTAAAGTCTG
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66732	64819	AAAAAGAAAATGTTAAAGTC
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66745	64832	CCTATTCTATACTAAAAAGA
66746	64833	ACCTATTCTATACTAAAAAG
66747	64834	GACCTATTCTATACTAAAAA
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115826	113913	ACATCATATTTGGTGCAAAA
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115829	113916	GATACATCATATTTGGTGCA
115830	113917	GGATACATCATATTTGGTGC
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115832	113919	CTGGATACATCATATTTGGT
115833	113920	ACTGGATACATCATATTTGG
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115842	113929	CTCACTGGGACTGGATACAT
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115845	113932	GGGCTCACTGGGACTGGATA
115846	113933	TGGGCTCACTGGGACTGGAT
115847	113934	CTGGGCTCACTGGGACTGGA
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115849	113936	GCCTGGGCTCACTGGGACTG
115850	113937	CGCCTGGGCTCACTGGGACT
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115855	113942	TTGCACGCCTGGGCTCACTG
115856	113943	CTTGCACGCCTGGGCTCACT
115857	113944	ACTTGCACGCCTGGGCTCAC
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115859	113946	TTACTTGCACGCCTGGGCTC
115860	113947	CTTACTTGCACGCCTGGGCT
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115863	113950	TGACTTACTTGCACGCCTGG
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115865	113952	TATGACTTACTTGCACGCCT
115866	113953	CTATGACTTACTTGCACGCC
115867	113954	TCTATGACTTACTTGCACGC
115868	113955	TTCTATGACTTACTTGCACG
115869	113956	ATTCTATGACTTACTTGCAC
115870	113957	AATTCTATGACTTACTTGCA
115871	113958	AAATTCTATGACTTACTTGC
115872	113959	CAAATTCTATGACTTACTTG
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115874	113961	ATCAAATTCTATGACTTACT
115875	113962	CATCAAATTCTATGACTTAC
115876	113963	ACATCAAATTCTATGACTTA
115877	113964	AACATCAAATTCTATGACTT
115878	113965	GAACATCAAATTCTATGACT
115879	113966	TGAACATCAAATTCTATGAC
115880	113967	GTGAACATCAAATTCTATGA
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115890	113977	GGGAGGCTAAGTGAACATCA
115891	113978	GGGGAGGCTAAGTGAACATC
115892	113979	TGGGGAGGCTAAGTGAACAT
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115895	113982	AATTGGGGAGGCTAAGTGAA

17602	15689	TTTGCCAAATCTGACAACCC
17603	15690	ATTTGCCAAATCTGACAACC
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17669	15756	AATTATACTAAAAAACTGGT
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17671	15758	ACAATTATACTAAAAAACTG
17672	15759	CACAATTATACTAAAAAACT

66749	64836	CTGACCTATTCTATACTAAA
66750	64837	ACTGACCTATTCTATACTAA
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66752	64839	AAACTGACCTATTCTATACT
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66770	64857	ATCTCATCAGAGGGAAAAAA
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66777	64864	GCATGGGATCTCATCAGAGG
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66783	64870	GAGTCAGCATGGGATCTCAT
66784	64871	AGAGTCAGCATGGGATCTCA
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66788	64875	ACTAAGAGTCAGCATGGGAT
66789	64876	AACTAAGAGTCAGCATGGGA
66790	64877	TAACTAAGAGTCAGCATGGG
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115896	113983	CAATTGGGGAGGCTAAGTGA
115897	113984	ACAATTGGGGAGGCTAAGTG
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115900	113987	CAAACAATTGGGGAGGCTAA
115901	113988	ACAAACAATTGGGGAGGCTA
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115919	114006	GAGTGCTTGGTGTCAGATAC
115920	114007	AGAGTGCTTGGTGTCAGATA
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115922	114009	AAAGAGTGCTTGGTGTCAGA
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115924	114011	CTAAAGAGTGCTTGGTGTCA
115925	114012	CCTAAAGAGTGCTTGGTGTC
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115940	114027	TCAAGTCACTGAAAACCTAA
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115944	114031	ACCCTCAAGTCACTGAAAAC
115945	114032	CACCCTCAAGTCACTGAAAA
115946	114033	ACACCCTCAAGTCACTGAAA
115947	114034	CACACCCTCAAGTCACTGAA
115948	114035	TCACACCCTCAAGTCACTGA
115949	114036	ATCACACCCTCAAGTCACTG
115950	114037	CATCACACCCTCAAGTCACT
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115962	114049	CATATGCATAACCATCACAC
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17673	15760	ACACAATTATACTAAAAAAC
17674	15761	TACACAATTATACTAAAAAA
17675	15762	ATACACAATTATACTAAAAA
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17678	15765	TTAATACACAATTATACTAA
17679	15766	TTTAATACACAATTATACTA
17680	15767	ATTTAATACACAATTATACT
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17683	15770	GCAATTTAATACACAATTAT
17684	15771	TGCAATTTAATACACAATTA
17685	15772	ATGCAATTTAATACACAATT
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17687	15774	CTATGCAATTTAATACACAA
17688	15775	TCTATGCAATTTAATACACA
17689	15776	TTCTATGCAATTTAATACAC
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17693	15780	TTTTTTCTATGCAATTTAAT
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17697	15784	TAACTTTTTTCTATGCAATT
17698	15785	ATAACTTTTTTCTATGCAAT
17699	15786	AATAACTTTTTTCTATGCAA
17700	15787	AAATAACTTTTTTCTATGCA
17701	15788	TAAATAACTTTTTTCTATGC
17702	15789	ATAAATAACTTTTTTCTATG
17703	15790	GATAAATAACTTTTTTCTAT
17704	15791	AGATAAATAACTTTTTTCTA
17705	15792	TAGATAAATAACTTTTTTCT
17706	15793	TTAGATAAATAACTTTTTTC
17707	15794	TTTAGATAAATAACTTTTTT
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17709	15796	ACTTTAGATAAATAACTTTT
17710	15797	AACTTTAGATAAATAACTTT
17711	15798	CAACTTTAGATAAATAACTT
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17721	15808	AGTTAAATTTCAACTTTAGA
17722	15809	CAGTTAAATTTCAACTTTAG
17723	15810	TCAGTTAAATTTCAACTTTA
17724	15811	CTCAGTTAAATTTCAACTTT
17725	15812	GCTCAGTTAAATTTCAACTT
17726	15813	TGCTCAGTTAAATTTCAACT
17727	15814	ATGCTCAGTTAAATTTCAAC
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17739	15826	ATAAAATACAAGATGCTCAG
17740	15827	GATAAAATACAAGATGCTCA
17741	15828	AGATAAAATACAAGATGCTC
17742	15829	CAGATAAAATACAAGATGCT
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66820	64907	CTAGCTCTTCTTCCAACCAA
66821	64908	ACTAGCTCTTCTTCCAACCA
66822	64909	CACTAGCTCTTCTTCCAACC
66823	64910	TCACTAGCTCTTCTTCCAAC
66824	64911	ATCACTAGCTCTTCTTCCAA
66825	64912	CATCACTAGCTCTTCTTCCA
66826	64913	ACATCACTAGCTCTTCTTCC
66827	64914	GACATCACTAGCTCTTCTTC
66828	64915	GGACATCACTAGCTCTTCTT
66829	64916	AGGACATCACTAGCTCTTCT
66830	64917	TAGGACATCACTAGCTCTTC
66831	64918	CTAGGACATCACTAGCTCTT
66832	64919	GCTAGGACATCACTAGCTCT
66833	64920	AGCTAGGACATCACTAGCTC
66834	64921	GAGCTAGGACATCACTAGCT
66835	64922	GGAGCTAGGACATCACTAGC
66836	64923	GGGAGCTAGGACATCACTAG
66837	64924	AGGGAGCTAGGACATCACTA
66838	64925	TAGGGAGCTAGGACATCACT
66839	64926	GTAGGGAGCTAGGACATCAC
66840	64927	AGTAGGGAGCTAGGACATCA
66841	64928	AAGTAGGGAGCTAGGACATC
66842	64929	TAAGTAGGGAGCTAGGACAT
66843	64930	GTAAGTAGGGAGCTAGGACA
66844	64931	AGTAAGTAGGGAGCTAGGAC
66845	64932	GAGTAAGTAGGGAGCTAGGA
66846	64933	GGAGTAAGTAGGGAGCTAGG
66847	64934	TGGAGTAAGTAGGGAGCTAG
66848	64935	GTGGAGTAAGTAGGGAGCTA
66849	64936	AGTGGAGTAAGTAGGGAGCT
66850	64937	AAGTGGAGTAAGTAGGGAGC
66851	64938	AAAGTGGAGTAAGTAGGGAG
66852	64939	GAAAGTGGAGTAAGTAGGGA
66853	64940	GGAAAGTGGAGTAAGTAGGG
66854	64941	GGGAAAGTGGAGTAAGTAGG
66855	64942	AGGGAAAGTGGAGTAAGTAG
66856	64943	AAGGGAAAGTGGAGTAAGTA
66857	64944	CAAGGGAAAGTGGAGTAAGT
66858	64945	GCAAGGGAAAGTGGAGTAAG
66859	64946	GGCAAGGGAAAGTGGAGTAA
66860	64947	AGGCAAGGGAAAGTGGAGTA
66861	64948	AAGGCAAGGGAAAGTGGAGT
66862	64949	GAAGGCAAGGGAAAGTGGAG
66863	64950	AGAAGGCAAGGGAAAGTGGA
66864	64951	CAGAAGGCAAGGGAAAGTGG
66865	64952	CCAGAAGGCAAGGGAAAGTG
66866	64953	CCCAGAAGGCAAGGGAAAGT
66867	64954	CCCCAGAAGGCAAGGGAAAG
66868	64955	ACCCCAGAAGGCAAGGGAAA
66869	64956	CACCCCAGAAGGCAAGGGAA
66870	64957	ACACCCCAGAAGGCAAGGGA
66871	64958	GACACCCCAGAAGGCAAGGG
66872	64959	GGACACCCCAGAAGGCAAGG
66873	64960	AGGACACCCCAGAAGGCAAG
66874	64961	CAGGACACCCCAGAAGGCAA
66875	64962	TCAGGACACCCCAGAAGGCA
66876	64963	TTCAGGACACCCCAGAAGGC
66877	64964	CTTCAGGACACCCCAGAAGG
66878	64965	TCTTCAGGACACCCCAGAAG
66879	64966	GTCTTCAGGACACCCCAGAA
66880	64967	TGTCTTCAGGACACCCCAGA
66881	64968	ATGTCTTCAGGACACCCCAG
66882	64969	GATGTCTTCAGGACACCCCA
66883	64970	TGATGTCTTCAGGACACCCC
66884	64971	ATGATGTCTTCAGGACACCC
66885	64972	TATGATGTCTTCAGGACACC
66886	64973	CTATGATGTCTTCAGGACAC
66887	64974	CCTATGATGTCTTCAGGACA
66888	64975	CCCTATGATGTCTTCAGGAC
66889	64976	ACCCTATGATGTCTTCAGGA
66890	64977	CACCCTATGATGTCTTCAGG

115967	114054	AAATGCATATGCATAACCAT
115968	114055	CAAATGCATATGCATAACCA
115969	114056	TCAAATGCATATGCATAACC
115970	114057	TTCAAATGCATATGCATAAC
115971	114058	TTTCAAATGCATATGCATAA
115972	114059	GTTTCAAATGCATATGCATA
115973	114060	TGTTTCAAATGCATATGCAT
115974	114061	CTGTTTCAAATGCATATGCA
115975	114062	TCTGTTTCAAATGCATATGC
115976	114063	GTCTGTTTCAAATGCATATG
115977	114064	TGTCTGTTTCAAATGCATAT
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115982	114069	ATGCCTGTCTGTTTCAAATG
115983	114070	CATGCCTGTCTGTTTCAAAT
115984	114071	GCATGCCTGTCTGTTTCAAA
115985	114072	TGCATGCCTGTCTGTTTCAA
115986	114073	CTGCATGCCTGTCTGTTTCA
115987	114074	TCTGCATGCCTGTCTGTTTC
115988	114075	CTCTGCATGCCTGTCTGTTT
115989	114076	TCTCTGCATGCCTGTCTGTT
115990	114077	ATCTCTGCATGCCTGTCTGT
115991	114078	AATCTCTGCATGCCTGTCTG
115992	114079	GAATCTCTGCATGCCTGTCT
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115996	114083	CACTGAATCTCTGCATGCCT
115997	114084	ACACTGAATCTCTGCATGCC
115998	114085	CACACTGAATCTCTGCATGC
115999	114086	ACACACTGAATCTCTGCATG
116000	114087	AACACACTGAATCTCTGCAT
116001	114088	CAACACACTGAATCTCTGCA
116002	114089	ACAACACACTGAATCTCTGC
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116010	114097	CATACTTAACAACACACTGA
116011	114098	TCATACTTAACAACACACTG
116012	114099	CTCATACTTAACAACACACT
116013	114100	CCTCATACTTAACAACACAC
116014	114101	TCCTCATACTTAACAACACA
116015	114102	GTCCTCATACTTAACAACAC
116016	114103	GGTCCTCATACTTAACAACA
116017	114104	AGGTCCTCATACTTAACAAC
116018	114105	TAGGTCCTCATACTTAACAA
116019	114106	TTAGGTCCTCATACTTAACA
116020	114107	TTTAGGTCCTCATACTTAAC
116021	114108	ATTTAGGTCCTCATACTTAA
116022	114109	GATTTAGGTCCTCATACTTA
116023	114110	AGATTTAGGTCCTCATACTT
116024	114111	CAGATTTAGGTCCTCATACT
116025	114112	TCAGATTTAGGTCCTCATAC
116026	114113	CTCAGATTTAGGTCCTCATA
116027	114114	TCTCAGATTTAGGTCCTCAT
116028	114115	TTCTCAGATTTAGGTCCTCA
116029	114116	ATTCTCAGATTTAGGTCCTC
116030	114117	CATTCTCAGATTTAGGTCCT
116031	114118	ACATTCTCAGATTTAGGTCC
116032	114119	AACATTCTCAGATTTAGGTC
116033	114120	AAACATTCTCAGATTTAGGT
116034	114121	AAAACATTCTCAGATTTAGG
116035	114122	GAAAACATTCTCAGATTTAG
116036	114123	AGAAAACATTCTCAGATTTA
116037	114124	CAGAAAACATTCTCAGATTT

17744	15831	GCCAGATAAAATACAAGATG
17745	15832	TGCCAGATAAAATACAAGAT
17746	15833	TTGCCAGATAAAATACAAGA
17747	15834	GTTGCCAGATAAAATACAAG
17748	15835	AGTTGCCAGATAAAATACAA
17749	15836	GAGTTGCCAGATAAAATACA
17750	15837	GGAGTTGCCAGATAAAATAC
17751	15838	TGGAGTTGCCAGATAAAATA
17752	15839	CTGGAGTTGCCAGATAAAAT
17753	15840	ACTGGAGTTGCCAGATAAAA
17754	15841	GACTGGAGTTGCCAGATAAA
17755	15842	AGACTGGAGTTGCCAGATAA
17756	15843	TAGACTGGAGTTGCCAGATA
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17758	15845	CTTAGACTGGAGTTGCCAGA
17759	15846	GCTTAGACTGGAGTTGCCAG
17760	15847	AGCTTAGACTGGAGTTGCCA
17761	15848	CAGCTTAGACTGGAGTTGCC
17762	15849	CCAGCTTAGACTGGAGTTGC
17763	15850	TCCAGCTTAGACTGGAGTTG
17764	15851	TTCCAGCTTAGACTGGAGTT
17765	15852	ATTCCAGCTTAGACTGGAGT
17766	15853	GATTCCAGCTTAGACTGGAG
17767	15854	TGATTCCAGCTTAGACTGGA
17768	15855	ATGATTCCAGCTTAGACTGG
17769	15856	CATGATTCCAGCTTAGACTG
17770	15857	CCATGATTCCAGCTTAGACT
17771	15858	ACCATGATTCCAGCTTAGAC
17772	15859	AACCATGATTCCAGCTTAGA
17773	15860	GAACCATGATTCCAGCTTAG
17774	15861	TGAACCATGATTCCAGCTTA
17775	15862	GTGAACCATGATTCCAGCTT
17776	15863	AGTGAACCATGATTCCAGCT
17777	15864	CAGTGAACCATGATTCCAGC
17778	15865	ACAGTGAACCATGATTCCAG
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17780	15867	AAACAGTGAACCATGATTCC
17781	15868	AAAACAGTGAACCATGATTC
17782	15869	AAAAACAGTGAACCATGATT
17783	15870	AAAAAACAGTGAACCATGAT
17784	15871	AAAAAAACAGTGAACCATGA
17785	15872	AAAAAAAACAGTGAACCATG
17786	15873	AAAAAAAAACAGTGAACCAT
17787	15874	AAAAAAAAAACAGTGAACCA
17788	15875	AAAAAAAAAAACAGTGAACC
17789	15876	AAAAAAAAAAAACAGTGAAC
17790	15877	AAAAAAAAAAAAACAGTGAA
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17792	15879	AAAAAAAAAAAAAAACAGTG
17793	15880	AAAAAAAAAAAAAAAACAGT
17794	15881	AAAAAAAAAAAAAAAAACAG
17795	15882	AAAAAAAAAAAAAAAAAACA
17796	15883	AAAAAAAAAAAAAAAAAAAC
17797	15884	AAAAAAAAAAAAAAAAAAAA
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17799	15886	AAAAAAAAAAAAAAAAAAAA
17800	15887	AAAAAAAAAAAAAAAAAAAA
17801	15888	AAAAAAAAAAAAAAAAAAAA
17802	15889	CAAAAAAAAAAAAAAAAAAA
17803	15890	TCAAAAAAAAAAAAAAAAAA
17804	15891	CTCAAAAAAAAAAAAAAAAA
17805	15892	ACTCAAAAAAAAAAAAAAAA
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17807	15894	CGACTCAAAAAAAAAAAAAA
17808	15895	CCGACTCAAAAAAAAAAAAA
17809	15896	TCCGACTCAAAAAAAAAAAA
17810	15897	CTCCGACTCAAAAAAAAAAA
17811	15898	ACTCCGACTCAAAAAAAAAA
17812	15899	GACTCCGACTCAAAAAAAAA
17813	15900	AGACTCCGACTCAAAAAAAA
17814	15901	AAGACTCCGACTCAAAAAAA

66891	64978	ACACCCTATGATGTCTTCAG
66892	64979	GACACCCTATGATGTCTTCA
66893	64980	TGACACCCTATGATGTCTTC
66894	64981	ATGACACCCTATGATGTCTT
66895	64982	CATGACACCCTATGATGTCT
66896	64983	TCATGACACCCTATGATGTC
66897	64984	TTCATGACACCCTATGATGT
66898	64985	CTTCATGACACCCTATGATG
66899	64986	ACTTCATGACACCCTATGAT
66900	64987	TACTTCATGACACCCTATGA
66901	64988	GTACTTCATGACACCCTATG
66902	64989	TGTACTTCATGACACCCTAT
66903	64990	CTGTACTTCATGACACCCTA
66904	64991	ACTGTACTTCATGACACCCT
66905	64992	AACTGTACTTCATGACACCC
66906	64993	CAACTGTACTTCATGACACC
66907	64994	CCAACTGTACTTCATGACAC
66908	64995	TCCAACTGTACTTCATGACA
66909	64996	CTCCAACTGTACTTCATGAC
66910	64997	TCTCCAACTGTACTTCATGA
66911	64998	TTCTCCAACTGTACTTCATG
66912	64999	GTTCTCCAACTGTACTTCAT
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66914	65001	TGGTTCTCCAACTGTACTTC
66915	65002	CTGGTTCTCCAACTGTACTT
66916	65003	ACTGGTTCTCCAACTGTACT
66917	65004	CACTGGTTCTCCAACTGTAC
66918	65005	CCACTGGTTCTCCAACTGTA
66919	65006	ACCACTGGTTCTCCAACTGT
66920	65007	GACCACTGGTTCTCCAACTG
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66928	65015	ATGATGGAGACCACTGGTTC
66929	65016	CATGATGGAGACCACTGGTT
66930	65017	ACATGATGGAGACCACTGGT
66931	65018	TACATGATGGAGACCACTGG
66932	65019	GTACATGATGGAGACCACTG
66933	65020	GGTACATGATGGAGACCACT
66934	65021	TGGTACATGATGGAGACCAC
66935	65022	TTGGTACATGATGGAGACCA
66936	65023	TTTGGTACATGATGGAGACC
66937	65024	GTTTGGTACATGATGGAGAC
66938	65025	TGTTTGGTACATGATGGAGA
66939	65026	GTGTTTGGTACATGATGGAG
66940	65027	AGTGTTTGGTACATGATGGA
66941	65028	GAGTGTTTGGTACATGATGG
66942	65029	TGAGTGTTTGGTACATGATG
66943	65030	ATGAGTGTTTGGTACATGAT
66944	65031	GATGAGTGTTTGGTACATGA
66945	65032	AGATGAGTGTTTGGTACATG
66946	65033	AAGATGAGTGTTTGGTACAT
66947	65034	GAAGATGAGTGTTTGGTACA
66948	65035	TGAAGATGAGTGTTTGGTAC
66949	65036	GTGAAGATGAGTGTTTGGTA
66950	65037	CGTGAAGATGAGTGTTTGGT
66951	65038	TCGTGAAGATGAGTGTTTGG
66952	65039	TTCGTGAAGATGAGTGTTTG
66953	65040	CTTCGTGAAGATGAGTGTTT
66954	65041	GCTTCGTGAAGATGAGTGTT
66955	65042	TGCTTCGTGAAGATGAGTGT
66956	65043	CTGCTTCGTGAAGATGAGTG
66957	65044	ACTGCTTCGTGAAGATGAGT
66958	65045	TACTGCTTCGTGAAGATGAG
66959	65046	ATACTGCTTCGTGAAGATGA
66960	65047	CATACTGCTTCGTGAAGATG
66961	65048	ACATACTGCTTCGTGAAGAT

116038	114125	ACAGAAAACATTCTCAGATT
116039	114126	CACAGAAAACATTCTCAGAT
116040	114127	TCACAGAAAACATTCTCAGA
116041	114128	TTCACAGAAAACATTCTCAG
116042	114129	TTTCACAGAAAACATTCTCA
116043	114130	TTTTCACAGAAAACATTCTC
116044	114131	TTTTTCACAGAAAACATTCT
116045	114132	CTTTTTCACAGAAAACATTC
116046	114133	TCTTTTTCACAGAAAACATT
116047	114134	ATCTTTTTCACAGAAAACAT
116048	114135	CATCTTTTTCACAGAAAACA
116049	114136	CCATCTTTTTCACAGAAAAC
116050	114137	ACCATCTTTTTCACAGAAAA
116051	114138	AACCATCTTTTTCACAGAAA
116052	114139	AAACCATCTTTTTCACAGAA
116053	114140	TAAACCATCTTTTTCACAGA
116054	114141	CTAAACCATCTTTTTCACAG
116055	114142	TCTAAACCATCTTTTTCACA
116056	114143	ATCTAAACCATCTTTTTCAC
116057	114144	AATCTAAACCATCTTTTTCA
116058	114145	AAATCTAAACCATCTTTTTC
116059	114146	TAAATCTAAACCATCTTTTT
116060	114147	GTAAATCTAAACCATCTTTT
116061	114148	AGTAAATCTAAACCATCTTT
116062	114149	CAGTAAATCTAAACCATCTT
116063	114150	ACAGTAAATCTAAACCATCT
116064	114151	TACAGTAAATCTAAACCATC
116065	114152	CTACAGTAAATCTAAACCAT
116066	114153	ACTACAGTAAATCTAAACCA
116067	114154	AACTACAGTAAATCTAAACC
116068	114155	AAACTACAGTAAATCTAAAC
116069	114156	CAAACTACAGTAAATCTAAA
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116071	114158	CCCAAACTACAGTAAATCTA
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116073	114160	ACCCCAAACTACAGTAAATC
116074	114161	AACCCCAAACTACAGTAAAT
116075	114162	AAACCCCAAACTACAGTAAA
116076	114163	CAAACCCCAAACTACAGTAA
116077	114164	ACAAACCCCAAACTACAGTA
116078	114165	AACAAACCCCAAACTACAGT
116079	114166	GAACAAACCCCAAACTACAG
116080	114167	GGAACAAACCCCAAACTACA
116081	114168	AGGAACAAACCCCAAACTAC
116082	114169	AAGGAACAAACCCCAAACTA
116083	114170	AAAGGAACAAACCCCAAACT
116084	114171	AAAAGGAACAAACCCCAAAC
116085	114172	TAAAAGGAACAAACCCCAAA
116086	114173	CTAAAAGGAACAAACCCCAA
116087	114174	GCTAAAAGGAACAAACCCCA
116088	114175	AGCTAAAAGGAACAAACCCC
116089	114176	CAGCTAAAAGGAACAAACCC
116090	114177	ACAGCTAAAAGGAACAAACC
116091	114178	CACAGCTAAAAGGAACAAAC
116092	114179	CCACAGCTAAAAGGAACAAA
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116094	114181	ACCCACAGCTAAAAGGAACA
116095	114182	TACCCACAGCTAAAAGGAAC
116096	114183	ATACCCACAGCTAAAAGGAA
116097	114184	CATACCCACAGCTAAAAGGA
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116099	114186	ATCATACCCACAGCTAAAAG
116100	114187	GATCATACCCACAGCTAAAA
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116102	114189	TAGATCATACCCACAGCTAA
116103	114190	TTAGATCATACCCACAGCTA
116104	114191	ATTAGATCATACCCACAGCT
116105	114192	AATTAGATCATACCCACAGC
116106	114193	AAATTAGATCATACCCACAG
116107	114194	AAAATTAGATCATACCCACA
116108	114195	AAAAATTAGATCATACCCAC

17815	15902	CAAGACTCCGACTCAAAAAA
17816	15903	GCAAGACTCCGACTCAAAAA
17817	15904	AGCAAGACTCCGACTCAAAA
17818	15905	CAGCAAGACTCCGACTCAAA
17819	15906	ACAGCAAGACTCCGACTCAA
17820	15907	CACAGCAAGACTCCGACTCA
17821	15908	ACACAGCAAGACTCCGACTC
17822	15909	AACACAGCAAGACTCCGACT
17823	15910	CAACACAGCAAGACTCCGAC
17824	15911	GCAACACAGCAAGACTCCGA
17825	15912	GGCAACACAGCAAGACTCCG
17826	15913	GGGCAACACAGCAAGACTCC
17827	15914	TGGGCAACACAGCAAGACTC
17828	15915	CTGGGCAACACAGCAAGACT
17829	15916	CCTGGGCAACACAGCAAGAC
17830	15917	GCCTGGGCAACACAGCAAGA
17831	15918	AGCCTGGGCAACACAGCAAG
17832	15919	CAGCCTGGGCAACACAGCAA
17833	15920	CCAGCCTGGGCAACACAGCA
17834	15921	TCCAGCCTGGGCAACACAGC
17835	15922	CTCCAGCCTGGGCAACACAG
17836	15923	ACTCCAGCCTGGGCAACACA
17837	15924	CACTCCAGCCTGGGCAACAC
17838	15925	GCACTCCAGCCTGGGCAACA
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17840	15927	TTGCACTCCAGCCTGGGCAA
17841	15928	ATTGCACTCCAGCCTGGGCA
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17844	15931	ACCATTGCACTCCAGCCTGG
17845	15932	CACCATTGCACTCCAGCCTG
17846	15933	GCACCATTGCACTCCAGCCT
17847	15934	CGCACCATTGCACTCCAGCC
17848	15935	TCGCACCATTGCACTCCAGC
17849	15936	ATCGCACCATTGCACTCCAG
17850	15937	GATCGCACCATTGCACTCCA
17851	15938	AGATCGCACCATTGCACTCC
17852	15939	AAGATCGCACCATTGCACTC
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17854	15941	CCAAGATCGCACCATTGCAC
17855	15942	GCCAAGATCGCACCATTGCA
17856	15943	AGCCAAGATCGCACCATTGC
17857	15944	GAGCCAAGATCGCACCATTG
17858	15945	TGAGCCAAGATCGCACCATT
17859	15946	GTGAGCCAAGATCGCACCAT
17860	15947	AGTGAGCCAAGATCGCACCA
17861	15948	CAGTGAGCCAAGATCGCACC
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17863	15950	TGCAGTGAGCCAAGATCGCA
17864	15951	TTGCAGTGAGCCAAGATCGC
17865	15952	GTTGCAGTGAGCCAAGATCG
17866	15953	GGTTGCAGTGAGCCAAGATC
17867	15954	AGGTTGCAGTGAGCCAAGAT
17868	15955	GAGGTTGCAGTGAGCCAAGA
17869	15956	GGAGGTTGCAGTGAGCCAAG
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17871	15958	GTGGAGGTTGCAGTGAGCCA
17872	15959	GGTGGAGGTTGCAGTGAGCC
17873	15960	AGGTGGAGGTTGCAGTGAGC
17874	15961	GAGGTGGAGGTTGCAGTGAG
17875	15962	GGAGGTGGAGGTTGCAGTGA
17876	15963	AGGAGGTGGAGGTTGCAGTG
17877	15964	CAGGAGGTGGAGGTTGCAGT
17878	15965	ACAGGAGGTGGAGGTTGCAG
17879	15966	CACAGGAGGTGGAGGTTGCA
17880	15967	ACACAGGAGGTGGAGGTTGC
17881	15968	AACACAGGAGGTGGAGGTTG
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17883	15970	TGAACACAGGAGGTGGAGGT
17884	15971	TTGAACACAGGAGGTGGAGG
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66962	65049	TACATACTGCTTCGTGAAGA
66963	65050	CTACATACTGCTTCGTGAAG
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66965	65052	CACTACATACTGCTTCGTGA
66966	65053	ACACTACATACTGCTTCGTG
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66974	65061	TAAAAAAGACACTACATACT
66975	65062	GTAAAAAAGACACTACATAC
66976	65063	GGTAAAAAAGACACTACATA
66977	65064	CGGTAAAAAAGACACTACAT
66978	65065	CCGGTAAAAAAGACACTACA
66979	65066	ACCGGTAAAAAAGACACTAC
66980	65067	TACCGGTAAAAAAGACACTA
66981	65068	ATACCGGTAAAAAAGACACT
66982	65069	TATACCGGTAAAAAAGACAC
66983	65070	ATATACCGGTAAAAAAGACA
66984	65071	AATATACCGGTAAAAAAGAC
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66986	65073	AAAATATACCGGTAAAAAAG
66987	65074	GAAAATATACCGGTAAAAAA
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66989	65076	GAGAAAATATACCGGTAAAA
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66991	65078	GAGAGAAAATATACCGGTAA
66992	65079	AGAGAGAAAATATACCGGTA
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66995	65082	GGGAGAGAGAAAATATACCG
66996	65083	TGGGAGAGAGAAAATATACC
66997	65084	TTGGGAGAGAGAAAATATAC
66998	65085	ATTGGGAGAGAGAAAATATA
66999	65086	CATTGGGAGAGAGAAAATAT
67000	65087	GCATTGGGAGAGAGAAAATA
67001	65088	TGCATTGGGAGAGAGAAAAT
67002	65089	ATGCATTGGGAGAGAGAAAA
67003	65090	AATGCATTGGGAGAGAGAAA
67004	65091	TAATGCATTGGGAGAGAGAA
67005	65092	TTAATGCATTGGGAGAGAGA
67006	65093	TTTAATGCATTGGGAGAGAG
67007	65094	GTTTAATGCATTGGGAGAGA
67008	65095	AGTTTAATGCATTGGGAGAG
67009	65096	AAGTTTAATGCATTGGGAGA
67010	65097	AAAGTTTAATGCATTGGGAG
67011	65098	AAAAGTTTAATGCATTGGGA
67012	65099	GAAAAGTTTAATGCATTGGG
67013	65100	AGAAAAGTTTAATGCATTGG
67014	65101	CAGAAAAGTTTAATGCATTG
67015	65102	CCAGAAAAGTTTAATGCATT
67016	65103	TCCAGAAAAGTTTAATGCAT
67017	65104	CTCCAGAAAAGTTTAATGCA
67018	65105	ACTCCAGAAAAGTTTAATGC
67019	65106	AACTCCAGAAAAGTTTAATG
67020	65107	GAACTCCAGAAAAGTTTAAT
67021	65108	TGAACTCCAGAAAAGTTTAA
67022	65109	CTGAACTCCAGAAAAGTTTA
67023	65110	TCTGAACTCCAGAAAAGTTT
67024	65111	TTCTGAACTCCAGAAAAGTT
67025	65112	TTTCTGAACTCCAGAAAAGT
67026	65113	TTTTCTGAACTCCAGAAAAG
67027	65114	GTTTTCTGAACTCCAGAAAA
67028	65115	TGTTTTCTGAACTCCAGAAA
67029	65116	TTGTTTTCTGAACTCCAGAA
67030	65117	TTTGTTTTCTGAACTCCAGA
67031	65118	ATTTGTTTTCTGAACTCCAG
67032	65119	AATTTGTTTTCTGAACTCCA

116109	114196	AAAAAATTAGATCATACCCA
116110	114197	TAAAAAATTAGATCATACCC
116111	114198	TTAAAAAATTAGATCATACC
116112	114199	ATTAAAAAATTAGATCATAC
116113	114200	CATTAAAAAATTAGATCATA
116114	114201	TCATTAAAAAATTAGATCAT
116115	114202	GTCATTAAAAAATTAGATCA
116116	114203	AGTCATTAAAAAATTAGATC
116117	114204	TAGTCATTAAAAAATTAGAT
116118	114205	TTAGTCATTAAAAAATTAGA
116119	114206	ATTAGTCATTAAAAAATTAG
116120	114207	CATTAGTCATTAAAAAATTA
116121	114208	CCATTAGTCATTAAAAAATT
116122	114209	TCCATTAGTCATTAAAAAAT
116123	114210	CTCCATTAGTCATTAAAAAA
116124	114211	TCTCCATTAGTCATTAAAAA
116125	114212	TTCTCCATTAGTCATTAAAA
116126	114213	ATTCTCCATTAGTCATTAAA
116127	114214	GATTCTCCATTAGTCATTAA
116128	114215	TGATTCTCCATTAGTCATTA
116129	114216	CTGATTCTCCATTAGTCATT
116130	114217	CCTGATTCTCCATTAGTCAT
116131	114218	TCCTGATTCTCCATTAGTCA
116132	114219	TTCCTGATTCTCCATTAGTC
116133	114220	TTTCCTGATTCTCCATTAGT
116134	114221	GTTTCCTGATTCTCCATTAG
116135	114222	GGTTTCCTGATTCTCCATTA
116136	114223	AGGTTTCCTGATTCTCCATT
116137	114224	AAGGTTTCCTGATTCTCCAT
116138	114225	GAAGGTTTCCTGATTCTCCA
116139	114226	AGAAGGTTTCCTGATTCTCC
116140	114227	GAGAAGGTTTCCTGATTCTC
116141	114228	TGAGAAGGTTTCCTGATTCT
116142	114229	ATGAGAAGGTTTCCTGATTC
116143	114230	CATGAGAAGGTTTCCTGATT
116144	114231	GCATGAGAAGGTTTCCTGAT
116145	114232	GGCATGAGAAGGTTTCCTGA
116146	114233	AGGCATGAGAAGGTTTCCTG
116147	114234	TAGGCATGAGAAGGTTTCCT
116148	114235	CTAGGCATGAGAAGGTTTCC
116149	114236	GCTAGGCATGAGAAGGTTTC
116150	114237	AGCTAGGCATGAGAAGGTTT
116151	114238	GAGCTAGGCATGAGAAGGTT
116152	114239	AGAGCTAGGCATGAGAAGGT
116153	114240	GAGAGCTAGGCATGAGAAGG
116154	114241	AGAGAGCTAGGCATGAGAAG
116155	114242	TAGAGAGCTAGGCATGAGAA
116156	114243	CTAGAGAGCTAGGCATGAGA
116157	114244	GCTAGAGAGCTAGGCATGAG
116158	114245	TGCTAGAGAGCTAGGCATGA
116159	114246	TTGCTAGAGAGCTAGGCATG
116160	114247	ATTGCTAGAGAGCTAGGCAT
116161	114248	TATTGCTAGAGAGCTAGGCA
116162	114249	ATATTGCTAGAGAGCTAGGC
116163	114250	TATATTGCTAGAGAGCTAGG
116164	114251	TTATATTGCTAGAGAGCTAG
116165	114252	TTTATATTGCTAGAGAGCTA
116166	114253	TTTTATATTGCTAGAGAGCT
116167	114254	GTTTTATATTGCTAGAGAGC
116168	114255	AGTTTTATATTGCTAGAGAG
116169	114256	TAGTTTTATATTGCTAGAGA
116170	114257	TTAGTTTTATATTGCTAGAG
116171	114258	CTTAGTTTTATATTGCTAGA
116172	114259	TCTTAGTTTTATATTGCTAG
116173	114260	CTCTTAGTTTTATATTGCTA
116174	114261	ACTCTTAGTTTTATATTGCT
116175	114262	CACTCTTAGTTTTATATTGC
116176	114263	TCACTCTTAGTTTTATATTG
116177	114264	GTCACTCTTAGTTTTATATT
116178	114265	TGTCACTCTTAGTTTTATAT
116179	114266	CTGTCACTCTTAGTTTTATA

17886	15973	ACTTGAACACAGGAGGTGGA
17887	15974	CACTTGAACACAGGAGGTGG
17888	15975	TCACTTGAACACAGGAGGTG
17889	15976	ATCACTTGAACACAGGAGGT
17890	15977	AATCACTTGAACACAGGAGG
17891	15978	GAATCACTTGAACACAGGAG
17892	15979	AGAATCACTTGAACACAGGA
17893	15980	GAGAATCACTTGAACACAGG
17894	15981	GGAGAATCACTTGAACACAG
17895	15982	AGGAGAATCACTTGAACACA
17896	15983	CAGGAGAATCACTTGAACAC
17897	15984	GCAGGAGAATCACTTGAACA
17898	15985	GGCAGGAGAATCACTTGAAC
17899	15986	AGGCAGGAGAATCACTTGAA
17900	15987	GAGGCAGGAGAATCACTTGA
17901	15988	TGAGGCAGGAGAATCACTTG
17902	15989	CTGAGGCAGGAGAATCACTT
17903	15990	GCTGAGGCAGGAGAATCACT
17904	15991	GGCTGAGGCAGGAGAATCAC
17905	15992	AGGCTGAGGCAGGAGAATCA
17906	15993	GAGGCTGAGGCAGGAGAATC
17907	15994	GGAGGCTGAGGCAGGAGAAT
17908	15995	AGGAGGCTGAGGCAGGAGAA
17909	15996	CAGGAGGCTGAGGCAGGAGA
17910	15997	TCAGGAGGCTGAGGCAGGAG
17911	15998	TTCAGGAGGCTGAGGCAGGA
17912	15999	ATTCAGGAGGCTGAGGCAGG
17913	16000	TATTCAGGAGGCTGAGGCAG
17914	16001	CTATTCAGGAGGCTGAGGCA
17915	16002	ACTATTCAGGAGGCTGAGGC
17916	16003	AACTATTCAGGAGGCTGAGG
17917	16004	CAACTATTCAGGAGGCTGAG
17918	16005	CCAACTATTCAGGAGGCTGA
17919	16006	CCCAACTATTCAGGAGGCTG
17920	16007	TCCCAACTATTCAGGAGGCT
17921	16008	ATCCCAACTATTCAGGAGGC
17922	16009	AATCCCAACTATTCAGGAGG
17923	16010	TAATCCCAACTATTCAGGAG
17924	16011	GTAATCCCAACTATTCAGGA
17925	16012	TGTAATCCCAACTATTCAGG
17926	16013	CTGTAATCCCAACTATTCAG
17927	16014	CCTGTAATCCCAACTATTCA
17928	16015	GCCTGTAATCCCAACTATTC
17929	16016	TGCCTGTAATCCCAACTATT
17930	16017	GTGCCTGTAATCCCAACTAT
17931	16018	GGTGCCTGTAATCCCAACTA
17932	16019	GGGTGCCTGTAATCCCAACT
17933	16020	TGGGTGCCTGTAATCCCAAC
17934	16021	GTGGGTGCCTGTAATCCCAA
17935	16022	GGTGGGTGCCTGTAATCCCA
17936	16023	TGGTGGGTGCCTGTAATCCC
17937	16024	GTGGTGGGTGCCTGTAATCC
17938	16025	GGTGGTGGGTGCCTGTAATC
17939	16026	TGGTGGTGGGTGCCTGTAAT
17940	16027	ATGGTGGTGGGTGCCTGTAA
17941	16028	CATGGTGGTGGGTGCCTGTA
17942	16029	GCATGGTGGTGGGTGCCTGT
17943	16030	GGCATGGTGGTGGGTGCCTG
17944	16031	GGGCATGGTGGTGGGTGCCT
17945	16032	TGGGCATGGTGGTGGGTGCC
17946	16033	CTGGGCATGGTGGTGGGTGC
17947	16034	GCTGGGCATGGTGGTGGGTG
17948	16035	AGCTGGGCATGGTGGTGGGT
17949	16036	TAGCTGGGCATGGTGGTGGG
17950	16037	TTAGCTGGGCATGGTGGTGG
17951	16038	ATTAGCTGGGCATGGTGGTG
17952	16039	AATTAGCTGGGCATGGTGGT
17953	16040	AAATTAGCTGGGCATGGTGG
17954	16041	AAAATTAGCTGGGCATGGTG
17955	16042	AAAAATTAGCTGGGCATGGT
17956	16043	TAAAAATTAGCTGGGCATGG

67033	65120	AAATTTGTTTTCTGAACTCC
67034	65121	TAAATTTGTTTTCTGAACTC
67035	65122	ATAAATTTGTTTTCTGAACT
67036	65123	TATAAATTTGTTTTCTGAAC
67037	65124	CTATAAATTTGTTTTCTGAA
67038	65125	TCTATAAATTTGTTTTCTGA
67039	65126	TTCTATAAATTTGTTTTCTG
67040	65127	ATTCTATAAATTTGTTTTCT
67041	65128	AATTCTATAAATTTGTTTTC
67042	65129	TAATTCTATAAATTTGTTTT
67043	65130	TTAATTCTATAAATTTGTTT
67044	65131	CTTAATTCTATAAATTTGTT
67045	65132	CCTTAATTCTATAAATTTGT
67046	65133	TCCTTAATTCTATAAATTTG
67047	65134	TTCCTTAATTCTATAAATTT
67048	65135	TTTCCTTAATTCTATAAATT
67049	65136	ATTTCCTTAATTCTATAAAT
67050	65137	CATTTCCTTAATTCTATAAA
67051	65138	GCATTTCCTTAATTCTATAA
67052	65139	CGCATTTCCTTAATTCTATA
67053	65140	ACGCATTTCCTTAATTCTAT
67054	65141	GACGCATTTCCTTAATTCTA
67055	65142	GGACGCATTTCCTTAATTCT
67056	65143	GGGACGCATTTCCTTAATTC
67057	65144	GGGGACGCATTTCCTTAATT
67058	65145	GGGGGACGCATTTCCTTAAT
67059	65146	GGGGGGACGCATTTCCTTAA
67060	65147	GGGGGGGACGCATTTCCTTA
67061	65148	TGGGGGGGACGCATTTCCTT
67062	65149	TTGGGGGGGACGCATTTCCT
67063	65150	GTTGGGGGGGACGCATTTCC
67064	65151	GGTTGGGGGGGACGCATTTC
67065	65152	TGGTTGGGGGGGACGCATTT
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67071	65158	ACACCATGGTTGGGGGGGAC
67072	65159	GACACCATGGTTGGGGGGGA
67073	65160	AGACACCATGGTTGGGGGGG
67074	65161	TAGACACCATGGTTGGGGGG
67075	65162	CTAGACACCATGGTTGGGGG
67076	65163	ACTAGACACCATGGTTGGGG
67077	65164	TACTAGACACCATGGTTGGG
67078	65165	ATACTAGACACCATGGTTGG
67079	65166	TATACTAGACACCATGGTTG
67080	65167	ATATACTAGACACCATGGTT
67081	65168	TATATACTAGACACCATGGT
67082	65169	ATATATACTAGACACCATGG
67083	65170	TATATATACTAGACACCATG
67084	65171	GTATATATACTAGACACCAT
67085	65172	TGTATATATACTAGACACCA
67086	65173	CTGTATATATACTAGACACC
67087	65174	ACTGTATATATACTAGACAC
67088	65175	CACTGTATATATACTAGACA
67089	65176	TCACTGTATATATACTAGAC
67090	65177	GTCACTGTATATATACTAGA
67091	65178	AGTCACTGTATATATACTAG
67092	65179	AAGTCACTGTATATATACTA
67093	65180	TAAGTCACTGTATATATACT
67094	65181	GTAAGTCACTGTATATATAC
67095	65182	TGTAAGTCACTGTATATATA
67096	65183	CTGTAAGTCACTGTATATAT
67097	65184	TCTGTAAGTCACTGTATATA
67098	65185	ATCTGTAAGTCACTGTATAT
67099	65186	TATCTGTAAGTCACTGTATA
67100	65187	TTATCTGTAAGTCACTGTAT
67101	65188	GTTATCTGTAAGTCACTGTA
67102	65189	TGTTATCTGTAAGTCACTGT
67103	65190	CTGTTATCTGTAAGTCACTG

116180	114267	TCTGTCACTCTTAGTTTTAT
116181	114268	TTCTGTCACTCTTAGTTTTA
116182	114269	ATTCTGTCACTCTTAGTTTT
116183	114270	TATTCTGTCACTCTTAGTTT
116184	114271	GTATTCTGTCACTCTTAGTT
116185	114272	GGTATTCTGTCACTCTTAGT
116186	114273	AGGTATTCTGTCACTCTTAG
116187	114274	AAGGTATTCTGTCACTCTTA
116188	114275	CAAGGTATTCTGTCACTCTT
116189	114276	ACAAGGTATTCTGTCACTCT
116190	114277	AACAAGGTATTCTGTCACTC
116191	114278	TAACAAGGTATTCTGTCACT
116192	114279	ATAACAAGGTATTCTGTCAC
116193	114280	AATAACAAGGTATTCTGTCA
116194	114281	TAATAACAAGGTATTCTGTC
116195	114282	ATAATAACAAGGTATTCTGT
116196	114283	GATAATAACAAGGTATTCTG
116197	114284	TGATAATAACAAGGTATTCT
116198	114285	ATGATAATAACAAGGTATTC
116199	114286	TATGATAATAACAAGGTATT
116200	114287	CTATGATAATAACAAGGTAT
116201	114288	CCTATGATAATAACAAGGTA
116202	114289	ACCTATGATAATAACAAGGT
116203	114290	CACCTATGATAATAACAAGG
116204	114291	GCACCTATGATAATAACAAG
116205	114292	GGCACCTATGATAATAACAA
116206	114293	AGGCACCTATGATAATAACA
116207	114294	TAGGCACCTATGATAATAAC
116208	114295	TTAGGCACCTATGATAATAA
116209	114296	ATTAGGCACCTATGATAATA
116210	114297	CATTAGGCACCTATGATAAT
116211	114298	ACATTAGGCACCTATGATAA
116212	114299	AACATTAGGCACCTATGATA
116213	114300	TAACATTAGGCACCTATGAT
116214	114301	TTAACATTAGGCACCTATGA
116215	114302	ATTAACATTAGGCACCTATG
116216	114303	AATTAACATTAGGCACCTAT
116217	114304	AAATTAACATTAGGCACCTA
116218	114305	AAAATTAACATTAGGCACCT
116219	114306	AAAAATTAACATTAGGCACC
116220	114307	AAAAAATTAACATTAGGCAC
116221	114308	AAAAAAATTAACATTAGGCA
116222	114309	AAAAAAAATTAACATTAGGC
116223	114310	AAAAAAAAATTAACATTAGG
116224	114311	AAAAAAAAAATTAACATTAG
116225	114312	TAAAAAAAAAATTAACATTA
116226	114313	TTAAAAAAAAAATTAACATT
116227	114314	ATTAAAAAAAAAATTAACAT
116228	114315	AATTAAAAAAAAAATTAACA
116229	114316	GAATTAAAAAAAAAATTAAC
116230	114317	AGAATTAAAAAAAAAATTAA
116231	114318	GAGAATTAAAAAAAAAATTA
116232	114319	AGAGAATTAAAAAAAAAATT
116233	114320	GAGAGAATTAAAAAAAAAAT
116234	114321	TGAGAGAATTAAAAAAAAAA
116235	114322	TTGAGAGAATTAAAAAAAAA
116236	114323	CTTGAGAGAATTAAAAAAAA
116237	114324	GCTTGAGAGAATTAAAAAAA
116238	114325	GGCTTGAGAGAATTAAAAAA
116239	114326	AGGCTTGAGAGAATTAAAAA
116240	114327	AAGGCTTGAGAGAATTAAAA
116241	114328	AAAGGCTTGAGAGAATTAAA
116242	114329	TAAAGGCTTGAGAGAATTAA
116243	114330	ATAAAGGCTTGAGAGAATTA
116244	114331	TATAAAGGCTTGAGAGAATT
116245	114332	GTATAAAGGCTTGAGAGAAT
116246	114333	GGTATAAAGGCTTGAGAGAA
116247	114334	GGGTATAAAGGCTTGAGAGA
116248	114335	TGGGTATAAAGGCTTGAGAG
116249	114336	TTGGGTATAAAGGCTTGAGA
116250	114337	ATTGGGTATAAAGGCTTGAG

17957	16044	ATAAAAATTAGCTGGGCATG
17958	16045	TATAAAAATTAGCTGGGCAT
17959	16046	ATATAAAAATTAGCTGGGCA
17960	16047	AATATAAAAATTAGCTGGGC
17961	16048	AAATATAAAAATTAGCTGGG
17962	16049	AAAATATAAAAATTAGCTGG
17963	16050	AAAAATATAAAAATTAGCTG
17964	16051	TAAAAATATAAAAATTAGCT
17965	16052	CTAAAAATATAAAAATTAGC
17966	16053	ACTAAAAATATAAAAATTAG
17967	16054	TACTAAAAATATAAAAATTA
17968	16055	CTACTAAAAATATAAAAATT
17969	16056	TCTACTAAAAATATAAAAAT
17970	16057	CTCTACTAAAAATATAAAAA
17971	16058	TCTCTACTAAAAATATAAAA
17972	16059	GTCTCTACTAAAAATATAAA
17973	16060	CGTCTCTACTAAAAATATAA
17974	16061	CCGTCTCTACTAAAAATATA
17975	16062	CCCGTCTCTACTAAAAATAT
17976	16063	CCCCGTCTCTACTAAAAATA
17977	16064	ACCCCGTCTCTACTAAAAAT
17978	16065	AACCCCGTCTCTACTAAAAA
17979	16066	AAACCCCGTCTCTACTAAAA
17980	16067	AAAACCCCGTCTCTACTAAA
17981	16068	GAAAACCCCGTCTCTACTAA
17982	16069	CGAAAACCCCGTCTCTACTA
17983	16070	GCGAAAACCCCGTCTCTACT
17984	16071	GGCGAAAACCCCGTCTCTAC
17985	16072	TGGCGAAAACCCCGTCTCTA
17986	16073	ATGGCGAAAACCCCGTCTCT
17987	16074	CATGGCGAAAACCCCGTCTC
17988	16075	ACATGGCGAAAACCCCGTCT
17989	16076	AACATGGCGAAAACCCCGTC
17990	16077	CAACATGGCGAAAACCCCGT
17991	16078	ACAACATGGCGAAAACCCCG
17992	16079	AACAACATGGCGAAAACCCC
17993	16080	GAACAACATGGCGAAAACCC
17994	16081	TGAACAACATGGCGAAAACC
17995	16082	CTGAACAACATGGCGAAAAC
17996	16083	CCTGAACAACATGGCGAAAA
17997	16084	GCCTGAACAACATGGCGAAA
17998	16085	AGCCTGAACAACATGGCGAA
17999	16086	CAGCCTGAACAACATGGCGA
18000	16087	CCAGCCTGAACAACATGGCG
18001	16088	ACCAGCCTGAACAACATGGC
18002	16089	GACCAGCCTGAACAACATGG
18003	16090	AGACCAGCCTGAACAACATG
18004	16091	AAGACCAGCCTGAACAACAT
18005	16092	CAAGACCAGCCTGAACAACA
18006	16093	TCAAGACCAGCCTGAACAAC
18007	16094	TTCAAGACCAGCCTGAACAA
18008	16095	GTTCAAGACCAGCCTGAACA
18009	16096	AGTTCAAGACCAGCCTGAAC
18010	16097	GAGTTCAAGACCAGCCTGAA
18011	16098	GGAGTTCAAGACCAGCCTGA
18012	16099	AGGAGTTCAAGACCAGCCTG
18013	16100	CAGGAGTTCAAGACCAGCCT
18014	16101	TCAGGAGTTCAAGACCAGCC
18015	16102	GTCAGGAGTTCAAGACCAGC
18016	16103	GGTCAGGAGTTCAAGACCAG
18017	16104	AGGTCAGGAGTTCAAGACCA
18018	16105	GAGGTCAGGAGTTCAAGACC
18019	16106	TGAGGTCAGGAGTTCAAGAC
18020	16107	CTGAGGTCAGGAGTTCAAGA
18021	16108	CCTGAGGTCAGGAGTTCAAG
18022	16109	ACCTGAGGTCAGGAGTTCAA
18023	16110	CACCTGAGGTCAGGAGTTCA
18024	16111	CCACCTGAGGTCAGGAGTTC
18025	16112	ACCACCTGAGGTCAGGAGTT
18026	16113	GACCACCTGAGGTCAGGAGT
18027	16114	GGACCACCTGAGGTCAGGAG

67104	65191	CCTGTTATCTGTAAGTCACT
67105	65192	ACCTGTTATCTGTAAGTCAC
67106	65193	CACCTGTTATCTGTAAGTCA
67107	65194	ACACCTGTTATCTGTAAGTC
67108	65195	AACACCTGTTATCTGTAAGT
67109	65196	GAACACCTGTTATCTGTAAG
67110	65197	TGAACACCTGTTATCTGTAA
67111	65198	TTGAACACCTGTTATCTGTA
67112	65199	GTTGAACACCTGTTATCTGT
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67115	65202	TATGTTGAACACCTGTTATC
67116	65203	ATATGTTGAACACCTGTTAT
67117	65204	TATATGTTGAACACCTGTTA
67118	65205	ATATATGTTGAACACCTGTT
67119	65206	TATATATGTTGAACACCTGT
67120	65207	ATATATATGTTGAACACCTG
67121	65208	TATATATATGTTGAACACCT
67122	65209	ATATATATATGTTGAACACC
67123	65210	AATATATATATGTTGAACAC
67124	65211	GAATATATATATGTTGAACA
67125	65212	GGAATATATATATGTTGAAC
67126	65213	AGGAATATATATATGTTGAA
67127	65214	AAGGAATATATATATGTTGA
67128	65215	AAAGGAATATATATATGTTG
67129	65216	CAAAGGAATATATATATGTT
67130	65217	TCAAAGGAATATATATATGT
67131	65218	ATCAAAGGAATATATATATG
67132	65219	AATCAAAGGAATATATATAT
67133	65220	CAATCAAAGGAATATATATA
67134	65221	TCAATCAAAGGAATATATAT
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67143	65230	TTTCAAAAATCAATCAAAGG
67144	65231	TTTTCAAAAATCAATCAAAG
67145	65232	CTTTTCAAAAATCAATCAAA
67146	65233	ACTTTTCAAAAATCAATCAA
67147	65234	AACTTTTCAAAAATCAATCA
67148	65235	AAACTTTTCAAAAATCAATC
67149	65236	TAAACTTTTCAAAAATCAAT
67150	65237	GTAAACTTTTCAAAAATCAA
67151	65238	TGTAAACTTTTCAAAAATCA
67152	65239	ATGTAAACTTTTCAAAAATC
67153	65240	CATGTAAACTTTTCAAAAAT
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67158	65245	ATATACATGTAAACTTTTCA
67159	65246	TATATACATGTAAACTTTTC
67160	65247	ATATATACATGTAAACTTTT
67161	65248	AATATATACATGTAAACTTT
67162	65249	AAATATATACATGTAAACTT
67163	65250	AAAATATATACATGTAAACT
67164	65251	AAAAATATATACATGTAAAC
67165	65252	AAAAAATATATACATGTAAA
67166	65253	TAAAAAATATATACATGTAA
67167	65254	ATAAAAAATATATACATGTA
67168	65255	TATAAAAAATATATACATGT
67169	65256	ATATAAAAAATATATACATG
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67171	65258	GTATATAAAAAATATATACA
67172	65259	CGTATATAAAAAATATATAC
67173	65260	CCGTATATAAAAAATATATA
67174	65261	CCCGTATATAAAAAATATAT

116251	114338	TATTGGGTATAAAGGCTTGA
116252	114339	GTATTGGGTATAAAGGCTTG
116253	114340	GGTATTGGGTATAAAGGCTT
116254	114341	AGGTATTGGGTATAAAGGCT
116255	114342	TAGGTATTGGGTATAAAGGC
116256	114343	ATAGGTATTGGGTATAAAGG
116257	114344	CATAGGTATTGGGTATAAAG
116258	114345	TCATAGGTATTGGGTATAAA
116259	114346	GTCATAGGTATTGGGTATAA
116260	114347	CGTCATAGGTATTGGGTATA
116261	114348	GCGTCATAGGTATTGGGTAT
116262	114349	GGCGTCATAGGTATTGGGTA
116263	114350	GGGCGTCATAGGTATTGGGT
116264	114351	TGGGCGTCATAGGTATTGGG
116265	114352	ATGGGCGTCATAGGTATTGG
116266	114353	CATGGGCGTCATAGGTATTG
116267	114354	GCATGGGCGTCATAGGTATT
116268	114355	GGCATGGGCGTCATAGGTAT
116269	114356	TGGCATGGGCGTCATAGGTA
116270	114357	CTGGCATGGGCGTCATAGGT
116271	114358	ACTGGCATGGGCGTCATAGG
116272	114359	CACTGGCATGGGCGTCATAG
116273	114360	TCACTGGCATGGGCGTCATA
116274	114361	TTCACTGGCATGGGCGTCAT
116275	114362	ATTCACTGGCATGGGCGTCA
116276	114363	GATTCACTGGCATGGGCGTC
116277	114364	TGATTCACTGGCATGGGCGT
116278	114365	TTGATTCACTGGCATGGGCG
116279	114366	CTTGATTCACTGGCATGGGC
116280	114367	GCTTGATTCACTGGCATGGG
116281	114368	GGCTTGATTCACTGGCATGG
116282	114369	TGGCTTGATTCACTGGCATG
116283	114370	TTGGCTTGATTCACTGGCAT
116284	114371	CTTGGCTTGATTCACTGGCA
116285	114372	TCTTGGCTTGATTCACTGGC
116286	114373	GTCTTGGCTTGATTCACTGG
116287	114374	TGTCTTGGCTTGATTCACTG
116288	114375	ATGTCTTGGCTTGATTCACT
116289	114376	TATGTCTTGGCTTGATTCAC
116290	114377	ATATGTCTTGGCTTGATTCA
116291	114378	TATATGTCTTGGCTTGATTC
116292	114379	CTATATGTCTTGGCTTGATT
116293	114380	TCTATATGTCTTGGCTTGAT
116294	114381	CTCTATATGTCTTGGCTTGA
116295	114382	GCTCTATATGTCTTGGCTTG
116296	114383	TGCTCTATATGTCTTGGCTT
116297	114384	CTGCTCTATATGTCTTGGCT
116298	114385	CCTGCTCTATATGTCTTGGC
116299	114386	ACCTGCTCTATATGTCTTGG
116300	114387	TACCTGCTCTATATGTCTTG
116301	114388	TTACCTGCTCTATATGTCTT
116302	114389	TTTACCTGCTCTATATGTCT
116303	114390	CTTTACCTGCTCTATATGTC
116304	114391	CCTTTACCTGCTCTATATGT
116305	114392	ACCTTTACCTGCTCTATATG
116306	114393	CACCTTTACCTGCTCTATAT
116307	114394	TCACCTTTACCTGCTCTATA
116308	114395	CTCACCTTTACCTGCTCTAT
116309	114396	TCTCACCTTTACCTGCTCTA
116310	114397	TTCTCACCTTTACCTGCTCT
116311	114398	ATTCTCACCTTTACCTGCTC
116312	114399	TATTCTCACCTTTACCTGCT
116313	114400	TTATTCTCACCTTTACCTGC
116314	114401	ATTATTCTCACCTTTACCTG
116315	114402	GATTATTCTCACCTTTACCT
116316	114403	GGATTATTCTCACCTTTACC
116317	114404	AGGATTATTCTCACCTTTAC
116318	114405	CAGGATTATTCTCACCTTTA
116319	114406	GCAGGATTATTCTCACCTTT
116320	114407	GGCAGGATTATTCTCACCTT
116321	114408	AGGCAGGATTATTCTCACCT

18028	16115	CGGACCACCTGAGGTCAGGA
18029	16116	GCGGACCACCTGAGGTCAGG
18030	16117	GGCGGACCACCTGAGGTCAG
18031	16118	GGGCGGACCACCTGAGGTCA
18032	16119	TGGGCGGACCACCTGAGGTC
18033	16120	GTGGGCGGACCACCTGAGGT
18034	16121	GGTGGGCGGACCACCTGAGG
18035	16122	AGGTGGGCGGACCACCTGAG
18036	16123	CAGGTGGGCGGACCACCTGA
18037	16124	CCAGGTGGGCGGACCACCTG
18038	16125	CCCAGGTGGGCGGACCACCT
18039	16126	GCCCAGGTGGGCGGACCACC
18040	16127	GGCCCAGGTGGGCGGACCAC
18041	16128	AGGCCCAGGTGGGCGGACCA
18042	16129	GAGGCCCAGGTGGGCGGACC
18043	16130	GGAGGCCCAGGTGGGCGGAC
18044	16131	GGGAGGCCCAGGTGGGCGGA
18045	16132	TGGGAGGCCCAGGTGGGCGG
18046	16133	TTGGGAGGCCCAGGTGGGCG
18047	16134	GTTGGGAGGCCCAGGTGGGC
18048	16135	CGTTGGGAGGCCCAGGTGGG
18049	16136	ACGTTGGGAGGCCCAGGTGG
18050	16137	CACGTTGGGAGGCCCAGGTG
18051	16138	GCACGTTGGGAGGCCCAGGT
18052	16139	AGCACGTTGGGAGGCCCAGG
18053	16140	CAGCACGTTGGGAGGCCCAG
18054	16141	CCAGCACGTTGGGAGGCCCA
18055	16142	CCCAGCACGTTGGGAGGCCC
18056	16143	TCCCAGCACGTTGGGAGGCC
18057	16144	ATCCCAGCACGTTGGGAGGC
18058	16145	AATCCCAGCACGTTGGGAGG
18059	16146	TAATCCCAGCACGTTGGGAG
18060	16147	GTAATCCCAGCACGTTGGGA
18061	16148	TGTAATCCCAGCACGTTGGG
18062	16149	CTGTAATCCCAGCACGTTGG
18063	16150	CCTGTAATCCCAGCACGTTG
18064	16151	GCCTGTAATCCCAGCACGTT
18065	16152	TGCCTGTAATCCCAGCACGT
18066	16153	ATGCCTGTAATCCCAGCACG
18067	16154	CATGCCTGTAATCCCAGCAC
18068	16155	TCATGCCTGTAATCCCAGCA
18069	16156	ATCATGCCTGTAATCCCAGC
18070	16157	GATCATGCCTGTAATCCCAG
18071	16158	AGATCATGCCTGTAATCCCA
18072	16159	TAGATCATGCCTGTAATCCC
18073	16160	GTAGATCATGCCTGTAATCC
18074	16161	GGTAGATCATGCCTGTAATC
18075	16162	CGGTAGATCATGCCTGTAAT
18076	16163	ACGGTAGATCATGCCTGTAA
18077	16164	CACGGTAGATCATGCCTGTA
18078	16165	GCACGGTAGATCATGCCTGT
18079	16166	GGCACGGTAGATCATGCCTG
18080	16167	AGGCACGGTAGATCATGCCT
18081	16168	CAGGCACGGTAGATCATGCC
18082	16169	CCAGGCACGGTAGATCATGC
18083	16170	GCCAGGCACGGTAGATCATG
18084	16171	GGCCAGGCACGGTAGATCAT
18085	16172	TGGCCAGGCACGGTAGATCA
18086	16173	ATGGCCAGGCACGGTAGATC
18087	16174	CATGGCCAGGCACGGTAGAT
18088	16175	CCATGGCCAGGCACGGTAGA
18089	16176	ACCATGGCCAGGCACGGTAG
18090	16177	AACCATGGCCAGGCACGGTA
18091	16178	GAACCATGGCCAGGCACGGT
18092	16179	TGAACCATGGCCAGGCACGG
18093	16180	GTGAACCATGGCCAGGCACG
18094	16181	AGTGAACCATGGCCAGGCAC
18095	16182	GAGTGAACCATGGCCAGGCA
18096	16183	AGAGTGAACCATGGCCAGGC
18097	16184	AAGAGTGAACCATGGCCAGG
18098	16185	GAAGAGTGAACCATGGCCAG

67175	65262	CCCCGTATATAAAAAATATA
67176	65263	ACCCCGTATATAAAAAATAT
67177	65264	GACCCCGTATATAAAAAATA
67178	65265	AGACCCCGTATATAAAAAAT
67179	65266	GAGACCCCGTATATAAAAAA
67180	65267	TGAGACCCCGTATATAAAAA
67181	65268	GTGAGACCCCGTATATAAAA
67182	65269	AGTGAGACCCCGTATATAAA
67183	65270	GAGTGAGACCCCGTATATAA
67184	65271	AGAGTGAGACCCCGTATATA
67185	65272	TAGAGTGAGACCCCGTATAT
67186	65273	ATAGAGTGAGACCCCGTATA
67187	65274	GATAGAGTGAGACCCCGTAT
67188	65275	TGATAGAGTGAGACCCCGTA
67189	65276	GTGATAGAGTGAGACCCCGT
67190	65277	AGTGATAGAGTGAGACCCCG
67191	65278	CAGTGATAGAGTGAGACCCC
67192	65279	TCAGTGATAGAGTGAGACCC
67193	65280	CTCAGTGATAGAGTGAGACC
67194	65281	CCTCAGTGATAGAGTGAGAC
67195	65282	ACCTCAGTGATAGAGTGAGA
67196	65283	AACCTCAGTGATAGAGTGAG
67197	65284	CAACCTCAGTGATAGAGTGA
67198	65285	CCAACCTCAGTGATAGAGTG
67199	65286	TCCAACCTCAGTGATAGAGT
67200	65287	CTCCAACCTCAGTGATAGAG
67201	65288	ACTCCAACCTCAGTGATAGA
67202	65289	CACTCCAACCTCAGTGATAG
67203	65290	ACACTCCAACCTCAGTGATA
67204	65291	CACACTCCAACCTCAGTGAT
67205	65292	CCACACTCCAACCTCAGTGA
67206	65293	ACCACACTCCAACCTCAGTG
67207	65294	CACCACACTCCAACCTCAGT
67208	65295	TCACCACACTCCAACCTCAG
67209	65296	ATCACCACACTCCAACCTCA
67210	65297	CATCACCACACTCCAACCTC
67211	65298	GCATCACCACACTCCAACCT
67212	65299	TGCATCACCACACTCCAACC
67213	65300	CTGCATCACCACACTCCAAC
67214	65301	TCTGCATCACCACACTCCAA
67215	65302	ATCTGCATCACCACACTCCA
67216	65303	GATCTGCATCACCACACTCC
67217	65304	AGATCTGCATCACCACACTC
67218	65305	AAGATCTGCATCACCACACT
67219	65306	CAAGATCTGCATCACCACAC
67220	65307	CCAAGATCTGCATCACCACA
67221	65308	GCCAAGATCTGCATCACCAC
67222	65309	AGCCAAGATCTGCATCACCA
67223	65310	GAGCCAAGATCTGCATCACC
67224	65311	TGAGCCAAGATCTGCATCAC
67225	65312	GTGAGCCAAGATCTGCATCA
67226	65313	GGTGAGCCAAGATCTGCATC
67227	65314	CGGTGAGCCAAGATCTGCAT
67228	65315	GCGGTGAGCCAAGATCTGCA
67229	65316	TGCGGTGAGCCAAGATCTGC
67230	65317	TTGCGGTGAGCCAAGATCTG
67231	65318	GTTGCGGTGAGCCAAGATCT
67232	65319	GGTTGCGGTGAGCCAAGATC
67233	65320	AGGTTGCGGTGAGCCAAGAT
67234	65321	GAGGTTGCGGTGAGCCAAGA
67235	65322	GGAGGTTGCGGTGAGCCAAG
67236	65323	AGGAGGTTGCGGTGAGCCAA
67237	65324	GAGGAGGTTGCGGTGAGCCA
67238	65325	GGAGGAGGTTGCGGTGAGCC
67239	65326	AGGAGGAGGTTGCGGTGAGC
67240	65327	GAGGAGGAGGTTGCGGTGAG
67241	65328	GGAGGAGGAGGTTGCGGTGA
67242	65329	GGGAGGAGGAGGTTGCGGTG
67243	65330	TGGGAGGAGGAGGTTGCGGT
67244	65331	CTGGGAGGAGGAGGTTGCGG
67245	65332	CCTGGGAGGAGGAGGTTGCG

116322	114409	CAGGCAGGATTATTCTCACC
116323	114410	ACAGGCAGGATTATTCTCAC
116324	114411	CACAGGCAGGATTATTCTCA
116325	114412	ACACAGGCAGGATTATTCTC
116326	114413	AACACAGGCAGGATTATTCT
116327	114414	AAACACAGGCAGGATTATTC
116328	114415	CAAACACAGGCAGGATTATT
116329	114416	GCAAACACAGGCAGGATTAT
116330	114417	AGCAAACACAGGCAGGATTA
116331	114418	AAGCAAACACAGGCAGGATT
116332	114419	CAAGCAAACACAGGCAGGAT
116333	114420	ACAAGCAAACACAGGCAGGA
116334	114421	TACAAGCAAACACAGGCAGG
116335	114422	CTACAAGCAAACACAGGCAG
116336	114423	ACTACAAGCAAACACAGGCA
116337	114424	AACTACAAGCAAACACAGGC
116338	114425	AAACTACAAGCAAACACAGG
116339	114426	CAAACTACAAGCAAACACAG
116340	114427	GCAAACTACAAGCAAACACA
116341	114428	TGCAAACTACAAGCAAACAC
116342	114429	ATGCAAACTACAAGCAAACA
116343	114430	CATGCAAACTACAAGCAAAC
116344	114431	GCATGCAAACTACAAGCAAA
116345	114432	AGCATGCAAACTACAAGCAA
116346	114433	CAGCATGCAAACTACAAGCA
116347	114434	GCAGCATGCAAACTACAAGC
116348	114435	TGCAGCATGCAAACTACAAG
116349	114436	ATGCAGCATGCAAACTACAA
116350	114437	CATGCAGCATGCAAACTACA
116351	114438	TCATGCAGCATGCAAACTAC
116352	114439	TTCATGCAGCATGCAAACTA
116353	114440	ATTCATGCAGCATGCAAACT
116354	114441	AATTCATGCAGCATGCAAAC
116355	114442	CAATTCATGCAGCATGCAAA
116356	114443	TCAATTCATGCAGCATGCAA
116357	114444	CTCAATTCATGCAGCATGCA
116358	114445	ACTCAATTCATGCAGCATGC
116359	114446	TACTCAATTCATGCAGCATG
116360	114447	TTACTCAATTCATGCAGCAT
116361	114448	GTTACTCAATTCATGCAGCA
116362	114449	AGTTACTCAATTCATGCAGC
116363	114450	TAGTTACTCAATTCATGCAG
116364	114451	TTAGTTACTCAATTCATGCA
116365	114452	CTTAGTTACTCAATTCATGC
116366	114453	ACTTAGTTACTCAATTCATG
116367	114454	AACTTAGTTACTCAATTCAT
116368	114455	AAACTTAGTTACTCAATTCA
116369	114456	TAAACTTAGTTACTCAATTC
116370	114457	ATAAACTTAGTTACTCAATT
116371	114458	TATAAACTTAGTTACTCAAT
116372	114459	TTATAAACTTAGTTACTCAA
116373	114460	ATTATAAACTTAGTTACTCA
116374	114461	CATTATAAACTTAGTTACTC
116375	114462	TCATTATAAACTTAGTTACT
116376	114463	TTCATTATAAACTTAGTTAC
116377	114464	ATTCATTATAAACTTAGTTA
116378	114465	TATTCATTATAAACTTAGTT
116379	114466	TTATTCATTATAAACTTAGT
116380	114467	TTTATTCATTATAAACTTAG
116381	114468	ATTTATTCATTATAAACTTA
116382	114469	TATTTATTCATTATAAACTT
116383	114470	CTATTTATTCATTATAAACT
116384	114471	ACTATTTATTCATTATAAAC
116385	114472	AACTATTTATTCATTATAAA
116386	114473	CAACTATTTATTCATTATAA
116387	114474	ACAACTATTTATTCATTATA
116388	114475	TACAACTATTTATTCATTAT
116389	114476	CTACAACTATTTATTCATTA
116390	114477	ACTACAACTATTTATTCATT
116391	114478	AACTACAACTATTTATTCAT
116392	114479	AAACTACAACTATTTATTCA

18099	16186	TGAAGAGTGAACCATGGCCA
18100	16187	CTGAAGAGTGAACCATGGCC
18101	16188	ACTGAAGAGTGAACCATGGC
18102	16189	TACTGAAGAGTGAACCATGG
18103	16190	TTACTGAAGAGTGAACCATG
18104	16191	GTTACTGAAGAGTGAACCAT
18105	16192	AGTTACTGAAGAGTGAACCA
18106	16193	TAGTTACTGAAGAGTGAACC
18107	16194	TTAGTTACTGAAGAGTGAAC
18108	16195	TTTAGTTACTGAAGAGTGAA
18109	16196	TTTTAGTTACTGAAGAGTGA
18110	16197	ATTTTAGTTACTGAAGAGTG
18111	16198	AATTTTAGTTACTGAAGAGT
18112	16199	AAATTTTAGTTACTGAAGAG
18113	16200	TAAATTTTAGTTACTGAAGA
18114	16201	TTAAATTTTAGTTACTGAAG
18115	16202	CTTAAATTTTAGTTACTGAA
18116	16203	GCTTAAATTTTAGTTACTGA
18117	16204	AGCTTAAATTTTAGTTACTG
18118	16205	GAGCTTAAATTTTAGTTACT
18119	16206	AGAGCTTAAATTTTAGTTAC
18120	16207	TAGAGCTTAAATTTTAGTTA
18121	16208	ATAGAGCTTAAATTTTAGTT
18122	16209	CATAGAGCTTAAATTTTAGT
18123	16210	TCATAGAGCTTAAATTTTAG
18124	16211	TTCATAGAGCTTAAATTTTA
18125	16212	TTTCATAGAGCTTAAATTTT
18126	16213	CTTTCATAGAGCTTAAATTT
18127	16214	GCTTTCATAGAGCTTAAATT
18128	16215	TGCTTTCATAGAGCTTAAAT
18129	16216	CTGCTTTCATAGAGCTTAAA
18130	16217	CCTGCTTTCATAGAGCTTAA
18131	16218	TCCTGCTTTCATAGAGCTTA
18132	16219	TTCCTGCTTTCATAGAGCTT
18133	16220	GTTCCTGCTTTCATAGAGCT
18134	16221	AGTTCCTGCTTTCATAGAGC
18135	16222	AAGTTCCTGCTTTCATAGAG
18136	16223	AAAGTTCCTGCTTTCATAGA
18137	16224	CAAAGTTCCTGCTTTCATAG
18138	16225	ACAAAGTTCCTGCTTTCATA
18139	16226	AACAAAGTTCCTGCTTTCAT
18140	16227	AAACAAAGTTCCTGCTTTCA
18141	16228	AAAACAAAGTTCCTGCTTTC
18142	16229	CAAAACAAAGTTCCTGCTTT
18143	16230	ACAAAACAAAGTTCCTGCTT
18144	16231	AACAAAACAAAGTTCCTGCT
18145	16232	GAACAAAACAAAGTTCCTGC
18146	16233	TGAACAAAACAAAGTTCCTG
18147	16234	GTGAACAAAACAAAGTTCCT
18148	16235	AGTGAACAAAACAAAGTTCC
18149	16236	TAGTGAACAAAACAAAGTTC
18150	16237	ATAGTGAACAAAACAAAGTT
18151	16238	AATAGTGAACAAAACAAAGT
18152	16239	CAATAGTGAACAAAACAAAG
18153	16240	TCAATAGTGAACAAAACAAA
18154	16241	ATCAATAGTGAACAAAACAA
18155	16242	AATCAATAGTGAACAAAACA
18156	16243	CAATCAATAGTGAACAAAAC
18157	16244	ACAATCAATAGTGAACAAAA
18158	16245	TACAATCAATAGTGAACAAA
18159	16246	ATACAATCAATAGTGAACAA
18160	16247	GATACAATCAATAGTGAACA
18161	16248	GGATACAATCAATAGTGAAC
18162	16249	GGGATACAATCAATAGTGAA
18163	16250	AGGGATACAATCAATAGTGA
18164	16251	TAGGGATACAATCAATAGTG
18165	16252	ATAGGGATACAATCAATAGT
18166	16253	AATAGGGATACAATCAATAG
18167	16254	AAATAGGGATACAATCAATA
18168	16255	GAAATAGGGATACAATCAAT
18169	16256	AGAAATAGGGATACAATCAA

67246	65333	GCCTGGGAGGAGGAGGTTGC
67247	65334	AGCCTGGGAGGAGGAGGTTG
67248	65335	GAGCCTGGGAGGAGGAGGTT
67249	65336	TGAGCCTGGGAGGAGGAGGT
67250	65337	TTGAGCCTGGGAGGAGGAGG
67251	65338	CTTGAGCCTGGGAGGAGGAG
67252	65339	ACTTGAGCCTGGGAGGAGGA
67253	65340	CACTTGAGCCTGGGAGGAGG
67254	65341	TCACTTGAGCCTGGGAGGAG
67255	65342	ATCACTTGAGCCTGGGAGGA
67256	65343	AATCACTTGAGCCTGGGAGG
67257	65344	GAATCACTTGAGCCTGGGAG
67258	65345	AGAATCACTTGAGCCTGGGA
67259	65346	GAGAATCACTTGAGCCTGGG
67260	65347	GGAGAATCACTTGAGCCTGG
67261	65348	GGGAGAATCACTTGAGCCTG
67262	65349	TGGGAGAATCACTTGAGCCT
67263	65350	GTGGGAGAATCACTTGAGCC
67264	65351	GGTGGGAGAATCACTTGAGC
67265	65352	AGGTGGGAGAATCACTTGAG
67266	65353	GAGGTGGGAGAATCACTTGA
67267	65354	TGAGGTGGGAGAATCACTTG
67268	65355	CTGAGGTGGGAGAATCACTT
67269	65356	GCTGAGGTGGGAGAATCACT
67270	65357	GGCTGAGGTGGGAGAATCAC
67271	65358	AGGCTGAGGTGGGAGAATCA
67272	65359	GAGGCTGAGGTGGGAGAATC
67273	65360	GGAGGCTGAGGTGGGAGAAT
67274	65361	GGGAGGCTGAGGTGGGAGAA
67275	65362	CGGGAGGCTGAGGTGGGAGA
67276	65363	TCGGGAGGCTGAGGTGGGAG
67277	65364	CTCGGGAGGCTGAGGTGGGA
67278	65365	ACTCGGGAGGCTGAGGTGGG
67279	65366	TACTCGGGAGGCTGAGGTGG
67280	65367	GTACTCGGGAGGCTGAGGTG
67281	65368	GGTACTCGGGAGGCTGAGGT
67282	65369	AGGTACTCGGGAGGCTGAGG
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67285	65372	CCCAGGTACTCGGGAGGCTG
67286	65373	TCCCAGGTACTCGGGAGGCT
67287	65374	GTCCCAGGTACTCGGGAGGC
67288	65375	GGTCCCAGGTACTCGGGAGG
67289	65376	TGGTCCCAGGTACTCGGGAG
67290	65377	GTGGTCCCAGGTACTCGGGA
67291	65378	TGTGGTCCCAGGTACTCGGG
67292	65379	CTGTGGTCCCAGGTACTCGG
67293	65380	CCTGTGGTCCCAGGTACTCG
67294	65381	ACCTGTGGTCCCAGGTACTC
67295	65382	CACCTGTGGTCCCAGGTACT
67296	65383	GCACCTGTGGTCCCAGGTAC
67297	65384	CGCACCTGTGGTCCCAGGTA
67298	65385	GCGCACCTGTGGTCCCAGGT
67299	65386	TGCGCACCTGTGGTCCCAGG
67300	65387	ATGCGCACCTGTGGTCCCAG
67301	65388	GATGCGCACCTGTGGTCCCA
67302	65389	TGATGCGCACCTGTGGTCCC
67303	65390	GTGATGCGCACCTGTGGTCC
67304	65391	GGTGATGCGCACCTGTGGTC
67305	65392	TGGTGATGCGCACCTGTGGT
67306	65393	ATGGTGATGCGCACCTGTGG
67307	65394	CATGGTGATGCGCACCTGTG
67308	65395	GCATGGTGATGCGCACCTGT
67309	65396	GGCATGGTGATGCGCACCTG
67310	65397	AGGCATGGTGATGCGCACCT
67311	65398	CAGGCATGGTGATGCGCACC
67312	65399	CCAGGCATGGTGATGCGCAC
67313	65400	GCCAGGCATGGTGATGCGCA
67314	65401	AGCCAGGCATGGTGATGCGC
67315	65402	TAGCCAGGCATGGTGATGCG
67316	65403	TTAGCCAGGCATGGTGATGC

116393	114480	TAAACTACAACTATTTATTC
116394	114481	CTAAACTACAACTATTTATT
116395	114482	GCTAAACTACAACTATTTAT
116396	114483	AGCTAAACTACAACTATTTA
116397	114484	GAGCTAAACTACAACTATTT
116398	114485	AGAGCTAAACTACAACTATT
116399	114486	CAGAGCTAAACTACAACTAT
116400	114487	TCAGAGCTAAACTACAACTA
116401	114488	GTCAGAGCTAAACTACAACT
116402	114489	AGTCAGAGCTAAACTACAAC
116403	114490	AAGTCAGAGCTAAACTACAA
116404	114491	AAAGTCAGAGCTAAACTACA
116405	114492	AAAAGTCAGAGCTAAACTAC
116406	114493	AAAAAGTCAGAGCTAAACTA
116407	114494	CAAAAAGTCAGAGCTAAACT
116408	114495	TCAAAAAGTCAGAGCTAAAC
116409	114496	ATCAAAAAGTCAGAGCTAAA
116410	114497	CATCAAAAAGTCAGAGCTAA
116411	114498	TCATCAAAAAGTCAGAGCTA
116412	114499	CTCATCAAAAAGTCAGAGCT
116413	114500	CCTCATCAAAAAGTCAGAGC
116414	114501	GCCTCATCAAAAAGTCAGAG
116415	114502	AGCCTCATCAAAAAGTCAGA
116416	114503	TAGCCTCATCAAAAAGTCAG
116417	114504	ATAGCCTCATCAAAAAGTCA
116418	114505	CATAGCCTCATCAAAAAGTC
116419	114506	GCATAGCCTCATCAAAAAGT
116420	114507	TGCATAGCCTCATCAAAAAG
116421	114508	ATGCATAGCCTCATCAAAAA
116422	114509	AATGCATAGCCTCATCAAAA
116423	114510	CAATGCATAGCCTCATCAAA
116424	114511	CCAATGCATAGCCTCATCAA
116425	114512	GCCAATGCATAGCCTCATCA
116426	114513	AGCCAATGCATAGCCTCATC
116427	114514	AAGCCAATGCATAGCCTCAT
116428	114515	AAAGCCAATGCATAGCCTCA
116429	114516	AAAAGCCAATGCATAGCCTC
116430	114517	CAAAAGCCAATGCATAGCCT
116431	114518	TCAAAAGCCAATGCATAGCC
116432	114519	ATCAAAAGCCAATGCATAGC
116433	114520	CATCAAAAGCCAATGCATAG
116434	114521	TCATCAAAAGCCAATGCATA
116435	114522	TTCATCAAAAGCCAATGCAT
116436	114523	GTTCATCAAAAGCCAATGCA
116437	114524	TGTTCATCAAAAGCCAATGC
116438	114525	TTGTTCATCAAAAGCCAATG
116439	114526	GTTGTTCATCAAAAGCCAAT
116440	114527	TGTTGTTCATCAAAAGCCAA
116441	114528	ATGTTGTTCATCAAAAGCCA
116442	114529	AATGTTGTTCATCAAAAGCC
116443	114530	TAATGTTGTTCATCAAAAGC
116444	114531	GTAATGTTGTTCATCAAAAG
116445	114532	TGTAATGTTGTTCATCAAAA
116446	114533	ATGTAATGTTGTTCATCAAA
116447	114534	TATGTAATGTTGTTCATCAA
116448	114535	CTATGTAATGTTGTTCATCA
116449	114536	TCTATGTAATGTTGTTCATC
116450	114537	ATCTATGTAATGTTGTTCAT
116451	114538	TATCTATGTAATGTTGTTCA
116452	114539	ATATCTATGTAATGTTGTTC
116453	114540	AATATCTATGTAATGTTGTT
116454	114541	GAATATCTATGTAATGTTGT
116455	114542	TGAATATCTATGTAATGTTG
116456	114543	GTGAATATCTATGTAATGTT
116457	114544	TGTGAATATCTATGTAATGT
116458	114545	ATGTGAATATCTATGTAATG
116459	114546	CATGTGAATATCTATGTAAT
116460	114547	CCATGTGAATATCTATGTAA
116461	114548	TCCATGTGAATATCTATGTA
116462	114549	ATCCATGTGAATATCTATGT
116463	114550	AATCCATGTGAATATCTATG

18170	16257	AAGAAATAGGGATACAATCA
18171	16258	CAAGAAATAGGGATACAATC
18172	16259	TCAAGAAATAGGGATACAAT
18173	16260	TTCAAGAAATAGGGATACAA
18174	16261	ATTCAAGAAATAGGGATACA
18175	16262	CATTCAAGAAATAGGGATAC
18176	16263	CCATTCAAGAAATAGGGATA
18177	16264	ACCATTCAAGAAATAGGGAT
18178	16265	AACCATTCAAGAAATAGGGA
18179	16266	CAACCATTCAAGAAATAGGG
18180	16267	CCAACCATTCAAGAAATAGG
18181	16268	GCCAACCATTCAAGAAATAG
18182	16269	TGCCAACCATTCAAGAAATA
18183	16270	GTGCCAACCATTCAAGAAAT
18184	16271	AGTGCCAACCATTCAAGAAA
18185	16272	AAGTGCCAACCATTCAAGAA
18186	16273	TAAGTGCCAACCATTCAAGA
18187	16274	TTAAGTGCCAACCATTCAAG
18188	16275	GTTAAGTGCCAACCATTCAA
18189	16276	AGTTAAGTGCCAACCATTCA
18190	16277	CAGTTAAGTGCCAACCATTC
18191	16278	GCAGTTAAGTGCCAACCATT
18192	16279	AGCAGTTAAGTGCCAACCAT
18193	16280	AAGCAGTTAAGTGCCAACCA
18194	16281	CAAGCAGTTAAGTGCCAACC
18195	16282	CCAAGCAGTTAAGTGCCAAC
18196	16283	ACCAAGCAGTTAAGTGCCAA
18197	16284	GACCAAGCAGTTAAGTGCCA
18198	16285	TGACCAAGCAGTTAAGTGCC
18199	16286	GTGACCAAGCAGTTAAGTGC
18200	16287	TGTGACCAAGCAGTTAAGTG
18201	16288	ATGTGACCAAGCAGTTAAGT
18202	16289	CATGTGACCAAGCAGTTAAG
18203	16290	ACATGTGACCAAGCAGTTAA
18204	16291	AACATGTGACCAAGCAGTTA
18205	16292	AAACATGTGACCAAGCAGTT
18206	16293	CAAACATGTGACCAAGCAGT
18207	16294	TCAAACATGTGACCAAGCAG
18208	16295	TTCAAACATGTGACCAAGCA
18209	16296	ATTCAAACATGTGACCAAGC
18210	16297	CATTCAAACATGTGACCAAG
18211	16298	CCATTCAAACATGTGACCAA
18212	16299	CCCATTCAAACATGTGACCA
18213	16300	GCCCATTCAAACATGTGACC
18214	16301	TGCCCATTCAAACATGTGAC
18215	16302	TTGCCCATTCAAACATGTGA
18216	16303	CTTGCCCATTCAAACATGTG
18217	16304	ACTTGCCCATTCAAACATGT
18218	16305	AACTTGCCCATTCAAACATG
18219	16306	TAACTTGCCCATTCAAACAT
18220	16307	GTAACTTGCCCATTCAAACA
18221	16308	AGTAACTTGCCCATTCAAAC
18222	16309	GAGTAACTTGCCCATTCAAA
18223	16310	TGAGTAACTTGCCCATTCAA
18224	16311	CTGAGTAACTTGCCCATTCA
18225	16312	GCTGAGTAACTTGCCCATTC
18226	16313	GGCTGAGTAACTTGCCCATT
18227	16314	TGGCTGAGTAACTTGCCCAT
18228	16315	GTGGCTGAGTAACTTGCCCA
18229	16316	AGTGGCTGAGTAACTTGCCC
18230	16317	GAGTGGCTGAGTAACTTGCC
18231	16318	AGAGTGGCTGAGTAACTTGC
18232	16319	GAGAGTGGCTGAGTAACTTG
18233	16320	TGAGAGTGGCTGAGTAACTT
18234	16321	CTGAGAGTGGCTGAGTAACT
18235	16322	CCTGAGAGTGGCTGAGTAAC
18236	16323	GCCTGAGAGTGGCTGAGTAA
18237	16324	AGCCTGAGAGTGGCTGAGTA
18238	16325	AAGCCTGAGAGTGGCTGAGT
18239	16326	TAAGCCTGAGAGTGGCTGAG
18240	16327	CTAAGCCTGAGAGTGGCTGA

67317	65404	ATTAGCCAGGCATGGTGATG
67318	65405	AATTAGCCAGGCATGGTGAT
67319	65406	AAATTAGCCAGGCATGGTGA
67320	65407	AAAATTAGCCAGGCATGGTG
67321	65408	AAAAATTAGCCAGGCATGGT
67322	65409	AAAAAATTAGCCAGGCATGG
67323	65410	TAAAAAATTAGCCAGGCATG
67324	65411	ATAAAAAATTAGCCAGGCAT
67325	65412	TATAAAAAATTAGCCAGGCA
67326	65413	ATATAAAAAATTAGCCAGGC
67327	65414	AATATAAAAAATTAGCCAGG
67328	65415	AAATATAAAAAATTAGCCAG
67329	65416	AAAATATAAAAAATTAGCCA
67330	65417	AAAAATATAAAAAATTAGCC
67331	65418	CAAAAATATAAAAAATTAGC
67332	65419	CCAAAAATATAAAAAATTAG
67333	65420	ACCAAAAATATAAAAAATTA
67334	65421	TACCAAAAATATAAAAAATT
67335	65422	CTACCAAAAATATAAAAAAT
67336	65423	TCTACCAAAAATATAAAAAA
67337	65424	CTCTACCAAAAATATAAAAA
67338	65425	TCTCTACCAAAAATATAAAA
67339	65426	GTCTCTACCAAAAATATAAA
67340	65427	TGTCTCTACCAAAAATATAA
67341	65428	CTGTCTCTACCAAAAATATA
67342	65429	CCTGTCTCTACCAAAAATAT
67343	65430	TCCTGTCTCTACCAAAAATA
67344	65431	ATCCTGTCTCTACCAAAAAT
67345	65432	AATCCTGTCTCTACCAAAAA
67346	65433	AAATCCTGTCTCTACCAAAA
67347	65434	AAAATCCTGTCTCTACCAAA
67348	65435	CAAAATCCTGTCTCTACCAA
67349	65436	GCAAAATCCTGTCTCTACCA
67350	65437	GGCAAAATCCTGTCTCTACC
67351	65438	CGGCAAAATCCTGTCTCTAC
67352	65439	ACGGCAAAATCCTGTCTCTA
67353	65440	CACGGCAAAATCCTGTCTCT
67354	65441	ACACGGCAAAATCCTGTCTC
67355	65442	AACACGGCAAAATCCTGTCT
67356	65443	CAACACGGCAAAATCCTGTC
67357	65444	GCAACACGGCAAAATCCTGT
67358	65445	GGCAACACGGCAAAATCCTG
67359	65446	GGGCAACACGGCAAAATCCT
67360	65447	TGGGCAACACGGCAAAATCC
67361	65448	CTGGGCAACACGGCAAAATC
67362	65449	CCTGGGCAACACGGCAAAAT
67363	65450	ACCTGGGCAACACGGCAAAA
67364	65451	AACCTGGGCAACACGGCAAA
67365	65452	CAACCTGGGCAACACGGCAA
67366	65453	CCAACCTGGGCAACACGGCA
67367	65454	ACCAACCTGGGCAACACGGC
67368	65455	AACCAACCTGGGCAACACGG
67369	65456	AAACCAACCTGGGCAACACG
67370	65457	GAAACCAACCTGGGCAACAC
67371	65458	CGAAACCAACCTGGGCAACA
67372	65459	TCGAAACCAACCTGGGCAAC
67373	65460	TTCGAAACCAACCTGGGCAA
67374	65461	GTTCGAAACCAACCTGGGCA
67375	65462	AGTTCGAAACCAACCTGGGC
67376	65463	GAGTTCGAAACCAACCTGGG
67377	65464	GGAGTTCGAAACCAACCTGG
67378	65465	AGGAGTTCGAAACCAACCTG
67379	65466	CAGGAGTTCGAAACCAACCT
67380	65467	TCAGGAGTTCGAAACCAACC
67381	65468	CTCAGGAGTTCGAAACCAAC
67382	65469	GCTCAGGAGTTCGAAACCAA
67383	65470	AGCTCAGGAGTTCGAAACCA
67384	65471	GAGCTCAGGAGTTCGAAACC
67385	65472	TGAGCTCAGGAGTTCGAAAC
67386	65473	CTGAGCTCAGGAGTTCGAAA
67387	65474	CCTGAGCTCAGGAGTTCGAA

116464	114551	AAATCCATGTGAATATCTAT
116465	114552	AAAATCCATGTGAATATCTA
116466	114553	TAAAATCCATGTGAATATCT
116467	114554	ATAAAATCCATGTGAATATC
116468	114555	CATAAAATCCATGTGAATAT
116469	114556	TCATAAAATCCATGTGAATA
116470	114557	TTCATAAAATCCATGTGAAT
116471	114558	CTTCATAAAATCCATGTGAA
116472	114559	TCTTCATAAAATCCATGTGA
116473	114560	TTCTTCATAAAATCCATGTG
116474	114561	TTTCTTCATAAAATCCATGT
116475	114562	TTTTCTTCATAAAATCCATG
116476	114563	TTTTTCTTCATAAAATCCAT
116477	114564	GTTTTTCTTCATAAAATCCA
116478	114565	TGTTTTTCTTCATAAAATCC
116479	114566	CTGTTTTTCTTCATAAAATC
116480	114567	CCTGTTTTTCTTCATAAAAT
116481	114568	CCCTGTTTTTCTTCATAAAA
116482	114569	CCCCTGTTTTTCTTCATAAA
116483	114570	TCCCCTGTTTTTCTTCATAA
116484	114571	CTCCCCTGTTTTTCTTCATA
116485	114572	TCTCCCCTGTTTTTCTTCAT
116486	114573	TTCTCCCCTGTTTTTCTTCA
116487	114574	TTTCTCCCCTGTTTTTCTTC
116488	114575	TTTTCTCCCCTGTTTTTCTT
116489	114576	TTTTTCTCCCCTGTTTTTCT
116490	114577	TTTTTTCTCCCCTGTTTTTC
116491	114578	ATTTTTTCTCCCCTGTTTTT
116492	114579	CATTTTTTCTCCCCTGTTTT
116493	114580	GCATTTTTTCTCCCCTGTTT
116494	114581	GGCATTTTTTCTCCCCTGTT
116495	114582	GGGCATTTTTTCTCCCCTGT
116496	114583	TGGGCATTTTTTCTCCCCTG
116497	114584	ATGGGCATTTTTTCTCCCCT
116498	114585	GATGGGCATTTTTTCTCCCC
116499	114586	TGATGGGCATTTTTTCTCCC
116500	114587	CTGATGGGCATTTTTTCTCC
116501	114588	ACTGATGGGCATTTTTTCTC
116502	114589	AACTGATGGGCATTTTTTCT
116503	114590	CAACTGATGGGCATTTTTTC
116504	114591	ACAACTGATGGGCATTTTTT
116505	114592	CACAACTGATGGGCATTTTT
116506	114593	TCACAACTGATGGGCATTTT
116507	114594	ATCACAACTGATGGGCATTT
116508	114595	AATCACAACTGATGGGCATT
116509	114596	TAATCACAACTGATGGGCAT
116510	114597	ATAATCACAACTGATGGGCA
116511	114598	TATAATCACAACTGATGGGC
116512	114599	ATATAATCACAACTGATGGG
116513	114600	TATATAATCACAACTGATGG
116514	114601	CTATATAATCACAACTGATG
116515	114602	ACTATATAATCACAACTGAT
116516	114603	TACTATATAATCACAACTGA
116517	114604	ATACTATATAATCACAACTG
116518	114605	GATACTATATAATCACAACT
116519	114606	GGATACTATATAATCACAAC
116520	114607	AGGATACTATATAATCACAA
116521	114608	GAGGATACTATATAATCACA
116522	114609	AGAGGATACTATATAATCAC
116523	114610	AAGAGGATACTATATAATCA
116524	114611	GAAGAGGATACTATATAATC
116525	114612	TGAAGAGGATACTATATAAT
116526	114613	TTGAAGAGGATACTATATAA
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116528	114615	TTTTGAAGAGGATACTATAT
116529	114616	TTTTTGAAGAGGATACTATA
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116531	114618	TCTTTTTGAAGAGGATACTA
116532	114619	CTCTTTTTGAAGAGGATACT
116533	114620	ACTCTTTTTGAAGAGGATAC
116534	114621	TACTCTTTTTGAAGAGGATA

18241	16328	ACTAAGCCTGAGAGTGGCTG
18242	16329	AACTAAGCCTGAGAGTGGCT
18243	16330	AAACTAAGCCTGAGAGTGGC
18244	16331	TAAACTAAGCCTGAGAGTGG
18245	16332	ATAAACTAAGCCTGAGAGTG
18246	16333	AATAAACTAAGCCTGAGAGT
18247	16334	AAATAAACTAAGCCTGAGAG
18248	16335	TAAATAAACTAAGCCTGAGA
18249	16336	GTAAATAAACTAAGCCTGAG
18250	16337	GGTAAATAAACTAAGCCTGA
18251	16338	AGGTAAATAAACTAAGCCTG
18252	16339	TAGGTAAATAAACTAAGCCT
18253	16340	ATAGGTAAATAAACTAAGCC
18254	16341	AATAGGTAAATAAACTAAGC
18255	16342	TAATAGGTAAATAAACTAAG
18256	16343	TTAATAGGTAAATAAACTAA
18257	16344	TTTAATAGGTAAATAAACTA
18258	16345	TTTTAATAGGTAAATAAACT
18259	16346	CTTTTAATAGGTAAATAAAC
18260	16347	TCTTTTAATAGGTAAATAAA
18261	16348	CTCTTTTAATAGGTAAATAA
18262	16349	TCTCTTTTAATAGGTAAATA
18263	16350	TTCTCTTTTAATAGGTAAAT
18264	16351	TTTCTCTTTTAATAGGTAAA
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18268	16355	ATTCTTTCTCTTTTAATAGG
18269	16356	TATTCTTTCTCTTTTAATAG
18270	16357	ATATTCTTTCTCTTTTAATA
18271	16358	GATATTCTTTCTCTTTTAAT
18272	16359	AGATATTCTTTCTCTTTTAA
18273	16360	AAGATATTCTTTCTCTTTTA
18274	16361	GAAGATATTCTTTCTCTTTT
18275	16362	GGAAGATATTCTTTCTCTTT
18276	16363	AGGAAGATATTCTTTCTCTT
18277	16364	AAGGAAGATATTCTTTCTCT
18278	16365	CAAGGAAGATATTCTTTCTC
18279	16366	CCAAGGAAGATATTCTTTCT
18280	16367	GCCAAGGAAGATATTCTTTC
18281	16368	AGCCAAGGAAGATATTCTTT
18282	16369	CAGCCAAGGAAGATATTCTT
18283	16370	CCAGCCAAGGAAGATATTCT
18284	16371	CCCAGCCAAGGAAGATATTC
18285	16372	GCCCAGCCAAGGAAGATATT
18286	16373	CGCCCAGCCAAGGAAGATAT
18287	16374	GCGCCCAGCCAAGGAAGATA
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18289	16376	CCGCGCCCAGCCAAGGAAGA
18290	16377	ACCGCGCCCAGCCAAGGAAG
18291	16378	CACCGCGCCCAGCCAAGGAA
18292	16379	CCACCGCGCCCAGCCAAGGA
18293	16380	GCCACCGCGCCCAGCCAAGG
18294	16381	AGCCACCGCGCCCAGCCAAG
18295	16382	GAGCCACCGCGCCCAGCCAA
18296	16383	TGAGCCACCGCGCCCAGCCA
18297	16384	GTGAGCCACCGCGCCCAGCC
18298	16385	CGTGAGCCACCGCGCCCAGC
18299	16386	GCGTGAGCCACCGCGCCCAG
18300	16387	GGCGTGAGCCACCGCGCCCA
18301	16388	AGGCGTGAGCCACCGCGCCC
18302	16389	TAGGCGTGAGCCACCGCGCC
18303	16390	ATAGGCGTGAGCCACCGCGC
18304	16391	TATAGGCGTGAGCCACCGCG
18305	16392	TTATAGGCGTGAGCCACCGC
18306	16393	ATTATAGGCGTGAGCCACCG
18307	16394	GATTATAGGCGTGAGCCACC
18308	16395	GGATTATAGGCGTGAGCCAC
18309	16396	GGGATTATAGGCGTGAGCCA
18310	16397	TGGGATTATAGGCGTGAGCC
18311	16398	CTGGGATTATAGGCGTGAGC

67388	65475	GCCTGAGCTCAGGAGTTCGA
67389	65476	TGCCTGAGCTCAGGAGTTCG
67390	65477	CTGCCTGAGCTCAGGAGTTC
67391	65478	ACTGCCTGAGCTCAGGAGTT
67392	65479	GACTGCCTGAGCTCAGGAGT
67393	65480	GGACTGCCTGAGCTCAGGAG
67394	65481	TGGACTGCCTGAGCTCAGGA
67395	65482	GTGGACTGCCTGAGCTCAGG
67396	65483	GGTGGACTGCCTGAGCTCAG
67397	65484	AGGTGGACTGCCTGAGCTCA
67398	65485	CAGGTGGACTGCCTGAGCTC
67399	65486	GCAGGTGGACTGCCTGAGCT
67400	65487	GGCAGGTGGACTGCCTGAGC
67401	65488	AGGCAGGTGGACTGCCTGAG
67402	65489	AAGGCAGGTGGACTGCCTGA
67403	65490	CAAGGCAGGTGGACTGCCTG
67404	65491	CCAAGGCAGGTGGACTGCCT
67405	65492	GCCAAGGCAGGTGGACTGCC
67406	65493	AGCCAAGGCAGGTGGACTGC
67407	65494	AAGCCAAGGCAGGTGGACTG
67408	65495	GAAGCCAAGGCAGGTGGACT
67409	65496	GGAAGCCAAGGCAGGTGGAC
67410	65497	GGGAAGCCAAGGCAGGTGGA
67411	65498	TGGGAAGCCAAGGCAGGTGG
67412	65499	TTGGGAAGCCAAGGCAGGTG
67413	65500	CTTGGGAAGCCAAGGCAGGT
67414	65501	ACTTGGGAAGCCAAGGCAGG
67415	65502	CACTTGGGAAGCCAAGGCAG
67416	65503	ACACTTGGGAAGCCAAGGCA
67417	65504	CACACTTGGGAAGCCAAGGC
67418	65505	TCACACTTGGGAAGCCAAGG
67419	65506	CTCACACTTGGGAAGCCAAG
67420	65507	GCTCACACTTGGGAAGCCAA
67421	65508	GGCTCACACTTGGGAAGCCA
67422	65509	TGGCTCACACTTGGGAAGCC
67423	65510	GTGGCTCACACTTGGGAAGC
67424	65511	GGTGGCTCACACTTGGGAAG
67425	65512	TGGTGGCTCACACTTGGGAA
67426	65513	GTGGTGGCTCACACTTGGGA
67427	65514	AGTGGTGGCTCACACTTGGG
67428	65515	CAGTGGTGGCTCACACTTGG
67429	65516	TCAGTGGTGGCTCACACTTG
67430	65517	TTCAGTGGTGGCTCACACTT
67431	65518	TTTCAGTGGTGGCTCACACT
67432	65519	ATTTCAGTGGTGGCTCACAC
67433	65520	TATTTCAGTGGTGGCTCACA
67434	65521	GTATTTCAGTGGTGGCTCAC
67435	65522	AGTATTTCAGTGGTGGCTCA
67436	65523	AAGTATTTCAGTGGTGGCTC
67437	65524	TAAGTATTTCAGTGGTGGCT
67438	65525	ATAAGTATTTCAGTGGTGGC
67439	65526	TATAAGTATTTCAGTGGTGG
67440	65527	ATATAAGTATTTCAGTGGTG
67441	65528	AATATAAGTATTTCAGTGGT
67442	65529	AAATATAAGTATTTCAGTGG
67443	65530	AAAATATAAGTATTTCAGTG
67444	65531	AAAAATATAAGTATTTCAGT
67445	65532	TAAAAATATAAGTATTTCAG
67446	65533	TTAAAAATATAAGTATTTCA
67447	65534	TTTAAAAATATAAGTATTTC
67448	65535	GTTTAAAAATATAAGTATTT
67449	65536	AGTTTAAAAATATAAGTATT
67450	65537	AAGTTTAAAAATATAAGTAT
67451	65538	TAAGTTTAAAAATATAAGTA
67452	65539	TTAAGTTTAAAAATATAAGT
67453	65540	ATTAAGTTTAAAAATATAAG
67454	65541	AATTAAGTTTAAAAATATAA
67455	65542	AAATTAAGTTTAAAAATATA
67456	65543	TAAATTAAGTTTAAAAATAT
67457	65544	ATAAATTAAGTTTAAAAATA
67458	65545	AATAAATTAAGTTTAAAAAT

116535	114622	TTACTCTTTTTGAAGAGGAT
116536	114623	ATTACTCTTTTTGAAGAGGA
116537	114624	AATTACTCTTTTTGAAGAGG
116538	114625	CAATTACTCTTTTTGAAGAG
116539	114626	CCAATTACTCTTTTTGAAGA
116540	114627	TCCAATTACTCTTTTTGAAG
116541	114628	CTCCAATTACTCTTTTTGAA
116542	114629	CCTCCAATTACTCTTTTTGA
116543	114630	GCCTCCAATTACTCTTTTTG
116544	114631	GGCCTCCAATTACTCTTTTT
116545	114632	AGGCCTCCAATTACTCTTTT
116546	114633	CAGGCCTCCAATTACTCTTT
116547	114634	CCAGGCCTCCAATTACTCTT
116548	114635	ACCAGGCCTCCAATTACTCT
116549	114636	CACCAGGCCTCCAATTACTC
116550	114637	ACACCAGGCCTCCAATTACT
116551	114638	CACACCAGGCCTCCAATTAC
116552	114639	TCACACCAGGCCTCCAATTA
116553	114640	ATCACACCAGGCCTCCAATT
116554	114641	CATCACACCAGGCCTCCAAT
116555	114642	CCATCACACCAGGCCTCCAA
116556	114643	GCCATCACACCAGGCCTCCA
116557	114644	AGCCATCACACCAGGCCTCC
116558	114645	GAGCCATCACACCAGGCCTC
116559	114646	TGAGCCATCACACCAGGCCT
116560	114647	GTGAGCCATCACACCAGGCC
116561	114648	TGTGAGCCATCACACCAGGC
116562	114649	GTGTGAGCCATCACACCAGG
116563	114650	GGTGTGAGCCATCACACCAG
116564	114651	AGGTGTGAGCCATCACACCA
116565	114652	CAGGTGTGAGCCATCACACC
116566	114653	ACAGGTGTGAGCCATCACAC
116567	114654	TACAGGTGTGAGCCATCACA
116568	114655	TTACAGGTGTGAGCCATCAC
116569	114656	ATTACAGGTGTGAGCCATCA
116570	114657	AATTACAGGTGTGAGCCATC
116571	114658	AAATTACAGGTGTGAGCCAT
116572	114659	AAAATTACAGGTGTGAGCCA
116573	114660	TAAAATTACAGGTGTGAGCC
116574	114661	CTAAAATTACAGGTGTGAGC
116575	114662	GCTAAAATTACAGGTGTGAG
116576	114663	TGCTAAAATTACAGGTGTGA
116577	114664	GTGCTAAAATTACAGGTGTG
116578	114665	AGTGCTAAAATTACAGGTGT
116579	114666	AAGTGCTAAAATTACAGGTG
116580	114667	AAAGTGCTAAAATTACAGGT
116581	114668	CAAAGTGCTAAAATTACAGG
116582	114669	CCAAAGTGCTAAAATTACAG
116583	114670	CCCAAAGTGCTAAAATTACA
116584	114671	TCCCAAAGTGCTAAAATTAC
116585	114672	CTCCCAAAGTGCTAAAATTA
116586	114673	CCTCCCAAAGTGCTAAAATT
116587	114674	GCCTCCCAAAGTGCTAAAAT
116588	114675	GGCCTCCCAAAGTGCTAAAA
116589	114676	TGGCCTCCCAAAGTGCTAAA
116590	114677	TTGGCCTCCCAAAGTGCTAA
116591	114678	CTTGGCCTCCCAAAGTGCTA
116592	114679	CCTTGGCCTCCCAAAGTGCT
116593	114680	GCCTTGGCCTCCCAAAGTGC
116594	114681	TGCCTTGGCCTCCCAAAGTG
116595	114682	CTGCCTTGGCCTCCCAAAGT
116596	114683	CCTGCCTTGGCCTCCCAAAG
116597	114684	TCCTGCCTTGGCCTCCCAAA
116598	114685	CTCCTGCCTTGGCCTCCCAA
116599	114686	CCTCCTGCCTTGGCCTCCCA
116600	114687	TCCTCCTGCCTTGGCCTCCC
116601	114688	ATCCTCCTGCCTTGGCCTCC
116602	114689	AATCCTCCTGCCTTGGCCTC
116603	114690	CAATCCTCCTGCCTTGGCCT
116604	114691	GCAATCCTCCTGCCTTGGCC
116605	114692	AGCAATCCTCCTGCCTTGGC

18312	16399	GCTGGGATTATAGGCGTGAG
18313	16400	TGCTGGGATTATAGGCGTGA
18314	16401	GTGCTGGGATTATAGGCGTG
18315	16402	AGTGCTGGGATTATAGGCGT
18316	16403	AAGTGCTGGGATTATAGGCG
18317	16404	AAAGTGCTGGGATTATAGGC
18318	16405	CAAAGTGCTGGGATTATAGG
18319	16406	CCAAAGTGCTGGGATTATAG
18320	16407	CCCAAAGTGCTGGGATTATA
18321	16408	TCCCAAAGTGCTGGGATTAT
18322	16409	CTCCCAAAGTGCTGGGATTA
18323	16410	CCTCCCAAAGTGCTGGGATT
18324	16411	GCCTCCCAAAGTGCTGGGAT
18325	16412	AGCCTCCCAAAGTGCTGGGA
18326	16413	CAGCCTCCCAAAGTGCTGGG
18327	16414	TCAGCCTCCCAAAGTGCTGG
18328	16415	CTCAGCCTCCCAAAGTGCTG
18329	16416	CCTCAGCCTCCCAAAGTGCT
18330	16417	GCCTCAGCCTCCCAAAGTGC
18331	16418	CGCCTCAGCCTCCCAAAGTG
18332	16419	CCGCCTCAGCCTCCCAAAGT
18333	16420	CCCGCCTCAGCCTCCCAAAG
18334	16421	ACCCGCCTCAGCCTCCCAAA
18335	16422	CACCCGCCTCAGCCTCCCAA
18336	16423	CCACCCGCCTCAGCCTCCCA
18337	16424	TCCACCCGCCTCAGCCTCCC
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18339	16426	GATCCACCCGCCTCAGCCTC
18340	16427	TGATCCACCCGCCTCAGCCT
18341	16428	GTGATCCACCCGCCTCAGCC
18342	16429	CGTGATCCACCCGCCTCAGC
18343	16430	TCGTGATCCACCCGCCTCAG
18344	16431	CTCGTGATCCACCCGCCTCA
18345	16432	CCTCGTGATCCACCCGCCTC
18346	16433	ACCTCGTGATCCACCCGCCT
18347	16434	GACCTCGTGATCCACCCGCC
18348	16435	TGACCTCGTGATCCACCCGC
18349	16436	CTGACCTCGTGATCCACCCG
18350	16437	CCTGACCTCGTGATCCACCC
18351	16438	TCCTGACCTCGTGATCCACC
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18353	16440	TCTCCTGACCTCGTGATCCA
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18357	16444	TCGATCTCCTGACCTCGTGA
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18360	16447	GTCTCGATCTCCTGACCTCG
18361	16448	GGTCTCGATCTCCTGACCTC
18362	16449	TGGTCTCGATCTCCTGACCT
18363	16450	TTGGTCTCGATCTCCTGACC
18364	16451	GTTGGTCTCGATCTCCTGAC
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18366	16453	AGGTTGGTCTCGATCTCCTG
18367	16454	CAGGTTGGTCTCGATCTCCT
18368	16455	CCAGGTTGGTCTCGATCTCC
18369	16456	CCCAGGTTGGTCTCGATCTC
18370	16457	GCCCAGGTTGGTCTCGATCT
18371	16458	TGCCCAGGTTGGTCTCGATC
18372	16459	TTGCCCAGGTTGGTCTCGAT
18373	16460	GTTGCCCAGGTTGGTCTCGA
18374	16461	TGTTGCCCAGGTTGGTCTCG
18375	16462	ATGTTGCCCAGGTTGGTCTC
18376	16463	AATGTTGCCCAGGTTGGTCT
18377	16464	CAATGTTGCCCAGGTTGGTC
18378	16465	ACAATGTTGCCCAGGTTGGT
18379	16466	CACAATGTTGCCCAGGTTGG
18380	16467	TCACAATGTTGCCCAGGTTG
18381	16468	TTCACAATGTTGCCCAGGTT
18382	16469	TTTCACAATGTTGCCCAGGT

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67460	65547	TAAATAAATTAAGTTTAAAA
67461	65548	ATAAATAAATTAAGTTTAAA
67462	65549	TATAAATAAATTAAGTTTAA
67463	65550	ATATAAATAAATTAAGTTTA
67464	65551	AATATAAATAAATTAAGTTT
67465	65552	AAATATAAATAAATTAAGTT
67466	65553	TAAATATAAATAAATTAAGT
67467	65554	ATAAATATAAATAAATTAAG
67468	65555	AATAAATATAAATAAATTAA
67469	65556	TAATAAATATAAATAAATTA
67470	65557	ATAATAAATATAAATAAATT
67471	65558	TATAATAAATATAAATAAAT
67472	65559	ATATAATAAATATAAATAAA
67473	65560	AATATAATAAATATAAATAA
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67476	65563	AAAAATATAATAAATATAAA
67477	65564	TAAAAATATAATAAATATAA
67478	65565	ATAAAAATATAATAAATATA
67479	65566	CATAAAAATATAATAAATAT
67480	65567	ACATAAAAATATAATAAATA
67481	65568	AACATAAAAATATAATAAAT
67482	65569	AAACATAAAAATATAATAAA
67483	65570	AAAACATAAAAATATAATAA
67484	65571	AAAAACATAAAAATATAATA
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67488	65575	ATATAAAAACATAAAAATAT
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67507	65594	TATAAAAATATTTTTTAAAA
67508	65595	GTATAAAAATATTTTTTAAA
67509	65596	AGTATAAAAATATTTTTTAA
67510	65597	GAGTATAAAAATATTTTTTA
67511	65598	TGAGTATAAAAATATTTTTT
67512	65599	GTGAGTATAAAAATATTTTT
67513	65600	AGTGAGTATAAAAATATTTT
67514	65601	TAGTGAGTATAAAAATATTT
67515	65602	CTAGTGAGTATAAAAATATT
67516	65603	TCTAGTGAGTATAAAAATAT
67517	65604	GTCTAGTGAGTATAAAAATA
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67525	65612	AAAATTGGGTCTAGTGAGTA
67526	65613	TAAAATTGGGTCTAGTGAGT
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67529	65616	GTATAAAATTGGGTCTAGTG

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116607	114694	CAAGCAATCCTCCTGCCTTG
116608	114695	TCAAGCAATCCTCCTGCCTT
116609	114696	CTCAAGCAATCCTCCTGCCT
116610	114697	GCTCAAGCAATCCTCCTGCC
116611	114698	AGCTCAAGCAATCCTCCTGC
116612	114699	GAGCTCAAGCAATCCTCCTG
116613	114700	TGAGCTCAAGCAATCCTCCT
116614	114701	CTGAGCTCAAGCAATCCTCC
116615	114702	CCTGAGCTCAAGCAATCCTC
116616	114703	TCCTGAGCTCAAGCAATCCT
116617	114704	CTCCTGAGCTCAAGCAATCC
116618	114705	GCTCCTGAGCTCAAGCAATC
116619	114706	GGCTCCTGAGCTCAAGCAAT
116620	114707	GGGCTCCTGAGCTCAAGCAA
116621	114708	TGGGCTCCTGAGCTCAAGCA
116622	114709	TTGGGCTCCTGAGCTCAAGC
116623	114710	CTTGGGCTCCTGAGCTCAAG
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116629	114716	GCTGATCTTGGGCTCCTGAG
116630	114717	GGCTGATCTTGGGCTCCTGA
116631	114718	AGGCTGATCTTGGGCTCCTG
116632	114719	CAGGCTGATCTTGGGCTCCT
116633	114720	CCAGGCTGATCTTGGGCTCC
116634	114721	TCCAGGCTGATCTTGGGCTC
116635	114722	GTCCAGGCTGATCTTGGGCT
116636	114723	TGTCCAGGCTGATCTTGGGC
116637	114724	TTGTCCAGGCTGATCTTGGG
116638	114725	GTTGTCCAGGCTGATCTTGG
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116640	114727	CTGTTGTCCAGGCTGATCTT
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116642	114729	CTCTGTTGTCCAGGCTGATC
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116648	114735	CAAAGTCTCTGTTGTCCAGG
116649	114736	ACAAAGTCTCTGTTGTCCAG
116650	114737	GACAAAGTCTCTGTTGTCCA
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116653	114740	AGAGACAAAGTCTCTGTTGT
116654	114741	TAGAGACAAAGTCTCTGTTG
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116670	114757	TTTTTTTGAATTTTAGTAGA
116671	114758	ATTTTTTTGAATTTTAGTAG
116672	114759	AATTTTTTTGAATTTTAGTA
116673	114760	TAATTTTTTTGAATTTTAGT
116674	114761	CTAATTTTTTTGAATTTTAG
116675	114762	GCTAATTTTTTTGAATTTTA
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18384	16471	GGTTTCACAATGTTGCCCAG
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18386	16473	GAGGTTTCACAATGTTGCCC
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18393	16480	TAGAGATGAGGTTTCACAAT
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18398	16485	TTTAGTAGAGATGAGGTTTC
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18406	16493	TTTTCTATTTTAGTAGAGAT
18407	16494	TTTTTCTATTTTAGTAGAGA
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18417	16504	CCCAGCTAATTTTTTCTATT
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18419	16506	TGCCCAGCTAATTTTTTCTA
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18422	16509	CCATGCCCAGCTAATTTTTT
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18434	16521	AGATGCGCACCACCATGCCC
18435	16522	CAGATGCGCACCACCATGCC
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18438	16525	CTACAGATGCGCACCACCAT
18439	16526	ACTACAGATGCGCACCACCA
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18442	16529	GGGACTACAGATGCGCACCA
18443	16530	TGGGACTACAGATGCGCACC
18444	16531	CTGGGACTACAGATGCGCAC
18445	16532	GCTGGGACTACAGATGCGCA
18446	16533	AGCTGGGACTACAGATGCGC
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18448	16535	GTAGCTGGGACTACAGATGC
18449	16536	AGTAGCTGGGACTACAGATG
18450	16537	GAGTAGCTGGGACTACAGAT
18451	16538	CGAGTAGCTGGGACTACAGA
18452	16539	TCGAGTAGCTGGGACTACAG
18453	16540	CTCGAGTAGCTGGGACTACA

67530	65617	AGTATAAAATTGGGTCTAGT
67531	65618	GAGTATAAAATTGGGTCTAG
67532	65619	GGAGTATAAAATTGGGTCTA
67533	65620	AGGAGTATAAAATTGGGTCT
67534	65621	TAGGAGTATAAAATTGGGTC
67535	65622	TTAGGAGTATAAAATTGGGT
67536	65623	TTTAGGAGTATAAAATTGGG
67537	65624	GTTTAGGAGTATAAAATTGG
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67539	65626	TGGTTTAGGAGTATAAAATT
67540	65627	CTGGTTTAGGAGTATAAAAT
67541	65628	CCTGGTTTAGGAGTATAAAA
67542	65629	CCCTGGTTTAGGAGTATAAA
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67545	65632	ATTCCCTGGTTTAGGAGTAT
67546	65633	TATTCCCTGGTTTAGGAGTA
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67568	65655	ATGTAAGAGAAAAAAAAAACA
67569	65656	TATGTAAGAGAAAAAAAAAC
67570	65657	CTATGTAAGAGAAAAAAAAA
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67573	65660	TGCCTATGTAAGAGAAAAAA
67574	65661	ATGCCTATGTAAGAGAAAAA
67575	65662	CATGCCTATGTAAGAGAAAA
67576	65663	TCATGCCTATGTAAGAGAAA
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67578	65665	TATCATGCCTATGTAAGAGA
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67587	65674	TGTCTATGGTATCATGCCTA
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67590	65677	CATTGTCTATGGTATCATGC
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67592	65679	ATCATTGTCTATGGTATCAT
67593	65680	AATCATTGTCTATGGTATCA
67594	65681	TAATCATTGTCTATGGTATC
67595	65682	TTAATCATTGTCTATGGTAT
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116677	114764	CAGCTAATTTTTTTGAATTT
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116680	114767	GCCCAGCTAATTTTTTTGAA
116681	114768	TGCCCAGCTAATTTTTTTGA
116682	114769	ATGCCCAGCTAATTTTTTTG
116683	114770	CATGCCCAGCTAATTTTTTT
116684	114771	CCATGCCCAGCTAATTTTTT
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116686	114773	CACCATGCCCAGCTAATTTT
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116694	114781	GCATATGCCACCATGCCCAG
116695	114782	GGCATATGCCACCATGCCCA
116696	114783	AGGCATATGCCACCATGCCC
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116700	114787	CTACAGGCATATGCCACCAT
116701	114788	GCTACAGGCATATGCCACCA
116702	114789	GGCTACAGGCATATGCCACC
116703	114790	GGGCTACAGGCATATGCCAC
116704	114791	GGGGCTACAGGCATATGCCA
116705	114792	TGGGGCTACAGGCATATGCC
116706	114793	CTGGGGCTACAGGCATATGC
116707	114794	GCTGGGGCTACAGGCATATG
116708	114795	AGCTGGGGCTACAGGCATAT
116709	114796	CAGCTGGGGCTACAGGCATA
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116711	114798	AACAGCTGGGGCTACAGGCA
116712	114799	AAACAGCTGGGGCTACAGGC
116713	114800	CAAACAGCTGGGGCTACAGG
116714	114801	CCAAACAGCTGGGGCTACAG
116715	114802	CCCAAACAGCTGGGGCTACA
116716	114803	CCCCAAACAGCTGGGGCTAC
116717	114804	CCCCCAAACAGCTGGGGCTA
116718	114805	TCCCCCAAACAGCTGGGGCT
116719	114806	GTCCCCCAAACAGCTGGGGC
116720	114807	AGTCCCCCAAACAGCTGGGG
116721	114808	CAGTCCCCCAAACAGCTGGG
116722	114809	TCAGTCCCCCAAACAGCTGG
116723	114810	CTCAGTCCCCCAAACAGCTG
116724	114811	CCTCAGTCCCCCAAACAGCT
116725	114812	GCCTCAGTCCCCCAAACAGC
116726	114813	CGCCTCAGTCCCCCAAACAG
116727	114814	TCGCCTCAGTCCCCCAAACA
116728	114815	CTCGCCTCAGTCCCCCAAAC
116729	114816	TCTCGCCTCAGTCCCCCAAA
116730	114817	CTCTCGCCTCAGTCCCCCAA
116731	114818	CCTCTCGCCTCAGTCCCCCA
116732	114819	TCCTCTCGCCTCAGTCCCCC
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116734	114821	GATCCTCTCGCCTCAGTCCC
116735	114822	TGATCCTCTCGCCTCAGTCC
116736	114823	GTGATCCTCTCGCCTCAGTC
116737	114824	AGTGATCCTCTCGCCTCAGT
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116740	114827	TCAAGTGATCCTCTCGCCTC
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116742	114829	GCTCAAGTGATCCTCTCGCC
116743	114830	GGCTCAAGTGATCCTCTCGC
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116745	114832	TGGGCTCAAGTGATCCTCTC
116746	114833	CTGGGCTCAAGTGATCCTCT
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18454	16541	TCTCGAGTAGCTGGGACTAC
18455	16542	CTCTCGAGTAGCTGGGACTA
18456	16543	CCTCTCGAGTAGCTGGGACT
18457	16544	GCCTCTCGAGTAGCTGGGAC
18458	16545	AGCCTCTCGAGTAGCTGGGA
18459	16546	CAGCCTCTCGAGTAGCTGGG
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18462	16549	CCTCAGCCTCTCGAGTAGCT
18463	16550	GCCTCAGCCTCTCGAGTAGC
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18465	16552	CTGCCTCAGCCTCTCGAGTA
18466	16553	CCTGCCTCAGCCTCTCGAGT
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18473	16560	CGATTCCCCTGCCTCAGCCT
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18477	16564	CAAGCGATTCCCCTGCCTCA
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18480	16567	GTTCAAGCGATTCCCCTGCC
18481	16568	GGTTCAAGCGATTCCCCTGC
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18483	16570	TGGGTTCAAGCGATTCCCCT
18484	16571	CTGGGTTCAAGCGATTCCCC
18485	16572	CCTGGGTTCAAGCGATTCCC
18486	16573	TCCTGGGTTCAAGCGATTCC
18487	16574	CTCCTGGGTTCAAGCGATTC
18488	16575	CCTCCTGGGTTCAAGCGATT
18489	16576	ACCTCCTGGGTTCAAGCGAT
18490	16577	CACCTCCTGGGTTCAAGCGA
18491	16578	CCACCTCCTGGGTTCAAGCG
18492	16579	TCCACCTCCTGGGTTCAAGC
18493	16580	CTCCACCTCCTGGGTTCAAG
18494	16581	CCTCCACCTCCTGGGTTCAA
18495	16582	ACCTCCACCTCCTGGGTTCA
18496	16583	AACCTCCACCTCCTGGGTTC
18497	16584	CAACCTCCACCTCCTGGGTT
18498	16585	GCAACCTCCACCTCCTGGGT
18499	16586	TGCAACCTCCACCTCCTGGG
18500	16587	CTGCAACCTCCACCTCCTGG
18501	16588	ACTGCAACCTCCACCTCCTG
18502	16589	CACTGCAACCTCCACCTCCT
18503	16590	TCACTGCAACCTCCACCTCC
18504	16591	CTCACTGCAACCTCCACCTC
18505	16592	GCTCACTGCAACCTCCACCT
18506	16593	GGCTCACTGCAACCTCCACC
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18508	16595	TTGGCTCACTGCAACCTCCA
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18510	16597	TCTTGGCTCACTGCAACCTC
18511	16598	ATCTTGGCTCACTGCAACCT
18512	16599	AATCTTGGCTCACTGCAACC
18513	16600	CAATCTTGGCTCACTGCAAC
18514	16601	ACAATCTTGGCTCACTGCAA
18515	16602	CACAATCTTGGCTCACTGCA
18516	16603	GCACAATCTTGGCTCACTGC
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18520	16607	AGTGGCACAATCTTGGCTCA
18521	16608	CAGTGGCACAATCTTGGCTC
18522	16609	GCAGTGGCACAATCTTGGCT
18523	16610	TGCAGTGGCACAATCTTGGC
18524	16611	GTGCAGTGGCACAATCTTGG

67601	65688	ACAATTTTAATCATTGTCTA
67602	65689	TACAATTTTAATCATTGTCT
67603	65690	TTACAATTTTAATCATTGTC
67604	65691	ATTACAATTTTAATCATTGT
67605	65692	AATTACAATTTTAATCATTG
67606	65693	TAATTACAATTTTAATCATT
67607	65694	GTAATTACAATTTTAATCAT
67608	65695	GGTAATTACAATTTTAATCA
67609	65696	TGGTAATTACAATTTTAATC
67610	65697	ATGGTAATTACAATTTTAAT
67611	65698	AATGGTAATTACAATTTTAA
67612	65699	GAATGGTAATTACAATTTTA
67613	65700	TGAATGGTAATTACAATTTT
67614	65701	ATGAATGGTAATTACAATTT
67615	65702	AATGAATGGTAATTACAATT
67616	65703	AAATGAATGGTAATTACAAT
67617	65704	GAAATGAATGGTAATTACAA
67618	65705	AGAAATGAATGGTAATTACA
67619	65706	AAGAAATGAATGGTAATTAC
67620	65707	TAAGAAATGAATGGTAATTA
67621	65708	CTAAGAAATGAATGGTAATT
67622	65709	ACTAAGAAATGAATGGTAAT
67623	65710	AACTAAGAAATGAATGGTAA
67624	65711	AAACTAAGAAATGAATGGTA
67625	65712	AAAACTAAGAAATGAATGGT
67626	65713	CAAAACTAAGAAATGAATGG
67627	65714	ACAAAACTAAGAAATGAATG
67628	65715	CACAAAACTAAGAAATGAAT
67629	65716	CCACAAAACTAAGAAATGAA
67630	65717	GCCACAAAACTAAGAAATGA
67631	65718	AGCCACAAAACTAAGAAATG
67632	65719	CAGCCACAAAACTAAGAAAT
67633	65720	CCAGCCACAAAACTAAGAAA
67634	65721	CCCAGCCACAAAACTAAGAA
67635	65722	TCCCAGCCACAAAACTAAGA
67636	65723	GTCCCAGCCACAAAACTAAG
67637	65724	TGTCCCAGCCACAAAACTAA
67638	65725	GTGTCCCAGCCACAAAACTA
67639	65726	AGTGTCCCAGCCACAAAACT
67640	65727	CAGTGTCCCAGCCACAAAAC
67641	65728	TCAGTGTCCCAGCCACAAAA
67642	65729	ATCAGTGTCCCAGCCACAAA
67643	65730	CATCAGTGTCCCAGCCACAA
67644	65731	ACATCAGTGTCCCAGCCACA
67645	65732	GACATCAGTGTCCCAGCCAC
67646	65733	AGACATCAGTGTCCCAGCCA
67647	65734	AAGACATCAGTGTCCCAGCC
67648	65735	GAAGACATCAGTGTCCCAGC
67649	65736	TGAAGACATCAGTGTCCCAG
67650	65737	TTGAAGACATCAGTGTCCCA
67651	65738	TTTGAAGACATCAGTGTCCC
67652	65739	ATTTGAAGACATCAGTGTCC
67653	65740	CATTTGAAGACATCAGTGTC
67654	65741	ACATTTGAAGACATCAGTGT
67655	65742	AACATTTGAAGACATCAGTG
67656	65743	TAACATTTGAAGACATCAGT
67657	65744	CTAACATTTGAAGACATCAG
67658	65745	ACTAACATTTGAAGACATCA
67659	65746	AACTAACATTTGAAGACATC
67660	65747	AAACTAACATTTGAAGACAT
67661	65748	CAAACTAACATTTGAAGACA
67662	65749	GCAAACTAACATTTGAAGAC
67663	65750	TGCAAACTAACATTTGAAGA
67664	65751	TTGCAAACTAACATTTGAAG
67665	65752	TTTGCAAACTAACATTTGAA
67666	65753	ATTTGCAAACTAACATTTGA
67667	65754	TATTTGCAAACTAACATTTG
67668	65755	GTATTTGCAAACTAACATTT
67669	65756	TGTATTTGCAAACTAACATT
67670	65757	CTGTATTTGCAAACTAACAT
67671	65758	ACTGTATTTGCAAACTAACA

116748	114835	TCCTGGGCTCAAGTGATCCT
116749	114836	TTCCTGGGCTCAAGTGATCC
116750	114837	CTTCCTGGGCTCAAGTGATC
116751	114838	ACTTCCTGGGCTCAAGTGAT
116752	114839	TACTTCCTGGGCTCAAGTGA
116753	114840	CTACTTCCTGGGCTCAAGTG
116754	114841	TCTACTTCCTGGGCTCAAGT
116755	114842	CTCTACTTCCTGGGCTCAAG
116756	114843	CCTCTACTTCCTGGGCTCAA
116757	114844	GCCTCTACTTCCTGGGCTCA
116758	114845	AGCCTCTACTTCCTGGGCTC
116759	114846	CAGCCTCTACTTCCTGGGCT
116760	114847	GCAGCCTCTACTTCCTGGGC
116761	114848	TGCAGCCTCTACTTCCTGGG
116762	114849	CTGCAGCCTCTACTTCCTGG
116763	114850	ACTGCAGCCTCTACTTCCTG
116764	114851	CACTGCAGCCTCTACTTCCT
116765	114852	TCACTGCAGCCTCTACTTCC
116766	114853	CTCACTGCAGCCTCTACTTC
116767	114854	GCTCACTGCAGCCTCTACTT
116768	114855	AGCTCACTGCAGCCTCTACT
116769	114856	CAGCTCACTGCAGCCTCTAC
116770	114857	ACAGCTCACTGCAGCCTCTA
116771	114858	CACAGCTCACTGCAGCCTCT
116772	114859	TCACAGCTCACTGCAGCCTC
116773	114860	ATCACAGCTCACTGCAGCCT
116774	114861	AATCACAGCTCACTGCAGCC
116775	114862	TAATCACAGCTCACTGCAGC
116776	114863	ATAATCACAGCTCACTGCAG
116777	114864	CATAATCACAGCTCACTGCA
116778	114865	GCATAATCACAGCTCACTGC
116779	114866	GGCATAATCACAGCTCACTG
116780	114867	TGGCATAATCACAGCTCACT
116781	114868	GTGGCATAATCACAGCTCAC
116782	114869	AGTGGCATAATCACAGCTCA
116783	114870	CAGTGGCATAATCACAGCTC
116784	114871	GCAGTGGCATAATCACAGCT
116785	114872	GGCAGTGGCATAATCACAGC
116786	114873	GGGCAGTGGCATAATCACAG
116787	114874	AGGGCAGTGGCATAATCACA
116788	114875	GAGGGCAGTGGCATAATCAC
116789	114876	GGAGGGCAGTGGCATAATCA
116790	114877	TGGAGGGCAGTGGCATAATC
116791	114878	CTGGAGGGCAGTGGCATAAT
116792	114879	GCTGGAGGGCAGTGGCATAA
116793	114880	GGCTGGAGGGCAGTGGCATA
116794	114881	AGGCTGGAGGGCAGTGGCAT
116795	114882	CAGGCTGGAGGGCAGTGGCA
116796	114883	CCAGGCTGGAGGGCAGTGGC
116797	114884	CCCAGGCTGGAGGGCAGTGG
116798	114885	GCCCAGGCTGGAGGGCAGTG
116799	114886	CGCCCAGGCTGGAGGGCAGT
116800	114887	TCGCCCAGGCTGGAGGGCAG
116801	114888	GTCGCCCAGGCTGGAGGGCA
116802	114889	TGTCGCCCAGGCTGGAGGGC
116803	114890	CTGTCGCCCAGGCTGGAGGG
116804	114891	TCTGTCGCCCAGGCTGGAGG
116805	114892	CTCTGTCGCCCAGGCTGGAG
116806	114893	ACTCTGTCGCCCAGGCTGGA
116807	114894	CACTCTGTCGCCCAGGCTGG
116808	114895	TCACTCTGTCGCCCAGGCTG
116809	114896	CTCACTCTGTCGCCCAGGCT
116810	114897	TCTCACTCTGTCGCCCAGGC
116811	114898	GTCTCACTCTGTCGCCCAGG
116812	114899	GGTCTCACTCTGTCGCCCAG
116813	114900	GGGTCTCACTCTGTCGCCCA
116814	114901	GGGGTCTCACTCTGTCGCCC
116815	114902	CGGGGTCTCACTCTGTCGCC
116816	114903	ACGGGGTCTCACTCTGTCGC
116817	114904	GACGGGGTCTCACTCTGTCG
116818	114905	AGACGGGGTCTCACTCTGTC

18525	16612	AGTGCAGTGGCACAATCTTG
18526	16613	GAGTGCAGTGGCACAATCTT
18527	16614	GGAGTGCAGTGGCACAATCT
18528	16615	TGGAGTGCAGTGGCACAATC
18529	16616	CTGGAGTGCAGTGGCACAAT
18530	16617	GCTGGAGTGCAGTGGCACAA
18531	16618	GGCTGGAGTGCAGTGGCACA
18532	16619	AGGCTGGAGTGCAGTGGCAC
18533	16620	CAGGCTGGAGTGCAGTGGCA
18534	16621	CCAGGCTGGAGTGCAGTGGC
18535	16622	CCCAGGCTGGAGTGCAGTGG
18536	16623	GCCCAGGCTGGAGTGCAGTG
18537	16624	CGCCCAGGCTGGAGTGCAGT
18538	16625	TCGCCCAGGCTGGAGTGCAG
18539	16626	GTCGCCCAGGCTGGAGTGCA
18540	16627	TGTCGCCCAGGCTGGAGTGC
18541	16628	CTGTCGCCCAGGCTGGAGTG
18542	16629	TCTGTCGCCCAGGCTGGAGT
18543	16630	TTCTGTCGCCCAGGCTGGAG
18544	16631	GTTCTGTCGCCCAGGCTGGA
18545	16632	CGTTCTGTCGCCCAGGCTGG
18546	16633	TCGTTCTGTCGCCCAGGCTG
18547	16634	CTCGTTCTGTCGCCCAGGCT
18548	16635	TCTCGTTCTGTCGCCCAGGC
18549	16636	GTCTCGTTCTGTCGCCCAGG
18550	16637	AGTCTCGTTCTGTCGCCCAG
18551	16638	GAGTCTCGTTCTGTCGCCCA
18552	16639	AGAGTCTCGTTCTGTCGCCC
18553	16640	CAGAGTCTCGTTCTGTCGCC
18554	16641	ACAGAGTCTCGTTCTGTCGC
18555	16642	GACAGAGTCTCGTTCTGTCG
18556	16643	AGACAGAGTCTCGTTCTGTC
18557	16644	GAGACAGAGTCTCGTTCTGT
18558	16645	GGAGACAGAGTCTCGTTCTG
18559	16646	TGGAGACAGAGTCTCGTTCT
18560	16647	TTGGAGACAGAGTCTCGTTC
18561	16648	TTTGGAGACAGAGTCTCGTT
18562	16649	TTTTGGAGACAGAGTCTCGT
18563	16650	TTTTTGGAGACAGAGTCTCG
18564	16651	TTTTTTGGAGACAGAGTCTC
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18566	16653	TTTTTTTTGGAGACAGAGTC
18567	16654	TTTTTTTTTGGAGACAGAGT
18568	16655	TTTTTTTTTTGGAGACAGAG
18569	16656	TTTTTTTTTTTGGAGACAGA
18570	16657	TTTTTTTTTTTTGGAGACAG
18571	16658	TTTTTTTTTTTTTGGAGACA
18572	16659	TTTTTTTTTTTTTTGGAGAC
18573	16660	TTTTTTTTTTTTTTTGGAGA
18574	16661	TTTTTTTTTTTTTTTTGGAG
18575	16662	GTTTTTTTTTTTTTTTTGGA
18576	16663	TGTTTTTTTTTTTTTTTTGG
18577	16664	TTGTTTTTTTTTTTTTTTTG
18578	16665	TTTGTTTTTTTTTTTTTTTT
18579	16666	GTTTGTTTTTTTTTTTTTTT
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18581	16668	TTGTTTGTTTTTTTTTTTTT
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18583	16670	TTTTGTTTGTTTTTTTTTTT
18584	16671	TTTTTGTTTGTTTTTTTTTT
18585	16672	TTTTTTGTTTGTTTTTTTTT
18586	16673	TTTTTTTGTTTGTTTTTTTT
18587	16674	TTTTTTTTGTTTGTTTTTTT
18588	16675	TTTTTTTTTGTTTGTTTTTT
18589	16676	TTTTTTTTTTGTTTGTTTTT
18590	16677	TTTTTTTTTTTGTTTGTTTT
18591	16678	GTTTTTTTTTTTGTTTGTTT
18592	16679	AGTTTTTTTTTTTGTTTGTT
18593	16680	CAGTTTTTTTTTTTGTTTGT
18594	16681	TCAGTTTTTTTTTTTTGTTTG
18595	16682	CTCAGTTTTTTTTTTTTGTTT

67672	65759	GACTGTATTTGCAAACTAAC
67673	65760	TGACTGTATTTGCAAACTAA
67674	65761	CTGACTGTATTTGCAAACTA
67675	65762	GCTGACTGTATTTGCAAACT
67676	65763	GGCTGACTGTATTTGCAAAC
67677	65764	GGGCTGACTGTATTTGCAAA
67678	65765	AGGGCTGACTGTATTTGCAA
67679	65766	GAGGGCTGACTGTATTTGCA
67680	65767	AGAGGGCTGACTGTATTTGC
67681	65768	GAGAGGGCTGACTGTATTTG
67682	65769	AGAGAGGGCTGACTGTATTT
67683	65770	TAGAGAGGGCTGACTGTATT
67684	65771	ATAGAGAGGGCTGACTGTAT
67685	65772	GATAGAGAGGGCTGACTGTA
67686	65773	GGATAGAGAGGGCTGACTGT
67687	65774	TGGATAGAGAGGGCTGACTG
67688	65775	ATGGATAGAGAGGGCTGACT
67689	65776	CATGGATAGAGAGGGCTGAC
67690	65777	CCATGGATAGAGAGGGCTGA
67691	65778	CCCATGGATAGAGAGGGCTG
67692	65779	ACCCATGGATAGAGAGGGCT
67693	65780	AACCCATGGATAGAGAGGGC
67694	65781	TAACCCATGGATAGAGAGGG
67695	65782	GTAACCCATGGATAGAGAGG
67696	65783	TGTAACCCATGGATAGAGAG
67697	65784	GTGTAACCCATGGATAGAGA
67698	65785	TGTGTAACCCATGGATAGAG
67699	65786	CTGTGTAACCCATGGATAGA
67700	65787	GCTGTGTAACCCATGGATAG
67701	65788	AGCTGTGTAACCCATGGATA
67702	65789	CAGCTGTGTAACCCATGGAT
67703	65790	ACAGCTGTGTAACCCATGGA
67704	65791	CACAGCTGTGTAACCCATGG
67705	65792	TCACAGCTGTGTAACCCATG
67706	65793	TTCACAGCTGTGTAACCCAT
67707	65794	ATTCACAGCTGTGTAACCCA
67708	65795	AATTCACAGCTGTGTAACCC
67709	65796	GAATTCACAGCTGTGTAACC
67710	65797	TGAATTCACAGCTGTGTAAC
67711	65798	TTGAATTCACAGCTGTGTAA
67712	65799	GTTGAATTCACAGCTGTGTA
67713	65800	GGTTGAATTCACAGCTGTGT
67714	65801	TGGTTGAATTCACAGCTGTG
67715	65802	TTGGTTGAATTCACAGCTGT
67716	65803	GTTGGTTGAATTCACAGCTG
67717	65804	GGTTGGTTGAATTCACAGCT
67718	65805	TGGTTGGTTGAATTCACAGC
67719	65806	ATGGTTGGTTGAATTCACAG
67720	65807	CATGGTTGGTTGAATTCACA
67721	65808	CCATGGTTGGTTGAATTCAC
67722	65809	TCCATGGTTGGTTGAATTCA
67723	65810	ATCCATGGTTGGTTGAATTC
67724	65811	GATCCATGGTTGGTTGAATT
67725	65812	GGATCCATGGTTGGTTGAAT
67726	65813	TGGATCCATGGTTGGTTGAA
67727	65814	TTGGATCCATGGTTGGTTGA
67728	65815	TTTGGATCCATGGTTGGTTG
67729	65816	TTTTGGATCCATGGTTGGTT
67730	65817	ATTTTGGATCCATGGTTGGT
67731	65818	TATTTTGGATCCATGGTTGG
67732	65819	ATATTTTGGATCCATGGTTG
67733	65820	TATATTTTGGATCCATGGTT
67734	65821	ATATATTTTGGATCCATGGT
67735	65822	CATATATTTTGGATCCATGG
67736	65823	CCATATATTTTGGATCCATG
67737	65824	CCCATATATTTTGGATCCAT
67738	65825	TCCCATATATTTTGGATCCA
67739	65826	TTCCCATATATTTTGGATCC
67740	65827	TTTCCCATATATTTTGGATC
67741	65828	ATTTCCCATATATTTTGGAT
67742	65829	TATTTCCCATATATTTTGGA

116819	114906	GAGACGGGGTCTCACTCTGT
116820	114907	TGAGACGGGGTCTCACTCTG
116821	114908	TTGAGACGGGGTCTCACTCT
116822	114909	TTTGAGACGGGGTCTCACTC
116823	114910	GTTTGAGACGGGGTCTCACT
116824	114911	TGTTTGAGACGGGGTCTCAC
116825	114912	ATGTTTGAGACGGGGTCTCA
116826	114913	TATGTTTGAGACGGGGTCTC
116827	114914	TTATGTTTGAGACGGGGTCT
116828	114915	TTTATGTTTGAGACGGGGTC
116829	114916	ATTTATGTTTGAGACGGGGT
116830	114917	TATTTATGTTTGAGACGGGG
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116833	114920	CAGTATTTATGTTTGAGACG
116834	114921	CCAGTATTTATGTTTGAGAC
116835	114922	GCCAGTATTTATGTTTGAGA
116836	114923	AGCCAGTATTTATGTTTGAG
116837	114924	CAGCCAGTATTTATGTTTGA
116838	114925	CCAGCCAGTATTTATGTTTG
116839	114926	CCCAGCCAGTATTTATGTTT
116840	114927	GCCCAGCCAGTATTTATGTT
116841	114928	TGCCCAGCCAGTATTTATGT
116842	114929	ATGCCCAGCCAGTATTTATG
116843	114930	CATGCCCAGCCAGTATTTAT
116844	114931	CCATGCCCAGCCAGTATTTA
116845	114932	ACCATGCCCAGCCAGTATTT
116846	114933	CACCATGCCCAGCCAGTATT
116847	114934	CCACCATGCCCAGCCAGTAT
116848	114935	GCCACCATGCCCAGCCAGTA
116849	114936	AGCCACCATGCCCAGCCAGT
116850	114937	AAGCCACCATGCCCAGCCAG
116851	114938	TAAGCCACCATGCCCAGCCA
116852	114939	ATAAGCCACCATGCCCAGCC
116853	114940	CATAAGCCACCATGCCCAGC
116854	114941	GCATAAGCCACCATGCCCAG
116855	114942	GGCATAAGCCACCATGCCCA
116856	114943	AGGCATAAGCCACCATGCCC
116857	114944	CAGGCATAAGCCACCATGCC
116858	114945	ACAGGCATAAGCCACCATGC
116859	114946	TACAGGCATAAGCCACCATG
116860	114947	TTACAGGCATAAGCCACCAT
116861	114948	ATTACAGGCATAAGCCACCA
116862	114949	GATTACAGGCATAAGCCACC
116863	114950	GGATTACAGGCATAAGCCAC
116864	114951	GGGATTACAGGCATAAGCCA
116865	114952	TGGGATTACAGGCATAAGCC
116866	114953	CTGGGATTACAGGCATAAGC
116867	114954	GCTGGGATTACAGGCATAAG
116868	114955	TGCTGGGATTACAGGCATAA
116869	114956	GTGCTGGGATTACAGGCATA
116870	114957	AGTGCTGGGATTACAGGCAT
116871	114958	AAGTGCTGGGATTACAGGCA
116872	114959	AAAGTGCTGGGATTACAGGC
116873	114960	CAAAGTGCTGGGATTACAGG
116874	114961	CCAAAGTGCTGGGATTACAG
116875	114962	CCCAAAGTGCTGGGATTACA
116876	114963	TCCCAAAGTGCTGGGATTAC
116877	114964	CTCCCAAAGTGCTGGGATTA
116878	114965	CCTCCCAAAGTGCTGGGATT
116879	114966	GCCTCCCAAAGTGCTGGGAT
116880	114967	GGCCTCCCAAAGTGCTGGGA
116881	114968	CGGCCTCCCAAAGTGCTGGG
116882	114969	TCGGCCTCCCAAAGTGCTGG
116883	114970	CTCGGCCTCCCAAAGTGCTG
116884	114971	CCTCGGCCTCCCAAAGTGCT
116885	114972	ACCTCGGCCTCCCAAAGTGC
116886	114973	CACCTCGGCCTCCCAAAGTG
116887	114974	CCACCTCGGCCTCCCAAAGT
116888	114975	CCCACCTCGGCCTCCCAAAG
116889	114976	ACCCACCTCGGCCTCCCAAA

18596	16683	TCTCAGTTTTTTTTTTTGTT
18597	16684	ATCTCAGTTTTTTTTTTGT
18598	16685	TATCTCAGTTTTTTTTTTG
18599	16686	GTATCTCAGTTTTTTTTTT
18600	16687	AGTATCTCAGTTTTTTTTT
18601	16688	CAGTATCTCAGTTTTTTTT
18602	16689	CCAGTATCTCAGTTTTTTT
18603	16690	GCCAGTATCTCAGTTTTTT
18604	16691	GGCCAGTATCTCAGTTTTT
18605	16692	CGGCCAGTATCTCAGTTTT
18606	16693	CCGGCCAGTATCTCAGTTT
18607	16694	CCCGGCCAGTATCTCAGTT
18608	16695	GCCCGGCCAGTATCTCAGT
18609	16696	CGCCCGGCCAGTATCTCAG
18610	16697	GCGCCCGGCCAGTATCTCAG
18611	16698	CGCGCCCGGCCAGTATCTCA
18612	16699	CCGCGCCCGGCCAGTATCTC
18613	16700	ACCGCGCCCGGCCAGTATCT
18614	16701	CACCGCGCCCGGCCAGTATC
18615	16702	CCACCGCGCCCGGCCAGTAT
18616	16703	GCCACCGCGCCCGGCCAGTA
18617	16704	AGCCACCGCGCCCGGCCAGT
18618	16705	GAGCCACCGCGCCCGGCCAG
18619	16706	CGAGCCACCGCGCCCGGCCA
18620	16707	ACGAGCCACCGCGCCCGGCC
18621	16708	CACGAGCCACCGCGCCCGGC
18622	16709	GCACGAGCCACCGCGCCCGG
18623	16710	GGCACGAGCCACCGCGCCCG
18624	16711	AGGCACGAGCCACCGCGCCC
18625	16712	CAGGCACGAGCCACCGCGCC
18626	16713	ACAGGCACGAGCCACCGCGC
18627	16714	TACAGGCACGAGCCACCGCG
18628	16715	TTACAGGCACGAGCCACCGC
18629	16716	ATTACAGGCACGAGCCACCG
18630	16717	GATTACAGGCACGAGCCACC
18631	16718	GGATTACAGGCACGAGCCAC
18632	16719	GGGATTACAGGCACGAGCCA
18633	16720	TGGGATTACAGGCACGAGCC
18634	16721	CTGGGATTACAGGCACGAGC
18635	16722	GCTGGGATTACAGGCACGAG
18636	16723	TGCTGGGATTACAGGCACGA
18637	16724	GTGCTGGGATTACAGGCACG
18638	16725	AGTGCTGGGATTACAGGCAC
18639	16726	AAGTGCTGGGATTACAGGCA
18640	16727	AAAGTGCTGGGATTACAGGC
18641	16728	CAAAGTGCTGGGATTACAGG
18642	16729	CCAAAGTGCTGGGATTACAG
18643	16730	TCCAAAGTGCTGGGATTACA
18644	16731	TTCCAAAGTGCTGGGATTAC
18645	16732	CTTCCAAAGTGCTGGGATTA
18646	16733	CCTTCCAAAGTGCTGGGATT
18647	16734	GCCTTCCAAAGTGCTGGGAT
18648	16735	GGCCTTCCAAAGTGCTGGGA
18649	16736	CGGCCTTCCAAAGTGCTGGG
18650	16737	TCGGCCTTCCAAAGTGCTGG
18651	16738	CTCGGCCTTCCAAAGTGCTG
18652	16739	CCTCGGCCTTCCAAAGTGCT
18653	16740	GCCTCGGCCTTCCAAAGTGC
18654	16741	CGCCTCGGCCTTCCAAAGTG
18655	16742	CCGCCTCGGCCTTCCAAAGT
18656	16743	CCCGCCTCGGCCTTCCAAAG
18657	16744	ACCCGCCTCGGCCTTCCAAA
18658	16745	CACCCGCCTCGGCCTTCCAA
18659	16746	CCACCCGCCTCGGCCTTCCA
18660	16747	TCCACCCGCCTCGGCCTTCC
18661	16748	ATCCACCCGCCTCGGCCTTC
18662	16749	GATCCACCCGCCTCGGCCTT
18663	16750	TGATCCACCCGCCTCGGCCT
18664	16751	GTGATCCACCCGCCTCGGCC
18665	16752	CGTGATCCACCCGCCTCGGC
18666	16753	TCGTGATCCACCCGCCTCGG

67743	65830	GTATTTCCCATATATTTTGG
67744	65831	CGTATTTCCCATATATTTTG
67745	65832	GCGTATTTCCCATATATTTT
67746	65833	AGCGTATTTCCCATATATTT
67747	65834	CAGCGTATTTCCCATATATT
67748	65835	CCAGCGTATTTCCCATATAT
67749	65836	CCCAGCGTATTTCCCATATA
67750	65837	CCCCAGCGTATTTCCCATAT
67751	65838	GCCCCAGCGTATTTCCCATA
67752	65839	AGCCCCAGCGTATTTCCCAT
67753	65840	CAGCCCCAGCGTATTTCCCA
67754	65841	ACAGCCCCAGCGTATTTCCC
67755	65842	CACAGCCCCAGCGTATTTCC
67756	65843	CCACAGCCCCAGCGTATTTC
67757	65844	CCCACAGCCCCAGCGTATTT
67758	65845	ACCCACAGCCCCAGCGTATT
67759	65846	GACCCACAGCCCCAGCGTAT
67760	65847	TGACCCACAGCCCCAGCGTA
67761	65848	GTGACCCACAGCCCCAGCGT
67762	65849	TGTGACCCACAGCCCCAGCG
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67765	65852	AGGTGTGACCCACAGCCCCA
67766	65853	CAGGTGTGACCCACAGCCCC
67767	65854	ACAGGTGTGACCCACAGCCC
67768	65855	TACAGGTGTGACCCACAGCC
67769	65856	TTACAGGTGTGACCCACAGC
67770	65857	ATTACAGGTGTGACCCACAG
67771	65858	AATTACAGGTGTGACCCACA
67772	65859	GAATTACAGGTGTGACCCAC
67773	65860	GGAATTACAGGTGTGACCCA
67774	65861	TGGAATTACAGGTGTGACCC
67775	65862	CTGGAATTACAGGTGTGACC
67776	65863	GCTGGAATTACAGGTGTGAC
67777	65864	TGCTGGAATTACAGGTGTGA
67778	65865	GTGCTGGAATTACAGGTGTG
67779	65866	AGTGCTGGAATTACAGGTGT
67780	65867	AAGTGCTGGAATTACAGGTG
67781	65868	TAAGTGCTGGAATTACAGGT
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67785	65872	TCCCTAAGTGCTGGAATTAC
67786	65873	CTCCCTAAGTGCTGGAATTA
67787	65874	CCTCCCTAAGTGCTGGAATT
67788	65875	GCCTCCCTAAGTGCTGGAAT
67789	65876	AGCCTCCCTAAGTGCTGGAA
67790	65877	CAGCCTCCCTAAGTGCTGGA
67791	65878	TCAGCCTCCCTAAGTGCTGG
67792	65879	CTCAGCCTCCCTAAGTGCTG
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67794	65881	GCCTCAGCCTCCCTAAGTGC
67795	65882	TGCCTCAGCCTCCCTAAGTG
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67798	65885	ATCTGCCTCAGCCTCCCTAA
67799	65886	CATCTGCCTCAGCCTCCCTA
67800	65887	CCATCTGCCTCAGCCTCCCT
67801	65888	TCCATCTGCCTCAGCCTCCC
67802	65889	ATCCATCTGCCTCAGCCTCC
67803	65890	GATCCATCTGCCTCAGCCTC
67804	65891	TGATCCATCTGCCTCAGCCT
67805	65892	GTGATCCATCTGCCTCAGCC
67806	65893	GGTGATCCATCTGCCTCAGC
67807	65894	AGGTGATCCATCTGCCTCAG
67808	65895	CAGGTGATCCATCTGCCTCA
67809	65896	TCAGGTGATCCATCTGCCTC
67810	65897	CTCAGGTGATCCATCTGCCT
67811	65898	CCTCAGGTGATCCATCTGCC
67812	65899	ACCTCAGGTGATCCATCTGC
67813	65900	GACCTCAGGTGATCCATCTG

116890	114977	CACCCACCTCGGCCTCCCAA
116891	114978	ACACCCACCTCGGCCTCCCA
116892	114979	TACACCCACCTCGGCCTCCC
116893	114980	ATACACCCACCTCGGCCTCC
116894	114981	GATACACCCACCTCGGCCTC
116895	114982	TGATACACCCACCTCGGCCT
116896	114983	GTGATACACCCACCTCGGCC
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116898	114985	AGGTGATACACCCACCTCGG
116899	114986	CAGGTGATACACCCACCTCG
116900	114987	TCAGGTGATACACCCACCTC
116901	114988	CTCAGGTGATACACCCACCT
116902	114989	CCTCAGGTGATACACCCACC
116903	114990	ACCTCAGGTGATACACCCAC
116904	114991	GACCTCAGGTGATACACCCA
116905	114992	TGACCTCAGGTGATACACCC
116906	114993	CTGACCTCAGGTGATACACC
116907	114994	ACTGACCTCAGGTGATACAC
116908	114995	TACTGACCTCAGGTGATACA
116909	114996	CTACTGACCTCAGGTGATAC
116910	114997	ACTACTGACCTCAGGTGATA
116911	114998	AACTACTGACCTCAGGTGAT
116912	114999	AAACTACTGACCTCAGGTGA
116913	115000	CAAACTACTGACCTCAGGTG
116914	115001	TCAAACTACTGACCTCAGGT
116915	115002	CTCAAACTACTGACCTCAGG
116916	115003	TCTCAAACTACTGACCTCAG
116917	115004	GTCTCAAACTACTGACCTCA
116918	115005	GGTCTCAAACTACTGACCTC
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116920	115007	CTGGTCTCAAACTACTGACC
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116933	115020	CATGTTGGCCAGGCTGGTCT
116934	115021	CCATGTTGGCCAGGCTGGTC
116935	115022	GCCATGTTGGCCAGGCTGGT
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116937	115024	TCGCCATGTTGGCCAGGCTG
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116939	115026	TTTCGCCATGTTGGCCAGGC
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116941	115028	GGTTTCGCCATGTTGGCCAG
116942	115029	GGGTTTCGCCATGTTGGCCA
116943	115030	GGGGTTTCGCCATGTTGGCC
116944	115031	TGGGGTTTCGCCATGTTGGC
116945	115032	ATGGGGTTTCGCCATGTTGG
116946	115033	GATGGGGTTTCGCCATGTTG
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18669	16756	ACCTCGTGATCCACCCGCCT
18670	16757	GACCTCGTGATCCACCCGCC
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18673	16760	CCTGACCTCGTGATCCACCC
18674	16761	TCCTGACCTCGTGATCCACC
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18682	16769	TCTCGATCTCCTGACCTCGT
18683	16770	GTCTCGATCTCCTGACCTCG
18684	16771	GGTCTCGATCTCCTGACCTC
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18710	16797	CAGGGTTTCCCCATGTTAGG
18711	16798	ACAGGGTTTCCCCATGTTAG
18712	16799	GACAGGGTTTCCCCATGTTA
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18717	16804	GTAGAGACAGGGTTTCCCCA
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18734	16821	AATTTTTTGTATTTTTAGTA
18735	16822	TAATTTTTTGTATTTTTAGT
18736	16823	CTAATTTTTTGTATTTTTAG
18737	16824	GCTAATTTTTTGTATTTTTA

67814	65901	TGACCTCAGGTGATCCATCT
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67826	65913	GTCTTGAACTCCTGACCTCA
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67874	65961	TTTTTGTACTTATAGTAGAG
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67877	65964	AATTTTTTGTACTTATAGTA
67878	65965	TAATTTTTTGTACTTATAGT
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67882	65969	CAGCTAATTTTTTGTACTTA
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67884	65971	GCCAGCTAATTTTTTGTACT

116961	115048	TTGTATTTTAGTAGAGATGG
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116963	115050	TTTTGTATTTTAGTAGAGAT
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116966	115053	AATTTTTGTATTTTAGTAGA
116967	115054	TAATTTTTGTATTTTAGTAG
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116972	115059	CCGGCTAATTTTTGTATTTT
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116974	115061	GTCCGGCTAATTTTTGTATT
116975	115062	TGTCCGGCTAATTTTTGTAT
116976	115063	ATGTCCGGCTAATTTTTGTA
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116979	115066	ACCATGTCCGGCTAATTTTT
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116982	115069	GCCACCATGTCCGGCTAATT
116983	115070	TGCCACCATGTCCGGCTAAT
116984	115071	GTGCCACCATGTCCGGCTAA
116985	115072	GGTGCCACCATGTCCGGCTA
116986	115073	AGGTGCCACCATGTCCGGCT
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116989	115076	GGCAGGTGCCACCATGTCCG
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117020	115107	TCAGCCCCACCTAGTAGCTG
117021	115108	CTCAGCCCCACCTAGTAGCT
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117029	115116	TCTCCTGCCTCAGCCCCACC
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18738	16825	GGCTAATTTTTTGTATTTTT
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67885	65972	GGCCAGCTAATTTTTTGTAC
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67889	65976	CCATGGCCAGCTAATTTTTT
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67898	65985	TGTGCACTACCATGGCCAGC
67899	65986	ATGTGCACTACCATGGCCAG
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67902	65989	CACATGTGCACTACCATGGC
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67905	65992	TTACACATGTGCACTACCAT
67906	65993	ATTACACATGTGCACTACCA
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67935	66022	TGCTTGTCTCAACCTCTCGA
67936	66023	TTGCTTGTCTCAACCTCTCG
67937	66024	ATTGCTTGTCTCAACCTCTC
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67939	66026	AAATTGCTTGTCTCAACCTC
67940	66027	CAAATTGCTTGTCTCAACCT
67941	66028	GCAAATTGCTTGTCTCAACC
67942	66029	AGCAAATTGCTTGTCTCAAC
67943	66030	AAGCAAATTGCTTGTCTCAA
67944	66031	CAAGCAAATTGCTTGTCTCA
67945	66032	TCAAGCAAATTGCTTGTCTC
67946	66033	TTCAAGCAAATTGCTTGTCT
67947	66034	GTTCAAGCAAATTGCTTGTC
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67949	66036	AGGTTCAAGCAAATTGCTTG
67950	66037	CAGGTTCAAGCAAATTGCTT
67951	66038	TCAGGTTCAAGCAAATTGCT
67952	66039	CTCAGGTTCAAGCAAATTGC
67953	66040	TCTCAGGTTCAAGCAAATTG
67954	66041	TTCTCAGGTTCAAGCAAATT
67955	66042	CTTCTCAGGTTCAAGCAAAT

117032	115119	AATTCTCCTGCCTCAGCCCC
117033	115120	CAATTCTCCTGCCTCAGCCC
117034	115121	GCAATTCTCCTGCCTCAGCC
117035	115122	AGCAATTCTCCTGCCTCAGC
117036	115123	AAGCAATTCTCCTGCCTCAG
117037	115124	CAAGCAATTCTCCTGCCTCA
117038	115125	TCAAGCAATTCTCCTGCCTC
117039	115126	TTCAAGCAATTCTCCTGCCT
117040	115127	GTTCAAGCAATTCTCCTGCC
117041	115128	GGTTCAAGCAATTCTCCTGC
117042	115129	GGGTTCAAGCAATTCTCCTG
117043	115130	CGGGTTCAAGCAATTCTCCT
117044	115131	CCGGGTTCAAGCAATTCTCC
117045	115132	CCCGGGTTCAAGCAATTCTC
117046	115133	TCCCGGGTTCAAGCAATTCT
117047	115134	CTCCCGGGTTCAAGCAATTC
117048	115135	CCTCCCGGGTTCAAGCAATT
117049	115136	GCCTCCCGGGTTCAAGCAAT
117050	115137	TGCCTCCCGGGTTCAAGCAA
117051	115138	CTGCCTCCCGGGTTCAAGCA
117052	115139	CCTGCCTCCCGGGTTCAAGC
117053	115140	CCCTGCCTCCCGGGTTCAAG
117054	115141	CCCCTGCCTCCCGGGTTCAA
117055	115142	ACCCCTGCCTCCCGGGTTCA
117056	115143	AACCCCTGCCTCCCGGGTTC
117057	115144	CAACCCCTGCCTCCCGGGTT
117058	115145	GCAACCCCTGCCTCCCGGGT
117059	115146	TGCAACCCCTGCCTCCCGGG
117060	115147	CTGCAACCCCTGCCTCCCGG
117061	115148	ACTGCAACCCCTGCCTCCCG
117062	115149	CACTGCAACCCCTGCCTCCC
117063	115150	TCACTGCAACCCCTGCCTCC
117064	115151	CTCACTGCAACCCCTGCCTC
117065	115152	GCTCACTGCAACCCCTGCCT
117066	115153	GGCTCACTGCAACCCCTGCC
117067	115154	TGGCTCACTGCAACCCCTGC
117068	115155	TTGGCTCACTGCAACCCCTG
117069	115156	CTTGGCTCACTGCAACCCCT
117070	115157	TCTTGGCTCACTGCAACCCC
117071	115158	ATCTTGGCTCACTGCAACCC
117072	115159	GATCTTGGCTCACTGCAACC
117073	115160	CGATCTTGGCTCACTGCAAC
117074	115161	ACGATCTTGGCTCACTGCAA
117075	115162	CACGATCTTGGCTCACTGCA
117076	115163	GCACGATCTTGGCTCACTGC
117077	115164	GGCACGATCTTGGCTCACTG
117078	115165	TGGCACGATCTTGGCTCACT
117079	115166	GTGGCACGATCTTGGCTCAC
117080	115167	AGTGGCACGATCTTGGCTCA
117081	115168	CAGTGGCACGATCTTGGCTC
117082	115169	GCAGTGGCACGATCTTGGCT
117083	115170	TGCAGTGGCACGATCTTGGC
117084	115171	GTGCAGTGGCACGATCTTGG
117085	115172	AGTGCAGTGGCACGATCTTG
117086	115173	AAGTGCAGTGGCACGATCTT
117087	115174	GAAGTGCAGTGGCACGATCT
117088	115175	TGAAGTGCAGTGGCACGATC
117089	115176	CTGAAGTGCAGTGGCACGAT
117090	115177	GCTGAAGTGCAGTGGCACGA
117091	115178	GGCTGAAGTGCAGTGGCACG
117092	115179	AGGCTGAAGTGCAGTGGCAC
117093	115180	CAGGCTGAAGTGCAGTGGCA
117094	115181	CCAGGCTGAAGTGCAGTGGC
117095	115182	CCCAGGCTGAAGTGCAGTGG
117096	115183	GCCCAGGCTGAAGTGCAGTG
117097	115184	TGCCCAGGCTGAAGTGCAGT
117098	115185	TTGCCCAGGCTGAAGTGCAG
117099	115186	GTTGCCCAGGCTGAAGTGCA
117100	115187	TGTTGCCCAGGCTGAAGTGC
117101	115188	CTGTTGCCCAGGCTGAAGTG
117102	115189	TCTGTTGCCCAGGCTGAAGT

18809	16896	CCCGGGTTCACGCCATTCTC
18810	16897	TCCCGGGTTCACGCCATTCT
18811	16898	CTCCCGGGTTCACGCCATTC
18812	16899	CCTCCCGGGTTCACGCCATT
18813	16900	GCCTCCCGGGTTCACGCCAT
18814	16901	TGCCTCCCGGGTTCACGCCA
18815	16902	CTGCCTCCCGGGTTCACGCC
18816	16903	TCTGCCTCCCGGGTTCACGC
18817	16904	CTCTGCCTCCCGGGTTCACG
18818	16905	GCTCTGCCTCCCGGGTTCAC
18819	16906	AGCTCTGCCTCCCGGGTTCA
18820	16907	AAGCTCTGCCTCCCGGGTTC
18821	16908	CAAGCTCTGCCTCCCGGGTT
18822	16909	GCAAGCTCTGCCTCCCGGGT
18823	16910	TGCAAGCTCTGCCTCCCGGG
18824	16911	CTGCAAGCTCTGCCTCCCGG
18825	16912	ACTGCAAGCTCTGCCTCCCG
18826	16913	CACTGCAAGCTCTGCCTCCC
18827	16914	TCACTGCAAGCTCTGCCTCC
18828	16915	CTCACTGCAAGCTCTGCCTC
18829	16916	GCTCACTGCAAGCTCTGCCT
18830	16917	CGCTCACTGCAAGCTCTGCC
18831	16918	CCGCTCACTGCAAGCTCTGC
18832	16919	TCCGCTCACTGCAAGCTCTG
18833	16920	CTCCGCTCACTGCAAGCTCT
18834	16921	TCTCCGCTCACTGCAAGCTC
18835	16922	ATCTCCGCTCACTGCAAGCT
18836	16923	CATCTCCGCTCACTGCAAGC
18837	16924	CCATCTCCGCTCACTGCAAG
18838	16925	ACCATCTCCGCTCACTGCAA
18839	16926	CACCATCTCCGCTCACTGCA
18840	16927	GCACCATCTCCGCTCACTGC
18841	16928	GGCACCATCTCCGCTCACTG
18842	16929	TGGCACCATCTCCGCTCACT
18843	16930	GTGGCACCATCTCCGCTCAC
18844	16931	AGTGGCACCATCTCCGCTCA
18845	16932	CAGTGGCACCATCTCCGCTC
18846	16933	GCAGTGGCACCATCTCCGCT
18847	16934	TGCAGTGGCACCATCTCCGC
18848	16935	GTGCAGTGGCACCATCTCCG
18849	16936	AGTGCAGTGGCACCATCTCC
18850	16937	GAGTGCAGTGGCACCATCTC
18851	16938	GGAGTGCAGTGGCACCATCT
18852	16939	TGGAGTGCAGTGGCACCATC
18853	16940	CTGGAGTGCAGTGGCACCAT
18854	16941	GCTGGAGTGCAGTGGCACCA
18855	16942	GGCTGGAGTGCAGTGGCACC
18856	16943	AGGCTGGAGTGCAGTGGCAC
18857	16944	CAGGCTGGAGTGCAGTGGCA
18858	16945	GCAGGCTGGAGTGCAGTGGC
18859	16946	AGCAGGCTGGAGTGCAGTGG
18860	16947	CAGCAGGCTGGAGTGCAGTG
18861	16948	CCAGCAGGCTGGAGTGCAGT
18862	16949	CCCAGCAGGCTGGAGTGCAG
18863	16950	GCCCAGCAGGCTGGAGTGCA
18864	16951	CGCCCAGCAGGCTGGAGTGC
18865	16952	TCGCCCAGCAGGCTGGAGTG
18866	16953	GTCGCCCAGCAGGCTGGAGT
18867	16954	TGTCGCCCAGCAGGCTGGAG
18868	16955	CTGTCGCCCAGCAGGCTGGA
18869	16956	TCTGTCGCCCAGCAGGCTGG
18870	16957	CTCTGTCGCCCAGCAGGCTG
18871	16958	GCTCTGTCGCCCAGCAGGCT
18872	16959	CGCTCTGTCGCCCAGCAGGC
18873	16960	TCGCTCTGTCGCCCAGCAGG
18874	16961	CTCGCTCTGTCGCCCAGCAG
18875	16962	TCTCGCTCTGTCGCCCAGCA
18876	16963	GTCTCGCTCTGTCGCCCAGC
18877	16964	AGTCTCGCTCTGTCGCCCAG
18878	16965	GAGTCTCGCTCTGTCGCCCA
18879	16966	GGAGTCTCGCTCTGTCGCCC

67956	66043	ACTTCTCAGGTTCAAGCAAA
67957	66044	TACTTCTCAGGTTCAAGCAA
67958	66045	CTACTTCTCAGGTTCAAGCA
67959	66046	TCTACTTCTCAGGTTCAAGC
67960	66047	CTCTACTTCTCAGGTTCAAG
67961	66048	CCTCTACTTCTCAGGTTCAA
67962	66049	ACCTCTACTTCTCAGGTTCA
67963	66050	AACCTCTACTTCTCAGGTTC
67964	66051	AAACCTCTACTTCTCAGGTT
67965	66052	GAAACCTCTACTTCTCAGGT
67966	66053	GGAAACCTCTACTTCTCAGG
67967	66054	TGGAAACCTCTACTTCTCAG
67968	66055	ATGGAAACCTCTACTTCTCA
67969	66056	CATGGAAACCTCTACTTCTC
67970	66057	TCATGGAAACCTCTACTTCT
67971	66058	CTCATGGAAACCTCTACTTC
67972	66059	GCTCATGGAAACCTCTACTT
67973	66060	AGCTCATGGAAACCTCTACT
67974	66061	CAGCTCATGGAAACCTCTAC
67975	66062	TCAGCTCATGGAAACCTCTA
67976	66063	CTCAGCTCATGGAAACCTCT
67977	66064	TCTCAGCTCATGGAAACCTC
67978	66065	ATCTCAGCTCATGGAAACCT
67979	66066	AATCTCAGCTCATGGAAACC
67980	66067	CAATCTCAGCTCATGGAAAC
67981	66068	ACAATCTCAGCTCATGGAAA
67982	66069	CACAATCTCAGCTCATGGAA
67983	66070	ACACAATCTCAGCTCATGGA
67984	66071	GACACAATCTCAGCTCATGG
67985	66072	TGACACAATCTCAGCTCATG
67986	66073	GTGACACAATCTCAGCTCAT
67987	66074	AGTGACACAATCTCAGCTCA
67988	66075	CAGTGACACAATCTCAGCTC
67989	66076	GCAGTGACACAATCTCAGCT
67990	66077	TGCAGTGACACAATCTCAGC
67991	66078	GTGCAGTGACACAATCTCAG
67992	66079	AGTGCAGTGACACAATCTCA
67993	66080	GAGTGCAGTGACACAATCTC
67994	66081	GGAGTGCAGTGACACAATCT
67995	66082	TGGAGTGCAGTGACACAATC
67996	66083	CTGGAGTGCAGTGACACAAT
67997	66084	GCTGGAGTGCAGTGACACAA
67998	66085	GGCTGGAGTGCAGTGACACA
67999	66086	AGGCTGGAGTGCAGTGACAC
68000	66087	CAGGCTGGAGTGCAGTGACA
68001	66088	GCAGGCTGGAGTGCAGTGAC
68002	66089	CGCAGGCTGGAGTGCAGTGA
68003	66090	GCGCAGGCTGGAGTGCAGTG
68004	66091	TGCGCAGGCTGGAGTGCAGT
68005	66092	TTGCGCAGGCTGGAGTGCAG
68006	66093	GTTGCGCAGGCTGGAGTGCA
68007	66094	TGTTGCGCAGGCTGGAGTGC
68008	66095	CTGTTGCGCAGGCTGGAGTG
68009	66096	TCTGTTGCGCAGGCTGGAGT
68010	66097	CTCTGTTGCGCAGGCTGGAG
68011	66098	ACTCTGTTGCGCAGGCTGGA
68012	66099	CACTCTGTTGCGCAGGCTGG
68013	66100	ACACTCTGTTGCGCAGGCTG
68014	66101	CACACTCTGTTGCGCAGGCT
68015	66102	TCACACTCTGTTGCGCAGGC
68016	66103	CTCACACTCTGTTGCGCAGG
68017	66104	TCTCACACTCTGTTGCGCAG
68018	66105	TTCTCACACTCTGTTGCGCA
68019	66106	CTTCTCACACTCTGTTGCGC
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68022	66109	TTTCTTCTCACACTCTGTTG
68023	66110	TTTTCTTCTCACACTCTGTT
68024	66111	CTTTTCTTCTCACACTCTGT
68025	66112	TCTTTTCTTCTCACACTCTG
68026	66113	TTCTTTTCTTCTCACACTCT

117103	115190	CTCTGTTGCCCAGGCTGAAG
117104	115191	ACTCTGTTGCCCAGGCTGAA
117105	115192	CACTCTGTTGCCCAGGCTGA
117106	115193	TCACTCTGTTGCCCAGGCTG
117107	115194	CTCACTCTGTTGCCCAGGCT
117108	115195	TCTCACTCTGTTGCCCAGGC
117109	115196	GTCTCACTCTGTTGCCCAGG
117110	115197	AGTCTCACTCTGTTGCCCAG
117111	115198	GAGTCTCACTCTGTTGCCCA
117112	115199	GGAGTCTCACTCTGTTGCCC
117113	115200	TGGAGTCTCACTCTGTTGCC
117114	115201	ATGGAGTCTCACTCTGTTGC
117115	115202	GATGGAGTCTCACTCTGTTG
117116	115203	AGATGGAGTCTCACTCTGTT
117117	115204	GAGATGGAGTCTCACTCTGT
117118	115205	TGAGATGGAGTCTCACTCTG
117119	115206	TTGAGATGGAGTCTCACTCT
117120	115207	TTTGAGATGGAGTCTCACTC
117121	115208	TTTTGAGATGGAGTCTCACT
117122	115209	GTTTTGAGATGGAGTCTCAC
117123	115210	TGTTTTGAGATGGAGTCTCA
117124	115211	TTGTTTTGAGATGGAGTCTC
117125	115212	TTTGTTTTGAGATGGAGTCT
117126	115213	GTTTGTTTTGAGATGGAGTC
117127	115214	TGTTTGTTTTGAGATGGAGT
117128	115215	TTGTTTGTTTTGAGATGGAG
117129	115216	TTTGTTTGTTTTGAGATGGA
117130	115217	GTTTGTTTGTTTTGAGATGG
117131	115218	TGTTTGTTTGTTTTGAGATG
117132	115219	TTGTTTGTTTGTTTTGAGAT
117133	115220	TTTGTTTGTTTGTTTTGAGA
117134	115221	GTTTGTTTGTTTGTTTTGAG
117135	115222	TGTTTGTTTGTTTGTTTTGA
117136	115223	TTGTTTGTTTGTTTGTTTTG
117137	115224	TTTGTTTGTTTGTTTGTTTT
117138	115225	TTTTGTTTGTTTGTTTGTTT
117139	115226	TTTTTGTTTGTTTGTTTGTT
117140	115227	TTTTTTGTTTGTTTGTTTGT
117141	115228	GTTTTTTGTTTGTTTGTTTG
117142	115229	TGTTTTTTGTTTGTTTGTTT
117143	115230	TTGTTTTTTGTTTGTTTGTT
117144	115231	TTTGTTTTTTGTTTGTTTGT
117145	115232	GTTTGTTTTTTGTTTGTTTG
117146	115233	TGTTTGTTTTTTGTTTGTTT
117147	115234	TTGTTTGTTTTTTGTTTGTT
117148	115235	TTTGTTTGTTTTTTGTTTGT
117149	115236	GTTTGTTTGTTTTTTGTTTG
117150	115237	TGTTTGTTTGTTTTTTGTTT
117151	115238	TTGTTTGTTTGTTTTTTGTT
117152	115239	TTTGTTTGTTTGTTTTTTGT
117153	115240	TTTTGTTTGTTTGTTTTTTG
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117155	115242	TTTTTTGTTTGTTTGTTTTT
117156	115243	TTTTTTTGTTTGTTTGTTTT
117157	115244	GTTTTTTTGTTTGTTTGTTT
117158	115245	GGTTTTTTTGTTTGTTTGTT
117159	115246	TGGTTTTTTTGTTTGTTTGT
117160	115247	CTGGTTTTTTTGTTTGTTTG
117161	115248	TCTGGTTTTTTTGTTTGTTT
117162	115249	GTCTGGTTTTTTTGTTTGTT
117163	115250	AGTCTGGTTTTTTTGTTTGT
117164	115251	TAGTCTGGTTTTTTTGTTTG
117165	115252	TTAGTCTGGTTTTTTTGTTT
117166	115253	ATTAGTCTGGTTTTTTTGTT
117167	115254	AATTAGTCTGGTTTTTTTGT
117168	115255	CAATTAGTCTGGTTTTTTTG
117169	115256	CCAATTAGTCTGGTTTTTTT
117170	115257	GCCAATTAGTCTGGTTTTTT
117171	115258	AGCCAATTAGTCTGGTTTTT
117172	115259	CAGCCAATTAGTCTGGTTTT
117173	115260	CCAGCCAATTAGTCTGGTTT

18880	16967	CGGAGTCTCGCTCTGTCGCC
18881	16968	ACGGAGTCTCGCTCTGTCGC
18882	16969	GACGGAGTCTCGCTCTGTCG
18883	16970	AGACGGAGTCTCGCTCTGTC
18884	16971	GAGACGGAGTCTCGCTCTGT
18885	16972	TGAGACGGAGTCTCGCTCTG
18886	16973	TTGAGACGGAGTCTCGCTCT
18887	16974	TTTGAGACGGAGTCTCGCTC
18888	16975	GTTTGAGACGGAGTCTCGCT
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18892	16979	GTTTGTTTGAGACGGAGTCT
18893	16980	TGTTTGTTTGAGACGGAGTC
18894	16981	TTGTTTGTTTGAGACGGAGT
18895	16982	TTTGTTTGTTTGAGACGGAG
18896	16983	GTTTGTTTGTTTGAGACGGA
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18898	16985	TTGTTTGTTTGTTTGAGACG
18899	16986	TTTGTTTGTTTGTTTGAGAC
18900	16987	GTTTGTTTGTTTGTTTGAGA
18901	16988	TGTTTGTTTGTTTGTTTGAG
18902	16989	TTGTTTGTTTGTTTGTTTGA
18903	16990	TTTGTTTGTTTGTTTGTTTG
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18905	16992	TGTTTGTTTGTTTGTTTGTT
18906	16993	TTGTTTGTTTGTTTGTTTGT
18907	16994	TTTGTTTGTTTGTTTGTTTG
18908	16995	TTTTGTTTGTTTGTTTGTTT
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18910	16997	TTTTTTGTTTGTTTGTTTGT
18911	16998	TTTTTTTGTTTGTTTGTTTG
18912	16999	GTTTTTTTGTTTGTTTGTTT
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18914	17001	CAGTTTTTTTGTTTGTTTGT
18915	17002	TCAGTTTTTTTGTTTGTTTG
18916	17003	CTCAGTTTTTTTGTTTGTTT
18917	17004	TCTCAGTTTTTTTGTTTGTT
18918	17005	ATCTCAGTTTTTTTGTTTGT
18919	17006	TATCTCAGTTTTTTTGTTTG
18920	17007	GTATCTCAGTTTTTTTGTTT
18921	17008	AGTATCTCAGTTTTTTTGTT
18922	17009	TAGTATCTCAGTTTTTTTGT
18923	17010	TTAGTATCTCAGTTTTTTTG
18924	17011	TTTAGTATCTCAGTTTTTTT
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18926	17013	ACTTTAGTATCTCAGTTTTT
18927	17014	GACTTTAGTATCTCAGTTTT
18928	17015	AGACTTTAGTATCTCAGTTT
18929	17016	AAGACTTTAGTATCTCAGTT
18930	17017	TAAGACTTTAGTATCTCAGT
18931	17018	TTAAGACTTTAGTATCTCAG
18932	17019	ATTAAGACTTTAGTATCTCA
18933	17020	TATTAAGACTTTAGTATCTC
18934	17021	ATATTAAGACTTTAGTATCT
18935	17022	AATATTAAGACTTTAGTATC
18936	17023	AAATATTAAGACTTTAGTAT
18937	17024	AAAATATTAAGACTTTAGTA
18938	17025	GAAAATATTAAGACTTTAGT
18939	17026	AGAAAATATTAAGACTTTAG
18940	17027	CAGAAAATATTAAGACTTTA
18941	17028	ACAGAAAATATTAAGACTTT
18942	17029	AACAGAAAATATTAAGACTT
18943	17030	AAACAGAAAATATTAAGACT
18944	17031	AAAACAGAAAATATTAAGAC
18945	17032	AAAAACAGAAAATATTAAGA
18946	17033	TAAAAACAGAAAATATTAAG
18947	17034	ATAAAAACAGAAAATATTAA
18948	17035	CATAAAAACAGAAAATATTA
18949	17036	ACATAAAAACAGAAAATATT
18950	17037	TACATAAAAACAGAAAATAT

68027	66114	TTTCTTTTCTTCTCACACTC
68028	66115	TTTTCTTTTCTTCTCACACT
68029	66116	TTTTTCTTTTCTTCTCACAC
68030	66117	TTTTTTCTTTTCTTCTCACA
68031	66118	TTTTTTTCTTTTCTTCTCAC
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68037	66124	GACAGTTTTTTTTCTTTTCT
68038	66125	AGACAGTTTTTTTTCTTTTC
68039	66126	CAGACAGTTTTTTTTCTTTT
68040	66127	TCAGACAGTTTTTTTTCTTT
68041	66128	TTCAGACAGTTTTTTTTCTT
68042	66129	TTTCAGACAGTTTTTTTTCT
68043	66130	TTTTCAGACAGTTTTTTTTC
68044	66131	CTTTTCAGACAGTTTTTTTT
68045	66132	TCTTTTCAGACAGTTTTTTT
68046	66133	TTCTTTTCAGACAGTTTTTT
68047	66134	TTTCTTTTCAGACAGTTTTT
68048	66135	TTTTCTTTTCAGACAGTTTT
68049	66136	TTTTTCTTTTCAGACAGTTT
68050	66137	TTTTTTCTTTTCAGACAGTT
68051	66138	TTTTTTTCTTTTCAGACAGT
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68053	66140	TTTTTTTTTCTTTTCAGACA
68054	66141	TTTTTTTTTTCTTTTCAGAC
68055	66142	TTTTTTTTTTTCTTTTCAGA
68056	66143	ATTTTTTTTTTTCTTTTCAG
68057	66144	AATTTTTTTTTTTCTTTTCA
68058	66145	TAATTTTTTTTTTTCTTTTC
68059	66146	ATAATTTTTTTTTTTTCTTT
68060	66147	TATAATTTTTTTTTTTCTTT
68061	66148	ATATAATTTTTTTTTTTCTT
68062	66149	CATATAATTTTTTTTTTTCT
68063	66150	CCATATAATTTTTTTTTTTC
68064	66151	CCCATATAATTTTTTTTTTT
68065	66152	TCCCATATAATTTTTTTTTT
68066	66153	TTCCCATATAATTTTTTTTT
68067	66154	TTTCCCATATAATTTTTTTT
68068	66155	ATTTCCCATATAATTTTTTT
68069	66156	GATTTCCCATATAATTTTTT
68070	66157	TGATTTCCCATATAATTTTT
68071	66158	TTGATTTCCCATATAATTTT
68072	66159	TTTGATTTCCCATATAATTT
68073	66160	TTTTGATTTCCCATATAATT
68074	66161	CTTTTGATTTCCCATATAAT
68075	66162	GCTTTTGATTTCCCATATAA
68076	66163	TGCTTTTGATTTCCCATATA
68077	66164	ATGCTTTTGATTTCCCATAT
68078	66165	GATGCTTTTGATTTCCCATA
68079	66166	AGATGCTTTTGATTTCCCAT
68080	66167	TAGATGCTTTTGATTTCCCA
68081	66168	ATAGATGCTTTTGATTTCCC
68082	66169	TATAGATGCTTTTGATTTCC
68083	66170	GTATAGATGCTTTTGATTTC
68084	66171	AGTATAGATGCTTTTGATTT
68085	66172	CAGTATAGATGCTTTTGATT
68086	66173	TCAGTATAGATGCTTTTGAT
68087	66174	TTCAGTATAGATGCTTTTGA
68088	66175	GTTCAGTATAGATGCTTTTG
68089	66176	TGTTCAGTATAGATGCTTTT
68090	66177	ATGTTCAGTATAGATGCTTT
68091	66178	CATGTTCAGTATAGATGCTT
68092	66179	ACATGTTCAGTATAGATGCT
68093	66180	TACATGTTCAGTATAGATGC
68094	66181	GTACATGTTCAGTATAGATG
68095	66182	TGTACATGTTCAGTATAGAT
68096	66183	CTGTACATGTTCAGTATAGA
68097	66184	TCTGTACATGTTCAGTATAG

117174	115261	TCCAGCCAATTAGTCTGGTT
117175	115262	GTCCAGCCAATTAGTCTGGT
117176	115263	TGTCCAGCCAATTAGTCTGG
117177	115264	GTGTCCAGCCAATTAGTCTG
117178	115265	TGTGTCCAGCCAATTAGTCT
117179	115266	CTGTGTCCAGCCAATTAGTC
117180	115267	ACTGTGTCCAGCCAATTAGT
117181	115268	CACTGTGTCCAGCCAATTAG
117182	115269	CCACTGTGTCCAGCCAATTA
117183	115270	GCCACTGTGTCCAGCCAATT
117184	115271	AGCCACTGTGTCCAGCCAAT
117185	115272	GAGCCACTGTGTCCAGCCAA
117186	115273	GGAGCCACTGTGTCCAGCCA
117187	115274	TGGAGCCACTGTGTCCAGCC
117188	115275	ATGGAGCCACTGTGTCCAGC
117189	115276	CATGGAGCCACTGTGTCCAG
117190	115277	GCATGGAGCCACTGTGTCCA
117191	115278	GGCATGGAGCCACTGTGTCC
117192	115279	AGGCATGGAGCCACTGTGTC
117193	115280	CAGGCATGGAGCCACTGTGT
117194	115281	TCAGGCATGGAGCCACTGTG
117195	115282	ATCAGGCATGGAGCCACTGT
117196	115283	TATCAGGCATGGAGCCACTG
117197	115284	ATATCAGGCATGGAGCCACT
117198	115285	GATATCAGGCATGGAGCCAC
117199	115286	GGATATCAGGCATGGAGCCA
117200	115287	GGGATATCAGGCATGGAGCC
117201	115288	TGGGATATCAGGCATGGAGC
117202	115289	CTGGGATATCAGGCATGGAG
117203	115290	GCTGGGATATCAGGCATGGA
117204	115291	AGCTGGGATATCAGGCATGG
117205	115292	CAGCTGGGATATCAGGCATG
117206	115293	CCAGCTGGGATATCAGGCAT
117207	115294	TCCAGCTGGGATATCAGGCA
117208	115295	CTCCAGCTGGGATATCAGGC
117209	115296	CCTCCAGCTGGGATATCAGG
117210	115297	TCCTCCAGCTGGGATATCAG
117211	115298	ATCCTCCAGCTGGGATATCA
117212	115299	CATCCTCCAGCTGGGATATC
117213	115300	TCATCCTCCAGCTGGGATAT
117214	115301	GTCATCCTCCAGCTGGGATA
117215	115302	AGTCATCCTCCAGCTGGGAT
117216	115303	AAGTCATCCTCCAGCTGGGA
117217	115304	CAAGTCATCCTCCAGCTGGG
117218	115305	TCAAGTCATCCTCCAGCTGG
117219	115306	TTCAAGTCATCCTCCAGCTG
117220	115307	GTTCAAGTCATCCTCCAGCT
117221	115308	GGTTCAAGTCATCCTCCAGC
117222	115309	GGGTTCAAGTCATCCTCCAG
117223	115310	TGGGTTCAAGTCATCCTCCA
117224	115311	ATGGGTTCAAGTCATCCTCC
117225	115312	CATGGGTTCAAGTCATCCTC
117226	115313	TCATGGGTTCAAGTCATCCT
117227	115314	CTCATGGGTTCAAGTCATCC
117228	115315	ACTCATGGGTTCAAGTCATC
117229	115316	AACTCATGGGTTCAAGTCAT
117230	115317	GAACTCATGGGTTCAAGTCA
117231	115318	CGAACTCATGGGTTCAAGTC
117232	115319	TCGAACTCATGGGTTCAAGT
117233	115320	CTCGAACTCATGGGTTCAAG
117234	115321	TCTCGAACTCATGGGTTCAA
117235	115322	CTCTCGAACTCATGGGTTCA
117236	115323	GCTCTCGAACTCATGGGTTC
117237	115324	TGCTCTCGAACTCATGGGTT
117238	115325	CTGCTCTCGAACTCATGGGT
117239	115326	GCTGCTCTCGAACTCATGGG
117240	115327	TGCTGCTCTCGAACTCATGG
117241	115328	ATGCTGCTCTCGAACTCATG
117242	115329	CATGCTGCTCTCGAACTCAT
117243	115330	CCATGCTGCTCTCGAACTCA
117244	115331	CCCATGCTGCTCTCGAACTC

18951	17038	ATACATAAAAACAGAAAATA
18952	17039	AATACATAAAAACAGAAAAT
18953	17040	AAATACATAAAAACAGAAAA
18954	17041	TAAATACATAAAAACAGAAA
18955	17042	ATAAATACATAAAAACAGAA
18956	17043	AATAAATACATAAAAACAGA
18957	17044	AAATAAATACATAAAAACAG
18958	17045	AAAATAAATACATAAAAACA
18959	17046	AAAAATAAATACATAAAAAC
18960	17047	AAAAAATAAATACATAAAAA
18961	17048	CAAAAAATAAATACATAAAA
18962	17049	TCAAAAAATAAATACATAAA
18963	17050	CTCAAAAAATAAATACATAA
18964	17051	TCTCAAAAAATAAATACATA
18965	17052	ATCTCAAAAAATAAATACAT
18966	17053	CATCTCAAAAAATAAATACA
18967	17054	CCATCTCAAAAAATAAATAC
18968	17055	CCCATCTCAAAAAATAAATA
18969	17056	TCCCATCTCAAAAAATAAAT
18970	17057	ATCCCATCTCAAAAAATAAA
18971	17058	GATCCCATCTCAAAAAATAA
18972	17059	AGATCCCATCTCAAAAAATA
18973	17060	AAGATCCCATCTCAAAAAAT
18974	17061	CAAGATCCCATCTCAAAAAA
18975	17062	GCAAGATCCCATCTCAAAAA
18976	17063	AGCAAGATCCCATCTCAAAA
18977	17064	CAGCAAGATCCCATCTCAAA
18978	17065	ACAGCAAGATCCCATCTCAA
18979	17066	TACAGCAAGATCCCATCTCA
18980	17067	ATACAGCAAGATCCCATCTC
18981	17068	AATACAGCAAGATCCCATCT
18982	17069	CAATACAGCAAGATCCCATC
18983	17070	GCAATACAGCAAGATCCCAT
18984	17071	GGCAATACAGCAAGATCCCA
18985	17072	GGGCAATACAGCAAGATCCC
18986	17073	TGGGCAATACAGCAAGATCC
18987	17074	CTGGGCAATACAGCAAGATC
18988	17075	CCTGGGCAATACAGCAAGAT
18989	17076	ACCTGGGCAATACAGCAAGA
18990	17077	AACCTGGGCAATACAGCAAG
18991	17078	CAACCTGGGCAATACAGCAA
18992	17079	CCAACCTGGGCAATACAGCA
18993	17080	TCCAACCTGGGCAATACAGC
18994	17081	CTCCAACCTGGGCAATACAG
18995	17082	ACTCCAACCTGGGCAATACA
18996	17083	TACTCCAACCTGGGCAATAC
18997	17084	GTACTCCAACCTGGGCAATA
18998	17085	TGTACTCCAACCTGGGCAAT
18999	17086	CTGTACTCCAACCTGGGCAA
19000	17087	ACTGTACTCCAACCTGGGCA
19001	17088	TACTGTACTCCAACCTGGGC
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19003	17090	AATACTGTACTCCAACCTGG
19004	17091	CAATACTGTACTCCAACCTG
19005	17092	ACAATACTGTACTCCAACCT
19006	17093	CACAATACTGTACTCCAACC
19007	17094	TCACAATACTGTACTCCAAC
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19009	17096	GATCACAATACTGTACTCCA
19010	17097	TGATCACAATACTGTACTCC
19011	17098	ATGATCACAATACTGTACTC
19012	17099	CATGATCACAATACTGTACT
19013	17100	CCATGATCACAATACTGTAC
19014	17101	GCCATGATCACAATACTGTA
19015	17102	AGCCATGATCACAATACTGT
19016	17103	AAGCCATGATCACAATACTG
19017	17104	TAAGCCATGATCACAATACT
19018	17105	ATAAGCCATGATCACAATAC
19019	17106	AATAAGCCATGATCACAATA
19020	17107	CAATAAGCCATGATCACAAT
19021	17108	GCAATAAGCCATGATCACAA

68098	66185	GTCTGTACATGTTCAGTATA
68099	66186	AGTCTGTACATGTTCAGTAT
68100	66187	AAGTCTGTACATGTTCAGTA
68101	66188	AAAGTCTGTACATGTTCAGT
68102	66189	AAAAGTCTGTACATGTTCAG
68103	66190	AAAAAGTCTGTACATGTTCA
68104	66191	AAAAAAGTCTGTACATGTTC
68105	66192	AAAAAAAGTCTGTACATGTT
68106	66193	GAAAAAAAGTCTGTACATGT
68107	66194	AGAAAAAAAGTCTGTACATG
68108	66195	AAGAAAAAAAGTCTGTACAT
68109	66196	CAAGAAAAAAAGTCTGTACA
68110	66197	ACAAGAAAAAAAGTCTGTAC
68111	66198	GACAAGAAAAAAAGTCTGTA
68112	66199	TGACAAGAAAAAAAGTCTGT
68113	66200	ATGACAAGAAAAAAAGTCTG
68114	66201	AATGACAAGAAAAAAAGTCT
68115	66202	TAATGACAAGAAAAAAAGTC
68116	66203	ATAATGACAAGAAAAAAAGT
68117	66204	AATAATGACAAGAAAAAAAG
68118	66205	GAATAATGACAAGAAAAAAA
68119	66206	GGAATAATGACAAGAAAAAA
68120	66207	AGGAATAATGACAAGAAAAA
68121	66208	AAGGAATAATGACAAGAAAA
68122	66209	TAAGGAATAATGACAAGAAA
68123	66210	TTAAGGAATAATGACAAGAA
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68125	66212	GCTTAAGGAATAATGACAAG
68126	66213	TGCTTAAGGAATAATGACAA
68127	66214	CTGCTTAAGGAATAATGACA
68128	66215	ACTGCTTAAGGAATAATGAC
68129	66216	TACTGCTTAAGGAATAATGA
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68132	66219	TGGTACTGCTTAAGGAATAA
68133	66220	GTGGTACTGCTTAAGGAATA
68134	66221	TGTGGTACTGCTTAAGGAAT
68135	66222	TTGTGGTACTGCTTAAGGAA
68136	66223	GTTGTGGTACTGCTTAAGGA
68137	66224	AGTTGTGGTACTGCTTAAGG
68138	66225	TAGTTGTGGTACTGCTTAAG
68139	66226	ATAGTTGTGGTACTGCTTAA
68140	66227	AATAGTTGTGGTACTGCTTA
68141	66228	AAATAGTTGTGGTACTGCTT
68142	66229	GAAATAGTTGTGGTACTGCT
68143	66230	GGAAATAGTTGTGGTACTGC
68144	66231	CGGAAATAGTTGTGGTACTG
68145	66232	ACGGAAATAGTTGTGGTACT
68146	66233	TACGGAAATAGTTGTGGTAC
68147	66234	CTACGGAAATAGTTGTGGTA
68148	66235	GCTACGGAAATAGTTGTGGT
68149	66236	TGCTACGGAAATAGTTGTGG
68150	66237	ATGCTACGGAAATAGTTGTG
68151	66238	AATGCTACGGAAATAGTTGT
68152	66239	AAATGCTACGGAAATAGTTG
68153	66240	TAAATGCTACGGAAATAGTT
68154	66241	GTAAATGCTACGGAAATAGT
68155	66242	AGTAAATGCTACGGAAATAG
68156	66243	AAGTAAATGCTACGGAAATA
68157	66244	AAAGTAAATGCTACGGAAAT
68158	66245	CAAAGTAAATGCTACGGAAA
68159	66246	ACAAAGTAAATGCTACGGAA
68160	66247	TACAAAGTAAATGCTACGGA
68161	66248	ATACAAAGTAAATGCTACGG
68162	66249	AATACAAAGTAAATGCTACG
68163	66250	TAATACAAAGTAAATGCTAC
68164	66251	CTAATACAAAGTAAATGCTA
68165	66252	CCTAATACAAAGTAAATGCT
68166	66253	ACCTAATACAAAGTAAATGC
68167	66254	TACCTAATACAAAGTAAATG
68168	66255	ATACCTAATACAAAGTAAAT

117245	115332	GCCCATGCTGCTCTCGAACT
117246	115333	TGCCCATGCTGCTCTCGAAC
117247	115334	TTGCCCATGCTGCTCTCGAA
117248	115335	ATTGCCCATGCTGCTCTCGA
117249	115336	TATTGCCCATGCTGCTCTCG
117250	115337	ATATTGCCCATGCTGCTCTC
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117252	115339	CTATATTGCCCATGCTGCTC
117253	115340	ACTATATTGCCCATGCTGCT
117254	115341	CACTATATTGCCCATGCTGC
117255	115342	TCACTATATTGCCCATGCTG
117256	115343	CTCACTATATTGCCCATGCT
117257	115344	TCTCACTATATTGCCCATGC
117258	115345	GTCTCACTATATTGCCCATG
117259	115346	GGTCTCACTATATTGCCCAT
117260	115347	GGGTCTCACTATATTGCCCA
117261	115348	AGGGTCTCACTATATTGCCC
117262	115349	TAGGGTCTCACTATATTGCC
117263	115350	ATAGGGTCTCACTATATTGC
117264	115351	GATAGGGTCTCACTATATTG
117265	115352	AGATAGGGTCTCACTATATT
117266	115353	GAGATAGGGTCTCACTATAT
117267	115354	TGAGATAGGGTCTCACTATA
117268	115355	TTGAGATAGGGTCTCACTAT
117269	115356	TTTGAGATAGGGTCTCACTA
117270	115357	TTTTGAGATAGGGTCTCACT
117271	115358	TTTTTGAGATAGGGTCTCAC
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117279	115366	TTTTTTTTTTTTTGAGATAG
117280	115367	TTTTTTTTTTTTTTGAGATA
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117283	115370	CTTTTTTTTTTTTTTTTGAG
117284	115371	ACTTTTTTTTTTTTTTTTGA
117285	115372	AACTTTTTTTTTTTTTTTTG
117286	115373	TAACTTTTTTTTTTTTTTTT
117287	115374	TTAACTTTTTTTTTTTTTTT
117288	115375	ATTAACTTTTTTTTTTTTTT
117289	115376	AATTAACTTTTTTTTTTTTT
117290	115377	GAATTAACTTTTTTTTTTTT
117291	115378	GGAATTAACTTTTTTTTTTT
117292	115379	TGGAATTAACTTTTTTTTTT
117293	115380	TTGGAATTAACTTTTTTTTT
117294	115381	TTTGGAATTAACTTTTTTTT
117295	115382	CTTTGGAATTAACTTTTTTT
117296	115383	GCTTTGGAATTAACTTTTTT
117297	115384	AGCTTTGGAATTAACTTTTT
117298	115385	AAGCTTTGGAATTAACTTTT
117299	115386	AAAGCTTTGGAATTAACTTT
117300	115387	AAAAGCTTTGGAATTAACTT
117301	115388	AAAAAGCTTTGGAATTAACT
117302	115389	CAAAAAGCTTTGGAATTAAC
117303	115390	TCAAAAAGCTTTGGAATTAA
117304	115391	ATCAAAAAGCTTTGGAATTA
117305	115392	GATCAAAAAGCTTTGGAATT
117306	115393	AGATCAAAAAGCTTTGGAAT
117307	115394	CAGATCAAAAAGCTTTGGAA
117308	115395	TCAGATCAAAAAGCTTTGGA
117309	115396	TTCAGATCAAAAAGCTTTGG
117310	115397	TTTCAGATCAAAAAGCTTTG
117311	115398	ATTTCAGATCAAAAAGCTTT
117312	115399	GATTTCAGATCAAAAAGCTT
117313	115400	AGATTTCAGATCAAAAAGCT
117314	115401	CAGATTTCAGATCAAAAAGC
117315	115402	TCAGATTTCAGATCAAAAAG

19022	17109	TGCAATAAGCCATGATCACA
19023	17110	CTGCAATAAGCCATGATCAC
19024	17111	GCTGCAATAAGCCATGATCA
19025	17112	GGCTGCAATAAGCCATGATC
19026	17113	AGGCTGCAATAAGCCATGAT
19027	17114	AAGGCTGCAATAAGCCATGA
19028	17115	AAAGGCTGCAATAAGCCATG
19029	17116	TAAAGGCTGCAATAAGCCAT
19030	17117	TTAAAGGCTGCAATAAGCCA
19031	17118	GTTAAAGGCTGCAATAAGCC
19032	17119	AGTTAAAGGCTGCAATAAGC
19033	17120	GAGTTAAAGGCTGCAATAAG
19034	17121	GGAGTTAAAGGCTGCAATAA
19035	17122	AGGAGTTAAAGGCTGCAATA
19036	17123	CAGGAGTTAAAGGCTGCAAT
19037	17124	CCAGGAGTTAAAGGCTGCAA
19038	17125	CCCAGGAGTTAAAGGCTGCA
19039	17126	ACCCAGGAGTTAAAGGCTGC
19040	17127	AACCCAGGAGTTAAAGGCTG
19041	17128	GAACCCAGGAGTTAAAGGCT
19042	17129	TGAACCCAGGAGTTAAAGGC
19043	17130	TTGAACCCAGGAGTTAAAGG
19044	17131	CTTGAACCCAGGAGTTAAAG
19045	17132	ACTTGAACCCAGGAGTTAAA
19046	17133	CACTTGAACCCAGGAGTTAA
19047	17134	TCACTTGAACCCAGGAGTTA
19048	17135	ATCACTTGAACCCAGGAGTT
19049	17136	GATCACTTGAACCCAGGAGT
19050	17137	GGATCACTTGAACCCAGGAG
19051	17138	AGGATCACTTGAACCCAGGA
19052	17139	GAGGATCACTTGAACCCAGG
19053	17140	GGAGGATCACTTGAACCCAG
19054	17141	GGGAGGATCACTTGAACCCA
19055	17142	TGGGAGGATCACTTGAACCC
19056	17143	GTGGGAGGATCACTTGAACC
19057	17144	GGTGGGAGGATCACTTGAAC
19058	17145	AGGTGGGAGGATCACTTGAA
19059	17146	GAGGTGGGAGGATCACTTGA
19060	17147	TGAGGTGGGAGGATCACTTG
19061	17148	CTGAGGTGGGAGGATCACTT
19062	17149	GCTGAGGTGGGAGGATCACT
19063	17150	GGCTGAGGTGGGAGGATCAC
19064	17151	AGGCTGAGGTGGGAGGATCA
19065	17152	GAGGCTGAGGTGGGAGGATC
19066	17153	GGAGGCTGAGGTGGGAGGAT
19067	17154	AGGAGGCTGAGGTGGGAGGA
19068	17155	CAGGAGGCTGAGGTGGGAGG
19069	17156	TCAGGAGGCTGAGGTGGGAG
19070	17157	CTCAGGAGGCTGAGGTGGGA
19071	17158	ACTCAGGAGGCTGAGGTGGG
19072	17159	TACTCAGGAGGCTGAGGTGG
19073	17160	CTACTCAGGAGGCTGAGGTG
19074	17161	GCTACTCAGGAGGCTGAGGT
19075	17162	AGCTACTCAGGAGGCTGAGG
19076	17163	CAGCTACTCAGGAGGCTGAG
19077	17164	CCAGCTACTCAGGAGGCTGA
19078	17165	CCCAGCTACTCAGGAGGCTG
19079	17166	TCCCAGCTACTCAGGAGGCT
19080	17167	GTCCCAGCTACTCAGGAGGC
19081	17168	GGTCCCAGCTACTCAGGAGG
19082	17169	TGGTCCCAGCTACTCAGGAG
19083	17170	GTGGTCCCAGCTACTCAGGA
19084	17171	TGTGGTCCCAGCTACTCAGG
19085	17172	CTGTGGTCCCAGCTACTCAG
19086	17173	CCTGTGGTCCCAGCTACTCA
19087	17174	GCCTGTGGTCCCAGCTACTC
19088	17175	TGCCTGTGGTCCCAGCTACT
19089	17176	GTGCCTGTGGTCCCAGCTAC
19090	17177	TGTGCCTGTGGTCCCAGCTA
19091	17178	ATGTGCCTGTGGTCCCAGCT
19092	17179	CATGTGCCTGTGGTCCCAGC

68169	66256	AATACCTAATACAAAGTAAA
68170	66257	TAATACCTAATACAAAGTAA
68171	66258	ATAATACCTAATACAAAGTA
68172	66259	TATAATACCTAATACAAAGT
68173	66260	CTATAATACCTAATACAAAG
68174	66261	CCTATAATACCTAATACAAA
68175	66262	ACCTATAATACCTAATACAA
68176	66263	TACCTATAATACCTAATACA
68177	66264	TTACCTATAATACCTAATAC
68178	66265	GTTACCTATAATACCTAATA
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68180	66267	AGGTTACCTATAATACCTAA
68181	66268	TAGGTTACCTATAATACCTA
68182	66269	CTAGGTTACCTATAATACCT
68183	66270	TCTAGGTTACCTATAATACC
68184	66271	CTCTAGGTTACCTATAATAC
68185	66272	CCTCTAGGTTACCTATAATA
68186	66273	ACCTCTAGGTTACCTATAAT
68187	66274	AACCTCTAGGTTACCTATAA
68188	66275	AAACCTCTAGGTTACCTATA
68189	66276	TAAACCTCTAGGTTACCTAT
68190	66277	TTAAACCTCTAGGTTACCTA
68191	66278	TTTAAACCTCTAGGTTACCT
68192	66279	CTTTAAACCTCTAGGTTACC
68193	66280	ACTTTAAACCTCTAGGTTAC
68194	66281	TACTTTAAACCTCTAGGTTA
68195	66282	ATACTTTAAACCTCTAGGTT
68196	66283	CATACTTTAAACCTCTAGGT
68197	66284	GCATACTTTAAACCTCTAGG
68198	66285	CGCATACTTTAAACCTCTAG
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68203	66290	ACTCTCGCATACTTTAAACC
68204	66291	TACTCTCGCATACTTTAAAC
68205	66292	ATACTCTCGCATACTTTAAA
68206	66293	CATACTCTCGCATACTTTAA
68207	66294	GCATACTCTCGCATACTTTA
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68209	66296	TTGCATACTCTCGCATACTT
68210	66297	TTTGCATACTCTCGCATACT
68211	66298	ATTTGCATACTCTCGCATAC
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68220	66307	TGGTGTAGTATTTGCATACT
68221	66308	GTGGTGTAGTATTTGCATAC
68222	66309	AGTGGTGTAGTATTTGCATA
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68224	66311	AAAGTGGTGTAGTATTTGCA
68225	66312	CAAAGTGGTGTAGTATTTGC
68226	66313	ACAAAGTGGTGTAGTATTTG
68227	66314	TACAAAGTGGTGTAGTATTT
68228	66315	ATACAAAGTGGTGTAGTATT
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68230	66317	TGATACAAAGTGGTGTAGTA
68231	66318	CTGATACAAAGTGGTGTAGT
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68233	66320	CCCTGATACAAAGTGGTGTA
68234	66321	TCCCTGATACAAAGTGGTGT
68235	66322	GTCCCTGATACAAAGTGGTG
68236	66323	AGTCCCTGATACAAAGTGGT
68237	66324	AAGTCCCTGATACAAAGTGG
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117316	115403	ATCAGATTTCAGATCAAAAA
117317	115404	AATCAGATTTCAGATCAAAA
117318	115405	AAATCAGATTTCAGATCAAA
117319	115406	TAAATCAGATTTCAGATCAA
117320	115407	TTAAATCAGATTTCAGATCA
117321	115408	TTTAAATCAGATTTCAGATC
117322	115409	ATTTAAATCAGATTTCAGAT
117323	115410	GATTTAAATCAGATTTCAGA
117324	115411	AGATTTAAATCAGATTTCAG
117325	115412	CAGATTTAAATCAGATTTCA
117326	115413	TCAGATTTAAATCAGATTTC
117327	115414	TTCAGATTTAAATCAGATTT
117328	115415	GTTCAGATTTAAATCAGATT
117329	115416	AGTTCAGATTTAAATCAGAT
117330	115417	AAGTTCAGATTTAAATCAGA
117331	115418	TAAGTTCAGATTTAAATCAG
117332	115419	TTAAGTTCAGATTTAAATCA
117333	115420	TTTAAGTTCAGATTTAAATC
117334	115421	ATTTAAGTTCAGATTTAAAT
117335	115422	AATTTAAGTTCAGATTTAAA
117336	115423	AAATTTAAGTTCAGATTTAA
117337	115424	CAAATTTAAGTTCAGATTTA
117338	115425	TCAAATTTAAGTTCAGATTT
117339	115426	TTCAAATTTAAGTTCAGATT
117340	115427	CTTCAAATTTAAGTTCAGAT
117341	115428	TCTTCAAATTTAAGTTCAGA
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117343	115430	CTTCTTCAAATTTAAGTTCA
117344	115431	TCTTCTTCAAATTTAAGTTC
117345	115432	CTCTTCTTCAAATTTAAGTT
117346	115433	CCTCTTCTTCAAATTTAAGT
117347	115434	CCCTCTTCTTCAAATTTAAG
117348	115435	ACCCTCTTCTTCAAATTTAA
117349	115436	AACCCTCTTCTTCAAATTTA
117350	115437	AAACCCTCTTCTTCAAATTT
117351	115438	CAAACCCTCTTCTTCAAATT
117352	115439	GCAAACCCTCTTCTTCAAAT
117353	115440	AGCAAACCCTCTTCTTCAAA
117354	115441	TAGCAAACCCTCTTCTTCAA
117355	115442	CTAGCAAACCCTCTTCTTCA
117356	115443	TCTAGCAAACCCTCTTCTTC
117357	115444	ATCTAGCAAACCCTCTTCTT
117358	115445	AATCTAGCAAACCCTCTTCT
117359	115446	TAATCTAGCAAACCCTCTTC
117360	115447	TTAATCTAGCAAACCCTCTT
117361	115448	ATTAATCTAGCAAACCCTCT
117362	115449	AATTAATCTAGCAAACCCTC
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117365	115452	GTAAATTAATCTAGCAAACC
117366	115453	AGTAAATTAATCTAGCAAAC
117367	115454	TAGTAAATTAATCTAGCAAA
117368	115455	CTAGTAAATTAATCTAGCAA
117369	115456	TCTAGTAAATTAATCTAGCA
117370	115457	ATCTAGTAAATTAATCTAGC
117371	115458	AATCTAGTAAATTAATCTAG
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117373	115460	GCAATCTAGTAAATTAATCT
117374	115461	AGCAATCTAGTAAATTAATC
117375	115462	TAGCAATCTAGTAAATTAAT
117376	115463	TTAGCAATCTAGTAAATTAA
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117381	115468	CAAGGTTAGCAATCTAGTAA
117382	115469	GCAAGGTTAGCAATCTAGTA
117383	115470	AGCAAGGTTAGCAATCTAGT
117384	115471	AAGCAAGGTTAGCAATCTAG
117385	115472	AAAGCAAGGTTAGCAATCTA
117386	115473	TAAAGCAAGGTTAGCAATCT

19093	17180	GCATGTGCCTGTGGTCCCAG
19094	17181	TGCATGTGCCTGTGGTCCCA
19095	17182	TTGCATGTGCCTGTGGTCCC
19096	17183	GTTGCATGTGCCTGTGGTCC
19097	17184	TGTTGCATGTGCCTGTGGTC
19098	17185	ATGTTGCATGTGCCTGTGGT
19099	17186	GATGTTGCATGTGCCTGTGG
19100	17187	TGATGTTGCATGTGCCTGTG
19101	17188	GTGATGTTGCATGTGCCTGT
19102	17189	TGTGATGTTGCATGTGCCTG
19103	17190	GTGTGATGTTGCATGTGCCT
19104	17191	GGTGTGATGTTGCATGTGCC
19105	17192	GGGTGTGATGTTGCATGTGC
19106	17193	AGGGTGTGATGTTGCATGTG
19107	17194	CAGGGTGTGATGTTGCATGT
19108	17195	GCAGGGTGTGATGTTGCATG
19109	17196	TGCAGGGTGTGATGTTGCAT
19110	17197	CTGCAGGGTGTGATGTTGCA
19111	17198	ACTGCAGGGTGTGATGTTGC
19112	17199	AACTGCAGGGTGTGATGTTG
19113	17200	GAACTGCAGGGTGTGATGTT
19114	17201	AGAACTGCAGGGTGTGATGT
19115	17202	AAGAACTGCAGGGTGTGATG
19116	17203	AAAGAACTGCAGGGTGTGAT
19117	17204	AAAAGAACTGCAGGGTGTGA
19118	17205	AAAAAGAACTGCAGGGTGTG
19119	17206	AAAAAAGAACTGCAGGGTGT
19120	17207	AAAAAAAGAACTGCAGGGTG
19121	17208	AAAAAAAAGAACTGCAGGGT
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19123	17210	AAAAAAAAAAGAACTGCAGG
19124	17211	AAAAAAAAAAAGAACTGCAG
19125	17212	AAAAAAAAAAAAGAACTGCA
19126	17213	AAAAAAAAAAAAAGAACTGC
19127	17214	CAAAAAAAAAAAAAGAACTG
19128	17215	TCAAAAAAAAAAAAAGAACT
19129	17216	CTCAAAAAAAAAAAAAGAAC
19130	17217	TCTCAAAAAAAAAAAAAGAA
19131	17218	GTCTCAAAAAAAAAAAAAGA
19132	17219	TGTCTCAAAAAAAAAAAAAG
19133	17220	GTGTCTCAAAAAAAAAAAAA
19134	17221	GGTGTCTCAAAAAAAAAAAA
19135	17222	CGGTGTCTCAAAAAAAAAAA
19136	17223	ACGGTGTCTCAAAAAAAAAA
19137	17224	GACGGTGTCTCAAAAAAAAA
19138	17225	AGACGGTGTCTCAAAAAAAA
19139	17226	GAGACGGTGTCTCAAAAAAA
19140	17227	CGAGACGGTGTCTCAAAAAA
19141	17228	GCGAGACGGTGTCTCAAAAA
19142	17229	AGCGAGACGGTGTCTCAAAA
19143	17230	AAGCGAGACGGTGTCTCAAA
19144	17231	AAAGCGAGACGGTGTCTCAA
19145	17232	CAAAGCGAGACGGTGTCTCA
19146	17233	ACAAAGCGAGACGGTGTCTC
19147	17234	GACAAAGCGAGACGGTGTCT
19148	17235	TGACAAAGCGAGACGGTGTC
19149	17236	GTGACAAAGCGAGACGGTGT
19150	17237	GGTGACAAAGCGAGACGGTG
19151	17238	GGGTGACAAAGCGAGACGGT
19152	17239	TGGGTGACAAAGCGAGACGG
19153	17240	CTGGGTGACAAAGCGAGACG
19154	17241	CCTGGGTGACAAAGCGAGAC
19155	17242	GCCTGGGTGACAAAGCGAGA
19156	17243	AGCCTGGGTGACAAAGCGAG
19157	17244	CAGCCTGGGTGACAAAGCGA
19158	17245	GCAGCCTGGGTGACAAAGCG
19159	17246	TGCAGCCTGGGTGACAAAGC
19160	17247	CTGCAGCCTGGGTGACAAAG
19161	17248	ACTGCAGCCTGGGTGACAAA
19162	17249	CACTGCAGCCTGGGTGACAA
19163	17250	GCACTGCAGCCTGGGTGACA

68240	66327	CTTAAGTCCCTGATACAAAG
68241	66328	GCTTAAGTCCCTGATACAAA
68242	66329	TGCTTAAGTCCCTGATACAA
68243	66330	ATGCTTAAGTCCCTGATACA
68244	66331	GATGCTTAAGTCCCTGATAC
68245	66332	GGATGCTTAAGTCCCTGATA
68246	66333	GGGATGCTTAAGTCCCTGAT
68247	66334	AGGGATGCTTAAGTCCCTGA
68248	66335	CAGGGATGCTTAAGTCCCTG
68249	66336	CCAGGGATGCTTAAGTCCCT
68250	66337	TCCAGGGATGCTTAAGTCCC
68251	66338	ATCCAGGGATGCTTAAGTCC
68252	66339	AATCCAGGGATGCTTAAGTC
68253	66340	AAATCCAGGGATGCTTAAGT
68254	66341	AAAATCCAGGGATGCTTAAG
68255	66342	CAAAATCCAGGGATGCTTAA
68256	66343	CCAAAATCCAGGGATGCTTA
68257	66344	ACCAAAATCCAGGGATGCTT
68258	66345	TACCAAAATCCAGGGATGCT
68259	66346	ATACCAAAATCCAGGGATGC
68260	66347	GATACCAAAATCCAGGGATG
68261	66348	GGATACCAAAATCCAGGGAT
68262	66349	GGGATACCAAAATCCAGGGA
68263	66350	AGGGATACCAAAATCCAGGG
68264	66351	TAGGGATACCAAAATCCAGG
68265	66352	CTAGGGATACCAAAATCCAG
68266	66353	CCTAGGGATACCAAAATCCA
68267	66354	CCCTAGGGATACCAAAATCC
68268	66355	CCCCTAGGGATACCAAAATC
68269	66356	CCCCCTAGGGATACCAAAAT
68270	66357	ACCCCCTAGGGATACCAAAA
68271	66358	TACCCCCTAGGGATACCAAA
68272	66359	ATACCCCCTAGGGATACCAA
68273	66360	AATACCCCCTAGGGATACCA
68274	66361	TAATACCCCCTAGGGATACC
68275	66362	CTAATACCCCCTAGGGATAC
68276	66363	TCTAATACCCCCTAGGGATA
68277	66364	TTCTAATACCCCCTAGGGAT
68278	66365	GTTCTAATACCCCCTAGGGA
68279	66366	GGTTCTAATACCCCCTAGGG
68280	66367	TGGTTCTAATACCCCCTAGG
68281	66368	TTGGTTCTAATACCCCCTAG
68282	66369	ATTGGTTCTAATACCCCCTA
68283	66370	GATTGGTTCTAATACCCCCT
68284	66371	GGATTGGTTCTAATACCCCC
68285	66372	GGGATTGGTTCTAATACCCC
68286	66373	GGGGATTGGTTCTAATACCC
68287	66374	GGGGGATTGGTTCTAATACC
68288	66375	TGGGGGATTGGTTCTAATAC
68289	66376	ATGGGGGATTGGTTCTAATA
68290	66377	TATGGGGGATTGGTTCTAAT
68291	66378	CTATGGGGGATTGGTTCTAA
68292	66379	TCTATGGGGGATTGGTTCTA
68293	66380	ATCTATGGGGGATTGGTTCT
68294	66381	CATCTATGGGGGATTGGTTC
68295	66382	GCATCTATGGGGGATTGGTT
68296	66383	AGCATCTATGGGGGATTGGT
68297	66384	CAGCATCTATGGGGGATTGG
68298	66385	TCAGCATCTATGGGGGATTG
68299	66386	TTCAGCATCTATGGGGGATT
68300	66387	CTTCAGCATCTATGGGGGAT
68301	66388	CCTTCAGCATCTATGGGGGA
68302	66389	TCCTTCAGCATCTATGGGGG
68303	66390	GTCCTTCAGCATCTATGGGG
68304	66391	TGTCCTTCAGCATCTATGGG
68305	66392	TTGTCCTTCAGCATCTATGG
68306	66393	GTTGTCCTTCAGCATCTATG
68307	66394	AGTTGTCCTTCAGCATCTAT
68308	66395	CAGTTGTCCTTCAGCATCTA
68309	66396	ACAGTTGTCCTTCAGCATCT
68310	66397	TACAGTTGTCCTTCAGCATC

117387	115474	ATAAAGCAAGGTTAGCAATC
117388	115475	TATAAAGCAAGGTTAGCAAT
117389	115476	ATATAAAGCAAGGTTAGCAA
117390	115477	TATATAAAGCAAGGTTAGCA
117391	115478	ATATATAAAGCAAGGTTAGC
117392	115479	TATATATAAAGCAAGGTTAG
117393	115480	GTATATATAAAGCAAGGTTA
117394	115481	GGTATATATAAAGCAAGGTT
117395	115482	AGGTATATATAAAGCAAGGT
117396	115483	TAGGTATATATAAAGCAAGG
117397	115484	GTAGGTATATATAAAGCAAG
117398	115485	TGTAGGTATATATAAAGCAA
117399	115486	CTGTAGGTATATATAAAGCA
117400	115487	ACTGTAGGTATATATAAAGC
117401	115488	AACTGTAGGTATATATAAAG
117402	115489	TAACTGTAGGTATATATAAA
117403	115490	ATAACTGTAGGTATATATAA
117404	115491	AATAACTGTAGGTATATATA
117405	115492	AAATAACTGTAGGTATATAT
117406	115493	GAAATAACTGTAGGTATATA
117407	115494	GGAAATAACTGTAGGTATAT
117408	115495	GGGAAATAACTGTAGGTATA
117409	115496	GGGGAAATAACTGTAGGTAT
117410	115497	TGGGGAAATAACTGTAGGTA
117411	115498	TTGGGGAAATAACTGTAGGT
117412	115499	TTTGGGGAAATAACTGTAGG
117413	115500	CTTTGGGGAAATAACTGTAG
117414	115501	GCTTTGGGGAAATAACTGTA
117415	115502	GGCTTTGGGGAAATAACTGT
117416	115503	TGGCTTTGGGGAAATAACTG
117417	115504	CTGGCTTTGGGGAAATAACT
117418	115505	TCTGGCTTTGGGGAAATAAC
117419	115506	TTCTGGCTTTGGGGAAATAA
117420	115507	ATTCTGGCTTTGGGGAAATA
117421	115508	AATTCTGGCTTTGGGGAAAT
117422	115509	AAATTCTGGCTTTGGGGAAA
117423	115510	GAAATTCTGGCTTTGGGGAA
117424	115511	AGAAATTCTGGCTTTGGGGA
117425	115512	AAGAAATTCTGGCTTTGGGG
117426	115513	AAAGAAATTCTGGCTTTGGG
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117428	115515	CAAAAGAAATTCTGGCTTTG
117429	115516	TCAAAAGAAATTCTGGCTTT
117430	115517	TTCAAAAGAAATTCTGGCTT
117431	115518	CTTCAAAAGAAATTCTGGCT
117432	115519	GCTTCAAAAGAAATTCTGGC
117433	115520	TGCTTCAAAAGAAATTCTGG
117434	115521	CTGCTTCAAAAGAAATTCTG
117435	115522	TCTGCTTCAAAAGAAATTCT
117436	115523	CTCTGCTTCAAAAGAAATTC
117437	115524	CCTCTGCTTCAAAAGAAATT
117438	115525	CCCTCTGCTTCAAAAGAAAT
117439	115526	CCCCTCTGCTTCAAAAGAAA
117440	115527	GCCCCTCTGCTTCAAAAGAA
117441	115528	TGCCCCTCTGCTTCAAAAGA
117442	115529	TTGCCCCTCTGCTTCAAAAG
117443	115530	GTTGCCCCTCTGCTTCAAAA
117444	115531	AGTTGCCCCTCTGCTTCAAA
117445	115532	TAGTTGCCCCTCTGCTTCAA
117446	115533	TTAGTTGCCCCTCTGCTTCA
117447	115534	GTTAGTTGCCCCTCTGCTTC
117448	115535	AGTTAGTTGCCCCTCTGCTT
117449	115536	AAGTTAGTTGCCCCTCTGCT
117450	115537	GAAGTTAGTTGCCCCTCTGC
117451	115538	TGAAGTTAGTTGCCCCTCTG
117452	115539	TTGAAGTTAGTTGCCCCTCT
117453	115540	GTTGAAGTTAGTTGCCCCTC
117454	115541	GGTTGAAGTTAGTTGCCCCT
117455	115542	TGGTTGAAGTTAGTTGCCCC
117456	115543	TTGGTTGAAGTTAGTTGCCC
117457	115544	ATTGGTTGAAGTTAGTTGCC

19164	17251	CGCACTGCAGCCTGGGTGAC
19165	17252	ACGCACTGCAGCCTGGGTGA
19166	17253	CACGCACTGCAGCCTGGGTG
19167	17254	CCACGCACTGCAGCCTGGGT
19168	17255	ACCACGCACTGCAGCCTGGG
19169	17256	CACCACGCACTGCAGCCTGG
19170	17257	GCACCACGCACTGCAGCCTG
19171	17258	TGCACCACGCACTGCAGCCT
19172	17259	TTGCACCACGCACTGCAGCC
19173	17260	ATTGCACCACGCACTGCAGC
19174	17261	AATTGCACCACGCACTGCAG
19175	17262	AAATTGCACCACGCACTGCA
19176	17263	GAAATTGCACCACGCACTGC
19177	17264	AGAAATTGCACCACGCACTG
19178	17265	CAGAAATTGCACCACGCACT
19179	17266	GCAGAAATTGCACCACGCAC
19180	17267	AGCAGAAATTGCACCACGCA
19181	17268	GAGCAGAAATTGCACCACGC
19182	17269	TGAGCAGAAATTGCACCACG
19183	17270	GTGAGCAGAAATTGCACCAC
19184	17271	AGTGAGCAGAAATTGCACCA
19185	17272	GAGTGAGCAGAAATTGCACC
19186	17273	AGAGTGAGCAGAAATTGCAC
19187	17274	TAGAGTGAGCAGAAATTGCA
19188	17275	TTAGAGTGAGCAGAAATTGC
19189	17276	GTTAGAGTGAGCAGAAATTG
19190	17277	GGTTAGAGTGAGCAGAAATT
19191	17278	AGGTTAGAGTGAGCAGAAAT
19192	17279	GAGGTTAGAGTGAGCAGAAA
19193	17280	GGAGGTTAGAGTGAGCAGAA
19194	17281	TGGAGGTTAGAGTGAGCAGA
19195	17282	GTGGAGGTTAGAGTGAGCAG
19196	17283	GGTGGAGGTTAGAGTGAGCA
19197	17284	AGGTGGAGGTTAGAGTGAGC
19198	17285	GAGGTGGAGGTTAGAGTGAG
19199	17286	GGAGGTGGAGGTTAGAGTGA
19200	17287	GGGAGGTGGAGGTTAGAGTG
19201	17288	CGGGAGGTGGAGGTTAGAGT
19202	17289	TCGGGAGGTGGAGGTTAGAG
19203	17290	CTCGGGAGGTGGAGGTTAGA
19204	17291	ACTCGGGAGGTGGAGGTTAG
19205	17292	AACTCGGGAGGTGGAGGTTA
19206	17293	GAACTCGGGAGGTGGAGGTT
19207	17294	TGAACTCGGGAGGTGGAGGT
19208	17295	TTGAACTCGGGAGGTGGAGG
19209	17296	CTTGAACTCGGGAGGTGGAG
19210	17297	GCTTGAACTCGGGAGGTGGA
19211	17298	TGCTTGAACTCGGGAGGTGG
19212	17299	CTGCTTGAACTCGGGAGGTG
19213	17300	ACTGCTTGAACTCGGGAGGT
19214	17301	AACTGCTTGAACTCGGGAGG
19215	17302	GAACTGCTTGAACTCGGGAG
19216	17303	AGAACTGCTTGAACTCGGGA
19217	17304	CAGAACTGCTTGAACTCGGG
19218	17305	GCAGAACTGCTTGAACTCGG
19219	17306	GGCAGAACTGCTTGAACTCG
19220	17307	AGGCAGAACTGCTTGAACTC
19221	17308	GAGGCAGAACTGCTTGAACT
19222	17309	TGAGGCAGAACTGCTTGAAC
19223	17310	CTGAGGCAGAACTGCTTGAA
19224	17311	GCTGAGGCAGAACTGCTTGA
19225	17312	GGCTGAGGCAGAACTGCTTG
19226	17313	AGGCTGAGGCAGAACTGCTT
19227	17314	GAGGCTGAGGCAGAACTGCT
19228	17315	GGAGGCTGAGGCAGAACTGC
19229	17316	AGGAGGCTGAGGCAGAACTG
19230	17317	CAGGAGGCTGAGGCAGAACT
19231	17318	TCAGGAGGCTGAGGCAGAAC
19232	17319	CTCAGGAGGCTGAGGCAGAA
19233	17320	ACTCAGGAGGCTGAGGCAGA
19234	17321	TACTCAGGAGGCTGAGGCAG

68311	66398	CTACAGTTGTCCTTCAGCAT
68312	66399	ACTACAGTTGTCCTTCAGCA
68313	66400	CACTACAGTTGTCCTTCAGC
68314	66401	ACACTACAGTTGTCCTTCAG
68315	66402	CACACTACAGTTGTCCTTCA
68316	66403	ACACACTACAGTTGTCCTTC
68317	66404	CACACACTACAGTTGTCCTT
68318	66405	ACACACACTACAGTTGTCCT
68319	66406	AACACACACTACAGTTGTCC
68320	66407	CAACACACACTACAGTTGTC
68321	66408	CCAACACACACTACAGTTGT
68322	66409	TCCAACACACACTACAGTTG
68323	66410	TTCCAACACACACTACAGTT
68324	66411	ATTCCAACACACACTACAGT
68325	66412	TATTCCAACACACACTACAG
68326	66413	TTATTCCAACACACACTACA
68327	66414	ATTATTCCAACACACACTAC
68328	66415	AATTATTCCAACACACACTA
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68330	66417	TAAATTATTCCAACACACAC
68331	66418	ATAAATTATTCCAACACACA
68332	66419	AATAAATTATTCCAACACAC
68333	66420	AAATAAATTATTCCAACACA
68334	66421	AAAATAAATTATTCCAACAC
68335	66422	GAAAATAAATTATTCCAACA
68336	66423	TGAAAATAAATTATTCCAAC
68337	66424	TTGAAAATAAATTATTCCAA
68338	66425	TTTGAAAATAAATTATTCCA
68339	66426	ATTTGAAAATAAATTATTCC
68340	66427	CATTTGAAAATAAATTATTC
68341	66428	CCATTTGAAAATAAATTATT
68342	66429	TCCATTTGAAAATAAATTAT
68343	66430	ATCCATTTGAAAATAAATTA
68344	66431	GATCCATTTGAAAATAAATT
68345	66432	TGATCCATTTGAAAATAAAT
68346	66433	ATGATCCATTTGAAAATAAA
68347	66434	AATGATCCATTTGAAAATAA
68348	66435	AAATGATCCATTTGAAAATA
68349	66436	CAAATGATCCATTTGAAAAT
68350	66437	CCAAATGATCCATTTGAAAA
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68355	66442	GTTCTCCAAATGATCCATTT
68356	66443	TGTTCTCCAAATGATCCATT
68357	66444	GTGTTCTCCAAATGATCCAT
68358	66445	AGTGTTCTCCAAATGATCCA
68359	66446	TAGTGTTCTCCAAATGATCC
68360	66447	ATAGTGTTCTCCAAATGATC
68361	66448	AATAGTGTTCTCCAAATGAT
68362	66449	GAATAGTGTTCTCCAAATGA
68363	66450	AGAATAGTGTTCTCCAAATG
68364	66451	AAGAATAGTGTTCTCCAAAT
68365	66452	AAAGAATAGTGTTCTCCAAA
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68368	66455	CCTAAAGAATAGTGTTCTCC
68369	66456	TCCTAAAGAATAGTGTTCTC
68370	66457	TTCCTAAAGAATAGTGTTCT
68371	66458	TTTCCTAAAGAATAGTGTTC
68372	66459	GTTTCCTAAAGAATAGTGTT
68373	66460	TGTTTCCTAAAGAATAGTGT
68374	66461	ATGTTTCCTAAAGAATAGTG
68375	66462	TATGTTTCCTAAAGAATAGT
68376	66463	CTATGTTTCCTAAAGAATAG
68377	66464	GCTATGTTTCCTAAAGAATA
68378	66465	GGCTATGTTTCCTAAAGAAT
68379	66466	AGGCTATGTTTCCTAAAGAA
68380	66467	GAGGCTATGTTTCCTAAAGA
68381	66468	GGAGGCTATGTTTCCTAAAG

117458	115545	CATTGGTTGAAGTTAGTTGC
117459	115546	ACATTGGTTGAAGTTAGTTG
117460	115547	AACATTGGTTGAAGTTAGTT
117461	115548	TAACATTGGTTGAAGTTAGT
117462	115549	TTAACATTGGTTGAAGTTAG
117463	115550	CTTAACATTGGTTGAAGTTA
117464	115551	TCTTAACATTGGTTGAAGTT
117465	115552	ATCTTAACATTGGTTGAAGT
117466	115553	GATCTTAACATTGGTTGAAG
117467	115554	GGATCTTAACATTGGTTGAA
117468	115555	AGGATCTTAACATTGGTTGA
117469	115556	TAGGATCTTAACATTGGTTG
117470	115557	ATAGGATCTTAACATTGGTT
117471	115558	AATAGGATCTTAACATTGGT
117472	115559	TAATAGGATCTTAACATTGG
117473	115560	CTAATAGGATCTTAACATTG
117474	115561	TCTAATAGGATCTTAACATT
117475	115562	TTCTAATAGGATCTTAACAT
117476	115563	CTTCTAATAGGATCTTAACA
117477	115564	CCTTCTAATAGGATCTTAAC
117478	115565	TCCTTCTAATAGGATCTTAA
117479	115566	ATCCTTCTAATAGGATCTTA
117480	115567	CATCCTTCTAATAGGATCTT
117481	115568	ACATCCTTCTAATAGGATCT
117482	115569	AACATCCTTCTAATAGGATC
117483	115570	AAACATCCTTCTAATAGGAT
117484	115571	GAAACATCCTTCTAATAGGA
117485	115572	CGAAACATCCTTCTAATAGG
117486	115573	CCGAAACATCCTTCTAATAG
117487	115574	GCCGAAACATCCTTCTAATA
117488	115575	AGCCGAAACATCCTTCTAAT
117489	115576	TAGCCGAAACATCCTTCTAA
117490	115577	CTAGCCGAAACATCCTTCTA
117491	115578	CCTAGCCGAAACATCCTTCT
117492	115579	GCCTAGCCGAAACATCCTTC
117493	115580	AGCCTAGCCGAAACATCCTT
117494	115581	AAGCCTAGCCGAAACATCCT
117495	115582	CAAGCCTAGCCGAAACATCC
117496	115583	CCAAGCCTAGCCGAAACATC
117497	115584	ACCAAGCCTAGCCGAAACAT
117498	115585	CACCAAGCCTAGCCGAAACA
117499	115586	CCACCAAGCCTAGCCGAAAC
117500	115587	GCCACCAAGCCTAGCCGAAA
117501	115588	AGCCACCAAGCCTAGCCGAA
117502	115589	GAGCCACCAAGCCTAGCCGA
117503	115590	TGAGCCACCAAGCCTAGCCG
117504	115591	GTGAGCCACCAAGCCTAGCC
117505	115592	CGTGAGCCACCAAGCCTAGC
117506	115593	ACGTGAGCCACCAAGCCTAG
117507	115594	CACGTGAGCCACCAAGCCTA
117508	115595	ACACGTGAGCCACCAAGCCT
117509	115596	TACACGTGAGCCACCAAGCC
117510	115597	TTACACGTGAGCCACCAAGC
117511	115598	ATTACACGTGAGCCACCAAG
117512	115599	AATTACACGTGAGCCACCAA
117513	115600	GAATTACACGTGAGCCACCA
117514	115601	GGAATTACACGTGAGCCACC
117515	115602	TGGAATTACACGTGAGCCAC
117516	115603	CTGGAATTACACGTGAGCCA
117517	115604	GCTGGAATTACACGTGAGCC
117518	115605	TGCTGGAATTACACGTGAGC
117519	115606	GTGCTGGAATTACACGTGAG
117520	115607	AGTGCTGGAATTACACGTGA
117521	115608	AAGTGCTGGAATTACACGTG
117522	115609	AAAGTGCTGGAATTACACGT
117523	115610	CAAAGTGCTGGAATTACACG
117524	115611	TCAAAGTGCTGGAATTACAC
117525	115612	CTCAAAGTGCTGGAATTACA
117526	115613	TCTCAAAGTGCTGGAATTAC
117527	115614	CTCTCAAAGTGCTGGAATTA
117528	115615	CCTCTCAAAGTGCTGGAATT

19235	17322	CTACTCAGGAGGCTGAGGCA
19236	17323	GCTACTCAGGAGGCTGAGGC
19237	17324	AGCTACTCAGGAGGCTGAGG
19238	17325	AAGCTACTCAGGAGGCTGAG
19239	17326	CAAGCTACTCAGGAGGCTGA
19240	17327	CCAAGCTACTCAGGAGGCTG
19241	17328	CCCAAGCTACTCAGGAGGCT
19242	17329	TCCCAAGCTACTCAGGAGGC
19243	17330	GTCCCAAGCTACTCAGGAGG
19244	17331	GGTCCCAAGCTACTCAGGAG
19245	17332	TGGTCCCAAGCTACTCAGGA
19246	17333	GTGGTCCCAAGCTACTCAGG
19247	17334	TGTGGTCCCAAGCTACTCAG
19248	17335	ATGTGGTCCCAAGCTACTCA
19249	17336	CATGTGGTCCCAAGCTACTC
19250	17337	ACATGTGGTCCCAAGCTACT
19251	17338	CACATGTGGTCCCAAGCTAC
19252	17339	ACACATGTGGTCCCAAGCTA
19253	17340	CACACATGTGGTCCCAAGCT
19254	17341	ACACACATGTGGTCCCAAGC
19255	17342	CACACACATGTGGTCCCAAG
19256	17343	GCACACACATGTGGTCCCAA
19257	17344	GGCACACACATGTGGTCCCA
19258	17345	TGGCACACACATGTGGTCCC
19259	17346	ATGGCACACACATGTGGTCC
19260	17347	GATGGCACACACATGTGGTC
19261	17348	TGATGGCACACACATGTGGT
19262	17349	ATGATGGCACACACATGTGG
19263	17350	CATGATGGCACACACATGTG
19264	17351	GCATGATGGCACACACATGT
19265	17352	GGCATGATGGCACACACATG
19266	17353	AGGCATGATGGCACACACAT
19267	17354	CAGGCATGATGGCACACACA
19268	17355	CCAGGCATGATGGCACACAC
19269	17356	ACCAGGCATGATGGCACACA
19270	17357	AACCAGGCATGATGGCACAC
19271	17358	TAACCAGGCATGATGGCACA
19272	17359	TTAACCAGGCATGATGGCAC
19273	17360	ATTAACCAGGCATGATGGCA
19274	17361	AATTAACCAGGCATGATGGC
19275	17362	AAATTAACCAGGCATGATGG
19276	17363	AAAATTAACCAGGCATGATG
19277	17364	AAAAATTAACCAGGCATGAT
19278	17365	AAAAAATTAACCAGGCATGA
19279	17366	CAAAAAATTAACCAGGCATG
19280	17367	ACAAAAAATTAACCAGGCAT
19281	17368	TACAAAAAATTAACCAGGCA
19282	17369	ATACAAAAAATTAACCAGGC
19283	17370	AATACAAAAAATTAACCAGG
19284	17371	AAATACAAAAAATTAACCAG
19285	17372	AAAATACAAAAAATTAACCA
19286	17373	AAAAATACAAAAAATTAACC
19287	17374	TAAAAATACAAAAAATTAAC
19288	17375	CTAAAAATACAAAAAATTAA
19289	17376	ACTAAAAATACAAAAAATTA
19290	17377	TACTAAAAATACAAAAAATT
19291	17378	CTACTAAAAATACAAAAAAT
19292	17379	ACTACTAAAAATACAAAAAA
19293	17380	CACTACTAAAAATACAAAAA
19294	17381	TCACTACTAAAAATACAAAA
19295	17382	GTCACTACTAAAAATACAAA
19296	17383	TGTCACTACTAAAAATACAA
19297	17384	CTGTCACTACTAAAAATACA
19298	17385	CCTGTCACTACTAAAAATAC
19299	17386	CCCTGTCACTACTAAAAATA
19300	17387	ACCCTGTCACTACTAAAAAT
19301	17388	GACCCTGTCACTACTAAAAA
19302	17389	AGACCCTGTCACTACTAAAA
19303	17390	AAGACCCTGTCACTACTAAA
19304	17391	TAAGACCCTGTCACTACTAA
19305	17392	GTAAGACCCTGTCACTACTA

68382	66469	AGGAGGCTATGTTTCCTAAA
68383	66470	TAGGAGGCTATGTTTCCTAA
68384	66471	TTAGGAGGCTATGTTTCCTA
68385	66472	CTTAGGAGGCTATGTTTCCT
68386	66473	ACTTAGGAGGCTATGTTTCC
68387	66474	AACTTAGGAGGCTATGTTTC
68388	66475	GAACTTAGGAGGCTATGTTT
68389	66476	AGAACTTAGGAGGCTATGTT
68390	66477	CAGAACTTAGGAGGCTATGT
68391	66478	ACAGAACTTAGGAGGCTATG
68392	66479	AACAGAACTTAGGAGGCTAT
68393	66480	GAACAGAACTTAGGAGGCTA
68394	66481	GGAACAGAACTTAGGAGGCT
68395	66482	TGGAACAGAACTTAGGAGGC
68396	66483	ATGGAACAGAACTTAGGAGG
68397	66484	TATGGAACAGAACTTAGGAG
68398	66485	GTATGGAACAGAACTTAGGA
68399	66486	TGTATGGAACAGAACTTAGG
68400	66487	ATGTATGGAACAGAACTTAG
68401	66488	GATGTATGGAACAGAACTTA
68402	66489	GGATGTATGGAACAGAACTT
68403	66490	GGGATGTATGGAACAGAACT
68404	66491	AGGGATGTATGGAACAGAAC
68405	66492	AAGGGATGTATGGAACAGAA
68406	66493	AAAGGGATGTATGGAACAGA
68407	66494	GAAAGGGATGTATGGAACAG
68408	66495	TGAAAGGGATGTATGGAACA
68409	66496	GTGAAAGGGATGTATGGAAC
68410	66497	GGTGAAAGGGATGTATGGAA
68411	66498	AGGTGAAAGGGATGTATGGA
68412	66499	GAGGTGAAAGGGATGTATGG
68413	66500	GGAGGTGAAAGGGATGTATG
68414	66501	TGGAGGTGAAAGGGATGTAT
68415	66502	GTGGAGGTGAAAGGGATGTA
68416	66503	CGTGGAGGTGAAAGGGATGT
68417	66504	CCGTGGAGGTGAAAGGGATG
68418	66505	GCCGTGGAGGTGAAAGGGAT
68419	66506	CGCCGTGGAGGTGAAAGGGA
68420	66507	ACGCCGTGGAGGTGAAAGGG
68421	66508	AACGCCGTGGAGGTGAAAGG
68422	66509	CAACGCCGTGGAGGTGAAAG
68423	66510	ACAACGCCGTGGAGGTGAAA
68424	66511	TACAACGCCGTGGAGGTGAA
68425	66512	CTACAACGCCGTGGAGGTGA
68426	66513	GCTACAACGCCGTGGAGGTG
68427	66514	TGCTACAACGCCGTGGAGGT
68428	66515	ATGCTACAACGCCGTGGAGG
68429	66516	GATGCTACAACGCCGTGGAG
68430	66517	GGATGCTACAACGCCGTGGA
68431	66518	AGGATGCTACAACGCCGTGG
68432	66519	CAGGATGCTACAACGCCGTG
68433	66520	GCAGGATGCTACAACGCCGT
68434	66521	AGCAGGATGCTACAACGCCG
68435	66522	AAGCAGGATGCTACAACGCC
68436	66523	AAAGCAGGATGCTACAACGC
68437	66524	GAAAGCAGGATGCTACAACG
68438	66525	TGAAAGCAGGATGCTACAAC
68439	66526	ATGAAAGCAGGATGCTACAA
68440	66527	CATGAAAGCAGGATGCTACA
68441	66528	TCATGAAAGCAGGATGCTAC
68442	66529	GTCATGAAAGCAGGATGCTA
68443	66530	AGTCATGAAAGCAGGATGCT
68444	66531	CAGTCATGAAAGCAGGATGC
68445	66532	ACAGTCATGAAAGCAGGATG
68446	66533	CACAGTCATGAAAGCAGGAT
68447	66534	ACACAGTCATGAAAGCAGGA
68448	66535	GACACAGTCATGAAAGCAGG
68449	66536	TGACACAGTCATGAAAGCAG
68450	66537	ATGACACAGTCATGAAAGCA
68451	66538	GATGACACAGTCATGAAAGC
68452	66539	TGATGACACAGTCATGAAAG

117529	115616	GCCTCTCAAAGTGCTGGAAT
117530	115617	AGCCTCTCAAAGTGCTGGAA
117531	115618	CAGCCTCTCAAAGTGCTGGA
117532	115619	TCAGCCTCTCAAAGTGCTGG
117533	115620	CTCAGCCTCTCAAAGTGCTG
117534	115621	CCTCAGCCTCTCAAAGTGCT
117535	115622	ACCTCAGCCTCTCAAAGTGC
117536	115623	CACCTCAGCCTCTCAAAGTG
117537	115624	CCACCTCAGCCTCTCAAAGT
117538	115625	CCCACCTCAGCCTCTCAAAG
117539	115626	GCCCACCTCAGCCTCTCAAA
117540	115627	TGCCCACCTCAGCCTCTCAA
117541	115628	CTGCCCACCTCAGCCTCTCA
117542	115629	TCTGCCCACCTCAGCCTCTC
117543	115630	ATCTGCCCACCTCAGCCTCT
117544	115631	GATCTGCCCACCTCAGCCTC
117545	115632	TGATCTGCCCACCTCAGCCT
117546	115633	GTGATCTGCCCACCTCAGCC
117547	115634	TGTGATCTGCCCACCTCAGC
117548	115635	ATGTGATCTGCCCACCTCAG
117549	115636	CATGTGATCTGCCCACCTCA
117550	115637	TCATGTGATCTGCCCACCTC
117551	115638	GTCATGTGATCTGCCCACCT
117552	115639	GGTCATGTGATCTGCCCACC
117553	115640	CGGTCATGTGATCTGCCCAC
117554	115641	CCGGTCATGTGATCTGCCCA
117555	115642	CCCGGTCATGTGATCTGCCC
117556	115643	TCCCGGTCATGTGATCTGCC
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117558	115645	ACTCCCGGTCATGTGATCTG
117559	115646	AACTCCCGGTCATGTGATCT
117560	115647	AAACTCCCGGTCATGTGATC
117561	115648	AAAACTCCCGGTCATGTGAT
117562	115649	TAAAACTCCCGGTCATGTGA
117563	115650	TTAAAACTCCCGGTCATGTG
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117566	115653	GTCTTAAAACTCCCGGTCAT
117567	115654	GGTCTTAAAACTCCCGGTCA
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117569	115656	CTGGTCTTAAAACTCCCGGT
117570	115657	GCTGGTCTTAAAACTCCCGG
117571	115658	GGCTGGTCTTAAAACTCCCG
117572	115659	AGGCTGGTCTTAAAACTCCC
117573	115660	CAGGCTGGTCTTAAAACTCC
117574	115661	CCAGGCTGGTCTTAAAACTC
117575	115662	CCCAGGCTGGTCTTAAAACT
117576	115663	GCCCAGGCTGGTCTTAAAAC
117577	115664	TGCCCAGGCTGGTCTTAAAA
117578	115665	TTGCCCAGGCTGGTCTTAAA
117579	115666	GTTGCCCAGGCTGGTCTTAA
117580	115667	TGTTGCCCAGGCTGGTCTTA
117581	115668	ATGTTGCCCAGGCTGGTCTT
117582	115669	CATGTTGCCCAGGCTGGTCT
117583	115670	CCATGTTGCCCAGGCTGGTC
117584	115671	GCCATGTTGCCCAGGCTGGT
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117586	115673	TTGCCATGTTGCCCAGGCTG
117587	115674	TTTGCCATGTTGCCCAGGCT
117588	115675	TTTTGCCATGTTGCCCAGGC
117589	115676	TTTTTGCCATGTTGCCCAGG
117590	115677	GTTTTTGCCATGTTGCCCAG
117591	115678	GGTTTTTGCCATGTTGCCCA
117592	115679	AGGTTTTTGCCATGTTGCCC
117593	115680	TAGGTTTTTGCCATGTTGCC
117594	115681	ATAGGTTTTTGCCATGTTGC
117595	115682	GATAGGTTTTTGCCATGTTG
117596	115683	AGATAGGTTTTTGCCATGTT
117597	115684	GAGATAGGTTTTTGCCATGT
117598	115685	AGAGATAGGTTTTTGCCATG
117599	115686	CAGAGATAGGTTTTTGCCAT

19306	17393	GGTAAGACCCTGTCACTACT
19307	17394	TGGTAAGACCCTGTCACTAC
19308	17395	ATGGTAAGACCCTGTCACTA
19309	17396	CATGGTAAGACCCTGTCACT
19310	17397	ACATGGTAAGACCCTGTCAC
19311	17398	AACATGGTAAGACCCTGTCA
19312	17399	CAACATGGTAAGACCCTGTC
19313	17400	GCAACATGGTAAGACCCTGT
19314	17401	GGCAACATGGTAAGACCCTG
19315	17402	GGGCAACATGGTAAGACCCT
19316	17403	TGGGCAACATGGTAAGACCC
19317	17404	CTGGGCAACATGGTAAGACC
19318	17405	CCTGGGCAACATGGTAAGAC
19319	17406	ACCTGGGCAACATGGTAAGA
19320	17407	AACCTGGGCAACATGGTAAG
19321	17408	CAACCTGGGCAACATGGTAA
19322	17409	CCAACCTGGGCAACATGGTA
19323	17410	ACCAACCTGGGCAACATGGT
19324	17411	GACCAACCTGGGCAACATGG
19325	17412	AGACCAACCTGGGCAACATG
19326	17413	GAGACCAACCTGGGCAACAT
19327	17414	TGAGACCAACCTGGGCAACA
19328	17415	TTGAGACCAACCTGGGCAAC
19329	17416	TTTGAGACCAACCTGGGCAA
19330	17417	GTTTGAGACCAACCTGGGCA
19331	17418	AGTTTGAGACCAACCTGGGC
19332	17419	GAGTTTGAGACCAACCTGGG
19333	17420	GGAGTTTGAGACCAACCTGG
19334	17421	AGGAGTTTGAGACCAACCTG
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19338	17425	GCTCAGGAGTTTGAGACCAA
19339	17426	AGCTCAGGAGTTTGAGACCA
19340	17427	GAGCTCAGGAGTTTGAGACC
19341	17428	TGAGCTCAGGAGTTTGAGAC
19342	17429	TTGAGCTCAGGAGTTTGAGA
19343	17430	CTTGAGCTCAGGAGTTTGAG
19344	17431	ACTTGAGCTCAGGAGTTTGA
19345	17432	CACTTGAGCTCAGGAGTTTG
19346	17433	TCACTTGAGCTCAGGAGTTT
19347	17434	ATCACTTGAGCTCAGGAGTT
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19350	17437	CAGATCACTTGAGCTCAGGA
19351	17438	GCAGATCACTTGAGCTCAGG
19352	17439	GGCAGATCACTTGAGCTCAG
19353	17440	GGGCAGATCACTTGAGCTCA
19354	17441	CGGGCAGATCACTTGAGCTC
19355	17442	GCGGGCAGATCACTTGAGCT
19356	17443	GGCGGGCAGATCACTTGAGC
19357	17444	AGGCGGGCAGATCACTTGAG
19358	17445	AAGGCGGGCAGATCACTTGA
19359	17446	GAAGGCGGGCAGATCACTTG
19360	17447	CGAAGGCGGGCAGATCACTT
19361	17448	GCGAAGGCGGGCAGATCACT
19362	17449	GGCGAAGGCGGGCAGATCAC
19363	17450	AGGCGAAGGCGGGCAGATCA
19364	17451	GAGGCGAAGGCGGGCAGATC
19365	17452	GGAGGCGAAGGCGGGCAGAT
19366	17453	GGGAGGCGAAGGCGGGCAGA
19367	17454	TGGGAGGCGAAGGCGGGCAG
19368	17455	TTGGGAGGCGAAGGCGGGCA
19369	17456	TTTGGGAGGCGAAGGCGGGC
19370	17457	CTTTGGGAGGCGAAGGCGGG
19371	17458	ACTTTGGGAGGCGAAGGCGG
19372	17459	CACTTTGGGAGGCGAAGGCG
19373	17460	ACACTTTGGGAGGCGAAGGC
19374	17461	GACACTTTGGGAGGCGAAGG
19375	17462	AGACACTTTGGGAGGCGAAG
19376	17463	CAGACACTTTGGGAGGCGAA

68453	66540	GTGATGACACAGTCATGAAA
68454	66541	AGTGATGACACAGTCATGAA
68455	66542	GAGTGATGACACAGTCATGA
68456	66543	CGAGTGATGACACAGTCATG
68457	66544	CCGAGTGATGACACAGTCAT
68458	66545	TCCGAGTGATGACACAGTCA
68459	66546	TTCCGAGTGATGACACAGTC
68460	66547	CTTCCGAGTGATGACACAGT
68461	66548	CCTTCCGAGTGATGACACAG
68462	66549	TCCTTCCGAGTGATGACACA
68463	66550	TTCCTTCCGAGTGATGACAC
68464	66551	GTTCCTTCCGAGTGATGACA
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68466	66553	CAGTTCCTTCCGAGTGATGA
68467	66554	GCAGTTCCTTCCGAGTGATG
68468	66555	AGCAGTTCCTTCCGAGTGAT
68469	66556	AAGCAGTTCCTTCCGAGTGA
68470	66557	GAAGCAGTTCCTTCCGAGTG
68471	66558	AGAAGCAGTTCCTTCCGAGT
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68473	66560	AGAGAAGCAGTTCCTTCCGA
68474	66561	AAGAGAAGCAGTTCCTTCCG
68475	66562	GAAGAGAAGCAGTTCCTTCC
68476	66563	GGAAGAGAAGCAGTTCCTTC
68477	66564	TGGAAGAGAAGCAGTTCCTT
68478	66565	CTGGAAGAGAAGCAGTTCCT
68479	66566	TCTGGAAGAGAAGCAGTTCC
68480	66567	TTCTGGAAGAGAAGCAGTTC
68481	66568	ATTCTGGAAGAGAAGCAGTT
68482	66569	CATTCTGGAAGAGAAGCAGT
68483	66570	GCATTCTGGAAGAGAAGCAG
68484	66571	AGCATTCTGGAAGAGAAGCA
68485	66572	AAGCATTCTGGAAGAGAAGC
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68488	66575	GAAAAGCATTCTGGAAGAGA
68489	66576	TGAAAAGCATTCTGGAAGAG
68490	66577	TTGAAAAGCATTCTGGAAGA
68491	66578	CTTGAAAAGCATTCTGGAAG
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68493	66580	ATCTTGAAAAGCATTCTGGA
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68495	66582	AGATCTTGAAAAGCATTCTG
68496	66583	TAGATCTTGAAAAGCATTCT
68497	66584	GTAGATCTTGAAAAGCATTC
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68500	66587	AGAGTAGATCTTGAAAAGCA
68501	66588	CAGAGTAGATCTTGAAAAGC
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68504	66591	GGTCAGAGTAGATCTTGAAA
68505	66592	TGGTCAGAGTAGATCTTGAA
68506	66593	GTGGTCAGAGTAGATCTTGA
68507	66594	TGTGGTCAGAGTAGATCTTG
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68510	66597	AGCTGTGGTCAGAGTAGATC
68511	66598	TAGCTGTGGTCAGAGTAGAT
68512	66599	ATAGCTGTGGTCAGAGTAGA
68513	66600	TATAGCTGTGGTCAGAGTAG
68514	66601	TTATAGCTGTGGTCAGAGTA
68515	66602	TTTATAGCTGTGGTCAGAGT
68516	66603	GTTTATAGCTGTGGTCAGAG
68517	66604	AGTTTATAGCTGTGGTCAGA
68518	66605	AAGTTTATAGCTGTGGTCAG
68519	66606	AAAGTTTATAGCTGTGGTCA
68520	66607	TAAAGTTTATAGCTGTGGTC
68521	66608	GTAAAGTTTATAGCTGTGGT
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117600	115687	GCAGAGATAGGTTTTTGCCA
117601	115688	TGCAGAGATAGGTTTTTGCC
117602	115689	TTGCAGAGATAGGTTTTTGC
117603	115690	TTTGCAGAGATAGGTTTTTG
117604	115691	TTTTGCAGAGATAGGTTTTT
117605	115692	TTTTTGCAGAGATAGGTTTT
117606	115693	TTTTTTGCAGAGATAGGTTT
117607	115694	TTTTTTTGCAGAGATAGGTT
117608	115695	TTTTTTTTGCAGAGATAGGT
117609	115696	TTTTTTTTTGCAGAGATAGG
117610	115697	TTTTTTTTTTGCAGAGATAG
117611	115698	ATTTTTTTTTTGCAGAGATA
117612	115699	TATTTTTTTTTTGCAGAGAT
117613	115700	CTATTTTTTTTTTGCAGAGA
117614	115701	TCTATTTTTTTTTTGCAGAG
117615	115702	TTCTATTTTTTTTTTGCAGA
117616	115703	TTTCTATTTTTTTTTTGCAG
117617	115704	ATTTCTATTTTTTTTTTGCA
117618	115705	GATTTCTATTTTTTTTTTGC
117619	115706	AGATTTCTATTTTTTTTTTG
117620	115707	AAGATTTCTATTTTTTTTTT
117621	115708	TAAGATTTCTATTTTTTTTT
117622	115709	CTAAGATTTCTATTTTTTTT
117623	115710	GCTAAGATTTCTATTTTTTT
117624	115711	GGCTAAGATTTCTATTTTTT
117625	115712	TGGCTAAGATTTCTATTTTT
117626	115713	CTGGCTAAGATTTCTATTTT
117627	115714	GCTGGCTAAGATTTCTATTT
117628	115715	GGCTGGCTAAGATTTCTATT
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117631	115718	GACGGCTGGCTAAGATTTCT
117632	115719	TGACGGCTGGCTAAGATTTC
117633	115720	ATGACGGCTGGCTAAGATTT
117634	115721	CATGACGGCTGGCTAAGATT
117635	115722	CCATGACGGCTGGCTAAGAT
117636	115723	ACCATGACGGCTGGCTAAGA
117637	115724	CACCATGACGGCTGGCTAAG
117638	115725	ACACCATGACGGCTGGCTAA
117639	115726	CACACCATGACGGCTGGCTA
117640	115727	GCACACCATGACGGCTGGCT
117641	115728	AGCACACCATGACGGCTGGC
117642	115729	GAGCACACCATGACGGCTGG
117643	115730	GGAGCACACCATGACGGCTG
117644	115731	AGGAGCACACCATGACGGCT
117645	115732	CAGGAGCACACCATGACGGC
117646	115733	ACAGGAGCACACCATGACGG
117647	115734	TACAGGAGCACACCATGACG
117648	115735	CTACAGGAGCACACCATGAC
117649	115736	ACTACAGGAGCACACCATGA
117650	115737	GACTACAGGAGCACACCATG
117651	115738	GGACTACAGGAGCACACCAT
117652	115739	AGGACTACAGGAGCACACCA
117653	115740	TAGGACTACAGGAGCACACC
117654	115741	CTAGGACTACAGGAGCACAC
117655	115742	GCTAGGACTACAGGAGCACA
117656	115743	AGCTAGGACTACAGGAGCAC
117657	115744	TAGCTAGGACTACAGGAGCA
117658	115745	GTAGCTAGGACTACAGGAGC
117659	115746	AGTAGCTAGGACTACAGGAG
117660	115747	AAGTAGCTAGGACTACAGGA
117661	115748	CAAGTAGCTAGGACTACAGG
117662	115749	CCAAGTAGCTAGGACTACAG
117663	115750	CCCAAGTAGCTAGGACTACA
117664	115751	TCCCAAGTAGCTAGGACTAC
117665	115752	CTCCCAAGTAGCTAGGACTA
117666	115753	TCTCCCAAGTAGCTAGGACT
117667	115754	GTCTCCCAAGTAGCTAGGAC
117668	115755	AGTCTCCCAAGTAGCTAGGA
117669	115756	CAGTCTCCCAAGTAGCTAGG
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19377	17464	GCAGACACTTTGGGAGGCGA
19378	17465	CGCAGACACTTTGGGAGGCG
19379	17466	GCGCAGACACTTTGGGAGGC
19380	17467	GGCGCAGACACTTTGGGAGG
19381	17468	GGGCGCAGACACTTTGGGAG
19382	17469	AGGGCGCAGACACTTTGGGA
19383	17470	TAGGGCGCAGACACTTTGGG
19384	17471	GTAGGGCGCAGACACTTTGG
19385	17472	TGTAGGGCGCAGACACTTTG
19386	17473	TTGTAGGGCGCAGACACTTT
19387	17474	ATTGTAGGGCGCAGACACTT
19388	17475	AATTGTAGGGCGCAGACACT
19389	17476	AAATTGTAGGGCGCAGACAC
19390	17477	TAAATTGTAGGGCGCAGACA
19391	17478	TTAAATTGTAGGGCGCAGAC
19392	17479	TTTAAATTGTAGGGCGCAGA
19393	17480	TTTTAAATTGTAGGGCGCAG
19394	17481	TTTTTAAATTGTAGGGCGCA
19395	17482	TTTTTTAAATTGTAGGGCGC
19396	17483	TTTTTTTAAATTGTAGGGCG
19397	17484	ATTTTTTTAAATTGTAGGGC
19398	17485	AATTTTTTTAAATTGTAGGG
19399	17486	AAATTTTTTTAAATTGTAGG
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19404	17491	TACAAAAATTTTTTTAAATT
19405	17492	CTACAAAAATTTTTTTAAAT
19406	17493	TCTACAAAAATTTTTTTAAA
19407	17494	CTCTACAAAAATTTTTTTAA
19408	17495	TCTCTACAAAAATTTTTTTA
19409	17496	GTCTCTACAAAAATTTTTTT
19410	17497	TGTCTCTACAAAAATTTTTT
19411	17498	CTGTCTCTACAAAAATTTTT
19412	17499	ACTGTCTCTACAAAAATTTT
19413	17500	GACTGTCTCTACAAAAATTT
19414	17501	AGACTGTCTCTACAAAAATT
19415	17502	GAGACTGTCTCTACAAAAAT
19416	17503	TGAGACTGTCTCTACAAAAA
19417	17504	GTGAGACTGTCTCTACAAAA
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19419	17506	CAGTGAGACTGTCTCTACAA
19420	17507	ACAGTGAGACTGTCTCTACA
19421	17508	AACAGTGAGACTGTCTCTAC
19422	17509	TAACAGTGAGACTGTCTCTA
19423	17510	GTAACAGTGAGACTGTCTCT
19424	17511	GGTAACAGTGAGACTGTCTC
19425	17512	GGGTAACAGTGAGACTGTCT
19426	17513	CGGGTAACAGTGAGACTGTC
19427	17514	CCGGGTAACAGTGAGACTGT
19428	17515	CCCGGGTAACAGTGAGACTG
19429	17516	GCCCGGGTAACAGTGAGACT
19430	17517	AGCCCGGGTAACAGTGAGAC
19431	17518	CAGCCCGGGTAACAGTGAGA
19432	17519	CCAGCCCGGGTAACAGTGAG
19433	17520	ACCAGCCCGGGTAACAGTGA
19434	17521	AACCAGCCCGGGTAACAGTG
19435	17522	AAACCAGCCCGGGTAACAGT
19436	17523	AAAACCAGCCCGGGTAACAG
19437	17524	CAAAACCAGCCCGGGTAACA
19438	17525	TCAAAACCAGCCCGGGTAAC
19439	17526	TTCAAAACCAGCCCGGGTAA
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19441	17528	AGTTCAAAACCAGCCCGGGT
19442	17529	AAGTTCAAAACCAGCCCGGG
19443	17530	GAAGTTCAAAACCAGCCCGG
19444	17531	AGAAGTTCAAAACCAGCCCG
19445	17532	CAGAAGTTCAAAACCAGCCC
19446	17533	GCAGAAGTTCAAAACCAGCC
19447	17534	GGCAGAAGTTCAAAACCAGC

68524	66611	AGTGTAAAGTTTATAGCTGT
68525	66612	AAGTGTAAAGTTTATAGCTG
68526	66613	GAAGTGTAAAGTTTATAGCT
68527	66614	AGAAGTGTAAAGTTTATAGC
68528	66615	TAGAAGTGTAAAGTTTATAG
68529	66616	ATAGAAGTGTAAAGTTTATA
68530	66617	AATAGAAGTGTAAAGTTTAT
68531	66618	GAATAGAAGTGTAAAGTTTA
68532	66619	AGAATAGAAGTGTAAAGTTT
68533	66620	GAGAATAGAAGTGTAAAGTT
68534	66621	AGAGAATAGAAGTGTAAAGT
68535	66622	AAGAGAATAGAAGTGTAAAG
68536	66623	GAAGAGAATAGAAGTGTAAA
68537	66624	AGAAGAGAATAGAAGTGTAA
68538	66625	AAGAAGAGAATAGAAGTGTA
68539	66626	CAAGAAGAGAATAGAAGTGT
68540	66627	GCAAGAAGAGAATAGAAGTG
68541	66628	GGCAAGAAGAGAATAGAAGT
68542	66629	GGGCAAGAAGAGAATAGAAG
68543	66630	GGGGCAAGAAGAGAATAGAA
68544	66631	AGGGGCAAGAAGAGAATAGA
68545	66632	GAGGGGCAAGAAGAGAATAG
68546	66633	TGAGGGGCAAGAAGAGAATA
68547	66634	GTGAGGGGCAAGAAGAGAAT
68548	66635	TGTGAGGGGCAAGAAGAGAA
68549	66636	CTGTGAGGGGCAAGAAGAGA
68550	66637	ACTGTGAGGGGCAAGAAGAG
68551	66638	CACTGTGAGGGGCAAGAAGA
68552	66639	ACACTGTGAGGGGCAAGAAG
68553	66640	AACACTGTGAGGGGCAAGAA
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68555	66642	AGAACACTGTGAGGGGCAAG
68556	66643	GAGAACACTGTGAGGGGCAA
68557	66644	AGAGAACACTGTGAGGGGCA
68558	66645	CAGAGAACACTGTGAGGGGC
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68560	66647	AACAGAGAACACTGTGAGGG
68561	66648	GAACAGAGAACACTGTGAGG
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68566	66653	TAGAGGAACAGAGAACACTG
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68568	66655	CTTAGAGGAACAGAGAACAC
68569	66656	TCTTAGAGGAACAGAGAACA
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68571	66658	GATCTTAGAGGAACAGAGAA
68572	66659	AGATCTTAGAGGAACAGAGA
68573	66660	AAGATCTTAGAGGAACAGAG
68574	66661	TAAGATCTTAGAGGAACAGA
68575	66662	TTAAGATCTTAGAGGAACAG
68576	66663	TTTAAGATCTTAGAGGAACA
68577	66664	GTTTAAGATCTTAGAGGAAC
68578	66665	AGTTTAAGATCTTAGAGGAA
68579	66666	GAGTTTAAGATCTTAGAGGA
68580	66667	AGAGTTTAAGATCTTAGAGG
68581	66668	CAGAGTTTAAGATCTTAGAG
68582	66669	ACAGAGTTTAAGATCTTAGA
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68584	66671	AGACAGAGTTTAAGATCTTA
68585	66672	TAGACAGAGTTTAAGATCTT
68586	66673	GTAGACAGAGTTTAAGATCT
68587	66674	AGTAGACAGAGTTTAAGATC
68588	66675	GAGTAGACAGAGTTTAAGAT
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68590	66677	AGGAGTAGACAGAGTTTAAG
68591	66678	TAGGAGTAGACAGAGTTTAA
68592	66679	TTAGGAGTAGACAGAGTTTA
68593	66680	ATTAGGAGTAGACAGAGTTT
68594	66681	GATTAGGAGTAGACAGAGTT

117671	115758	CTCAGTCTCCCAAGTAGCTA
117672	115759	CCTCAGTCTCCCAAGTAGCT
117673	115760	ACCTCAGTCTCCCAAGTAGC
117674	115761	CACCTCAGTCTCCCAAGTAG
117675	115762	CCACCTCAGTCTCCCAAGTA
117676	115763	CCCACCTCAGTCTCCCAAGT
117677	115764	TCCCACCTCAGTCTCCCAAG
117678	115765	CTCCCACCTCAGTCTCCCAA
117679	115766	CCTCCCACCTCAGTCTCCCA
117680	115767	TCCTCCCACCTCAGTCTCCC
117681	115768	ATCCTCCCACCTCAGTCTCC
117682	115769	GATCCTCCCACCTCAGTCTC
117683	115770	TGATCCTCCCACCTCAGTCT
117684	115771	TTGATCCTCCCACCTCAGTC
117685	115772	ATTGATCCTCCCACCTCAGT
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117688	115775	TCAATTGATCCTCCCACCTC
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117691	115778	GTTTCAATTGATCCTCCCAC
117692	115779	GGTTTCAATTGATCCTCCCA
117693	115780	TGGTTTCAATTGATCCTCCC
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117695	115782	TCTGGTTTCAATTGATCCTC
117696	115783	TTCTGGTTTCAATTGATCCT
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117711	115798	CCTGCAGCCTGGACCTTCTG
117712	115799	CCCTGCAGCCTGGACCTTCT
117713	115800	TCCCTGCAGCCTGGACCTTC
117714	115801	TTCCCTGCAGCCTGGACCTT
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117716	115803	AGTTCCCTGCAGCCTGGACC
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117718	115805	ACAGTTCCCTGCAGCCTGGA
117719	115806	CACAGTTCCCTGCAGCCTGG
117720	115807	TCACAGTTCCCTGCAGCCTG
117721	115808	GTCACAGTTCCCTGCAGCCT
117722	115809	AGTCACAGTTCCCTGCAGCC
117723	115810	CAGTCACAGTTCCCTGCAGC
117724	115811	GCAGTCACAGTTCCCTGCAG
117725	115812	TGCAGTCACAGTTCCCTGCA
117726	115813	GTGCAGTCACAGTTCCCTGC
117727	115814	GGTGCAGTCACAGTTCCCTG
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117729	115816	GTGGTGCAGTCACAGTTCCC
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117731	115818	CAGTGGTGCAGTCACAGTTC
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117737	115824	GGAGCCCAGTGGTGCAGTCA
117738	115825	TGGAGCCCAGTGGTGCAGTC
117739	115826	CTGGAGCCCAGTGGTGCAGT
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117741	115828	AGCTGGAGCCCAGTGGTGCA

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19450	17537	GAGGGCAGAAGTTCAAAACC
19451	17538	TGAGGGCAGAAGTTCAAAAC
19452	17539	TTGAGGGCAGAAGTTCAAAA
19453	17540	CTTGAGGGCAGAAGTTCAAA
19454	17541	ACTTGAGGGCAGAAGTTCAA
19455	17542	TACTTGAGGGCAGAAGTTCA
19456	17543	GTACTTGAGGGCAGAAGTTC
19457	17544	AGTACTTGAGGGCAGAAGTT
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19459	17546	GGAGTACTTGAGGGCAGAAG
19460	17547	AGGAGTACTTGAGGGCAGAA
19461	17548	GAGGAGTACTTGAGGGCAGA
19462	17549	AGAGGAGTACTTGAGGGCAG
19463	17550	AAGAGGAGTACTTGAGGGCA
19464	17551	CAAGAGGAGTACTTGAGGGC
19465	17552	GCAAGAGGAGTACTTGAGGG
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19469	17556	CAAGGCAAGAGGAGTACTTG
19470	17557	CCAAGGCAAGAGGAGTACTT
19471	17558	GCCAAGGCAAGAGGAGTACT
19472	17559	GGCCAAGGCAAGAGGAGTAC
19473	17560	AGGCCAAGGCAAGAGGAGTA
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19475	17562	GGAGGCCAAGGCAAGAGGAG
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19487	17574	TTCAATACTTTGGGAGGCCA
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19493	17580	CTTAATTTCAATACTTTGGG
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19515	17602	GCTGGGTGTGCTGCCTCATG
19516	17603	GGCTGGGTGTGCTGCCTCAT
19517	17604	AGGCTGGGTGTGCTGCCTCA
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68595	66682	GGATTAGGAGTAGACAGAGT
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68599	66686	GGCTGGATTAGGAGTAGACA
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68601	66688	CAGGCTGGATTAGGAGTAGA
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68615	66702	CCAGCCACACCCAGCAGGCT
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68618	66705	TCTCCAGCCACACCCAGCAG
68619	66706	TTCTCCAGCCACACCCAGCA
68620	66707	TTTCTCCAGCCACACCCAGC
68621	66708	CTTTCTCCAGCCACACCCAG
68622	66709	ACTTTCTCCAGCCACACCCA
68623	66710	GACTTTCTCCAGCCACACCC
68624	66711	GGACTTTCTCCAGCCACACC
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68637	66724	CAGCCCCCCAGTGGGACTTT
68638	66725	TCAGCCCCCCAGTGGGACTT
68639	66726	ATCAGCCCCCCAGTGGGACT
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68644	66731	AACTAATCAGCCCCCCAGTG
68645	66732	TAACTAATCAGCCCCCCAGT
68646	66733	CTAACTAATCAGCCCCCCAG
68647	66734	CCTAACTAATCAGCCCCCCA
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68656	66743	CCCTACATTCCTAACTAATC
68657	66744	ACCCTACATTCCTAACTAAT
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68659	66746	AAACCCTACATTCCTAACTA
68660	66747	GAAACCCTACATTCCTAACT
68661	66748	GGAAACCCTACATTCCTAAC
68662	66749	TGGAAACCCTACATTCCTAA
68663	66750	CTGGAAACCCTACATTCCTA
68664	66751	GCTGGAAACCCTACATTCCT
68665	66752	AGCTGGAAACCCTACATTCC

117742	115829	AAGCTGGAGCCCAGTGGTGC
117743	115830	CAAGCTGGAGCCCAGTGGTG
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117745	115832	CCCAAGCTGGAGCCCAGTGG
117746	115833	ACCCAAGCTGGAGCCCAGTG
117747	115834	CACCCAAGCTGGAGCCCAGT
117748	115835	TCACCCAAGCTGGAGCCCAG
117749	115836	TTCACCCAAGCTGGAGCCCA
117750	115837	TTTCACCCAAGCTGGAGCCC
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117756	115843	TCGCTCTTTCACCCAAGCTG
117757	115844	TTCGCTCTTTCACCCAAGCT
117758	115845	TTTCGCTCTTTCACCCAAGC
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117761	115848	GGGTTTCGCTCTTTCACCCA
117762	115849	AGGGTTTCGCTCTTTCACCC
117763	115850	CAGGGTTTCGCTCTTTCACC
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117765	115852	GGCAGGGTTTCGCTCTTTCA
117766	115853	AGGCAGGGTTTCGCTCTTTC
117767	115854	GAGGCAGGGTTTCGCTCTTT
117768	115855	TGAGGCAGGGTTTCGCTCTT
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117770	115857	TTTGAGGCAGGGTTTCGCTC
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117773	115860	CTTTTTGAGGCAGGGTTTCG
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117777	115864	TTTTCTTTTTGAGGCAGGGT
117778	115865	TTTTTCTTTTTGAGGCAGGG
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117786	115873	CCATCTTATTTTTCTTTTTG
117787	115874	TCCATCTTATTTTTCTTTTT
117788	115875	ATCCATCTTATTTTTCTTTT
117789	115876	CATCCATCTTATTTTTCTTT
117790	115877	ACATCCATCTTATTTTTCTT
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117800	115887	TAATGCAGAAACATCCATCT
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19519	17606	TTAGGCTGGGTGTGCTGCCT
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19523	17610	GAATTTAGGCTGGGTGTGCT
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19526	17613	GAAGAATTTAGGCTGGGTGT
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19537	17624	ACAGAACATAAGAAGAATTT
19538	17625	AACAGAACATAAGAAGAATT
19539	17626	GAACAGAACATAAGAAGAAT
19540	17627	AGAACAGAACATAAGAAGAA
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19542	17629	CAAGAACAGAACATAAGAAG
19543	17630	CCAAGAACAGAACATAAGAA
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19545	17632	TGCCAAGAACAGAACATAAG
19546	17633	GTGCCAAGAACAGAACATAA
19547	17634	TGTGCCAAGAACAGAACATA
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19549	17636	TATGTGCCAAGAACAGAACA
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19556	17643	CATCTACTATGTGCCAAGAA
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19569	17656	CTACATTGTTGAACATCTAC
19570	17657	TCTACATTGTTGAACATCTA
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19574	17661	TGACTCTACATTGTTGAACA
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68666	66753	GAGCTGGAAACCCTACATTC
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68669	66756	CAAGAGCTGGAAACCCTACA
68670	66757	GCAAGAGCTGGAAACCCTAC
68671	66758	AGCAAGAGCTGGAAACCCTA
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68673	66760	CCAGCAAGAGCTGGAAACCC
68674	66761	TCCAGCAAGAGCTGGAAACC
68675	66762	CTCCAGCAAGAGCTGGAAAC
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68678	66765	AGGCTCCAGCAAGAGCTGGA
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68680	66767	TGAGGCTCCAGCAAGAGCTG
68681	66768	CTGAGGCTCCAGCAAGAGCT
68682	66769	TCTGAGGCTCCAGCAAGAGC
68683	66770	TTCTGAGGCTCCAGCAAGAG
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68685	66772	TCTTCTGAGGCTCCAGCAAG
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68688	66775	AACTCTTCTGAGGCTCCAGC
68689	66776	GAACTCTTCTGAGGCTCCAG
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68712	66799	AAAAAAAAAAAAAAAAGTCT
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68722	66809	GTTTAAGGAAAAAAAAAAAA
68723	66810	GGTTTAAGGAAAAAAAAAAA
68724	66811	AGGTTTAAGGAAAAAAAAAA
68725	66812	TAGGTTTAAGGAAAAAAAAA
68726	66813	ATAGGTTTAAGGAAAAAAAA
68727	66814	AATAGGTTTAAGGAAAAAAA
68728	66815	AAATAGGTTTAAGGAAAAAA
68729	66816	GAAATAGGTTTAAGGAAAAA
68730	66817	AGAAATAGGTTTAAGGAAAA
68731	66818	CAGAAATAGGTTTAAGGAAA
68732	66819	GCAGAAATAGGTTTAAGGAA
68733	66820	TGCAGAAATAGGTTTAAGGA
68734	66821	CTGCAGAAATAGGTTTAAGG
68735	66822	GCTGCAGAAATAGGTTTAAG
68736	66823	GGCTGCAGAAATAGGTTTAA

117813	115900	AACTCCCTAATTTTAATGCA
117814	115901	CAACTCCCTAATTTTAATGC
117815	115902	ACAACTCCCTAATTTTAATG
117816	115903	GACAACTCCCTAATTTTAAT
117817	115904	CGACAACTCCCTAATTTTAA
117818	115905	ACGACAACTCCCTAATTTTA
117819	115906	TACGACAACTCCCTAATTTT
117820	115907	ATACGACAACTCCCTAATTT
117821	115908	TATACGACAACTCCCTAATT
117822	115909	TTATACGACAACTCCCTAAT
117823	115910	ATTATACGACAACTCCCTAA
117824	115911	CATTATACGACAACTCCCTA
117825	115912	ACATTATACGACAACTCCCT
117826	115913	TACATTATACGACAACTCCC
117827	115914	CTACATTATACGACAACTCC
117828	115915	ACTACATTATACGACAACTC
117829	115916	AACTACATTATACGACAACT
117830	115917	CAACTACATTATACGACAAC
117831	115918	GCAACTACATTATACGACAA
117832	115919	TGCAACTACATTATACGACA
117833	115920	ATGCAACTACATTATACGAC
117834	115921	TATGCAACTACATTATACGA
117835	115922	TTATGCAACTACATTATACG
117836	115923	TTTATGCAACTACATTATAC
117837	115924	GTTTATGCAACTACATTATA
117838	115925	AGTTTATGCAACTACATTAT
117839	115926	TAGTTTATGCAACTACATTA
117840	115927	CTAGTTTATGCAACTACATT
117841	115928	ACTAGTTTATGCAACTACAT
117842	115929	TACTAGTTTATGCAACTACA
117843	115930	ATACTAGTTTATGCAACTAC
117844	115931	AATACTAGTTTATGCAACTA
117845	115932	GAATACTAGTTTATGCAACT
117846	115933	AGAATACTAGTTTATGCAAC
117847	115934	CAGAATACTAGTTTATGCAA
117848	115935	ACAGAATACTAGTTTATGCA
117849	115936	CACAGAATACTAGTTTATGC
117850	115937	GCACAGAATACTAGTTTATG
117851	115938	AGCACAGAATACTAGTTTAT
117852	115939	AAGCACAGAATACTAGTTTA
117853	115940	CAAGCACAGAATACTAGTTT
117854	115941	ACAAGCACAGAATACTAGTT
117855	115942	CACAAGCACAGAATACTAGT
117856	115943	ACACAAGCACAGAATACTAG
117857	115944	CACACAAGCACAGAATACTA
117858	115945	CCACACAAGCACAGAATACT
117859	115946	ACCACACAAGCACAGAATAC
117860	115947	AACCACACAAGCACAGAATA
117861	115948	TAACCACACAAGCACAGAAT
117862	115949	TTAACCACACAAGCACAGAA
117863	115950	TTTAACCACACAAGCACAGA
117864	115951	CTTTAACCACACAAGCACAG
117865	115952	TCTTTAACCACACAAGCACA
117866	115953	CTCTTTAACCACACAAGCAC
117867	115954	GCTCTTTAACCACACAAGCA
117868	115955	GGCTCTTTAACCACACAAGC
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117872	115959	CGAAGGCTCTTTAACCACAC
117873	115960	ACGAAGGCTCTTTAACCACA
117874	115961	TACGAAGGCTCTTTAACCAC
117875	115962	CTACGAAGGCTCTTTAACCA
117876	115963	TCTACGAAGGCTCTTTAACC
117877	115964	TTCTACGAAGGCTCTTTAAC
117878	115965	TTTCTACGAAGGCTCTTTAA
117879	115966	TTTTCTACGAAGGCTCTTTA
117880	115967	TTTTTCTACGAAGGCTCTTT
117881	115968	TTTTTTCTACGAAGGCTCTT
117882	115969	ATTTTTTCTACGAAGGCTCT
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19590	17677	CAACTCCAAATGCGTTTGAC
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19592	17679	TCCAACTCCAAATGCGTTTG
19593	17680	TTCCAACTCCAAATGCGTTT
19594	17681	ATTCCAACTCCAAATGCGTT
19595	17682	CATTCCAACTCCAAATGCGT
19596	17683	CCATTCCAACTCCAAATGCG
19597	17684	GCCATTCCAACTCCAAATGC
19598	17685	AGCCATTCCAACTCCAAATG
19599	17686	GAGCCATTCCAACTCCAAAT
19600	17687	AGAGCCATTCCAACTCCAAA
19601	17688	CAGAGCCATTCCAACTCCAA
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19603	17690	ACCAGAGCCATTCCAACTCC
19604	17691	CACCAGAGCCATTCCAACTC
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19606	17693	AACACCAGAGCCATTCCAAC
19607	17694	AAACACCAGAGCCATTCCAA
19608	17695	AAAACACCAGAGCCATTCCA
19609	17696	AAAAACACCAGAGCCATTCC
19610	17697	AAAAAACACCAGAGCCATTC
19611	17698	AAAAAAACACCAGAGCCATT
19612	17699	AAAAAAAACACCAGAGCCAT
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19614	17701	AAAAAAAAAACACCAGAGCC
19615	17702	AAAAAAAAAAACACCAGAGC
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19634	17721	CGTGTTTCTGGTTTAAAAAA
19635	17722	ACGTGTTTCTGGTTTAAAAA
19636	17723	CACGTGTTTCTGGTTTAAAA
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19638	17725	TGCACGTGTTTCTGGTTTAA
19639	17726	CTGCACGTGTTTCTGGTTTA
19640	17727	ACTGCACGTGTTTCTGGTTT
19641	17728	AACTGCACGTGTTTCTGGTT
19642	17729	AAACTGCACGTGTTTCTGGT
19643	17730	TAAACTGCACGTGTTTCTGG
19644	17731	ATAAACTGCACGTGTTTCTG
19645	17732	AATAAACTGCACGTGTTTCT
19646	17733	CAATAAACTGCACGTGTTTC
19647	17734	TCAATAAACTGCACGTGTTT
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19649	17736	ATTCAATAAACTGCACGTGT
19650	17737	CATTCAATAAACTGCACGTG
19651	17738	GCATTCAATAAACTGCACGT
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19655	17742	AATGGCATTCAATAAACTGC
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19657	17744	ACAATGGCATTCAATAAACT
19658	17745	TACAATGGCATTCAATAAAC
19659	17746	CTACAATGGCATTCAATAAA
19660	17747	TCTACAATGGCATTCAATAA

68737	66824	AGGCTGCAGAAATAGGTTTA
68738	66825	AAGGCTGCAGAAATAGGTTT
68739	66826	CAAGGCTGCAGAAATAGGTT
68740	66827	TCAAGGCTGCAGAAATAGGT
68741	66828	ATCAAGGCTGCAGAAATAGG
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68744	66831	GTCATCAAGGCTGCAGAAAT
68745	66832	GGTCATCAAGGCTGCAGAAA
68746	66833	TGGTCATCAAGGCTGCAGAA
68747	66834	GTGGTCATCAAGGCTGCAGA
68748	66835	AGTGGTCATCAAGGCTGCAG
68749	66836	GAGTGGTCATCAAGGCTGCA
68750	66837	GGAGTGGTCATCAAGGCTGC
68751	66838	AGGAGTGGTCATCAAGGCTG
68752	66839	AAGGAGTGGTCATCAAGGCT
68753	66840	GAAGGAGTGGTCATCAAGGC
68754	66841	GGAAGGAGTGGTCATCAAGG
68755	66842	TGGAAGGAGTGGTCATCAAG
68756	66843	CTGGAAGGAGTGGTCATCAA
68757	66844	ACTGGAAGGAGTGGTCATCA
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68760	66847	GGGACTGGAAGGAGTGGTCA
68761	66848	AGGGACTGGAAGGAGTGGTC
68762	66849	GAGGGACTGGAAGGAGTGGT
68763	66850	TGAGGGACTGGAAGGAGTGG
68764	66851	GTGAGGGACTGGAAGGAGTG
68765	66852	GGTGAGGGACTGGAAGGAGT
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68769	66856	AATAGGTGAGGGACTGGAAG
68770	66857	AAATAGGTGAGGGACTGGAA
68771	66858	CAAATAGGTGAGGGACTGGA
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68774	66861	AAGCAAATAGGTGAGGGACT
68775	66862	AAAGCAAATAGGTGAGGGAC
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68778	66865	AATAAAGCAAATAGGTGAGG
68779	66866	GAATAAAGCAAATAGGTGAG
68780	66867	TGAATAAAGCAAATAGGTGA
68781	66868	ATGAATAAAGCAAATAGGTG
68782	66869	CATGAATAAAGCAAATAGGT
68783	66870	CCATGAATAAAGCAAATAGG
68784	66871	GCCATGAATAAAGCAAATAG
68785	66872	TGCCATGAATAAAGCAAATA
68786	66873	CTGCCATGAATAAAGCAAAT
68787	66874	TCTGCCATGAATAAAGCAAA
68788	66875	CTCTGCCATGAATAAAGCAA
68789	66876	CCTCTGCCATGAATAAAGCA
68790	66877	GCCTCTGCCATGAATAAAGC
68791	66878	AGCCTCTGCCATGAATAAAG
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68794	66881	AAGAGCCTCTGCCATGAATA
68795	66882	AAAGAGCCTCTGCCATGAAT
68796	66883	GAAAGAGCCTCTGCCATGAA
68797	66884	AGAAAGAGCCTCTGCCATGA
68798	66885	AAGAAAGAGCCTCTGCCATG
68799	66886	GAAGAAAGAGCCTCTGCCAT
68800	66887	GGAAGAAAGAGCCTCTGCCA
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68803	66890	GCAGGAAGAAAGAGCCTCTG
68804	66891	AGCAGGAAGAAAGAGCCTCT
68805	66892	AAGCAGGAAGAAAGAGCCTC
68806	66893	CAAGCAGGAAGAAAGAGCCT
68807	66894	ACAAGCAGGAAGAAAGAGCC

117884	115971	GGATTTTTTCTACGAAGGCT
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117886	115973	TGGGATTTTTTCTACGAAGG
117887	115974	GTGGGATTTTTTCTACGAAG
117888	115975	TGTGGGATTTTTTCTACGAA
117889	115976	ATGTGGGATTTTTTCTACGA
117890	115977	AATGTGGGATTTTTTCTACG
117891	115978	AAATGTGGGATTTTTTCTAC
117892	115979	AAAATGTGGGATTTTTTCTA
117893	115980	AAAAATGTGGGATTTTTTCT
117894	115981	GAAAAATGTGGGATTTTTTC
117895	115982	AGAAAAATGTGGGATTTTTT
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117897	115984	TAAGAAAAATGTGGGATTTT
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117899	115986	TTTAAGAAAAATGTGGGATT
117900	115987	TTTTAAGAAAAATGTGGGAT
117901	115988	CTTTTAAGAAAAATGTGGGA
117902	115989	CCTTTTAAGAAAAATGTGGG
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117904	115991	TTCCTTTTAAGAAAAATGTG
117905	115992	TTTCCTTTTAAGAAAAATGT
117906	115993	ATTTCCTTTTAAGAAAAATG
117907	115994	GATTTCCTTTTAAGAAAAAT
117908	115995	AGATTTCCTTTTAAGAAAAA
117909	115996	AAGATTTCCTTTTAAGAAAA
117910	115997	AAAGATTTCCTTTTAAGAAA
117911	115998	AAAAGATTTCCTTTTAAGAA
117912	115999	CAAAAGATTTCCTTTTAAGA
117913	116000	CCAAAAGATTTCCTTTTAAG
117914	116001	GCCAAAAGATTTCCTTTTAA
117915	116002	GGCCAAAAGATTTCCTTTTA
117916	116003	TGGCCAAAAGATTTCCTTTT
117917	116004	CTGGCCAAAAGATTTCCTTT
117918	116005	CCTGGCCAAAAGATTTCCTT
117919	116006	ACCTGGCCAAAAGATTTCCT
117920	116007	CACCTGGCCAAAAGATTTCC
117921	116008	ACACCTGGCCAAAAGATTTC
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117923	116010	CCACACCTGGCCAAAAGATT
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117925	116012	CACCACACCTGGCCAAAAGA
117926	116013	CCACCACACCTGGCCAAAAG
117927	116014	GCCACCACACCTGGCCAAAA
117928	116015	AGCCACCACACCTGGCCAAA
117929	116016	GAGCCACCACACCTGGCCAA
117930	116017	TGAGCCACCACACCTGGCCA
117931	116018	GTGAGCCACCACACCTGGCC
117932	116019	TGTGAGCCACCACACCTGGC
117933	116020	ATGTGAGCCACCACACCTGG
117934	116021	GATGTGAGCCACCACACCTG
117935	116022	AGATGTGAGCCACCACACCT
117936	116023	CAGATGTGAGCCACCACACC
117937	116024	ACAGATGTGAGCCACCACAC
117938	116025	TACAGATGTGAGCCACCACA
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117940	116027	CTTACAGATGTGAGCCACCA
117941	116028	GCTTACAGATGTGAGCCACC
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117943	116030	GGGCTTACAGATGTGAGCCA
117944	116031	TGGGCTTACAGATGTGAGCC
117945	116032	TTGGGCTTACAGATGTGAGC
117946	116033	GTTGGGCTTACAGATGTGAG
117947	116034	TGTTGGGCTTACAGATGTGA
117948	116035	GTGTTGGGCTTACAGATGTG
117949	116036	AGTGTTGGGCTTACAGATGT
117950	116037	GAGTGTTGGGCTTACAGATG
117951	116038	AGAGTGTTGGGCTTACAGAT
117952	116039	CAGAGTGTTGGGCTTACAGA
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117954	116041	CCCAGAGTGTTGGGCTTACA

19661	17748	TTCTACAATGGCATTCAATA
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19663	17750	TTTTCTACAATGGCATTCAA
19664	17751	CTTTTCTACAATGGCATTCA
19665	17752	ACTTTTCTACAATGGCATTC
19666	17753	CACTTTTCTACAATGGCATT
19667	17754	ACACTTTTCTACAATGGCAT
19668	17755	CACACTTTTCTACAATGGCA
19669	17756	ACACACTTTTCTACAATGGC
19670	17757	CACACACTTTTCTACAATGG
19671	17758	TCACACACTTTTCTACAATG
19672	17759	CTCACACACTTTTCTACAAT
19673	17760	CCTCACACACTTTTCTACAA
19674	17761	TCCTCACACACTTTTCTACA
19675	17762	ATCCTCACACACTTTTCTAC
19676	17763	TATCCTCACACACTTTTCTA
19677	17764	TTATCCTCACACACTTTTCT
19678	17765	TTTATCCTCACACACTTTTC
19679	17766	GTTTATCCTCACACACTTTT
19680	17767	CGTTTATCCTCACACACTTT
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19682	17769	GCCGTTTATCCTCACACACT
19683	17770	AGCCGTTTATCCTCACACAC
19684	17771	CAGCCGTTTATCCTCACACA
19685	17772	TCAGCCGTTTATCCTCACAC
19686	17773	ATCAGCCGTTTATCCTCACA
19687	17774	TATCAGCCGTTTATCCTCAC
19688	17775	CTATCAGCCGTTTATCCTCA
19689	17776	TCTATCAGCCGTTTATCCTC
19690	17777	CTCTATCAGCCGTTTATCCT
19691	17778	TCTCTATCAGCCGTTTATCC
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19693	17780	GTTCTCTATCAGCCGTTTAT
19694	17781	AGTTCTCTATCAGCCGTTTA
19695	17782	AAGTTCTCTATCAGCCGTTT
19696	17783	CAAGTTCTCTATCAGCCGTT
19697	17784	CCAAGTTCTCTATCAGCCGT
19698	17785	GCCAAGTTCTCTATCAGCCG
19699	17786	AGCCAAGTTCTCTATCAGCC
19700	17787	GAGCCAAGTTCTCTATCAGC
19701	17788	AGAGCCAAGTTCTCTATCAG
19702	17789	CAGAGCCAAGTTCTCTATCA
19703	17790	CCAGAGCCAAGTTCTCTATC
19704	17791	CCCAGAGCCAAGTTCTCTAT
19705	17792	CCCCAGAGCCAAGTTCTCTA
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19707	17794	GCCCCCAGAGCCAAGTTCTC
19708	17795	TGCCCCCAGAGCCAAGTTCT
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19712	17799	GCCCTGCCCCCAGAGCCAAG
19713	17800	CGCCCTGCCCCCAGAGCCAA
19714	17801	TCGCCCTGCCCCCAGAGCCA
19715	17802	CTCGCCCTGCCCCCAGAGCC
19716	17803	CCTCGCCCTGCCCCCAGAGC
19717	17804	TCCTCGCCCTGCCCCCAGAG
19718	17805	TTCCTCGCCCTGCCCCCAGA
19719	17806	ATTCCTCGCCCTGCCCCCAG
19720	17807	CATTCCTCGCCCTGCCCCCA
19721	17808	CCATTCCTCGCCCTGCCCCC
19722	17809	TCCATTCCTCGCCCTGCCCC
19723	17810	CTCCATTCCTCGCCCTGCCC
19724	17811	CCTCCATTCCTCGCCCTGCC
19725	17812	CCCTCCATTCCTCGCCCTGC
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68808	66895	GACAAGCAGGAAGAAAGAGC
68809	66896	TGACAAGCAGGAAGAAAGAG
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68815	66902	TTGTACTGACAAGCAGGAAG
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68819	66906	CTCTTTGTACTGACAAGCAG
68820	66907	CCTCTTTGTACTGACAAGCA
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68823	66910	CTGCCTCTTTGTACTGACAA
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68841	66928	AGATCCAGGTGAAGAATCCT
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68844	66931	CACAGATCCAGGTGAAGAAT
68845	66932	CCACAGATCCAGGTGAAGAA
68846	66933	TCCACAGATCCAGGTGAAGA
68847	66934	ATCCACAGATCCAGGTGAAG
68848	66935	AATCCACAGATCCAGGTGAA
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68850	66937	AGAATCCACAGATCCAGGTG
68851	66938	GAGAATCCACAGATCCAGGT
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68853	66940	TTGAGAATCCACAGATCCAG
68854	66941	TTTGAGAATCCACAGATCCA
68855	66942	CTTTGAGAATCCACAGATCC
68856	66943	TCTTTGAGAATCCACAGATC
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68858	66945	ATTCTTTGAGAATCCACAGA
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68861	66948	CAAATTCTTTGAGAATCCAC
68862	66949	ACAAATTCTTTGAGAATCCA
68863	66950	CACAAATTCTTTGAGAATCC
68864	66951	CCACAAATTCTTTGAGAATC
68865	66952	TCCACAAATTCTTTGAGAAT
68866	66953	CTCCACAAATTCTTTGAGAA
68867	66954	TCTCCACAAATTCTTTGAGA
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68870	66957	TTCTCTCCACAAATTCTTTG
68871	66958	ATTCTCTCCACAAATTCTTT
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68874	66961	TGAATTCTCTCCACAAATTC
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68876	66963	CCTGAATTCTCTCCACAAAT
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117955	116042	TCCCAGAGTGTTGGGCTTAC
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117958	116045	GCTTCCCAGAGTGTTGGGCT
117959	116046	GGCTTCCCAGAGTGTTGGGC
117960	116047	CGGCTTCCCAGAGTGTTGGG
117961	116048	TCGGCTTCCCAGAGTGTTGG
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117963	116050	CCTCGGCTTCCCAGAGTGTT
117964	116051	ACCTCGGCTTCCCAGAGTGT
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117968	116055	GCCCACCTCGGCTTCCCAGA
117969	116056	TGCCCACCTCGGCTTCCCAG
117970	116057	CTGCCCACCTCGGCTTCCCA
117971	116058	TCTGCCCACCTCGGCTTCCC
117972	116059	ATCTGCCCACCTCGGCTTCC
117973	116060	GATCTGCCCACCTCGGCTTC
117974	116061	TGATCTGCCCACCTCGGCTT
117975	116062	GTGATCTGCCCACCTCGGCT
117976	116063	AGTGATCTGCCCACCTCGGC
117977	116064	AAGTGATCTGCCCACCTCGG
117978	116065	CAAGTGATCTGCCCACCTCG
117979	116066	TCAAGTGATCTGCCCACCTC
117980	116067	CTCAAGTGATCTGCCCACCT
117981	116068	CCTCAAGTGATCTGCCCACC
117982	116069	ACCTCAAGTGATCTGCCCAC
117983	116070	GACCTCAAGTGATCTGCCCA
117984	116071	TGACCTCAAGTGATCTGCCC
117985	116072	CTGACCTCAAGTGATCTGCC
117986	116073	CCTGACCTCAAGTGATCTGC
117987	116074	TCCTGACCTCAAGTGATCTG
117988	116075	CTCCTGACCTCAAGTGATCT
117989	116076	ACTCCTGACCTCAAGTGATC
117990	116077	TACTCCTGACCTCAAGTGAT
117991	116078	GTACTCCTGACCTCAAGTGA
117992	116079	TGTACTCCTGACCTCAAGTG
117993	116080	TTGTACTCCTGACCTCAAGT
117994	116081	TTTGTACTCCTGACCTCAAG
117995	116082	TTTTGTACTCCTGACCTCAA
117996	116083	GTTTTGTACTCCTGACCTCA
117997	116084	GGTTTTGTACTCCTGACCTC
117998	116085	TGGTTTTGTACTCCTGACCT
117999	116086	ATGGTTTTGTACTCCTGACC
118000	116087	GATGGTTTTGTACTCCTGAC
118001	116088	GGATGGTTTTGTACTCCTGA
118002	116089	AGGATGGTTTTGTACTCCTG
118003	116090	CAGGATGGTTTTGTACTCCT
118004	116091	CCAGGATGGTTTTGTACTCC
118005	116092	GCCAGGATGGTTTTGTACTC
118006	116093	GGCCAGGATGGTTTTGTACT
118007	116094	TGGCCAGGATGGTTTTGTAC
118008	116095	TTGGCCAGGATGGTTTTGTA
118009	116096	GTTGGCCAGGATGGTTTTGT
118010	116097	TGTTGGCCAGGATGGTTTTG
118011	116098	ATGTTGGCCAGGATGGTTTT
118012	116099	CATGTTGGCCAGGATGGTTT
118013	116100	CCATGTTGGCCAGGATGGTT
118014	116101	ACCATGTTGGCCAGGATGGT
118015	116102	CACCATGTTGGCCAGGATGG
118016	116103	TCACCATGTTGGCCAGGATG
118017	116104	TTCACCATGTTGGCCAGGAT
118018	116105	TTTCACCATGTTGGCCAGGA
118019	116106	TTTTCACCATGTTGGCCAGG
118020	116107	GTTTTCACCATGTTGGCCAG
118021	116108	GGTTTTCACCATGTTGGCCA
118022	116109	GGGTTTTCACCATGTTGGCC
118023	116110	CGGGTTTTCACCATGTTGGC
118024	116111	ACGGGTTTTCACCATGTTGG
118025	116112	GACGGGTTTTCACCATGTTG

19732	17819	CCATCCACCCTCCATTCCTC
19733	17820	TCCATCCACCCTCCATTCCT
19734	17821	CTCCATCCACCCTCCATTCC
19735	17822	ACTCCATCCACCCTCCATTC
19736	17823	TACTCCATCCACCCTCCATT
19737	17824	GTACTCCATCCACCCTCCAT
19738	17825	TGTACTCCATCCACCCTCCA
19739	17826	ATGTACTCCATCCACCCTCC
19740	17827	CATGTACTCCATCCACCCTC
19741	17828	CCATGTACTCCATCCACCCT
19742	17829	CCCATGTACTCCATCCACCC
19743	17830	TCCCATGTACTCCATCCACC
19744	17831	TTCCCATGTACTCCATCCAC
19745	17832	ATTCCCATGTACTCCATCCA
19746	17833	GATTCCCATGTACTCCATCC
19747	17834	TGATTCCCATGTACTCCATC
19748	17835	CTGATTCCCATGTACTCCAT
19749	17836	TCTGATTCCCATGTACTCCA
19750	17837	ATCTGATTCCCATGTACTCC
19751	17838	GATCTGATTCCCATGTACTC
19752	17839	TGATCTGATTCCCATGTACT
19753	17840	GTGATCTGATTCCCATGTAC
19754	17841	CGTGATCTGATTCCCATGTA
19755	17842	CCGTGATCTGATTCCCATGT
19756	17843	CCCGTGATCTGATTCCCATG
19757	17844	GCCCGTGATCTGATTCCCAT
19758	17845	TGCCCGTGATCTGATTCCCA
19759	17846	CTGCCCGTGATCTGATTCCC
19760	17847	TCTGCCCGTGATCTGATTCC
19761	17848	CTCTGCCCGTGATCTGATTC
19762	17849	GCTCTGCCCGTGATCTGATT
19763	17850	AGCTCTGCCCGTGATCTGAT
19764	17851	GAGCTCTGCCCGTGATCTGA
19765	17852	GGAGCTCTGCCCGTGATCTG
19766	17853	AGGAGCTCTGCCCGTGATCT
19767	17854	CAGGAGCTCTGCCCGTGATC
19768	17855	CCAGGAGCTCTGCCCGTGAT
19769	17856	GCCAGGAGCTCTGCCCGTGA
19770	17857	GGCCAGGAGCTCTGCCCGTG
19771	17858	AGGCCAGGAGCTCTGCCCGT
19772	17859	TAGGCCAGGAGCTCTGCCCG
19773	17860	CTAGGCCAGGAGCTCTGCCC
19774	17861	TCTAGGCCAGGAGCTCTGCC
19775	17862	ATCTAGGCCAGGAGCTCTGC
19776	17863	TATCTAGGCCAGGAGCTCTG
19777	17864	TTATCTAGGCCAGGAGCTCT
19778	17865	ATTATCTAGGCCAGGAGCTC
19779	17866	CATTATCTAGGCCAGGAGCT
19780	17867	GCATTATCTAGGCCAGGAGC
19781	17868	GGCATTATCTAGGCCAGGAG
19782	17869	AGGCATTATCTAGGCCAGGA
19783	17870	GAGGCATTATCTAGGCCAGG
19784	17871	GGAGGCATTATCTAGGCCAG
19785	17872	AGGAGGCATTATCTAGGCCA
19786	17873	CAGGAGGCATTATCTAGGCC
19787	17874	TCAGGAGGCATTATCTAGGC
19788	17875	ATCAGGAGGCATTATCTAGG
19789	17876	GATCAGGAGGCATTATCTAG
19790	17877	AGATCAGGAGGCATTATCTA
19791	17878	CAGATCAGGAGGCATTATCT
19792	17879	ACAGATCAGGAGGCATTATC
19793	17880	AACAGATCAGGAGGCATTAT
19794	17881	CAACAGATCAGGAGGCATTA
19795	17882	TCAACAGATCAGGAGGCATT
19796	17883	ATCAACAGATCAGGAGGCAT
19797	17884	TATCAACAGATCAGGAGGCA
19798	17885	CTATCAACAGATCAGGAGGC
19799	17886	TCTATCAACAGATCAGGAGG
19800	17887	GTCTATCAACAGATCAGGAG
19801	17888	AGTCTATCAACAGATCAGGA
19802	17889	AAGTCTATCAACAGATCAGG

68879	66966	TGCCCTGAATTCTCTCCACA
68880	66967	ATGCCCTGAATTCTCTCCAC
68881	66968	AATGCCCTGAATTCTCTCCA
68882	66969	CAATGCCCTGAATTCTCTCC
68883	66970	TCAATGCCCTGAATTCTCTC
68884	66971	ATCAATGCCCTGAATTCTCT
68885	66972	CATCAATGCCCTGAATTCTC
68886	66973	TCATCAATGCCCTGAATTCT
68887	66974	GTCATCAATGCCCTGAATTC
68888	66975	GGTCATCAATGCCCTGAATT
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68892	66979	CCAAGGTCATCAATGCCCTG
68893	66980	TCCAAGGTCATCAATGCCCT
68894	66981	ATCCAAGGTCATCAATGCCC
68895	66982	CATCCAAGGTCATCAATGCC
68896	66983	TCATCCAAGGTCATCAATGC
68897	66984	TTCATCCAAGGTCATCAATG
68898	66985	CTTCATCCAAGGTCATCAAT
68899	66986	TCTTCATCCAAGGTCATCAA
68900	66987	CTCTTCATCCAAGGTCATCA
68901	66988	TCTCTTCATCCAAGGTCATC
68902	66989	TTCTCTTCATCCAAGGTCAT
68903	66990	TTTCTCTTCATCCAAGGTCA
68904	66991	ATTTCTCTTCATCCAAGGTC
68905	66992	AATTTCTCTTCATCCAAGGT
68906	66993	AAATTTCTCTTCATCCAAGG
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68913	67000	AAGATGTAAATTTCTCTTCA
68914	67001	AAAGATGTAAATTTCTCTTC
68915	67002	TAAAGATGTAAATTTCTCTT
68916	67003	ATAAAGATGTAAATTTCTCT
68917	67004	AATAAAGATGTAAATTTCTC
68918	67005	AAATAAAGATGTAAATTTCT
68919	67006	TAAATAAAGATGTAAATTTC
68920	67007	GTAAATAAAGATGTAAATTT
68921	67008	TGTAAATAAAGATGTAAATT
68922	67009	GTGTAAATAAAGATGTAAAT
68923	67010	AGTGTAAATAAAGATGTAAA
68924	67011	TAGTGTAAATAAAGATGTAA
68925	67012	TTAGTGTAAATAAAGATGTA
68926	67013	GTTAGTGTAAATAAAGATGT
68927	67014	GGTTAGTGTAAATAAAGATG
68928	67015	AGGTTAGTGTAAATAAAGAT
68929	67016	AAGGTTAGTGTAAATAAAGA
68930	67017	GAAGGTTAGTGTAAATAAAG
68931	67018	TGAAGGTTAGTGTAAATAAA
68932	67019	TTGAAGGTTAGTGTAAATAA
68933	67020	CTTGAAGGTTAGTGTAAATA
68934	67021	ACTTGAAGGTTAGTGTAAAT
68935	67022	CACTTGAAGGTTAGTGTAAA
68936	67023	TCACTTGAAGGTTAGTGTAA
68937	67024	TTCACTTGAAGGTTAGTGTA
68938	67025	TTTCACTTGAAGGTTAGTGT
68939	67026	ATTTCACTTGAAGGTTAGTG
68940	67027	AATTTCACTTGAAGGTTAGT
68941	67028	AAATTTCACTTGAAGGTTAG
68942	67029	TAAATTTCACTTGAAGGTTA
68943	67030	CTAAATTTCACTTGAAGGTT
68944	67031	GCTAAATTTCACTTGAAGGT
68945	67032	TGCTAAATTTCACTTGAAGG
68946	67033	ATGCTAAATTTCACTTGAAG
68947	67034	AATGCTAAATTTCACTTGAA
68948	67035	AAATGCTAAATTTCACTTGA
68949	67036	AAAATGCTAAATTTCACTTG

118026	116113	AGACGGGTTTTCACCATGTT
118027	116114	GAGACGGGTTTTCACCATGT
118028	116115	AGAGACGGGTTTTCACCATG
118029	116116	TAGAGACGGGTTTTCACCAT
118030	116117	GTAGAGACGGGTTTTCACCA
118031	116118	AGTAGAGACGGGTTTTCACC
118032	116119	TAGTAGAGACGGGTTTTCAC
118033	116120	TTAGTAGAGACGGGTTTTCA
118034	116121	TTTAGTAGAGACGGGTTTTC
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118036	116123	TTTTTAGTAGAGACGGGTTT
118037	116124	ATTTTTAGTAGAGACGGGTT
118038	116125	TATTTTTAGTAGAGACGGGT
118039	116126	GTATTTTTAGTAGAGACGGG
118040	116127	TGTATTTTTAGTAGAGACGG
118041	116128	TTGTATTTTTAGTAGAGACG
118042	116129	TTTGTATTTTTAGTAGAGAC
118043	116130	CTTTGTATTTTTAGTAGAGA
118044	116131	TCTTTGTATTTTTAGTAGAG
118045	116132	ATCTTTGTATTTTTAGTAGA
118046	116133	GATCTTTGTATTTTTAGTAG
118047	116134	TGATCTTTGTATTTTTAGTA
118048	116135	CTGATCTTTGTATTTTTAGT
118049	116136	GCTGATCTTTGTATTTTTAG
118050	116137	AGCTGATCTTTGTATTTTTA
118051	116138	CAGCTGATCTTTGTATTTTT
118052	116139	CCAGCTGATCTTTGTATTTT
118053	116140	CCCAGCTGATCTTTGTATTT
118054	116141	GCCCAGCTGATCTTTGTATT
118055	116142	TGCCCAGCTGATCTTTGTAT
118056	116143	ATGCCCAGCTGATCTTTGTA
118057	116144	CATGCCCAGCTGATCTTTGT
118058	116145	CCATGCCCAGCTGATCTTTG
118059	116146	ACCATGCCCAGCTGATCTTT
118060	116147	CACCATGCCCAGCTGATCTT
118061	116148	CCACCATGCCCAGCTGATCT
118062	116149	ACCACCATGCCCAGCTGATC
118063	116150	CACCACCATGCCCAGCTGAT
118064	116151	GCACCACCATGCCCAGCTGA
118065	116152	CGCACCACCATGCCCAGCTG
118066	116153	ACGCACCACCATGCCCAGCT
118067	116154	CACGCACCACCATGCCCAGC
118068	116155	GCACGCACCACCATGCCCAG
118069	116156	GGCACGCACCACCATGCCCA
118070	116157	AGGCACGCACCACCATGCCC
118071	116158	CAGGCACGCACCACCATGCC
118072	116159	CCAGGCACGCACCACCATGC
118073	116160	CCCAGGCACGCACCACCATG
118074	116161	ACCCAGGCACGCACCACCAT
118075	116162	CACCCAGGCACGCACCACCA
118076	116163	TCACCCAGGCACGCACCACC
118077	116164	GTCACCCAGGCACGCACCAC
118078	116165	TGTCACCCAGGCACGCACCA
118079	116166	CTGTCACCCAGGCACGCACC
118080	116167	TCTGTCACCCAGGCACGCAC
118081	116168	CTCTGTCACCCAGGCACGCA
118082	116169	GCTCTGTCACCCAGGCACGC
118083	116170	CGCTCTGTCACCCAGGCACG
118084	116171	TCGCTCTGTCACCCAGGCAC
118085	116172	CTCGCTCTGTCACCCAGGCA
118086	116173	TCTCGCTCTGTCACCCAGGC
118087	116174	GTCTCGCTCTGTCACCCAGG
118088	116175	AGTCTCGCTCTGTCACCCAG
118089	116176	GAGTCTCGCTCTGTCACCCA
118090	116177	GGAGTCTCGCTCTGTCACCC
118091	116178	CGGAGTCTCGCTCTGTCACC
118092	116179	ACGGAGTCTCGCTCTGTCAC
118093	116180	GACGGAGTCTCGCTCTGTCA
118094	116181	GGACGGAGTCTCGCTCTGTC
118095	116182	TGGACGGAGTCTCGCTCTGT
118096	116183	TTGGACGGAGTCTCGCTCTG

19803	17890	CAAGTCTATCAACAGATCAG
19804	17891	TCAAGTCTATCAACAGATCA
19805	17892	TTCAAGTCTATCAACAGATC
19806	17893	TTTCAAGTCTATCAACAGAT
19807	17894	CTTTCAAGTCTATCAACAGA
19808	17895	TCTTTCAAGTCTATCAACAG
19809	17896	ATCTTTCAAGTCTATCAACA
19810	17897	GATCTTTCAAGTCTATCAAC
19811	17898	TGATCTTTCAAGTCTATCAA
19812	17899	TTGATCTTTCAAGTCTATCA
19813	17900	GTTGATCTTTCAAGTCTATC
19814	17901	TGTTGATCTTTCAAGTCTAT
19815	17902	GTGTTGATCTTTCAAGTCTA
19816	17903	AGTGTTGATCTTTCAAGTCT
19817	17904	CAGTGTTGATCTTTCAAGTC
19818	17905	CCAGTGTTGATCTTTCAAGT
19819	17906	CCCAGTGTTGATCTTTCAAG
19820	17907	TCCCAGTGTTGATCTTTCAA
19821	17908	ATCCCAGTGTTGATCTTTCA
19822	17909	CATCCCAGTGTTGATCTTTC
19823	17910	TCATCCCAGTGTTGATCTTT
19824	17911	ATCATCCCAGTGTTGATCTT
19825	17912	CATCATCCCAGTGTTGATCT
19826	17913	GCATCATCCCAGTGTTGATC
19827	17914	AGCATCATCCCAGTGTTGAT
19828	17915	CAGCATCATCCCAGTGTTGA
19829	17916	TCAGCATCATCCCAGTGTTG
19830	17917	CTCAGCATCATCCCAGTGTT
19831	17918	GCTCAGCATCATCCCAGTGT
19832	17919	TGCTCAGCATCATCCCAGTG
19833	17920	CTGCTCAGCATCATCCCAGT
19834	17921	TCTGCTCAGCATCATCCCAG
19835	17922	TTCTGCTCAGCATCATCCCA
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19839	17926	ACCATTCTGCTCAGCATCAT
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19841	17928	CGACCATTCTGCTCAGCATC
19842	17929	ACGACCATTCTGCTCAGCAT
19843	17930	TACGACCATTCTGCTCAGCA
19844	17931	TTACGACCATTCTGCTCAGC
19845	17932	ATTACGACCATTCTGCTCAG
19846	17933	CATTACGACCATTCTGCTCA
19847	17934	TCATTACGACCATTCTGCTC
19848	17935	ATCATTACGACCATTCTGCT
19849	17936	CATCATTACGACCATTCTGC
19850	17937	GCATCATTACGACCATTCTG
19851	17938	CGCATCATTACGACCATTCT
19852	17939	GCGCATCATTACGACCATTC
19853	17940	TGCGCATCATTACGACCATT
19854	17941	GTGCGCATCATTACGACCAT
19855	17942	TGTGCGCATCATTACGACCA
19856	17943	TTGTGCGCATCATTACGACC
19857	17944	ATTGTGCGCATCATTACGAC
19858	17945	GATTGTGCGCATCATTACGA
19859	17946	TGATTGTGCGCATCATTACG
19860	17947	CTGATTGTGCGCATCATTAC
19861	17948	CCTGATTGTGCGCATCATTA
19862	17949	CCCTGATTGTGCGCATCATT
19863	17950	GCCCTGATTGTGCGCATCAT
19864	17951	GGCCCTGATTGTGCGCATCA
19865	17952	GGGCCCTGATTGTGCGCATC
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19869	17956	ATCTGGGCCCTGATTGTGCG
19870	17957	CATCTGGGCCCTGATTGTGC
19871	17958	ACATCTGGGCCCTGATTGTG
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19873	17960	GAACATCTGGGCCCTGATTG

68950	67037	AAAAATGCTAAATTTCACTT
68951	67038	AAAAAATGCTAAATTTCACT
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68953	67040	GCAAAAAATGCTAAATTTCA
68954	67041	GGCAAAAAATGCTAAATTTC
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68967	67054	CATATTTTTAAATGGCAAAA
68968	67055	CCATATTTTTAAATGGCAAA
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68970	67057	GCCCATATTTTTAAATGGCA
68971	67058	TGCCCATATTTTTAAATGGC
68972	67059	TTGCCCATATTTTTAAATGG
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68974	67061	TGTTGCCCATATTTTTAAAT
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68977	67064	GTTTGTTGCCCATATTTTTA
68978	67065	TGTTTGTTGCCCATATTTTT
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68992	67079	CTAATACTACTAGTTGTTTG
68993	67080	GCTAATACTACTAGTTGTTT
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68995	67082	CTGCTAATACTACTAGTTGT
68996	67083	ACTGCTAATACTACTAGTTG
68997	67084	TACTGCTAATACTACTAGTT
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69000	67087	AAATACTGCTAATACTACTA
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69002	67089	ATAAATACTGCTAATACTAC
69003	67090	CATAAATACTGCTAATACTA
69004	67091	TCATAAATACTGCTAATACT
69005	67092	GTCATAAATACTGCTAATAC
69006	67093	AGTCATAAATACTGCTAATA
69007	67094	AAGTCATAAATACTGCTAAT
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69009	67096	TTAAGTCATAAATACTGCTA
69010	67097	CTTAAGTCATAAATACTGCT
69011	67098	GCTTAAGTCATAAATACTGC
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69013	67100	GTGCTTAAGTCATAAATACT
69014	67101	GGTGCTTAAGTCATAAATAC
69015	67102	AGGTGCTTAAGTCATAAATA
69016	67103	TAGGTGCTTAAGTCATAAAT
69017	67104	ATAGGTGCTTAAGTCATAAA
69018	67105	TATAGGTGCTTAAGTCATAA
69019	67106	CTATAGGTGCTTAAGTCATA
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118097	116184	TTTGGACGGAGTCTCGCTCT
118098	116185	TTTTGGACGGAGTCTCGCTC
118099	116186	TTTTTGGACGGAGTCTCGCT
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118114	116201	TTTTTTTTTTTTTTTTTTTT
118115	116202	TTTTTTTTTTTTTTTTTTTT
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118119	116206	ACTCTTTTTTTTTTTTTTTT
118120	116207	AACTCTTTTTTTTTTTTTTT
118121	116208	GAACTCTTTTTTTTTTTTTT
118122	116209	AGAACTCTTTTTTTTTTTTT
118123	116210	AAGAACTCTTTTTTTTTTTT
118124	116211	AAAGAACTCTTTTTTTTTTT
118125	116212	AAAAGAACTCTTTTTTTTTT
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118131	116218	AACATTAAAAGAACTCTTTT
118132	116219	CAACATTAAAAGAACTCTTT
118133	116220	CCAACATTAAAAGAACTCTT
118134	116221	TCCAACATTAAAAGAACTCT
118135	116222	TTCCAACATTAAAAGAACTC
118136	116223	TTTCCAACATTAAAAGAACT
118137	116224	TTTTCCAACATTAAAAGAAC
118138	116225	ATTTTCCAACATTAAAAGAA
118139	116226	CATTTTCCAACATTAAAAGA
118140	116227	GCATTTTCCAACATTAAAAG
118141	116228	AGCATTTTCCAACATTAAAA
118142	116229	TAGCATTTTCCAACATTAAA
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118144	116231	TTTAGCATTTTCCAACATTA
118145	116232	CTTTAGCATTTTCCAACATT
118146	116233	CCTTTAGCATTTTCCAACAT
118147	116234	CCCTTTAGCATTTTCCAACA
118148	116235	ACCCTTTAGCATTTTCCAAC
118149	116236	AACCCTTTAGCATTTTCCAA
118150	116237	AAACCCTTTAGCATTTTCCA
118151	116238	AAAACCCTTTAGCATTTTCC
118152	116239	AAAAACCCTTTAGCATTTTC
118153	116240	AAAAAACCCTTTAGCATTTT
118154	116241	AAAAAAACCCTTTAGCATTT
118155	116242	AAAAAAAACCCTTTAGCATT
118156	116243	AAAAAAAAACCCTTTAGCAT
118157	116244	AAAAAAAAAACCCTTTAGCA
118158	116245	CAAAAAAAAAACCCTTTAGC
118159	116246	GCAAAAAAAAAACCCTTTAG
118160	116247	GGCAAAAAAAAAACCCTTTA
118161	116248	TGGCAAAAAAAAAACCCTTT
118162	116249	TTGGCAAAAAAAAAACCCTT
118163	116250	GTTGGCAAAAAAAAAACCCT
118164	116251	GGTTGGCAAAAAAAAAACCC
118165	116252	TGGTTGGCAAAAAAAAAACC
118166	116253	CTGGTTGGCAAAAAAAAAAC
118167	116254	ACTGGTTGGCAAAAAAAAAA

19874	17961	TGAACATCTGGGCCCTGATT
19875	17962	CTGAACATCTGGGCCCTGAT
19876	17963	CCTGAACATCTGGGCCCTGA
19877	17964	GCCTGAACATCTGGGCCCTG
19878	17965	TGCCTGAACATCTGGGCCCT
19879	17966	GTGCCTGAACATCTGGGCCC
19880	17967	AGTGCCTGAACATCTGGGCC
19881	17968	AAGTGCCTGAACATCTGGGC
19882	17969	CAAGTGCCTGAACATCTGGG
19883	17970	CCAAGTGCCTGAACATCTGG
19884	17971	GCCAAGTGCCTGAACATCTG
19885	17972	CGCCAAGTGCCTGAACATCT
19886	17973	CCGCCAAGTGCCTGAACATC
19887	17974	ACCGCCAAGTGCCTGAACAT
19888	17975	TACCGCCAAGTGCCTGAACA
19889	17976	TTACCGCCAAGTGCCTGAAC
19890	17977	TTTACCGCCAAGTGCCTGAA
19891	17978	CTTTACCGCCAAGTGCCTGA
19892	17979	CCTTTACCGCCAAGTGCCTG
19893	17980	GCCTTTACCGCCAAGTGCCT
19894	17981	TGCCTTTACCGCCAAGTGCC
19895	17982	ATGCCTTTACCGCCAAGTGC
19896	17983	TATGCCTTTACCGCCAAGTG
19897	17984	CTATGCCTTTACCGCCAAGT
19898	17985	CCTATGCCTTTACCGCCAAG
19899	17986	GCCTATGCCTTTACCGCCAA
19900	17987	GGCCTATGCCTTTACCGCCA
19901	17988	AGGCCTATGCCTTTACCGCC
19902	17989	CAGGCCTATGCCTTTACCGC
19903	17990	CCAGGCCTATGCCTTTACCG
19904	17991	CCCAGGCCTATGCCTTTACC
19905	17992	GCCCAGGCCTATGCCTTTAC
19906	17993	GGCCCAGGCCTATGCCTTTA
19907	17994	GGGCCCAGGCCTATGCCTTT
19908	17995	AGGGCCCAGGCCTATGCCTT
19909	17996	CAGGGCCCAGGCCTATGCCT
19910	17997	TCAGGGCCCAGGCCTATGCC
19911	17998	ATCAGGGCCCAGGCCTATGC
19912	17999	GATCAGGGCCCAGGCCTATG
19913	18000	TGATCAGGGCCCAGGCCTAT
19914	18001	CTGATCAGGGCCCAGGCCTA
19915	18002	CCTGATCAGGGCCCAGGCCT
19916	18003	ACCTGATCAGGGCCCAGGCC
19917	18004	GACCTGATCAGGGCCCAGGC
19918	18005	CGACCTGATCAGGGCCCAGG
19919	18006	GCGACCTGATCAGGGCCCAG
19920	18007	GGCGACCTGATCAGGGCCCA
19921	18008	TGGCGACCTGATCAGGGCCC
19922	18009	TTGGCGACCTGATCAGGGCC
19923	18010	GTTGGCGACCTGATCAGGGC
19924	18011	GGTTGGCGACCTGATCAGGG
19925	18012	TGGTTGGCGACCTGATCAGG
19926	18013	ATGGTTGGCGACCTGATCAG
19927	18014	GATGGTTGGCGACCTGATCA
19928	18015	AGATGGTTGGCGACCTGATC
19929	18016	AAGATGGTTGGCGACCTGAT
19930	18017	GAAGATGGTTGGCGACCTGA
19931	18018	AGAAGATGGTTGGCGACCTG
19932	18019	AAGAAGATGGTTGGCGACCT
19933	18020	CAAGAAGATGGTTGGCGACC
19934	18021	ACAAGAAGATGGTTGGCGAC
19935	18022	GACAAGAAGATGGTTGGCGA
19936	18023	GGACAAGAAGATGGTTGGCG
19937	18024	GGGACAAGAAGATGGTTGGC
19938	18025	AGGGACAAGAAGATGGTTGG
19939	18026	TAGGGACAAGAAGATGGTTG
19940	18027	CTAGGGACAAGAAGATGGTT
19941	18028	TCTAGGGACAAGAAGATGGT
19942	18029	GTCTAGGGACAAGAAGATGG
19943	18030	AGTCTAGGGACAAGAAGATG
19944	18031	AAGTCTAGGGACAAGAAGAT

69021	67108	TTCTATAGGTGCTTAAGTCA
69022	67109	GTTCTATAGGTGCTTAAGTC
69023	67110	AGTTCTATAGGTGCTTAAGT
69024	67111	GAGTTCTATAGGTGCTTAAG
69025	67112	TGAGTTCTATAGGTGCTTAA
69026	67113	CTGAGTTCTATAGGTGCTTA
69027	67114	ACTGAGTTCTATAGGTGCTT
69028	67115	AACTGAGTTCTATAGGTGCT
69029	67116	TAACTGAGTTCTATAGGTGC
69030	67117	TTAACTGAGTTCTATAGGTG
69031	67118	ATTAACTGAGTTCTATAGGT
69032	67119	AATTAACTGAGTTCTATAGG
69033	67120	AAATTAACTGAGTTCTATAG
69034	67121	GAAATTAACTGAGTTCTATA
69035	67122	TGAAATTAACTGAGTTCTAT
69036	67123	ATGAAATTAACTGAGTTCTA
69037	67124	TATGAAATTAACTGAGTTCT
69038	67125	ATATGAAATTAACTGAGTTC
69039	67126	GATATGAAATTAACTGAGTT
69040	67127	CGATATGAAATTAACTGAGT
69041	67128	GCGATATGAAATTAACTGAG
69042	67129	AGCGATATGAAATTAACTGA
69043	67130	AAGCGATATGAAATTAACTG
69044	67131	CAAGCGATATGAAATTAACT
69045	67132	TCAAGCGATATGAAATTAAC
69046	67133	ATCAAGCGATATGAAATTAA
69047	67134	CATCAAGCGATATGAAATTA
69048	67135	ACATCAAGCGATATGAAATT
69049	67136	AACATCAAGCGATATGAAAT
69050	67137	TAACATCAAGCGATATGAAA
69051	67138	ATAACATCAAGCGATATGAA
69052	67139	CATAACATCAAGCGATATGA
69053	67140	CCATAACATCAAGCGATATG
69054	67141	CCCATAACATCAAGCGATAT
69055	67142	ACCCATAACATCAAGCGATA
69056	67143	TACCCATAACATCAAGCGAT
69057	67144	ATACCCATAACATCAAGCGA
69058	67145	GATACCCATAACATCAAGCG
69059	67146	AGATACCCATAACATCAAGC
69060	67147	GAGATACCCATAACATCAAG
69061	67148	TGAGATACCCATAACATCAA
69062	67149	TTGAGATACCCATAACATCA
69063	67150	TTTGAGATACCCATAACATC
69064	67151	ATTTGAGATACCCATAACAT
69065	67152	AATTTGAGATACCCATAACA
69066	67153	TAATTTGAGATACCCATAAC
69067	67154	ATAATTTGAGATACCCATAA
69068	67155	AATAATTTGAGATACCCATA
69069	67156	TAATAATTTGAGATACCCAT
69070	67157	ATAATAATTTGAGATACCCA
69071	67158	AATAATAATTTGAGATACCC
69072	67159	AAATAATAATTTGAGATACC
69073	67160	AAAATAATAATTTGAGATAC
69074	67161	TAAAATAATAATTTGAGATA
69075	67162	ATAAAATAATAATTTGAGAT
69076	67163	CATAAAATAATAATTTGAGA
69077	67164	ACATAAAATAATAATTTGAG
69078	67165	TACATAAAATAATAATTTGA
69079	67166	ATACATAAAATAATAATTTG
69080	67167	TATACATAAAATAATAATTT
69081	67168	ATATACATAAAATAATAATT
69082	67169	TATATACATAAAATAATAAT
69083	67170	ATATATACATAAAATAATAA
69084	67171	TATATATACATAAAATAATA
69085	67172	ATATATATACATAAAATAAT
69086	67173	AATATATATACATAAAATAA
69087	67174	AAATATATATACATAAAATA
69088	67175	AAAATATATATACATAAAAT
69089	67176	AAAAATATATATACATAAAA
69090	67177	CAAAAATATATATACATAAA
69091	67178	TCAAAAATATATATACATAA

118168	116255	AACTGGTTGGCAAAAAAAAA
118169	116256	TAACTGGTTGGCAAAAAAAA
118170	116257	TTAACTGGTTGGCAAAAAAA
118171	116258	ATTAACTGGTTGGCAAAAAA
118172	116259	AATTAACTGGTTGGCAAAAA
118173	116260	AAATTAACTGGTTGGCAAAA
118174	116261	TAAATTAACTGGTTGGCAAA
118175	116262	CTAAATTAACTGGTTGGCAA
118176	116263	TCTAAATTAACTGGTTGGCA
118177	116264	CTCTAAATTAACTGGTTGGC
118178	116265	ACTCTAAATTAACTGGTTGG
118179	116266	CACTCTAAATTAACTGGTTG
118180	116267	TCACTCTAAATTAACTGGTT
118181	116268	ATCACTCTAAATTAACTGGT
118182	116269	AATCACTCTAAATTAACTGG
118183	116270	TAATCACTCTAAATTAACTG
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118185	116272	GTTAATCACTCTAAATTAAC
118186	116273	AGTTAATCACTCTAAATTAA
118187	116274	CAGTTAATCACTCTAAATTA
118188	116275	GCAGTTAATCACTCTAAATT
118189	116276	AGCAGTTAATCACTCTAAAT
118190	116277	TAGCAGTTAATCACTCTAAA
118191	116278	ATAGCAGTTAATCACTCTAA
118192	116279	GATAGCAGTTAATCACTCTA
118193	116280	TGATAGCAGTTAATCACTCT
118194	116281	CTGATAGCAGTTAATCACTC
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118199	116286	CTCAACTGATAGCAGTTAAT
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118201	116288	TTCTCAACTGATAGCAGTTA
118202	116289	TTTCTCAACTGATAGCAGTT
118203	116290	GTTTCTCAACTGATAGCAGT
118204	116291	AGTTTCTCAACTGATAGCAG
118205	116292	TAGTTTCTCAACTGATAGCA
118206	116293	ATAGTTTCTCAACTGATAGC
118207	116294	TATAGTTTCTCAACTGATAG
118208	116295	CTATAGTTTCTCAACTGATA
118209	116296	TCTATAGTTTCTCAACTGAT
118210	116297	TTCTATAGTTTCTCAACTGA
118211	116298	TTTCTATAGTTTCTCAACTG
118212	116299	CTTTCTATAGTTTCTCAACT
118213	116300	ACTTTCTATAGTTTCTCAAC
118214	116301	TACTTTCTATAGTTTCTCAA
118215	116302	CTACTTTCTATAGTTTCTCA
118216	116303	TCTACTTTCTATAGTTTCTC
118217	116304	TTCTACTTTCTATAGTTTCT
118218	116305	ATTCTACTTTCTATAGTTTC
118219	116306	TATTCTACTTTCTATAGTTT
118220	116307	TTATTCTACTTTCTATAGTT
118221	116308	ATTATTCTACTTTCTATAGT
118222	116309	AATTATTCTACTTTCTATAG
118223	116310	AAATTATTCTACTTTCTATA
118224	116311	TAAATTATTCTACTTTCTAT
118225	116312	ATAAATTATTCTACTTTCTA
118226	116313	TATAAATTATTCTACTTTCT
118227	116314	GTATAAATTATTCTACTTTC
118228	116315	TGTATAAATTATTCTACTTT
118229	116316	CTGTATAAATTATTCTACTT
118230	116317	TCTGTATAAATTATTCTACT
118231	116318	TTCTGTATAAATTATTCTAC
118232	116319	TTTCTGTATAAATTATTCTA
118233	116320	TTTTCTGTATAAATTATTCT
118234	116321	CTTTTCTGTATAAATTATTC
118235	116322	TCTTTTCTGTATAAATTATT
118236	116323	GTCTTTTCTGTATAAATTAT
118237	116324	TGTCTTTTCTGTATAAATTA
118238	116325	ATGTCTTTTCTGTATAAATT

19945	18032	GAAGTCTAGGGACAAGAAGA
19946	18033	TGAAGTCTAGGGACAAGAAG
19947	18034	GTGAAGTCTAGGGACAAGAA
19948	18035	CGTGAAGTCTAGGGACAAGA
19949	18036	CCGTGAAGTCTAGGGACAAG
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19951	18038	CTCCGTGAAGTCTAGGGACA
19952	18039	ACTCCGTGAAGTCTAGGGAC
19953	18040	TACTCCGTGAAGTCTAGGGA
19954	18041	CTACTCCGTGAAGTCTAGGG
19955	18042	CCTACTCCGTGAAGTCTAGG
19956	18043	GCCTACTCCGTGAAGTCTAG
19957	18044	GGCCTACTCCGTGAAGTCTA
19958	18045	TGGCCTACTCCGTGAAGTCT
19959	18046	TTGGCCTACTCCGTGAAGTC
19960	18047	ATTGGCCTACTCCGTGAAGT
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19962	18049	GCATTGGCCTACTCCGTGAA
19963	18050	AGCATTGGCCTACTCCGTGA
19964	18051	TAGCATTGGCCTACTCCGTG
19965	18052	ATAGCATTGGCCTACTCCGT
19966	18053	CATAGCATTGGCCTACTCCG
19967	18054	TCATAGCATTGGCCTACTCC
19968	18055	TTCATAGCATTGGCCTACTC
19969	18056	CTTCATAGCATTGGCCTACT
19970	18057	GCTTCATAGCATTGGCCTAC
19971	18058	GGCTTCATAGCATTGGCCTA
19972	18059	GGGCTTCATAGCATTGGCCT
19973	18060	TGGGCTTCATAGCATTGGCC
19974	18061	CTGGGCTTCATAGCATTGGC
19975	18062	CCTGGGCTTCATAGCATTGG
19976	18063	GCCTGGGCTTCATAGCATTG
19977	18064	TGCCTGGGCTTCATAGCATT
19978	18065	CTGCCTGGGCTTCATAGCAT
19979	18066	GCTGCCTGGGCTTCATAGCA
19980	18067	TGCTGCCTGGGCTTCATAGC
19981	18068	CTGCTGCCTGGGCTTCATAG
19982	18069	CCTGCTGCCTGGGCTTCATA
19983	18070	TCCTGCTGCCTGGGCTTCAT
19984	18071	CTCCTGCTGCCTGGGCTTCA
19985	18072	ACTCCTGCTGCCTGGGCTTC
19986	18073	AACTCCTGCTGCCTGGGCTT
19987	18074	GAACTCCTGCTGCCTGGGCT
19988	18075	TGAACTCCTGCTGCCTGGGC
19989	18076	ATGAACTCCTGCTGCCTGGG
19990	18077	CATGAACTCCTGCTGCCTGG
19991	18078	TCATGAACTCCTGCTGCCTG
19992	18079	TTCATGAACTCCTGCTGCCT
19993	18080	CTTCATGAACTCCTGCTGCC
19994	18081	ACTTCATGAACTCCTGCTGC
19995	18082	CACTTCATGAACTCCTGCTG
19996	18083	CCACTTCATGAACTCCTGCT
19997	18084	CCCACTTCATGAACTCCTGC
19998	18085	ACCCACTTCATGAACTCCTG
19999	18086	CACCCACTTCATGAACTCCT
20000	18087	ACACCCACTTCATGAACTCC
20001	18088	AACACCCACTTCATGAACTC
20002	18089	CAACACCCACTTCATGAACT
20003	18090	TCAACACCCACTTCATGAAC
20004	18091	TTCAACACCCACTTCATGAA
20005	18092	GTTCAACACCCACTTCATGA
20006	18093	TGTTCAACACCCACTTCATG
20007	18094	CTGTTCAACACCCACTTCAT
20008	18095	CCTGTTCAACACCCACTTCA
20009	18096	CCCTGTTCAACACCCACTTC
20010	18097	TCCCTGTTCAACACCCACTT
20011	18098	GTCCCTGTTCAACACCCACT
20012	18099	GGTCCCTGTTCAACACCCAC
20013	18100	TGGTCCCTGTTCAACACCCA
20014	18101	CTGGTCCCTGTTCAACACCC
20015	18102	TCTGGTCCCTGTTCAACACC

69092	67179	CTCAAAAATATATATACATA
69093	67180	TCTCAAAAATATATATACAT
69094	67181	ATCTCAAAAATATATATACA
69095	67182	CATCTCAAAAATATATATAC
69096	67183	CCATCTCAAAAATATATATA
69097	67184	TCCATCTCAAAAATATATAT
69098	67185	CTCCATCTCAAAAATATATA
69099	67186	ACTCCATCTCAAAAATATAT
69100	67187	GACTCCATCTCAAAAATATA
69101	67188	AGACTCCATCTCAAAAATAT
69102	67189	GAGACTCCATCTCAAAAATA
69103	67190	CGAGACTCCATCTCAAAAAT
69104	67191	GCGAGACTCCATCTCAAAAA
69105	67192	AGCGAGACTCCATCTCAAAA
69106	67193	GAGCGAGACTCCATCTCAAA
69107	67194	AGAGCGAGACTCCATCTCAA
69108	67195	CAGAGCGAGACTCCATCTCA
69109	67196	ACAGAGCGAGACTCCATCTC
69110	67197	GACAGAGCGAGACTCCATCT
69111	67198	AGACAGAGCGAGACTCCATC
69112	67199	GAGACAGAGCGAGACTCCAT
69113	67200	GGAGACAGAGCGAGACTCCA
69114	67201	GGGAGACAGAGCGAGACTCC
69115	67202	TGGGAGACAGAGCGAGACTC
69116	67203	CTGGGAGACAGAGCGAGACT
69117	67204	CCTGGGAGACAGAGCGAGAC
69118	67205	GCCTGGGAGACAGAGCGAGA
69119	67206	AGCCTGGGAGACAGAGCGAG
69120	67207	CAGCCTGGGAGACAGAGCGA
69121	67208	TCAGCCTGGGAGACAGAGCG
69122	67209	CTCAGCCTGGGAGACAGAGC
69123	67210	ACTCAGCCTGGGAGACAGAG
69124	67211	CACTCAGCCTGGGAGACAGA
69125	67212	GCACTCAGCCTGGGAGACAG
69126	67213	TGCACTCAGCCTGGGAGACA
69127	67214	CTGCACTCAGCCTGGGAGAC
69128	67215	ACTGCACTCAGCCTGGGAGA
69129	67216	CACTGCACTCAGCCTGGGAG
69130	67217	CCACTGCACTCAGCCTGGGA
69131	67218	ACCACTGCACTCAGCCTGGG
69132	67219	CACCACTGCACTCAGCCTGG
69133	67220	GCACCACTGCACTCAGCCTG
69134	67221	TGCACCACTGCACTCAGCCT
69135	67222	CTGCACCACTGCACTCAGCC
69136	67223	ACTGCACCACTGCACTCAGC
69137	67224	GACTGCACCACTGCACTCAG
69138	67225	AGACTGCACCACTGCACTCA
69139	67226	GAGACTGCACCACTGCACTC
69140	67227	TGAGACTGCACCACTGCACT
69141	67228	CTGAGACTGCACCACTGCAC
69142	67229	GCTGAGACTGCACCACTGCA
69143	67230	GGCTGAGACTGCACCACTGC
69144	67231	GGGCTGAGACTGCACCACTG
69145	67232	TGGGCTGAGACTGCACCACT
69146	67233	ATGGGCTGAGACTGCACCAC
69147	67234	AATGGGCTGAGACTGCACCA
69148	67235	CAATGGGCTGAGACTGCACC
69149	67236	GCAATGGGCTGAGACTGCAC
69150	67237	TGCAATGGGCTGAGACTGCA
69151	67238	TTGCAATGGGCTGAGACTGC
69152	67239	GTTGCAATGGGCTGAGACTG
69153	67240	GGTTGCAATGGGCTGAGACT
69154	67241	AGGTTGCAATGGGCTGAGAC
69155	67242	GAGGTTGCAATGGGCTGAGA
69156	67243	AGAGGTTGCAATGGGCTGAG
69157	67244	CAGAGGTTGCAATGGGCTGA
69158	67245	GCAGAGGTTGCAATGGGCTG
69159	67246	GGCAGAGGTTGCAATGGGCT
69160	67247	AGGCAGAGGTTGCAATGGGC
69161	67248	GAGGCAGAGGTTGCAATGGG
69162	67249	GGAGGCAGAGGTTGCAATGG

118239	116326	AATGTCTTTTCTGTATAAAT
118240	116327	AAATGTCTTTTCTGTATAAA
118241	116328	GAAATGTCTTTTCTGTATAA
118242	116329	AGAAATGTCTTTTCTGTATA
118243	116330	GAGAAATGTCTTTTCTGTAT
118244	116331	TGAGAAATGTCTTTTCTGTA
118245	116332	CTGAGAAATGTCTTTTCTGT
118246	116333	ACTGAGAAATGTCTTTTCTG
118247	116334	CACTGAGAAATGTCTTTTCT
118248	116335	GCACTGAGAAATGTCTTTTC
118249	116336	GGCACTGAGAAATGTCTTTT
118250	116337	GGGCACTGAGAAATGTCTTT
118251	116338	TGGGCACTGAGAAATGTCTT
118252	116339	TTGGGCACTGAGAAATGTCT
118253	116340	ATTGGGCACTGAGAAATGTC
118254	116341	TATTGGGCACTGAGAAATGT
118255	116342	TTATTGGGCACTGAGAAATG
118256	116343	ATTATTGGGCACTGAGAAAT
118257	116344	AATTATTGGGCACTGAGAAA
118258	116345	CAATTATTGGGCACTGAGAA
118259	116346	GCAATTATTGGGCACTGAGA
118260	116347	GGCAATTATTGGGCACTGAG
118261	116348	AGGCAATTATTGGGCACTGA
118262	116349	AAGGCAATTATTGGGCACTG
118263	116350	AAAGGCAATTATTGGGCACT
118264	116351	GAAAGGCAATTATTGGGCAC
118265	116352	AGAAAGGCAATTATTGGGCA
118266	116353	CAGAAAGGCAATTATTGGGC
118267	116354	TCAGAAAGGCAATTATTGGG
118268	116355	GTCAGAAAGGCAATTATTGG
118269	116356	TGTCAGAAAGGCAATTATTG
118270	116357	ATGTCAGAAAGGCAATTATT
118271	116358	TATGTCAGAAAGGCAATTAT
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118275	116362	ACTTTATGTCAGAAAGGCAA
118276	116363	AACTTTATGTCAGAAAGGCA
118277	116364	AAACTTTATGTCAGAAAGGC
118278	116365	AAAACTTTATGTCAGAAAGG
118279	116366	GAAAACTTTATGTCAGAAAG
118280	116367	TGAAAACTTTATGTCAGAAA
118281	116368	ATGAAAACTTTATGTCAGAA
118282	116369	AATGAAAACTTTATGTCAGA
118283	116370	AAATGAAAACTTTATGTCAG
118284	116371	AAAATGAAAACTTTATGTCA
118285	116372	AAAAATGAAAACTTTATGTC
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118287	116374	GGAAAAATGAAAACTTTATG
118288	116375	AGGAAAAATGAAAACTTTAT
118289	116376	CAGGAAAAATGAAAACTTTA
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118291	116378	TTCAGGAAAAATGAAAACTT
118292	116379	ATTCAGGAAAAATGAAAACT
118293	116380	AATTCAGGAAAAATGAAAAC
118294	116381	TAATTCAGGAAAAATGAAAA
118295	116382	TTAATTCAGGAAAAATGAAA
118296	116383	ATTAATTCAGGAAAAATGAA
118297	116384	TATTAATTCAGGAAAAATGA
118298	116385	TTATTAATTCAGGAAAAATG
118299	116386	CTTATTAATTCAGGAAAAAT
118300	116387	TCTTATTAATTCAGGAAAAA
118301	116388	ATCTTATTAATTCAGGAAAA
118302	116389	AATCTTATTAATTCAGGAAA
118303	116390	AAATCTTATTAATTCAGGAA
118304	116391	GAAATCTTATTAATTCAGGA
118305	116392	GGAAATCTTATTAATTCAGG
118306	116393	AGGAAATCTTATTAATTCAG
118307	116394	GAGGAAATCTTATTAATTCA
118308	116395	TGAGGAAATCTTATTAATTC
118309	116396	TTGAGGAAATCTTATTAATT

20016	18103	GTCTGGTCCCTGTTCAACAC
20017	18104	CGTCTGGTCCCTGTTCAACA
20018	18105	TCGTCTGGTCCCTGTTCAAC
20019	18106	GTCGTCTGGTCCCTGTTCAA
20020	18107	TGTCGTCTGGTCCCTGTTCA
20021	18108	ATGTCGTCTGGTCCCTGTTC
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20024	18111	ACCATGTCGTCTGGTCCCTG
20025	18112	GACCATGTCGTCTGGTCCCT
20026	18113	CGACCATGTCGTCTGGTCCC
20027	18114	CCGACCATGTCGTCTGGTCC
20028	18115	CCCGACCATGTCGTCTGGTC
20029	18116	GCCCGACCATGTCGTCTGGT
20030	18117	TGCCCGACCATGTCGTCTGG
20031	18118	GTGCCCGACCATGTCGTCTG
20032	18119	CGTGCCCGACCATGTCGTCT
20033	18120	CCGTGCCCGACCATGTCGTC
20034	18121	TCCGTGCCCGACCATGTCGT
20035	18122	CTCCGTGCCCGACCATGTCG
20036	18123	ACTCCGTGCCCGACCATGTC
20037	18124	AACTCCGTGCCCGACCATGT
20038	18125	GAACTCCGTGCCCGACCATG
20039	18126	AGAACTCCGTGCCCGACCAT
20040	18127	GAGAACTCCGTGCCCGACCA
20041	18128	CGAGAACTCCGTGCCCGACC
20042	18129	GCGAGAACTCCGTGCCCGAC
20043	18130	AGCGAGAACTCCGTGCCCGA
20044	18131	CAGCGAGAACTCCGTGCCCG
20045	18132	ACAGCGAGAACTCCGTGCCC
20046	18133	CACAGCGAGAACTCCGTGCC
20047	18134	CCACAGCGAGAACTCCGTGC
20048	18135	TCCACAGCGAGAACTCCGTG
20049	18136	ATCCACAGCGAGAACTCCGT
20050	18137	CATCCACAGCGAGAACTCCG
20051	18138	CCATCCACAGCGAGAACTCC
20052	18139	CCCATCCACAGCGAGAACTC
20053	18140	CCCCATCCACAGCGAGAACT
20054	18141	TCCCCATCCACAGCGAGAAC
20055	18142	ATCCCCATCCACAGCGAGAA
20056	18143	GATCCCCATCCACAGCGAGA
20057	18144	TGATCCCCATCCACAGCGAG
20058	18145	GTGATCCCCATCCACAGCGA
20059	18146	CGTGATCCCCATCCACAGCG
20060	18147	CCGTGATCCCCATCCACAGC
20061	18148	ACCGTGATCCCCATCCACAG
20062	18149	CACCGTGATCCCCATCCACA
20063	18150	CCACCGTGATCCCCATCCAC
20064	18151	TCCACCGTGATCCCCATCCA
20065	18152	GTCCACCGTGATCCCCATCC
20066	18153	TGTCCACCGTGATCCCCATC
20067	18154	ATGTCCACCGTGATCCCCAT
20068	18155	AATGTCCACCGTGATCCCCA
20069	18156	CAATGTCCACCGTGATCCCC
20070	18157	CCAATGTCCACCGTGATCCC
20071	18158	CCCAATGTCCACCGTGATCC
20072	18159	CCCCAATGTCCACCGTGATC
20073	18160	CCCCCAATGTCCACCGTGAT
20074	18161	TCCCCCAATGTCCACCGTGA
20075	18162	CTCCCCCAATGTCCACCGTG
20076	18163	GCTCCCCCAATGTCCACCGT
20077	18164	TGCTCCCCCAATGTCCACCG
20078	18165	CTGCTCCCCCAATGTCCACC
20079	18166	CCTGCTCCCCCAATGTCCAC
20080	18167	CCCTGCTCCCCCAATGTCCA
20081	18168	ACCCTGCTCCCCCAATGTCC
20082	18169	AACCCTGCTCCCCCAATGTC
20083	18170	CAACCCTGCTCCCCCAATGT
20084	18171	ACAACCCTGCTCCCCCAATG
20085	18172	CACAACCCTGCTCCCCCAAT
20086	18173	CCACAACCCTGCTCCCCCAA

69163	67250	AGGAGGCAGAGGTTGCAATG
69164	67251	CAGGAGGCAGAGGTTGCAAT
69165	67252	CCAGGAGGCAGAGGTTGCAA
69166	67253	CCCAGGAGGCAGAGGTTGCA
69167	67254	ACCCAGGAGGCAGAGGTTGC
69168	67255	AACCCAGGAGGCAGAGGTTG
69169	67256	GAACCCAGGAGGCAGAGGTT
69170	67257	TGAACCCAGGAGGCAGAGGT
69171	67258	TTGAACCCAGGAGGCAGAGG
69172	67259	TTTGAACCCAGGAGGCAGAG
69173	67260	GTTTGAACCCAGGAGGCAGA
69174	67261	CGTTTGAACCCAGGAGGCAG
69175	67262	TCGTTTGAACCCAGGAGGCA
69176	67263	ATCGTTTGAACCCAGGAGGC
69177	67264	AATCGTTTGAACCCAGGAGG
69178	67265	GAATCGTTTGAACCCAGGAG
69179	67266	AGAATCGTTTGAACCCAGGA
69180	67267	GAGAATCGTTTGAACCCAGG
69181	67268	GGAGAATCGTTTGAACCCAG
69182	67269	AGGAGAATCGTTTGAACCCA
69183	67270	CAGGAGAATCGTTTGAACCC
69184	67271	GCAGGAGAATCGTTTGAACC
69185	67272	GGCAGGAGAATCGTTTGAAC
69186	67273	AGGCAGGAGAATCGTTTGAA
69187	67274	GAGGCAGGAGAATCGTTTGA
69188	67275	TGAGGCAGGAGAATCGTTTG
69189	67276	CTGAGGCAGGAGAATCGTTT
69190	67277	GCTGAGGCAGGAGAATCGTT
69191	67278	GGCTGAGGCAGGAGAATCGT
69192	67279	AGGCTGAGGCAGGAGAATCG
69193	67280	GAGGCTGAGGCAGGAGAATC
69194	67281	GGAGGCTGAGGCAGGAGAAT
69195	67282	AGGAGGCTGAGGCAGGAGAA
69196	67283	CAGGAGGCTGAGGCAGGAGA
69197	67284	TCAGGAGGCTGAGGCAGGAG
69198	67285	CTCAGGAGGCTGAGGCAGGA
69199	67286	ACTCAGGAGGCTGAGGCAGG
69200	67287	TACTCAGGAGGCTGAGGCAG
69201	67288	CTACTCAGGAGGCTGAGGCA
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69203	67290	AGCTACTCAGGAGGCTGAGG
69204	67291	CAGCTACTCAGGAGGCTGAG
69205	67292	CCAGCTACTCAGGAGGCTGA
69206	67293	CCCAGCTACTCAGGAGGCTG
69207	67294	TCCCAGCTACTCAGGAGGCT
69208	67295	ATCCCAGCTACTCAGGAGGC
69209	67296	AATCCCAGCTACTCAGGAGG
69210	67297	TAATCCCAGCTACTCAGGAG
69211	67298	GTAATCCCAGCTACTCAGGA
69212	67299	TGTAATCCCAGCTACTCAGG
69213	67300	CTGTAATCCCAGCTACTCAG
69214	67301	CCTGTAATCCCAGCTACTCA
69215	67302	GCCTGTAATCCCAGCTACTC
69216	67303	CGCCTGTAATCCCAGCTACT
69217	67304	GCGCCTGTAATCCCAGCTAC
69218	67305	TGCGCCTGTAATCCCAGCTA
69219	67306	GTGCGCCTGTAATCCCAGCT
69220	67307	TGTGCGCCTGTAATCCCAGC
69221	67308	GTGTGCGCCTGTAATCCCAG
69222	67309	GGTGTGCGCCTGTAATCCCA
69223	67310	TGGTGTGCGCCTGTAATCCC
69224	67311	GTGGTGTGCGCCTGTAATCC
69225	67312	GGTGGTGTGCGCCTGTAATC
69226	67313	TGGTGGTGTGCGCCTGTAAT
69227	67314	GTGGTGGTGTGCGCCTGTAA
69228	67315	CGTGGTGGTGTGCGCCTGTA
69229	67316	GCGTGGTGGTGTGCGCCTGT
69230	67317	GGCGTGGTGGTGTGCGCCTG
69231	67318	AGGCGTGGTGGTGTGCGCCT
69232	67319	TAGGCGTGGTGGTGTGCGCC
69233	67320	CTAGGCGTGGTGGTGTGCGC

118310	116397	ATTGAGGAAATCTTATTAAT
118311	116398	CATTGAGGAAATCTTATTAA
118312	116399	ACATTGAGGAAATCTTATTA
118313	116400	CACATTGAGGAAATCTTATT
118314	116401	ACACATTGAGGAAATCTTAT
118315	116402	AACACATTGAGGAAATCTTA
118316	116403	AAACACATTGAGGAAATCTT
118317	116404	AAAACACATTGAGGAAATCT
118318	116405	AAAAACACATTGAGGAAATC
118319	116406	AAAAAACACATTGAGGAAAT
118320	116407	AAAAAAACACATTGAGGAAA
118321	116408	CAAAAAAACACATTGAGGAA
118322	116409	CCAAAAAAACACATTGAGGA
118323	116410	CCCAAAAAAACACATTGAGG
118324	116411	ACCCAAAAAAACACATTGAG
118325	116412	CACCCAAAAAAACACATTGA
118326	116413	ACACCCAAAAAAACACATTG
118327	116414	AACACCCAAAAAAACACATT
118328	116415	AAACACCCAAAAAAACACAT
118329	116416	AAAACACCCAAAAAAACACA
118330	116417	CAAAACACCCAAAAAAACAC
118331	116418	ACAAAACACCCAAAAAAACA
118332	116419	CACAAAACACCCAAAAAAAC
118333	116420	ACACAAAACACCCAAAAAAA
118334	116421	CACACAAAACACCCAAAAAA
118335	116422	ACACACAAAACACCCAAAAA
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118337	116424	ACACACACAAAACACCCAAA
118338	116425	CACACACACAAAACACCCAA
118339	116426	ACACACACACAAAACACCCA
118340	116427	CACACACACACAAAACACCC
118341	116428	ACACACACACACAAAACACC
118342	116429	CACACACACACACAAAACAC
118343	116430	ACACACACACACACAAAACA
118344	116431	CACACACACACACACAAAAC
118345	116432	ACACACACACACACACAAAA
118346	116433	CACACACACACACACACAAA
118347	116434	ACACACACACACACACACAA
118348	116435	CACACACACACACACACACA
118349	116436	ACACACACACACACACACAC
118350	116437	CACACACACACACACACACA
118351	116438	ACACACACACACACACACAC
118352	116439	CACACACACACACACACACA
118353	116440	ACACACACACACACACACAC
118354	116441	CACACACACACACACACACA
118355	116442	ACACACACACACACACACAC
118356	116443	CACACACACACACACACACA
118357	116444	ACACACACACACACACACAC
118358	116445	CACACACACACACACACACA
118359	116446	ACACACACACACACACACAC
118360	116447	CACACACACACACACACACA
118361	116448	ACACACACACACACACACAC
118362	116449	CACACACACACACACACACA
118363	116450	ACACACACACACACACACAC
118364	116451	CACACACACACACACACACA
118365	116452	ACACACACACACACACACAC
118366	116453	CACACACACACACACACACA
118367	116454	ACACACACACACACACACAC
118368	116455	CACACACACACACACACACA
118369	116456	ACACACACACACACACACAC
118370	116457	CACACACACACACACACACA
118371	116458	ACACACACACACACACACAC
118372	116459	CACACACACACACACACACA
118373	116460	ACACACACACACACACACAC
118374	116461	TACACACACACACACACACA
118375	116462	ATACACACACACACACACAC
118376	116463	CATACACACACACACACACA
118377	116464	ACATACACACACACACACAC
118378	116465	CACATACACACACACACACA
118379	116466	ACACATACACACACACACAC
118380	116467	AACACATACACACACACACA

20087	18174	CCCACAACCCTGCTCCCCCA
20088	18175	CCCCACAACCCTGCTCCCCC
20089	18176	ACCCCACAACCCTGCTCCCC
20090	18177	CACCCCACAACCCTGCTCCC
20091	18178	GCACCCCACAACCCTGCTCC
20092	18179	GGCACCCCACAACCCTGCTC
20093	18180	GGGCACCCCACAACCCTGCT
20094	18181	GGGGCACCCCACAACCCTGC
20095	18182	GGGGGCACCCCACAACCCTG
20096	18183	TGGGGGCACCCCACAACCCT
20097	18184	CTGGGGGCACCCCACAACCC
20098	18185	GCTGGGGGCACCCCACAACC
20099	18186	TGCTGGGGGCACCCCACAAC
20100	18187	GTGCTGGGGGCACCCCACAA
20101	18188	TGTGCTGGGGGCACCCCACA
20102	18189	CTGTGCTGGGGGCACCCCAC
20103	18190	GCTGTGCTGGGGGCACCCCA
20104	18191	GGCTGTGCTGGGGGCACCCC
20105	18192	TGGCTGTGCTGGGGGCACCC
20106	18193	GTGGCTGTGCTGGGGGCACC
20107	18194	GGTGGCTGTGCTGGGGGCAC
20108	18195	AGGTGGCTGTGCTGGGGGCA
20109	18196	GAGGTGGCTGTGCTGGGGGC
20110	18197	AGAGGTGGCTGTGCTGGGGG
20111	18198	AAGAGGTGGCTGTGCTGGGG
20112	18199	CAAGAGGTGGCTGTGCTGGG
20113	18200	GCAAGAGGTGGCTGTGCTGG
20114	18201	AGCAAGAGGTGGCTGTGCTG
20115	18202	GAGCAAGAGGTGGCTGTGCT
20116	18203	GGAGCAAGAGGTGGCTGTGC
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20118	18205	GAGGAGCAAGAGGTGGCTGT
20119	18206	GGAGGAGCAAGAGGTGGCTG
20120	18207	AGGAGGAGCAAGAGGTGGCT
20121	18208	AAGGAGGAGCAAGAGGTGGC
20122	18209	CAAGGAGGAGCAAGAGGTGG
20123	18210	TCAAGGAGGAGCAAGAGGTG
20124	18211	CTCAAGGAGGAGCAAGAGGT
20125	18212	GCTCAAGGAGGAGCAAGAGG
20126	18213	TGCTCAAGGAGGAGCAAGAG
20127	18214	ATGCTCAAGGAGGAGCAAGA
20128	18215	GATGCTCAAGGAGGAGCAAG
20129	18216	AGATGCTCAAGGAGGAGCAA
20130	18217	GAGATGCTCAAGGAGGAGCA
20131	18218	TGAGATGCTCAAGGAGGAGC
20132	18219	ATGAGATGCTCAAGGAGGAG
20133	18220	TATGAGATGCTCAAGGAGGA
20134	18221	CTATGAGATGCTCAAGGAGG
20135	18222	ACTATGAGATGCTCAAGGAG
20136	18223	AACTATGAGATGCTCAAGGA
20137	18224	TAACTATGAGATGCTCAAGG
20138	18225	CTAACTATGAGATGCTCAAG
20139	18226	CCTAACTATGAGATGCTCAA
20140	18227	CCCTAACTATGAGATGCTCA
20141	18228	CCCCTAACTATGAGATGCTC
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20143	18230	TCCCCCTAACTATGAGATGC
20144	18231	ATCCCCCTAACTATGAGATG
20145	18232	CATCCCCCTAACTATGAGAT
20146	18233	CCATCCCCCTAACTATGAGA
20147	18234	GCCATCCCCCTAACTATGAG
20148	18235	GGCCATCCCCCTAACTATGA
20149	18236	CGGCCATCCCCCTAACTATG
20150	18237	TCGGCCATCCCCCTAACTAT
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20152	18239	CATCGGCCATCCCCCTAACT
20153	18240	ACATCGGCCATCCCCCTAAC
20154	18241	AACATCGGCCATCCCCCTAA
20155	18242	CAACATCGGCCATCCCCCTA
20156	18243	CCAACATCGGCCATCCCCCT
20157	18244	GCCAACATCGGCCATCCCCC

69234	67321	GCTAGGCGTGGTGGTGTGCG
69235	67322	AGCTAGGCGTGGTGGTGTGC
69236	67323	TAGCTAGGCGTGGTGGTGTG
69237	67324	TTAGCTAGGCGTGGTGGTGT
69238	67325	ATTAGCTAGGCGTGGTGGTG
69239	67326	CATTAGCTAGGCGTGGTGGT
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69244	67331	ACAAACATTAGCTAGGCGTG
69245	67332	TACAAACATTAGCTAGGCGT
69246	67333	ATACAAACATTAGCTAGGCG
69247	67334	AATACAAACATTAGCTAGGC
69248	67335	AAATACAAACATTAGCTAGG
69249	67336	AAAATACAAACATTAGCTAG
69250	67337	GAAAATACAAACATTAGCTA
69251	67338	TGAAAATACAAACATTAGCT
69252	67339	CTGAAAATACAAACATTAGC
69253	67340	ACTGAAAATACAAACATTAG
69254	67341	TACTGAAAATACAAACATTA
69255	67342	CTACTGAAAATACAAACATT
69256	67343	TCTACTGAAAATACAAACAT
69257	67344	CTCTACTGAAAATACAAACA
69258	67345	TCTCTACTGAAAATACAAAC
69259	67346	TTCTCTACTGAAAATACAAA
69260	67347	CTTCTCTACTGAAAATACAA
69261	67348	CCTTCTCTACTGAAAATACA
69262	67349	CCCTTCTCTACTGAAAATAC
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69264	67351	ACCCCTTCTCTACTGAAAAT
69265	67352	AACCCCTTCTCTACTGAAAA
69266	67353	AAACCCCTTCTCTACTGAAA
69267	67354	GAAACCCCTTCTCTACTGAA
69268	67355	TGAAACCCCTTCTCTACTGA
69269	67356	GTGAAACCCCTTCTCTACTG
69270	67357	GGTGAAACCCCTTCTCTACT
69271	67358	TGGTGAAACCCCTTCTCTAC
69272	67359	ATGGTGAAACCCCTTCTCTA
69273	67360	TATGGTGAAACCCCTTCTCT
69274	67361	ATATGGTGAAACCCCTTCTC
69275	67362	AATATGGTGAAACCCCTTCT
69276	67363	CAATATGGTGAAACCCCTTC
69277	67364	CCAATATGGTGAAACCCCTT
69278	67365	GCCAATATGGTGAAACCCCT
69279	67366	GGCCAATATGGTGAAACCCC
69280	67367	TGGCCAATATGGTGAAACCC
69281	67368	CTGGCCAATATGGTGAAACC
69282	67369	CCTGGCCAATATGGTGAAAC
69283	67370	GCCTGGCCAATATGGTGAAA
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69285	67372	CAGCCTGGCCAATATGGTGA
69286	67373	CCAGCCTGGCCAATATGGTG
69287	67374	ACCAGCCTGGCCAATATGGT
69288	67375	GACCAGCCTGGCCAATATGG
69289	67376	TGACCAGCCTGGCCAATATG
69290	67377	GTGACCAGCCTGGCCAATAT
69291	67378	GGTGACCAGCCTGGCCAATA
69292	67379	TGGTGACCAGCCTGGCCAAT
69293	67380	TTGGTGACCAGCCTGGCCAA
69294	67381	GTTGGTGACCAGCCTGGCCA
69295	67382	AGTTGGTGACCAGCCTGGCC
69296	67383	GAGTTGGTGACCAGCCTGGC
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69298	67385	AGGAGTTGGTGACCAGCCTG
69299	67386	CAGGAGTTGGTGACCAGCCT
69300	67387	TCAGGAGTTGGTGACCAGCC
69301	67388	GTCAGGAGTTGGTGACCAGC
69302	67389	GGTCAGGAGTTGGTGACCAG
69303	67390	AGGTCAGGAGTTGGTGACCA
69304	67391	GAGGTCAGGAGTTGGTGACC

118381	116468	AAACACATACACACACACAC
118382	116469	CAAACACATACACACACACA
118383	116470	TCAAACACATACACACACAC
118384	116471	ATCAAACACATACACACACA
118385	116472	TATCAAACACATACACACAC
118386	116473	GTATCAAACACATACACACA
118387	116474	TGTATCAAACACATACACAC
118388	116475	CTGTATCAAACACATACACA
118389	116476	CCTGTATCAAACACATACAC
118390	116477	CCCTGTATCAAACACATACA
118391	116478	ACCCTGTATCAAACACATAC
118392	116479	GACCCTGTATCAAACACATA
118393	116480	AGACCCTGTATCAAACACAT
118394	116481	AAGACCCTGTATCAAACACA
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118396	116483	GCAAGACCCTGTATCAAACA
118397	116484	AGCAAGACCCTGTATCAAAC
118398	116485	AAGCAAGACCCTGTATCAAA
118399	116486	AAAGCAAGACCCTGTATCAA
118400	116487	CAAAGCAAGACCCTGTATCA
118401	116488	GCAAAGCAAGACCCTGTATC
118402	116489	AGCAAAGCAAGACCCTGTAT
118403	116490	CAGCAAAGCAAGACCCTGTA
118404	116491	GCAGCAAAGCAAGACCCTGT
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118406	116493	CAGCAGCAAAGCAAGACCCT
118407	116494	TCAGCAGCAAAGCAAGACCC
118408	116495	CTCAGCAGCAAAGCAAGACC
118409	116496	CCTCAGCAGCAAAGCAAGAC
118410	116497	GCCTCAGCAGCAAAGCAAGA
118411	116498	AGCCTCAGCAGCAAAGCAAG
118412	116499	CAGCCTCAGCAGCAAAGCAA
118413	116500	CCAGCCTCAGCAGCAAAGCA
118414	116501	TCCAGCCTCAGCAGCAAAGC
118415	116502	TTCCAGCCTCAGCAGCAAAG
118416	116503	GTTCCAGCCTCAGCAGCAAA
118417	116504	CGTTCCAGCCTCAGCAGCAA
118418	116505	GCGTTCCAGCCTCAGCAGCA
118419	116506	TGCGTTCCAGCCTCAGCAGC
118420	116507	CTGCGTTCCAGCCTCAGCAG
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118426	116513	GCGCCACTGCGTTCCAGCCT
118427	116514	AGCGCCACTGCGTTCCAGCC
118428	116515	TAGCGCCACTGCGTTCCAGC
118429	116516	ATAGCGCCACTGCGTTCCAG
118430	116517	GATAGCGCCACTGCGTTCCA
118431	116518	TGATAGCGCCACTGCGTTCC
118432	116519	ATGATAGCGCCACTGCGTTC
118433	116520	CATGATAGCGCCACTGCGTT
118434	116521	CCATGATAGCGCCACTGCGT
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118440	116527	ATTGAGCCATGATAGCGCCA
118441	116528	CATTGAGCCATGATAGCGCC
118442	116529	GCATTGAGCCATGATAGCGC
118443	116530	TGCATTGAGCCATGATAGCG
118444	116531	CTGCATTGAGCCATGATAGC
118445	116532	GCTGCATTGAGCCATGATAG
118446	116533	GGCTGCATTGAGCCATGATA
118447	116534	AGGCTGCATTGAGCCATGAT
118448	116535	AAGGCTGCATTGAGCCATGA
118449	116536	CAAGGCTGCATTGAGCCATG
118450	116537	TCAAGGCTGCATTGAGCCAT
118451	116538	GTCAAGGCTGCATTGAGCCA

20158	18245	TGCCAACATCGGCCATCCCC
20159	18246	CTGCCAACATCGGCCATCCC
20160	18247	CCTGCCAACATCGGCCATCC
20161	18248	TCCTGCCAACATCGGCCATC
20162	18249	CTCCTGCCAACATCGGCCAT
20163	18250	ACTCCTGCCAACATCGGCCA
20164	18251	CACTCCTGCCAACATCGGCC
20165	18252	TCACTCCTGCCAACATCGGC
20166	18253	TTCACTCCTGCCAACATCGG
20167	18254	CTTCACTCCTGCCAACATCG
20168	18255	TCTTCACTCCTGCCAACATC
20169	18256	CTCTTCACTCCTGCCAACAT
20170	18257	CCTCTTCACTCCTGCCAACA
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20172	18259	AACCTCTTCACTCCTGCCAA
20173	18260	AAACCTCTTCACTCCTGCCA
20174	18261	CAAACCTCTTCACTCCTGCC
20175	18262	CCAAACCTCTTCACTCCTGC
20176	18263	TCCAAACCTCTTCACTCCTG
20177	18264	GTCCAAACCTCTTCACTCCT
20178	18265	TGTCCAAACCTCTTCACTCC
20179	18266	ATGTCCAAACCTCTTCACTC
20180	18267	AATGTCCAAACCTCTTCACT
20181	18268	CAATGTCCAAACCTCTTCAC
20182	18269	ACAATGTCCAAACCTCTTCA
20183	18270	CACAATGTCCAAACCTCTTC
20184	18271	CCACAATGTCCAAACCTCTT
20185	18272	ACCACAATGTCCAAACCTCT
20186	18273	AACCACAATGTCCAAACCTC
20187	18274	GAACCACAATGTCCAAACCT
20188	18275	TGAACCACAATGTCCAAACC
20189	18276	ATGAACCACAATGTCCAAAC
20190	18277	CATGAACCACAATGTCCAAA
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20192	18279	ACCATGAACCACAATGTCCA
20193	18280	CACCATGAACCACAATGTCC
20194	18281	ACACCATGAACCACAATGTC
20195	18282	GACACCATGAACCACAATGT
20196	18283	GGACACCATGAACCACAATG
20197	18284	TGGACACCATGAACCACAAT
20198	18285	CTGGACACCATGAACCACAA
20199	18286	CCTGGACACCATGAACCACA
20200	18287	CCCTGGACACCATGAACCAC
20201	18288	TCCCTGGACACCATGAACCA
20202	18289	TTCCCTGGACACCATGAACC
20203	18290	CTTCCCTGGACACCATGAAC
20204	18291	TCTTCCCTGGACACCATGAA
20205	18292	GTCTTCCCTGGACACCATGA
20206	18293	GGTCTTCCCTGGACACCATG
20207	18294	TGGTCTTCCCTGGACACCAT
20208	18295	CTGGTCTTCCCTGGACACCA
20209	18296	GCTGGTCTTCCCTGGACACC
20210	18297	AGCTGGTCTTCCCTGGACAC
20211	18298	CAGCTGGTCTTCCCTGGACA
20212	18299	ACAGCTGGTCTTCCCTGGAC
20213	18300	CACAGCTGGTCTTCCCTGGA
20214	18301	CCACAGCTGGTCTTCCCTGG
20215	18302	ACCACAGCTGGTCTTCCCTG
20216	18303	GACCACAGCTGGTCTTCCCT
20217	18304	CGACCACAGCTGGTCTTCCC
20218	18305	CCGACCACAGCTGGTCTTCC
20219	18306	CCCGACCACAGCTGGTCTTC
20220	18307	ACCCGACCACAGCTGGTCTT
20221	18308	AACCCGACCACAGCTGGTCT
20222	18309	CAACCCGACCACAGCTGGTC
20223	18310	GCAACCCGACCACAGCTGGT
20224	18311	AGCAACCCGACCACAGCTGG
20225	18312	CAGCAACCCGACCACAGCTG
20226	18313	CCAGCAACCCGACCACAGCT
20227	18314	CCCAGCAACCCGACCACAGC
20228	18315	CCCCAGCAACCCGACCACAG

69305	67392	TGAGGTCAGGAGTTGGTGAC
69306	67393	TTGAGGTCAGGAGTTGGTGA
69307	67394	CTTGAGGTCAGGAGTTGGTG
69308	67395	ACTTGAGGTCAGGAGTTGGT
69309	67396	CACTTGAGGTCAGGAGTTGG
69310	67397	TCACTTGAGGTCAGGAGTTG
69311	67398	ATCACTTGAGGTCAGGAGTT
69312	67399	GATCACTTGAGGTCAGGAGT
69313	67400	GGATCACTTGAGGTCAGGAG
69314	67401	CGGATCACTTGAGGTCAGGA
69315	67402	GCGGATCACTTGAGGTCAGG
69316	67403	GGCGGATCACTTGAGGTCAG
69317	67404	AGGCGGATCACTTGAGGTCA
69318	67405	CAGGCGGATCACTTGAGGTC
69319	67406	GCAGGCGGATCACTTGAGGT
69320	67407	GGCAGGCGGATCACTTGAGG
69321	67408	AGGCAGGCGGATCACTTGAG
69322	67409	AAGGCAGGCGGATCACTTGA
69323	67410	CAAGGCAGGCGGATCACTTG
69324	67411	CCAAGGCAGGCGGATCACTT
69325	67412	GCCAAGGCAGGCGGATCACT
69326	67413	AGCCAAGGCAGGCGGATCAC
69327	67414	AAGCCAAGGCAGGCGGATCA
69328	67415	GAAGCCAAGGCAGGCGGATC
69329	67416	GGAAGCCAAGGCAGGCGGAT
69330	67417	TGGAAGCCAAGGCAGGCGGA
69331	67418	TTGGAAGCCAAGGCAGGCGG
69332	67419	TTTGGAAGCCAAGGCAGGCG
69333	67420	CTTTGGAAGCCAAGGCAGGC
69334	67421	ACTTTGGAAGCCAAGGCAGG
69335	67422	CACTTTGGAAGCCAAGGCAG
69336	67423	GCACTTTGGAAGCCAAGGCA
69337	67424	AGCACTTTGGAAGCCAAGGC
69338	67425	CAGCACTTTGGAAGCCAAGG
69339	67426	CCAGCACTTTGGAAGCCAAG
69340	67427	CCCAGCACTTTGGAAGCCAA
69341	67428	TCCCAGCACTTTGGAAGCCA
69342	67429	ATCCCAGCACTTTGGAAGCC
69343	67430	AATCCCAGCACTTTGGAAGC
69344	67431	TAATCCCAGCACTTTGGAAG
69345	67432	GTAATCCCAGCACTTTGGAA
69346	67433	TGTAATCCCAGCACTTTGGA
69347	67434	CTGTAATCCCAGCACTTTGG
69348	67435	CCTGTAATCCCAGCACTTTG
69349	67436	ACCTGTAATCCCAGCACTTT
69350	67437	CACCTGTAATCCCAGCACTT
69351	67438	ACACCTGTAATCCCAGCACT
69352	67439	CACACCTGTAATCCCAGCAC
69353	67440	TCACACCTGTAATCCCAGCA
69354	67441	CTCACACCTGTAATCCCAGC
69355	67442	GCTCACACCTGTAATCCCAG
69356	67443	GGCTCACACCTGTAATCCCA
69357	67444	TGGCTCACACCTGTAATCCC
69358	67445	GTGGCTCACACCTGTAATCC
69359	67446	GGTGGCTCACACCTGTAATC
69360	67447	CGGTGGCTCACACCTGTAAT
69361	67448	GCGGTGGCTCACACCTGTAA
69362	67449	TGCGGTGGCTCACACCTGTA
69363	67450	GTGCGGTGGCTCACACCTGT
69364	67451	GGTGCGGTGGCTCACACCTG
69365	67452	GGGTGCGGTGGCTCACACCT
69366	67453	CGGGTGCGGTGGCTCACACC
69367	67454	CCGGGTGCGGTGGCTCACAC
69368	67455	GCCGGGTGCGGTGGCTCACA
69369	67456	GGCCGGGTGCGGTGGCTCAC
69370	67457	AGGCCGGGTGCGGTGGCTCA
69371	67458	GAGGCCGGGTGCGGTGGCTC
69372	67459	TGAGGCCGGGTGCGGTGGCT
69373	67460	TTGAGGCCGGGTGCGGTGGC
69374	67461	TTTGAGGCCGGGTGCGGTGG
69375	67462	ATTTGAGGCCGGGTGCGGTG

118452	116539	GGTCAAGGCTGCATTGAGCC
118453	116540	AGGTCAAGGCTGCATTGAGC
118454	116541	GAGGTCAAGGCTGCATTGAG
118455	116542	GGAGGTCAAGGCTGCATTGA
118456	116543	AGGAGGTCAAGGCTGCATTG
118457	116544	CAGGAGGTCAAGGCTGCATT
118458	116545	CCAGGAGGTCAAGGCTGCAT
118459	116546	CCCAGGAGGTCAAGGCTGCA
118460	116547	GCCCAGGAGGTCAAGGCTGC
118461	116548	AGCCCAGGAGGTCAAGGCTG
118462	116549	GAGCCCAGGAGGTCAAGGCT
118463	116550	TGAGCCCAGGAGGTCAAGGC
118464	116551	TTGAGCCCAGGAGGTCAAGG
118465	116552	CTTGAGCCCAGGAGGTCAAG
118466	116553	GCTTGAGCCCAGGAGGTCAA
118467	116554	CGCTTGAGCCCAGGAGGTCA
118468	116555	TCGCTTGAGCCCAGGAGGTC
118469	116556	ATCGCTTGAGCCCAGGAGGT
118470	116557	GATCGCTTGAGCCCAGGAGG
118471	116558	GGATCGCTTGAGCCCAGGAG
118472	116559	AGGATCGCTTGAGCCCAGGA
118473	116560	GAGGATCGCTTGAGCCCAGG
118474	116561	GGAGGATCGCTTGAGCCCAG
118475	116562	GGGAGGATCGCTTGAGCCCA
118476	116563	AGGGAGGATCGCTTGAGCCC
118477	116564	AAGGGAGGATCGCTTGAGCC
118478	116565	GAAGGGAGGATCGCTTGAGC
118479	116566	AGAAGGGAGGATCGCTTGAG
118480	116567	GAGAAGGGAGGATCGCTTGA
118481	116568	TGAGAAGGGAGGATCGCTTG
118482	116569	CTGAGAAGGGAGGATCGCTT
118483	116570	ACTGAGAAGGGAGGATCGCT
118484	116571	GACTGAGAAGGGAGGATCGC
118485	116572	GGACTGAGAAGGGAGGATCG
118486	116573	GGGACTGAGAAGGGAGGATC
118487	116574	GGGGACTGAGAAGGGAGGAT
118488	116575	AGGGGACTGAGAAGGGAGGA
118489	116576	CAGGGGACTGAGAAGGGAGG
118490	116577	CCAGGGGACTGAGAAGGGAG
118491	116578	TCCAGGGGACTGAGAAGGGA
118492	116579	ATCCAGGGGACTGAGAAGGG
118493	116580	TATCCAGGGGACTGAGAAGG
118494	116581	CTATCCAGGGGACTGAGAAG
118495	116582	GCTATCCAGGGGACTGAGAA
118496	116583	CGCTATCCAGGGGACTGAGA
118497	116584	CCGCTATCCAGGGGACTGAG
118498	116585	CCCGCTATCCAGGGGACTGA
118499	116586	CCCCGCTATCCAGGGGACTG
118500	116587	CCCCCGCTATCCAGGGGACT
118501	116588	GCCCCCGCTATCCAGGGGAC
118502	116589	AGCCCCCGCTATCCAGGGGA
118503	116590	TAGCCCCCGCTATCCAGGGG
118504	116591	GTAGCCCCCGCTATCCAGGG
118505	116592	TGTAGCCCCCGCTATCCAGG
118506	116593	CTGTAGCCCCCGCTATCCAG
118507	116594	CCTGTAGCCCCCGCTATCCA
118508	116595	ACCTGTAGCCCCCGCTATCC
118509	116596	CACCTGTAGCCCCCGCTATC
118510	116597	GCACCTGTAGCCCCCGCTAT
118511	116598	TGCACCTGTAGCCCCCGCTA
118512	116599	GTGCACCTGTAGCCCCCGCT
118513	116600	TGTGCACCTGTAGCCCCCGC
118514	116601	GTGTGCACCTGTAGCCCCCG
118515	116602	GGTGTGCACCTGTAGCCCCC
118516	116603	TGGTGTGCACCTGTAGCCCC
118517	116604	GTGGTGTGCACCTGTAGCCC
118518	116605	GGTGGTGTGCACCTGTAGCC
118519	116606	TGGTGGTGTGCACCTGTAGC
118520	116607	GTGGTGGTGTGCACCTGTAG
118521	116608	TGTGGTGGTGTGCACCTGTA
118522	116609	GTGTGGTGGTGTGCACCTGT

20229	18316	ACCCCAGCAACCCGACCACA
20230	18317	CACCCCAGCAACCCGACCAC
20231	18318	CCACCCCAGCAACCCGACCA
20232	18319	ACCACCCCAGCAACCCGACC
20233	18320	AACCACCCCAGCAACCCGAC
20234	18321	GAACCACCCCAGCAACCCGA
20235	18322	AGAACCACCCCAGCAACCCG
20236	18323	GAGAACCACCCCAGCAACCC
20237	18324	TGAGAACCACCCCAGCAACC
20238	18325	CTGAGAACCACCCCAGCAAC
20239	18326	ACTGAGAACCACCCCAGCAA
20240	18327	CACTGAGAACCACCCCAGCA
20241	18328	CCACTGAGAACCACCCCAGC
20242	18329	CCCACTGAGAACCACCCCAG
20243	18330	GCCCACTGAGAACCACCCCA
20244	18331	GGCCCACTGAGAACCACCCC
20245	18332	GGGCCCACTGAGAACCACCC
20246	18333	GGGGCCCACTGAGAACCACC
20247	18334	AGGGGCCCACTGAGAACCAC
20248	18335	GAGGGGCCCACTGAGAACCA
20249	18336	GGAGGGGCCCACTGAGAACC
20250	18337	GGGAGGGGCCCACTGAGAAC
20251	18338	AGGGAGGGGCCCACTGAGAA
20252	18339	AAGGGAGGGGCCCACTGAGA
20253	18340	AAAGGGAGGGGCCCACTGAG
20254	18341	GAAAGGGAGGGGCCCACTGA
20255	18342	GGAAAGGGAGGGGCCCACTG
20256	18343	GGGAAAGGGAGGGGCCCACT
20257	18344	AGGGAAAGGGAGGGGCCCAC
20258	18345	CAGGGAAAGGGAGGGGCCCA
20259	18346	CCAGGGAAAGGGAGGGGCCC
20260	18347	ACCAGGGAAAGGGAGGGGCC
20261	18348	TACCAGGGAAAGGGAGGGGC
20262	18349	CTACCAGGGAAAGGGAGGGG
20263	18350	ACTACCAGGGAAAGGGAGGG
20264	18351	AACTACCAGGGAAAGGGAGG
20265	18352	AAACTACCAGGGAAAGGGAG
20266	18353	CAAACTACCAGGGAAAGGGA
20267	18354	CCAAACTACCAGGGAAAGGG
20268	18355	TCCAAACTACCAGGGAAAGG
20269	18356	ATCCAAACTACCAGGGAAAG
20270	18357	AATCCAAACTACCAGGGAAA
20271	18358	AAATCCAAACTACCAGGGAA
20272	18359	GAAATCCAAACTACCAGGGA
20273	18360	AGAAATCCAAACTACCAGGG
20274	18361	GAGAAATCCAAACTACCAGG
20275	18362	AGAGAAATCCAAACTACCAG
20276	18363	CAGAGAAATCCAAACTACCA
20277	18364	CCAGAGAAATCCAAACTACC
20278	18365	GCCAGAGAAATCCAAACTAC
20279	18366	AGCCAGAGAAATCCAAACTA
20280	18367	GAGCCAGAGAAATCCAAACT
20281	18368	AGAGCCAGAGAAATCCAAAC
20282	18369	CAGAGCCAGAGAAATCCAAA
20283	18370	CCAGAGCCAGAGAAATCCAA
20284	18371	ACCAGAGCCAGAGAAATCCA
20285	18372	CACCAGAGCCAGAGAAATCC
20286	18373	CCACCAGAGCCAGAGAAATC
20287	18374	ACCACCAGAGCCAGAGAAAT
20288	18375	AACCACCAGAGCCAGAGAAA
20289	18376	AAACCACCAGAGCCAGAGAA
20290	18377	AAAACCACCAGAGCCAGAGA
20291	18378	AAAAACCACCAGAGCCAGAG
20292	18379	AAAAAACCACCAGAGCCAGA
20293	18380	TAAAAAACCACCAGAGCCAG
20294	18381	CTAAAAAACCACCAGAGCCA
20295	18382	ACTAAAAAACCACCAGAGCC
20296	18383	TACTAAAAAACCACCAGAGC
20297	18384	GTACTAAAAAACCACCAGAG
20298	18385	AGTACTAAAAAACCACCAGA
20299	18386	GAGTACTAAAAAACCACCAG

69376	67463	AATTTGAGGCCGGGTGCGGT
69377	67464	TAATTTGAGGCCGGGTGCGG
69378	67465	ATAATTTGAGGCCGGGTGCG
69379	67466	AATAATTTGAGGCCGGGTGC
69380	67467	AAATAATTTGAGGCCGGGTG
69381	67468	AAAATAATTTGAGGCCGGGT
69382	67469	AAAAATAATTTGAGGCCGGG
69383	67470	TAAAAATAATTTGAGGCCGG
69384	67471	CTAAAAATAATTTGAGGCCG
69385	67472	TCTAAAAATAATTTGAGGCC
69386	67473	TTCTAAAAATAATTTGAGGC
69387	67474	TTTCTAAAAATAATTTGAGG
69388	67475	GTTTCTAAAAATAATTTGAG
69389	67476	TGTTTCTAAAAATAATTTGA
69390	67477	CTGTTTCTAAAAATAATTTG
69391	67478	TCTGTTTCTAAAAATAATTT
69392	67479	TTCTGTTTCTAAAAATAATT
69393	67480	ATTCTGTTTCTAAAAATAAT
69394	67481	GATTCTGTTTCTAAAAATAA
69395	67482	AGATTCTGTTTCTAAAAATA
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69398	67485	TCAAGATTCTGTTTCTAAAA
69399	67486	ATCAAGATTCTGTTTCTAAA
69400	67487	TATCAAGATTCTGTTTCTAA
69401	67488	ATATCAAGATTCTGTTTCTA
69402	67489	CATATCAAGATTCTGTTTCT
69403	67490	CCATATCAAGATTCTGTTTC
69404	67491	ACCATATCAAGATTCTGTTT
69405	67492	TACCATATCAAGATTCTGTT
69406	67493	ATACCATATCAAGATTCTGT
69407	67494	GATACCATATCAAGATTCTG
69408	67495	GGATACCATATCAAGATTCT
69409	67496	CGGATACCATATCAAGATTC
69410	67497	GCGGATACCATATCAAGATT
69411	67498	AGCGGATACCATATCAAGAT
69412	67499	GAGCGGATACCATATCAAGA
69413	67500	AGAGCGGATACCATATCAAG
69414	67501	CAGAGCGGATACCATATCAA
69415	67502	CCAGAGCGGATACCATATCA
69416	67503	GCCAGAGCGGATACCATATC
69417	67504	GGCCAGAGCGGATACCATAT
69418	67505	AGGCCAGAGCGGATACCATA
69419	67506	AAGGCCAGAGCGGATACCAT
69420	67507	CAAGGCCAGAGCGGATACCA
69421	67508	TCAAGGCCAGAGCGGATACC
69422	67509	TTCAAGGCCAGAGCGGATAC
69423	67510	GTTCAAGGCCAGAGCGGATA
69424	67511	AGTTCAAGGCCAGAGCGGAT
69425	67512	AAGTTCAAGGCCAGAGCGGA
69426	67513	CAAGTTCAAGGCCAGAGCGG
69427	67514	ACAAGTTCAAGGCCAGAGCG
69428	67515	CACAAGTTCAAGGCCAGAGC
69429	67516	CCACAAGTTCAAGGCCAGAG
69430	67517	CCCACAAGTTCAAGGCCAGA
69431	67518	GCCCACAAGTTCAAGGCCAG
69432	67519	AGCCCACAAGTTCAAGGCCA
69433	67520	GAGCCCACAAGTTCAAGGCC
69434	67521	TGAGCCCACAAGTTCAAGGC
69435	67522	CTGAGCCCACAAGTTCAAGG
69436	67523	CCTGAGCCCACAAGTTCAAG
69437	67524	GCCTGAGCCCACAAGTTCAA
69438	67525	TGCCTGAGCCCACAAGTTCA
69439	67526	CTGCCTGAGCCCACAAGTTC
69440	67527	ACTGCCTGAGCCCACAAGTT
69441	67528	GACTGCCTGAGCCCACAAGT
69442	67529	GGACTGCCTGAGCCCACAAG
69443	67530	AGGACTGCCTGAGCCCACAA
69444	67531	GAGGACTGCCTGAGCCCACA
69445	67532	GGAGGACTGCCTGAGCCCAC
69446	67533	GGGAGGACTGCCTGAGCCCA

118523	116610	GGTGTGGTGGTGTGCACCTG
118524	116611	AGGTGTGGTGGTGTGCACCT
118525	116612	TAGGTGTGGTGGTGTGCACC
118526	116613	CTAGGTGTGGTGGTGTGCAC
118527	116614	GCTAGGTGTGGTGGTGTGCA
118528	116615	AGCTAGGTGTGGTGGTGTGC
118529	116616	TAGCTAGGTGTGGTGGTGTG
118530	116617	TTAGCTAGGTGTGGTGGTGT
118531	116618	ATTAGCTAGGTGTGGTGGTG
118532	116619	AATTAGCTAGGTGTGGTGGT
118533	116620	AAATTAGCTAGGTGTGGTGG
118534	116621	AAAATTAGCTAGGTGTGGTG
118535	116622	AAAAATTAGCTAGGTGTGGT
118536	116623	CAAAAATTAGCTAGGTGTGG
118537	116624	ACAAAAATTAGCTAGGTGTG
118538	116625	TACAAAAATTAGCTAGGTGT
118539	116626	ATACAAAAATTAGCTAGGTG
118540	116627	AATACAAAAATTAGCTAGGT
118541	116628	AAATACAAAAATTAGCTAGG
118542	116629	AAAATACAAAAATTAGCTAG
118543	116630	AAAAATACAAAAATTAGCTA
118544	116631	AAAAAATACAAAAATTAGCT
118545	116632	CAAAAAATACAAAAATTAGC
118546	116633	ACAAAAAATACAAAAATTAG
118547	116634	TACAAAAAATACAAAAATTA
118548	116635	CTACAAAAAATACAAAAATT
118549	116636	TCTACAAAAAATACAAAAAT
118550	116637	CTCTACAAAAAATACAAAAA
118551	116638	TCTCTACAAAAAATACAAAA
118552	116639	ATCTCTACAAAAAATACAAA
118553	116640	CATCTCTACAAAAAATACAA
118554	116641	CCATCTCTACAAAAAATACA
118555	116642	CCCATCTCTACAAAAAATAC
118556	116643	ACCCATCTCTACAAAAAATA
118557	116644	AACCCATCTCTACAAAAAAT
118558	116645	AAACCCATCTCTACAAAAAA
118559	116646	AAAACCCATCTCTACAAAAA
118560	116647	CAAAACCCATCTCTACAAAA
118561	116648	GCAAAACCCATCTCTACAAA
118562	116649	GGCAAAACCCATCTCTACAA
118563	116650	TGGCAAAACCCATCTCTACA
118564	116651	ATGGCAAAACCCATCTCTAC
118565	116652	CATGGCAAAACCCATCTCTA
118566	116653	ACATGGCAAAACCCATCTCT
118567	116654	AACATGGCAAAACCCATCTC
118568	116655	CAACATGGCAAAACCCATCT
118569	116656	GCAACATGGCAAAACCCATC
118570	116657	GGCAACATGGCAAAACCCAT
118571	116658	AGGCAACATGGCAAAACCCA
118572	116659	TAGGCAACATGGCAAAACCC
118573	116660	CTAGGCAACATGGCAAAACC
118574	116661	CCTAGGCAACATGGCAAAAC
118575	116662	GCCTAGGCAACATGGCAAAA
118576	116663	AGCCTAGGCAACATGGCAAA
118577	116664	CAGCCTAGGCAACATGGCAA
118578	116665	CCAGCCTAGGCAACATGGCA
118579	116666	ACCAGCCTAGGCAACATGGC
118580	116667	GACCAGCCTAGGCAACATGG
118581	116668	AGACCAGCCTAGGCAACATG
118582	116669	GAGACCAGCCTAGGCAACAT
118583	116670	TGAGACCAGCCTAGGCAACA
118584	116671	TTGAGACCAGCCTAGGCAAC
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118587	116674	AGTTTGAGACCAGCCTAGGC
118588	116675	GAGTTTGAGACCAGCCTAGG
118589	116676	GGAGTTTGAGACCAGCCTAG
118590	116677	AGGAGTTTGAGACCAGCCTA
118591	116678	CAGGAGTTTGAGACCAGCCT
118592	116679	CCAGGAGTTTGAGACCAGCC
118593	116680	CCCAGGAGTTTGAGACCAGC

20300	18387	TGAGTACTAAAAAACCACCA
20301	18388	ATGAGTACTAAAAAACCACC
20302	18389	AATGAGTACTAAAAAACCAC
20303	18390	GAATGAGTACTAAAAAACCA
20304	18391	AGAATGAGTACTAAAAAACC
20305	18392	TAGAATGAGTACTAAAAAAC
20306	18393	ATAGAATGAGTACTAAAAAA
20307	18394	AATAGAATGAGTACTAAAAA
20308	18395	AAATAGAATGAGTACTAAAA
20309	18396	TAAATAGAATGAGTACTAAA
20310	18397	GTAAATAGAATGAGTACTAA
20311	18398	CGTAAATAGAATGAGTACTA
20312	18399	CCGTAAATAGAATGAGTACT
20313	18400	CCCGTAAATAGAATGAGTAC
20314	18401	ACCCGTAAATAGAATGAGTA
20315	18402	CACCCGTAAATAGAATGAGT
20316	18403	TCACCCGTAAATAGAATGAG
20317	18404	TTCACCCGTAAATAGAATGA
20318	18405	CTTCACCCGTAAATAGAATG
20319	18406	TCTTCACCCGTAAATAGAAT
20320	18407	TTCTTCACCCGTAAATAGAA
20321	18408	TTTCTTCACCCGTAAATAGA
20322	18409	ATTTCTTCACCCGTAAATAG
20323	18410	AATTTCTTCACCCGTAAATA
20324	18411	CAATTTCTTCACCCGTAAAT
20325	18412	TCAATTTCTTCACCCGTAAA
20326	18413	CTCAATTTCTTCACCCGTAA
20327	18414	TCTCAATTTCTTCACCCGTA
20328	18415	GTCTCAATTTCTTCACCCGT
20329	18416	GGTCTCAATTTCTTCACCCG
20330	18417	TGGTCTCAATTTCTTCACCC
20331	18418	TTGGTCTCAATTTCTTCACC
20332	18419	CTTGGTCTCAATTTCTTCAC
20333	18420	TCTTGGTCTCAATTTCTTCA
20334	18421	CTCTTGGTCTCAATTTCTTC
20335	18422	CCTCTTGGTCTCAATTTCTT
20336	18423	CCCTCTTGGTCTCAATTTCT
20337	18424	ACCCTCTTGGTCTCAATTTC
20338	18425	AACCCTCTTGGTCTCAATTT
20339	18426	TAACCCTCTTGGTCTCAATT
20340	18427	ATAACCCTCTTGGTCTCAAT
20341	18428	AATAACCCTCTTGGTCTCAA
20342	18429	AAATAACCCTCTTGGTCTCA
20343	18430	TAAATAACCCTCTTGGTCTC
20344	18431	GTAAATAACCCTCTTGGTCT
20345	18432	GGTAAATAACCCTCTTGGTC
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20347	18434	CTGGTAAATAACCCTCTTGG
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20350	18437	ACTCTGGTAAATAACCCTCT
20351	18438	TACTCTGGTAAATAACCCTC
20352	18439	ATACTCTGGTAAATAACCCT
20353	18440	GATACTCTGGTAAATAACCC
20354	18441	AGATACTCTGGTAAATAACC
20355	18442	GAGATACTCTGGTAAATAAC
20356	18443	TGAGATACTCTGGTAAATAA
20357	18444	ATGAGATACTCTGGTAAATA
20358	18445	GATGAGATACTCTGGTAAAT
20359	18446	TGATGAGATACTCTGGTAAA
20360	18447	ATGATGAGATACTCTGGTAA
20361	18448	AATGATGAGATACTCTGGTA
20362	18449	CAATGATGAGATACTCTGGT
20363	18450	CCAATGATGAGATACTCTGG
20364	18451	GCCAATGATGAGATACTCTG
20365	18452	AGCCAATGATGAGATACTCT
20366	18453	CAGCCAATGATGAGATACTC
20367	18454	GCAGCCAATGATGAGATACT
20368	18455	TGCAGCCAATGATGAGATAC
20369	18456	ATGCAGCCAATGATGAGATA
20370	18457	TATGCAGCCAATGATGAGAT

69447	67534	TGGGAGGACTGCCTGAGCCC
69448	67535	GTGGGAGGACTGCCTGAGCC
69449	67536	GGTGGGAGGACTGCCTGAGC
69450	67537	AGGTGGGAGGACTGCCTGAG
69451	67538	GAGGTGGGAGGACTGCCTGA
69452	67539	TGAGGTGGGAGGACTGCCTG
69453	67540	CTGAGGTGGGAGGACTGCCT
69454	67541	GCTGAGGTGGGAGGACTGCC
69455	67542	GGCTGAGGTGGGAGGACTGC
69456	67543	AGGCTGAGGTGGGAGGACTG
69457	67544	GAGGCTGAGGTGGGAGGACT
69458	67545	GGAGGCTGAGGTGGGAGGAC
69459	67546	AGGAGGCTGAGGTGGGAGGA
69460	67547	CAGGAGGCTGAGGTGGGAGG
69461	67548	TCAGGAGGCTGAGGTGGGAG
69462	67549	CTCAGGAGGCTGAGGTGGGA
69463	67550	ACTCAGGAGGCTGAGGTGGG
69464	67551	TACTCAGGAGGCTGAGGTGG
69465	67552	CTACTCAGGAGGCTGAGGTG
69466	67553	GCTACTCAGGAGGCTGAGGT
69467	67554	AGCTACTCAGGAGGCTGAGG
69468	67555	CAGCTACTCAGGAGGCTGAG
69469	67556	CCAGCTACTCAGGAGGCTGA
69470	67557	CCCAGCTACTCAGGAGGCTG
69471	67558	TCCCAGCTACTCAGGAGGCT
69472	67559	ATCCCAGCTACTCAGGAGGC
69473	67560	AATCCCAGCTACTCAGGAGG
69474	67561	TAATCCCAGCTACTCAGGAG
69475	67562	ATAATCCCAGCTACTCAGGA
69476	67563	TATAATCCCAGCTACTCAGG
69477	67564	CTATAATCCCAGCTACTCAG
69478	67565	CCTATAATCCCAGCTACTCA
69479	67566	GCCTATAATCCCAGCTACTC
69480	67567	TGCCTATAATCCCAGCTACT
69481	67568	ATGCCTATAATCCCAGCTAC
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69515	67602	ATACATAATAATTTGAAGCC
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118596	116683	GAGCCCAGGAGTTTGAGACC
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118598	116685	TTGAGCCCAGGAGTTTGAGA
118599	116686	CTTGAGCCCAGGAGTTTGAG
118600	116687	GCTTGAGCCCAGGAGTTTGA
118601	116688	CGCTTGAGCCCAGGAGTTTG
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118607	116694	GCAGATCGCTTGAGCCCAGG
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118609	116696	AGGCAGATCGCTTGAGCCCA
118610	116697	CAGGCAGATCGCTTGAGCCC
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118612	116699	GCCAGGCAGATCGCTTGAGC
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118614	116701	GAGCCAGGCAGATCGCTTGA
118615	116702	AGAGCCAGGCAGATCGCTTG
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69527	67614	GAGGTGATGAACATACATAA
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118745	116832	GTTCCAAGGCTAAAAAAAAA
118746	116833	TGTTCCAAGGCTAAAAAAAA
118747	116834	ATGTTCCAAGGCTAAAAAAA
118748	116835	TATGTTCCAAGGCTAAAAAA
118749	116836	ATATGTTCCAAGGCTAAAAA
118750	116837	CATATGTTCCAAGGCTAAAA
118751	116838	TCATATGTTCCAAGGCTAAA
118752	116839	TTCATATGTTCCAAGGCTAA
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118754	116841	GGTTCATATGTTCCAAGGCT
118755	116842	AGGTTCATATGTTCCAAGGC
118756	116843	CAGGTTCATATGTTCCAAGG
118757	116844	ACAGGTTCATATGTTCCAAG
118758	116845	AACAGGTTCATATGTTCCAA
118759	116846	CAACAGGTTCATATGTTCCA
118760	116847	TCAACAGGTTCATATGTTCC
118761	116848	TTCAACAGGTTCATATGTTC
118762	116849	TTTCAACAGGTTCATATGTT
118763	116850	CTTTCAACAGGTTCATATGT
118764	116851	TCTTTCAACAGGTTCATATG
118765	116852	TTCTTTCAACAGGTTCATAT
118766	116853	GTTCTTTCAACAGGTTCATA
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118768	116855	GAGTTCTTTCAACAGGTTCA
118769	116856	AGAGTTCTTTCAACAGGTTC
118770	116857	CAGAGTTCTTTCAACAGGTT
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118774	116861	CAGGCAGAGTTCTTTCAACA
118775	116862	TCAGGCAGAGTTCTTTCAAC
118776	116863	TTCAGGCAGAGTTCTTTCAA
118777	116864	TTTCAGGCAGAGTTCTTTCA
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118780	116867	TTATTTCAGGCAGAGTTCTT
118781	116868	ATTATTTCAGGCAGAGTTCT
118782	116869	CATTATTTCAGGCAGAGTTC
118783	116870	ACATTATTTCAGGCAGAGTT
118784	116871	TACATTATTTCAGGCAGAGT
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118786	116873	ATTACATTATTTCAGGCAGA
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118788	116875	TGATTACATTATTTCAGGCA
118789	116876	TTGATTACATTATTTCAGGC
118790	116877	TTTGATTACATTATTTCAGG
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118793	116880	TAATTTGATTACATTATTTC
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118795	116882	TATAATTTGATTACATTATT
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118797	116884	TCTATAATTTGATTACATTA
118798	116885	CTCTATAATTTGATTACATT
118799	116886	ACTCTATAATTTGATTACAT
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118803	116890	TTAAACTCTATAATTTGATT
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118806	116893	AGATTAAACTCTATAATTTG

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20514	18601	TGAACCCAGGAGGTGGAGGT
20515	18602	TTGAACCCAGGAGGTGGAGG
20516	18603	CTTGAACCCAGGAGGTGGAG
20517	18604	GCTTGAACCCAGGAGGTGGA
20518	18605	AGCTTGAACCCAGGAGGTGG
20519	18606	TAGCTTGAACCCAGGAGGTG
20520	18607	ATAGCTTGAACCCAGGAGGT
20521	18608	AATAGCTTGAACCCAGGAGG
20522	18609	GAATAGCTTGAACCCAGGAG
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20524	18611	AGGAATAGCTTGAACCCAGG
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20526	18613	ACAGGAATAGCTTGAACCCA
20527	18614	GACAGGAATAGCTTGAACCC
20528	18615	AGACAGGAATAGCTTGAACC
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20535	18622	GAGGCTGAGACAGGAATAGC
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20548	18635	CCCAGCTACTTGGGAGGCTG
20549	18636	TCCCAGCTACTTGGGAGGCT
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20559	18646	GTGCCTGTAGTCCCAGCTAC
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20563	18650	GCAGGTGCCTGTAGTCCCAG
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20565	18652	TGGCAGGTGCCTGTAGTCCC
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20567	18654	GGTGGCAGGTGCCTGTAGTC
20568	18655	TGGTGGCAGGTGCCTGTAGT
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20577	18664	AGCCGGCTGTGGTGGCAGGT
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20579	18666	CTAGCCGGCTGTGGTGGCAG
20580	18667	CCTAGCCGGCTGTGGTGGCA
20581	18668	ACCTAGCCGGCTGTGGTGGC
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69660	67747	TGAGAACAAGTAACAATGAA
69661	67748	ATGAGAACAAGTAACAATGA
69662	67749	AATGAGAACAAGTAACAATG
69663	67750	AAATGAGAACAAGTAACAAT
69664	67751	CAAATGAGAACAAGTAACAA
69665	67752	TCAAATGAGAACAAGTAACA
69666	67753	ATCAAATGAGAACAAGTAAC
69667	67754	AATCAAATGAGAACAAGTAA
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69669	67756	GAAATCAAATGAGAACAAGT
69670	67757	GGAAATCAAATGAGAACAAG
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69674	67761	CACAGGAAATCAAATGAGAA
69675	67762	ACACAGGAAATCAAATGAGA
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69677	67764	ATACACAGGAAATCAAATGA
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69681	67768	TAAAATACACAGGAAATCAA
69682	67769	GTAAAATACACAGGAAATCA
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69719	67806	AAGCCTATGAAACCGTATTC
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69723	67810	AGGGAAGCCTATGAAACCGT
69724	67811	TAGGGAAGCCTATGAAACCG
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69726	67813	TTTAGGGAAGCCTATGAAAC
69727	67814	TTTTAGGGAAGCCTATGAAA
69728	67815	ATTTTAGGGAAGCCTATGAA
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118811	116898	AAATAAGATTAAACTCTATA
118812	116899	AAAATAAGATTAAACTCTAT
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118814	116901	TCAAAATAAGATTAAACTCT
118815	116902	CTCAAAATAAGATTAAACTC
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118820	116907	AGGCCCTCAAAATAAGATTA
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118835	116922	TCTCAGAATTTCTAAAGGCC
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118844	116931	CCACTTTCTTCTCAGAATTT
118845	116932	CCCACTTTCTTCTCAGAATT
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118847	116934	AACCCACTTTCTTCTCAGAA
118848	116935	AAACCCACTTTCTTCTCAGA
118849	116936	AAAACCCACTTTCTTCTCAG
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118875	116962	ACTACATTAAAATGGCAGTA
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20584	18671	AAAACCTAGCCGGCTGTGGT
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20588	18675	ATACAAAACCTAGCCGGCTG
20589	18676	AATACAAAACCTAGCCGGCT
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20622	18709	CTGGCCAACATGGTGCTACC
20623	18710	CCTGGCCAACATGGTGCTAC
20624	18711	GCCTGGCCAACATGGTGCTA
20625	18712	AGCCTGGCCAACATGGTGCT
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20628	18715	ACCAGCCTGGCCAACATGGT
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20630	18717	AGACCAGCCTGGCCAACATG
20631	18718	GAGACCAGCCTGGCCAACAT
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20634	18721	TTCGAGACCAGCCTGGCCAA
20635	18722	GTTCGAGACCAGCCTGGCCA
20636	18723	AGTTCGAGACCAGCCTGGCC
20637	18724	GAGTTCGAGACCAGCCTGGC
20638	18725	TGAGTTCGAGACCAGCCTGG
20639	18726	ATGAGTTCGAGACCAGCCTG
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69795	67882	GAGGACTGTGGGGAGCCTCT
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118886	116973	AACACCTTAACACTACATTA
118887	116974	GAACACCTTAACACTACATT
118888	116975	TGAACACCTTAACACTACAT
118889	116976	ATGAACACCTTAACACTACA
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118893	116980	ATACATGAACACCTTAACAC
118894	116981	GATACATGAACACCTTAACA
118895	116982	TGATACATGAACACCTTAAC
118896	116983	GTGATACATGAACACCTTAA
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118898	116985	TGGTGATACATGAACACCTT
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118900	116987	GCTGGTGATACATGAACACC
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118914	117001	AAACAGCTACACCTGCTGGT
118915	117002	AAAACAGCTACACCTGCTGG
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118918	117005	TTGAAAACAGCTACACCTGC
118919	117006	ATTGAAAACAGCTACACCTG
118920	117007	CATTGAAAACAGCTACACCT
118921	117008	TCATTGAAAACAGCTACACC
118922	117009	ATCATTGAAAACAGCTACAC
118923	117010	AATCATTGAAAACAGCTACA
118924	117011	TAATCATTGAAAACAGCTAC
118925	117012	GTAATCATTGAAAACAGCTA
118926	117013	AGTAATCATTGAAAACAGCT
118927	117014	AAGTAATCATTGAAAACAGC
118928	117015	TAAGTAATCATTGAAAACAG
118929	117016	TTAAGTAATCATTGAAAACA
118930	117017	TTTAAGTAATCATTGAAAAC
118931	117018	TTTTAAGTAATCATTGAAAA
118932	117019	GTTTTAAGTAATCATTGAAA
118933	117020	TGTTTTAAGTAATCATTGAA
118934	117021	TTGTTTTAAGTAATCATTGA
118935	117022	ATTGTTTTAAGTAATCATTG
118936	117023	CATTGTTTTAAGTAATCATT
118937	117024	GCATTGTTTTAAGTAATCAT
118938	117025	TGCATTGTTTTAAGTAATCA
118939	117026	TTGCATTGTTTTAAGTAATC
118940	117027	ATTGCATTGTTTTAAGTAAT
118941	117028	CATTGCATTGTTTTAAGTAA
118942	117029	CCATTGCATTGTTTTAAGTA
118943	117030	CCCATTGCATTGTTTTAAGT
118944	117031	TCCCATTGCATTGTTTTAAG
118945	117032	TTCCCATTGCATTGTTTTAA
118946	117033	GTTCCCATTGCATTGTTTTA
118947	117034	AGTTCCCATTGCATTGTTTT
118948	117035	AAGTTCCCATTGCATTGTTT

20655	18742	TGGATCACCTGAGGTCATGA
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20657	18744	GGTGGATCACCTGAGGTCAT
20658	18745	AGGTGGATCACCTGAGGTCA
20659	18746	CAGGTGGATCACCTGAGGTC
20660	18747	GCAGGTGGATCACCTGAGGT
20661	18748	GGCAGGTGGATCACCTGAGG
20662	18749	AGGCAGGTGGATCACCTGAG
20663	18750	GAGGCAGGTGGATCACCTGA
20664	18751	CGAGGCAGGTGGATCACCTG
20665	18752	CCGAGGCAGGTGGATCACCT
20666	18753	GCCGAGGCAGGTGGATCACC
20667	18754	GGCCGAGGCAGGTGGATCAC
20668	18755	AGGCCGAGGCAGGTGGATCA
20669	18756	GAGGCCGAGGCAGGTGGATC
20670	18757	GGAGGCCGAGGCAGGTGGAT
20671	18758	GGGAGGCCGAGGCAGGTGGA
20672	18759	TGGGAGGCCGAGGCAGGTGG
20673	18760	CTGGGAGGCCGAGGCAGGTG
20674	18761	ACTGGGAGGCCGAGGCAGGT
20675	18762	CACTGGGAGGCCGAGGCAGG
20676	18763	GCACTGGGAGGCCGAGGCAG
20677	18764	AGCACTGGGAGGCCGAGGCA
20678	18765	CAGCACTGGGAGGCCGAGGC
20679	18766	CCAGCACTGGGAGGCCGAGG
20680	18767	CCCAGCACTGGGAGGCCGAG
20681	18768	TCCCAGCACTGGGAGGCCGA
20682	18769	ATCCCAGCACTGGGAGGCCG
20683	18770	AATCCCAGCACTGGGAGGCC
20684	18771	TAATCCCAGCACTGGGAGGC
20685	18772	ATAATCCCAGCACTGGGAGG
20686	18773	TATAATCCCAGCACTGGGAG
20687	18774	CTATAATCCCAGCACTGGGA
20688	18775	CCTATAATCCCAGCACTGGG
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20690	18777	TGCCTATAATCCCAGCACTG
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20692	18779	CATGCCTATAATCCCAGCAC
20693	18780	TCATGCCTATAATCCCAGCA
20694	18781	CTCATGCCTATAATCCCAGC
20695	18782	GCTCATGCCTATAATCCCAG
20696	18783	GGCTCATGCCTATAATCCCA
20697	18784	TGGCTCATGCCTATAATCCC
20698	18785	GTGGCTCATGCCTATAATCC
20699	18786	GGTGGCTCATGCCTATAATC
20700	18787	TGGTGGCTCATGCCTATAAT
20701	18788	ATGGTGGCTCATGCCTATAA
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20703	18790	GCATGGTGGCTCATGCCTAT
20704	18791	GGCATGGTGGCTCATGCCTA
20705	18792	AGGCATGGTGGCTCATGCCT
20706	18793	CAGGCATGGTGGCTCATGCC
20707	18794	CCAGGCATGGTGGCTCATGC
20708	18795	GCCAGGCATGGTGGCTCATG
20709	18796	GGCCAGGCATGGTGGCTCAT
20710	18797	AGGCCAGGCATGGTGGCTCA
20711	18798	AAGGCCAGGCATGGTGGCTC
20712	18799	AAAGGCCAGGCATGGTGGCT
20713	18800	GAAAGGCCAGGCATGGTGGC
20714	18801	AGAAAGGCCAGGCATGGTGG
20715	18802	AAGAAAGGCCAGGCATGGTG
20716	18803	AAAGAAAGGCCAGGCATGGT
20717	18804	CAAAGAAAGGCCAGGCATGG
20718	18805	ACAAAGAAAGGCCAGGCATG
20719	18806	GACAAAGAAAGGCCAGGCAT
20720	18807	CGACAAAGAAAGGCCAGGCA
20721	18808	ACGACAAAGAAAGGCCAGGC
20722	18809	AACGACAAAGAAAGGCCAGG
20723	18810	AAACGACAAAGAAAGGCCAG
20724	18811	GAAACGACAAAGAAAGGCCA
20725	18812	GGAAACGACAAAGAAAGGCC

69802	67889	GACAAAAGAGGACTGTGGGG
69803	67890	TGACAAAAGAGGACTGTGGG
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69805	67892	GATGACAAAAGAGGACTGTG
69806	67893	TGATGACAAAAGAGGACTGT
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69812	67899	GGGGTATGATGACAAAAGAG
69813	67900	AGGGGTATGATGACAAAAGA
69814	67901	TAGGGGTATGATGACAAAAG
69815	67902	GTAGGGGTATGATGACAAAA
69816	67903	GGTAGGGGTATGATGACAAA
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69818	67905	GGGGTAGGGGTATGATGACA
69819	67906	TGGGGTAGGGGTATGATGAC
69820	67907	ATGGGGTAGGGGTATGATGA
69821	67908	AATGGGGTAGGGGTATGATG
69822	67909	GAATGGGGTAGGGGTATGAT
69823	67910	AGAATGGGGTAGGGGTATGA
69824	67911	TAGAATGGGGTAGGGGTATG
69825	67912	CTAGAATGGGGTAGGGGTAT
69826	67913	GCTAGAATGGGGTAGGGGTA
69827	67914	GGCTAGAATGGGGTAGGGGT
69828	67915	AGGCTAGAATGGGGTAGGGG
69829	67916	CAGGCTAGAATGGGGTAGGG
69830	67917	TCAGGCTAGAATGGGGTAGG
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69837	67924	ACGCTCCTCAGGCTAGAATG
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69839	67926	CCACGCTCCTCAGGCTAGAA
69840	67927	GCCACGCTCCTCAGGCTAGA
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69842	67929	GAGCCACGCTCCTCAGGCTA
69843	67930	GGAGCCACGCTCCTCAGGCT
69844	67931	TGGAGCCACGCTCCTCAGGC
69845	67932	GTGGAGCCACGCTCCTCAGG
69846	67933	GGTGGAGCCACGCTCCTCAG
69847	67934	AGGTGGAGCCACGCTCCTCA
69848	67935	CAGGTGGAGCCACGCTCCTC
69849	67936	ACAGGTGGAGCCACGCTCCT
69850	67937	CACAGGTGGAGCCACGCTCC
69851	67938	GCACAGGTGGAGCCACGCTC
69852	67939	GGCACAGGTGGAGCCACGCT
69853	67940	GGGCACAGGTGGAGCCACGC
69854	67941	AGGGCACAGGTGGAGCCACG
69855	67942	AAGGGCACAGGTGGAGCCAC
69856	67943	CAAGGGCACAGGTGGAGCCA
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69858	67945	ACCAAGGGCACAGGTGGAGC
69859	67946	AACCAAGGGCACAGGTGGAG
69860	67947	AAACCAAGGGCACAGGTGGA
69861	67948	AAAACCAAGGGCACAGGTGG
69862	67949	CAAAACCAAGGGCACAGGTG
69863	67950	ACAAAACCAAGGGCACAGGT
69864	67951	AACAAAACCAAGGGCACAGG
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69867	67954	AACAACAAAACCAAGGGCAC
69868	67955	GAACAACAAAACCAAGGGCA
69869	67956	GGAACAACAAAACCAAGGGC
69870	67957	TGGAACAACAAAACCAAGGG
69871	67958	CTGGAACAACAAAACCAAGG
69872	67959	ACTGGAACAACAAAACCAAG

118949	117036	AAAGTTCCCATTGCATTGTT
118950	117037	AAAAGTTCCCATTGCATTGT
118951	117038	AAAAAGTTCCCATTGCATTG
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118953	117040	ACAAAAAGTTCCCATTGCAT
118954	117041	AACAAAAAGTTCCCATTGCA
118955	117042	CAACAAAAAGTTCCCATTGC
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118958	117045	TGACAACAAAAAGTTCCCAT
118959	117046	ATGACAACAAAAAGTTCCCA
118960	117047	AATGACAACAAAAAGTTCCC
118961	117048	TAATGACAACAAAAAGTTCC
118962	117049	TTAATGACAACAAAAAGTTC
118963	117050	TTTAATGACAACAAAAAGTT
118964	117051	TTTTAATGACAACAAAAAGT
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118966	117053	TATTTTAATGACAACAAAAA
118967	117054	ATATTTTAATGACAACAAAA
118968	117055	TATATTTTAATGACAACAAA
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118970	117057	TTTATATTTTAATGACAACA
118971	117058	TTTTATATTTTAATGACAAC
118972	117059	CTTTTATATTTTAATGACAA
118973	117060	CCTTTTATATTTTAATGACA
118974	117061	ACCTTTTATATTTTAATGAC
118975	117062	AACCTTTTATATTTTAATGA
118976	117063	TAACCTTTTATATTTTAATG
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118978	117065	AGTAACCTTTTATATTTTAA
118979	117066	CAGTAACCTTTTATATTTTA
118980	117067	ACAGTAACCTTTTATATTTT
118981	117068	TACAGTAACCTTTTATATTT
118982	117069	CTACAGTAACCTTTTATATT
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118984	117071	TACTACAGTAACCTTTTATA
118985	117072	TTACTACAGTAACCTTTTAT
118986	117073	CTTACTACAGTAACCTTTTA
118987	117074	TCTTACTACAGTAACCTTTT
118988	117075	CTCTTACTACAGTAACCTTT
118989	117076	GCTCTTACTACAGTAACCTT
118990	117077	TGCTCTTACTACAGTAACCT
118991	117078	TTGCTCTTACTACAGTAACC
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118993	117080	GCTTGCTCTTACTACAGTAA
118994	117081	TGCTTGCTCTTACTACAGTA
118995	117082	ATGCTTGCTCTTACTACAGT
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118999	117086	TGTCATGCTTGCTCTTACTA
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119014	117101	ATCAGATAGCCAAACTGTCA
119015	117102	CATCAGATAGCCAAACTGTC
119016	117103	CCATCAGATAGCCAAACTGT
119017	117104	CCCATCAGATAGCCAAACTG
119018	117105	TCCCATCAGATAGCCAAACT
119019	117106	CTCCCATCAGATAGCCAAAC

20726	18813	AGGAAACGACAAAGAAAGGC
20727	18814	AAGGAAACGACAAAGAAAGG
20728	18815	AAAGGAAACGACAAAGAAAG
20729	18816	GAAAGGAAACGACAAAGAAA
20730	18817	AGAAAGGAAACGACAAAGAA
20731	18818	AAGAAAGGAAACGACAAAGA
20732	18819	AAAGAAAGGAAACGACAAAG
20733	18820	GAAAGAAAGGAAACGACAAA
20734	18821	AGAAAGAAAGGAAACGACAA
20735	18822	GAGAAAGAAAGGAAACGACA
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20737	18824	AAGAGAAAGAAAGGAAACGA
20738	18825	GAAGAGAAAGAAAGGAAACG
20739	18826	TGAAGAGAAAGAAAGGAAAC
20740	18827	ATGAAGAGAAAGAAAGGAAA
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20743	18830	GGGATGAAGAGAAAGAAAGG
20744	18831	AGGGATGAAGAGAAAGAAAG
20745	18832	GAGGGATGAAGAGAAAGAAA
20746	18833	GGAGGGATGAAGAGAAAGAA
20747	18834	AGGAGGGATGAAGAGAAAGA
20748	18835	GAGGAGGGATGAAGAGAAAG
20749	18836	AGAGGAGGGATGAAGAGAAA
20750	18837	GAGAGGAGGGATGAAGAGAA
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20754	18841	AAAGGAGAGGAGGGATGAAG
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20769	18856	AGCGGGGAGGGGAAAAAAGG
20770	18857	CAGCGGGGAGGGGAAAAAAG
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20784	18871	AAGACAGGAGGAGGCAGCGG
20785	18872	GAAGACAGGAGGAGGCAGCG
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20787	18874	GGGAAGACAGGAGGAGGCAG
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20789	18876	AAGGGAAGACAGGAGGAGGC
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69873	67960	GACTGGAACAACAAAACCAA
69874	67961	GGACTGGAACAACAAAACCA
69875	67962	TGGACTGGAACAACAAAACC
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69877	67964	TATGGACTGGAACAACAAAA
69878	67965	GTATGGACTGGAACAACAAA
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69891	67978	AAGGGTGCAGGATGTATGGA
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69898	67985	CACAGTTAAGGGTGCAGGAT
69899	67986	ACACAGTTAAGGGTGCAGGA
69900	67987	AACACAGTTAAGGGTGCAGG
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69902	67989	GAAACACAGTTAAGGGTGCA
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69904	67991	AAGAAACACAGTTAAGGGTG
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69907	67994	GATAAGAAACACAGTTAAGG
69908	67995	GGATAAGAAACACAGTTAAG
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69916	68003	CAAGTTGGGGATAAGAAACA
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69918	68005	AACAAGTTGGGGATAAGAAA
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69920	68007	GAAACAAGTTGGGGATAAGA
69921	68008	AGAAACAAGTTGGGGATAAG
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69923	68010	AAAGAAACAAGTTGGGGATA
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69926	68013	CACAAAGAAACAAGTTGGGG
69927	68014	ACACAAAGAAACAAGTTGGG
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69929	68016	TAACACAAAGAAACAAGTTG
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69932	68019	GAATAACACAAAGAAACAAG
69933	68020	AGAATAACACAAAGAAACAA
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69936	68023	TGAAGAATAACACAAAGAAA
69937	68024	CTGAAGAATAACACAAAGAA
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69940	68027	ATACTGAAGAATAACACAAA
69941	68028	AATACTGAAGAATAACACAA
69942	68029	TAATACTGAAGAATAACACA
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119020	117107	TCTCCCATCAGATAGCCAAA
119021	117108	CTCTCCCATCAGATAGCCAA
119022	117109	ACTCTCCCATCAGATAGCCA
119023	117110	GACTCTCCCATCAGATAGCC
119024	117111	TGACTCTCCCATCAGATAGC
119025	117112	GTGACTCTCCCATCAGATAG
119026	117113	TGTGACTCTCCCATCAGATA
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119028	117115	AATGTGACTCTCCCATCAGA
119029	117116	GAATGTGACTCTCCCATCAG
119030	117117	AGAATGTGACTCTCCCATCA
119031	117118	TAGAATGTGACTCTCCCATC
119032	117119	TTAGAATGTGACTCTCCCAT
119033	117120	GTTAGAATGTGACTCTCCCA
119034	117121	AGTTAGAATGTGACTCTCCC
119035	117122	AAGTTAGAATGTGACTCTCC
119036	117123	GAAGTTAGAATGTGACTCTC
119037	117124	TGAAGTTAGAATGTGACTCT
119038	117125	CTGAAGTTAGAATGTGACTC
119039	117126	CCTGAAGTTAGAATGTGACT
119040	117127	TCCTGAAGTTAGAATGTGAC
119041	117128	CTCCTGAAGTTAGAATGTGA
119042	117129	CCTCCTGAAGTTAGAATGTG
119043	117130	ACCTCCTGAAGTTAGAATGT
119044	117131	TACCTCCTGAAGTTAGAATG
119045	117132	GTACCTCCTGAAGTTAGAAT
119046	117133	AGTACCTCCTGAAGTTAGAA
119047	117134	CAGTACCTCCTGAAGTTAGA
119048	117135	ACAGTACCTCCTGAAGTTAG
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119051	117138	AAGACAGTACCTCCTGAAGT
119052	117139	AAAGACAGTACCTCCTGAAG
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119055	117142	TAAAAAGACAGTACCTCCTG
119056	117143	TTAAAAAGACAGTACCTCCT
119057	117144	ATTAAAAAGACAGTACCTCC
119058	117145	TATTAAAAAGACAGTACCTC
119059	117146	CTATTAAAAAGACAGTACCT
119060	117147	TCTATTAAAAAGACAGTACC
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119062	117149	TTTCTATTAAAAAGACAGTA
119063	117150	ATTTCTATTAAAAAGACAGT
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119067	117154	TATCATTTCTATTAAAAAGA
119068	117155	ATATCATTTCTATTAAAAAG
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119070	117157	GTATATCATTTCTATTAAAA
119071	117158	AGTATATCATTTCTATTAAA
119072	117159	GAGTATATCATTTCTATTAA
119073	117160	TGAGTATATCATTTCTATTA
119074	117161	CTGAGTATATCATTTCTATT
119075	117162	TCTGAGTATATCATTTCTAT
119076	117163	CTCTGAGTATATCATTTCTA
119077	117164	ACTCTGAGTATATCATTTCT
119078	117165	GACTCTGAGTATATCATTTC
119079	117166	AGACTCTGAGTATATCATTT
119080	117167	CAGACTCTGAGTATATCATT
119081	117168	CCAGACTCTGAGTATATCAT
119082	117169	CCCAGACTCTGAGTATATCA
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119084	117171	TGCCCAGACTCTGAGTATAT
119085	117172	GTGCCCAGACTCTGAGTATA
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119087	117174	CCGTGCCCAGACTCTGAGTA
119088	117175	ACCGTGCCCAGACTCTGAGT
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20800	18887	AGGAAGGAAAGAAGGGAAGA
20801	18888	AAGGAAGGAAAGAAGGGAAG
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20804	18891	AGAAAGGAAGGAAAGAAGGG
20805	18892	GAGAAAGGAAGGAAAGAAGG
20806	18893	AGAGAAAGGAAGGAAAGAAG
20807	18894	GAGAGAAAGGAAGGAAAGAA
20808	18895	GGAGAGAAAGGAAGGAAAGA
20809	18896	AGGAGAGAAAGGAAGGAAAG
20810	18897	AAGGAGAGAAAGGAAGGAAA
20811	18898	AAAGGAGAGAAAGGAAGGAA
20812	18899	AAAAGGAGAGAAAGGAAGGA
20813	18900	AAAAAGGAGAGAAAGGAAGG
20814	18901	TAAAAAGGAGAGAAAGGAAG
20815	18902	ATAAAAAGGAGAGAAAGGAA
20816	18903	AATAAAAAGGAGAGAAAGGA
20817	18904	AAATAAAAAGGAGAGAAAGG
20818	18905	AAAATAAAAAGGAGAGAAAG
20819	18906	AAAAATAAAAAGGAGAGAAA
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20821	18908	GAAAAAATAAAAAGGAGAGA
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20823	18910	AGGAAAAAATAAAAAGGAGA
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20825	18912	AAAGGAAAAAATAAAAAGGA
20826	18913	GAAAGGAAAAAATAAAAAGG
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20828	18915	AAGAAAGGAAAAAATAAAAA
20829	18916	AAAGAAAGGAAAAAATAAAA
20830	18917	AAAAGAAAGGAAAAAATAAA
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20832	18919	GAAAAAGAAAGGAAAAAATA
20833	18920	AGAAAAAGAAAGGAAAAAAT
20834	18921	AAGAAAAAGAAAGGAAAAAA
20835	18922	AAAGAAAAAGAAAGGAAAAA
20836	18923	GAAAGAAAAAGAAAGGAAAA
20837	18924	AGAAAGAAAAAGAAAGGAAA
20838	18925	GAGAAAGAAAAAGAAAGGAA
20839	18926	AGAGAAAGAAAAAGAAAGGA
20840	18927	CAGAGAAAGAAAAAGAAAGG
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20842	18929	GACAGAGAAAGAAAAAGAAA
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20844	18931	GAGACAGAGAAAGAAAAAGA
20845	18932	AGAGACAGAGAAAGAAAAAG
20846	18933	GAGAGACAGAGAAAGAAAAA
20847	18934	GGAGAGACAGAGAAAGAAAA
20848	18935	GGGAGAGACAGAGAAAGAAA
20849	18936	TGGGAGAGACAGAGAAAGAA
20850	18937	TTGGGAGAGACAGAGAAAGA
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20852	18939	GGTTGGGAGAGACAGAGAAA
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20854	18941	AGGGTTGGGAGAGACAGAGA
20855	18942	AAGGGTTGGGAGAGACAGAG
20856	18943	GAAGGGTTGGGAGAGACAGA
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20858	18945	AGGAAGGGTTGGGAGAGACA
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20860	18947	AGAGGAAGGGTTGGGAGAGA
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20863	18950	GAGAGAGGAAGGGTTGGGAG
20864	18951	GGAGAGAGGAAGGGTTGGGA
20865	18952	GGGAGAGAGGAAGGGTTGGG
20866	18953	AGGGAGAGAGGAAGGGTTGG
20867	18954	GAGGGAGAGAGGAAGGGTTG

69944	68031	TATAATACTGAAGAATAACA
69945	68032	CTATAATACTGAAGAATAAC
69946	68033	ACTATAATACTGAAGAATAA
69947	68034	GACTATAATACTGAAGAATA
69948	68035	AGACTATAATACTGAAGAAT
69949	68036	AAGACTATAATACTGAAGAA
69950	68037	AAAGACTATAATACTGAAGA
69951	68038	TAAAGACTATAATACTGAAG
69952	68039	TTAAAGACTATAATACTGAA
69953	68040	ATTAAAGACTATAATACTGA
69954	68041	TATTAAAGACTATAATACTG
69955	68042	ATATTAAAGACTATAATACT
69956	68043	TATATTAAAGACTATAATAC
69957	68044	TTATATTAAAGACTATAATA
69958	68045	ATTATATTAAAGACTATAAT
69959	68046	GATTATATTAAAGACTATAA
69960	68047	AGATTATATTAAAGACTATA
69961	68048	CAGATTATATTAAAGACTAT
69962	68049	ACAGATTATATTAAAGACTA
69963	68050	TACAGATTATATTAAAGACT
69964	68051	ATACAGATTATATTAAAGAC
69965	68052	TATACAGATTATATTAAAGA
69966	68053	TTATACAGATTATATTAAAG
69967	68054	ATTATACAGATTATATTAAA
69968	68055	TATTATACAGATTATATTAA
69969	68056	GTATTATACAGATTATATTA
69970	68057	TGTATTATACAGATTATATT
69971	68058	ATGTATTATACAGATTATAT
69972	68059	CATGTATTATACAGATTATA
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69974	68061	ACCATGTATTATACAGATTA
69975	68062	CACCATGTATTATACAGATT
69976	68063	ACACCATGTATTATACAGAT
69977	68064	TACACCATGTATTATACAGA
69978	68065	CTACACCATGTATTATACAG
69979	68066	ACTACACCATGTATTATACA
69980	68067	TACTACACCATGTATTATAC
69981	68068	CTACTACACCATGTATTATA
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69983	68070	TACTACTACACCATGTATTA
69984	68071	ATACTACTACACCATGTATT
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69986	68073	ATATACTACTACACCATGTA
69987	68074	CATATACTACTACACCATGT
69988	68075	GCATATACTACTACACCATG
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69990	68077	GAGCATATACTACTACACCA
69991	68078	CGAGCATATACTACTACACC
69992	68079	ACGAGCATATACTACTACAC
69993	68080	TACGAGCATATACTACTACA
69994	68081	CTACGAGCATATACTACTAC
69995	68082	ACTACGAGCATATACTACTA
69996	68083	TACTACGAGCATATACTACT
69997	68084	ATACTACGAGCATATACTAC
69998	68085	TATACTACGAGCATATACTA
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70001	68088	TTGTATACTACGAGCATATA
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70007	68094	ACTGAATTGTATACTACGAG
70008	68095	AACTGAATTGTATACTACGA
70009	68096	TAACTGAATTGTATACTACG
70010	68097	CTAACTGAATTGTATACTAC
70011	68098	TCTAACTGAATTGTATACTA
70012	68099	TTCTAACTGAATTGTATACT
70013	68100	GTTCTAACTGAATTGTATAC
70014	68101	TGTTCTAACTGAATTGTATA

119091	117178	GCCACCGTGCCCAGACTCTG
119092	117179	AGCCACCGTGCCCAGACTCT
119093	117180	GAGCCACCGTGCCCAGACTC
119094	117181	TGAGCCACCGTGCCCAGACT
119095	117182	GTGAGCCACCGTGCCCAGAC
119096	117183	CGTGAGCCACCGTGCCCAGA
119097	117184	GCGTGAGCCACCGTGCCCAG
119098	117185	GGCGTGAGCCACCGTGCCCA
119099	117186	AGGCGTGAGCCACCGTGCCC
119100	117187	CAGGCGTGAGCCACCGTGCC
119101	117188	ACAGGCGTGAGCCACCGTGC
119102	117189	TACAGGCGTGAGCCACCGTG
119103	117190	TTACAGGCGTGAGCCACCGT
119104	117191	ATTACAGGCGTGAGCCACCG
119105	117192	GATTACAGGCGTGAGCCACC
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119107	117194	TGGATTACAGGCGTGAGCCA
119108	117195	CTGGATTACAGGCGTGAGCC
119109	117196	GCTGGATTACAGGCGTGAGC
119110	117197	TGCTGGATTACAGGCGTGAG
119111	117198	GTGCTGGATTACAGGCGTGA
119112	117199	AGTGCTGGATTACAGGCGTG
119113	117200	AAGTGCTGGATTACAGGCGT
119114	117201	AAAGTGCTGGATTACAGGCG
119115	117202	CAAAGTGCTGGATTACAGGC
119116	117203	CCAAAGTGCTGGATTACAGG
119117	117204	CCCAAAGTGCTGGATTACAG
119118	117205	TCCCAAAGTGCTGGATTACA
119119	117206	CTCCCAAAGTGCTGGATTAC
119120	117207	CCTCCCAAAGTGCTGGATTA
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119122	117209	GGCCTCCCAAAGTGCTGGAT
119123	117210	CGGCCTCCCAAAGTGCTGGA
119124	117211	TCGGCCTCCCAAAGTGCTGG
119125	117212	CTCGGCCTCCCAAAGTGCTG
119126	117213	CCTCGGCCTCCCAAAGTGCT
119127	117214	ACCTCGGCCTCCCAAAGTGC
119128	117215	CACCTCGGCCTCCCAAAGTG
119129	117216	CCACCTCGGCCTCCCAAAGT
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119131	117218	GCCCACCTCGGCCTCCCAAA
119132	117219	TGCCCACCTCGGCCTCCCAA
119133	117220	CTGCCCACCTCGGCCTCCCA
119134	117221	TCTGCCCACCTCGGCCTCCC
119135	117222	ATCTGCCCACCTCGGCCTCC
119136	117223	GATCTGCCCACCTCGGCCTC
119137	117224	TGATCTGCCCACCTCGGCCT
119138	117225	GTGATCTGCCCACCTCGGCC
119139	117226	CGTGATCTGCCCACCTCGGC
119140	117227	TCGTGATCTGCCCACCTCGG
119141	117228	CTCGTGATCTGCCCACCTCG
119142	117229	CCTCGTGATCTGCCCACCTC
119143	117230	ACCTCGTGATCTGCCCACCT
119144	117231	GACCTCGTGATCTGCCCACC
119145	117232	TGACCTCGTGATCTGCCCAC
119146	117233	CTGACCTCGTGATCTGCCCA
119147	117234	CCTGACCTCGTGATCTGCCC
119148	117235	TCCTGACCTCGTGATCTGCC
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119150	117237	TCTCCTGACCTCGTGATCTG
119151	117238	ATCTCCTGACCTCGTGATCT
119152	117239	GATCTCCTGACCTCGTGATC
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119158	117245	GGTCTTGATCTCCTGACCTC
119159	117246	TGGTCTTGATCTCCTGACCT
119160	117247	ATGGTCTTGATCTCCTGACC
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20868	18955	GGAGGGAGAGAGGAAGGGTT
20869	18956	GGGAGGGAGAGAGGAAGGGT
20870	18957	AGGGAGGGAGAGAGGAAGGG
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20874	18961	AGGGAGGGAGGGAGAGAGGA
20875	18962	GAGGGAGGGAGGGAGAGAGG
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20877	18964	GGGAGGGAGGGAGGGAGAGA
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20879	18966	AGGGGAGGGAGGGAGGGAGA
20880	18967	AAGGGGAGGGAGGGAGGGAG
20881	18968	GAAGGGGAGGGAGGGAGGGA
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20884	18971	AGAGAAGGGGAGGGAGGGAG
20885	18972	GAGAGAAGGGGAGGGAGGGA
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20887	18974	GAGAGAGAAGGGGAGGGAGG
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20895	18982	GAGGGGGGGAGAGAGAAGGG
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20917	19004	GAGGGGGAGAGAGAAGGGGA
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20919	19006	GGGAGGGGGAGAGAGAAGGG
20920	19007	GGGGAGGGGGAGAGAGAAGG
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20925	19012	CAAAAGGGGAGGGGGAGAGA
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20927	19014	AACAAAAGGGGAGGGGGAGA
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20929	19016	GGAACAAAAGGGGAGGGGGA
20930	19017	AGGAACAAAAGGGGAGGGGG
20931	19018	TAGGAACAAAAGGGGAGGGG
20932	19019	TTAGGAACAAAAGGGGAGGG
20933	19020	CTTAGGAACAAAAGGGGAGG
20934	19021	TCTTAGGAACAAAAGGGGAG
20935	19022	CTCTTAGGAACAAAAGGGGA
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20937	19024	GTCTCTTAGGAACAAAAGGG
20938	19025	TGTCTCTTAGGAACAAAAGG

70015	68102	CTGTTCTAACTGAATTGTAT
70016	68103	TCTGTTCTAACTGAATTGTA
70017	68104	ATCTGTTCTAACTGAATTGT
70018	68105	CATCTGTTCTAACTGAATTG
70019	68106	TCATCTGTTCTAACTGAATT
70020	68107	CTCATCTGTTCTAACTGAAT
70021	68108	ACTCATCTGTTCTAACTGAA
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70023	68110	ATACTCATCTGTTCTAACTG
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70025	68112	GAATACTCATCTGTTCTAAC
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70027	68114	TTGAATACTCATCTGTTCTA
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70029	68116	CATTGAATACTCATCTGTTC
70030	68117	TCATTGAATACTCATCTGTT
70031	68118	TTCATTGAATACTCATCTGT
70032	68119	TTTCATTGAATACTCATCTG
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70035	68122	TCTTTTCATTGAATACTCAT
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70037	68124	TATCTTTTCATTGAATACTC
70038	68125	TTATCTTTTCATTGAATACT
70039	68126	ATTATCTTTTCATTGAATAC
70040	68127	GATTATCTTTTCATTGAATA
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70042	68129	GAGATTATCTTTTCATTGAA
70043	68130	GGAGATTATCTTTTCATTGA
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70047	68134	GAGAGGAGATTATCTTTTCA
70048	68135	AGAGAGGAGATTATCTTTTC
70049	68136	TAGAGAGGAGATTATCTTTT
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70051	68138	GTTAGAGAGGAGATTATCTT
70052	68139	GGTTAGAGAGGAGATTATCT
70053	68140	GGGTTAGAGAGGAGATTATC
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70061	68148	GGGACTGGGGGTTAGAGAGG
70062	68149	TGGGACTGGGGGTTAGAGAG
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70066	68153	GAAGTGGGACTGGGGGTTAG
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70075	68162	TTCCCCAGGGAAGTGGGACT
70076	68163	CTTCCCCAGGGAAGTGGGAC
70077	68164	GCTTCCCCAGGGAAGTGGGA
70078	68165	GGCTTCCCCAGGGAAGTGGG
70079	68166	AGGCTTCCCCAGGGAAGTGG
70080	68167	CAGGCTTCCCCAGGGAAGTG
70081	68168	ACAGGCTTCCCCAGGGAAGT
70082	68169	CACAGGCTTCCCCAGGGAAG
70083	68170	ACACAGGCTTCCCCAGGGAA
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119162	117249	GGATGGTCTTGATCTCCTGA
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119165	117252	CCAGGATGGTCTTGATCTCC
119166	117253	GCCAGGATGGTCTTGATCTC
119167	117254	AGCCAGGATGGTCTTGATCT
119168	117255	TAGCCAGGATGGTCTTGATC
119169	117256	TTAGCCAGGATGGTCTTGAT
119170	117257	ATTAGCCAGGATGGTCTTGA
119171	117258	TATTAGCCAGGATGGTCTTG
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119173	117260	TGTATTAGCCAGGATGGTCT
119174	117261	CTGTATTAGCCAGGATGGTC
119175	117262	ACTGTATTAGCCAGGATGGT
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119177	117264	TCACTGTATTAGCCAGGATG
119178	117265	TTCACTGTATTAGCCAGGAT
119179	117266	TTTCACTGTATTAGCCAGGA
119180	117267	GTTTCACTGTATTAGCCAGG
119181	117268	GGTTTCACTGTATTAGCCAG
119182	117269	CGGTTTCACTGTATTAGCCA
119183	117270	ACGGTTTCACTGTATTAGCC
119184	117271	CACGGTTTCACTGTATTAGC
119185	117272	ACACGGTTTCACTGTATTAG
119186	117273	GACACGGTTTCACTGTATTA
119187	117274	AGACACGGTTTCACTGTATT
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119189	117276	AGAGACACGGTTTCACTGTA
119190	117277	TAGAGACACGGTTTCACTGT
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119194	117281	TTAGTAGAGACACGGTTTCA
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119198	117285	ATTTTTAGTAGAGACACGGT
119199	117286	TATTTTTAGTAGAGACACGG
119200	117287	GTATTTTTAGTAGAGACACG
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119202	117289	TTGTATTTTTAGTAGAGACA
119203	117290	TTTGTATTTTTAGTAGAGAC
119204	117291	GTTTGTATTTTTAGTAGAGA
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119208	117295	AATTGTTTGTATTTTTAGTA
119209	117296	TAATTGTTTGTATTTTTAGT
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119211	117298	GCTAATTGTTTGTATTTTTA
119212	117299	AGCTAATTGTTTGTATTTTT
119213	117300	CAGCTAATTGTTTGTATTTT
119214	117301	TCAGCTAATTGTTTGTATTT
119215	117302	CTCAGCTAATTGTTTGTATT
119216	117303	GCTCAGCTAATTGTTTGTAT
119217	117304	CGCTCAGCTAATTGTTTGTA
119218	117305	ACGCTCAGCTAATTGTTTGT
119219	117306	CACGCTCAGCTAATTGTTTG
119220	117307	CCACGCTCAGCTAATTGTTT
119221	117308	ACCACGCTCAGCTAATTGTT
119222	117309	CACCACGCTCAGCTAATTGT
119223	117310	CCACCACGCTCAGCTAATTG
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119225	117312	TGCCACCACGCTCAGCTAAT
119226	117313	CTGCCACCACGCTCAGCTAA
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20939	19026	CTGTCTCTTAGGAACAAAAG
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20942	19029	ACCCTGTCTCTTAGGAACAA
20943	19030	GACCCTGTCTCTTAGGAACA
20944	19031	AGACCCTGTCTCTTAGGAAC
20945	19032	GAGACCCTGTCTCTTAGGAA
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20947	19034	AGGAGACCCTGTCTCTTAGG
20948	19035	AAGGAGACCCTGTCTCTTAG
20949	19036	TAAGGAGACCCTGTCTCTTA
20950	19037	ATAAGGAGACCCTGTCTCTT
20951	19038	CATAAGGAGACCCTGTCTCT
20952	19039	ACATAAGGAGACCCTGTCTC
20953	19040	AACATAAGGAGACCCTGTCT
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20955	19042	GCAACATAAGGAGACCCTGT
20956	19043	AGCAACATAAGGAGACCCTG
20957	19044	CAGCAACATAAGGAGACCCT
20958	19045	TCAGCAACATAAGGAGACCC
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20961	19048	GCCTCAGCAACATAAGGAGA
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20963	19050	CAGCCTCAGCAACATAAGGA
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20965	19052	GTCAGCCTCAGCAACATAAG
20966	19053	GGTCAGCCTCAGCAACATAA
20967	19054	AGGTCAGCCTCAGCAACATA
20968	19055	AAGGTCAGCCTCAGCAACAT
20969	19056	CAAGGTCAGCCTCAGCAACA
20970	19057	TCAAGGTCAGCCTCAGCAAC
20971	19058	TTCAAGGTCAGCCTCAGCAA
20972	19059	GTTCAAGGTCAGCCTCAGCA
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20976	19063	AGGAGTTCAAGGTCAGCCTC
20977	19064	CAGGAGTTCAAGGTCAGCCT
20978	19065	TCAGGAGTTCAAGGTCAGCC
20979	19066	CTCAGGAGTTCAAGGTCAGC
20980	19067	GCTCAGGAGTTCAAGGTCAG
20981	19068	GGCTCAGGAGTTCAAGGTCA
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20985	19072	TCTGGGCTCAGGAGTTCAAG
20986	19073	ATCTGGGCTCAGGAGTTCAA
20987	19074	CATCTGGGCTCAGGAGTTCA
20988	19075	TCATCTGGGCTCAGGAGTTC
20989	19076	ATCATCTGGGCTCAGGAGTT
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20991	19078	GAATCATCTGGGCTCAGGAG
20992	19079	AGAATCATCTGGGCTCAGGA
20993	19080	CAGAATCATCTGGGCTCAGG
20994	19081	GCAGAATCATCTGGGCTCAG
20995	19082	GGCAGAATCATCTGGGCTCA
20996	19083	AGGCAGAATCATCTGGGCTC
20997	19084	GAGGCAGAATCATCTGGGCT
20998	19085	GGAGGCAGAATCATCTGGGC
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21000	19087	AAGGAGGCAGAATCATCTGG
21001	19088	TAAGGAGGCAGAATCATCTG
21002	19089	CTAAGGAGGCAGAATCATCT
21003	19090	ACTAAGGAGGCAGAATCATC
21004	19091	TACTAAGGAGGCAGAATCAT
21005	19092	CTACTAAGGAGGCAGAATCA
21006	19093	GCTACTAAGGAGGCAGAATC
21007	19094	AGCTACTAAGGAGGCAGAAT
21008	19095	CAGCTACTAAGGAGGCAGAA
21009	19096	CCAGCTACTAAGGAGGCAGA

70086	68173	AGAACACAGGCTTCCCCAGG
70087	68174	AAGAACACAGGCTTCCCCAG
70088	68175	CAAGAACACAGGCTTCCCCA
70089	68176	ACAAGAACACAGGCTTCCCC
70090	68177	CACAAGAACACAGGCTTCCC
70091	68178	ACACAAGAACACAGGCTTCC
70092	68179	TACACAAGAACACAGGCTTC
70093	68180	GTACACAAGAACACAGGCTT
70094	68181	TGTACACAAGAACACAGGCT
70095	68182	TTGTACACAAGAACACAGGC
70096	68183	ATTGTACACAAGAACACAGG
70097	68184	AATTGTACACAAGAACACAG
70098	68185	GAATTGTACACAAGAACACA
70099	68186	TGAATTGTACACAAGAACAC
70100	68187	CTGAATTGTACACAAGAACA
70101	68188	TCTGAATTGTACACAAGAAC
70102	68189	TTCTGAATTGTACACAAGAA
70103	68190	TTTCTGAATTGTACACAAGA
70104	68191	TTTTCTGAATTGTACACAAG
70105	68192	ATTTTCTGAATTGTACACAA
70106	68193	CATTTTCTGAATTGTACACA
70107	68194	ACATTTTCTGAATTGTACAC
70108	68195	AACATTTTCTGAATTGTACA
70109	68196	AAACATTTTCTGAATTGTAC
70110	68197	TAAACATTTTCTGAATTGTA
70111	68198	ATAAACATTTTCTGAATTGT
70112	68199	TATAAACATTTTCTGAATTG
70113	68200	GTATAAACATTTTCTGAATT
70114	68201	TGTATAAACATTTTCTGAAT
70115	68202	GTGTATAAACATTTTCTGAA
70116	68203	TGTGTATAAACATTTTCTGA
70117	68204	ATGTGTATAAACATTTTCTG
70118	68205	TATGTGTATAAACATTTTCT
70119	68206	ATATGTGTATAAACATTTTC
70120	68207	AATATGTGTATAAACATTTT
70121	68208	AAATATGTGTATAAACATTT
70122	68209	AAAATATGTGTATAAACATT
70123	68210	AAAAATATGTGTATAAACAT
70124	68211	AAAAAATATGTGTATAAACA
70125	68212	TAAAAAATATGTGTATAAAC
70126	68213	ATAAAAAATATGTGTATAAA
70127	68214	AATAAAAAATATGTGTATAA
70128	68215	AAATAAAAAATATGTGTATA
70129	68216	TAAATAAAAAATATGTGTAT
70130	68217	ATAAATAAAAAATATGTGTA
70131	68218	AATAAATAAAAAATATGTGT
70132	68219	AAATAAATAAAAAATATGTG
70133	68220	TAAATAAATAAAAAATATGT
70134	68221	ATAAATAAATAAAAAATATG
70135	68222	AATAAATAAATAAAAAATAT
70136	68223	AAATAAATAAATAAAAAATA
70137	68224	AAAATAAATAAATAAAAAAT
70138	68225	AAAAATAAATAAATAAAAAA
70139	68226	AAAAAATAAATAAATAAAAA
70140	68227	CAAAAAATAAATAAATAAAA
70141	68228	TCAAAAAATAAATAAATAAA
70142	68229	CTCAAAAAATAAATAAATAA
70143	68230	TCTCAAAAAATAAATAAATA
70144	68231	GTCTCAAAAAATAAATAAAT
70145	68232	CGTCTCAAAAAATAAATAAA
70146	68233	CCGTCTCAAAAAATAAATAA
70147	68234	TCCGTCTCAAAAAATAAATA
70148	68235	CTCCGTCTCAAAAAATAAAT
70149	68236	ACTCCGTCTCAAAAAATAAA
70150	68237	GACTCCGTCTCAAAAAATAA
70151	68238	AGACTCCGTCTCAAAAAATA
70152	68239	GAGACTCCGTCTCAAAAAAT
70153	68240	CGAGACTCCGTCTCAAAAAA
70154	68241	GCGAGACTCCGTCTCAAAAA
70155	68242	AGCGAGACTCCGTCTCAAAA
70156	68243	GAGCGAGACTCCGTCTCAAA

119233	117320	TAGGCACCTGCCACCACGCT
119234	117321	ATAGGCACCTGCCACCACGC
119235	117322	TATAGGCACCTGCCACCACG
119236	117323	CTATAGGCACCTGCCACCAC
119237	117324	ACTATAGGCACCTGCCACCA
119238	117325	GACTATAGGCACCTGCCACC
119239	117326	GGACTATAGGCACCTGCCAC
119240	117327	GGGACTATAGGCACCTGCCA
119241	117328	TGGGACTATAGGCACCTGCC
119242	117329	CTGGGACTATAGGCACCTGC
119243	117330	GCTGGGACTATAGGCACCTG
119244	117331	AGCTGGGACTATAGGCACCT
119245	117332	TAGCTGGGACTATAGGCACC
119246	117333	GTAGCTGGGACTATAGGCAC
119247	117334	AGTAGCTGGGACTATAGGCA
119248	117335	GAGTAGCTGGGACTATAGGC
119249	117336	CGAGTAGCTGGGACTATAGG
119250	117337	CCGAGTAGCTGGGACTATAG
119251	117338	CCCGAGTAGCTGGGACTATA
119252	117339	TCCCGAGTAGCTGGGACTAT
119253	117340	CTCCCGAGTAGCTGGGACTA
119254	117341	CCTCCCGAGTAGCTGGGACT
119255	117342	GCCTCCCGAGTAGCTGGGAC
119256	117343	AGCCTCCCGAGTAGCTGGGA
119257	117344	CAGCCTCCCGAGTAGCTGGG
119258	117345	TCAGCCTCCCGAGTAGCTGG
119259	117346	CTCAGCCTCCCGAGTAGCTG
119260	117347	CCTCAGCCTCCCGAGTAGCT
119261	117348	GCCTCAGCCTCCCGAGTAGC
119262	117349	TGCCTCAGCCTCCCGAGTAG
119263	117350	CTGCCTCAGCCTCCCGAGTA
119264	117351	CCTGCCTCAGCCTCCCGAGT
119265	117352	TCCTGCCTCAGCCTCCCGAG
119266	117353	CTCCTGCCTCAGCCTCCCGA
119267	117354	TCTCCTGCCTCAGCCTCCCG
119268	117355	TTCTCCTGCCTCAGCCTCCC
119269	117356	ATTCTCCTGCCTCAGCCTCC
119270	117357	CATTCTCCTGCCTCAGCCTC
119271	117358	CCATTCTCCTGCCTCAGCCT
119272	117359	GCCATTCTCCTGCCTCAGCC
119273	117360	TGCCATTCTCCTGCCTCAGC
119274	117361	ATGCCATTCTCCTGCCTCAG
119275	117362	CATGCCATTCTCCTGCCTCA
119276	117363	TCATGCCATTCTCCTGCCTC
119277	117364	TTCATGCCATTCTCCTGCCT
119278	117365	GTTCATGCCATTCTCCTGCC
119279	117366	GGTTCATGCCATTCTCCTGC
119280	117367	AGGTTCATGCCATTCTCCTG
119281	117368	CAGGTTCATGCCATTCTCCT
119282	117369	CCAGGTTCATGCCATTCTCC
119283	117370	CCCAGGTTCATGCCATTCTC
119284	117371	TCCCAGGTTCATGCCATTCT
119285	117372	CTCCCAGGTTCATGCCATTC
119286	117373	CCTCCCAGGTTCATGCCATT
119287	117374	GCCTCCCAGGTTCATGCCAT
119288	117375	TGCCTCCCAGGTTCATGCCA
119289	117376	CTGCCTCCCAGGTTCATGCC
119290	117377	TCTGCCTCCCAGGTTCATGC
119291	117378	CTCTGCCTCCCAGGTTCATG
119292	117379	GCTCTGCCTCCCAGGTTCAT
119293	117380	AGCTCTGCCTCCCAGGTTCA
119294	117381	CAGCTCTGCCTCCCAGGTTC
119295	117382	CCAGCTCTGCCTCCCAGGTT
119296	117383	GCCAGCTCTGCCTCCCAGGT
119297	117384	TGCCAGCTCTGCCTCCCAGG
119298	117385	CTGCCAGCTCTGCCTCCCAG
119299	117386	ACTGCCAGCTCTGCCTCCCA
119300	117387	CACTGCCAGCTCTGCCTCCC
119301	117388	TCACTGCCAGCTCTGCCTCC
119302	117389	CTCACTGCCAGCTCTGCCTC
119303	117390	GCTCACTGCCAGCTCTGCCT

21010	19097	CCCAGCTACTAAGGAGGCAG
21011	19098	TCCCAGCTACTAAGGAGGCA
21012	19099	GTCCCAGCTACTAAGGAGGC
21013	19100	AGTCCCAGCTACTAAGGAGG
21014	19101	TAGTCCCAGCTACTAAGGAG
21015	19102	GTAGTCCCAGCTACTAAGGA
21016	19103	TGTAGTCCCAGCTACTAAGG
21017	19104	GTGTAGTCCCAGCTACTAAG
21018	19105	GGTGTAGTCCCAGCTACTAA
21019	19106	GGGTGTAGTCCCAGCTACTA
21020	19107	TGGGTGTAGTCCCAGCTACT
21021	19108	GTGGGTGTAGTCCCAGCTAC
21022	19109	GGTGGGTGTAGTCCCAGCTA
21023	19110	AGGTGGGTGTAGTCCCAGCT
21024	19111	GAGGTGGGTGTAGTCCCAGC
21025	19112	GGAGGTGGGTGTAGTCCCAG
21026	19113	GGGAGGTGGGTGTAGTCCCA
21027	19114	CGGGAGGTGGGTGTAGTCCC
21028	19115	ACGGGAGGTGGGTGTAGTCC
21029	19116	AACGGGAGGTGGGTGTAGTC
21030	19117	GAACGGGAGGTGGGTGTAGT
21031	19118	GGAACGGGAGGTGGGTGTAG
21032	19119	CGGAACGGGAGGTGGGTGTA
21033	19120	ACGGAACGGGAGGTGGGTGT
21034	19121	AACGGAACGGGAGGTGGGTG
21035	19122	CAACGGAACGGGAGGTGGGT
21036	19123	ACAACGGAACGGGAGGTGGG
21037	19124	GACAACGGAACGGGAGGTGG
21038	19125	TGACAACGGAACGGGAGGTG
21039	19126	ATGACAACGGAACGGGAGGT
21040	19127	GATGACAACGGAACGGGAGG
21041	19128	AGATGACAACGGAACGGGAG
21042	19129	AAGATGACAACGGAACGGGA
21043	19130	AAAGATGACAACGGAACGGG
21044	19131	AAAAGATGACAACGGAACGG
21045	19132	AAAAAGATGACAACGGAACG
21046	19133	AAAAAAGATGACAACGGAAC
21047	19134	AAAAAAAGATGACAACGGAA
21048	19135	AAAAAAAAGATGACAACGGA
21049	19136	AAAAAAAAAGATGACAACGG
21050	19137	AAAAAAAAAAGATGACAACG
21051	19138	AAAAAAAAAAAGATGACAAC
21052	19139	AAAAAAAAAAAAGATGACAA
21053	19140	AAAAAAAAAAAAAGATGACA
21054	19141	AAAAAAAAAAAAAAGATGAC
21055	19142	GAAAAAAAAAAAAAAGATGA
21056	19143	AGAAAAAAAAAAAAAAGATG
21057	19144	AAGAAAAAAAAAAAAAAGAT
21058	19145	AAAGAAAAAAAAAAAAAAGA
21059	19146	AAAAGAAAAAAAAAAAAAAG
21060	19147	AAAAAGAAAAAAAAAAAAAA
21061	19148	AAAAAAGAAAAAAAAAAAAA
21062	19149	CAAAAAAGAAAAAAAAAAAA
21063	19150	CCAAAAAAGAAAAAAAAAAA
21064	19151	TCCAAAAAAGAAAAAAAAAA
21065	19152	CTCCAAAAAAGAAAAAAAAA
21066	19153	TCTCCAAAAAAGAAAAAAAA
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21069	19156	CTGTCTCCAAAAAAGAAAAA
21070	19157	TCTGTCTCCAAAAAAGAAAA
21071	19158	TTCTGTCTCCAAAAAAGAAA
21072	19159	ATTCTGTCTCCAAAAAAGAA
21073	19160	GATTCTGTCTCCAAAAAAGA
21074	19161	AGATTCTGTCTCCAAAAAAG
21075	19162	AAGATTCTGTCTCCAAAAAA
21076	19163	GAAGATTCTGTCTCCAAAAA
21077	19164	GGAAGATTCTGTCTCCAAAA
21078	19165	AGGAAGATTCTGTCTCCAAA
21079	19166	GAGGAAGATTCTGTCTCCAA
21080	19167	AGAGGAAGATTCTGTCTCCA

70157	68244	AGAGCGAGACTCCGTCTCAA
70158	68245	GAGAGCGAGACTCCGTCTCA
70159	68246	CGAGAGCGAGACTCCGTCTC
70160	68247	GCGAGAGCGAGACTCCGTCT
70161	68248	GGCGAGAGCGAGACTCCGTC
70162	68249	TGGCGAGAGCGAGACTCCGT
70163	68250	CTGGCGAGAGCGAGACTCCG
70164	68251	CCTGGCGAGAGCGAGACTCC
70165	68252	ACCTGGCGAGAGCGAGACTC
70166	68253	AACCTGGCGAGAGCGAGACT
70167	68254	CAACCTGGCGAGAGCGAGAC
70168	68255	CCAACCTGGCGAGAGCGAGA
70169	68256	TCCAACCTGGCGAGAGCGAG
70170	68257	CTCCAACCTGGCGAGAGCGA
70171	68258	ACTCCAACCTGGCGAGAGCG
70172	68259	CACTCCAACCTGGCGAGAGC
70173	68260	GCACTCCAACCTGGCGAGAG
70174	68261	TGCACTCCAACCTGGCGAGA
70175	68262	CTGCACTCCAACCTGGCGAG
70176	68263	ACTGCACTCCAACCTGGCGA
70177	68264	CACTGCACTCCAACCTGGCG
70178	68265	CCACTGCACTCCAACCTGGC
70179	68266	GCCACTGCACTCCAACCTGG
70180	68267	CGCCACTGCACTCCAACCTG
70181	68268	GCGCCACTGCACTCCAACCT
70182	68269	TGCGCCACTGCACTCCAACC
70183	68270	TTGCGCCACTGCACTCCAAC
70184	68271	ATTGCGCCACTGCACTCCAA
70185	68272	GATTGCGCCACTGCACTCCA
70186	68273	AGATTGCGCCACTGCACTCC
70187	68274	AAGATTGCGCCACTGCACTC
70188	68275	CAAGATTGCGCCACTGCACT
70189	68276	CCAAGATTGCGCCACTGCAC
70190	68277	GCCAAGATTGCGCCACTGCA
70191	68278	AGCCAAGATTGCGCCACTGC
70192	68279	GAGCCAAGATTGCGCCACTG
70193	68280	TGAGCCAAGATTGCGCCACT
70194	68281	GTGAGCCAAGATTGCGCCAC
70195	68282	AGTGAGCCAAGATTGCGCCA
70196	68283	TAGTGAGCCAAGATTGCGCC
70197	68284	GTAGTGAGCCAAGATTGCGC
70198	68285	TGTAGTGAGCCAAGATTGCG
70199	68286	TTGTAGTGAGCCAAGATTGC
70200	68287	GTTGTAGTGAGCCAAGATTG
70201	68288	GGTTGTAGTGAGCCAAGATT
70202	68289	AGGTTGTAGTGAGCCAAGAT
70203	68290	GAGGTTGTAGTGAGCCAAGA
70204	68291	GGAGGTTGTAGTGAGCCAAG
70205	68292	CGGAGGTTGTAGTGAGCCAA
70206	68293	GCGGAGGTTGTAGTGAGCCA
70207	68294	GGCGGAGGTTGTAGTGAGCC
70208	68295	AGGCGGAGGTTGTAGTGAGC
70209	68296	GAGGCGGAGGTTGTAGTGAG
70210	68297	GGAGGCGGAGGTTGTAGTGA
70211	68298	GGGAGGCGGAGGTTGTAGTG
70212	68299	AGGGAGGCGGAGGTTGTAGT
70213	68300	TAGGGAGGCGGAGGTTGTAG
70214	68301	CTAGGGAGGCGGAGGTTGTA
70215	68302	ACTAGGGAGGCGGAGGTTGT
70216	68303	TACTAGGGAGGCGGAGGTTG
70217	68304	CTACTAGGGAGGCGGAGGTT
70218	68305	ACTACTAGGGAGGCGGAGGT
70219	68306	AACTACTAGGGAGGCGGAGG
70220	68307	GAACTACTAGGGAGGCGGAG
70221	68308	TGAACTACTAGGGAGGCGGA
70222	68309	TTGAACTACTAGGGAGGCGG
70223	68310	CTTGAACTACTAGGGAGGCG
70224	68311	GCTTGAACTACTAGGGAGGC
70225	68312	TGCTTGAACTACTAGGGAGG
70226	68313	TTGCTTGAACTACTAGGGAG
70227	68314	ATTGCTTGAACTACTAGGGA

119304	117391	AGCTCACTGCCAGCTCTGCC
119305	117392	CAGCTCACTGCCAGCTCTGC
119306	117393	TCAGCTCACTGCCAGCTCTG
119307	117394	CTCAGCTCACTGCCAGCTCT
119308	117395	TCTCAGCTCACTGCCAGCTC
119309	117396	ATCTCAGCTCACTGCCAGCT
119310	117397	CATCTCAGCTCACTGCCAGC
119311	117398	CCATCTCAGCTCACTGCCAG
119312	117399	ACCATCTCAGCTCACTGCCA
119313	117400	CACCATCTCAGCTCACTGCC
119314	117401	GCACCATCTCAGCTCACTGC
119315	117402	GGCACCATCTCAGCTCACTG
119316	117403	TGGCACCATCTCAGCTCACT
119317	117404	GTGGCACCATCTCAGCTCAC
119318	117405	AGTGGCACCATCTCAGCTCA
119319	117406	CAGTGGCACCATCTCAGCTC
119320	117407	GCAGTGGCACCATCTCAGCT
119321	117408	TGCAGTGGCACCATCTCAGC
119322	117409	GTGCAGTGGCACCATCTCAG
119323	117410	AGTGCAGTGGCACCATCTCA
119324	117411	GAGTGCAGTGGCACCATCTC
119325	117412	GGAGTGCAGTGGCACCATCT
119326	117413	TGGAGTGCAGTGGCACCATC
119327	117414	CTGGAGTGCAGTGGCACCAT
119328	117415	GCTGGAGTGCAGTGGCACCA
119329	117416	GGCTGGAGTGCAGTGGCACC
119330	117417	AGGCTGGAGTGCAGTGGCAC
119331	117418	CAGGCTGGAGTGCAGTGGCA
119332	117419	CCAGGCTGGAGTGCAGTGGC
119333	117420	CCCAGGCTGGAGTGCAGTGG
119334	117421	ACCCAGGCTGGAGTGCAGTG
119335	117422	CACCCAGGCTGGAGTGCAGT
119336	117423	TCACCCAGGCTGGAGTGCAG
119337	117424	GTCACCCAGGCTGGAGTGCA
119338	117425	TGTCACCCAGGCTGGAGTGC
119339	117426	CTGTCACCCAGGCTGGAGTG
119340	117427	TCTGTCACCCAGGCTGGAGT
119341	117428	CTCTGTCACCCAGGCTGGAG
119342	117429	GCTCTGTCACCCAGGCTGGA
119343	117430	CGCTCTGTCACCCAGGCTGG
119344	117431	TCGCTCTGTCACCCAGGCTG
119345	117432	CTCGCTCTGTCACCCAGGCT
119346	117433	TCTCGCTCTGTCACCCAGGC
119347	117434	GTCTCGCTCTGTCACCCAGG
119348	117435	AGTCTCGCTCTGTCACCCAG
119349	117436	GAGTCTCGCTCTGTCACCCA
119350	117437	GGAGTCTCGCTCTGTCACCC
119351	117438	CGGAGTCTCGCTCTGTCACC
119352	117439	ACGGAGTCTCGCTCTGTCAC
119353	117440	GACGGAGTCTCGCTCTGTCA
119354	117441	AGACGGAGTCTCGCTCTGTC
119355	117442	GAGACGGAGTCTCGCTCTGT
119356	117443	TGAGACGGAGTCTCGCTCTG
119357	117444	TTGAGACGGAGTCTCGCTCT
119358	117445	TTTGAGACGGAGTCTCGCTC
119359	117446	TTTTGAGACGGAGTCTCGCT
119360	117447	TTTTTGAGACGGAGTCTCGC
119361	117448	TTTTTTGAGACGGAGTCTCG
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119363	117450	TTTTTTTTGAGACGGAGTCT
119364	117451	TTTTTTTTTGAGACGGAGTC
119365	117452	TTTTTTTTTTGAGACGGAGT
119366	117453	TTTTTTTTTTTGAGACGGAG
119367	117454	TTTTTTTTTTTTGAGACGGA
119368	117455	TTTTTTTTTTTTTGAGACGG
119369	117456	TTTTTTTTTTTTTTGAGACG
119370	117457	TTTTTTTTTTTTTTTGAGAC
119371	117458	TTTTTTTTTTTTTTTTGAGA
119372	117459	TTTTTTTTTTTTTTTTTGAG
119373	117460	TTTTTTTTTTTTTTTTTTGA
119374	117461	TTTTTTTTTTTTTTTTTTTG

21081	19168	CAGAGGAAGATTCTGTCTCC
21082	19169	ACAGAGGAAGATTCTGTCTC
21083	19170	AACAGAGGAAGATTCTGTCT
21084	19171	CAACAGAGGAAGATTCTGTC
21085	19172	GCAACAGAGGAAGATTCTGT
21086	19173	AGCAACAGAGGAAGATTCTG
21087	19174	GAGCAACAGAGGAAGATTCT
21088	19175	TGAGCAACAGAGGAAGATTC
21089	19176	CTGAGCAACAGAGGAAGATT
21090	19177	CCTGAGCAACAGAGGAAGAT
21091	19178	CCCTGAGCAACAGAGGAAGA
21092	19179	ACCCTGAGCAACAGAGGAAG
21093	19180	CACCCTGAGCAACAGAGGAA
21094	19181	CCACCCTGAGCAACAGAGGA
21095	19182	TCCACCCTGAGCAACAGAGG
21096	19183	CTCCACCCTGAGCAACAGAG
21097	19184	ACTCCACCCTGAGCAACAGA
21098	19185	CACTCCACCCTGAGCAACAG
21099	19186	ACACTCCACCCTGAGCAACA
21100	19187	TACACTCCACCCTGAGCAAC
21101	19188	CTACACTCCACCCTGAGCAA
21102	19189	ACTACACTCCACCCTGAGCA
21103	19190	CACTACACTCCACCCTGAGC
21104	19191	CCACTACACTCCACCCTGAG
21105	19192	GCCACTACACTCCACCCTGA
21106	19193	TGCCACTACACTCCACCCTG
21107	19194	GTGCCACTACACTCCACCCT
21108	19195	CGTGCCACTACACTCCACCC
21109	19196	TCGTGCCACTACACTCCACC
21110	19197	ATCGTGCCACTACACTCCAC
21111	19198	GATCGTGCCACTACACTCCA
21112	19199	TGATCGTGCCACTACACTCC
21113	19200	ATGATCGTGCCACTACACTC
21114	19201	TATGATCGTGCCACTACACT
21115	19202	CTATGATCGTGCCACTACAC
21116	19203	GCTATGATCGTGCCACTACA
21117	19204	AGCTATGATCGTGCCACTAC
21118	19205	AAGCTATGATCGTGCCACTA
21119	19206	TAAGCTATGATCGTGCCACT
21120	19207	GTAAGCTATGATCGTGCCAC
21121	19208	AGTAAGCTATGATCGTGCCA
21122	19209	CAGTAAGCTATGATCGTGCC
21123	19210	ACAGTAAGCTATGATCGTGC
21124	19211	TACAGTAAGCTATGATCGTG
21125	19212	TTACAGTAAGCTATGATCGT
21126	19213	GTTACAGTAAGCTATGATCG
21127	19214	AGTTACAGTAAGCTATGATC
21128	19215	CAGTTACAGTAAGCTATGAT
21129	19216	ACAGTTACAGTAAGCTATGA
21130	19217	CACAGTTACAGTAAGCTATG
21131	19218	ACACAGTTACAGTAAGCTAT
21132	19219	TACACAGTTACAGTAAGCTA
21133	19220	TTACACAGTTACAGTAAGCT
21134	19221	GTTACACAGTTACAGTAAGC
21135	19222	GGTTACACAGTTACAGTAAG
21136	19223	AGGTTACACAGTTACAGTAA
21137	19224	GAGGTTACACAGTTACAGTA
21138	19225	CGAGGTTACACAGTTACAGT
21139	19226	TCGAGGTTACACAGTTACAG
21140	19227	TTCGAGGTTACACAGTTACA
21141	19228	ATTCGAGGTTACACAGTTAC
21142	19229	AATTCGAGGTTACACAGTTA
21143	19230	GAATTCGAGGTTACACAGTT
21144	19231	AGAATTCGAGGTTACACAGT
21145	19232	AAGAATTCGAGGTTACACAG
21146	19233	CAAGAATTCGAGGTTACACA
21147	19234	CCAAGAATTCGAGGTTACAC
21148	19235	CCCAAGAATTCGAGGTTACA
21149	19236	GCCCAAGAATTCGAGGTTAC
21150	19237	AGCCCAAGAATTCGAGGTTA
21151	19238	GAGCCCAAGAATTCGAGGTT

70228	68315	AATTGCTTGAACTACTAGGG
70229	68316	GAATTGCTTGAACTACTAGG
70230	68317	TGAATTGCTTGAACTACTAG
70231	68318	TTGAATTGCTTGAACTACTA
70232	68319	CTTGAATTGCTTGAACTACT
70233	68320	CCTTGAATTGCTTGAACTAC
70234	68321	ACCTTGAATTGCTTGAACTA
70235	68322	AACCTTGAATTGCTTGAACT
70236	68323	GAACCTTGAATTGCTTGAAC
70237	68324	TGAACCTTGAATTGCTTGAA
70238	68325	TTGAACCTTGAATTGCTTGA
70239	68326	CTTGAACCTTGAATTGCTTG
70240	68327	GCTTGAACCTTGAATTGCTT
70241	68328	TGCTTGAACCTTGAATTGCT
70242	68329	TTGCTTGAACCTTGAATTGC
70243	68330	ATTGCTTGAACCTTGAATTG
70244	68331	AATTGCTTGAACCTTGAATT
70245	68332	GAATTGCTTGAACCTTGAAT
70246	68333	CGAATTGCTTGAACCTTGAA
70247	68334	GCGAATTGCTTGAACCTTGA
70248	68335	GGCGAATTGCTTGAACCTTG
70249	68336	AGGCGAATTGCTTGAACCTT
70250	68337	CAGGCGAATTGCTTGAACCT
70251	68338	GCAGGCGAATTGCTTGAACC
70252	68339	GGCAGGCGAATTGCTTGAAC
70253	68340	AGGCAGGCGAATTGCTTGAA
70254	68341	GAGGCAGGCGAATTGCTTGA
70255	68342	TGAGGCAGGCGAATTGCTTG
70256	68343	CTGAGGCAGGCGAATTGCTT
70257	68344	GCTGAGGCAGGCGAATTGCT
70258	68345	GGCTGAGGCAGGCGAATTGC
70259	68346	AGGCTGAGGCAGGCGAATTG
70260	68347	GAGGCTGAGGCAGGCGAATT
70261	68348	GGAGGCTGAGGCAGGCGAAT
70262	68349	GGGAGGCTGAGGCAGGCGAA
70263	68350	CGGGAGGCTGAGGCAGGCGA
70264	68351	TCGGGAGGCTGAGGCAGGCG
70265	68352	CTCGGGAGGCTGAGGCAGGC
70266	68353	ACTCGGGAGGCTGAGGCAGG
70267	68354	TACTCGGGAGGCTGAGGCAG
70268	68355	CTACTCGGGAGGCTGAGGCA
70269	68356	GCTACTCGGGAGGCTGAGGC
70270	68357	AGCTACTCGGGAGGCTGAGG
70271	68358	CAGCTACTCGGGAGGCTGAG
70272	68359	CCAGCTACTCGGGAGGCTGA
70273	68360	CCCAGCTACTCGGGAGGCTG
70274	68361	TCCCAGCTACTCGGGAGGCT
70275	68362	GTCCCAGCTACTCGGGAGGC
70276	68363	AGTCCCAGCTACTCGGGAGG
70277	68364	TAGTCCCAGCTACTCGGGAG
70278	68365	ATAGTCCCAGCTACTCGGGA
70279	68366	TATAGTCCCAGCTACTCGGG
70280	68367	CTATAGTCCCAGCTACTCGG
70281	68368	CCTATAGTCCCAGCTACTCG
70282	68369	GCCTATAGTCCCAGCTACTC
70283	68370	CGCCTATAGTCCCAGCTACT
70284	68371	ACGCCTATAGTCCCAGCTAC
70285	68372	CACGCCTATAGTCCCAGCTA
70286	68373	ACACGCCTATAGTCCCAGCT
70287	68374	TACACGCCTATAGTCCCAGC
70288	68375	GTACACGCCTATAGTCCCAG
70289	68376	GGTACACGCCTATAGTCCCA
70290	68377	TGGTACACGCCTATAGTCCC
70291	68378	GTGGTACACGCCTATAGTCC
70292	68379	GGTGGTACACGCCTATAGTC
70293	68380	TGGTGGTACACGCCTATAGT
70294	68381	GTGGTGGTACACGCCTATAG
70295	68382	CGTGGTGGTACACGCCTATA
70296	68383	GCGTGGTGGTACACGCCTAT
70297	68384	GGCGTGGTGGTACACGCCTA
70298	68385	AGGCGTGGTGGTACACGCCT

119375	117462	TTTTTTTTTTTTTTTTTTT
119376	117463	TTTTTTTTTTTTTTTTTTT
119377	117464	TTTTTTTTTTTTTTTTTTT
119378	117465	ATTTTTTTTTTTTTTTTTT
119379	117466	TATTTTTTTTTTTTTTTTT
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119382	117469	TACTATTTTTTTTTTTTTT
119383	117470	CTACTATTTTTTTTTTTTT
119384	117471	TCTACTATTTTTTTTTTTT
119385	117472	CTCTACTATTTTTTTTTTT
119386	117473	TCTCTACTATTTTTTTTTT
119387	117474	TTCTCTACTATTTTTTTTT
119388	117475	TTTCTCTACTATTTTTTTT
119389	117476	CTTTCTCTACTATTTTTTT
119390	117477	CCTTTCTCTACTATTTTTT
119391	117478	CCCTTTCTCTACTATTTTT
119392	117479	GCCCTTTCTCTACTATTTT
119393	117480	AGCCCTTTCTCTACTATTT
119394	117481	AAGCCCTTTCTCTACTATT
119395	117482	AAAGCCCTTTCTCTACTAT
119396	117483	CAAAGCCCTTTCTCTACTA
119397	117484	GCAAAGCCCTTTCTCTACT
119398	117485	GGCAAAGCCCTTTCTCTAC
119399	117486	TGGCAAAGCCCTTTCTCTA
119400	117487	ATGGCAAAGCCCTTTCTCT
119401	117488	CATGGCAAAGCCCTTTCTC
119402	117489	ACATGGCAAAGCCCTTTCT
119403	117490	AACATGGCAAAGCCCTTTC
119404	117491	CAACATGGCAAAGCCCTTT
119405	117492	CCAACATGGCAAAGCCCTT
119406	117493	GCCAACATGGCAAAGCCCT
119407	117494	GGCCAACATGGCAAAGCCC
119408	117495	CGGCCAACATGGCAAAGCC
119409	117496	CCGGCCAACATGGCAAAGC
119410	117497	CCCGGCCAACATGGCAAAG
119411	117498	GCCCGGCCAACATGGCAAA
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119413	117500	CAGCCCGGCCAACATGGCA
119414	117501	CCAGCCCGGCCAACATGGC
119415	117502	ACCAGCCCGGCCAACATGG
119416	117503	GACCAGCCCGGCCAACATG
119417	117504	AGACCAGCCCGGCCAACAT
119418	117505	AAGACCAGCCCGGCCAACA
119419	117506	CAAGACCAGCCCGGCCAAC
119420	117507	TCAAGACCAGCCCGGCCAA
119421	117508	TTCAAGACCAGCCCGGCCA
119422	117509	GTTCAAGACCAGCCCGGCC
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119424	117511	GAGTTCAAGACCAGCCCGG
119425	117512	GGAGTTCAAGACCAGCCCG
119426	117513	AGGAGTTCAAGACCAGCCC
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119428	117515	CCAGGAGTTCAAGACCAGC
119429	117516	GCCAGGAGTTCAAGACCAGC
119430	117517	GGCCAGGAGTTCAAGACCAG
119431	117518	AGGCCAGGAGTTCAAGACCA
119432	117519	GAGGCCAGGAGTTCAAGACC
119433	117520	TGAGGCCAGGAGTTCAAGAC
119434	117521	TTGAGGCCAGGAGTTCAAGA
119435	117522	CTTGAGGCCAGGAGTTCAAG
119436	117523	ACTTGAGGCCAGGAGTTCAA
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119438	117525	TCACTTGAGGCCAGGAGTTC
119439	117526	ATCACTTGAGGCCAGGAGTT
119440	117527	GATCACTTGAGGCCAGGAGT
119441	117528	GGATCACTTGAGGCCAGGAG
119442	117529	TGGATCACTTGAGGCCAGGA
119443	117530	GTGGATCACTTGAGGCCAGG
119444	117531	GGTGGATCACTTGAGGCCAG
119445	117532	AGGTGGATCACTTGAGGCCA

21152	19239	TGAGCCCAAGAATTCGAGGT
21153	19240	TTGAGCCCAAGAATTCGAGG
21154	19241	CTTGAGCCCAAGAATTCGAG
21155	19242	GCTTGAGCCCAAGAATTCGA
21156	19243	TGCTTGAGCCCAAGAATTCG
21157	19244	TTGCTTGAGCCCAAGAATTC
21158	19245	ATTGCTTGAGCCCAAGAATT
21159	19246	GATTGCTTGAGCCCAAGAAT
21160	19247	TGATTGCTTGAGCCCAAGAA
21161	19248	ATGATTGCTTGAGCCCAAGA
21162	19249	GATGATTGCTTGAGCCCAAG
21163	19250	GGATGATTGCTTGAGCCCAA
21164	19251	GGGATGATTGCTTGAGCCCA
21165	19252	TGGGATGATTGCTTGAGCCC
21166	19253	ATGGGATGATTGCTTGAGCC
21167	19254	GATGGGATGATTGCTTGAGC
21168	19255	TGATGGGATGATTGCTTGAG
21169	19256	ATGATGGGATGATTGCTTGA
21170	19257	GATGATGGGATGATTGCTTG
21171	19258	GGATGATGGGATGATTGCTT
21172	19259	GGGATGATGGGATGATTGCT
21173	19260	TGGGATGATGGGATGATTGC
21174	19261	GTGGGATGATGGGATGATTG
21175	19262	GGTGGGATGATGGGATGATT
21176	19263	AGGTGGGATGATGGGATGAT
21177	19264	GAGGTGGGATGATGGGATGA
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21180	19267	GCTGAGGTGGGATGATGGGA
21181	19268	AGCTGAGGTGGGATGATGGG
21182	19269	AAGCTGAGGTGGGATGATGG
21183	19270	CAAGCTGAGGTGGGATGATG
21184	19271	GCAAGCTGAGGTGGGATGAT
21185	19272	AGCAAGCTGAGGTGGGATGA
21186	19273	CAGCAAGCTGAGGTGGGATG
21187	19274	TCAGCAAGCTGAGGTGGGAT
21188	19275	CTCAGCAAGCTGAGGTGGGA
21189	19276	ACTCAGCAAGCTGAGGTGGG
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21191	19278	GTACTCAGCAAGCTGAGGTG
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21193	19280	AGGTACTCAGCAAGCTGAGG
21194	19281	CAGGTACTCAGCAAGCTGAG
21195	19282	CCAGGTACTCAGCAAGCTGA
21196	19283	CCCAGGTACTCAGCAAGCTG
21197	19284	CCCCAGGTACTCAGCAAGCT
21198	19285	GCCCCAGGTACTCAGCAAGC
21199	19286	AGCCCCAGGTACTCAGCAAG
21200	19287	TAGCCCCAGGTACTCAGCAA
21201	19288	GTAGCCCCAGGTACTCAGCA
21202	19289	TGTAGCCCCAGGTACTCAGC
21203	19290	CTGTAGCCCCAGGTACTCAG
21204	19291	CCTGTAGCCCCAGGTACTCA
21205	19292	ACCTGTAGCCCCAGGTACTC
21206	19293	CACCTGTAGCCCCAGGTACT
21207	19294	ACACCTGTAGCCCCAGGTAC
21208	19295	CACACCTGTAGCCCCAGGTA
21209	19296	ACACACCTGTAGCCCCAGGT
21210	19297	TACACACCTGTAGCCCCAGG
21211	19298	GTACACACCTGTAGCCCCAG
21212	19299	GGTACACACCTGTAGCCCCA
21213	19300	TGGTACACACCTGTAGCCCC
21214	19301	GTGGTACACACCTGTAGCCC
21215	19302	GGTGGTACACACCTGTAGCC
21216	19303	TGGTGGTACACACCTGTAGC
21217	19304	ATGGTGGTACACACCTGTAG
21218	19305	CATGGTGGTACACACCTGTA
21219	19306	ACATGGTGGTACACACCTGT
21220	19307	GACATGGTGGTACACACCTG
21221	19308	GGACATGGTGGTACACACCT
21222	19309	CGGACATGGTGGTACACACC

70299	68386	TAGGCGTGGTGGTACACGCC
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70301	68388	GGTAGGCGTGGTGGTACACG
70302	68389	AGGTAGGCGTGGTGGTACAC
70303	68390	TAGGTAGGCGTGGTGGTACA
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70305	68392	ATTAGGTAGGCGTGGTGGTA
70306	68393	AATTAGGTAGGCGTGGTGGT
70307	68394	AAATTAGGTAGGCGTGGTGG
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70333	68420	AAACCCTGTCTCTACTAAAA
70334	68421	GAAACCCTGTCTCTACTAAA
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70336	68423	GTGAAACCCTGTCTCTACTA
70337	68424	GGTGAAACCCTGTCTCTACT
70338	68425	TGGTGAAACCCTGTCTCTAC
70339	68426	ATGGTGAAACCCTGTCTCTA
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70342	68429	AACATGGTGAAACCCTGTCT
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70350	68437	TCCTGGCCAACATGGTGAAA
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70352	68439	CATCCTGGCCAACATGGTGA
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70356	68443	AGACCATCCTGGCCAACATG
70357	68444	GAGACCATCCTGGCCAACAT
70358	68445	CGAGACCATCCTGGCCAACA
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70360	68447	ATCGAGACCATCCTGGCCAA
70361	68448	GATCGAGACCATCCTGGCCA
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70363	68450	GAGATCGAGACCATCCTGGC
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70365	68452	AAGAGATCGAGACCATCCTG
70366	68453	CAAGAGATCGAGACCATCCT
70367	68454	TCAAGAGATCGAGACCATCC
70368	68455	GTCAAGAGATCGAGACCATC
70369	68456	GGTCAAGAGATCGAGACCAT

119446	117533	GAGGTGGATCACTTGAGGCC
119447	117534	GGAGGTGGATCACTTGAGGC
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119449	117536	AGGGAGGTGGATCACTTGAG
119450	117537	GAGGGAGGTGGATCACTTGA
119451	117538	CGAGGGAGGTGGATCACTTG
119452	117539	CCGAGGGAGGTGGATCACTT
119453	117540	GCCGAGGGAGGTGGATCACT
119454	117541	GGCCGAGGGAGGTGGATCAC
119455	117542	AGGCCGAGGGAGGTGGATCA
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119457	117544	GGAGGCCGAGGGAGGTGGAT
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119468	117555	CCAGCACTTTGGGAGGCCGA
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119471	117558	ATCCCAGCACTTTGGGAGGC
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119473	117560	TAATCCCAGCACTTTGGGAG
119474	117561	GTAATCCCAGCACTTTGGGA
119475	117562	TGTAATCCCAGCACTTTGGG
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119484	117571	GCTCACACCTGTAATCCCAG
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119488	117575	AGTGGCTCACACCTGTAATC
119489	117576	CAGTGGCTCACACCTGTAAT
119490	117577	GCAGTGGCTCACACCTGTAA
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119492	117579	GAGCAGTGGCTCACACCTGT
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21223	19310	CCGGACATGGTGGTACACAC
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21228	19315	ATTAGCCGGACATGGTGGTA
21229	19316	AATTAGCCGGACATGGTGGT
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21235	19322	AAAAGTAATTAGCCGGACAT
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21237	19324	AGAAAAGTAATTAGCCGGAC
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21241	19328	AATAAGAAAAGTAATTAGCC
21242	19329	AAATAAGAAAAGTAATTAGC
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21245	19332	TAAAAATAAGAAAAGTAATT
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21268	19355	GCAAGATCCTATCTCCGAAA
21269	19356	AGCAAGATCCTATCTCCGAA
21270	19357	GAGCAAGATCCTATCTCCGA
21271	19358	AGAGCAAGATCCTATCTCCG
21272	19359	CAGAGCAAGATCCTATCTCC
21273	19360	ACAGAGCAAGATCCTATCTC
21274	19361	AACAGAGCAAGATCCTATCT
21275	19362	CAACAGAGCAAGATCCTATC
21276	19363	GCAACAGAGCAAGATCCTAT
21277	19364	GGCAACAGAGCAAGATCCTA
21278	19365	GGGCAACAGAGCAAGATCCT
21279	19366	TGGGCAACAGAGCAAGATCC
21280	19367	CTGGGCAACAGAGCAAGATC
21281	19368	CCTGGGCAACAGAGCAAGAT
21282	19369	GCCTGGGCAACAGAGCAAGA
21283	19370	AGCCTGGGCAACAGAGCAAG
21284	19371	CAGCCTGGGCAACAGAGCAA
21285	19372	CCAGCCTGGGCAACAGAGCA
21286	19373	ACCAGCCTGGGCAACAGAGC
21287	19374	CACCAGCCTGGGCAACAGAG
21288	19375	ACACCAGCCTGGGCAACAGA
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70370	68457	AGGTCAAGAGATCGAGACCA
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70373	68460	ATGAGGTCAAGAGATCGAGA
70374	68461	CATGAGGTCAAGAGATCGAG
70375	68462	TCATGAGGTCAAGAGATCGA
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70388	68475	TGAGGCGGGTGGATCATGAG
70389	68476	CTGAGGCGGGTGGATCATGA
70390	68477	GCTGAGGCGGGTGGATCATG
70391	68478	GGCTGAGGCGGGTGGATCAT
70392	68479	AGGCTGAGGCGGGTGGATCA
70393	68480	GAGGCTGAGGCGGGTGGATC
70394	68481	GGAGGCTGAGGCGGGTGGAT
70395	68482	GGGAGGCTGAGGCGGGTGGA
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70397	68484	TTGGGAGGCTGAGGCGGGTG
70398	68485	TTTGGGAGGCTGAGGCGGGT
70399	68486	CTTTGGGAGGCTGAGGCGGG
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70407	68494	TCCCAGCACTTTGGGAGGCT
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70410	68497	TAATCCCAGCACTTTGGGAG
70411	68498	GTAATCCCAGCACTTTGGGA
70412	68499	TGTAATCCCAGCACTTTGGG
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70414	68501	TCTGTAATCCCAGCACTTTG
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70419	68506	TCACATCTGTAATCCCAGCA
70420	68507	CTCACATCTGTAATCCCAGC
70421	68508	GCTCACATCTGTAATCCCAG
70422	68509	GGCTCACATCTGTAATCCCA
70423	68510	TGGCTCACATCTGTAATCCC
70424	68511	GTGGCTCACATCTGTAATCC
70425	68512	AGTGGCTCACATCTGTAATC
70426	68513	CAGTGGCTCACATCTGTAAT
70427	68514	ACAGTGGCTCACATCTGTAA
70428	68515	CACAGTGGCTCACATCTGTA
70429	68516	GCACAGTGGCTCACATCTGT
70430	68517	GGCACAGTGGCTCACATCTG
70431	68518	GGGCACAGTGGCTCACATCT
70432	68519	TGGGCACAGTGGCTCACATC
70433	68520	CTGGGCACAGTGGCTCACAT
70434	68521	GCTGGGCACAGTGGCTCACA
70435	68522	GGCTGGGCACAGTGGCTCAC
70436	68523	AGGCTGGGCACAGTGGCTCA
70437	68524	CAGGCTGGGCACAGTGGCTC
70438	68525	ACAGGCTGGGCACAGTGGCT
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119517	117604	GGTAAAAGTGGTATATTCAG
119518	117605	AGGTAAAAGTGGTATATTCA
119519	117606	TAGGTAAAAGTGGTATATTC
119520	117607	ATAGGTAAAAGTGGTATATT
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119522	117609	TGATAGGTAAAAGTGGTATA
119523	117610	ATGATAGGTAAAAGTGGTAT
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119529	117616	CAACTGATGATAGGTAAAAG
119530	117617	TCAACTGATGATAGGTAAAA
119531	117618	ATCAACTGATGATAGGTAAA
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119534	117621	TTCATCAACTGATGATAGGT
119535	117622	GTTCATCAACTGATGATAGG
119536	117623	TGTTCATCAACTGATGATAG
119537	117624	ATGTTCATCAACTGATGATA
119538	117625	AATGTTCATCAACTGATGAT
119539	117626	AAATGTTCATCAACTGATGA
119540	117627	CAAATGTTCATCAACTGATG
119541	117628	CCAAATGTTCATCAACTGAT
119542	117629	TCCAAATGTTCATCAACTGA
119543	117630	ATCCAAATGTTCATCAACTG
119544	117631	AATCCAAATGTTCATCAACT
119545	117632	TAATCCAAATGTTCATCAAC
119546	117633	ATAATCCAAATGTTCATCAA
119547	117634	AATAATCCAAATGTTCATCA
119548	117635	AAATAATCCAAATGTTCATC
119549	117636	GAAATAATCCAAATGTTCAT
119550	117637	GGAAATAATCCAAATGTTCA
119551	117638	AGGAAATAATCCAAATGTTC
119552	117639	AAGGAAATAATCCAAATGTT
119553	117640	AAAGGAAATAATCCAAATGT
119554	117641	AAAAGGAAATAATCCAAATG
119555	117642	AAAAAGGAAATAATCCAAAT
119556	117643	GAAAAAGGAAATAATCCAAA
119557	117644	AGAAAAAGGAAATAATCCAA
119558	117645	CAGAAAAAGGAAATAATCCA
119559	117646	CCAGAAAAAGGAAATAATCC
119560	117647	GCCAGAAAAAGGAAATAATC
119561	117648	TGCCAGAAAAAGGAAATAAT
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119563	117650	ATTGCCAGAAAAAGGAAATA
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119565	117652	TCATTGCCAGAAAAAGGAAA
119566	117653	CTCATTGCCAGAAAAAGGAA
119567	117654	ACTCATTGCCAGAAAAAGGA
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119569	117656	TTACTCATTGCCAGAAAAAG
119570	117657	ATTACTCATTGCCAGAAAAA
119571	117658	CATTACTCATTGCCAGAAAA
119572	117659	GCATTACTCATTGCCAGAAA
119573	117660	AGCATTACTCATTGCCAGAA
119574	117661	AAGCATTACTCATTGCCAGA
119575	117662	AAAGCATTACTCATTGCCAG
119576	117663	AAAAGCATTACTCATTGCCA
119577	117664	CAAAAGCATTACTCATTGCC
119578	117665	ACAAAAGCATTACTCATTGC
119579	117666	CACAAAAGCATTACTCATTG
119580	117667	CCACAAAAGCATTACTCATT
119581	117668	TCCACAAAAGCATTACTCAT
119582	117669	ATCCACAAAAGCATTACTCA
119583	117670	AATCCACAAAAGCATTACTC
119584	117671	AAATCCACAAAAGCATTACT
119585	117672	AAAATCCACAAAAGCATTAC
119586	117673	GAAAATCCACAAAAGCATTA
119587	117674	TGAAAATCCACAAAAGCATT

21294	19381	AGTTTGACACCAGCCTGGGC
21295	19382	GAGTTTGACACCAGCCTGGG
21296	19383	GGAGTTTGACACCAGCCTGG
21297	19384	AGGAGTTTGACACCAGCCTG
21298	19385	CAGGAGTTTGACACCAGCCT
21299	19386	CCAGGAGTTTGACACCAGCC
21300	19387	CCCAGGAGTTTGACACCAGC
21301	19388	GCCCAGGAGTTTGACACCAG
21302	19389	AGCCCAGGAGTTTGACACCA
21303	19390	GAGCCCAGGAGTTTGACACC
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21305	19392	TTGAGCCCAGGAGTTTGACA
21306	19393	CTTGAGCCCAGGAGTTTGAC
21307	19394	ACTTGAGCCCAGGAGTTTGA
21308	19395	CACTTGAGCCCAGGAGTTTG
21309	19396	TCACTTGAGCCCAGGAGTTT
21310	19397	TTCACTTGAGCCCAGGAGTT
21311	19398	TTTCACTTGAGCCCAGGAGT
21312	19399	GTTTCACTTGAGCCCAGGAG
21313	19400	AGTTTCACTTGAGCCCAGGA
21314	19401	GAGTTTCACTTGAGCCCAGG
21315	19402	AGAGTTTCACTTGAGCCCAG
21316	19403	AAGAGTTTCACTTGAGCCCA
21317	19404	CAAGAGTTTCACTTGAGCCC
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21319	19406	GGCAAGAGTTTCACTTGAGC
21320	19407	AGGCAAGAGTTTCACTTGAG
21321	19408	AAGGCAAGAGTTTCACTTGA
21322	19409	CAAGGCAAGAGTTTCACTTG
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21325	19412	GGCCAAGGCAAGAGTTTCAC
21326	19413	AGGCCAAGGCAAGAGTTTCA
21327	19414	GAGGCCAAGGCAAGAGTTTC
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21332	19419	TTTGGGAGGCCAAGGCAAGA
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21334	19421	ACTTTGGGAGGCCAAGGCAA
21335	19422	CACTTTGGGAGGCCAAGGCA
21336	19423	ACACTTTGGGAGGCCAAGGC
21337	19424	AACACTTTGGGAGGCCAAGG
21338	19425	CAACACTTTGGGAGGCCAAG
21339	19426	CCAACACTTTGGGAGGCCAA
21340	19427	CCCAACACTTTGGGAGGCCA
21341	19428	TCCCAACACTTTGGGAGGCC
21342	19429	CTCCCAACACTTTGGGAGGC
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21344	19431	CCCTCCCAACACTTTGGGAG
21345	19432	TCCCTCCCAACACTTTGGGA
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21349	19436	GTAATCCCTCCCAACACTTT
21350	19437	TGTAATCCCTCCCAACACTT
21351	19438	CTGTAATCCCTCCCAACACT
21352	19439	CCTGTAATCCCTCCCAACAC
21353	19440	GCCTGTAATCCCTCCCAACA
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21355	19442	ATGCCTGTAATCCCTCCCAA
21356	19443	CATGCCTGTAATCCCTCCCA
21357	19444	TCATGCCTGTAATCCCTCCC
21358	19445	CTCATGCCTGTAATCCCTCC
21359	19446	GCTCATGCCTGTAATCCCTC
21360	19447	GGCTCATGCCTGTAATCCCT
21361	19448	TGGCTCATGCCTGTAATCCC
21362	19449	GTGGCTCATGCCTGTAATCC
21363	19450	AGTGGCTCATGCCTGTAATC
21364	19451	CAGTGGCTCATGCCTGTAAT

70441	68528	TCAACAGGCTGGGCACAGTG
70442	68529	ATCAACAGGCTGGGCACAGT
70443	68530	AATCAACAGGCTGGGCACAG
70444	68531	AAATCAACAGGCTGGGCACA
70445	68532	TAAATCAACAGGCTGGGCAC
70446	68533	TTAAATCAACAGGCTGGGCA
70447	68534	ATTAAATCAACAGGCTGGGC
70448	68535	AATTAAATCAACAGGCTGGG
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70450	68537	AAAATTAAATCAACAGGCTG
70451	68538	TAAAATTAAATCAACAGGCT
70452	68539	TTAAAATTAAATCAACAGGC
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70454	68541	GTTTAAAATTAAATCAACAG
70455	68542	TGTTTAAAATTAAATCAACA
70456	68543	CTGTTTAAAATTAAATCAAC
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70459	68546	ACTCTGTTTAAAATTAAATC
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70461	68548	AAACTCTGTTTAAAATTAAA
70462	68549	GAAACTCTGTTTAAAATTAA
70463	68550	CGAAACTCTGTTTAAAATTA
70464	68551	GCGAAACTCTGTTTAAAATT
70465	68552	AGCGAAACTCTGTTTAAAAT
70466	68553	GAGCGAAACTCTGTTTAAAA
70467	68554	AGAGCGAAACTCTGTTTAAA
70468	68555	AAGAGCGAAACTCTGTTTAA
70469	68556	CAAGAGCGAAACTCTGTTTA
70470	68557	ACAAGAGCGAAACTCTGTTT
70471	68558	AACAAGAGCGAAACTCTGTT
70472	68559	TAACAAGAGCGAAACTCTGT
70473	68560	GTAACAAGAGCGAAACTCTG
70474	68561	GGTAACAAGAGCGAAACTCT
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70476	68563	TGGGTAACAAGAGCGAAACT
70477	68564	CTGGGTAACAAGAGCGAAAC
70478	68565	CCTGGGTAACAAGAGCGAAA
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70481	68568	CAGCCTGGGTAACAAGAGCG
70482	68569	CCAGCCTGGGTAACAAGAGC
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70493	68580	ACCATTGCACTCCAGCCTGG
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70495	68582	GCACCATTGCACTCCAGCCT
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70498	68585	ATCGCACCATTGCACTCCAG
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70500	68587	AGATCGCACCATTGCACTCC
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70505	68592	AGCCGAGATCGCACCATTGC
70506	68593	GAGCCGAGATCGCACCATTG
70507	68594	TGAGCCGAGATCGCACCATT
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70509	68596	GGTGAGCCGAGATCGCACCA
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119588	117675	ATGAAAATCCACAAAAGCAT
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119594	117681	TTGTACATGAAAATCCACAA
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119597	117684	AATTTGTACATGAAAATCCA
119598	117685	AAATTTGTACATGAAAATCC
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119601	117688	TGAAAATTTGTACATGAAAA
119602	117689	ATGAAAATTTGTACATGAAA
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119619	117706	ACTGCTCCCAGCCTCATATG
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119621	117708	CCACTGCTCCCAGCCTCATA
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119625	117712	TGAGCCACTGCTCCCAGCCT
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119629	117716	GGCATGAGCCACTGCTCCCA
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119633	117720	TATAGGCATGAGCCACTGCT
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119636	117723	GATTATAGGCATGAGCCACT
119637	117724	GGATTATAGGCATGAGCCAC
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21366	19453	TGCAGTGGCTCATGCCTGTA
21367	19454	GTGCAGTGGCTCATGCCTGT
21368	19455	GGTGCAGTGGCTCATGCCTG
21369	19456	GGGTGCAGTGGCTCATGCCT
21370	19457	TGGGTGCAGTGGCTCATGCC
21371	19458	CTGGGTGCAGTGGCTCATGC
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21373	19460	GGCTGGGTGCAGTGGCTCAT
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21378	19465	GAGGAGGCTGGGTGCAGTGG
21379	19466	AGAGGAGGCTGGGTGCAGTG
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21382	19469	GAAAGAGGAGGCTGGGTGCA
21383	19470	AGAAAGAGGAGGCTGGGTGC
21384	19471	AAGAAAGAGGAGGCTGGGTG
21385	19472	GAAGAAAGAGGAGGCTGGGT
21386	19473	GGAAGAAAGAGGAGGCTGGG
21387	19474	GGGAAGAAAGAGGAGGCTGG
21388	19475	TGGGAAGAAAGAGGAGGCTG
21389	19476	ATGGGAAGAAAGAGGAGGCT
21390	19477	AATGGGAAGAAAGAGGAGGC
21391	19478	AAATGGGAAGAAAGAGGAGG
21392	19479	TAAATGGGAAGAAAGAGGAG
21393	19480	TTAAATGGGAAGAAAGAGGA
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21425	19512	TCTGCAGACAGAAAGTTCGG
21426	19513	CTCTGCAGACAGAAAGTTCG
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21429	19516	CCTCTCTGCAGACAGAAAGT
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21431	19518	CTCCTCTCTGCAGACAGAAA
21432	19519	GCTCCTCTCTGCAGACAGAA
21433	19520	TGCTCCTCTCTGCAGACAGA
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21435	19522	AATGCTCCTCTCTGCAGACA

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70513	68600	CTGCGGTGAGCCGAGATCGC
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70515	68602	GGCTGCGGTGAGCCGAGATC
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70520	68607	GCAGAGGCTGCGGTGAGCCG
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70540	68627	GAATCACTTGAACCTGGGAG
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70542	68629	GAGAATCACTTGAACCTGGG
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70544	68631	AGGAGAATCACTTGAACCTG
70545	68632	CAGGAGAATCACTTGAACCT
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70550	68637	TGAAGCAGGAGAATCACTTG
70551	68638	CTGAAGCAGGAGAATCACTT
70552	68639	GCTGAAGCAGGAGAATCACT
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70563	68650	CTGCTCGGGAGGCTGAAGCA
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70569	68656	TCCCAGCTGCTCGGGAGGCT
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70572	68659	TAATCCCAGCTGCTCGGGAG
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70574	68661	TGTAATCCCAGCTGCTCGGG
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119659	117746	ACCTCAGCCTCCCAGACTGC
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119663	117750	GCCCACCTCAGCCTCCCAGA
119664	117751	TGCCCACCTCAGCCTCCCAG
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119673	117760	CAAGTCATCTGCCCACCTCA
119674	117761	TCAAGTCATCTGCCCACCTC
119675	117762	CTCAAGTCATCTGCCCACCT
119676	117763	CCTCAAGTCATCTGCCCACC
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119683	117770	CTCCTGACCTCAAGTCATCT
119684	117771	ACTCCTGACCTCAAGTCATC
119685	117772	AACTCCTGACCTCAAGTCAT
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119689	117776	CTCAAACTCCTGACCTCAAG
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119700	117787	GCCAGGCTGGTCTCAAACTC
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119707	117794	CATGTTGGCCAGGCTGGTCT
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119709	117796	ACCATGTTGGCCAGGCTGGT
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119711	117798	TCACCATGTTGGCCAGGCTG
119712	117799	TTCACCATGTTGGCCAGGCT
119713	117800	TTTCACCATGTTGGCCAGGC
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119720	117807	GATGGGATTTCACCATGTTG
119721	117808	AGATGGGATTTCACCATGTT
119722	117809	GAGATGGGATTTCACCATGT
119723	117810	AGAGATGGGATTTCACCATG
119724	117811	TAGAGATGGGATTTCACCAT
119725	117812	GTAGAGATGGGATTTCACCA
119726	117813	AGTAGAGATGGGATTTCACC
119727	117814	TAGTAGAGATGGGATTTCAC
119728	117815	TTAGTAGAGATGGGATTTCA
119729	117816	TTTAGTAGAGATGGGATTTC

21436	19523	CAATGCTCCTCTCTGCAGAC
21437	19524	CCAATGCTCCTCTCTGCAGA
21438	19525	ACCAATGCTCCTCTCTGCAG
21439	19526	GACCAATGCTCCTCTCTGCA
21440	19527	TGACCAATGCTCCTCTCTGC
21441	19528	CTGACCAATGCTCCTCTCTG
21442	19529	GCTGACCAATGCTCCTCTCT
21443	19530	TGCTGACCAATGCTCCTCTC
21444	19531	CTGCTGACCAATGCTCCTCT
21445	19532	ACTGCTGACCAATGCTCCTC
21446	19533	AACTGCTGACCAATGCTCCT
21447	19534	GAACTGCTGACCAATGCTCC
21448	19535	TGAACTGCTGACCAATGCTC
21449	19536	GTGAACTGCTGACCAATGCT
21450	19537	TGTGAACTGCTGACCAATGC
21451	19538	TTGTGAACTGCTGACCAATG
21452	19539	TTTGTGAACTGCTGACCAAT
21453	19540	TTTTGTGAACTGCTGACCAA
21454	19541	ATTTTGTGAACTGCTGACCA
21455	19542	CATTTTGTGAACTGCTGACC
21456	19543	CCATTTTGTGAACTGCTGAC
21457	19544	GCCATTTTGTGAACTGCTGA
21458	19545	AGCCATTTTGTGAACTGCTG
21459	19546	TAGCCATTTTGTGAACTGCT
21460	19547	CTAGCCATTTTGTGAACTGC
21461	19548	CCTAGCCATTTTGTGAACTG
21462	19549	ACCTAGCCATTTTGTGAACT
21463	19550	CACCTAGCCATTTTGTGAAC
21464	19551	ACACCTAGCCATTTTGTGAA
21465	19552	CACACCTAGCCATTTTGTGA
21466	19553	TCACACCTAGCCATTTTGTG
21467	19554	ATCACACCTAGCCATTTTGT
21468	19555	CATCACACCTAGCCATTTTG
21469	19556	CCATCACACCTAGCCATTTT
21470	19557	GCCATCACACCTAGCCATTT
21471	19558	CGCCATCACACCTAGCCATT
21472	19559	ACGCCATCACACCTAGCCAT
21473	19560	CACGCCATCACACCTAGCCA
21474	19561	GCACGCCATCACACCTAGCC
21475	19562	TGCACGCCATCACACCTAGC
21476	19563	GTGCACGCCATCACACCTAG
21477	19564	GGTGCACGCCATCACACCTA
21478	19565	GGGTGCACGCCATCACACCT
21479	19566	TGGGTGCACGCCATCACACC
21480	19567	ATGGGTGCACGCCATCACAC
21481	19568	TATGGGTGCACGCCATCACA
21482	19569	CTATGGGTGCACGCCATCAC
21483	19570	ACTATGGGTGCACGCCATCA
21484	19571	GACTATGGGTGCACGCCATC
21485	19572	GGACTATGGGTGCACGCCAT
21486	19573	GGGACTATGGGTGCACGCCA
21487	19574	TGGGACTATGGGTGCACGCC
21488	19575	CTGGGACTATGGGTGCACGC
21489	19576	GCTGGGACTATGGGTGCACG
21490	19577	AGCTGGGACTATGGGTGCAC
21491	19578	TAGCTGGGACTATGGGTGCA
21492	19579	GTAGCTGGGACTATGGGTGC
21493	19580	AGTAGCTGGGACTATGGGTG
21494	19581	AAGTAGCTGGGACTATGGGT
21495	19582	CAAGTAGCTGGGACTATGGG
21496	19583	CCAAGTAGCTGGGACTATGG
21497	19584	CCCAAGTAGCTGGGACTATG
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21499	19586	TCCCCAAGTAGCTGGGACTA
21500	19587	CTCCCCAAGTAGCTGGGACT
21501	19588	GCTCCCCAAGTAGCTGGGAC
21502	19589	AGCTCCCCAAGTAGCTGGGA
21503	19590	CAGCTCCCCAAGTAGCTGGG
21504	19591	TCAGCTCCCCAAGTAGCTGG
21505	19592	CTCAGCTCCCCAAGTAGCTG
21506	19593	CCTCAGCTCCCCAAGTAGCT

70583	68670	GTGCATGCCTGTAATCCCAG
70584	68671	GGTGCATGCCTGTAATCCCA
70585	68672	TGGTGCATGCCTGTAATCCC
70586	68673	GTGGTGCATGCCTGTAATCC
70587	68674	GGTGGTGCATGCCTGTAATC
70588	68675	TGGTGGTGCATGCCTGTAAT
70589	68676	ATGGTGGTGCATGCCTGTAA
70590	68677	CATGGTGGTGCATGCCTGTA
70591	68678	GCATGGTGGTGCATGCCTGT
70592	68679	TGCATGGTGGTGCATGCCTG
70593	68680	GTGCATGGTGGTGCATGCCT
70594	68681	TGTGCATGGTGGTGCATGCC
70595	68682	CTGTGCATGGTGGTGCATGC
70596	68683	GCTGTGCATGGTGGTGCATG
70597	68684	AGCTGTGCATGGTGGTGCAT
70598	68685	TAGCTGTGCATGGTGGTGCA
70599	68686	ATAGCTGTGCATGGTGGTGC
70600	68687	TATAGCTGTGCATGGTGGTG
70601	68688	ATATAGCTGTGCATGGTGGT
70602	68689	AATATAGCTGTGCATGGTGG
70603	68690	AAATATAGCTGTGCATGGTG
70604	68691	TAAATATAGCTGTGCATGGT
70605	68692	CTAAATATAGCTGTGCATGG
70606	68693	ACTAAATATAGCTGTGCATG
70607	68694	TACTAAATATAGCTGTGCAT
70608	68695	CTACTAAATATAGCTGTGCA
70609	68696	TCTACTAAATATAGCTGTGC
70610	68697	CTCTACTAAATATAGCTGTG
70611	68698	TCTCTACTAAATATAGCTGT
70612	68699	ATCTCTACTAAATATAGCTG
70613	68700	CATCTCTACTAAATATAGCT
70614	68701	CCATCTCTACTAAATATAGC
70615	68702	CCCATCTCTACTAAATATAG
70616	68703	CCCCATCTCTACTAAATATA
70617	68704	CCCCCATCTCTACTAAATAT
70618	68705	ACCCCCATCTCTACTAAATA
70619	68706	AACCCCCATCTCTACTAAAT
70620	68707	AAACCCCCATCTCTACTAAA
70621	68708	GAAACCCCCATCTCTACTAA
70622	68709	AGAAACCCCCATCTCTACTA
70623	68710	GAGAAACCCCCATCTCTACT
70624	68711	GGAGAAACCCCCATCTCTAC
70625	68712	TGGAGAAACCCCCATCTCTA
70626	68713	ATGGAGAAACCCCCATCTCT
70627	68714	CATGGAGAAACCCCCATCTC
70628	68715	ACATGGAGAAACCCCCATCT
70629	68716	AACATGGAGAAACCCCCATC
70630	68717	CAACATGGAGAAACCCCCAT
70631	68718	CCAACATGGAGAAACCCCCA
70632	68719	ACCAACATGGAGAAACCCCC
70633	68720	GACCAACATGGAGAAACCCC
70634	68721	TGACCAACATGGAGAAACCC
70635	68722	CTGACCAACATGGAGAAACC
70636	68723	CCTGACCAACATGGAGAAAC
70637	68724	GCCTGACCAACATGGAGAAA
70638	68725	AGCCTGACCAACATGGAGAA
70639	68726	CAGCCTGACCAACATGGAGA
70640	68727	CCAGCCTGACCAACATGGAG
70641	68728	ACCAGCCTGACCAACATGGA
70642	68729	GACCAGCCTGACCAACATGG
70643	68730	AGACCAGCCTGACCAACATG
70644	68731	GAGACCAGCCTGACCAACAT
70645	68732	CGAGACCAGCCTGACCAACA
70646	68733	TCGAGACCAGCCTGACCAAC
70647	68734	TTCGAGACCAGCCTGACCAA
70648	68735	GTTCGAGACCAGCCTGACCA
70649	68736	AGTTCGAGACCAGCCTGACC
70650	68737	GAGTTCGAGACCAGCCTGAC
70651	68738	GGAGTTCGAGACCAGCCTGA
70652	68739	CGGAGTTCGAGACCAGCCTG
70653	68740	CCGGAGTTCGAGACCAGCCT

119730	117817	TTTTAGTAGAGATGGGATTT
119731	117818	TTTTTAGTAGAGATGGGATT
119732	117819	ATTTTTAGTAGAGATGGGAT
119733	117820	TATTTTTAGTAGAGATGGGA
119734	117821	GTATTTTTAGTAGAGATGGG
119735	117822	TGTATTTTTAGTAGAGATGG
119736	117823	TTGTATTTTTAGTAGAGATG
119737	117824	TTTGTATTTTTAGTAGAGAT
119738	117825	TTTTGTATTTTTAGTAGAGA
119739	117826	TTTTTGTATTTTTAGTAGAG
119740	117827	ATTTTTGTATTTTTAGTAGA
119741	117828	AATTTTTGTATTTTTAGTAG
119742	117829	TAATTTTTGTATTTTTAGTA
119743	117830	GTAATTTTTGTATTTTTAGT
119744	117831	TGTAATTTTTGTATTTTTAG
119745	117832	GTGTAATTTTTGTATTTTTA
119746	117833	AGTGTAATTTTTGTATTTTT
119747	117834	CAGTGTAATTTTTGTATTTT
119748	117835	CCAGTGTAATTTTTGTATTT
119749	117836	GCCAGTGTAATTTTTGTATT
119750	117837	TGCCAGTGTAATTTTTGTAT
119751	117838	ATGCCAGTGTAATTTTTGTA
119752	117839	CATGCCAGTGTAATTTTTGT
119753	117840	CCATGCCAGTGTAATTTTTG
119754	117841	ACCATGCCAGTGTAATTTTT
119755	117842	TACCATGCCAGTGTAATTTT
119756	117843	CTACCATGCCAGTGTAATTT
119757	117844	GCTACCATGCCAGTGTAATT
119758	117845	CGCTACCATGCCAGTGTAAT
119759	117846	ACGCTACCATGCCAGTGTAA
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119761	117848	GCACGCTACCATGCCAGTGT
119762	117849	TGCACGCTACCATGCCAGTG
119763	117850	GTGCACGCTACCATGCCAGT
119764	117851	GGTGCACGCTACCATGCCAG
119765	117852	AGGTGCACGCTACCATGCCA
119766	117853	TAGGTGCACGCTACCATGCC
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119769	117856	TTATAGGTGCACGCTACCAT
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119771	117858	GATTATAGGTGCACGCTACC
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119773	117860	GGGATTATAGGTGCACGCTA
119774	117861	TGGGATTATAGGTGCACGCT
119775	117862	CTGGGATTATAGGTGCACGC
119776	117863	GCTGGGATTATAGGTGCACG
119777	117864	AGCTGGGATTATAGGTGCAC
119778	117865	TAGCTGGGATTATAGGTGCA
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119782	117869	TGAATAGCTGGGATTATAGG
119783	117870	CTGAATAGCTGGGATTATAG
119784	117871	CCTGAATAGCTGGGATTATA
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119787	117874	CCTCCTGAATAGCTGGGATT
119788	117875	GCCTCCTGAATAGCTGGGAT
119789	117876	AGCCTCCTGAATAGCTGGGA
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119791	117878	TCAGCCTCCTGAATAGCTGG
119792	117879	CTCAGCCTCCTGAATAGCTG
119793	117880	CCTCAGCCTCCTGAATAGCT
119794	117881	GCCTCAGCCTCCTGAATAGC
119795	117882	TGCCTCAGCCTCCTGAATAG
119796	117883	CTGCCTCAGCCTCCTGAATA
119797	117884	CCTGCCTCAGCCTCCTGAAT
119798	117885	TCCTGCCTCAGCCTCCTGAA
119799	117886	CTCCTGCCTCAGCCTCCTGA
119800	117887	GCTCCTGCCTCAGCCTCCTG

21507	19594	ACCTCAGCTCCCCAAGTAGC
21508	19595	CACCTCAGCTCCCCAAGTAG
21509	19596	CCACCTCAGCTCCCCAAGTA
21510	19597	CCCACCTCAGCTCCCCAAGT
21511	19598	TCCCACCTCAGCTCCCCAAG
21512	19599	CTCCCACCTCAGCTCCCCAA
21513	19600	CCTCCCACCTCAGCTCCCCA
21514	19601	TCCTCCCACCTCAGCTCCCC
21515	19602	ATCCTCCCACCTCAGCTCCC
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21517	19604	CGATCCTCCCACCTCAGCTC
21518	19605	GCGATCCTCCCACCTCAGCT
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21522	19609	TCCAGCGATCCTCCCACCTC
21523	19610	CTCCAGCGATCCTCCCACCT
21524	19611	GCTCCAGCGATCCTCCCACC
21525	19612	GGCTCCAGCGATCCTCCCAC
21526	19613	GGGCTCCAGCGATCCTCCCA
21527	19614	TGGGCTCCAGCGATCCTCCC
21528	19615	CTGGGCTCCAGCGATCCTCC
21529	19616	CCTGGGCTCCAGCGATCCTC
21530	19617	TCCTGGGCTCCAGCGATCCT
21531	19618	CTCCTGGGCTCCAGCGATCC
21532	19619	ACTCCTGGGCTCCAGCGATC
21533	19620	AACTCCTGGGCTCCAGCGAT
21534	19621	GAACTCCTGGGCTCCAGCGA
21535	19622	TGAACTCCTGGGCTCCAGCG
21536	19623	TTGAACTCCTGGGCTCCAGC
21537	19624	CTTGAACTCCTGGGCTCCAG
21538	19625	CCTTGAACTCCTGGGCTCCA
21539	19626	GCCTTGAACTCCTGGGCTCC
21540	19627	GGCCTTGAACTCCTGGGCTC
21541	19628	GGGCCTTGAACTCCTGGGCT
21542	19629	AGGGCCTTGAACTCCTGGGC
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21544	19631	CCAGGGCCTTGAACTCCTGG
21545	19632	CCCAGGGCCTTGAACTCCTG
21546	19633	GCCCAGGGCCTTGAACTCCT
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21548	19635	TTGCCCAGGGCCTTGAACTC
21549	19636	GTTGCCCAGGGCCTTGAACT
21550	19637	TGTTGCCCAGGGCCTTGAAC
21551	19638	GTGTTGCCCAGGGCCTTGAA
21552	19639	TGTGTTGCCCAGGGCCTTGA
21553	19640	CTGTGTTGCCCAGGGCCTTG
21554	19641	GCTGTGTTGCCCAGGGCCTT
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21556	19643	TTGCTGTGTTGCCCAGGGCC
21557	19644	CTTGCTGTGTTGCCCAGGGC
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21559	19646	GTCTTGCTGTGTTGCCCAGG
21560	19647	GGTCTTGCTGTGTTGCCCAG
21561	19648	AGGTCTTGCTGTGTTGCCCA
21562	19649	AAGGTCTTGCTGTGTTGCCC
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21564	19651	ATAAGGTCTTGCTGTGTTGC
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21566	19653	AGATAAGGTCTTGCTGTGTT
21567	19654	GAGATAAGGTCTTGCTGTGT
21568	19655	AGAGATAAGGTCTTGCTGTG
21569	19656	CAGAGATAAGGTCTTGCTGT
21570	19657	CCAGAGATAAGGTCTTGCTG
21571	19658	GCCAGAGATAAGGTCTTGCT
21572	19659	AGCCAGAGATAAGGTCTTGC
21573	19660	CAGCCAGAGATAAGGTCTTG
21574	19661	CCAGCCAGAGATAAGGTCTT
21575	19662	CCCAGCCAGAGATAAGGTCT
21576	19663	GCCCAGCCAGAGATAAGGTC
21577	19664	GGCCCAGCCAGAGATAAGGT

70654	68741	TCCGGAGTTCGAGACCAGCC
70655	68742	GTCCGGAGTTCGAGACCAGC
70656	68743	GGTCCGGAGTTCGAGACCAG
70657	68744	AGGTCCGGAGTTCGAGACCA
70658	68745	GAGGTCCGGAGTTCGAGACC
70659	68746	TGAGGTCCGGAGTTCGAGAC
70660	68747	CTGAGGTCCGGAGTTCGAGA
70661	68748	CCTGAGGTCCGGAGTTCGAG
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70663	68750	CACCTGAGGTCCGGAGTTCG
70664	68751	TCACCTGAGGTCCGGAGTTC
70665	68752	ATCACCTGAGGTCCGGAGTT
70666	68753	GATCACCTGAGGTCCGGAGT
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70668	68755	CGGATCACCTGAGGTCCGGA
70669	68756	GCGGATCACCTGAGGTCCGG
70670	68757	GGCGGATCACCTGAGGTCCG
70671	68758	GGGCGGATCACCTGAGGTCC
70672	68759	CGGGCGGATCACCTGAGGTC
70673	68760	GCGGGCGGATCACCTGAGGT
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70675	68762	AGGCGGGCGGATCACCTGAG
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70677	68764	CGAGGCGGGCGGATCACCTG
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70679	68766	GCCGAGGCGGGCGGATCACC
70680	68767	GGCCGAGGCGGGCGGATCAC
70681	68768	AGGCCGAGGCGGGCGGATCA
70682	68769	GAGGCCGAGGCGGGCGGATC
70683	68770	GGAGGCCGAGGCGGGCGGAT
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70686	68773	TTGGGAGGCCGAGGCGGGCG
70687	68774	TTTGGGAGGCCGAGGCGGGC
70688	68775	CTTTGGGAGGCCGAGGCGGG
70689	68776	ACTTTGGGAGGCCGAGGCGG
70690	68777	CACTTTGGGAGGCCGAGGCG
70691	68778	TCACTTTGGGAGGCCGAGGC
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70695	68782	CCCATCACTTTGGGAGGCCG
70696	68783	TCCCATCACTTTGGGAGGCC
70697	68784	ATCCCATCACTTTGGGAGGC
70698	68785	AATCCCATCACTTTGGGAGG
70699	68786	TAATCCCATCACTTTGGGAG
70700	68787	GTAATCCCATCACTTTGGGA
70701	68788	TGTAATCCCATCACTTTGGG
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70703	68790	CCTGTAATCCCATCACTTTG
70704	68791	GCCTGTAATCCCATCACTTT
70705	68792	CGCCTGTAATCCCATCACTT
70706	68793	ACGCCTGTAATCCCATCACT
70707	68794	GACGCCTGTAATCCCATCAC
70708	68795	TGACGCCTGTAATCCCATCA
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70710	68797	GCTGACGCCTGTAATCCCAT
70711	68798	GGCTGACGCCTGTAATCCCA
70712	68799	TGGCTGACGCCTGTAATCCC
70713	68800	GTGGCTGACGCCTGTAATCC
70714	68801	AGTGGCTGACGCCTGTAATC
70715	68802	CAGTGGCTGACGCCTGTAAT
70716	68803	GCAGTGGCTGACGCCTGTAA
70717	68804	TGCAGTGGCTGACGCCTGTA
70718	68805	GTGCAGTGGCTGACGCCTGT
70719	68806	GGTGCAGTGGCTGACGCCTG
70720	68807	GGGTGCAGTGGCTGACGCCT
70721	68808	GGGGTGCAGTGGCTGACGCC
70722	68809	CGGGGTGCAGTGGCTGACGC
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119801	117888	TGCTCCTGCCTCAGCCTCCT
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119805	117892	CTGATGCTCCTGCCTCAGCC
119806	117893	TCTGATGCTCCTGCCTCAGC
119807	117894	TTCTGATGCTCCTGCCTCAG
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119810	117897	CGATTCTGATGCTCCTGCCT
119811	117898	GCGATTCTGATGCTCCTGCC
119812	117899	AGCGATTCTGATGCTCCTGC
119813	117900	AAGCGATTCTGATGCTCCTG
119814	117901	CAAGCGATTCTGATGCTCCT
119815	117902	TCAAGCGATTCTGATGCTCC
119816	117903	TTCAAGCGATTCTGATGCTC
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119818	117905	GGTTCAAGCGATTCTGATGC
119819	117906	AGGTTCAAGCGATTCTGATG
119820	117907	CAGGTTCAAGCGATTCTGAT
119821	117908	CCAGGTTCAAGCGATTCTGA
119822	117909	CCCAGGTTCAAGCGATTCTG
119823	117910	TCCCAGGTTCAAGCGATTCT
119824	117911	CTCCCAGGTTCAAGCGATTC
119825	117912	CCTCCCAGGTTCAAGCGATT
119826	117913	GCCTCCCAGGTTCAAGCGAT
119827	117914	CGCCTCCCAGGTTCAAGCGA
119828	117915	CCGCCTCCCAGGTTCAAGCG
119829	117916	TCCGCCTCCCAGGTTCAAGC
119830	117917	CTCCGCCTCCCAGGTTCAAG
119831	117918	CCTCCGCCTCCCAGGTTCAA
119832	117919	GCCTCCGCCTCCCAGGTTCA
119833	117920	AGCCTCCGCCTCCCAGGTTC
119834	117921	CAGCCTCCGCCTCCCAGGTT
119835	117922	GCAGCCTCCGCCTCCCAGGT
119836	117923	TGCAGCCTCCGCCTCCCAGG
119837	117924	CTGCAGCCTCCGCCTCCCAG
119838	117925	ACTGCAGCCTCCGCCTCCCA
119839	117926	CACTGCAGCCTCCGCCTCCC
119840	117927	TCACTGCAGCCTCCGCCTCC
119841	117928	CTCACTGCAGCCTCCGCCTC
119842	117929	GCTCACTGCAGCCTCCGCCT
119843	117930	AGCTCACTGCAGCCTCCGCC
119844	117931	CAGCTCACTGCAGCCTCCGC
119845	117932	TCAGCTCACTGCAGCCTCCG
119846	117933	CTCAGCTCACTGCAGCCTCC
119847	117934	TCTCAGCTCACTGCAGCCTC
119848	117935	ATCTCAGCTCACTGCAGCCT
119849	117936	GATCTCAGCTCACTGCAGCC
119850	117937	TGATCTCAGCTCACTGCAGC
119851	117938	GTGATCTCAGCTCACTGCAG
119852	117939	TGTGATCTCAGCTCACTGCA
119853	117940	GTGTGATCTCAGCTCACTGC
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119855	117942	TGGTGTGATCTCAGCTCACT
119856	117943	GTGGTGTGATCTCAGCTCAC
119857	117944	AGTGGTGTGATCTCAGCTCA
119858	117945	CAGTGGTGTGATCTCAGCTC
119859	117946	GCAGTGGTGTGATCTCAGCT
119860	117947	TGCAGTGGTGTGATCTCAGC
119861	117948	GTGCAGTGGTGTGATCTCAG
119862	117949	GGTGCAGTGGTGTGATCTCA
119863	117950	GGGTGCAGTGGTGTGATCTC
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119865	117952	TGGGGTGCAGTGGTGTGATC
119866	117953	CTGGGGTGCAGTGGTGTGAT
119867	117954	GCTGGGGTGCAGTGGTGTGA
119868	117955	GGCTGGGGTGCAGTGGTGTG
119869	117956	AGGCTGGGGTGCAGTGGTGT
119870	117957	CAGGCTGGGGTGCAGTGGTG
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21578	19665	GGGCCCAGCCAGAGATAAGG
21579	19666	TGGGCCCAGCCAGAGATAAG
21580	19667	CTGGGCCCAGCCAGAGATAA
21581	19668	ACTGGGCCCAGCCAGAGATA
21582	19669	CACTGGGCCCAGCCAGAGAT
21583	19670	CCACTGGGCCCAGCCAGAGA
21584	19671	GCCACTGGGCCCAGCCAGAG
21585	19672	AGCCACTGGGCCCAGCCAGA
21586	19673	GAGCCACTGGGCCCAGCCAG
21587	19674	TGAGCCACTGGGCCCAGCCA
21588	19675	GTGAGCCACTGGGCCCAGCC
21589	19676	CGTGAGCCACTGGGCCCAGC
21590	19677	GCGTGAGCCACTGGGCCCAG
21591	19678	GGCGTGAGCCACTGGGCCCA
21592	19679	AGGCGTGAGCCACTGGGCCC
21593	19680	CAGGCGTGAGCCACTGGGCC
21594	19681	ACAGGCGTGAGCCACTGGGC
21595	19682	TACAGGCGTGAGCCACTGGG
21596	19683	TTACAGGCGTGAGCCACTGG
21597	19684	ATTACAGGCGTGAGCCACTG
21598	19685	GATTACAGGCGTGAGCCACT
21599	19686	GGATTACAGGCGTGAGCCAC
21600	19687	GGGATTACAGGCGTGAGCCA
21601	19688	TGGGATTACAGGCGTGAGCC
21602	19689	CTGGGATTACAGGCGTGAGC
21603	19690	GCTGGGATTACAGGCGTGAG
21604	19691	TGCTGGGATTACAGGCGTGA
21605	19692	GTGCTGGGATTACAGGCGTG
21606	19693	AGTGCTGGGATTACAGGCGT
21607	19694	AAGTGCTGGGATTACAGGCG
21608	19695	AAAGTGCTGGGATTACAGGC
21609	19696	CAAAGTGCTGGGATTACAGG
21610	19697	CCAAAGTGCTGGGATTACAG
21611	19698	CCCAAAGTGCTGGGATTACA
21612	19699	TCCCAAAGTGCTGGGATTAC
21613	19700	CTCCCAAAGTGCTGGGATTA
21614	19701	CCTCCCAAAGTGCTGGGATT
21615	19702	GCCTCCCAAAGTGCTGGGAT
21616	19703	AGCCTCCCAAAGTGCTGGGA
21617	19704	CAGCCTCCCAAAGTGCTGGG
21618	19705	TCAGCCTCCCAAAGTGCTGG
21619	19706	CTCAGCCTCCCAAAGTGCTG
21620	19707	CCTCAGCCTCCCAAAGTGCT
21621	19708	ACCTCAGCCTCCCAAAGTGC
21622	19709	CACCTCAGCCTCCCAAAGTG
21623	19710	CCACCTCAGCCTCCCAAAGT
21624	19711	CCCACCTCAGCCTCCCAAAG
21625	19712	ACCCACCTCAGCCTCCCAAA
21626	19713	CACCCACCTCAGCCTCCCAA
21627	19714	CCACCCACCTCAGCCTCCCA
21628	19715	TCCACCCACCTCAGCCTCCC
21629	19716	ATCCACCCACCTCAGCCTCC
21630	19717	GATCCACCCACCTCAGCCTC
21631	19718	TGATCCACCCACCTCAGCCT
21632	19719	GTGATCCACCCACCTCAGCC
21633	19720	GGTGATCCACCCACCTCAGC
21634	19721	AGGTGATCCACCCACCTCAG
21635	19722	CAGGTGATCCACCCACCTCA
21636	19723	TCAGGTGATCCACCCACCTC
21637	19724	CTCAGGTGATCCACCCACCT
21638	19725	CCTCAGGTGATCCACCCACC
21639	19726	ACCTCAGGTGATCCACCCAC
21640	19727	GACCTCAGGTGATCCACCCA
21641	19728	TGACCTCAGGTGATCCACCC
21642	19729	CTGACCTCAGGTGATCCACC
21643	19730	CCTGACCTCAGGTGATCCAC
21644	19731	TCCTGACCTCAGGTGATCCA
21645	19732	CTCCTGACCTCAGGTGATCC
21646	19733	ACTCCTGACCTCAGGTGATC
21647	19734	AACTCCTGACCTCAGGTGAT
21648	19735	GAACTCCTGACCTCAGGTGA

70725	68812	AGGCGGGGTGCAGTGGCTGA
70726	68813	TAGGCGGGGTGCAGTGGCTG
70727	68814	ATAGGCGGGGTGCAGTGGCT
70728	68815	TATAGGCGGGGTGCAGTGGC
70729	68816	GTATAGGCGGGGTGCAGTGG
70730	68817	TGTATAGGCGGGGTGCAGTG
70731	68818	GTGTATAGGCGGGGTGCAGT
70732	68819	TGTGTATAGGCGGGGTGCAG
70733	68820	ATGTGTATAGGCGGGGTGCA
70734	68821	AATGTGTATAGGCGGGGTGC
70735	68822	AAATGTGTATAGGCGGGGTG
70736	68823	AAAATGTGTATAGGCGGGGT
70737	68824	AAAAATGTGTATAGGCGGGG
70738	68825	AAAAAATGTGTATAGGCGGG
70739	68826	AAAAAAATGTGTATAGGCGG
70740	68827	CAAAAAAATGTGTATAGGCG
70741	68828	ACAAAAAAATGTGTATAGGC
70742	68829	AACAAAAAAATGTGTATAGG
70743	68830	AAACAAAAAAATGTGTATAG
70744	68831	AAAACAAAAAAATGTGTATA
70745	68832	AAAAACAAAAAAATGTGTAT
70746	68833	AAAAAACAAAAAAATGTGTA
70747	68834	CAAAAAACAAAAAAATGTGT
70748	68835	ACAAAAAACAAAAAAATGTG
70749	68836	AACAAAAAACAAAAAAATGT
70750	68837	AAACAAAAAACAAAAAAATG
70751	68838	AAAACAAAAAACAAAAAAAT
70752	68839	AAAAACAAAAAACAAAAAAA
70753	68840	AAAAAACAAAAAACAAAAAA
70754	68841	AAAAAAACAAAAAACAAAAA
70755	68842	CAAAAAAACAAAAAACAAAA
70756	68843	TCAAAAAAACAAAAAACAAA
70757	68844	CTCAAAAAAACAAAAAACAA
70758	68845	TCTCAAAAAAACAAAAAACA
70759	68846	ATCTCAAAAAAACAAAAAAC
70760	68847	CATCTCAAAAAAACAAAAAA
70761	68848	CCATCTCAAAAAAACAAAAA
70762	68849	TCCATCTCAAAAAAACAAAA
70763	68850	CTCCATCTCAAAAAAACAAA
70764	68851	ACTCCATCTCAAAAAAACAA
70765	68852	GACTCCATCTCAAAAAAACA
70766	68853	AGACTCCATCTCAAAAAAAC
70767	68854	GAGACTCCATCTCAAAAAAA
70768	68855	CGAGACTCCATCTCAAAAAA
70769	68856	GCGAGACTCCATCTCAAAAA
70770	68857	AGCGAGACTCCATCTCAAAA
70771	68858	GAGCGAGACTCCATCTCAAA
70772	68859	AGAGCGAGACTCCATCTCAA
70773	68860	CAGAGCGAGACTCCATCTCA
70774	68861	ACAGAGCGAGACTCCATCTC
70775	68862	AACAGAGCGAGACTCCATCT
70776	68863	CAACAGAGCGAGACTCCATC
70777	68864	ACAACAGAGCGAGACTCCAT
70778	68865	GACAACAGAGCGAGACTCCA
70779	68866	GGACAACAGAGCGAGACTCC
70780	68867	TGGACAACAGAGCGAGACTC
70781	68868	CTGGACAACAGAGCGAGACT
70782	68869	CCTGGACAACAGAGCGAGAC
70783	68870	GCCTGGACAACAGAGCGAGA
70784	68871	AGCCTGGACAACAGAGCGAG
70785	68872	CAGCCTGGACAACAGAGCGA
70786	68873	CCAGCCTGGACAACAGAGCG
70787	68874	TCCAGCCTGGACAACAGAGC
70788	68875	CTCCAGCCTGGACAACAGAG
70789	68876	ACTCCAGCCTGGACAACAGA
70790	68877	CACTCCAGCCTGGACAACAG
70791	68878	GCACTCCAGCCTGGACAACA
70792	68879	TGCACTCCAGCCTGGACAAC
70793	68880	CTGCACTCCAGCCTGGACAA
70794	68881	ACTGCACTCCAGCCTGGACA
70795	68882	CACTGCACTCCAGCCTGGAC

119872	117959	CTCAGGCTGGGGTGCAGTGG
119873	117960	ACTCAGGCTGGGGTGCAGTG
119874	117961	CACTCAGGCTGGGGTGCAGT
119875	117962	TCACTCAGGCTGGGGTGCAG
119876	117963	TTCACTCAGGCTGGGGTGCA
119877	117964	TTTCACTCAGGCTGGGGTGC
119878	117965	CTTTCACTCAGGCTGGGGTG
119879	117966	TCTTTCACTCAGGCTGGGGT
119880	117967	CTCTTTCACTCAGGCTGGGG
119881	117968	ACTCTTTCACTCAGGCTGGG
119882	117969	CACTCTTTCACTCAGGCTGG
119883	117970	TCACTCTTTCACTCAGGCTG
119884	117971	CTCACTCTTTCACTCAGGCT
119885	117972	ACTCACTCTTTCACTCAGGC
119886	117973	GACTCACTCTTTCACTCAGG
119887	117974	AGACTCACTCTTTCACTCAG
119888	117975	GAGACTCACTCTTTCACTCA
119889	117976	TGAGACTCACTCTTTCACTC
119890	117977	TTGAGACTCACTCTTTCACT
119891	117978	TTTGAGACTCACTCTTTCAC
119892	117979	TTTTGAGACTCACTCTTTCA
119893	117980	TTTTTGAGACTCACTCTTTC
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119898	117985	TTTATTTTTTGAGACTCACT
119899	117986	TTTTATTTTTTGAGACTCAC
119900	117987	TTTTTATTTTTTGAGACTCA
119901	117988	TTTTTTATTTTTTGAGACTC
119902	117989	ATTTTTTATTTTTTGAGACT
119903	117990	TATTTTTTATTTTTTGAGAC
119904	117991	TTATTTTTTATTTTTTGAGA
119905	117992	TTTATTTTTTATTTTTTGAG
119906	117993	TTTTATTTTTTATTTTTTGA
119907	117994	ATTTTATTTTTTATTTTTTG
119908	117995	AATTTTATTTTTTATTTTTT
119909	117996	AAATTTTATTTTTTATTTTT
119910	117997	AAAATTTTATTTTTTATTTT
119911	117998	AAAAATTTTATTTTTTATTT
119912	117999	AAAAAATTTTATTTTTTATT
119913	118000	AAAAAAATTTTATTTTTTAT
119914	118001	AAAAAAAATTTTATTTTTTA
119915	118002	GAAAAAAAATTTTATTTTTT
119916	118003	TGAAAAAAAATTTTATTTTT
119917	118004	ATGAAAAAAAATTTTATTTT
119918	118005	CATGAAAAAAAATTTTATTT
119919	118006	ACATGAAAAAAAATTTTATT
119920	118007	CACATGAAAAAAAATTTTAT
119921	118008	CCACATGAAAAAAAATTTTA
119922	118009	GCCACATGAAAAAAAATTTT
119923	118010	GGCCACATGAAAAAAAATTT
119924	118011	AGGCCACATGAAAAAAAATT
119925	118012	AAGGCCACATGAAAAAAAAT
119926	118013	TAAGGCCACATGAAAAAAAA
119927	118014	CTAAGGCCACATGAAAAAAA
119928	118015	TCTAAGGCCACATGAAAAAA
119929	118016	ATCTAAGGCCACATGAAAAA
119930	118017	AATCTAAGGCCACATGAAAA
119931	118018	AAATCTAAGGCCACATGAAA
119932	118019	AAAATCTAAGGCCACATGAA
119933	118020	GAAAATCTAAGGCCACATGA
119934	118021	TGAAAATCTAAGGCCACATG
119935	118022	ATGAAAATCTAAGGCCACAT
119936	118023	AATGAAAATCTAAGGCCACA
119937	118024	AAATGAAAATCTAAGGCCAC
119938	118025	GAAATGAAAATCTAAGGCCA
119939	118026	AGAAATGAAAATCTAAGGCC
119940	118027	GAGAAATGAAAATCTAAGGC
119941	118028	GGAGAAATGAAAATCTAAGG
119942	118029	AGGAGAAATGAAAATCTAAG

21649	19736	CGAACTCCTGACCTCAGGTG
21650	19737	TCGAACTCCTGACCTCAGGT
21651	19738	CTCGAACTCCTGACCTCAGG
21652	19739	TCTCGAACTCCTGACCTCAG
21653	19740	GTCTCGAACTCCTGACCTCA
21654	19741	GGTCTCGAACTCCTGACCTC
21655	19742	TGGTCTCGAACTCCTGACCT
21656	19743	CTGGTCTCGAACTCCTGACC
21657	19744	GCTGGTCTCGAACTCCTGAC
21658	19745	GGCTGGTCTCGAACTCCTGA
21659	19746	AGGCTGGTCTCGAACTCCTG
21660	19747	CAGGCTGGTCTCGAACTCCT
21661	19748	CCAGGCTGGTCTCGAACTCC
21662	19749	GCCAGGCTGGTCTCGAACTC
21663	19750	GGCCAGGCTGGTCTCGAACT
21664	19751	TGGCCAGGCTGGTCTCGAAC
21665	19752	TTGGCCAGGCTGGTCTCGAA
21666	19753	GTTGGCCAGGCTGGTCTCGA
21667	19754	TGTTGGCCAGGCTGGTCTCG
21668	19755	ATGTTGGCCAGGCTGGTCTC
21669	19756	CATGTTGGCCAGGCTGGTCT
21670	19757	CCATGTTGGCCAGGCTGGTC
21671	19758	ACCATGTTGGCCAGGCTGGT
21672	19759	CACCATGTTGGCCAGGCTGG
21673	19760	TCACCATGTTGGCCAGGCTG
21674	19761	CTCACCATGTTGGCCAGGCT
21675	19762	TCTCACCATGTTGGCCAGGC
21676	19763	GTCTCACCATGTTGGCCAGG
21677	19764	GGTCTCACCATGTTGGCCAG
21678	19765	GGGTCTCACCATGTTGGCCA
21679	19766	AGGGTCTCACCATGTTGGCC
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21681	19768	ACAGGGTCTCACCATGTTGG
21682	19769	CACAGGGTCTCACCATGTTG
21683	19770	ACACAGGGTCTCACCATGTT
21684	19771	GACACAGGGTCTCACCATGT
21685	19772	AGACACAGGGTCTCACCATG
21686	19773	TAGACACAGGGTCTCACCAT
21687	19774	GTAGACACAGGGTCTCACCA
21688	19775	AGTAGACACAGGGTCTCACC
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21690	19777	TTAGTAGACACAGGGTCTCA
21691	19778	TTTAGTAGACACAGGGTCTC
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21693	19780	CTTTTAGTAGACACAGGGTC
21694	19781	ACTTTTAGTAGACACAGGGT
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21696	19783	GTACTTTTAGTAGACACAGG
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21698	19785	TTGTACTTTTAGTAGACACA
21699	19786	TTTGTACTTTTAGTAGACAC
21700	19787	TTTTGTACTTTTAGTAGACA
21701	19788	TTTTTGTACTTTTAGTAGAC
21702	19789	ATTTTTGTACTTTTAGTAGA
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21704	19791	TAATTTTTGTACTTTTAGTA
21705	19792	CTAATTTTTGTACTTTTAGT
21706	19793	GCTAATTTTTGTACTTTTAG
21707	19794	GGCTAATTTTTGTACTTTTA
21708	19795	TGGCTAATTTTTGTACTTTT
21709	19796	CTGGCTAATTTTTGTACTTT
21710	19797	CCTGGCTAATTTTTGTACTT
21711	19798	GCCTGGCTAATTTTTGTACT
21712	19799	TGCCTGGCTAATTTTTGTAC
21713	19800	GTGCCTGGCTAATTTTTGTA
21714	19801	CGTGCCTGGCTAATTTTTGT
21715	19802	CCGTGCCTGGCTAATTTTTG
21716	19803	ACCGTGCCTGGCTAATTTTT
21717	19804	CACCGTGCCTGGCTAATTTT
21718	19805	CCACCGTGCCTGGCTAATTT
21719	19806	GCCACCGTGCCTGGCTAATT

70796	68883	CCACTGCACTCCAGCCTGGA
70797	68884	GCCACTGCACTCCAGCCTGG
70798	68885	CGCCACTGCACTCCAGCCTG
70799	68886	GCGCCACTGCACTCCAGCCT
70800	68887	CGCGCCACTGCACTCCAGCC
70801	68888	TCGCGCCACTGCACTCCAGC
70802	68889	ATCGCGCCACTGCACTCCAG
70803	68890	GATCGCGCCACTGCACTCCA
70804	68891	AGATCGCGCCACTGCACTCC
70805	68892	GAGATCGCGCCACTGCACTC
70806	68893	AGAGATCGCGCCACTGCACT
70807	68894	CAGAGATCGCGCCACTGCAC
70808	68895	GCAGAGATCGCGCCACTGCA
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70810	68897	GAGCAGAGATCGCGCCACTG
70811	68898	TGAGCAGAGATCGCGCCACT
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70813	68900	AGTGAGCAGAGATCGCGCCA
70814	68901	CAGTGAGCAGAGATCGCGCC
70815	68902	GCAGTGAGCAGAGATCGCGC
70816	68903	TGCAGTGAGCAGAGATCGCG
70817	68904	TTGCAGTGAGCAGAGATCGC
70818	68905	CTTGCAGTGAGCAGAGATCG
70819	68906	GCTTGCAGTGAGCAGAGATC
70820	68907	AGCTTGCAGTGAGCAGAGAT
70821	68908	GAGCTTGCAGTGAGCAGAGA
70822	68909	AGAGCTTGCAGTGAGCAGAG
70823	68910	CAGAGCTTGCAGTGAGCAGA
70824	68911	GCAGAGCTTGCAGTGAGCAG
70825	68912	GGCAGAGCTTGCAGTGAGCA
70826	68913	AGGCAGAGCTTGCAGTGAGC
70827	68914	GAGGCAGAGCTTGCAGTGAG
70828	68915	GGAGGCAGAGCTTGCAGTGA
70829	68916	GGGAGGCAGAGCTTGCAGTG
70830	68917	AGGGAGGCAGAGCTTGCAGT
70831	68918	CAGGGAGGCAGAGCTTGCAG
70832	68919	CCAGGGAGGCAGAGCTTGCA
70833	68920	ACCAGGGAGGCAGAGCTTGC
70834	68921	AACCAGGGAGGCAGAGCTTG
70835	68922	GAACCAGGGAGGCAGAGCTT
70836	68923	TGAACCAGGGAGGCAGAGCT
70837	68924	GTGAACCAGGGAGGCAGAGC
70838	68925	TGTGAACCAGGGAGGCAGAG
70839	68926	GTGTGAACCAGGGAGGCAGA
70840	68927	GGTGTGAACCAGGGAGGCAG
70841	68928	TGGTGTGAACCAGGGAGGCA
70842	68929	ATGGTGTGAACCAGGGAGGC
70843	68930	AATGGTGTGAACCAGGGAGG
70844	68931	GAATGGTGTGAACCAGGGAG
70845	68932	AGAATGGTGTGAACCAGGGA
70846	68933	GAGAATGGTGTGAACCAGGG
70847	68934	GGAGAATGGTGTGAACCAGG
70848	68935	AGGAGAATGGTGTGAACCAG
70849	68936	CAGGAGAATGGTGTGAACCA
70850	68937	GCAGGAGAATGGTGTGAACC
70851	68938	GGCAGGAGAATGGTGTGAAC
70852	68939	AGGCAGGAGAATGGTGTGAA
70853	68940	GAGGCAGGAGAATGGTGTGA
70854	68941	TGAGGCAGGAGAATGGTGTG
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70856	68943	GCTGAGGCAGGAGAATGGTG
70857	68944	GGCTGAGGCAGGAGAATGGT
70858	68945	AGGCTGAGGCAGGAGAATGG
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70860	68947	GGAGGCTGAGGCAGGAGAAT
70861	68948	GGGAGGCTGAGGCAGGAGAA
70862	68949	CGGGAGGCTGAGGCAGGAGA
70863	68950	TCGGGAGGCTGAGGCAGGAG
70864	68951	CTCGGGAGGCTGAGGCAGGA
70865	68952	ACTCGGGAGGCTGAGGCAGG
70866	68953	TACTCGGGAGGCTGAGGCAG

119943	118030	TAGGAGAAATGAAAATCTAA
119944	118031	TTAGGAGAAATGAAAATCTA
119945	118032	TTTAGGAGAAATGAAAATCT
119946	118033	CTTTAGGAGAAATGAAAATC
119947	118034	ACTTTAGGAGAAATGAAAAT
119948	118035	TACTTTAGGAGAAATGAAAA
119949	118036	CTACTTTAGGAGAAATGAAA
119950	118037	TCTACTTTAGGAGAAATGAA
119951	118038	TTCTACTTTAGGAGAAATGA
119952	118039	TTTCTACTTTAGGAGAAATG
119953	118040	ATTTCTACTTTAGGAGAAAT
119954	118041	CATTTCTACTTTAGGAGAAA
119955	118042	GCATTTCTACTTTAGGAGAA
119956	118043	AGCATTTCTACTTTAGGAGA
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119958	118045	ACAGCATTTCTACTTTAGGA
119959	118046	CACAGCATTTCTACTTTAGG
119960	118047	TCACAGCATTTCTACTTTAG
119961	118048	ATCACAGCATTTCTACTTTA
119962	118049	CATCACAGCATTTCTACTTT
119963	118050	CCATCACAGCATTTCTACTT
119964	118051	TCCATCACAGCATTTCTACT
119965	118052	TTCCATCACAGCATTTCTAC
119966	118053	GTTCCATCACAGCATTTCTA
119967	118054	AGTTCCATCACAGCATTTCT
119968	118055	CAGTTCCATCACAGCATTTC
119969	118056	GCAGTTCCATCACAGCATTT
119970	118057	GGCAGTTCCATCACAGCATT
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119973	118060	TTTGGCAGTTCCATCACAGC
119974	118061	GTTTGGCAGTTCCATCACAG
119975	118062	AGTTTGGCAGTTCCATCACA
119976	118063	AAGTTTGGCAGTTCCATCAC
119977	118064	AAAGTTTGGCAGTTCCATCA
119978	118065	AAAAGTTTGGCAGTTCCATC
119979	118066	GAAAAGTTTGGCAGTTCCAT
119980	118067	GGAAAAGTTTGGCAGTTCCA
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119982	118069	TTGGAAAAGTTTGGCAGTTC
119983	118070	TTTGGAAAAGTTTGGCAGTT
119984	118071	CTTTGGAAAAGTTTGGCAGT
119985	118072	GCTTTGGAAAAGTTTGGCAG
119986	118073	TGCTTTGGAAAAGTTTGGCA
119987	118074	CTGCTTTGGAAAAGTTTGGC
119988	118075	GCTGCTTTGGAAAAGTTTGG
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119992	118079	TGCAGCTGCTTTGGAAAAGT
119993	118080	ATGCAGCTGCTTTGGAAAAG
119994	118081	GATGCAGCTGCTTTGGAAAA
119995	118082	TGATGCAGCTGCTTTGGAAA
119996	118083	ATGATGCAGCTGCTTTGGAA
119997	118084	AATGATGCAGCTGCTTTGGA
119998	118085	AAATGATGCAGCTGCTTTGG
119999	118086	AAAATGATGCAGCTGCTTTG
120000	118087	CAAAATGATGCAGCTGCTTT
120001	118088	ACAAAATGATGCAGCTGCTT
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120003	118090	ATACAAAATGATGCAGCTGC
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120005	118092	AAATACAAAATGATGCAGCT
120006	118093	GAAATACAAAATGATGCAGC
120007	118094	AGAAATACAAAATGATGCAG
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120009	118096	GTAGAAATACAAAATGATGC
120010	118097	GGTAGAAATACAAAATGATG
120011	118098	TGGTAGAAATACAAAATGAT
120012	118099	CTGGTAGAAATACAAAATGA
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21720	19807	CGCCACCGTGCCTGGCTAAT
21721	19808	GCGCCACCGTGCCTGGCTAA
21722	19809	CGCGCCACCGTGCCTGGCTA
21723	19810	GCGCGCCACCGTGCCTGGCT
21724	19811	AGCGCGCCACCGTGCCTGGC
21725	19812	GAGCGCGCCACCGTGCCTGG
21726	19813	GGAGCGCGCCACCGTGCCTG
21727	19814	AGGAGCGCGCCACCGTGCCT
21728	19815	CAGGAGCGCGCCACCGTGCC
21729	19816	ACAGGAGCGCGCCACCGTGC
21730	19817	TACAGGAGCGCGCCACCGTG
21731	19818	TTACAGGAGCGCGCCACCGT
21732	19819	ATTACAGGAGCGCGCCACCG
21733	19820	GATTACAGGAGCGCGCCACC
21734	19821	GGATTACAGGAGCGCGCCAC
21735	19822	GGGATTACAGGAGCGCGCCA
21736	19823	TGGGATTACAGGAGCGCGCC
21737	19824	CTGGGATTACAGGAGCGCGC
21738	19825	GCTGGGATTACAGGAGCGCG
21739	19826	AGCTGGGATTACAGGAGCGC
21740	19827	TAGCTGGGATTACAGGAGCG
21741	19828	GTAGCTGGGATTACAGGAGC
21742	19829	AGTAGCTGGGATTACAGGAG
21743	19830	GAGTAGCTGGGATTACAGGA
21744	19831	CGAGTAGCTGGGATTACAGG
21745	19832	CCGAGTAGCTGGGATTACAG
21746	19833	CCCGAGTAGCTGGGATTACA
21747	19834	CCCCGAGTAGCTGGGATTAC
21748	19835	CCCCCGAGTAGCTGGGATTA
21749	19836	CCCCCCGAGTAGCTGGGATT
21750	19837	CCCCCCCGAGTAGCTGGGAT
21751	19838	GCCCCCCCGAGTAGCTGGGA
21752	19839	AGCCCCCCCGAGTAGCTGGG
21753	19840	CAGCCCCCCCGAGTAGCTGG
21754	19841	TCAGCCCCCCCGAGTAGCTG
21755	19842	CTCAGCCCCCCCGAGTAGCT
21756	19843	TCTCAGCCCCCCCGAGTAGC
21757	19844	GTCTCAGCCCCCCCGAGTAG
21758	19845	TGTCTCAGCCCCCCCGAGTA
21759	19846	CTGTCTCAGCCCCCCCGAGT
21760	19847	CCTGTCTCAGCCCCCCCGAG
21761	19848	TCCTGTCTCAGCCCCCCCGA
21762	19849	CTCCTGTCTCAGCCCCCCCG
21763	19850	TCTCCTGTCTCAGCCCCCCC
21764	19851	TTCTCCTGTCTCAGCCCCCC
21765	19852	ATTCTCCTGTCTCAGCCCCC
21766	19853	GATTCTCCTGTCTCAGCCCC
21767	19854	TGATTCTCCTGTCTCAGCCC
21768	19855	GTGATTCTCCTGTCTCAGCC
21769	19856	AGTGATTCTCCTGTCTCAGC
21770	19857	AAGTGATTCTCCTGTCTCAG
21771	19858	CAAGTGATTCTCCTGTCTCA
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21773	19860	TTCAAGTGATTCTCCTGTCT
21774	19861	GTTCAAGTGATTCTCCTGTC
21775	19862	GGTTCAAGTGATTCTCCTGT
21776	19863	GGGTTCAAGTGATTCTCCTG
21777	19864	TGGGTTCAAGTGATTCTCCT
21778	19865	CTGGGTTCAAGTGATTCTCC
21779	19866	CCTGGGTTCAAGTGATTCTC
21780	19867	TCCTGGGTTCAAGTGATTCT
21781	19868	CTCCTGGGTTCAAGTGATTC
21782	19869	CCTCCTGGGTTCAAGTGATT
21783	19870	TCCTCCTGGGTTCAAGTGAT
21784	19871	CTCCTCCTGGGTTCAAGTGA
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21787	19874	CTCCTCCTCCTGGGTTCAAG
21788	19875	CCTCCTCCTCCTGGGTTCAA
21789	19876	ACCTCCTCCTCCTGGGTTCA
21790	19877	AACCTCCTCCTCCTGGGTTC

70867	68954	CTACTCGGGAGGCTGAGGCA
70868	68955	GCTACTCGGGAGGCTGAGGC
70869	68956	AGCTACTCGGGAGGCTGAGG
70870	68957	CAGCTACTCGGGAGGCTGAG
70871	68958	CCAGCTACTCGGGAGGCTGA
70872	68959	CCCAGCTACTCGGGAGGCTG
70873	68960	TCCCAGCTACTCGGGAGGCT
70874	68961	ATCCCAGCTACTCGGGAGGC
70875	68962	AATCCCAGCTACTCGGGAGG
70876	68963	TAATCCCAGCTACTCGGGAG
70877	68964	GTAATCCCAGCTACTCGGGA
70878	68965	TGTAATCCCAGCTACTCGGG
70879	68966	CTGTAATCCCAGCTACTCGG
70880	68967	CCTGTAATCCCAGCTACTCG
70881	68968	GCCTGTAATCCCAGCTACTC
70882	68969	CGCCTGTAATCCCAGCTACT
70883	68970	GCGCCTGTAATCCCAGCTAC
70884	68971	GGCGCCTGTAATCCCAGCTA
70885	68972	CGGCGCCTGTAATCCCAGCT
70886	68973	CCGGCGCCTGTAATCCCAGC
70887	68974	GCCGGCGCCTGTAATCCCAG
70888	68975	GGCCGGCGCCTGTAATCCCA
70889	68976	TGGCCGGCGCCTGTAATCCC
70890	68977	GTGGCCGGCGCCTGTAATCC
70891	68978	AGTGGCCGGCGCCTGTAATC
70892	68979	TAGTGGCCGGCGCCTGTAAT
70893	68980	GTAGTGGCCGGCGCCTGTAA
70894	68981	CGTAGTGGCCGGCGCCTGTA
70895	68982	GCGTAGTGGCCGGCGCCTGT
70896	68983	GGCGTAGTGGCCGGCGCCTG
70897	68984	GGGCGTAGTGGCCGGCGCCT
70898	68985	TGGGCGTAGTGGCCGGCGCC
70899	68986	ATGGGCGTAGTGGCCGGCGC
70900	68987	GATGGGCGTAGTGGCCGGCG
70901	68988	AGATGGGCGTAGTGGCCGGC
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70903	68990	TTAGATGGGCGTAGTGGCCG
70904	68991	GTTAGATGGGCGTAGTGGCC
70905	68992	AGTTAGATGGGCGTAGTGGC
70906	68993	AAGTTAGATGGGCGTAGTGG
70907	68994	AAAGTTAGATGGGCGTAGTG
70908	68995	AAAAGTTAGATGGGCGTAGT
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70911	68998	ACAAAAAGTTAGATGGGCGT
70912	68999	TACAAAAAGTTAGATGGGCG
70913	69000	ATACAAAAAGTTAGATGGGC
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70915	69002	AAATACAAAAAGTTAGATGG
70916	69003	AAAATACAAAAAGTTAGATG
70917	69004	AAAAATACAAAAAGTTAGAT
70918	69005	TAAAAATACAAAAAGTTAGA
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70920	69007	ACTAAAAATACAAAAAGTTA
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70923	69010	TCTACTAAAAATACAAAAAG
70924	69011	CTCTACTAAAAATACAAAAA
70925	69012	TCTCTACTAAAAATACAAAA
70926	69013	ATCTCTACTAAAAATACAAA
70927	69014	CATCTCTACTAAAAATACAA
70928	69015	CCATCTCTACTAAAAATACA
70929	69016	CCCATCTCTACTAAAAATAC
70930	69017	CCCCATCTCTACTAAAAATA
70931	69018	ACCCCATCTCTACTAAAAAT
70932	69019	AACCCCATCTCTACTAAAAA
70933	69020	AAACCCCATCTCTACTAAAA
70934	69021	GAAACCCCATCTCTACTAAA
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70937	69024	GGTGAAACCCCATCTCTACT

120014	118101	TACTGGTAGAAATACAAAAT
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120016	118103	ATTACTGGTAGAAATACAAA
120017	118104	CATTACTGGTAGAAATACAA
120018	118105	ACATTACTGGTAGAAATACA
120019	118106	TACATTACTGGTAGAAATAC
120020	118107	GTACATTACTGGTAGAAATA
120021	118108	TGTACATTACTGGTAGAAAT
120022	118109	TTGTACATTACTGGTAGAAA
120023	118110	CTTGTACATTACTGGTAGAA
120024	118111	ACTTGTACATTACTGGTAGA
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120026	118113	ACACTTGTACATTACTGGTA
120027	118114	AACACTTGTACATTACTGGT
120028	118115	GAACACTTGTACATTACTGG
120029	118116	GGAACACTTGTACATTACTG
120030	118117	TGGAACACTTGTACATTACT
120031	118118	CTGGAACACTTGTACATTAC
120032	118119	ACTGGAACACTTGTACATTA
120033	118120	AACTGGAACACTTGTACATT
120034	118121	AAACTGGAACACTTGTACAT
120035	118122	GAAACTGGAACACTTGTACA
120036	118123	AGAAACTGGAACACTTGTAC
120037	118124	GAGAAACTGGAACACTTGTA
120038	118125	GGAGAAACTGGAACACTTGT
120039	118126	TGGAGAAACTGGAACACTTG
120040	118127	GTGGAGAAACTGGAACACTT
120041	118128	TGTGGAGAAACTGGAACACT
120042	118129	ATGTGGAGAAACTGGAACAC
120043	118130	GATGTGGAGAAACTGGAACA
120044	118131	GGATGTGGAGAAACTGGAAC
120045	118132	AGGATGTGGAGAAACTGGAA
120046	118133	GAGGATGTGGAGAAACTGGA
120047	118134	TGAGGATGTGGAGAAACTGG
120048	118135	ATGAGGATGTGGAGAAACTG
120049	118136	TATGAGGATGTGGAGAAACT
120050	118137	TTATGAGGATGTGGAGAAAC
120051	118138	TTTATGAGGATGTGGAGAAA
120052	118139	ATTTATGAGGATGTGGAGAA
120053	118140	TATTTATGAGGATGTGGAGA
120054	118141	TTATTTATGAGGATGTGGAG
120055	118142	GTTATTTATGAGGATGTGGA
120056	118143	GGTTATTTATGAGGATGTGG
120057	118144	CGGTTATTTATGAGGATGTG
120058	118145	TCGGTTATTTATGAGGATGT
120059	118146	ATCGGTTATTTATGAGGATG
120060	118147	TATCGGTTATTTATGAGGAT
120061	118148	ATATCGGTTATTTATGAGGA
120062	118149	CATATCGGTTATTTATGAGG
120063	118150	ACATATCGGTTATTTATGAG
120064	118151	GACATATCGGTTATTTATGA
120065	118152	AGACATATCGGTTATTTATG
120066	118153	AAGACATATCGGTTATTTAT
120067	118154	AAAGACATATCGGTTATTTA
120068	118155	CAAAGACATATCGGTTATTT
120069	118156	CCAAAGACATATCGGTTATT
120070	118157	ACCAAAGACATATCGGTTAT
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120073	118160	CAAACCAAAGACATATCGGT
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120075	118162	CCCAAACCAAAGACATATCG
120076	118163	ACCCAAACCAAAGACATATC
120077	118164	AACCCAAACCAAAGACATAT
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120080	118167	CATAACCCAAACCAAAGACA
120081	118168	ACATAACCCAAACCAAAGAC
120082	118169	GACATAACCCAAACCAAAGA
120083	118170	GGACATAACCCAAACCAAAG
120084	118171	TGGACATAACCCAAACCAAA

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21792	19879	GCAACCTCCTCCTCCTGGGT
21793	19880	TGCAACCTCCTCCTCCTGGG
21794	19881	CTGCAACCTCCTCCTCCTGG
21795	19882	ACTGCAACCTCCTCCTCCTG
21796	19883	CACTGCAACCTCCTCCTCCT
21797	19884	TCACTGCAACCTCCTCCTCC
21798	19885	TTCACTGCAACCTCCTCCTC
21799	19886	GTTCACTGCAACCTCCTCCT
21800	19887	GGTTCACTGCAACCTCCTCC
21801	19888	TGGTTCACTGCAACCTCCTC
21802	19889	TTGGTTCACTGCAACCTCCT
21803	19890	CTTGGTTCACTGCAACCTCC
21804	19891	TCTTGGTTCACTGCAACCTC
21805	19892	TTCTTGGTTCACTGCAACCT
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21807	19894	TGTTCTTGGTTCACTGCAAC
21808	19895	GTGTTCTTGGTTCACTGCAA
21809	19896	CGTGTTCTTGGTTCACTGCA
21810	19897	GCGTGTTCTTGGTTCACTGC
21811	19898	GGCGTGTTCTTGGTTCACTG
21812	19899	TGGCGTGTTCTTGGTTCACT
21813	19900	GTGGCGTGTTCTTGGTTCAC
21814	19901	AGTGGCGTGTTCTTGGTTCA
21815	19902	CAGTGGCGTGTTCTTGGTTC
21816	19903	GCAGTGGCGTGTTCTTGGTT
21817	19904	TGCAGTGGCGTGTTCTTGGT
21818	19905	GTGCAGTGGCGTGTTCTTGG
21819	19906	AGTGCAGTGGCGTGTTCTTG
21820	19907	GAGTGCAGTGGCGTGTTCTT
21821	19908	GGAGTGCAGTGGCGTGTTCT
21822	19909	TGGAGTGCAGTGGCGTGTTC
21823	19910	CTGGAGTGCAGTGGCGTGTT
21824	19911	GCTGGAGTGCAGTGGCGTGT
21825	19912	GGCTGGAGTGCAGTGGCGTG
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21831	19918	CACCCAGGCTGGAGTGCAGT
21832	19919	TCACCCAGGCTGGAGTGCAG
21833	19920	GTCACCCAGGCTGGAGTGCA
21834	19921	TGTCACCCAGGCTGGAGTGC
21835	19922	ATGTCACCCAGGCTGGAGTG
21836	19923	TATGTCACCCAGGCTGGAGT
21837	19924	CTATGTCACCCAGGCTGGAG
21838	19925	ACTATGTCACCCAGGCTGGA
21839	19926	CACTATGTCACCCAGGCTGG
21840	19927	TCACTATGTCACCCAGGCTG
21841	19928	CTCACTATGTCACCCAGGCT
21842	19929	TCTCACTATGTCACCCAGGC
21843	19930	GTCTCACTATGTCACCCAGG
21844	19931	AGTCTCACTATGTCACCCAG
21845	19932	GAGTCTCACTATGTCACCCA
21846	19933	AGAGTCTCACTATGTCACCC
21847	19934	AAGAGTCTCACTATGTCACC
21848	19935	TAAGAGTCTCACTATGTCAC
21849	19936	ATAAGAGTCTCACTATGTCA
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21852	19939	GAGATAAGAGTCTCACTATG
21853	19940	TGAGATAAGAGTCTCACTAT
21854	19941	TTGAGATAAGAGTCTCACTA
21855	19942	TTTGAGATAAGAGTCTCACT
21856	19943	TTTTGAGATAAGAGTCTCAC
21857	19944	TTTTTGAGATAAGAGTCTCA
21858	19945	TTTTTTGAGATAAGAGTCTC
21859	19946	TTTTTTTGAGATAAGAGTCT
21860	19947	TTTTTTTTGAGATAAGAGTC
21861	19948	TTTTTTTTTGAGATAAGAGT

70938	69025	CGGTGAAACCCCATCTCTAC
70939	69026	ACGGTGAAACCCCATCTCTA
70940	69027	CACGGTGAAACCCCATCTCT
70941	69028	ACACGGTGAAACCCCATCTC
70942	69029	AACACGGTGAAACCCCATCT
70943	69030	TAACACGGTGAAACCCCATC
70944	69031	TTAACACGGTGAAACCCCAT
70945	69032	GTTAACACGGTGAAACCCCA
70946	69033	GGTTAACACGGTGAAACCCC
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70948	69035	CTGGTTAACACGGTGAAACC
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70957	69044	AAGACCATCCTGGTTAACAC
70958	69045	CAAGACCATCCTGGTTAACA
70959	69046	TCAAGACCATCCTGGTTAAC
70960	69047	ATCAAGACCATCCTGGTTAA
70961	69048	GATCAAGACCATCCTGGTTA
70962	69049	AGATCAAGACCATCCTGGTT
70963	69050	GAGATCAAGACCATCCTGGT
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70967	69054	TCAGGAGATCAAGACCATCC
70968	69055	GTCAGGAGATCAAGACCATC
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70970	69057	AGGTCAGGAGATCAAGACCA
70971	69058	GAGGTCAGGAGATCAAGACC
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70974	69061	CACGAGGTCAGGAGATCAAG
70975	69062	TCACGAGGTCAGGAGATCAA
70976	69063	ATCACGAGGTCAGGAGATCA
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70979	69066	CAGATCACGAGGTCAGGAGA
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70981	69068	GGCAGATCACGAGGTCAGGA
70982	69069	AGGCAGATCACGAGGTCAGG
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70988	69075	CCAGTCAGGCAGATCACGAG
70989	69076	CCCAGTCAGGCAGATCACGA
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71003	69090	AGCATTTTGGGAGGCCCAGT
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71005	69092	TCAGCATTTTGGGAGGCCCA
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71008	69095	ATCTCAGCATTTTGGGAGGC

120085	118172	ATGGACATAACCCAAACCAA
120086	118173	AATGGACATAACCCAAACCA
120087	118174	GAATGGACATAACCCAAACC
120088	118175	AGAATGGACATAACCCAAAC
120089	118176	TAGAATGGACATAACCCAAA
120090	118177	CTAGAATGGACATAACCCAA
120091	118178	ACTAGAATGGACATAACCCA
120092	118179	CACTAGAATGGACATAACCC
120093	118180	CCACTAGAATGGACATAACC
120094	118181	ACCACTAGAATGGACATAAC
120095	118182	AACCACTAGAATGGACATAA
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120098	118185	CATAACCACTAGAATGGACA
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120102	118189	ACTTCATAACCACTAGAATG
120103	118190	CACTTCATAACCACTAGAAT
120104	118191	ACACTTCATAACCACTAGAA
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120107	118194	ATGACACTTCATAACCACTA
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120109	118196	CAATGACACTTCATAACCAC
120110	118197	ACAATGACACTTCATAACCA
120111	118198	CACAATGACACTTCATAACC
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120113	118200	ACCACAATGACACTTCATAA
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120121	118208	AACAAAAAACCACAATGACA
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120124	118211	AAAAACAAAAAACCACAATG
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120127	118214	CAAAAAAACAAAAAACCACA
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120129	118216	TACAAAAAAACAAAAAACCA
120130	118217	ATACAAAAAAACAAAAAACC
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120132	118219	CAATACAAAAAAACAAAAAA
120133	118220	ACAATACAAAAAAACAAAAA
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120136	118223	AAAACAATACAAAAAAACAA
120137	118224	CAAAACAATACAAAAAAACA
120138	118225	TCAAAACAATACAAAAAAAC
120139	118226	CTCAAAACAATACAAAAAAA
120140	118227	TCTCAAAACAATACAAAAAA
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120142	118229	GATCTCAAAACAATACAAAA
120143	118230	CGATCTCAAAACAATACAAA
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120145	118232	CACGATCTCAAAACAATACA
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120147	118234	GGCACGATCTCAAAACAATA
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120149	118236	TGGGCACGATCTCAAAACAA
120150	118237	CTGGGCACGATCTCAAAACA
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21862	19949	TTTTTTTTTTGAGATAAGAG
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21865	19952	TTTTTTTTTTTGAGATAA
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21868	19955	TTTTTTTTTTTTTTTGAGA
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21870	19957	CCTTTTTTTTTTTTTTTGA
21871	19958	ACCTTTTTTTTTTTTTTTG
21872	19959	GACCTTTTTTTTTTTTTTT
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21876	19963	AGACGACCTTTTTTTTTTT
21877	19964	CAGACGACCTTTTTTTTTT
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21879	19966	TACAGACGACCTTTTTTTT
21880	19967	GTACAGACGACCTTTTTTT
21881	19968	AGTACAGACGACCTTTTTT
21882	19969	TAGTACAGACGACCTTTTT
21883	19970	ATAGTACAGACGACCTTTT
21884	19971	AATAGTACAGACGACCTTT
21885	19972	CAATAGTACAGACGACCTT
21886	19973	GCAATAGTACAGACGACCTT
21887	19974	TGCAATAGTACAGACGACCT
21888	19975	ATGCAATAGTACAGACGACC
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21891	19978	AACATGCAATAGTACAGACG
21892	19979	TAACATGCAATAGTACAGAC
21893	19980	CTAACATGCAATAGTACAGA
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21901	19988	AGAAACTACTAACATGCAAT
21902	19989	AAGAAACTACTAACATGCAA
21903	19990	AAAGAAACTACTAACATGCA
21904	19991	GAAAGAAACTACTAACATGC
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21906	19993	CAGAAAGAAACTACTAACAT
21907	19994	GCAGAAAGAAACTACTAACA
21908	19995	AGCAGAAAGAAACTACTAAC
21909	19996	AAGCAGAAAGAAACTACTAA
21910	19997	TAAGCAGAAAGAAACTACTA
21911	19998	ATAAGCAGAAAGAAACTACT
21912	19999	AATAAGCAGAAAGAAACTAC
21913	20000	CAATAAGCAGAAAGAAACTA
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21915	20002	AACAATAAGCAGAAAGAAAC
21916	20003	CAACAATAAGCAGAAAGAAA
21917	20004	TCAACAATAAGCAGAAAGAA
21918	20005	CTCAACAATAAGCAGAAAGA
21919	20006	ACTCAACAATAAGCAGAAAG
21920	20007	TACTCAACAATAAGCAGAAA
21921	20008	CTACTCAACAATAAGCAGAA
21922	20009	ACTACTCAACAATAAGCAGA
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21924	20011	CTACTACTCAACAATAAGCA
21925	20012	ACTACTACTCAACAATAAGC
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71009	69096	AATCTCAGCATTTTGGGAGG
71010	69097	TAATCTCAGCATTTTGGGAG
71011	69098	GTAATCTCAGCATTTTGGGA
71012	69099	TGTAATCTCAGCATTTTGGG
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71015	69102	GCCTGTAATCTCAGCATTTT
71016	69103	CGCCTGTAATCTCAGCATTT
71017	69104	ACGCCTGTAATCTCAGCATT
71018	69105	CACGCCTGTAATCTCAGCAT
71019	69106	TCACGCCTGTAATCTCAGCA
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71021	69108	GCTCACGCCTGTAATCTCAG
71022	69109	GGCTCACGCCTGTAATCTCA
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71024	69111	GTGGCTCACGCCTGTAATCT
71025	69112	GGTGGCTCACGCCTGTAATC
71026	69113	CGGTGGCTCACGCCTGTAAT
71027	69114	GCGGTGGCTCACGCCTGTAA
71028	69115	AGCGGTGGCTCACGCCTGTA
71029	69116	GAGCGGTGGCTCACGCCTGT
71030	69117	GGAGCGGTGGCTCACGCCTG
71031	69118	GGGAGCGGTGGCTCACGCCT
71032	69119	TGGGAGCGGTGGCTCACGCC
71033	69120	CTGGGAGCGGTGGCTCACGC
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71035	69122	AGCTGGGAGCGGTGGCTCAC
71036	69123	TAGCTGGGAGCGGTGGCTCA
71037	69124	ATAGCTGGGAGCGGTGGCTC
71038	69125	TATAGCTGGGAGCGGTGGCT
71039	69126	GTATAGCTGGGAGCGGTGGC
71040	69127	TGTATAGCTGGGAGCGGTGG
71041	69128	GTGTATAGCTGGGAGCGGTG
71042	69129	CGTGTATAGCTGGGAGCGGT
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71044	69131	TACGTGTATAGCTGGGAGCG
71045	69132	ATACGTGTATAGCTGGGAGC
71046	69133	AATACGTGTATAGCTGGGAG
71047	69134	AAATACGTGTATAGCTGGGA
71048	69135	AAAATACGTGTATAGCTGGG
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71050	69137	TAAAAATACGTGTATAGCTG
71051	69138	TTAAAAATACGTGTATAGCT
71052	69139	ATTAAAAATACGTGTATAGC
71053	69140	CATTAAAAATACGTGTATAG
71054	69141	GCATTAAAAATACGTGTATA
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71056	69143	TGGCATTAAAAATACGTGTA
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71058	69145	AGTGGCATTAAAAATACGTG
71059	69146	GAGTGGCATTAAAAATACGT
71060	69147	GGAGTGGCATTAAAAATACG
71061	69148	TGGAGTGGCATTAAAAATAC
71062	69149	CTGGAGTGGCATTAAAAATA
71063	69150	ACTGGAGTGGCATTAAAAAT
71064	69151	GACTGGAGTGGCATTAAAAA
71065	69152	AGACTGGAGTGGCATTAAAA
71066	69153	TAGACTGGAGTGGCATTAAA
71067	69154	ATAGACTGGAGTGGCATTAA
71068	69155	CATAGACTGGAGTGGCATTA
71069	69156	ACATAGACTGGAGTGGCATT
71070	69157	AACATAGACTGGAGTGGCAT
71071	69158	CAACATAGACTGGAGTGGCA
71072	69159	CCAACATAGACTGGAGTGGC
71073	69160	TCCAACATAGACTGGAGTGG
71074	69161	TTCCAACATAGACTGGAGTG
71075	69162	GTTCCAACATAGACTGGAGT
71076	69163	GGTTCCAACATAGACTGGAG
71077	69164	TGGTTCCAACATAGACTGGA
71078	69165	ATGGTTCCAACATAGACTGG
71079	69166	AATGGTTCCAACATAGACTG

120156	118243	TCCAGCCTGGGCACGATCTC
120157	118244	CTCCAGCCTGGGCACGATCT
120158	118245	GCTCCAGCCTGGGCACGATC
120159	118246	TGCTCCAGCCTGGGCACGAT
120160	118247	GTGCTCCAGCCTGGGCACGA
120161	118248	TGTGCTCCAGCCTGGGCACG
120162	118249	CTGTGCTCCAGCCTGGGCAC
120163	118250	ACTGTGCTCCAGCCTGGGCA
120164	118251	CACTGTGCTCCAGCCTGGGC
120165	118252	CCACTGTGCTCCAGCCTGGG
120166	118253	GCCACTGTGCTCCAGCCTGG
120167	118254	TGCCACTGTGCTCCAGCCTG
120168	118255	GTGCCACTGTGCTCCAGCCT
120169	118256	TGTGCCACTGTGCTCCAGCC
120170	118257	TTGTGCCACTGTGCTCCAGC
120171	118258	ATTGTGCCACTGTGCTCCAG
120172	118259	GATTGTGCCACTGTGCTCCA
120173	118260	AGATTGTGCCACTGTGCTCC
120174	118261	GAGATTGTGCCACTGTGCTC
120175	118262	CGAGATTGTGCCACTGTGCT
120176	118263	CCGAGATTGTGCCACTGTGC
120177	118264	GCCGAGATTGTGCCACTGTG
120178	118265	AGCCGAGATTGTGCCACTGT
120179	118266	GAGCCGAGATTGTGCCACTG
120180	118267	TGAGCCGAGATTGTGCCACT
120181	118268	GTGAGCCGAGATTGTGCCAC
120182	118269	AGTGAGCCGAGATTGTGCCA
120183	118270	CAGTGAGCCGAGATTGTGCC
120184	118271	GCAGTGAGCCGAGATTGTGC
120185	118272	TGCAGTGAGCCGAGATTGTG
120186	118273	CTGCAGTGAGCCGAGATTGT
120187	118274	GCTGCAGTGAGCCGAGATTG
120188	118275	GGCTGCAGTGAGCCGAGATT
120189	118276	AGGCTGCAGTGAGCCGAGAT
120190	118277	AAGGCTGCAGTGAGCCGAGA
120191	118278	GAAGGCTGCAGTGAGCCGAG
120192	118279	CGAAGGCTGCAGTGAGCCGA
120193	118280	GCGAAGGCTGCAGTGAGCCG
120194	118281	AGCGAAGGCTGCAGTGAGCC
120195	118282	AAGCGAAGGCTGCAGTGAGC
120196	118283	GAAGCGAAGGCTGCAGTGAG
120197	118284	GGAAGCGAAGGCTGCAGTGA
120198	118285	AGGAAGCGAAGGCTGCAGTG
120199	118286	CAGGAAGCGAAGGCTGCAGT
120200	118287	CCAGGAAGCGAAGGCTGCAG
120201	118288	CCCAGGAAGCGAAGGCTGCA
120202	118289	ACCCAGGAAGCGAAGGCTGC
120203	118290	AACCCAGGAAGCGAAGGCTG
120204	118291	GAACCCAGGAAGCGAAGGCT
120205	118292	TGAACCCAGGAAGCGAAGGC
120206	118293	TTGAACCCAGGAAGCGAAGG
120207	118294	CTTGAACCCAGGAAGCGAAG
120208	118295	GCTTGAACCCAGGAAGCGAA
120209	118296	TGCTTGAACCCAGGAAGCGA
120210	118297	TTGCTTGAACCCAGGAAGCG
120211	118298	ATTGCTTGAACCCAGGAAGC
120212	118299	AATTGCTTGAACCCAGGAAG
120213	118300	GAATTGCTTGAACCCAGGAA
120214	118301	AGAATTGCTTGAACCCAGGA
120215	118302	GAGAATTGCTTGAACCCAGG
120216	118303	GGAGAATTGCTTGAACCCAG
120217	118304	AGGAGAATTGCTTGAACCCA
120218	118305	CAGGAGAATTGCTTGAACCC
120219	118306	GCAGGAGAATTGCTTGAACC
120220	118307	GGCAGGAGAATTGCTTGAAC
120221	118308	AGGCAGGAGAATTGCTTGAA
120222	118309	GAGGCAGGAGAATTGCTTGA
120223	118310	TGAGGCAGGAGAATTGCTTG
120224	118311	GTGAGGCAGGAGAATTGCTT
120225	118312	GGTGAGGCAGGAGAATTGCT
120226	118313	GGGTGAGGCAGGAGAATTGC

21933	20020	TACAATAGACTACTACTCAA
21934	20021	ATACAATAGACTACTACTCA
21935	20022	CATACAATAGACTACTACTC
21936	20023	GCATACAATAGACTACTACT
21937	20024	TGCATACAATAGACTACTAC
21938	20025	ATGCATACAATAGACTACTA
21939	20026	CATGCATACAATAGACTACT
21940	20027	ACATGCATACAATAGACTAC
21941	20028	TACATGCATACAATAGACTA
21942	20029	GTACATGCATACAATAGACT
21943	20030	GGTACATGCATACAATAGAC
21944	20031	TGGTACATGCATACAATAGA
21945	20032	CTGGTACATGCATACAATAG
21946	20033	ACTGGTACATGCATACAATA
21947	20034	AACTGGTACATGCATACAAT
21948	20035	AAACTGGTACATGCATACAA
21949	20036	CAAACTGGTACATGCATACA
21950	20037	ACAAACTGGTACATGCATAC
21951	20038	AACAAACTGGTACATGCATA
21952	20039	GAACAAACTGGTACATGCAT
21953	20040	TGAACAAACTGGTACATGCA
21954	20041	ATGAACAAACTGGTACATGC
21955	20042	GATGAACAAACTGGTACATG
21956	20043	AGATGAACAAACTGGTACAT
21957	20044	TAGATGAACAAACTGGTACA
21958	20045	CTAGATGAACAAACTGGTAC
21959	20046	ACTAGATGAACAAACTGGTA
21960	20047	CACTAGATGAACAAACTGGT
21961	20048	CCACTAGATGAACAAACTGG
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21963	20050	CACCACTAGATGAACAAACT
21964	20051	CCACCACTAGATGAACAAAC
21965	20052	TCCACCACTAGATGAACAAA
21966	20053	GTCCACCACTAGATGAACAA
21967	20054	TGTCCACCACTAGATGAACA
21968	20055	ATGTCCACCACTAGATGAAC
21969	20056	AATGTCCACCACTAGATGAA
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21971	20058	TCAATGTCCACCACTAGATG
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21973	20060	ACTCAATGTCCACCACTAGA
21974	20061	AACTCAATGTCCACCACTAG
21975	20062	TAACTCAATGTCCACCACTA
21976	20063	CTAACTCAATGTCCACCACT
21977	20064	GCTAACTCAATGTCCACCAC
21978	20065	TGCTAACTCAATGTCCACCA
21979	20066	CTGCTAACTCAATGTCCACC
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21981	20068	ACCTGCTAACTCAATGTCCA
21982	20069	AACCTGCTAACTCAATGTCC
21983	20070	AAACCTGCTAACTCAATGTC
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21986	20073	CCAAAACCTGCTAACTCAAT
21987	20074	GCCAAAACCTGCTAACTCAA
21988	20075	AGCCAAAACCTGCTAACTCA
21989	20076	TAGCCAAAACCTGCTAACTC
21990	20077	ATAGCCAAAACCTGCTAACT
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21992	20079	TAATAGCCAAAACCTGCTAA
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21995	20082	TTTTAATAGCCAAAACCTGC
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21997	20084	ATTTTTAATAGCCAAAACCT
21998	20085	TATTTTTAATAGCCAAAACC
21999	20086	TTATTTTTAATAGCCAAAAC
22000	20087	TTTATTTTTAATAGCCAAAA
22001	20088	CTTTATTTTTAATAGCCAAA
22002	20089	GCTTTATTTTTAATAGCCAA
22003	20090	AGCTTTATTTTTAATAGCCA

71080	69167	AAATGGTTCCAACATAGACT
71081	69168	AAAATGGTTCCAACATAGAC
71082	69169	TAAAATGGTTCCAACATAGA
71083	69170	GTAAAATGGTTCCAACATAG
71084	69171	AGTAAAATGGTTCCAACATA
71085	69172	AAGTAAAATGGTTCCAACAT
71086	69173	GAAGTAAAATGGTTCCAACA
71087	69174	GGAAGTAAAATGGTTCCAAC
71088	69175	GGGAAGTAAAATGGTTCCAA
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71090	69177	AGGGGAAGTAAAATGGTTCC
71091	69178	AAGGGGAAGTAAAATGGTTC
71092	69179	AAAGGGGAAGTAAAATGGTT
71093	69180	GAAAGGGGAAGTAAAATGGT
71094	69181	AGAAAGGGGAAGTAAAATGG
71095	69182	AAGAAAGGGGAAGTAAAATG
71096	69183	TAAGAAAGGGGAAGTAAAAT
71097	69184	ATAAGAAAGGGGAAGTAAAA
71098	69185	AATAAGAAAGGGGAAGTAAA
71099	69186	AAATAAGAAAGGGGAAGTAA
71100	69187	AAAATAAGAAAGGGGAAGTA
71101	69188	GAAAATAAGAAAGGGGAAGT
71102	69189	AGAAAATAAGAAAGGGGAAG
71103	69190	AAGAAAATAAGAAAGGGGAA
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71105	69192	AGAAGAAAATAAGAAAGGGG
71106	69193	AAGAAGAAAATAAGAAAGGG
71107	69194	CAAGAAGAAAATAAGAAAGG
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71112	69199	GAACACAAGAAGAAAATAAG
71113	69200	AGAACACAAGAAGAAAATAA
71114	69201	AAGAACACAAGAAGAAAATA
71115	69202	CAAGAACACAAGAAGAAAAT
71116	69203	TCAAGAACACAAGAAGAAAA
71117	69204	TTCAAGAACACAAGAAGAAA
71118	69205	CTTCAAGAACACAAGAAGAA
71119	69206	CCTTCAAGAACACAAGAAGA
71120	69207	GCCTTCAAGAACACAAGAAG
71121	69208	GGCCTTCAAGAACACAAGAA
71122	69209	AGGCCTTCAAGAACACAAGA
71123	69210	TAGGCCTTCAAGAACACAAG
71124	69211	CTAGGCCTTCAAGAACACAA
71125	69212	TCTAGGCCTTCAAGAACACA
71126	69213	ATCTAGGCCTTCAAGAACAC
71127	69214	GATCTAGGCCTTCAAGAACA
71128	69215	TGATCTAGGCCTTCAAGAAC
71129	69216	CTGATCTAGGCCTTCAAGAA
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71136	69223	GCAACAGCTGATCTAGGCCT
71137	69224	AGCAACAGCTGATCTAGGCC
71138	69225	CAGCAACAGCTGATCTAGGC
71139	69226	TCAGCAACAGCTGATCTAGG
71140	69227	ATCAGCAACAGCTGATCTAG
71141	69228	TATCAGCAACAGCTGATCTA
71142	69229	CTATCAGCAACAGCTGATCT
71143	69230	CCTATCAGCAACAGCTGATC
71144	69231	GCCTATCAGCAACAGCTGAT
71145	69232	AGCCTATCAGCAACAGCTGA
71146	69233	CAGCCTATCAGCAACAGCTG
71147	69234	ACAGCCTATCAGCAACAGCT
71148	69235	GACAGCCTATCAGCAACAGC
71149	69236	TGACAGCCTATCAGCAACAG
71150	69237	GTGACAGCCTATCAGCAACA

120227	118314	AGGGTGAGGCAGGAGAATTG
120228	118315	GAGGGTGAGGCAGGAGAATT
120229	118316	GGAGGGTGAGGCAGGAGAAT
120230	118317	GGGAGGGTGAGGCAGGAGAA
120231	118318	TGGGAGGGTGAGGCAGGAGA
120232	118319	CTGGGAGGGTGAGGCAGGAG
120233	118320	TCTGGGAGGGTGAGGCAGGA
120234	118321	ATCTGGGAGGGTGAGGCAGG
120235	118322	TATCTGGGAGGGTGAGGCAG
120236	118323	CTATCTGGGAGGGTGAGGCA
120237	118324	GCTATCTGGGAGGGTGAGGC
120238	118325	AGCTATCTGGGAGGGTGAGG
120239	118326	CAGCTATCTGGGAGGGTGAG
120240	118327	CCAGCTATCTGGGAGGGTGA
120241	118328	CCCAGCTATCTGGGAGGGTG
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120243	118330	GCCCCAGCTATCTGGGAGGG
120244	118331	AGCCCCAGCTATCTGGGAGG
120245	118332	CAGCCCCAGCTATCTGGGAG
120246	118333	GCAGCCCCAGCTATCTGGGA
120247	118334	TGCAGCCCCAGCTATCTGGG
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120249	118336	CCTGCAGCCCCAGCTATCTG
120250	118337	GCCTGCAGCCCCAGCTATCT
120251	118338	TGCCTGCAGCCCCAGCTATC
120252	118339	ATGCCTGCAGCCCCAGCTAT
120253	118340	TATGCCTGCAGCCCCAGCTA
120254	118341	GTATGCCTGCAGCCCCAGCT
120255	118342	CGTATGCCTGCAGCCCCAGC
120256	118343	GCGTATGCCTGCAGCCCCAG
120257	118344	GGCGTATGCCTGCAGCCCCA
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120259	118346	GTGGCGTATGCCTGCAGCCC
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120261	118348	TGGTGGCGTATGCCTGCAGC
120262	118349	GTGGTGGCGTATGCCTGCAG
120263	118350	TGTGGTGGCGTATGCCTGCA
120264	118351	GTGTGGTGGCGTATGCCTGC
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120266	118353	TGGTGTGGTGGCGTATGCCT
120267	118354	CTGGTGTGGTGGCGTATGCC
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120269	118356	GCCTGGTGTGGTGGCGTATG
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120271	118358	TAGCCTGGTGTGGTGGCGTA
120272	118359	TTAGCCTGGTGTGGTGGCGT
120273	118360	ATTAGCCTGGTGTGGTGGCG
120274	118361	AATTAGCCTGGTGTGGTGGC
120275	118362	AAATTAGCCTGGTGTGGTGG
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120280	118367	TATAAAAATTAGCCTGGTGT
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120287	118374	CAAAAAATATAAAAATTAGC
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120293	118380	TCTCTACAAAAAATATAAAA
120294	118381	ATCTCTACAAAAAATATAAA
120295	118382	CATCTCTACAAAAAATATAA
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22004	20091	CAGCTTTATTTTTAATAGCC
22005	20092	CCAGCTTTATTTTTAATAGC
22006	20093	TCCAGCTTTATTTTTAATAG
22007	20094	CTCCAGCTTTATTTTTAATA
22008	20095	CCTCCAGCTTTATTTTTAAT
22009	20096	GCCTCCAGCTTTATTTTTAA
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22020	20107	CATCGCACCCGGCCTCCAGC
22021	20108	ACATCGCACCCGGCCTCCAG
22022	20109	GACATCGCACCCGGCCTCCA
22023	20110	AGACATCGCACCCGGCCTCC
22024	20111	GAGACATCGCACCCGGCCTC
22025	20112	TGAGACATCGCACCCGGCCT
22026	20113	GTGAGACATCGCACCCGGCC
22027	20114	CGTGAGACATCGCACCCGGC
22028	20115	GCGTGAGACATCGCACCCGG
22029	20116	GGCGTGAGACATCGCACCCG
22030	20117	AGGCGTGAGACATCGCACCC
22031	20118	CAGGCGTGAGACATCGCACC
22032	20119	ACAGGCGTGAGACATCGCAC
22033	20120	TACAGGCGTGAGACATCGCA
22034	20121	TTACAGGCGTGAGACATCGC
22035	20122	ATTACAGGCGTGAGACATCG
22036	20123	GATTACAGGCGTGAGACATC
22037	20124	GGATTACAGGCGTGAGACAT
22038	20125	GGGATTACAGGCGTGAGACA
22039	20126	TGGGATTACAGGCGTGAGAC
22040	20127	CTGGGATTACAGGCGTGAGA
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22042	20129	TGCTGGGATTACAGGCGTGA
22043	20130	ATGCTGGGATTACAGGCGTG
22044	20131	AATGCTGGGATTACAGGCGT
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22049	20136	TCCAAAATGCTGGGATTACA
22050	20137	TTCCAAAATGCTGGGATTAC
22051	20138	CTTCCAAAATGCTGGGATTA
22052	20139	CCTTCCAAAATGCTGGGATT
22053	20140	GCCTTCCAAAATGCTGGGAT
22054	20141	GGCCTTCCAAAATGCTGGGA
22055	20142	CGGCCTTCCAAAATGCTGGG
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22061	20148	CTGCCTCGGCCTTCCAAAAT
22062	20149	CCTGCCTCGGCCTTCCAAAA
22063	20150	GCCTGCCTCGGCCTTCCAAA
22064	20151	CGCCTGCCTCGGCCTTCCAA
22065	20152	CCGCCTGCCTCGGCCTTCCA
22066	20153	TCCGCCTGCCTCGGCCTTCC
22067	20154	ATCCGCCTGCCTCGGCCTTC
22068	20155	GATCCGCCTGCCTCGGCCTT
22069	20156	TGATCCGCCTGCCTCGGCCT
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22071	20158	GGTGATCCGCCTGCCTCGGC
22072	20159	AGGTGATCCGCCTGCCTCGG
22073	20160	TAGGTGATCCGCCTGCCTCG
22074	20161	TTAGGTGATCCGCCTGCCTC

71151	69238	AGTGACAGCCTATCAGCAAC
71152	69239	CAGTGACAGCCTATCAGCAA
71153	69240	ACAGTGACAGCCTATCAGCA
71154	69241	GACAGTGACAGCCTATCAGC
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71170	69257	CTGGGCTTTCTAAAGTGACA
71171	69258	TCTGGGCTTTCTAAAGTGAC
71172	69259	CTCTGGGCTTTCTAAAGTGA
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71181	69268	AACAAAAGGCTCTGGGCTTT
71182	69269	GAACAAAAGGCTCTGGGCTT
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71184	69271	AGGAACAAAAGGCTCTGGGC
71185	69272	AAGGAACAAAAGGCTCTGGG
71186	69273	TAAGGAACAAAAGGCTCTGG
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71196	69283	AACAAAGTTCTAAGGAACAA
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71198	69285	AAAACAAAGTTCTAAGGAAC
71199	69286	AAAAACAAAGTTCTAAGGAA
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71201	69288	TTAAAAACAAAGTTCTAAGG
71202	69289	ATTAAAAACAAAGTTCTAAG
71203	69290	AATTAAAAACAAAGTTCTAA
71204	69291	CAATTAAAAACAAAGTTCTA
71205	69292	ACAATTAAAAACAAAGTTCT
71206	69293	TACAATTAAAAACAAAGTTC
71207	69294	ATACAATTAAAAACAAAGTT
71208	69295	AATACAATTAAAAACAAAGT
71209	69296	CAATACAATTAAAAACAAAG
71210	69297	ACAATACAATTAAAAACAAA
71211	69298	TACAATACAATTAAAAACAA
71212	69299	CTACAATACAATTAAAAACA
71213	69300	GCTACAATACAATTAAAAAC
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71216	69303	AGTGCTACAATACAATTAAA
71217	69304	GAGTGCTACAATACAATTAA
71218	69305	TGAGTGCTACAATACAATTA
71219	69306	ATGAGTGCTACAATACAATT
71220	69307	AATGAGTGCTACAATACAAT
71221	69308	CAATGAGTGCTACAATACAA

120298	118385	CTCCATCTCTACAAAAAATA
120299	118386	GCTCCATCTCTACAAAAAAT
120300	118387	AGCTCCATCTCTACAAAAAA
120301	118388	AAGCTCCATCTCTACAAAAA
120302	118389	GAAGCTCCATCTCTACAAAA
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120305	118392	GGAGAAGCTCCATCTCTACA
120306	118393	CGGAGAAGCTCCATCTCTAC
120307	118394	ACGGAGAAGCTCCATCTCTA
120308	118395	CACGGAGAAGCTCCATCTCT
120309	118396	GCACGGAGAAGCTCCATCTC
120310	118397	AGCACGGAGAAGCTCCATCT
120311	118398	AAGCACGGAGAAGCTCCATC
120312	118399	GAAGCACGGAGAAGCTCCAT
120313	118400	GGAAGCACGGAGAAGCTCCA
120314	118401	GGGAAGCACGGAGAAGCTCC
120315	118402	TGGGAAGCACGGAGAAGCTC
120316	118403	CTGGGAAGCACGGAGAAGCT
120317	118404	CCTGGGAAGCACGGAGAAGC
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120319	118406	AGCCTGGGAAGCACGGAGAA
120320	118407	CAGCCTGGGAAGCACGGAGA
120321	118408	CCAGCCTGGGAAGCACGGAG
120322	118409	ACCAGCCTGGGAAGCACGGA
120323	118410	GACCAGCCTGGGAAGCACGG
120324	118411	AGACCAGCCTGGGAAGCACG
120325	118412	GAGACCAGCCTGGGAAGCAC
120326	118413	CGAGACCAGCCTGGGAAGCA
120327	118414	TCGAGACCAGCCTGGGAAGC
120328	118415	TTCGAGACCAGCCTGGGAAG
120329	118416	ATTCGAGACCAGCCTGGGAA
120330	118417	AATTCGAGACCAGCCTGGGA
120331	118418	GAATTCGAGACCAGCCTGGG
120332	118419	GGAATTCGAGACCAGCCTGG
120333	118420	AGGAATTCGAGACCAGCCTG
120334	118421	CAGGAATTCGAGACCAGCCT
120335	118422	TCAGGAATTCGAGACCAGCC
120336	118423	CTCAGGAATTCGAGACCAGC
120337	118424	GCTCAGGAATTCGAGACCAG
120338	118425	AGCTCAGGAATTCGAGACCA
120339	118426	GAGCTCAGGAATTCGAGACC
120340	118427	TGAGCTCAGGAATTCGAGAC
120341	118428	TTGAGCTCAGGAATTCGAGA
120342	118429	CTTGAGCTCAGGAATTCGAG
120343	118430	GCTTGAGCTCAGGAATTCGA
120344	118431	CGCTTGAGCTCAGGAATTCG
120345	118432	TCGCTTGAGCTCAGGAATTC
120346	118433	ATCGCTTGAGCTCAGGAATT
120347	118434	GATCGCTTGAGCTCAGGAAT
120348	118435	GGATCGCTTGAGCTCAGGAA
120349	118436	GGGATCGCTTGAGCTCAGGA
120350	118437	GGGGATCGCTTGAGCTCAGG
120351	118438	GGGGGATCGCTTGAGCTCAG
120352	118439	AGGGGGATCGCTTGAGCTCA
120353	118440	CAGGGGGATCGCTTGAGCTC
120354	118441	GCAGGGGGATCGCTTGAGCT
120355	118442	CGCAGGGGGATCGCTTGAGC
120356	118443	ACGCAGGGGGATCGCTTGAG
120357	118444	GACGCAGGGGGATCGCTTGA
120358	118445	TGACGCAGGGGGATCGCTTG
120359	118446	CTGACGCAGGGGGATCGCTT
120360	118447	GCTGACGCAGGGGGATCGCT
120361	118448	GGCTGACGCAGGGGGATCGC
120362	118449	AGGCTGACGCAGGGGGATCG
120363	118450	GAGGCTGACGCAGGGGGATC
120364	118451	GGAGGCTGACGCAGGGGGAT
120365	118452	TGGAGGCTGACGCAGGGGGA
120366	118453	CTGGAGGCTGACGCAGGGGG
120367	118454	TCTGGAGGCTGACGCAGGGG
120368	118455	CTCTGGAGGCTGACGCAGGG

22075	20162	CTTAGGTGATCCGCCTGCCT
22076	20163	CCTTAGGTGATCCGCCTGCC
22077	20164	ACCTTAGGTGATCCGCCTGC
22078	20165	AACCTTAGGTGATCCGCCTG
22079	20166	CAACCTTAGGTGATCCGCCT
22080	20167	CCAACCTTAGGTGATCCGCC
22081	20168	CCCAACCTTAGGTGATCCGC
22082	20169	TCCCAACCTTAGGTGATCCG
22083	20170	CTCCCAACCTTAGGTGATCC
22084	20171	ACTCCCAACCTTAGGTGATC
22085	20172	AACTCCCAACCTTAGGTGAT
22086	20173	AAACTCCCAACCTTAGGTGA
22087	20174	CAAACTCCCAACCTTAGGTG
22088	20175	TCAAACTCCCAACCTTAGGT
22089	20176	CTCAAACTCCCAACCTTAGG
22090	20177	TCTCAAACTCCCAACCTTAG
22091	20178	GTCTCAAACTCCCAACCTTA
22092	20179	GGTCTCAAACTCCCAACCTT
22093	20180	TGGTCTCAAACTCCCAACCT
22094	20181	CTGGTCTCAAACTCCCAACC
22095	20182	GCTGGTCTCAAACTCCCAAC
22096	20183	GGCTGGTCTCAAACTCCCAA
22097	20184	AGGCTGGTCTCAAACTCCCA
22098	20185	CAGGCTGGTCTCAAACTCCC
22099	20186	TCAGGCTGGTCTCAAACTCC
22100	20187	GTCAGGCTGGTCTCAAACTC
22101	20188	GGTCAGGCTGGTCTCAAACT
22102	20189	TGGTCAGGCTGGTCTCAAAC
22103	20190	TTGGTCAGGCTGGTCTCAAA
22104	20191	GTTGGTCAGGCTGGTCTCAA
22105	20192	TGTTGGTCAGGCTGGTCTCA
22106	20193	ATGTTGGTCAGGCTGGTCTC
22107	20194	CATGTTGGTCAGGCTGGTCT
22108	20195	CCATGTTGGTCAGGCTGGTC
22109	20196	TCCATGTTGGTCAGGCTGGT
22110	20197	CTCCATGTTGGTCAGGCTGG
22111	20198	TCTCCATGTTGGTCAGGCTG
22112	20199	TTCTCCATGTTGGTCAGGCT
22113	20200	TTTCTCCATGTTGGTCAGGC
22114	20201	GTTTCTCCATGTTGGTCAGG
22115	20202	GGTTTCTCCATGTTGGTCAG
22116	20203	GGGTTTCTCCATGTTGGTCA
22117	20204	GGGGTTTCTCCATGTTGGTC
22118	20205	TGGGGTTTCTCCATGTTGGT
22119	20206	ATGGGGTTTCTCCATGTTGG
22120	20207	GATGGGGTTTCTCCATGTTG
22121	20208	AGATGGGGTTTCTCCATGTT
22122	20209	GAGATGGGGTTTCTCCATGT
22123	20210	AGAGATGGGGTTTCTCCATG
22124	20211	TAGAGATGGGGTTTCTCCAT
22125	20212	GTAGAGATGGGGTTTCTCCA
22126	20213	AGTAGAGATGGGGTTTCTCC
22127	20214	TAGTAGAGATGGGGTTTCTC
22128	20215	TTAGTAGAGATGGGGTTTCT
22129	20216	TTTAGTAGAGATGGGGTTTC
22130	20217	TTTTAGTAGAGATGGGGTTT
22131	20218	TTTTTAGTAGAGATGGGGTT
22132	20219	ATTTTTAGTAGAGATGGGGT
22133	20220	TATTTTTAGTAGAGATGGGG
22134	20221	GTATTTTTAGTAGAGATGGG
22135	20222	TGTATTTTTAGTAGAGATGG
22136	20223	TTGTATTTTTAGTAGAGATG
22137	20224	TTTGTATTTTTAGTAGAGAT
22138	20225	TTTTGTATTTTTAGTAGAGA
22139	20226	ATTTTGTATTTTTAGTAGAG
22140	20227	AATTTTGTATTTTTAGTAGA
22141	20228	TAATTTTGTATTTTTAGTAG
22142	20229	CTAATTTTGTATTTTTAGTA
22143	20230	GCTAATTTTGTATTTTTAGT
22144	20231	GGCTAATTTTGTATTTTTAG
22145	20232	TGGCTAATTTTGTATTTTTA

71222	69309	ACAATGAGTGCTACAATACA
71223	69310	TACAATGAGTGCTACAATAC
71224	69311	ATACAATGAGTGCTACAATA
71225	69312	AATACAATGAGTGCTACAAT
71226	69313	GAATACAATGAGTGCTACAA
71227	69314	CGAATACAATGAGTGCTACA
71228	69315	TCGAATACAATGAGTGCTAC
71229	69316	ATCGAATACAATGAGTGCTA
71230	69317	AATCGAATACAATGAGTGCT
71231	69318	GAATCGAATACAATGAGTGC
71232	69319	AGAATCGAATACAATGAGTG
71233	69320	TAGAATCGAATACAATGAGT
71234	69321	TTAGAATCGAATACAATGAG
71235	69322	TTTAGAATCGAATACAATGA
71236	69323	TTTTAGAATCGAATACAATG
71237	69324	CTTTTAGAATCGAATACAAT
71238	69325	TCTTTTAGAATCGAATACAA
71239	69326	ATCTTTTAGAATCGAATACA
71240	69327	AATCTTTTAGAATCGAATAC
71241	69328	AAATCTTTTAGAATCGAATA
71242	69329	CAAATCTTTTAGAATCGAAT
71243	69330	GCAAATCTTTTAGAATCGAA
71244	69331	AGCAAATCTTTTAGAATCGA
71245	69332	AAGCAAATCTTTTAGAATCG
71246	69333	GAAGCAAATCTTTTAGAATC
71247	69334	TGAAGCAAATCTTTTAGAAT
71248	69335	ATGAAGCAAATCTTTTAGAA
71249	69336	AATGAAGCAAATCTTTTAGA
71250	69337	AAATGAAGCAAATCTTTTAG
71251	69338	GAAATGAAGCAAATCTTTTA
71252	69339	AGAAATGAAGCAAATCTTTT
71253	69340	CAGAAATGAAGCAAATCTTT
71254	69341	ACAGAAATGAAGCAAATCTT
71255	69342	TACAGAAATGAAGCAAATCT
71256	69343	TTACAGAAATGAAGCAAATC
71257	69344	GTTACAGAAATGAAGCAAAT
71258	69345	AGTTACAGAAATGAAGCAAA
71259	69346	TAGTTACAGAAATGAAGCAA
71260	69347	CTAGTTACAGAAATGAAGCA
71261	69348	ACTAGTTACAGAAATGAAGC
71262	69349	GACTAGTTACAGAAATGAAG
71263	69350	AGACTAGTTACAGAAATGAA
71264	69351	GAGACTAGTTACAGAAATGA
71265	69352	AGAGACTAGTTACAGAAATG
71266	69353	AAGAGACTAGTTACAGAAAT
71267	69354	TAAGAGACTAGTTACAGAAA
71268	69355	GTAAGAGACTAGTTACAGAA
71269	69356	TGTAAGAGACTAGTTACAGA
71270	69357	GTGTAAGAGACTAGTTACAG
71271	69358	GGTGTAAGAGACTAGTTACA
71272	69359	GGGTGTAAGAGACTAGTTAC
71273	69360	TGGGTGTAAGAGACTAGTTA
71274	69361	CTGGGTGTAAGAGACTAGTT
71275	69362	CCTGGGTGTAAGAGACTAGT
71276	69363	TCCTGGGTGTAAGAGACTAG
71277	69364	CTCCTGGGTGTAAGAGACTA
71278	69365	GCTCCTGGGTGTAAGAGACT
71279	69366	AGCTCCTGGGTGTAAGAGAC
71280	69367	GAGCTCCTGGGTGTAAGAGA
71281	69368	GGAGCTCCTGGGTGTAAGAG
71282	69369	AGGAGCTCCTGGGTGTAAGA
71283	69370	TAGGAGCTCCTGGGTGTAAG
71284	69371	CTAGGAGCTCCTGGGTGTAA
71285	69372	ACTAGGAGCTCCTGGGTGTA
71286	69373	AACTAGGAGCTCCTGGGTGT
71287	69374	GAACTAGGAGCTCCTGGGTG
71288	69375	GGAACTAGGAGCTCCTGGGT
71289	69376	AGGAACTAGGAGCTCCTGGG
71290	69377	TAGGAACTAGGAGCTCCTGG
71291	69378	GTAGGAACTAGGAGCTCCTG
71292	69379	TGTAGGAACTAGGAGCTCCT

120369	118456	ACTCTGGAGGCTGACGCAGG
120370	118457	TACTCTGGAGGCTGACGCAG
120371	118458	CTACTCTGGAGGCTGACGCA
120372	118459	GCTACTCTGGAGGCTGACGC
120373	118460	AGCTACTCTGGAGGCTGACG
120374	118461	CAGCTACTCTGGAGGCTGAC
120375	118462	CCAGCTACTCTGGAGGCTGA
120376	118463	CCCAGCTACTCTGGAGGCTG
120377	118464	CCCCAGCTACTCTGGAGGCT
120378	118465	ACCCCAGCTACTCTGGAGGC
120379	118466	AACCCCAGCTACTCTGGAGG
120380	118467	TAACCCCAGCTACTCTGGAG
120381	118468	ATAACCCCAGCTACTCTGGA
120382	118469	TATAACCCCAGCTACTCTGG
120383	118470	CTATAACCCCAGCTACTCTG
120384	118471	CCTATAACCCCAGCTACTCT
120385	118472	GCCTATAACCCCAGCTACTC
120386	118473	CGCCTATAACCCCAGCTACT
120387	118474	ACGCCTATAACCCCAGCTAC
120388	118475	CACGCCTATAACCCCAGCTA
120389	118476	GCACGCCTATAACCCCAGCT
120390	118477	TGCACGCCTATAACCCCAGC
120391	118478	GTGCACGCCTATAACCCCAG
120392	118479	GGTGCACGCCTATAACCCCA
120393	118480	TGGTGCACGCCTATAACCCC
120394	118481	GTGGTGCACGCCTATAACCC
120395	118482	GGTGGTGCACGCCTATAACC
120396	118483	CGGTGGTGCACGCCTATAAC
120397	118484	GCGGTGGTGCACGCCTATAA
120398	118485	CGCGGTGGTGCACGCCTATA
120399	118486	GCGCGGTGGTGCACGCCTAT
120400	118487	AGCGCGGTGGTGCACGCCTA
120401	118488	GAGCGCGGTGGTGCACGCCT
120402	118489	CGAGCGCGGTGGTGCACGCC
120403	118490	CCGAGCGCGGTGGTGCACGC
120404	118491	GCCGAGCGCGGTGGTGCACG
120405	118492	GGCCGAGCGCGGTGGTGCAC
120406	118493	GGGCCGAGCGCGGTGGTGCA
120407	118494	TGGGCCGAGCGCGGTGGTGC
120408	118495	ATGGGCCGAGCGCGGTGGTG
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120410	118497	AAATGGGCCGAGCGCGGTGG
120411	118498	AAAATGGGCCGAGCGCGGTG
120412	118499	AAAAATGGGCCGAGCGCGGT
120413	118500	CAAAAATGGGCCGAGCGCGG
120414	118501	ACAAAAATGGGCCGAGCGCG
120415	118502	TACAAAAATGGGCCGAGCGC
120416	118503	ATACAAAAATGGGCCGAGCG
120417	118504	AATACAAAAATGGGCCGAGC
120418	118505	AAATACAAAAATGGGCCGAG
120419	118506	AAAATACAAAAATGGGCCGA
120420	118507	AAAAATACAAAAATGGGCCG
120421	118508	TAAAAATACAAAAATGGGCC
120422	118509	CTAAAAATACAAAAATGGGC
120423	118510	ACTAAAAATACAAAAATGGG
120424	118511	TACTAAAAATACAAAAATGG
120425	118512	CTACTAAAAATACAAAAATG
120426	118513	TCTACTAAAAATACAAAAAT
120427	118514	CTCTACTAAAAATACAAAAA
120428	118515	TCTCTACTAAAAATACAAAA
120429	118516	ATCTCTACTAAAAATACAAA
120430	118517	CATCTCTACTAAAAATACAA
120431	118518	CCATCTCTACTAAAAATACA
120432	118519	TCCATCTCTACTAAAAATAC
120433	118520	TTCCATCTCTACTAAAAATA
120434	118521	ATTCCATCTCTACTAAAAAT
120435	118522	AATTCCATCTCTACTAAAAA
120436	118523	AAATTCCATCTCTACTAAAA
120437	118524	GAAATTCCATCTCTACTAAA
120438	118525	TGAAATTCCATCTCTACTAA
120439	118526	GTGAAATTCCATCTCTACTA

22146	20233	CTGGCTAATTTTGTATTTTT
22147	20234	CCTGGCTAATTTTGTATTTT
22148	20235	GCCTGGCTAATTTTGTATTT
22149	20236	CGCCTGGCTAATTTTGTATT
22150	20237	ACGCCTGGCTAATTTTGTAT
22151	20238	CACGCCTGGCTAATTTTGTA
22152	20239	CCACGCCTGGCTAATTTTGT
22153	20240	ACCACGCCTGGCTAATTTTG
22154	20241	CACCACGCCTGGCTAATTTT
22155	20242	CCACCACGCCTGGCTAATTT
22156	20243	GCCACCACGCCTGGCTAATT
22157	20244	CGCCACCACGCCTGGCTAAT
22158	20245	GCGCCACCACGCCTGGCTAA
22159	20246	TGCGCCACCACGCCTGGCTA
22160	20247	ATGCGCCACCACGCCTGGCT
22161	20248	CATGCGCCACCACGCCTGGC
22162	20249	GCATGCGCCACCACGCCTGG
22163	20250	GGCATGCGCCACCACGCCTG
22164	20251	AGGCATGCGCCACCACGCCT
22165	20252	CAGGCATGCGCCACCACGCC
22166	20253	ACAGGCATGCGCCACCACGC
22167	20254	TACAGGCATGCGCCACCACG
22168	20255	TTACAGGCATGCGCCACCAC
22169	20256	ATTACAGGCATGCGCCACCA
22170	20257	GATTACAGGCATGCGCCACC
22171	20258	GGATTACAGGCATGCGCCAC
22172	20259	AGGATTACAGGCATGCGCCA
22173	20260	TAGGATTACAGGCATGCGCC
22174	20261	CTAGGATTACAGGCATGCGC
22175	20262	GCTAGGATTACAGGCATGCG
22176	20263	AGCTAGGATTACAGGCATGC
22177	20264	TAGCTAGGATTACAGGCATG
22178	20265	GTAGCTAGGATTACAGGCAT
22179	20266	AGTAGCTAGGATTACAGGCA
22180	20267	GAGTAGCTAGGATTACAGGC
22181	20268	TGAGTAGCTAGGATTACAGG
22182	20269	CTGAGTAGCTAGGATTACAG
22183	20270	CCTGAGTAGCTAGGATTACA
22184	20271	TCCTGAGTAGCTAGGATTAC
22185	20272	CTCCTGAGTAGCTAGGATTA
22186	20273	CCTCCTGAGTAGCTAGGATT
22187	20274	GCCTCCTGAGTAGCTAGGAT
22188	20275	AGCCTCCTGAGTAGCTAGGA
22189	20276	CAGCCTCCTGAGTAGCTAGG
22190	20277	TCAGCCTCCTGAGTAGCTAG
22191	20278	CTCAGCCTCCTGAGTAGCTA
22192	20279	CCTCAGCCTCCTGAGTAGCT
22193	20280	GCCTCAGCCTCCTGAGTAGC
22194	20281	TGCCTCAGCCTCCTGAGTAG
22195	20282	CTGCCTCAGCCTCCTGAGTA
22196	20283	CCTGCCTCAGCCTCCTGAGT
22197	20284	TCCTGCCTCAGCCTCCTGAG
22198	20285	CTCCTGCCTCAGCCTCCTGA
22199	20286	TCTCCTGCCTCAGCCTCCTG
22200	20287	TTCTCCTGCCTCAGCCTCCT
22201	20288	ATTCTCCTGCCTCAGCCTCC
22202	20289	GATTCTCCTGCCTCAGCCTC
22203	20290	CGATTCTCCTGCCTCAGCCT
22204	20291	GCGATTCTCCTGCCTCAGCC
22205	20292	AGCGATTCTCCTGCCTCAGC
22206	20293	AAGCGATTCTCCTGCCTCAG
22207	20294	CAAGCGATTCTCCTGCCTCA
22208	20295	TCAAGCGATTCTCCTGCCTC
22209	20296	TTCAAGCGATTCTCCTGCCT
22210	20297	GTTCAAGCGATTCTCCTGCC
22211	20298	GGTTCAAGCGATTCTCCTGC
22212	20299	GGGTTCAAGCGATTCTCCTG
22213	20300	CGGGTTCAAGCGATTCTCCT
22214	20301	CCGGGTTCAAGCGATTCTCC
22215	20302	CCCGGGTTCAAGCGATTCTC
22216	20303	TCCCGGGTTCAAGCGATTCT

71293	69380	CTGTAGGAACTAGGAGCTCC
71294	69381	CCTGTAGGAACTAGGAGCTC
71295	69382	TCCTGTAGGAACTAGGAGCT
71296	69383	TTCCTGTAGGAACTAGGAGC
71297	69384	TTTCCTGTAGGAACTAGGAG
71298	69385	ATTTCCTGTAGGAACTAGGA
71299	69386	CATTTCCTGTAGGAACTAGG
71300	69387	GCATTTCCTGTAGGAACTAG
71301	69388	AGCATTTCCTGTAGGAACTA
71302	69389	CAGCATTTCCTGTAGGAACT
71303	69390	CCAGCATTTCCTGTAGGAAC
71304	69391	CCCAGCATTTCCTGTAGGAA
71305	69392	TCCCAGCATTTCCTGTAGGA
71306	69393	TTCCCAGCATTTCCTGTAGG
71307	69394	ATTCCCAGCATTTCCTGTAG
71308	69395	AATTCCCAGCATTTCCTGTA
71309	69396	CAATTCCCAGCATTTCCTGT
71310	69397	ACAATTCCCAGCATTTCCTG
71311	69398	TACAATTCCCAGCATTTCCT
71312	69399	ATACAATTCCCAGCATTTCC
71313	69400	GATACAATTCCCAGCATTTC
71314	69401	TGATACAATTCCCAGCATTT
71315	69402	CTGATACAATTCCCAGCATT
71316	69403	ACTGATACAATTCCCAGCAT
71317	69404	GACTGATACAATTCCCAGCA
71318	69405	TGACTGATACAATTCCCAGC
71319	69406	TTGACTGATACAATTCCCAG
71320	69407	TTTGACTGATACAATTCCCA
71321	69408	ATTTGACTGATACAATTCCC
71322	69409	CATTTGACTGATACAATTCC
71323	69410	ACATTTGACTGATACAATTC
71324	69411	CACATTTGACTGATACAATT
71325	69412	TCACATTTGACTGATACAAT
71326	69413	TTCACATTTGACTGATACAA
71327	69414	ATTCACATTTGACTGATACA
71328	69415	GATTCACATTTGACTGATAC
71329	69416	GGATTCACATTTGACTGATA
71330	69417	GGGATTCACATTTGACTGAT
71331	69418	GGGGATTCACATTTGACTGA
71332	69419	TGGGGATTCACATTTGACTG
71333	69420	GTGGGGATTCACATTTGACT
71334	69421	GGTGGGGATTCACATTTGAC
71335	69422	AGGTGGGGATTCACATTTGA
71336	69423	GAGGTGGGGATTCACATTTG
71337	69424	CGAGGTGGGGATTCACATTT
71338	69425	ACGAGGTGGGGATTCACATT
71339	69426	GACGAGGTGGGGATTCACAT
71340	69427	GGACGAGGTGGGGATTCACA
71341	69428	TGGACGAGGTGGGGATTCAC
71342	69429	CTGGACGAGGTGGGGATTCA
71343	69430	TCTGGACGAGGTGGGGATTC
71344	69431	GTCTGGACGAGGTGGGGATT
71345	69432	AGTCTGGACGAGGTGGGGAT
71346	69433	AAGTCTGGACGAGGTGGGGA
71347	69434	TAAGTCTGGACGAGGTGGGG
71348	69435	ATAAGTCTGGACGAGGTGGG
71349	69436	CATAAGTCTGGACGAGGTGG
71350	69437	TCATAAGTCTGGACGAGGTG
71351	69438	CTCATAAGTCTGGACGAGGT
71352	69439	ACTCATAAGTCTGGACGAGG
71353	69440	CACTCATAAGTCTGGACGAG
71354	69441	GCACTCATAAGTCTGGACGA
71355	69442	TGCACTCATAAGTCTGGACG
71356	69443	ATGCACTCATAAGTCTGGAC
71357	69444	AATGCACTCATAAGTCTGGA
71358	69445	CAATGCACTCATAAGTCTGG
71359	69446	ACAATGCACTCATAAGTCTG
71360	69447	TACAATGCACTCATAAGTCT
71361	69448	CTACAATGCACTCATAAGTC
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71363	69450	ACCTACAATGCACTCATAAG

120440	118527	GGTGAAATTCCATCTCTACT
120441	118528	TGGTGAAATTCCATCTCTAC
120442	118529	ATGGTGAAATTCCATCTCTA
120443	118530	CATGGTGAAATTCCATCTCT
120444	118531	ACATGGTGAAATTCCATCTC
120445	118532	AACATGGTGAAATTCCATCT
120446	118533	CAACATGGTGAAATTCCATC
120447	118534	CCAACATGGTGAAATTCCAT
120448	118535	GCCAACATGGTGAAATTCCA
120449	118536	GGCCAACATGGTGAAATTCC
120450	118537	TGGCCAACATGGTGAAATTC
120451	118538	CTGGCCAACATGGTGAAATT
120452	118539	CCTGGCCAACATGGTGAAAT
120453	118540	GCCTGGCCAACATGGTGAAA
120454	118541	AGCCTGGCCAACATGGTGAA
120455	118542	CAGCCTGGCCAACATGGTGA
120456	118543	CCAGCCTGGCCAACATGGTG
120457	118544	ACCAGCCTGGCCAACATGGT
120458	118545	GACCAGCCTGGCCAACATGG
120459	118546	AGACCAGCCTGGCCAACATG
120460	118547	AAGACCAGCCTGGCCAACAT
120461	118548	CAAGACCAGCCTGGCCAACA
120462	118549	TCAAGACCAGCCTGGCCAAC
120463	118550	TTCAAGACCAGCCTGGCCAA
120464	118551	GTTCAAGACCAGCCTGGCCA
120465	118552	AGTTCAAGACCAGCCTGGCC
120466	118553	GAGTTCAAGACCAGCCTGGC
120467	118554	GGAGTTCAAGACCAGCCTGG
120468	118555	AGGAGTTCAAGACCAGCCTG
120469	118556	CAGGAGTTCAAGACCAGCCT
120470	118557	TCAGGAGTTCAAGACCAGCC
120471	118558	GTCAGGAGTTCAAGACCAGC
120472	118559	GGTCAGGAGTTCAAGACCAG
120473	118560	AGGTCAGGAGTTCAAGACCA
120474	118561	GAGGTCAGGAGTTCAAGACC
120475	118562	TGAGGTCAGGAGTTCAAGAC
120476	118563	TTGAGGTCAGGAGTTCAAGA
120477	118564	TTTGAGGTCAGGAGTTCAAG
120478	118565	ATTTGAGGTCAGGAGTTCAA
120479	118566	CATTTGAGGTCAGGAGTTCA
120480	118567	TCATTTGAGGTCAGGAGTTC
120481	118568	ATCATTTGAGGTCAGGAGTT
120482	118569	GATCATTTGAGGTCAGGAGT
120483	118570	GGATCATTTGAGGTCAGGAG
120484	118571	CGGATCATTTGAGGTCAGGA
120485	118572	GCGGATCATTTGAGGTCAGG
120486	118573	GGCGGATCATTTGAGGTCAG
120487	118574	AGGCGGATCATTTGAGGTCA
120488	118575	CAGGCGGATCATTTGAGGTC
120489	118576	GCAGGCGGATCATTTGAGGT
120490	118577	GGCAGGCGGATCATTTGAGG
120491	118578	AGGCAGGCGGATCATTTGAG
120492	118579	GAGGCAGGCGGATCATTTGA
120493	118580	TGAGGCAGGCGGATCATTTG
120494	118581	GTGAGGCAGGCGGATCATTT
120495	118582	GGTGAGGCAGGCGGATCATT
120496	118583	AGGTGAGGCAGGCGGATCAT
120497	118584	AAGGTGAGGCAGGCGGATCA
120498	118585	GAAGGTGAGGCAGGCGGATC
120499	118586	GGAAGGTGAGGCAGGCGGAT
120500	118587	GGGAAGGTGAGGCAGGCGGA
120501	118588	TGGGAAGGTGAGGCAGGCGG
120502	118589	TTGGGAAGGTGAGGCAGGCG
120503	118590	TTTGGGAAGGTGAGGCAGGC
120504	118591	CTTTGGGAAGGTGAGGCAGG
120505	118592	ACTTTGGGAAGGTGAGGCAG
120506	118593	CACTTTGGGAAGGTGAGGCA
120507	118594	GCACTTTGGGAAGGTGAGGC
120508	118595	AGCACTTTGGGAAGGTGAGG
120509	118596	CAGCACTTTGGGAAGGTGAG
120510	118597	TCAGCACTTTGGGAAGGTGA

22217	20304	CTCCCGGGTTCAAGCGATTC
22218	20305	CCTCCCGGGTTCAAGCGATT
22219	20306	GCCTCCCGGGTTCAAGCGAT
22220	20307	TGCCTCCCGGGTTCAAGCGA
22221	20308	CTGCCTCCCGGGTTCAAGCG
22222	20309	TCTGCCTCCCGGGTTCAAGC
22223	20310	CTCTGCCTCCCGGGTTCAAG
22224	20311	CCTCTGCCTCCCGGGTTCAA
22225	20312	ACCTCTGCCTCCCGGGTTCA
22226	20313	AACCTCTGCCTCCCGGGTTC
22227	20314	CAACCTCTGCCTCCCGGGTT
22228	20315	ACAACCTCTGCCTCCCGGGT
22229	20316	CACAACCTCTGCCTCCCGGG
22230	20317	CCACAACCTCTGCCTCCCGG
22231	20318	ACCACAACCTCTGCCTCCCG
22232	20319	CACCACAACCTCTGCCTCCC
22233	20320	TCACCACAACCTCTGCCTCC
22234	20321	CTCACCACAACCTCTGCCTC
22235	20322	GCTCACCACAACCTCTGCCT
22236	20323	GGCTCACCACAACCTCTGCC
22237	20324	TGGCTCACCACAACCTCTGC
22238	20325	TTGGCTCACCACAACCTCTG
22239	20326	CTTGGCTCACCACAACCTCT
22240	20327	TCTTGGCTCACCACAACCTC
22241	20328	ATCTTGGCTCACCACAACCT
22242	20329	AATCTTGGCTCACCACAACC
22243	20330	CAATCTTGGCTCACCACAAC
22244	20331	GCAATCTTGGCTCACCACAA
22245	20332	TGCAATCTTGGCTCACCACA
22246	20333	GTGCAATCTTGGCTCACCAC
22247	20334	GGTGCAATCTTGGCTCACCA
22248	20335	TGGTGCAATCTTGGCTCACC
22249	20336	ATGGTGCAATCTTGGCTCAC
22250	20337	AATGGTGCAATCTTGGCTCA
22251	20338	CAATGGTGCAATCTTGGCTC
22252	20339	GCAATGGTGCAATCTTGGCT
22253	20340	TGCAATGGTGCAATCTTGGC
22254	20341	GTGCAATGGTGCAATCTTGG
22255	20342	AGTGCAATGGTGCAATCTTG
22256	20343	GAGTGCAATGGTGCAATCTT
22257	20344	GGAGTGCAATGGTGCAATCT
22258	20345	TGGAGTGCAATGGTGCAATC
22259	20346	CTGGAGTGCAATGGTGCAAT
22260	20347	GCTGGAGTGCAATGGTGCAA
22261	20348	GGCTGGAGTGCAATGGTGCA
22262	20349	AGGCTGGAGTGCAATGGTGC
22263	20350	CAGGCTGGAGTGCAATGGTG
22264	20351	CCAGGCTGGAGTGCAATGGT
22265	20352	CCCAGGCTGGAGTGCAATGG
22266	20353	GCCCAGGCTGGAGTGCAATG
22267	20354	TGCCCAGGCTGGAGTGCAAT
22268	20355	ATGCCCAGGCTGGAGTGCAA
22269	20356	GATGCCCAGGCTGGAGTGCA
22270	20357	TGATGCCCAGGCTGGAGTGC
22271	20358	TTGATGCCCAGGCTGGAGTG
22272	20359	CTTGATGCCCAGGCTGGAGT
22273	20360	TCTTGATGCCCAGGCTGGAG
22274	20361	CTCTTGATGCCCAGGCTGGA
22275	20362	ACTCTTGATGCCCAGGCTGG
22276	20363	CACTCTTGATGCCCAGGCTG
22277	20364	TCACTCTTGATGCCCAGGCT
22278	20365	TTCACTCTTGATGCCCAGGC
22279	20366	TTTCACTCTTGATGCCCAGG
22280	20367	GTTTCACTCTTGATGCCCAG
22281	20368	AGTTTCACTCTTGATGCCCA
22282	20369	GAGTTTCACTCTTGATGCCC
22283	20370	GGAGTTTCACTCTTGATGCC
22284	20371	CGGAGTTTCACTCTTGATGC
22285	20372	ACGGAGTTTCACTCTTGATG
22286	20373	GACGGAGTTTCACTCTTGAT
22287	20374	AGACGGAGTTTCACTCTTGA

71364	69451	TACCTACAATGCACTCATAA
71365	69452	GTACCTACAATGCACTCATA
71366	69453	AGTACCTACAATGCACTCAT
71367	69454	GAGTACCTACAATGCACTCA
71368	69455	TGAGTACCTACAATGCACTC
71369	69456	CTGAGTACCTACAATGCACT
71370	69457	ACTGAGTACCTACAATGCAC
71371	69458	TACTGAGTACCTACAATGCA
71372	69459	TTACTGAGTACCTACAATGC
71373	69460	CTTACTGAGTACCTACAATG
71374	69461	ACTTACTGAGTACCTACAAT
71375	69462	CACTTACTGAGTACCTACAA
71376	69463	GCACTTACTGAGTACCTACA
71377	69464	AGCACTTACTGAGTACCTAC
71378	69465	TAGCACTTACTGAGTACCTA
71379	69466	TTAGCACTTACTGAGTACCT
71380	69467	TTTAGCACTTACTGAGTACC
71381	69468	TTTTAGCACTTACTGAGTAC
71382	69469	TTTTTAGCACTTACTGAGTA
71383	69470	ATTTTTAGCACTTACTGAGT
71384	69471	CATTTTTAGCACTTACTGAG
71385	69472	TCATTTTTAGCACTTACTGA
71386	69473	GTCATTTTTAGCACTTACTG
71387	69474	AGTCATTTTTAGCACTTACT
71388	69475	TAGTCATTTTTAGCACTTAC
71389	69476	TTAGTCATTTTTAGCACTTA
71390	69477	TTTAGTCATTTTTAGCACTT
71391	69478	ATTTAGTCATTTTTAGCACT
71392	69479	TATTTAGTCATTTTTAGCAC
71393	69480	CTATTTAGTCATTTTTAGCA
71394	69481	ACTATTTAGTCATTTTTAGC
71395	69482	GACTATTTAGTCATTTTTAG
71396	69483	GGACTATTTAGTCATTTTTA
71397	69484	GGGACTATTTAGTCATTTTT
71398	69485	TGGGACTATTTAGTCATTTT
71399	69486	GTGGGACTATTTAGTCATTT
71400	69487	AGTGGGACTATTTAGTCATT
71401	69488	CAGTGGGACTATTTAGTCAT
71402	69489	TCAGTGGGACTATTTAGTCA
71403	69490	ATCAGTGGGACTATTTAGTC
71404	69491	TATCAGTGGGACTATTTAGT
71405	69492	GTATCAGTGGGACTATTTAG
71406	69493	GGTATCAGTGGGACTATTTA
71407	69494	TGGTATCAGTGGGACTATTT
71408	69495	TTGGTATCAGTGGGACTATT
71409	69496	ATTGGTATCAGTGGGACTAT
71410	69497	GATTGGTATCAGTGGGACTA
71411	69498	AGATTGGTATCAGTGGGACT
71412	69499	TAGATTGGTATCAGTGGGAC
71413	69500	ATAGATTGGTATCAGTGGGA
71414	69501	TATAGATTGGTATCAGTGGG
71415	69502	ATATAGATTGGTATCAGTGG
71416	69503	TATATAGATTGGTATCAGTG
71417	69504	GTATATAGATTGGTATCAGT
71418	69505	AGTATATAGATTGGTATCAG
71419	69506	CAGTATATAGATTGGTATCA
71420	69507	TCAGTATATAGATTGGTATC
71421	69508	ATCAGTATATAGATTGGTAT
71422	69509	TATCAGTATATAGATTGGTA
71423	69510	GTATCAGTATATAGATTGGT
71424	69511	AGTATCAGTATATAGATTGG
71425	69512	AAGTATCAGTATATAGATTG
71426	69513	AAAGTATCAGTATATAGATT
71427	69514	TAAAGTATCAGTATATAGAT
71428	69515	ATAAAGTATCAGTATATAGA
71429	69516	TATAAAGTATCAGTATATAG
71430	69517	ATATAAAGTATCAGTATATA
71431	69518	TATATAAAGTATCAGTATAT
71432	69519	CTATATAAAGTATCAGTATA
71433	69520	ACTATATAAAGTATCAGTAT
71434	69521	TACTATATAAAGTATCAGTA

120511	118598	CTCAGCACTTTGGGAAGGTG
120512	118599	TCTCAGCACTTTGGGAAGGT
120513	118600	ATCTCAGCACTTTGGGAAGG
120514	118601	AATCTCAGCACTTTGGGAAG
120515	118602	AAATCTCAGCACTTTGGGAA
120516	118603	AAAATCTCAGCACTTTGGGA
120517	118604	TAAAATCTCAGCACTTTGGG
120518	118605	CTAAAATCTCAGCACTTTGG
120519	118606	TCTAAAATCTCAGCACTTTG
120520	118607	GTCTAAAATCTCAGCACTTT
120521	118608	CGTCTAAAATCTCAGCACTT
120522	118609	GCGTCTAAAATCTCAGCACT
120523	118610	CGCGTCTAAAATCTCAGCAC
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120526	118613	GTTCGCGTCTAAAATCTCAG
120527	118614	GGTTCGCGTCTAAAATCTCA
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120532	118619	ATGGTGGTTCGCGTCTAAAA
120533	118620	CATGGTGGTTCGCGTCTAAA
120534	118621	GCATGGTGGTTCGCGTCTAA
120535	118622	GGCATGGTGGTTCGCGTCTA
120536	118623	GGGCATGGTGGTTCGCGTCT
120537	118624	AGGGCATGGTGGTTCGCGTC
120538	118625	CAGGGCATGGTGGTTCGCGT
120539	118626	TCAGGGCATGGTGGTTCGCG
120540	118627	GTCAGGGCATGGTGGTTCGC
120541	118628	AGTCAGGGCATGGTGGTTCG
120542	118629	TAGTCAGGGCATGGTGGTTC
120543	118630	ATAGTCAGGGCATGGTGGTT
120544	118631	TATAGTCAGGGCATGGTGGT
120545	118632	CTATAGTCAGGGCATGGTGG
120546	118633	CCTATAGTCAGGGCATGGTG
120547	118634	ACCTATAGTCAGGGCATGGT
120548	118635	AACCTATAGTCAGGGCATGG
120549	118636	TAACCTATAGTCAGGGCATG
120550	118637	ATAACCTATAGTCAGGGCAT
120551	118638	GATAACCTATAGTCAGGGCA
120552	118639	AGATAACCTATAGTCAGGGC
120553	118640	AAGATAACCTATAGTCAGGG
120554	118641	AAAGATAACCTATAGTCAGG
120555	118642	AAAAGATAACCTATAGTCAG
120556	118643	AAAAAGATAACCTATAGTCA
120557	118644	TAAAAAGATAACCTATAGTC
120558	118645	GTAAAAAGATAACCTATAGT
120559	118646	AGTAAAAAGATAACCTATAG
120560	118647	AAGTAAAAAGATAACCTATA
120561	118648	CAAGTAAAAAGATAACCTAT
120562	118649	GCAAGTAAAAAGATAACCTA
120563	118650	AGCAAGTAAAAAGATAACCT
120564	118651	AAGCAAGTAAAAAGATAACC
120565	118652	CAAGCAAGTAAAAAGATAAC
120566	118653	TCAAGCAAGTAAAAAGATAA
120567	118654	ATCAAGCAAGTAAAAAGATA
120568	118655	CATCAAGCAAGTAAAAAGAT
120569	118656	CCATCAAGCAAGTAAAAAGA
120570	118657	ACCATCAAGCAAGTAAAAAG
120571	118658	CACCATCAAGCAAGTAAAAA
120572	118659	ACACCATCAAGCAAGTAAAA
120573	118660	AACACCATCAAGCAAGTAAA
120574	118661	GAACACCATCAAGCAAGTAA
120575	118662	AGAACACCATCAAGCAAGTA
120576	118663	AAGAACACCATCAAGCAAGT
120577	118664	AAAGAACACCATCAAGCAAG
120578	118665	CAAAGAACACCATCAAGCAA
120579	118666	ACAAAGAACACCATCAAGCA
120580	118667	TACAAAGAACACCATCAAGC
120581	118668	TTACAAAGAACACCATCAAG

22288	20375	GAGACGGAGTTTCACTCTTG
22289	20376	TGAGACGGAGTTTCACTCTT
22290	20377	TTGAGACGGAGTTTCACTCT
22291	20378	TTTGAGACGGAGTTTCACTC
22292	20379	TTTTGAGACGGAGTTTCACT
22293	20380	TTTTTGAGACGGAGTTTCAC
22294	20381	TTTTTTGAGACGGAGTTTCA
22295	20382	TTTTTTTGAGACGGAGTTTC
22296	20383	ATTTTTTTGAGACGGAGTTT
22297	20384	TATTTTTTTGAGACGGAGTT
22298	20385	TTATTTTTTTGAGACGGAGT
22299	20386	TTTATTTTTTTGAGACGGAG
22300	20387	ATTTATTTTTTTGAGACGGA
22301	20388	TATTTATTTTTTTGAGACGG
22302	20389	TTATTTATTTTTTTGAGACG
22303	20390	TTTATTTATTTTTTTGAGAC
22304	20391	ATTTATTTATTTTTTTGAGA
22305	20392	TATTTATTTATTTTTTTGAG
22306	20393	TTATTTATTTATTTTTTTGA
22307	20394	TTTATTTATTTATTTTTTTG
22308	20395	CTTTATTTATTTATTTTTTT
22309	20396	GCTTTATTTATTTATTTTTT
22310	20397	AGCTTTATTTATTTATTTTT
22311	20398	CAGCTTTATTTATTTATTTT
22312	20399	CCAGCTTTATTTATTTATTT
22313	20400	ACCAGCTTTATTTATTTATT
22314	20401	TACCAGCTTTATTTATTTAT
22315	20402	ATACCAGCTTTATTTATTTA
22316	20403	CATACCAGCTTTATTTATTT
22317	20404	TCATACCAGCTTTATTTATT
22318	20405	TTCATACCAGCTTTATTTAT
22319	20406	ATTCATACCAGCTTTATTTA
22320	20407	TATTCATACCAGCTTTATTT
22321	20408	ATATTCATACCAGCTTTATT
22322	20409	AATATTCATACCAGCTTTAT
22323	20410	AAATATTCATACCAGCTTTA
22324	20411	TAAATATTCATACCAGCTTT
22325	20412	ATAAATATTCATACCAGCTT
22326	20413	CATAAATATTCATACCAGCT
22327	20414	ACATAAATATTCATACCAGC
22328	20415	TACATAAATATTCATACCAG
22329	20416	GTACATAAATATTCATACCA
22330	20417	TGTACATAAATATTCATACC
22331	20418	CTGTACATAAATATTCATAC
22332	20419	CCTGTACATAAATATTCATA
22333	20420	ACCTGTACATAAATATTCAT
22334	20421	AACCTGTACATAAATATTCA
22335	20422	AAACCTGTACATAAATATTC
22336	20423	AAAACCTGTACATAAATATT
22337	20424	CAAAACCTGTACATAAATAT
22338	20425	ACAAAACCTGTACATAAATA
22339	20426	CACAAAACCTGTACATAAAT
22340	20427	ACACAAAACCTGTACATAAA
22341	20428	CACACAAAACCTGTACATAA
22342	20429	TCACACAAAACCTGTACATA
22343	20430	TTCACACAAAACCTGTACAT
22344	20431	GTTCACACAAAACCTGTACA
22345	20432	TGTTCACACAAAACCTGTAC
22346	20433	ATGTTCACACAAAACCTGTA
22347	20434	TATGTTCACACAAAACCTGT
22348	20435	ATATGTTCACACAAAACCTG
22349	20436	CATATGTTCACACAAAACCT
22350	20437	TCATATGTTCACACAAAACC
22351	20438	ATCATATGTTCACACAAAAC
22352	20439	AATCATATGTTCACACAAAA
22353	20440	AAATCATATGTTCACACAAA
22354	20441	AAAATCATATGTTCACACAA
22355	20442	TAAAATCATATGTTCACACA
22356	20443	ATAAAATCATATGTTCACAC
22357	20444	AATAAAATCATATGTTCACA
22358	20445	AAATAAAATCATATGTTCAC

71435	69522	ATACTATATAAAGTATCAGT
71436	69523	TATACTATATAAAGTATCAG
71437	69524	ATATACTATATAAAGTATCA
71438	69525	TATATACTATATAAAGTATC
71439	69526	CTATATACTATATAAAGTAT
71440	69527	TCTATATACTATATAAAGTA
71441	69528	ATCTATATACTATATAAAGT
71442	69529	AATCTATATACTATATAAAG
71443	69530	CAATCTATATACTATATAAA
71444	69531	CCAATCTATATACTATATAA
71445	69532	ACCAATCTATATACTATATA
71446	69533	GACCAATCTATATACTATAT
71447	69534	GGACCAATCTATATACTATA
71448	69535	TGGACCAATCTATATACTAT
71449	69536	GTGGACCAATCTATATACTA
71450	69537	TGTGGACCAATCTATATACT
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71454	69541	TATATGTGGACCAATCTATA
71455	69542	TTATATGTGGACCAATCTAT
71456	69543	GTTATATGTGGACCAATCTA
71457	69544	CGTTATATGTGGACCAATCT
71458	69545	TCGTTATATGTGGACCAATC
71459	69546	ATCGTTATATGTGGACCAAT
71460	69547	CATCGTTATATGTGGACCAA
71461	69548	TCATCGTTATATGTGGACCA
71462	69549	GTCATCGTTATATGTGGACC
71463	69550	TGTCATCGTTATATGTGGAC
71464	69551	GTGTCATCGTTATATGTGGA
71465	69552	TGTGTCATCGTTATATGTGG
71466	69553	ATGTGTCATCGTTATATGTG
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71470	69557	CATTATGTGTCATCGTTATA
71471	69558	TCATTATGTGTCATCGTTAT
71472	69559	CTCATTATGTGTCATCGTTA
71473	69560	TCTCATTATGTGTCATCGTT
71474	69561	TTCTCATTATGTGTCATCGT
71475	69562	TTTCTCATTATGTGTCATCG
71476	69563	GTTTCTCATTATGTGTCATC
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71490	69577	AACTTTTTAAGACAGTTTCT
71491	69578	CAACTTTTTAAGACAGTTTC
71492	69579	ACAACTTTTTAAGACAGTTT
71493	69580	AACAACTTTTTAAGACAGTT
71494	69581	CAACAACTTTTTAAGACAGT
71495	69582	TCAACAACTTTTTAAGACAG
71496	69583	TTCAACAACTTTTTAAGACA
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71501	69588	GCACTTTCAACAACTTTTTA
71502	69589	GGCACTTTCAACAACTTTTT
71503	69590	CGGCACTTTCAACAACTTTT
71504	69591	GCGGCACTTTCAACAACTTT
71505	69592	TGCGGCACTTTCAACAACTT

120582	118669	GTTACAAAGAACACCATCAA
120583	118670	TGTTACAAAGAACACCATCA
120584	118671	GTGTTACAAAGAACACCATC
120585	118672	TGTGTTACAAAGAACACCAT
120586	118673	CTGTGTTACAAAGAACACCA
120587	118674	ACTGTGTTACAAAGAACACC
120588	118675	AACTGTGTTACAAAGAACAC
120589	118676	AAACTGTGTTACAAAGAACA
120590	118677	AAAACTGTGTTACAAAGAAC
120591	118678	AAAAACTGTGTTACAAAGAA
120592	118679	TAAAAACTGTGTTACAAAGA
120593	118680	TTAAAAACTGTGTTACAAAG
120594	118681	ATTAAAAACTGTGTTACAAA
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120596	118683	AAATTAAAAACTGTGTTACA
120597	118684	AAAATTAAAAACTGTGTTAC
120598	118685	CAAAATTAAAAACTGTGTTA
120599	118686	TCAAAATTAAAAACTGTGTT
120600	118687	ATCAAAATTAAAAACTGTGT
120601	118688	CATCAAAATTAAAAACTGTG
120602	118689	TCATCAAAATTAAAAACTGT
120603	118690	TTCATCAAAATTAAAAACTG
120604	118691	CTTCATCAAAATTAAAAACT
120605	118692	ACTTCATCAAAATTAAAAAC
120606	118693	AACTTCATCAAAATTAAAAA
120607	118694	GAACTTCATCAAAATTAAAA
120608	118695	TGAACTTCATCAAAATTAAA
120609	118696	TTGAACTTCATCAAAATTAA
120610	118697	ATTGAACTTCATCAAAATTA
120611	118698	AATTGAACTTCATCAAAATT
120612	118699	AAATTGAACTTCATCAAAAT
120613	118700	TAAATTGAACTTCATCAAAA
120614	118701	ATAAATTGAACTTCATCAAA
120615	118702	GATAAATTGAACTTCATCAA
120616	118703	AGATAAATTGAACTTCATCA
120617	118704	CAGATAAATTGAACTTCATC
120618	118705	ACAGATAAATTGAACTTCAT
120619	118706	AACAGATAAATTGAACTTCA
120620	118707	AAACAGATAAATTGAACTTC
120621	118708	CAAACAGATAAATTGAACTT
120622	118709	ACAAACAGATAAATTGAACT
120623	118710	AACAAACAGATAAATTGAAC
120624	118711	AAACAAACAGATAAATTGAA
120625	118712	AAAACAAACAGATAAATTGA
120626	118713	AAAAACAAACAGATAAATTG
120627	118714	AAAAAACAAACAGATAAATT
120628	118715	GAAAAAACAAACAGATAAAT
120629	118716	AGAAAAAACAAACAGATAAA
120630	118717	AAGAAAAAACAAACAGATAA
120631	118718	AAAGAAAAAACAAACAGATA
120632	118719	AAAAGAAAAAACAAACAGAT
120633	118720	CAAAAGAAAAAACAAACAGA
120634	118721	ACAAAAGAAAAAACAAACAG
120635	118722	AACAAAAGAAAAAACAAACA
120636	118723	CAACAAAAGAAAAAACAAAC
120637	118724	GCAACAAAAGAAAAAACAAA
120638	118725	AGCAACAAAAGAAAAAACAA
120639	118726	CAGCAACAAAAGAAAAAACA
120640	118727	ACAGCAACAAAAGAAAAAAC
120641	118728	AACAGCAACAAAAGAAAAAA
120642	118729	CAACAGCAACAAAAGAAAAA
120643	118730	GCAACAGCAACAAAAGAAAA
120644	118731	AGCAACAGCAACAAAAGAAA
120645	118732	GAGCAACAGCAACAAAAGAA
120646	118733	GGAGCAACAGCAACAAAAGA
120647	118734	AGGAGCAACAGCAACAAAAG
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120649	118736	TCAGGAGCAACAGCAACAAA
120650	118737	ATCAGGAGCAACAGCAACAA
120651	118738	CATCAGGAGCAACAGCAACA
120652	118739	ACATCAGGAGCAACAGCAAC

22359	20446	GAAATAAAATCATATGTTCA
22360	20447	AGAAATAAAATCATATGTTC
22361	20448	GAGAAATAAAATCATATGTT
22362	20449	AGAGAAATAAAATCATATGT
22363	20450	AAGAGAAATAAAATCATATG
22364	20451	CAAGAGAAATAAAATCATAT
22365	20452	CCAAGAGAAATAAAATCATA
22366	20453	ACCAAGAGAAATAAAATCAT
22367	20454	AACCAAGAGAAATAAAATCA
22368	20455	CAACCAAGAGAAATAAAATC
22369	20456	CCAACCAAGAGAAATAAAAT
22370	20457	TCCAACCAAGAGAAATAAAA
22371	20458	TTCCAACCAAGAGAAATAAA
22372	20459	ATTCCAACCAAGAGAAATAA
22373	20460	CATTCCAACCAAGAGAAATA
22374	20461	GCATTCCAACCAAGAGAAAT
22375	20462	TGCATTCCAACCAAGAGAAA
22376	20463	ATGCATTCCAACCAAGAGAA
22377	20464	TATGCATTCCAACCAAGAGA
22378	20465	CTATGCATTCCAACCAAGAG
22379	20466	TCTATGCATTCCAACCAAGA
22380	20467	TTCTATGCATTCCAACCAAG
22381	20468	TTTCTATGCATTCCAACCAA
22382	20469	ATTTCTATGCATTCCAACCA
22383	20470	CATTTCTATGCATTCCAACC
22384	20471	TCATTTCTATGCATTCCAAC
22385	20472	CTCATTTCTATGCATTCCAA
22386	20473	TCTCATTTCTATGCATTCCA
22387	20474	ATCTCATTTCTATGCATTCC
22388	20475	AATCTCATTTCTATGCATTC
22389	20476	CAATCTCATTTCTATGCATT
22390	20477	GCAATCTCATTTCTATGCAT
22391	20478	AGCAATCTCATTTCTATGCA
22392	20479	CAGCAATCTCATTTCTATGC
22393	20480	CCAGCAATCTCATTTCTATG
22394	20481	CCCAGCAATCTCATTTCTAT
22395	20482	ACCCAGCAATCTCATTTCTA
22396	20483	AACCCAGCAATCTCATTTCT
22397	20484	AAACCCAGCAATCTCATTTC
22398	20485	AAAACCCAGCAATCTCATTT
22399	20486	CAAAACCCAGCAATCTCATT
22400	20487	ACAAAACCCAGCAATCTCAT
22401	20488	CACAAAACCCAGCAATCTCA
22402	20489	CCACAAAACCCAGCAATCTC
22403	20490	GCCACAAAACCCAGCAATCT
22404	20491	TGCCACAAAACCCAGCAATC
22405	20492	TTGCCACAAAACCCAGCAAT
22406	20493	CTTGCCACAAAACCCAGCAA
22407	20494	ACTTGCCACAAAACCCAGCA
22408	20495	CACTTGCCACAAAACCCAGC
22409	20496	ACACTTGCCACAAAACCCAG
22410	20497	AACACTTGCCACAAAACCCA
22411	20498	AAACACTTGCCACAAAACCC
22412	20499	TAAACACTTGCCACAAAACC
22413	20500	ATAAACACTTGCCACAAAAC
22414	20501	AATAAACACTTGCCACAAAA
22415	20502	AAATAAACACTTGCCACAAA
22416	20503	AAAATAAACACTTGCCACAA
22417	20504	AAAAATAAACACTTGCCACA
22418	20505	GAAAAATAAACACTTGCCAC
22419	20506	GGAAAAATAAACACTTGCCA
22420	20507	TGGAAAAATAAACACTTGCC
22421	20508	CTGGAAAAATAAACACTTGC
22422	20509	CCTGGAAAAATAAACACTTG
22423	20510	CCCTGGAAAAATAAACACTT
22424	20511	ACCCTGGAAAAATAAACACT
22425	20512	TACCCTGGAAAAATAAACAC
22426	20513	GTACCCTGGAAAAATAAACA
22427	20514	TGTACCCTGGAAAAATAAAC
22428	20515	ATGTACCCTGGAAAAATAAA
22429	20516	TATGTACCCTGGAAAAATAA

71506	69593	CTGCGGCACTTTCAACAACT
71507	69594	CCTGCGGCACTTTCAACAAC
71508	69595	TCCTGCGGCACTTTCAACAA
71509	69596	TTCCTGCGGCACTTTCAACA
71510	69597	ATTCCTGCGGCACTTTCAAC
71511	69598	TATTCCTGCGGCACTTTCAA
71512	69599	CTATTCCTGCGGCACTTTCA
71513	69600	CCTATTCCTGCGGCACTTTC
71514	69601	TCCTATTCCTGCGGCACTTT
71515	69602	TTCCTATTCCTGCGGCACTT
71516	69603	ATTCCTATTCCTGCGGCACT
71517	69604	AATTCCTATTCCTGCGGCAC
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71520	69607	ATCAATTCCTATTCCTGCGG
71521	69608	GATCAATTCCTATTCCTGCG
71522	69609	TGATCAATTCCTATTCCTGC
71523	69610	TTGATCAATTCCTATTCCTG
71524	69611	TTTGATCAATTCCTATTCCT
71525	69612	TTTTGATCAATTCCTATTCC
71526	69613	GTTTTGATCAATTCCTATTC
71527	69614	TGTTTTGATCAATTCCTATT
71528	69615	TTGTTTTGATCAATTCCTAT
71529	69616	ATTGTTTTGATCAATTCCTA
71530	69617	TATTGTTTTGATCAATTCCT
71531	69618	ATATTGTTTTGATCAATTCC
71532	69619	CATATTGTTTTGATCAATTC
71533	69620	TCATATTGTTTTGATCAATT
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71536	69623	AAATCATATTGTTTTGATCA
71537	69624	AAAATCATATTGTTTTGATC
71538	69625	AAAAATCATATTGTTTTGAT
71539	69626	AAAAAATCATATTGTTTTGA
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71542	69629	CCTAAAAAATCATATTGTTT
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71548	69635	TATAAACCTAAAAAATCATA
71549	69636	ATATAAACCTAAAAAATCAT
71550	69637	CATATAAACCTAAAAAATCA
71551	69638	CCATATAAACCTAAAAAATC
71552	69639	TCCATATAAACCTAAAAAAT
71553	69640	TTCCATATAAACCTAAAAAA
71554	69641	GTTCCATATAAACCTAAAAA
71555	69642	AGTTCCATATAAACCTAAAA
71556	69643	AAGTTCCATATAAACCTAAA
71557	69644	AAAGTTCCATATAAACCTAA
71558	69645	CAAAGTTCCATATAAACCTA
71559	69646	TCAAAGTTCCATATAAACCT
71560	69647	ATCAAAGTTCCATATAAACC
71561	69648	CATCAAAGTTCCATATAAAC
71562	69649	ACATCAAAGTTCCATATAAA
71563	69650	AACATCAAAGTTCCATATAA
71564	69651	AAACATCAAAGTTCCATATA
71565	69652	CAAACATCAAAGTTCCATAT
71566	69653	TCAAACATCAAAGTTCCATA
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71572	69659	CTTTTCTCAAACATCAAAGT
71573	69660	CCTTTTCTCAAACATCAAAG
71574	69661	GCCTTTTCTCAAACATCAAA
71575	69662	AGCCTTTTCTCAAACATCAA
71576	69663	CAGCCTTTTCTCAAACATCA

120653	118740	GACATCAGGAGCAACAGCAA
120654	118741	TGACATCAGGAGCAACAGCA
120655	118742	ATGACATCAGGAGCAACAGC
120656	118743	TATGACATCAGGAGCAACAG
120657	118744	ATATGACATCAGGAGCAACA
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120659	118746	TGATATGACATCAGGAGCAA
120660	118747	CTGATATGACATCAGGAGCA
120661	118748	TCTGATATGACATCAGGAGC
120662	118749	GTCTGATATGACATCAGGAG
120663	118750	TGTCTGATATGACATCAGGA
120664	118751	TTGTCTGATATGACATCAGG
120665	118752	TTTGTCTGATATGACATCAG
120666	118753	CTTTGTCTGATATGACATCA
120667	118754	GCTTTGTCTGATATGACATC
120668	118755	TGCTTTGTCTGATATGACAT
120669	118756	ATGCTTTGTCTGATATGACA
120670	118757	AATGCTTTGTCTGATATGAC
120671	118758	CAATGCTTTGTCTGATATGA
120672	118759	GCAATGCTTTGTCTGATATG
120673	118760	GGCAATGCTTTGTCTGATAT
120674	118761	AGGCAATGCTTTGTCTGATA
120675	118762	TAGGCAATGCTTTGTCTGAT
120676	118763	TTAGGCAATGCTTTGTCTGA
120677	118764	GTTAGGCAATGCTTTGTCTG
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120681	118768	TTGAGTTAGGCAATGCTTTG
120682	118769	CTTGAGTTAGGCAATGCTTT
120683	118770	CCTTGAGTTAGGCAATGCTT
120684	118771	GCCTTGAGTTAGGCAATGCT
120685	118772	GGCCTTGAGTTAGGCAATGC
120686	118773	TGGCCTTGAGTTAGGCAATG
120687	118774	GTGGCCTTGAGTTAGGCAAT
120688	118775	TGTGGCCTTGAGTTAGGCAA
120689	118776	CTGTGGCCTTGAGTTAGGCA
120690	118777	TCTGTGGCCTTGAGTTAGGC
120691	118778	CTCTGTGGCCTTGAGTTAGG
120692	118779	TCTCTGTGGCCTTGAGTTAG
120693	118780	ATCTCTGTGGCCTTGAGTTA
120694	118781	AATCTCTGTGGCCTTGAGTT
120695	118782	AAATCTCTGTGGCCTTGAGT
120696	118783	TAAATCTCTGTGGCCTTGAG
120697	118784	GTAAATCTCTGTGGCCTTGA
120698	118785	AGTAAATCTCTGTGGCCTTG
120699	118786	GAGTAAATCTCTGTGGCCTT
120700	118787	GGAGTAAATCTCTGTGGCCT
120701	118788	AGGAGTAAATCTCTGTGGCC
120702	118789	TAGGAGTAAATCTCTGTGGC
120703	118790	ATAGGAGTAAATCTCTGTGG
120704	118791	CATAGGAGTAAATCTCTGTG
120705	118792	TCATAGGAGTAAATCTCTGT
120706	118793	TTCATAGGAGTAAATCTCTG
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120710	118797	GCGTTTCATAGGAGTAAATC
120711	118798	GGCGTTTCATAGGAGTAAAT
120712	118799	AGGCGTTTCATAGGAGTAAA
120713	118800	TAGGCGTTTCATAGGAGTAA
120714	118801	ATAGGCGTTTCATAGGAGTA
120715	118802	TATAGGCGTTTCATAGGAGT
120716	118803	TTATAGGCGTTTCATAGGAG
120717	118804	TTTATAGGCGTTTCATAGGA
120718	118805	TTTTATAGGCGTTTCATAGG
120719	118806	GTTTTATAGGCGTTTCATAG
120720	118807	AGTTTTATAGGCGTTTCATA
120721	118808	GAGTTTTATAGGCGTTTCAT
120722	118809	GGAGTTTTATAGGCGTTTCA
120723	118810	AGGAGTTTTATAGGCGTTTC

22430	20517	ATATGTACCCTGGAAAAATA
22431	20518	TATATGTACCCTGGAAAAAT
22432	20519	TTATATGTACCCTGGAAAAA
22433	20520	ATTATATGTACCCTGGAAAA
22434	20521	GATTATATGTACCCTGGAAA
22435	20522	GGATTATATGTACCCTGGAA
22436	20523	AGGATTATATGTACCCTGGA
22437	20524	CAGGATTATATGTACCCTGG
22438	20525	ACAGGATTATATGTACCCTG
22439	20526	CACAGGATTATATGTACCCT
22440	20527	TCACAGGATTATATGTACCC
22441	20528	CTCACAGGATTATATGTACC
22442	20529	ACTCACAGGATTATATGTAC
22443	20530	CACTCACAGGATTATATGTA
22444	20531	ACACTCACAGGATTATATGT
22445	20532	AACACTCACAGGATTATATG
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22453	20540	ATTAAATAAACACTCACAGG
22454	20541	AATTAAATAAACACTCACAG
22455	20542	AAATTAAATAAACACTCACA
22456	20543	AAAATTAAATAAACACTCAC
22457	20544	TAAAATTAAATAAACACTCA
22458	20545	TTAAAATTAAATAAACACTC
22459	20546	TTTAAAATTAAATAAACACT
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22461	20548	CTTTTAAAATTAAATAAACA
22462	20549	ACTTTTAAAATTAAATAAAC
22463	20550	TACTTTTAAAATTAAATAAA
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22465	20552	ATTACTTTTAAAATTAAATA
22466	20553	AATTACTTTTAAAATTAAAT
22467	20554	CAATTACTTTTAAAATTAAA
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22472	20559	TTTAGCAATTACTTTTAAAA
22473	20560	GTTTAGCAATTACTTTTAAA
22474	20561	AGTTTAGCAATTACTTTTAA
22475	20562	CAGTTTAGCAATTACTTTTA
22476	20563	ACAGTTTAGCAATTACTTTT
22477	20564	AACAGTTTAGCAATTACTTT
22478	20565	AAACAGTTTAGCAATTACTT
22479	20566	CAAACAGTTTAGCAATTACT
22480	20567	GCAAACAGTTTAGCAATTAC
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22489	20576	GTCACTTTAGCAAACAGTTT
22490	20577	AGTCACTTTAGCAAACAGTT
22491	20578	CAGTCACTTTAGCAAACAGT
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22493	20580	AGCAGTCACTTTAGCAAACA
22494	20581	TAGCAGTCACTTTAGCAAAC
22495	20582	ATAGCAGTCACTTTAGCAAA
22496	20583	TATAGCAGTCACTTTAGCAA
22497	20584	ATATAGCAGTCACTTTAGCA
22498	20585	AATATAGCAGTCACTTTAGC
22499	20586	AAATATAGCAGTCACTTTAG
22500	20587	AAAATATAGCAGTCACTTTA

71577	69664	TCAGCCTTTTCTCAAACATC
71578	69665	ATCAGCCTTTTCTCAAACAT
71579	69666	AATCAGCCTTTTCTCAAACA
71580	69667	AAATCAGCCTTTTCTCAAAC
71581	69668	TAAATCAGCCTTTTCTCAAA
71582	69669	CTAAATCAGCCTTTTCTCAA
71583	69670	ACTAAATCAGCCTTTTCTCA
71584	69671	AACTAAATCAGCCTTTTCTC
71585	69672	CAACTAAATCAGCCTTTTCT
71586	69673	TCAACTAAATCAGCCTTTTC
71587	69674	CTCAACTAAATCAGCCTTTT
71588	69675	TCTCAACTAAATCAGCCTTT
71589	69676	TTCTCAACTAAATCAGCCTT
71590	69677	CTTCTCAACTAAATCAGCCT
71591	69678	TCTTCTCAACTAAATCAGCC
71592	69679	TTCTTCTCAACTAAATCAGC
71593	69680	TTTCTTCTCAACTAAATCAG
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71595	69682	CATTTCTTCTCAACTAAATC
71596	69683	CCATTTCTTCTCAACTAAAT
71597	69684	ACCATTTCTTCTCAACTAAA
71598	69685	AACCATTTCTTCTCAACTAA
71599	69686	TAACCATTTCTTCTCAACTA
71600	69687	CTAACCATTTCTTCTCAACT
71601	69688	GCTAACCATTTCTTCTCAAC
71602	69689	AGCTAACCATTTCTTCTCAA
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71609	69696	AATCCTCAGCTAACCATTTC
71610	69697	AAATCCTCAGCTAACCATTT
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71612	69699	CAAAATCCTCAGCTAACCAT
71613	69700	TCAAAATCCTCAGCTAACCA
71614	69701	ATCAAAATCCTCAGCTAACC
71615	69702	CATCAAAATCCTCAGCTAAC
71616	69703	TCATCAAAATCCTCAGCTAA
71617	69704	GTCATCAAAATCCTCAGCTA
71618	69705	AGTCATCAAAATCCTCAGCT
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71620	69707	GAAGTCATCAAAATCCTCAG
71621	69708	AGAAGTCATCAAAATCCTCA
71622	69709	GAGAAGTCATCAAAATCCTC
71623	69710	AGAGAAGTCATCAAAATCCT
71624	69711	CAGAGAAGTCATCAAAATCC
71625	69712	CCAGAGAAGTCATCAAAATC
71626	69713	TCCAGAGAAGTCATCAAAAT
71627	69714	TTCCAGAGAAGTCATCAAAA
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71636	69723	CAAATGTGCTTCCAGAGAAG
71637	69724	TCAAATGTGCTTCCAGAGAA
71638	69725	CTCAAATGTGCTTCCAGAGA
71639	69726	CCTCAAATGTGCTTCCAGAG
71640	69727	CCCTCAAATGTGCTTCCAGA
71641	69728	ACCCTCAAATGTGCTTCCAG
71642	69729	AACCCTCAAATGTGCTTCCA
71643	69730	AAACCCTCAAATGTGCTTCC
71644	69731	CAAACCCTCAAATGTGCTTC
71645	69732	ACAAACCCTCAAATGTGCTT
71646	69733	CACAAACCCTCAAATGTGCT
71647	69734	TCACAAACCCTCAAATGTGC

120724	118811	TAGGAGTTTTATAGGCGTTT
120725	118812	ATAGGAGTTTTATAGGCGTT
120726	118813	CATAGGAGTTTTATAGGCGT
120727	118814	TCATAGGAGTTTTATAGGCG
120728	118815	ATCATAGGAGTTTTATAGGC
120729	118816	AATCATAGGAGTTTTATAGG
120730	118817	AAATCATAGGAGTTTTATAG
120731	118818	AAAATCATAGGAGTTTTATA
120732	118819	AAAAATCATAGGAGTTTTAT
120733	118820	TAAAAATCATAGGAGTTTTA
120734	118821	ATAAAAATCATAGGAGTTTT
120735	118822	TATAAAAATCATAGGAGTTT
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120739	118826	AAACTATAAAAATCATAGGA
120740	118827	TAAACTATAAAAATCATAGG
120741	118828	CTAAACTATAAAAATCATAG
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120754	118841	TAAATGTTAAGAGCTAAACT
120755	118842	TTAAATGTTAAGAGCTAAAC
120756	118843	CTTAAATGTTAAGAGCTAAA
120757	118844	ACTTAAATGTTAAGAGCTAA
120758	118845	GACTTAAATGTTAAGAGCTA
120759	118846	AGACTTAAATGTTAAGAGCT
120760	118847	TAGACTTAAATGTTAAGAGC
120761	118848	GTAGACTTAAATGTTAAGAG
120762	118849	TGTAGACTTAAATGTTAAGA
120763	118850	TTGTAGACTTAAATGTTAAG
120764	118851	ATTGTAGACTTAAATGTTAA
120765	118852	GATTGTAGACTTAAATGTTA
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120767	118854	GAGATTGTAGACTTAAATGT
120768	118855	AGAGATTGTAGACTTAAATG
120769	118856	AAGAGATTGTAGACTTAAAT
120770	118857	AAAGAGATTGTAGACTTAAA
120771	118858	AAAAGAGATTGTAGACTTAA
120772	118859	CAAAAGAGATTGTAGACTTA
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120774	118861	CTCAAAAGAGATTGTAGACT
120775	118862	ACTCAAAAGAGATTGTAGAC
120776	118863	AACTCAAAAGAGATTGTAGA
120777	118864	TAACTCAAAAGAGATTGTAG
120778	118865	TTAACTCAAAAGAGATTGTA
120779	118866	ATTAACTCAAAAGAGATTGT
120780	118867	AATTAACTCAAAAGAGATTG
120781	118868	AAATTAACTCAAAAGAGATT
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22501	20588	GAAAATATAGCAGTCACTTT
22502	20589	AGAAAATATAGCAGTCACTT
22503	20590	AAGAAAATATAGCAGTCACT
22504	20591	AAAGAAAATATAGCAGTCAC
22505	20592	GAAAGAAAATATAGCAGTCA
22506	20593	GGAAAGAAAATATAGCAGTC
22507	20594	GGGAAAGAAAATATAGCAGT
22508	20595	AGGGAAAGAAAATATAGCAG
22509	20596	TAGGGAAAGAAAATATAGCA
22510	20597	CTAGGGAAAGAAAATATAGC
22511	20598	GCTAGGGAAAGAAAATATAG
22512	20599	TGCTAGGGAAAGAAAATATA
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22514	20601	ACTGCTAGGGAAAGAAAATA
22515	20602	CACTGCTAGGGAAAGAAAAT
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22521	20608	TTCATACACTGCTAGGGAAA
22522	20609	ATTCATACACTGCTAGGGAA
22523	20610	AATTCATACACTGCTAGGGA
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22525	20612	AAAATTCATACACTGCTAGG
22526	20613	AAAAATTCATACACTGCTAG
22527	20614	AAAAAATTCATACACTGCTA
22528	20615	AAAAAAATTCATACACTGCT
22529	20616	AAAAAAAATTCATACACTGC
22530	20617	AAAAAAAAATTCATACACTG
22531	20618	CAAAAAAAAATTCATACACT
22532	20619	TCAAAAAAAAATTCATACAC
22533	20620	CTCAAAAAAAAAATTCATACA
22534	20621	CCTCAAAAAAAAAATTCATAC
22535	20622	GCCTCAAAAAAAAAATTCATA
22536	20623	TGCCTCAAAAAAAAAATTCAT
22537	20624	CTGCCTCAAAAAAAAAATTCA
22538	20625	CCTGCCTCAAAAAAAAAATTC
22539	20626	CCCTGCCTCAAAAAAAAATT
22540	20627	ACCCTGCCTCAAAAAAAAAT
22541	20628	GACCCTGCCTCAAAAAAAAA
22542	20629	AGACCCTGCCTCAAAAAAAA
22543	20630	AAGACCCTGCCTCAAAAAAA
22544	20631	CAAGACCCTGCCTCAAAAAA
22545	20632	GCAAGACCCTGCCTCAAAAA
22546	20633	AGCAAGACCCTGCCTCAAAA
22547	20634	GAGCAAGACCCTGCCTCAAA
22548	20635	AGAGCAAGACCCTGCCTCAA
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22551	20638	GACAGAGCAAGACCCTGCCT
22552	20639	TGACAGAGCAAGACCCTGCC
22553	20640	GTGACAGAGCAAGACCCTGC
22554	20641	GGTGACAGAGCAAGACCCTG
22555	20642	GGGTGACAGAGCAAGACCCT
22556	20643	TGGGTGACAGAGCAAGACCC
22557	20644	CTGGGTGACAGAGCAAGACC
22558	20645	CCTGGGTGACAGAGCAAGAC
22559	20646	CCCTGGGTGACAGAGCAAGA
22560	20647	ACCCTGGGTGACAGAGCAAG
22561	20648	CACCCTGGGTGACAGAGCAA
22562	20649	CCACCCTGGGTGACAGAGCA
22563	20650	TCCACCCTGGGTGACAGAGC
22564	20651	CTCCACCCTGGGTGACAGAG
22565	20652	ACTCCACCCTGGGTGACAGA
22566	20653	CACTCCACCCTGGGTGACAG
22567	20654	GCACTCCACCCTGGGTGACA
22568	20655	TGCACTCCACCCTGGGTGAC
22569	20656	CTGCACTCCACCCTGGGTGA
22570	20657	ACTGCACTCCACCCTGGGTG
22571	20658	CACTGCACTCCACCCTGGGT

71648	69735	ATCACAAACCCTCAAATGTG
71649	69736	CATCACAAACCCTCAAATGT
71650	69737	ACATCACAAACCCTCAAATG
71651	69738	AACATCACAAACCCTCAAAT
71652	69739	TAACATCACAAACCCTCAAA
71653	69740	TTAACATCACAAACCCTCAA
71654	69741	TTTAACATCACAAACCCTCA
71655	69742	ATTTAACATCACAAACCCTC
71656	69743	GATTTAACATCACAAACCCT
71657	69744	AGATTTAACATCACAAACCC
71658	69745	CAGATTTAACATCACAAACC
71659	69746	TCAGATTTAACATCACAAAC
71660	69747	ATCAGATTTAACATCACAAA
71661	69748	CATCAGATTTAACATCACAA
71662	69749	ACATCAGATTTAACATCACA
71663	69750	AACATCAGATTTAACATCAC
71664	69751	TAACATCAGATTTAACATCA
71665	69752	TTAACATCAGATTTAACATC
71666	69753	ATTAACATCAGATTTAACAT
71667	69754	CATTAACATCAGATTTAACA
71668	69755	TCATTAACATCAGATTTAAC
71669	69756	ATCATTAACATCAGATTTAA
71670	69757	AATCATTAACATCAGATTTA
71671	69758	TAATCATTAACATCAGATTT
71672	69759	ATAATCATTAACATCAGATT
71673	69760	AATAATCATTAACATCAGAT
71674	69761	AAATAATCATTAACATCAGA
71675	69762	GAAATAATCATTAACATCAG
71676	69763	TGAAATAATCATTAACATCA
71677	69764	ATGAAATAATCATTAACATC
71678	69765	GATGAAATAATCATTAACAT
71679	69766	GGATGAAATAATCATTAACA
71680	69767	TGGATGAAATAATCATTAAC
71681	69768	CTGGATGAAATAATCATTAA
71682	69769	ACTGGATGAAATAATCATTA
71683	69770	AACTGGATGAAATAATCATT
71684	69771	AAACTGGATGAAATAATCAT
71685	69772	AAAACTGGATGAAATAATCA
71686	69773	TAAAACTGGATGAAATAATC
71687	69774	ATAAAACTGGATGAAATAAT
71688	69775	CATAAAACTGGATGAAATAA
71689	69776	ACATAAAACTGGATGAAATA
71690	69777	GACATAAAACTGGATGAAAT
71691	69778	TGACATAAAACTGGATGAAA
71692	69779	ATGACATAAAACTGGATGAA
71693	69780	AATGACATAAAACTGGATGA
71694	69781	AAATGACATAAAACTGGATG
71695	69782	AAAATGACATAAAACTGGAT
71696	69783	TAAAATGACATAAAACTGGA
71697	69784	ATAAAATGACATAAAACTGG
71698	69785	TATAAAATGACATAAAACTG
71699	69786	CTATAAAATGACATAAAACT
71700	69787	ACTATAAAATGACATAAAAC
71701	69788	AACTATAAAATGACATAAAA
71702	69789	AAACTATAAAATGACATAAA
71703	69790	AAAACTATAAAATGACATAA
71704	69791	AAAAACTATAAAATGACATA
71705	69792	TAAAAACTATAAAATGACAT
71706	69793	ATAAAAACTATAAAATGACA
71707	69794	TATAAAAACTATAAAATGAC
71708	69795	GTATAAAAACTATAAAATGA
71709	69796	TGTATAAAAACTATAAAATG
71710	69797	ATGTATAAAAACTATAAAAT
71711	69798	AATGTATAAAAACTATAAAA
71712	69799	AAATGTATAAAAACTATAAA
71713	69800	TAAATGTATAAAAACTATAA
71714	69801	TTAAATGTATAAAAACTATA
71715	69802	CTTAAATGTATAAAAACTAT
71716	69803	ACTTAAATGTATAAAAACTA
71717	69804	TACTTAAATGTATAAAAACT
71718	69805	ATACTTAAATGTATAAAAAC

120795	118882	CATCTCATACACAAAAATTA
120796	118883	TCATCTCATACACAAAAATT
120797	118884	CTCATCTCATACACAAAAAT
120798	118885	TCTCATCTCATACACAAAAA
120799	118886	CTCTCATCTCATACACAAAA
120800	118887	ACTCTCATCTCATACACAAA
120801	118888	TACTCTCATCTCATACACAA
120802	118889	CTACTCTCATCTCATACACA
120803	118890	ACTACTCTCATCTCATACAC
120804	118891	CACTACTCTCATCTCATACA
120805	118892	CCACTACTCTCATCTCATAC
120806	118893	ACCACTACTCTCATCTCATA
120807	118894	GACCACTACTCTCATCTCAT
120808	118895	GGACCACTACTCTCATCTCA
120809	118896	TGGACCACTACTCTCATCTC
120810	118897	CTGGACCACTACTCTCATCT
120811	118898	CCTGGACCACTACTCTCATC
120812	118899	ACCTGGACCACTACTCTCAT
120813	118900	AACCTGGACCACTACTCTCA
120814	118901	AAACCTGGACCACTACTCTC
120815	118902	AAAACCTGGACCACTACTCT
120816	118903	AAAAACCTGGACCACTACTC
120817	118904	GAAAAACCTGGACCACTACT
120818	118905	GGAAAAACCTGGACCACTAC
120819	118906	AGGAAAAACCTGGACCACTA
120820	118907	AAGGAAAAACCTGGACCACT
120821	118908	AAAGGAAAAACCTGGACCAC
120822	118909	AAAAGGAAAAACCTGGACCA
120823	118910	CAAAAGGAAAAACCTGGACC
120824	118911	GCAAAAGGAAAAACCTGGAC
120825	118912	AGCAAAAGGAAAAACCTGGA
120826	118913	AAGCAAAAGGAAAAACCTGG
120827	118914	CAAGCAAAAGGAAAAACCTG
120828	118915	ACAAGCAAAAGGAAAAACCT
120829	118916	CACAAGCAAAAGGAAAAACC
120830	118917	CCACAAGCAAAAGGAAAAAC
120831	118918	TCCACAAGCAAAAGGAAAAA
120832	118919	ATCCACAAGCAAAAGGAAAA
120833	118920	TATCCACAAGCAAAAGGAAA
120834	118921	ATATCCACAAGCAAAAGGAA
120835	118922	GATATCCACAAGCAAAAGGA
120836	118923	GGATATCCACAAGCAAAAGG
120837	118924	CGGATATCCACAAGCAAAAG
120838	118925	ACGGATATCCACAAGCAAAA
120839	118926	AACGGATATCCACAAGCAAA
120840	118927	CAACGGATATCCACAAGCAA
120841	118928	ACAACGGATATCCACAAGCA
120842	118929	GACAACGGATATCCACAAGC
120843	118930	GGACAACGGATATCCACAAG
120844	118931	GGGACAACGGATATCCACAA
120845	118932	GGGGACAACGGATATCCACA
120846	118933	TGGGGACAACGGATATCCAC
120847	118934	GTGGGGACAACGGATATCCA
120848	118935	GGTGGGGACAACGGATATCC
120849	118936	AGGTGGGGACAACGGATATC
120850	118937	GAGGTGGGGACAACGGATAT
120851	118938	TGAGGTGGGGACAACGGATA
120852	118939	ATGAGGTGGGGACAACGGAT
120853	118940	AATGAGGTGGGGACAACGGA
120854	118941	AAATGAGGTGGGGACAACGG
120855	118942	CAAATGAGGTGGGGACAACG
120856	118943	ACAAATGAGGTGGGGACAAC
120857	118944	AACAAATGAGGTGGGGACAA
120858	118945	CAACAAATGAGGTGGGGACA
120859	118946	TCAACAAATGAGGTGGGGAC
120860	118947	TTCAACAAATGAGGTGGGGA
120861	118948	TTTCAACAAATGAGGTGGGG
120862	118949	TTTTCAACAAATGAGGTGGG
120863	118950	CTTTTCAACAAATGAGGTGG
120864	118951	TCTTTTCAACAAATGAGGTG
120865	118952	GTCTTTTCAACAAATGAGGT

22572	20659	CCACTGCACTCCACCCTGGG
22573	20660	ACCACTGCACTCCACCCTGG
22574	20661	CACCACTGCACTCCACCCTG
22575	20662	GCACCACTGCACTCCACCCT
22576	20663	CGCACCACTGCACTCCACCC
22577	20664	TCGCACCACTGCACTCCACC
22578	20665	ATCGCACCACTGCACTCCAC
22579	20666	TATCGCACCACTGCACTCCA
22580	20667	ATATCGCACCACTGCACTCC
22581	20668	AATATCGCACCACTGCACTC
22582	20669	CAATATCGCACCACTGCACT
22583	20670	ACAATATCGCACCACTGCAC
22584	20671	GACAATATCGCACCACTGCA
22585	20672	AGACAATATCGCACCACTGC
22586	20673	CAGACAATATCGCACCACTG
22587	20674	TCAGACAATATCGCACCACT
22588	20675	GTCAGACAATATCGCACCAC
22589	20676	AGTCAGACAATATCGCACCA
22590	20677	CAGTCAGACAATATCGCACC
22591	20678	GCAGTCAGACAATATCGCAC
22592	20679	TGCAGTCAGACAATATCGCA
22593	20680	TTGCAGTCAGACAATATCGC
22594	20681	GTTGCAGTCAGACAATATCG
22595	20682	TGTTGCAGTCAGACAATATC
22596	20683	ATGTTGCAGTCAGACAATAT
22597	20684	AATGTTGCAGTCAGACAATA
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22600	20687	GTCAATGTTGCAGTCAGACA
22601	20688	GGTCAATGTTGCAGTCAGAC
22602	20689	AGGTCAATGTTGCAGTCAGA
22603	20690	GAGGTCAATGTTGCAGTCAG
22604	20691	GGAGGTCAATGTTGCAGTCA
22605	20692	AGGAGGTCAATGTTGCAGTC
22606	20693	CAGGAGGTCAATGTTGCAGT
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22608	20695	CCCAGGAGGTCAATGTTGCA
22609	20696	GCCCAGGAGGTCAATGTTGC
22610	20697	AGCCCAGGAGGTCAATGTTG
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22612	20699	TGAGCCCAGGAGGTCAATGT
22613	20700	TTGAGCCCAGGAGGTCAATG
22614	20701	CTTGAGCCCAGGAGGTCAAT
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22622	20709	GAGGATCACTTGAGCCCAGG
22623	20710	GGAGGATCACTTGAGCCCAG
22624	20711	AGGAGGATCACTTGAGCCCA
22625	20712	CAGGAGGATCACTTGAGCCC
22626	20713	GCAGGAGGATCACTTGAGCC
22627	20714	GGCAGGAGGATCACTTGAGC
22628	20715	AGGCAGGAGGATCACTTGAG
22629	20716	GAGGCAGGAGGATCACTTGA
22630	20717	TGAGGCAGGAGGATCACTTG
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22633	20720	GGCTGAGGCAGGAGGATCAC
22634	20721	AGGCTGAGGCAGGAGGATCA
22635	20722	GAGGCTGAGGCAGGAGGATC
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22637	20724	AGGAGGCTGAGGCAGGAGGA
22638	20725	CAGGAGGCTGAGGCAGGAGG
22639	20726	CCAGGAGGCTGAGGCAGGAG
22640	20727	GCCAGGAGGCTGAGGCAGGA
22641	20728	AGCCAGGAGGCTGAGGCAGG
22642	20729	CAGCCAGGAGGCTGAGGCAG

71719	69806	TATACTTAAATGTATAAAAA
71720	69807	ATATACTTAAATGTATAAAA
71721	69808	AATATACTTAAATGTATAAA
71722	69809	AAATATACTTAAATGTATAA
71723	69810	TAAATATACTTAAATGTATA
71724	69811	ATAAATATACTTAAATGTAT
71725	69812	AATAAATATACTTAAATGTA
71726	69813	AAATAAATATACTTAAATGT
71727	69814	GAAATAAATATACTTAAATG
71728	69815	AGAAATAAATATACTTAAAT
71729	69816	TAGAAATAAATATACTTAAA
71730	69817	TTAGAAATAAATATACTTAA
71731	69818	ATTAGAAATAAATATACTTA
71732	69819	CATTAGAAATAAATATACTT
71733	69820	ACATTAGAAATAAATATACT
71734	69821	AACATTAGAAATAAATATAC
71735	69822	AAACATTAGAAATAAATATA
71736	69823	TAAACATTAGAAATAAATAT
71737	69824	TTAAACATTAGAAATAAATA
71738	69825	GTTAAACATTAGAAATAAAT
71739	69826	TGTTAAACATTAGAAATAAA
71740	69827	GTGTTAAACATTAGAAATAA
71741	69828	AGTGTTAAACATTAGAAATA
71742	69829	TAGTGTTAAACATTAGAAAT
71743	69830	GTAGTGTTAAACATTAGAAA
71744	69831	GGTAGTGTTAAACATTAGAA
71745	69832	TGGTAGTGTTAAACATTAGA
71746	69833	ATGGTAGTGTTAAACATTAG
71747	69834	AATGGTAGTGTTAAACATTA
71748	69835	AAATGGTAGTGTTAAACATT
71749	69836	AAAATGGTAGTGTTAAACAT
71750	69837	TAAAATGGTAGTGTTAAACA
71751	69838	CTAAAATGGTAGTGTTAAAC
71752	69839	ACTAAAATGGTAGTGTTAAA
71753	69840	AACTAAAATGGTAGTGTTAA
71754	69841	TAACTAAAATGGTAGTGTTA
71755	69842	ATAACTAAAATGGTAGTGTT
71756	69843	AATAACTAAAATGGTAGTGT
71757	69844	AAATAACTAAAATGGTAGTG
71758	69845	CAAATAACTAAAATGGTAGT
71759	69846	TCAAATAACTAAAATGGTAG
71760	69847	GTCAAATAACTAAAATGGTA
71761	69848	GGTCAAATAACTAAAATGGT
71762	69849	TGGTCAAATAACTAAAATGG
71763	69850	ATGGTCAAATAACTAAAATG
71764	69851	AATGGTCAAATAACTAAAAT
71765	69852	TAATGGTCAAATAACTAAAA
71766	69853	ATAATGGTCAAATAACTAAA
71767	69854	AATAATGGTCAAATAACTAA
71768	69855	GAATAATGGTCAAATAACTA
71769	69856	AGAATAATGGTCAAATAACT
71770	69857	CAGAATAATGGTCAAATAAC
71771	69858	CCAGAATAATGGTCAAATAA
71772	69859	GCCAGAATAATGGTCAAATA
71773	69860	GGCCAGAATAATGGTCAAAT
71774	69861	GGGCCAGAATAATGGTCAAA
71775	69862	AGGGCCAGAATAATGGTCAA
71776	69863	AAGGGCCAGAATAATGGTCA
71777	69864	AAAGGGCCAGAATAATGGTC
71778	69865	TAAAGGGCCAGAATAATGGT
71779	69866	TTAAAGGGCCAGAATAATGG
71780	69867	TTTAAAGGGCCAGAATAATG
71781	69868	TTTTAAAGGGCCAGAATAAT
71782	69869	TTTTTAAAGGGCCAGAATAA
71783	69870	TTTTTTAAAGGGCCAGAATA
71784	69871	ATTTTTTAAAGGGCCAGAAT
71785	69872	CATTTTTTAAAGGGCCAGAA
71786	69873	GCATTTTTTAAAGGGCCAGA
71787	69874	AGCATTTTTTAAAGGGCCAG
71788	69875	GAGCATTTTTTAAAGGGCCA
71789	69876	TGAGCATTTTTTAAAGGGCC

120866	118953	AGTCTTTTCAACAAATGAGG
120867	118954	TAGTCTTTTCAACAAATGAG
120868	118955	ATAGTCTTTTCAACAAATGA
120869	118956	AATAGTCTTTTCAACAAATG
120870	118957	GAATAGTCTTTTCAACAAAT
120871	118958	AGAATAGTCTTTTCAACAAA
120872	118959	AAGAATAGTCTTTTCAACAA
120873	118960	AAAGAATAGTCTTTTCAACA
120874	118961	GAAAGAATAGTCTTTTCAAC
120875	118962	GGAAAGAATAGTCTTTTCAA
120876	118963	AGGAAAGAATAGTCTTTTCA
120877	118964	GAGGAAAGAATAGTCTTTTC
120878	118965	AGAGGAAAGAATAGTCTTTT
120879	118966	AAGAGGAAAGAATAGTCTTT
120880	118967	TAAGAGGAAAGAATAGTCTT
120881	118968	TTAAGAGGAAAGAATAGTCT
120882	118969	TTTAAGAGGAAAGAATAGTC
120883	118970	ATTTAAGAGGAAAGAATAGT
120884	118971	AATTTAAGAGGAAAGAATAG
120885	118972	CAATTTAAGAGGAAAGAATA
120886	118973	ACAATTTAAGAGGAAAGAAT
120887	118974	AACAATTTAAGAGGAAAGAA
120888	118975	AAACAATTTAAGAGGAAAGA
120889	118976	CAAACAATTTAAGAGGAAAG
120890	118977	ACAAACAATTTAAGAGGAAA
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120893	118980	CAAACAAACAATTTAAGAGG
120894	118981	ACAAACAAACAATTTAAGAG
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120896	118983	AAACAAACAAACAATTTAAG
120897	118984	TAAACAAACAAACAATTTAA
120898	118985	ATAAACAAACAAACAATTTA
120899	118986	AATAAACAAACAAACAATTT
120900	118987	AAATAAACAAACAAACAATT
120901	118988	TAAATAAACAAACAAACAAT
120902	118989	ATAAATAAACAAACAAACAA
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120905	118992	AAAATAAATAAACAAACAAA
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120907	118994	CAAAAATAAATAAACAAACA
120908	118995	TCAAAAATAAATAAACAAAC
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120912	118999	CATCTCAAAAATAAATAAAC
120913	119000	CCATCTCAAAAATAAATAAA
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120919	119006	GACACTCCATCTCAAAAATA
120920	119007	CGACACTCCATCTCAAAAAT
120921	119008	GCGACACTCCATCTCAAAAA
120922	119009	AGCGACACTCCATCTCAAAA
120923	119010	GAGCGACACTCCATCTCAAA
120924	119011	AGAGCGACACTCCATCTCAA
120925	119012	CAGAGCGACACTCCATCTCA
120926	119013	TCAGAGCGACACTCCATCTC
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120928	119015	CATCAGAGCGACACTCCATC
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120932	119019	ACTCCATCAGAGCGACACTC
120933	119020	CACTCCATCAGAGCGACACT
120934	119021	CCACTCCATCAGAGCGACAC
120935	119022	GCCACTCCATCAGAGCGACA
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22643	20730	CCAGCCAGGAGGCTGAGGCA
22644	20731	CCCAGCCAGGAGGCTGAGGC
22645	20732	TCCCAGCCAGGAGGCTGAGG
22646	20733	GTCCCAGCCAGGAGGCTGAG
22647	20734	GGTCCCAGCCAGGAGGCTGA
22648	20735	TGGTCCCAGCCAGGAGGCTG
22649	20736	GTGGTCCCAGCCAGGAGGCT
22650	20737	TGTGGTCCCAGCCAGGAGGC
22651	20738	CTGTGGTCCCAGCCAGGAGG
22652	20739	CCTGTGGTCCCAGCCAGGAG
22653	20740	GCCTGTGGTCCCAGCCAGGA
22654	20741	TGCCTGTGGTCCCAGCCAGG
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22656	20743	CATGCCTGTGGTCCCAGCCA
22657	20744	ACATGCCTGTGGTCCCAGCC
22658	20745	TACATGCCTGTGGTCCCAGC
22659	20746	GTACATGCCTGTGGTCCCAG
22660	20747	GGTACATGCCTGTGGTCCCA
22661	20748	TGGTACATGCCTGTGGTCCC
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22663	20750	GGTGGTACATGCCTGTGGTC
22664	20751	TGGTGGTACATGCCTGTGGT
22665	20752	GTGGTGGTACATGCCTGTGG
22666	20753	TGTGGTGGTACATGCCTGTG
22667	20754	GTGTGGTGGTACATGCCTGT
22668	20755	GGTGTGGTGGTACATGCCTG
22669	20756	AGGTGTGGTGGTACATGCCT
22670	20757	CAGGTGTGGTGGTACATGCC
22671	20758	CCAGGTGTGGTGGTACATGC
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22673	20760	TACCAGGTGTGGTGGTACAT
22674	20761	CTACCAGGTGTGGTGGTACA
22675	20762	ACTACCAGGTGTGGTGGTAC
22676	20763	AACTACCAGGTGTGGTGGTA
22677	20764	AAACTACCAGGTGTGGTGGT
22678	20765	CAAACTACCAGGTGTGGTGG
22679	20766	GCAAACTACCAGGTGTGGTG
22680	20767	AGCAAACTACCAGGTGTGGT
22681	20768	AAGCAAACTACCAGGTGTGG
22682	20769	AAAGCAAACTACCAGGTGTG
22683	20770	CAAAGCAAACTACCAGGTGT
22684	20771	TCAAAGCAAACTACCAGGTG
22685	20772	ATCAAAGCAAACTACCAGGT
22686	20773	AATCAAAGCAAACTACCAGG
22687	20774	AAATCAAAGCAAACTACCAG
22688	20775	AAAATCAAAGCAAACTACCA
22689	20776	AAAAATCAAAGCAAACTACC
22690	20777	TAAAAATCAAAGCAAACTAC
22691	20778	CTAAAAATCAAAGCAAACTA
22692	20779	ACTAAAAATCAAAGCAAACT
22693	20780	TACTAAAAATCAAAGCAAAC
22694	20781	CTACTAAAAATCAAAGCAAA
22695	20782	TCTACTAAAAATCAAAGCAA
22696	20783	CTCTACTAAAAATCAAAGCA
22697	20784	TCTCTACTAAAAATCAAAGC
22698	20785	TTCTCTACTAAAAATCAAAG
22699	20786	CTTCTCTACTAAAAATCAAA
22700	20787	TCTTCTCTACTAAAAATCAA
22701	20788	CTCTTCTCTACTAAAAATCA
22702	20789	CCTCTTCTCTACTAAAAATC
22703	20790	ACCTCTTCTCTACTAAAAAT
22704	20791	GACCTCTTCTCTACTAAAAA
22705	20792	AGACCTCTTCTCTACTAAAA
22706	20793	GAGACCTCTTCTCTACTAAA
22707	20794	TGAGACCTCTTCTCTACTAA
22708	20795	GTGAGACCTCTTCTCTACTA
22709	20796	AGTGAGACCTCTTCTCTACT
22710	20797	TAGTGAGACCTCTTCTCTAC
22711	20798	ATAGTGAGACCTCTTCTCTA
22712	20799	CATAGTGAGACCTCTTCTCT
22713	20800	ACATAGTGAGACCTCTTCTC

71790	69877	CTGAGCATTTTTTAAAGGGC
71791	69878	TCTGAGCATTTTTTAAAGGG
71792	69879	GTCTGAGCATTTTTTAAAGG
71793	69880	TGTCTGAGCATTTTTTAAAG
71794	69881	TTGTCTGAGCATTTTTTAAA
71795	69882	CTTGTCTGAGCATTTTTTAA
71796	69883	ACTTGTCTGAGCATTTTTTA
71797	69884	AACTTGTCTGAGCATTTTTT
71798	69885	AAACTTGTCTGAGCATTTTT
71799	69886	CAAACTTGTCTGAGCATTTT
71800	69887	TCAAACTTGTCTGAGCATTT
71801	69888	TTCAAACTTGTCTGAGCATT
71802	69889	ATTCAAACTTGTCTGAGCAT
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71804	69891	TCATTCAAACTTGTCTGAGC
71805	69892	ATCATTCAAACTTGTCTGAG
71806	69893	AATCATTCAAACTTGTCTGA
71807	69894	AAATCATTCAAACTTGTCTG
71808	69895	AAAATCATTCAAACTTGTCT
71809	69896	AAAAATCATTCAAACTTGTC
71810	69897	GAAAAATCATTCAAACTTGT
71811	69898	TGAAAAATCATTCAAACTTG
71812	69899	CTGAAAAATCATTCAAACTT
71813	69900	TCTGAAAAATCATTCAAACT
71814	69901	CTCTGAAAAATCATTCAAAC
71815	69902	CCTCTGAAAAATCATTCAAA
71816	69903	GCCTCTGAAAAATCATTCAA
71817	69904	TGCCTCTGAAAAATCATTCA
71818	69905	ATGCCTCTGAAAAATCATTC
71819	69906	AATGCCTCTGAAAAATCATT
71820	69907	TAATGCCTCTGAAAAATCAT
71821	69908	ATAATGCCTCTGAAAAATCA
71822	69909	AATAATGCCTCTGAAAAATC
71823	69910	CAATAATGCCTCTGAAAAAT
71824	69911	CCAATAATGCCTCTGAAAAA
71825	69912	GCCAATAATGCCTCTGAAAA
71826	69913	AGCCAATAATGCCTCTGAAA
71827	69914	GAGCCAATAATGCCTCTGAA
71828	69915	TGAGCCAATAATGCCTCTGA
71829	69916	CTGAGCCAATAATGCCTCTG
71830	69917	TCTGAGCCAATAATGCCTCT
71831	69918	CTCTGAGCCAATAATGCCTC
71832	69919	CCTCTGAGCCAATAATGCCT
71833	69920	ACCTCTGAGCCAATAATGCC
71834	69921	TACCTCTGAGCCAATAATGC
71835	69922	TTACCTCTGAGCCAATAATG
71836	69923	TTTACCTCTGAGCCAATAAT
71837	69924	TTTTACCTCTGAGCCAATAA
71838	69925	CTTTTACCTCTGAGCCAATA
71839	69926	TCTTTTACCTCTGAGCCAAT
71840	69927	CTCTTTTACCTCTGAGCCAA
71841	69928	CCTCTTTTACCTCTGAGCCA
71842	69929	TCCTCTTTTACCTCTGAGCC
71843	69930	TTCCTCTTTTACCTCTGAGC
71844	69931	TTTCCTCTTTTACCTCTGAG
71845	69932	CTTTCCTCTTTTACCTCTGA
71846	69933	TCTTTCCTCTTTTACCTCTG
71847	69934	ATCTTTCCTCTTTTACCTCT
71848	69935	AATCTTTCCTCTTTTACCTC
71849	69936	CAATCTTTCCTCTTTTACCT
71850	69937	TCAATCTTTCCTCTTTTACC
71851	69938	CTCAATCTTTCCTCTTTTAC
71852	69939	TCTCAATCTTTCCTCTTTTA
71853	69940	TTCTCAATCTTTCCTCTTTT
71854	69941	CTTCTCAATCTTTCCTCTTT
71855	69942	GCTTCTCAATCTTTCCTCTT
71856	69943	AGCTTCTCAATCTTTCCTCT
71857	69944	CAGCTTCTCAATCTTTCCTC
71858	69945	TCAGCTTCTCAATCTTTCCT
71859	69946	TTCAGCTTCTCAATCTTTCC
71860	69947	ATTCAGCTTCTCAATCTTTC

120937	119024	GCGCCACTCCATCAGAGCGA
120938	119025	AGCGCCACTCCATCAGAGCG
120939	119026	TAGCGCCACTCCATCAGAGC
120940	119027	TTAGCGCCACTCCATCAGAG
120941	119028	GTTAGCGCCACTCCATCAGA
120942	119029	AGTTAGCGCCACTCCATCAG
120943	119030	AAGTTAGCGCCACTCCATCA
120944	119031	TAAGTTAGCGCCACTCCATC
120945	119032	CTAAGTTAGCGCCACTCCAT
120946	119033	GCTAAGTTAGCGCCACTCCA
120947	119034	AGCTAAGTTAGCGCCACTCC
120948	119035	AAGCTAAGTTAGCGCCACTC
120949	119036	GAAGCTAAGTTAGCGCCACT
120950	119037	TGAAGCTAAGTTAGCGCCAC
120951	119038	GTGAAGCTAAGTTAGCGCCA
120952	119039	AGTGAAGCTAAGTTAGCGCC
120953	119040	CAGTGAAGCTAAGTTAGCGC
120954	119041	GCAGTGAAGCTAAGTTAGCG
120955	119042	TGCAGTGAAGCTAAGTTAGC
120956	119043	TTGCAGTGAAGCTAAGTTAG
120957	119044	GTTGCAGTGAAGCTAAGTTA
120958	119045	GGTTGCAGTGAAGCTAAGTT
120959	119046	AGGTTGCAGTGAAGCTAAGT
120960	119047	GAGGTTGCAGTGAAGCTAAG
120961	119048	GGAGGTTGCAGTGAAGCTAA
120962	119049	CGGAGGTTGCAGTGAAGCTA
120963	119050	GCGGAGGTTGCAGTGAAGCT
120964	119051	GGCGGAGGTTGCAGTGAAGC
120965	119052	AGGCGGAGGTTGCAGTGAAG
120966	119053	GAGGCGGAGGTTGCAGTGAA
120967	119054	AGAGGCGGAGGTTGCAGTGA
120968	119055	GAGAGGCGGAGGTTGCAGTG
120969	119056	TGAGAGGCGGAGGTTGCAGT
120970	119057	CTGAGAGGCGGAGGTTGCAG
120971	119058	TCTGAGAGGCGGAGGTTGCA
120972	119059	ATCTGAGAGGCGGAGGTTGC
120973	119060	AATCTGAGAGGCGGAGGTTG
120974	119061	GAATCTGAGAGGCGGAGGTT
120975	119062	TGAATCTGAGAGGCGGAGGT
120976	119063	TTGAATCTGAGAGGCGGAGG
120977	119064	CTTGAATCTGAGAGGCGGAG
120978	119065	GCTTGAATCTGAGAGGCGGA
120979	119066	CGCTTGAATCTGAGAGGCGG
120980	119067	TCGCTTGAATCTGAGAGGCG
120981	119068	ATCGCTTGAATCTGAGAGGC
120982	119069	AATCGCTTGAATCTGAGAGG
120983	119070	GAATCGCTTGAATCTGAGAG
120984	119071	GGAATCGCTTGAATCTGAGA
120985	119072	GGGAATCGCTTGAATCTGAG
120986	119073	GGGGAATCGCTTGAATCTGA
120987	119074	AGGGGAATCGCTTGAATCTG
120988	119075	CAGGGGAATCGCTTGAATCT
120989	119076	GCAGGGGAATCGCTTGAATC
120990	119077	GGCAGGGGAATCGCTTGAAT
120991	119078	AGGCAGGGGAATCGCTTGAA
120992	119079	GAGGCAGGGGAATCGCTTGA
120993	119080	TGAGGCAGGGGAATCGCTTG
120994	119081	CTGAGGCAGGGGAATCGCTT
120995	119082	GCTGAGGCAGGGGAATCGCT
120996	119083	GGCTGAGGCAGGGGAATCGC
120997	119084	AGGCTGAGGCAGGGGAATCG
120998	119085	GAGGCTGAGGCAGGGGAATC
120999	119086	GGAGGCTGAGGCAGGGGAAT
121000	119087	AGGAGGCTGAGGCAGGGGAA
121001	119088	CAGGAGGCTGAGGCAGGGGA
121002	119089	TCAGGAGGCTGAGGCAGGGG
121003	119090	CTCAGGAGGCTGAGGCAGGG
121004	119091	ACTCAGGAGGCTGAGGCAGG
121005	119092	TACTCAGGAGGCTGAGGCAG
121006	119093	CTACTCAGGAGGCTGAGGCA
121007	119094	GCTACTCAGGAGGCTGAGGC

22714	20801	AACATAGTGAGACCTCTTCT
22715	20802	CAACATAGTGAGACCTCTTC
22716	20803	GCAACATAGTGAGACCTCTT
22717	20804	GGCAACATAGTGAGACCTCT
22718	20805	GGGCAACATAGTGAGACCTC
22719	20806	AGGGCAACATAGTGAGACCT
22720	20807	CAGGGCAACATAGTGAGACC
22721	20808	CCAGGGCAACATAGTGAGAC
22722	20809	CCCAGGGCAACATAGTGAGA
22723	20810	ACCCAGGGCAACATAGTGAG
22724	20811	CACCCAGGGCAACATAGTGA
22725	20812	CCACCCAGGGCAACATAGTG
22726	20813	ACCACCCAGGGCAACATAGT
22727	20814	CACCACCCAGGGCAACATAG
22728	20815	ACACCACCCAGGGCAACATA
22729	20816	AACACCACCCAGGGCAACAT
22730	20817	CAACACCACCCAGGGCAACA
22731	20818	TCAACACCACCCAGGGCAAC
22732	20819	TTCAACACCACCCAGGGCAA
22733	20820	GTTCAACACCACCCAGGGCA
22734	20821	AGTTCAACACCACCCAGGGC
22735	20822	GAGTTCAACACCACCCAGGG
22736	20823	GGAGTTCAACACCACCCAGG
22737	20824	AGGAGTTCAACACCACCCAG
22738	20825	CAGGAGTTCAACACCACCCA
22739	20826	CCAGGAGTTCAACACCACCC
22740	20827	CCCAGGAGTTCAACACCACC
22741	20828	GCCCAGGAGTTCAACACCAC
22742	20829	AGCCCAGGAGTTCAACACCA
22743	20830	GAGCCCAGGAGTTCAACACC
22744	20831	TGAGCCCAGGAGTTCAACAC
22745	20832	TTGAGCCCAGGAGTTCAACA
22746	20833	CTTGAGCCCAGGAGTTCAAC
22747	20834	ACTTGAGCCCAGGAGTTCAA
22748	20835	CACTTGAGCCCAGGAGTTCA
22749	20836	TCACTTGAGCCCAGGAGTTC
22750	20837	ATCACTTGAGCCCAGGAGTT
22751	20838	AATCACTTGAGCCCAGGAGT
22752	20839	GAATCACTTGAGCCCAGGAG
22753	20840	TGAATCACTTGAGCCCAGGA
22754	20841	ATGAATCACTTGAGCCCAGG
22755	20842	GATGAATCACTTGAGCCCAG
22756	20843	AGATGAATCACTTGAGCCCA
22757	20844	TAGATGAATCACTTGAGCCC
22758	20845	GTAGATGAATCACTTGAGCC
22759	20846	GGTAGATGAATCACTTGAGC
22760	20847	AGGTAGATGAATCACTTGAG
22761	20848	GAGGTAGATGAATCACTTGA
22762	20849	TGAGGTAGATGAATCACTTG
22763	20850	CTGAGGTAGATGAATCACTT
22764	20851	GCTGAGGTAGATGAATCACT
22765	20852	GGCTGAGGTAGATGAATCAC
22766	20853	AGGCTGAGGTAGATGAATCA
22767	20854	GAGGCTGAGGTAGATGAATC
22768	20855	GGAGGCTGAGGTAGATGAAT
22769	20856	GGGAGGCTGAGGTAGATGAA
22770	20857	TGGGAGGCTGAGGTAGATGA
22771	20858	TTGGGAGGCTGAGGTAGATG
22772	20859	TTTGGGAGGCTGAGGTAGAT
22773	20860	CTTTGGGAGGCTGAGGTAGA
22774	20861	ACTTTGGGAGGCTGAGGTAG
22775	20862	CACTTTGGGAGGCTGAGGTA
22776	20863	GCACTTTGGGAGGCTGAGGT
22777	20864	AGCACTTTGGGAGGCTGAGG
22778	20865	CAGCACTTTGGGAGGCTGAG
22779	20866	CCAGCACTTTGGGAGGCTGA
22780	20867	CCCAGCACTTTGGGAGGCTG
22781	20868	TCCCAGCACTTTGGGAGGCT
22782	20869	ATCCCAGCACTTTGGGAGGC
22783	20870	AATCCCAGCACTTTGGGAGG
22784	20871	TAATCCCAGCACTTTGGGAG

71861	69948	TATTCAGCTTCTCAATCTTT
71862	69949	ATATTCAGCTTCTCAATCTT
71863	69950	CATATTCAGCTTCTCAATCT
71864	69951	ACATATTCAGCTTCTCAATC
71865	69952	TACATATTCAGCTTCTCAAT
71866	69953	GTACATATTCAGCTTCTCAA
71867	69954	AGTACATATTCAGCTTCTCA
71868	69955	GAGTACATATTCAGCTTCTC
71869	69956	AGAGTACATATTCAGCTTCT
71870	69957	CAGAGTACATATTCAGCTTC
71871	69958	ACAGAGTACATATTCAGCTT
71872	69959	AACAGAGTACATATTCAGCT
71873	69960	AAACAGAGTACATATTCAGC
71874	69961	GAAACAGAGTACATATTCAG
71875	69962	GGAAACAGAGTACATATTCA
71876	69963	AGGAAACAGAGTACATATTC
71877	69964	CAGGAAACAGAGTACATATT
71878	69965	CCAGGAAACAGAGTACATAT
71879	69966	CCCAGGAAACAGAGTACATA
71880	69967	ACCCAGGAAACAGAGTACAT
71881	69968	TACCCAGGAAACAGAGTACA
71882	69969	ATACCCAGGAAACAGAGTAC
71883	69970	CATACCCAGGAAACAGAGTA
71884	69971	CCATACCCAGGAAACAGAGT
71885	69972	CCCATACCCAGGAAACAGAG
71886	69973	CCCCATACCCAGGAAACAGA
71887	69974	GCCCCATACCCAGGAAACAG
71888	69975	AGCCCCATACCCAGGAAACA
71889	69976	CAGCCCCATACCCAGGAAAC
71890	69977	CCAGCCCCATACCCAGGAAA
71891	69978	CCCAGCCCCATACCCAGGAA
71892	69979	CCCCAGCCCCATACCCAGGA
71893	69980	TCCCCAGCCCCATACCCAGG
71894	69981	ATCCCCAGCCCCATACCCAG
71895	69982	TATCCCCAGCCCCATACCCA
71896	69983	GTATCCCCAGCCCCATACCC
71897	69984	GGTATCCCCAGCCCCATACC
71898	69985	GGGTATCCCCAGCCCCATAC
71899	69986	TGGGTATCCCCAGCCCCATA
71900	69987	CTGGGTATCCCCAGCCCCAT
71901	69988	TCTGGGTATCCCCAGCCCCA
71902	69989	TTCTGGGTATCCCCAGCCCC
71903	69990	CTTCTGGGTATCCCCAGCCC
71904	69991	TCTTCTGGGTATCCCCAGCC
71905	69992	CTCTTCTGGGTATCCCCAGC
71906	69993	CCTCTTCTGGGTATCCCCAG
71907	69994	ACCTCTTCTGGGTATCCCCA
71908	69995	AACCTCTTCTGGGTATCCCC
71909	69996	GAACCTCTTCTGGGTATCCC
71910	69997	TGAACCTCTTCTGGGTATCC
71911	69998	GTGAACCTCTTCTGGGTATC
71912	69999	TGTGAACCTCTTCTGGGTAT
71913	70000	GTGTGAACCTCTTCTGGGTA
71914	70001	CGTGTGAACCTCTTCTGGGT
71915	70002	ACGTGTGAACCTCTTCTGGG
71916	70003	AACGTGTGAACCTCTTCTGG
71917	70004	CAACGTGTGAACCTCTTCTG
71918	70005	CCAACGTGTGAACCTCTTCT
71919	70006	ACCAACGTGTGAACCTCTTC
71920	70007	GACCAACGTGTGAACCTCTT
71921	70008	CGACCAACGTGTGAACCTCT
71922	70009	TCGACCAACGTGTGAACCTC
71923	70010	CTCGACCAACGTGTGAACCT
71924	70011	TCTCGACCAACGTGTGAACC
71925	70012	GTCTCGACCAACGTGTGAAC
71926	70013	TGTCTCGACCAACGTGTGAA
71927	70014	ATGTCTCGACCAACGTGTGA
71928	70015	AATGTCTCGACCAACGTGTG
71929	70016	AAATGTCTCGACCAACGTGT
71930	70017	GAAATGTCTCGACCAACGTG
71931	70018	AGAAATGTCTCGACCAACGT

121008	119095	AGCTACTCAGGAGGCTGAGG
121009	119096	CAGCTACTCAGGAGGCTGAG
121010	119097	CCAGCTACTCAGGAGGCTGA
121011	119098	TCCAGCTACTCAGGAGGCTG
121012	119099	TTCCAGCTACTCAGGAGGCT
121013	119100	ATTCCAGCTACTCAGGAGGC
121014	119101	AATTCCAGCTACTCAGGAGG
121015	119102	TAATTCCAGCTACTCAGGAG
121016	119103	GTAATTCCAGCTACTCAGGA
121017	119104	TGTAATTCCAGCTACTCAGG
121018	119105	CTGTAATTCCAGCTACTCAG
121019	119106	CCTGTAATTCCAGCTACTCA
121020	119107	CCCTGTAATTCCAGCTACTC
121021	119108	CCCCTGTAATTCCAGCTACT
121022	119109	ACCCCTGTAATTCCAGCTAC
121023	119110	CACCCCTGTAATTCCAGCTA
121024	119111	GCACCCCTGTAATTCCAGCT
121025	119112	CGCACCCCTGTAATTCCAGC
121026	119113	GCGCACCCCTGTAATTCCAG
121027	119114	GGCGCACCCCTGTAATTCCA
121028	119115	TGGCGCACCCCTGTAATTCC
121029	119116	GTGGCGCACCCCTGTAATTC
121030	119117	GGTGGCGCACCCCTGTAATT
121031	119118	TGGTGGCGCACCCCTGTAAT
121032	119119	GTGGTGGCGCACCCCTGTAA
121033	119120	TGTGGTGGCGCACCCCTGTA
121034	119121	GTGTGGTGGCGCACCCCTGT
121035	119122	GGTGTGGTGGCGCACCCCTG
121036	119123	GGGTGTGGTGGCGCACCCCT
121037	119124	TGGGTGTGGTGGCGCACCCC
121038	119125	CTGGGTGTGGTGGCGCACCC
121039	119126	GCTGGGTGTGGTGGCGCACC
121040	119127	AGCTGGGTGTGGTGGCGCAC
121041	119128	TAGCTGGGTGTGGTGGCGCA
121042	119129	TTAGCTGGGTGTGGTGGCGC
121043	119130	ATTAGCTGGGTGTGGTGGCG
121044	119131	AATTAGCTGGGTGTGGTGGC
121045	119132	AAATTAGCTGGGTGTGGTGG
121046	119133	AAAATTAGCTGGGTGTGGTG
121047	119134	AAAAATTAGCTGGGTGTGGT
121048	119135	CAAAAATTAGCTGGGTGTGG
121049	119136	ACAAAAATTAGCTGGGTGTG
121050	119137	TACAAAAATTAGCTGGGTGT
121051	119138	ATACAAAAATTAGCTGGGTG
121052	119139	AATACAAAAATTAGCTGGGT
121053	119140	AAATACAAAAATTAGCTGGG
121054	119141	AAAATACAAAAATTAGCTGG
121055	119142	AAAAATACAAAAATTAGCTG
121056	119143	TAAAAATACAAAAATTAGCT
121057	119144	CTAAAAATACAAAAATTAGC
121058	119145	ACTAAAAATACAAAAATTAG
121059	119146	TACTAAAAATACAAAAATTA
121060	119147	CTACTAAAAATACAAAAATT
121061	119148	TCTACTAAAAATACAAAAAT
121062	119149	CTCTACTAAAAATACAAAAA
121063	119150	TCTCTACTAAAAATACAAAA
121064	119151	GTCTCTACTAAAAATACAAA
121065	119152	CGTCTCTACTAAAAATACAA
121066	119153	CCGTCTCTACTAAAAATACA
121067	119154	CCCGTCTCTACTAAAAATAC
121068	119155	CCCCGTCTCTACTAAAAATA
121069	119156	ACCCCGTCTCTACTAAAAAT
121070	119157	AACCCCGTCTCTACTAAAAA
121071	119158	AAACCCCGTCTCTACTAAAA
121072	119159	AAAACCCCGTCTCTACTAAA
121073	119160	TAAAACCCCGTCTCTACTAA
121074	119161	GTAAAACCCCGTCTCTACTA
121075	119162	GGTAAAACCCCGTCTCTACT
121076	119163	CGGTAAAACCCCGTCTCTAC
121077	119164	ACGGTAAAACCCCGTCTCTA
121078	119165	CACGGTAAAACCCCGTCTCT

22785	20872	ATAATCCCAGCACTTTGGGA
22786	20873	TATAATCCCAGCACTTTGGG
22787	20874	CTATAATCCCAGCACTTTGG
22788	20875	TCTATAATCCCAGCACTTTG
22789	20876	ATCTATAATCCCAGCACTTT
22790	20877	TATCTATAATCCCAGCACTT
22791	20878	ATATCTATAATCCCAGCACT
22792	20879	CATATCTATAATCCCAGCAC
22793	20880	TCATATCTATAATCCCAGCA
22794	20881	CTCATATCTATAATCCCAGC
22795	20882	GCTCATATCTATAATCCCAG
22796	20883	GGCTCATATCTATAATCCCA
22797	20884	GGGCTCATATCTATAATCCC
22798	20885	GGGGCTCATATCTATAATCC
22799	20886	AGGGGCTCATATCTATAATC
22800	20887	CAGGGGCTCATATCTATAAT
22801	20888	ACAGGGGCTCATATCTATAA
22802	20889	CACAGGGGCTCATATCTATA
22803	20890	GCACAGGGGCTCATATCTAT
22804	20891	GGCACAGGGGCTCATATCTA
22805	20892	AGGCACAGGGGCTCATATCT
22806	20893	CAGGCACAGGGGCTCATATC
22807	20894	CCAGGCACAGGGGCTCATAT
22808	20895	GCCAGGCACAGGGGCTCATA
22809	20896	GGCCAGGCACAGGGGCTCAT
22810	20897	AGGCCAGGCACAGGGGCTCA
22811	20898	GAGGCCAGGCACAGGGGCTC
22812	20899	TGAGGCCAGGCACAGGGGCT
22813	20900	ATGAGGCCAGGCACAGGGGC
22814	20901	AATGAGGCCAGGCACAGGGG
22815	20902	CAATGAGGCCAGGCACAGGG
22816	20903	ACAATGAGGCCAGGCACAGG
22817	20904	CACAATGAGGCCAGGCACAG
22818	20905	CCACAATGAGGCCAGGCACA
22819	20906	ACCACAATGAGGCCAGGCAC
22820	20907	AACCACAATGAGGCCAGGCA
22821	20908	AAACCACAATGAGGCCAGGC
22822	20909	AAAACCACAATGAGGCCAGG
22823	20910	TAAAACCACAATGAGGCCAG
22824	20911	TTAAAACCACAATGAGGCCA
22825	20912	ATTAAAACCACAATGAGGCC
22826	20913	AATTAAAACCACAATGAGGC
22827	20914	AAATTAAAACCACAATGAGG
22828	20915	CAAATTAAAACCACAATGAG
22829	20916	GCAAATTAAAACCACAATGA
22830	20917	TGCAAATTAAAACCACAATG
22831	20918	ATGCAAATTAAAACCACAAT
22832	20919	AATGCAAATTAAAACCACAA
22833	20920	AAATGCAAATTAAAACCACA
22834	20921	GAAATGCAAATTAAAACCAC
22835	20922	GGAAATGCAAATTAAAACCA
22836	20923	GGGAAATGCAAATTAAAACC
22837	20924	AGGGAAATGCAAATTAAAAC
22838	20925	TAGGGAAATGCAAATTAAAA
22839	20926	TTAGGGAAATGCAAATTAAA
22840	20927	ATTAGGGAAATGCAAATTAA
22841	20928	CATTAGGGAAATGCAAATTA
22842	20929	GCATTAGGGAAATGCAAATT
22843	20930	GGCATTAGGGAAATGCAAAT
22844	20931	GGGCATTAGGGAAATGCAAA
22845	20932	TGGGCATTAGGGAAATGCAA
22846	20933	CTGGGCATTAGGGAAATGCA
22847	20934	ACTGGGCATTAGGGAAATGC
22848	20935	CACTGGGCATTAGGGAAATG
22849	20936	TCACTGGGCATTAGGGAAAT
22850	20937	ATCACTGGGCATTAGGGAAA
22851	20938	TATCACTGGGCATTAGGGAA
22852	20939	ATATCACTGGGCATTAGGGA
22853	20940	AATATCACTGGGCATTAGGG
22854	20941	CAATATCACTGGGCATTAGG
22855	20942	TCAATATCACTGGGCATTAG

71932	70019	AAGAAATGTCTCGACCAACG
71933	70020	AAAGAAATGTCTCGACCAAC
71934	70021	TAAAGAAATGTCTCGACCAA
71935	70022	ATAAAGAAATGTCTCGACCA
71936	70023	CATAAAGAAATGTCTCGACC
71937	70024	TCATAAAGAAATGTCTCGAC
71938	70025	GTCATAAAGAAATGTCTCGA
71939	70026	GGTCATAAAGAAATGTCTCG
71940	70027	TGGTCATAAAGAAATGTCTC
71941	70028	GTGGTCATAAAGAAATGTCT
71942	70029	GGTGGTCATAAAGAAATGTC
71943	70030	TGGTGGTCATAAAGAAATGT
71944	70031	CTGGTGGTCATAAAGAAATG
71945	70032	GCTGGTGGTCATAAAGAAAT
71946	70033	TGCTGGTGGTCATAAAGAAA
71947	70034	CTGCTGGTGGTCATAAAGAA
71948	70035	CCTGCTGGTGGTCATAAAGA
71949	70036	ACCTGCTGGTGGTCATAAAG
71950	70037	CACCTGCTGGTGGTCATAAA
71951	70038	CCACCTGCTGGTGGTCATAA
71952	70039	GCCACCTGCTGGTGGTCATA
71953	70040	TGCCACCTGCTGGTGGTCAT
71954	70041	ATGCCACCTGCTGGTGGTCA
71955	70042	GATGCCACCTGCTGGTGGTC
71956	70043	TGATGCCACCTGCTGGTGGT
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71958	70045	GGTGATGCCACCTGCTGGTG
71959	70046	CGGTGATGCCACCTGCTGGT
71960	70047	CCGGTGATGCCACCTGCTGG
71961	70048	GCCGGTGATGCCACCTGCTG
71962	70049	GGCCGGTGATGCCACCTGCT
71963	70050	GGGCCGGTGATGCCACCTGC
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71965	70052	TTGGGCCGGTGATGCCACCT
71966	70053	TTTGGGCCGGTGATGCCACC
71967	70054	TTTTGGGCCGGTGATGCCAC
71968	70055	ATTTTGGGCCGGTGATGCCA
71969	70056	CATTTTGGGCCGGTGATGCC
71970	70057	TCATTTTGGGCCGGTGATGC
71971	70058	GTCATTTTGGGCCGGTGATG
71972	70059	AGTCATTTTGGGCCGGTGAT
71973	70060	TAGTCATTTTGGGCCGGTGA
71974	70061	TTAGTCATTTTGGGCCGGTG
71975	70062	CTTAGTCATTTTGGGCCGGT
71976	70063	ACTTAGTCATTTTGGGCCGG
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71978	70065	AAACTTAGTCATTTTGGGCC
71979	70066	GAAACTTAGTCATTTTGGGC
71980	70067	AGAAACTTAGTCATTTTGGG
71981	70068	CAGAAACTTAGTCATTTTGG
71982	70069	GCAGAAACTTAGTCATTTTG
71983	70070	GGCAGAAACTTAGTCATTTT
71984	70071	GGGCAGAAACTTAGTCATTT
71985	70072	TGGGCAGAAACTTAGTCATT
71986	70073	CTGGGCAGAAACTTAGTCAT
71987	70074	TCTGGGCAGAAACTTAGTCA
71988	70075	TTCTGGGCAGAAACTTAGTC
71989	70076	ATTCTGGGCAGAAACTTAGT
71990	70077	GATTCTGGGCAGAAACTTAG
71991	70078	TGATTCTGGGCAGAAACTTA
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71993	70080	TCTGATTCTGGGCAGAAACT
71994	70081	TTCTGATTCTGGGCAGAAAC
71995	70082	CTTCTGATTCTGGGCAGAAA
71996	70083	TCTTCTGATTCTGGGCAGAA
71997	70084	CTCTTCTGATTCTGGGCAGA
71998	70085	TCTCTTCTGATTCTGGGCAG
71999	70086	TTCTCTTCTGATTCTGGGCA
72000	70087	CTTCTCTTCTGATTCTGGGC
72001	70088	CCTTCTCTTCTGATTCTGGG
72002	70089	ACCTTCTCTTCTGATTCTGG

121079	119166	ACACGGTAAAACCCCGTCTC
121080	119167	AACACGGTAAAACCCCGTCT
121081	119168	CAACACGGTAAAACCCCGTC
121082	119169	CCAACACGGTAAAACCCCGT
121083	119170	ACCAACACGGTAAAACCCCG
121084	119171	GACCAACACGGTAAAACCCC
121085	119172	TGACCAACACGGTAAAACCC
121086	119173	CTGACCAACACGGTAAAACC
121087	119174	CCTGACCAACACGGTAAAAC
121088	119175	GCCTGACCAACACGGTAAAA
121089	119176	AGCCTGACCAACACGGTAAA
121090	119177	CAGCCTGACCAACACGGTAA
121091	119178	CCAGCCTGACCAACACGGTA
121092	119179	ACCAGCCTGACCAACACGGT
121093	119180	GACCAGCCTGACCAACACGG
121094	119181	AGACCAGCCTGACCAACACG
121095	119182	GAGACCAGCCTGACCAACAC
121096	119183	CGAGACCAGCCTGACCAACA
121097	119184	TCGAGACCAGCCTGACCAAC
121098	119185	TTCGAGACCAGCCTGACCAA
121099	119186	GTTCGAGACCAGCCTGACCA
121100	119187	AGTTCGAGACCAGCCTGACC
121101	119188	GAGTTCGAGACCAGCCTGAC
121102	119189	GGAGTTCGAGACCAGCCTGA
121103	119190	AGGAGTTCGAGACCAGCCTG
121104	119191	CAGGAGTTCGAGACCAGCCT
121105	119192	TCAGGAGTTCGAGACCAGCC
121106	119193	ATCAGGAGTTCGAGACCAGC
121107	119194	GATCAGGAGTTCGAGACCAG
121108	119195	AGATCAGGAGTTCGAGACCA
121109	119196	GAGATCAGGAGTTCGAGACC
121110	119197	CGAGATCAGGAGTTCGAGAC
121111	119198	ACGAGATCAGGAGTTCGAGA
121112	119199	CACGAGATCAGGAGTTCGAG
121113	119200	TCACGAGATCAGGAGTTCGA
121114	119201	ATCACGAGATCAGGAGTTCG
121115	119202	GATCACGAGATCAGGAGTTC
121116	119203	AGATCACGAGATCAGGAGTT
121117	119204	CAGATCACGAGATCAGGAGT
121118	119205	GCAGATCACGAGATCAGGAG
121119	119206	GGCAGATCACGAGATCAGGA
121120	119207	AGGCAGATCACGAGATCAGG
121121	119208	CAGGCAGATCACGAGATCAG
121122	119209	ACAGGCAGATCACGAGATCA
121123	119210	GACAGGCAGATCACGAGATC
121124	119211	AGACAGGCAGATCACGAGAT
121125	119212	GAGACAGGCAGATCACGAGA
121126	119213	GGAGACAGGCAGATCACGAG
121127	119214	AGGAGACAGGCAGATCACGA
121128	119215	CAGGAGACAGGCAGATCACG
121129	119216	CCAGGAGACAGGCAGATCAC
121130	119217	GCCAGGAGACAGGCAGATCA
121131	119218	TGCCAGGAGACAGGCAGATC
121132	119219	GTGCCAGGAGACAGGCAGAT
121133	119220	GGTGCCAGGAGACAGGCAGA
121134	119221	GGGTGCCAGGAGACAGGCAG
121135	119222	AGGGTGCCAGGAGACAGGCA
121136	119223	CAGGGTGCCAGGAGACAGGC
121137	119224	CCAGGGTGCCAGGAGACAGG
121138	119225	CCCAGGGTGCCAGGAGACAG
121139	119226	TCCCAGGGTGCCAGGAGACA
121140	119227	CTCCCAGGGTGCCAGGAGAC
121141	119228	CCTCCCAGGGTGCCAGGAGA
121142	119229	GCCTCCCAGGGTGCCAGGAG
121143	119230	AGCCTCCCAGGGTGCCAGGA
121144	119231	CAGCCTCCCAGGGTGCCAGG
121145	119232	TCAGCCTCCCAGGGTGCCAG
121146	119233	CTCAGCCTCCCAGGGTGCCA
121147	119234	TCTCAGCCTCCCAGGGTGCC
121148	119235	CTCTCAGCCTCCCAGGGTGC
121149	119236	CCTCTCAGCCTCCCAGGGTG

22856	20943	CTCAATATCACTGGGCATTA
22857	20944	GCTCAATATCACTGGGCATT
22858	20945	TGCTCAATATCACTGGGCAT
22859	20946	ATGCTCAATATCACTGGGCA
22860	20947	AATGCTCAATATCACTGGGC
22861	20948	AAATGCTCAATATCACTGGG
22862	20949	AAAATGCTCAATATCACTGG
22863	20950	AAAAATGCTCAATATCACTG
22864	20951	AAAAAATGCTCAATATCACT
22865	20952	GAAAAAATGCTCAATATCAC
22866	20953	TGAAAAAATGCTCAATATCA
22867	20954	ATGAAAAAATGCTCAATATC
22868	20955	CATGAAAAAATGCTCAATAT
22869	20956	ACATGAAAAAATGCTCAATA
22870	20957	CACATGAAAAAATGCTCAAT
22871	20958	ACACATGAAAAAATGCTCAA
22872	20959	AACACATGAAAAAATGCTCA
22873	20960	AAACACATGAAAAAATGCTC
22874	20961	TAAACACATGAAAAAATGCT
22875	20962	ATAAACACATGAAAAAATGC
22876	20963	AATAAACACATGAAAAAATG
22877	20964	AAATAAACACATGAAAAAAT
22878	20965	CAAATAAACACATGAAAAAA
22879	20966	TCAAATAAACACATGAAAAA
22880	20967	GTCAAATAAACACATGAAAA
22881	20968	TGTCAAATAAACACATGAAA
22882	20969	ATGTCAAATAAACACATGAA
22883	20970	AATGTCAAATAAACACATGA
22884	20971	GAATGTCAAATAAACACATG
22885	20972	TGAATGTCAAATAAACACAT
22886	20973	ATGAATGTCAAATAAACACA
22887	20974	TATGAATGTCAAATAAACAC
22888	20975	GTATGAATGTCAAATAAACA
22889	20976	GGTATGAATGTCAAATAAAC
22890	20977	TGGTATGAATGTCAAATAAA
22891	20978	ATGGTATGAATGTCAAATAA
22892	20979	GATGGTATGAATGTCAAATA
22893	20980	AGATGGTATGAATGTCAAAT
22894	20981	AAGATGGTATGAATGTCAAA
22895	20982	AAAGATGGTATGAATGTCAA
22896	20983	CAAAGATGGTATGAATGTCA
22897	20984	CCAAAGATGGTATGAATGTC
22898	20985	ACCAAAGATGGTATGAATGT
22899	20986	CACCAAAGATGGTATGAATG
22900	20987	TCACCAAAGATGGTATGAAT
22901	20988	ATCACCAAAGATGGTATGAA
22902	20989	CATCACCAAAGATGGTATGA
22903	20990	TCATCACCAAAGATGGTATG
22904	20991	CTCATCACCAAAGATGGTAT
22905	20992	TCTCATCACCAAAGATGGTA
22906	20993	TTCTCATCACCAAAGATGGT
22907	20994	TTTCTCATCACCAAAGATGG
22908	20995	GTTTCTCATCACCAAAGATG
22909	20996	AGTTTCTCATCACCAAAGAT
22910	20997	TAGTTTCTCATCACCAAAGA
22911	20998	ATAGTTTCTCATCACCAAAG
22912	20999	CATAGTTTCTCATCACCAAA
22913	21000	ACATAGTTTCTCATCACCAA
22914	21001	AACATAGTTTCTCATCACCA
22915	21002	AAACATAGTTTCTCATCACC
22916	21003	TAAACATAGTTTCTCATCAC
22917	21004	ATAAACATAGTTTCTCATCA
22918	21005	CATAAACATAGTTTCTCATC
22919	21006	GCATAAACATAGTTTCTCAT
22920	21007	TGCATAAACATAGTTTCTCA
22921	21008	ATGCATAAACATAGTTTCTC
22922	21009	AATGCATAAACATAGTTTCT
22923	21010	CAATGCATAAACATAGTTTC
22924	21011	GCAATGCATAAACATAGTTT
22925	21012	AGCAATGCATAAACATAGTT
22926	21013	AAGCAATGCATAAACATAGT

72003	70090	CACCTTCTCTTCTGATTCTG
72004	70091	ACACCTTCTCTTCTGATTCT
72005	70092	AACACCTTCTCTTCTGATTC
72006	70093	CAACACCTTCTCTTCTGATT
72007	70094	TCAACACCTTCTCTTCTGAT
72008	70095	CTCAACACCTTCTCTTCTGA
72009	70096	TCTCAACACCTTCTCTTCTG
72010	70097	CTCTCAACACCTTCTCTTCT
72011	70098	GCTCTCAACACCTTCTCTTC
72012	70099	GGCTCTCAACACCTTCTCTT
72013	70100	GGGCTCTCAACACCTTCTCT
72014	70101	TGGGCTCTCAACACCTTCTC
72015	70102	GTGGGCTCTCAACACCTTCT
72016	70103	AGTGGGCTCTCAACACCTTC
72017	70104	CAGTGGGCTCTCAACACCTT
72018	70105	GCAGTGGGCTCTCAACACCT
72019	70106	AGCAGTGGGCTCTCAACACC
72020	70107	CAGCAGTGGGCTCTCAACAC
72021	70108	ACAGCAGTGGGCTCTCAACA
72022	70109	CACAGCAGTGGGCTCTCAAC
72023	70110	CCACAGCAGTGGGCTCTCAA
72024	70111	CCCACAGCAGTGGGCTCTCA
72025	70112	CCCCACAGCAGTGGGCTCTC
72026	70113	CCCCCACAGCAGTGGGCTCT
72027	70114	ACCCCCACAGCAGTGGGCTC
72028	70115	TACCCCCACAGCAGTGGGCT
72029	70116	CTACCCCCACAGCAGTGGGC
72030	70117	GCTACCCCCACAGCAGTGGG
72031	70118	TGCTACCCCCACAGCAGTGG
72032	70119	ATGCTACCCCCACAGCAGTG
72033	70120	CATGCTACCCCCACAGCAGT
72034	70121	CCATGCTACCCCCACAGCAG
72035	70122	TCCATGCTACCCCCACAGCA
72036	70123	CTCCATGCTACCCCCACAGC
72037	70124	CCTCCATGCTACCCCCACAG
72038	70125	ACCTCCATGCTACCCCCACA
72039	70126	CACCTCCATGCTACCCCCAC
72040	70127	CCACCTCCATGCTACCCCCA
72041	70128	CCCACCTCCATGCTACCCCC
72042	70129	TCCCACCTCCATGCTACCCC
72043	70130	ATCCCACCTCCATGCTACCC
72044	70131	TATCCCACCTCCATGCTACC
72045	70132	GTATCCCACCTCCATGCTAC
72046	70133	TGTATCCCACCTCCATGCTA
72047	70134	CTGTATCCCACCTCCATGCT
72048	70135	CCTGTATCCCACCTCCATGC
72049	70136	CCCTGTATCCCACCTCCATG
72050	70137	CCCCTGTATCCCACCTCCAT
72051	70138	GCCCCTGTATCCCACCTCCA
72052	70139	AGCCCCTGTATCCCACCTCC
72053	70140	CAGCCCCTGTATCCCACCTC
72054	70141	CCAGCCCCTGTATCCCACCT
72055	70142	TCCAGCCCCTGTATCCCACC
72056	70143	CTCCAGCCCCTGTATCCCAC
72057	70144	CCTCCAGCCCCTGTATCCCA
72058	70145	ACCTCCAGCCCCTGTATCCC
72059	70146	CACCTCCAGCCCCTGTATCC
72060	70147	TCACCTCCAGCCCCTGTATC
72061	70148	ATCACCTCCAGCCCCTGTAT
72062	70149	TATCACCTCCAGCCCCTGTA
72063	70150	GTATCACCTCCAGCCCCTGT
72064	70151	TGTATCACCTCCAGCCCCTG
72065	70152	TTGTATCACCTCCAGCCCCT
72066	70153	ATTGTATCACCTCCAGCCCC
72067	70154	AATTGTATCACCTCCAGCCC
72068	70155	AAATTGTATCACCTCCAGCC
72069	70156	AAAATTGTATCACCTCCAGC
72070	70157	CAAAATTGTATCACCTCCAG
72071	70158	ACAAAATTGTATCACCTCCA
72072	70159	AACAAAATTGTATCACCTCC
72073	70160	AAACAAAATTGTATCACCTC

121150	119237	GCCTCTCAGCCTCCCAGGGT
121151	119238	AGCCTCTCAGCCTCCCAGGG
121152	119239	CAGCCTCTCAGCCTCCCAGG
121153	119240	TCAGCCTCTCAGCCTCCCAG
121154	119241	CTCAGCCTCTCAGCCTCCCA
121155	119242	CCTCAGCCTCTCAGCCTCCC
121156	119243	ACCTCAGCCTCTCAGCCTCC
121157	119244	CACCTCAGCCTCTCAGCCTC
121158	119245	CCACCTCAGCCTCTCAGCCT
121159	119246	CCCACCTCAGCCTCTCAGCC
121160	119247	TCCCACCTCAGCCTCTCAGC
121161	119248	CTCCCACCTCAGCCTCTCAG
121162	119249	CCTCCCACCTCAGCCTCTCA
121163	119250	TCCTCCCACCTCAGCCTCTC
121164	119251	ATCCTCCCACCTCAGCCTCT
121165	119252	GATCCTCCCACCTCAGCCTC
121166	119253	TGATCCTCCCACCTCAGCCT
121167	119254	GTGATCCTCCCACCTCAGCC
121168	119255	AGTGATCCTCCCACCTCAGC
121169	119256	AAGTGATCCTCCCACCTCAG
121170	119257	CAAGTGATCCTCCCACCTCA
121171	119258	TCAAGTGATCCTCCCACCTC
121172	119259	CTCAAGTGATCCTCCCACCT
121173	119260	GCTCAAGTGATCCTCCCACC
121174	119261	AGCTCAAGTGATCCTCCCAC
121175	119262	GAGCTCAAGTGATCCTCCCA
121176	119263	TGAGCTCAAGTGATCCTCCC
121177	119264	CTGAGCTCAAGTGATCCTCC
121178	119265	CCTGAGCTCAAGTGATCCTC
121179	119266	TCCTGAGCTCAAGTGATCCT
121180	119267	CTCCTGAGCTCAAGTGATCC
121181	119268	ACTCCTGAGCTCAAGTGATC
121182	119269	AACTCCTGAGCTCAAGTGAT
121183	119270	AAACTCCTGAGCTCAAGTGA
121184	119271	CAAACTCCTGAGCTCAAGTG
121185	119272	TCAAACTCCTGAGCTCAAGT
121186	119273	CTCAAACTCCTGAGCTCAAG
121187	119274	TCTCAAACTCCTGAGCTCAA
121188	119275	GTCTCAAACTCCTGAGCTCA
121189	119276	GGTCTCAAACTCCTGAGCTC
121190	119277	TGGTCTCAAACTCCTGAGCT
121191	119278	CTGGTCTCAAACTCCTGAGC
121192	119279	GCTGGTCTCAAACTCCTGAG
121193	119280	GGCTGGTCTCAAACTCCTGA
121194	119281	AGGCTGGTCTCAAACTCCTG
121195	119282	CAGGCTGGTCTCAAACTCCT
121196	119283	ACAGGCTGGTCTCAAACTCC
121197	119284	TACAGGCTGGTCTCAAACTC
121198	119285	GTACAGGCTGGTCTCAAACT
121199	119286	GGTACAGGCTGGTCTCAAAC
121200	119287	TGGTACAGGCTGGTCTCAAA
121201	119288	ATGGTACAGGCTGGTCTCAA
121202	119289	AATGGTACAGGCTGGTCTCA
121203	119290	TAATGGTACAGGCTGGTCTC
121204	119291	ATAATGGTACAGGCTGGTCT
121205	119292	CATAATGGTACAGGCTGGTC
121206	119293	GCATAATGGTACAGGCTGGT
121207	119294	GGCATAATGGTACAGGCTGG
121208	119295	AGGCATAATGGTACAGGCTG
121209	119296	CAGGCATAATGGTACAGGCT
121210	119297	CCAGGCATAATGGTACAGGC
121211	119298	GCCAGGCATAATGGTACAGG
121212	119299	AGCCAGGCATAATGGTACAG
121213	119300	TAGCCAGGCATAATGGTACA
121214	119301	TTAGCCAGGCATAATGGTAC
121215	119302	ATTAGCCAGGCATAATGGTA
121216	119303	AATTAGCCAGGCATAATGGT
121217	119304	AAATTAGCCAGGCATAATGG
121218	119305	AAAATTAGCCAGGCATAATG
121219	119306	TAAAATTAGCCAGGCATAAT
121220	119307	CTAAAATTAGCCAGGCATAA

22927	21014	TAAGCAATGCATAAACATAG
22928	21015	TTAAGCAATGCATAAACATA
22929	21016	ATTAAGCAATGCATAAACAT
22930	21017	CATTAAGCAATGCATAAACA
22931	21018	TCATTAAGCAATGCATAAAC
22932	21019	ATCATTAAGCAATGCATAAA
22933	21020	CATCATTAAGCAATGCATAA
22934	21021	CCATCATTAAGCAATGCATA
22935	21022	CCCATCATTAAGCAATGCAT
22936	21023	CCCCATCATTAAGCAATGCA
22937	21024	TCCCCATCATTAAGCAATGC
22938	21025	ATCCCCATCATTAAGCAATG
22939	21026	CATCCCCATCATTAAGCAAT
22940	21027	ACATCCCCATCATTAAGCAA
22941	21028	CACATCCCCATCATTAAGCA
22942	21029	ACACATCCCCATCATTAAGC
22943	21030	AACACATCCCCATCATTAAG
22944	21031	AAACACATCCCCATCATTAA
22945	21032	AAAACACATCCCCATCATTA
22946	21033	CAAAACACATCCCCATCATT
22947	21034	TCAAAACACATCCCCATCAT
22948	21035	CTCAAAACACATCCCCATCA
22949	21036	TCTCAAAACACATCCCCATC
22950	21037	TTCTCAAAACACATCCCCAT
22951	21038	TTTCTCAAAACACATCCCCA
22952	21039	ATTTCTCAAAACACATCCCC
22953	21040	AATTTCTCAAAACACATCCC
22954	21041	AAATTTCTCAAAACACATCC
22955	21042	AAAATTTCTCAAAACACATC
22956	21043	AAAAATTTCTCAAAACACAT
22957	21044	AAAAAATTTCTCAAAACACA
22958	21045	GAAAAAATTTCTCAAAACAC
22959	21046	CGAAAAAATTTCTCAAAACA
22960	21047	CCGAAAAAATTTCTCAAAAC
22961	21048	ACCGAAAAAATTTCTCAAAA
22962	21049	CACCGAAAAAATTTCTCAAA
22963	21050	TCACCGAAAAAATTTCTCAA
22964	21051	ATCACCGAAAAAATTTCTCA
22965	21052	GATCACCGAAAAAATTTCTC
22966	21053	AGATCACCGAAAAAATTTCT
22967	21054	AAGATCACCGAAAAAATTTC
22968	21055	TAAGATCACCGAAAAAATTT
22969	21056	ATAAGATCACCGAAAAAATT
22970	21057	GATAAGATCACCGAAAAAAT
22971	21058	TGATAAGATCACCGAAAAAA
22972	21059	ATGATAAGATCACCGAAAAA
22973	21060	AATGATAAGATCACCGAAAA
22974	21061	CAATGATAAGATCACCGAAA
22975	21062	ACAATGATAAGATCACCGAA
22976	21063	TACAATGATAAGATCACCGA
22977	21064	GTACAATGATAAGATCACCG
22978	21065	TGTACAATGATAAGATCACC
22979	21066	TTGTACAATGATAAGATCAC
22980	21067	TTTGTACAATGATAAGATCA
22981	21068	ATTTGTACAATGATAAGATC
22982	21069	TATTTGTACAATGATAAGAT
22983	21070	ATATTTGTACAATGATAAGA
22984	21071	TATATTTGTACAATGATAAG
22985	21072	CTATATTTGTACAATGATAA
22986	21073	TCTATATTTGTACAATGATA
22987	21074	CTCTATATTTGTACAATGAT
22988	21075	ACTCTATATTTGTACAATGA
22989	21076	AACTCTATATTTGTACAATG
22990	21077	AAACTCTATATTTGTACAAT
22991	21078	TAAACTCTATATTTGTACAA
22992	21079	GTAAACTCTATATTTGTACA
22993	21080	AGTAAACTCTATATTTGTAC
22994	21081	AAGTAAACTCTATATTTGTA
22995	21082	TAAGTAAACTCTATATTTGT
22996	21083	GTAAGTAAACTCTATATTTG
22997	21084	TGTAAGTAAACTCTATATTT

72074	70161	GAAACAAAATTGTATCACCT
72075	70162	AGAAACAAAATTGTATCACC
72076	70163	AAGAAACAAAATTGTATCAC
72077	70164	GAAGAAACAAAATTGTATCA
72078	70165	GGAAGAAACAAAATTGTATC
72079	70166	AGGAAGAAACAAAATTGTAT
72080	70167	GAGGAAGAAACAAAATTGTA
72081	70168	GGAGGAAGAAACAAAATTGT
72082	70169	TGGAGGAAGAAACAAAATTG
72083	70170	TTGGAGGAAGAAACAAAATT
72084	70171	GTTGGAGGAAGAAACAAAAT
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72087	70174	GATGTTGGAGGAAGAAACAA
72088	70175	CGATGTTGGAGGAAGAAACA
72089	70176	GCGATGTTGGAGGAAGAAAC
72090	70177	GGCGATGTTGGAGGAAGAAA
72091	70178	AGGCGATGTTGGAGGAAGAA
72092	70179	CAGGCGATGTTGGAGGAAGA
72093	70180	GCAGGCGATGTTGGAGGAAG
72094	70181	AGCAGGCGATGTTGGAGGAA
72095	70182	TAGCAGGCGATGTTGGAGGA
72096	70183	CTAGCAGGCGATGTTGGAGG
72097	70184	ACTAGCAGGCGATGTTGGAG
72098	70185	GACTAGCAGGCGATGTTGGA
72099	70186	AGACTAGCAGGCGATGTTGG
72100	70187	TAGACTAGCAGGCGATGTTG
72101	70188	CTAGACTAGCAGGCGATGTT
72102	70189	TCTAGACTAGCAGGCGATGT
72103	70190	CTCTAGACTAGCAGGCGATG
72104	70191	CCTCTAGACTAGCAGGCGAT
72105	70192	GCCTCTAGACTAGCAGGCGA
72106	70193	AGCCTCTAGACTAGCAGGCG
72107	70194	AAGCCTCTAGACTAGCAGGC
72108	70195	AAAGCCTCTAGACTAGCAGG
72109	70196	AAAAGCCTCTAGACTAGCAG
72110	70197	TAAAAGCCTCTAGACTAGCA
72111	70198	ATAAAAGCCTCTAGACTAGC
72112	70199	TATAAAAGCCTCTAGACTAG
72113	70200	TTATAAAAGCCTCTAGACTA
72114	70201	TTTATAAAAGCCTCTAGACT
72115	70202	ATTTATAAAAGCCTCTAGAC
72116	70203	AATTTATAAAAGCCTCTAGA
72117	70204	CAATTTATAAAAGCCTCTAG
72118	70205	TCAATTTATAAAAGCCTCTA
72119	70206	TTCAATTTATAAAAGCCTCT
72120	70207	TTTCAATTTATAAAAGCCTC
72121	70208	TTTTCAATTTATAAAAGCCT
72122	70209	TTTTTCAATTTATAAAAGCC
72123	70210	GTTTTTCAATTTATAAAAGC
72124	70211	AGTTTTTCAATTTATAAAAG
72125	70212	TAGTTTTTCAATTTATAAAA
72126	70213	TTAGTTTTTCAATTTATAAA
72127	70214	ATTAGTTTTTCAATTTATAA
72128	70215	AATTAGTTTTTCAATTTATA
72129	70216	GAATTAGTTTTTCAATTTAT
72130	70217	AGAATTAGTTTTTCAATTTA
72131	70218	AAGAATTAGTTTTTCAATTT
72132	70219	AAAGAATTAGTTTTTCAATT
72133	70220	TAAAGAATTAGTTTTTCAAT
72134	70221	ATAAAGAATTAGTTTTTCAA
72135	70222	GATAAAGAATTAGTTTTTCA
72136	70223	TGATAAAGAATTAGTTTTTC
72137	70224	ATGATAAAGAATTAGTTTTT
72138	70225	GATGATAAAGAATTAGTTTT
72139	70226	AGATGATAAAGAATTAGTTT
72140	70227	GAGATGATAAAGAATTAGTT
72141	70228	TGAGATGATAAAGAATTAGT
72142	70229	ATGAGATGATAAAGAATTAG
72143	70230	GATGAGATGATAAAGAATTA
72144	70231	AGATGAGATGATAAAGAATT

121221	119308	TCTAAAATTAGCCAGGCATA
121222	119309	TTCTAAAATTAGCCAGGCAT
121223	119310	ATTCTAAAATTAGCCAGGCA
121224	119311	AATTCTAAAATTAGCCAGGC
121225	119312	AAATTCTAAAATTAGCCAGG
121226	119313	TAAATTCTAAAATTAGCCAG
121227	119314	ATAAATTCTAAAATTAGCCA
121228	119315	GATAAATTCTAAAATTAGCC
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121232	119319	TTAAGATAAATTCTAAAATT
121233	119320	TTTAAGATAAATTCTAAAAT
121234	119321	CTTTAAGATAAATTCTAAAA
121235	119322	ACTTTAAGATAAATTCTAAA
121236	119323	TACTTTAAGATAAATTCTAA
121237	119324	ATACTTTAAGATAAATTCTA
121238	119325	TATACTTTAAGATAAATTCT
121239	119326	TTATACTTTAAGATAAATTC
121240	119327	TTTATACTTTAAGATAAATT
121241	119328	TTTTATACTTTAAGATAAAT
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121243	119330	CATTTTATACTTTAAGATAA
121244	119331	ACATTTTATACTTTAAGATA
121245	119332	CACATTTTATACTTTAAGAT
121246	119333	TCACATTTTATACTTTAAGA
121247	119334	TTCACATTTTATACTTTAAG
121248	119335	ATTCACATTTTATACTTTAA
121249	119336	GATTCACATTTTATACTTTA
121250	119337	GGATTCACATTTTATACTTT
121251	119338	TGGATTCACATTTTATACTT
121252	119339	TTGGATTCACATTTTATACT
121253	119340	ATTGGATTCACATTTTATAC
121254	119341	AATTGGATTCACATTTTATA
121255	119342	AAATTGGATTCACATTTTAT
121256	119343	TAAATTGGATTCACATTTTA
121257	119344	ATAAATTGGATTCACATTTT
121258	119345	GATAAATTGGATTCACATTT
121259	119346	AGATAAATTGGATTCACATT
121260	119347	AAGATAAATTGGATTCACAT
121261	119348	CAAGATAAATTGGATTCACA
121262	119349	ACAAGATAAATTGGATTCAC
121263	119350	AACAAGATAAATTGGATTCA
121264	119351	GAACAAGATAAATTGGATTC
121265	119352	AGAACAAGATAAATTGGATT
121266	119353	TAGAACAAGATAAATTGGAT
121267	119354	TTAGAACAAGATAAATTGGA
121268	119355	TTTAGAACAAGATAAATTGG
121269	119356	ATTTAGAACAAGATAAATTG
121270	119357	CATTTAGAACAAGATAAATT
121271	119358	TCATTTAGAACAAGATAAAT
121272	119359	GTCATTTAGAACAAGATAAA
121273	119360	AGTCATTTAGAACAAGATAA
121274	119361	TAGTCATTTAGAACAAGATA
121275	119362	ATAGTCATTTAGAACAAGAT
121276	119363	GATAGTCATTTAGAACAAGA
121277	119364	GGATAGTCATTTAGAACAAG
121278	119365	TGGATAGTCATTTAGAACAA
121279	119366	TTGGATAGTCATTTAGAACA
121280	119367	TTTGGATAGTCATTTAGAAC
121281	119368	TTTTGGATAGTCATTTAGAA
121282	119369	ATTTTGGATAGTCATTTAGA
121283	119370	CATTTTGGATAGTCATTTAG
121284	119371	ACATTTTGGATAGTCATTTA
121285	119372	AACATTTTGGATAGTCATTT
121286	119373	AAACATTTTGGATAGTCATT
121287	119374	AAAACATTTTGGATAGTCAT
121288	119375	TAAAACATTTTGGATAGTCA
121289	119376	TTAAAACATTTTGGATAGTC
121290	119377	GTTAAAACATTTTGGATAGT
121291	119378	GGTTAAAACATTTTGGATAG

22998	21085	GTGTAAGTAAACTCTATATT
22999	21086	TGTGTAAGTAAACTCTATAT
23000	21087	TTGTGTAAGTAAACTCTATA
23001	21088	CTTGTGTAAGTAAACTCTAT
23002	21089	GCTTGTGTAAGTAAACTCTA
23003	21090	GGCTTGTGTAAGTAAACTCT
23004	21091	AGGCTTGTGTAAGTAAACTC
23005	21092	TAGGCTTGTGTAAGTAAACT
23006	21093	CTAGGCTTGTGTAAGTAAAC
23007	21094	TCTAGGCTTGTGTAAGTAAA
23008	21095	ATCTAGGCTTGTGTAAGTAA
23009	21096	CATCTAGGCTTGTGTAAGTA
23010	21097	CCATCTAGGCTTGTGTAAGT
23011	21098	ACCATCTAGGCTTGTGTAAG
23012	21099	TACCATCTAGGCTTGTGTAA
23013	21100	ATACCATCTAGGCTTGTGTA
23014	21101	TATACCATCTAGGCTTGTGT
23015	21102	GTATACCATCTAGGCTTGTG
23016	21103	GGTATACCATCTAGGCTTGT
23017	21104	AGGTATACCATCTAGGCTTG
23018	21105	TAGGTATACCATCTAGGCTT
23019	21106	GTAGGTATACCATCTAGGCT
23020	21107	AGTAGGTATACCATCTAGGC
23021	21108	TAGTAGGTATACCATCTAGG
23022	21109	CTAGTAGGTATACCATCTAG
23023	21110	TCTAGTAGGTATACCATCTA
23024	21111	GTCTAGTAGGTATACCATCT
23025	21112	TGTCTAGTAGGTATACCATC
23026	21113	GTGTCTAGTAGGTATACCAT
23027	21114	TGTGTCTAGTAGGTATACCA
23028	21115	ATGTGTCTAGTAGGTATACC
23029	21116	TATGTGTCTAGTAGGTATAC
23030	21117	CTATGTGTCTAGTAGGTATA
23031	21118	CCTATGTGTCTAGTAGGTAT
23032	21119	GCCTATGTGTCTAGTAGGTA
23033	21120	AGCCTATGTGTCTAGTAGGT
23034	21121	CAGCCTATGTGTCTAGTAGG
23035	21122	ACAGCCTATGTGTCTAGTAG
23036	21123	GACAGCCTATGTGTCTAGTA
23037	21124	CGACAGCCTATGTGTCTAGT
23038	21125	ACGACAGCCTATGTGTCTAG
23039	21126	TACGACAGCCTATGTGTCTA
23040	21127	GTACGACAGCCTATGTGTCT
23041	21128	TGTACGACAGCCTATGTGTC
23042	21129	CTGTACGACAGCCTATGTGT
23043	21130	TCTGTACGACAGCCTATGTG
23044	21131	CTCTGTACGACAGCCTATGT
23045	21132	ACTCTGTACGACAGCCTATG
23046	21133	TACTCTGTACGACAGCCTAT
23047	21134	ATACTCTGTACGACAGCCTA
23048	21135	AATACTCTGTACGACAGCCT
23049	21136	TAATACTCTGTACGACAGCC
23050	21137	GTAATACTCTGTACGACAGC
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23052	21139	GAGTAATACTCTGTACGACA
23053	21140	AGAGTAATACTCTGTACGAC
23054	21141	AAGAGTAATACTCTGTACGA
23055	21142	TAAGAGTAATACTCTGTACG
23056	21143	CTAAGAGTAATACTCTGTAC
23057	21144	CCTAAGAGTAATACTCTGTA
23058	21145	GCCTAAGAGTAATACTCTGT
23059	21146	AGCCTAAGAGTAATACTCTG
23060	21147	TAGCCTAAGAGTAATACTCT
23061	21148	GTAGCCTAAGAGTAATACTC
23062	21149	TGTAGCCTAAGAGTAATACT
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23064	21151	TTTGTAGCCTAAGAGTAATA
23065	21152	ATTTGTAGCCTAAGAGTAAT
23066	21153	GATTTGTAGCCTAAGAGTAA
23067	21154	AGATTTGTAGCCTAAGAGTA
23068	21155	CAGATTTGTAGCCTAAGAGT

72145	70232	CAGATGAGATGATAAAGAAT
72146	70233	TCAGATGAGATGATAAAGAA
72147	70234	ATCAGATGAGATGATAAAGA
72148	70235	CATCAGATGAGATGATAAAG
72149	70236	CCATCAGATGAGATGATAAA
72150	70237	ACCATCAGATGAGATGATAA
72151	70238	AACCATCAGATGAGATGATA
72152	70239	AAACCATCAGATGAGATGAT
72153	70240	AAAACCATCAGATGAGATGA
72154	70241	AAAAACCATCAGATGAGATG
72155	70242	TAAAAACCATCAGATGAGAT
72156	70243	ATAAAAACCATCAGATGAGA
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72158	70245	ACATAAAAACCATCAGATGA
72159	70246	AACATAAAAACCATCAGATG
72160	70247	AAACATAAAAACCATCAGAT
72161	70248	AAAACATAAAAACCATCAGA
72162	70249	AAAAACATAAAAACCATCAG
72163	70250	GAAAAACATAAAAACCATCA
72164	70251	GGAAAAACATAAAAACCATC
72165	70252	AGGAAAAACATAAAAACCAT
72166	70253	AAGGAAAAACATAAAAACCA
72167	70254	AAAGGAAAAACATAAAAACC
72168	70255	AAAAGGAAAAACATAAAAAC
72169	70256	AAAAAGGAAAAACATAAAAA
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72172	70259	AGAAAAAAGGAAAAACATAA
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72183	70270	CAGGTATAGAGAGAAAAAAG
72184	70271	ACAGGTATAGAGAGAAAAAA
72185	70272	TACAGGTATAGAGAGAAAAA
72186	70273	CTACAGGTATAGAGAGAAAA
72187	70274	ACTACAGGTATAGAGAGAAA
72188	70275	AACTACAGGTATAGAGAGAA
72189	70276	GAACTACAGGTATAGAGAGA
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72192	70279	AAGGAACTACAGGTATAGAG
72193	70280	GAAGGAACTACAGGTATAGA
72194	70281	TGAAGGAACTACAGGTATAG
72195	70282	CTGAAGGAACTACAGGTATA
72196	70283	TCTGAAGGAACTACAGGTAT
72197	70284	TTCTGAAGGAACTACAGGTA
72198	70285	TTTCTGAAGGAACTACAGGT
72199	70286	GTTTCTGAAGGAACTACAGG
72200	70287	TGTTTCTGAAGGAACTACAG
72201	70288	CTGTTTCTGAAGGAACTACA
72202	70289	CCTGTTTCTGAAGGAACTAC
72203	70290	ACCTGTTTCTGAAGGAACTA
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72205	70292	TTACCTGTTTCTGAAGGAAC
72206	70293	GTTACCTGTTTCTGAAGGAA
72207	70294	TGTTACCTGTTTCTGAAGGA
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72209	70296	AGTGTTACCTGTTTCTGAAG
72210	70297	AAGTGTTACCTGTTTCTGAA
72211	70298	AAAGTGTTACCTGTTTCTGA
72212	70299	AAAAGTGTTACCTGTTTCTG
72213	70300	GAAAAGTGTTACCTGTTTCT
72214	70301	AGAAAAGTGTTACCTGTTTC
72215	70302	TAGAAAAGTGTTACCTGTTT

121292	119379	TGGTTAAAACATTTTGGATA
121293	119380	CTGGTTAAAACATTTTGGAT
121294	119381	ACTGGTTAAAACATTTTGGA
121295	119382	AACTGGTTAAAACATTTTGG
121296	119383	AAACTGGTTAAAACATTTTG
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121298	119385	TAAAACTGGTTAAAACATTT
121299	119386	ATAAAACTGGTTAAAACATT
121300	119387	AATAAAACTGGTTAAAACAT
121301	119388	TAATAAAACTGGTTAAAACA
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121303	119390	ACTAATAAAACTGGTTAAAA
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121306	119393	CAGACTAATAAAACTGGTTA
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121308	119395	TACAGACTAATAAAACTGGT
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121310	119397	ATTACAGACTAATAAAACTG
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121313	119400	TAAATTACAGACTAATAAAA
121314	119401	GTAAATTACAGACTAATAAA
121315	119402	TGTAAATTACAGACTAATAA
121316	119403	ATGTAAATTACAGACTAATA
121317	119404	TATGTAAATTACAGACTAAT
121318	119405	GTATGTAAATTACAGACTAA
121319	119406	TGTATGTAAATTACAGACTA
121320	119407	TTGTATGTAAATTACAGACT
121321	119408	CTTGTATGTAAATTACAGAC
121322	119409	TCTTGTATGTAAATTACAGA
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121324	119411	TTTCTTGTATGTAAATTACA
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121333	119420	GATGAGCATTTTCTTGTATG
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121335	119422	AAGATGAGCATTTTCTTGTA
121336	119423	AAAGATGAGCATTTTCTTGT
121337	119424	AAAAGATGAGCATTTTCTTG
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121339	119426	TAAAAAGATGAGCATTTTCT
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121345	119432	TAAACATAAAAAGATGAGCA
121346	119433	GTAAACATAAAAAGATGAGC
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121356	119443	TCATTAAAATGTAAACATAA
121357	119444	CTCATTAAAATGTAAACATA
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121359	119446	AACTCATTAAAATGTAAACA
121360	119447	AAACTCATTAAAATGTAAAC
121361	119448	AAAACTCATTAAAATGTAAA
121362	119449	CAAAACTCATTAAAATGTAA

23069	21156	ACAGATTTGTAGCCTAAGAG
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23071	21158	ATACAGATTTGTAGCCTAAG
23072	21159	TATACAGATTTGTAGCCTAA
23073	21160	CTATACAGATTTGTAGCCTA
23074	21161	GCTATACAGATTTGTAGCCT
23075	21162	TGCTATACAGATTTGTAGCC
23076	21163	ATGCTATACAGATTTGTAGC
23077	21164	CATGCTATACAGATTTGTAG
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23082	21169	CGCAACATGCTATACAGATT
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23084	21171	ACCGCAACATGCTATACAGA
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23086	21173	GTACCGCAACATGCTATACA
23087	21174	AGTACCGCAACATGCTATAC
23088	21175	CAGTACCGCAACATGCTATA
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23090	21177	TTCAGTACCGCAACATGCTA
23091	21178	GTTCAGTACCGCAACATGCT
23092	21179	TGTTCAGTACCGCAACATGC
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23099	21186	CCAACAGTGTTCAGTACCGC
23100	21187	GCCAACAGTGTTCAGTACCG
23101	21188	TGCCAACAGTGTTCAGTACC
23102	21189	CTGCCAACAGTGTTCAGTAC
23103	21190	TCTGCCAACAGTGTTCAGTA
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23105	21192	CATCTGCCAACAGTGTTCAG
23106	21193	ACATCTGCCAACAGTGTTCA
23107	21194	TACATCTGCCAACAGTGTTC
23108	21195	TTACATCTGCCAACAGTGTT
23109	21196	GTTACATCTGCCAACAGTGT
23110	21197	TGTTACATCTGCCAACAGTG
23111	21198	ATGTTACATCTGCCAACAGT
23112	21199	TATGTTACATCTGCCAACAG
23113	21200	TTATGTTACATCTGCCAACA
23114	21201	ATTATGTTACATCTGCCAAC
23115	21202	CATTATGTTACATCTGCCAA
23116	21203	ACATTATGTTACATCTGCCA
23117	21204	AACATTATGTTACATCTGCC
23118	21205	TAACATTATGTTACATCTGC
23119	21206	TTAACATTATGTTACATCTG
23120	21207	CTTAACATTATGTTACATCT
23121	21208	ACTTAACATTATGTTACATC
23122	21209	TACTTAACATTATGTTACAT
23123	21210	ATACTTAACATTATGTTACA
23124	21211	AATACTTAACATTATGTTAC
23125	21212	AAATACTTAACATTATGTTA
23126	21213	CAAATACTTAACATTATGTT
23127	21214	ACAAATACTTAACATTATGT
23128	21215	CACAAATACTTAACATTATG
23129	21216	TCACAAATACTTAACATTAT
23130	21217	TTCACAAATACTTAACATTA
23131	21218	ATTCACAAATACTTAACATT
23132	21219	GATTCACAAATACTTAACAT
23133	21220	AGATTCACAAATACTTAACA
23134	21221	TAGATTCACAAATACTTAAC
23135	21222	TTAGATTCACAAATACTTAA
23136	21223	TTTAGATTCACAAATACTTA
23137	21224	GTTTAGATTCACAAATACTT
23138	21225	TGTTTAGATTCACAAATACT
23139	21226	ATGTTTAGATTCACAAATAC

72216	70303	TTAGAAAAGTGTTACCTGTT
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72219	70306	CTATTAGAAAAGTGTTACCT
72220	70307	ACTATTAGAAAAGTGTTACC
72221	70308	GACTATTAGAAAAGTGTTAC
72222	70309	TGACTATTAGAAAAGTGTTA
72223	70310	GTGACTATTAGAAAAGTGTT
72224	70311	CGTGACTATTAGAAAAGTGT
72225	70312	ACGTGACTATTAGAAAAGTG
72226	70313	AACGTGACTATTAGAAAAGT
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72229	70316	TACAACGTGACTATTAGAAA
72230	70317	ATACAACGTGACTATTAGAA
72231	70318	AATACAACGTGACTATTAGA
72232	70319	GAATACAACGTGACTATTAG
72233	70320	AGAATACAACGTGACTATTA
72234	70321	AAGAATACAACGTGACTATT
72235	70322	CAAGAATACAACGTGACTAT
72236	70323	GCAAGAATACAACGTGACTA
72237	70324	TGCAAGAATACAACGTGACT
72238	70325	ATGCAAGAATACAACGTGAC
72239	70326	GATGCAAGAATACAACGTGA
72240	70327	AGATGCAAGAATACAACGTG
72241	70328	AAGATGCAAGAATACAACGT
72242	70329	CAAGATGCAAGAATACAACG
72243	70330	ACAAGATGCAAGAATACAAC
72244	70331	AACAAGATGCAAGAATACAA
72245	70332	CAACAAGATGCAAGAATACA
72246	70333	ACAACAAGATGCAAGAATAC
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72252	70339	ATTGTAACAACAAGATGCAA
72253	70340	CATTGTAACAACAAGATGCA
72254	70341	GCATTGTAACAACAAGATGC
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72258	70345	AAAAGCATTGTAACAACAAG
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72263	70350	GAAACAAAAGCATTGTAACA
72264	70351	AGAAACAAAAGCATTGTAAC
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72273	70360	CCTATGGTGAGAAACAAAAG
72274	70361	CCCTATGGTGAGAAACAAAA
72275	70362	CCCCTATGGTGAGAAACAAA
72276	70363	TCCCCTATGGTGAGAAACAA
72277	70364	ATCCCCTATGGTGAGAAACA
72278	70365	CATCCCCTATGGTGAGAAAC
72279	70366	TCATCCCCTATGGTGAGAAA
72280	70367	ATCATCCCCTATGGTGAGAA
72281	70368	CATCATCCCCTATGGTGAGA
72282	70369	CCATCATCCCCTATGGTGAG
72283	70370	TCCATCATCCCCTATGGTGA
72284	70371	TTCCATCATCCCCTATGGTG
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121363	119450	TCAAAACTCATTAAAATGTA
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121375	119462	CAAATATATTTGTCAAAACT
121376	119463	GCAAATATATTTGTCAAAAC
121377	119464	AGCAAATATATTTGTCAAAA
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121379	119466	TGAGCAAATATATTTGTCAA
121380	119467	ATGAGCAAATATATTTGTCA
121381	119468	CATGAGCAAATATATTTGTC
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121384	119471	TTACATGAGCAAATATATTT
121385	119472	GTTACATGAGCAAATATATT
121386	119473	AGTTACATGAGCAAATATAT
121387	119474	TAGTTACATGAGCAAATATA
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121389	119476	AGTAGTTACATGAGCAAATA
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121391	119478	CAAGTAGTTACATGAGCAAA
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121393	119480	AGCAAGTAGTTACATGAGCA
121394	119481	AAGCAAGTAGTTACATGAGC
121395	119482	GAAGCAAGTAGTTACATGAG
121396	119483	TGAAGCAAGTAGTTACATGA
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121400	119487	CTGATGAAGCAAGTAGTTAC
121401	119488	ACTGATGAAGCAAGTAGTTA
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121403	119490	TCACTGATGAAGCAAGTAGT
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121405	119492	CTTCACTGATGAAGCAAGTA
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121414	119501	GTTTTCCATCTTCACTGATG
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121416	119503	ATGTTTTCCATCTTCACTGA
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121419	119506	ACAATGTTTTCCATCTTCAC
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23140	21227	TATGTTTAGATTCACAAATA
23141	21228	ATATGTTTAGATTCACAAAT
23142	21229	GATATGTTTAGATTCACAAA
23143	21230	AGATATGTTTAGATTCACAA
23144	21231	TAGATATGTTTAGATTCACA
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23146	21233	TTTAGATATGTTTAGATTCA
23147	21234	GTTTAGATATGTTTAGATTC
23148	21235	TGTTTAGATATGTTTAGATT
23149	21236	ATGTTTAGATATGTTTAGAT
23150	21237	TATGTTTAGATATGTTTAGA
23151	21238	CTATGTTTAGATATGTTTAG
23152	21239	TCTATGTTTAGATATGTTTA
23153	21240	TTCTATGTTTAGATATGTTT
23154	21241	TTTCTATGTTTAGATATGTT
23155	21242	TTTTCTATGTTTAGATATGT
23156	21243	CTTTTCTATGTTTAGATATG
23157	21244	CCTTTTCTATGTTTAGATAT
23158	21245	ACCTTTTCTATGTTTAGATA
23159	21246	CACCTTTTCTATGTTTAGAT
23160	21247	TCACCTTTTCTATGTTTAGA
23161	21248	CTCACCTTTTCTATGTTTAG
23162	21249	ACTCACCTTTTCTATGTTTA
23163	21250	TACTCACCTTTTCTATGTTT
23164	21251	TTACTCACCTTTTCTATGTT
23165	21252	TTTACTCACCTTTTCTATGT
23166	21253	TTTTACTCACCTTTTCTATG
23167	21254	TTTTTACTCACCTTTTCTAT
23168	21255	ATTTTTACTCACCTTTTCTA
23169	21256	TATTTTTACTCACCTTTTCT
23170	21257	GTATTTTTACTCACCTTTTC
23171	21258	TGTATTTTTACTCACCTTTT
23172	21259	CTGTATTTTTACTCACCTTT
23173	21260	GCTGTATTTTTACTCACCTT
23174	21261	CGCTGTATTTTTACTCACCT
23175	21262	ACGCTGTATTTTTACTCACC
23176	21263	TACGCTGTATTTTTACTCAC
23177	21264	TTACGCTGTATTTTTACTCA
23178	21265	TTTACGCTGTATTTTTACTC
23179	21266	TTTTACGCTGTATTTTTACT
23180	21267	CTTTTACGCTGTATTTTTAC
23181	21268	TCTTTTACGCTGTATTTTTA
23182	21269	ATCTTTTACGCTGTATTTTT
23183	21270	TATCTTTTACGCTGTATTTT
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23185	21272	TTTATCTTTTACGCTGTATT
23186	21273	TTTTATCTTTTACGCTGTAT
23187	21274	CTTTTATCTTTTACGCTGTA
23188	21275	ACTTTTATCTTTTACGCTGT
23189	21276	CACTTTTATCTTTTACGCTG
23190	21277	CCACTTTTATCTTTTACGCT
23191	21278	ACCACTTTTATCTTTTACGC
23192	21279	TACCACTTTTATCTTTTACG
23193	21280	ATACCACTTTTATCTTTTAC
23194	21281	TATACCACTTTTATCTTTTA
23195	21282	ATATACCACTTTTATCTTTT
23196	21283	GATATACCACTTTTATCTTT
23197	21284	AGATATACCACTTTTATCTT
23198	21285	CAGATATACCACTTTTATCT
23199	21286	TCAGATATACCACTTTTATC
23200	21287	TTCAGATATACCACTTTTAT
23201	21288	ATTCAGATATACCACTTTTA
23202	21289	TATTCAGATATACCACTTTT
23203	21290	CTATTCAGATATACCACTTT
23204	21291	CCTATTCAGATATACCACTT
23205	21292	ACCTATTCAGATATACCACT
23206	21293	GACCTATTCAGATATACCAC
23207	21294	TGACCTATTCAGATATACCA
23208	21295	GTGACCTATTCAGATATACC
23209	21296	AGTGACCTATTCAGATATAC
23210	21297	AAGTGACCTATTCAGATATA

72287	70374	ATTTTCCATCATCCCCTATG
72288	70375	AATTTTCCATCATCCCCTAT
72289	70376	TAATTTTCCATCATCCCCTA
72290	70377	TTAATTTTCCATCATCCCCT
72291	70378	ATTAATTTTCCATCATCCCC
72292	70379	TATTAATTTTCCATCATCCC
72293	70380	ATATTAATTTTCCATCATCC
72294	70381	AATATTAATTTTCCATCATC
72295	70382	GAATATTAATTTTCCATCAT
72296	70383	AGAATATTAATTTTCCATCA
72297	70384	AAGAATATTAATTTTCCATC
72298	70385	AAAGAATATTAATTTTCCAT
72299	70386	CAAAGAATATTAATTTTCCA
72300	70387	TCAAAGAATATTAATTTTCC
72301	70388	GTCAAAGAATATTAATTTTC
72302	70389	AGTCAAAGAATATTAATTTT
72303	70390	AAGTCAAAGAATATTAATTT
72304	70391	TAAGTCAAAGAATATTAATT
72305	70392	ATAAGTCAAAGAATATTAAT
72306	70393	CATAAGTCAAAGAATATTAA
72307	70394	CCATAAGTCAAAGAATATTA
72308	70395	GCCATAAGTCAAAGAATATT
72309	70396	TGCCATAAGTCAAAGAATAT
72310	70397	ATGCCATAAGTCAAAGAATA
72311	70398	AATGCCATAAGTCAAAGAAT
72312	70399	CAATGCCATAAGTCAAAGAA
72313	70400	CCAATGCCATAAGTCAAAGA
72314	70401	ACCAATGCCATAAGTCAAAG
72315	70402	TACCAATGCCATAAGTCAAA
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72317	70404	TTTACCAATGCCATAAGTCA
72318	70405	TTTTACCAATGCCATAAGTC
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72320	70407	GATTTTACCAATGCCATAAG
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72324	70411	TGCAGATTTTACCAATGCCA
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72327	70414	GCATGCAGATTTTACCAATG
72328	70415	TGCATGCAGATTTTACCAAT
72329	70416	TTGCATGCAGATTTTACCAA
72330	70417	TTTGCATGCAGATTTTACCA
72331	70418	ATTTGCATGCAGATTTTACC
72332	70419	AATTTGCATGCAGATTTTAC
72333	70420	GAATTTGCATGCAGATTTTA
72334	70421	GGAATTTGCATGCAGATTTT
72335	70422	GGGAATTTGCATGCAGATTT
72336	70423	TGGGAATTTGCATGCAGATT
72337	70424	GTGGGAATTTGCATGCAGAT
72338	70425	TGTGGGAATTTGCATGCAGA
72339	70426	CTGTGGGAATTTGCATGCAG
72340	70427	ACTGTGGGAATTTGCATGCA
72341	70428	AACTGTGGGAATTTGCATGC
72342	70429	CAACTGTGGGAATTTGCATG
72343	70430	GCAACTGTGGGAATTTGCAT
72344	70431	GGCAACTGTGGGAATTTGCA
72345	70432	AGGCAACTGTGGGAATTTGC
72346	70433	CAGGCAACTGTGGGAATTTG
72347	70434	ACAGGCAACTGTGGGAATTT
72348	70435	TACAGGCAACTGTGGGAATT
72349	70436	CTACAGGCAACTGTGGGAAT
72350	70437	TCTACAGGCAACTGTGGGAA
72351	70438	ATCTACAGGCAACTGTGGGA
72352	70439	AATCTACAGGCAACTGTGGG
72353	70440	TAATCTACAGGCAACTGTGG
72354	70441	CTAATCTACAGGCAACTGTG
72355	70442	TCTAATCTACAGGCAACTGT
72356	70443	CTCTAATCTACAGGCAACTG
72357	70444	GCTCTAATCTACAGGCAACT

121434	119521	AGAAGAGGAACAGGCACAAT
121435	119522	GAGAAGAGGAACAGGCACAA
121436	119523	AGAGAAGAGGAACAGGCACA
121437	119524	CAGAGAAGAGGAACAGGCAC
121438	119525	ACAGAGAAGAGGAACAGGCA
121439	119526	GACAGAGAAGAGGAACAGGC
121440	119527	GGACAGAGAAGAGGAACAGG
121441	119528	TGGACAGAGAAGAGGAACAG
121442	119529	TTGGACAGAGAAGAGGAACA
121443	119530	GTTGGACAGAGAAGAGGAAC
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121449	119536	AGTACAGTTGGACAGAGAAG
121450	119537	AAGTACAGTTGGACAGAGAA
121451	119538	AAAGTACAGTTGGACAGAGA
121452	119539	TAAAGTACAGTTGGACAGAG
121453	119540	ATAAAGTACAGTTGGACAGA
121454	119541	AATAAAGTACAGTTGGACAG
121455	119542	TAATAAAGTACAGTTGGACA
121456	119543	GTAATAAAGTACAGTTGGAC
121457	119544	GGTAATAAAGTACAGTTGGA
121458	119545	TGGTAATAAAGTACAGTTGG
121459	119546	GTGGTAATAAAGTACAGTTG
121460	119547	AGTGGTAATAAAGTACAGTT
121461	119548	TAGTGGTAATAAAGTACAGT
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121463	119550	GCTAGTGGTAATAAAGTACA
121464	119551	AGCTAGTGGTAATAAAGTAC
121465	119552	GAGCTAGTGGTAATAAAGTA
121466	119553	GGAGCTAGTGGTAATAAAGT
121467	119554	TGGAGCTAGTGGTAATAAAG
121468	119555	CTGGAGCTAGTGGTAATAAA
121469	119556	ACTGGAGCTAGTGGTAATAA
121470	119557	AACTGGAGCTAGTGGTAATA
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121476	119563	CTGGTTAACTGGAGCTAGTG
121477	119564	ACTGGTTAACTGGAGCTAGT
121478	119565	TACTGGTTAACTGGAGCTAG
121479	119566	TTACTGGTTAACTGGAGCTA
121480	119567	ATTACTGGTTAACTGGAGCT
121481	119568	GATTACTGGTTAACTGGAGC
121482	119569	AGATTACTGGTTAACTGGAG
121483	119570	CAGATTACTGGTTAACTGGA
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121485	119572	GGCAGATTACTGGTTAACTG
121486	119573	AGGCAGATTACTGGTTAACT
121487	119574	AAGGCAGATTACTGGTTAAC
121488	119575	GAAGGCAGATTACTGGTTAA
121489	119576	AGAAGGCAGATTACTGGTTA
121490	119577	AAGAAGGCAGATTACTGGTT
121491	119578	AAAGAAGGCAGATTACTGGT
121492	119579	AAAAGAAGGCAGATTACTGG
121493	119580	TAAAAGAAGGCAGATTACTG
121494	119581	GTAAAAGAAGGCAGATTACT
121495	119582	AGTAAAAGAAGGCAGATTAC
121496	119583	TAGTAAAAGAAGGCAGATTA
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121498	119585	TATAGTAAAAGAAGGCAGAT
121499	119586	CTATAGTAAAAGAAGGCAGA
121500	119587	TCTATAGTAAAAGAAGGCAG
121501	119588	ATCTATAGTAAAAGAAGGCA
121502	119589	AATCTATAGTAAAAGAAGGC
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23211	21298	TAAGTGACCTATTCAGATAT
23212	21299	GTAAGTGACCTATTCAGATA
23213	21300	GGTAAGTGACCTATTCAGAT
23214	21301	TGGTAAGTGACCTATTCAGA
23215	21302	ATGGTAAGTGACCTATTCAG
23216	21303	CATGGTAAGTGACCTATTCA
23217	21304	TCATGGTAAGTGACCTATTC
23218	21305	TTCATGGTAAGTGACCTATT
23219	21306	ATTCATGGTAAGTGACCTAT
23220	21307	CATTCATGGTAAGTGACCTA
23221	21308	CCATTCATGGTAAGTGACCT
23222	21309	TCCATTCATGGTAAGTGACC
23223	21310	CTCCATTCATGGTAAGTGAC
23224	21311	GCTCCATTCATGGTAAGTGA
23225	21312	AGCTCCATTCATGGTAAGTG
23226	21313	AAGCTCCATTCATGGTAAGT
23227	21314	CAAGCTCCATTCATGGTAAG
23228	21315	GCAAGCTCCATTCATGGTAA
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23238	21325	TTCCTGTCCTGCAAGCTCCA
23239	21326	CTTCCTGTCCTGCAAGCTCC
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23242	21329	CAACTTCCTGTCCTGCAAGC
23243	21330	GCAACTTCCTGTCCTGCAAG
23244	21331	AGCAACTTCCTGTCCTGCAA
23245	21332	AAGCAACTTCCTGTCCTGCA
23246	21333	CAAGCAACTTCCTGTCCTGC
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23248	21335	CCCAAGCAACTTCCTGTCCT
23249	21336	TCCCAAGCAACTTCCTGTCC
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23252	21339	TCATCCCAAGCAACTTCCTG
23253	21340	CTCATCCCAAGCAACTTCCT
23254	21341	ACTCATCCCAAGCAACTTCC
23255	21342	GACTCATCCCAAGCAACTTC
23256	21343	TGACTCATCCCAAGCAACTT
23257	21344	ATGACTCATCCCAAGCAACT
23258	21345	AATGACTCATCCCAAGCAAC
23259	21346	AAATGACTCATCCCAAGCAA
23260	21347	TAAATGACTCATCCCAAGCA
23261	21348	ATAAATGACTCATCCCAAGC
23262	21349	GATAAATGACTCATCCCAAG
23263	21350	TGATAAATGACTCATCCCAA
23264	21351	CTGATAAATGACTCATCCCA
23265	21352	ACTGATAAATGACTCATCCC
23266	21353	CACTGATAAATGACTCATCC
23267	21354	CCACTGATAAATGACTCATC
23268	21355	ACCACTGATAAATGACTCAT
23269	21356	CACCACTGATAAATGACTCA
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23278	21365	ACATTCACACACCACTGATA
23279	21366	CACATTCACACACCACTGAT
23280	21367	GCACATTCACACACCACTGA
23281	21368	TGCACATTCACACACCACTG

72358	70445	GGCTCTAATCTACAGGCAAC
72359	70446	TGGCTCTAATCTACAGGCAA
72360	70447	CTGGCTCTAATCTACAGGCA
72361	70448	ACTGGCTCTAATCTACAGGC
72362	70449	AACTGGCTCTAATCTACAGG
72363	70450	CAACTGGCTCTAATCTACAG
72364	70451	ACAACTGGCTCTAATCTACA
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72366	70453	AAACAACTGGCTCTAATCTA
72367	70454	AAAACAACTGGCTCTAATCT
72368	70455	AAAAACAACTGGCTCTAATC
72369	70456	AAAAAACAACTGGCTCTAAT
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72371	70458	GAAAAAAACAACTGGCTCTA
72372	70459	AGAAAAAAACAACTGGCTCT
72373	70460	GAGAAAAAAACAACTGGCTC
72374	70461	TGAGAAAAAAACAACTGGCT
72375	70462	TTGAGAAAAAAACAACTGGC
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72378	70465	AAGTTGAGAAAAAAACAACT
72379	70466	AAAGTTGAGAAAAAAACAAC
72380	70467	CAAAGTTGAGAAAAAAACAA
72381	70468	GCAAAGTTGAGAAAAAAACA
72382	70469	TGCAAAGTTGAGAAAAAAAC
72383	70470	CTGCAAAGTTGAGAAAAAAA
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72387	70474	ATTCCTGCAAAGTTGAGAAA
72388	70475	GATTCCTGCAAAGTTGAGAA
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72392	70479	CCAGGATTCCTGCAAAGTTG
72393	70480	ACCAGGATTCCTGCAAAGTT
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72396	70483	GTAACCAGGATTCCTGCAAA
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72398	70485	TTGTAACCAGGATTCCTGCA
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72402	70489	AATGTTGTAACCAGGATTCC
72403	70490	CAATGTTGTAACCAGGATTC
72404	70491	ACAATGTTGTAACCAGGATT
72405	70492	TACAATGTTGTAACCAGGAT
72406	70493	GTACAATGTTGTAACCAGGA
72407	70494	AGTACAATGTTGTAACCAGG
72408	70495	TAGTACAATGTTGTAACCAG
72409	70496	ATAGTACAATGTTGTAACCA
72410	70497	AATAGTACAATGTTGTAACC
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72412	70499	TAAATAGTACAATGTTGTAA
72413	70500	GTAAATAGTACAATGTTGTA
72414	70501	AGTAAATAGTACAATGTTGT
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121505	119592	TCTAATCTATAGTAAAAGAA
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121512	119599	GGATAAATCTAATCTATAGT
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121514	119601	GAGGATAAATCTAATCTATA
121515	119602	AGAGGATAAATCTAATCTAT
121516	119603	AAGAGGATAAATCTAATCTA
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121519	119606	CTAAAGAGGATAAATCTAAT
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121523	119610	AAATCTAAAGAGGATAAATC
121524	119611	GAAATCTAAAGAGGATAAAT
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23282	21369	CTGCACATTCACACACCACT
23283	21370	CCTGCACATTCACACACCAC
23284	21371	GCCTGCACATTCACACACCA
23285	21372	GGCCTGCACATTCACACACC
23286	21373	AGGCCTGCACATTCACACAC
23287	21374	TAGGCCTGCACATTCACACA
23288	21375	CTAGGCCTGCACATTCACAC
23289	21376	CCTAGGCCTGCACATTCACA
23290	21377	TCCTAGGCCTGCACATTCAC
23291	21378	GTCCTAGGCCTGCACATTCA
23292	21379	TGTCCTAGGCCTGCACATTC
23293	21380	ATGTCCTAGGCCTGCACATT
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23298	21385	CAGTAATGTCCTAGGCCTGC
23299	21386	ACAGTAATGTCCTAGGCCTG
23300	21387	TACAGTAATGTCCTAGGCCT
23301	21388	ATACAGTAATGTCCTAGGCC
23302	21389	CATACAGTAATGTCCTAGGC
23303	21390	GCATACAGTAATGTCCTAGG
23304	21391	AGCATACAGTAATGTCCTAG
23305	21392	TAGCATACAGTAATGTCCTA
23306	21393	GTAGCATACAGTAATGTCCT
23307	21394	AGTAGCATACAGTAATGTCC
23308	21395	CAGTAGCATACAGTAATGTC
23309	21396	ACAGTAGCATACAGTAATGT
23310	21397	TACAGTAGCATACAGTAATG
23311	21398	CTACAGTAGCATACAGTAAT
23312	21399	TCTACAGTAGCATACAGTAA
23313	21400	GTCTACAGTAGCATACAGTA
23314	21401	TGTCTACAGTAGCATACAGT
23315	21402	TTGTCTACAGTAGCATACAG
23316	21403	TTTGTCTACAGTAGCATACA
23317	21404	GTTTGTCTACAGTAGCATAC
23318	21405	TGTTTGTCTACAGTAGCATA
23319	21406	GTGTTTGTCTACAGTAGCAT
23320	21407	AGTGTTTGTCTACAGTAGCA
23321	21408	CAGTGTTTGTCTACAGTAGC
23322	21409	TCAGTGTTTGTCTACAGTAG
23323	21410	TTCAGTGTTTGTCTACAGTA
23324	21411	GTTCAGTGTTTGTCTACAGT
23325	21412	TGTTCAGTGTTTGTCTACAG
23326	21413	CTGTTCAGTGTTTGTCTACA
23327	21414	ACTGTTCAGTGTTTGTCTAC
23328	21415	AACTGTTCAGTGTTTGTCTA
23329	21416	TAACTGTTCAGTGTTTGTCT
23330	21417	CTAACTGTTCAGTGTTTGTC
23331	21418	CCTAACTGTTCAGTGTTTGT
23332	21419	TCCTAACTGTTCAGTGTTTG
23333	21420	ATCCTAACTGTTCAGTGTTT
23334	21421	TATCCTAACTGTTCAGTGTT
23335	21422	GTATCCTAACTGTTCAGTGT
23336	21423	TGTATCCTAACTGTTCAGTG
23337	21424	GTGTATCCTAACTGTTCAGT
23338	21425	AGTGTATCCTAACTGTTCAG
23339	21426	TAGTGTATCCTAACTGTTCA
23340	21427	TTAGTGTATCCTAACTGTTC
23341	21428	TTTAGTGTATCCTAACTGTT
23342	21429	ATTTAGTGTATCCTAACTGT
23343	21430	AATTTAGTGTATCCTAACTG
23344	21431	CAATTTAGTGTATCCTAACT
23345	21432	TCAATTTAGTGTATCCTAAC
23346	21433	ATCAATTTAGTGTATCCTAA
23347	21434	TATCAATTTAGTGTATCCTA
23348	21435	TTATCAATTTAGTGTATCCT
23349	21436	TTTATCAATTTAGTGTATCC
23350	21437	ATTTATCAATTTAGTGTATC
23351	21438	TATTTATCAATTTAGTGTAT
23352	21439	ATATTTATCAATTTAGTGTA

72429	70516	AAAAACACTGTTGGTAGTAA
72430	70517	AAAAAACACTGTTGGTAGTA
72431	70518	AAAAAAACACTGTTGGTAGT
72432	70519	AAAAAAAACACTGTTGGTAG
72433	70520	AAAAAAAAACACTGTTGGTA
72434	70521	AAAAAAAAAACACTGTTGGT
72435	70522	AAAAAAAAAAACACTGTTGG
72436	70523	AAAAAAAAAAAACACTGTTG
72437	70524	TAAAAAAAAAAAACACTGTT
72438	70525	TTAAAAAAAAAAAACACTGT
72439	70526	TTTAAAAAAAAAAAACACTG
72440	70527	TTTTAAAAAAAAAAAACACT
72441	70528	ATTTTAAAAAAAAAAAACAC
72442	70529	GATTTTAAAAAAAAAAAACA
72443	70530	GGATTTTAAAAAAAAAAAAC
72444	70531	TGGATTTTAAAAAAAAAAAA
72445	70532	CTGGATTTTAAAAAAAAAAA
72446	70533	TCTGGATTTTAAAAAAAAAA
72447	70534	GTCTGGATTTTAAAAAAAAA
72448	70535	AGTCTGGATTTTAAAAAAAA
72449	70536	AAGTCTGGATTTTAAAAAAA
72450	70537	CAAGTCTGGATTTTAAAAAA
72451	70538	GCAAGTCTGGATTTTAAAAA
72452	70539	AGCAAGTCTGGATTTTAAAA
72453	70540	CAGCAAGTCTGGATTTTAAA
72454	70541	CCAGCAAGTCTGGATTTTAA
72455	70542	CCCAGCAAGTCTGGATTTTA
72456	70543	GCCCAGCAAGTCTGGATTTT
72457	70544	TGCCCAGCAAGTCTGGATTT
72458	70545	ATGCCCAGCAAGTCTGGATT
72459	70546	TATGCCCAGCAAGTCTGGAT
72460	70547	CTATGCCCAGCAAGTCTGGA
72461	70548	ACTATGCCCAGCAAGTCTGG
72462	70549	CACTATGCCCAGCAAGTCTG
72463	70550	CCACTATGCCCAGCAAGTCT
72464	70551	GCCACTATGCCCAGCAAGTC
72465	70552	AGCCACTATGCCCAGCAAGT
72466	70553	GAGCCACTATGCCCAGCAAG
72467	70554	TGAGCCACTATGCCCAGCAA
72468	70555	ATGAGCCACTATGCCCAGCA
72469	70556	CATGAGCCACTATGCCCAGC
72470	70557	GCATGAGCCACTATGCCCAG
72471	70558	GGCATGAGCCACTATGCCCA
72472	70559	AGGCATGAGCCACTATGCCC
72473	70560	CAGGCATGAGCCACTATGCC
72474	70561	ACAGGCATGAGCCACTATGC
72475	70562	TACAGGCATGAGCCACTATG
72476	70563	TTACAGGCATGAGCCACTAT
72477	70564	ATTACAGGCATGAGCCACTA
72478	70565	GATTACAGGCATGAGCCACT
72479	70566	AGATTACAGGCATGAGCCAC
72480	70567	GAGATTACAGGCATGAGCCA
72481	70568	TGAGATTACAGGCATGAGCC
72482	70569	CTGAGATTACAGGCATGAGC
72483	70570	GCTGAGATTACAGGCATGAG
72484	70571	CGCTGAGATTACAGGCATGA
72485	70572	TCGCTGAGATTACAGGCATG
72486	70573	GTCGCTGAGATTACAGGCAT
72487	70574	AGTCGCTGAGATTACAGGCA
72488	70575	AAGTCGCTGAGATTACAGGC
72489	70576	CAAGTCGCTGAGATTACAGG
72490	70577	CCAAGTCGCTGAGATTACAG
72491	70578	CCCAAGTCGCTGAGATTACA
72492	70579	TCCCAAGTCGCTGAGATTAC
72493	70580	CTCCCAAGTCGCTGAGATTA
72494	70581	CCTCCCAAGTCGCTGAGATT
72495	70582	GCCTCCCAAGTCGCTGAGAT
72496	70583	AGCCTCCCAAGTCGCTGAGA
72497	70584	CAGCCTCCCAAGTCGCTGAG
72498	70585	TCAGCCTCCCAAGTCGCTGA
72499	70586	CTCAGCCTCCCAAGTCGCTG

121576	119663	TTTACGTAAAAAAAGAAAAA
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121578	119665	TTTTTACGTAAAAAAAGAAA
121579	119666	TTTTTTACGTAAAAAAAGAA
121580	119667	TTTTTTTACGTAAAAAAAGA
121581	119668	ATTTTTTTACGTAAAAAAAG
121582	119669	GATTTTTTTACGTAAAAAAA
121583	119670	AGATTTTTTTACGTAAAAAA
121584	119671	AAGATTTTTTTACGTAAAAA
121585	119672	AAAGATTTTTTTACGTAAAA
121586	119673	AAAAGATTTTTTTACGTAAA
121587	119674	AAAAAGATTTTTTTACGTAA
121588	119675	AAAAAAGATTTTTTTACGTA
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121590	119677	CAAAAAAAGATTTTTTTACG
121591	119678	CCAAAAAAAGATTTTTTTAC
121592	119679	TCCAAAAAAAGATTTTTTTA
121593	119680	CTCCAAAAAAAGATTTTTTT
121594	119681	TCTCCAAAAAAAGATTTTTT
121595	119682	GTCTCCAAAAAAAGATTTTT
121596	119683	CGTCTCCAAAAAAAGATTTT
121597	119684	ACGTCTCCAAAAAAAGATTT
121598	119685	GACGTCTCCAAAAAAAGATT
121599	119686	AGACGTCTCCAAAAAAAGAT
121600	119687	GAGACGTCTCCAAAAAAAGA
121601	119688	TGAGACGTCTCCAAAAAAAG
121602	119689	ATGAGACGTCTCCAAAAAAA
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121604	119691	TAATGAGACGTCTCCAAAAA
121605	119692	ATAATGAGACGTCTCCAAAA
121606	119693	TATAATGAGACGTCTCCAAA
121607	119694	ATATAATGAGACGTCTCCAA
121608	119695	AATATAATGAGACGTCTCCA
121609	119696	CAATATAATGAGACGTCTCC
121610	119697	GCAATATAATGAGACGTCTC
121611	119698	GGCAATATAATGAGACGTCT
121612	119699	GGGCAATATAATGAGACGTC
121613	119700	TGGGCAATATAATGAGACGT
121614	119701	CTGGGCAATATAATGAGACG
121615	119702	CCTGGGCAATATAATGAGAC
121616	119703	ACCTGGGCAATATAATGAGA
121617	119704	AACCTGGGCAATATAATGAG
121618	119705	CAACCTGGGCAATATAATGA
121619	119706	CCAACCTGGGCAATATAATG
121620	119707	ACCAACCTGGGCAATATAAT
121621	119708	GACCAACCTGGGCAATATAA
121622	119709	AGACCAACCTGGGCAATATA
121623	119710	GAGACCAACCTGGGCAATAT
121624	119711	CGAGACCAACCTGGGCAATA
121625	119712	TCGAGACCAACCTGGGCAAT
121626	119713	TTCGAGACCAACCTGGGCAA
121627	119714	GTTCGAGACCAACCTGGGCA
121628	119715	AGTTCGAGACCAACCTGGGC
121629	119716	GAGTTCGAGACCAACCTGGG
121630	119717	AGAGTTCGAGACCAACCTGG
121631	119718	AAGAGTTCGAGACCAACCTG
121632	119719	CAAGAGTTCGAGACCAACCT
121633	119720	TCAAGAGTTCGAGACCAACC
121634	119721	CTCAAGAGTTCGAGACCAAC
121635	119722	GCTCAAGAGTTCGAGACCAA
121636	119723	AGCTCAAGAGTTCGAGACCA
121637	119724	GAGCTCAAGAGTTCGAGACC
121638	119725	TGAGCTCAAGAGTTCGAGAC
121639	119726	GTGAGCTCAAGAGTTCGAGA
121640	119727	GGTGAGCTCAAGAGTTCGAG
121641	119728	AGGTGAGCTCAAGAGTTCGA
121642	119729	GAGGTGAGCTCAAGAGTTCG
121643	119730	TGAGGTGAGCTCAAGAGTTC
121644	119731	CTGAGGTGAGCTCAAGAGTT
121645	119732	GCTGAGGTGAGCTCAAGAGT
121646	119733	GGCTGAGGTGAGCTCAAGAG

23353	21440	GATATTTATCAATTTAGTGT
23354	21441	AGATATTTATCAATTTAGTG
23355	21442	AAGATATTTATCAATTTAGT
23356	21443	AAAGATATTTATCAATTTAG
23357	21444	GAAAGATATTTATCAATTTA
23358	21445	AGAAAGATATTTATCAATTT
23359	21446	AAGAAAGATATTTATCAATT
23360	21447	TAAGAAAGATATTTATCAAT
23361	21448	ATAAGAAAGATATTTATCAA
23362	21449	AATAAGAAAGATATTTATCA
23363	21450	AAATAAGAAAGATATTTATC
23364	21451	AAAATAAGAAAGATATTTAT
23365	21452	CAAAATAAGAAAGATATTTA
23366	21453	ACAAAATAAGAAAGATATTT
23367	21454	AACAAAATAAGAAAGATATT
23368	21455	AAACAAAATAAGAAAGATAT
23369	21456	AAAACAAAATAAGAAAGATA
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23371	21458	AAAAAACAAAATAAGAAAGA
23372	21459	CAAAAAACAAAATAAGAAAG
23373	21460	TCAAAAAACAAAATAAGAAA
23374	21461	CTCAAAAAACAAAATAAGAA
23375	21462	TCTCAAAAAACAAAATAAGA
23376	21463	ATCTCAAAAAACAAAATAAG
23377	21464	CATCTCAAAAAACAAAATAA
23378	21465	CCATCTCAAAAAACAAAATA
23379	21466	TCCATCTCAAAAAACAAAAT
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23381	21468	ACTCCATCTCAAAAAACAAA
23382	21469	GACTCCATCTCAAAAAACAA
23383	21470	AGACTCCATCTCAAAAAACA
23384	21471	GAGACTCCATCTCAAAAAAC
23385	21472	CGAGACTCCATCTCAAAAAA
23386	21473	GCGAGACTCCATCTCAAAAA
23387	21474	AGCGAGACTCCATCTCAAAA
23388	21475	GAGCGAGACTCCATCTCAAA
23389	21476	AGAGCGAGACTCCATCTCAA
23390	21477	TAGAGCGAGACTCCATCTCA
23391	21478	ATAGAGCGAGACTCCATCTC
23392	21479	GATAGAGCGAGACTCCATCT
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23394	21481	GCGATAGAGCGAGACTCCAT
23395	21482	GGCGATAGAGCGAGACTCCA
23396	21483	GGGCGATAGAGCGAGACTCC
23397	21484	TGGGCGATAGAGCGAGACTC
23398	21485	CTGGGCGATAGAGCGAGACT
23399	21486	CCTGGGCGATAGAGCGAGAC
23400	21487	GCCTGGGCGATAGAGCGAGA
23401	21488	AGCCTGGGCGATAGAGCGAG
23402	21489	CAGCCTGGGCGATAGAGCGA
23403	21490	CCAGCCTGGGCGATAGAGCG
23404	21491	TCCAGCCTGGGCGATAGAGC
23405	21492	CTCCAGCCTGGGCGATAGAG
23406	21493	ACTCCAGCCTGGGCGATAGA
23407	21494	CACTCCAGCCTGGGCGATAG
23408	21495	ACACTCCAGCCTGGGCGATA
23409	21496	TACACTCCAGCCTGGGCGAT
23410	21497	CTACACTCCAGCCTGGGCGA
23411	21498	ACTACACTCCAGCCTGGGCG
23412	21499	CACTACACTCCAGCCTGGGC
23413	21500	CCACTACACTCCAGCCTGGG
23414	21501	GCCACTACACTCCAGCCTGG
23415	21502	CGCCACTACACTCCAGCCTG
23416	21503	ACGCCACTACACTCCAGCCT
23417	21504	CACGCCACTACACTCCAGCC
23418	21505	TCACGCCACTACACTCCAGC
23419	21506	ATCACGCCACTACACTCCAG
23420	21507	CATCACGCCACTACACTCCA
23421	21508	ACATCACGCCACTACACTCC
23422	21509	AACATCACGCCACTACACTC
23423	21510	CAACATCACGCCACTACACT

72500	70587	CCTCAGCCTCCCAAGTCGCT
72501	70588	ACCTCAGCCTCCCAAGTCGC
72502	70589	CACCTCAGCCTCCCAAGTCG
72503	70590	CCACCTCAGCCTCCCAAGTC
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72505	70592	TCCCACCTCAGCCTCCCAAG
72506	70593	CTCCCACCTCAGCCTCCCAA
72507	70594	CCTCCCACCTCAGCCTCCCA
72508	70595	TCCTCCCACCTCAGCCTCCC
72509	70596	ATCCTCCCACCTCAGCCTCC
72510	70597	AATCCTCCCACCTCAGCCTC
72511	70598	CAATCCTCCCACCTCAGCCT
72512	70599	GCAATCCTCCCACCTCAGCC
72513	70600	AGCAATCCTCCCACCTCAGC
72514	70601	AAGCAATCCTCCCACCTCAG
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72516	70603	TCAAGCAATCCTCCCACCTC
72517	70604	CTCAAGCAATCCTCCCACCT
72518	70605	GCTCAAGCAATCCTCCCACC
72519	70606	GGCTCAAGCAATCCTCCCAC
72520	70607	GGGCTCAAGCAATCCTCCCA
72521	70608	TGGGCTCAAGCAATCCTCCC
72522	70609	CTGGGCTCAAGCAATCCTCC
72523	70610	CCTGGGCTCAAGCAATCCTC
72524	70611	CCCTGGGCTCAAGCAATCCT
72525	70612	GCCCTGGGCTCAAGCAATCC
72526	70613	AGCCCTGGGCTCAAGCAATC
72527	70614	CAGCCCTGGGCTCAAGCAAT
72528	70615	GCAGCCCTGGGCTCAAGCAA
72529	70616	TGCAGCCCTGGGCTCAAGCA
72530	70617	CTGCAGCCCTGGGCTCAAGC
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72532	70619	CACTGCAGCCCTGGGCTCAA
72533	70620	TCACTGCAGCCCTGGGCTCA
72534	70621	ATCACTGCAGCCCTGGGCTC
72535	70622	AATCACTGCAGCCCTGGGCT
72536	70623	CAATCACTGCAGCCCTGGGC
72537	70624	GCAATCACTGCAGCCCTGGG
72538	70625	CGCAATCACTGCAGCCCTGG
72539	70626	CCGCAATCACTGCAGCCCTG
72540	70627	GCCGCAATCACTGCAGCCCT
72541	70628	TGCCGCAATCACTGCAGCCC
72542	70629	GTGCCGCAATCACTGCAGCC
72543	70630	AGTGCCGCAATCACTGCAGC
72544	70631	TAGTGCCGCAATCACTGCAG
72545	70632	GTAGTGCCGCAATCACTGCA
72546	70633	TGTAGTGCCGCAATCACTGC
72547	70634	GTGTAGTGCCGCAATCACTG
72548	70635	AGTGTAGTGCCGCAATCACT
72549	70636	GAGTGTAGTGCCGCAATCAC
72550	70637	GGAGTGTAGTGCCGCAATCA
72551	70638	TGGAGTGTAGTGCCGCAATC
72552	70639	CTGGAGTGTAGTGCCGCAAT
72553	70640	GCTGGAGTGTAGTGCCGCAA
72554	70641	TGCTGGAGTGTAGTGCCGCA
72555	70642	ATGCTGGAGTGTAGTGCCGC
72556	70643	CATGCTGGAGTGTAGTGCCG
72557	70644	TCATGCTGGAGTGTAGTGCC
72558	70645	CTCATGCTGGAGTGTAGTGC
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72560	70647	CACTCATGCTGGAGTGTAGT
72561	70648	TCACTCATGCTGGAGTGTAG
72562	70649	GTCACTCATGCTGGAGTGTA
72563	70650	TGTCACTCATGCTGGAGTGT
72564	70651	TTGTCACTCATGCTGGAGTG
72565	70652	TTTGTCACTCATGCTGGAGT
72566	70653	CTTTGTCACTCATGCTGGAG
72567	70654	TCTTTGTCACTCATGCTGGA
72568	70655	GTCTTTGTCACTCATGCTGG
72569	70656	GGTCTTTGTCACTCATGCTG
72570	70657	GGGTCTTTGTCACTCATGCT

121647	119734	AGGCTGAGGTGAGCTCAAGA
121648	119735	GAGGCTGAGGTGAGCTCAAG
121649	119736	GGAGGCTGAGGTGAGCTCAA
121650	119737	GGGAGGCTGAGGTGAGCTCA
121651	119738	TGGGAGGCTGAGGTGAGCTC
121652	119739	CTGGGAGGCTGAGGTGAGCT
121653	119740	TCTGGGAGGCTGAGGTGAGC
121654	119741	CTCTGGGAGGCTGAGGTGAG
121655	119742	ACTCTGGGAGGCTGAGGTGA
121656	119743	CACTCTGGGAGGCTGAGGTG
121657	119744	GCACTCTGGGAGGCTGAGGT
121658	119745	AGCACTCTGGGAGGCTGAGG
121659	119746	TAGCACTCTGGGAGGCTGAG
121660	119747	CTAGCACTCTGGGAGGCTGA
121661	119748	CCTAGCACTCTGGGAGGCTG
121662	119749	TCCTAGCACTCTGGGAGGCT
121663	119750	ATCCTAGCACTCTGGGAGGC
121664	119751	AATCCTAGCACTCTGGGAGG
121665	119752	TAATCCTAGCACTCTGGGAG
121666	119753	GTAATCCTAGCACTCTGGGA
121667	119754	TGTAATCCTAGCACTCTGGG
121668	119755	CTGTAATCCTAGCACTCTGG
121669	119756	TCTGTAATCCTAGCACTCTG
121670	119757	ATCTGTAATCCTAGCACTCT
121671	119758	CATCTGTAATCCTAGCACTC
121672	119759	ACATCTGTAATCCTAGCACT
121673	119760	CACATCTGTAATCCTAGCAC
121674	119761	TCACATCTGTAATCCTAGCA
121675	119762	CTCACATCTGTAATCCTAGC
121676	119763	GCTCACATCTGTAATCCTAG
121677	119764	GGCTCACATCTGTAATCCTA
121678	119765	TGGCTCACATCTGTAATCCT
121679	119766	GTGGCTCACATCTGTAATCC
121680	119767	GGTGGCTCACATCTGTAATC
121681	119768	AGGTGGCTCACATCTGTAAT
121682	119769	GAGGTGGCTCACATCTGTAA
121683	119770	TGAGGTGGCTCACATCTGTA
121684	119771	CTGAGGTGGCTCACATCTGT
121685	119772	GCTGAGGTGGCTCACATCTG
121686	119773	GGCTGAGGTGGCTCACATCT
121687	119774	TGGCTGAGGTGGCTCACATC
121688	119775	CTGGCTGAGGTGGCTCACAT
121689	119776	GCTGGCTGAGGTGGCTCACA
121690	119777	GGCTGGCTGAGGTGGCTCAC
121691	119778	GGGCTGGCTGAGGTGGCTCA
121692	119779	GGGGCTGGCTGAGGTGGCTC
121693	119780	AGGGGCTGGCTGAGGTGGCT
121694	119781	TAGGGGCTGGCTGAGGTGGC
121695	119782	CTAGGGGCTGGCTGAGGTGG
121696	119783	TCTAGGGGCTGGCTGAGGTG
121697	119784	ATCTAGGGGCTGGCTGAGGT
121698	119785	AATCTAGGGGCTGGCTGAGG
121699	119786	AAATCTAGGGGCTGGCTGAG
121700	119787	AAAATCTAGGGGCTGGCTGA
121701	119788	AAAAATCTAGGGGCTGGCTG
121702	119789	AAAAAATCTAGGGGCTGGCT
121703	119790	AAAAAAATCTAGGGGCTGGC
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121705	119792	AAAAAAAAATCTAGGGGCTG
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121712	119799	AAAAAAAAAAAAAAAATCTA
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23424	21511	CCAACATCACGCCACTACAC
23425	21512	GCCAACATCACGCCACTACA
23426	21513	AGCCAACATCACGCCACTAC
23427	21514	GAGCCAACATCACGCCACTA
23428	21515	TGAGCCAACATCACGCCACT
23429	21516	GTGAGCCAACATCACGCCAC
23430	21517	AGTGAGCCAACATCACGCCA
23431	21518	CAGTGAGCCAACATCACGCC
23432	21519	GCAGTGAGCCAACATCACGC
23433	21520	TGCAGTGAGCCAACATCACG
23434	21521	CTGCAGTGAGCCAACATCAC
23435	21522	ACTGCAGTGAGCCAACATCA
23436	21523	GACTGCAGTGAGCCAACATC
23437	21524	AGACTGCAGTGAGCCAACAT
23438	21525	GAGACTGCAGTGAGCCAACA
23439	21526	AGAGACTGCAGTGAGCCAAC
23440	21527	CAGAGACTGCAGTGAGCCAA
23441	21528	GCAGAGACTGCAGTGAGCCA
23442	21529	GGCAGAGACTGCAGTGAGCC
23443	21530	AGGCAGAGACTGCAGTGAGC
23444	21531	AAGGCAGAGACTGCAGTGAG
23445	21532	GAAGGCAGAGACTGCAGTGA
23446	21533	AGAAGGCAGAGACTGCAGTG
23447	21534	CAGAAGGCAGAGACTGCAGT
23448	21535	CCAGAAGGCAGAGACTGCAG
23449	21536	CCCAGAAGGCAGAGACTGCA
23450	21537	ACCCAGAAGGCAGAGACTGC
23451	21538	AACCCAGAAGGCAGAGACTG
23452	21539	GAACCCAGAAGGCAGAGACT
23453	21540	TGAACCCAGAAGGCAGAGAC
23454	21541	TTGAACCCAGAAGGCAGAGA
23455	21542	CTTGAACCCAGAAGGCAGAG
23456	21543	GCTTGAACCCAGAAGGCAGA
23457	21544	CGCTTGAACCCAGAAGGCAG
23458	21545	TCGCTTGAACCCAGAAGGCA
23459	21546	ATCGCTTGAACCCAGAAGGC
23460	21547	AATCGCTTGAACCCAGAAGG
23461	21548	GAATCGCTTGAACCCAGAAG
23462	21549	AGAATCGCTTGAACCCAGAA
23463	21550	GAGAATCGCTTGAACCCAGA
23464	21551	GGAGAATCGCTTGAACCCAG
23465	21552	AGGAGAATCGCTTGAACCCA
23466	21553	CAGGAGAATCGCTTGAACCC
23467	21554	GCAGGAGAATCGCTTGAACC
23468	21555	GGCAGGAGAATCGCTTGAAC
23469	21556	AGGCAGGAGAATCGCTTGAA
23470	21557	GAGGCAGGAGAATCGCTTGA
23471	21558	TGAGGCAGGAGAATCGCTTG
23472	21559	TTGAGGCAGGAGAATCGCTT
23473	21560	GTTGAGGCAGGAGAATCGCT
23474	21561	GGTTGAGGCAGGAGAATCGC
23475	21562	AGGTTGAGGCAGGAGAATCG
23476	21563	GAGGTTGAGGCAGGAGAATC
23477	21564	GGAGGTTGAGGCAGGAGAAT
23478	21565	AGGAGGTTGAGGCAGGAGAA
23479	21566	CAGGAGGTTGAGGCAGGAGA
23480	21567	TCAGGAGGTTGAGGCAGGAG
23481	21568	TTCAGGAGGTTGAGGCAGGA
23482	21569	ATTCAGGAGGTTGAGGCAGG
23483	21570	TATTCAGGAGGTTGAGGCAG
23484	21571	CTATTCAGGAGGTTGAGGCA
23485	21572	GCTATTCAGGAGGTTGAGGC
23486	21573	AGCTATTCAGGAGGTTGAGG
23487	21574	CAGCTATTCAGGAGGTTGAG
23488	21575	CCAGCTATTCAGGAGGTTGA
23489	21576	CCCAGCTATTCAGGAGGTTG
23490	21577	TCCCAGCTATTCAGGAGGTT
23491	21578	ATCCCAGCTATTCAGGAGGT
23492	21579	AATCCCAGCTATTCAGGAGG
23493	21580	TAATCCCAGCTATTCAGGAG
23494	21581	GTAATCCCAGCTATTCAGGA

72571	70658	GGGGTCTTTGTCACTCATGC
72572	70659	TGGGGTCTTTGTCACTCATG
72573	70660	ATGGGGTCTTTGTCACTCAT
72574	70661	GATGGGGTCTTTGTCACTCA
72575	70662	AGATGGGGTCTTTGTCACTC
72576	70663	GAGATGGGGTCTTTGTCACT
72577	70664	AGAGATGGGGTCTTTGTCAC
72578	70665	CAGAGATGGGGTCTTTGTCA
72579	70666	TCAGAGATGGGGTCTTTGTC
72580	70667	TTCAGAGATGGGGTCTTTGT
72581	70668	TTTCAGAGATGGGGTCTTTG
72582	70669	TTTTCAGAGATGGGGTCTTT
72583	70670	TTTTTCAGAGATGGGGTCTT
72584	70671	TTTTTTCAGAGATGGGGTCT
72585	70672	GTTTTTTCAGAGATGGGGTC
72586	70673	TGTTTTTTCAGAGATGGGGT
72587	70674	TTGTTTTTTCAGAGATGGGG
72588	70675	TTTGTTTTTTCAGAGATGGG
72589	70676	TTTTGTTTTTTCAGAGATGG
72590	70677	TTTTTGTTTTTTCAGAGATG
72591	70678	GTTTTTGTTTTTTCAGAGAT
72592	70679	TGTTTTTGTTTTTTCAGAGA
72593	70680	TTGTTTTTGTTTTTTCAGAG
72594	70681	TTTGTTTTTGTTTTTTCAGA
72595	70682	TTTTGTTTTTGTTTTTTCAG
72596	70683	TTTTTGTTTTTGTTTTTTCA
72597	70684	GTTTTTGTTTTTGTTTTTTC
72598	70685	TGTTTTTGTTTTTGTTTTTT
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72600	70687	TTTGTTTTTGTTTTTGTTTT
72601	70688	ATTTGTTTTTGTTTTTGTTT
72602	70689	AATTTGTTTTTGTTTTTGTT
72603	70690	AAATTTGTTTTTGTTTTTGT
72604	70691	AAAATTTGTTTTTGTTTTTG
72605	70692	AAAAATTTGTTTTTGTTTTT
72606	70693	AAAAAATTTGTTTTTGTTTT
72607	70694	AAAAAAATTTGTTTTTGTTT
72608	70695	AAAAAAAATTTGTTTTTGTT
72609	70696	TAAAAAAAATTTGTTTTTGT
72610	70697	TTAAAAAAAATTTGTTTTTG
72611	70698	TTTAAAAAAAATTTGTTTTT
72612	70699	CTTTAAAAAAAATTTGTTTT
72613	70700	TCTTTAAAAAAAATTTGTTT
72614	70701	TTCTTTAAAAAAAATTTGTT
72615	70702	TTTCTTTAAAAAAAATTTGT
72616	70703	GTTTCTTTAAAAAAAATTTG
72617	70704	TGTTTCTTTAAAAAAAATTT
72618	70705	CTGTTTCTTTAAAAAAAATT
72619	70706	TCTGTTTCTTTAAAAAAAAT
72620	70707	TTCTGTTTCTTTAAAAAAAA
72621	70708	TTTCTGTTTCTTTAAAAAAA
72622	70709	GTTTCTGTTTCTTTAAAAAA
72623	70710	TGTTTCTGTTTCTTTAAAAA
72624	70711	TTGTTTCTGTTTCTTTAAAA
72625	70712	TTTGTTTCTGTTTCTTTAAA
72626	70713	TTTTGTTTCTGTTTCTTTAA
72627	70714	TTTTTGTTTCTGTTTCTTTA
72628	70715	ATTTTTGTTTCTGTTTCTTT
72629	70716	GATTTTTGTTTCTGTTTCTT
72630	70717	GGATTTTTGTTTCTGTTTCT
72631	70718	TGGATTTTTGTTTCTGTTTC
72632	70719	TTGGATTTTTGTTTCTGTTT
72633	70720	TTTGGATTTTTGTTTCTGTT
72634	70721	GTTTGGATTTTTGTTTCTGT
72635	70722	AGTTTGGATTTTTGTTTCTG
72636	70723	AAGTTTGGATTTTTGTTTCT
72637	70724	CAAGTTTGGATTTTTGTTTC
72638	70725	ACAAGTTTGGATTTTTGTTT
72639	70726	TACAAGTTTGGATTTTTGTT
72640	70727	TTACAAGTTTGGATTTTTGT
72641	70728	GTTACAAGTTTGGATTTTTG

121718	119805	TTTATTAAAAAAAAAAAAAA
121719	119806	ATTTATTAAAAAAAAAAAAA
121720	119807	CATTTATTAAAAAAAAAAAA
121721	119808	CCATTTATTAAAAAAAAAAA
121722	119809	TCCATTTATTAAAAAAAAAA
121723	119810	TTCCATTTATTAAAAAAAAA
121724	119811	ATTCCATTTATTAAAAAAAA
121725	119812	GATTCCATTTATTAAAAAAA
121726	119813	TGATTCCATTTATTAAAAAA
121727	119814	TTGATTCCATTTATTAAAAA
121728	119815	TTTGATTCCATTTATTAAAA
121729	119816	GTTTGATTCCATTTATTAAA
121730	119817	TGTTTGATTCCATTTATTAA
121731	119818	CTGTTTGATTCCATTTATTA
121732	119819	GCTGTTTGATTCCATTTATT
121733	119820	CGCTGTTTGATTCCATTTAT
121734	119821	ACGCTGTTTGATTCCATTTA
121735	119822	CACGCTGTTTGATTCCATTT
121736	119823	ACACGCTGTTTGATTCCATT
121737	119824	TACACGCTGTTTGATTCCAT
121738	119825	TTACACGCTGTTTGATTCCA
121739	119826	GTTACACGCTGTTTGATTCC
121740	119827	TGTTACACGCTGTTTGATTC
121741	119828	CTGTTACACGCTGTTTGATT
121742	119829	TCTGTTACACGCTGTTTGAT
121743	119830	CTCTGTTACACGCTGTTTGA
121744	119831	CCTCTGTTACACGCTGTTTG
121745	119832	ACCTCTGTTACACGCTGTTT
121746	119833	CACCTCTGTTACACGCTGTT
121747	119834	ACACCTCTGTTACACGCTGT
121748	119835	AACACCTCTGTTACACGCTG
121749	119836	GAACACCTCTGTTACACGCT
121750	119837	TGAACACCTCTGTTACACGC
121751	119838	TTGAACACCTCTGTTACACG
121752	119839	ATTGAACACCTCTGTTACAC
121753	119840	GATTGAACACCTCTGTTACA
121754	119841	AGATTGAACACCTCTGTTAC
121755	119842	AAGATTGAACACCTCTGTTA
121756	119843	AAAGATTGAACACCTCTGTT
121757	119844	AAAAGATTGAACACCTCTGT
121758	119845	CAAAAGATTGAACACCTCTG
121759	119846	CCAAAAGATTGAACACCTCT
121760	119847	GCCAAAAGATTGAACACCTC
121761	119848	AGCCAAAAGATTGAACACCT
121762	119849	AAGCCAAAAGATTGAACACC
121763	119850	GAAGCCAAAAGATTGAACAC
121764	119851	GGAAGCCAAAAGATTGAACA
121765	119852	GGGAAGCCAAAAGATTGAAC
121766	119853	AGGGAAGCCAAAAGATTGAA
121767	119854	CAGGGAAGCCAAAAGATTGA
121768	119855	CCAGGGAAGCCAAAAGATTG
121769	119856	CCCAGGGAAGCCAAAAGATT
121770	119857	ACCCAGGGAAGCCAAAAGAT
121771	119858	GACCCAGGGAAGCCAAAAGA
121772	119859	TGACCCAGGGAAGCCAAAAG
121773	119860	ATGACCCAGGGAAGCCAAAA
121774	119861	TATGACCCAGGGAAGCCAAA
121775	119862	ATATGACCCAGGGAAGCCAA
121776	119863	AATATGACCCAGGGAAGCCA
121777	119864	CAATATGACCCAGGGAAGCC
121778	119865	CCAATATGACCCAGGGAAGC
121779	119866	TCCAATATGACCCAGGGAAG
121780	119867	TTCCAATATGACCCAGGGAA
121781	119868	CTTCCAATATGACCCAGGGA
121782	119869	TCTTCCAATATGACCCAGGG
121783	119870	TTCTTCCAATATGACCCAGG
121784	119871	CTTCTTCCAATATGACCCAG
121785	119872	TCTTCTTCCAATATGACCCA
121786	119873	TTCTTCTTCCAATATGACCC
121787	119874	ATTCTTCTTCCAATATGACC
121788	119875	AATTCTTCTTCCAATATGAC

23495	21582	TGTAATCCCAGCTATTCAGG
23496	21583	CTGTAATCCCAGCTATTCAG
23497	21584	CCTGTAATCCCAGCTATTCA
23498	21585	ACCTGTAATCCCAGCTATTC
23499	21586	CACCTGTAATCCCAGCTATT
23500	21587	GCACCTGTAATCCCAGCTAT
23501	21588	CGCACCTGTAATCCCAGCTA
23502	21589	ACGCACCTGTAATCCCAGCT
23503	21590	CACGCACCTGTAATCCCAGC
23504	21591	GCACGCACCTGTAATCCCAG
23505	21592	GGCACGCACCTGTAATCCCA
23506	21593	TGGCACGCACCTGTAATCCC
23507	21594	GTGGCACGCACCTGTAATCC
23508	21595	GGTGGCACGCACCTGTAATC
23509	21596	TGGTGGCACGCACCTGTAAT
23510	21597	GTGGTGGCACGCACCTGTAA
23511	21598	TGTGGTGGCACGCACCTGTA
23512	21599	GTGTGGTGGCACGCACCTGT
23513	21600	GGTGTGGTGGCACGCACCTG
23514	21601	AGGTGTGGTGGCACGCACCT
23515	21602	CAGGTGTGGTGGCACGCACC
23516	21603	CCAGGTGTGGTGGCACGCAC
23517	21604	GCCAGGTGTGGTGGCACGCA
23518	21605	AGCCAGGTGTGGTGGCACGC
23519	21606	TAGCCAGGTGTGGTGGCACG
23520	21607	TTAGCCAGGTGTGGTGGCAC
23521	21608	ATTAGCCAGGTGTGGTGGCA
23522	21609	AATTAGCCAGGTGTGGTGGC
23523	21610	AAATTAGCCAGGTGTGGTGG
23524	21611	AAAATTAGCCAGGTGTGGTG
23525	21612	AAAAATTAGCCAGGTGTGGT
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23527	21614	ACAAAAATTAGCCAGGTGTG
23528	21615	TACAAAAATTAGCCAGGTGT
23529	21616	ATACAAAAATTAGCCAGGTG
23530	21617	AATACAAAAATTAGCCAGGT
23531	21618	AAATACAAAAATTAGCCAGG
23532	21619	AAAATACAAAAATTAGCCAG
23533	21620	AAAAATACAAAAATTAGCCA
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23535	21622	CTAAAAATACAAAAATTAGC
23536	21623	ACTAAAAATACAAAAATTAG
23537	21624	TACTAAAAATACAAAAATTA
23538	21625	CTACTAAAAATACAAAAATT
23539	21626	TCTACTAAAAATACAAAAAT
23540	21627	CTCTACTAAAAATACAAAAA
23541	21628	TCTCTACTAAAAATACAAAA
23542	21629	GTCTCTACTAAAAATACAAA
23543	21630	CGTCTCTACTAAAAATACAA
23544	21631	CCGTCTCTACTAAAAATACA
23545	21632	CCCGTCTCTACTAAAAATAC
23546	21633	CCCCGTCTCTACTAAAAATA
23547	21634	CCCCCGTCTCTACTAAAAAT
23548	21635	ACCCCCGTCTCTACTAAAAA
23549	21636	AACCCCCGTCTCTACTAAAA
23550	21637	AAACCCCCGTCTCTACTAAA
23551	21638	GAAACCCCCGTCTCTACTAA
23552	21639	TGAAACCCCCGTCTCTACTA
23553	21640	GTGAAACCCCCGTCTCTACT
23554	21641	GGTGAAACCCCCGTCTCTAC
23555	21642	TGGTGAAACCCCCGTCTCTA
23556	21643	ATGGTGAAACCCCCGTCTCT
23557	21644	CATGGTGAAACCCCCGTCTC
23558	21645	ACATGGTGAAACCCCCGTCT
23559	21646	AACATGGTGAAACCCCCGTC
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23561	21648	CCAACATGGTGAAACCCCCG
23562	21649	GCCAACATGGTGAAACCCCC
23563	21650	GGCCAACATGGTGAAACCCC
23564	21651	TGGCCAACATGGTGAAACCC
23565	21652	CTGGCCAACATGGTGAAACC

72642	70729	GGTTACAAGTTTGGATTTTT
72643	70730	TGGTTACAAGTTTGGATTTT
72644	70731	GTGGTTACAAGTTTGGATTT
72645	70732	AGTGGTTACAAGTTTGGATT
72646	70733	CAGTGGTTACAAGTTTGGAT
72647	70734	ACAGTGGTTACAAGTTTGGA
72648	70735	TACAGTGGTTACAAGTTTGG
72649	70736	TTACAGTGGTTACAAGTTTG
72650	70737	TTTACAGTGGTTACAAGTTT
72651	70738	TTTTACAGTGGTTACAAGTT
72652	70739	GTTTTACAGTGGTTACAAGT
72653	70740	TGTTTTACAGTGGTTACAAG
72654	70741	TTGTTTTACAGTGGTTACAA
72655	70742	TTTGTTTTACAGTGGTTACA
72656	70743	ATTTGTTTTACAGTGGTTAC
72657	70744	GATTTGTTTTACAGTGGTTA
72658	70745	TGATTTGTTTTACAGTGGTT
72659	70746	CTGATTTGTTTTACAGTGGT
72660	70747	TCTGATTTGTTTTACAGTGG
72661	70748	TTCTGATTTGTTTTACAGTG
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72664	70751	AAATTCTGATTTGTTTTACA
72665	70752	TAAATTCTGATTTGTTTTAC
72666	70753	GTAAATTCTGATTTGTTTTA
72667	70754	CGTAAATTCTGATTTGTTTT
72668	70755	TCGTAAATTCTGATTTGTTT
72669	70756	ATCGTAAATTCTGATTTGTT
72670	70757	TATCGTAAATTCTGATTTGT
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72674	70761	CCACTATCGTAAATTCTGAT
72675	70762	TCCACTATCGTAAATTCTGA
72676	70763	ATCCACTATCGTAAATTCTG
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72678	70765	ATATCCACTATCGTAAATTC
72679	70766	AATATCCACTATCGTAAATT
72680	70767	TAATATCCACTATCGTAAAT
72681	70768	ATAATATCCACTATCGTAAA
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72683	70770	TAATAATATCCACTATCGTA
72684	70771	TTAATAATATCCACTATCGT
72685	70772	ATTAATAATATCCACTATCG
72686	70773	TATTAATAATATCCACTATC
72687	70774	CTATTAATAATATCCACTAT
72688	70775	ACTATTAATAATATCCACTA
72689	70776	CACTATTAATAATATCCACT
72690	70777	GCACTATTAATAATATCCAC
72691	70778	TGCACTATTAATAATATCCA
72692	70779	CTGCACTATTAATAATATCC
72693	70780	TCTGCACTATTAATAATATC
72694	70781	TTCTGCACTATTAATAATAT
72695	70782	ATTCTGCACTATTAATAATA
72696	70783	CATTCTGCACTATTAATAAT
72697	70784	CCATTCTGCACTATTAATAA
72698	70785	TCCATTCTGCACTATTAATA
72699	70786	ATCCATTCTGCACTATTAAT
72700	70787	TATCCATTCTGCACTATTAA
72701	70788	GTATCCATTCTGCACTATTA
72702	70789	GGTATCCATTCTGCACTATT
72703	70790	GGGTATCCATTCTGCACTAT
72704	70791	TGGGTATCCATTCTGCACTA
72705	70792	CTGGGTATCCATTCTGCACT
72706	70793	TCTGGGTATCCATTCTGCAC
72707	70794	ATCTGGGTATCCATTCTGCA
72708	70795	GATCTGGGTATCCATTCTGC
72709	70796	AGATCTGGGTATCCATTCTG
72710	70797	AAGATCTGGGTATCCATTCT
72711	70798	CAAGATCTGGGTATCCATTC
72712	70799	GCAAGATCTGGGTATCCATT

121789	119876	CAATTCTTCTTCCAATATGA
121790	119877	ACAATTCTTCTTCCAATATG
121791	119878	CACAATTCTTCTTCCAATAT
121792	119879	ACACAATTCTTCTTCCAATA
121793	119880	AACACAATTCTTCTTCCAAT
121794	119881	CAACACAATTCTTCTTCCAA
121795	119882	CCAACACAATTCTTCTTCCA
121796	119883	CCCAACACAATTCTTCTTCC
121797	119884	GCCCAACACAATTCTTCTTC
121798	119885	GGCCCAACACAATTCTTCTT
121799	119886	TGGCCCAACACAATTCTTCT
121800	119887	GTGGCCCAACACAATTCTTC
121801	119888	TGTGGCCCAACACAATTCTT
121802	119889	GTGTGGCCCAACACAATTCT
121803	119890	TGTGTGGCCCAACACAATTC
121804	119891	ATGTGTGGCCCAACACAATT
121805	119892	TATGTGTGGCCCAACACAAT
121806	119893	TTATGTGTGGCCCAACACAA
121807	119894	TTTATGTGTGGCCCAACACA
121808	119895	TTTTATGTGTGGCCCAACAC
121809	119896	ATTTTATGTGTGGCCCAACA
121810	119897	TATTTTATGTGTGGCCCAAC
121811	119898	GTATTTTATGTGTGGCCCAA
121812	119899	TGTATTTTATGTGTGGCCCA
121813	119900	CTGTATTTTATGTGTGGCCC
121814	119901	ACTGTATTTTATGTGTGGCC
121815	119902	TACTGTATTTTATGTGTGGC
121816	119903	TTACTGTATTTTATGTGTGG
121817	119904	GTTACTGTATTTTATGTGTG
121818	119905	TGTTACTGTATTTTATGTGT
121819	119906	GTGTTACTGTATTTTATGTG
121820	119907	AGTGTTACTGTATTTTATGT
121821	119908	TAGTGTTACTGTATTTTATG
121822	119909	TTAGTGTTACTGTATTTTAT
121823	119910	ATTAGTGTTACTGTATTTTA
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121825	119912	TCATTAGTGTTACTGTATTT
121826	119913	ATCATTAGTGTTACTGTATT
121827	119914	TATCATTAGTGTTACTGTAT
121828	119915	CTATCATTAGTGTTACTGTA
121829	119916	GCTATCATTAGTGTTACTGT
121830	119917	AGCTATCATTAGTGTTACTG
121831	119918	CAGCTATCATTAGTGTTACT
121832	119919	TCAGCTATCATTAGTGTTAC
121833	119920	ATCAGCTATCATTAGTGTTA
121834	119921	CATCAGCTATCATTAGTGTT
121835	119922	TCATCAGCTATCATTAGTGT
121836	119923	TTCATCAGCTATCATTAGTG
121837	119924	GTTCATCAGCTATCATTAGT
121838	119925	TGTTCATCAGCTATCATTAG
121839	119926	TTGTTCATCAGCTATCATTA
121840	119927	TTTGTTCATCAGCTATCATT
121841	119928	TTTTGTTCATCAGCTATCAT
121842	119929	GTTTTGTTCATCAGCTATCA
121843	119930	TGTTTTGTTCATCAGCTATC
121844	119931	TTGTTTTGTTCATCAGCTAT
121845	119932	TTTGTTTTGTTCATCAGCTA
121846	119933	TTTTGTTTTGTTCATCAGCT
121847	119934	TTTTTGTTTTGTTCATCAGC
121848	119935	TTTTTTGTTTTGTTCATCAG
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121854	119941	CTATTTTTTTTTGTTTTGTT
121855	119942	GCTATTTTTTTTTGTTTTGT
121856	119943	TGCTATTTTTTTTTGTTTTG
121857	119944	TTGCTATTTTTTTTTGTTTT
121858	119945	TTTGCTATTTTTTTTTGTTT
121859	119946	TTTTGCTATTTTTTTTTGTT

23566	21653	CCTGGCCAACATGGTGAAAC
23567	21654	GCCTGGCCAACATGGTGAAA
23568	21655	AGCCTGGCCAACATGGTGAA
23569	21656	CAGCCTGGCCAACATGGTGA
23570	21657	CCAGCCTGGCCAACATGGTG
23571	21658	ACCAGCCTGGCCAACATGGT
23572	21659	GACCAGCCTGGCCAACATGG
23573	21660	AGACCAGCCTGGCCAACATG
23574	21661	GAGACCAGCCTGGCCAACAT
23575	21662	CGAGACCAGCCTGGCCAACA
23576	21663	TCGAGACCAGCCTGGCCAAC
23577	21664	TTCGAGACCAGCCTGGCCAA
23578	21665	GTTCGAGACCAGCCTGGCCA
23579	21666	AGTTCGAGACCAGCCTGGCC
23580	21667	GAGTTCGAGACCAGCCTGGC
23581	21668	GGAGTTCGAGACCAGCCTGG
23582	21669	AGGAGTTCGAGACCAGCCTG
23583	21670	CAGGAGTTCGAGACCAGCCT
23584	21671	TCAGGAGTTCGAGACCAGCC
23585	21672	GTCAGGAGTTCGAGACCAGC
23586	21673	GGTCAGGAGTTCGAGACCAG
23587	21674	AGGTCAGGAGTTCGAGACCA
23588	21675	GAGGTCAGGAGTTCGAGACC
23589	21676	TGAGGTCAGGAGTTCGAGAC
23590	21677	CTGAGGTCAGGAGTTCGAGA
23591	21678	CCTGAGGTCAGGAGTTCGAG
23592	21679	ACCTGAGGTCAGGAGTTCGA
23593	21680	CACCTGAGGTCAGGAGTTCG
23594	21681	TCACCTGAGGTCAGGAGTTC
23595	21682	ATCACCTGAGGTCAGGAGTT
23596	21683	GATCACCTGAGGTCAGGAGT
23597	21684	GGATCACCTGAGGTCAGGAG
23598	21685	TGGATCACCTGAGGTCAGGA
23599	21686	GTGGATCACCTGAGGTCAGG
23600	21687	GGTGGATCACCTGAGGTCAG
23601	21688	GGGTGGATCACCTGAGGTCA
23602	21689	CGGGTGGATCACCTGAGGTC
23603	21690	GCGGGTGGATCACCTGAGGT
23604	21691	GGCGGGTGGATCACCTGAGG
23605	21692	CGGCGGGTGGATCACCTGAG
23606	21693	ACGGCGGGTGGATCACCTGA
23607	21694	CACGGCGGGTGGATCACCTG
23608	21695	CCACGGCGGGTGGATCACCT
23609	21696	GCCACGGCGGGTGGATCACC
23610	21697	GGCCACGGCGGGTGGATCAC
23611	21698	AGGCCACGGCGGGTGGATCA
23612	21699	GAGGCCACGGCGGGTGGATC
23613	21700	GGAGGCCACGGCGGGTGGAT
23614	21701	GGGAGGCCACGGCGGGTGGA
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23616	21703	TTGGGAGGCCACGGCGGGTG
23617	21704	TTTGGGAGGCCACGGCGGGT
23618	21705	CTTTGGGAGGCCACGGCGGG
23619	21706	ACTTTGGGAGGCCACGGCGG
23620	21707	CACTTTGGGAGGCCACGGCG
23621	21708	GCACTTTGGGAGGCCACGGC
23622	21709	AGCACTTTGGGAGGCCACGG
23623	21710	CAGCACTTTGGGAGGCCACG
23624	21711	CCAGCACTTTGGGAGGCCAC
23625	21712	CCCAGCACTTTGGGAGGCCA
23626	21713	TCCCAGCACTTTGGGAGGCC
23627	21714	ATCCCAGCACTTTGGGAGGC
23628	21715	AATCCCAGCACTTTGGGAGG
23629	21716	TAATCCCAGCACTTTGGGAG
23630	21717	GTAATCCCAGCACTTTGGGA
23631	21718	TGTAATCCCAGCACTTTGGG
23632	21719	CTGTAATCCCAGCACTTTGG
23633	21720	TCTGTAATCCCAGCACTTTG
23634	21721	ATCTGTAATCCCAGCACTTT
23635	21722	CATCTGTAATCCCAGCACTT
23636	21723	ACATCTGTAATCCCAGCACT

72713	70800	AGCAAGATCTGGGTATCCAT
72714	70801	AAGCAAGATCTGGGTATCCA
72715	70802	GAAGCAAGATCTGGGTATCC
72716	70803	GGAAGCAAGATCTGGGTATC
72717	70804	AGGAAGCAAGATCTGGGTAT
72718	70805	AAGGAAGCAAGATCTGGGTA
72719	70806	AAAGGAAGCAAGATCTGGGT
72720	70807	GAAAGGAAGCAAGATCTGGG
72721	70808	AGAAAGGAAGCAAGATCTGG
72722	70809	TAGAAAGGAAGCAAGATCTG
72723	70810	CTAGAAAGGAAGCAAGATCT
72724	70811	GCTAGAAAGGAAGCAAGATC
72725	70812	AGCTAGAAAGGAAGCAAGAT
72726	70813	TAGCTAGAAAGGAAGCAAGA
72727	70814	TTAGCTAGAAAGGAAGCAAG
72728	70815	ATTAGCTAGAAAGGAAGCAA
72729	70816	CATTAGCTAGAAAGGAAGCA
72730	70817	TCATTAGCTAGAAAGGAAGC
72731	70818	ATCATTAGCTAGAAAGGAAG
72732	70819	CATCATTAGCTAGAAAGGAA
72733	70820	GCATCATTAGCTAGAAAGGA
72734	70821	TGCATCATTAGCTAGAAAGG
72735	70822	TTGCATCATTAGCTAGAAAG
72736	70823	ATTGCATCATTAGCTAGAAA
72737	70824	CATTGCATCATTAGCTAGAA
72738	70825	ACATTGCATCATTAGCTAGA
72739	70826	AACATTGCATCATTAGCTAG
72740	70827	CAACATTGCATCATTAGCTA
72741	70828	CCAACATTGCATCATTAGCT
72742	70829	GCCAACATTGCATCATTAGC
72743	70830	GGCCAACATTGCATCATTAG
72744	70831	AGGCCAACATTGCATCATTA
72745	70832	CAGGCCAACATTGCATCATT
72746	70833	TCAGGCCAACATTGCATCAT
72747	70834	TTCAGGCCAACATTGCATCA
72748	70835	TTTCAGGCCAACATTGCATC
72749	70836	ATTTCAGGCCAACATTGCAT
72750	70837	CATTTCAGGCCAACATTGCA
72751	70838	GCATTTCAGGCCAACATTGC
72752	70839	TGCATTTCAGGCCAACATTG
72753	70840	ATGCATTTCAGGCCAACATT
72754	70841	AATGCATTTCAGGCCAACAT
72755	70842	TAATGCATTTCAGGCCAACA
72756	70843	GTAATGCATTTCAGGCCAAC
72757	70844	AGTAATGCATTTCAGGCCAA
72758	70845	AAGTAATGCATTTCAGGCCA
72759	70846	TAAGTAATGCATTTCAGGCC
72760	70847	ATAAGTAATGCATTTCAGGC
72761	70848	TATAAGTAATGCATTTCAGG
72762	70849	CTATAAGTAATGCATTTCAG
72763	70850	GCTATAAGTAATGCATTTCA
72764	70851	GGCTATAAGTAATGCATTTC
72765	70852	TGGCTATAAGTAATGCATTT
72766	70853	CTGGCTATAAGTAATGCATT
72767	70854	CCTGGCTATAAGTAATGCAT
72768	70855	CCCTGGCTATAAGTAATGCA
72769	70856	TCCCTGGCTATAAGTAATGC
72770	70857	ATCCCTGGCTATAAGTAATG
72771	70858	AATCCCTGGCTATAAGTAAT
72772	70859	AAATCCCTGGCTATAAGTAA
72773	70860	AAAATCCCTGGCTATAAGTA
72774	70861	GAAAATCCCTGGCTATAAGT
72775	70862	AGAAAATCCCTGGCTATAAG
72776	70863	GAGAAAATCCCTGGCTATAA
72777	70864	TGAGAAAATCCCTGGCTATA
72778	70865	CTGAGAAAATCCCTGGCTAT
72779	70866	GCTGAGAAAATCCCTGGCTA
72780	70867	TGCTGAGAAAATCCCTGGCT
72781	70868	ATGCTGAGAAAATCCCTGGC
72782	70869	GATGCTGAGAAAATCCCTGG
72783	70870	GGATGCTGAGAAAATCCCTG

121860	119947	GTTTTGCTATTTTTTTTTGT
121861	119948	AGTTTTGCTATTTTTTTTTG
121862	119949	AAGTTTTGCTATTTTTTTTT
121863	119950	TAAGTTTTGCTATTTTTTTT
121864	119951	ATAAGTTTTGCTATTTTTTT
121865	119952	TATAAGTTTTGCTATTTTTT
121866	119953	TTATAAGTTTTGCTATTTTT
121867	119954	ATTATAAGTTTTGCTATTTT
121868	119955	CATTATAAGTTTTGCTATTT
121869	119956	ACATTATAAGTTTTGCTATT
121870	119957	AACATTATAAGTTTTGCTAT
121871	119958	AAACATTATAAGTTTTGCTA
121872	119959	AAAACATTATAAGTTTTGCT
121873	119960	TAAAACATTATAAGTTTTGC
121874	119961	TTAAAACATTATAAGTTTTG
121875	119962	CTTAAAACATTATAAGTTTT
121876	119963	TCTTAAAACATTATAAGTTT
121877	119964	TTCTTAAAACATTATAAGTT
121878	119965	TTTCTTAAAACATTATAAGT
121879	119966	CTTTCTTAAAACATTATAAG
121880	119967	ACTTTCTTAAAACATTATAA
121881	119968	AACTTTCTTAAAACATTATA
121882	119969	AAACTTTCTTAAAACATTAT
121883	119970	TAAACTTTCTTAAAACATTA
121884	119971	ATAAACTTTCTTAAAACATT
121885	119972	CATAAACTTTCTTAAAACAT
121886	119973	TCATAAACTTTCTTAAAACA
121887	119974	TTCATAAACTTTCTTAAAAC
121888	119975	ATTCATAAACTTTCTTAAAA
121889	119976	AATTCATAAACTTTCTTAAA
121890	119977	AAATTCATAAACTTTCTTAA
121891	119978	CAAATTCATAAACTTTCTTA
121892	119979	ACAAATTCATAAACTTTCTT
121893	119980	CACAAATTCATAAACTTTCT
121894	119981	ACACAAATTCATAAACTTTC
121895	119982	AACACAAATTCATAAACTTT
121896	119983	CAACACAAATTCATAAACTT
121897	119984	CCAACACAAATTCATAAACT
121898	119985	CCCAACACAAATTCATAAAC
121899	119986	GCCCAACACAAATTCATAAA
121900	119987	GGCCCAACACAAATTCATAA
121901	119988	TGGCCCAACACAAATTCATA
121902	119989	GTGGCCCAACACAAATTCAT
121903	119990	TGTGGCCCAACACAAATTCA
121904	119991	ATGTGGCCCAACACAAATTC
121905	119992	AATGTGGCCCAACACAAATT
121906	119993	GAATGTGGCCCAACACAAAT
121907	119994	TGAATGTGGCCCAACACAAA
121908	119995	TTGAATGTGGCCCAACACAA
121909	119996	TTTGAATGTGGCCCAACACA
121910	119997	CTTTGAATGTGGCCCAACAC
121911	119998	GCTTTGAATGTGGCCCAACA
121912	119999	GGCTTTGAATGTGGCCCAAC
121913	120000	CGGCTTTGAATGTGGCCCAA
121914	120001	ACGGCTTTGAATGTGGCCCA
121915	120002	GACGGCTTTGAATGTGGCCC
121916	120003	GGACGGCTTTGAATGTGGCC
121917	120004	GGGACGGCTTTGAATGTGGC
121918	120005	TGGGACGGCTTTGAATGTGG
121919	120006	CTGGGACGGCTTTGAATGTG
121920	120007	CCTGGGACGGCTTTGAATGT
121921	120008	TCCTGGGACGGCTTTGAATG
121922	120009	GTCCTGGGACGGCTTTGAAT
121923	120010	CGTCCTGGGACGGCTTTGAA
121924	120011	GCGTCCTGGGACGGCTTTGA
121925	120012	TGCGTCCTGGGACGGCTTTG
121926	120013	TTGCGTCCTGGGACGGCTTT
121927	120014	CTTGCGTCCTGGGACGGCTT
121928	120015	ACTTGCGTCCTGGGACGGCT
121929	120016	AACTTGCGTCCTGGGACGGC
121930	120017	CAACTTGCGTCCTGGGACGG

23637	21724	CACATCTGTAATCCCAGCAC
23638	21725	TCACATCTGTAATCCCAGCA
23639	21726	CTCACATCTGTAATCCCAGC
23640	21727	GCTCACATCTGTAATCCCAG
23641	21728	GGCTCACATCTGTAATCCCA
23642	21729	TGGCTCACATCTGTAATCCC
23643	21730	GTGGCTCACATCTGTAATCC
23644	21731	GGTGGCTCACATCTGTAATC
23645	21732	CGGTGGCTCACATCTGTAAT
23646	21733	GCGGTGGCTCACATCTGTAA
23647	21734	TGCGGTGGCTCACATCTGTA
23648	21735	GTGCGGTGGCTCACATCTGT
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23650	21737	AGGTGCGGTGGCTCACATCT
23651	21738	CAGGTGCGGTGGCTCACATC
23652	21739	CCAGGTGCGGTGGCTCACAT
23653	21740	GCCAGGTGCGGTGGCTCACA
23654	21741	GGCCAGGTGCGGTGGCTCAC
23655	21742	TGGCCAGGTGCGGTGGCTCA
23656	21743	CTGGCCAGGTGCGGTGGCTC
23657	21744	TCTGGCCAGGTGCGGTGGCT
23658	21745	CTCTGGCCAGGTGCGGTGGC
23659	21746	TCTCTGGCCAGGTGCGGTGG
23660	21747	ATCTCTGGCCAGGTGCGGTG
23661	21748	CATCTCTGGCCAGGTGCGGT
23662	21749	TCATCTCTGGCCAGGTGCGG
23663	21750	CTCATCTCTGGCCAGGTGCG
23664	21751	CCTCATCTCTGGCCAGGTGC
23665	21752	ACCTCATCTCTGGCCAGGTG
23666	21753	GACCTCATCTCTGGCCAGGT
23667	21754	AGACCTCATCTCTGGCCAGG
23668	21755	AAGACCTCATCTCTGGCCAG
23669	21756	CAAGACCTCATCTCTGGCCA
23670	21757	GCAAGACCTCATCTCTGGCC
23671	21758	AGCAAGACCTCATCTCTGGC
23672	21759	CAGCAAGACCTCATCTCTGG
23673	21760	ACAGCAAGACCTCATCTCTG
23674	21761	TACAGCAAGACCTCATCTCT
23675	21762	ATACAGCAAGACCTCATCTC
23676	21763	AATACAGCAAGACCTCATCT
23677	21764	CAATACAGCAAGACCTCATC
23678	21765	GCAATACAGCAAGACCTCAT
23679	21766	GGCAATACAGCAAGACCTCA
23680	21767	GGGCAATACAGCAAGACCTC
23681	21768	TGGGCAATACAGCAAGACCT
23682	21769	CTGGGCAATACAGCAAGACC
23683	21770	CCTGGGCAATACAGCAAGAC
23684	21771	CCCTGGGCAATACAGCAAGA
23685	21772	GCCCTGGGCAATACAGCAAG
23686	21773	CGCCCTGGGCAATACAGCAA
23687	21774	ACGCCCTGGGCAATACAGCA
23688	21775	AACGCCCTGGGCAATACAGC
23689	21776	CAACGCCCTGGGCAATACAG
23690	21777	TCAACGCCCTGGGCAATACA
23691	21778	TTCAACGCCCTGGGCAATAC
23692	21779	GTTCAACGCCCTGGGCAATA
23693	21780	AGTTCAACGCCCTGGGCAAT
23694	21781	GAGTTCAACGCCCTGGGCAA
23695	21782	GGAGTTCAACGCCCTGGGCA
23696	21783	AGGAGTTCAACGCCCTGGGC
23697	21784	CAGGAGTTCAACGCCCTGGG
23698	21785	CCAGGAGTTCAACGCCCTGG
23699	21786	CCCAGGAGTTCAACGCCCTG
23700	21787	GCCCAGGAGTTCAACGCCCT
23701	21788	AGCCCAGGAGTTCAACGCCC
23702	21789	GAGCCCAGGAGTTCAACGCC
23703	21790	GGAGCCCAGGAGTTCAACGC
23704	21791	TGGAGCCCAGGAGTTCAACG
23705	21792	CTGGAGCCCAGGAGTTCAAC
23706	21793	GCTGGAGCCCAGGAGTTCAA
23707	21794	TGCTGGAGCCCAGGAGTTCA

72784	70871	AGGATGCTGAGAAAATCCCT
72785	70872	CAGGATGCTGAGAAAATCCC
72786	70873	TCAGGATGCTGAGAAAATCC
72787	70874	ATCAGGATGCTGAGAAAATC
72788	70875	CATCAGGATGCTGAGAAAAT
72789	70876	TCATCAGGATGCTGAGAAAA
72790	70877	ATCATCAGGATGCTGAGAAA
72791	70878	TATCATCAGGATGCTGAGAA
72792	70879	ATATCATCAGGATGCTGAGA
72793	70880	TATATCATCAGGATGCTGAG
72794	70881	CTATATCATCAGGATGCTGA
72795	70882	GCTATATCATCAGGATGCTG
72796	70883	GGCTATATCATCAGGATGCT
72797	70884	AGGCTATATCATCAGGATGC
72798	70885	GAGGCTATATCATCAGGATG
72799	70886	TGAGGCTATATCATCAGGAT
72800	70887	ATGAGGCTATATCATCAGGA
72801	70888	AATGAGGCTATATCATCAGG
72802	70889	AAATGAGGCTATATCATCAG
72803	70890	GAAATGAGGCTATATCATCA
72804	70891	CGAAATGAGGCTATATCATC
72805	70892	ACGAAATGAGGCTATATCAT
72806	70893	CACGAAATGAGGCTATATCA
72807	70894	GCACGAAATGAGGCTATATC
72808	70895	AGCACGAAATGAGGCTATAT
72809	70896	TAGCACGAAATGAGGCTATA
72810	70897	TTAGCACGAAATGAGGCTAT
72811	70898	GTTAGCACGAAATGAGGCTA
72812	70899	AGTTAGCACGAAATGAGGCT
72813	70900	GAGTTAGCACGAAATGAGGC
72814	70901	AGAGTTAGCACGAAATGAGG
72815	70902	GAGAGTTAGCACGAAATGAG
72816	70903	GGAGAGTTAGCACGAAATGA
72817	70904	TGGAGAGTTAGCACGAAATG
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72825	70912	TGCAGAAGTGGAGAGTTAGC
72826	70913	GTGCAGAAGTGGAGAGTTAG
72827	70914	TGTGCAGAAGTGGAGAGTTA
72828	70915	ATGTGCAGAAGTGGAGAGTT
72829	70916	GATGTGCAGAAGTGGAGAGT
72830	70917	AGATGTGCAGAAGTGGAGAG
72831	70918	AAGATGTGCAGAAGTGGAGA
72832	70919	GAAGATGTGCAGAAGTGGAG
72833	70920	GGAAGATGTGCAGAAGTGGA
72834	70921	GGGAAGATGTGCAGAAGTGG
72835	70922	GGGGAAGATGTGCAGAAGTG
72836	70923	AGGGGAAGATGTGCAGAAGT
72837	70924	TAGGGGAAGATGTGCAGAAG
72838	70925	TTAGGGGAAGATGTGCAGAA
72839	70926	CTTAGGGGAAGATGTGCAGA
72840	70927	ACTTAGGGGAAGATGTGCAG
72841	70928	GACTTAGGGGAAGATGTGCA
72842	70929	GGACTTAGGGGAAGATGTGC
72843	70930	AGGACTTAGGGGAAGATGTG
72844	70931	AAGGACTTAGGGGAAGATGT
72845	70932	AAAGGACTTAGGGGAAGATG
72846	70933	TAAAGGACTTAGGGGAAGAT
72847	70934	GTAAAGGACTTAGGGGAAGA
72848	70935	AGTAAAGGACTTAGGGGAAG
72849	70936	GAGTAAAGGACTTAGGGGAA
72850	70937	TGAGTAAAGGACTTAGGGGA
72851	70938	ATGAGTAAAGGACTTAGGGG
72852	70939	GATGAGTAAAGGACTTAGGG
72853	70940	AGATGAGTAAAGGACTTAGG
72854	70941	AAGATGAGTAAAGGACTTAG

121931	120018	CCAACTTGCGTCCTGGGACG
121932	120019	TCCAACTTGCGTCCTGGGAC
121933	120020	GTCCAACTTGCGTCCTGGGA
121934	120021	TGTCCAACTTGCGTCCTGGG
121935	120022	TTGTCCAACTTGCGTCCTGG
121936	120023	CTTGTCCAACTTGCGTCCTG
121937	120024	GCTTGTCCAACTTGCGTCCT
121938	120025	AGCTTGTCCAACTTGCGTCC
121939	120026	AAGCTTGTCCAACTTGCGTC
121940	120027	CAAGCTTGTCCAACTTGCGT
121941	120028	CCAAGCTTGTCCAACTTGCG
121942	120029	ACCAAGCTTGTCCAACTTGC
121943	120030	TACCAAGCTTGTCCAACTTG
121944	120031	ATACCAAGCTTGTCCAACTT
121945	120032	TATACCAAGCTTGTCCAACT
121946	120033	ATATACCAAGCTTGTCCAAC
121947	120034	TATATACCAAGCTTGTCCAA
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121950	120037	AATTATATACCAAGCTTGTC
121951	120038	AAATTATATACCAAGCTTGT
121952	120039	GAAATTATATACCAAGCTTG
121953	120040	TGAAATTATATACCAAGCTT
121954	120041	ATGAAATTATATACCAAGCT
121955	120042	TATGAAATTATATACCAAGC
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121957	120044	CATATGAAATTATATACCAA
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121959	120046	CACATATGAAATTATATACC
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121966	120053	TAGGACACACATATGAAATT
121967	120054	TTAGGACACACATATGAAAT
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121972	120059	ACTGTTTAGGACACACATAT
121973	120060	CACTGTTTAGGACACACATA
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121981	120068	AATTACTACACTGTTTAGGA
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121983	120070	CAAATTACTACACTGTTTAG
121984	120071	TCAAATTACTACACTGTTTA
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121989	120076	GAAATTCAAATTACTACACT
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121991	120078	ATGAAATTCAAATTACTACA
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121995	120082	TAACATGAAATTCAAATTAC
121996	120083	CTAACATGAAATTCAAATTA
121997	120084	ACTAACATGAAATTCAAATT
121998	120085	TACTAACATGAAATTCAAAT
121999	120086	ATACTAACATGAAATTCAAA
122000	120087	GATACTAACATGAAATTCAA
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23708	21795	TTGCTGGAGCCCAGGAGTTC
23709	21796	ATTGCTGGAGCCCAGGAGTT
23710	21797	GATTGCTGGAGCCCAGGAGT
23711	21798	GGATTGCTGGAGCCCAGGAG
23712	21799	AGGATTGCTGGAGCCCAGGA
23713	21800	GAGGATTGCTGGAGCCCAGG
23714	21801	GGAGGATTGCTGGAGCCCAG
23715	21802	GGGAGGATTGCTGGAGCCCA
23716	21803	TGGGAGGATTGCTGGAGCCC
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23718	21805	GGTGGGAGGATTGCTGGAGC
23719	21806	AGGTGGGAGGATTGCTGGAG
23720	21807	GAGGTGGGAGGATTGCTGGA
23721	21808	TGAGGTGGGAGGATTGCTGG
23722	21809	CTGAGGTGGGAGGATTGCTG
23723	21810	GCTGAGGTGGGAGGATTGCT
23724	21811	AGCTGAGGTGGGAGGATTGC
23725	21812	AAGCTGAGGTGGGAGGATTG
23726	21813	GAAGCTGAGGTGGGAGGATT
23727	21814	GGAAGCTGAGGTGGGAGGAT
23728	21815	GGGAAGCTGAGGTGGGAGGA
23729	21816	TGGGAAGCTGAGGTGGGAGG
23730	21817	GTGGGAAGCTGAGGTGGGAG
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23732	21819	ACGTGGGAAGCTGAGGTGGG
23733	21820	TACGTGGGAAGCTGAGGTGG
23734	21821	CTACGTGGGAAGCTGAGGTG
23735	21822	GCTACGTGGGAAGCTGAGGT
23736	21823	AGCTACGTGGGAAGCTGAGG
23737	21824	CAGCTACGTGGGAAGCTGAG
23738	21825	CCAGCTACGTGGGAAGCTGA
23739	21826	CCCAGCTACGTGGGAAGCTG
23740	21827	TCCCAGCTACGTGGGAAGCT
23741	21828	GTCCCAGCTACGTGGGAAGC
23742	21829	AGTCCCAGCTACGTGGGAAG
23743	21830	CAGTCCCAGCTACGTGGGAA
23744	21831	ACAGTCCCAGCTACGTGGGA
23745	21832	CACAGTCCCAGCTACGTGGG
23746	21833	CCACAGTCCCAGCTACGTGG
23747	21834	CCCACAGTCCCAGCTACGTG
23748	21835	ACCCACAGTCCCAGCTACGT
23749	21836	CACCCACAGTCCCAGCTACG
23750	21837	GCACCCACAGTCCCAGCTAC
23751	21838	TGCACCCACAGTCCCAGCTA
23752	21839	GTGCACCCACAGTCCCAGCT
23753	21840	CGTGCACCCACAGTCCCAGC
23754	21841	GCGTGCACCCACAGTCCCAG
23755	21842	GGCGTGCACCCACAGTCCCA
23756	21843	TGGCGTGCACCCACAGTCCC
23757	21844	ATGGCGTGCACCCACAGTCC
23758	21845	GATGGCGTGCACCCACAGTC
23759	21846	TGATGGCGTGCACCCACAGT
23760	21847	ATGATGGCGTGCACCCACAG
23761	21848	CATGATGGCGTGCACCCACA
23762	21849	GCATGATGGCGTGCACCCAC
23763	21850	GGCATGATGGCGTGCACCCA
23764	21851	AGGCATGATGGCGTGCACCC
23765	21852	TAGGCATGATGGCGTGCACC
23766	21853	CTAGGCATGATGGCGTGCAC
23767	21854	GCTAGGCATGATGGCGTGCA
23768	21855	GGCTAGGCATGATGGCGTGC
23769	21856	CGGCTAGGCATGATGGCGTG
23770	21857	ACGGCTAGGCATGATGGCGT
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23772	21859	AAACGGCTAGGCATGATGGC
23773	21860	AAAACGGCTAGGCATGATGG
23774	21861	CAAAACGGCTAGGCATGATG
23775	21862	ACAAAACGGCTAGGCATGAT
23776	21863	CACAAAACGGCTAGGCATGA
23777	21864	TCACAAAACGGCTAGGCATG
23778	21865	TTCACAAAACGGCTAGGCAT

72855	70942	AAAGATGAGTAAAGGACTTA
72856	70943	TAAAGATGAGTAAAGGACTT
72857	70944	CTAAAGATGAGTAAAGGACT
72858	70945	TCTAAAGATGAGTAAAGGAC
72859	70946	TTCTAAAGATGAGTAAAGGA
72860	70947	TTTCTAAAGATGAGTAAAGG
72861	70948	CTTTCTAAAGATGAGTAAAG
72862	70949	TCTTTCTAAAGATGAGTAAA
72863	70950	CTCTTTCTAAAGATGAGTAA
72864	70951	GCTCTTTCTAAAGATGAGTA
72865	70952	AGCTCTTTCTAAAGATGAGT
72866	70953	TAGCTCTTTCTAAAGATGAG
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72868	70955	AGTAGCTCTTTCTAAAGATG
72869	70956	AAGTAGCTCTTTCTAAAGAT
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72872	70959	CAAAAGTAGCTCTTTCTAAA
72873	70960	CCAAAAGTAGCTCTTTCTAA
72874	70961	ACCAAAAGTAGCTCTTTCTA
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72876	70963	TCACCAAAAGTAGCTCTTTC
72877	70964	TTCACCAAAAGTAGCTCTTT
72878	70965	TTTCACCAAAAGTAGCTCTT
72879	70966	ATTTCACCAAAAGTAGCTCT
72880	70967	AATTTCACCAAAAGTAGCTC
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72882	70969	AAAATTTCACCAAAAGTAGC
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72884	70971	TTAAAATTTCACCAAAAGTA
72885	70972	TTTAAAATTTCACCAAAAGT
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72893	70980	TCCTTGGTTTTAAAATTTCA
72894	70981	TTCCTTGGTTTTAAAATTTC
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72896	70983	TATTCCTTGGTTTTAAAATT
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72898	70985	GATATTCCTTGGTTTTAAAA
72899	70986	TGATATTCCTTGGTTTTAAA
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72901	70988	AATGATATTCCTTGGTTTTA
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72903	70990	AGAATGATATTCCTTGGTTT
72904	70991	AAGAATGATATTCCTTGGTT
72905	70992	AAAGAATGATATTCCTTGGT
72906	70993	TAAAGAATGATATTCCTTGG
72907	70994	ATAAAGAATGATATTCCTTG
72908	70995	TATAAAGAATGATATTCCTT
72909	70996	CTATAAAGAATGATATTCCT
72910	70997	TCTATAAAGAATGATATTCC
72911	70998	TTCTATAAAGAATGATATTC
72912	70999	ATTCTATAAAGAATGATATT
72913	71000	GATTCTATAAAGAATGATAT
72914	71001	TGATTCTATAAAGAATGATA
72915	71002	GTGATTCTATAAAGAATGAT
72916	71003	TGTGATTCTATAAAGAATGA
72917	71004	GTGTGATTCTATAAAGAATG
72918	71005	AGTGTGATTCTATAAAGAAT
72919	71006	AAGTGTGATTCTATAAAGAA
72920	71007	GAAGTGTGATTCTATAAAGA
72921	71008	AGAAGTGTGATTCTATAAAG
72922	71009	CAGAAGTGTGATTCTATAAA
72923	71010	ACAGAAGTGTGATTCTATAA
72924	71011	CACAGAAGTGTGATTCTATA
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122002	120089	CTGATACTAACATGAAATTC
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122004	120091	AGCTGATACTAACATGAAAT
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122006	120093	TAAGCTGATACTAACATGAA
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122008	120095	AATAAGCTGATACTAACATG
122009	120096	GAATAAGCTGATACTAACAT
122010	120097	GGAATAAGCTGATACTAACA
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122012	120099	AAGGAATAAGCTGATACTAA
122013	120100	AAAGGAATAAGCTGATACTA
122014	120101	AAAAGGAATAAGCTGATACT
122015	120102	AAAAAGGAATAAGCTGATAC
122016	120103	CAAAAAGGAATAAGCTGATA
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122018	120105	AACAAAAAGGAATAAGCTGA
122019	120106	AAACAAAAAGGAATAAGCTG
122020	120107	CAAACAAAAAGGAATAAGCT
122021	120108	ACAAACAAAAAGGAATAAGC
122022	120109	AACAAACAAAAAGGAATAAG
122023	120110	AAACAAACAAAAAGGAATAA
122024	120111	CAAACAAACAAAAAGGAATA
122025	120112	ACAAACAAACAAAAAGGAAT
122026	120113	AACAAACAAACAAAAAGGAA
122027	120114	AAACAAACAAACAAAAAGGA
122028	120115	CAAACAAACAAACAAAAAGG
122029	120116	ACAAACAAACAAACAAAAAG
122030	120117	AACAAACAAACAAACAAAAA
122031	120118	AAACAAACAAACAAACAAAA
122032	120119	AAAACAAACAAACAAACAAA
122033	120120	AAAAACAAACAAACAAACAA
122034	120121	CAAAAACAAACAAACAAACA
122035	120122	TCAAAAACAAACAAACAAAC
122036	120123	CTCAAAAACAAACAAACAAA
122037	120124	TCTCAAAAACAAACAAACAA
122038	120125	ATCTCAAAAACAAACAAACA
122039	120126	CATCTCAAAAACAAACAAAC
122040	120127	CCATCTCAAAAACAAACAAA
122041	120128	TCCATCTCAAAAACAAACAA
122042	120129	CTCCATCTCAAAAACAAACA
122043	120130	ACTCCATCTCAAAAACAAAC
122044	120131	GACTCCATCTCAAAAACAAA
122045	120132	AGACTCCATCTCAAAAACAA
122046	120133	AAGACTCCATCTCAAAAACA
122047	120134	CAAGACTCCATCTCAAAAAC
122048	120135	ACAAGACTCCATCTCAAAAA
122049	120136	AACAAGACTCCATCTCAAAA
122050	120137	GAACAAGACTCCATCTCAAA
122051	120138	AGAACAAGACTCCATCTCAA
122052	120139	CAGAACAAGACTCCATCTCA
122053	120140	ACAGAACAAGACTCCATCTC
122054	120141	CACAGAACAAGACTCCATCT
122055	120142	ACACAGAACAAGACTCCATC
122056	120143	GACACAGAACAAGACTCCAT
122057	120144	GGACACAGAACAAGACTCCA
122058	120145	GGGACACAGAACAAGACTCC
122059	120146	TGGGACACAGAACAAGACTC
122060	120147	CTGGGACACAGAACAAGACT
122061	120148	TCTGGGACACAGAACAAGAC
122062	120149	TTCTGGGACACAGAACAAGA
122063	120150	ATTCTGGGACACAGAACAAG
122064	120151	AATTCTGGGACACAGAACAA
122065	120152	CAATTCTGGGACACAGAACA
122066	120153	CCAATTCTGGGACACAGAAC
122067	120154	ACCAATTCTGGGACACAGAA
122068	120155	GACCAATTCTGGGACACAGA
122069	120156	AGACCAATTCTGGGACACAG
122070	120157	CAGACCAATTCTGGGACACA
122071	120158	GCAGACCAATTCTGGGACAC
122072	120159	TGCAGACCAATTCTGGGACA

23779	21866	GTTCACAAAACGGCTAGGCA
23780	21867	AGTTCACAAAACGGCTAGGC
23781	21868	CAGTTCACAAAACGGCTAGG
23782	21869	ACAGTTCACAAAACGGCTAG
23783	21870	AACAGTTCACAAAACGGCTA
23784	21871	CAACAGTTCACAAAACGGCT
23785	21872	TCAACAGTTCACAAAACGGC
23786	21873	GTCAACAGTTCACAAAACGG
23787	21874	GGTCAACAGTTCACAAAACG
23788	21875	TGGTCAACAGTTCACAAAAC
23789	21876	TTGGTCAACAGTTCACAAAA
23790	21877	ATTGGTCAACAGTTCACAAA
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23794	21881	GAGCATTGGTCAACAGTTCA
23795	21882	AGAGCATTGGTCAACAGTTC
23796	21883	AAGAGCATTGGTCAACAGTT
23797	21884	AAAGAGCATTGGTCAACAGT
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23815	21902	GAACTTTCTGTCTGCAGAAA
23816	21903	TGAACTTTCTGTCTGCAGAA
23817	21904	GTGAACTTTCTGTCTGCAGA
23818	21905	AGTGAACTTTCTGTCTGCAG
23819	21906	CAGTGAACTTTCTGTCTGCA
23820	21907	ACAGTGAACTTTCTGTCTGC
23821	21908	CACAGTGAACTTTCTGTCTG
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23825	21912	TAACCACAGTGAACTTTCTG
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23831	21918	AACTCCTAACCACAGTGAAC
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23835	21922	TCTTAACTCCTAACCACAGT
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23837	21924	AGTCTTAACTCCTAACCACA
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23839	21926	AAAGTCTTAACTCCTAACCA
23840	21927	AAAAGTCTTAACTCCTAACC
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23848	21935	CAGAGGTTAAAAGTCTTAAC
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72928	71015	AAAACACAGAAGTGTGATTC
72929	71016	GAAAACACAGAAGTGTGATT
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72934	71021	AAGGGGAAAACACAGAAGTG
72935	71022	GAAGGGGAAAACACAGAAGT
72936	71023	GGAAGGGGAAAACACAGAAG
72937	71024	GGGAAGGGGAAAACACAGAA
72938	71025	GGGGAAGGGGAAAACACAGA
72939	71026	TGGGGAAGGGGAAAACACAG
72940	71027	ATGGGGAAGGGGAAAACACA
72941	71028	AATGGGGAAGGGGAAAACAC
72942	71029	AAATGGGGAAGGGGAAAACA
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72945	71032	CAGAAATGGGGAAGGGGAAA
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72948	71035	AGACAGAAATGGGGAAGGGG
72949	71036	GAGACAGAAATGGGGAAGGG
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72951	71038	TCGAGACAGAAATGGGGAAG
72952	71039	TTCGAGACAGAAATGGGGAA
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72956	71043	CGCTTTCGAGACAGAAATGG
72957	71044	TCGCTTTCGAGACAGAAATG
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72964	71051	CAGTCTGTCGCTTTCGAGAC
72965	71052	GCAGTCTGTCGCTTTCGAGA
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72967	71054	TAGCAGTCTGTCGCTTTCGA
72968	71055	GTAGCAGTCTGTCGCTTTCG
72969	71056	TGTAGCAGTCTGTCGCTTTC
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122075	120162	AATTGCAGACCAATTCTGGG
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122080	120167	AGTGGAATTGCAGACCAATT
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122089	120176	GGCTGAGGCAGTGGAATTGC
122090	120177	AGGCTGAGGCAGTGGAATTG
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122096	120183	CTTGGGAGGCTGAGGCAGTG
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122099	120186	CTACTTGGGAGGCTGAGGCA
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122101	120188	AGCTACTTGGGAGGCTGAGG
122102	120189	CAGCTACTTGGGAGGCTGAG
122103	120190	CCAGCTACTTGGGAGGCTGA
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122120	120207	GGCACGTGCCTGTAATCCCA
122121	120208	TGGCACGTGCCTGTAATCCC
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122125	120212	GTGGTGGCACGTGCCTGTAA
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122130	120217	CAGGTGTGGTGGCACGTGCC
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122134	120221	TAGCCAGGTGTGGTGGCACG
122135	120222	TTAGCCAGGTGTGGTGGCAC
122136	120223	ATTAGCCAGGTGTGGTGGCA
122137	120224	AATTAGCCAGGTGTGGTGGC
122138	120225	AAATTAGCCAGGTGTGGTGG
122139	120226	AAAATTAGCCAGGTGTGGTG
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23862	21949	AGATCACTTGAGGTCAGAGG
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23866	21953	GGGCAGATCACTTGAGGTCA
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23868	21955	GTGGGCAGATCACTTGAGGT
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23870	21957	AGGTGGGCAGATCACTTGAG
23871	21958	AAGGTGGGCAGATCACTTGA
23872	21959	CAAGGTGGGCAGATCACTTG
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23874	21961	GTCAAGGTGGGCAGATCACT
23875	21962	GGTCAAGGTGGGCAGATCAC
23876	21963	AGGTCAAGGTGGGCAGATCA
23877	21964	GAGGTCAAGGTGGGCAGATC
23878	21965	GGAGGTCAAGGTGGGCAGAT
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23906	21993	GGCTCACACCTGTAATCCCA
23907	21994	TGGCTCACACCTGTAATCCC
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23909	21996	GATGGCTCACACCTGTAATC
23910	21997	TGATGGCTCACACCTGTAAT
23911	21998	GTGATGGCTCACACCTGTAA
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23916	22003	CAGGCGTGATGGCTCACACC
23917	22004	CCAGGCGTGATGGCTCACAC
23918	22005	ACCAGGCGTGATGGCTCACA
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23920	22007	TGACCAGGCGTGATGGCTCA

72997	71084	TTTTTTAAAAAAAAGTATTC
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122146	120233	AGAGACAAAAATTAGCCAGG
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122153	120240	AAGAGAGAGAGACAAAAATT
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122200	120287	CATGGTGAAATCCCGTCTCT
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122209	120296	CCTGGCCAACATGGTGAAAT
122210	120297	GCCTGGCCAACATGGTGAAA
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122212	120299	CAGCCTGGCCAACATGGTGA
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23921	22008	TTGACCAGGCGTGATGGCTC
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23923	22010	TTTTGACCAGGCGTGATGGC
23924	22011	TTTTTGACCAGGCGTGATGG
23925	22012	ATTTTTGACCAGGCGTGATG
23926	22013	TATTTTTGACCAGGCGTGAT
23927	22014	ATATTTTTGACCAGGCGTGA
23928	22015	GATATTTTTGACCAGGCGTG
23929	22016	AGATATTTTTGACCAGGCGT
23930	22017	AAGATATTTTTGACCAGGCG
23931	22018	AAAGATATTTTTGACCAGGC
23932	22019	GAAAGATATTTTTGACCAGG
23933	22020	AGAAAGATATTTTTGACCAG
23934	22021	AAGAAAGATATTTTTGACCA
23935	22022	AAAGAAAGATATTTTTGACC
23936	22023	TAAAGAAAGATATTTTTGAC
23937	22024	TTAAAGAAAGATATTTTTGA
23938	22025	CTTAAAGAAAGATATTTTTG
23939	22026	TCTTAAAGAAAGATATTTTT
23940	22027	CTCTTAAAGAAAGATATTTT
23941	22028	ACTCTTAAAGAAAGATATTT
23942	22029	TACTCTTAAAGAAAGATATT
23943	22030	TTACTCTTAAAGAAAGATAT
23944	22031	TTTACTCTTAAAGAAAGATA
23945	22032	ATTTACTCTTAAAGAAAGAT
23946	22033	AATTTACTCTTAAAGAAAGA
23947	22034	AAATTTACTCTTAAAGAAAG
23948	22035	TAAATTTACTCTTAAAGAAA
23949	22036	GTAAATTTACTCTTAAAGAA
23950	22037	GGTAAATTTACTCTTAAAGA
23951	22038	AGGTAAATTTACTCTTAAAG
23952	22039	AAGGTAAATTTACTCTTAAA
23953	22040	TAAGGTAAATTTACTCTTAA
23954	22041	TTAAGGTAAATTTACTCTTA
23955	22042	GTTAAGGTAAATTTACTCTT
23956	22043	AGTTAAGGTAAATTTACTCT
23957	22044	AAGTTAAGGTAAATTTACTC
23958	22045	TAAGTTAAGGTAAATTTACT
23959	22046	GTAAGTTAAGGTAAATTTAC
23960	22047	AGTAAGTTAAGGTAAATTTA
23961	22048	CAGTAAGTTAAGGTAAATTT
23962	22049	CCAGTAAGTTAAGGTAAATT
23963	22050	ACCAGTAAGTTAAGGTAAAT
23964	22051	AACCAGTAAGTTAAGGTAAA
23965	22052	CAACCAGTAAGTTAAGGTAA
23966	22053	TCAACCAGTAAGTTAAGGTA
23967	22054	ATCAACCAGTAAGTTAAGGT
23968	22055	GATCAACCAGTAAGTTAAGG
23969	22056	TGATCAACCAGTAAGTTAAG
23970	22057	ATGATCAACCAGTAAGTTAA
23971	22058	AATGATCAACCAGTAAGTTA
23972	22059	CAATGATCAACCAGTAAGTT
23973	22060	ACAATGATCAACCAGTAAGT
23974	22061	TACAATGATCAACCAGTAAG
23975	22062	ATACAATGATCAACCAGTAA
23976	22063	TATACAATGATCAACCAGTA
23977	22064	ATATACAATGATCAACCAGT
23978	22065	TATATACAATGATCAACCAG
23979	22066	CTATATACAATGATCAACCA
23980	22067	CCTATATACAATGATCAACC
23981	22068	ACCTATATACAATGATCAAC
23982	22069	GACCTATATACAATGATCAA
23983	22070	AGACCTATATACAATGATCA
23984	22071	CAGACCTATATACAATGATC
23985	22072	ACAGACCTATATACAATGAT
23986	22073	AACAGACCTATATACAATGA
23987	22074	CAACAGACCTATATACAATG
23988	22075	ACAACAGACCTATATACAAT
23989	22076	AACAACAGACCTATATACAA
23990	22077	TAACAACAGACCTATATACA
23991	22078	TTAACAACAGACCTATATAC

73068	71155	GCATTATTAATAAATCTATT
73069	71156	GGCATTATTAATAAATCTAT
73070	71157	GGGCATTATTAATAAATCTA
73071	71158	AGGGCATTATTAATAAATCT
73072	71159	GAGGGCATTATTAATAAATC
73073	71160	AGAGGGCATTATTAATAAAT
73074	71161	AAGAGGGCATTATTAATAAA
73075	71162	TAAGAGGGCATTATTAATAA
73076	71163	TTAAGAGGGCATTATTAATA
73077	71164	GTTAAGAGGGCATTATTAAT
73078	71165	TGTTAAGAGGGCATTATTAA
73079	71166	GTGTTAAGAGGGCATTATTA
73080	71167	TGTGTTAAGAGGGCATTATT
73081	71168	TTGTGTTAAGAGGGCATTAT
73082	71169	GTTGTGTTAAGAGGGCATTA
73083	71170	GGTTGTGTTAAGAGGGCATT
73084	71171	AGGTTGTGTTAAGAGGGCAT
73085	71172	TAGGTTGTGTTAAGAGGGCA
73086	71173	TTAGGTTGTGTTAAGAGGGC
73087	71174	TTTAGGTTGTGTTAAGAGGG
73088	71175	ATTTAGGTTGTGTTAAGAGG
73089	71176	AATTTAGGTTGTGTTAAGAG
73090	71177	GAATTTAGGTTGTGTTAAGA
73091	71178	AGAATTTAGGTTGTGTTAAG
73092	71179	CAGAATTTAGGTTGTGTTAA
73093	71180	CCAGAATTTAGGTTGTGTTA
73094	71181	ACCAGAATTTAGGTTGTGTT
73095	71182	GACCAGAATTTAGGTTGTGT
73096	71183	TGACCAGAATTTAGGTTGTG
73097	71184	CTGACCAGAATTTAGGTTGT
73098	71185	ACTGACCAGAATTTAGGTTG
73099	71186	CACTGACCAGAATTTAGGTT
73100	71187	CCACTGACCAGAATTTAGGT
73101	71188	TCCACTGACCAGAATTTAGG
73102	71189	TTCCACTGACCAGAATTTAG
73103	71190	ATTCCACTGACCAGAATTTA
73104	71191	TATTCCACTGACCAGAATTT
73105	71192	TTATTCCACTGACCAGAATT
73106	71193	TTTATTCCACTGACCAGAAT
73107	71194	CTTTATTCCACTGACCAGAA
73108	71195	GCTTTATTCCACTGACCAGA
73109	71196	GGCTTTATTCCACTGACCAG
73110	71197	AGGCTTTATTCCACTGACCA
73111	71198	CAGGCTTTATTCCACTGACC
73112	71199	CCAGGCTTTATTCCACTGAC
73113	71200	CCCAGGCTTTATTCCACTGA
73114	71201	ACCCAGGCTTTATTCCACTG
73115	71202	GACCCAGGCTTTATTCCACT
73116	71203	GGACCCAGGCTTTATTCCAC
73117	71204	AGGACCCAGGCTTTATTCCA
73118	71205	TAGGACCCAGGCTTTATTCC
73119	71206	TTAGGACCCAGGCTTTATTC
73120	71207	TTTAGGACCCAGGCTTTATT
73121	71208	CTTTAGGACCCAGGCTTTAT
73122	71209	ACTTTAGGACCCAGGCTTTA
73123	71210	AACTTTAGGACCCAGGCTTT
73124	71211	AAACTTTAGGACCCAGGCTT
73125	71212	AAAACTTTAGGACCCAGGCT
73126	71213	TAAAACTTTAGGACCCAGGC
73127	71214	CTAAAACTTTAGGACCCAGG
73128	71215	TCTAAAACTTTAGGACCCAG
73129	71216	GTCTAAAACTTTAGGACCCA
73130	71217	CGTCTAAAACTTTAGGACCC
73131	71218	GCGTCTAAAACTTTAGGACC
73132	71219	AGCGTCTAAAACTTTAGGAC
73133	71220	AAGCGTCTAAAACTTTAGGA
73134	71221	CAAGCGTCTAAAACTTTAGG
73135	71222	GCAAGCGTCTAAAACTTTAG
73136	71223	AGCAAGCGTCTAAAACTTTA
73137	71224	AAGCAAGCGTCTAAAACTTT
73138	71225	CAAGCAAGCGTCTAAAACTT

122215	120302	GACCAGCCTGGCCAACATGG
122216	120303	AGACCAGCCTGGCCAACATG
122217	120304	GAGACCAGCCTGGCCAACAT
122218	120305	TGAGACCAGCCTGGCCAACA
122219	120306	TTGAGACCAGCCTGGCCAAC
122220	120307	TTTGAGACCAGCCTGGCCAA
122221	120308	GTTTGAGACCAGCCTGGCCA
122222	120309	AGTTTGAGACCAGCCTGGCC
122223	120310	GAGTTTGAGACCAGCCTGGC
122224	120311	GGAGTTTGAGACCAGCCTGG
122225	120312	AGGAGTTTGAGACCAGCCTG
122226	120313	CAGGAGTTTGAGACCAGCCT
122227	120314	TCAGGAGTTTGAGACCAGCC
122228	120315	GTCAGGAGTTTGAGACCAGC
122229	120316	GGTCAGGAGTTTGAGACCAG
122230	120317	GGGTCAGGAGTTTGAGACCA
122231	120318	GGGGTCAGGAGTTTGAGACC
122232	120319	TGGGGTCAGGAGTTTGAGAC
122233	120320	TTGGGGTCAGGAGTTTGAGA
122234	120321	TTTGGGGTCAGGAGTTTGAG
122235	120322	ATTTGGGGTCAGGAGTTTGA
122236	120323	CATTTGGGGTCAGGAGTTTG
122237	120324	TCATTTGGGGTCAGGAGTTT
122238	120325	ATCATTTGGGGTCAGGAGTT
122239	120326	GATCATTTGGGGTCAGGAGT
122240	120327	GGATCATTTGGGGTCAGGAG
122241	120328	TGGATCATTTGGGGTCAGGA
122242	120329	GTGGATCATTTGGGGTCAGG
122243	120330	GGTGGATCATTTGGGGTCAG
122244	120331	AGGTGGATCATTTGGGGTCA
122245	120332	CAGGTGGATCATTTGGGGTC
122246	120333	GCAGGTGGATCATTTGGGGT
122247	120334	GGCAGGTGGATCATTTGGGG
122248	120335	AGGCAGGTGGATCATTTGGG
122249	120336	AAGGCAGGTGGATCATTTGG
122250	120337	CAAGGCAGGTGGATCATTTG
122251	120338	CCAAGGCAGGTGGATCATTT
122252	120339	GCCAAGGCAGGTGGATCATT
122253	120340	GGCCAAGGCAGGTGGATCAT
122254	120341	AGGCCAAGGCAGGTGGATCA
122255	120342	GAGGCCAAGGCAGGTGGATC
122256	120343	GGAGGCCAAGGCAGGTGGAT
122257	120344	GGGAGGCCAAGGCAGGTGGA
122258	120345	TGGGAGGCCAAGGCAGGTGG
122259	120346	TTGGGAGGCCAAGGCAGGTG
122260	120347	TTTGGGAGGCCAAGGCAGGT
122261	120348	CTTTGGGAGGCCAAGGCAGG
122262	120349	ACTTTGGGAGGCCAAGGCAG
122263	120350	CACTTTGGGAGGCCAAGGCA
122264	120351	GCACTTTGGGAGGCCAAGGC
122265	120352	AGCACTTTGGGAGGCCAAGG
122266	120353	CAGCACTTTGGGAGGCCAAG
122267	120354	CCAGCACTTTGGGAGGCCAA
122268	120355	CCCAGCACTTTGGGAGGCCA
122269	120356	TCCCAGCACTTTGGGAGGCC
122270	120357	ATCCCAGCACTTTGGGAGGC
122271	120358	AATCCCAGCACTTTGGGAGG
122272	120359	TAATCCCAGCACTTTGGGAG
122273	120360	GTAATCCCAGCACTTTGGGA
122274	120361	TGTAATCCCAGCACTTTGGG
122275	120362	CTGTAATCCCAGCACTTTGG
122276	120363	CCTGTAATCCCAGCACTTTG
122277	120364	ACCTGTAATCCCAGCACTTT
122278	120365	CACCTGTAATCCCAGCACTT
122279	120366	ACACCTGTAATCCCAGCACT
122280	120367	CACACCTGTAATCCCAGCAC
122281	120368	TCACACCTGTAATCCCAGCA
122282	120369	CTCACACCTGTAATCCCAGC
122283	120370	ACTCACACCTGTAATCCCAG
122284	120371	GACTCACACCTGTAATCCCA
122285	120372	TGACTCACACCTGTAATCCC

23992	22079	ATTAACAACAGACCTATATA
23993	22080	AATTAACAACAGACCTATAT
23994	22081	CAATTAACAACAGACCTATA
23995	22082	TCAATTAACAACAGACCTAT
23996	22083	TTCAATTAACAACAGACCTA
23997	22084	TTTCAATTAACAACAGACCT
23998	22085	GTTTCAATTAACAACAGACC
23999	22086	TGTTTCAATTAACAACAGAC
24000	22087	ATGTTTCAATTAACAACAGA
24001	22088	CATGTTTCAATTAACAACAG
24002	22089	GCATGTTTCAATTAACAACA
24003	22090	CGCATGTTTCAATTAACAAC
24004	22091	CCGCATGTTTCAATTAACAA
24005	22092	CCCGCATGTTTCAATTAACA
24006	22093	GCCCGCATGTTTCAATTAAC
24007	22094	GGCCCGCATGTTTCAATTAA
24008	22095	CGGCCCGCATGTTTCAATTA
24009	22096	CCGGCCCGCATGTTTCAATT
24010	22097	CCCGGCCCGCATGTTTCAAT
24011	22098	GCCCGGCCCGCATGTTTCAA
24012	22099	GGCCCGGCCCGCATGTTTCA
24013	22100	GGGCCCGGCCCGCATGTTTC
24014	22101	CGGGCCCGGCCCGCATGTTT
24015	22102	CCGGGCCCGGCCCGCATGTT
24016	22103	ACCGGGCCCGGCCCGCATGT
24017	22104	CACCGGGCCCGGCCCGCATG
24018	22105	CCACCGGGCCCGGCCCGCAT
24019	22106	GCCACCGGGCCCGGCCCGCA
24020	22107	AGCCACCGGGCCCGGCCCGC
24021	22108	GAGCCACCGGGCCCGGCCCG
24022	22109	TGAGCCACCGGGCCCGGCCC
24023	22110	ATGAGCCACCGGGCCCGGCC
24024	22111	CATGAGCCACCGGGCCCGGC
24025	22112	GCATGAGCCACCGGGCCCGG
24026	22113	GGCATGAGCCACCGGGCCCG
24027	22114	AGGCATGAGCCACCGGGCCC
24028	22115	CAGGCATGAGCCACCGGGCC
24029	22116	ACAGGCATGAGCCACCGGGC
24030	22117	TACAGGCATGAGCCACCGGG
24031	22118	TTACAGGCATGAGCCACCGG
24032	22119	ATTACAGGCATGAGCCACCG
24033	22120	GATTACAGGCATGAGCCACC
24034	22121	GGATTACAGGCATGAGCCAC
24035	22122	GGGATTACAGGCATGAGCCA
24036	22123	TGGGATTACAGGCATGAGCC
24037	22124	CTGGGATTACAGGCATGAGC
24038	22125	GCTGGGATTACAGGCATGAG
24039	22126	TGCTGGGATTACAGGCATGA
24040	22127	GTGCTGGGATTACAGGCATG
24041	22128	AGTGCTGGGATTACAGGCAT
24042	22129	AAGTGCTGGGATTACAGGCA
24043	22130	AAAGTGCTGGGATTACAGGC
24044	22131	CAAAGTGCTGGGATTACAGG
24045	22132	CCAAAGTGCTGGGATTACAG
24046	22133	CCCAAAGTGCTGGGATTACA
24047	22134	TCCCAAAGTGCTGGGATTAC
24048	22135	CTCCCAAAGTGCTGGGATTA
24049	22136	CCTCCCAAAGTGCTGGGATT
24050	22137	GCCTCCCAAAGTGCTGGGAT
24051	22138	GGCCTCCCAAAGTGCTGGGA
24052	22139	CGGCCTCCCAAAGTGCTGGG
24053	22140	TCGGCCTCCCAAAGTGCTGG
24054	22141	CTCGGCCTCCCAAAGTGCTG
24055	22142	CCTCGGCCTCCCAAAGTGCT
24056	22143	GCCTCGGCCTCCCAAAGTGC
24057	22144	CGCCTCGGCCTCCCAAAGTG
24058	22145	CCGCCTCGGCCTCCCAAAGT
24059	22146	CCCGCCTCGGCCTCCCAAAG
24060	22147	ACCCGCCTCGGCCTCCCAAA
24061	22148	CACCCGCCTCGGCCTCCCAA
24062	22149	CCACCCGCCTCGGCCTCCCA

73139	71226	GCAAGCAAGCGTCTAAAACT
73140	71227	AGCAAGCAAGCGTCTAAAAC
73141	71228	AAGCAAGCAAGCGTCTAAAA
73142	71229	AAAGCAAGCAAGCGTCTAAA
73143	71230	AAAAGCAAGCAAGCGTCTAA
73144	71231	GAAAAGCAAGCAAGCGTCTA
73145	71232	GGAAAAGCAAGCAAGCGTCT
73146	71233	TGGAAAAGCAAGCAAGCGTC
73147	71234	GTGGAAAAGCAAGCAAGCGT
73148	71235	TGTGGAAAAGCAAGCAAGCG
73149	71236	GTGTGGAAAAGCAAGCAAGC
73150	71237	AGTGTGGAAAAGCAAGCAAG
73151	71238	CAGTGTGGAAAAGCAAGCAA
73152	71239	CCAGTGTGGAAAAGCAAGCA
73153	71240	GCCAGTGTGGAAAAGCAAGC
73154	71241	AGCCAGTGTGGAAAAGCAAG
73155	71242	GAGCCAGTGTGGAAAAGCAA
73156	71243	AGAGCCAGTGTGGAAAAGCA
73157	71244	AAGAGCCAGTGTGGAAAAGC
73158	71245	TAAGAGCCAGTGTGGAAAAG
73159	71246	GTAAGAGCCAGTGTGGAAAA
73160	71247	AGTAAGAGCCAGTGTGGAAA
73161	71248	AAGTAAGAGCCAGTGTGGAA
73162	71249	CAAGTAAGAGCCAGTGTGGA
73163	71250	CCAAGTAAGAGCCAGTGTGG
73164	71251	CCCAAGTAAGAGCCAGTGTG
73165	71252	CCCCAAGTAAGAGCCAGTGT
73166	71253	TCCCCAAGTAAGAGCCAGTG
73167	71254	ATCCCCAAGTAAGAGCCAGT
73168	71255	GATCCCCAAGTAAGAGCCAG
73169	71256	GGATCCCCAAGTAAGAGCCA
73170	71257	AGGATCCCCAAGTAAGAGCC
73171	71258	AAGGATCCCCAAGTAAGAGC
73172	71259	AAAGGATCCCCAAGTAAGAG
73173	71260	AAAAGGATCCCCAAGTAAGA
73174	71261	TAAAAGGATCCCCAAGTAAG
73175	71262	CTAAAAGGATCCCCAAGTAA
73176	71263	TCTAAAAGGATCCCCAAGTA
73177	71264	TTCTAAAAGGATCCCCAAGT
73178	71265	TTTCTAAAAGGATCCCCAAG
73179	71266	ATTTCTAAAAGGATCCCCAA
73180	71267	AATTTCTAAAAGGATCCCCA
73181	71268	AAATTTCTAAAAGGATCCCC
73182	71269	CAAATTTCTAAAAGGATCCC
73183	71270	ACAAATTTCTAAAAGGATCC
73184	71271	AACAAATTTCTAAAAGGATC
73185	71272	AAACAAATTTCTAAAAGGAT
73186	71273	TAAACAAATTTCTAAAAGGA
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73190	71277	ATTCTAAACAAATTTCTAAA
73191	71278	TATTCTAAACAAATTTCTAA
73192	71279	TTATTCTAAACAAATTTCTA
73193	71280	ATTATTCTAAACAAATTTCT
73194	71281	TATTATTCTAAACAAATTTC
73195	71282	GTATTATTCTAAACAAATTT
73196	71283	AGTATTATTCTAAACAAATT
73197	71284	CAGTATTATTCTAAACAAAT
73198	71285	ACAGTATTATTCTAAACAAA
73199	71286	TACAGTATTATTCTAAACAA
73200	71287	TTACAGTATTATTCTAAACA
73201	71288	TTTACAGTATTATTCTAAAC
73202	71289	TTTTACAGTATTATTCTAAA
73203	71290	TTTTTACAGTATTATTCTAA
73204	71291	GTTTTTACAGTATTATTCTA
73205	71292	TGTTTTTACAGTATTATTCT
73206	71293	ATGTTTTTACAGTATTATTC
73207	71294	TATGTTTTTACAGTATTATT
73208	71295	ATATGTTTTTACAGTATTAT
73209	71296	AATATGTTTTTACAGTATTA

122286	120373	GTGACTCACACCTGTAATCC
122287	120374	GGTGACTCACACCTGTAATC
122288	120375	CGGTGACTCACACCTGTAAT
122289	120376	ACGGTGACTCACACCTGTAA
122290	120377	CACGGTGACTCACACCTGTA
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122292	120379	GGCACGGTGACTCACACCTG
122293	120380	GGGCACGGTGACTCACACCT
122294	120381	TGGGCACGGTGACTCACACC
122295	120382	CTGGGCACGGTGACTCACAC
122296	120383	GCTGGGCACGGTGACTCACA
122297	120384	GGCTGGGCACGGTGACTCAC
122298	120385	TGGCTGGGCACGGTGACTCA
122299	120386	CTGGCTGGGCACGGTGACTC
122300	120387	GCTGGCTGGGCACGGTGACT
122301	120388	AGCTGGCTGGGCACGGTGAC
122302	120389	AAGCTGGCTGGGCACGGTGA
122303	120390	TAAGCTGGCTGGGCACGGTG
122304	120391	ATAAGCTGGCTGGGCACGGT
122305	120392	AATAAGCTGGCTGGGCACGG
122306	120393	GAATAAGCTGGCTGGGCACG
122307	120394	GGAATAAGCTGGCTGGGCAC
122308	120395	AGGAATAAGCTGGCTGGGCA
122309	120396	AAGGAATAAGCTGGCTGGGC
122310	120397	AAAGGAATAAGCTGGCTGGG
122311	120398	AAAAGGAATAAGCTGGCTGG
122312	120399	AAAAAGGAATAAGCTGGCTG
122313	120400	TAAAAAGGAATAAGCTGGCT
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122316	120403	CAATAAAAAGGAATAAGCTG
122317	120404	GCAATAAAAAGGAATAAGCT
122318	120405	AGCAATAAAAAGGAATAAGC
122319	120406	CAGCAATAAAAAGGAATAAG
122320	120407	CCAGCAATAAAAAGGAATAA
122321	120408	CCCAGCAATAAAAAGGAATA
122322	120409	ACCCAGCAATAAAAAGGAAT
122323	120410	TACCCAGCAATAAAAAGGAA
122324	120411	CTACCCAGCAATAAAAAGGA
122325	120412	GCTACCCAGCAATAAAAAGG
122326	120413	TGCTACCCAGCAATAAAAAG
122327	120414	ATGCTACCCAGCAATAAAAA
122328	120415	AATGCTACCCAGCAATAAAA
122329	120416	AAATGCTACCCAGCAATAAA
122330	120417	GAAATGCTACCCAGCAATAA
122331	120418	TGAAATGCTACCCAGCAATA
122332	120419	ATGAAATGCTACCCAGCAAT
122333	120420	AATGAAATGCTACCCAGCAA
122334	120421	AAATGAAATGCTACCCAGCA
122335	120422	AAAATGAAATGCTACCCAGC
122336	120423	TAAAATGAAATGCTACCCAG
122337	120424	ATAAAATGAAATGCTACCCA
122338	120425	CATAAAATGAAATGCTACCC
122339	120426	TCATAAAATGAAATGCTACC
122340	120427	ATCATAAAATGAAATGCTAC
122341	120428	AATCATAAAATGAAATGCTA
122342	120429	TAATCATAAAATGAAATGCT
122343	120430	ATAATCATAAAATGAAATGC
122344	120431	TATAATCATAAAATGAAATG
122345	120432	GTATAATCATAAAATGAAAT
122346	120433	GGTATAATCATAAAATGAAA
122347	120434	TGGTATAATCATAAAATGAA
122348	120435	GTGGTATAATCATAAAATGA
122349	120436	TGTGGTATAATCATAAAATG
122350	120437	CTGTGGTATAATCATAAAAT
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122352	120439	AACTGTGGTATAATCATAAA
122353	120440	TAACTGTGGTATAATCATAA
122354	120441	TTAACTGTGGTATAATCATA
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24063	22150	TCCACCCGCCTCGGCCTCCC
24064	22151	ATCCACCCGCCTCGGCCTCC
24065	22152	GATCCACCCGCCTCGGCCTC
24066	22153	TGATCCACCCGCCTCGGCCT
24067	22154	GTGATCCACCCGCCTCGGCC
24068	22155	TGTGATCCACCCGCCTCGGC
24069	22156	TTGTGATCCACCCGCCTCGG
24070	22157	CTTGTGATCCACCCGCCTCG
24071	22158	CCTTGTGATCCACCCGCCTC
24072	22159	ACCTTGTGATCCACCCGCCT
24073	22160	GACCTTGTGATCCACCCGCC
24074	22161	TGACCTTGTGATCCACCCGC
24075	22162	CTGACCTTGTGATCCACCCG
24076	22163	CCTGACCTTGTGATCCACCC
24077	22164	TCCTGACCTTGTGATCCACC
24078	22165	CTCCTGACCTTGTGATCCAC
24079	22166	TCTCCTGACCTTGTGATCCA
24080	22167	ATCTCCTGACCTTGTGATCC
24081	22168	GATCTCCTGACCTTGTGATC
24082	22169	CGATCTCCTGACCTTGTGAT
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24092	22179	AGGATGGTCTCGATCTCCTG
24093	22180	CAGGATGGTCTCGATCTCCT
24094	22181	CCAGGATGGTCTCGATCTCC
24095	22182	GCCAGGATGGTCTCGATCTC
24096	22183	AGCCAGGATGGTCTCGATCT
24097	22184	TAGCCAGGATGGTCTCGATC
24098	22185	TTAGCCAGGATGGTCTCGAT
24099	22186	GTTAGCCAGGATGGTCTCGA
24100	22187	TGTTAGCCAGGATGGTCTCG
24101	22188	GTGTTAGCCAGGATGGTCTC
24102	22189	CGTGTTAGCCAGGATGGTCT
24103	22190	CCGTGTTAGCCAGGATGGTC
24104	22191	ACCGTGTTAGCCAGGATGGT
24105	22192	CACCGTGTTAGCCAGGATGG
24106	22193	TCACCGTGTTAGCCAGGATG
24107	22194	TTCACCGTGTTAGCCAGGAT
24108	22195	TTTCACCGTGTTAGCCAGGA
24109	22196	GTTTCACCGTGTTAGCCAGG
24110	22197	GGTTTCACCGTGTTAGCCAG
24111	22198	GGGTTTCACCGTGTTAGCCA
24112	22199	GGGGTTTCACCGTGTTAGCC
24113	22200	CGGGGTTTCACCGTGTTAGC
24114	22201	ACGGGGTTTCACCGTGTTAG
24115	22202	GACGGGGTTTCACCGTGTTA
24116	22203	AGACGGGGTTTCACCGTGTT
24117	22204	GAGACGGGGTTTCACCGTGT
24118	22205	AGAGACGGGGTTTCACCGTG
24119	22206	TAGAGACGGGGTTTCACCGT
24120	22207	GTAGAGACGGGGTTTCACCG
24121	22208	AGTAGAGACGGGGTTTCACC
24122	22209	TAGTAGAGACGGGGTTTCAC
24123	22210	TTAGTAGAGACGGGGTTTCA
24124	22211	TTTAGTAGAGACGGGGTTTC
24125	22212	TTTTAGTAGAGACGGGGTTT
24126	22213	TTTTTAGTAGAGACGGGGTT
24127	22214	ATTTTTAGTAGAGACGGGGT
24128	22215	TATTTTTAGTAGAGACGGGG
24129	22216	GTATTTTTAGTAGAGACGGG
24130	22217	AGTATTTTTAGTAGAGACGG
24131	22218	TAGTATTTTTAGTAGAGACG
24132	22219	TTAGTATTTTTAGTAGAGAC
24133	22220	TTTAGTATTTTTAGTAGAGA

73210	71297	AAATATGTTTTTACAGTATT
73211	71298	TAAATATGTTTTTACAGTAT
73212	71299	TTAAATATGTTTTTACAGTA
73213	71300	CTTAAATATGTTTTTACAGT
73214	71301	GCTTAAATATGTTTTTACAG
73215	71302	AGCTTAAATATGTTTTTACA
73216	71303	TAGCTTAAATATGTTTTTAC
73217	71304	GTAGCTTAAATATGTTTTTA
73218	71305	AGTAGCTTAAATATGTTTTT
73219	71306	AAGTAGCTTAAATATGTTTT
73220	71307	AAAGTAGCTTAAATATGTTT
73221	71308	CAAAGTAGCTTAAATATGTT
73222	71309	ACAAAGTAGCTTAAATATGT
73223	71310	CACAAAGTAGCTTAAATATG
73224	71311	ACACAAAGTAGCTTAAATAT
73225	71312	CACACAAAGTAGCTTAAATA
73226	71313	ACACACAAAGTAGCTTAAAT
73227	71314	TACACACAAAGTAGCTTAAA
73228	71315	GTACACACAAAGTAGCTTAA
73229	71316	TGTACACACAAAGTAGCTTA
73230	71317	ATGTACACACAAAGTAGCTT
73231	71318	AATGTACACACAAAGTAGCT
73232	71319	AAATGTACACACAAAGTAGC
73233	71320	CAAATGTACACACAAAGTAG
73234	71321	CCAAATGTACACACAAAGTA
73235	71322	CCCAAATGTACACACAAAGT
73236	71323	TCCCAAATGTACACACAAAG
73237	71324	ATCCCAAATGTACACACAAA
73238	71325	GATCCCAAATGTACACACAA
73239	71326	AGATCCCAAATGTACACACA
73240	71327	AAGATCCCAAATGTACACAC
73241	71328	AAAGATCCCAAATGTACACA
73242	71329	AAAAGATCCCAAATGTACAC
73243	71330	CAAAAGATCCCAAATGTACA
73244	71331	CCAAAAGATCCCAAATGTAC
73245	71332	ACCAAAAGATCCCAAATGTA
73246	71333	AACCAAAAGATCCCAAATGT
73247	71334	AAACCAAAAGATCCCAAATG
73248	71335	CAAACCAAAAGATCCCAAAT
73249	71336	TCAAACCAAAAGATCCCAAA
73250	71337	TTCAAACCAAAAGATCCCAA
73251	71338	CTTCAAACCAAAAGATCCCA
73252	71339	TCTTCAAACCAAAAGATCCC
73253	71340	GTCTTCAAACCAAAAGATCC
73254	71341	CGTCTTCAAACCAAAAGATC
73255	71342	CCGTCTTCAAACCAAAAGAT
73256	71343	GCCGTCTTCAAACCAAAAGA
73257	71344	AGCCGTCTTCAAACCAAAAG
73258	71345	AAGCCGTCTTCAAACCAAAA
73259	71346	CAAGCCGTCTTCAAACCAAA
73260	71347	TCAAGCCGTCTTCAAACCAA
73261	71348	GTCAAGCCGTCTTCAAACCA
73262	71349	AGTCAAGCCGTCTTCAAACC
73263	71350	GAGTCAAGCCGTCTTCAAAC
73264	71351	TGAGTCAAGCCGTCTTCAAA
73265	71352	TTGAGTCAAGCCGTCTTCAA
73266	71353	CTTGAGTCAAGCCGTCTTCA
73267	71354	TCTTGAGTCAAGCCGTCTTC
73268	71355	GTCTTGAGTCAAGCCGTCTT
73269	71356	AGTCTTGAGTCAAGCCGTCT
73270	71357	AAGTCTTGAGTCAAGCCGTC
73271	71358	AAAGTCTTGAGTCAAGCCGT
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73274	71361	TAGAAAGTCTTGAGTCAAGC
73275	71362	TTAGAAAGTCTTGAGTCAAG
73276	71363	TTTAGAAAGTCTTGAGTCAA
73277	71364	ATTTAGAAAGTCTTGAGTCA
73278	71365	TATTTAGAAAGTCTTGAGTC
73279	71366	ATATTTAGAAAGTCTTGAGT
73280	71367	AATATTTAGAAAGTCTTGAG

122357	120444	AAATTAACTGTGGTATAATC
122358	120445	TAAATTAACTGTGGTATAAT
122359	120446	GTAAATTAACTGTGGTATAA
122360	120447	GGTAAATTAACTGTGGTATA
122361	120448	GGGTAAATTAACTGTGGTAT
122362	120449	TGGGTAAATTAACTGTGGTA
122363	120450	ATGGGTAAATTAACTGTGGT
122364	120451	AATGGGTAAATTAACTGTGG
122365	120452	TAATGGGTAAATTAACTGTG
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122368	120455	TAGTAATGGGTAAATTAACT
122369	120456	CTAGTAATGGGTAAATTAAC
122370	120457	ACTAGTAATGGGTAAATTAA
122371	120458	GACTAGTAATGGGTAAATTA
122372	120459	CGACTAGTAATGGGTAAATT
122373	120460	TCGACTAGTAATGGGTAAAT
122374	120461	ATCGACTAGTAATGGGTAAA
122375	120462	CATCGACTAGTAATGGGTAA
122376	120463	CCATCGACTAGTAATGGGTA
122377	120464	CCCATCGACTAGTAATGGGT
122378	120465	GCCCATCGACTAGTAATGGG
122379	120466	TGCCCATCGACTAGTAATGG
122380	120467	ATGCCCATCGACTAGTAATG
122381	120468	AATGCCCATCGACTAGTAAT
122382	120469	AAATGCCCATCGACTAGTAA
122383	120470	CAAATGCCCATCGACTAGTA
122384	120471	TCAAATGCCCATCGACTAGT
122385	120472	CTCAAATGCCCATCGACTAG
122386	120473	ACTCAAATGCCCATCGACTA
122387	120474	AACTCAAATGCCCATCGACT
122388	120475	TAACTCAAATGCCCATCGAC
122389	120476	ATAACTCAAATGCCCATCGA
122390	120477	AATAACTCAAATGCCCATCG
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122392	120479	GCAATAACTCAAATGCCCAT
122393	120480	GGCAATAACTCAAATGCCCA
122394	120481	TGGCAATAACTCAAATGCCC
122395	120482	CTGGCAATAACTCAAATGCC
122396	120483	GCTGGCAATAACTCAAATGC
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122398	120485	AAGCTGGCAATAACTCAAAT
122399	120486	AAAGCTGGCAATAACTCAAA
122400	120487	AAAAGCTGGCAATAACTCAA
122401	120488	CAAAAGCTGGCAATAACTCA
122402	120489	CCAAAAGCTGGCAATAACTC
122403	120490	GCCAAAAGCTGGCAATAACT
122404	120491	AGCCAAAAGCTGGCAATAAC
122405	120492	TAGCCAAAAGCTGGCAATAA
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122408	120495	TAATAGCCAAAAGCTGGCAA
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122410	120497	CATAATAGCCAAAAGCTGGC
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122413	120500	ATTCATAATAGCCAAAAGCT
122414	120501	CATTCATAATAGCCAAAAGC
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122416	120503	TTCATTCATAATAGCCAAAA
122417	120504	CTTCATTCATAATAGCCAAA
122418	120505	GCTTCATTCATAATAGCCAA
122419	120506	AGCTTCATTCATAATAGCCA
122420	120507	CAGCTTCATTCATAATAGCC
122421	120508	GCAGCTTCATTCATAATAGC
122422	120509	AGCAGCTTCATTCATAATAG
122423	120510	CAGCAGCTTCATTCATAATA
122424	120511	ACAGCAGCTTCATTCATAAT
122425	120512	CACAGCAGCTTCATTCATAA
122426	120513	TCACAGCAGCTTCATTCATA
122427	120514	CTCACAGCAGCTTCATTCAT

24134	22221	TTTTAGTATTTTTAGTAGAG
24135	22222	TTTTTAGTATTTTTAGTAGA
24136	22223	ATTTTTAGTATTTTTAGTAG
24137	22224	AATTTTTAGTATTTTTAGTA
24138	22225	TAATTTTTAGTATTTTTAGT
24139	22226	TTAATTTTTAGTATTTTTAG
24140	22227	GTTAATTTTTAGTATTTTTA
24141	22228	GGTTAATTTTTAGTATTTTT
24142	22229	CGGTTAATTTTTAGTATTTT
24143	22230	CCGGTTAATTTTTAGTATTT
24144	22231	CCCGGTTAATTTTTAGTATT
24145	22232	ACCCGGTTAATTTTTAGTAT
24146	22233	CACCCGGTTAATTTTTAGTA
24147	22234	ACACCCGGTTAATTTTTAGT
24148	22235	CACACCCGGTTAATTTTTAG
24149	22236	CCACACCCGGTTAATTTTTA
24150	22237	ACCACACCCGGTTAATTTTT
24151	22238	CACCACACCCGGTTAATTTT
24152	22239	CCACCACACCCGGTTAATTT
24153	22240	GCCACCACACCCGGTTAATT
24154	22241	CGCCACCACACCCGGTTAAT
24155	22242	CCGCCACCACACCCGGTTAA
24156	22243	CCCGCCACCACACCCGGTTA
24157	22244	GCCCGCCACCACACCCGGTT
24158	22245	CGCCCGCCACCACACCCGGT
24159	22246	GCGCCCGCCACCACACCCGG
24160	22247	GGCGCCCGCCACCACACCCG
24161	22248	AGGCGCCCGCCACCACACCC
24162	22249	CAGGCGCCCGCCACCACACC
24163	22250	ACAGGCGCCCGCCACCACAC
24164	22251	TACAGGCGCCCGCCACCACA
24165	22252	TTACAGGCGCCCGCCACCAC
24166	22253	ATTACAGGCGCCCGCCACCA
24167	22254	GATTACAGGCGCCCGCCACC
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24169	22256	GGGATTACAGGCGCCCGCCA
24170	22257	TGGGATTACAGGCGCCCGCC
24171	22258	CTGGGATTACAGGCGCCCGC
24172	22259	GCTGGGATTACAGGCGCCCG
24173	22260	AGCTGGGATTACAGGCGCCC
24174	22261	TAGCTGGGATTACAGGCGCC
24175	22262	GTAGCTGGGATTACAGGCGC
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24177	22264	GAGTAGCTGGGATTACAGGC
24178	22265	CGAGTAGCTGGGATTACAGG
24179	22266	CCGAGTAGCTGGGATTACAG
24180	22267	CCCGAGTAGCTGGGATTACA
24181	22268	TCCCGAGTAGCTGGGATTAC
24182	22269	CTCCCGAGTAGCTGGGATTA
24183	22270	CCTCCCGAGTAGCTGGGATT
24184	22271	GCCTCCCGAGTAGCTGGGAT
24185	22272	AGCCTCCCGAGTAGCTGGGA
24186	22273	CAGCCTCCCGAGTAGCTGGG
24187	22274	TCAGCCTCCCGAGTAGCTGG
24188	22275	CTCAGCCTCCCGAGTAGCTG
24189	22276	CCTCAGCCTCCCGAGTAGCT
24190	22277	GCCTCAGCCTCCCGAGTAGC
24191	22278	TGCCTCAGCCTCCCGAGTAG
24192	22279	CTGCCTCAGCCTCCCGAGTA
24193	22280	CCTGCCTCAGCCTCCCGAGT
24194	22281	TCCTGCCTCAGCCTCCCGAG
24195	22282	CTCCTGCCTCAGCCTCCCGA
24196	22283	TCTCCTGCCTCAGCCTCCCG
24197	22284	TTCTCCTGCCTCAGCCTCCC
24198	22285	ATTCTCCTGCCTCAGCCTCC
24199	22286	CATTCTCCTGCCTCAGCCTC
24200	22287	CCATTCTCCTGCCTCAGCCT
24201	22288	GCCATTCTCCTGCCTCAGCC
24202	22289	CGCCATTCTCCTGCCTCAGC
24203	22290	ACGCCATTCTCCTGCCTCAG
24204	22291	CACGCCATTCTCCTGCCTCA

73281	71368	AAATATTTAGAAAGTCTTGA
73282	71369	AAAATATTTAGAAAGTCTTG
73283	71370	GAAAATATTTAGAAAGTCTT
73284	71371	TGAAAATATTTAGAAAGTCT
73285	71372	GTGAAAATATTTAGAAAGTC
73286	71373	TGTGAAAATATTTAGAAAGT
73287	71374	GTGTGAAAATATTTAGAAAG
73288	71375	TGTGTGAAAATATTTAGAAA
73289	71376	GTGTGTGAAAATATTTAGAA
73290	71377	TGTGTGTGAAAATATTTAGA
73291	71378	GTGTGTGTGAAAATATTTAG
73292	71379	TGTGTGTGTGAAAATATTTA
73293	71380	GTGTGTGTGTGAAAATATTT
73294	71381	TGTGTGTGTGTGAAAATATT
73295	71382	GTGTGTGTGTGTGAAAATAT
73296	71383	TGTGTGTGTGTGTGAAAATA
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73298	71385	TATGTGTGTGTGTGTGAAAA
73299	71386	GTATGTGTGTGTGTGTGAAA
73300	71387	GGTATGTGTGTGTGTGTGAA
73301	71388	GGGTATGTGTGTGTGTGTGA
73302	71389	AGGGTATGTGTGTGTGTGTG
73303	71390	CAGGGTATGTGTGTGTGTGT
73304	71391	ACAGGGTATGTGTGTGTGTG
73305	71392	TACAGGGTATGTGTGTGTGT
73306	71393	CTACAGGGTATGTGTGTGTG
73307	71394	ACTACAGGGTATGTGTGTGT
73308	71395	CACTACAGGGTATGTGTGTG
73309	71396	TCACTACAGGGTATGTGTGT
73310	71397	CTCACTACAGGGTATGTGTG
73311	71398	TCTCACTACAGGGTATGTGT
73312	71399	TTCTCACTACAGGGTATGTG
73313	71400	TTTCTCACTACAGGGTATGT
73314	71401	TTTTCTCACTACAGGGTATG
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73319	71406	GATTTTTTTCTCACTACAGG
73320	71407	GGATTTTTTTCTCACTACAG
73321	71408	CGGATTTTTTTCTCACTACA
73322	71409	ACGGATTTTTTTCTCACTAC
73323	71410	AACGGATTTTTTTCTCACTA
73324	71411	AAACGGATTTTTTTCTCACT
73325	71412	TAAACGGATTTTTTTCTCAC
73326	71413	ATAAACGGATTTTTTTCTCA
73327	71414	TATAAACGGATTTTTTTCTC
73328	71415	ATATAAACGGATTTTTTTCT
73329	71416	CATATAAACGGATTTTTTTC
73330	71417	CCATATAAACGGATTTTTTT
73331	71418	ACCATATAAACGGATTTTTT
73332	71419	AACCATATAAACGGATTTTT
73333	71420	GAACCATATAAACGGATTTT
73334	71421	AGAACCATATAAACGGATTT
73335	71422	TAGAACCATATAAACGGATT
73336	71423	ATAGAACCATATAAACGGAT
73337	71424	TATAGAACCATATAAACGGA
73338	71425	TTATAGAACCATATAAACGG
73339	71426	TTTATAGAACCATATAAACG
73340	71427	TTTTATAGAACCATATAAAC
73341	71428	TTTTTATAGAACCATATAAA
73342	71429	ATTTTTATAGAACCATATAA
73343	71430	GATTTTTATAGAACCATATA
73344	71431	AGATTTTTATAGAACCATAT
73345	71432	GAGATTTTTATAGAACCATA
73346	71433	AGAGATTTTTATAGAACCAT
73347	71434	TAGAGATTTTTATAGAACCA
73348	71435	CTAGAGATTTTTATAGAACC
73349	71436	GCTAGAGATTTTTATAGAAC
73350	71437	AGCTAGAGATTTTTATAGAA
73351	71438	CAGCTAGAGATTTTTATAGA

122428	120515	GCTCACAGCAGCTTCATTCA
122429	120516	TGCTCACAGCAGCTTCATTC
122430	120517	ATGCTCACAGCAGCTTCATT
122431	120518	AATGCTCACAGCAGCTTCAT
122432	120519	AAATGCTCACAGCAGCTTCA
122433	120520	CAAATGCTCACAGCAGCTTC
122434	120521	ACAAATGCTCACAGCAGCTT
122435	120522	CACAAATGCTCACAGCAGCT
122436	120523	ACACAAATGCTCACAGCAGC
122437	120524	TACACAAATGCTCACAGCAG
122438	120525	GTACACAAATGCTCACAGCA
122439	120526	TGTACACAAATGCTCACAGC
122440	120527	TTGTACACAAATGCTCACAG
122441	120528	CTTGTACACAAATGCTCACA
122442	120529	ACTTGTACACAAATGCTCAC
122443	120530	CACTTGTACACAAATGCTCA
122444	120531	ACACTTGTACACAAATGCTC
122445	120532	AACACTTGTACACAAATGCT
122446	120533	AAACACTTGTACACAAATGC
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122448	120535	ACAAACACTTGTACACAAAT
122449	120536	CACAAACACTTGTACACAAA
122450	120537	ACACAAACACTTGTACACAA
122451	120538	AACACAAACACTTGTACACA
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122453	120540	AAAACACAAACACTTGTACA
122454	120541	AAAAACACAAACACTTGTAC
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122462	120549	AAAGAAATAAAAACACAAAC
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122474	120561	GGTATTTAACTAAAAGAAAT
122475	120562	AGGTATTTAACTAAAAGAAA
122476	120563	TAGGTATTTAACTAAAAGAA
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122478	120565	TCTAGGTATTTAACTAAAAG
122479	120566	TTCTAGGTATTTAACTAAAA
122480	120567	ATTCTAGGTATTTAACTAAA
122481	120568	AATTCTAGGTATTTAACTAA
122482	120569	CAATTCTAGGTATTTAACTA
122483	120570	CCAATTCTAGGTATTTAACT
122484	120571	TCCAATTCTAGGTATTTAAC
122485	120572	TTCCAATTCTAGGTATTTAA
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122496	120583	TACCTCAGCAATTCCAATTC
122497	120584	ATACCTCAGCAATTCCAATT
122498	120585	CATACCTCAGCAATTCCAAT

24205	22292	TCACGCCATTCTCCTGCCTC
24206	22293	TTCACGCCATTCTCCTGCCT
24207	22294	GTTCACGCCATTCTCCTGCC
24208	22295	GGTTCACGCCATTCTCCTGC
24209	22296	GGGTTCACGCCATTCTCCTG
24210	22297	CGGGTTCACGCCATTCTCCT
24211	22298	CCGGGTTCACGCCATTCTCC
24212	22299	CCCGGGTTCACGCCATTCTC
24213	22300	TCCCGGGTTCACGCCATTCT
24214	22301	CTCCCGGGTTCACGCCATTC
24215	22302	CCTCCCGGGTTCACGCCATT
24216	22303	GCCTCCCGGGTTCACGCCAT
24217	22304	CGCCTCCCGGGTTCACGCCA
24218	22305	CCGCCTCCCGGGTTCACGCC
24219	22306	TCCGCCTCCCGGGTTCACGC
24220	22307	CTCCGCCTCCCGGGTTCACG
24221	22308	GCTCCGCCTCCCGGGTTCAC
24222	22309	AGCTCCGCCTCCCGGGTTCA
24223	22310	AAGCTCCGCCTCCCGGGTTC
24224	22311	CAAGCTCCGCCTCCCGGGTT
24225	22312	GCAAGCTCCGCCTCCCGGGT
24226	22313	TGCAAGCTCCGCCTCCCGGG
24227	22314	CTGCAAGCTCCGCCTCCCGG
24228	22315	ACTGCAAGCTCCGCCTCCCG
24229	22316	CACTGCAAGCTCCGCCTCCC
24230	22317	TCACTGCAAGCTCCGCCTCC
24231	22318	CTCACTGCAAGCTCCGCCTC
24232	22319	GCTCACTGCAAGCTCCGCCT
24233	22320	GGCTCACTGCAAGCTCCGCC
24234	22321	CGGCTCACTGCAAGCTCCGC
24235	22322	TCGGCTCACTGCAAGCTCCG
24236	22323	CTCGGCTCACTGCAAGCTCC
24237	22324	TCTCGGCTCACTGCAAGCTC
24238	22325	ATCTCGGCTCACTGCAAGCT
24239	22326	GATCTCGGCTCACTGCAAGC
24240	22327	CGATCTCGGCTCACTGCAAG
24241	22328	ACGATCTCGGCTCACTGCAA
24242	22329	CACGATCTCGGCTCACTGCA
24243	22330	GCACGATCTCGGCTCACTGC
24244	22331	GGCACGATCTCGGCTCACTG
24245	22332	TGGCACGATCTCGGCTCACT
24246	22333	GTGGCACGATCTCGGCTCAC
24247	22334	AGTGGCACGATCTCGGCTCA
24248	22335	CAGTGGCACGATCTCGGCTC
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24250	22337	TGCAGTGGCACGATCTCGGC
24251	22338	GTGCAGTGGCACGATCTCGG
24252	22339	AGTGCAGTGGCACGATCTCG
24253	22340	GAGTGCAGTGGCACGATCTC
24254	22341	GGAGTGCAGTGGCACGATCT
24255	22342	TGGAGTGCAGTGGCACGATC
24256	22343	CTGGAGTGCAGTGGCACGAT
24257	22344	GCTGGAGTGCAGTGGCACGA
24258	22345	GGCTGGAGTGCAGTGGCACG
24259	22346	AGGCTGGAGTGCAGTGGCAC
24260	22347	CAGGCTGGAGTGCAGTGGCA
24261	22348	CCAGGCTGGAGTGCAGTGGC
24262	22349	CCCAGGCTGGAGTGCAGTGG
24263	22350	GCCCAGGCTGGAGTGCAGTG
24264	22351	TGCCCAGGCTGGAGTGCAGT
24265	22352	TTGCCCAGGCTGGAGTGCAG
24266	22353	GTTGCCCAGGCTGGAGTGCA
24267	22354	TGTTGCCCAGGCTGGAGTGC
24268	22355	CTGTTGCCCAGGCTGGAGTG
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24270	22357	CTCTGTTGCCCAGGCTGGAG
24271	22358	GCTCTGTTGCCCAGGCTGGA
24272	22359	CGCTCTGTTGCCCAGGCTGG
24273	22360	TCGCTCTGTTGCCCAGGCTG
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24275	22362	TCTCGCTCTGTTGCCCAGGC

73352	71439	GCAGCTAGAGATTTTTATAG
73353	71440	AGCAGCTAGAGATTTTTATA
73354	71441	AAGCAGCTAGAGATTTTTAT
73355	71442	GAAGCAGCTAGAGATTTTTA
73356	71443	CGAAGCAGCTAGAGATTTTT
73357	71444	TCGAAGCAGCTAGAGATTTT
73358	71445	CTCGAAGCAGCTAGAGATTT
73359	71446	GCTCGAAGCAGCTAGAGATT
73360	71447	AGCTCGAAGCAGCTAGAGAT
73361	71448	AAGCTCGAAGCAGCTAGAGA
73362	71449	AAAGCTCGAAGCAGCTAGAG
73363	71450	TAAAGCTCGAAGCAGCTAGA
73364	71451	TTAAAGCTCGAAGCAGCTAG
73365	71452	ATTAAAGCTCGAAGCAGCTA
73366	71453	AATTAAAGCTCGAAGCAGCT
73367	71454	AAATTAAAGCTCGAAGCAGC
73368	71455	GAAATTAAAGCTCGAAGCAG
73369	71456	AGAAATTAAAGCTCGAAGCA
73370	71457	AAGAAATTAAAGCTCGAAGC
73371	71458	CAAGAAATTAAAGCTCGAAG
73372	71459	TCAAGAAATTAAAGCTCGAA
73373	71460	TTCAAGAAATTAAAGCTCGA
73374	71461	ATTCAAGAAATTAAAGCTCG
73375	71462	GATTCAAGAAATTAAAGCTC
73376	71463	TGATTCAAGAAATTAAAGCT
73377	71464	TTGATTCAAGAAATTAAAGC
73378	71465	TTTGATTCAAGAAATTAAAG
73379	71466	TTTTGATTCAAGAAATTAAA
73380	71467	CTTTTGATTCAAGAAATTAA
73381	71468	TCTTTTGATTCAAGAAATTA
73382	71469	CTCTTTTGATTCAAGAAATT
73383	71470	ACTCTTTTGATTCAAGAAAT
73384	71471	TACTCTTTTGATTCAAGAAA
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73399	71486	CAGTATTAAAAACAATACTC
73400	71487	TCAGTATTAAAAACAATACT
73401	71488	CTCAGTATTAAAAACAATAC
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73403	71490	AGCTCAGTATTAAAAACAAT
73404	71491	AAGCTCAGTATTAAAAACAA
73405	71492	GAAGCTCAGTATTAAAAACA
73406	71493	AGAAGCTCAGTATTAAAAAC
73407	71494	TAGAAGCTCAGTATTAAAAA
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73409	71496	GATAGAAGCTCAGTATTAAA
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73411	71498	TAGATAGAAGCTCAGTATTA
73412	71499	TTAGATAGAAGCTCAGTATT
73413	71500	TTTAGATAGAAGCTCAGTAT
73414	71501	ATTTAGATAGAAGCTCAGTA
73415	71502	TATTTAGATAGAAGCTCAGT
73416	71503	TTATTTAGATAGAAGCTCAG
73417	71504	TTTATTTAGATAGAAGCTCA
73418	71505	ATTTATTTAGATAGAAGCTC
73419	71506	CATTTATTTAGATAGAAGCT
73420	71507	GCATTTATTTAGATAGAAGC
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73422	71509	AAGCATTTATTTAGATAGAA

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122500	120587	ACCATACCTCAGCAATTCCA
122501	120588	TACCATACCTCAGCAATTCC
122502	120589	TTACCATACCTCAGCAATTC
122503	120590	CTTACCATACCTCAGCAATT
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122505	120592	CACTTACCATACCTCAGCAA
122506	120593	GCACTTACCATACCTCAGCA
122507	120594	TGCACTTACCATACCTCAGC
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122509	120596	TATGCACTTACCATACCTCA
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122520	120607	AAAAAATGAAATATGCACTT
122521	120608	AAAAAAATGAAATATGCACT
122522	120609	TAAAAAAATGAAATATGCAC
122523	120610	TTAAAAAAATGAAATATGCA
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122536	120623	TAAAATAAATTTTTTAAAAA
122537	120624	ATAAAATAAATTTTTTAAAA
122538	120625	AATAAAATAAATTTTTTAAA
122539	120626	AAATAAAATAAATTTTTTAA
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122545	120632	AATAAAAAATAAAATAAATT
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122557	120644	AAAAAATAAATAAATAAAAA
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122567	120654	TTCATCTCAAAAAAAATAAA
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122569	120656	ACTTCATCTCAAAAAAAATA

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24277	22364	AGTCTCGCTCTGTTGCCCAG
24278	22365	GAGTCTCGCTCTGTTGCCCA
24279	22366	AGAGTCTCGCTCTGTTGCCC
24280	22367	CAGAGTCTCGCTCTGTTGCC
24281	22368	ACAGAGTCTCGCTCTGTTGC
24282	22369	GACAGAGTCTCGCTCTGTTG
24283	22370	AGACAGAGTCTCGCTCTGTT
24284	22371	GAGACAGAGTCTCGCTCTGT
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24296	22383	TTTATTTATTTTGAGACAGA
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24298	22385	TATTTATTTATTTTGAGACA
24299	22386	TTATTTATTTATTTTGAGAC
24300	22387	TTTATTTATTTATTTTGAGA
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24334	22421	AACACATGCACCGCATGTTT
24335	22422	AAACACATGCACCGCATGTT
24336	22423	TAAACACATGCACCGCATGT
24337	22424	ATAAACACATGCACCGCATG
24338	22425	AATAAACACATGCACCGCAT
24339	22426	AAATAAACACATGCACCGCA
24340	22427	CAAATAAACACATGCACCGC
24341	22428	GCAAATAAACACATGCACCG
24342	22429	CGCAAATAAACACATGCACC
24343	22430	TCGCAAATAAACACATGCAC
24344	22431	ATCGCAAATAAACACATGCA
24345	22432	GATCGCAAATAAACACATGC
24346	22433	AGATCGCAAATAAACACATG

73423	71510	AAAGCATTTATTTAGATAGA
73424	71511	TAAAGCATTTATTTAGATAG
73425	71512	ATAAAGCATTTATTTAGATA
73426	71513	AATAAAGCATTTATTTAGAT
73427	71514	AAATAAAGCATTTATTTAGA
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73429	71516	GTAAATAAAGCATTTATTTA
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73431	71518	AAGTAAATAAAGCATTTATT
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73433	71520	TTAAGTAAATAAAGCATTTA
73434	71521	TTTAAGTAAATAAAGCATTT
73435	71522	ATTTAAGTAAATAAAGCATT
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73438	71525	CACATTTAAGTAAATAAAGC
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73464	71551	TTAATCATACTAGTTTTTGA
73465	71552	CTTAATCATACTAGTTTTTG
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73468	71555	TGTCTTAATCATACTAGTTT
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73470	71557	AATGTCTTAATCATACTAGT
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73473	71560	GTTAATGTCTTAATCATACT
73474	71561	TGTTAATGTCTTAATCATAC
73475	71562	CTGTTAATGTCTTAATCATA
73476	71563	CCTGTTAATGTCTTAATCAT
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73478	71565	ATCCTGTTAATGTCTTAATC
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73481	71568	AAGATCCTGTTAATGTCTTA
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73493	71580	TCCTTTACGTCTAAGATCCT

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122612	120699	CTGAAATCACGCCACTGAAC
122613	120700	GCTGAAATCACGCCACTGAA
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122615	120702	GAGCTGAAATCACGCCACTG
122616	120703	TGAGCTGAAATCACGCCACT
122617	120704	ATGAGCTGAAATCACGCCAC
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122622	120709	TTGCCATGAGCTGAAATCAC
122623	120710	GTTGCCATGAGCTGAAATCA
122624	120711	GGTTGCCATGAGCTGAAATC
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122626	120713	GAGGTTGCCATGAGCTGAAA
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24347	22434	CAGATCGCAAATAAACACAT
24348	22435	TCAGATCGCAAATAAACACA
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24350	22437	AGTCAGATCGCAAATAAACA
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24374	22461	AGATAATGCAAATATTTCCA
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24376	22463	GAAGATAATGCAAATATTTC
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24378	22465	AGGAAGATAATGCAAATATT
24379	22466	AAGGAAGATAATGCAAATAT
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24382	22469	TAGAAGGAAGATAATGCAAA
24383	22470	CTAGAAGGAAGATAATGCAA
24384	22471	TCTAGAAGGAAGATAATGCA
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24388	22475	TAAATCTAGAAGGAAGATAA
24389	22476	CTAAATCTAGAAGGAAGATA
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24391	22478	CTCTAAATCTAGAAGGAAGA
24392	22479	GCTCTAAATCTAGAAGGAAG
24393	22480	TGCTCTAAATCTAGAAGGAA
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24395	22482	GATGCTCTAAATCTAGAAGG
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24397	22484	AAGATGCTCTAAATCTAGAA
24398	22485	CAAGATGCTCTAAATCTAGA
24399	22486	TCAAGATGCTCTAAATCTAG
24400	22487	GTCAAGATGCTCTAAATCTA
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24414	22501	CACTTGTTCCTACTGTCAAG
24415	22502	ACACTTGTTCCTACTGTCAA
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73494	71581	TTCCTTTACGTCTAAGATCC
73495	71582	GTTCCTTTACGTCTAAGATC
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73499	71586	GACTGTTCCTTTACGTCTAA
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73518	71605	CTTCTGGAAGAAGCAACAGG
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73520	71607	ATCTTCTGGAAGAAGCAACA
73521	71608	TATCTTCTGGAAGAAGCAAC
73522	71609	TTATCTTCTGGAAGAAGCAA
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73524	71611	TATTATCTTCTGGAAGAAGC
73525	71612	ATATTATCTTCTGGAAGAAG
73526	71613	CATATTATCTTCTGGAAGAA
73527	71614	TCATATTATCTTCTGGAAGA
73528	71615	GTCATATTATCTTCTGGAAG
73529	71616	AGTCATATTATCTTCTGGAA
73530	71617	GAGTCATATTATCTTCTGGA
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73533	71620	AACGAGTCATATTATCTTCT
73534	71621	AAACGAGTCATATTATCTTC
73535	71622	CAAACGAGTCATATTATCTT
73536	71623	CCAAACGAGTCATATTATCT
73537	71624	TCCAAACGAGTCATATTATC
73538	71625	TTCCAAACGAGTCATATTAT
73539	71626	ATTCCAAACGAGTCATATTA
73540	71627	AATTCCAAACGAGTCATATT
73541	71628	AAATTCCAAACGAGTCATAT
73542	71629	AAAATTCCAAACGAGTCATA
73543	71630	GAAAATTCCAAACGAGTCAT
73544	71631	GGAAAATTCCAAACGAGTCA
73545	71632	AGGAAAATTCCAAACGAGTC
73546	71633	TAGGAAAATTCCAAACGAGT
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73555	71642	ACTACACTATAGGAAAATTC
73556	71643	AACTACACTATAGGAAAATT
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73560	71647	AAAAAACTACACTATAGGAA
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73562	71649	ACAAAAAACTACACTATAGG
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122644	120731	GCTTGAACCCGGGACAGGGA
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122646	120733	TTGCTTGAACCCGGGACAGG
122647	120734	ATTGCTTGAACCCGGGACAG
122648	120735	AATTGCTTGAACCCGGGACA
122649	120736	GAATTGCTTGAACCCGGGAC
122650	120737	AGAATTGCTTGAACCCGGGA
122651	120738	GAGAATTGCTTGAACCCGGG
122652	120739	GGAGAATTGCTTGAACCCGG
122653	120740	GGGAGAATTGCTTGAACCCG
122654	120741	CGGGAGAATTGCTTGAACCC
122655	120742	GCGGGAGAATTGCTTGAACC
122656	120743	GGCGGGAGAATTGCTTGAAC
122657	120744	AGGCGGGAGAATTGCTTGAA
122658	120745	GAGGCGGGAGAATTGCTTGA
122659	120746	TGAGGCGGGAGAATTGCTTG
122660	120747	CTGAGGCGGGAGAATTGCTT
122661	120748	GCTGAGGCGGGAGAATTGCT
122662	120749	GGCTGAGGCGGGAGAATTGC
122663	120750	AGGCTGAGGCGGGAGAATTG
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122665	120752	GGAGGCTGAGGCGGGAGAAT
122666	120753	GGGAGGCTGAGGCGGGAGAA
122667	120754	TGGGAGGCTGAGGCGGGAGA
122668	120755	TTGGGAGGCTGAGGCGGGAG
122669	120756	CTTGGGAGGCTGAGGCGGGA
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122671	120758	TACTTGGGAGGCTGAGGCGG
122672	120759	CTACTTGGGAGGCTGAGGCG
122673	120760	GCTACTTGGGAGGCTGAGGC
122674	120761	AGCTACTTGGGAGGCTGAGG
122675	120762	CAGCTACTTGGGAGGCTGAG
122676	120763	CCAGCTACTTGGGAGGCTGA
122677	120764	CCCAGCTACTTGGGAGGCTG
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73574	71661	TCACAACACTAGACAAAAAA
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73624	71711	GAAAACATCAAATAATAACC
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73629	71716	TCCAAGAAAACATCAAATAA
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73634	71721	AATGTTCCAAGAAAACATCA
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122747	120834	ACGTGGTGAAACCCCGTCTC
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122781	120868	ACTTGTGGTCAGGAGTTCGA
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24513	22600	CCTCGGCCTCCCAAAGTGCT
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24521	22608	TCTGCCCGCCTCGGCCTCCC
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24524	22611	TGATCTGCCCGCCTCGGCCT
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73696	71783	CTTAAAGTTATGTGGATTGC
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73703	71790	ACATTATCTTAAAGTTATGT
73704	71791	TACATTATCTTAAAGTTATG
73705	71792	CTACATTATCTTAAAGTTAT
73706	71793	TCTACATTATCTTAAAGTTA

122783	120870	TCACTTGTGGTCAGGAGTTC
122784	120871	ATCACTTGTGGTCAGGAGTT
122785	120872	GATCACTTGTGGTCAGGAGT
122786	120873	GGATCACTTGTGGTCAGGAG
122787	120874	TGGATCACTTGTGGTCAGGA
122788	120875	GTGGATCACTTGTGGTCAGG
122789	120876	GGTGGATCACTTGTGGTCAG
122790	120877	GGGTGGATCACTTGTGGTCA
122791	120878	CGGGTGGATCACTTGTGGTC
122792	120879	GCGGGTGGATCACTTGTGGT
122793	120880	GGCGGGTGGATCACTTGTGG
122794	120881	GGGCGGGTGGATCACTTGTG
122795	120882	GGGGCGGGTGGATCACTTGT
122796	120883	TGGGGCGGGTGGATCACTTG
122797	120884	CTGGGGCGGGTGGATCACTT
122798	120885	GCTGGGGCGGGTGGATCACT
122799	120886	GGCTGGGGCGGGTGGATCAC
122800	120887	AGGCTGGGGCGGGTGGATCA
122801	120888	GAGGCTGGGGCGGGTGGATC
122802	120889	GGAGGCTGGGGCGGGTGGAT
122803	120890	GGGAGGCTGGGGCGGGTGGA
122804	120891	TGGGAGGCTGGGGCGGGTGG
122805	120892	TTGGGAGGCTGGGGCGGGTG
122806	120893	TTTGGGAGGCTGGGGCGGGT
122807	120894	CTTTGGGAGGCTGGGGCGGG
122808	120895	ACTTTGGGAGGCTGGGGCGG
122809	120896	CACTTTGGGAGGCTGGGGCG
122810	120897	ACACTTTGGGAGGCTGGGGC
122811	120898	AACACTTTGGGAGGCTGGGG
122812	120899	CAACACTTTGGGAGGCTGGG
122813	120900	CCAACACTTTGGGAGGCTGG
122814	120901	CCCAACACTTTGGGAGGCTG
122815	120902	TCCCAACACTTTGGGAGGCT
122816	120903	ATCCCAACACTTTGGGAGGC
122817	120904	AATCCCAACACTTTGGGAGG
122818	120905	TAATCCCAACACTTTGGGAG
122819	120906	GTAATCCCAACACTTTGGGA
122820	120907	TGTAATCCCAACACTTTGGG
122821	120908	CTGTAATCCCAACACTTTGG
122822	120909	TCTGTAATCCCAACACTTTG
122823	120910	ATCTGTAATCCCAACACTTT
122824	120911	CATCTGTAATCCCAACACTT
122825	120912	ACATCTGTAATCCCAACACT
122826	120913	CACATCTGTAATCCCAACAC
122827	120914	TCACATCTGTAATCCCAACA
122828	120915	CTCACATCTGTAATCCCAAC
122829	120916	GCTCACATCTGTAATCCCAA
122830	120917	GGCTCACATCTGTAATCCCA
122831	120918	TGGCTCACATCTGTAATCCC
122832	120919	GTGGCTCACATCTGTAATCC
122833	120920	GGTGGCTCACATCTGTAATC
122834	120921	TGGTGGCTCACATCTGTAAT
122835	120922	GTGGTGGCTCACATCTGTAA
122836	120923	TGTGGTGGCTCACATCTGTA
122837	120924	GTGTGGTGGCTCACATCTGT
122838	120925	TGTGTGGTGGCTCACATCTG
122839	120926	GTGTGTGGTGGCTCACATCT
122840	120927	AGTGTGTGGTGGCTCACATC
122841	120928	CAGTGTGTGGTGGCTCACAT
122842	120929	GCAGTGTGTGGTGGCTCACA
122843	120930	GGCAGTGTGTGGTGGCTCAC
122844	120931	AGGCAGTGTGTGGTGGCTCA
122845	120932	CAGGCAGTGTGTGGTGGCTC
122846	120933	CCAGGCAGTGTGTGGTGGCT
122847	120934	ACCAGGCAGTGTGTGGTGGC
122848	120935	TACCAGGCAGTGTGTGGTGG
122849	120936	TTACCAGGCAGTGTGTGGTG
122850	120937	TTTACCAGGCAGTGTGTGGT
122851	120938	ATTTACCAGGCAGTGTGTGG
122852	120939	TATTTACCAGGCAGTGTGTG
122853	120940	GTATTTACCAGGCAGTGTGT

24560	22647	CGTTGGCCACGCTGGTCTCG
24561	22648	ACGTTGGCCACGCTGGTCTC
24562	22649	CACGTTGGCCACGCTGGTCT
24563	22650	CCACGTTGGCCACGCTGGTC
24564	22651	ACCACGTTGGCCACGCTGGT
24565	22652	CACCACGTTGGCCACGCTGG
24566	22653	TCACCACGTTGGCCACGCTG
24567	22654	TTCACCACGTTGGCCACGCT
24568	22655	TTTCACCACGTTGGCCACGC
24569	22656	GTTTCACCACGTTGGCCACG
24570	22657	GGTTTCACCACGTTGGCCAC
24571	22658	GGGTTTCACCACGTTGGCCA
24572	22659	AGGGTTTCACCACGTTGGCC
24573	22660	CAGGGTTTCACCACGTTGGC
24574	22661	CCAGGGTTTCACCACGTTGG
24575	22662	CCCAGGGTTTCACCACGTTG
24576	22663	ACCCAGGGTTTCACCACGTT
24577	22664	AACCCAGGGTTTCACCACGT
24578	22665	AAACCCAGGGTTTCACCACG
24579	22666	CAAACCCAGGGTTTCACCAC
24580	22667	ACAAACCCAGGGTTTCACCA
24581	22668	AACAAACCCAGGGTTTCACC
24582	22669	AAACAAACCCAGGGTTTCAC
24583	22670	CAAACAAACCCAGGGTTTCA
24584	22671	ACAAACAAACCCAGGGTTTC
24585	22672	AACAAACAAACCCAGGGTTT
24586	22673	AAACAAACAAACCCAGGGTT
24587	22674	CAAACAAACAAACCCAGGGT
24588	22675	ACAAACAAACAAACCCAGGG
24589	22676	AACAAACAAACAAACCCAGG
24590	22677	AAACAAACAAACAAACCCAG
24591	22678	TAAACAAACAAACAAACCCA
24592	22679	ATAAACAAACAAACAAACCC
24593	22680	AATAAACAAACAAACAAACC
24594	22681	AAATAAACAAACAAACAAAC
24595	22682	TAAATAAACAAACAAACAAA
24596	22683	ATAAATAAACAAACAAACAA
24597	22684	AATAAATAAACAAACAAACA
24598	22685	AAATAAATAAACAAACAAAC
24599	22686	TAAATAAATAAACAAACAAA
24600	22687	ATAAATAAATAAACAAACAA
24601	22688	AATAAATAAATAAACAAACA
24602	22689	AAATAAATAAATAAACAAAC
24603	22690	TAAATAAATAAATAAACAAA
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24605	22692	AATAAATAAATAAATAAACA
24606	22693	AAATAAATAAATAAATAAAC
24607	22694	AAAATAAATAAATAAATAAA
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24609	22696	AAAAAATAAATAAATAAATA
24610	22697	CAAAAAATAAATAAATAAAT
24611	22698	CCAAAAAATAAATAAATAAA
24612	22699	TCCAAAAAATAAATAAATAA
24613	22700	CTCCAAAAAATAAATAAATA
24614	22701	TCTCCAAAAAATAAATAAAT
24615	22702	GTCTCCAAAAAATAAATAAA
24616	22703	CGTCTCCAAAAAATAAATAA
24617	22704	CCGTCTCCAAAAAATAAATA
24618	22705	TCCGTCTCCAAAAAATAAAT
24619	22706	CTCCGTCTCCAAAAAATAAA
24620	22707	ACTCCGTCTCCAAAAAATAA
24621	22708	GACTCCGTCTCCAAAAAATA
24622	22709	AGACTCCGTCTCCAAAAAAT
24623	22710	GAGACTCCGTCTCCAAAAAA
24624	22711	CGAGACTCCGTCTCCAAAAA
24625	22712	GCGAGACTCCGTCTCCAAAA
24626	22713	AGCGAGACTCCGTCTCCAAA
24627	22714	GAGCGAGACTCCGTCTCCAA
24628	22715	AGAGCGAGACTCCGTCTCCA
24629	22716	CAGAGCGAGACTCCGTCTCC
24630	22717	ACAGAGCGAGACTCCGTCTC

73707	71794	CTCTACATTATCTTAAAGTT
73708	71795	TCTCTACATTATCTTAAAGT
73709	71796	TTCTCTACATTATCTTAAAG
73710	71797	CTTCTCTACATTATCTTAAA
73711	71798	TCTTCTCTACATTATCTTAA
73712	71799	TTCTTCTCTACATTATCTTA
73713	71800	GTTCTTCTCTACATTATCTT
73714	71801	CGTTCTTCTCTACATTATCT
73715	71802	ACGTTCTTCTCTACATTATC
73716	71803	CACGTTCTTCTCTACATTAT
73717	71804	TCACGTTCTTCTCTACATTA
73718	71805	ATCACGTTCTTCTCTACATT
73719	71806	AATCACGTTCTTCTCTACAT
73720	71807	GAATCACGTTCTTCTCTACA
73721	71808	TGAATCACGTTCTTCTCTAC
73722	71809	CTGAATCACGTTCTTCTCTA
73723	71810	CCTGAATCACGTTCTTCTCT
73724	71811	ACCTGAATCACGTTCTTCTC
73725	71812	AACCTGAATCACGTTCTTCT
73726	71813	TAACCTGAATCACGTTCTTC
73727	71814	CTAACCTGAATCACGTTCTT
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73729	71816	TACTAACCTGAATCACGTTC
73730	71817	ATACTAACCTGAATCACGTT
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73732	71819	TGATACTAACCTGAATCACG
73733	71820	TTGATACTAACCTGAATCAC
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73739	71826	CCTTATTTGATACTAACCTG
73740	71827	ACCTTATTTGATACTAACCT
73741	71828	GACCTTATTTGATACTAACC
73742	71829	TGACCTTATTTGATACTAAC
73743	71830	CTGACCTTATTTGATACTAA
73744	71831	TCTGACCTTATTTGATACTA
73745	71832	ATCTGACCTTATTTGATACT
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73748	71835	GAAATCTGACCTTATTTGAT
73749	71836	AGAAATCTGACCTTATTTGA
73750	71837	TAGAAATCTGACCTTATTTG
73751	71838	CTAGAAATCTGACCTTATTT
73752	71839	ACTAGAAATCTGACCTTATT
73753	71840	CACTAGAAATCTGACCTTAT
73754	71841	GCACTAGAAATCTGACCTTA
73755	71842	GGCACTAGAAATCTGACCTT
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73758	71845	GATGGCACTAGAAATCTGAC
73759	71846	TGATGGCACTAGAAATCTGA
73760	71847	CTGATGGCACTAGAAATCTG
73761	71848	ACTGATGGCACTAGAAATCT
73762	71849	TACTGATGGCACTAGAAATC
73763	71850	CTACTGATGGCACTAGAAAT
73764	71851	GCTACTGATGGCACTAGAAA
73765	71852	AGCTACTGATGGCACTAGAA
73766	71853	AAGCTACTGATGGCACTAGA
73767	71854	AAAGCTACTGATGGCACTAG
73768	71855	GAAAGCTACTGATGGCACTA
73769	71856	TGAAAGCTACTGATGGCACT
73770	71857	CTGAAAGCTACTGATGGCAC
73771	71858	GCTGAAAGCTACTGATGGCA
73772	71859	TGCTGAAAGCTACTGATGGC
73773	71860	TTGCTGAAAGCTACTGATGG
73774	71861	TTTGCTGAAAGCTACTGATG
73775	71862	CTTTGCTGAAAGCTACTGAT
73776	71863	TCTTTGCTGAAAGCTACTGA
73777	71864	ATCTTTGCTGAAAGCTACTG

122854	120941	TGTATTTACCAGGCAGTGTG
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122856	120943	TATGTATTTACCAGGCAGTG
122857	120944	ATATGTATTTACCAGGCAGT
122858	120945	AATATGTATTTACCAGGCAG
122859	120946	AAATATGTATTTACCAGGCA
122860	120947	GAAATATGTATTTACCAGGC
122861	120948	TGAAATATGTATTTACCAGG
122862	120949	TTGAAATATGTATTTACCAG
122863	120950	ATTGAAATATGTATTTACCA
122864	120951	AATTGAAATATGTATTTACC
122865	120952	TAATTGAAATATGTATTTAC
122866	120953	TTAATTGAAATATGTATTTA
122867	120954	ATTAATTGAAATATGTATTT
122868	120955	TATTAATTGAAATATGTATT
122869	120956	TTATTAATTGAAATATGTAT
122870	120957	CTTATTAATTGAAATATGTA
122871	120958	TCTTATTAATTGAAATATGT
122872	120959	TTCTTATTAATTGAAATATG
122873	120960	TTTCTTATTAATTGAAATAT
122874	120961	GTTTCTTATTAATTGAAATA
122875	120962	AGTTTCTTATTAATTGAAAT
122876	120963	TAGTTTCTTATTAATTGAAA
122877	120964	CTAGTTTCTTATTAATTGAA
122878	120965	GCTAGTTTCTTATTAATTGA
122879	120966	TGCTAGTTTCTTATTAATTG
122880	120967	TTGCTAGTTTCTTATTAATT
122881	120968	ATTGCTAGTTTCTTATTAAT
122882	120969	GATTGCTAGTTTCTTATTAA
122883	120970	AGATTGCTAGTTTCTTATTA
122884	120971	AAGATTGCTAGTTTCTTATT
122885	120972	GAAGATTGCTAGTTTCTTAT
122886	120973	AGAAGATTGCTAGTTTCTTA
122887	120974	TAGAAGATTGCTAGTTTCTT
122888	120975	TTAGAAGATTGCTAGTTTCT
122889	120976	TTTAGAAGATTGCTAGTTTC
122890	120977	CTTTAGAAGATTGCTAGTTT
122891	120978	ACTTTAGAAGATTGCTAGTT
122892	120979	CACTTTAGAAGATTGCTAGT
122893	120980	TCACTTTAGAAGATTGCTAG
122894	120981	ATCACTTTAGAAGATTGCTA
122895	120982	AATCACTTTAGAAGATTGCT
122896	120983	CAATCACTTTAGAAGATTGC
122897	120984	ACAATCACTTTAGAAGATTG
122898	120985	CACAATCACTTTAGAAGATT
122899	120986	ACACAATCACTTTAGAAGAT
122900	120987	GACACAATCACTTTAGAAGA
122901	120988	TGACACAATCACTTTAGAAG
122902	120989	ATGACACAATCACTTTAGAA
122903	120990	AATGACACAATCACTTTAGA
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122905	120992	AAAATGACACAATCACTTTA
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122907	120994	GTAAAATGACACAATCACTT
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122910	120997	AATGTAAAATGACACAATCA
122911	120998	GAATGTAAAATGACACAATC
122912	120999	GGAATGTAAAATGACACAAT
122913	121000	TGGAATGTAAAATGACACAA
122914	121001	TTGGAATGTAAAATGACACA
122915	121002	GTTGGAATGTAAAATGACAC
122916	121003	AGTTGGAATGTAAAATGACA
122917	121004	CAGTTGGAATGTAAAATGAC
122918	121005	TCAGTTGGAATGTAAAATGA
122919	121006	ATCAGTTGGAATGTAAAATG
122920	121007	GATCAGTTGGAATGTAAAAT
122921	121008	TGATCAGTTGGAATGTAAAA
122922	121009	CTGATCAGTTGGAATGTAAA
122923	121010	CCTGATCAGTTGGAATGTAA
122924	121011	ACCTGATCAGTTGGAATGTA

24631	22718	GACAGAGCGAGACTCCGTCT
24632	22719	CGACAGAGCGAGACTCCGTC
24633	22720	GCGACAGAGCGAGACTCCGT
24634	22721	GGCGACAGAGCGAGACTCCG
24635	22722	GGGCGACAGAGCGAGACTCC
24636	22723	TGGGCGACAGAGCGAGACTC
24637	22724	CTGGGCGACAGAGCGAGACT
24638	22725	CCTGGGCGACAGAGCGAGAC
24639	22726	GCCTGGGCGACAGAGCGAGA
24640	22727	AGCCTGGGCGACAGAGCGAG
24641	22728	CAGCCTGGGCGACAGAGCGA
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24643	22730	TCCAGCCTGGGCGACAGAGC
24644	22731	CTCCAGCCTGGGCGACAGAG
24645	22732	ACTCCAGCCTGGGCGACAGA
24646	22733	CACTCCAGCCTGGGCGACAG
24647	22734	GCACTCCAGCCTGGGCGACA
24648	22735	TGCACTCCAGCCTGGGCGAC
24649	22736	CTGCACTCCAGCCTGGGCGA
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24651	22738	CACTGCACTCCAGCCTGGGC
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24653	22740	GCCACTGCACTCCAGCCTGG
24654	22741	CGCCACTGCACTCCAGCCTG
24655	22742	ACGCCACTGCACTCCAGCCT
24656	22743	CACGCCACTGCACTCCAGCC
24657	22744	TCACGCCACTGCACTCCAGC
24658	22745	ATCACGCCACTGCACTCCAG
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24661	22748	GAGATCACGCCACTGCACTC
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24663	22750	CCGAGATCACGCCACTGCAC
24664	22751	GCCGAGATCACGCCACTGCA
24665	22752	AGCCGAGATCACGCCACTGC
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24668	22755	GTGAGCCGAGATCACGCCAC
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24674	22761	GTTGCAGTGAGCCGAGATCA
24675	22762	GGTTGCAGTGAGCCGAGATC
24676	22763	AGGTTGCAGTGAGCCGAGAT
24677	22764	GAGGTTGCAGTGAGCCGAGA
24678	22765	GGAGGTTGCAGTGAGCCGAG
24679	22766	CGGAGGTTGCAGTGAGCCGA
24680	22767	TCGGAGGTTGCAGTGAGCCG
24681	22768	GTCGGAGGTTGCAGTGAGCC
24682	22769	AGTCGGAGGTTGCAGTGAGC
24683	22770	GAGTCGGAGGTTGCAGTGAG
24684	22771	GGAGTCGGAGGTTGCAGTGA
24685	22772	GGGAGTCGGAGGTTGCAGTG
24686	22773	TGGGAGTCGGAGGTTGCAGT
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24688	22775	CCTGGGAGTCGGAGGTTGCA
24689	22776	ACCTGGGAGTCGGAGGTTGC
24690	22777	AACCTGGGAGTCGGAGGTTG
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24692	22779	TGAACCTGGGAGTCGGAGGT
24693	22780	ATGAACCTGGGAGTCGGAGG
24694	22781	CATGAACCTGGGAGTCGGAG
24695	22782	GCATGAACCTGGGAGTCGGA
24696	22783	GGCATGAACCTGGGAGTCGG
24697	22784	TGGCATGAACCTGGGAGTCG
24698	22785	ATGGCATGAACCTGGGAGTC
24699	22786	AATGGCATGAACCTGGGAGT
24700	22787	GAATGGCATGAACCTGGGAG
24701	22788	AGAATGGCATGAACCTGGGA

73778	71865	CATCTTTGCTGAAAGCTACT
73779	71866	TCATCTTTGCTGAAAGCTAC
73780	71867	CTCATCTTTGCTGAAAGCTA
73781	71868	CCTCATCTTTGCTGAAAGCT
73782	71869	ACCTCATCTTTGCTGAAAGC
73783	71870	CACCTCATCTTTGCTGAAAG
73784	71871	ACACCTCATCTTTGCTGAAA
73785	71872	AACACCTCATCTTTGCTGAA
73786	71873	CAACACCTCATCTTTGCTGA
73787	71874	CCAACACCTCATCTTTGCTG
73788	71875	ACCAACACCTCATCTTTGCT
73789	71876	TACCAACACCTCATCTTTGC
73790	71877	TTACCAACACCTCATCTTTG
73791	71878	CTTACCAACACCTCATCTTT
73792	71879	TCTTACCAACACCTCATCTT
73793	71880	ATCTTACCAACACCTCATCT
73794	71881	TATCTTACCAACACCTCATC
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73797	71884	TGCTATCTTACCAACACCTC
73798	71885	ATGCTATCTTACCAACACCT
73799	71886	AATGCTATCTTACCAACACC
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73801	71888	CTAATGCTATCTTACCAACA
73802	71889	ACTAATGCTATCTTACCAAC
73803	71890	GACTAATGCTATCTTACCAA
73804	71891	AGACTAATGCTATCTTACCA
73805	71892	GAGACTAATGCTATCTTACC
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73807	71894	AAGAGACTAATGCTATCTTA
73808	71895	TAAGAGACTAATGCTATCTT
73809	71896	CTAAGAGACTAATGCTATCT
73810	71897	TCTAAGAGACTAATGCTATC
73811	71898	TTCTAAGAGACTAATGCTAT
73812	71899	ATTCTAAGAGACTAATGCTA
73813	71900	GATTCTAAGAGACTAATGCT
73814	71901	AGATTCTAAGAGACTAATGC
73815	71902	GAGATTCTAAGAGACTAATG
73816	71903	AGAGATTCTAAGAGACTAAT
73817	71904	AAGAGATTCTAAGAGACTAA
73818	71905	TAAGAGATTCTAAGAGACTA
73819	71906	CTAAGAGATTCTAAGAGACT
73820	71907	TCTAAGAGATTCTAAGAGAC
73821	71908	CTCTAAGAGATTCTAAGAGA
73822	71909	TCTCTAAGAGATTCTAAGAG
73823	71910	CTCTCTAAGAGATTCTAAGA
73824	71911	TCTCTCTAAGAGATTCTAAG
73825	71912	ATCTCTCTAAGAGATTCTAA
73826	71913	AATCTCTCTAAGAGATTCTA
73827	71914	AAATCTCTCTAAGAGATTCT
73828	71915	AAAATCTCTCTAAGAGATTC
73829	71916	GAAAATCTCTCTAAGAGATT
73830	71917	GGAAAATCTCTCTAAGAGAT
73831	71918	TGGAAAATCTCTCTAAGAGA
73832	71919	TTGGAAAATCTCTCTAAGAG
73833	71920	TTTGGAAAATCTCTCTAAGA
73834	71921	TTTTGGAAAATCTCTCTAAG
73835	71922	ATTTTGGAAAATCTCTCTAA
73836	71923	AATTTTGGAAAATCTCTCTA
73837	71924	GAATTTTGGAAAATCTCTCT
73838	71925	TGAATTTTGGAAAATCTCTC
73839	71926	CTGAATTTTGGAAAATCTCT
73840	71927	GCTGAATTTTGGAAAATCTC
73841	71928	GGCTGAATTTTGGAAAATCT
73842	71929	TGGCTGAATTTTGGAAAATC
73843	71930	ATGGCTGAATTTTGGAAAAT
73844	71931	AATGGCTGAATTTTGGAAAA
73845	71932	AAATGGCTGAATTTTGGAAA
73846	71933	GAAATGGCTGAATTTTGGAA
73847	71934	AGAAATGGCTGAATTTTGGA
73848	71935	TAGAAATGGCTGAATTTTGG

122925	121012	TACCTGATCAGTTGGAATGT
122926	121013	GTACCTGATCAGTTGGAATG
122927	121014	TGTACCTGATCAGTTGGAAT
122928	121015	ATGTACCTGATCAGTTGGAA
122929	121016	CATGTACCTGATCAGTTGGA
122930	121017	ACATGTACCTGATCAGTTGG
122931	121018	CACATGTACCTGATCAGTTG
122932	121019	ACACATGTACCTGATCAGTT
122933	121020	TACACATGTACCTGATCAGT
122934	121021	CTACACATGTACCTGATCAG
122935	121022	CCTACACATGTACCTGATCA
122936	121023	ACCTACACATGTACCTGATC
122937	121024	AACCTACACATGTACCTGAT
122938	121025	GAACCTACACATGTACCTGA
122939	121026	GGAACCTACACATGTACCTG
122940	121027	TGGAACCTACACATGTACCT
122941	121028	ATGGAACCTACACATGTACC
122942	121029	CATGGAACCTACACATGTAC
122943	121030	ACATGGAACCTACACATGTA
122944	121031	CACATGGAACCTACACATGT
122945	121032	ACACATGGAACCTACACATG
122946	121033	AACACATGGAACCTACACAT
122947	121034	GAACACATGGAACCTACACA
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122949	121036	CAGAACACATGGAACCTACA
122950	121037	GCAGAACACATGGAACCTAC
122951	121038	TGCAGAACACATGGAACCTA
122952	121039	ATGCAGAACACATGGAACCT
122953	121040	GATGCAGAACACATGGAACC
122954	121041	GGATGCAGAACACATGGAAC
122955	121042	AGGATGCAGAACACATGGAA
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122957	121044	CAAGGATGCAGAACACATGG
122958	121045	GCAAGGATGCAGAACACATG
122959	121046	GGCAAGGATGCAGAACACAT
122960	121047	TGGCAAGGATGCAGAACACA
122961	121048	TTGGCAAGGATGCAGAACAC
122962	121049	GTTGGCAAGGATGCAGAACA
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122965	121052	AGTGTTGGCAAGGATGCAGA
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122967	121054	CAAGTGTTGGCAAGGATGCA
122968	121055	CCAAGTGTTGGCAAGGATGC
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122975	121062	CACAATACCAAGTGTTGGCA
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122977	121064	AACACAATACCAAGTGTTGG
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122980	121067	GATAACACAATACCAAGTGT
122981	121068	AGATAACACAATACCAAGTG
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122983	121070	AAAGATAACACAATACCAAG
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122985	121072	AAAAAGATAACACAATACCA
122986	121073	TAAAAAGATAACACAATACC
122987	121074	TTAAAAAGATAACACAATAC
122988	121075	ATTAAAAAGATAACACAATA
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122991	121078	GAAATTAAAAAGATAACACA
122992	121079	TGAAATTAAAAAGATAACAC
122993	121080	TTGAAATTAAAAAGATAACA
122994	121081	GTTGAAATTAAAAAGATAAC
122995	121082	TGTTGAAATTAAAAAGATAA

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24703	22790	GGAGAATGGCATGAACCTGG
24704	22791	AGGAGAATGGCATGAACCTG
24705	22792	CAGGAGAATGGCATGAACCT
24706	22793	GCAGGAGAATGGCATGAACC
24707	22794	GGCAGGAGAATGGCATGAAC
24708	22795	AGGCAGGAGAATGGCATGAA
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24710	22797	TGAGGCAGGAGAATGGCATG
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24713	22800	GGCTGAGGCAGGAGAATGGC
24714	22801	AGGCTGAGGCAGGAGAATGG
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24716	22803	GGAGGCTGAGGCAGGAGAAT
24717	22804	GGGAGGCTGAGGCAGGAGAA
24718	22805	TGGGAGGCTGAGGCAGGAGA
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24722	22809	TACTTGGGAGGCTGAGGCAG
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24726	22813	CAGCTACTTGGGAGGCTGAG
24727	22814	CCAGCTACTTGGGAGGCTGA
24728	22815	CCCAGCTACTTGGGAGGCTG
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24759	22846	TTAGCCAGGCATGGTGGCGG
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24769	22856	AATAAAAAAATTAGCCAGGC
24770	22857	AAATAAAAAAATTAGCCAGG
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73853	71940	TTCACTAGAAATGGCTGAAT
73854	71941	ATTCACTAGAAATGGCTGAA
73855	71942	CATTCACTAGAAATGGCTGA
73856	71943	GCATTCACTAGAAATGGCTG
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73858	71945	GAGCATTCACTAGAAATGGC
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73861	71948	ATGGAGCATTCACTAGAAAT
73862	71949	AATGGAGCATTCACTAGAAA
73863	71950	GAATGGAGCATTCACTAGAA
73864	71951	GGAATGGAGCATTCACTAGA
73865	71952	TGGAATGGAGCATTCACTAG
73866	71953	GTGGAATGGAGCATTCACTA
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73868	71955	GGGTGGAATGGAGCATTCAC
73869	71956	GGGGTGGAATGGAGCATTCA
73870	71957	GGGGGTGGAATGGAGCATTC
73871	71958	TGGGGGTGGAATGGAGCATT
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73874	71961	AGCTGGGGGTGGAATGGAGC
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73876	71963	TCAGCTGGGGGTGGAATGGA
73877	71964	CTCAGCTGGGGGTGGAATGG
73878	71965	ACTCAGCTGGGGGTGGAATG
73879	71966	GACTCAGCTGGGGGTGGAAT
73880	71967	GGACTCAGCTGGGGGTGGAA
73881	71968	AGGACTCAGCTGGGGGTGGA
73882	71969	CAGGACTCAGCTGGGGGTGG
73883	71970	GCAGGACTCAGCTGGGGGTG
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73885	71972	CAGCAGGACTCAGCTGGGGG
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73889	71976	AGAGCAGCAGGACTCAGCTG
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73892	71979	CCCAGAGCAGCAGGACTCAG
73893	71980	CCCCAGAGCAGCAGGACTCA
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73897	71984	AGTTCCCCAGAGCAGCAGGA
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73906	71993	TGCTGAGGGAGTTCCCCAGA
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73908	71995	TGTGCTGAGGGAGTTCCCCA
73909	71996	GTGTGCTGAGGGAGTTCCCC
73910	71997	AGTGTGCTGAGGGAGTTCCC
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73912	71999	AGAGTGTGCTGAGGGAGTTC
73913	72000	AAGAGTGTGCTGAGGGAGTT
73914	72001	CAAGAGTGTGCTGAGGGAGT
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73916	72003	GCCAAGAGTGTGCTGAGGGA
73917	72004	AGCCAAGAGTGTGCTGAGGG
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73919	72006	AGAGCCAAGAGTGTGCTGAG

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122999	121086	GACCTGTTGAAATTAAAAAG
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123001	121088	TAGACCTGTTGAAATTAAAA
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123023	121110	TGAGATACCATAAGACACCC
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123026	121113	CAATGAGATACCATAAGACA
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123030	121117	ATCACAATGAGATACCATAA
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123037	121124	ATTTAAGATCACAATGAGAT
123038	121125	CATTTAAGATCACAATGAGA
123039	121126	ACATTTAAGATCACAATGAG
123040	121127	TACATTTAAGATCACAATGA
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123042	121129	TGTACATTTAAGATCACAAT
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123044	121131	AATGTACATTTAAGATCACA
123045	121132	AAATGTACATTTAAGATCAC
123046	121133	GAAATGTACATTTAAGATCA
123047	121134	AGAAATGTACATTTAAGATC
123048	121135	GAGAAATGTACATTTAAGAT
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123051	121138	TCAGAGAAATGTACATTTAA
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123060	121147	CAGTCATCATCAGAGAAATG
123061	121148	TCAGTCATCATCAGAGAAAT
123062	121149	ATCAGTCATCATCAGAGAAA
123063	121150	GATCAGTCATCATCAGAGAA
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24780	22867	TCTCTACTAAAAATAAAAAA
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24784	22871	CCCATCTCTACTAAAAATAA
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24789	22876	GAAACCCCATCTCTACTAAA
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24794	22881	ACGGCGAAACCCCATCTCTA
24795	22882	CACGGCGAAACCCCATCTCT
24796	22883	ACACGGCGAAACCCCATCTC
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24799	22886	ATAACACGGCGAAACCCCAT
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24824	22911	AGTCAGGAGTTCGAGACCAT
24825	22912	AAGTCAGGAGTTCGAGACCA
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24830	22917	TCACAAAGTCAGGAGTTCGA
24831	22918	ATCACAAAGTCAGGAGTTCG
24832	22919	GATCACAAAGTCAGGAGTTC
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24834	22921	CGGATCACAAAGTCAGGAGT
24835	22922	GCGGATCACAAAGTCAGGAG
24836	22923	GGCGGATCACAAAGTCAGGA
24837	22924	GGGCGGATCACAAAGTCAGG
24838	22925	CGGGCGGATCACAAAGTCAG
24839	22926	GCGGGCGGATCACAAAGTCA
24840	22927	GGCGGGCGGATCACAAAGTC
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24843	22930	CGAGGCGGGCGGATCACAAA

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73921	72008	TAAGAGCCAAGAGTGTGCTG
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73923	72010	TCTAAGAGCCAAGAGTGTGC
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73946	72033	GCACTACTCCCATTGCTAGC
73947	72034	AGCACTACTCCCATTGCTAG
73948	72035	CAGCACTACTCCCATTGCTA
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73950	72037	AGCAGCACTACTCCCATTGC
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73954	72041	CACCAGCAGCACTACTCCCA
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73959	72046	AGCTCCACCAGCAGCACTAC
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123120	121207	TTTACTAAAAAAAGGTTGAC
123121	121208	ATTTACTAAAAAAAGGTTGA
123122	121209	CATTTACTAAAAAAAGGTTG
123123	121210	CCATTTACTAAAAAAAGGTT
123124	121211	ACCATTTACTAAAAAAAGGT
123125	121212	AACCATTTACTAAAAAAAGG
123126	121213	GAACCATTTACTAAAAAAAG
123127	121214	TGAACCATTTACTAAAAAAA
123128	121215	TTGAACCATTTACTAAAAAA
123129	121216	TTTGAACCATTTACTAAAAA
123130	121217	ATTTGAACCATTTACTAAAA
123131	121218	GATTTGAACCATTTACTAAA
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123134	121221	AAAGATTTGAACCATTTACT
123135	121222	AAAAGATTTGAACCATTTAC
123136	121223	AAAAAGATTTGAACCATTTA
123137	121224	AAAAAAGATTTGAACCATTT

24844	22931	CCGAGGCGGGCGGATCACAA
24845	22932	GCCGAGGCGGGCGGATCACA
24846	22933	GGCCGAGGCGGGCGGATCAC
24847	22934	AGGCCGAGGCGGGCGGATCA
24848	22935	GAGGCCGAGGCGGGCGGATC
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24850	22937	GGGAGGCCGAGGCGGGCGGA
24851	22938	TGGGAGGCCGAGGCGGGCGG
24852	22939	TTGGGAGGCCGAGGCGGGCG
24853	22940	TTTGGGAGGCCGAGGCGGGC
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24855	22942	ACTTTGGGAGGCCGAGGCGG
24856	22943	AACTTTGGGAGGCCGAGGCG
24857	22944	GAACTTTGGGAGGCCGAGGC
24858	22945	AGAACTTTGGGAGGCCGAGG
24859	22946	CAGAACTTTGGGAGGCCGAG
24860	22947	CCAGAACTTTGGGAGGCCGA
24861	22948	CCCAGAACTTTGGGAGGCCG
24862	22949	TCCCAGAACTTTGGGAGGCC
24863	22950	ATCCCAGAACTTTGGGAGGC
24864	22951	AATCCCAGAACTTTGGGAGG
24865	22952	TAATCCCAGAACTTTGGGAG
24866	22953	GTAATCCCAGAACTTTGGGA
24867	22954	TGTAATCCCAGAACTTTGGG
24868	22955	CTGTAATCCCAGAACTTTGG
24869	22956	CCTGTAATCCCAGAACTTTG
24870	22957	GCCTGTAATCCCAGAACTTT
24871	22958	CGCCTGTAATCCCAGAACTT
24872	22959	ACGCCTGTAATCCCAGAACT
24873	22960	CACGCCTGTAATCCCAGAAC
24874	22961	TCACGCCTGTAATCCCAGAA
24875	22962	CTCACGCCTGTAATCCCAGA
24876	22963	GCTCACGCCTGTAATCCCAG
24877	22964	GGCTCACGCCTGTAATCCCA
24878	22965	TGGCTCACGCCTGTAATCCC
24879	22966	GTGGCTCACGCCTGTAATCC
24880	22967	GGTGGCTCACGCCTGTAATC
24881	22968	TGGTGGCTCACGCCTGTAAT
24882	22969	GTGGTGGCTCACGCCTGTAA
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24884	22971	GTGTGGTGGCTCACGCCTGT
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24886	22973	AGGTGTGGTGGCTCACGCCT
24887	22974	CAGGTGTGGTGGCTCACGCC
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24890	22977	GGCCAGGTGTGGTGGCTCAC
24891	22978	AGGCCAGGTGTGGTGGCTCA
24892	22979	TAGGCCAGGTGTGGTGGCTC
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24896	22983	AGGGTAGGCCAGGTGTGGTG
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24899	22986	CACAGGGTAGGCCAGGTGTG
24900	22987	ACACAGGGTAGGCCAGGTGT
24901	22988	AACACAGGGTAGGCCAGGTG
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24903	22990	TAAACACAGGGTAGGCCAGG
24904	22991	ATAAACACAGGGTAGGCCAG
24905	22992	AATAAACACAGGGTAGGCCA
24906	22993	TAATAAACACAGGGTAGGCC
24907	22994	GTAATAAACACAGGGTAGGC
24908	22995	TGTAATAAACACAGGGTAGG
24909	22996	TTGTAATAAACACAGGGTAG
24910	22997	TTTGTAATAAACACAGGGTA
24911	22998	ATTTGTAATAAACACAGGGT
24912	22999	TATTTGTAATAAACACAGGG
24913	23000	GTATTTGTAATAAACACAGG
24914	23001	TGTATTTGTAATAAACACAG

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73992	72079	AAAAGCATTAATCCACCTCT
73993	72080	TAAAAGCATTAATCCACCTC
73994	72081	ATAAAAGCATTAATCCACCT
73995	72082	AATAAAAGCATTAATCCACC
73996	72083	GAATAAAAGCATTAATCCAC
73997	72084	GGAATAAAAGCATTAATCCA
73998	72085	GGGAATAAAAGCATTAATCC
73999	72086	AGGGAATAAAAGCATTAATC
74000	72087	CAGGGAATAAAAGCATTAAT
74001	72088	TCAGGGAATAAAAGCATTAA
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74003	72090	CATCAGGGAATAAAAGCATT
74004	72091	ACATCAGGGAATAAAAGCAT
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74009	72096	CCTGTACATCAGGGAATAAA
74010	72097	ACCTGTACATCAGGGAATAA
74011	72098	TACCTGTACATCAGGGAATA
74012	72099	GTACCTGTACATCAGGGAAT
74013	72100	TGTACCTGTACATCAGGGAA
74014	72101	GTGTACCTGTACATCAGGGA
74015	72102	TGTGTACCTGTACATCAGGG
74016	72103	GTGTGTACCTGTACATCAGG
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74019	72106	AGTGTGTGTACCTGTACATC
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74021	72108	TGAGTGTGTGTACCTGTACA
74022	72109	ATGAGTGTGTGTACCTGTAC
74023	72110	TATGAGTGTGTGTACCTGTA
74024	72111	GTATGAGTGTGTGTACCTGT
74025	72112	GGTATGAGTGTGTGTACCTG
74026	72113	AGGTATGAGTGTGTGTACCT
74027	72114	TAGGTATGAGTGTGTGTACC
74028	72115	GTAGGTATGAGTGTGTGTAC
74029	72116	GGTAGGTATGAGTGTGTGTA
74030	72117	GGGTAGGTATGAGTGTGTGT
74031	72118	TGGGTAGGTATGAGTGTGTG
74032	72119	GTGGGTAGGTATGAGTGTGT
74033	72120	TGTGGGTAGGTATGAGTGTG
74034	72121	GTGTGGGTAGGTATGAGTGT
74035	72122	GGTGTGGGTAGGTATGAGTG
74036	72123	AGGTGTGGGTAGGTATGAGT
74037	72124	TAGGTGTGGGTAGGTATGAG
74038	72125	CTAGGTGTGGGTAGGTATGA
74039	72126	ACTAGGTGTGGGTAGGTATG
74040	72127	AACTAGGTGTGGGTAGGTAT
74041	72128	AAACTAGGTGTGGGTAGGTA
74042	72129	CAAACTAGGTGTGGGTAGGT
74043	72130	CCAAACTAGGTGTGGGTAGG
74044	72131	CCCAAACTAGGTGTGGGTAG
74045	72132	TCCCAAACTAGGTGTGGGTA
74046	72133	ATCCCAAACTAGGTGTGGGT
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74052	72139	CTTCTTATCCCAAACTAGGT
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74055	72142	CCTCTTCTTATCCCAAACTA
74056	72143	ACCTCTTCTTATCCCAAACT
74057	72144	AACCTCTTCTTATCCCAAAC
74058	72145	TAACCTCTTCTTATCCCAAA
74059	72146	CTAACCTCTTCTTATCCCAA
74060	72147	TCTAACCTCTTCTTATCCCA
74061	72148	TTCTAACCTCTTCTTATCCC

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123142	121229	AATGGAAAAAAGATTTGAAC
123143	121230	AAATGGAAAAAAGATTTGAA
123144	121231	AAAATGGAAAAAAGATTTGA
123145	121232	TAAAATGGAAAAAAGATTTG
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123147	121234	AATAAAATGGAAAAAAGATT
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123149	121236	TAAATAAAATGGAAAAAAGA
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123153	121240	TAAATAAATAAAATGGAAAA
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123155	121242	AATAAATAAATAAAATGGAA
123156	121243	AAATAAATAAATAAAATGGA
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123158	121245	ATAAATAAATAAATAAAATG
123159	121246	AATAAATAAATAAATAAAAT
123160	121247	AAATAAATAAATAAATAAAA
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123166	121253	TCAAATAAATAAATAAATAA
123167	121254	ATCAAATAAATAAATAAATA
123168	121255	CATCAAATAAATAAATAAAT
123169	121256	CCATCAAATAAATAAATAAA
123170	121257	TCCATCAAATAAATAAATAA
123171	121258	TTCCATCAAATAAATAAATA
123172	121259	ATTCCATCAAATAAATAAAT
123173	121260	GATTCCATCAAATAAATAAA
123174	121261	AGATTCCATCAAATAAATAA
123175	121262	GAGATTCCATCAAATAAATA
123176	121263	TGAGATTCCATCAAATAAAT
123177	121264	GTGAGATTCCATCAAATAAA
123178	121265	AGTGAGATTCCATCAAATAA
123179	121266	GAGTGAGATTCCATCAAATA
123180	121267	AGAGTGAGATTCCATCAAAT
123181	121268	TAGAGTGAGATTCCATCAAA
123182	121269	ATAGAGTGAGATTCCATCAA
123183	121270	AATAGAGTGAGATTCCATCA
123184	121271	CAATAGAGTGAGATTCCATC
123185	121272	GCAATAGAGTGAGATTCCAT
123186	121273	GGCAATAGAGTGAGATTCCA
123187	121274	GGGCAATAGAGTGAGATTCC
123188	121275	TGGGCAATAGAGTGAGATTC
123189	121276	CTGGGCAATAGAGTGAGATT
123190	121277	CCTGGGCAATAGAGTGAGAT
123191	121278	GCCTGGGCAATAGAGTGAGA
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123193	121280	CAGCCTGGGCAATAGAGTGA
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123197	121284	GTTCCAGCCTGGGCAATAGA
123198	121285	CGTTCCAGCCTGGGCAATAG
123199	121286	GCGTTCCAGCCTGGGCAATA
123200	121287	TGCGTTCCAGCCTGGGCAAT
123201	121288	CTGCGTTCCAGCCTGGGCAA
123202	121289	ACTGCGTTCCAGCCTGGGCA
123203	121290	CACTGCGTTCCAGCCTGGGC
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123206	121293	CACCACTGCGTTCCAGCCTG
123207	121294	GCACCACTGCGTTCCAGCCT
123208	121295	GGCACCACTGCGTTCCAGCC

24915	23002	GTGTATTTGTAATAAACACA
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24917	23004	TTGTGTATTTGTAATAAACA
24918	23005	TTTGTGTATTTGTAATAAAC
24919	23006	ATTTGTGTATTTGTAATAAA
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24921	23008	CAATTTGTGTATTTGTAATA
24922	23009	CCAATTTGTGTATTTGTAAT
24923	23010	GCCAATTTGTGTATTTGTAA
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24935	23022	CACGCACAAATGGCCAATTT
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24937	23024	GCCACGCACAAATGGCCAAT
24938	23025	AGCCACGCACAAATGGCCAA
24939	23026	GAGCCACGCACAAATGGCCA
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24941	23028	ATGAGCCACGCACAAATGGC
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24943	23030	AGATGAGCCACGCACAAATG
24944	23031	TAGATGAGCCACGCACAAAT
24945	23032	GTAGATGAGCCACGCACAAA
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24947	23034	CTGTAGATGAGCCACGCACA
24948	23035	ACTGTAGATGAGCCACGCAC
24949	23036	GACTGTAGATGAGCCACGCA
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24953	23040	CTGAGACTGTAGATGAGCCA
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24955	23042	CACTGAGACTGTAGATGAGC
24956	23043	TCACTGAGACTGTAGATGAG
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24960	23047	TGAGTCACTGAGACTGTAGA
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24962	23049	TCTGAGTCACTGAGACTGTA
24963	23050	TTCTGAGTCACTGAGACTGT
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24965	23052	CCTTCTGAGTCACTGAGACT
24966	23053	GCCTTCTGAGTCACTGAGAC
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24969	23056	TCAGCCTTCTGAGTCACTGA
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24972	23059	GCCTCAGCCTTCTGAGTCAC
24973	23060	TGCCTCAGCCTTCTGAGTCA
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24977	23064	CTCCTGCCTCAGCCTTCTGA
24978	23065	TCTCCTGCCTCAGCCTTCTG
24979	23066	TTCTCCTGCCTCAGCCTTCT
24980	23067	ATTCTCCTGCCTCAGCCTTC
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24982	23069	AGATTCTCCTGCCTCAGCCT
24983	23070	GAGATTCTCCTGCCTCAGCC
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24985	23072	AAGAGATTCTCCTGCCTCAG

74062	72149	ATTCTAACCTCTTCTTATCC
74063	72150	AATTCTAACCTCTTCTTATC
74064	72151	TAATTCTAACCTCTTCTTAT
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74073	72160	AAGCCTAGCTAATTCTAACC
74074	72161	CAAGCCTAGCTAATTCTAAC
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74076	72163	TTCAAGCCTAGCTAATTCTA
74077	72164	CTTCAAGCCTAGCTAATTCT
74078	72165	ACTTCAAGCCTAGCTAATTC
74079	72166	AACTTCAAGCCTAGCTAATT
74080	72167	GAACTTCAAGCCTAGCTAAT
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74082	72169	TGGAACTTCAAGCCTAGCTA
74083	72170	ATGGAACTTCAAGCCTAGCT
74084	72171	CATGGAACTTCAAGCCTAGC
74085	72172	GCATGGAACTTCAAGCCTAG
74086	72173	AGCATGGAACTTCAAGCCTA
74087	72174	AAGCATGGAACTTCAAGCCT
74088	72175	TAAGCATGGAACTTCAAGCC
74089	72176	TTAAGCATGGAACTTCAAGC
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74096	72183	AGCAAATTTAAGCATGGAAC
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74106	72193	AATCTGAGCCAGCAAATTTA
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74109	72196	AGAAATCTGAGCCAGCAAAT
74110	72197	AAGAAATCTGAGCCAGCAAA
74111	72198	TAAGAAATCTGAGCCAGCAA
74112	72199	ATAAGAAATCTGAGCCAGCA
74113	72200	AATAAGAAATCTGAGCCAGC
74114	72201	AAATAAGAAATCTGAGCCAG
74115	72202	AAAATAAGAAATCTGAGCCA
74116	72203	CAAAATAAGAAATCTGAGCC
74117	72204	CCAAAATAAGAAATCTGAGC
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74121	72208	GATGCCAAAATAAGAAATCT
74122	72209	TGATGCCAAAATAAGAAATC
74123	72210	GTGATGCCAAAATAAGAAAT
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74125	72212	AAGTGATGCCAAAATAAGAA
74126	72213	AAAGTGATGCCAAAATAAGA
74127	72214	CAAAGTGATGCCAAAATAAG
74128	72215	GCAAAGTGATGCCAAAATAA
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74130	72217	GGGCAAAGTGATGCCAAAAT
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123209	121296	TGGCACCACTGCGTTCCAGC
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123213	121300	AAGATGGCACCACTGCGTTC
123214	121301	CAAGATGGCACCACTGCGTT
123215	121302	CCAAGATGGCACCACTGCGT
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123217	121304	AGCCAAGATGGCACCACTGC
123218	121305	GAGCCAAGATGGCACCACTG
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123220	121307	GTGAGCCAAGATGGCACCAC
123221	121308	AGTGAGCCAAGATGGCACCA
123222	121309	CAGTGAGCCAAGATGGCACC
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123226	121313	GTTGCAGTGAGCCAAGATGG
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123230	121317	GGAGGTTGCAGTGAGCCAAG
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123232	121319	GCGGAGGTTGCAGTGAGCCA
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123234	121321	AGGCGGAGGTTGCAGTGAGC
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123236	121323	GGAGGCGGAGGTTGCAGTGA
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123240	121327	CCTGGGAGGCGGAGGTTGCA
123241	121328	ACCTGGGAGGCGGAGGTTGC
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123243	121330	GAACCTGGGAGGCGGAGGTT
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123247	121334	GCTTGAACCTGGGAGGCGGA
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123251	121338	AATTGCTTGAACCTGGGAGG
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123253	121340	AGAATTGCTTGAACCTGGGA
123254	121341	AAGAATTGCTTGAACCTGGG
123255	121342	TAAGAATTGCTTGAACCTGG
123256	121343	GTAAGAATTGCTTGAACCTG
123257	121344	CGTAAGAATTGCTTGAACCT
123258	121345	GCGTAAGAATTGCTTGAACC
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123260	121347	AGGCGTAAGAATTGCTTGAA
123261	121348	AAGGCGTAAGAATTGCTTGA
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123278	121365	CAGCTACTTGGGAGGCTAAG
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24986	23073	CAAGAGATTCTCCTGCCTCA
24987	23074	TCAAGAGATTCTCCTGCCTC
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24989	23076	GTTCAAGAGATTCTCCTGCC
24990	23077	GGTTCAAGAGATTCTCCTGC
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24992	23079	CGGGTTCAAGAGATTCTCCT
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24994	23081	CCCGGGTTCAAGAGATTCTC
24995	23082	TCCCGGGTTCAAGAGATTCT
24996	23083	CTCCCGGGTTCAAGAGATTC
24997	23084	CCTCCCGGGTTCAAGAGATT
24998	23085	GCCTCCCGGGTTCAAGAGAT
24999	23086	TGCCTCCCGGGTTCAAGAGA
25000	23087	CTGCCTCCCGGGTTCAAGAG
25001	23088	TCTGCCTCCCGGGTTCAAGA
25002	23089	CTCTGCCTCCCGGGTTCAAG
25003	23090	CCTCTGCCTCCCGGGTTCAA
25004	23091	ACCTCTGCCTCCCGGGTTCA
25005	23092	AACCTCTGCCTCCCGGGTTC
25006	23093	CAACCTCTGCCTCCCGGGTT
25007	23094	GCAACCTCTGCCTCCCGGGT
25008	23095	TGCAACCTCTGCCTCCCGGG
25009	23096	CTGCAACCTCTGCCTCCCGG
25010	23097	ACTGCAACCTCTGCCTCCCG
25011	23098	CACTGCAACCTCTGCCTCCC
25012	23099	TCACTGCAACCTCTGCCTCC
25013	23100	CTCACTGCAACCTCTGCCTC
25014	23101	GCTCACTGCAACCTCTGCCT
25015	23102	TGCTCACTGCAACCTCTGCC
25016	23103	CTGCTCACTGCAACCTCTGC
25017	23104	TCTGCTCACTGCAACCTCTG
25018	23105	CTCTGCTCACTGCAACCTCT
25019	23106	TCTCTGCTCACTGCAACCTC
25020	23107	ATCTCTGCTCACTGCAACCT
25021	23108	GATCTCTGCTCACTGCAACC
25022	23109	CGATCTCTGCTCACTGCAAC
25023	23110	ACGATCTCTGCTCACTGCAA
25024	23111	CACGATCTCTGCTCACTGCA
25025	23112	GCACGATCTCTGCTCACTGC
25026	23113	GGCACGATCTCTGCTCACTG
25027	23114	TGGCACGATCTCTGCTCACT
25028	23115	GTGGCACGATCTCTGCTCAC
25029	23116	AGTGGCACGATCTCTGCTCA
25030	23117	CAGTGGCACGATCTCTGCTC
25031	23118	ACAGTGGCACGATCTCTGCT
25032	23119	TACAGTGGCACGATCTCTGC
25033	23120	GTACAGTGGCACGATCTCTG
25034	23121	AGTACAGTGGCACGATCTCT
25035	23122	AAGTACAGTGGCACGATCTC
25036	23123	GAAGTACAGTGGCACGATCT
25037	23124	TGAAGTACAGTGGCACGATC
25038	23125	CTGAAGTACAGTGGCACGAT
25039	23126	GCTGAAGTACAGTGGCACGA
25040	23127	GGCTGAAGTACAGTGGCACG
25041	23128	AGGCTGAAGTACAGTGGCAC
25042	23129	CAGGCTGAAGTACAGTGGCA
25043	23130	CCAGGCTGAAGTACAGTGGC
25044	23131	CCCAGGCTGAAGTACAGTGG
25045	23132	ACCCAGGCTGAAGTACAGTG
25046	23133	CACCCAGGCTGAAGTACAGT
25047	23134	TCACCCAGGCTGAAGTACAG
25048	23135	GTCACCCAGGCTGAAGTACA
25049	23136	TGTCACCCAGGCTGAAGTAC
25050	23137	CTGTCACCCAGGCTGAAGTA
25051	23138	TCTGTCACCCAGGCTGAAGT
25052	23139	CTCTGTCACCCAGGCTGAAG
25053	23140	ACTCTGTCACCCAGGCTGAA
25054	23141	CACTCTGTCACCCAGGCTGA
25055	23142	TCACTCTGTCACCCAGGCTG
25056	23143	CTCACTCTGTCACCCAGGCT

74133	72220	AATGGGCAAAGTGATGCCAA
74134	72221	TAATGGGCAAAGTGATGCCA
74135	72222	CTAATGGGCAAAGTGATGCC
74136	72223	CCTAATGGGCAAAGTGATGC
74137	72224	CCCTAATGGGCAAAGTGATG
74138	72225	TCCCTAATGGGCAAAGTGAT
74139	72226	CTCCCTAATGGGCAAAGTGA
74140	72227	TCTCCCTAATGGGCAAAGTG
74141	72228	GTCTCCCTAATGGGCAAAGT
74142	72229	TGTCTCCCTAATGGGCAAAG
74143	72230	TTGTCTCCCTAATGGGCAAA
74144	72231	ATTGTCTCCCTAATGGGCAA
74145	72232	CATTGTCTCCCTAATGGGCA
74146	72233	TCATTGTCTCCCTAATGGGC
74147	72234	GTCATTGTCTCCCTAATGGG
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74150	72237	ACTGTCATTGTCTCCCTAAT
74151	72238	AACTGTCATTGTCTCCCTAA
74152	72239	TAACTGTCATTGTCTCCCTA
74153	72240	ATAACTGTCATTGTCTCCCT
74154	72241	TATAACTGTCATTGTCTCCC
74155	72242	CTATAACTGTCATTGTCTCC
74156	72243	TCTATAACTGTCATTGTCTC
74157	72244	TTCTATAACTGTCATTGTCT
74158	72245	CTTCTATAACTGTCATTGTC
74159	72246	GCTTCTATAACTGTCATTGT
74160	72247	TGCTTCTATAACTGTCATTG
74161	72248	ATGCTTCTATAACTGTCATT
74162	72249	AATGCTTCTATAACTGTCAT
74163	72250	CAATGCTTCTATAACTGTCA
74164	72251	GCAATGCTTCTATAACTGTC
74165	72252	GGCAATGCTTCTATAACTGT
74166	72253	TGGCAATGCTTCTATAACTG
74167	72254	TTGGCAATGCTTCTATAACT
74168	72255	TTTGGCAATGCTTCTATAAC
74169	72256	ATTTGGCAATGCTTCTATAA
74170	72257	TATTTGGCAATGCTTCTATA
74171	72258	TTATTTGGCAATGCTTCTAT
74172	72259	TTTATTTGGCAATGCTTCTA
74173	72260	TTTTATTTGGCAATGCTTCT
74174	72261	TTTTTATTTGGCAATGCTTC
74175	72262	TTTTTTATTTGGCAATGCTT
74176	72263	ATTTTTTATTTGGCAATGCT
74177	72264	GATTTTTTATTTGGCAATGC
74178	72265	GGATTTTTTATTTGGCAATG
74179	72266	TGGATTTTTTATTTGGCAAT
74180	72267	ATGGATTTTTTATTTGGCAA
74181	72268	GATGGATTTTTTATTTGGCA
74182	72269	AGATGGATTTTTTATTTGGC
74183	72270	CAGATGGATTTTTTATTTGG
74184	72271	CCAGATGGATTTTTTATTTG
74185	72272	TCCAGATGGATTTTTTATTT
74186	72273	TTCCAGATGGATTTTTTATT
74187	72274	ATTCCAGATGGATTTTTTAT
74188	72275	TATTCCAGATGGATTTTTTA
74189	72276	TTATTCCAGATGGATTTTTT
74190	72277	GTTATTCCAGATGGATTTTT
74191	72278	GGTTATTCCAGATGGATTTT
74192	72279	AGGTTATTCCAGATGGATTT
74193	72280	GAGGTTATTCCAGATGGATT
74194	72281	AGAGGTTATTCCAGATGGAT
74195	72282	AAGAGGTTATTCCAGATGGA
74196	72283	AAAGAGGTTATTCCAGATGG
74197	72284	AAAAGAGGTTATTCCAGATG
74198	72285	CAAAAGAGGTTATTCCAGAT
74199	72286	ACAAAAGAGGTTATTCCAGA
74200	72287	TACAAAAGAGGTTATTCCAG
74201	72288	CTACAAAAGAGGTTATTCCA
74202	72289	CCTACAAAAGAGGTTATTCC
74203	72290	TCCTACAAAAGAGGTTATTC

123280	121367	CCCAGCTACTTGGGAGGCTA
123281	121368	TCCCAGCTACTTGGGAGGCT
123282	121369	ATCCCAGCTACTTGGGAGGC
123283	121370	AATCCCAGCTACTTGGGAGG
123284	121371	TAATCCCAGCTACTTGGGAG
123285	121372	GTAATCCCAGCTACTTGGGA
123286	121373	TGTAATCCCAGCTACTTGGG
123287	121374	CTGTAATCCCAGCTACTTGG
123288	121375	CCTGTAATCCCAGCTACTTG
123289	121376	GCCTGTAATCCCAGCTACTT
123290	121377	TGCCTGTAATCCCAGCTACT
123291	121378	ATGCCTGTAATCCCAGCTAC
123292	121379	CATGCCTGTAATCCCAGCTA
123293	121380	GCATGCCTGTAATCCCAGCT
123294	121381	CGCATGCCTGTAATCCCAGC
123295	121382	GCGCATGCCTGTAATCCCAG
123296	121383	GGCGCATGCCTGTAATCCCA
123297	121384	TGGCGCATGCCTGTAATCCC
123298	121385	GTGGCGCATGCCTGTAATCC
123299	121386	GGTGGCGCATGCCTGTAATC
123300	121387	TGGTGGCGCATGCCTGTAAT
123301	121388	ATGGTGGCGCATGCCTGTAA
123302	121389	CATGGTGGCGCATGCCTGTA
123303	121390	GCATGGTGGCGCATGCCTGT
123304	121391	GGCATGGTGGCGCATGCCTG
123305	121392	AGGCATGGTGGCGCATGCCT
123306	121393	CAGGCATGGTGGCGCATGCC
123307	121394	CCAGGCATGGTGGCGCATGC
123308	121395	GCCAGGCATGGTGGCGCATG
123309	121396	AGCCAGGCATGGTGGCGCAT
123310	121397	TAGCCAGGCATGGTGGCGCA
123311	121398	TTAGCCAGGCATGGTGGCGC
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123314	121401	AAATTAGCCAGGCATGGTGG
123315	121402	AAAATTAGCCAGGCATGGTG
123316	121403	CAAAATTAGCCAGGCATGGT
123317	121404	ACAAAATTAGCCAGGCATGG
123318	121405	TACAAAATTAGCCAGGCATG
123319	121406	ATACAAAATTAGCCAGGCAT
123320	121407	AATACAAAATTAGCCAGGCA
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123322	121409	AAAATACAAAATTAGCCAGG
123323	121410	AAAAATACAAAATTAGCCAG
123324	121411	TAAAAATACAAAATTAGCCA
123325	121412	CTAAAAATACAAAATTAGCC
123326	121413	ACTAAAAATACAAAATTAGC
123327	121414	CACTAAAAATACAAAATTAG
123328	121415	ACACTAAAAATACAAAATTA
123329	121416	TACACTAAAAATACAAAATT
123330	121417	CTACACTAAAAATACAAAAT
123331	121418	CCTACACTAAAAATACAAAA
123332	121419	ACCTACACTAAAAATACAAA
123333	121420	CACCTACACTAAAAATACAA
123334	121421	CCACCTACACTAAAAATACA
123335	121422	CCCACCTACACTAAAAATAC
123336	121423	CCCCACCTACACTAAAAATA
123337	121424	ACCCCACCTACACTAAAAAT
123338	121425	AACCCCACCTACACTAAAAA
123339	121426	AAACCCCACCTACACTAAAA
123340	121427	GAAACCCCACCTACACTAAA
123341	121428	TGAAACCCCACCTACACTAA
123342	121429	GTGAAACCCCACCTACACTA
123343	121430	GGTGAAACCCCACCTACACT
123344	121431	TGGTGAAACCCCACCTACAC
123345	121432	ATGGTGAAACCCCACCTACA
123346	121433	CATGGTGAAACCCCACCTAC
123347	121434	ACATGGTGAAACCCCACCTA
123348	121435	AACATGGTGAAACCCCACCT
123349	121436	CAACATGGTGAAACCCCACC
123350	121437	CCAACATGGTGAAACCCCAC

25057	23144	TCTCACTCTGTCACCCAGGC
25058	23145	GTCTCACTCTGTCACCCAGG
25059	23146	AGTCTCACTCTGTCACCCAG
25060	23147	CAGTCTCACTCTGTCACCCA
25061	23148	ACAGTCTCACTCTGTCACCC
25062	23149	CACAGTCTCACTCTGTCACC
25063	23150	ACACAGTCTCACTCTGTCAC
25064	23151	GACACAGTCTCACTCTGTCA
25065	23152	AGACACAGTCTCACTCTGTC
25066	23153	GAGACACAGTCTCACTCTGT
25067	23154	TGAGACACAGTCTCACTCTG
25068	23155	TTGAGACACAGTCTCACTCT
25069	23156	TTTGAGACACAGTCTCACTC
25070	23157	TTTTGAGACACAGTCTCACT
25071	23158	ATTTTGAGACACAGTCTCAC
25072	23159	TATTTTGAGACACAGTCTCA
25073	23160	TTATTTTGAGACACAGTCTC
25074	23161	ATTATTTTGAGACACAGTCT
25075	23162	TATTATTTTGAGACACAGTC
25076	23163	TTATTATTTTGAGACACAGT
25077	23164	ATTATTATTTTGAGACACAG
25078	23165	TATTATTATTTTGAGACACA
25079	23166	TTATTATTATTTTGAGACAC
25080	23167	ATTATTATTATTTTGAGACA
25081	23168	TATTATTATTATTTTGAGAC
25082	23169	TTATTATTATTATTTTGAGA
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25084	23171	AATTATTATTATTATTTTGA
25085	23172	AAATTATTATTATTATTTTG
25086	23173	CAAATTATTATTATTATTTT
25087	23174	ACAAATTATTATTATTATTT
25088	23175	AACAAATTATTATTATTATT
25089	23176	CAACAAATTATTATTATTAT
25090	23177	TCAACAAATTATTATTATTA
25091	23178	TTCAACAAATTATTATTATT
25092	23179	ATTCAACAAATTATTATTAT
25093	23180	TATTCAACAAATTATTATTA
25094	23181	ATATTCAACAAATTATTATT
25095	23182	CATATTCAACAAATTATTAT
25096	23183	ACATATTCAACAAATTATTA
25097	23184	CACATATTCAACAAATTATT
25098	23185	TCACATATTCAACAAATTAT
25099	23186	GTCACATATTCAACAAATTA
25100	23187	AGTCACATATTCAACAAATT
25101	23188	CAGTCACATATTCAACAAAT
25102	23189	ACAGTCACATATTCAACAAA
25103	23190	AACAGTCACATATTCAACAA
25104	23191	CAACAGTCACATATTCAACA
25105	23192	CCAACAGTCACATATTCAAC
25106	23193	ACCAACAGTCACATATTCAA
25107	23194	AACCAACAGTCACATATTCA
25108	23195	AAACCAACAGTCACATATTC
25109	23196	TAAACCAACAGTCACATATT
25110	23197	TTAAACCAACAGTCACATAT
25111	23198	ATTAAACCAACAGTCACATA
25112	23199	AATTAAACCAACAGTCACAT
25113	23200	AAATTAAACCAACAGTCACA
25114	23201	AAAATTAAACCAACAGTCAC
25115	23202	AAAAATTAAACCAACAGTCA
25116	23203	TAAAAATTAAACCAACAGTC
25117	23204	ATAAAAATTAAACCAACAGT
25118	23205	AATAAAAATTAAACCAACAG
25119	23206	AAATAAAAATTAAACCAACA
25120	23207	AAAATAAAAATTAAACCAAC
25121	23208	AAAAATAAAAATTAAACCAA
25122	23209	TAAAAATAAAAATTAAACCA
25123	23210	ATAAAAATAAAAATTAAACC
25124	23211	CATAAAAATAAAAATTAAAC
25125	23212	TCATAAAAATAAAAATTAAA
25126	23213	CTCATAAAAATAAAAATTAA
25127	23214	TCTCATAAAAATAAAAATTA

74204	72291	CTCCTACAAAAGAGGTTATT
74205	72292	ACTCCTACAAAAGAGGTTAT
74206	72293	TACTCCTACAAAAGAGGTTA
74207	72294	ATACTCCTACAAAAGAGGTT
74208	72295	AATACTCCTACAAAAGAGGT
74209	72296	CAATACTCCTACAAAAGAGG
74210	72297	ACAATACTCCTACAAAAGAG
74211	72298	CACAATACTCCTACAAAAGA
74212	72299	ACACAATACTCCTACAAAAG
74213	72300	CACACAATACTCCTACAAAA
74214	72301	ACACACAATACTCCTACAAA
74215	72302	AACACACAATACTCCTACAA
74216	72303	AAACACACAATACTCCTACA
74217	72304	TAAACACACAATACTCCTAC
74218	72305	CTAAACACACAATACTCCTA
74219	72306	ACTAAACACACAATACTCCT
74220	72307	AACTAAACACACAATACTCC
74221	72308	CAACTAAACACACAATACTC
74222	72309	ACAACTAAACACACAATACT
74223	72310	AACAACTAAACACACAATAC
74224	72311	CAACAACTAAACACACAATA
74225	72312	TCAACAACTAAACACACAAT
74226	72313	ATCAACAACTAAACACACAA
74227	72314	AATCAACAACTAAACACACA
74228	72315	GAATCAACAACTAAACACAC
74229	72316	CGAATCAACAACTAAACACA
74230	72317	ACGAATCAACAACTAAACAC
74231	72318	GACGAATCAACAACTAAACA
74232	72319	GGACGAATCAACAACTAAAC
74233	72320	GGGACGAATCAACAACTAAA
74234	72321	AGGGACGAATCAACAACTAA
74235	72322	AAGGGACGAATCAACAACTA
74236	72323	GAAGGGACGAATCAACAACT
74237	72324	GGAAGGGACGAATCAACAAC
74238	72325	AGGAAGGGACGAATCAACAA
74239	72326	GAGGAAGGGACGAATCAACA
74240	72327	GGAGGAAGGGACGAATCAAC
74241	72328	AGGAGGAAGGGACGAATCAA
74242	72329	GAGGAGGAAGGGACGAATCA
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74246	72333	CTAAGAGGAGGAAGGGACGA
74247	72334	ACTAAGAGGAGGAAGGGACG
74248	72335	CACTAAGAGGAGGAAGGGAC
74249	72336	CCACTAAGAGGAGGAAGGGA
74250	72337	GCCACTAAGAGGAGGAAGGG
74251	72338	TGCCACTAAGAGGAGGAAGG
74252	72339	TTGCCACTAAGAGGAGGAAG
74253	72340	GTTGCCACTAAGAGGAGGAA
74254	72341	AGTTGCCACTAAGAGGAGGA
74255	72342	AAGTTGCCACTAAGAGGAGG
74256	72343	TAAGTTGCCACTAAGAGGAG
74257	72344	GTAAGTTGCCACTAAGAGGA
74258	72345	TGTAAGTTGCCACTAAGAGG
74259	72346	CTGTAAGTTGCCACTAAGAG
74260	72347	ACTGTAAGTTGCCACTAAGA
74261	72348	TACTGTAAGTTGCCACTAAG
74262	72349	GTACTGTAAGTTGCCACTAA
74263	72350	AGTACTGTAAGTTGCCACTA
74264	72351	CAGTACTGTAAGTTGCCACT
74265	72352	CCAGTACTGTAAGTTGCCAC
74266	72353	CCCAGTACTGTAAGTTGCCA
74267	72354	TCCCAGTACTGTAAGTTGCC
74268	72355	TTCCCAGTACTGTAAGTTGC
74269	72356	CTTCCCAGTACTGTAAGTTG
74270	72357	CCTTCCCAGTACTGTAAGTT
74271	72358	TCCTTCCCAGTACTGTAAGT
74272	72359	TTCCTTCCCAGTACTGTAAG
74273	72360	GTTCCTTCCCAGTACTGTAA
74274	72361	TGTTCCTTCCCAGTACTGTA

123351	121438	ACCAACATGGTGAAACCCCA
123352	121439	GACCAACATGGTGAAACCCC
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123354	121441	ATGACCAACATGGTGAAACC
123355	121442	CATGACCAACATGGTGAAAC
123356	121443	GCATGACCAACATGGTGAAA
123357	121444	AGCATGACCAACATGGTGAA
123358	121445	CAGCATGACCAACATGGTGA
123359	121446	CCAGCATGACCAACATGGTG
123360	121447	ACCAGCATGACCAACATGGT
123361	121448	GACCAGCATGACCAACATGG
123362	121449	AGACCAGCATGACCAACATG
123363	121450	GAGACCAGCATGACCAACAT
123364	121451	AGAGACCAGCATGACCAACA
123365	121452	TAGAGACCAGCATGACCAAC
123366	121453	TTAGAGACCAGCATGACCAA
123367	121454	GTTAGAGACCAGCATGACCA
123368	121455	AGTTAGAGACCAGCATGACC
123369	121456	GAGTTAGAGACCAGCATGAC
123370	121457	GGAGTTAGAGACCAGCATGA
123371	121458	AGGAGTTAGAGACCAGCATG
123372	121459	CAGGAGTTAGAGACCAGCAT
123373	121460	TCAGGAGTTAGAGACCAGCA
123374	121461	GTCAGGAGTTAGAGACCAGC
123375	121462	GGTCAGGAGTTAGAGACCAG
123376	121463	AGGTCAGGAGTTAGAGACCA
123377	121464	GAGGTCAGGAGTTAGAGACC
123378	121465	TGAGGTCAGGAGTTAGAGAC
123379	121466	CTGAGGTCAGGAGTTAGAGA
123380	121467	CCTGAGGTCAGGAGTTAGAG
123381	121468	ACCTGAGGTCAGGAGTTAGA
123382	121469	CACCTGAGGTCAGGAGTTAG
123383	121470	TCACCTGAGGTCAGGAGTTA
123384	121471	ATCACCTGAGGTCAGGAGTT
123385	121472	GATCACCTGAGGTCAGGAGT
123386	121473	AGATCACCTGAGGTCAGGAG
123387	121474	TAGATCACCTGAGGTCAGGA
123388	121475	GTAGATCACCTGAGGTCAGG
123389	121476	GGTAGATCACCTGAGGTCAG
123390	121477	AGGTAGATCACCTGAGGTCA
123391	121478	CAGGTAGATCACCTGAGGTC
123392	121479	GCAGGTAGATCACCTGAGGT
123393	121480	GGCAGGTAGATCACCTGAGG
123394	121481	AGGCAGGTAGATCACCTGAG
123395	121482	GAGGCAGGTAGATCACCTGA
123396	121483	CGAGGCAGGTAGATCACCTG
123397	121484	CCGAGGCAGGTAGATCACCT
123398	121485	GCCGAGGCAGGTAGATCACC
123399	121486	GGCCGAGGCAGGTAGATCAC
123400	121487	AGGCCGAGGCAGGTAGATCA
123401	121488	GAGGCCGAGGCAGGTAGATC
123402	121489	GGAGGCCGAGGCAGGTAGAT
123403	121490	GGGAGGCCGAGGCAGGTAGA
123404	121491	TGGGAGGCCGAGGCAGGTAG
123405	121492	TTGGGAGGCCGAGGCAGGTA
123406	121493	TTTGGGAGGCCGAGGCAGGT
123407	121494	CTTTGGGAGGCCGAGGCAGG
123408	121495	ACTTTGGGAGGCCGAGGCAG
123409	121496	CACTTTGGGAGGCCGAGGCA
123410	121497	GCACTTTGGGAGGCCGAGGC
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123412	121499	CAGCACTTTGGGAGGCCGAG
123413	121500	TCAGCACTTTGGGAGGCCGA
123414	121501	CTCAGCACTTTGGGAGGCCG
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123420	121507	TGTAATCTCAGCACTTTGGG
123421	121508	CTGTAATCTCAGCACTTTGG

25128	23215	ATCTCATAAAAATAAAAATT
25129	23216	CATCTCATAAAAATAAAAAT
25130	23217	CCATCTCATAAAAATAAAAA
25131	23218	TCCATCTCATAAAAATAAAA
25132	23219	CTCCATCTCATAAAAATAAA
25133	23220	ACTCCATCTCATAAAAATAA
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25135	23222	AGACTCCATCTCATAAAAAT
25136	23223	GAGACTCCATCTCATAAAAA
25137	23224	TGAGACTCCATCTCATAAAA
25138	23225	GTGAGACTCCATCTCATAAA
25139	23226	AGTGAGACTCCATCTCATAA
25140	23227	GAGTGAGACTCCATCTCATA
25141	23228	AGAGTGAGACTCCATCTCAT
25142	23229	CAGAGTGAGACTCCATCTCA
25143	23230	ACAGAGTGAGACTCCATCTC
25144	23231	AACAGAGTGAGACTCCATCT
25145	23232	CAACAGAGTGAGACTCCATC
25146	23233	GCAACAGAGTGAGACTCCAT
25147	23234	GGCAACAGAGTGAGACTCCA
25148	23235	GGGCAACAGAGTGAGACTCC
25149	23236	TGGGCAACAGAGTGAGACTC
25150	23237	CTGGGCAACAGAGTGAGACT
25151	23238	CCTGGGCAACAGAGTGAGAC
25152	23239	ACCTGGGCAACAGAGTGAGA
25153	23240	AACCTGGGCAACAGAGTGAG
25154	23241	CAACCTGGGCAACAGAGTGA
25155	23242	CCAACCTGGGCAACAGAGTG
25156	23243	TCCAACCTGGGCAACAGAGT
25157	23244	CTCCAACCTGGGCAACAGAG
25158	23245	ACTCCAACCTGGGCAACAGA
25159	23246	TACTCCAACCTGGGCAACAG
25160	23247	GTACTCCAACCTGGGCAACA
25161	23248	TGTACTCCAACCTGGGCAAC
25162	23249	CTGTACTCCAACCTGGGCAA
25163	23250	ACTGTACTCCAACCTGGGCA
25164	23251	CACTGTACTCCAACCTGGGC
25165	23252	CCACTGTACTCCAACCTGGG
25166	23253	GCCACTGTACTCCAACCTGG
25167	23254	CGCCACTGTACTCCAACCTG
25168	23255	ACGCCACTGTACTCCAACCT
25169	23256	CACGCCACTGTACTCCAACC
25170	23257	GCACGCCACTGTACTCCAAC
25171	23258	TGCACGCCACTGTACTCCAA
25172	23259	CTGCACGCCACTGTACTCCA
25173	23260	ACTGCACGCCACTGTACTCC
25174	23261	CACTGCACGCCACTGTACTC
25175	23262	CCACTGCACGCCACTGTACT
25176	23263	GCCACTGCACGCCACTGTAC
25177	23264	CGCCACTGCACGCCACTGTA
25178	23265	GCGCCACTGCACGCCACTGT
25179	23266	TGCGCCACTGCACGCCACTG
25180	23267	TTGCGCCACTGCACGCCACT
25181	23268	ATTGCGCCACTGCACGCCAC
25182	23269	GATTGCGCCACTGCACGCCA
25183	23270	AGATTGCGCCACTGCACGCC
25184	23271	AAGATTGCGCCACTGCACGC
25185	23272	TAAGATTGCGCCACTGCACG
25186	23273	CTAAGATTGCGCCACTGCAC
25187	23274	GCTAAGATTGCGCCACTGCA
25188	23275	AGCTAAGATTGCGCCACTGC
25189	23276	GAGCTAAGATTGCGCCACTG
25190	23277	TGAGCTAAGATTGCGCCACT
25191	23278	GTGAGCTAAGATTGCGCCAC
25192	23279	AGTGAGCTAAGATTGCGCCA
25193	23280	CAGTGAGCTAAGATTGCGCC
25194	23281	GCAGTGAGCTAAGATTGCGC
25195	23282	TGCAGTGAGCTAAGATTGCG
25196	23283	TTGCAGTGAGCTAAGATTGC
25197	23284	GTTGCAGTGAGCTAAGATTG
25198	23285	GGTTGCAGTGAGCTAAGATT

74275	72362	CTGTTCCTTCCCAGTACTGT
74276	72363	ACTGTTCCTTCCCAGTACTG
74277	72364	CACTGTTCCTTCCCAGTACT
74278	72365	CCACTGTTCCTTCCCAGTAC
74279	72366	GCCACTGTTCCTTCCCAGTA
74280	72367	AGCCACTGTTCCTTCCCAGT
74281	72368	CAGCCACTGTTCCTTCCCAG
74282	72369	CCAGCCACTGTTCCTTCCCA
74283	72370	CCCAGCCACTGTTCCTTCCC
74284	72371	TCCCAGCCACTGTTCCTTCC
74285	72372	CTCCCAGCCACTGTTCCTTC
74286	72373	GCTCCCAGCCACTGTTCCTT
74287	72374	AGCTCCCAGCCACTGTTCCT
74288	72375	AAGCTCCCAGCCACTGTTCC
74289	72376	TAAGCTCCCAGCCACTGTTC
74290	72377	ATAAGCTCCCAGCCACTGTT
74291	72378	TATAAGCTCCCAGCCACTGT
74292	72379	ATATAAGCTCCCAGCCACTG
74293	72380	AATATAAGCTCCCAGCCACT
74294	72381	GAATATAAGCTCCCAGCCAC
74295	72382	GGAATATAAGCTCCCAGCCA
74296	72383	AGGAATATAAGCTCCCAGCC
74297	72384	GAGGAATATAAGCTCCCAGC
74298	72385	TGAGGAATATAAGCTCCCAG
74299	72386	CTGAGGAATATAAGCTCCCA
74300	72387	GCTGAGGAATATAAGCTCCC
74301	72388	TGCTGAGGAATATAAGCTCC
74302	72389	CTGCTGAGGAATATAAGCTC
74303	72390	TCTGCTGAGGAATATAAGCT
74304	72391	CTCTGCTGAGGAATATAAGC
74305	72392	GCTCTGCTGAGGAATATAAG
74306	72393	GGCTCTGCTGAGGAATATAA
74307	72394	TGGCTCTGCTGAGGAATATA
74308	72395	CTGGCTCTGCTGAGGAATAT
74309	72396	TCTGGCTCTGCTGAGGAATA
74310	72397	ATCTGGCTCTGCTGAGGAAT
74311	72398	GATCTGGCTCTGCTGAGGAA
74312	72399	TGATCTGGCTCTGCTGAGGA
74313	72400	CTGATCTGGCTCTGCTGAGG
74314	72401	GCTGATCTGGCTCTGCTGAG
74315	72402	TGCTGATCTGGCTCTGCTGA
74316	72403	CTGCTGATCTGGCTCTGCTG
74317	72404	TCTGCTGATCTGGCTCTGCT
74318	72405	TTCTGCTGATCTGGCTCTGC
74319	72406	CTTCTGCTGATCTGGCTCTG
74320	72407	ACTTCTGCTGATCTGGCTCT
74321	72408	TACTTCTGCTGATCTGGCTC
74322	72409	ATACTTCTGCTGATCTGGCT
74323	72410	AATACTTCTGCTGATCTGGC
74324	72411	TAATACTTCTGCTGATCTGG
74325	72412	GTAATACTTCTGCTGATCTG
74326	72413	AGTAATACTTCTGCTGATCT
74327	72414	GAGTAATACTTCTGCTGATC
74328	72415	GGAGTAATACTTCTGCTGAT
74329	72416	AGGAGTAATACTTCTGCTGA
74330	72417	AAGGAGTAATACTTCTGCTG
74331	72418	TAAGGAGTAATACTTCTGCT
74332	72419	CTAAGGAGTAATACTTCTGC
74333	72420	ACTAAGGAGTAATACTTCTG
74334	72421	AACTAAGGAGTAATACTTCT
74335	72422	GAACTAAGGAGTAATACTTC
74336	72423	CGAACTAAGGAGTAATACTT
74337	72424	ACGAACTAAGGAGTAATACT
74338	72425	TACGAACTAAGGAGTAATAC
74339	72426	CTACGAACTAAGGAGTAATA
74340	72427	ACTACGAACTAAGGAGTAAT
74341	72428	TACTACGAACTAAGGAGTAA
74342	72429	CTACTACGAACTAAGGAGTA
74343	72430	CCTACTACGAACTAAGGAGT
74344	72431	ACCTACTACGAACTAAGGAG
74345	72432	CACCTACTACGAACTAAGGA

123422	121509	CCTGTAATCTCAGCACTTTG
123423	121510	ACCTGTAATCTCAGCACTTT
123424	121511	CACCTGTAATCTCAGCACTT
123425	121512	ACACCTGTAATCTCAGCACT
123426	121513	CACACCTGTAATCTCAGCAC
123427	121514	TCACACCTGTAATCTCAGCA
123428	121515	CTCACACCTGTAATCTCAGC
123429	121516	GCTCACACCTGTAATCTCAG
123430	121517	GGCTCACACCTGTAATCTCA
123431	121518	TGGCTCACACCTGTAATCTC
123432	121519	GTGGCTCACACCTGTAATCT
123433	121520	AGTGGCTCACACCTGTAATC
123434	121521	CAGTGGCTCACACCTGTAAT
123435	121522	GCAGTGGCTCACACCTGTAA
123436	121523	CGCAGTGGCTCACACCTGTA
123437	121524	GCGCAGTGGCTCACACCTGT
123438	121525	GGCGCAGTGGCTCACACCTG
123439	121526	AGGCGCAGTGGCTCACACCT
123440	121527	CAGGCGCAGTGGCTCACACC
123441	121528	ACAGGCGCAGTGGCTCACAC
123442	121529	GACAGGCGCAGTGGCTCACA
123443	121530	GGACAGGCGCAGTGGCTCAC
123444	121531	AGGACAGGCGCAGTGGCTCA
123445	121532	TAGGACAGGCGCAGTGGCTC
123446	121533	TTAGGACAGGCGCAGTGGCT
123447	121534	ATTAGGACAGGCGCAGTGGC
123448	121535	TATTAGGACAGGCGCAGTGG
123449	121536	TTATTAGGACAGGCGCAGTG
123450	121537	ATTATTAGGACAGGCGCAGT
123451	121538	AATTATTAGGACAGGCGCAG
123452	121539	AAATTATTAGGACAGGCGCA
123453	121540	GAAATTATTAGGACAGGCGC
123454	121541	AGAAATTATTAGGACAGGCG
123455	121542	AAGAAATTATTAGGACAGGC
123456	121543	AAAGAAATTATTAGGACAGG
123457	121544	AAAAGAAATTATTAGGACAG
123458	121545	AAAAAGAAATTATTAGGACA
123459	121546	CAAAAAGAAATTATTAGGAC
123460	121547	ACAAAAAGAAATTATTAGGA
123461	121548	GACAAAAAGAAATTATTAGG
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123463	121550	GAGACAAAAAGAAATTATTA
123464	121551	TGAGACAAAAAGAAATTATT
123465	121552	TTGAGACAAAAAGAAATTAT
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123468	121555	ACATTGAGACAAAAAGAAAT
123469	121556	AACATTGAGACAAAAAGAAA
123470	121557	AAACATTGAGACAAAAAGAA
123471	121558	GAAACATTGAGACAAAAAGA
123472	121559	AGAAACATTGAGACAAAAAG
123473	121560	CAGAAACATTGAGACAAAAA
123474	121561	GCAGAAACATTGAGACAAAA
123475	121562	GGCAGAAACATTGAGACAAA
123476	121563	AGGCAGAAACATTGAGACAA
123477	121564	CAGGCAGAAACATTGAGACA
123478	121565	CCAGGCAGAAACATTGAGAC
123479	121566	CCCAGGCAGAAACATTGAGA
123480	121567	ACCCAGGCAGAAACATTGAG
123481	121568	CACCCAGGCAGAAACATTGA
123482	121569	GCACCCAGGCAGAAACATTG
123483	121570	TGCACCCAGGCAGAAACATT
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123485	121572	AGTGCACCCAGGCAGAAACA
123486	121573	CAGTGCACCCAGGCAGAAAC
123487	121574	CCAGTGCACCCAGGCAGAAA
123488	121575	GCCAGTGCACCCAGGCAGAA
123489	121576	AGCCAGTGCACCCAGGCAGA
123490	121577	GAGCCAGTGCACCCAGGCAG
123491	121578	TGAGCCAGTGCACCCAGGCA
123492	121579	GTGAGCCAGTGCACCCAGGC

25199	23286	AGGTTGCAGTGAGCTAAGAT
25200	23287	GAGGTTGCAGTGAGCTAAGA
25201	23288	GGAGGTTGCAGTGAGCTAAG
25202	23289	CGGAGGTTGCAGTGAGCTAA
25203	23290	GCGGAGGTTGCAGTGAGCTA
25204	23291	GGCGGAGGTTGCAGTGAGCT
25205	23292	AGGCGGAGGTTGCAGTGAGC
25206	23293	GAGGCGGAGGTTGCAGTGAG
25207	23294	GGAGGCGGAGGTTGCAGTGA
25208	23295	AGGAGGCGGAGGTTGCAGTG
25209	23296	CAGGAGGCGGAGGTTGCAGT
25210	23297	ACAGGAGGCGGAGGTTGCAG
25211	23298	CACAGGAGGCGGAGGTTGCA
25212	23299	ACACAGGAGGCGGAGGTTGC
25213	23300	AACACAGGAGGCGGAGGTTG
25214	23301	GAACACAGGAGGCGGAGGTT
25215	23302	TGAACACAGGAGGCGGAGGT
25216	23303	CTGAACACAGGAGGCGGAGG
25217	23304	CCTGAACACAGGAGGCGGAG
25218	23305	ACCTGAACACAGGAGGCGGA
25219	23306	CACCTGAACACAGGAGGCGG
25220	23307	TCACCTGAACACAGGAGGCG
25221	23308	ATCACCTGAACACAGGAGGC
25222	23309	AATCACCTGAACACAGGAGG
25223	23310	GAATCACCTGAACACAGGAG
25224	23311	TGAATCACCTGAACACAGGA
25225	23312	CTGAATCACCTGAACACAGG
25226	23313	GCTGAATCACCTGAACACAG
25227	23314	GGCTGAATCACCTGAACACA
25228	23315	AGGCTGAATCACCTGAACAC
25229	23316	GAGGCTGAATCACCTGAACA
25230	23317	GGAGGCTGAATCACCTGAAC
25231	23318	GGGAGGCTGAATCACCTGAA
25232	23319	TGGGAGGCTGAATCACCTGA
25233	23320	TTGGGAGGCTGAATCACCTG
25234	23321	CTTGGGAGGCTGAATCACCT
25235	23322	ACTTGGGAGGCTGAATCACC
25236	23323	TACTTGGGAGGCTGAATCAC
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25238	23325	GGTACTTGGGAGGCTGAATC
25239	23326	AGGTACTTGGGAGGCTGAAT
25240	23327	CAGGTACTTGGGAGGCTGAA
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25244	23331	GTCTCAGGTACTTGGGAGGC
25245	23332	AGTCTCAGGTACTTGGGAGG
25246	23333	TAGTCTCAGGTACTTGGGAG
25247	23334	GTAGTCTCAGGTACTTGGGA
25248	23335	TGTAGTCTCAGGTACTTGGG
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25250	23337	TCTGTAGTCTCAGGTACTTG
25251	23338	GTCTGTAGTCTCAGGTACTT
25252	23339	CGTCTGTAGTCTCAGGTACT
25253	23340	ACGTCTGTAGTCTCAGGTAC
25254	23341	CACGTCTGTAGTCTCAGGTA
25255	23342	GCACGTCTGTAGTCTCAGGT
25256	23343	TGCACGTCTGTAGTCTCAGG
25257	23344	GTGCACGTCTGTAGTCTCAG
25258	23345	AGTGCACGTCTGTAGTCTCA
25259	23346	TAGTGCACGTCTGTAGTCTC
25260	23347	GTAGTGCACGTCTGTAGTCT
25261	23348	GGTAGTGCACGTCTGTAGTC
25262	23349	CGGTAGTGCACGTCTGTAGT
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25264	23351	CACGGTAGTGCACGTCTGTA
25265	23352	GCACGGTAGTGCACGTCTGT
25266	23353	GGCACGGTAGTGCACGTCTG
25267	23354	AGGCACGGTAGTGCACGTCT
25268	23355	CAGGCACGGTAGTGCACGTC
25269	23356	TCAGGCACGGTAGTGCACGT

74346	72433	CCACCTACTACGAACTAAGG
74347	72434	ACCACCTACTACGAACTAAG
74348	72435	TACCACCTACTACGAACTAA
74349	72436	GTACCACCTACTACGAACTA
74350	72437	GGTACCACCTACTACGAACT
74351	72438	GGGTACCACCTACTACGAAC
74352	72439	AGGGTACCACCTACTACGAA
74353	72440	TAGGGTACCACCTACTACGA
74354	72441	ATAGGGTACCACCTACTACG
74355	72442	CATAGGGTACCACCTACTAC
74356	72443	CCATAGGGTACCACCTACTA
74357	72444	CCCATAGGGTACCACCTACT
74358	72445	ACCCATAGGGTACCACCTAC
74359	72446	GACCCATAGGGTACCACCTA
74360	72447	GGACCCATAGGGTACCACCT
74361	72448	TGGACCCATAGGGTACCACC
74362	72449	CTGGACCCATAGGGTACCAC
74363	72450	ACTGGACCCATAGGGTACCA
74364	72451	GACTGGACCCATAGGGTACC
74365	72452	TGACTGGACCCATAGGGTAC
74366	72453	ATGACTGGACCCATAGGGTA
74367	72454	AATGACTGGACCCATAGGGT
74368	72455	AAATGACTGGACCCATAGGG
74369	72456	TAAATGACTGGACCCATAGG
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74371	72458	TTTAAATGACTGGACCCATA
74372	72459	ATTTAAATGACTGGACCCAT
74373	72460	CATTTAAATGACTGGACCCA
74374	72461	GCATTTAAATGACTGGACCC
74375	72462	TGCATTTAAATGACTGGACC
74376	72463	TTGCATTTAAATGACTGGAC
74377	72464	CTTGCATTTAAATGACTGGA
74378	72465	GCTTGCATTTAAATGACTGG
74379	72466	GGCTTGCATTTAAATGACTG
74380	72467	AGGCTTGCATTTAAATGACT
74381	72468	CAGGCTTGCATTTAAATGAC
74382	72469	ACAGGCTTGCATTTAAATGA
74383	72470	TACAGGCTTGCATTTAAATG
74384	72471	ATACAGGCTTGCATTTAAAT
74385	72472	GATACAGGCTTGCATTTAAA
74386	72473	AGATACAGGCTTGCATTTAA
74387	72474	TAGATACAGGCTTGCATTTA
74388	72475	GTAGATACAGGCTTGCATTT
74389	72476	TGTAGATACAGGCTTGCATT
74390	72477	CTGTAGATACAGGCTTGCAT
74391	72478	TCTGTAGATACAGGCTTGCA
74392	72479	CTCTGTAGATACAGGCTTGC
74393	72480	GCTCTGTAGATACAGGCTTG
74394	72481	CGCTCTGTAGATACAGGCTT
74395	72482	ACGCTCTGTAGATACAGGCT
74396	72483	AACGCTCTGTAGATACAGGC
74397	72484	AAACGCTCTGTAGATACAGG
74398	72485	GAAACGCTCTGTAGATACAG
74399	72486	GGAAACGCTCTGTAGATACA
74400	72487	AGGAAACGCTCTGTAGATAC
74401	72488	TAGGAAACGCTCTGTAGATA
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74403	72490	ACTAGGAAACGCTCTGTAGA
74404	72491	CACTAGGAAACGCTCTGTAG
74405	72492	GCACTAGGAAACGCTCTGTA
74406	72493	GGCACTAGGAAACGCTCTGT
74407	72494	TGGCACTAGGAAACGCTCTG
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74409	72496	GATGGCACTAGGAAACGCTC
74410	72497	TGATGGCACTAGGAAACGCT
74411	72498	ATGATGGCACTAGGAAACGC
74412	72499	AATGATGGCACTAGGAAACG
74413	72500	CAATGATGGCACTAGGAAAC
74414	72501	GCAATGATGGCACTAGGAAA
74415	72502	GGCAATGATGGCACTAGGAA
74416	72503	GGGCAATGATGGCACTAGGA

123493	121580	CGTGAGCCAGTGCACCCAGG
123494	121581	GCGTGAGCCAGTGCACCCAG
123495	121582	GGCGTGAGCCAGTGCACCCA
123496	121583	AGGCGTGAGCCAGTGCACCC
123497	121584	CAGGCGTGAGCCAGTGCACC
123498	121585	ACAGGCGTGAGCCAGTGCAC
123499	121586	TACAGGCGTGAGCCAGTGCA
123500	121587	TTACAGGCGTGAGCCAGTGC
123501	121588	ATTACAGGCGTGAGCCAGTG
123502	121589	AATTACAGGCGTGAGCCAGT
123503	121590	GAATTACAGGCGTGAGCCAG
123504	121591	GGAATTACAGGCGTGAGCCA
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123506	121593	CTGGAATTACAGGCGTGAGC
123507	121594	GCTGGAATTACAGGCGTGAG
123508	121595	TGCTGGAATTACAGGCGTGA
123509	121596	GTGCTGGAATTACAGGCGTG
123510	121597	AGTGCTGGAATTACAGGCGT
123511	121598	AAGTGCTGGAATTACAGGCG
123512	121599	AAAGTGCTGGAATTACAGGC
123513	121600	CAAAGTGCTGGAATTACAGG
123514	121601	CCAAAGTGCTGGAATTACAG
123515	121602	CCCAAAGTGCTGGAATTACA
123516	121603	TCCCAAAGTGCTGGAATTAC
123517	121604	CTCCCAAAGTGCTGGAATTA
123518	121605	CCTCCCAAAGTGCTGGAATT
123519	121606	GCCTCCCAAAGTGCTGGAAT
123520	121607	GGCCTCCCAAAGTGCTGGAA
123521	121608	TGGCCTCCCAAAGTGCTGGA
123522	121609	TTGGCCTCCCAAAGTGCTGG
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123525	121612	AGGTTGGCCTCCCAAAGTGC
123526	121613	CAGGTTGGCCTCCCAAAGTG
123527	121614	CCAGGTTGGCCTCCCAAAGT
123528	121615	TCCAGGTTGGCCTCCCAAAG
123529	121616	ATCCAGGTTGGCCTCCCAAA
123530	121617	CATCCAGGTTGGCCTCCCAA
123531	121618	CCATCCAGGTTGGCCTCCCA
123532	121619	TCCATCCAGGTTGGCCTCCC
123533	121620	ATCCATCCAGGTTGGCCTCC
123534	121621	GATCCATCCAGGTTGGCCTC
123535	121622	TGATCCATCCAGGTTGGCCT
123536	121623	ATGATCCATCCAGGTTGGCC
123537	121624	AATGATCCATCCAGGTTGGC
123538	121625	AAATGATCCATCCAGGTTGG
123539	121626	CAAATGATCCATCCAGGTTG
123540	121627	TCAAATGATCCATCCAGGTT
123541	121628	CTCAAATGATCCATCCAGGT
123542	121629	GCTCAAATGATCCATCCAGG
123543	121630	GGCTCAAATGATCCATCCAG
123544	121631	TGGCTCAAATGATCCATCCA
123545	121632	TTGGCTCAAATGATCCATCC
123546	121633	GTTGGCTCAAATGATCCATC
123547	121634	TGTTGGCTCAAATGATCCAT
123548	121635	CTGTTGGCTCAAATGATCCA
123549	121636	ACTGTTGGCTCAAATGATCC
123550	121637	AACTGTTGGCTCAAATGATC
123551	121638	AAACTGTTGGCTCAAATGAT
123552	121639	CAAACTGTTGGCTCAAATGA
123553	121640	TCAAACTGTTGGCTCAAATG
123554	121641	CTCAAACTGTTGGCTCAAAT
123555	121642	TCTCAAACTGTTGGCTCAAA
123556	121643	GTCTCAAACTGTTGGCTCAA
123557	121644	GGTCTCAAACTGTTGGCTCA
123558	121645	TGGTCTCAAACTGTTGGCTC
123559	121646	CTGGTCTCAAACTGTTGGCT
123560	121647	GCTGGTCTCAAACTGTTGGC
123561	121648	GGCTGGTCTCAAACTGTTGG
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123563	121650	CAGGCTGGTCTCAAACTGTT

25270	23357	GTCAGGCACGGTAGTGCACG
25271	23358	AGTCAGGCACGGTAGTGCAC
25272	23359	TAGTCAGGCACGGTAGTGCA
25273	23360	TTAGTCAGGCACGGTAGTGC
25274	23361	ATTAGTCAGGCACGGTAGTG
25275	23362	AATTAGTCAGGCACGGTAGT
25276	23363	AAATTAGTCAGGCACGGTAG
25277	23364	AAAATTAGTCAGGCACGGTA
25278	23365	AAAAATTAGTCAGGCACGGT
25279	23366	CAAAAATTAGTCAGGCACGG
25280	23367	ACAAAAATTAGTCAGGCACG
25281	23368	TACAAAAATTAGTCAGGCAC
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25283	23370	AATACAAAAATTAGTCAGGC
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25285	23372	AAAATACAAAAATTAGTCAG
25286	23373	AAAAATACAAAAATTAGTCA
25287	23374	TAAAAATACAAAAATTAGTC
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25291	23378	CTACTAAAAATACAAAAATT
25292	23379	TCTACTAAAAATACAAAAAT
25293	23380	TTCTACTAAAAATACAAAAA
25294	23381	TTTCTACTAAAAATACAAAA
25295	23382	ATTTCTACTAAAAATACAAA
25296	23383	CATTTCTACTAAAAATACAA
25297	23384	CCATTTCTACTAAAAATACA
25298	23385	CCCATTTCTACTAAAAATAC
25299	23386	CCCCATTTCTACTAAAAATA
25300	23387	ACCCCATTTCTACTAAAAAT
25301	23388	AACCCCATTTCTACTAAAAA
25302	23389	AAACCCCATTTCTACTAAAA
25303	23390	GAAACCCCATTTCTACTAAA
25304	23391	TGAAACCCCATTTCTACTAA
25305	23392	GTGAAACCCCATTTCTACTA
25306	23393	GGTGAAACCCCATTTCTACT
25307	23394	TGGTGAAACCCCATTTCTAC
25308	23395	ATGGTGAAACCCCATTTCTA
25309	23396	CATGGTGAAACCCCATTTCT
25310	23397	ACATGGTGAAACCCCATTTC
25311	23398	AACATGGTGAAACCCCATTT
25312	23399	CAACATGGTGAAACCCCATT
25313	23400	CCAACATGGTGAAACCCCAT
25314	23401	ACCAACATGGTGAAACCCCA
25315	23402	GACCAACATGGTGAAACCCC
25316	23403	TGACCAACATGGTGAAACCC
25317	23404	CTGACCAACATGGTGAAACC
25318	23405	GCTGACCAACATGGTGAAAC
25319	23406	GGCTGACCAACATGGTGAAA
25320	23407	AGGCTGACCAACATGGTGAA
25321	23408	CAGGCTGACCAACATGGTGA
25322	23409	CCAGGCTGACCAACATGGTG
25323	23410	ACCAGGCTGACCAACATGGT
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25327	23414	TGAGACCAGGCTGACCAACA
25328	23415	TTGAGACCAGGCTGACCAAC
25329	23416	TTTGAGACCAGGCTGACCAA
25330	23417	GTTTGAGACCAGGCTGACCA
25331	23418	AGTTTGAGACCAGGCTGACC
25332	23419	GAGTTTGAGACCAGGCTGAC
25333	23420	GGAGTTTGAGACCAGGCTGA
25334	23421	AGGAGTTTGAGACCAGGCTG
25335	23422	TAGGAGTTTGAGACCAGGCT
25336	23423	ATAGGAGTTTGAGACCAGGC
25337	23424	AATAGGAGTTTGAGACCAGG
25338	23425	GAATAGGAGTTTGAGACCAG
25339	23426	AGAATAGGAGTTTGAGACCA
25340	23427	GAGAATAGGAGTTTGAGACC

74417	72504	TGGGCAATGATGGCACTAGG
74418	72505	CTGGGCAATGATGGCACTAG
74419	72506	ACTGGGCAATGATGGCACTA
74420	72507	CACTGGGCAATGATGGCACT
74421	72508	CCACTGGGCAATGATGGCAC
74422	72509	CCCACTGGGCAATGATGGCA
74423	72510	GCCCACTGGGCAATGATGGC
74424	72511	GGCCCACTGGGCAATGATGG
74425	72512	AGGCCCACTGGGCAATGATG
74426	72513	AAGGCCCACTGGGCAATGAT
74427	72514	AAAGGCCCACTGGGCAATGA
74428	72515	TAAAGGCCCACTGGGCAATG
74429	72516	ATAAAGGCCCACTGGGCAAT
74430	72517	AATAAAGGCCCACTGGGCAA
74431	72518	AAATAAAGGCCCACTGGGCA
74432	72519	TAAATAAAGGCCCACTGGGC
74433	72520	CTAAATAAAGGCCCACTGGG
74434	72521	GCTAAATAAAGGCCCACTGG
74435	72522	AGCTAAATAAAGGCCCACTG
74436	72523	CAGCTAAATAAAGGCCCACT
74437	72524	TCAGCTAAATAAAGGCCCAC
74438	72525	CTCAGCTAAATAAAGGCCCA
74439	72526	ACTCAGCTAAATAAAGGCCC
74440	72527	GACTCAGCTAAATAAAGGCC
74441	72528	AGACTCAGCTAAATAAAGGC
74442	72529	TAGACTCAGCTAAATAAAGG
74443	72530	TTAGACTCAGCTAAATAAAG
74444	72531	GTTAGACTCAGCTAAATAAA
74445	72532	AGTTAGACTCAGCTAAATAA
74446	72533	GAGTTAGACTCAGCTAAATA
74447	72534	GGAGTTAGACTCAGCTAAAT
74448	72535	GGGAGTTAGACTCAGCTAAA
74449	72536	TGGGAGTTAGACTCAGCTAA
74450	72537	TTGGGAGTTAGACTCAGCTA
74451	72538	GTTGGGAGTTAGACTCAGCT
74452	72539	AGTTGGGAGTTAGACTCAGC
74453	72540	TAGTTGGGAGTTAGACTCAG
74454	72541	CTAGTTGGGAGTTAGACTCA
74455	72542	TCTAGTTGGGAGTTAGACTC
74456	72543	CTCTAGTTGGGAGTTAGACT
74457	72544	TCTCTAGTTGGGAGTTAGAC
74458	72545	TTCTCTAGTTGGGAGTTAGA
74459	72546	TTTCTCTAGTTGGGAGTTAG
74460	72547	TTTTCTCTAGTTGGGAGTTA
74461	72548	ATTTTCTCTAGTTGGGAGTT
74462	72549	AATTTTCTCTAGTTGGGAGT
74463	72550	AAATTTTCTCTAGTTGGGAG
74464	72551	GAAATTTTCTCTAGTTGGGA
74465	72552	GGAAATTTTCTCTAGTTGGG
74466	72553	AGGAAATTTTCTCTAGTTGG
74467	72554	CAGGAAATTTTCTCTAGTTG
74468	72555	ACAGGAAATTTTCTCTAGTT
74469	72556	CACAGGAAATTTTCTCTAGT
74470	72557	GCACAGGAAATTTTCTCTAG
74471	72558	GGCACAGGAAATTTTCTCTA
74472	72559	TGGCACAGGAAATTTTCTCT
74473	72560	CTGGCACAGGAAATTTTCTC
74474	72561	TCTGGCACAGGAAATTTTCT
74475	72562	GTCTGGCACAGGAAATTTTC
74476	72563	TGTCTGGCACAGGAAATTTT
74477	72564	CTGTCTGGCACAGGAAATTT
74478	72565	GCTGTCTGGCACAGGAAATT
74479	72566	TGCTGTCTGGCACAGGAAAT
74480	72567	CTGCTGTCTGGCACAGGAAA
74481	72568	ACTGCTGTCTGGCACAGGAA
74482	72569	TACTGCTGTCTGGCACAGGA
74483	72570	ATACTGCTGTCTGGCACAGG
74484	72571	CATACTGCTGTCTGGCACAG
74485	72572	CCATACTGCTGTCTGGCACA
74486	72573	ACCATACTGCTGTCTGGCAC
74487	72574	GACCATACTGCTGTCTGGCA

123564	121651	TCAGGCTGGTCTCAAACTGT
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123566	121653	CCTCAGGCTGGTCTCAAACT
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123568	121655	TTCCTCAGGCTGGTCTCAAA
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123570	121657	TGTTCCTCAGGCTGGTCTCA
123571	121658	ATGTTCCTCAGGCTGGTCTC
123572	121659	CATGTTCCTCAGGCTGGTCT
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123576	121663	TTGTCATGTTCCTCAGGCTG
123577	121664	TTTGTCATGTTCCTCAGGCT
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123581	121668	GGGTTTTGTCATGTTCCTCA
123582	121669	AGGGTTTTGTCATGTTCCTC
123583	121670	CAGGGTTTTGTCATGTTCCT
123584	121671	ACAGGGTTTTGTCATGTTCC
123585	121672	GACAGGGTTTTGTCATGTTC
123586	121673	AGACAGGGTTTTGTCATGTT
123587	121674	AAGACAGGGTTTTGTCATGT
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123589	121676	CAAAGACAGGGTTTTGTCAT
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123591	121678	TGCAAAGACAGGGTTTTGTC
123592	121679	TTGCAAAGACAGGGTTTTGT
123593	121680	TTTGCAAAGACAGGGTTTTG
123594	121681	TTTTGCAAAGACAGGGTTTT
123595	121682	TTTTTGCAAAGACAGGGTTT
123596	121683	TTTTTTGCAAAGACAGGGTT
123597	121684	TTTTTTTGCAAAGACAGGGT
123598	121685	TTTTTTTTGCAAAGACAGGG
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123601	121688	TTTTTTTTTTTGCAAAGACA
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123607	121694	TTTTCTTTTTTTTTTTTGCA
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123612	121699	TTCTTTTTTCTTTTTTTTTT
123613	121700	TTTCTTTTTTCTTTTTTTTT
123614	121701	TTTTCTTTTTTCTTTTTTTT
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123616	121703	ATTTTTCTTTTTTCTTTTTT
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123618	121705	TAATTTTTCTTTTTTCTTTT
123619	121706	CTAATTTTTCTTTTTTCTTT
123620	121707	GCTAATTTTTCTTTTTTCTT
123621	121708	GGCTAATTTTTCTTTTTTCT
123622	121709	TGGCTAATTTTTCTTTTTTC
123623	121710	CTGGCTAATTTTTCTTTTTT
123624	121711	CCTGGCTAATTTTTCTTTTT
123625	121712	GCCTGGCTAATTTTTCTTTT
123626	121713	TGCCTGGCTAATTTTTCTTT
123627	121714	GTGCCTGGCTAATTTTTCTT
123628	121715	TGTGCCTGGCTAATTTTTCT
123629	121716	CTGTGCCTGGCTAATTTTTC
123630	121717	TCTGTGCCTGGCTAATTTTT
123631	121718	TTCTGTGCCTGGCTAATTTT
123632	121719	CTTCTGTGCCTGGCTAATTT
123633	121720	GCTTCTGTGCCTGGCTAATT
123634	121721	CGCTTCTGTGCCTGGCTAAT

25341	23428	TGAGAATAGGAGTTTGAGAC
25342	23429	TTGAGAATAGGAGTTTGAGA
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25344	23431	ACTTGAGAATAGGAGTTTGA
25345	23432	CACTTGAGAATAGGAGTTTG
25346	23433	TCACTTGAGAATAGGAGTTT
25347	23434	ATCACTTGAGAATAGGAGTT
25348	23435	GATCACTTGAGAATAGGAGT
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25350	23437	CGGATCACTTGAGAATAGGA
25351	23438	GCGGATCACTTGAGAATAGG
25352	23439	GGCGGATCACTTGAGAATAG
25353	23440	AGGCGGATCACTTGAGAATA
25354	23441	TAGGCGGATCACTTGAGAAT
25355	23442	GTAGGCGGATCACTTGAGAA
25356	23443	GGTAGGCGGATCACTTGAGA
25357	23444	AGGTAGGCGGATCACTTGAG
25358	23445	GAGGTAGGCGGATCACTTGA
25359	23446	CGAGGTAGGCGGATCACTTG
25360	23447	TCGAGGTAGGCGGATCACTT
25361	23448	GTCGAGGTAGGCGGATCACT
25362	23449	GGTCGAGGTAGGCGGATCAC
25363	23450	AGGTCGAGGTAGGCGGATCA
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25366	23453	GGAAGGTCGAGGTAGGCGGA
25367	23454	TGGAAGGTCGAGGTAGGCGG
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25372	23459	CACTTTGGAAGGTCGAGGTA
25373	23460	CCACTTTGGAAGGTCGAGGT
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25376	23463	CCGCCACTTTGGAAGGTCGA
25377	23464	TCCGCCACTTTGGAAGGTCG
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25382	23469	ATAATTCCGCCACTTTGGAA
25383	23470	TATAATTCCGCCACTTTGGA
25384	23471	CTATAATTCCGCCACTTTGG
25385	23472	CCTATAATTCCGCCACTTTG
25386	23473	ACCTATAATTCCGCCACTTT
25387	23474	CACCTATAATTCCGCCACTT
25388	23475	ACACCTATAATTCCGCCACT
25389	23476	CACACCTATAATTCCGCCAC
25390	23477	TCACACCTATAATTCCGCCA
25391	23478	CTCACACCTATAATTCCGCC
25392	23479	GCTCACACCTATAATTCCGC
25393	23480	GGCTCACACCTATAATTCCG
25394	23481	CGGCTCACACCTATAATTCC
25395	23482	ACGGCTCACACCTATAATTC
25396	23483	CACGGCTCACACCTATAATT
25397	23484	CCACGGCTCACACCTATAAT
25398	23485	ACCACGGCTCACACCTATAA
25399	23486	CACCACGGCTCACACCTATA
25400	23487	GCACCACGGCTCACACCTAT
25401	23488	GGCACCACGGCTCACACCTA
25402	23489	GGGCACCACGGCTCACACCT
25403	23490	CGGGCACCACGGCTCACACC
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25405	23492	GCCGGGCACCACGGCTCACA
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25407	23494	TGGCCGGGCACCACGGCTCA
25408	23495	CTGGCCGGGCACCACGGCTC
25409	23496	TCTGGCCGGGCACCACGGCT
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25411	23498	AGTCTGGCCGGGCACCACGG

74488	72575	TGACCATACTGCTGTCTGGC
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74492	72579	TAGCTGACCATACTGCTGTC
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74498	72585	ACATGTTAGCTGACCATACT
74499	72586	CACATGTTAGCTGACCATAC
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74501	72588	TCCACATGTTAGCTGACCAT
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74503	72590	CATCCACATGTTAGCTGACC
74504	72591	GCATCCACATGTTAGCTGAC
74505	72592	AGCATCCACATGTTAGCTGA
74506	72593	TAGCATCCACATGTTAGCTG
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74508	72595	TGTAGCATCCACATGTTAGC
74509	72596	ATGTAGCATCCACATGTTAG
74510	72597	AATGTAGCATCCACATGTTA
74511	72598	AAATGTAGCATCCACATGTT
74512	72599	CAAATGTAGCATCCACATGT
74513	72600	GCAAATGTAGCATCCACATG
74514	72601	AGCAAATGTAGCATCCACAT
74515	72602	AAGCAAATGTAGCATCCACA
74516	72603	AAAGCAAATGTAGCATCCAC
74517	72604	GAAAGCAAATGTAGCATCCA
74518	72605	TGAAAGCAAATGTAGCATCC
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74532	72619	AGAGTACTGACTTATGAAAG
74533	72620	AAGAGTACTGACTTATGAAA
74534	72621	GAAGAGTACTGACTTATGAA
74535	72622	TGAAGAGTACTGACTTATGA
74536	72623	TTGAAGAGTACTGACTTATG
74537	72624	ATTGAAGAGTACTGACTTAT
74538	72625	TATTGAAGAGTACTGACTTA
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74541	72628	TGTTATTGAAGAGTACTGAC
74542	72629	ATGTTATTGAAGAGTACTGA
74543	72630	AATGTTATTGAAGAGTACTG
74544	72631	TAATGTTATTGAAGAGTACT
74545	72632	CTAATGTTATTGAAGAGTAC
74546	72633	ACTAATGTTATTGAAGAGTA
74547	72634	TACTAATGTTATTGAAGAGT
74548	72635	CTACTAATGTTATTGAAGAG
74549	72636	TCTACTAATGTTATTGAAGA
74550	72637	TTCTACTAATGTTATTGAAG
74551	72638	CTTCTACTAATGTTATTGAA
74552	72639	TCTTCTACTAATGTTATTGA
74553	72640	CTCTTCTACTAATGTTATTG
74554	72641	TCTCTTCTACTAATGTTATT
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74556	72643	CTTCTCTTCTACTAATGTTA
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74558	72645	CTCTTCTCTTCTACTAATGT

123635	121722	GCGCTTCTGTGCCTGGCTAA
123636	121723	TGCGCTTCTGTGCCTGGCTA
123637	121724	ATGCGCTTCTGTGCCTGGCT
123638	121725	AATGCGCTTCTGTGCCTGGC
123639	121726	GAATGCGCTTCTGTGCCTGG
123640	121727	GGAATGCGCTTCTGTGCCTG
123641	121728	AGGAATGCGCTTCTGTGCCT
123642	121729	TAGGAATGCGCTTCTGTGCC
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123644	121731	CATAGGAATGCGCTTCTGTG
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123646	121733	ACCATAGGAATGCGCTTCTG
123647	121734	GACCATAGGAATGCGCTTCT
123648	121735	GGACCATAGGAATGCGCTTC
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123650	121737	TGGGACCATAGGAATGCGCT
123651	121738	CTGGGACCATAGGAATGCGC
123652	121739	GCTGGGACCATAGGAATGCG
123653	121740	AGCTGGGACCATAGGAATGC
123654	121741	TAGCTGGGACCATAGGAATG
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123656	121743	AGTAGCTGGGACCATAGGAA
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123658	121745	CAAGTAGCTGGGACCATAGG
123659	121746	CCAAGTAGCTGGGACCATAG
123660	121747	CCCAAGTAGCTGGGACCATA
123661	121748	CCCCAAGTAGCTGGGACCAT
123662	121749	CCCCCAAGTAGCTGGGACCA
123663	121750	CCCCCCAAGTAGCTGGGACC
123664	121751	GCCCCCCAAGTAGCTGGGAC
123665	121752	AGCCCCCCAAGTAGCTGGGA
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123671	121758	CACCTCAGCCCCCCAAGTAG
123672	121759	CCACCTCAGCCCCCCAAGTA
123673	121760	CCCACCTCAGCCCCCCAAGT
123674	121761	TCCCACCTCAGCCCCCCAAG
123675	121762	GTCCCACCTCAGCCCCCCAA
123676	121763	TGTCCCACCTCAGCCCCCCA
123677	121764	TTGTCCCACCTCAGCCCCCC
123678	121765	ATTGTCCCACCTCAGCCCCC
123679	121766	GATTGTCCCACCTCAGCCCC
123680	121767	CGATTGTCCCACCTCAGCCC
123681	121768	GCGATTGTCCCACCTCAGCC
123682	121769	AGCGATTGTCCCACCTCAGC
123683	121770	AAGCGATTGTCCCACCTCAG
123684	121771	CAAGCGATTGTCCCACCTCA
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123688	121775	CGCTCAAGCGATTGTCCCAC
123689	121776	TCGCTCAAGCGATTGTCCCA
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123692	121779	ACCTCGCTCAAGCGATTGTC
123693	121780	AACCTCGCTCAAGCGATTGT
123694	121781	CAACCTCGCTCAAGCGATTG
123695	121782	GCAACCTCGCTCAAGCGATT
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123697	121784	CCGCAACCTCGCTCAAGCGA
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123702	121789	AACCCCCGCAACCTCGCTCA
123703	121790	AAACCCCCGCAACCTCGCTC
123704	121791	CAAACCCCCGCAACCTCGCT
123705	121792	CCAAACCCCCGCAACCTCGC

25412	23499	TAGTCTGGCCGGGCACCACG
25413	23500	ATAGTCTGGCCGGGCACCAC
25414	23501	AATAGTCTGGCCGGGCACCA
25415	23502	CAATAGTCTGGCCGGGCACC
25416	23503	CCAATAGTCTGGCCGGGCAC
25417	23504	ACCAATAGTCTGGCCGGGCA
25418	23505	AACCAATAGTCTGGCCGGGC
25419	23506	AAACCAATAGTCTGGCCGGG
25420	23507	CAAACCAATAGTCTGGCCGG
25421	23508	CCAAACCAATAGTCTGGCCG
25422	23509	ACCAAACCAATAGTCTGGCC
25423	23510	AACCAAACCAATAGTCTGGC
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25425	23512	CAAACCAAACCAATAGTCTG
25426	23513	CCAAACCAAACCAATAGTCT
25427	23514	ACCAAACCAAACCAATAGTC
25428	23515	CACCAAACCAAACCAATAGT
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25432	23519	ATCACACCAAACCAAACCAA
25433	23520	CATCACACCAAACCAAACCA
25434	23521	ACATCACACCAAACCAAACC
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25436	23523	TAACATCACACCAAACCAAA
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25438	23525	CATAACATCACACCAAACCA
25439	23526	ACATAACATCACACCAAACC
25440	23527	AACATAACATCACACCAAAC
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25443	23530	CATAACATAACATCACACCA
25444	23531	ACATAACATAACATCACACC
25445	23532	AACATAACATAACATCACAC
25446	23533	TAACATAACATAACATCACA
25447	23534	ATAACATAACATAACATCAC
25448	23535	CATAACATAACATAACATCA
25449	23536	ACATAACATAACATAACATC
25450	23537	AACATAACATAACATAACAT
25451	23538	TAACATAACATAACATAACA
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25453	23540	CATAACATAACATAACATAA
25454	23541	ACATAACATAACATAACATA
25455	23542	AACATAACATAACATAACAT
25456	23543	TAACATAACATAACATAACA
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25458	23545	CATAACATAACATAACATAA
25459	23546	ACATAACATAACATAACATA
25460	23547	AACATAACATAACATAACAT
25461	23548	TAACATAACATAACATAACA
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25463	23550	CATAACATAACATAACATAA
25464	23551	ACATAACATAACATAACATA
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25466	23553	TAACATAACATAACATAACA
25467	23554	ATAACATAACATAACATAAC
25468	23555	CATAACATAACATAACATAA
25469	23556	ACATAACATAACATAACATA
25470	23557	AACATAACATAACATAACAT
25471	23558	TAACATAACATAACATAACA
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25473	23560	CATAACATAACATAACATAA
25474	23561	ACATAACATAACATAACATA
25475	23562	AACATAACATAACATAACAT
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25479	23566	ACATAACATAACATAACATA
25480	23567	AACATAACATAACATAACAT
25481	23568	TAACATAACATAACATAACA
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74559	72646	CCTCTTCTCTTCTACTAATG
74560	72647	TCCTCTTCTCTTCTACTAAT
74561	72648	GTCCTCTTCTCTTCTACTAA
74562	72649	TGTCCTCTTCTCTTCTACTA
74563	72650	GTGTCCTCTTCTCTTCTACT
74564	72651	TGTGTCCTCTTCTCTTCTAC
74565	72652	TTGTGTCCTCTTCTCTTCTA
74566	72653	TTTGTGTCCTCTTCTCTTCT
74567	72654	CTTTGTGTCCTCTTCTCTTC
74568	72655	ACTTTGTGTCCTCTTCTCTT
74569	72656	CACTTTGTGTCCTCTTCTCT
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74588	72675	CTTCCTATTAACACACTCTC
74589	72676	ACTTCCTATTAACACACTCT
74590	72677	GACTTCCTATTAACACACTC
74591	72678	GGACTTCCTATTAACACACT
74592	72679	TGGACTTCCTATTAACACAC
74593	72680	CTGGACTTCCTATTAACACA
74594	72681	CCTGGACTTCCTATTAACAC
74595	72682	ACCTGGACTTCCTATTAACA
74596	72683	TACCTGGACTTCCTATTAAC
74597	72684	ATACCTGGACTTCCTATTAA
74598	72685	CATACCTGGACTTCCTATTA
74599	72686	GCATACCTGGACTTCCTATT
74600	72687	GGCATACCTGGACTTCCTAT
74601	72688	AGGCATACCTGGACTTCCTA
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74607	72694	GGTAGCAGGCATACCTGGAC
74608	72695	AGGTAGCAGGCATACCTGGA
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74610	72697	TCAGGTAGCAGGCATACCTG
74611	72698	TTCAGGTAGCAGGCATACCT
74612	72699	GTTCAGGTAGCAGGCATACC
74613	72700	AGTTCAGGTAGCAGGCATAC
74614	72701	AAGTTCAGGTAGCAGGCATA
74615	72702	AAAGTTCAGGTAGCAGGCAT
74616	72703	GAAAGTTCAGGTAGCAGGCA
74617	72704	AGAAAGTTCAGGTAGCAGGC
74618	72705	CAGAAAGTTCAGGTAGCAGG
74619	72706	TCAGAAAGTTCAGGTAGCAG
74620	72707	CTCAGAAAGTTCAGGTAGCA
74621	72708	TCTCAGAAAGTTCAGGTAGC
74622	72709	GTCTCAGAAAGTTCAGGTAG
74623	72710	TGTCTCAGAAAGTTCAGGTA
74624	72711	CTGTCTCAGAAAGTTCAGGT
74625	72712	CCTGTCTCAGAAAGTTCAGG
74626	72713	ACCTGTCTCAGAAAGTTCAG
74627	72714	TACCTGTCTCAGAAAGTTCA
74628	72715	TTACCTGTCTCAGAAAGTTC
74629	72716	ATTACCTGTCTCAGAAAGTT

123706	121793	TCCAAACCCCCGCAACCTCG
123707	121794	CTCCAAACCCCCGCAACCTC
123708	121795	CCTCCAAACCCCCGCAACCT
123709	121796	CCCTCCAAACCCCCGCAACC
123710	121797	GCCCTCCAAACCCCCGCAAC
123711	121798	CGCCCTCCAAACCCCCGCAA
123712	121799	TCGCCCTCCAAACCCCCGCA
123713	121800	ATCGCCCTCCAAACCCCCGC
123714	121801	CATCGCCCTCCAAACCCCCG
123715	121802	CCATCGCCCTCCAAACCCCC
123716	121803	TCCATCGCCCTCCAAACCCC
123717	121804	CTCCATCGCCCTCCAAACCC
123718	121805	CCTCCATCGCCCTCCAAACC
123719	121806	CCCTCCATCGCCCTCCAAAC
123720	121807	CCCCTCCATCGCCCTCCAAA
123721	121808	ACCCCTCCATCGCCCTCCAA
123722	121809	CACCCCTCCATCGCCCTCCA
123723	121810	TCACCCCTCCATCGCCCTCC
123724	121811	ATCACCCCTCCATCGCCCTC
123725	121812	GATCACCCCTCCATCGCCCT
123726	121813	CGATCACCCCTCCATCGCCC
123727	121814	TCGATCACCCCTCCATCGCC
123728	121815	CTCGATCACCCCTCCATCGC
123729	121816	CCTCGATCACCCCTCCATCG
123730	121817	ACCTCGATCACCCCTCCATC
123731	121818	AACCTCGATCACCCCTCCAT
123732	121819	CAACCTCGATCACCCCTCCA
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123734	121821	TGCAACCTCGATCACCCCTC
123735	121822	CTGCAACCTCGATCACCCCT
123736	121823	ACTGCAACCTCGATCACCCC
123737	121824	CACTGCAACCTCGATCACCC
123738	121825	TCACTGCAACCTCGATCACC
123739	121826	CTCACTGCAACCTCGATCAC
123740	121827	GCTCACTGCAACCTCGATCA
123741	121828	AGCTCACTGCAACCTCGATC
123742	121829	CAGCTCACTGCAACCTCGAT
123743	121830	TCAGCTCACTGCAACCTCGA
123744	121831	CTCAGCTCACTGCAACCTCG
123745	121832	TCTCAGCTCACTGCAACCTC
123746	121833	ATCTCAGCTCACTGCAACCT
123747	121834	AATCTCAGCTCACTGCAACC
123748	121835	CAATCTCAGCTCACTGCAAC
123749	121836	GCAATCTCAGCTCACTGCAA
123750	121837	TGCAATCTCAGCTCACTGCA
123751	121838	GTGCAATCTCAGCTCACTGC
123752	121839	AGTGCAATCTCAGCTCACTG
123753	121840	TAGTGCAATCTCAGCTCACT
123754	121841	GTAGTGCAATCTCAGCTCAC
123755	121842	AGTAGTGCAATCTCAGCTCA
123756	121843	CAGTAGTGCAATCTCAGCTC
123757	121844	GCAGTAGTGCAATCTCAGCT
123758	121845	TGCAGTAGTGCAATCTCAGC
123759	121846	GTGCAGTAGTGCAATCTCAG
123760	121847	AGTGCAGTAGTGCAATCTCA
123761	121848	GAGTGCAGTAGTGCAATCTC
123762	121849	GGAGTGCAGTAGTGCAATCT
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123764	121851	CTGGAGTGCAGTAGTGCAAT
123765	121852	GCTGGAGTGCAGTAGTGCAA
123766	121853	GGCTGGAGTGCAGTAGTGCA
123767	121854	AGGCTGGAGTGCAGTAGTGC
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123770	121857	CCCAGGCTGGAGTGCAGTAG
123771	121858	GCCCAGGCTGGAGTGCAGTA
123772	121859	TGCCCAGGCTGGAGTGCAGT
123773	121860	TTGCCCAGGCTGGAGTGCAG
123774	121861	ATTGCCCAGGCTGGAGTGCA
123775	121862	TATTGCCCAGGCTGGAGTGC
123776	121863	CTATTGCCCAGGCTGGAGTG

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25486	23573	TAAAATAACATAACATAACA
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25489	23576	TCTTAAAATAACATAACATA
25490	23577	GTCTTAAAATAACATAACAT
25491	23578	TGTCTTAAAATAACATAACA
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25499	23586	ACAAACTCTGTCTTAAAATA
25500	23587	GACAAACTCTGTCTTAAAAT
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25522	23609	CACTCCAGCCTGGGCGACAA
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25539	23626	CCGAGATCATGCCGCTGCAC
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25550	23637	GTTGCAGTAAGCCGAGATCA
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74631	72718	GTATTACCTGTCTCAGAAAG
74632	72719	AGTATTACCTGTCTCAGAAA
74633	72720	CAGTATTACCTGTCTCAGAA
74634	72721	ACAGTATTACCTGTCTCAGA
74635	72722	TACAGTATTACCTGTCTCAG
74636	72723	CTACAGTATTACCTGTCTCA
74637	72724	CCTACAGTATTACCTGTCTC
74638	72725	CCCTACAGTATTACCTGTCT
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74643	72730	TCAGGCCCTACAGTATTACC
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74647	72734	AAGTTCAGGCCCTACAGTAT
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74680	72767	ACCCACTTCTTCATATATAA
74681	72768	AACCCACTTCTTCATATATA
74682	72769	GAACCCACTTCTTCATATAT
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74684	72771	CAGAACCCACTTCTTCATAT
74685	72772	CCAGAACCCACTTCTTCATA
74686	72773	CCCAGAACCCACTTCTTCAT
74687	72774	TCCCAGAACCCACTTCTTCA
74688	72775	CTCCCAGAACCCACTTCTTC
74689	72776	CCTCCCAGAACCCACTTCTT
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74696	72783	TTTAACCCCTCCCAGAACCC
74697	72784	GTTTAACCCCTCCCAGAACC
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74699	72786	TGGTTTAACCCCTCCCAGAA
74700	72787	GTGGTTTAACCCCTCCCAGA

123777	121864	TCTATTGCCCAGGCTGGAGT
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123781	121868	TGGCTCTATTGCCCAGGCTG
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123783	121870	TCTGGCTCTATTGCCCAGGC
123784	121871	GTCTGGCTCTATTGCCCAGG
123785	121872	GGTCTGGCTCTATTGCCCAG
123786	121873	GGGTCTGGCTCTATTGCCCA
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123789	121876	ACAGGGTCTGGCTCTATTGC
123790	121877	GACAGGGTCTGGCTCTATTG
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123793	121880	TGAGACAGGGTCTGGCTCTA
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123796	121883	TTGTGAGACAGGGTCTGGCT
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123798	121885	TTTTGTGAGACAGGGTCTGG
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123800	121887	TTTTTTGTGAGACAGGGTCT
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123805	121892	TTCTTTTTTTTGTGAGACAG
123806	121893	TTTCTTTTTTTTGTGAGACA
123807	121894	TTTTCTTTTTTTTGTGAGAC
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123820	121907	AAACATGACTTTTTTTTTCTT
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123824	121911	AAAGAAACATGACTTTTTTT
123825	121912	AAAAGAAACATGACTTTTTT
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123827	121914	AGAAAAGAAACATGACTTTT
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123829	121916	TAAGAAAAGAAACATGACTT
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123839	121926	ATTTTCACAGTAAGAAAAGA
123840	121927	TATTTTCACAGTAAGAAAAG
123841	121928	TTATTTTCACAGTAAGAAAA
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123844	121931	ACTTTATTTTCACAGTAAGA
123845	121932	AACTTTATTTTCACAGTAAG
123846	121933	TAACTTTATTTTCACAGTAA
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25556	23643	GCGGAGGTTGCAGTAAGCCG
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25574	23661	ATCACTTGAACCTGGGAGGC
25575	23662	AATCACTTGAACCTGGGAGG
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25577	23664	AGAATCACTTGAACCTGGGA
25578	23665	GAGAATCACTTGAACCTGGG
25579	23666	GGAGAATCACTTGAACCTGG
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25581	23668	CAGGAGAATCACTTGAACCT
25582	23669	ACAGGAGAATCACTTGAACC
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25584	23671	AGACAGGAGAATCACTTGAA
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25586	23673	TAAGACAGGAGAATCACTTG
25587	23674	CTAAGACAGGAGAATCACTT
25588	23675	GCTAAGACAGGAGAATCACT
25589	23676	GGCTAAGACAGGAGAATCAC
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25595	23682	TTGGGAGGCTAAGACAGGAG
25596	23683	CTTGGGAGGCTAAGACAGGA
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25599	23686	CTACTTGGGAGGCTAAGACA
25600	23687	GCTACTTGGGAGGCTAAGAC
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25606	23693	ATCCCAGCTACTTGGGAGGC
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25608	23695	TAATCCCAGCTACTTGGGAG
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25612	23699	CCTGTAATCCCAGCTACTTG
25613	23700	GCCTGTAATCCCAGCTACTT
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25615	23702	GCGCCTGTAATCCCAGCTAC
25616	23703	GGCGCCTGTAATCCCAGCTA
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25619	23706	GTGGGCGCCTGTAATCCCAG
25620	23707	GGTGGGCGCCTGTAATCCCA
25621	23708	TGGTGGGCGCCTGTAATCCC
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25623	23710	GGTGGTGGGCGCCTGTAATC
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74701	72788	AGTGGTTTAACCCCTCCCAG
74702	72789	AAGTGGTTTAACCCCTCCCA
74703	72790	TAAGTGGTTTAACCCCTCCC
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74705	72792	TCTAAGTGGTTTAACCCCTC
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74707	72794	ATTCTAAGTGGTTTAACCCC
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74710	72797	GCCATTCTAAGTGGTTTAAC
74711	72798	AGCCATTCTAAGTGGTTTAA
74712	72799	AAGCCATTCTAAGTGGTTTA
74713	72800	GAAGCCATTCTAAGTGGTTT
74714	72801	TGAAGCCATTCTAAGTGGTT
74715	72802	ATGAAGCCATTCTAAGTGGT
74716	72803	AATGAAGCCATTCTAAGTGG
74717	72804	AAATGAAGCCATTCTAAGTG
74718	72805	TAAATGAAGCCATTCTAAGT
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74720	72807	AGTAAATGAAGCCATTCTAA
74721	72808	TAGTAAATGAAGCCATTCTA
74722	72809	TTAGTAAATGAAGCCATTCT
74723	72810	ATTAGTAAATGAAGCCATTC
74724	72811	CATTAGTAAATGAAGCCATT
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74726	72813	GCCATTAGTAAATGAAGCCA
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74729	72816	CTTGCCATTAGTAAATGAAG
74730	72817	TCTTGCCATTAGTAAATGAA
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74741	72828	TCCCAGCAAACTCTTGCCAT
74742	72829	ATCCCAGCAAACTCTTGCCA
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74744	72831	ATATCCCAGCAAACTCTTGC
74745	72832	AATATCCCAGCAAACTCTTG
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74747	72834	TCAATATCCCAGCAAACTCT
74748	72835	GTCAATATCCCAGCAAACTC
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74755	72842	TACAGTGGTCAATATCCCAG
74756	72843	GTACAGTGGTCAATATCCCA
74757	72844	TGTACAGTGGTCAATATCCC
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74759	72846	TATGTACAGTGGTCAATATC
74760	72847	CTATGTACAGTGGTCAATAT
74761	72848	TCTATGTACAGTGGTCAATA
74762	72849	GTCTATGTACAGTGGTCAAT
74763	72850	TGTCTATGTACAGTGGTCAA
74764	72851	ATGTCTATGTACAGTGGTCA
74765	72852	CATGTCTATGTACAGTGGTC
74766	72853	TCATGTCTATGTACAGTGGT
74767	72854	TTCATGTCTATGTACAGTGG
74768	72855	ATTCATGTCTATGTACAGTG
74769	72856	TATTCATGTCTATGTACAGT
74770	72857	ATATTCATGTCTATGTACAG
74771	72858	CATATTCATGTCTATGTACA

123848	121935	AGTAACTTTATTTTCACAGT
123849	121936	TAGTAACTTTATTTTCACAG
123850	121937	GTAGTAACTTTATTTTCACA
123851	121938	AGTAGTAACTTTATTTTCAC
123852	121939	AAGTAGTAACTTTATTTTCA
123853	121940	AAAGTAGTAACTTTATTTTC
123854	121941	AAAAGTAGTAACTTTATTTT
123855	121942	TAAAAGTAGTAACTTTATTT
123856	121943	CTAAAAGTAGTAACTTTATT
123857	121944	ACTAAAAGTAGTAACTTTAT
123858	121945	TACTAAAAGTAGTAACTTTA
123859	121946	TTACTAAAAGTAGTAACTTT
123860	121947	TTTACTAAAAGTAGTAACTT
123861	121948	ATTTACTAAAAGTAGTAACT
123862	121949	AATTTACTAAAAGTAGTAAC
123863	121950	TAATTTACTAAAAGTAGTAA
123864	121951	ATAATTTACTAAAAGTAGTA
123865	121952	AATAATTTACTAAAAGTAGT
123866	121953	AAATAATTTACTAAAAGTAG
123867	121954	AAAATAATTTACTAAAAGTA
123868	121955	TAAAATAATTTACTAAAAGT
123869	121956	TTAAAATAATTTACTAAAAG
123870	121957	CTTAAAATAATTTACTAAAA
123871	121958	ACTTAAAATAATTTACTAAA
123872	121959	AACTTAAAATAATTTACTAA
123873	121960	TAACTTAAAATAATTTACTA
123874	121961	ATAACTTAAAATAATTTACT
123875	121962	AATAACTTAAAATAATTTAC
123876	121963	AAATAACTTAAAATAATTTA
123877	121964	TAAATAACTTAAAATAATTT
123878	121965	ATAAATAACTTAAAATAATT
123879	121966	TATAAATAACTTAAAATAAT
123880	121967	ATATAAATAACTTAAAATAA
123881	121968	TATATAAATAACTTAAAATA
123882	121969	ATATATAAATAACTTAAAAT
123883	121970	AATATATAAATAACTTAAAA
123884	121971	GAATATATAAATAACTTAAA
123885	121972	AGAATATATAAATAACTTAA
123886	121973	CAGAATATATAAATAACTTA
123887	121974	CCAGAATATATAAATAACTT
123888	121975	ACCAGAATATATAAATAACT
123889	121976	AACCAGAATATATAAATAAC
123890	121977	TAACCAGAATATATAAATAA
123891	121978	GTAACCAGAATATATAAATA
123892	121979	TGTAACCAGAATATATAAAT
123893	121980	TTGTAACCAGAATATATAAA
123894	121981	CTTGTAACCAGAATATATAA
123895	121982	ACTTGTAACCAGAATATATA
123896	121983	GACTTGTAACCAGAATATAT
123897	121984	GGACTTGTAACCAGAATATA
123898	121985	AGGACTTGTAACCAGAATAT
123899	121986	AAGGACTTGTAACCAGAATA
123900	121987	AAAGGACTTGTAACCAGAAT
123901	121988	GAAAGGACTTGTAACCAGAA
123902	121989	AGAAAGGACTTGTAACCAGA
123903	121990	GAGAAAGGACTTGTAACCAG
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123905	121992	CTGAGAAAGGACTTGTAACC
123906	121993	TCTGAGAAAGGACTTGTAAC
123907	121994	TTCTGAGAAAGGACTTGTAA
123908	121995	ATTCTGAGAAAGGACTTGTA
123909	121996	TATTCTGAGAAAGGACTTGT
123910	121997	ATATTCTGAGAAAGGACTTG
123911	121998	AATATTCTGAGAAAGGACTT
123912	121999	CAATATTCTGAGAAAGGACT
123913	122000	ACAATATTCTGAGAAAGGAC
123914	122001	CACAATATTCTGAGAAAGGA
123915	122002	TCACAATATTCTGAGAAAGG
123916	122003	TTCACAATATTCTGAGAAAG
123917	122004	ATTCACAATATTCTGAGAAA
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25626	23713	CACGGTGGTGGGCGCCTGTA
25627	23714	GCACGGTGGTGGGCGCCTGT
25628	23715	GGCACGGTGGTGGGCGCCTG
25629	23716	AGGCACGGTGGTGGGCGCCT
25630	23717	CAGGCACGGTGGTGGGCGCC
25631	23718	CCAGGCACGGTGGTGGGCGC
25632	23719	GCCAGGCACGGTGGTGGGCG
25633	23720	AGCCAGGCACGGTGGTGGGC
25634	23721	TAGCCAGGCACGGTGGTGGG
25635	23722	TTAGCCAGGCACGGTGGTGG
25636	23723	ATTAGCCAGGCACGGTGGTG
25637	23724	AATTAGCCAGGCACGGTGGT
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25640	23727	AAAAATTAGCCAGGCACGGT
25641	23728	CAAAAATTAGCCAGGCACGG
25642	23729	ACAAAAATTAGCCAGGCACG
25643	23730	TACAAAAATTAGCCAGGCAC
25644	23731	ATACAAAAATTAGCCAGGCA
25645	23732	AATACAAAAATTAGCCAGGC
25646	23733	AAATACAAAAATTAGCCAGG
25647	23734	AAAATACAAAAATTAGCCAG
25648	23735	AAAAATACAAAAATTAGCCA
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25655	23742	CTCTACTAAAAATACAAAAA
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25661	23748	CCCTGTCTCTACTAAAAATA
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25664	23751	AAACCCTGTCTCTACTAAAA
25665	23752	GAAACCCTGTCTCTACTAAA
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25667	23754	GTGAAACCCTGTCTCTACTA
25668	23755	GGTGAAACCCTGTCTCTACT
25669	23756	TGGTGAAACCCTGTCTCTAC
25670	23757	ATGGTGAAACCCTGTCTCTA
25671	23758	GATGGTGAAACCCTGTCTCT
25672	23759	AGATGGTGAAACCCTGTCTC
25673	23760	AAGATGGTGAAACCCTGTCT
25674	23761	CAAGATGGTGAAACCCTGTC
25675	23762	CCAAGATGGTGAAACCCTGT
25676	23763	GCCAAGATGGTGAAACCCTG
25677	23764	GGCCAAGATGGTGAAACCCT
25678	23765	TGGCCAAGATGGTGAAACCC
25679	23766	CTGGCCAAGATGGTGAAACC
25680	23767	CCTGGCCAAGATGGTGAAAC
25681	23768	GCCTGGCCAAGATGGTGAAA
25682	23769	AGCCTGGCCAAGATGGTGAA
25683	23770	CAGCCTGGCCAAGATGGTGA
25684	23771	ACAGCCTGGCCAAGATGGTG
25685	23772	AACAGCCTGGCCAAGATGGT
25686	23773	GAACAGCCTGGCCAAGATGG
25687	23774	AGAACAGCCTGGCCAAGATG
25688	23775	CAGAACAGCCTGGCCAAGAT
25689	23776	CCAGAACAGCCTGGCCAAGA
25690	23777	TCCAGAACAGCCTGGCCAAG
25691	23778	TTCCAGAACAGCCTGGCCAA
25692	23779	GTTCCAGAACAGCCTGGCCA
25693	23780	AGTTCCAGAACAGCCTGGCC
25694	23781	GAGTTCCAGAACAGCCTGGC
25695	23782	GGAGTTCCAGAACAGCCTGG

74772	72859	CCATATTCATGTCTATGTAC
74773	72860	TCCATATTCATGTCTATGTA
74774	72861	TTCCATATTCATGTCTATGT
74775	72862	TTTCCATATTCATGTCTATG
74776	72863	CTTTCCATATTCATGTCTAT
74777	72864	ACTTTCCATATTCATGTCTA
74778	72865	AACTTTCCATATTCATGTCT
74779	72866	TAACTTTCCATATTCATGTC
74780	72867	TTAACTTTCCATATTCATGT
74781	72868	TTTAACTTTCCATATTCATG
74782	72869	TTTTAACTTTCCATATTCAT
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74785	72872	TGTTTTTAACTTTCCATATT
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74787	72874	TTTGTTTTTAACTTTCCATA
74788	72875	TTTTGTTTTTAACTTTCCAT
74789	72876	ATTTTGTTTTTAACTTTCCA
74790	72877	GATTTTGTTTTTAACTTTCC
74791	72878	GGATTTTGTTTTTAACTTTC
74792	72879	TGGATTTTGTTTTTAACTTT
74793	72880	GTGGATTTTGTTTTTAACTT
74794	72881	TGTGGATTTTGTTTTTAACT
74795	72882	ATGTGGATTTTGTTTTTAAC
74796	72883	TATGTGGATTTTGTTTTTAA
74797	72884	ATATGTGGATTTTGTTTTTA
74798	72885	TATATGTGGATTTTGTTTTT
74799	72886	ATATATGTGGATTTTGTTTT
74800	72887	AATATATGTGGATTTTGTTT
74801	72888	AAATATATGTGGATTTTGTT
74802	72889	CAAATATATGTGGATTTTGT
74803	72890	CCAAATATATGTGGATTTTG
74804	72891	GCCAAATATATGTGGATTTT
74805	72892	AGCCAAATATATGTGGATTT
74806	72893	CAGCCAAATATATGTGGATT
74807	72894	GCAGCCAAATATATGTGGAT
74808	72895	TGCAGCCAAATATATGTGGA
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74810	72897	CTTGCAGCCAAATATATGTG
74811	72898	ACTTGCAGCCAAATATATGT
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74819	72906	TTCGGAGTACTTGCAGCCAA
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74821	72908	CCTTCGGAGTACTTGCAGCC
74822	72909	ACCTTCGGAGTACTTGCAGC
74823	72910	TACCTTCGGAGTACTTGCAG
74824	72911	ATACCTTCGGAGTACTTGCA
74825	72912	TATACCTTCGGAGTACTTGC
74826	72913	ATATACCTTCGGAGTACTTG
74827	72914	GATATACCTTCGGAGTACTT
74828	72915	AGATATACCTTCGGAGTACT
74829	72916	TAGATATACCTTCGGAGTAC
74830	72917	TTAGATATACCTTCGGAGTA
74831	72918	ATTAGATATACCTTCGGAGT
74832	72919	AATTAGATATACCTTCGGAG
74833	72920	TAATTAGATATACCTTCGGA
74834	72921	CTAATTAGATATACCTTCGG
74835	72922	ACTAATTAGATATACCTTCG
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74838	72925	TGCACTAATTAGATATACCT
74839	72926	ATGCACTAATTAGATATACC
74840	72927	GATGCACTAATTAGATATAC
74841	72928	GGATGCACTAATTAGATATA
74842	72929	TGGATGCACTAATTAGATAT

123919	122006	ATATTCACAATATTCTGAGA
123920	122007	AATATTCACAATATTCTGAG
123921	122008	AAATATTCACAATATTCTGA
123922	122009	AAAATATTCACAATATTCTG
123923	122010	GAAAATATTCACAATATTCT
123924	122011	AGAAAATATTCACAATATTC
123925	122012	GAGAAAATATTCACAATATT
123926	122013	GGAGAAAATATTCACAATAT
123927	122014	GGGAGAAAATATTCACAATA
123928	122015	TGGGAGAAAATATTCACAAT
123929	122016	CTGGGAGAAAATATTCACAA
123930	122017	ACTGGGAGAAAATATTCACA
123931	122018	GACTGGGAGAAAATATTCAC
123932	122019	AGACTGGGAGAAAATATTCA
123933	122020	CAGACTGGGAGAAAATATTC
123934	122021	GCAGACTGGGAGAAAATATT
123935	122022	CGCAGACTGGGAGAAAATAT
123936	122023	CCGCAGACTGGGAGAAAATA
123937	122024	ACCGCAGACTGGGAGAAAAT
123938	122025	AACCGCAGACTGGGAGAAAA
123939	122026	AAACCGCAGACTGGGAGAAA
123940	122027	AAAACCGCAGACTGGGAGAA
123941	122028	AAAAACCGCAGACTGGGAGA
123942	122029	AAAAAACCGCAGACTGGGAG
123943	122030	AAAAAAACCGCAGACTGGGA
123944	122031	AAAAAAAACCGCAGACTGGG
123945	122032	CAAAAAAAACCGCAGACTGG
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123947	122034	TTCAAAAAAAACCGCAGACT
123948	122035	CTTCAAAAAAAACCGCAGAC
123949	122036	TCTTCAAAAAAAACCGCAGA
123950	122037	CTCTTCAAAAAAAACCGCAG
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123952	122039	GGCTCTTCAAAAAAAACCGC
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123954	122041	CTGGCTCTTCAAAAAAAACC
123955	122042	ACTGGCTCTTCAAAAAAAAC
123956	122043	TACTGGCTCTTCAAAAAAAA
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123962	122049	TAACAATACTGGCTCTTCAA
123963	122050	TTAACAATACTGGCTCTTCA
123964	122051	ATTAACAATACTGGCTCTTC
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123967	122054	AAAATTAACAATACTGGCTC
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123969	122056	TTAAAATTAACAATACTGGC
123970	122057	ATTAAAATTAACAATACTGG
123971	122058	CATTAAAATTAACAATACTG
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123973	122060	TTCATTAAAATTAACAATAC
123974	122061	CTTCATTAAAATTAACAATA
123975	122062	GCTTCATTAAAATTAACAAT
123976	122063	GGCTTCATTAAAATTAACAA
123977	122064	AGGCTTCATTAAAATTAACA
123978	122065	AAGGCTTCATTAAAATTAAC
123979	122066	TAAGGCTTCATTAAAATTAA
123980	122067	ATAAGGCTTCATTAAAATTA
123981	122068	AATAAGGCTTCATTAAAATT
123982	122069	AAATAAGGCTTCATTAAAAT
123983	122070	TAAATAAGGCTTCATTAAAA
123984	122071	ATAAATAAGGCTTCATTAAA
123985	122072	GATAAATAAGGCTTCATTAA
123986	122073	TGATAAATAAGGCTTCATTA
123987	122074	TTGATAAATAAGGCTTCATT
123988	122075	CTTGATAAATAAGGCTTCAT
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25696	23783	AGGAGTTCCAGAACAGCCTG
25697	23784	CAGGAGTTCCAGAACAGCCT
25698	23785	TCAGGAGTTCCAGAACAGCC
25699	23786	GTCAGGAGTTCCAGAACAGC
25700	23787	GGTCAGGAGTTCCAGAACAG
25701	23788	AGGTCAGGAGTTCCAGAACA
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25703	23790	TGAGGTCAGGAGTTCCAGAA
25704	23791	ATGAGGTCAGGAGTTCCAGA
25705	23792	CATGAGGTCAGGAGTTCCAG
25706	23793	TCATGAGGTCAGGAGTTCCA
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25708	23795	GATCATGAGGTCAGGAGTTC
25709	23796	GGATCATGAGGTCAGGAGTT
25710	23797	TGGATCATGAGGTCAGGAGT
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25712	23799	GGTGGATCATGAGGTCAGGA
25713	23800	GGGTGGATCATGAGGTCAGG
25714	23801	CGGGTGGATCATGAGGTCAG
25715	23802	GCGGGTGGATCATGAGGTCA
25716	23803	GGCGGGTGGATCATGAGGTC
25717	23804	AGGCGGGTGGATCATGAGGT
25718	23805	AAGGCGGGTGGATCATGAGG
25719	23806	CAAGGCGGGTGGATCATGAG
25720	23807	CCAAGGCGGGTGGATCATGA
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25723	23810	AGGCCAAGGCGGGTGGATCA
25724	23811	GAGGCCAAGGCGGGTGGATC
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25728	23815	TTGGGAGGCCAAGGCGGGTG
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25733	23820	GCACTTTGGGAGGCCAAGGC
25734	23821	AGCACTTTGGGAGGCCAAGG
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25752	23839	GCTCACGCCTGTAATCCCAG
25753	23840	GGCTCACGCCTGTAATCCCA
25754	23841	TGGCTCACGCCTGTAATCCC
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25756	23843	AGTGGCTCACGCCTGTAATC
25757	23844	CAGTGGCTCACGCCTGTAAT
25758	23845	GCAGTGGCTCACGCCTGTAA
25759	23846	CGCAGTGGCTCACGCCTGTA
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25761	23848	GGCGCAGTGGCTCACGCCTG
25762	23849	AGGCGCAGTGGCTCACGCCT
25763	23850	CAGGCGCAGTGGCTCACGCC
25764	23851	CCAGGCGCAGTGGCTCACGC
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74843	72930	ATGGATGCACTAATTAGATA
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74846	72933	TTAATGGATGCACTAATTAG
74847	72934	TTTAATGGATGCACTAATTA
74848	72935	GTTTAATGGATGCACTAATT
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74893	72980	GATTACAGGTGTGAGCAACC
74894	72981	GGATTACAGGTGTGAGCAAC
74895	72982	GGGATTACAGGTGTGAGCAA
74896	72983	TGGGATTACAGGTGTGAGCA
74897	72984	CTGGGATTACAGGTGTGAGC
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74901	72988	AGTGCTGGGATTACAGGTGT
74902	72989	AAGTGCTGGGATTACAGGTG
74903	72990	AAAGTGCTGGGATTACAGGT
74904	72991	CAAAGTGCTGGGATTACAGG
74905	72992	CCAAAGTGCTGGGATTACAG
74906	72993	CCCAAAGTGCTGGGATTACA
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123990	122077	AGCTTGATAAATAAGGCTTC
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123993	122080	AAAAGCTTGATAAATAAGGC
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123995	122082	AGAAAAGCTTGATAAATAAG
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123997	122084	AGAGAAAAGCTTGATAAATA
123998	122085	AAGAGAAAAGCTTGATAAAT
123999	122086	TAAGAGAAAAGCTTGATAAA
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124001	122088	CTTAAGAGAAAAGCTTGATA
124002	122089	CCTTAAGAGAAAAGCTTGAT
124003	122090	ACCTTAAGAGAAAAGCTTGA
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124007	122094	ATGAACCTTAAGAGAAAAGC
124008	122095	CATGAACCTTAAGAGAAAAG
124009	122096	GCATGAACCTTAAGAGAAAA
124010	122097	AGCATGAACCTTAAGAGAAA
124011	122098	AAGCATGAACCTTAAGAGAA
124012	122099	AAAGCATGAACCTTAAGAGA
124013	122100	AAAAGCATGAACCTTAAGAG
124014	122101	AAAAAGCATGAACCTTAAGA
124015	122102	AAAAAAGCATGAACCTTAAG
124016	122103	CAAAAAAGCATGAACCTTAA
124017	122104	ACAAAAAAGCATGAACCTTA
124018	122105	TACAAAAAAGCATGAACCTT
124019	122106	ATACAAAAAAGCATGAACCT
124020	122107	GATACAAAAAAGCATGAACC
124021	122108	TGATACAAAAAAGCATGAAC
124022	122109	ATGATACAAAAAAGCATGAA
124023	122110	TATGATACAAAAAAGCATGA
124024	122111	TTATGATACAAAAAAGCATG
124025	122112	ATTATGATACAAAAAAGCAT
124026	122113	TATTATGATACAAAAAAGCA
124027	122114	TTATTATGATACAAAAAAGC
124028	122115	CTTATTATGATACAAAAAAG
124029	122116	TCTTATTATGATACAAAAAA
124030	122117	TTCTTATTATGATACAAAAA
124031	122118	TTTCTTATTATGATACAAAA
124032	122119	ATTTCTTATTATGATACAAA
124033	122120	GATTTCTTATTATGATACAA
124034	122121	AGATTTCTTATTATGATACA
124035	122122	AAGATTTCTTATTATGATAC
124036	122123	AAAGATTTCTTATTATGATA
124037	122124	AAAAGATTTCTTATTATGAT
124038	122125	TAAAAGATTTCTTATTATGA
124039	122126	GTAAAAGATTTCTTATTATG
124040	122127	CGTAAAAGATTTCTTATTAT
124041	122128	ACGTAAAAGATTTCTTATTA
124042	122129	TACGTAAAAGATTTCTTATT
124043	122130	GTACGTAAAAGATTTCTTAT
124044	122131	GGTACGTAAAAGATTTCTTA
124045	122132	GGGTACGTAAAAGATTTCTT
124046	122133	AGGGTACGTAAAAGATTTCT
124047	122134	TAGGGTACGTAAAAGATTTC
124048	122135	CTAGGGTACGTAAAAGATTT
124049	122136	CCTAGGGTACGTAAAAGATT
124050	122137	ACCTAGGGTACGTAAAAGAT
124051	122138	AACCTAGGGTACGTAAAAGA
124052	122139	TAACCTAGGGTACGTAAAAG
124053	122140	ATAACCTAGGGTACGTAAAA
124054	122141	CATAACCTAGGGTACGTAAA
124055	122142	TCATAACCTAGGGTACGTAA
124056	122143	TTCATAACCTAGGGTACGTA
124057	122144	ATTCATAACCTAGGGTACGT
124058	122145	CATTCATAACCTAGGGTACG
124059	122146	ACATTCATAACCTAGGGTAC
124060	122147	AACATTCATAACCTAGGGTA

25767	23854	CAGCCAGGCGCAGTGGCTCA
25768	23855	TCAGCCAGGCGCAGTGGCTC
25769	23856	GTCAGCCAGGCGCAGTGGCT
25770	23857	AGTCAGCCAGGCGCAGTGGC
25771	23858	TAGTCAGCCAGGCGCAGTGG
25772	23859	ATAGTCAGCCAGGCGCAGTG
25773	23860	AATAGTCAGCCAGGCGCAGT
25774	23861	CAATAGTCAGCCAGGCGCAG
25775	23862	CCAATAGTCAGCCAGGCGCA
25776	23863	ACCAATAGTCAGCCAGGCGC
25777	23864	AACCAATAGTCAGCCAGGCG
25778	23865	AAACCAATAGTCAGCCAGGC
25779	23866	AAAACCAATAGTCAGCCAGG
25780	23867	TAAAACCAATAGTCAGCCAG
25781	23868	ATAAAACCAATAGTCAGCCA
25782	23869	AATAAAACCAATAGTCAGCC
25783	23870	TAATAAAACCAATAGTCAGC
25784	23871	ATAATAAAACCAATAGTCAG
25785	23872	AATAATAAAACCAATAGTCA
25786	23873	TAATAATAAAACCAATAGTC
25787	23874	TTAATAATAAAACCAATAGT
25788	23875	CTTAATAATAAAACCAATAG
25789	23876	GCTTAATAATAAAACCAATA
25790	23877	TGCTTAATAATAAAACCAAT
25791	23878	CTGCTTAATAATAAAACCAA
25792	23879	ACTGCTTAATAATAAAACCA
25793	23880	TACTGCTTAATAATAAAACC
25794	23881	CTACTGCTTAATAATAAAAC
25795	23882	ACTACTGCTTAATAATAAAA
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25798	23885	ACTACTACTGCTTAATAATA
25799	23886	AACTACTACTGCTTAATAAT
25800	23887	CAACTACTACTGCTTAATAA
25801	23888	TCAACTACTACTGCTTAATA
25802	23889	GTCAACTACTACTGCTTAAT
25803	23890	GGTCAACTACTACTGCTTAA
25804	23891	GGGTCAACTACTACTGCTTA
25805	23892	AGGGTCAACTACTACTGCTT
25806	23893	CAGGGTCAACTACTACTGCT
25807	23894	ACAGGGTCAACTACTACTGC
25808	23895	GACAGGGTCAACTACTACTG
25809	23896	TGACAGGGTCAACTACTACT
25810	23897	ATGACAGGGTCAACTACTAC
25811	23898	CATGACAGGGTCAACTACTA
25812	23899	ACATGACAGGGTCAACTACT
25813	23900	TACATGACAGGGTCAACTAC
25814	23901	CTACATGACAGGGTCAACTA
25815	23902	TCTACATGACAGGGTCAACT
25816	23903	TTCTACATGACAGGGTCAAC
25817	23904	TTTCTACATGACAGGGTCAA
25818	23905	CTTTCTACATGACAGGGTCA
25819	23906	GCTTTCTACATGACAGGGTC
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25822	23909	CATGCTTTCTACATGACAGG
25823	23910	CCATGCTTTCTACATGACAG
25824	23911	GCCATGCTTTCTACATGACA
25825	23912	TGCCATGCTTTCTACATGAC
25826	23913	ATGCCATGCTTTCTACATGA
25827	23914	AATGCCATGCTTTCTACATG
25828	23915	AAATGCCATGCTTTCTACAT
25829	23916	TAAATGCCATGCTTTCTACA
25830	23917	ATAAATGCCATGCTTTCTAC
25831	23918	TATAAATGCCATGCTTTCTA
25832	23919	CTATAAATGCCATGCTTTCT
25833	23920	CCTATAAATGCCATGCTTTC
25834	23921	GCCTATAAATGCCATGCTTT
25835	23922	TGCCTATAAATGCCATGCTT
25836	23923	ATGCCTATAAATGCCATGCT
25837	23924	TATGCCTATAAATGCCATGC

74914	73001	CTTGGCCTCCCAAAGTGCTG
74915	73002	CCTTGGCCTCCCAAAGTGCT
74916	73003	ACCTTGGCCTCCCAAAGTGC
74917	73004	CACCTTGGCCTCCCAAAGTG
74918	73005	CCACCTTGGCCTCCCAAAGT
74919	73006	CCCACCTTGGCCTCCCAAAG
74920	73007	ACCCACCTTGGCCTCCCAAA
74921	73008	CACCCACCTTGGCCTCCCAA
74922	73009	CCACCCACCTTGGCCTCCCA
74923	73010	TCCACCCACCTTGGCCTCCC
74924	73011	ATCCACCCACCTTGGCCTCC
74925	73012	GATCCACCCACCTTGGCCTC
74926	73013	TGATCCACCCACCTTGGCCT
74927	73014	GTGATCCACCCACCTTGGCC
74928	73015	GGTGATCCACCCACCTTGGC
74929	73016	AGGTGATCCACCCACCTTGG
74930	73017	CAGGTGATCCACCCACCTTG
74931	73018	TCAGGTGATCCACCCACCTT
74932	73019	CTCAGGTGATCCACCCACCT
74933	73020	CCTCAGGTGATCCACCCACC
74934	73021	ACCTCAGGTGATCCACCCAC
74935	73022	GACCTCAGGTGATCCACCCA
74936	73023	TGACCTCAGGTGATCCACCC
74937	73024	CTGACCTCAGGTGATCCACC
74938	73025	CCTGACCTCAGGTGATCCAC
74939	73026	TCCTGACCTCAGGTGATCCA
74940	73027	CTCCTGACCTCAGGTGATCC
74941	73028	ACTCCTGACCTCAGGTGATC
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74949	73036	GGTCTCGAACTCCTGACCTC
74950	73037	TGGTCTCGAACTCCTGACCT
74951	73038	CTGGTCTCGAACTCCTGACC
74952	73039	GCTGGTCTCGAACTCCTGAC
74953	73040	GGCTGGTCTCGAACTCCTGA
74954	73041	AGGCTGGTCTCGAACTCCTG
74955	73042	CAGGCTGGTCTCGAACTCCT
74956	73043	CCAGGCTGGTCTCGAACTCC
74957	73044	GCCAGGCTGGTCTCGAACTC
74958	73045	GGCCAGGCTGGTCTCGAACT
74959	73046	TGGCCAGGCTGGTCTCGAAC
74960	73047	TTGGCCAGGCTGGTCTCGAA
74961	73048	GTTGGCCAGGCTGGTCTCGA
74962	73049	TGTTGGCCAGGCTGGTCTCG
74963	73050	ATGTTGGCCAGGCTGGTCTC
74964	73051	CATGTTGGCCAGGCTGGTCT
74965	73052	CCATGTTGGCCAGGCTGGTC
74966	73053	ACCATGTTGGCCAGGCTGGT
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74968	73055	TCACCATGTTGGCCAGGCTG
74969	73056	TTCACCATGTTGGCCAGGCT
74970	73057	TTTCACCATGTTGGCCAGGC
74971	73058	GTTTCACCATGTTGGCCAGG
74972	73059	GGTTTCACCATGTTGGCCAG
74973	73060	GGGTTTCACCATGTTGGCCA
74974	73061	AGGGTTTCACCATGTTGGCC
74975	73062	CAGGGTTTCACCATGTTGGC
74976	73063	ACAGGGTTTCACCATGTTGG
74977	73064	GACAGGGTTTCACCATGTTG
74978	73065	AGACAGGGTTTCACCATGTT
74979	73066	GAGACAGGGTTTCACCATGT
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74981	73068	CAGAGACAGGGTTTCACCAT
74982	73069	GCAGAGACAGGGTTTCACCA
74983	73070	AGCAGAGACAGGGTTTCACC
74984	73071	TAGCAGAGACAGGGTTTCAC

124061	122148	AAACATTCATAACCTAGGGT
124062	122149	AAAACATTCATAACCTAGGG
124063	122150	AAAAACATTCATAACCTAGG
124064	122151	TAAAAACATTCATAACCTAG
124065	122152	ATAAAAACATTCATAACCTA
124066	122153	CATAAAAACATTCATAACCT
124067	122154	CCATAAAAACATTCATAACC
124068	122155	ACCATAAAAACATTCATAAC
124069	122156	AACCATAAAAACATTCATAA
124070	122157	TAACCATAAAAACATTCATA
124071	122158	CTAACCATAAAAACATTCAT
124072	122159	CCTAACCATAAAAACATTCA
124073	122160	ACCTAACCATAAAAACATTC
124074	122161	TACCTAACCATAAAAACATT
124075	122162	ATACCTAACCATAAAAACAT
124076	122163	TATACCTAACCATAAAAACA
124077	122164	ATATACCTAACCATAAAAAC
124078	122165	CATATACCTAACCATAAAAA
124079	122166	CCATATACCTAACCATAAAA
124080	122167	ACCATATACCTAACCATAAA
124081	122168	AACCATATACCTAACCATAA
124082	122169	CAACCATATACCTAACCATA
124083	122170	TCAACCATATACCTAACCAT
124084	122171	ATCAACCATATACCTAACCA
124085	122172	AATCAACCATATACCTAACC
124086	122173	AAATCAACCATATACCTAAC
124087	122174	GAAATCAACCATATACCTAA
124088	122175	TGAAATCAACCATATACCTA
124089	122176	CTGAAATCAACCATATACCT
124090	122177	CCTGAAATCAACCATATACC
124091	122178	ACCTGAAATCAACCATATAC
124092	122179	AACCTGAAATCAACCATATA
124093	122180	TAACCTGAAATCAACCATAT
124094	122181	CTAACCTGAAATCAACCATA
124095	122182	CCTAACCTGAAATCAACCAT
124096	122183	ACCTAACCTGAAATCAACCA
124097	122184	AACCTAACCTGAAATCAACC
124098	122185	AAACCTAACCTGAAATCAAC
124099	122186	AAAACCTAACCTGAAATCAA
124100	122187	CAAAACCTAACCTGAAATCA
124101	122188	ACAAAACCTAACCTGAAATC
124102	122189	CACAAAACCTAACCTGAAAT
124103	122190	ACACAAAACCTAACCTGAAA
124104	122191	TACACAAAACCTAACCTGAA
124105	122192	CTACACAAAACCTAACCTGA
124106	122193	CCTACACAAAACCTAACCTG
124107	122194	CCCTACACAAAACCTAACCT
124108	122195	ACCCTACACAAAACCTAACC
124109	122196	CACCCTACACAAAACCTAAC
124110	122197	ACACCCTACACAAAACCTAA
124111	122198	CACACCCTACACAAAACCTA
124112	122199	TCACACCCTACACAAAACCT
124113	122200	ATCACACCCTACACAAAACC
124114	122201	CATCACACCCTACACAAAAC
124115	122202	ACATCACACCCTACACAAAA
124116	122203	TACATCACACCCTACACAAA
124117	122204	TTACATCACACCCTACACAA
124118	122205	TTTACATCACACCCTACACA
124119	122206	CTTTACATCACACCCTACAC
124120	122207	CCTTTACATCACACCCTACA
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124122	122209	GACCTTTACATCACACCCTA
124123	122210	AGACCTTTACATCACACCCT
124124	122211	TAGACCTTTACATCACACCC
124125	122212	CTAGACCTTTACATCACACC
124126	122213	GCTAGACCTTTACATCACAC
124127	122214	AGCTAGACCTTTACATCACA
124128	122215	AAGCTAGACCTTTACATCAC
124129	122216	GAAGCTAGACCTTTACATCA
124130	122217	TGAAGCTAGACCTTTACATC
124131	122218	ATGAAGCTAGACCTTTACAT

25838	23925	GTATGCCTATAAATGCCATG
25839	23926	GGTATGCCTATAAATGCCAT
25840	23927	TGGTATGCCTATAAATGCCA
25841	23928	GTGGTATGCCTATAAATGCC
25842	23929	CGTGGTATGCCTATAAATGC
25843	23930	ACGTGGTATGCCTATAAATG
25844	23931	AACGTGGTATGCCTATAAAT
25845	23932	AAACGTGGTATGCCTATAAA
25846	23933	TAAACGTGGTATGCCTATAA
25847	23934	TTAAACGTGGTATGCCTATA
25848	23935	ATTAAACGTGGTATGCCTAT
25849	23936	AATTAAACGTGGTATGCCTA
25850	23937	AAATTAAACGTGGTATGCCT
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25852	23939	GGAAATTAAACGTGGTATGC
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25854	23941	GAGGAAATTAAACGTGGTAT
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25856	23943	GGGAGGAAATTAAACGTGGT
25857	23944	GGGGAGGAAATTAAACGTGG
25858	23945	AGGGGAGGAAATTAAACGTG
25859	23946	AAGGGGAGGAAATTAAACGT
25860	23947	AAAGGGGAGGAAATTAAACG
25861	23948	AAAAGGGGAGGAAATTAAAC
25862	23949	AAAAAGGGGAGGAAATTAAA
25863	23950	AAAAAAGGGGAGGAAATTAA
25864	23951	AAAAAAAGGGGAGGAAATTA
25865	23952	TAAAAAAAGGGGAGGAAATT
25866	23953	ATAAAAAAAGGGGAGGAAAT
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25874	23961	CTCCAAAAATAAAAAAAGGG
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25878	23965	GGTACTCCAAAAATAAAAAA
25879	23966	AGGTACTCCAAAAATAAAAA
25880	23967	GAGGTACTCCAAAAATAAAA
25881	23968	GGAGGTACTCCAAAAATAAA
25882	23969	AGGAGGTACTCCAAAAATAA
25883	23970	CAGGAGGTACTCCAAAAATA
25884	23971	GCAGGAGGTACTCCAAAAAT
25885	23972	AGCAGGAGGTACTCCAAAAA
25886	23973	AAGCAGGAGGTACTCCAAAA
25887	23974	CAAGCAGGAGGTACTCCAAA
25888	23975	ACAAGCAGGAGGTACTCCAA
25889	23976	CACAAGCAGGAGGTACTCCA
25890	23977	TCACAAGCAGGAGGTACTCC
25891	23978	CTCACAAGCAGGAGGTACTC
25892	23979	CCTCACAAGCAGGAGGTACT
25893	23980	GCCTCACAAGCAGGAGGTAC
25894	23981	AGCCTCACAAGCAGGAGGTA
25895	23982	AAGCCTCACAAGCAGGAGGT
25896	23983	CAAGCCTCACAAGCAGGAGG
25897	23984	CCAAGCCTCACAAGCAGGAG
25898	23985	CCCAAGCCTCACAAGCAGGA
25899	23986	TCCCAAGCCTCACAAGCAGG
25900	23987	TTCCCAAGCCTCACAAGCAG
25901	23988	ATTCCCAAGCCTCACAAGCA
25902	23989	TATTCCCAAGCCTCACAAGC
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25904	23991	TGTATTCCCAAGCCTCACAA
25905	23992	CTGTATTCCCAAGCCTCACA
25906	23993	ACTGTATTCCCAAGCCTCAC
25907	23994	TACTGTATTCCCAAGCCTCA
25908	23995	CTACTGTATTCCCAAGCCTC

74985	73072	TTAGCAGAGACAGGGTTTCA
74986	73073	TTTAGCAGAGACAGGGTTTC
74987	73074	TTTTAGCAGAGACAGGGTTT
74988	73075	TTTTTAGCAGAGACAGGGTT
74989	73076	ATTTTTAGCAGAGACAGGGT
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74993	73080	TTGTATTTTTAGCAGAGACA
74994	73081	TTTGTATTTTTAGCAGAGAC
74995	73082	GTTTGTATTTTTAGCAGAGA
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74997	73084	ATGTTTGTATTTTTAGCAGA
74998	73085	AATGTTTGTATTTTTAGCAG
74999	73086	TAATGTTTGTATTTTTAGCA
75000	73087	CTAATGTTTGTATTTTTAGC
75001	73088	GCTAATGTTTGTATTTTTAG
75002	73089	AGCTAATGTTTGTATTTTTA
75003	73090	CAGCTAATGTTTGTATTTTT
75004	73091	CCAGCTAATGTTTGTATTTT
75005	73092	CCCAGCTAATGTTTGTATTT
75006	73093	GCCCAGCTAATGTTTGTATT
75007	73094	CGCCCAGCTAATGTTTGTAT
75008	73095	ACGCCCAGCTAATGTTTGTA
75009	73096	CACGCCCAGCTAATGTTTGT
75010	73097	ACACGCCCAGCTAATGTTTG
75011	73098	AACACGCCCAGCTAATGTTT
75012	73099	CAACACGCCCAGCTAATGTT
75013	73100	CCAACACGCCCAGCTAATGT
75014	73101	ACCAACACGCCCAGCTAATG
75015	73102	CACCAACACGCCCAGCTAAT
75016	73103	CCACCAACACGCCCAGCTAA
75017	73104	CCCACCAACACGCCCAGCTA
75018	73105	GCCCACCAACACGCCCAGCT
75019	73106	CGCCCACCAACACGCCCAGC
75020	73107	GCGCCCACCAACACGCCCAG
75021	73108	GGCGCCCACCAACACGCCCA
75022	73109	AGGCGCCCACCAACACGCCC
75023	73110	CAGGCGCCCACCAACACGCC
75024	73111	ACAGGCGCCCACCAACACGC
75025	73112	TACAGGCGCCCACCAACACG
75026	73113	TTACAGGCGCCCACCAACAC
75027	73114	ATTACAGGCGCCCACCAACA
75028	73115	GATTACAGGCGCCCACCAAC
75029	73116	AGATTACAGGCGCCCACCAA
75030	73117	AAGATTACAGGCGCCCACCA
75031	73118	TAAGATTACAGGCGCCCACC
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75035	73122	TAGCTAAGATTACAGGCGCC
75036	73123	GTAGCTAAGATTACAGGCGC
75037	73124	AGTAGCTAAGATTACAGGCG
75038	73125	AAGTAGCTAAGATTACAGGC
75039	73126	CAAGTAGCTAAGATTACAGG
75040	73127	CCAAGTAGCTAAGATTACAG
75041	73128	CCCAAGTAGCTAAGATTACA
75042	73129	TCCCAAGTAGCTAAGATTAC
75043	73130	CTCCCAAGTAGCTAAGATTA
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75045	73132	GCCTCCCAAGTAGCTAAGAT
75046	73133	AGCCTCCCAAGTAGCTAAGA
75047	73134	CAGCCTCCCAAGTAGCTAAG
75048	73135	TCAGCCTCCCAAGTAGCTAA
75049	73136	CTCAGCCTCCCAAGTAGCTA
75050	73137	CCTCAGCCTCCCAAGTAGCT
75051	73138	GCCTCAGCCTCCCAAGTAGC
75052	73139	TGCCTCAGCCTCCCAAGTAG
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124132	122219	AATGAAGCTAGACCTTTACA
124133	122220	AAATGAAGCTAGACCTTTAC
124134	122221	AAAATGAAGCTAGACCTTTA
124135	122222	GAAAATGAAGCTAGACCTTT
124136	122223	AGAAAATGAAGCTAGACCTT
124137	122224	GAGAAAATGAAGCTAGACCT
124138	122225	GGAGAAAATGAAGCTAGACC
124139	122226	TGGAGAAAATGAAGCTAGAC
124140	122227	GTGGAGAAAATGAAGCTAGA
124141	122228	GGTGGAGAAAATGAAGCTAG
124142	122229	TGGTGGAGAAAATGAAGCTA
124143	122230	ATGGTGGAGAAAATGAAGCT
124144	122231	TATGGTGGAGAAAATGAAGC
124145	122232	TTATGGTGGAGAAAATGAAG
124146	122233	TTTATGGTGGAGAAAATGAA
124147	122234	ATTTATGGTGGAGAAAATGA
124148	122235	TATTTATGGTGGAGAAAATG
124149	122236	ATATTTATGGTGGAGAAAAT
124150	122237	AATATTTATGGTGGAGAAAA
124151	122238	AAATATTTATGGTGGAGAAA
124152	122239	TAAATATTTATGGTGGAGAA
124153	122240	GTAAATATTTATGGTGGAGA
124154	122241	AGTAAATATTTATGGTGGAG
124155	122242	GAGTAAATATTTATGGTGGA
124156	122243	CGAGTAAATATTTATGGTGG
124157	122244	CCGAGTAAATATTTATGGTG
124158	122245	ACCGAGTAAATATTTATGGT
124159	122246	AACCGAGTAAATATTTATGG
124160	122247	AAACCGAGTAAATATTTATG
124161	122248	GAAACCGAGTAAATATTTAT
124162	122249	AGAAACCGAGTAAATATTTA
124163	122250	GAGAAACCGAGTAAATATTT
124164	122251	AGAGAAACCGAGTAAATATT
124165	122252	CAGAGAAACCGAGTAAATAT
124166	122253	CCAGAGAAACCGAGTAAATA
124167	122254	GCCAGAGAAACCGAGTAAAT
124168	122255	TGCCAGAGAAACCGAGTAAA
124169	122256	GTGCCAGAGAAACCGAGTAA
124170	122257	GGTGCCAGAGAAACCGAGTA
124171	122258	TGGTGCCAGAGAAACCGAGT
124172	122259	CTGGTGCCAGAGAAACCGAG
124173	122260	GCTGGTGCCAGAGAAACCGA
124174	122261	GGCTGGTGCCAGAGAAACCG
124175	122262	AGGCTGGTGCCAGAGAAACC
124176	122263	GAGGCTGGTGCCAGAGAAAC
124177	122264	AGAGGCTGGTGCCAGAGAAA
124178	122265	CAGAGGCTGGTGCCAGAGAA
124179	122266	ACAGAGGCTGGTGCCAGAGA
124180	122267	AACAGAGGCTGGTGCCAGAG
124181	122268	AAACAGAGGCTGGTGCCAGA
124182	122269	AAAACAGAGGCTGGTGCCAG
124183	122270	GAAAACAGAGGCTGGTGCCA
124184	122271	GGAAAACAGAGGCTGGTGCC
124185	122272	TGGAAAACAGAGGCTGGTGC
124186	122273	ATGGAAAACAGAGGCTGGTG
124187	122274	AATGGAAAACAGAGGCTGGT
124188	122275	CAATGGAAAACAGAGGCTGG
124189	122276	CCAATGGAAAACAGAGGCTG
124190	122277	ACCAATGGAAAACAGAGGCT
124191	122278	CACCAATGGAAAACAGAGGC
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124193	122280	GCCACCAATGGAAAACAGAG
124194	122281	AGCCACCAATGGAAAACAGA
124195	122282	AAGCCACCAATGGAAAACAG
124196	122283	AAAGCCACCAATGGAAAACA
124197	122284	TAAAGCCACCAATGGAAAAC
124198	122285	ATAAAGCCACCAATGGAAAA
124199	122286	AATAAAGCCACCAATGGAAA
124200	122287	AAATAAAGCCACCAATGGAA
124201	122288	AAAATAAAGCCACCAATGGA
124202	122289	AAAAATAAAGCCACCAATGG

25909	23996	ACTACTGTATTCCCAAGCCT
25910	23997	CACTACTGTATTCCCAAGCC
25911	23998	TCACTACTGTATTCCCAAGC
25912	23999	TTCACTACTGTATTCCCAAG
25913	24000	ATTCACTACTGTATTCCCAA
25914	24001	TATTCACTACTGTATTCCCA
25915	24002	TTATTCACTACTGTATTCCC
25916	24003	CTTATTCACTACTGTATTCC
25917	24004	GCTTATTCACTACTGTATTC
25918	24005	GGCTTATTCACTACTGTATT
25919	24006	TGGCTTATTCACTACTGTAT
25920	24007	CTGGCTTATTCACTACTGTA
25921	24008	TCTGGCTTATTCACTACTGT
25922	24009	ATCTGGCTTATTCACTACTG
25923	24010	CATCTGGCTTATTCACTACT
25924	24011	TCATCTGGCTTATTCACTAC
25925	24012	CTCATCTGGCTTATTCACTA
25926	24013	CCTCATCTGGCTTATTCACT
25927	24014	ACCTCATCTGGCTTATTCAC
25928	24015	GACCTCATCTGGCTTATTCA
25929	24016	AGACCTCATCTGGCTTATTC
25930	24017	GAGACCTCATCTGGCTTATT
25931	24018	AGAGACCTCATCTGGCTTAT
25932	24019	GAGAGACCTCATCTGGCTTA
25933	24020	AGAGAGACCTCATCTGGCTT
25934	24021	GAGAGAGACCTCATCTGGCT
25935	24022	AGAGAGAGACCTCATCTGGC
25936	24023	AAGAGAGAGACCTCATCTGG
25937	24024	AAAGAGAGAGACCTCATCTG
25938	24025	AAAAGAGAGAGACCTCATCT
25939	24026	AAAAAGAGAGAGACCTCATC
25940	24027	CAAAAAGAGAGAGACCTCAT
25941	24028	CCAAAAAGAGAGAGACCTCA
25942	24029	TCCAAAAAGAGAGAGACCTC
25943	24030	CTCCAAAAAGAGAGAGACCT
25944	24031	GCTCCAAAAAGAGAGAGACC
25945	24032	AGCTCCAAAAAGAGAGAGAC
25946	24033	AAGCTCCAAAAAGAGAGAGA
25947	24034	TAAGCTCCAAAAAGAGAGAG
25948	24035	ATAAGCTCCAAAAAGAGAGA
25949	24036	CATAAGCTCCAAAAAGAGAG
25950	24037	ACATAAGCTCCAAAAAGAGA
25951	24038	CACATAAGCTCCAAAAAGAG
25952	24039	CCACATAAGCTCCAAAAAGA
25953	24040	ACCACATAAGCTCCAAAAAG
25954	24041	TACCACATAAGCTCCAAAAA
25955	24042	CTACCACATAAGCTCCAAAA
25956	24043	ACTACCACATAAGCTCCAAA
25957	24044	TACTACCACATAAGCTCCAA
25958	24045	ATACTACCACATAAGCTCCA
25959	24046	TATACTACCACATAAGCTCC
25960	24047	CTATACTACCACATAAGCTC
25961	24048	TCTATACTACCACATAAGCT
25962	24049	GTCTATACTACCACATAAGC
25963	24050	AGTCTATACTACCACATAAG
25964	24051	TAGTCTATACTACCACATAA
25965	24052	CTAGTCTATACTACCACATA
25966	24053	CCTAGTCTATACTACCACAT
25967	24054	GCCTAGTCTATACTACCACA
25968	24055	TGCCTAGTCTATACTACCAC
25969	24056	CTGCCTAGTCTATACTACCA
25970	24057	TCTGCCTAGTCTATACTACC
25971	24058	TTCTGCCTAGTCTATACTAC
25972	24059	TTTCTGCCTAGTCTATACTA
25973	24060	CTTTCTGCCTAGTCTATACT
25974	24061	ACTTTCTGCCTAGTCTATAC
25975	24062	AACTTTCTGCCTAGTCTATA
25976	24063	GAACTTTCTGCCTAGTCTAT
25977	24064	AGAACTTTCTGCCTAGTCTA
25978	24065	GAGAACTTTCTGCCTAGTCT
25979	24066	TGAGAACTTTCTGCCTAGTC

75056	73143	CTCCTGCCTCAGCCTCCCAA
75057	73144	TCTCCTGCCTCAGCCTCCCA
75058	73145	ATCTCCTGCCTCAGCCTCCC
75059	73146	AATCTCCTGCCTCAGCCTCC
75060	73147	GAATCTCCTGCCTCAGCCTC
75061	73148	GGAATCTCCTGCCTCAGCCT
75062	73149	GGGAATCTCCTGCCTCAGCC
75063	73150	AGGGAATCTCCTGCCTCAGC
75064	73151	AAGGGAATCTCCTGCCTCAG
75065	73152	CAAGGGAATCTCCTGCCTCA
75066	73153	TCAAGGGAATCTCCTGCCTC
75067	73154	TTCAAGGGAATCTCCTGCCT
75068	73155	GTTCAAGGGAATCTCCTGCC
75069	73156	GGTTCAAGGGAATCTCCTGC
75070	73157	AGGTTCAAGGGAATCTCCTG
75071	73158	CAGGTTCAAGGGAATCTCCT
75072	73159	CCAGGTTCAAGGGAATCTCC
75073	73160	TCCAGGTTCAAGGGAATCTC
75074	73161	TTCCAGGTTCAAGGGAATCT
75075	73162	CTTCCAGGTTCAAGGGAATC
75076	73163	CCTTCCAGGTTCAAGGGAAT
75077	73164	ACCTTCCAGGTTCAAGGGAA
75078	73165	CACCTTCCAGGTTCAAGGGA
75079	73166	CCACCTTCCAGGTTCAAGGG
75080	73167	TCCACCTTCCAGGTTCAAGG
75081	73168	ATCCACCTTCCAGGTTCAAG
75082	73169	CATCCACCTTCCAGGTTCAA
75083	73170	ACATCCACCTTCCAGGTTCA
75084	73171	AACATCCACCTTCCAGGTTC
75085	73172	CAACATCCACCTTCCAGGTT
75086	73173	GCAACATCCACCTTCCAGGT
75087	73174	TGCAACATCCACCTTCCAGG
75088	73175	CTGCAACATCCACCTTCCAG
75089	73176	CCTGCAACATCCACCTTCCA
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75091	73178	TCCCTGCAACATCCACCTTC
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75093	73180	GCTCCCTGCAACATCCACCT
75094	73181	GGCTCCCTGCAACATCCACC
75095	73182	CGGCTCCCTGCAACATCCAC
75096	73183	TCGGCTCCCTGCAACATCCA
75097	73184	CTCGGCTCCCTGCAACATCC
75098	73185	TCTCGGCTCCCTGCAACATC
75099	73186	ATCTCGGCTCCCTGCAACAT
75100	73187	CATCTCGGCTCCCTGCAACA
75101	73188	CCATCTCGGCTCCCTGCAAC
75102	73189	ACCATCTCGGCTCCCTGCAA
75103	73190	CACCATCTCGGCTCCCTGCA
75104	73191	ACACCATCTCGGCTCCCTGC
75105	73192	GACACCATCTCGGCTCCCTG
75106	73193	TGACACCATCTCGGCTCCCT
75107	73194	GTGACACCATCTCGGCTCCC
75108	73195	AGTGACACCATCTCGGCTCC
75109	73196	CAGTGACACCATCTCGGCTC
75110	73197	GCAGTGACACCATCTCGGCT
75111	73198	TGCAGTGACACCATCTCGGC
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75115	73202	GGAGTGCAGTGACACCATCT
75116	73203	CGGAGTGCAGTGACACCATC
75117	73204	CCGGAGTGCAGTGACACCAT
75118	73205	ACCGGAGTGCAGTGACACCA
75119	73206	GACCGGAGTGCAGTGACACC
75120	73207	AGACCGGAGTGCAGTGACAC
75121	73208	CAGACCGGAGTGCAGTGACA
75122	73209	CCAGACCGGAGTGCAGTGAC
75123	73210	CCCAGACCGGAGTGCAGTGA
75124	73211	ACCCAGACCGGAGTGCAGTG
75125	73212	CACCCAGACCGGAGTGCAGT
75126	73213	TCACCCAGACCGGAGTGCAG

124203	122290	AAAAAATAAAGCCACCAATG
124204	122291	AAAAAAATAAAGCCACCAAT
124205	122292	AAAAAAAATAAAGCCACCAA
124206	122293	GAAAAAAAATAAAGCCACCA
124207	122294	AGAAAAAAAATAAAGCCACC
124208	122295	CAGAAAAAAAATAAAGCCAC
124209	122296	ACAGAAAAAAAATAAAGCCA
124210	122297	AACAGAAAAAAAATAAAGCC
124211	122298	GAACAGAAAAAAAATAAAGC
124212	122299	AGAACAGAAAAAAAATAAAG
124213	122300	AAGAACAGAAAAAAAATAAA
124214	122301	CAAGAACAGAAAAAAAATAA
124215	122302	TCAAGAACAGAAAAAAAATA
124216	122303	TTCAAGAACAGAAAAAAAAT
124217	122304	TTTCAAGAACAGAAAAAAAA
124218	122305	GTTTCAAGAACAGAAAAAAA
124219	122306	TGTTTCAAGAACAGAAAAAA
124220	122307	TTGTTTCAAGAACAGAAAAA
124221	122308	CTTGTTTCAAGAACAGAAAA
124222	122309	TCTTGTTTCAAGAACAGAAA
124223	122310	CTCTTGTTTCAAGAACAGAA
124224	122311	ACTCTTGTTTCAAGAACAGA
124225	122312	GACTCTTGTTTCAAGAACAG
124226	122313	AGACTCTTGTTTCAAGAACA
124227	122314	GAGACTCTTGTTTCAAGAAC
124228	122315	CGAGACTCTTGTTTCAAGAA
124229	122316	TCGAGACTCTTGTTTCAAGA
124230	122317	ATCGAGACTCTTGTTTCAAG
124231	122318	GATCGAGACTCTTGTTTCAA
124232	122319	AGATCGAGACTCTTGTTTCA
124233	122320	AAGATCGAGACTCTTGTTTC
124234	122321	CAAGATCGAGACTCTTGTTT
124235	122322	ACAAGATCGAGACTCTTGTT
124236	122323	AACAAGATCGAGACTCTTGT
124237	122324	TAACAAGATCGAGACTCTTG
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124241	122328	TGGGTAACAAGATCGAGACT
124242	122329	CTGGGTAACAAGATCGAGAC
124243	122330	CCTGGGTAACAAGATCGAGA
124244	122331	GCCTGGGTAACAAGATCGAG
124245	122332	AGCCTGGGTAACAAGATCGA
124246	122333	CAGCCTGGGTAACAAGATCG
124247	122334	CCAGCCTGGGTAACAAGATC
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124252	122339	GCACTCCAGCCTGGGTAACA
124253	122340	TGCACTCCAGCCTGGGTAAC
124254	122341	CTGCACTCCAGCCTGGGTAA
124255	122342	ACTGCACTCCAGCCTGGGTA
124256	122343	TACTGCACTCCAGCCTGGGT
124257	122344	CTACTGCACTCCAGCCTGGG
124258	122345	ACTACTGCACTCCAGCCTGG
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124261	122348	CACACTACTGCACTCCAGCC
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124263	122350	GTCACACTACTGCACTCCAG
124264	122351	GGTCACACTACTGCACTCCA
124265	122352	AGGTCACACTACTGCACTCC
124266	122353	AAGGTCACACTACTGCACTC
124267	122354	CAAGGTCACACTACTGCACT
124268	122355	CCAAGGTCACACTACTGCAC
124269	122356	GCCAAGGTCACACTACTGCA
124270	122357	AGCCAAGGTCACACTACTGC
124271	122358	GAGCCAAGGTCACACTACTG
124272	122359	TGAGCCAAGGTCACACTACT
124273	122360	GTGAGCCAAGGTCACACTAC

25980	24067	ATGAGAACTTTCTGCCTAGT
25981	24068	AATGAGAACTTTCTGCCTAG
25982	24069	CAATGAGAACTTTCTGCCTA
25983	24070	GCAATGAGAACTTTCTGCCT
25984	24071	GGCAATGAGAACTTTCTGCC
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25992	24079	GTGGCAGGGGCAATGAGAAC
25993	24080	GGTGGCAGGGGCAATGAGAA
25994	24081	AGGTGGCAGGGGCAATGAGA
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25996	24083	TAAGGTGGCAGGGGCAATGA
25997	24084	ATAAGGTGGCAGGGGCAATG
25998	24085	CATAAGGTGGCAGGGGCAAT
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26014	24101	TCAAACACCTCAATGCCATA
26015	24102	CTCAAACACCTCAATGCCAT
26016	24103	TCTCAAACACCTCAATGCCA
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26018	24105	CATCTCAAACACCTCAATGC
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26020	24107	AGCATCTCAAACACCTCAAT
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26022	24109	TCAGCATCTCAAACACCTCA
26023	24110	ATCAGCATCTCAAACACCTC
26024	24111	CATCAGCATCTCAAACACCT
26025	24112	ACATCAGCATCTCAAACACC
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26027	24114	AAACATCAGCATCTCAAACA
26028	24115	TAAACATCAGCATCTCAAAC
26029	24116	GTAAACATCAGCATCTCAAA
26030	24117	AGTAAACATCAGCATCTCAA
26031	24118	AAGTAAACATCAGCATCTCA
26032	24119	GAAGTAAACATCAGCATCTC
26033	24120	AGAAGTAAACATCAGCATCT
26034	24121	CAGAAGTAAACATCAGCATC
26035	24122	ACAGAAGTAAACATCAGCAT
26036	24123	GACAGAAGTAAACATCAGCA
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26039	24126	TGAGACAGAAGTAAACATCA
26040	24127	ATGAGACAGAAGTAAACATC
26041	24128	TATGAGACAGAAGTAAACAT
26042	24129	TTATGAGACAGAAGTAAACA
26043	24130	TTTATGAGACAGAAGTAAAC
26044	24131	TTTTATGAGACAGAAGTAAA
26045	24132	ATTTTATGAGACAGAAGTAA
26046	24133	GATTTTATGAGACAGAAGTA
26047	24134	AGATTTTATGAGACAGAAGT
26048	24135	AAGATTTTATGAGACAGAAG
26049	24136	CAAGATTTTATGAGACAGAA
26050	24137	TCAAGATTTTATGAGACAGA

75127	73214	TTCACCCAGACCGGAGTGCA
75128	73215	TTTCACCCAGACCGGAGTGC
75129	73216	CTTTCACCCAGACCGGAGTG
75130	73217	TCTTTCACCCAGACCGGAGT
75131	73218	CTCTTTCACCCAGACCGGAG
75132	73219	GCTCTTTCACCCAGACCGGA
75133	73220	TGCTCTTTCACCCAGACCGG
75134	73221	TTGCTCTTTCACCCAGACCG
75135	73222	CTTGCTCTTTCACCCAGACC
75136	73223	GCTTGCTCTTTCACCCAGAC
75137	73224	AGCTTGCTCTTTCACCCAGA
75138	73225	GAGCTTGCTCTTTCACCCAG
75139	73226	GGAGCTTGCTCTTTCACCCA
75140	73227	TGGAGCTTGCTCTTTCACCC
75141	73228	ATGGAGCTTGCTCTTTCACC
75142	73229	GATGGAGCTTGCTCTTTCAC
75143	73230	AGATGGAGCTTGCTCTTTCA
75144	73231	GAGATGGAGCTTGCTCTTTC
75145	73232	TGAGATGGAGCTTGCTCTTT
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75154	73241	TTTCTTTTTTGAGATGGAGC
75155	73242	TTTTCTTTTTTGAGATGGAG
75156	73243	TTTTTCTTTTTTGAGATGGA
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75158	73245	TTTTTTTCTTTTTTGAGATG
75159	73246	TTTTTTTTCTTTTTTGAGAT
75160	73247	TTTTTTTTTCTTTTTTGAGA
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75174	73261	AAAATATCTCTTTTTTTTTT
75175	73262	AAAAATATCTCTTTTTTTTT
75176	73263	CAAAAATATCTCTTTTTTTT
75177	73264	TCAAAAATATCTCTTTTTTT
75178	73265	ATCAAAAATATCTCTTTTTT
75179	73266	CATCAAAAATATCTCTTTTT
75180	73267	CCATCAAAAATATCTCTTTT
75181	73268	TCCATCAAAAATATCTCTTT
75182	73269	ATCCATCAAAAATATCTCTT
75183	73270	AATCCATCAAAAATATCTCT
75184	73271	CAATCCATCAAAAATATCTC
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75194	73281	AAATTTCTATCAATCCATCA
75195	73282	AAAATTTCTATCAATCCATC
75196	73283	GAAAATTTCTATCAATCCAT
75197	73284	AGAAAATTTCTATCAATCCA

124274	122361	AGTGAGCCAAGGTCACACTA
124275	122362	CAGTGAGCCAAGGTCACACT
124276	122363	GCAGTGAGCCAAGGTCACAC
124277	122364	TGCAGTGAGCCAAGGTCACA
124278	122365	TTGCAGTGAGCCAAGGTCAC
124279	122366	GTTGCAGTGAGCCAAGGTCA
124280	122367	GGTTGCAGTGAGCCAAGGTC
124281	122368	AGGTTGCAGTGAGCCAAGGT
124282	122369	GAGGTTGCAGTGAGCCAAGG
124283	122370	GGAGGTTGCAGTGAGCCAAG
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124286	122373	AGTGGAGGTTGCAGTGAGCC
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124288	122375	GAAGTGGAGGTTGCAGTGAG
124289	122376	GGAAGTGGAGGTTGCAGTGA
124290	122377	GGGAAGTGGAGGTTGCAGTG
124291	122378	TGGGAAGTGGAGGTTGCAGT
124292	122379	CTGGGAAGTGGAGGTTGCAG
124293	122380	CCTGGGAAGTGGAGGTTGCA
124294	122381	CCCTGGGAAGTGGAGGTTGC
124295	122382	ACCCTGGGAAGTGGAGGTTG
124296	122383	GACCCTGGGAAGTGGAGGTT
124297	122384	TGACCCTGGGAAGTGGAGGT
124298	122385	TTGACCCTGGGAAGTGGAGG
124299	122386	CTTGACCCTGGGAAGTGGAG
124300	122387	GCTTGACCCTGGGAAGTGGA
124301	122388	CGCTTGACCCTGGGAAGTGG
124302	122389	TCGCTTGACCCTGGGAAGTG
124303	122390	ATCGCTTGACCCTGGGAAGT
124304	122391	AATCGCTTGACCCTGGGAAG
124305	122392	GAATCGCTTGACCCTGGGAA
124306	122393	AGAATCGCTTGACCCTGGGA
124307	122394	CAGAATCGCTTGACCCTGGG
124308	122395	GCAGAATCGCTTGACCCTGG
124309	122396	GGCAGAATCGCTTGACCCTG
124310	122397	AGGCAGAATCGCTTGACCCT
124311	122398	GAGGCAGAATCGCTTGACCC
124312	122399	TGAGGCAGAATCGCTTGACC
124313	122400	CTGAGGCAGAATCGCTTGAC
124314	122401	GCTGAGGCAGAATCGCTTGA
124315	122402	GGCTGAGGCAGAATCGCTTG
124316	122403	AGGCTGAGGCAGAATCGCTT
124317	122404	GAGGCTGAGGCAGAATCGCT
124318	122405	AGAGGCTGAGGCAGAATCGC
124319	122406	GAGAGGCTGAGGCAGAATCG
124320	122407	CGAGAGGCTGAGGCAGAATC
124321	122408	TCGAGAGGCTGAGGCAGAAT
124322	122409	CTCGAGAGGCTGAGGCAGAA
124323	122410	ACTCGAGAGGCTGAGGCAGA
124324	122411	TACTCGAGAGGCTGAGGCAG
124325	122412	CTACTCGAGAGGCTGAGGCA
124326	122413	GCTACTCGAGAGGCTGAGGC
124327	122414	AGCTACTCGAGAGGCTGAGG
124328	122415	TAGCTACTCGAGAGGCTGAG
124329	122416	CTAGCTACTCGAGAGGCTGA
124330	122417	CCTAGCTACTCGAGAGGCTG
124331	122418	TCCTAGCTACTCGAGAGGCT
124332	122419	ATCCTAGCTACTCGAGAGGC
124333	122420	AATCCTAGCTACTCGAGAGG
124334	122421	TAATCCTAGCTACTCGAGAG
124335	122422	GTAATCCTAGCTACTCGAGA
124336	122423	TGTAATCCTAGCTACTCGAG
124337	122424	CTGTAATCCTAGCTACTCGA
124338	122425	CCTGTAATCCTAGCTACTCG
124339	122426	ACCTGTAATCCTAGCTACTC
124340	122427	CACCTGTAATCCTAGCTACT
124341	122428	GCACCTGTAATCCTAGCTAC
124342	122429	GGCACCTGTAATCCTAGCTA
124343	122430	GGGCACCTGTAATCCTAGCT
124344	122431	CGGGCACCTGTAATCCTAGC

26051	24138	TTCAAGATTTTATGAGACAG
26052	24139	TTTCAAGATTTTATGAGACA
26053	24140	CTTTCAAGATTTTATGAGAC
26054	24141	CCTTTCAAGATTTTATGAGA
26055	24142	TCCTTTCAAGATTTTATGAG
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26058	24145	AACTCCTTTCAAGATTTTAT
26059	24146	GAACTCCTTTCAAGATTTTA
26060	24147	AGAACTCCTTTCAAGATTTT
26061	24148	AAGAACTCCTTTCAAGATTT
26062	24149	AAAGAACTCCTTTCAAGATT
26063	24150	AAAAGAACTCCTTTCAAGAT
26064	24151	TAAAAGAACTCCTTTCAAGA
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26067	24154	ATCTAAAAGAACTCCTTTCA
26068	24155	CATCTAAAAGAACTCCTTTC
26069	24156	TCATCTAAAAGAACTCCTTT
26070	24157	TTCATCTAAAAGAACTCCTT
26071	24158	CTTCATCTAAAAGAACTCCT
26072	24159	TCTTCATCTAAAAGAACTCC
26073	24160	CTCTTCATCTAAAAGAACTC
26074	24161	CCTCTTCATCTAAAAGAACT
26075	24162	TCCTCTTCATCTAAAAGAAC
26076	24163	TTCCTCTTCATCTAAAAGAA
26077	24164	TTTCCTCTTCATCTAAAAGA
26078	24165	TTTTCCTCTTCATCTAAAAG
26079	24166	GTTTTCCTCTTCATCTAAAA
26080	24167	TGTTTTCCTCTTCATCTAAA
26081	24168	TTGTTTTCCTCTTCATCTAA
26082	24169	TTTGTTTTCCTCTTCATCTA
26083	24170	TTTTGTTTTCCTCTTCATCT
26084	24171	ATTTTGTTTTCCTCTTCATC
26085	24172	GATTTTGTTTTCCTCTTCAT
26086	24173	TGATTTTGTTTTCCTCTTCA
26087	24174	CTGATTTTGTTTTCCTCTTC
26088	24175	TCTGATTTTGTTTTCCTCTT
26089	24176	TTCTGATTTTGTTTTCCTCT
26090	24177	CTTCTGATTTTGTTTTCCTC
26091	24178	TCTTCTGATTTTGTTTTCCT
26092	24179	TTCTTCTGATTTTGTTTTCC
26093	24180	ATTCTTCTGATTTTGTTTTC
26094	24181	CATTCTTCTGATTTTGTTTT
26095	24182	CCATTCTTCTGATTTTGTTT
26096	24183	CCCATTCTTCTGATTTTGTT
26097	24184	GCCCATTCTTCTGATTTTGT
26098	24185	GGCCCATTCTTCTGATTTTG
26099	24186	AGGCCCATTCTTCTGATTTT
26100	24187	CAGGCCCATTCTTCTGATTT
26101	24188	CCAGGCCCATTCTTCTGATT
26102	24189	CCCAGGCCCATTCTTCTGAT
26103	24190	ACCCAGGCCCATTCTTCTGA
26104	24191	GACCCAGGCCCATTCTTCTG
26105	24192	TGACCCAGGCCCATTCTTCT
26106	24193	ATGACCCAGGCCCATTCTTC
26107	24194	CATGACCCAGGCCCATTCTT
26108	24195	ACATGACCCAGGCCCATTCT
26109	24196	GACATGACCCAGGCCCATTC
26110	24197	AGACATGACCCAGGCCCATT
26111	24198	CAGACATGACCCAGGCCCAT
26112	24199	ACAGACATGACCCAGGCCCA
26113	24200	TACAGACATGACCCAGGCCC
26114	24201	TTACAGACATGACCCAGGCC
26115	24202	TTTACAGACATGACCCAGGC
26116	24203	GTTTACAGACATGACCCAGG
26117	24204	GGTTTACAGACATGACCCAG
26118	24205	AGGTTTACAGACATGACCCA
26119	24206	GAGGTTTACAGACATGACCC
26120	24207	GGAGGTTTACAGACATGACC
26121	24208	GGGAGGTTTACAGACATGAC

75198	73285	AAGAAAATTTCTATCAATCC
75199	73286	AAAGAAAATTTCTATCAATC
75200	73287	AAAAGAAAATTTCTATCAAT
75201	73288	AAAAAGAAAATTTCTATCAA
75202	73289	GAAAAAGAAAATTTCTATCA
75203	73290	AGAAAAAGAAAATTTCTATC
75204	73291	AAGAAAAAGAAAATTTCTAT
75205	73292	AAAGAAAAAGAAAATTTCTA
75206	73293	AAAAGAAAAAGAAAATTTCT
75207	73294	AAAAAGAAAAAGAAAATTTC
75208	73295	AAAAAAGAAAAAGAAAATTT
75209	73296	AAAAAAAGAAAAAGAAAATT
75210	73297	AAAAAAAAGAAAAAGAAAAT
75211	73298	AAAAAAAAAGAAAAAGAAAA
75212	73299	AAAAAAAAAAGAAAAAGAAA
75213	73300	AAAAAAAAAAAGAAAAAGAA
75214	73301	CAAAAAAAAAAAGAAAAAGA
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75217	73304	TCTCAAAAAAAAAAAGAAAA
75218	73305	GTCTCAAAAAAAAAAAGAAA
75219	73306	TGTCTCAAAAAAAAAAAGAA
75220	73307	CTGTCTCAAAAAAAAAAAGA
75221	73308	CCTGTCTCAAAAAAAAAAAG
75222	73309	CCCTGTCTCAAAAAAAAAAA
75223	73310	ACCCTGTCTCAAAAAAAAAA
75224	73311	GACCCTGTCTCAAAAAAAAA
75225	73312	AGACCCTGTCTCAAAAAAAA
75226	73313	GAGACCCTGTCTCAAAAAAA
75227	73314	TGAGACCCTGTCTCAAAAAA
75228	73315	GTGAGACCCTGTCTCAAAAA
75229	73316	AGTGAGACCCTGTCTCAAAA
75230	73317	GAGTGAGACCCTGTCTCAAA
75231	73318	AGAGTGAGACCCTGTCTCAA
75232	73319	CAGAGTGAGACCCTGTCTCA
75233	73320	ACAGAGTGAGACCCTGTCTC
75234	73321	GACAGAGTGAGACCCTGTCT
75235	73322	CGACAGAGTGAGACCCTGTC
75236	73323	GCGACAGAGTGAGACCCTGT
75237	73324	GGCGACAGAGTGAGACCCTG
75238	73325	TGGCGACAGAGTGAGACCCT
75239	73326	CTGGCGACAGAGTGAGACCC
75240	73327	CCTGGCGACAGAGTGAGACC
75241	73328	GCCTGGCGACAGAGTGAGAC
75242	73329	AGCCTGGCGACAGAGTGAGA
75243	73330	CAGCCTGGCGACAGAGTGAG
75244	73331	CCAGCCTGGCGACAGAGTGA
75245	73332	TCCAGCCTGGCGACAGAGTG
75246	73333	CTCCAGCCTGGCGACAGAGT
75247	73334	GCTCCAGCCTGGCGACAGAG
75248	73335	TGCTCCAGCCTGGCGACAGA
75249	73336	GTGCTCCAGCCTGGCGACAG
75250	73337	TGTGCTCCAGCCTGGCGACA
75251	73338	CTGTGCTCCAGCCTGGCGAC
75252	73339	ACTGTGCTCCAGCCTGGCGA
75253	73340	CACTGTGCTCCAGCCTGGCG
75254	73341	CCACTGTGCTCCAGCCTGGC
75255	73342	GCCACTGTGCTCCAGCCTGG
75256	73343	CGCCACTGTGCTCCAGCCTG
75257	73344	ACGCCACTGTGCTCCAGCCT
75258	73345	CACGCCACTGTGCTCCAGCC
75259	73346	TCACGCCACTGTGCTCCAGC
75260	73347	ATCACGCCACTGTGCTCCAG
75261	73348	GATCACGCCACTGTGCTCCA
75262	73349	AGATCACGCCACTGTGCTCC
75263	73350	GAGATCACGCCACTGTGCTC
75264	73351	GGAGATCACGCCACTGTGCT
75265	73352	TGGAGATCACGCCACTGTGC
75266	73353	ATGGAGATCACGCCACTGTG
75267	73354	AATGGAGATCACGCCACTGT
75268	73355	GAATGGAGATCACGCCACTG

124345	122432	GCGGGCACCTGTAATCCTAG
124346	122433	GGCGGGCACCTGTAATCCTA
124347	122434	TGGCGGGCACCTGTAATCCT
124348	122435	GTGGCGGGCACCTGTAATCC
124349	122436	AGTGGCGGGCACCTGTAATC
124350	122437	TAGTGGCGGGCACCTGTAAT
124351	122438	GTAGTGGCGGGCACCTGTAA
124352	122439	TGTAGTGGCGGGCACCTGTA
124353	122440	GTGTAGTGGCGGGCACCTGT
124354	122441	GGTGTAGTGGCGGGCACCTG
124355	122442	GGGTGTAGTGGCGGGCACCT
124356	122443	TGGGTGTAGTGGCGGGCACC
124357	122444	CTGGGTGTAGTGGCGGGCAC
124358	122445	GCTGGGTGTAGTGGCGGGCA
124359	122446	AGCTGGGTGTAGTGGCGGGC
124360	122447	TAGCTGGGTGTAGTGGCGGG
124361	122448	TTAGCTGGGTGTAGTGGCGG
124362	122449	ATTAGCTGGGTGTAGTGGCG
124363	122450	AATTAGCTGGGTGTAGTGGC
124364	122451	AAATTAGCTGGGTGTAGTGG
124365	122452	CAAATTAGCTGGGTGTAGTG
124366	122453	ACAAATTAGCTGGGTGTAGT
124367	122454	TACAAATTAGCTGGGTGTAG
124368	122455	ATACAAATTAGCTGGGTGTA
124369	122456	AATACAAATTAGCTGGGTGT
124370	122457	AAATACAAATTAGCTGGGTG
124371	122458	AAAATACAAATTAGCTGGGT
124372	122459	AAAAATACAAATTAGCTGGG
124373	122460	AAAAAATACAAATTAGCTGG
124374	122461	AAAAAAATACAAATTAGCTG
124375	122462	AAAAAAAATACAAATTAGCT
124376	122463	AAAAAAAAATACAAATTAGC
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124378	122465	AAAAAAAAAAATACAAATTA
124379	122466	AAAAAAAAAAAATACAAATT
124380	122467	AAAAAAAAAAAAATACAAAT
124381	122468	AAAAAAAAAAAAAATACAAA
124382	122469	AAAAAAAAAAAAAAATACAA
124383	122470	AAAAAAAAAAAAAAAATACA
124384	122471	AAAAAAAAAAAAAAAAATAC
124385	122472	AAAAAAAAAAAAAAAAAATA
124386	122473	AAAAAAAAAAAAAAAAAAAT
124387	122474	AAAAAAAAAAAAAAAAAAAA
124388	122475	TAAAAAAAAAAAAAAAAAAA
124389	122476	CTAAAAAAAAAAAAAAAAAA
124390	122477	ACTAAAAAAAAAAAAAAAAA
124391	122478	TACTAAAAAAAAAAAAAAAA
124392	122479	CTACTAAAAAAAAAAAAAAA
124393	122480	TCTACTAAAAAAAAAAAAAA
124394	122481	CTCTACTAAAAAAAAAAAAA
124395	122482	TCTCTACTAAAAAAAAAAAA
124396	122483	GTCTCTACTAAAAAAAAAAA
124397	122484	TGTCTCTACTAAAAAAAAAA
124398	122485	CTGTCTCTACTAAAAAAAAA
124399	122486	CCTGTCTCTACTAAAAAAAA
124400	122487	CCCTGTCTCTACTAAAAAAA
124401	122488	ACCCTGTCTCTACTAAAAAA
124402	122489	GACCCTGTCTCTACTAAAAA
124403	122490	AGACCCTGTCTCTACTAAAA
124404	122491	GAGACCCTGTCTCTACTAAA
124405	122492	TGAGACCCTGTCTCTACTAA
124406	122493	GTGAGACCCTGTCTCTACTA
124407	122494	GGTGAGACCCTGTCTCTACT
124408	122495	TGGTGAGACCCTGTCTCTAC
124409	122496	ATGGTGAGACCCTGTCTCTA
124410	122497	CATGGTGAGACCCTGTCTCT
124411	122498	ACATGGTGAGACCCTGTCTC
124412	122499	AACATGGTGAGACCCTGTCT
124413	122500	CAACATGGTGAGACCCTGTC
124414	122501	CCAACATGGTGAGACCCTGT
124415	122502	GCCAACATGGTGAGACCCTG

26122	24209	GGGGAGGTTTACAGACATGA
26123	24210	TGGGGAGGTTTACAGACATG
26124	24211	GTGGGGAGGTTTACAGACAT
26125	24212	CGTGGGGAGGTTTACAGACA
26126	24213	ACGTGGGGAGGTTTACAGAC
26127	24214	GACGTGGGGAGGTTTACAGA
26128	24215	TGACGTGGGGAGGTTTACAG
26129	24216	ATGACGTGGGGAGGTTTACA
26130	24217	CATGACGTGGGGAGGTTTAC
26131	24218	CCATGACGTGGGGAGGTTTA
26132	24219	CCCATGACGTGGGGAGGTTT
26133	24220	CCCCATGACGTGGGGAGGTT
26134	24221	TCCCCATGACGTGGGGAGGT
26135	24222	CTCCCCATGACGTGGGGAGG
26136	24223	CCTCCCCATGACGTGGGGAG
26137	24224	GCCTCCCCATGACGTGGGGA
26138	24225	AGCCTCCCCATGACGTGGGG
26139	24226	CAGCCTCCCCATGACGTGGG
26140	24227	TCAGCCTCCCCATGACGTGG
26141	24228	TTCAGCCTCCCCATGACGTG
26142	24229	TTTCAGCCTCCCCATGACGT
26143	24230	ATTTCAGCCTCCCCATGACG
26144	24231	CATTTCAGCCTCCCCATGAC
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26146	24233	CCCATTTCAGCCTCCCCATG
26147	24234	TCCCATTTCAGCCTCCCCAT
26148	24235	TTCCCATTTCAGCCTCCCCA
26149	24236	CTTCCCATTTCAGCCTCCCC
26150	24237	CCTTCCCATTTCAGCCTCCC
26151	24238	CCCTTCCCATTTCAGCCTCC
26152	24239	GCCCTTCCCATTTCAGCCTC
26153	24240	GGCCCTTCCCATTTCAGCCT
26154	24241	TGGCCCTTCCCATTTCAGCC
26155	24242	CTGGCCCTTCCCATTTCAGC
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26159	24246	ACTCCTGGCCCTTCCCATTT
26160	24247	AACTCCTGGCCCTTCCCATT
26161	24248	GAACTCCTGGCCCTTCCCAT
26162	24249	TGAACTCCTGGCCCTTCCCA
26163	24250	TTGAACTCCTGGCCCTTCCC
26164	24251	CTTGAACTCCTGGCCCTTCC
26165	24252	TCTTGAACTCCTGGCCCTTC
26166	24253	GTCTTGAACTCCTGGCCCTT
26167	24254	GGTCTTGAACTCCTGGCCCT
26168	24255	TGGTCTTGAACTCCTGGCCC
26169	24256	CTGGTCTTGAACTCCTGGCC
26170	24257	CCTGGTCTTGAACTCCTGGC
26171	24258	GCCTGGTCTTGAACTCCTGG
26172	24259	AGCCTGGTCTTGAACTCCTG
26173	24260	CAGCCTGGTCTTGAACTCCT
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26175	24262	CTCAGCCTGGTCTTGAACTC
26176	24263	TCTCAGCCTGGTCTTGAACT
26177	24264	TTCTCAGCCTGGTCTTGAAC
26178	24265	TTTCTCAGCCTGGTCTTGAA
26179	24266	GTTTCTCAGCCTGGTCTTGA
26180	24267	TGTTTCTCAGCCTGGTCTTG
26181	24268	ATGTTTCTCAGCCTGGTCTT
26182	24269	TATGTTTCTCAGCCTGGTCT
26183	24270	TTATGTTTCTCAGCCTGGTC
26184	24271	GTTATGTTTCTCAGCCTGGT
26185	24272	TGTTATGTTTCTCAGCCTGG
26186	24273	TTGTTATGTTTCTCAGCCTG
26187	24274	CTTGTTATGTTTCTCAGCCT
26188	24275	TCTTGTTATGTTTCTCAGCC
26189	24276	GTCTTGTTATGTTTCTCAGC
26190	24277	GGTCTTGTTATGTTTCTCAG
26191	24278	GGGTCTTGTTATGTTTCTCA
26192	24279	GGGGTCTTGTTATGTTTCTC

75269	73356	TGAATGGAGATCACGCCACT
75270	73357	ATGAATGGAGATCACGCCAC
75271	73358	AATGAATGGAGATCACGCCA
75272	73359	CAATGAATGGAGATCACGCC
75273	73360	GCAATGAATGGAGATCACGC
75274	73361	TGCAATGAATGGAGATCACG
75275	73362	TTGCAATGAATGGAGATCAC
75276	73363	GTTGCAATGAATGGAGATCA
75277	73364	GGTTGCAATGAATGGAGATC
75278	73365	AGGTTGCAATGAATGGAGAT
75279	73366	GAGGTTGCAATGAATGGAGA
75280	73367	GGAGGTTGCAATGAATGGAG
75281	73368	TGGAGGTTGCAATGAATGGA
75282	73369	GTGGAGGTTGCAATGAATGG
75283	73370	GGTGGAGGTTGCAATGAATG
75284	73371	AGGTGGAGGTTGCAATGAAT
75285	73372	GAGGTGGAGGTTGCAATGAA
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75288	73375	CGGGAGGTGGAGGTTGCAAT
75289	73376	CCGGGAGGTGGAGGTTGCAA
75290	73377	CCCGGGAGGTGGAGGTTGCA
75291	73378	ACCCGGGAGGTGGAGGTTGC
75292	73379	AACCCGGGAGGTGGAGGTTG
75293	73380	GAACCCGGGAGGTGGAGGTT
75294	73381	TGAACCCGGGAGGTGGAGGT
75295	73382	TTGAACCCGGGAGGTGGAGG
75296	73383	TTTGAACCCGGGAGGTGGAG
75297	73384	GTTTGAACCCGGGAGGTGGA
75298	73385	CGTTTGAACCCGGGAGGTGG
75299	73386	TCGTTTGAACCCGGGAGGTG
75300	73387	ATCGTTTGAACCCGGGAGGT
75301	73388	AATCGTTTGAACCCGGGAGG
75302	73389	GAATCGTTTGAACCCGGGAG
75303	73390	AGAATCGTTTGAACCCGGGA
75304	73391	GAGAATCGTTTGAACCCGGG
75305	73392	GGAGAATCGTTTGAACCCGG
75306	73393	AGGAGAATCGTTTGAACCCG
75307	73394	AAGGAGAATCGTTTGAACCC
75308	73395	GAAGGAGAATCGTTTGAACC
75309	73396	GGAAGGAGAATCGTTTGAAC
75310	73397	AGGAAGGAGAATCGTTTGAA
75311	73398	GAGGAAGGAGAATCGTTTGA
75312	73399	TGAGGAAGGAGAATCGTTTG
75313	73400	CTGAGGAAGGAGAATCGTTT
75314	73401	GCTGAGGAAGGAGAATCGTT
75315	73402	GGCTGAGGAAGGAGAATCGT
75316	73403	AGGCTGAGGAAGGAGAATCG
75317	73404	GAGGCTGAGGAAGGAGAATC
75318	73405	GGAGGCTGAGGAAGGAGAAT
75319	73406	GGGAGGCTGAGGAAGGAGAA
75320	73407	CGGGAGGCTGAGGAAGGAGA
75321	73408	TCGGGAGGCTGAGGAAGGAG
75322	73409	CTCGGGAGGCTGAGGAAGGA
75323	73410	ACTCGGGAGGCTGAGGAAGG
75324	73411	TACTCGGGAGGCTGAGGAAG
75325	73412	CTACTCGGGAGGCTGAGGAA
75326	73413	GCTACTCGGGAGGCTGAGGA
75327	73414	AGCTACTCGGGAGGCTGAGG
75328	73415	CAGCTACTCGGGAGGCTGAG
75329	73416	CCAGCTACTCGGGAGGCTGA
75330	73417	CCCAGCTACTCGGGAGGCTG
75331	73418	TCCCAGCTACTCGGGAGGCT
75332	73419	GTCCCAGCTACTCGGGAGGC
75333	73420	AGTCCCAGCTACTCGGGAGG
75334	73421	TAGTCCCAGCTACTCGGGAG
75335	73422	GTAGTCCCAGCTACTCGGGA
75336	73423	TGTAGTCCCAGCTACTCGGG
75337	73424	CTGTAGTCCCAGCTACTCGG
75338	73425	CCTGTAGTCCCAGCTACTCG
75339	73426	GCCTGTAGTCCCAGCTACTC

124416	122503	GGCCAACATGGTGAGACCCT
124417	122504	TGGCCAACATGGTGAGACCC
124418	122505	CTGGCCAACATGGTGAGACC
124419	122506	CCTGGCCAACATGGTGAGAC
124420	122507	GCCTGGCCAACATGGTGAGA
124421	122508	AGCCTGGCCAACATGGTGAG
124422	122509	TAGCCTGGCCAACATGGTGA
124423	122510	CTAGCCTGGCCAACATGGTG
124424	122511	ACTAGCCTGGCCAACATGGT
124425	122512	GACTAGCCTGGCCAACATGG
124426	122513	AGACTAGCCTGGCCAACATG
124427	122514	GAGACTAGCCTGGCCAACAT
124428	122515	CGAGACTAGCCTGGCCAACA
124429	122516	TCGAGACTAGCCTGGCCAAC
124430	122517	TTCGAGACTAGCCTGGCCAA
124431	122518	GTTCGAGACTAGCCTGGCCA
124432	122519	AGTTCGAGACTAGCCTGGCC
124433	122520	GAGTTCGAGACTAGCCTGGC
124434	122521	GGAGTTCGAGACTAGCCTGG
124435	122522	AGGAGTTCGAGACTAGCCTG
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124439	122526	GGTCAGGAGTTCGAGACTAG
124440	122527	AGGTCAGGAGTTCGAGACTA
124441	122528	GAGGTCAGGAGTTCGAGACT
124442	122529	TGAGGTCAGGAGTTCGAGAC
124443	122530	CTGAGGTCAGGAGTTCGAGA
124444	122531	CCTGAGGTCAGGAGTTCGAG
124445	122532	ACCTGAGGTCAGGAGTTCGA
124446	122533	CACCTGAGGTCAGGAGTTCG
124447	122534	TCACCTGAGGTCAGGAGTTC
124448	122535	ATCACCTGAGGTCAGGAGTT
124449	122536	GATCACCTGAGGTCAGGAGT
124450	122537	AGATCACCTGAGGTCAGGAG
124451	122538	CAGATCACCTGAGGTCAGGA
124452	122539	GCAGATCACCTGAGGTCAGG
124453	122540	AGCAGATCACCTGAGGTCAG
124454	122541	GAGCAGATCACCTGAGGTCA
124455	122542	TGAGCAGATCACCTGAGGTC
124456	122543	ATGAGCAGATCACCTGAGGT
124457	122544	GATGAGCAGATCACCTGAGG
124458	122545	AGATGAGCAGATCACCTGAG
124459	122546	GAGATGAGCAGATCACCTGA
124460	122547	TGAGATGAGCAGATCACCTG
124461	122548	CTGAGATGAGCAGATCACCT
124462	122549	GCTGAGATGAGCAGATCACC
124463	122550	GGCTGAGATGAGCAGATCAC
124464	122551	AGGCTGAGATGAGCAGATCA
124465	122552	GAGGCTGAGATGAGCAGATC
124466	122553	GGAGGCTGAGATGAGCAGAT
124467	122554	GGGAGGCTGAGATGAGCAGA
124468	122555	TGGGAGGCTGAGATGAGCAG
124469	122556	TTGGGAGGCTGAGATGAGCA
124470	122557	TTTGGGAGGCTGAGATGAGC
124471	122558	CTTTGGGAGGCTGAGATGAG
124472	122559	ACTTTGGGAGGCTGAGATGA
124473	122560	AACTTTGGGAGGCTGAGATG
124474	122561	GAACTTTGGGAGGCTGAGAT
124475	122562	AGAACTTTGGGAGGCTGAGA
124476	122563	CAGAACTTTGGGAGGCTGAG
124477	122564	CCAGAACTTTGGGAGGCTGA
124478	122565	CCCAGAACTTTGGGAGGCTG
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124480	122567	ATCCCAGAACTTTGGGAGGC
124481	122568	AATCCCAGAACTTTGGGAGG
124482	122569	TAATCCCAGAACTTTGGGAG
124483	122570	GTAATCCCAGAACTTTGGGA
124484	122571	TGTAATCCCAGAACTTTGGG
124485	122572	CTGTAATCCCAGAACTTTGG
124486	122573	CCTGTAATCCCAGAACTTTG

26193	24280	TGGGGTCTTGTTATGTTTCT
26194	24281	ATGGGGTCTTGTTATGTTTC
26195	24282	GATGGGGTCTTGTTATGTTT
26196	24283	AGATGGGGTCTTGTTATGTT
26197	24284	GAGATGGGGTCTTGTTATGT
26198	24285	AGAGATGGGGTCTTGTTATG
26199	24286	TAGAGATGGGGTCTTGTTAT
26200	24287	GTAGAGATGGGGTCTTGTTA
26201	24288	TGTAGAGATGGGGTCTTGTT
26202	24289	TTGTAGAGATGGGGTCTTGT
26203	24290	TTTGTAGAGATGGGGTCTTG
26204	24291	TTTTGTAGAGATGGGGTCTT
26205	24292	TTTTTGTAGAGATGGGGTCT
26206	24293	TTTTTTGTAGAGATGGGGTC
26207	24294	ATTTTTTGTAGAGATGGGGT
26208	24295	TATTTTTTGTAGAGATGGGG
26209	24296	ATATTTTTTGTAGAGATGGG
26210	24297	AATATTTTTTGTAGAGATGG
26211	24298	AAATATTTTTTGTAGAGATG
26212	24299	AAAATATTTTTTGTAGAGAT
26213	24300	AAAAATATTTTTTGTAGAGA
26214	24301	AAAAAATATTTTTTGTAGAG
26215	24302	TAAAAAATATTTTTTGTAGA
26216	24303	TTAAAAAATATTTTTTGTAG
26217	24304	ATTAAAAAAATATTTTTTGTA
26218	24305	AATTAAAAAAATATTTTTTGT
26219	24306	TAATTAAAAAATATTTTTTG
26220	24307	TTAATTAAAAAATATTTTTT
26221	24308	ATTAATTAAAAAATATTTTT
26222	24309	CATTAATTAAAAAATATTTT
26223	24310	CCATTAATTAAAAAATATTT
26224	24311	CCCATTAATTAAAAAATATT
26225	24312	CCCCATTAATTAAAAAATAT
26226	24313	CCCCCATTAATTAAAAAATA
26227	24314	TCCCCCATTAATTAAAAAAT
26228	24315	ATCCCCCATTAATTAAAAAA
26229	24316	CATCCCCCATTAATTAAAAA
26230	24317	CCATCCCCCATTAATTAAAA
26231	24318	GCCATCCCCCATTAATTAAA
26232	24319	TGCCATCCCCCATTAATTAA
26233	24320	CTGCCATCCCCCATTAATTA
26234	24321	GCTGCCATCCCCCATTAATT
26235	24322	TGCTGCCATCCCCCATTAAT
26236	24323	GTGCTGCCATCCCCCATTAA
26237	24324	TGTGCTGCCATCCCCCATTA
26238	24325	GTGTGCTGCCATCCCCCATT
26239	24326	TGTGTGCTGCCATCCCCCAT
26240	24327	GTGTGTGCTGCCATCCCCCA
26241	24328	GGTGTGTGCTGCCATCCCCC
26242	24329	AGGTGTGTGCTGCCATCCCC
26243	24330	CAGGTGTGTGCTGCCATCCC
26244	24331	ACAGGTGTGTGCTGCCATCC
26245	24332	TACAGGTGTGTGCTGCCATC
26246	24333	CTACAGGTGTGTGCTGCCAT
26247	24334	ACTACAGGTGTGTGCTGCCA
26248	24335	GACTACAGGTGTGTGCTGCC
26249	24336	CGACTACAGGTGTGTGCTGC
26250	24337	GCGACTACAGGTGTGTGCTG
26251	24338	TGCGACTACAGGTGTGTGCT
26252	24339	CTGCGACTACAGGTGTGTGC
26253	24340	GCTGCGACTACAGGTGTGTG
26254	24341	AGCTGCGACTACAGGTGTGT
26255	24342	TAGCTGCGACTACAGGTGTG
26256	24343	GTAGCTGCGACTACAGGTGT
26257	24344	AGTAGCTGCGACTACAGGTG
26258	24345	TAGTAGCTGCGACTACAGGT
26259	24346	GTAGTAGCTGCGACTACAGG
26260	24347	CGTAGTAGCTGCGACTACAG
26261	24348	TCGTAGTAGCTGCGACTACA
26262	24349	CTCGTAGTAGCTGCGACTAC
26263	24350	CCTCGTAGTAGCTGCGACTA

75340	73427	TGCCTGTAGTCCCAGCTACT
75341	73428	ATGCCTGTAGTCCCAGCTAC
75342	73429	CATGCCTGTAGTCCCAGCTA
75343	73430	ACATGCCTGTAGTCCCAGCT
75344	73431	CACATGCCTGTAGTCCCAGC
75345	73432	GCACATGCCTGTAGTCCCAG
75346	73433	GGCACATGCCTGTAGTCCCA
75347	73434	TGGCACATGCCTGTAGTCCC
75348	73435	GTGGCACATGCCTGTAGTCC
75349	73436	GGTGGCACATGCCTGTAGTC
75350	73437	TGGTGGCACATGCCTGTAGT
75351	73438	ATGGTGGCACATGCCTGTAG
75352	73439	CATGGTGGCACATGCCTGTA
75353	73440	GCATGGTGGCACATGCCTGT
75354	73441	GGCATGGTGGCACATGCCTG
75355	73442	GGGCATGGTGGCACATGCCT
75356	73443	TGGGCATGGTGGCACATGCC
75357	73444	TTGGGCATGGTGGCACATGC
75358	73445	GTTGGGCATGGTGGCACATG
75359	73446	AGTTGGGCATGGTGGCACAT
75360	73447	TAGTTGGGCATGGTGGCACA
75361	73448	TTAGTTGGGCATGGTGGCAC
75362	73449	ATTAGTTGGGCATGGTGGCA
75363	73450	AATTAGTTGGGCATGGTGGC
75364	73451	AAATTAGTTGGGCATGGTGG
75365	73452	AAAATTAGTTGGGCATGGTG
75366	73453	AAAAATTAGTTGGGCATGGT
75367	73454	CAAAAATTAGTTGGGCATGG
75368	73455	ACAAAAATTAGTTGGGCATG
75369	73456	TACAAAAATTAGTTGGGCAT
75370	73457	ATACAAAAATTAGTTGGGCA
75371	73458	AATACAAAAATTAGTTGGGC
75372	73459	AAATACAAAAATTAGTTGGG
75373	73460	AAAATACAAAAATTAGTTGG
75374	73461	AAAAATACAAAAATTAGTTG
75375	73462	TAAAAATACAAAAATTAGTT
75376	73463	CTAAAAATACAAAAATTAGT
75377	73464	ACTAAAAATACAAAAATTAG
75378	73465	TACTAAAAATACAAAAATTA
75379	73466	CTACTAAAAATACAAAAATT
75380	73467	TCTACTAAAAATACAAAAAT
75381	73468	CTCTACTAAAAATACAAAAA
75382	73469	TCTCTACTAAAAATACAAAA
75383	73470	CTCTCTACTAAAAATACAAA
75384	73471	TCTCTCTACTAAAAATACAA
75385	73472	CTCTCTCTACTAAAAATACA
75386	73473	CCTCTCTCTACTAAAAATAC
75387	73474	CCCTCTCTCTACTAAAAATA
75388	73475	ACCCTCTCTCTACTAAAAAT
75389	73476	AACCCTCTCTCTACTAAAAA
75390	73477	AAACCCTCTCTCTACTAAAA
75391	73478	GAAACCCTCTCTCTACTAAA
75392	73479	TGAAACCCTCTCTCTACTAA
75393	73480	GTGAAACCCTCTCTCTACTA
75394	73481	GGTGAAACCCTCTCTCTACT
75395	73482	TGGTGAAACCCTCTCTCTAC
75396	73483	ATGGTGAAACCCTCTCTCTA
75397	73484	CATGGTGAAACCCTCTCTCT
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75399	73486	AACATGGTGAAACCCTCTCT
75400	73487	CAACATGGTGAAACCCTCTC
75401	73488	CCAACATGGTGAAACCCTCT
75402	73489	GCCAACATGGTGAAACCCTC
75403	73490	GGCCAACATGGTGAAACCCT
75404	73491	TGGCCAACATGGTGAAACCC
75405	73492	CTGGCCAACATGGTGAAACC
75406	73493	CCTGGCCAACATGGTGAAAC
75407	73494	TCCTGGCCAACATGGTGAAA
75408	73495	ATCCTGGCCAACATGGTGAA
75409	73496	CATCCTGGCCAACATGGTGA
75410	73497	CCATCCTGGCCAACATGGTG

124487	122574	GCCTGTAATCCCAGAACTTT
124488	122575	TGCCTGTAATCCCAGAACTT
124489	122576	ATGCCTGTAATCCCAGAACT
124490	122577	CATGCCTGTAATCCCAGAAC
124491	122578	TCATGCCTGTAATCCCAGAA
124492	122579	CTCATGCCTGTAATCCCAGA
124493	122580	GCTCATGCCTGTAATCCCAG
124494	122581	GGCTCATGCCTGTAATCCCA
124495	122582	TGGCTCATGCCTGTAATCCC
124496	122583	GTGGCTCATGCCTGTAATCC
124497	122584	AGTGGCTCATGCCTGTAATC
124498	122585	CAGTGGCTCATGCCTGTAAT
124499	122586	GCAGTGGCTCATGCCTGTAA
124500	122587	CGCAGTGGCTCATGCCTGTA
124501	122588	GCGCAGTGGCTCATGCCTGT
124502	122589	GGCGCAGTGGCTCATGCCTG
124503	122590	GGGCGCAGTGGCTCATGCCT
124504	122591	TGGGCGCAGTGGCTCATGCC
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124507	122594	GGCTGGGCGCAGTGGCTCAT
124508	122595	TGGCTGGGCGCAGTGGCTCA
124509	122596	ATGGCTGGGCGCAGTGGCTC
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124512	122599	ACTATGGCTGGGCGCAGTGG
124513	122600	TACTATGGCTGGGCGCAGTG
124514	122601	CTACTATGGCTGGGCGCAGT
124515	122602	GCTACTATGGCTGGGCGCAG
124516	122603	AGCTACTATGGCTGGGCGCA
124517	122604	AAGCTACTATGGCTGGGCGC
124518	122605	AAAGCTACTATGGCTGGGCG
124519	122606	TAAAGCTACTATGGCTGGGC
124520	122607	ATAAAGCTACTATGGCTGGG
124521	122608	AATAAAGCTACTATGGCTGG
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124529	122616	CTGAATTCAATAAAGCTACT
124530	122617	ACTGAATTCAATAAAGCTAC
124531	122618	AACTGAATTCAATAAAGCTA
124532	122619	CAACTGAATTCAATAAAGCT
124533	122620	TCAACTGAATTCAATAAAGC
124534	122621	GTCAACTGAATTCAATAAAG
124535	122622	AGTCAACTGAATTCAATAAA
124536	122623	CAGTCAACTGAATTCAATAA
124537	122624	ACAGTCAACTGAATTCAATA
124538	122625	TACAGTCAACTGAATTCAAT
124539	122626	ATACAGTCAACTGAATTCAA
124540	122627	AATACAGTCAACTGAATTCA
124541	122628	CAATACAGTCAACTGAATTC
124542	122629	ACAATACAGTCAACTGAATT
124543	122630	TACAATACAGTCAACTGAAT
124544	122631	ATACAATACAGTCAACTGAA
124545	122632	CATACAATACAGTCAACTGA
124546	122633	ACATACAATACAGTCAACTG
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124552	122639	AGACACACATACAATACAGT
124553	122640	TAGACACACATACAATACAG
124554	122641	ATAGACACACATACAATACA
124555	122642	AATAGACACACATACAATAC
124556	122643	AAATAGACACACATACAATA
124557	122644	CAAATAGACACACATACAAT

26264	24351	GCCTCGTAGTAGCTGCGACT
26265	24352	AGCCTCGTAGTAGCTGCGAC
26266	24353	CAGCCTCGTAGTAGCTGCGA
26267	24354	TCAGCCTCGTAGTAGCTGCG
26268	24355	TTCAGCCTCGTAGTAGCTGC
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26270	24357	GCTTCAGCCTCGTAGTAGCT
26271	24358	CGCTTCAGCCTCGTAGTAGC
26272	24359	TCGCTTCAGCCTCGTAGTAG
26273	24360	CTCGCTTCAGCCTCGTAGTA
26274	24361	TCTCGCTTCAGCCTCGTAGT
26275	24362	CTCTCGCTTCAGCCTCGTAG
26276	24363	CCTCTCGCTTCAGCCTCGTA
26277	24364	TCCTCTCGCTTCAGCCTCGT
26278	24365	ATCCTCTCGCTTCAGCCTCG
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26282	24369	AGCAATCCTCTCGCTTCAGC
26283	24370	AAGCAATCCTCTCGCTTCAG
26284	24371	CAAGCAATCCTCTCGCTTCA
26285	24372	TCAAGCAATCCTCTCGCTTC
26286	24373	CTCAAGCAATCCTCTCGCTT
26287	24374	GCTCAAGCAATCCTCTCGCT
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26294	24381	CTCCTGAGCTCAAGCAATCC
26295	24382	ACTCCTGAGCTCAAGCAATC
26296	24383	AACTCCTGAGCTCAAGCAAT
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26302	24389	ATCTTTAACTCCTGAGCTCA
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26304	24391	CAATCTTTAACTCCTGAGCT
26305	24392	GCAATCTTTAACTCCTGAGC
26306	24393	TGCAATCTTTAACTCCTGAG
26307	24394	CTGCAATCTTTAACTCCTGA
26308	24395	CCTGCAATCTTTAACTCCTG
26309	24396	TCCTGCAATCTTTAACTCCT
26310	24397	CTCCTGCAATCTTTAACTCC
26311	24398	GCTCCTGCAATCTTTAACTC
26312	24399	AGCTCCTGCAATCTTTAACT
26313	24400	TAGCTCCTGCAATCTTTAAC
26314	24401	ATAGCTCCTGCAATCTTTAA
26315	24402	CATAGCTCCTGCAATCTTTA
26316	24403	TCATAGCTCCTGCAATCTTT
26317	24404	ATCATAGCTCCTGCAATCTT
26318	24405	GATCATAGCTCCTGCAATCT
26319	24406	TGATCATAGCTCCTGCAATC
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26321	24408	TGTGATCATAGCTCCTGCAA
26322	24409	CTGTGATCATAGCTCCTGCA
26323	24410	GCTGTGATCATAGCTCCTGC
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26325	24412	GTGCTGTGATCATAGCTCCT
26326	24413	AGTGCTGTGATCATAGCTCC
26327	24414	CAGTGCTGTGATCATAGCTC
26328	24415	GCAGTGCTGTGATCATAGCT
26329	24416	CGCAGTGCTGTGATCATAGC
26330	24417	GCGCAGTGCTGTGATCATAG
26331	24418	AGCGCAGTGCTGTGATCATA
26332	24419	GAGCGCAGTGCTGTGATCAT
26333	24420	GGAGCGCAGTGCTGTGATCA
26334	24421	TGGAGCGCAGTGCTGTGATC

75411	73498	ACCATCCTGGCCAACATGGT
75412	73499	GACCATCCTGGCCAACATGG
75413	73500	AGACCATCCTGGCCAACATG
75414	73501	GAGACCATCCTGGCCAACAT
75415	73502	CGAGACCATCCTGGCCAACA
75416	73503	TCGAGACCATCCTGGCCAAC
75417	73504	ATCGAGACCATCCTGGCCAA
75418	73505	GATCGAGACCATCCTGGCCA
75419	73506	AGATCGAGACCATCCTGGCC
75420	73507	GAGATCGAGACCATCCTGGC
75421	73508	AGAGATCGAGACCATCCTGG
75422	73509	AAGAGATCGAGACCATCCTG
75423	73510	TAAGAGATCGAGACCATCCT
75424	73511	TTAAGAGATCGAGACCATCC
75425	73512	GTTAAGAGATCGAGACCATC
75426	73513	GGTTAAGAGATCGAGACCAT
75427	73514	AGGTTAAGAGATCGAGACCA
75428	73515	GAGGTTAAGAGATCGAGACC
75429	73516	TGAGGTTAAGAGATCGAGAC
75430	73517	ATGAGGTTAAGAGATCGAGA
75431	73518	CATGAGGTTAAGAGATCGAG
75432	73519	TCATGAGGTTAAGAGATCGA
75433	73520	ATCATGAGGTTAAGAGATCG
75434	73521	GATCATGAGGTTAAGAGATC
75435	73522	GGATCATGAGGTTAAGAGAT
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75439	73526	AGGTGGATCATGAGGTTAAG
75440	73527	CAGGTGGATCATGAGGTTAA
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75443	73530	AGGCAGGTGGATCATGAGGT
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75463	73550	ACCAGCACTTTGGGAGGCCC
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75465	73552	ATACCAGCACTTTGGGAGGC
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75467	73554	TAATACCAGCACTTTGGGAG
75468	73555	GTAATACCAGCACTTTGGGA
75469	73556	TGTAATACCAGCACTTTGGG
75470	73557	CTGTAATACCAGCACTTTGG
75471	73558	CCTGTAATACCAGCACTTTG
75472	73559	GCCTGTAATACCAGCACTTT
75473	73560	TGCCTGTAATACCAGCACTT
75474	73561	ATGCCTGTAATACCAGCACT
75475	73562	CATGCCTGTAATACCAGCAC
75476	73563	TCATGCCTGTAATACCAGCA
75477	73564	CTCATGCCTGTAATACCAGC
75478	73565	GCTCATGCCTGTAATACCAG
75479	73566	GGCTCATGCCTGTAATACCA
75480	73567	TGGCTCATGCCTGTAATACC
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124558	122645	ACAAATAGACACACATACAA
124559	122646	CACAAATAGACACACATACA
124560	122647	TCACAAATAGACACACATAC
124561	122648	TTCACAAATAGACACACATA
124562	122649	GTTCACAAATAGACACACAT
124563	122650	AGTTCACAAATAGACACACA
124564	122651	CAGTTCACAAATAGACACAC
124565	122652	ACAGTTCACAAATAGACACA
124566	122653	AACAGTTCACAAATAGACAC
124567	122654	AAACAGTTCACAAATAGACA
124568	122655	AAAACAGTTCACAAATAGAC
124569	122656	CAAAACAGTTCACAAATAGA
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124571	122658	AACAAAACAGTTCACAAATA
124572	122659	CAACAAAACAGTTCACAAAT
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124574	122661	TACAACAAAACAGTTCACAA
124575	122662	ATACAACAAAACAGTTCACA
124576	122663	AATACAACAAAACAGTTCAC
124577	122664	CAATACAACAAAACAGTTCA
124578	122665	TCAATACAACAAAACAGTTC
124579	122666	ATCAATACAACAAAACAGTT
124580	122667	GATCAATACAACAAAACAGT
124581	122668	AGATCAATACAACAAAACAG
124582	122669	AAGATCAATACAACAAAACA
124583	122670	AAAGATCAATACAACAAAAC
124584	122671	CAAAGATCAATACAACAAAA
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124590	122677	TATATACAAAGATCAATACA
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124594	122681	AGGATATATACAAAGATCAA
124595	122682	AAGGATATATACAAAGATCA
124596	122683	TAAGGATATATACAAAGATC
124597	122684	ATAAGGATATATACAAAGAT
124598	122685	CATAAGGATATATACAAAGA
124599	122686	GCATAAGGATATATACAAAG
124600	122687	GGCATAAGGATATATACAAA
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124611	122698	AAGAGAGAATTGGCATAAGG
124612	122699	AAAGAGAGAATTGGCATAAG
124613	122700	TAAAGAGAGAATTGGCATAA
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124615	122702	AATAAAGAGAGAATTGGCAT
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124619	122706	CAGCAATAAAGAGAGAATTG
124620	122707	ACAGCAATAAAGAGAGAATT
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124623	122710	GTAACAGCAATAAAGAGAGA
124624	122711	AGTAACAGCAATAAAGAGAG
124625	122712	AAGTAACAGCAATAAAGAGA
124626	122713	AAAGTAACAGCAATAAAGAG
124627	122714	CAAAGTAACAGCAATAAAGA
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26335	24422	CTGGAGCGCAGTGCTGTGAT
26336	24423	GCTGGAGCGCAGTGCTGTGA
26337	24424	GGCTGGAGCGCAGTGCTGTG
26338	24425	GGGCTGGAGCGCAGTGCTGT
26339	24426	GGGGCTGGAGCGCAGTGCTG
26340	24427	AGGGGCTGGAGCGCAGTGCT
26341	24428	GAGGGGCTGGAGCGCAGTGC
26342	24429	AGAGGGGCTGGAGCGCAGTG
26343	24430	AAGAGGGGCTGGAGCGCAGT
26344	24431	TAAGAGGGGCTGGAGCGCAG
26345	24432	ATAAGAGGGGCTGGAGCGCA
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26351	24438	CTGCTGATAAGAGGGGCTGG
26352	24439	ACTGCTGATAAGAGGGGCTG
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26354	24441	AGACTGCTGATAAGAGGGGC
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26356	24443	CCAGACTGCTGATAAGAGGG
26357	24444	ACCAGACTGCTGATAAGAGG
26358	24445	TACCAGACTGCTGATAAGAG
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26362	24449	AACATACCAGACTGCTGATA
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26369	24456	CCTTAGCAACATACCAGACT
26370	24457	CCCTTAGCAACATACCAGAC
26371	24458	ACCCTTAGCAACATACCAGA
26372	24459	GACCCTTAGCAACATACCAG
26373	24460	AGACCCTTAGCAACATACCA
26374	24461	AAGACCCTTAGCAACATACC
26375	24462	CAAGACCCTTAGCAACATAC
26376	24463	ACAAGACCCTTAGCAACATA
26377	24464	AACAAGACCCTTAGCAACAT
26378	24465	GAACAAGACCCTTAGCAACA
26379	24466	AGAACAAGACCCTTAGCAAC
26380	24467	AAGAACAAGACCCTTAGCAA
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26382	24469	AAAAGAACAAGACCCTTAGC
26383	24470	AAAAAGAACAAGACCCTTAG
26384	24471	TAAAAAGAACAAGACCCTTA
26385	24472	CTAAAAAGAACAAGACCCTT
26386	24473	ACTAAAAAGAACAAGACCCT
26387	24474	CACTAAAAAGAACAAGACCC
26388	24475	GCACTAAAAAGAACAAGACC
26389	24476	AGCACTAAAAAGAACAAGAC
26390	24477	AAGCACTAAAAAGAACAAGA
26391	24478	GAAGCACTAAAAAGAACAAG
26392	24479	TGAAGCACTAAAAAGAACAA
26393	24480	CTGAAGCACTAAAAAGAACA
26394	24481	CCTGAAGCACTAAAAAGAAC
26395	24482	CCCTGAAGCACTAAAAAGAA
26396	24483	TCCCTGAAGCACTAAAAAGA
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26399	24486	CTGTCCCTGAAGCACTAAAA
26400	24487	GCTGTCCCTGAAGCACTAAA
26401	24488	GGCTGTCCCTGAAGCACTAA
26402	24489	TGGCTGTCCCTGAAGCACTA
26403	24490	GTGGCTGTCCCTGAAGCACT
26404	24491	AGTGGCTGTCCCTGAAGCAC
26405	24492	CAGTGGCTGTCCCTGAAGCA

75482	73569	GGTGGCTCATGCCTGTAATA
75483	73570	TGGTGGCTCATGCCTGTAAT
75484	73571	GTGGTGGCTCATGCCTGTAA
75485	73572	TGTGGTGGCTCATGCCTGTA
75486	73573	ATGTGGTGGCTCATGCCTGT
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75488	73575	AGATGTGGTGGCTCATGCCT
75489	73576	CAGATGTGGTGGCTCATGCC
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75492	73579	GGCCAGATGTGGTGGCTCAT
75493	73580	TGGCCAGATGTGGTGGCTCA
75494	73581	CTGGCCAGATGTGGTGGCTC
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75496	73583	TTCTGGCCAGATGTGGTGGC
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75498	73585	ATTTCTGGCCAGATGTGGTG
75499	73586	AATTTCTGGCCAGATGTGGT
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75504	73591	AAGAAAATTTCTGGCCAGAT
75505	73592	CAAGAAAATTTCTGGCCAGA
75506	73593	CCAAGAAAATTTCTGGCCAG
75507	73594	ACCAAGAAAATTTCTGGCCA
75508	73595	GACCAAGAAAATTTCTGGCC
75509	73596	TGACCAAGAAAATTTCTGGC
75510	73597	GTGACCAAGAAAATTTCTGG
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75513	73600	GAAGTGACCAAGAAAATTTC
75514	73601	AGAAGTGACCAAGAAAATTT
75515	73602	CAGAAGTGACCAAGAAAATT
75516	73603	TCAGAAGTGACCAAGAAAAT
75517	73604	CTCAGAAGTGACCAAGAAAA
75518	73605	TCTCAGAAGTGACCAAGAAA
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75522	73609	CATGTCTCAGAAGTGACCAA
75523	73610	GCATGTCTCAGAAGTGACCA
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75526	73613	TCTGCATGTCTCAGAAGTGA
75527	73614	CTCTGCATGTCTCAGAAGTG
75528	73615	ACTCTGCATGTCTCAGAAGT
75529	73616	TACTCTGCATGTCTCAGAAG
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75531	73618	ATTACTCTGCATGTCTCAGA
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75533	73620	TAATTACTCTGCATGTCTCA
75534	73621	GTAATTACTCTGCATGTCTC
75535	73622	GGTAATTACTCTGCATGTCT
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124634	122721	TTGGTTACAAAGTAACAGCA
124635	122722	GTTGGTTACAAAGTAACAGC
124636	122723	GGTTGGTTACAAAGTAACAG
124637	122724	AGGTTGGTTACAAAGTAACA
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124639	122726	AAAGGTTGGTTACAAAGTAA
124640	122727	TAAAGGTTGGTTACAAAGTA
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124658	122745	GGGAGACTCATATGAACTTA
124659	122746	TGGGAGACTCATATGAACTT
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26412	24499	GCATAGCCAGTGGCTGTCCC
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26527	24614	TAAACTCACGGTAGCGTCCG
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75683	73770	TGTTAGCCAGGCTGGTCTTG
75684	73771	GTGTTAGCCAGGCTGGTCTT
75685	73772	CGTGTTAGCCAGGCTGGTCT
75686	73773	CCGTGTTAGCCAGGCTGGTC
75687	73774	ACCGTGTTAGCCAGGCTGGT
75688	73775	CACCGTGTTAGCCAGGCTGG
75689	73776	TCACCGTGTTAGCCAGGCTG
75690	73777	TTCACCGTGTTAGCCAGGCT
75691	73778	TTTCACCGTGTTAGCCAGGC
75692	73779	GTTTCACCGTGTTAGCCAGG
75693	73780	GGTTTCACCGTGTTAGCCAG
75694	73781	GGGTTTCACCGTGTTAGCCA

124771	122858	TATTTCTCCCAGAACTGATA
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124773	122860	GATATTTCTCCCAGAACTGA
124774	122861	AGATATTTCTCCCAGAACTG
124775	122862	AAGATATTTCTCCCAGAACT
124776	122863	TAAGATATTTCTCCCAGAAC
124777	122864	TTAAGATATTTCTCCCAGAA
124778	122865	GTTAAGATATTTCTCCCAGA
124779	122866	TGTTAAGATATTTCTCCCAG
124780	122867	TTGTTAAGATATTTCTCCCA
124781	122868	ATTGTTAAGATATTTCTCCC
124782	122869	TATTGTTAAGATATTTCTCC
124783	122870	ATATTGTTAAGATATTTCTC
124784	122871	CATATTGTTAAGATATTTCT
124785	122872	CCATATTGTTAAGATATTTC
124786	122873	TCCATATTGTTAAGATATTT
124787	122874	TTCCATATTGTTAAGATATT
124788	122875	ATTCCATATTGTTAAGATAT
124789	122876	GATTCCATATTGTTAAGATA
124790	122877	AGATTCCATATTGTTAAGAT
124791	122878	AAGATTCCATATTGTTAAGA
124792	122879	GAAGATTCCATATTGTTAAG
124793	122880	TGAAGATTCCATATTGTTAA
124794	122881	ATGAAGATTCCATATTGTTA
124795	122882	AATGAAGATTCCATATTGTT
124796	122883	CAATGAAGATTCCATATTGT
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124799	122886	CCTCAATGAAGATTCCATAT
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124807	122894	TATGATGACCTCAATGAAGA
124808	122895	ATATGATGACCTCAATGAAG
124809	122896	TATATGATGACCTCAATGAA
124810	122897	GTATATGATGACCTCAATGA
124811	122898	AGTATATGATGACCTCAATG
124812	122899	CAGTATATGATGACCTCAAT
124813	122900	GCAGTATATGATGACCTCAA
124814	122901	AGCAGTATATGATGACCTCA
124815	122902	GAGCAGTATATGATGACCTC
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124817	122904	TGGAGCAGTATATGATGACC
124818	122905	ATGGAGCAGTATATGATGAC
124819	122906	AATGGAGCAGTATATGATGA
124820	122907	AAATGGAGCAGTATATGATG
124821	122908	TAAATGGAGCAGTATATGAT
124822	122909	ATAAATGGAGCAGTATATGA
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124824	122911	AAATAAATGGAGCAGTATAT
124825	122912	TAAATAAATGGAGCAGTATA
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124827	122914	CTTAAATAAATGGAGCAGTA
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124841	122928	GGTGAAACTTAAGACTTAAA

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26550	24637	AGATTATGTATGCCCTGGGA
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26559	24646	AATCACATGAGATTATGTAT
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26569	24656	GCTATGTGGTAATCACATGA
26570	24657	GGCTATGTGGTAATCACATG
26571	24658	GGGCTATGTGGTAATCACAT
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26574	24661	ACAGGGCTATGTGGTAATCA
26575	24662	AACAGGGCTATGTGGTAATC
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26597	24684	AGGACAGGATAACAGATTAT
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26599	24686	TGAGGACAGGATAACAGATT
26600	24687	ATGAGGACAGGATAACAGAT
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26615	24702	TTCCTCATGGGTAAAATGAG
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26617	24704	ATTTCCTCATGGGTAAAATG
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75695	73782	GGGGTTTCACCGTGTTAGCC
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75718	73805	AATTTTTTGTATTTTTAGTA
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75720	73807	ATAATTTTTTGTATTTTTAG
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75725	73812	CCCGGATAATTTTTTGTATT
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75746	73833	CTACAGGTGTGTACCACCAC
75747	73834	ACTACAGGTGTGTACCACCA
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75754	73841	AGCTGGGACTACAGGTGTGT
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75761	73848	CCCGAGTAGCTGGGACTACA
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75764	73851	TCTCCCGAGTAGCTGGGACT
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124857	122944	AAAACTAGAAAACACTGGTG
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124865	122952	ATACAAAGAAAACTAGAAAA
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124869	122956	ACTGATACAAAGAAAACTAG
124870	122957	AACTGATACAAAGAAAACTA
124871	122958	AAACTGATACAAAGAAAACT
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26619	24706	TCATTTCCTCATGGGTAAAA
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26626	24713	TGGGCCTTCATTTCCTCATG
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26637	24724	TTTAACCTCTCTGGGCCTTC
26638	24725	ATTTAACCTCTCTGGGCCTT
26639	24726	CATTTAACCTCTCTGGGCCT
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75796	73883	CCTCCCGGGTTCAAGCGATT
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75799	73886	CTGCCTCCCGGGTTCAAGCG
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75806	73893	GCAACCTCTGCCTCCCGGGT
75807	73894	TGCAACCTCTGCCTCCCGGG
75808	73895	CTGCAACCTCTGCCTCCCGG
75809	73896	ACTGCAACCTCTGCCTCCCG
75810	73897	CACTGCAACCTCTGCCTCCC
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75812	73899	CTCACTGCAACCTCTGCCTC
75813	73900	GCTCACTGCAACCTCTGCCT
75814	73901	GGCTCACTGCAACCTCTGCC
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75817	73904	CTCGGCTCACTGCAACCTCT
75818	73905	TCTCGGCTCACTGCAACCTC
75819	73906	ATCTCGGCTCACTGCAACCT
75820	73907	GATCTCGGCTCACTGCAACC
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75822	73909	GTGATCTCGGCTCACTGCAA
75823	73910	CGTGATCTCGGCTCACTGCA
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124920	123007	GCACAAAACAGATGAAATAT
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124923	123010	ACAGCACAAAACAGATGAAA
124924	123011	AACAGCACAAAACAGATGAA
124925	123012	CAACAGCACAAAACAGATGA
124926	123013	ACAACAGCACAAAACAGATG
124927	123014	CACAACAGCACAAAACAGAT
124928	123015	TCACAACAGCACAAAACAGA
124929	123016	CTCACAACAGCACAAAACAG
124930	123017	ACTCACAACAGCACAAAACA
124931	123018	AACTCACAACAGCACAAAAC
124932	123019	TAACTCACAACAGCACAAAA
124933	123020	ATAACTCACAACAGCACAAA
124934	123021	TATAACTCACAACAGCACAA
124935	123022	ATATAACTCACAACAGCACA
124936	123023	AATATAACTCACAACAGCAC
124937	123024	AAATATAACTCACAACAGCA
124938	123025	AAAATATAACTCACAACAGC
124939	123026	TAAAATATAACTCACAACAG
124940	123027	TTAAAATATAACTCACAACA
124941	123028	TTTAAAATATAACTCACAAC
124942	123029	TTTTAAAATATAACTCACAA
124943	123030	TTTTTAAAATATAACTCACA
124944	123031	GTTTTTAAAATATAACTCAC
124945	123032	AGTTTTTAAAATATAACTCA
124946	123033	AAGTTTTTAAAATATAACTC
124947	123034	AAAGTTTTTAAAATATAACT
124948	123035	GAAAGTTTTTAAAATATAAC
124949	123036	TGAAAGTTTTTAAAATATAA
124950	123037	TTGAAAGTTTTTAAAATATA
124951	123038	GTTGAAAGTTTTTAAAATAT
124952	123039	CGTTGAAAGTTTTTAAAATA
124953	123040	ACGTTGAAAGTTTTTAAAAT
124954	123041	AACGTTGAAAGTTTTTAAAA
124955	123042	AAACGTTGAAAGTTTTTAAA
124956	123043	CAAACGTTGAAAGTTTTTAA
124957	123044	ACAAACGTTGAAAGTTTTTA
124958	123045	AACAAACGTTGAAAGTTTTT
124959	123046	AAACAAACGTTGAAAGTTTT
124960	123047	TAAACAAACGTTGAAAGTTT
124961	123048	ATAAACAAACGTTGAAAGTT
124962	123049	AATAAACAAACGTTGAAAGT
124963	123050	GAATAAACAAACGTTGAAAG
124964	123051	CGAATAAACAAACGTTGAAA
124965	123052	ACGAATAAACAAACGTTGAA
124966	123053	TACGAATAAACAAACGTTGA
124967	123054	TTACGAATAAACAAACGTTG
124968	123055	TTTACGAATAAACAAACGTT
124969	123056	ATTTACGAATAAACAAACGT
124970	123057	TATTTACGAATAAACAAACG
124971	123058	CTATTTACGAATAAACAAAC
124972	123059	TCTATTTACGAATAAACAAA
124973	123060	CTCTATTTACGAATAAACAA
124974	123061	TCTCTATTTACGAATAAACA
124975	123062	ATCTCTATTTACGAATAAAC
124976	123063	CATCTCTATTTACGAATAAA
124977	123064	GCATCTCTATTTACGAATAA
124978	123065	TGCATCTCTATTTACGAATA
124979	123066	GTGCATCTCTATTTACGAAT
124980	123067	AGTGCATCTCTATTTACGAA
124981	123068	AAGTGCATCTCTATTTACGA
124982	123069	CAAGTGCATCTCTATTTACG
124983	123070	TCAAGTGCATCTCTATTTAC

26690	24777	TACAATGATAGTAACTCATC
26691	24778	ATACAATGATAGTAACTCAT
26692	24779	AATACAATGATAGTAACTCA
26693	24780	AAATACAATGATAGTAACTC
26694	24781	AAAATACAATGATAGTAACT
26695	24782	CAAAATACAATGATAGTAAC
26696	24783	CCAAAATACAATGATAGTAA
26697	24784	TCCAAAATACAATGATAGTA
26698	24785	ATCCAAAATACAATGATAGT
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26700	24787	AGATCCAAAATACAATGATA
26701	24788	GAGATCCAAAATACAATGAT
26702	24789	AGAGATCCAAAATACAATGA
26703	24790	CAGAGATCCAAAATACAATG
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26705	24792	TCCAGAGATCCAAAATACAA
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26707	24794	TTTCCAGAGATCCAAAATAC
26708	24795	CTTTCCAGAGATCCAAAATA
26709	24796	TCTTTCCAGAGATCCAAAAT
26710	24797	TTCTTTCCAGAGATCCAAAA
26711	24798	TTTCTTTCCAGAGATCCAAA
26712	24799	CTTTCTTTCCAGAGATCCAA
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26715	24802	TTTCTTTCTTTCCAGAGATC
26716	24803	TTTTCTTTCTTTCCAGAGAT
26717	24804	GTTTTCTTTCTTTCCAGAGA
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26719	24806	TAGTTTTCTTTCTTTCCAGA
26720	24807	CTAGTTTTCTTTCTTTCCAG
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26722	24809	CACTAGTTTTCTTTCTTTCC
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26724	24811	ATCACTAGTTTTCTTTCTTT
26725	24812	CATCACTAGTTTTCTTTCTT
26726	24813	CCATCACTAGTTTTCTTTCT
26727	24814	ACCATCACTAGTTTTCTTTC
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26735	24822	TTTTTAATACCATCACTAGT
26736	24823	TTTTTTAATACCATCACTAG
26737	24824	ATTTTTTAATACCATCACTA
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26739	24826	ACATTTTTTAATACCATCAC
26740	24827	AACATTTTTTAATACCATCA
26741	24828	TAACATTTTTTAATACCATC
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26748	24835	CTATTAATAACATTTTTTAA
26749	24836	ACTATTAATAACATTTTTTA
26750	24837	AACTATTAATAACATTTTTT
26751	24838	AAACTATTAATAACATTTTT
26752	24839	GAAACTATTAATAACATTTT
26753	24840	AGAAACTATTAATAACATTT
26754	24841	AAGAAACTATTAATAACATT
26755	24842	AAAGAAACTATTAATAACAT
26756	24843	AAAAGAAACTATTAATAACA
26757	24844	TAAAAGAAACTATTAATAAC
26758	24845	TTAAAAGAAACTATTAATAA
26759	24846	ATTAAAAGAAACTATTAATA
26760	24847	GATTAAAAGAAACTATTAAT

75837	73924	CTGGAATGCAGTGGCGTGAT
75838	73925	GCTGGAATGCAGTGGCGTGA
75839	73926	GGCTGGAATGCAGTGGCGTG
75840	73927	AGGCTGGAATGCAGTGGCGT
75841	73928	CAGGCTGGAATGCAGTGGCG
75842	73929	CCAGGCTGGAATGCAGTGGC
75843	73930	CCCAGGCTGGAATGCAGTGG
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75845	73932	TGCCCAGGCTGGAATGCAGT
75846	73933	TTGCCCAGGCTGGAATGCAG
75847	73934	GTTGCCCAGGCTGGAATGCA
75848	73935	TGTTGCCCAGGCTGGAATGC
75849	73936	CTGTTGCCCAGGCTGGAATG
75850	73937	TCTGTTGCCCAGGCTGGAAT
75851	73938	TTCTGTTGCCCAGGCTGGAA
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75853	73940	CGTTCTGTTGCCCAGGCTGG
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75859	73946	GAGTCTCGTTCTGTTGCCCA
75860	73947	AGAGTCTCGTTCTGTTGCCC
75861	73948	TAGAGTCTCGTTCTGTTGCC
75862	73949	ATAGAGTCTCGTTCTGTTGC
75863	73950	GATAGAGTCTCGTTCTGTTG
75864	73951	AGATAGAGTCTCGTTCTGTT
75865	73952	GAGATAGAGTCTCGTTCTGT
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75878	73965	TTTTTTTTTTTTTGAGATAG
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75884	73971	GCATTTTTTTTTTTTTTTTG
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75888	73975	CGAAGCATTTTTTTTTTTTT
75889	73976	ACGAAGCATTTTTTTTTTTT
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75891	73978	ACACGAAGCATTTTTTTTTT
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75894	73981	GCCACACGAAGCATTTTTTT
75895	73982	AGCCACACGAAGCATTTTTT
75896	73983	AAGCCACACGAAGCATTTTT
75897	73984	TAAGCCACACGAAGCATTTT
75898	73985	TTAAGCCACACGAAGCATTT
75899	73986	TTTAAGCCACACGAAGCATT
75900	73987	TTTTAAGCCACACGAAGCAT
75901	73988	ATTTTAAGCCACACGAAGCA
75902	73989	AATTTTAAGCCACACGAAGC
75903	73990	TAATTTTAAGCCACACGAAG
75904	73991	ATAATTTTAAGCCACACGAA
75905	73992	TATAATTTTAAGCCACACGA
75906	73993	ATATAATTTTAAGCCACACG
75907	73994	CATATAATTTTAAGCCACAC

124984	123071	ATCAAGTGCATCTCTATTTA
124985	123072	AATCAAGTGCATCTCTATTT
124986	123073	AAATCAAGTGCATCTCTATT
124987	123074	AAAATCAAGTGCATCTCTAT
124988	123075	AAAAATCAAGTGCATCTCTA
124989	123076	CAAAAATCAAGTGCATCTCT
124990	123077	TCAAAAATCAAGTGCATCTC
124991	123078	TTCAAAAATCAAGTGCATCT
124992	123079	ATTCAAAAATCAAGTGCATC
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125002	123089	CAAGGTCAATATTCAAAAAT
125003	123090	ACAAGGTCAATATTCAAAAA
125004	123091	CACAAGGTCAATATTCAAAA
125005	123092	ACACAAGGTCAATATTCAAA
125006	123093	GACACAAGGTCAATATTCAA
125007	123094	AGACACAAGGTCAATATTCA
125008	123095	AAGACACAAGGTCAATATTC
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125010	123097	TCAAGACACAAGGTCAATAT
125011	123098	ATCAAGACACAAGGTCAATA
125012	123099	CATCAAGACACAAGGTCAAT
125013	123100	ACATCAAGACACAAGGTCAA
125014	123101	CACATCAAGACACAAGGTCA
125015	123102	ACACATCAAGACACAAGGTC
125016	123103	AACACATCAAGACACAAGGT
125017	123104	CAACACATCAAGACACAAGG
125018	123105	CCAACACATCAAGACACAAG
125019	123106	ACCAACACATCAAGACACAA
125020	123107	TACCAACACATCAAGACACA
125021	123108	TTACCAACACATCAAGACAC
125022	123109	TTTACCAACACATCAAGACA
125023	123110	GTTTACCAACACATCAAGAC
125024	123111	GGTTTACCAACACATCAAGA
125025	123112	GGGTTTACCAACACATCAAG
125026	123113	TGGGTTTACCAACACATCAA
125027	123114	GTGGGTTTACCAACACATCA
125028	123115	AGTGGGTTTACCAACACATC
125029	123116	CAGTGGGTTTACCAACACAT
125030	123117	ACAGTGGGTTTACCAACACA
125031	123118	AACAGTGGGTTTACCAACAC
125032	123119	AAACAGTGGGTTTACCAACA
125033	123120	GAAACAGTGGGTTTACCAAC
125034	123121	AGAAACAGTGGGTTTACCAA
125035	123122	CAGAAACAGTGGGTTTACCA
125036	123123	CCAGAAACAGTGGGTTTACC
125037	123124	GCCAGAAACAGTGGGTTTAC
125038	123125	TGCCAGAAACAGTGGGTTTA
125039	123126	CTGCCAGAAACAGTGGGTTT
125040	123127	GCTGCCAGAAACAGTGGGTT
125041	123128	GGCTGCCAGAAACAGTGGGT
125042	123129	GGGCTGCCAGAAACAGTGGG
125043	123130	AGGGCTGCCAGAAACAGTGG
125044	123131	AAGGGCTGCCAGAAACAGTG
125045	123132	AAAGGGCTGCCAGAAACAGT
125046	123133	TAAAGGGCTGCCAGAAACAG
125047	123134	TTAAAGGGCTGCCAGAAACA
125048	123135	CTTAAAGGGCTGCCAGAAAC
125049	123136	TCTTAAAGGGCTGCCAGAAA
125050	123137	GTCTTAAAGGGCTGCCAGAA
125051	123138	AGTCTTAAAGGGCTGCCAGA
125052	123139	AAGTCTTAAAGGGCTGCCAG
125053	123140	TAAGTCTTAAAGGGCTGCCA
125054	123141	TTAAGTCTTAAAGGGCTGCC

26761	24848	TGATTAAAAGAAACTATTAA
26762	24849	TTGATTAAAAGAAACTATTA
26763	24850	GTTGATTAAAAGAAACTATT
26764	24851	GGTTGATTAAAAGAAACTAT
26765	24852	TGGTTGATTAAAAGAAACTA
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26769	24856	TTCCTGGTTGATTAAAAGAA
26770	24857	GTTCCTGGTTGATTAAAAGA
26771	24858	AGTTCCTGGTTGATTAAAAG
26772	24859	AAGTTCCTGGTTGATTAAAA
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26774	24861	TCAAGTTCCTGGTTGATTAA
26775	24862	CTCAAGTTCCTGGTTGATTA
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26778	24865	TGACTCAAGTTCCTGGTTGA
26779	24866	GTGACTCAAGTTCCTGGTTG
26780	24867	AGTGACTCAAGTTCCTGGTT
26781	24868	TAGTGACTCAAGTTCCTGGT
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26784	24871	AGCTAGTGACTCAAGTTCCT
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26787	24874	AGAAGCTAGTGACTCAAGTT
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26789	24876	AGAGAAGCTAGTGACTCAAG
26790	24877	CAGAGAAGCTAGTGACTCAA
26791	24878	CCAGAGAAGCTAGTGACTCA
26792	24879	CCCAGAGAAGCTAGTGACTC
26793	24880	ACCCAGAGAAGCTAGTGACT
26794	24881	CACCCAGAGAAGCTAGTGAC
26795	24882	TCACCCAGAGAAGCTAGTGA
26796	24883	TTCACCCAGAGAAGCTAGTG
26797	24884	CTTCACCCAGAGAAGCTAGT
26798	24885	CCTTCACCCAGAGAAGCTAG
26799	24886	TCCTTCACCCAGAGAAGCTA
26800	24887	GTCCTTCACCCAGAGAAGCT
26801	24888	AGTCCTTCACCCAGAGAAGC
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26803	24890	ATAGTCCTTCACCCAGAGAA
26804	24891	TATAGTCCTTCACCCAGAGA
26805	24892	GTATAGTCCTTCACCCAGAG
26806	24893	AGTATAGTCCTTCACCCAGA
26807	24894	AAGTATAGTCCTTCACCCAG
26808	24895	GAAGTATAGTCCTTCACCCA
26809	24896	TGAAGTATAGTCCTTCACCC
26810	24897	TTGAAGTATAGTCCTTCACC
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26812	24899	TGTTGAAGTATAGTCCTTCA
26813	24900	CTGTTGAAGTATAGTCCTTC
26814	24901	ACTGTTGAAGTATAGTCCTT
26815	24902	TACTGTTGAAGTATAGTCCT
26816	24903	ATACTGTTGAAGTATAGTCC
26817	24904	CATACTGTTGAAGTATAGTC
26818	24905	TCATACTGTTGAAGTATAGT
26819	24906	TTCATACTGTTGAAGTATAG
26820	24907	TTTCATACTGTTGAAGTATA
26821	24908	TTTTCATACTGTTGAAGTAT
26822	24909	TTTTTCATACTGTTGAAGTA
26823	24910	GTTTTTCATACTGTTGAAGT
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26825	24912	CCGTTTTTCATACTGTTGAA
26826	24913	TCCGTTTTTCATACTGTTGA
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26828	24915	TTTCCGTTTTTCATACTGTT
26829	24916	TTTTCCGTTTTTCATACTGT
26830	24917	CTTTTCCGTTTTTCATACTG
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75908	73995	TCATATAATTTTAAGCCACA
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75910	73997	TTTCATATAATTTTAAGCCA
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75916	74003	TTTTCTTTTCATATAATTTT
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75918	74005	TATTTTCTTTTCATATAATT
75919	74006	GTATTTTCTTTTCATATAAT
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75925	74012	GTAAAGGTATTTTCTTTTCA
75926	74013	AGTAAAGGTATTTTCTTTTC
75927	74014	CAGTAAAGGTATTTTCTTTT
75928	74015	TCAGTAAAGGTATTTTCTTT
75929	74016	ATCAGTAAAGGTATTTTCTT
75930	74017	TATCAGTAAAGGTATTTTCT
75931	74018	CTATCAGTAAAGGTATTTTC
75932	74019	ACTATCAGTAAAGGTATTTT
75933	74020	GACTATCAGTAAAGGTATTT
75934	74021	TGACTATCAGTAAAGGTATT
75935	74022	ATGACTATCAGTAAAGGTAT
75936	74023	GATGACTATCAGTAAAGGTA
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75938	74025	CAGATGACTATCAGTAAAGG
75939	74026	ACAGATGACTATCAGTAAAG
75940	74027	CACAGATGACTATCAGTAAA
75941	74028	TCACAGATGACTATCAGTAA
75942	74029	ATCACAGATGACTATCAGTA
75943	74030	AATCACAGATGACTATCAGT
75944	74031	GAATCACAGATGACTATCAG
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75946	74033	TGGAATCACAGATGACTATC
75947	74034	ATGGAATCACAGATGACTAT
75948	74035	AATGGAATCACAGATGACTA
75949	74036	AAATGGAATCACAGATGACT
75950	74037	CAAATGGAATCACAGATGAC
75951	74038	GCAAATGGAATCACAGATGA
75952	74039	AGCAAATGGAATCACAGATG
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75954	74041	TTAGCAAATGGAATCACAGA
75955	74042	TTTAGCAAATGGAATCACAG
75956	74043	ATTTAGCAAATGGAATCACA
75957	74044	AATTTAGCAAATGGAATCAC
75958	74045	TAATTTAGCAAATGGAATCA
75959	74046	TTAATTTAGCAAATGGAATC
75960	74047	TTTAATTTAGCAAATGGAAT
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75974	74061	AGTATGCTTTCACGTTTAAT
75975	74062	AAGTATGCTTTCACGTTTAA
75976	74063	AAAGTATGCTTTCACGTTTA
75977	74064	AAAAGTATGCTTTCACGTTT
75978	74065	TAAAAGTATGCTTTCACGTT

125055	123142	TTTAAGTCTTAAAGGGCTGC
125056	123143	GTTTAAGTCTTAAAGGGCTG
125057	123144	TGTTTAAGTCTTAAAGGGCT
125058	123145	ATGTTTAAGTCTTAAAGGGC
125059	123146	TATGTTTAAGTCTTAAAGGG
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125065	123152	TGATTGTATGTTTAAGTCTT
125066	123153	ATGATTGTATGTTTAAGTCT
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125070	123157	GATCATGATTGTATGTTTAA
125071	123158	AGATCATGATTGTATGTTTA
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125074	123161	ATTAGATCATGATTGTATGT
125075	123162	GATTAGATCATGATTGTATG
125076	123163	TGATTAGATCATGATTGTAT
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125086	123173	ACCAACATGGTGATTAGATC
125087	123174	CACCAACATGGTGATTAGAT
125088	123175	ACACCAACATGGTGATTAGA
125089	123176	AACACCAACATGGTGATTAG
125090	123177	AAACACCAACATGGTGATTA
125091	123178	AAAACACCAACATGGTGATT
125092	123179	AAAAACACCAACATGGTGAT
125093	123180	CAAAAACACCAACATGGTGA
125094	123181	CCAAAAACACCAACATGGTG
125095	123182	CCCAAAAACACCAACATGGT
125096	123183	ACCCAAAAACACCAACATGG
125097	123184	AACCCAAAAACACCAACATG
125098	123185	AAACCCAAAAACACCAACAT
125099	123186	AAAACCCAAAAACACCAACA
125100	123187	AAAAACCCAAAAACACCAAC
125101	123188	AAAAAACCCAAAAACACCAA
125102	123189	AAAAAAACCCAAAAACACCA
125103	123190	AAAAAAAACCCAAAAACACC
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125105	123192	AAAAAAAAAACCCAAAAACA
125106	123193	AAAAAAAAAAACCCAAAAAC
125107	123194	AAAAAAAAAAAACCCAAAAA
125108	123195	CAAAAAAAAAAAACCCAAAA
125109	123196	ACAAAAAAAAAAAACCCAAA
125110	123197	GACAAAAAAAAAAAACCCAA
125111	123198	AGACAAAAAAAAAAAACCCA
125112	123199	AAGACAAAAAAAAAAAACCC
125113	123200	TAAGACAAAAAAAAAAAACC
125114	123201	ATAAGACAAAAAAAAAAAAC
125115	123202	AATAAGACAAAAAAAAAAAA
125116	123203	CAATAAGACAAAAAAAAAAA
125117	123204	ACAATAAGACAAAAAAAAAA
125118	123205	TACAATAAGACAAAAAAAAA
125119	123206	GTACAATAAGACAAAAAAAA
125120	123207	AGTACAATAAGACAAAAAAA
125121	123208	CAGTACAATAAGACAAAAAA
125122	123209	CCAGTACAATAAGACAAAAA
125123	123210	ACCAGTACAATAAGACAAAA
125124	123211	CACCAGTACAATAAGACAAA
125125	123212	GCACCAGTACAATAAGACAA

26832	24919	TTCTTTTCCGTTTTTCATAC
26833	24920	TTTCTTTTCCGTTTTTCATA
26834	24921	TTTTCTTTTCCGTTTTTCAT
26835	24922	ATTTTCTTTTCCGTTTTTCA
26836	24923	CATTTTCTTTTCCGTTTTTC
26837	24924	TCATTTTCTTTTCCGTTTTT
26838	24925	CTCATTTTCTTTTCCGTTTT
26839	24926	CCTCATTTTCTTTTCCGTTT
26840	24927	TCCTCATTTTCTTTTCCGTT
26841	24928	TTCCTCATTTTCTTTTCCGT
26842	24929	ATTCCTCATTTTCTTTTCCG
26843	24930	AATTCCTCATTTTCTTTTCC
26844	24931	AAATTCCTCATTTTCTTTTC
26845	24932	AAAATTCCTCATTTTCTTTT
26846	24933	CAAAATTCCTCATTTTCTTT
26847	24934	CCAAAATTCCTCATTTTCTT
26848	24935	GCCAAAATTCCTCATTTTCT
26849	24936	AGCCAAAATTCCTCATTTTC
26850	24937	CAGCCAAAATTCCTCATTTT
26851	24938	CCAGCCAAAATTCCTCATTT
26852	24939	CCCAGCCAAAATTCCTCATT
26853	24940	GCCCAGCCAAAATTCCTCAT
26854	24941	TGCCCAGCCAAAATTCCTCA
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26858	24945	ACTGTGCCCAGCCAAAATTC
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26866	24953	TGTGAGCCACTGTGCCCAGC
26867	24954	GTGTGAGCCACTGTGCCCAG
26868	24955	GGTGTGAGCCACTGTGCCCA
26869	24956	AGGTGTGAGCCACTGTGCCC
26870	24957	CAGGTGTGAGCCACTGTGCC
26871	24958	ACAGGTGTGAGCCACTGTGC
26872	24959	TACAGGTGTGAGCCACTGTG
26873	24960	TTACAGGTGTGAGCCACTGT
26874	24961	ATTACAGGTGTGAGCCACTG
26875	24962	AATTACAGGTGTGAGCCACT
26876	24963	GAATTACAGGTGTGAGCCAC
26877	24964	AGAATTACAGGTGTGAGCCA
26878	24965	TAGAATTACAGGTGTGAGCC
26879	24966	CTAGAATTACAGGTGTGAGC
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26881	24968	TGCTAGAATTACAGGTGTGA
26882	24969	GTGCTAGAATTACAGGTGTG
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26884	24971	AAGTGCTAGAATTACAGGTG
26885	24972	AAAGTGCTAGAATTACAGGT
26886	24973	CAAAGTGCTAGAATTACAGG
26887	24974	CCAAAGTGCTAGAATTACAG
26888	24975	CCCAAAGTGCTAGAATTACA
26889	24976	TCCCAAAGTGCTAGAATTAC
26890	24977	TTCCCAAAGTGCTAGAATTA
26891	24978	CTTCCCAAAGTGCTAGAATT
26892	24979	GCTTCCCAAAGTGCTAGAAT
26893	24980	GGCTTCCCAAAGTGCTAGAA
26894	24981	TGGCTTCCCAAAGTGCTAGA
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26898	24985	CCCTTGGCTTCCCAAAGTGC
26899	24986	TCCCTTGGCTTCCCAAAGTG
26900	24987	CTCCCTTGGCTTCCCAAAGT
26901	24988	CCTCCCTTGGCTTCCCAAAG
26902	24989	TCCTCCCTTGGCTTCCCAAA

75979	74066	GTAAAAGTATGCTTTCACGT
75980	74067	AGTAAAAGTATGCTTTCACG
75981	74068	CAGTAAAAGTATGCTTTCAC
75982	74069	TCAGTAAAAGTATGCTTTCA
75983	74070	TTCAGTAAAAGTATGCTTTC
75984	74071	ATTCAGTAAAAGTATGCTTT
75985	74072	TATTCAGTAAAAGTATGCTT
75986	74073	GTATTCAGTAAAAGTATGCT
75987	74074	AGTATTCAGTAAAAGTATGC
75988	74075	TAGTATTCAGTAAAAGTATG
75989	74076	ATAGTATTCAGTAAAAGTAT
75990	74077	TATAGTATTCAGTAAAAGTA
75991	74078	ATATAGTATTCAGTAAAAGT
75992	74079	TATATAGTATTCAGTAAAAG
75993	74080	ATATATAGTATTCAGTAAAA
75994	74081	AATATATAGTATTCAGTAAA
75995	74082	GAATATATAGTATTCAGTAA
75996	74083	GGAATATATAGTATTCAGTA
75997	74084	CGGAATATATAGTATTCAGT
75998	74085	ACGGAATATATAGTATTCAG
75999	74086	TACGGAATATATAGTATTCA
76000	74087	ATACGGAATATATAGTATTC
76001	74088	GATACGGAATATATAGTATT
76002	74089	TGATACGGAATATATAGTAT
76003	74090	CTGATACGGAATATATAGTA
76004	74091	ACTGATACGGAATATATAGT
76005	74092	AACTGATACGGAATATATAG
76006	74093	AAACTGATACGGAATATATA
76007	74094	TAAACTGATACGGAATATAT
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76009	74096	TCTAAACTGATACGGAATAT
76010	74097	ATCTAAACTGATACGGAATA
76011	74098	TATCTAAACTGATACGGAAT
76012	74099	CTATCTAAACTGATACGGAA
76013	74100	GCTATCTAAACTGATACGGA
76014	74101	TGCTATCTAAACTGATACGG
76015	74102	CTGCTATCTAAACTGATACG
76016	74103	ACTGCTATCTAAACTGATAC
76017	74104	AACTGCTATCTAAACTGATA
76018	74105	AAACTGCTATCTAAACTGAT
76019	74106	TAAACTGCTATCTAAACTGA
76020	74107	ATAAACTGCTATCTAAACTG
76021	74108	GATAAACTGCTATCTAAACT
76022	74109	AGATAAACTGCTATCTAAAC
76023	74110	AAGATAAACTGCTATCTAAA
76024	74111	GAAGATAAACTGCTATCTAA
76025	74112	TGAAGATAAACTGCTATCTA
76026	74113	GTGAAGATAAACTGCTATCT
76027	74114	TGTGAAGATAAACTGCTATC
76028	74115	ATGTGAAGATAAACTGCTAT
76029	74116	TATGTGAAGATAAACTGCTA
76030	74117	GTATGTGAAGATAAACTGCT
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76033	74120	TATGTATGTGAAGATAAACT
76034	74121	TTATGTATGTGAAGATAAAC
76035	74122	CTTATGTATGTGAAGATAAA
76036	74123	ACTTATGTATGTGAAGATAA
76037	74124	AACTTATGTATGTGAAGATA
76038	74125	AAACTTATGTATGTGAAGAT
76039	74126	AAAACTTATGTATGTGAAGA
76040	74127	TAAAACTTATGTATGTGAAG
76041	74128	TTAAAACTTATGTATGTGAA
76042	74129	CTTAAAACTTATGTATGTGA
76043	74130	ACTTAAAACTTATGTATGTG
76044	74131	AACTTAAAACTTATGTATGT
76045	74132	AAACTTAAAACTTATGTATG
76046	74133	TAAACTTAAAACTTATGTAT
76047	74134	GTAAACTTAAAACTTATGTA
76048	74135	GGTAAACTTAAAACTTATGT
76049	74136	AGGTAAACTTAAAACTTATG

125126	123213	TGCACCAGTACAATAAGACA
125127	123214	ATGCACCAGTACAATAAGAC
125128	123215	AATGCACCAGTACAATAAGA
125129	123216	TAATGCACCAGTACAATAAG
125130	123217	GTAATGCACCAGTACAATAA
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125132	123219	CAGTAATGCACCAGTACAAT
125133	123220	TCAGTAATGCACCAGTACAA
125134	123221	TTCAGTAATGCACCAGTACA
125135	123222	TTTCAGTAATGCACCAGTAC
125136	123223	TTTTCAGTAATGCACCAGTA
125137	123224	TTTTTCAGTAATGCACCAGT
125138	123225	CTTTTTCAGTAATGCACCAG
125139	123226	CCTTTTTCAGTAATGCACCA
125140	123227	GCCTTTTTCAGTAATGCACC
125141	123228	TGCCTTTTTCAGTAATGCAC
125142	123229	ATGCCTTTTTCAGTAATGCA
125143	123230	CATGCCTTTTTCAGTAATGC
125144	123231	TCATGCCTTTTTCAGTAATG
125145	123232	CTCATGCCTTTTTCAGTAAT
125146	123233	TCTCATGCCTTTTTCAGTAA
125147	123234	ATCTCATGCCTTTTTCAGTA
125148	123235	AATCTCATGCCTTTTTCAGT
125149	123236	AAATCTCATGCCTTTTTCAG
125150	123237	AAAATCTCATGCCTTTTTCA
125151	123238	CAAAATCTCATGCCTTTTTC
125152	123239	GCAAAATCTCATGCCTTTTT
125153	123240	GGCAAAATCTCATGCCTTTT
125154	123241	TGGCAAAATCTCATGCCTTT
125155	123242	ATGGCAAAATCTCATGCCTT
125156	123243	CATGGCAAAATCTCATGCCT
125157	123244	GCATGGCAAAATCTCATGCC
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125159	123246	GAGCATGGCAAAATCTCATG
125160	123247	GGAGCATGGCAAAATCTCAT
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125163	123250	ATGGGAGCATGGCAAAATCT
125164	123251	AATGGGAGCATGGCAAAATC
125165	123252	AAATGGGAGCATGGCAAAAT
125166	123253	AAAATGGGAGCATGGCAAAA
125167	123254	AAAAATGGGAGCATGGCAAA
125168	123255	TAAAAATGGGAGCATGGCAA
125169	123256	CTAAAAATGGGAGCATGGCA
125170	123257	CCTAAAAATGGGAGCATGGC
125171	123258	CCCTAAAAATGGGAGCATGG
125172	123259	CCCCTAAAAATGGGAGCATG
125173	123260	ACCCCTAAAAATGGGAGCAT
125174	123261	CACCCCTAAAAATGGGAGCA
125175	123262	TCACCCCTAAAAATGGGAGC
125176	123263	CTCACCCCTAAAAATGGGAG
125177	123264	TCTCACCCCTAAAAATGGGA
125178	123265	GTCTCACCCCTAAAAATGGG
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125186	123273	AAGACAATGTCTCACCCCTA
125187	123274	AAAGACAATGTCTCACCCCT
125188	123275	GAAAGACAATGTCTCACCCC
125189	123276	TGAAAGACAATGTCTCACCC
125190	123277	GTGAAAGACAATGTCTCACC
125191	123278	AGTGAAAGACAATGTCTCAC
125192	123279	TAGTGAAAGACAATGTCTCA
125193	123280	ATAGTGAAAGACAATGTCTC
125194	123281	AATAGTGAAAGACAATGTCT
125195	123282	TAATAGTGAAAGACAATGTC
125196	123283	TTAATAGTGAAAGACAATGT

26903	24990	CTCCTCCCTTGGCTTCCCAA
26904	24991	CCTCCTCCCTTGGCTTCCCA
26905	24992	CCCTCCTCCCTTGGCTTCCC
26906	24993	ACCCTCCTCCCTTGGCTTCC
26907	24994	GACCCTCCTCCCTTGGCTTC
26908	24995	CGACCCTCCTCCCTTGGCTT
26909	24996	GCGACCCTCCTCCCTTGGCT
26910	24997	AGCGACCCTCCTCCCTTGGC
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26913	25000	TCAAGCGACCCTCCTCCCTT
26914	25001	CTCAAGCGACCCTCCTCCCT
26915	25002	GCTCAAGCGACCCTCCTCCC
26916	25003	AGCTCAAGCGACCCTCCTCC
26917	25004	GAGCTCAAGCGACCCTCCTC
26918	25005	TGAGCTCAAGCGACCCTCCT
26919	25006	CTGAGCTCAAGCGACCCTCC
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26921	25008	TCCTGAGCTCAAGCGACCCT
26922	25009	TTCCTGAGCTCAAGCGACCC
26923	25010	ATTCCTGAGCTCAAGCGACC
26924	25011	AATTCCTGAGCTCAAGCGAC
26925	25012	GAATTCCTGAGCTCAAGCGA
26926	25013	TGAATTCCTGAGCTCAAGCG
26927	25014	TTGAATTCCTGAGCTCAAGC
26928	25015	CTTGAATTCCTGAGCTCAAG
26929	25016	TCTTGAATTCCTGAGCTCAA
26930	25017	ATCTTGAATTCCTGAGCTCA
26931	25018	GATCTTGAATTCCTGAGCTC
26932	25019	TGATCTTGAATTCCTGAGCT
26933	25020	CTGATCTTGAATTCCTGAGC
26934	25021	GCTGATCTTGAATTCCTGAG
26935	25022	GGCTGATCTTGAATTCCTGA
26936	25023	AGGCTGATCTTGAATTCCTG
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26938	25025	CTAGGCTGATCTTGAATTCC
26939	25026	CCTAGGCTGATCTTGAATTC
26940	25027	GCCTAGGCTGATCTTGAATT
26941	25028	TGCCTAGGCTGATCTTGAAT
26942	25029	TTGCCTAGGCTGATCTTGAA
26943	25030	GTTGCCTAGGCTGATCTTGA
26944	25031	TGTTGCCTAGGCTGATCTTG
26945	25032	ATGTTGCCTAGGCTGATCTT
26946	25033	TATGTTGCCTAGGCTGATCT
26947	25034	CTATGTTGCCTAGGCTGATC
26948	25035	ACTATGTTGCCTAGGCTGAT
26949	25036	CACTATGTTGCCTAGGCTGA
26950	25037	TCACTATGTTGCCTAGGCTG
26951	25038	CTCACTATGTTGCCTAGGCT
26952	25039	CCTCACTATGTTGCCTAGGC
26953	25040	GCCTCACTATGTTGCCTAGG
26954	25041	GGCCTCACTATGTTGCCTAG
26955	25042	GGGCCTCACTATGTTGCCTA
26956	25043	GGGGCCTCACTATGTTGCCT
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26958	25045	ATGGGGCCTCACTATGTTGC
26959	25046	GATGGGGCCTCACTATGTTG
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26961	25048	GAGATGGGGCCTCACTATGT
26962	25049	AGAGATGGGGCCTCACTATG
26963	25050	TAGAGATGGGGCCTCACTAT
26964	25051	GTAGAGATGGGGCCTCACTA
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26966	25053	TTGTAGAGATGGGGCCTCAC
26967	25054	TTTGTAGAGATGGGGCCTCA
26968	25055	TTTTGTAGAGATGGGGCCTC
26969	25056	TTTTTGTAGAGATGGGGCCT
26970	25057	ATTTTTGTAGAGATGGGGCC
26971	25058	TATTTTTGTAGAGATGGGGC
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26973	25060	TTTATTTTTGTAGAGATGGG

76050	74137	AAGGTAAACTTAAAACTTAT
76051	74138	AAAGGTAAACTTAAAACTTA
76052	74139	TAAAGGTAAACTTAAAACTT
76053	74140	ATAAAGGTAAACTTAAAACT
76054	74141	AATAAAGGTAAACTTAAAAC
76055	74142	TAATAAAGGTAAACTTAAAA
76056	74143	ATAATAAAGGTAAACTTAAA
76057	74144	TATAATAAAGGTAAACTTAA
76058	74145	CTATAATAAAGGTAAACTTA
76059	74146	ACTATAATAAAGGTAAACTT
76060	74147	CACTATAATAAAGGTAAACT
76061	74148	GCACTATAATAAAGGTAAAC
76062	74149	TGCACTATAATAAAGGTAAA
76063	74150	ATGCACTATAATAAAGGTAA
76064	74151	AATGCACTATAATAAAGGTA
76065	74152	CAATGCACTATAATAAAGGT
76066	74153	CCAATGCACTATAATAAAGG
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76068	74155	GACCAATGCACTATAATAAA
76069	74156	AGACCAATGCACTATAATAA
76070	74157	AAGACCAATGCACTATAATA
76071	74158	AAAGACCAATGCACTATAAT
76072	74159	AAAAGACCAATGCACTATAA
76073	74160	CAAAAGACCAATGCACTATA
76074	74161	ACAAAAGACCAATGCACTAT
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76093	74180	ATAATTTAGGTTGATGAAAA
76094	74181	CATAATTTAGGTTGATGAAA
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76103	74190	TTTATTGAACATAATTTAGG
76104	74191	ATTTATTGAACATAATTTAG
76105	74192	CATTTATTGAACATAATTTA
76106	74193	ACATTTATTGAACATAATTT
76107	74194	AACATTTATTGAACATAATT
76108	74195	AAACATTTATTGAACATAAT
76109	74196	GAAACATTTATTGAACATAA
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76113	74200	AACAGAAACATTTATTGAAC
76114	74201	TAACAGAAACATTTATTGAA
76115	74202	CTAACAGAAACATTTATTGA
76116	74203	TCTAACAGAAACATTTATTG
76117	74204	ATCTAACAGAAACATTTATT
76118	74205	AATCTAACAGAAACATTTAT
76119	74206	AAATCTAACAGAAACATTTA
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125197	123284	CTTAATAGTGAAAGACAATG
125198	123285	GCTTAATAGTGAAAGACAAT
125199	123286	TGCTTAATAGTGAAAGACAA
125200	123287	ATGCTTAATAGTGAAAGACA
125201	123288	TATGCTTAATAGTGAAAGAC
125202	123289	GTATGCTTAATAGTGAAAGA
125203	123290	TGTATGCTTAATAGTGAAAG
125204	123291	CTGTATGCTTAATAGTGAAA
125205	123292	ACTGTATGCTTAATAGTGAA
125206	123293	AACTGTATGCTTAATAGTGA
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125208	123295	CTAACTGTATGCTTAATAGT
125209	123296	CCTAACTGTATGCTTAATAG
125210	123297	ACCTAACTGTATGCTTAATA
125211	123298	CACCTAACTGTATGCTTAAT
125212	123299	ACACCTAACTGTATGCTTAA
125213	123300	AACACCTAACTGTATGCTTA
125214	123301	TAACACCTAACTGTATGCTT
125215	123302	GTAACACCTAACTGTATGCT
125216	123303	AGTAACACCTAACTGTATGC
125217	123304	AAGTAACACCTAACTGTATG
125218	123305	GAAGTAACACCTAACTGTAT
125219	123306	TGAAGTAACACCTAACTGTA
125220	123307	CTGAAGTAACACCTAACTGT
125221	123308	ACTGAAGTAACACCTAACTG
125222	123309	AACTGAAGTAACACCTAACT
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125227	123314	TTAGGAACTGAAGTAACACC
125228	123315	ATTAGGAACTGAAGTAACAC
125229	123316	AATTAGGAACTGAAGTAACA
125230	123317	AAATTAGGAACTGAAGTAAC
125231	123318	CAAATTAGGAACTGAAGTAA
125232	123319	GCAAATTAGGAACTGAAGTA
125233	123320	TGCAAATTAGGAACTGAAGT
125234	123321	CTGCAAATTAGGAACTGAAG
125235	123322	TCTGCAAATTAGGAACTGAA
125236	123323	CTCTGCAAATTAGGAACTGA
125237	123324	CCTCTGCAAATTAGGAACTG
125238	123325	ACCTCTGCAAATTAGGAACT
125239	123326	CACCTCTGCAAATTAGGAAC
125240	123327	CCACCTCTGCAAATTAGGAA
125241	123328	CCCACCTCTGCAAATTAGGA
125242	123329	ACCCACCTCTGCAAATTAGG
125243	123330	AACCCACCTCTGCAAATTAG
125244	123331	AAACCCACCTCTGCAAATTA
125245	123332	CAAACCCACCTCTGCAAATT
125246	123333	ACAAACCCACCTCTGCAAAT
125247	123334	AACAAACCCACCTCTGCAAA
125248	123335	AAACAAACCCACCTCTGCAA
125249	123336	AAAACAAACCCACCTCTGCA
125250	123337	GAAAACAAACCCACCTCTGC
125251	123338	AGAAAACAAACCCACCTCTG
125252	123339	AAGAAAACAAACCCACCTCT
125253	123340	AAAGAAAACAAACCCACCTC
125254	123341	AAAAGAAAACAAACCCACCT
125255	123342	AAAAAGAAAACAAACCCACC
125256	123343	TAAAAAGAAAACAAACCCAC
125257	123344	TTAAAAAGAAAACAAACCCA
125258	123345	ATTAAAAAGAAAACAAACCC
125259	123346	GATTAAAAAGAAAACAAACC
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125261	123348	ATGATTAAAAAGAAAACAAA
125262	123349	CATGATTAAAAAGAAAACAA
125263	123350	TCATGATTAAAAAGAAAACA
125264	123351	TTCATGATTAAAAAGAAAAC
125265	123352	ATTCATGATTAAAAAGAAAA
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26974	25061	ATTTATTTTTGTAGAGATGG
26975	25062	AATTTATTTTTGTAGAGATG
26976	25063	TAATTTATTTTTGTAGAGAT
26977	25064	CTAATTTATTTTTGTAGAGA
26978	25065	GCTAATTTATTTTTGTAGAG
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26980	25067	CAGCTAATTTATTTTTGTAG
26981	25068	CCAGCTAATTTATTTTTGTA
26982	25069	CCCAGCTAATTTATTTTTGT
26983	25070	GCCCAGCTAATTTATTTTTG
26984	25071	TGCCCAGCTAATTTATTTTT
26985	25072	ATGCCCAGCTAATTTATTTT
26986	25073	CATGCCCAGCTAATTTATTT
26987	25074	CCATGCCCAGCTAATTTATT
26988	25075	ACCATGCCCAGCTAATTTAT
26989	25076	CACCATGCCCAGCTAATTTA
26990	25077	CCACCATGCCCAGCTAATTT
26991	25078	ACCACCATGCCCAGCTAATT
26992	25079	CACCACCATGCCCAGCTAAT
26993	25080	GCACCACCATGCCCAGCTAA
26994	25081	TGCACCACCATGCCCAGCTA
26995	25082	ATGCACCACCATGCCCAGCT
26996	25083	CATGCACCACCATGCCCAGC
26997	25084	GCATGCACCACCATGCCCAG
26998	25085	CGCATGCACCACCATGCCCA
26999	25086	ACGCATGCACCACCATGCCC
27000	25087	TACGCATGCACCACCATGCC
27001	25088	ATACGCATGCACCACCATGC
27002	25089	TATACGCATGCACCACCATG
27003	25090	CTATACGCATGCACCACCAT
27004	25091	ACTATACGCATGCACCACCA
27005	25092	GACTATACGCATGCACCACC
27006	25093	AGACTATACGCATGCACCAC
27007	25094	GAGACTATACGCATGCACCA
27008	25095	TGAGACTATACGCATGCACC
27009	25096	CTGAGACTATACGCATGCAC
27010	25097	GCTGAGACTATACGCATGCA
27011	25098	AGCTGAGACTATACGCATGC
27012	25099	TAGCTGAGACTATACGCATG
27013	25100	GTAGCTGAGACTATACGCAT
27014	25101	AGTAGCTGAGACTATACGCA
27015	25102	AAGTAGCTGAGACTATACGC
27016	25103	CAAGTAGCTGAGACTATACG
27017	25104	CCAAGTAGCTGAGACTATAC
27018	25105	CCCAAGTAGCTGAGACTATA
27019	25106	TCCCAAGTAGCTGAGACTAT
27020	25107	CTCCCAAGTAGCTGAGACTA
27021	25108	CCTCCCAAGTAGCTGAGACT
27022	25109	GCCTCCCAAGTAGCTGAGAC
27023	25110	AGCCTCCCAAGTAGCTGAGA
27024	25111	CAGCCTCCCAAGTAGCTGAG
27025	25112	TCAGCCTCCCAAGTAGCTGA
27026	25113	GTCAGCCTCCCAAGTAGCTG
27027	25114	AGTCAGCCTCCCAAGTAGCT
27028	25115	GAGTCAGCCTCCCAAGTAGC
27029	25116	TGAGTCAGCCTCCCAAGTAG
27030	25117	CTGAGTCAGCCTCCCAAGTA
27031	25118	CCTGAGTCAGCCTCCCAAGT
27032	25119	TCCTGAGTCAGCCTCCCAAG
27033	25120	CTCCTGAGTCAGCCTCCCAA
27034	25121	CCTCCTGAGTCAGCCTCCCA
27035	25122	CCCTCCTGAGTCAGCCTCCC
27036	25123	ACCCTCCTGAGTCAGCCTCC
27037	25124	GACCCTCCTGAGTCAGCCTC
27038	25125	TGACCCTCCTGAGTCAGCCT
27039	25126	GTGACCCTCCTGAGTCAGCC
27040	25127	AGTGACCCTCCTGAGTCAGC
27041	25128	AAGTGACCCTCCTGAGTCAG
27042	25129	TAAGTGACCCTCCTGAGTCA
27043	25130	TTAAGTGACCCTCCTGAGTC
27044	25131	TTTAAGTGACCCTCCTGAGT

76121	74208	TAAAATCTAACAGAAACATT
76122	74209	TTAAAATCTAACAGAAACAT
76123	74210	CTTAAAATCTAACAGAAACA
76124	74211	ACTTAAAATCTAACAGAAAC
76125	74212	AACTTAAAATCTAACAGAAA
76126	74213	TAACTTAAAATCTAACAGAA
76127	74214	TTAACTTAAAATCTAACAGA
76128	74215	TTTAACTTAAAATCTAACAG
76129	74216	GTTTAACTTAAAATCTAACA
76130	74217	TGTTTAACTTAAAATCTAAC
76131	74218	TTGTTTAACTTAAAATCTAA
76132	74219	ATTGTTTAACTTAAAATCTA
76133	74220	AATTGTTTAACTTAAAATCT
76134	74221	TAATTGTTTAACTTAAAATC
76135	74222	ATAATTGTTTAACTTAAAAT
76136	74223	CATAATTGTTTAACTTAAAA
76137	74224	ACATAATTGTTTAACTTAAA
76138	74225	CACATAATTGTTTAACTTAA
76139	74226	TCACATAATTGTTTAACTTA
76140	74227	TTCACATAATTGTTTAACTT
76141	74228	TTTCACATAATTGTTTAACT
76142	74229	ATTTCACATAATTGTTTAAC
76143	74230	AATTTCACATAATTGTTTAA
76144	74231	GAATTTCACATAATTGTTTA
76145	74232	TGAATTTCACATAATTGTTT
76146	74233	ATGAATTTCACATAATTGTT
76147	74234	AATGAATTTCACATAATTGT
76148	74235	AAATGAATTTCACATAATTG
76149	74236	AAAATGAATTTCACATAATT
76150	74237	AAAAATGAATTTCACATAAT
76151	74238	GAAAAATGAATTTCACATAA
76152	74239	CGAAAAATGAATTTCACATA
76153	74240	ACGAAAAATGAATTTCACAT
76154	74241	TACGAAAAATGAATTTCACA
76155	74242	TTACGAAAAATGAATTTCAC
76156	74243	ATTACGAAAAATGAATTTCA
76157	74244	AATTACGAAAAATGAATTTC
76158	74245	CAATTACGAAAAATGAATTT
76159	74246	ACAATTACGAAAAATGAATT
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76161	74248	AAACAATTACGAAAAATGAA
76162	74249	AAAACAATTACGAAAAATGA
76163	74250	AAAAACAATTACGAAAAATG
76164	74251	AAAAAACAATTACGAAAAAT
76165	74252	TAAAAAACAATTACGAAAAA
76166	74253	TTAAAAAACAATTACGAAAA
76167	74254	GTTAAAAAACAATTACGAAA
76168	74255	TGTTAAAAAACAATTACGAA
76169	74256	ATGTTAAAAAACAATTACGA
76170	74257	TATGTTAAAAAACAATTACG
76171	74258	ATATGTTAAAAAACAATTAC
76172	74259	CATATGTTAAAAAACAATTA
76173	74260	ACATATGTTAAAAAACAATT
76174	74261	GACATATGTTAAAAAACAAT
76175	74262	AGACATATGTTAAAAAACAA
76176	74263	AAGACATATGTTAAAAAACA
76177	74264	AAAGACATATGTTAAAAAAC
76178	74265	CAAAGACATATGTTAAAAAA
76179	74266	ACAAAGACATATGTTAAAAA
76180	74267	AACAAAGACATATGTTAAAA
76181	74268	CAACAAAGACATATGTTAAA
76182	74269	CCAACAAAGACATATGTTAA
76183	74270	ACCAACAAAGACATATGTTA
76184	74271	TACCAACAAAGACATATGTT
76185	74272	TTACCAACAAAGACATATGT
76186	74273	ATTACCAACAAAGACATATG
76187	74274	AATTACCAACAAAGACATAT
76188	74275	GAATTACCAACAAAGACATA
76189	74276	TGAATTACCAACAAAGACAT
76190	74277	GTGAATTACCAACAAAGACA
76191	74278	CGTGAATTACCAACAAAGAC

125268	123355	ACCATTCATGATTAAAAAGA
125269	123356	AACCATTCATGATTAAAAAG
125270	123357	CAACCATTCATGATTAAAAA
125271	123358	ACAACCATTCATGATTAAAA
125272	123359	AACAACCATTCATGATTAAA
125273	123360	CAACAACCATTCATGATTAA
125274	123361	CCAACAACCATTCATGATTA
125275	123362	TCCAACAACCATTCATGATT
125276	123363	ATCCAACAACCATTCATGAT
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125279	123366	ATAATCCAACAACCATTCAT
125280	123367	CATAATCCAACAACCATTCA
125281	123368	ACATAATCCAACAACCATTC
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125286	123373	TTTGAACATAATCCAACAAC
125287	123374	ATTTGAACATAATCCAACAA
125288	123375	TATTTGAACATAATCCAACA
125289	123376	GTATTTGAACATAATCCAAC
125290	123377	AGTATTTGAACATAATCCAA
125291	123378	AAGTATTTGAACATAATCCA
125292	123379	TAAGTATTTGAACATAATCC
125293	123380	ATAAGTATTTGAACATAATC
125294	123381	GATAAGTATTTGAACATAAT
125295	123382	TGATAAGTATTTGAACATAA
125296	123383	ATGATAAGTATTTGAACATA
125297	123384	GATGATAAGTATTTGAACAT
125298	123385	AGATGATAAGTATTTGAACA
125299	123386	TAGATGATAAGTATTTGAAC
125300	123387	GTAGATGATAAGTATTTGAA
125301	123388	AGTAGATGATAAGTATTTGA
125302	123389	TAGTAGATGATAAGTATTTG
125303	123390	TTAGTAGATGATAAGTATTT
125304	123391	CTTAGTAGATGATAAGTATT
125305	123392	ACTTAGTAGATGATAAGTAT
125306	123393	TACTTAGTAGATGATAAGTA
125307	123394	ATACTTAGTAGATGATAAGT
125308	123395	TATACTTAGTAGATGATAAG
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125313	123400	TATGATATACTTAGTAGATG
125314	123401	ATATGATATACTTAGTAGAT
125315	123402	AATATGATATACTTAGTAGA
125316	123403	CAATATGATATACTTAGTAG
125317	123404	TCAATATGATATACTTAGTA
125318	123405	GTCAATATGATATACTTAGT
125319	123406	GGTCAATATGATATACTTAG
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125321	123408	CTGGTCAATATGATATACTT
125322	123409	CCTGGTCAATATGATATACT
125323	123410	TCCTGGTCAATATGATATAC
125324	123411	TTCCTGGTCAATATGATATA
125325	123412	GTTCCTGGTCAATATGATAT
125326	123413	TGTTCCTGGTCAATATGATA
125327	123414	CTGTTCCTGGTCAATATGAT
125328	123415	ACTGTTCCTGGTCAATATGA
125329	123416	CACTGTTCCTGGTCAATATG
125330	123417	CCACTGTTCCTGGTCAATAT
125331	123418	GCCACTGTTCCTGGTCAATA
125332	123419	AGCCACTGTTCCTGGTCAAT
125333	123420	GAGCCACTGTTCCTGGTCAA
125334	123421	TGAGCCACTGTTCCTGGTCA
125335	123422	ATGAGCCACTGTTCCTGGTC
125336	123423	TATGAGCCACTGTTCCTGGT
125337	123424	GTATGAGCCACTGTTCCTGG
125338	123425	GGTATGAGCCACTGTTCCTG

27045	25132	GTTTAAGTGACCCTCCTGAG
27046	25133	GGTTTAAGTGACCCTCCTGA
27047	25134	GGGTTTAAGTGACCCTCCTG
27048	25135	TGGGTTTAAGTGACCCTCCT
27049	25136	CTGGGTTTAAGTGACCCTCC
27050	25137	CCTGGGTTTAAGTGACCCTC
27051	25138	TCCTGGGTTTAAGTGACCCT
27052	25139	TTCCTGGGTTTAAGTGACCC
27053	25140	ATTCCTGGGTTTAAGTGACC
27054	25141	AATTCCTGGGTTTAAGTGAC
27055	25142	CAATTCCTGGGTTTAAGTGA
27056	25143	CCAATTCCTGGGTTTAAGTG
27057	25144	TCCAATTCCTGGGTTTAAGT
27058	25145	CTCCAATTCCTGGGTTTAAG
27059	25146	CCTCCAATTCCTGGGTTTAA
27060	25147	ACCTCCAATTCCTGGGTTTA
27061	25148	AACCTCCAATTCCTGGGTTT
27062	25149	CAACCTCCAATTCCTGGGTT
27063	25150	GCAACCTCCAATTCCTGGGT
27064	25151	TGCAACCTCCAATTCCTGGG
27065	25152	CTGCAACCTCCAATTCCTGG
27066	25153	ACTGCAACCTCCAATTCCTG
27067	25154	CACTGCAACCTCCAATTCCT
27068	25155	TCACTGCAACCTCCAATTCC
27069	25156	CTCACTGCAACCTCCAATTC
27070	25157	GCTCACTGCAACCTCCAATT
27071	25158	AGCTCACTGCAACCTCCAAT
27072	25159	TAGCTCACTGCAACCTCCAA
27073	25160	ATAGCTCACTGCAACCTCCA
27074	25161	CATAGCTCACTGCAACCTCC
27075	25162	TCATAGCTCACTGCAACCTC
27076	25163	ATCATAGCTCACTGCAACCT
27077	25164	AATCATAGCTCACTGCAACC
27078	25165	CAATCATAGCTCACTGCAAC
27079	25166	GCAATCATAGCTCACTGCAA
27080	25167	CGCAATCATAGCTCACTGCA
27081	25168	GCGCAATCATAGCTCACTGC
27082	25169	GGCGCAATCATAGCTCACTG
27083	25170	TGGCGCAATCATAGCTCACT
27084	25171	GTGGCGCAATCATAGCTCAC
27085	25172	AGTGGCGCAATCATAGCTCA
27086	25173	CAGTGGCGCAATCATAGCTC
27087	25174	ACAGTGGCGCAATCATAGCT
27088	25175	TACAGTGGCGCAATCATAGC
27089	25176	ATACAGTGGCGCAATCATAG
27090	25177	TATACAGTGGCGCAATCATA
27091	25178	GTATACAGTGGCGCAATCAT
27092	25179	GGTATACAGTGGCGCAATCA
27093	25180	TGGTATACAGTGGCGCAATC
27094	25181	ATGGTATACAGTGGCGCAAT
27095	25182	GATGGTATACAGTGGCGCAA
27096	25183	GGATGGTATACAGTGGCGCA
27097	25184	GGGATGGTATACAGTGGCGC
27098	25185	TGGGATGGTATACAGTGGCG
27099	25186	CTGGGATGGTATACAGTGGC
27100	25187	CCTGGGATGGTATACAGTGG
27101	25188	GCCTGGGATGGTATACAGTG
27102	25189	CGCCTGGGATGGTATACAGT
27103	25190	TCGCCTGGGATGGTATACAG
27104	25191	GTCGCCTGGGATGGTATACA
27105	25192	TGTCGCCTGGGATGGTATAC
27106	25193	CTGTCGCCTGGGATGGTATA
27107	25194	TCTGTCGCCTGGGATGGTAT
27108	25195	CTCTGTCGCCTGGGATGGTA
27109	25196	ACTCTGTCGCCTGGGATGGT
27110	25197	CACTCTGTCGCCTGGGATGG
27111	25198	TCACTCTGTCGCCTGGGATG
27112	25199	CTCACTCTGTCGCCTGGGAT
27113	25200	TCTCACTCTGTCGCCTGGGA
27114	25201	GTCTCACTCTGTCGCCTGGG
27115	25202	GGTCTCACTCTGTCGCCTGG

76192	74279	ACGTGAATTACCAACAAAGA
76193	74280	CACGTGAATTACCAACAAAG
76194	74281	ACACGTGAATTACCAACAAA
76195	74282	CACACGTGAATTACCAACAA
76196	74283	ACACACGTGAATTACCAACA
76197	74284	CACACACGTGAATTACCAAC
76198	74285	TCACACACGTGAATTACCAA
76199	74286	CTCACACACGTGAATTACCA
76200	74287	ACTCACACACGTGAATTACC
76201	74288	CACTCACACACGTGAATTAC
76202	74289	ACACTCACACACGTGAATTA
76203	74290	TACACTCACACACGTGAATT
76204	74291	TTACACTCACACACGTGAAT
76205	74292	GTTACACTCACACACGTGAA
76206	74293	AGTTACACTCACACACGTGA
76207	74294	CAGTTACACTCACACACGTG
76208	74295	TCAGTTACACTCACACACGT
76209	74296	ATCAGTTACACTCACACACG
76210	74297	AATCAGTTACACTCACACAC
76211	74298	CAATCAGTTACACTCACACA
76212	74299	GCAATCAGTTACACTCACAC
76213	74300	GGCAATCAGTTACACTCACA
76214	74301	TGGCAATCAGTTACACTCAC
76215	74302	CTGGCAATCAGTTACACTCA
76216	74303	TCTGGCAATCAGTTACACTC
76217	74304	ATCTGGCAATCAGTTACACT
76218	74305	AATCTGGCAATCAGTTACAC
76219	74306	TAATCTGGCAATCAGTTACA
76220	74307	ATAATCTGGCAATCAGTTAC
76221	74308	TATAATCTGGCAATCAGTTA
76222	74309	ATATAATCTGGCAATCAGTT
76223	74310	TATATAATCTGGCAATCAGT
76224	74311	TTATATAATCTGGCAATCAG
76225	74312	TTTATATAATCTGGCAATCA
76226	74313	GTTTATATAATCTGGCAATC
76227	74314	AGTTTATATAATCTGGCAAT
76228	74315	AAGTTTATATAATCTGGCAA
76229	74316	AAAGTTTATATAATCTGGCA
76230	74317	GAAAGTTTATATAATCTGGC
76231	74318	TGAAAGTTTATATAATCTGG
76232	74319	TTGAAAGTTTATATAATCTG
76233	74320	GTTGAAAGTTTATATAATCT
76234	74321	GGTTGAAAGTTTATATAATC
76235	74322	TGGTTGAAAGTTTATATAAT
76236	74323	TTGGTTGAAAGTTTATATAA
76237	74324	TTTGGTTGAAAGTTTATATA
76238	74325	TTTTGGTTGAAAGTTTATAT
76239	74326	GTTTTGGTTGAAAGTTTATA
76240	74327	GGTTTTGGTTGAAAGTTTAT
76241	74328	TGGTTTTGGTTGAAAGTTTA
76242	74329	ATGGTTTTGGTTGAAAGTTT
76243	74330	AATGGTTTTGGTTGAAAGTT
76244	74331	GAATGGTTTTGGTTGAAAGT
76245	74332	AGAATGGTTTTGGTTGAAAG
76246	74333	AAGAATGGTTTTGGTTGAAA
76247	74334	AAAGAATGGTTTTGGTTGAA
76248	74335	CAAAGAATGGTTTTGGTTGA
76249	74336	GCAAAGAATGGTTTTGGTTG
76250	74337	TGCAAAGAATGGTTTTGGTT
76251	74338	CTGCAAAGAATGGTTTTGGT
76252	74339	TCTGCAAAGAATGGTTTTGG
76253	74340	ATCTGCAAAGAATGGTTTTG
76254	74341	CATCTGCAAAGAATGGTTTT
76255	74342	GCATCTGCAAAGAATGGTTT
76256	74343	AGCATCTGCAAAGAATGGTT
76257	74344	AAGCATCTGCAAAGAATGGT
76258	74345	AAAGCATCTGCAAAGAATGG
76259	74346	AAAAGCATCTGCAAAGAATG
76260	74347	TAAAAGCATCTGCAAAGAAT
76261	74348	GTAAAAGCATCTGCAAAGAA
76262	74349	AGTAAAAGCATCTGCAAAGA

125339	123426	AGGTATGAGCCACTGTTCCT
125340	123427	CAGGTATGAGCCACTGTTCC
125341	123428	ACAGGTATGAGCCACTGTTC
125342	123429	TACAGGTATGAGCCACTGTT
125343	123430	TTACAGGTATGAGCCACTGT
125344	123431	GTTACAGGTATGAGCCACTG
125345	123432	GGTTACAGGTATGAGCCACT
125346	123433	AGGTTACAGGTATGAGCCAC
125347	123434	GAGGTTACAGGTATGAGCCA
125348	123435	TGAGGTTACAGGTATGAGCC
125349	123436	CTGAGGTTACAGGTATGAGC
125350	123437	TCTGAGGTTACAGGTATGAG
125351	123438	CTCTGAGGTTACAGGTATGA
125352	123439	GCTCTGAGGTTACAGGTATG
125353	123440	AGCTCTGAGGTTACAGGTAT
125354	123441	AAGCTCTGAGGTTACAGGTA
125355	123442	AAAGCTCTGAGGTTACAGGT
125356	123443	CAAAGCTCTGAGGTTACAGG
125357	123444	CCAAAGCTCTGAGGTTACAG
125358	123445	CCCAAAGCTCTGAGGTTACA
125359	123446	TCCCAAAGCTCTGAGGTTAC
125360	123447	CTCCCAAAGCTCTGAGGTTA
125361	123448	CCTCCCAAAGCTCTGAGGTT
125362	123449	GCCTCCCAAAGCTCTGAGGT
125363	123450	GGCCTCCCAAAGCTCTGAGG
125364	123451	TGGCCTCCCAAAGCTCTGAG
125365	123452	TTGGCCTCCCAAAGCTCTGA
125366	123453	CTTGGCCTCCCAAAGCTCTG
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125369	123456	TGCCTTGGCCTCCCAAAGCT
125370	123457	CTGCCTTGGCCTCCCAAAGC
125371	123458	CCTGCCTTGGCCTCCCAAAG
125372	123459	TCCTGCCTTGGCCTCCCAAA
125373	123460	CTCCTGCCTTGGCCTCCCAA
125374	123461	CCTCCTGCCTTGGCCTCCCA
125375	123462	TCCTCCTGCCTTGGCCTCCC
125376	123463	ATCCTCCTGCCTTGGCCTCC
125377	123464	GATCCTCCTGCCTTGGCCTC
125378	123465	CGATCCTCCTGCCTTGGCCT
125379	123466	GCGATCCTCCTGCCTTGGCC
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125383	123470	TCAAGCGATCCTCCTGCCTT
125384	123471	CTCAAGCGATCCTCCTGCCT
125385	123472	CCTCAAGCGATCCTCCTGCC
125386	123473	GCCTCAAGCGATCCTCCTGC
125387	123474	GGCCTCAAGCGATCCTCCTG
125388	123475	TGGCCTCAAGCGATCCTCCT
125389	123476	CTGGCCTCAAGCGATCCTCC
125390	123477	CCTGGCCTCAAGCGATCCTC
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125405	123492	GGTTGGTCTTGAACTCCTGG
125406	123493	AGGTTGGTCTTGAACTCCTG
125407	123494	CAGGTTGGTCTTGAACTCCT
125408	123495	CCAGGTTGGTCTTGAACTCC
125409	123496	CCCAGGTTGGTCTTGAACTC

27116	25203	GGGTCTCACTCTGTCGCCTG
27117	25204	AGGGTCTCACTCTGTCGCCT
27118	25205	TAGGGTCTCACTCTGTCGCC
27119	25206	ATAGGGTCTCACTCTGTCGC
27120	25207	GATAGGGTCTCACTCTGTCG
27121	25208	GGATAGGGTCTCACTCTGTC
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27123	25210	GGGGATAGGGTCTCACTCTG
27124	25211	GGGGGATAGGGTCTCACTCT
27125	25212	GGGGGGATAGGGTCTCACTC
27126	25213	TGGGGGGATAGGGTCTCACT
27127	25214	GTGGGGGGATAGGGTCTCAC
27128	25215	GGTGGGGGGATAGGGTCTCA
27129	25216	CGGTGGGGGGATAGGGTCTC
27130	25217	GCGGTGGGGGGATAGGGTCT
27131	25218	GGCGGTGGGGGGATAGGGTC
27132	25219	TGGCGGTGGGGGGATAGGGT
27133	25220	TTGGCGGTGGGGGGATAGGG
27134	25221	TTTGGCGGTGGGGGGATAGG
27135	25222	TTTTGGCGGTGGGGGGATAG
27136	25223	TTTTTGGCGGTGGGGGGATA
27137	25224	TTTTTTGGCGGTGGGGGGAT
27138	25225	TTTTTTTGGCGGTGGGGGGA
27139	25226	TTTTTTTTGGCGGTGGGGGG
27140	25227	CTTTTTTTTGGCGGTGGGGG
27141	25228	TCTTTTTTTTGGCGGTGGGG
27142	25229	TTCTTTTTTTTGGCGGTGGG
27143	25230	TTTCTTTTTTTTGGCGGTGG
27144	25231	TTTTCTTTTTTTTGGCGGTG
27145	25232	CTTTTCTTTTTTTTGGCGGT
27146	25233	TCTTTTCTTTTTTTTGGCGG
27147	25234	TTCTTTTCTTTTTTTTGGCG
27148	25235	TTTCTTTTCTTTTTTTTGGC
27149	25236	TTTTCTTTTCTTTTTTTTGG
27150	25237	ATTTTCTTTTCTTTTTTTTG
27151	25238	CATTTTCTTTTCTTTTTTTT
27152	25239	TCATTTTCTTTTCTTTTTTT
27153	25240	CTCATTTTCTTTTCTTTTTT
27154	25241	CCTCATTTTCTTTTCTTTTT
27155	25242	TCCTCATTTTCTTTTCTTTT
27156	25243	TTCCTCATTTTCTTTTCTTT
27157	25244	ATTCCTCATTTTCTTTTCTT
27158	25245	AATTCCTCATTTTCTTTTCT
27159	25246	AAATTCCTCATTTTCTTTTC
27160	25247	TAAATTCCTCATTTTCTTTT
27161	25248	GTAAATTCCTCATTTTCTTT
27162	25249	TGTAAATTCCTCATTTTCTT
27163	25250	ATGTAAATTCCTCATTTTCT
27164	25251	AATGTAAATTCCTCATTTTC
27165	25252	AAATGTAAATTCCTCATTTT
27166	25253	CAAATGTAAATTCCTCATTT
27167	25254	ACAAATGTAAATTCCTCATT
27168	25255	CACAAATGTAAATTCCTCAT
27169	25256	TCACAAATGTAAATTCCTCA
27170	25257	GTCACAAATGTAAATTCCTC
27171	25258	TGTCACAAATGTAAATTCCT
27172	25259	CTGTCACAAATGTAAATTCC
27173	25260	TCTGTCACAAATGTAAATTC
27174	25261	ATCTGTCACAAATGTAAATT
27175	25262	TATCTGTCACAAATGTAAAT
27176	25263	GTATCTGTCACAAATGTAAA
27177	25264	CGTATCTGTCACAAATGTAA
27178	25265	CCGTATCTGTCACAAATGTA
27179	25266	TCCGTATCTGTCACAAATGT
27180	25267	TTCCGTATCTGTCACAAATG
27181	25268	ATTCCGTATCTGTCACAAAT
27182	25269	AATTCCGTATCTGTCACAAA
27183	25270	GAATTCCGTATCTGTCACAA
27184	25271	TGAATTCCGTATCTGTCACA
27185	25272	CTGAATTCCGTATCTGTCAC
27186	25273	CCTGAATTCCGTATCTGTCA

76263	74350	CAGTAAAAGCATCTGCAAAG
76264	74351	TCAGTAAAAGCATCTGCAAA
76265	74352	GTCAGTAAAAGCATCTGCAA
76266	74353	AGTCAGTAAAAGCATCTGCA
76267	74354	GAGTCAGTAAAAGCATCTGC
76268	74355	AGAGTCAGTAAAAGCATCTG
76269	74356	CAGAGTCAGTAAAAGCATCT
76270	74357	GCAGAGTCAGTAAAAGCATC
76271	74358	AGCAGAGTCAGTAAAAGCAT
76272	74359	TAGCAGAGTCAGTAAAAGCA
76273	74360	ATAGCAGAGTCAGTAAAAGC
76274	74361	GATAGCAGAGTCAGTAAAAG
76275	74362	TGATAGCAGAGTCAGTAAAA
76276	74363	CTGATAGCAGAGTCAGTAAA
76277	74364	ACTGATAGCAGAGTCAGTAA
76278	74365	CACTGATAGCAGAGTCAGTA
76279	74366	GCACTGATAGCAGAGTCAGT
76280	74367	AGCACTGATAGCAGAGTCAG
76281	74368	TAGCACTGATAGCAGAGTCA
76282	74369	TTAGCACTGATAGCAGAGTC
76283	74370	TTTAGCACTGATAGCAGAGT
76284	74371	CTTTAGCACTGATAGCAGAG
76285	74372	ACTTTAGCACTGATAGCAGA
76286	74373	CACTTTAGCACTGATAGCAG
76287	74374	TCACTTTAGCACTGATAGCA
76288	74375	TTCACTTTAGCACTGATAGC
76289	74376	ATTCACTTTAGCACTGATAG
76290	74377	CATTCACTTTAGCACTGATA
76291	74378	CCATTCACTTTAGCACTGAT
76292	74379	GCCATTCACTTTAGCACTGA
76293	74380	CGCCATTCACTTTAGCACTG
76294	74381	TCGCCATTCACTTTAGCACT
76295	74382	TTCGCCATTCACTTTAGCAC
76296	74383	GTTCGCCATTCACTTTAGCA
76297	74384	TGTTCGCCATTCACTTTAGC
76298	74385	GTGTTCGCCATTCACTTTAG
76299	74386	TGTGTTCGCCATTCACTTTA
76300	74387	TTGTGTTCGCCATTCACTTT
76301	74388	TTTGTGTTCGCCATTCACTT
76302	74389	CTTTGTGTTCGCCATTCACT
76303	74390	TCTTTGTGTTCGCCATTCAC
76304	74391	CTCTTTGTGTTCGCCATTCA
76305	74392	TCTCTTTGTGTTCGCCATTC
76306	74393	TTCTCTTTGTGTTCGCCATT
76307	74394	CTTCTCTTTGTGTTCGCCAT
76308	74395	CCTTCTCTTTGTGTTCGCCA
76309	74396	TCCTTCTCTTTGTGTTCGCC
76310	74397	GTCCTTCTCTTTGTGTTCGC
76311	74398	GGTCCTTCTCTTTGTGTTCG
76312	74399	AGGTCCTTCTCTTTGTGTTC
76313	74400	CAGGTCCTTCTCTTTGTGTT
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76321	74408	CAGGGCTCCAGGTCCTTCTC
76322	74409	CCAGGGCTCCAGGTCCTTCT
76323	74410	CCCAGGGCTCCAGGTCCTTC
76324	74411	TCCCAGGGCTCCAGGTCCTT
76325	74412	ATCCCAGGGCTCCAGGTCCT
76326	74413	CATCCCAGGGCTCCAGGTCC
76327	74414	GCATCCCAGGGCTCCAGGTC
76328	74415	TGCATCCCAGGGCTCCAGGT
76329	74416	CTGCATCCCAGGGCTCCAGG
76330	74417	CCTGCATCCCAGGGCTCCAG
76331	74418	ACCTGCATCCCAGGGCTCCA
76332	74419	CACCTGCATCCCAGGGCTCC
76333	74420	TCACCTGCATCCCAGGGCTC

125410	123497	ACCCAGGTTGGTCTTGAACT
125411	123498	CACCCAGGTTGGTCTTGAAC
125412	123499	TCACCCAGGTTGGTCTTGAA
125413	123500	ATCACCCAGGTTGGTCTTGA
125414	123501	CATCACCCAGGTTGGTCTTG
125415	123502	ACATCACCCAGGTTGGTCTT
125416	123503	TACATCACCCAGGTTGGTCT
125417	123504	CTACATCACCCAGGTTGGTC
125418	123505	CCTACATCACCCAGGTTGGT
125419	123506	TCCTACATCACCCAGGTTGG
125420	123507	TTCCTACATCACCCAGGTTG
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125423	123510	GTTTTCCTACATCACCCAGG
125424	123511	GGTTTTCCTACATCACCCAG
125425	123512	GGGTTTTCCTACATCACCCA
125426	123513	GGGGTTTTCCTACATCACCC
125427	123514	TGGGGTTTTCCTACATCACC
125428	123515	ATGGGGTTTTCCTACATCAC
125429	123516	TATGGGGTTTTCCTACATCA
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125432	123519	AGATATGGGGTTTTCCTACA
125433	123520	TAGATATGGGGTTTTCCTAC
125434	123521	GTAGATATGGGGTTTTCCTA
125435	123522	TGTAGATATGGGGTTTTCCT
125436	123523	TTGTAGATATGGGGTTTTCC
125437	123524	TTTGTAGATATGGGGTTTTC
125438	123525	TTTTGTAGATATGGGGTTTT
125439	123526	GTTTTGTAGATATGGGGTTT
125440	123527	TGTTTTGTAGATATGGGGTT
125441	123528	TTGTTTTGTAGATATGGGGT
125442	123529	ATTGTTTTGTAGATATGGGG
125443	123530	AATTGTTTTGTAGATATGGG
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125447	123534	TTTAAATTGTTTTGTAGATA
125448	123535	TTTTAAATTGTTTTGTAGAT
125449	123536	TTTTTAAATTGTTTTGTAGA
125450	123537	ATTTTTAAATTGTTTTGTAG
125451	123538	AATTTTTAAATTGTTTTGTA
125452	123539	AAATTTTTAAATTGTTTTGT
125453	123540	CAAATTTTTAAATTGTTTTG
125454	123541	GCAAATTTTTAAATTGTTTT
125455	123542	AGCAAATTTTTAAATTGTTT
125456	123543	CAGCAAATTTTTAAATTGTT
125457	123544	CCAGCAAATTTTTAAATTGT
125458	123545	CCCAGCAAATTTTTAAATTG
125459	123546	ACCCAGCAAATTTTTAAATT
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125461	123548	ACACCCAGCAAATTTTTAAA
125462	123549	CACACCCAGCAAATTTTTAA
125463	123550	CCACACCCAGCAAATTTTTA
125464	123551	ACCACACCCAGCAAATTTTT
125465	123552	CACCACACCCAGCAAATTTT
125466	123553	CCACCACACCCAGCAAATTT
125467	123554	GCCACCACACCCAGCAAATT
125468	123555	TGCCACCACACCCAGCAAAT
125469	123556	GTGCCACCACACCCAGCAAA
125470	123557	TGTGCCACCACACCCAGCAA
125471	123558	GTGTGCCACCACACCCAGCA
125472	123559	TGTGTGCCACCACACCCAGC
125473	123560	GTGTGTGCCACCACACCCAG
125474	123561	GGTGTGTGCCACCACACCCA
125475	123562	AGGTGTGTGCCACCACACCC
125476	123563	CAGGTGTGTGCCACCACACC
125477	123564	ACAGGTGTGTGCCACCACAC
125478	123565	TACAGGTGTGTGCCACCACA
125479	123566	CTACAGGTGTGTGCCACCAC
125480	123567	ACTACAGGTGTGTGCCACCA

27187	25274	CCCTGAATTCCGTATCTGTC
27188	25275	TCCCTGAATTCCGTATCTGT
27189	25276	TTCCCTGAATTCCGTATCTG
27190	25277	ATTCCCTGAATTCCGTATCT
27191	25278	AATTCCCTGAATTCCGTATC
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27194	25281	CTAAATTCCCTGAATTCCGT
27195	25282	ACTAAATTCCCTGAATTCCG
27196	25283	AACTAAATTCCCTGAATTCC
27197	25284	CAACTAAATTCCCTGAATTC
27198	25285	ACAACTAAATTCCCTGAATT
27199	25286	AACAACTAAATTCCCTGAAT
27200	25287	GAACAACTAAATTCCCTGAA
27201	25288	TGAACAACTAAATTCCCTGA
27202	25289	ATGAACAACTAAATTCCCTG
27203	25290	TATGAACAACTAAATTCCCT
27204	25291	CTATGAACAACTAAATTCCC
27205	25292	ACTATGAACAACTAAATTCC
27206	25293	GACTATGAACAACTAAATTC
27207	25294	AGACTATGAACAACTAAATT
27208	25295	TAGACTATGAACAACTAAAT
27209	25296	ATAGACTATGAACAACTAAA
27210	25297	TATAGACTATGAACAACTAA
27211	25298	TTATAGACTATGAACAACTA
27212	25299	TTTATAGACTATGAACAACT
27213	25300	ATTTATAGACTATGAACAAC
27214	25301	CATTTATAGACTATGAACAA
27215	25302	GCATTTATAGACTATGAACA
27216	25303	AGCATTTATAGACTATGAAC
27217	25304	TAGCATTTATAGACTATGAA
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27219	25306	TATAGCATTTATAGACTATG
27220	25307	TTATAGCATTTATAGACTAT
27221	25308	CTTATAGCATTTATAGACTA
27222	25309	TCTTATAGCATTTATAGACT
27223	25310	TTCTTATAGCATTTATAGAC
27224	25311	CTTCTTATAGCATTTATAGA
27225	25312	ACTTCTTATAGCATTTATAG
27226	25313	GACTTCTTATAGCATTTATA
27227	25314	AGACTTCTTATAGCATTTAT
27228	25315	GAGACTTCTTATAGCATTTA
27229	25316	GGAGACTTCTTATAGCATTT
27230	25317	TGGAGACTTCTTATAGCATT
27231	25318	ATGGAGACTTCTTATAGCAT
27232	25319	TATGGAGACTTCTTATAGCA
27233	25320	GTATGGAGACTTCTTATAGC
27234	25321	GGTATGGAGACTTCTTATAG
27235	25322	AGGTATGGAGACTTCTTATA
27236	25323	AAGGTATGGAGACTTCTTAT
27237	25324	AAAGGTATGGAGACTTCTTA
27238	25325	AAAAGGTATGGAGACTTCTT
27239	25326	AAAAAGGTATGGAGACTTCT
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27241	25328	AAAAAAAGGTATGGAGACTT
27242	25329	AAAAAAAAGGTATGGAGACT
27243	25330	AAAAAAAAAGGTATGGAGAC
27244	25331	AAAAAAAAAAGGTATGGAGA
27245	25332	AAAAAAAAAAAGGTATGGAG
27246	25333	AAAAAAAAAAAAGGTATGGA
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27248	25335	AAAAAAAAAAAAAAGGTATG
27249	25336	AAAAAAAAAAAAAAAGGTAT
27250	25337	AAAAAAAAAAAAAAAAGGTA
27251	25338	AAAAAAAAAAAAAAAAAGGT
27252	25339	AAAAAAAAAAAAAAAAAAGG
27253	25340	AAAAAAAAAAAAAAAAAAAG
27254	25341	AAAAAAAAAAAAAAAAAAAA
27255	25342	AAAAAAAAAAAAAAAAAAAA
27256	25343	AAAAAAAAAAAAAAAAAAAA
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76334	74421	TTCACCTGCATCCCAGGGCT
76335	74422	GTTCACCTGCATCCCAGGGC
76336	74423	AGTTCACCTGCATCCCAGGG
76337	74424	GAGTTCACCTGCATCCCAGG
76338	74425	TGAGTTCACCTGCATCCCAG
76339	74426	GTGAGTTCACCTGCATCCCA
76340	74427	TGTGAGTTCACCTGCATCCC
76341	74428	CTGTGAGTTCACCTGCATCC
76342	74429	GCTGTGAGTTCACCTGCATC
76343	74430	GGCTGTGAGTTCACCTGCAT
76344	74431	TGGCTGTGAGTTCACCTGCA
76345	74432	TTGGCTGTGAGTTCACCTGC
76346	74433	ATTGGCTGTGAGTTCACCTG
76347	74434	CATTGGCTGTGAGTTCACCT
76348	74435	TCATTGGCTGTGAGTTCACC
76349	74436	CTCATTGGCTGTGAGTTCAC
76350	74437	CCTCATTGGCTGTGAGTTCA
76351	74438	TCCTCATTGGCTGTGAGTTC
76352	74439	TTCCTCATTGGCTGTGAGTT
76353	74440	GTTCCTCATTGGCTGTGAGT
76354	74441	AGTTCCTCATTGGCTGTGAG
76355	74442	AAGTTCCTCATTGGCTGTGA
76356	74443	CAAGTTCCTCATTGGCTGTG
76357	74444	TCAAGTTCCTCATTGGCTGT
76358	74445	CTCAAGTTCCTCATTGGCTG
76359	74446	CCTCAAGTTCCTCATTGGCT
76360	74447	GCCTCAAGTTCCTCATTGGC
76361	74448	AGCCTCAAGTTCCTCATTGG
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76376	74463	TACGTCATTTTCCAAAGCCT
76377	74464	CTACGTCATTTTCCAAAGCC
76378	74465	ACTACGTCATTTTCCAAAGC
76379	74466	TACTACGTCATTTTCCAAAG
76380	74467	TTACTACGTCATTTTCCAAA
76381	74468	CTTACTACGTCATTTTCCAA
76382	74469	ACTTACTACGTCATTTTCCA
76383	74470	TACTTACTACGTCATTTTCC
76384	74471	TTACTTACTACGTCATTTTC
76385	74472	GTTACTTACTACGTCATTTT
76386	74473	TGTTACTTACTACGTCATTT
76387	74474	ATGTTACTTACTACGTCATT
76388	74475	GATGTTACTTACTACGTCAT
76389	74476	AGATGTTACTTACTACGTCA
76390	74477	AAGATGTTACTTACTACGTC
76391	74478	AAAGATGTTACTTACTACGT
76392	74479	CAAAGATGTTACTTACTACG
76393	74480	ACAAAGATGTTACTTACTAC
76394	74481	TACAAAGATGTTACTTACTA
76395	74482	TTACAAAGATGTTACTTACT
76396	74483	ATTACAAAGATGTTACTTAC
76397	74484	AATTACAAAGATGTTACTTA
76398	74485	TAATTACAAAGATGTTACTT
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76400	74487	AATAATTACAAAGATGTTAC
76401	74488	CAATAATTACAAAGATGTTA
76402	74489	GCAATAATTACAAAGATGTT
76403	74490	AGCAATAATTACAAAGATGT
76404	74491	TAGCAATAATTACAAAGATG

125481	123568	GACTACAGGTGTGTGCCACC
125482	123569	GGACTACAGGTGTGTGCCAC
125483	123570	AGGACTACAGGTGTGTGCCA
125484	123571	TAGGACTACAGGTGTGTGCC
125485	123572	TTAGGACTACAGGTGTGTGC
125486	123573	GTTAGGACTACAGGTGTGTG
125487	123574	AGTTAGGACTACAGGTGTGT
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125491	123578	AAGTAGTTAGGACTACAGGT
125492	123579	CAAGTAGTTAGGACTACAGG
125493	123580	TCAAGTAGTTAGGACTACAG
125494	123581	CTCAAGTAGTTAGGACTACA
125495	123582	TCTCAAGTAGTTAGGACTAC
125496	123583	CTCTCAAGTAGTTAGGACTA
125497	123584	CCTCTCAAGTAGTTAGGACT
125498	123585	GCCTCTCAAGTAGTTAGGAC
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125504	123591	TCCTCAGCCTCTCAAGTAGT
125505	123592	TTCCTCAGCCTCTCAAGTAG
125506	123593	CTTCCTCAGCCTCTCAAGTA
125507	123594	CCTTCCTCAGCCTCTCAAGT
125508	123595	TCCTTCCTCAGCCTCTCAAG
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125510	123597	TCTCCTTCCTCAGCCTCTCA
125511	123598	TTCTCCTTCCTCAGCCTCTC
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125514	123601	CAATTCTCCTTCCTCAGCCT
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125516	123603	AGCAATTCTCCTTCCTCAGC
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125518	123605	CAAGCAATTCTCCTTCCTCA
125519	123606	TCAAGCAATTCTCCTTCCTC
125520	123607	CTCAAGCAATTCTCCTTCCT
125521	123608	GCTCAAGCAATTCTCCTTCC
125522	123609	GGCTCAAGCAATTCTCCTTC
125523	123610	GGGCTCAAGCAATTCTCCTT
125524	123611	TGGGCTCAAGCAATTCTCCT
125525	123612	CTGGGCTCAAGCAATTCTCC
125526	123613	ACTGGGCTCAAGCAATTCTC
125527	123614	TACTGGGCTCAAGCAATTCT
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125541	123628	CTGCTGCTTTAAACTACTGG
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125543	123630	CACTGCTGCTTTAAACTACT
125544	123631	TCACTGCTGCTTTAAACTAC
125545	123632	CTCACTGCTGCTTTAAACTA
125546	123633	GCTCACTGCTGCTTTAAACT
125547	123634	AGCTCACTGCTGCTTTAAAC
125548	123635	CAGCTCACTGCTGCTTTAAA
125549	123636	ACAGCTCACTGCTGCTTTAA
125550	123637	CACAGCTCACTGCTGCTTTA
125551	123638	TCACAGCTCACTGCTGCTTT

27258	25345	AAAAAAAAAAAAAAAAAAA
27259	25346	AAAAAAAAAAAAAAAAAAA
27260	25347	CAAAAAAAAAAAAAAAAAA
27261	25348	CCAAAAAAAAAAAAAAAAA
27262	25349	TCCAAAAAAAAAAAAAAAA
27263	25350	CTCCAAAAAAAAAAAAAAA
27264	25351	TCTCCAAAAAAAAAAAAAA
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27269	25356	CTCTGTCTCCAAAAAAAAA
27270	25357	ACTCTGTCTCCAAAAAAAA
27271	25358	GACTCTGTCTCCAAAAAAA
27272	25359	AGACTCTGTCTCCAAAAAA
27273	25360	AAGACTCTGTCTCCAAAAA
27274	25361	CAAGACTCTGTCTCCAAAA
27275	25362	GCAAGACTCTGTCTCCAAA
27276	25363	AGCAAGACTCTGTCTCCAA
27277	25364	GAGCAAGACTCTGTCTCCA
27278	25365	AGAGCAAGACTCTGTCTCC
27279	25366	CAGAGCAAGACTCTGTCTC
27280	25367	ACAGAGCAAGACTCTGTCT
27281	25368	GACAGAGCAAGACTCTGTC
27282	25369	CGACAGAGCAAGACTCTGT
27283	25370	GCGACAGAGCAAGACTCTG
27284	25371	GGCGACAGAGCAAGACTCT
27285	25372	GGGCGACAGAGCAAGACTC
27286	25373	TGGGCGACAGAGCAAGACT
27287	25374	CTGGGCGACAGAGCAAGAC
27288	25375	CCTGGGCGACAGAGCAAGA
27289	25376	GCCTGGGCGACAGAGCAAG
27290	25377	AGCCTGGGCGACAGAGCAA
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27292	25379	CCAGCCTGGGCGACAGAGC
27293	25380	TCCAGCCTGGGCGACAGAG
27294	25381	CTCCAGCCTGGGCGACAGA
27295	25382	ACTCCAGCCTGGGCGACAG
27296	25383	CACTCCAGCCTGGGCGACA
27297	25384	GCACTCCAGCCTGGGCGAC
27298	25385	TGCACTCCAGCCTGGGCGA
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27304	25391	CACCACTGCACTCCAGCCT
27305	25392	GCACCACTGCACTCCAGCC
27306	25393	CGCACCACTGCACTCCAGC
27307	25394	TCGCACCACTGCACTCCAG
27308	25395	ATCGCACCACTGCACTCCA
27309	25396	GATCGCACCACTGCACTCC
27310	25397	AGATCGCACCACTGCACTC
27311	25398	AAGATCGCACCACTGCACT
27312	25399	CAAGATCGCACCACTGCAC
27313	25400	CCAAGATCGCACCACTGCA
27314	25401	GCCAAGATCGCACCACTGC
27315	25402	AGCCAAGATCGCACCACTG
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27317	25404	TGAGCCAAGATCGCACCAC
27318	25405	GTGAGCCAAGATCGCACCA
27319	25406	AGTGAGCCAAGATCGCACC
27320	25407	TAGTGAGCCAAGATCGCAC
27321	25408	GTAGTGAGCCAAGATCGCA
27322	25409	TGTAGTGAGCCAAGATCGC
27323	25410	TTGTAGTGAGCCAAGATCG
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27325	25412	GCTTGTAGTGAGCCAAGAT
27326	25413	AGCTTGTAGTGAGCCAAGA
27327	25414	GAGCTTGTAGTGAGCCAAG
27328	25415	AGAGCTTGTAGTGAGCCAAG

76405	74492	CTAGCAATAATTACAAAGAT
76406	74493	TCTAGCAATAATTACAAAGA
76407	74494	GTCTAGCAATAATTACAAAG
76408	74495	AGTCTAGCAATAATTACAAA
76409	74496	GAGTCTAGCAATAATTACAA
76410	74497	AGAGTCTAGCAATAATTACA
76411	74498	CAGAGTCTAGCAATAATTAC
76412	74499	CCAGAGTCTAGCAATAATTA
76413	74500	ACCAGAGTCTAGCAATAATT
76414	74501	GACCAGAGTCTAGCAATAAT
76415	74502	TGACCAGAGTCTAGCAATAA
76416	74503	CTGACCAGAGTCTAGCAATA
76417	74504	ACTGACCAGAGTCTAGCAAT
76418	74505	TACTGACCAGAGTCTAGCAA
76419	74506	ATACTGACCAGAGTCTAGCA
76420	74507	CATACTGACCAGAGTCTAGC
76421	74508	TCATACTGACCAGAGTCTAG
76422	74509	GTCATACTGACCAGAGTCTA
76423	74510	TGTCATACTGACCAGAGTCT
76424	74511	ATGTCATACTGACCAGAGTC
76425	74512	GATGTCATACTGACCAGAGT
76426	74513	GGATGTCATACTGACCAGAG
76427	74514	AGGATGTCATACTGACCAGA
76428	74515	CAGGATGTCATACTGACCAG
76429	74516	ACAGGATGTCATACTGACCA
76430	74517	GACAGGATGTCATACTGACC
76431	74518	TGACAGGATGTCATACTGAC
76432	74519	GTGACAGGATGTCATACTGA
76433	74520	AGTGACAGGATGTCATACTG
76434	74521	AAGTGACAGGATGTCATACT
76435	74522	CAAGTGACAGGATGTCATAC
76436	74523	CCAAGTGACAGGATGTCATA
76437	74524	ACCAAGTGACAGGATGTCAT
76438	74525	AACCAAGTGACAGGATGTCA
76439	74526	CAACCAAGTGACAGGATGTC
76440	74527	ACAACCAAGTGACAGGATGT
76441	74528	TACAACCAAGTGACAGGATG
76442	74529	TTACAACCAAGTGACAGGAT
76443	74530	ATTACAACCAAGTGACAGGA
76444	74531	AATTACAACCAAGTGACAGG
76445	74532	AAATTACAACCAAGTGACAG
76446	74533	TAAATTACAACCAAGTGACA
76447	74534	TTAAATTACAACCAAGTGAC
76448	74535	TTTAAATTACAACCAAGTGA
76449	74536	ATTTAAATTACAACCAAGTG
76450	74537	CATTTAAATTACAACCAAGT
76451	74538	ACATTTAAATTACAACCAAG
76452	74539	CACATTTAAATTACAACCAA
76453	74540	GCACATTTAAATTACAACCA
76454	74541	AGCACATTTAAATTACAACC
76455	74542	AAGCACATTTAAATTACAAC
76456	74543	AAAGCACATTTAAATTACAA
76457	74544	AAAAGCACATTTAAATTACA
76458	74545	CAAAAGCACATTTAAATTAC
76459	74546	ACAAAAGCACATTTAAATTA
76460	74547	AACAAAAGCACATTTAAATT
76461	74548	CAACAAAAGCACATTTAAAT
76462	74549	ACAACAAAAGCACATTTAAA
76463	74550	AACAACAAAAGCACATTTAA
76464	74551	CAACAACAAAAGCACATTTA
76465	74552	ACAACAACAAAAGCACATTT
76466	74553	AACAACAACAAAAGCACATT
76467	74554	CAACAACAACAAAAGCACAT
76468	74555	ACAACAACAACAAAAGCACA
76469	74556	AACAACAACAACAAAAGCAC
76470	74557	TAACAACAACAACAAAAGCA
76471	74558	ATAACAACAACAACAAAAGC
76472	74559	AATAACAACAACAACAAAAG
76473	74560	CAATAACAACAACAACAAAA
76474	74561	ACAATAACAACAACAACAAA
76475	74562	TACAATAACAACAACAACAA

125552	123639	ATCACAGCTCACTGCTGCTT
125553	123640	AATCACAGCTCACTGCTGCT
125554	123641	CAATCACAGCTCACTGCTGC
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125556	123643	TACAATCACAGCTCACTGCT
125557	123644	GTACAATCACAGCTCACTGC
125558	123645	GGTACAATCACAGCTCACTG
125559	123646	TGGTACAATCACAGCTCACT
125560	123647	GTGGTACAATCACAGCTCAC
125561	123648	AGTGGTACAATCACAGCTCA
125562	123649	CAGTGGTACAATCACAGCTC
125563	123650	ACAGTGGTACAATCACAGCT
125564	123651	TACAGTGGTACAATCACAGC
125565	123652	GTACAGTGGTACAATCACAG
125566	123653	AGTACAGTGGTACAATCACA
125567	123654	GAGTACAGTGGTACAATCAC
125568	123655	GGAGTACAGTGGTACAATCA
125569	123656	TGGAGTACAGTGGTACAATC
125570	123657	CTGGAGTACAGTGGTACAAT
125571	123658	GCTGGAGTACAGTGGTACAA
125572	123659	GGCTGGAGTACAGTGGTACA
125573	123660	AGGCTGGAGTACAGTGGTAC
125574	123661	CAGGCTGGAGTACAGTGGTA
125575	123662	CCAGGCTGGAGTACAGTGGT
125576	123663	CCCAGGCTGGAGTACAGTGG
125577	123664	ACCCAGGCTGGAGTACAGTG
125578	123665	CACCCAGGCTGGAGTACAGT
125579	123666	TCACCCAGGCTGGAGTACAG
125580	123667	GTCACCCAGGCTGGAGTACA
125581	123668	TGTCACCCAGGCTGGAGTAC
125582	123669	CTGTCACCCAGGCTGGAGTA
125583	123670	TCTGTCACCCAGGCTGGAGT
125584	123671	TTCTGTCACCCAGGCTGGAG
125585	123672	CTTCTGTCACCCAGGCTGGA
125586	123673	CCTTCTGTCACCCAGGCTGG
125587	123674	TCCTTCTGTCACCCAGGCTG
125588	123675	CTCCTTCTGTCACCCAGGCT
125589	123676	TCTCCTTCTGTCACCCAGGC
125590	123677	GTCTCCTTCTGTCACCCAGG
125591	123678	GGTCTCCTTCTGTCACCCAG
125592	123679	GGGTCTCCTTCTGTCACCCA
125593	123680	AGGGTCTCCTTCTGTCACCC
125594	123681	CAGGGTCTCCTTCTGTCACC
125595	123682	ACAGGGTCTCCTTCTGTCAC
125596	123683	TACAGGGTCTCCTTCTGTCA
125597	123684	ATACAGGGTCTCCTTCTGTC
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125599	123686	AAATACAGGGTCTCCTTCTG
125600	123687	TAAATACAGGGTCTCCTTCT
125601	123688	TTAAATACAGGGTCTCCTTC
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125604	123691	ACTTTAAATACAGGGTCTCC
125605	123692	CACTTTAAATACAGGGTCTC
125606	123693	ACACTTTAAATACAGGGTCT
125607	123694	CACACTTTAAATACAGGGTC
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125611	123698	CACACACACTTTAAATACAG
125612	123699	ACACACACACTTTAAATACA
125613	123700	TACACACACACTTTAAATAC
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125618	123705	ACGCATACACACACACTTTA
125619	123706	CACGCATACACACACACTTT
125620	123707	GCACGCATACACACACACTT
125621	123708	CGCACGCATACACACACACT
125622	123709	GCGCACGCATACACACACAC

27329	25416	CAGAGCTTGTAGTGAGCCAA
27330	25417	GCAGAGCTTGTAGTGAGCCA
27331	25418	GGCAGAGCTTGTAGTGAGCC
27332	25419	AGGCAGAGCTTGTAGTGAGC
27333	25420	GAGGCAGAGCTTGTAGTGAG
27334	25421	AGAGGCAGAGCTTGTAGTGA
27335	25422	GAGAGGCAGAGCTTGTAGTG
27336	25423	CGAGAGGCAGAGCTTGTAGT
27337	25424	CCGAGAGGCAGAGCTTGTAG
27338	25425	CCCGAGAGGCAGAGCTTGTA
27339	25426	ACCCGAGAGGCAGAGCTTGT
27340	25427	AACCCGAGAGGCAGAGCTTG
27341	25428	GAACCCGAGAGGCAGAGCTT
27342	25429	TGAACCCGAGAGGCAGAGCT
27343	25430	GTGAACCCGAGAGGCAGAGC
27344	25431	CGTGAACCCGAGAGGCAGAG
27345	25432	GCGTGAACCCGAGAGGCAGA
27346	25433	GGCGTGAACCCGAGAGGCAG
27347	25434	TGGCGTGAACCCGAGAGGCA
27348	25435	ATGGCGTGAACCCGAGAGGC
27349	25436	AATGGCGTGAACCCGAGAGG
27350	25437	GAATGGCGTGAACCCGAGAG
27351	25438	AGAATGGCGTGAACCCGAGA
27352	25439	GAGAATGGCGTGAACCCGAG
27353	25440	GGAGAATGGCGTGAACCCGA
27354	25441	AGGAGAATGGCGTGAACCCG
27355	25442	CAGGAGAATGGCGTGAACCC
27356	25443	GCAGGAGAATGGCGTGAACC
27357	25444	GGCAGGAGAATGGCGTGAAC
27358	25445	AGGCAGGAGAATGGCGTGAA
27359	25446	GAGGCAGGAGAATGGCGTGA
27360	25447	GGAGGCAGGAGAATGGCGTG
27361	25448	TGGAGGCAGGAGAATGGCGT
27362	25449	GTGGAGGCAGGAGAATGGCG
27363	25450	GGTGGAGGCAGGAGAATGGC
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27365	25452	GAGGTGGAGGCAGGAGAATG
27366	25453	GGAGGTGGAGGCAGGAGAAT
27367	25454	GGGAGGTGGAGGCAGGAGAA
27368	25455	CGGGAGGTGGAGGCAGGAGA
27369	25456	TCGGGAGGTGGAGGCAGGAG
27370	25457	CTCGGGAGGTGGAGGCAGGA
27371	25458	ACTCGGGAGGTGGAGGCAGG
27372	25459	TACTCGGGAGGTGGAGGCAG
27373	25460	CTACTCGGGAGGTGGAGGCA
27374	25461	GCTACTCGGGAGGTGGAGGC
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27376	25463	CAGCTACTCGGGAGGTGGAG
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27381	25468	AGTCCCAGCTACTCGGGAGG
27382	25469	TAGTCCCAGCTACTCGGGAG
27383	25470	GTAGTCCCAGCTACTCGGGA
27384	25471	TGTAGTCCCAGCTACTCGGG
27385	25472	CTGTAGTCCCAGCTACTCGG
27386	25473	CCTGTAGTCCCAGCTACTCG
27387	25474	ACCTGTAGTCCCAGCTACTC
27388	25475	CACCTGTAGTCCCAGCTACT
27389	25476	GCACCTGTAGTCCCAGCTAC
27390	25477	GGCACCTGTAGTCCCAGCTA
27391	25478	GGGCACCTGTAGTCCCAGCT
27392	25479	CGGGCACCTGTAGTCCCAGC
27393	25480	GCGGGCACCTGTAGTCCCAG
27394	25481	GGCGGGCACCTGTAGTCCCA
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27396	25483	GTGGCGGGCACCTGTAGTCC
27397	25484	GGTGGCGGGCACCTGTAGTC
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27399	25486	GTGGTGGCGGGCACCTGTAG

76476	74563	CTACAATAACAACAACAACA
76477	74564	ACTACAATAACAACAACAAC
76478	74565	CACTACAATAACAACAACAA
76479	74566	TCACTACAATAACAACAACA
76480	74567	CTCACTACAATAACAACAAC
76481	74568	ACTCACTACAATAACAACAA
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76484	74571	TACACTCACTACAATAACAA
76485	74572	ATACACTCACTACAATAACA
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76491	74578	CTCTAAATACACTCACTACA
76492	74579	GCTCTAAATACACTCACTAC
76493	74580	TGCTCTAAATACACTCACTA
76494	74581	CTGCTCTAAATACACTCACT
76495	74582	GCTGCTCTAAATACACTCAC
76496	74583	TGCTGCTCTAAATACACTCA
76497	74584	CTGCTGCTCTAAATACACTC
76498	74585	CCTGCTGCTCTAAATACACT
76499	74586	ACCTGCTGCTCTAAATACAC
76500	74587	AACCTGCTGCTCTAAATACA
76501	74588	AAACCTGCTGCTCTAAATAC
76502	74589	CAAACCTGCTGCTCTAAATA
76503	74590	ACAAACCTGCTGCTCTAAAT
76504	74591	AACAAACCTGCTGCTCTAAA
76505	74592	CAACAAACCTGCTGCTCTAA
76506	74593	ACAACAAACCTGCTGCTCTA
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76508	74595	ATACAACAAACCTGCTGCTC
76509	74596	TATACAACAAACCTGCTGCT
76510	74597	TTATACAACAAACCTGCTGC
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76514	74601	CTAGTTATACAACAAACCTG
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76516	74603	CTCTAGTTATACAACAAACC
76517	74604	TCTCTAGTTATACAACAAAC
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76519	74606	AGTCTCTAGTTATACAACAA
76520	74607	AAGTCTCTAGTTATACAACA
76521	74608	AAAGTCTCTAGTTATACAAC
76522	74609	GAAAGTCTCTAGTTATACAA
76523	74610	AGAAAGTCTCTAGTTATACA
76524	74611	GAGAAAGTCTCTAGTTATAC
76525	74612	GGAGAAAGTCTCTAGTTATA
76526	74613	GGGAGAAAGTCTCTAGTTAT
76527	74614	TGGGAGAAAGTCTCTAGTTA
76528	74615	TTGGGAGAAAGTCTCTAGTT
76529	74616	CTTGGGAGAAAGTCTCTAGT
76530	74617	GCTTGGGAGAAAGTCTCTAG
76531	74618	TGCTTGGGAGAAAGTCTCTA
76532	74619	TTGCTTGGGAGAAAGTCTCT
76533	74620	ATTGCTTGGGAGAAAGTCTC
76534	74621	TATTGCTTGGGAGAAAGTCT
76535	74622	ATATTGCTTGGGAGAAAGTC
76536	74623	TATATTGCTTGGGAGAAAGT
76537	74624	ATATATTGCTTGGGAGAAAG
76538	74625	TATATATTGCTTGGGAGAAA
76539	74626	TTATATATTGCTTGGGAGAA
76540	74627	TTTATATATTGCTTGGGAGA
76541	74628	CTTTATATATTGCTTGGGAG
76542	74629	TCTTTATATATTGCTTGGGA
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76545	74632	TTTTCTTTATATATTGCTTG
76546	74633	TTTTTCTTTATATATTGCTT

125623	123710	TGCGCACGCATACACACACA
125624	123711	ATGCGCACGCATACACACAC
125625	123712	TATGCGCACGCATACACACA
125626	123713	CTATGCGCACGCATACACAC
125627	123714	TCTATGCGCACGCATACACA
125628	123715	ATCTATGCGCACGCATACAC
125629	123716	CATCTATGCGCACGCATACA
125630	123717	CCATCTATGCGCACGCATAC
125631	123718	TCCATCTATGCGCACGCATA
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125634	123721	CTATCCATCTATGCGCACGC
125635	123722	TCTATCCATCTATGCGCACG
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125637	123724	TATCTATCCATCTATGCGCA
125638	123725	TTATCTATCCATCTATGCGC
125639	123726	ATTATCTATCCATCTATGCG
125640	123727	TATTATCTATCCATCTATGC
125641	123728	TTATTATCTATCCATCTATG
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125644	123731	ACATTATTATCTATCCATCT
125645	123732	TACATTATTATCTATCCATC
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125653	123740	AATGGAATTACATTATTATC
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125665	123752	TTGTATGACCATAATGGAAT
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125667	123754	GTTTGTATGACCATAATGGA
125668	123755	AGTTTGTATGACCATAATGG
125669	123756	CAGTTTGTATGACCATAATG
125670	123757	TCAGTTTGTATGACCATAAT
125671	123758	ATCAGTTTGTATGACCATAA
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125674	123761	CATATCAGTTTGTATGACCA
125675	123762	TCATATCAGTTTGTATGACC
125676	123763	TTCATATCAGTTTGTATGAC
125677	123764	TTTCATATCAGTTTGTATGA
125678	123765	ATTTCATATCAGTTTGTATG
125679	123766	CATTTCATATCAGTTTGTAT
125680	123767	GCATTTCATATCAGTTTGTA
125681	123768	GGCATTTCATATCAGTTTGT
125682	123769	TGGCATTTCATATCAGTTTG
125683	123770	ATGGCATTTCATATCAGTTT
125684	123771	AATGGCATTTCATATCAGTT
125685	123772	AAATGGCATTTCATATCAGT
125686	123773	AAAATGGCATTTCATATCAG
125687	123774	TAAAATGGCATTTCATATCA
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27400	25487	CGTGGTGGCGGGCACCTGTA
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27402	25489	GGCGTGGTGGCGGGCACCTG
27403	25490	GGGCGTGGTGGCGGGCACCT
27404	25491	CGGGCGTGGTGGCGGGCACC
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27406	25493	GCCGGGCGTGGTGGCGGGCA
27407	25494	AGCCGGGCGTGGTGGCGGGC
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27418	25505	ACAAAAAAATTAGCCGGGCG
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27435	25522	TCATCTCTACCAAAAATACA
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27437	25524	CCTCATCTCTACCAAAAATA
27438	25525	ACCTCATCTCTACCAAAAAT
27439	25526	AACCTCATCTCTACCAAAAA
27440	25527	AAACCTCATCTCTACCAAAA
27441	25528	GAAACCTCATCTCTACCAAA
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27443	25530	GTGAAACCTCATCTCTACCA
27444	25531	AGTGAAACCTCATCTCTACC
27445	25532	CAGTGAAACCTCATCTCTAC
27446	25533	ACAGTGAAACCTCATCTCTA
27447	25534	CACAGTGAAACCTCATCTCT
27448	25535	ACACAGTGAAACCTCATCTC
27449	25536	AACACAGTGAAACCTCATCT
27450	25537	TAACACAGTGAAACCTCATC
27451	25538	CTAACACAGTGAAACCTCAT
27452	25539	GCTAACACAGTGAAACCTCA
27453	25540	GGCTAACACAGTGAAACCTC
27454	25541	TGGCTAACACAGTGAAACCT
27455	25542	GTGGCTAACACAGTGAAACC
27456	25543	TGTGGCTAACACAGTGAAAC
27457	25544	CTGTGGCTAACACAGTGAAA
27458	25545	TCTGTGGCTAACACAGTGAA
27459	25546	ATCTGTGGCTAACACAGTGA
27460	25547	GATCTGTGGCTAACACAGTG
27461	25548	GGATCTGTGGCTAACACAGT
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27463	25550	CGGGATCTGTGGCTAACACA
27464	25551	TCGGGATCTGTGGCTAACAC
27465	25552	GTCGGGATCTGTGGCTAACA
27466	25553	GGTCGGGATCTGTGGCTAAC
27467	25554	AGGTCGGGATCTGTGGCTAA
27468	25555	GAGGTCGGGATCTGTGGCTA
27469	25556	TGAGGTCGGGATCTGTGGCT
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76547	74634	ATTTTTCTTTATATATTGCT
76548	74635	CATTTTTCTTTATATATTGC
76549	74636	ACATTTTTCTTTATATATTG
76550	74637	AACATTTTTCTTTATATATT
76551	74638	AAACATTTTTCTTTATATAT
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76558	74645	AAATGACAAACATTTTTCTT
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76560	74647	TAAAATGACAAACATTTTTC
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76562	74649	AGTAAAATGACAAACATTTT
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76566	74653	TACAAGTAAAATGACAAACA
76567	74654	CTACAAGTAAAATGACAAAC
76568	74655	CCTACAAGTAAAATGACAAA
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76570	74657	CCCCTACAAGTAAAATGACA
76571	74658	ACCCCTACAAGTAAAATGAC
76572	74659	AACCCCTACAAGTAAAATGA
76573	74660	TAACCCCTACAAGTAAAATG
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76575	74662	CTTAACCCCTACAAGTAAAA
76576	74663	GCTTAACCCCTACAAGTAAA
76577	74664	TGCTTAACCCCTACAAGTAA
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76583	74670	TACTCCTGCTTAACCCCTAC
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76586	74673	CAGTACTCCTGCTTAACCCC
76587	74674	ACAGTACTCCTGCTTAACCC
76588	74675	GACAGTACTCCTGCTTAACC
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76590	74677	CAGACAGTACTCCTGCTTAA
76591	74678	ACAGACAGTACTCCTGCTTA
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76593	74680	GAACAGACAGTACTCCTGCT
76594	74681	AGAACAGACAGTACTCCTGC
76595	74682	AAGAACAGACAGTACTCCTG
76596	74683	CAAGAACAGACAGTACTCCT
76597	74684	ACAAGAACAGACAGTACTCC
76598	74685	CACAAGAACAGACAGTACTC
76599	74686	CCACAAGAACAGACAGTACT
76600	74687	TCCACAAGAACAGACAGTAC
76601	74688	ATCCACAAGAACAGACAGTA
76602	74689	CATCCACAAGAACAGACAGT
76603	74690	GCATCCACAAGAACAGACAG
76604	74691	AGCATCCACAAGAACAGACA
76605	74692	GAGCATCCACAAGAACAGAC
76606	74693	TGAGCATCCACAAGAACAGA
76607	74694	ATGAGCATCCACAAGAACAG
76608	74695	CATGAGCATCCACAAGAACA
76609	74696	TCATGAGCATCCACAAGAAC
76610	74697	TTCATGAGCATCCACAAGAA
76611	74698	ATTCATGAGCATCCACAAGA
76612	74699	AATTCATGAGCATCCACAAG
76613	74700	TAATTCATGAGCATCCACAA
76614	74701	GTAATTCATGAGCATCCACA
76615	74702	AGTAATTCATGAGCATCCAC
76616	74703	AAGTAATTCATGAGCATCCA
76617	74704	GAAGTAATTCATGAGCATCC

125694	123781	TATATGATAAAATGGCATTT
125695	123782	TTATATGATAAAATGGCATT
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125697	123784	TGTTATATGATAAAATGGCA
125698	123785	TTGTTATATGATAAAATGGC
125699	123786	CTTGTTATATGATAAAATGG
125700	123787	ACTTGTTATATGATAAAATG
125701	123788	CACTTGTTATATGATAAAAT
125702	123789	ACACTTGTTATATGATAAAA
125703	123790	GACACTTGTTATATGATAAA
125704	123791	AGACACTTGTTATATGATAA
125705	123792	AAGACACTTGTTATATGATA
125706	123793	AAAGACACTTGTTATATGAT
125707	123794	AAAAGACACTTGTTATATGA
125708	123795	AAAAAGACACTTGTTATATG
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125713	123800	ACCACAAAAAGACACTTGTT
125714	123801	AACCACAAAAAGACACTTGT
125715	123802	CAACCACAAAAAGACACTTG
125716	123803	TCAACCACAAAAAGACACTT
125717	123804	TTCAACCACAAAAAGACACT
125718	123805	ATTCAACCACAAAAAGACAC
125719	123806	AATTCAACCACAAAAAGACA
125720	123807	AAATTCAACCACAAAAAGAC
125721	123808	CAAATTCAACCACAAAAAGA
125722	123809	ACAAATTCAACCACAAAAAG
125723	123810	AACAAATTCAACCACAAAAA
125724	123811	AAACAAATTCAACCACAAAA
125725	123812	GAAACAAATTCAACCACAAA
125726	123813	AGAAACAAATTCAACCACAA
125727	123814	CAGAAACAAATTCAACCACA
125728	123815	CCAGAAACAAATTCAACCAC
125729	123816	TCCAGAAACAAATTCAACCA
125730	123817	ATCCAGAAACAAATTCAACC
125731	123818	AATCCAGAAACAAATTCAAC
125732	123819	AAATCCAGAAACAAATTCAA
125733	123820	AAAATCCAGAAACAAATTCA
125734	123821	AAAAATCCAGAAACAAATTC
125735	123822	GAAAAATCCAGAAACAAATT
125736	123823	TGAAAAATCCAGAAACAAAT
125737	123824	GTGAAAAATCCAGAAACAAA
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125739	123826	GAGTGAAAAATCCAGAAACA
125740	123827	AGAGTGAAAAATCCAGAAAC
125741	123828	CAGAGTGAAAAATCCAGAAA
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125743	123830	AGCAGAGTGAAAAATCCAGA
125744	123831	AAGCAGAGTGAAAAATCCAG
125745	123832	GAAGCAGAGTGAAAAATCCA
125746	123833	TGAAGCAGAGTGAAAAATCC
125747	123834	GTGAAGCAGAGTGAAAAATC
125748	123835	AGTGAAGCAGAGTGAAAAAT
125749	123836	TAGTGAAGCAGAGTGAAAAA
125750	123837	TTAGTGAAGCAGAGTGAAAA
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125759	123846	CCTATTAGATTAGTGAAGCA
125760	123847	TCCTATTAGATTAGTGAAGC
125761	123848	GTCCTATTAGATTAGTGAAG
125762	123849	AGTCCTATTAGATTAGTGAA
125763	123850	TAGTCCTATTAGATTAGTGA
125764	123851	GTAGTCCTATTAGATTAGTG

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27472	25559	TCATGAGGTCGGGATCTGTG
27473	25560	ATCATGAGGTCGGGATCTGT
27474	25561	GATCATGAGGTCGGGATCTG
27475	25562	AGATCATGAGGTCGGGATCT
27476	25563	CAGATCATGAGGTCGGGATC
27477	25564	ACAGATCATGAGGTCGGGAT
27478	25565	GACAGATCATGAGGTCGGGA
27479	25566	AGACAGATCATGAGGTCGGG
27480	25567	CAGACAGATCATGAGGTCGG
27481	25568	GCAGACAGATCATGAGGTCG
27482	25569	GGCAGACAGATCATGAGGTC
27483	25570	AGGCAGACAGATCATGAGGT
27484	25571	GAGGCAGACAGATCATGAGG
27485	25572	TGAGGCAGACAGATCATGAG
27486	25573	CTGAGGCAGACAGATCATGA
27487	25574	GCTGAGGCAGACAGATCATG
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27490	25577	GAGGCTGAGGCAGACAGATC
27491	25578	GGAGGCTGAGGCAGACAGAT
27492	25579	GGGAGGCTGAGGCAGACAGA
27493	25580	TGGGAGGCTGAGGCAGACAG
27494	25581	TTGGGAGGCTGAGGCAGACA
27495	25582	TTTGGGAGGCTGAGGCAGAC
27496	25583	CTTTGGGAGGCTGAGGCAGA
27497	25584	ACTTTGGGAGGCTGAGGCAG
27498	25585	CACTTTGGGAGGCTGAGGCA
27499	25586	GCACTTTGGGAGGCTGAGGC
27500	25587	AGCACTTTGGGAGGCTGAGG
27501	25588	CAGCACTTTGGGAGGCTGAG
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27505	25592	ATCCCAGCACTTTGGGAGGC
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27508	25595	GCAATCCCAGCACTTTGGGA
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27517	25604	TTCAAGCCTGCAATCCCAGC
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27520	25607	TGATTCAAGCCTGCAATCCC
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27536	25623	TTCCGGCCGGGTGCGGTGAT
27537	25624	CTTCCGGCCGGGTGCGGTGA
27538	25625	ACTTCCGGCCGGGTGCGGTG
27539	25626	GACTTCCGGCCGGGTGCGGT
27540	25627	AGACTTCCGGCCGGGTGCGG
27541	25628	GAGACTTCCGGCCGGGTGCG

76618	74705	AGAAGTAATTCATGAGCATC
76619	74706	AAGAAGTAATTCATGAGCAT
76620	74707	AAAGAAGTAATTCATGAGCA
76621	74708	CAAAGAAGTAATTCATGAGC
76622	74709	ACAAAGAAGTAATTCATGAG
76623	74710	CACAAAGAAGTAATTCATGA
76624	74711	TCACAAAGAAGTAATTCATG
76625	74712	ATCACAAAGAAGTAATTCAT
76626	74713	AATCACAAAGAAGTAATTCA
76627	74714	TAATCACAAAGAAGTAATTC
76628	74715	TTAATCACAAAGAAGTAATT
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76633	74720	TTATTTTAATCACAAAGAAG
76634	74721	TTTATTTTAATCACAAAGAA
76635	74722	ATTTATTTTAATCACAAAGA
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76638	74725	ATTATTTATTTTAATCACAA
76639	74726	TATTATTTATTTTAATCACA
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76641	74728	CTTATTATTTATTTTAATCA
76642	74729	TCTTATTATTTATTTTAATC
76643	74730	TTCTTATTATTTATTTTAAT
76644	74731	CTTCTTATTATTTATTTTAA
76645	74732	ACTTCTTATTATTTATTTTA
76646	74733	TACTTCTTATTATTTATTTT
76647	74734	CTACTTCTTATTATTTATTT
76648	74735	GCTACTTCTTATTATTTATT
76649	74736	AGCTACTTCTTATTATTTAT
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76658	74745	TTTAATTTAAGCTACTTCTT
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76663	74750	CTAATTTTAATTTAAGCTAC
76664	74751	TCTAATTTTAATTTAAGCTA
76665	74752	TTCTAATTTTAATTTAAGCT
76666	74753	TTTCTAATTTTAATTTAAGC
76667	74754	GTTTCTAATTTTAATTTAAG
76668	74755	GGTTTCTAATTTTAATTTAA
76669	74756	TGGTTTCTAATTTTAATTTA
76670	74757	ATGGTTTCTAATTTTAATTT
76671	74758	CATGGTTTCTAATTTTAATT
76672	74759	CCATGGTTTCTAATTTTAAT
76673	74760	CCCATGGTTTCTAATTTTAA
76674	74761	TCCCATGGTTTCTAATTTTA
76675	74762	TTCCCATGGTTTCTAATTTT
76676	74763	TTTCCCATGGTTTCTAATTT
76677	74764	ATTTCCCATGGTTTCTAATT
76678	74765	CATTTCCCATGGTTTCTAAT
76679	74766	GCATTTCCCATGGTTTCTAA
76680	74767	GGCATTTCCCATGGTTTCTA
76681	74768	CGGCATTTCCCATGGTTTCT
76682	74769	CCGGCATTTCCCATGGTTTC
76683	74770	ACCGGCATTTCCCATGGTTT
76684	74771	CACCGGCATTTCCCATGGTT
76685	74772	ACACCGGCATTTCCCATGGT
76686	74773	CACACCGGCATTTCCCATGG
76687	74774	ACACACCGGCATTTCCCATG
76688	74775	AACACACCGGCATTTCCCAT

125765	123852	GGTAGTCCTATTAGATTAGT
125766	123853	AGGTAGTCCTATTAGATTAG
125767	123854	AAGGTAGTCCTATTAGATTA
125768	123855	GAAGGTAGTCCTATTAGATT
125769	123856	AGAAGGTAGTCCTATTAGAT
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125771	123858	TGAGAAGGTAGTCCTATTAG
125772	123859	ATGAGAAGGTAGTCCTATTA
125773	123860	GATGAGAAGGTAGTCCTATT
125774	123861	GGATGAGAAGGTAGTCCTAT
125775	123862	TGGATGAGAAGGTAGTCCTA
125776	123863	GTGGATGAGAAGGTAGTCCT
125777	123864	AGTGGATGAGAAGGTAGTCC
125778	123865	GAGTGGATGAGAAGGTAGTC
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125780	123867	GTGAGTGGATGAGAAGGTAG
125781	123868	AGTGAGTGGATGAGAAGGTA
125782	123869	CAGTGAGTGGATGAGAAGGT
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125785	123872	TGGCAGTGAGTGGATGAGAA
125786	123873	TTGGCAGTGAGTGGATGAGA
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125788	123875	TGTTGGCAGTGAGTGGATGA
125789	123876	ATGTTGGCAGTGAGTGGATG
125790	123877	AATGTTGGCAGTGAGTGGAT
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125792	123879	TCAATGTTGGCAGTGAGTGG
125793	123880	ATCAATGTTGGCAGTGAGTG
125794	123881	AATCAATGTTGGCAGTGAGT
125795	123882	AAATCAATGTTGGCAGTGAG
125796	123883	AAAATCAATGTTGGCAGTGA
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125798	123885	AAAAAATCAATGTTGGCAGT
125799	123886	AAAAAAATCAATGTTGGCAG
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125813	123900	AAGGTAATCTGAAAAAAAAA
125814	123901	CAAGGTAATCTGAAAAAAAA
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125820	123907	AAAATTCAAGGTAATCTGAA
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125822	123909	AGAAAATTCAAGGTAATCTG
125823	123910	CAGAAAATTCAAGGTAATCT
125824	123911	ACAGAAAATTCAAGGTAATC
125825	123912	AACAGAAAATTCAAGGTAAT
125826	123913	AAACAGAAAATTCAAGGTAA
125827	123914	TAAACAGAAAATTCAAGGTA
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125829	123916	AATAAACAGAAAATTCAAGG
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27542	25629	GGAGACTTCCGGCCGGGTGC
27543	25630	TGGAGACTTCCGGCCGGGTG
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27545	25632	TATGGAGACTTCCGGCCGGG
27546	25633	GTATGGAGACTTCCGGCCGG
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27548	25635	AAGTATGGAGACTTCCGGCC
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27561	25648	AGATTGGGTTAAAAAGTATG
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27576	25663	TTTCCTTACCATTTTAGATT
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27579	25666	ATATTTCCTTACCATTTTAG
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27588	25675	CATTCTTATATATTTCCTTA
27589	25676	ACATTCTTATATATTTCCTT
27590	25677	GACATTCTTATATATTTCCT
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27594	25681	AATAGACATTCTTATATATT
27595	25682	AAATAGACATTCTTATATAT
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27607	25694	AAATTTAATAATAAATAGAC
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76689	74776	AAACACACCGGCATTTCCCA
76690	74777	AAAACACACCGGCATTTCCC
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76692	74779	GCAAAACACACCGGCATTTC
76693	74780	AGCAAAACACACCGGCATTT
76694	74781	AAGCAAAACACACCGGCATT
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76696	74783	TAAAGCAAAACACACCGGCA
76697	74784	TTAAAGCAAAACACACCGGC
76698	74785	GTTAAAGCAAAACACACCGG
76699	74786	TGTTAAAGCAAAACACACCG
76700	74787	GTGTTAAAGCAAAACACACC
76701	74788	GGTGTTAAAGCAAAACACAC
76702	74789	GGGTGTTAAAGCAAAACACA
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76704	74791	CTGGGTGTTAAAGCAAAACA
76705	74792	GCTGGGTGTTAAAGCAAAAC
76706	74793	GGCTGGGTGTTAAAGCAAAA
76707	74794	TGGCTGGGTGTTAAAGCAAA
76708	74795	TTGGCTGGGTGTTAAAGCAA
76709	74796	TTTGGCTGGGTGTTAAAGCA
76710	74797	ATTTGGCTGGGTGTTAAAGC
76711	74798	TATTTGGCTGGGTGTTAAAG
76712	74799	TTATTTGGCTGGGTGTTAAA
76713	74800	CTTATTTGGCTGGGTGTTAA
76714	74801	CCTTATTTGGCTGGGTGTTA
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76716	74803	TACCTTATTTGGCTGGGTGT
76717	74804	CTACCTTATTTGGCTGGGTG
76718	74805	GCTACCTTATTTGGCTGGGT
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76734	74821	ACACCACTTTCCTTAGGCTA
76735	74822	GACACCACTTTCCTTAGGCT
76736	74823	AGACACCACTTTCCTTAGGC
76737	74824	AAGACACCACTTTCCTTAGG
76738	74825	TAAGACACCACTTTCCTTAG
76739	74826	TTAAGACACCACTTTCCTTA
76740	74827	ATTAAGACACCACTTTCCTT
76741	74828	AATTAAGACACCACTTTCCT
76742	74829	CAATTAAGACACCACTTTCC
76743	74830	ACAATTAAGACACCACTTTC
76744	74831	AACAATTAAGACACCACTTT
76745	74832	CAACAATTAAGACACCACTT
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76747	74834	GTCAACAATTAAGACACCAC
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76751	74838	TGAAGTCAACAATTAAGACA
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76755	74842	TAGGTGAAGTCAACAATTAA
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125839	123926	CATATGGAAAAATAAACAGA
125840	123927	TCATATGGAAAAATAAACAG
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125843	123930	AGTTCATATGGAAAAATAAA
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125846	123933	TAGAGTTCATATGGAAAAAT
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126012	124099	CTCAACTCAACTACAACTTC
126013	124100	TCTCAACTCAACTACAACTT
126014	124101	ATCTCAACTCAACTACAACT
126015	124102	AATCTCAACTCAACTACAAC
126016	124103	CAATCTCAACTCAACTACAA
126017	124104	GCAATCTCAACTCAACTACA
126018	124105	CGCAATCTCAACTCAACTAC
126019	124106	GCGCAATCTCAACTCAACTA
126020	124107	TGCGCAATCTCAACTCAACT
126021	124108	GTGCGCAATCTCAACTCAAC
126022	124109	GGTGCGCAATCTCAACTCAA
126023	124110	AGGTGCGCAATCTCAACTCA
126024	124111	CAGGTGCGCAATCTCAACTC
126025	124112	ACAGGTGCGCAATCTCAACT
126026	124113	TACAGGTGCGCAATCTCAAC
126027	124114	GTACAGGTGCGCAATCTCAA
126028	124115	AGTACAGGTGCGCAATCTCA
126029	124116	GAGTACAGGTGCGCAATCTC
126030	124117	GGAGTACAGGTGCGCAATCT
126031	124118	TGGAGTACAGGTGCGCAATC
126032	124119	CTGGAGTACAGGTGCGCAAT
126033	124120	GCTGGAGTACAGGTGCGCAA
126034	124121	GGCTGGAGTACAGGTGCGCA
126035	124122	AGGCTGGAGTACAGGTGCGC
126036	124123	CAGGCTGGAGTACAGGTGCG
126037	124124	CCAGGCTGGAGTACAGGTGC
126038	124125	CCCAGGCTGGAGTACAGGTG
126039	124126	ACCCAGGCTGGAGTACAGGT
126040	124127	CACCCAGGCTGGAGTACAGG
126041	124128	TCACCCAGGCTGGAGTACAG
126042	124129	GTCACCCAGGCTGGAGTACA
126043	124130	TGTCACCCAGGCTGGAGTAC
126044	124131	CTGTCACCCAGGCTGGAGTA
126045	124132	TCTGTCACCCAGGCTGGAGT
126046	124133	CTCTGTCACCCAGGCTGGAG
126047	124134	GCTCTGTCACCCAGGCTGGA
126048	124135	TGCTCTGTCACCCAGGCTGG

27755	25842	ACCTAAATAAAATGTTCATC
27756	25843	TACCTAAATAAAATGTTCAT
27757	25844	TTACCTAAATAAAATGTTCA
27758	25845	ATTACCTAAATAAAATGTTC
27759	25846	TATTACCTAAATAAAATGTT
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27761	25848	TTTATTACCTAAATAAAATG
27762	25849	ATTTATTACCTAAATAAAAT
27763	25850	CATTTATTACCTAAATAAAA
27764	25851	ACATTTATTACCTAAATAAA
27765	25852	AACATTTATTACCTAAATAA
27766	25853	TAACATTTATTACCTAAATA
27767	25854	ATAACATTTATTACCTAAAT
27768	25855	CATAACATTTATTACCTAAA
27769	25856	ACATAACATTTATTACCTAA
27770	25857	GACATAACATTTATTACCTA
27771	25858	TGACATAACATTTATTACCT
27772	25859	ATGACATAACATTTATTACC
27773	25860	TATGACATAACATTTATTAC
27774	25861	TTATGACATAACATTTATTA
27775	25862	TTTATGACATAACATTTATT
27776	25863	TTTTATGACATAACATTTAT
27777	25864	ATTTTATGACATAACATTTA
27778	25865	TATTTTATGACATAACATTT
27779	25866	GTATTTTATGACATAACATT
27780	25867	GGTATTTTATGACATAACAT
27781	25868	TGGTATTTTATGACATAACA
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27787	25874	AATAAATGGTATTTTATGAC
27788	25875	CAATAAATGGTATTTTATGA
27789	25876	ACAATAAATGGTATTTTATG
27790	25877	CACAATAAATGGTATTTTAT
27791	25878	ACACAATAAATGGTATTTTA
27792	25879	CACACAATAAATGGTATTTT
27793	25880	GCACACAATAAATGGTATTT
27794	25881	GGCACACAATAAATGGTATT
27795	25882	AGGCACACAATAAATGGTAT
27796	25883	TAGGCACACAATAAATGGTA
27797	25884	ATAGGCACACAATAAATGGT
27798	25885	AATAGGCACACAATAAATGG
27799	25886	TAATAGGCACACAATAAATG
27800	25887	CTAATAGGCACACAATAAAT
27801	25888	CCTAATAGGCACACAATAAA
27802	25889	ACCTAATAGGCACACAATAA
27803	25890	AACCTAATAGGCACACAATA
27804	25891	AAACCTAATAGGCACACAAT
27805	25892	GAAACCTAATAGGCACACAA
27806	25893	TGAAACCTAATAGGCACACA
27807	25894	CTGAAACCTAATAGGCACAC
27808	25895	CCTGAAACCTAATAGGCACA
27809	25896	TCCTGAAACCTAATAGGCAC
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27811	25898	TCTCCTGAAACCTAATAGGC
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27813	25900	GCTCTCCTGAAACCTAATAG
27814	25901	AGCTCTCCTGAAACCTAATA
27815	25902	CAGCTCTCCTGAAACCTAAT
27816	25903	ACAGCTCTCCTGAAACCTAA
27817	25904	CACAGCTCTCCTGAAACCTA
27818	25905	GCACAGCTCTCCTGAAACCT
27819	25906	GGCACAGCTCTCCTGAAACC
27820	25907	TGGCACAGCTCTCCTGAAAC
27821	25908	TTGGCACAGCTCTCCTGAAA
27822	25909	CTTGGCACAGCTCTCCTGAA
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76902	74989	AATAAAAGAATTTTGTGGAG
76903	74990	AAATAAAAGAATTTTGTGGA
76904	74991	GAAATAAAAGAATTTTGTGG
76905	74992	AGAAATAAAAGAATTTTGTG
76906	74993	TAGAAATAAAAGAATTTTGT
76907	74994	TTAGAAATAAAAGAATTTTG
76908	74995	TTTAGAAATAAAAGAATTTT
76909	74996	TTTTAGAAATAAAAGAATTT
76910	74997	GTTTTAGAAATAAAAGAATT
76911	74998	CGTTTTAGAAATAAAAGAAT
76912	74999	GCGTTTTAGAAATAAAAGAA
76913	75000	GGCGTTTTAGAAATAAAAGA
76914	75001	AGGCGTTTTAGAAATAAAAG
76915	75002	GAGGCGTTTTAGAAATAAAA
76916	75003	AGAGGCGTTTTAGAAATAAA
76917	75004	AAGAGGCGTTTTAGAAATAA
76918	75005	CAAGAGGCGTTTTAGAAATA
76919	75006	ACAAGAGGCGTTTTAGAAAT
76920	75007	GACAAGAGGCGTTTTAGAAA
76921	75008	TGACAAGAGGCGTTTTAGAA
76922	75009	GTGACAAGAGGCGTTTTAGA
76923	75010	TGTGACAAGAGGCGTTTTAG
76924	75011	ATGTGACAAGAGGCGTTTTA
76925	75012	TATGTGACAAGAGGCGTTTT
76926	75013	GTATGTGACAAGAGGCGTTT
76927	75014	AGTATGTGACAAGAGGCGTT
76928	75015	TAGTATGTGACAAGAGGCGT
76929	75016	CTAGTATGTGACAAGAGGCG
76930	75017	ACTAGTATGTGACAAGAGGC
76931	75018	AACTAGTATGTGACAAGAGG
76932	75019	AAACTAGTATGTGACAAGAG
76933	75020	AAAACTAGTATGTGACAAGA
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76944	75031	AAGAGAGAAACAAAACTAGT
76945	75032	AAAGAGAGAAACAAAACTAG
76946	75033	TAAAGAGAGAAACAAAACTA
76947	75034	TTAAAGAGAGAAACAAAACT
76948	75035	ATTAAAGAGAGAAACAAAAC
76949	75036	CATTAAAGAGAGAAACAAAA
76950	75037	GCATTAAAGAGAGAAACAAA
76951	75038	TGCATTAAAGAGAGAAACAA
76952	75039	ATGCATTAAAGAGAGAAACA
76953	75040	AATGCATTAAAGAGAGAAAC
76954	75041	TAATGCATTAAAGAGAGAAA
76955	75042	ATAATGCATTAAAGAGAGAA
76956	75043	GATAATGCATTAAAGAGAGA
76957	75044	AGATAATGCATTAAAGAGAG
76958	75045	CAGATAATGCATTAAAGAGA
76959	75046	ACAGATAATGCATTAAAGAG
76960	75047	TACAGATAATGCATTAAAGA
76961	75048	GTACAGATAATGCATTAAAG
76962	75049	AGTACAGATAATGCATTAAA
76963	75050	AAGTACAGATAATGCATTAA
76964	75051	CAAGTACAGATAATGCATTA
76965	75052	TCAAGTACAGATAATGCATT
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76967	75054	CTTCAAGTACAGATAATGCA
76968	75055	ACTTCAAGTACAGATAATGC
76969	75056	CACTTCAAGTACAGATAATG
76970	75057	GCACTTCAAGTACAGATAAT
76971	75058	AGCACTTCAAGTACAGATAA
76972	75059	AAGCACTTCAAGTACAGATA

126049	124136	TTGCTCTGTCACCCAGGCTG
126050	124137	CTTGCTCTGTCACCCAGGCT
126051	124138	TCTTGCTCTGTCACCCAGGC
126052	124139	ATCTTGCTCTGTCACCCAGG
126053	124140	AATCTTGCTCTGTCACCCAG
126054	124141	GAATCTTGCTCTGTCACCCA
126055	124142	GGAATCTTGCTCTGTCACCC
126056	124143	GGGAATCTTGCTCTGTCACC
126057	124144	AGGGAATCTTGCTCTGTCAC
126058	124145	GAGGGAATCTTGCTCTGTCA
126059	124146	AGAGGGAATCTTGCTCTGTC
126060	124147	AAGAGGGAATCTTGCTCTGT
126061	124148	TAAGAGGGAATCTTGCTCTG
126062	124149	TTAAGAGGGAATCTTGCTCT
126063	124150	TTTAAGAGGGAATCTTGCTC
126064	124151	TTTTAAGAGGGAATCTTGCT
126065	124152	TTTTTAAGAGGGAATCTTGC
126066	124153	TTTTTTAAGAGGGAATCTTG
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126071	124158	TTTTTTTTTTTAAGAGGGAA
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126074	124161	TTTTTTTTTTTTTTAAGAGG
126075	124162	TTTTTTTTTTTTTTTAAGAG
126076	124163	TTTTTTTTTTTTTTTTAAGA
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126080	124167	TTTTTTTTTTTTTTTTTTTT
126081	124168	CTTTTTTTTTTTTTTTTTTT
126082	124169	TCTTTTTTTTTTTTTTTTTT
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126085	124172	GTTTCTTTTTTTTTTTTTTT
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126088	124175	TCTGTTTCTTTTTTTTTTTT
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126091	124178	TTTTCTGTTTCTTTTTTTTT
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126094	124181	ATCTTTTCTGTTTCTTTTTT
126095	124182	TATCTTTTCTGTTTCTTTTT
126096	124183	TTATCTTTTCTGTTTCTTTT
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126098	124185	ATTTATCTTTTCTGTTTCTT
126099	124186	GATTTATCTTTTCTGTTTCT
126100	124187	AGATTTATCTTTTCTGTTTC
126101	124188	AAGATTTATCTTTTCTGTTT
126102	124189	AAAGATTTATCTTTTCTGTT
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126105	124192	TAAAAAGATTTATCTTTTCT
126106	124193	GTAAAAAGATTTATCTTTTC
126107	124194	TGTAAAAAGATTTATCTTTT
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126109	124196	ATTGTAAAAAGATTTATCTT
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126113	124200	AATTATTGTAAAAAGATTTA
126114	124201	AAATTATTGTAAAAAGATTT
126115	124202	CAAATTATTGTAAAAAGATT
126116	124203	ACAAATTATTGTAAAAAGAT
126117	124204	AACAAATTATTGTAAAAAGA
126118	124205	GAACAAATTATTGTAAAAAG
126119	124206	GGAACAAATTATTGTAAAAA

27826	25913	TGCTCTTGGCACAGCTCTCC
27827	25914	ATGCTCTTGGCACAGCTCTC
27828	25915	AATGCTCTTGGCACAGCTCT
27829	25916	TAATGCTCTTGGCACAGCTC
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27831	25918	AGTAATGCTCTTGGCACAGC
27832	25919	AAGTAATGCTCTTGGCACAG
27833	25920	CAAGTAATGCTCTTGGCACA
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27835	25922	TACAAGTAATGCTCTTGGCA
27836	25923	ATACAAGTAATGCTCTTGGC
27837	25924	TATACAAGTAATGCTCTTGG
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27841	25928	AAGATATACAAGTAATGCTC
27842	25929	AAAGATATACAAGTAATGCT
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27846	25933	CTTAAAAGATATACAAGTAA
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27848	25935	GGCTTAAAAGATATACAAGT
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27850	25937	AAGGCTTAAAAGATATACAA
27851	25938	TAAGGCTTAAAAGATATACA
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27868	25955	GACAGGCTGGGCTGTTGTAA
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27873	25960	AGCCTGACAGGCTGGGCTGT
27874	25961	CAGCCTGACAGGCTGGGCTG
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27876	25963	ACCAGCCTGACAGGCTGGGC
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27878	25965	CTACCAGCCTGACAGGCTGG
27879	25966	ACTACCAGCCTGACAGGCTG
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27881	25968	GCACTACCAGCCTGACAGGC
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27884	25971	ATGGCACTACCAGCCTGACA
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27893	25980	AAAACAGATATGGCACTACC
27894	25981	TAAAACAGATATGGCACTAC
27895	25982	GTAAAACAGATATGGCACTA
27896	25983	TGTAAAACAGATATGGCACT

76973	75060	TAAGCACTTCAAGTACAGAT
76974	75061	CTAAGCACTTCAAGTACAGA
76975	75062	GCTAAGCACTTCAAGTACAG
76976	75063	AGCTAAGCACTTCAAGTACA
76977	75064	CAGCTAAGCACTTCAAGTAC
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76982	75069	ATACCCAGCTAAGCACTTCA
76983	75070	CATACCCAGCTAAGCACTTC
76984	75071	GCATACCCAGCTAAGCACTT
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76986	75073	CAGCATACCCAGCTAAGCAC
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76989	75076	TGCCAGCATACCCAGCTAAG
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76995	75082	GGCATGTGCCAGCATACCCA
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76999	75086	TGCAGGCATGTGCCAGCATA
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77008	75095	AGCTGGGACTGCAGGCATGT
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77016	75103	TCCCAAGTAGCTGGGACTGC
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77019	75106	GCCTCCCAAGTAGCTGGGAC
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77024	75111	CTTCAGCCTCCCAAGTAGCT
77025	75112	GCTTCAGCCTCCCAAGTAGC
77026	75113	TGCTTCAGCCTCCCAAGTAG
77027	75114	CTGCTTCAGCCTCCCAAGTA
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77031	75118	CCTCCTGCTTCAGCCTCCCA
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77039	75126	CAAGTGATCCTCCTGCTTCA
77040	75127	TCAAGTGATCCTCCTGCTTC
77041	75128	CTCAAGTGATCCTCCTGCTT
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126120	124207	TGGAACAAATTATTGTAAAA
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126123	124210	AATTGGAACAAATTATTGTA
126124	124211	TAATTGGAACAAATTATTGT
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126128	124215	ACCCTAATTGGAACAAATTA
126129	124216	GACCCTAATTGGAACAAATT
126130	124217	GGACCCTAATTGGAACAAAT
126131	124218	TGGACCCTAATTGGAACAAA
126132	124219	TTGGACCCTAATTGGAACAA
126133	124220	CTTGGACCCTAATTGGAACA
126134	124221	ACTTGGACCCTAATTGGAAC
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126137	124224	CTGACTTGGACCCTAATTGG
126138	124225	CCTGACTTGGACCCTAATTG
126139	124226	GCCTGACTTGGACCCTAATT
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126141	124228	AAGCCTGACTTGGACCCTAA
126142	124229	CAAGCCTGACTTGGACCCTA
126143	124230	GCAAGCCTGACTTGGACCCT
126144	124231	TGCAAGCCTGACTTGGACCC
126145	124232	TTGCAAGCCTGACTTGGACC
126146	124233	ATTGCAAGCCTGACTTGGAC
126147	124234	AATTGCAAGCCTGACTTGGA
126148	124235	AAATTGCAAGCCTGACTTGG
126149	124236	CAAATTGCAAGCCTGACTTG
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126152	124239	ATCCAAATTGCAAGCCTGAC
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126155	124242	CAAATCCAAATTGCAAGCCT
126156	124243	ACAAATCCAAATTGCAAGCC
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126159	124246	TAAACAAATCCAAATTGCAA
126160	124247	ATAAACAAATCCAAATTGCA
126161	124248	TATAAACAAATCCAAATTGC
126162	124249	ATATAAACAAATCCAAATTG
126163	124250	CATATAAACAAATCCAAATT
126164	124251	ACATATAAACAAATCCAAAT
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126166	124253	CAACATATAAACAAATCCAA
126167	124254	TCAACATATAAACAAATCCA
126168	124255	TTCAACATATAAACAAATCC
126169	124256	CTTCAACATATAAACAAATC
126170	124257	ACTTCAACATATAAACAAAT
126171	124258	GACTTCAACATATAAACAAA
126172	124259	AGACTTCAACATATAAACAA
126173	124260	AAGACTTCAACATATAAACA
126174	124261	AAAGACTTCAACATATAAAC
126175	124262	AAAAGACTTCAACATATAAA
126176	124263	AAAAAGACTTCAACATATAA
126177	124264	AAAAAAGACTTCAACATATA
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126189	124276	CAATTAAAAAAAAAAAAAGA
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27897	25984	CTGTAAAACAGATATGGCAC
27898	25985	TCTGTAAAACAGATATGGCA
27899	25986	ATCTGTAAAACAGATATGGC
27900	25987	CATCTGTAAAACAGATATGG
27901	25988	TCATCTGTAAAACAGATATG
27902	25989	CTCATCTGTAAAACAGATAT
27903	25990	CCTCATCTGTAAAACAGATA
27904	25991	TCCTCATCTGTAAAACAGAT
27905	25992	TTCCTCATCTGTAAAACAGA
27906	25993	CTTCCTCATCTGTAAAACAG
27907	25994	ACTTCCTCATCTGTAAAACA
27908	25995	CACTTCCTCATCTGTAAAAC
27909	25996	TCACTTCCTCATCTGTAAAA
27910	25997	ATCACTTCCTCATCTGTAAA
27911	25998	CATCACTTCCTCATCTGTAA
27912	25999	CCATCACTTCCTCATCTGTA
27913	26000	TCCATCACTTCCTCATCTGT
27914	26001	ATCCATCACTTCCTCATCTG
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27917	26004	CCAATCCATCACTTCCTCAT
27918	26005	TCCAATCCATCACTTCCTCA
27919	26006	CTCCAATCCATCACTTCCTC
27920	26007	TCTCCAATCCATCACTTCCT
27921	26008	TTCTCCAATCCATCACTTCC
27922	26009	TTTCTCCAATCCATCACTTC
27923	26010	ATTTCTCCAATCCATCACTT
27924	26011	AATTTCTCCAATCCATCACT
27925	26012	TAATTTCTCCAATCCATCAC
27926	26013	TTAATTTCTCCAATCCATCA
27927	26014	CTTAATTTCTCCAATCCATC
27928	26015	CCTTAATTTCTCCAATCCAT
27929	26016	TCCTTAATTTCTCCAATCCA
27930	26017	TTCCTTAATTTCTCCAATCC
27931	26018	TTTCCTTAATTTCTCCAATC
27932	26019	ATTTCCTTAATTTCTCCAAT
27933	26020	AATTTCCTTAATTTCTCCAA
27934	26021	CAATTTCCTTAATTTCTCCA
27935	26022	GCAATTTCCTTAATTTCTCC
27936	26023	GGCAATTTCCTTAATTTCTC
27937	26024	AGGCAATTTCCTTAATTTCT
27938	26025	AAGGCAATTTCCTTAATTTC
27939	26026	AAAGGCAATTTCCTTAATTT
27940	26027	TAAAGGCAATTTCCTTAATT
27941	26028	CTAAAGGCAATTTCCTTAAT
27942	26029	CCTAAAGGCAATTTCCTTAA
27943	26030	ACCTAAAGGCAATTTCCTTA
27944	26031	GACCTAAAGGCAATTTCCTT
27945	26032	TGACCTAAAGGCAATTTCCT
27946	26033	TTGACCTAAAGGCAATTTCC
27947	26034	TTTGACCTAAAGGCAATTTC
27948	26035	CTTTGACCTAAAGGCAATTT
27949	26036	TCTTTGACCTAAAGGCAATT
27950	26037	CTCTTTGACCTAAAGGCAAT
27951	26038	TCTCTTTGACCTAAAGGCAA
27952	26039	ATCTCTTTGACCTAAAGGCA
27953	26040	TATCTCTTTGACCTAAAGGC
27954	26041	CTATCTCTTTGACCTAAAGG
27955	26042	CCTATCTCTTTGACCTAAAG
27956	26043	TCCTATCTCTTTGACCTAAA
27957	26044	TTCCTATCTCTTTGACCTAA
27958	26045	CTTCCTATCTCTTTGACCTA
27959	26046	ACTTCCTATCTCTTTGACCT
27960	26047	CACTTCCTATCTCTTTGACC
27961	26048	TCACTTCCTATCTCTTTGAC
27962	26049	GTCACTTCCTATCTCTTTGA
27963	26050	TGTCACTTCCTATCTCTTTG
27964	26051	TTGTCACTTCCTATCTCTTT
27965	26052	TTTGTCACTTCCTATCTCTT
27966	26053	CTTTGTCACTTCCTATCTCT
27967	26054	GCTTTGTCACTTCCTATCTC

77044	75131	GGGCTCAAGTGATCCTCCTG
77045	75132	TGGGCTCAAGTGATCCTCCT
77046	75133	CTGGGCTCAAGTGATCCTCC
77047	75134	CCTGGGCTCAAGTGATCCTC
77048	75135	TCCTGGGCTCAAGTGATCCT
77049	75136	CTCCTGGGCTCAAGTGATCC
77050	75137	ACTCCTGGGCTCAAGTGATC
77051	75138	AACTCCTGGGCTCAAGTGAT
77052	75139	CAACTCCTGGGCTCAAGTGA
77053	75140	CCAACTCCTGGGCTCAAGTG
77054	75141	TCCAACTCCTGGGCTCAAGT
77055	75142	CTCCAACTCCTGGGCTCAAG
77056	75143	ACTCCAACTCCTGGGCTCAA
77057	75144	GACTCCAACTCCTGGGCTCA
77058	75145	GGACTCCAACTCCTGGGCTC
77059	75146	TGGACTCCAACTCCTGGGCT
77060	75147	CTGGACTCCAACTCCTGGGC
77061	75148	GCTGGACTCCAACTCCTGGG
77062	75149	GGCTGGACTCCAACTCCTGG
77063	75150	AGGCTGGACTCCAACTCCTG
77064	75151	CAGGCTGGACTCCAACTCCT
77065	75152	TCAGGCTGGACTCCAACTCC
77066	75153	TTCAGGCTGGACTCCAACTC
77067	75154	ATTCAGGCTGGACTCCAACT
77068	75155	CATTCAGGCTGGACTCCAAC
77069	75156	TCATTCAGGCTGGACTCCAA
77070	75157	GTCATTCAGGCTGGACTCCA
77071	75158	TGTCATTCAGGCTGGACTCC
77072	75159	ATGTCATTCAGGCTGGACTC
77073	75160	TATGTCATTCAGGCTGGACT
77074	75161	TTATGTCATTCAGGCTGGAC
77075	75162	CTTATGTCATTCAGGCTGGA
77076	75163	CCTTATGTCATTCAGGCTGG
77077	75164	TCCTTATGTCATTCAGGCTG
77078	75165	CTCCTTATGTCATTCAGGCT
77079	75166	TCTCCTTATGTCATTCAGGC
77080	75167	GTCTCCTTATGTCATTCAGG
77081	75168	GGTCTCCTTATGTCATTCAG
77082	75169	GGGTCTCCTTATGTCATTCA
77083	75170	GGGGTCTCCTTATGTCATTC
77084	75171	AGGGGTCTCCTTATGTCATT
77085	75172	AAGGGGTCTCCTTATGTCAT
77086	75173	GAAGGGGTCTCCTTATGTCA
77087	75174	AGAAGGGGTCTCCTTATGTC
77088	75175	GAGAAGGGGTCTCCTTATGT
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77090	75177	TAGAGAAGGGGTCTCCTTAT
77091	75178	TTAGAGAAGGGGTCTCCTTA
77092	75179	CTTAGAGAAGGGGTCTCCTT
77093	75180	TCTTAGAGAAGGGGTCTCCT
77094	75181	TTCTTAGAGAAGGGGTCTCC
77095	75182	TTTCTTAGAGAAGGGGTCTC
77096	75183	ATTTCTTAGAGAAGGGGTCT
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77098	75185	TTATTTCTTAGAGAAGGGGT
77099	75186	TTTATTTCTTAGAGAAGGGG
77100	75187	TTTTATTTCTTAGAGAAGGG
77101	75188	TTTTTATTTCTTAGAGAAGG
77102	75189	ATTTTTATTTCTTAGAGAAG
77103	75190	TATTTTTATTTCTTAGAGAA
77104	75191	TTATTTTTATTTCTTAGAGA
77105	75192	TTTATTTTTATTTCTTAGAG
77106	75193	TTTTATTTTTATTTCTTAGA
77107	75194	TTTTTATTTTTATTTCTTAG
77108	75195	GTTTTTATTTTTATTTCTTA
77109	75196	TGTTTTTATTTTTATTTCTT
77110	75197	TTGTTTTTATTTTTATTTCT
77111	75198	TTTGTTTTTATTTTTATTTC
77112	75199	ATTTGTTTTTATTTTTATTT
77113	75200	TATTTGTTTTTATTTTTATT
77114	75201	GTATTTGTTTTTATTTTTAT

126191	124278	AACAATTAAAAAAAAAAAAA
126192	124279	AAACAATTAAAAAAAAAAAA
126193	124280	GAAACAATTAAAAAAAAAAA
126194	124281	TGAAACAATTAAAAAAAAAA
126195	124282	ATGAAACAATTAAAAAAAAA
126196	124283	TATGAAACAATTAAAAAAAA
126197	124284	ATATGAAACAATTAAAAAAA
126198	124285	AATATGAAACAATTAAAAAA
126199	124286	CAATATGAAACAATTAAAAA
126200	124287	ACAATATGAAACAATTAAAA
126201	124288	CACAATATGAAACAATTAAA
126202	124289	CCACAATATGAAACAATTAA
126203	124290	ACCACAATATGAAACAATTA
126204	124291	TACCACAATATGAAACAATT
126205	124292	TTACCACAATATGAAACAAT
126206	124293	GTTACCACAATATGAAACAA
126207	124294	AGTTACCACAATATGAAACA
126208	124295	AAGTTACCACAATATGAAAC
126209	124296	AAAGTTACCACAATATGAAA
126210	124297	AAAAGTTACCACAATATGAA
126211	124298	AAAAAGTTACCACAATATGA
126212	124299	AAAAAAGTTACCACAATATG
126213	124300	AAAAAAAGTTACCACAATAT
126214	124301	AAAAAAAAGTTACCACAATA
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126220	124307	AAAAAAAAAAAAAAGTTACC
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126222	124309	AAAAAAAAAAAAAAAAGTTA
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126224	124311	CAAAAAAAAAAAAAAAAAGT
126225	124312	TCAAAAAAAAAAAAAAAAAG
126226	124313	CTCAAAAAAAAAAAAAAAAA
126227	124314	TCTCAAAAAAAAAAAAAAAA
126228	124315	ATCTCAAAAAAAAAAAAAAA
126229	124316	CATCTCAAAAAAAAAAAAAA
126230	124317	CCATCTCAAAAAAAAAAAAA
126231	124318	TCCATCTCAAAAAAAAAAAA
126232	124319	TTCCATCTCAAAAAAAAAAA
126233	124320	ATTCCATCTCAAAAAAAAAA
126234	124321	GATTCCATCTCAAAAAAAAA
126235	124322	AGATTCCATCTCAAAAAAAA
126236	124323	AAGATTCCATCTCAAAAAAA
126237	124324	CAAGATTCCATCTCAAAAAA
126238	124325	CCAAGATTCCATCTCAAAAA
126239	124326	GCCAAGATTCCATCTCAAAA
126240	124327	AGCCAAGATTCCATCTCAAA
126241	124328	GAGCCAAGATTCCATCTCAA
126242	124329	AGAGCCAAGATTCCATCTCA
126243	124330	CAGAGCCAAGATTCCATCTC
126244	124331	ACAGAGCCAAGATTCCATCT
126245	124332	GACAGAGCCAAGATTCCATC
126246	124333	TGACAGAGCCAAGATTCCAT
126247	124334	GTGACAGAGCCAAGATTCCA
126248	124335	GGTGACAGAGCCAAGATTCC
126249	124336	AGGTGACAGAGCCAAGATTC
126250	124337	TAGGTGACAGAGCCAAGATT
126251	124338	CTAGGTGACAGAGCCAAGAT
126252	124339	CCTAGGTGACAGAGCCAAGA
126253	124340	GCCTAGGTGACAGAGCCAAG
126254	124341	AGCCTAGGTGACAGAGCCAA
126255	124342	CAGCCTAGGTGACAGAGCCA
126256	124343	CCAGCCTAGGTGACAGAGCC
126257	124344	TCCAGCCTAGGTGACAGAGC
126258	124345	CTCCAGCCTAGGTGACAGAG
126259	124346	ACTCCAGCCTAGGTGACAGA
126260	124347	TACTCCAGCCTAGGTGACAG
126261	124348	GTACTCCAGCCTAGGTGACA

27968	26055	AGCTTTGTCACTTCCTATCT
27969	26056	CAGCTTTGTCACTTCCTATC
27970	26057	TCAGCTTTGTCACTTCCTAT
27971	26058	CTCAGCTTTGTCACTTCCTA
27972	26059	TCTCAGCTTTGTCACTTCCT
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27979	26066	TTAAAAATCTCAGCTTTGTC
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27981	26068	GGTTAAAAATCTCAGCTTTG
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27994	26081	TGAAATCTCACAAGGTTAAA
27995	26082	TTGAAATCTCACAAGGTTAA
27996	26083	TTTGAAATCTCACAAGGTTA
27997	26084	CTTTGAAATCTCACAAGGTT
27998	26085	ACTTTGAAATCTCACAAGGT
27999	26086	GACTTTGAAATCTCACAAGG
28000	26087	AGACTTTGAAATCTCACAAG
28001	26088	AAGACTTTGAAATCTCACAA
28002	26089	AAAGACTTTGAAATCTCACA
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28004	26091	GCAAAGACTTTGAAATCTCA
28005	26092	AGCAAAGACTTTGAAATCTC
28006	26093	AAGCAAAGACTTTGAAATCT
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28015	26102	GTTATTAAAAAGCAAAGACT
28016	26103	AGTTATTAAAAAGCAAAGAC
28017	26104	CAGTTATTAAAAAGCAAAGA
28018	26105	ACAGTTATTAAAAAGCAAAG
28019	26106	AACAGTTATTAAAAAGCAAA
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28021	26108	GGAACAGTTATTAAAAAGCA
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28028	26115	AAGCAATGGAACAGTTATTA
28029	26116	GAAGCAATGGAACAGTTATT
28030	26117	AGAAGCAATGGAACAGTTAT
28031	26118	TAGAAGCAATGGAACAGTTA
28032	26119	TTAGAAGCAATGGAACAGTT
28033	26120	ATTAGAAGCAATGGAACAGT
28034	26121	TATTAGAAGCAATGGAACAG
28035	26122	ATATTAGAAGCAATGGAACA
28036	26123	TATATTAGAAGCAATGGAAC
28037	26124	CTATATTAGAAGCAATGGAA
28038	26125	TCTATATTAGAAGCAATGGA

77115	75202	AGTATTTGTTTTTATTTTTA
77116	75203	AAGTATTTGTTTTTATTTTT
77117	75204	TAAGTATTTGTTTTTATTTT
77118	75205	TTAAGTATTTGTTTTTATTT
77119	75206	ATTAAGTATTTGTTTTTATT
77120	75207	TATTAAGTATTTGTTTTTAT
77121	75208	TTATTAAGTATTTGTTTTTA
77122	75209	TTTATTAAGTATTTGTTTTT
77123	75210	CTTTATTAAGTATTTGTTTT
77124	75211	TCTTTATTAAGTATTTGTTT
77125	75212	GTCTTTATTAAGTATTTGTT
77126	75213	AGTCTTTATTAAGTATTTGT
77127	75214	GAGTCTTTATTAAGTATTTG
77128	75215	AGAGTCTTTATTAAGTATTT
77129	75216	CAGAGTCTTTATTAAGTATT
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77131	75218	GACAGAGTCTTTATTAAGTA
77132	75219	AGACAGAGTCTTTATTAAGT
77133	75220	AAGACAGAGTCTTTATTAAG
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77136	75223	CTAAAGACAGAGTCTTTATT
77137	75224	CCTAAAGACAGAGTCTTTAT
77138	75225	TCCTAAAGACAGAGTCTTTA
77139	75226	ATCCTAAAGACAGAGTCTTT
77140	75227	TATCCTAAAGACAGAGTCTT
77141	75228	CTATCCTAAAGACAGAGTCT
77142	75229	TCTATCCTAAAGACAGAGTC
77143	75230	CTCTATCCTAAAGACAGAGT
77144	75231	TCTCTATCCTAAAGACAGAG
77145	75232	CTCTCTATCCTAAAGACAGA
77146	75233	GCTCTCTATCCTAAAGACAG
77147	75234	TGCTCTCTATCCTAAAGACA
77148	75235	ATGCTCTCTATCCTAAAGAC
77149	75236	TATGCTCTCTATCCTAAAGA
77150	75237	CTATGCTCTCTATCCTAAAG
77151	75238	TCTATGCTCTCTATCCTAAA
77152	75239	CTCTATGCTCTCTATCCTAA
77153	75240	TCTCTATGCTCTCTATCCTA
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77155	75242	TATCTCTATGCTCTCTATCC
77156	75243	ATATCTCTATGCTCTCTATC
77157	75244	TATATCTCTATGCTCTCTAT
77158	75245	TTATATCTCTATGCTCTCTA
77159	75246	TTTATATCTCTATGCTCTCT
77160	75247	CTTTATATCTCTATGCTCTC
77161	75248	GCTTTATATCTCTATGCTCT
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77168	75255	ACACTTTGCTTTATATCTCT
77169	75256	GACACTTTGCTTTATATCTC
77170	75257	AGACACTTTGCTTTATATCT
77171	75258	AAGACACTTTGCTTTATATC
77172	75259	CAAGACACTTTGCTTTATAT
77173	75260	GCAAGACACTTTGCTTTATA
77174	75261	GGCAAGACACTTTGCTTTAT
77175	75262	TGGCAAGACACTTTGCTTTA
77176	75263	TTGGCAAGACACTTTGCTTT
77177	75264	TTTGGCAAGACACTTTGCTT
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77179	75266	TTTTTGGCAAGACACTTTGC
77180	75267	ATTTTTGGCAAGACACTTTG
77181	75268	CATTTTTGGCAAGACACTTT
77182	75269	TCATTTTTGGCAAGACACTT
77183	75270	CTCATTTTTGGCAAGACACT
77184	75271	ACTCATTTTTGGCAAGACAC
77185	75272	CACTCATTTTTGGCAAGACA

126262	124349	TGTACTCCAGCCTAGGTGAC
126263	124350	CTGTACTCCAGCCTAGGTGA
126264	124351	ACTGTACTCCAGCCTAGGTG
126265	124352	CACTGTACTCCAGCCTAGGT
126266	124353	CCACTGTACTCCAGCCTAGG
126267	124354	GCCACTGTACTCCAGCCTAG
126268	124355	TGCCACTGTACTCCAGCCTA
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126270	124357	TGTGCCACTGTACTCCAGCC
126271	124358	TTGTGCCACTGTACTCCAGC
126272	124359	ATTGTGCCACTGTACTCCAG
126273	124360	GATTGTGCCACTGTACTCCA
126274	124361	AGATTGTGCCACTGTACTCC
126275	124362	GAGATTGTGCCACTGTACTC
126276	124363	TGAGATTGTGCCACTGTACT
126277	124364	TTGAGATTGTGCCACTGTAC
126278	124365	GTTGAGATTGTGCCACTGTA
126279	124366	AGTTGAGATTGTGCCACTGT
126280	124367	GAGTTGAGATTGTGCCACTG
126281	124368	TGAGTTGAGATTGTGCCACT
126282	124369	GTGAGTTGAGATTGTGCCAC
126283	124370	AGTGAGTTGAGATTGTGCCA
126284	124371	CAGTGAGTTGAGATTGTGCC
126285	124372	GCAGTGAGTTGAGATTGTGC
126286	124373	TGCAGTGAGTTGAGATTGTG
126287	124374	TTGCAGTGAGTTGAGATTGT
126288	124375	GTTGCAGTGAGTTGAGATTG
126289	124376	GGTTGCAGTGAGTTGAGATT
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126291	124378	GAGGTTGCAGTGAGTTGAGA
126292	124379	GGAGGTTGCAGTGAGTTGAG
126293	124380	GGGAGGTTGCAGTGAGTTGA
126294	124381	GGGGAGGTTGCAGTGAGTTG
126295	124382	GGGGGAGGTTGCAGTGAGTT
126296	124383	AGGGGGAGGTTGCAGTGAGT
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126298	124385	AGAGGGGGAGGTTGCAGTGA
126299	124386	CAGAGGGGGAGGTTGCAGTG
126300	124387	CCAGAGGGGGAGGTTGCAGT
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126302	124389	CCCCAGAGGGGGAGGTTGCA
126303	124390	ACCCCAGAGGGGGAGGTTGC
126304	124391	AACCCCAGAGGGGGAGGTTG
126305	124392	GAACCCCAGAGGGGGAGGTT
126306	124393	TGAACCCCAGAGGGGGAGGT
126307	124394	TTGAACCCCAGAGGGGGAGG
126308	124395	CTTGAACCCCAGAGGGGGAG
126309	124396	GCTTGAACCCCAGAGGGGGA
126310	124397	TGCTTGAACCCCAGAGGGGG
126311	124398	TTGCTTGAACCCCAGAGGGG
126312	124399	ATTGCTTGAACCCCAGAGGG
126313	124400	AATTGCTTGAACCCCAGAGG
126314	124401	GAATTGCTTGAACCCCAGAG
126315	124402	AGAATTGCTTGAACCCCAGA
126316	124403	GAGAATTGCTTGAACCCCAG
126317	124404	GGAGAATTGCTTGAACCCCA
126318	124405	AGGAGAATTGCTTGAACCCC
126319	124406	CAGGAGAATTGCTTGAACCC
126320	124407	GCAGGAGAATTGCTTGAACC
126321	124408	GGCAGGAGAATTGCTTGAAC
126322	124409	AGGCAGGAGAATTGCTTGAA
126323	124410	GAGGCAGGAGAATTGCTTGA
126324	124411	TGAGGCAGGAGAATTGCTTG
126325	124412	CTGAGGCAGGAGAATTGCTT
126326	124413	GCTGAGGCAGGAGAATTGCT
126327	124414	GGCTGAGGCAGGAGAATTGC
126328	124415	AGGCTGAGGCAGGAGAATTG
126329	124416	GAGGCTGAGGCAGGAGAATT
126330	124417	GGAGGCTGAGGCAGGAGAAT
126331	124418	GGGAGGCTGAGGCAGGAGAA
126332	124419	TGGGAGGCTGAGGCAGGAGA

28039	26126	CTCTATATTAGAAGCAATGG
28040	26127	TCTCTATATTAGAAGCAATG
28041	26128	ATCTCTATATTAGAAGCAAT
28042	26129	TATCTCTATATTAGAAGCAA
28043	26130	ATATCTCTATATTAGAAGCA
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28045	26132	TCATATCTCTATATTAGAAG
28046	26133	GTCATATCTCTATATTAGAA
28047	26134	TGTCATATCTCTATATTAGA
28048	26135	TTGTCATATCTCTATATTAG
28049	26136	TTTGTCATATCTCTATATTA
28050	26137	TTTTGTCATATCTCTATATT
28051	26138	TTTTTGTCATATCTCTATAT
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28067	26154	CACTGATTTTTACTTGTTTT
28068	26155	TCACTGATTTTTACTTGTTT
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28071	26158	TCTTCACTGATTTTTACTTG
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28075	26162	GCCTTCTTCACTGATTTTTA
28076	26163	AGCCTTCTTCACTGATTTTT
28077	26164	CAGCCTTCTTCACTGATTTT
28078	26165	CCAGCCTTCTTCACTGATTT
28079	26166	CCCAGCCTTCTTCACTGATT
28080	26167	TCCCAGCCTTCTTCACTGAT
28081	26168	CTCCCAGCCTTCTTCACTGA
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28083	26170	TGCTCCCAGCCTTCTTCACT
28084	26171	CTGCTCCCAGCCTTCTTCAC
28085	26172	ACTGCTCCCAGCCTTCTTCA
28086	26173	GACTGCTCCCAGCCTTCTTC
28087	26174	CGACTGCTCCCAGCCTTCTT
28088	26175	GCGACTGCTCCCAGCCTTCT
28089	26176	AGCGACTGCTCCCAGCCTTC
28090	26177	AAGCGACTGCTCCCAGCCTT
28091	26178	TAAGCGACTGCTCCCAGCCT
28092	26179	ATAAGCGACTGCTCCCAGCC
28093	26180	CATAAGCGACTGCTCCCAGC
28094	26181	GCATAAGCGACTGCTCCCAG
28095	26182	GGCATAAGCGACTGCTCCCA
28096	26183	AGGCATAAGCGACTGCTCCC
28097	26184	CAGGCATAAGCGACTGCTCC
28098	26185	ACAGGCATAAGCGACTGCTC
28099	26186	TACAGGCATAAGCGACTGCT
28100	26187	TTACAGGCATAAGCGACTGC
28101	26188	ATTACAGGCATAAGCGACTG
28102	26189	GATTACAGGCATAAGCGACT
28103	26190	GGATTACAGGCATAAGCGAC
28104	26191	GGGATTACAGGCATAAGCGA
28105	26192	TGGGATTACAGGCATAAGCG
28106	26193	CTGGGATTACAGGCATAAGC
28107	26194	GCTGGGATTACAGGCATAAG
28108	26195	TGCTGGGATTACAGGCATAA
28109	26196	CTGCTGGGATTACAGGCATA

77186	75273	ACACTCATTTTTGGCAAGAC
77187	75274	AACACTCATTTTTGGCAAGA
77188	75275	TAACACTCATTTTTGGCAAG
77189	75276	ATAACACTCATTTTTGGCAA
77190	75277	CATAACACTCATTTTTGGCA
77191	75278	CCATAACACTCATTTTTGGC
77192	75279	ACCATAACACTCATTTTTGG
77193	75280	TACCATAACACTCATTTTTG
77194	75281	GTACCATAACACTCATTTTT
77195	75282	GGTACCATAACACTCATTTT
77196	75283	TGGTACCATAACACTCATTT
77197	75284	TTGGTACCATAACACTCATT
77198	75285	ATTGGTACCATAACACTCAT
77199	75286	TATTGGTACCATAACACTCA
77200	75287	ATATTGGTACCATAACACTC
77201	75288	AATATTGGTACCATAACACT
77202	75289	AAATATTGGTACCATAACAC
77203	75290	CAAATATTGGTACCATAACA
77204	75291	TCAAATATTGGTACCATAAC
77205	75292	CTCAAATATTGGTACCATAA
77206	75293	ACTCAAATATTGGTACCATA
77207	75294	TACTCAAATATTGGTACCAT
77208	75295	CTACTCAAATATTGGTACCA
77209	75296	TCTACTCAAATATTGGTACC
77210	75297	TTCTACTCAAATATTGGTAC
77211	75298	ATTCTACTCAAATATTGGTA
77212	75299	CATTCTACTCAAATATTGGT
77213	75300	TCATTCTACTCAAATATTGG
77214	75301	TTCATTCTACTCAAATATTG
77215	75302	CTTCATTCTACTCAAATATT
77216	75303	TCTTCATTCTACTCAAATAT
77217	75304	TTCTTCATTCTACTCAAATA
77218	75305	ATTCTTCATTCTACTCAAAT
77219	75306	GATTCTTCATTCTACTCAAA
77220	75307	AGATTCTTCATTCTACTCAA
77221	75308	AAGATTCTTCATTCTACTCA
77222	75309	GAAGATTCTTCATTCTACTC
77223	75310	GGAAGATTCTTCATTCTACT
77224	75311	TGGAAGATTCTTCATTCTAC
77225	75312	ATGGAAGATTCTTCATTCTA
77226	75313	AATGGAAGATTCTTCATTCT
77227	75314	CAATGGAAGATTCTTCATTC
77228	75315	TCAATGGAAGATTCTTCATT
77229	75316	CTCAATGGAAGATTCTTCAT
77230	75317	ACTCAATGGAAGATTCTTCA
77231	75318	TACTCAATGGAAGATTCTTC
77232	75319	CTACTCAATGGAAGATTCTT
77233	75320	TCTACTCAATGGAAGATTCT
77234	75321	TTCTACTCAATGGAAGATTC
77235	75322	TTTCTACTCAATGGAAGATT
77236	75323	CTTTCTACTCAATGGAAGAT
77237	75324	TCTTTCTACTCAATGGAAGA
77238	75325	CTCTTTCTACTCAATGGAAG
77239	75326	TCTCTTTCTACTCAATGGAA
77240	75327	TTCTCTTTCTACTCAATGGA
77241	75328	ATTCTCTTTCTACTCAATGG
77242	75329	AATTCTCTTTCTACTCAATG
77243	75330	AAATTCTCTTTCTACTCAAT
77244	75331	CAAATTCTCTTTCTACTCAA
77245	75332	ACAAATTCTCTTTCTACTCA
77246	75333	TACAAATTCTCTTTCTACTC
77247	75334	TTACAAATTCTCTTTCTACT
77248	75335	GTTACAAATTCTCTTTCTAC
77249	75336	TGTTACAAATTCTCTTTCTA
77250	75337	ATGTTACAAATTCTCTTTCT
77251	75338	TATGTTACAAATTCTCTTTC
77252	75339	ATATGTTACAAATTCTCTTT
77253	75340	GATATGTTACAAATTCTCTT
77254	75341	AGATATGTTACAAATTCTCT
77255	75342	CAGATATGTTACAAATTCTC
77256	75343	ACAGATATGTTACAAATTCT

126333	124420	TTGGGAGGCTGAGGCAGGAG
126334	124421	CTTGGGAGGCTGAGGCAGGA
126335	124422	ACTTGGGAGGCTGAGGCAGG
126336	124423	TACTTGGGAGGCTGAGGCAG
126337	124424	CTACTTGGGAGGCTGAGGCA
126338	124425	GCTACTTGGGAGGCTGAGGC
126339	124426	GGCTACTTGGGAGGCTGAGG
126340	124427	GGGCTACTTGGGAGGCTGAG
126341	124428	TGGGCTACTTGGGAGGCTGA
126342	124429	CTGGGCTACTTGGGAGGCTG
126343	124430	GCTGGGCTACTTGGGAGGCT
126344	124431	GGCTGGGCTACTTGGGAGGC
126345	124432	AGGCTGGGCTACTTGGGAGG
126346	124433	AAGGCTGGGCTACTTGGGAG
126347	124434	AAAGGCTGGGCTACTTGGGA
126348	124435	AAAAGGCTGGGCTACTTGGG
126349	124436	AAAAAGGCTGGGCTACTTGG
126350	124437	AAAAAAGGCTGGGCTACTTG
126351	124438	AAAAAAAGGCTGGGCTACTT
126352	124439	AAAAAAAAGGCTGGGCTACT
126353	124440	AAAAAAAAAGGCTGGGCTAC
126354	124441	AAAAAAAAAAGGCTGGGCTA
126355	124442	CAAAAAAAAAAGGCTGGGCT
126356	124443	TCAAAAAAAAAAGGCTGGGC
126357	124444	CTCAAAAAAAAAAGGCTGGG
126358	124445	TCTCAAAAAAAAAAGGCTGG
126359	124446	GTCTCAAAAAAAAAAGGCTG
126360	124447	TGTCTCAAAAAAAAAAGGCT
126361	124448	CTGTCTCAAAAAAAAAAGGC
126362	124449	TCTGTCTCAAAAAAAAAAGG
126363	124450	CTCTGTCTCAAAAAAAAAAG
126364	124451	ACTCTGTCTCAAAAAAAAAA
126365	124452	GACTCTGTCTCAAAAAAAAA
126366	124453	AGACTCTGTCTCAAAAAAAA
126367	124454	GAGACTCTGTCTCAAAAAAA
126368	124455	CGAGACTCTGTCTCAAAAAA
126369	124456	GCGAGACTCTGTCTCAAAAA
126370	124457	AGCGAGACTCTGTCTCAAAA
126371	124458	GAGCGAGACTCTGTCTCAAA
126372	124459	AGAGCGAGACTCTGTCTCAA
126373	124460	CAGAGCGAGACTCTGTCTCA
126374	124461	ACAGAGCGAGACTCTGTCTC
126375	124462	AACAGAGCGAGACTCTGTCT
126376	124463	CAACAGAGCGAGACTCTGTC
126377	124464	GCAACAGAGCGAGACTCTGT
126378	124465	GGCAACAGAGCGAGACTCTG
126379	124466	GGGCAACAGAGCGAGACTCT
126380	124467	TGGGCAACAGAGCGAGACTC
126381	124468	CTGGGCAACAGAGCGAGACT
126382	124469	CCTGGGCAACAGAGCGAGAC
126383	124470	GCCTGGGCAACAGAGCGAGA
126384	124471	AGCCTGGGCAACAGAGCGAG
126385	124472	CAGCCTGGGCAACAGAGCGA
126386	124473	CCAGCCTGGGCAACAGAGCG
126387	124474	TCCAGCCTGGGCAACAGAGC
126388	124475	CTCCAGCCTGGGCAACAGAG
126389	124476	ACTCCAGCCTGGGCAACAGA
126390	124477	CACTCCAGCCTGGGCAACAG
126391	124478	GCACTCCAGCCTGGGCAACA
126392	124479	TGCACTCCAGCCTGGGCAAC
126393	124480	CTGCACTCCAGCCTGGGCAA
126394	124481	ACTGCACTCCAGCCTGGGCA
126395	124482	CACTGCACTCCAGCCTGGGC
126396	124483	TCACTGCACTCCAGCCTGGG
126397	124484	ATCACTGCACTCCAGCCTGG
126398	124485	CATCACTGCACTCCAGCCTG
126399	124486	GCATCACTGCACTCCAGCCT
126400	124487	CGCATCACTGCACTCCAGCC
126401	124488	TCGCATCACTGCACTCCAGC
126402	124489	ATCGCATCACTGCACTCCAG
126403	124490	GATCGCATCACTGCACTCCA

28110	26197	ACTGCTGGGATTACAGGCAT
28111	26198	AACTGCTGGGATTACAGGCA
28112	26199	AAACTGCTGGGATTACAGGC
28113	26200	CAAACTGCTGGGATTACAGG
28114	26201	CCAAACTGCTGGGATTACAG
28115	26202	CCCAAACTGCTGGGATTACA
28116	26203	TCCCAAACTGCTGGGATTAC
28117	26204	CTCCCAAACTGCTGGGATTA
28118	26205	CCTCCCAAACTGCTGGGATT
28119	26206	GCCTCCCAAACTGCTGGGAT
28120	26207	GGCCTCCCAAACTGCTGGGA
28121	26208	CGGCCTCCCAAACTGCTGGG
28122	26209	TCGGCCTCCCAAACTGCTGG
28123	26210	CTCGGCCTCCCAAACTGCTG
28124	26211	CCTCGGCCTCCCAAACTGCT
28125	26212	GCCTCGGCCTCCCAAACTGC
28126	26213	CGCCTCGGCCTCCCAAACTG
28127	26214	ACGCCTCGGCCTCCCAAACT
28128	26215	CACGCCTCGGCCTCCCAAAC
28129	26216	ACACGCCTCGGCCTCCCAAA
28130	26217	CACACGCCTCGGCCTCCCAA
28131	26218	CCACACGCCTCGGCCTCCCA
28132	26219	TCCACACGCCTCGGCCTCCC
28133	26220	ATCCACACGCCTCGGCCTCC
28134	26221	GATCCACACGCCTCGGCCTC
28135	26222	CGATCCACACGCCTCGGCCT
28136	26223	GCGATCCACACGCCTCGGCC
28137	26224	GGCGATCCACACGCCTCGGC
28138	26225	AGGCGATCCACACGCCTCGG
28139	26226	CAGGCGATCCACACGCCTCG
28140	26227	TCAGGCGATCCACACGCCTC
28141	26228	CTCAGGCGATCCACACGCCT
28142	26229	CCTCAGGCGATCCACACGCC
28143	26230	ACCTCAGGCGATCCACACGC
28144	26231	GACCTCAGGCGATCCACACG
28145	26232	TGACCTCAGGCGATCCACAC
28146	26233	CTGACCTCAGGCGATCCACA
28147	26234	CCTGACCTCAGGCGATCCAC
28148	26235	TCCTGACCTCAGGCGATCCA
28149	26236	TTCCTGACCTCAGGCGATCC
28150	26237	ATTCCTGACCTCAGGCGATC
28151	26238	AATTCCTGACCTCAGGCGAT
28152	26239	AAATTCCTGACCTCAGGCGA
28153	26240	CAAATTCCTGACCTCAGGCG
28154	26241	TCAAATTCCTGACCTCAGGC
28155	26242	CTCAAATTCCTGACCTCAGG
28156	26243	TCTCAAATTCCTGACCTCAG
28157	26244	GTCTCAAATTCCTGACCTCA
28158	26245	GGTCTCAAATTCCTGACCTC
28159	26246	TGGTCTCAAATTCCTGACCT
28160	26247	CTGGTCTCAAATTCCTGACC
28161	26248	GCTGGTCTCAAATTCCTGAC
28162	26249	GGCTGGTCTCAAATTCCTGA
28163	26250	AGGCTGGTCTCAAATTCCTG
28164	26251	CAGGCTGGTCTCAAATTCCT
28165	26252	CCAGGCTGGTCTCAAATTCC
28166	26253	GCCAGGCTGGTCTCAAATTC
28167	26254	GGCCAGGCTGGTCTCAAATT
28168	26255	TGGCCAGGCTGGTCTCAAAT
28169	26256	TTGGCCAGGCTGGTCTCAAA
28170	26257	GTTGGCCAGGCTGGTCTCAA
28171	26258	TGTTGGCCAGGCTGGTCTCA
28172	26259	ATGTTGGCCAGGCTGGTCTC
28173	26260	CATGTTGGCCAGGCTGGTCT
28174	26261	TCATGTTGGCCAGGCTGGTC
28175	26262	GTCATGTTGGCCAGGCTGGT
28176	26263	TGTCATGTTGGCCAGGCTGG
28177	26264	TTGTCATGTTGGCCAGGCTG
28178	26265	TTTGTCATGTTGGCCAGGCT
28179	26266	TTTTGTCATGTTGGCCAGGC
28180	26267	GTTTTGTCATGTTGGCCAGG

77257	75344	CACAGATATGTTACAAATTC
77258	75345	ACACAGATATGTTACAAATT
77259	75346	AACACAGATATGTTACAAAT
77260	75347	AAACACAGATATGTTACAAA
77261	75348	CAAACACAGATATGTTACAA
77262	75349	TCAAACACAGATATGTTACA
77263	75350	ATCAAACACAGATATGTTAC
77264	75351	CATCAAACACAGATATGTTA
77265	75352	ACATCAAACACAGATATGTT
77266	75353	AACATCAAACACAGATATGT
77267	75354	AAACATCAAACACAGATATG
77268	75355	TAAACATCAAACACAGATAT
77269	75356	TTAAACATCAAACACAGATA
77270	75357	CTTAAACATCAAACACAGAT
77271	75358	CCTTAAACATCAAACACAGA
77272	75359	GCCTTAAACATCAAACACAG
77273	75360	TGCCTTAAACATCAAACACA
77274	75361	ATGCCTTAAACATCAAACAC
77275	75362	TATGCCTTAAACATCAAACA
77276	75363	TTATGCCTTAAACATCAAAC
77277	75364	GTTATGCCTTAAACATCAAA
77278	75365	TGTTATGCCTTAAACATCAA
77279	75366	CTGTTATGCCTTAAACATCA
77280	75367	GCTGTTATGCCTTAAACATC
77281	75368	AGCTGTTATGCCTTAAACAT
77282	75369	AAGCTGTTATGCCTTAAACA
77283	75370	TAAGCTGTTATGCCTTAAAC
77284	75371	TTAAGCTGTTATGCCTTAAA
77285	75372	ATTAAGCTGTTATGCCTTAA
77286	75373	TATTAAGCTGTTATGCCTTA
77287	75374	TTATTAAGCTGTTATGCCTT
77288	75375	ATTATTAAGCTGTTATGCCT
77289	75376	CATTATTAAGCTGTTATGCC
77290	75377	TCATTATTAAGCTGTTATGC
77291	75378	GTCATTATTAAGCTGTTATG
77292	75379	TGTCATTATTAAGCTGTTAT
77293	75380	GTGTCATTATTAAGCTGTTA
77294	75381	AGTGTCATTATTAAGCTGTT
77295	75382	GAGTGTCATTATTAAGCTGT
77296	75383	AGAGTGTCATTATTAAGCTG
77297	75384	AAGAGTGTCATTATTAAGCT
77298	75385	GAAGAGTGTCATTATTAAGC
77299	75386	GGAAGAGTGTCATTATTAAG
77300	75387	AGGAAGAGTGTCATTATTAA
77301	75388	GAGGAAGAGTGTCATTATTA
77302	75389	TGAGGAAGAGTGTCATTATT
77303	75390	CTGAGGAAGAGTGTCATTAT
77304	75391	TCTGAGGAAGAGTGTCATTA
77305	75392	GTCTGAGGAAGAGTGTCATT
77306	75393	TGTCTGAGGAAGAGTGTCAT
77307	75394	CTGTCTGAGGAAGAGTGTCA
77308	75395	CCTGTCTGAGGAAGAGTGTC
77309	75396	TCCTGTCTGAGGAAGAGTGT
77310	75397	TTCCTGTCTGAGGAAGAGTG
77311	75398	CTTCCTGTCTGAGGAAGAGT
77312	75399	GCTTCCTGTCTGAGGAAGAG
77313	75400	GGCTTCCTGTCTGAGGAAGA
77314	75401	AGGCTTCCTGTCTGAGGAAG
77315	75402	CAGGCTTCCTGTCTGAGGAA
77316	75403	TCAGGCTTCCTGTCTGAGGA
77317	75404	TTCAGGCTTCCTGTCTGAGG
77318	75405	TTTCAGGCTTCCTGTCTGAG
77319	75406	ATTTCAGGCTTCCTGTCTGA
77320	75407	CATTTCAGGCTTCCTGTCTG
77321	75408	ACATTTCAGGCTTCCTGTCT
77322	75409	GACATTTCAGGCTTCCTGTC
77323	75410	GGACATTTCAGGCTTCCTGT
77324	75411	AGGACATTTCAGGCTTCCTG
77325	75412	TAGGACATTTCAGGCTTCCT
77326	75413	GTAGGACATTTCAGGCTTCC
77327	75414	AGTAGGACATTTCAGGCTTC

126404	124491	AGATCGCATCACTGCACTCC
126405	124492	GAGATCGCATCACTGCACTC
126406	124493	CGAGATCGCATCACTGCACT
126407	124494	CCGAGATCGCATCACTGCAC
126408	124495	GCCGAGATCGCATCACTGCA
126409	124496	AGCCGAGATCGCATCACTGC
126410	124497	GAGCCGAGATCGCATCACTG
126411	124498	TGAGCCGAGATCGCATCACT
126412	124499	GTGAGCCGAGATCGCATCAC
126413	124500	AGTGAGCCGAGATCGCATCA
126414	124501	CAGTGAGCCGAGATCGCATC
126415	124502	GCAGTGAGCCGAGATCGCAT
126416	124503	TGCAGTGAGCCGAGATCGCA
126417	124504	TTGCAGTGAGCCGAGATCGC
126418	124505	CTTGCAGTGAGCCGAGATCG
126419	124506	GCTTGCAGTGAGCCGAGATC
126420	124507	AGCTTGCAGTGAGCCGAGAT
126421	124508	GAGCTTGCAGTGAGCCGAGA
126422	124509	GGAGCTTGCAGTGAGCCGAG
126423	124510	CGGAGCTTGCAGTGAGCCGA
126424	124511	GCGGAGCTTGCAGTGAGCCG
126425	124512	GGCGGAGCTTGCAGTGAGCC
126426	124513	AGGCGGAGCTTGCAGTGAGC
126427	124514	GAGGCGGAGCTTGCAGTGAG
126428	124515	AGAGGCGGAGCTTGCAGTGA
126429	124516	AAGAGGCGGAGCTTGCAGTG
126430	124517	CAAGAGGCGGAGCTTGCAGT
126431	124518	CCAAGAGGCGGAGCTTGCAG
126432	124519	CCCAAGAGGCGGAGCTTGCA
126433	124520	ACCCAAGAGGCGGAGCTTGC
126434	124521	AACCCAAGAGGCGGAGCTTG
126435	124522	GAACCCAAGAGGCGGAGCTT
126436	124523	TGAACCCAAGAGGCGGAGCT
126437	124524	ATGAACCCAAGAGGCGGAGC
126438	124525	CATGAACCCAAGAGGCGGAG
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126440	124527	GGCATGAACCCAAGAGGCGG
126441	124528	TGGCATGAACCCAAGAGGCG
126442	124529	ATGGCATGAACCCAAGAGGC
126443	124530	AATGGCATGAACCCAAGAGG
126444	124531	GAATGGCATGAACCCAAGAG
126445	124532	AGAATGGCATGAACCCAAGA
126446	124533	GAGAATGGCATGAACCCAAG
126447	124534	GGAGAATGGCATGAACCCAA
126448	124535	AGGAGAATGGCATGAACCCA
126449	124536	CAGGAGAATGGCATGAACCC
126450	124537	GCAGGAGAATGGCATGAACC
126451	124538	GGCAGGAGAATGGCATGAAC
126452	124539	AGGCAGGAGAATGGCATGAA
126453	124540	GAGGCAGGAGAATGGCATGA
126454	124541	TGAGGCAGGAGAATGGCATG
126455	124542	CTGAGGCAGGAGAATGGCAT
126456	124543	GCTGAGGCAGGAGAATGGCA
126457	124544	GGCTGAGGCAGGAGAATGGC
126458	124545	AGGCTGAGGCAGGAGAATGG
126459	124546	GAGGCTGAGGCAGGAGAATG
126460	124547	GGAGGCTGAGGCAGGAGAAT
126461	124548	AGGAGGCTGAGGCAGGAGAA
126462	124549	CAGGAGGCTGAGGCAGGAGA
126463	124550	TCAGGAGGCTGAGGCAGGAG
126464	124551	CTCAGGAGGCTGAGGCAGGA
126465	124552	ACTCAGGAGGCTGAGGCAGG
126466	124553	TACTCAGGAGGCTGAGGCAG
126467	124554	CTACTCAGGAGGCTGAGGCA
126468	124555	GCTACTCAGGAGGCTGAGGC
126469	124556	AGCTACTCAGGAGGCTGAGG
126470	124557	CAGCTACTCAGGAGGCTGAG
126471	124558	CCAGCTACTCAGGAGGCTGA
126472	124559	CCCAGCTACTCAGGAGGCTG
126473	124560	TCCCAGCTACTCAGGAGGCT
126474	124561	GTCCCAGCTACTCAGGAGGC

28181	26268	AGTTTTGTCATGTTGGCCAG
28182	26269	GAGTTTTGTCATGTTGGCCA
28183	26270	GGAGTTTTGTCATGTTGGCC
28184	26271	CGGAGTTTTGTCATGTTGGC
28185	26272	ACGGAGTTTTGTCATGTTGG
28186	26273	GACGGAGTTTTGTCATGTTG
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28188	26275	GAGACGGAGTTTTGTCATGT
28189	26276	AGAGACGGAGTTTTGTCATG
28190	26277	TAGAGACGGAGTTTTGTCAT
28191	26278	GTAGAGACGGAGTTTTGTCA
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28194	26281	TTAGTAGAGACGGAGTTTTG
28195	26282	TTTAGTAGAGACGGAGTTTT
28196	26283	TTTTAGTAGAGACGGAGTTT
28197	26284	TTTTTAGTAGAGACGGAGTT
28198	26285	ATTTTTAGTAGAGACGGAGT
28199	26286	TATTTTTAGTAGAGACGGAG
28200	26287	GTATTTTTAGTAGAGACGGA
28201	26288	TGTATTTTTAGTAGAGACGG
28202	26289	TTGTATTTTTAGTAGAGACG
28203	26290	TTTGTATTTTTAGTAGAGAC
28204	26291	TTTTGTATTTTTAGTAGAGA
28205	26292	TTTTTGTATTTTTAGTAGAG
28206	26293	TTTTTTGTATTTTTAGTAGA
28207	26294	CTTTTTTGTATTTTTAGTAG
28208	26295	ACTTTTTTGTATTTTTAGTA
28209	26296	AACTTTTTTGTATTTTTAGT
28210	26297	TAACTTTTTTGTATTTTTAG
28211	26298	CTAACTTTTTTGTATTTTTA
28212	26299	GCTAACTTTTTTGTATTTTT
28213	26300	GGCTAACTTTTTTGTATTTT
28214	26301	TGGCTAACTTTTTTGTATTT
28215	26302	CTGGCTAACTTTTTTGTATT
28216	26303	CCTGGCTAACTTTTTTGTAT
28217	26304	GCCTGGCTAACTTTTTTGTA
28218	26305	CGCCTGGCTAACTTTTTTGT
28219	26306	ACGCCTGGCTAACTTTTTTG
28220	26307	CACGCCTGGCTAACTTTTTT
28221	26308	CCACGCCTGGCTAACTTTTT
28222	26309	ACCACGCCTGGCTAACTTTT
28223	26310	CACCACGCCTGGCTAACTTT
28224	26311	TCACCACGCCTGGCTAACTT
28225	26312	GTCACCACGCCTGGCTAACT
28226	26313	TGTCACCACGCCTGGCTAAC
28227	26314	TTGTCACCACGCCTGGCTAA
28228	26315	CTTGTCACCACGCCTGGCTA
28229	26316	GCTTGTCACCACGCCTGGCT
28230	26317	TGCTTGTCACCACGCCTGGC
28231	26318	GTGCTTGTCACCACGCCTGG
28232	26319	GGTGCTTGTCACCACGCCTG
28233	26320	AGGTGCTTGTCACCACGCCT
28234	26321	CAGGTGCTTGTCACCACGCC
28235	26322	ACAGGTGCTTGTCACCACGC
28236	26323	TACAGGTGCTTGTCACCACG
28237	26324	TTACAGGTGCTTGTCACCAC
28238	26325	ATTACAGGTGCTTGTCACCA
28239	26326	GATTACAGGTGCTTGTCACC
28240	26327	GGATTACAGGTGCTTGTCAC
28241	26328	GGGATTACAGGTGCTTGTCA
28242	26329	TGGGATTACAGGTGCTTGTC
28243	26330	CTGGGATTACAGGTGCTTGT
28244	26331	GCTGGGATTACAGGTGCTTG
28245	26332	AGCTGGGATTACAGGTGCTT
28246	26333	TAGCTGGGATTACAGGTGCT
28247	26334	GTAGCTGGGATTACAGGTGC
28248	26335	AGTAGCTGGGATTACAGGTG
28249	26336	GAGTAGCTGGGATTACAGGT
28250	26337	TGAGTAGCTGGGATTACAGG
28251	26338	CTGAGTAGCTGGGATTACAG

77328	75415	AAGTAGGACATTTCAGGCTT
77329	75416	AAAGTAGGACATTTCAGGCT
77330	75417	CAAAGTAGGACATTTCAGGC
77331	75418	TCAAAGTAGGACATTTCAGG
77332	75419	GTCAAAGTAGGACATTTCAG
77333	75420	GGTCAAAGTAGGACATTTCA
77334	75421	AGGTCAAAGTAGGACATTTC
77335	75422	TAGGTCAAAGTAGGACATTT
77336	75423	TTAGGTCAAAGTAGGACATT
77337	75424	TTTAGGTCAAAGTAGGACAT
77338	75425	CTTTAGGTCAAAGTAGGACA
77339	75426	ACTTTAGGTCAAAGTAGGAC
77340	75427	GACTTTAGGTCAAAGTAGGA
77341	75428	AGACTTTAGGTCAAAGTAGG
77342	75429	TAGACTTTAGGTCAAAGTAG
77343	75430	CTAGACTTTAGGTCAAAGTA
77344	75431	ACTAGACTTTAGGTCAAAGT
77345	75432	TACTAGACTTTAGGTCAAAG
77346	75433	TTACTAGACTTTAGGTCAAA
77347	75434	ATTACTAGACTTTAGGTCAA
77348	75435	TATTACTAGACTTTAGGTCA
77349	75436	TTATTACTAGACTTTAGGTC
77350	75437	TTTATTACTAGACTTTAGGT
77351	75438	TTTTATTACTAGACTTTAGG
77352	75439	GTTTTATTACTAGACTTTAG
77353	75440	AGTTTTATTACTAGACTTTA
77354	75441	CAGTTTTATTACTAGACTTT
77355	75442	CCAGTTTTATTACTAGACTT
77356	75443	TCCAGTTTTATTACTAGACT
77357	75444	GTCCAGTTTTATTACTAGAC
77358	75445	TGTCCAGTTTTATTACTAGA
77359	75446	ATGTCCAGTTTTATTACTAG
77360	75447	TATGTCCAGTTTTATTACTA
77361	75448	GTATGTCCAGTTTTATTACT
77362	75449	TGTATGTCCAGTTTTATTAC
77363	75450	GTGTATGTCCAGTTTTATTA
77364	75451	TGTGTATGTCCAGTTTTATT
77365	75452	CTGTGTATGTCCAGTTTTAT
77366	75453	CCTGTGTATGTCCAGTTTTA
77367	75454	GCCTGTGTATGTCCAGTTTT
77368	75455	TGCCTGTGTATGTCCAGTTT
77369	75456	TTGCCTGTGTATGTCCAGTT
77370	75457	GTTGCCTGTGTATGTCCAGT
77371	75458	TGTTGCCTGTGTATGTCCAG
77372	75459	ATGTTGCCTGTGTATGTCCA
77373	75460	CATGTTGCCTGTGTATGTCC
77374	75461	ACATGTTGCCTGTGTATGTC
77375	75462	GACATGTTGCCTGTGTATGT
77376	75463	TGACATGTTGCCTGTGTATG
77377	75464	ATGACATGTTGCCTGTGTAT
77378	75465	AATGACATGTTGCCTGTGTA
77379	75466	TAATGACATGTTGCCTGTGT
77380	75467	TTAATGACATGTTGCCTGTG
77381	75468	ATTAATGACATGTTGCCTGT
77382	75469	AATTAATGACATGTTGCCTG
77383	75470	GAATTAATGACATGTTGCCT
77384	75471	AGAATTAATGACATGTTGCC
77385	75472	GAGAATTAATGACATGTTGC
77386	75473	TGAGAATTAATGACATGTTG
77387	75474	TTGAGAATTAATGACATGTT
77388	75475	TTTGAGAATTAATGACATGT
77389	75476	GTTTGAGAATTAATGACATG
77390	75477	AGTTTGAGAATTAATGACAT
77391	75478	AAGTTTGAGAATTAATGACA
77392	75479	AAAGTTTGAGAATTAATGAC
77393	75480	TAAAGTTTGAGAATTAATGA
77394	75481	TTAAAGTTTGAGAATTAATG
77395	75482	GTTAAAGTTTGAGAATTAAT
77396	75483	TGTTAAAGTTTGAGAATTAA
77397	75484	TTGTTAAAGTTTGAGAATTA
77398	75485	TTTGTTAAAGTTTGAGAATT

126475	124562	AGTCCCAGCTACTCAGGAGG
126476	124563	TAGTCCCAGCTACTCAGGAG
126477	124564	GTAGTCCCAGCTACTCAGGA
126478	124565	TGTAGTCCCAGCTACTCAGG
126479	124566	ATGTAGTCCCAGCTACTCAG
126480	124567	AATGTAGTCCCAGCTACTCA
126481	124568	GAATGTAGTCCCAGCTACTC
126482	124569	CGAATGTAGTCCCAGCTACT
126483	124570	GCGAATGTAGTCCCAGCTAC
126484	124571	GGCGAATGTAGTCCCAGCTA
126485	124572	GGGCGAATGTAGTCCCAGCT
126486	124573	CGGGCGAATGTAGTCCCAGC
126487	124574	GCGGGCGAATGTAGTCCCAG
126488	124575	GGCGGGCGAATGTAGTCCCA
126489	124576	TGGCGGGCGAATGTAGTCCC
126490	124577	GTGGCGGGCGAATGTAGTCC
126491	124578	GGTGGCGGGCGAATGTAGTC
126492	124579	TGGTGGCGGGCGAATGTAGT
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126494	124581	TGTGGTGGCGGGCGAATGTA
126495	124582	GTGTGGTGGCGGGCGAATGT
126496	124583	GGTGTGGTGGCGGGCGAATG
126497	124584	GGGTGTGGTGGCGGGCGAAT
126498	124585	CGGGTGTGGTGGCGGGCGAA
126499	124586	CCGGGTGTGGTGGCGGGCGA
126500	124587	GCCGGGTGTGGTGGCGGGCG
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126503	124590	TTAGCCGGGTGTGGTGGCGG
126504	124591	ATTAGCCGGGTGTGGTGGCG
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126512	124599	ACAAAAAAATTAGCCGGGTG
126513	124600	TACAAAAAAATTAGCCGGGT
126514	124601	ATACAAAAAAATTAGCCGGG
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126535	124622	GAAACCCTGTCTCTACTAAA
126536	124623	TGAAACCCTGTCTCTACTAA
126537	124624	GTGAAACCCTGTCTCTACTA
126538	124625	GGTGAAACCCTGTCTCTACT
126539	124626	CGGTGAAACCCTGTCTCTAC
126540	124627	ACGGTGAAACCCTGTCTCTA
126541	124628	CACGGTGAAACCCTGTCTCT
126542	124629	ACACGGTGAAACCCTGTCTC
126543	124630	AACACGGTGAAACCCTGTCT
126544	124631	TAACACGGTGAAACCCTGTC
126545	124632	CTAACACGGTGAAACCCTGT

28252	26339	ACTGAGTAGCTGGGATTACA
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28254	26341	CTACTGAGTAGCTGGGATTA
28255	26342	CCTACTGAGTAGCTGGGATT
28256	26343	GCCTACTGAGTAGCTGGGAT
28257	26344	AGCCTACTGAGTAGCTGGGA
28258	26345	CAGCCTACTGAGTAGCTGGG
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28261	26348	CCTCAGCCTACTGAGTAGCT
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28263	26350	TGCCTCAGCCTACTGAGTAG
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28269	26356	TCTCCTTGCCTCAGCCTACT
28270	26357	TTCTCCTTGCCTCAGCCTAC
28271	26358	ATTCTCCTTGCCTCAGCCTA
28272	26359	GATTCTCCTTGCCTCAGCCT
28273	26360	CGATTCTCCTTGCCTCAGCC
28274	26361	GCGATTCTCCTTGCCTCAGC
28275	26362	AGCGATTCTCCTTGCCTCAG
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28278	26365	TCAAGCGATTCTCCTTGCCT
28279	26366	TTCAAGCGATTCTCCTTGCC
28280	26367	GTTCAAGCGATTCTCCTTGC
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28282	26369	AGGTTCAAGCGATTCTCCTT
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28285	26372	CCCAGGTTCAAGCGATTCTC
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28294	26381	CCTCCACCTCCCAGGTTCAA
28295	26382	ACCTCCACCTCCCAGGTTCA
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28300	26387	CTGCAACCTCCACCTCCCAG
28301	26388	ACTGCAACCTCCACCTCCCA
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28306	26393	AGCTCACTGCAACCTCCACC
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28312	26399	GATCTCAGCTCACTGCAACC
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28315	26402	AGCGATCTCAGCTCACTGCA
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28318	26405	TGGAGCGATCTCAGCTCACT
28319	26406	ATGGAGCGATCTCAGCTCAC
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28322	26409	GCAATGGAGCGATCTCAGCT

77399	75486	ATTTGTTAAAGTTTGAGAAT
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77411	75498	AGGTTATATATGATTTGTTA
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77413	75500	TTAGGTTATATATGATTTGT
77414	75501	ATTAGGTTATATATGATTTG
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77423	75510	AACCATTATATTAGGTTATA
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77425	75512	AGAACCATTATATTAGGTTA
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77427	75514	TGAGAACCATTATATTAGGT
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77442	75529	CGTGATGTACAGACTTGAGA
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77444	75531	GACGTGATGTACAGACTTGA
77445	75532	TGACGTGATGTACAGACTTG
77446	75533	GTGACGTGATGTACAGACTT
77447	75534	GGTGACGTGATGTACAGACT
77448	75535	AGGTGACGTGATGTACAGAC
77449	75536	CAGGTGACGTGATGTACAGA
77450	75537	ACAGGTGACGTGATGTACAG
77451	75538	TACAGGTGACGTGATGTACA
77452	75539	ATACAGGTGACGTGATGTAC
77453	75540	CATACAGGTGACGTGATGTA
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77461	75548	ATATTTTTCATACAGGTGAC
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77464	75551	CTCATATTTTTCATACAGGT
77465	75552	CCTCATATTTTTCATACAGG
77466	75553	TCCTCATATTTTTCATACAG
77467	75554	TTCCTCATATTTTTCATACA
77468	75555	TTTCCTCATATTTTTCATAC
77469	75556	GTTTCCTCATATTTTTCATA

126546	124633	GCTAACACGGTGAAACCCTG
126547	124634	GGCTAACACGGTGAAACCCT
126548	124635	TGGCTAACACGGTGAAACCC
126549	124636	CTGGCTAACACGGTGAAACC
126550	124637	CCTGGCTAACACGGTGAAAC
126551	124638	TCCTGGCTAACACGGTGAAA
126552	124639	ATCCTGGCTAACACGGTGAA
126553	124640	CATCCTGGCTAACACGGTGA
126554	124641	CCATCCTGGCTAACACGGTG
126555	124642	ACCATCCTGGCTAACACGGT
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126558	124645	GATACCATCCTGGCTAACAC
126559	124646	CGATACCATCCTGGCTAACA
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126568	124655	TCAGGAGATCGATACCATCC
126569	124656	GTCAGGAGATCGATACCATC
126570	124657	GGTCAGGAGATCGATACCAT
126571	124658	AGGTCAGGAGATCGATACCA
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126573	124660	CGAGGTCAGGAGATCGATAC
126574	124661	ACGAGGTCAGGAGATCGATA
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126576	124663	TCACGAGGTCAGGAGATCGA
126577	124664	ATCACGAGGTCAGGAGATCG
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126580	124667	CGGATCACGAGGTCAGGAGA
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126582	124669	GGCGGATCACGAGGTCAGGA
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126585	124672	GCGGGCGGATCACGAGGTCA
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126587	124674	AGGCGGGCGGATCACGAGGT
126588	124675	GAGGCGGGCGGATCACGAGG
126589	124676	CGAGGCGGGCGGATCACGAG
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126593	124680	AGGCCGAGGCGGGCGGATCA
126594	124681	GAGGCCGAGGCGGGCGGATC
126595	124682	GGAGGCCGAGGCGGGCGGAT
126596	124683	GGGAGGCCGAGGCGGGCGGA
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126598	124685	TTGGGAGGCCGAGGCGGGCG
126599	124686	TTTGGGAGGCCGAGGCGGGC
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126615	124702	CCTGTAATCCCAGCACTTTG
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28323	26410	TGCAATGGAGCGATCTCAGC
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28326	26413	GAGTGCAATGGAGCGATCTC
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28350	26437	AGTCTTGCTTTGTTGCCTAC
28351	26438	GAGTCTTGCTTTGTTGCCTA
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77470	75557	TGTTTCCTCATATTTTTCAT
77471	75558	CTGTTTCCTCATATTTTTCA
77472	75559	TCTGTTTCCTCATATTTTTC
77473	75560	CTCTGTTTCCTCATATTTTT
77474	75561	TCTCTGTTTCCTCATATTTT
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77476	75563	AGTCTCTGTTTCCTCATATT
77477	75564	AAGTCTCTGTTTCCTCATAT
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77482	75569	AAAAGAAGTCTCTGTTTCCT
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77488	75575	TAGTGTAAAAGAAGTCTCTG
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77490	75577	AATAGTGTAAAAGAAGTCTC
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77494	75581	CACCAATAGTGTAAAAGAAG
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77501	75588	TCCACCTCACCAATAGTGTA
77502	75589	ATCCACCTCACCAATAGTGT
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77507	75594	AATTTATCCACCTCACCAAT
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77510	75597	ATCAATTTATCCACCTCACC
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77512	75599	CTATCAATTTATCCACCTCA
77513	75600	TCTATCAATTTATCCACCTC
77514	75601	CTCTATCAATTTATCCACCT
77515	75602	ACTCTATCAATTTATCCACC
77516	75603	GACTCTATCAATTTATCCAC
77517	75604	AGACTCTATCAATTTATCCA
77518	75605	AAGACTCTATCAATTTATCC
77519	75606	AAAGACTCTATCAATTTATC
77520	75607	GAAAGACTCTATCAATTTAT
77521	75608	AGAAAGACTCTATCAATTTA
77522	75609	CAGAAAGACTCTATCAATTT
77523	75610	CCAGAAAGACTCTATCAATT
77524	75611	TCCAGAAAGACTCTATCAAT
77525	75612	CTCCAGAAAGACTCTATCAA
77526	75613	TCTCCAGAAAGACTCTATCA
77527	75614	CTCTCCAGAAAGACTCTATC
77528	75615	TCTCTCCAGAAAGACTCTAT
77529	75616	TTCTCTCCAGAAAGACTCTA
77530	75617	ATTCTCTCCAGAAAGACTCT
77531	75618	GATTCTCTCCAGAAAGACTC
77532	75619	AGATTCTCTCCAGAAAGACT
77533	75620	CAGATTCTCTCCAGAAAGAC
77534	75621	CCAGATTCTCTCCAGAAAGA
77535	75622	GCCAGATTCTCTCCAGAAAG
77536	75623	TGCCAGATTCTCTCCAGAAA
77537	75624	TTGCCAGATTCTCTCCAGAA
77538	75625	ATTGCCAGATTCTCTCCAGA
77539	75626	CATTGCCAGATTCTCTCCAG
77540	75627	GCATTGCCAGATTCTCTCCA

126617	124704	CACCTGTAATCCCAGCACTT
126618	124705	ACACCTGTAATCCCAGCACT
126619	124706	CACACCTGTAATCCCAGCAC
126620	124707	TCACACCTGTAATCCCAGCA
126621	124708	CTCACACCTGTAATCCCAGC
126622	124709	GCTCACACCTGTAATCCCAG
126623	124710	GGCTCACACCTGTAATCCCA
126624	124711	TGGCTCACACCTGTAATCCC
126625	124712	GTGGCTCACACCTGTAATCC
126626	124713	AGTGGCTCACACCTGTAATC
126627	124714	CAGTGGCTCACACCTGTAAT
126628	124715	GCAGTGGCTCACACCTGTAA
126629	124716	CGCAGTGGCTCACACCTGTA
126630	124717	GCGCAGTGGCTCACACCTGT
126631	124718	GGCGCAGTGGCTCACACCTG
126632	124719	GGGCGCAGTGGCTCACACCT
126633	124720	CGGGCGCAGTGGCTCACACC
126634	124721	CCGGGCGCAGTGGCTCACAC
126635	124722	GCCGGGCGCAGTGGCTCACA
126636	124723	GGCCGGGCGCAGTGGCTCAC
126637	124724	AGGCCGGGCGCAGTGGCTCA
126638	124725	AAGGCCGGGCGCAGTGGCTC
126639	124726	CAAGGCCGGGCGCAGTGGCT
126640	124727	ACAAGGCCGGGCGCAGTGGC
126641	124728	TACAAGGCCGGGCGCAGTGG
126642	124729	ATACAAGGCCGGGCGCAGTG
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126645	124732	AAAATACAAGGCCGGGCGCA
126646	124733	AAAAATACAAGGCCGGGCGC
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126651	124738	CTATTAAAAATACAAGGCCG
126652	124739	TCTATTAAAAATACAAGGCC
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126657	124744	CCATCTCTATTAAAAATACA
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126659	124746	CCCCATCTCTATTAAAAATA
126660	124747	ACCCCATCTCTATTAAAAAT
126661	124748	AACCCCATCTCTATTAAAAA
126662	124749	AAACCCCATCTCTATTAAAA
126663	124750	GAAACCCCATCTCTATTAAA
126664	124751	TGAAACCCCATCTCTATTAA
126665	124752	GTGAAACCCCATCTCTATTA
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126667	124754	TGGTGAAACCCCATCTCTAT
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126669	124756	CATGGTGAAACCCCATCTCT
126670	124757	ACATGGTGAAACCCCATCTC
126671	124758	AACATGGTGAAACCCCATCT
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126679	124766	GGCTGGCCAACATGGTGAAA
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126681	124768	CGGGCTGGCCAACATGGTGA
126682	124769	CCGGGCTGGCCAACATGGTG
126683	124770	ACCGGGCTGGCCAACATGGT
126684	124771	GACCGGGCTGGCCAACATGG
126685	124772	AGACCGGGCTGGCCAACATG
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28394	26481	TTGTTATTATTTTTATTTAT
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28397	26484	TTATTGTTATTATTTTTATT
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28458	26545	TAAAGCATGGTTGATTGAAG
28459	26546	CTAAAGCATGGTTGATTGAA
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28461	26548	GACTAAAGCATGGTTGATTG
28462	26549	GGACTAAAGCATGGTTGATT
28463	26550	AGGACTAAAGCATGGTTGAT
28464	26551	CAGGACTAAAGCATGGTTGA

77541	75628	AGCATTGCCAGATTCTCTCC
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77544	75631	ATTAGCATTGCCAGATTCTC
77545	75632	GATTAGCATTGCCAGATTCT
77546	75633	TGATTAGCATTGCCAGATTC
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77551	75638	AATTTTGATTAGCATTGCCA
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77574	75661	GAACAAAGTGTATGTGCATT
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77576	75663	TGGAACAAAGTGTATGTGCA
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77591	75678	TAGAGATAGAACTGCTGGAA
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77596	75683	ATTACTAGAGATAGAACTGC
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77599	75686	TAAATTACTAGAGATAGAAC
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77601	75688	AATAAATTACTAGAGATAGA
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77605	75692	CAAAAATAAATTACTAGAGA
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126689	124776	TTCAAGACCGGGCTGGCCAA
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126694	124781	AGGAGTTCAAGACCGGGCTG
126695	124782	CAGGAGTTCAAGACCGGGCT
126696	124783	TCAGGAGTTCAAGACCGGGC
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126699	124786	AGGTCAGGAGTTCAAGACCG
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126713	124800	GGGTGGATCATTTGAGGTCA
126714	124801	CGGGTGGATCATTTGAGGTC
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126717	124804	AGGCGGGTGGATCATTTGAG
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126721	124808	GCCGAGGCGGGTGGATCATT
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126724	124811	GAGGCCGAGGCGGGTGGATC
126725	124812	GGAGGCCGAGGCGGGTGGAT
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126746	124833	ACCTGTAATCCCAGCACTTT
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77614	75701	ATATGAGGGCAAAAATAAAT
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77619	75706	TGGATATATGAGGGCAAAAA
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77623	75710	CTTATGGATATATGAGGGCA
77624	75711	TCTTATGGATATATGAGGGC
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77629	75716	GCATGTCTTATGGATATATG
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77674	75761	CTCTGCAGAAAAAGAAAAAA
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77678	75765	CTGTCTCTGCAGAAAAAGAA
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77680	75767	CCCTGTCTCTGCAGAAAAAG
77681	75768	ACCCTGTCTCTGCAGAAAAA
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126759	124846	AGCGATGGCTCACACCTGTA
126760	124847	GAGCGATGGCTCACACCTGT
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126763	124850	TGAGAGCGATGGCTCACACC
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126776	124863	GTTACCGCAAGGCTGAGAGC
126777	124864	AGTTACCGCAAGGCTGAGAG
126778	124865	AAGTTACCGCAAGGCTGAGA
126779	124866	AAAGTTACCGCAAGGCTGAG
126780	124867	AAAAGTTACCGCAAGGCTGA
126781	124868	AAAAAGTTACCGCAAGGCTG
126782	124869	TAAAAAGTTACCGCAAGGCT
126783	124870	ATAAAAAGTTACCGCAAGGC
126784	124871	AATAAAAAGTTACCGCAAGG
126785	124872	TAATAAAAAGTTACCGCAAG
126786	124873	GTAATAAAAAGTTACCGCAA
126787	124874	CGTAATAAAAAGTTACCGCA
126788	124875	TCGTAATAAAAAGTTACCGC
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126790	124877	ATTCGTAATAAAAAGTTACC
126791	124878	CATTCGTAATAAAAAGTTAC
126792	124879	ACATTCGTAATAAAAAGTTA
126793	124880	TACATTCGTAATAAAAAGTT
126794	124881	ATACATTCGTAATAAAAAGT
126795	124882	AATACATTCGTAATAAAAAG
126796	124883	CAATACATTCGTAATAAAAA
126797	124884	TCAATACATTCGTAATAAAA
126798	124885	CTCAATACATTCGTAATAAA
126799	124886	TCTCAATACATTCGTAATAA
126800	124887	GTCTCAATACATTCGTAATA
126801	124888	TGTCTCAATACATTCGTAAT
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126803	124890	AATGTCTCAATACATTCGTA
126804	124891	TAATGTCTCAATACATTCGT
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126806	124893	ATTAATGTCTCAATACATTC
126807	124894	TATTAATGTCTCAATACATT
126808	124895	TTATTAATGTCTCAATACAT
126809	124896	GTTATTAATGTCTCAATACA
126810	124897	GGTTATTAATGTCTCAATAC
126811	124898	AGGTTATTAATGTCTCAATA
126812	124899	TAGGTTATTAATGTCTCAAT
126813	124900	CTAGGTTATTAATGTCTCAA
126814	124901	CCTAGGTTATTAATGTCTCA
126815	124902	GCCTAGGTTATTAATGTCTC
126816	124903	GGCCTAGGTTATTAATGTCT
126817	124904	TGGCCTAGGTTATTAATGTC
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126819	124906	ACTGGCCTAGGTTATTAATG
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126821	124908	TGACTGGCCTAGGTTATTAA
126822	124909	ATGACTGGCCTAGGTTATTA
126823	124910	CATGACTGGCCTAGGTTATT
126824	124911	ACATGACTGGCCTAGGTTAT
126825	124912	AACATGACTGGCCTAGGTTA
126826	124913	AAACATGACTGGCCTAGGTT
126827	124914	GAAACATGACTGGCCTAGGT
126828	124915	TGAAACATGACTGGCCTAGG
126829	124916	ATGAAACATGACTGGCCTAG

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28538	26625	CCAAATTTCAAAATTTTAAA
28539	26626	TCCAAATTTCAAAATTTTAA
28540	26627	TTCCAAATTTCAAAATTTTA
28541	26628	TTTCCAAATTTCAAAATTTT
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28543	26630	TGTTTCCAAATTTCAAAATT
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28561	26648	AACCATCATTTATGATGTTG
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28578	26665	GGGAGCTGCAGAAAACTAAC
28579	26666	AGGGAGCTGCAGAAAACTAA
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28582	26669	AATAGGGAGCTGCAGAAAAC
28583	26670	AAATAGGGAGCTGCAGAAAA
28584	26671	AAAATAGGGAGCTGCAGAAA
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28588	26675	TGCCAAAATAGGGAGCTGCA
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28598	26685	ACAGACTATCTGCCAAAATA
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77685	75772	TAAAACCCTGTCTCTGCAGA
77686	75773	GTAAAACCCTGTCTCTGCAG
77687	75774	GGTAAAACCCTGTCTCTGCA
77688	75775	TGGTAAAACCCTGTCTCTGC
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77690	75777	CATGGTAAAACCCTGTCTCT
77691	75778	ACATGGTAAAACCCTGTCTC
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77693	75780	CAACATGGTAAAACCCTGTC
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77695	75782	GGCAACATGGTAAAACCCTG
77696	75783	GGGCAACATGGTAAAACCCT
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77705	75792	GATCACCCTGGGCAACATGG
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77718	75805	CTCAGGAGTTCCAGATCACC
77719	75806	GCTCAGGAGTTCCAGATCAC
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77729	75816	GATTACCTGAGCTCAGGAGT
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77740	75827	TGAGGTGGGTGGATTACCTG
77741	75828	CTGAGGTGGGTGGATTACCT
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77745	75832	GAGGCTGAGGTGGGTGGATT
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126836	124923	GGTAGGGATGAAACATGACT
126837	124924	GGGTAGGGATGAAACATGAC
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126839	124926	ATGGGTAGGGATGAAACATG
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126841	124928	CAATGGGTAGGGATGAAACA
126842	124929	ACAATGGGTAGGGATGAAAC
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126845	124932	GAGACAATGGGTAGGGATGA
126846	124933	AGAGACAATGGGTAGGGATG
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126850	124937	TTTAAGAGACAATGGGTAGG
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126855	124942	AAGCTTTTAAGAGACAATGG
126856	124943	AAAGCTTTTAAGAGACAATG
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126859	124946	CTCAAAGCTTTTAAGAGACA
126860	124947	ACTCAAAGCTTTTAAGAGAC
126861	124948	GACTCAAAGCTTTTAAGAGA
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126874	124961	GAATAATCCAGTGGACTCAA
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126895	124982	CAATGTCTAGAATTTGCTTC
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126899	124986	GATGCAATGTCTAGAATTTG
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28607	26694	TGAGTAACAACAGACTATCT
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28644	26731	ATATCGTACAACACTACTTT
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28648	26735	CATGATATCGTACAACACTA
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28651	26738	GCCCATGATATCGTACAACA
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28658	26745	ATTCACAGCCCATGATATCG
28659	26746	CATTCACAGCCCATGATATC
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28663	26750	AACACATTCACAGCCCATGA
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28665	26752	CAAACACATTCACAGCCCAT
28666	26753	ACAAACACATTCACAGCCCA
28667	26754	CACAAACACATTCACAGCCC
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28669	26756	GTCACAAACACATTCACAGC
28670	26757	AGTCACAAACACATTCACAG
28671	26758	AAGTCACAAACACATTCACA
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28673	26760	TCAAGTCACAAACACATTCA
28674	26761	ATCAAGTCACAAACACATTC
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77754	75841	GCACTTTGGGAGGCTGAGGT
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77760	75847	ATCCCAGCACTTTGGGAGGC
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77784	75871	CAGGCATGATGGCTCACACC
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77823	75910	AACAAAAGAAATAATGCTGA
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126901	124988	CTGATGCAATGTCTAGAATT
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126935	125022	CTTAAAGATACACACTAAAA
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126937	125024	AACTTAAAGATACACACTAA
126938	125025	CAACTTAAAGATACACACTA
126939	125026	CCAACTTAAAGATACACACT
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126941	125028	AACCAACTTAAAGATACACA
126942	125029	AAACCAACTTAAAGATACAC
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126954	125041	AAAACAAAACCAAAACCAAC
126955	125042	AAAAACAAAACCAAAACCAA
126956	125043	AAAAAACAAAACCAAAACCA
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126961	125048	AAAACAAAAAACAAAACCAA
126962	125049	AAAAACAAAAAACAAAACCA
126963	125050	CAAAAACAAAAAACAAAACC
126964	125051	TCAAAAACAAAAAACAAAAC
126965	125052	CTCAAAAACAAAAAACAAAA
126966	125053	TCTCAAAAACAAAAAACAAA
126967	125054	ATCTCAAAAACAAAAAACAA
126968	125055	CATCTCAAAAACAAAAAACA
126969	125056	CCATCTCAAAAACAAAAAAC
126970	125057	CCCATCTCAAAAACAAAAAA
126971	125058	CCCCATCTCAAAAACAAAAA

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28679	26766	CTCAGATCAAGTCACAAACA
28680	26767	TCTCAGATCAAGTCACAAAC
28681	26768	TTCTCAGATCAAGTCACAAA
28682	26769	GTTCTCAGATCAAGTCACAA
28683	26770	GGTTCTCAGATCAAGTCACA
28684	26771	GGGTTCTCAGATCAAGTCAC
28685	26772	TGGGTTCTCAGATCAAGTCA
28686	26773	GTGGGTTCTCAGATCAAGTC
28687	26774	TGTGGGTTCTCAGATCAAGT
28688	26775	GTGTGGGTTCTCAGATCAAG
28689	26776	TGTGTGGGTTCTCAGATCAA
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28691	26778	GGTGTGTGGGTTCTCAGATC
28692	26779	TGGTGTGTGGGTTCTCAGAT
28693	26780	GTGGTGTGTGGGTTCTCAGA
28694	26781	AGTGGTGTGTGGGTTCTCAG
28695	26782	AAGTGGTGTGTGGGTTCTCA
28696	26783	TAAGTGGTGTGTGGGTTCTC
28697	26784	CTAAGTGGTGTGTGGGTTCT
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28700	26787	ATCCTAAGTGGTGTGTGGGT
28701	26788	CATCCTAAGTGGTGTGTGGG
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28703	26790	AGCATCCTAAGTGGTGTGTG
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28705	26792	GAAGCATCCTAAGTGGTGTG
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28708	26795	ACAGAAGCATCCTAAGTGGT
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28713	26800	TTCCTACAGAAGCATCCTAA
28714	26801	TTTCCTACAGAAGCATCCTA
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28716	26803	ATTTTCCTACAGAAGCATCC
28717	26804	AATTTTCCTACAGAAGCATC
28718	26805	TAATTTTCCTACAGAAGCAT
28719	26806	CTAATTTTCCTACAGAAGCA
28720	26807	TCTAATTTTCCTACAGAAGC
28721	26808	CTCTAATTTTCCTACAGAAG
28722	26809	ACTCTAATTTTCCTACAGAA
28723	26810	TACTCTAATTTTCCTACAGA
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28725	26812	CATACTCTAATTTTCCTACA
28726	26813	CCATACTCTAATTTTCCTAC
28727	26814	TCCATACTCTAATTTTCCTA
28728	26815	TTCCATACTCTAATTTTCCT
28729	26816	GTTCCATACTCTAATTTTCC
28730	26817	AGTTCCATACTCTAATTTTC
28731	26818	GAGTTCCATACTCTAATTTT
28732	26819	TGAGTTCCATACTCTAATTT
28733	26820	GTGAGTTCCATACTCTAATT
28734	26821	AGTGAGTTCCATACTCTAAT
28735	26822	AAGTGAGTTCCATACTCTAA
28736	26823	CAAGTGAGTTCCATACTCTA
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28739	26826	GGGCAAGTGAGTTCCATACT
28740	26827	TGGGCAAGTGAGTTCCATAC
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28743	26830	GCGTGGGCAAGTGAGTTCCA
28744	26831	AGCGTGGGCAAGTGAGTTCC
28745	26832	AAGCGTGGGCAAGTGAGTTC
28746	26833	AAAGCGTGGGCAAGTGAGTT
28747	26834	GAAAGCGTGGGCAAGTGAGT
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77835	75922	AACAGCAACAACAACAAAAG
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77837	75924	ACAACAGCAACAACAACAAA
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77839	75926	AAACAACAGCAACAACAACA
77840	75927	AAAACAACAGCAACAACAAC
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77842	75929	TCAAAACAACAGCAACAACA
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77844	75931	TCTCAAAACAACAGCAACAA
77845	75932	CTCTCAAAACAACAGCAACA
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77847	75934	ATCTCTCAAAACAACAGCAA
77848	75935	CATCTCTCAAAACAACAGCA
77849	75936	CCATCTCTCAAAACAACAGC
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77851	75938	CTCCATCTCTCAAAACAACA
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77873	75960	CAGTCTGGGTGACAGAGTGA
77874	75961	CCAGTCTGGGTGACAGAGTG
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77876	75963	CTCCAGTCTGGGTGACAGAG
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77878	75965	CACTCCAGTCTGGGTGACAG
77879	75966	GCACTCCAGTCTGGGTGACA
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77894	75981	CGAGATCGCACCACTGCACT
77895	75982	CCGAGATCGCACCACTGCAC

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126975	125062	CAGACCCCATCTCAAAAACA
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126977	125064	GCCAGACCCCATCTCAAAAA
126978	125065	AGCCAGACCCCATCTCAAAA
126979	125066	AAGCCAGACCCCATCTCAAA
126980	125067	AAAGCCAGACCCCATCTCAA
126981	125068	CAAAGCCAGACCCCATCTCA
126982	125069	ACAAAGCCAGACCCCATCTC
126983	125070	AACAAAGCCAGACCCCATCT
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126985	125072	GCAACAAAGCCAGACCCCAT
126986	125073	GGCAACAAAGCCAGACCCCA
126987	125074	GGGCAACAAAGCCAGACCCC
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127020	125107	TGAGCTATGATTGCACTACT
127021	125108	GTGAGCTATGATTGCACTAC
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127023	125110	CAGTGAGCTATGATTGCACT
127024	125111	GCAGTGAGCTATGATTGCAC
127025	125112	AGCAGTGAGCTATGATTGCA
127026	125113	CAGCAGTGAGCTATGATTGC
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127031	125118	CGCAGCAGCAGTGAGCTATG
127032	125119	TCGCAGCAGCAGTGAGCTAT
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127035	125122	AATTCGCAGCAGCAGTGAGC
127036	125123	GAATTCGCAGCAGCAGTGAG
127037	125124	GGAATTCGCAGCAGCAGTGA
127038	125125	AGGAATTCGCAGCAGCAGTG
127039	125126	CAGGAATTCGCAGCAGCAGT
127040	125127	CCAGGAATTCGCAGCAGCAG
127041	125128	ACCAGGAATTCGCAGCAGCA
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28749	26836	GGGAAAGCGTGGGCAAGTGA
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28752	26839	ACAGGGAAAGCGTGGGCAAG
28753	26840	GACAGGGAAAGCGTGGGCAA
28754	26841	AGACAGGGAAAGCGTGGGCA
28755	26842	GAGACAGGGAAAGCGTGGGC
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28757	26844	CTGAGACAGGGAAAGCGTGG
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28768	26855	ACCAACATGGACTGAGACAG
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28770	26857	CTACCAACATGGACTGAGAC
28771	26858	CCTACCAACATGGACTGAGA
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28813	26900	CTGAAGTCTTGTTCAGTGTC
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28815	26902	TGCTGAAGTCTTGTTCAGTG
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77896	75983	GCCGAGATCGCACCACTGCA
77897	75984	AGCCGAGATCGCACCACTGC
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77899	75986	GGAGCCGAGATCGCACCACT
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77918	76005	CAGGAGGTGGAGGTTACAGG
77919	76006	CCAGGAGGTGGAGGTTACAG
77920	76007	CCCAGGAGGTGGAGGTTACA
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77922	76009	AACCCAGGAGGTGGAGGTTA
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77924	76011	TGAACCCAGGAGGTGGAGGT
77925	76012	TTGAACCCAGGAGGTGGAGG
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77940	76027	AGGCAGTAGAATCACTTGAA
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77942	76029	TGAGGCAGTAGAATCACTTG
77943	76030	CTGAGGCAGTAGAATCACTT
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77945	76032	AGCTGAGGCAGTAGAATCAC
77946	76033	AAGCTGAGGCAGTAGAATCA
77947	76034	AAAGCTGAGGCAGTAGAATC
77948	76035	GAAAGCTGAGGCAGTAGAAT
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77950	76037	TGGAAAGCTGAGGCAGTAGA
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77963	76050	AGTCCCAGCTGCTTGGAAAG
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127043	125130	AGACCAGGAATTCGCAGCAG
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127050	125137	TCCTTTGAGACCAGGAATTC
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127060	125147	GGAGGGAGGATCCTTTGAGA
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127081	125168	CACAGTTACTTGAGAGGCTG
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127085	125172	TAGTCACAGTTACTTGAGAG
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127089	125176	CCTGTAGTCACAGTTACTTG
127090	125177	GCCTGTAGTCACAGTTACTT
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127092	125179	GTGCCTGTAGTCACAGTTAC
127093	125180	TGTGCCTGTAGTCACAGTTA
127094	125181	ATGTGCCTGTAGTCACAGTT
127095	125182	CATGTGCCTGTAGTCACAGT
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127097	125184	GGCATGTGCCTGTAGTCACA
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127110	125197	AAGCTGGCAAGGTGGCATGT
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28820	26907	TGTACTGCTGAAGTCTTGTT
28821	26908	ATGTACTGCTGAAGTCTTGT
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28823	26910	ACATGTACTGCTGAAGTCTT
28824	26911	AACATGTACTGCTGAAGTCT
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28827	26914	ACTAACATGTACTGCTGAAG
28828	26915	GACTAACATGTACTGCTGAA
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28831	26918	GAAGACTAACATGTACTGCT
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28845	26932	ATTCCTTCCCTCTGGAAGAC
28846	26933	TATTCCTTCCCTCTGGAAGA
28847	26934	ATATTCCTTCCCTCTGGAAG
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28855	26942	CAACTATTATATTCCTTCCC
28856	26943	TCAACTATTATATTCCTTCC
28857	26944	CTCAACTATTATATTCCTTC
28858	26945	TCTCAACTATTATATTCCTT
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28870	26957	AAGGAATTATTCTCTCAACT
28871	26958	AAAGGAATTATTCTCTCAAC
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28874	26961	AGGAAAGGAATTATTCTCTC
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28886	26973	CTAAAGTCACAGAGGAAAGG
28887	26974	CCTAAAGTCACAGAGGAAAG
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77969	76056	GCCTATAGTCCCAGCTGCTT
77970	76057	CGCCTATAGTCCCAGCTGCT
77971	76058	ACGCCTATAGTCCCAGCTGC
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77973	76060	GCACGCCTATAGTCCCAGCT
77974	76061	CGCACGCCTATAGTCCCAGC
77975	76062	GCGCACGCCTATAGTCCCAG
77976	76063	GGCGCACGCCTATAGTCCCA
77977	76064	TGGCGCACGCCTATAGTCCC
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77979	76066	GGTGGCGCACGCCTATAGTC
77980	76067	TGGTGGCGCACGCCTATAGT
77981	76068	GTGGTGGCGCACGCCTATAG
77982	76069	TGTGGTGGCGCACGCCTATA
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77984	76071	GGTGTGGTGGCGCACGCCTA
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77986	76073	TGGGTGTGGTGGCGCACGCC
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77989	76076	AGCTGGGTGTGGTGGCGCAC
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78021	76108	GAAACCCCGTCTCTACTAAA
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28942	27029	TACAACCTCCTGATATTGTT
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78055	76142	CAGGAGTTCAAGACCAGCCT
78056	76143	TCAGGAGTTCAAGACCAGCC
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78059	76146	AGGTCAGGAGTTCAAGACCA
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78062	76149	CTGAGGTCAGGAGTTCAAGA
78063	76150	CCTGAGGTCAGGAGTTCAAG
78064	76151	ACCTGAGGTCAGGAGTTCAA
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28962	27049	CAGTAATTAAGAATAAAATG
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29032	27119	CACAAGTAGAGTTGAAGTCT

78109	76196	CACGCCTATAATCTCAGCAC
78110	76197	TCACGCCTATAATCTCAGCA
78111	76198	TTCACGCCTATAATCTCAGC
78112	76199	GTTCACGCCTATAATCTCAG
78113	76200	GGTTCACGCCTATAATCTCA
78114	76201	TGGTTCACGCCTATAATCTC
78115	76202	GTGGTTCACGCCTATAATCT
78116	76203	GGTGGTTCACGCCTATAATC
78117	76204	TGGTGGTTCACGCCTATAAT
78118	76205	ATGGTGGTTCACGCCTATAA
78119	76206	CATGGTGGTTCACGCCTATA
78120	76207	GCATGGTGGTTCACGCCTAT
78121	76208	GGCATGGTGGTTCACGCCTA
78122	76209	AGGCATGGTGGTTCACGCCT
78123	76210	CAGGCATGGTGGTTCACGCC
78124	76211	CCAGGCATGGTGGTTCACGC
78125	76212	GCCAGGCATGGTGGTTCACG
78126	76213	GGCCAGGCATGGTGGTTCAC
78127	76214	TGGCCAGGCATGGTGGTTCA
78128	76215	ATGGCCAGGCATGGTGGTTC
78129	76216	TATGGCCAGGCATGGTGGTT
78130	76217	CTATGGCCAGGCATGGTGGT
78131	76218	GCTATGGCCAGGCATGGTGG
78132	76219	TGCTATGGCCAGGCATGGTG
78133	76220	ATGCTATGGCCAGGCATGGT
78134	76221	AATGCTATGGCCAGGCATGG
78135	76222	TAATGCTATGGCCAGGCATG
78136	76223	ATAATGCTATGGCCAGGCAT
78137	76224	AATAATGCTATGGCCAGGCA
78138	76225	AAATAATGCTATGGCCAGGC
78139	76226	GAAATAATGCTATGGCCAGG
78140	76227	AGAAATAATGCTATGGCCAG
78141	76228	TAGAAATAATGCTATGGCCA
78142	76229	TTAGAAATAATGCTATGGCC
78143	76230	ATTAGAAATAATGCTATGGC
78144	76231	TATTAGAAATAATGCTATGG
78145	76232	CTATTAGAAATAATGCTATG
78146	76233	ACTATTAGAAATAATGCTAT
78147	76234	CACTATTAGAAATAATGCTA
78148	76235	TCACTATTAGAAATAATGCT
78149	76236	TTCACTATTAGAAATAATGC
78150	76237	TTTCACTATTAGAAATAATG
78151	76238	TTTTCACTATTAGAAATAAT
78152	76239	TTTTTCACTATTAGAAATAA
78153	76240	ATTTTTCACTATTAGAAATA
78154	76241	AATTTTTCACTATTAGAAAT
78155	76242	CAATTTTTCACTATTAGAAA
78156	76243	CCAATTTTTCACTATTAGAA
78157	76244	TCCAATTTTTCACTATTAGA
78158	76245	TTCCAATTTTTCACTATTAG
78159	76246	TTTCCAATTTTTCACTATTA
78160	76247	GTTTCCAATTTTTCACTATT
78161	76248	TGTTTCCAATTTTTCACTAT
78162	76249	ATGTTTCCAATTTTTCACTA
78163	76250	CATGTTTCCAATTTTTCACT
78164	76251	GCATGTTTCCAATTTTTCAC
78165	76252	AGCATGTTTCCAATTTTTCA
78166	76253	TAGCATGTTTCCAATTTTTC
78167	76254	TTAGCATGTTTCCAATTTTT
78168	76255	CTTAGCATGTTTCCAATTTT
78169	76256	ACTTAGCATGTTTCCAATTT
78170	76257	CACTTAGCATGTTTCCAATT
78171	76258	ACACTTAGCATGTTTCCAAT
78172	76259	GACACTTAGCATGTTTCCAA
78173	76260	AGACACTTAGCATGTTTCCA
78174	76261	TAGACACTTAGCATGTTTCC
78175	76262	ATAGACACTTAGCATGTTTC
78176	76263	GATAGACACTTAGCATGTTT
78177	76264	TGATAGACACTTAGCATGTT
78178	76265	TTGATAGACACTTAGCATGT
78179	76266	ATTGATAGACACTTAGCATG

127256	125343	TTAGGAGGCTGAGGTAGAAA
127257	125344	TTTAGGAGGCTGAGGTAGAA
127258	125345	CTTTAGGAGGCTGAGGTAGA
127259	125346	ACTTTAGGAGGCTGAGGTAG
127260	125347	CACTTTAGGAGGCTGAGGTA
127261	125348	GCACTTTAGGAGGCTGAGGT
127262	125349	AGCACTTTAGGAGGCTGAGG
127263	125350	TAGCACTTTAGGAGGCTGAG
127264	125351	CTAGCACTTTAGGAGGCTGA
127265	125352	CCTAGCACTTTAGGAGGCTG
127266	125353	TCCTAGCACTTTAGGAGGCT
127267	125354	ATCCTAGCACTTTAGGAGGC
127268	125355	AATCCTAGCACTTTAGGAGG
127269	125356	TAATCCTAGCACTTTAGGAG
127270	125357	GTAATCCTAGCACTTTAGGA
127271	125358	TGTAATCCTAGCACTTTAGG
127272	125359	CTGTAATCCTAGCACTTTAG
127273	125360	CCTGTAATCCTAGCACTTTA
127274	125361	GCCTGTAATCCTAGCACTTT
127275	125362	GGCCTGTAATCCTAGCACTT
127276	125363	TGGCCTGTAATCCTAGCACT
127277	125364	CTGGCCTGTAATCCTAGCAC
127278	125365	GCTGGCCTGTAATCCTAGCA
127279	125366	TGCTGGCCTGTAATCCTAGC
127280	125367	GTGCTGGCCTGTAATCCTAG
127281	125368	AGTGCTGGCCTGTAATCCTA
127282	125369	AAGTGCTGGCCTGTAATCCT
127283	125370	AAAGTGCTGGCCTGTAATCC
127284	125371	TAAAGTGCTGGCCTGTAATC
127285	125372	CTAAAGTGCTGGCCTGTAAT
127286	125373	CCTAAAGTGCTGGCCTGTAA
127287	125374	TCCTAAAGTGCTGGCCTGTA
127288	125375	CTCCTAAAGTGCTGGCCTGT
127289	125376	CCTCCTAAAGTGCTGGCCTG
127290	125377	ACCTCCTAAAGTGCTGGCCT
127291	125378	CACCTCCTAAAGTGCTGGCC
127292	125379	GCACCTCCTAAAGTGCTGGC
127293	125380	AGCACCTCCTAAAGTGCTGG
127294	125381	CAGCACCTCCTAAAGTGCTG
127295	125382	CCAGCACCTCCTAAAGTGCT
127296	125383	TCCAGCACCTCCTAAAGTGC
127297	125384	ATCCAGCACCTCCTAAAGTG
127298	125385	CATCCAGCACCTCCTAAAGT
127299	125386	TCATCCAGCACCTCCTAAAG
127300	125387	CTCATCCAGCACCTCCTAAA
127301	125388	GCTCATCCAGCACCTCCTAA
127302	125389	GGCTCATCCAGCACCTCCTA
127303	125390	TGGCTCATCCAGCACCTCCT
127304	125391	ATGGCTCATCCAGCACCTCC
127305	125392	GATGGCTCATCCAGCACCTC
127306	125393	TGATGGCTCATCCAGCACCT
127307	125394	GTGATGGCTCATCCAGCACC
127308	125395	TGTGATGGCTCATCCAGCAC
127309	125396	GTGTGATGGCTCATCCAGCA
127310	125397	GGTGTGATGGCTCATCCAGC
127311	125398	GGGTGTGATGGCTCATCCAG
127312	125399	TGGGTGTGATGGCTCATCCA
127313	125400	CTGGGTGTGATGGCTCATCC
127314	125401	GCTGGGTGTGATGGCTCATC
127315	125402	GGCTGGGTGTGATGGCTCAT
127316	125403	TGGCTGGGTGTGATGGCTCA
127317	125404	TTGGCTGGGTGTGATGGCTC
127318	125405	CTTGGCTGGGTGTGATGGCT
127319	125406	ACTTGGCTGGGTGTGATGGC
127320	125407	GACTTGGCTGGGTGTGATGG
127321	125408	TGACTTGGCTGGGTGTGATG
127322	125409	ATGACTTGGCTGGGTGTGAT
127323	125410	TATGACTTGGCTGGGTGTGA
127324	125411	CTATGACTTGGCTGGGTGTG
127325	125412	CCTATGACTTGGCTGGGTGT
127326	125413	ACCTATGACTTGGCTGGGTG

29033	27120	ACACAAGTAGAGTTGAAGTC
29034	27121	AACACAAGTAGAGTTGAAGT
29035	27122	CAACACAAGTAGAGTTGAAG
29036	27123	CCAACACAAGTAGAGTTGAA
29037	27124	CCCAACACAAGTAGAGTTGA
29038	27125	ACCCAACACAAGTAGAGTTG
29039	27126	AACCCAACACAAGTAGAGTT
29040	27127	TAACCCAACACAAGTAGAGT
29041	27128	GTAACCCAACACAAGTAGAG
29042	27129	GGTAACCCAACACAAGTAGA
29043	27130	GGGTAACCCAACACAAGTAG
29044	27131	GGGGTAACCCAACACAAGTA
29045	27132	AGGGGTAACCCAACACAAGT
29046	27133	GAGGGGTAACCCAACACAAG
29047	27134	AGAGGGGTAACCCAACACAA
29048	27135	CAGAGGGGTAACCCAACACA
29049	27136	GCAGAGGGGTAACCCAACAC
29050	27137	AGCAGAGGGGTAACCCAACA
29051	27138	AAGCAGAGGGGTAACCCAAC
29052	27139	TAAGCAGAGGGGTAACCCAA
29053	27140	TTAAGCAGAGGGGTAACCCA
29054	27141	TTTAAGCAGAGGGGTAACCC
29055	27142	TTTTAAGCAGAGGGGTAACC
29056	27143	TTTTTAAGCAGAGGGGTAAC
29057	27144	ATTTTTAAGCAGAGGGGTAA
29058	27145	GATTTTTAAGCAGAGGGGTA
29059	27146	TGATTTTTAAGCAGAGGGGT
29060	27147	GTGATTTTTAAGCAGAGGGG
29061	27148	GGTGATTTTTAAGCAGAGGG
29062	27149	GGGTGATTTTTAAGCAGAGG
29063	27150	AGGGTGATTTTTAAGCAGAG
29064	27151	TAGGGTGATTTTTAAGCAGA
29065	27152	ATAGGGTGATTTTTAAGCAG
29066	27153	AATAGGGTGATTTTTAAGCA
29067	27154	GAATAGGGTGATTTTTAAGC
29068	27155	GGAATAGGGTGATTTTTAAG
29069	27156	GGGAATAGGGTGATTTTTAA
29070	27157	TGGGAATAGGGTGATTTTTA
29071	27158	TTGGGAATAGGGTGATTTTT
29072	27159	CTTGGGAATAGGGTGATTTT
29073	27160	GCTTGGGAATAGGGTGATTT
29074	27161	GGCTTGGGAATAGGGTGATT
29075	27162	AGGCTTGGGAATAGGGTGAT
29076	27163	CAGGCTTGGGAATAGGGTGA
29077	27164	TCAGGCTTGGGAATAGGGTG
29078	27165	CTCAGGCTTGGGAATAGGGT
29079	27166	CCTCAGGCTTGGGAATAGGG
29080	27167	CCCTCAGGCTTGGGAATAGG
29081	27168	TCCCTCAGGCTTGGGAATAG
29082	27169	CTCCCTCAGGCTTGGGAATA
29083	27170	ACTCCCTCAGGCTTGGGAAT
29084	27171	GACTCCCTCAGGCTTGGGAA
29085	27172	AGACTCCCTCAGGCTTGGGA
29086	27173	TAGACTCCCTCAGGCTTGGG
29087	27174	GTAGACTCCCTCAGGCTTGG
29088	27175	GGTAGACTCCCTCAGGCTTG
29089	27176	AGGTAGACTCCCTCAGGCTT
29090	27177	AAGGTAGACTCCCTCAGGCT
29091	27178	GAAGGTAGACTCCCTCAGGC
29092	27179	TGAAGGTAGACTCCCTCAGG
29093	27180	TTGAAGGTAGACTCCCTCAG
29094	27181	TTTGAAGGTAGACTCCCTCA
29095	27182	CTTTGAAGGTAGACTCCCTC
29096	27183	GCTTTGAAGGTAGACTCCCT
29097	27184	AGCTTTGAAGGTAGACTCCC
29098	27185	AAGCTTTGAAGGTAGACTCC
29099	27186	AAAGCTTTGAAGGTAGACTC
29100	27187	GAAAGCTTTGAAGGTAGACT
29101	27188	AGAAAGCTTTGAAGGTAGAC
29102	27189	TAGAAAGCTTTGAAGGTAGA
29103	27190	ATAGAAAGCTTTGAAGGTAG

78180	76267	TATTGATAGACACTTAGCAT
78181	76268	ATATTGATAGACACTTAGCA
78182	76269	TATATTGATAGACACTTAGC
78183	76270	CTATATTGATAGACACTTAG
78184	76271	GCTATATTGATAGACACTTA
78185	76272	TGCTATATTGATAGACACTT
78186	76273	ATGCTATATTGATAGACACT
78187	76274	CATGCTATATTGATAGACAC
78188	76275	TCATGCTATATTGATAGACA
78189	76276	CTCATGCTATATTGATAGAC
78190	76277	ACTCATGCTATATTGATAGA
78191	76278	AACTCATGCTATATTGATAG
78192	76279	TAACTCATGCTATATTGATA
78193	76280	CTAACTCATGCTATATTGAT
78194	76281	TCTAACTCATGCTATATTGA
78195	76282	ATCTAACTCATGCTATATTG
78196	76283	AATCTAACTCATGCTATATT
78197	76284	AAATCTAACTCATGCTATAT
78198	76285	TAAATCTAACTCATGCTATA
78199	76286	ATAAATCTAACTCATGCTAT
78200	76287	CATAAATCTAACTCATGCTA
78201	76288	TCATAAATCTAACTCATGCT
78202	76289	ATCATAAATCTAACTCATGC
78203	76290	CATCATAAATCTAACTCATG
78204	76291	ACATCATAAATCTAACTCAT
78205	76292	GACATCATAAATCTAACTCA
78206	76293	TGACATCATAAATCTAACTC
78207	76294	GTGACATCATAAATCTAACT
78208	76295	GGTGACATCATAAATCTAAC
78209	76296	TGGTGACATCATAAATCTAA
78210	76297	ATGGTGACATCATAAATCTA
78211	76298	AATGGTGACATCATAAATCT
78212	76299	GAATGGTGACATCATAAATC
78213	76300	TGAATGGTGACATCATAAAT
78214	76301	TTGAATGGTGACATCATAAA
78215	76302	ATTGAATGGTGACATCATAA
78216	76303	AATTGAATGGTGACATCATA
78217	76304	CAATTGAATGGTGACATCAT
78218	76305	TCAATTGAATGGTGACATCA
78219	76306	TTCAATTGAATGGTGACATC
78220	76307	TTTCAATTGAATGGTGACAT
78221	76308	GTTTCAATTGAATGGTGACA
78222	76309	TGTTTCAATTGAATGGTGAC
78223	76310	GTGTTTCAATTGAATGGTGA
78224	76311	AGTGTTTCAATTGAATGGTG
78225	76312	TAGTGTTTCAATTGAATGGT
78226	76313	GTAGTGTTTCAATTGAATGG
78227	76314	TGTAGTGTTTCAATTGAATG
78228	76315	ATGTAGTGTTTCAATTGAAT
78229	76316	TATGTAGTGTTTCAATTGAA
78230	76317	ATATGTAGTGTTTCAATTGA
78231	76318	GATATGTAGTGTTTCAATTG
78232	76319	AGATATGTAGTGTTTCAATT
78233	76320	GAGATATGTAGTGTTTCAAT
78234	76321	GGAGATATGTAGTGTTTCAA
78235	76322	GGGAGATATGTAGTGTTTCA
78236	76323	TGGGAGATATGTAGTGTTTC
78237	76324	TTGGGAGATATGTAGTGTTT
78238	76325	TTTGGGAGATATGTAGTGTT
78239	76326	TTTTGGGAGATATGTAGTGT
78240	76327	TTTTTGGGAGATATGTAGTG
78241	76328	CTTTTTGGGAGATATGTAGT
78242	76329	TCTTTTTGGGAGATATGTAG
78243	76330	TTCTTTTTGGGAGATATGTA
78244	76331	ATTCTTTTTGGGAGATATGT
78245	76332	CATTCTTTTTGGGAGATATG
78246	76333	CCATTCTTTTTGGGAGATAT
78247	76334	ACCATTCTTTTTGGGAGATA
78248	76335	CACCATTCTTTTTGGGAGAT
78249	76336	ACACCATTCTTTTTGGGAGA
78250	76337	AACACCATTCTTTTTGGGAG

127327	125414	AACCTATGACTTGGCTGGGT
127328	125415	AAACCTATGACTTGGCTGGG
127329	125416	AAAACCTATGACTTGGCTGG
127330	125417	AAAAACCTATGACTTGGCTG
127331	125418	AAAAAACCTATGACTTGGCT
127332	125419	AAAAAAACCTATGACTTGGC
127333	125420	CAAAAAAACCTATGACTTGG
127334	125421	ACAAAAAAACCTATGACTTG
127335	125422	AACAAAAAAACCTATGACTT
127336	125423	AAACAAAAAAACCTATGACT
127337	125424	CAAACAAAAAAACCTATGAC
127338	125425	ACAAACAAAAAAACCTATGA
127339	125426	AACAAACAAAAAAACCTATG
127340	125427	AAACAAACAAAAAAACCTAT
127341	125428	CAAACAAACAAAAAAACCTA
127342	125429	ACAAACAAACAAAAAAACCT
127343	125430	AACAAACAAACAAAAAAACC
127344	125431	AAACAAACAAACAAAAAAAC
127345	125432	AAAACAAACAAACAAAAAAA
127346	125433	AAAAACAAACAAACAAAAAA
127347	125434	AAAAAACAAACAAACAAAAA
127348	125435	CAAAAAACAAACAAACAAAA
127349	125436	TCAAAAAACAAACAAACAAA
127350	125437	CTCAAAAAACAAACAAACAA
127351	125438	TCTCAAAAAACAAACAAACA
127352	125439	GTCTCAAAAAACAAACAAAC
127353	125440	TGTCTCAAAAAACAAACAAA
127354	125441	CTGTCTCAAAAAACAAACAA
127355	125442	ACTGTCTCAAAAAACAAACA
127356	125443	CACTGTCTCAAAAAACAAAC
127357	125444	ACACTGTCTCAAAAAACAAA
127358	125445	GACACTGTCTCAAAAAACAA
127359	125446	AGACACTGTCTCAAAAAACA
127360	125447	TAGACACTGTCTCAAAAAAC
127361	125448	TTAGACACTGTCTCAAAAAA
127362	125449	GTTAGACACTGTCTCAAAAA
127363	125450	AGTTAGACACTGTCTCAAAA
127364	125451	GAGTTAGACACTGTCTCAAA
127365	125452	AGAGTTAGACACTGTCTCAA
127366	125453	CAGAGTTAGACACTGTCTCA
127367	125454	ACAGAGTTAGACACTGTCTC
127368	125455	GACAGAGTTAGACACTGTCT
127369	125456	TGACAGAGTTAGACACTGTC
127370	125457	GTGACAGAGTTAGACACTGT
127371	125458	GGTGACAGAGTTAGACACTG
127372	125459	GGGTGACAGAGTTAGACACT
127373	125460	TGGGTGACAGAGTTAGACAC
127374	125461	TTGGGTGACAGAGTTAGACA
127375	125462	CTTGGGTGACAGAGTTAGAC
127376	125463	GCTTGGGTGACAGAGTTAGA
127377	125464	AGCTTGGGTGACAGAGTTAG
127378	125465	CAGCTTGGGTGACAGAGTTA
127379	125466	CCAGCTTGGGTGACAGAGTT
127380	125467	TCCAGCTTGGGTGACAGAGT
127381	125468	CTCCAGCTTGGGTGACAGAG
127382	125469	ACTCCAGCTTGGGTGACAGA
127383	125470	CACTCCAGCTTGGGTGACAG
127384	125471	GCACTCCAGCTTGGGTGACA
127385	125472	TGCACTCCAGCTTGGGTGAC
127386	125473	CTGCACTCCAGCTTGGGTGA
127387	125474	ACTGCACTCCAGCTTGGGTG
127388	125475	CACTGCACTCCAGCTTGGGT
127389	125476	CCACTGCACTCCAGCTTGGG
127390	125477	GCCACTGCACTCCAGCTTGG
127391	125478	TGCCACTGCACTCCAGCTTG
127392	125479	ATGCCACTGCACTCCAGCTT
127393	125480	CATGCCACTGCACTCCAGCT
127394	125481	TCATGCCACTGCACTCCAGC
127395	125482	ATCATGCCACTGCACTCCAG
127396	125483	AATCATGCCACTGCACTCCA
127397	125484	AAATCATGCCACTGCACTCC

29104	27191	CATAGAAAGCTTTGAAGGTA
29105	27192	TCATAGAAAGCTTTGAAGGT
29106	27193	GTCATAGAAAGCTTTGAAGG
29107	27194	GGTCATAGAAAGCTTTGAAG
29108	27195	AGGTCATAGAAAGCTTTGAA
29109	27196	TAGGTCATAGAAAGCTTTGA
29110	27197	TTAGGTCATAGAAAGCTTTG
29111	27198	ATTAGGTCATAGAAAGCTTT
29112	27199	GATTAGGTCATAGAAAGCTT
29113	27200	GGATTAGGTCATAGAAAGCT
29114	27201	TGGATTAGGTCATAGAAAGC
29115	27202	TTGGATTAGGTCATAGAAAG
29116	27203	CTTGGATTAGGTCATAGAAA
29117	27204	CCTTGGATTAGGTCATAGAA
29118	27205	GCCTTGGATTAGGTCATAGA
29119	27206	GGCCTTGGATTAGGTCATAG
29120	27207	AGGCCTTGGATTAGGTCATA
29121	27208	CAGGCCTTGGATTAGGTCAT
29122	27209	ACAGGCCTTGGATTAGGTCA
29123	27210	GACAGGCCTTGGATTAGGTC
29124	27211	TGACAGGCCTTGGATTAGGT
29125	27212	TTGACAGGCCTTGGATTAGG
29126	27213	TTTGACAGGCCTTGGATTAG
29127	27214	GTTTGACAGGCCTTGGATTA
29128	27215	AGTTTGACAGGCCTTGGATT
29129	27216	AAGTTTGACAGGCCTTGGAT
29130	27217	GAAGTTTGACAGGCCTTGGA
29131	27218	CGAAGTTTGACAGGCCTTGG
29132	27219	ACGAAGTTTGACAGGCCTTG
29133	27220	TACGAAGTTTGACAGGCCTT
29134	27221	TTACGAAGTTTGACAGGCCT
29135	27222	TTTACGAAGTTTGACAGGCC
29136	27223	CTTTACGAAGTTTGACAGGC
29137	27224	CCTTTACGAAGTTTGACAGG
29138	27225	CCCTTTACGAAGTTTGACAG
29139	27226	GCCCTTTACGAAGTTTGACA
29140	27227	GGCCCTTTACGAAGTTTGAC
29141	27228	TGGCCCTTTACGAAGTTTGA
29142	27229	CTGGCCCTTTACGAAGTTTG
29143	27230	TCTGGCCCTTTACGAAGTTT
29144	27231	ATCTGGCCCTTTACGAAGTT
29145	27232	TATCTGGCCCTTTACGAAGT
29146	27233	CTATCTGGCCCTTTACGAAG
29147	27234	ACTATCTGGCCCTTTACGAA
29148	27235	TACTATCTGGCCCTTTACGA
29149	27236	TTACTATCTGGCCCTTTACG
29150	27237	TTTACTATCTGGCCCTTTAC
29151	27238	ATTTACTATCTGGCCCTTTA
29152	27239	AATTTACTATCTGGCCCTTT
29153	27240	AAATTTACTATCTGGCCCTT
29154	27241	CAAATTTACTATCTGGCCCT
29155	27242	ACAAATTTACTATCTGGCCC
29156	27243	AACAAATTTACTATCTGGCC
29157	27244	AAACAAATTTACTATCTGGC
29158	27245	AAAACAAATTTACTATCTGG
29159	27246	AAAAACAAATTTACTATCTG
29160	27247	AAAAAACAAATTTACTATCT
29161	27248	AAAAAAACAAATTTACTATC
29162	27249	AAAAAAAACAAATTTACTAT
29163	27250	AAAAAAAAACAAATTTACTA
29164	27251	AAAAAAAAAACAAATTTACT
29165	27252	AAAAAAAAAAACAAATTTAC
29166	27253	AAAAAAAAAAAACAAATTTA
29167	27254	CAAAAAAAAAAAACAAATTT
29168	27255	TCAAAAAAAAAAAACAAATT
29169	27256	CTCAAAAAAAAAAAACAAAT
29170	27257	TCTCAAAAAAAAAAAACAAA
29171	27258	ATCTCAAAAAAAAAAAACAA
29172	27259	CATCTCAAAAAAAAAAAACA
29173	27260	CCATCTCAAAAAAAAAAAAC
29174	27261	TCCATCTCAAAAAAAAAAAA

78251	76338	GAACACCATTCTTTTTGGGA
78252	76339	GGAACACCATTCTTTTTGGG
78253	76340	TGGAACACCATTCTTTTTGG
78254	76341	TTGGAACACCATTCTTTTTG
78255	76342	ATTGGAACACCATTCTTTTT
78256	76343	TATTGGAACACCATTCTTTT
78257	76344	ATATTGGAACACCATTCTTT
78258	76345	CATATTGGAACACCATTCTT
78259	76346	CCATATTGGAACACCATTCT
78260	76347	TCCATATTGGAACACCATTC
78261	76348	TTCCATATTGGAACACCATT
78262	76349	TTTCCATATTGGAACACCAT
78263	76350	CTTTCCATATTGGAACACCA
78264	76351	TCTTTCCATATTGGAACACC
78265	76352	ATCTTTCCATATTGGAACAC
78266	76353	TATCTTTCCATATTGGAACA
78267	76354	ATATCTTTCCATATTGGAAC
78268	76355	GATATCTTTCCATATTGGAA
78269	76356	AGATATCTTTCCATATTGGA
78270	76357	TAGATATCTTTCCATATTGG
78271	76358	TTAGATATCTTTCCATATTG
78272	76359	CTTAGATATCTTTCCATATT
78273	76360	TCTTAGATATCTTTCCATAT
78274	76361	ATCTTAGATATCTTTCCATA
78275	76362	AATCTTAGATATCTTTCCAT
78276	76363	AAATCTTAGATATCTTTCCA
78277	76364	TAAATCTTAGATATCTTTCC
78278	76365	ATAAATCTTAGATATCTTTC
78279	76366	AATAAATCTTAGATATCTTT
78280	76367	TAATAAATCTTAGATATCTT
78281	76368	TTAATAAATCTTAGATATCT
78282	76369	CTTAATAAATCTTAGATATC
78283	76370	TCTTAATAAATCTTAGATAT
78284	76371	CTCTTAATAAATCTTAGATA
78285	76372	TCTCTTAATAAATCTTAGAT
78286	76373	TTCTCTTAATAAATCTTAGA
78287	76374	TTTCTCTTAATAAATCTTAG
78288	76375	TTTTCTCTTAATAAATCTTA
78289	76376	TTTTTCTCTTAATAAATCTT
78290	76377	CTTTTTCTCTTAATAAATCT
78291	76378	GCTTTTTCTCTTAATAAATC
78292	76379	TGCTTTTTCTCTTAATAAAT
78293	76380	GTGCTTTTTCTCTTAATAAA
78294	76381	TGTGCTTTTTCTCTTAATAA
78295	76382	ATGTGCTTTTTCTCTTAATA
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78297	76384	CAATGTGCTTTTTCTCTTAA
78298	76385	GCAATGTGCTTTTTCTCTTA
78299	76386	TGCAATGTGCTTTTTCTCTT
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78301	76388	TCTGCAATGTGCTTTTTCTC
78302	76389	TTCTGCAATGTGCTTTTTCT
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78304	76391	TGTTCTGCAATGTGCTTTTT
78305	76392	GTGTTCTGCAATGTGCTTTT
78306	76393	AGTGTTCTGCAATGTGCTTT
78307	76394	CAGTGTTCTGCAATGTGCTT
78308	76395	CCAGTGTTCTGCAATGTGCT
78309	76396	CCCAGTGTTCTGCAATGTGC
78310	76397	TCCCAGTGTTCTGCAATGTG
78311	76398	ATCCCAGTGTTCTGCAATGT
78312	76399	GATCCCAGTGTTCTGCAATG
78313	76400	GGATCCCAGTGTTCTGCAAT
78314	76401	AGGATCCCAGTGTTCTGCAA
78315	76402	TAGGATCCCAGTGTTCTGCA
78316	76403	ATAGGATCCCAGTGTTCTGC
78317	76404	AATAGGATCCCAGTGTTCTG
78318	76405	AAATAGGATCCCAGTGTTCT
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78320	76407	GCAAATAGGATCCCAGTGTT
78321	76408	AGCAAATAGGATCCCAGTGT

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127399	125486	TGAAATCATGCCACTGCACT
127400	125487	CTGAAATCATGCCACTGCAC
127401	125488	GCTGAAATCATGCCACTGCA
127402	125489	AGCTGAAATCATGCCACTGC
127403	125490	GAGCTGAAATCATGCCACTG
127404	125491	TGAGCTGAAATCATGCCACT
127405	125492	CTGAGCTGAAATCATGCCAC
127406	125493	ACTGAGCTGAAATCATGCCA
127407	125494	CACTGAGCTGAAATCATGCC
127408	125495	GCACTGAGCTGAAATCATGC
127409	125496	TGCACTGAGCTGAAATCATG
127410	125497	CTGCACTGAGCTGAAATCAT
127411	125498	ACTGCACTGAGCTGAAATCA
127412	125499	GACTGCACTGAGCTGAAATC
127413	125500	AGACTGCACTGAGCTGAAAT
127414	125501	GAGACTGCACTGAGCTGAAA
127415	125502	AGAGACTGCACTGAGCTGAA
127416	125503	TAGAGACTGCACTGAGCTGA
127417	125504	GTAGAGACTGCACTGAGCTG
127418	125505	GGTAGAGACTGCACTGAGCT
127419	125506	TGGTAGAGACTGCACTGAGC
127420	125507	TTGGTAGAGACTGCACTGAG
127421	125508	ATTGGTAGAGACTGCACTGA
127422	125509	AATTGGTAGAGACTGCACTG
127423	125510	CAATTGGTAGAGACTGCACT
127424	125511	CCAATTGGTAGAGACTGCAC
127425	125512	CCCAATTGGTAGAGACTGCA
127426	125513	GCCCAATTGGTAGAGACTGC
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127435	125522	ACCACCTAAGCCCAATTGGT
127436	125523	GACCACCTAAGCCCAATTGG
127437	125524	GGACCACCTAAGCCCAATTG
127438	125525	AGGACCACCTAAGCCCAATT
127439	125526	GAGGACCACCTAAGCCCAAT
127440	125527	GGAGGACCACCTAAGCCCAA
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127442	125529	TGGGAGGACCACCTAAGCCC
127443	125530	GTGGGAGGACCACCTAAGCC
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127445	125532	AGGTGGGAGGACCACCTAAG
127446	125533	GAGGTGGGAGGACCACCTAA
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127448	125535	TTGAGGTGGGAGGACCACCT
127449	125536	GTTGAGGTGGGAGGACCACC
127450	125537	GGTTGAGGTGGGAGGACCAC
127451	125538	AGGTTGAGGTGGGAGGACCA
127452	125539	GAGGTTGAGGTGGGAGGACC
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127464	125551	CCAGCTACTTGGGAGGTTGA
127465	125552	CCCAGCTACTTGGGAGGTTG
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29185	27272	AAGAGCAAAACTCCATCTCA
29186	27273	CAAGAGCAAAACTCCATCTC
29187	27274	ACAAGAGCAAAACTCCATCT
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29189	27276	TGACAAGAGCAAAACTCCAT
29190	27277	GTGACAAGAGCAAAACTCCA
29191	27278	GGTGACAAGAGCAAAACTCC
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29193	27280	TGGGTGACAAGAGCAAAACT
29194	27281	CTGGGTGACAAGAGCAAAAC
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29203	27290	CACTCCAGCCTGGGTGACAA
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29216	27303	GATGGCACCATTGCACTCCA
29217	27304	AGATGGCACCATTGCACTCC
29218	27305	AAGATGGCACCATTGCACTC
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29225	27312	GTGAGCCAAGATGGCACCAT
29226	27313	AGTGAGCCAAGATGGCACCA
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29237	27324	GCAGAGGTTGCAGTGAGCCA
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78388	76475	TTGAACCCGGGAGGCGGAGG
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127476	125563	GCACCTTTAGTCCCAGCTAC
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127490	125577	AGGTATGGTGGCGCGCACCT
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78396	76483	AGAATCGCTTGAACCCGGGA
78397	76484	GAGAATCGCTTGAACCCGGG
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78399	76486	AGGAGAATCGCTTGAACCCG
78400	76487	CAGGAGAATCGCTTGAACCC
78401	76488	GCAGGAGAATCGCTTGAACC
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78405	76492	TGAGGCAGGAGAATCGCTTG
78406	76493	CTGAGGCAGGAGAATCGCTT
78407	76494	GCTGAGGCAGGAGAATCGCT
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78409	76496	AGGCTGAGGCAGGAGAATCG
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78413	76500	CAGGAGGCTGAGGCAGGAGA
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78415	76502	CTCAGGAGGCTGAGGCAGGA
78416	76503	ACTCAGGAGGCTGAGGCAGG
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78422	76509	GCAGCTACTCAGGAGGCTGA
78423	76510	GGCAGCTACTCAGGAGGCTG
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78425	76512	GTGGCAGCTACTCAGGAGGC
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78429	76516	CATGGTGGCAGCTACTCAGG
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78433	76520	TGGGCATGGTGGCAGCTACT
78434	76521	CTGGGCATGGTGGCAGCTAC
78435	76522	GCTGGGCATGGTGGCAGCTA
78436	76523	AGCTGGGCATGGTGGCAGCT
78437	76524	TAGCTGGGCATGGTGGCAGC
78438	76525	TTAGCTGGGCATGGTGGCAG
78439	76526	ATTAGCTGGGCATGGTGGCA
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78442	76529	AAAATTAGCTGGGCATGGTG
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78445	76532	ACAAAAATTAGCTGGGCATG
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78455	76542	TACTAAAAACACAAAAATTA
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78459	76546	TCTCTACTAAAAACACAAAA
78460	76547	TTCTCTACTAAAAACACAAA
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127542	125629	TTGAGCTCAGGAATTCGAAA
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127546	125633	CTGCTTGAGCTCAGGAATTC
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127552	125639	GGCAGACTGCTTGAGCTCAG
127553	125640	AGGCAGACTGCTTGAGCTCA
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127558	125645	AAGGCAGGCAGACTGCTTGA
127559	125646	CAAGGCAGGCAGACTGCTTG
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127562	125649	AGTCAAGGCAGGCAGACTGC
127563	125650	GAGTCAAGGCAGGCAGACTG
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127737	125824	GGACAGAAGTCTACTTTAAA
127738	125825	GGGACAGAAGTCTACTTTAA
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127743	125830	TACAGGGGACAGAAGTCTAC
127744	125831	TTACAGGGGACAGAAGTCTA
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78736	76823	TGAACCTGGAAGGCAGAGGT
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29612	27699	GAGCCAAGATTGCACCACTG
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29615	27702	AGTGAGCCAAGATTGCACCA
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29784	27871	GAGGTGGGCAGATCACCTGA
29785	27872	AGAGGTGGGCAGATCACCTG
29786	27873	CAGAGGTGGGCAGATCACCT
29787	27874	GCAGAGGTGGGCAGATCACC
29788	27875	GGCAGAGGTGGGCAGATCAC
29789	27876	AGGCAGAGGTGGGCAGATCA
29790	27877	GAGGCAGAGGTGGGCAGATC
29791	27878	GGAGGCAGAGGTGGGCAGAT
29792	27879	GGGAGGCAGAGGTGGGCAGA
29793	27880	TGGGAGGCAGAGGTGGGCAG
29794	27881	TTGGGAGGCAGAGGTGGGCA
29795	27882	TTTGGGAGGCAGAGGTGGGC
29796	27883	CTTTGGGAGGCAGAGGTGGG
29797	27884	ACTTTGGGAGGCAGAGGTGG
29798	27885	CACTTTGGGAGGCAGAGGTG
29799	27886	GCACTTTGGGAGGCAGAGGT
29800	27887	AGCACTTTGGGAGGCAGAGG
29801	27888	CAGCACTTTGGGAGGCAGAG
29802	27889	CCAGCACTTTGGGAGGCAGA
29803	27890	CCCAGCACTTTGGGAGGCAG
29804	27891	TCCCAGCACTTTGGGAGGCA
29805	27892	ATCCCAGCACTTTGGGAGGC
29806	27893	AATCCCAGCACTTTGGGAGG
29807	27894	TAATCCCAGCACTTTGGGAG
29808	27895	GTAATCCCAGCACTTTGGGA
29809	27896	TGTAATCCCAGCACTTTGGG
29810	27897	CTGTAATCCCAGCACTTTGG
29811	27898	CCTGTAATCCCAGCACTTTG
29812	27899	ACCTGTAATCCCAGCACTTT
29813	27900	CACCTGTAATCCCAGCACTT

78890	76977	CAAGGTGGGTGGATCACCTG
78891	76978	CCAAGGTGGGTGGATCACCT
78892	76979	GCCAAGGTGGGTGGATCACC
78893	76980	GGCCAAGGTGGGTGGATCAC
78894	76981	AGGCCAAGGTGGGTGGATCA
78895	76982	GAGGCCAAGGTGGGTGGATC
78896	76983	AGAGGCCAAGGTGGGTGGAT
78897	76984	GAGAGGCCAAGGTGGGTGGA
78898	76985	TGAGAGGCCAAGGTGGGTGG
78899	76986	TTGAGAGGCCAAGGTGGGTG
78900	76987	TTTGAGAGGCCAAGGTGGGT
78901	76988	CTTTGAGAGGCCAAGGTGGG
78902	76989	ACTTTGAGAGGCCAAGGTGG
78903	76990	CACTTTGAGAGGCCAAGGTG
78904	76991	GCACTTTGAGAGGCCAAGGT
78905	76992	AGCACTTTGAGAGGCCAAGG
78906	76993	CAGCACTTTGAGAGGCCAAG
78907	76994	CCAGCACTTTGAGAGGCCAA
78908	76995	CCCAGCACTTTGAGAGGCCA
78909	76996	TCCCAGCACTTTGAGAGGCC
78910	76997	ATCCCAGCACTTTGAGAGGC
78911	76998	AATCCCAGCACTTTGAGAGG
78912	76999	TAATCCCAGCACTTTGAGAG
78913	77000	GTAATCCCAGCACTTTGAGA
78914	77001	TGTAATCCCAGCACTTTGAG
78915	77002	CTGTAATCCCAGCACTTTGA
78916	77003	CCTGTAATCCCAGCACTTTG
78917	77004	GCCTGTAATCCCAGCACTTT
78918	77005	TGCCTGTAATCCCAGCACTT
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78921	77008	TCATGCCTGTAATCCCAGCA
78922	77009	CTCATGCCTGTAATCCCAGC
78923	77010	GCTCATGCCTGTAATCCCAG
78924	77011	GGCTCATGCCTGTAATCCCA
78925	77012	TGGCTCATGCCTGTAATCCC
78926	77013	GTGGCTCATGCCTGTAATCC
78927	77014	AGTGGCTCATGCCTGTAATC
78928	77015	CAGTGGCTCATGCCTGTAAT
78929	77016	GCAGTGGCTCATGCCTGTAA
78930	77017	CGCAGTGGCTCATGCCTGTA
78931	77018	GCGCAGTGGCTCATGCCTGT
78932	77019	GGCGCAGTGGCTCATGCCTG
78933	77020	GGGCGCAGTGGCTCATGCCT
78934	77021	CGGGCGCAGTGGCTCATGCC
78935	77022	CCGGGCGCAGTGGCTCATGC
78936	77023	GCCGGGCGCAGTGGCTCATG
78937	77024	AGCCGGGCGCAGTGGCTCAT
78938	77025	CAGCCGGGCGCAGTGGCTCA
78939	77026	TCAGCCGGGCGCAGTGGCTC
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78942	77029	GTTTCAGCCGGGCGCAGTGG
78943	77030	AGTTTCAGCCGGGCGCAGTG
78944	77031	GAGTTTCAGCCGGGCGCAGT
78945	77032	AGAGTTTCAGCCGGGCGCAG
78946	77033	AAGAGTTTCAGCCGGGCGCA
78947	77034	AAAGAGTTTCAGCCGGGCGC
78948	77035	AAAAGAGTTTCAGCCGGGCG
78949	77036	AAAAAGAGTTTCAGCCGGGC
78950	77037	AAAAAAGAGTTTCAGCCGGG
78951	77038	AAAAAAAGAGTTTCAGCCGG
78952	77039	AAAAAAAAGAGTTTCAGCCG
78953	77040	AAAAAAAAAGAGTTTCAGCC
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78955	77042	AGAAAAAAAAAGAGTTTCAG
78956	77043	AAGAAAAAAAAAGAGTTTCA
78957	77044	AAAGAAAAAAAAAGAGTTTC
78958	77045	AAAAGAAAAAAAAAGAGTTT
78959	77046	TAAAAGAAAAAAAAAGAGTT
78960	77047	TTAAAAGAAAAAAAAAGAGT

128037	126124	ATGAAAGGAAAAGAATGTCA
128038	126125	GATGAAAGGAAAAGAATGTC
128039	126126	GGATGAAAGGAAAAGAATGT
128040	126127	GGGATGAAAGGAAAAGAATG
128041	126128	AGGGATGAAAGGAAAAGAAT
128042	126129	AAGGGATGAAAGGAAAAGAA
128043	126130	GAAGGGATGAAAGGAAAAGA
128044	126131	AGAAGGGATGAAAGGAAAAG
128045	126132	AAGAAGGGATGAAAGGAAAA
128046	126133	GAAGAAGGGATGAAAGGAAA
128047	126134	TGAAGAAGGGATGAAAGGAA
128048	126135	TTGAAGAAGGGATGAAAGGA
128049	126136	ATTGAAGAAGGGATGAAAGG
128050	126137	AATTGAAGAAGGGATGAAAG
128051	126138	TAATTGAAGAAGGGATGAAA
128052	126139	ATAATTGAAGAAGGGATGAA
128053	126140	AATAATTGAAGAAGGGATGA
128054	126141	CAATAATTGAAGAAGGGATG
128055	126142	GCAATAATTGAAGAAGGGAT
128056	126143	GGCAATAATTGAAGAAGGGA
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128058	126145	CAGGCAATAATTGAAGAAGG
128059	126146	CCAGGCAATAATTGAAGAAG
128060	126147	TCCAGGCAATAATTGAAGAA
128061	126148	TTCCAGGCAATAATTGAAGA
128062	126149	ATTCCAGGCAATAATTGAAG
128063	126150	TATTCCAGGCAATAATTGAA
128064	126151	ATATTCCAGGCAATAATTGA
128065	126152	AATATTCCAGGCAATAATTG
128066	126153	AAATATTCCAGGCAATAATT
128067	126154	GAAATATTCCAGGCAATAAT
128068	126155	AGAAATATTCCAGGCAATAA
128069	126156	TAGAAATATTCCAGGCAATA
128070	126157	ATAGAAATATTCCAGGCAAT
128071	126158	TATAGAAATATTCCAGGCAA
128072	126159	TTATAGAAATATTCCAGGCA
128073	126160	TTTATAGAAATATTCCAGGC
128074	126161	CTTTATAGAAATATTCCAGG
128075	126162	TCTTTATAGAAATATTCCAG
128076	126163	TTCTTTATAGAAATATTCCA
128077	126164	TTTCTTTATAGAAATATTCC
128078	126165	TTTTCTTTATAGAAATATTC
128079	126166	TTTTTCTTTATAGAAATATT
128080	126167	GTTTTTCTTTATAGAAATAT
128081	126168	AGTTTTTCTTTATAGAAATA
128082	126169	AAGTTTTTCTTTATAGAAAT
128083	126170	AAAGTTTTTCTTTATAGAAA
128084	126171	GAAAGTTTTTCTTTATAGAA
128085	126172	GGAAAGTTTTTCTTTATAGA
128086	126173	GGGAAAGTTTTTCTTTATAG
128087	126174	TGGGAAAGTTTTTCTTTATA
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128089	126176	TATGGGAAAGTTTTTCTTTA
128090	126177	ATATGGGAAAGTTTTTCTTT
128091	126178	GATATGGGAAAGTTTTTCTT
128092	126179	GGATATGGGAAAGTTTTTCT
128093	126180	TGGATATGGGAAAGTTTTTC
128094	126181	CTGGATATGGGAAAGTTTTT
128095	126182	GCTGGATATGGGAAAGTTTT
128096	126183	AGCTGGATATGGGAAAGTTT
128097	126184	CAGCTGGATATGGGAAAGTT
128098	126185	ACAGCTGGATATGGGAAAGT
128099	126186	AACAGCTGGATATGGGAAAG
128100	126187	AAACAGCTGGATATGGGAAA
128101	126188	CAAACAGCTGGATATGGGAA
128102	126189	CCAAACAGCTGGATATGGGA
128103	126190	ACCAAACAGCTGGATATGGG
128104	126191	AACCAAACAGCTGGATATGG
128105	126192	TAACCAAACAGCTGGATATG
128106	126193	GTAACCAAACAGCTGGATAT
128107	126194	GGTAACCAAACAGCTGGATA

29814	27901	ACACCTGTAATCCCAGCACT
29815	27902	CACACCTGTAATCCCAGCAC
29816	27903	TCACACCTGTAATCCCAGCA
29817	27904	CTCACACCTGTAATCCCAGC
29818	27905	GCTCACACCTGTAATCCCAG
29819	27906	GGCTCACACCTGTAATCCCA
29820	27907	TGGCTCACACCTGTAATCCC
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29822	27909	GGTGGCTCACACCTGTAATC
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29827	27914	GGCACGGTGGCTCACACCTG
29828	27915	AGGCACGGTGGCTCACACCT
29829	27916	CAGGCACGGTGGCTCACACC
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29842	27929	AGAGCTTTTAGGTCAGGCAC
29843	27930	AAGAGCTTTTAGGTCAGGCA
29844	27931	AAAGAGCTTTTAGGTCAGGC
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29846	27933	GTAAAGAGCTTTTAGGTCAG
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29857	27944	TTTTTTACACTGTAAAGAGC
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29861	27948	AATATTTTTTACACTGTAAA
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29863	27950	AGAATATTTTTTACACTGTA
29864	27951	CAGAATATTTTTTACACTGT
29865	27952	TCAGAATATTTTTTACACTG
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29867	27954	GCTCAGAATATTTTTTACAC
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29869	27956	AAGCTCAGAATATTTTTTAC
29870	27957	AAAGCTCAGAATATTTTTTA
29871	27958	TAAAGCTCAGAATATTTTTT
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29873	27960	CTTAAAGCTCAGAATATTTT
29874	27961	GCTTAAAGCTCAGAATATTT
29875	27962	GGCTTAAAGCTCAGAATATT
29876	27963	TGGCTTAAAGCTCAGAATAT
29877	27964	ATGGCTTAAAGCTCAGAATA
29878	27965	CATGGCTTAAAGCTCAGAAT
29879	27966	ACATGGCTTAAAGCTCAGAA
29880	27967	CACATGGCTTAAAGCTCAGA
29881	27968	TCACATGGCTTAAAGCTCAG
29882	27969	TTCACATGGCTTAAAGCTCA
29883	27970	TTTCACATGGCTTAAAGCTC
29884	27971	TTTTCACATGGCTTAAAGCT

78961	77048	CTTAAAAGAAAAAAAAAGAG
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78963	77050	ATCTTAAAAGAAAAAAAAAG
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78966	77053	TCCATCTTAAAAGAAAAAAA
78967	77054	CTCCATCTTAAAAGAAAAAA
78968	77055	ACTCCATCTTAAAAGAAAAA
78969	77056	GACTCCATCTTAAAAGAAAA
78970	77057	AGACTCCATCTTAAAAGAAA
78971	77058	GAGACTCCATCTTAAAAGAA
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78974	77061	AGCGAGACTCCATCTTAAAA
78975	77062	GAGCGAGACTCCATCTTAAA
78976	77063	AGAGCGAGACTCCATCTTAA
78977	77064	CAGAGCGAGACTCCATCTTA
78978	77065	ACAGAGCGAGACTCCATCTT
78979	77066	GACAGAGCGAGACTCCATCT
78980	77067	CGACAGAGCGAGACTCCATC
78981	77068	GCGACAGAGCGAGACTCCAT
78982	77069	GGCGACAGAGCGAGACTCCA
78983	77070	GGGCGACAGAGCGAGACTCC
78984	77071	TGGGCGACAGAGCGAGACTC
78985	77072	CTGGGCGACAGAGCGAGACT
78986	77073	TCTGGGCGACAGAGCGAGAC
78987	77074	GTCTGGGCGACAGAGCGAGA
78988	77075	AGTCTGGGCGACAGAGCGAG
78989	77076	AAGTCTGGGCGACAGAGCGA
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78991	77078	TCAAGTCTGGGCGACAGAGC
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79015	77102	TGAGCTGAGATCACACCACT
79016	77103	GTGAGCTGAGATCACACCAC
79017	77104	AGTGAGCTGAGATCACACCA
79018	77105	CAGTGAGCTGAGATCACACC
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79022	77109	CTTGCAGTGAGCTGAGATCA
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79028	77115	GCAGAGCTTGCAGTGAGCTG
79029	77116	GGCAGAGCTTGCAGTGAGCT
79030	77117	AGGCAGAGCTTGCAGTGAGC
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128111	126198	TCAGGGTAACCAAACAGCTG
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128115	126202	TACCTCAGGGTAACCAAACA
128116	126203	ATACCTCAGGGTAACCAAAC
128117	126204	TATACCTCAGGGTAACCAAA
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128119	126206	GCTATACCTCAGGGTAACCA
128120	126207	AGCTATACCTCAGGGTAACC
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128123	126210	GAAAGCTATACCTCAGGGTA
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128127	126214	CTAAGAAAGCTATACCTCAG
128128	126215	CCTAAGAAAGCTATACCTCA
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128133	126220	CTTTTCCTAAGAAAGCTATA
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128143	126230	TTTTAAATTACTTTTCCTAA
128144	126231	ATTTTAAATTACTTTTCCTA
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128146	126233	ACATTTTAAATTACTTTTCC
128147	126234	AACATTTTAAATTACTTTTC
128148	126235	TAACATTTTAAATTACTTTT
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29898	27985	ATGCCCATGGCCTATTTTCA
29899	27986	AATGCCCATGGCCTATTTTC
29900	27987	AAATGCCCATGGCCTATTTT
29901	27988	CAAATGCCCATGGCCTATTT
29902	27989	GCAAATGCCCATGGCCTATT
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29907	27994	GGTCAGCAAATGCCCATGGC
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29909	27996	GGGGTCAGCAAATGCCCATG
29910	27997	AGGGGTCAGCAAATGCCCAT
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29916	28003	TCTATTAGGGGTCAGCAAAT
29917	28004	TTCTATTAGGGGTCAGCAAA
29918	28005	GTTCTATTAGGGGTCAGCAA
29919	28006	AGTTCTATTAGGGGTCAGCA
29920	28007	GAGTTCTATTAGGGGTCAGC
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29923	28010	ATGGAGTTCTATTAGGGGTC
29924	28011	AATGGAGTTCTATTAGGGGT
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29926	28013	AAAATGGAGTTCTATTAGGG
29927	28014	TAAAATGGAGTTCTATTAGG
29928	28015	GTAAAATGGAGTTCTATTAG
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29934	28021	AGAAAGGTAAAATGGAGTTC
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29936	28023	TCAGAAAGGTAAAATGGAGT
29937	28024	ATCAGAAAGGTAAAATGGAG
29938	28025	GATCAGAAAGGTAAAATGGA
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29940	28027	ATGATCAGAAAGGTAAAATG
29941	28028	CATGATCAGAAAGGTAAAAT
29942	28029	ACATGATCAGAAAGGTAAAA
29943	28030	AACATGATCAGAAAGGTAAA
29944	28031	AAACATGATCAGAAAGGTAA
29945	28032	GAAACATGATCAGAAAGGTA
29946	28033	GGAAACATGATCAGAAAGGT
29947	28034	GGGAAACATGATCAGAAAGG
29948	28035	TGGGAAACATGATCAGAAAG
29949	28036	ATGGGAAACATGATCAGAAA
29950	28037	AATGGGAAACATGATCAGAA
29951	28038	TAATGGGAAACATGATCAGA
29952	28039	TTAATGGGAAACATGATCAG
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29954	28041	AGTTAATGGGAAACATGATC
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79032	77119	GGAGGCAGAGCTTGCAGTGA
79033	77120	GGGAGGCAGAGCTTGCAGTG
79034	77121	CGGGAGGCAGAGCTTGCAGT
79035	77122	CCGGGAGGCAGAGCTTGCAG
79036	77123	CCCGGGAGGCAGAGCTTGCA
79037	77124	ACCCGGGAGGCAGAGCTTGC
79038	77125	AACCCGGGAGGCAGAGCTTG
79039	77126	GAACCCGGGAGGCAGAGCTT
79040	77127	TGAACCCGGGAGGCAGAGCT
79041	77128	GTGAACCCGGGAGGCAGAGC
79042	77129	TGTGAACCCGGGAGGCAGAG
79043	77130	GTGTGAACCCGGGAGGCAGA
79044	77131	GGTGTGAACCCGGGAGGCAG
79045	77132	TGGTGTGAACCCGGGAGGCA
79046	77133	ATGGTGTGAACCCGGGAGGC
79047	77134	AATGGTGTGAACCCGGGAGG
79048	77135	GAATGGTGTGAACCCGGGAG
79049	77136	AGAATGGTGTGAACCCGGGA
79050	77137	GAGAATGGTGTGAACCCGGG
79051	77138	GGAGAATGGTGTGAACCCGG
79052	77139	AGGAGAATGGTGTGAACCCG
79053	77140	CAGGAGAATGGTGTGAACCC
79054	77141	GCAGGAGAATGGTGTGAACC
79055	77142	GGCAGGAGAATGGTGTGAAC
79056	77143	GGGCAGGAGAATGGTGTGAA
79057	77144	AGGGCAGGAGAATGGTGTGA
79058	77145	TAGGGCAGGAGAATGGTGTG
79059	77146	CTAGGGCAGGAGAATGGTGT
79060	77147	GCTAGGGCAGGAGAATGGTG
79061	77148	GGCTAGGGCAGGAGAATGGT
79062	77149	AGGCTAGGGCAGGAGAATGG
79063	77150	GAGGCTAGGGCAGGAGAATG
79064	77151	GGAGGCTAGGGCAGGAGAAT
79065	77152	GGGAGGCTAGGGCAGGAGAA
79066	77153	TGGGAGGCTAGGGCAGGAGA
79067	77154	TTGGGAGGCTAGGGCAGGAG
79068	77155	CTTGGGAGGCTAGGGCAGGA
79069	77156	ACTTGGGAGGCTAGGGCAGG
79070	77157	TACTTGGGAGGCTAGGGCAG
79071	77158	CTACTTGGGAGGCTAGGGCA
79072	77159	GCTACTTGGGAGGCTAGGGC
79073	77160	AGCTACTTGGGAGGCTAGGG
79074	77161	CAGCTACTTGGGAGGCTAGG
79075	77162	CCAGCTACTTGGGAGGCTAG
79076	77163	CCCAGCTACTTGGGAGGCTA
79077	77164	TCCCAGCTACTTGGGAGGCT
79078	77165	GTCCCAGCTACTTGGGAGGC
79079	77166	AGTCCCAGCTACTTGGGAGG
79080	77167	TAGTCCCAGCTACTTGGGAG
79081	77168	GTAGTCCCAGCTACTTGGGA
79082	77169	TGTAGTCCCAGCTACTTGGG
79083	77170	CTGTAGTCCCAGCTACTTGG
79084	77171	CCTGTAGTCCCAGCTACTTG
79085	77172	GCCTGTAGTCCCAGCTACTT
79086	77173	AGCCTGTAGTCCCAGCTACT
79087	77174	GAGCCTGTAGTCCCAGCTAC
79088	77175	GGAGCCTGTAGTCCCAGCTA
79089	77176	GGGAGCCTGTAGTCCCAGCT
79090	77177	CGGGAGCCTGTAGTCCCAGC
79091	77178	GCGGGAGCCTGTAGTCCCAG
79092	77179	GGCGGGAGCCTGTAGTCCCA
79093	77180	TGGCGGGAGCCTGTAGTCCC
79094	77181	GTGGCGGGAGCCTGTAGTCC
79095	77182	GGTGGCGGGAGCCTGTAGTC
79096	77183	TGGTGGCGGGAGCCTGTAGT
79097	77184	GTGGTGGCGGGAGCCTGTAG
79098	77185	TGTGGTGGCGGGAGCCTGTA
79099	77186	GTGTGGTGGCGGGAGCCTGT
79100	77187	GGTGTGGTGGCGGGAGCCTG
79101	77188	AGGTGTGGTGGCGGGAGCCT
79102	77189	CAGGTGTGGTGGCGGGAGCC

128179	126266	TTTTGAAGACTGCCTTAAAA
128180	126267	ATTTTGAAGACTGCCTTAAA
128181	126268	TATTTTGAAGACTGCCTTAA
128182	126269	TTATTTTGAAGACTGCCTTA
128183	126270	ATTATTTTGAAGACTGCCTT
128184	126271	CATTATTTTGAAGACTGCCT
128185	126272	TCATTATTTTGAAGACTGCC
128186	126273	CTCATTATTTTGAAGACTGC
128187	126274	ACTCATTATTTTGAAGACTG
128188	126275	AACTCATTATTTTGAAGACT
128189	126276	CAACTCATTATTTTGAAGAC
128190	126277	CCAACTCATTATTTTGAAGA
128191	126278	ACCAACTCATTATTTTGAAG
128192	126279	AACCAACTCATTATTTTGAA
128193	126280	AAACCAACTCATTATTTTGA
128194	126281	AAAACCAACTCATTATTTTG
128195	126282	GAAAACCAACTCATTATTTT
128196	126283	AGAAAACCAACTCATTATTT
128197	126284	CAGAAAACCAACTCATTATT
128198	126285	ACAGAAAACCAACTCATTAT
128199	126286	AACAGAAAACCAACTCATTA
128200	126287	TAACAGAAAACCAACTCATT
128201	126288	ATAACAGAAAACCAACTCAT
128202	126289	GATAACAGAAAACCAACTCA
128203	126290	GGATAACAGAAAACCAACTC
128204	126291	AGGATAACAGAAAACCAACT
128205	126292	GAGGATAACAGAAAACCAAC
128206	126293	GGAGGATAACAGAAAACCAA
128207	126294	TGGAGGATAACAGAAAACCA
128208	126295	TTGGAGGATAACAGAAAACC
128209	126296	TTTGGAGGATAACAGAAAAC
128210	126297	CTTTGGAGGATAACAGAAAA
128211	126298	CCTTTGGAGGATAACAGAAA
128212	126299	ACCTTTGGAGGATAACAGAA
128213	126300	TACCTTTGGAGGATAACAGA
128214	126301	TTACCTTTGGAGGATAACAG
128215	126302	GTTACCTTTGGAGGATAACA
128216	126303	GGTTACCTTTGGAGGATAAC
128217	126304	TGGTTACCTTTGGAGGATAA
128218	126305	CTGGTTACCTTTGGAGGATA
128219	126306	ACTGGTTACCTTTGGAGGAT
128220	126307	CACTGGTTACCTTTGGAGGA
128221	126308	TCACTGGTTACCTTTGGAGG
128222	126309	CTCACTGGTTACCTTTGGAG
128223	126310	CCTCACTGGTTACCTTTGGA
128224	126311	ACCTCACTGGTTACCTTTGG
128225	126312	CACCTCACTGGTTACCTTTG
128226	126313	CCACCTCACTGGTTACCTTT
128227	126314	ACCACCTCACTGGTTACCTT
128228	126315	AACCACCTCACTGGTTACCT
128229	126316	AAACCACCTCACTGGTTACC
128230	126317	AAAACCACCTCACTGGTTAC
128231	126318	AAAAACCACCTCACTGGTTA
128232	126319	AAAAAACCACCTCACTGGTT
128233	126320	AAAAAAACCACCTCACTGGT
128234	126321	CAAAAAAACCACCTCACTGG
128235	126322	ACAAAAAAACCACCTCACTG
128236	126323	GACAAAAAAACCACCTCACT
128237	126324	CGACAAAAAAACCACCTCAC
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128239	126326	AACGACAAAAAAACCACCTC
128240	126327	CAACGACAAAAAAACCACCT
128241	126328	CCAACGACAAAAAAACCACC
128242	126329	ACCAACGACAAAAAAACCAC
128243	126330	AACCAACGACAAAAAAACCA
128244	126331	GAACCAACGACAAAAAAACC
128245	126332	AGAACCAACGACAAAAAAAC
128246	126333	AAGAACCAACGACAAAAAAA
128247	126334	TAAGAACCAACGACAAAAAA
128248	126335	GTAAGAACCAACGACAAAAA
128249	126336	AGTAAGAACCAACGACAAAA

29956	28043	AGAGTTAATGGGAAACATGA
29957	28044	AAGAGTTAATGGGAAACATG
29958	28045	GAAGAGTTAATGGGAAACAT
29959	28046	TGAAGAGTTAATGGGAAACA
29960	28047	TTGAAGAGTTAATGGGAAAC
29961	28048	TTTGAAGAGTTAATGGGAAA
29962	28049	TTTTGAAGAGTTAATGGGAA
29963	28050	TTTTTGAAGAGTTAATGGGA
29964	28051	ATTTTTGAAGAGTTAATGGG
29965	28052	TATTTTTGAAGAGTTAATGG
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29969	28056	GTCATATTTTTGAAGAGTTA
29970	28057	GGTCATATTTTTGAAGAGTT
29971	28058	AGGTCATATTTTTGAAGAGT
29972	28059	GAGGTCATATTTTTGAAGAG
29973	28060	GGAGGTCATATTTTTGAAGA
29974	28061	TGGAGGTCATATTTTTGAAG
29975	28062	ATGGAGGTCATATTTTTGAA
29976	28063	AATGGAGGTCATATTTTTGA
29977	28064	AAATGGAGGTCATATTTTTG
29978	28065	TAAATGGAGGTCATATTTTT
29979	28066	TTAAATGGAGGTCATATTTT
29980	28067	TTTAAATGGAGGTCATATTT
29981	28068	ATTTAAATGGAGGTCATATT
29982	28069	GATTTAAATGGAGGTCATAT
29983	28070	TGATTTAAATGGAGGTCATA
29984	28071	TTGATTTAAATGGAGGTCAT
29985	28072	CTTGATTTAAATGGAGGTCA
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29988	28075	CATCTTGATTTAAATGGAGG
29989	28076	CCATCTTGATTTAAATGGAG
29990	28077	ACCATCTTGATTTAAATGGA
29991	28078	GACCATCTTGATTTAAATGG
29992	28079	AGACCATCTTGATTTAAATG
29993	28080	GAGACCATCTTGATTTAAAT
29994	28081	GGAGACCATCTTGATTTAAA
29995	28082	AGGAGACCATCTTGATTTAA
29996	28083	AAGGAGACCATCTTGATTTA
29997	28084	GAAGGAGACCATCTTGATTT
29998	28085	GGAAGGAGACCATCTTGATT
29999	28086	AGGAAGGAGACCATCTTGAT
30000	28087	GAGGAAGGAGACCATCTTGA
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30007	28094	AAGCAGTGAGGAAGGAGACC
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30010	28097	CACAAGCAGTGAGGAAGGAG
30011	28098	CCACAAGCAGTGAGGAAGGA
30012	28099	TCCACAAGCAGTGAGGAAGG
30013	28100	CTCCACAAGCAGTGAGGAAG
30014	28101	CCTCCACAAGCAGTGAGGAA
30015	28102	ACCTCCACAAGCAGTGAGGA
30016	28103	GACCTCCACAAGCAGTGAGG
30017	28104	GGACCTCCACAAGCAGTGAG
30018	28105	TGGACCTCCACAAGCAGTGA
30019	28106	CTGGACCTCCACAAGCAGTG
30020	28107	ACTGGACCTCCACAAGCAGT
30021	28108	CACTGGACCTCCACAAGCAG
30022	28109	GCACTGGACCTCCACAAGCA
30023	28110	GGCACTGGACCTCCACAAGC
30024	28111	GGGCACTGGACCTCCACAAG
30025	28112	TGGGCACTGGACCTCCACAA
30026	28113	CTGGGCACTGGACCTCCACA

79103	77190	CCAGGTGTGGTGGCGGGAGC
79104	77191	GCCAGGTGTGGTGGCGGGAG
79105	77192	AGCCAGGTGTGGTGGCGGGA
79106	77193	TAGCCAGGTGTGGTGGCGGG
79107	77194	TTAGCCAGGTGTGGTGGCGG
79108	77195	ATTAGCCAGGTGTGGTGGCG
79109	77196	AATTAGCCAGGTGTGGTGGC
79110	77197	AAATTAGCCAGGTGTGGTGG
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79115	77202	ACAAAAAATTAGCCAGGTGT
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79118	77205	AATACAAAAAATTAGCCAGG
79119	77206	AAATACAAAAAATTAGCCAG
79120	77207	AAAATACAAAAAATTAGCCA
79121	77208	AAAAATACAAAAAATTAGCC
79122	77209	TAAAAATACAAAAAATTAGC
79123	77210	CTAAAAATACAAAAAATTAG
79124	77211	ACTAAAAATACAAAAAATTA
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79127	77214	TCTACTAAAAATACAAAAAA
79128	77215	CTCTACTAAAAATACAAAAA
79129	77216	TCTCTACTAAAAATACAAAA
79130	77217	GTCTCTACTAAAAATACAAA
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79132	77219	CTGTCTCTACTAAAAATACA
79133	77220	CCTGTCTCTACTAAAAATAC
79134	77221	CCCTGTCTCTACTAAAAATA
79135	77222	ACCCTGTCTCTACTAAAAAT
79136	77223	AACCCTGTCTCTACTAAAAA
79137	77224	AAACCCTGTCTCTACTAAAA
79138	77225	GAAACCCTGTCTCTACTAAA
79139	77226	TGAAACCCTGTCTCTACTAA
79140	77227	GTGAAACCCTGTCTCTACTA
79141	77228	GGTGAAACCCTGTCTCTACT
79142	77229	TGGTGAAACCCTGTCTCTAC
79143	77230	ATGGTGAAACCCTGTCTCTA
79144	77231	CATGGTGAAACCCTGTCTCT
79145	77232	ACATGGTGAAACCCTGTCTC
79146	77233	AACATGGTGAAACCCTGTCT
79147	77234	TAACATGGTGAAACCCTGTC
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79151	77238	TGGCTAACATGGTGAAACCC
79152	77239	CTGGCTAACATGGTGAAACC
79153	77240	GCTGGCTAACATGGTGAAAC
79154	77241	TGCTGGCTAACATGGTGAAA
79155	77242	ATGCTGGCTAACATGGTGAA
79156	77243	CATGCTGGCTAACATGGTGA
79157	77244	CCATGCTGGCTAACATGGTG
79158	77245	ACCATGCTGGCTAACATGGT
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79162	77249	TGAGACCATGCTGGCTAACA
79163	77250	TTGAGACCATGCTGGCTAAC
79164	77251	ATTGAGACCATGCTGGCTAA
79165	77252	GATTGAGACCATGCTGGCTA
79166	77253	AGATTGAGACCATGCTGGCT
79167	77254	GAGATTGAGACCATGCTGGC
79168	77255	GGAGATTGAGACCATGCTGG
79169	77256	AGGAGATTGAGACCATGCTG
79170	77257	CAGGAGATTGAGACCATGCT
79171	77258	TCAGGAGATTGAGACCATGC
79172	77259	GTCAGGAGATTGAGACCATG
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128250	126337	TAGTAAGAACCAACGACAAA
128251	126338	ATAGTAAGAACCAACGACAA
128252	126339	GATAGTAAGAACCAACGACA
128253	126340	TGATAGTAAGAACCAACGAC
128254	126341	CTGATAGTAAGAACCAACGA
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128256	126343	TACTGATAGTAAGAACCAAC
128257	126344	ATACTGATAGTAAGAACCAA
128258	126345	TATACTGATAGTAAGAACCA
128259	126346	TTATACTGATAGTAAGAACC
128260	126347	TTTATACTGATAGTAAGAAC
128261	126348	GTTTATACTGATAGTAAGAA
128262	126349	AGTTTATACTGATAGTAAGA
128263	126350	AAGTTTATACTGATAGTAAG
128264	126351	GAAGTTTATACTGATAGTAA
128265	126352	AGAAGTTTATACTGATAGTA
128266	126353	CAGAAGTTTATACTGATAGT
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128268	126355	TCCAGAAGTTTATACTGATA
128269	126356	TTCCAGAAGTTTATACTGAT
128270	126357	ATTCCAGAAGTTTATACTGA
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128272	126359	AAATTCCAGAAGTTTATACT
128273	126360	AAAATTCCAGAAGTTTATAC
128274	126361	AAAAATTCCAGAAGTTTATA
128275	126362	AAAAAATTCCAGAAGTTTAT
128276	126363	AAAAAAATTCCAGAAGTTTA
128277	126364	AAAAAAAATTCCAGAAGTTT
128278	126365	AAAAAAAAATTCCAGAAGTT
128279	126366	AAAAAAAAAATTCCAGAAGT
128280	126367	AAAAAAAAAAATTCCAGAAG
128281	126368	AAAAAAAAAAAATTCCAGAA
128282	126369	AAAAAAAAAAAAATTCCAGA
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128284	126371	AAAAAAAAAAAAAAATTCCA
128285	126372	AAAAAAAAAAAAAAAATTCC
128286	126373	TAAAAAAAAAAAAAAAATTC
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128289	126376	AATTAAAAAAAAAAAAAAAA
128290	126377	AAATTAAAAAAAAAAAAAAA
128291	126378	AAAATTAAAAAAAAAAAAAA
128292	126379	AAAAATTAAAAAAAAAAAAA
128293	126380	AAAAAATTAAAAAAAAAAAA
128294	126381	CAAAAAATTAAAAAAAAAAA
128295	126382	CCAAAAAATTAAAAAAAAAA
128296	126383	TCCAAAAAATTAAAAAAAAA
128297	126384	CTCCAAAAAATTAAAAAAAA
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128299	126386	GTCTCCAAAAAATTAAAAAA
128300	126387	TGTCTCCAAAAAATTAAAAA
128301	126388	TTGTCTCCAAAAAATTAAAA
128302	126389	CTTGTCTCCAAAAAATTAAA
128303	126390	CCTTGTCTCCAAAAAATTAA
128304	126391	ACCTTGTCTCCAAAAAATTA
128305	126392	GACCTTGTCTCCAAAAAATT
128306	126393	AGACCTTGTCTCCAAAAAAT
128307	126394	CAGACCTTGTCTCCAAAAAA
128308	126395	CCAGACCTTGTCTCCAAAAA
128309	126396	GCCAGACCTTGTCTCCAAAA
128310	126397	AGCCAGACCTTGTCTCCAAA
128311	126398	GAGCCAGACCTTGTCTCCAA
128312	126399	AGAGCCAGACCTTGTCTCCA
128313	126400	CAGAGCCAGACCTTGTCTCC
128314	126401	ACAGAGCCAGACCTTGTCTC
128315	126402	AACAGAGCCAGACCTTGTCT
128316	126403	TAACAGAGCCAGACCTTGTC
128317	126404	GTAACAGAGCCAGACCTTGT
128318	126405	GGTAACAGAGCCAGACCTTG
128319	126406	AGGTAACAGAGCCAGACCTT
128320	126407	TAGGTAACAGAGCCAGACCT

30027	28114	ACTGGGCACTGGACCTCCAC
30028	28115	CACTGGGCACTGGACCTCCA
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30030	28117	GACACTGGGCACTGGACCTC
30031	28118	AGACACTGGGCACTGGACCT
30032	28119	CAGACACTGGGCACTGGACC
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30034	28121	GGCAGACACTGGGCACTGGA
30035	28122	AGGCAGACACTGGGCACTGG
30036	28123	GAGGCAGACACTGGGCACTG
30037	28124	AGAGGCAGACACTGGGCACT
30038	28125	AAGAGGCAGACACTGGGCAC
30039	28126	CAAGAGGCAGACACTGGGCA
30040	28127	GCAAGAGGCAGACACTGGGC
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30043	28130	CAAGCAAGAGGCAGACACTG
30044	28131	GCAAGCAAGAGGCAGACACT
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30046	28133	GAGCAAGCAAGAGGCAGACA
30047	28134	GGAGCAAGCAAGAGGCAGAC
30048	28135	AGGAGCAAGCAAGAGGCAGA
30049	28136	GAGGAGCAAGCAAGAGGCAG
30050	28137	GGAGGAGCAAGCAAGAGGCA
30051	28138	TGGAGGAGCAAGCAAGAGGC
30052	28139	ATGGAGGAGCAAGCAAGAGG
30053	28140	GATGGAGGAGCAAGCAAGAG
30054	28141	TGATGGAGGAGCAAGCAAGA
30055	28142	ATGATGGAGGAGCAAGCAAG
30056	28143	AATGATGGAGGAGCAAGCAA
30057	28144	CAATGATGGAGGAGCAAGCA
30058	28145	ACAATGATGGAGGAGCAAGC
30059	28146	AACAATGATGGAGGAGCAAG
30060	28147	GAACAATGATGGAGGAGCAA
30061	28148	AGAACAATGATGGAGGAGCA
30062	28149	CAGAACAATGATGGAGGAGC
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30065	28152	TGGCAGAACAATGATGGAGG
30066	28153	ATGGCAGAACAATGATGGAG
30067	28154	AATGGCAGAACAATGATGGA
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30070	28157	TCGAATGGCAGAACAATGAT
30071	28158	CTCGAATGGCAGAACAATGA
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30076	28163	AGGATCTCGAATGGCAGAAC
30077	28164	GAGGATCTCGAATGGCAGAA
30078	28165	TGAGGATCTCGAATGGCAGA
30079	28166	ATGAGGATCTCGAATGGCAG
30080	28167	TATGAGGATCTCGAATGGCA
30081	28168	GTATGAGGATCTCGAATGGC
30082	28169	AGTATGAGGATCTCGAATGG
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30093	28180	CTTAAAGGGTAAGTATGAGG
30094	28181	TCTTAAAGGGTAAGTATGAG
30095	28182	ATCTTAAAGGGTAAGTATGA
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79174	77261	AAGTCAGGAGATTGAGACCA
79175	77262	GAAGTCAGGAGATTGAGACC
79176	77263	CGAAGTCAGGAGATTGAGAC
79177	77264	ACGAAGTCAGGAGATTGAGA
79178	77265	CACGAAGTCAGGAGATTGAG
79179	77266	TCACGAAGTCAGGAGATTGA
79180	77267	ATCACGAAGTCAGGAGATTG
79181	77268	GATCACGAAGTCAGGAGATT
79182	77269	GGATCACGAAGTCAGGAGAT
79183	77270	AGGATCACGAAGTCAGGAGA
79184	77271	GAGGATCACGAAGTCAGGAG
79185	77272	GGAGGATCACGAAGTCAGGA
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79191	77278	GAGGCAGGAGGATCACGAAG
79192	77279	CGAGGCAGGAGGATCACGAA
79193	77280	CCGAGGCAGGAGGATCACGA
79194	77281	GCCGAGGCAGGAGGATCACG
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79197	77284	GAGGCCGAGGCAGGAGGATC
79198	77285	GGAGGCCGAGGCAGGAGGAT
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79200	77287	TGGGAGGCCGAGGCAGGAGG
79201	77288	TTGGGAGGCCGAGGCAGGAG
79202	77289	TTTGGGAGGCCGAGGCAGGA
79203	77290	CTTTGGGAGGCCGAGGCAGG
79204	77291	ACTTTGGGAGGCCGAGGCAG
79205	77292	CACTTTGGGAGGCCGAGGCA
79206	77293	GCACTTTGGGAGGCCGAGGC
79207	77294	AGCACTTTGGGAGGCCGAGG
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79215	77302	GGTATCCCAGCACTTTGGGA
79216	77303	TGGTATCCCAGCACTTTGGG
79217	77304	CTGGTATCCCAGCACTTTGG
79218	77305	CCTGGTATCCCAGCACTTTG
79219	77306	GCCTGGTATCCCAGCACTTT
79220	77307	TGCCTGGTATCCCAGCACTT
79221	77308	ATGCCTGGTATCCCAGCACT
79222	77309	CATGCCTGGTATCCCAGCAC
79223	77310	TCATGCCTGGTATCCCAGCA
79224	77311	CTCATGCCTGGTATCCCAGC
79225	77312	GCTCATGCCTGGTATCCCAG
79226	77313	GGCTCATGCCTGGTATCCCA
79227	77314	TGGCTCATGCCTGGTATCCC
79228	77315	GTGGCTCATGCCTGGTATCC
79229	77316	GGTGGCTCATGCCTGGTATC
79230	77317	CGGTGGCTCATGCCTGGTAT
79231	77318	ACGGTGGCTCATGCCTGGTA
79232	77319	CACGGTGGCTCATGCCTGGT
79233	77320	GCACGGTGGCTCATGCCTGG
79234	77321	GGCACGGTGGCTCATGCCTG
79235	77322	GGGCACGGTGGCTCATGCCT
79236	77323	CGGGCACGGTGGCTCATGCC
79237	77324	CCGGGCACGGTGGCTCATGC
79238	77325	GCCGGGCACGGTGGCTCATG
79239	77326	GGCCGGGCACGGTGGCTCAT
79240	77327	TGGCCGGGCACGGTGGCTCA
79241	77328	CTGGCCGGGCACGGTGGCTC
79242	77329	TCTGGCCGGGCACGGTGGCT
79243	77330	TTCTGGCCGGGCACGGTGGC
79244	77331	GTTCTGGCCGGGCACGGTGG

128321	126408	CTAGGTAACAGAGCCAGACC
128322	126409	CCTAGGTAACAGAGCCAGAC
128323	126410	GCCTAGGTAACAGAGCCAGA
128324	126411	AGCCTAGGTAACAGAGCCAG
128325	126412	CAGCCTAGGTAACAGAGCCA
128326	126413	CCAGCCTAGGTAACAGAGCC
128327	126414	TCCAGCCTAGGTAACAGAGC
128328	126415	CTCCAGCCTAGGTAACAGAG
128329	126416	ACTCCAGCCTAGGTAACAGA
128330	126417	CACTCCAGCCTAGGTAACAG
128331	126418	GCACTCCAGCCTAGGTAACA
128332	126419	TGCACTCCAGCCTAGGTAAC
128333	126420	CTGCACTCCAGCCTAGGTAA
128334	126421	ACTGCACTCCAGCCTAGGTA
128335	126422	CACTGCACTCCAGCCTAGGT
128336	126423	CCACTGCACTCCAGCCTAGG
128337	126424	CCCACTGCACTCCAGCCTAG
128338	126425	TCCCACTGCACTCCAGCCTA
128339	126426	ATCCCACTGCACTCCAGCCT
128340	126427	CATCCCACTGCACTCCAGCC
128341	126428	TCATCCCACTGCACTCCAGC
128342	126429	ATCATCCCACTGCACTCCAG
128343	126430	GATCATCCCACTGCACTCCA
128344	126431	AGATCATCCCACTGCACTCC
128345	126432	CAGATCATCCCACTGCACTC
128346	126433	CCAGATCATCCCACTGCACT
128347	126434	CCCAGATCATCCCACTGCAC
128348	126435	GCCCAGATCATCCCACTGCA
128349	126436	TGCCCAGATCATCCCACTGC
128350	126437	ATGCCCAGATCATCCCACTG
128351	126438	TATGCCCAGATCATCCCACT
128352	126439	GTATGCCCAGATCATCCCAC
128353	126440	AGTATGCCCAGATCATCCCA
128354	126441	CAGTATGCCCAGATCATCCC
128355	126442	GCAGTATGCCCAGATCATCC
128356	126443	TGCAGTATGCCCAGATCATC
128357	126444	CTGCAGTATGCCCAGATCAT
128358	126445	GCTGCAGTATGCCCAGATCA
128359	126446	GGCTGCAGTATGCCCAGATC
128360	126447	AGGCTGCAGTATGCCCAGAT
128361	126448	GAGGCTGCAGTATGCCCAGA
128362	126449	TGAGGCTGCAGTATGCCCAG
128363	126450	TTGAGGCTGCAGTATGCCCA
128364	126451	GTTGAGGCTGCAGTATGCCC
128365	126452	AGTTGAGGCTGCAGTATGCC
128366	126453	AAGTTGAGGCTGCAGTATGC
128367	126454	GAAGTTGAGGCTGCAGTATG
128368	126455	GGAAGTTGAGGCTGCAGTAT
128369	126456	GGGAAGTTGAGGCTGCAGTA
128370	126457	CGGGAAGTTGAGGCTGCAGT
128371	126458	TCGGGAAGTTGAGGCTGCAG
128372	126459	CTCGGGAAGTTGAGGCTGCA
128373	126460	GCTCGGGAAGTTGAGGCTGC
128374	126461	AGCTCGGGAAGTTGAGGCTG
128375	126462	TAGCTCGGGAAGTTGAGGCT
128376	126463	TTAGCTCGGGAAGTTGAGGC
128377	126464	CTTAGCTCGGGAAGTTGAGG
128378	126465	CCTTAGCTCGGGAAGTTGAG
128379	126466	GCCTTAGCTCGGGAAGTTGA
128380	126467	TGCCTTAGCTCGGGAAGTTG
128381	126468	TTGCCTTAGCTCGGGAAGTT
128382	126469	ATTGCCTTAGCTCGGGAAGT
128383	126470	GATTGCCTTAGCTCGGGAAG
128384	126471	GGATTGCCTTAGCTCGGGAA
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128387	126474	GGGGGATTGCCTTAGCTCGG
128388	126475	GGGGGGATTGCCTTAGCTCG
128389	126476	TGGGGGGATTGCCTTAGCTC
128390	126477	GTGGGGGGATTGCCTTAGCT
128391	126478	GGTGGGGGGATTGCCTTAGC

30098	28185	TAGATCTTAAAGGGTAAGTA
30099	28186	CTAGATCTTAAAGGGTAAGT
30100	28187	GCTAGATCTTAAAGGGTAAG
30101	28188	GGCTAGATCTTAAAGGGTAA
30102	28189	GGGCTAGATCTTAAAGGGTA
30103	28190	TGGGCTAGATCTTAAAGGGT
30104	28191	TTGGGCTAGATCTTAAAGGG
30105	28192	TTTGGGCTAGATCTTAAAGG
30106	28193	ATTTGGGCTAGATCTTAAAG
30107	28194	AATTTGGGCTAGATCTTAAA
30108	28195	AAATTTGGGCTAGATCTTAA
30109	28196	AAAATTTGGGCTAGATCTTA
30110	28197	GAAAATTTGGGCTAGATCTT
30111	28198	GGAAAATTTGGGCTAGATCT
30112	28199	TGGAAAATTTGGGCTAGATC
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30114	28201	CATGGAAAATTTGGGCTAGA
30115	28202	TCATGGAAAATTTGGGCTAG
30116	28203	TTCATGGAAAATTTGGGCTA
30117	28204	TTTCATGGAAAATTTGGGCT
30118	28205	GTTTCATGGAAAATTTGGGC
30119	28206	AGTTTCATGGAAAATTTGGG
30120	28207	TAGTTTCATGGAAAATTTGG
30121	28208	TTAGTTTCATGGAAAATTTG
30122	28209	ATTAGTTTCATGGAAAATTT
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30126	28213	TAGAATTAGTTTCATGGAAA
30127	28214	TTAGAATTAGTTTCATGGAA
30128	28215	ATTAGAATTAGTTTCATGGA
30129	28216	TATTAGAATTAGTTTCATGG
30130	28217	TTATTAGAATTAGTTTCATG
30131	28218	ATTATTAGAATTAGTTTCAT
30132	28219	AATTATTAGAATTAGTTTCA
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30134	28221	TTAATTATTAGAATTAGTTT
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30136	28223	TTTTAATTATTAGAATTAGT
30137	28224	TTTTTAATTATTAGAATTAG
30138	28225	GTTTTTAATTATTAGAATTA
30139	28226	AGTTTTTAATTATTAGAATT
30140	28227	AAGTTTTTAATTATTAGAAT
30141	28228	GAAGTTTTTAATTATTAGAA
30142	28229	GGAAGTTTTTAATTATTAGA
30143	28230	AGGAAGTTTTTAATTATTAG
30144	28231	CAGGAAGTTTTTAATTATTA
30145	28232	ACAGGAAGTTTTTAATTATT
30146	28233	TACAGGAAGTTTTTAATTAT
30147	28234	CTACAGGAAGTTTTTAATTA
30148	28235	TCTACAGGAAGTTTTTAATT
30149	28236	TTCTACAGGAAGTTTTTAAT
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30156	28243	AGTTAAGTTCTACAGGAAGT
30157	28244	AAGTTAAGTTCTACAGGAAG
30158	28245	AAAGTTAAGTTCTACAGGAA
30159	28246	CAAAGTTAAGTTCTACAGGA
30160	28247	ACAAAGTTAAGTTCTACAGG
30161	28248	GACAAAGTTAAGTTCTACAG
30162	28249	AGACAAAGTTAAGTTCTACA
30163	28250	TAGACAAAGTTAAGTTCTAC
30164	28251	CTAGACAAAGTTAAGTTCTA
30165	28252	ACTAGACAAAGTTAAGTTCT
30166	28253	TACTAGACAAAGTTAAGTTC
30167	28254	GTACTAGACAAAGTTAAGTT
30168	28255	TGTACTAGACAAAGTTAAGT

79245	77332	AGTTCTGGCCGGGCACGGTG
79246	77333	GAGTTCTGGCCGGGCACGGT
79247	77334	AGAGTTCTGGCCGGGCACGG
79248	77335	AAGAGTTCTGGCCGGGCACG
79249	77336	TAAGAGTTCTGGCCGGGCAC
79250	77337	TTAAGAGTTCTGGCCGGGCA
79251	77338	ATTAAGAGTTCTGGCCGGGC
79252	77339	TATTAAGAGTTCTGGCCGGG
79253	77340	CTATTAAGAGTTCTGGCCGG
79254	77341	ACTATTAAGAGTTCTGGCCG
79255	77342	TACTATTAAGAGTTCTGGCC
79256	77343	CTACTATTAAGAGTTCTGGC
79257	77344	ACTACTATTAAGAGTTCTGG
79258	77345	AACTACTATTAAGAGTTCTG
79259	77346	TAACTACTATTAAGAGTTCT
79260	77347	ATAACTACTATTAAGAGTTC
79261	77348	AATAACTACTATTAAGAGTT
79262	77349	AAATAACTACTATTAAGAGT
79263	77350	TAAATAACTACTATTAAGAG
79264	77351	ATAAATAACTACTATTAAGA
79265	77352	CATAAATAACTACTATTAAG
79266	77353	GCATAAATAACTACTATTAA
79267	77354	TGCATAAATAACTACTATTA
79268	77355	GTGCATAAATAACTACTATT
79269	77356	CGTGCATAAATAACTACTAT
79270	77357	GCGTGCATAAATAACTACTA
79271	77358	AGCGTGCATAAATAACTACT
79272	77359	CAGCGTGCATAAATAACTAC
79273	77360	CCAGCGTGCATAAATAACTA
79274	77361	CCCAGCGTGCATAAATAACT
79275	77362	TCCCAGCGTGCATAAATAAC
79276	77363	ATCCCAGCGTGCATAAATAA
79277	77364	AATCCCAGCGTGCATAAATA
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79282	77369	CTTCCAATCCCAGCGTGCAT
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79286	77373	ATGTCTTCCAATCCCAGCGT
79287	77374	AATGTCTTCCAATCCCAGCG
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79289	77376	TAAATGTCTTCCAATCCCAG
79290	77377	GTAAATGTCTTCCAATCCCA
79291	77378	AGTAAATGTCTTCCAATCCC
79292	77379	AAGTAAATGTCTTCCAATCC
79293	77380	AAAGTAAATGTCTTCCAATC
79294	77381	AAAAGTAAATGTCTTCCAAT
79295	77382	AAAAAGTAAATGTCTTCCAA
79296	77383	TAAAAAGTAAATGTCTTCCA
79297	77384	GTAAAAAGTAAATGTCTTCC
79298	77385	AGTAAAAAGTAAATGTCTTC
79299	77386	CAGTAAAAAGTAAATGTCTT
79300	77387	CCAGTAAAAAGTAAATGTCT
79301	77388	TCCAGTAAAAAGTAAATGTC
79302	77389	ATCCAGTAAAAAGTAAATGT
79303	77390	CATCCAGTAAAAAGTAAATG
79304	77391	ACATCCAGTAAAAAGTAAAT
79305	77392	GACATCCAGTAAAAAGTAAA
79306	77393	AGACATCCAGTAAAAAGTAA
79307	77394	AAGACATCCAGTAAAAAGTA
79308	77395	AAAGACATCCAGTAAAAAGT
79309	77396	GAAAGACATCCAGTAAAAAG
79310	77397	GGAAAGACATCCAGTAAAAA
79311	77398	CGGAAAGACATCCAGTAAAA
79312	77399	ACGGAAAGACATCCAGTAAA
79313	77400	TACGGAAAGACATCCAGTAA
79314	77401	ATACGGAAAGACATCCAGTA
79315	77402	AATACGGAAAGACATCCAGT

128392	126479	AGGTGGGGGGATTGCCTTAG
128393	126480	GAGGTGGGGGGATTGCCTTA
128394	126481	TGAGGTGGGGGGATTGCCTT
128395	126482	CTGAGGTGGGGGGATTGCCT
128396	126483	GCTGAGGTGGGGGGATTGCC
128397	126484	GGCTGAGGTGGGGGGATTGC
128398	126485	AGGCTGAGGTGGGGGGATTG
128399	126486	GAGGCTGAGGTGGGGGGATT
128400	126487	GGAGGCTGAGGTGGGGGGAT
128401	126488	GGGAGGCTGAGGTGGGGGGA
128402	126489	TGGGAGGCTGAGGTGGGGGG
128403	126490	TTGGGAGGCTGAGGTGGGGG
128404	126491	CTTGGGAGGCTGAGGTGGGG
128405	126492	ACTTGGGAGGCTGAGGTGGG
128406	126493	TACTTGGGAGGCTGAGGTGG
128407	126494	CTACTTGGGAGGCTGAGGTG
128408	126495	GCTACTTGGGAGGCTGAGGT
128409	126496	AGCTACTTGGGAGGCTGAGG
128410	126497	CAGCTACTTGGGAGGCTGAG
128411	126498	CCAGCTACTTGGGAGGCTGA
128412	126499	CCCAGCTACTTGGGAGGCTG
128413	126500	TCCCAGCTACTTGGGAGGCT
128414	126501	GTCCCAGCTACTTGGGAGGC
128415	126502	AGTCCCAGCTACTTGGGAGG
128416	126503	TAGTCCCAGCTACTTGGGAG
128417	126504	GTAGTCCCAGCTACTTGGGA
128418	126505	TGTAGTCCCAGCTACTTGGG
128419	126506	CTGTAGTCCCAGCTACTTGG
128420	126507	CCTGTAGTCCCAGCTACTTG
128421	126508	GCCTGTAGTCCCAGCTACTT
128422	126509	TGCCTGTAGTCCCAGCTACT
128423	126510	TTGCCTGTAGTCCCAGCTAC
128424	126511	CTTGCCTGTAGTCCCAGCTA
128425	126512	GCTTGCCTGTAGTCCCAGCT
128426	126513	TGCTTGCCTGTAGTCCCAGC
128427	126514	GTGCTTGCCTGTAGTCCCAG
128428	126515	GGTGCTTGCCTGTAGTCCCA
128429	126516	TGGTGCTTGCCTGTAGTCCC
128430	126517	GTGGTGCTTGCCTGTAGTCC
128431	126518	GGTGGTGCTTGCCTGTAGTC
128432	126519	CGGTGGTGCTTGCCTGTAGT
128433	126520	ACGGTGGTGCTTGCCTGTAG
128434	126521	CACGGTGGTGCTTGCCTGTA
128435	126522	GCACGGTGGTGCTTGCCTGT
128436	126523	GGCACGGTGGTGCTTGCCTG
128437	126524	AGGCACGGTGGTGCTTGCCT
128438	126525	CAGGCACGGTGGTGCTTGCC
128439	126526	CCAGGCACGGTGGTGCTTGC
128440	126527	GCCAGGCACGGTGGTGCTTG
128441	126528	AGCCAGGCACGGTGGTGCTT
128442	126529	AAGCCAGGCACGGTGGTGCT
128443	126530	TAAGCCAGGCACGGTGGTGC
128444	126531	TTAAGCCAGGCACGGTGGTG
128445	126532	ATTAAGCCAGGCACGGTGGT
128446	126533	AATTAAGCCAGGCACGGTGG
128447	126534	AAATTAAGCCAGGCACGGTG
128448	126535	AAAATTAAGCCAGGCACGGT
128449	126536	AAAAATTAAGCCAGGCACGG
128450	126537	CAAAAATTAAGCCAGGCACG
128451	126538	ACAAAAATTAAGCCAGGCAC
128452	126539	TACAAAAATTAAGCCAGGCA
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128454	126541	TATACAAAAATTAAGCCAGG
128455	126542	ATATACAAAAATTAAGCCAG
128456	126543	AATATACAAAAATTAAGCCA
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128458	126545	AAAATATACAAAAATTAAGC
128459	126546	CAAAATATACAAAAATTAAG
128460	126547	GCAAAATATACAAAAATTAA
128461	126548	TGCAAAATATACAAAAATTA
128462	126549	CTGCAAAATATACAAAAATT

30169	28256	TTGTACTAGACAAAGTTAAG
30170	28257	CTTGTACTAGACAAAGTTAA
30171	28258	ACTTGTACTAGACAAAGTTA
30172	28259	AACTTGTACTAGACAAAGTT
30173	28260	TAACTTGTACTAGACAAAGT
30174	28261	CTAACTTGTACTAGACAAAG
30175	28262	GCTAACTTGTACTAGACAAA
30176	28263	AGCTAACTTGTACTAGACAA
30177	28264	AAGCTAACTTGTACTAGACA
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30179	28266	GAAAGCTAACTTGTACTAGA
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30181	28268	AAGAAAGCTAACTTGTACTA
30182	28269	TAAGAAAGCTAACTTGTACT
30183	28270	ATAAGAAAGCTAACTTGTAC
30184	28271	AATAAGAAAGCTAACTTGTA
30185	28272	GAATAAGAAAGCTAACTTGT
30186	28273	TGAATAAGAAAGCTAACTTG
30187	28274	CTGAATAAGAAAGCTAACTT
30188	28275	ACTGAATAAGAAAGCTAACT
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30194	28281	GCTACTACTGAATAAGAAAG
30195	28282	AGCTACTACTGAATAAGAAA
30196	28283	AAGCTACTACTGAATAAGAA
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30198	28285	GTAAGCTACTACTGAATAAG
30199	28286	AGTAAGCTACTACTGAATAA
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30209	28296	TGTAATTTATAGTAAGCTAC
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30213	28300	TTCTTGTAATTTATAGTAAG
30214	28301	ATTCTTGTAATTTATAGTAA
30215	28302	TATTCTTGTAATTTATAGTA
30216	28303	TTATTCTTGTAATTTATAGT
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30218	28305	TTTTATTCTTGTAATTTATA
30219	28306	TTTTTATTCTTGTAATTTAT
30220	28307	CTTTTTATTCTTGTAATTTA
30221	28308	TCTTTTTATTCTTGTAATTT
30222	28309	ATCTTTTTATTCTTGTAATT
30223	28310	AATCTTTTTATTCTTGTAAT
30224	28311	TAATCTTTTTATTCTTGTAA
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30227	28314	TGGTAATCTTTTTATTCTTG
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30229	28316	AATGGTAATCTTTTTATTCT
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30231	28318	AAAATGGTAATCTTTTTATT
30232	28319	GAAAATGGTAATCTTTTTAT
30233	28320	GGAAAATGGTAATCTTTTTA
30234	28321	GGGAAAATGGTAATCTTTTT
30235	28322	AGGGAAAATGGTAATCTTTT
30236	28323	GAGGGAAAATGGTAATCTTT
30237	28324	TGAGGGAAAATGGTAATCTT
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79316	77403	CAATACGGAAAGACATCCAG
79317	77404	ACAATACGGAAAGACATCCA
79318	77405	CACAATACGGAAAGACATCC
79319	77406	ACACAATACGGAAAGACATC
79320	77407	CACACAATACGGAAAGACAT
79321	77408	GCACACAATACGGAAAGACA
79322	77409	AGCACACAATACGGAAAGAC
79323	77410	AAGCACACAATACGGAAAGA
79324	77411	AAAGCACACAATACGGAAAG
79325	77412	AAAAGCACACAATACGGAAA
79326	77413	AAAAAGCACACAATACGGAA
79327	77414	AAAAAAGCACACAATACGGA
79328	77415	AAAAAAAGCACACAATACGG
79329	77416	AAAAAAAAGCACACAATACG
79330	77417	AAAAAAAAAGCACACAATAC
79331	77418	AAAAAAAAAAGCACACAATA
79332	77419	AAAAAAAAAAAGCACACAAT
79333	77420	AAAAAAAAAAAAGCACACAA
79334	77421	AAAAAAAAAAAAAGCACACA
79335	77422	AAAAAAAAAAAAAAGCACAC
79336	77423	AAAAAAAAAAAAAAAGCACA
79337	77424	AAAAAAAAAAAAAAAAGCAC
79338	77425	AAAAAAAAAAAAAAAAAGCA
79339	77426	AAAAAAAAAAAAAAAAAAGC
79340	77427	TAAAAAAAAAAAAAAAAAAG
79341	77428	ATAAAAAAAAAAAAAAAAAA
79342	77429	CATAAAAAAAAAAAAAAAAA
79343	77430	ACATAAAAAAAAAAAAAAAA
79344	77431	TACATAAAAAAAAAAAAAAA
79345	77432	CTACATAAAAAAAAAAAAAA
79346	77433	CCTACATAAAAAAAAAAAAA
79347	77434	CCCTACATAAAAAAAAAAAA
79348	77435	GCCCTACATAAAAAAAAAAA
79349	77436	TGCCCTACATAAAAAAAAAA
79350	77437	ATGCCCTACATAAAAAAAAA
79351	77438	TATGCCCTACATAAAAAAAA
79352	77439	GTATGCCCTACATAAAAAAA
79353	77440	TGTATGCCCTACATAAAAAA
79354	77441	ATGTATGCCCTACATAAAAA
79355	77442	AATGTATGCCCTACATAAAA
79356	77443	TAATGTATGCCCTACATAAA
79357	77444	GTAATGTATGCCCTACATAA
79358	77445	AGTAATGTATGCCCTACATA
79359	77446	AAGTAATGTATGCCCTACAT
79360	77447	TAAGTAATGTATGCCCTACA
79361	77448	TTAAGTAATGTATGCCCTAC
79362	77449	CTTAAGTAATGTATGCCCTA
79363	77450	ACTTAAGTAATGTATGCCCT
79364	77451	TACTTAAGTAATGTATGCCC
79365	77452	TTACTTAAGTAATGTATGCC
79366	77453	ATTACTTAAGTAATGTATGC
79367	77454	AATTACTTAAGTAATGTATG
79368	77455	AAATTACTTAAGTAATGTAT
79369	77456	AAAATTACTTAAGTAATGTA
79370	77457	TAAAATTACTTAAGTAATGT
79371	77458	TTAAAATTACTTAAGTAATG
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79373	77460	CTTTAAAATTACTTAAGTAA
79374	77461	GCTTTAAAATTACTTAAGTA
79375	77462	GGCTTTAAAATTACTTAAGT
79376	77463	AGGCTTTAAAATTACTTAAG
79377	77464	GAGGCTTTAAAATTACTTAA
79378	77465	GGAGGCTTTAAAATTACTTA
79379	77466	TGGAGGCTTTAAAATTACTT
79380	77467	ATGGAGGCTTTAAAATTACT
79381	77468	TATGGAGGCTTTAAAATTAC
79382	77469	TTATGGAGGCTTTAAAATTA
79383	77470	CTTATGGAGGCTTTAAAATT
79384	77471	ACTTATGGAGGCTTTAAAAT
79385	77472	TACTTATGGAGGCTTTAAAA
79386	77473	TTACTTATGGAGGCTTTAAA

128463	126550	TCTGCAAAATATACAAAAAT
128464	126551	CTCTGCAAAATATACAAAAA
128465	126552	TCTCTGCAAAATATACAAAA
128466	126553	GTCTCTGCAAAATATACAAA
128467	126554	TGTCTCTGCAAAATATACAA
128468	126555	CTGTCTCTGCAAAATATACA
128469	126556	CCTGTCTCTGCAAAATATAC
128470	126557	CCCTGTCTCTGCAAAATATA
128471	126558	ACCCTGTCTCTGCAAAATAT
128472	126559	AACCCTGTCTCTGCAAAATA
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128474	126561	GAAACCCTGTCTCTGCAAAA
128475	126562	TGAAACCCTGTCTCTGCAAA
128476	126563	GTGAAACCCTGTCTCTGCAA
128477	126564	GGTGAAACCCTGTCTCTGCA
128478	126565	TGGTGAAACCCTGTCTCTGC
128479	126566	ATGGTGAAACCCTGTCTCTG
128480	126567	CATGGTGAAACCCTGTCTCT
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128482	126569	AACATGGTGAAACCCTGTCT
128483	126570	CAACATGGTGAAACCCTGTC
128484	126571	GCAACATGGTGAAACCCTGT
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128486	126573	GGGCAACATGGTGAAACCCT
128487	126574	TGGGCAACATGGTGAAACCC
128488	126575	CTGGGCAACATGGTGAAACC
128489	126576	CCTGGGCAACATGGTGAAAC
128490	126577	GCCTGGGCAACATGGTGAAA
128491	126578	AGCCTGGGCAACATGGTGAA
128492	126579	CAGCCTGGGCAACATGGTGA
128493	126580	CCAGCCTGGGCAACATGGTG
128494	126581	ACCAGCCTGGGCAACATGGT
128495	126582	CACCAGCCTGGGCAACATGG
128496	126583	ACACCAGCCTGGGCAACATG
128497	126584	GACACCAGCCTGGGCAACAT
128498	126585	CGACACCAGCCTGGGCAACA
128499	126586	TCGACACCAGCCTGGGCAAC
128500	126587	TTCGACACCAGCCTGGGCAA
128501	126588	GTTCGACACCAGCCTGGGCA
128502	126589	AGTTCGACACCAGCCTGGGC
128503	126590	GAGTTCGACACCAGCCTGGG
128504	126591	GGAGTTCGACACCAGCCTGG
128505	126592	AGGAGTTCGACACCAGCCTG
128506	126593	CAGGAGTTCGACACCAGCCT
128507	126594	TCAGGAGTTCGACACCAGCC
128508	126595	CTCAGGAGTTCGACACCAGC
128509	126596	GCTCAGGAGTTCGACACCAG
128510	126597	AGCTCAGGAGTTCGACACCA
128511	126598	GAGCTCAGGAGTTCGACACC
128512	126599	TGAGCTCAGGAGTTCGACAC
128513	126600	TTGAGCTCAGGAGTTCGACA
128514	126601	CTTGAGCTCAGGAGTTCGAC
128515	126602	GCTTGAGCTCAGGAGTTCGA
128516	126603	TGCTTGAGCTCAGGAGTTCG
128517	126604	CTGCTTGAGCTCAGGAGTTC
128518	126605	ACTGCTTGAGCTCAGGAGTT
128519	126606	GACTGCTTGAGCTCAGGAGT
128520	126607	AGACTGCTTGAGCTCAGGAG
128521	126608	CAGACTGCTTGAGCTCAGGA
128522	126609	GCAGACTGCTTGAGCTCAGG
128523	126610	GGCAGACTGCTTGAGCTCAG
128524	126611	AGGCAGACTGCTTGAGCTCA
128525	126612	CAGGCAGACTGCTTGAGCTC
128526	126613	ACAGGCAGACTGCTTGAGCT
128527	126614	CACAGGCAGACTGCTTGAGC
128528	126615	ACACAGGCAGACTGCTTGAG
128529	126616	GACACAGGCAGACTGCTTGA
128530	126617	TGACACAGGCAGACTGCTTG
128531	126618	CTGACACAGGCAGACTGCTT
128532	126619	GCTGACACAGGCAGACTGCT
128533	126620	GGCTGACACAGGCAGACTGC

30240	28327	GTGTGAGGGAAAATGGTAAT
30241	28328	AGTGTGAGGGAAAATGGTAA
30242	28329	CAGTGTGAGGGAAAATGGTA
30243	28330	ACAGTGTGAGGGAAAATGGT
30244	28331	AACAGTGTGAGGGAAAATGG
30245	28332	AAACAGTGTGAGGGAAAATG
30246	28333	AAAACAGTGTGAGGGAAAAT
30247	28334	CAAAACAGTGTGAGGGAAAA
30248	28335	ACAAAACAGTGTGAGGGAAA
30249	28336	CACAAAACAGTGTGAGGGAA
30250	28337	CCACAAAACAGTGTGAGGGA
30251	28338	TCCACAAAACAGTGTGAGGG
30252	28339	CTCCACAAAACAGTGTGAGG
30253	28340	TCTCCACAAAACAGTGTGAG
30254	28341	TTCTCCACAAAACAGTGTGA
30255	28342	ATTCTCCACAAAACAGTGTG
30256	28343	CATTCTCCACAAAACAGTGT
30257	28344	GCATTCTCCACAAAACAGTG
30258	28345	GGCATTCTCCACAAAACAGT
30259	28346	AGGCATTCTCCACAAAACAG
30260	28347	TAGGCATTCTCCACAAAACA
30261	28348	TTAGGCATTCTCCACAAAAC
30262	28349	TTTAGGCATTCTCCACAAAA
30263	28350	CTTTAGGCATTCTCCACAAA
30264	28351	ACTTTAGGCATTCTCCACAA
30265	28352	AACTTTAGGCATTCTCCACA
30266	28353	TAACTTTAGGCATTCTCCAC
30267	28354	GTAACTTTAGGCATTCTCCA
30268	28355	AGTAACTTTAGGCATTCTCC
30269	28356	AAGTAACTTTAGGCATTCTC
30270	28357	AAAGTAACTTTAGGCATTCT
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30276	28363	AAAGAAAAAGTAACTTTAGG
30277	28364	AAAAGAAAAAGTAACTTTAG
30278	28365	AAAAAGAAAAAGTAACTTTA
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30281	28368	TGTAAAAAGAAAAAGTAACT
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30294	28381	AGGAATACTGACCTGTAAAA
30295	28382	TAGGAATACTGACCTGTAAA
30296	28383	ATAGGAATACTGACCTGTAA
30297	28384	AATAGGAATACTGACCTGTA
30298	28385	AAATAGGAATACTGACCTGT
30299	28386	CAAATAGGAATACTGACCTG
30300	28387	CCAAATAGGAATACTGACCT
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30303	28390	ATGCCAAATAGGAATACTGA
30304	28391	GATGCCAAATAGGAATACTG
30305	28392	GGATGCCAAATAGGAATACT
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30307	28394	TAGGATGCCAAATAGGAATA
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79387	77474	CTTACTTATGGAGGCTTTAA
79388	77475	ACTTACTTATGGAGGCTTTA
79389	77476	CACTTACTTATGGAGGCTTT
79390	77477	ACACTTACTTATGGAGGCTT
79391	77478	CACACTTACTTATGGAGGCT
79392	77479	TCACACTTACTTATGGAGGC
79393	77480	ATCACACTTACTTATGGAGG
79394	77481	AATCACACTTACTTATGGAG
79395	77482	AAATCACACTTACTTATGGA
79396	77483	GAAATCACACTTACTTATGG
79397	77484	GGAAATCACACTTACTTATG
79398	77485	AGGAAATCACACTTACTTAT
79399	77486	CAGGAAATCACACTTACTTA
79400	77487	GCAGGAAATCACACTTACTT
79401	77488	GGCAGGAAATCACACTTACT
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79403	77490	TGGGCAGGAAATCACACTTA
79404	77491	ATGGGCAGGAAATCACACTT
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79407	77494	CACATGGGCAGGAAATCACA
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79409	77496	AACACATGGGCAGGAAATCA
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79411	77498	CAAACACATGGGCAGGAAAT
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79415	77502	TTGCCAAACACATGGGCAGG
79416	77503	TTTGCCAAACACATGGGCAG
79417	77504	TTTTGCCAAACACATGGGCA
79418	77505	CTTTTGCCAAACACATGGGC
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79422	77509	ATTCCTTTTGCCAAACACAT
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79429	77516	CAATGCAATTCCTTTTGCCA
79430	77517	CCAATGCAATTCCTTTTGCC
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79432	77519	CACCAATGCAATTCCTTTTG
79433	77520	CCACCAATGCAATTCCTTTT
79434	77521	ACCACCAATGCAATTCCTTT
79435	77522	TACCACCAATGCAATTCCTT
79436	77523	CTACCACCAATGCAATTCCT
79437	77524	TCTACCACCAATGCAATTCC
79438	77525	GTCTACCACCAATGCAATTC
79439	77526	AGTCTACCACCAATGCAATT
79440	77527	AAGTCTACCACCAATGCAAT
79441	77528	TAAGTCTACCACCAATGCAA
79442	77529	GTAAGTCTACCACCAATGCA
79443	77530	TGTAAGTCTACCACCAATGC
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79445	77532	AATGTAAGTCTACCACCAAT
79446	77533	TAATGTAAGTCTACCACCAA
79447	77534	ATAATGTAAGTCTACCACCA
79448	77535	TATAATGTAAGTCTACCACC
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79451	77538	GACTATAATGTAAGTCTACC
79452	77539	AGACTATAATGTAAGTCTAC
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79454	77541	TAAGACTATAATGTAAGTCT
79455	77542	GTAAGACTATAATGTAAGTC
79456	77543	GGTAAGACTATAATGTAAGT
79457	77544	AGGTAAGACTATAATGTAAG

128534	126621	AGGCTGACACAGGCAGACTG
128535	126622	GAGGCTGACACAGGCAGACT
128536	126623	TGAGGCTGACACAGGCAGAC
128537	126624	GTGAGGCTGACACAGGCAGA
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128539	126626	TTGTGAGGCTGACACAGGCA
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128545	126632	ACCACTTTGTGAGGCTGACA
128546	126633	CACCACTTTGTGAGGCTGAC
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128548	126635	CCCACCACTTTGTGAGGCTG
128549	126636	TCCCACCACTTTGTGAGGCT
128550	126637	GTCCCACCACTTTGTGAGGC
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128552	126639	TAGTCCCACCACTTTGTGAG
128553	126640	GTAGTCCCACCACTTTGTGA
128554	126641	TGTAGTCCCACCACTTTGTG
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128556	126643	CCTGTAGTCCCACCACTTTG
128557	126644	GCCTGTAGTCCCACCACTTT
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128560	126647	CATGCCTGTAGTCCCACCAC
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128577	126664	GGCCTGCCATGGTGGCTCAT
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128593	126680	AGTTTATTGTGATTCTGGCC
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128601	126688	AATTTATAAGTTTATTGTGA
128602	126689	TAATTTATAAGTTTATTGTG
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30311	28398	GGATTAGGATGCCAAATAGG
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30315	28402	AAGGGGATTAGGATGCCAAA
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30328	28415	TTCAGATTTGGGAAAGGGGA
30329	28416	ATTCAGATTTGGGAAAGGGG
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30332	28419	AAAATTCAGATTTGGGAAAG
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30351	28438	AATGCAAGCTTCAAATCCCA
30352	28439	AAATGCAAGCTTCAAATCCC
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30378	28465	CAACAAGGAAGACAAATCAT
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30380	28467	TACAACAAGGAAGACAAATC
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79458	77545	CAGGTAAGACTATAATGTAA
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79460	77547	TCCAGGTAAGACTATAATGT
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79462	77549	ACTCCAGGTAAGACTATAAT
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79464	77551	CTACTCCAGGTAAGACTATA
79465	77552	GCTACTCCAGGTAAGACTAT
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79475	77562	GTCCTCCTGTGCTACTCCAG
79476	77563	GGTCCTCCTGTGCTACTCCA
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79502	77589	GCCTCGAAGTTCACCTATTA
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79506	77593	GCTTGCCTCGAAGTTCACCT
79507	77594	GGCTTGCCTCGAAGTTCACC
79508	77595	AGGCTTGCCTCGAAGTTCAC
79509	77596	AAGGCTTGCCTCGAAGTTCA
79510	77597	TAAGGCTTGCCTCGAAGTTC
79511	77598	CTAAGGCTTGCCTCGAAGTT
79512	77599	GCTAAGGCTTGCCTCGAAGT
79513	77600	TGCTAAGGCTTGCCTCGAAG
79514	77601	ATGCTAAGGCTTGCCTCGAA
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79516	77603	CAATGCTAAGGCTTGCCTCG
79517	77604	TCAATGCTAAGGCTTGCCTC
79518	77605	CTCAATGCTAAGGCTTGCCT
79519	77606	CCTCAATGCTAAGGCTTGCC
79520	77607	ACCTCAATGCTAAGGCTTGC
79521	77608	AACCTCAATGCTAAGGCTTG
79522	77609	CAACCTCAATGCTAAGGCTT
79523	77610	GCAACCTCAATGCTAAGGCT
79524	77611	GGCAACCTCAATGCTAAGGC
79525	77612	TGGCAACCTCAATGCTAAGG
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128605	126692	AGTTAATTTATAAGTTTATT
128606	126693	AAGTTAATTTATAAGTTTAT
128607	126694	CAAGTTAATTTATAAGTTTA
128608	126695	TCAAGTTAATTTATAAGTTT
128609	126696	CTCAAGTTAATTTATAAGTT
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128616	126703	ATTTCTTCTCAAGTTAATTT
128617	126704	CATTTCTTCTCAAGTTAATT
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128628	126715	AAGACATCAATCATTTCTTC
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128631	126718	ATGAAGACATCAATCATTTC
128632	126719	CATGAAGACATCAATCATTT
128633	126720	TCATGAAGACATCAATCATT
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128636	126723	ACATCATGAAGACATCAATC
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128639	126726	TCAACATCATGAAGACATCA
128640	126727	CTCAACATCATGAAGACATC
128641	126728	ACTCAACATCATGAAGACAT
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128643	126730	AGACTCAACATCATGAAGAC
128644	126731	AAGACTCAACATCATGAAGA
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128646	126733	GGAAGACTCAACATCATGAA
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128649	126736	ACAGGAAGACTCAACATCAT
128650	126737	AACAGGAAGACTCAACATCA
128651	126738	GAACAGGAAGACTCAACATC
128652	126739	TGAACAGGAAGACTCAACAT
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128659	126746	TTGTTCTTGAACAGGAAGAC
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128673	126760	ATTGAAGGTATACTTTGTTC
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128675	126762	CTATTGAAGGTATACTTTGT

30382	28469	TGTACAACAAGGAAGACAAA
30383	28470	GTGTACAACAAGGAAGACAA
30384	28471	TGTGTACAACAAGGAAGACA
30385	28472	CTGTGTACAACAAGGAAGAC
30386	28473	CCTGTGTACAACAAGGAAGA
30387	28474	TCCTGTGTACAACAAGGAAG
30388	28475	CTCCTGTGTACAACAAGGAA
30389	28476	GCTCCTGTGTACAACAAGGA
30390	28477	TGCTCCTGTGTACAACAAGG
30391	28478	CTGCTCCTGTGTACAACAAG
30392	28479	CCTGCTCCTGTGTACAACAA
30393	28480	CCCTGCTCCTGTGTACAACA
30394	28481	TCCCTGCTCCTGTGTACAAC
30395	28482	GTCCCTGCTCCTGTGTACAA
30396	28483	AGTCCCTGCTCCTGTGTACA
30397	28484	AAGTCCCTGCTCCTGTGTAC
30398	28485	AAAGTCCCTGCTCCTGTGTA
30399	28486	TAAAGTCCCTGCTCCTGTGT
30400	28487	GTAAAGTCCCTGCTCCTGTG
30401	28488	TGTAAAGTCCCTGCTCCTGT
30402	28489	TTGTAAAGTCCCTGCTCCTG
30403	28490	ATTGTAAAGTCCCTGCTCCT
30404	28491	AATTGTAAAGTCCCTGCTCC
30405	28492	TAATTGTAAAGTCCCTGCTC
30406	28493	CTAATTGTAAAGTCCCTGCT
30407	28494	ACTAATTGTAAAGTCCCTGC
30408	28495	TACTAATTGTAAAGTCCCTG
30409	28496	ATACTAATTGTAAAGTCCCT
30410	28497	AATACTAATTGTAAAGTCCC
30411	28498	GAATACTAATTGTAAAGTCC
30412	28499	CGAATACTAATTGTAAAGTC
30413	28500	GCGAATACTAATTGTAAAGT
30414	28501	TGCGAATACTAATTGTAAAG
30415	28502	ATGCGAATACTAATTGTAAA
30416	28503	GATGCGAATACTAATTGTAA
30417	28504	GGATGCGAATACTAATTGTA
30418	28505	GGGATGCGAATACTAATTGT
30419	28506	AGGGATGCGAATACTAATTG
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30421	28508	GCAGGGATGCGAATACTAAT
30422	28509	AGCAGGGATGCGAATACTAA
30423	28510	GAGCAGGGATGCGAATACTA
30424	28511	GGAGCAGGGATGCGAATACT
30425	28512	AGGAGCAGGGATGCGAATAC
30426	28513	AAGGAGCAGGGATGCGAATA
30427	28514	GAAGGAGCAGGGATGCGAAT
30428	28515	TGAAGGAGCAGGGATGCGAA
30429	28516	ATGAAGGAGCAGGGATGCGA
30430	28517	TATGAAGGAGCAGGGATGCG
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30432	28519	AGTATGAAGGAGCAGGGATG
30433	28520	AAGTATGAAGGAGCAGGGAT
30434	28521	GAAGTATGAAGGAGCAGGGA
30435	28522	CGAAGTATGAAGGAGCAGGG
30436	28523	ACGAAGTATGAAGGAGCAGG
30437	28524	CACGAAGTATGAAGGAGCAG
30438	28525	TCACGAAGTATGAAGGAGCA
30439	28526	ATCACGAAGTATGAAGGAGC
30440	28527	CATCACGAAGTATGAAGGAG
30441	28528	ACATCACGAAGTATGAAGGA
30442	28529	TACATCACGAAGTATGAAGG
30443	28530	TTACATCACGAAGTATGAAG
30444	28531	CTTACATCACGAAGTATGAA
30445	28532	CCTTACATCACGAAGTATGA
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30447	28534	TGCCTTACATCACGAAGTAT
30448	28535	TTGCCTTACATCACGAAGTA
30449	28536	CTTGCCTTACATCACGAAGT
30450	28537	ACTTGCCTTACATCACGAAG
30451	28538	AACTTGCCTTACATCACGAA
30452	28539	TAACTTGCCTTACATCACGA

79529	77616	CTGATGGCAACCTCAATGCT
79530	77617	GCTGATGGCAACCTCAATGC
79531	77618	TGCTGATGGCAACCTCAATG
79532	77619	ATGCTGATGGCAACCTCAAT
79533	77620	AATGCTGATGGCAACCTCAA
79534	77621	CAATGCTGATGGCAACCTCA
79535	77622	GCAATGCTGATGGCAACCTC
79536	77623	AGCAATGCTGATGGCAACCT
79537	77624	AAGCAATGCTGATGGCAACC
79538	77625	CAAGCAATGCTGATGGCAAC
79539	77626	CCAAGCAATGCTGATGGCAA
79540	77627	ACCAAGCAATGCTGATGGCA
79541	77628	AACCAAGCAATGCTGATGGC
79542	77629	CAACCAAGCAATGCTGATGG
79543	77630	TCAACCAAGCAATGCTGATG
79544	77631	ATCAACCAAGCAATGCTGAT
79545	77632	CATCAACCAAGCAATGCTGA
79546	77633	ACATCAACCAAGCAATGCTG
79547	77634	CACATCAACCAAGCAATGCT
79548	77635	ACACATCAACCAAGCAATGC
79549	77636	AACACATCAACCAAGCAATG
79550	77637	GAACACATCAACCAAGCAAT
79551	77638	TGAACACATCAACCAAGCAA
79552	77639	ATGAACACATCAACCAAGCA
79553	77640	AATGAACACATCAACCAAGC
79554	77641	GAATGAACACATCAACCAAG
79555	77642	AGAATGAACACATCAACCAA
79556	77643	AAGAATGAACACATCAACCA
79557	77644	GAAGAATGAACACATCAACC
79558	77645	AGAAGAATGAACACATCAAC
79559	77646	CAGAAGAATGAACACATCAA
79560	77647	CCAGAAGAATGAACACATCA
79561	77648	CCCAGAAGAATGAACACATC
79562	77649	TCCCAGAAGAATGAACACAT
79563	77650	ATCCCAGAAGAATGAACACA
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79565	77652	CCATCCCAGAAGAATGAACA
79566	77653	TCCATCCCAGAAGAATGAAC
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79569	77656	TAATCCATCCCAGAAGAATG
79570	77657	GTAATCCATCCCAGAAGAAT
79571	77658	TGTAATCCATCCCAGAAGAA
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79574	77661	GGTTGTAATCCATCCCAGAA
79575	77662	AGGTTGTAATCCATCCCAGA
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79577	77664	AAAGGTTGTAATCCATCCCA
79578	77665	TAAAGGTTGTAATCCATCCC
79579	77666	GTAAAGGTTGTAATCCATCC
79580	77667	AGTAAAGGTTGTAATCCATC
79581	77668	CAGTAAAGGTTGTAATCCAT
79582	77669	CCAGTAAAGGTTGTAATCCA
79583	77670	TCCAGTAAAGGTTGTAATCC
79584	77671	GTCCAGTAAAGGTTGTAATC
79585	77672	AGTCCAGTAAAGGTTGTAAT
79586	77673	AAGTCCAGTAAAGGTTGTAA
79587	77674	AAAGTCCAGTAAAGGTTGTA
79588	77675	TAAAGTCCAGTAAAGGTTGT
79589	77676	ATAAAGTCCAGTAAAGGTTG
79590	77677	TATAAAGTCCAGTAAAGGTT
79591	77678	GTATAAAGTCCAGTAAAGGT
79592	77679	AGTATAAAGTCCAGTAAAGG
79593	77680	AAGTATAAAGTCCAGTAAAG
79594	77681	AAAGTATAAAGTCCAGTAAA
79595	77682	AAAAGTATAAAGTCCAGTAA
79596	77683	GAAAAGTATAAAGTCCAGTA
79597	77684	TGAAAAGTATAAAGTCCAGT
79598	77685	GTGAAAAGTATAAAGTCCAG
79599	77686	GGTGAAAAGTATAAAGTCCA

128676	126763	GCTATTGAAGGTATACTTTG
128677	126764	TGCTATTGAAGGTATACTTT
128678	126765	ATGCTATTGAAGGTATACTT
128679	126766	TATGCTATTGAAGGTATACT
128680	126767	ATATGCTATTGAAGGTATAC
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128682	126769	TAATATGCTATTGAAGGTAT
128683	126770	TTAATATGCTATTGAAGGTA
128684	126771	TTTAATATGCTATTGAAGGT
128685	126772	CTTTAATATGCTATTGAAGG
128686	126773	ACTTTAATATGCTATTGAAG
128687	126774	AACTTTAATATGCTATTGAA
128688	126775	AAACTTTAATATGCTATTGA
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128690	126777	ATAAACTTTAATATGCTATT
128691	126778	GATAAACTTTAATATGCTAT
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128693	126780	AGGATAAACTTTAATATGCT
128694	126781	AAGGATAAACTTTAATATGC
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128698	126785	AGCCAAGGATAAACTTTAAT
128699	126786	CAGCCAAGGATAAACTTTAA
128700	126787	CCAGCCAAGGATAAACTTTA
128701	126788	TCCAGCCAAGGATAAACTTT
128702	126789	ATCCAGCCAAGGATAAACTT
128703	126790	CATCCAGCCAAGGATAAACT
128704	126791	GCATCCAGCCAAGGATAAAC
128705	126792	TGCATCCAGCCAAGGATAAA
128706	126793	CTGCATCCAGCCAAGGATAA
128707	126794	ACTGCATCCAGCCAAGGATA
128708	126795	CACTGCATCCAGCCAAGGAT
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128712	126799	CAGCCACTGCATCCAGCCAA
128713	126800	TCAGCCACTGCATCCAGCCA
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128715	126802	CGTCAGCCACTGCATCCAGC
128716	126803	GCGTCAGCCACTGCATCCAG
128717	126804	GGCGTCAGCCACTGCATCCA
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128720	126807	ACAGGCGTCAGCCACTGCAT
128721	126808	TACAGGCGTCAGCCACTGCA
128722	126809	TTACAGGCGTCAGCCACTGC
128723	126810	ATTACAGGCGTCAGCCACTG
128724	126811	GATTACAGGCGTCAGCCACT
128725	126812	GGATTACAGGCGTCAGCCAC
128726	126813	GGGATTACAGGCGTCAGCCA
128727	126814	TGGGATTACAGGCGTCAGCC
128728	126815	GTGGGATTACAGGCGTCAGC
128729	126816	GGTGGGATTACAGGCGTCAG
128730	126817	AGGTGGGATTACAGGCGTCA
128731	126818	GAGGTGGGATTACAGGCGTC
128732	126819	AGAGGTGGGATTACAGGCGT
128733	126820	AAGAGGTGGGATTACAGGCG
128734	126821	AAAGAGGTGGGATTACAGGC
128735	126822	CAAAGAGGTGGGATTACAGG
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128737	126824	CCCAAAGAGGTGGGATTACA
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128739	126826	CTCCCAAAGAGGTGGGATTA
128740	126827	CCTCCCAAAGAGGTGGGATT
128741	126828	GCCTCCCAAAGAGGTGGGAT
128742	126829	TGCCTCCCAAAGAGGTGGGA
128743	126830	CTGCCTCCCAAAGAGGTGGG
128744	126831	TCTGCCTCCCAAAGAGGTGG
128745	126832	CTCTGCCTCCCAAAGAGGTG
128746	126833	CCTCTGCCTCCCAAAGAGGT

30453	28540	ATAACTTGCCTTACATCACG
30454	28541	AATAACTTGCCTTACATCAC
30455	28542	AAATAACTTGCCTTACATCA
30456	28543	AAAATAACTTGCCTTACATC
30457	28544	GAAAATAACTTGCCTTACAT
30458	28545	TGAAAATAACTTGCCTTACA
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30460	28547	AGTGAAAATAACTTGCCTTA
30461	28548	AAGTGAAAATAACTTGCCTT
30462	28549	TAAGTGAAAATAACTTGCCT
30463	28550	ATAAGTGAAAATAACTTGCC
30464	28551	CATAAGTGAAAATAACTTGC
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30466	28553	AGCATAAGTGAAAATAACTT
30467	28554	AAGCATAAGTGAAAATAACT
30468	28555	TAAGCATAAGTGAAAATAAC
30469	28556	TTAAGCATAAGTGAAAATAA
30470	28557	CTTAAGCATAAGTGAAAATA
30471	28558	ACTTAAGCATAAGTGAAAAT
30472	28559	AACTTAAGCATAAGTGAAAA
30473	28560	AAACTTAAGCATAAGTGAAA
30474	28561	GAAACTTAAGCATAAGTGAA
30475	28562	AGAAACTTAAGCATAAGTGA
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30485	28572	TTACAGGGGAAGAAACTTAA
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30487	28574	TTTTACAGGGGAAGAAACTT
30488	28575	TTTTTACAGGGGAAGAAACT
30489	28576	CTTTTTACAGGGGAAGAAAC
30490	28577	CCTTTTTACAGGGGAAGAAA
30491	28578	CCCTTTTTACAGGGGAAGAA
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30494	28581	ATCCCCTTTTTACAGGGGAA
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30499	28586	CTTCCATCCCCTTTTTACAG
30500	28587	TCTTCCATCCCCTTTTTACA
30501	28588	CTCTTCCATCCCCTTTTTAC
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30507	28594	TTAATCCTCTTCCATCCCCT
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30509	28596	ATTTAATCCTCTTCCATCCC
30510	28597	CATTTAATCCTCTTCCATCC
30511	28598	TCATTTAATCCTCTTCCATC
30512	28599	TTCATTTAATCCTCTTCCAT
30513	28600	ATTCATTTAATCCTCTTCCA
30514	28601	AATTCATTTAATCCTCTTCC
30515	28602	TAATTCATTTAATCCTCTTC
30516	28603	TTAATTCATTTAATCCTCTT
30517	28604	TTTAATTCATTTAATCCTCT
30518	28605	GTTTAATTCATTTAATCCTC
30519	28606	TGTTTAATTCATTTAATCCT
30520	28607	ATGTTTAATTCATTTAATCC
30521	28608	CATGTTTAATTCATTTAATC
30522	28609	ACATGTTTAATTCATTTAAT
30523	28610	TACATGTTTAATTCATTTAA

79600	77687	TGGTGAAAAGTATAAAGTCC
79601	77688	CTGGTGAAAAGTATAAAGTC
79602	77689	ACTGGTGAAAAGTATAAAGT
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79606	77693	CCTTACTGGTGAAAAGTATA
79607	77694	GCCTTACTGGTGAAAAGTAT
79608	77695	AGCCTTACTGGTGAAAAGTA
79609	77696	AAGCCTTACTGGTGAAAAGT
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79611	77698	TAAAGCCTTACTGGTGAAAA
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79618	77705	CCTTTTTTAAAGCCTTACTG
79619	77706	TCCTTTTTTAAAGCCTTACT
79620	77707	CTCCTTTTTTAAAGCCTTAC
79621	77708	ACTCCTTTTTTAAAGCCTTA
79622	77709	AACTCCTTTTTTAAAGCCTT
79623	77710	CAACTCCTTTTTTAAAGCCT
79624	77711	TCAACTCCTTTTTTAAAGCC
79625	77712	TTCAACTCCTTTTTTAAAGC
79626	77713	TTTCAACTCCTTTTTTAAAG
79627	77714	GTTTCAACTCCTTTTTTAAA
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79629	77716	ATGTTTCAACTCCTTTTTTA
79630	77717	AATGTTTCAACTCCTTTTTT
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79632	77719	CTAATGTTTCAACTCCTTTT
79633	77720	TCTAATGTTTCAACTCCTTT
79634	77721	CTCTAATGTTTCAACTCCTT
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79637	77724	ATTCTCTAATGTTTCAACTC
79638	77725	TATTCTCTAATGTTTCAACT
79639	77726	TTATTCTCTAATGTTTCAAC
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79663	77750	CAGTGAATATTACTGCCTGG
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128747	126834	ACCTCTGCCTCCCAAAGAGG
128748	126835	CACCTCTGCCTCCCAAAGAG
128749	126836	CCACCTCTGCCTCCCAAAGA
128750	126837	CCCACCTCTGCCTCCCAAAG
128751	126838	GCCCACCTCTGCCTCCCAAA
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128753	126840	CTGCCCACCTCTGCCTCCCA
128754	126841	TCTGCCCACCTCTGCCTCCC
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128756	126843	GATCTGCCCACCTCTGCCTC
128757	126844	TGATCTGCCCACCTCTGCCT
128758	126845	GTGATCTGCCCACCTCTGCC
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128762	126849	TCAGGTGATCTGCCCACCTC
128763	126850	CTCAGGTGATCTGCCCACCT
128764	126851	CCTCAGGTGATCTGCCCACC
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128768	126855	CAGACCTCAGGTGATCTGCC
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128779	126866	GTCTCGAACTCCAGACCTCA
128780	126867	GGTCTCGAACTCCAGACCTC
128781	126868	TGGTCTCGAACTCCAGACCT
128782	126869	CTGGTCTCGAACTCCAGACC
128783	126870	GCTGGTCTCGAACTCCAGAC
128784	126871	GGCTGGTCTCGAACTCCAGA
128785	126872	AGGCTGGTCTCGAACTCCAG
128786	126873	CAGGCTGGTCTCGAACTCCA
128787	126874	CCAGGCTGGTCTCGAACTCC
128788	126875	GCCAGGCTGGTCTCGAACTC
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128795	126882	CATGTTGGCCAGGCTGGTCT
128796	126883	CCATGTTGGCCAGGCTGGTC
128797	126884	ACCATGTTGGCCAGGCTGGT
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128799	126886	TCACCATGTTGGCCAGGCTG
128800	126887	TTCACCATGTTGGCCAGGCT
128801	126888	TTTCACCATGTTGGCCAGGC
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128803	126890	GGTTTCACCATGTTGGCCAG
128804	126891	GGGTTTCACCATGTTGGCCA
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128807	126894	ACGGGGTTTCACCATGTTGG
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128810	126897	GAGACGGGGTTTCACCATGT
128811	126898	AGAGACGGGGTTTCACCATG
128812	126899	TAGAGACGGGGTTTCACCAT
128813	126900	GTAGAGACGGGGTTTCACCA
128814	126901	AGTAGAGACGGGGTTTCACC
128815	126902	TAGTAGAGACGGGGTTTCAC
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30524	28611	TTACATGTTTAATTCATTTA
30525	28612	GTTACATGTTTAATTCATTT
30526	28613	TGTTACATGTTTAATTCATT
30527	28614	GTGTTACATGTTTAATTCAT
30528	28615	CGTGTTACATGTTTAATTCA
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30532	28619	TAAGCGTGTTACATGTTTAA
30533	28620	TTAAGCGTGTTACATGTTTA
30534	28621	TTTAAGCGTGTTACATGTTT
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30536	28623	GCTTTAAGCGTGTTACATGT
30537	28624	TGCTTTAAGCGTGTTACATG
30538	28625	TTGCTTTAAGCGTGTTACAT
30539	28626	ATTGCTTTAAGCGTGTTACA
30540	28627	CATTGCTTTAAGCGTGTTAC
30541	28628	GCATTGCTTTAAGCGTGTTA
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30544	28631	CAGGCATTGCTTTAAGCGTG
30545	28632	CCAGGCATTGCTTTAAGCGT
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30548	28635	TTGCCAGGCATTGCTTTAAG
30549	28636	CTTGCCAGGCATTGCTTTAA
30550	28637	ACTTGCCAGGCATTGCTTTA
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30552	28639	TTACTTGCCAGGCATTGCTT
30553	28640	ATTACTTGCCAGGCATTGCT
30554	28641	TATTACTTGCCAGGCATTGC
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30582	28669	TAAGAACAGCTAAAAGTTAC
30583	28670	ATAAGAACAGCTAAAAGTTA
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30585	28672	TAATAAGAACAGCTAAAAGT
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30587	28674	GCTAATAAGAACAGCTAAAA
30588	28675	TGCTAATAAGAACAGCTAAA
30589	28676	ATGCTAATAAGAACAGCTAA
30590	28677	CATGCTAATAAGAACAGCTA
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79674	77761	AGACTATTTACCAGTGAATA
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79676	77763	GAAGACTATTTACCAGTGAA
79677	77764	GGAAGACTATTTACCAGTGA
79678	77765	TGGAAGACTATTTACCAGTG
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79680	77767	GCTGGAAGACTATTTACCAG
79681	77768	GGCTGGAAGACTATTTACCA
79682	77769	AGGCTGGAAGACTATTTACC
79683	77770	CAGGCTGGAAGACTATTTAC
79684	77771	ACAGGCTGGAAGACTATTTA
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79686	77773	CCACAGGCTGGAAGACTATT
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79688	77775	GGCCACAGGCTGGAAGACTA
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79733	77820	AGCAGCTGAGGCTGCATTCT
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79738	77825	GGCAGAGCAGCTGAGGCTGC
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79740	77827	TAGGCAGAGCAGCTGAGGCT
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128831	126918	TTTTTTAAAATATTTTTAGT
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128842	126929	CAGCTAATACTTTTTTTAAA
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79757	77844	AAAAGAATCCTACTCCATAG
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128889	126976	CTACCTCAGCCTCCAGAGTA
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128919	127006	CTCTCTGCCTCCTGGGTTCA
128920	127007	ACTCTCTGCCTCCTGGGTTC
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128923	127010	TGCACTCTCTGCCTCCTGGG
128924	127011	CTGCACTCTCTGCCTCCTGG
128925	127012	ACTGCACTCTCTGCCTCCTG
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128928	127015	CTCACTGCACTCTCTGCCTC
128929	127016	ACTCACTGCACTCTCTGCCT
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128931	127018	TGACTCACTGCACTCTCTGC
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128933	127020	CTTGACTCACTGCACTCTCT
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128939	127026	TGCAATCTTGACTCACTGCA
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30677	28764	TGTAGCCATTCATACTGTAC
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30686	28773	ACGCTAAACTGTAGCCATTC
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30717	28804	AATGAATTAATGAATATACA
30718	28805	TAATGAATTAATGAATATAC
30719	28806	GTAATGAATTAATGAATATA
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30723	28810	ATGTGTAATGAATTAATGAA
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30725	28812	AAATGTGTAATGAATTAATG
30726	28813	CAAATGTGTAATGAATTAAT
30727	28814	TCAAATGTGTAATGAATTAA
30728	28815	ATCAAATGTGTAATGAATTA
30729	28816	CATCAAATGTGTAATGAATT
30730	28817	GCATCAAATGTGTAATGAAT
30731	28818	AGCATCAAATGTGTAATGAA
30732	28819	CAGCATCAAATGTGTAATGA
30733	28820	ACAGCATCAAATGTGTAATG
30734	28821	GACAGCATCAAATGTGTAAT
30735	28822	TGACAGCATCAAATGTGTAA
30736	28823	CTGACAGCATCAAATGTGTA

79813	77900	CTTCTTTTTTTGGTGGGGGG
79814	77901	CCTTCTTTTTTTGGTGGGGG
79815	77902	GCCTTCTTTTTTTGGTGGGG
79816	77903	TGCCTTCTTTTTTTGGTGGG
79817	77904	CTGCCTTCTTTTTTTGGTGG
79818	77905	GCTGCCTTCTTTTTTTGGTG
79819	77906	GGCTGCCTTCTTTTTTTGGT
79820	77907	AGGCTGCCTTCTTTTTTTGG
79821	77908	GAGGCTGCCTTCTTTTTTTG
79822	77909	GGAGGCTGCCTTCTTTTTTT
79823	77910	GGGAGGCTGCCTTCTTTTTT
79824	77911	AGGGAGGCTGCCTTCTTTTT
79825	77912	AAGGGAGGCTGCCTTCTTTT
79826	77913	AAAGGGAGGCTGCCTTCTTT
79827	77914	AAAAGGGAGGCTGCCTTCTT
79828	77915	CAAAAGGGAGGCTGCCTTCT
79829	77916	GCAAAAGGGAGGCTGCCTTC
79830	77917	CGCAAAAGGGAGGCTGCCTT
79831	77918	TCGCAAAAGGGAGGCTGCCT
79832	77919	TTCGCAAAAGGGAGGCTGCC
79833	77920	ATTCGCAAAAGGGAGGCTGC
79834	77921	CATTCGCAAAAGGGAGGCTG
79835	77922	CCATTCGCAAAAGGGAGGCT
79836	77923	ACCATTCGCAAAAGGGAGGC
79837	77924	TACCATTCGCAAAAGGGAGG
79838	77925	TTACCATTCGCAAAAGGGAG
79839	77926	ATTACCATTCGCAAAAGGGA
79840	77927	AATTACCATTCGCAAAAGGG
79841	77928	AAATTACCATTCGCAAAAGG
79842	77929	GAAATTACCATTCGCAAAAG
79843	77930	GGAAATTACCATTCGCAAAA
79844	77931	AGGAAATTACCATTCGCAAA
79845	77932	TAGGAAATTACCATTCGCAA
79846	77933	ATAGGAAATTACCATTCGCA
79847	77934	TATAGGAAATTACCATTCGC
79848	77935	CTATAGGAAATTACCATTCG
79849	77936	ACTATAGGAAATTACCATTC
79850	77937	AACTATAGGAAATTACCATT
79851	77938	AAACTATAGGAAATTACCAT
79852	77939	GAAACTATAGGAAATTACCA
79853	77940	GGAAACTATAGGAAATTACC
79854	77941	AGGAAACTATAGGAAATTAC
79855	77942	GAGGAAACTATAGGAAATTA
79856	77943	CGAGGAAACTATAGGAAATT
79857	77944	ACGAGGAAACTATAGGAAAT
79858	77945	TACGAGGAAACTATAGGAAA
79859	77946	CTACGAGGAAACTATAGGAA
79860	77947	TCTACGAGGAAACTATAGGA
79861	77948	TTCTACGAGGAAACTATAGG
79862	77949	ATTCTACGAGGAAACTATAG
79863	77950	AATTCTACGAGGAAACTATA
79864	77951	CAATTCTACGAGGAAACTAT
79865	77952	ACAATTCTACGAGGAAACTA
79866	77953	CACAATTCTACGAGGAAACT
79867	77954	CCACAATTCTACGAGGAAAC
79868	77955	TCCACAATTCTACGAGGAAA
79869	77956	CTCCACAATTCTACGAGGAA
79870	77957	ACTCCACAATTCTACGAGGA
79871	77958	AACTCCACAATTCTACGAGG
79872	77959	TAACTCCACAATTCTACGAG
79873	77960	GTAACTCCACAATTCTACGA
79874	77961	GGTAACTCCACAATTCTACG
79875	77962	AGGTAACTCCACAATTCTAC
79876	77963	TAGGTAACTCCACAATTCTA
79877	77964	ATAGGTAACTCCACAATTCT
79878	77965	CATAGGTAACTCCACAATTC
79879	77966	GCATAGGTAACTCCACAATT
79880	77967	AGCATAGGTAACTCCACAAT
79881	77968	CAGCATAGGTAACTCCACAA
79882	77969	TCAGCATAGGTAACTCCACA
79883	77970	CTCAGCATAGGTAACTCCAC

128960	127047	GCCCAAGCTGGAGTGCAGTG
128961	127048	TGCCCAAGCTGGAGTGCAGT
128962	127049	TTGCCCAAGCTGGAGTGCAG
128963	127050	GTTGCCCAAGCTGGAGTGCA
128964	127051	GGTTGCCCAAGCTGGAGTGC
128965	127052	CGGTTGCCCAAGCTGGAGTG
128966	127053	TCGGTTGCCCAAGCTGGAGT
128967	127054	CTCGGTTGCCCAAGCTGGAG
128968	127055	GCTCGGTTGCCCAAGCTGGA
128969	127056	CGCTCGGTTGCCCAAGCTGG
128970	127057	TCGCTCGGTTGCCCAAGCTG
128971	127058	GTCGCTCGGTTGCCCAAGCT
128972	127059	TGTCGCTCGGTTGCCCAAGC
128973	127060	GTGTCGCTCGGTTGCCCAAG
128974	127061	AGTGTCGCTCGGTTGCCCAA
128975	127062	GAGTGTCGCTCGGTTGCCCA
128976	127063	AGAGTGTCGCTCGGTTGCCC
128977	127064	CAGAGTGTCGCTCGGTTGCC
128978	127065	ACAGAGTGTCGCTCGGTTGC
128979	127066	GACAGAGTGTCGCTCGGTTG
128980	127067	AGACAGAGTGTCGCTCGGTT
128981	127068	GAGACAGAGTGTCGCTCGGT
128982	127069	TGAGACAGAGTGTCGCTCGG
128983	127070	TTGAGACAGAGTGTCGCTCG
128984	127071	TTTGAGACAGAGTGTCGCTC
128985	127072	CTTTGAGACAGAGTGTCGCT
128986	127073	TCTTTGAGACAGAGTGTCGC
128987	127074	TTCTTTGAGACAGAGTGTCG
128988	127075	TTTCTTTGAGACAGAGTGTC
128989	127076	TTTTCTTTGAGACAGAGTGT
128990	127077	ATTTTCTTTGAGACAGAGTG
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128995	127082	TATTTATTTTCTTTGAGACA
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129017	127104	AAAGATAAACTTTATTTTTA
129018	127105	TAAAGATAAACTTTATTTTT
129019	127106	TTAAAGATAAACTTTATTTT
129020	127107	CTTAAAGATAAACTTTATTT
129021	127108	CCTTAAAGATAAACTTTATT
129022	127109	ACCTTAAAGATAAACTTTAT
129023	127110	AACCTTAAAGATAAACTTTA
129024	127111	AAACCTTAAAGATAAACTTT
129025	127112	AAAACCTTAAAGATAAACTT
129026	127113	CAAAACCTTAAAGATAAACT
129027	127114	ACAAAACCTTAAAGATAAAC
129028	127115	TACAAAACCTTAAAGATAAA
129029	127116	GTACAAAACCTTAAAGATAA
129030	127117	TGTACAAAACCTTAAAGATA

30737	28824	TCTGACAGCATCAAATGTGT
30738	28825	GTCTGACAGCATCAAATGTG
30739	28826	AGTCTGACAGCATCAAATGT
30740	28827	TAGTCTGACAGCATCAAATG
30741	28828	CTAGTCTGACAGCATCAAAT
30742	28829	CCTAGTCTGACAGCATCAAA
30743	28830	TCCTAGTCTGACAGCATCAA
30744	28831	GTCCTAGTCTGACAGCATCA
30745	28832	TGTCCTAGTCTGACAGCATC
30746	28833	CTGTCCTAGTCTGACAGCAT
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30757	28844	CATCTTTGTCTCTGTCCTAG
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30759	28846	TTCATCTTTGTCTCTGTCCT
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30770	28857	ATAATGTTTCATTCATCTTT
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30773	28860	GAGATAATGTTTCATTCATC
30774	28861	AGAGATAATGTTTCATTCAT
30775	28862	CAGAGATAATGTTTCATTCA
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30777	28864	AGCAGAGATAATGTTTCATT
30778	28865	AAGCAGAGATAATGTTTCAT
30779	28866	GAAGCAGAGATAATGTTTCA
30780	28867	GGAAGCAGAGATAATGTTTC
30781	28868	TGGAAGCAGAGATAATGTTT
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30784	28871	ACCTGGAAGCAGAGATAATG
30785	28872	AACCTGGAAGCAGAGATAAT
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30789	28876	GGGTAACCTGGAAGCAGAGA
30790	28877	TGGGTAACCTGGAAGCAGAG
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30793	28880	CACTGGGTAACCTGGAAGCA
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30797	28884	ACTACACTGGGTAACCTGGA
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30799	28886	CTACTACACTGGGTAACCTG
30800	28887	TCTACTACACTGGGTAACCT
30801	28888	CTCTACTACACTGGGTAACC
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30805	28892	CCTTCTCTACTACACTGGGT
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79884	77971	CCTCAGCATAGGTAACTCCA
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79886	77973	AACCTCAGCATAGGTAACTC
79887	77974	TAACCTCAGCATAGGTAACT
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79890	77977	CTATAACCTCAGCATAGGTA
79891	77978	CCTATAACCTCAGCATAGGT
79892	77979	ACCTATAACCTCAGCATAGG
79893	77980	AACCTATAACCTCAGCATAG
79894	77981	TAACCTATAACCTCAGCATA
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79900	77987	ATACCCTAACCTATAACCTC
79901	77988	AATACCCTAACCTATAACCT
79902	77989	CAATACCCTAACCTATAACC
79903	77990	TCAATACCCTAACCTATAAC
79904	77991	CTCAATACCCTAACCTATAA
79905	77992	TCTCAATACCCTAACCTATA
79906	77993	ATCTCAATACCCTAACCTAT
79907	77994	GATCTCAATACCCTAACCTA
79908	77995	GGATCTCAATACCCTAACCT
79909	77996	TGGATCTCAATACCCTAACC
79910	77997	CTGGATCTCAATACCCTAAC
79911	77998	TCTGGATCTCAATACCCTAA
79912	77999	CTCTGGATCTCAATACCCTA
79913	78000	ACTCTGGATCTCAATACCCT
79914	78001	AACTCTGGATCTCAATACCC
79915	78002	CAACTCTGGATCTCAATACC
79916	78003	GCAACTCTGGATCTCAATAC
79917	78004	GGCAACTCTGGATCTCAATA
79918	78005	TGGCAACTCTGGATCTCAAT
79919	78006	GTGGCAACTCTGGATCTCAA
79920	78007	AGTGGCAACTCTGGATCTCA
79921	78008	AAGTGGCAACTCTGGATCTC
79922	78009	GAAGTGGCAACTCTGGATCT
79923	78010	AGAAGTGGCAACTCTGGATC
79924	78011	CAGAAGTGGCAACTCTGGAT
79925	78012	TCAGAAGTGGCAACTCTGGA
79926	78013	CTCAGAAGTGGCAACTCTGG
79927	78014	CCTCAGAAGTGGCAACTCTG
79928	78015	ACCTCAGAAGTGGCAACTCT
79929	78016	CACCTCAGAAGTGGCAACTC
79930	78017	ACACCTCAGAAGTGGCAACT
79931	78018	GACACCTCAGAAGTGGCAAC
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79933	78020	GTGACACCTCAGAAGTGGCA
79934	78021	TGTGACACCTCAGAAGTGGC
79935	78022	TTGTGACACCTCAGAAGTGG
79936	78023	GTTGTGACACCTCAGAAGTG
79937	78024	AGTTGTGACACCTCAGAAGT
79938	78025	CAGTTGTGACACCTCAGAAG
79939	78026	GCAGTTGTGACACCTCAGAA
79940	78027	AGCAGTTGTGACACCTCAGA
79941	78028	TAGCAGTTGTGACACCTCAG
79942	78029	TTAGCAGTTGTGACACCTCA
79943	78030	ATTAGCAGTTGTGACACCTC
79944	78031	CATTAGCAGTTGTGACACCT
79945	78032	CCATTAGCAGTTGTGACACC
79946	78033	ACCATTAGCAGTTGTGACAC
79947	78034	TACCATTAGCAGTTGTGACA
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79949	78036	TTTACCATTAGCAGTTGTGA
79950	78037	TTTTACCATTAGCAGTTGTG
79951	78038	GTTTTACCATTAGCAGTTGT
79952	78039	GGTTTTACCATTAGCAGTTG
79953	78040	TGGTTTTACCATTAGCAGTT
79954	78041	ATGGTTTTACCATTAGCAGT

129031	127118	ATGTACAAAACCTTAAAGAT
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129037	127124	AAAAAAATGTACAAAACCTT
129038	127125	GAAAAAAATGTACAAAACCT
129039	127126	TGAAAAAAATGTACAAAACC
129040	127127	CTGAAAAAAATGTACAAAAC
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129059	127146	AACCTACCTAAGGCATACAC
129060	127147	GAACCTACCTAAGGCATACA
129061	127148	AGAACCTACCTAAGGCATAC
129062	127149	AAGAACCTACCTAAGGCATA
129063	127150	AAAGAACCTACCTAAGGCAT
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129071	127158	ACATTAAAAAAGAACCTACC
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129079	127166	TTACACTAACATTAAAAAAG
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129089	127176	AGTCCCTGGGTTACACTAAC
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129091	127178	GAAGTCCCTGGGTTACACTA
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129100	127187	AATGGAAGAGAAGTCCCTGG
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30808	28895	CTGCCTTCTCTACTACACTG
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30811	28898	TGCCTGCCTTCTCTACTACA
30812	28899	ATGCCTGCCTTCTCTACTAC
30813	28900	CATGCCTGCCTTCTCTACTA
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30815	28902	TGCATGCCTGCCTTCTCTAC
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30818	28905	ATCTGCATGCCTGCCTTCTC
30819	28906	TATCTGCATGCCTGCCTTCT
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30827	28914	ATTTAAACTATCTGCATGCC
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30830	28917	CCAATTTAAACTATCTGCAT
30831	28918	ACCAATTTAAACTATCTGCA
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30840	28927	CCCAGTGCTACCAATTTAAA
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30842	28929	CTCCCAGTGCTACCAATTTA
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30844	28931	CCCTCCCAGTGCTACCAATT
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30846	28933	TCCCCTCCCAGTGCTACCAA
30847	28934	GTCCCCTCCCAGTGCTACCA
30848	28935	AGTCCCCTCCCAGTGCTACC
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30850	28937	GCAGTCCCCTCCCAGTGCTA
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30852	28939	TGGCAGTCCCCTCCCAGTGC
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30855	28942	CCATGGCAGTCCCCTCCCAG
30856	28943	CCCATGGCAGTCCCCTCCCA
30857	28944	ACCCATGGCAGTCCCCTCCC
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30860	28947	CCCACCCATGGCAGTCCCCT
30861	28948	GCCCACCCATGGCAGTCCCC
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30864	28951	ACTGCCCACCCATGGCAGTC
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30874	28961	CTTTTTCTTCACTGCCCACC
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30876	28963	CCCTTTTTCTTCACTGCCCA
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30878	28965	AGCCCTTTTTCTTCACTGCC

79955	78042	AATGGTTTTACCATTAGCAG
79956	78043	AAATGGTTTTACCATTAGCA
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79958	78045	AGAAATGGTTTTACCATTAG
79959	78046	TAGAAATGGTTTTACCATTA
79960	78047	TTAGAAATGGTTTTACCATT
79961	78048	TTTAGAAATGGTTTTACCAT
79962	78049	CTTTAGAAATGGTTTTACCA
79963	78050	GCTTTAGAAATGGTTTTACC
79964	78051	GGCTTTAGAAATGGTTTTAC
79965	78052	GGGCTTTAGAAATGGTTTTA
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79967	78054	CTGGGCTTTAGAAATGGTTT
79968	78055	ACTGGGCTTTAGAAATGGTT
79969	78056	AACTGGGCTTTAGAAATGGT
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79975	78062	CACAAGAACTGGGCTTTAGA
79976	78063	TCACAAGAACTGGGCTTTAG
79977	78064	GTCACAAGAACTGGGCTTTA
79978	78065	AGTCACAAGAACTGGGCTTT
79979	78066	AAGTCACAAGAACTGGGCTT
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79981	78068	CAAAGTCACAAGAACTGGGC
79982	78069	ACAAAGTCACAAGAACTGGG
79983	78070	GACAAAGTCACAAGAACTGG
79984	78071	GGACAAAGTCACAAGAACTG
79985	78072	TGGACAAAGTCACAAGAACT
79986	78073	CTGGACAAAGTCACAAGAAC
79987	78074	ACTGGACAAAGTCACAAGAA
79988	78075	CACTGGACAAAGTCACAAGA
79989	78076	TCACTGGACAAAGTCACAAG
79990	78077	ATCACTGGACAAAGTCACAA
79991	78078	AATCACTGGACAAAGTCACA
79992	78079	CAATCACTGGACAAAGTCAC
79993	78080	GCAATCACTGGACAAAGTCA
79994	78081	GGCAATCACTGGACAAAGTC
79995	78082	AGGCAATCACTGGACAAAGT
79996	78083	CAGGCAATCACTGGACAAAG
79997	78084	ACAGGCAATCACTGGACAAA
79998	78085	AACAGGCAATCACTGGACAA
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80000	78087	TGAACAGGCAATCACTGGAC
80001	78088	GTGAACAGGCAATCACTGGA
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80007	78094	GAAACGGTGAACAGGCAATC
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80016	78103	AGGCAGCATGAAACGGTGAA
80017	78104	AAGGCAGCATGAAACGGTGA
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80021	78108	TGGGAAGGCAGCATGAAACG
80022	78109	ATGGGAAGGCAGCATGAAAC
80023	78110	AATGGGAAGGCAGCATGAAA
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80025	78112	CAAATGGGAAGGCAGCATGA

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129103	127190	TGCAATGGAAGAGAAGTCCC
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129105	127192	GATGCAATGGAAGAGAAGTC
129106	127193	AGATGCAATGGAAGAGAAGT
129107	127194	AAGATGCAATGGAAGAGAAG
129108	127195	GAAGATGCAATGGAAGAGAA
129109	127196	AGAAGATGCAATGGAAGAGA
129110	127197	TAGAAGATGCAATGGAAGAG
129111	127198	TTAGAAGATGCAATGGAAGA
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129123	127210	ATAAGTAATTACTTAGAAGA
129124	127211	CATAAGTAATTACTTAGAAG
129125	127212	TCATAAGTAATTACTTAGAA
129126	127213	TTCATAAGTAATTACTTAGA
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129165	127252	AACTAACATATAAACAGCAA
129166	127253	AAACTAACATATAAACAGCA
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129169	127256	TAAAAACTAACATATAAACA
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30881	28968	TGAAGCCCTTTTTCTTCACT
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30905	28992	GATCCATCTCAACTCTCATT
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30921	29008	GCTTATCTTCCTTGAAGATC
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30930	29017	CTGAAAACTGCTTATCTTCC
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80026	78113	TCAAATGGGAAGGCAGCATG
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80048	78135	CTCCCCTTCCTCCTGGGAAT
80049	78136	CCTCCCCTTCCTCCTGGGAA
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129182	127269	TAAAGGAGCAGGGTAAAAAC
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80106	78193	GCTTTCCCTCATATTCAACG
80107	78194	CGCTTTCCCTCATATTCAAC
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80161	78248	TTTTTAACAGCCAAAAATAC
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80164	78251	TGCTTTTTAACAGCCAAAAA
80165	78252	GTGCTTTTTAACAGCCAAAA
80166	78253	GGTGCTTTTTAACAGCCAAA
80167	78254	GGGTGCTTTTTAACAGCCAA

129244	127331	GCCTGTTATTTGAAAAATGC
129245	127332	TGCCTGTTATTTGAAAAATG
129246	127333	CTGCCTGTTATTTGAAAAAT
129247	127334	TCTGCCTGTTATTTGAAAAA
129248	127335	CTCTGCCTGTTATTTGAAAA
129249	127336	ACTCTGCCTGTTATTTGAAA
129250	127337	GACTCTGCCTGTTATTTGAA
129251	127338	TGACTCTGCCTGTTATTTGA
129252	127339	TTGACTCTGCCTGTTATTTG
129253	127340	CTTGACTCTGCCTGTTATTT
129254	127341	CCTTGACTCTGCCTGTTATT
129255	127342	CCCTTGACTCTGCCTGTTAT
129256	127343	GCCCTTGACTCTGCCTGTTA
129257	127344	AGCCCTTGACTCTGCCTGTT
129258	127345	AAGCCCTTGACTCTGCCTGT
129259	127346	CAAGCCCTTGACTCTGCCTG
129260	127347	CCAAGCCCTTGACTCTGCCT
129261	127348	ACCAAGCCCTTGACTCTGCC
129262	127349	AACCAAGCCCTTGACTCTGC
129263	127350	AAACCAAGCCCTTGACTCTG
129264	127351	GAAACCAAGCCCTTGACTCT
129265	127352	AGAAACCAAGCCCTTGACTC
129266	127353	AAGAAACCAAGCCCTTGACT
129267	127354	AAAGAAACCAAGCCCTTGAC
129268	127355	AAAAGAAACCAAGCCCTTGA
129269	127356	GAAAAGAAACCAAGCCCTTG
129270	127357	AGAAAAGAAACCAAGCCCTT
129271	127358	AAGAAAAGAAACCAAGCCCT
129272	127359	GAAGAAAAGAAACCAAGCCC
129273	127360	GGAAGAAAAGAAACCAAGCC
129274	127361	GGGAAGAAAAGAAACCAAGC
129275	127362	GGGGAAGAAAAGAAACCAAG
129276	127363	AGGGGAAGAAAAGAAACCAA
129277	127364	GAGGGGAAGAAAAGAAACCA
129278	127365	GGAGGGGAAGAAAAGAAACC
129279	127366	AGGAGGGGAAGAAAAGAAAC
129280	127367	CAGGAGGGGAAGAAAAGAAA
129281	127368	ACAGGAGGGGAAGAAAAGAA
129282	127369	GACAGGAGGGGAAGAAAAGA
129283	127370	GGACAGGAGGGGAAGAAAAG
129284	127371	GGGACAGGAGGGGAAGAAAA
129285	127372	GGGGACAGGAGGGGAAGAAA
129286	127373	AGGGGACAGGAGGGGAAGAA
129287	127374	TAGGGGACAGGAGGGGAAGA
129288	127375	GTAGGGGACAGGAGGGGAAG
129289	127376	GGTAGGGGACAGGAGGGGAA
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129291	127378	AGGGTAGGGGACAGGAGGGG
129292	127379	GAGGGTAGGGGACAGGAGGG
129293	127380	GGAGGGTAGGGGACAGGAGG
129294	127381	GGGAGGGTAGGGGACAGGAG
129295	127382	GGGGAGGGTAGGGGACAGGA
129296	127383	AGGGGAGGGTAGGGGACAGG
129297	127384	AAGGGGAGGGTAGGGGACAG
129298	127385	AAAGGGGAGGGTAGGGGACA
129299	127386	AAAAGGGGAGGGTAGGGGAC
129300	127387	AAAAAGGGGAGGGTAGGGGA
129301	127388	AAAAAAGGGGAGGGTAGGGG
129302	127389	CAAAAAAGGGGAGGGTAGGG
129303	127390	TCAAAAAAGGGGAGGGTAGG
129304	127391	CTCAAAAAAGGGGAGGGTAG
129305	127392	TCTCAAAAAAGGGGAGGGTA
129306	127393	GTCTCAAAAAAGGGGAGGGT
129307	127394	TGTCTCAAAAAAGGGGAGGG
129308	127395	CTGTCTCAAAAAAGGGGAGG
129309	127396	CCTGTCTCAAAAAAGGGGAG
129310	127397	CCCTGTCTCAAAAAAGGGGA
129311	127398	ACCCTGTCTCAAAAAAGGGG
129312	127399	GACCCTGTCTCAAAAAAGGG
129313	127400	AGACCCTGTCTCAAAAAAGG
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31021	29108	ATTTTTTCTACATACACCAT
31022	29109	AATTTTTTCTACATACACCA
31023	29110	AAATTTTTTCTACATACACC
31024	29111	CAAATTTTTTCTACATACAC
31025	29112	CCAAATTTTTTCTACATACA
31026	29113	ACCAAATTTTTTCTACATAC
31027	29114	AACCAAATTTTTTCTACATA
31028	29115	GAACCAAATTTTTTCTACAT
31029	29116	TGAACCAAATTTTTTCTACA
31030	29117	GTGAACCAAATTTTTTCTAC
31031	29118	TGTGAACCAAATTTTTTCTA
31032	29119	CTGTGAACCAAATTTTTTCT
31033	29120	ACTGTGAACCAAATTTTTTC
31034	29121	CACTGTGAACCAAATTTTTT
31035	29122	ACACTGTGAACCAAATTTTT
31036	29123	CACACTGTGAACCAAATTTT
31037	29124	TCACACTGTGAACCAAATTT
31038	29125	ATCACACTGTGAACCAAATT
31039	29126	TATCACACTGTGAACCAAAT
31040	29127	CTATCACACTGTGAACCAAA
31041	29128	TCTATCACACTGTGAACCAA
31042	29129	TTCTATCACACTGTGAACCA
31043	29130	CTTCTATCACACTGTGAACC
31044	29131	TCTTCTATCACACTGTGAAC
31045	29132	TTCTTCTATCACACTGTGAA
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31047	29134	AATTCTTCTATCACACTGTG
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31049	29136	CCAATTCTTCTATCACACTG
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31056	29143	ACCCCCTCCAATTCTTCTAT
31057	29144	GACCCCCTCCAATTCTTCTA
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31060	29147	GAGGACCCCCTCCAATTCTT
31061	29148	TGAGGACCCCCTCCAATTCT
31062	29149	GTGAGGACCCCCTCCAATTC
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31068	29155	CTTTCAGTGAGGACCCCCTC
31069	29156	ACTTTCAGTGAGGACCCCCT
31070	29157	TACTTTCAGTGAGGACCCCC
31071	29158	TTACTTTCAGTGAGGACCCC
31072	29159	CTTACTTTCAGTGAGGACCC
31073	29160	CCTTACTTTCAGTGAGGACC
31074	29161	TCCTTACTTTCAGTGAGGAC
31075	29162	TTCCTTACTTTCAGTGAGGA
31076	29163	TTTCCTTACTTTCAGTGAGG
31077	29164	GTTTCCTTACTTTCAGTGAG
31078	29165	TGTTTCCTTACTTTCAGTGA
31079	29166	GTGTTTCCTTACTTTCAGTG
31080	29167	TGTGTTTCCTTACTTTCAGT
31081	29168	ATGTGTTTCCTTACTTTCAG
31082	29169	AATGTGTTTCCTTACTTTCA
31083	29170	AAATGTGTTTCCTTACTTTC
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31085	29172	CCAAATGTGTTTCCTTACTT
31086	29173	TCCAAATGTGTTTCCTTACT
31087	29174	TTCCAAATGTGTTTCCTTAC
31088	29175	CTTCCAAATGTGTTTCCTTA
31089	29176	TCTTCCAAATGTGTTTCCTT
31090	29177	TTCTTCCAAATGTGTTTCCT
31091	29178	ATTCTTCCAAATGTGTTTCC

80168	78255	GGGGTGCTTTTTAACAGCCA
80169	78256	AGGGGTGCTTTTTAACAGCC
80170	78257	AAGGGGTGCTTTTTAACAGC
80171	78258	CAAGGGGTGCTTTTTAACAG
80172	78259	ACAAGGGGTGCTTTTTAACA
80173	78260	AACAAGGGGTGCTTTTTAAC
80174	78261	GAACAAGGGGTGCTTTTTAA
80175	78262	GGAACAAGGGGTGCTTTTTA
80176	78263	TGGAACAAGGGGTGCTTTTT
80177	78264	ATGGAACAAGGGGTGCTTTT
80178	78265	CATGGAACAAGGGGTGCTTT
80179	78266	ACATGGAACAAGGGGTGCTT
80180	78267	CACATGGAACAAGGGGTGCT
80181	78268	CCACATGGAACAAGGGGTGC
80182	78269	TCCACATGGAACAAGGGGTG
80183	78270	TTCCACATGGAACAAGGGGT
80184	78271	ATTCCACATGGAACAAGGGG
80185	78272	GATTCCACATGGAACAAGGG
80186	78273	GGATTCCACATGGAACAAGG
80187	78274	GGGATTCCACATGGAACAAG
80188	78275	AGGGATTCCACATGGAACAA
80189	78276	AAGGGATTCCACATGGAACA
80190	78277	CAAGGGATTCCACATGGAAC
80191	78278	ACAAGGGATTCCACATGGAA
80192	78279	AACAAGGGATTCCACATGGA
80193	78280	AAACAAGGGATTCCACATGG
80194	78281	TAAACAAGGGATTCCACATG
80195	78282	TTAAACAAGGGATTCCACAT
80196	78283	TTTAAACAAGGGATTCCACA
80197	78284	TTTTAAACAAGGGATTCCAC
80198	78285	CTTTTAAACAAGGGATTCCA
80199	78286	TCTTTTAAACAAGGGATTCC
80200	78287	TTCTTTTAAACAAGGGATTC
80201	78288	CTTCTTTTAAACAAGGGATT
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80208	78295	TATTTTACTTCTTTTAAACA
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80210	78297	CATATTTTACTTCTTTTAAA
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80212	78299	TACATATTTTACTTCTTTTA
80213	78300	GTACATATTTTACTTCTTTT
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80215	78302	AGGTACATATTTTACTTCTT
80216	78303	GAGGTACATATTTTACTTCT
80217	78304	GGAGGTACATATTTTACTTC
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80219	78306	CAGGAGGTACATATTTTACT
80220	78307	ACAGGAGGTACATATTTTAC
80221	78308	GACAGGAGGTACATATTTTA
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80224	78311	GAGGACAGGAGGTACATATT
80225	78312	GGAGGACAGGAGGTACATAT
80226	78313	TGGAGGACAGGAGGTACATA
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80228	78315	TGTGGAGGACAGGAGGTACA
80229	78316	CTGTGGAGGACAGGAGGTAC
80230	78317	TCTGTGGAGGACAGGAGGTA
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80235	78322	TCAGGTCTGTGGAGGACAGG
80236	78323	CTCAGGTCTGTGGAGGACAG
80237	78324	CCTCAGGTCTGTGGAGGACA
80238	78325	TCCTCAGGTCTGTGGAGGAC

129315	127402	TGAGACCCTGTCTCAAAAAA
129316	127403	GTGAGACCCTGTCTCAAAAA
129317	127404	AGTGAGACCCTGTCTCAAAA
129318	127405	AAGTGAGACCCTGTCTCAAA
129319	127406	GAAGTGAGACCCTGTCTCAA
129320	127407	AGAAGTGAGACCCTGTCTCA
129321	127408	AAGAAGTGAGACCCTGTCTC
129322	127409	GAAGAAGTGAGACCCTGTCT
129323	127410	CGAAGAAGTGAGACCCTGTC
129324	127411	GCGAAGAAGTGAGACCCTGT
129325	127412	GGCGAAGAAGTGAGACCCTG
129326	127413	CGGCGAAGAAGTGAGACCCT
129327	127414	TCGGCGAAGAAGTGAGACCC
129328	127415	CTCGGCGAAGAAGTGAGACC
129329	127416	CCTCGGCGAAGAAGTGAGAC
129330	127417	GCCTCGGCGAAGAAGTGAGA
129331	127418	AGCCTCGGCGAAGAAGTGAG
129332	127419	CAGCCTCGGCGAAGAAGTGA
129333	127420	CCAGCCTCGGCGAAGAAGTG
129334	127421	TCCAGCCTCGGCGAAGAAGT
129335	127422	CTCCAGCCTCGGCGAAGAAG
129336	127423	ACTCCAGCCTCGGCGAAGAA
129337	127424	CACTCCAGCCTCGGCGAAGA
129338	127425	GCACTCCAGCCTCGGCGAAG
129339	127426	TGCACTCCAGCCTCGGCGAA
129340	127427	CTGCACTCCAGCCTCGGCGA
129341	127428	ACTGCACTCCAGCCTCGGCG
129342	127429	CACTGCACTCCAGCCTCGGC
129343	127430	CCACTGCACTCCAGCCTCGG
129344	127431	ACCACTGCACTCCAGCCTCG
129345	127432	CACCACTGCACTCCAGCCTC
129346	127433	GCACCACTGCACTCCAGCCT
129347	127434	TGCACCACTGCACTCCAGCC
129348	127435	CTGCACCACTGCACTCCAGC
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129350	127437	AACTGCACCACTGCACTCCA
129351	127438	TAACTGCACCACTGCACTCC
129352	127439	GTAACTGCACCACTGCACTC
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129354	127441	CCGTAACTGCACCACTGCAC
129355	127442	GCCGTAACTGCACCACTGCA
129356	127443	AGCCGTAACTGCACCACTGC
129357	127444	AAGCCGTAACTGCACCACTG
129358	127445	TAAGCCGTAACTGCACCACT
129359	127446	GTAAGCCGTAACTGCACCAC
129360	127447	GGTAAGCCGTAACTGCACCA
129361	127448	CGGTAAGCCGTAACTGCACC
129362	127449	GCGGTAAGCCGTAACTGCAC
129363	127450	CGCGGTAAGCCGTAACTGCA
129364	127451	CCGCGGTAAGCCGTAACTGC
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129367	127454	ATGCCGCGGTAAGCCGTAAC
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129370	127457	CAGATGCCGCGGTAAGCCGT
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129372	127459	GGCAGATGCCGCGGTAAGCC
129373	127460	AGGCAGATGCCGCGGTAAGC
129374	127461	GAGGCAGATGCCGCGGTAAG
129375	127462	GGAGGCAGATGCCGCGGTAA
129376	127463	GGGAGGCAGATGCCGCGGTA
129377	127464	AGGGAGGCAGATGCCGCGGT
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129379	127466	CCAGGGAGGCAGATGCCGCG
129380	127467	GCCAGGGAGGCAGATGCCGC
129381	127468	AGCCAGGGAGGCAGATGCCG
129382	127469	CAGCCAGGGAGGCAGATGCC
129383	127470	TCAGCCAGGGAGGCAGATGC
129384	127471	TTCAGCCAGGGAGGCAGATG
129385	127472	TTTCAGCCAGGGAGGCAGAT

31092	29179	TATTCTTCCAAATGTGTTTC
31093	29180	ATATTCTTCCAAATGTGTTT
31094	29181	CATATTCTTCCAAATGTGTT
31095	29182	ACATATTCTTCCAAATGTGT
31096	29183	AACATATTCTTCCAAATGTG
31097	29184	AAACATATTCTTCCAAATGT
31098	29185	GAAACATATTCTTCCAAATG
31099	29186	TGAAACATATTCTTCCAAAT
31100	29187	CTGAAACATATTCTTCCAAA
31101	29188	ACTGAAACATATTCTTCCAA
31102	29189	AACTGAAACATATTCTTCCA
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31104	29191	CTAACTGAAACATATTCTTC
31105	29192	TCTAACTGAAACATATTCTT
31106	29193	TTCTAACTGAAACATATTCT
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31119	29206	AGCTCATTTCATTTTCTAAC
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31139	29226	CCTTATTAGCGTTTACTTTA
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31141	29228	AACCTTATTAGCGTTTACTT
31142	29229	AAACCTTATTAGCGTTTACT
31143	29230	AAAACCTTATTAGCGTTTAC
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31145	29232	TAAAAACCTTATTAGCGTTT
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31148	29235	TTTTAAAAACCTTATTAGCG
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31158	29245	AAATTTTACATTTTAAAAAC
31159	29246	GAAATTTTACATTTTAAAAA
31160	29247	TGAAATTTTACATTTTAAAA
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31162	29249	GTTGAAATTTTACATTTTAA

80239	78326	GTCCTCAGGTCTGTGGAGGA
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80242	78329	CTGGTCCTCAGGTCTGTGGA
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80246	78333	CACACTGGTCCTCAGGTCTG
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80251	78338	GAGATCACACTGGTCCTCAG
80252	78339	TGAGATCACACTGGTCCTCA
80253	78340	TTGAGATCACACTGGTCCTC
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80255	78342	TCTTGAGATCACACTGGTCC
80256	78343	TTCTTGAGATCACACTGGTC
80257	78344	CTTCTTGAGATCACACTGGT
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80260	78347	AACCTTCTTGAGATCACACT
80261	78348	TAACCTTCTTGAGATCACAC
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80264	78351	CTGTAACCTTCTTGAGATCA
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80271	78358	CATTTACCTGTAACCTTCTT
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80282	78369	AGAGACATCTACATTTACCT
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80285	78372	GTTAGAGACATCTACATTTA
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80287	78374	CAGTTAGAGACATCTACATT
80288	78375	TCAGTTAGAGACATCTACAT
80289	78376	TTCAGTTAGAGACATCTACA
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80291	78378	CTTTCAGTTAGAGACATCTA
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80293	78380	ACCTTTCAGTTAGAGACATC
80294	78381	CACCTTTCAGTTAGAGACAT
80295	78382	CCACCTTTCAGTTAGAGACA
80296	78383	GCCACCTTTCAGTTAGAGAC
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80301	78388	TAAAAGCCACCTTTCAGTTA
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80303	78390	TGTAAAAGCCACCTTTCAGT
80304	78391	CTGTAAAAGCCACCTTTCAG
80305	78392	CCTGTAAAAGCCACCTTTCA
80306	78393	ACCTGTAAAAGCCACCTTTC
80307	78394	AACCTGTAAAAGCCACCTTT
80308	78395	TAACCTGTAAAAGCCACCTT
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129386	127473	TTTTCAGCCAGGGAGGCAGA
129387	127474	CTTTTCAGCCAGGGAGGCAG
129388	127475	ACTTTTCAGCCAGGGAGGCA
129389	127476	AACTTTTCAGCCAGGGAGGC
129390	127477	GAACTTTTCAGCCAGGGAGG
129391	127478	GGAACTTTTCAGCCAGGGAG
129392	127479	AGGAACTTTTCAGCCAGGGA
129393	127480	GAGGAACTTTTCAGCCAGGG
129394	127481	GGAGGAACTTTTCAGCCAGG
129395	127482	GGGAGGAACTTTTCAGCCAG
129396	127483	TGGGAGGAACTTTTCAGCCA
129397	127484	GTGGGAGGAACTTTTCAGCC
129398	127485	GGTGGGAGGAACTTTTCAGC
129399	127486	AGGTGGGAGGAACTTTTCAG
129400	127487	GAGGTGGGAGGAACTTTTCA
129401	127488	TGAGGTGGGAGGAACTTTTC
129402	127489	CTGAGGTGGGAGGAACTTTT
129403	127490	GCTGAGGTGGGAGGAACTTT
129404	127491	GGCTGAGGTGGGAGGAACTT
129405	127492	AGGCTGAGGTGGGAGGAACT
129406	127493	GAGGCTGAGGTGGGAGGAAC
129407	127494	GGAGGCTGAGGTGGGAGGAA
129408	127495	AGGAGGCTGAGGTGGGAGGA
129409	127496	CAGGAGGCTGAGGTGGGAGG
129410	127497	TCAGGAGGCTGAGGTGGGAG
129411	127498	CTCAGGAGGCTGAGGTGGGA
129412	127499	ACTCAGGAGGCTGAGGTGGG
129413	127500	TACTCAGGAGGCTGAGGTGG
129414	127501	CTACTCAGGAGGCTGAGGTG
129415	127502	GCTACTCAGGAGGCTGAGGT
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129417	127504	CAGCTACTCAGGAGGCTGAG
129418	127505	CCAGCTACTCAGGAGGCTGA
129419	127506	CCCAGCTACTCAGGAGGCTG
129420	127507	TCCCAGCTACTCAGGAGGCT
129421	127508	GTCCCAGCTACTCAGGAGGC
129422	127509	GGTCCCAGCTACTCAGGAGG
129423	127510	TGGTCCCAGCTACTCAGGAG
129424	127511	ATGGTCCCAGCTACTCAGGA
129425	127512	TATGGTCCCAGCTACTCAGG
129426	127513	CTATGGTCCCAGCTACTCAG
129427	127514	TCTATGGTCCCAGCTACTCA
129428	127515	ATCTATGGTCCCAGCTACTC
129429	127516	CATCTATGGTCCCAGCTACT
129430	127517	GCATCTATGGTCCCAGCTAC
129431	127518	TGCATCTATGGTCCCAGCTA
129432	127519	GTGCATCTATGGTCCCAGCT
129433	127520	TGTGCATCTATGGTCCCAGC
129434	127521	CTGTGCATCTATGGTCCCAG
129435	127522	GCTGTGCATCTATGGTCCCA
129436	127523	TGCTGTGCATCTATGGTCCC
129437	127524	GTGCTGTGCATCTATGGTCC
129438	127525	GGTGCTGTGCATCTATGGTC
129439	127526	CGGTGCTGTGCATCTATGGT
129440	127527	GCGGTGCTGTGCATCTATGG
129441	127528	TGCGGTGCTGTGCATCTATG
129442	127529	CTGCGGTGCTGTGCATCTAT
129443	127530	GCTGCGGTGCTGTGCATCTA
129444	127531	AGCTGCGGTGCTGTGCATCT
129445	127532	CAGCTGCGGTGCTGTGCATC
129446	127533	CCAGCTGCGGTGCTGTGCAT
129447	127534	GCCAGCTGCGGTGCTGTGCA
129448	127535	AGCCAGCTGCGGTGCTGTGC
129449	127536	TAGCCAGCTGCGGTGCTGTG
129450	127537	TTAGCCAGCTGCGGTGCTGT
129451	127538	ATTAGCCAGCTGCGGTGCTG
129452	127539	TATTAGCCAGCTGCGGTGCT
129453	127540	ATATTAGCCAGCTGCGGTGC
129454	127541	AATATTAGCCAGCTGCGGTG
129455	127542	AAATATTAGCCAGCTGCGGT
129456	127543	AAAATATTAGCCAGCTGCGG

31163	29250	CGTTGAAATTTTACATTTTA
31164	29251	ACGTTGAAATTTTACATTTT
31165	29252	TACGTTGAAATTTTACATTT
31166	29253	ATACGTTGAAATTTTACATT
31167	29254	AATACGTTGAAATTTTACAT
31168	29255	AAATACGTTGAAATTTTACA
31169	29256	TAAATACGTTGAAATTTTAC
31170	29257	CTAAATACGTTGAAATTTTA
31171	29258	TCTAAATACGTTGAAATTTT
31172	29259	TTCTAAATACGTTGAAATTT
31173	29260	TTTCTAAATACGTTGAAATT
31174	29261	CTTTCTAAATACGTTGAAAT
31175	29262	TCTTTCTAAATACGTTGAAA
31176	29263	CTCTTTCTAAATACGTTGAA
31177	29264	TCTCTTTCTAAATACGTTGA
31178	29265	TTCTCTTTCTAAATACGTTG
31179	29266	GTTCTCTTTCTAAATACGTT
31180	29267	TGTTCTCTTTCTAAATACGT
31181	29268	CTGTTCTCTTTCTAAATACG
31182	29269	GCTGTTCTCTTTCTAAATAC
31183	29270	AGCTGTTCTCTTTCTAAATA
31184	29271	CAGCTGTTCTCTTTCTAAAT
31185	29272	CCAGCTGTTCTCTTTCTAAA
31186	29273	TCCAGCTGTTCTCTTTCTAA
31187	29274	ATCCAGCTGTTCTCTTTCTA
31188	29275	CATCCAGCTGTTCTCTTTCT
31189	29276	TCATCCAGCTGTTCTCTTTC
31190	29277	TTCATCCAGCTGTTCTCTTT
31191	29278	ATTCATCCAGCTGTTCTCTT
31192	29279	GATTCATCCAGCTGTTCTCT
31193	29280	AGATTCATCCAGCTGTTCTC
31194	29281	AAGATTCATCCAGCTGTTCT
31195	29282	TAAGATTCATCCAGCTGTTC
31196	29283	ATAAGATTCATCCAGCTGTT
31197	29284	CATAAGATTCATCCAGCTGT
31198	29285	ACATAAGATTCATCCAGCTG
31199	29286	TACATAAGATTCATCCAGCT
31200	29287	GTACATAAGATTCATCCAGC
31201	29288	GGTACATAAGATTCATCCAG
31202	29289	AGGTACATAAGATTCATCCA
31203	29290	CAGGTACATAAGATTCATCC
31204	29291	ACAGGTACATAAGATTCATC
31205	29292	GACAGGTACATAAGATTCAT
31206	29293	TGACAGGTACATAAGATTCA
31207	29294	GTGACAGGTACATAAGATTC
31208	29295	AGTGACAGGTACATAAGATT
31209	29296	GAGTGACAGGTACATAAGAT
31210	29297	TGAGTGACAGGTACATAAGA
31211	29298	CTGAGTGACAGGTACATAAG
31212	29299	GCTGAGTGACAGGTACATAA
31213	29300	AGCTGAGTGACAGGTACATA
31214	29301	AAGCTGAGTGACAGGTACAT
31215	29302	AAAGCTGAGTGACAGGTACA
31216	29303	TAAAGCTGAGTGACAGGTAC
31217	29304	CTAAAGCTGAGTGACAGGTA
31218	29305	GCTAAAGCTGAGTGACAGGT
31219	29306	TGCTAAAGCTGAGTGACAGG
31220	29307	CTGCTAAAGCTGAGTGACAG
31221	29308	ACTGCTAAAGCTGAGTGACA
31222	29309	AACTGCTAAAGCTGAGTGAC
31223	29310	TAACTGCTAAAGCTGAGTGA
31224	29311	ATAACTGCTAAAGCTGAGTG
31225	29312	GATAACTGCTAAAGCTGAGT
31226	29313	TGATAACTGCTAAAGCTGAG
31227	29314	CTGATAACTGCTAAAGCTGA
31228	29315	ACTGATAACTGCTAAAGCTG
31229	29316	TACTGATAACTGCTAAAGCT
31230	29317	TTACTGATAACTGCTAAAGC
31231	29318	TTTACTGATAACTGCTAAAG
31232	29319	ATTTACTGATAACTGCTAAA
31233	29320	CATTTACTGATAACTGCTAA

80310	78397	TCTAACCTGTAAAAGCCACC
80311	78398	CTCTAACCTGTAAAAGCCAC
80312	78399	TCTCTAACCTGTAAAAGCCA
80313	78400	TTCTCTAACCTGTAAAAGCC
80314	78401	TTTCTCTAACCTGTAAAAGC
80315	78402	TTTTCTCTAACCTGTAAAAG
80316	78403	CTTTTCTCTAACCTGTAAAA
80317	78404	TCTTTTCTCTAACCTGTAAA
80318	78405	CTCTTTTCTCTAACCTGTAA
80319	78406	TCTCTTTTCTCTAACCTGTA
80320	78407	CTCTCTTTTCTCTAACCTGT
80321	78408	TCTCTCTTTTCTCTAACCTG
80322	78409	TTCTCTCTTTTCTCTAACCT
80323	78410	GTTCTCTCTTTTCTCTAACC
80324	78411	GGTTCTCTCTTTTCTCTAAC
80325	78412	GGGTTCTCTCTTTTCTCTAA
80326	78413	AGGGTTCTCTCTTTTCTCTA
80327	78414	CAGGGTTCTCTCTTTTCTCT
80328	78415	TCAGGGTTCTCTCTTTTCTC
80329	78416	ATCAGGGTTCTCTCTTTTCT
80330	78417	GATCAGGGTTCTCTCTTTTC
80331	78418	AGATCAGGGTTCTCTCTTTT
80332	78419	CAGATCAGGGTTCTCTCTTT
80333	78420	TCAGATCAGGGTTCTCTCTT
80334	78421	TTCAGATCAGGGTTCTCTCT
80335	78422	CTTCAGATCAGGGTTCTCTC
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80337	78424	GCCTTCAGATCAGGGTTCTC
80338	78425	AGCCTTCAGATCAGGGTTCT
80339	78426	TAGCCTTCAGATCAGGGTTC
80340	78427	ATAGCCTTCAGATCAGGGTT
80341	78428	AATAGCCTTCAGATCAGGGT
80342	78429	AAATAGCCTTCAGATCAGGG
80343	78430	AAAATAGCCTTCAGATCAGG
80344	78431	TAAAATAGCCTTCAGATCAG
80345	78432	ATAAAATAGCCTTCAGATCA
80346	78433	CATAAAATAGCCTTCAGATC
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80348	78435	TTCATAAAATAGCCTTCAGA
80349	78436	CTTCATAAAATAGCCTTCAG
80350	78437	ACTTCATAAAATAGCCTTCA
80351	78438	TACTTCATAAAATAGCCTTC
80352	78439	TTACTTCATAAAATAGCCTT
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80356	78443	TTAATTACTTCATAAAATAG
80357	78444	TTTAATTACTTCATAAAATA
80358	78445	TTTTAATTACTTCATAAAAT
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80360	78447	CATTTTAATTACTTCATAAA
80361	78448	ACATTTTAATTACTTCATAA
80362	78449	AACATTTTAATTACTTCATA
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80365	78452	TAGAACATTTTAATTACTTC
80366	78453	TTAGAACATTTTAATTACTT
80367	78454	TTTAGAACATTTTAATTACT
80368	78455	GTTTAGAACATTTTAATTAC
80369	78456	AGTTTAGAACATTTTAATTA
80370	78457	AAGTTTAGAACATTTTAATT
80371	78458	AAAGTTTAGAACATTTTAAT
80372	78459	TAAAGTTTAGAACATTTTAA
80373	78460	TTAAAGTTTAGAACATTTTA
80374	78461	TTTAAAGTTTAGAACATTTT
80375	78462	TTTTAAAGTTTAGAACATTT
80376	78463	TTTTTAAAGTTTAGAACATT
80377	78464	ATTTTTAAAGTTTAGAACAT
80378	78465	TATTTTTAAAGTTTAGAACA
80379	78466	TTATTTTTAAAGTTTAGAAC
80380	78467	GTTATTTTTAAAGTTTAGAA

129457	127544	AAAAATATTAGCCAGCTGCG
129458	127545	CAAAAATATTAGCCAGCTGC
129459	127546	ACAAAAATATTAGCCAGCTG
129460	127547	TACAAAAATATTAGCCAGCT
129461	127548	ATACAAAAATATTAGCCAGC
129462	127549	AATACAAAAATATTAGCCAG
129463	127550	AAATACAAAAATATTAGCCA
129464	127551	AAAATACAAAAATATTAGCC
129465	127552	AAAAATACAAAAATATTAGC
129466	127553	AAAAAATACAAAAATATTAG
129467	127554	CAAAAAATACAAAAATATTA
129468	127555	ACAAAAAATACAAAAATATT
129469	127556	CACAAAAAATACAAAAATAT
129470	127557	CCACAAAAAATACAAAAATA
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129473	127560	CCTCCACAAAAAATACAAAA
129474	127561	GCCTCCACAAAAAATACAAA
129475	127562	TGCCTCCACAAAAAATACAA
129476	127563	CTGCCTCCACAAAAAATACA
129477	127564	ACTGCCTCCACAAAAAATAC
129478	127565	CACTGCCTCCACAAAAAATA
129479	127566	ACACTGCCTCCACAAAAAAT
129480	127567	GACACTGCCTCCACAAAAAA
129481	127568	AGACACTGCCTCCACAAAAA
129482	127569	GAGACACTGCCTCCACAAAA
129483	127570	GGAGACACTGCCTCCACAAA
129484	127571	GGGAGACACTGCCTCCACAA
129485	127572	GGGGAGACACTGCCTCCACA
129486	127573	TGGGGAGACACTGCCTCCAC
129487	127574	ATGGGGAGACACTGCCTCCA
129488	127575	CATGGGGAGACACTGCCTCC
129489	127576	ACATGGGGAGACACTGCCTC
129490	127577	AACATGGGGAGACACTGCCT
129491	127578	CAACATGGGGAGACACTGCC
129492	127579	GCAACATGGGGAGACACTGC
129493	127580	GGCAACATGGGGAGACACTG
129494	127581	GGGCAACATGGGGAGACACT
129495	127582	TGGGCAACATGGGGAGACAC
129496	127583	CTGGGCAACATGGGGAGACA
129497	127584	CCTGGGCAACATGGGGAGAC
129498	127585	CCCTGGGCAACATGGGGAGA
129499	127586	ACCCTGGGCAACATGGGGAG
129500	127587	CACCCTGGGCAACATGGGGA
129501	127588	CCACCCTGGGCAACATGGGG
129502	127589	ACCACCCTGGGCAACATGGG
129503	127590	GACCACCCTGGGCAACATGG
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129506	127593	TGGGACCACCCTGGGCAACA
129507	127594	TTGGGACCACCCTGGGCAAC
129508	127595	TTTGGGACCACCCTGGGCAA
129509	127596	GTTTGGGACCACCCTGGGCA
129510	127597	AGTTTGGGACCACCCTGGGC
129511	127598	GAGTTTGGGACCACCCTGGG
129512	127599	TGAGTTTGGGACCACCCTGG
129513	127600	ATGAGTTTGGGACCACCCTG
129514	127601	CATGAGTTTGGGACCACCCT
129515	127602	TCATGAGTTTGGGACCACCC
129516	127603	CTCATGAGTTTGGGACCACC
129517	127604	GCTCATGAGTTTGGGACCAC
129518	127605	AGCTCATGAGTTTGGGACCA
129519	127606	GAGCTCATGAGTTTGGGACC
129520	127607	TGAGCTCATGAGTTTGGGAC
129521	127608	TTGAGCTCATGAGTTTGGGA
129522	127609	CTTGAGCTCATGAGTTTGGG
129523	127610	GCTTGAGCTCATGAGTTTGG
129524	127611	TGCTTGAGCTCATGAGTTTG
129525	127612	CTGCTTGAGCTCATGAGTTT
129526	127613	ACTGCTTGAGCTCATGAGTT
129527	127614	GACTGCTTGAGCTCATGAGT

31234	29321	CCATTTACTGATAACTGCTA
31235	29322	GCCATTTACTGATAACTGCT
31236	29323	GGCCATTTACTGATAACTGC
31237	29324	TGGCCATTTACTGATAACTG
31238	29325	TTGGCCATTTACTGATAACT
31239	29326	GTTGGCCATTTACTGATAAC
31240	29327	CGTTGGCCATTTACTGATAA
31241	29328	ACGTTGGCCATTTACTGATA
31242	29329	AACGTTGGCCATTTACTGAT
31243	29330	CAACGTTGGCCATTTACTGA
31244	29331	ACAACGTTGGCCATTTACTG
31245	29332	AACAACGTTGGCCATTTACT
31246	29333	AAACAACGTTGGCCATTTAC
31247	29334	GAAACAACGTTGGCCATTTA
31248	29335	TGAAACAACGTTGGCCATTT
31249	29336	CTGAAACAACGTTGGCCATT
31250	29337	GCTGAAACAACGTTGGCCAT
31251	29338	AGCTGAAACAACGTTGGCCA
31252	29339	TAGCTGAAACAACGTTGGCC
31253	29340	ATAGCTGAAACAACGTTGGC
31254	29341	TATAGCTGAAACAACGTTGG
31255	29342	GTATAGCTGAAACAACGTTG
31256	29343	AGTATAGCTGAAACAACGTT
31257	29344	GAGTATAGCTGAAACAACGT
31258	29345	GGAGTATAGCTGAAACAACG
31259	29346	GGGAGTATAGCTGAAACAAC
31260	29347	GGGGAGTATAGCTGAAACAA
31261	29348	AGGGGAGTATAGCTGAAACA
31262	29349	GAGGGGAGTATAGCTGAAAC
31263	29350	AGAGGGGAGTATAGCTGAAA
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31265	29352	GGAGAGGGGAGTATAGCTGA
31266	29353	AGGAGAGGGGAGTATAGCTG
31267	29354	GAGGAGAGGGGAGTATAGCT
31268	29355	GGAGGAGAGGGGAGTATAGC
31269	29356	TGGAGGAGAGGGGAGTATAG
31270	29357	GTGGAGGAGAGGGGAGTATA
31271	29358	AGTGGAGGAGAGGGGAGTAT
31272	29359	CAGTGGAGGAGAGGGGAGTA
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31275	29362	TATCAGTGGAGGAGAGGGGA
31276	29363	CTATCAGTGGAGGAGAGGGG
31277	29364	ACTATCAGTGGAGGAGAGGG
31278	29365	GACTATCAGTGGAGGAGAGG
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31280	29367	AAGACTATCAGTGGAGGAGA
31281	29368	AAAGACTATCAGTGGAGGAG
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31285	29372	TTCAAAAGACTATCAGTGGA
31286	29373	CTTCAAAAGACTATCAGTGG
31287	29374	CCTTCAAAAGACTATCAGTG
31288	29375	CCCTTCAAAAGACTATCAGT
31289	29376	CCCCTTCAAAAGACTATCAG
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31291	29378	TTCCCCTTCAAAAGACTATC
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31293	29380	TATTCCCCTTCAAAAGACTA
31294	29381	GTATTCCCCTTCAAAAGACT
31295	29382	TGTATTCCCCTTCAAAAGAC
31296	29383	TTGTATTCCCCTTCAAAAGA
31297	29384	ATTGTATTCCCCTTCAAAAG
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31299	29386	CAATTGTATTCCCCTTCAAA
31300	29387	ACAATTGTATTCCCCTTCAA
31301	29388	AACAATTGTATTCCCCTTCA
31302	29389	AAACAATTGTATTCCCCTTC
31303	29390	AAAACAATTGTATTCCCCTT
31304	29391	CAAAACAATTGTATTCCCCT

80381	78468	AGTTATTTTTAAAGTTTAGA
80382	78469	CAGTTATTTTTAAAGTTTAG
80383	78470	GCAGTTATTTTTAAAGTTTA
80384	78471	AGCAGTTATTTTTAAAGTTT
80385	78472	GAGCAGTTATTTTTAAAGTT
80386	78473	TGAGCAGTTATTTTTAAAGT
80387	78474	TTGAGCAGTTATTTTTAAAG
80388	78475	TTTGAGCAGTTATTTTTAAA
80389	78476	ATTTGAGCAGTTATTTTTAA
80390	78477	TATTTGAGCAGTTATTTTTA
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80392	78479	ATTATTTGAGCAGTTATTTT
80393	78480	AATTATTTGAGCAGTTATTT
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80395	78482	ACAATTATTTGAGCAGTTAT
80396	78483	CACAATTATTTGAGCAGTTA
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80398	78485	AACACAATTATTTGAGCAGT
80399	78486	CAACACAATTATTTGAGCAG
80400	78487	ACAACACAATTATTTGAGCA
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80404	78491	CTATACAACACAATTATTTG
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80406	78493	AACTATACAACACAATTATT
80407	78494	TAACTATACAACACAATTAT
80408	78495	GTAACTATACAACACAATTA
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80410	78497	AAGTAACTATACAACACAAT
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80412	78499	ATAAGTAACTATACAACACA
80413	78500	GATAAGTAACTATACAACAC
80414	78501	TGATAAGTAACTATACAACA
80415	78502	TTGATAAGTAACTATACAAC
80416	78503	GTTGATAAGTAACTATACAA
80417	78504	AGTTGATAAGTAACTATACA
80418	78505	CAGTTGATAAGTAACTATAC
80419	78506	CCAGTTGATAAGTAACTATA
80420	78507	TCCAGTTGATAAGTAACTAT
80421	78508	CTCCAGTTGATAAGTAACTA
80422	78509	CCTCCAGTTGATAAGTAACT
80423	78510	CCCTCCAGTTGATAAGTAAC
80424	78511	CCCCTCCAGTTGATAAGTAA
80425	78512	GCCCCTCCAGTTGATAAGTA
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80428	78515	TCAGCCCCTCCAGTTGATAA
80429	78516	ATCAGCCCCTCCAGTTGATA
80430	78517	TATCAGCCCCTCCAGTTGAT
80431	78518	TTATCAGCCCCTCCAGTTGA
80432	78519	CTTATCAGCCCCTCCAGTTG
80433	78520	ACTTATCAGCCCCTCCAGTT
80434	78521	TACTTATCAGCCCCTCCAGT
80435	78522	ATACTTATCAGCCCCTCCAG
80436	78523	AATACTTATCAGCCCCTCCA
80437	78524	AAATACTTATCAGCCCCTCC
80438	78525	AAAATACTTATCAGCCCCTC
80439	78526	AAAAATACTTATCAGCCCCT
80440	78527	GAAAAATACTTATCAGCCCC
80441	78528	AGAAAAATACTTATCAGCCC
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80443	78530	TTAGAAAAATACTTATCAGC
80444	78531	TTTAGAAAAATACTTATCAG
80445	78532	TTTTAGAAAAATACTTATCA
80446	78533	GTTTTAGAAAAATACTTATC
80447	78534	TGTTTTAGAAAAATACTTAT
80448	78535	ATGTTTTAGAAAAATACTTA
80449	78536	AATGTTTTAGAAAAATACTT
80450	78537	AAATGTTTTAGAAAAATACT
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129528	127615	GGACTGCTTGAGCTCATGAG
129529	127616	CGGACTGCTTGAGCTCATGA
129530	127617	GCGGACTGCTTGAGCTCATG
129531	127618	AGCGGACTGCTTGAGCTCAT
129532	127619	GAGCGGACTGCTTGAGCTCA
129533	127620	CGAGCGGACTGCTTGAGCTC
129534	127621	GCGAGCGGACTGCTTGAGCT
129535	127622	GGCGAGCGGACTGCTTGAGC
129536	127623	GGGCGAGCGGACTGCTTGAG
129537	127624	AGGGCGAGCGGACTGCTTGA
129538	127625	CAGGGCGAGCGGACTGCTTG
129539	127626	CCAGGGCGAGCGGACTGCTT
129540	127627	GCCAGGGCGAGCGGACTGCT
129541	127628	GGCCAGGGCGAGCGGACTGC
129542	127629	AGGCCAGGGCGAGCGGACTG
129543	127630	GAGGCCAGGGCGAGCGGACT
129544	127631	GGAGGCCAGGGCGAGCGGAC
129545	127632	AGGAGGCCAGGGCGAGCGGA
129546	127633	TAGGAGGCCAGGGCGAGCGG
129547	127634	TTAGGAGGCCAGGGCGAGCG
129548	127635	TTTAGGAGGCCAGGGCGAGC
129549	127636	CTTTAGGAGGCCAGGGCGAG
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129552	127639	ACACTTTAGGAGGCCAGGGC
129553	127640	TACACTTTAGGAGGCCAGGG
129554	127641	CTACACTTTAGGAGGCCAGG
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129556	127643	CCCTACACTTTAGGAGGCCA
129557	127644	TCCCTACACTTTAGGAGGCC
129558	127645	ATCCCTACACTTTAGGAGGC
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129560	127647	TAATCCCTACACTTTAGGAG
129561	127648	ATAATCCCTACACTTTAGGA
129562	127649	TATAATCCCTACACTTTAGG
129563	127650	TTATAATCCCTACACTTTAG
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129565	127652	GCTTATAATCCCTACACTTT
129566	127653	CGCTTATAATCCCTACACTT
129567	127654	ACGCTTATAATCCCTACACT
129568	127655	CACGCTTATAATCCCTACAC
129569	127656	TCACGCTTATAATCCCTACA
129570	127657	CTCACGCTTATAATCCCTAC
129571	127658	GCTCACGCTTATAATCCCTA
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129573	127660	TGGCTCACGCTTATAATCCC
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129575	127662	AGTGGCTCACGCTTATAATC
129576	127663	CAGTGGCTCACGCTTATAAT
129577	127664	GCAGTGGCTCACGCTTATAA
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129581	127668	AGGCGCAGTGGCTCACGCTT
129582	127669	CAGGCGCAGTGGCTCACGCT
129583	127670	CCAGGCGCAGTGGCTCACGC
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129585	127672	GGCCAGGCGCAGTGGCTCAC
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129594	127681	TGATCCCCAGGCCAGGCGCA
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129596	127683	CATGATCCCCAGGCCAGGCG
129597	127684	ACATGATCCCCAGGCCAGGC
129598	127685	AACATGATCCCCAGGCCAGG

31305	29392	ACAAAACAATTGTATTCCCC
31306	29393	CACAAAACAATTGTATTCCC
31307	29394	CCACAAAACAATTGTATTCC
31308	29395	GCCACAAAACAATTGTATTC
31309	29396	GGCCACAAAACAATTGTATT
31310	29397	AGGCCACAAAACAATTGTAT
31311	29398	GAGGCCACAAAACAATTGTA
31312	29399	GGAGGCCACAAAACAATTGT
31313	29400	TGGAGGCCACAAAACAATTG
31314	29401	CTGGAGGCCACAAAACAATT
31315	29402	TCTGGAGGCCACAAAACAAT
31316	29403	TTCTGGAGGCCACAAAACAA
31317	29404	TTTCTGGAGGCCACAAAACA
31318	29405	CTTTCTGGAGGCCACAAAAC
31319	29406	CCTTTCTGGAGGCCACAAAA
31320	29407	CCCTTTCTGGAGGCCACAAA
31321	29408	TCCCTTTCTGGAGGCCACAA
31322	29409	ATCCCTTTCTGGAGGCCACA
31323	29410	TATCCCTTTCTGGAGGCCAC
31324	29411	TTATCCCTTTCTGGAGGCCA
31325	29412	CTTATCCCTTTCTGGAGGCC
31326	29413	ACTTATCCCTTTCTGGAGGC
31327	29414	AACTTATCCCTTTCTGGAGG
31328	29415	AAACTTATCCCTTTCTGGAG
31329	29416	TAAACTTATCCCTTTCTGGA
31330	29417	ATAAACTTATCCCTTTCTGG
31331	29418	CATAAACTTATCCCTTTCTG
31332	29419	TCATAAACTTATCCCTTTCT
31333	29420	CTCATAAACTTATCCCTTTC
31334	29421	GCTCATAAACTTATCCCTTT
31335	29422	TGCTCATAAACTTATCCCTT
31336	29423	TTGCTCATAAACTTATCCCT
31337	29424	GTTGCTCATAAACTTATCCC
31338	29425	CGTTGCTCATAAACTTATCC
31339	29426	CCGTTGCTCATAAACTTATC
31340	29427	CCCGTTGCTCATAAACTTAT
31341	29428	ACCCGTTGCTCATAAACTTA
31342	29429	TACCCGTTGCTCATAAACTT
31343	29430	CTACCCGTTGCTCATAAACT
31344	29431	TCTACCCGTTGCTCATAAAC
31345	29432	ATCTACCCGTTGCTCATAAA
31346	29433	GATCTACCCGTTGCTCATAA
31347	29434	CGATCTACCCGTTGCTCATA
31348	29435	ACGATCTACCCGTTGCTCAT
31349	29436	AACGATCTACCCGTTGCTCA
31350	29437	CAACGATCTACCCGTTGCTC
31351	29438	CCAACGATCTACCCGTTGCT
31352	29439	CCCAACGATCTACCCGTTGC
31353	29440	TCCCAACGATCTACCCGTTG
31354	29441	CTCCCAACGATCTACCCGTT
31355	29442	TCTCCCAACGATCTACCCGT
31356	29443	CTCTCCCAACGATCTACCCG
31357	29444	TCTCTCCCAACGATCTACCC
31358	29445	GTCTCTCCCAACGATCTACC
31359	29446	AGTCTCTCCCAACGATCTAC
31360	29447	AAGTCTCTCCCAACGATCTA
31361	29448	CAAGTCTCTCCCAACGATCT
31362	29449	TCAAGTCTCTCCCAACGATC
31363	29450	CTCAAGTCTCTCCCAACGAT
31364	29451	ACTCAAGTCTCTCCCAACGA
31365	29452	AACTCAAGTCTCTCCCAACG
31366	29453	AAACTCAAGTCTCTCCCAAC
31367	29454	GAAACTCAAGTCTCTCCCAA
31368	29455	GGAAACTCAAGTCTCTCCCA
31369	29456	AGGAAACTCAAGTCTCTCCC
31370	29457	CAGGAAACTCAAGTCTCTCC
31371	29458	ACAGGAAACTCAAGTCTCTC
31372	29459	GACAGGAAACTCAAGTCTCT
31373	29460	TGACAGGAAACTCAAGTCTC
31374	29461	CTGACAGGAAACTCAAGTCT
31375	29462	CCTGACAGGAAACTCAAGTC

80452	78539	AAAAATGTTTTAGAAAAATA
80453	78540	TAAAAATGTTTTAGAAAAAT
80454	78541	TTAAAAATGTTTTAGAAAAA
80455	78542	CTTAAAAATGTTTTAGAAAA
80456	78543	CCTTAAAAATGTTTTAGAAA
80457	78544	TCCTTAAAAATGTTTTAGAA
80458	78545	TTCCTTAAAAATGTTTTAGA
80459	78546	TTTCCTTAAAAATGTTTTAG
80460	78547	ATTTCCTTAAAAATGTTTTA
80461	78548	AATTTCCTTAAAAATGTTTT
80462	78549	AAATTTCCTTAAAAATGTTT
80463	78550	AAAATTTCCTTAAAAATGTT
80464	78551	AAAAATTTCCTTAAAAATGT
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80470	78557	ATAGGAAAAAATTTCCTTAA
80471	78558	AATAGGAAAAAATTTCCTTA
80472	78559	AAATAGGAAAAAATTTCCTT
80473	78560	AAAATAGGAAAAAATTTCCT
80474	78561	GAAAATAGGAAAAAATTTCC
80475	78562	AGAAAATAGGAAAAAATTTC
80476	78563	TAGAAAATAGGAAAAAATTT
80477	78564	TTAGAAAATAGGAAAAAATT
80478	78565	ATTAGAAAATAGGAAAAAAT
80479	78566	AATTAGAAAATAGGAAAAAA
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80514	78601	ACAATATCTAACAAACTACT
80515	78602	AACAATATCTAACAAACTAC
80516	78603	TAACAATATCTAACAAACTA
80517	78604	TTAACAATATCTAACAAACT
80518	78605	ATTAACAATATCTAACAAAC
80519	78606	TATTAACAATATCTAACAAA
80520	78607	ATATTAACAATATCTAACAA
80521	78608	TATATTAACAATATCTAACA
80522	78609	CTATATTAACAATATCTAAC

129599	127686	AAACATGATCCCCAGGCCAG
129600	127687	AAAACATGATCCCCAGGCCA
129601	127688	TAAAACATGATCCCCAGGCC
129602	127689	TTAAAACATGATCCCCAGGC
129603	127690	GTTAAAACATGATCCCCAGG
129604	127691	TGTTAAAACATGATCCCCAG
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129606	127693	CATGTTAAAACATGATCCCC
129607	127694	TCATGTTAAAACATGATCCC
129608	127695	CTCATGTTAAAACATGATCC
129609	127696	TCTCATGTTAAAACATGATC
129610	127697	TTCTCATGTTAAAACATGAT
129611	127698	ATTCTCATGTTAAAACATGA
129612	127699	AATTCTCATGTTAAAACATG
129613	127700	TAATTCTCATGTTAAAACAT
129614	127701	CTAATTCTCATGTTAAAACA
129615	127702	ACTAATTCTCATGTTAAAAC
129616	127703	CACTAATTCTCATGTTAAAA
129617	127704	CCACTAATTCTCATGTTAAA
129618	127705	TCCACTAATTCTCATGTTAA
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129626	127713	TGTTTGTCTCCACTAATTCT
129627	127714	GTGTTTGTCTCCACTAATTC
129628	127715	TGTGTTTGTCTCCACTAATT
129629	127716	ATGTGTTTGTCTCCACTAAT
129630	127717	CATGTGTTTGTCTCCACTAA
129631	127718	TCATGTGTTTGTCTCCACTA
129632	127719	ATCATGTGTTTGTCTCCACT
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129637	127724	TAGATATCATGTGTTTGTCT
129638	127725	TTAGATATCATGTGTTTGTC
129639	127726	TTTAGATATCATGTGTTTGT
129640	127727	ATTTAGATATCATGTGTTTG
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129643	127730	ATTATTTAGATATCATGTGT
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129649	127736	GGTGCTATTATTTAGATATC
129650	127737	TGGTGCTATTATTTAGATAT
129651	127738	ATGGTGCTATTATTTAGATA
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129664	127751	AGTCAAGTATACTATGGTGC
129665	127752	TAGTCAAGTATACTATGGTG
129666	127753	CTAGTCAAGTATACTATGGT
129667	127754	GCTAGTCAAGTATACTATGG
129668	127755	AGCTAGTCAAGTATACTATG
129669	127756	AAGCTAGTCAAGTATACTAT

31376	29463	TCCTGACAGGAAACTCAAGT
31377	29464	TTCCTGACAGGAAACTCAAG
31378	29465	CTTCCTGACAGGAAACTCAA
31379	29466	GCTTCCTGACAGGAAACTCA
31380	29467	TGCTTCCTGACAGGAAACTC
31381	29468	ATGCTTCCTGACAGGAAACT
31382	29469	AATGCTTCCTGACAGGAAAC
31383	29470	GAATGCTTCCTGACAGGAAA
31384	29471	AGAATGCTTCCTGACAGGAA
31385	29472	AAGAATGCTTCCTGACAGGA
31386	29473	CAAGAATGCTTCCTGACAGG
31387	29474	CCAAGAATGCTTCCTGACAG
31388	29475	ACCAAGAATGCTTCCTGACA
31389	29476	CACCAAGAATGCTTCCTGAC
31390	29477	GCACCAAGAATGCTTCCTGA
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31394	29481	TTATGCACCAAGAATGCTTC
31395	29482	CTTATGCACCAAGAATGCTT
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31397	29484	GACTTATGCACCAAGAATGC
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31399	29486	CTGACTTATGCACCAAGAAT
31400	29487	TCTGACTTATGCACCAAGAA
31401	29488	CTCTGACTTATGCACCAAGA
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31406	29493	ATCACCTCTGACTTATGCAC
31407	29494	TATCACCTCTGACTTATGCA
31408	29495	ATATCACCTCTGACTTATGC
31409	29496	CATATCACCTCTGACTTATG
31410	29497	TCATATCACCTCTGACTTAT
31411	29498	TTCATATCACCTCTGACTTA
31412	29499	ATTCATATCACCTCTGACTT
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31414	29501	GCATTCATATCACCTCTGAC
31415	29502	GGCATTCATATCACCTCTGA
31416	29503	CGGCATTCATATCACCTCTG
31417	29504	ACGGCATTCATATCACCTCT
31418	29505	CACGGCATTCATATCACCTC
31419	29506	CCACGGCATTCATATCACCT
31420	29507	TCCACGGCATTCATATCACC
31421	29508	TTCCACGGCATTCATATCAC
31422	29509	CTTCCACGGCATTCATATCA
31423	29510	CCTTCCACGGCATTCATATC
31424	29511	CCCTTCCACGGCATTCATAT
31425	29512	CCCCTTCCACGGCATTCATA
31426	29513	CCCCCTTCCACGGCATTCAT
31427	29514	ACCCCCTTCCACGGCATTCA
31428	29515	CACCCCCTTCCACGGCATTC
31429	29516	CCACCCCCTTCCACGGCATT
31430	29517	GCCACCCCCTTCCACGGCAT
31431	29518	AGCCACCCCCTTCCACGGCA
31432	29519	AAGCCACCCCCTTCCACGGC
31433	29520	TAAGCCACCCCCTTCCACGG
31434	29521	GTAAGCCACCCCCTTCCACG
31435	29522	AGTAAGCCACCCCCTTCCAC
31436	29523	CAGTAAGCCACCCCCTTCCA
31437	29524	ACAGTAAGCCACCCCCTTCC
31438	29525	GACAGTAAGCCACCCCCTTC
31439	29526	AGACAGTAAGCCACCCCCTT
31440	29527	CAGACAGTAAGCCACCCCCT
31441	29528	CCAGACAGTAAGCCACCCCC
31442	29529	TCCAGACAGTAAGCCACCCC
31443	29530	CTCCAGACAGTAAGCCACCC
31444	29531	TCTCCAGACAGTAAGCCACC
31445	29532	TTCTCCAGACAGTAAGCCAC
31446	29533	GTTCTCCAGACAGTAAGCCA

80523	78610	TCTATATTAACAATATCTAA
80524	78611	ATCTATATTAACAATATCTA
80525	78612	CATCTATATTAACAATATCT
80526	78613	ACATCTATATTAACAATATC
80527	78614	AACATCTATATTAACAATAT
80528	78615	CAACATCTATATTAACAATA
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80530	78617	ACCAACATCTATATTAACAA
80531	78618	AACCAACATCTATATTAACA
80532	78619	TAACCAACATCTATATTAAC
80533	78620	ATAACCAACATCTATATTAA
80534	78621	TATAACCAACATCTATATTA
80535	78622	TTATAACCAACATCTATATT
80536	78623	GTTATAACCAACATCTATAT
80537	78624	AGTTATAACCAACATCTATA
80538	78625	CAGTTATAACCAACATCTAT
80539	78626	TCAGTTATAACCAACATCTA
80540	78627	TTCAGTTATAACCAACATCT
80541	78628	ATTCAGTTATAACCAACATC
80542	78629	CATTCAGTTATAACCAACAT
80543	78630	TCATTCAGTTATAACCAACA
80544	78631	TTCATTCAGTTATAACCAAC
80545	78632	TTTCATTCAGTTATAACCAA
80546	78633	CTTTCATTCAGTTATAACCA
80547	78634	CCTTTCATTCAGTTATAACC
80548	78635	CCCTTTCATTCAGTTATAAC
80549	78636	TCCCTTTCATTCAGTTATAA
80550	78637	TTCCCTTTCATTCAGTTATA
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80552	78639	TGTTCCCTTTCATTCAGTTA
80553	78640	TTGTTCCCTTTCATTCAGTT
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80558	78645	AGTAGTTGTTCCCTTTCATT
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80560	78647	AAAGTAGTTGTTCCCTTTCA
80561	78648	CAAAGTAGTTGTTCCCTTTC
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80563	78650	GTCAAAGTAGTTGTTCCCTT
80564	78651	TGTCAAAGTAGTTGTTCCCT
80565	78652	ATGTCAAAGTAGTTGTTCCC
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80567	78654	AAATGTCAAAGTAGTTGTTC
80568	78655	AAAATGTCAAAGTAGTTGTT
80569	78656	CAAAATGTCAAAGTAGTTGT
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80573	78660	TTTTCAAAATGTCAAAGTAG
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80575	78662	GTTTTTCAAAATGTCAAAGT
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80577	78664	TTGTTTTTCAAAATGTCAAA
80578	78665	CTTGTTTTTCAAAATGTCAA
80579	78666	GCTTGTTTTTCAAAATGTCA
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80583	78670	TGAAGCTTGTTTTTCAAAAT
80584	78671	ATGAAGCTTGTTTTTCAAAA
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80587	78674	AAAATGAAGCTTGTTTTTCA
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80589	78676	AGAAAATGAAGCTTGTTTTT
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129670	127757	AAAGCTAGTCAAGTATACTA
129671	127758	AAAAGCTAGTCAAGTATACT
129672	127759	AAAAAGCTAGTCAAGTATAC
129673	127760	TAAAAAGCTAGTCAAGTATA
129674	127761	TTAAAAAGCTAGTCAAGTAT
129675	127762	ATTAAAAAGCTAGTCAAGTA
129676	127763	AATTAAAAAGCTAGTCAAGT
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129678	127765	ATAATTAAAAAGCTAGTCAA
129679	127766	AATAATTAAAAAGCTAGTCA
129680	127767	AAATAATTAAAAAGCTAGTC
129681	127768	AAAATAATTAAAAAGCTAGT
129682	127769	AAAAATAATTAAAAAGCTAG
129683	127770	AAAAAATAATTAAAAAGCTA
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129685	127772	TTAAAAAATAATTAAAAAGC
129686	127773	TTTAAAAAATAATTAAAAAG
129687	127774	ATTTAAAAAATAATTAAAAA
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129689	127776	ATATTTAAAAAATAATTAAA
129690	127777	TATATTTAAAAAATAATTAA
129691	127778	GTATATTTAAAAAATAATTA
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129696	127783	TTCCTGTATATTTAAAAAAT
129697	127784	CTTCCTGTATATTTAAAAAA
129698	127785	CCTTCCTGTATATTTAAAAA
129699	127786	ACCTTCCTGTATATTTAAAA
129700	127787	TACCTTCCTGTATATTTAAA
129701	127788	TTACCTTCCTGTATATTTAA
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129706	127793	ACTTATTACCTTCCTGTATA
129707	127794	TACTTATTACCTTCCTGTAT
129708	127795	TTACTTATTACCTTCCTGTA
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129712	127799	TTTGTTACTTATTACCTTCC
129713	127800	CTTTGTTACTTATTACCTTC
129714	127801	ACTTTGTTACTTATTACCTT
129715	127802	TACTTTGTTACTTATTACCT
129716	127803	TTACTTTGTTACTTATTACC
129717	127804	ATTACTTTGTTACTTATTAC
129718	127805	TATTACTTTGTTACTTATTA
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129725	127812	TCACTATTATTACTTTGTTA
129726	127813	TTCACTATTATTACTTTGTT
129727	127814	ATTCACTATTATTACTTTGT
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129729	127816	CTATTCACTATTATTACTTT
129730	127817	ACTATTCACTATTATTACTT
129731	127818	AACTATTCACTATTATTACT
129732	127819	AAACTATTCACTATTATTAC
129733	127820	TAAACTATTCACTATTATTA
129734	127821	TTAAACTATTCACTATTATT
129735	127822	CTTAAACTATTCACTATTAT
129736	127823	GCTTAAACTATTCACTATTA
129737	127824	AGCTTAAACTATTCACTATT
129738	127825	GAGCTTAAACTATTCACTAT
129739	127826	TGAGCTTAAACTATTCACTA
129740	127827	CTGAGCTTAAACTATTCACT

31447	29534	AGTTCTCCAGACAGTAAGCC
31448	29535	GAGTTCTCCAGACAGTAAGC
31449	29536	CGAGTTCTCCAGACAGTAAG
31450	29537	TCGAGTTCTCCAGACAGTAA
31451	29538	CTCGAGTTCTCCAGACAGTA
31452	29539	TCTCGAGTTCTCCAGACAGT
31453	29540	TTCTCGAGTTCTCCAGACAG
31454	29541	CTTCTCGAGTTCTCCAGACA
31455	29542	TCTTCTCGAGTTCTCCAGAC
31456	29543	ATCTTCTCGAGTTCTCCAGA
31457	29544	CATCTTCTCGAGTTCTCCAG
31458	29545	CCATCTTCTCGAGTTCTCCA
31459	29546	CCCATCTTCTCGAGTTCTCC
31460	29547	TCCCATCTTCTCGAGTTCTC
31461	29548	TTCCCATCTTCTCGAGTTCT
31462	29549	ATTCCCATCTTCTCGAGTTC
31463	29550	CATTCCCATCTTCTCGAGTT
31464	29551	CCATTCCCATCTTCTCGAGT
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31466	29553	GCCCATTCCCATCTTCTCGA
31467	29554	TGCCCATTCCCATCTTCTCG
31468	29555	GTGCCCATTCCCATCTTCTC
31469	29556	AGTGCCCATTCCCATCTTCT
31470	29557	CAGTGCCCATTCCCATCTTC
31471	29558	ACAGTGCCCATTCCCATCTT
31472	29559	GACAGTGCCCATTCCCATCT
31473	29560	GGACAGTGCCCATTCCCATC
31474	29561	TGGACAGTGCCCATTCCCAT
31475	29562	CTGGACAGTGCCCATTCCCA
31476	29563	ACTGGACAGTGCCCATTCCC
31477	29564	TACTGGACAGTGCCCATTCC
31478	29565	ATACTGGACAGTGCCCATTC
31479	29566	AATACTGGACAGTGCCCATT
31480	29567	CAATACTGGACAGTGCCCAT
31481	29568	ACAATACTGGACAGTGCCCA
31482	29569	CACAATACTGGACAGTGCCC
31483	29570	CCACAATACTGGACAGTGCC
31484	29571	GCCACAATACTGGACAGTGC
31485	29572	AGCCACAATACTGGACAGTG
31486	29573	TAGCCACAATACTGGACAGT
31487	29574	GTAGCCACAATACTGGACAG
31488	29575	AGTAGCCACAATACTGGACA
31489	29576	AAGTAGCCACAATACTGGAC
31490	29577	GAAGTAGCCACAATACTGGA
31491	29578	GGAAGTAGCCACAATACTGG
31492	29579	TGGAAGTAGCCACAATACTG
31493	29580	GTGGAAGTAGCCACAATACT
31494	29581	TGTGGAAGTAGCCACAATAC
31495	29582	GTGTGGAAGTAGCCACAATA
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31497	29584	ATGTGTGGAAGTAGCCACAA
31498	29585	CATGTGTGGAAGTAGCCACA
31499	29586	CCATGTGTGGAAGTAGCCAC
31500	29587	ACCATGTGTGGAAGTAGCCA
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31505	29592	AAAGAACCATGTGTGGAAGT
31506	29593	TAAAGAACCATGTGTGGAAG
31507	29594	TTAAAGAACCATGTGTGGAA
31508	29595	TTTAAAGAACCATGTGTGGA
31509	29596	ATTTAAAGAACCATGTGTGG
31510	29597	AATTTAAAGAACCATGTGTG
31511	29598	AAATTTAAAGAACCATGTGT
31512	29599	TAAATTTAAAGAACCATGTG
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31514	29601	TTTAAATTTAAAGAACCATG
31515	29602	TTTTAAATTTAAAGAACCAT
31516	29603	ATTTTAAATTTAAAGAACCA
31517	29604	AATTTTAAATTTAAAGAACC

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80596	78683	GACTAGAAGAAAATGAAGCT
80597	78684	AGACTAGAAGAAAATGAAGC
80598	78685	TAGACTAGAAGAAAATGAAG
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80602	78689	CCATTAGACTAGAAGAAAAT
80603	78690	TCCATTAGACTAGAAGAAAA
80604	78691	ATCCATTAGACTAGAAGAAA
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80606	78693	CCATCCATTAGACTAGAAGA
80607	78694	CCCATCCATTAGACTAGAAG
80608	78695	TCCCATCCATTAGACTAGAA
80609	78696	ATCCCATCCATTAGACTAGA
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80613	78700	TGGGATCCCATCCATTAGAC
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80617	78704	TCATTGGGATCCCATCCATT
80618	78705	ATCATTGGGATCCCATCCAT
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80627	78714	TCGAAACATATCATTGGGAT
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129741	127828	ACTGAGCTTAAACTATTCAC
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129743	127830	TAACTGAGCTTAAACTATTC
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129748	127835	TATGCTAACTGAGCTTAAAC
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129766	127853	AATGAAAGTTTGCCCGATTA
129767	127854	AAATGAAAGTTTGCCCGATT
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129769	127856	TCAAATGAAAGTTTGCCCGA
129770	127857	ATCAAATGAAAGTTTGCCCG
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129773	127860	TTTATCAAATGAAAGTTTGC
129774	127861	TTTTATCAAATGAAAGTTTG
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129784	127871	TACTTATCACTTTTATCAAA
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129786	127873	ACTACTTATCACTTTTATCA
129787	127874	AACTACTTATCACTTTTATC
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31520	29607	CATAATTTTAAATTTAAAGA
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31522	29609	AACATAATTTTAAATTTAAA
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31524	29611	TCAACATAATTTTAAATTTA
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31584	29671	GCAGCTAAGCACTTGAAATA
31585	29672	GGCAGCTAAGCACTTGAAAT
31586	29673	TGGCAGCTAAGCACTTGAAA
31587	29674	GTGGCAGCTAAGCACTTGAA
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80688	78775	ACGTATACGAAGATAAACTG
80689	78776	TACGTATACGAAGATAAACT
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80701	78788	ACTTTTCAAACTTACGTATA
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80725	78812	ACAAATGCACTAAAATAAAA
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80727	78814	AGACAAATGCACTAAAATAA
80728	78815	AAGACAAATGCACTAAAATA
80729	78816	AAAGACAAATGCACTAAAAT
80730	78817	CAAAGACAAATGCACTAAAA
80731	78818	TCAAAGACAAATGCACTAAA
80732	78819	ATCAAAGACAAATGCACTAA
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80734	78821	AAATCAAAGACAAATGCACT
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129812	127899	TCTGGTAAACAAAAAAGCCA
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129820	127907	CACCTCCTTCTGGTAAACAA
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129839	127926	GATGCACGTATTTAAAAACC
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129845	127932	ATCTTGGATGCACGTATTTA
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129847	127934	TTATCTTGGATGCACGTATT
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129849	127936	TTTTATCTTGGATGCACGTA
129850	127937	ATTTTATCTTGGATGCACGT
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129865	127952	TGAACATTTTTTTATATTTT
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129881	127968	TGTAGGAAAGCAAACCTGAA
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31589	29676	ATGTGGCAGCTAAGCACTTG
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31593	29680	GCACATGTGGCAGCTAAGCA
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31596	29683	TAGGCACATGTGGCAGCTAA
31597	29684	TTAGGCACATGTGGCAGCTA
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31610	29697	AATATTGCAGCCATTAGGCA
31611	29698	CAATATTGCAGCCATTAGGC
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31613	29700	TCCAATATTGCAGCCATTAG
31614	29701	GTCCAATATTGCAGCCATTA
31615	29702	TGTCCAATATTGCAGCCATT
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31626	29713	CTATGTCATGCTGTCCAATA
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31647	29734	TTGTACAATGATGAAGATGT
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31649	29736	CTTTGTACAATGATGAAGAT
31650	29737	ACTTTGTACAATGATGAAGA
31651	29738	AACTTTGTACAATGATGAAG
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31656	29743	AAGAGAACTTTGTACAATGA
31657	29744	CAAGAGAACTTTGTACAATG
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31659	29746	TCCAAGAGAACTTTGTACAA

80736	78823	GAAAATCAAAGACAAATGCA
80737	78824	TGAAAATCAAAGACAAATGC
80738	78825	ATGAAAATCAAAGACAAATG
80739	78826	GATGAAAATCAAAGACAAAT
80740	78827	TGATGAAAATCAAAGACAAA
80741	78828	CTGATGAAAATCAAAGACAA
80742	78829	GCTGATGAAAATCAAAGACA
80743	78830	AGCTGATGAAAATCAAAGAC
80744	78831	AAGCTGATGAAAATCAAAGA
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80746	78833	TTAAGCTGATGAAAATCAAA
80747	78834	ATTAAGCTGATGAAAATCAA
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80757	78844	TTCATCATAAATTAAGCTGA
80758	78845	ATTCATCATAAATTAAGCTG
80759	78846	TATTCATCATAAATTAAGCT
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80762	78849	ATTTATTCATCATAAATTAA
80763	78850	CATTTATTCATCATAAATTA
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80766	78853	AAACATTTATTCATCATAAA
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80769	78856	AACAAACATTTATTCATCAT
80770	78857	TAACAAACATTTATTCATCA
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80789	78876	AATTGTTTAACTTAAAAACT
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129887	127974	TATCTATGTAGGAAAGCAAA
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129889	127976	TTTATCTATGTAGGAAAGCA
129890	127977	TTTTATCTATGTAGGAAAGC
129891	127978	ATTTTATCTATGTAGGAAAG
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129919	128006	TGAAATTTGGGAGAGCTAGT
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129952	128039	CAAATTTGTGGCTAAACATT
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31663	29750	GCTGTCCAAGAGAACTTTGT
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31668	29755	CCCATGCTGTCCAAGAGAAC
31669	29756	TCCCATGCTGTCCAAGAGAA
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31684	29771	ATCTTAGGGCTCTAGTCCCA
31685	29772	GATCTTAGGGCTCTAGTCCC
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31688	29775	AAGGATCTTAGGGCTCTAGT
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31709	29796	ATCCAAACAACTCAGGTAGA
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80837	78924	TAATGGAAATTTATCACAGT
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31734	29821	AGATCCAACCTAGACACACC
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80908	78995	AAAAGACAAAACCAAAATTT
80909	78996	AAAAAGACAAAACCAAAATT
80910	78997	AAAAAAGACAAAACCAAAAT
80911	78998	AAAAAAAGACAAAACCAAAA
80912	78999	AAAAAAAAGACAAAACCAAA
80913	79000	AAAAAAAAAGACAAAACCAA
80914	79001	GAAAAAAAAAGACAAAACCA
80915	79002	AGAAAAAAAAAGACAAAACC
80916	79003	AAGAAAAAAAAAGACAAAAC
80917	79004	AAAGAAAAAAAAAGACAAAA
80918	79005	AAAAGAAAAAAAAAGACAAA
80919	79006	CAAAAGAAAAAAAAAGACAA
80920	79007	TCAAAAGAAAAAAAAAGACA
80921	79008	CTCAAAAGAAAAAAAAAGAC
80922	79009	TCTCAAAAGAAAAAAAAAGA
80923	79010	CTCTCAAAAGAAAAAAAAAG
80924	79011	CCTCTCAAAAGAAAAAAAAA
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80926	79013	TCCCTCTCAAAAGAAAAAAA
80927	79014	TTCCCTCTCAAAAGAAAAAA
80928	79015	ATTCCCTCTCAAAAGAAAAA
80929	79016	GATTCCCTCTCAAAAGAAAA
80930	79017	AGATTCCCTCTCAAAAGAAA
80931	79018	GAGATTCCCTCTCAAAAGAA
80932	79019	CGAGATTCCCTCTCAAAAGA
80933	79020	GCGAGATTCCCTCTCAAAAG
80934	79021	AGCGAGATTCCCTCTCAAAA
80935	79022	CAGCGAGATTCCCTCTCAAA
80936	79023	ACAGCGAGATTCCCTCTCAA
80937	79024	CACAGCGAGATTCCCTCTCA
80938	79025	ACACAGCGAGATTCCCTCTC
80939	79026	GACACAGCGAGATTCCCTCT
80940	79027	AGACACAGCGAGATTCCCTC
80941	79028	GAGACACAGCGAGATTCCCT
80942	79029	GGAGACACAGCGAGATTCCC
80943	79030	TGGAGACACAGCGAGATTCC
80944	79031	CTGGAGACACAGCGAGATTC
80945	79032	CCTGGAGACACAGCGAGATT
80946	79033	GCCTGGAGACACAGCGAGAT
80947	79034	AGCCTGGAGACACAGCGAGA
80948	79035	CAGCCTGGAGACACAGCGAG

130025	128112	ACAACTAGGTATAAGGCACA
130026	128113	TACAACTAGGTATAAGGCAC
130027	128114	TTACAACTAGGTATAAGGCA
130028	128115	CTTACAACTAGGTATAAGGC
130029	128116	GCTTACAACTAGGTATAAGG
130030	128117	TGCTTACAACTAGGTATAAG
130031	128118	CTGCTTACAACTAGGTATAA
130032	128119	ACTGCTTACAACTAGGTATA
130033	128120	GACTGCTTACAACTAGGTAT
130034	128121	TGACTGCTTACAACTAGGTA
130035	128122	ATGACTGCTTACAACTAGGT
130036	128123	AATGACTGCTTACAACTAGG
130037	128124	GAATGACTGCTTACAACTAG
130038	128125	GGAATGACTGCTTACAACTA
130039	128126	TGGAATGACTGCTTACAACT
130040	128127	GTGGAATGACTGCTTACAAC
130041	128128	TGTGGAATGACTGCTTACAA
130042	128129	TTGTGGAATGACTGCTTACA
130043	128130	ATTGTGGAATGACTGCTTAC
130044	128131	AATTGTGGAATGACTGCTTA
130045	128132	TAATTGTGGAATGACTGCTT
130046	128133	ATAATTGTGGAATGACTGCT
130047	128134	AATAATTGTGGAATGACTGC
130048	128135	AAATAATTGTGGAATGACTG
130049	128136	AAAATAATTGTGGAATGACT
130050	128137	GAAAATAATTGTGGAATGAC
130051	128138	GGAAAATAATTGTGGAATGA
130052	128139	AGGAAAATAATTGTGGAATG
130053	128140	CAGGAAAATAATTGTGGAAT
130054	128141	TCAGGAAAATAATTGTGGAA
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130057	128144	ACTTCAGGAAAATAATTGTG
130058	128145	CACTTCAGGAAAATAATTGT
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130062	128149	AAGCCACTTCAGGAAAATAA
130063	128150	CAAGCCACTTCAGGAAAATA
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130066	128153	AACCAAGCCACTTCAGGAAA
130067	128154	TAACCAAGCCACTTCAGGAA
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130069	128156	ATTAACCAAGCCACTTCAGG
130070	128157	CATTAACCAAGCCACTTCAG
130071	128158	GCATTAACCAAGCCACTTCA
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130084	128171	TGTTTCTGGTGTGGCATTAA
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130092	128179	CTGTGACCTGTTTCTGGTGT
130093	128180	TCTGTGACCTGTTTCTGGTG
130094	128181	GTCTGTGACCTGTTTCTGGT
130095	128182	TGTCTGTGACCTGTTTCTGG

31802	29889	GTGCCTTTACCCCTTGAGTC
31803	29890	AGTGCCTTTACCCCTTGAGT
31804	29891	CAGTGCCTTTACCCCTTGAG
31805	29892	TCAGTGCCTTTACCCCTTGA
31806	29893	TTCAGTGCCTTTACCCCTTG
31807	29894	CTTCAGTGCCTTTACCCCTT
31808	29895	CCTTCAGTGCCTTTACCCCT
31809	29896	CCCTTCAGTGCCTTTACCCC
31810	29897	CCCCTTCAGTGCCTTTACCC
31811	29898	ACCCCTTCAGTGCCTTTACC
31812	29899	TACCCCTTCAGTGCCTTTAC
31813	29900	TTACCCCTTCAGTGCCTTTA
31814	29901	TTTACCCCTTCAGTGCCTTT
31815	29902	TTTTACCCCTTCAGTGCCTT
31816	29903	GTTTTACCCCTTCAGTGCCT
31817	29904	AGTTTTACCCCTTCAGTGCC
31818	29905	AAGTTTTACCCCTTCAGTGC
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31825	29912	TCATATGAAGTTTTACCCCT
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31829	29916	CTCTTCATATGAAGTTTTAC
31830	29917	ACTCTTCATATGAAGTTTTA
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31835	29922	ACCACACTCTTCATATGAAG
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31839	29926	CACCACCACACTCTTCATAT
31840	29927	CCACCACCACACTCTTCATA
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31843	29930	CCACCACCACCACACTCTTC
31844	29931	ACCACCACCACCACACTCTT
31845	29932	CACCACCACCACCACACTCT
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31847	29934	ACCACCACCACCACCACACT
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31869	29956	GAGCGAGACCCTGTCTTAAA
31870	29957	AGAGCGAGACCCTGTCTTAA
31871	29958	CAGAGCGAGACCCTGTCTTA
31872	29959	ACAGAGCGAGACCCTGTCTT

80949	79036	CCAGCCTGGAGACACAGCGA
80950	79037	TCCAGCCTGGAGACACAGCG
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80954	79041	GCACTCCAGCCTGGAGACAC
80955	79042	TGCACTCCAGCCTGGAGACA
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80968	79055	GAGATTGCACCACTGCACTC
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80971	79058	GCCGAGATTGCACCACTGCA
80972	79059	AGCCGAGATTGCACCACTGC
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80974	79061	TGAGCCGAGATTGCACCACT
80975	79062	GTGAGCCGAGATTGCACCAC
80976	79063	AGTGAGCCGAGATTGCACCA
80977	79064	CAGTGAGCCGAGATTGCACC
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80986	79073	CAGAGGTTGCAGTGAGCCGA
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81003	79090	CGCTTGAACCCGGGATGCAG
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81008	79095	AGAATCGCTTGAACCCGGGA
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81015	79102	AGGCAGGAGAATCGCTTGAA
81016	79103	GAGGCAGGAGAATCGCTTGA
81017	79104	TGAGGCAGGAGAATCGCTTG
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130096	128183	TTGTCTGTGACCTGTTTCTG
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130098	128185	TATTGTCTGTGACCTGTTTC
130099	128186	CTATTGTCTGTGACCTGTTT
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130106	128193	TACAGCACTATTGTCTGTGA
130107	128194	TTACAGCACTATTGTCTGTG
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130115	128202	CACATTTCTTACAGCACTAT
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130118	128205	TCACACATTTCTTACAGCAC
130119	128206	CTCACACATTTCTTACAGCA
130120	128207	CCTCACACATTTCTTACAGC
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130122	128209	TTCCTCACACATTTCTTACA
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130131	128218	TGTGCCTCTTTCCTCACACA
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130136	128223	TCCCATGTGCCTCTTTCCTC
130137	128224	TTCCCATGTGCCTCTTTCCT
130138	128225	CTTCCCATGTGCCTCTTTCC
130139	128226	ACTTCCCATGTGCCTCTTTC
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130141	128228	CTACTTCCCATGTGCCTCTT
130142	128229	GCTACTTCCCATGTGCCTCT
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130145	128232	CTAGCTACTTCCCATGTGCC
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31873	29960	GACAGAGCGAGACCCTGTCT
31874	29961	TGACAGAGCGAGACCCTGTC
31875	29962	GTGACAGAGCGAGACCCTGT
31876	29963	AGTGACAGAGCGAGACCCTG
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31879	29966	CTGAGTGACAGAGCGAGACC
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31881	29968	GCCTGAGTGACAGAGCGAGA
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31884	29971	CCAGCCTGAGTGACAGAGCG
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31887	29974	ACTCCAGCCTGAGTGACAGA
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31915	30002	CTGCAGTGAGCCAGGATCAT
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31917	30004	GGCTGCAGTGAGCCAGGATC
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31919	30006	GAGGCTGCAGTGAGCCAGGA
31920	30007	CGAGGCTGCAGTGAGCCAGG
31921	30008	TCGAGGCTGCAGTGAGCCAG
31922	30009	GTCGAGGCTGCAGTGAGCCA
31923	30010	AGTCGAGGCTGCAGTGAGCC
31924	30011	AAGTCGAGGCTGCAGTGAGC
31925	30012	GAAGTCGAGGCTGCAGTGAG
31926	30013	GGAAGTCGAGGCTGCAGTGA
31927	30014	AGGAAGTCGAGGCTGCAGTG
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31931	30018	GCCCAGGAAGTCGAGGCTGC
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31937	30024	ACTTAAGCCCAGGAAGTCGA
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31939	30026	TCACTTAAGCCCAGGAAGTC
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81021	79108	AGGCTGAGGCAGGAGAATCG
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81033	79120	CAGCTACTCGGGAGGCTGAG
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81037	79124	GTCCCAGCTACTCGGGAGGC
81038	79125	AGTCCCAGCTACTCGGGAGG
81039	79126	TAGTCCCAGCTACTCGGGAG
81040	79127	ATAGTCCCAGCTACTCGGGA
81041	79128	TATAGTCCCAGCTACTCGGG
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81043	79130	CCTATAGTCCCAGCTACTCG
81044	79131	GCCTATAGTCCCAGCTACTC
81045	79132	CGCCTATAGTCCCAGCTACT
81046	79133	GCGCCTATAGTCCCAGCTAC
81047	79134	CGCGCCTATAGTCCCAGCTA
81048	79135	ACGCGCCTATAGTCCCAGCT
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81050	79137	GCACGCGCCTATAGTCCCAG
81051	79138	AGCACGCGCCTATAGTCCCA
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81060	79147	GGGCATGGTAGCACGCGCCT
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81063	79150	GATGGGCATGGTAGCACGCG
81064	79151	AGATGGGCATGGTAGCACGC
81065	79152	TAGATGGGCATGGTAGCACG
81066	79153	TTAGATGGGCATGGTAGCAC
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81068	79155	AATTAGATGGGCATGGTAGC
81069	79156	AAATTAGATGGGCATGGTAG
81070	79157	GAAATTAGATGGGCATGGTA
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81073	79160	ACAGAAATTAGATGGGCATG
81074	79161	TACAGAAATTAGATGGGCAT
81075	79162	ATACAGAAATTAGATGGGCA
81076	79163	AATACAGAAATTAGATGGGC
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81078	79165	AAAATACAGAAATTAGATGG
81079	79166	AAAAATACAGAAATTAGATG
81080	79167	TAAAAATACAGAAATTAGAT
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81083	79170	TACTAAAAATACAGAAATTA
81084	79171	CTACTAAAAATACAGAAATT
81085	79172	TCTACTAAAAATACAGAAAT
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130167	128254	TTTCCAGTTCCTCCAGCACG
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130170	128257	TTTTTTCCAGTTCCTCCAGC
130171	128258	TTTTTTTCCAGTTCCTCCAG
130172	128259	GTTTTTTTCCAGTTCCTCCA
130173	128260	GGTTTTTTTCCAGTTCCTCC
130174	128261	AGGTTTTTTTCCAGTTCCTC
130175	128262	GAGGTTTTTTTCCAGTTCCT
130176	128263	TGAGGTTTTTTTCCAGTTCC
130177	128264	GTGAGGTTTTTTTCCAGTTC
130178	128265	TGTGAGGTTTTTTTCCAGTT
130179	128266	ATGTGAGGTTTTTTTCCAGT
130180	128267	CATGTGAGGTTTTTTTCCAG
130181	128268	CCATGTGAGGTTTTTTTCCA
130182	128269	CCCATGTGAGGTTTTTTTCC
130183	128270	TCCCATGTGAGGTTTTTTTC
130184	128271	CTCCCATGTGAGGTTTTTTT
130185	128272	TCTCCCATGTGAGGTTTTTT
130186	128273	ATCTCCCATGTGAGGTTTTT
130187	128274	CATCTCCCATGTGAGGTTTT
130188	128275	TCATCTCCCATGTGAGGTTT
130189	128276	GTCATCTCCCATGTGAGGTT
130190	128277	TGTCATCTCCCATGTGAGGT
130191	128278	CTGTCATCTCCCATGTGAGG
130192	128279	ACTGTCATCTCCCATGTGAG
130193	128280	AACTGTCATCTCCCATGTGA
130194	128281	CAACTGTCATCTCCCATGTG
130195	128282	TCAACTGTCATCTCCCATGT
130196	128283	CTCAACTGTCATCTCCCATG
130197	128284	GCTCAACTGTCATCTCCCAT
130198	128285	AGCTCAACTGTCATCTCCCA
130199	128286	CAGCTCAACTGTCATCTCCC
130200	128287	TCAGCTCAACTGTCATCTCC
130201	128288	TTCAGCTCAACTGTCATCTC
130202	128289	ATTCAGCTCAACTGTCATCT
130203	128290	AATTCAGCTCAACTGTCATC
130204	128291	GAATTCAGCTCAACTGTCAT
130205	128292	AGAATTCAGCTCAACTGTCA
130206	128293	AAGAATTCAGCTCAACTGTC
130207	128294	TAAGAATTCAGCTCAACTGT
130208	128295	TTAAGAATTCAGCTCAACTG
130209	128296	GTTAAGAATTCAGCTCAACT
130210	128297	AGTTAAGAATTCAGCTCAAC
130211	128298	TAGTTAAGAATTCAGCTCAA
130212	128299	CTAGTTAAGAATTCAGCTCA
130213	128300	TCTAGTTAAGAATTCAGCTC
130214	128301	CTCTAGTTAAGAATTCAGCT
130215	128302	ACTCTAGTTAAGAATTCAGC
130216	128303	AACTCTAGTTAAGAATTCAG
130217	128304	CAACTCTAGTTAAGAATTCA
130218	128305	ACAACTCTAGTTAAGAATTC
130219	128306	TACAACTCTAGTTAAGAATT
130220	128307	TTACAACTCTAGTTAAGAAT
130221	128308	GTTACAACTCTAGTTAAGAA
130222	128309	TGTTACAACTCTAGTTAAGA
130223	128310	CTGTTACAACTCTAGTTAAG
130224	128311	CCTGTTACAACTCTAGTTAA
130225	128312	CCCTGTTACAACTCTAGTTA
130226	128313	GCCCTGTTACAACTCTAGTT
130227	128314	CGCCCTGTTACAACTCTAGT
130228	128315	TCGCCCTGTTACAACTCTAG
130229	128316	CTCGCCCTGTTACAACTCTA
130230	128317	CCTCGCCCTGTTACAACTCT
130231	128318	GCCTCGCCCTGTTACAACTC
130232	128319	GGCCTCGCCCTGTTACAACT
130233	128320	GGGCCTCGCCCTGTTACAAC
130234	128321	AGGGCCTCGCCCTGTTACAA
130235	128322	AAGGGCCTCGCCCTGTTACA
130236	128323	TAAGGGCCTCGCCCTGTTAC
130237	128324	GTAAGGGCCTCGCCCTGTTA

31944	30031	GAGGATCACTTAAGCCCAGG
31945	30032	GGAGGATCACTTAAGCCCAG
31946	30033	GGGAGGATCACTTAAGCCCA
31947	30034	TGGGAGGATCACTTAAGCCC
31948	30035	GTGGGAGGATCACTTAAGCC
31949	30036	GGTGGGAGGATCACTTAAGC
31950	30037	AGGTGGGAGGATCACTTAAG
31951	30038	GAGGTGGGAGGATCACTTAA
31952	30039	TGAGGTGGGAGGATCACTTA
31953	30040	CTGAGGTGGGAGGATCACTT
31954	30041	GCTGAGGTGGGAGGATCACT
31955	30042	AGCTGAGGTGGGAGGATCAC
31956	30043	GAGCTGAGGTGGGAGGATCA
31957	30044	GGAGCTGAGGTGGGAGGATC
31958	30045	GGGAGCTGAGGTGGGAGGAT
31959	30046	TGGGAGCTGAGGTGGGAGGA
31960	30047	TTGGGAGCTGAGGTGGGAGG
31961	30048	CTTGGGAGCTGAGGTGGGAG
31962	30049	ACTTGGGAGCTGAGGTGGGA
31963	30050	TACTTGGGAGCTGAGGTGGG
31964	30051	TTACTTGGGAGCTGAGGTGG
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31966	30053	AGTTACTTGGGAGCTGAGGT
31967	30054	CAGTTACTTGGGAGCTGAGG
31968	30055	CCAGTTACTTGGGAGCTGAG
31969	30056	TCCAGTTACTTGGGAGCTGA
31970	30057	TTCCAGTTACTTGGGAGCTG
31971	30058	GTTCCAGTTACTTGGGAGCT
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31973	30060	CAGTTCCAGTTACTTGGGAG
31974	30061	ACAGTTCCAGTTACTTGGGA
31975	30062	TACAGTTCCAGTTACTTGGG
31976	30063	CTACAGTTCCAGTTACTTGG
31977	30064	CCTACAGTTCCAGTTACTTG
31978	30065	GCCTACAGTTCCAGTTACTT
31979	30066	TGCCTACAGTTCCAGTTACT
31980	30067	ATGCCTACAGTTCCAGTTAC
31981	30068	CATGCCTACAGTTCCAGTTA
31982	30069	TCATGCCTACAGTTCCAGTT
31983	30070	CTCATGCCTACAGTTCCAGT
31984	30071	GCTCATGCCTACAGTTCCAG
31985	30072	GGCTCATGCCTACAGTTCCA
31986	30073	TGGCTCATGCCTACAGTTCC
31987	30074	GTGGCTCATGCCTACAGTTC
31988	30075	GGTGGCTCATGCCTACAGTT
31989	30076	TGGTGGCTCATGCCTACAGT
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31991	30078	TGTGGTGGCTCATGCCTACA
31992	30079	GTGTGGTGGCTCATGCCTAC
31993	30080	GGTGTGGTGGCTCATGCCTA
31994	30081	AGGTGTGGTGGCTCATGCCT
31995	30082	CAGGTGTGGTGGCTCATGCC
31996	30083	GCAGGTGTGGTGGCTCATGC
31997	30084	GGCAGGTGTGGTGGCTCATG
31998	30085	AGGCAGGTGTGGTGGCTCAT
31999	30086	TAGGCAGGTGTGGTGGCTCA
32000	30087	TTAGGCAGGTGTGGTGGCTC
32001	30088	ATTAGGCAGGTGTGGTGGCT
32002	30089	AATTAGGCAGGTGTGGTGGC
32003	30090	AAATTAGGCAGGTGTGGTGG
32004	30091	AAAATTAGGCAGGTGTGGTG
32005	30092	AAAAATTAGGCAGGTGTGGT
32006	30093	TAAAAATTAGGCAGGTGTGG
32007	30094	TTAAAAATTAGGCAGGTGTG
32008	30095	TTTAAAAATTAGGCAGGTGT
32009	30096	TTTTAAAAATTAGGCAGGTG
32010	30097	GTTTTAAAAATTAGGCAGGT
32011	30098	AGTTTTAAAAATTAGGCAGG
32012	30099	AAGTTTTAAAAATTAGGCAG
32013	30100	AAAGTTTTAAAAATTAGGCA
32014	30101	GAAAGTTTTAAAAATTAGGC

81091	79178	CCCGTCTCTACTAAAAATAC
81092	79179	CCCCGTCTCTACTAAAAATA
81093	79180	ACCCCGTCTCTACTAAAAAT
81094	79181	AACCCCGTCTCTACTAAAAA
81095	79182	AAACCCCGTCTCTACTAAAA
81096	79183	GAAACCCCGTCTCTACTAAA
81097	79184	TGAAACCCCGTCTCTACTAA
81098	79185	GTGAAACCCCGTCTCTACTA
81099	79186	GGTGAAACCCCGTCTCTACT
81100	79187	TGGTGAAACCCCGTCTCTAC
81101	79188	ATGGTGAAACCCCGTCTCTA
81102	79189	CATGGTGAAACCCCGTCTCT
81103	79190	ACATGGTGAAACCCCGTCTC
81104	79191	AACATGGTGAAACCCCGTCT
81105	79192	CAACATGGTGAAACCCCGTC
81106	79193	CCAACATGGTGAAACCCCGT
81107	79194	GCCAACATGGTGAAACCCCG
81108	79195	GGCCAACATGGTGAAACCCC
81109	79196	TGGCCAACATGGTGAAACCC
81110	79197	CTGGCCAACATGGTGAAACC
81111	79198	CCTGGCCAACATGGTGAAAC
81112	79199	TCCTGGCCAACATGGTGAAA
81113	79200	ATCCTGGCCAACATGGTGAA
81114	79201	TATCCTGGCCAACATGGTGA
81115	79202	CTATCCTGGCCAACATGGTG
81116	79203	ACTATCCTGGCCAACATGGT
81117	79204	GACTATCCTGGCCAACATGG
81118	79205	AGACTATCCTGGCCAACATG
81119	79206	GAGACTATCCTGGCCAACAT
81120	79207	CGAGACTATCCTGGCCAACA
81121	79208	TCGAGACTATCCTGGCCAAC
81122	79209	ATCGAGACTATCCTGGCCAA
81123	79210	GATCGAGACTATCCTGGCCA
81124	79211	AGATCGAGACTATCCTGGCC
81125	79212	GAGATCGAGACTATCCTGGC
81126	79213	AGAGATCGAGACTATCCTGG
81127	79214	AAGAGATCGAGACTATCCTG
81128	79215	GAAGAGATCGAGACTATCCT
81129	79216	TGAAGAGATCGAGACTATCC
81130	79217	GTGAAGAGATCGAGACTATC
81131	79218	GGTGAAGAGATCGAGACTAT
81132	79219	AGGTGAAGAGATCGAGACTA
81133	79220	GAGGTGAAGAGATCGAGACT
81134	79221	CGAGGTGAAGAGATCGAGAC
81135	79222	ACGAGGTGAAGAGATCGAGA
81136	79223	CACGAGGTGAAGAGATCGAG
81137	79224	TCACGAGGTGAAGAGATCGA
81138	79225	ATCACGAGGTGAAGAGATCG
81139	79226	GATCACGAGGTGAAGAGATC
81140	79227	GGATCACGAGGTGAAGAGAT
81141	79228	TGGATCACGAGGTGAAGAGA
81142	79229	GTGGATCACGAGGTGAAGAG
81143	79230	GGTGGATCACGAGGTGAAGA
81144	79231	AGGTGGATCACGAGGTGAAG
81145	79232	CAGGTGGATCACGAGGTGAA
81146	79233	GCAGGTGGATCACGAGGTGA
81147	79234	GGCAGGTGGATCACGAGGTG
81148	79235	AGGCAGGTGGATCACGAGGT
81149	79236	GAGGCAGGTGGATCACGAGG
81150	79237	CGAGGCAGGTGGATCACGAG
81151	79238	CCGAGGCAGGTGGATCACGA
81152	79239	GCCGAGGCAGGTGGATCACG
81153	79240	GGCCGAGGCAGGTGGATCAC
81154	79241	AGGCCGAGGCAGGTGGATCA
81155	79242	GAGGCCGAGGCAGGTGGATC
81156	79243	GGAGGCCGAGGCAGGTGGAT
81157	79244	GGGAGGCCGAGGCAGGTGGA
81158	79245	TGGGAGGCCGAGGCAGGTGG
81159	79246	TTGGGAGGCCGAGGCAGGTG
81160	79247	TTTGGGAGGCCGAGGCAGGT
81161	79248	CTTTGGGAGGCCGAGGCAGG

130238	128325	TGTAAGGGCCTCGCCCTGTT
130239	128326	ATGTAAGGGCCTCGCCCTGT
130240	128327	CATGTAAGGGCCTCGCCCTG
130241	128328	GCATGTAAGGGCCTCGCCCT
130242	128329	TGCATGTAAGGGCCTCGCCC
130243	128330	CTGCATGTAAGGGCCTCGCC
130244	128331	TCTGCATGTAAGGGCCTCGC
130245	128332	GTCTGCATGTAAGGGCCTCG
130246	128333	GGTCTGCATGTAAGGGCCTC
130247	128334	TGGTCTGCATGTAAGGGCCT
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130249	128336	GGTGGTCTGCATGTAAGGGC
130250	128337	AGGTGGTCTGCATGTAAGGG
130251	128338	CAGGTGGTCTGCATGTAAGG
130252	128339	ACAGGTGGTCTGCATGTAAG
130253	128340	CACAGGTGGTCTGCATGTAA
130254	128341	ACACAGGTGGTCTGCATGTA
130255	128342	CACACAGGTGGTCTGCATGT
130256	128343	CCACACAGGTGGTCTGCATG
130257	128344	TCCACACAGGTGGTCTGCAT
130258	128345	ATCCACACAGGTGGTCTGCA
130259	128346	AATCCACACAGGTGGTCTGC
130260	128347	TAATCCACACAGGTGGTCTG
130261	128348	TTAATCCACACAGGTGGTCT
130262	128349	CTTAATCCACACAGGTGGTC
130263	128350	TCTTAATCCACACAGGTGGT
130264	128351	ATCTTAATCCACACAGGTGG
130265	128352	TATCTTAATCCACACAGGTG
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130267	128354	CTTATCTTAATCCACACAGG
130268	128355	TCTTATCTTAATCCACACAG
130269	128356	GTCTTATCTTAATCCACACA
130270	128357	TGTCTTATCTTAATCCACAC
130271	128358	ATGTCTTATCTTAATCCACA
130272	128359	TATGTCTTATCTTAATCCAC
130273	128360	TTATGTCTTATCTTAATCCA
130274	128361	TTTATGTCTTATCTTAATCC
130275	128362	CTTTATGTCTTATCTTAATC
130276	128363	ACTTTATGTCTTATCTTAAT
130277	128364	TACTTTATGTCTTATCTTAA
130278	128365	TTACTTTATGTCTTATCTTA
130279	128366	ATTACTTTATGTCTTATCTT
130280	128367	GATTACTTTATGTCTTATCT
130281	128368	AGATTACTTTATGTCTTATC
130282	128369	AAGATTACTTTATGTCTTAT
130283	128370	AAAGATTACTTTATGTCTTA
130284	128371	AAAAGATTACTTTATGTCTT
130285	128372	TAAAAGATTACTTTATGTCT
130286	128373	TTAAAAGATTACTTTATGTC
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130288	128375	TTTTAAAAGATTACTTTATG
130289	128376	CTTTTAAAAGATTACTTTAT
130290	128377	TCTTTTAAAAGATTACTTTA
130291	128378	TTCTTTTAAAAGATTACTTT
130292	128379	GTTCTTTTAAAAGATTACTT
130293	128380	AGTTCTTTTAAAAGATTACT
130294	128381	TAGTTCTTTTAAAAGATTAC
130295	128382	ATAGTTCTTTTAAAAGATTA
130296	128383	AATAGTTCTTTTAAAAGATT
130297	128384	TAATAGTTCTTTTAAAAGAT
130298	128385	ATAATAGTTCTTTTAAAAGA
130299	128386	AATAATAGTTCTTTTAAAAG
130300	128387	AAATAATAGTTCTTTTAAAA
130301	128388	TAAATAATAGTTCTTTTAAA
130302	128389	CTAAATAATAGTTCTTTTAA
130303	128390	TCTAAATAATAGTTCTTTTA
130304	128391	TTCTAAATAATAGTTCTTTT
130305	128392	TTTCTAAATAATAGTTCTTT
130306	128393	GTTTCTAAATAATAGTTCTT
130307	128394	GGTTTCTAAATAATAGTTCT
130308	128395	AGGTTTCTAAATAATAGTTC

32015	30102	AGAAAGTTTTAAAAATTAGG
32016	30103	CAGAAAGTTTTAAAAATTAG
32017	30104	ACAGAAAGTTTTAAAAATTA
32018	30105	TACAGAAAGTTTTAAAAATT
32019	30106	CTACAGAAAGTTTTAAAAAT
32020	30107	TCTACAGAAAGTTTTAAAAA
32021	30108	CTCTACAGAAAGTTTTAAAA
32022	30109	TCTCTACAGAAAGTTTTAAA
32023	30110	GTCTCTACAGAAAGTTTTAA
32024	30111	CGTCTCTACAGAAAGTTTTA
32025	30112	TCGTCTCTACAGAAAGTTTT
32026	30113	CTCGTCTCTACAGAAAGTTT
32027	30114	TCTCGTCTCTACAGAAAGTT
32028	30115	ATCTCGTCTCTACAGAAAGT
32029	30116	AATCTCGTCTCTACAGAAAG
32030	30117	AAATCTCGTCTCTACAGAAA
32031	30118	GAAATCTCGTCTCTACAGAA
32032	30119	CGAAATCTCGTCTCTACAGA
32033	30120	GCGAAATCTCGTCTCTACAG
32034	30121	GGCGAAATCTCGTCTCTACA
32035	30122	TGGCGAAATCTCGTCTCTAC
32036	30123	ATGGCGAAATCTCGTCTCTA
32037	30124	CATGGCGAAATCTCGTCTCT
32038	30125	ACATGGCGAAATCTCGTCTC
32039	30126	AACATGGCGAAATCTCGTCT
32040	30127	CAACATGGCGAAATCTCGTC
32041	30128	ACAACATGGCGAAATCTCGT
32042	30129	GACAACATGGCGAAATCTCG
32043	30130	GGACAACATGGCGAAATCTC
32044	30131	TGGACAACATGGCGAAATCT
32045	30132	CTGGACAACATGGCGAAATC
32046	30133	CCTGGACAACATGGCGAAAT
32047	30134	GCCTGGACAACATGGCGAAA
32048	30135	AGCCTGGACAACATGGCGAA
32049	30136	CAGCCTGGACAACATGGCGA
32050	30137	CCAGCCTGGACAACATGGCG
32051	30138	ACCAGCCTGGACAACATGGC
32052	30139	GACCAGCCTGGACAACATGG
32053	30140	AGACCAGCCTGGACAACATG
32054	30141	GAGACCAGCCTGGACAACAT
32055	30142	TGAGACCAGCCTGGACAACA
32056	30143	TTGAGACCAGCCTGGACAAC
32057	30144	TTTGAGACCAGCCTGGACAA
32058	30145	ATTTGAGACCAGCCTGGACA
32059	30146	AATTTGAGACCAGCCTGGAC
32060	30147	GAATTTGAGACCAGCCTGGA
32061	30148	GGAATTTGAGACCAGCCTGG
32062	30149	AGGAATTTGAGACCAGCCTG
32063	30150	CAGGAATTTGAGACCAGCCT
32064	30151	CCAGGAATTTGAGACCAGCC
32065	30152	TCCAGGAATTTGAGACCAGC
32066	30153	GTCCAGGAATTTGAGACCAG
32067	30154	AGTCCAGGAATTTGAGACCA
32068	30155	GAGTCCAGGAATTTGAGACC
32069	30156	TGAGTCCAGGAATTTGAGAC
32070	30157	GTGAGTCCAGGAATTTGAGA
32071	30158	GGTGAGTCCAGGAATTTGAG
32072	30159	AGGTGAGTCCAGGAATTTGA
32073	30160	AAGGTGAGTCCAGGAATTTG
32074	30161	CAAGGTGAGTCCAGGAATTT
32075	30162	CCAAGGTGAGTCCAGGAATT
32076	30163	GCCAAGGTGAGTCCAGGAAT
32077	30164	GGCCAAGGTGAGTCCAGGAA
32078	30165	AGGCCAAGGTGAGTCCAGGA
32079	30166	GAGGCCAAGGTGAGTCCAGG
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32082	30169	TGGGAGGCCAAGGTGAGTCC
32083	30170	CTGGGAGGCCAAGGTGAGTC
32084	30171	TCTGGGAGGCCAAGGTGAGT
32085	30172	CTCTGGGAGGCCAAGGTGAG

81162	79249	ACTTTGGGAGGCCGAGGCAG
81163	79250	CACTTTGGGAGGCCGAGGCA
81164	79251	GCACTTTGGGAGGCCGAGGC
81165	79252	AGCACTTTGGGAGGCCGAGG
81166	79253	CAGCACTTTGGGAGGCCGAG
81167	79254	CCAGCACTTTGGGAGGCCGA
81168	79255	CCCAGCACTTTGGGAGGCCG
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81170	79257	ATCCCAGCACTTTGGGAGGC
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81172	79259	TAATCCCAGCACTTTGGGAG
81173	79260	GTAATCCCAGCACTTTGGGA
81174	79261	TGTAATCCCAGCACTTTGGG
81175	79262	CTGTAATCCCAGCACTTTGG
81176	79263	CCTGTAATCCCAGCACTTTG
81177	79264	ACCTGTAATCCCAGCACTTT
81178	79265	CACCTGTAATCCCAGCACTT
81179	79266	ACACCTGTAATCCCAGCACT
81180	79267	CACACCTGTAATCCCAGCAC
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81182	79269	CTCACACCTGTAATCCCAGC
81183	79270	GCTCACACCTGTAATCCCAG
81184	79271	GGCTCACACCTGTAATCCCA
81185	79272	TGGCTCACACCTGTAATCCC
81186	79273	GTGGCTCACACCTGTAATCC
81187	79274	AGTGGCTCACACCTGTAATC
81188	79275	CAGTGGCTCACACCTGTAAT
81189	79276	ACAGTGGCTCACACCTGTAA
81190	79277	CACAGTGGCTCACACCTGTA
81191	79278	GCACAGTGGCTCACACCTGT
81192	79279	GGCACAGTGGCTCACACCTG
81193	79280	AGGCACAGTGGCTCACACCT
81194	79281	CAGGCACAGTGGCTCACACC
81195	79282	CCAGGCACAGTGGCTCACAC
81196	79283	GCCAGGCACAGTGGCTCACA
81197	79284	GGCCAGGCACAGTGGCTCAC
81198	79285	CGGCCAGGCACAGTGGCTCA
81199	79286	CCGGCCAGGCACAGTGGCTC
81200	79287	ACCGGCCAGGCACAGTGGCT
81201	79288	AACCGGCCAGGCACAGTGGC
81202	79289	AAACCGGCCAGGCACAGTGG
81203	79290	AAAACCGGCCAGGCACAGTG
81204	79291	CAAAACCGGCCAGGCACAGT
81205	79292	ACAAAACCGGCCAGGCACAG
81206	79293	GACAAAACCGGCCAGGCACA
81207	79294	AGACAAAACCGGCCAGGCAC
81208	79295	AAGACAAAACCGGCCAGGCA
81209	79296	GAAGACAAAACCGGCCAGGC
81210	79297	AGAAGACAAAACCGGCCAGG
81211	79298	TAGAAGACAAAACCGGCCAG
81212	79299	TTAGAAGACAAAACCGGCCA
81213	79300	CTTAGAAGACAAAACCGGCC
81214	79301	ACTTAGAAGACAAAACCGGC
81215	79302	AACTTAGAAGACAAAACCGG
81216	79303	CAACTTAGAAGACAAAACCG
81217	79304	ACAACTTAGAAGACAAAACC
81218	79305	AACAACTTAGAAGACAAAAC
81219	79306	TAACAACTTAGAAGACAAAA
81220	79307	TTAACAACTTAGAAGACAAA
81221	79308	TTTAACAACTTAGAAGACAA
81222	79309	TTTTAACAACTTAGAAGACA
81223	79310	TTTTTAACAACTTAGAAGAC
81224	79311	TTTTTTAACAACTTAGAAGA
81225	79312	ATTTTTTAACAACTTAGAAG
81226	79313	TATTTTTTAACAACTTAGAA
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81228	79315	GATATTTTTTAACAACTTAG
81229	79316	AGATATTTTTTAACAACTTA
81230	79317	TAGATATTTTTTAACAACTT
81231	79318	TTAGATATTTTTTAACAACT
81232	79319	TTTAGATATTTTTTAACAAC

130309	128396	CAGGTTTCTAAATAATAGTT
130310	128397	CCAGGTTTCTAAATAATAGT
130311	128398	ACCAGGTTTCTAAATAATAG
130312	128399	TACCAGGTTTCTAAATAATA
130313	128400	ATACCAGGTTTCTAAATAAT
130314	128401	TATACCAGGTTTCTAAATAA
130315	128402	ATATACCAGGTTTCTAAATA
130316	128403	CATATACCAGGTTTCTAAAT
130317	128404	GCATATACCAGGTTTCTAAA
130318	128405	AGCATATACCAGGTTTCTAA
130319	128406	TAGCATATACCAGGTTTCTA
130320	128407	GTAGCATATACCAGGTTTCT
130321	128408	TGTAGCATATACCAGGTTTC
130322	128409	ATGTAGCATATACCAGGTTT
130323	128410	CATGTAGCATATACCAGGTT
130324	128411	CCATGTAGCATATACCAGGT
130325	128412	ACCATGTAGCATATACCAGG
130326	128413	CACCATGTAGCATATACCAG
130327	128414	GCACCATGTAGCATATACCA
130328	128415	AGCACCATGTAGCATATACC
130329	128416	CAGCACCATGTAGCATATAC
130330	128417	ACAGCACCATGTAGCATATA
130331	128418	CACAGCACCATGTAGCATAT
130332	128419	ACACAGCACCATGTAGCATA
130333	128420	AACACAGCACCATGTAGCAT
130334	128421	TAACACAGCACCATGTAGCA
130335	128422	ATAACACAGCACCATGTAGC
130336	128423	TATAACACAGCACCATGTAG
130337	128424	GTATAACACAGCACCATGTA
130338	128425	AGTATAACACAGCACCATGT
130339	128426	CAGTATAACACAGCACCATG
130340	128427	CCAGTATAACACAGCACCAT
130341	128428	CCCAGTATAACACAGCACCA
130342	128429	ACCCAGTATAACACAGCACC
130343	128430	AACCCAGTATAACACAGCAC
130344	128431	AAACCCAGTATAACACAGCA
130345	128432	CAAACCCAGTATAACACAGC
130346	128433	TCAAACCCAGTATAACACAG
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130348	128435	TCTCAAACCCAGTATAACAC
130349	128436	TTCTCAAACCCAGTATAACA
130350	128437	TTTCTCAAACCCAGTATAAC
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130353	128440	TTCTTTCTCAAACCCAGTAT
130354	128441	ATTCTTTCTCAAACCCAGTA
130355	128442	CATTCTTTCTCAAACCCAGT
130356	128443	CCATTCTTTCTCAAACCCAG
130357	128444	CCCATTCTTTCTCAAACCCA
130358	128445	TCCCATTCTTTCTCAAACCC
130359	128446	TTCCCATTCTTTCTCAAACC
130360	128447	CTTCCCATTCTTTCTCAAAC
130361	128448	ACTTCCCATTCTTTCTCAAA
130362	128449	CACTTCCCATTCTTTCTCAA
130363	128450	ACACTTCCCATTCTTTCTCA
130364	128451	AACACTTCCCATTCTTTCTC
130365	128452	TAACACTTCCCATTCTTTCT
130366	128453	GTAACACTTCCCATTCTTTC
130367	128454	TGTAACACTTCCCATTCTTT
130368	128455	TTGTAACACTTCCCATTCTT
130369	128456	CTTGTAACACTTCCCATTCT
130370	128457	CCTTGTAACACTTCCCATTC
130371	128458	TCCTTGTAACACTTCCCATT
130372	128459	ATCCTTGTAACACTTCCCAT
130373	128460	AATCCTTGTAACACTTCCCA
130374	128461	GAATCCTTGTAACACTTCCC
130375	128462	TGAATCCTTGTAACACTTCC
130376	128463	CTGAATCCTTGTAACACTTC
130377	128464	ACTGAATCCTTGTAACACTT
130378	128465	CACTGAATCCTTGTAACACT
130379	128466	CCACTGAATCCTTGTAACAC

32086	30173	ACTCTGGGAGGCCAAGGTGA
32087	30174	CACTCTGGGAGGCCAAGGTG
32088	30175	GCACTCTGGGAGGCCAAGGT
32089	30176	AGCACTCTGGGAGGCCAAGG
32090	30177	CAGCACTCTGGGAGGCCAAG
32091	30178	CCAGCACTCTGGGAGGCCAA
32092	30179	CCCAGCACTCTGGGAGGCCA
32093	30180	TCCCAGCACTCTGGGAGGCC
32094	30181	ATCCCAGCACTCTGGGAGGC
32095	30182	AATCCCAGCACTCTGGGAGG
32096	30183	CAATCCCAGCACTCTGGGAG
32097	30184	GCAATCCCAGCACTCTGGGA
32098	30185	TGCAATCCCAGCACTCTGGG
32099	30186	CTGCAATCCCAGCACTCTGG
32100	30187	CCTGCAATCCCAGCACTCTG
32101	30188	ACCTGCAATCCCAGCACTCT
32102	30189	CACCTGCAATCCCAGCACTC
32103	30190	ACACCTGCAATCCCAGCACT
32104	30191	CACACCTGCAATCCCAGCAC
32105	30192	CCACACCTGCAATCCCAGCA
32106	30193	CCCACACCTGCAATCCCAGC
32107	30194	GCCCACACCTGCAATCCCAG
32108	30195	GGCCCACACCTGCAATCCCA
32109	30196	TGGCCCACACCTGCAATCCC
32110	30197	GTGGCCCACACCTGCAATCC
32111	30198	AGTGGCCCACACCTGCAATC
32112	30199	CAGTGGCCCACACCTGCAAT
32113	30200	GCAGTGGCCCACACCTGCAA
32114	30201	CGCAGTGGCCCACACCTGCA
32115	30202	TCGCAGTGGCCCACACCTGC
32116	30203	GTCGCAGTGGCCCACACCTG
32117	30204	AGTCGCAGTGGCCCACACCT
32118	30205	CAGTCGCAGTGGCCCACACC
32119	30206	CCAGTCGCAGTGGCCCACAC
32120	30207	GCCAGTCGCAGTGGCCCACA
32121	30208	GGCCAGTCGCAGTGGCCCAC
32122	30209	AGGCCAGTCGCAGTGGCCCA
32123	30210	AAGGCCAGTCGCAGTGGCCC
32124	30211	AAAGGCCAGTCGCAGTGGCC
32125	30212	AAAAGGCCAGTCGCAGTGGC
32126	30213	AAAAAGGCCAGTCGCAGTGG
32127	30214	AAAAAAGGCCAGTCGCAGTG
32128	30215	AAAAAAAGGCCAGTCGCAGT
32129	30216	AAAAAAAAGGCCAGTCGCAG
32130	30217	GAAAAAAAAGGCCAGTCGCA
32131	30218	AGAAAAAAAAGGCCAGTCGC
32132	30219	GAGAAAAAAAAGGCCAGTCG
32133	30220	GGAGAAAAAAAAGGCCAGTC
32134	30221	AGGAGAAAAAAAAGGCCAGT
32135	30222	AAGGAGAAAAAAAAGGCCAG
32136	30223	AAAGGAGAAAAAAAAGGCCA
32137	30224	TAAAGGAGAAAAAAAAGGCC
32138	30225	GTAAAGGAGAAAAAAAAGGC
32139	30226	AGTAAAGGAGAAAAAAAAGG
32140	30227	TAGTAAAGGAGAAAAAAAAG
32141	30228	GTAGTAAAGGAGAAAAAAAA
32142	30229	AGTAGTAAAGGAGAAAAAAA
32143	30230	GAGTAGTAAAGGAGAAAAAA
32144	30231	AGAGTAGTAAAGGAGAAAAA
32145	30232	TAGAGTAGTAAAGGAGAAAA
32146	30233	CTAGAGTAGTAAAGGAGAAA
32147	30234	ACTAGAGTAGTAAAGGAGAA
32148	30235	CACTAGAGTAGTAAAGGAGA
32149	30236	ACACTAGAGTAGTAAAGGAG
32150	30237	TACACTAGAGTAGTAAAGGA
32151	30238	ATACACTAGAGTAGTAAAGG
32152	30239	CATACACTAGAGTAGTAAAG
32153	30240	GCATACACTAGAGTAGTAAA
32154	30241	AGCATACACTAGAGTAGTAA
32155	30242	CAGCATACACTAGAGTAGTA
32156	30243	CCAGCATACACTAGAGTAGT

81233	79320	ATTTAGATATTTTTTAACAA
81234	79321	AATTTAGATATTTTTTAACA
81235	79322	AAATTTAGATATTTTTTAAC
81236	79323	CAAATTTAGATATTTTTTAA
81237	79324	GCAAATTTAGATATTTTTTA
81238	79325	TGCAAATTTAGATATTTTTT
81239	79326	TTGCAAATTTAGATATTTTT
81240	79327	CTTGCAAATTTAGATATTTT
81241	79328	CCTTGCAAATTTAGATATTT
81242	79329	CCCTTGCAAATTTAGATATT
81243	79330	GCCCTTGCAAATTTAGATAT
81244	79331	TGCCCTTGCAAATTTAGATA
81245	79332	CTGCCCTTGCAAATTTAGAT
81246	79333	TCTGCCCTTGCAAATTTAGA
81247	79334	CTCTGCCCTTGCAAATTTAG
81248	79335	TCTCTGCCCTTGCAAATTTA
81249	79336	ATCTCTGCCCTTGCAAATTT
81250	79337	AATCTCTGCCCTTGCAAATT
81251	79338	TAATCTCTGCCCTTGCAAAT
81252	79339	ATAATCTCTGCCCTTGCAAA
81253	79340	CATAATCTCTGCCCTTGCAA
81254	79341	CCATAATCTCTGCCCTTGCA
81255	79342	ACCATAATCTCTGCCCTTGC
81256	79343	CACCATAATCTCTGCCCTTG
81257	79344	TCACCATAATCTCTGCCCTT
81258	79345	TTCACCATAATCTCTGCCCT
81259	79346	GTTCACCATAATCTCTGCCC
81260	79347	TGTTCACCATAATCTCTGCC
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81279	79366	TTTCAAAAACTGGTTAAACT
81280	79367	ATTTCAAAAACTGGTTAAAC
81281	79368	TATTTCAAAAACTGGTTAAA
81282	79369	ATATTTCAAAAACTGGTTAA
81283	79370	CATATTTCAAAAACTGGTTA
81284	79371	ACATATTTCAAAAACTGGTT
81285	79372	AACATATTTCAAAAACTGGT
81286	79373	GAACATATTTCAAAAACTGG
81287	79374	GGAACATATTTCAAAAACTG
81288	79375	AGGAACATATTTCAAAAACT
81289	79376	GAGGAACATATTTCAAAAAC
81290	79377	AGAGGAACATATTTCAAAAA
81291	79378	CAGAGGAACATATTTCAAAA
81292	79379	CCAGAGGAACATATTTCAAA
81293	79380	TCCAGAGGAACATATTTCAA
81294	79381	CTCCAGAGGAACATATTTCA
81295	79382	TCTCCAGAGGAACATATTTC
81296	79383	TTCTCCAGAGGAACATATTT
81297	79384	TTTCTCCAGAGGAACATATT
81298	79385	TTTTCTCCAGAGGAACATAT
81299	79386	CTTTTCTCCAGAGGAACATA
81300	79387	CCTTTTCTCCAGAGGAACAT
81301	79388	ACCTTTTCTCCAGAGGAACA
81302	79389	TACCTTTTCTCCAGAGGAAC
81303	79390	TTACCTTTTCTCCAGAGGAA

130380	128467	ACCACTGAATCCTTGTAACA
130381	128468	AACCACTGAATCCTTGTAAC
130382	128469	CAACCACTGAATCCTTGTAA
130383	128470	CCAACCACTGAATCCTTGTA
130384	128471	TCCAACCACTGAATCCTTGT
130385	128472	TTCCAACCACTGAATCCTTG
130386	128473	TTTCCAACCACTGAATCCTT
130387	128474	ATTTCCAACCACTGAATCCT
130388	128475	AATTTCCAACCACTGAATCC
130389	128476	TAATTTCCAACCACTGAATC
130390	128477	TTAATTTCCAACCACTGAAT
130391	128478	CTTAATTTCCAACCACTGAA
130392	128479	CCTTAATTTCCAACCACTGA
130393	128480	TCCTTAATTTCCAACCACTG
130394	128481	TTCCTTAATTTCCAACCACT
130395	128482	CTTCCTTAATTTCCAACCAC
130396	128483	TCTTCCTTAATTTCCAACCA
130397	128484	ATCTTCCTTAATTTCCAACC
130398	128485	TATCTTCCTTAATTTCCAAC
130399	128486	CTATCTTCCTTAATTTCCAA
130400	128487	TCTATCTTCCTTAATTTCCA
130401	128488	TTCTATCTTCCTTAATTTCC
130402	128489	TTTCTATCTTCCTTAATTTC
130403	128490	CTTTCTATCTTCCTTAATTT
130404	128491	ACTTTCTATCTTCCTTAATT
130405	128492	AACTTTCTATCTTCCTTAAT
130406	128493	TAACTTTCTATCTTCCTTAA
130407	128494	CTAACTTTCTATCTTCCTTA
130408	128495	ACTAACTTTCTATCTTCCTT
130409	128496	CACTAACTTTCTATCTTCCT
130410	128497	ACACTAACTTTCTATCTTCC
130411	128498	AACACTAACTTTCTATCTTC
130412	128499	CAACACTAACTTTCTATCTT
130413	128500	CCAACACTAACTTTCTATCT
130414	128501	TCCAACACTAACTTTCTATC
130415	128502	ATCCAACACTAACTTTCTAT
130416	128503	GATCCAACACTAACTTTCTA
130417	128504	AGATCCAACACTAACTTTCT
130418	128505	CAGATCCAACACTAACTTTC
130419	128506	ACAGATCCAACACTAACTTT
130420	128507	AACAGATCCAACACTAACTT
130421	128508	AAACAGATCCAACACTAACT
130422	128509	AAAACAGATCCAACACTAAC
130423	128510	CAAAACAGATCCAACACTAA
130424	128511	CCAAAACAGATCCAACACTA
130425	128512	GCCAAAACAGATCCAACACT
130426	128513	AGCCAAAACAGATCCAACAC
130427	128514	GAGCCAAAACAGATCCAACA
130428	128515	AGAGCCAAAACAGATCCAAC
130429	128516	AAGAGCCAAAACAGATCCAA
130430	128517	AAAGAGCCAAAACAGATCCA
130431	128518	CAAAGAGCCAAAACAGATCC
130432	128519	CCAAAGAGCCAAAACAGATC
130433	128520	ACCAAAGAGCCAAAACAGAT
130434	128521	GACCAAAGAGCCAAAACAGA
130435	128522	TGACCAAAGAGCCAAAACAG
130436	128523	ATGACCAAAGAGCCAAAACA
130437	128524	CATGACCAAAGAGCCAAAAC
130438	128525	GCATGACCAAAGAGCCAAAA
130439	128526	GGCATGACCAAAGAGCCAAA
130440	128527	AGGCATGACCAAAGAGCCAA
130441	128528	AAGGCATGACCAAAGAGCCA
130442	128529	AAAGGCATGACCAAAGAGCC
130443	128530	CAAAGGCATGACCAAAGAGC
130444	128531	ACAAAGGCATGACCAAAGAG
130445	128532	AACAAAGGCATGACCAAAGA
130446	128533	AAACAAAGGCATGACCAAAG
130447	128534	AAAACAAAGGCATGACCAAA
130448	128535	AAAAACAAAGGCATGACCAA
130449	128536	GAAAAACAAAGGCATGACCA
130450	128537	AGAAAAACAAAGGCATGACC

32157	30244	TCCAGCATACACTAGAGTAG
32158	30245	TTCCAGCATACACTAGAGTA
32159	30246	ATTCCAGCATACACTAGAGT
32160	30247	TATTCCAGCATACACTAGAG
32161	30248	ATATTCCAGCATACACTAGA
32162	30249	CATATTCCAGCATACACTAG
32163	30250	TCATATTCCAGCATACACTA
32164	30251	CTCATATTCCAGCATACACT
32165	30252	CCTCATATTCCAGCATACAC
32166	30253	TCCTCATATTCCAGCATACA
32167	30254	TTCCTCATATTCCAGCATAC
32168	30255	TTTCCTCATATTCCAGCATA
32169	30256	ATTTCCTCATATTCCAGCAT
32170	30257	TATTTCCTCATATTCCAGCA
32171	30258	TTATTTCCTCATATTCCAGC
32172	30259	ATTATTTCCTCATATTCCAG
32173	30260	AATTATTTCCTCATATTCCA
32174	30261	TAATTATTTCCTCATATTCC
32175	30262	ATAATTATTTCCTCATATTC
32176	30263	TATAATTATTTCCTCATATT
32177	30264	ATATAATTATTTCCTCATAT
32178	30265	AATATAATTATTTCCTCATA
32179	30266	TAATATAATTATTTCCTCAT
32180	30267	CTAATATAATTATTTCCTCA
32181	30268	GCTAATATAATTATTTCCTC
32182	30269	AGCTAATATAATTATTTCCT
32183	30270	TAGCTAATATAATTATTTCC
32184	30271	CTAGCTAATATAATTATTTC
32185	30272	GCTAGCTAATATAATTATTT
32186	30273	TGCTAGCTAATATAATTATT
32187	30274	CTGCTAGCTAATATAATTAT
32188	30275	ACTGCTAGCTAATATAATTA
32189	30276	AACTGCTAGCTAATATAATT
32190	30277	TAACTGCTAGCTAATATAAT
32191	30278	ATAACTGCTAGCTAATATAA
32192	30279	AATAACTGCTAGCTAATATA
32193	30280	TAATAACTGCTAGCTAATAT
32194	30281	TTAATAACTGCTAGCTAATA
32195	30282	TTTAATAACTGCTAGCTAAT
32196	30283	GTTTAATAACTGCTAGCTAA
32197	30284	TGTTTAATAACTGCTAGCTA
32198	30285	GTGTTTAATAACTGCTAGCT
32199	30286	AGTGTTTAATAACTGCTAGC
32200	30287	AAGTGTTTAATAACTGCTAG
32201	30288	TAAGTGTTTAATAACTGCTA
32202	30289	TTAAGTGTTTAATAACTGCT
32203	30290	ATTAAGTGTTTAATAACTGC
32204	30291	TATTAAGTGTTTAATAACTG
32205	30292	TTATTAAGTGTTTAATAACT
32206	30293	GTTATTAAGTGTTTAATAAC
32207	30294	TGTTATTAAGTGTTTAATAA
32208	30295	ATGTTATTAAGTGTTTAATA
32209	30296	TATGTTATTAAGTGTTTAAT
32210	30297	GTATGTTATTAAGTGTTTAA
32211	30298	GGTATGTTATTAAGTGTTTA
32212	30299	TGGTATGTTATTAAGTGTTT
32213	30300	CTGGTATGTTATTAAGTGTT
32214	30301	CCTGGTATGTTATTAAGTGT
32215	30302	GCCTGGTATGTTATTAAGTG
32216	30303	TGCCTGGTATGTTATTAAGT
32217	30304	GTGCCTGGTATGTTATTAAG
32218	30305	AGTGCCTGGTATGTTATTAA
32219	30306	CAGTGCCTGGTATGTTATTA
32220	30307	ACAGTGCCTGGTATGTTATT
32221	30308	AACAGTGCCTGGTATGTTAT
32222	30309	AAACAGTGCCTGGTATGTTA
32223	30310	AAAACAGTGCCTGGTATGTT
32224	30311	TAAAACAGTGCCTGGTATGT
32225	30312	TTAAAACAGTGCCTGGTATG
32226	30313	CTTAAAACAGTGCCTGGTAT
32227	30314	GCTTAAAACAGTGCCTGGTA

81304	79391	GTTACCTTTTCTCCAGAGGA
81305	79392	TGTTACCTTTTCTCCAGAGG
81306	79393	CTGTTACCTTTTCTCCAGAG
81307	79394	TCTGTTACCTTTTCTCCAGA
81308	79395	TTCTGTTACCTTTTCTCCAG
81309	79396	TTTCTGTTACCTTTTCTCCA
81310	79397	TTTTCTGTTACCTTTTCTCC
81311	79398	TTTTTCTGTTACCTTTTCTC
81312	79399	TTTTTTCTGTTACCTTTTCT
81313	79400	TTTTTTTCTGTTACCTTTTC
81314	79401	TTTTTTTTCTGTTACCTTTT
81315	79402	CTTTTTTTTCTGTTACCTTT
81316	79403	ACTTTTTTTTCTGTTACCTT
81317	79404	AACTTTTTTTTTCTGTTACCT
81318	79405	TAACTTTTTTTTTCTGTTACC
81319	79406	CTAACTTTTTTTTCTGTTAC
81320	79407	TCTAACTTTTTTTTCTGTTA
81321	79408	TTCTAACTTTTTTTTCTGTT
81322	79409	ATTCTAACTTTTTTTTCTGT
81323	79410	AATTCTAACTTTTTTTTCTG
81324	79411	AAATTCTAACTTTTTTTTCT
81325	79412	AAAATTCTAACTTTTTTTTC
81326	79413	CAAAATTCTAACTTTTTTTT
81327	79414	TCAAAATTCTAACTTTTTTT
81328	79415	ATCAAAATTCTAACTTTTTT
81329	79416	AATCAAAATTCTAACTTTTT
81330	79417	AAATCAAAATTCTAACTTTT
81331	79418	TAAATCAAAATTCTAACTTT
81332	79419	ATAAATCAAAATTCTAACTT
81333	79420	TATAAATCAAAATTCTAACT
81334	79421	TTATAAATCAAAATTCTAAC
81335	79422	TTTATAAATCAAAATTCTAA
81336	79423	ATTTATAAATCAAAATTCTA
81337	79424	TATTTATAAATCAAAATTCT
81338	79425	GTATTTATAAATCAAAATTC
81339	79426	TGTATTTATAAATCAAAATT
81340	79427	GTGTATTTATAAATCAAAAT
81341	79428	TGTGTATTTATAAATCAAAA
81342	79429	CTGTGTATTTATAAATCAAA
81343	79430	TCTGTGTATTTATAAATCAA
81344	79431	ATCTGTGTATTTATAAATCA
81345	79432	GATCTGTGTATTTATAAATC
81346	79433	TGATCTGTGTATTTATAAAT
81347	79434	GTGATCTGTGTATTTATAAA
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81349	79436	TAGTGATCTGTGTATTTATA
81350	79437	ATAGTGATCTGTGTATTTAT
81351	79438	TATAGTGATCTGTGTATTTA
81352	79439	TTATAGTGATCTGTGTATTT
81353	79440	GTTATAGTGATCTGTGTATT
81354	79441	AGTTATAGTGATCTGTGTAT
81355	79442	AAGTTATAGTGATCTGTGTA
81356	79443	AAAGTTATAGTGATCTGTGT
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81360	79447	ACTAAAAGTTATAGTGATCT
81361	79448	AACTAAAAGTTATAGTGATC
81362	79449	AAACTAAAAGTTATAGTGAT
81363	79450	AAAACTAAAAGTTATAGTGA
81364	79451	TAAAACTAAAAGTTATAGTG
81365	79452	CTAAAACTAAAAGTTATAGT
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81367	79454	AACTAAAACTAAAAGTTATA
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81370	79457	TAAAACTAAAACTAAAAGTT
81371	79458	CTAAAACTAAAACTAAAAGT
81372	79459	ACTAAAACTAAAACTAAAAG
81373	79460	AACTAAAACTAAAACTAAAA
81374	79461	AAACTAAAACTAAAACTAAA

130451	128538	GAGAAAAACAAAGGCATGAC
130452	128539	TGAGAAAAACAAAGGCATGA
130453	128540	TTGAGAAAAACAAAGGCATG
130454	128541	TTTGAGAAAAACAAAGGCAT
130455	128542	TTTTGAGAAAAACAAAGGCA
130456	128543	ATTTTGAGAAAAACAAAGGC
130457	128544	CATTTTGAGAAAAACAAAGG
130458	128545	TCATTTTGAGAAAAACAAAG
130459	128546	TTCATTTTGAGAAAAACAAA
130460	128547	ATTCATTTTGAGAAAAACAA
130461	128548	CATTCATTTTGAGAAAAACA
130462	128549	GCATTCATTTTGAGAAAAAC
130463	128550	TGCATTCATTTTGAGAAAAA
130464	128551	CTGCATTCATTTTGAGAAAA
130465	128552	ACTGCATTCATTTTGAGAAA
130466	128553	CACTGCATTCATTTTGAGAA
130467	128554	GCACTGCATTCATTTTGAGA
130468	128555	GGCACTGCATTCATTTTGAG
130469	128556	GGGCACTGCATTCATTTTGA
130470	128557	CGGGCACTGCATTCATTTTG
130471	128558	ACGGGCACTGCATTCATTTT
130472	128559	GACGGGCACTGCATTCATTT
130473	128560	GGACGGGCACTGCATTCATT
130474	128561	GGGACGGGCACTGCATTCAT
130475	128562	TGGGACGGGCACTGCATTCA
130476	128563	CTGGGACGGGCACTGCATTC
130477	128564	TCTGGGACGGGCACTGCATT
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130479	128566	TTTCTGGGACGGGCACTGCA
130480	128567	TTTTCTGGGACGGGCACTGC
130481	128568	ATTTTCTGGGACGGGCACTG
130482	128569	TATTTTCTGGGACGGGCACT
130483	128570	GTATTTTCTGGGACGGGCAC
130484	128571	GGTATTTTCTGGGACGGGCA
130485	128572	TGGTATTTTCTGGGACGGGC
130486	128573	ATGGTATTTTCTGGGACGGG
130487	128574	TATGGTATTTTCTGGGACGG
130488	128575	ATATGGTATTTTCTGGGACG
130489	128576	CATATGGTATTTTCTGGGAC
130490	128577	TCATATGGTATTTTCTGGGA
130491	128578	CTCATATGGTATTTTCTGGG
130492	128579	TCTCATATGGTATTTTCTGG
130493	128580	TTCTCATATGGTATTTTCTG
130494	128581	CTTCTCATATGGTATTTTCT
130495	128582	GCTTCTCATATGGTATTTTC
130496	128583	CGCTTCTCATATGGTATTTT
130497	128584	TCGCTTCTCATATGGTATTT
130498	128585	ATCGCTTCTCATATGGTATT
130499	128586	AATCGCTTCTCATATGGTAT
130500	128587	AAATCGCTTCTCATATGGTA
130501	128588	GAAATCGCTTCTCATATGGT
130502	128589	TGAAATCGCTTCTCATATGG
130503	128590	ATGAAATCGCTTCTCATATG
130504	128591	TATGAAATCGCTTCTCATAT
130505	128592	TTATGAAATCGCTTCTCATA
130506	128593	ATTATGAAATCGCTTCTCAT
130507	128594	CATTATGAAATCGCTTCTCA
130508	128595	GCATTATGAAATCGCTTCTC
130509	128596	AGCATTATGAAATCGCTTCT
130510	128597	CAGCATTATGAAATCGCTTC
130511	128598	ACAGCATTATGAAATCGCTT
130512	128599	CACAGCATTATGAAATCGCT
130513	128600	TCACAGCATTATGAAATCGC
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130516	128603	CTCTCACAGCATTATGAAAT
130517	128604	ACTCTCACAGCATTATGAAA
130518	128605	GACTCTCACAGCATTATGAA
130519	128606	AGACTCTCACAGCATTATGA
130520	128607	CAGACTCTCACAGCATTATG
130521	128608	ACAGACTCTCACAGCATTAT

32228	30315	AGCTTAAAACAGTGCCTGGT
32229	30316	TAGCTTAAAACAGTGCCTGG
32230	30317	ATAGCTTAAAACAGTGCCTG
32231	30318	CATAGCTTAAAACAGTGCCT
32232	30319	GCATAGCTTAAAACAGTGCC
32233	30320	CGCATAGCTTAAAACAGTGC
32234	30321	TCGCATAGCTTAAAACAGTG
32235	30322	ATCGCATAGCTTAAAACAGT
32236	30323	GATCGCATAGCTTAAAACAG
32237	30324	AGATCGCATAGCTTAAAACA
32238	30325	CAGATCGCATAGCTTAAAAC
32239	30326	ACAGATCGCATAGCTTAAAA
32240	30327	TACAGATCGCATAGCTTAAA
32241	30328	ATACAGATCGCATAGCTTAA
32242	30329	CATACAGATCGCATAGCTTA
32243	30330	CCATACAGATCGCATAGCTT
32244	30331	TCCATACAGATCGCATAGCT
32245	30332	TTCCATACAGATCGCATAGC
32246	30333	ATTCCATACAGATCGCATAG
32247	30334	TATTCCATACAGATCGCATA
32248	30335	ATATTCCATACAGATCGCAT
32249	30336	AATATTCCATACAGATCGCA
32250	30337	TAATATTCCATACAGATCGC
32251	30338	GTAATATTCCATACAGATCG
32252	30339	AGTAATATTCCATACAGATC
32253	30340	AAGTAATATTCCATACAGAT
32254	30341	TAAGTAATATTCCATACAGA
32255	30342	TTAAGTAATATTCCATACAG
32256	30343	ATTAAGTAATATTCCATACA
32257	30344	AATTAAGTAATATTCCATAC
32258	30345	AAATTAAGTAATATTCCATA
32259	30346	GAAATTAAGTAATATTCCAT
32260	30347	GGAAATTAAGTAATATTCCA
32261	30348	TGGAAATTAAGTAATATTCC
32262	30349	GTGGAAATTAAGTAATATTC
32263	30350	TGTGGAAATTAAGTAATATT
32264	30351	TTGTGGAAATTAAGTAATAT
32265	30352	GTTGTGGAAATTAAGTAATA
32266	30353	GGTTGTGGAAATTAAGTAAT
32267	30354	AGGTTGTGGAAATTAAGTAA
32268	30355	AAGGTTGTGGAAATTAAGTA
32269	30356	TAAGGTTGTGGAAATTAAGT
32270	30357	ATAAGGTTGTGGAAATTAAG
32271	30358	CATAAGGTTGTGGAAATTAA
32272	30359	TCATAAGGTTGTGGAAATTA
32273	30360	TTCATAAGGTTGTGGAAATT
32274	30361	TTTCATAAGGTTGTGGAAAT
32275	30362	TTTTCATAAGGTTGTGGAAA
32276	30363	CTTTTCATAAGGTTGTGGAA
32277	30364	TCTTTTCATAAGGTTGTGGA
32278	30365	ATCTTTTCATAAGGTTGTGG
32279	30366	TATCTTTTCATAAGGTTGTG
32280	30367	GTATCTTTTCATAAGGTTGT
32281	30368	AGTATCTTTTCATAAGGTTG
32282	30369	TAGTATCTTTTCATAAGGTT
32283	30370	ATAGTATCTTTTCATAAGGT
32284	30371	AATAGTATCTTTTCATAAGG
32285	30372	AAATAGTATCTTTTCATAAG
32286	30373	AAAATAGTATCTTTTCATAA
32287	30374	AAAAATAGTATCTTTTCATA
32288	30375	AAAAAATAGTATCTTTTCAT
32289	30376	AAAAAAATAGTATCTTTTCA
32290	30377	AAAAAAAATAGTATCTTTTC
32291	30378	GAAAAAAAATAGTATCTTTT
32292	30379	AGAAAAAAAATAGTATCTTT
32293	30380	AAGAAAAAAAATAGTATCTT
32294	30381	AAAGAAAAAAAATAGTATCT
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32296	30383	CAAAAGAAAAAAAATAGTAT
32297	30384	TCAAAAGAAAAAAAATAGTA
32298	30385	CTCAAAAGAAAAAAAATAGT

81375	79462	AAAACTAAAACTAAAACTAA
81376	79463	TAAAACTAAAACTAAAACTA
81377	79464	CTAAAACTAAAACTAAAACT
81378	79465	ACTAAAACTAAAACTAAAAC
81379	79466	AACTAAAACTAAAACTAAAA
81380	79467	AAACTAAAACTAAAACTAAA
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81382	79469	AGAAACTAAAACTAAAACTA
81383	79470	CAGAAACTAAAACTAAAACT
81384	79471	ACAGAAACTAAAACTAAAAC
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81387	79474	AAAACAGAAACTAAAACTAA
81388	79475	AAAAACAGAAACTAAAACTA
81389	79476	TAAAAACAGAAACTAAAACT
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81391	79478	GGTAAAAACAGAAACTAAAA
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81394	79481	ACTGGTAAAAACAGAAACTA
81395	79482	TACTGGTAAAAACAGAAACT
81396	79483	ATACTGGTAAAAACAGAAAC
81397	79484	AATACTGGTAAAAACAGAAA
81398	79485	GAATACTGGTAAAAACAGAA
81399	79486	AGAATACTGGTAAAAACAGA
81400	79487	TAGAATACTGGTAAAAACAG
81401	79488	TTAGAATACTGGTAAAAACA
81402	79489	TTTAGAATACTGGTAAAAAC
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81409	79496	TTTAGAGTTTAGAATACTGG
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81412	79499	AAGTTTAGAGTTTAGAATAC
81413	79500	AAAGTTTAGAGTTTAGAATA
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81419	79506	ACTAAGAAAGTTTAGAGTTT
81420	79507	TACTAAGAAAGTTTAGAGTT
81421	79508	CTACTAAGAAAGTTTAGAGT
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81423	79510	AACTACTAAGAAAGTTTAGA
81424	79511	CAACTACTAAGAAAGTTTAG
81425	79512	TCAACTACTAAGAAAGTTTA
81426	79513	ATCAACTACTAAGAAAGTTT
81427	79514	AATCAACTACTAAGAAAGTT
81428	79515	TAATCAACTACTAAGAAAGT
81429	79516	ATAATCAACTACTAAGAAAG
81430	79517	CATAATCAACTACTAAGAAA
81431	79518	TCATAATCAACTACTAAGAA
81432	79519	GTCATAATCAACTACTAAGA
81433	79520	TGTCATAATCAACTACTAAG
81434	79521	CTGTCATAATCAACTACTAA
81435	79522	TCTGTCATAATCAACTACTA
81436	79523	ATCTGTCATAATCAACTACT
81437	79524	TATCTGTCATAATCAACTAC
81438	79525	GTATCTGTCATAATCAACTA
81439	79526	TGTATCTGTCATAATCAACT
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81442	79529	TTATGTATCTGTCATAATCA
81443	79530	TTTATGTATCTGTCATAATC
81444	79531	GTTTATGTATCTGTCATAAT
81445	79532	AGTTTATGTATCTGTCATAA

130522	128609	AACAGACTCTCACAGCATTA
130523	128610	TAACAGACTCTCACAGCATT
130524	128611	GTAACAGACTCTCACAGCAT
130525	128612	TGTAACAGACTCTCACAGCA
130526	128613	CTGTAACAGACTCTCACAGC
130527	128614	CCTGTAACAGACTCTCACAG
130528	128615	CCCTGTAACAGACTCTCACA
130529	128616	TCCCTGTAACAGACTCTCAC
130530	128617	GTCCCTGTAACAGACTCTCA
130531	128618	AGTCCCTGTAACAGACTCTC
130532	128619	AAGTCCCTGTAACAGACTCT
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130534	128621	TCAAGTCCCTGTAACAGACT
130535	128622	ATCAAGTCCCTGTAACAGAC
130536	128623	GATCAAGTCCCTGTAACAGA
130537	128624	TGATCAAGTCCCTGTAACAG
130538	128625	TTGATCAAGTCCCTGTAACA
130539	128626	CTTGATCAAGTCCCTGTAAC
130540	128627	ACTTGATCAAGTCCCTGTAA
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130543	128630	CAGACTTGATCAAGTCCCTG
130544	128631	TCAGACTTGATCAAGTCCCT
130545	128632	CTCAGACTTGATCAAGTCCC
130546	128633	CCTCAGACTTGATCAAGTCC
130547	128634	CCCTCAGACTTGATCAAGTC
130548	128635	GCCCTCAGACTTGATCAAGT
130549	128636	GGCCCTCAGACTTGATCAAG
130550	128637	TGGCCCTCAGACTTGATCAA
130551	128638	ATGGCCCTCAGACTTGATCA
130552	128639	CATGGCCCTCAGACTTGATC
130553	128640	TCATGGCCCTCAGACTTGAT
130554	128641	CTCATGGCCCTCAGACTTGA
130555	128642	TCTCATGGCCCTCAGACTTG
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130557	128644	TCTCTCATGGCCCTCAGACT
130558	128645	TTCTCTCATGGCCCTCAGAC
130559	128646	TTTCTCTCATGGCCCTCAGA
130560	128647	CTTTCTCTCATGGCCCTCAG
130561	128648	ACTTTCTCTCATGGCCCTCA
130562	128649	GACTTTCTCTCATGGCCCTC
130563	128650	GGACTTTCTCTCATGGCCCT
130564	128651	GGGACTTTCTCTCATGGCCC
130565	128652	AGGGACTTTCTCTCATGGCC
130566	128653	GAGGGACTTTCTCTCATGGC
130567	128654	AGAGGGACTTTCTCTCATGG
130568	128655	CAGAGGGACTTTCTCTCATG
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130578	128665	GCAACTTCCTCAGAGGGACT
130579	128666	AGCAACTTCCTCAGAGGGAC
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130582	128669	GAAAGCAACTTCCTCAGAGG
130583	128670	TGAAAGCAACTTCCTCAGAG
130584	128671	TTGAAAGCAACTTCCTCAGA
130585	128672	CTTGAAAGCAACTTCCTCAG
130586	128673	GCTTGAAAGCAACTTCCTCA
130587	128674	AGCTTGAAAGCAACTTCCTC
130588	128675	CAGCTTGAAAGCAACTTCCT
130589	128676	TCAGCTTGAAAGCAACTTCC
130590	128677	GTCAGCTTGAAAGCAACTTC
130591	128678	TGTCAGCTTGAAAGCAACTT
130592	128679	GTGTCAGCTTGAAAGCAACT

32299	30386	TCTCAAAAGAAAAAAAATAG
32300	30387	TTCTCAAAAGAAAAAAAATA
32301	30388	CTTCTCAAAAGAAAAAAAAT
32302	30389	CCTTCTCAAAAGAAAAAAAA
32303	30390	ACCTTCTCAAAAGAAAAAAA
32304	30391	TACCTTCTCAAAAGAAAAAA
32305	30392	GTACCTTCTCAAAAGAAAAA
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32307	30394	TAGTACCTTCTCAAAAGAAA
32308	30395	ATAGTACCTTCTCAAAAGAA
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32310	30397	AAATAGTACCTTCTCAAAAG
32311	30398	AAAATAGTACCTTCTCAAAA
32312	30399	GAAAATAGTACCTTCTCAAA
32313	30400	TGAAAATAGTACCTTCTCAA
32314	30401	ATGAAAATAGTACCTTCTCA
32315	30402	GATGAAAATAGTACCTTCTC
32316	30403	AGATGAAAATAGTACCTTCT
32317	30404	AAGATGAAAATAGTACCTTC
32318	30405	GAAGATGAAAATAGTACCTT
32319	30406	TGAAGATGAAAATAGTACCT
32320	30407	ATGAAGATGAAAATAGTACC
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32322	30409	AAATGAAGATGAAAATAGTA
32323	30410	GAAATGAAGATGAAAATAGT
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32325	30412	ATGAAATGAAGATGAAAATA
32326	30413	TATGAAATGAAGATGAAAAT
32327	30414	CTATGAAATGAAGATGAAAA
32328	30415	TCTATGAAATGAAGATGAAA
32329	30416	ATCTATGAAATGAAGATGAA
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32338	30425	AATTTCAACATCTATGAAAT
32339	30426	CAATTTCAACATCTATGAAA
32340	30427	TCAATTTCAACATCTATGAA
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32342	30429	TTTCAATTTCAACATCTATG
32343	30430	GTTTCAATTTCAACATCTAT
32344	30431	TGTTTCAATTTCAACATCTA
32345	30432	GTGTTTCAATTTCAACATCT
32346	30433	TGTGTTTCAATTTCAACATC
32347	30434	CTGTGTTTCAATTTCAACAT
32348	30435	TCTGTGTTTCAATTTCAACA
32349	30436	CTCTGTGTTTCAATTTCAAC
32350	30437	TCTCTGTGTTTCAATTTCAA
32351	30438	CTCTCTGTGTTTCAATTTCA
32352	30439	GCTCTCTGTGTTTCAATTTC
32353	30440	AGCTCTCTGTGTTTCAATTT
32354	30441	CAGCTCTCTGTGTTTCAATT
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32356	30443	TTCAGCTCTCTGTGTTTCAA
32357	30444	CTTCAGCTCTCTGTGTTTCA
32358	30445	ACTTCAGCTCTCTGTGTTTC
32359	30446	GACTTCAGCTCTCTGTGTTT
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32361	30448	GTGACTTCAGCTCTCTGTGT
32362	30449	TGTGACTTCAGCTCTCTGTG
32363	30450	CTGTGACTTCAGCTCTCTGT
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32365	30452	TCCTGTGACTTCAGCTCTCT
32366	30453	ATCCTGTGACTTCAGCTCTC
32367	30454	AATCCTGTGACTTCAGCTCT
32368	30455	TAATCCTGTGACTTCAGCTC
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81446	79533	CAGTTTATGTATCTGTCATA
81447	79534	ACAGTTTATGTATCTGTCAT
81448	79535	CACAGTTTATGTATCTGTCA
81449	79536	CCACAGTTTATGTATCTGTC
81450	79537	GCCACAGTTTATGTATCTGT
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81452	79539	AAGCCACAGTTTATGTATCT
81453	79540	AAAGCCACAGTTTATGTATC
81454	79541	TAAAGCCACAGTTTATGTAT
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81456	79543	TTTAAAGCCACAGTTTATGT
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81460	79547	GTCCTTTAAAGCCACAGTTT
81461	79548	AGTCCTTTAAAGCCACAGTT
81462	79549	GAGTCCTTTAAAGCCACAGT
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81464	79551	ATGAGTCCTTTAAAGCCACA
81465	79552	AATGAGTCCTTTAAAGCCAC
81466	79553	AAATGAGTCCTTTAAAGCCA
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81468	79555	CAAAATGAGTCCTTTAAAGC
81469	79556	GCAAAATGAGTCCTTTAAAG
81470	79557	AGCAAAATGAGTCCTTTAAA
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81498	79585	GGGCACTCTGAAACATGAGG
81499	79586	AGGGCACTCTGAAACATGAG
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81503	79590	TCTAAGGGCACTCTGAAACA
81504	79591	TTCTAAGGGCACTCTGAAAC
81505	79592	TTTCTAAGGGCACTCTGAAA
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81513	79600	GTTATCTCTTTCTAAGGGCA
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130593	128680	GGTGTCAGCTTGAAAGCAAC
130594	128681	AGGTGTCAGCTTGAAAGCAA
130595	128682	CAGGTGTCAGCTTGAAAGCA
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130598	128685	CTTCAGGTGTCAGCTTGAAA
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130600	128687	TCCTTCAGGTGTCAGCTTGA
130601	128688	ATCCTTCAGGTGTCAGCTTG
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130613	128700	TAATTCTGCTTCATCCTTCA
130614	128701	ATAATTCTGCTTCATCCTTC
130615	128702	GATAATTCTGCTTCATCCTT
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130617	128704	GGGATAATTCTGCTTCATCC
130618	128705	TGGGATAATTCTGCTTCATC
130619	128706	CTGGGATAATTCTGCTTCAT
130620	128707	GCTGGGATAATTCTGCTTCA
130621	128708	AGCTGGGATAATTCTGCTTC
130622	128709	CAGCTGGGATAATTCTGCTT
130623	128710	CCAGCTGGGATAATTCTGCT
130624	128711	CCCAGCTGGGATAATTCTGC
130625	128712	TCCCAGCTGGGATAATTCTG
130626	128713	ATCCCAGCTGGGATAATTCT
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130629	128716	CAAATCCCAGCTGGGATAAT
130630	128717	CCAAATCCCAGCTGGGATAA
130631	128718	CCCAAATCCCAGCTGGGATA
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130635	128722	AGTTCCCAAATCCCAGCTGG
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130639	128726	CACCAGTTCCCAAATCCCAG
130640	128727	ACACCAGTTCCCAAATCCCA
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130643	128730	CAAACACCAGTTCCCAAATC
130644	128731	TCAAACACCAGTTCCCAAAT
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130647	128734	GCCTCAAACACCAGTTCCCA
130648	128735	AGCCTCAAACACCAGTTCCC
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130650	128737	TCAGCCTCAAACACCAGTTC
130651	128738	CTCAGCCTCAAACACCAGTT
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130661	128748	CATGCTAGTCCTCAGCCTCA
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32370	30457	CTTAATCCTGTGACTTCAGC
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32372	30459	GCCTTAATCCTGTGACTTCA
32373	30460	GGCCTTAATCCTGTGACTTC
32374	30461	TGGCCTTAATCCTGTGACTT
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32376	30463	TGTGGCCTTAATCCTGTGAC
32377	30464	CTGTGGCCTTAATCCTGTGA
32378	30465	TCTGTGGCCTTAATCCTGTG
32379	30466	CTCTGTGGCCTTAATCCTGT
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32381	30468	AGCTCTGTGGCCTTAATCCT
32382	30469	CAGCTCTGTGGCCTTAATCC
32383	30470	TCAGCTCTGTGGCCTTAATC
32384	30471	CTCAGCTCTGTGGCCTTAAT
32385	30472	TCTCAGCTCTGTGGCCTTAA
32386	30473	TTCTCAGCTCTGTGGCCTTA
32387	30474	CTTCTCAGCTCTGTGGCCTT
32388	30475	ACTTCTCAGCTCTGTGGCCT
32389	30476	CACTTCTCAGCTCTGTGGCC
32390	30477	TCACTTCTCAGCTCTGTGGC
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32392	30479	CATCACTTCTCAGCTCTGTG
32393	30480	CCATCACTTCTCAGCTCTGT
32394	30481	TCCATCACTTCTCAGCTCTG
32395	30482	CTCCATCACTTCTCAGCTCT
32396	30483	GCTCCATCACTTCTCAGCTC
32397	30484	GGCTCCATCACTTCTCAGCT
32398	30485	CGGCTCCATCACTTCTCAGC
32399	30486	CCGGCTCCATCACTTCTCAG
32400	30487	TCCGGCTCCATCACTTCTCA
32401	30488	TTCCGGCTCCATCACTTCTC
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32406	30493	TCAAATTCCGGCTCCATCAC
32407	30494	TTCAAATTCCGGCTCCATCA
32408	30495	GTTCAAATTCCGGCTCCATC
32409	30496	GGTTCAAATTCCGGCTCCAT
32410	30497	GGGTTCAAATTCCGGCTCCA
32411	30498	TGGGTTCAAATTCCGGCTCC
32412	30499	TTGGGTTCAAATTCCGGCTC
32413	30500	CTTGGGTTCAAATTCCGGCT
32414	30501	GCTTGGGTTCAAATTCCGGC
32415	30502	TGCTTGGGTTCAAATTCCGG
32416	30503	TTGCTTGGGTTCAAATTCCG
32417	30504	ATTGCTTGGGTTCAAATTCC
32418	30505	AATTGCTTGGGTTCAAATTC
32419	30506	TAATTGCTTGGGTTCAAATT
32420	30507	TTAATTGCTTGGGTTCAAAT
32421	30508	ATTAATTGCTTGGGTTCAAA
32422	30509	CATTAATTGCTTGGGTTCAA
32423	30510	GCATTAATTGCTTGGGTTCA
32424	30511	AGCATTAATTGCTTGGGTTC
32425	30512	CAGCATTAATTGCTTGGGTT
32426	30513	TCAGCATTAATTGCTTGGGT
32427	30514	ATCAGCATTAATTGCTTGGG
32428	30515	TATCAGCATTAATTGCTTGG
32429	30516	ATATCAGCATTAATTGCTTG
32430	30517	AATATCAGCATTAATTGCTT
32431	30518	TAATATCAGCATTAATTGCT
32432	30519	CTAATATCAGCATTAATTGC
32433	30520	ACTAATATCAGCATTAATTG
32434	30521	AACTAATATCAGCATTAATT
32435	30522	GAACTAATATCAGCATTAAT
32436	30523	AGAACTAATATCAGCATTAA
32437	30524	AAGAACTAATATCAGCATTA
32438	30525	CAAGAACTAATATCAGCATT
32439	30526	ACAAGAACTAATATCAGCAT
32440	30527	CACAAGAACTAATATCAGCA

81517	79604	CTGAGTTATCTCTTTCTAAG
81518	79605	TCTGAGTTATCTCTTTCTAA
81519	79606	TTCTGAGTTATCTCTTTCTA
81520	79607	CTTCTGAGTTATCTCTTTCT
81521	79608	TCTTCTGAGTTATCTCTTTC
81522	79609	TTCTTCTGAGTTATCTCTTT
81523	79610	ATTCTTCTGAGTTATCTCTT
81524	79611	AATTCTTCTGAGTTATCTCT
81525	79612	AAATTCTTCTGAGTTATCTC
81526	79613	AAAATTCTTCTGAGTTATCT
81527	79614	AAAAATTCTTCTGAGTTATC
81528	79615	TAAAAATTCTTCTGAGTTAT
81529	79616	TTAAAAATTCTTCTGAGTTA
81530	79617	TTTAAAAATTCTTCTGAGTT
81531	79618	TTTTAAAAATTCTTCTGAGT
81532	79619	GTTTTAAAAATTCTTCTGAG
81533	79620	CGTTTTAAAAATTCTTCTGA
81534	79621	CCGTTTTAAAAATTCTTCTG
81535	79622	CCCGTTTTAAAAATTCTTCT
81536	79623	TCCCGTTTTAAAAATTCTTC
81537	79624	TTCCCGTTTTAAAAATTCTT
81538	79625	CTTCCCGTTTTAAAAATTCT
81539	79626	GCTTCCCGTTTTAAAAATTC
81540	79627	TGCTTCCCGTTTTAAAAATT
81541	79628	TTGCTTCCCGTTTTAAAAAT
81542	79629	CTTGCTTCCCGTTTTAAAAA
81543	79630	CCTTGCTTCCCGTTTTAAAA
81544	79631	CCCTTGCTTCCCGTTTTAAA
81545	79632	GCCCTTGCTTCCCGTTTTAA
81546	79633	TGCCCTTGCTTCCCGTTTTA
81547	79634	TTGCCCTTGCTTCCCGTTTT
81548	79635	TTTGCCCTTGCTTCCCGTTT
81549	79636	GTTTGCCCTTGCTTCCCGTT
81550	79637	GGTTTGCCCTTGCTTCCCGT
81551	79638	TGGTTTGCCCTTGCTTCCCG
81552	79639	CTGGTTTGCCCTTGCTTCCC
81553	79640	ACTGGTTTGCCCTTGCTTCC
81554	79641	AACTGGTTTGCCCTTGCTTC
81555	79642	TAACTGGTTTGCCCTTGCTT
81556	79643	CTAACTGGTTTGCCCTTGCT
81557	79644	GCTAACTGGTTTGCCCTTGC
81558	79645	TGCTAACTGGTTTGCCCTTG
81559	79646	CTGCTAACTGGTTTGCCCTT
81560	79647	TCTGCTAACTGGTTTGCCCT
81561	79648	TTCTGCTAACTGGTTTGCCC
81562	79649	CTTCTGCTAACTGGTTTGCC
81563	79650	TCTTCTGCTAACTGGTTTGC
81564	79651	TTCTTCTGCTAACTGGTTTG
81565	79652	TTTCTTCTGCTAACTGGTTT
81566	79653	ATTTCTTCTGCTAACTGGTT
81567	79654	AATTTCTTCTGCTAACTGGT
81568	79655	CAATTTCTTCTGCTAACTGG
81569	79656	TCAATTTCTTCTGCTAACTG
81570	79657	CTCAATTTCTTCTGCTAACT
81571	79658	ACTCAATTTCTTCTGCTAAC
81572	79659	GACTCAATTTCTTCTGCTAA
81573	79660	TGACTCAATTTCTTCTGCTA
81574	79661	TTGACTCAATTTCTTCTGCT
81575	79662	CTTGACTCAATTTCTTCTGC
81576	79663	ACTTGACTCAATTTCTTCTG
81577	79664	CACTTGACTCAATTTCTTCT
81578	79665	GCACTTGACTCAATTTCTTC
81579	79666	GGCACTTGACTCAATTTCTT
81580	79667	GGGCACTTGACTCAATTTCT
81581	79668	TGGGCACTTGACTCAATTTC
81582	79669	CTGGGCACTTGACTCAATTT
81583	79670	ACTGGGCACTTGACTCAATT
81584	79671	TACTGGGCACTTGACTCAAT
81585	79672	GTACTGGGCACTTGACTCAA
81586	79673	TGTACTGGGCACTTGACTCA
81587	79674	TTGTACTGGGCACTTGACTC

130664	128751	ATGCATGCTAGTCCTCAGCC
130665	128752	CATGCATGCTAGTCCTCAGC
130666	128753	TCATGCATGCTAGTCCTCAG
130667	128754	ATCATGCATGCTAGTCCTCA
130668	128755	TATCATGCATGCTAGTCCTC
130669	128756	CTATCATGCATGCTAGTCCT
130670	128757	CCTATCATGCATGCTAGTCC
130671	128758	TCCTATCATGCATGCTAGTC
130672	128759	TTCCTATCATGCATGCTAGT
130673	128760	TTTCCTATCATGCATGCTAG
130674	128761	TTTTCCTATCATGCATGCTA
130675	128762	ATTTTCCTATCATGCATGCT
130676	128763	TATTTTCCTATCATGCATGC
130677	128764	TTATTTTCCTATCATGCATG
130678	128765	GTTATTTTCCTATCATGCAT
130679	128766	GGTTATTTTCCTATCATGCA
130680	128767	GGGTTATTTTCCTATCATGC
130681	128768	TGGGTTATTTTCCTATCATG
130682	128769	CTGGGTTATTTTCCTATCAT
130683	128770	TCTGGGTTATTTTCCTATCA
130684	128771	CTCTGGGTTATTTTCCTATC
130685	128772	ACTCTGGGTTATTTTCCTAT
130686	128773	CACTCTGGGTTATTTTCCTA
130687	128774	CCACTCTGGGTTATTTTCCT
130688	128775	GCCACTCTGGGTTATTTTCC
130689	128776	TGCCACTCTGGGTTATTTTC
130690	128777	CTGCCACTCTGGGTTATTTT
130691	128778	TCTGCCACTCTGGGTTATTT
130692	128779	TTCTGCCACTCTGGGTTATT
130693	128780	CTTCTGCCACTCTGGGTTAT
130694	128781	ACTTCTGCCACTCTGGGTTA
130695	128782	CACTTCTGCCACTCTGGGTT
130696	128783	CCACTTCTGCCACTCTGGGT
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130702	128789	CCACTCCCACTTCTGCCACT
130703	128790	ACCACTCCCACTTCTGCCAC
130704	128791	TACCACTCCCACTTCTGCCA
130705	128792	ATACCACTCCCACTTCTGCC
130706	128793	CATACCACTCCCACTTCTGC
130707	128794	TCATACCACTCCCACTTCTG
130708	128795	CTCATACCACTCCCACTTCT
130709	128796	TCTCATACCACTCCCACTTC
130710	128797	ATCTCATACCACTCCCACTT
130711	128798	CATCTCATACCACTCCCACT
130712	128799	CCATCTCATACCACTCCCAC
130713	128800	GCCATCTCATACCACTCCCA
130714	128801	TGCCATCTCATACCACTCCC
130715	128802	ATGCCATCTCATACCACTCC
130716	128803	GATGCCATCTCATACCACTC
130717	128804	TGATGCCATCTCATACCACT
130718	128805	CTGATGCCATCTCATACCAC
130719	128806	TCTGATGCCATCTCATACCA
130720	128807	CTCTGATGCCATCTCATACC
130721	128808	TCTCTGATGCCATCTCATAC
130722	128809	GTCTCTGATGCCATCTCATA
130723	128810	CGTCTCTGATGCCATCTCAT
130724	128811	GCGTCTCTGATGCCATCTCA
130725	128812	TGCGTCTCTGATGCCATCTC
130726	128813	CTGCGTCTCTGATGCCATCT
130727	128814	TCTGCGTCTCTGATGCCATC
130728	128815	ATCTGCGTCTCTGATGCCAT
130729	128816	AATCTGCGTCTCTGATGCCA
130730	128817	GAATCTGCGTCTCTGATGCC
130731	128818	TGAATCTGCGTCTCTGATGC
130732	128819	CTGAATCTGCGTCTCTGATG
130733	128820	CCTGAATCTGCGTCTCTGAT
130734	128821	CCCTGAATCTGCGTCTCTGA

32441	30528	ACACAAGAACTAATATCAGC
32442	30529	CACACAAGAACTAATATCAG
32443	30530	TCACACAAGAACTAATATCA
32444	30531	TTCACACAAGAACTAATATC
32445	30532	ATTCACACAAGAACTAATAT
32446	30533	CATTCACACAAGAACTAATA
32447	30534	CCATTCACACAAGAACTAAT
32448	30535	ACCATTCACACAAGAACTAA
32449	30536	TACCATTCACACAAGAACTA
32450	30537	TTACCATTCACACAAGAACT
32451	30538	ATTACCATTCACACAAGAAC
32452	30539	AATTACCATTCACACAAGAA
32453	30540	CAATTACCATTCACACAAGA
32454	30541	ACAATTACCATTCACACAAG
32455	30542	AACAATTACCATTCACACAA
32456	30543	AAACAATTACCATTCACACA
32457	30544	AAAACAATTACCATTCACAC
32458	30545	CAAAACAATTACCATTCACA
32459	30546	TCAAAACAATTACCATTCAC
32460	30547	TTCAAAACAATTACCATTCA
32461	30548	TTTCAAAACAATTACCATTC
32462	30549	GTTTCAAAACAATTACCATT
32463	30550	TGTTTCAAAACAATTACCAT
32464	30551	TTGTTTCAAAACAATTACCA
32465	30552	ATTGTTTCAAAACAATTACC
32466	30553	CATTGTTTCAAAACAATTAC
32467	30554	TCATTGTTTCAAAACAATTA
32468	30555	ATCATTGTTTCAAAACAATT
32469	30556	GATCATTGTTTCAAAACAAT
32470	30557	GGATCATTGTTTCAAAACAA
32471	30558	AGGATCATTGTTTCAAAACA
32472	30559	TAGGATCATTGTTTCAAAAC
32473	30560	CTAGGATCATTGTTTCAAAA
32474	30561	TCTAGGATCATTGTTTCAAA
32475	30562	ATCTAGGATCATTGTTTCAA
32476	30563	CATCTAGGATCATTGTTTCA
32477	30564	TCATCTAGGATCATTGTTTC
32478	30565	ATCATCTAGGATCATTGTTT
32479	30566	AATCATCTAGGATCATTGTT
32480	30567	TAATCATCTAGGATCATTGT
32481	30568	ATAATCATCTAGGATCATTG
32482	30569	TATAATCATCTAGGATCATT
32483	30570	ATATAATCATCTAGGATCAT
32484	30571	CATATAATCATCTAGGATCA
32485	30572	TCATATAATCATCTAGGATC
32486	30573	GTCATATAATCATCTAGGAT
32487	30574	GGTCATATAATCATCTAGGA
32488	30575	CGGTCATATAATCATCTAGG
32489	30576	CCGGTCATATAATCATCTAG
32490	30577	TCCGGTCATATAATCATCTA
32491	30578	ATCCGGTCATATAATCATCT
32492	30579	AATCCGGTCATATAATCATC
32493	30580	TAATCCGGTCATATAATCAT
32494	30581	TTAATCCGGTCATATAATCA
32495	30582	ATTAATCCGGTCATATAATC
32496	30583	GATTAATCCGGTCATATAAT
32497	30584	AGATTAATCCGGTCATATAA
32498	30585	CAGATTAATCCGGTCATATA
32499	30586	CCAGATTAATCCGGTCATAT
32500	30587	GCCAGATTAATCCGGTCATA
32501	30588	TGCCAGATTAATCCGGTCAT
32502	30589	CTGCCAGATTAATCCGGTCA
32503	30590	ACTGCCAGATTAATCCGGTC
32504	30591	AACTGCCAGATTAATCCGGT
32505	30592	CAACTGCCAGATTAATCCGG
32506	30593	ACAACTGCCAGATTAATCCG
32507	30594	AACAACTGCCAGATTAATCC
32508	30595	GAACAACTGCCAGATTAATC
32509	30596	AGAACAACTGCCAGATTAAT
32510	30597	CAGAACAACTGCCAGATTAA
32511	30598	ACAGAACAACTGCCAGATTA

81588	79675	TTTGTACTGGGCACTTGACT
81589	79676	CTTTGTACTGGGCACTTGAC
81590	79677	GCTTTGTACTGGGCACTTGA
81591	79678	AGCTTTGTACTGGGCACTTG
81592	79679	GAGCTTTGTACTGGGCACTT
81593	79680	CGAGCTTTGTACTGGGCACT
81594	79681	TCGAGCTTTGTACTGGGCAC
81595	79682	CTCGAGCTTTGTACTGGGCA
81596	79683	ACTCGAGCTTTGTACTGGGC
81597	79684	CACTCGAGCTTTGTACTGGG
81598	79685	CCACTCGAGCTTTGTACTGG
81599	79686	GCCACTCGAGCTTTGTACTG
81600	79687	GGCCACTCGAGCTTTGTACT
81601	79688	GGGCCACTCGAGCTTTGTAC
81602	79689	AGGGCCACTCGAGCTTTGTA
81603	79690	CAGGGCCACTCGAGCTTTGT
81604	79691	CCAGGGCCACTCGAGCTTTG
81605	79692	TCCAGGGCCACTCGAGCTTT
81606	79693	TTCCAGGGCCACTCGAGCTT
81607	79694	TTTCCAGGGCCACTCGAGCT
81608	79695	TTTTCCAGGGCCACTCGAGC
81609	79696	ATTTTCCAGGGCCACTCGAG
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81611	79698	TCATTTTCCAGGGCCACTCG
81612	79699	ATCATTTTCCAGGGCCACTC
81613	79700	CATCATTTTCCAGGGCCACT
81614	79701	TCATCATTTTCCAGGGCCAC
81615	79702	ATCATCATTTTCCAGGGCCA
81616	79703	TATCATCATTTTCCAGGGCC
81617	79704	CTATCATCATTTTCCAGGGC
81618	79705	CCTATCATCATTTTCCAGGG
81619	79706	TCCTATCATCATTTTCCAGG
81620	79707	CTCCTATCATCATTTTCCAG
81621	79708	ACTCCTATCATCATTTTCCA
81622	79709	CACTCCTATCATCATTTTCC
81623	79710	TCACTCCTATCATCATTTTC
81624	79711	CTCACTCCTATCATCATTTT
81625	79712	CCTCACTCCTATCATCATTT
81626	79713	TCCTCACTCCTATCATCATT
81627	79714	TTCCTCACTCCTATCATCAT
81628	79715	CTTCCTCACTCCTATCATCA
81629	79716	TCTTCCTCACTCCTATCATC
81630	79717	TTCTTCCTCACTCCTATCAT
81631	79718	TTTCTTCCTCACTCCTATCA
81632	79719	TTTTCTTCCTCACTCCTATC
81633	79720	TTTTTCTTCCTCACTCCTAT
81634	79721	ATTTTTCTTCCTCACTCCTA
81635	79722	TATTTTTCTTCCTCACTCCT
81636	79723	GTATTTTTCTTCCTCACTCC
81637	79724	TGTATTTTTCTTCCTCACTC
81638	79725	GTGTATTTTTCTTCCTCACT
81639	79726	TGTGTATTTTTCTTCCTCAC
81640	79727	CTGTGTATTTTTCTTCCTCA
81641	79728	GCTGTGTATTTTTCTTCCTC
81642	79729	TGCTGTGTATTTTTCTTCCT
81643	79730	CTGCTGTGTATTTTTCTTCC
81644	79731	ACTGCTGTGTATTTTTCTTC
81645	79732	AACTGCTGTGTATTTTTCTT
81646	79733	GAACTGCTGTGTATTTTTCT
81647	79734	TGAACTGCTGTGTATTTTTC
81648	79735	CTGAACTGCTGTGTATTTTT
81649	79736	TCTGAACTGCTGTGTATTTT
81650	79737	CTCTGAACTGCTGTGTATTT
81651	79738	TCTCTGAACTGCTGTGTATT
81652	79739	TTCTCTGAACTGCTGTGTAT
81653	79740	TTTCTCTGAACTGCTGTGTA
81654	79741	ATTTCTCTGAACTGCTGTGT
81655	79742	AATTTCTCTGAACTGCTGTG
81656	79743	GAATTTCTCTGAACTGCTGT
81657	79744	GGAATTTCTCTGAACTGCTG
81658	79745	TGGAATTTCTCTGAACTGCT

130735	128822	ACCCTGAATCTGCGTCTCTG
130736	128823	GACCCTGAATCTGCGTCTCT
130737	128824	TGACCCTGAATCTGCGTCTC
130738	128825	TTGACCCTGAATCTGCGTCT
130739	128826	TTTGACCCTGAATCTGCGTC
130740	128827	ATTTGACCCTGAATCTGCGT
130741	128828	GATTTGACCCTGAATCTGCG
130742	128829	TGATTTGACCCTGAATCTGC
130743	128830	ATGATTTGACCCTGAATCTG
130744	128831	AATGATTTGACCCTGAATCT
130745	128832	GAATGATTTGACCCTGAATC
130746	128833	TGAATGATTTGACCCTGAAT
130747	128834	CTGAATGATTTGACCCTGAA
130748	128835	TCTGAATGATTTGACCCTGA
130749	128836	CTCTGAATGATTTGACCCTG
130750	128837	GCTCTGAATGATTTGACCCT
130751	128838	GGCTCTGAATGATTTGACCC
130752	128839	AGGCTCTGAATGATTTGACC
130753	128840	GAGGCTCTGAATGATTTGAC
130754	128841	GGAGGCTCTGAATGATTTGA
130755	128842	AGGAGGCTCTGAATGATTTG
130756	128843	TAGGAGGCTCTGAATGATTT
130757	128844	CTAGGAGGCTCTGAATGATT
130758	128845	TCTAGGAGGCTCTGAATGAT
130759	128846	GTCTAGGAGGCTCTGAATGA
130760	128847	GGTCTAGGAGGCTCTGAATG
130761	128848	TGGTCTAGGAGGCTCTGAAT
130762	128849	ATGGTCTAGGAGGCTCTGAA
130763	128850	CATGGTCTAGGAGGCTCTGA
130764	128851	ACATGGTCTAGGAGGCTCTG
130765	128852	CACATGGTCTAGGAGGCTCT
130766	128853	TCACATGGTCTAGGAGGCTC
130767	128854	TTCACATGGTCTAGGAGGCT
130768	128855	GTTCACATGGTCTAGGAGGC
130769	128856	TGTTCACATGGTCTAGGAGG
130770	128857	GTGTTCACATGGTCTAGGAG
130771	128858	TGTGTTCACATGGTCTAGGA
130772	128859	ATGTGTTCACATGGTCTAGG
130773	128860	CATGTGTTCACATGGTCTAG
130774	128861	ACATGTGTTCACATGGTCTA
130775	128862	TACATGTGTTCACATGGTCT
130776	128863	ATACATGTGTTCACATGGTC
130777	128864	AATACATGTGTTCACATGGT
130778	128865	TAATACATGTGTTCACATGG
130779	128866	ATAATACATGTGTTCACATG
130780	128867	CATAATACATGTGTTCACAT
130781	128868	GCATAATACATGTGTTCACA
130782	128869	AGCATAATACATGTGTTCAC
130783	128870	CAGCATAATACATGTGTTCA
130784	128871	ACAGCATAATACATGTGTTC
130785	128872	CACAGCATAATACATGTGTT
130786	128873	CCACAGCATAATACATGTGT
130787	128874	TCCACAGCATAATACATGTG
130788	128875	CTCCACAGCATAATACATGT
130789	128876	TCTCCACAGCATAATACATG
130790	128877	ATCTCCACAGCATAATACAT
130791	128878	TATCTCCACAGCATAATACA
130792	128879	GTATCTCCACAGCATAATAC
130793	128880	AGTATCTCCACAGCATAATA
130794	128881	CAGTATCTCCACAGCATAAT
130795	128882	ACAGTATCTCCACAGCATAA
130796	128883	AACAGTATCTCCACAGCATA
130797	128884	AAACAGTATCTCCACAGCAT
130798	128885	TAAACAGTATCTCCACAGCA
130799	128886	TTAAACAGTATCTCCACAGC
130800	128887	ATTAAACAGTATCTCCACAG
130801	128888	TATTAAACAGTATCTCCACA
130802	128889	CTATTAAACAGTATCTCCAC
130803	128890	CCTATTAAACAGTATCTCCA
130804	128891	GCCTATTAAACAGTATCTCC
130805	128892	TGCCTATTAAACAGTATCTC

32512	30599	CACAGAACAACTGCCAGATT
32513	30600	ACACAGAACAACTGCCAGAT
32514	30601	CACACAGAACAACTGCCAGA
32515	30602	TCACACAGAACAACTGCCAG
32516	30603	TTCACACAGAACAACTGCCA
32517	30604	ATTCACACAGAACAACTGCC
32518	30605	AATTCACACAGAACAACTGC
32519	30606	AAATTCACACAGAACAACTG
32520	30607	TAAATTCACACAGAACAACT
32521	30608	CTAAATTCACACAGAACAAC
32522	30609	TCTAAATTCACACAGAACAA
32523	30610	CTCTAAATTCACACAGAACA
32524	30611	ACTCTAAATTCACACAGAAC
32525	30612	AACTCTAAATTCACACAGAA
32526	30613	CAACTCTAAATTCACACAGA
32527	30614	GCAACTCTAAATTCACACAG
32528	30615	GGCAACTCTAAATTCACACA
32529	30616	AGGCAACTCTAAATTCACAC
32530	30617	AAGGCAACTCTAAATTCACA
32531	30618	GAAGGCAACTCTAAATTCAC
32532	30619	GGAAGGCAACTCTAAATTCA
32533	30620	GGGAAGGCAACTCTAAATTC
32534	30621	TGGGAAGGCAACTCTAAATT
32535	30622	GTGGGAAGGCAACTCTAAAT
32536	30623	GGTGGGAAGGCAACTCTAAA
32537	30624	AGGTGGGAAGGCAACTCTAA
32538	30625	GAGGTGGGAAGGCAACTCTA
32539	30626	TGAGGTGGGAAGGCAACTCT
32540	30627	CTGAGGTGGGAAGGCAACTC
32541	30628	ACTGAGGTGGGAAGGCAACT
32542	30629	AACTGAGGTGGGAAGGCAAC
32543	30630	AAACTGAGGTGGGAAGGCAA
32544	30631	GAAACTGAGGTGGGAAGGCA
32545	30632	GGAAACTGAGGTGGGAAGGC
32546	30633	AGGAAACTGAGGTGGGAAGG
32547	30634	TAGGAAACTGAGGTGGGAAG
32548	30635	TTAGGAAACTGAGGTGGGAA
32549	30636	TTTAGGAAACTGAGGTGGGA
32550	30637	TTTTAGGAAACTGAGGTGGG
32551	30638	TTTTTAGGAAACTGAGGTGG
32552	30639	GTTTTTAGGAAACTGAGGTG
32553	30640	TGTTTTTAGGAAACTGAGGT
32554	30641	TTGTTTTTAGGAAACTGAGG
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32558	30645	TGTTTTGTTTTTAGGAAACT
32559	30646	TTGTTTTGTTTTTAGGAAAC
32560	30647	TTTGTTTTGTTTTTAGGAAA
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32562	30649	GTTTTGTTTTGTTTTTAGGA
32563	30650	TGTTTTGTTTTGTTTTTAGG
32564	30651	TTGTTTTGTTTTGTTTTTAG
32565	30652	TTTGTTTTGTTTTGTTTTTA
32566	30653	TTTTGTTTTGTTTTGTTTTT
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32568	30655	TGTTTTGTTTTGTTTTGTTT
32569	30656	TTGTTTTGTTTTGTTTTGTT
32570	30657	TTTGTTTTGTTTTGTTTTGT
32571	30658	TTTTGTTTTGTTTTGTTTTG
32572	30659	GTTTTGTTTTGTTTTGTTTT
32573	30660	TGTTTTGTTTTGTTTTGTTT
32574	30661	TTGTTTTGTTTTGTTTTGTT
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32576	30663	TTTTGTTTTGTTTTGTTTTG
32577	30664	TTTTTGTTTTGTTTTGTTTT
32578	30665	TTTTTTGTTTTGTTTTGTTT
32579	30666	TTTTTTTGTTTTGTTTTGTT
32580	30667	TTTTTTTTGTTTTGTTTTGT
32581	30668	GTTTTTTTTGTTTTGTTTTG
32582	30669	AGTTTTTTTTGTTTTGTTTT

81659	79746	CTGGAATTTCTCTGAACTGC
81660	79747	ACTGGAATTTCTCTGAACTG
81661	79748	CACTGGAATTTCTCTGAACT
81662	79749	TCACTGGAATTTCTCTGAAC
81663	79750	TTCACTGGAATTTCTCTGAA
81664	79751	GTTCACTGGAATTTCTCTGA
81665	79752	CGTTCACTGGAATTTCTCTG
81666	79753	ACGTTCACTGGAATTTCTCT
81667	79754	CACGTTCACTGGAATTTCTC
81668	79755	TCACGTTCACTGGAATTTCT
81669	79756	CTCACGTTCACTGGAATTTC
81670	79757	CCTCACGTTCACTGGAATTT
81671	79758	CCCTCACGTTCACTGGAATT
81672	79759	CCCCTCACGTTCACTGGAAT
81673	79760	GCCCCTCACGTTCACTGGAA
81674	79761	TGCCCCTCACGTTCACTGGA
81675	79762	GTGCCCCTCACGTTCACTGG
81676	79763	TGTGCCCCTCACGTTCACTG
81677	79764	CTGTGCCCCTCACGTTCACT
81678	79765	GCTGTGCCCCTCACGTTCAC
81679	79766	TGCTGTGCCCCTCACGTTCA
81680	79767	ATGCTGTGCCCCTCACGTTC
81681	79768	TATGCTGTGCCCCTCACGTT
81682	79769	TTATGCTGTGCCCCTCACGT
81683	79770	TTTATGCTGTGCCCCTCACG
81684	79771	GTTTATGCTGTGCCCCTCAC
81685	79772	TGTTTATGCTGTGCCCCTCA
81686	79773	GTGTTTATGCTGTGCCCCTC
81687	79774	AGTGTTTATGCTGTGCCCCT
81688	79775	TAGTGTTTATGCTGTGCCCC
81689	79776	CTAGTGTTTATGCTGTGCCC
81690	79777	CCTAGTGTTTATGCTGTGCC
81691	79778	ACCTAGTGTTTATGCTGTGC
81692	79779	TACCTAGTGTTTATGCTGTG
81693	79780	ATACCTAGTGTTTATGCTGT
81694	79781	AATACCTAGTGTTTATGCTG
81695	79782	AAATACCTAGTGTTTATGCT
81696	79783	TAAATACCTAGTGTTTATGC
81697	79784	TTAAATACCTAGTGTTTATG
81698	79785	TTTAAATACCTAGTGTTTAT
81699	79786	CTTTAAATACCTAGTGTTTA
81700	79787	CCTTTAAATACCTAGTGTTT
81701	79788	TCCTTTAAATACCTAGTGTT
81702	79789	TTCCTTTAAATACCTAGTGT
81703	79790	TTTCCTTTAAATACCTAGTG
81704	79791	ATTTCCTTTAAATACCTAGT
81705	79792	GATTTCCTTTAAATACCTAG
81706	79793	TGATTTCCTTTAAATACCTA
81707	79794	ATGATTTCCTTTAAATACCT
81708	79795	CATGATTTCCTTTAAATACC
81709	79796	TCATGATTTCCTTTAAATAC
81710	79797	ATCATGATTTCCTTTAAATA
81711	79798	CATCATGATTTCCTTTAAAT
81712	79799	GCATCATGATTTCCTTTAAA
81713	79800	TGCATCATGATTTCCTTTAA
81714	79801	CTGCATCATGATTTCCTTTA
81715	79802	ACTGCATCATGATTTCCTTT
81716	79803	TACTGCATCATGATTTCCTT
81717	79804	ATACTGCATCATGATTTCCT
81718	79805	AATACTGCATCATGATTTCC
81719	79806	AAATACTGCATCATGATTTC
81720	79807	AAAATACTGCATCATGATTT
81721	79808	CAAAATACTGCATCATGATT
81722	79809	CCAAAATACTGCATCATGAT
81723	79810	TCCAAAATACTGCATCATGA
81724	79811	ATCCAAAATACTGCATCATG
81725	79812	TATCCAAAATACTGCATCAT
81726	79813	GTATCCAAAATACTGCATCA
81727	79814	TGTATCCAAAATACTGCATC
81728	79815	GTGTATCCAAAATACTGCAT
81729	79816	TGTGTATCCAAAATACTGCA

130806	128893	CTGCCTATTAAACAGTATCT
130807	128894	ACTGCCTATTAAACAGTATC
130808	128895	GACTGCCTATTAAACAGTAT
130809	128896	AGACTGCCTATTAAACAGTA
130810	128897	CAGACTGCCTATTAAACAGT
130811	128898	GCAGACTGCCTATTAAACAG
130812	128899	AGCAGACTGCCTATTAAACA
130813	128900	AAGCAGACTGCCTATTAAAC
130814	128901	AAAGCAGACTGCCTATTAAA
130815	128902	AAAAGCAGACTGCCTATTAA
130816	128903	AAAAAGCAGACTGCCTATTA
130817	128904	AAAAAAGCAGACTGCCTATT
130818	128905	AAAAAAAGCAGACTGCCTAT
130819	128906	AAAAAAAAGCAGACTGCCTA
130820	128907	GAAAAAAAAGCAGACTGCCT
130821	128908	AGAAAAAAAAGCAGACTGCC
130822	128909	CAGAAAAAAAAGCAGACTGC
130823	128910	GCAGAAAAAAAAGCAGACTG
130824	128911	TGCAGAAAAAAAAGCAGACT
130825	128912	CTGCAGAAAAAAAAGCAGAC
130826	128913	ACTGCAGAAAAAAAAGCAGA
130827	128914	TACTGCAGAAAAAAAAGCAG
130828	128915	GTACTGCAGAAAAAAAAGCA
130829	128916	GGTACTGCAGAAAAAAAAGC
130830	128917	TGGTACTGCAGAAAAAAAAG
130831	128918	TTGGTACTGCAGAAAAAAAA
130832	128919	TTTGGTACTGCAGAAAAAAA
130833	128920	ATTTGGTACTGCAGAAAAAA
130834	128921	TATTTGGTACTGCAGAAAAA
130835	128922	ATATTTGGTACTGCAGAAAA
130836	128923	CATATTTGGTACTGCAGAAA
130837	128924	GCATATTTGGTACTGCAGAA
130838	128925	GGCATATTTGGTACTGCAGA
130839	128926	GGGCATATTTGGTACTGCAG
130840	128927	GGGGCATATTTGGTACTGCA
130841	128928	TGGGGCATATTTGGTACTGC
130842	128929	TTGGGGCATATTTGGTACTG
130843	128930	GTTGGGGCATATTTGGTACT
130844	128931	TGTTGGGGCATATTTGGTAC
130845	128932	CTGTTGGGGCATATTTGGTA
130846	128933	GCTGTTGGGGCATATTTGGT
130847	128934	CGCTGTTGGGGCATATTTGG
130848	128935	CCGCTGTTGGGGCATATTTG
130849	128936	GCCGCTGTTGGGGCATATTT
130850	128937	TGCCGCTGTTGGGGCATATT
130851	128938	TTGCCGCTGTTGGGGCATAT
130852	128939	CTTGCCGCTGTTGGGGCATA
130853	128940	TCTTGCCGCTGTTGGGGCAT
130854	128941	GTCTTGCCGCTGTTGGGGCA
130855	128942	GGTCTTGCCGCTGTTGGGGC
130856	128943	TGGTCTTGCCGCTGTTGGGG
130857	128944	CTGGTCTTGCCGCTGTTGGG
130858	128945	GCTGGTCTTGCCGCTGTTGG
130859	128946	TGCTGGTCTTGCCGCTGTTG
130860	128947	ATGCTGGTCTTGCCGCTGTT
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130862	128949	TGATGCTGGTCTTGCCGCTG
130863	128950	ATGATGCTGGTCTTGCCGCT
130864	128951	GATGATGCTGGTCTTGCCGC
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130866	128953	CTGATGATGCTGGTCTTGCC
130867	128954	TCTGATGATGCTGGTCTTGC
130868	128955	CTCTGATGATGCTGGTCTTG
130869	128956	ACTCTGATGATGCTGGTCTT
130870	128957	CACTCTGATGATGCTGGTCT
130871	128958	GCACTCTGATGATGCTGGTC
130872	128959	GGCACTCTGATGATGCTGGT
130873	128960	TGGCACTCTGATGATGCTGG
130874	128961	ATGGCACTCTGATGATGCTG
130875	128962	CATGGCACTCTGATGATGCT
130876	128963	TCATGGCACTCTGATGATGC

32583	30670	GAGTTTTTTTTGTTTTGTTT
32584	30671	AGAGTTTTTTTTGTTTTGTT
32585	30672	TAGAGTTTTTTTTGTTTTGT
32586	30673	CTAGAGTTTTTTTTGTTTTG
32587	30674	GCTAGAGTTTTTTTTGTTTT
32588	30675	AGCTAGAGTTTTTTTTGTTT
32589	30676	AAGCTAGAGTTTTTTTTGTT
32590	30677	GAAGCTAGAGTTTTTTTTGT
32591	30678	TGAAGCTAGAGTTTTTTTTG
32592	30679	GTGAAGCTAGAGTTTTTTTT
32593	30680	AGTGAAGCTAGAGTTTTTTT
32594	30681	CAGTGAAGCTAGAGTTTTTT
32595	30682	ACAGTGAAGCTAGAGTTTTT
32596	30683	CACAGTGAAGCTAGAGTTTT
32597	30684	ACACAGTGAAGCTAGAGTTT
32598	30685	AACACAGTGAAGCTAGAGTT
32599	30686	AAACACAGTGAAGCTAGAGT
32600	30687	CAAACACAGTGAAGCTAGAG
32601	30688	CCAAACACAGTGAAGCTAGA
32602	30689	CCCAAACACAGTGAAGCTAG
32603	30690	ACCCAAACACAGTGAAGCTA
32604	30691	AACCCAAACACAGTGAAGCT
32605	30692	CAACCCAAACACAGTGAAGC
32606	30693	ACAACCCAAACACAGTGAAG
32607	30694	GACAACCCAAACACAGTGAA
32608	30695	TGACAACCCAAACACAGTGA
32609	30696	ATGACAACCCAAACACAGTG
32610	30697	CATGACAACCCAAACACAGT
32611	30698	CCATGACAACCCAAACACAG
32612	30699	GCCATGACAACCCAAACACA
32613	30700	GGCCATGACAACCCAAACAC
32614	30701	AGGCCATGACAACCCAAACA
32615	30702	TAGGCCATGACAACCCAAAC
32616	30703	GTAGGCCATGACAACCCAAA
32617	30704	GGTAGGCCATGACAACCCAA
32618	30705	GGGTAGGCCATGACAACCCA
32619	30706	GGGGTAGGCCATGACAACCC
32620	30707	GGGGGTAGGCCATGACAACC
32621	30708	AGGGGGTAGGCCATGACAAC
32622	30709	GAGGGGGTAGGCCATGACAA
32623	30710	AGAGGGGGTAGGCCATGACA
32624	30711	AAGAGGGGGTAGGCCATGAC
32625	30712	CAAGAGGGGGTAGGCCATGA
32626	30713	GCAAGAGGGGGTAGGCCATG
32627	30714	GGCAAGAGGGGGTAGGCCAT
32628	30715	TGGCAAGAGGGGGTAGGCCA
32629	30716	GTGGCAAGAGGGGGTAGGCC
32630	30717	GGTGGCAAGAGGGGGTAGGC
32631	30718	AGGTGGCAAGAGGGGGTAGG
32632	30719	GAGGTGGCAAGAGGGGGTAG
32633	30720	TGAGGTGGCAAGAGGGGGTA
32634	30721	ATGAGGTGGCAAGAGGGGGT
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32639	30726	GTCAAATGAGGTGGCAAGAG
32640	30727	AGTCAAATGAGGTGGCAAGA
32641	30728	GAGTCAAATGAGGTGGCAAG
32642	30729	TGAGTCAAATGAGGTGGCAA
32643	30730	TTGAGTCAAATGAGGTGGCA
32644	30731	GTTGAGTCAAATGAGGTGGC
32645	30732	AGTTGAGTCAAATGAGGTGG
32646	30733	AAGTTGAGTCAAATGAGGTG
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32650	30737	TAAAAAGTTGAGTCAAATGA
32651	30738	CTAAAAAGTTGAGTCAAATG
32652	30739	CCTAAAAAGTTGAGTCAAAT
32653	30740	CCCTAAAAAGTTGAGTCAAA

81730	79817	TTGTGTATCCAAAATACTGC
81731	79818	GTTGTGTATCCAAAATACTG
81732	79819	AGTTGTGTATCCAAAATACT
81733	79820	GAGTTGTGTATCCAAAATAC
81734	79821	TGAGTTGTGTATCCAAAATA
81735	79822	TTGAGTTGTGTATCCAAAAT
81736	79823	CTTGAGTTGTGTATCCAAAA
81737	79824	CCTTGAGTTGTGTATCCAAA
81738	79825	ACCTTGAGTTGTGTATCCAA
81739	79826	GACCTTGAGTTGTGTATCCA
81740	79827	AGACCTTGAGTTGTGTATCC
81741	79828	CAGACCTTGAGTTGTGTATC
81742	79829	ACAGACCTTGAGTTGTGTAT
81743	79830	CACAGACCTTGAGTTGTGTA
81744	79831	ACACAGACCTTGAGTTGTGT
81745	79832	CACACAGACCTTGAGTTGTG
81746	79833	TCACACAGACCTTGAGTTGT
81747	79834	CTCACACAGACCTTGAGTTG
81748	79835	TCTCACACAGACCTTGAGTT
81749	79836	GTCTCACACAGACCTTGAGT
81750	79837	CGTCTCACACAGACCTTGAG
81751	79838	CCGTCTCACACAGACCTTGA
81752	79839	ACCGTCTCACACAGACCTTG
81753	79840	CACCGTCTCACACAGACCTT
81754	79841	ACACCGTCTCACACAGACCT
81755	79842	TACACCGTCTCACACAGACC
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81757	79844	AATACACCGTCTCACACAGA
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81759	79846	ACAATACACCGTCTCACACA
81760	79847	AACAATACACCGTCTCACAC
81761	79848	TAACAATACACCGTCTCACA
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81763	79850	AATAACAATACACCGTCTCA
81764	79851	TAATAACAATACACCGTCTC
81765	79852	ATAATAACAATACACCGTCT
81766	79853	TATAATAACAATACACCGTC
81767	79854	ATATAATAACAATACACCGT
81768	79855	AATATAATAACAATACACCG
81769	79856	AAATATAATAACAATACACC
81770	79857	GAAATATAATAACAATACAC
81771	79858	GGAAATATAATAACAATACA
81772	79859	AGGAAATATAATAACAATAC
81773	79860	GAGGAAATATAATAACAATA
81774	79861	AGAGGAAATATAATAACAAT
81775	79862	AAGAGGAAATATAATAACAA
81776	79863	GAAGAGGAAATATAATAACA
81777	79864	GGAAGAGGAAATATAATAAC
81778	79865	AGGAAGAGGAAATATAATAA
81779	79866	AAGGAAGAGGAAATATAATA
81780	79867	AAAGGAAGAGGAAATATAAT
81781	79868	TAAAGGAAGAGGAAATATAA
81782	79869	TTAAAGGAAGAGGAAATATA
81783	79870	ATTAAAGGAAGAGGAAATAT
81784	79871	TATTAAAGGAAGAGGAAATA
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81786	79873	TATATTAAAGGAAGAGGAAA
81787	79874	CTATATTAAAGGAAGAGGAA
81788	79875	GCTATATTAAAGGAAGAGGA
81789	79876	AGCTATATTAAAGGAAGAGG
81790	79877	AAGCTATATTAAAGGAAGAG
81791	79878	TAAGCTATATTAAAGGAAGA
81792	79879	CTAAGCTATATTAAAGGAAG
81793	79880	CCTAAGCTATATTAAAGGAA
81794	79881	ACCTAAGCTATATTAAAGGA
81795	79882	TACCTAAGCTATATTAAAGG
81796	79883	CTACCTAAGCTATATTAAAG
81797	79884	TCTACCTAAGCTATATTAAA
81798	79885	CTCTACCTAAGCTATATTAA
81799	79886	TCTCTACCTAAGCTATATTA
81800	79887	TTCTCTACCTAAGCTATATT

130877	128964	ATCATGGCACTCTGATGATG
130878	128965	CATCATGGCACTCTGATGAT
130879	128966	GCATCATGGCACTCTGATGA
130880	128967	TGCATCATGGCACTCTGATG
130881	128968	GTGCATCATGGCACTCTGAT
130882	128969	GGTGCATCATGGCACTCTGA
130883	128970	GGGTGCATCATGGCACTCTG
130884	128971	TGGGTGCATCATGGCACTCT
130885	128972	CTGGGTGCATCATGGCACTC
130886	128973	GCTGGGTGCATCATGGCACT
130887	128974	CGCTGGGTGCATCATGGCAC
130888	128975	ACGCTGGGTGCATCATGGCA
130889	128976	GACGCTGGGTGCATCATGGC
130890	128977	TGACGCTGGGTGCATCATGG
130891	128978	CTGACGCTGGGTGCATCATG
130892	128979	GCTGACGCTGGGTGCATCAT
130893	128980	TGCTGACGCTGGGTGCATCA
130894	128981	CTGCTGACGCTGGGTGCATC
130895	128982	GCTGCTGACGCTGGGTGCAT
130896	128983	CGCTGCTGACGCTGGGTGCA
130897	128984	CCGCTGCTGACGCTGGGTGC
130898	128985	CCCGCTGCTGACGCTGGGTG
130899	128986	GCCCGCTGCTGACGCTGGGT
130900	128987	GGCCCGCTGCTGACGCTGGG
130901	128988	GGGCCCGCTGCTGACGCTGG
130902	128989	TGGGCCCGCTGCTGACGCTG
130903	128990	GTGGGCCCGCTGCTGACGCT
130904	128991	GGTGGGCCCGCTGCTGACGC
130905	128992	CGGTGGGCCCGCTGCTGACG
130906	128993	TCGGTGGGCCCGCTGCTGAC
130907	128994	ATCGGTGGGCCCGCTGCTGA
130908	128995	AATCGGTGGGCCCGCTGCTG
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130910	128997	GCAATCGGTGGGCCCGCTGC
130911	128998	TGCAATCGGTGGGCCCGCTG
130912	128999	CTGCAATCGGTGGGCCCGCT
130913	129000	GCTGCAATCGGTGGGCCCGC
130914	129001	GGCTGCAATCGGTGGGCCCG
130915	129002	TGGCTGCAATCGGTGGGCCC
130916	129003	GTGGCTGCAATCGGTGGGCC
130917	129004	GGTGGCTGCAATCGGTGGGC
130918	129005	GGGTGGCTGCAATCGGTGGG
130919	129006	GGGGTGGCTGCAATCGGTGG
130920	129007	TGGGGTGGCTGCAATCGGTG
130921	129008	GTGGGGTGGCTGCAATCGGT
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130923	129010	TGGTGGGGTGGCTGCAATCG
130924	129011	CTGGTGGGGTGGCTGCAATC
130925	129012	GCTGGTGGGGTGGCTGCAAT
130926	129013	AGCTGGTGGGGTGGCTGCAA
130927	129014	AAGCTGGTGGGGTGGCTGCA
130928	129015	TAAGCTGGTGGGGTGGCTGC
130929	129016	GTAAGCTGGTGGGGTGGCTG
130930	129017	AGTAAGCTGGTGGGGTGGCT
130931	129018	GAGTAAGCTGGTGGGGTGGC
130932	129019	GGAGTAAGCTGGTGGGGTGG
130933	129020	TGGAGTAAGCTGGTGGGGTG
130934	129021	GTGGAGTAAGCTGGTGGGGT
130935	129022	CGTGGAGTAAGCTGGTGGGG
130936	129023	GCGTGGAGTAAGCTGGTGGG
130937	129024	TGCGTGGAGTAAGCTGGTGG
130938	129025	TTGCGTGGAGTAAGCTGGTG
130939	129026	ATTGCGTGGAGTAAGCTGGT
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130941	129028	ATATTGCGTGGAGTAAGCTG
130942	129029	CATATTGCGTGGAGTAAGCT
130943	129030	ACATATTGCGTGGAGTAAGC
130944	129031	AACATATTGCGTGGAGTAAG
130945	129032	CAACATATTGCGTGGAGTAA
130946	129033	GCAACATATTGCGTGGAGTA
130947	129034	GGCAACATATTGCGTGGAGT

32654	30741	TCCCTAAAAAGTTGAGTCAA
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32656	30743	TCTCCCTAAAAAGTTGAGTC
32657	30744	TTCTCCCTAAAAAGTTGAGT
32658	30745	TTTCTCCCTAAAAAGTTGAG
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32660	30747	ATTTTCTCCCTAAAAAGTTG
32661	30748	TATTTTCTCCCTAAAAAGTT
32662	30749	ATATTTTCTCCCTAAAAAGT
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32664	30751	GAATATTTTCTCCCTAAAAA
32665	30752	TGAATATTTTCTCCCTAAAA
32666	30753	TTGAATATTTTCTCCCTAAA
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32668	30755	TATTGAATATTTTCTCCCTA
32669	30756	GTATTGAATATTTTCTCCCT
32670	30757	CGTATTGAATATTTTCTCCC
32671	30758	ACGTATTGAATATTTTCTCC
32672	30759	CACGTATTGAATATTTTCTC
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32674	30761	ACCACGTATTGAATATTTTC
32675	30762	TACCACGTATTGAATATTTT
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32677	30764	TATACCACGTATTGAATATT
32678	30765	CTATACCACGTATTGAATAT
32679	30766	CCTATACCACGTATTGAATA
32680	30767	TCCTATACCACGTATTGAAT
32681	30768	ATCCTATACCACGTATTGAA
32682	30769	AATCCTATACCACGTATTGA
32683	30770	AAATCCTATACCACGTATTG
32684	30771	GAAATCCTATACCACGTATT
32685	30772	GGAAATCCTATACCACGTAT
32686	30773	GGGAAATCCTATACCACGTA
32687	30774	AGGGAAATCCTATACCACGT
32688	30775	AAGGGAAATCCTATACCACG
32689	30776	AAAGGGAAATCCTATACCAC
32690	30777	GAAAGGGAAATCCTATACCA
32691	30778	AGAAAGGGAAATCCTATACC
32692	30779	TAGAAAGGGAAATCCTATAC
32693	30780	TTAGAAAGGGAAATCCTATA
32694	30781	ATTAGAAAGGGAAATCCTAT
32695	30782	TATTAGAAAGGGAAATCCTA
32696	30783	TTATTAGAAAGGGAAATCCT
32697	30784	ATTATTAGAAAGGGAAATCC
32698	30785	TATTATTAGAAAGGGAAATC
32699	30786	TTATTATTAGAAAGGGAAAT
32700	30787	ATTATTATTAGAAAGGGAAA
32701	30788	CATTATTATTAGAAAGGGAA
32702	30789	ACATTATTATTAGAAAGGGA
32703	30790	TACATTATTATTAGAAAGGG
32704	30791	TTACATTATTATTAGAAAGG
32705	30792	TTTACATTATTATTAGAAAG
32706	30793	GTTTACATTATTATTAGAAA
32707	30794	TGTTTACATTATTATTAGAA
32708	30795	TTGTTTACATTATTATTAGA
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32710	30797	TGTTGTTTACATTATTATTA
32711	30798	TTGTTGTTTACATTATTATT
32712	30799	GTTGTTGTTTACATTATTAT
32713	30800	TGTTGTTGTTTACATTATTA
32714	30801	TTGTTGTTGTTTACATTATT
32715	30802	CTTGTTGTTGTTTACATTAT
32716	30803	TCTTGTTGTTGTTTACATTA
32717	30804	TTCTTGTTGTTGTTTACATT
32718	30805	CTTCTTGTTGTTGTTTACAT
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32720	30807	GACTTCTTGTTGTTGTTTAC
32721	30808	AGACTTCTTGTTGTTGTTTA
32722	30809	CAGACTTCTTGTTGTTGTTT
32723	30810	TCAGACTTCTTGTTGTTGTT
32724	30811	TTCAGACTTCTTGTTGTTGT

81801	79888	ATTCTCTACCTAAGCTATAT
81802	79889	CATTCTCTACCTAAGCTATA
81803	79890	GCATTCTCTACCTAAGCTAT
81804	79891	TGCATTCTCTACCTAAGCTA
81805	79892	TTGCATTCTCTACCTAAGCT
81806	79893	CTTGCATTCTCTACCTAAGC
81807	79894	ACTTGCATTCTCTACCTAAG
81808	79895	TACTTGCATTCTCTACCTAA
81809	79896	CTACTTGCATTCTCTACCTA
81810	79897	TCTACTTGCATTCTCTACCT
81811	79898	TTCTACTTGCATTCTCTACC
81812	79899	ATTCTACTTGCATTCTCTAC
81813	79900	AATTCTACTTGCATTCTCTA
81814	79901	CAATTCTACTTGCATTCTCT
81815	79902	CCAATTCTACTTGCATTCTC
81816	79903	ACCAATTCTACTTGCATTCT
81817	79904	AACCAATTCTACTTGCATTC
81818	79905	AAACCAATTCTACTTGCATT
81819	79906	TAAACCAATTCTACTTGCAT
81820	79907	TTAAACCAATTCTACTTGCA
81821	79908	CTTAAACCAATTCTACTTGC
81822	79909	TCTTAAACCAATTCTACTTG
81823	79910	ATCTTAAACCAATTCTACTT
81824	79911	GATCTTAAACCAATTCTACT
81825	79912	AGATCTTAAACCAATTCTAC
81826	79913	CAGATCTTAAACCAATTCTA
81827	79914	ACAGATCTTAAACCAATTCT
81828	79915	AACAGATCTTAAACCAATTC
81829	79916	TAACAGATCTTAAACCAATT
81830	79917	CTAACAGATCTTAAACCAAT
81831	79918	TCTAACAGATCTTAAACCAA
81832	79919	CTCTAACAGATCTTAAACCA
81833	79920	TCTCTAACAGATCTTAAACC
81834	79921	TTCTCTAACAGATCTTAAAC
81835	79922	TTTCTCTAACAGATCTTAAA
81836	79923	TTTTCTCTAACAGATCTTAA
81837	79924	CTTTTCTCTAACAGATCTTA
81838	79925	CCTTTTCTCTAACAGATCTT
81839	79926	ACCTTTTCTCTAACAGATCT
81840	79927	AACCTTTTCTCTAACAGATC
81841	79928	TAACCTTTTCTCTAACAGAT
81842	79929	ATAACCTTTTCTCTAACAGA
81843	79930	CATAACCTTTTCTCTAACAG
81844	79931	CCATAACCTTTTCTCTAACA
81845	79932	ACCATAACCTTTTCTCTAAC
81846	79933	CACCATAACCTTTTCTCTAA
81847	79934	TCACCATAACCTTTTCTCTA
81848	79935	ATCACCATAACCTTTTCTCT
81849	79936	GATCACCATAACCTTTTCTC
81850	79937	AGATCACCATAACCTTTTCT
81851	79938	AAGATCACCATAACCTTTTC
81852	79939	CAAGATCACCATAACCTTTT
81853	79940	CCAAGATCACCATAACCTTT
81854	79941	TCCAAGATCACCATAACCTT
81855	79942	TTCCAAGATCACCATAACCT
81856	79943	TTTCCAAGATCACCATAACC
81857	79944	TTTTCCAAGATCACCATAAC
81858	79945	ATTTTCCAAGATCACCATAA
81859	79946	TATTTTCCAAGATCACCATA
81860	79947	ATATTTTCCAAGATCACCAT
81861	79948	CATATTTTCCAAGATCACCA
81862	79949	GCATATTTTCCAAGATCACC
81863	79950	AGCATATTTTCCAAGATCAC
81864	79951	AAGCATATTTTCCAAGATCA
81865	79952	AAAGCATATTTTCCAAGATC
81866	79953	AAAAGCATATTTTCCAAGAT
81867	79954	CAAAAGCATATTTTCCAAGA
81868	79955	TCAAAAGCATATTTTCCAAG
81869	79956	CTCAAAAGCATATTTTCCAA
81870	79957	TCTCAAAAGCATATTTTCCA
81871	79958	CTCTCAAAAGCATATTTTCC

130948	129035	AGGCAACATATTGCGTGGAG
130949	129036	TAGGCAACATATTGCGTGGA
130950	129037	GTAGGCAACATATTGCGTGG
130951	129038	TGTAGGCAACATATTGCGTG
130952	129039	CTGTAGGCAACATATTGCGT
130953	129040	ACTGTAGGCAACATATTGCG
130954	129041	GACTGTAGGCAACATATTGC
130955	129042	GGACTGTAGGCAACATATTG
130956	129043	AGGACTGTAGGCAACATATT
130957	129044	GAGGACTGTAGGCAACATAT
130958	129045	TGAGGACTGTAGGCAACATA
130959	129046	CTGAGGACTGTAGGCAACAT
130960	129047	GCTGAGGACTGTAGGCAACA
130961	129048	TGCTGAGGACTGTAGGCAAC
130962	129049	CTGCTGAGGACTGTAGGCAA
130963	129050	ACTGCTGAGGACTGTAGGCA
130964	129051	AACTGCTGAGGACTGTAGGC
130965	129052	GAACTGCTGAGGACTGTAGG
130966	129053	GGAACTGCTGAGGACTGTAG
130967	129054	GGGAACTGCTGAGGACTGTA
130968	129055	TGGGAACTGCTGAGGACTGT
130969	129056	TTGGGAACTGCTGAGGACTG
130970	129057	TTTGGGAACTGCTGAGGACT
130971	129058	ATTTGGGAACTGCTGAGGAC
130972	129059	GATTTGGGAACTGCTGAGGA
130973	129060	TGATTTGGGAACTGCTGAGG
130974	129061	CTGATTTGGGAACTGCTGAG
130975	129062	GCTGATTTGGGAACTGCTGA
130976	129063	GGCTGATTTGGGAACTGCTG
130977	129064	GGGCTGATTTGGGAACTGCT
130978	129065	GGGGCTGATTTGGGAACTGC
130979	129066	AGGGGCTGATTTGGGAACTG
130980	129067	AAGGGGCTGATTTGGGAACT
130981	129068	CAAGGGGCTGATTTGGGAAC
130982	129069	ACAAGGGGCTGATTTGGGAA
130983	129070	AACAAGGGGCTGATTTGGGA
130984	129071	GAACAAGGGGCTGATTTGGG
130985	129072	TGAACAAGGGGCTGATTTGG
130986	129073	CTGAACAAGGGGCTGATTTG
130987	129074	GCTGAACAAGGGGCTGATTT
130988	129075	TGCTGAACAAGGGGCTGATT
130989	129076	ATGCTGAACAAGGGGCTGAT
130990	129077	CATGCTGAACAAGGGGCTGA
130991	129078	ACATGCTGAACAAGGGGCTG
130992	129079	CACATGCTGAACAAGGGGCT
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130999	129086	AATGTGGCACATGCTGAACA
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131001	129088	ATAATGTGGCACATGCTGAA
131002	129089	GATAATGTGGCACATGCTGA
131003	129090	TGATAATGTGGCACATGCTG
131004	129091	CTGATAATGTGGCACATGCT
131005	129092	ACTGATAATGTGGCACATGC
131006	129093	GACTGATAATGTGGCACATG
131007	129094	AGACTGATAATGTGGCACAT
131008	129095	GAGACTGATAATGTGGCACA
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131010	129097	CTGAGACTGATAATGTGGCA
131011	129098	CCTGAGACTGATAATGTGGC
131012	129099	ACCTGAGACTGATAATGTGG
131013	129100	TACCTGAGACTGATAATGTG
131014	129101	TTACCTGAGACTGATAATGT
131015	129102	CTTACCTGAGACTGATAATG
131016	129103	CCTTACCTGAGACTGATAAT
131017	129104	GCCTTACCTGAGACTGATAA
131018	129105	AGCCTTACCTGAGACTGATA

32725	30812	TTTCAGACTTCTTGTTGTTG
32726	30813	ATTTCAGACTTCTTGTTGTT
32727	30814	AATTTCAGACTTCTTGTTGT
32728	30815	CAATTTCAGACTTCTTGTTG
32729	30816	CCAATTTCAGACTTCTTGTT
32730	30817	TCCAATTTCAGACTTCTTGT
32731	30818	TTCCAATTTCAGACTTCTTG
32732	30819	CTTCCAATTTCAGACTTCTT
32733	30820	TCTTCCAATTTCAGACTTCT
32734	30821	TTCTTCCAATTTCAGACTTC
32735	30822	GTTCTTCCAATTTCAGACTT
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32737	30824	TTGTTCTTCCAATTTCAGAC
32738	30825	TTTGTTCTTCCAATTTCAGA
32739	30826	TTTTGTTCTTCCAATTTCAG
32740	30827	ATTTTGTTCTTCCAATTTCA
32741	30828	CATTTTGTTCTTCCAATTTC
32742	30829	TCATTTTGTTCTTCCAATTT
32743	30830	GTCATTTTGTTCTTCCAATT
32744	30831	AGTCATTTTGTTCTTCCAAT
32745	30832	GAGTCATTTTGTTCTTCCAA
32746	30833	TGAGTCATTTTGTTCTTCCA
32747	30834	GTGAGTCATTTTGTTCTTCC
32748	30835	GGTGAGTCATTTTGTTCTTC
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32750	30837	TAGGTGAGTCATTTTGTTCT
32751	30838	TTAGGTGAGTCATTTTGTTC
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32753	30840	ACTTAGGTGAGTCATTTTGT
32754	30841	CACTTAGGTGAGTCATTTTG
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32757	30844	ACTCACTTAGGTGAGTCATT
32758	30845	AACTCACTTAGGTGAGTCAT
32759	30846	TAACTCACTTAGGTGAGTCA
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32761	30848	GTTAACTCACTTAGGTGAGT
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32763	30850	AGGTTAACTCACTTAGGTGA
32764	30851	AAGGTTAACTCACTTAGGTG
32765	30852	TAAGGTTAACTCACTTAGGT
32766	30853	TTAAGGTTAACTCACTTAGG
32767	30854	CTTAAGGTTAACTCACTTAG
32768	30855	TCTTAAGGTTAACTCACTTA
32769	30856	CTCTTAAGGTTAACTCACTT
32770	30857	CCTCTTAAGGTTAACTCACT
32771	30858	ACCTCTTAAGGTTAACTCAC
32772	30859	CACCTCTTAAGGTTAACTCA
32773	30860	CCACCTCTTAAGGTTAACTC
32774	30861	TCCACCTCTTAAGGTTAACT
32775	30862	TTCCACCTCTTAAGGTTAAC
32776	30863	GTTCCACCTCTTAAGGTTAA
32777	30864	AGTTCCACCTCTTAAGGTTA
32778	30865	AAGTTCCACCTCTTAAGGTT
32779	30866	CAAGTTCCACCTCTTAAGGT
32780	30867	TCAAGTTCCACCTCTTAAGG
32781	30868	ATCAAGTTCCACCTCTTAAG
32782	30869	AATCAAGTTCCACCTCTTAA
32783	30870	AAATCAAGTTCCACCTCTTA
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32786	30873	TAGAAATCAAGTTCCACCTC
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32788	30875	TCTAGAAATCAAGTTCCACC
32789	30876	ATCTAGAAATCAAGTTCCAC
32790	30877	AATCTAGAAATCAAGTTCCA
32791	30878	AAATCTAGAAATCAAGTTCC
32792	30879	AAAATCTAGAAATCAAGTTC
32793	30880	TAAAATCTAGAAATCAAGTT
32794	30881	CTAAAATCTAGAAATCAAGT
32795	30882	ACTAAAATCTAGAAATCAAG

81872	79959	ACTCTCAAAAGCATATTTTC
81873	79960	TACTCTCAAAAGCATATTTT
81874	79961	TTACTCTCAAAAGCATATTT
81875	79962	CTTACTCTCAAAAGCATATT
81876	79963	GCTTACTCTCAAAAGCATAT
81877	79964	AGCTTACTCTCAAAAGCATA
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81879	79966	AGAGCTTACTCTCAAAAGCA
81880	79967	CAGAGCTTACTCTCAAAAGC
81881	79968	ACAGAGCTTACTCTCAAAAG
81882	79969	CACAGAGCTTACTCTCAAAA
81883	79970	CCACAGAGCTTACTCTCAAA
81884	79971	TCCACAGAGCTTACTCTCAA
81885	79972	CTCCACAGAGCTTACTCTCA
81886	79973	GCTCCACAGAGCTTACTCTC
81887	79974	GGCTCCACAGAGCTTACTCT
81888	79975	TGGCTCCACAGAGCTTACTC
81889	79976	TTGGCTCCACAGAGCTTACT
81890	79977	CTTGGCTCCACAGAGCTTAC
81891	79978	ACTTGGCTCCACAGAGCTTA
81892	79979	CACTTGGCTCCACAGAGCTT
81893	79980	ACACTTGGCTCCACAGAGCT
81894	79981	AACACTTGGCTCCACAGAGC
81895	79982	CAACACTTGGCTCCACAGAG
81896	79983	CCAACACTTGGCTCCACAGA
81897	79984	ACCAACACTTGGCTCCACAG
81898	79985	TACCAACACTTGGCTCCACA
81899	79986	ATACCAACACTTGGCTCCAC
81900	79987	TATACCAACACTTGGCTCCA
81901	79988	ATATACCAACACTTGGCTCC
81902	79989	GATATACCAACACTTGGCTC
81903	79990	TGATATACCAACACTTGGCT
81904	79991	GTGATATACCAACACTTGGC
81905	79992	CGTGATATACCAACACTTGG
81906	79993	CCGTGATATACCAACACTTG
81907	79994	ACCGTGATATACCAACACTT
81908	79995	CACCGTGATATACCAACACT
81909	79996	TCACCGTGATATACCAACAC
81910	79997	CTCACCGTGATATACCAACA
81911	79998	GCTCACCGTGATATACCAAC
81912	79999	TGCTCACCGTGATATACCAA
81913	80000	TTGCTCACCGTGATATACCA
81914	80001	ATTGCTCACCGTGATATACC
81915	80002	GATTGCTCACCGTGATATAC
81916	80003	GGATTGCTCACCGTGATATA
81917	80004	TGGATTGCTCACCGTGATAT
81918	80005	TTGGATTGCTCACCGTGATA
81919	80006	CTTGGATTGCTCACCGTGAT
81920	80007	TCTTGGATTGCTCACCGTGA
81921	80008	ATCTTGGATTGCTCACCGTG
81922	80009	GATCTTGGATTGCTCACCGT
81923	80010	AGATCTTGGATTGCTCACCG
81924	80011	AAGATCTTGGATTGCTCACC
81925	80012	CAAGATCTTGGATTGCTCAC
81926	80013	TCAAGATCTTGGATTGCTCA
81927	80014	TTCAAGATCTTGGATTGCTC
81928	80015	CTTCAAGATCTTGGATTGCT
81929	80016	TCTTCAAGATCTTGGATTGC
81930	80017	CTCTTCAAGATCTTGGATTG
81931	80018	GCTCTTCAAGATCTTGGATT
81932	80019	AGCTCTTCAAGATCTTGGAT
81933	80020	AAGCTCTTCAAGATCTTGGA
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81935	80022	ACAAGCTCTTCAAGATCTTG
81936	80023	AACAAGCTCTTCAAGATCTT
81937	80024	TAACAAGCTCTTCAAGATCT
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81939	80026	TTTAACAAGCTCTTCAAGAT
81940	80027	TTTTAACAAGCTCTTCAAGA
81941	80028	ATTTTAACAAGCTCTTCAAG
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131019	129106	CAGCCTTACCTGAGACTGAT
131020	129107	CCAGCCTTACCTGAGACTGA
131021	129108	ACCAGCCTTACCTGAGACTG
131022	129109	TACCAGCCTTACCTGAGACT
131023	129110	TTACCAGCCTTACCTGAGAC
131024	129111	CTTACCAGCCTTACCTGAGA
131025	129112	CCTTACCAGCCTTACCTGAG
131026	129113	GCCTTACCAGCCTTACCTGA
131027	129114	GGCCTTACCAGCCTTACCTG
131028	129115	AGGCCTTACCAGCCTTACCT
131029	129116	TAGGCCTTACCAGCCTTACC
131030	129117	TTAGGCCTTACCAGCCTTAC
131031	129118	GTTAGGCCTTACCAGCCTTA
131032	129119	AGTTAGGCCTTACCAGCCTT
131033	129120	GAGTTAGGCCTTACCAGCCT
131034	129121	AGAGTTAGGCCTTACCAGCC
131035	129122	AAGAGTTAGGCCTTACCAGC
131036	129123	TAAGAGTTAGGCCTTACCAG
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131038	129125	ATTAAGAGTTAGGCCTTACC
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131040	129127	AAATTAAGAGTTAGGCCTTA
131041	129128	AAAATTAAGAGTTAGGCCTT
131042	129129	AAAAATTAAGAGTTAGGCCT
131043	129130	CAAAAATTAAGAGTTAGGCC
131044	129131	ACAAAAATTAAGAGTTAGGC
131045	129132	TACAAAAATTAAGAGTTAGG
131046	129133	GTACAAAAATTAAGAGTTAG
131047	129134	GGTACAAAAATTAAGAGTTA
131048	129135	TGGTACAAAAATTAAGAGTT
131049	129136	ATGGTACAAAAATTAAGAGT
131050	129137	TATGGTACAAAAATTAAGAG
131051	129138	ATATGGTACAAAAATTAAGA
131052	129139	TATATGGTACAAAAATTAAG
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131054	129141	TTTATATGGTACAAAAATTA
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131056	129143	TTTTTATATGGTACAAAAAT
131057	129144	TTTTTTATATGGTACAAAAA
131058	129145	TTTTTTTATATGGTACAAAA
131059	129146	GTTTTTTTATATGGTACAAA
131060	129147	AGTTTTTTTATATGGTACAA
131061	129148	AAGTTTTTTTATATGGTACA
131062	129149	AAAGTTTTTTTATATGGTAC
131063	129150	AAAAGTTTTTTTATATGGTA
131064	129151	TAAAAGTTTTTTTATATGGT
131065	129152	TTAAAAGTTTTTTTATATGG
131066	129153	ATTAAAAGTTTTTTTATATG
131067	129154	TATTAAAAGTTTTTTTATAT
131068	129155	ATATTAAAAGTTTTTTTATA
131069	129156	CATATTAAAAGTTTTTTTAT
131070	129157	CCATATTAAAAGTTTTTTTA
131071	129158	ACCATATTAAAAGTTTTTTT
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131073	129160	TTACCATATTAAAAGTTTTT
131074	129161	TTTACCATATTAAAAGTTTT
131075	129162	CTTTACCATATTAAAAGTTT
131076	129163	CCTTTACCATATTAAAAGTT
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131078	129165	TCCCTTTACCATATTAAAAG
131079	129166	ATCCCTTTACCATATTAAAA
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131082	129169	AAAATCCCTTTACCATATTA
131083	129170	GAAAATCCCTTTACCATATT
131084	129171	GGAAAATCCCTTTACCATAT
131085	129172	AGGAAAATCCCTTTACCATA
131086	129173	AAGGAAAATCCCTTTACCAT
131087	129174	AAAGGAAAATCCCTTTACCA
131088	129175	TAAAGGAAAATCCCTTTACC
131089	129176	ATAAAGGAAAATCCCTTTAC

32796	30883	AACTAAAATCTAGAAATCAA
32797	30884	TAACTAAAATCTAGAAATCA
32798	30885	TTAACTAAAATCTAGAAATC
32799	30886	ATTAACTAAAATCTAGAAAT
32800	30887	AATTAACTAAAATCTAGAAA
32801	30888	CAATTAACTAAAATCTAGAA
32802	30889	ACAATTAACTAAAATCTAGA
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32804	30891	AGACAATTAACTAAAATCTA
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32806	30893	TTAGACAATTAACTAAAATC
32807	30894	GTTAGACAATTAACTAAAAT
32808	30895	AGTTAGACAATTAACTAAAA
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32810	30897	TCAGTTAGACAATTAACTAA
32811	30898	ATCAGTTAGACAATTAACTA
32812	30899	CATCAGTTAGACAATTAACT
32813	30900	ACATCAGTTAGACAATTAAC
32814	30901	TACATCAGTTAGACAATTAA
32815	30902	GTACATCAGTTAGACAATTA
32816	30903	AGTACATCAGTTAGACAATT
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32818	30905	TTAGTACATCAGTTAGACAA
32819	30906	TTTAGTACATCAGTTAGACA
32820	30907	ATTTAGTACATCAGTTAGAC
32821	30908	TATTTAGTACATCAGTTAGA
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32823	30910	AATATTTAGTACATCAGTTA
32824	30911	TAATATTTAGTACATCAGTT
32825	30912	CTAATATTTAGTACATCAGT
32826	30913	ACTAATATTTAGTACATCAG
32827	30914	AACTAATATTTAGTACATCA
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32833	30920	TTAAGTAACTAATATTTAGT
32834	30921	CTTAAGTAACTAATATTTAG
32835	30922	ACTTAAGTAACTAATATTTA
32836	30923	TACTTAAGTAACTAATATTT
32837	30924	ATACTTAAGTAACTAATATT
32838	30925	AATACTTAAGTAACTAATAT
32839	30926	TAATACTTAAGTAACTAATA
32840	30927	TTAATACTTAAGTAACTAAT
32841	30928	TTTAATACTTAAGTAACTAA
32842	30929	TTTTAATACTTAAGTAACTA
32843	30930	GTTTTAATACTTAAGTAACT
32844	30931	CGTTTTAATACTTAAGTAAC
32845	30932	CCGTTTTAATACTTAAGTAA
32846	30933	CCCGTTTTAATACTTAAGTA
32847	30934	ACCCGTTTTAATACTTAAGT
32848	30935	TACCCGTTTTAATACTTAAG
32849	30936	CTACCCGTTTTAATACTTAA
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32855	30942	TTATGTCTACCCGTTTTAAT
32856	30943	ATTATGTCTACCCGTTTTAA
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32859	30946	ACTATTATGTCTACCCGTTT
32860	30947	AACTATTATGTCTACCCGTT
32861	30948	CAACTATTATGTCTACCCGT
32862	30949	CCAACTATTATGTCTACCCG
32863	30950	CCCAACTATTATGTCTACCC
32864	30951	CCCCAACTATTATGTCTACC
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81943	80030	CTATTTTAACAAGCTCTTCA
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81946	80033	TAACTATTTTAACAAGCTCT
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81949	80036	AGATAACTATTTTAACAAGC
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81959	80046	GTCCCCCACCAGATAACTAT
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81982	80069	GTACTGCTGTGATTGTTACA
81983	80070	TGTACTGCTGTGATTGTTAC
81984	80071	TTGTACTGCTGTGATTGTTA
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81993	80080	CAAATCATATTGTACTGCTG
81994	80081	GCAAATCATATTGTACTGCT
81995	80082	AGCAAATCATATTGTACTGC
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81997	80084	CAAGCAAATCATATTGTACT
81998	80085	CCAAGCAAATCATATTGTAC
81999	80086	ACCAAGCAAATCATATTGTA
82000	80087	AACCAAGCAAATCATATTGT
82001	80088	TAACCAAGCAAATCATATTG
82002	80089	TTAACCAAGCAAATCATATT
82003	80090	TTTAACCAAGCAAATCATAT
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82007	80094	TGCCTTTAACCAAGCAAATC
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82010	80097	ACATGCCTTTAACCAAGCAA
82011	80098	AACATGCCTTTAACCAAGCA
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131090	129177	TATAAAGGAAAATCCCTTTA
131091	129178	TTATAAAGGAAAATCCCTTT
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131093	129180	AATTATAAAGGAAAATCCCT
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131096	129183	AAAAATTATAAAGGAAAATC
131097	129184	CAAAAATTATAAAGGAAAAT
131098	129185	GCAAAAATTATAAAGGAAAA
131099	129186	AGCAAAAATTATAAAGGAAA
131100	129187	AAGCAAAAATTATAAAGGAA
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131102	129189	AAAAGCAAAAATTATAAAGG
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131104	129191	ACAAAAGCAAAAATTATAAA
131105	129192	CACAAAAGCAAAAATTATAA
131106	129193	ACACAAAAGCAAAAATTATA
131107	129194	CACACAAAAGCAAAAATTAT
131108	129195	TCACACAAAAGCAAAAATTA
131109	129196	ATCACACAAAAGCAAAAATT
131110	129197	CATCACACAAAAGCAAAAAT
131111	129198	CCATCACACAAAAGCAAAAA
131112	129199	ACCATCACACAAAAGCAAAA
131113	129200	TACCATCACACAAAAGCAAA
131114	129201	CTACCATCACACAAAAGCAA
131115	129202	CCTACCATCACACAAAAGCA
131116	129203	CCCTACCATCACACAAAAGC
131117	129204	ACCCTACCATCACACAAAAG
131118	129205	TACCCTACCATCACACAAAA
131119	129206	CTACCCTACCATCACACAAA
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131121	129208	ATCTACCCTACCATCACACA
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131123	129210	CTATCTACCCTACCATCACA
131124	129211	GCTATCTACCCTACCATCAC
131125	129212	AGCTATCTACCCTACCATCA
131126	129213	TAGCTATCTACCCTACCATC
131127	129214	TTAGCTATCTACCCTACCAT
131128	129215	CTTAGCTATCTACCCTACCA
131129	129216	CCTTAGCTATCTACCCTACC
131130	129217	TCCTTAGCTATCTACCCTAC
131131	129218	GTCCTTAGCTATCTACCCTA
131132	129219	AGTCCTTAGCTATCTACCCT
131133	129220	AAGTCCTTAGCTATCTACCC
131134	129221	CAAGTCCTTAGCTATCTACC
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131136	129223	CCCAAGTCCTTAGCTATCTA
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131138	129225	TCCCCAAGTCCTTAGCTATC
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131140	129227	GGTCCCCAAGTCCTTAGCTA
131141	129228	GGGTCCCCAAGTCCTTAGCT
131142	129229	AGGGTCCCCAAGTCCTTAGC
131143	129230	AAGGGTCCCCAAGTCCTTAG
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131145	129232	AAAAGGGTCCCCAAGTCCTT
131146	129233	GAAAAGGGTCCCCAAGTCCT
131147	129234	TGAAAAGGGTCCCCAAGTCC
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131159	129246	TCGAATATATATTGAAAAGG
131160	129247	TTCGAATATATATTGAAAAG

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32869	30956	CAGCTCCCCAACTATTATGT
32870	30957	GCAGCTCCCCAACTATTATG
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32873	30960	ACAGCAGCTCCCCAACTATT
32874	30961	TACAGCAGCTCCCCAACTAT
32875	30962	CTACAGCAGCTCCCCAACTA
32876	30963	TCTACAGCAGCTCCCCAACT
32877	30964	CTCTACAGCAGCTCCCCAAC
32878	30965	CCTCTACAGCAGCTCCCCAA
32879	30966	CCCTCTACAGCAGCTCCCCA
32880	30967	CCCCTCTACAGCAGCTCCCC
32881	30968	CCCCCTCTACAGCAGCTCCC
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32883	30970	TACCCCCTCTACAGCAGCTC
32884	30971	CTACCCCCTCTACAGCAGCT
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32916	31003	AAATGTCACCTCCTGAAAGA
32917	31004	TAAATGTCACCTCCTGAAAG
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32931	31018	GTTAGTTACCAACTTAAATG
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32937	31024	TTTCTTGTTAGTTACCAACT

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82016	80103	CTTTGAACATGCCTTTAACC
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82018	80105	TACTTTGAACATGCCTTTAA
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82022	80109	CTAGTACTTTGAACATGCCT
82023	80110	CCTAGTACTTTGAACATGCC
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131164	129251	AACCTTCGAATATATATTGA
131165	129252	TAACCTTCGAATATATATTG
131166	129253	GTAACCTTCGAATATATATT
131167	129254	AGTAACCTTCGAATATATAT
131168	129255	CAGTAACCTTCGAATATATA
131169	129256	TCAGTAACCTTCGAATATAT
131170	129257	ATCAGTAACCTTCGAATATA
131171	129258	CATCAGTAACCTTCGAATAT
131172	129259	TCATCAGTAACCTTCGAATA
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131174	129261	AATCATCAGTAACCTTCGAA
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131182	129269	CCTCTTACAATCATCAGTAA
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131186	129273	TGAACCTCTTACAATCATCA
131187	129274	CTGAACCTCTTACAATCATC
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131191	129278	TCCTCTGAACCTCTTACAAT
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131195	129282	TGTTTCCTCTGAACCTCTTA
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131204	129291	TTTCTTGGCTGTTTCCTCTG
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131206	129293	TCTTTCTTGGCTGTTTCCTC
131207	129294	ATCTTTCTTGGCTGTTTCCT
131208	129295	AATCTTTCTTGGCTGTTTCC
131209	129296	AAATCTTTCTTGGCTGTTTC
131210	129297	CAAATCTTTCTTGGCTGTTT
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131212	129299	CTCAAATCTTTCTTGGCTGT
131213	129300	TCTCAAATCTTTCTTGGCTG
131214	129301	CTCTCAAATCTTTCTTGGCT
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131218	129305	TAAACTCTCAAATCTTTCTT
131219	129306	GTAAACTCTCAAATCTTTCT
131220	129307	TGTAAACTCTCAAATCTTTC
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131224	129311	CAGCTGTAAACTCTCAAATC
131225	129312	ACAGCTGTAAACTCTCAAAT
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131227	129314	AAACAGCTGTAAACTCTCAA
131228	129315	GAAACAGCTGTAAACTCTCA
131229	129316	AGAAACAGCTGTAAACTCTC
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32938	31025	CTTTCTTGTTAGTTACCAAC
32939	31026	CCTTTCTTGTTAGTTACCAA
32940	31027	CCCTTTCTTGTTAGTTACCA
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32943	31030	TGCCCCTTTCTTGTTAGTTA
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32998	31085	AACCCCCTTCCAGTAAAACT
32999	31086	TAACCCCCTTCCAGTAAAAC
33000	31087	CTAACCCCCTTCCAGTAAAA
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33004	31091	ACCTCTAACCCCCTTCCAGT
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82088	80175	CACCTCCTCAATGAGGTTTT
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131232	129319	TCCAGAAACAGCTGTAAACT
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131239	129326	CCAGATTTCCAGAAACAGCT
131240	129327	TCCAGATTTCCAGAAACAGC
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131243	129330	GTTTCCAGATTTCCAGAAAC
131244	129331	GGTTTCCAGATTTCCAGAAA
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131246	129333	ATGGTTTCCAGATTTCCAGA
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131256	129343	TTTTAACTCCATGGTTTCCA
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131270	129357	ACTTTAGTTAAGATTTTTAA
131271	129358	GACTTTAGTTAAGATTTTTA
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131273	129360	CAGACTTTAGTTAAGATTTT
131274	129361	GCAGACTTTAGTTAAGATTT
131275	129362	AGCAGACTTTAGTTAAGATT
131276	129363	AAGCAGACTTTAGTTAAGAT
131277	129364	CAAGCAGACTTTAGTTAAGA
131278	129365	CCAAGCAGACTTTAGTTAAG
131279	129366	GCCAAGCAGACTTTAGTTAA
131280	129367	AGCCAAGCAGACTTTAGTTA
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131282	129369	AGAGCCAAGCAGACTTTAGT
131283	129370	TAGAGCCAAGCAGACTTTAG
131284	129371	ATAGAGCCAAGCAGACTTTA
131285	129372	AATAGAGCCAAGCAGACTTT
131286	129373	AAATAGAGCCAAGCAGACTT
131287	129374	CAAATAGAGCCAAGCAGACT
131288	129375	GCAAATAGAGCCAAGCAGAC
131289	129376	TGCAAATAGAGCCAAGCAGA
131290	129377	CTGCAAATAGAGCCAAGCAG
131291	129378	ACTGCAAATAGAGCCAAGCA
131292	129379	CACTGCAAATAGAGCCAAGC
131293	129380	ACACTGCAAATAGAGCCAAG
131294	129381	AACACTGCAAATAGAGCCAA
131295	129382	TAACACTGCAAATAGAGCCA
131296	129383	TTAACACTGCAAATAGAGCC
131297	129384	ATTAACACTGCAAATAGAGC
131298	129385	CATTAACACTGCAAATAGAG
131299	129386	ACATTAACACTGCAAATAGA
131300	129387	CACATTAACACTGCAAATAG
131301	129388	GCACATTAACACTGCAAATA
131302	129389	AGCACATTAACACTGCAAAT

33009	31096	CACATACCTCTAACCCCCTT
33010	31097	CCACATACCTCTAACCCCCT
33011	31098	ACCACATACCTCTAACCCCC
33012	31099	TACCACATACCTCTAACCCC
33013	31100	GTACCACATACCTCTAACCC
33014	31101	GGTACCACATACCTCTAACC
33015	31102	GGGTACCACATACCTCTAAC
33016	31103	AGGGTACCACATACCTCTAA
33017	31104	AAGGGTACCACATACCTCTA
33018	31105	TAAGGGTACCACATACCTCT
33019	31106	ATAAGGGTACCACATACCTC
33020	31107	CATAAGGGTACCACATACCT
33021	31108	GCATAAGGGTACCACATACC
33022	31109	GGCATAAGGGTACCACATAC
33023	31110	TGGCATAAGGGTACCACATA
33024	31111	TTGGCATAAGGGTACCACAT
33025	31112	TTTGGCATAAGGGTACCACA
33026	31113	CTTTGGCATAAGGGTACCAC
33027	31114	TCTTTGGCATAAGGGTACCA
33028	31115	TTCTTTGGCATAAGGGTACC
33029	31116	TTTCTTTGGCATAAGGGTAC
33030	31117	TTTTCTTTGGCATAAGGGTA
33031	31118	ATTTTCTTTGGCATAAGGGT
33032	31119	AATTTTCTTTGGCATAAGGG
33033	31120	TAATTTTCTTTGGCATAAGG
33034	31121	CTAATTTTCTTTGGCATAAG
33035	31122	ACTAATTTTCTTTGGCATAA
33036	31123	AACTAATTTTCTTTGGCATA
33037	31124	TAACTAATTTTCTTTGGCAT
33038	31125	GTAACTAATTTTCTTTGGCA
33039	31126	AGTAACTAATTTTCTTTGGC
33040	31127	AAGTAACTAATTTTCTTTGG
33041	31128	GAAGTAACTAATTTTCTTTG
33042	31129	AGAAGTAACTAATTTTCTTT
33043	31130	TAGAAGTAACTAATTTTCTT
33044	31131	ATAGAAGTAACTAATTTTCT
33045	31132	TATAGAAGTAACTAATTTTC
33046	31133	GTATAGAAGTAACTAATTTT
33047	31134	TGTATAGAAGTAACTAATTT
33048	31135	TTGTATAGAAGTAACTAATT
33049	31136	GTTGTATAGAAGTAACTAAT
33050	31137	GGTTGTATAGAAGTAACTAA
33051	31138	TGGTTGTATAGAAGTAACTA
33052	31139	CTGGTTGTATAGAAGTAACT
33053	31140	ACTGGTTGTATAGAAGTAAC
33054	31141	GACTGGTTGTATAGAAGTAA
33055	31142	AGACTGGTTGTATAGAAGTA
33056	31143	CAGACTGGTTGTATAGAAGT
33057	31144	TCAGACTGGTTGTATAGAAG
33058	31145	ATCAGACTGGTTGTATAGAA
33059	31146	AATCAGACTGGTTGTATAGA
33060	31147	GAATCAGACTGGTTGTATAG
33061	31148	AGAATCAGACTGGTTGTATA
33062	31149	TAGAATCAGACTGGTTGTAT
33063	31150	CTAGAATCAGACTGGTTGTA
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33070	31157	CAGGTTTCTAGAATCAGACT
33071	31158	CCAGGTTTCTAGAATCAGAC
33072	31159	TCCAGGTTTCTAGAATCAGA
33073	31160	ATCCAGGTTTCTAGAATCAG
33074	31161	GATCCAGGTTTCTAGAATCA
33075	31162	TGATCCAGGTTTCTAGAATC
33076	31163	TTGATCCAGGTTTCTAGAAT
33077	31164	ATTGATCCAGGTTTCTAGAA
33078	31165	CATTGATCCAGGTTTCTAGA
33079	31166	TCATTGATCCAGGTTTCTAG

82156	80243	CAGGTGATAAACTCTTCTCC
82157	80244	TCAGGTGATAAACTCTTCTC
82158	80245	ATCAGGTGATAAACTCTTCT
82159	80246	CATCAGGTGATAAACTCTTC
82160	80247	TCATCAGGTGATAAACTCTT
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82163	80250	TTTTCATCAGGTGATAAACT
82164	80251	CTTTTCATCAGGTGATAAAC
82165	80252	GCTTTTCATCAGGTGATAAA
82166	80253	GGCTTTTCATCAGGTGATAA
82167	80254	TGGCTTTTCATCAGGTGATA
82168	80255	ATGGCTTTTCATCAGGTGAT
82169	80256	CATGGCTTTTCATCAGGTGA
82170	80257	ACATGGCTTTTCATCAGGTG
82171	80258	TACATGGCTTTTCATCAGGT
82172	80259	GTACATGGCTTTTCATCAGG
82173	80260	TGTACATGGCTTTTCATCAG
82174	80261	TTGTACATGGCTTTTCATCA
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82177	80264	TGCTTGTACATGGCTTTTCA
82178	80265	ATGCTTGTACATGGCTTTTC
82179	80266	CATGCTTGTACATGGCTTTT
82180	80267	CCATGCTTGTACATGGCTTT
82181	80268	GCCATGCTTGTACATGGCTT
82182	80269	AGCCATGCTTGTACATGGCT
82183	80270	TAGCCATGCTTGTACATGGC
82184	80271	ATAGCCATGCTTGTACATGG
82185	80272	CATAGCCATGCTTGTACATG
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82187	80274	CTCATAGCCATGCTTGTACA
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82198	80285	GGCCAAATTTTCTCATAGCC
82199	80286	TGGCCAAATTTTCTCATAGC
82200	80287	CTGGCCAAATTTTCTCATAG
82201	80288	GCTGGCCAAATTTTCTCATA
82202	80289	AGCTGGCCAAATTTTCTCAT
82203	80290	GAGCTGGCCAAATTTTCTCA
82204	80291	TGAGCTGGCCAAATTTTCTC
82205	80292	CTGAGCTGGCCAAATTTTCT
82206	80293	CCTGAGCTGGCCAAATTTTC
82207	80294	TCCTGAGCTGGCCAAATTTT
82208	80295	CTCCTGAGCTGGCCAAATTT
82209	80296	TCTCCTGAGCTGGCCAAATT
82210	80297	CTCTCCTGAGCTGGCCAAAT
82211	80298	CCTCTCCTGAGCTGGCCAAA
82212	80299	CCCTCTCCTGAGCTGGCCAA
82213	80300	GCCCTCTCCTGAGCTGGCCA
82214	80301	AGCCCTCTCCTGAGCTGGCC
82215	80302	CAGCCCTCTCCTGAGCTGGC
82216	80303	CCAGCCCTCTCCTGAGCTGG
82217	80304	ACCAGCCCTCTCCTGAGCTG
82218	80305	AACCAGCCCTCTCCTGAGCT
82219	80306	CAACCAGCCCTCTCCTGAGC
82220	80307	ACAACCAGCCCTCTCCTGAG
82221	80308	AACAACCAGCCCTCTCCTGA
82222	80309	CAACAACCAGCCCTCTCCTG
82223	80310	GCAACAACCAGCCCTCTCCT
82224	80311	TGCAACAACCAGCCCTCTCC
82225	80312	ATGCAACAACCAGCCCTCTC
82226	80313	CATGCAACAACCAGCCCTCT

131303	129390	AAGCACATTAACACTGCAAA
131304	129391	AAAGCACATTAACACTGCAA
131305	129392	GAAAGCACATTAACACTGCA
131306	129393	AGAAAGCACATTAACACTGC
131307	129394	AAGAAAGCACATTAACACTG
131308	129395	AAAGAAAGCACATTAACACT
131309	129396	TAAAGAAAGCACATTAACAC
131310	129397	ATAAAGAAAGCACATTAACA
131311	129398	AATAAAGAAAGCACATTAAC
131312	129399	AAATAAAGAAAGCACATTAA
131313	129400	AAAATAAAGAAAGCACATTA
131314	129401	AAAAATAAAGAAAGCACATT
131315	129402	AAAAAATAAAGAAAGCACAT
131316	129403	CAAAAAATAAAGAAAGCACA
131317	129404	ACAAAAAATAAAGAAAGCAC
131318	129405	AACAAAAAATAAAGAAAGCA
131319	129406	AAACAAAAAATAAAGAAAGC
131320	129407	CAAACAAAAAATAAAGAAAG
131321	129408	TCAAACAAAAAATAAAGAAA
131322	129409	TTCAAACAAAAAATAAAGAA
131323	129410	GTTCAAACAAAAAATAAAGA
131324	129411	TGTTCAAACAAAAAATAAAG
131325	129412	GTGTTCAAACAAAAAATAAA
131326	129413	TGTGTTCAAACAAAAAATAA
131327	129414	CTGTGTTCAAACAAAAAATA
131328	129415	GCTGTGTTCAAACAAAAAAT
131329	129416	TGCTGTGTTCAAACAAAAAA
131330	129417	ATGCTGTGTTCAAACAAAAA
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131332	129419	GGATGCTGTGTTCAAACAAA
131333	129420	AGGATGCTGTGTTCAAACAA
131334	129421	GAGGATGCTGTGTTCAAACA
131335	129422	TGAGGATGCTGTGTTCAAAC
131336	129423	ATGAGGATGCTGTGTTCAAA
131337	129424	CATGAGGATGCTGTGTTCAA
131338	129425	ACATGAGGATGCTGTGTTCA
131339	129426	GACATGAGGATGCTGTGTTC
131340	129427	AGACATGAGGATGCTGTGTT
131341	129428	TAGACATGAGGATGCTGTGT
131342	129429	ATAGACATGAGGATGCTGTG
131343	129430	TATAGACATGAGGATGCTGT
131344	129431	CTATAGACATGAGGATGCTG
131345	129432	ACTATAGACATGAGGATGCT
131346	129433	GACTATAGACATGAGGATGC
131347	129434	GGACTATAGACATGAGGATG
131348	129435	AGGACTATAGACATGAGGAT
131349	129436	CAGGACTATAGACATGAGGA
131350	129437	ACAGGACTATAGACATGAGG
131351	129438	TACAGGACTATAGACATGAG
131352	129439	TTACAGGACTATAGACATGA
131353	129440	ATTACAGGACTATAGACATG
131354	129441	TATTACAGGACTATAGACAT
131355	129442	GTATTACAGGACTATAGACA
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131357	129444	CTGTATTACAGGACTATAGA
131358	129445	CCTGTATTACAGGACTATAG
131359	129446	CCCTGTATTACAGGACTATA
131360	129447	ACCCTGTATTACAGGACTAT
131361	129448	TACCCTGTATTACAGGACTA
131362	129449	TTACCCTGTATTACAGGACT
131363	129450	ATTACCCTGTATTACAGGAC
131364	129451	CATTACCCTGTATTACAGGA
131365	129452	GCATTACCCTGTATTACAGG
131366	129453	AGCATTACCCTGTATTACAG
131367	129454	TAGCATTACCCTGTATTACA
131368	129455	CTAGCATTACCCTGTATTAC
131369	129456	TCTAGCATTACCCTGTATTA
131370	129457	TTCTAGCATTACCCTGTATT
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131372	129459	CATTCTAGCATTACCCTGTA
131373	129460	TCATTCTAGCATTACCCTGT

33080	31167	TTCATTGATCCAGGTTTCTA
33081	31168	TTTCATTGATCCAGGTTTCT
33082	31169	ATTTCATTGATCCAGGTTTC
33083	31170	TATTTCATTGATCCAGGTTT
33084	31171	ATATTTCATTGATCCAGGTT
33085	31172	AATATTTCATTGATCCAGGT
33086	31173	AAATATTTCATTGATCCAGG
33087	31174	AAAATATTTCATTGATCCAG
33088	31175	CAAAATATTTCATTGATCCA
33089	31176	TCAAAATATTTCATTGATCC
33090	31177	ATCAAAATATTTCATTGATC
33091	31178	AATCAAAATATTTCATTGAT
33092	31179	TAATCAAAATATTTCATTGA
33093	31180	ATAATCAAAATATTTCATTG
33094	31181	TATAATCAAAATATTTCATT
33095	31182	ATATAATCAAAATATTTCAT
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33102	31189	TTTTTTTATATAATCAAAAT
33103	31190	ATTTTTTTATATAATCAAAA
33104	31191	GATTTTTTTATATAATCAAA
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33106	31193	CAGATTTTTTTATATAATCA
33107	31194	ACAGATTTTTTTATATAATC
33108	31195	AACAGATTTTTTTATATAAT
33109	31196	TAACAGATTTTTTTATATAA
33110	31197	GTAACAGATTTTTTTATATA
33111	31198	GGTAACAGATTTTTTTATAT
33112	31199	GGGTAACAGATTTTTTTATA
33113	31200	TGGGTAACAGATTTTTTTAT
33114	31201	CTGGGTAACAGATTTTTTTA
33115	31202	CCTGGGTAACAGATTTTTTT
33116	31203	ACCTGGGTAACAGATTTTTT
33117	31204	GACCTGGGTAACAGATTTTT
33118	31205	AGACCTGGGTAACAGATTTT
33119	31206	AAGACCTGGGTAACAGATTT
33120	31207	CAAGACCTGGGTAACAGATT
33121	31208	ACAAGACCTGGGTAACAGAT
33122	31209	AACAAGACCTGGGTAACAGA
33123	31210	CAACAAGACCTGGGTAACAG
33124	31211	TCAACAAGACCTGGGTAACA
33125	31212	TTCAACAAGACCTGGGTAAC
33126	31213	TTTCAACAAGACCTGGGTAA
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33136	31223	TCTAATGCTATTTCAACAAG
33137	31224	TTCTAATGCTATTTCAACAA
33138	31225	TTTCTAATGCTATTTCAACA
33139	31226	GTTTCTAATGCTATTTCAAC
33140	31227	AGTTTCTAATGCTATTTCAA
33141	31228	TAGTTTCTAATGCTATTTCA
33142	31229	GTAGTTTCTAATGCTATTTC
33143	31230	AGTAGTTTCTAATGCTATTT
33144	31231	CAGTAGTTTCTAATGCTATT
33145	31232	TCAGTAGTTTCTAATGCTAT
33146	31233	TTCAGTAGTTTCTAATGCTA
33147	31234	CTTCAGTAGTTTCTAATGCT
33148	31235	CCTTCAGTAGTTTCTAATGC
33149	31236	TCCTTCAGTAGTTTCTAATG
33150	31237	GTCCTTCAGTAGTTTCTAAT

82227	80314	ACATGCAACAACCAGCCCTC
82228	80315	CACATGCAACAACCAGCCCT
82229	80316	ACACATGCAACAACCAGCCC
82230	80317	GACACATGCAACAACCAGCC
82231	80318	AGACACATGCAACAACCAGC
82232	80319	CAGACACATGCAACAACCAG
82233	80320	CCAGACACATGCAACAACCA
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82235	80322	TTCCAGACACATGCAACAAC
82236	80323	GTTCCAGACACATGCAACAA
82237	80324	TGTTCCAGACACATGCAACA
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82239	80326	TGTGTTCCAGACACATGCAA
82240	80327	CTGTGTTCCAGACACATGCA
82241	80328	CCTGTGTTCCAGACACATGC
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82244	80331	GATCCTGTGTTCCAGACACA
82245	80332	AGATCCTGTGTTCCAGACAC
82246	80333	CAGATCCTGTGTTCCAGACA
82247	80334	ACAGATCCTGTGTTCCAGAC
82248	80335	CACAGATCCTGTGTTCCAGA
82249	80336	ACACAGATCCTGTGTTCCAG
82250	80337	GACACAGATCCTGTGTTCCA
82251	80338	TGACACAGATCCTGTGTTCC
82252	80339	CTGACACAGATCCTGTGTTC
82253	80340	CCTGACACAGATCCTGTGTT
82254	80341	ACCTGACACAGATCCTGTGT
82255	80342	CACCTGACACAGATCCTGTG
82256	80343	GCACCTGACACAGATCCTGT
82257	80344	TGCACCTGACACAGATCCTG
82258	80345	CTGCACCTGACACAGATCCT
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82260	80347	TGCTGCACCTGACACAGATC
82261	80348	CTGCTGCACCTGACACAGAT
82262	80349	ACTGCTGCACCTGACACAGA
82263	80350	CACTGCTGCACCTGACACAG
82264	80351	CCACTGCTGCACCTGACACA
82265	80352	GCCACTGCTGCACCTGACAC
82266	80353	TGCCACTGCTGCACCTGACA
82267	80354	CTGCCACTGCTGCACCTGAC
82268	80355	ACTGCCACTGCTGCACCTGA
82269	80356	AACTGCCACTGCTGCACCTG
82270	80357	CAACTGCCACTGCTGCACCT
82271	80358	TCAACTGCCACTGCTGCACC
82272	80359	ATCAACTGCCACTGCTGCAC
82273	80360	TATCAACTGCCACTGCTGCA
82274	80361	CTATCAACTGCCACTGCTGC
82275	80362	ACTATCAACTGCCACTGCTG
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82279	80366	TCCTACTATCAACTGCCACT
82280	80367	TTCCTACTATCAACTGCCAC
82281	80368	GTTCCTACTATCAACTGCCA
82282	80369	AGTTCCTACTATCAACTGCC
82283	80370	CAGTTCCTACTATCAACTGC
82284	80371	TCAGTTCCTACTATCAACTG
82285	80372	CTCAGTTCCTACTATCAACT
82286	80373	CCTCAGTTCCTACTATCAAC
82287	80374	ACCTCAGTTCCTACTATCAA
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82292	80379	TAATGACCTCAGTTCCTACT
82293	80380	TTAATGACCTCAGTTCCTAC
82294	80381	TTTAATGACCTCAGTTCCTA
82295	80382	CTTTAATGACCTCAGTTCCT
82296	80383	CCTTTAATGACCTCAGTTCC
82297	80384	TCCTTTAATGACCTCAGTTC

131374	129461	ATCATTCTAGCATTACCCTG
131375	129462	CATCATTCTAGCATTACCCT
131376	129463	CCATCATTCTAGCATTACCC
131377	129464	GCCATCATTCTAGCATTACC
131378	129465	TGCCATCATTCTAGCATTAC
131379	129466	GTGCCATCATTCTAGCATTA
131380	129467	GGTGCCATCATTCTAGCATT
131381	129468	TGGTGCCATCATTCTAGCAT
131382	129469	GTGGTGCCATCATTCTAGCA
131383	129470	GGTGGTGCCATCATTCTAGC
131384	129471	TGGTGGTGCCATCATTCTAG
131385	129472	TTGGTGGTGCCATCATTCTA
131386	129473	GTTGGTGGTGCCATCATTCT
131387	129474	TGTTGGTGGTGCCATCATTC
131388	129475	GTGTTGGTGGTGCCATCATT
131389	129476	TGTGTTGGTGGTGCCATCAT
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131391	129478	CGTGTGTTGGTGGTGCCATC
131392	129479	GCGTGTGTTGGTGGTGCCAT
131393	129480	GGCGTGTGTTGGTGGTGCCA
131394	129481	GGGCGTGTGTTGGTGGTGCC
131395	129482	TGGGCGTGTGTTGGTGGTGC
131396	129483	CTGGGCGTGTGTTGGTGGTG
131397	129484	GCTGGGCGTGTGTTGGTGGT
131398	129485	GGCTGGGCGTGTGTTGGTGG
131399	129486	AGGCTGGGCGTGTGTTGGTG
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131403	129490	AACCAGGCTGGGCGTGTGTT
131404	129491	AAACCAGGCTGGGCGTGTGT
131405	129492	TAAACCAGGCTGGGCGTGTG
131406	129493	CTAAACCAGGCTGGGCGTGT
131407	129494	ACTAAACCAGGCTGGGCGTG
131408	129495	TACTAAACCAGGCTGGGCGT
131409	129496	ATACTAAACCAGGCTGGGCG
131410	129497	GATACTAAACCAGGCTGGGC
131411	129498	AGATACTAAACCAGGCTGGG
131412	129499	AAGATACTAAACCAGGCTGG
131413	129500	GAAGATACTAAACCAGGCTG
131414	129501	AGAAGATACTAAACCAGGCT
131415	129502	AAGAAGATACTAAACCAGGC
131416	129503	GAAGAAGATACTAAACCAGG
131417	129504	TGAAGAAGATACTAAACCAG
131418	129505	CTGAAGAAGATACTAAACCA
131419	129506	GCTGAAGAAGATACTAAACC
131420	129507	TGCTGAAGAAGATACTAAAC
131421	129508	TTGCTGAAGAAGATACTAAA
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131423	129510	AGTTGCTGAAGAAGATACTA
131424	129511	GAGTTGCTGAAGAAGATACT
131425	129512	TGAGTTGCTGAAGAAGATAC
131426	129513	CTGAGTTGCTGAAGAAGATA
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131428	129515	TACTGAGTTGCTGAAGAAGA
131429	129516	GTACTGAGTTGCTGAAGAAG
131430	129517	CGTACTGAGTTGCTGAAGAA
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131433	129520	CCCCGTACTGAGTTGCTGAA
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131438	129525	ATGAGCCCCGTACTGAGTTG
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131440	129527	TCATGAGCCCCGTACTGAGT
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131442	129529	GCTCATGAGCCCCGTACTGA
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33151	31238	TGTCCTTCAGTAGTTTCTAA
33152	31239	ATGTCCTTCAGTAGTTTCTA
33153	31240	TATGTCCTTCAGTAGTTTCT
33154	31241	ATATGTCCTTCAGTAGTTTC
33155	31242	TATATGTCCTTCAGTAGTTT
33156	31243	CTATATGTCCTTCAGTAGTT
33157	31244	TCTATATGTCCTTCAGTAGT
33158	31245	CTCTATATGTCCTTCAGTAG
33159	31246	CCTCTATATGTCCTTCAGTA
33160	31247	TCCTCTATATGTCCTTCAGT
33161	31248	CTCCTCTATATGTCCTTCAG
33162	31249	CCTCCTCTATATGTCCTTCA
33163	31250	TCCTCCTCTATATGTCCTTC
33164	31251	CTCCTCCTCTATATGTCCTT
33165	31252	ACTCCTCCTCTATATGTCCT
33166	31253	CACTCCTCCTCTATATGTCC
33167	31254	ACACTCCTCCTCTATATGTC
33168	31255	AACACTCCTCCTCTATATGT
33169	31256	CAACACTCCTCCTCTATATG
33170	31257	TCAACACTCCTCCTCTATAT
33171	31258	TTCAACACTCCTCCTCTATA
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33176	31263	CATTTTTCAACACTCCTCCT
33177	31264	CCATTTTTCAACACTCCTCC
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33181	31268	ATCACCATTTTTCAACACTC
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33183	31270	CCATCACCATTTTTCAACAC
33184	31271	TCCATCACCATTTTTCAACA
33185	31272	ATCCATCACCATTTTTCAAC
33186	31273	CATCCATCACCATTTTTCAA
33187	31274	TCATCCATCACCATTTTTCA
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33190	31277	TGCTCATCCATCACCATTTT
33191	31278	CTGCTCATCCATCACCATTT
33192	31279	TCTGCTCATCCATCACCATT
33193	31280	TTCTGCTCATCCATCACCAT
33194	31281	ATTCTGCTCATCCATCACCA
33195	31282	CATTCTGCTCATCCATCACC
33196	31283	CCATTCTGCTCATCCATCAC
33197	31284	ACCATTCTGCTCATCCATCA
33198	31285	CACCATTCTGCTCATCCATC
33199	31286	TCACCATTCTGCTCATCCAT
33200	31287	TTCACCATTCTGCTCATCCA
33201	31288	TTTCACCATTCTGCTCATCC
33202	31289	TTTTCACCATTCTGCTCATC
33203	31290	TTTTTCACCATTCTGCTCAT
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33209	31296	TTTTTATTTTTCACCATTCT
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33212	31299	GTCTTTTTATTTTTCACCAT
33213	31300	TGTCTTTTTATTTTTCACCA
33214	31301	ATGTCTTTTTATTTTTCACC
33215	31302	CATGTCTTTTTATTTTTCAC
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33217	31304	TTCATGTCTTTTTATTTTTC
33218	31305	CTTCATGTCTTTTTATTTTT
33219	31306	GCTTCATGTCTTTTTATTTT
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33221	31308	GAGCTTCATGTCTTTTTATT

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82299	80386	AGTCCTTTAATGACCTCAGT
82300	80387	AAGTCCTTTAATGACCTCAG
82301	80388	CAAGTCCTTTAATGACCTCA
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82304	80391	TGCCAAGTCCTTTAATGACC
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82306	80393	CATGCCAAGTCCTTTAATGA
82307	80394	ACATGCCAAGTCCTTTAATG
82308	80395	GACATGCCAAGTCCTTTAAT
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82310	80397	ATGACATGCCAAGTCCTTTA
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82312	80399	GCATGACATGCCAAGTCCTT
82313	80400	AGCATGACATGCCAAGTCCT
82314	80401	TAGCATGACATGCCAAGTCC
82315	80402	TTAGCATGACATGCCAAGTC
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82317	80404	CTTTAGCATGACATGCCAAG
82318	80405	TCTTTAGCATGACATGCCAA
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82320	80407	GCTCTTTAGCATGACATGCC
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82335	80422	TCCTTCCAACAGGGTGCTCT
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82346	80433	TTCACCCCATCTCCTTCCAA
82347	80434	ATTCACCCCATCTCCTTCCA
82348	80435	TATTCACCCCATCTCCTTCC
82349	80436	TTATTCACCCCATCTCCTTC
82350	80437	TTTATTCACCCCATCTCCTT
82351	80438	GTTTATTCACCCCATCTCCT
82352	80439	GGTTTATTCACCCCATCTCC
82353	80440	GGGTTTATTCACCCCATCTC
82354	80441	AGGGTTTATTCACCCCATCT
82355	80442	CAGGGTTTATTCACCCCATC
82356	80443	CCAGGGTTTATTCACCCCAT
82357	80444	CCCAGGGTTTATTCACCCCA
82358	80445	CCCCAGGGTTTATTCACCCC
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82360	80447	TGCCCCAGGGTTTATTCACC
82361	80448	ATGCCCCAGGGTTTATTCAC
82362	80449	AATGCCCCAGGGTTTATTCA
82363	80450	CAATGCCCCAGGGTTTATTC
82364	80451	TCAATGCCCCAGGGTTTATT
82365	80452	CTCAATGCCCCAGGGTTTAT
82366	80453	CCTCAATGCCCCAGGGTTTA
82367	80454	TCCTCAATGCCCCAGGGTTT
82368	80455	GTCCTCAATGCCCCAGGGTT

131445	129532	TCTGCTCATGAGCCCCGTAC
131446	129533	GTCTGCTCATGAGCCCCGTA
131447	129534	CGTCTGCTCATGAGCCCCGT
131448	129535	GCGTCTGCTCATGAGCCCCG
131449	129536	TGCGTCTGCTCATGAGCCCC
131450	129537	ATGCGTCTGCTCATGAGCCC
131451	129538	CATGCGTCTGCTCATGAGCC
131452	129539	GCATGCGTCTGCTCATGAGC
131453	129540	CGCATGCGTCTGCTCATGAG
131454	129541	TCGCATGCGTCTGCTCATGA
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131456	129543	CATCGCATGCGTCTGCTCAT
131457	129544	ACATCGCATGCGTCTGCTCA
131458	129545	TACATCGCATGCGTCTGCTC
131459	129546	ATACATCGCATGCGTCTGCT
131460	129547	CATACATCGCATGCGTCTGC
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131462	129549	ACCATACATCGCATGCGTCT
131463	129550	TACCATACATCGCATGCGTC
131464	129551	CTACCATACATCGCATGCGT
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131466	129553	TCCTACCATACATCGCATGC
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131468	129555	CTTCCTACCATACATCGCAT
131469	129556	GCTTCCTACCATACATCGCA
131470	129557	TGCTTCCTACCATACATCGC
131471	129558	GTGCTTCCTACCATACATCG
131472	129559	AGTGCTTCCTACCATACATC
131473	129560	AAGTGCTTCCTACCATACAT
131474	129561	AAAGTGCTTCCTACCATACA
131475	129562	CAAAGTGCTTCCTACCATAC
131476	129563	ACAAAGTGCTTCCTACCATA
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131478	129565	AAACAAAGTGCTTCCTACCA
131479	129566	CAAACAAAGTGCTTCCTACC
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131483	129570	GAGACAAACAAAGTGCTTCC
131484	129571	AGAGACAAACAAAGTGCTTC
131485	129572	AAGAGACAAACAAAGTGCTT
131486	129573	GAAGAGACAAACAAAGTGCT
131487	129574	GGAAGAGACAAACAAAGTGC
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131491	129578	CACTGGAAGAGACAAACAAA
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131507	129594	TAAGAAGAGTCACACACACT
131508	129595	TTAAGAAGAGTCACACACAC
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131510	129597	AATTAAGAAGAGTCACACAC
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131513	129600	TTAAATTAAGAAGAGTCACA
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131515	129602	ACTTAAATTAAGAAGAGTCA

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33223	31310	TAGAGCTTCATGTCTTTTTA
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33226	31313	TTATAGAGCTTCATGTCTTT
33227	31314	ATTATAGAGCTTCATGTCTT
33228	31315	AATTATAGAGCTTCATGTCT
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33239	31326	CCATACAATATAATTATAGA
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33244	31331	TGTCACCATACAATATAATT
33245	31332	CTGTCACCATACAATATAAT
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33269	31356	AAAAACATGCAATCTCTATT
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33271	31358	GAAAAAACATGCAATCTCTA
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33278	31365	CTGGGGAGAAAAAACATGCA
33279	31366	ACTGGGGAGAAAAAACATGC
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82369	80456	AGTCCTCAATGCCCCAGGGT
82370	80457	CAGTCCTCAATGCCCCAGGG
82371	80458	CCAGTCCTCAATGCCCCAGG
82372	80459	GCCAGTCCTCAATGCCCCAG
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82374	80461	CAGCCAGTCCTCAATGCCCC
82375	80462	TCAGCCAGTCCTCAATGCCC
82376	80463	CTCAGCCAGTCCTCAATGCC
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82379	80466	TGTCTCAGCCAGTCCTCAAT
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82384	80471	CTCTGTGTCTCAGCCAGTCC
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82413	80500	AGTTGAACTATTTCAGTGCA
82414	80501	CAGTTGAACTATTTCAGTGC
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131516	129603	AACTTAAATTAAGAAGAGTC
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131520	129607	CAGAAACTTAAATTAAGAAG
131521	129608	TCAGAAACTTAAATTAAGAA
131522	129609	TTCAGAAACTTAAATTAAGA
131523	129610	TTTCAGAAACTTAAATTAAG
131524	129611	TTTTCAGAAACTTAAATTAA
131525	129612	GTTTTCAGAAACTTAAATTA
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131532	129619	AGAGTATGTTTTCAGAAACT
131533	129620	TAGAGTATGTTTTCAGAAAC
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131536	129623	AGATAGAGTATGTTTTCAGA
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131571	129658	TGACCCTCAATGTCATAAAA
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131576	129663	ATTCTTGACCCTCAATGTCA
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131582	129669	CTTCAGATTCTTGACCCTCA
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33293	31380	AAACAAAAAAAAAAACTGGG
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33295	31382	CAAAACAAAAAAAAAACTG
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33297	31384	AACAAAACAAAAAAAAAAC
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33323	31410	AGTGAGACTCTGTCTCAAAA
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33325	31412	ACAGTGAGACTCTGTCTCAA
33326	31413	CACAGTGAGACTCTGTCTCA
33327	31414	ACACAGTGAGACTCTGTCTC
33328	31415	GACACAGTGAGACTCTGTCT
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33330	31417	GTGACACAGTGAGACTCTGT
33331	31418	AGTGACACAGTGAGACTCTG
33332	31419	GAGTGACACAGTGAGACTCT
33333	31420	TGAGTGACACAGTGAGACTC
33334	31421	CTGAGTGACACAGTGAGACT
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33336	31423	GCCTGAGTGACACAGTGAGA
33337	31424	AGCCTGAGTGACACAGTGAG
33338	31425	CAGCCTGAGTGACACAGTGA
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33341	31428	CTCCAGCCTGAGTGACACAG
33342	31429	ACTCCAGCCTGAGTGACACA
33343	31430	CACTCCAGCCTGAGTGACAC
33344	31431	GCACTCCAGCCTGAGTGACA
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33346	31433	ATGCACTCCAGCCTGAGTGA
33347	31434	AATGCACTCCAGCCTGAGTG
33348	31435	CAATGCACTCCAGCCTGAGT
33349	31436	ACAATGCACTCCAGCCTGAG
33350	31437	GACAATGCACTCCAGCCTGA
33351	31438	CGACAATGCACTCCAGCCTG
33352	31439	ACGACAATGCACTCCAGCCT
33353	31440	CACGACAATGCACTCCAGCC
33354	31441	TCACGACAATGCACTCCAGC
33355	31442	ATCACGACAATGCACTCCAG
33356	31443	TATCACGACAATGCACTCCA
33357	31444	ATATCACGACAATGCACTCC
33358	31445	AATATCACGACAATGCACTC
33359	31446	CAATATCACGACAATGCACT
33360	31447	CCAATATCACGACAATGCAC
33361	31448	GCCAATATCACGACAATGCA
33362	31449	AGCCAATATCACGACAATGC
33363	31450	AAGCCAATATCACGACAATG

82440	80527	TTAACTAGGTGGTTACCAAA
82441	80528	CTTAACTAGGTGGTTACCAA
82442	80529	CCTTAACTAGGTGGTTACCA
82443	80530	CCCTTAACTAGGTGGTTACC
82444	80531	TCCCTTAACTAGGTGGTTAC
82445	80532	ATCCCTTAACTAGGTGGTTA
82446	80533	CATCCCTTAACTAGGTGGTT
82447	80534	TCATCCCTTAACTAGGTGGT
82448	80535	CTCATCCCTTAACTAGGTGG
82449	80536	GCTCATCCCTTAACTAGGTG
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82451	80538	AGGCTCATCCCTTAACTAGG
82452	80539	CAGGCTCATCCCTTAACTAG
82453	80540	TCAGGCTCATCCCTTAACTA
82454	80541	CTCAGGCTCATCCCTTAACT
82455	80542	CCTCAGGCTCATCCCTTAAC
82456	80543	ACCTCAGGCTCATCCCTTAA
82457	80544	AACCTCAGGCTCATCCCTTA
82458	80545	AAACCTCAGGCTCATCCCTT
82459	80546	TAAACCTCAGGCTCATCCCT
82460	80547	ATAAACCTCAGGCTCATCCC
82461	80548	AATAAACCTCAGGCTCATCC
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82463	80550	CAAATAAACCTCAGGCTCAT
82464	80551	TCAAATAAACCTCAGGCTCA
82465	80552	ATCAAATAAACCTCAGGCTC
82466	80553	TATCAAATAAACCTCAGGCT
82467	80554	TTATCAAATAAACCTCAGGC
82468	80555	GTTATCAAATAAACCTCAGG
82469	80556	AGTTATCAAATAAACCTCAG
82470	80557	TAGTTATCAAATAAACCTCA
82471	80558	TTAGTTATCAAATAAACCTC
82472	80559	CTTAGTTATCAAATAAACCT
82473	80560	ACTTAGTTATCAAATAAACC
82474	80561	CACTTAGTTATCAAATAAAC
82475	80562	TCACTTAGTTATCAAATAAA
82476	80563	GTCACTTAGTTATCAAATAA
82477	80564	AGTCACTTAGTTATCAAATA
82478	80565	AAGTCACTTAGTTATCAAAT
82479	80566	TAAGTCACTTAGTTATCAAA
82480	80567	TTAAGTCACTTAGTTATCAA
82481	80568	ATTAAGTCACTTAGTTATCA
82482	80569	CATTAAGTCACTTAGTTATC
82483	80570	CCATTAAGTCACTTAGTTAT
82484	80571	TCCATTAAGTCACTTAGTTA
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82486	80573	CATCCATTAAGTCACTTAGT
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82489	80576	GTACATCCATTAAGTCACTT
82490	80577	AGTACATCCATTAAGTCACT
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82495	80582	TTACCAGTACATCCATTAAG
82496	80583	CTTACCAGTACATCCATTAA
82497	80584	TCTTACCAGTACATCCATTA
82498	80585	CTCTTACCAGTACATCCATT
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82500	80587	CTCTCTTACCAGTACATCCA
82501	80588	TCTCTCTTACCAGTACATCC
82502	80589	CTCTCTCTTACCAGTACATC
82503	80590	TCTCTCTCTTACCAGTACAT
82504	80591	CTCTCTCTCTTACCAGTACA
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82506	80593	TCCTCTCTCTCTTACCAGTA
82507	80594	TTCCTCTCTCTCTTACCAGT
82508	80595	TTTCCTCTCTCTCTTACCAG
82509	80596	GTTTCCTCTCTCTCTTACCA
82510	80597	TGTTTCCTCTCTCTCTTACC

131587	129674	TTTTCCTTCAGATTCTTGAC
131588	129675	CTTTTCCTTCAGATTCTTGA
131589	129676	TCTTTTCCTTCAGATTCTTG
131590	129677	ATCTTTTCCTTCAGATTCTT
131591	129678	CATCTTTTCCTTCAGATTCT
131592	129679	TCATCTTTTCCTTCAGATTC
131593	129680	TTCATCTTTTCCTTCAGATT
131594	129681	GTTCATCTTTTCCTTCAGAT
131595	129682	GGTTCATCTTTTCCTTCAGA
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131597	129684	TGGGTTCATCTTTTCCTTCA
131598	129685	ATGGGTTCATCTTTTCCTTC
131599	129686	AATGGGTTCATCTTTTCCTT
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131601	129688	GAAATGGGTTCATCTTTTCC
131602	129689	AGAAATGGGTTCATCTTTTC
131603	129690	AAGAAATGGGTTCATCTTTT
131604	129691	AAAGAAATGGGTTCATCTTT
131605	129692	CAAAGAAATGGGTTCATCTT
131606	129693	GCAAAGAAATGGGTTCATCT
131607	129694	GGCAAAGAAATGGGTTCATC
131608	129695	AGGCAAAGAAATGGGTTCAT
131609	129696	CAGGCAAAGAAATGGGTTCA
131610	129697	TCAGGCAAAGAAATGGGTTC
131611	129698	GTCAGGCAAAGAAATGGGTT
131612	129699	AGTCAGGCAAAGAAATGGGT
131613	129700	AAGTCAGGCAAAGAAATGGG
131614	129701	CAAGTCAGGCAAAGAAATGG
131615	129702	GCAAGTCAGGCAAAGAAATG
131616	129703	AGCAAGTCAGGCAAAGAAAT
131617	129704	AAGCAAGTCAGGCAAAGAAA
131618	129705	AAAGCAAGTCAGGCAAAGAA
131619	129706	TAAAGCAAGTCAGGCAAAGA
131620	129707	ATAAAGCAAGTCAGGCAAAG
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131623	129710	GTTATAAAGCAAGTCAGGCA
131624	129711	AGTTATAAAGCAAGTCAGGC
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131626	129713	AAAGTTATAAAGCAAGTCAG
131627	129714	AAAAGTTATAAAGCAAGTCA
131628	129715	CAAAAGTTATAAAGCAAGTC
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131630	129717	GCCAAAAGTTATAAAGCAAG
131631	129718	TGCCAAAAGTTATAAAGCAA
131632	129719	TTGCCAAAAGTTATAAAGCA
131633	129720	TTTGCCAAAAGTTATAAAGC
131634	129721	ATTTGCCAAAAGTTATAAAG
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131637	129724	ACTATTTGCCAAAAGTTATA
131638	129725	AACTATTTGCCAAAAGTTAT
131639	129726	AAACTATTTGCCAAAAGTTA
131640	129727	GAAACTATTTGCCAAAAGTT
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131642	129729	TAGAAACTATTTGCCAAAAG
131643	129730	GTAGAAACTATTTGCCAAAA
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131646	129733	GAAGTAGAAACTATTTGCCA
131647	129734	AGAAGTAGAAACTATTTGCC
131648	129735	CAGAAGTAGAAACTATTTGC
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131650	129737	TACAGAAGTAGAAACTATTT
131651	129738	GTACAGAAGTAGAAACTATT
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131653	129740	AGGTACAGAAGTAGAAACTA
131654	129741	CAGGTACAGAAGTAGAAACT
131655	129742	CCAGGTACAGAAGTAGAAAC
131656	129743	ACCAGGTACAGAAGTAGAAA
131657	129744	GACCAGGTACAGAAGTAGAA

33364	31451	TAAGCCAATATCACGACAAT
33365	31452	GTAAGCCAATATCACGACAA
33366	31453	AGTAAGCCAATATCACGACA
33367	31454	CAGTAAGCCAATATCACGAC
33368	31455	GCAGTAAGCCAATATCACGA
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33371	31458	GTTGCAGTAAGCCAATATCA
33372	31459	GGTTGCAGTAAGCCAATATC
33373	31460	AGGTTGCAGTAAGCCAATAT
33374	31461	GAGGTTGCAGTAAGCCAATA
33375	31462	AGAGGTTGCAGTAAGCCAAT
33376	31463	CAGAGGTTGCAGTAAGCCAA
33377	31464	GCAGAGGTTGCAGTAAGCCA
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33383	31470	CAGGAAGCAGAGGTTGCAGT
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33385	31472	CCCAGGAAGCAGAGGTTGCA
33386	31473	ACCCAGGAAGCAGAGGTTGC
33387	31474	AACCCAGGAAGCAGAGGTTG
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33406	31493	GAGGCAGGAGAATCGCTTGA
33407	31494	TGAGGCAGGAGAATCGCTTG
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33409	31496	GCTGAGGCAGGAGAATCGCT
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33414	31501	AGGAGGCTGAGGCAGGAGAA
33415	31502	CAGGAGGCTGAGGCAGGAGA
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33417	31504	CTCAGGAGGCTGAGGCAGGA
33418	31505	ACTCAGGAGGCTGAGGCAGG
33419	31506	TACTCAGGAGGCTGAGGCAG
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33421	31508	GCTACTCAGGAGGCTGAGGC
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33423	31510	CAGCTACTCAGGAGGCTGAG
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33431	31518	TGTAATCCCAGCTACTCAGG
33432	31519	CTGTAATCCCAGCTACTCAG
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82514	80601	TCCATGTTTCCTCTCTCTCT
82515	80602	CTCCATGTTTCCTCTCTCTC
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82523	80610	CAAACTTGCTCCATGTTTCC
82524	80611	TCAAACTTGCTCCATGTTTC
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82534	80621	GTTTTTCCCCTCAAACTTGC
82535	80622	TGTTTTTCCCCTCAAACTTG
82536	80623	CTGTTTTTCCCCTCAAACTT
82537	80624	ACTGTTTTTCCCCTCAAACT
82538	80625	CACTGTTTTTCCCCTCAAAC
82539	80626	TCACTGTTTTTCCCCTCAAA
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82547	80634	AAACGGAGTCACTGTTTTTC
82548	80635	CAAACGGAGTCACTGTTTTT
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82550	80637	CACAAACGGAGTCACTGTTT
82551	80638	GCACAAACGGAGTCACTGTT
82552	80639	TGCACAAACGGAGTCACTGT
82553	80640	CTGCACAAACGGAGTCACTG
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82561	80648	GCAATTAGCTGCACAAACGG
82562	80649	TGCAATTAGCTGCACAAACG
82563	80650	ATGCAATTAGCTGCACAAAC
82564	80651	TATGCAATTAGCTGCACAAA
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82566	80653	CATATGCAATTAGCTGCACA
82567	80654	ACATATGCAATTAGCTGCAC
82568	80655	CACATATGCAATTAGCTGCA
82569	80656	CCACATATGCAATTAGCTGC
82570	80657	CCCACATATGCAATTAGCTG
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82572	80659	AGCCCACATATGCAATTAGC
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82577	80664	CCACAAGCCCACATATGCAA
82578	80665	CCCACAAGCCCACATATGCA
82579	80666	ACCCACAAGCCCACATATGC
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131658	129745	AGACCAGGTACAGAAGTAGA
131659	129746	AAGACCAGGTACAGAAGTAG
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131661	129748	TGAAGACCAGGTACAGAAGT
131662	129749	CTGAAGACCAGGTACAGAAG
131663	129750	TCTGAAGACCAGGTACAGAA
131664	129751	ATCTGAAGACCAGGTACAGA
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131670	129757	AAAGAGATCTGAAGACCAGG
131671	129758	GAAAGAGATCTGAAGACCAG
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131673	129760	AGGAAAGAGATCTGAAGACC
131674	129761	CAGGAAAGAGATCTGAAGAC
131675	129762	GCAGGAAAGAGATCTGAAGA
131676	129763	AGCAGGAAAGAGATCTGAAG
131677	129764	AAGCAGGAAAGAGATCTGAA
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131679	129766	TAAAGCAGGAAAGAGATCTG
131680	129767	TTAAAGCAGGAAAGAGATCT
131681	129768	GTTAAAGCAGGAAAGAGATC
131682	129769	AGTTAAAGCAGGAAAGAGAT
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131690	129777	TACATTTTAGTTAAAGCAGG
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131694	129781	TCATTACATTTTAGTTAAAG
131695	129782	ATCATTACATTTTAGTTAAA
131696	129783	CATCATTACATTTTAGTTAA
131697	129784	ACATCATTACATTTTAGTTA
131698	129785	TACATCATTACATTTTAGTT
131699	129786	ATACATCATTACATTTTAGT
131700	129787	TATACATCATTACATTTTAG
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131702	129789	TATATACATCATTACATTTT
131703	129790	TTATATACATCATTACATTT
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131705	129792	CATTATATACATCATTACAT
131706	129793	CCATTATATACATCATTACA
131707	129794	GCCATTATATACATCATTAC
131708	129795	TGCCATTATATACATCATTA
131709	129796	TTGCCATTATATACATCATT
131710	129797	TTTGCCATTATATACATCAT
131711	129798	CTTTGCCATTATATACATCA
131712	129799	GCTTTGCCATTATATACATC
131713	129800	TGCTTTGCCATTATATACAT
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131715	129802	GATGCTTTGCCATTATATAC
131716	129803	AGATGCTTTGCCATTATATA
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131720	129807	ACAAAGATGCTTTGCCATTA
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131723	129810	TCCACAAAGATGCTTTGCCA
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131727	129814	TTTCTCCACAAAGATGCTTT
131728	129815	CTTTCTCCACAAAGATGCTT

33435	31522	TGCCTGTAATCCCAGCTACT
33436	31523	ATGCCTGTAATCCCAGCTAC
33437	31524	CATGCCTGTAATCCCAGCTA
33438	31525	ACATGCCTGTAATCCCAGCT
33439	31526	CACATGCCTGTAATCCCAGC
33440	31527	GCACATGCCTGTAATCCCAG
33441	31528	GGCACATGCCTGTAATCCCA
33442	31529	TGGCACATGCCTGTAATCCC
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33444	31531	GGTGGCACATGCCTGTAATC
33445	31532	TGGTGGCACATGCCTGTAAT
33446	31533	GTGGTGGCACATGCCTGTAA
33447	31534	CGTGGTGGCACATGCCTGTA
33448	31535	GCGTGGTGGCACATGCCTGT
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33453	31540	GCCGGGCGTGGTGGCACATG
33454	31541	AGCCGGGCGTGGTGGCACAT
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33457	31544	ATTAGCCGGGCGTGGTGGCA
33458	31545	AATTAGCCGGGCGTGGTGGC
33459	31546	AAATTAGCCGGGCGTGGTGG
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33461	31548	AAAAATTAGCCGGGCGTGGT
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33464	31551	TACAAAAATTAGCCGGGCGT
33465	31552	ATACAAAAATTAGCCGGGCG
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33468	31555	AAAATACAAAAATTAGCCGG
33469	31556	AAAAATACAAAAATTAGCCG
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33473	31560	AAATAAAAATACAAAAATTA
33474	31561	CAAATAAAAATACAAAAATT
33475	31562	TCAAATAAAAATACAAAAAT
33476	31563	CTCAAATAAAAATACAAAAA
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33491	31578	ATGGTGAAATCCCCTCTCAA
33492	31579	CATGGTGAAATCCCCTCTCA
33493	31580	ACATGGTGAAATCCCCTCTC
33494	31581	AACATGGTGAAATCCCCTCT
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33499	31586	TTGCCAACATGGTGAAATCC
33500	31587	CTTGCCAACATGGTGAAATC
33501	31588	CCTTGCCAACATGGTGAAAT
33502	31589	GCCTTGCCAACATGGTGAAA
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82582	80669	AAGACCCACAAGCCCACATA
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82584	80671	GAAAGACCCACAAGCCCACA
82585	80672	TGAAAGACCCACAAGCCCAC
82586	80673	ATGAAAGACCCACAAGCCCA
82587	80674	AATGAAAGACCCACAAGCCC
82588	80675	AAATGAAAGACCCACAAGCC
82589	80676	TAAATGAAAGACCCACAAGC
82590	80677	ATAAATGAAAGACCCACAAG
82591	80678	AATAAATGAAAGACCCACAA
82592	80679	GAATAAATGAAAGACCCACA
82593	80680	TGAATAAATGAAAGACCCAC
82594	80681	ATGAATAAATGAAAGACCCA
82595	80682	TATGAATAAATGAAAGACCC
82596	80683	TTATGAATAAATGAAAGACC
82597	80684	TTTATGAATAAATGAAAGAC
82598	80685	GTTTATGAATAAATGAAAGA
82599	80686	CGTTTATGAATAAATGAAAG
82600	80687	ACGTTTATGAATAAATGAAA
82601	80688	CACGTTTATGAATAAATGAA
82602	80689	ACACGTTTATGAATAAATGA
82603	80690	AACACGTTTATGAATAAATG
82604	80691	CAACACGTTTATGAATAAAT
82605	80692	TCAACACGTTTATGAATAAA
82606	80693	CTCAACACGTTTATGAATAA
82607	80694	TCTCAACACGTTTATGAATA
82608	80695	TTCTCAACACGTTTATGAAT
82609	80696	TTTCTCAACACGTTTATGAA
82610	80697	ATTTCTCAACACGTTTATGA
82611	80698	TATTTCTCAACACGTTTATG
82612	80699	GTATTTCTCAACACGTTTAT
82613	80700	GGTATTTCTCAACACGTTTA
82614	80701	AGGTATTTCTCAACACGTTT
82615	80702	CAGGTATTTCTCAACACGTT
82616	80703	GCAGGTATTTCTCAACACGT
82617	80704	AGCAGGTATTTCTCAACACG
82618	80705	TAGCAGGTATTTCTCAACAC
82619	80706	GTAGCAGGTATTTCTCAACA
82620	80707	GGTAGCAGGTATTTCTCAAC
82621	80708	AGGTAGCAGGTATTTCTCAA
82622	80709	TAGGTAGCAGGTATTTCTCA
82623	80710	ATAGGTAGCAGGTATTTCTC
82624	80711	GATAGGTAGCAGGTATTTCT
82625	80712	AGATAGGTAGCAGGTATTTC
82626	80713	TAGATAGGTAGCAGGTATTT
82627	80714	CTAGATAGGTAGCAGGTATT
82628	80715	ACTAGATAGGTAGCAGGTAT
82629	80716	TACTAGATAGGTAGCAGGTA
82630	80717	TTACTAGATAGGTAGCAGGT
82631	80718	TTTACTAGATAGGTAGCAGG
82632	80719	CTTTACTAGATAGGTAGCAG
82633	80720	ACTTTACTAGATAGGTAGCA
82634	80721	TACTTTACTAGATAGGTAGC
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82636	80723	CTTACTTTACTAGATAGGTA
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82639	80726	TCTCTTACTTTACTAGATAG
82640	80727	ATCTCTTACTTTACTAGATA
82641	80728	CATCTCTTACTTTACTAGAT
82642	80729	GCATCTCTTACTTTACTAGA
82643	80730	TGCATCTCTTACTTTACTAG
82644	80731	ATGCATCTCTTACTTTACTA
82645	80732	GATGCATCTCTTACTTTACT
82646	80733	GGATGCATCTCTTACTTTAC
82647	80734	AGGATGCATCTCTTACTTTA
82648	80735	GAGGATGCATCTCTTACTTT
82649	80736	AGAGGATGCATCTCTTACTT
82650	80737	GAGAGGATGCATCTCTTACT
82651	80738	AGAGAGGATGCATCTCTTAC
82652	80739	AAGAGAGGATGCATCTCTTA

131729	129816	CCTTTCTCCACAAAGATGCT
131730	129817	ACCTTTCTCCACAAAGATGC
131731	129818	TACCTTTCTCCACAAAGATG
131732	129819	GTACCTTTCTCCACAAAGAT
131733	129820	GGTACCTTTCTCCACAAAGA
131734	129821	AGGTACCTTTCTCCACAAAG
131735	129822	AAGGTACCTTTCTCCACAAA
131736	129823	AAAGGTACCTTTCTCCACAA
131737	129824	GAAAGGTACCTTTCTCCACA
131738	129825	AGAAAGGTACCTTTCTCCAC
131739	129826	GAGAAAGGTACCTTTCTCCA
131740	129827	GGAGAAAGGTACCTTTCTCC
131741	129828	AGGAGAAAGGTACCTTTCTC
131742	129829	GAGGAGAAAGGTACCTTTCT
131743	129830	AGAGGAGAAAGGTACCTTTC
131744	129831	AAGAGGAGAAAGGTACCTTT
131745	129832	GAAGAGGAGAAAGGTACCTT
131746	129833	GGAAGAGGAGAAAGGTACCT
131747	129834	AGGAAGAGGAGAAAGGTACC
131748	129835	GAGGAAGAGGAGAAAGGTAC
131749	129836	TGAGGAAGAGGAGAAAGGTA
131750	129837	ATGAGGAAGAGGAGAAAGGT
131751	129838	GATGAGGAAGAGGAGAAAGG
131752	129839	TGATGAGGAAGAGGAGAAAG
131753	129840	TTGATGAGGAAGAGGAGAAA
131754	129841	ATTGATGAGGAAGAGGAGAA
131755	129842	TATTGATGAGGAAGAGGAGA
131756	129843	ATATTGATGAGGAAGAGGAG
131757	129844	AATATTGATGAGGAAGAGGA
131758	129845	TAATATTGATGAGGAAGAGG
131759	129846	ATAATATTGATGAGGAAGAG
131760	129847	CATAATATTGATGAGGAAGA
131761	129848	GCATAATATTGATGAGGAAG
131762	129849	AGCATAATATTGATGAGGAA
131763	129850	AAGCATAATATTGATGAGGA
131764	129851	AAAGCATAATATTGATGAGG
131765	129852	CAAAGCATAATATTGATGAG
131766	129853	CCAAAGCATAATATTGATGA
131767	129854	ACCAAAGCATAATATTGATG
131768	129855	TACCAAAGCATAATATTGAT
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131771	129858	ATATACCAAAGCATAATATT
131772	129859	GATATACCAAAGCATAATAT
131773	129860	GGATATACCAAAGCATAATA
131774	129861	AGGATATACCAAAGCATAAT
131775	129862	CAGGATATACCAAAGCATAA
131776	129863	GCAGGATATACCAAAGCATA
131777	129864	GGCAGGATATACCAAAGCAT
131778	129865	AGGCAGGATATACCAAAGCA
131779	129866	TAGGCAGGATATACCAAAGC
131780	129867	GTAGGCAGGATATACCAAAG
131781	129868	CGTAGGCAGGATATACCAAA
131782	129869	TCGTAGGCAGGATATACCAA
131783	129870	GTCGTAGGCAGGATATACCA
131784	129871	TGTCGTAGGCAGGATATACC
131785	129872	ATGTCGTAGGCAGGATATAC
131786	129873	CATGTCGTAGGCAGGATATA
131787	129874	GCATGTCGTAGGCAGGATAT
131788	129875	TGCATGTCGTAGGCAGGATA
131789	129876	TTGCATGTCGTAGGCAGGAT
131790	129877	CTTGCATGTCGTAGGCAGGA
131791	129878	TCTTGCATGTCGTAGGCAGG
131792	129879	CTCTTGCATGTCGTAGGCAG
131793	129880	TCTCTTGCATGTCGTAGGCA
131794	129881	TTCTCTTGCATGTCGTAGGC
131795	129882	ATTCTCTTGCATGTCGTAGG
131796	129883	AATTCTCTTGCATGTCGTAG
131797	129884	AAATTCTCTTGCATGTCGTA
131798	129885	AAAATTCTCTTGCATGTCGT
131799	129886	TAAAATTCTCTTGCATGTCG

33506	31593	ACCAGCCTTGCCAACATGGT
33507	31594	GACCAGCCTTGCCAACATGG
33508	31595	AGACCAGCCTTGCCAACATG
33509	31596	AAGACCAGCCTTGCCAACAT
33510	31597	CAAGACCAGCCTTGCCAACA
33511	31598	TCAAGACCAGCCTTGCCAAC
33512	31599	CTCAAGACCAGCCTTGCCAA
33513	31600	ACTCAAGACCAGCCTTGCCA
33514	31601	AACTCAAGACCAGCCTTGCC
33515	31602	GAACTCAAGACCAGCCTTGC
33516	31603	GGAACTCAAGACCAGCCTTG
33517	31604	AGGAACTCAAGACCAGCCTT
33518	31605	CAGGAACTCAAGACCAGCCT
33519	31606	TCAGGAACTCAAGACCAGCC
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33522	31609	AGGTCAGGAACTCAAGACCA
33523	31610	GAGGTCAGGAACTCAAGACC
33524	31611	TGAGGTCAGGAACTCAAGAC
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33529	31616	TTATCTGAGGTCAGGAACTC
33530	31617	ATTATCTGAGGTCAGGAACT
33531	31618	GATTATCTGAGGTCAGGAAC
33532	31619	GGATTATCTGAGGTCAGGAA
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33535	31622	GGTGGATTATCTGAGGTCAG
33536	31623	AGGTGGATTATCTGAGGTCA
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33542	31629	TGAGGCAGGTGGATTATCTG
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33544	31631	GCTGAGGCAGGTGGATTATC
33545	31632	GGCTGAGGCAGGTGGATTAT
33546	31633	AGGCTGAGGCAGGTGGATTA
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33549	31636	GGGAGGCTGAGGCAGGTGGA
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33554	31641	ACTTTGGGAGGCTGAGGCAG
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33556	31643	GCACTTTGGGAGGCTGAGGC
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33558	31645	CGGCACTTTGGGAGGCTGAG
33559	31646	CCGGCACTTTGGGAGGCTGA
33560	31647	CCCGGCACTTTGGGAGGCTG
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33563	31650	AATCCCGGCACTTTGGGAGG
33564	31651	TAATCCCGGCACTTTGGGAG
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33566	31653	TGTAATCCCGGCACTTTGGG
33567	31654	CTGTAATCCCGGCACTTTGG
33568	31655	CCTGTAATCCCGGCACTTTG
33569	31656	ACCTGTAATCCCGGCACTTT
33570	31657	CACCTGTAATCCCGGCACTT
33571	31658	ACACCTGTAATCCCGGCACT
33572	31659	CACACCTGTAATCCCGGCAC
33573	31660	TCACACCTGTAATCCCGGCA
33574	31661	CTCACACCTGTAATCCCGGC
33575	31662	GCTCACACCTGTAATCCCGG
33576	31663	GGCTCACACCTGTAATCCCG

82653	80740	TAAGAGAGGATGCATCTCTT
82654	80741	TTAAGAGAGGATGCATCTCT
82655	80742	TTTAAGAGAGGATGCATCTC
82656	80743	CTTTAAGAGAGGATGCATCT
82657	80744	CCTTTAAGAGAGGATGCATC
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82664	80751	CTGACTGCCTTTAAGAGAGG
82665	80752	GCTGACTGCCTTTAAGAGAG
82666	80753	AGCTGACTGCCTTTAAGAGA
82667	80754	AAGCTGACTGCCTTTAAGAG
82668	80755	TAAGCTGACTGCCTTTAAGA
82669	80756	CTAAGCTGACTGCCTTTAAG
82670	80757	TCTAAGCTGACTGCCTTTAA
82671	80758	CTCTAAGCTGACTGCCTTTA
82672	80759	ACTCTAAGCTGACTGCCTTT
82673	80760	GACTCTAAGCTGACTGCCTT
82674	80761	AGACTCTAAGCTGACTGCCT
82675	80762	CAGACTCTAAGCTGACTGCC
82676	80763	CCAGACTCTAAGCTGACTGC
82677	80764	ACCAGACTCTAAGCTGACTG
82678	80765	CACCAGACTCTAAGCTGACT
82679	80766	TCACCAGACTCTAAGCTGAC
82680	80767	ATCACCAGACTCTAAGCTGA
82681	80768	AATCACCAGACTCTAAGCTG
82682	80769	AAATCACCAGACTCTAAGCT
82683	80770	CAAATCACCAGACTCTAAGC
82684	80771	TCAAATCACCAGACTCTAAG
82685	80772	TTCAAATCACCAGACTCTAA
82686	80773	ATTCAAATCACCAGACTCTA
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82688	80775	CAATTCAAATCACCAGACTC
82689	80776	TCAATTCAAATCACCAGACT
82690	80777	GTCAATTCAAATCACCAGAC
82691	80778	TGTCAATTCAAATCACCAGA
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82693	80780	CATGTCAATTCAAATCACCA
82694	80781	ACATGTCAATTCAAATCACC
82695	80782	GACATGTCAATTCAAATCAC
82696	80783	GGACATGTCAATTCAAATCA
82697	80784	TGGACATGTCAATTCAAATC
82698	80785	GTGGACATGTCAATTCAAAT
82699	80786	AGTGGACATGTCAATTCAAA
82700	80787	CAGTGGACATGTCAATTCAA
82701	80788	TCAGTGGACATGTCAATTCA
82702	80789	ATCAGTGGACATGTCAATTC
82703	80790	TATCAGTGGACATGTCAATT
82704	80791	CTATCAGTGGACATGTCAAT
82705	80792	TCTATCAGTGGACATGTCAA
82706	80793	ATCTATCAGTGGACATGTCA
82707	80794	CATCTATCAGTGGACATGTC
82708	80795	ACATCTATCAGTGGACATGT
82709	80796	AACATCTATCAGTGGACATG
82710	80797	CAACATCTATCAGTGGACAT
82711	80798	TCAACATCTATCAGTGGACA
82712	80799	GTCAACATCTATCAGTGGAC
82713	80800	TGTCAACATCTATCAGTGGA
82714	80801	GTGTCAACATCTATCAGTGG
82715	80802	AGTGTCAACATCTATCAGTG
82716	80803	CAGTGTCAACATCTATCAGT
82717	80804	ACAGTGTCAACATCTATCAG
82718	80805	CACAGTGTCAACATCTATCA
82719	80806	TCACAGTGTCAACATCTATC
82720	80807	CTCACAGTGTCAACATCTAT
82721	80808	TCTCACAGTGTCAACATCTA
82722	80809	GTCTCACAGTGTCAACATCT
82723	80810	AGTCTCACAGTGTCAACATC

131800	129887	ATAAAATTCTCTTGCATGTC
131801	129888	TATAAAATTCTCTTGCATGT
131802	129889	TTATAAAATTCTCTTGCATG
131803	129890	ATTATAAAATTCTCTTGCAT
131804	129891	TATTATAAAATTCTCTTGCA
131805	129892	TTATTATAAAATTCTCTTGC
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131807	129894	TATTATTATAAAATTCTCTT
131808	129895	TTATTATTATAAAATTCTCT
131809	129896	TTTATTATTATAAAATTCTC
131810	129897	TTTTATTATTATAAAATTCT
131811	129898	CTTTTATTATTATAAAATTC
131812	129899	GCTTTTATTATTATAAAATT
131813	129900	TGCTTTTATTATTATAAAAT
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131818	129905	CTTTATGCTTTTATTATTAT
131819	129906	CCTTTATGCTTTTATTATTA
131820	129907	ACCTTTATGCTTTTATTATT
131821	129908	CACCTTTATGCTTTTATTAT
131822	129909	ACACCTTTATGCTTTTATTA
131823	129910	AACACCTTTATGCTTTTATT
131824	129911	GAACACCTTTATGCTTTTAT
131825	129912	AGAACACCTTTATGCTTTTA
131826	129913	GAGAACACCTTTATGCTTTT
131827	129914	GGAGAACACCTTTATGCTTT
131828	129915	TGGAGAACACCTTTATGCTT
131829	129916	CTGGAGAACACCTTTATGCT
131830	129917	GCTGGAGAACACCTTTATGC
131831	129918	TGCTGGAGAACACCTTTATG
131832	129919	ATGCTGGAGAACACCTTTAT
131833	129920	CATGCTGGAGAACACCTTTA
131834	129921	TCATGCTGGAGAACACCTTT
131835	129922	TTCATGCTGGAGAACACCTT
131836	129923	TTTCATGCTGGAGAACACCT
131837	129924	TTTTCATGCTGGAGAACACC
131838	129925	GTTTTCATGCTGGAGAACAC
131839	129926	TGTTTTCATGCTGGAGAACA
131840	129927	ATGTTTTCATGCTGGAGAAC
131841	129928	AATGTTTTCATGCTGGAGAA
131842	129929	AAATGTTTTCATGCTGGAGA
131843	129930	AAAATGTTTTCATGCTGGAG
131844	129931	CAAAATGTTTTCATGCTGGA
131845	129932	GCAAAATGTTTTCATGCTGG
131846	129933	AGCAAAATGTTTTCATGCTG
131847	129934	AAGCAAAATGTTTTCATGCT
131848	129935	GAAGCAAAATGTTTTCATGC
131849	129936	TGAAGCAAAATGTTTTCATG
131850	129937	GTGAAGCAAAATGTTTTCAT
131851	129938	AGTGAAGCAAAATGTTTTCA
131852	129939	TAGTGAAGCAAAATGTTTTC
131853	129940	GTAGTGAAGCAAAATGTTTT
131854	129941	AGTAGTGAAGCAAAATGTTT
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131856	129943	CAAGTAGTGAAGCAAAATGT
131857	129944	TCAAGTAGTGAAGCAAAATG
131858	129945	ATCAAGTAGTGAAGCAAAAT
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131866	129953	ACCCTCAGATCAAGTAGTGA
131867	129954	GACCCTCAGATCAAGTAGTG
131868	129955	TGACCCTCAGATCAAGTAGT
131869	129956	GTGACCCTCAGATCAAGTAG
131870	129957	AGTGACCCTCAGATCAAGTA

33577	31664	TGGCTCACACCTGTAATCCC
33578	31665	GTGGCTCACACCTGTAATCC
33579	31666	AGTGGCTCACACCTGTAATC
33580	31667	CAGTGGCTCACACCTGTAAT
33581	31668	GCAGTGGCTCACACCTGTAA
33582	31669	CGCAGTGGCTCACACCTGTA
33583	31670	GCGCAGTGGCTCACACCTGT
33584	31671	GGCGCAGTGGCTCACACCTG
33585	31672	GGGCGCAGTGGCTCACACCT
33586	31673	CGGGCGCAGTGGCTCACACC
33587	31674	CCGGGCGCAGTGGCTCACAC
33588	31675	GCCGGGCGCAGTGGCTCACA
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33598	31685	ACTGGGGGAGGCCGGGCGCA
33599	31686	AACTGGGGGAGGCCGGGCGC
33600	31687	CAACTGGGGGAGGCCGGGCG
33601	31688	ACAACTGGGGGAGGCCGGGC
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33603	31690	CAACAACTGGGGGAGGCCGG
33604	31691	TCAACAACTGGGGGAGGCCG
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33606	31693	TTTCAACAACTGGGGGAGGC
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33608	31695	TGTTTCAACAACTGGGGGAG
33609	31696	TTGTTTCAACAACTGGGGGA
33610	31697	ATTGTTTCAACAACTGGGGG
33611	31698	TATTGTTTCAACAACTGGGG
33612	31699	TTATTGTTTCAACAACTGGG
33613	31700	ATTATTGTTTCAACAACTGG
33614	31701	CATTATTGTTTCAACAACTG
33615	31702	CCATTATTGTTTCAACAACT
33616	31703	TCCATTATTGTTTCAACAAC
33617	31704	TTCCATTATTGTTTCAACAA
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33621	31708	TACCTTCCATTATTGTTTCA
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33623	31710	ATTACCTTCCATTATTGTTT
33624	31711	AATTACCTTCCATTATTGTT
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33626	31713	AAAATTACCTTCCATTATTG
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33628	31715	ATAAAATTACCTTCCATTAT
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33630	31717	GAATAAAATTACCTTCCATT
33631	31718	AGAATAAAATTACCTTCCAT
33632	31719	AAGAATAAAATTACCTTCCA
33633	31720	TAAGAATAAAATTACCTTCC
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33635	31722	TCTAAGAATAAAATTACCTT
33636	31723	ATCTAAGAATAAAATTACCT
33637	31724	AATCTAAGAATAAAATTACC
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33639	31726	ATAATCTAAGAATAAAATTA
33640	31727	AATAATCTAAGAATAAAATT
33641	31728	AAATAATCTAAGAATAAAAT
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33643	31730	TTAAATAATCTAAGAATAAA
33644	31731	ATTAAATAATCTAAGAATAA
33645	31732	CATTAAATAATCTAAGAATA
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33647	31734	AACATTAAATAATCTAAGAA

82724	80811	CAGTCTCACAGTGTCAACAT
82725	80812	CCAGTCTCACAGTGTCAACA
82726	80813	GCCAGTCTCACAGTGTCAAC
82727	80814	CGCCAGTCTCACAGTGTCAA
82728	80815	CCGCCAGTCTCACAGTGTCA
82729	80816	ACCGCCAGTCTCACAGTGTC
82730	80817	AACCGCCAGTCTCACAGTGT
82731	80818	GAACCGCCAGTCTCACAGTG
82732	80819	TGAACCGCCAGTCTCACAGT
82733	80820	CTGAACCGCCAGTCTCACAG
82734	80821	ACTGAACCGCCAGTCTCACA
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82736	80823	AAACTGAACCGCCAGTCTCA
82737	80824	CAAACTGAACCGCCAGTCTC
82738	80825	TCAAACTGAACCGCCAGTCT
82739	80826	CTCAAACTGAACCGCCAGTC
82740	80827	CCTCAAACTGAACCGCCAGT
82741	80828	ACCTCAAACTGAACCGCCAG
82742	80829	AACCTCAAACTGAACCGCCA
82743	80830	AAACCTCAAACTGAACCGCC
82744	80831	GAAACCTCAAACTGAACCGC
82745	80832	TGAAACCTCAAACTGAACCG
82746	80833	ATGAAACCTCAAACTGAACC
82747	80834	GATGAAACCTCAAACTGAAC
82748	80835	TGATGAAACCTCAAACTGAA
82749	80836	CTGATGAAACCTCAAACTGA
82750	80837	GCTGATGAAACCTCAAACTG
82751	80838	TGCTGATGAAACCTCAAACT
82752	80839	ATGCTGATGAAACCTCAAAC
82753	80840	AATGCTGATGAAACCTCAAA
82754	80841	CAATGCTGATGAAACCTCAA
82755	80842	GCAATGCTGATGAAACCTCA
82756	80843	GGCAATGCTGATGAAACCTC
82757	80844	CGGCAATGCTGATGAAACCT
82758	80845	TCGGCAATGCTGATGAAACC
82759	80846	ATCGGCAATGCTGATGAAAC
82760	80847	TATCGGCAATGCTGATGAAA
82761	80848	ATATCGGCAATGCTGATGAA
82762	80849	AATATCGGCAATGCTGATGA
82763	80850	CAATATCGGCAATGCTGATG
82764	80851	CCAATATCGGCAATGCTGAT
82765	80852	TCCAATATCGGCAATGCTGA
82766	80853	CTCCAATATCGGCAATGCTG
82767	80854	GCTCCAATATCGGCAATGCT
82768	80855	GGCTCCAATATCGGCAATGC
82769	80856	TGGCTCCAATATCGGCAATG
82770	80857	ATGGCTCCAATATCGGCAAT
82771	80858	CATGGCTCCAATATCGGCAA
82772	80859	TCATGGCTCCAATATCGGCA
82773	80860	TTCATGGCTCCAATATCGGC
82774	80861	TTTCATGGCTCCAATATCGG
82775	80862	TTTTCATGGCTCCAATATCG
82776	80863	TTTTTCATGGCTCCAATATC
82777	80864	GTTTTTCATGGCTCCAATAT
82778	80865	GGTTTTTCATGGCTCCAATA
82779	80866	TGGTTTTTCATGGCTCCAAT
82780	80867	TTGGTTTTTCATGGCTCCAA
82781	80868	TTTGGTTTTTCATGGCTCCA
82782	80869	CTTTGGTTTTTCATGGCTCC
82783	80870	TCTTTGGTTTTTCATGGCTC
82784	80871	TTCTTTGGTTTTTCATGGCT
82785	80872	GTTCTTTGGTTTTTCATGGC
82786	80873	TGTTCTTTGGTTTTTCATGG
82787	80874	CTGTTCTTTGGTTTTTCATG
82788	80875	GCTGTTCTTTGGTTTTTCAT
82789	80876	GGCTGTTCTTTGGTTTTTCA
82790	80877	TGGCTGTTCTTTGGTTTTTC
82791	80878	CTGGCTGTTCTTTGGTTTTT
82792	80879	ACTGGCTGTTCTTTGGTTTT
82793	80880	CACTGGCTGTTCTTTGGTTT
82794	80881	TCACTGGCTGTTCTTTGGTT

131871	129958	CAGTGACCCTCAGATCAAGT
131872	129959	CCAGTGACCCTCAGATCAAG
131873	129960	GCCAGTGACCCTCAGATCAA
131874	129961	TGCCAGTGACCCTCAGATCA
131875	129962	ATGCCAGTGACCCTCAGATC
131876	129963	AATGCCAGTGACCCTCAGAT
131877	129964	TAATGCCAGTGACCCTCAGA
131878	129965	GTAATGCCAGTGACCCTCAG
131879	129966	TGTAATGCCAGTGACCCTCA
131880	129967	ATGTAATGCCAGTGACCCTC
131881	129968	TATGTAATGCCAGTGACCCT
131882	129969	ATATGTAATGCCAGTGACCC
131883	129970	AATATGTAATGCCAGTGACC
131884	129971	AAATATGTAATGCCAGTGAC
131885	129972	AAAATATGTAATGCCAGTGA
131886	129973	AAAAATATGTAATGCCAGTG
131887	129974	AAAAAATATGTAATGCCAGT
131888	129975	AAAAAAATATGTAATGCCAG
131889	129976	AAAAAAAATATGTAATGCCA
131890	129977	CAAAAAAAATATGTAATGCC
131891	129978	GCAAAAAAAATATGTAATGC
131892	129979	AGCAAAAAAAATATGTAATG
131893	129980	CAGCAAAAAAAATATGTAAT
131894	129981	ACAGCAAAAAAAATATGTAA
131895	129982	AACAGCAAAAAAAATATGTA
131896	129983	AAACAGCAAAAAAAATATGT
131897	129984	CAAACAGCAAAAAAAATATG
131898	129985	ACAAACAGCAAAAAAAATAT
131899	129986	AACAAACAGCAAAAAAAATA
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131901	129988	ATAACAAACAGCAAAAAAAA
131902	129989	TATAACAAACAGCAAAAAAA
131903	129990	TTATAACAAACAGCAAAAAA
131904	129991	ATTATAACAAACAGCAAAAA
131905	129992	CATTATAACAAACAGCAAAA
131906	129993	TCATTATAACAAACAGCAAA
131907	129994	ATCATTATAACAAACAGCAA
131908	129995	TATCATTATAACAAACAGCA
131909	129996	TTATCATTATAACAAACAGC
131910	129997	ATTATCATTATAACAAACAG
131911	129998	TATTATCATTATAACAAACA
131912	129999	GTATTATCATTATAACAAAC
131913	130000	AGTATTATCATTATAACAAA
131914	130001	TAGTATTATCATTATAACAA
131915	130002	ATAGTATTATCATTATAACA
131916	130003	CATAGTATTATCATTATAAC
131917	130004	ACATAGTATTATCATTATAA
131918	130005	AACATAGTATTATCATTATA
131919	130006	AAACATAGTATTATCATTAT
131920	130007	GAAACATAGTATTATCATTA
131921	130008	AGAAACATAGTATTATCATT
131922	130009	TAGAAACATAGTATTATCAT
131923	130010	GTAGAAACATAGTATTATCA
131924	130011	TGTAGAAACATAGTATTATC
131925	130012	ATGTAGAAACATAGTATTAT
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131927	130014	TGATGTAGAAACATAGTATT
131928	130015	ATGATGTAGAAACATAGTAT
131929	130016	CATGATGTAGAAACATAGTA
131930	130017	GCATGATGTAGAAACATAGT
131931	130018	AGCATGATGTAGAAACATAG
131932	130019	CAGCATGATGTAGAAACATA
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131934	130021	TACAGCATGATGTAGAAACA
131935	130022	ATACAGCATGATGTAGAAAC
131936	130023	AATACAGCATGATGTAGAAA
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131938	130025	AAAATACAGCATGATGTAGA
131939	130026	TAAAATACAGCATGATGTAG
131940	130027	TTAAAATACAGCATGATGTA
131941	130028	ATTAAAATACAGCATGATGT

33648	31735	AAACATTAAATAATCTAAGA
33649	31736	AAAACATTAAATAATCTAAG
33650	31737	AAAAACATTAAATAATCTAA
33651	31738	GAAAAACATTAAATAATCTA
33652	31739	TGAAAAACATTAAATAATCT
33653	31740	CTGAAAAACATTAAATAATC
33654	31741	ACTGAAAAACATTAAATAAT
33655	31742	AACTGAAAAACATTAAATAA
33656	31743	TAACTGAAAAACATTAAATA
33657	31744	ATAACTGAAAAACATTAAAT
33658	31745	GATAACTGAAAAACATTAAA
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33661	31748	CCTGATAACTGAAAAACATT
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33682	31769	TACACAAACAATCTAACACA
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33685	31772	ATATACACAAACAATCTAAC
33686	31773	AATATACACAAACAATCTAA
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33694	31781	AGCAAAACAATATACACAAA
33695	31782	AAGCAAAACAATATACACAA
33696	31783	CAAGCAAAACAATATACACA
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33698	31785	AACAAGCAAAACAATATACA
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33706	31793	ACTTAATTAACAAGCAAAAC
33707	31794	TACTTAATTAACAAGCAAAA
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33709	31796	GTTACTTAATTAACAAGCAA
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33715	31802	CACTGTGTTACTTAATTAAC
33716	31803	TCACTGTGTTACTTAATTAA
33717	31804	TTCACTGTGTTACTTAATTA
33718	31805	ATTCACTGTGTTACTTAATT

82795	80882	CTCACTGGCTGTTCTTTGGT
82796	80883	TCTCACTGGCTGTTCTTTGG
82797	80884	CTCTCACTGGCTGTTCTTTG
82798	80885	TCTCTCACTGGCTGTTCTTT
82799	80886	TTCTCTCACTGGCTGTTCTT
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82815	80902	TTTTCTCTGAGATCTCTTCT
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82818	80905	TTATTTTCTCTGAGATCTCT
82819	80906	TTTATTTTCTCTGAGATCTC
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82821	80908	ATTTTATTTTCTCTGAGATC
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82823	80910	CAATTTTATTTTCTCTGAGA
82824	80911	TCAATTTTATTTTCTCTGAG
82825	80912	CTCAATTTTATTTTCTCTGA
82826	80913	TCTCAATTTTATTTTCTCTG
82827	80914	TTCTCAATTTTATTTTCTCT
82828	80915	TTTCTCAATTTTATTTTCTC
82829	80916	CTTTCTCAATTTTATTTTCT
82830	80917	ACTTTCTCAATTTTATTTTC
82831	80918	CACTTTCTCAATTTTATTTT
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82833	80920	TTCACTTTCTCAATTTTATT
82834	80921	CTTCACTTTCTCAATTTTAT
82835	80922	CCTTCACTTTCTCAATTTTA
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82837	80924	GTCCTTCACTTTCTCAATTT
82838	80925	TGTCCTTCACTTTCTCAATT
82839	80926	TTGTCCTTCACTTTCTCAAT
82840	80927	TTTGTCCTTCACTTTCTCAA
82841	80928	TTTTGTCCTTCACTTTCTCA
82842	80929	TTTTTGTCCTTCACTTTCTC
82843	80930	TTTTTTGTCCTTCACTTTCT
82844	80931	ATTTTTTGTCCTTCACTTTC
82845	80932	CATTTTTTGTCCTTCACTTT
82846	80933	ACATTTTTTGTCCTTCACTT
82847	80934	AACATTTTTTGTCCTTCACT
82848	80935	CAACATTTTTTGTCCTTCAC
82849	80936	ACAACATTTTTTGTCCTTCA
82850	80937	CACAACATTTTTTGTCCTTC
82851	80938	TCACAACATTTTTTGTCCTT
82852	80939	TTCACAACATTTTTTGTCCT
82853	80940	CTTCACAACATTTTTTGTCC
82854	80941	TCTTCACAACATTTTTTGTC
82855	80942	ATCTTCACAACATTTTTTGT
82856	80943	TATCTTCACAACATTTTTTG
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82859	80946	GTCTATCTTCACAACATTTT
82860	80947	GGTCTATCTTCACAACATTT
82861	80948	TGGTCTATCTTCACAACATT
82862	80949	TTGGTCTATCTTCACAACAT
82863	80950	CTTGGTCTATCTTCACAACA
82864	80951	TCTTGGTCTATCTTCACAAC
82865	80952	ATCTTGGTCTATCTTCACAA

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131943	130030	CCATTAAAATACAGCATGAT
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131945	130032	AACCATTAAAATACAGCATG
131946	130033	CAACCATTAAAATACAGCAT
131947	130034	TCAACCATTAAAATACAGCA
131948	130035	TTCAACCATTAAAATACAGC
131949	130036	ATTCAACCATTAAAATACAG
131950	130037	TATTCAACCATTAAAATACA
131951	130038	ATATTCAACCATTAAAATAC
131952	130039	AATATTCAACCATTAAAATA
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131955	130042	CATAATATTCAACCATTAAA
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131957	130044	GACATAATATTCAACCATTA
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131959	130046	ATGACATAATATTCAACCAT
131960	130047	TATGACATAATATTCAACCA
131961	130048	ATATGACATAATATTCAACC
131962	130049	AATATGACATAATATTCAAC
131963	130050	TAATATGACATAATATTCAA
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131965	130052	TCTAATATGACATAATATTC
131966	130053	ATCTAATATGACATAATATT
131967	130054	TATCTAATATGACATAATAT
131968	130055	ATATCTAATATGACATAATA
131969	130056	TATATCTAATATGACATAAT
131970	130057	ATATATCTAATATGACATAA
131971	130058	AATATATCTAATATGACATA
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131975	130062	CTAAAATATATCTAATATGA
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131979	130066	ATGTCTAAAATATATCTAAT
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131981	130068	TCATGTCTAAAATATATCTA
131982	130069	CTCATGTCTAAAATATATCT
131983	130070	ACTCATGTCTAAAATATATC
131984	130071	GACTCATGTCTAAAATATAT
131985	130072	TGACTCATGTCTAAAATATA
131986	130073	GTGACTCATGTCTAAAATAT
131987	130074	TGTGACTCATGTCTAAAATA
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131989	130076	AGTGTGACTCATGTCTAAAA
131990	130077	AAGTGTGACTCATGTCTAAA
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131992	130079	TAAAGTGTGACTCATGTCTA
131993	130080	TTAAAGTGTGACTCATGTCT
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132005	130092	CATTGGTTATATTTAAAGTG
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33719	31806	TATTCACTGTGTTACTTAAT
33720	31807	TTATTCACTGTGTTACTTAA
33721	31808	CTTATTCACTGTGTTACTTA
33722	31809	TCTTATTCACTGTGTTACTT
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33739	31826	TTTCGTATGTTTGTCTGTCT
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33758	31845	AAATAAAATAAATGTACATT
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33787	31874	TCCAGCCTGGGCAACAGACT
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82866	80953	AATCTTGGTCTATCTTCACA
82867	80954	CAATCTTGGTCTATCTTCAC
82868	80955	TCAATCTTGGTCTATCTTCA
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82886	80973	TCTCTATGGCTGATTCCATC
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82898	80985	TCCCACTTGACCTCTCTATG
82899	80986	ATCCCACTTGACCTCTCTAT
82900	80987	CATCCCACTTGACCTCTCTA
82901	80988	TCATCCCACTTGACCTCTCT
82902	80989	CTCATCCCACTTGACCTCTC
82903	80990	TCTCATCCCACTTGACCTCT
82904	80991	TTCTCATCCCACTTGACCTC
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82914	81001	TGCGTGCTCATTCTCATCCC
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82917	81004	AGATGCGTGCTCATTCTCAT
82918	81005	CAGATGCGTGCTCATTCTCA
82919	81006	ACAGATGCGTGCTCATTCTC
82920	81007	AACAGATGCGTGCTCATTCT
82921	81008	TAACAGATGCGTGCTCATTC
82922	81009	TTAACAGATGCGTGCTCATT
82923	81010	TTTAACAGATGCGTGCTCAT
82924	81011	GTTTAACAGATGCGTGCTCA
82925	81012	AGTTTAACAGATGCGTGCTC
82926	81013	AAGTTTAACAGATGCGTGCT
82927	81014	AAAGTTTAACAGATGCGTGC
82928	81015	CAAAGTTTAACAGATGCGTG
82929	81016	ACAAAGTTTAACAGATGCGT
82930	81017	CACAAAGTTTAACAGATGCG
82931	81018	GCACAAAGTTTAACAGATGC
82932	81019	AGCACAAAGTTTAACAGATG
82933	81020	AAGCACAAAGTTTAACAGAT
82934	81021	TAAGCACAAAGTTTAACAGA
82935	81022	CTAAGCACAAAGTTTAACAG
82936	81023	CCTAAGCACAAAGTTTAACA

132013	130100	TCTGTTCACATTGGTTATAT
132014	130101	TTCTGTTCACATTGGTTATA
132015	130102	ATTCTGTTCACATTGGTTAT
132016	130103	CATTCTGTTCACATTGGTTA
132017	130104	GCATTCTGTTCACATTGGTT
132018	130105	AGCATTCTGTTCACATTGGT
132019	130106	CAGCATTCTGTTCACATTGG
132020	130107	TCAGCATTCTGTTCACATTG
132021	130108	TTCAGCATTCTGTTCACATT
132022	130109	TTTCAGCATTCTGTTCACAT
132023	130110	ATTTCAGCATTCTGTTCACA
132024	130111	CATTTCAGCATTCTGTTCAC
132025	130112	TCATTTCAGCATTCTGTTCA
132026	130113	TTCATTTCAGCATTCTGTTC
132027	130114	TTTCATTTCAGCATTCTGTT
132028	130115	TTTTCATTTCAGCATTCTGT
132029	130116	ATTTTCATTTCAGCATTCTG
132030	130117	CATTTTCATTTCAGCATTCT
132031	130118	TCATTTTCATTTCAGCATTC
132032	130119	CTCATTTTCATTTCAGCATT
132033	130120	TCTCATTTTCATTTCAGCAT
132034	130121	TTCTCATTTTCATTTCAGCA
132035	130122	CTTCTCATTTTCATTTCAGC
132036	130123	ACTTCTCATTTTCATTTCAG
132037	130124	TACTTCTCATTTTCATTTCA
132038	130125	ATACTTCTCATTTTCATTTC
132039	130126	AATACTTCTCATTTTCATTT
132040	130127	AAATACTTCTCATTTTCATT
132041	130128	AAAATACTTCTCATTTTCAT
132042	130129	TAAAATACTTCTCATTTTCA
132043	130130	ATAAAATACTTCTCATTTTC
132044	130131	CATAAAATACTTCTCATTTT
132045	130132	ACATAAAATACTTCTCATTT
132046	130133	TACATAAAATACTTCTCATT
132047	130134	TTACATAAAATACTTCTCAT
132048	130135	TTTACATAAAATACTTCTCA
132049	130136	TTTTACATAAAATACTTCTC
132050	130137	GTTTTACATAAAATACTTCT
132051	130138	AGTTTTACATAAAATACTTC
132052	130139	TAGTTTTACATAAAATACTT
132053	130140	TTAGTTTTACATAAAATACT
132054	130141	CTTAGTTTTACATAAAATAC
132055	130142	GCTTAGTTTTACATAAAATA
132056	130143	TGCTTAGTTTTACATAAAAT
132057	130144	CTGCTTAGTTTTACATAAAA
132058	130145	ACTGCTTAGTTTTACATAAA
132059	130146	TACTGCTTAGTTTTACATAA
132060	130147	ATACTGCTTAGTTTTACATA
132061	130148	AATACTGCTTAGTTTTACAT
132062	130149	AAATACTGCTTAGTTTTACA
132063	130150	TAAATACTGCTTAGTTTTAC
132064	130151	ATAAATACTGCTTAGTTTTA
132065	130152	TATAAATACTGCTTAGTTTT
132066	130153	ATATAAATACTGCTTAGTTT
132067	130154	CATATAAATACTGCTTAGTT
132068	130155	ACATATAAATACTGCTTAGT
132069	130156	CACATATAAATACTGCTTAG
132070	130157	TCACATATAAATACTGCTTA
132071	130158	CTCACATATAAATACTGCTT
132072	130159	TCTCACATATAAATACTGCT
132073	130160	TTCTCACATATAAATACTGC
132074	130161	ATTCTCACATATAAATACTG
132075	130162	TATTCTCACATATAAATACT
132076	130163	TTATTCTCACATATAAATAC
132077	130164	ATTATTCTCACATATAAATA
132078	130165	TATTATTCTCACATATAAAT
132079	130166	TTATTATTCTCACATATAAA
132080	130167	CTTATTATTCTCACATATAA
132081	130168	GCTTATTATTCTCACATATA
132082	130169	TGCTTATTATTCTCACATAT
132083	130170	TTGCTTATTATTCTCACATA

33790	31877	CACTCCAGCCTGGGCAACAG
33791	31878	GCACTCCAGCCTGGGCAACA
33792	31879	TGCACTCCAGCCTGGGCAAC
33793	31880	CTGCACTCCAGCCTGGGCAA
33794	31881	ACTGCACTCCAGCCTGGGCA
33795	31882	CACTGCACTCCAGCCTGGGC
33796	31883	CCACTGCACTCCAGCCTGGG
33797	31884	GCCACTGCACTCCAGCCTGG
33798	31885	GGCCACTGCACTCCAGCCTG
33799	31886	GGGCCACTGCACTCCAGCCT
33800	31887	TGGGCCACTGCACTCCAGCC
33801	31888	TTGGGCCACTGCACTCCAGC
33802	31889	ATTGGGCCACTGCACTCCAG
33803	31890	GATTGGGCCACTGCACTCCA
33804	31891	AGATTGGGCCACTGCACTCC
33805	31892	GAGATTGGGCCACTGCACTC
33806	31893	CGAGATTGGGCCACTGCACT
33807	31894	CCGAGATTGGGCCACTGCAC
33808	31895	GCCGAGATTGGGCCACTGCA
33809	31896	GGCCGAGATTGGGCCACTGC
33810	31897	GGGCCGAGATTGGGCCACTG
33811	31898	TGGGCCGAGATTGGGCCACT
33812	31899	GTGGGCCGAGATTGGGCCAC
33813	31900	AGTGGGCCGAGATTGGGCCA
33814	31901	CAGTGGGCCGAGATTGGGCC
33815	31902	GCAGTGGGCCGAGATTGGGC
33816	31903	TGCAGTGGGCCGAGATTGGG
33817	31904	TTGCAGTGGGCCGAGATTGG
33818	31905	GTTGCAGTGGGCCGAGATTG
33819	31906	GGTTGCAGTGGGCCGAGATT
33820	31907	AGGTTGCAGTGGGCCGAGAT
33821	31908	GAGGTTGCAGTGGGCCGAGA
33822	31909	AGAGGTTGCAGTGGGCCGAG
33823	31910	CAGAGGTTGCAGTGGGCCGA
33824	31911	GCAGAGGTTGCAGTGGGCCG
33825	31912	GGCAGAGGTTGCAGTGGGCC
33826	31913	AGGCAGAGGTTGCAGTGGGC
33827	31914	GAGGCAGAGGTTGCAGTGGG
33828	31915	GGAGGCAGAGGTTGCAGTGG
33829	31916	AGGAGGCAGAGGTTGCAGTG
33830	31917	CAGGAGGCAGAGGTTGCAGT
33831	31918	TCAGGAGGCAGAGGTTGCAG
33832	31919	CTCAGGAGGCAGAGGTTGCA
33833	31920	ACTCAGGAGGCAGAGGTTGC
33834	31921	AACTCAGGAGGCAGAGGTTG
33835	31922	CAACTCAGGAGGCAGAGGTT
33836	31923	TCAACTCAGGAGGCAGAGGT
33837	31924	TTCAACTCAGGAGGCAGAGG
33838	31925	CTTCAACTCAGGAGGCAGAG
33839	31926	GCTTCAACTCAGGAGGCAGA
33840	31927	CGCTTCAACTCAGGAGGCAG
33841	31928	TCGCTTCAACTCAGGAGGCA
33842	31929	ATCGCTTCAACTCAGGAGGC
33843	31930	AATCGCTTCAACTCAGGAGG
33844	31931	GAATCGCTTCAACTCAGGAG
33845	31932	AGAATCGCTTCAACTCAGGA
33846	31933	GAGAATCGCTTCAACTCAGG
33847	31934	AGAGAATCGCTTCAACTCAG
33848	31935	AAGAGAATCGCTTCAACTCA
33849	31936	CAAGAGAATCGCTTCAACTC
33850	31937	ACAAGAGAATCGCTTCAACT
33851	31938	CACAAGAGAATCGCTTCAAC
33852	31939	ACACAAGAGAATCGCTTCAA
33853	31940	GACACAAGAGAATCGCTTCA
33854	31941	TGACACAAGAGAATCGCTTC
33855	31942	CTGACACAAGAGAATCGCTT
33856	31943	GCTGACACAAGAGAATCGCT
33857	31944	GGCTGACACAAGAGAATCGC
33858	31945	AGGCTGACACAAGAGAATCG
33859	31946	GAGGCTGACACAAGAGAATC
33860	31947	TGAGGCTGACACAAGAGAAT

82937	81024	TCCTAAGCACAAAGTTTAAC
82938	81025	CTCCTAAGCACAAAGTTTAA
82939	81026	GCTCCTAAGCACAAAGTTTA
82940	81027	TGCTCCTAAGCACAAAGTTT
82941	81028	CTGCTCCTAAGCACAAAGTT
82942	81029	TCTGCTCCTAAGCACAAAGT
82943	81030	TTCTGCTCCTAAGCACAAAG
82944	81031	ATTCTGCTCCTAAGCACAAA
82945	81032	GATTCTGCTCCTAAGCACAA
82946	81033	AGATTCTGCTCCTAAGCACA
82947	81034	TAGATTCTGCTCCTAAGCAC
82948	81035	TTAGATTCTGCTCCTAAGCA
82949	81036	CTTAGATTCTGCTCCTAAGC
82950	81037	CCTTAGATTCTGCTCCTAAG
82951	81038	CCCTTAGATTCTGCTCCTAA
82952	81039	TCCCTTAGATTCTGCTCCTA
82953	81040	TTCCCTTAGATTCTGCTCCT
82954	81041	CTTCCCTTAGATTCTGCTCC
82955	81042	CCTTCCCTTAGATTCTGCTC
82956	81043	CCCTTCCCTTAGATTCTGCT
82957	81044	TCCCTTCCCTTAGATTCTGC
82958	81045	GTCCCTTCCCTTAGATTCTG
82959	81046	TGTCCCTTCCCTTAGATTCT
82960	81047	CTGTCCCTTCCCTTAGATTC
82961	81048	ACTGTCCCTTCCCTTAGATT
82962	81049	GACTGTCCCTTCCCTTAGAT
82963	81050	GGACTGTCCCTTCCCTTAGA
82964	81051	TGGACTGTCCCTTCCCTTAG
82965	81052	CTGGACTGTCCCTTCCCTTA
82966	81053	TCTGGACTGTCCCTTCCCTT
82967	81054	CTCTGGACTGTCCCTTCCCT
82968	81055	CCTCTGGACTGTCCCTTCCC
82969	81056	ACCTCTGGACTGTCCCTTCC
82970	81057	AACCTCTGGACTGTCCCTTC
82971	81058	TAACCTCTGGACTGTCCCTT
82972	81059	CTAACCTCTGGACTGTCCCT
82973	81060	TCTAACCTCTGGACTGTCCC
82974	81061	TTCTAACCTCTGGACTGTCC
82975	81062	GTTCTAACCTCTGGACTGTC
82976	81063	AGTTCTAACCTCTGGACTGT
82977	81064	GAGTTCTAACCTCTGGACTG
82978	81065	TGAGTTCTAACCTCTGGACT
82979	81066	CTGAGTTCTAACCTCTGGAC
82980	81067	CCTGAGTTCTAACCTCTGGA
82981	81068	CCCTGAGTTCTAACCTCTGG
82982	81069	ACCCTGAGTTCTAACCTCTG
82983	81070	TACCCTGAGTTCTAACCTCT
82984	81071	TTACCCTGAGTTCTAACCTC
82985	81072	CTTACCCTGAGTTCTAACCT
82986	81073	TCTTACCCTGAGTTCTAACC
82987	81074	ATCTTACCCTGAGTTCTAAC
82988	81075	CATCTTACCCTGAGTTCTAA
82989	81076	CCATCTTACCCTGAGTTCTA
82990	81077	TCCATCTTACCCTGAGTTCT
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82992	81079	CTTCCATCTTACCCTGAGTT
82993	81080	TCTTCCATCTTACCCTGAGT
82994	81081	TTCTTCCATCTTACCCTGAG
82995	81082	GTTCTTCCATCTTACCCTGA
82996	81083	TGTTCTTCCATCTTACCCTG
82997	81084	CTGTTCTTCCATCTTACCCT
82998	81085	CCTGTTCTTCCATCTTACCC
82999	81086	CCCTGTTCTTCCATCTTACC
83000	81087	CCCCTGTTCTTCCATCTTAC
83001	81088	GCCCCTGTTCTTCCATCTTA
83002	81089	TGCCCCTGTTCTTCCATCTT
83003	81090	ATGCCCCTGTTCTTCCATCT
83004	81091	GATGCCCCTGTTCTTCCATC
83005	81092	AGATGCCCCTGTTCTTCCAT
83006	81093	CAGATGCCCCTGTTCTTCCA
83007	81094	CCAGATGCCCCTGTTCTTCC

132084	130171	TTTGCTTATTATTCTCACAT
132085	130172	TTTTGCTTATTATTCTCACA
132086	130173	TTTTTGCTTATTATTCTCAC
132087	130174	TTTTTTGCTTATTATTCTCA
132088	130175	TTTTTTTGCTTATTATTCTC
132089	130176	GTTTTTTTGCTTATTATTCT
132090	130177	GGTTTTTTTGCTTATTATTC
132091	130178	GGGTTTTTTTGCTTATTATT
132092	130179	TGGGTTTTTTTGCTTATTAT
132093	130180	ATGGGTTTTTTTGCTTATTA
132094	130181	GATGGGTTTTTTTGCTTATT
132095	130182	AGATGGGTTTTTTTGCTTAT
132096	130183	AAGATGGGTTTTTTTGCTTA
132097	130184	GAAGATGGGTTTTTTTGCTT
132098	130185	CGAAGATGGGTTTTTTTGCT
132099	130186	ACGAAGATGGGTTTTTTTGC
132100	130187	AACGAAGATGGGTTTTTTTG
132101	130188	AAACGAAGATGGGTTTTTTT
132102	130189	AAAACGAAGATGGGTTTTTT
132103	130190	CAAAACGAAGATGGGTTTTT
132104	130191	ACAAAACGAAGATGGGTTTT
132105	130192	CACAAAACGAAGATGGGTTT
132106	130193	TCACAAAACGAAGATGGGTT
132107	130194	GTCACAAAACGAAGATGGGT
132108	130195	AGTCACAAAACGAAGATGGG
132109	130196	TAGTCACAAAACGAAGATGG
132110	130197	TTAGTCACAAAACGAAGATG
132111	130198	TTTAGTCACAAAACGAAGAT
132112	130199	GTTTAGTCACAAAACGAAGA
132113	130200	TGTTTAGTCACAAAACGAAG
132114	130201	CTGTTTAGTCACAAAACGAA
132115	130202	TCTGTTTAGTCACAAAACGA
132116	130203	CTCTGTTTAGTCACAAAACG
132117	130204	TCTCTGTTTAGTCACAAAAC
132118	130205	TTCTCTGTTTAGTCACAAAA
132119	130206	TTTCTCTGTTTAGTCACAAA
132120	130207	ATTTCTCTGTTTAGTCACAA
132121	130208	AATTTCTCTGTTTAGTCACA
132122	130209	AAATTTCTCTGTTTAGTCAC
132123	130210	CAAATTTCTCTGTTTAGTCA
132124	130211	ACAAATTTCTCTGTTTAGTC
132125	130212	CACAAATTTCTCTGTTTAGT
132126	130213	ACACAAATTTCTCTGTTTAG
132127	130214	TACACAAATTTCTCTGTTTA
132128	130215	CTACACAAATTTCTCTGTTT
132129	130216	TCTACACAAATTTCTCTGTT
132130	130217	ATCTACACAAATTTCTCTGT
132131	130218	GATCTACACAAATTTCTCTG
132132	130219	TGATCTACACAAATTTCTCT
132133	130220	TTGATCTACACAAATTTCTC
132134	130221	GTTGATCTACACAAATTTCT
132135	130222	AGTTGATCTACACAAATTTC
132136	130223	AAGTTGATCTACACAAATTT
132137	130224	TAAGTTGATCTACACAAATT
132138	130225	CTAAGTTGATCTACACAAAT
132139	130226	GCTAAGTTGATCTACACAAA
132140	130227	TGCTAAGTTGATCTACACAA
132141	130228	CTGCTAAGTTGATCTACACA
132142	130229	GCTGCTAAGTTGATCTACAC
132143	130230	AGCTGCTAAGTTGATCTACA
132144	130231	CAGCTGCTAAGTTGATCTAC
132145	130232	ACAGCTGCTAAGTTGATCTA
132146	130233	GACAGCTGCTAAGTTGATCT
132147	130234	AGACAGCTGCTAAGTTGATC
132148	130235	TAGACAGCTGCTAAGTTGAT
132149	130236	TTAGACAGCTGCTAAGTTGA
132150	130237	TTTAGACAGCTGCTAAGTTG
132151	130238	CTTTAGACAGCTGCTAAGTT
132152	130239	ACTTTAGACAGCTGCTAAGT
132153	130240	TACTTTAGACAGCTGCTAAG
132154	130241	GTACTTTAGACAGCTGCTAA

33861	31948	ATGAGGCTGACACAAGAGAA
33862	31949	CATGAGGCTGACACAAGAGA
33863	31950	TCATGAGGCTGACACAAGAG
33864	31951	CTCATGAGGCTGACACAAGA
33865	31952	ACTCATGAGGCTGACACAAG
33866	31953	TACTCATGAGGCTGACACAA
33867	31954	CTACTCATGAGGCTGACACA
33868	31955	GCTACTCATGAGGCTGACAC
33869	31956	AGCTACTCATGAGGCTGACA
33870	31957	CAGCTACTCATGAGGCTGAC
33871	31958	CCAGCTACTCATGAGGCTGA
33872	31959	CCCAGCTACTCATGAGGCTG
33873	31960	CCCCAGCTACTCATGAGGCT
33874	31961	GCCCCAGCTACTCATGAGGC
33875	31962	GGCCCCAGCTACTCATGAGG
33876	31963	TGGCCCCAGCTACTCATGAG
33877	31964	ATGGCCCCAGCTACTCATGA
33878	31965	CATGGCCCCAGCTACTCATG
33879	31966	CCATGGCCCCAGCTACTCAT
33880	31967	CCCATGGCCCCAGCTACTCA
33881	31968	ACCCATGGCCCCAGCTACTC
33882	31969	CACCCATGGCCCCAGCTACT
33883	31970	GCACCCATGGCCCCAGCTAC
33884	31971	TGCACCCATGGCCCCAGCTA
33885	31972	GTGCACCCATGGCCCCAGCT
33886	31973	CGTGCACCCATGGCCCCAGC
33887	31974	GCGTGCACCCATGGCCCCAG
33888	31975	GGCGTGCACCCATGGCCCCA
33889	31976	TGGCGTGCACCCATGGCCCC
33890	31977	GTGGCGTGCACCCATGGCCC
33891	31978	GGTGGCGTGCACCCATGGCC
33892	31979	TGGTGGCGTGCACCCATGGC
33893	31980	ATGGTGGCGTGCACCCATGG
33894	31981	TATGGTGGCGTGCACCCATG
33895	31982	GTATGGTGGCGTGCACCCAT
33896	31983	GGTATGGTGGCGTGCACCCA
33897	31984	GGGTATGGTGGCGTGCACCC
33898	31985	CGGGTATGGTGGCGTGCACC
33899	31986	CCGGGTATGGTGGCGTGCAC
33900	31987	GCCGGGTATGGTGGCGTGCA
33901	31988	AGCCGGGTATGGTGGCGTGC
33902	31989	TAGCCGGGTATGGTGGCGTG
33903	31990	TTAGCCGGGTATGGTGGCGT
33904	31991	ATTAGCCGGGTATGGTGGCG
33905	31992	AATTAGCCGGGTATGGTGGC
33906	31993	AAATTAGCCGGGTATGGTGG
33907	31994	AAAATTAGCCGGGTATGGTG
33908	31995	AAAAATTAGCCGGGTATGGT
33909	31996	TAAAAATTAGCCGGGTATGG
33910	31997	ATAAAAATTAGCCGGGTATG
33911	31998	TATAAAAATTAGCCGGGTAT
33912	31999	ATATAAAAATTAGCCGGGTA
33913	32000	AATATAAAAATTAGCCGGGT
33914	32001	AAATATAAAAATTAGCCGGG
33915	32002	AAAATATAAAAATTAGCCGG
33916	32003	AAAAATATAAAAATTAGCCG
33917	32004	TAAAAATATAAAAATTAGCC
33918	32005	CTAAAAATATAAAAATTAGC
33919	32006	ACTAAAAATATAAAAATTAG
33920	32007	TACTAAAAATATAAAAATTA
33921	32008	CTACTAAAAATATAAAAATT
33922	32009	TCTACTAAAAATATAAAAAT
33923	32010	CTCTACTAAAAATATAAAAA
33924	32011	TCTCTACTAAAAATATAAAA
33925	32012	ATCTCTACTAAAAATATAAA
33926	32013	CATCTCTACTAAAAATATAA
33927	32014	CCATCTCTACTAAAAATATA
33928	32015	CCCATCTCTACTAAAAATAT
33929	32016	CCCCATCTCTACTAAAAATA
33930	32017	ACCCCATCTCTACTAAAAAT
33931	32018	AACCCCATCTCTACTAAAAA

83008	81095	CCCAGATGCCCCTGTTCTTC
83009	81096	TCCCAGATGCCCCTGTTCTT
83010	81097	CTCCCAGATGCCCCTGTTCT
83011	81098	ACTCCCAGATGCCCCTGTTC
83012	81099	CACTCCCAGATGCCCCTGTT
83013	81100	TCACTCCCAGATGCCCCTGT
83014	81101	CTCACTCCCAGATGCCCCTG
83015	81102	CCTCACTCCCAGATGCCCCT
83016	81103	GCCTCACTCCCAGATGCCCC
83017	81104	TGCCTCACTCCCAGATGCCC
83018	81105	CTGCCTCACTCCCAGATGCC
83019	81106	ACTGCCTCACTCCCAGATGC
83020	81107	AACTGCCTCACTCCCAGATG
83021	81108	AAACTGCCTCACTCCCAGAT
83022	81109	CAAACTGCCTCACTCCCAGA
83023	81110	CCAAACTGCCTCACTCCCAG
83024	81111	ACCAAACTGCCTCACTCCCA
83025	81112	AACCAAACTGCCTCACTCCC
83026	81113	AAACCAAACTGCCTCACTCC
83027	81114	TAAACCAAACTGCCTCACTC
83028	81115	CTAAACCAAACTGCCTCACT
83029	81116	ACTAAACCAAACTGCCTCAC
83030	81117	CACTAAACCAAACTGCCTCA
83031	81118	ACACTAAACCAAACTGCCTC
83032	81119	TACACTAAACCAAACTGCCT
83033	81120	CTACACTAAACCAAACTGCC
83034	81121	TCTACACTAAACCAAACTGC
83035	81122	TTCTACACTAAACCAAACTG
83036	81123	GTTCTACACTAAACCAAACT
83037	81124	GGTTCTACACTAAACCAAAC
83038	81125	AGGTTCTACACTAAACCAAA
83039	81126	AAGGTTCTACACTAAACCAA
83040	81127	AAAGGTTCTACACTAAACCA
83041	81128	AAAAGGTTCTACACTAAACC
83042	81129	AAAAAGGTTCTACACTAAAC
83043	81130	CAAAAAGGTTCTACACTAAA
83044	81131	ACAAAAAGGTTCTACACTAA
83045	81132	TACAAAAAGGTTCTACACTA
83046	81133	TTACAAAAAGGTTCTACACT
83047	81134	GTTACAAAAAGGTTCTACAC
83048	81135	TGTTACAAAAAGGTTCTACA
83049	81136	TTGTTACAAAAAGGTTCTAC
83050	81137	CTTGTTACAAAAAGGTTCTA
83051	81138	GCTTGTTACAAAAAGGTTCT
83052	81139	TGCTTGTTACAAAAAGGTTC
83053	81140	ATGCTTGTTACAAAAAGGTT
83054	81141	AATGCTTGTTACAAAAAGGT
83055	81142	GAATGCTTGTTACAAAAAGG
83056	81143	GGAATGCTTGTTACAAAAAG
83057	81144	GGGAATGCTTGTTACAAAAA
83058	81145	AGGGAATGCTTGTTACAAAA
83059	81146	AAGGGAATGCTTGTTACAAA
83060	81147	GAAGGGAATGCTTGTTACAA
83061	81148	AGAAGGGAATGCTTGTTACA
83062	81149	CAGAAGGGAATGCTTGTTAC
83063	81150	ACAGAAGGGAATGCTTGTTA
83064	81151	GACAGAAGGGAATGCTTGTT
83065	81152	AGACAGAAGGGAATGCTTGT
83066	81153	TAGACAGAAGGGAATGCTTG
83067	81154	CTAGACAGAAGGGAATGCTT
83068	81155	TCTAGACAGAAGGGAATGCT
83069	81156	ATCTAGACAGAAGGGAATGC
83070	81157	CATCTAGACAGAAGGGAATG
83071	81158	TCATCTAGACAGAAGGGAAT
83072	81159	GTCATCTAGACAGAAGGGAA
83073	81160	AGTCATCTAGACAGAAGGGA
83074	81161	AAGTCATCTAGACAGAAGGG
83075	81162	AAAGTCATCTAGACAGAAGG
83076	81163	AAAAGTCATCTAGACAGAAG
83077	81164	TAAAAGTCATCTAGACAGAA
83078	81165	CTAAAAGTCATCTAGACAGA

132155	130242	GGTACTTTAGACAGCTGCTA
132156	130243	TGGTACTTTAGACAGCTGCT
132157	130244	TTGGTACTTTAGACAGCTGC
132158	130245	TTTGGTACTTTAGACAGCTG
132159	130246	TTTTGGTACTTTAGACAGCT
132160	130247	ATTTTGGTACTTTAGACAGC
132161	130248	TATTTTGGTACTTTAGACAG
132162	130249	TTATTTTGGTACTTTAGACA
132163	130250	ATTATTTTGGTACTTTAGAC
132164	130251	TATTATTTTGGTACTTTAGA
132165	130252	CTATTATTTTGGTACTTTAG
132166	130253	TCTATTATTTTGGTACTTTA
132167	130254	ATCTATTATTTTGGTACTTT
132168	130255	AATCTATTATTTTGGTACTT
132169	130256	AAATCTATTATTTTGGTACT
132170	130257	AAAATCTATTATTTTGGTAC
132171	130258	AAAAATCTATTATTTTGGTA
132172	130259	GAAAAATCTATTATTTTGGT
132173	130260	TGAAAAATCTATTATTTTGG
132174	130261	GTGAAAAATCTATTATTTTG
132175	130262	AGTGAAAAATCTATTATTTT
132176	130263	CAGTGAAAAATCTATTATTT
132177	130264	ACAGTGAAAAATCTATTATT
132178	130265	AACAGTGAAAAATCTATTAT
132179	130266	CAACAGTGAAAAATCTATTA
132180	130267	TCAACAGTGAAAAATCTATT
132181	130268	ATCAACAGTGAAAAATCTAT
132182	130269	TATCAACAGTGAAAAATCTA
132183	130270	TTATCAACAGTGAAAAATCT
132184	130271	ATTATCAACAGTGAAAAATC
132185	130272	AATTATCAACAGTGAAAAAT
132186	130273	AAATTATCAACAGTGAAAAA
132187	130274	TAAATTATCAACAGTGAAAA
132188	130275	TTAAATTATCAACAGTGAAA
132189	130276	TTTAAATTATCAACAGTGAA
132190	130277	TTTTAAATTATCAACAGTGA
132191	130278	ATTTTAAATTATCAACAGTG
132192	130279	TATTTTAAATTATCAACAGT
132193	130280	TTATTTTAAATTATCAACAG
132194	130281	TTTATTTTAAATTATCAACA
132195	130282	TTTTATTTTAAATTATCAAC
132196	130283	ATTTTATTTTAAATTATCAA
132197	130284	CATTTTATTTTAAATTATCA
132198	130285	ACATTTTATTTTAAATTATC
132199	130286	GACATTTTATTTTAAATTAT
132200	130287	GGACATTTTATTTTAAATTA
132201	130288	TGGACATTTTATTTTAAATT
132202	130289	ATGGACATTTTATTTTAAAT
132203	130290	AATGGACATTTTATTTTAAA
132204	130291	AAATGGACATTTTATTTTAA
132205	130292	CAAATGGACATTTTATTTTA
132206	130293	ACAAATGGACATTTTATTTT
132207	130294	TACAAATGGACATTTTATTT
132208	130295	ATACAAATGGACATTTTATT
132209	130296	TATACAAATGGACATTTTAT
132210	130297	ATATACAAATGGACATTTTA
132211	130298	GATATACAAATGGACATTTT
132212	130299	AGATATACAAATGGACATTT
132213	130300	AAGATATACAAATGGACATT
132214	130301	TAAGATATACAAATGGACAT
132215	130302	ATAAGATATACAAATGGACA
132216	130303	CATAAGATATACAAATGGAC
132217	130304	TCATAAGATATACAAATGGA
132218	130305	ATCATAAGATATACAAATGG
132219	130306	TATCATAAGATATACAAATG
132220	130307	GTATCATAAGATATACAAAT
132221	130308	TGTATCATAAGATATACAAA
132222	130309	CTGTATCATAAGATATACAA
132223	130310	TCTGTATCATAAGATATACA
132224	130311	TTCTGTATCATAAGATATAC
132225	130312	ATTCTGTATCATAAGATATA

33932	32019	AAACCCCATCTCTACTAAAA
33933	32020	GAAACCCCATCTCTACTAAA
33934	32021	TGAAACCCCATCTCTACTAA
33935	32022	GTGAAACCCCATCTCTACTA
33936	32023	GGTGAAACCCCATCTCTACT
33937	32024	TGGTGAAACCCCATCTCTAC
33938	32025	ATGGTGAAACCCCATCTCTA
33939	32026	TATGGTGAAACCCCATCTCT
33940	32027	ATATGGTGAAACCCCATCTC
33941	32028	AATATGGTGAAACCCCATCT
33942	32029	CAATATGGTGAAACCCCATC
33943	32030	CCAATATGGTGAAACCCCAT
33944	32031	GCCAATATGGTGAAACCCCA
33945	32032	GGCCAATATGGTGAAACCCC
33946	32033	TGGCCAATATGGTGAAACCC
33947	32034	CTGGCCAATATGGTGAAACC
33948	32035	CCTGGCCAATATGGTGAAAC
33949	32036	GCCTGGCCAATATGGTGAAA
33950	32037	AGCCTGGCCAATATGGTGAA
33951	32038	CAGCCTGGCCAATATGGTGA
33952	32039	CCAGCCTGGCCAATATGGTG
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33955	32042	AGACCAGCCTGGCCAATATG
33956	32043	GAGACCAGCCTGGCCAATAT
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33962	32049	GAATTCGAGACCAGCCTGGC
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33965	32052	CAGGAATTCGAGACCAGCCT
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33967	32054	GTCAGGAATTCGAGACCAGC
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33970	32057	GAGGTCAGGAATTCGAGACC
33971	32058	TGAGGTCAGGAATTCGAGAC
33972	32059	CTGAGGTCAGGAATTCGAGA
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33974	32061	ACCTGAGGTCAGGAATTCGA
33975	32062	CACCTGAGGTCAGGAATTCG
33976	32063	TCACCTGAGGTCAGGAATTC
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33978	32065	GATCACCTGAGGTCAGGAAT
33979	32066	AGATCACCTGAGGTCAGGAA
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33981	32068	GCAGATCACCTGAGGTCAGG
33982	32069	GGCAGATCACCTGAGGTCAG
33983	32070	GGGCAGATCACCTGAGGTCA
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33985	32072	GCGGGCAGATCACCTGAGGT
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33987	32074	AGGCGGGCAGATCACCTGAG
33988	32075	AAGGCGGGCAGATCACCTGA
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33998	32085	TTGGGAGACCAAGGCGGGCA
33999	32086	TTTGGGAGACCAAGGCGGGC
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34002	32089	CACTTTGGGAGACCAAGGCG

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83081	81168	TATCTAAAAGTCATCTAGAC
83082	81169	ATATCTAAAAGTCATCTAGA
83083	81170	CATATCTAAAAGTCATCTAG
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83085	81172	AACATATCTAAAAGTCATCT
83086	81173	AAACATATCTAAAAGTCATC
83087	81174	GAAACATATCTAAAAGTCAT
83088	81175	TGAAACATATCTAAAAGTCA
83089	81176	ATGAAACATATCTAAAAGTC
83090	81177	AATGAAACATATCTAAAAGT
83091	81178	CAATGAAACATATCTAAAAG
83092	81179	CCAATGAAACATATCTAAAA
83093	81180	GCCAATGAAACATATCTAAA
83094	81181	AGCCAATGAAACATATCTAA
83095	81182	AAGCCAATGAAACATATCTA
83096	81183	CAAGCCAATGAAACATATCT
83097	81184	CCAAGCCAATGAAACATATC
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83101	81188	GGTACCAAGCCAATGAAACA
83102	81189	AGGTACCAAGCCAATGAAAC
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83107	81194	CTAAAAGGTACCAAGCCAAT
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83115	81202	ATTTTATTCTAAAAGGTACC
83116	81203	CATTTTATTCTAAAAGGTAC
83117	81204	TCATTTTATTCTAAAAGGTA
83118	81205	ATCATTTTATTCTAAAAGGT
83119	81206	AATCATTTTATTCTAAAAGG
83120	81207	AAATCATTTTATTCTAAAAG
83121	81208	TAAATCATTTTATTCTAAAA
83122	81209	CTAAATCATTTTATTCTAAA
83123	81210	TCTAAATCATTTTATTCTAA
83124	81211	CTCTAAATCATTTTATTCTA
83125	81212	CCTCTAAATCATTTTATTCT
83126	81213	TCCTCTAAATCATTTTATTC
83127	81214	ATCCTCTAAATCATTTTATT
83128	81215	GATCCTCTAAATCATTTTAT
83129	81216	AGATCCTCTAAATCATTTTA
83130	81217	GAGATCCTCTAAATCATTTT
83131	81218	AGAGATCCTCTAAATCATTT
83132	81219	GAGAGATCCTCTAAATCATT
83133	81220	TGAGAGATCCTCTAAATCAT
83134	81221	ATGAGAGATCCTCTAAATCA
83135	81222	AATGAGAGATCCTCTAAATC
83136	81223	AAATGAGAGATCCTCTAAAT
83137	81224	AAAATGAGAGATCCTCTAAA
83138	81225	GAAAATGAGAGATCCTCTAA
83139	81226	TGAAAATGAGAGATCCTCTA
83140	81227	CTGAAAATGAGAGATCCTCT
83141	81228	CCTGAAAATGAGAGATCCTC
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83143	81230	TCCCTGAAAATGAGAGATCC
83144	81231	TTCCCTGAAAATGAGAGATC
83145	81232	TTTCCCTGAAAATGAGAGAT
83146	81233	TTTTCCCTGAAAATGAGAGA
83147	81234	ATTTTCCCTGAAAATGAGAG
83148	81235	TATTTTCCCTGAAAATGAGA
83149	81236	TTATTTTCCCTGAAAATGAG

132226	130313	AATTCTGTATCATAAGATAT
132227	130314	TAATTCTGTATCATAAGATA
132228	130315	TTAATTCTGTATCATAAGAT
132229	130316	ATTAATTCTGTATCATAAGA
132230	130317	CATTAATTCTGTATCATAAG
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132234	130321	AATCCATTAATTCTGTATCA
132235	130322	CAATCCATTAATTCTGTATC
132236	130323	GCAATCCATTAATTCTGTAT
132237	130324	AGCAATCCATTAATTCTGTA
132238	130325	AAGCAATCCATTAATTCTGT
132239	130326	GAAGCAATCCATTAATTCTG
132240	130327	TGAAGCAATCCATTAATTCT
132241	130328	TTGAAGCAATCCATTAATTC
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132262	130349	AAAACATATTCTGAAAAACA
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132264	130351	TAAAAACATATTCTGAAAAA
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132267	130354	ATTTAAAAACATATTCTGAA
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132276	130363	ATCAGTACTATTTAAAAACA
132277	130364	AATCAGTACTATTTAAAAAC
132278	130365	AAATCAGTACTATTTAAAAA
132279	130366	GAAATCAGTACTATTTAAAA
132280	130367	TGAAATCAGTACTATTTAAA
132281	130368	ATGAAATCAGTACTATTTAA
132282	130369	AATGAAATCAGTACTATTTA
132283	130370	TAATGAAATCAGTACTATTT
132284	130371	TTAATGAAATCAGTACTATT
132285	130372	CTTAATGAAATCAGTACTAT
132286	130373	TCTTAATGAAATCAGTACTA
132287	130374	ATCTTAATGAAATCAGTACT
132288	130375	CATCTTAATGAAATCAGTAC
132289	130376	ACATCTTAATGAAATCAGTA
132290	130377	AACATCTTAATGAAATCAGT
132291	130378	AAACATCTTAATGAAATCAG
132292	130379	AAAACATCTTAATGAAATCA
132293	130380	CAAAACATCTTAATGAAATC
132294	130381	ACAAAACATCTTAATGAAAT
132295	130382	AACAAAACATCTTAATGAAA
132296	130383	GAACAAAACATCTTAATGAA

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34004	32091	AGCACTTTGGGAGACCAAGG
34005	32092	CAGCACTTTGGGAGACCAAG
34006	32093	CCAGCACTTTGGGAGACCAA
34007	32094	CCCAGCACTTTGGGAGACCA
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34010	32097	AGTCCCAGCACTTTGGGAGA
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34012	32099	GTAGTCCCAGCACTTTGGGA
34013	32100	TGTAGTCCCAGCACTTTGGG
34014	32101	CTGTAGTCCCAGCACTTTGG
34015	32102	CCTGTAGTCCCAGCACTTTG
34016	32103	GCCTGTAGTCCCAGCACTTT
34017	32104	TGCCTGTAGTCCCAGCACTT
34018	32105	ATGCCTGTAGTCCCAGCACT
34019	32106	CATGCCTGTAGTCCCAGCAC
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34022	32109	GCTCATGCCTGTAGTCCCAG
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34026	32113	AGTGGCTCATGCCTGTAGTC
34027	32114	CAGTGGCTCATGCCTGTAGT
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34036	32123	GGCCTGGCACAGTGGCTCAT
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34045	32132	AAATGAAATGGCCTGGCACA
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34058	32145	AAGAACGTTCCAAAAATGAA
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34062	32149	AAAAAAGAACGTTCCAAAAA
34063	32150	AAAAAAAGAACGTTCCAAAA
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83150	81237	TTTATTTTCCCTGAAAATGA
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83154	81241	TATATTTATTTTCCCTGAAA
83155	81242	ATATATTTATTTTCCCTGAA
83156	81243	AATATATTTATTTTCCCTGA
83157	81244	GAATATATTTATTTTCCCTG
83158	81245	GGAATATATTTATTTTCCCT
83159	81246	AGGAATATATTTATTTTCCC
83160	81247	GAGGAATATATTTATTTTCC
83161	81248	GGAGGAATATATTTATTTTC
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83166	81253	GTCCAGGAGGAATATATTTA
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83169	81256	TTTGTCCAGGAGGAATATAT
83170	81257	CTTTGTCCAGGAGGAATATA
83171	81258	TCTTTGTCCAGGAGGAATAT
83172	81259	TTCTTTGTCCAGGAGGAATA
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83174	81261	ATTTCTTTGTCCAGGAGGAA
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83183	81270	GACTTCTCTATTTCTTTGTC
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83187	81274	ATATGACTTCTCTATTTCTT
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83207	81294	CTGTCTCCCACTTCCCCAGG
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83209	81296	TTCTGTCTCCCACTTCCCCA
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83211	81298	AATTCTGTCTCCCACTTCCC
83212	81299	GAATTCTGTCTCCCACTTCC
83213	81300	TGAATTCTGTCTCCCACTTC
83214	81301	GTGAATTCTGTCTCCCACTT
83215	81302	GGTGAATTCTGTCTCCCACT
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83217	81304	GCGGTGAATTCTGTCTCCCA
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132297	130384	AGAACAAAACATCTTAATGA
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132300	130387	TTCAGAACAAAACATCTTAA
132301	130388	ATTCAGAACAAAACATCTTA
132302	130389	TATTCAGAACAAAACATCTT
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132304	130391	AATATTCAGAACAAAACATC
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132306	130393	GAAATATTCAGAACAAAACA
132307	130394	AGAAATATTCAGAACAAAAC
132308	130395	CAGAAATATTCAGAACAAAA
132309	130396	TCAGAAATATTCAGAACAAA
132310	130397	CTCAGAAATATTCAGAACAA
132311	130398	TCTCAGAAATATTCAGAACA
132312	130399	TTCTCAGAAATATTCAGAAC
132313	130400	GTTCTCAGAAATATTCAGAA
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132315	130402	TAGTTCTCAGAAATATTCAG
132316	130403	GTAGTTCTCAGAAATATTCA
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132318	130405	CGGTAGTTCTCAGAAATATT
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132320	130407	TACGGTAGTTCTCAGAAATA
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132323	130410	CACTACGGTAGTTCTCAGAA
132324	130411	ACACTACGGTAGTTCTCAGA
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132326	130413	CGACACTACGGTAGTTCTCA
132327	130414	ACGACACTACGGTAGTTCTC
132328	130415	AACGACACTACGGTAGTTCT
132329	130416	AAACGACACTACGGTAGTTC
132330	130417	TAAACGACACTACGGTAGTT
132331	130418	CTAAACGACACTACGGTAGT
132332	130419	ACTAAACGACACTACGGTAG
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132335	130422	AAAACTAAACGACACTACGG
132336	130423	GAAAACTAAACGACACTACG
132337	130424	GGAAAACTAAACGACACTAC
132338	130425	AGGAAAACTAAACGACACTA
132339	130426	TAGGAAAACTAAACGACACT
132340	130427	ATAGGAAAACTAAACGACAC
132341	130428	AATAGGAAAACTAAACGACA
132342	130429	AAATAGGAAAACTAAACGAC
132343	130430	CAAATAGGAAAACTAAACGA
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132345	130432	CGCAAATAGGAAAACTAAAC
132346	130433	ACGCAAATAGGAAAACTAAA
132347	130434	AACGCAAATAGGAAAACTAA
132348	130435	AAACGCAAATAGGAAAACTA
132349	130436	AAAACGCAAATAGGAAAACT
132350	130437	AAAAACGCAAATAGGAAAAC
132351	130438	CAAAAACGCAAATAGGAAAA
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132353	130440	ACCAAAAACGCAAATAGGAA
132354	130441	AACCAAAAACGCAAATAGGA
132355	130442	CAACCAAAAACGCAAATAGG
132356	130443	ACAACCAAAAACGCAAATAG
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132366	130453	CCTACTCCAAACAACCAAAA
132367	130454	CCCTACTCCAAACAACCAAA

34074	32161	CATTTCAAAAAAAAAAAAGA
34075	32162	CCATTTCAAAAAAAAAAAAG
34076	32163	CCCATTTCAAAAAAAAAAAA
34077	32164	CCCCATTTCAAAAAAAAAAA
34078	32165	ACCCCATTTCAAAAAAAAAA
34079	32166	GACCCCATTTCAAAAAAAAA
34080	32167	AGACCCCATTTCAAAAAAAA
34081	32168	GAGACCCCATTTCAAAAAAA
34082	32169	CGAGACCCCATTTCAAAAAA
34083	32170	GCGAGACCCCATTTCAAAAA
34084	32171	AGCGAGACCCCATTTCAAAA
34085	32172	GAGCGAGACCCCATTTCAAA
34086	32173	AGAGCGAGACCCCATTTCAA
34087	32174	CAGAGCGAGACCCCATTTCA
34088	32175	ACAGAGCGAGACCCCATTTC
34089	32176	GACAGAGCGAGACCCCATTT
34090	32177	AGACAGAGCGAGACCCCATT
34091	32178	GAGACAGAGCGAGACCCCAT
34092	32179	GGAGACAGAGCGAGACCCCA
34093	32180	GGGAGACAGAGCGAGACCCC
34094	32181	TGGGAGACAGAGCGAGACCC
34095	32182	CTGGGAGACAGAGCGAGACC
34096	32183	CCTGGGAGACAGAGCGAGAC
34097	32184	GCCTGGGAGACAGAGCGAGA
34098	32185	AGCCTGGGAGACAGAGCGAG
34099	32186	CAGCCTGGGAGACAGAGCGA
34100	32187	CCAGCCTGGGAGACAGAGCG
34101	32188	TCCAGCCTGGGAGACAGAGC
34102	32189	CTCCAGCCTGGGAGACAGAG
34103	32190	ACTCCAGCCTGGGAGACAGA
34104	32191	CACTCCAGCCTGGGAGACAG
34105	32192	GCACTCCAGCCTGGGAGACA
34106	32193	TGCACTCCAGCCTGGGAGAC
34107	32194	CTGCACTCCAGCCTGGGAGA
34108	32195	ACTGCACTCCAGCCTGGGAG
34109	32196	CACTGCACTCCAGCCTGGGA
34110	32197	CCACTGCACTCCAGCCTGGG
34111	32198	GCCACTGCACTCCAGCCTGG
34112	32199	AGCCACTGCACTCCAGCCTG
34113	32200	GAGCCACTGCACTCCAGCCT
34114	32201	TGAGCCACTGCACTCCAGCC
34115	32202	TTGAGCCACTGCACTCCAGC
34116	32203	ATTGAGCCACTGCACTCCAG
34117	32204	GATTGAGCCACTGCACTCCA
34118	32205	AGATTGAGCCACTGCACTCC
34119	32206	GAGATTGAGCCACTGCACTC
34120	32207	TGAGATTGAGCCACTGCACT
34121	32208	CTGAGATTGAGCCACTGCAC
34122	32209	GCTGAGATTGAGCCACTGCA
34123	32210	AGCTGAGATTGAGCCACTGC
34124	32211	AAGCTGAGATTGAGCCACTG
34125	32212	TAAGCTGAGATTGAGCCACT
34126	32213	GTAAGCTGAGATTGAGCCAC
34127	32214	AGTAAGCTGAGATTGAGCCA
34128	32215	CAGTAAGCTGAGATTGAGCC
34129	32216	GCAGTAAGCTGAGATTGAGC
34130	32217	TGCAGTAAGCTGAGATTGAG
34131	32218	TTGCAGTAAGCTGAGATTGA
34132	32219	GTTGCAGTAAGCTGAGATTG
34133	32220	GGTTGCAGTAAGCTGAGATT
34134	32221	AGGTTGCAGTAAGCTGAGAT
34135	32222	GAGGTTGCAGTAAGCTGAGA
34136	32223	AGAGGTTGCAGTAAGCTGAG
34137	32224	CAGAGGTTGCAGTAAGCTGA
34138	32225	GCAGAGGTTGCAGTAAGCTG
34139	32226	GGCAGAGGTTGCAGTAAGCT
34140	32227	AGGCAGAGGTTGCAGTAAGC
34141	32228	AAGGCAGAGGTTGCAGTAAG
34142	32229	GAAGGCAGAGGTTGCAGTAA
34143	32230	GGAAGGCAGAGGTTGCAGTA
34144	32231	CGGAAGGCAGAGGTTGCAGT

83221	81308	ATACGCGGTGAATTCTGTCT
83222	81309	CATACGCGGTGAATTCTGTC
83223	81310	CCATACGCGGTGAATTCTGT
83224	81311	CCCATACGCGGTGAATTCTG
83225	81312	GCCCATACGCGGTGAATTCT
83226	81313	GGCCCATACGCGGTGAATTC
83227	81314	TGGCCCATACGCGGTGAATT
83228	81315	CTGGCCCATACGCGGTGAAT
83229	81316	GCTGGCCCATACGCGGTGAA
83230	81317	GGCTGGCCCATACGCGGTGA
83231	81318	AGGCTGGCCCATACGCGGTG
83232	81319	CAGGCTGGCCCATACGCGGT
83233	81320	CCAGGCTGGCCCATACGCGG
83234	81321	TCCAGGCTGGCCCATACGCG
83235	81322	ATCCAGGCTGGCCCATACGC
83236	81323	GATCCAGGCTGGCCCATACG
83237	81324	CGATCCAGGCTGGCCCATAC
83238	81325	CCGATCCAGGCTGGCCCATA
83239	81326	CCCGATCCAGGCTGGCCCAT
83240	81327	GCCCGATCCAGGCTGGCCCA
83241	81328	AGCCCGATCCAGGCTGGCCC
83242	81329	GAGCCCGATCCAGGCTGGCC
83243	81330	GGAGCCCGATCCAGGCTGGC
83244	81331	TGGAGCCCGATCCAGGCTGG
83245	81332	ATGGAGCCCGATCCAGGCTG
83246	81333	CATGGAGCCCGATCCAGGCT
83247	81334	GCATGGAGCCCGATCCAGGC
83248	81335	GGCATGGAGCCCGATCCAGG
83249	81336	TGGCATGGAGCCCGATCCAG
83250	81337	ATGGCATGGAGCCCGATCCA
83251	81338	GATGGCATGGAGCCCGATCC
83252	81339	TGATGGCATGGAGCCCGATC
83253	81340	TTGATGGCATGGAGCCCGAT
83254	81341	CTTGATGGCATGGAGCCCGA
83255	81342	TCTTGATGGCATGGAGCCCG
83256	81343	ATCTTGATGGCATGGAGCCC
83257	81344	GATCTTGATGGCATGGAGCC
83258	81345	GGATCTTGATGGCATGGAGC
83259	81346	TGGATCTTGATGGCATGGAG
83260	81347	GTGGATCTTGATGGCATGGA
83261	81348	AGTGGATCTTGATGGCATGG
83262	81349	AAGTGGATCTTGATGGCATG
83263	81350	GAAGTGGATCTTGATGGCAT
83264	81351	AGAAGTGGATCTTGATGGCA
83265	81352	GAGAAGTGGATCTTGATGGC
83266	81353	TGAGAAGTGGATCTTGATGG
83267	81354	GTGAGAAGTGGATCTTGATG
83268	81355	TGTGAGAAGTGGATCTTGAT
83269	81356	GTGTGAGAAGTGGATCTTGA
83270	81357	AGTGTGAGAAGTGGATCTTG
83271	81358	AAGTGTGAGAAGTGGATCTT
83272	81359	GAAGTGTGAGAAGTGGATCT
83273	81360	TGAAGTGTGAGAAGTGGATC
83274	81361	CTGAAGTGTGAGAAGTGGAT
83275	81362	TCTGAAGTGTGAGAAGTGGA
83276	81363	ATCTGAAGTGTGAGAAGTGG
83277	81364	AATCTGAAGTGTGAGAAGTG
83278	81365	AAATCTGAAGTGTGAGAAGT
83279	81366	GAAATCTGAAGTGTGAGAAG
83280	81367	TGAAATCTGAAGTGTGAGAA
83281	81368	TTGAAATCTGAAGTGTGAGA
83282	81369	GTTGAAATCTGAAGTGTGAG
83283	81370	GGTTGAAATCTGAAGTGTGA
83284	81371	GGGTTGAAATCTGAAGTGTG
83285	81372	CGGGTTGAAATCTGAAGTGT
83286	81373	TCGGGTTGAAATCTGAAGTG
83287	81374	TTCGGGTTGAAATCTGAAGT
83288	81375	ATTCGGGTTGAAATCTGAAG
83289	81376	AATTCGGGTTGAAATCTGAA
83290	81377	GAATTCGGGTTGAAATCTGA
83291	81378	AGAATTCGGGTTGAAATCTG

132368	130455	CCCCTACTCCAAACAACCAA
132369	130456	TCCCCTACTCCAAACAACCA
132370	130457	ATCCCCTACTCCAAACAACC
132371	130458	TATCCCCTACTCCAAACAAC
132372	130459	TTATCCCCTACTCCAAACAA
132373	130460	ATTATCCCCTACTCCAAACA
132374	130461	AATTATCCCCTACTCCAAAC
132375	130462	AAATTATCCCCTACTCCAAA
132376	130463	AAAATTATCCCCTACTCCAA
132377	130464	CAAAATTATCCCCTACTCCA
132378	130465	CCAAAATTATCCCCTACTCC
132379	130466	ACCAAAATTATCCCCTACTC
132380	130467	AACCAAAATTATCCCCTACT
132381	130468	AAACCAAAATTATCCCCTAC
132382	130469	TAAACCAAAATTATCCCCTA
132383	130470	ATAAACCAAAATTATCCCCT
132384	130471	AATAAACCAAAATTATCCCC
132385	130472	GAATAAACCAAAATTATCCC
132386	130473	TGAATAAACCAAAATTATCC
132387	130474	ATGAATAAACCAAAATTATC
132388	130475	TATGAATAAACCAAAATTAT
132389	130476	GTATGAATAAACCAAAATTA
132390	130477	TGTATGAATAAACCAAAATT
132391	130478	CTGTATGAATAAACCAAAAT
132392	130479	ACTGTATGAATAAACCAAAA
132393	130480	AACTGTATGAATAAACCAAA
132394	130481	CAACTGTATGAATAAACCAA
132395	130482	TCAACTGTATGAATAAACCA
132396	130483	TTCAACTGTATGAATAAACC
132397	130484	TTTCAACTGTATGAATAAAC
132398	130485	TTTTCAACTGTATGAATAAA
132399	130486	CTTTTCAACTGTATGAATAA
132400	130487	ACTTTTCAACTGTATGAATA
132401	130488	CACTTTTCAACTGTATGAAT
132402	130489	ACACTTTTCAACTGTATGAA
132403	130490	TACACTTTTCAACTGTATGA
132404	130491	GTACACTTTTCAACTGTATG
132405	130492	AGTACACTTTTCAACTGTAT
132406	130493	CAGTACACTTTTCAACTGTA
132407	130494	GCAGTACACTTTTCAACTGT
132408	130495	AGCAGTACACTTTTCAACTG
132409	130496	TAGCAGTACACTTTTCAACT
132410	130497	ATAGCAGTACACTTTTCAAC
132411	130498	CATAGCAGTACACTTTTCAA
132412	130499	TCATAGCAGTACACTTTTCA
132413	130500	CTCATAGCAGTACACTTTTC
132414	130501	TCTCATAGCAGTACACTTTT
132415	130502	TTCTCATAGCAGTACACTTT
132416	130503	ATTCTCATAGCAGTACACTT
132417	130504	CATTCTCATAGCAGTACACT
132418	130505	TCATTCTCATAGCAGTACAC
132419	130506	CTCATTCTCATAGCAGTACA
132420	130507	TCTCATTCTCATAGCAGTAC
132421	130508	ATCTCATTCTCATAGCAGTA
132422	130509	AATCTCATTCTCATAGCAGT
132423	130510	TAATCTCATTCTCATAGCAG
132424	130511	ATAATCTCATTCTCATAGCA
132425	130512	CATAATCTCATTCTCATAGC
132426	130513	CCATAATCTCATTCTCATAG
132427	130514	ACCATAATCTCATTCTCATA
132428	130515	AACCATAATCTCATTCTCAT
132429	130516	TAACCATAATCTCATTCTCA
132430	130517	GTAACCATAATCTCATTCTC
132431	130518	TGTAACCATAATCTCATTCT
132432	130519	ATGTAACCATAATCTCATTC
132433	130520	CATGTAACCATAATCTCATT
132434	130521	ACATGTAACCATAATCTCAT
132435	130522	TACATGTAACCATAATCTCA
132436	130523	TTACATGTAACCATAATCTC
132437	130524	GTTACATGTAACCATAATCT
132438	130525	AGTTACATGTAACCATAATC

34145	32232	CCGGAAGGCAGAGGTTGCAG
34146	32233	CCCGGAAGGCAGAGGTTGCA
34147	32234	ACCCGGAAGGCAGAGGTTGC
34148	32235	AACCCGGAAGGCAGAGGTTG
34149	32236	GAACCCGGAAGGCAGAGGTT
34150	32237	TGAACCCGGAAGGCAGAGGT
34151	32238	TTGAACCCGGAAGGCAGAGG
34152	32239	CTTGAACCCGGAAGGCAGAG
34153	32240	ACTTGAACCCGGAAGGCAGA
34154	32241	CACTTGAACCCGGAAGGCAG
34155	32242	TCACTTGAACCCGGAAGGCA
34156	32243	ATCACTTGAACCCGGAAGGC
34157	32244	AATCACTTGAACCCGGAAGG
34158	32245	GAATCACTTGAACCCGGAAG
34159	32246	AGAATCACTTGAACCCGGAA
34160	32247	GAGAATCACTTGAACCCGGA
34161	32248	GGAGAATCACTTGAACCCGG
34162	32249	AGGAGAATCACTTGAACCCG
34163	32250	CAGGAGAATCACTTGAACCC
34164	32251	GCAGGAGAATCACTTGAACC
34165	32252	GGCAGGAGAATCACTTGAAC
34166	32253	AGGCAGGAGAATCACTTGAA
34167	32254	GAGGCAGGAGAATCACTTGA
34168	32255	TGAGGCAGGAGAATCACTTG
34169	32256	CTGAGGCAGGAGAATCACTT
34170	32257	GCTGAGGCAGGAGAATCACT
34171	32258	GGCTGAGGCAGGAGAATCAC
34172	32259	AGGCTGAGGCAGGAGAATCA
34173	32260	GAGGCTGAGGCAGGAGAATC
34174	32261	GGAGGCTGAGGCAGGAGAAT
34175	32262	AGGAGGCTGAGGCAGGAGAA
34176	32263	CAGGAGGCTGAGGCAGGAGA
34177	32264	TCAGGAGGCTGAGGCAGGAG
34178	32265	CTCAGGAGGCTGAGGCAGGA
34179	32266	ACTCAGGAGGCTGAGGCAGG
34180	32267	TACTCAGGAGGCTGAGGCAG
34181	32268	ATACTCAGGAGGCTGAGGCA
34182	32269	GATACTCAGGAGGCTGAGGC
34183	32270	AGATACTCAGGAGGCTGAGG
34184	32271	CAGATACTCAGGAGGCTGAG
34185	32272	CCAGATACTCAGGAGGCTGA
34186	32273	CCCAGATACTCAGGAGGCTG
34187	32274	TCCCAGATACTCAGGAGGCT
34188	32275	GTCCCAGATACTCAGGAGGC
34189	32276	AGTCCCAGATACTCAGGAGG
34190	32277	TAGTCCCAGATACTCAGGAG
34191	32278	GTAGTCCCAGATACTCAGGA
34192	32279	TGTAGTCCCAGATACTCAGG
34193	32280	CTGTAGTCCCAGATACTCAG
34194	32281	CCTGTAGTCCCAGATACTCA
34195	32282	ACCTGTAGTCCCAGATACTC
34196	32283	CACCTGTAGTCCCAGATACT
34197	32284	GCACCTGTAGTCCCAGATAC
34198	32285	TGCACCTGTAGTCCCAGATA
34199	32286	ATGCACCTGTAGTCCCAGAT
34200	32287	CATGCACCTGTAGTCCCAGA
34201	32288	GCATGCACCTGTAGTCCCAG
34202	32289	GGCATGCACCTGTAGTCCCA
34203	32290	TGGCATGCACCTGTAGTCCC
34204	32291	GTGGCATGCACCTGTAGTCC
34205	32292	GGTGGCATGCACCTGTAGTC
34206	32293	TGGTGGCATGCACCTGTAGT
34207	32294	GTGGTGGCATGCACCTGTAG
34208	32295	CGTGGTGGCATGCACCTGTA
34209	32296	GCGTGGTGGCATGCACCTGT
34210	32297	GGCGTGGTGGCATGCACCTG
34211	32298	TGGCGTGGTGGCATGCACCT
34212	32299	CTGGCGTGGTGGCATGCACC
34213	32300	CCTGGCGTGGTGGCATGCAC
34214	32301	GCCTGGCGTGGTGGCATGCA
34215	32302	AGCCTGGCGTGGTGGCATGC

83292	81379	CAGAATTCGGGTTGAAATCT
83293	81380	CCAGAATTCGGGTTGAAATC
83294	81381	ACCAGAATTCGGGTTGAAAT
83295	81382	AACCAGAATTCGGGTTGAAA
83296	81383	GAACCAGAATTCGGGTTGAA
83297	81384	TGAACCAGAATTCGGGTTGA
83298	81385	CTGAACCAGAATTCGGGTTG
83299	81386	TCTGAACCAGAATTCGGGTT
83300	81387	GTCTGAACCAGAATTCGGGT
83301	81388	GGTCTGAACCAGAATTCGGG
83302	81389	TGGTCTGAACCAGAATTCGG
83303	81390	TTGGTCTGAACCAGAATTCG
83304	81391	TTTGGTCTGAACCAGAATTC
83305	81392	CTTTGGTCTGAACCAGAATT
83306	81393	TCTTTGGTCTGAACCAGAAT
83307	81394	CTCTTTGGTCTGAACCAGAA
83308	81395	ACTCTTTGGTCTGAACCAGA
83309	81396	TACTCTTTGGTCTGAACCAG
83310	81397	CTACTCTTTGGTCTGAACCA
83311	81398	ACTACTCTTTGGTCTGAACC
83312	81399	AACTACTCTTTGGTCTGAAC
83313	81400	TAACTACTCTTTGGTCTGAA
83314	81401	TTAACTACTCTTTGGTCTGA
83315	81402	ATTAACTACTCTTTGGTCTG
83316	81403	CATTAACTACTCTTTGGTCT
83317	81404	CCATTAACTACTCTTTGGTC
83318	81405	TCCATTAACTACTCTTTGGT
83319	81406	CTCCATTAACTACTCTTTGG
83320	81407	CCTCCATTAACTACTCTTTG
83321	81408	GCCTCCATTAACTACTCTTT
83322	81409	TGCCTCCATTAACTACTCTT
83323	81410	TTGCCTCCATTAACTACTCT
83324	81411	CTTGCCTCCATTAACTACTC
83325	81412	ACTTGCCTCCATTAACTACT
83326	81413	TACTTGCCTCCATTAACTAC
83327	81414	ATACTTGCCTCCATTAACTA
83328	81415	AATACTTGCCTCCATTAACT
83329	81416	AAATACTTGCCTCCATTAAC
83330	81417	AAAATACTTGCCTCCATTAA
83331	81418	CAAAATACTTGCCTCCATTA
83332	81419	TCAAAATACTTGCCTCCATT
83333	81420	GTCAAAATACTTGCCTCCAT
83334	81421	GGTCAAAATACTTGCCTCCA
83335	81422	TGGTCAAAATACTTGCCTCC
83336	81423	CTGGTCAAAATACTTGCCTC
83337	81424	TCTGGTCAAAATACTTGCCT
83338	81425	GTCTGGTCAAAATACTTGCC
83339	81426	AGTCTGGTCAAAATACTTGC
83340	81427	AAGTCTGGTCAAAATACTTG
83341	81428	CAAGTCTGGTCAAAATACTT
83342	81429	ACAAGTCTGGTCAAAATACT
83343	81430	GACAAGTCTGGTCAAAATAC
83344	81431	TGACAAGTCTGGTCAAAATA
83345	81432	TTGACAAGTCTGGTCAAAAT
83346	81433	ATTGACAAGTCTGGTCAAAA
83347	81434	TATTGACAAGTCTGGTCAAA
83348	81435	ATATTGACAAGTCTGGTCAA
83349	81436	GATATTGACAAGTCTGGTCA
83350	81437	TGATATTGACAAGTCTGGTC
83351	81438	ATGATATTGACAAGTCTGGT
83352	81439	AATGATATTGACAAGTCTGG
83353	81440	CAATGATATTGACAAGTCTG
83354	81441	TCAATGATATTGACAAGTCT
83355	81442	ATCAATGATATTGACAAGTC
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83358	81445	TTTATCAATGATATTGACAA
83359	81446	TTTTATCAATGATATTGACA
83360	81447	ATTTTATCAATGATATTGAC
83361	81448	TATTTTATCAATGATATTGA
83362	81449	CTATTTTATCAATGATATTG

132439	130526	TAGTTACATGTAACCATAAT
132440	130527	GTAGTTACATGTAACCATAA
132441	130528	TGTAGTTACATGTAACCATA
132442	130529	ATGTAGTTACATGTAACCAT
132443	130530	CATGTAGTTACATGTAACCA
132444	130531	CCATGTAGTTACATGTAACC
132445	130532	CCCATGTAGTTACATGTAAC
132446	130533	GCCCATGTAGTTACATGTAA
132447	130534	TGCCCATGTAGTTACATGTA
132448	130535	ATGCCCATGTAGTTACATGT
132449	130536	AATGCCCATGTAGTTACATG
132450	130537	AAATGCCCATGTAGTTACAT
132451	130538	GAAATGCCCATGTAGTTACA
132452	130539	TGAAATGCCCATGTAGTTAC
132453	130540	ATGAAATGCCCATGTAGTTA
132454	130541	AATGAAATGCCCATGTAGTT
132455	130542	AAATGAAATGCCCATGTAGT
132456	130543	AAAATGAAATGCCCATGTAG
132457	130544	AAAAATGAAATGCCCATGTA
132458	130545	TAAAAATGAAATGCCCATGT
132459	130546	TTAAAAATGAAATGCCCATG
132460	130547	TTTAAAAATGAAATGCCCAT
132461	130548	CTTTAAAAATGAAATGCCCA
132462	130549	GCTTTAAAAATGAAATGCCC
132463	130550	GGCTTTAAAAATGAAATGCC
132464	130551	AGGCTTTAAAAATGAAATGC
132465	130552	GAGGCTTTAAAAATGAAATG
132466	130553	AGAGGCTTTAAAAATGAAAT
132467	130554	AAGAGGCTTTAAAAATGAAA
132468	130555	AAAGAGGCTTTAAAAATGAA
132469	130556	CAAAGAGGCTTTAAAAATGA
132470	130557	TCAAAGAGGCTTTAAAAATG
132471	130558	TTCAAAGAGGCTTTAAAAAT
132472	130559	GTTCAAAGAGGCTTTAAAAA
132473	130560	AGTTCAAAGAGGCTTTAAAA
132474	130561	AAGTTCAAAGAGGCTTTAAA
132475	130562	AAAGTTCAAAGAGGCTTTAA
132476	130563	AAAAGTTCAAAGAGGCTTTA
132477	130564	AAAAAGTTCAAAGAGGCTTT
132478	130565	CAAAAAGTTCAAAGAGGCTT
132479	130566	TCAAAAAGTTCAAAGAGGCT
132480	130567	TTCAAAAAGTTCAAAGAGGC
132481	130568	TTTCAAAAAGTTCAAAGAGG
132482	130569	ATTTCAAAAAGTTCAAAGAG
132483	130570	TATTTCAAAAAGTTCAAAGA
132484	130571	GTATTTCAAAAAGTTCAAAG
132485	130572	AGTATTTCAAAAAGTTCAAA
132486	130573	TAGTATTTCAAAAAGTTCAA
132487	130574	TTAGTATTTCAAAAAGTTCA
132488	130575	CTTAGTATTTCAAAAAGTTC
132489	130576	TCTTAGTATTTCAAAAAGTT
132490	130577	TTCTTAGTATTTCAAAAAGT
132491	130578	ATTCTTAGTATTTCAAAAAG
132492	130579	TATTCTTAGTATTTCAAAAA
132493	130580	ATATTCTTAGTATTTCAAAA
132494	130581	TATATTCTTAGTATTTCAAA
132495	130582	TTATATTCTTAGTATTTCAA
132496	130583	TTTATATTCTTAGTATTTCA
132497	130584	TTTTATATTCTTAGTATTTC
132498	130585	ATTTTATATTCTTAGTATTT
132499	130586	AATTTTATATTCTTAGTATT
132500	130587	AAATTTTATATTCTTAGTAT
132501	130588	AAAATTTTATATTCTTAGTA
132502	130589	AAAAATTTTATATTCTTAGT
132503	130590	TAAAAATTTTATATTCTTAG
132504	130591	ATAAAAATTTTATATTCTTA
132505	130592	AATAAAAATTTTATATTCTT
132506	130593	AAATAAAAATTTTATATTCT
132507	130594	AAAATAAAAATTTTATATTC
132508	130595	AAAAATAAAAATTTTATATT
132509	130596	AAAAAATAAAAATTTTATAT

34216	32303	TAGCCTGGCGTGGTGGCATG
34217	32304	TTAGCCTGGCGTGGTGGCAT
34218	32305	ATTAGCCTGGCGTGGTGGCA
34219	32306	AATTAGCCTGGCGTGGTGGC
34220	32307	AAATTAGCCTGGCGTGGTGG
34221	32308	AAAATTAGCCTGGCGTGGTG
34222	32309	AAAAATTAGCCTGGCGTGGT
34223	32310	CAAAAATTAGCCTGGCGTGG
34224	32311	ACAAAAATTAGCCTGGCGTG
34225	32312	TACAAAAATTAGCCTGGCGT
34226	32313	ATACAAAAATTAGCCTGGCG
34227	32314	AATACAAAAATTAGCCTGGC
34228	32315	AAATACAAAAATTAGCCTGG
34229	32316	AAAATACAAAAATTAGCCTG
34230	32317	AAAAATACAAAAATTAGCCT
34231	32318	TAAAAATACAAAAATTAGCC
34232	32319	CTAAAAATACAAAAATTAGC
34233	32320	ACTAAAAATACAAAAATTAG
34234	32321	TACTAAAAATACAAAAATTA
34235	32322	CTACTAAAAATACAAAAATT
34236	32323	TCTACTAAAAATACAAAAAT
34237	32324	CTCTACTAAAAATACAAAAA
34238	32325	TCTCTACTAAAAATACAAAA
34239	32326	GTCTCTACTAAAAATACAAA
34240	32327	CGTCTCTACTAAAAATACAA
34241	32328	CCGTCTCTACTAAAAATACA
34242	32329	CCCGTCTCTACTAAAAATAC
34243	32330	CCCCGTCTCTACTAAAAATA
34244	32331	ACCCCGTCTCTACTAAAAAT
34245	32332	AACCCCGTCTCTACTAAAAA
34246	32333	AAACCCCGTCTCTACTAAAA
34247	32334	GAAACCCCGTCTCTACTAAA
34248	32335	TGAAACCCCGTCTCTACTAA
34249	32336	GTGAAACCCCGTCTCTACTA
34250	32337	GGTGAAACCCCGTCTCTACT
34251	32338	TGGTGAAACCCCGTCTCTAC
34252	32339	ATGGTGAAACCCCGTCTCTA
34253	32340	TATGGTGAAACCCCGTCTCT
34254	32341	ATATGGTGAAACCCCGTCTC
34255	32342	AATATGGTGAAACCCCGTCT
34256	32343	CAATATGGTGAAACCCCGTC
34257	32344	CCAATATGGTGAAACCCCGT
34258	32345	ACCAATATGGTGAAACCCCG
34259	32346	CACCAATATGGTGAAACCCC
34260	32347	TCACCAATATGGTGAAACCC
34261	32348	CTCACCAATATGGTGAAACC
34262	32349	CCTCACCAATATGGTGAAAC
34263	32350	GCCTCACCAATATGGTGAAA
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34265	32352	CAGCCTCACCAATATGGTGA
34266	32353	CCAGCCTCACCAATATGGTG
34267	32354	ACCAGCCTCACCAATATGGT
34268	32355	GACCAGCCTCACCAATATGG
34269	32356	AGACCAGCCTCACCAATATG
34270	32357	AAGACCAGCCTCACCAATAT
34271	32358	CAAGACCAGCCTCACCAATA
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34273	32360	TTCAAGACCAGCCTCACCAA
34274	32361	GTTCAAGACCAGCCTCACCA
34275	32362	AGTTCAAGACCAGCCTCACC
34276	32363	GAGTTCAAGACCAGCCTCAC
34277	32364	GGAGTTCAAGACCAGCCTCA
34278	32365	AGGAGTTCAAGACCAGCCTC
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34280	32367	CCAGGAGTTCAAGACCAGCC
34281	32368	GCCAGGAGTTCAAGACCAGC
34282	32369	AGCCAGGAGTTCAAGACCAG
34283	32370	AAGCCAGGAGTTCAAGACCA
34284	32371	GAAGCCAGGAGTTCAAGACC
34285	32372	CGAAGCCAGGAGTTCAAGAC
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83363	81450	ACTATTTTATCAATGATATT
83364	81451	AACTATTTTATCAATGATAT
83365	81452	AAACTATTTTATCAATGATA
83366	81453	AAAACTATTTTATCAATGAT
83367	81454	GAAAACTATTTTATCAATGA
83368	81455	AGAAAACTATTTTATCAATG
83369	81456	TAGAAAACTATTTTATCAAT
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83373	81460	TATTTAGAAAACTATTTTAT
83374	81461	GTATTTAGAAAACTATTTTA
83375	81462	AGTATTTAGAAAACTATTTT
83376	81463	AAGTATTTAGAAAACTATTT
83377	81464	TAAGTATTTAGAAAACTATT
83378	81465	TTAAGTATTTAGAAAACTAT
83379	81466	TTTAAGTATTTAGAAAACTA
83380	81467	TTTTAAGTATTTAGAAAACT
83381	81468	ATTTTAAGTATTTAGAAAAC
83382	81469	TATTTTAAGTATTTAGAAAA
83383	81470	GTATTTTAAGTATTTAGAAA
83384	81471	AGTATTTTAAGTATTTAGAA
83385	81472	AAGTATTTTAAGTATTTAGA
83386	81473	TAAGTATTTTAAGTATTTAG
83387	81474	TTAAGTATTTTAAGTATTTA
83388	81475	TTTAAGTATTTTAAGTATTT
83389	81476	TTTTAAGTATTTTAAGTATT
83390	81477	ATTTTAAGTATTTTAAGTAT
83391	81478	TATTTTAAGTATTTTAAGTA
83392	81479	CTATTTTAAGTATTTTAAGT
83393	81480	ACTATTTTAAGTATTTTAAG
83394	81481	AACTATTTTAAGTATTTTAA
83395	81482	AAACTATTTTAAGTATTTTA
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83398	81485	TGTAAACTATTTTAAGTATT
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83400	81487	TATGTAAACTATTTTAAGTA
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83405	81492	TCAGTTATGTAAACTATTTT
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83411	81498	TTCATATCAGTTATGTAAAC
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83413	81500	CATTCATATCAGTTATGTAA
83414	81501	ACATTCATATCAGTTATGTA
83415	81502	CACATTCATATCAGTTATGT
83416	81503	GCACATTCATATCAGTTATG
83417	81504	TGCACATTCATATCAGTTAT
83418	81505	GTGCACATTCATATCAGTTA
83419	81506	AGTGCACATTCATATCAGTT
83420	81507	AAGTGCACATTCATATCAGT
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83422	81509	TAAAGTGCACATTCATATCA
83423	81510	TTAAAGTGCACATTCATATC
83424	81511	ATTAAAGTGCACATTCATAT
83425	81512	CATTAAAGTGCACATTCATA
83426	81513	TCATTAAAGTGCACATTCAT
83427	81514	ATCATTAAAGTGCACATTCA
83428	81515	AATCATTAAAGTGCACATTC
83429	81516	AAATCATTAAAGTGCACATT
83430	81517	CAAATCATTAAAGTGCACAT
83431	81518	CCAAATCATTAAAGTGCACA
83432	81519	ACCAAATCATTAAAGTGCAC
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132512	130599	CTTAAAAAATAAAAATTTTA
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132515	130602	AAACTTAAAAAATAAAAATT
132516	130603	TAAACTTAAAAAATAAAAAT
132517	130604	CTAAACTTAAAAAATAAAAA
132518	130605	TCTAAACTTAAAAAATAAAA
132519	130606	ATCTAAACTTAAAAAATAAA
132520	130607	CATCTAAACTTAAAAAATAA
132521	130608	ACATCTAAACTTAAAAAATA
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132523	130610	GGACATCTAAACTTAAAAAA
132524	130611	AGGACATCTAAACTTAAAAA
132525	130612	CAGGACATCTAAACTTAAAA
132526	130613	TCAGGACATCTAAACTTAAA
132527	130614	TTCAGGACATCTAAACTTAA
132528	130615	GTTCAGGACATCTAAACTTA
132529	130616	CGTTCAGGACATCTAAACTT
132530	130617	TCGTTCAGGACATCTAAACT
132531	130618	CTCGTTCAGGACATCTAAAC
132532	130619	ACTCGTTCAGGACATCTAAA
132533	130620	TACTCGTTCAGGACATCTAA
132534	130621	ATACTCGTTCAGGACATCTA
132535	130622	CATACTCGTTCAGGACATCT
132536	130623	ACATACTCGTTCAGGACATC
132537	130624	AACATACTCGTTCAGGACAT
132538	130625	AAACATACTCGTTCAGGACA
132539	130626	TAAACATACTCGTTCAGGAC
132540	130627	CTAAACATACTCGTTCAGGA
132541	130628	CCTAAACATACTCGTTCAGG
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132544	130631	TTGCCTAAACATACTCGTTC
132545	130632	TTTGCCTAAACATACTCGTT
132546	130633	TTTTGCCTAAACATACTCGT
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132548	130635	AATTTTGCCTAAACATACTC
132549	130636	CAATTTTGCCTAAACATACT
132550	130637	TCAATTTTGCCTAAACATAC
132551	130638	CTCAATTTTGCCTAAACATA
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132553	130640	AACTCAATTTTGCCTAAACA
132554	130641	TAACTCAATTTTGCCTAAAC
132555	130642	ATAACTCAATTTTGCCTAAA
132556	130643	AATAACTCAATTTTGCCTAA
132557	130644	AAATAACTCAATTTTGCCTA
132558	130645	TAAATAACTCAATTTTGCCT
132559	130646	TTAAATAACTCAATTTTGCC
132560	130647	CTTAAATAACTCAATTTTGC
132561	130648	TCTTAAATAACTCAATTTTG
132562	130649	TTCTTAAATAACTCAATTTT
132563	130650	ATTCTTAAATAACTCAATTT
132564	130651	AATTCTTAAATAACTCAATT
132565	130652	AAATTCTTAAATAACTCAAT
132566	130653	TAAATTCTTAAATAACTCAA
132567	130654	ATAAATTCTTAAATAACTCA
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132570	130657	CCTATAAATTCTTAAATAAC
132571	130658	GCCTATAAATTCTTAAATAA
132572	130659	AGCCTATAAATTCTTAAATA
132573	130660	CAGCCTATAAATTCTTAAAT
132574	130661	CCAGCCTATAAATTCTTAAA
132575	130662	CCCAGCCTATAAATTCTTAA
132576	130663	GCCCAGCCTATAAATTCTTA
132577	130664	CGCCCAGCCTATAAATTCTT
132578	130665	GCGCCCAGCCTATAAATTCT
132579	130666	TGCGCCCAGCCTATAAATTC
132580	130667	CTGCGCCCAGCCTATAAATT

34287	32374	CACGAAGCCAGGAGTTCAAG
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34293	32380	GCAGATCACGAAGCCAGGAG
34294	32381	GGCAGATCACGAAGCCAGGA
34295	32382	GGGCAGATCACGAAGCCAGG
34296	32383	CGGGCAGATCACGAAGCCAG
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34301	32388	TGAGGCGGGCAGATCACGAA
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34304	32391	AGTTGAGGCGGGCAGATCAC
34305	32392	AAGTTGAGGCGGGCAGATCA
34306	32393	GAAGTTGAGGCGGGCAGATC
34307	32394	CGAAGTTGAGGCGGGCAGAT
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34312	32399	CTTTGCGAAGTTGAGGCGGG
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34321	32408	ATCCCAGCACTTTGCGAAGT
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34326	32413	TTGTAATCCCAGCACTTTGC
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34336	32423	TGGCTCACACTTGTAATCCC
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34338	32425	GGTGGCTCACACTTGTAATC
34339	32426	TGGTGGCTCACACTTGTAAT
34340	32427	GTGGTGGCTCACACTTGTAA
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34345	32432	CGGGCGTGGTGGCTCACACT
34346	32433	CCGGGCGTGGTGGCTCACAC
34347	32434	GCCGGGCGTGGTGGCTCACA
34348	32435	GGCCGGGCGTGGTGGCTCAC
34349	32436	AGGCCGGGCGTGGTGGCTCA
34350	32437	CAGGCCGGGCGTGGTGGCTC
34351	32438	ACAGGCCGGGCGTGGTGGCT
34352	32439	AACAGGCCGGGCGTGGTGGC
34353	32440	AAACAGGCCGGGCGTGGTGG
34354	32441	GAAACAGGCCGGGCGTGGTG
34355	32442	AGAAACAGGCCGGGCGTGGT
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34357	32444	CCAGAAACAGGCCGGGCGTG

83434	81521	TCACCAAATCATTAAAGTGC
83435	81522	CTCACCAAATCATTAAAGTG
83436	81523	ACTCACCAAATCATTAAAGT
83437	81524	TACTCACCAAATCATTAAAG
83438	81525	CTACTCACCAAATCATTAAA
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83440	81527	AGCTACTCACCAAATCATTA
83441	81528	AAGCTACTCACCAAATCATT
83442	81529	AAAGCTACTCACCAAATCAT
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83444	81531	TGAAAGCTACTCACCAAATC
83445	81532	GTGAAAGCTACTCACCAAAT
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83449	81536	TGAAGTGAAAGCTACTCACC
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83453	81540	ATGCTGAAGTGAAAGCTACT
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83456	81543	GTAATGCTGAAGTGAAAGCT
83457	81544	AGTAATGCTGAAGTGAAAGC
83458	81545	AAGTAATGCTGAAGTGAAAG
83459	81546	TAAGTAATGCTGAAGTGAAA
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83462	81549	TTTTAAGTAATGCTGAAGTG
83463	81550	ATTTTAAGTAATGCTGAAGT
83464	81551	AATTTTAAGTAATGCTGAAG
83465	81552	CAATTTTAAGTAATGCTGAA
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83467	81554	GCCAATTTTAAGTAATGCTG
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83469	81556	AAGCCAATTTTAAGTAATGC
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83476	81563	TCCACAAAAGCCAATTTTAA
83477	81564	ATCCACAAAAGCCAATTTTA
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83480	81567	AATATCCACAAAAGCCAATT
83481	81568	TAATATCCACAAAAGCCAAT
83482	81569	TTAATATCCACAAAAGCCAA
83483	81570	TTTAATATCCACAAAAGCCA
83484	81571	ATTTAATATCCACAAAAGCC
83485	81572	AATTTAATATCCACAAAAGC
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83487	81574	CTAATTTAATATCCACAAAA
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83490	81577	TTACTAATTTAATATCCACA
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83492	81579	TTTTACTAATTTAATATCCA
83493	81580	GTTTTACTAATTTAATATCC
83494	81581	TGTTTTACTAATTTAATATC
83495	81582	ATGTTTTACTAATTTAATAT
83496	81583	AATGTTTTACTAATTTAATA
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83498	81585	ACAATGTTTTACTAATTTAA
83499	81586	TACAATGTTTTACTAATTTA
83500	81587	ATACAATGTTTTACTAATTT
83501	81588	TATACAATGTTTTACTAATT
83502	81589	ATATACAATGTTTTACTAAT
83503	81590	CATATACAATGTTTTACTAA
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132581	130668	ACTGCGCCCAGCCTATAAAT
132582	130669	CACTGCGCCCAGCCTATAAA
132583	130670	CCACTGCGCCCAGCCTATAA
132584	130671	GCCACTGCGCCCAGCCTATA
132585	130672	AGCCACTGCGCCCAGCCTAT
132586	130673	GAGCCACTGCGCCCAGCCTA
132587	130674	TGAGCCACTGCGCCCAGCCT
132588	130675	GTGAGCCACTGCGCCCAGCC
132589	130676	CGTGAGCCACTGCGCCCAGC
132590	130677	GCGTGAGCCACTGCGCCCAG
132591	130678	GGCGTGAGCCACTGCGCCCA
132592	130679	AGGCGTGAGCCACTGCGCCC
132593	130680	CAGGCGTGAGCCACTGCGCC
132594	130681	ACAGGCGTGAGCCACTGCGC
132595	130682	TACAGGCGTGAGCCACTGCG
132596	130683	TTACAGGCGTGAGCCACTGC
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132598	130685	GATTACAGGCGTGAGCCACT
132599	130686	GGATTACAGGCGTGAGCCAC
132600	130687	GGGATTACAGGCGTGAGCCA
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132603	130690	GCTGGGATTACAGGCGTGAG
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132608	130695	AAAGTGCTGGGATTACAGGC
132609	130696	CAAAGTGCTGGGATTACAGG
132610	130697	CCAAAGTGCTGGGATTACAG
132611	130698	CCCAAAGTGCTGGGATTACA
132612	130699	TCCCAAAGTGCTGGGATTAC
132613	130700	CTCCCAAAGTGCTGGGATTA
132614	130701	CCTCCCAAAGTGCTGGGATT
132615	130702	GCCTCCCAAAGTGCTGGGAT
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132621	130708	GCCTTGGCCTCCCAAAGTGC
132622	130709	AGCCTTGGCCTCCCAAAGTG
132623	130710	CAGCCTTGGCCTCCCAAAGT
132624	130711	CCAGCCTTGGCCTCCCAAAG
132625	130712	GCCAGCCTTGGCCTCCCAAA
132626	130713	CGCCAGCCTTGGCCTCCCAA
132627	130714	CCGCCAGCCTTGGCCTCCCA
132628	130715	TCCGCCAGCCTTGGCCTCCC
132629	130716	ATCCGCCAGCCTTGGCCTCC
132630	130717	GATCCGCCAGCCTTGGCCTC
132631	130718	TGATCCGCCAGCCTTGGCCT
132632	130719	ATGATCCGCCAGCCTTGGCC
132633	130720	CATGATCCGCCAGCCTTGGC
132634	130721	TCATGATCCGCCAGCCTTGG
132635	130722	CTCATGATCCGCCAGCCTTG
132636	130723	CCTCATGATCCGCCAGCCTT
132637	130724	ACCTCATGATCCGCCAGCCT
132638	130725	GACCTCATGATCCGCCAGCC
132639	130726	TGACCTCATGATCCGCCAGC
132640	130727	CTGACCTCATGATCCGCCAG
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132649	130736	CTCGATCTCCTGACCTCATG
132650	130737	TCTCGATCTCCTGACCTCAT
132651	130738	GTCTCGATCTCCTGACCTCA

34358	32445	TCCAGAAACAGGCCGGGCGT
34359	32446	TTCCAGAAACAGGCCGGGCG
34360	32447	ATTCCAGAAACAGGCCGGGC
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34362	32449	ATATTCCAGAAACAGGCCGG
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34367	32454	TATGAATATTCCAGAAACAG
34368	32455	TTATGAATATTCCAGAAACA
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34370	32457	GATTATGAATATTCCAGAAA
34371	32458	AGATTATGAATATTCCAGAA
34372	32459	AAGATTATGAATATTCCAGA
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34374	32461	AAAAGATTATGAATATTCCA
34375	32462	CAAAAGATTATGAATATTCC
34376	32463	ACAAAAGATTATGAATATTC
34377	32464	AACAAAAGATTATGAATATT
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34381	32468	TGACAACAAAAGATTATGAA
34382	32469	ATGACAACAAAAGATTATGA
34383	32470	AATGACAACAAAAGATTATG
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34386	32473	TGAAATGACAACAAAAGATT
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34388	32475	GTTGAAATGACAACAAAAGA
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34390	32477	CTGTTGAAATGACAACAAAA
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34395	32482	GAGCACTGTTGAAATGACAA
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34400	32487	GCTGTGAGCACTGTTGAAAT
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34406	32493	GAAGCTGCTGTGAGCACTGT
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34409	32496	GGTGAAGCTGCTGTGAGCAC
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34412	32499	CCTGGTGAAGCTGCTGTGAG
34413	32500	ACCTGGTGAAGCTGCTGTGA
34414	32501	CACCTGGTGAAGCTGCTGTG
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34416	32503	TACACCTGGTGAAGCTGCTG
34417	32504	CTACACCTGGTGAAGCTGCT
34418	32505	TCTACACCTGGTGAAGCTGC
34419	32506	ATCTACACCTGGTGAAGCTG
34420	32507	AATCTACACCTGGTGAAGCT
34421	32508	GAATCTACACCTGGTGAAGC
34422	32509	GGAATCTACACCTGGTGAAG
34423	32510	TGGAATCTACACCTGGTGAA
34424	32511	ATGGAATCTACACCTGGTGA
34425	32512	GATGGAATCTACACCTGGTG
34426	32513	AGATGGAATCTACACCTGGT
34427	32514	AAGATGGAATCTACACCTGG
34428	32515	TAAGATGGAATCTACACCTG

83505	81592	GACATATACAATGTTTTACT
83506	81593	TGACATATACAATGTTTTAC
83507	81594	ATGACATATACAATGTTTTA
83508	81595	AATGACATATACAATGTTTT
83509	81596	CAATGACATATACAATGTTT
83510	81597	TCAATGACATATACAATGTT
83511	81598	GTCAATGACATATACAATGT
83512	81599	TGTCAATGACATATACAATG
83513	81600	ATGTCAATGACATATACAAT
83514	81601	TATGTCAATGACATATACAA
83515	81602	ATATGTCAATGACATATACA
83516	81603	TATATGTCAATGACATATAC
83517	81604	ATATATGTCAATGACATATA
83518	81605	TATATATGTCAATGACATAT
83519	81606	ATATATATGTCAATGACATA
83520	81607	AATATATATGTCAATGACAT
83521	81608	TAATATATATGTCAATGACA
83522	81609	ATAATATATATGTCAATGAC
83523	81610	AATAATATATATGTCAATGA
83524	81611	AAATAATATATATGTCAATG
83525	81612	TAAATAATATATATGTCAAT
83526	81613	CTAAATAATATATATGTCAA
83527	81614	GCTAAATAATATATATGTCA
83528	81615	TGCTAAATAATATATATGTC
83529	81616	ATGCTAAATAATATATATGT
83530	81617	CATGCTAAATAATATATATG
83531	81618	TCATGCTAAATAATATATAT
83532	81619	ATCATGCTAAATAATATATA
83533	81620	CATCATGCTAAATAATATAT
83534	81621	TCATCATGCTAAATAATATA
83535	81622	TTCATCATGCTAAATAATAT
83536	81623	TTTCATCATGCTAAATAATA
83537	81624	ATTTCATCATGCTAAATAAT
83538	81625	TATTTCATCATGCTAAATAA
83539	81626	ATATTTCATCATGCTAAATA
83540	81627	AATATTTCATCATGCTAAAT
83541	81628	GAATATTTCATCATGCTAAA
83542	81629	TGAATATTTCATCATGCTAA
83543	81630	ATGAATATTTCATCATGCTA
83544	81631	CATGAATATTTCATCATGCT
83545	81632	TCATGAATATTTCATCATGC
83546	81633	ATCATGAATATTTCATCATG
83547	81634	CATCATGAATATTTCATCAT
83548	81635	ACATCATGAATATTTCATCA
83549	81636	TACATCATGAATATTTCATC
83550	81637	GTACATCATGAATATTTCAT
83551	81638	AGTACATCATGAATATTTCA
83552	81639	TAGTACATCATGAATATTTC
83553	81640	TTAGTACATCATGAATATTT
83554	81641	CTTAGTACATCATGAATATT
83555	81642	TCTTAGTACATCATGAATAT
83556	81643	ATCTTAGTACATCATGAATA
83557	81644	TATCTTAGTACATCATGAAT
83558	81645	TTATCTTAGTACATCATGAA
83559	81646	TTTATCTTAGTACATCATGA
83560	81647	CTTTATCTTAGTACATCATG
83561	81648	ACTTTATCTTAGTACATCAT
83562	81649	CACTTTATCTTAGTACATCA
83563	81650	GCACTTTATCTTAGTACATC
83564	81651	AGCACTTTATCTTAGTACAT
83565	81652	TAGCACTTTATCTTAGTACA
83566	81653	GTAGCACTTTATCTTAGTAC
83567	81654	TGTAGCACTTTATCTTAGTA
83568	81655	ATGTAGCACTTTATCTTAGT
83569	81656	AATGTAGCACTTTATCTTAG
83570	81657	AAATGTAGCACTTTATCTTA
83571	81658	TAAATGTAGCACTTTATCTT
83572	81659	TTAAATGTAGCACTTTATCT
83573	81660	GTTAAATGTAGCACTTTATC
83574	81661	GGTTAAATGTAGCACTTTAT
83575	81662	GGGTTAAATGTAGCACTTTA

132652	130739	GGTCTCGATCTCCTGACCTC
132653	130740	TGGTCTCGATCTCCTGACCT
132654	130741	CTGGTCTCGATCTCCTGACC
132655	130742	GCTGGTCTCGATCTCCTGAC
132656	130743	GGCTGGTCTCGATCTCCTGA
132657	130744	AGGCTGGTCTCGATCTCCTG
132658	130745	CAGGCTGGTCTCGATCTCCT
132659	130746	CCAGGCTGGTCTCGATCTCC
132660	130747	GCCAGGCTGGTCTCGATCTC
132661	130748	GGCCAGGCTGGTCTCGATCT
132662	130749	TGGCCAGGCTGGTCTCGATC
132663	130750	TTGGCCAGGCTGGTCTCGAT
132664	130751	GTTGGCCAGGCTGGTCTCGA
132665	130752	TGTTGGCCAGGCTGGTCTCG
132666	130753	ATGTTGGCCAGGCTGGTCTC
132667	130754	CATGTTGGCCAGGCTGGTCT
132668	130755	CCATGTTGGCCAGGCTGGTC
132669	130756	ACCATGTTGGCCAGGCTGGT
132670	130757	CACCATGTTGGCCAGGCTGG
132671	130758	TCACCATGTTGGCCAGGCTG
132672	130759	TTCACCATGTTGGCCAGGCT
132673	130760	TTTCACCATGTTGGCCAGGC
132674	130761	GTTTCACCATGTTGGCCAGG
132675	130762	GGTTTCACCATGTTGGCCAG
132676	130763	GGGTTTCACCATGTTGGCCA
132677	130764	GGGGTTTCACCATGTTGGCC
132678	130765	TGGGGTTTCACCATGTTGGC
132679	130766	ATGGGGTTTCACCATGTTGG
132680	130767	GATGGGGTTTCACCATGTTG
132681	130768	AGATGGGGTTTCACCATGTT
132682	130769	GAGATGGGGTTTCACCATGT
132683	130770	AGAGATGGGGTTTCACCATG
132684	130771	TAGAGATGGGGTTTCACCAT
132685	130772	GTAGAGATGGGGTTTCACCA
132686	130773	AGTAGAGATGGGGTTTCACC
132687	130774	TAGTAGAGATGGGGTTTCAC
132688	130775	TTAGTAGAGATGGGGTTTCA
132689	130776	TTTAGTAGAGATGGGGTTTC
132690	130777	TTTTAGTAGAGATGGGGTTT
132691	130778	TTTTTAGTAGAGATGGGGTT
132692	130779	ATTTTTAGTAGAGATGGGGT
132693	130780	GATTTTTAGTAGAGATGGGG
132694	130781	GGATTTTTAGTAGAGATGGG
132695	130782	TGGATTTTTAGTAGAGATGG
132696	130783	TTGGATTTTTAGTAGAGATG
132697	130784	TTTGGATTTTTAGTAGAGAT
132698	130785	TTTTGGATTTTTAGTAGAGA
132699	130786	TTTTTGGATTTTTAGTAGAG
132700	130787	TTTTTTGGATTTTTAGTAGA
132701	130788	ATTTTTTGGATTTTTAGTAG
132702	130789	AATTTTTTGGATTTTTAGTA
132703	130790	CAATTTTTTGGATTTTTAGT
132704	130791	CCAATTTTTTGGATTTTTAG
132705	130792	GCCAATTTTTTGGATTTTTA
132706	130793	GGCCAATTTTTTGGATTTTT
132707	130794	CGGCCAATTTTTTGGATTTT
132708	130795	CCGGCCAATTTTTTGGATTT
132709	130796	CCCGGCCAATTTTTTGGATT
132710	130797	ACCCGGCCAATTTTTTGGAT
132711	130798	CACCCGGCCAATTTTTTGGA
132712	130799	ACACCCGGCCAATTTTTTGG
132713	130800	CACACCCGGCCAATTTTTTG
132714	130801	CCACACCCGGCCAATTTTTT
132715	130802	ACCACACCCGGCCAATTTTT
132716	130803	CACCACACCCGGCCAATTTT
132717	130804	CCACCACACCCGGCCAATTT
132718	130805	GCCACCACACCCGGCCAATT
132719	130806	TGCCACCACACCCGGCCAAT
132720	130807	ATGCCACCACACCCGGCCAA
132721	130808	CATGCCACCACACCCGGCCA
132722	130809	ACATGCCACCACACCCGGCC

34429	32516	TTAAGATGGAATCTACACCT
34430	32517	CTTAAGATGGAATCTACACC
34431	32518	TCTTAAGATGGAATCTACAC
34432	32519	TTCTTAAGATGGAATCTACA
34433	32520	TTTCTTAAGATGGAATCTAC
34434	32521	GTTTCTTAAGATGGAATCTA
34435	32522	GGTTTCTTAAGATGGAATCT
34436	32523	TGGTTTCTTAAGATGGAATC
34437	32524	GTGGTTTCTTAAGATGGAAT
34438	32525	AGTGGTTTCTTAAGATGGAA
34439	32526	AAGTGGTTTCTTAAGATGGA
34440	32527	AAAGTGGTTTCTTAAGATGG
34441	32528	GAAAGTGGTTTCTTAAGATG
34442	32529	AGAAAGTGGTTTCTTAAGAT
34443	32530	AAGAAAGTGGTTTCTTAAGA
34444	32531	AAAGAAAGTGGTTTCTTAAG
34445	32532	CAAAGAAAGTGGTTTCTTAA
34446	32533	GCAAAGAAAGTGGTTTCTTA
34447	32534	AGCAAAGAAAGTGGTTTCTT
34448	32535	AAGCAAAGAAAGTGGTTTCT
34449	32536	TAAGCAAAGAAAGTGGTTTC
34450	32537	ATAAGCAAAGAAAGTGGTTT
34451	32538	GATAAGCAAAGAAAGTGGTT
34452	32539	GGATAAGCAAAGAAAGTGGT
34453	32540	TGGATAAGCAAAGAAAGTGG
34454	32541	ATGGATAAGCAAAGAAAGTG
34455	32542	CATGGATAAGCAAAGAAAGT
34456	32543	TCATGGATAAGCAAAGAAAG
34457	32544	CTCATGGATAAGCAAAGAAA
34458	32545	TCTCATGGATAAGCAAAGAA
34459	32546	TTCTCATGGATAAGCAAAGA
34460	32547	CTTCTCATGGATAAGCAAAG
34461	32548	GCTTCTCATGGATAAGCAAA
34462	32549	TGCTTCTCATGGATAAGCAA
34463	32550	TTGCTTCTCATGGATAAGCA
34464	32551	GTTGCTTCTCATGGATAAGC
34465	32552	TGTTGCTTCTCATGGATAAG
34466	32553	GTGTTGCTTCTCATGGATAA
34467	32554	GGTGTTGCTTCTCATGGATA
34468	32555	AGGTGTTGCTTCTCATGGAT
34469	32556	GAGGTGTTGCTTCTCATGGA
34470	32557	TGAGGTGTTGCTTCTCATGG
34471	32558	ATGAGGTGTTGCTTCTCATG
34472	32559	GATGAGGTGTTGCTTCTCAT
34473	32560	AGATGAGGTGTTGCTTCTCA
34474	32561	TAGATGAGGTGTTGCTTCTC
34475	32562	ATAGATGAGGTGTTGCTTCT
34476	32563	AATAGATGAGGTGTTGCTTC
34477	32564	GAATAGATGAGGTGTTGCTT
34478	32565	TGAATAGATGAGGTGTTGCT
34479	32566	TTGAATAGATGAGGTGTTGC
34480	32567	CTTGAATAGATGAGGTGTTG
34481	32568	ACTTGAATAGATGAGGTGTT
34482	32569	AACTTGAATAGATGAGGTGT
34483	32570	AAACTTGAATAGATGAGGTG
34484	32571	AAAACTTGAATAGATGAGGT
34485	32572	TAAAACTTGAATAGATGAGG
34486	32573	ATAAAACTTGAATAGATGAG
34487	32574	GATAAAACTTGAATAGATGA
34488	32575	TGATAAAACTTGAATAGATG
34489	32576	ATGATAAAACTTGAATAGAT
34490	32577	CATGATAAAACTTGAATAGA
34491	32578	TCATGATAAAACTTGAATAG
34492	32579	CTCATGATAAAACTTGAATA
34493	32580	TCTCATGATAAAACTTGAAT
34494	32581	ATCTCATGATAAAACTTGAA
34495	32582	AATCTCATGATAAAACTTGA
34496	32583	CAATCTCATGATAAAACTTG
34497	32584	GCAATCTCATGATAAAACTT
34498	32585	TGCAATCTCATGATAAAACT
34499	32586	CTGCAATCTCATGATAAAAC

83576	81663	TGGGTTAAATGTAGCACTTT
83577	81664	TTGGGTTAAATGTAGCACTT
83578	81665	CTTGGGTTAAATGTAGCACT
83579	81666	TCTTGGGTTAAATGTAGCAC
83580	81667	GTCTTGGGTTAAATGTAGCA
83581	81668	TGTCTTGGGTTAAATGTAGC
83582	81669	TTGTCTTGGGTTAAATGTAG
83583	81670	ATTGTCTTGGGTTAAATGTA
83584	81671	GATTGTCTTGGGTTAAATGT
83585	81672	TGATTGTCTTGGGTTAAATG
83586	81673	GTGATTGTCTTGGGTTAAAT
83587	81674	AGTGATTGTCTTGGGTTAAA
83588	81675	AAGTGATTGTCTTGGGTTAA
83589	81676	CAAGTGATTGTCTTGGGTTA
83590	81677	CCAAGTGATTGTCTTGGGTT
83591	81678	GCCAAGTGATTGTCTTGGGT
83592	81679	GGCCAAGTGATTGTCTTGGG
83593	81680	TGGCCAAGTGATTGTCTTGG
83594	81681	TTGGCCAAGTGATTGTCTTG
83595	81682	TTTGGCCAAGTGATTGTCTT
83596	81683	TTTTGGCCAAGTGATTGTCT
83597	81684	TTTTTGGCCAAGTGATTGTC
83598	81685	GTTTTTGGCCAAGTGATTGT
83599	81686	TGTTTTTGGCCAAGTGATTG
83600	81687	GTGTTTTTGGCCAAGTGATT
83601	81688	AGTGTTTTTGGCCAAGTGAT
83602	81689	AAGTGTTTTTGGCCAAGTGA
83603	81690	GAAGTGTTTTTGGCCAAGTG
83604	81691	TGAAGTGTTTTTGGCCAAGT
83605	81692	GTGAAGTGTTTTTGGCCAAG
83606	81693	TGTGAAGTGTTTTTGGCCAA
83607	81694	ATGTGAAGTGTTTTTGGCCA
83608	81695	TATGTGAAGTGTTTTTGGCC
83609	81696	ATATGTGAAGTGTTTTTGGC
83610	81697	TATATGTGAAGTGTTTTTGG
83611	81698	TTATATGTGAAGTGTTTTTG
83612	81699	TTTATATGTGAAGTGTTTTT
83613	81700	CTTTATATGTGAAGTGTTTT
83614	81701	TCTTTATATGTGAAGTGTTT
83615	81702	TTCTTTATATGTGAAGTGTT
83616	81703	TTTCTTTATATGTGAAGTGT
83617	81704	ATTTCTTTATATGTGAAGTG
83618	81705	AATTTCTTTATATGTGAAGT
83619	81706	CAATTTCTTTATATGTGAAG
83620	81707	CCAATTTCTTTATATGTGAA
83621	81708	TCCAATTTCTTTATATGTGA
83622	81709	TTCCAATTTCTTTATATGTG
83623	81710	TTTCCAATTTCTTTATATGT
83624	81711	GTTTCCAATTTCTTTATATG
83625	81712	AGTTTCCAATTTCTTTATAT
83626	81713	AAGTTTCCAATTTCTTTATA
83627	81714	AAAGTTTCCAATTTCTTTAT
83628	81715	CAAAGTTTCCAATTTCTTTA
83629	81716	CCAAAGTTTCCAATTTCTTT
83630	81717	CCCAAAGTTTCCAATTTCTT
83631	81718	ACCCAAAGTTTCCAATTTCT
83632	81719	TACCCAAAGTTTCCAATTTC
83633	81720	CTACCCAAAGTTTCCAATTT
83634	81721	CCTACCCAAAGTTTCCAATT
83635	81722	ACCTACCCAAAGTTTCCAAT
83636	81723	AACCTACCCAAAGTTTCCAA
83637	81724	GAACCTACCCAAAGTTTCCA
83638	81725	AGAACCTACCCAAAGTTTCC
83639	81726	GAGAACCTACCCAAAGTTTC
83640	81727	TGAGAACCTACCCAAAGTTT
83641	81728	TTGAGAACCTACCCAAAGTT
83642	81729	ATTGAGAACCTACCCAAAGT
83643	81730	AATTGAGAACCTACCCAAAG
83644	81731	AAATTGAGAACCTACCCAAA
83645	81732	AAAATTGAGAACCTACCCAA
83646	81733	TAAAATTGAGAACCTACCCA

132723	130810	CACATGCCACCACACCCGGC
132724	130811	GCACATGCCACCACACCCGG
132725	130812	GGCACATGCCACCACACCCG
132726	130813	AGGCACATGCCACCACACCC
132727	130814	CAGGCACATGCCACCACACC
132728	130815	ACAGGCACATGCCACCACAC
132729	130816	TACAGGCACATGCCACCACA
132730	130817	CTACAGGCACATGCCACCAC
132731	130818	ACTACAGGCACATGCCACCA
132732	130819	GACTACAGGCACATGCCACC
132733	130820	GGACTACAGGCACATGCCAC
132734	130821	GGGACTACAGGCACATGCCA
132735	130822	CGGGACTACAGGCACATGCC
132736	130823	CCGGGACTACAGGCACATGC
132737	130824	GCCGGGACTACAGGCACATG
132738	130825	AGCCGGGACTACAGGCACAT
132739	130826	TAGCCGGGACTACAGGCACA
132740	130827	GTAGCCGGGACTACAGGCAC
132741	130828	AGTAGCCGGGACTACAGGCA
132742	130829	AAGTAGCCGGGACTACAGGC
132743	130830	GAAGTAGCCGGGACTACAGG
132744	130831	CGAAGTAGCCGGGACTACAG
132745	130832	CCGAAGTAGCCGGGACTACA
132746	130833	TCCGAAGTAGCCGGGACTAC
132747	130834	CTCCGAAGTAGCCGGGACTA
132748	130835	CCTCCGAAGTAGCCGGGACT
132749	130836	GCCTCCGAAGTAGCCGGGAC
132750	130837	AGCCTCCGAAGTAGCCGGGA
132751	130838	CAGCCTCCGAAGTAGCCGGG
132752	130839	TCAGCCTCCGAAGTAGCCGG
132753	130840	CTCAGCCTCCGAAGTAGCCG
132754	130841	CCTCAGCCTCCGAAGTAGCC
132755	130842	GCCTCAGCCTCCGAAGTAGC
132756	130843	TGCCTCAGCCTCCGAAGTAG
132757	130844	TTGCCTCAGCCTCCGAAGTA
132758	130845	GTTGCCTCAGCCTCCGAAGT
132759	130846	TGTTGCCTCAGCCTCCGAAG
132760	130847	CTGTTGCCTCAGCCTCCGAA
132761	130848	TCTGTTGCCTCAGCCTCCGA
132762	130849	TTCTGTTGCCTCAGCCTCCG
132763	130850	ATTCTGTTGCCTCAGCCTCC
132764	130851	AATTCTGTTGCCTCAGCCTC
132765	130852	CAATTCTGTTGCCTCAGCCT
132766	130853	GCAATTCTGTTGCCTCAGCC
132767	130854	AGCAATTCTGTTGCCTCAGC
132768	130855	AAGCAATTCTGTTGCCTCAG
132769	130856	CAAGCAATTCTGTTGCCTCA
132770	130857	TCAAGCAATTCTGTTGCCTC
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132772	130859	GTTCAAGCAATTCTGTTGCC
132773	130860	GGTTCAAGCAATTCTGTTGC
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132775	130862	CGGGTTCAAGCAATTCTGTT
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132779	130866	CTCCCGGGTTCAAGCAATTC
132780	130867	CCTCCCGGGTTCAAGCAATT
132781	130868	GCCTCCCGGGTTCAAGCAAT
132782	130869	TGCCTCCCGGGTTCAAGCAA
132783	130870	CTGCCTCCCGGGTTCAAGCA
132784	130871	TCTGCCTCCCGGGTTCAAGC
132785	130872	CTCTGCCTCCCGGGTTCAAG
132786	130873	CCTCTGCCTCCCGGGTTCAA
132787	130874	ACCTCTGCCTCCCGGGTTCA
132788	130875	AACCTCTGCCTCCCGGGTTC
132789	130876	CAACCTCTGCCTCCCGGGTT
132790	130877	GCAACCTCTGCCTCCCGGGT
132791	130878	TGCAACCTCTGCCTCCCGGG
132792	130879	CTGCAACCTCTGCCTCCCGG
132793	130880	ACTGCAACCTCTGCCTCCCG

34500	32587	GCTGCAATCTCATGATAAAA
34501	32588	TGCTGCAATCTCATGATAAA
34502	32589	TTGCTGCAATCTCATGATAA
34503	32590	ATTGCTGCAATCTCATGATA
34504	32591	AATTGCTGCAATCTCATGAT
34505	32592	GAATTGCTGCAATCTCATGA
34506	32593	TGAATTGCTGCAATCTCATG
34507	32594	CTGAATTGCTGCAATCTCAT
34508	32595	ACTGAATTGCTGCAATCTCA
34509	32596	AACTGAATTGCTGCAATCTC
34510	32597	TAACTGAATTGCTGCAATCT
34511	32598	GTAACTGAATTGCTGCAATC
34512	32599	TGTAACTGAATTGCTGCAAT
34513	32600	ATGTAACTGAATTGCTGCAA
34514	32601	GATGTAACTGAATTGCTGCA
34515	32602	AGATGTAACTGAATTGCTGC
34516	32603	AAGATGTAACTGAATTGCTG
34517	32604	GAAGATGTAACTGAATTGCT
34518	32605	AGAAGATGTAACTGAATTGC
34519	32606	CAGAAGATGTAACTGAATTG
34520	32607	TCAGAAGATGTAACTGAATT
34521	32608	GTCAGAAGATGTAACTGAAT
34522	32609	GGTCAGAAGATGTAACTGAA
34523	32610	GGGTCAGAAGATGTAACTGA
34524	32611	GGGGTCAGAAGATGTAACTG
34525	32612	TGGGGTCAGAAGATGTAACT
34526	32613	GTGGGGTCAGAAGATGTAAC
34527	32614	AGTGGGGTCAGAAGATGTAA
34528	32615	AAGTGGGGTCAGAAGATGTA
34529	32616	GAAGTGGGGTCAGAAGATGT
34530	32617	AGAAGTGGGGTCAGAAGATG
34531	32618	TAGAAGTGGGGTCAGAAGAT
34532	32619	TTAGAAGTGGGGTCAGAAGA
34533	32620	ATTAGAAGTGGGGTCAGAAG
34534	32621	AATTAGAAGTGGGGTCAGAA
34535	32622	AAATTAGAAGTGGGGTCAGA
34536	32623	AAAATTAGAAGTGGGGTCAG
34537	32624	TAAAATTAGAAGTGGGGTCA
34538	32625	CTAAAATTAGAAGTGGGGTC
34539	32626	ACTAAAATTAGAAGTGGGGT
34540	32627	AACTAAAATTAGAAGTGGGG
34541	32628	GAACTAAAATTAGAAGTGGG
34542	32629	AGAACTAAAATTAGAAGTGG
34543	32630	GAGAACTAAAATTAGAAGTG
34544	32631	AGAGAACTAAAATTAGAAGT
34545	32632	AAGAGAACTAAAATTAGAAG
34546	32633	CAAGAGAACTAAAATTAGAA
34547	32634	GCAAGAGAACTAAAATTAGA
34548	32635	AGCAAGAGAACTAAAATTAG
34549	32636	AAGCAAGAGAACTAAAATTA
34550	32637	AAAGCAAGAGAACTAAAATT
34551	32638	AAAAGCAAGAGAACTAAAAT
34552	32639	AAAAAGCAAGAGAACTAAAA
34553	32640	AAAAAAGCAAGAGAACTAAA
34554	32641	TAAAAAAGCAAGAGAACTAA
34555	32642	GTAAAAAAGCAAGAGAACTA
34556	32643	GGTAAAAAAGCAAGAGAACT
34557	32644	TGGTAAAAAAGCAAGAGAAC
34558	32645	GTGGTAAAAAAGCAAGAGAA
34559	32646	TGTGGTAAAAAAGCAAGAGA
34560	32647	ATGTGGTAAAAAAGCAAGAG
34561	32648	GATGTGGTAAAAAAGCAAGA
34562	32649	AGATGTGGTAAAAAAGCAAG
34563	32650	CAGATGTGGTAAAAAAGCAA
34564	32651	GCAGATGTGGTAAAAAAGCA
34565	32652	TGCAGATGTGGTAAAAAAGC
34566	32653	CTGCAGATGTGGTAAAAAAG
34567	32654	ACTGCAGATGTGGTAAAAAA
34568	32655	AACTGCAGATGTGGTAAAAA
34569	32656	TAACTGCAGATGTGGTAAAA
34570	32657	GTAACTGCAGATGTGGTAAA

83647	81734	TTAAAATTGAGAACCTACCC
83648	81735	TTTAAAATTGAGAACCTACC
83649	81736	TTTTAAAATTGAGAACCTAC
83650	81737	TTTTTAAAATTGAGAACCTA
83651	81738	GTTTTTAAAATTGAGAACCT
83652	81739	TGTTTTTAAAATTGAGAACC
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83655	81742	CAGTGTTTTTAAAATTGAGA
83656	81743	CCAGTGTTTTTAAAATTGAG
83657	81744	TCCAGTGTTTTTAAAATTGA
83658	81745	ATCCAGTGTTTTTAAAATTG
83659	81746	TATCCAGTGTTTTTAAAATT
83660	81747	TTATCCAGTGTTTTTAAAAT
83661	81748	ATTATCCAGTGTTTTTAAAA
83662	81749	TATTATCCAGTGTTTTTAAA
83663	81750	TTATTATCCAGTGTTTTTAA
83664	81751	TTTATTATCCAGTGTTTTTA
83665	81752	TTTTATTATCCAGTGTTTTT
83666	81753	ATTTTATTATCCAGTGTTTT
83667	81754	AATTTTATTATCCAGTGTTT
83668	81755	AAATTTTATTATCCAGTGTT
83669	81756	AAAATTTTATTATCCAGTGT
83670	81757	AAAAATTTTATTATCCAGTG
83671	81758	AAAAAATTTTATTATCCAGT
83672	81759	TAAAAAATTTTATTATCCAG
83673	81760	CTAAAAAATTTTATTATCCA
83674	81761	TCTAAAAAATTTTATTATCC
83675	81762	GTCTAAAAAATTTTATTATC
83676	81763	TGTCTAAAAAATTTTATTAT
83677	81764	ATGTCTAAAAAATTTTATTA
83678	81765	TATGTCTAAAAAATTTTATT
83679	81766	TTATGTCTAAAAAATTTTAT
83680	81767	ATTATGTCTAAAAAATTTTA
83681	81768	AATTATGTCTAAAAAATTTT
83682	81769	AAATTATGTCTAAAAAATTT
83683	81770	TAAATTATGTCTAAAAAATT
83684	81771	ATAAATTATGTCTAAAAAAT
83685	81772	TATAAATTATGTCTAAAAAA
83686	81773	ATATAAATTATGTCTAAAAA
83687	81774	CATATAAATTATGTCTAAAA
83688	81775	CCATATAAATTATGTCTAAA
83689	81776	TCCATATAAATTATGTCTAA
83690	81777	TTCCATATAAATTATGTCTA
83691	81778	TTTCCATATAAATTATGTCT
83692	81779	TTTTCCATATAAATTATGTC
83693	81780	ATTTTCCATATAAATTATGT
83694	81781	AATTTTCCATATAAATTATG
83695	81782	GAATTTTCCATATAAATTAT
83696	81783	AGAATTTTCCATATAAATTA
83697	81784	TAGAATTTTCCATATAAATT
83698	81785	TTAGAATTTTCCATATAAAT
83699	81786	GTTAGAATTTTCCATATAAA
83700	81787	GGTTAGAATTTTCCATATAA
83701	81788	AGGTTAGAATTTTCCATATA
83702	81789	TAGGTTAGAATTTTCCATAT
83703	81790	ATAGGTTAGAATTTTCCATA
83704	81791	CATAGGTTAGAATTTTCCAT
83705	81792	ACATAGGTTAGAATTTTCCA
83706	81793	CACATAGGTTAGAATTTTCC
83707	81794	GCACATAGGTTAGAATTTTC
83708	81795	TGCACATAGGTTAGAATTTT
83709	81796	TTGCACATAGGTTAGAATTT
83710	81797	GTTGCACATAGGTTAGAATT
83711	81798	TGTTGCACATAGGTTAGAAT
83712	81799	GTGTTGCACATAGGTTAGAA
83713	81800	AGTGTTGCACATAGGTTAGA
83714	81801	CAGTGTTGCACATAGGTTAG
83715	81802	ACAGTGTTGCACATAGGTTA
83716	81803	CACAGTGTTGCACATAGGTT
83717	81804	CCACAGTGTTGCACATAGGT

132794	130881	CACTGCAACCTCTGCCTCCC
132795	130882	TCACTGCAACCTCTGCCTCC
132796	130883	CTCACTGCAACCTCTGCCTC
132797	130884	GCTCACTGCAACCTCTGCCT
132798	130885	GGCTCACTGCAACCTCTGCC
132799	130886	CGGCTCACTGCAACCTCTGC
132800	130887	TCGGCTCACTGCAACCTCTG
132801	130888	CTCGGCTCACTGCAACCTCT
132802	130889	TCTCGGCTCACTGCAACCTC
132803	130890	ATCTCGGCTCACTGCAACCT
132804	130891	GATCTCGGCTCACTGCAACC
132805	130892	CGATCTCGGCTCACTGCAAC
132806	130893	GCGATCTCGGCTCACTGCAA
132807	130894	CGCGATCTCGGCTCACTGCA
132808	130895	GCGCGATCTCGGCTCACTGC
132809	130896	GGCGCGATCTCGGCTCACTG
132810	130897	TGGCGCGATCTCGGCTCACT
132811	130898	GTGGCGCGATCTCGGCTCAC
132812	130899	AGTGGCGCGATCTCGGCTCA
132813	130900	TAGTGGCGCGATCTCGGCTC
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132816	130903	GTGTAGTGGCGCGATCTCGG
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132819	130906	AGAGTGTAGTGGCGCGATCT
132820	130907	TAGAGTGTAGTGGCGCGATC
132821	130908	CTAGAGTGTAGTGGCGCGAT
132822	130909	GCTAGAGTGTAGTGGCGCGA
132823	130910	GGCTAGAGTGTAGTGGCGCG
132824	130911	AGGCTAGAGTGTAGTGGCGC
132825	130912	CAGGCTAGAGTGTAGTGGCG
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132827	130914	CTCAGGCTAGAGTGTAGTGG
132828	130915	GCTCAGGCTAGAGTGTAGTG
132829	130916	CGCTCAGGCTAGAGTGTAGT
132830	130917	TCGCTCAGGCTAGAGTGTAG
132831	130918	GTCGCTCAGGCTAGAGTGTA
132832	130919	TGTCGCTCAGGCTAGAGTGT
132833	130920	CTGTCGCTCAGGCTAGAGTG
132834	130921	TCTGTCGCTCAGGCTAGAGT
132835	130922	CTCTGTCGCTCAGGCTAGAG
132836	130923	ACTCTGTCGCTCAGGCTAGA
132837	130924	CACTCTGTCGCTCAGGCTAG
132838	130925	TCACTCTGTCGCTCAGGCTA
132839	130926	CTCACTCTGTCGCTCAGGCT
132840	130927	TCTCACTCTGTCGCTCAGGC
132841	130928	GTCTCACTCTGTCGCTCAGG
132842	130929	AGTCTCACTCTGTCGCTCAG
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132847	130934	GATGGAGTCTCACTCTGTCG
132848	130935	AGATGGAGTCTCACTCTGTC
132849	130936	GAGATGGAGTCTCACTCTGT
132850	130937	GGAGATGGAGTCTCACTCTG
132851	130938	TGGAGATGGAGTCTCACTCT
132852	130939	TTGGAGATGGAGTCTCACTC
132853	130940	TTTGGAGATGGAGTCTCACT
132854	130941	TTTTGGAGATGGAGTCTCAC
132855	130942	TTTTTGGAGATGGAGTCTCA
132856	130943	TTTTTTGGAGATGGAGTCTC
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132858	130945	TTTTTTTTGGAGATGGAGTC
132859	130946	TTTTTTTTTGGAGATGGAGT
132860	130947	TTTTTTTTTTGGAGATGGAG
132861	130948	TTTTTTTTTTTGGAGATGGA
132862	130949	TTTTTTTTTTTTGGAGATGG
132863	130950	TTTTTTTTTTTTTGGAGATG
132864	130951	TTTTTTTTTTTTTTGGAGAT

34571	32658	AGTAACTGCAGATGTGGTAA
34572	32659	AAGTAACTGCAGATGTGGTA
34573	32660	CAAGTAACTGCAGATGTGGT
34574	32661	GCAAGTAACTGCAGATGTGG
34575	32662	AGCAAGTAACTGCAGATGTG
34576	32663	GAGCAAGTAACTGCAGATGT
34577	32664	AGAGCAAGTAACTGCAGATG
34578	32665	TAGAGCAAGTAACTGCAGAT
34579	32666	GTAGAGCAAGTAACTGCAGA
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34581	32668	CAGTAGAGCAAGTAACTGCA
34582	32669	TCAGTAGAGCAAGTAACTGC
34583	32670	TTCAGTAGAGCAAGTAACTG
34584	32671	CTTCAGTAGAGCAAGTAACT
34585	32672	ACTTCAGTAGAGCAAGTAAC
34586	32673	GACTTCAGTAGAGCAAGTAA
34587	32674	GGACTTCAGTAGAGCAAGTA
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34593	32680	GGTTCAGGACTTCAGTAGAG
34594	32681	GGGTTCAGGACTTCAGTAGA
34595	32682	GGGGTTCAGGACTTCAGTAG
34596	32683	AGGGGTTCAGGACTTCAGTA
34597	32684	GAGGGGTTCAGGACTTCAGT
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34599	32686	TTGAGGGGTTCAGGACTTCA
34600	32687	TTTGAGGGGTTCAGGACTTC
34601	32688	TTTTGAGGGGTTCAGGACTT
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34603	32690	GATTTTGAGGGGTTCAGGAC
34604	32691	TGATTTTGAGGGGTTCAGGA
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34606	32693	AATGATTTTGAGGGGTTCAG
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34610	32697	CATGAATGATTTTGAGGGGT
34611	32698	TCATGAATGATTTTGAGGGG
34612	32699	CTCATGAATGATTTTGAGGG
34613	32700	ACTCATGAATGATTTTGAGG
34614	32701	TACTCATGAATGATTTTGAG
34615	32702	ATACTCATGAATGATTTTGA
34616	32703	AATACTCATGAATGATTTTG
34617	32704	TAATACTCATGAATGATTTT
34618	32705	CTAATACTCATGAATGATTT
34619	32706	TCTAATACTCATGAATGATT
34620	32707	TTCTAATACTCATGAATGAT
34621	32708	CTTCTAATACTCATGAATGA
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34627	32714	AAATTGCTTCTAATACTCAT
34628	32715	GAAATTGCTTCTAATACTCA
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34630	32717	AGGAAATTGCTTCTAATACT
34631	32718	CAGGAAATTGCTTCTAATAC
34632	32719	CCAGGAAATTGCTTCTAATA
34633	32720	ACCAGGAAATTGCTTCTAAT
34634	32721	AACCAGGAAATTGCTTCTAA
34635	32722	CAACCAGGAAATTGCTTCTA
34636	32723	CCAACCAGGAAATTGCTTCT
34637	32724	CCCAACCAGGAAATTGCTTC
34638	32725	GCCCAACCAGGAAATTGCTT
34639	32726	TGCCCAACCAGGAAATTGCT
34640	32727	GTGCCCAACCAGGAAATTGC
34641	32728	CGTGCCCAACCAGGAAATTG

83718	81805	ACCACAGTGTTGCACATAGG
83719	81806	AACCACAGTGTTGCACATAG
83720	81807	TAACCACAGTGTTGCACATA
83721	81808	TTAACCACAGTGTTGCACAT
83722	81809	ATTAACCACAGTGTTGCACA
83723	81810	TATTAACCACAGTGTTGCAC
83724	81811	ATATTAACCACAGTGTTGCA
83725	81812	TATATTAACCACAGTGTTGC
83726	81813	CTATATTAACCACAGTGTTG
83727	81814	TCTATATTAACCACAGTGTT
83728	81815	ATCTATATTAACCACAGTGT
83729	81816	GATCTATATTAACCACAGTG
83730	81817	TGATCTATATTAACCACAGT
83731	81818	TTGATCTATATTAACCACAG
83732	81819	ATTGATCTATATTAACCACA
83733	81820	AATTGATCTATATTAACCAC
83734	81821	AAATTGATCTATATTAACCA
83735	81822	AAAATTGATCTATATTAACC
83736	81823	GAAAATTGATCTATATTAAC
83737	81824	TGAAAATTGATCTATATTAA
83738	81825	ATGAAAATTGATCTATATTA
83739	81826	AATGAAAATTGATCTATATT
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83744	81831	CAAATAATGAAAATTGATCT
83745	81832	ACAAATAATGAAAATTGATC
83746	81833	AACAAATAATGAAAATTGAT
83747	81834	AAACAAATAATGAAAATTGA
83748	81835	GAAACAAATAATGAAAATTG
83749	81836	AGAAACAAATAATGAAAATT
83750	81837	TAGAAACAAATAATGAAAAT
83751	81838	ATAGAAACAAATAATGAAAA
83752	81839	TATAGAAACAAATAATGAAA
83753	81840	ATATAGAAACAAATAATGAA
83754	81841	AATATAGAAACAAATAATGA
83755	81842	TAATATAGAAACAAATAATG
83756	81843	ATAATATAGAAACAAATAAT
83757	81844	CATAATATAGAAACAAATAA
83758	81845	GCATAATATAGAAACAAATA
83759	81846	AGCATAATATAGAAACAAAT
83760	81847	AAGCATAATATAGAAACAAA
83761	81848	TAAGCATAATATAGAAACAA
83762	81849	GTAAGCATAATATAGAAACA
83763	81850	AGTAAGCATAATATAGAAAC
83764	81851	AAGTAAGCATAATATAGAAA
83765	81852	GAAGTAAGCATAATATAGAA
83766	81853	TGAAGTAAGCATAATATAGA
83767	81854	TTGAAGTAAGCATAATATAG
83768	81855	CTTGAAGTAAGCATAATATA
83769	81856	TCTTGAAGTAAGCATAATAT
83770	81857	TTCTTGAAGTAAGCATAATA
83771	81858	TTTCTTGAAGTAAGCATAAT
83772	81859	CTTTCTTGAAGTAAGCATAA
83773	81860	CCTTTCTTGAAGTAAGCATA
83774	81861	TCCTTTCTTGAAGTAAGCAT
83775	81862	ATCCTTTCTTGAAGTAAGCA
83776	81863	GATCCTTTCTTGAAGTAAGC
83777	81864	AGATCCTTTCTTGAAGTAAG
83778	81865	CAGATCCTTTCTTGAAGTAA
83779	81866	TCAGATCCTTTCTTGAAGTA
83780	81867	CTCAGATCCTTTCTTGAAGT
83781	81868	CCTCAGATCCTTTCTTGAAG
83782	81869	ACCTCAGATCCTTTCTTGAA
83783	81870	TACCTCAGATCCTTTCTTGA
83784	81871	TTACCTCAGATCCTTTCTTG
83785	81872	GTTACCTCAGATCCTTTCTT
83786	81873	AGTTACCTCAGATCCTTTCT
83787	81874	AAGTTACCTCAGATCCTTTC
83788	81875	TAAGTTACCTCAGATCCTTT

132865	130952	TTTTTTTTTTTTTTGGAGA
132866	130953	TTTTTTTTTTTTTTTGGAG
132867	130954	TTTTTTTTTTTTTTTTGGA
132868	130955	TTTTTTTTTTTTTTTTGG
132869	130956	TTTTTTTTTTTTTTTTTG
132870	130957	TTTTTTTTTTTTTTTTTT
132871	130958	TTTTTTTTTTTTTTTTTT
132872	130959	CTTTTTTTTTTTTTTTTT
132873	130960	TCTTTTTTTTTTTTTTTT
132874	130961	TTCTTTTTTTTTTTTTTT
132875	130962	ATTCTTTTTTTTTTTTTT
132876	130963	AATTCTTTTTTTTTTTTT
132877	130964	AAATTCTTTTTTTTTTTT
132878	130965	TAAATTCTTTTTTTTTTT
132879	130966	GTAAATTCTTTTTTTTTT
132880	130967	TGTAAATTCTTTTTTTTT
132881	130968	CTGTAAATTCTTTTTTTT
132882	130969	TCTGTAAATTCTTTTTTT
132883	130970	ATCTGTAAATTCTTTTTTT
132884	130971	AATCTGTAAATTCTTTTTT
132885	130972	AAATCTGTAAATTCTTTTT
132886	130973	GAAATCTGTAAATTCTTTT
132887	130974	AGAAATCTGTAAATTCTTT
132888	130975	CAGAAATCTGTAAATTCTT
132889	130976	CCAGAAATCTGTAAATTCT
132890	130977	GCCAGAAATCTGTAAATTC
132891	130978	TGCCAGAAATCTGTAAATTC
132892	130979	TTGCCAGAAATCTGTAAATT
132893	130980	TTTGCCAGAAATCTGTAAAT
132894	130981	GTTTGCCAGAAATCTGTAAA
132895	130982	GGTTTGCCAGAAATCTGTAA
132896	130983	AGGTTTGCCAGAAATCTGTA
132897	130984	AAGGTTTGCCAGAAATCTGT
132898	130985	GAAGGTTTGCCAGAAATCTG
132899	130986	AGAAGGTTTGCCAGAAATCT
132900	130987	AAGAAGGTTTGCCAGAAATC
132901	130988	GAAGAAGGTTTGCCAGAAAT
132902	130989	AGAAGAAGGTTTGCCAGAAA
132903	130990	AAGAAGAAGGTTTGCCAGAA
132904	130991	CAAGAAGAAGGTTTGCCAGA
132905	130992	TCAAGAAGAAGGTTTGCCAG
132906	130993	CTCAAGAAGAAGGTTTGCCA
132907	130994	TCTCAAGAAGAAGGTTTGCC
132908	130995	GTCTCAAGAAGAAGGTTTGC
132909	130996	TGTCTCAAGAAGAAGGTTTG
132910	130997	ATGTCTCAAGAAGAAGGTTT
132911	130998	AATGTCTCAAGAAGAAGGTT
132912	130999	TAATGTCTCAAGAAGAAGGT
132913	131000	GTAATGTCTCAAGAAGAAGG
132914	131001	AGTAATGTCTCAAGAAGAAG
132915	131002	TAGTAATGTCTCAAGAAGAA
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132917	131004	AGTAGTAATGTCTCAAGAAG
132918	131005	AAGTAGTAATGTCTCAAGAA
132919	131006	AAAGTAGTAATGTCTCAAGA
132920	131007	AAAAGTAGTAATGTCTCAAG
132921	131008	GAAAAGTAGTAATGTCTCAA
132922	131009	TGAAAAGTAGTAATGTCTCA
132923	131010	ATGAAAAGTAGTAATGTCTC
132924	131011	TATGAAAAGTAGTAATGTCT
132925	131012	GTATGAAAAGTAGTAATGTC
132926	131013	GGTATGAAAAGTAGTAATGT
132927	131014	TGGTATGAAAAGTAGTAATG
132928	131015	GTGGTATGAAAAGTAGTAAT
132929	131016	GGTGGTATGAAAAGTAGTAA
132930	131017	AGGTGGTATGAAAAGTAGTA
132931	131018	GAGGTGGTATGAAAAGTAGT
132932	131019	AGAGGTGGTATGAAAAGTAG
132933	131020	CAGAGGTGGTATGAAAAGTA
132934	131021	ACAGAGGTGGTATGAAAAGT
132935	131022	GACAGAGGTGGTATGAAAAG

34642	32729	CCGTGCCCAACCAGGAAATT
34643	32730	ACCGTGCCCAACCAGGAAAT
34644	32731	CACCGTGCCCAACCAGGAAA
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34646	32733	GCCACCGTGCCCAACCAGGA
34647	32734	AGCCACCGTGCCCAACCAGG
34648	32735	GAGCCACCGTGCCCAACCAG
34649	32736	TGAGCCACCGTGCCCAACCA
34650	32737	ATGAGCCACCGTGCCCAACC
34651	32738	CATGAGCCACCGTGCCCAAC
34652	32739	GCATGAGCCACCGTGCCCAA
34653	32740	GGCATGAGCCACCGTGCCCA
34654	32741	AGGCATGAGCCACCGTGCCC
34655	32742	CAGGCATGAGCCACCGTGCC
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34657	32744	TACAGGCATGAGCCACCGTG
34658	32745	TTACAGGCATGAGCCACCGT
34659	32746	ATTACAGGCATGAGCCACCG
34660	32747	GATTACAGGCATGAGCCACC
34661	32748	GGATTACAGGCATGAGCCAC
34662	32749	GGGATTACAGGCATGAGCCA
34663	32750	TGGGATTACAGGCATGAGCC
34664	32751	CTGGGATTACAGGCATGAGC
34665	32752	ACTGGGATTACAGGCATGAG
34666	32753	TACTGGGATTACAGGCATGA
34667	32754	GTACTGGGATTACAGGCATG
34668	32755	AGTACTGGGATTACAGGCAT
34669	32756	AAGTACTGGGATTACAGGCA
34670	32757	AAAGTACTGGGATTACAGGC
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34673	32760	CCCAAAGTACTGGGATTACA
34674	32761	TCCCAAAGTACTGGGATTAC
34675	32762	CTCCCAAAGTACTGGGATTA
34676	32763	CCTCCCAAAGTACTGGGATT
34677	32764	GCCTCCCAAAGTACTGGGAT
34678	32765	GGCCTCCCAAAGTACTGGGA
34679	32766	TGGCCTCCCAAAGTACTGGG
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34683	32770	TCCTTGGCCTCCCAAAGTAC
34684	32771	CTCCTTGGCCTCCCAAAGTA
34685	32772	CCTCCTTGGCCTCCCAAAGT
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34688	32775	CGCCCTCCTTGGCCTCCCAA
34689	32776	CCGCCCTCCTTGGCCTCCCA
34690	32777	TCCGCCCTCCTTGGCCTCCC
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34693	32780	TGATCCGCCCTCCTTGGCCT
34694	32781	GTGATCCGCCCTCCTTGGCC
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34697	32784	CAGGTGATCCGCCCTCCTTG
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34707	32794	CTCCTGACTTCAGGTGATCC
34708	32795	ACTCCTGACTTCAGGTGATC
34709	32796	AACTCCTGACTTCAGGTGAT
34710	32797	GAACTCCTGACTTCAGGTGA
34711	32798	TGAACTCCTGACTTCAGGTG
34712	32799	TTGAACTCCTGACTTCAGGT

83789	81876	ATAAGTTACCTCAGATCCTT
83790	81877	TATAAGTTACCTCAGATCCT
83791	81878	TTATAAGTTACCTCAGATCC
83792	81879	ATTATAAGTTACCTCAGATC
83793	81880	TATTATAAGTTACCTCAGAT
83794	81881	GTATTATAAGTTACCTCAGA
83795	81882	TGTATTATAAGTTACCTCAG
83796	81883	TTGTATTATAAGTTACCTCA
83797	81884	CTTGTATTATAAGTTACCTC
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83815	81902	CATGACTCTTGATCATGTCT
83816	81903	ACATGACTCTTGATCATGTC
83817	81904	CACATGACTCTTGATCATGT
83818	81905	TCACATGACTCTTGATCATG
83819	81906	TTCACATGACTCTTGATCAT
83820	81907	CTTCACATGACTCTTGATCA
83821	81908	TCTTCACATGACTCTTGATC
83822	81909	TTCTTCACATGACTCTTGAT
83823	81910	TTTCTTCACATGACTCTTGA
83824	81911	CTTTCTTCACATGACTCTTG
83825	81912	ACTTTCTTCACATGACTCTT
83826	81913	CACTTTCTTCACATGACTCT
83827	81914	TCACTTTCTTCACATGACTC
83828	81915	GTCACTTTCTTCACATGACT
83829	81916	AGTCACTTTCTTCACATGAC
83830	81917	TAGTCACTTTCTTCACATGA
83831	81918	CTAGTCACTTTCTTCACATG
83832	81919	TCTAGTCACTTTCTTCACAT
83833	81920	CTCTAGTCACTTTCTTCACA
83834	81921	TCTCTAGTCACTTTCTTCAC
83835	81922	TTCTCTAGTCACTTTCTTCA
83836	81923	TTTCTCTAGTCACTTTCTTC
83837	81924	ATTTCTCTAGTCACTTTCTT
83838	81925	AATTTCTCTAGTCACTTTCT
83839	81926	AAATTTCTCTAGTCACTTTC
83840	81927	CAAATTTCTCTAGTCACTTT
83841	81928	GCAAATTTCTCTAGTCACTT
83842	81929	AGCAAATTTCTCTAGTCACT
83843	81930	AAGCAAATTTCTCTAGTCAC
83844	81931	TAAGCAAATTTCTCTAGTCA
83845	81932	TTAAGCAAATTTCTCTAGTC
83846	81933	TTTAAGCAAATTTCTCTAGT
83847	81934	TTTTAAGCAAATTTCTCTAG
83848	81935	TTTTTAAGCAAATTTCTCTA
83849	81936	TTTTTTAAGCAAATTTCTCT
83850	81937	GTTTTTTAAGCAAATTTCTC
83851	81938	TGTTTTTTAAGCAAATTTCT
83852	81939	TTGTTTTTTAAGCAAATTTC
83853	81940	GTTGTTTTTTAAGCAAATTT
83854	81941	TGTTGTTTTTTAAGCAAATT
83855	81942	TTGTTGTTTTTTAAGCAAAT
83856	81943	TTTGTTGTTTTTTAAGCAAA
83857	81944	TTTTGTTGTTTTTTAAGCAA
83858	81945	TTTTTGTTGTTTTTTAAGCA
83859	81946	GTTTTTGTTGTTTTTTAAGC

132936	131023	GGACAGAGGTGGTATGAAAA
132937	131024	AGGACAGAGGTGGTATGAAA
132938	131025	AAGGACAGAGGTGGTATGAA
132939	131026	AAAGGACAGAGGTGGTATGA
132940	131027	AAAAGGACAGAGGTGGTATG
132941	131028	AAAAAGGACAGAGGTGGTAT
132942	131029	CAAAAAGGACAGAGGTGGTA
132943	131030	TCAAAAAGGACAGAGGTGGT
132944	131031	TTCAAAAAGGACAGAGGTGG
132945	131032	CTTCAAAAAGGACAGAGGTG
132946	131033	TCTTCAAAAAGGACAGAGGT
132947	131034	TTCTTCAAAAAGGACAGAGG
132948	131035	ATTCTTCAAAAAGGACAGAG
132949	131036	TATTCTTCAAAAAGGACAGA
132950	131037	TTATTCTTCAAAAAGGACAG
132951	131038	TTTATTCTTCAAAAAGGACA
132952	131039	TTTTATTCTTCAAAAAGGAC
132953	131040	CTTTTATTCTTCAAAAAGGA
132954	131041	ACTTTTATTCTTCAAAAAGG
132955	131042	AACTTTTATTCTTCAAAAAG
132956	131043	AAACTTTTATTCTTCAAAAA
132957	131044	AAAACTTTTATTCTTCAAAA
132958	131045	TAAAACTTTTATTCTTCAAA
132959	131046	TTAAAACTTTTATTCTTCAA
132960	131047	GTTAAAACTTTTATTCTTCA
132961	131048	TGTTAAAACTTTTATTCTTC
132962	131049	ATGTTAAAACTTTTATTCTT
132963	131050	AATGTTAAAACTTTTATTCT
132964	131051	GAATGTTAAAACTTTTATTC
132965	131052	GGAATGTTAAAACTTTTATT
132966	131053	CGGAATGTTAAAACTTTTAT
132967	131054	ACGGAATGTTAAAACTTTTA
132968	131055	TACGGAATGTTAAAACTTTT
132969	131056	CTACGGAATGTTAAAACTTT
132970	131057	CCTACGGAATGTTAAAACTT
132971	131058	ACCTACGGAATGTTAAAACT
132972	131059	AACCTACGGAATGTTAAAAC
132973	131060	TAACCTACGGAATGTTAAAA
132974	131061	TTAACCTACGGAATGTTAAA
132975	131062	ATTAACCTACGGAATGTTAA
132976	131063	CATTAACCTACGGAATGTTA
132977	131064	TCATTAACCTACGGAATGTT
132978	131065	CTCATTAACCTACGGAATGT
132979	131066	TCTCATTAACCTACGGAATG
132980	131067	TTCTCATTAACCTACGGAAT
132981	131068	ATTCTCATTAACCTACGGAA
132982	131069	TATTCTCATTAACCTACGGA
132983	131070	CTATTCTCATTAACCTACGG
132984	131071	CCTATTCTCATTAACCTACG
132985	131072	TCCTATTCTCATTAACCTAC
132986	131073	GTCCTATTCTCATTAACCTA
132987	131074	AGTCCTATTCTCATTAACCT
132988	131075	AAGTCCTATTCTCATTAACC
132989	131076	CAAGTCCTATTCTCATTAAC
132990	131077	CCAAGTCCTATTCTCATTAA
132991	131078	CCCAAGTCCTATTCTCATTA
132992	131079	GCCCAAGTCCTATTCTCATT
132993	131080	TGCCCAAGTCCTATTCTCAT
132994	131081	CTGCCCAAGTCCTATTCTCA
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133000	131087	TTGCTGCTGCCCAAGTCCTA
133001	131088	ATTGCTGCTGCCCAAGTCCT
133002	131089	GATTGCTGCTGCCCAAGTCC
133003	131090	TGATTGCTGCTGCCCAAGTC
133004	131091	ATGATTGCTGCTGCCCAAGT
133005	131092	GATGATTGCTGCTGCCCAAG
133006	131093	GGATGATTGCTGCTGCCCAA

34713	32800	CTTGAACTCCTGACTTCAGG
34714	32801	TCTTGAACTCCTGACTTCAG
34715	32802	GTCTTGAACTCCTGACTTCA
34716	32803	GGTCTTGAACTCCTGACTTC
34717	32804	TGGTCTTGAACTCCTGACTT
34718	32805	CTGGTCTTGAACTCCTGACT
34719	32806	ACTGGTCTTGAACTCCTGAC
34720	32807	GACTGGTCTTGAACTCCTGA
34721	32808	AGACTGGTCTTGAACTCCTG
34722	32809	CAGACTGGTCTTGAACTCCT
34723	32810	CCAGACTGGTCTTGAACTCC
34724	32811	GCCAGACTGGTCTTGAACTC
34725	32812	TGCCAGACTGGTCTTGAACT
34726	32813	TTGCCAGACTGGTCTTGAAC
34727	32814	TTTGCCAGACTGGTCTTGAA
34728	32815	GTTTGCCAGACTGGTCTTGA
34729	32816	CGTTTGCCAGACTGGTCTTG
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34735	32822	TCACCACGTTTGCCAGACTG
34736	32823	TTCACCACGTTTGCCAGACT
34737	32824	TTTCACCACGTTTGCCAGAC
34738	32825	GTTTCACCACGTTTGCCAGA
34739	32826	GGTTTCACCACGTTTGCCAG
34740	32827	GGGTTTCACCACGTTTGCCA
34741	32828	GGGGTTTCACCACGTTTGCC
34742	32829	CGGGGTTTCACCACGTTTGC
34743	32830	ACGGGGTTTCACCACGTTTG
34744	32831	AACGGGGTTTCACCACGTTT
34745	32832	AAACGGGGTTTCACCACGTT
34746	32833	GAAACGGGGTTTCACCACGT
34747	32834	AGAAACGGGGTTTCACCACG
34748	32835	TAGAAACGGGGTTTCACCAC
34749	32836	GTAGAAACGGGGTTTCACCA
34750	32837	AGTAGAAACGGGGTTTCACC
34751	32838	TAGTAGAAACGGGGTTTCAC
34752	32839	TTAGTAGAAACGGGGTTTCA
34753	32840	TTTAGTAGAAACGGGGTTTC
34754	32841	TTTTAGTAGAAACGGGGTTT
34755	32842	TTTTTAGTAGAAACGGGGTT
34756	32843	ATTTTTAGTAGAAACGGGGT
34757	32844	TATTTTTAGTAGAAACGGGG
34758	32845	GTATTTTTAGTAGAAACGGG
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34762	32849	TTTTGTATTTTTAGTAGAAA
34763	32850	TTTTTGTATTTTTAGTAGAA
34764	32851	ATTTTTGTATTTTTAGTAGA
34765	32852	AATTTTTGTATTTTTAGTAG
34766	32853	TAATTTTTGTATTTTTAGTA
34767	32854	CTAATTTTTGTATTTTTAGT
34768	32855	GCTAATTTTTGTATTTTTAG
34769	32856	CGCTAATTTTTGTATTTTTA
34770	32857	CCGCTAATTTTTGTATTTTT
34771	32858	CCCGCTAATTTTTGTATTTT
34772	32859	CCCCGCTAATTTTTGTATTT
34773	32860	TCCCCGCTAATTTTTGTATT
34774	32861	ATCCCCGCTAATTTTTGTAT
34775	32862	CATCCCCGCTAATTTTTGTA
34776	32863	ACATCCCCGCTAATTTTTGT
34777	32864	CACATCCCCGCTAATTTTTG
34778	32865	CCACATCCCCGCTAATTTTT
34779	32866	ACCACATCCCCGCTAATTTT
34780	32867	CACCACATCCCCGCTAATTT
34781	32868	CCACCACATCCCCGCTAATT
34782	32869	GCCACCACATCCCCGCTAAT
34783	32870	CGCCACCACATCCCCGCTAA

83860	81947	TGTTTTTGTTGTTTTTTAAG
83861	81948	TTGTTTTTGTTGTTTTTTAA
83862	81949	GTTGTTTTTGTTGTTTTTTA
83863	81950	GGTTGTTTTTGTTGTTTTTT
83864	81951	GGGTTGTTTTTGTTGTTTTT
83865	81952	AGGGTTGTTTTTGTTGTTTT
83866	81953	AAGGGTTGTTTTTGTTGTTT
83867	81954	TAAGGGTTGTTTTTGTTGTT
83868	81955	CTAAGGGTTGTTTTTGTTGT
83869	81956	ACTAAGGGTTGTTTTTGTTG
83870	81957	GACTAAGGGTTGTTTTTGTT
83871	81958	AGACTAAGGGTTGTTTTTGT
83872	81959	TAGACTAAGGGTTGTTTTTG
83873	81960	TTAGACTAAGGGTTGTTTTT
83874	81961	CTTAGACTAAGGGTTGTTTT
83875	81962	CCTTAGACTAAGGGTTGTTT
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83877	81964	ACCCTTAGACTAAGGGTTGT
83878	81965	CACCCTTAGACTAAGGGTTG
83879	81966	CCACCCTTAGACTAAGGGTT
83880	81967	TCCACCCTTAGACTAAGGGT
83881	81968	ATCCACCCTTAGACTAAGGG
83882	81969	CATCCACCCTTAGACTAAGG
83883	81970	ACATCCACCCTTAGACTAAG
83884	81971	AACATCCACCCTTAGACTAA
83885	81972	TAACATCCACCCTTAGACTA
83886	81973	GTAACATCCACCCTTAGACT
83887	81974	TGTAACATCCACCCTTAGAC
83888	81975	CTGTAACATCCACCCTTAGA
83889	81976	ACTGTAACATCCACCCTTAG
83890	81977	AACTGTAACATCCACCCTTA
83891	81978	AAACTGTAACATCCACCCTT
83892	81979	TAAACTGTAACATCCACCCT
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83894	81981	GCTAAACTGTAACATCCACC
83895	81982	TGCTAAACTGTAACATCCAC
83896	81983	TTGCTAAACTGTAACATCCA
83897	81984	GTTGCTAAACTGTAACATCC
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83902	81989	CTTAAGTTGCTAAACTGTAA
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83904	81991	TACTTAAGTTGCTAAACTGT
83905	81992	TTACTTAAGTTGCTAAACTG
83906	81993	TTTACTTAAGTTGCTAAACT
83907	81994	TTTTACTTAAGTTGCTAAAC
83908	81995	CTTTTACTTAAGTTGCTAAA
83909	81996	TCTTTTACTTAAGTTGCTAA
83910	81997	TTCTTTTACTTAAGTTGCTA
83911	81998	TTTCTTTTACTTAAGTTGCT
83912	81999	GTTTCTTTTACTTAAGTTGC
83913	82000	GGTTTCTTTTACTTAAGTTG
83914	82001	AGGTTTCTTTTACTTAAGTT
83915	82002	CAGGTTTCTTTTACTTAAGT
83916	82003	TCAGGTTTCTTTTACTTAAG
83917	82004	TTCAGGTTTCTTTTACTTAA
83918	82005	ATTCAGGTTTCTTTTACTTA
83919	82006	GATTCAGGTTTCTTTTACTT
83920	82007	AGATTCAGGTTTCTTTTACT
83921	82008	AAGATTCAGGTTTCTTTTAC
83922	82009	AAAGATTCAGGTTTCTTTTA
83923	82010	TAAAGATTCAGGTTTCTTTT
83924	82011	CTAAAGATTCAGGTTTCTTT
83925	82012	ACTAAAGATTCAGGTTTCTT
83926	82013	TACTAAAGATTCAGGTTTCT
83927	82014	CTACTAAAGATTCAGGTTTC
83928	82015	CCTACTAAAGATTCAGGTTT
83929	82016	TCCTACTAAAGATTCAGGTT
83930	82017	TTCCTACTAAAGATTCAGGT

133007	131094	AGGATGATTGCTGCTGCCCA
133008	131095	AAGGATGATTGCTGCTGCCC
133009	131096	GAAGGATGATTGCTGCTGCC
133010	131097	GGAAGGATGATTGCTGCTGC
133011	131098	AGGAAGGATGATTGCTGCTG
133012	131099	CAGGAAGGATGATTGCTGCT
133013	131100	ACAGGAAGGATGATTGCTGC
133014	131101	GACAGGAAGGATGATTGCTG
133015	131102	TGACAGGAAGGATGATTGCT
133016	131103	GTGACAGGAAGGATGATTGC
133017	131104	GGTGACAGGAAGGATGATTG
133018	131105	AGGTGACAGGAAGGATGATT
133019	131106	CAGGTGACAGGAAGGATGAT
133020	131107	ACAGGTGACAGGAAGGATGA
133021	131108	TACAGGTGACAGGAAGGATG
133022	131109	TTACAGGTGACAGGAAGGAT
133023	131110	GTTACAGGTGACAGGAAGGA
133024	131111	GGTTACAGGTGACAGGAAGG
133025	131112	GGGTTACAGGTGACAGGAAG
133026	131113	TGGGTTACAGGTGACAGGAA
133027	131114	GTGGGTTACAGGTGACAGGA
133028	131115	TGTGGGTTACAGGTGACAGG
133029	131116	CTGTGGGTTACAGGTGACAG
133030	131117	GCTGTGGGTTACAGGTGACA
133031	131118	AGCTGTGGGTTACAGGTGAC
133032	131119	AAGCTGTGGGTTACAGGTGA
133033	131120	TAAGCTGTGGGTTACAGGTG
133034	131121	ATAAGCTGTGGGTTACAGGT
133035	131122	CATAAGCTGTGGGTTACAGG
133036	131123	GCATAAGCTGTGGGTTACAG
133037	131124	AGCATAAGCTGTGGGTTACA
133038	131125	AAGCATAAGCTGTGGGTTAC
133039	131126	AAAGCATAAGCTGTGGGTTA
133040	131127	GAAAGCATAAGCTGTGGGTT
133041	131128	AGAAAGCATAAGCTGTGGGT
133042	131129	AAGAAAGCATAAGCTGTGGG
133043	131130	GAAGAAAGCATAAGCTGTGG
133044	131131	GGAAGAAAGCATAAGCTGTG
133045	131132	AGGAAGAAAGCATAAGCTGT
133046	131133	CAGGAAGAAAGCATAAGCTG
133047	131134	CCAGGAAGAAAGCATAAGCT
133048	131135	TCCAGGAAGAAAGCATAAGC
133049	131136	CTCCAGGAAGAAAGCATAAG
133050	131137	CCTCCAGGAAGAAAGCATAA
133051	131138	ACCTCCAGGAAGAAAGCATA
133052	131139	AACCTCCAGGAAGAAAGCAT
133053	131140	GAACCTCCAGGAAGAAAGCA
133054	131141	AGAACCTCCAGGAAGAAAGC
133055	131142	AAGAACCTCCAGGAAGAAAG
133056	131143	CAAGAACCTCCAGGAAGAAA
133057	131144	ACAAGAACCTCCAGGAAGAA
133058	131145	GACAAGAACCTCCAGGAAGA
133059	131146	AGACAAGAACCTCCAGGAAG
133060	131147	CAGACAAGAACCTCCAGGAA
133061	131148	GCAGACAAGAACCTCCAGGA
133062	131149	GGCAGACAAGAACCTCCAGG
133063	131150	TGGCAGACAAGAACCTCCAG
133064	131151	GTGGCAGACAAGAACCTCCA
133065	131152	TGTGGCAGACAAGAACCTCC
133066	131153	TTGTGGCAGACAAGAACCTC
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133068	131155	CTTTGTGGCAGACAAGAACC
133069	131156	CCTTTGTGGCAGACAAGAAC
133070	131157	GCCTTTGTGGCAGACAAGAA
133071	131158	AGCCTTTGTGGCAGACAAGA
133072	131159	GAGCCTTTGTGGCAGACAAG
133073	131160	TGAGCCTTTGTGGCAGACAA
133074	131161	GTGAGCCTTTGTGGCAGACA
133075	131162	AGTGAGCCTTTGTGGCAGAC
133076	131163	CAGTGAGCCTTTGTGGCAGA
133077	131164	GCAGTGAGCCTTTGTGGCAG

34784	32871	CCGCCACCACATCCCCGCTA
34785	32872	CCCGCCACCACATCCCCGCT
34786	32873	GCCCGCCACCACATCCCCGC
34787	32874	CGCCCGCCACCACATCCCCG
34788	32875	GCGCCCGCCACCACATCCCC
34789	32876	GGCGCCCGCCACCACATCCC
34790	32877	AGGCGCCCGCCACCACATCC
34791	32878	TAGGCGCCCGCCACCACATC
34792	32879	ATAGGCGCCCGCCACCACAT
34793	32880	TATAGGCGCCCGCCACCACA
34794	32881	TTATAGGCGCCCGCCACCAC
34795	32882	ATTATAGGCGCCCGCCACCA
34796	32883	GATTATAGGCGCCCGCCACC
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34798	32885	GGGATTATAGGCGCCCGCCA
34799	32886	TGGGATTATAGGCGCCCGCC
34800	32887	CTGGGATTATAGGCGCCCGC
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34806	32893	AAGTAGCTGGGATTATAGGC
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34808	32895	CCAAGTAGCTGGGATTATAG
34809	32896	CCCAAGTAGCTGGGATTATA
34810	32897	TCCCAAGTAGCTGGGATTAT
34811	32898	CTCCCAAGTAGCTGGGATTA
34812	32899	TCTCCCAAGTAGCTGGGATT
34813	32900	GTCTCCCAAGTAGCTGGGAT
34814	32901	AGTCTCCCAAGTAGCTGGGA
34815	32902	CAGTCTCCCAAGTAGCTGGG
34816	32903	TCAGTCTCCCAAGTAGCTGG
34817	32904	CTCAGTCTCCCAAGTAGCTG
34818	32905	CCTCAGTCTCCCAAGTAGCT
34819	32906	GCCTCAGTCTCCCAAGTAGC
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34824	32911	CTCCTGCCTCAGTCTCCCAA
34825	32912	TCTCCTGCCTCAGTCTCCCA
34826	32913	TTCTCCTGCCTCAGTCTCCC
34827	32914	ATTCTCCTGCCTCAGTCTCC
34828	32915	GATTCTCCTGCCTCAGTCTC
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34830	32917	GCGATTCTCCTGCCTCAGTC
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34837	32924	GGTTCAAGCGATTCTCCTGC
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34839	32926	CAGGTTCAAGCGATTCTCCT
34840	32927	CCAGGTTCAAGCGATTCTCC
34841	32928	CCCAGGTTCAAGCGATTCTC
34842	32929	TCCCAGGTTCAAGCGATTCT
34843	32930	CTCCCAGGTTCAAGCGATTC
34844	32931	CCTCCCAGGTTCAAGCGATT
34845	32932	ACCTCCCAGGTTCAAGCGAT
34846	32933	CACCTCCCAGGTTCAAGCGA
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34849	32936	CTCCACCTCCCAGGTTCAAG
34850	32937	CCTCCACCTCCCAGGTTCAA
34851	32938	ACCTCCACCTCCCAGGTTCA
34852	32939	AACCTCCACCTCCCAGGTTC
34853	32940	CAACCTCCACCTCCCAGGTT
34854	32941	GCAACCTCCACCTCCCAGGT

83931	82018	CTTCCTACTAAAGATTCAGG
83932	82019	TCTTCCTACTAAAGATTCAG
83933	82020	GTCTTCCTACTAAAGATTCA
83934	82021	TGTCTTCCTACTAAAGATTC
83935	82022	ATGTCTTCCTACTAAAGATT
83936	82023	AATGTCTTCCTACTAAAGAT
83937	82024	AAATGTCTTCCTACTAAAGA
83938	82025	AAAATGTCTTCCTACTAAAG
83939	82026	AAAAATGTCTTCCTACTAAA
83940	82027	AAAAAATGTCTTCCTACTAA
83941	82028	TAAAAAATGTCTTCCTACTA
83942	82029	GTAAAAAATGTCTTCCTACT
83943	82030	AGTAAAAAATGTCTTCCTAC
83944	82031	GAGTAAAAAATGTCTTCCTA
83945	82032	AGAGTAAAAAATGTCTTCCT
83946	82033	TAGAGTAAAAAATGTCTTCC
83947	82034	GTAGAGTAAAAAATGTCTTC
83948	82035	GGTAGAGTAAAAAATGTCTT
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83950	82037	GAGGTAGAGTAAAAAATGTC
83951	82038	AGAGGTAGAGTAAAAAATGT
83952	82039	TAGAGGTAGAGTAAAAAATG
83953	82040	TTAGAGGTAGAGTAAAAAAT
83954	82041	TTTAGAGGTAGAGTAAAAAA
83955	82042	ATTTAGAGGTAGAGTAAAAA
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83958	82045	TAGATTTAGAGGTAGAGTAA
83959	82046	CTAGATTTAGAGGTAGAGTA
83960	82047	CCTAGATTTAGAGGTAGAGT
83961	82048	ACCTAGATTTAGAGGTAGAG
83962	82049	AACCTAGATTTAGAGGTAGA
83963	82050	CAACCTAGATTTAGAGGTAG
83964	82051	TCAACCTAGATTTAGAGGTA
83965	82052	TTCAACCTAGATTTAGAGGT
83966	82053	ATTCAACCTAGATTTAGAGG
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83968	82055	ATATTCAACCTAGATTTAGA
83969	82056	TATATTCAACCTAGATTTAG
83970	82057	ATATATTCAACCTAGATTTA
83971	82058	GATATATTCAACCTAGATTT
83972	82059	AGATATATTCAACCTAGATT
83973	82060	AAGATATATTCAACCTAGAT
83974	82061	CAAGATATATTCAACCTAGA
83975	82062	ACAAGATATATTCAACCTAG
83976	82063	TACAAGATATATTCAACCTA
83977	82064	CTACAAGATATATTCAACCT
83978	82065	CCTACAAGATATATTCAACC
83979	82066	ACCTACAAGATATATTCAAC
83980	82067	AACCTACAAGATATATTCAA
83981	82068	CAACCTACAAGATATATTCA
83982	82069	ACAACCTACAAGATATATTC
83983	82070	CACAACCTACAAGATATATT
83984	82071	CCACAACCTACAAGATATAT
83985	82072	TCCACAACCTACAAGATATA
83986	82073	ATCCACAACCTACAAGATAT
83987	82074	GATCCACAACCTACAAGATA
83988	82075	AGATCCACAACCTACAAGAT
83989	82076	AAGATCCACAACCTACAAGA
83990	82077	AAAGATCCACAACCTACAAG
83991	82078	AAAAGATCCACAACCTACAA
83992	82079	GAAAAGATCCACAACCTACA
83993	82080	GGAAAAGATCCACAACCTAC
83994	82081	TGGAAAAGATCCACAACCTA
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83996	82083	TATGGAAAAGATCCACAACC
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83998	82085	TTTATGGAAAAGATCCACAA
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84000	82087	GATTTATGGAAAAGATCCAC
84001	82088	TGATTTATGGAAAAGATCCA

133078	131165	AGCAGTGAGCCTTTGTGGCA
133079	131166	CAGCAGTGAGCCTTTGTGGC
133080	131167	TCAGCAGTGAGCCTTTGTGG
133081	131168	ATCAGCAGTGAGCCTTTGTG
133082	131169	TATCAGCAGTGAGCCTTTGT
133083	131170	CTATCAGCAGTGAGCCTTTG
133084	131171	CCTATCAGCAGTGAGCCTTT
133085	131172	TCCTATCAGCAGTGAGCCTT
133086	131173	TTCCTATCAGCAGTGAGCCT
133087	131174	ATTCCTATCAGCAGTGAGCC
133088	131175	AATTCCTATCAGCAGTGAGC
133089	131176	AAATTCCTATCAGCAGTGAG
133090	131177	CAAATTCCTATCAGCAGTGA
133091	131178	ACAAATTCCTATCAGCAGTG
133092	131179	TACAAATTCCTATCAGCAGT
133093	131180	ATACAAATTCCTATCAGCAG
133094	131181	TATACAAATTCCTATCAGCA
133095	131182	ATATACAAATTCCTATCAGC
133096	131183	CATATACAAATTCCTATCAG
133097	131184	TCATATACAAATTCCTATCA
133098	131185	ATCATATACAAATTCCTATC
133099	131186	GATCATATACAAATTCCTAT
133100	131187	TGATCATATACAAATTCCTA
133101	131188	TTGATCATATACAAATTCCT
133102	131189	TTTGATCATATACAAATTCC
133103	131190	CTTTGATCATATACAAATTC
133104	131191	CCTTTGATCATATACAAATT
133105	131192	ACCTTTGATCATATACAAAT
133106	131193	CACCTTTGATCATATACAAA
133107	131194	ACACCTTTGATCATATACAA
133108	131195	AACACCTTTGATCATATACA
133109	131196	AAACACCTTTGATCATATAC
133110	131197	TAAACACCTTTGATCATATA
133111	131198	CTAAACACCTTTGATCATAT
133112	131199	ACTAAACACCTTTGATCATA
133113	131200	AACTAAACACCTTTGATCAT
133114	131201	AAACTAAACACCTTTGATCA
133115	131202	AAAACTAAACACCTTTGATC
133116	131203	TAAAACTAAACACCTTTGAT
133117	131204	ATAAAACTAAACACCTTTGA
133118	131205	TATAAAACTAAACACCTTTG
133119	131206	TTATAAAACTAAACACCTTT
133120	131207	TTTATAAAACTAAACACCTT
133121	131208	TTTTATAAAACTAAACACCT
133122	131209	GTTTTATAAAACTAAACACC
133123	131210	TGTTTTATAAAACTAAACAC
133124	131211	CTGTTTTATAAAACTAAACA
133125	131212	ACTGTTTTATAAAACTAAAC
133126	131213	AACTGTTTTATAAAACTAAA
133127	131214	TAACTGTTTTATAAAACTAA
133128	131215	TTAACTGTTTTATAAAACTA
133129	131216	CTTAACTGTTTTATAAAACT
133130	131217	ACTTAACTGTTTTATAAAAC
133131	131218	GACTTAACTGTTTTATAAAA
133132	131219	GGACTTAACTGTTTTATAAA
133133	131220	TGGACTTAACTGTTTTATAA
133134	131221	CTGGACTTAACTGTTTTATA
133135	131222	ACTGGACTTAACTGTTTTAT
133136	131223	GACTGGACTTAACTGTTTTA
133137	131224	AGACTGGACTTAACTGTTTT
133138	131225	AAGACTGGACTTAACTGTTT
133139	131226	TAAGACTGGACTTAACTGTT
133140	131227	TTAAGACTGGACTTAACTGT
133141	131228	ATTAAGACTGGACTTAACTG
133142	131229	AATTAAGACTGGACTTAACT
133143	131230	AAATTAAGACTGGACTTAAC
133144	131231	AAAATTAAGACTGGACTTAA
133145	131232	GAAAATTAAGACTGGACTTA
133146	131233	GGAAAATTAAGACTGGACTT
133147	131234	TGGAAAATTAAGACTGGACT
133148	131235	GTGGAAAATTAAGACTGGAC

34855	32942	TGCAACCTCCACCTCCCAGG
34856	32943	CTGCAACCTCCACCTCCCAG
34857	32944	ACTGCAACCTCCACCTCCCA
34858	32945	CACTGCAACCTCCACCTCCC
34859	32946	TCACTGCAACCTCCACCTCC
34860	32947	CTCACTGCAACCTCCACCTC
34861	32948	ACTCACTGCAACCTCCACCT
34862	32949	AACTCACTGCAACCTCCACC
34863	32950	CAACTCACTGCAACCTCCAC
34864	32951	TCAACTCACTGCAACCTCCA
34865	32952	CTCAACTCACTGCAACCTCC
34866	32953	TCTCAACTCACTGCAACCTC
34867	32954	ATCTCAACTCACTGCAACCT
34868	32955	AATCTCAACTCACTGCAACC
34869	32956	CAATCTCAACTCACTGCAAC
34870	32957	ACAATCTCAACTCACTGCAA
34871	32958	CACAATCTCAACTCACTGCA
34872	32959	GCACAATCTCAACTCACTGC
34873	32960	GGCACAATCTCAACTCACTG
34874	32961	GGGCACAATCTCAACTCACT
34875	32962	AGGGCACAATCTCAACTCAC
34876	32963	AAGGGCACAATCTCAACTCA
34877	32964	CAAGGGCACAATCTCAACTC
34878	32965	GCAAGGGCACAATCTCAACT
34879	32966	TGCAAGGGCACAATCTCAAC
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34881	32968	AGTGCAAGGGCACAATCTCA
34882	32969	GAGTGCAAGGGCACAATCTC
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34885	32972	CTGGAGTGCAAGGGCACAAT
34886	32973	GCTGGAGTGCAAGGGCACAA
34887	32974	GGCTGGAGTGCAAGGGCACA
34888	32975	AGGCTGGAGTGCAAGGGCAC
34889	32976	CAGGCTGGAGTGCAAGGGCA
34890	32977	CCAGGCTGGAGTGCAAGGGC
34891	32978	CCCAGGCTGGAGTGCAAGGG
34892	32979	GCCCAGGCTGGAGTGCAAGG
34893	32980	TGCCCAGGCTGGAGTGCAAG
34894	32981	TTGCCCAGGCTGGAGTGCAA
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34897	32984	CTGTTGCCCAGGCTGGAGTG
34898	32985	CCTGTTGCCCAGGCTGGAGT
34899	32986	TCCTGTTGCCCAGGCTGGAG
34900	32987	CTCCTGTTGCCCAGGCTGGA
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34902	32989	CGCTCCTGTTGCCCAGGCTG
34903	32990	TCGCTCCTGTTGCCCAGGCT
34904	32991	TTCGCTCCTGTTGCCCAGGC
34905	32992	TTTCGCTCCTGTTGCCCAGG
34906	32993	GTTTCGCTCCTGTTGCCCAG
34907	32994	AGTTTCGCTCCTGTTGCCCA
34908	32995	GAGTTTCGCTCCTGTTGCCC
34909	32996	AGAGTTTCGCTCCTGTTGCC
34910	32997	TAGAGTTTCGCTCCTGTTGC
34911	32998	ATAGAGTTTCGCTCCTGTTG
34912	32999	GATAGAGTTTCGCTCCTGTT
34913	33000	AGATAGAGTTTCGCTCCTGT
34914	33001	AAGATAGAGTTTCGCTCCTG
34915	33002	TAAGATAGAGTTTCGCTCCT
34916	33003	TTAAGATAGAGTTTCGCTCC
34917	33004	TTTAAGATAGAGTTTCGCTC
34918	33005	TTTTAAGATAGAGTTTCGCT
34919	33006	TTTTTAAGATAGAGTTTCGC
34920	33007	TTTTTTAAGATAGAGTTTCG
34921	33008	TTTTTTTAAGATAGAGTTTC
34922	33009	TTTTTTTTAAGATAGAGTTT
34923	33010	TTTTTTTTTAAGATAGAGTT
34924	33011	TTTTTTTTTTAAGATAGAGT
34925	33012	TTTTTTTTTTTAAGATAGAG

84002	82089	CTGATTTATGGAAAAGATCC
84003	82090	CCTGATTTATGGAAAAGATC
84004	82091	CCCTGATTTATGGAAAAGAT
84005	82092	TCCCTGATTTATGGAAAAGA
84006	82093	ATCCCTGATTTATGGAAAAG
84007	82094	TATCCCTGATTTATGGAAAA
84008	82095	GTATCCCTGATTTATGGAAA
84009	82096	AGTATCCCTGATTTATGGAA
84010	82097	CAGTATCCCTGATTTATGGA
84011	82098	TCAGTATCCCTGATTTATGG
84012	82099	TTCAGTATCCCTGATTTATG
84013	82100	GTTCAGTATCCCTGATTTAT
84014	82101	TGTTCAGTATCCCTGATTTA
84015	82102	TTGTTCAGTATCCCTGATTT
84016	82103	GTTGTTCAGTATCCCTGATT
84017	82104	TGTTGTTCAGTATCCCTGAT
84018	82105	CTGTTGTTCAGTATCCCTGA
84019	82106	ACTGTTGTTCAGTATCCCTG
84020	82107	AACTGTTGTTCAGTATCCCT
84021	82108	GAACTGTTGTTCAGTATCCC
84022	82109	AGAACTGTTGTTCAGTATCC
84023	82110	TAGAACTGTTGTTCAGTATC
84024	82111	ATAGAACTGTTGTTCAGTAT
84025	82112	CATAGAACTGTTGTTCAGTA
84026	82113	CCATAGAACTGTTGTTCAGT
84027	82114	TCCATAGAACTGTTGTTCAG
84028	82115	ATCCATAGAACTGTTGTTCA
84029	82116	CATCCATAGAACTGTTGTTC
84030	82117	CCATCCATAGAACTGTTGTT
84031	82118	ACCATCCATAGAACTGTTGT
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84036	82123	TCCATACCATCCATAGAACT
84037	82124	TTCCATACCATCCATAGAAC
84038	82125	TTTCCATACCATCCATAGAA
84039	82126	ATTTCCATACCATCCATAGA
84040	82127	TATTTCCATACCATCCATAG
84041	82128	CTATTTCCATACCATCCATA
84042	82129	ACTATTTCCATACCATCCAT
84043	82130	TACTATTTCCATACCATCCA
84044	82131	TTACTATTTCCATACCATCC
84045	82132	ATTACTATTTCCATACCATC
84046	82133	TATTACTATTTCCATACCAT
84047	82134	CTATTACTATTTCCATACCA
84048	82135	GCTATTACTATTTCCATACC
84049	82136	TGCTATTACTATTTCCATAC
84050	82137	TTGCTATTACTATTTCCATA
84051	82138	ATTGCTATTACTATTTCCAT
84052	82139	TATTGCTATTACTATTTCCA
84053	82140	CTATTGCTATTACTATTTCC
84054	82141	ACTATTGCTATTACTATTTC
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84056	82143	ATACTATTGCTATTACTATT
84057	82144	CATACTATTGCTATTACTAT
84058	82145	ACATACTATTGCTATTACTA
84059	82146	AACATACTATTGCTATTACT
84060	82147	TAACATACTATTGCTATTAC
84061	82148	GTAACATACTATTGCTATTA
84062	82149	AGTAACATACTATTGCTATT
84063	82150	TAGTAACATACTATTGCTAT
84064	82151	TTAGTAACATACTATTGCTA
84065	82152	GTTAGTAACATACTATTGCT
84066	82153	AGTTAGTAACATACTATTGC
84067	82154	AAGTTAGTAACATACTATTG
84068	82155	AAAGTTAGTAACATACTATT
84069	82156	CAAAGTTAGTAACATACTAT
84070	82157	ACAAAGTTAGTAACATACTA
84071	82158	CACAAAGTTAGTAACATACT
84072	82159	CCACAAAGTTAGTAACATAC

133149	131236	TGTGGAAAATTAAGACTGGA
133150	131237	ATGTGGAAAATTAAGACTGG
133151	131238	AATGTGGAAAATTAAGACTG
133152	131239	TAATGTGGAAAATTAAGACT
133153	131240	ATAATGTGGAAAATTAAGAC
133154	131241	GATAATGTGGAAAATTAAGA
133155	131242	TGATAATGTGGAAAATTAAG
133156	131243	GTGATAATGTGGAAAATTAA
133157	131244	AGTGATAATGTGGAAAATTA
133158	131245	AAGTGATAATGTGGAAAATT
133159	131246	AAAGTGATAATGTGGAAAAT
133160	131247	GAAAGTGATAATGTGGAAAA
133161	131248	TGAAAGTGATAATGTGGAAA
133162	131249	TTGAAAGTGATAATGTGGAA
133163	131250	ATTGAAAGTGATAATGTGGA
133164	131251	AATTGAAAGTGATAATGTGG
133165	131252	AAATTGAAAGTGATAATGTG
133166	131253	AAAATTGAAAGTGATAATGT
133167	131254	CAAAATTGAAAGTGATAATG
133168	131255	ACAAAATTGAAAGTGATAAT
133169	131256	TACAAAATTGAAAGTGATAA
133170	131257	ATACAAAATTGAAAGTGATA
133171	131258	AATACAAAATTGAAAGTGAT
133172	131259	CAATACAAAATTGAAAGTGA
133173	131260	ACAATACAAAATTGAAAGTG
133174	131261	CACAATACAAAATTGAAAGT
133175	131262	CCACAATACAAAATTGAAAG
133176	131263	TCCACAATACAAAATTGAAA
133177	131264	ATCCACAATACAAAATTGAA
133178	131265	AATCCACAATACAAAATTGA
133179	131266	TAATCCACAATACAAAATTG
133180	131267	GTAATCCACAATACAAAATT
133181	131268	CGTAATCCACAATACAAAAT
133182	131269	GCGTAATCCACAATACAAAA
133183	131270	TGCGTAATCCACAATACAAA
133184	131271	ATGCGTAATCCACAATACAA
133185	131272	AATGCGTAATCCACAATACA
133186	131273	AAATGCGTAATCCACAATAC
133187	131274	AAAATGCGTAATCCACAATA
133188	131275	TAAAATGCGTAATCCACAAT
133189	131276	TTAAAATGCGTAATCCACAA
133190	131277	TTTAAAATGCGTAATCCACA
133191	131278	ATTTAAAATGCGTAATCCAC
133192	131279	TATTTAAAATGCGTAATCCA
133193	131280	TTATTTAAAATGCGTAATCC
133194	131281	TTTATTTAAAATGCGTAATC
133195	131282	TTTTATTTAAAATGCGTAAT
133196	131283	TTTTTATTTAAAATGCGTAA
133197	131284	TTTTTTATTTAAAATGCGTA
133198	131285	ATTTTTTATTTAAAATGCGT
133199	131286	AATTTTTTATTTAAAATGCG
133200	131287	CAATTTTTTATTTAAAATGC
133201	131288	ACAATTTTTTATTTAAAATG
133202	131289	CACAATTTTTTATTTAAAAT
133203	131290	ACACAATTTTTTATTTAAAA
133204	131291	CACACAATTTTTTATTTAAA
133205	131292	TCACACAATTTTTTATTTAA
133206	131293	ATCACACAATTTTTTATTTA
133207	131294	AATCACACAATTTTTTATTT
133208	131295	CAATCACACAATTTTTTATT
133209	131296	GCAATCACACAATTTTTTAT
133210	131297	AGCAATCACACAATTTTTTA
133211	131298	TAGCAATCACACAATTTTTT
133212	131299	GTAGCAATCACACAATTTTT
133213	131300	TGTAGCAATCACACAATTTT
133214	131301	ATGTAGCAATCACACAATTT
133215	131302	AATGTAGCAATCACACAATT
133216	131303	AAATGTAGCAATCACACAAT
133217	131304	AAAATGTAGCAATCACACAA
133218	131305	CAAAATGTAGCAATCACACA
133219	131306	CCAAAATGTAGCAATCACAC

34926	33013	TTTTTTTTTTTTAAGATAGA
34927	33014	TTTTTTTTTTTTAAGATAG
34928	33015	TTTTTTTTTTTTTAAGATA
34929	33016	TTTTTTTTTTTTTAAGAT
34930	33017	CTTTTTTTTTTTTTTAAGA
34931	33018	TCTTTTTTTTTTTTTTAAG
34932	33019	TTCTTTTTTTTTTTTTTAA
34933	33020	TTTCTTTTTTTTTTTTTTA
34934	33021	TTTTCTTTTTTTTTTTTTT
34935	33022	CTTTTCTTTTTTTTTTTTT
34936	33023	GCTTTTCTTTTTTTTTTTT
34937	33024	TGCTTTTCTTTTTTTTTTT
34938	33025	TTGCTTTTCTTTTTTTTTT
34939	33026	ATTGCTTTTCTTTTTTTTT
34940	33027	AATTGCTTTTCTTTTTTTT
34941	33028	AAATTGCTTTTCTTTTTTT
34942	33029	GAAATTGCTTTTCTTTTTT
34943	33030	GGAAATTGCTTTTCTTTTT
34944	33031	AGGAAATTGCTTTTCTTTT
34945	33032	GAGGAAATTGCTTTTCTTTT
34946	33033	AGAGGAAATTGCTTTTCTTT
34947	33034	TAGAGGAAATTGCTTTTCTT
34948	33035	TTAGAGGAAATTGCTTTTCT
34949	33036	TTTAGAGGAAATTGCTTTTC
34950	33037	TTTTAGAGGAAATTGCTTTT
34951	33038	GTTTTAGAGGAAATTGCTTT
34952	33039	AGTTTTAGAGGAAATTGCTT
34953	33040	GAGTTTTAGAGGAAATTGCT
34954	33041	GGAGTTTTAGAGGAAATTGC
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34961	33048	ATTAACAGGAGTTTTAGAGG
34962	33049	CATTAACAGGAGTTTTAGAG
34963	33050	ACATTAACAGGAGTTTTAGA
34964	33051	AACATTAACAGGAGTTTTAG
34965	33052	CAACATTAACAGGAGTTTTA
34966	33053	TCAACATTAACAGGAGTTTT
34967	33054	ATCAACATTAACAGGAGTTT
34968	33055	CATCAACATTAACAGGAGTT
34969	33056	ACATCAACATTAACAGGAGT
34970	33057	AACATCAACATTAACAGGAG
34971	33058	AAACATCAACATTAACAGGA
34972	33059	AAAACATCAACATTAACAGG
34973	33060	TAAAACATCAACATTAACAG
34974	33061	TTAAAACATCAACATTAACA
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34976	33063	GGTTAAAACATCAACATTAA
34977	33064	AGGTTAAAACATCAACATTA
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34986	33073	CATGGGAGGAGGTTAAAACA
34987	33074	GCATGGGAGGAGGTTAAAAC
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34992	33079	CATGAGCATGGGAGGAGGTT
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34994	33081	TCCATGAGCATGGGAGGAGG
34995	33082	ATCCATGAGCATGGGAGGAG
34996	33083	CATCCATGAGCATGGGAGGA

84073	82160	CCCACAAAGTTAGTAACATA
84074	82161	TCCCACAAAGTTAGTAACAT
84075	82162	TTCCCACAAAGTTAGTAACA
84076	82163	TTTCCCACAAAGTTAGTAAC
84077	82164	TTTTCCCACAAAGTTAGTAA
84078	82165	CTTTTCCCACAAAGTTAGTA
84079	82166	TCTTTTCCCACAAAGTTAGT
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84081	82168	ACTCTTTTCCCACAAAGTTA
84082	82169	CACTCTTTTCCCACAAAGTT
84083	82170	CCACTCTTTTCCCACAAAGT
84084	82171	TCCACTCTTTTCCCACAAAG
84085	82172	GTCCACTCTTTTCCCACAAA
84086	82173	TGTCCACTCTTTTCCCACAA
84087	82174	ATGTCCACTCTTTTCCCACA
84088	82175	AATGTCCACTCTTTTCCCAC
84089	82176	GAATGTCCACTCTTTTCCCA
84090	82177	TGAATGTCCACTCTTTTCCC
84091	82178	TTGAATGTCCACTCTTTTCC
84092	82179	ATTGAATGTCCACTCTTTTC
84093	82180	AATTGAATGTCCACTCTTTT
84094	82181	AAATTGAATGTCCACTCTTT
84095	82182	AAAATTGAATGTCCACTCTT
84096	82183	TAAAATTGAATGTCCACTCT
84097	82184	CTAAAATTGAATGTCCACTC
84098	82185	GCTAAAATTGAATGTCCACT
84099	82186	AGCTAAAATTGAATGTCCAC
84100	82187	TAGCTAAAATTGAATGTCCA
84101	82188	ATAGCTAAAATTGAATGTCC
84102	82189	AATAGCTAAAATTGAATGTC
84103	82190	AAATAGCTAAAATTGAATGT
84104	82191	TAAATAGCTAAAATTGAATG
84105	82192	TTAAATAGCTAAAATTGAAT
84106	82193	TTTAAATAGCTAAAATTGAA
84107	82194	ATTTAAATAGCTAAAATTGA
84108	82195	AATTTAAATAGCTAAAATTG
84109	82196	AAATTTAAATAGCTAAAATT
84110	82197	CAAATTTAAATAGCTAAAAT
84111	82198	CCAAATTTAAATAGCTAAAA
84112	82199	TCCAAATTTAAATAGCTAAA
84113	82200	TTCCAAATTTAAATAGCTAA
84114	82201	TTTCCAAATTTAAATAGCTA
84115	82202	CTTTCCAAATTTAAATAGCT
84116	82203	ACTTTCCAAATTTAAATAGC
84117	82204	AACTTTCCAAATTTAAATAG
84118	82205	TAACTTTCCAAATTTAAATA
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84120	82207	TCTAACTTTCCAAATTTAAA
84121	82208	ATCTAACTTTCCAAATTTAA
84122	82209	CATCTAACTTTCCAAATTTA
84123	82210	TCATCTAACTTTCCAAATTT
84124	82211	TTCATCTAACTTTCCAAATT
84125	82212	TTTCATCTAACTTTCCAAAT
84126	82213	TTTTCATCTAACTTTCCAAA
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84130	82217	TCTATTTTCATCTAACTTTC
84131	82218	CTCTATTTTCATCTAACTTT
84132	82219	TCTCTATTTTCATCTAACTT
84133	82220	TTCTCTATTTTCATCTAACT
84134	82221	GTTCTCTATTTTCATCTAAC
84135	82222	TGTTCTCTATTTTCATCTAA
84136	82223	GTGTTCTCTATTTTCATCTA
84137	82224	AGTGTTCTCTATTTTCATCT
84138	82225	TAGTGTTCTCTATTTTCATC
84139	82226	TTAGTGTTCTCTATTTTCAT
84140	82227	CTTAGTGTTCTCTATTTTCA
84141	82228	ACTTAGTGTTCTCTATTTTC
84142	82229	AACTTAGTGTTCTCTATTTT
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133220	131307	TCCAAAATGTAGCAATCACA
133221	131308	TTCCAAAATGTAGCAATCAC
133222	131309	TTTCCAAAATGTAGCAATCA
133223	131310	TTTTCCAAAATGTAGCAATC
133224	131311	GTTTTCCAAAATGTAGCAAT
133225	131312	TGTTTTCCAAAATGTAGCAA
133226	131313	ATGTTTTCCAAAATGTAGCA
133227	131314	AATGTTTTCCAAAATGTAGC
133228	131315	AAATGTTTTCCAAAATGTAG
133229	131316	AAAATGTTTTCCAAAATGTA
133230	131317	AAAAATGTTTTCCAAAATGT
133231	131318	AAAAAATGTTTTCCAAAATG
133232	131319	AAAAAAATGTTTTCCAAAAT
133233	131320	GAAAAAAATGTTTTCCAAAA
133234	131321	TGAAAAAAATGTTTTCCAAA
133235	131322	TTGAAAAAAATGTTTTCCAA
133236	131323	CTTGAAAAAAATGTTTTCCA
133237	131324	TCTTGAAAAAAATGTTTTCC
133238	131325	CTCTTGAAAAAAATGTTTTC
133239	131326	CCTCTTGAAAAAAATGTTTT
133240	131327	GCCTCTTGAAAAAAATGTTT
133241	131328	GGCCTCTTGAAAAAAATGTT
133242	131329	GGGCCTCTTGAAAAAAATGT
133243	131330	TGGGCCTCTTGAAAAAAATG
133244	131331	ATGGGCCTCTTGAAAAAAAT
133245	131332	GATGGGCCTCTTGAAAAAAA
133246	131333	GGATGGGCCTCTTGAAAAAA
133247	131334	CGGATGGGCCTCTTGAAAAA
133248	131335	ACGGATGGGCCTCTTGAAAA
133249	131336	TACGGATGGGCCTCTTGAAA
133250	131337	TTACGGATGGGCCTCTTGAA
133251	131338	ATTACGGATGGGCCTCTTGA
133252	131339	AATTACGGATGGGCCTCTTG
133253	131340	AAATTACGGATGGGCCTCTT
133254	131341	TAAATTACGGATGGGCCTCT
133255	131342	TTAAATTACGGATGGGCCTC
133256	131343	ATTAAATTACGGATGGGCCT
133257	131344	AATTAAATTACGGATGGGCC
133258	131345	CAATTAAATTACGGATGGGC
133259	131346	ACAATTAAATTACGGATGGG
133260	131347	TACAATTAAATTACGGATGG
133261	131348	TTACAATTAAATTACGGATG
133262	131349	TTTACAATTAAATTACGGAT
133263	131350	TTTTACAATTAAATTACGGA
133264	131351	CTTTTACAATTAAATTACGG
133265	131352	TCTTTTACAATTAAATTACG
133266	131353	ATCTTTTACAATTAAATTAC
133267	131354	TATCTTTTACAATTAAATTA
133268	131355	GTATCTTTTACAATTAAATT
133269	131356	AGTATCTTTTACAATTAAAT
133270	131357	CAGTATCTTTTACAATTAAA
133271	131358	TCAGTATCTTTTACAATTAA
133272	131359	GTCAGTATCTTTTACAATTA
133273	131360	TGTCAGTATCTTTTACAATT
133274	131361	TTGTCAGTATCTTTTACAAT
133275	131362	TTTGTCAGTATCTTTTACAA
133276	131363	GTTTGTCAGTATCTTTTACA
133277	131364	AGTTTGTCAGTATCTTTTAC
133278	131365	TAGTTTGTCAGTATCTTTTA
133279	131366	TTAGTTTGTCAGTATCTTTT
133280	131367	GTTAGTTTGTCAGTATCTTT
133281	131368	AGTTAGTTTGTCAGTATCTT
133282	131369	AAGTTAGTTTGTCAGTATCT
133283	131370	CAAGTTAGTTTGTCAGTATC
133284	131371	CCAAGTTAGTTTGTCAGTAT
133285	131372	ACCAAGTTAGTTTGTCAGTA
133286	131373	AACCAAGTTAGTTTGTCAGT
133287	131374	AAACCAAGTTAGTTTGTCAG
133288	131375	TAAACCAAGTTAGTTTGTCA
133289	131376	ATAAACCAAGTTAGTTTGTC
133290	131377	AATAAACCAAGTTAGTTTGT

34997	33084	CCATCCATGAGCATGGGAGG
34998	33085	GCCATCCATGAGCATGGGAG
34999	33086	TGCCATCCATGAGCATGGGA
35000	33087	ATGCCATCCATGAGCATGGG
35001	33088	AATGCCATCCATGAGCATGG
35002	33089	GAATGCCATCCATGAGCATG
35003	33090	AGAATGCCATCCATGAGCAT
35004	33091	GAGAATGCCATCCATGAGCA
35005	33092	TGAGAATGCCATCCATGAGC
35006	33093	CTGAGAATGCCATCCATGAG
35007	33094	ACTGAGAATGCCATCCATGA
35008	33095	CACTGAGAATGCCATCCATG
35009	33096	CCACTGAGAATGCCATCCAT
35010	33097	GCCACTGAGAATGCCATCCA
35011	33098	TGCCACTGAGAATGCCATCC
35012	33099	ATGCCACTGAGAATGCCATC
35013	33100	GATGCCACTGAGAATGCCAT
35014	33101	AGATGCCACTGAGAATGCCA
35015	33102	TAGATGCCACTGAGAATGCC
35016	33103	CTAGATGCCACTGAGAATGC
35017	33104	TCTAGATGCCACTGAGAATG
35018	33105	TTCTAGATGCCACTGAGAAT
35019	33106	ATTCTAGATGCCACTGAGAA
35020	33107	CATTCTAGATGCCACTGAGA
35021	33108	CCATTCTAGATGCCACTGAG
35022	33109	ACCATTCTAGATGCCACTGA
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35024	33111	TCACCATTCTAGATGCCACT
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35026	33113	ATTCACCATTCTAGATGCCA
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35028	33115	GTATTCACCATTCTAGATGC
35029	33116	AGTATTCACCATTCTAGATG
35030	33117	AAGTATTCACCATTCTAGAT
35031	33118	AAAGTATTCACCATTCTAGA
35032	33119	AAAAGTATTCACCATTCTAG
35033	33120	AAAAAGTATTCACCATTCTA
35034	33121	TAAAAAGTATTCACCATTCT
35035	33122	CTAAAAAGTATTCACCATTC
35036	33123	TCTAAAAAGTATTCACCATT
35037	33124	TTCTAAAAAGTATTCACCAT
35038	33125	TTTCTAAAAAGTATTCACCA
35039	33126	CTTTCTAAAAAGTATTCACC
35040	33127	ACTTTCTAAAAAGTATTCAC
35041	33128	AACTTTCTAAAAAGTATTCA
35042	33129	AAACTTTCTAAAAAGTATTC
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35044	33131	GAAAACTTTCTAAAAAGTAT
35045	33132	TGAAAACTTTCTAAAAAGTA
35046	33133	TTGAAAACTTTCTAAAAAGT
35047	33134	ATTGAAAACTTTCTAAAAAG
35048	33135	AATTGAAAACTTTCTAAAAA
35049	33136	AAATTGAAAACTTTCTAAAA
35050	33137	TAAATTGAAAACTTTCTAAA
35051	33138	ATAAATTGAAAACTTTCTAA
35052	33139	AATAAATTGAAAACTTTCTA
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35054	33141	AAAATAAATTGAAAACTTTC
35055	33142	CAAAATAAATTGAAAACTTT
35056	33143	GCAAAATAAATTGAAAACTT
35057	33144	GGCAAAATAAATTGAAAACT
35058	33145	TGGCAAAATAAATTGAAAAC
35059	33146	ATGGCAAAATAAATTGAAAA
35060	33147	GATGGCAAAATAAATTGAAA
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35062	33149	CTGATGGCAAAATAAATTGA
35063	33150	TCTGATGGCAAAATAAATTG
35064	33151	CTCTGATGGCAAAATAAATT
35065	33152	TCTCTGATGGCAAAATAAAT
35066	33153	TTCTCTGATGGCAAAATAAA
35067	33154	ATTCTCTGATGGCAAAATAA

84144	82231	GAAACTTAGTGTTCTCTATT
84145	82232	GGAAACTTAGTGTTCTCTAT
84146	82233	TGGAAACTTAGTGTTCTCTA
84147	82234	TTGGAAACTTAGTGTTCTCT
84148	82235	ATTGGAAACTTAGTGTTCTC
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84150	82237	AAATTGGAAACTTAGTGTTC
84151	82238	GAAATTGGAAACTTAGTGTT
84152	82239	TGAAATTGGAAACTTAGTGT
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84154	82241	AATGAAATTGGAAACTTAGT
84155	82242	AAATGAAATTGGAAACTTAG
84156	82243	CAAATGAAATTGGAAACTTA
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84159	82246	AAACAAATGAAATTGGAAAC
84160	82247	AAAACAAATGAAATTGGAAA
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84164	82251	AATGAAAACAAATGAAATTG
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84168	82255	ACTCAATGAAAACAAATGAA
84169	82256	GACTCAATGAAAACAAATGA
84170	82257	AGACTCAATGAAAACAAATG
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84172	82259	AAAGACTCAATGAAAACAAA
84173	82260	AAAAGACTCAATGAAAACAA
84174	82261	GAAAAGACTCAATGAAAACA
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84176	82263	GAGAAAAGACTCAATGAAAA
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84178	82265	TGGAGAAAAGACTCAATGAA
84179	82266	CTGGAGAAAAGACTCAATGA
84180	82267	TCTGGAGAAAAGACTCAATG
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84186	82273	AGGAATTCTGGAGAAAAGAC
84187	82274	GAGGAATTCTGGAGAAAAGA
84188	82275	AGAGGAATTCTGGAGAAAAG
84189	82276	GAGAGGAATTCTGGAGAAAA
84190	82277	GGAGAGGAATTCTGGAGAAA
84191	82278	TGGAGAGGAATTCTGGAGAA
84192	82279	TTGGAGAGGAATTCTGGAGA
84193	82280	TTTGGAGAGGAATTCTGGAG
84194	82281	ATTTGGAGAGGAATTCTGGA
84195	82282	CATTTGGAGAGGAATTCTGG
84196	82283	CCATTTGGAGAGGAATTCTG
84197	82284	TCCATTTGGAGAGGAATTCT
84198	82285	GTCCATTTGGAGAGGAATTC
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84201	82288	AGTGTCCATTTGGAGAGGAA
84202	82289	GAGTGTCCATTTGGAGAGGA
84203	82290	AGAGTGTCCATTTGGAGAGG
84204	82291	AAGAGTGTCCATTTGGAGAG
84205	82292	CAAGAGTGTCCATTTGGAGA
84206	82293	TCAAGAGTGTCCATTTGGAG
84207	82294	CTCAAGAGTGTCCATTTGGA
84208	82295	ACTCAAGAGTGTCCATTTGG
84209	82296	TACTCAAGAGTGTCCATTTG
84210	82297	ATACTCAAGAGTGTCCATTT
84211	82298	AATACTCAAGAGTGTCCATT
84212	82299	AAATACTCAAGAGTGTCCAT
84213	82300	AAAATACTCAAGAGTGTCCA
84214	82301	GAAAATACTCAAGAGTGTCC

133291	131378	TAATAAACCAAGTTAGTTTG
133292	131379	ATAATAAACCAAGTTAGTTT
133293	131380	AATAATAAACCAAGTTAGTT
133294	131381	AAATAATAAACCAAGTTAGT
133295	131382	AAAATAATAAACCAAGTTAG
133296	131383	CAAAATAATAAACCAAGTTA
133297	131384	CCAAAATAATAAACCAAGTT
133298	131385	ACCAAAATAATAAACCAAGT
133299	131386	AACCAAAATAATAAACCAAG
133300	131387	TAACCAAAATAATAAACCAA
133301	131388	ATAACCAAAATAATAAACCA
133302	131389	CATAACCAAAATAATAAACC
133303	131390	TCATAACCAAAATAATAAAC
133304	131391	GTCATAACCAAAATAATAAA
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133306	131393	GGGTCATAACCAAAATAATA
133307	131394	GGGGTCATAACCAAAATAAT
133308	131395	CGGGGTCATAACCAAAATAA
133309	131396	ACGGGGTCATAACCAAAATA
133310	131397	GACGGGGTCATAACCAAAAT
133311	131398	TGACGGGGTCATAACCAAAA
133312	131399	ATGACGGGGTCATAACCAAA
133313	131400	AATGACGGGGTCATAACCAA
133314	131401	AAATGACGGGGTCATAACCA
133315	131402	CAAATGACGGGGTCATAACC
133316	131403	TCAAATGACGGGGTCATAAC
133317	131404	GTCAAATGACGGGGTCATAA
133318	131405	AGTCAAATGACGGGGTCATA
133319	131406	AAGTCAAATGACGGGGTCAT
133320	131407	CAAGTCAAATGACGGGGTCA
133321	131408	ACAAGTCAAATGACGGGGTC
133322	131409	GACAAGTCAAATGACGGGGT
133323	131410	AGACAAGTCAAATGACGGGG
133324	131411	AAGACAAGTCAAATGACGGG
133325	131412	AAAGACAAGTCAAATGACGG
133326	131413	TAAAGACAAGTCAAATGACG
133327	131414	CTAAAGACAAGTCAAATGAC
133328	131415	ACTAAAGACAAGTCAAATGA
133329	131416	AACTAAAGACAAGTCAAATG
133330	131417	CAACTAAAGACAAGTCAAAT
133331	131418	ACAACTAAAGACAAGTCAAA
133332	131419	GACAACTAAAGACAAGTCAA
133333	131420	AGACAACTAAAGACAAGTCA
133334	131421	AAGACAACTAAAGACAAGTC
133335	131422	TAAGACAACTAAAGACAAGT
133336	131423	TTAAGACAACTAAAGACAAG
133337	131424	GTTAAGACAACTAAAGACAA
133338	131425	CGTTAAGACAACTAAAGACA
133339	131426	CCGTTAAGACAACTAAAGAC
133340	131427	CCCGTTAAGACAACTAAAGA
133341	131428	CCCCGTTAAGACAACTAAAG
133342	131429	TCCCCGTTAAGACAACTAAA
133343	131430	GTCCCCGTTAAGACAACTAA
133344	131431	AGTCCCCGTTAAGACAACTA
133345	131432	CAGTCCCCGTTAAGACAACT
133346	131433	TCAGTCCCCGTTAAGACAAC
133347	131434	TTCAGTCCCCGTTAAGACAA
133348	131435	ATTCAGTCCCCGTTAAGACA
133349	131436	TATTCAGTCCCCGTTAAGAC
133350	131437	ATATTCAGTCCCCGTTAAGA
133351	131438	CATATTCAGTCCCCGTTAAG
133352	131439	GCATATTCAGTCCCCGTTAA
133353	131440	CGCATATTCAGTCCCCGTTA
133354	131441	ACGCATATTCAGTCCCCGTT
133355	131442	CACGCATATTCAGTCCCCGT
133356	131443	GCACGCATATTCAGTCCCCG
133357	131444	TGCACGCATATTCAGTCCCC
133358	131445	TTGCACGCATATTCAGTCCC
133359	131446	TTTGCACGCATATTCAGTCC
133360	131447	CTTTGCACGCATATTCAGTC
133361	131448	CCTTTGCACGCATATTCAGT

35068	33155	CATTCTCTGATGGCAAAATA
35069	33156	CCATTCTCTGATGGCAAAAT
35070	33157	GCCATTCTCTGATGGCAAAA
35071	33158	AGCCATTCTCTGATGGCAAA
35072	33159	TAGCCATTCTCTGATGGCAA
35073	33160	ATAGCCATTCTCTGATGGCA
35074	33161	CATAGCCATTCTCTGATGGC
35075	33162	TCATAGCCATTCTCTGATGG
35076	33163	TTCATAGCCATTCTCTGATG
35077	33164	ATTCATAGCCATTCTCTGAT
35078	33165	CATTCATAGCCATTCTCTGA
35079	33166	CCATTCATAGCCATTCTCTG
35080	33167	GCCATTCATAGCCATTCTCT
35081	33168	TGCCATTCATAGCCATTCTC
35082	33169	CTGCCATTCATAGCCATTCT
35083	33170	ACTGCCATTCATAGCCATTC
35084	33171	TACTGCCATTCATAGCCATT
35085	33172	CTACTGCCATTCATAGCCAT
35086	33173	ACTACTGCCATTCATAGCCA
35087	33174	TACTACTGCCATTCATAGCC
35088	33175	CTACTACTGCCATTCATAGC
35089	33176	GCTACTACTGCCATTCATAG
35090	33177	GGCTACTACTGCCATTCATA
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35092	33179	AAGGCTACTACTGCCATTCA
35093	33180	TAAGGCTACTACTGCCATTC
35094	33181	GTAAGGCTACTACTGCCATT
35095	33182	TGTAAGGCTACTACTGCCAT
35096	33183	CTGTAAGGCTACTACTGCCA
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35098	33185	TTCTGTAAGGCTACTACTGC
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35100	33187	CATTCTGTAAGGCTACTACT
35101	33188	ACATTCTGTAAGGCTACTAC
35102	33189	TACATTCTGTAAGGCTACTA
35103	33190	ATACATTCTGTAAGGCTACT
35104	33191	AATACATTCTGTAAGGCTAC
35105	33192	AAATACATTCTGTAAGGCTA
35106	33193	GAAATACATTCTGTAAGGCT
35107	33194	AGAAATACATTCTGTAAGGC
35108	33195	AAGAAATACATTCTGTAAGG
35109	33196	AAAGAAATACATTCTGTAAG
35110	33197	AAAAGAAATACATTCTGTAA
35111	33198	AAAAAGAAATACATTCTGTA
35112	33199	AAAAAAGAAATACATTCTGT
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35114	33201	AAAAAAAAGAAATACATTCT
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35124	33211	AAAAGAAAAAAAAAAAAAGA
35125	33212	AAAAAGAAAAAAAAAAAAAG
35126	33213	AAAAAAGAAAAAAAAAAAAA
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35130	33217	CAAAAAAAAAGAAAAAAAAA
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35134	33221	ATCTCAAAAAAAAAGAAAAA
35135	33222	CATCTCAAAAAAAAAGAAAA
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84215	82302	TGAAAATACTCAAGAGTGTC
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84219	82306	GTACTGAAAATACTCAAGAG
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84230	82317	CCCAATATTAAGTACTGAAA
84231	82318	CCCCAATATTAAGTACTGAA
84232	82319	CCCCCAATATTAAGTACTGA
84233	82320	ACCCCCAATATTAAGTACTG
84234	82321	CACCCCCAATATTAAGTACT
84235	82322	TCACCCCCAATATTAAGTAC
84236	82323	TTCACCCCCAATATTAAGTA
84237	82324	TTTCACCCCCAATATTAAGT
84238	82325	ATTTCACCCCCAATATTAAG
84239	82326	AATTTCACCCCCAATATTAA
84240	82327	AAATTTCACCCCCAATATTA
84241	82328	GAAATTTCACCCCCAATATT
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84246	82333	GCAAAGAAATTTCACCCCCA
84247	82334	AGCAAAGAAATTTCACCCCC
84248	82335	GAGCAAAGAAATTTCACCCC
84249	82336	TGAGCAAAGAAATTTCACCC
84250	82337	GTGAGCAAAGAAATTTCACC
84251	82338	AGTGAGCAAAGAAATTTCAC
84252	82339	CAGTGAGCAAAGAAATTTCA
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84271	82358	AACAACTAAAATCTTTCCTC
84272	82359	AAACAACTAAAATCTTTCCT
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84274	82361	ATAAACAACTAAAATCTTTC
84275	82362	TATAAACAACTAAAATCTTT
84276	82363	TTATAAACAACTAAAATCTT
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84281	82368	TCTGTTTATAAACAACTAAA
84282	82369	TTCTGTTTATAAACAACTAA
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84285	82372	AAATTCTGTTTATAAACAAC

133362	131449	GCCTTTGCACGCATATTCAG
133363	131450	TGCCTTTGCACGCATATTCA
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133365	131452	CGTGCCTTTGCACGCATATT
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133369	131456	CAATCGTGCCTTTGCACGCA
133370	131457	TCAATCGTGCCTTTGCACGC
133371	131458	ATCAATCGTGCCTTTGCACG
133372	131459	AATCAATCGTGCCTTTGCAC
133373	131460	AAATCAATCGTGCCTTTGCA
133374	131461	TAAATCAATCGTGCCTTTGC
133375	131462	ATAAATCAATCGTGCCTTTG
133376	131463	GATAAATCAATCGTGCCTTT
133377	131464	TGATAAATCAATCGTGCCTT
133378	131465	ATGATAAATCAATCGTGCCT
133379	131466	CATGATAAATCAATCGTGCC
133380	131467	GCATGATAAATCAATCGTGC
133381	131468	AGCATGATAAATCAATCGTG
133382	131469	CAGCATGATAAATCAATCGT
133383	131470	CCAGCATGATAAATCAATCG
133384	131471	GCCAGCATGATAAATCAATC
133385	131472	AGCCAGCATGATAAATCAAT
133386	131473	AAGCCAGCATGATAAATCAA
133387	131474	AAAGCCAGCATGATAAATCA
133388	131475	AAAAGCCAGCATGATAAATC
133389	131476	TAAAAGCCAGCATGATAAAT
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133395	131482	GTTGCATAAAAGCCAGCATG
133396	131483	AGTTGCATAAAAGCCAGCAT
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133398	131485	CAAGTTGCATAAAAGCCAGC
133399	131486	ACAAGTTGCATAAAAGCCAG
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133402	131489	TATACAAGTTGCATAAAAGC
133403	131490	ATATACAAGTTGCATAAAAG
133404	131491	TATATACAAGTTGCATAAAA
133405	131492	ATATATACAAGTTGCATAAA
133406	131493	AATATATACAAGTTGCATAA
133407	131494	AAATATATACAAGTTGCATA
133408	131495	AAAATATATACAAGTTGCAT
133409	131496	TAAAATATATACAAGTTGCA
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133411	131498	GTTAAAATATATACAAGTTG
133412	131499	TGTTAAAATATATACAAGTT
133413	131500	TTGTTAAAATATATACAAGT
133414	131501	ATTGTTAAAATATATACAAG
133415	131502	AATTGTTAAAATATATACAA
133416	131503	AAATTGTTAAAATATATACA
133417	131504	AAAATTGTTAAAATATATAC
133418	131505	GAAAATTGTTAAAATATATA
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133420	131507	AGGAAAATTGTTAAAATATA
133421	131508	CAGGAAAATTGTTAAAATAT
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133424	131511	AAACAGGAAAATTGTTAAAA
133425	131512	CAAACAGGAAAATTGTTAAA
133426	131513	GCAAACAGGAAAATTGTTAA
133427	131514	AGCAAACAGGAAAATTGTTA
133428	131515	TAGCAAACAGGAAAATTGTT
133429	131516	TTAGCAAACAGGAAAATTGT
133430	131517	TTTAGCAAACAGGAAAATTG
133431	131518	CTTTAGCAAACAGGAAAATT
133432	131519	CCTTTAGCAAACAGGAAAAT

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35140	33227	AACTCCATCTCAAAAAAAA
35141	33228	AAACTCCATCTCAAAAAAA
35142	33229	AAAACTCCATCTCAAAAAA
35143	33230	AAAAACTCCATCTCAAAAA
35144	33231	AAAAAACTCCATCTCAAAA
35145	33232	AAAAAAACTCCATCTCAAA
35146	33233	AAAAAAAACTCCATCTCAA
35147	33234	CAAAAAAAACTCCATCTCAA
35148	33235	GCAAAAAAAACTCCATCTCA
35149	33236	AGCAAAAAAAACTCCATCTC
35150	33237	GAGCAAAAAAAACTCCATCT
35151	33238	AGAGCAAAAAAAACTCCATC
35152	33239	AAGAGCAAAAAAAACTCCAT
35153	33240	CAAGAGCAAAAAAAACTCCA
35154	33241	ACAAGAGCAAAAAAAACTCC
35155	33242	GACAAGAGCAAAAAAAACTC
35156	33243	TGACAAGAGCAAAAAAAACT
35157	33244	GTGACAAGAGCAAAAAAAAC
35158	33245	GGTGACAAGAGCAAAAAAAA
35159	33246	GGGTGACAAGAGCAAAAAAA
35160	33247	TGGGTGACAAGAGCAAAAAA
35161	33248	CTGGGTGACAAGAGCAAAAA
35162	33249	CCTGGGTGACAAGAGCAAAA
35163	33250	GCCTGGGTGACAAGAGCAAA
35164	33251	AGCCTGGGTGACAAGAGCAA
35165	33252	CAGCCTGGGTGACAAGAGCA
35166	33253	CCAGCCTGGGTGACAAGAGC
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35168	33255	CTCCAGCCTGGGTGACAAGA
35169	33256	ACTCCAGCCTGGGTGACAAG
35170	33257	CACTCCAGCCTGGGTGACAA
35171	33258	GCACTCCAGCCTGGGTGACA
35172	33259	TGCACTCCAGCCTGGGTGAC
35173	33260	CTGCACTCCAGCCTGGGTGA
35174	33261	ACTGCACTCCAGCCTGGGTG
35175	33262	CACTGCACTCCAGCCTGGGT
35176	33263	CCACTGCACTCCAGCCTGGG
35177	33264	GCCACTGCACTCCAGCCTGG
35178	33265	TGCCACTGCACTCCAGCCTG
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35181	33268	GCATGCCACTGCACTCCAGC
35182	33269	AGCATGCCACTGCACTCCAG
35183	33270	TAGCATGCCACTGCACTCCA
35184	33271	ATAGCATGCCACTGCACTCC
35185	33272	GATAGCATGCCACTGCACTC
35186	33273	AGATAGCATGCCACTGCACT
35187	33274	GAGATAGCATGCCACTGCAC
35188	33275	CGAGATAGCATGCCACTGCA
35189	33276	CCGAGATAGCATGCCACTGC
35190	33277	GCCGAGATAGCATGCCACTG
35191	33278	AGCCGAGATAGCATGCCACT
35192	33279	GAGCCGAGATAGCATGCCAC
35193	33280	TGAGCCGAGATAGCATGCCA
35194	33281	GTGAGCCGAGATAGCATGCC
35195	33282	GGTGAGCCGAGATAGCATGC
35196	33283	CGGTGAGCCGAGATAGCATG
35197	33284	GCGGTGAGCCGAGATAGCAT
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35200	33287	GTTGCGGTGAGCCGAGATAG
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35206	33293	GCGGAGGTTGCGGTGAGCCG
35207	33294	GGCGGAGGTTGCGGTGAGCC
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84288	82375	TTAAAATTCTGTTTATAAAC
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84315	82402	TCTCAGCCCCCTTCAGGTTT
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84328	82415	AGTATCATATATTTCTCAGC
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84335	82422	ACACTTAAGTATCATATATT
84336	82423	CACACTTAAGTATCATATAT
84337	82424	ACACACTTAAGTATCATATA
84338	82425	CACACACTTAAGTATCATAT
84339	82426	CCACACACTTAAGTATCATA
84340	82427	TCCACACACTTAAGTATCAT
84341	82428	TTCCACACACTTAAGTATCA
84342	82429	GTTCCACACACTTAAGTATC
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84345	82432	AGGGTTCCACACACTTAAGT
84346	82433	TAGGGTTCCACACACTTAAG
84347	82434	ATAGGGTTCCACACACTTAA
84348	82435	CATAGGGTTCCACACACTTA
84349	82436	CCATAGGGTTCCACACACTT
84350	82437	TCCATAGGGTTCCACACACT
84351	82438	CTCCATAGGGTTCCACACAC
84352	82439	TCTCCATAGGGTTCCACACA
84353	82440	CTCTCCATAGGGTTCCACAC
84354	82441	CCTCTCCATAGGGTTCCACA
84355	82442	TCCTCTCCATAGGGTTCCAC
84356	82443	CTCCTCTCCATAGGGTTCCA

133433	131520	GCCTTTAGCAAACAGGAAAA
133434	131521	AGCCTTTAGCAAACAGGAAA
133435	131522	AAGCCTTTAGCAAACAGGAA
133436	131523	TAAGCCTTTAGCAAACAGGA
133437	131524	CTAAGCCTTTAGCAAACAGG
133438	131525	CCTAAGCCTTTAGCAAACAG
133439	131526	ACCTAAGCCTTTAGCAAACA
133440	131527	AACCTAAGCCTTTAGCAAAC
133441	131528	TAACCTAAGCCTTTAGCAAA
133442	131529	TTAACCTAAGCCTTTAGCAA
133443	131530	TTTAACCTAAGCCTTTAGCA
133444	131531	TTTTAACCTAAGCCTTTAGC
133445	131532	CTTTTAACCTAAGCCTTTAG
133446	131533	ACTTTTAACCTAAGCCTTTA
133447	131534	AACTTTTAACCTAAGCCTTT
133448	131535	GAACTTTTAACCTAAGCCTT
133449	131536	TGAACTTTTAACCTAAGCCT
133450	131537	ATGAACTTTTAACCTAAGCC
133451	131538	AATGAACTTTTAACCTAAGC
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133453	131540	ATAATGAACTTTTAACCTAA
133454	131541	CATAATGAACTTTTAACCTA
133455	131542	TCATAATGAACTTTTAACCT
133456	131543	ATCATAATGAACTTTTAACC
133457	131544	AATCATAATGAACTTTTAAC
133458	131545	CAATCATAATGAACTTTTAA
133459	131546	ACAATCATAATGAACTTTTA
133460	131547	AACAATCATAATGAACTTTT
133461	131548	AAACAATCATAATGAACTTT
133462	131549	TAAACAATCATAATGAACTT
133463	131550	ATAAACAATCATAATGAACT
133464	131551	TATAAACAATCATAATGAAC
133465	131552	GTATAAACAATCATAATGAA
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133467	131554	ATGTATAAACAATCATAATG
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133469	131556	AAATGTATAAACAATCATAA
133470	131557	GAAATGTATAAACAATCATA
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133476	131563	TCACCAGAAATGTATAAACA
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133480	131567	GTATTCACCAGAAATGTATA
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133482	131569	ATGTATTCACCAGAAATGTA
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133485	131572	ATGATGTATTCACCAGAAAT
133486	131573	CATGATGTATTCACCAGAAA
133487	131574	TCATGATGTATTCACCAGAA
133488	131575	ATCATGATGTATTCACCAGA
133489	131576	AATCATGATGTATTCACCAG
133490	131577	AAATCATGATGTATTCACCA
133491	131578	TAAATCATGATGTATTCACC
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133493	131580	GTTAAATCATGATGTATTCA
133494	131581	TGTTAAATCATGATGTATTC
133495	131582	TTGTTAAATCATGATGTATT
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133498	131585	CACTTGTTAAATCATGATGT
133499	131586	CCACTTGTTAAATCATGATG
133500	131587	TCCACTTGTTAAATCATGAT
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35210	33297	GGAGGCGGAGGTTGCGGTGA
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35212	33299	CGGGAGGCGGAGGTTGCGGT
35213	33300	CCGGGAGGCGGAGGTTGCGG
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35219	33306	TTGAACCCGGGAGGCGGAGG
35220	33307	CTTGAACCCGGGAGGCGGAG
35221	33308	GCTTGAACCCGGGAGGCGGA
35222	33309	TGCTTGAACCCGGGAGGCGG
35223	33310	TTGCTTGAACCCGGGAGGCG
35224	33311	ATTGCTTGAACCCGGGAGGC
35225	33312	AATTGCTTGAACCCGGGAGG
35226	33313	GAATTGCTTGAACCCGGGAG
35227	33314	AGAATTGCTTGAACCCGGGA
35228	33315	GAGAATTGCTTGAACCCGGG
35229	33316	GGAGAATTGCTTGAACCCGG
35230	33317	AGGAGAATTGCTTGAACCCG
35231	33318	CAGGAGAATTGCTTGAACCC
35232	33319	GCAGGAGAATTGCTTGAACC
35233	33320	GGCAGGAGAATTGCTTGAAC
35234	33321	AGGCAGGAGAATTGCTTGAA
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35236	33323	TGAGGCAGGAGAATTGCTTG
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35239	33326	GGCTGAGGCAGGAGAATTGC
35240	33327	AGGCTGAGGCAGGAGAATTG
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35244	33331	CAGGAGGCTGAGGCAGGAGA
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35253	33340	CCAGCTACTCAGGAGGCTGA
35254	33341	CCCAGCTACTCAGGAGGCTG
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35262	33349	CCTGTAATCCCAGCTACTCA
35263	33350	GCCTGTAATCCCAGCTACTC
35264	33351	TGCCTGTAATCCCAGCTACT
35265	33352	ATGCCTGTAATCCCAGCTAC
35266	33353	CATGCCTGTAATCCCAGCTA
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35268	33355	TGCATGCCTGTAATCCCAGC
35269	33356	GTGCATGCCTGTAATCCCAG
35270	33357	GGTGCATGCCTGTAATCCCA
35271	33358	TGGTGCATGCCTGTAATCCC
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35273	33360	GGTGGTGCATGCCTGTAATC
35274	33361	TGGTGGTGCATGCCTGTAAT
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35276	33363	CATGGTGGTGCATGCCTGTA
35277	33364	GCATGGTGGTGCATGCCTGT
35278	33365	GGCATGGTGGTGCATGCCTG
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35280	33367	TGGGCATGGTGGTGCATGCC

84357	82444	TCTCCTCTCCATAGGGTTCC
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84363	82450	TCCAGGTCTCCTCTCCATAG
84364	82451	GTCCAGGTCTCCTCTCCATA
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84366	82453	CAGTCCAGGTCTCCTCTCCA
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84377	82464	ATCTTATCAAACAGTCCAGG
84378	82465	AATCTTATCAAACAGTCCAG
84379	82466	TAATCTTATCAAACAGTCCA
84380	82467	TTAATCTTATCAAACAGTCC
84381	82468	CTTAATCTTATCAAACAGTC
84382	82469	CCTTAATCTTATCAAACAGT
84383	82470	ACCTTAATCTTATCAAACAG
84384	82471	TACCTTAATCTTATCAAACA
84385	82472	TTACCTTAATCTTATCAAAC
84386	82473	CTTACCTTAATCTTATCAAA
84387	82474	ACTTACCTTAATCTTATCAA
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84390	82477	ATCACTTACCTTAATCTTAT
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84406	82493	GTATTTAACATTACATATCA
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84411	82498	AGCTAGTATTTAACATTACA
84412	82499	CAGCTAGTATTTAACATTAC
84413	82500	ACAGCTAGTATTTAACATTA
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84416	82503	GATACAGCTAGTATTTAACA
84417	82504	AGATACAGCTAGTATTTAAC
84418	82505	AAGATACAGCTAGTATTTAA
84419	82506	AAAGATACAGCTAGTATTTA
84420	82507	TAAAGATACAGCTAGTATTT
84421	82508	GTAAAGATACAGCTAGTATT
84422	82509	GGTAAAGATACAGCTAGTAT
84423	82510	AGGTAAAGATACAGCTAGTA
84424	82511	TAGGTAAAGATACAGCTAGT
84425	82512	CTAGGTAAAGATACAGCTAG
84426	82513	CCTAGGTAAAGATACAGCTA
84427	82514	GCCTAGGTAAAGATACAGCT

133504	131591	TCTTTCCACTTGTTAAATCA
133505	131592	TTCTTTCCACTTGTTAAATC
133506	131593	GTTCTTTCCACTTGTTAAAT
133507	131594	TGTTCTTTCCACTTGTTAAA
133508	131595	ATGTTCTTTCCACTTGTTAA
133509	131596	GATGTTCTTTCCACTTGTTA
133510	131597	AGATGTTCTTTCCACTTGTT
133511	131598	GAGATGTTCTTTCCACTTGT
133512	131599	AGAGATGTTCTTTCCACTTG
133513	131600	AAGAGATGTTCTTTCCACTT
133514	131601	AAAGAGATGTTCTTTCCACT
133515	131602	GAAAGAGATGTTCTTTCCAC
133516	131603	GGAAAGAGATGTTCTTTCCA
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133518	131605	AAGGAAAGAGATGTTCTTTC
133519	131606	GAAGGAAAGAGATGTTCTTT
133520	131607	GGAAGGAAAGAGATGTTCTT
133521	131608	TGGAAGGAAAGAGATGTTCT
133522	131609	ATGGAAGGAAAGAGATGTTC
133523	131610	AATGGAAGGAAAGAGATGTT
133524	131611	AAATGGAAGGAAAGAGATGT
133525	131612	AAAATGGAAGGAAAGAGATG
133526	131613	GAAAATGGAAGGAAAGAGAT
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133533	131620	TATGCCAGAAAATGGAAGGA
133534	131621	GTATGCCAGAAAATGGAAGG
133535	131622	AGTATGCCAGAAAATGGAAG
133536	131623	GAGTATGCCAGAAAATGGAA
133537	131624	GGAGTATGCCAGAAAATGGA
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133539	131626	GGGGAGTATGCCAGAAAATG
133540	131627	AGGGGAGTATGCCAGAAAAT
133541	131628	AAGGGGAGTATGCCAGAAAA
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133544	131631	TCCAAGGGGAGTATGCCAGA
133545	131632	TTCCAAGGGGAGTATGCCAG
133546	131633	ATTCCAAGGGGAGTATGCCA
133547	131634	GATTCCAAGGGGAGTATGCC
133548	131635	TGATTCCAAGGGGAGTATGC
133549	131636	CTGATTCCAAGGGGAGTATG
133550	131637	TCTGATTCCAAGGGGAGTAT
133551	131638	ATCTGATTCCAAGGGGAGTA
133552	131639	GATCTGATTCCAAGGGGAGT
133553	131640	AGATCTGATTCCAAGGGGAG
133554	131641	CAGATCTGATTCCAAGGGGA
133555	131642	TCAGATCTGATTCCAAGGGG
133556	131643	TTCAGATCTGATTCCAAGGG
133557	131644	TTTCAGATCTGATTCCAAGG
133558	131645	GTTTCAGATCTGATTCCAAG
133559	131646	AGTTTCAGATCTGATTCCAA
133560	131647	AAGTTTCAGATCTGATTCCA
133561	131648	AAAGTTTCAGATCTGATTCC
133562	131649	AAAAGTTTCAGATCTGATTC
133563	131650	TAAAAGTTTCAGATCTGATT
133564	131651	TTAAAAGTTTCAGATCTGAT
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133570	131657	TTTAGCTTAAAAGTTTCAGA
133571	131658	TTTTAGCTTAAAAGTTTCAG
133572	131659	ATTTTAGCTTAAAAGTTTCA
133573	131660	AATTTTAGCTTAAAAGTTTC
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35281	33368	GTGGGCATGGTGGTGCATGC
35282	33369	GGTGGGCATGGTGGTGCATG
35283	33370	AGGTGGGCATGGTGGTGCAT
35284	33371	TAGGTGGGCATGGTGGTGCA
35285	33372	TTAGGTGGGCATGGTGGTGC
35286	33373	ATTAGGTGGGCATGGTGGTG
35287	33374	AATTAGGTGGGCATGGTGGT
35288	33375	AAATTAGGTGGGCATGGTGG
35289	33376	AAAATTAGGTGGGCATGGTG
35290	33377	CAAAATTAGGTGGGCATGGT
35291	33378	ACAAAATTAGGTGGGCATGG
35292	33379	TACAAAATTAGGTGGGCATG
35293	33380	ATACAAAATTAGGTGGGCAT
35294	33381	AATACAAAATTAGGTGGGCA
35295	33382	AAATACAAAATTAGGTGGGC
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35297	33384	AAAAATACAAAATTAGGTGG
35298	33385	TAAAAATACAAAATTAGGTG
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35301	33388	TACTAAAAATACAAAATTAG
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35303	33390	TCTACTAAAAATACAAAATT
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35308	33395	CCGCCTCTACTAAAAATACA
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35314	33401	GAAACCCCGCCTCTACTAAA
35315	33402	AGAAACCCCGCCTCTACTAA
35316	33403	GAGAAACCCCGCCTCTACTA
35317	33404	GGAGAAACCCCGCCTCTACT
35318	33405	TGGAGAAACCCCGCCTCTAC
35319	33406	ATGGAGAAACCCCGCCTCTA
35320	33407	CATGGAGAAACCCCGCCTCT
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35322	33409	AACATGGAGAAACCCCGCCT
35323	33410	CAACATGGAGAAACCCCGCC
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35327	33414	TGACCAACATGGAGAAACCC
35328	33415	CTGACCAACATGGAGAAACC
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35334	33421	ACCAGCCTGACCAACATGGA
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35336	33423	AGACCAGCCTGACCAACATG
35337	33424	AAGACCAGCCTGACCAACAT
35338	33425	CAAGACCAGCCTGACCAACA
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35340	33427	TTCAAGACCAGCCTGACCAA
35341	33428	GTTCAAGACCAGCCTGACCA
35342	33429	AGTTCAAGACCAGCCTGACC
35343	33430	GAGTTCAAGACCAGCCTGAC
35344	33431	GGAGTTCAAGACCAGCCTGA
35345	33432	GGGAGTTCAAGACCAGCCTG
35346	33433	CGGGAGTTCAAGACCAGCCT
35347	33434	TCGGGAGTTCAAGACCAGCC
35348	33435	ATCGGGAGTTCAAGACCAGC
35349	33436	GATCGGGAGTTCAAGACCAG
35350	33437	AGATCGGGAGTTCAAGACCA
35351	33438	GAGATCGGGAGTTCAAGACC

84428	82515	TGCCTAGGTAAAGATACAGC
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84430	82517	TATGCCTAGGTAAAGATACA
84431	82518	ATATGCCTAGGTAAAGATAC
84432	82519	GATATGCCTAGGTAAAGATA
84433	82520	GGATATGCCTAGGTAAAGAT
84434	82521	TGGATATGCCTAGGTAAAGA
84435	82522	ATGGATATGCCTAGGTAAAG
84436	82523	GATGGATATGCCTAGGTAAA
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84438	82525	CTGATGGATATGCCTAGGTA
84439	82526	ACTGATGGATATGCCTAGGT
84440	82527	TACTGATGGATATGCCTAGG
84441	82528	ATACTGATGGATATGCCTAG
84442	82529	TATACTGATGGATATGCCTA
84443	82530	TTATACTGATGGATATGCCT
84444	82531	TTTATACTGATGGATATGCC
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84446	82533	AATTTATACTGATGGATATG
84447	82534	AAATTTATACTGATGGATAT
84448	82535	TAAATTTATACTGATGGATA
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84453	82540	CCAAATAAATTTATACTGAT
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84463	82550	GCAGTCATCACCAAATAAAT
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84473	82560	CAACTACAAAGCAGTCATCA
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84476	82563	CTGCAACTACAAAGCAGTCA
84477	82564	ACTGCAACTACAAAGCAGTC
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84480	82567	AATACTGCAACTACAAAGCA
84481	82568	AAATACTGCAACTACAAAGC
84482	82569	TAAATACTGCAACTACAAAG
84483	82570	ATAAATACTGCAACTACAAA
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84485	82572	TAATAAATACTGCAACTACA
84486	82573	TTAATAAATACTGCAACTAC
84487	82574	CTTAATAAATACTGCAACTA
84488	82575	GCTTAATAAATACTGCAACT
84489	82576	TGCTTAATAAATACTGCAAC
84490	82577	CTGCTTAATAAATACTGCAA
84491	82578	ACTGCTTAATAAATACTGCA
84492	82579	GACTGCTTAATAAATACTGC
84493	82580	CGACTGCTTAATAAATACTG
84494	82581	GCGACTGCTTAATAAATACT
84495	82582	AGCGACTGCTTAATAAATAC
84496	82583	AAGCGACTGCTTAATAAATA
84497	82584	TAAGCGACTGCTTAATAAAT
84498	82585	CTAAGCGACTGCTTAATAAA

133575	131662	GAAATTTTAGCTTAAAAGTT
133576	131663	GGAAATTTTAGCTTAAAAGT
133577	131664	TGGAAATTTTAGCTTAAAAG
133578	131665	ATGGAAATTTTAGCTTAAAA
133579	131666	AATGGAAATTTTAGCTTAAA
133580	131667	CAATGGAAATTTTAGCTTAA
133581	131668	GCAATGGAAATTTTAGCTTA
133582	131669	TGCAATGGAAATTTTAGCTT
133583	131670	ATGCAATGGAAATTTTAGCT
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133585	131672	AAATGCAATGGAAATTTTAG
133586	131673	CAAATGCAATGGAAATTTTA
133587	131674	CCAAATGCAATGGAAATTTT
133588	131675	TCCAAATGCAATGGAAATTT
133589	131676	CTCCAAATGCAATGGAAATT
133590	131677	TCTCCAAATGCAATGGAAAT
133591	131678	CTCTCCAAATGCAATGGAAA
133592	131679	ACTCTCCAAATGCAATGGAA
133593	131680	TACTCTCCAAATGCAATGGA
133594	131681	CTACTCTCCAAATGCAATGG
133595	131682	ACTACTCTCCAAATGCAATG
133596	131683	AACTACTCTCCAAATGCAAT
133597	131684	TAACTACTCTCCAAATGCAA
133598	131685	ATAACTACTCTCCAAATGCA
133599	131686	AATAACTACTCTCCAAATGC
133600	131687	AAATAACTACTCTCCAAATG
133601	131688	CAAATAACTACTCTCCAAAT
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133603	131690	CACAAATAACTACTCTCCAA
133604	131691	ACACAAATAACTACTCTCCA
133605	131692	TACACAAATAACTACTCTCC
133606	131693	ATACACAAATAACTACTCTC
133607	131694	CATACACAAATAACTACTCT
133608	131695	GCATACACAAATAACTACTC
133609	131696	TGCATACACAAATAACTACT
133610	131697	ATGCATACACAAATAACTAC
133611	131698	CATGCATACACAAATAACTA
133612	131699	GCATGCATACACAAATAACT
133613	131700	AGCATGCATACACAAATAAC
133614	131701	AAGCATGCATACACAAATAA
133615	131702	AAAGCATGCATACACAAATA
133616	131703	AAAAGCATGCATACACAAAT
133617	131704	CAAAAGCATGCATACACAAA
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133619	131706	CTCAAAAGCATGCATACACA
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133621	131708	GTCTCAAAAGCATGCATACA
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133625	131712	CAATGTCTCAAAAGCATGCA
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133633	131720	TATTGCTACAATGTCTCAAA
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133638	131725	AGTATTATTGCTACAATGTC
133639	131726	CAGTATTATTGCTACAATGT
133640	131727	ACAGTATTATTGCTACAATG
133641	131728	TACAGTATTATTGCTACAAT
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35352	33439	TGAGATCGGGAGTTCAAGAC
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35356	33443	CACCTGAGATCGGGAGTTCA
35357	33444	TCACCTGAGATCGGGAGTTC
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35359	33446	GATCACCTGAGATCGGGAGT
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35362	33449	GCAGATCACCTGAGATCGGG
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35366	33453	GCAGGCAGATCACCTGAGAT
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35369	33456	GAGGCAGGCAGATCACCTGA
35370	33457	CGAGGCAGGCAGATCACCTG
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35372	33459	GCCGAGGCAGGCAGATCACC
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35374	33461	AGGCCGAGGCAGGCAGATCA
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35387	33474	TCAACACTTCGGAAGGCCGA
35388	33475	CTCAACACTTCGGAAGGCCG
35389	33476	TCTCAACACTTCGGAAGGCC
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35393	33480	GTAATCTCAACACTTCGGAA
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35400	33487	CACGCCTGTAATCTCAACAC
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35410	33497	CGCGGTGGCTCACGCCTGTA
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35420	33507	TACGGCCGGGCGCGGTGGCT
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84499	82586	TCTAAGCGACTGCTTAATAA
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84506	82593	ACACTTATCTAAGCGACTGC
84507	82594	AACACTTATCTAAGCGACTG
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84518	82605	TTATACAGTTAAACACTTAT
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84527	82614	CTAAATAATTTATACAGTTA
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84536	82623	GGAGACCTTCTAAATAATTT
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84542	82629	AAAAAGGGAGACCTTCTAAA
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84544	82631	AGAAAAAGGGAGACCTTCTA
84545	82632	TAGAAAAAGGGAGACCTTCT
84546	82633	CTAGAAAAAGGGAGACCTTC
84547	82634	ACTAGAAAAAGGGAGACCTT
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84549	82636	AAACTAGAAAAAGGGAGACC
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84556	82643	CCTCATTAAACTAGAAAAAG
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133646	131733	AACATTACAGTATTATTGCT
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133657	131744	AGATTCGGCTCAACATTACA
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133659	131746	AAAGATTCGGCTCAACATTA
133660	131747	GAAAGATTCGGCTCAACATT
133661	131748	AGAAAGATTCGGCTCAACAT
133662	131749	GAGAAAGATTCGGCTCAACA
133663	131750	GGAGAAAGATTCGGCTCAAC
133664	131751	AGGAGAAAGATTCGGCTCAA
133665	131752	GAGGAGAAAGATTCGGCTCA
133666	131753	TGAGGAGAAAGATTCGGCTC
133667	131754	ATGAGGAGAAAGATTCGGCT
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133669	131756	CAATGAGGAGAAAGATTCGG
133670	131757	ACAATGAGGAGAAAGATTCG
133671	131758	CACAATGAGGAGAAAGATTC
133672	131759	ACACAATGAGGAGAAAGATT
133673	131760	AACACAATGAGGAGAAAGAT
133674	131761	GAACACAATGAGGAGAAAGA
133675	131762	TGAACACAATGAGGAGAAAG
133676	131763	ATGAACACAATGAGGAGAAA
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133678	131765	GAATGAACACAATGAGGAGA
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133680	131767	GTGAATGAACACAATGAGGA
133681	131768	AGTGAATGAACACAATGAGG
133682	131769	CAGTGAATGAACACAATGAG
133683	131770	GCAGTGAATGAACACAATGA
133684	131771	GGCAGTGAATGAACACAATG
133685	131772	TGGCAGTGAATGAACACAAT
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133687	131774	GTTGGCAGTGAATGAACACA
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133689	131776	ATGTTGGCAGTGAATGAACA
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133691	131778	AGATGTTGGCAGTGAATGAA
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133693	131780	CCAGATGTTGGCAGTGAATG
133694	131781	GCCAGATGTTGGCAGTGAAT
133695	131782	AGCCAGATGTTGGCAGTGAA
133696	131783	AAGCCAGATGTTGGCAGTGA
133697	131784	GAAGCCAGATGTTGGCAGTG
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133699	131786	ATGAAGCCAGATGTTGGCAG
133700	131787	GATGAAGCCAGATGTTGGCA
133701	131788	AGATGAAGCCAGATGTTGGC
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133708	131795	ATCCAAAAGATGAAGCCAGA
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133714	131801	ACATTCATCCAAAAGATGAA
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35423	33510	AAATACGGCCGGGCGCGGTG
35424	33511	GAAATACGGCCGGGCGCGGT
35425	33512	AGAAATACGGCCGGGCGCGG
35426	33513	AAGAAATACGGCCGGGCGCG
35427	33514	TAAGAAATACGGCCGGGCGC
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35439	33526	AGCCATTTTATTTAAGAAAT
35440	33527	AAGCCATTTTATTTAAGAAA
35441	33528	TAAGCCATTTTATTTAAGAA
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35444	33531	GTTTAAGCCATTTTATTTAA
35445	33532	CGTTTAAGCCATTTTATTTA
35446	33533	ACGTTTAAGCCATTTTATTT
35447	33534	GACGTTTAAGCCATTTTATT
35448	33535	TGACGTTTAAGCCATTTTAT
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35456	33543	GATAATTTTGACGTTTAAGC
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35460	33547	AAGGGATAATTTTGACGTTT
35461	33548	CAAGGGATAATTTTGACGTT
35462	33549	TCAAGGGATAATTTTGACGT
35463	33550	ATCAAGGGATAATTTTGACG
35464	33551	GATCAAGGGATAATTTTGAC
35465	33552	GGATCAAGGGATAATTTTGA
35466	33553	GGGATCAAGGGATAATTTTG
35467	33554	AGGGATCAAGGGATAATTTT
35468	33555	CAGGGATCAAGGGATAATTT
35469	33556	CCAGGGATCAAGGGATAATT
35470	33557	CCCAGGGATCAAGGGATAAT
35471	33558	GCCCAGGGATCAAGGGATAA
35472	33559	AGCCCAGGGATCAAGGGATA
35473	33560	TAGCCCAGGGATCAAGGGAT
35474	33561	ATAGCCCAGGGATCAAGGGA
35475	33562	CATAGCCCAGGGATCAAGGG
35476	33563	CCATAGCCCAGGGATCAAGG
35477	33564	TCCATAGCCCAGGGATCAAG
35478	33565	GTCCATAGCCCAGGGATCAA
35479	33566	AGTCCATAGCCCAGGGATCA
35480	33567	CAGTCCATAGCCCAGGGATC
35481	33568	TCAGTCCATAGCCCAGGGAT
35482	33569	ATCAGTCCATAGCCCAGGGA
35483	33570	AATCAGTCCATAGCCCAGGG
35484	33571	GAATCAGTCCATAGCCCAGG
35485	33572	AGAATCAGTCCATAGCCCAG
35486	33573	AAGAATCAGTCCATAGCCCA
35487	33574	CAAGAATCAGTCCATAGCCC
35488	33575	ACAAGAATCAGTCCATAGCC
35489	33576	CACAAGAATCAGTCCATAGC
35490	33577	ACACAAGAATCAGTCCATAG
35491	33578	AACACAAGAATCAGTCCATA
35492	33579	TAACACAAGAATCAGTCCAT
35493	33580	CTAACACAAGAATCAGTCCA

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84573	82660	CAAAAAAAAAGTCTTGACCT
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84583	82670	ATTGCTATTTCAAAAAAAAA
84584	82671	CATTGCTATTTCAAAAAAAA
84585	82672	TCATTGCTATTTCAAAAAAA
84586	82673	TTCATTGCTATTTCAAAAAA
84587	82674	ATTCATTGCTATTTCAAAAA
84588	82675	TATTCATTGCTATTTCAAAA
84589	82676	ATATTCATTGCTATTTCAAA
84590	82677	AATATTCATTGCTATTTCAA
84591	82678	TAATATTCATTGCTATTTCA
84592	82679	ATAATATTCATTGCTATTTC
84593	82680	GATAATATTCATTGCTATTT
84594	82681	TGATAATATTCATTGCTATT
84595	82682	ATGATAATATTCATTGCTAT
84596	82683	AATGATAATATTCATTGCTA
84597	82684	AAATGATAATATTCATTGCT
84598	82685	CAAATGATAATATTCATTGC
84599	82686	TCAAATGATAATATTCATTG
84600	82687	ATCAAATGATAATATTCATT
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84606	82693	GTGAGTATCAAATGATAATA
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84608	82695	CTGTGAGTATCAAATGATAA
84609	82696	CCTGTGAGTATCAAATGATA
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84612	82699	ACTCCTGTGAGTATCAAATG
84613	82700	GACTCCTGTGAGTATCAAAT
84614	82701	TGACTCCTGTGAGTATCAAA
84615	82702	GTGACTCCTGTGAGTATCAA
84616	82703	TGTGACTCCTGTGAGTATCA
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84622	82709	AGAGTTTGTGACTCCTGTGA
84623	82710	TAGAGTTTGTGACTCCTGTG
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84630	82717	ACTCTTCTAGAGTTTGTGAC
84631	82718	TACTCTTCTAGAGTTTGTGA
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84633	82720	ATTACTCTTCTAGAGTTTGT
84634	82721	CATTACTCTTCTAGAGTTTG
84635	82722	ACATTACTCTTCTAGAGTTT
84636	82723	AACATTACTCTTCTAGAGTT
84637	82724	AAACATTACTCTTCTAGAGT
84638	82725	AAAACATTACTCTTCTAGAG
84639	82726	TAAAACATTACTCTTCTAGA
84640	82727	ATAAAACATTACTCTTCTAG

133717	131804	TGAACATTCATCCAAAAGAT
133718	131805	ATGAACATTCATCCAAAAGA
133719	131806	AATGAACATTCATCCAAAAG
133720	131807	CAATGAACATTCATCCAAAA
133721	131808	CCAATGAACATTCATCCAAA
133722	131809	ACCAATGAACATTCATCCAA
133723	131810	AACCAATGAACATTCATCCA
133724	131811	AAACCAATGAACATTCATCC
133725	131812	AAAACCAATGAACATTCATC
133726	131813	CAAAACCAATGAACATTCAT
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133728	131815	TTCAAAACCAATGAACATTC
133729	131816	TTTCAAAACCAATGAACATT
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133731	131818	TGTTTCAAAACCAATGAACA
133732	131819	CTGTTTCAAAACCAATGAAC
133733	131820	GCTGTTTCAAAACCAATGAA
133734	131821	GGCTGTTTCAAAACCAATGA
133735	131822	AGGCTGTTTCAAAACCAATG
133736	131823	TAGGCTGTTTCAAAACCAAT
133737	131824	ATAGGCTGTTTCAAAACCAA
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133739	131826	CTATAGGCTGTTTCAAAACC
133740	131827	CCTATAGGCTGTTTCAAAAC
133741	131828	CCCTATAGGCTGTTTCAAAA
133742	131829	ACCCTATAGGCTGTTTCAAA
133743	131830	TACCCTATAGGCTGTTTCAA
133744	131831	TTACCCTATAGGCTGTTTCA
133745	131832	TTTACCCTATAGGCTGTTTC
133746	131833	ATTTACCCTATAGGCTGTTT
133747	131834	TATTTACCCTATAGGCTGTT
133748	131835	GTATTTACCCTATAGGCTGT
133749	131836	AGTATTTACCCTATAGGCTG
133750	131837	CAGTATTTACCCTATAGGCT
133751	131838	ACAGTATTTACCCTATAGGC
133752	131839	CACAGTATTTACCCTATAGG
133753	131840	ACACAGTATTTACCCTATAG
133754	131841	AACACAGTATTTACCCTATA
133755	131842	AAACACAGTATTTACCCTAT
133756	131843	CAAACACAGTATTTACCCTA
133757	131844	TCAAACACAGTATTTACCCT
133758	131845	CTCAAACACAGTATTTACCC
133759	131846	CCTCAAACACAGTATTTACC
133760	131847	ACCTCAAACACAGTATTTAC
133761	131848	TACCTCAAACACAGTATTTA
133762	131849	GTACCTCAAACACAGTATTT
133763	131850	TGTACCTCAAACACAGTATT
133764	131851	CTGTACCTCAAACACAGTAT
133765	131852	TCTGTACCTCAAACACAGTA
133766	131853	ATCTGTACCTCAAACACAGT
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133769	131856	ATCATCTGTACCTCAAACAC
133770	131857	AATCATCTGTACCTCAAACA
133771	131858	AAATCATCTGTACCTCAAAC
133772	131859	AAAATCATCTGTACCTCAAA
133773	131860	GAAAATCATCTGTACCTCAA
133774	131861	TGAAAATCATCTGTACCTCA
133775	131862	ATGAAAATCATCTGTACCTC
133776	131863	TATGAAAATCATCTGTACCT
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133779	131866	AGTTATGAAAATCATCTGTA
133780	131867	TAGTTATGAAAATCATCTGT
133781	131868	GTAGTTATGAAAATCATCTG
133782	131869	AGTAGTTATGAAAATCATCT
133783	131870	AAGTAGTTATGAAAATCATC
133784	131871	GAAGTAGTTATGAAAATCAT
133785	131872	GGAAGTAGTTATGAAAATCA
133786	131873	AGGAAGTAGTTATGAAAATC
133787	131874	TAGGAAGTAGTTATGAAAAT

35494	33581	GCTAACACAAGAATCAGTCC
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35500	33587	ATAACTGCTAACACAAGAAT
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84661	82748	GCAAGTCCCATTTAAGTAGA
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84664	82751	TAAGCAAGTCCCATTTAAGT
84665	82752	TTAAGCAAGTCCCATTTAAG
84666	82753	ATTAAGCAAGTCCCATTTAA
84667	82754	TATTAAGCAAGTCCCATTTA
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84669	82756	CTTATTAAGCAAGTCCCATT
84670	82757	TCTTATTAAGCAAGTCCCAT
84671	82758	ATCTTATTAAGCAAGTCCCA
84672	82759	AATCTTATTAAGCAAGTCCC
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84698	82785	ACACTTGAACCCAGAACTCA
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133788	131875	CTAGGAAGTAGTTATGAAAA
133789	131876	TCTAGGAAGTAGTTATGAAA
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133793	131880	ATGTTCTAGGAAGTAGTTAT
133794	131881	CATGTTCTAGGAAGTAGTTA
133795	131882	ACATGTTCTAGGAAGTAGTT
133796	131883	GACATGTTCTAGGAAGTAGT
133797	131884	GGACATGTTCTAGGAAGTAG
133798	131885	TGGACATGTTCTAGGAAGTA
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133800	131887	AATGGACATGTTCTAGGAAG
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133805	131892	CTTCAAATGGACATGTTCTA
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133808	131895	GCTCTTCAAATGGACATGTT
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133811	131898	ACTGCTCTTCAAATGGACAT
133812	131899	CACTGCTCTTCAAATGGACA
133813	131900	CCACTGCTCTTCAAATGGAC
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133816	131903	GCCCCACTGCTCTTCAAATG
133817	131904	GGCCCCACTGCTCTTCAAAT
133818	131905	AGGCCCCACTGCTCTTCAAA
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133820	131907	TAAGGCCCCACTGCTCTTCA
133821	131908	CTAAGGCCCCACTGCTCTTC
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133823	131910	GTCTAAGGCCCCACTGCTCT
133824	131911	GGTCTAAGGCCCCACTGCTC
133825	131912	GGGTCTAAGGCCCCACTGCT
133826	131913	GGGGTCTAAGGCCCCACTGC
133827	131914	TGGGGTCTAAGGCCCCACTG
133828	131915	TTGGGGTCTAAGGCCCCACT
133829	131916	TTTGGGGTCTAAGGCCCCAC
133830	131917	CTTTGGGGTCTAAGGCCCCA
133831	131918	ACTTTGGGGTCTAAGGCCCC
133832	131919	GACTTTGGGGTCTAAGGCCC
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133834	131921	TGGACTTTGGGGTCTAAGGC
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133840	131927	CATAAATGGACTTTGGGGTC
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133847	131934	GCCCACACATAAATGGACTT
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133852	131939	TATTTGCCCACACATAAATG
133853	131940	CTATTTGCCCACACATAAAT
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35565	33652	AAAAAAAAATTACTTCTCAT
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35567	33654	AAAAAAAAAATTACTTCTC
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35574	33661	TCAAAAAAAAAAAAAAATT
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35576	33663	TCTCAAAAAAAAAAAAAAA
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35593	33680	AACAGAGTGAGATTCTGTCT
35594	33681	AAACAGAGTGAGATTCTGTC
35595	33682	GAAACAGAGTGAGATTCTGT
35596	33683	GGAAACAGAGTGAGATTCTG
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35619	33706	TCATGCCACTGCACTCCACG
35620	33707	ATCATGCCACTGCACTCCAC
35621	33708	GATCATGCCACTGCACTCCA
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35625	33712	CTGAGATCATGCCACTGCAC
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35628	33715	GAGCTGAGATCATGCCACTG
35629	33716	TGAGCTGAGATCATGCCACT
35630	33717	CTGAGCTGAGATCATGCCAC
35631	33718	ACTGAGCTGAGATCATGCCA
35632	33719	CACTGAGCTGAGATCATGCC
35633	33720	GCACTGAGCTGAGATCATGC
35634	33721	TGCACTGAGCTGAGATCATG
35635	33722	ATGCACTGAGCTGAGATCAT

84712	82799	TTTTCATCAGGTTTACACTT
84713	82800	ATTTTCATCAGGTTTACACT
84714	82801	GATTTTCATCAGGTTTACAC
84715	82802	TGATTTTCATCAGGTTTACA
84716	82803	ATGATTTTCATCAGGTTTAC
84717	82804	TATGATTTTCATCAGGTTTA
84718	82805	CTATGATTTTCATCAGGTTT
84719	82806	TCTATGATTTTCATCAGGTT
84720	82807	ATCTATGATTTTCATCAGGT
84721	82808	TATCTATGATTTTCATCAGG
84722	82809	TTATCTATGATTTTCATCAG
84723	82810	ATTATCTATGATTTTCATCA
84724	82811	AATTATCTATGATTTTCATC
84725	82812	CAATTATCTATGATTTTCAT
84726	82813	ACAATTATCTATGATTTTCA
84727	82814	TACAATTATCTATGATTTTC
84728	82815	TTACAATTATCTATGATTTT
84729	82816	CTTACAATTATCTATGATTT
84730	82817	CCTTACAATTATCTATGATT
84731	82818	TCCTTACAATTATCTATGAT
84732	82819	TTCCTTACAATTATCTATGA
84733	82820	GTTCCTTACAATTATCTATG
84734	82821	GGTTCCTTACAATTATCTAT
84735	82822	TGGTTCCTTACAATTATCTA
84736	82823	CTGGTTCCTTACAATTATCT
84737	82824	GCTGGTTCCTTACAATTATC
84738	82825	TGCTGGTTCCTTACAATTAT
84739	82826	ATGCTGGTTCCTTACAATTA
84740	82827	AATGCTGGTTCCTTACAATT
84741	82828	AAATGCTGGTTCCTTACAAT
84742	82829	GAAATGCTGGTTCCTTACAA
84743	82830	AGAAATGCTGGTTCCTTACA
84744	82831	TAGAAATGCTGGTTCCTTAC
84745	82832	TTAGAAATGCTGGTTCCTTA
84746	82833	ATTAGAAATGCTGGTTCCTT
84747	82834	AATTAGAAATGCTGGTTCCT
84748	82835	CAATTAGAAATGCTGGTTCC
84749	82836	CCAATTAGAAATGCTGGTTC
84750	82837	TCCAATTAGAAATGCTGGTT
84751	82838	ATCCAATTAGAAATGCTGGT
84752	82839	TATCCAATTAGAAATGCTGG
84753	82840	ATATCCAATTAGAAATGCTG
84754	82841	TATATCCAATTAGAAATGCT
84755	82842	TTATATCCAATTAGAAATGC
84756	82843	ATTATATCCAATTAGAAATG
84757	82844	TATTATATCCAATTAGAAAT
84758	82845	CTATTATATCCAATTAGAAA
84759	82846	GCTATTATATCCAATTAGAA
84760	82847	AGCTATTATATCCAATTAGA
84761	82848	TAGCTATTATATCCAATTAG
84762	82849	GTAGCTATTATATCCAATTA
84763	82850	AGTAGCTATTATATCCAATT
84764	82851	CAGTAGCTATTATATCCAAT
84765	82852	GCAGTAGCTATTATATCCAA
84766	82853	AGCAGTAGCTATTATATCCA
84767	82854	AAGCAGTAGCTATTATATCC
84768	82855	TAAGCAGTAGCTATTATATC
84769	82856	ATAAGCAGTAGCTATTATAT
84770	82857	AATAAGCAGTAGCTATTATA
84771	82858	AAATAAGCAGTAGCTATTAT
84772	82859	AAAATAAGCAGTAGCTATTA
84773	82860	GAAAATAAGCAGTAGCTATT
84774	82861	CGAAAATAAGCAGTAGCTAT
84775	82862	ACGAAAATAAGCAGTAGCTA
84776	82863	AACGAAAATAAGCAGTAGCT
84777	82864	TAACGAAAATAAGCAGTAGC
84778	82865	ATAACGAAAATAAGCAGTAG
84779	82866	CATAACGAAAATAAGCAGTA
84780	82867	GCATAACGAAAATAAGCAGT
84781	82868	GGCATAACGAAAATAAGCAG
84782	82869	AGGCATAACGAAAATAAGCA

133859	131946	CATTTCCTATTTGCCCACAC
133860	131947	ACATTTCCTATTTGCCCACA
133861	131948	AACATTTCCTATTTGCCCAC
133862	131949	CAACATTTCCTATTTGCCCA
133863	131950	GCAACATTTCCTATTTGCCC
133864	131951	TGCAACATTTCCTATTTGCC
133865	131952	TTGCAACATTTCCTATTTGC
133866	131953	TTTGCAACATTTCCTATTTG
133867	131954	GTTTGCAACATTTCCTATTT
133868	131955	TGTTTGCAACATTTCCTATT
133869	131956	TTGTTTGCAACATTTCCTAT
133870	131957	TTTGTTTGCAACATTTCCTA
133871	131958	TTTTGTTTGCAACATTTCCT
133872	131959	GTTTTGTTTGCAACATTTCC
133873	131960	TGTTTTGTTTGCAACATTTC
133874	131961	TTGTTTTGTTTGCAACATTT
133875	131962	TTTGTTTTGTTTGCAACATT
133876	131963	CTTTGTTTTGTTTGCAACAT
133877	131964	GCTTTGTTTTGTTTGCAACA
133878	131965	TGCTTTGTTTTGTTTGCAAC
133879	131966	GTGCTTTGTTTTGTTTGCAA
133880	131967	AGTGCTTTGTTTTGTTTGCA
133881	131968	TAGTGCTTTGTTTTGTTTGC
133882	131969	CTAGTGCTTTGTTTTGTTTG
133883	131970	TCTAGTGCTTTGTTTTGTTT
133884	131971	ATCTAGTGCTTTGTTTTGTT
133885	131972	GATCTAGTGCTTTGTTTTGT
133886	131973	AGATCTAGTGCTTTGTTTTG
133887	131974	TAGATCTAGTGCTTTGTTTT
133888	131975	TTAGATCTAGTGCTTTGTTT
133889	131976	ATTAGATCTAGTGCTTTGTT
133890	131977	CATTAGATCTAGTGCTTTGT
133891	131978	ACATTAGATCTAGTGCTTTG
133892	131979	GACATTAGATCTAGTGCTTT
133893	131980	GGACATTAGATCTAGTGCTT
133894	131981	TGGACATTAGATCTAGTGCT
133895	131982	CTGGACATTAGATCTAGTGC
133896	131983	ACTGGACATTAGATCTAGTG
133897	131984	CACTGGACATTAGATCTAGT
133898	131985	TCACTGGACATTAGATCTAG
133899	131986	TTCACTGGACATTAGATCTA
133900	131987	TTTCACTGGACATTAGATCT
133901	131988	ATTTCACTGGACATTAGATC
133902	131989	GATTTCACTGGACATTAGAT
133903	131990	AGATTTCACTGGACATTAGA
133904	131991	CAGATTTCACTGGACATTAG
133905	131992	CCAGATTTCACTGGACATTA
133906	131993	TCCAGATTTCACTGGACATT
133907	131994	TTCCAGATTTCACTGGACAT
133908	131995	ATTCCAGATTTCACTGGACA
133909	131996	CATTCCAGATTTCACTGGAC
133910	131997	TCATTCCAGATTTCACTGGA
133911	131998	TTCATTCCAGATTTCACTGG
133912	131999	GTTCATTCCAGATTTCACTG
133913	132000	AGTTCATTCCAGATTTCACT
133914	132001	TAGTTCATTCCAGATTTCAC
133915	132002	CTAGTTCATTCCAGATTTCA
133916	132003	ACTAGTTCATTCCAGATTTC
133917	132004	GACTAGTTCATTCCAGATTT
133918	132005	TGACTAGTTCATTCCAGATT
133919	132006	ATGACTAGTTCATTCCAGAT
133920	132007	AATGACTAGTTCATTCCAGA
133921	132008	TAATGACTAGTTCATTCCAG
133922	132009	CTAATGACTAGTTCATTCCA
133923	132010	TCTAATGACTAGTTCATTCC
133924	132011	CTCTAATGACTAGTTCATTC
133925	132012	GCTCTAATGACTAGTTCATT
133926	132013	GGCTCTAATGACTAGTTCAT
133927	132014	CGGCTCTAATGACTAGTTCA
133928	132015	CCGGCTCTAATGACTAGTTC
133929	132016	ACCGGCTCTAATGACTAGTT

35636	33723	GATGCACTGAGCTGAGATCA
35637	33724	GGATGCACTGAGCTGAGATC
35638	33725	AGGATGCACTGAGCTGAGAT
35639	33726	TAGGATGCACTGAGCTGAGA
35640	33727	GTAGGATGCACTGAGCTGAG
35641	33728	TGTAGGATGCACTGAGCTGA
35642	33729	TTGTAGGATGCACTGAGCTG
35643	33730	GTTGTAGGATGCACTGAGCT
35644	33731	AGTTGTAGGATGCACTGAGC
35645	33732	GAGTTGTAGGATGCACTGAG
35646	33733	AGAGTTGTAGGATGCACTGA
35647	33734	CAGAGTTGTAGGATGCACTG
35648	33735	TCAGAGTTGTAGGATGCACT
35649	33736	CTCAGAGTTGTAGGATGCAC
35650	33737	CCTCAGAGTTGTAGGATGCA
35651	33738	ACCTCAGAGTTGTAGGATGC
35652	33739	AACCTCAGAGTTGTAGGATG
35653	33740	GAACCTCAGAGTTGTAGGAT
35654	33741	TGAACCTCAGAGTTGTAGGA
35655	33742	TTGAACCTCAGAGTTGTAGG
35656	33743	CTTGAACCTCAGAGTTGTAG
35657	33744	GCTTGAACCTCAGAGTTGTA
35658	33745	TGCTTGAACCTCAGAGTTGT
35659	33746	TTGCTTGAACCTCAGAGTTG
35660	33747	ATTGCTTGAACCTCAGAGTT
35661	33748	AATTGCTTGAACCTCAGAGT
35662	33749	GAATTGCTTGAACCTCAGAG
35663	33750	AGAATTGCTTGAACCTCAGA
35664	33751	GAGAATTGCTTGAACCTCAG
35665	33752	CGAGAATTGCTTGAACCTCA
35666	33753	ACGAGAATTGCTTGAACCTC
35667	33754	CACGAGAATTGCTTGAACCT
35668	33755	GCACGAGAATTGCTTGAACC
35669	33756	GGCACGAGAATTGCTTGAAC
35670	33757	AGGCACGAGAATTGCTTGAA
35671	33758	GAGGCACGAGAATTGCTTGA
35672	33759	TGAGGCACGAGAATTGCTTG
35673	33760	CTGAGGCACGAGAATTGCTT
35674	33761	GCTGAGGCACGAGAATTGCT
35675	33762	AGCTGAGGCACGAGAATTGC
35676	33763	AAGCTGAGGCACGAGAATTG
35677	33764	TAAGCTGAGGCACGAGAATT
35678	33765	GTAAGCTGAGGCACGAGAAT
35679	33766	AGTAAGCTGAGGCACGAGAA
35680	33767	CAGTAAGCTGAGGCACGAGA
35681	33768	TCAGTAAGCTGAGGCACGAG
35682	33769	CTCAGTAAGCTGAGGCACGA
35683	33770	ACTCAGTAAGCTGAGGCACG
35684	33771	TACTCAGTAAGCTGAGGCAC
35685	33772	CTACTCAGTAAGCTGAGGCA
35686	33773	GCTACTCAGTAAGCTGAGGC
35687	33774	AGCTACTCAGTAAGCTGAGG
35688	33775	CAGCTACTCAGTAAGCTGAG
35689	33776	CCAGCTACTCAGTAAGCTGA
35690	33777	CCCAGCTACTCAGTAAGCTG
35691	33778	TCCCAGCTACTCAGTAAGCT
35692	33779	ATCCCAGCTACTCAGTAAGC
35693	33780	AATCCCAGCTACTCAGTAAG
35694	33781	TAATCCCAGCTACTCAGTAA
35695	33782	GTAATCCCAGCTACTCAGTA
35696	33783	TGTAATCCCAGCTACTCAGT
35697	33784	CTGTAATCCCAGCTACTCAG
35698	33785	CCTGTAATCCCAGCTACTCA
35699	33786	GCCTGTAATCCCAGCTACTC
35700	33787	CGCCTGTAATCCCAGCTACT
35701	33788	GCGCCTGTAATCCCAGCTAC
35702	33789	GGCGCCTGTAATCCCAGCTA
35703	33790	GGGCGCCTGTAATCCCAGCT
35704	33791	TGGGCGCCTGTAATCCCAGC
35705	33792	GTGGGCGCCTGTAATCCCAG
35706	33793	GGTGGGCGCCTGTAATCCCA

84783	82870	GAGGCATAACGAAAATAAGC
84784	82871	TGAGGCATAACGAAAATAAG
84785	82872	CTGAGGCATAACGAAAATAA
84786	82873	TCTGAGGCATAACGAAAATA
84787	82874	CTCTGAGGCATAACGAAAAT
84788	82875	ACTCTGAGGCATAACGAAAA
84789	82876	AACTCTGAGGCATAACGAAA
84790	82877	TAACTCTGAGGCATAACGAA
84791	82878	TTAACTCTGAGGCATAACGA
84792	82879	TTTAACTCTGAGGCATAACG
84793	82880	TTTTAACTCTGAGGCATAAC
84794	82881	GTTTTAACTCTGAGGCATAA
84795	82882	AGTTTTAACTCTGAGGCATA
84796	82883	TAGTTTTAACTCTGAGGCAT
84797	82884	TTAGTTTTAACTCTGAGGCA
84798	82885	ATTAGTTTTAACTCTGAGGC
84799	82886	TATTAGTTTTAACTCTGAGG
84800	82887	GTATTAGTTTTAACTCTGAG
84801	82888	TGTATTAGTTTTAACTCTGA
84802	82889	CTGTATTAGTTTTAACTCTG
84803	82890	ACTGTATTAGTTTTAACTCT
84804	82891	TACTGTATTAGTTTTAACTC
84805	82892	TTACTGTATTAGTTTTAACT
84806	82893	TTTACTGTATTAGTTTTAAC
84807	82894	ATTTACTGTATTAGTTTTAA
84808	82895	TATTTACTGTATTAGTTTTA
84809	82896	TTATTTACTGTATTAGTTTT
84810	82897	ATTATTTACTGTATTAGTTT
84811	82898	GATTATTTACTGTATTAGTT
84812	82899	AGATTATTTACTGTATTAGT
84813	82900	AAGATTATTTACTGTATTAG
84814	82901	TAAGATTATTTACTGTATTA
84815	82902	GTAAGATTATTTACTGTATT
84816	82903	AGTAAGATTATTTACTGTAT
84817	82904	GAGTAAGATTATTTACTGTA
84818	82905	GGAGTAAGATTATTTACTGT
84819	82906	AGGAGTAAGATTATTTACTG
84820	82907	CAGGAGTAAGATTATTTACT
84821	82908	TCAGGAGTAAGATTATTTAC
84822	82909	CTCAGGAGTAAGATTATTTA
84823	82910	ACTCAGGAGTAAGATTATTT
84824	82911	TACTCAGGAGTAAGATTATT
84825	82912	CTACTCAGGAGTAAGATTAT
84826	82913	CCTACTCAGGAGTAAGATTA
84827	82914	TCCTACTCAGGAGTAAGATT
84828	82915	TTCCTACTCAGGAGTAAGAT
84829	82916	ATTCCTACTCAGGAGTAAGA
84830	82917	AATTCCTACTCAGGAGTAAG
84831	82918	TAATTCCTACTCAGGAGTAA
84832	82919	ATAATTCCTACTCAGGAGTA
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84834	82921	CAATAATTCCTACTCAGGAG
84835	82922	ACAATAATTCCTACTCAGGA
84836	82923	CACAATAATTCCTACTCAGG
84837	82924	TCACAATAATTCCTACTCAG
84838	82925	ATCACAATAATTCCTACTCA
84839	82926	AATCACAATAATTCCTACTC
84840	82927	AAATCACAATAATTCCTACT
84841	82928	TAAATCACAATAATTCCTAC
84842	82929	ATAAATCACAATAATTCCTA
84843	82930	AATAAATCACAATAATTCCT
84844	82931	TAATAAATCACAATAATTCC
84845	82932	ATAATAAATCACAATAATTC
84846	82933	CATAATAAATCACAATAATT
84847	82934	ACATAATAAATCACAATAAT
84848	82935	CACATAATAAATCACAATAA
84849	82936	TCACATAATAAATCACAATA
84850	82937	TTCACATAATAAATCACAAT
84851	82938	TTTCACATAATAAATCACAA
84852	82939	ATTTCACATAATAAATCACA
84853	82940	AATTTCACATAATAAATCAC

133930	132017	AACCGGCTCTAATGACTAGT
133931	132018	GAACCGGCTCTAATGACTAG
133932	132019	AGAACCGGCTCTAATGACTA
133933	132020	AAGAACCGGCTCTAATGACT
133934	132021	AAAGAACCGGCTCTAATGAC
133935	132022	GAAAGAACCGGCTCTAATGA
133936	132023	TGAAAGAACCGGCTCTAATG
133937	132024	ATGAAAGAACCGGCTCTAAT
133938	132025	CATGAAAGAACCGGCTCTAA
133939	132026	GCATGAAAGAACCGGCTCTA
133940	132027	GGCATGAAAGAACCGGCTCT
133941	132028	TGGCATGAAAGAACCGGCTC
133942	132029	CTGGCATGAAAGAACCGGCT
133943	132030	CCTGGCATGAAAGAACCGGC
133944	132031	TCCTGGCATGAAAGAACCGG
133945	132032	TTCCTGGCATGAAAGAACCG
133946	132033	TTTCCTGGCATGAAAGAACC
133947	132034	TTTTCCTGGCATGAAAGAAC
133948	132035	TTTTTCCTGGCATGAAAGAA
133949	132036	CTTTTTCCTGGCATGAAAGA
133950	132037	ACTTTTTCCTGGCATGAAAG
133951	132038	AACTTTTTCCTGGCATGAAA
133952	132039	TAACTTTTTCCTGGCATGAA
133953	132040	GTAACTTTTTCCTGGCATGA
133954	132041	AGTAACTTTTTCCTGGCATG
133955	132042	GAGTAACTTTTTCCTGGCAT
133956	132043	TGAGTAACTTTTTCCTGGCA
133957	132044	CTGAGTAACTTTTTCCTGGC
133958	132045	GCTGAGTAACTTTTTCCTGG
133959	132046	GGCTGAGTAACTTTTTCCTG
133960	132047	TGGCTGAGTAACTTTTTCCT
133961	132048	TTGGCTGAGTAACTTTTTCC
133962	132049	TTTGGCTGAGTAACTTTTTC
133963	132050	ATTTGGCTGAGTAACTTTTT
133964	132051	GATTTGGCTGAGTAACTTTT
133965	132052	AGATTTGGCTGAGTAACTTT
133966	132053	CAGATTTGGCTGAGTAACTT
133967	132054	TCAGATTTGGCTGAGTAACT
133968	132055	TTCAGATTTGGCTGAGTAAC
133969	132056	GTTCAGATTTGGCTGAGTAA
133970	132057	AGTTCAGATTTGGCTGAGTA
133971	132058	TAGTTCAGATTTGGCTGAGT
133972	132059	GTAGTTCAGATTTGGCTGAG
133973	132060	AGTAGTTCAGATTTGGCTGA
133974	132061	GAGTAGTTCAGATTTGGCTG
133975	132062	AGAGTAGTTCAGATTTGGCT
133976	132063	GAGAGTAGTTCAGATTTGGC
133977	132064	GGAGAGTAGTTCAGATTTGG
133978	132065	AGGAGAGTAGTTCAGATTTG
133979	132066	CAGGAGAGTAGTTCAGATTT
133980	132067	GCAGGAGAGTAGTTCAGATT
133981	132068	TGCAGGAGAGTAGTTCAGAT
133982	132069	CTGCAGGAGAGTAGTTCAGA
133983	132070	ACTGCAGGAGAGTAGTTCAG
133984	132071	AACTGCAGGAGAGTAGTTCA
133985	132072	AAACTGCAGGAGAGTAGTTC
133986	132073	TAAACTGCAGGAGAGTAGTT
133987	132074	GTAAACTGCAGGAGAGTAGT
133988	132075	TGTAAACTGCAGGAGAGTAG
133989	132076	GTGTAAACTGCAGGAGAGTA
133990	132077	TGTGTAAACTGCAGGAGAGT
133991	132078	CTGTGTAAACTGCAGGAGAG
133992	132079	CCTGTGTAAACTGCAGGAGA
133993	132080	ACCTGTGTAAACTGCAGGAG
133994	132081	CACCTGTGTAAACTGCAGGA
133995	132082	CCACCTGTGTAAACTGCAGG
133996	132083	ACCACCTGTGTAAACTGCAG
133997	132084	TACCACCTGTGTAAACTGCA
133998	132085	ATACCACCTGTGTAAACTGC
133999	132086	AATACCACCTGTGTAAACTG
134000	132087	AAATACCACCTGTGTAAACT

35707	33794	TGGTGGGCGCCTGTAATCCC
35708	33795	GTGGTGGGCGCCTGTAATCC
35709	33796	GGTGGTGGGCGCCTGTAATC
35710	33797	TGGTGGTGGGCGCCTGTAAT
35711	33798	GTGGTGGTGGGCGCCTGTAA
35712	33799	CGTGGTGGTGGGCGCCTGTA
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35714	33801	GACGTGGTGGTGGGCGCCTG
35715	33802	AGACGTGGTGGTGGGCGCCT
35716	33803	CAGACGTGGTGGTGGGCGCC
35717	33804	CCAGACGTGGTGGTGGGCGC
35718	33805	GCCAGACGTGGTGGTGGGCG
35719	33806	AGCCAGACGTGGTGGTGGGC
35720	33807	TAGCCAGACGTGGTGGTGGG
35721	33808	TTAGCCAGACGTGGTGGTGG
35722	33809	ATTAGCCAGACGTGGTGGTG
35723	33810	AATTAGCCAGACGTGGTGGT
35724	33811	AAATTAGCCAGACGTGGTGG
35725	33812	AAAATTAGCCAGACGTGGTG
35726	33813	AAAAATTAGCCAGACGTGGT
35727	33814	CAAAAATTAGCCAGACGTGG
35728	33815	ACAAAAATTAGCCAGACGTG
35729	33816	TACAAAAATTAGCCAGACGT
35730	33817	ATACAAAAATTAGCCAGACG
35731	33818	AATACAAAAATTAGCCAGAC
35732	33819	AAATACAAAAATTAGCCAGA
35733	33820	AAAATACAAAAATTAGCCAG
35734	33821	AAAAATACAAAAATTAGCCA
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35736	33823	CTAAAAATACAAAAATTAGC
35737	33824	ACTAAAAATACAAAAATTAG
35738	33825	TACTAAAAATACAAAAATTA
35739	33826	CTACTAAAAATACAAAAATT
35740	33827	TCTACTAAAAATACAAAAAT
35741	33828	CTCTACTAAAAATACAAAAA
35742	33829	TCTCTACTAAAAATACAAAA
35743	33830	ATCTCTACTAAAAATACAAA
35744	33831	CATCTCTACTAAAAATACAA
35745	33832	CCATCTCTACTAAAAATACA
35746	33833	CCCATCTCTACTAAAAATAC
35747	33834	CCCCATCTCTACTAAAAATA
35748	33835	ACCCCATCTCTACTAAAAAT
35749	33836	AACCCCATCTCTACTAAAAA
35750	33837	AAACCCCATCTCTACTAAAA
35751	33838	GAAACCCCATCTCTACTAAA
35752	33839	TGAAACCCCATCTCTACTAA
35753	33840	GTGAAACCCCATCTCTACTA
35754	33841	CGTGAAACCCCATCTCTACT
35755	33842	TCGTGAAACCCCATCTCTAC
35756	33843	ATCGTGAAACCCCATCTCTA
35757	33844	CATCGTGAAACCCCATCTCT
35758	33845	ACATCGTGAAACCCCATCTC
35759	33846	AACATCGTGAAACCCCATCT
35760	33847	CAACATCGTGAAACCCCATC
35761	33848	CCAACATCGTGAAACCCCAT
35762	33849	GCCAACATCGTGAAACCCCA
35763	33850	GGCCAACATCGTGAAACCCC
35764	33851	TGGCCAACATCGTGAAACCC
35765	33852	CTGGCCAACATCGTGAAACC
35766	33853	CCTGGCCAACATCGTGAAAC
35767	33854	GCCTGGCCAACATCGTGAAA
35768	33855	AGCCTGGCCAACATCGTGAA
35769	33856	CAGCCTGGCCAACATCGTGA
35770	33857	CCAGCCTGGCCAACATCGTG
35771	33858	CCCAGCCTGGCCAACATCGT
35772	33859	GCCCAGCCTGGCCAACATCG
35773	33860	AGCCCAGCCTGGCCAACATC
35774	33861	GAGCCCAGCCTGGCCAACAT
35775	33862	CGAGCCCAGCCTGGCCAACA
35776	33863	TCGAGCCCAGCCTGGCCAAC
35777	33864	TTCGAGCCCAGCCTGGCCAA

84854	82941	TAATTTCACATAATAAATCA
84855	82942	ATAATTTCACATAATAAATC
84856	82943	GATAATTTCACATAATAAAT
84857	82944	AGATAATTTCACATAATAAA
84858	82945	TAGATAATTTCACATAATAA
84859	82946	CTAGATAATTTCACATAATA
84860	82947	ACTAGATAATTTCACATAAT
84861	82948	CACTAGATAATTTCACATAA
84862	82949	ACACTAGATAATTTCACATA
84863	82950	TACACTAGATAATTTCACAT
84864	82951	ATACACTAGATAATTTCACA
84865	82952	CATACACTAGATAATTTCAC
84866	82953	ACATACACTAGATAATTTCA
84867	82954	AACATACACTAGATAATTTC
84868	82955	TAACATACACTAGATAATTT
84869	82956	ATAACATACACTAGATAATT
84870	82957	TATAACATACACTAGATAAT
84871	82958	ATATAACATACACTAGATAA
84872	82959	AATATAACATACACTAGATA
84873	82960	GAATATAACATACACTAGAT
84874	82961	GGAATATAACATACACTAGA
84875	82962	AGGAATATAACATACACTAG
84876	82963	AAGGAATATAACATACACTA
84877	82964	AAAGGAATATAACATACACT
84878	82965	TAAAGGAATATAACATACAC
84879	82966	TTAAAGGAATATAACATACA
84880	82967	TTTAAAGGAATATAACATAC
84881	82968	GTTTAAAGGAATATAACATA
84882	82969	TGTTTAAAGGAATATAACAT
84883	82970	TTGTTTAAAGGAATATAACA
84884	82971	GTTGTTTAAAGGAATATAAC
84885	82972	GGTTGTTTAAAGGAATATAA
84886	82973	TGGTTGTTTAAAGGAATATA
84887	82974	CTGGTTGTTTAAAGGAATAT
84888	82975	ACTGGTTGTTTAAAGGAATA
84889	82976	AACTGGTTGTTTAAAGGAAT
84890	82977	TAACTGGTTGTTTAAAGGAA
84891	82978	GTAACTGGTTGTTTAAAGGA
84892	82979	AGTAACTGGTTGTTTAAAGG
84893	82980	CAGTAACTGGTTGTTTAAAG
84894	82981	TCAGTAACTGGTTGTTTAAA
84895	82982	CTCAGTAACTGGTTGTTTAA
84896	82983	TCTCAGTAACTGGTTGTTTA
84897	82984	TTCTCAGTAACTGGTTGTTT
84898	82985	TTTCTCAGTAACTGGTTGTT
84899	82986	GTTTCTCAGTAACTGGTTGT
84900	82987	TGTTTCTCAGTAACTGGTTG
84901	82988	CTGTTTCTCAGTAACTGGTT
84902	82989	ACTGTTTCTCAGTAACTGGT
84903	82990	AACTGTTTCTCAGTAACTGG
84904	82991	TAACTGTTTCTCAGTAACTG
84905	82992	ATAACTGTTTCTCAGTAACT
84906	82993	TATAACTGTTTCTCAGTAAC
84907	82994	CTATAACTGTTTCTCAGTAA
84908	82995	TCTATAACTGTTTCTCAGTA
84909	82996	TTCTATAACTGTTTCTCAGT
84910	82997	CTTCTATAACTGTTTCTCAG
84911	82998	GCTTCTATAACTGTTTCTCA
84912	82999	TGCTTCTATAACTGTTTCTC
84913	83000	CTGCTTCTATAACTGTTTCT
84914	83001	CCTGCTTCTATAACTGTTTC
84915	83002	TCCTGCTTCTATAACTGTTT
84916	83003	ATCCTGCTTCTATAACTGTT
84917	83004	AATCCTGCTTCTATAACTGT
84918	83005	TAATCCTGCTTCTATAACTG
84919	83006	TTAATCCTGCTTCTATAACT
84920	83007	ATTAATCCTGCTTCTATAAC
84921	83008	TATTAATCCTGCTTCTATAA
84922	83009	CTATTAATCCTGCTTCTATA
84923	83010	CCTATTAATCCTGCTTCTAT
84924	83011	GCCTATTAATCCTGCTTCTA

134001	132088	TAAATACCACCTGTGTAAAC
134002	132089	TTAAATACCACCTGTGTAAA
134003	132090	ATTAAATACCACCTGTGTAA
134004	132091	AATTAAATACCACCTGTGTA
134005	132092	CAATTAAATACCACCTGTGT
134006	132093	GCAATTAAATACCACCTGTG
134007	132094	AGCAATTAAATACCACCTGT
134008	132095	CAGCAATTAAATACCACCTG
134009	132096	ACAGCAATTAAATACCACCT
134010	132097	GACAGCAATTAAATACCACC
134011	132098	AGACAGCAATTAAATACCAC
134012	132099	CAGACAGCAATTAAATACCA
134013	132100	ACAGACAGCAATTAAATACC
134014	132101	TACAGACAGCAATTAAATAC
134015	132102	ATACAGACAGCAATTAAATA
134016	132103	CATACAGACAGCAATTAAAT
134017	132104	CCATACAGACAGCAATTAAA
134018	132105	TCCATACAGACAGCAATTAA
134019	132106	CTCCATACAGACAGCAATTA
134020	132107	CCTCCATACAGACAGCAATT
134021	132108	GCCTCCATACAGACAGCAAT
134022	132109	TGCCTCCATACAGACAGCAA
134023	132110	CTGCCTCCATACAGACAGCA
134024	132111	CCTGCCTCCATACAGACAGC
134025	132112	GCCTGCCTCCATACAGACAG
134026	132113	AGCCTGCCTCCATACAGACA
134027	132114	TAGCCTGCCTCCATACAGAC
134028	132115	CTAGCCTGCCTCCATACAGA
134029	132116	CCTAGCCTGCCTCCATACAG
134030	132117	TCCTAGCCTGCCTCCATACA
134031	132118	CTCCTAGCCTGCCTCCATAC
134032	132119	GCTCCTAGCCTGCCTCCATA
134033	132120	TGCTCCTAGCCTGCCTCCAT
134034	132121	TTGCTCCTAGCCTGCCTCCA
134035	132122	CTTGCTCCTAGCCTGCCTCC
134036	132123	CCTTGCTCCTAGCCTGCCTC
134037	132124	GCCTTGCTCCTAGCCTGCCT
134038	132125	AGCCTTGCTCCTAGCCTGCC
134039	132126	CAGCCTTGCTCCTAGCCTGC
134040	132127	ACAGCCTTGCTCCTAGCCTG
134041	132128	CACAGCCTTGCTCCTAGCCT
134042	132129	CCACAGCCTTGCTCCTAGCC
134043	132130	TCCACAGCCTTGCTCCTAGC
134044	132131	GTCCACAGCCTTGCTCCTAG
134045	132132	AGTCCACAGCCTTGCTCCTA
134046	132133	AAGTCCACAGCCTTGCTCCT
134047	132134	CAAGTCCACAGCCTTGCTCC
134048	132135	ACAAGTCCACAGCCTTGCTC
134049	132136	AACAAGTCCACAGCCTTGCT
134050	132137	CAACAAGTCCACAGCCTTGC
134051	132138	ACAACAAGTCCACAGCCTTG
134052	132139	CACAACAAGTCCACAGCCTT
134053	132140	TCACAACAAGTCCACAGCCT
134054	132141	ATCACAACAAGTCCACAGCC
134055	132142	AATCACAACAAGTCCACAGC
134056	132143	CAATCACAACAAGTCCACAG
134057	132144	ACAATCACAACAAGTCCACA
134058	132145	GACAATCACAACAAGTCCAC
134059	132146	TGACAATCACAACAAGTCCA
134060	132147	GTGACAATCACAACAAGTCC
134061	132148	AGTGACAATCACAACAAGTC
134062	132149	TAGTGACAATCACAACAAGT
134063	132150	CTAGTGACAATCACAACAAG
134064	132151	ACTAGTGACAATCACAACAA
134065	132152	AACTAGTGACAATCACAACA
134066	132153	TAACTAGTGACAATCACAAC
134067	132154	TTAACTAGTGACAATCACAA
134068	132155	ATTAACTAGTGACAATCACA
134069	132156	GATTAACTAGTGACAATCAC
134070	132157	TGATTAACTAGTGACAATCA
134071	132158	TTGATTAACTAGTGACAATC

35778	33865	GTTCGAGCCCAGCCTGGCCA
35779	33866	AGTTCGAGCCCAGCCTGGCC
35780	33867	GAGTTCGAGCCCAGCCTGGC
35781	33868	GGAGTTCGAGCCCAGCCTGG
35782	33869	AGGAGTTCGAGCCCAGCCTG
35783	33870	CAGGAGTTCGAGCCCAGCCT
35784	33871	CCAGGAGTTCGAGCCCAGCC
35785	33872	GCCAGGAGTTCGAGCCCAGC
35786	33873	AGCCAGGAGTTCGAGCCCAG
35787	33874	AAGCCAGGAGTTCGAGCCCA
35788	33875	GAAGCCAGGAGTTCGAGCCC
35789	33876	TGAAGCCAGGAGTTCGAGCC
35790	33877	TTGAAGCCAGGAGTTCGAGC
35791	33878	CTTGAAGCCAGGAGTTCGAG
35792	33879	ACTTGAAGCCAGGAGTTCGA
35793	33880	CACTTGAAGCCAGGAGTTCG
35794	33881	TCACTTGAAGCCAGGAGTTC
35795	33882	ATCACTTGAAGCCAGGAGTT
35796	33883	GATCACTTGAAGCCAGGAGT
35797	33884	GGATCACTTGAAGCCAGGAG
35798	33885	TGGATCACTTGAAGCCAGGA
35799	33886	GTGGATCACTTGAAGCCAGG
35800	33887	GGTGGATCACTTGAAGCCAG
35801	33888	AGGTGGATCACTTGAAGCCA
35802	33889	CAGGTGGATCACTTGAAGCC
35803	33890	GCAGGTGGATCACTTGAAGC
35804	33891	GGCAGGTGGATCACTTGAAG
35805	33892	AGGCAGGTGGATCACTTGAA
35806	33893	AAGGCAGGTGGATCACTTGA
35807	33894	CAAGGCAGGTGGATCACTTG
35808	33895	CCAAGGCAGGTGGATCACTT
35809	33896	GCCAAGGCAGGTGGATCACT
35810	33897	GGCCAAGGCAGGTGGATCAC
35811	33898	AGGCCAAGGCAGGTGGATCA
35812	33899	GAGGCCAAGGCAGGTGGATC
35813	33900	GGAGGCCAAGGCAGGTGGAT
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35817	33904	TTTGGGAGGCCAAGGCAGGT
35818	33905	CTTTGGGAGGCCAAGGCAGG
35819	33906	ACTTTGGGAGGCCAAGGCAG
35820	33907	CACTTTGGGAGGCCAAGGCA
35821	33908	GCACTTTGGGAGGCCAAGGC
35822	33909	AGCACTTTGGGAGGCCAAGG
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35827	33914	ATCCCAGCACTTTGGGAGGC
35828	33915	AATCCCAGCACTTTGGGAGG
35829	33916	CAATCCCAGCACTTTGGGAG
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35833	33920	CCTACAATCCCAGCACTTTG
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35835	33922	CACCTACAATCCCAGCACTT
35836	33923	ACACCTACAATCCCAGCACT
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35838	33925	TCACACCTACAATCCCAGCA
35839	33926	CTCACACCTACAATCCCAGC
35840	33927	GCTCACACCTACAATCCCAG
35841	33928	GGCTCACACCTACAATCCCA
35842	33929	TGGCTCACACCTACAATCCC
35843	33930	GTGGCTCACACCTACAATCC
35844	33931	AGTGGCTCACACCTACAATC
35845	33932	TAGTGGCTCACACCTACAAT
35846	33933	ATAGTGGCTCACACCTACAA
35847	33934	CATAGTGGCTCACACCTACA
35848	33935	GCATAGTGGCTCACACCTAC

84925	83012	TGCCTATTAATCCTGCTTCT
84926	83013	TTGCCTATTAATCCTGCTTC
84927	83014	TTTGCCTATTAATCCTGCTT
84928	83015	CTTTGCCTATTAATCCTGCT
84929	83016	ACTTTGCCTATTAATCCTGC
84930	83017	GACTTTGCCTATTAATCCTG
84931	83018	AGACTTTGCCTATTAATCCT
84932	83019	AAGACTTTGCCTATTAATCC
84933	83020	TAAGACTTTGCCTATTAATC
84934	83021	TTAAGACTTTGCCTATTAAT
84935	83022	GTTAAGACTTTGCCTATTAA
84936	83023	AGTTAAGACTTTGCCTATTA
84937	83024	CAGTTAAGACTTTGCCTATT
84938	83025	ACAGTTAAGACTTTGCCTAT
84939	83026	GACAGTTAAGACTTTGCCTA
84940	83027	AGACAGTTAAGACTTTGCCT
84941	83028	AAGACAGTTAAGACTTTGCC
84942	83029	GAAGACAGTTAAGACTTTGC
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84944	83031	AAGAAGACAGTTAAGACTTT
84945	83032	GAAGAAGACAGTTAAGACTT
84946	83033	TGAAGAAGACAGTTAAGACT
84947	83034	TTGAAGAAGACAGTTAAGAC
84948	83035	ATTGAAGAAGACAGTTAAGA
84949	83036	TATTGAAGAAGACAGTTAAG
84950	83037	CTATTGAAGAAGACAGTTAA
84951	83038	ACTATTGAAGAAGACAGTTA
84952	83039	CACTATTGAAGAAGACAGTT
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84955	83042	ACACACTATTGAAGAAGACA
84956	83043	TACACACTATTGAAGAAGAC
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84963	83050	GGATCTATACACACTATTGA
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84965	83052	TAGGATCTATACACACTATT
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84967	83054	ATTAGGATCTATACACACTA
84968	83055	AATTAGGATCTATACACACT
84969	83056	TAATTAGGATCTATACACAC
84970	83057	TTAATTAGGATCTATACACA
84971	83058	GTTAATTAGGATCTATACAC
84972	83059	GGTTAATTAGGATCTATACA
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84974	83061	AGGGTTAATTAGGATCTATA
84975	83062	AAGGGTTAATTAGGATCTAT
84976	83063	AAAGGGTTAATTAGGATCTA
84977	83064	CAAAGGGTTAATTAGGATCT
84978	83065	CCAAAGGGTTAATTAGGATC
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84985	83072	CACGTTCCCAAAGGGTTAAT
84986	83073	ACACGTTCCCAAAGGGTTAA
84987	83074	TACACGTTCCCAAAGGGTTA
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84989	83076	AATACACGTTCCCAAAGGGT
84990	83077	GAATACACGTTCCCAAAGGG
84991	83078	TGAATACACGTTCCCAAAGG
84992	83079	ATGAATACACGTTCCCAAAG
84993	83080	AATGAATACACGTTCCCAAA
84994	83081	AAATGAATACACGTTCCCAA
84995	83082	TAAATGAATACACGTTCCCA

134072	132159	CTTGATTAACTAGTGACAAT
134073	132160	TCTTGATTAACTAGTGACAA
134074	132161	ATCTTGATTAACTAGTGACA
134075	132162	AATCTTGATTAACTAGTGAC
134076	132163	GAATCTTGATTAACTAGTGA
134077	132164	GGAATCTTGATTAACTAGTG
134078	132165	GGGAATCTTGATTAACTAGT
134079	132166	AGGGAATCTTGATTAACTAG
134080	132167	AAGGGAATCTTGATTAACTA
134081	132168	AAAGGGAATCTTGATTAACT
134082	132169	CAAAGGGAATCTTGATTAAC
134083	132170	ACAAAGGGAATCTTGATTAA
134084	132171	CACAAAGGGAATCTTGATTA
134085	132172	CCACAAAGGGAATCTTGATT
134086	132173	ACCACAAAGGGAATCTTGAT
134087	132174	CACCACAAAGGGAATCTTGA
134088	132175	GCACCACAAAGGGAATCTTG
134089	132176	AGCACCACAAAGGGAATCTT
134090	132177	AAGCACCACAAAGGGAATCT
134091	132178	TAAGCACCACAAAGGGAATC
134092	132179	TTAAGCACCACAAAGGGAAT
134093	132180	CTTAAGCACCACAAAGGGAA
134094	132181	TCTTAAGCACCACAAAGGGA
134095	132182	GTCTTAAGCACCACAAAGGG
134096	132183	GGTCTTAAGCACCACAAAGG
134097	132184	GGGTCTTAAGCACCACAAAG
134098	132185	AGGGTCTTAAGCACCACAAA
134099	132186	TAGGGTCTTAAGCACCACAA
134100	132187	TTAGGGTCTTAAGCACCACA
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134102	132189	TTTTAGGGTCTTAAGCACCA
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134105	132192	CCTTTTTAGGGTCTTAAGCA
134106	132193	TCCTTTTTAGGGTCTTAAGC
134107	132194	GTCCTTTTTAGGGTCTTAAG
134108	132195	TGTCCTTTTTAGGGTCTTAA
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134110	132197	AGTGTCCTTTTTAGGGTCTT
134111	132198	TAGTGTCCTTTTTAGGGTCT
134112	132199	CTAGTGTCCTTTTTAGGGTC
134113	132200	CCTAGTGTCCTTTTTAGGGT
134114	132201	TCCTAGTGTCCTTTTTAGGG
134115	132202	CTCCTAGTGTCCTTTTTAGG
134116	132203	GCTCCTAGTGTCCTTTTTAG
134117	132204	AGCTCCTAGTGTCCTTTTTA
134118	132205	CAGCTCCTAGTGTCCTTTTT
134119	132206	CCAGCTCCTAGTGTCCTTTT
134120	132207	CCCAGCTCCTAGTGTCCTTT
134121	132208	GCCCAGCTCCTAGTGTCCTT
134122	132209	TGCCCAGCTCCTAGTGTCCT
134123	132210	ATGCCCAGCTCCTAGTGTCC
134124	132211	CATGCCCAGCTCCTAGTGTC
134125	132212	CCATGCCCAGCTCCTAGTGT
134126	132213	ACCATGCCCAGCTCCTAGTG
134127	132214	CACCATGCCCAGCTCCTAGT
134128	132215	CCACCATGCCCAGCTCCTAG
134129	132216	GCCACCATGCCCAGCTCCTA
134130	132217	AGCCACCATGCCCAGCTCCT
134131	132218	CAGCCACCATGCCCAGCTCC
134132	132219	TCAGCCACCATGCCCAGCTC
134133	132220	GTCAGCCACCATGCCCAGCT
134134	132221	TGTCAGCCACCATGCCCAGC
134135	132222	GTGTCAGCCACCATGCCCAG
134136	132223	GGTGTCAGCCACCATGCCCA
134137	132224	AGGTGTCAGCCACCATGCCC
134138	132225	CAGGTGTCAGCCACCATGCC
134139	132226	ACAGGTGTCAGCCACCATGC
134140	132227	TACAGGTGTCAGCCACCATG
134141	132228	TTACAGGTGTCAGCCACCAT
134142	132229	ATTACAGGTGTCAGCCACCA

35849	33936	GGCATAGTGGCTCACACCTA
35850	33937	AGGCATAGTGGCTCACACCT
35851	33938	CAGGCATAGTGGCTCACACC
35852	33939	CCAGGCATAGTGGCTCACAC
35853	33940	GCCAGGCATAGTGGCTCACA
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35855	33942	AGGCCAGGCATAGTGGCTCA
35856	33943	TAGGCCAGGCATAGTGGCTC
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35859	33946	AATTAGGCCAGGCATAGTGG
35860	33947	CAATTAGGCCAGGCATAGTG
35861	33948	CCAATTAGGCCAGGCATAGT
35862	33949	GCCAATTAGGCCAGGCATAG
35863	33950	GGCCAATTAGGCCAGGCATA
35864	33951	AGGCCAATTAGGCCAGGCAT
35865	33952	TAGGCCAATTAGGCCAGGCA
35866	33953	TTAGGCCAATTAGGCCAGGC
35867	33954	ATTAGGCCAATTAGGCCAGG
35868	33955	AATTAGGCCAATTAGGCCAG
35869	33956	AAATTAGGCCAATTAGGCCA
35870	33957	GAAATTAGGCCAATTAGGCC
35871	33958	TGAAATTAGGCCAATTAGGC
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35873	33960	ATTGAAATTAGGCCAATTAG
35874	33961	TATTGAAATTAGGCCAATTA
35875	33962	ATATTGAAATTAGGCCAATT
35876	33963	AATATTGAAATTAGGCCAAT
35877	33964	CAATATTGAAATTAGGCCAA
35878	33965	ACAATATTGAAATTAGGCCA
35879	33966	AACAATATTGAAATTAGGCC
35880	33967	TAACAATATTGAAATTAGGC
35881	33968	ATAACAATATTGAAATTAGG
35882	33969	TATAACAATATTGAAATTAG
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35884	33971	GATATAACAATATTGAAATT
35885	33972	AGATATAACAATATTGAAAT
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35888	33975	CTGAGATATAACAATATTGA
35889	33976	CCTGAGATATAACAATATTG
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35893	33980	ATTCCCTGAGATATAACAAT
35894	33981	TATTCCCTGAGATATAACAA
35895	33982	CTATTCCCTGAGATATAACA
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35897	33984	CTCTATTCCCTGAGATATAA
35898	33985	TCTCTATTCCCTGAGATATA
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35900	33987	CCTCTCTATTCCCTGAGATA
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35902	33989	TGCCTCTCTATTCCCTGAGA
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35905	33992	TCGTGCCTCTCTATTCCCTG
35906	33993	CTCGTGCCTCTCTATTCCCT
35907	33994	CCTCGTGCCTCTCTATTCCC
35908	33995	TCCTCGTGCCTCTCTATTCC
35909	33996	CTCCTCGTGCCTCTCTATTC
35910	33997	TCTCCTCGTGCCTCTCTATT
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35913	34000	CTTTCTCCTCGTGCCTCTCT
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84996	83083	TTAAATGAATACACGTTCCC
84997	83084	TTTAAATGAATACACGTTCC
84998	83085	GTTTAAATGAATACACGTTC
84999	83086	TGTTTAAATGAATACACGTT
85000	83087	CTGTTTAAATGAATACACGT
85001	83088	TCTGTTTAAATGAATACACG
85002	83089	GTCTGTTTAAATGAATACAC
85003	83090	AGTCTGTTTAAATGAATACA
85004	83091	AAGTCTGTTTAAATGAATAC
85005	83092	TAAGTCTGTTTAAATGAATA
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85007	83094	ATTAAGTCTGTTTAAATGAA
85008	83095	GATTAAGTCTGTTTAAATGA
85009	83096	AGATTAAGTCTGTTTAAATG
85010	83097	AAGATTAAGTCTGTTTAAAT
85011	83098	TAAGATTAAGTCTGTTTAAA
85012	83099	TTAAGATTAAGTCTGTTTAA
85013	83100	CTTAAGATTAAGTCTGTTTA
85014	83101	CCTTAAGATTAAGTCTGTTT
85015	83102	TCCTTAAGATTAAGTCTGTT
85016	83103	CTCCTTAAGATTAAGTCTGT
85017	83104	CCTCCTTAAGATTAAGTCTG
85018	83105	ACCTCCTTAAGATTAAGTCT
85019	83106	AACCTCCTTAAGATTAAGTC
85020	83107	TAACCTCCTTAAGATTAAGT
85021	83108	TTAACCTCCTTAAGATTAAG
85022	83109	TTTAACCTCCTTAAGATTAA
85023	83110	CTTTAACCTCCTTAAGATTA
85024	83111	ACTTTAACCTCCTTAAGATT
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85028	83115	TTTTACTTTAACCTCCTTAA
85029	83116	ATTTTACTTTAACCTCCTTA
85030	83117	CATTTTACTTTAACCTCCTT
85031	83118	ACATTTTACTTTAACCTCCT
85032	83119	CACATTTTACTTTAACCTCC
85033	83120	TCACATTTTACTTTAACCTC
85034	83121	TTCACATTTTACTTTAACCT
85035	83122	ATTCACATTTTACTTTAACC
85036	83123	AATTCACATTTTACTTTAAC
85037	83124	AAATTCACATTTTACTTTAA
85038	83125	TAAATTCACATTTTACTTTA
85039	83126	ATAAATTCACATTTTACTTT
85040	83127	CATAAATTCACATTTTACTT
85041	83128	ACATAAATTCACATTTTACT
85042	83129	GACATAAATTCACATTTTAC
85043	83130	TGACATAAATTCACATTTTA
85044	83131	CTGACATAAATTCACATTTT
85045	83132	ACTGACATAAATTCACATTT
85046	83133	AACTGACATAAATTCACATT
85047	83134	TAACTGACATAAATTCACAT
85048	83135	TTAACTGACATAAATTCACA
85049	83136	CTTAACTGACATAAATTCAC
85050	83137	ACTTAACTGACATAAATTCA
85051	83138	AACTTAACTGACATAAATTC
85052	83139	TAACTTAACTGACATAAATT
85053	83140	ATAACTTAACTGACATAAAT
85054	83141	CATAACTTAACTGACATAAA
85055	83142	GCATAACTTAACTGACATAA
85056	83143	AGCATAACTTAACTGACATA
85057	83144	TAGCATAACTTAACTGACAT
85058	83145	TTAGCATAACTTAACTGACA
85059	83146	TTTAGCATAACTTAACTGAC
85060	83147	TTTTAGCATAACTTAACTGA
85061	83148	GTTTTAGCATAACTTAACTG
85062	83149	AGTTTTAGCATAACTTAACT
85063	83150	AAGTTTTAGCATAACTTAAC
85064	83151	TAAGTTTTAGCATAACTTAA
85065	83152	ATAAGTTTTAGCATAACTTA
85066	83153	GATAAGTTTTAGCATAACTT

134143	132230	GATTACAGGTGTCAGCCACC
134144	132231	GGATTACAGGTGTCAGCCAC
134145	132232	TGGATTACAGGTGTCAGCCA
134146	132233	TTGGATTACAGGTGTCAGCC
134147	132234	CTTGGATTACAGGTGTCAGC
134148	132235	TCTTGGATTACAGGTGTCAG
134149	132236	TTCTTGGATTACAGGTGTCA
134150	132237	GTTCTTGGATTACAGGTGTC
134151	132238	AGTTCTTGGATTACAGGTGT
134152	132239	AAGTTCTTGGATTACAGGTG
134153	132240	CAAGTTCTTGGATTACAGGT
134154	132241	CCAAGTTCTTGGATTACAGG
134155	132242	CCCAAGTTCTTGGATTACAG
134156	132243	CCCCAAGTTCTTGGATTACA
134157	132244	TCCCCAAGTTCTTGGATTAC
134158	132245	CTCCCCAAGTTCTTGGATTA
134159	132246	CCTCCCCAAGTTCTTGGATT
134160	132247	GCCTCCCCAAGTTCTTGGAT
134161	132248	AGCCTCCCCAAGTTCTTGGA
134162	132249	CAGCCTCCCCAAGTTCTTGG
134163	132250	TCAGCCTCCCCAAGTTCTTG
134164	132251	TTCAGCCTCCCCAAGTTCTT
134165	132252	CTTCAGCCTCCCCAAGTTCT
134166	132253	ACTTCAGCCTCCCCAAGTTC
134167	132254	CACTTCAGCCTCCCCAAGTT
134168	132255	CCACTTCAGCCTCCCCAAGT
134169	132256	TCCACTTCAGCCTCCCCAAG
134170	132257	CTCCACTTCAGCCTCCCCAA
134171	132258	CCTCCACTTCAGCCTCCCCA
134172	132259	TCCTCCACTTCAGCCTCCCC
134173	132260	ATCCTCCACTTCAGCCTCCC
134174	132261	GATCCTCCACTTCAGCCTCC
134175	132262	CGATCCTCCACTTCAGCCTC
134176	132263	GCGATCCTCCACTTCAGCCT
134177	132264	AGCGATCCTCCACTTCAGCC
134178	132265	AAGCGATCCTCCACTTCAGC
134179	132266	TAAGCGATCCTCCACTTCAG
134180	132267	CTAAGCGATCCTCCACTTCA
134181	132268	GCTAAGCGATCCTCCACTTC
134182	132269	GGCTAAGCGATCCTCCACTT
134183	132270	GGGCTAAGCGATCCTCCACT
134184	132271	TGGGCTAAGCGATCCTCCAC
134185	132272	CTGGGCTAAGCGATCCTCCA
134186	132273	CCTGGGCTAAGCGATCCTCC
134187	132274	ACCTGGGCTAAGCGATCCTC
134188	132275	CACCTGGGCTAAGCGATCCT
134189	132276	ACACCTGGGCTAAGCGATCC
134190	132277	AACACCTGGGCTAAGCGATC
134191	132278	GAACACCTGGGCTAAGCGAT
134192	132279	TGAACACCTGGGCTAAGCGA
134193	132280	TTGAACACCTGGGCTAAGCG
134194	132281	CTTGAACACCTGGGCTAAGC
134195	132282	TCTTGAACACCTGGGCTAAG
134196	132283	GTCTTGAACACCTGGGCTAA
134197	132284	GGTCTTGAACACCTGGGCTA
134198	132285	TGGTCTTGAACACCTGGGCT
134199	132286	CTGGTCTTGAACACCTGGGC
134200	132287	ACTGGTCTTGAACACCTGGG
134201	132288	GACTGGTCTTGAACACCTGG
134202	132289	AGACTGGTCTTGAACACCTG
134203	132290	TAGACTGGTCTTGAACACCT
134204	132291	CTAGACTGGTCTTGAACACC
134205	132292	CCTAGACTGGTCTTGAACAC
134206	132293	GCCTAGACTGGTCTTGAACA
134207	132294	TGCCTAGACTGGTCTTGAAC
134208	132295	TTGCCTAGACTGGTCTTGAA
134209	132296	CTTGCCTAGACTGGTCTTGA
134210	132297	TCTTGCCTAGACTGGTCTTG
134211	132298	ATCTTGCCTAGACTGGTCTT
134212	132299	CATCTTGCCTAGACTGGTCT
134213	132300	CCATCTTGCCTAGACTGGTC

35920	34007	TGTCTCTCTTTCTCCTCGTG
35921	34008	TTGTCTCTCTTTCTCCTCGT
35922	34009	CTTGTCTCTCTTTCTCCTCG
35923	34010	GCTTGTCTCTCTTTCTCCTC
35924	34011	AGCTTGTCTCTCTTTCTCCT
35925	34012	CAGCTTGTCTCTCTTTCTCC
35926	34013	TCAGCTTGTCTCTCTTTCTC
35927	34014	GTCAGCTTGTCTCTCTTTCT
35928	34015	AGTCAGCTTGTCTCTCTTTC
35929	34016	CAGTCAGCTTGTCTCTCTTT
35930	34017	GCAGTCAGCTTGTCTCTCTT
35931	34018	AGCAGTCAGCTTGTCTCTCT
35932	34019	CAGCAGTCAGCTTGTCTCTC
35933	34020	CCAGCAGTCAGCTTGTCTCT
35934	34021	ACCAGCAGTCAGCTTGTCTC
35935	34022	AACCAGCAGTCAGCTTGTCT
35936	34023	GAACCAGCAGTCAGCTTGTC
35937	34024	CGAACCAGCAGTCAGCTTGT
35938	34025	ACGAACCAGCAGTCAGCTTG
35939	34026	CACGAACCAGCAGTCAGCTT
35940	34027	CCACGAACCAGCAGTCAGCT
35941	34028	TCCACGAACCAGCAGTCAGC
35942	34029	CTCCACGAACCAGCAGTCAG
35943	34030	ACTCCACGAACCAGCAGTCA
35944	34031	TACTCCACGAACCAGCAGTC
35945	34032	CTACTCCACGAACCAGCAGT
35946	34033	ACTACTCCACGAACCAGCAG
35947	34034	GACTACTCCACGAACCAGCA
35948	34035	TGACTACTCCACGAACCAGC
35949	34036	ATGACTACTCCACGAACCAG
35950	34037	TATGACTACTCCACGAACCA
35951	34038	TTATGACTACTCCACGAACC
35952	34039	GTTATGACTACTCCACGAAC
35953	34040	TGTTATGACTACTCCACGAA
35954	34041	GTGTTATGACTACTCCACGA
35955	34042	TGTGTTATGACTACTCCACG
35956	34043	GTGTGTTATGACTACTCCAC
35957	34044	TGTGTGTTATGACTACTCCA
35958	34045	TTGTGTGTTATGACTACTCC
35959	34046	GTTGTGTGTTATGACTACTC
35960	34047	TGTTGTGTGTTATGACTACT
35961	34048	ATGTTGTGTGTTATGACTAC
35962	34049	AATGTTGTGTGTTATGACTA
35963	34050	AAATGTTGTGTGTTATGACT
35964	34051	TAAATGTTGTGTGTTATGAC
35965	34052	ATAAATGTTGTGTGTTATGA
35966	34053	AATAAATGTTGTGTGTTATG
35967	34054	TAATAAATGTTGTGTGTTAT
35968	34055	TTAATAAATGTTGTGTGTTA
35969	34056	CTTAATAAATGTTGTGTGTT
35970	34057	TCTTAATAAATGTTGTGTGT
35971	34058	ATCTTAATAAATGTTGTGTG
35972	34059	AATCTTAATAAATGTTGTGT
35973	34060	CAATCTTAATAAATGTTGTG
35974	34061	GCAATCTTAATAAATGTTGT
35975	34062	AGCAATCTTAATAAATGTTG
35976	34063	CAGCAATCTTAATAAATGTT
35977	34064	ACAGCAATCTTAATAAATGT
35978	34065	GACAGCAATCTTAATAAATG
35979	34066	AGACAGCAATCTTAATAAAT
35980	34067	AAGACAGCAATCTTAATAAA
35981	34068	TAAGACAGCAATCTTAATAA
35982	34069	ATAAGACAGCAATCTTAATA
35983	34070	TATAAGACAGCAATCTTAAT
35984	34071	ATATAAGACAGCAATCTTAA
35985	34072	CATATAAGACAGCAATCTTA
35986	34073	CCATATAAGACAGCAATCTT
35987	34074	TCCATATAAGACAGCAATCT
35988	34075	GTCCATATAAGACAGCAATC
35989	34076	GGTCCATATAAGACAGCAAT
35990	34077	CGGTCCATATAAGACAGCAA

85067	83154	TGATAAGTTTTAGCATAACT
85068	83155	GTGATAAGTTTTAGCATAAC
85069	83156	TGTGATAAGTTTTAGCATAA
85070	83157	TTGTGATAAGTTTTAGCATA
85071	83158	TTTGTGATAAGTTTTAGCAT
85072	83159	ATTTGTGATAAGTTTTAGCA
85073	83160	GATTTGTGATAAGTTTTAGC
85074	83161	TGATTTGTGATAAGTTTTAG
85075	83162	TTGATTTGTGATAAGTTTTA
85076	83163	TTTGATTTGTGATAAGTTTT
85077	83164	ATTTGATTTGTGATAAGTTT
85078	83165	CATTTGATTTGTGATAAGTT
85079	83166	TCATTTGATTTGTGATAAGT
85080	83167	GTCATTTGATTTGTGATAAG
85081	83168	AGTCATTTGATTTGTGATAA
85082	83169	CAGTCATTTGATTTGTGATA
85083	83170	ACAGTCATTTGATTTGTGAT
85084	83171	GACAGTCATTTGATTTGTGA
85085	83172	GGACAGTCATTTGATTTGTG
85086	83173	AGGACAGTCATTTGATTTGT
85087	83174	GAGGACAGTCATTTGATTTG
85088	83175	TGAGGACAGTCATTTGATTT
85089	83176	TTGAGGACAGTCATTTGATT
85090	83177	TTTGAGGACAGTCATTTGAT
85091	83178	CTTTGAGGACAGTCATTTGA
85092	83179	CCTTTGAGGACAGTCATTTG
85093	83180	CCCTTTGAGGACAGTCATTT
85094	83181	ACCCTTTGAGGACAGTCATT
85095	83182	AACCCTTTGAGGACAGTCAT
85096	83183	TAACCCTTTGAGGACAGTCA
85097	83184	TTAACCCTTTGAGGACAGTC
85098	83185	TTTAACCCTTTGAGGACAGT
85099	83186	TTTTAACCCTTTGAGGACAG
85100	83187	ATTTTAACCCTTTGAGGACA
85101	83188	CATTTTAACCCTTTGAGGAC
85102	83189	ACATTTTAACCCTTTGAGGA
85103	83190	TACATTTTAACCCTTTGAGG
85104	83191	GTACATTTTAACCCTTTGAG
85105	83192	TGTACATTTTAACCCTTTGA
85106	83193	TTGTACATTTTAACCCTTTG
85107	83194	CTTGTACATTTTAACCCTTT
85108	83195	TCTTGTACATTTTAACCCTT
85109	83196	TTCTTGTACATTTTAACCCT
85110	83197	TTTCTTGTACATTTTAACCC
85111	83198	ATTTCTTGTACATTTTAACC
85112	83199	GATTTCTTGTACATTTTAAC
85113	83200	TGATTTCTTGTACATTTTAA
85114	83201	ATGATTTCTTGTACATTTTA
85115	83202	AATGATTTCTTGTACATTTT
85116	83203	AAATGATTTCTTGTACATTT
85117	83204	AAAATGATTTCTTGTACATT
85118	83205	AAAAATGATTTCTTGTACAT
85119	83206	CAAAAATGATTTCTTGTACA
85120	83207	ACAAAAATGATTTCTTGTAC
85121	83208	GACAAAAATGATTTCTTGTA
85122	83209	TGACAAAAATGATTTCTTGT
85123	83210	ATGACAAAAATGATTTCTTG
85124	83211	AATGACAAAAATGATTTCTT
85125	83212	AAATGACAAAAATGATTTCT
85126	83213	AAAATGACAAAAATGATTTC
85127	83214	TAAAATGACAAAAATGATTT
85128	83215	GTAAAATGACAAAAATGATT
85129	83216	AGTAAAATGACAAAAATGAT
85130	83217	AAGTAAAATGACAAAAATGA
85131	83218	AAAGTAAAATGACAAAAATG
85132	83219	AAAAGTAAAATGACAAAAAT
85133	83220	AAAAAGTAAAATGACAAAAA
85134	83221	AAAAAAGTAAAATGACAAAA
85135	83222	AAAAAAAGTAAAATGACAAA
85136	83223	GAAAAAAAGTAAAATGACAA
85137	83224	AGAAAAAAAGTAAAATGACA

134214	132301	GCCATCTTGCCTAGACTGGT
134215	132302	CGCCATCTTGCCTAGACTGG
134216	132303	TCGCCATCTTGCCTAGACTG
134217	132304	CTCGCCATCTTGCCTAGACT
134218	132305	TCTCGCCATCTTGCCTAGAC
134219	132306	ATCTCGCCATCTTGCCTAGA
134220	132307	GATCTCGCCATCTTGCCTAG
134221	132308	GGATCTCGCCATCTTGCCTA
134222	132309	GGGATCTCGCCATCTTGCCT
134223	132310	TGGGATCTCGCCATCTTGCC
134224	132311	ATGGGATCTCGCCATCTTGC
134225	132312	GATGGGATCTCGCCATCTTG
134226	132313	AGATGGGATCTCGCCATCTT
134227	132314	GAGATGGGATCTCGCCATCT
134228	132315	AGAGATGGGATCTCGCCATC
134229	132316	TAGAGATGGGATCTCGCCAT
134230	132317	GTAGAGATGGGATCTCGCCA
134231	132318	GGTAGAGATGGGATCTCGCC
134232	132319	TGGTAGAGATGGGATCTCGC
134233	132320	TTGGTAGAGATGGGATCTCG
134234	132321	TTTGGTAGAGATGGGATCTC
134235	132322	TTTTGGTAGAGATGGGATCT
134236	132323	TTTTTGGTAGAGATGGGATC
134237	132324	TTTTTTGGTAGAGATGGGAT
134238	132325	TTTTTTTGGTAGAGATGGGA
134239	132326	TTTTTTTTGGTAGAGATGGG
134240	132327	TTTTTTTTTGGTAGAGATGG
134241	132328	TTTTTTTTTTGGTAGAGATG
134242	132329	TTTTTTTTTTTGGTAGAGAT
134243	132330	TTTTTTTTTTTTGGTAGAGA
134244	132331	TTTTTTTTTTTTTGGTAGAG
134245	132332	TTTTTTTTTTTTTTGGTAGA
134246	132333	TTTTTTTTTTTTTTTGGTAG
134247	132334	TTTTTTTTTTTTTTTTGGTA
134248	132335	TTTTTTTTTTTTTTTTTGGT
134249	132336	TTTTTTTTTTTTTTTTTTGG
134250	132337	TTTTTTTTTTTTTTTTTTTG
134251	132338	TTTTTTTTTTTTTTTTTTTT
134252	132339	TTTTTTTTTTTTTTTTTTTT
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134259	132346	TTTTTTTTTTTTTTTTTTTT
134260	132347	TTTTTTTTTTTTTTTTTTTT
134261	132348	CTTTTTTTTTTTTTTTTTTT
134262	132349	GCTTTTTTTTTTTTTTTTTT
134263	132350	GGCTTTTTTTTTTTTTTTTT
134264	132351	GGGCTTTTTTTTTTTTTTTT
134265	132352	TGGGCTTTTTTTTTTTTTTT
134266	132353	CTGGGCTTTTTTTTTTTTTT
134267	132354	ACTGGGCTTTTTTTTTTTTT
134268	132355	GACTGGGCTTTTTTTTTTTT
134269	132356	TGACTGGGCTTTTTTTTTTT
134270	132357	ATGACTGGGCTTTTTTTTTT
134271	132358	CATGACTGGGCTTTTTTTTT
134272	132359	CCATGACTGGGCTTTTTTTT
134273	132360	ACCATGACTGGGCTTTTTTT
134274	132361	CACCATGACTGGGCTTTTTT
134275	132362	CCACCATGACTGGGCTTTTT
134276	132363	GCCACCATGACTGGGCTTTT
134277	132364	TGCCACCATGACTGGGCTTT
134278	132365	GTGCCACCATGACTGGGCTT
134279	132366	TGTGCCACCATGACTGGGCT
134280	132367	ATGTGCCACCATGACTGGGC
134281	132368	CATGTGCCACCATGACTGGG
134282	132369	GCATGTGCCACCATGACTGG
134283	132370	GGCATGTGCCACCATGACTG
134284	132371	AGGCATGTGCCACCATGACT

35991	34078	ACGGTCCATATAAGACAGCA
35992	34079	AACGGTCCATATAAGACAGC
35993	34080	AAACGGTCCATATAAGACAG
35994	34081	CAAACGGTCCATATAAGACA
35995	34082	ACAAACGGTCCATATAAGAC
35996	34083	CACAAACGGTCCATATAAGA
35997	34084	CCACAAACGGTCCATATAAG
35998	34085	ACCACAAACGGTCCATATAA
35999	34086	CACCACAAACGGTCCATATA
36000	34087	GCACCACAAACGGTCCATAT
36001	34088	GGCACCACAAACGGTCCATA
36002	34089	AGGCACCACAAACGGTCCAT
36003	34090	AAGGCACCACAAACGGTCCA
36004	34091	TAAGGCACCACAAACGGTCC
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36010	34097	TTCTTTTAAGGCACCACAAA
36011	34098	TTTCTTTTAAGGCACCACAA
36012	34099	ATTTCTTTTAAGGCACCACA
36013	34100	GATTTCTTTTAAGGCACCAC
36014	34101	TGATTTCTTTTAAGGCACCA
36015	34102	CTGATTTCTTTTAAGGCACC
36016	34103	CCTGATTTCTTTTAAGGCAC
36017	34104	CCCTGATTTCTTTTAAGGCA
36018	34105	ACCCTGATTTCTTTTAAGGC
36019	34106	TACCCTGATTTCTTTTAAGG
36020	34107	TTACCCTGATTTCTTTTAAG
36021	34108	GTTACCCTGATTTCTTTTAA
36022	34109	TGTTACCCTGATTTCTTTTA
36023	34110	ATGTTACCCTGATTTCTTTT
36024	34111	GATGTTACCCTGATTTCTTT
36025	34112	TGATGTTACCCTGATTTCTT
36026	34113	TTGATGTTACCCTGATTTCT
36027	34114	GTTGATGTTACCCTGATTTC
36028	34115	CGTTGATGTTACCCTGATTT
36029	34116	TCGTTGATGTTACCCTGATT
36030	34117	ATCGTTGATGTTACCCTGAT
36031	34118	AATCGTTGATGTTACCCTGA
36032	34119	TAATCGTTGATGTTACCCTG
36033	34120	GTAATCGTTGATGTTACCCT
36034	34121	AGTAATCGTTGATGTTACCC
36035	34122	CAGTAATCGTTGATGTTACC
36036	34123	TCAGTAATCGTTGATGTTAC
36037	34124	ATCAGTAATCGTTGATGTTA
36038	34125	AATCAGTAATCGTTGATGTT
36039	34126	TAATCAGTAATCGTTGATGT
36040	34127	GTAATCAGTAATCGTTGATG
36041	34128	TGTAATCAGTAATCGTTGAT
36042	34129	CTGTAATCAGTAATCGTTGA
36043	34130	TCTGTAATCAGTAATCGTTG
36044	34131	ATCTGTAATCAGTAATCGTT
36045	34132	AATCTGTAATCAGTAATCGT
36046	34133	TAATCTGTAATCAGTAATCG
36047	34134	GTAATCTGTAATCAGTAATC
36048	34135	AGTAATCTGTAATCAGTAAT
36049	34136	TAGTAATCTGTAATCAGTAA
36050	34137	ATAGTAATCTGTAATCAGTA
36051	34138	TATAGTAATCTGTAATCAGT
36052	34139	TTATAGTAATCTGTAATCAG
36053	34140	GTTATAGTAATCTGTAATCA
36054	34141	TGTTATAGTAATCTGTAATC
36055	34142	CTGTTATAGTAATCTGTAAT
36056	34143	TCTGTTATAGTAATCTGTAA
36057	34144	ATCTGTTATAGTAATCTGTA
36058	34145	TATCTGTTATAGTAATCTGT
36059	34146	GTATCTGTTATAGTAATCTG
36060	34147	TGTATCTGTTATAGTAATCT
36061	34148	TTGTATCTGTTATAGTAATC

85138	83225	CAGAAAAAAAGTAAAATGAC
85139	83226	ACAGAAAAAAAGTAAAATGA
85140	83227	AACAGAAAAAAAGTAAAATG
85141	83228	AAACAGAAAAAAAGTAAAAT
85142	83229	TAAACAGAAAAAAAGTAAAA
85143	83230	GTAAACAGAAAAAAAGTAAA
85144	83231	AGTAAACAGAAAAAAAGTAA
85145	83232	AAGTAAACAGAAAAAAAGTA
85146	83233	AAAGTAAACAGAAAAAAAGT
85147	83234	AAAAGTAAACAGAAAAAAAG
85148	83235	AAAAAGTAAACAGAAAAAAA
85149	83236	AAAAAAGTAAACAGAAAAAA
85150	83237	GAAAAAAGTAAACAGAAAAA
85151	83238	GGAAAAAAGTAAACAGAAAA
85152	83239	GGGAAAAAAGTAAACAGAAA
85153	83240	AGGGAAAAAAGTAAACAGAA
85154	83241	GAGGGAAAAAAGTAAACAGA
85155	83242	TGAGGGAAAAAAGTAAACAG
85156	83243	ATGAGGGAAAAAAGTAAACA
85157	83244	AATGAGGGAAAAAAGTAAAC
85158	83245	AAATGAGGGAAAAAAGTAAA
85159	83246	AAAATGAGGGAAAAAAGTAA
85160	83247	AAAAATGAGGGAAAAAAGTA
85161	83248	AAAAAATGAGGGAAAAAAGT
85162	83249	AAAAAAATGAGGGAAAAAAG
85163	83250	GAAAAAAATGAGGGAAAAAA
85164	83251	AGAAAAAAATGAGGGAAAAA
85165	83252	AAGAAAAAAATGAGGGAAAA
85166	83253	AAAGAAAAAAATGAGGGAAA
85167	83254	TAAAGAAAAAAATGAGGGAA
85168	83255	CTAAAGAAAAAAATGAGGGA
85169	83256	ACTAAAGAAAAAAATGAGGG
85170	83257	AACTAAAGAAAAAAATGAGG
85171	83258	AAACTAAAGAAAAAAATGAG
85172	83259	AAAACTAAAGAAAAAAATGA
85173	83260	AAAAACTAAAGAAAAAAATG
85174	83261	TAAAAACTAAAGAAAAAAAT
85175	83262	ATAAAAACTAAAGAAAAAAA
85176	83263	TATAAAAACTAAAGAAAAAA
85177	83264	GTATAAAAACTAAAGAAAAA
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85180	83267	AAAGTATAAAAACTAAAGAA
85181	83268	GAAAGTATAAAAACTAAAGA
85182	83269	GGAAAGTATAAAAACTAAAG
85183	83270	AGGAAAGTATAAAAACTAAA
85184	83271	AAGGAAAGTATAAAAACTAA
85185	83272	GAAGGAAAGTATAAAAACTA
85186	83273	TGAAGGAAAGTATAAAAACT
85187	83274	ATGAAGGAAAGTATAAAAAC
85188	83275	TATGAAGGAAAGTATAAAAA
85189	83276	ATATGAAGGAAAGTATAAAA
85190	83277	GATATGAAGGAAAGTATAAA
85191	83278	TGATATGAAGGAAAGTATAA
85192	83279	ATGATATGAAGGAAAGTATA
85193	83280	AATGATATGAAGGAAAGTAT
85194	83281	AAATGATATGAAGGAAAGTA
85195	83282	CAAATGATATGAAGGAAAGT
85196	83283	ACAAATGATATGAAGGAAAG
85197	83284	AACAAATGATATGAAGGAAA
85198	83285	GAACAAATGATATGAAGGAA
85199	83286	AGAACAAATGATATGAAGGA
85200	83287	CAGAACAAATGATATGAAGG
85201	83288	ACAGAACAAATGATATGAAG
85202	83289	GACAGAACAAATGATATGAA
85203	83290	TGACAGAACAAATGATATGA
85204	83291	CTGACAGAACAAATGATATG
85205	83292	CCTGACAGAACAAATGATAT
85206	83293	ACCTGACAGAACAAATGATA
85207	83294	CACCTGACAGAACAAATGAT
85208	83295	ACACCTGACAGAACAAATGA

134285	132372	CAGGCATGTGCCACCATGAC
134286	132373	ACAGGCATGTGCCACCATGA
134287	132374	TACAGGCATGTGCCACCATG
134288	132375	CTACAGGCATGTGCCACCAT
134289	132376	ACTACAGGCATGTGCCACCA
134290	132377	GACTACAGGCATGTGCCACC
134291	132378	GGACTACAGGCATGTGCCAC
134292	132379	GGGACTACAGGCATGTGCCA
134293	132380	TGGGACTACAGGCATGTGCC
134294	132381	GTGGGACTACAGGCATGTGC
134295	132382	GGTGGGACTACAGGCATGTG
134296	132383	AGGTGGGACTACAGGCATGT
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134298	132385	GTAGGTGGGACTACAGGCAT
134299	132386	TGTAGGTGGGACTACAGGCA
134300	132387	GTGTAGGTGGGACTACAGGC
134301	132388	TGTGTAGGTGGGACTACAGG
134302	132389	CTGTGTAGGTGGGACTACAG
134303	132390	CCTGTGTAGGTGGGACTACA
134304	132391	TCCTGTGTAGGTGGGACTAC
134305	132392	TTCCTGTGTAGGTGGGACTA
134306	132393	CTTCCTGTGTAGGTGGGACT
134307	132394	GCTTCCTGTGTAGGTGGGAC
134308	132395	AGCTTCCTGTGTAGGTGGGA
134309	132396	CAGCTTCCTGTGTAGGTGGG
134310	132397	TCAGCTTCCTGTGTAGGTGG
134311	132398	CTCAGCTTCCTGTGTAGGTG
134312	132399	TCTCAGCTTCCTGTGTAGGT
134313	132400	ATCTCAGCTTCCTGTGTAGG
134314	132401	CATCTCAGCTTCCTGTGTAG
134315	132402	CCATCTCAGCTTCCTGTGTA
134316	132403	CCCATCTCAGCTTCCTGTGT
134317	132404	TCCCATCTCAGCTTCCTGTG
134318	132405	CTCCCATCTCAGCTTCCTGT
134319	132406	CCTCCCATCTCAGCTTCCTG
134320	132407	TCCTCCCATCTCAGCTTCCT
134321	132408	ATCCTCCCATCTCAGCTTCC
134322	132409	GATCCTCCCATCTCAGCTTC
134323	132410	TGATCCTCCCATCTCAGCTT
134324	132411	GTGATCCTCCCATCTCAGCT
134325	132412	AGTGATCCTCCCATCTCAGC
134326	132413	AAGTGATCCTCCCATCTCAG
134327	132414	CAAGTGATCCTCCCATCTCA
134328	132415	TCAAGTGATCCTCCCATCTC
134329	132416	CTCAAGTGATCCTCCCATCT
134330	132417	ACTCAAGTGATCCTCCCATC
134331	132418	GACTCAAGTGATCCTCCCAT
134332	132419	GGACTCAAGTGATCCTCCCA
134333	132420	TGGACTCAAGTGATCCTCCC
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134335	132422	CCTGGACTCAAGTGATCCTC
134336	132423	TCCTGGACTCAAGTGATCCT
134337	132424	GTCCTGGACTCAAGTGATCC
134338	132425	AGTCCTGGACTCAAGTGATC
134339	132426	AAGTCCTGGACTCAAGTGAT
134340	132427	AAAGTCCTGGACTCAAGTGA
134341	132428	CAAAGTCCTGGACTCAAGTG
134342	132429	TCAAAGTCCTGGACTCAAGT
134343	132430	CTCAAAGTCCTGGACTCAAG
134344	132431	CCTCAAAGTCCTGGACTCAA
134345	132432	GCCTCAAAGTCCTGGACTCA
134346	132433	AGCCTCAAAGTCCTGGACTC
134347	132434	TAGCCTCAAAGTCCTGGACT
134348	132435	GTAGCCTCAAAGTCCTGGAC
134349	132436	TGTAGCCTCAAAGTCCTGGA
134350	132437	CTGTAGCCTCAAAGTCCTGG
134351	132438	ACTGTAGCCTCAAAGTCCTG
134352	132439	CACTGTAGCCTCAAAGTCCT
134353	132440	TCACTGTAGCCTCAAAGTCC
134354	132441	CTCACTGTAGCCTCAAAGTC
134355	132442	GCTCACTGTAGCCTCAAAGT

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36063	34150	TATTGTATCTGTTATAGTAA
36064	34151	TTATTGTATCTGTTATAGTA
36065	34152	ATTATTGTATCTGTTATAGT
36066	34153	TATTATTGTATCTGTTATAG
36067	34154	TTATTATTGTATCTGTTATA
36068	34155	ATTATTATTGTATCTGTTAT
36069	34156	AATTATTATTGTATCTGTTA
36070	34157	CAATTATTATTGTATCTGTT
36071	34158	ACAATTATTATTGTATCTGT
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36073	34160	TTACAATTATTATTGTATCT
36074	34161	TTTACAATTATTATTGTATC
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36077	34164	TAATTTACAATTATTATTGT
36078	34165	ATAATTTACAATTATTATTG
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36088	34175	ATTGTAAATAATAATTTACA
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36092	34179	TACAATTGTAAATAATAATT
36093	34180	TTACAATTGTAAATAATAAT
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36106	34193	AAAAGATTGTATTTTACAAT
36107	34194	GAAAAGATTGTATTTTACAA
36108	34195	AGAAAAGATTGTATTTTACA
36109	34196	AAGAAAAGATTGTATTTTAC
36110	34197	AAAGAAAAGATTGTATTTTA
36111	34198	TAAAGAAAAGATTGTATTTT
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36113	34200	AATAAAGAAAAGATTGTATT
36114	34201	TAATAAAGAAAAGATTGTAT
36115	34202	ATAATAAAGAAAAGATTGTA
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36121	34208	TTGTAAATAATAAAGAAAAG
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36123	34210	AATTGTAAATAATAAAGAAA
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36125	34212	ATAATTGTAAATAATAAAGA
36126	34213	AATAATTGTAAATAATAAAG
36127	34214	CAATAATTGTAAATAATAAA
36128	34215	ACAATAATTGTAAATAATAA
36129	34216	TACAATAATTGTAAATAATA
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36131	34218	TTTACAATAATTGTAAATAA
36132	34219	TTTTACAATAATTGTAAATA

85209	83296	AACACCTGACAGAACAAATG
85210	83297	GAACACCTGACAGAACAAAT
85211	83298	GGAACACCTGACAGAACAAA
85212	83299	GGGAACACCTGACAGAACAA
85213	83300	AGGGAACACCTGACAGAACA
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85215	83302	CCAGGGAACACCTGACAGAA
85216	83303	GCCAGGGAACACCTGACAGA
85217	83304	GGCCAGGGAACACCTGACAG
85218	83305	TGGCCAGGGAACACCTGACA
85219	83306	ATGGCCAGGGAACACCTGAC
85220	83307	GATGGCCAGGGAACACCTGA
85221	83308	CGATGGCCAGGGAACACCTG
85222	83309	GCGATGGCCAGGGAACACCT
85223	83310	GGCGATGGCCAGGGAACACC
85224	83311	AGGCGATGGCCAGGGAACAC
85225	83312	AAGGCGATGGCCAGGGAACA
85226	83313	CAAGGCGATGGCCAGGGAAC
85227	83314	GCAAGGCGATGGCCAGGGAA
85228	83315	GGCAAGGCGATGGCCAGGGA
85229	83316	GGGCAAGGCGATGGCCAGGG
85230	83317	TGGGCAAGGCGATGGCCAGG
85231	83318	ATGGGCAAGGCGATGGCCAG
85232	83319	GATGGGCAAGGCGATGGCCA
85233	83320	AGATGGGCAAGGCGATGGCC
85234	83321	GAGATGGGCAAGGCGATGGC
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85236	83323	AGGAGATGGGCAAGGCGATG
85237	83324	AAGGAGATGGGCAAGGCGAT
85238	83325	GAAGGAGATGGGCAAGGCGA
85239	83326	GGAAGGAGATGGGCAAGGCG
85240	83327	AGGAAGGAGATGGGCAAGGC
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85243	83330	GAGAGGAAGGAGATGGGCAA
85244	83331	CGAGAGGAAGGAGATGGGCA
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85252	83339	AAGGTGGGCGAGAGGAAGGA
85253	83340	GAAGGTGGGCGAGAGGAAGG
85254	83341	AGAAGGTGGGCGAGAGGAAG
85255	83342	GAGAAGGTGGGCGAGAGGAA
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85258	83345	AGCGAGAAGGTGGGCGAGAG
85259	83346	TAGCGAGAAGGTGGGCGAGA
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85273	83360	TGGGACCTGACTGGTAGCGA
85274	83361	TTGGGACCTGACTGGTAGCG
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85276	83363	AGTTGGGACCTGACTGGTAG
85277	83364	GAGTTGGGACCTGACTGGTA
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134356	132443	AGCTCACTGTAGCCTCAAAG
134357	132444	TAGCTCACTGTAGCCTCAAA
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134359	132446	GATAGCTCACTGTAGCCTCA
134360	132447	TGATAGCTCACTGTAGCCTC
134361	132448	ATGATAGCTCACTGTAGCCT
134362	132449	CATGATAGCTCACTGTAGCC
134363	132450	CCATGATAGCTCACTGTAGC
134364	132451	GCCATGATAGCTCACTGTAG
134365	132452	TGCCATGATAGCTCACTGTA
134366	132453	GTGCCATGATAGCTCACTGT
134367	132454	GGTGCCATGATAGCTCACTG
134368	132455	TGGTGCCATGATAGCTCACT
134369	132456	GTGGTGCCATGATAGCTCAC
134370	132457	AGTGGTGCCATGATAGCTCA
134371	132458	CAGTGGTGCCATGATAGCTC
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134373	132460	TACAGTGGTGCCATGATAGC
134374	132461	TTACAGTGGTGCCATGATAG
134375	132462	ATTACAGTGGTGCCATGATA
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134377	132464	GGATTACAGTGGTGCCATGA
134378	132465	TGGATTACAGTGGTGCCATG
134379	132466	CTGGATTACAGTGGTGCCAT
134380	132467	GCTGGATTACAGTGGTGCCA
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134382	132469	AGGCTGGATTACAGTGGTGC
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134385	132472	CCCAGGCTGGATTACAGTGG
134386	132473	ACCCAGGCTGGATTACAGTG
134387	132474	CACCCAGGCTGGATTACAGT
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134400	132487	GGTCTTGCTCTGTCACCCAG
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134406	132493	AGACAGGGTCTTGCTCTGTC
134407	132494	GAGACAGGGTCTTGCTCTGT
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134412	132499	AAATAGAGACAGGGTCTTGC
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134415	132502	TTTAAATAGAGACAGGGTCT
134416	132503	TTTTAAATAGAGACAGGGTC
134417	132504	TTTTTAAATAGAGACAGGGT
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134421	132508	CTTTTTTTTAAATAGAGACA
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134425	132512	TTTTCTTTTTTTTAAATAGA
134426	132513	GTTTTCTTTTTTTTAAATAG

36133	34220	ATTTTACAATAATTGTAAAT
36134	34221	TATTTTACAATAATTGTAAA
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36136	34223	TGTATTTTACAATAATTGTA
36137	34224	TTGTATTTTACAATAATTGT
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36140	34227	AGATTGTATTTTACAATAAT
36141	34228	CAGATTGTATTTTACAATAA
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36145	34232	TAATCAGATTGTATTTTACA
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36147	34234	TGTAATCAGATTGTATTTTA
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36156	34243	ATAGTAATCTGTAATCAGAT
36157	34244	TATAGTAATCTGTAATCAGA
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36159	34246	GTTATAGTAATCTGTAATCA
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36183	34270	AACTTTTCCACTATTATTGT
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36193	34280	AATATTTTCAAACTTTTCCA
36194	34281	CAATATTTTCAAACTTTTCC
36195	34282	ACAATATTTTCAAACTTTTC
36196	34283	CACAATATTTTCAAACTTTT
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36198	34285	CTCACAATATTTTCAAACTT
36199	34286	TCTCACAATATTTTCAAACT
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36201	34288	AATCTCACAATATTTTCAAA
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85280	83367	AGAGAGTTGGGACCTGACTG
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85283	83370	GGAAGAGAGTTGGGACCTGA
85284	83371	TGGAAGAGAGTTGGGACCTG
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85310	83397	GGCCGTGTAGGGGTGGCTGC
85311	83398	CGGCCGTGTAGGGGTGGCTG
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85313	83400	GGCGGCCGTGTAGGGGTGGC
85314	83401	GGGCGGCCGTGTAGGGGTGG
85315	83402	AGGGCGGCCGTGTAGGGGTG
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85317	83404	GGAGGGCGGCCGTGTAGGGG
85318	83405	TGGAGGGCGGCCGTGTAGGG
85319	83406	CTGGAGGGCGGCCGTGTAGG
85320	83407	CCTGGAGGGCGGCCGTGTAG
85321	83408	GCCTGGAGGGCGGCCGTGTA
85322	83409	GGCCTGGAGGGCGGCCGTGT
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85324	83411	GGGGCCTGGAGGGCGGCCGT
85325	83412	GGGGGCCTGGAGGGCGGCCG
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85333	83420	GCCGCGAGGGGGGCCTGGAG
85334	83421	GGCCGCGAGGGGGGCCTGGA
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85337	83424	GATGGCCGCGAGGGGGGCCT
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85339	83426	TGGATGGCCGCGAGGGGGGC
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85341	83428	TCTGGATGGCCGCGAGGGGG
85342	83429	GTCTGGATGGCCGCGAGGGG
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134427	132514	TGTTTTCTTTTTTTTAAATA
134428	132515	ATGTTTTCTTTTTTTTAAAT
134429	132516	TATGTTTTCTTTTTTTTAAA
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134431	132518	CTTATGTTTTCTTTTTTTTA
134432	132519	TCTTATGTTTTCTTTTTTTT
134433	132520	TTCTTATGTTTTCTTTTTTT
134434	132521	TTTCTTATGTTTTCTTTTTT
134435	132522	CTTTCTTATGTTTTCTTTTT
134436	132523	TCTTTCTTATGTTTTCTTTT
134437	132524	TTCTTTCTTATGTTTTCTTT
134438	132525	ATTCTTTCTTATGTTTTCTT
134439	132526	AATTCTTTCTTATGTTTTCT
134440	132527	CAATTCTTTCTTATGTTTTC
134441	132528	ACAATTCTTTCTTATGTTTT
134442	132529	AACAATTCTTTCTTATGTTT
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134444	132531	AAAACAATTCTTTCTTATGT
134445	132532	CAAAACAATTCTTTCTTATG
134446	132533	ACAAAACAATTCTTTCTTAT
134447	132534	AACAAAACAATTCTTTCTTA
134448	132535	GAACAAAACAATTCTTTCTT
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134450	132537	TAGAACAAAACAATTCTTTC
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134452	132539	CATAGAACAAAACAATTCTT
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134454	132541	GGCATAGAACAAAACAATTC
134455	132542	TGGCATAGAACAAAACAATT
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134458	132545	TGATGGCATAGAACAAAACA
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134460	132547	TATGATGGCATAGAACAAAA
134461	132548	TTATGATGGCATAGAACAAA
134462	132549	CTTATGATGGCATAGAACAA
134463	132550	GCTTATGATGGCATAGAACA
134464	132551	GGCTTATGATGGCATAGAAC
134465	132552	TGGCTTATGATGGCATAGAA
134466	132553	ATGGCTTATGATGGCATAGA
134467	132554	TATGGCTTATGATGGCATAG
134468	132555	TTATGGCTTATGATGGCATA
134469	132556	ATTATGGCTTATGATGGCAT
134470	132557	AATTATGGCTTATGATGGCA
134471	132558	AAATTATGGCTTATGATGGC
134472	132559	TAAATTATGGCTTATGATGG
134473	132560	TTAAATTATGGCTTATGATG
134474	132561	ATTAAATTATGGCTTATGAT
134475	132562	GATTAAATTATGGCTTATGA
134476	132563	AGATTAAATTATGGCTTATG
134477	132564	CAGATTAAATTATGGCTTAT
134478	132565	GCAGATTAAATTATGGCTTA
134479	132566	AGCAGATTAAATTATGGCTT
134480	132567	AAGCAGATTAAATTATGGCT
134481	132568	TAAGCAGATTAAATTATGGC
134482	132569	TTAAGCAGATTAAATTATGG
134483	132570	CTTAAGCAGATTAAATTATG
134484	132571	GCTTAAGCAGATTAAATTAT
134485	132572	TGCTTAAGCAGATTAAATTA
134486	132573	ATGCTTAAGCAGATTAAATT
134487	132574	CATGCTTAAGCAGATTAAAT
134488	132575	ACATGCTTAAGCAGATTAAA
134489	132576	AACATGCTTAAGCAGATTAA
134490	132577	GAACATGCTTAAGCAGATTA
134491	132578	AGAACATGCTTAAGCAGATT
134492	132579	AAGAACATGCTTAAGCAGAT
134493	132580	GAAGAACATGCTTAAGCAGA
134494	132581	TGAAGAACATGCTTAAGCAG
134495	132582	ATGAAGAACATGCTTAAGCA
134496	132583	AATGAAGAACATGCTTAAGC
134497	132584	TAATGAAGAACATGCTTAAG

36204	34291	ATAAATCTCACAATATTTTC
36205	34292	CATAAATCTCACAATATTTT
36206	34293	TCATAAATCTCACAATATTT
36207	34294	CTCATAAATCTCACAATATT
36208	34295	TCTCATAAATCTCACAATAT
36209	34296	TTCTCATAAATCTCACAATA
36210	34297	ATTCTCATAAATCTCACAAT
36211	34298	CATTCTCATAAATCTCACAA
36212	34299	ACATTCTCATAAATCTCACA
36213	34300	CACATTCTCATAAATCTCAC
36214	34301	TCACATTCTCATAAATCTCA
36215	34302	GTCACATTCTCATAAATCTC
36216	34303	TGTCACATTCTCATAAATCT
36217	34304	GTGTCACATTCTCATAAATC
36218	34305	TGTGTCACATTCTCATAAAT
36219	34306	CTGTGTCACATTCTCATAAA
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36221	34308	GCCTGTGTCACATTCTCATA
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36223	34310	GCGCCTGTGTCACATTCTCA
36224	34311	TGCGCCTGTGTCACATTCTC
36225	34312	TTGCGCCTGTGTCACATTCT
36226	34313	TTTGCGCCTGTGTCACATTC
36227	34314	CTTTGCGCCTGTGTCACATT
36228	34315	TCTTTGCGCCTGTGTCACAT
36229	34316	CTCTTTGCGCCTGTGTCACA
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36232	34319	GCTCTCTTTGCGCCTGTGTC
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36235	34322	TGTGCTCTCTTTGCGCCTGT
36236	34323	ATGTGCTCTCTTTGCGCCTG
36237	34324	CATGTGCTCTCTTTGCGCCT
36238	34325	ACATGTGCTCTCTTTGCGCC
36239	34326	AACATGTGCTCTCTTTGCGC
36240	34327	TAACATGTGCTCTCTTTGCG
36241	34328	GTAACATGTGCTCTCTTTGC
36242	34329	AGTAACATGTGCTCTCTTTG
36243	34330	CAGTAACATGTGCTCTCTTT
36244	34331	CCAGTAACATGTGCTCTCTT
36245	34332	TCCAGTAACATGTGCTCTCT
36246	34333	TTCCAGTAACATGTGCTCTC
36247	34334	TTTCCAGTAACATGTGCTCT
36248	34335	ATTTCCAGTAACATGTGCTC
36249	34336	TATTTCCAGTAACATGTGCT
36250	34337	GTATTTCCAGTAACATGTGC
36251	34338	CGTATTTCCAGTAACATGTG
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36253	34340	GCCGTATTTCCAGTAACATG
36254	34341	TGCCGTATTTCCAGTAACAT
36255	34342	GTGCCGTATTTCCAGTAACA
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36257	34344	TAGTGCCGTATTTCCAGTAA
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36259	34346	ATTAGTGCCGTATTTCCAGT
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36261	34348	CCATTAGTGCCGTATTTCCA
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36271	34358	TCGGGCAAGTCCATTAGTGC
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85351	83438	GAGACGGGGGTCTGGATGGC
85352	83439	TGAGACGGGGGTCTGGATGG
85353	83440	GTGAGACGGGGGTCTGGATG
85354	83441	GGTGAGACGGGGGTCTGGAT
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85359	83446	AGAGGGGTGAGACGGGGGTC
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85366	83453	CATGAGCAGAGGGGTGAGAC
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85374	83461	TGGAGAACCATGAGCAGAGG
85375	83462	CTGGAGAACCATGAGCAGAG
85376	83463	GCTGGAGAACCATGAGCAGA
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85379	83466	GGAGCTGGAGAACCATGAGC
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85383	83470	GACAGGAGCTGGAGAACCAT
85384	83471	AGACAGGAGCTGGAGAACCA
85385	83472	GAGACAGGAGCTGGAGAACC
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85394	83481	GGCATAGTAGAGACAGGAGC
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85401	83488	GCGTTTAGGCATAGTAGAGA
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85403	83490	ATGCGTTTAGGCATAGTAGA
85404	83491	CATGCGTTTAGGCATAGTAG
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85406	83493	GACATGCGTTTAGGCATAGT
85407	83494	AGACATGCGTTTAGGCATAG
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85410	83497	TGAAGACATGCGTTTAGGCA
85411	83498	CTGAAGACATGCGTTTAGGC
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85413	83500	TTCTGAAGACATGCGTTTAG
85414	83501	CTTCTGAAGACATGCGTTTA
85415	83502	CCTTCTGAAGACATGCGTTT
85416	83503	ACCTTCTGAAGACATGCGTT
85417	83504	TACCTTCTGAAGACATGCGT
85418	83505	GTACCTTCTGAAGACATGCG
85419	83506	TGTACCTTCTGAAGACATGC
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85421	83508	ATTGTACCTTCTGAAGACAT

134498	132585	TTAATGAAGAACATGCTTAA
134499	132586	TTTAATGAAGAACATGCTTA
134500	132587	ATTTAATGAAGAACATGCTT
134501	132588	GATTTAATGAAGAACATGCT
134502	132589	AGATTTAATGAAGAACATGC
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134505	132592	TGCAGATTTAATGAAGAACA
134506	132593	CTGCAGATTTAATGAAGAAC
134507	132594	ACTGCAGATTTAATGAAGAA
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134510	132597	ATCACTGCAGATTTAATGAA
134511	132598	AATCACTGCAGATTTAATGA
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134514	132601	ATAAATCACTGCAGATTTAA
134515	132602	AATAAATCACTGCAGATTTA
134516	132603	AAATAAATCACTGCAGATTT
134517	132604	CAAATAAATCACTGCAGATT
134518	132605	TCAAATAAATCACTGCAGAT
134519	132606	TTCAAATAAATCACTGCAGA
134520	132607	ATTCAAATAAATCACTGCAG
134521	132608	AATTCAAATAAATCACTGCA
134522	132609	TAATTCAAATAAATCACTGC
134523	132610	ATAATTCAAATAAATCACTG
134524	132611	AATAATTCAAATAAATCACT
134525	132612	TAATAATTCAAATAAATCAC
134526	132613	CTAATAATTCAAATAAATCA
134527	132614	TCTAATAATTCAAATAAATC
134528	132615	GTCTAATAATTCAAATAAAT
134529	132616	AGTCTAATAATTCAAATAAA
134530	132617	AAGTCTAATAATTCAAATAA
134531	132618	AAAGTCTAATAATTCAAATA
134532	132619	GAAAGTCTAATAATTCAAAT
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134535	132622	TTTGAAAGTCTAATAATTCA
134536	132623	CTTTGAAAGTCTAATAATTC
134537	132624	GCTTTGAAAGTCTAATAATT
134538	132625	GGCTTTGAAAGTCTAATAAT
134539	132626	AGGCTTTGAAAGTCTAATAA
134540	132627	AAGGCTTTGAAAGTCTAATA
134541	132628	TAAGGCTTTGAAAGTCTAAT
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134544	132631	TAATAAGGCTTTGAAAGTCT
134545	132632	ATAATAAGGCTTTGAAAGTC
134546	132633	TATAATAAGGCTTTGAAAGT
134547	132634	ATATAATAAGGCTTTGAAAG
134548	132635	GATATAATAAGGCTTTGAAA
134549	132636	TGATATAATAAGGCTTTGAA
134550	132637	TTGATATAATAAGGCTTTGA
134551	132638	TTTGATATAATAAGGCTTTG
134552	132639	ATTTGATATAATAAGGCTTT
134553	132640	TATTTGATATAATAAGGCTT
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134558	132645	GTTTATATTTGATATAATAA
134559	132646	TGTTTATATTTGATATAATA
134560	132647	TTGTTTATATTTGATATAAT
134561	132648	TTTGTTTATATTTGATATAA
134562	132649	TTTTGTTTATATTTGATATA
134563	132650	ATTTTGTTTATATTTGATAT
134564	132651	AATTTTGTTTATATTTGATA
134565	132652	AAATTTTGTTTATATTTGAT
134566	132653	CAAATTTTGTTTATATTTGA
134567	132654	TCAAATTTTGTTTATATTTG
134568	132655	TTCAAATTTTGTTTATATTT

36275	34362	CGAGTCGGGCAAGTCCATTA
36276	34363	CCGAGTCGGGCAAGTCCATT
36277	34364	CCCGAGTCGGGCAAGTCCAT
36278	34365	CCCCGAGTCGGGCAAGTCCA
36279	34366	ACCCCGAGTCGGGCAAGTCC
36280	34367	AACCCCGAGTCGGGCAAGTC
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36282	34369	GAAACCCCGAGTCGGGCAAG
36283	34370	GGAAACCCCGAGTCGGGCAA
36284	34371	TGGAAACCCCGAGTCGGGCA
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36288	34375	TCTGTGGAAACCCCGAGTCG
36289	34376	GTCTGTGGAAACCCCGAGTC
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36300	34387	ACAAGCTGACCGTCTGTGGA
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36317	34404	CAGATGCTGCATTTTTGACA
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36319	34406	CACAGATGCTGCATTTTTGA
36320	34407	TCACAGATGCTGCATTTTTG
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36322	34409	ATTCACAGATGCTGCATTTT
36323	34410	AATTCACAGATGCTGCATTT
36324	34411	AAATTCACAGATGCTGCATT
36325	34412	GAAATTCACAGATGCTGCAT
36326	34413	TGAAATTCACAGATGCTGCA
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36333	34420	GCTTTATTGAAATTCACAGA
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85422	83509	TATTGTACCTTCTGAAGACA
85423	83510	GTATTGTACCTTCTGAAGAC
85424	83511	GGTATTGTACCTTCTGAAGA
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85450	83537	GACAAACAAAAACATGAACA
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85452	83539	AAGACAAACAAAAACATGAA
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85462	83549	GAGTTAAACAAAGACAAACA
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85465	83552	TAGGAGTTAAACAAAGACAA
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85468	83555	ACATAGGAGTTAAACAAAGA
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85470	83557	TCACATAGGAGTTAAACAAA
85471	83558	CTCACATAGGAGTTAAACAA
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85474	83561	AAACTCACATAGGAGTTAAA
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85476	83563	ATAAACTCACATAGGAGTTA
85477	83564	TATAAACTCACATAGGAGTT
85478	83565	TTATAAACTCACATAGGAGT
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134569	132656	CTTCAAATTTTGTTTATATT
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134571	132658	TACTTCAAATTTTGTTTATA
134572	132659	GTACTTCAAATTTTGTTTAT
134573	132660	TGTACTTCAAATTTTGTTTA
134574	132661	ATGTACTTCAAATTTTGTTT
134575	132662	AATGTACTTCAAATTTTGTT
134576	132663	GAATGTACTTCAAATTTTGT
134577	132664	AGAATGTACTTCAAATTTTG
134578	132665	AAGAATGTACTTCAAATTTT
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134580	132667	ATAAGAATGTACTTCAAATT
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134583	132670	TTTATAAGAATGTACTTCAA
134584	132671	GTTTATAAGAATGTACTTCA
134585	132672	AGTTTATAAGAATGTACTTC
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134591	132678	TGTTGTAGTTTATAAGAATG
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134593	132680	TTTGTTGTAGTTTATAAGAA
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134595	132682	AGTTTGTTGTAGTTTATAAG
134596	132683	AAGTTTGTTGTAGTTTATAA
134597	132684	TAAGTTTGTTGTAGTTTATA
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134599	132686	TGTAAGTTTGTTGTAGTTTA
134600	132687	ATGTAAGTTTGTTGTAGTTT
134601	132688	TATGTAAGTTTGTTGTAGTT
134602	132689	CTATGTAAGTTTGTTGTAGT
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134604	132691	TTCTATGTAAGTTTGTTGTA
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134607	132694	CACTTCTATGTAAGTTTGTT
134608	132695	ACACTTCTATGTAAGTTTGT
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134611	132698	TTAACACTTCTATGTAAGTT
134612	132699	ATTAACACTTCTATGTAAGT
134613	132700	AATTAACACTTCTATGTAAG
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134616	132703	TAAAATTAACACTTCTATGT
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134618	132705	TATAAAATTAACACTTCTAT
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134620	132707	AGTATAAAATTAACACTTCT
134621	132708	GAGTATAAAATTAACACTTC
134622	132709	TGAGTATAAAATTAACACTT
134623	132710	ATGAGTATAAAATTAACACT
134624	132711	GATGAGTATAAAATTAACAC
134625	132712	AGATGAGTATAAAATTAACA
134626	132713	AAGATGAGTATAAAATTAAC
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134631	132718	CAGGGAAGATGAGTATAAAA
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134633	132720	TTCAGGGAAGATGAGTATAA
134634	132721	GTTCAGGGAAGATGAGTATA
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134636	132723	TTGTTCAGGGAAGATGAGTA
134637	132724	ATTGTTCAGGGAAGATGAGT
134638	132725	AATTGTTCAGGGAAGATGAG
134639	132726	AAATTGTTCAGGGAAGATGA

36346	34433	TTTATTCTGCTTTGCTTTAT
36347	34434	TTTTATTCTGCTTTGCTTTA
36348	34435	ATTTTATTCTGCTTTGCTTT
36349	34436	CATTTTATTCTGCTTTGCTT
36350	34437	TCATTTTATTCTGCTTTGCT
36351	34438	CTCATTTTATTCTGCTTTGC
36352	34439	CCTCATTTTATTCTGCTTTG
36353	34440	ACCTCATTTTATTCTGCTTT
36354	34441	TACCTCATTTTATTCTGCTT
36355	34442	ATACCTCATTTTATTCTGCT
36356	34443	CATACCTCATTTTATTCTGC
36357	34444	GCATACCTCATTTTATTCTG
36358	34445	TGCATACCTCATTTTATTCT
36359	34446	ATGCATACCTCATTTTATTC
36360	34447	CATGCATACCTCATTTTATT
36361	34448	ACATGCATACCTCATTTTAT
36362	34449	TACATGCATACCTCATTTTA
36363	34450	ATACATGCATACCTCATTTT
36364	34451	AATACATGCATACCTCATTT
36365	34452	CAATACATGCATACCTCATT
36366	34453	GCAATACATGCATACCTCAT
36367	34454	GGCAATACATGCATACCTCA
36368	34455	TGGCAATACATGCATACCTC
36369	34456	ATGGCAATACATGCATACCT
36370	34457	GATGGCAATACATGCATACC
36371	34458	TGATGGCAATACATGCATAC
36372	34459	GTGATGGCAATACATGCATA
36373	34460	TGTGATGGCAATACATGCAT
36374	34461	ATGTGATGGCAATACATGCA
36375	34462	CATGTGATGGCAATACATGC
36376	34463	ACATGTGATGGCAATACATG
36377	34464	TACATGTGATGGCAATACAT
36378	34465	GTACATGTGATGGCAATACA
36379	34466	TGTACATGTGATGGCAATAC
36380	34467	GTGTACATGTGATGGCAATA
36381	34468	AGTGTACATGTGATGGCAAT
36382	34469	TAGTGTACATGTGATGGCAA
36383	34470	CTAGTGTACATGTGATGGCA
36384	34471	ACTAGTGTACATGTGATGGC
36385	34472	TACTAGTGTACATGTGATGG
36386	34473	TTACTAGTGTACATGTGATG
36387	34474	TTTACTAGTGTACATGTGAT
36388	34475	TTTTACTAGTGTACATGTGA
36389	34476	ATTTTACTAGTGTACATGTG
36390	34477	TATTTTACTAGTGTACATGT
36391	34478	GTATTTTACTAGTGTACATG
36392	34479	CGTATTTTACTAGTGTACAT
36393	34480	ACGTATTTTACTAGTGTACA
36394	34481	AACGTATTTTACTAGTGTAC
36395	34482	AAACGTATTTTACTAGTGTA
36396	34483	AAAACGTATTTTACTAGTGT
36397	34484	AAAAACGTATTTTACTAGTG
36398	34485	AAAAAACGTATTTTACTAGT
36399	34486	AAAAAAACGTATTTTACTAG
36400	34487	AAAAAAAACGTATTTTACTA
36401	34488	AAAAAAAAACGTATTTTACT
36402	34489	AAAAAAAAAACGTATTTTAC
36403	34490	GAAAAAAAAAACGTATTTTA
36404	34491	TGAAAAAAAAAACGTATTTT
36405	34492	CTGAAAAAAAAAACGTATTT
36406	34493	ACTGAAAAAAAAAACGTATT
36407	34494	TACTGAAAAAAAAAACGTAT
36408	34495	CTACTGAAAAAAAAAACGTA
36409	34496	CCTACTGAAAAAAAAAACGT
36410	34497	ACCTACTGAAAAAAAAAACG
36411	34498	CACCTACTGAAAAAAAAAAC
36412	34499	CCACCTACTGAAAAAAAAAA
36413	34500	TCCACCTACTGAAAAAAAAA
36414	34501	ATCCACCTACTGAAAAAAAA
36415	34502	GATCCACCTACTGAAAAAAA
36416	34503	TGATCCACCTACTGAAAAAA

85493	83580	GAAACTATTTTGTAATTATA
85494	83581	GGAAACTATTTTGTAATTAT
85495	83582	AGGAAACTATTTTGTAATTA
85496	83583	GAGGAAACTATTTTGTAATT
85497	83584	AGAGGAAACTATTTTGTAAT
85498	83585	AAGAGGAAACTATTTTGTAA
85499	83586	GAAGAGGAAACTATTTTGTA
85500	83587	TGAAGAGGAAACTATTTTGT
85501	83588	ATGAAGAGGAAACTATTTTG
85502	83589	AATGAAGAGGAAACTATTTT
85503	83590	TAATGAAGAGGAAACTATTT
85504	83591	ATAATGAAGAGGAAACTATT
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85506	83593	AAATAATGAAGAGGAAACTA
85507	83594	TAAATAATGAAGAGGAAACT
85508	83595	TTAAATAATGAAGAGGAAAC
85509	83596	ATTAAATAATGAAGAGGAAA
85510	83597	TATTAAATAATGAAGAGGAA
85511	83598	TTATTAAATAATGAAGAGGA
85512	83599	GTTATTAAATAATGAAGAGG
85513	83600	GGTTATTAAATAATGAAGAG
85514	83601	AGGTTATTAAATAATGAAGA
85515	83602	TAGGTTATTAAATAATGAAG
85516	83603	ATAGGTTATTAAATAATGAA
85517	83604	TATAGGTTATTAAATAATGA
85518	83605	TTATAGGTTATTAAATAATG
85519	83606	ATTATAGGTTATTAAATAAT
85520	83607	AATTATAGGTTATTAAATAA
85521	83608	AAATTATAGGTTATTAAATA
85522	83609	GAAATTATAGGTTATTAAAT
85523	83610	AGAAATTATAGGTTATTAAA
85524	83611	CAGAAATTATAGGTTATTAA
85525	83612	ACAGAAATTATAGGTTATTA
85526	83613	CACAGAAATTATAGGTTATT
85527	83614	ACACAGAAATTATAGGTTAT
85528	83615	AACACAGAAATTATAGGTTA
85529	83616	AAACACAGAAATTATAGGTT
85530	83617	AAAACACAGAAATTATAGGT
85531	83618	TAAAACACAGAAATTATAGG
85532	83619	TTAAAACACAGAAATTATAG
85533	83620	GTTAAAACACAGAAATTATA
85534	83621	AGTTAAAACACAGAAATTAT
85535	83622	AAGTTAAAACACAGAAATTA
85536	83623	AAAGTTAAAACACAGAAATT
85537	83624	TAAAGTTAAAACACAGAAAT
85538	83625	CTAAAGTTAAAACACAGAAA
85539	83626	ACTAAAGTTAAAACACAGAA
85540	83627	AACTAAAGTTAAAACACAGA
85541	83628	AAACTAAAGTTAAAACACAG
85542	83629	TAAACTAAAGTTAAAACACA
85543	83630	ATAAACTAAAGTTAAAACAC
85544	83631	AATAAACTAAAGTTAAAACA
85545	83632	TAATAAACTAAAGTTAAAAC
85546	83633	TTAATAAACTAAAGTTAAAA
85547	83634	TTTAATAAACTAAAGTTAAA
85548	83635	TTTTAATAAACTAAAGTTAA
85549	83636	GTTTTAATAAACTAAAGTTA
85550	83637	AGTTTTAATAAACTAAAGTT
85551	83638	TAGTTTTAATAAACTAAAGT
85552	83639	ATAGTTTTAATAAACTAAAG
85553	83640	AATAGTTTTAATAAACTAAA
85554	83641	AAATAGTTTTAATAAACTAA
85555	83642	GAAATAGTTTTAATAAACTA
85556	83643	AGAAATAGTTTTAATAAACT
85557	83644	TAGAAATAGTTTTAATAAAC
85558	83645	ATAGAAATAGTTTTAATAAA
85559	83646	AATAGAAATAGTTTTAATAA
85560	83647	TAATAGAAATAGTTTTAATA
85561	83648	TTAATAGAAATAGTTTTAAT
85562	83649	GTTAATAGAAATAGTTTTAA
85563	83650	GGTTAATAGAAATAGTTTTA

134640	132727	TAAATTGTTCAGGGAAGATG
134641	132728	ATAAATTGTTCAGGGAAGAT
134642	132729	TATAAATTGTTCAGGGAAGA
134643	132730	ATATAAATTGTTCAGGGAAG
134644	132731	AATATAAATTGTTCAGGGAA
134645	132732	AAATATAAATTGTTCAGGGA
134646	132733	AAAATATAAATTGTTCAGGG
134647	132734	TAAAATATAAATTGTTCAGG
134648	132735	ATAAAATATAAATTGTTCAG
134649	132736	TATAAAATATAAATTGTTCA
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134656	132743	ATATATTTATAAAATATAAA
134657	132744	AATATATTTATAAAATATAA
134658	132745	TAATATATTTATAAAATATA
134659	132746	TTAATATATTTATAAAATAT
134660	132747	TTTAATATATTTATAAAATA
134661	132748	ATTTAATATATTTATAAAAT
134662	132749	TATTTAATATATTTATAAAA
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134665	132752	ATATATTTAATATATTTATA
134666	132753	AATATATTTAATATATTTAT
134667	132754	CAATATATTTAATATATTTA
134668	132755	ACAATATATTTAATATATTT
134669	132756	GACAATATATTTAATATATT
134670	132757	TGACAATATATTTAATATAT
134671	132758	ATGACAATATATTTAATATA
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134675	132762	ATTTATGACAATATATTTAA
134676	132763	AATTTATGACAATATATTTA
134677	132764	AAATTTATGACAATATATTT
134678	132765	AAAATTTATGACAATATATT
134679	132766	GAAAATTTATGACAATATAT
134680	132767	AGAAAATTTATGACAATATA
134681	132768	GAGAAAATTTATGACAATAT
134682	132769	TGAGAAAATTTATGACAATA
134683	132770	TTGAGAAAATTTATGACAAT
134684	132771	TTTGAGAAAATTTATGACAA
134685	132772	CTTTGAGAAAATTTATGACA
134686	132773	CCTTTGAGAAAATTTATGAC
134687	132774	TCCTTTGAGAAAATTTATGA
134688	132775	TTCCTTTGAGAAAATTTATG
134689	132776	GTTCCTTTGAGAAAATTTAT
134690	132777	GGTTCCTTTGAGAAAATTTA
134691	132778	TGGTTCCTTTGAGAAAATTT
134692	132779	TTGGTTCCTTTGAGAAAATT
134693	132780	TTTGGTTCCTTTGAGAAAAT
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134695	132782	TATTTGGTTCCTTTGAGAAA
134696	132783	GTATTTGGTTCCTTTGAGAA
134697	132784	AGTATTTGGTTCCTTTGAGA
134698	132785	AAGTATTTGGTTCCTTTGAG
134699	132786	AAAGTATTTGGTTCCTTTGA
134700	132787	CAAAGTATTTGGTTCCTTTG
134701	132788	TCAAAGTATTTGGTTCCTTT
134702	132789	CTCAAAGTATTTGGTTCCTT
134703	132790	ACTCAAAGTATTTGGTTCCT
134704	132791	TACTCAAAGTATTTGGTTCC
134705	132792	ATACTCAAAGTATTTGGTTC
134706	132793	CATACTCAAAGTATTTGGTT
134707	132794	TCATACTCAAAGTATTTGGT
134708	132795	TTCATACTCAAAGTATTTGG
134709	132796	ATTCATACTCAAAGTATTTG
134710	132797	AATTCATACTCAAAGTATTT

36417	34504	TTGATCCACCTACTGAAAAA
36418	34505	GTTGATCCACCTACTGAAAA
36419	34506	GGTTGATCCACCTACTGAAA
36420	34507	AGGTTGATCCACCTACTGAA
36421	34508	GAGGTTGATCCACCTACTGA
36422	34509	TGAGGTTGATCCACCTACTG
36423	34510	TTGAGGTTGATCCACCTACT
36424	34511	TTTGAGGTTGATCCACCTAC
36425	34512	ATTTGAGGTTGATCCACCTA
36426	34513	AATTTGAGGTTGATCCACCT
36427	34514	AAATTTGAGGTTGATCCACC
36428	34515	AAAATTTGAGGTTGATCCAC
36429	34516	TAAAATTTGAGGTTGATCCA
36430	34517	TTAAAATTTGAGGTTGATCC
36431	34518	ATTAAAATTTGAGGTTGATC
36432	34519	TATTAAAATTTGAGGTTGAT
36433	34520	ATATTAAAATTTGAGGTTGA
36434	34521	TATATTAAAATTTGAGGTTG
36435	34522	TTATATTAAAATTTGAGGTT
36436	34523	TTTATATTAAAATTTGAGGT
36437	34524	CTTTATATTAAAATTTGAGG
36438	34525	GCTTTATATTAAAATTTGAG
36439	34526	TGCTTTATATTAAAATTTGA
36440	34527	ATGCTTTATATTAAAATTTG
36441	34528	AATGCTTTATATTAAAATTT
36442	34529	TAATGCTTTATATTAAAATT
36443	34530	GTAATGCTTTATATTAAAAT
36444	34531	AGTAATGCTTTATATTAAAA
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36446	34533	TAAGTAATGCTTTATATTAA
36447	34534	TTAAGTAATGCTTTATATTA
36448	34535	TTTAAGTAATGCTTTATATT
36449	34536	CTTTAAGTAATGCTTTATAT
36450	34537	CCTTTAAGTAATGCTTTATA
36451	34538	TCCTTTAAGTAATGCTTTAT
36452	34539	CTCCTTTAAGTAATGCTTTA
36453	34540	TCTCCTTTAAGTAATGCTTT
36454	34541	TTCTCCTTTAAGTAATGCTT
36455	34542	ATTCTCCTTTAAGTAATGCT
36456	34543	TATTCTCCTTTAAGTAATGC
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36459	34546	CCATATTCTCCTTTAAGTAA
36460	34547	CCCATATTCTCCTTTAAGTA
36461	34548	CCCCATATTCTCCTTTAAGT
36462	34549	TCCCCATATTCTCCTTTAAG
36463	34550	GTCCCCATATTCTCCTTTAA
36464	34551	TGTCCCCATATTCTCCTTTA
36465	34552	ATGTCCCCATATTCTCCTTT
36466	34553	AATGTCCCCATATTCTCCTT
36467	34554	GAATGTCCCCATATTCTCCT
36468	34555	TGAATGTCCCCATATTCTCC
36469	34556	ATGAATGTCCCCATATTCTC
36470	34557	CATGAATGTCCCCATATTCT
36471	34558	TCATGAATGTCCCCATATTC
36472	34559	GTCATGAATGTCCCCATATT
36473	34560	TGTCATGAATGTCCCCATAT
36474	34561	ATGTCATGAATGTCCCCATA
36475	34562	AATGTCATGAATGTCCCCAT
36476	34563	AAATGTCATGAATGTCCCCA
36477	34564	GAAATGTCATGAATGTCCCC
36478	34565	AGAAATGTCATGAATGTCCC
36479	34566	AAGAAATGTCATGAATGTCC
36480	34567	TAAGAAATGTCATGAATGTC
36481	34568	ATAAGAAATGTCATGAATGT
36482	34569	TATAAGAAATGTCATGAATG
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36484	34571	CATATAAGAAATGTCATGAA
36485	34572	ACATATAAGAAATGTCATGA
36486	34573	TACATATAAGAAATGTCATG
36487	34574	GTACATATAAGAAATGTCAT

85564	83651	AGGTTAATAGAAATAGTTTT
85565	83652	AAGGTTAATAGAAATAGTTT
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85567	83654	AAAAGGTTAATAGAAATAGT
85568	83655	CAAAAGGTTAATAGAAATAG
85569	83656	ACAAAAGGTTAATAGAAATA
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85573	83660	ATGAACAAAAGGTTAATAGA
85574	83661	AATGAACAAAAGGTTAATAG
85575	83662	TAATGAACAAAAGGTTAATA
85576	83663	CTAATGAACAAAAGGTTAAT
85577	83664	TCTAATGAACAAAAGGTTAA
85578	83665	CTCTAATGAACAAAAGGTTA
85579	83666	TCTCTAATGAACAAAAGGTT
85580	83667	CTCTCTAATGAACAAAAGGT
85581	83668	TCTCTCTAATGAACAAAAGG
85582	83669	TTCTCTCTAATGAACAAAAG
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85586	83673	AAATTTCTCTCTAATGAACA
85587	83674	CAAATTTCTCTCTAATGAAC
85588	83675	TCAAATTTCTCTCTAATGAA
85589	83676	ATCAAATTTCTCTCTAATGA
85590	83677	TATCAAATTTCTCTCTAATG
85591	83678	TTATCAAATTTCTCTCTAAT
85592	83679	TTTATCAAATTTCTCTCTAA
85593	83680	ATTTATCAAATTTCTCTCTA
85594	83681	CATTTATCAAATTTCTCTCT
85595	83682	ACATTTATCAAATTTCTCTC
85596	83683	CACATTTATCAAATTTCTCT
85597	83684	ACACATTTATCAAATTTCTC
85598	83685	CACACATTTATCAAATTTCT
85599	83686	TCACACATTTATCAAATTTC
85600	83687	TTCACACATTTATCAAATTT
85601	83688	CTTCACACATTTATCAAATT
85602	83689	GCTTCACACATTTATCAAAT
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85604	83691	TAGCTTCACACATTTATCAA
85605	83692	ATAGCTTCACACATTTATCA
85606	83693	TATAGCTTCACACATTTATC
85607	83694	TTATAGCTTCACACATTTAT
85608	83695	TTTATAGCTTCACACATTTA
85609	83696	GTTTATAGCTTCACACATTT
85610	83697	AGTTTATAGCTTCACACATT
85611	83698	GAGTTTATAGCTTCACACAT
85612	83699	AGAGTTTATAGCTTCACACA
85613	83700	GAGAGTTTATAGCTTCACAC
85614	83701	AGAGAGTTTATAGCTTCACA
85615	83702	AAGAGAGTTTATAGCTTCAC
85616	83703	CAAGAGAGTTTATAGCTTCA
85617	83704	TCAAGAGAGTTTATAGCTTC
85618	83705	TTCAAGAGAGTTTATAGCTT
85619	83706	ATTCAAGAGAGTTTATAGCT
85620	83707	AATTCAAGAGAGTTTATAGC
85621	83708	CAATTCAAGAGAGTTTATAG
85622	83709	ACAATTCAAGAGAGTTTATA
85623	83710	AACAATTCAAGAGAGTTTAT
85624	83711	CAACAATTCAAGAGAGTTTA
85625	83712	ACAACAATTCAAGAGAGTTT
85626	83713	AACAACAATTCAAGAGAGTT
85627	83714	TAACAACAATTCAAGAGAGT
85628	83715	TTAACAACAATTCAAGAGAG
85629	83716	TTTAACAACAATTCAAGAGA
85630	83717	TTTTAACAACAATTCAAGAG
85631	83718	TTTTTAACAACAATTCAAGA
85632	83719	CTTTTTAACAACAATTCAAG
85633	83720	CCTTTTTAACAACAATTCAA
85634	83721	CCCTTTTTAACAACAATTCA

134711	132798	CAATTCATACTCAAAGTATT
134712	132799	ACAATTCATACTCAAAGTAT
134713	132800	CACAATTCATACTCAAAGTA
134714	132801	GCACAATTCATACTCAAAGT
134715	132802	AGCACAATTCATACTCAAAG
134716	132803	AAGCACAATTCATACTCAAA
134717	132804	AAAGCACAATTCATACTCAA
134718	132805	AAAAGCACAATTCATACTCA
134719	132806	GAAAAGCACAATTCATACTC
134720	132807	AGAAAAGCACAATTCATACT
134721	132808	AAGAAAAGCACAATTCATAC
134722	132809	AAAGAAAAGCACAATTCATA
134723	132810	AAAAGAAAAGCACAATTCAT
134724	132811	AAAAAGAAAAGCACAATTCA
134725	132812	TAAAAAGAAAAGCACAATTC
134726	132813	TTAAAAAGAAAAGCACAATT
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134730	132817	TAGCTTAAAAAGAAAAGCAC
134731	132818	GTAGCTTAAAAAGAAAAGCA
134732	132819	TGTAGCTTAAAAAGAAAAGC
134733	132820	ATGTAGCTTAAAAAGAAAAG
134734	132821	GATGTAGCTTAAAAAGAAAA
134735	132822	TGATGTAGCTTAAAAAGAAA
134736	132823	ATGATGTAGCTTAAAAAGAA
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134738	132825	ATATGATGTAGCTTAAAAAG
134739	132826	GATATGATGTAGCTTAAAAA
134740	132827	AGATATGATGTAGCTTAAAA
134741	132828	TAGATATGATGTAGCTTAAA
134742	132829	CTAGATATGATGTAGCTTAA
134743	132830	CCTAGATATGATGTAGCTTA
134744	132831	ACCTAGATATGATGTAGCTT
134745	132832	AACCTAGATATGATGTAGCT
134746	132833	AAACCTAGATATGATGTAGC
134747	132834	AAAACCTAGATATGATGTAG
134748	132835	AAAAACCTAGATATGATGTA
134749	132836	TAAAAACCTAGATATGATGT
134750	132837	TTAAAAACCTAGATATGATG
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134753	132840	GTTTTAAAAACCTAGATATG
134754	132841	TGTTTTAAAAACCTAGATAT
134755	132842	ATGTTTTAAAAACCTAGATA
134756	132843	AATGTTTTAAAAACCTAGAT
134757	132844	AAATGTTTTAAAAACCTAGA
134758	132845	TAAATGTTTTAAAAACCTAG
134759	132846	TTAAATGTTTTAAAAACCTA
134760	132847	ATTAAATGTTTTAAAAACCT
134761	132848	CATTAAATGTTTTAAAAACC
134762	132849	GCATTAAATGTTTTAAAAAC
134763	132850	TGCATTAAATGTTTTAAAAA
134764	132851	TTGCATTAAATGTTTTAAAA
134765	132852	TTTGCATTAAATGTTTTAAA
134766	132853	GTTTGCATTAAATGTTTTAA
134767	132854	TGTTTGCATTAAATGTTTTA
134768	132855	CTGTTTGCATTAAATGTTTT
134769	132856	TCTGTTTGCATTAAATGTTT
134770	132857	TTCTGTTTGCATTAAATGTT
134771	132858	CTTCTGTTTGCATTAAATGT
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134778	132865	GCATGTTCTTCTGTTTGCAT
134779	132866	TGCATGTTCTTCTGTTTGCA
134780	132867	GTGCATGTTCTTCTGTTTGC
134781	132868	GGTGCATGTTCTTCTGTTTG

36488	34575	TGTACATATAAGAAATGTCA
36489	34576	ATGTACATATAAGAAATGTC
36490	34577	TATGTACATATAAGAAATGT
36491	34578	TTATGTACATATAAGAAATG
36492	34579	TTTATGTACATATAAGAAAT
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36495	34582	AGTTTTATGTACATATAAGA
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36498	34585	TGAAGTTTTATGTACATATA
36499	34586	ATGAAGTTTTATGTACATAT
36500	34587	CATGAAGTTTTATGTACATA
36501	34588	TCATGAAGTTTTATGTACAT
36502	34589	TTCATGAAGTTTTATGTACA
36503	34590	TTTCATGAAGTTTTATGTAC
36504	34591	TTTTCATGAAGTTTTATGTA
36505	34592	ATTTTCATGAAGTTTTATGT
36506	34593	TATTTTCATGAAGTTTTATG
36507	34594	TTATTTTCATGAAGTTTTAT
36508	34595	ATTATTTTCATGAAGTTTTA
36509	34596	AATTATTTTCATGAAGTTTT
36510	34597	AAATTATTTTCATGAAGTTT
36511	34598	TAAATTATTTTCATGAAGTT
36512	34599	TTAAATTATTTTCATGAAGT
36513	34600	ATTAAATTATTTTCATGAAG
36514	34601	CATTAAATTATTTTCATGAA
36515	34602	GCATTAAATTATTTTCATGA
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36518	34605	ATAGCATTAAATTATTTTCA
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36548	34635	GCCTCCAGTACTTCTAAAAT
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36552	34639	CCTAGCCTCCAGTACTTCTA
36553	34640	GCCTAGCCTCCAGTACTTCT
36554	34641	TGCCTAGCCTCCAGTACTTC
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36556	34643	CATGCCTAGCCTCCAGTACT
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85647	83734	GCAGAGATAAACCCCCTTTT
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85704	83791	GAGGGGGAAGGCTGTGGGGC
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134785	132872	TCTGGGTGCATGTTCTTCTG
134786	132873	ATCTGGGTGCATGTTCTTCT
134787	132874	CATCTGGGTGCATGTTCTTC
134788	132875	ACATCTGGGTGCATGTTCTT
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134790	132877	CAACATCTGGGTGCATGTTC
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134799	132886	AATTGTCACCAACATCTGGG
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134801	132888	AAAATTGTCACCAACATCTG
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134807	132894	TGACATAAAATTGTCACCAA
134808	132895	GTGACATAAAATTGTCACCA
134809	132896	GGTGACATAAAATTGTCACC
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134812	132899	AAAGGTGACATAAAATTGTC
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134849	132936	TGCCTTTGGCTATGGCTATA
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134890	132977	AGGATTTCATTTTGCAGTCA
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36630	34717	GTCTCCAGCTCCTGAACTCA
36631	34718	GGTCTCCAGCTCCTGAACTC
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36633	34720	CTGGTCTCCAGCTCCTGAAC
36634	34721	GCTGGTCTCCAGCTCCTGAA
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36636	34723	AAGCTGGTCTCCAGCTCCTG
36637	34724	CAAGCTGGTCTCCAGCTCCT
36638	34725	CCAAGCTGGTCTCCAGCTCC
36639	34726	CCCAAGCTGGTCTCCAGCTC
36640	34727	GCCCAAGCTGGTCTCCAGCT
36641	34728	TGCCCAAGCTGGTCTCCAGC
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36670	34757	TCTTTTGTAGAGATGGGGTC
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36674	34761	TTTCTCTTTTGTAGAGATGG
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36685	34772	CCAGTACTTCTTTTCTCTTT
36686	34773	TCCAGTACTTCTTTTCTCTT
36687	34774	CTCCAGTACTTCTTTTCTCT
36688	34775	ACTCCAGTACTTCTTTTCTC
36689	34776	CACTCCAGTACTTCTTTTCT
36690	34777	ACACTCCAGTACTTCTTTTC
36691	34778	AACACTCCAGTACTTCTTTT
36692	34779	CAACACTCCAGTACTTCTTT
36693	34780	GCAACACTCCAGTACTTCTT
36694	34781	TGCAACACTCCAGTACTTCT
36695	34782	CTGCAACACTCCAGTACTTC
36696	34783	GCTGCAACACTCCAGTACTT
36697	34784	AGCTGCAACACTCCAGTACT
36698	34785	GAGCTGCAACACTCCAGTAC
36699	34786	AGAGCTGCAACACTCCAGTA
36700	34787	AAGAGCTGCAACACTCCAGT

85777	83864	GTAAAATGAACCTAAGTTCA
85778	83865	TGTAAAATGAACCTAAGTTC
85779	83866	CTGTAAAATGAACCTAAGTT
85780	83867	GCTGTAAAATGAACCTAAGT
85781	83868	AGCTGTAAAATGAACCTAAG
85782	83869	GAGCTGTAAAATGAACCTAA
85783	83870	AGAGCTGTAAAATGAACCTA
85784	83871	AAGAGCTGTAAAATGAACCT
85785	83872	AAAGAGCTGTAAAATGAACC
85786	83873	CAAAGAGCTGTAAAATGAAC
85787	83874	CCAAAGAGCTGTAAAATGAA
85788	83875	GCCAAAGAGCTGTAAAATGA
85789	83876	GGCCAAAGAGCTGTAAAATG
85790	83877	TGGCCAAAGAGCTGTAAAAT
85791	83878	TTGGCCAAAGAGCTGTAAAA
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85793	83880	CCTTGGCCAAAGAGCTGTAA
85794	83881	ACCTTGGCCAAAGAGCTGTA
85795	83882	GACCTTGGCCAAAGAGCTGT
85796	83883	GGACCTTGGCCAAAGAGCTG
85797	83884	AGGACCTTGGCCAAAGAGCT
85798	83885	TAGGACCTTGGCCAAAGAGC
85799	83886	CTAGGACCTTGGCCAAAGAG
85800	83887	ACTAGGACCTTGGCCAAAGA
85801	83888	CACTAGGACCTTGGCCAAAG
85802	83889	TCACTAGGACCTTGGCCAAA
85803	83890	TTCACTAGGACCTTGGCCAA
85804	83891	GTTCACTAGGACCTTGGCCA
85805	83892	GGTTCACTAGGACCTTGGCC
85806	83893	AGGTTCACTAGGACCTTGGC
85807	83894	AAGGTTCACTAGGACCTTGG
85808	83895	GAAGGTTCACTAGGACCTTG
85809	83896	GGAAGGTTCACTAGGACCTT
85810	83897	AGGAAGGTTCACTAGGACCT
85811	83898	TAGGAAGGTTCACTAGGACC
85812	83899	ATAGGAAGGTTCACTAGGAC
85813	83900	AATAGGAAGGTTCACTAGGA
85814	83901	CAATAGGAAGGTTCACTAGG
85815	83902	CCAATAGGAAGGTTCACTAG
85816	83903	GCCAATAGGAAGGTTCACTA
85817	83904	GGCCAATAGGAAGGTTCACT
85818	83905	TGGCCAATAGGAAGGTTCAC
85819	83906	ATGGCCAATAGGAAGGTTCA
85820	83907	TATGGCCAATAGGAAGGTTC
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85822	83909	CTTATGGCCAATAGGAAGGT
85823	83910	GCTTATGGCCAATAGGAAGG
85824	83911	TGCTTATGGCCAATAGGAAG
85825	83912	CTGCTTATGGCCAATAGGAA
85826	83913	CCTGCTTATGGCCAATAGGA
85827	83914	CCCTGCTTATGGCCAATAGG
85828	83915	TCCCTGCTTATGGCCAATAG
85829	83916	ATCCCTGCTTATGGCCAATA
85830	83917	CATCCCTGCTTATGGCCAAT
85831	83918	CCATCCCTGCTTATGGCCAA
85832	83919	ACCATCCCTGCTTATGGCCA
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85835	83922	AACACCATCCCTGCTTATGG
85836	83923	AAACACCATCCCTGCTTATG
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85839	83926	AGAAAACACCATCCCTGCTT
85840	83927	CAGAAAACACCATCCCTGCT
85841	83928	CCAGAAAACACCATCCCTGC
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85843	83930	ACCCAGAAAACACCATCCCT
85844	83931	GACCCAGAAAACACCATCCC
85845	83932	AGACCCAGAAAACACCATCC
85846	83933	AAGACCCAGAAAACACCATC
85847	83934	AAAGACCCAGAAAACACCAT

134924	133011	TATTAAACATACTAAAAATT
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134926	133013	TGTATTAAACATACTAAAAA
134927	133014	GTGTATTAAACATACTAAAA
134928	133015	TGTGTATTAAACATACTAAA
134929	133016	ATGTGTATTAAACATACTAA
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134932	133019	CATATGTGTATTAAACATAC
134933	133020	GCATATGTGTATTAAACATA
134934	133021	AGCATATGTGTATTAAACAT
134935	133022	TAGCATATGTGTATTAAACA
134936	133023	TTAGCATATGTGTATTAAAC
134937	133024	GTTAGCATATGTGTATTAAA
134938	133025	TGTTAGCATATGTGTATTAA
134939	133026	ATGTTAGCATATGTGTATTA
134940	133027	AATGTTAGCATATGTGTATT
134941	133028	TAATGTTAGCATATGTGTAT
134942	133029	GTAATGTTAGCATATGTGTA
134943	133030	AGTAATGTTAGCATATGTGT
134944	133031	CAGTAATGTTAGCATATGTG
134945	133032	TCAGTAATGTTAGCATATGT
134946	133033	TTCAGTAATGTTAGCATATG
134947	133034	GTTCAGTAATGTTAGCATAT
134948	133035	TGTTCAGTAATGTTAGCATA
134949	133036	CTGTTCAGTAATGTTAGCAT
134950	133037	ACTGTTCAGTAATGTTAGCA
134951	133038	AACTGTTCAGTAATGTTAGC
134952	133039	TAACTGTTCAGTAATGTTAG
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134955	133042	ATTTAACTGTTCAGTAATGT
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134957	133044	TCATTTAACTGTTCAGTAAT
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134963	133050	ATTTTATCATTTAACTGTTC
134964	133051	TATTTTATCATTTAACTGTT
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134968	133055	ATCCTATTTTATCATTTAAC
134969	133056	TATCCTATTTTATCATTTAA
134970	133057	TTATCCTATTTTATCATTTA
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134972	133059	AATTATCCTATTTTATCATT
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134974	133061	ATAATTATCCTATTTTATCA
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134976	133063	AAATAATTATCCTATTTTAT
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134982	133069	AGAATAAAATAATTATCCTA
134983	133070	TAGAATAAAATAATTATCCT
134984	133071	TTAGAATAAAATAATTATCC
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134986	133073	TTTTAGAATAAAATAATTAT
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134988	133075	TTTTTTAGAATAAAATAATT
134989	133076	CTTTTTTAGAATAAAATAAT
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134991	133078	TACTTTTTTAGAATAAAATA
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134993	133080	AATACTTTTTTAGAATAAAA
134994	133081	CAATACTTTTTTAGAATAAA

36701	34788	TAAGAGCTGCAACACTCCAG
36702	34789	GTAAGAGCTGCAACACTCCA
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36704	34791	CTGTAAGAGCTGCAACACTC
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36707	34794	ATTCTGTAAGAGCTGCAACA
36708	34795	AATTCTGTAAGAGCTGCAAC
36709	34796	AAATTCTGTAAGAGCTGCAA
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36711	34798	ACAAATTCTGTAAGAGCTGC
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36713	34800	AGACAAATTCTGTAAGAGCT
36714	34801	TAGACAAATTCTGTAAGAGC
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36717	34804	TGCTAGACAAATTCTGTAAG
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36749	34836	ATGGGGGCATTTCTGGTAAA
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36761	34848	TACTACTTCTGCATGGGGGC
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36764	34851	ATTTACTACTTCTGCATGGG
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36768	34855	CAGTATTTACTACTTCTGCA
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36771	34858	AATCAGTATTTACTACTTCT

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85864	83951	GGGCTGTCGCTCTCAAAAAA
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85869	83956	TACATGGGCTGTCGCTCTCA
85870	83957	CTACATGGGCTGTCGCTCTC
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85874	83961	TCAGCTACATGGGCTGTCGC
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85878	83965	AAAGTCAGCTACATGGGCTG
85879	83966	CAAAGTCAGCTACATGGGCT
85880	83967	GCAAAGTCAGCTACATGGGC
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85887	83974	CAGACACGCAAAGTCAGCTA
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85889	83976	GGCAGACACGCAAAGTCAGC
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85894	83981	CTAAGGGCAGACACGCAAAG
85895	83982	TCTAAGGGCAGACACGCAAA
85896	83983	ATCTAAGGGCAGACACGCAA
85897	83984	AATCTAAGGGCAGACACGCA
85898	83985	TAATCTAAGGGCAGACACGC
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85900	83987	TTTAATCTAAGGGCAGACAC
85901	83988	CTTTAATCTAAGGGCAGACA
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85903	83990	TACTTTAATCTAAGGGCAGA
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85905	83992	ACTACTTTAATCTAAGGGCA
85906	83993	AACTACTTTAATCTAAGGGC
85907	83994	CAACTACTTTAATCTAAGGG
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85918	84005	ATTCTAAAAATCAACTACTT

134995	133082	TCAATACTTTTTTAGAATAA
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135004	133091	AGGTCAAGGTCAATACTTTT
135005	133092	GAGGTCAAGGTCAATACTTT
135006	133093	AGAGGTCAAGGTCAATACTT
135007	133094	AAGAGGTCAAGGTCAATACT
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135011	133098	TAGAAAGAGGTCAAGGTCAA
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135013	133100	GCTAGAAAGAGGTCAAGGTC
135014	133101	AGCTAGAAAGAGGTCAAGGT
135015	133102	TAGCTAGAAAGAGGTCAAGG
135016	133103	ATAGCTAGAAAGAGGTCAAG
135017	133104	GATAGCTAGAAAGAGGTCAA
135018	133105	AGATAGCTAGAAAGAGGTCA
135019	133106	AAGATAGCTAGAAAGAGGTC
135020	133107	TAAGATAGCTAGAAAGAGGT
135021	133108	CTAAGATAGCTAGAAAGAGG
135022	133109	TCTAAGATAGCTAGAAAGAG
135023	133110	TTCTAAGATAGCTAGAAAGA
135024	133111	TTTCTAAGATAGCTAGAAAG
135025	133112	CTTTCTAAGATAGCTAGAAA
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135027	133114	CCCTTTCTAAGATAGCTAGA
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135031	133118	AAAGCCCTTTCTAAGATAGC
135032	133119	AAAAGCCCTTTCTAAGATAG
135033	133120	CAAAAGCCCTTTCTAAGATA
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135049	133136	GAGATAAGGTTTTTGACAAA
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135051	133138	AAGAGATAAGGTTTTTGACA
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135054	133141	TCAAAGAGATAAGGTTTTTG
135055	133142	ATCAAAGAGATAAGGTTTTT
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135057	133144	ACATCAAAGAGATAAGGTTT
135058	133145	GACATCAAAGAGATAAGGTT
135059	133146	AGACATCAAAGAGATAAGGT
135060	133147	GAGACATCAAAGAGATAAGG
135061	133148	AGAGACATCAAAGAGATAAG
135062	133149	AAGAGACATCAAAGAGATAA
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36772	34859	GAATCAGTATTTACTACTTC
36773	34860	TGAATCAGTATTTACTACTT
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36775	34862	CATGAATCAGTATTTACTAC
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36784	34871	ATTATTTTACATGAATCAGT
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36788	34875	GTTTATTATTTTACATGAAT
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36795	34882	TAAAGTTGTTTATTATTTTA
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36806	34893	AAACTGAAAGATAAAGTTGT
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36822	34909	AGACCCTGTCTTTTAAAAAC
36823	34910	AAGACCCTGTCTTTTAAAAA
36824	34911	CAAGACCCTGTCTTTTAAAA
36825	34912	ACAAGACCCTGTCTTTTAAA
36826	34913	TACAAGACCCTGTCTTTTAA
36827	34914	TTACAAGACCCTGTCTTTTA
36828	34915	GTTACAAGACCCTGTCTTTT
36829	34916	CGTTACAAGACCCTGTCTTT
36830	34917	ACGTTACAAGACCCTGTCTT
36831	34918	AACGTTACAAGACCCTGTCT
36832	34919	CAACGTTACAAGACCCTGTC
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85919	84006	CATTCTAAAAATCAACTACT
85920	84007	GCATTCTAAAAATCAACTAC
85921	84008	GGCATTCTAAAAATCAACTA
85922	84009	TGGCATTCTAAAAATCAACT
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85935	84022	TTTAGAATTCTTCTGGCATT
85936	84023	ATTTAGAATTCTTCTGGCAT
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85939	84026	TAAATTTAGAATTCTTCTGG
85940	84027	TTAAATTTAGAATTCTTCTG
85941	84028	GTTAAATTTAGAATTCTTCT
85942	84029	AGTTAAATTTAGAATTCTTC
85943	84030	CAGTTAAATTTAGAATTCTT
85944	84031	TCAGTTAAATTTAGAATTCT
85945	84032	CTCAGTTAAATTTAGAATTC
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85947	84034	TACTCAGTTAAATTTAGAAT
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85949	84036	ATTACTCAGTTAAATTTAGA
85950	84037	AATTACTCAGTTAAATTTAG
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85959	84046	CTTTAAAAAAATTACTCAGT
85960	84047	ACTTTAAAAAAATTACTCAG
85961	84048	AACTTTAAAAAAATTACTCA
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85963	84050	CTAACTTTAAAAAAATTACT
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85967	84054	AAAGCTAACTTTAAAAAAAT
85968	84055	CAAAGCTAACTTTAAAAAAA
85969	84056	GCAAAGCTAACTTTAAAAAA
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85972	84059	ATTGCAAAGCTAACTTTAAA
85973	84060	GATTGCAAAGCTAACTTTAA
85974	84061	AGATTGCAAAGCTAACTTTA
85975	84062	AAGATTGCAAAGCTAACTTT
85976	84063	TAAGATTGCAAAGCTAACTT
85977	84064	GTAAGATTGCAAAGCTAACT
85978	84065	TGTAAGATTGCAAAGCTAAC
85979	84066	ATGTAAGATTGCAAAGCTAA
85980	84067	TATGTAAGATTGCAAAGCTA
85981	84068	CTATGTAAGATTGCAAAGCT
85982	84069	ACTATGTAAGATTGCAAAGC
85983	84070	CACTATGTAAGATTGCAAAG
85984	84071	TCACTATGTAAGATTGCAAA
85985	84072	TTCACTATGTAAGATTGCAA
85986	84073	TTTCACTATGTAAGATTGCA
85987	84074	CTTTCACTATGTAAGATTGC
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85989	84076	GCCTTTCACTATGTAAGATT

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135067	133154	AAAAAAAGAGACATCAAAGA
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135069	133156	TCAAAAAAAGAGACATCAAA
135070	133157	CTCAAAAAAAGAGACATCAA
135071	133158	TCTCAAAAAAAGAGACATCA
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135074	133161	CCATCTCAAAAAAAGAGACA
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135076	133163	CTCCATCTCAAAAAAAGAGA
135077	133164	ACTCCATCTCAAAAAAAGAG
135078	133165	GACTCCATCTCAAAAAAAGA
135079	133166	AGACTCCATCTCAAAAAAAG
135080	133167	GAGACTCCATCTCAAAAAAA
135081	133168	AGAGACTCCATCTCAAAAAA
135082	133169	GAGAGACTCCATCTCAAAAA
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135084	133171	GGGAGAGACTCCATCTCAAA
135085	133172	AGGGAGAGACTCCATCTCAA
135086	133173	CAGGGAGAGACTCCATCTCA
135087	133174	ACAGGGAGAGACTCCATCTC
135088	133175	GACAGGGAGAGACTCCATCT
135089	133176	CGACAGGGAGAGACTCCATC
135090	133177	GCGACAGGGAGAGACTCCAT
135091	133178	GGCGACAGGGAGAGACTCCA
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135095	133182	CCTGGGCGACAGGGAGAGAC
135096	133183	GCCTGGGCGACAGGGAGAGA
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135098	133185	CAGCCTGGGCGACAGGGAGA
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135103	133190	CACTCCAGCCTGGGCGACAG
135104	133191	GCACTCCAGCCTGGGCGACA
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135106	133193	CTGCACTCCAGCCTGGGCGA
135107	133194	ACTGCACTCCAGCCTGGGCG
135108	133195	CACTGCACTCCAGCCTGGGC
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135110	133197	GCCACTGCACTCCAGCCTGG
135111	133198	CGCCACTGCACTCCAGCCTG
135112	133199	ACGCCACTGCACTCCAGCCT
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135118	133205	GAGATCACGCCACTGCACTC
135119	133206	TGAGATCACGCCACTGCACT
135120	133207	CTGAGATCACGCCACTGCAC
135121	133208	GCTGAGATCACGCCACTGCA
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135123	133210	GAGCTGAGATCACGCCACTG
135124	133211	TGAGCTGAGATCACGCCACT
135125	133212	GTGAGCTGAGATCACGCCAC
135126	133213	AGTGAGCTGAGATCACGCCA
135127	133214	CAGTGAGCTGAGATCACGCC
135128	133215	GCAGTGAGCTGAGATCACGC
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135130	133217	GTGCAGTGAGCTGAGATCAC
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135133	133220	AGCGTGCAGTGAGCTGAGAT
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135136	133223	CGGAGCGTGCAGTGAGCTGA

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36844	34931	GGCCAGTCTGGGCAACGTTA
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36846	34933	AAGGCCAGTCTGGGCAACGT
36847	34934	AAAGGCCAGTCTGGGCAACG
36848	34935	TAAAGGCCAGTCTGGGCAAC
36849	34936	TTAAAGGCCAGTCTGGGCAA
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36854	34941	AGGAATTAAAGGCCAGTCTG
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36879	34966	TCAGGTGAGAGGATCGCTTG
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36884	34971	AAGGCTCAGGTGAGAGGATC
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36910	34997	TGCAGCCTGTAGTCTCAGCT
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86004	84091	TTCCAGATTAAAGCAGCCTT
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86006	84093	TCTTCCAGATTAAAGCAGCC
86007	84094	TTCTTCCAGATTAAAGCAGC
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86010	84097	GACTTCTTCCAGATTAAAGC
86011	84098	GGACTTCTTCCAGATTAAAG
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86014	84101	CAAGGACTTCTTCCAGATTA
86015	84102	TCAAGGACTTCTTCCAGATT
86016	84103	ATCAAGGACTTCTTCCAGAT
86017	84104	GATCAAGGACTTCTTCCAGA
86018	84105	AGATCAAGGACTTCTTCCAG
86019	84106	CAGATCAAGGACTTCTTCCA
86020	84107	TCAGATCAAGGACTTCTTCC
86021	84108	CTCAGATCAAGGACTTCTTC
86022	84109	TCTCAGATCAAGGACTTCTT
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86024	84111	TATCTCAGATCAAGGACTTC
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86027	84114	TTTTATCTCAGATCAAGGAC
86028	84115	ATTTTATCTCAGATCAAGGA
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86036	84123	TTTTATCAATTTTATCTCAG
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86041	84128	GTCGTTTTTATCAATTTTAT
86042	84129	TGTCGTTTTTATCAATTTTA
86043	84130	ATGTCGTTTTTATCAATTTT
86044	84131	TATGTCGTTTTTATCAATTT
86045	84132	ATATGTCGTTTTTATCAATT
86046	84133	CATATGTCGTTTTTATCAAT
86047	84134	TCATATGTCGTTTTTATCAA
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86049	84136	ATTCATATGTCGTTTTTATC
86050	84137	AATTCATATGTCGTTTTTAT
86051	84138	AAATTCATATGTCGTTTTTA
86052	84139	CAAATTCATATGTCGTTTTT
86053	84140	TCAAATTCATATGTCGTTTT
86054	84141	TTCAAATTCATATGTCGTTT
86055	84142	ATTCAAATTCATATGTCGTT
86056	84143	TATTCAAATTCATATGTCGT
86057	84144	ATATTCAAATTCATATGTCG
86058	84145	AATATTCAAATTCATATGTC
86059	84146	AAATATTCAAATTCATATGT
86060	84147	TAAATATTCAAATTCATATG

135137	133224	GCGGAGCGTGCAGTGAGCTG
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135139	133226	AGGCGGAGCGTGCAGTGAGC
135140	133227	GAGGCGGAGCGTGCAGTGAG
135141	133228	GGAGGCGGAGCGTGCAGTGA
135142	133229	AGGAGGCGGAGCGTGCAGTG
135143	133230	CAGGAGGCGGAGCGTGCAGT
135144	133231	GCAGGAGGCGGAGCGTGCAG
135145	133232	CGCAGGAGGCGGAGCGTGCA
135146	133233	ACGCAGGAGGCGGAGCGTGC
135147	133234	AACGCAGGAGGCGGAGCGTG
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135149	133236	TGAACGCAGGAGGCGGAGCG
135150	133237	GTGAACGCAGGAGGCGGAGC
135151	133238	CGTGAACGCAGGAGGCGGAG
135152	133239	GCGTGAACGCAGGAGGCGGA
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135161	133248	AGGAGAATGGCGTGAACGCA
135162	133249	TAGGAGAATGGCGTGAACGC
135163	133250	GTAGGAGAATGGCGTGAACG
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135167	133254	TGAGGTAGGAGAATGGCGTG
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135169	133256	GCTGAGGTAGGAGAATGGCG
135170	133257	GGCTGAGGTAGGAGAATGGC
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135172	133259	GAGGCTGAGGTAGGAGAATG
135173	133260	GGAGGCTGAGGTAGGAGAAT
135174	133261	GGGAGGCTGAGGTAGGAGAA
135175	133262	CGGGAGGCTGAGGTAGGAGA
135176	133263	TCGGGAGGCTGAGGTAGGAG
135177	133264	CTCGGGAGGCTGAGGTAGGA
135178	133265	ACTCGGGAGGCTGAGGTAGG
135179	133266	TACTCGGGAGGCTGAGGTAG
135180	133267	CTACTCGGGAGGCTGAGGTA
135181	133268	GCTACTCGGGAGGCTGAGGT
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135184	133271	CTAGCTACTCGGGAGGCTGA
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135189	133276	TAGTCCTAGCTACTCGGGAG
135190	133277	GTAGTCCTAGCTACTCGGGA
135191	133278	TGTAGTCCTAGCTACTCGGG
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135197	133284	GGCGCCTGTAGTCCTAGCTA
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135199	133286	CGGGCGCCTGTAGTCCTAGC
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36914	35001	GAGGTGCAGCCTGTAGTCTC
36915	35002	AGAGGTGCAGCCTGTAGTCT
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36922	35009	CAGGTGCAGAGGTGCAGCCT
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36924	35011	GCCAGGTGCAGAGGTGCAGC
36925	35012	AGCCAGGTGCAGAGGTGCAG
36926	35013	GAGCCAGGTGCAGAGGTGCA
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36931	35018	AAGCAGAGCCAGGTGCAGAG
36932	35019	CAAGCAGAGCCAGGTGCAGA
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36934	35021	ATCAAGCAGAGCCAGGTGCA
36935	35022	AATCAAGCAGAGCCAGGTGC
36936	35023	AAATCAAGCAGAGCCAGGTG
36937	35024	AAAATCAAGCAGAGCCAGGT
36938	35025	AAAAATCAAGCAGAGCCAGG
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86061	84148	CTAAATATTCAAATTCATAT
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86065	84152	ATAGCTAAATATTCAAATTC
86066	84153	AATAGCTAAATATTCAAATT
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86078	84165	GACGAGGAAAGAAATAGCTA
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86096	84183	GATTTTATTCTTATTTTTGA
86097	84184	AGATTTTATTCTTATTTTTG
86098	84185	AAGATTTTATTCTTATTTTT
86099	84186	CAAGATTTTATTCTTATTTT
86100	84187	ACAAGATTTTATTCTTATTT
86101	84188	TACAAGATTTTATTCTTATT
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86108	84195	TAAGAATTACAAGATTTTAT
86109	84196	ATAAGAATTACAAGATTTTA
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86112	84199	TGAATAAGAATTACAAGATT
86113	84200	CTGAATAAGAATTACAAGAT
86114	84201	ACTGAATAAGAATTACAAGA
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86117	84204	AATACTGAATAAGAATTACA
86118	84205	AAATACTGAATAAGAATTAC
86119	84206	CAAATACTGAATAAGAATTA
86120	84207	CCAAATACTGAATAAGAATT
86121	84208	GCCAAATACTGAATAAGAAT
86122	84209	CGCCAAATACTGAATAAGAA
86123	84210	GCGCCAAATACTGAATAAGA
86124	84211	AGCGCCAAATACTGAATAAG
86125	84212	TAGCGCCAAATACTGAATAA
86126	84213	TTAGCGCCAAATACTGAATA
86127	84214	TTTAGCGCCAAATACTGAAT
86128	84215	ATTTAGCGCCAAATACTGAA
86129	84216	GATTTAGCGCCAAATACTGA
86130	84217	GGATTTAGCGCCAAATACTG
86131	84218	TGGATTTAGCGCCAAATACT

135208	133295	GCATGGTGGCGGGCGCCTGT
135209	133296	GGCATGGTGGCGGGCGCCTG
135210	133297	GGGCATGGTGGCGGGCGCCT
135211	133298	CGGGCATGGTGGCGGGCGCC
135212	133299	CCGGGCATGGTGGCGGGCGC
135213	133300	GCCGGGCATGGTGGCGGGCG
135214	133301	AGCCGGGCATGGTGGCGGGC
135215	133302	TAGCCGGGCATGGTGGCGGG
135216	133303	TTAGCCGGGCATGGTGGCGG
135217	133304	ATTAGCCGGGCATGGTGGCG
135218	133305	AATTAGCCGGGCATGGTGGC
135219	133306	AAATTAGCCGGGCATGGTGG
135220	133307	AAAATTAGCCGGGCATGGTG
135221	133308	AAAAATTAGCCGGGCATGGT
135222	133309	AAAAAATTAGCCGGGCATGG
135223	133310	CAAAAAATTAGCCGGGCATG
135224	133311	ACAAAAAATTAGCCGGGCAT
135225	133312	TACAAAAAATTAGCCGGGCA
135226	133313	ATACAAAAAATTAGCCGGGC
135227	133314	AATACAAAAAATTAGCCGGG
135228	133315	AAATACAAAAAATTAGCCGG
135229	133316	AAAATACAAAAAATTAGCCG
135230	133317	CAAAATACAAAAAATTAGCC
135231	133318	ACAAAATACAAAAAATTAGC
135232	133319	AACAAAATACAAAAAATTAG
135233	133320	AAACAAAATACAAAAAATTA
135234	133321	TAAACAAAATACAAAAAATT
135235	133322	CTAAACAAAATACAAAAAAT
135236	133323	ACTAAACAAAATACAAAAAA
135237	133324	TACTAAACAAAATACAAAAA
135238	133325	CTACTAAACAAAATACAAAA
135239	133326	TCTACTAAACAAAATACAAA
135240	133327	CTCTACTAAACAAAATACAA
135241	133328	TCTCTACTAAACAAAATACA
135242	133329	ATCTCTACTAAACAAAATAC
135243	133330	CATCTCTACTAAACAAAATA
135244	133331	CCATCTCTACTAAACAAAAT
135245	133332	CCCATCTCTACTAAACAAAA
135246	133333	CCCCATCTCTACTAAACAAA
135247	133334	ACCCCATCTCTACTAAACAA
135248	133335	AACCCCATCTCTACTAAACA
135249	133336	AAACCCCATCTCTACTAAAC
135250	133337	GAAACCCCATCTCTACTAAA
135251	133338	TGAAACCCCATCTCTACTAA
135252	133339	GTGAAACCCCATCTCTACTA
135253	133340	AGTGAAACCCCATCTCTACT
135254	133341	CAGTGAAACCCCATCTCTAC
135255	133342	ACAGTGAAACCCCATCTCTA
135256	133343	CACAGTGAAACCCCATCTCT
135257	133344	ACACAGTGAAACCCCATCTC
135258	133345	AACACAGTGAAACCCCATCT
135259	133346	TAACACAGTGAAACCCCATC
135260	133347	CTAACACAGTGAAACCCCAT
135261	133348	GCTAACACAGTGAAACCCCA
135262	133349	GGCTAACACAGTGAAACCCC
135263	133350	TGGCTAACACAGTGAAACCC
135264	133351	CTGGCTAACACAGTGAAACC
135265	133352	CCTGGCTAACACAGTGAAAC
135266	133353	TCCTGGCTAACACAGTGAAA
135267	133354	ATCCTGGCTAACACAGTGAA
135268	133355	CATCCTGGCTAACACAGTGA
135269	133356	CCATCCTGGCTAACACAGTG
135270	133357	ACCATCCTGGCTAACACAGT
135271	133358	GACCATCCTGGCTAACACAG
135272	133359	AGACCATCCTGGCTAACACA
135273	133360	AAGACCATCCTGGCTAACAC
135274	133361	CAAGACCATCCTGGCTAACA
135275	133362	TCAAGACCATCCTGGCTAAC
135276	133363	ATCAAGACCATCCTGGCTAA
135277	133364	GATCAAGACCATCCTGGCTA
135278	133365	AGATCAAGACCATCCTGGCT

36985	35072	ACACTGAAGAAAAAAAAAAA
36986	35073	CACACTGAAGAAAAAAAAAA
36987	35074	TCACACTGAAGAAAAAAAAA
36988	35075	CTCACACTGAAGAAAAAAAA
36989	35076	CCTCACACTGAAGAAAAAAA
36990	35077	TCCTCACACTGAAGAAAAAA
36991	35078	ATCCTCACACTGAAGAAAAA
36992	35079	CATCCTCACACTGAAGAAAA
36993	35080	CCATCCTCACACTGAAGAAA
36994	35081	CCCATCCTCACACTGAAGAA
36995	35082	GCCCATCCTCACACTGAAGA
36996	35083	TGCCCATCCTCACACTGAAG
36997	35084	TTGCCCATCCTCACACTGAA
36998	35085	TTTGCCCATCCTCACACTGA
36999	35086	GTTTGCCCATCCTCACACTG
37000	35087	AGTTTGCCCATCCTCACACT
37001	35088	AAGTTTGCCCATCCTCACAC
37002	35089	AAAGTTTGCCCATCCTCACA
37003	35090	AAAAGTTTGCCCATCCTCAC
37004	35091	AAAAAGTTTGCCCATCCTCA
37005	35092	TAAAAAGTTTGCCCATCCTC
37006	35093	ATAAAAAGTTTGCCCATCCT
37007	35094	CATAAAAAGTTTGCCCATCC
37008	35095	ACATAAAAAGTTTGCCCATC
37009	35096	TACATAAAAAGTTTGCCCAT
37010	35097	TTACATAAAAAGTTTGCCCA
37011	35098	TTTACATAAAAAGTTTGCCC
37012	35099	CTTTACATAAAAAGTTTGCC
37013	35100	ACTTTACATAAAAAGTTTGC
37014	35101	GACTTTACATAAAAAGTTTG
37015	35102	AGACTTTACATAAAAAGTTT
37016	35103	GAGACTTTACATAAAAAGTT
37017	35104	TGAGACTTTACATAAAAAGT
37018	35105	CTGAGACTTTACATAAAAAG
37019	35106	CCTGAGACTTTACATAAAAA
37020	35107	ACCTGAGACTTTACATAAAA
37021	35108	TACCTGAGACTTTACATAAA
37022	35109	TTACCTGAGACTTTACATAA
37023	35110	ATTACCTGAGACTTTACATA
37024	35111	TATTACCTGAGACTTTACAT
37025	35112	TTATTACCTGAGACTTTACA
37026	35113	CTTATTACCTGAGACTTTAC
37027	35114	ACTTATTACCTGAGACTTTA
37028	35115	TACTTATTACCTGAGACTTT
37029	35116	ATACTTATTACCTGAGACTT
37030	35117	AATACTTATTACCTGAGACT
37031	35118	AAATACTTATTACCTGAGAC
37032	35119	AAAATACTTATTACCTGAGA
37033	35120	TAAAATACTTATTACCTGAG
37034	35121	CTAAAATACTTATTACCTGA
37035	35122	CCTAAAATACTTATTACCTG
37036	35123	GCCTAAAATACTTATTACCT
37037	35124	AGCCTAAAATACTTATTACC
37038	35125	GAGCCTAAAATACTTATTAC
37039	35126	AGAGCCTAAAATACTTATTA
37040	35127	TAGAGCCTAAAATACTTATT
37041	35128	CTAGAGCCTAAAATACTTAT
37042	35129	CCTAGAGCCTAAAATACTTA
37043	35130	CCCTAGAGCCTAAAATACTT
37044	35131	GCCCTAGAGCCTAAAATACT
37045	35132	GGCCCTAGAGCCTAAAATAC
37046	35133	TGGCCCTAGAGCCTAAAATA
37047	35134	ATGGCCCTAGAGCCTAAAAT
37048	35135	TATGGCCCTAGAGCCTAAAA
37049	35136	ATATGGCCCTAGAGCCTAAA
37050	35137	TATATGGCCCTAGAGCCTAA
37051	35138	CTATATGGCCCTAGAGCCTA
37052	35139	GCTATATGGCCCTAGAGCCT
37053	35140	AGCTATATGGCCCTAGAGCC
37054	35141	AAGCTATATGGCCCTAGAGC
37055	35142	GAAGCTATATGGCCCTAGAG

86132	84219	ATGGATTTAGCGCCAAATAC
86133	84220	GATGGATTTAGCGCCAAATA
86134	84221	TGATGGATTTAGCGCCAAAT
86135	84222	ATGATGGATTTAGCGCCAAA
86136	84223	AATGATGGATTTAGCGCCAA
86137	84224	CAATGATGGATTTAGCGCCA
86138	84225	GCAATGATGGATTTAGCGCC
86139	84226	GGCAATGATGGATTTAGCGC
86140	84227	TGGCAATGATGGATTTAGCG
86141	84228	GTGGCAATGATGGATTTAGC
86142	84229	TGTGGCAATGATGGATTTAG
86143	84230	ATGTGGCAATGATGGATTTA
86144	84231	TATGTGGCAATGATGGATTT
86145	84232	ATATGTGGCAATGATGGATT
86146	84233	GATATGTGGCAATGATGGAT
86147	84234	TGATATGTGGCAATGATGGA
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86151	84238	TATTTGATATGTGGCAATGA
86152	84239	GTATTTGATATGTGGCAATG
86153	84240	TGTATTTGATATGTGGCAAT
86154	84241	CTGTATTTGATATGTGGCAA
86155	84242	CCTGTATTTGATATGTGGCA
86156	84243	CCCTGTATTTGATATGTGGC
86157	84244	TCCCTGTATTTGATATGTGG
86158	84245	ATCCCTGTATTTGATATGTG
86159	84246	TATCCCTGTATTTGATATGT
86160	84247	ATATCCCTGTATTTGATATG
86161	84248	CATATCCCTGTATTTGATAT
86162	84249	ACATATCCCTGTATTTGATA
86163	84250	AACATATCCCTGTATTTGAT
86164	84251	CAACATATCCCTGTATTTGA
86165	84252	ACAACATATCCCTGTATTTG
86166	84253	TACAACATATCCCTGTATTT
86167	84254	CTACAACATATCCCTGTATT
86168	84255	TCTACAACATATCCCTGTAT
86169	84256	TTCTACAACATATCCCTGTA
86170	84257	TTTCTACAACATATCCCTGT
86171	84258	CTTTCTACAACATATCCCTG
86172	84259	CCTTTCTACAACATATCCCT
86173	84260	ACCTTTCTACAACATATCCC
86174	84261	TACCTTTCTACAACATATCC
86175	84262	TTACCTTTCTACAACATATC
86176	84263	GTTACCTTTCTACAACATAT
86177	84264	TGTTACCTTTCTACAACATA
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86181	84268	AGAATGTTACCTTTCTACAA
86182	84269	TAGAATGTTACCTTTCTACA
86183	84270	TTAGAATGTTACCTTTCTAC
86184	84271	ATTAGAATGTTACCTTTCTA
86185	84272	AATTAGAATGTTACCTTTCT
86186	84273	AAATTAGAATGTTACCTTTC
86187	84274	TAAATTAGAATGTTACCTTT
86188	84275	TTAAATTAGAATGTTACCTT
86189	84276	TTTAAATTAGAATGTTACCT
86190	84277	ATTTAAATTAGAATGTTACC
86191	84278	CATTTAAATTAGAATGTTAC
86192	84279	GCATTTAAATTAGAATGTTA
86193	84280	GGCATTTAAATTAGAATGTT
86194	84281	TGGCATTTAAATTAGAATGT
86195	84282	GTGGCATTTAAATTAGAATG
86196	84283	GGTGGCATTTAAATTAGAAT
86197	84284	GGGTGGCATTTAAATTAGAA
86198	84285	TGGGTGGCATTTAAATTAGA
86199	84286	ATGGGTGGCATTTAAATTAG
86200	84287	TATGGGTGGCATTTAAATTA
86201	84288	ATATGGGTGGCATTTAAATT
86202	84289	TATATGGGTGGCATTTAAAT

135279	133366	GAGATCAAGACCATCCTGGC
135280	133367	GGAGATCAAGACCATCCTGG
135281	133368	AGGAGATCAAGACCATCCTG
135282	133369	CAGGAGATCAAGACCATCCT
135283	133370	TCAGGAGATCAAGACCATCC
135284	133371	GTCAGGAGATCAAGACCATC
135285	133372	GGTCAGGAGATCAAGACCAT
135286	133373	AGGTCAGGAGATCAAGACCA
135287	133374	GAGGTCAGGAGATCAAGACC
135288	133375	CGAGGTCAGGAGATCAAGAC
135289	133376	ACGAGGTCAGGAGATCAAGA
135290	133377	CACGAGGTCAGGAGATCAAG
135291	133378	TCACGAGGTCAGGAGATCAA
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135293	133380	GATCACGAGGTCAGGAGATC
135294	133381	GGATCACGAGGTCAGGAGAT
135295	133382	CGGATCACGAGGTCAGGAGA
135296	133383	GCGGATCACGAGGTCAGGAG
135297	133384	GGCGGATCACGAGGTCAGGA
135298	133385	AGGCGGATCACGAGGTCAGG
135299	133386	CAGGCGGATCACGAGGTCAG
135300	133387	GCAGGCGGATCACGAGGTCA
135301	133388	GGCAGGCGGATCACGAGGTC
135302	133389	AGGCAGGCGGATCACGAGGT
135303	133390	GAGGCAGGCGGATCACGAGG
135304	133391	TGAGGCAGGCGGATCACGAG
135305	133392	CTGAGGCAGGCGGATCACGA
135306	133393	GCTGAGGCAGGCGGATCACG
135307	133394	GGCTGAGGCAGGCGGATCAC
135308	133395	AGGCTGAGGCAGGCGGATCA
135309	133396	GAGGCTGAGGCAGGCGGATC
135310	133397	GGAGGCTGAGGCAGGCGGAT
135311	133398	GGGAGGCTGAGGCAGGCGGA
135312	133399	TGGGAGGCTGAGGCAGGCGG
135313	133400	TTGGGAGGCTGAGGCAGGCG
135314	133401	TTTGGGAGGCTGAGGCAGGC
135315	133402	CTTTGGGAGGCTGAGGCAGG
135316	133403	ACTTTGGGAGGCTGAGGCAG
135317	133404	CACTTTGGGAGGCTGAGGCA
135318	133405	GCACTTTGGGAGGCTGAGGC
135319	133406	AGCACTTTGGGAGGCTGAGG
135320	133407	CAGCACTTTGGGAGGCTGAG
135321	133408	CCAGCACTTTGGGAGGCTGA
135322	133409	CCCAGCACTTTGGGAGGCTG
135323	133410	TCCCAGCACTTTGGGAGGCT
135324	133411	ATCCCAGCACTTTGGGAGGC
135325	133412	AATCCCAGCACTTTGGGAGG
135326	133413	TAATCCCAGCACTTTGGGAG
135327	133414	GTAATCCCAGCACTTTGGGA
135328	133415	TGTAATCCCAGCACTTTGGG
135329	133416	CTGTAATCCCAGCACTTTGG
135330	133417	CCTGTAATCCCAGCACTTTG
135331	133418	GCCTGTAATCCCAGCACTTT
135332	133419	CGCCTGTAATCCCAGCACTT
135333	133420	ACGCCTGTAATCCCAGCACT
135334	133421	CACGCCTGTAATCCCAGCAC
135335	133422	TCACGCCTGTAATCCCAGCA
135336	133423	CTCACGCCTGTAATCCCAGC
135337	133424	GCTCACGCCTGTAATCCCAG
135338	133425	GGCTCACGCCTGTAATCCCA
135339	133426	TGGCTCACGCCTGTAATCCC
135340	133427	GTGGCTCACGCCTGTAATCC
135341	133428	AGTGGCTCACGCCTGTAATC
135342	133429	CAGTGGCTCACGCCTGTAAT
135343	133430	ACAGTGGCTCACGCCTGTAA
135344	133431	CACAGTGGCTCACGCCTGTA
135345	133432	GCACAGTGGCTCACGCCTGT
135346	133433	GGCACAGTGGCTCACGCCTG
135347	133434	GGGCACAGTGGCTCACGCCT
135348	133435	TGGGCACAGTGGCTCACGCC
135349	133436	CTGGGCACAGTGGCTCACGC

37056	35143	AGAAGCTATATGGCCCTAGA
37057	35144	GAGAAGCTATATGGCCCTAG
37058	35145	AGAGAAGCTATATGGCCCTA
37059	35146	CAGAGAAGCTATATGGCCCT
37060	35147	ACAGAGAAGCTATATGGCCC
37061	35148	AACAGAGAAGCTATATGGCC
37062	35149	CAACAGAGAAGCTATATGGC
37063	35150	GCAACAGAGAAGCTATATGG
37064	35151	TGCAACAGAGAAGCTATATG
37065	35152	ATGCAACAGAGAAGCTATAT
37066	35153	TATGCAACAGAGAAGCTATA
37067	35154	ATATGCAACAGAGAAGCTAT
37068	35155	GATATGCAACAGAGAAGCTA
37069	35156	GGATATGCAACAGAGAAGCT
37070	35157	AGGATATGCAACAGAGAAGC
37071	35158	AAGGATATGCAACAGAGAAG
37072	35159	AAAGGATATGCAACAGAGAA
37073	35160	AAAAGGATATGCAACAGAGA
37074	35161	AAAAAGGATATGCAACAGAG
37075	35162	AAAAAAGGATATGCAACAGA
37076	35163	AAAAAAAGGATATGCAACAG
37077	35164	AAAAAAAAGGATATGCAACA
37078	35165	AAAAAAAAAGGATATGCAAC
37079	35166	AAAAAAAAAAGGATATGCAA
37080	35167	AAAAAAAAAAAGGATATGCA
37081	35168	AAAAAAAAAAAAGGATATGC
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37083	35170	GAAAAAAAAAAAAAGGATAT
37084	35171	GGAAAAAAAAAAAAAGGATA
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37086	35173	ATGGAAAAAAAAAAAAAGGA
37087	35174	AATGGAAAAAAAAAAAAAGG
37088	35175	AAATGGAAAAAAAAAAAAAG
37089	35176	GAAATGGAAAAAAAAAAAAA
37090	35177	GGAAATGGAAAAAAAAAAAA
37091	35178	GGGAAATGGAAAAAAAAAAA
37092	35179	GGGGAAATGGAAAAAAAAAA
37093	35180	AGGGGAAATGGAAAAAAAAA
37094	35181	GAGGGGAAATGGAAAAAAAA
37095	35182	TGAGGGGAAATGGAAAAAAA
37096	35183	TTGAGGGGAAATGGAAAAAA
37097	35184	TTTGAGGGGAAATGGAAAAA
37098	35185	ATTTGAGGGGAAATGGAAAA
37099	35186	AATTTGAGGGGAAATGGAAA
37100	35187	GAATTTGAGGGGAAATGGAA
37101	35188	GGAATTTGAGGGGAAATGGA
37102	35189	AGGAATTTGAGGGGAAATGG
37103	35190	AAGGAATTTGAGGGGAAATG
37104	35191	AAAGGAATTTGAGGGGAAAT
37105	35192	AAAAGGAATTTGAGGGGAAA
37106	35193	TAAAAGGAATTTGAGGGGAA
37107	35194	GTAAAAGGAATTTGAGGGGA
37108	35195	GGTAAAAGGAATTTGAGGGG
37109	35196	TGGTAAAAGGAATTTGAGGG
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37111	35198	TATGGTAAAAGGAATTTGAG
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37113	35200	CTTATGGTAAAAGGAATTTG
37114	35201	GCTTATGGTAAAAGGAATTT
37115	35202	TGCTTATGGTAAAAGGAATT
37116	35203	TTGCTTATGGTAAAAGGAAT
37117	35204	GTTGCTTATGGTAAAAGGAA
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37119	35206	GAGTTGCTTATGGTAAAAGG
37120	35207	AGAGTTGCTTATGGTAAAAG
37121	35208	AAGAGTTGCTTATGGTAAAA
37122	35209	CAAGAGTTGCTTATGGTAAA
37123	35210	TCAAGAGTTGCTTATGGTAA
37124	35211	CTCAAGAGTTGCTTATGGTA
37125	35212	CCTCAAGAGTTGCTTATGGT
37126	35213	TCCTCAAGAGTTGCTTATGG

86203	84290	ATATATGGGTGGCATTTAAA
86204	84291	AATATATGGGTGGCATTTAA
86205	84292	TAATATATGGGTGGCATTTA
86206	84293	TTAATATATGGGTGGCATTT
86207	84294	TTTAATATATGGGTGGCATT
86208	84295	TTTTAATATATGGGTGGCAT
86209	84296	TTTTTAATATATGGGTGGCA
86210	84297	GTTTTTAATATATGGGTGGC
86211	84298	GGTTTTTAATATATGGGTGG
86212	84299	AGGTTTTTAATATATGGGTG
86213	84300	CAGGTTTTTAATATATGGGT
86214	84301	ACAGGTTTTTAATATATGGG
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86218	84305	GAAAACAGGTTTTTAATATA
86219	84306	AGAAAACAGGTTTTTAATAT
86220	84307	CAGAAAACAGGTTTTTAATA
86221	84308	TCAGAAAACAGGTTTTTAAT
86222	84309	TTCAGAAAACAGGTTTTTAA
86223	84310	ATTCAGAAAACAGGTTTTTA
86224	84311	GATTCAGAAAACAGGTTTTT
86225	84312	TGATTCAGAAAACAGGTTTT
86226	84313	ATGATTCAGAAAACAGGTTT
86227	84314	TATGATTCAGAAAACAGGTT
86228	84315	TTATGATTCAGAAAACAGGT
86229	84316	ATTATGATTCAGAAAACAGG
86230	84317	CATTATGATTCAGAAAACAG
86231	84318	ACATTATGATTCAGAAAACA
86232	84319	GACATTATGATTCAGAAAAC
86233	84320	GGACATTATGATTCAGAAAA
86234	84321	AGGACATTATGATTCAGAAA
86235	84322	AAGGACATTATGATTCAGAA
86236	84323	AAAGGACATTATGATTCAGA
86237	84324	AAAAGGACATTATGATTCAG
86238	84325	CAAAAGGACATTATGATTCA
86239	84326	TCAAAAGGACATTATGATTC
86240	84327	ATCAAAAGGACATTATGATT
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86243	84330	AGTATCAAAAGGACATTATG
86244	84331	TAGTATCAAAAGGACATTAT
86245	84332	CTAGTATCAAAAGGACATTA
86246	84333	ACTAGTATCAAAAGGACATT
86247	84334	AACTAGTATCAAAAGGACAT
86248	84335	GAACTAGTATCAAAAGGACA
86249	84336	AGAACTAGTATCAAAAGGAC
86250	84337	CAGAACTAGTATCAAAAGGA
86251	84338	TCAGAACTAGTATCAAAAGG
86252	84339	TTCAGAACTAGTATCAAAAG
86253	84340	ATTCAGAACTAGTATCAAAA
86254	84341	TATTCAGAACTAGTATCAAA
86255	84342	ATATTCAGAACTAGTATCAA
86256	84343	AATATTCAGAACTAGTATCA
86257	84344	AAATATTCAGAACTAGTATC
86258	84345	CAAATATTCAGAACTAGTAT
86259	84346	ACAAATATTCAGAACTAGTA
86260	84347	CACAAATATTCAGAACTAGT
86261	84348	ACACAAATATTCAGAACTAG
86262	84349	AACACAAATATTCAGAACTA
86263	84350	TAACACAAATATTCAGAACT
86264	84351	TTAACACAAATATTCAGAAC
86265	84352	TTTAACACAAATATTCAGAA
86266	84353	TTTTAACACAAATATTCAGA
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86269	84356	AAATTTTAACACAAATATTC
86270	84357	AAAATTTTAACACAAATATT
86271	84358	TAAAATTTTAACACAAATAT
86272	84359	TTAAAATTTTAACACAAATA
86273	84360	ATTAAAATTTTAACACAAAT

135350	133437	GCTGGGCACAGTGGCTCACG
135351	133438	GGCTGGGCACAGTGGCTCAC
135352	133439	AGGCTGGGCACAGTGGCTCA
135353	133440	GAGGCTGGGCACAGTGGCTC
135354	133441	AGAGGCTGGGCACAGTGGCT
135355	133442	AAGAGGCTGGGCACAGTGGC
135356	133443	AAAGAGGCTGGGCACAGTGG
135357	133444	AAAAGAGGCTGGGCACAGTG
135358	133445	AAAAAGAGGCTGGGCACAGT
135359	133446	AAAAAAGAGGCTGGGCACAG
135360	133447	AAAAAAAGAGGCTGGGCACA
135361	133448	AAAAAAAAGAGGCTGGGCAC
135362	133449	AAAAAAAAAGAGGCTGGGCA
135363	133450	AAAAAAAAAAGAGGCTGGGC
135364	133451	AAAAAAAAAAAGAGGCTGGG
135365	133452	AAAAAAAAAAAAGAGGCTGG
135366	133453	AAAAAAAAAAAAAGAGGCTG
135367	133454	TAAAAAAAAAAAAAGAGGCT
135368	133455	ATAAAAAAAAAAAAAGAGGC
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135370	133457	AAATAAAAAAAAAAAAAGAG
135371	133458	AAAATAAAAAAAAAAAAAGA
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135373	133460	AAAAAATAAAAAAAAAAAAA
135374	133461	TAAAAAATAAAAAAAAAAAA
135375	133462	ATAAAAAATAAAAAAAAAAA
135376	133463	AATAAAAAATAAAAAAAAAA
135377	133464	AAATAAAAAATAAAAAAAAA
135378	133465	TAAATAAAAAATAAAAAAAA
135379	133466	ATAAATAAAAAATAAAAAAA
135380	133467	AATAAATAAAAAATAAAAAA
135381	133468	AAATAAATAAAAAATAAAAA
135382	133469	AAAATAAATAAAAAATAAAA
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135385	133472	TAAAAAATAAATAAAAAATA
135386	133473	ATAAAAAATAAATAAAAAAT
135387	133474	AATAAAAAATAAATAAAAAA
135388	133475	AAATAAAAAATAAATAAAAA
135389	133476	AAAATAAAAAATAAATAAAA
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135392	133479	AAAAAAATAAAAAATAAATA
135393	133480	AAAAAAAATAAAAAATAAAT
135394	133481	AAAAAAAAATAAAAAATAAA
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135396	133483	TAAAAAAAAAATAAAAAATA
135397	133484	TTAAAAAAAAAATAAAAAAT
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135401	133488	AAAATTAAAAAAAAAATAAA
135402	133489	AAAAATTAAAAAAAAAATAA
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135405	133492	CTCAAAAATTAAAAAAAAAA
135406	133493	TCTCAAAAATTAAAAAAAAA
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135408	133495	CTTCTCAAAAATTAAAAAAA
135409	133496	CCTTCTCAAAAATTAAAAAA
135410	133497	TCCTTCTCAAAAATTAAAAA
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135414	133501	AGACTCCTTCTCAAAAATTA
135415	133502	GAGACTCCTTCTCAAAAATT
135416	133503	GGAGACTCCTTCTCAAAAAT
135417	133504	GGGAGACTCCTTCTCAAAAA
135418	133505	AGGGAGACTCCTTCTCAAAA
135419	133506	GAGGGAGACTCCTTCTCAAA
135420	133507	AGAGGGAGACTCCTTCTCAA

37127	35214	TTCCTCAAGAGTTGCTTATG
37128	35215	GTTCCTCAAGAGTTGCTTAT
37129	35216	TGTTCCTCAAGAGTTGCTTA
37130	35217	ATGTTCCTCAAGAGTTGCTT
37131	35218	TATGTTCCTCAAGAGTTGCT
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37133	35220	TTTATGTTCCTCAAGAGTTG
37134	35221	TTTTATGTTCCTCAAGAGTT
37135	35222	TTTTTATGTTCCTCAAGAGT
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37137	35224	GATTTTTATGTTCCTCAAGA
37138	35225	TGATTTTTATGTTCCTCAAG
37139	35226	ATGATTTTTATGTTCCTCAA
37140	35227	AATGATTTTTATGTTCCTCA
37141	35228	GAATGATTTTTATGTTCCTC
37142	35229	AGAATGATTTTTATGTTCCT
37143	35230	AAGAATGATTTTTATGTTCC
37144	35231	TAAGAATGATTTTTATGTTC
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37146	35233	GCTAAGAATGATTTTTATGT
37147	35234	GGCTAAGAATGATTTTTATG
37148	35235	GGGCTAAGAATGATTTTTAT
37149	35236	TGGGCTAAGAATGATTTTTA
37150	35237	CTGGGCTAAGAATGATTTTT
37151	35238	TCTGGGCTAAGAATGATTTT
37152	35239	TTCTGGGCTAAGAATGATTT
37153	35240	CTTCTGGGCTAAGAATGATT
37154	35241	GCTTCTGGGCTAAGAATGAT
37155	35242	GGCTTCTGGGCTAAGAATGA
37156	35243	TGGCTTCTGGGCTAAGAATG
37157	35244	CTGGCTTCTGGGCTAAGAAT
37158	35245	TCTGGCTTCTGGGCTAAGAA
37159	35246	GTCTGGCTTCTGGGCTAAGA
37160	35247	GGTCTGGCTTCTGGGCTAAG
37161	35248	TGGTCTGGCTTCTGGGCTAA
37162	35249	TTGGTCTGGCTTCTGGGCTA
37163	35250	TTTGGTCTGGCTTCTGGGCT
37164	35251	TTTTGGTCTGGCTTCTGGGC
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37166	35253	TGTTTTGGTCTGGCTTCTGG
37167	35254	CTGTTTTGGTCTGGCTTCTG
37168	35255	CCTGTTTTGGTCTGGCTTCT
37169	35256	ACCTGTTTTGGTCTGGCTTC
37170	35257	AACCTGTTTTGGTCTGGCTT
37171	35258	CAACCTGTTTTGGTCTGGCT
37172	35259	ACAACCTGTTTTGGTCTGGC
37173	35260	CACAACCTGTTTTGGTCTGG
37174	35261	CCACAACCTGTTTTGGTCTG
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37176	35263	GCCCACAACCTGTTTTGGTC
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37179	35266	ACAGCCCACAACCTGTTTTG
37180	35267	TACAGCCCACAACCTGTTTT
37181	35268	CTACAGCCCACAACCTGTTT
37182	35269	ACTACAGCCCACAACCTGTT
37183	35270	CACTACAGCCCACAACCTGT
37184	35271	ACACTACAGCCCACAACCTG
37185	35272	GACACTACAGCCCACAACCT
37186	35273	GGACACTACAGCCCACAACC
37187	35274	AGGACACTACAGCCCACAAC
37188	35275	CAGGACACTACAGCCCACAA
37189	35276	TCAGGACACTACAGCCCACA
37190	35277	GTCAGGACACTACAGCCCAC
37191	35278	GGTCAGGACACTACAGCCCA
37192	35279	GGGTCAGGACACTACAGCCC
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37194	35281	AGGGGTCAGGACACTACAGC
37195	35282	CAGGGGTCAGGACACTACAG
37196	35283	TCAGGGGTCAGGACACTACA
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86276	84363	CAGATTAAAATTTTAACACA
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86278	84365	ATCAGATTAAAATTTTAACA
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86282	84369	ACAAATCAGATTAAAATTTT
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86295	84382	CTAATTTTAATGAACAAATC
86296	84383	ACTAATTTTAATGAACAAAT
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86299	84386	TTAACTAATTTTAATGAACA
86300	84387	ATTAACTAATTTTAATGAAC
86301	84388	TATTAACTAATTTTAATGAA
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86303	84390	AATATTAACTAATTTTAATG
86304	84391	CAATATTAACTAATTTTAAT
86305	84392	GCAATATTAACTAATTTTAA
86306	84393	AGCAATATTAACTAATTTTA
86307	84394	AAGCAATATTAACTAATTTT
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86309	84396	ATAAGCAATATTAACTAATT
86310	84397	CATAAGCAATATTAACTAAT
86311	84398	ACATAAGCAATATTAACTAA
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86325	84412	CTTTATTAGTCCCAACATAA
86326	84413	ACTTTATTAGTCCCAACATA
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86328	84415	AAACTTTATTAGTCCCAACA
86329	84416	AAAACTTTATTAGTCCCAAC
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86334	84421	TGCGGAAAACTTTATTAGTC
86335	84422	GTGCGGAAAACTTTATTAGT
86336	84423	TGTGCGGAAAACTTTATTAG
86337	84424	TTGTGCGGAAAACTTTATTA
86338	84425	TTTGTGCGGAAAACTTTATT
86339	84426	TTTTGTGCGGAAAACTTTAT
86340	84427	ATTTTGTGCGGAAAACTTTA
86341	84428	CATTTTGTGCGGAAAACTTT
86342	84429	ACATTTTGTGCGGAAAACTT
86343	84430	CACATTTTGTGCGGAAAACT
86344	84431	ACACATTTTGTGCGGAAAAC

135421	133508	CAGAGGGAGACTCCTTCTCA
135422	133509	GCAGAGGGAGACTCCTTCTC
135423	133510	GGCAGAGGGAGACTCCTTCT
135424	133511	TGGCAGAGGGAGACTCCTTC
135425	133512	GTGGCAGAGGGAGACTCCTT
135426	133513	GGTGGCAGAGGGAGACTCCT
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135429	133516	CTGGGTGGCAGAGGGAGACT
135430	133517	CCTGGGTGGCAGAGGGAGAC
135431	133518	GCCTGGGTGGCAGAGGGAGA
135432	133519	AGCCTGGGTGGCAGAGGGAG
135433	133520	CAGCCTGGGTGGCAGAGGGA
135434	133521	CCAGCCTGGGTGGCAGAGGG
135435	133522	TCCAGCCTGGGTGGCAGAGG
135436	133523	CTCCAGCCTGGGTGGCAGAG
135437	133524	ACTCCAGCCTGGGTGGCAGA
135438	133525	CACTCCAGCCTGGGTGGCAG
135439	133526	GCACTCCAGCCTGGGTGGCA
135440	133527	TGCACTCCAGCCTGGGTGGC
135441	133528	CTGCACTCCAGCCTGGGTGG
135442	133529	ACTGCACTCCAGCCTGGGTG
135443	133530	CACTGCACTCCAGCCTGGGT
135444	133531	CCACTGCACTCCAGCCTGGG
135445	133532	GCCACTGCACTCCAGCCTGG
135446	133533	CGCCACTGCACTCCAGCCTG
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135449	133536	TCGCGCCACTGCACTCCAGC
135450	133537	ATCGCGCCACTGCACTCCAG
135451	133538	GATCGCGCCACTGCACTCCA
135452	133539	AGATCGCGCCACTGCACTCC
135453	133540	GAGATCGCGCCACTGCACTC
135454	133541	TGAGATCGCGCCACTGCACT
135455	133542	CTGAGATCGCGCCACTGCAC
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135459	133546	GGAGCTGAGATCGCGCCACT
135460	133547	GGGAGCTGAGATCGCGCCAC
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135463	133550	GCAGGGAGCTGAGATCGCGC
135464	133551	TGCAGGGAGCTGAGATCGCG
135465	133552	TTGCAGGGAGCTGAGATCGC
135466	133553	TTTGCAGGGAGCTGAGATCG
135467	133554	GTTTGCAGGGAGCTGAGATC
135468	133555	AGTTTGCAGGGAGCTGAGAT
135469	133556	GAGTTTGCAGGGAGCTGAGA
135470	133557	GGAGTTTGCAGGGAGCTGAG
135471	133558	CGGAGTTTGCAGGGAGCTGA
135472	133559	GCGGAGTTTGCAGGGAGCTG
135473	133560	GGCGGAGTTTGCAGGGAGCT
135474	133561	AGGCGGAGTTTGCAGGGAGC
135475	133562	GAGGCGGAGTTTGCAGGGAG
135476	133563	GGAGGCGGAGTTTGCAGGGA
135477	133564	AGGAGGCGGAGTTTGCAGGG
135478	133565	CAGGAGGCGGAGTTTGCAGG
135479	133566	CCAGGAGGCGGAGTTTGCAG
135480	133567	CCCAGGAGGCGGAGTTTGCA
135481	133568	ACCCAGGAGGCGGAGTTTGC
135482	133569	AACCCAGGAGGCGGAGTTTG
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135485	133572	TTGAACCCAGGAGGCGGAGT
135486	133573	CTTGAACCCAGGAGGCGGAG
135487	133574	GCTTGAACCCAGGAGGCGGA
135488	133575	TGCTTGAACCCAGGAGGCGG
135489	133576	CTGCTTGAACCCAGGAGGCG
135490	133577	ACTGCTTGAACCCAGGAGGC
135491	133578	AACTGCTTGAACCCAGGAGG

37198	35285	AATCAGGGGTCAGGACACTA
37199	35286	AAATCAGGGGTCAGGACACT
37200	35287	TAAATCAGGGGTCAGGACAC
37201	35288	TTAAATCAGGGGTCAGGACA
37202	35289	TTTAAATCAGGGGTCAGGAC
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37204	35291	TCTTTAAATCAGGGGTCAGG
37205	35292	ATCTTTAAATCAGGGGTCAG
37206	35293	AATCTTTAAATCAGGGGTCA
37207	35294	CAATCTTTAAATCAGGGGTC
37208	35295	TCAATCTTTAAATCAGGGGT
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37214	35301	AAGCTATCAATCTTTAAATC
37215	35302	AAAGCTATCAATCTTTAAAT
37216	35303	CAAAGCTATCAATCTTTAAA
37217	35304	TCAAAGCTATCAATCTTTAA
37218	35305	TTCAAAGCTATCAATCTTTA
37219	35306	TTTCAAAGCTATCAATCTTT
37220	35307	ATTTCAAAGCTATCAATCTT
37221	35308	CATTTCAAAGCTATCAATCT
37222	35309	CCATTTCAAAGCTATCAATC
37223	35310	TCCATTTCAAAGCTATCAAT
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37232	35319	TTAAAACTTTCCATTTCAAA
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37237	35324	GAAAGTTAAAACTTTCCATT
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37239	35326	AAGAAAGTTAAAACTTTCCA
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37245	35332	AAAAAAAAGAAAGTTAAAAC
37246	35333	AAAAAAAAAGAAAGTTAAAA
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37251	35338	GAAAGAAAAAAAAAGAAAGT
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37256	35343	CAAGGGAAAGAAAAAAAAAG
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37261	35348	CAGAACAAGGGAAAGAAAAA
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37264	35351	AATCAGAACAAGGGAAAGAA
37265	35352	CAATCAGAACAAGGGAAAGA
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37267	35354	CCCAATCAGAACAAGGGAAA
37268	35355	GCCCAATCAGAACAAGGGAA

86345	84432	AACACATTTTGTGCGGAAAA
86346	84433	AAACACATTTTGTGCGGAAA
86347	84434	GAAACACATTTTGTGCGGAA
86348	84435	AGAAACACATTTTGTGCGGA
86349	84436	GAGAAACACATTTTGTGCGG
86350	84437	GGAGAAACACATTTTGTGCG
86351	84438	AGGAGAAACACATTTTGTGC
86352	84439	CAGGAGAAACACATTTTGTG
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86360	84447	CAGGGAAGCAGGAGAAACAC
86361	84448	CCAGGGAAGCAGGAGAAACA
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86363	84450	CTCCAGGGAAGCAGGAGAAA
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86365	84452	TTCTCCAGGGAAGCAGGAGA
86366	84453	TTTCTCCAGGGAAGCAGGAG
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86370	84457	CAGTTTTCTCCAGGGAAGCA
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86373	84460	ATACAGTTTTCTCCAGGGAA
86374	84461	AATACAGTTTTCTCCAGGGA
86375	84462	CAATACAGTTTTCTCCAGGG
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86378	84465	AGCCAATACAGTTTTCTCCA
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86380	84467	GTAGCCAATACAGTTTTCTC
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86412	84499	TGCCTGCTTAGATGGTAACA
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135492	133579	GAACTGCTTGAACCCAGGAG
135493	133580	AGAACTGCTTGAACCCAGGA
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135495	133582	GGAGAACTGCTTGAACCCAG
135496	133583	AGGAGAACTGCTTGAACCCA
135497	133584	CAGGAGAACTGCTTGAACCC
135498	133585	GCAGGAGAACTGCTTGAACC
135499	133586	GGCAGGAGAACTGCTTGAAC
135500	133587	AGGCAGGAGAACTGCTTGAA
135501	133588	GAGGCAGGAGAACTGCTTGA
135502	133589	TGAGGCAGGAGAACTGCTTG
135503	133590	CTGAGGCAGGAGAACTGCTT
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135505	133592	GGCTGAGGCAGGAGAACTGC
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135510	133597	CAGGAGGCTGAGGCAGGAGA
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135512	133599	CTCAGGAGGCTGAGGCAGGA
135513	133600	ACTCAGGAGGCTGAGGCAGG
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135515	133602	CTACTCAGGAGGCTGAGGCA
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135519	133606	CCAGCTACTCAGGAGGCTGA
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135522	133609	GTCCCAGCTACTCAGGAGGC
135523	133610	AGTCCCAGCTACTCAGGAGG
135524	133611	TAGTCCCAGCTACTCAGGAG
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135528	133615	CCTGTAGTCCCAGCTACTCA
135529	133616	ACCTGTAGTCCCAGCTACTC
135530	133617	CACCTGTAGTCCCAGCTACT
135531	133618	GCACCTGTAGTCCCAGCTAC
135532	133619	GGCACCTGTAGTCCCAGCTA
135533	133620	GGGCACCTGTAGTCCCAGCT
135534	133621	CGGGCACCTGTAGTCCCAGC
135535	133622	GCGGGCACCTGTAGTCCCAG
135536	133623	GGCGGGCACCTGTAGTCCCA
135537	133624	TGGCGGGCACCTGTAGTCCC
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135539	133626	GGTGGCGGGCACCTGTAGTC
135540	133627	TGGTGGCGGGCACCTGTAGT
135541	133628	GTGGTGGCGGGCACCTGTAG
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135544	133631	GGTGTGGTGGCGGGCACCTG
135545	133632	AGGTGTGGTGGCGGGCACCT
135546	133633	CAGGTGTGGTGGCGGGCACC
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135548	133635	GCCAGGTGTGGTGGCGGGCA
135549	133636	AGCCAGGTGTGGTGGCGGGC
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135551	133638	TTAGCCAGGTGTGGTGGCGG
135552	133639	ATTAGCCAGGTGTGGTGGCG
135553	133640	AATTAGCCAGGTGTGGTGGC
135554	133641	AAATTAGCCAGGTGTGGTGG
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135556	133643	AAAAATTAGCCAGGTGTGGT
135557	133644	CAAAAATTAGCCAGGTGTGG
135558	133645	ACAAAAATTAGCCAGGTGTG
135559	133646	CACAAAAATTAGCCAGGTGT
135560	133647	ACACAAAAATTAGCCAGGTG
135561	133648	AACACAAAAATTAGCCAGGT
135562	133649	AAACACAAAAATTAGCCAGG

37269	35356	AGCCCAATCAGAACAAGGGA
37270	35357	CAGCCCAATCAGAACAAGGG
37271	35358	ACAGCCCAATCAGAACAAGG
37272	35359	AACAGCCCAATCAGAACAAG
37273	35360	TAACAGCCCAATCAGAACAA
37274	35361	TTAACAGCCCAATCAGAACA
37275	35362	ATTAACAGCCCAATCAGAAC
37276	35363	AATTAACAGCCCAATCAGAA
37277	35364	GAATTAACAGCCCAATCAGA
37278	35365	TGAATTAACAGCCCAATCAG
37279	35366	ATGAATTAACAGCCCAATCA
37280	35367	AATGAATTAACAGCCCAATC
37281	35368	TAATGAATTAACAGCCCAAT
37282	35369	CTAATGAATTAACAGCCCAA
37283	35370	CCTAATGAATTAACAGCCCA
37284	35371	ACCTAATGAATTAACAGCCC
37285	35372	TACCTAATGAATTAACAGCC
37286	35373	ATACCTAATGAATTAACAGC
37287	35374	AATACCTAATGAATTAACAG
37288	35375	AAATACCTAATGAATTAACA
37289	35376	TAAATACCTAATGAATTAAC
37290	35377	GTAAATACCTAATGAATTAA
37291	35378	AGTAAATACCTAATGAATTA
37292	35379	GAGTAAATACCTAATGAATT
37293	35380	TGAGTAAATACCTAATGAAT
37294	35381	CTGAGTAAATACCTAATGAA
37295	35382	ACTGAGTAAATACCTAATGA
37296	35383	CACTGAGTAAATACCTAATG
37297	35384	ACACTGAGTAAATACCTAAT
37298	35385	CACACTGAGTAAATACCTAA
37299	35386	ACACACTGAGTAAATACCTA
37300	35387	TACACACTGAGTAAATACCT
37301	35388	ATACACACTGAGTAAATACC
37302	35389	GATACACACTGAGTAAATAC
37303	35390	TGATACACACTGAGTAAATA
37304	35391	ATGATACACACTGAGTAAAT
37305	35392	TATGATACACACTGAGTAAA
37306	35393	ATATGATACACACTGAGTAA
37307	35394	CATATGATACACACTGAGTA
37308	35395	TCATATGATACACACTGAGT
37309	35396	CTCATATGATACACACTGAG
37310	35397	CCTCATATGATACACACTGA
37311	35398	GCCTCATATGATACACACTG
37312	35399	TGCCTCATATGATACACACT
37313	35400	ATGCCTCATATGATACACAC
37314	35401	CATGCCTCATATGATACACA
37315	35402	TCATGCCTCATATGATACAC
37316	35403	ATCATGCCTCATATGATACA
37317	35404	AATCATGCCTCATATGATAC
37318	35405	GAATCATGCCTCATATGATA
37319	35406	GGAATCATGCCTCATATGAT
37320	35407	AGGAATCATGCCTCATATGA
37321	35408	GAGGAATCATGCCTCATATG
37322	35409	AGAGGAATCATGCCTCATAT
37323	35410	CAGAGGAATCATGCCTCATA
37324	35411	GCAGAGGAATCATGCCTCAT
37325	35412	AGCAGAGGAATCATGCCTCA
37326	35413	TAGCAGAGGAATCATGCCTC
37327	35414	TTAGCAGAGGAATCATGCCT
37328	35415	ATTAGCAGAGGAATCATGCC
37329	35416	AATTAGCAGAGGAATCATGC
37330	35417	AAATTAGCAGAGGAATCATG
37331	35418	AAAATTAGCAGAGGAATCAT
37332	35419	CAAAATTAGCAGAGGAATCA
37333	35420	CCAAAATTAGCAGAGGAATC
37334	35421	ACCAAAATTAGCAGAGGAAT
37335	35422	TACCAAAATTAGCAGAGGAA
37336	35423	CTACCAAAATTAGCAGAGGA
37337	35424	ACTACCAAAATTAGCAGAGG
37338	35425	CACTACCAAAATTAGCAGAG
37339	35426	CCACTACCAAAATTAGCAGA

86416	84503	GACCTGCCTGCTTAGATGGT
86417	84504	TGACCTGCCTGCTTAGATGG
86418	84505	ATGACCTGCCTGCTTAGATG
86419	84506	TATGACCTGCCTGCTTAGAT
86420	84507	ATATGACCTGCCTGCTTAGA
86421	84508	CATATGACCTGCCTGCTTAG
86422	84509	TCATATGACCTGCCTGCTTA
86423	84510	GTCATATGACCTGCCTGCTT
86424	84511	AGTCATATGACCTGCCTGCT
86425	84512	AAGTCATATGACCTGCCTGC
86426	84513	AAAGTCATATGACCTGCCTG
86427	84514	CAAAGTCATATGACCTGCCT
86428	84515	TCAAAGTCATATGACCTGCC
86429	84516	GTCAAAGTCATATGACCTGC
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86431	84518	CAGTCAAAGTCATATGACCT
86432	84519	TCAGTCAAAGTCATATGACC
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86436	84523	TGCTTCAGTCAAAGTCATAT
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86439	84526	AGATGCTTCAGTCAAAGTCA
86440	84527	TAGATGCTTCAGTCAAAGTC
86441	84528	TTAGATGCTTCAGTCAAAGT
86442	84529	GTTAGATGCTTCAGTCAAAG
86443	84530	GGTTAGATGCTTCAGTCAAA
86444	84531	AGGTTAGATGCTTCAGTCAA
86445	84532	AAGGTTAGATGCTTCAGTCA
86446	84533	CAAGGTTAGATGCTTCAGTC
86447	84534	TCAAGGTTAGATGCTTCAGT
86448	84535	TTCAAGGTTAGATGCTTCAG
86449	84536	CTTCAAGGTTAGATGCTTCA
86450	84537	TCTTCAAGGTTAGATGCTTC
86451	84538	CTCTTCAAGGTTAGATGCTT
86452	84539	GCTCTTCAAGGTTAGATGCT
86453	84540	TGCTCTTCAAGGTTAGATGC
86454	84541	TTGCTCTTCAAGGTTAGATG
86455	84542	CTTGCTCTTCAAGGTTAGAT
86456	84543	ACTTGCTCTTCAAGGTTAGA
86457	84544	AACTTGCTCTTCAAGGTTAG
86458	84545	GAACTTGCTCTTCAAGGTTA
86459	84546	GGAACTTGCTCTTCAAGGTT
86460	84547	TGGAACTTGCTCTTCAAGGT
86461	84548	GTGGAACTTGCTCTTCAAGG
86462	84549	AGTGGAACTTGCTCTTCAAG
86463	84550	CAGTGGAACTTGCTCTTCAA
86464	84551	TCAGTGGAACTTGCTCTTCA
86465	84552	ATCAGTGGAACTTGCTCTTC
86466	84553	AATCAGTGGAACTTGCTCTT
86467	84554	AAATCAGTGGAACTTGCTCT
86468	84555	AAAATCAGTGGAACTTGCTC
86469	84556	GAAAATCAGTGGAACTTGCT
86470	84557	TGAAAATCAGTGGAACTTGC
86471	84558	TTGAAAATCAGTGGAACTTG
86472	84559	CTTGAAAATCAGTGGAACTT
86473	84560	CCTTGAAAATCAGTGGAACT
86474	84561	ACCTTGAAAATCAGTGGAAC
86475	84562	CACCTTGAAAATCAGTGGAA
86476	84563	TCACCTTGAAAATCAGTGGA
86477	84564	GTCACCTTGAAAATCAGTGG
86478	84565	AGTCACCTTGAAAATCAGTG
86479	84566	AAGTCACCTTGAAAATCAGT
86480	84567	GAAGTCACCTTGAAAATCAG
86481	84568	AGAAGTCACCTTGAAAATCA
86482	84569	AAGAAGTCACCTTGAAAATC
86483	84570	AAAGAAGTCACCTTGAAAAT
86484	84571	CAAAGAAGTCACCTTGAAAA
86485	84572	GCAAAGAAGTCACCTTGAAA
86486	84573	AGCAAAGAAGTCACCTTGAA

135563	133650	AAAACACAAAAATTAGCCAG
135564	133651	AAAAACACAAAAATTAGCCA
135565	133652	TAAAAACACAAAAATTAGCC
135566	133653	CTAAAAACACAAAAATTAGC
135567	133654	ACTAAAAACACAAAAATTAG
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135571	133658	CTCTACTAAAAACACAAAAA
135572	133659	TCTCTACTAAAAACACAAAA
135573	133660	GTCTCTACTAAAAACACAAA
135574	133661	TGTCTCTACTAAAAACACAA
135575	133662	CTGTCTCTACTAAAAACACA
135576	133663	CCTGTCTCTACTAAAAACAC
135577	133664	CCCTGTCTCTACTAAAAACA
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135580	133667	AAACCCTGTCTCTACTAAAA
135581	133668	GAAACCCTGTCTCTACTAAA
135582	133669	TGAAACCCTGTCTCTACTAA
135583	133670	GTGAAACCCTGTCTCTACTA
135584	133671	GGTGAAACCCTGTCTCTACT
135585	133672	TGGTGAAACCCTGTCTCTAC
135586	133673	ATGGTGAAACCCTGTCTCTA
135587	133674	CATGGTGAAACCCTGTCTCT
135588	133675	ACATGGTGAAACCCTGTCTC
135589	133676	AACATGGTGAAACCCTGTCT
135590	133677	CAACATGGTGAAACCCTGTC
135591	133678	CCAACATGGTGAAACCCTGT
135592	133679	ACCAACATGGTGAAACCCTG
135593	133680	GACCAACATGGTGAAACCCT
135594	133681	TGACCAACATGGTGAAACCC
135595	133682	CTGACCAACATGGTGAAACC
135596	133683	CCTGACCAACATGGTGAAAC
135597	133684	GCCTGACCAACATGGTGAAA
135598	133685	AGCCTGACCAACATGGTGAA
135599	133686	CAGCCTGACCAACATGGTGA
135600	133687	CCAGCCTGACCAACATGGTG
135601	133688	ACCAGCCTGACCAACATGGT
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135606	133693	TCAAGACCAGCCTGACCAAC
135607	133694	TTCAAGACCAGCCTGACCAA
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135609	133696	AATTCAAGACCAGCCTGACC
135610	133697	GAATTCAAGACCAGCCTGAC
135611	133698	GGAATTCAAGACCAGCCTGA
135612	133699	GGGAATTCAAGACCAGCCTG
135613	133700	CGGGAATTCAAGACCAGCCT
135614	133701	TCGGGAATTCAAGACCAGCC
135615	133702	GTCGGGAATTCAAGACCAGC
135616	133703	GGTCGGGAATTCAAGACCAG
135617	133704	AGGTCGGGAATTCAAGACCA
135618	133705	GAGGTCGGGAATTCAAGACC
135619	133706	TGAGGTCGGGAATTCAAGAC
135620	133707	CTGAGGTCGGGAATTCAAGA
135621	133708	CCTGAGGTCGGGAATTCAAG
135622	133709	ACCTGAGGTCGGGAATTCAA
135623	133710	CACCTGAGGTCGGGAATTCA
135624	133711	TCACCTGAGGTCGGGAATTC
135625	133712	ATCACCTGAGGTCGGGAATT
135626	133713	GATCACCTGAGGTCGGGAAT
135627	133714	GGATCACCTGAGGTCGGGAA
135628	133715	TGGATCACCTGAGGTCGGGA
135629	133716	GTGGATCACCTGAGGTCGGG
135630	133717	GGTGGATCACCTGAGGTCGG
135631	133718	GGGTGGATCACCTGAGGTCG
135632	133719	TGGGTGGATCACCTGAGGTC
135633	133720	GTGGGTGGATCACCTGAGGT

37340	35427	ACCACTACCAAAATTAGCAG
37341	35428	TACCACTACCAAAATTAGCA
37342	35429	CTACCACTACCAAAATTAGC
37343	35430	TCTACCACTACCAAAATTAG
37344	35431	TTCTACCACTACCAAAATTA
37345	35432	TTTCTACCACTACCAAAATT
37346	35433	CTTTCTACCACTACCAAAAT
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37348	35435	ATCTTTCTACCACTACCAAA
37349	35436	TATCTTTCTACCACTACCAA
37350	35437	GTATCTTTCTACCACTACCA
37351	35438	AGTATCTTTCTACCACTACC
37352	35439	AAGTATCTTTCTACCACTAC
37353	35440	AAAGTATCTTTCTACCACTA
37354	35441	AAAAGTATCTTTCTACCACT
37355	35442	CAAAAGTATCTTTCTACCAC
37356	35443	GCAAAAGTATCTTTCTACCA
37357	35444	GGCAAAAGTATCTTTCTACC
37358	35445	TGGCAAAAGTATCTTTCTAC
37359	35446	TTGGCAAAAGTATCTTTCTA
37360	35447	CTTGGCAAAAGTATCTTTCT
37361	35448	GCTTGGCAAAAGTATCTTTC
37362	35449	AGCTTGGCAAAAGTATCTTT
37363	35450	AAGCTTGGCAAAAGTATCTT
37364	35451	CAAGCTTGGCAAAAGTATCT
37365	35452	CCAAGCTTGGCAAAAGTATC
37366	35453	ACCAAGCTTGGCAAAAGTAT
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37373	35460	CCTAACAACCAAGCTTGGCA
37374	35461	ACCTAACAACCAAGCTTGGC
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37376	35463	AAACCTAACAACCAAGCTTG
37377	35464	AAAACCTAACAACCAAGCTT
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37380	35467	ATGAAAACCTAACAACCAAG
37381	35468	AATGAAAACCTAACAACCAA
37382	35469	AAATGAAAACCTAACAACCA
37383	35470	CAAATGAAAACCTAACAACC
37384	35471	ACAAATGAAAACCTAACAAC
37385	35472	GACAAATGAAAACCTAACAA
37386	35473	GGACAAATGAAAACCTAACA
37387	35474	TGGACAAATGAAAACCTAAC
37388	35475	TTGGACAAATGAAAACCTAA
37389	35476	CTTGGACAAATGAAAACCTA
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37391	35478	CTCTTGGACAAATGAAAACC
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37393	35480	AACTCTTGGACAAATGAAAA
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37395	35482	GGAACTCTTGGACAAATGAA
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37398	35485	TCAGGAACTCTTGGACAAAT
37399	35486	GTCAGGAACTCTTGGACAAA
37400	35487	GGTCAGGAACTCTTGGACAA
37401	35488	TGGTCAGGAACTCTTGGACA
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37403	35490	CTTGGTCAGGAACTCTTGGA
37404	35491	ACTTGGTCAGGAACTCTTGG
37405	35492	CACTTGGTCAGGAACTCTTG
37406	35493	ACACTTGGTCAGGAACTCTT
37407	35494	CACACTTGGTCAGGAACTCT
37408	35495	TCACACTTGGTCAGGAACTC
37409	35496	TTCACACTTGGTCAGGAACT
37410	35497	ATTCACACTTGGTCAGGAAC

86487	84574	GAGCAAAGAAGTCACCTTGA
86488	84575	TGAGCAAAGAAGTCACCTTG
86489	84576	TTGAGCAAAGAAGTCACCTT
86490	84577	TTTGAGCAAAGAAGTCACCT
86491	84578	TTTTGAGCAAAGAAGTCACC
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86493	84580	CCTTTTGAGCAAAGAAGTCA
86494	84581	CCCTTTTGAGCAAAGAAGTC
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86497	84584	AGGCCCTTTTGAGCAAAGAA
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86502	84589	TATTAAGGCCCTTTTGAGCA
86503	84590	CTATTAAGGCCCTTTTGAGC
86504	84591	ACTATTAAGGCCCTTTTGAG
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86506	84593	CCACTATTAAGGCCCTTTTG
86507	84594	ACCACTATTAAGGCCCTTTT
86508	84595	GACCACTATTAAGGCCCTTT
86509	84596	TGACCACTATTAAGGCCCTT
86510	84597	GTGACCACTATTAAGGCCCT
86511	84598	AGTGACCACTATTAAGGCCC
86512	84599	TAGTGACCACTATTAAGGCC
86513	84600	TTAGTGACCACTATTAAGGC
86514	84601	TTTAGTGACCACTATTAAGG
86515	84602	ATTTAGTGACCACTATTAAG
86516	84603	CATTTAGTGACCACTATTAA
86517	84604	GCATTTAGTGACCACTATTA
86518	84605	TGCATTTAGTGACCACTATT
86519	84606	TTGCATTTAGTGACCACTAT
86520	84607	TTTGCATTTAGTGACCACTA
86521	84608	TTTTGCATTTAGTGACCACT
86522	84609	ATTTTGCATTTAGTGACCAC
86523	84610	AATTTTGCATTTAGTGACCA
86524	84611	GAATTTTGCATTTAGTGACC
86525	84612	AGAATTTTGCATTTAGTGAC
86526	84613	CAGAATTTTGCATTTAGTGA
86527	84614	ACAGAATTTTGCATTTAGTG
86528	84615	AACAGAATTTTGCATTTAGT
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86530	84617	TCAACAGAATTTTGCATTTA
86531	84618	ATCAACAGAATTTTGCATTT
86532	84619	TATCAACAGAATTTTGCATT
86533	84620	ATATCAACAGAATTTTGCAT
86534	84621	AATATCAACAGAATTTTGCA
86535	84622	AAATATCAACAGAATTTTGC
86536	84623	AAAATATCAACAGAATTTTG
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86547	84634	GGACTACAAGAAAAATATCA
86548	84635	TGGACTACAAGAAAAATATC
86549	84636	ATGGACTACAAGAAAAATAT
86550	84637	GATGGACTACAAGAAAAATA
86551	84638	TGATGGACTACAAGAAAAAT
86552	84639	ATGATGGACTACAAGAAAAA
86553	84640	AATGATGGACTACAAGAAAA
86554	84641	AAATGATGGACTACAAGAAA
86555	84642	CAAATGATGGACTACAAGAA
86556	84643	TCAAATGATGGACTACAAGA
86557	84644	CTCAAATGATGGACTACAAG

135634	133721	GGTGGGTGGATCACCTGAGG
135635	133722	AGGTGGGTGGATCACCTGAG
135636	133723	GAGGTGGGTGGATCACCTGA
135637	133724	TGAGGTGGGTGGATCACCTG
135638	133725	CTGAGGTGGGTGGATCACCT
135639	133726	GCTGAGGTGGGTGGATCACC
135640	133727	GGCTGAGGTGGGTGGATCAC
135641	133728	AGGCTGAGGTGGGTGGATCA
135642	133729	GAGGCTGAGGTGGGTGGATC
135643	133730	GGAGGCTGAGGTGGGTGGAT
135644	133731	GGGAGGCTGAGGTGGGTGGA
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135647	133734	TTTGGGAGGCTGAGGTGGGT
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135653	133740	CAGCACTTTGGGAGGCTGAG
135654	133741	CCAGCACTTTGGGAGGCTGA
135655	133742	CCCAGCACTTTGGGAGGCTG
135656	133743	TCCCAGCACTTTGGGAGGCT
135657	133744	ATCCCAGCACTTTGGGAGGC
135658	133745	AATCCCAGCACTTTGGGAGG
135659	133746	TAATCCCAGCACTTTGGGAG
135660	133747	GTAATCCCAGCACTTTGGGA
135661	133748	TGTAATCCCAGCACTTTGGG
135662	133749	CTGTAATCCCAGCACTTTGG
135663	133750	CCTGTAATCCCAGCACTTTG
135664	133751	GCCTGTAATCCCAGCACTTT
135665	133752	CGCCTGTAATCCCAGCACTT
135666	133753	ACGCCTGTAATCCCAGCACT
135667	133754	CACGCCTGTAATCCCAGCAC
135668	133755	TCACGCCTGTAATCCCAGCA
135669	133756	CTCACGCCTGTAATCCCAGC
135670	133757	GCTCACGCCTGTAATCCCAG
135671	133758	GGCTCACGCCTGTAATCCCA
135672	133759	TGGCTCACGCCTGTAATCCC
135673	133760	GTGGCTCACGCCTGTAATCC
135674	133761	AGTGGCTCACGCCTGTAATC
135675	133762	CAGTGGCTCACGCCTGTAAT
135676	133763	GCAGTGGCTCACGCCTGTAA
135677	133764	GGCAGTGGCTCACGCCTGTA
135678	133765	GGGCAGTGGCTCACGCCTGT
135679	133766	GGGGCAGTGGCTCACGCCTG
135680	133767	CGGGGCAGTGGCTCACGCCT
135681	133768	CCGGGGCAGTGGCTCACGCC
135682	133769	GCCGGGGCAGTGGCTCACGC
135683	133770	GGCCGGGGCAGTGGCTCACG
135684	133771	AGGCCGGGGCAGTGGCTCAC
135685	133772	GAGGCCGGGGCAGTGGCTCA
135686	133773	AGAGGCCGGGGCAGTGGCTC
135687	133774	AAGAGGCCGGGGCAGTGGCT
135688	133775	AAAGAGGCCGGGGCAGTGGC
135689	133776	CAAAGAGGCCGGGGCAGTGG
135690	133777	TCAAAGAGGCCGGGGCAGTG
135691	133778	ATCAAAGAGGCCGGGGCAGT
135692	133779	CATCAAAGAGGCCGGGGCAG
135693	133780	ACATCAAAGAGGCCGGGGCA
135694	133781	GACATCAAAGAGGCCGGGGC
135695	133782	AGACATCAAAGAGGCCGGGG
135696	133783	GAGACATCAAAGAGGCCGGG
135697	133784	AGAGACATCAAAGAGGCCGG
135698	133785	AAGAGACATCAAAGAGGCCG
135699	133786	TAAGAGACATCAAAGAGGCC
135700	133787	TTAAGAGACATCAAAGAGGC
135701	133788	ATTAAGAGACATCAAAGAGG
135702	133789	GATTAAGAGACATCAAAGAG
135703	133790	AGATTAAGAGACATCAAAGA
135704	133791	TAGATTAAGAGACATCAAAG

37411	35498	CATTCACACTTGGTCAGGAA
37412	35499	CCATTCACACTTGGTCAGGA
37413	35500	TCCATTCACACTTGGTCAGG
37414	35501	ATCCATTCACACTTGGTCAG
37415	35502	CATCCATTCACACTTGGTCA
37416	35503	ACATCCATTCACACTTGGTC
37417	35504	AACATCCATTCACACTTGGT
37418	35505	CAACATCCATTCACACTTGG
37419	35506	TCAACATCCATTCACACTTG
37420	35507	TTCAACATCCATTCACACTT
37421	35508	TTTCAACATCCATTCACACT
37422	35509	ATTTCAACATCCATTCACAC
37423	35510	GATTTCAACATCCATTCACA
37424	35511	TGATTTCAACATCCATTCAC
37425	35512	TTGATTTCAACATCCATTCA
37426	35513	CTTGATTTCAACATCCATTC
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37428	35515	ACCTTGATTTCAACATCCAT
37429	35516	CACCTTGATTTCAACATCCA
37430	35517	ACACCTTGATTTCAACATCC
37431	35518	AACACCTTGATTTCAACATC
37432	35519	AAACACCTTGATTTCAACAT
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37435	35522	AAGAAACACCTTGATTTCAA
37436	35523	AAAGAAACACCTTGATTTCA
37437	35524	CAAAGAAACACCTTGATTTC
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37439	35526	GCCAAAGAAACACCTTGATT
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37442	35529	GTGGCCAAAGAAACACCTTG
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37445	35532	TGTGTGGCCAAAGAAACACC
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37447	35534	ATTGTGTGGCCAAAGAAACA
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37451	35538	GCACATTGTGTGGCCAAAGA
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37471	35558	CATAGATATAGCCCCCAAAG
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37474	35561	GCACATAGATATAGCCCCCA
37475	35562	AGCACATAGATATAGCCCCC
37476	35563	AAGCACATAGATATAGCCCC
37477	35564	GAAGCACATAGATATAGCCC
37478	35565	AGAAGCACATAGATATAGCC
37479	35566	CAGAAGCACATAGATATAGC
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86576	84663	ATTAAATAAACATCGCTTAC
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86579	84666	CTCATTAAATAAACATCGCT
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135716	133803	AATGATGGAAGTTAGATTAA
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135722	133809	AGAGGCAATGATGGAAGTTA
135723	133810	TAGAGGCAATGATGGAAGTT
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135726	133813	GGGTAGAGGCAATGATGGAA
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135730	133817	GATGGGGTAGAGGCAATGAT
135731	133818	GGATGGGGTAGAGGCAATGA
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135734	133821	AAGGGATGGGGTAGAGGCAA
135735	133822	GAAGGGATGGGGTAGAGGCA
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135746	133833	GTAACTTCTTAGAAGGGATG
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37529	35616	AAACAGTGTGGTCGGCAAGC
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37531	35618	CAAAACAGTGTGGTCGGCAA
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135845	133932	TCGCACCGCTGCACTTCAGA
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37609	35696	CCATCACCTGACCATATTAT
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37611	35698	GACCATCACCTGACCATATT
37612	35699	GGACCATCACCTGACCATAT
37613	35700	AGGACCATCACCTGACCATA
37614	35701	CAGGACCATCACCTGACCAT
37615	35702	TCAGGACCATCACCTGACCA
37616	35703	CTCAGGACCATCACCTGACC
37617	35704	ACTCAGGACCATCACCTGAC
37618	35705	TACTCAGGACCATCACCTGA
37619	35706	CTACTCAGGACCATCACCTG
37620	35707	ACTACTCAGGACCATCACCT
37621	35708	CACTACTCAGGACCATCACC
37622	35709	CCACTACTCAGGACCATCAC
37623	35710	CCCACTACTCAGGACCATCA

86700	84787	AACATCTCTGAATGACACAG
86701	84788	CAACATCTCTGAATGACACA
86702	84789	TCAACATCTCTGAATGACAC
86703	84790	TTCAACATCTCTGAATGACA
86704	84791	ATTCAACATCTCTGAATGAC
86705	84792	TATTCAACATCTCTGAATGA
86706	84793	ATATTCAACATCTCTGAATG
86707	84794	AATATTCAACATCTCTGAAT
86708	84795	AAATATTCAACATCTCTGAA
86709	84796	GAAATATTCAACATCTCTGA
86710	84797	GGAAATATTCAACATCTCTG
86711	84798	TGGAAATATTCAACATCTCT
86712	84799	ATGGAAATATTCAACATCTC
86713	84800	AATGGAAATATTCAACATCT
86714	84801	AAATGGAAATATTCAACATC
86715	84802	CAAATGGAAATATTCAACAT
86716	84803	TCAAATGGAAATATTCAACA
86717	84804	TTCAAATGGAAATATTCAAC
86718	84805	TTTCAAATGGAAATATTCAA
86719	84806	TTTTCAAATGGAAATATTCA
86720	84807	ATTTTCAAATGGAAATATTC
86721	84808	AATTTTCAAATGGAAATATT
86722	84809	TAATTTTCAAATGGAAATAT
86723	84810	ATAATTTTCAAATGGAAATA
86724	84811	TATAATTTTCAAATGGAAAT
86725	84812	CTATAATTTTCAAATGGAAA
86726	84813	ACTATAATTTTCAAATGGAA
86727	84814	CACTATAATTTTCAAATGGA
86728	84815	ACACTATAATTTTCAAATGG
86729	84816	TACACTATAATTTTCAAATG
86730	84817	ATACACTATAATTTTCAAAT
86731	84818	TATACACTATAATTTTCAAA
86732	84819	TTATACACTATAATTTTCAA
86733	84820	GTTATACACTATAATTTTCA
86734	84821	TGTTATACACTATAATTTTC
86735	84822	ATGTTATACACTATAATTTT
86736	84823	AATGTTATACACTATAATTT
86737	84824	TAATGTTATACACTATAATT
86738	84825	CTAATGTTATACACTATAAT
86739	84826	GCTAATGTTATACACTATAA
86740	84827	TGCTAATGTTATACACTATA
86741	84828	ATGCTAATGTTATACACTAT
86742	84829	AATGCTAATGTTATACACTA
86743	84830	GAATGCTAATGTTATACACT
86744	84831	AGAATGCTAATGTTATACAC
86745	84832	AAGAATGCTAATGTTATACA
86746	84833	GAAGAATGCTAATGTTATAC
86747	84834	AGAAGAATGCTAATGTTATA
86748	84835	TAGAAGAATGCTAATGTTAT
86749	84836	TTAGAAGAATGCTAATGTTA
86750	84837	TTTAGAAGAATGCTAATGTT
86751	84838	CTTTAGAAGAATGCTAATGT
86752	84839	TCTTTAGAAGAATGCTAATG
86753	84840	ATCTTTAGAAGAATGCTAAT
86754	84841	GATCTTTAGAAGAATGCTAA
86755	84842	TGATCTTTAGAAGAATGCTA
86756	84843	ATGATCTTTAGAAGAATGCT
86757	84844	CATGATCTTTAGAAGAATGC
86758	84845	ACATGATCTTTAGAAGAATG
86759	84846	AACATGATCTTTAGAAGAAT
86760	84847	GAACATGATCTTTAGAAGAA
86761	84848	CGAACATGATCTTTAGAAGA
86762	84849	ACGAACATGATCTTTAGAAG
86763	84850	CACGAACATGATCTTTAGAA
86764	84851	ACACGAACATGATCTTTAGA
86765	84852	AACACGAACATGATCTTTAG
86766	84853	AAACACGAACATGATCTTTA
86767	84854	TAAACACGAACATGATCTTT
86768	84855	TTAAACACGAACATGATCTT
86769	84856	TTTAAACACGAACATGATCT
86770	84857	ATTTAAACACGAACATGATC

135847	133934	GATCGCACCGCTGCACTTCA
135848	133935	AGATCGCACCGCTGCACTTC
135849	133936	GAGATCGCACCGCTGCACTT
135850	133937	TGAGATCGCACCGCTGCACT
135851	133938	CTGAGATCGCACCGCTGCAC
135852	133939	GCTGAGATCGCACCGCTGCA
135853	133940	AGCTGAGATCGCACCGCTGC
135854	133941	GAGCTGAGATCGCACCGCTG
135855	133942	TGAGCTGAGATCGCACCGCT
135856	133943	GTGAGCTGAGATCGCACCGC
135857	133944	AGTGAGCTGAGATCGCACCG
135858	133945	CAGTGAGCTGAGATCGCACC
135859	133946	GCAGTGAGCTGAGATCGCAC
135860	133947	TGCAGTGAGCTGAGATCGCA
135861	133948	TTGCAGTGAGCTGAGATCGC
135862	133949	GTTGCAGTGAGCTGAGATCG
135863	133950	TGTTGCAGTGAGCTGAGATC
135864	133951	ATGTTGCAGTGAGCTGAGAT
135865	133952	GATGTTGCAGTGAGCTGAGA
135866	133953	AGATGTTGCAGTGAGCTGAG
135867	133954	CAGATGTTGCAGTGAGCTGA
135868	133955	GCAGATGTTGCAGTGAGCTG
135869	133956	GGCAGATGTTGCAGTGAGCT
135870	133957	AGGCAGATGTTGCAGTGAGC
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135872	133959	GGAGGCAGATGTTGCAGTGA
135873	133960	GGGAGGCAGATGTTGCAGTG
135874	133961	TGGGAGGCAGATGTTGCAGT
135875	133962	CTGGGAGGCAGATGTTGCAG
135876	133963	CCTGGGAGGCAGATGTTGCA
135877	133964	ACCTGGGAGGCAGATGTTGC
135878	133965	AACCTGGGAGGCAGATGTTG
135879	133966	GAACCTGGGAGGCAGATGTT
135880	133967	TGAACCTGGGAGGCAGATGT
135881	133968	TTGAACCTGGGAGGCAGATG
135882	133969	CTTGAACCTGGGAGGCAGAT
135883	133970	GCTTGAACCTGGGAGGCAGA
135884	133971	CGCTTGAACCTGGGAGGCAG
135885	133972	CCGCTTGAACCTGGGAGGCA
135886	133973	ACCGCTTGAACCTGGGAGGC
135887	133974	AACCGCTTGAACCTGGGAGG
135888	133975	AAACCGCTTGAACCTGGGAG
135889	133976	AAAACCGCTTGAACCTGGGA
135890	133977	AAAAACCGCTTGAACCTGGG
135891	133978	GAAAAACCGCTTGAACCTGG
135892	133979	AGAAAAACCGCTTGAACCTG
135893	133980	CAGAAAAACCGCTTGAACCT
135894	133981	GCAGAAAAACCGCTTGAACC
135895	133982	GGCAGAAAAACCGCTTGAAC
135896	133983	AGGCAGAAAAACCGCTTGAA
135897	133984	GAGGCAGAAAAACCGCTTGA
135898	133985	TGAGGCAGAAAAACCGCTTG
135899	133986	CTGAGGCAGAAAAACCGCTT
135900	133987	GCTGAGGCAGAAAAACCGCT
135901	133988	GGCTGAGGCAGAAAAACCGC
135902	133989	AGGCTGAGGCAGAAAAACCG
135903	133990	GAGGCTGAGGCAGAAAAACC
135904	133991	GGAGGCTGAGGCAGAAAAAC
135905	133992	GGGAGGCTGAGGCAGAAAAA
135906	133993	CGGGAGGCTGAGGCAGAAAA
135907	133994	TCGGGAGGCTGAGGCAGAAA
135908	133995	CTCGGGAGGCTGAGGCAGAA
135909	133996	ACTCGGGAGGCTGAGGCAGA
135910	133997	TACTCGGGAGGCTGAGGCAG
135911	133998	CTACTCGGGAGGCTGAGGCA
135912	133999	CCTACTCGGGAGGCTGAGGC
135913	134000	ACCTACTCGGGAGGCTGAGG
135914	134001	CACCTACTCGGGAGGCTGAG
135915	134002	CCACCTACTCGGGAGGCTGA
135916	134003	CCCACCTACTCGGGAGGCTG
135917	134004	TCCCACCTACTCGGGAGGCT

37624	35711	ACCCACTACTCAGGACCATC
37625	35712	TACCCACTACTCAGGACCAT
37626	35713	ATACCCACTACTCAGGACCA
37627	35714	TATACCCACTACTCAGGACC
37628	35715	ATATACCCACTACTCAGGAC
37629	35716	CATATACCCACTACTCAGGA
37630	35717	TCATATACCCACTACTCAGG
37631	35718	GTCATATACCCACTACTCAG
37632	35719	TGTCATATACCCACTACTCA
37633	35720	CTGTCATATACCCACTACTC
37634	35721	TCTGTCATATACCCACTACT
37635	35722	ATCTGTCATATACCCACTAC
37636	35723	TATCTGTCATATACCCACTA
37637	35724	GTATCTGTCATATACCCACT
37638	35725	TGTATCTGTCATATACCCAC
37639	35726	GTGTATCTGTCATATACCCA
37640	35727	AGTGTATCTGTCATATACCC
37641	35728	TAGTGTATCTGTCATATACC
37642	35729	CTAGTGTATCTGTCATATAC
37643	35730	ACTAGTGTATCTGTCATATA
37644	35731	TACTAGTGTATCTGTCATAT
37645	35732	TTACTAGTGTATCTGTCATA
37646	35733	ATTACTAGTGTATCTGTCAT
37647	35734	AATTACTAGTGTATCTGTCA
37648	35735	TAATTACTAGTGTATCTGTC
37649	35736	ATAATTACTAGTGTATCTGT
37650	35737	TATAATTACTAGTGTATCTG
37651	35738	TTATAATTACTAGTGTATCT
37652	35739	ATTATAATTACTAGTGTATC
37653	35740	TATTATAATTACTAGTGTAT
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37655	35742	TGTATTATAATTACTAGTGT
37656	35743	CTGTATTATAATTACTAGTG
37657	35744	TCTGTATTATAATTACTAGT
37658	35745	ATCTGTATTATAATTACTAG
37659	35746	GATCTGTATTATAATTACTA
37660	35747	AGATCTGTATTATAATTACT
37661	35748	TAGATCTGTATTATAATTAC
37662	35749	TTAGATCTGTATTATAATTA
37663	35750	TTTAGATCTGTATTATAATT
37664	35751	GTTTAGATCTGTATTATAAT
37665	35752	AGTTTAGATCTGTATTATAA
37666	35753	CAGTTTAGATCTGTATTATA
37667	35754	CCAGTTTAGATCTGTATTAT
37668	35755	TCCAGTTTAGATCTGTATTA
37669	35756	CTCCAGTTTAGATCTGTATT
37670	35757	TCTCCAGTTTAGATCTGTAT
37671	35758	CTCTCCAGTTTAGATCTGTA
37672	35759	ACTCTCCAGTTTAGATCTGT
37673	35760	AACTCTCCAGTTTAGATCTG
37674	35761	CAACTCTCCAGTTTAGATCT
37675	35762	TCAACTCTCCAGTTTAGATC
37676	35763	TTCAACTCTCCAGTTTAGAT
37677	35764	TTTCAACTCTCCAGTTTAGA
37678	35765	TTTTCAACTCTCCAGTTTAG
37679	35766	GTTTTCAACTCTCCAGTTTA
37680	35767	TGTTTTCAACTCTCCAGTTT
37681	35768	CTGTTTTCAACTCTCCAGTT
37682	35769	GCTGTTTTCAACTCTCCAGT
37683	35770	TGCTGTTTTCAACTCTCCAG
37684	35771	ATGCTGTTTTCAACTCTCCA
37685	35772	GATGCTGTTTTCAACTCTCC
37686	35773	CGATGCTGTTTTCAACTCTC
37687	35774	ACGATGCTGTTTTCAACTCT
37688	35775	TACGATGCTGTTTTCAACTC
37689	35776	ATACGATGCTGTTTTCAACT
37690	35777	TATACGATGCTGTTTTCAAC
37691	35778	ATATACGATGCTGTTTTCAA
37692	35779	AATATACGATGCTGTTTTCA
37693	35780	AAATATACGATGCTGTTTTC
37694	35781	CAAATATACGATGCTGTTTT

86771	84858	AATTTAAACACGAACATGAT
86772	84859	GAATTTAAACACGAACATGA
86773	84860	GGAATTTAAACACGAACATG
86774	84861	AGGAATTTAAACACGAACAT
86775	84862	CAGGAATTTAAACACGAACA
86776	84863	ACAGGAATTTAAACACGAAC
86777	84864	AACAGGAATTTAAACACGAA
86778	84865	CAACAGGAATTTAAACACGA
86779	84866	CCAACAGGAATTTAAACACG
86780	84867	TCCAACAGGAATTTAAACAC
86781	84868	TTCCAACAGGAATTTAAACA
86782	84869	CTTCCAACAGGAATTTAAAC
86783	84870	GCTTCCAACAGGAATTTAAA
86784	84871	GGCTTCCAACAGGAATTTAA
86785	84872	TGGCTTCCAACAGGAATTTA
86786	84873	CTGGCTTCCAACAGGAATTT
86787	84874	CCTGGCTTCCAACAGGAATT
86788	84875	GCCTGGCTTCCAACAGGAAT
86789	84876	TGCCTGGCTTCCAACAGGAA
86790	84877	ATGCCTGGCTTCCAACAGGA
86791	84878	CATGCCTGGCTTCCAACAGG
86792	84879	CCATGCCTGGCTTCCAACAG
86793	84880	ACCATGCCTGGCTTCCAACA
86794	84881	CACCATGCCTGGCTTCCAAC
86795	84882	CCACCATGCCTGGCTTCCAA
86796	84883	GCCACCATGCCTGGCTTCCA
86797	84884	AGCCACCATGCCTGGCTTCC
86798	84885	TAGCCACCATGCCTGGCTTC
86799	84886	TTAGCCACCATGCCTGGCTT
86800	84887	GTTAGCCACCATGCCTGGCT
86801	84888	CGTTAGCCACCATGCCTGGC
86802	84889	GCGTTAGCCACCATGCCTGG
86803	84890	GGCGTTAGCCACCATGCCTG
86804	84891	AGGCGTTAGCCACCATGCCT
86805	84892	CAGGCGTTAGCCACCATGCC
86806	84893	ACAGGCGTTAGCCACCATGC
86807	84894	TACAGGCGTTAGCCACCATG
86808	84895	TTACAGGCGTTAGCCACCAT
86809	84896	ATTACAGGCGTTAGCCACCA
86810	84897	GATTACAGGCGTTAGCCACC
86811	84898	AGATTACAGGCGTTAGCCAC
86812	84899	GAGATTACAGGCGTTAGCCA
86813	84900	TGAGATTACAGGCGTTAGCC
86814	84901	CTGAGATTACAGGCGTTAGC
86815	84902	GCTGAGATTACAGGCGTTAG
86816	84903	TGCTGAGATTACAGGCGTTA
86817	84904	GTGCTGAGATTACAGGCGTT
86818	84905	AGTGCTGAGATTACAGGCGT
86819	84906	AAGTGCTGAGATTACAGGCG
86820	84907	AAAGTGCTGAGATTACAGGC
86821	84908	CAAAGTGCTGAGATTACAGG
86822	84909	CCAAAGTGCTGAGATTACAG
86823	84910	CCCAAAGTGCTGAGATTACA
86824	84911	TCCCAAAGTGCTGAGATTAC
86825	84912	CTCCCAAAGTGCTGAGATTA
86826	84913	CCTCCCAAAGTGCTGAGATT
86827	84914	GCCTCCCAAAGTGCTGAGAT
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86830	84917	TCAGCCTCCCAAAGTGCTGA
86831	84918	CTCAGCCTCCCAAAGTGCTG
86832	84919	CCTCAGCCTCCCAAAGTGCT
86833	84920	GCCTCAGCCTCCCAAAGTGC
86834	84921	TGCCTCAGCCTCCCAAAGTG
86835	84922	CTGCCTCAGCCTCCCAAAGT
86836	84923	CCTGCCTCAGCCTCCCAAAG
86837	84924	ACCTGCCTCAGCCTCCCAAA
86838	84925	CACCTGCCTCAGCCTCCCAA
86839	84926	CCACCTGCCTCAGCCTCCCA
86840	84927	TCCACCTGCCTCAGCCTCCC
86841	84928	ATCCACCTGCCTCAGCCTCC

135918	134005	GTCCCACCTACTCGGGAGGC
135919	134006	AGTCCCACCTACTCGGGAGG
135920	134007	TAGTCCCACCTACTCGGGAG
135921	134008	GTAGTCCCACCTACTCGGGA
135922	134009	TGTAGTCCCACCTACTCGGG
135923	134010	CTGTAGTCCCACCTACTCGG
135924	134011	CCTGTAGTCCCACCTACTCG
135925	134012	ACCTGTAGTCCCACCTACTC
135926	134013	CACCTGTAGTCCCACCTACT
135927	134014	ACACCTGTAGTCCCACCTAC
135928	134015	CACACCTGTAGTCCCACCTA
135929	134016	GCACACCTGTAGTCCCACCT
135930	134017	CGCACACCTGTAGTCCCACC
135931	134018	GCGCACACCTGTAGTCCCAC
135932	134019	GGCGCACACCTGTAGTCCCA
135933	134020	TGGCGCACACCTGTAGTCCC
135934	134021	GTGGCGCACACCTGTAGTCC
135935	134022	GGTGGCGCACACCTGTAGTC
135936	134023	TGGTGGCGCACACCTGTAGT
135937	134024	GTGGTGGCGCACACCTGTAG
135938	134025	CGTGGTGGCGCACACCTGTA
135939	134026	TCGTGGTGGCGCACACCTGT
135940	134027	GTCGTGGTGGCGCACACCTG
135941	134028	GGTCGTGGTGGCGCACACCT
135942	134029	CGGTCGTGGTGGCGCACACC
135943	134030	CCGGTCGTGGTGGCGCACAC
135944	134031	GCCGGTCGTGGTGGCGCACA
135945	134032	GGCCGGTCGTGGTGGCGCAC
135946	134033	TGGCCGGTCGTGGTGGCGCA
135947	134034	TTGGCCGGTCGTGGTGGCGC
135948	134035	ATTGGCCGGTCGTGGTGGCG
135949	134036	AATTGGCCGGTCGTGGTGGC
135950	134037	AAATTGGCCGGTCGTGGTGG
135951	134038	AAAATTGGCCGGTCGTGGTG
135952	134039	AAAAATTGGCCGGTCGTGGT
135953	134040	CAAAAATTGGCCGGTCGTGG
135954	134041	ACAAAAATTGGCCGGTCGTG
135955	134042	TACAAAAATTGGCCGGTCGT
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135957	134044	AATACAAAAATTGGCCGGTC
135958	134045	AAATACAAAAATTGGCCGGT
135959	134046	AAAATACAAAAATTGGCCGG
135960	134047	AAAAATACAAAAATTGGCCG
135961	134048	TAAAAATACAAAAATTGGCC
135962	134049	CTAAAAATACAAAAATTGGC
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135964	134051	TACTAAAAATACAAAAATTG
135965	134052	CTACTAAAAATACAAAAATT
135966	134053	TCTACTAAAAATACAAAAAT
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135971	134058	CCGTCTCTACTAAAAATACA
135972	134059	CCCGTCTCTACTAAAAATAC
135973	134060	CCCCGTCTCTACTAAAAATA
135974	134061	ACCCCGTCTCTACTAAAAAT
135975	134062	AACCCCGTCTCTACTAAAAA
135976	134063	AAACCCCGTCTCTACTAAAA
135977	134064	GAAACCCCGTCTCTACTAAA
135978	134065	TGAAACCCCGTCTCTACTAA
135979	134066	GTGAAACCCCGTCTCTACTA
135980	134067	GGTGAAACCCCGTCTCTACT
135981	134068	CGGTGAAACCCCGTCTCTAC
135982	134069	ACGGTGAAACCCCGTCTCTA
135983	134070	GACGGTGAAACCCCGTCTCT
135984	134071	AGACGGTGAAACCCCGTCTC
135985	134072	AAGACGGTGAAACCCCGTCT
135986	134073	CAAGACGGTGAAACCCCGTC
135987	134074	CCAAGACGGTGAAACCCCGT
135988	134075	GCCAAGACGGTGAAACCCCG

37695	35782	TCAAATATACGATGCTGTTT
37696	35783	ATCAAATATACGATGCTGTT
37697	35784	AATCAAATATACGATGCTGT
37698	35785	CAATCAAATATACGATGCTG
37699	35786	TCAATCAAATATACGATGCT
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37702	35789	ATCTCAATCAAATATACGAT
37703	35790	TATCTCAATCAAATATACGA
37704	35791	TTATCTCAATCAAATATACG
37705	35792	ATTATCTCAATCAAATATAC
37706	35793	GATTATCTCAATCAAATATA
37707	35794	CGATTATCTCAATCAAATAT
37708	35795	TCGATTATCTCAATCAAATA
37709	35796	TTCGATTATCTCAATCAAAT
37710	35797	CTTCGATTATCTCAATCAAA
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37712	35799	TCCTTCGATTATCTCAATCA
37713	35800	TTCCTTCGATTATCTCAATC
37714	35801	CTTCCTTCGATTATCTCAAT
37715	35802	TCTTCCTTCGATTATCTCAA
37716	35803	GTCTTCCTTCGATTATCTCA
37717	35804	AGTCTTCCTTCGATTATCTC
37718	35805	AAGTCTTCCTTCGATTATCT
37719	35806	GAAGTCTTCCTTCGATTATC
37720	35807	GGAAGTCTTCCTTCGATTAT
37721	35808	AGGAAGTCTTCCTTCGATTA
37722	35809	CAGGAAGTCTTCCTTCGATT
37723	35810	TCAGGAAGTCTTCCTTCGAT
37724	35811	TTCAGGAAGTCTTCCTTCGA
37725	35812	TTTCAGGAAGTCTTCCTTCG
37726	35813	TTTTCAGGAAGTCTTCCTTC
37727	35814	CTTTTCAGGAAGTCTTCCTT
37728	35815	TCTTTTCAGGAAGTCTTCCT
37729	35816	ATCTTTTCAGGAAGTCTTCC
37730	35817	CATCTTTTCAGGAAGTCTTC
37731	35818	CCATCTTTTCAGGAAGTCTT
37732	35819	GCCATCTTTTCAGGAAGTCT
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37734	35821	ATGCCATCTTTTCAGGAAGT
37735	35822	AATGCCATCTTTTCAGGAAG
37736	35823	AAATGCCATCTTTTCAGGAA
37737	35824	CAAATGCCATCTTTTCAGGA
37738	35825	TCAAATGCCATCTTTTCAGG
37739	35826	CTCAAATGCCATCTTTTCAG
37740	35827	ACTCAAATGCCATCTTTTCA
37741	35828	AACTCAAATGCCATCTTTTC
37742	35829	AAACTCAAATGCCATCTTTT
37743	35830	GAAACTCAAATGCCATCTTT
37744	35831	TGAAACTCAAATGCCATCTT
37745	35832	TTGAAACTCAAATGCCATCT
37746	35833	CTTGAAACTCAAATGCCATC
37747	35834	CCTTGAAACTCAAATGCCAT
37748	35835	GCCTTGAAACTCAAATGCCA
37749	35836	AGCCTTGAAACTCAAATGCC
37750	35837	CAGCCTTGAAACTCAAATGC
37751	35838	TCAGCCTTGAAACTCAAATG
37752	35839	CTCAGCCTTGAAACTCAAAT
37753	35840	ACTCAGCCTTGAAACTCAAA
37754	35841	TACTCAGCCTTGAAACTCAA
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37760	35847	TAATCCTACTCAGCCTTGAA
37761	35848	TTAATCCTACTCAGCCTTGA
37762	35849	CTTAATCCTACTCAGCCTTG
37763	35850	ACTTAATCCTACTCAGCCTT
37764	35851	TACTTAATCCTACTCAGCCT
37765	35852	ATACTTAATCCTACTCAGCC

86842	84929	GATCCACCTGCCTCAGCCTC
86843	84930	TGATCCACCTGCCTCAGCCT
86844	84931	GTGATCCACCTGCCTCAGCC
86845	84932	AGTGATCCACCTGCCTCAGC
86846	84933	AAGTGATCCACCTGCCTCAG
86847	84934	CAAGTGATCCACCTGCCTCA
86848	84935	TCAAGTGATCCACCTGCCTC
86849	84936	CTCAAGTGATCCACCTGCCT
86850	84937	CCTCAAGTGATCCACCTGCC
86851	84938	ACCTCAAGTGATCCACCTGC
86852	84939	GACCTCAAGTGATCCACCTG
86853	84940	TGACCTCAAGTGATCCACCT
86854	84941	CTGACCTCAAGTGATCCACC
86855	84942	CCTGACCTCAAGTGATCCAC
86856	84943	TCCTGACCTCAAGTGATCCA
86857	84944	CTCCTGACCTCAAGTGATCC
86858	84945	ACTCCTGACCTCAAGTGATC
86859	84946	AACTCCTGACCTCAAGTGAT
86860	84947	AAACTCCTGACCTCAAGTGA
86861	84948	CAAACTCCTGACCTCAAGTG
86862	84949	TCAAACTCCTGACCTCAAGT
86863	84950	CTCAAACTCCTGACCTCAAG
86864	84951	TCTCAAACTCCTGACCTCAA
86865	84952	GTCTCAAACTCCTGACCTCA
86866	84953	GGTCTCAAACTCCTGACCTC
86867	84954	TGGTCTCAAACTCCTGACCT
86868	84955	CTGGTCTCAAACTCCTGACC
86869	84956	GCTGGTCTCAAACTCCTGAC
86870	84957	GGCTGGTCTCAAACTCCTGA
86871	84958	AGGCTGGTCTCAAACTCCTG
86872	84959	CAGGCTGGTCTCAAACTCCT
86873	84960	CCAGGCTGGTCTCAAACTCC
86874	84961	GCCAGGCTGGTCTCAAACTC
86875	84962	GGCCAGGCTGGTCTCAAACT
86876	84963	TGGCCAGGCTGGTCTCAAAC
86877	84964	TTGGCCAGGCTGGTCTCAAA
86878	84965	GTTGGCCAGGCTGGTCTCAA
86879	84966	TGTTGGCCAGGCTGGTCTCA
86880	84967	ATGTTGGCCAGGCTGGTCTC
86881	84968	CATGTTGGCCAGGCTGGTCT
86882	84969	CCATGTTGGCCAGGCTGGTC
86883	84970	ACCATGTTGGCCAGGCTGGT
86884	84971	CACCATGTTGGCCAGGCTGG
86885	84972	TCACCATGTTGGCCAGGCTG
86886	84973	TTCACCATGTTGGCCAGGCT
86887	84974	TTTCACCATGTTGGCCAGGC
86888	84975	GTTTCACCATGTTGGCCAGG
86889	84976	GGTTTCACCATGTTGGCCAG
86890	84977	AGGTTTCACCATGTTGGCCA
86891	84978	GAGGTTTCACCATGTTGGCC
86892	84979	CGAGGTTTCACCATGTTGGC
86893	84980	ACGAGGTTTCACCATGTTGG
86894	84981	GACGAGGTTTCACCATGTTG
86895	84982	AGACGAGGTTTCACCATGTT
86896	84983	GAGACGAGGTTTCACCATGT
86897	84984	AGAGACGAGGTTTCACCATG
86898	84985	TAGAGACGAGGTTTCACCAT
86899	84986	GTAGAGACGAGGTTTCACCA
86900	84987	AGTAGAGACGAGGTTTCACC
86901	84988	TAGTAGAGACGAGGTTTCAC
86902	84989	TTAGTAGAGACGAGGTTTCA
86903	84990	TTTAGTAGAGACGAGGTTTC
86904	84991	TTTTAGTAGAGACGAGGTTT
86905	84992	TTTTTAGTAGAGACGAGGTT
86906	84993	ATTTTTAGTAGAGACGAGGT
86907	84994	TATTTTTAGTAGAGACGAGG
86908	84995	GTATTTTTAGTAGAGACGAG
86909	84996	GGTATTTTTAGTAGAGACGA
86910	84997	GGGTATTTTTAGTAGAGACG
86911	84998	TGGGTATTTTTAGTAGAGAC
86912	84999	CTGGGTATTTTTAGTAGAGA

135989	134076	GGCCAAGACGGTGAAACCCC
135990	134077	TGGCCAAGACGGTGAAACCC
135991	134078	CTGGCCAAGACGGTGAAACC
135992	134079	CCTGGCCAAGACGGTGAAAC
135993	134080	GCCTGGCCAAGACGGTGAAA
135994	134081	AGCCTGGCCAAGACGGTGAA
135995	134082	CAGCCTGGCCAAGACGGTGA
135996	134083	TCAGCCTGGCCAAGACGGTG
135997	134084	ATCAGCCTGGCCAAGACGGT
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135999	134086	AGATCAGCCTGGCCAAGACG
136000	134087	GAGATCAGCCTGGCCAAGAC
136001	134088	CGAGATCAGCCTGGCCAAGA
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136003	134090	TTCGAGATCAGCCTGGCCAA
136004	134091	GTTCGAGATCAGCCTGGCCA
136005	134092	AGTTCGAGATCAGCCTGGCC
136006	134093	AAGTTCGAGATCAGCCTGGC
136007	134094	GAAGTTCGAGATCAGCCTGG
136008	134095	AGAAGTTCGAGATCAGCCTG
136009	134096	CAGAAGTTCGAGATCAGCCT
136010	134097	TCAGAAGTTCGAGATCAGCC
136011	134098	GTCAGAAGTTCGAGATCAGC
136012	134099	GGTCAGAAGTTCGAGATCAG
136013	134100	AGGTCAGAAGTTCGAGATCA
136014	134101	AAGGTCAGAAGTTCGAGATC
136015	134102	CAAGGTCAGAAGTTCGAGAT
136016	134103	ACAAGGTCAGAAGTTCGAGA
136017	134104	CACAAGGTCAGAAGTTCGAG
136018	134105	TCACAAGGTCAGAAGTTCGA
136019	134106	ATCACAAGGTCAGAAGTTCG
136020	134107	AATCACAAGGTCAGAAGTTC
136021	134108	AAATCACAAGGTCAGAAGTT
136022	134109	CAAATCACAAGGTCAGAAGT
136023	134110	ACAAATCACAAGGTCAGAAG
136024	134111	GACAAATCACAAGGTCAGAA
136025	134112	AGACAAATCACAAGGTCAGA
136026	134113	CAGACAAATCACAAGGTCAG
136027	134114	GCAGACAAATCACAAGGTCA
136028	134115	GGCAGACAAATCACAAGGTC
136029	134116	AGGCAGACAAATCACAAGGT
136030	134117	TAGGCAGACAAATCACAAGG
136031	134118	CTAGGCAGACAAATCACAAG
136032	134119	CCTAGGCAGACAAATCACAA
136033	134120	GCCTAGGCAGACAAATCACA
136034	134121	GGCCTAGGCAGACAAATCAC
136035	134122	AGGCCTAGGCAGACAAATCA
136036	134123	GAGGCCTAGGCAGACAAATC
136037	134124	GGAGGCCTAGGCAGACAAAT
136038	134125	GGGAGGCCTAGGCAGACAAA
136039	134126	TGGGAGGCCTAGGCAGACAA
136040	134127	TTGGGAGGCCTAGGCAGACA
136041	134128	TTTGGGAGGCCTAGGCAGAC
136042	134129	CTTTGGGAGGCCTAGGCAGA
136043	134130	ACTTTGGGAGGCCTAGGCAG
136044	134131	CACTTTGGGAGGCCTAGGCA
136045	134132	GCACTTTGGGAGGCCTAGGC
136046	134133	AGCACTTTGGGAGGCCTAGG
136047	134134	CAGCACTTTGGGAGGCCTAG
136048	134135	CCAGCACTTTGGGAGGCCTA
136049	134136	CCCAGCACTTTGGGAGGCCT
136050	134137	TCCCAGCACTTTGGGAGGCC
136051	134138	ATCCCAGCACTTTGGGAGGC
136052	134139	AATCCCAGCACTTTGGGAGG
136053	134140	TAATCCCAGCACTTTGGGAG
136054	134141	GTAATCCCAGCACTTTGGGA
136055	134142	TGTAATCCCAGCACTTTGGG
136056	134143	CTGTAATCCCAGCACTTTGG
136057	134144	TCTGTAATCCCAGCACTTTG
136058	134145	ATCTGTAATCCCAGCACTTT
136059	134146	CATCTGTAATCCCAGCACTT

37766	35853	AATACTTAATCCTACTCAGC
37767	35854	TAATACTTAATCCTACTCAG
37768	35855	ATAATACTTAATCCTACTCA
37769	35856	AATAATACTTAATCCTACTC
37770	35857	TAATAATACTTAATCCTACT
37771	35858	ATAATAATACTTAATCCTAC
37772	35859	AATAATAATACTTAATCCTA
37773	35860	AAATAATAATACTTAATCCT
37774	35861	TAAATAATAATACTTAATCC
37775	35862	TTAAATAATAATACTTAATC
37776	35863	TTTAAATAATAATACTTAAT
37777	35864	TTTTAAATAATAATACTTAA
37778	35865	TTTTTAAATAATAATACTTA
37779	35866	TTTTTTAAATAATAATACTT
37780	35867	ATTTTTTAAATAATAATACT
37781	35868	CATTTTTTAAATAATAATAC
37782	35869	GCATTTTTTAAATAATAATA
37783	35870	GGCATTTTTTAAATAATAAT
37784	35871	AGGCATTTTTTAAATAATAA
37785	35872	AAGGCATTTTTTAAATAATA
37786	35873	CAAGGCATTTTTTAAATAAT
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37788	35875	TCCAAGGCATTTTTTAAATA
37789	35876	GTCCAAGGCATTTTTTAAAT
37790	35877	TGTCCAAGGCATTTTTTAAA
37791	35878	TTGTCCAAGGCATTTTTTAA
37792	35879	ATTGTCCAAGGCATTTTTTA
37793	35880	CATTGTCCAAGGCATTTTTT
37794	35881	GCATTGTCCAAGGCATTTTT
37795	35882	TGCATTGTCCAAGGCATTTT
37796	35883	ATGCATTGTCCAAGGCATTT
37797	35884	AATGCATTGTCCAAGGCATT
37798	35885	TAATGCATTGTCCAAGGCAT
37799	35886	TTAATGCATTGTCCAAGGCA
37800	35887	TTTAATGCATTGTCCAAGGC
37801	35888	ATTTAATGCATTGTCCAAGG
37802	35889	TATTTAATGCATTGTCCAAG
37803	35890	CTATTTAATGCATTGTCCAA
37804	35891	TCTATTTAATGCATTGTCCA
37805	35892	CTCTATTTAATGCATTGTCC
37806	35893	ACTCTATTTAATGCATTGTC
37807	35894	AACTCTATTTAATGCATTGT
37808	35895	TAACTCTATTTAATGCATTG
37809	35896	TTAACTCTATTTAATGCATT
37810	35897	GTTAACTCTATTTAATGCAT
37811	35898	TGTTAACTCTATTTAATGCA
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37814	35901	ATTTGTTAACTCTATTTAAT
37815	35902	GATTTGTTAACTCTATTTAA
37816	35903	TGATTTGTTAACTCTATTTA
37817	35904	GTGATTTGTTAACTCTATTT
37818	35905	TGTGATTTGTTAACTCTATT
37819	35906	ATGTGATTTGTTAACTCTAT
37820	35907	GATGTGATTTGTTAACTCTA
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37824	35911	AAGTGATGTGATTTGTTAAC
37825	35912	TAAGTGATGTGATTTGTTAA
37826	35913	ATAAGTGATGTGATTTGTTA
37827	35914	TATAAGTGATGTGATTTGTT
37828	35915	CTATAAGTGATGTGATTTGT
37829	35916	ACTATAAGTGATGTGATTTG
37830	35917	GACTATAAGTGATGTGATTT
37831	35918	AGACTATAAGTGATGTGATT
37832	35919	GAGACTATAAGTGATGTGAT
37833	35920	GGAGACTATAAGTGATGTGA
37834	35921	TGGAGACTATAAGTGATGTG
37835	35922	TTGGAGACTATAAGTGATGT
37836	35923	ATTGGAGACTATAAGTGATG

86913	85000	GCTGGGTATTTTTAGTAGAG
86914	85001	AGCTGGGTATTTTTAGTAGA
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86916	85003	GTAGCTGGGTATTTTTAGTA
86917	85004	AGTAGCTGGGTATTTTTAGT
86918	85005	AAGTAGCTGGGTATTTTTAG
86919	85006	CAAGTAGCTGGGTATTTTTA
86920	85007	CCAAGTAGCTGGGTATTTTT
86921	85008	CCCAAGTAGCTGGGTATTTT
86922	85009	TCCCAAGTAGCTGGGTATTT
86923	85010	CTCCCAAGTAGCTGGGTATT
86924	85011	CCTCCCAAGTAGCTGGGTAT
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86926	85013	AGCCTCCCAAGTAGCTGGGT
86927	85014	CAGCCTCCCAAGTAGCTGGG
86928	85015	TCAGCCTCCCAAGTAGCTGG
86929	85016	CTCAGCCTCCCAAGTAGCTG
86930	85017	CCTCAGCCTCCCAAGTAGCT
86931	85018	GCCTCAGCCTCCCAAGTAGC
86932	85019	TGCCTCAGCCTCCCAAGTAG
86933	85020	CTGCCTCAGCCTCCCAAGTA
86934	85021	CCTGCCTCAGCCTCCCAAGT
86935	85022	TCCTGCCTCAGCCTCCCAAG
86936	85023	CTCCTGCCTCAGCCTCCCAA
86937	85024	TCTCCTGCCTCAGCCTCCCA
86938	85025	TTCTCCTGCCTCAGCCTCCC
86939	85026	ATTCTCCTGCCTCAGCCTCC
86940	85027	GATTCTCCTGCCTCAGCCTC
86941	85028	TGATTCTCCTGCCTCAGCCT
86942	85029	GTGATTCTCCTGCCTCAGCC
86943	85030	AGTGATTCTCCTGCCTCAGC
86944	85031	AAGTGATTCTCCTGCCTCAG
86945	85032	CAAGTGATTCTCCTGCCTCA
86946	85033	TCAAGTGATTCTCCTGCCTC
86947	85034	TTCAAGTGATTCTCCTGCCT
86948	85035	GTTCAAGTGATTCTCCTGCC
86949	85036	GGTTCAAGTGATTCTCCTGC
86950	85037	AGGTTCAAGTGATTCTCCTG
86951	85038	CAGGTTCAAGTGATTCTCCT
86952	85039	CCAGGTTCAAGTGATTCTCC
86953	85040	CCCAGGTTCAAGTGATTCTC
86954	85041	TCCCAGGTTCAAGTGATTCT
86955	85042	CTCCCAGGTTCAAGTGATTC
86956	85043	CCTCCCAGGTTCAAGTGATT
86957	85044	GCCTCCCAGGTTCAAGTGAT
86958	85045	TGCCTCCCAGGTTCAAGTGA
86959	85046	CTGCCTCCCAGGTTCAAGTG
86960	85047	TCTGCCTCCCAGGTTCAAGT
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86968	85055	CTGCAACCTCTGCCTCCCAG
86969	85056	ACTGCAACCTCTGCCTCCCA
86970	85057	CACTGCAACCTCTGCCTCCC
86971	85058	TCACTGCAACCTCTGCCTCC
86972	85059	CTCACTGCAACCTCTGCCTC
86973	85060	ACTCACTGCAACCTCTGCCT
86974	85061	AACTCACTGCAACCTCTGCC
86975	85062	CAACTCACTGCAACCTCTGC
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86977	85064	CTCAACTCACTGCAACCTCT
86978	85065	TCTCAACTCACTGCAACCTC
86979	85066	ATCTCAACTCACTGCAACCT
86980	85067	GATCTCAACTCACTGCAACC
86981	85068	CGATCTCAACTCACTGCAAC
86982	85069	ACGATCTCAACTCACTGCAA
86983	85070	TACGATCTCAACTCACTGCA

136060	134147	ACATCTGTAATCCCAGCACT
136061	134148	CACATCTGTAATCCCAGCAC
136062	134149	TCACATCTGTAATCCCAGCA
136063	134150	CTCACATCTGTAATCCCAGC
136064	134151	GCTCACATCTGTAATCCCAG
136065	134152	GGCTCACATCTGTAATCCCA
136066	134153	TGGCTCACATCTGTAATCCC
136067	134154	GTGGCTCACATCTGTAATCC
136068	134155	GGTGGCTCACATCTGTAATC
136069	134156	TGGTGGCTCACATCTGTAAT
136070	134157	GTGGTGGCTCACATCTGTAA
136071	134158	CGTGGTGGCTCACATCTGTA
136072	134159	GCGTGGTGGCTCACATCTGT
136073	134160	GGCGTGGTGGCTCACATCTG
136074	134161	GGGCGTGGTGGCTCACATCT
136075	134162	TGGGCGTGGTGGCTCACATC
136076	134163	CTGGGCGTGGTGGCTCACAT
136077	134164	GCTGGGCGTGGTGGCTCACA
136078	134165	GGCTGGGCGTGGTGGCTCAC
136079	134166	AGGCTGGGCGTGGTGGCTCA
136080	134167	GAGGCTGGGCGTGGTGGCTC
136081	134168	TGAGGCTGGGCGTGGTGGCT
136082	134169	GTGAGGCTGGGCGTGGTGGC
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136088	134175	GTAGATGTGAGGCTGGGCGT
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136092	134179	AAGAGTAGATGTGAGGCTGG
136093	134180	GAAGAGTAGATGTGAGGCTG
136094	134181	AGAAGAGTAGATGTGAGGCT
136095	134182	TAGAAGAGTAGATGTGAGGC
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136097	134184	ATTAGAAGAGTAGATGTGAG
136098	134185	GATTAGAAGAGTAGATGTGA
136099	134186	GGATTAGAAGAGTAGATGTG
136100	134187	TGGATTAGAAGAGTAGATGT
136101	134188	ATGGATTAGAAGAGTAGATG
136102	134189	GATGGATTAGAAGAGTAGAT
136103	134190	AGATGGATTAGAAGAGTAGA
136104	134191	TAGATGGATTAGAAGAGTAG
136105	134192	TTAGATGGATTAGAAGAGTA
136106	134193	ATTAGATGGATTAGAAGAGT
136107	134194	AATTAGATGGATTAGAAGAG
136108	134195	AAATTAGATGGATTAGAAGA
136109	134196	AAAATTAGATGGATTAGAAG
136110	134197	CAAAATTAGATGGATTAGAA
136111	134198	ACAAAATTAGATGGATTAGA
136112	134199	AACAAAATTAGATGGATTAG
136113	134200	AAACAAAATTAGATGGATTA
136114	134201	AAAACAAAATTAGATGGATT
136115	134202	TAAAACAAAATTAGATGGAT
136116	134203	ATAAAACAAAATTAGATGGA
136117	134204	CATAAAACAAAATTAGATGG
136118	134205	CCATAAAACAAAATTAGATG
136119	134206	ACCATAAAACAAAATTAGAT
136120	134207	CACCATAAAACAAAATTAGA
136121	134208	TCACCATAAAACAAAATTAG
136122	134209	ATCACCATAAAACAAAATTA
136123	134210	CATCACCATAAAACAAAATT
136124	134211	GCATCACCATAAAACAAAAT
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136126	134213	AAGCATCACCATAAAACAAA
136127	134214	AAAGCATCACCATAAAACAA
136128	134215	AAAAGCATCACCATAAAACA
136129	134216	TAAAAGCATCACCATAAAAC
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37837	35924	AATTGGAGACTATAAGTGAT
37838	35925	TAATTGGAGACTATAAGTGA
37839	35926	TTAATTGGAGACTATAAGTG
37840	35927	TTTAATTGGAGACTATAAGT
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37843	35930	GTTTTTAATTGGAGACTATA
37844	35931	TGTTTTTAATTGGAGACTAT
37845	35932	ATGTTTTTAATTGGAGACTA
37846	35933	AATGTTTTTAATTGGAGACT
37847	35934	AAATGTTTTTAATTGGAGAC
37848	35935	AAAATGTTTTTAATTGGAGA
37849	35936	TAAAATGTTTTTAATTGGAG
37850	35937	GTAAAATGTTTTTAATTGGA
37851	35938	AGTAAAATGTTTTTAATTGG
37852	35939	AAGTAAAATGTTTTTAATTG
37853	35940	TAAGTAAAATGTTTTTAATT
37854	35941	TTAAGTAAAATGTTTTTAAT
37855	35942	TTTAAGTAAAATGTTTTTAA
37856	35943	GTTTAAGTAAAATGTTTTTA
37857	35944	TGTTTAAGTAAAATGTTTTT
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37859	35946	TATGTTTAAGTAAAATGTTT
37860	35947	TTATGTTTAAGTAAAATGTT
37861	35948	ATTATGTTTAAGTAAAATGT
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37863	35950	AAATTATGTTTAAGTAAAAT
37864	35951	AAAATTATGTTTAAGTAAAA
37865	35952	TAAAATTATGTTTAAGTAAA
37866	35953	CTAAAATTATGTTTAAGTAA
37867	35954	TCTAAAATTATGTTTAAGTA
37868	35955	GTCTAAAATTATGTTTAAGT
37869	35956	AGTCTAAAATTATGTTTAAG
37870	35957	AAGTCTAAAATTATGTTTAA
37871	35958	AAAGTCTAAAATTATGTTTA
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37874	35961	CTAAAAGTCTAAAATTATGT
37875	35962	TCTAAAAGTCTAAAATTATG
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37881	35968	AATTTTTCTAAAAGTCTAAA
37882	35969	CAATTTTTCTAAAAGTCTAA
37883	35970	GCAATTTTTCTAAAAGTCTA
37884	35971	TGCAATTTTTCTAAAAGTCT
37885	35972	TTGCAATTTTTCTAAAAGTC
37886	35973	TTTGCAATTTTTCTAAAAGT
37887	35974	CTTTGCAATTTTTCTAAAAG
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37893	35980	TAATATCTTTGCAATTTTTC
37894	35981	ATAATATCTTTGCAATTTTT
37895	35982	TATAATATCTTTGCAATTTT
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37897	35984	TTTATAATATCTTTGCAATT
37898	35985	CTTTATAATATCTTTGCAAT
37899	35986	TCTTTATAATATCTTTGCAA
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37901	35988	ATTCTTTATAATATCTTTGC
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37903	35990	GAATTCTTTATAATATCTTT
37904	35991	AGAATTCTTTATAATATCTT
37905	35992	GAGAATTCTTTATAATATCT
37906	35993	GGAGAATTCTTTATAATATC
37907	35994	AGGAGAATTCTTTATAATAT

86984	85071	GTACGATCTCAACTCACTGC
86985	85072	GGTACGATCTCAACTCACTG
86986	85073	TGGTACGATCTCAACTCACT
86987	85074	GTGGTACGATCTCAACTCAC
86988	85075	AGTGGTACGATCTCAACTCA
86989	85076	CAGTGGTACGATCTCAACTC
86990	85077	GCAGTGGTACGATCTCAACT
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86992	85079	GTGCAGTGGTACGATCTCAA
86993	85080	AGTGCAGTGGTACGATCTCA
86994	85081	GAGTGCAGTGGTACGATCTC
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86999	85086	GGCTGGAGTGCAGTGGTACG
87000	85087	AGGCTGGAGTGCAGTGGTAC
87001	85088	CAGGCTGGAGTGCAGTGGTA
87002	85089	CCAGGCTGGAGTGCAGTGGT
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87004	85091	GCCCAGGCTGGAGTGCAGTG
87005	85092	CGCCCAGGCTGGAGTGCAGT
87006	85093	TCGCCCAGGCTGGAGTGCAG
87007	85094	GTCGCCCAGGCTGGAGTGCA
87008	85095	TGTCGCCCAGGCTGGAGTGC
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87010	85097	TCTGTCGCCCAGGCTGGAGT
87011	85098	CTCTGTCGCCCAGGCTGGAG
87012	85099	TCTCTGTCGCCCAGGCTGGA
87013	85100	GTCTCTGTCGCCCAGGCTGG
87014	85101	TGTCTCTGTCGCCCAGGCTG
87015	85102	CTGTCTCTGTCGCCCAGGCT
87016	85103	TCTGTCTCTGTCGCCCAGGC
87017	85104	GTCTGTCTCTGTCGCCCAGG
87018	85105	AGTCTGTCTCTGTCGCCCAG
87019	85106	GAGTCTGTCTCTGTCGCCCA
87020	85107	AGAGTCTGTCTCTGTCGCCC
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87023	85110	GACAGAGTCTGTCTCTGTCG
87024	85111	AGACAGAGTCTGTCTCTGTC
87025	85112	AAGACAGAGTCTGTCTCTGT
87026	85113	TAAGACAGAGTCTGTCTCTG
87027	85114	ATAAGACAGAGTCTGTCTCT
87028	85115	TATAAGACAGAGTCTGTCTC
87029	85116	TTATAAGACAGAGTCTGTCT
87030	85117	TTTATAAGACAGAGTCTGTC
87031	85118	TTTTATAAGACAGAGTCTGT
87032	85119	TTTTTATAAGACAGAGTCTG
87033	85120	ATTTTTATAAGACAGAGTCT
87034	85121	TATTTTTATAAGACAGAGTC
87035	85122	TTATTTTTATAAGACAGAGT
87036	85123	TTTATTTTTATAAGACAGAG
87037	85124	TTTTATTTTTATAAGACAGA
87038	85125	TTTTTATTTTTATAAGACAG
87039	85126	ATTTTTATTTTTATAAGACA
87040	85127	TATTTTTATTTTTATAAGAC
87041	85128	TTATTTTTATTTTTATAAGA
87042	85129	TTTATTTTTATTTTTATAAG
87043	85130	TTTTATTTTTATTTTTATAA
87044	85131	ATTTTATTTTTATTTTTATA
87045	85132	TATTTTATTTTTATTTTTAT
87046	85133	TTATTTTATTTTTATTTTTA
87047	85134	ATTATTTTATTTTTATTTTT
87048	85135	TATTATTTTATTTTTATTTT
87049	85136	TTATTATTTTATTTTTATTT
87050	85137	ATTATTATTTTATTTTTATT
87051	85138	AATTATTATTTTATTTTTAT
87052	85139	GAATTATTATTTTATTTTTA
87053	85140	AGAATTATTATTTTATTTTT
87054	85141	TAGAATTATTATTTTATTTT

136131	134218	GGTAAAAGCATCACCATAAA
136132	134219	AGGTAAAAGCATCACCATAA
136133	134220	AAGGTAAAAGCATCACCATA
136134	134221	AAAGGTAAAAGCATCACCAT
136135	134222	GAAAGGTAAAAGCATCACCA
136136	134223	TGAAAGGTAAAAGCATCACC
136137	134224	CTGAAAGGTAAAAGCATCAC
136138	134225	TCTGAAAGGTAAAAGCATCA
136139	134226	TTCTGAAAGGTAAAAGCATC
136140	134227	TTTCTGAAAGGTAAAAGCAT
136141	134228	GTTTCTGAAAGGTAAAAGCA
136142	134229	TGTTTCTGAAAGGTAAAAGC
136143	134230	CTGTTTCTGAAAGGTAAAAG
136144	134231	ACTGTTTCTGAAAGGTAAAA
136145	134232	TACTGTTTCTGAAAGGTAAA
136146	134233	TTACTGTTTCTGAAAGGTAA
136147	134234	ATTACTGTTTCTGAAAGGTA
136148	134235	TATTACTGTTTCTGAAAGGT
136149	134236	TTATTACTGTTTCTGAAAGG
136150	134237	ATTATTACTGTTTCTGAAAG
136151	134238	TATTATTACTGTTTCTGAAA
136152	134239	GTATTATTACTGTTTCTGAA
136153	134240	TGTATTATTACTGTTTCTGA
136154	134241	TTGTATTATTACTGTTTCTG
136155	134242	GTTGTATTATTACTGTTTCT
136156	134243	AGTTGTATTATTACTGTTTC
136157	134244	AAGTTGTATTATTACTGTTT
136158	134245	AAAGTTGTATTATTACTGTT
136159	134246	AAAAGTTGTATTATTACTGT
136160	134247	GAAAAGTTGTATTATTACTG
136161	134248	GGAAAAGTTGTATTATTACT
136162	134249	CGGAAAAGTTGTATTATTAC
136163	134250	TCGGAAAAGTTGTATTATTA
136164	134251	GTCGGAAAAGTTGTATTATT
136165	134252	AGTCGGAAAAGTTGTATTAT
136166	134253	TAGTCGGAAAAGTTGTATTA
136167	134254	TTAGTCGGAAAAGTTGTATT
136168	134255	GTTAGTCGGAAAAGTTGTAT
136169	134256	AGTTAGTCGGAAAAGTTGTA
136170	134257	TAGTTAGTCGGAAAAGTTGT
136171	134258	CTAGTTAGTCGGAAAAGTTG
136172	134259	TCTAGTTAGTCGGAAAAGTT
136173	134260	CTCTAGTTAGTCGGAAAAGT
136174	134261	GCTCTAGTTAGTCGGAAAAG
136175	134262	GGCTCTAGTTAGTCGGAAAA
136176	134263	TGGCTCTAGTTAGTCGGAAA
136177	134264	ATGGCTCTAGTTAGTCGGAA
136178	134265	AATGGCTCTAGTTAGTCGGA
136179	134266	TAATGGCTCTAGTTAGTCGG
136180	134267	CTAATGGCTCTAGTTAGTCG
136181	134268	CCTAATGGCTCTAGTTAGTC
136182	134269	TCCTAATGGCTCTAGTTAGT
136183	134270	TTCCTAATGGCTCTAGTTAG
136184	134271	CTTCCTAATGGCTCTAGTTA
136185	134272	TCTTCCTAATGGCTCTAGTT
136186	134273	TTCTTCCTAATGGCTCTAGT
136187	134274	ATTCTTCCTAATGGCTCTAG
136188	134275	AATTCTTCCTAATGGCTCTA
136189	134276	TAATTCTTCCTAATGGCTCT
136190	134277	CTAATTCTTCCTAATGGCTC
136191	134278	TCTAATTCTTCCTAATGGCT
136192	134279	ATCTAATTCTTCCTAATGGC
136193	134280	GATCTAATTCTTCCTAATGG
136194	134281	GGATCTAATTCTTCCTAATG
136195	134282	TGGATCTAATTCTTCCTAAT
136196	134283	CTGGATCTAATTCTTCCTAA
136197	134284	TCTGGATCTAATTCTTCCTA
136198	134285	TTCTGGATCTAATTCTTCCT
136199	134286	ATTCTGGATCTAATTCTTCC
136200	134287	GATTCTGGATCTAATTCTTC
136201	134288	GGATTCTGGATCTAATTCTT

37908	35995	TAGGAGAATTCTTTATAATA
37909	35996	ATAGGAGAATTCTTTATAAT
37910	35997	TATAGGAGAATTCTTTATAA
37911	35998	ATATAGGAGAATTCTTTATA
37912	35999	TATATAGGAGAATTCTTTAT
37913	36000	ATATATAGGAGAATTCTTTA
37914	36001	GATATATAGGAGAATTCTTT
37915	36002	AGATATATAGGAGAATTCTT
37916	36003	GAGATATATAGGAGAATTCT
37917	36004	TGAGATATATAGGAGAATTC
37918	36005	GTGAGATATATAGGAGAATT
37919	36006	GGTGAGATATATAGGAGAAT
37920	36007	AGGTGAGATATATAGGAGAA
37921	36008	CAGGTGAGATATATAGGAGA
37922	36009	ACAGGTGAGATATATAGGAG
37923	36010	TACAGGTGAGATATATAGGA
37924	36011	ATACAGGTGAGATATATAGG
37925	36012	AATACAGGTGAGATATATAG
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37929	36016	GAAGAATACAGGTGAGATAT
37930	36017	TGAAGAATACAGGTGAGATA
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37939	36026	AATGTTACTTGAAGAATACA
37940	36027	AAATGTTACTTGAAGAATAC
37941	36028	AAAATGTTACTTGAAGAATA
37942	36029	TAAAATGTTACTTGAAGAAT
37943	36030	GTAAAATGTTACTTGAAGAA
37944	36031	GGTAAAATGTTACTTGAAGA
37945	36032	TGGTAAAATGTTACTTGAAG
37946	36033	ATGGTAAAATGTTACTTGAA
37947	36034	TATGGTAAAATGTTACTTGA
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37949	36036	AATATGGTAAAATGTTACTT
37950	36037	GAATATGGTAAAATGTTACT
37951	36038	TGAATATGGTAAAATGTTAC
37952	36039	GTGAATATGGTAAAATGTTA
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37954	36041	AGGTGAATATGGTAAAATGT
37955	36042	AAGGTGAATATGGTAAAATG
37956	36043	TAAGGTGAATATGGTAAAAT
37957	36044	TTAAGGTGAATATGGTAAAA
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37959	36046	TGTTAAGGTGAATATGGTAA
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37968	36055	CAGAGAAAATGTTAAGGTGA
37969	36056	ACAGAGAAAATGTTAAGGTG
37970	36057	TACAGAGAAAATGTTAAGGT
37971	36058	ATACAGAGAAAATGTTAAGG
37972	36059	AATACAGAGAAAATGTTAAG
37973	36060	CAATACAGAGAAAATGTTAA
37974	36061	CCAATACAGAGAAAATGTTA
37975	36062	ACCAATACAGAGAAAATGTT
37976	36063	TACCAATACAGAGAAAATGT
37977	36064	TTACCAATACAGAGAAAATG
37978	36065	ATTACCAATACAGAGAAAAT

87055	85142	ATAGAATTATTATTTTATTT
87056	85143	AATAGAATTATTATTTTATT
87057	85144	CAATAGAATTATTATTTTAT
87058	85145	CCAATAGAATTATTATTTTA
87059	85146	GCCAATAGAATTATTATTTT
87060	85147	TGCCAATAGAATTATTATTT
87061	85148	TTGCCAATAGAATTATTATT
87062	85149	GTTGCCAATAGAATTATTAT
87063	85150	TGTTGCCAATAGAATTATTA
87064	85151	ATGTTGCCAATAGAATTATT
87065	85152	TATGTTGCCAATAGAATTAT
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87068	85155	ATATATGTTGCCAATAGAAT
87069	85156	AATATATGTTGCCAATAGAA
87070	85157	TAATATATGTTGCCAATAGA
87071	85158	TTAATATATGTTGCCAATAG
87072	85159	ATTAATATATGTTGCCAATA
87073	85160	AATTAATATATGTTGCCAAT
87074	85161	AAATTAATATATGTTGCCAA
87075	85162	CAAATTAATATATGTTGCCA
87076	85163	TCAAATTAATATATGTTGCC
87077	85164	TTCAAATTAATATATGTTGC
87078	85165	CTTCAAATTAATATATGTTG
87079	85166	ACTTCAAATTAATATATGTT
87080	85167	AACTTCAAATTAATATATGT
87081	85168	GAACTTCAAATTAATATATG
87082	85169	AGAACTTCAAATTAATATAT
87083	85170	TAGAACTTCAAATTAATATA
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87085	85172	TTTAGAACTTCAAATTAATA
87086	85173	CTTTAGAACTTCAAATTAAT
87087	85174	TCTTTAGAACTTCAAATTAA
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87096	85183	CTGCCAAACTCTTTAGAACT
87097	85184	GCTGCCAAACTCTTTAGAAC
87098	85185	GGCTGCCAAACTCTTTAGAA
87099	85186	CGGCTGCCAAACTCTTTAGA
87100	85187	CCGGCTGCCAAACTCTTTAG
87101	85188	CCCGGCTGCCAAACTCTTTA
87102	85189	ACCCGGCTGCCAAACTCTTT
87103	85190	CACCCGGCTGCCAAACTCTT
87104	85191	TCACCCGGCTGCCAAACTCT
87105	85192	CTCACCCGGCTGCCAAACTC
87106	85193	TCTCACCCGGCTGCCAAACT
87107	85194	CTCTCACCCGGCTGCCAAAC
87108	85195	TCTCTCACCCGGCTGCCAAA
87109	85196	CTCTCTCACCCGGCTGCCAA
87110	85197	ACTCTCTCACCCGGCTGCCA
87111	85198	CACTCTCTCACCCGGCTGCC
87112	85199	TCACTCTCTCACCCGGCTGC
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87121	85208	CAAATCTCCTCACTCTCTCA
87122	85209	CCAAATCTCCTCACTCTCTC
87123	85210	GCCAAATCTCCTCACTCTCT
87124	85211	AGCCAAATCTCCTCACTCTC
87125	85212	AAGCCAAATCTCCTCACTCT

136202	134289	AGGATTCTGGATCTAATTCT
136203	134290	AAGGATTCTGGATCTAATTC
136204	134291	AAAGGATTCTGGATCTAATT
136205	134292	AAAAGGATTCTGGATCTAAT
136206	134293	AAAAAGGATTCTGGATCTAA
136207	134294	AAAAAAGGATTCTGGATCTA
136208	134295	CAAAAAAGGATTCTGGATCT
136209	134296	TCAAAAAAGGATTCTGGATC
136210	134297	ATCAAAAAAGGATTCTGGAT
136211	134298	AATCAAAAAAGGATTCTGGA
136212	134299	AAATCAAAAAAGGATTCTGG
136213	134300	CAAATCAAAAAAGGATTCTG
136214	134301	ACAAATCAAAAAAGGATTCT
136215	134302	AACAAATCAAAAAAGGATTC
136216	134303	AAACAAATCAAAAAAGGATT
136217	134304	AAAACAAATCAAAAAAGGAT
136218	134305	AAAAACAAATCAAAAAAGGA
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136220	134307	CCAAAAACAAATCAAAAAAG
136221	134308	ACCAAAAACAAATCAAAAAA
136222	134309	TACCAAAAACAAATCAAAAA
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136224	134311	ACTACCAAAAACAAATCAAA
136225	134312	AACTACCAAAAACAAATCAA
136226	134313	AAACTACCAAAAACAAATCA
136227	134314	TAAACTACCAAAAACAAATC
136228	134315	TTAAACTACCAAAAACAAAT
136229	134316	ATTAAACTACCAAAAACAAA
136230	134317	CATTAAACTACCAAAAACAA
136231	134318	GCATTAAACTACCAAAAACA
136232	134319	TGCATTAAACTACCAAAAAC
136233	134320	CTGCATTAAACTACCAAAAA
136234	134321	TCTGCATTAAACTACCAAAA
136235	134322	ATCTGCATTAAACTACCAAA
136236	134323	TATCTGCATTAAACTACCAA
136237	134324	TTATCTGCATTAAACTACCA
136238	134325	CTTATCTGCATTAAACTACC
136239	134326	ACTTATCTGCATTAAACTAC
136240	134327	TACTTATCTGCATTAAACTA
136241	134328	TTACTTATCTGCATTAAACT
136242	134329	CTTACTTATCTGCATTAAAC
136243	134330	TCTTACTTATCTGCATTAAA
136244	134331	TTCTTACTTATCTGCATTAA
136245	134332	TTTCTTACTTATCTGCATTA
136246	134333	TTTTCTTACTTATCTGCATT
136247	134334	ATTTTCTTACTTATCTGCAT
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136251	134338	CTATATTTTCTTACTTATCT
136252	134339	ACTATATTTTCTTACTTATC
136253	134340	AACTATATTTTCTTACTTAT
136254	134341	TAACTATATTTTCTTACTTA
136255	134342	TTAACTATATTTTCTTACTT
136256	134343	CTTAACTATATTTTCTTACT
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136258	134345	AACTTAACTATATTTTCTTA
136259	134346	TAACTTAACTATATTTTCTT
136260	134347	TTAACTTAACTATATTTTCT
136261	134348	TTTAACTTAACTATATTTTC
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136263	134350	TTTTTAACTTAACTATATTT
136264	134351	TTTTTTAACTTAACTATATT
136265	134352	TTTTTTTAACTTAACTATAT
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136269	134356	TTTTTTTTTTTAACTTAACT
136270	134357	TTTTTTTTTTTTAACTTAAC
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37979	36066	AATTACCAATACAGAGAAAA
37980	36067	CAATTACCAATACAGAGAAA
37981	36068	ACAATTACCAATACAGAGAA
37982	36069	TACAATTACCAATACAGAGA
37983	36070	ATACAATTACCAATACAGAG
37984	36071	TATACAATTACCAATACAGA
37985	36072	ATATACAATTACCAATACAG
37986	36073	CATATACAATTACCAATACA
37987	36074	ACATATACAATTACCAATAC
37988	36075	TACATATACAATTACCAATA
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37991	36078	TCTTACATATACAATTACCA
37992	36079	ATCTTACATATACAATTACC
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37994	36081	AAATCTTACATATACAATTA
37995	36082	TAAATCTTACATATACAATT
37996	36083	TTAAATCTTACATATACAAT
37997	36084	ATTAAATCTTACATATACAA
37998	36085	TATTAAATCTTACATATACA
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38001	36088	TTATATTAAATCTTACATAT
38002	36089	TTTATATTAAATCTTACATA
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38023	36110	ATGTTTAATAAGAATTTTTA
38024	36111	TATGTTTAATAAGAATTTTT
38025	36112	ATATGTTTAATAAGAATTTT
38026	36113	CATATGTTTAATAAGAATTT
38027	36114	TCATATGTTTAATAAGAATT
38028	36115	CTCATATGTTTAATAAGAAT
38029	36116	TCTCATATGTTTAATAAGAA
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38032	36119	GTCTCTCATATGTTTAATAA
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38035	36122	CATGTCTCTCATATGTTTAA
38036	36123	TCATGTCTCTCATATGTTTA
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38046	36133	TAAAGAGGCATCATGTCTCT
38047	36134	CTAAAGAGGCATCATGTCTC
38048	36135	GCTAAAGAGGCATCATGTCT
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87126	85213	AAAGCCAAATCTCCTCACTC
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87128	85215	TCAAAGCCAAATCTCCTCAC
87129	85216	GTCAAAGCCAAATCTCCTCA
87130	85217	TGTCAAAGCCAAATCTCCTC
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87135	85222	CCTAATGTCAAAGCCAAATC
87136	85223	CCCTAATGTCAAAGCCAAAT
87137	85224	TCCCTAATGTCAAAGCCAAA
87138	85225	TTCCCTAATGTCAAAGCCAA
87139	85226	CTTCCCTAATGTCAAAGCCA
87140	85227	ACTTCCCTAATGTCAAAGCC
87141	85228	AACTTCCCTAATGTCAAAGC
87142	85229	AAACTTCCCTAATGTCAAAG
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87145	85232	CGAAAACTTCCCTAATGTCA
87146	85233	GCGAAAACTTCCCTAATGTC
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87151	85238	ACCAAGCGAAAACTTCCCTA
87152	85239	CACCAAGCGAAAACTTCCCT
87153	85240	ACACCAAGCGAAAACTTCCC
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87155	85242	TAACACCAAGCGAAAACTTC
87156	85243	TTAACACCAAGCGAAAACTT
87157	85244	GTTAACACCAAGCGAAAACT
87158	85245	TGTTAACACCAAGCGAAAAC
87159	85246	GTGTTAACACCAAGCGAAAA
87160	85247	GGTGTTAACACCAAGCGAAA
87161	85248	TGGTGTTAACACCAAGCGAA
87162	85249	CTGGTGTTAACACCAAGCGA
87163	85250	ACTGGTGTTAACACCAAGCG
87164	85251	TACTGGTGTTAACACCAAGC
87165	85252	CTACTGGTGTTAACACCAAG
87166	85253	CCTACTGGTGTTAACACCAA
87167	85254	GCCTACTGGTGTTAACACCA
87168	85255	AGCCTACTGGTGTTAACACC
87169	85256	AAGCCTACTGGTGTTAACAC
87170	85257	GAAGCCTACTGGTGTTAACA
87171	85258	AGAAGCCTACTGGTGTTAAC
87172	85259	GAGAAGCCTACTGGTGTTAA
87173	85260	AGAGAAGCCTACTGGTGTTA
87174	85261	CAGAGAAGCCTACTGGTGTT
87175	85262	TCAGAGAAGCCTACTGGTGT
87176	85263	ATCAGAGAAGCCTACTGGTG
87177	85264	CATCAGAGAAGCCTACTGGT
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87180	85267	CCTCATCAGAGAAGCCTACT
87181	85268	CCCTCATCAGAGAAGCCTAC
87182	85269	GCCCTCATCAGAGAAGCCTA
87183	85270	GGCCCTCATCAGAGAAGCCT
87184	85271	TGGCCCTCATCAGAGAAGCC
87185	85272	ATGGCCCTCATCAGAGAAGC
87186	85273	AATGGCCCTCATCAGAGAAG
87187	85274	GAATGGCCCTCATCAGAGAA
87188	85275	AGAATGGCCCTCATCAGAGA
87189	85276	CAGAATGGCCCTCATCAGAG
87190	85277	ACAGAATGGCCCTCATCAGA
87191	85278	GACAGAATGGCCCTCATCAG
87192	85279	GGACAGAATGGCCCTCATCA
87193	85280	TGGACAGAATGGCCCTCATC
87194	85281	GTGGACAGAATGGCCCTCAT
87195	85282	AGTGGACAGAATGGCCCTCA
87196	85283	GAGTGGACAGAATGGCCCTC

136273	134360	ATTTTTTTTTTTTTTAACTT
136274	134361	CATTTTTTTTTTTTTTAACT
136275	134362	TCATTTTTTTTTTTTTTAAC
136276	134363	TTCATTTTTTTTTTTTTTAA
136277	134364	TTTCATTTTTTTTTTTTTTA
136278	134365	TTTTCATTTTTTTTTTTTTT
136279	134366	CTTTTCATTTTTTTTTTTTT
136280	134367	GCTTTTCATTTTTTTTTTTT
136281	134368	TGCTTTTCATTTTTTTTTTT
136282	134369	ATGCTTTTCATTTTTTTTTT
136283	134370	GATGCTTTTCATTTTTTTTT
136284	134371	GGATGCTTTTCATTTTTTTT
136285	134372	TGGATGCTTTTCATTTTTTT
136286	134373	ATGGATGCTTTTCATTTTTT
136287	134374	TATGGATGCTTTTCATTTTT
136288	134375	TTATGGATGCTTTTCATTTT
136289	134376	ATTATGGATGCTTTTCATTT
136290	134377	GATTATGGATGCTTTTCATT
136291	134378	GGATTATGGATGCTTTTCAT
136292	134379	GGGATTATGGATGCTTTTCA
136293	134380	AGGGATTATGGATGCTTTTC
136294	134381	GAGGGATTATGGATGCTTTT
136295	134382	GGAGGGATTATGGATGCTTT
136296	134383	TGGAGGGATTATGGATGCTT
136297	134384	GTGGAGGGATTATGGATGCT
136298	134385	GGTGGAGGGATTATGGATGC
136299	134386	AGGTGGAGGGATTATGGATG
136300	134387	CAGGTGGAGGGATTATGGAT
136301	134388	TCAGGTGGAGGGATTATGGA
136302	134389	GTCAGGTGGAGGGATTATGG
136303	134390	TGTCAGGTGGAGGGATTATG
136304	134391	TTGTCAGGTGGAGGGATTAT
136305	134392	GTTGTCAGGTGGAGGGATTA
136306	134393	AGTTGTCAGGTGGAGGGATT
136307	134394	CAGTTGTCAGGTGGAGGGAT
136308	134395	GCAGTTGTCAGGTGGAGGGA
136309	134396	GGCAGTTGTCAGGTGGAGGG
136310	134397	AGGCAGTTGTCAGGTGGAGG
136311	134398	AAGGCAGTTGTCAGGTGGAG
136312	134399	AAAGGCAGTTGTCAGGTGGA
136313	134400	AAAAGGCAGTTGTCAGGTGG
136314	134401	TAAAAGGCAGTTGTCAGGTG
136315	134402	TTAAAAGGCAGTTGTCAGGT
136316	134403	GTTAAAAGGCAGTTGTCAGG
136317	134404	TGTTAAAAGGCAGTTGTCAG
136318	134405	ATGTTAAAAGGCAGTTGTCA
136319	134406	AATGTTAAAAGGCAGTTGTC
136320	134407	AAATGTTAAAAGGCAGTTGT
136321	134408	AAAATGTTAAAAGGCAGTTG
136322	134409	CAAAATGTTAAAAGGCAGTT
136323	134410	TCAAAATGTTAAAAGGCAGT
136324	134411	ATCAAAATGTTAAAAGGCAG
136325	134412	CATCAAAATGTTAAAAGGCA
136326	134413	ACATCAAAATGTTAAAAGGC
136327	134414	CACATCAAAATGTTAAAAGG
136328	134415	ACACATCAAAATGTTAAAAG
136329	134416	TACACATCAAAATGTTAAAA
136330	134417	ATACACATCAAAATGTTAAA
136331	134418	GATACACATCAAAATGTTAA
136332	134419	GGATACACATCAAAATGTTA
136333	134420	AGGATACACATCAAAATGTT
136334	134421	AAGGATACACATCAAAATGT
136335	134422	GAAGGATACACATCAAAATG
136336	134423	GGAAGGATACACATCAAAAT
136337	134424	TGGAAGGATACACATCAAAA
136338	134425	CTGGAAGGATACACATCAAA
136339	134426	CCTGGAAGGATACACATCAA
136340	134427	ACCTGGAAGGATACACATCA
136341	134428	CACCTGGAAGGATACACATC
136342	134429	ACACCTGGAAGGATACACAT
136343	134430	TACACCTGGAAGGATACACA

38050	36137	GGGCTAAAGAGGCATCATGT
38051	36138	AGGGCTAAAGAGGCATCATG
38052	36139	TAGGGCTAAAGAGGCATCAT
38053	36140	TTAGGGCTAAAGAGGCATCA
38054	36141	TTTAGGGCTAAAGAGGCATC
38055	36142	ATTTAGGGCTAAAGAGGCAT
38056	36143	TATTTAGGGCTAAAGAGGCA
38057	36144	GTATTTAGGGCTAAAGAGGC
38058	36145	AGTATTTAGGGCTAAAGAGG
38059	36146	AAGTATTTAGGGCTAAAGAG
38060	36147	GAAGTATTTAGGGCTAAAGA
38061	36148	TGAAGTATTTAGGGCTAAAG
38062	36149	TTGAAGTATTTAGGGCTAAA
38063	36150	GTTGAAGTATTTAGGGCTAA
38064	36151	AGTTGAAGTATTTAGGGCTA
38065	36152	AAGTTGAAGTATTTAGGGCT
38066	36153	CAAGTTGAAGTATTTAGGGC
38067	36154	ACAAGTTGAAGTATTTAGGG
38068	36155	TACAAGTTGAAGTATTTAGG
38069	36156	ATACAAGTTGAAGTATTTAG
38070	36157	CATACAAGTTGAAGTATTTA
38071	36158	ACATACAAGTTGAAGTATTT
38072	36159	TACATACAAGTTGAAGTATT
38073	36160	GTACATACAAGTTGAAGTAT
38074	36161	AGTACATACAAGTTGAAGTA
38075	36162	TAGTACATACAAGTTGAAGT
38076	36163	TTAGTACATACAAGTTGAAG
38077	36164	ATTAGTACATACAAGTTGAA
38078	36165	TATTAGTACATACAAGTTGA
38079	36166	TTATTAGTACATACAAGTTG
38080	36167	GTTATTAGTACATACAAGTT
38081	36168	TGTTATTAGTACATACAAGT
38082	36169	TTGTTATTAGTACATACAAG
38083	36170	CTTGTTATTAGTACATACAA
38084	36171	CCTTGTTATTAGTACATACA
38085	36172	CCCTTGTTATTAGTACATAC
38086	36173	GCCCTTGTTATTAGTACATA
38087	36174	TGCCCTTGTTATTAGTACAT
38088	36175	ATGCCCTTGTTATTAGTACA
38089	36176	AATGCCCTTGTTATTAGTAC
38090	36177	GAATGCCCTTGTTATTAGTA
38091	36178	AGAATGCCCTTGTTATTAGT
38092	36179	TAGAATGCCCTTGTTATTAG
38093	36180	ATAGAATGCCCTTGTTATTA
38094	36181	AATAGAATGCCCTTGTTATT
38095	36182	AAATAGAATGCCCTTGTTAT
38096	36183	GAAATAGAATGCCCTTGTTA
38097	36184	TGAAATAGAATGCCCTTGTT
38098	36185	TTGAAATAGAATGCCCTTGT
38099	36186	TTTGAAATAGAATGCCCTTG
38100	36187	TTTTGAAATAGAATGCCCTT
38101	36188	GTTTTGAAATAGAATGCCCT
38102	36189	GGTTTTGAAATAGAATGCCC
38103	36190	TGGTTTTGAAATAGAATGCC
38104	36191	GTGGTTTTGAAATAGAATGC
38105	36192	TGTGGTTTTGAAATAGAATG
38106	36193	CTGTGGTTTTGAAATAGAAT
38107	36194	ACTGTGGTTTTGAAATAGAA
38108	36195	TACTGTGGTTTTGAAATAGA
38109	36196	GTACTGTGGTTTTGAAATAG
38110	36197	TGTACTGTGGTTTTGAAATA
38111	36198	CTGTACTGTGGTTTTGAAAT
38112	36199	ACTGTACTGTGGTTTTGAAA
38113	36200	AACTGTACTGTGGTTTTGAA
38114	36201	CAACTGTACTGTGGTTTTGA
38115	36202	ACAACTGTACTGTGGTTTTG
38116	36203	GACAACTGTACTGTGGTTTT
38117	36204	TGACAACTGTACTGTGGTTT
38118	36205	TTGACAACTGTACTGTGGTT
38119	36206	TTTGACAACTGTACTGTGGT
38120	36207	TTTTGACAACTGTACTGTGG

87197	85284	AGAGTGGACAGAATGGCCCT
87198	85285	AAGAGTGGACAGAATGGCCC
87199	85286	AAAGAGTGGACAGAATGGCC
87200	85287	AAAAGAGTGGACAGAATGGC
87201	85288	TAAAAGAGTGGACAGAATGG
87202	85289	GTAAAAGAGTGGACAGAATG
87203	85290	GGTAAAAGAGTGGACAGAAT
87204	85291	AGGTAAAAGAGTGGACAGAA
87205	85292	CAGGTAAAAGAGTGGACAGA
87206	85293	TCAGGTAAAAGAGTGGACAG
87207	85294	ATCAGGTAAAAGAGTGGACA
87208	85295	TATCAGGTAAAAGAGTGGAC
87209	85296	CTATCAGGTAAAAGAGTGGA
87210	85297	TCTATCAGGTAAAAGAGTGG
87211	85298	ATCTATCAGGTAAAAGAGTG
87212	85299	AATCTATCAGGTAAAAGAGT
87213	85300	CAATCTATCAGGTAAAAGAG
87214	85301	CCAATCTATCAGGTAAAAGA
87215	85302	ACCAATCTATCAGGTAAAAG
87216	85303	GACCAATCTATCAGGTAAAA
87217	85304	AGACCAATCTATCAGGTAAA
87218	85305	TAGACCAATCTATCAGGTAA
87219	85306	TTAGACCAATCTATCAGGTA
87220	85307	ATTAGACCAATCTATCAGGT
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87222	85309	GCATTAGACCAATCTATCAG
87223	85310	TGCATTAGACCAATCTATCA
87224	85311	GTGCATTAGACCAATCTATC
87225	85312	TGTGCATTAGACCAATCTAT
87226	85313	CTGTGCATTAGACCAATCTA
87227	85314	ACTGTGCATTAGACCAATCT
87228	85315	TACTGTGCATTAGACCAATC
87229	85316	CTACTGTGCATTAGACCAAT
87230	85317	TCTACTGTGCATTAGACCAA
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87232	85319	AGTCTACTGTGCATTAGACC
87233	85320	CAGTCTACTGTGCATTAGAC
87234	85321	TCAGTCTACTGTGCATTAGA
87235	85322	ATCAGTCTACTGTGCATTAG
87236	85323	AATCAGTCTACTGTGCATTA
87237	85324	AAATCAGTCTACTGTGCATT
87238	85325	TAAATCAGTCTACTGTGCAT
87239	85326	CTAAATCAGTCTACTGTGCA
87240	85327	TCTAAATCAGTCTACTGTGC
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87243	85330	CTTTCTAAATCAGTCTACTG
87244	85331	TCTTTCTAAATCAGTCTACT
87245	85332	CTCTTTCTAAATCAGTCTAC
87246	85333	ACTCTTTCTAAATCAGTCTA
87247	85334	TACTCTTTCTAAATCAGTCT
87248	85335	CTACTCTTTCTAAATCAGTC
87249	85336	ACTACTCTTTCTAAATCAGT
87250	85337	GACTACTCTTTCTAAATCAG
87251	85338	TGACTACTCTTTCTAAATCA
87252	85339	GTGACTACTCTTTCTAAATC
87253	85340	AGTGACTACTCTTTCTAAAT
87254	85341	TAGTGACTACTCTTTCTAAA
87255	85342	CTAGTGACTACTCTTTCTAA
87256	85343	ACTAGTGACTACTCTTTCTA
87257	85344	CACTAGTGACTACTCTTTCT
87258	85345	CCACTAGTGACTACTCTTTC
87259	85346	GCCACTAGTGACTACTCTTT
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87261	85348	ATGCCACTAGTGACTACTCT
87262	85349	CATGCCACTAGTGACTACTC
87263	85350	CCATGCCACTAGTGACTACT
87264	85351	GCCATGCCACTAGTGACTAC
87265	85352	TGCCATGCCACTAGTGACTA
87266	85353	CTGCCATGCCACTAGTGACT
87267	85354	TCTGCCATGCCACTAGTGAC

136344	134431	ATACACCTGGAAGGATACAC
136345	134432	AATACACCTGGAAGGATACA
136346	134433	AAATACACCTGGAAGGATAC
136347	134434	TAAATACACCTGGAAGGATA
136348	134435	TTAAATACACCTGGAAGGAT
136349	134436	TTTAAATACACCTGGAAGGA
136350	134437	ATTTAAATACACCTGGAAGG
136351	134438	TATTTAAATACACCTGGAAG
136352	134439	GTATTTAAATACACCTGGAA
136353	134440	TGTATTTAAATACACCTGGA
136354	134441	GTGTATTTAAATACACCTGG
136355	134442	AGTGTATTTAAATACACCTG
136356	134443	GAGTGTATTTAAATACACCT
136357	134444	TGAGTGTATTTAAATACACC
136358	134445	TTGAGTGTATTTAAATACAC
136359	134446	TTTGAGTGTATTTAAATACA
136360	134447	ATTTGAGTGTATTTAAATAC
136361	134448	TATTTGAGTGTATTTAAATA
136362	134449	GTATTTGAGTGTATTTAAAT
136363	134450	GGTATTTGAGTGTATTTAAA
136364	134451	GGGTATTTGAGTGTATTTAA
136365	134452	AGGGTATTTGAGTGTATTTA
136366	134453	TAGGGTATTTGAGTGTATTT
136367	134454	GTAGGGTATTTGAGTGTATT
136368	134455	GGTAGGGTATTTGAGTGTAT
136369	134456	GGGTAGGGTATTTGAGTGTA
136370	134457	GGGGTAGGGTATTTGAGTGT
136371	134458	AGGGGTAGGGTATTTGAGTG
136372	134459	AAGGGGTAGGGTATTTGAGT
136373	134460	AAAGGGGTAGGGTATTTGAG
136374	134461	TAAAGGGGTAGGGTATTTGA
136375	134462	ATAAAGGGGTAGGGTATTTG
136376	134463	CATAAAGGGGTAGGGTATTT
136377	134464	ACATAAAGGGGTAGGGTATT
136378	134465	TACATAAAGGGGTAGGGTAT
136379	134466	CTACATAAAGGGGTAGGGTA
136380	134467	TCTACATAAAGGGGTAGGGT
136381	134468	GTCTACATAAAGGGGTAGGG
136382	134469	TGTCTACATAAAGGGGTAGG
136383	134470	ATGTCTACATAAAGGGGTAG
136384	134471	CATGTCTACATAAAGGGGTA
136385	134472	ACATGTCTACATAAAGGGGT
136386	134473	AACATGTCTACATAAAGGGG
136387	134474	AAACATGTCTACATAAAGGG
136388	134475	AAAACATGTCTACATAAAGG
136389	134476	TAAAACATGTCTACATAAAG
136390	134477	TTAAAACATGTCTACATAAA
136391	134478	ATTAAAACATGTCTACATAA
136392	134479	TATTAAAACATGTCTACATA
136393	134480	TTATTAAAACATGTCTACAT
136394	134481	CTTATTAAAACATGTCTACA
136395	134482	TCTTATTAAAACATGTCTAC
136396	134483	TTCTTATTAAAACATGTCTA
136397	134484	TTTCTTATTAAAACATGTCT
136398	134485	ATTTCTTATTAAAACATGTC
136399	134486	TATTTCTTATTAAAACATGT
136400	134487	TTATTTCTTATTAAAACATG
136401	134488	ATTATTTCTTATTAAAACAT
136402	134489	TATTATTTCTTATTAAAACA
136403	134490	ATATTATTTCTTATTAAAAC
136404	134491	AATATTATTTCTTATTAAAA
136405	134492	GAATATTATTTCTTATTAAA
136406	134493	TGAATATTATTTCTTATTAA
136407	134494	ATGAATATTATTTCTTATTA
136408	134495	CATGAATATTATTTCTTATT
136409	134496	ACATGAATATTATTTCTTAT
136410	134497	AACATGAATATTATTTCTTA
136411	134498	AAACATGAATATTATTTCTT
136412	134499	TAAACATGAATATTATTTCT
136413	134500	ATAAACATGAATATTATTTC
136414	134501	TATAAACATGAATATTATTT

38121	36208	ATTTTGACAACTGTACTGTG
38122	36209	TATTTTGACAACTGTACTGT
38123	36210	TTATTTTGACAACTGTACTG
38124	36211	CTTATTTTGACAACTGTACT
38125	36212	CCTTATTTTGACAACTGTAC
38126	36213	TCCTTATTTTGACAACTGTA
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38130	36217	AATTTCCTTATTTTGACAAC
38131	36218	TAATTTCCTTATTTTGACAA
38132	36219	TTAATTTCCTTATTTTGACA
38133	36220	ATTAATTTCCTTATTTTGAC
38134	36221	TATTAATTTCCTTATTTTGA
38135	36222	TTATTAATTTCCTTATTTTG
38136	36223	ATTATTAATTTCCTTATTTT
38137	36224	AATTATTAATTTCCTTATTT
38138	36225	CAATTATTAATTTCCTTATT
38139	36226	ACAATTATTAATTTCCTTAT
38140	36227	CACAATTATTAATTTCCTTA
38141	36228	ACACAATTATTAATTTCCTT
38142	36229	GACACAATTATTAATTTCCT
38143	36230	TGACACAATTATTAATTTCC
38144	36231	TTGACACAATTATTAATTTC
38145	36232	TTTGACACAATTATTAATTT
38146	36233	GTTTGACACAATTATTAATT
38147	36234	AGTTTGACACAATTATTAAT
38148	36235	CAGTTTGACACAATTATTAA
38149	36236	ACAGTTTGACACAATTATTA
38150	36237	AACAGTTTGACACAATTATT
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38154	36241	GAATAACAGTTTGACACAAT
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38156	36243	CAGAATAACAGTTTGACACA
38157	36244	ACAGAATAACAGTTTGACAC
38158	36245	AACAGAATAACAGTTTGACA
38159	36246	AAACAGAATAACAGTTTGAC
38160	36247	TAAACAGAATAACAGTTTGA
38161	36248	ATAAACAGAATAACAGTTTG
38162	36249	TATAAACAGAATAACAGTTT
38163	36250	CTATAAACAGAATAACAGTT
38164	36251	TCTATAAACAGAATAACAGT
38165	36252	GTCTATAAACAGAATAACAG
38166	36253	GGTCTATAAACAGAATAACA
38167	36254	AGGTCTATAAACAGAATAAC
38168	36255	AAGGTCTATAAACAGAATAA
38169	36256	GAAGGTCTATAAACAGAATA
38170	36257	AGAAGGTCTATAAACAGAAT
38171	36258	TAGAAGGTCTATAAACAGAA
38172	36259	TTAGAAGGTCTATAAACAGA
38173	36260	ATTAGAAGGTCTATAAACAG
38174	36261	CATTAGAAGGTCTATAAACA
38175	36262	ACATTAGAAGGTCTATAAAC
38176	36263	GACATTAGAAGGTCTATAAA
38177	36264	GGACATTAGAAGGTCTATAA
38178	36265	AGGACATTAGAAGGTCTATA
38179	36266	AAGGACATTAGAAGGTCTAT
38180	36267	AAAGGACATTAGAAGGTCTA
38181	36268	TAAAGGACATTAGAAGGTCT
38182	36269	TTAAAGGACATTAGAAGGTC
38183	36270	TTTAAAGGACATTAGAAGGT
38184	36271	TTTTAAAGGACATTAGAAGG
38185	36272	GTTTTAAAGGACATTAGAAG
38186	36273	TGTTTTAAAGGACATTAGAA
38187	36274	TTGTTTTAAAGGACATTAGA
38188	36275	ATTGTTTTAAAGGACATTAG
38189	36276	GATTGTTTTAAAGGACATTA
38190	36277	TGATTGTTTTAAAGGACATT
38191	36278	TTGATTGTTTTAAAGGACAT

87268	85355	TTCTGCCATGCCACTAGTGA
87269	85356	ATTCTGCCATGCCACTAGTG
87270	85357	GATTCTGCCATGCCACTAGT
87271	85358	TGATTCTGCCATGCCACTAG
87272	85359	TTGATTCTGCCATGCCACTA
87273	85360	ATTGATTCTGCCATGCCACT
87274	85361	TATTGATTCTGCCATGCCAC
87275	85362	TTATTGATTCTGCCATGCCA
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87277	85364	CATTATTGATTCTGCCATGC
87278	85365	ACATTATTGATTCTGCCATG
87279	85366	TACATTATTGATTCTGCCAT
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87284	85371	AATTCTACATTATTGATTCT
87285	85372	AAATTCTACATTATTGATTC
87286	85373	AAAATTCTACATTATTGATT
87287	85374	CAAAATTCTACATTATTGAT
87288	85375	TCAAAATTCTACATTATTGA
87289	85376	GTCAAAATTCTACATTATTG
87290	85377	TGTCAAAATTCTACATTATT
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87295	85382	TGAATTGTCAAAATTCTACA
87296	85383	ATGAATTGTCAAAATTCTAC
87297	85384	TATGAATTGTCAAAATTCTA
87298	85385	ATATGAATTGTCAAAATTCT
87299	85386	TATATGAATTGTCAAAATTC
87300	85387	CTATATGAATTGTCAAAATT
87301	85388	ACTATATGAATTGTCAAAAT
87302	85389	CACTATATGAATTGTCAAAA
87303	85390	GCACTATATGAATTGTCAAA
87304	85391	AGCACTATATGAATTGTCAA
87305	85392	CAGCACTATATGAATTGTCA
87306	85393	TCAGCACTATATGAATTGTC
87307	85394	ATCAGCACTATATGAATTGT
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87315	85402	GGGGAGAAATCAGCACTATA
87316	85403	GGGGGAGAAATCAGCACTAT
87317	85404	TGGGGGAGAAATCAGCACTA
87318	85405	TTGGGGGAGAAATCAGCACT
87319	85406	TTTGGGGGAGAAATCAGCAC
87320	85407	ATTTGGGGGAGAAATCAGCA
87321	85408	CATTTGGGGGAGAAATCAGC
87322	85409	ACATTTGGGGGAGAAATCAG
87323	85410	GACATTTGGGGGAGAAATCA
87324	85411	TGACATTTGGGGGAGAAATC
87325	85412	CTGACATTTGGGGGAGAAAT
87326	85413	ACTGACATTTGGGGGAGAAA
87327	85414	AACTGACATTTGGGGGAGAA
87328	85415	TAACTGACATTTGGGGGAGA
87329	85416	ATAACTGACATTTGGGGGAG
87330	85417	AATAACTGACATTTGGGGGA
87331	85418	AAATAACTGACATTTGGGGG
87332	85419	AAAATAACTGACATTTGGGG
87333	85420	CAAAATAACTGACATTTGGG
87334	85421	CCAAAATAACTGACATTTGG
87335	85422	ACCAAAATAACTGACATTTG
87336	85423	GACCAAAATAACTGACATTT
87337	85424	TGACCAAAATAACTGACATT
87338	85425	ATGACCAAAATAACTGACAT

136415	134502	ATATAAACATGAATATTATT
136416	134503	AATATAAACATGAATATTAT
136417	134504	GAATATAAACATGAATATTA
136418	134505	AGAATATAAACATGAATATT
136419	134506	AAGAATATAAACATGAATAT
136420	134507	CAAGAATATAAACATGAATA
136421	134508	GCAAGAATATAAACATGAAT
136422	134509	AGCAAGAATATAAACATGAA
136423	134510	TAGCAAGAATATAAACATGA
136424	134511	ATAGCAAGAATATAAACATG
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136426	134513	TCATAGCAAGAATATAAACA
136427	134514	ATCATAGCAAGAATATAAAC
136428	134515	GATCATAGCAAGAATATAAA
136429	134516	GGATCATAGCAAGAATATAA
136430	134517	AGGATCATAGCAAGAATATA
136431	134518	TAGGATCATAGCAAGAATAT
136432	134519	TTAGGATCATAGCAAGAATA
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136436	134523	AAATTTAGGATCATAGCAAG
136437	134524	AAAATTTAGGATCATAGCAA
136438	134525	AAAAATTTAGGATCATAGCA
136439	134526	CAAAAATTTAGGATCATAGC
136440	134527	CCAAAAATTTAGGATCATAG
136441	134528	TCCAAAAATTTAGGATCATA
136442	134529	ATCCAAAAATTTAGGATCAT
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136445	134532	TGGATCCAAAAATTTAGGAT
136446	134533	ATGGATCCAAAAATTTAGGA
136447	134534	AATGGATCCAAAAATTTAGG
136448	134535	TAATGGATCCAAAAATTTAG
136449	134536	GTAATGGATCCAAAAATTTA
136450	134537	AGTAATGGATCCAAAAATTT
136451	134538	TAGTAATGGATCCAAAAATT
136452	134539	CTAGTAATGGATCCAAAAAT
136453	134540	TCTAGTAATGGATCCAAAAA
136454	134541	ATCTAGTAATGGATCCAAAA
136455	134542	TATCTAGTAATGGATCCAAA
136456	134543	TTATCTAGTAATGGATCCAA
136457	134544	ATTATCTAGTAATGGATCCA
136458	134545	GATTATCTAGTAATGGATCC
136459	134546	AGATTATCTAGTAATGGATC
136460	134547	AAGATTATCTAGTAATGGAT
136461	134548	AAAGATTATCTAGTAATGGA
136462	134549	GAAAGATTATCTAGTAATGG
136463	134550	TGAAAGATTATCTAGTAATG
136464	134551	CTGAAAGATTATCTAGTAAT
136465	134552	CCTGAAAGATTATCTAGTAA
136466	134553	TCCTGAAAGATTATCTAGTA
136467	134554	ATCCTGAAAGATTATCTAGT
136468	134555	TATCCTGAAAGATTATCTAG
136469	134556	TTATCCTGAAAGATTATCTA
136470	134557	ATTATCCTGAAAGATTATCT
136471	134558	CATTATCCTGAAAGATTATC
136472	134559	TCATTATCCTGAAAGATTAT
136473	134560	GTCATTATCCTGAAAGATTA
136474	134561	TGTCATTATCCTGAAAGATT
136475	134562	ATGTCATTATCCTGAAAGAT
136476	134563	AATGTCATTATCCTGAAAGA
136477	134564	AAATGTCATTATCCTGAAAG
136478	134565	GAAATGTCATTATCCTGAAA
136479	134566	GGAAATGTCATTATCCTGAA
136480	134567	TGGAAATGTCATTATCCTGA
136481	134568	ATGGAAATGTCATTATCCTG
136482	134569	AATGGAAATGTCATTATCCT
136483	134570	TAATGGAAATGTCATTATCC
136484	134571	CTAATGGAAATGTCATTATC
136485	134572	ACTAATGGAAATGTCATTAT

38192	36279	GTTGATTGTTTTAAAGGACA
38193	36280	TGTTGATTGTTTTAAAGGAC
38194	36281	TTGTTGATTGTTTTAAAGGA
38195	36282	TTTGTTGATTGTTTTAAAGG
38196	36283	ATTTGTTGATTGTTTTAAAG
38197	36284	GATTTGTTGATTGTTTTAAA
38198	36285	TGATTTGTTGATTGTTTTAA
38199	36286	TTGATTTGTTGATTGTTTTA
38200	36287	GTTGATTTGTTGATTGTTTT
38201	36288	TGTTGATTTGTTGATTGTTT
38202	36289	ATGTTGATTTGTTGATTGTT
38203	36290	AATGTTGATTTGTTGATTGT
38204	36291	AAATGTTGATTTGTTGATTG
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38206	36293	AAAAATGTTGATTTGTTGAT
38207	36294	GAAAAATGTTGATTTGTTGA
38208	36295	AGAAAAATGTTGATTTGTTG
38209	36296	CAGAAAAATGTTGATTTGTT
38210	36297	CCAGAAAAATGTTGATTTGT
38211	36298	ACCAGAAAAATGTTGATTTG
38212	36299	GACCAGAAAAATGTTGATTT
38213	36300	TGACCAGAAAAATGTTGATT
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38216	36303	TCTTGACCAGAAAAATGTTG
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38219	36306	GGTTCTTGACCAGAAAAATG
38220	36307	TGGTTCTTGACCAGAAAAAT
38221	36308	CTGGTTCTTGACCAGAAAAA
38222	36309	ACTGGTTCTTGACCAGAAAA
38223	36310	TACTGGTTCTTGACCAGAAA
38224	36311	TTACTGGTTCTTGACCAGAA
38225	36312	TTTACTGGTTCTTGACCAGA
38226	36313	ATTTACTGGTTCTTGACCAG
38227	36314	TATTTACTGGTTCTTGACCA
38228	36315	ATATTTACTGGTTCTTGACC
38229	36316	CATATTTACTGGTTCTTGAC
38230	36317	ACATATTTACTGGTTCTTGA
38231	36318	TACATATTTACTGGTTCTTG
38232	36319	ATACATATTTACTGGTTCTT
38233	36320	TATACATATTTACTGGTTCT
38234	36321	ATATACATATTTACTGGTTC
38235	36322	AATATACATATTTACTGGTT
38236	36323	GAATATACATATTTACTGGT
38237	36324	AGAATATACATATTTACTGG
38238	36325	TAGAATATACATATTTACTG
38239	36326	GTAGAATATACATATTTACT
38240	36327	TGTAGAATATACATATTTAC
38241	36328	ATGTAGAATATACATATTTA
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38243	36330	ATATGTAGAATATACATATT
38244	36331	TATATGTAGAATATACATAT
38245	36332	ATATATGTAGAATATACATA
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38254	36341	TGTGTATATATATATGTAGA
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38256	36343	TATGTGTATATATATATGTA
38257	36344	ATATGTGTATATATATATGT
38258	36345	TATATGTGTATATATATATG
38259	36346	ATATATGTGTATATATATAT
38260	36347	TATATATGTGTATATATATA
38261	36348	ATATATATGTGTATATATAT
38262	36349	TATATATATGTGTATATATA

87339	85426	GATGACCAAAATAACTGACA
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87341	85428	TAGATGACCAAAATAACTGA
87342	85429	ATAGATGACCAAAATAACTG
87343	85430	AATAGATGACCAAAATAACT
87344	85431	TAATAGATGACCAAAATAAC
87345	85432	TTAATAGATGACCAAAATAA
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87348	85435	CTATTAATAGATGACCAAAA
87349	85436	TCTATTAATAGATGACCAAA
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87355	85442	TATTAGTCTATTAATAGATG
87356	85443	GTATTAGTCTATTAATAGAT
87357	85444	TGTATTAGTCTATTAATAGA
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87359	85446	CTTGTATTAGTCTATTAATA
87360	85447	ACTTGTATTAGTCTATTAAT
87361	85448	GACTTGTATTAGTCTATTAA
87362	85449	TGACTTGTATTAGTCTATTA
87363	85450	ATGACTTGTATTAGTCTATT
87364	85451	GATGACTTGTATTAGTCTAT
87365	85452	GGATGACTTGTATTAGTCTA
87366	85453	GGGATGACTTGTATTAGTCT
87367	85454	AGGGATGACTTGTATTAGTC
87368	85455	AAGGGATGACTTGTATTAGT
87369	85456	AAAGGGATGACTTGTATTAG
87370	85457	TAAAGGGATGACTTGTATTA
87371	85458	TTAAAGGGATGACTTGTATT
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87385	85472	AGCTGAAAATTCTATTAAAG
87386	85473	GAGCTGAAAATTCTATTAAA
87387	85474	TGAGCTGAAAATTCTATTAA
87388	85475	GTGAGCTGAAAATTCTATTA
87389	85476	TGTGAGCTGAAAATTCTATT
87390	85477	CTGTGAGCTGAAAATTCTAT
87391	85478	GCTGTGAGCTGAAAATTCTA
87392	85479	GGCTGTGAGCTGAAAATTCT
87393	85480	AGGCTGTGAGCTGAAAATTC
87394	85481	CAGGCTGTGAGCTGAAAATT
87395	85482	GCAGGCTGTGAGCTGAAAAT
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87402	85489	AGGCTTAGCAGGCTGTGAGC
87403	85490	TAGGCTTAGCAGGCTGTGAG
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87405	85492	CTTAGGCTTAGCAGGCTGTG
87406	85493	TCTTAGGCTTAGCAGGCTGT
87407	85494	TTCTTAGGCTTAGCAGGCTG
87408	85495	TTTCTTAGGCTTAGCAGGCT
87409	85496	GTTTCTTAGGCTTAGCAGGC

136486	134573	TACTAATGGAAATGTCATTA
136487	134574	TTACTAATGGAAATGTCATT
136488	134575	ATTACTAATGGAAATGTCAT
136489	134576	CATTACTAATGGAAATGTCA
136490	134577	ACATTACTAATGGAAATGTC
136491	134578	AACATTACTAATGGAAATGT
136492	134579	AAACATTACTAATGGAAATG
136493	134580	AAAACATTACTAATGGAAAT
136494	134581	AAAAACATTACTAATGGAAA
136495	134582	CAAAAACATTACTAATGGAA
136496	134583	GCAAAAACATTACTAATGGA
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136499	134586	TTTGCAAAAACATTACTAAT
136500	134587	TTTTGCAAAAACATTACTAA
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136503	134590	CAATTTTGCAAAAACATTAC
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136506	134593	ACACAATTTTGCAAAAACAT
136507	134594	CACACAATTTTGCAAAAACA
136508	134595	ACACACAATTTTGCAAAAAC
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136510	134597	AGACACACAATTTTGCAAAA
136511	134598	TAGACACACAATTTTGCAAA
136512	134599	ATAGACACACAATTTTGCAA
136513	134600	AATAGACACACAATTTTGCA
136514	134601	CAATAGACACACAATTTTGC
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136516	134603	TTCAATAGACACACAATTTT
136517	134604	ATTCAATAGACACACAATTT
136518	134605	AATTCAATAGACACACAATT
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136520	134607	TTAATTCAATAGACACACAA
136521	134608	TTTAATTCAATAGACACACA
136522	134609	GTTTAATTCAATAGACACAC
136523	134610	AGTTTAATTCAATAGACACA
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136525	134612	CAAGTTTAATTCAATAGACA
136526	134613	ACAAGTTTAATTCAATAGAC
136527	134614	TACAAGTTTAATTCAATAGA
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136529	134616	TTTACAAGTTTAATTCAATA
136530	134617	TTTTACAAGTTTAATTCAAT
136531	134618	ATTTTACAAGTTTAATTCAA
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136536	134623	AAACTATTTTACAAGTTTAA
136537	134624	AAAACTATTTTACAAGTTTA
136538	134625	TAAAACTATTTTACAAGTTT
136539	134626	ATAAAACTATTTTACAAGTT
136540	134627	AATAAAACTATTTTACAAGT
136541	134628	AAATAAAACTATTTTACAAG
136542	134629	AAAATAAAACTATTTTACAA
136543	134630	CAAAATAAAACTATTTTACA
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136545	134632	ACCAAAATAAAACTATTTTA
136546	134633	TACCAAAATAAAACTATTTT
136547	134634	GTACCAAAATAAAACTATTT
136548	134635	TGTACCAAAATAAAACTATT
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136550	134637	CATGTACCAAAATAAAACTA
136551	134638	TCATGTACCAAAATAAAACT
136552	134639	ATCATGTACCAAAATAAAAC
136553	134640	AATCATGTACCAAAATAAAA
136554	134641	AAATCATGTACCAAAATAAA
136555	134642	TAAATCATGTACCAAAATAA
136556	134643	ATAAATCATGTACCAAAATA

38263	36350	GTATATATATGTGTATATAT
38264	36351	TGTATATATATGTGTATATA
38265	36352	GTGTATATATATGTGTATAT
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38277	36364	TAGAATATATGTGTGTATAT
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38286	36373	ATATATATGTAGAATATATG
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38288	36375	ACATATATATGTAGAATATA
38289	36376	CACATATATATGTAGAATAT
38290	36377	CCACATATATATGTAGAATA
38291	36378	TCCACATATATATGTAGAAT
38292	36379	TTCCACATATATATGTAGAA
38293	36380	ATTCCACATATATATGTAGA
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38295	36382	ATATTCCACATATATATGTA
38296	36383	TATATTCCACATATATATGT
38297	36384	GTATATTCCACATATATATG
38298	36385	CGTATATTCCACATATATAT
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38300	36387	TACGTATATTCCACATATAT
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38302	36389	AATACGTATATTCCACATAT
38303	36390	AAATACGTATATTCCACATA
38304	36391	TAAATACGTATATTCCACAT
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38306	36393	AGTAAATACGTATATTCCAC
38307	36394	GAGTAAATACGTATATTCCA
38308	36395	GGAGTAAATACGTATATTCC
38309	36396	GGGAGTAAATACGTATATTC
38310	36397	AGGGAGTAAATACGTATATT
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38312	36399	AGAGGGAGTAAATACGTATA
38313	36400	CAGAGGGAGTAAATACGTAT
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38315	36402	GACAGAGGGAGTAAATACGT
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38317	36404	TGGACAGAGGGAGTAAATAC
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38319	36406	CTTGGACAGAGGGAGTAAAT
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38322	36409	GTTCTTGGACAGAGGGAGTA
38323	36410	GGTTCTTGGACAGAGGGAGT
38324	36411	TGGTTCTTGGACAGAGGGAG
38325	36412	TTGGTTCTTGGACAGAGGGA
38326	36413	ATTGGTTCTTGGACAGAGGG
38327	36414	GATTGGTTCTTGGACAGAGG
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38329	36416	TGGATTGGTTCTTGGACAGA
38330	36417	CTGGATTGGTTCTTGGACAG
38331	36418	CCTGGATTGGTTCTTGGACA
38332	36419	TCCTGGATTGGTTCTTGGAC
38333	36420	ATCCTGGATTGGTTCTTGGA

87410	85497	AGTTTCTTAGGCTTAGCAGG
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87412	85499	GCAGTTTCTTAGGCTTAGCA
87413	85500	AGCAGTTTCTTAGGCTTAGC
87414	85501	AAGCAGTTTCTTAGGCTTAG
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87416	85503	GTAAGCAGTTTCTTAGGCTT
87417	85504	TGTAAGCAGTTTCTTAGGCT
87418	85505	CTGTAAGCAGTTTCTTAGGC
87419	85506	CCTGTAAGCAGTTTCTTAGG
87420	85507	ACCTGTAAGCAGTTTCTTAG
87421	85508	AACCTGTAAGCAGTTTCTTA
87422	85509	TAACCTGTAAGCAGTTTCTT
87423	85510	GTAACCTGTAAGCAGTTTCT
87424	85511	AGTAACCTGTAAGCAGTTTC
87425	85512	CAGTAACCTGTAAGCAGTTT
87426	85513	GCAGTAACCTGTAAGCAGTT
87427	85514	AGCAGTAACCTGTAAGCAGT
87428	85515	AAGCAGTAACCTGTAAGCAG
87429	85516	TAAGCAGTAACCTGTAAGCA
87430	85517	GTAAGCAGTAACCTGTAAGC
87431	85518	AGTAAGCAGTAACCTGTAAG
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87435	85522	AAACAGTAAGCAGTAACCTG
87436	85523	AAAACAGTAAGCAGTAACCT
87437	85524	TAAAACAGTAAGCAGTAACC
87438	85525	TTAAAACAGTAAGCAGTAAC
87439	85526	CTTAAAACAGTAAGCAGTAA
87440	85527	GCTTAAAACAGTAAGCAGTA
87441	85528	GGCTTAAAACAGTAAGCAGT
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87443	85530	TCGGCTTAAAACAGTAAGCA
87444	85531	CTCGGCTTAAAACAGTAAGC
87445	85532	ACTCGGCTTAAAACAGTAAG
87446	85533	AACTCGGCTTAAAACAGTAA
87447	85534	AAACTCGGCTTAAAACAGTA
87448	85535	AAAACTCGGCTTAAAACAGT
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87450	85537	TTAAAACTCGGCTTAAAACA
87451	85538	TTTAAAACTCGGCTTAAAAC
87452	85539	TTTTAAAACTCGGCTTAAAA
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87454	85541	AATTTTAAAACTCGGCTTAA
87455	85542	CAATTTTAAAACTCGGCTTA
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87463	85550	ATGATCATCAATTTTAAAAC
87464	85551	CATGATCATCAATTTTAAAA
87465	85552	TCATGATCATCAATTTTAAA
87466	85553	ATCATGATCATCAATTTTAA
87467	85554	TATCATGATCATCAATTTTA
87468	85555	CTATCATGATCATCAATTTT
87469	85556	TCTATCATGATCATCAATTT
87470	85557	TTCTATCATGATCATCAATT
87471	85558	CTTCTATCATGATCATCAAT
87472	85559	TCTTCTATCATGATCATCAA
87473	85560	CTCTTCTATCATGATCATCA
87474	85561	TCTCTTCTATCATGATCATC
87475	85562	ATCTCTTCTATCATGATCAT
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87477	85564	TTATCTCTTCTATCATGATC
87478	85565	TTTATCTCTTCTATCATGAT
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87480	85567	TATTTATCTCTTCTATCATG

136557	134644	TATAAATCATGTACCAAAAT
136558	134645	ATATAAATCATGTACCAAAA
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136560	134647	TGATATAAATCATGTACCAA
136561	134648	TTGATATAAATCATGTACCA
136562	134649	CTTGATATAAATCATGTACC
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136565	134652	AACCTTGATATAAATCATGT
136566	134653	CAACCTTGATATAAATCATG
136567	134654	ACAACCTTGATATAAATCAT
136568	134655	AACAACCTTGATATAAATCA
136569	134656	GAACAACCTTGATATAAATC
136570	134657	TGAACAACCTTGATATAAAT
136571	134658	CTGAACAACCTTGATATAAA
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136577	134664	ATTCTACTGAACAACCTTGA
136578	134665	CATTCTACTGAACAACCTTG
136579	134666	GCATTCTACTGAACAACCTT
136580	134667	GGCATTCTACTGAACAACCT
136581	134668	TGGCATTCTACTGAACAACC
136582	134669	ATGGCATTCTACTGAACAAC
136583	134670	CATGGCATTCTACTGAACAA
136584	134671	ACATGGCATTCTACTGAACA
136585	134672	AACATGGCATTCTACTGAAC
136586	134673	CAACATGGCATTCTACTGAA
136587	134674	CCAACATGGCATTCTACTGA
136588	134675	ACCAACATGGCATTCTACTG
136589	134676	CACCAACATGGCATTCTACT
136590	134677	ACACCAACATGGCATTCTAC
136591	134678	AACACCAACATGGCATTCTA
136592	134679	AAACACCAACATGGCATTCT
136593	134680	AAAACACCAACATGGCATTC
136594	134681	AAAAACACCAACATGGCATT
136595	134682	TAAAAACACCAACATGGCAT
136596	134683	ATAAAAACACCAACATGGCA
136597	134684	AATAAAAACACCAACATGGC
136598	134685	TAATAAAAACACCAACATGG
136599	134686	CTAATAAAAACACCAACATG
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136603	134690	TTATCTAATAAAAACACCAA
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136607	134694	ATCATTATCTAATAAAAACA
136608	134695	AATCATTATCTAATAAAAAC
136609	134696	AAATCATTATCTAATAAAAA
136610	134697	AAAATCATTATCTAATAAAA
136611	134698	TAAAATCATTATCTAATAAA
136612	134699	ATAAAATCATTATCTAATAA
136613	134700	AATAAAATCATTATCTAATA
136614	134701	GAATAAAATCATTATCTAAT
136615	134702	GGAATAAAATCATTATCTAA
136616	134703	AGGAATAAAATCATTATCTA
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136618	134705	AAAGGAATAAAATCATTATC
136619	134706	AAAAGGAATAAAATCATTAT
136620	134707	TAAAAGGAATAAAATCATTA
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136623	134710	AAGTAAAAGGAATAAAATCA
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136625	134712	AAAAGTAAAAGGAATAAAAT
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38334	36421	AATCCTGGATTGGTTCTTGG
38335	36422	CAATCCTGGATTGGTTCTTG
38336	36423	ACAATCCTGGATTGGTTCTT
38337	36424	AACAATCCTGGATTGGTTCT
38338	36425	TAACAATCCTGGATTGGTTC
38339	36426	GTAACAATCCTGGATTGGTT
38340	36427	GGTAACAATCCTGGATTGGT
38341	36428	AGGTAACAATCCTGGATTGG
38342	36429	AAGGTAACAATCCTGGATTG
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38350	36437	GATAACCGAAGGTAACAATC
38351	36438	TGATAACCGAAGGTAACAAT
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38384	36471	AACTGCTTTGGATTAAAGGA
38385	36472	AAACTGCTTTGGATTAAAGG
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38388	36475	AAGAAACTGCTTTGGATTAA
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38390	36477	CAAAGAAACTGCTTTGGATT
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38527	36614	CACACAAATCATTTCTGTTG
38528	36615	ACACACAAATCATTTCTGTT
38529	36616	AACACACAAATCATTTCTGT
38530	36617	AAACACACAAATCATTTCTG
38531	36618	AAAACACACAAATCATTTCT
38532	36619	AAAAACACACAAATCATTTC
38533	36620	GAAAAACACACAAATCATTT
38534	36621	AGAAAAACACACAAATCATT
38535	36622	GAGAAAAACACACAAATCAT
38536	36623	TGAGAAAAACACACAAATCA
38537	36624	ATGAGAAAAACACACAAATC
38538	36625	AATGAGAAAAACACACAAAT
38539	36626	CAATGAGAAAAACACACAAA
38540	36627	GCAATGAGAAAAACACACAA
38541	36628	TGCAATGAGAAAAACACACA
38542	36629	ATGCAATGAGAAAAACACAC
38543	36630	CATGCAATGAGAAAAACACA
38544	36631	TCATGCAATGAGAAAAACAC
38545	36632	ATCATGCAATGAGAAAAACA
38546	36633	TATCATGCAATGAGAAAAAC

87623	85710	TACCTTTCCCTGACCCGAAT
87624	85711	TTACCTTTCCCTGACCCGAA
87625	85712	TTTACCTTTCCCTGACCCGA
87626	85713	TTTTACCTTTCCCTGACCCG
87627	85714	ATTTTACCTTTCCCTGACCC
87628	85715	TATTTTACCTTTCCCTGACC
87629	85716	ATATTTTACCTTTCCCTGAC
87630	85717	TATATTTTACCTTTCCCTGA
87631	85718	ATATATTTTACCTTTCCCTG
87632	85719	CATATATTTTACCTTTCCCT
87633	85720	CCATATATTTTACCTTTCCC
87634	85721	TCCATATATTTTACCTTTCC
87635	85722	TTCCATATATTTTACCTTTC
87636	85723	TTTCCATATATTTTACCTTT
87637	85724	CTTTCCATATATTTTACCTT
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87640	85727	TAACTTTCCATATATTTTAC
87641	85728	TTAACTTTCCATATATTTTA
87642	85729	TTTAACTTTCCATATATTTT
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87644	85731	TTTTTAACTTTCCATATATT
87645	85732	ATTTTTAACTTTCCATATAT
87646	85733	TATTTTTAACTTTCCATATA
87647	85734	ATATTTTTAACTTTCCATAT
87648	85735	AATATTTTTAACTTTCCATA
87649	85736	AAATATTTTTAACTTTCCAT
87650	85737	AAAATATTTTTAACTTTCCA
87651	85738	TAAAATATTTTTAACTTTCC
87652	85739	ATAAAATATTTTTAACTTTC
87653	85740	GATAAAATATTTTTAACTTT
87654	85741	TGATAAAATATTTTTAACTT
87655	85742	ATGATAAAATATTTTTAACT
87656	85743	CATGATAAAATATTTTTAAC
87657	85744	ACATGATAAAATATTTTTAA
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87666	85753	ATTATGACTACATGATAAAA
87667	85754	AATTATGACTACATGATAAA
87668	85755	AAATTATGACTACATGATAA
87669	85756	GAAATTATGACTACATGATA
87670	85757	AGAAATTATGACTACATGAT
87671	85758	TAGAAATTATGACTACATGA
87672	85759	CTAGAAATTATGACTACATG
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87674	85761	TACTAGAAATTATGACTACA
87675	85762	TTACTAGAAATTATGACTAC
87676	85763	GTTACTAGAAATTATGACTA
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87678	85765	ATGTTACTAGAAATTATGAC
87679	85766	TATGTTACTAGAAATTATGA
87680	85767	ATATGTTACTAGAAATTATG
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87683	85770	GAAATATGTTACTAGAAATT
87684	85771	AGAAATATGTTACTAGAAAT
87685	85772	AAGAAATATGTTACTAGAAA
87686	85773	AAAGAAATATGTTACTAGAA
87687	85774	TAAAGAAATATGTTACTAGA
87688	85775	GTAAAGAAATATGTTACTAG
87689	85776	TGTAAAGAAATATGTTACTA
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87691	85778	TTTGTAAAGAAATATGTTAC
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136770	134857	ATTTCTTTTTGTATTCATGC
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136772	134859	TAATTTCTTTTTGTATTCAT
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136775	134862	TAGTAATTTCTTTTTGTATT
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136784	134871	TTGACATATTAGTAATTTCT
136785	134872	GTTGACATATTAGTAATTTC
136786	134873	GGTTGACATATTAGTAATTT
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136790	134877	GAAAGGTTGACATATTAGTA
136791	134878	GGAAAGGTTGACATATTAGT
136792	134879	TGGAAAGGTTGACATATTAG
136793	134880	CTGGAAAGGTTGACATATTA
136794	134881	TCTGGAAAGGTTGACATATT
136795	134882	TTCTGGAAAGGTTGACATAT
136796	134883	TTTCTGGAAAGGTTGACATA
136797	134884	TTTTCTGGAAAGGTTGACAT
136798	134885	ATTTTCTGGAAAGGTTGACA
136799	134886	AATTTTCTGGAAAGGTTGAC
136800	134887	AAATTTTCTGGAAAGGTTGA
136801	134888	CAAATTTTCTGGAAAGGTTG
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136808	134895	CATTTTCCAAATTTTCTGGA
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136811	134898	GTGCATTTTCCAAATTTTCT
136812	134899	TGTGCATTTTCCAAATTTTC
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136815	134902	AGGTGTGCATTTTCCAAATT
136816	134903	GAGGTGTGCATTTTCCAAAT
136817	134904	TGAGGTGTGCATTTTCCAAA
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136819	134906	TTTGAGGTGTGCATTTTCCA
136820	134907	TTTTGAGGTGTGCATTTTCC
136821	134908	CTTTTGAGGTGTGCATTTTC
136822	134909	CCTTTTGAGGTGTGCATTTT
136823	134910	GCCTTTTGAGGTGTGCATTT
136824	134911	AGCCTTTTGAGGTGTGCATT
136825	134912	TAGCCTTTTGAGGTGTGCAT
136826	134913	TTAGCCTTTTGAGGTGTGCA
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136829	134916	AAATTAGCCTTTTGAGGTGT
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136836	134923	GAAAGGTAAATTAGCCTTTT
136837	134924	AGAAAGGTAAATTAGCCTTT
136838	134925	TAGAAAGGTAAATTAGCCTT
136839	134926	ATAGAAAGGTAAATTAGCCT
136840	134927	AATAGAAAGGTAAATTAGCC

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38548	36635	GATATCATGCAATGAGAAAA
38549	36636	TGATATCATGCAATGAGAAA
38550	36637	CTGATATCATGCAATGAGAA
38551	36638	TCTGATATCATGCAATGAGA
38552	36639	TTCTGATATCATGCAATGAG
38553	36640	TTTCTGATATCATGCAATGA
38554	36641	CTTTCTGATATCATGCAATG
38555	36642	ACTTTCTGATATCATGCAAT
38556	36643	CACTTTCTGATATCATGCAA
38557	36644	GCACTTTCTGATATCATGCA
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38569	36656	AATATATACAATGCACTTTC
38570	36657	AAATATATACAATGCACTTT
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38573	36660	GATAAATATATACAATGCAC
38574	36661	GGATAAATATATACAATGCA
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38597	36684	CAAAGTTAACAACCCCAGTA
38598	36685	TCAAAGTTAACAACCCCAGT
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38607	36694	ACCAAGTGATCAAAGTTAAC
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38612	36699	CTCTAACCAAGTGATCAAAG
38613	36700	ACTCTAACCAAGTGATCAAA
38614	36701	AACTCTAACCAAGTGATCAA
38615	36702	CAACTCTAACCAAGTGATCA
38616	36703	ACAACTCTAACCAAGTGATC
38617	36704	CACAACTCTAACCAAGTGAT

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87696	85783	TCTTATTTGTAAAGAAATAT
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87704	85791	CAACTATGTCTTATTTGTAA
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87710	85797	CTGTTTCAACTATGTCTTAT
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87717	85804	TAGCAATCTGTTTCAACTAT
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87719	85806	TGTAGCAATCTGTTTCAACT
87720	85807	CTGTAGCAATCTGTTTCAAC
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87722	85809	AACTGTAGCAATCTGTTTCA
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87738	85825	TGTCAACTCTTAAAAGAACT
87739	85826	ATGTCAACTCTTAAAAGAAC
87740	85827	GATGTCAACTCTTAAAAGAA
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87743	85830	TAAGATGTCAACTCTTAAAA
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87745	85832	AATAAGATGTCAACTCTTAA
87746	85833	CAATAAGATGTCAACTCTTA
87747	85834	ACAATAAGATGTCAACTCTT
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87761	85848	GTGGTAAGAAATCAACAATA
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136841	134928	AAATAGAAAGGTAAATTAGC
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136862	134949	TTGGGACATGCTGAATTTGG
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136871	134958	TATGGTAATTTGGGACATGC
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136892	134979	GAAGGGCTTGTCTCCTTGTT
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136901	134988	AAGTAGAAAGAAGGGCTTGT
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38621	36708	TAGACACAACTCTAACCAAG
38622	36709	GTAGACACAACTCTAACCAA
38623	36710	AGTAGACACAACTCTAACCA
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38627	36714	ACTTAGTAGACACAACTCTA
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38687	36774	GTAACTCCCCACAAGATACT
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87765	85852	GTTGGTGGTAAGAAATCAAC
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87768	85855	GAAGTTGGTGGTAAGAAATC
87769	85856	TGAAGTTGGTGGTAAGAAAT
87770	85857	ATGAAGTTGGTGGTAAGAAA
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87773	85860	GGGATGAAGTTGGTGGTAAG
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87779	85866	AAGGGAGGGATGAAGTTGGT
87780	85867	AAAGGGAGGGATGAAGTTGG
87781	85868	GAAAGGGAGGGATGAAGTTG
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87783	85870	AAGAAAGGGAGGGATGAAGT
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87787	85874	TTTAAAGAAAGGGAGGGATG
87788	85875	TTTTAAAGAAAGGGAGGGAT
87789	85876	TTTTTAAAGAAAGGGAGGGA
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87793	85880	TTTATTTTTAAAGAAAGGGA
87794	85881	CTTTATTTTTAAAGAAAGGG
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87796	85883	CCCTTTATTTTTAAAGAAAG
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136916	135003	CCCAACTCACTGGCAAAGTA
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136918	135005	AACCCAACTCACTGGCAAAG
136919	135006	AAACCCAACTCACTGGCAAA
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87837	85924	TGTGGAATGCCACAAAGTTT
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87922	86009	CTACAGTTTTTCCTTGGTTA
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87952	86039	CACACACACATGCACACACA
87953	86040	TCACACACACATGCACACAC
87954	86041	TTCACACACACATGCACACA
87955	86042	ATTCACACACACATGCACAC
87956	86043	CATTCACACACACATGCACA
87957	86044	CCATTCACACACACATGCAC
87958	86045	CCCATTCACACACACATGCA
87959	86046	ACCCATTCACACACACATGC
87960	86047	CACCCATTCACACACACATG
87961	86048	ACACCCATTCACACACACAT
87962	86049	TACACCCATTCACACACACA
87963	86050	ATACACCCATTCACACACAC
87964	86051	AATACACCCATTCACACACA
87965	86052	AAATACACCCATTCACACAC
87966	86053	TAAATACACCCATTCACACA
87967	86054	CTAAATACACCCATTCACAC
87968	86055	GCTAAATACACCCATTCACA
87969	86056	TGCTAAATACACCCATTCAC
87970	86057	CTGCTAAATACACCCATTCA
87971	86058	TCTGCTAAATACACCCATTC
87972	86059	TTCTGCTAAATACACCCATT
87973	86060	TTTCTGCTAAATACACCCAT
87974	86061	TTTTCTGCTAAATACACCCA
87975	86062	CTTTTCTGCTAAATACACCC
87976	86063	ACTTTTCTGCTAAATACACC
87977	86064	TACTTTTCTGCTAAATACAC

137054	135141	AAAACTGAATTATTTATATA
137055	135142	AAAAACTGAATTATTTATAT
137056	135143	TAAAAACTGAATTATTTATA
137057	135144	TTAAAAACTGAATTATTTAT
137058	135145	TTTAAAAACTGAATTATTTA
137059	135146	TTTTAAAAACTGAATTATTT
137060	135147	ATTTTAAAAACTGAATTATT
137061	135148	CATTTTAAAAACTGAATTAT
137062	135149	CCATTTTAAAAACTGAATTA
137063	135150	TCCATTTTAAAAACTGAATT
137064	135151	TTCCATTTTAAAAACTGAAT
137065	135152	TTTCCATTTTAAAAACTGAA
137066	135153	ATTTCCATTTTAAAAACTGA
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137068	135155	GTATTTCCATTTTAAAAACT
137069	135156	GGTATTTCCATTTTAAAAAC
137070	135157	GGGTATTTCCATTTTAAAAA
137071	135158	TGGGTATTTCCATTTTAAAA
137072	135159	TTGGGTATTTCCATTTTAAA
137073	135160	ATTGGGTATTTCCATTTTAA
137074	135161	AATTGGGTATTTCCATTTTA
137075	135162	AAATTGGGTATTTCCATTTT
137076	135163	TAAATTGGGTATTTCCATTT
137077	135164	TTAAATTGGGTATTTCCATT
137078	135165	CTTAAATTGGGTATTTCCAT
137079	135166	TCTTAAATTGGGTATTTCCA
137080	135167	TTCTTAAATTGGGTATTTCC
137081	135168	CTTCTTAAATTGGGTATTTC
137082	135169	CCTTCTTAAATTGGGTATTT
137083	135170	GCCTTCTTAAATTGGGTATT
137084	135171	AGCCTTCTTAAATTGGGTAT
137085	135172	CAGCCTTCTTAAATTGGGTA
137086	135173	CCAGCCTTCTTAAATTGGGT
137087	135174	TCCAGCCTTCTTAAATTGGG
137088	135175	CTCCAGCCTTCTTAAATTGG
137089	135176	ACTCCAGCCTTCTTAAATTG
137090	135177	AACTCCAGCCTTCTTAAATT
137091	135178	TAACTCCAGCCTTCTTAAAT
137092	135179	TTAACTCCAGCCTTCTTAAA
137093	135180	ATTAACTCCAGCCTTCTTAA
137094	135181	CATTAACTCCAGCCTTCTTA
137095	135182	TCATTAACTCCAGCCTTCTT
137096	135183	TTCATTAACTCCAGCCTTCT
137097	135184	TTTCATTAACTCCAGCCTTC
137098	135185	TTTTCATTAACTCCAGCCTT
137099	135186	TTTTTCATTAACTCCAGCCT
137100	135187	ATTTTTCATTAACTCCAGCC
137101	135188	CATTTTTCATTAACTCCAGC
137102	135189	CCATTTTTCATTAACTCCAG
137103	135190	TCCATTTTTCATTAACTCCA
137104	135191	CTCCATTTTTCATTAACTCC
137105	135192	ACTCCATTTTTCATTAACTC
137106	135193	AACTCCATTTTTCATTAACT
137107	135194	CAACTCCATTTTTCATTAAC
137108	135195	ACAACTCCATTTTTCATTAA
137109	135196	AACAACTCCATTTTTCATTA
137110	135197	AAACAACTCCATTTTTCATT
137111	135198	GAAACAACTCCATTTTTCAT
137112	135199	TGAAACAACTCCATTTTTCA
137113	135200	CTGAAACAACTCCATTTTTC
137114	135201	TCTGAAACAACTCCATTTTT
137115	135202	TTCTGAAACAACTCCATTTT
137116	135203	TTTCTGAAACAACTCCATTT
137117	135204	ATTTCTGAAACAACTCCATT
137118	135205	GATTTCTGAAACAACTCCAT
137119	135206	TGATTTCTGAAACAACTCCA
137120	135207	TTGATTTCTGAAACAACTCC
137121	135208	ATTGATTTCTGAAACAACTC
137122	135209	AATTGATTTCTGAAACAACT
137123	135210	AAATTGATTTCTGAAACAAC
137124	135211	AAAATTGATTTCTGAAACAA

38831	36918	AAAAAAAAATGTAGACAGAA
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38833	36920	AAAAAAAAAATGTAGACAG
38834	36921	AAAAAAAAAAATGTAGACA
38835	36922	AAAAAAAAAAAATGTAGAC
38836	36923	AAAAAAAAAAAAATGTAGA
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38838	36925	AAAAAAAAAAAAAAATGTA
38839	36926	AAAAAAAAAAAAAAAATGT
38840	36927	AAAAAAAAAAAAAAAAATG
38841	36928	AAAAAAAAAAAAAAAAAAT
38842	36929	AAAAAAAAAAAAAAAAAAA
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38845	36932	AAAAAAAAAAAAAAAAAAA
38846	36933	AAAAAAAAAAAAAAAAAAA
38847	36934	AAAAAAAAAAAAAAAAAAA
38848	36935	CAAAAAAAAAAAAAAAAAA
38849	36936	TCAAAAAAAAAAAAAAAAA
38850	36937	CTCAAAAAAAAAAAAAAAA
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38852	36939	ATCTCAAAAAAAAAAAAAA
38853	36940	CATCTCAAAAAAAAAAAAA
38854	36941	CCATCTCAAAAAAAAAAAA
38855	36942	TCCATCTCAAAAAAAAAAA
38856	36943	CTCCATCTCAAAAAAAAAA
38857	36944	ACTCCATCTCAAAAAAAAA
38858	36945	AACTCCATCTCAAAAAAAA
38859	36946	AAACTCCATCTCAAAAAAA
38860	36947	GAAACTCCATCTCAAAAAA
38861	36948	CGAAACTCCATCTCAAAAA
38862	36949	GCGAAACTCCATCTCAAAA
38863	36950	AGCGAAACTCCATCTCAAA
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38865	36952	AGAGCGAAACTCCATCTCA
38866	36953	AAGAGCGAAACTCCATCTCA
38867	36954	TAAGAGCGAAACTCCATCTC
38868	36955	ATAAGAGCGAAACTCCATCT
38869	36956	AATAAGAGCGAAACTCCATC
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38871	36958	GCAATAAGAGCGAAACTCCA
38872	36959	GGCAATAAGAGCGAAACTCC
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38874	36961	TGGGCAATAAGAGCGAAACT
38875	36962	CTGGGCAATAAGAGCGAAAC
38876	36963	CCTGGGCAATAAGAGCGAAA
38877	36964	GCCTGGGCAATAAGAGCGAA
38878	36965	AGCCTGGGCAATAAGAGCGA
38879	36966	CAGCCTGGGCAATAAGAGCG
38880	36967	CCAGCCTGGGCAATAAGAGC
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38883	36970	ACTCCAGCCTGGGCAATAAG
38884	36971	CACTCCAGCCTGGGCAATAA
38885	36972	GCACTCCAGCCTGGGCAATA
38886	36973	CGCACTCCAGCCTGGGCAAT
38887	36974	CCGCACTCCAGCCTGGGCAA
38888	36975	ACCGCACTCCAGCCTGGGCA
38889	36976	CACCGCACTCCAGCCTGGGC
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38893	36980	AGGCCACCGCACTCCAGCCT
38894	36981	CAGGCCACCGCACTCCAGCC
38895	36982	TCAGGCCACCGCACTCCAGC
38896	36983	ATCAGGCCACCGCACTCCAG
38897	36984	GATCAGGCCACCGCACTCCA
38898	36985	AGATCAGGCCACCGCACTCC
38899	36986	AAGATCAGGCCACCGCACTC
38900	36987	CAAGATCAGGCCACCGCACT
38901	36988	CCAAGATCAGGCCACCGCAC

87978	86065	CTACTTTTCTGCTAAATACA
87979	86066	ACTACTTTTCTGCTAAATAC
87980	86067	TACTACTTTTCTGCTAAATA
87981	86068	GTACTACTTTTCTGCTAAAT
87982	86069	AGTACTACTTTTCTGCTAAA
87983	86070	CAGTACTACTTTTCTGCTAA
87984	86071	TCAGTACTACTTTTCTGCTA
87985	86072	ATCAGTACTACTTTTCTGCT
87986	86073	CATCAGTACTACTTTTCTGC
87987	86074	TCATCAGTACTACTTTTCTG
87988	86075	TTCATCAGTACTACTTTTCT
87989	86076	ATTCATCAGTACTACTTTTC
87990	86077	TATTCATCAGTACTACTTTT
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87993	86080	TGATATTCATCAGTACTACT
87994	86081	ATGATATTCATCAGTACTAC
87995	86082	CATGATATTCATCAGTACTA
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87997	86084	TCCATGATATTCATCAGTAC
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87999	86086	ATTCCATGATATTCATCAGT
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88008	86095	ATCACATAAATTCCATGATA
88009	86096	CATCACATAAATTCCATGAT
88010	86097	ACATCACATAAATTCCATGA
88011	86098	AACATCACATAAATTCCATG
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88013	86100	TGAACATCACATAAATTCCA
88014	86101	GTGAACATCACATAAATTCC
88015	86102	AGTGAACATCACATAAATTC
88016	86103	CAGTGAACATCACATAAATT
88017	86104	ACAGTGAACATCACATAAAT
88018	86105	AACAGTGAACATCACATAAA
88019	86106	AAACAGTGAACATCACATAA
88020	86107	GAAACAGTGAACATCACATA
88021	86108	AGAAACAGTGAACATCACAT
88022	86109	AAGAAACAGTGAACATCACA
88023	86110	GAAGAAACAGTGAACATCAC
88024	86111	GGAAGAAACAGTGAACATCA
88025	86112	AGGAAGAAACAGTGAACATC
88026	86113	AAGGAAGAAACAGTGAACAT
88027	86114	TAAGGAAGAAACAGTGAACA
88028	86115	CTAAGGAAGAAACAGTGAAC
88029	86116	CCTAAGGAAGAAACAGTGAA
88030	86117	CCCTAAGGAAGAAACAGTGA
88031	86118	GCCCTAAGGAAGAAACAGTG
88032	86119	GGCCCTAAGGAAGAAACAGT
88033	86120	AGGCCCTAAGGAAGAAACAG
88034	86121	GAGGCCCTAAGGAAGAAACA
88035	86122	GGAGGCCCTAAGGAAGAAAC
88036	86123	TGGAGGCCCTAAGGAAGAAA
88037	86124	TTGGAGGCCCTAAGGAAGAA
88038	86125	CTTGGAGGCCCTAAGGAAGA
88039	86126	CCTTGGAGGCCCTAAGGAAG
88040	86127	TCCTTGGAGGCCCTAAGGAA
88041	86128	ATCCTTGGAGGCCCTAAGGA
88042	86129	CATCCTTGGAGGCCCTAAGG
88043	86130	ACATCCTTGGAGGCCCTAAG
88044	86131	GACATCCTTGGAGGCCCTAA
88045	86132	GGACATCCTTGGAGGCCCTA
88046	86133	GGGACATCCTTGGAGGCCCT
88047	86134	GGGGACATCCTTGGAGGCCC
88048	86135	TGGGGACATCCTTGGAGGCC

137125	135212	AAAAATTGATTTCTGAAACA
137126	135213	CAAAAATTGATTTCTGAAAC
137127	135214	GCAAAAATTGATTTCTGAAA
137128	135215	TGCAAAAATTGATTTCTGAA
137129	135216	ATGCAAAAATTGATTTCTGA
137130	135217	TATGCAAAAATTGATTTCTG
137131	135218	GTATGCAAAAATTGATTTCT
137132	135219	GGTATGCAAAAATTGATTTC
137133	135220	TGGTATGCAAAAATTGATTT
137134	135221	TTGGTATGCAAAAATTGATT
137135	135222	CTTGGTATGCAAAAATTGAT
137136	135223	GCTTGGTATGCAAAAATTGA
137137	135224	TGCTTGGTATGCAAAAATTG
137138	135225	TTGCTTGGTATGCAAAAATT
137139	135226	TTTGCTTGGTATGCAAAAAT
137140	135227	ATTTGCTTGGTATGCAAAAA
137141	135228	CATTTGCTTGGTATGCAAAA
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137143	135230	CACATTTGCTTGGTATGCAA
137144	135231	TCACATTTGCTTGGTATGCA
137145	135232	GTCACATTTGCTTGGTATGC
137146	135233	AGTCACATTTGCTTGGTATG
137147	135234	CAGTCACATTTGCTTGGTAT
137148	135235	CCAGTCACATTTGCTTGGTA
137149	135236	CCCAGTCACATTTGCTTGGT
137150	135237	TCCCAGTCACATTTGCTTGG
137151	135238	TTCCCAGTCACATTTGCTTG
137152	135239	TTTCCCAGTCACATTTGCTT
137153	135240	ATTTCCCAGTCACATTTGCT
137154	135241	CATTTCCCAGTCACATTTGC
137155	135242	GCATTTCCCAGTCACATTTG
137156	135243	GGCATTTCCCAGTCACATTT
137157	135244	AGGCATTTCCCAGTCACATT
137158	135245	TAGGCATTTCCCAGTCACAT
137159	135246	TTAGGCATTTCCCAGTCACA
137160	135247	ATTAGGCATTTCCCAGTCAC
137161	135248	TATTAGGCATTTCCCAGTCA
137162	135249	ATATTAGGCATTTCCCAGTC
137163	135250	AATATTAGGCATTTCCCAGT
137164	135251	AAATATTAGGCATTTCCCAG
137165	135252	AAAATATTAGGCATTTCCCA
137166	135253	GAAAATATTAGGCATTTCCC
137167	135254	GGAAAATATTAGGCATTTCC
137168	135255	AGGAAAATATTAGGCATTTC
137169	135256	AAGGAAAATATTAGGCATTT
137170	135257	CAAGGAAAATATTAGGCATT
137171	135258	ACAAGGAAAATATTAGGCAT
137172	135259	AACAAGGAAAATATTAGGCA
137173	135260	TAACAAGGAAAATATTAGGC
137174	135261	CTAACAAGGAAAATATTAGG
137175	135262	TCTAACAAGGAAAATATTAG
137176	135263	CTCTAACAAGGAAAATATTA
137177	135264	TCTCTAACAAGGAAAATATT
137178	135265	TTCTCTAACAAGGAAAATAT
137179	135266	TTTCTCTAACAAGGAAAATA
137180	135267	GTTTCTCTAACAAGGAAAAT
137181	135268	AGTTTCTCTAACAAGGAAAA
137182	135269	AAGTTTCTCTAACAAGGAAA
137183	135270	GAAGTTTCTCTAACAAGGAA
137184	135271	GGAAGTTTCTCTAACAAGGA
137185	135272	AGGAAGTTTCTCTAACAAGG
137186	135273	TAGGAAGTTTCTCTAACAAG
137187	135274	TTAGGAAGTTTCTCTAACAA
137188	135275	TTTAGGAAGTTTCTCTAACA
137189	135276	GTTTAGGAAGTTTCTCTAAC
137190	135277	TGTTTAGGAAGTTTCTCTAA
137191	135278	CTGTTTAGGAAGTTTCTCTA
137192	135279	GCTGTTTAGGAAGTTTCTCT
137193	135280	AGCTGTTTAGGAAGTTTCTC
137194	135281	AAGCTGTTTAGGAAGTTTCT
137195	135282	AAAGCTGTTTAGGAAGTTTC

38902	36989	GCCAAGATCAGGCCACCGCA
38903	36990	AGCCAAGATCAGGCCACCGC
38904	36991	GAGCCAAGATCAGGCCACCG
38905	36992	TGAGCCAAGATCAGGCCACC
38906	36993	GTGAGCCAAGATCAGGCCAC
38907	36994	AGTGAGCCAAGATCAGGCCA
38908	36995	CAGTGAGCCAAGATCAGGCC
38909	36996	GCAGTGAGCCAAGATCAGGC
38910	36997	TGCAGTGAGCCAAGATCAGG
38911	36998	TTGCAGTGAGCCAAGATCAG
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38916	37003	AGAGGTTGCAGTGAGCCAAG
38917	37004	CAGAGGTTGCAGTGAGCCAA
38918	37005	GCAGAGGTTGCAGTGAGCCA
38919	37006	GGCAGAGGTTGCAGTGAGCC
38920	37007	AGGCAGAGGTTGCAGTGAGC
38921	37008	GAGGCAGAGGTTGCAGTGAG
38922	37009	GGAGGCAGAGGTTGCAGTGA
38923	37010	GGGAGGCAGAGGTTGCAGTG
38924	37011	CGGGAGGCAGAGGTTGCAGT
38925	37012	CCGGGAGGCAGAGGTTGCAG
38926	37013	CCCGGGAGGCAGAGGTTGCA
38927	37014	ACCCGGGAGGCAGAGGTTGC
38928	37015	AACCCGGGAGGCAGAGGTTG
38929	37016	GAACCCGGGAGGCAGAGGTT
38930	37017	TGAACCCGGGAGGCAGAGGT
38931	37018	TTGAACCCGGGAGGCAGAGG
38932	37019	CTTGAACCCGGGAGGCAGAG
38933	37020	GCTTGAACCCGGGAGGCAGA
38934	37021	TGCTTGAACCCGGGAGGCAG
38935	37022	CTGCTTGAACCCGGGAGGCA
38936	37023	ACTGCTTGAACCCGGGAGGC
38937	37024	AACTGCTTGAACCCGGGAGG
38938	37025	GAACTGCTTGAACCCGGGAG
38939	37026	AGAACTGCTTGAACCCGGGA
38940	37027	GAGAACTGCTTGAACCCGGG
38941	37028	GGAGAACTGCTTGAACCCGG
38942	37029	AGGAGAACTGCTTGAACCCG
38943	37030	CAGGAGAACTGCTTGAACCC
38944	37031	GCAGGAGAACTGCTTGAACC
38945	37032	CGCAGGAGAACTGCTTGAAC
38946	37033	ACGCAGGAGAACTGCTTGAA
38947	37034	GACGCAGGAGAACTGCTTGA
38948	37035	TGACGCAGGAGAACTGCTTG
38949	37036	CTGACGCAGGAGAACTGCTT
38950	37037	GCTGACGCAGGAGAACTGCT
38951	37038	GGCTGACGCAGGAGAACTGC
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38953	37040	GAGGCTGACGCAGGAGAACT
38954	37041	GGAGGCTGACGCAGGAGAAC
38955	37042	GGGAGGCTGACGCAGGAGAA
38956	37043	CGGGAGGCTGACGCAGGAGA
38957	37044	TCGGGAGGCTGACGCAGGAG
38958	37045	CTCGGGAGGCTGACGCAGGA
38959	37046	ACTCGGGAGGCTGACGCAGG
38960	37047	TACTCGGGAGGCTGACGCAG
38961	37048	CTACTCGGGAGGCTGACGCA
38962	37049	GCTACTCGGGAGGCTGACGC
38963	37050	AGCTACTCGGGAGGCTGACG
38964	37051	CAGCTACTCGGGAGGCTGAC
38965	37052	CCAGCTACTCGGGAGGCTGA
38966	37053	CCCAGCTACTCGGGAGGCTG
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38969	37056	AATCCCAGCTACTCGGGAGG
38970	37057	TAATCCCAGCTACTCGGGAG
38971	37058	GTAATCCCAGCTACTCGGGA
38972	37059	TGTAATCCCAGCTACTCGGG

88049	86136	TTGGGGACATCCTTGGAGGC
88050	86137	TTTGGGGACATCCTTGGAGG
88051	86138	CTTTGGGGACATCCTTGGAG
88052	86139	CCTTTGGGGACATCCTTGGA
88053	86140	GCCTTTGGGGACATCCTTGG
88054	86141	GGCCTTTGGGGACATCCTTG
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88058	86145	GCTGGGCCTTTGGGGACATC
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88061	86148	GTCGCTGGGCCTTTGGGGAC
88062	86149	TGTCGCTGGGCCTTTGGGGA
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88064	86151	GATGTCGCTGGGCCTTTGGG
88065	86152	GGATGTCGCTGGGCCTTTGG
88066	86153	AGGATGTCGCTGGGCCTTTG
88067	86154	GAGGATGTCGCTGGGCCTTT
88068	86155	CGAGGATGTCGCTGGGCCTT
88069	86156	TCGAGGATGTCGCTGGGCCT
88070	86157	TTCGAGGATGTCGCTGGGCC
88071	86158	TTTCGAGGATGTCGCTGGGC
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88074	86161	TGATTTCGAGGATGTCGCTG
88075	86162	GTGATTTCGAGGATGTCGCT
88076	86163	TGTGATTTCGAGGATGTCGC
88077	86164	CTGTGATTTCGAGGATGTCG
88078	86165	TCTGTGATTTCGAGGATGTC
88079	86166	CTCTGTGATTTCGAGGATGT
88080	86167	ACTCTGTGATTTCGAGGATG
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88082	86169	AAACTCTGTGATTTCGAGGA
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88085	86172	CAGAAACTCTGTGATTTCGA
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88087	86174	AGCAGAAACTCTGTGATTTC
88088	86175	CAGCAGAAACTCTGTGATTT
88089	86176	CCAGCAGAAACTCTGTGATT
88090	86177	CCCAGCAGAAACTCTGTGAT
88091	86178	TCCCAGCAGAAACTCTGTGA
88092	86179	CTCCCAGCAGAAACTCTGTG
88093	86180	CCTCCCAGCAGAAACTCTGT
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88095	86182	CCCCTCCCAGCAGAAACTCT
88096	86183	ACCCCTCCCAGCAGAAACTC
88097	86184	AACCCCTCCCAGCAGAAACT
88098	86185	GAACCCCTCCCAGCAGAAAC
88099	86186	GGAACCCCTCCCAGCAGAAA
88100	86187	TGGAACCCCTCCCAGCAGAA
88101	86188	ATGGAACCCCTCCCAGCAGA
88102	86189	TATGGAACCCCTCCCAGCAG
88103	86190	ATATGGAACCCCTCCCAGCA
88104	86191	GATATGGAACCCCTCCCAGC
88105	86192	GGATATGGAACCCCTCCCAG
88106	86193	TGGATATGGAACCCCTCCCA
88107	86194	CTGGATATGGAACCCCTCCC
88108	86195	ACTGGATATGGAACCCCTCC
88109	86196	CACTGGATATGGAACCCCTC
88110	86197	CCACTGGATATGGAACCCCT
88111	86198	GCCACTGGATATGGAACCCC
88112	86199	GGCCACTGGATATGGAACCC
88113	86200	AGGCCACTGGATATGGAACC
88114	86201	TAGGCCACTGGATATGGAAC
88115	86202	CTAGGCCACTGGATATGGAA
88116	86203	TCTAGGCCACTGGATATGGA
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88119	86206	AATTCTAGGCCACTGGATAT

137196	135283	TAAAGCTGTTTAGGAAGTTT
137197	135284	ATAAAGCTGTTTAGGAAGTT
137198	135285	TATAAAGCTGTTTAGGAAGT
137199	135286	GTATAAAGCTGTTTAGGAAG
137200	135287	TGTATAAAGCTGTTTAGGAA
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137202	135289	TGTGTATAAAGCTGTTTAGG
137203	135290	GTGTGTATAAAGCTGTTTAG
137204	135291	TGTGTGTATAAAGCTGTTTA
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137210	135297	TGTGTGTGTGTGTATAAAGC
137211	135298	GTGTGTGTGTGTGTATAAAG
137212	135299	TGTGTGTGTGTGTGTATAAA
137213	135300	GTGTGTGTGTGTGTGTATAA
137214	135301	TGTGTGTGTGTGTGTGTATA
137215	135302	GTGTGTGTGTGTGTGTGTAT
137216	135303	TGTGTGTGTGTGTGTGTGTA
137217	135304	GTGTGTGTGTGTGTGTGTGT
137218	135305	TGTGTGTGTGTGTGTGTGTG
137219	135306	GTGTGTGTGTGTGTGTGTGT
137220	135307	TGTGTGTGTGTGTGTGTGTG
137221	135308	GTGTGTGTGTGTGTGTGTGT
137222	135309	TGTGTGTGTGTGTGTGTGTG
137223	135310	GTGTGTGTGTGTGTGTGTGT
137224	135311	TGTGTGTGTGTGTGTGTGTG
137225	135312	GTGTGTGTGTGTGTGTGTGT
137226	135313	TGTGTGTGTGTGTGTGTGTG
137227	135314	GTGTGTGTGTGTGTGTGTGT
137228	135315	TGTGTGTGTGTGTGTGTGTG
137229	135316	GTGTGTGTGTGTGTGTGTGT
137230	135317	TGTGTGTGTGTGTGTGTGTG
137231	135318	GTGTGTGTGTGTGTGTGTGT
137232	135319	TGTGTGTGTGTGTGTGTGTG
137233	135320	TTGTGTGTGTGTGTGTGTGT
137234	135321	TTTGTGTGTGTGTGTGTGTG
137235	135322	GTTTGTGTGTGTGTGTGTGT
137236	135323	TGTTTGTGTGTGTGTGTGTG
137237	135324	GTGTTTGTGTGTGTGTGTGT
137238	135325	TGTGTTTGTGTGTGTGTGTG
137239	135326	GTGTGTTTGTGTGTGTGTGT
137240	135327	TGTGTGTTTGTGTGTGTGTG
137241	135328	GTGTGTGTTTGTGTGTGTGT
137242	135329	TGTGTGTGTTTGTGTGTGTG
137243	135330	GTGTGTGTGTTTGTGTGTGT
137244	135331	GGTGTGTGTGTTTGTGTGTG
137245	135332	GGGTGTGTGTGTTTGTGTGT
137246	135333	TGGGTGTGTGTGTTTGTGTG
137247	135334	TTGGGTGTGTGTGTTTGTGT
137248	135335	CTTGGGTGTGTGTGTTTGTG
137249	135336	GCTTGGGTGTGTGTGTTTGT
137250	135337	GGCTTGGGTGTGTGTGTTTG
137251	135338	TGGCTTGGGTGTGTGTGTTT
137252	135339	GTGGCTTGGGTGTGTGTGTT
137253	135340	TGTGGCTTGGGTGTGTGTGT
137254	135341	TTGTGGCTTGGGTGTGTGTG
137255	135342	CTTGTGGCTTGGGTGTGTGT
137256	135343	GCTTGTGGCTTGGGTGTGTG
137257	135344	AGCTTGTGGCTTGGGTGTGT
137258	135345	AAGCTTGTGGCTTGGGTGTG
137259	135346	CAAGCTTGTGGCTTGGGTGT
137260	135347	CCAAGCTTGTGGCTTGGGTG
137261	135348	ACCAAGCTTGTGGCTTGGGT
137262	135349	TACCAAGCTTGTGGCTTGGG
137263	135350	ATACCAAGCTTGTGGCTTGG
137264	135351	TATACCAAGCTTGTGGCTTG
137265	135352	TTATACCAAGCTTGTGGCTT
137266	135353	TTTATACCAAGCTTGTGGCT

38973	37060	CTGTAATCCCAGCTACTCGG
38974	37061	TCTGTAATCCCAGCTACTCG
38975	37062	GTCTGTAATCCCAGCTACTC
38976	37063	TGTCTGTAATCCCAGCTACT
38977	37064	ATGTCTGTAATCCCAGCTAC
38978	37065	CATGTCTGTAATCCCAGCTA
38979	37066	GCATGTCTGTAATCCCAGCT
38980	37067	CGCATGTCTGTAATCCCAGC
38981	37068	GCGCATGTCTGTAATCCCAG
38982	37069	GGCGCATGTCTGTAATCCCA
38983	37070	TGGCGCATGTCTGTAATCCC
38984	37071	GTGGCGCATGTCTGTAATCC
38985	37072	GGTGGCGCATGTCTGTAATC
38986	37073	TGGTGGCGCATGTCTGTAAT
38987	37074	GTGGTGGCGCATGTCTGTAA
38988	37075	AGTGGTGGCGCATGTCTGTA
38989	37076	GAGTGGTGGCGCATGTCTGT
38990	37077	GGAGTGGTGGCGCATGTCTG
38991	37078	AGGAGTGGTGGCGCATGTCT
38992	37079	CAGGAGTGGTGGCGCATGTC
38993	37080	CCAGGAGTGGTGGCGCATGT
38994	37081	GCCAGGAGTGGTGGCGCATG
38995	37082	AGCCAGGAGTGGTGGCGCAT
38996	37083	TAGCCAGGAGTGGTGGCGCA
38997	37084	TTAGCCAGGAGTGGTGGCGC
38998	37085	ATTAGCCAGGAGTGGTGGCG
38999	37086	AATTAGCCAGGAGTGGTGGC
39000	37087	AAATTAGCCAGGAGTGGTGG
39001	37088	AAAATTAGCCAGGAGTGGTG
39002	37089	CAAAATTAGCCAGGAGTGGT
39003	37090	ACAAAATTAGCCAGGAGTGG
39004	37091	TACAAAATTAGCCAGGAGTG
39005	37092	ATACAAAATTAGCCAGGAGT
39006	37093	CATACAAAATTAGCCAGGAG
39007	37094	ACATACAAAATTAGCCAGGA
39008	37095	AACATACAAAATTAGCCAGG
39009	37096	GAACATACAAAATTAGCCAG
39010	37097	TGAACATACAAAATTAGCCA
39011	37098	CTGAACATACAAAATTAGCC
39012	37099	ACTGAACATACAAAATTAGC
39013	37100	TACTGAACATACAAAATTAG
39014	37101	CTACTGAACATACAAAATTA
39015	37102	TCTACTGAACATACAAAATT
39016	37103	CTCTACTGAACATACAAAAT
39017	37104	TCTCTACTGAACATACAAAA
39018	37105	GTCTCTACTGAACATACAAA
39019	37106	TGTCTCTACTGAACATACAA
39020	37107	CTGTCTCTACTGAACATACA
39021	37108	CCTGTCTCTACTGAACATAC
39022	37109	TCCTGTCTCTACTGAACATA
39023	37110	ATCCTGTCTCTACTGAACAT
39024	37111	AATCCTGTCTCTACTGAACA
39025	37112	AAATCCTGTCTCTACTGAAC
39026	37113	AAAATCCTGTCTCTACTGAA
39027	37114	AAAAATCCTGTCTCTACTGA
39028	37115	GAAAAATCCTGTCTCTACTG
39029	37116	GGAAAAATCCTGTCTCTACT
39030	37117	TGGAAAAATCCTGTCTCTAC
39031	37118	ATGGAAAAATCCTGTCTCTA
39032	37119	CATGGAAAAATCCTGTCTCT
39033	37120	ACATGGAAAAATCCTGTCTC
39034	37121	AACATGGAAAAATCCTGTCT
39035	37122	CAACATGGAAAAATCCTGTC
39036	37123	CCAACATGGAAAAATCCTGT
39037	37124	ACCAACATGGAAAAATCCTG
39038	37125	GACCAACATGGAAAAATCCT
39039	37126	TGACCAACATGGAAAAATCC
39040	37127	CTGACCAACATGGAAAAATC
39041	37128	CCTGACCAACATGGAAAAAT
39042	37129	GCCTGACCAACATGGAAAAA
39043	37130	AGCCTGACCAACATGGAAAA

88120	86207	AAATTCTAGGCCACTGGATA
88121	86208	CAAATTCTAGGCCACTGGAT
88122	86209	ACAAATTCTAGGCCACTGGA
88123	86210	TACAAATTCTAGGCCACTGG
88124	86211	ATACAAATTCTAGGCCACTG
88125	86212	GATACAAATTCTAGGCCACT
88126	86213	GGATACAAATTCTAGGCCAC
88127	86214	GGGATACAAATTCTAGGCCA
88128	86215	TGGGATACAAATTCTAGGCC
88129	86216	GTGGGATACAAATTCTAGGC
88130	86217	TGTGGGATACAAATTCTAGG
88131	86218	TTGTGGGATACAAATTCTAG
88132	86219	GTTGTGGGATACAAATTCTA
88133	86220	GGTTGTGGGATACAAATTCT
88134	86221	GGGTTGTGGGATACAAATTC
88135	86222	TGGGTTGTGGGATACAAATT
88136	86223	GTGGGTTGTGGGATACAAAT
88137	86224	GGTGGGTTGTGGGATACAAA
88138	86225	GGGTGGGTTGTGGGATACAA
88139	86226	TGGGTGGGTTGTGGGATACA
88140	86227	CTGGGTGGGTTGTGGGATAC
88141	86228	ACTGGGTGGGTTGTGGGATA
88142	86229	CACTGGGTGGGTTGTGGGAT
88143	86230	TCACTGGGTGGGTTGTGGGA
88144	86231	TTCACTGGGTGGGTTGTGGG
88145	86232	CTTCACTGGGTGGGTTGTGG
88146	86233	GCTTCACTGGGTGGGTTGTG
88147	86234	TGCTTCACTGGGTGGGTTGT
88148	86235	CTGCTTCACTGGGTGGGTTG
88149	86236	GCTGCTTCACTGGGTGGGTT
88150	86237	AGCTGCTTCACTGGGTGGGT
88151	86238	TAGCTGCTTCACTGGGTGGG
88152	86239	GTAGCTGCTTCACTGGGTGG
88153	86240	AGTAGCTGCTTCACTGGGTG
88154	86241	GAGTAGCTGCTTCACTGGGT
88155	86242	GGAGTAGCTGCTTCACTGGG
88156	86243	AGGAGTAGCTGCTTCACTGG
88157	86244	GAGGAGTAGCTGCTTCACTG
88158	86245	GGAGGAGTAGCTGCTTCACT
88159	86246	TGGAGGAGTAGCTGCTTCAC
88160	86247	CTGGAGGAGTAGCTGCTTCA
88161	86248	ACTGGAGGAGTAGCTGCTTC
88162	86249	TACTGGAGGAGTAGCTGCTT
88163	86250	CTACTGGAGGAGTAGCTGCT
88164	86251	GCTACTGGAGGAGTAGCTGC
88165	86252	TGCTACTGGAGGAGTAGCTG
88166	86253	TTGCTACTGGAGGAGTAGCT
88167	86254	CTTGCTACTGGAGGAGTAGC
88168	86255	CCTTGCTACTGGAGGAGTAG
88169	86256	TCCTTGCTACTGGAGGAGTA
88170	86257	GTCCTTGCTACTGGAGGAGT
88171	86258	GGTCCTTGCTACTGGAGGAG
88172	86259	TGGTCCTTGCTACTGGAGGA
88173	86260	CTGGTCCTTGCTACTGGAGG
88174	86261	ACTGGTCCTTGCTACTGGAG
88175	86262	GACTGGTCCTTGCTACTGGA
88176	86263	GGACTGGTCCTTGCTACTGG
88177	86264	GGGACTGGTCCTTGCTACTG
88178	86265	AGGGACTGGTCCTTGCTACT
88179	86266	GAGGGACTGGTCCTTGCTAC
88180	86267	CGAGGGACTGGTCCTTGCTA
88181	86268	CCGAGGGACTGGTCCTTGCT
88182	86269	CCCGAGGGACTGGTCCTTGC
88183	86270	CCCCGAGGGACTGGTCCTTG
88184	86271	CCCCCGAGGGACTGGTCCTT
88185	86272	CCCCCCGAGGGACTGGTCCT
88186	86273	TCCCCCCGAGGGACTGGTCC
88187	86274	TTCCCCCCGAGGGACTGGTC
88188	86275	GTTCCCCCCGAGGGACTGGT
88189	86276	CGTTCCCCCCGAGGGACTGG
88190	86277	ACGTTCCCCCCGAGGGACTG

137267	135354	ATTTATACCAAGCTTGTGGC
137268	135355	AATTTATACCAAGCTTGTGG
137269	135356	AAATTTATACCAAGCTTGTG
137270	135357	TAAATTTATACCAAGCTTGT
137271	135358	TTAAATTTATACCAAGCTTG
137272	135359	TTTAAATTTATACCAAGCTT
137273	135360	TTTTAAATTTATACCAAGCT
137274	135361	ATTTTAAATTTATACCAAGC
137275	135362	CATTTTAAATTTATACCAAG
137276	135363	ACATTTTAAATTTATACCAA
137277	135364	AACATTTTAAATTTATACCA
137278	135365	AAACATTTTAAATTTATACC
137279	135366	TAAACATTTTAAATTTATAC
137280	135367	ATAAACATTTTAAATTTATA
137281	135368	AATAAACATTTTAAATTTAT
137282	135369	AAATAAACATTTTAAATTTA
137283	135370	TAAATAAACATTTTAAATTT
137284	135371	ATAAATAAACATTTTAAATT
137285	135372	TATAAATAAACATTTTAAAT
137286	135373	GTATAAATAAACATTTTAAA
137287	135374	TGTATAAATAAACATTTTAA
137288	135375	GTGTATAAATAAACATTTTA
137289	135376	TGTGTATAAATAAACATTTT
137290	135377	GTGTGTATAAATAAACATTT
137291	135378	TGTGTGTATAAATAAACATT
137292	135379	GTGTGTGTATAAATAAACAT
137293	135380	TGTGTGTGTATAAATAAACA
137294	135381	GTGTGTGTGTATAAATAAAC
137295	135382	TGTGTGTGTGTATAAATAAA
137296	135383	GTGTGTGTGTGTATAAATAA
137297	135384	TGTGTGTGTGTGTATAAATA
137298	135385	GTGTGTGTGTGTGTATAAAT
137299	135386	TGTGTGTGTGTGTGTATAAA
137300	135387	GTGTGTGTGTGTGTGTATAA
137301	135388	TGTGTGTGTGTGTGTGTATA
137302	135389	GTGTGTGTGTGTGTGTGTAT
137303	135390	TGTGTGTGTGTGTGTGTGTA
137304	135391	GTGTGTGTGTGTGTGTGTGT
137305	135392	TGTGTGTGTGTGTGTGTGTG
137306	135393	GTGTGTGTGTGTGTGTGTGT
137307	135394	TGTGTGTGTGTGTGTGTGTG
137308	135395	GTGTGTGTGTGTGTGTGTGT
137309	135396	TGTGTGTGTGTGTGTGTGTG
137310	135397	GTGTGTGTGTGTGTGTGTGT
137311	135398	TGTGTGTGTGTGTGTGTGTG
137312	135399	GTGTGTGTGTGTGTGTGTGT
137313	135400	TGTGTGTGTGTGTGTGTGTG
137314	135401	GTGTGTGTGTGTGTGTGTGT
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137316	135403	GTGTGTGTGTGTGTGTGTGT
137317	135404	TGTGTGTGTGTGTGTGTGTG
137318	135405	GTGTGTGTGTGTGTGTGTGT
137319	135406	TGTGTGTGTGTGTGTGTGTG
137320	135407	GTGTGTGTGTGTGTGTGTGT
137321	135408	GGTGTGTGTGTGTGTGTGTG
137322	135409	GGGTGTGTGTGTGTGTGTGT
137323	135410	GGGGTGTGTGTGTGTGTGTG
137324	135411	TGGGGTGTGTGTGTGTGTGT
137325	135412	TTGGGGTGTGTGTGTGTGTG
137326	135413	CTTGGGGTGTGTGTGTGTGT
137327	135414	GCTTGGGGTGTGTGTGTGTG
137328	135415	GGCTTGGGGTGTGTGTGTGT
137329	135416	TGGCTTGGGGTGTGTGTGTG
137330	135417	GTGGCTTGGGGTGTGTGTGT
137331	135418	TGTGGCTTGGGGTGTGTGTG
137332	135419	TTGTGGCTTGGGGTGTGTGT
137333	135420	CTTGTGGCTTGGGGTGTGTG
137334	135421	GCTTGTGGCTTGGGGTGTGT
137335	135422	AGCTTGTGGCTTGGGGTGTG
137336	135423	AAGCTTGTGGCTTGGGGTGT
137337	135424	CAAGCTTGTGGCTTGGGGTG

39044	37131	CAGCCTGACCAACATGGAAA
39045	37132	CCAGCCTGACCAACATGGAA
39046	37133	ACCAGCCTGACCAACATGGA
39047	37134	GACCAGCCTGACCAACATGG
39048	37135	AGACCAGCCTGACCAACATG
39049	37136	GAGACCAGCCTGACCAACAT
39050	37137	GGAGACCAGCCTGACCAACA
39051	37138	TGGAGACCAGCCTGACCAAC
39052	37139	TTGGAGACCAGCCTGACCAA
39053	37140	GTTGGAGACCAGCCTGACCA
39054	37141	AGTTGGAGACCAGCCTGACC
39055	37142	GAGTTGGAGACCAGCCTGAC
39056	37143	GGAGTTGGAGACCAGCCTGA
39057	37144	GGGAGTTGGAGACCAGCCTG
39058	37145	CGGGAGTTGGAGACCAGCCT
39059	37146	TCGGGAGTTGGAGACCAGCC
39060	37147	GTCGGGAGTTGGAGACCAGC
39061	37148	GGTCGGGAGTTGGAGACCAG
39062	37149	AGGTCGGGAGTTGGAGACCA
39063	37150	GAGGTCGGGAGTTGGAGACC
39064	37151	TGAGGTCGGGAGTTGGAGAC
39065	37152	CTGAGGTCGGGAGTTGGAGA
39066	37153	CCTGAGGTCGGGAGTTGGAG
39067	37154	ACCTGAGGTCGGGAGTTGGA
39068	37155	CACCTGAGGTCGGGAGTTGG
39069	37156	TCACCTGAGGTCGGGAGTTG
39070	37157	ATCACCTGAGGTCGGGAGTT
39071	37158	GATCACCTGAGGTCGGGAGT
39072	37159	GGATCACCTGAGGTCGGGAG
39073	37160	TGGATCACCTGAGGTCGGGA
39074	37161	GTGGATCACCTGAGGTCGGG
39075	37162	GGTGGATCACCTGAGGTCGG
39076	37163	GGGTGGATCACCTGAGGTCG
39077	37164	TGGGTGGATCACCTGAGGTC
39078	37165	GTGGGTGGATCACCTGAGGT
39079	37166	GGTGGGTGGATCACCTGAGG
39080	37167	AGGTGGGTGGATCACCTGAG
39081	37168	GAGGTGGGTGGATCACCTGA
39082	37169	TGAGGTGGGTGGATCACCTG
39083	37170	CTGAGGTGGGTGGATCACCT
39084	37171	GCTGAGGTGGGTGGATCACC
39085	37172	GGCTGAGGTGGGTGGATCAC
39086	37173	AGGCTGAGGTGGGTGGATCA
39087	37174	GAGGCTGAGGTGGGTGGATC
39088	37175	GGAGGCTGAGGTGGGTGGAT
39089	37176	GGGAGGCTGAGGTGGGTGGA
39090	37177	TGGGAGGCTGAGGTGGGTGG
39091	37178	CTGGGAGGCTGAGGTGGGTG
39092	37179	TCTGGGAGGCTGAGGTGGGT
39093	37180	CTCTGGGAGGCTGAGGTGGG
39094	37181	ACTCTGGGAGGCTGAGGTGG
39095	37182	CACTCTGGGAGGCTGAGGTG
39096	37183	GCACTCTGGGAGGCTGAGGT
39097	37184	AGCACTCTGGGAGGCTGAGG
39098	37185	TAGCACTCTGGGAGGCTGAG
39099	37186	CTAGCACTCTGGGAGGCTGA
39100	37187	CCTAGCACTCTGGGAGGCTG
39101	37188	TCCTAGCACTCTGGGAGGCT
39102	37189	ATCCTAGCACTCTGGGAGGC
39103	37190	AATCCTAGCACTCTGGGAGG
39104	37191	TAATCCTAGCACTCTGGGAG
39105	37192	GTAATCCTAGCACTCTGGGA
39106	37193	TGTAATCCTAGCACTCTGGG
39107	37194	CTGTAATCCTAGCACTCTGG
39108	37195	CCTGTAATCCTAGCACTCTG
39109	37196	GCCTGTAATCCTAGCACTCT
39110	37197	CGCCTGTAATCCTAGCACTC
39111	37198	ACGCCTGTAATCCTAGCACT
39112	37199	CACGCCTGTAATCCTAGCAC
39113	37200	TCACGCCTGTAATCCTAGCA
39114	37201	CTCACGCCTGTAATCCTAGC

88191	86278	CACGTTCCCCCCGAGGGACT
88192	86279	CCACGTTCCCCCCGAGGGAC
88193	86280	ACCACGTTCCCCCCGAGGGA
88194	86281	GACCACGTTCCCCCCGAGGG
88195	86282	TGACCACGTTCCCCCCGAGG
88196	86283	ATGACCACGTTCCCCCCGAG
88197	86284	GATGACCACGTTCCCCCCGA
88198	86285	TGATGACCACGTTCCCCCCG
88199	86286	CTGATGACCACGTTCCCCCC
88200	86287	ACTGATGACCACGTTCCCCC
88201	86288	CACTGATGACCACGTTCCCC
88202	86289	CCACTGATGACCACGTTCCC
88203	86290	ACCACTGATGACCACGTTCC
88204	86291	GACCACTGATGACCACGTTC
88205	86292	TGACCACTGATGACCACGTT
88206	86293	CTGACCACTGATGACCACGT
88207	86294	ACTGACCACTGATGACCACG
88208	86295	CACTGACCACTGATGACCAC
88209	86296	CCACTGACCACTGATGACCA
88210	86297	CCCACTGACCACTGATGACC
88211	86298	CCCCACTGACCACTGATGAC
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88213	86300	ACCCCCACTGACCACTGATG
88214	86301	TACCCCCACTGACCACTGAT
88215	86302	CTACCCCCACTGACCACTGA
88216	86303	CCTACCCCCACTGACCACTG
88217	86304	ACCTACCCCCACTGACCACT
88218	86305	TACCTACCCCCACTGACCAC
88219	86306	TTACCTACCCCCACTGACCA
88220	86307	GTTACCTACCCCCACTGACC
88221	86308	TGTTACCTACCCCCACTGAC
88222	86309	GTGTTACCTACCCCCACTGA
88223	86310	AGTGTTACCTACCCCCACTG
88224	86311	AAGTGTTACCTACCCCCACT
88225	86312	CAAGTGTTACCTACCCCCAC
88226	86313	CCAAGTGTTACCTACCCCCA
88227	86314	CCCAAGTGTTACCTACCCCC
88228	86315	GCCCAAGTGTTACCTACCCC
88229	86316	TGCCCAAGTGTTACCTACCC
88230	86317	ATGCCCAAGTGTTACCTACC
88231	86318	TATGCCCAAGTGTTACCTAC
88232	86319	TTATGCCCAAGTGTTACCTA
88233	86320	ATTATGCCCAAGTGTTACCT
88234	86321	CATTATGCCCAAGTGTTACC
88235	86322	TCATTATGCCCAAGTGTTAC
88236	86323	ATCATTATGCCCAAGTGTTA
88237	86324	CATCATTATGCCCAAGTGTT
88238	86325	CCATCATTATGCCCAAGTGT
88239	86326	ACCATCATTATGCCCAAGTG
88240	86327	TACCATCATTATGCCCAAGT
88241	86328	GTACCATCATTATGCCCAAG
88242	86329	AGTACCATCATTATGCCCAA
88243	86330	GAGTACCATCATTATGCCCA
88244	86331	TGAGTACCATCATTATGCCC
88245	86332	ATGAGTACCATCATTATGCC
88246	86333	AATGAGTACCATCATTATGC
88247	86334	AAATGAGTACCATCATTATG
88248	86335	AAAATGAGTACCATCATTAT
88249	86336	CAAAATGAGTACCATCATTA
88250	86337	ACAAAATGAGTACCATCATT
88251	86338	GACAAAATGAGTACCATCAT
88252	86339	TGACAAAATGAGTACCATCA
88253	86340	ATGACAAAATGAGTACCATC
88254	86341	AATGACAAAATGAGTACCAT
88255	86342	TAATGACAAAATGAGTACCA
88256	86343	GTAATGACAAAATGAGTACC
88257	86344	TGTAATGACAAAATGAGTAC
88258	86345	GTGTAATGACAAAATGAGTA
88259	86346	AGTGTAATGACAAAATGAGT
88260	86347	TAGTGTAATGACAAAATGAG
88261	86348	CTAGTGTAATGACAAAATGA

137338	135425	CCAAGCTTGTGGCTTGGGGT
137339	135426	ACCAAGCTTGTGGCTTGGGG
137340	135427	TACCAAGCTTGTGGCTTGGG
137341	135428	ATACCAAGCTTGTGGCTTGG
137342	135429	TATACCAAGCTTGTGGCTTG
137343	135430	TTATACCAAGCTTGTGGCTT
137344	135431	TTTATACCAAGCTTGTGGCT
137345	135432	GTTTATACCAAGCTTGTGGC
137346	135433	AGTTTATACCAAGCTTGTGG
137347	135434	AAGTTTATACCAAGCTTGTG
137348	135435	TAAGTTTATACCAAGCTTGT
137349	135436	TTAAGTTTATACCAAGCTTG
137350	135437	TTTAAGTTTATACCAAGCTT
137351	135438	TTTTAAGTTTATACCAAGCT
137352	135439	ATTTTAAGTTTATACCAAGC
137353	135440	CATTTTAAGTTTATACCAAG
137354	135441	ACATTTTAAGTTTATACCAA
137355	135442	AACATTTTAAGTTTATACCA
137356	135443	AAACATTTTAAGTTTATACC
137357	135444	TAAACATTTTAAGTTTATAC
137358	135445	ATAAACATTTTAAGTTTATA
137359	135446	AATAAACATTTTAAGTTTAT
137360	135447	AAATAAACATTTTAAGTTTA
137361	135448	TAAATAAACATTTTAAGTTT
137362	135449	ATAAATAAACATTTTAAGTT
137363	135450	TATAAATAAACATTTTAAGT
137364	135451	ATATAAATAAACATTTTAAG
137365	135452	AATATAAATAAACATTTTAA
137366	135453	GAATATAAATAAACATTTTA
137367	135454	AGAATATAAATAAACATTTT
137368	135455	CAGAATATAAATAAACATTT
137369	135456	TCAGAATATAAATAAACATT
137370	135457	ATCAGAATATAAATAAACAT
137371	135458	TATCAGAATATAAATAAACA
137372	135459	TTATCAGAATATAAATAAAC
137373	135460	CTTATCAGAATATAAATAAA
137374	135461	TCTTATCAGAATATAAATAA
137375	135462	ATCTTATCAGAATATAAATA
137376	135463	CATCTTATCAGAATATAAAT
137377	135464	TCATCTTATCAGAATATAAA
137378	135465	TTCATCTTATCAGAATATAA
137379	135466	TTTCATCTTATCAGAATATA
137380	135467	ATTTCATCTTATCAGAATAT
137381	135468	AATTTCATCTTATCAGAATA
137382	135469	AAATTTCATCTTATCAGAAT
137383	135470	TAAATTTCATCTTATCAGAA
137384	135471	ATAAATTTCATCTTATCAGA
137385	135472	CATAAATTTCATCTTATCAG
137386	135473	GCATAAATTTCATCTTATCA
137387	135474	GGCATAAATTTCATCTTATC
137388	135475	AGGCATAAATTTCATCTTAT
137389	135476	TAGGCATAAATTTCATCTTA
137390	135477	GTAGGCATAAATTTCATCTT
137391	135478	GGTAGGCATAAATTTCATCT
137392	135479	TGGTAGGCATAAATTTCATC
137393	135480	CTGGTAGGCATAAATTTCAT
137394	135481	CCTGGTAGGCATAAATTTCA
137395	135482	TCCTGGTAGGCATAAATTTC
137396	135483	ATCCTGGTAGGCATAAATTT
137397	135484	AATCCTGGTAGGCATAAATT
137398	135485	AAATCCTGGTAGGCATAAAT
137399	135486	AAAATCCTGGTAGGCATAAA
137400	135487	AAAAATCCTGGTAGGCATAA
137401	135488	TAAAAATCCTGGTAGGCATA
137402	135489	TTAAAAATCCTGGTAGGCAT
137403	135490	ATTAAAAATCCTGGTAGGCA
137404	135491	AATTAAAAATCCTGGTAGGC
137405	135492	CAATTAAAAATCCTGGTAGG
137406	135493	TCAATTAAAAATCCTGGTAG
137407	135494	TTCAATTAAAAATCCTGGTA
137408	135495	ATTCAATTAAAAATCCTGGT

39115	37202	GCTCACGCCTGTAATCCTAG
39116	37203	AGCTCACGCCTGTAATCCTA
39117	37204	CAGCTCACGCCTGTAATCCT
39118	37205	GCAGCTCACGCCTGTAATCC
39119	37206	GGCAGCTCACGCCTGTAATC
39120	37207	TGGCAGCTCACGCCTGTAAT
39121	37208	GTGGCAGCTCACGCCTGTAA
39122	37209	TGTGGCAGCTCACGCCTGTA
39123	37210	GTGTGGCAGCTCACGCCTGT
39124	37211	GGTGTGGCAGCTCACGCCTG
39125	37212	TGGTGTGGCAGCTCACGCCT
39126	37213	CTGGTGTGGCAGCTCACGCC
39127	37214	CCTGGTGTGGCAGCTCACGC
39128	37215	GCCTGGTGTGGCAGCTCACG
39129	37216	GGCCTGGTGTGGCAGCTCAC
39130	37217	AGGCCTGGTGTGGCAGCTCA
39131	37218	AAGGCCTGGTGTGGCAGCTC
39132	37219	GAAGGCCTGGTGTGGCAGCT
39133	37220	AGAAGGCCTGGTGTGGCAGC
39134	37221	AAGAAGGCCTGGTGTGGCAG
39135	37222	AAAGAAGGCCTGGTGTGGCA
39136	37223	AAAAGAAGGCCTGGTGTGGC
39137	37224	AAAAAGAAGGCCTGGTGTGG
39138	37225	GAAAAAGAAGGCCTGGTGTG
39139	37226	AGAAAAAGAAGGCCTGGTGT
39140	37227	GAGAAAAAGAAGGCCTGGTG
39141	37228	AGAGAAAAAGAAGGCCTGGT
39142	37229	AAGAGAAAAAGAAGGCCTGG
39143	37230	AAAGAGAAAAAGAAGGCCTG
39144	37231	AAAAGAGAAAAAGAAGGCCT
39145	37232	TAAAAGAGAAAAAGAAGGCC
39146	37233	TTAAAAGAGAAAAAGAAGGC
39147	37234	CTTAAAAGAGAAAAAGAAGG
39148	37235	TCTTAAAAGAGAAAAAGAAG
39149	37236	CTCTTAAAAGAGAAAAAGAA
39150	37237	TCTCTTAAAAGAGAAAAAGA
39151	37238	ATCTCTTAAAAGAGAAAAAG
39152	37239	TATCTCTTAAAAGAGAAAAA
39153	37240	CTATCTCTTAAAAGAGAAAA
39154	37241	TCTATCTCTTAAAAGAGAAA
39155	37242	CTCTATCTCTTAAAAGAGAA
39156	37243	ACTCTATCTCTTAAAAGAGA
39157	37244	GACTCTATCTCTTAAAAGAG
39158	37245	GGACTCTATCTCTTAAAAGA
39159	37246	AGGACTCTATCTCTTAAAAG
39160	37247	CAGGACTCTATCTCTTAAAA
39161	37248	GCAGGACTCTATCTCTTAAA
39162	37249	AGCAGGACTCTATCTCTTAA
39163	37250	AAGCAGGACTCTATCTCTTA
39164	37251	AAAGCAGGACTCTATCTCTT
39165	37252	CAAAGCAGGACTCTATCTCT
39166	37253	ACAAAGCAGGACTCTATCTC
39167	37254	GACAAAGCAGGACTCTATCT
39168	37255	TGACAAAGCAGGACTCTATC
39169	37256	GTGACAAAGCAGGACTCTAT
39170	37257	GGTGACAAAGCAGGACTCTA
39171	37258	TGGTGACAAAGCAGGACTCT
39172	37259	TTGGTGACAAAGCAGGACTC
39173	37260	CTTGGTGACAAAGCAGGACT
39174	37261	CCTTGGTGACAAAGCAGGAC
39175	37262	GCCTTGGTGACAAAGCAGGA
39176	37263	AGCCTTGGTGACAAAGCAGG
39177	37264	CAGCCTTGGTGACAAAGCAG
39178	37265	CCAGCCTTGGTGACAAAGCA
39179	37266	TCCAGCCTTGGTGACAAAGC
39180	37267	CTCCAGCCTTGGTGACAAAG
39181	37268	ACTCCAGCCTTGGTGACAAA
39182	37269	CACTCCAGCCTTGGTGACAA
39183	37270	GCACTCCAGCCTTGGTGACA
39184	37271	TGCACTCCAGCCTTGGTGAC
39185	37272	CTGCACTCCAGCCTTGGTGA

88262	86349	TCTAGTGTAATGACAAAATG
88263	86350	ATCTAGTGTAATGACAAAAT
88264	86351	TATCTAGTGTAATGACAAAA
88265	86352	ATATCTAGTGTAATGACAAA
88266	86353	TATATCTAGTGTAATGACAA
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88268	86355	TTTATATCTAGTGTAATGAC
88269	86356	CTTTATATCTAGTGTAATGA
88270	86357	TCTTTATATCTAGTGTAATG
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88272	86359	CCTCTTTATATCTAGTGTAA
88273	86360	CCCTCTTTATATCTAGTGTA
88274	86361	GCCCTCTTTATATCTAGTGT
88275	86362	AGCCCTCTTTATATCTAGTG
88276	86363	CAGCCCTCTTTATATCTAGT
88277	86364	TCAGCCCTCTTTATATCTAG
88278	86365	CTCAGCCCTCTTTATATCTA
88279	86366	GCTCAGCCCTCTTTATATCT
88280	86367	AGCTCAGCCCTCTTTATATC
88281	86368	TAGCTCAGCCCTCTTTATAT
88282	86369	GTAGCTCAGCCCTCTTTATA
88283	86370	TGTAGCTCAGCCCTCTTTAT
88284	86371	TTGTAGCTCAGCCCTCTTTA
88285	86372	GTTGTAGCTCAGCCCTCTTT
88286	86373	AGTTGTAGCTCAGCCCTCTT
88287	86374	GAGTTGTAGCTCAGCCCTCT
88288	86375	AGAGTTGTAGCTCAGCCCTC
88289	86376	CAGAGTTGTAGCTCAGCCCT
88290	86377	ACAGAGTTGTAGCTCAGCCC
88291	86378	AACAGAGTTGTAGCTCAGCC
88292	86379	AAACAGAGTTGTAGCTCAGC
88293	86380	CAAACAGAGTTGTAGCTCAG
88294	86381	TCAAACAGAGTTGTAGCTCA
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88301	86388	CACTTCCTCAAACAGAGTTG
88302	86389	ACACTTCCTCAAACAGAGTT
88303	86390	TACACTTCCTCAAACAGAGT
88304	86391	TTACACTTCCTCAAACAGAG
88305	86392	CTTACACTTCCTCAAACAGA
88306	86393	ACTTACACTTCCTCAAACAG
88307	86394	TACTTACACTTCCTCAAACA
88308	86395	ATACTTACACTTCCTCAAAC
88309	86396	CATACTTACACTTCCTCAAA
88310	86397	ACATACTTACACTTCCTCAA
88311	86398	TACATACTTACACTTCCTCA
88312	86399	ATACATACTTACACTTCCTC
88313	86400	TATACATACTTACACTTCCT
88314	86401	ATATACATACTTACACTTCC
88315	86402	CATATACATACTTACACTTC
88316	86403	ACATATACATACTTACACTT
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88318	86405	TAACATATACATACTTACAC
88319	86406	TTAACATATACATACTTACA
88320	86407	TTTAACATATACATACTTAC
88321	86408	TTTTAACATATACATACTTA
88322	86409	TTTTTAACATATACATACTT
88323	86410	ATTTTTAACATATACATACT
88324	86411	TATTTTTAACATATACATAC
88325	86412	CTATTTTTAACATATACATA
88326	86413	ACTATTTTTAACATATACAT
88327	86414	TACTATTTTTAACATATACA
88328	86415	CTACTATTTTTAACATATAC
88329	86416	TCTACTATTTTTAACATATA
88330	86417	TTCTACTATTTTTAACATAT
88331	86418	ATTCTACTATTTTTAACATA
88332	86419	GATTCTACTATTTTTAACAT

137409	135496	TATTCAATTAAAAATCCTGG
137410	135497	CTATTCAATTAAAAATCCTG
137411	135498	CCTATTCAATTAAAAATCCT
137412	135499	TCCTATTCAATTAAAAATCC
137413	135500	ATCCTATTCAATTAAAAATC
137414	135501	AATCCTATTCAATTAAAAAT
137415	135502	CAATCCTATTCAATTAAAAA
137416	135503	TCAATCCTATTCAATTAAAA
137417	135504	ATCAATCCTATTCAATTAAA
137418	135505	CATCAATCCTATTCAATTAA
137419	135506	TCATCAATCCTATTCAATTA
137420	135507	TTCATCAATCCTATTCAATT
137421	135508	TTTCATCAATCCTATTCAAT
137422	135509	ATTTCATCAATCCTATTCAA
137423	135510	TATTTCATCAATCCTATTCA
137424	135511	GTATTTCATCAATCCTATTC
137425	135512	AGTATTTCATCAATCCTATT
137426	135513	TAGTATTTCATCAATCCTAT
137427	135514	TTAGTATTTCATCAATCCTA
137428	135515	CTTAGTATTTCATCAATCCT
137429	135516	CCTTAGTATTTCATCAATCC
137430	135517	CCCTTAGTATTTCATCAATC
137431	135518	TCCCTTAGTATTTCATCAAT
137432	135519	TTCCCTTAGTATTTCATCAA
137433	135520	TTTCCCTTAGTATTTCATCA
137434	135521	TTTTCCCTTAGTATTTCATC
137435	135522	TTTTTCCCTTAGTATTTCAT
137436	135523	GTTTTTCCCTTAGTATTTCA
137437	135524	AGTTTTTCCCTTAGTATTTC
137438	135525	AAGTTTTTCCCTTAGTATTT
137439	135526	AAAGTTTTTCCCTTAGTATT
137440	135527	AAAAGTTTTTCCCTTAGTAT
137441	135528	GAAAAGTTTTTCCCTTAGTA
137442	135529	TGAAAAGTTTTTCCCTTAGT
137443	135530	CTGAAAAGTTTTTCCCTTAG
137444	135531	ACTGAAAAGTTTTTCCCTTA
137445	135532	GACTGAAAAGTTTTTCCCTT
137446	135533	GGACTGAAAAGTTTTTCCCT
137447	135534	AGGACTGAAAAGTTTTTCCC
137448	135535	CAGGACTGAAAAGTTTTTCC
137449	135536	ACAGGACTGAAAAGTTTTTC
137450	135537	CACAGGACTGAAAAGTTTTT
137451	135538	GCACAGGACTGAAAAGTTTT
137452	135539	TGCACAGGACTGAAAAGTTT
137453	135540	ATGCACAGGACTGAAAAGTT
137454	135541	CATGCACAGGACTGAAAAGT
137455	135542	CCATGCACAGGACTGAAAAG
137456	135543	GCCATGCACAGGACTGAAAA
137457	135544	AGCCATGCACAGGACTGAAA
137458	135545	TAGCCATGCACAGGACTGAA
137459	135546	TTAGCCATGCACAGGACTGA
137460	135547	TTTAGCCATGCACAGGACTG
137461	135548	CTTTAGCCATGCACAGGACT
137462	135549	CCTTTAGCCATGCACAGGAC
137463	135550	ACCTTTAGCCATGCACAGGA
137464	135551	AACCTTTAGCCATGCACAGG
137465	135552	AAACCTTTAGCCATGCACAG
137466	135553	TAAACCTTTAGCCATGCACA
137467	135554	TTAAACCTTTAGCCATGCAC
137468	135555	TTTAAACCTTTAGCCATGCA
137469	135556	TTTTAAACCTTTAGCCATGC
137470	135557	ATTTTAAACCTTTAGCCATG
137471	135558	TATTTTAAACCTTTAGCCAT
137472	135559	GTATTTTAAACCTTTAGCCA
137473	135560	AGTATTTTAAACCTTTAGCC
137474	135561	GAGTATTTTAAACCTTTAGC
137475	135562	TGAGTATTTTAAACCTTTAG
137476	135563	CTGAGTATTTTAAACCTTTA
137477	135564	CCTGAGTATTTTAAACCTTT
137478	135565	TCCTGAGTATTTTAAACCTT
137479	135566	TTCCTGAGTATTTTAAACCT

39186	37273	ACTGCACTCCAGCCTTGGTG
39187	37274	CACTGCACTCCAGCCTTGGT
39188	37275	CCACTGCACTCCAGCCTTGG
39189	37276	GCCACTGCACTCCAGCCTTG
39190	37277	TGCCACTGCACTCCAGCCTT
39191	37278	ATGCCACTGCACTCCAGCCT
39192	37279	CATGCCACTGCACTCCAGCC
39193	37280	TCATGCCACTGCACTCCAGC
39194	37281	ATCATGCCACTGCACTCCAG
39195	37282	CATCATGCCACTGCACTCCA
39196	37283	TCATCATGCCACTGCACTCC
39197	37284	ATCATCATGCCACTGCACTC
39198	37285	TATCATCATGCCACTGCACT
39199	37286	CTATCATCATGCCACTGCAC
39200	37287	ACTATCATCATGCCACTGCA
39201	37288	AACTATCATCATGCCACTGC
39202	37289	GAACTATCATCATGCCACTG
39203	37290	TGAACTATCATCATGCCACT
39204	37291	GTGAACTATCATCATGCCAC
39205	37292	AGTGAACTATCATCATGCCA
39206	37293	CAGTGAACTATCATCATGCC
39207	37294	GCAGTGAACTATCATCATGC
39208	37295	TGCAGTGAACTATCATCATG
39209	37296	CTGCAGTGAACTATCATCAT
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39220	37307	GGAGTTTGAGGCTGCAGTGA
39221	37308	AGGAGTTTGAGGCTGCAGTG
39222	37309	CAGGAGTTTGAGGCTGCAGT
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39224	37311	CCCAGGAGTTTGAGGCTGCA
39225	37312	GCCCAGGAGTTTGAGGCTGC
39226	37313	AGCCCAGGAGTTTGAGGCTG
39227	37314	GAGCCCAGGAGTTTGAGGCT
39228	37315	TGAGCCCAGGAGTTTGAGGC
39229	37316	TTGAGCCCAGGAGTTTGAGG
39230	37317	CTTGAGCCCAGGAGTTTGAG
39231	37318	ACTTGAGCCCAGGAGTTTGA
39232	37319	CACTTGAGCCCAGGAGTTTG
39233	37320	TCACTTGAGCCCAGGAGTTT
39234	37321	TTCACTTGAGCCCAGGAGTT
39235	37322	GTTCACTTGAGCCCAGGAGT
39236	37323	GGTTCACTTGAGCCCAGGAG
39237	37324	AGGTTCACTTGAGCCCAGGA
39238	37325	GAGGTTCACTTGAGCCCAGG
39239	37326	GGAGGTTCACTTGAGCCCAG
39240	37327	GGGAGGTTCACTTGAGCCCA
39241	37328	TGGGAGGTTCACTTGAGCCC
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39243	37330	GATGGGAGGTTCACTTGAGC
39244	37331	AGATGGGAGGTTCACTTGAG
39245	37332	CAGATGGGAGGTTCACTTGA
39246	37333	ACAGATGGGAGGTTCACTTG
39247	37334	TACAGATGGGAGGTTCACTT
39248	37335	CTACAGATGGGAGGTTCACT
39249	37336	GCTACAGATGGGAGGTTCAC
39250	37337	AGCTACAGATGGGAGGTTCA
39251	37338	CAGCTACAGATGGGAGGTTC
39252	37339	CCAGCTACAGATGGGAGGTT
39253	37340	CCCAGCTACAGATGGGAGGT
39254	37341	TCCCAGCTACAGATGGGAGG
39255	37342	GTCCCAGCTACAGATGGGAG
39256	37343	AGTCCCAGCTACAGATGGGA

88333	86420	TGATTCTACTATTTTTAACA
88334	86421	GTGATTCTACTATTTTTAAC
88335	86422	GGTGATTCTACTATTTTTAA
88336	86423	TGGTGATTCTACTATTTTTA
88337	86424	CTGGTGATTCTACTATTTTT
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88339	86426	TCCTGGTGATTCTACTATTT
88340	86427	TTCCTGGTGATTCTACTATT
88341	86428	ATTCCTGGTGATTCTACTAT
88342	86429	AATTCCTGGTGATTCTACTA
88343	86430	CAATTCCTGGTGATTCTACT
88344	86431	CCAATTCCTGGTGATTCTAC
88345	86432	CCCAATTCCTGGTGATTCTA
88346	86433	TCCCAATTCCTGGTGATTCT
88347	86434	TTCCCAATTCCTGGTGATTC
88348	86435	TTTCCCAATTCCTGGTGATT
88349	86436	GTTTCCCAATTCCTGGTGAT
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88353	86440	ATGGGTTTCCCAATTCCTGG
88354	86441	TATGGGTTTCCCAATTCCTG
88355	86442	ATATGGGTTTCCCAATTCCT
88356	86443	AATATGGGTTTCCCAATTCC
88357	86444	AAATATGGGTTTCCCAATTC
88358	86445	AAAATATGGGTTTCCCAATT
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88360	86447	TAAAAATATGGGTTTCCCAA
88361	86448	ATAAAAATATGGGTTTCCCA
88362	86449	AATAAAAATATGGGTTTCCC
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88364	86451	AGAATAAAAATATGGGTTTC
88365	86452	CAGAATAAAAATATGGGTTT
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88367	86454	CCCAGAATAAAAATATGGGT
88368	86455	GCCCAGAATAAAAATATGGG
88369	86456	AGCCCAGAATAAAAATATGG
88370	86457	GAGCCCAGAATAAAAATATG
88371	86458	AGAGCCCAGAATAAAAATAT
88372	86459	TAGAGCCCAGAATAAAAATA
88373	86460	GTAGAGCCCAGAATAAAAAT
88374	86461	GGTAGAGCCCAGAATAAAAA
88375	86462	TGGTAGAGCCCAGAATAAAA
88376	86463	GTGGTAGAGCCCAGAATAAA
88377	86464	AGTGGTAGAGCCCAGAATAA
88378	86465	AAGTGGTAGAGCCCAGAATA
88379	86466	TAAGTGGTAGAGCCCAGAAT
88380	86467	ATAAGTGGTAGAGCCCAGAA
88381	86468	AATAAGTGGTAGAGCCCAGA
88382	86469	GAATAAGTGGTAGAGCCCAG
88383	86470	TGAATAAGTGGTAGAGCCCA
88384	86471	ATGAATAAGTGGTAGAGCCC
88385	86472	GATGAATAAGTGGTAGAGCC
88386	86473	TGATGAATAAGTGGTAGAGC
88387	86474	ATGATGAATAAGTGGTAGAG
88388	86475	TATGATGAATAAGTGGTAGA
88389	86476	ATATGATGAATAAGTGGTAG
88390	86477	TATATGATGAATAAGTGGTA
88391	86478	ATATATGATGAATAAGTGGT
88392	86479	AATATATGATGAATAAGTGG
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88399	86486	TTGCTTTAATATATGATGAA
88400	86487	CTTGCTTTAATATATGATGA
88401	86488	ACTTGCTTTAATATATGATG
88402	86489	GACTTGCTTTAATATATGAT
88403	86490	TGACTTGCTTTAATATATGA

137480	135567	CTTCCTGAGTATTTTAAACC
137481	135568	CCTTCCTGAGTATTTTAAAC
137482	135569	CCCTTCCTGAGTATTTTAAA
137483	135570	GCCCTTCCTGAGTATTTTAA
137484	135571	GGCCCTTCCTGAGTATTTTA
137485	135572	TGGCCCTTCCTGAGTATTTT
137486	135573	CTGGCCCTTCCTGAGTATTT
137487	135574	CCTGGCCCTTCCTGAGTATT
137488	135575	GCCTGGCCCTTCCTGAGTAT
137489	135576	TGCCTGGCCCTTCCTGAGTA
137490	135577	GTGCCTGGCCCTTCCTGAGT
137491	135578	CGTGCCTGGCCCTTCCTGAG
137492	135579	CCGTGCCTGGCCCTTCCTGA
137493	135580	ACCGTGCCTGGCCCTTCCTG
137494	135581	CACCGTGCCTGGCCCTTCCT
137495	135582	CCACCGTGCCTGGCCCTTCC
137496	135583	GCCACCGTGCCTGGCCCTTC
137497	135584	AGCCACCGTGCCTGGCCCTT
137498	135585	GAGCCACCGTGCCTGGCCCT
137499	135586	TGAGCCACCGTGCCTGGCCC
137500	135587	GTGAGCCACCGTGCCTGGCC
137501	135588	TGTGAGCCACCGTGCCTGGC
137502	135589	GTGTGAGCCACCGTGCCTGG
137503	135590	GGTGTGAGCCACCGTGCCTG
137504	135591	AGGTGTGAGCCACCGTGCCT
137505	135592	CAGGTGTGAGCCACCGTGCC
137506	135593	ACAGGTGTGAGCCACCGTGC
137507	135594	TACAGGTGTGAGCCACCGTG
137508	135595	TTACAGGTGTGAGCCACCGT
137509	135596	ATTACAGGTGTGAGCCACCG
137510	135597	GATTACAGGTGTGAGCCACC
137511	135598	GGATTACAGGTGTGAGCCAC
137512	135599	GGGATTACAGGTGTGAGCCA
137513	135600	TGGGATTACAGGTGTGAGCC
137514	135601	CTGGGATTACAGGTGTGAGC
137515	135602	ACTGGGATTACAGGTGTGAG
137516	135603	CACTGGGATTACAGGTGTGA
137517	135604	GCACTGGGATTACAGGTGTG
137518	135605	AGCACTGGGATTACAGGTGT
137519	135606	AAGCACTGGGATTACAGGTG
137520	135607	AAAGCACTGGGATTACAGGT
137521	135608	CAAAGCACTGGGATTACAGG
137522	135609	CCAAAGCACTGGGATTACAG
137523	135610	CCCAAAGCACTGGGATTACA
137524	135611	TCCCAAAGCACTGGGATTAC
137525	135612	CTCCCAAAGCACTGGGATTA
137526	135613	CCTCCCAAAGCACTGGGATT
137527	135614	GCCTCCCAAAGCACTGGGAT
137528	135615	AGCCTCCCAAAGCACTGGGA
137529	135616	CAGCCTCCCAAAGCACTGGG
137530	135617	TCAGCCTCCCAAAGCACTGG
137531	135618	CTCAGCCTCCCAAAGCACTG
137532	135619	CCTCAGCCTCCCAAAGCACT
137533	135620	GCCTCAGCCTCCCAAAGCAC
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137535	135622	CCGCCTCAGCCTCCCAAAGC
137536	135623	CCCGCCTCAGCCTCCCAAAG
137537	135624	ACCCGCCTCAGCCTCCCAAA
137538	135625	CACCCGCCTCAGCCTCCCAA
137539	135626	CCACCCGCCTCAGCCTCCCA
137540	135627	TCCACCCGCCTCAGCCTCCC
137541	135628	ATCCACCCGCCTCAGCCTCC
137542	135629	GATCCACCCGCCTCAGCCTC
137543	135630	TGATCCACCCGCCTCAGCCT
137544	135631	ATGATCCACCCGCCTCAGCC
137545	135632	GATGATCCACCCGCCTCAGC
137546	135633	AGATGATCCACCCGCCTCAG
137547	135634	CAGATGATCCACCCGCCTCA
137548	135635	TCAGATGATCCACCCGCCTC
137549	135636	CTCAGATGATCCACCCGCCT
137550	135637	CCTCAGATGATCCACCCGCC

39257	37344	TAGTCCCAGCTACAGATGGG
39258	37345	GTAGTCCCAGCTACAGATGG
39259	37346	TGTAGTCCCAGCTACAGATG
39260	37347	CTGTAGTCCCAGCTACAGAT
39261	37348	CCTGTAGTCCCAGCTACAGA
39262	37349	GCCTGTAGTCCCAGCTACAG
39263	37350	TGCCTGTAGTCCCAGCTACA
39264	37351	GTGCCTGTAGTCCCAGCTAC
39265	37352	GGTGCCTGTAGTCCCAGCTA
39266	37353	AGGTGCCTGTAGTCCCAGCT
39267	37354	CAGGTGCCTGTAGTCCCAGC
39268	37355	GCAGGTGCCTGTAGTCCCAG
39269	37356	TGCAGGTGCCTGTAGTCCCA
39270	37357	ATGCAGGTGCCTGTAGTCCC
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39272	37359	TTATGCAGGTGCCTGTAGTC
39273	37360	GTTATGCAGGTGCCTGTAGT
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39275	37362	GTGTTATGCAGGTGCCTGTA
39276	37363	GGTGTTATGCAGGTGCCTGT
39277	37364	AGGTGTTATGCAGGTGCCTG
39278	37365	CAGGTGTTATGCAGGTGCCT
39279	37366	TCAGGTGTTATGCAGGTGCC
39280	37367	GTCAGGTGTTATGCAGGTGC
39281	37368	AGTCAGGTGTTATGCAGGTG
39282	37369	CAGTCAGGTGTTATGCAGGT
39283	37370	ACAGTCAGGTGTTATGCAGG
39284	37371	AACAGTCAGGTGTTATGCAG
39285	37372	AAACAGTCAGGTGTTATGCA
39286	37373	AAAACAGTCAGGTGTTATGC
39287	37374	AAAAACAGTCAGGTGTTATG
39288	37375	AAAAAACAGTCAGGTGTTAT
39289	37376	TAAAAAACAGTCAGGTGTTA
39290	37377	TTAAAAAACAGTCAGGTGTT
39291	37378	TTTAAAAAACAGTCAGGTGT
39292	37379	TTTTAAAAAACAGTCAGGTG
39293	37380	GTTTTAAAAAACAGTCAGGT
39294	37381	AGTTTTAAAAAACAGTCAGG
39295	37382	TAGTTTTAAAAAACAGTCAG
39296	37383	ATAGTTTTAAAAAACAGTCA
39297	37384	AATAGTTTTAAAAAACAGTC
39298	37385	AAATAGTTTTAAAAAACAGT
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39300	37387	TAAAATAGTTTTAAAAAACA
39301	37388	CTAAAATAGTTTTAAAAAAC
39302	37389	TCTAAAATAGTTTTAAAAAA
39303	37390	CTCTAAAATAGTTTTAAAAA
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39305	37392	ATCTCTAAAATAGTTTTAAA
39306	37393	CATCTCTAAAATAGTTTTAA
39307	37394	CCATCTCTAAAATAGTTTTA
39308	37395	CCCATCTCTAAAATAGTTTT
39309	37396	CCCCATCTCTAAAATAGTTT
39310	37397	ACCCCATCTCTAAAATAGTT
39311	37398	GACCCCATCTCTAAAATAGT
39312	37399	AGACCCCATCTCTAAAATAG
39313	37400	AAGACCCCATCTCTAAAATA
39314	37401	CAAGACCCCATCTCTAAAAT
39315	37402	GCAAGACCCCATCTCTAAAA
39316	37403	CGCAAGACCCCATCTCTAAA
39317	37404	TCGCAAGACCCCATCTCTAA
39318	37405	TTCGCAAGACCCCATCTCTA
39319	37406	CTTCGCAAGACCCCATCTCT
39320	37407	ACTTCGCAAGACCCCATCTC
39321	37408	AACTTCGCAAGACCCCATCT
39322	37409	CAACTTCGCAAGACCCCATC
39323	37410	GCAACTTCGCAAGACCCCAT
39324	37411	AGCAACTTCGCAAGACCCCA
39325	37412	GAGCAACTTCGCAAGACCCC
39326	37413	TGAGCAACTTCGCAAGACCC
39327	37414	CTGAGCAACTTCGCAAGACC

88404	86491	CTGACTTGCTTTAATATATG
88405	86492	TCTGACTTGCTTTAATATAT
88406	86493	GTCTGACTTGCTTTAATATA
88407	86494	TGTCTGACTTGCTTTAATAT
88408	86495	GTGTCTGACTTGCTTTAATA
88409	86496	AGTGTCTGACTTGCTTTAAT
88410	86497	GAGTGTCTGACTTGCTTTAA
88411	86498	TGAGTGTCTGACTTGCTTTA
88412	86499	ATGAGTGTCTGACTTGCTTT
88413	86500	AATGAGTGTCTGACTTGCTT
88414	86501	GAATGAGTGTCTGACTTGCT
88415	86502	AGAATGAGTGTCTGACTTGC
88416	86503	CAGAATGAGTGTCTGACTTG
88417	86504	TCAGAATGAGTGTCTGACTT
88418	86505	TTCAGAATGAGTGTCTGACT
88419	86506	CTTCAGAATGAGTGTCTGAC
88420	86507	ACTTCAGAATGAGTGTCTGA
88421	86508	AACTTCAGAATGAGTGTCTG
88422	86509	CAACTTCAGAATGAGTGTCT
88423	86510	TCAACTTCAGAATGAGTGTC
88424	86511	CTCAACTTCAGAATGAGTGT
88425	86512	TCTCAACTTCAGAATGAGTG
88426	86513	ATCTCAACTTCAGAATGAGT
88427	86514	AATCTCAACTTCAGAATGAG
88428	86515	AAATCTCAACTTCAGAATGA
88429	86516	GAAATCTCAACTTCAGAATG
88430	86517	CGAAATCTCAACTTCAGAAT
88431	86518	GCGAAATCTCAACTTCAGAA
88432	86519	TGCGAAATCTCAACTTCAGA
88433	86520	CTGCGAAATCTCAACTTCAG
88434	86521	ACTGCGAAATCTCAACTTCA
88435	86522	CACTGCGAAATCTCAACTTC
88436	86523	TCACTGCGAAATCTCAACTT
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88444	86531	CACTTTACTCACTGCGAAAT
88445	86532	ACACTTTACTCACTGCGAAA
88446	86533	AACACTTTACTCACTGCGAA
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88449	86536	ATTAACACTTTACTCACTGC
88450	86537	TATTAACACTTTACTCACTG
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88456	86543	AAGAATTATTAACACTTTAC
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88458	86545	GCAAGAATTATTAACACTTT
88459	86546	GGCAAGAATTATTAACACTT
88460	86547	AGGCAAGAATTATTAACACT
88461	86548	TAGGCAAGAATTATTAACAC
88462	86549	CTAGGCAAGAATTATTAACA
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88465	86552	AGACTAGGCAAGAATTATTA
88466	86553	TAGACTAGGCAAGAATTATT
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88469	86556	ATGTAGACTAGGCAAGAATT
88470	86557	AATGTAGACTAGGCAAGAAT
88471	86558	TAATGTAGACTAGGCAAGAA
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88473	86560	CATAATGTAGACTAGGCAAG
88474	86561	CCATAATGTAGACTAGGCAA

137551	135638	ACCTCAGATGATCCACCCGC
137552	135639	GACCTCAGATGATCCACCCG
137553	135640	TGACCTCAGATGATCCACCC
137554	135641	CTGACCTCAGATGATCCACC
137555	135642	GCTGACCTCAGATGATCCAC
137556	135643	TGCTGACCTCAGATGATCCA
137557	135644	CTGCTGACCTCAGATGATCC
137558	135645	ACTGCTGACCTCAGATGATC
137559	135646	AACTGCTGACCTCAGATGAT
137560	135647	GAACTGCTGACCTCAGATGA
137561	135648	TGAACTGCTGACCTCAGATG
137562	135649	TTGAACTGCTGACCTCAGAT
137563	135650	CTTGAACTGCTGACCTCAGA
137564	135651	TCTTGAACTGCTGACCTCAG
137565	135652	GTCTTGAACTGCTGACCTCA
137566	135653	GGTCTTGAACTGCTGACCTC
137567	135654	TGGTCTTGAACTGCTGACCT
137568	135655	CTGGTCTTGAACTGCTGACC
137569	135656	GCTGGTCTTGAACTGCTGAC
137570	135657	GGCTGGTCTTGAACTGCTGA
137571	135658	AGGCTGGTCTTGAACTGCTG
137572	135659	TAGGCTGGTCTTGAACTGCT
137573	135660	CTAGGCTGGTCTTGAACTGC
137574	135661	GCTAGGCTGGTCTTGAACTG
137575	135662	GGCTAGGCTGGTCTTGAACT
137576	135663	TGGCTAGGCTGGTCTTGAAC
137577	135664	TTGGCTAGGCTGGTCTTGAA
137578	135665	GTTGGCTAGGCTGGTCTTGA
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137580	135667	ATGTTGGCTAGGCTGGTCTT
137581	135668	CATGTTGGCTAGGCTGGTCT
137582	135669	CCATGTTGGCTAGGCTGGTC
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137584	135671	TACCATGTTGGCTAGGCTGG
137585	135672	TTACCATGTTGGCTAGGCTG
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137588	135675	GTTTTACCATGTTGGCTAGG
137589	135676	AGTTTTACCATGTTGGCTAG
137590	135677	GAGTTTTACCATGTTGGCTA
137591	135678	GGAGTTTTACCATGTTGGCT
137592	135679	TGGAGTTTTACCATGTTGGC
137593	135680	ATGGAGTTTTACCATGTTGG
137594	135681	GATGGAGTTTTACCATGTTG
137595	135682	AGATGGAGTTTTACCATGTT
137596	135683	GAGATGGAGTTTTACCATGT
137597	135684	AGAGATGGAGTTTTACCATG
137598	135685	TAGAGATGGAGTTTTACCAT
137599	135686	GTAGAGATGGAGTTTTACCA
137600	135687	AGTAGAGATGGAGTTTTACC
137601	135688	TAGTAGAGATGGAGTTTTAC
137602	135689	TTAGTAGAGATGGAGTTTTA
137603	135690	TTTAGTAGAGATGGAGTTTT
137604	135691	TTTTAGTAGAGATGGAGTTT
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137606	135693	TTTTTTAGTAGAGATGGAGT
137607	135694	ATTTTTTAGTAGAGATGGAG
137608	135695	TATTTTTTAGTAGAGATGGA
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137610	135697	TGTATTTTTTAGTAGAGATG
137611	135698	TTGTATTTTTTAGTAGAGAT
137612	135699	TTTGTATTTTTTAGTAGAGA
137613	135700	TTTTGTATTTTTTAGTAGAG
137614	135701	TTTTTGTATTTTTTAGTAGA
137615	135702	ATTTTTGTATTTTTTAGTAG
137616	135703	GATTTTTGTATTTTTTAGTA
137617	135704	TGATTTTTGTATTTTTTAGT
137618	135705	CTGATTTTTGTATTTTTTAG
137619	135706	GCTGATTTTTGTATTTTTTA
137620	135707	GGCTGATTTTTGTATTTTTT
137621	135708	TGGCTGATTTTTGTATTTTT

39328	37415	CCTGAGCAACTTCGCAAGAC
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39330	37417	ATCCTGAGCAACTTCGCAAG
39331	37418	CATCCTGAGCAACTTCGCAA
39332	37419	CCATCCTGAGCAACTTCGCA
39333	37420	ACCATCCTGAGCAACTTCGC
39334	37421	GACCATCCTGAGCAACTTCG
39335	37422	AGACCATCCTGAGCAACTTC
39336	37423	AAGACCATCCTGAGCAACTT
39337	37424	CAAGACCATCCTGAGCAACT
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39342	37429	GAGTTCAAGACCATCCTGAG
39343	37430	GGAGTTCAAGACCATCCTGA
39344	37431	CGGAGTTCAAGACCATCCTG
39345	37432	CCGGAGTTCAAGACCATCCT
39346	37433	CCCGGAGTTCAAGACCATCC
39347	37434	ACCCGGAGTTCAAGACCATC
39348	37435	GACCCGGAGTTCAAGACCAT
39349	37436	AGACCCGGAGTTCAAGACCA
39350	37437	AAGACCCGGAGTTCAAGACC
39351	37438	TAAGACCCGGAGTTCAAGAC
39352	37439	TTAAGACCCGGAGTTCAAGA
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39356	37443	CCACTTAAGACCCGGAGTTC
39357	37444	ACCACTTAAGACCCGGAGTT
39358	37445	GACCACTTAAGACCCGGAGT
39359	37446	GGACCACTTAAGACCCGGAG
39360	37447	AGGACCACTTAAGACCCGGA
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39363	37450	AGAAGGACCACTTAAGACCC
39364	37451	CAGAAGGACCACTTAAGACC
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39367	37454	AGGCAGAAGGACCACTTAAG
39368	37455	GAGGCAGAAGGACCACTTAA
39369	37456	TGAGGCAGAAGGACCACTTA
39370	37457	CTGAGGCAGAAGGACCACTT
39371	37458	GCTGAGGCAGAAGGACCACT
39372	37459	GGCTGAGGCAGAAGGACCAC
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39374	37461	GAGGCTGAGGCAGAAGGACC
39375	37462	AGAGGCTGAGGCAGAAGGAC
39376	37463	CAGAGGCTGAGGCAGAAGGA
39377	37464	CCAGAGGCTGAGGCAGAAGG
39378	37465	TCCAGAGGCTGAGGCAGAAG
39379	37466	ATCCAGAGGCTGAGGCAGAA
39380	37467	AATCCAGAGGCTGAGGCAGA
39381	37468	TAATCCAGAGGCTGAGGCAG
39382	37469	CTAATCCAGAGGCTGAGGCA
39383	37470	ACTAATCCAGAGGCTGAGGC
39384	37471	AACTAATCCAGAGGCTGAGG
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39386	37473	CCAACTAATCCAGAGGCTGA
39387	37474	GCCAACTAATCCAGAGGCTG
39388	37475	TGCCAACTAATCCAGAGGCT
39389	37476	ATGCCAACTAATCCAGAGGC
39390	37477	AATGCCAACTAATCCAGAGG
39391	37478	TAATGCCAACTAATCCAGAG
39392	37479	GTAATGCCAACTAATCCAGA
39393	37480	TGTAATGCCAACTAATCCAG
39394	37481	CTGTAATGCCAACTAATCCA
39395	37482	CCTGTAATGCCAACTAATCC
39396	37483	GCCTGTAATGCCAACTAATC
39397	37484	TGCCTGTAATGCCAACTAAT
39398	37485	ATGCCTGTAATGCCAACTAA

88475	86562	CCCATAATGTAGACTAGGCA
88476	86563	TCCCATAATGTAGACTAGGC
88477	86564	ATCCCATAATGTAGACTAGG
88478	86565	AATCCCATAATGTAGACTAG
88479	86566	CAATCCCATAATGTAGACTA
88480	86567	ACAATCCCATAATGTAGACT
88481	86568	CACAATCCCATAATGTAGAC
88482	86569	TCACAATCCCATAATGTAGA
88483	86570	ATCACAATCCCATAATGTAG
88484	86571	CATCACAATCCCATAATGTA
88485	86572	TCATCACAATCCCATAATGT
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88495	86582	TATAGGAATCTCATCACAAT
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88497	86584	CTTATAGGAATCTCATCACA
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88499	86586	ACCTTATAGGAATCTCATCA
88500	86587	AACCTTATAGGAATCTCATC
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88506	86593	TTTATGAACCTTATAGGAAT
88507	86594	ATTTATGAACCTTATAGGAA
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88515	86602	ATATCTGTATTTATGAACCT
88516	86603	TATATCTGTATTTATGAACC
88517	86604	ATATATCTGTATTTATGAAC
88518	86605	AATATATCTGTATTTATGAA
88519	86606	CAATATATCTGTATTTATGA
88520	86607	ACAATATATCTGTATTTATG
88521	86608	TACAATATATCTGTATTTAT
88522	86609	TTACAATATATCTGTATTTA
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88525	86612	GTTTTACAATATATCTGTAT
88526	86613	AGTTTTACAATATATCTGTA
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88536	86623	AAAACTTTATAGTTTTACAA
88537	86624	CAAAACTTTATAGTTTTACA
88538	86625	ACAAAACTTTATAGTTTTAC
88539	86626	TACAAAACTTTATAGTTTTA
88540	86627	TTACAAAACTTTATAGTTTT
88541	86628	TTTACAAAACTTTATAGTTT
88542	86629	CTTTACAAAACTTTATAGTT
88543	86630	ACTTTACAAAACTTTATAGT
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88545	86632	GTACTTTACAAAACTTTATA

137622	135709	ATGGCTGATTTTTGTATTTT
137623	135710	CATGGCTGATTTTTGTATTT
137624	135711	GCATGGCTGATTTTTGTATT
137625	135712	TGCATGGCTGATTTTTGTAT
137626	135713	ATGCATGGCTGATTTTTGTA
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137628	135715	GCATGCATGGCTGATTTTTG
137629	135716	AGCATGCATGGCTGATTTTT
137630	135717	CAGCATGCATGGCTGATTTT
137631	135718	CCAGCATGCATGGCTGATTT
137632	135719	GCCAGCATGCATGGCTGATT
137633	135720	TGCCAGCATGCATGGCTGAT
137634	135721	ATGCCAGCATGCATGGCTGA
137635	135722	CATGCCAGCATGCATGGCTG
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137637	135724	CGCATGCCAGCATGCATGGC
137638	135725	GCGCATGCCAGCATGCATGG
137639	135726	GGCGCATGCCAGCATGCATG
137640	135727	AGGCGCATGCCAGCATGCAT
137641	135728	TAGGCGCATGCCAGCATGCA
137642	135729	ATAGGCGCATGCCAGCATGC
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137644	135731	TTATAGGCGCATGCCAGCAT
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137646	135733	GATTATAGGCGCATGCCAGC
137647	135734	AGATTATAGGCGCATGCCAG
137648	135735	GAGATTATAGGCGCATGCCA
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137650	135737	CTGAGATTATAGGCGCATGC
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137652	135739	AGCTGAGATTATAGGCGCAT
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137658	135745	CCTAGTAGCTGAGATTATAG
137659	135746	CCCTAGTAGCTGAGATTATA
137660	135747	TCCCTAGTAGCTGAGATTAT
137661	135748	CTCCCTAGTAGCTGAGATTA
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137663	135750	GCCTCCCTAGTAGCTGAGAT
137664	135751	AGCCTCCCTAGTAGCTGAGA
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137666	135753	TCAGCCTCCCTAGTAGCTGA
137667	135754	CTCAGCCTCCCTAGTAGCTG
137668	135755	TCTCAGCCTCCCTAGTAGCT
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137674	135761	CTCCTGTCTCAGCCTCCCTA
137675	135762	TCTCCTGTCTCAGCCTCCCT
137676	135763	TTCTCCTGTCTCAGCCTCCC
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137678	135765	AATTCTCCTGTCTCAGCCTC
137679	135766	CAATTCTCCTGTCTCAGCCT
137680	135767	GCAATTCTCCTGTCTCAGCC
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137685	135772	TTCAAGCAATTCTCCTGTCT
137686	135773	GTTCAAGCAATTCTCCTGTC
137687	135774	AGTTCAAGCAATTCTCCTGT
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137689	135776	CAAGTTCAAGCAATTCTCCT
137690	135777	CCAAGTTCAAGCAATTCTCC
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39399	37486	CATGCCTGTAATGCCAACTA
39400	37487	TCATGCCTGTAATGCCAACT
39401	37488	CTCATGCCTGTAATGCCAAC
39402	37489	GCTCATGCCTGTAATGCCAA
39403	37490	GGCTCATGCCTGTAATGCCA
39404	37491	TGGCTCATGCCTGTAATGCC
39405	37492	ATGGCTCATGCCTGTAATGC
39406	37493	AATGGCTCATGCCTGTAATG
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39408	37495	ACAATGGCTCATGCCTGTAA
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39411	37498	GGTACAATGGCTCATGCCTG
39412	37499	AGGTACAATGGCTCATGCCT
39413	37500	CAGGTACAATGGCTCATGCC
39414	37501	CCAGGTACAATGGCTCATGC
39415	37502	GCCAGGTACAATGGCTCATG
39416	37503	TGCCAGGTACAATGGCTCAT
39417	37504	TTGCCAGGTACAATGGCTCA
39418	37505	CTTGCCAGGTACAATGGCTC
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39420	37507	CACTTGCCAGGTACAATGGC
39421	37508	GCACTTGCCAGGTACAATGG
39422	37509	TGCACTTGCCAGGTACAATG
39423	37510	ATGCACTTGCCAGGTACAAT
39424	37511	TATGCACTTGCCAGGTACAA
39425	37512	ATATGCACTTGCCAGGTACA
39426	37513	AATATGCACTTGCCAGGTAC
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39430	37517	AGAAAATATGCACTTGCCAG
39431	37518	AAGAAAATATGCACTTGCCA
39432	37519	AAAGAAAATATGCACTTGCC
39433	37520	AAAAGAAAATATGCACTTGC
39434	37521	AAAAAGAAAATATGCACTTG
39435	37522	AAAAAAGAAAATATGCACTT
39436	37523	AAAAAAAGAAAATATGCACT
39437	37524	AAAAAAAAGAAAATATGCAC
39438	37525	AAAAAAAAAGAAAATATGCA
39439	37526	AAAAAAAAAAGAAAATATGC
39440	37527	AAAAAAAAAAAGAAAATATG
39441	37528	AAAAAAAAAAAAGAAAATAT
39442	37529	AAAAAAAAAAAAAGAAAATA
39443	37530	TAAAAAAAAAAAAAGAAAAT
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39451	37538	CTCCACCTTAAAAAAAAAAA
39452	37539	ACTCCACCTTAAAAAAAAAA
39453	37540	GACTCCACCTTAAAAAAAAA
39454	37541	AGACTCCACCTTAAAAAAAA
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39456	37543	CGAGACTCCACCTTAAAAAA
39457	37544	TCGAGACTCCACCTTAAAAA
39458	37545	CTCGAGACTCCACCTTAAAA
39459	37546	CCTCGAGACTCCACCTTAAA
39460	37547	GCCTCGAGACTCCACCTTAA
39461	37548	GGCCTCGAGACTCCACCTTA
39462	37549	CGGCCTCGAGACTCCACCTT
39463	37550	CCGGCCTCGAGACTCCACCT
39464	37551	CCCGGCCTCGAGACTCCACC
39465	37552	GCCCGGCCTCGAGACTCCAC
39466	37553	CGCCCGGCCTCGAGACTCCA
39467	37554	GCGCCCGGCCTCGAGACTCC
39468	37555	TGCGCCCGGCCTCGAGACTC
39469	37556	CTGCGCCCGGCCTCGAGACT

88546	86633	GGTACTTTACAAAACTTTAT
88547	86634	AGGTACTTTACAAAACTTTA
88548	86635	GAGGTACTTTACAAAACTTT
88549	86636	AGAGGTACTTTACAAAACTT
88550	86637	GAGAGGTACTTTACAAAACT
88551	86638	AGAGAGGTACTTTACAAAAC
88552	86639	TAGAGAGGTACTTTACAAAA
88553	86640	TTAGAGAGGTACTTTACAAA
88554	86641	ATTAGAGAGGTACTTTACAA
88555	86642	TATTAGAGAGGTACTTTACA
88556	86643	ATATTAGAGAGGTACTTTAC
88557	86644	CATATTAGAGAGGTACTTTA
88558	86645	TCATATTAGAGAGGTACTTT
88559	86646	CTCATATTAGAGAGGTACTT
88560	86647	CCTCATATTAGAGAGGTACT
88561	86648	GCCTCATATTAGAGAGGTAC
88562	86649	TGCCTCATATTAGAGAGGTA
88563	86650	TTGCCTCATATTAGAGAGGT
88564	86651	TTTGCCTCATATTAGAGAGG
88565	86652	GTTTGCCTCATATTAGAGAG
88566	86653	TGTTTGCCTCATATTAGAGA
88567	86654	GTGTTTGCCTCATATTAGAG
88568	86655	TGTGTTTGCCTCATATTAGA
88569	86656	CTGTGTTTGCCTCATATTAG
88570	86657	ACTGTGTTTGCCTCATATTA
88571	86658	TACTGTGTTTGCCTCATATT
88572	86659	ATACTGTGTTTGCCTCATAT
88573	86660	CATACTGTGTTTGCCTCATA
88574	86661	ACATACTGTGTTTGCCTCAT
88575	86662	TACATACTGTGTTTGCCTCA
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88578	86665	TGTTACATACTGTGTTTGCC
88579	86666	GTGTTACATACTGTGTTTGC
88580	86667	AGTGTTACATACTGTGTTTG
88581	86668	TAGTGTTACATACTGTGTTT
88582	86669	ATAGTGTTACATACTGTGTT
88583	86670	AATAGTGTTACATACTGTGT
88584	86671	AAATAGTGTTACATACTGTG
88585	86672	CAAATAGTGTTACATACTGT
88586	86673	CCAAATAGTGTTACATACTG
88587	86674	TCCAAATAGTGTTACATACT
88588	86675	CTCCAAATAGTGTTACATAC
88589	86676	CCTCCAAATAGTGTTACATA
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88592	86679	GTCCCTCCAAATAGTGTTAC
88593	86680	GGTCCCTCCAAATAGTGTTA
88594	86681	CGGTCCCTCCAAATAGTGTT
88595	86682	ACGGTCCCTCCAAATAGTGT
88596	86683	TACGGTCCCTCCAAATAGTG
88597	86684	ATACGGTCCCTCCAAATAGT
88598	86685	AATACGGTCCCTCCAAATAG
88599	86686	AAATACGGTCCCTCCAAATA
88600	86687	GAAATACGGTCCCTCCAAAT
88601	86688	GGAAATACGGTCCCTCCAAA
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88603	86690	AAGGAAATACGGTCCCTCCA
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88605	86692	ATAAGGAAATACGGTCCCTC
88606	86693	GATAAGGAAATACGGTCCCT
88607	86694	AGATAAGGAAATACGGTCCC
88608	86695	AAGATAAGGAAATACGGTCC
88609	86696	AAAGATAAGGAAATACGGTC
88610	86697	AAAAGATAAGGAAATACGGT
88611	86698	AAAAAGATAAGGAAATACGG
88612	86699	TAAAAAGATAAGGAAATACG
88613	86700	CTAAAAAGATAAGGAAATAC
88614	86701	GCTAAAAAGATAAGGAAATA
88615	86702	TGCTAAAAAGATAAGGAAAT
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137693	135780	CTCCCAAGTTCAAGCAATTC
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137695	135782	GCCTCCCAAGTTCAAGCAAT
137696	135783	TGCCTCCCAAGTTCAAGCAA
137697	135784	CTGCCTCCCAAGTTCAAGCA
137698	135785	TCTGCCTCCCAAGTTCAAGC
137699	135786	CTCTGCCTCCCAAGTTCAAG
137700	135787	CCTCTGCCTCCCAAGTTCAA
137701	135788	ACCTCTGCCTCCCAAGTTCA
137702	135789	AACCTCTGCCTCCCAAGTTC
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137706	135793	CTGCAACCTCTGCCTCCCAA
137707	135794	ACTGCAACCTCTGCCTCCCA
137708	135795	CACTGCAACCTCTGCCTCCC
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137710	135797	CTCACTGCAACCTCTGCCTC
137711	135798	GCTCACTGCAACCTCTGCCT
137712	135799	GGCTCACTGCAACCTCTGCC
137713	135800	CGGCTCACTGCAACCTCTGC
137714	135801	TCGGCTCACTGCAACCTCTG
137715	135802	TTCGGCTCACTGCAACCTCT
137716	135803	CTTCGGCTCACTGCAACCTC
137717	135804	ACTTCGGCTCACTGCAACCT
137718	135805	GACTTCGGCTCACTGCAACC
137719	135806	CGACTTCGGCTCACTGCAAC
137720	135807	ACGACTTCGGCTCACTGCAA
137721	135808	CACGACTTCGGCTCACTGCA
137722	135809	GCACGACTTCGGCTCACTGC
137723	135810	GGCACGACTTCGGCTCACTG
137724	135811	TGGCACGACTTCGGCTCACT
137725	135812	GTGGCACGACTTCGGCTCAC
137726	135813	AGTGGCACGACTTCGGCTCA
137727	135814	GAGTGGCACGACTTCGGCTC
137728	135815	GGAGTGGCACGACTTCGGCT
137729	135816	TGGAGTGGCACGACTTCGGC
137730	135817	GTGGAGTGGCACGACTTCGG
137731	135818	AGTGGAGTGGCACGACTTCG
137732	135819	GAGTGGAGTGGCACGACTTC
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137735	135822	CTGGAGTGGAGTGGCACGAC
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137737	135824	GGCTGGAGTGGAGTGGCACG
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137741	135828	CCCAGGCTGGAGTGGAGTGG
137742	135829	ACCCAGGCTGGAGTGGAGTG
137743	135830	CACCCAGGCTGGAGTGGAGT
137744	135831	CCACCCAGGCTGGAGTGGAG
137745	135832	GCCACCCAGGCTGGAGTGGA
137746	135833	TGCCACCCAGGCTGGAGTGG
137747	135834	CTGCCACCCAGGCTGGAGTG
137748	135835	TCTGCCACCCAGGCTGGAGT
137749	135836	CTCTGCCACCCAGGCTGGAG
137750	135837	GCTCTGCCACCCAGGCTGGA
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137754	135841	TTTCGCTCTGCCACCCAGGC
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137756	135843	AATTTCGCTCTGCCACCCAG
137757	135844	GAATTTCGCTCTGCCACCCA
137758	135845	AGAATTTCGCTCTGCCACCC
137759	135846	CAGAATTTCGCTCTGCCACC
137760	135847	ACAGAATTTCGCTCTGCCAC
137761	135848	GACAGAATTTCGCTCTGCCA
137762	135849	AGACAGAATTTCGCTCTGCC
137763	135850	GAGACAGAATTTCGCTCTGC

39470	37557	ACTGCGCCCGGCCTCGAGAC
39471	37558	CACTGCGCCCGGCCTCGAGA
39472	37559	CCACTGCGCCCGGCCTCGAG
39473	37560	GCCACTGCGCCCGGCCTCGA
39474	37561	AGCCACTGCGCCCGGCCTCG
39475	37562	GAGCCACTGCGCCCGGCCTC
39476	37563	TGAGCCACTGCGCCCGGCCT
39477	37564	GTGAGCCACTGCGCCCGGCC
39478	37565	TGTGAGCCACTGCGCCCGGC
39479	37566	GTGTGAGCCACTGCGCCCGG
39480	37567	GGTGTGAGCCACTGCGCCCG
39481	37568	AGGTGTGAGCCACTGCGCCC
39482	37569	CAGGTGTGAGCCACTGCGCC
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39516	37603	CCACCCACCTCGGCCTTCCA
39517	37604	TCCACCCACCTCGGCCTTCC
39518	37605	ATCCACCCACCTCGGCCTTC
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39520	37607	TGATCCACCCACCTCGGCCT
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39525	37612	CCTCTTGATCCACCCACCTC
39526	37613	ACCTCTTGATCCACCCACCT
39527	37614	GACCTCTTGATCCACCCACC
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39529	37616	CTGACCTCTTGATCCACCCA
39530	37617	CCTGACCTCTTGATCCACCC
39531	37618	TCCTGACCTCTTGATCCACC
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39533	37620	TCTCCTGACCTCTTGATCCA
39534	37621	ATCTCCTGACCTCTTGATCC
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88617	86704	GCTGCTAAAAAGATAAGGAA
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88630	86717	ACTGATAAACAAAGCTGCTA
88631	86718	TACTGATAAACAAAGCTGCT
88632	86719	GTACTGATAAACAAAGCTGC
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88635	86722	AATGTACTGATAAACAAAGC
88636	86723	GAATGTACTGATAAACAAAG
88637	86724	AGAATGTACTGATAAACAAA
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88639	86726	ATAGAATGTACTGATAAACA
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88644	86731	TGTTTATAGAATGTACTGAT
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88670	86757	ACACTACAATGTAAGCCAAA
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88675	86762	GAAACACACTACAATGTAAG
88676	86763	AGAAACACACTACAATGTAA
88677	86764	TAGAAACACACTACAATGTA
88678	86765	ATAGAAACACACTACAATGT
88679	86766	TATAGAAACACACTACAATG
88680	86767	CTATAGAAACACACTACAAT
88681	86768	GCTATAGAAACACACTACAA
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88684	86771	GATGCTATAGAAACACACTA
88685	86772	AGATGCTATAGAAACACACT
88686	86773	CAGATGCTATAGAAACACAC
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137764	135851	TGAGACAGAATTTCGCTCTG
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137766	135853	TTTGAGACAGAATTTCGCTC
137767	135854	TTTTGAGACAGAATTTCGCT
137768	135855	TTTTTGAGACAGAATTTCGC
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137770	135857	ATTTTTTGAGACAGAATTTC
137771	135858	TATTTTTTGAGACAGAATTT
137772	135859	TTATTTTTTGAGACAGAATT
137773	135860	TTTATTTTTTGAGACAGAAT
137774	135861	TTTTATTTTTTGAGACAGAA
137775	135862	ATTTTATTTTTTGAGACAGA
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137777	135864	ATATTTTATTTTTTGAGACA
137778	135865	AATATTTTATTTTTTGAGAC
137779	135866	GAATATTTTATTTTTTGAGA
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137782	135869	CCTGAATATTTTATTTTTTG
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137789	135876	TCTGCTTCCTGAATATTTTA
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137791	135878	GGTCTGCTTCCTGAATATTT
137792	135879	GGGTCTGCTTCCTGAATATT
137793	135880	GGGGTCTGCTTCCTGAATAT
137794	135881	AGGGGTCTGCTTCCTGAATA
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137796	135883	TGAGGGGTCTGCTTCCTGAA
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137807	135894	TCAAGATATCCTGAGGGGTC
137808	135895	CTCAAGATATCCTGAGGGGT
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137810	135897	AGCTCAAGATATCCTGAGGG
137811	135898	AAGCTCAAGATATCCTGAGG
137812	135899	TAAGCTCAAGATATCCTGAG
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137815	135902	GCTTAAGCTCAAGATATCCT
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137823	135910	GATCTCTTGCTTAAGCTCAA
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137830	135917	AGGTCATGATCTCTTGCTTA
137831	135918	GAGGTCATGATCTCTTGCTT
137832	135919	AGAGGTCATGATCTCTTGCT
137833	135920	GAGAGGTCATGATCTCTTGC
137834	135921	TGAGAGGTCATGATCTCTTG

39541	37628	GGTCTCGATCTCCTGACCTC
39542	37629	TGGTCTCGATCTCCTGACCT
39543	37630	ATGGTCTCGATCTCCTGACC
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39545	37632	GGATGGTCTCGATCTCCTGA
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39547	37634	CAGGATGGTCTCGATCTCCT
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39552	37639	TTAGCCAGGATGGTCTCGAT
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39561	37648	TTCACCATGTTAGCCAGGAT
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39568	37655	ACAGGGTTTCACCATGTTAG
39569	37656	GACAGGGTTTCACCATGTTA
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39573	37660	TAGAGACAGGGTTTCACCAT
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39575	37662	AGTAGAGACAGGGTTTCACC
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39577	37664	TTAGTAGAGACAGGGTTTCA
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39579	37666	TTTTAGTAGAGACAGGGTTT
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39582	37669	TATTTTTAGTAGAGACAGGG
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39585	37672	TTGTATTTTTAGTAGAGACA
39586	37673	TTTGTATTTTTAGTAGAGAC
39587	37674	TTTTGTATTTTTAGTAGAGA
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39589	37676	TTTTTTGTATTTTTAGTAGA
39590	37677	ATTTTTTGTATTTTTAGTAG
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39594	37681	GTTAATTTTTTGTATTTTTA
39595	37682	AGTTAATTTTTTGTATTTTT
39596	37683	CAGTTAATTTTTTGTATTTT
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39598	37685	CCCAGTTAATTTTTTGTATT
39599	37686	GCCCAGTTAATTTTTTGTAT
39600	37687	TGCCCAGTTAATTTTTTGTA
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88688	86775	TACAGATGCTATAGAAACAC
88689	86776	ATACAGATGCTATAGAAACA
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88701	86788	AATTAGTGCCATATACAGAT
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88704	86791	GGGAATTAGTGCCATATACA
88705	86792	TGGGAATTAGTGCCATATAC
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88709	86796	TAGTTGGGAATTAGTGCCAT
88710	86797	ATAGTTGGGAATTAGTGCCA
88711	86798	TATAGTTGGGAATTAGTGCC
88712	86799	ATATAGTTGGGAATTAGTGC
88713	86800	AATATAGTTGGGAATTAGTG
88714	86801	AAATATAGTTGGGAATTAGT
88715	86802	GAAATATAGTTGGGAATTAG
88716	86803	GGAAATATAGTTGGGAATTA
88717	86804	TGGAAATATAGTTGGGAATT
88718	86805	ATGGAAATATAGTTGGGAAT
88719	86806	TATGGAAATATAGTTGGGAA
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88721	86808	ATTATGGAAATATAGTTGGG
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88723	86810	TTATTATGGAAATATAGTTG
88724	86811	CTTATTATGGAAATATAGTT
88725	86812	CCTTATTATGGAAATATAGT
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88727	86814	TTCCTTATTATGGAAATATA
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88729	86816	TATTCCTTATTATGGAAATA
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88740	86827	TTTGTATTTGATATTCCTTA
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88742	86829	TATTTGTATTTGATATTCCT
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88744	86831	TTTATTTGTATTTGATATTC
88745	86832	CTTTATTTGTATTTGATATT
88746	86833	CCTTTATTTGTATTTGATAT
88747	86834	CCCTTTATTTGTATTTGATA
88748	86835	ACCCTTTATTTGTATTTGAT
88749	86836	GACCCTTTATTTGTATTTGA
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88751	86838	TGGACCCTTTATTTGTATTT
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88754	86841	ACTTGGACCCTTTATTTGTA
88755	86842	AACTTGGACCCTTTATTTGT
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137837	135924	ACCTGAGAGGTCATGATCTC
137838	135925	GACCTGAGAGGTCATGATCT
137839	135926	TGACCTGAGAGGTCATGATC
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137842	135929	TAATGACCTGAGAGGTCATG
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137848	135935	CCAAGATAATGACCTGAGAG
137849	135936	TCCAAGATAATGACCTGAGA
137850	135937	GTCCAAGATAATGACCTGAG
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137856	135943	TGTGCTGTCCAAGATAATGA
137857	135944	CTGTGCTGTCCAAGATAATG
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137859	135946	ACCTGTGCTGTCCAAGATAA
137860	135947	GACCTGTGCTGTCCAAGATA
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137862	135949	GGGACCTGTGCTGTCCAAGA
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137864	135951	AGGGGACCTGTGCTGTCCAA
137865	135952	GAGGGGACCTGTGCTGTCCA
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137900	135987	GAGCAACTATTTCTGTACTT
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39615	37702	AGGCGTGTGCCACCATGCCC
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39619	37706	CTACAGGCGTGTGCCACCAT
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39623	37710	GGGACTACAGGCGTGTGCCA
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88784	86871	AGCATATTCCTTATGCTAAT
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88787	86874	GTCAGCATATTCCTTATGCT
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88817	86904	CAGCCTAATTTTTATACTTT
88818	86905	CCAGCCTAATTTTTATACTT
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88820	86907	ACCCAGCCTAATTTTTATAC
88821	86908	CACCCAGCCTAATTTTTATA
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88823	86910	CACACCCAGCCTAATTTTTA
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88825	86912	ACCACACCCAGCCTAATTTT
88826	86913	CACCACACCCAGCCTAATTT
88827	86914	CCACCACACCCAGCCTAATT
88828	86915	GCCACCACACCCAGCCTAAT
88829	86916	AGCCACCACACCCAGCCTAA

137906	135993	ATGAAGGAGCAACTATTTCT
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137909	135996	TCCATGAAGGAGCAACTATT
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137912	135999	TTCTCCATGAAGGAGCAACT
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137930	136017	GAAAGCTCTGCCCAGACTTT
137931	136018	AGAAAGCTCTGCCCAGACTT
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137934	136021	AGAAGAAAGCTCTGCCCAGA
137935	136022	CAGAAGAAAGCTCTGCCCAG
137936	136023	CCAGAAGAAAGCTCTGCCCA
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137945	136032	AGTTCATTTCCAGAAGAAAG
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137968	136055	AAATAGGAAAAATGTACCTT
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39696	37783	CATGATCTTGACTCACTGCA
39697	37784	GCATGATCTTGACTCACTGC
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39705	37792	GTGCAGTGGCATGATCTTGA
39706	37793	AGTGCAGTGGCATGATCTTG
39707	37794	GAGTGCAGTGGCATGATCTT
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88830	86917	GAGCCACCACACCCAGCCTA
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88834	86921	GCGTGAGCCACCACACCCAG
88835	86922	GGCGTGAGCCACCACACCCA
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88878	86965	TTGTGATCCGCCCACCTCAG
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88880	86967	CCTTGTGATCCGCCCACCTC
88881	86968	ACCTTGTGATCCGCCCACCT
88882	86969	GACCTTGTGATCCGCCCACC
88883	86970	TGACCTTGTGATCCGCCCAC
88884	86971	CTGACCTTGTGATCCGCCCA
88885	86972	CCTGACCTTGTGATCCGCCC
88886	86973	TCCTGACCTTGTGATCCGCC
88887	86974	CTCCTGACCTTGTGATCCGC
88888	86975	TCTCCTGACCTTGTGATCCG
88889	86976	ATCTCCTGACCTTGTGATCC
88890	86977	GATCTCCTGACCTTGTGATC
88891	86978	CGATCTCCTGACCTTGTGAT
88892	86979	TCGATCTCCTGACCTTGTGA
88893	86980	CTCGATCTCCTGACCTTGTG
88894	86981	TCTCGATCTCCTGACCTTGT
88895	86982	GTCTCGATCTCCTGACCTTG
88896	86983	GGTCTCGATCTCCTGACCTT
88897	86984	TGGTCTCGATCTCCTGACCT
88898	86985	ATGGTCTCGATCTCCTGACC
88899	86986	GATGGTCTCGATCTCCTGAC
88900	86987	GGATGGTCTCGATCTCCTGA

137977	136064	TTGCCCTACAAATAGGAAAA
137978	136065	ATTGCCCTACAAATAGGAAA
137979	136066	AATTGCCCTACAAATAGGAA
137980	136067	AAATTGCCCTACAAATAGGA
137981	136068	CAAATTGCCCTACAAATAGG
137982	136069	ACAAATTGCCCTACAAATAG
137983	136070	TACAAATTGCCCTACAAATA
137984	136071	TTACAAATTGCCCTACAAAT
137985	136072	TTTACAAATTGCCCTACAAA
137986	136073	TTTTACAAATTGCCCTACAA
137987	136074	TTTTTACAAATTGCCCTACA
137988	136075	ATTTTTACAAATTGCCCTAC
137989	136076	TATTTTTACAAATTGCCCTA
137990	136077	TTATTTTTACAAATTGCCCT
137991	136078	CTTATTTTTACAAATTGCCC
137992	136079	CCTTATTTTTACAAATTGCC
137993	136080	CCCTTATTTTTACAAATTGC
137994	136081	GCCCTTATTTTTACAAATTG
137995	136082	GGCCCTTATTTTTACAAATT
137996	136083	CGGCCCTTATTTTTACAAAT
137997	136084	CCGGCCCTTATTTTTACAAA
137998	136085	TCCGGCCCTTATTTTTACAA
137999	136086	GTCCGGCCCTTATTTTTACA
138000	136087	CGTCCGGCCCTTATTTTTAC
138001	136088	ACGTCCGGCCCTTATTTTTA
138002	136089	CACGTCCGGCCCTTATTTTT
138003	136090	CCACGTCCGGCCCTTATTTT
138004	136091	ACCACGTCCGGCCCTTATTT
138005	136092	CACCACGTCCGGCCCTTATT
138006	136093	CCACCACGTCCGGCCCTTAT
138007	136094	GCCACCACGTCCGGCCCTTA
138008	136095	AGCCACCACGTCCGGCCCTT
138009	136096	GAGCCACCACGTCCGGCCCT
138010	136097	TGAGCCACCACGTCCGGCCC
138011	136098	GTGAGCCACCACGTCCGGCC
138012	136099	CGTGAGCCACCACGTCCGGC
138013	136100	GCGTGAGCCACCACGTCCGG
138014	136101	GGCGTGAGCCACCACGTCCG
138015	136102	AGGCGTGAGCCACCACGTCC
138016	136103	CAGGCGTGAGCCACCACGTC
138017	136104	ACAGGCGTGAGCCACCACGT
138018	136105	TACAGGCGTGAGCCACCACG
138019	136106	TTACAGGCGTGAGCCACCAC
138020	136107	ATTACAGGCGTGAGCCACCA
138021	136108	GATTACAGGCGTGAGCCACC
138022	136109	GGATTACAGGCGTGAGCCAC
138023	136110	GGGATTACAGGCGTGAGCCA
138024	136111	TGGGATTACAGGCGTGAGCC
138025	136112	CTGGGATTACAGGCGTGAGC
138026	136113	ACTGGGATTACAGGCGTGAG
138027	136114	TACTGGGATTACAGGCGTGA
138028	136115	GTACTGGGATTACAGGCGTG
138029	136116	AGTACTGGGATTACAGGCGT
138030	136117	AAGTACTGGGATTACAGGCG
138031	136118	AAAGTACTGGGATTACAGGC
138032	136119	CAAAGTACTGGGATTACAGG
138033	136120	CCAAAGTACTGGGATTACAG
138034	136121	CCCAAAGTACTGGGATTACA
138035	136122	TCCCAAAGTACTGGGATTAC
138036	136123	CTCCCAAAGTACTGGGATTA
138037	136124	CCTCCCAAAGTACTGGGATT
138038	136125	GCCTCCCAAAGTACTGGGAT
138039	136126	GGCCTCCCAAAGTACTGGGA
138040	136127	CGGCCTCCCAAAGTACTGGG
138041	136128	TCGGCCTCCCAAAGTACTGG
138042	136129	CTCGGCCTCCCAAAGTACTG
138043	136130	CCTCGGCCTCCCAAAGTACT
138044	136131	ACCTCGGCCTCCCAAAGTAC
138045	136132	CACCTCGGCCTCCCAAAGTA
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138047	136134	CCCACCTCGGCCTCCCAAAG

39754	37841	TCTTTCTGTTTTTTTTGAGA
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39756	37843	CGTCTTTCTGTTTTTTTTGA
39757	37844	CCGTCTTTCTGTTTTTTTTG
39758	37845	TCCGTCTTTCTGTTTTTTTT
39759	37846	CTCCGTCTTTCTGTTTTTTT
39760	37847	ACTCCGTCTTTCTGTTTTTT
39761	37848	GACTCCGTCTTTCTGTTTTT
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39765	37852	GCAAGACTCCGTCTTTCTGT
39766	37853	AGCAAGACTCCGTCTTTCTG
39767	37854	GAGCAAGACTCCGTCTTTCT
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39769	37856	CAGAGCAAGACTCCGTCTTT
39770	37857	ACAGAGCAAGACTCCGTCTT
39771	37858	GACAGAGCAAGACTCCGTCT
39772	37859	TGACAGAGCAAGACTCCGTC
39773	37860	GTGACAGAGCAAGACTCCGT
39774	37861	GGTGACAGAGCAAGACTCCG
39775	37862	GGGTGACAGAGCAAGACTCC
39776	37863	TGGGTGACAGAGCAAGACTC
39777	37864	CTGGGTGACAGAGCAAGACT
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39794	37881	TGCCACTGCAATGCAGCCTG
39795	37882	ATGCCACTGCAATGCAGCCT
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39803	37890	CGGAGTTCATGCCACTGCAA
39804	37891	GCGGAGTTCATGCCACTGCA
39805	37892	GGCGGAGTTCATGCCACTGC
39806	37893	AGGCGGAGTTCATGCCACTG
39807	37894	GAGGCGGAGTTCATGCCACT
39808	37895	GGAGGCGGAGTTCATGCCAC
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39813	37900	ACTCAGGAGGCGGAGTTCAT
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39815	37902	GAACTCAGGAGGCGGAGTTC
39816	37903	TGAACTCAGGAGGCGGAGTT
39817	37904	TTGAACTCAGGAGGCGGAGT
39818	37905	CTTGAACTCAGGAGGCGGAG
39819	37906	GCTTGAACTCAGGAGGCGGA
39820	37907	TGCTTGAACTCAGGAGGCGG
39821	37908	TTGCTTGAACTCAGGAGGCG
39822	37909	ATTGCTTGAACTCAGGAGGC
39823	37910	AATTGCTTGAACTCAGGAGG
39824	37911	GAATTGCTTGAACTCAGGAG

88901	86988	AGGATGGTCTCGATCTCCTG
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88904	86991	GCCAGGATGGTCTCGATCTC
88905	86992	AGCCAGGATGGTCTCGATCT
88906	86993	TAGCCAGGATGGTCTCGATC
88907	86994	TTAGCCAGGATGGTCTCGAT
88908	86995	GTTAGCCAGGATGGTCTCGA
88909	86996	TGTTAGCCAGGATGGTCTCG
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88912	86999	CCGTGTTAGCCAGGATGGTC
88913	87000	ACCGTGTTAGCCAGGATGGT
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88915	87002	TCACCGTGTTAGCCAGGATG
88916	87003	TTCACCGTGTTAGCCAGGAT
88917	87004	TTTCACCGTGTTAGCCAGGA
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88924	87011	GACGGGGTTTCACCGTGTTA
88925	87012	GGACGGGGTTTCACCGTGTT
88926	87013	GGGACGGGGTTTCACCGTGT
88927	87014	AGGGACGGGGTTTCACCGTG
88928	87015	TAGGGACGGGGTTTCACCGT
88929	87016	GTAGGGACGGGGTTTCACCG
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88936	87023	ACTTTTAGTAGGGACGGGGT
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88942	87029	TTTTGTACTTTTAGTAGGGA
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88944	87031	TTTTTTGTACTTTTAGTAGG
88945	87032	TTTTTTTGTACTTTTAGTAG
88946	87033	TTTTTTTTGTACTTTTAGTA
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88948	87035	AATTTTTTTTGTACTTTTAG
88949	87036	TAATTTTTTTTGTACTTTTA
88950	87037	CTAATTTTTTTTGTACTTTT
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88952	87039	GGCTAATTTTTTTTGTACTT
88953	87040	CGGCTAATTTTTTTTGTACT
88954	87041	CCGGCTAATTTTTTTTGTAC
88955	87042	CCCGGCTAATTTTTTTTGTA
88956	87043	GCCCGGCTAATTTTTTTTGT
88957	87044	TGCCCGGCTAATTTTTTTTG
88958	87045	ATGCCCGGCTAATTTTTTTT
88959	87046	CATGCCCGGCTAATTTTTTT
88960	87047	CCATGCCCGGCTAATTTTTT
88961	87048	ACCATGCCCGGCTAATTTTT
88962	87049	CACCATGCCCGGCTAATTTT
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88964	87051	GCCACCATGCCCGGCTAATT
88965	87052	CGCCACCATGCCCGGCTAAT
88966	87053	CCGCCACCATGCCCGGCTAA
88967	87054	CCCGCCACCATGCCCGGCTA
88968	87055	ACCCGCCACCATGCCCGGCT
88969	87056	CACCCGCCACCATGCCCGGC
88970	87057	GCACCCGCCACCATGCCCGG
88971	87058	GGCACCCGCCACCATGCCCG

138048	136135	ACCCACCTCGGCCTCCCAAA
138049	136136	CACCCACCTCGGCCTCCCAA
138050	136137	CCACCCACCTCGGCCTCCCA
138051	136138	TCCACCCACCTCGGCCTCCC
138052	136139	ATCCACCCACCTCGGCCTCC
138053	136140	AATCCACCCACCTCGGCCTC
138054	136141	CAATCCACCCACCTCGGCCT
138055	136142	GCAATCCACCCACCTCGGCC
138056	136143	AGCAATCCACCCACCTCGGC
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138058	136145	CAAGCAATCCACCCACCTCG
138059	136146	TCAAGCAATCCACCCACCTC
138060	136147	CTCAAGCAATCCACCCACCT
138061	136148	CCTCAAGCAATCCACCCACC
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138063	136150	GGCCTCAAGCAATCCACCCA
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138067	136154	TCCTGGCCTCAAGCAATCCA
138068	136155	CTCCTGGCCTCAAGCAATCC
138069	136156	ACTCCTGGCCTCAAGCAATC
138070	136157	AACTCCTGGCCTCAAGCAAT
138071	136158	GAACTCCTGGCCTCAAGCAA
138072	136159	CGAACTCCTGGCCTCAAGCA
138073	136160	TCGAACTCCTGGCCTCAAGC
138074	136161	CTCGAACTCCTGGCCTCAAG
138075	136162	TCTCGAACTCCTGGCCTCAA
138076	136163	TTCTCGAACTCCTGGCCTCA
138077	136164	GTTCTCGAACTCCTGGCCTC
138078	136165	TGTTCTCGAACTCCTGGCCT
138079	136166	CTGTTCTCGAACTCCTGGCC
138080	136167	GCTGTTCTCGAACTCCTGGC
138081	136168	GGCTGTTCTCGAACTCCTGG
138082	136169	AGGCTGTTCTCGAACTCCTG
138083	136170	CAGGCTGTTCTCGAACTCCT
138084	136171	CCAGGCTGTTCTCGAACTCC
138085	136172	GCCAGGCTGTTCTCGAACTC
138086	136173	GGCCAGGCTGTTCTCGAACT
138087	136174	TGGCCAGGCTGTTCTCGAAC
138088	136175	TTGGCCAGGCTGTTCTCGAA
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138093	136180	CCATGTTGGCCAGGCTGTTC
138094	136181	ACCATGTTGGCCAGGCTGTT
138095	136182	CACCATGTTGGCCAGGCTGT
138096	136183	TCACCATGTTGGCCAGGCTG
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138098	136185	TTTCACCATGTTGGCCAGGC
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138101	136188	GGGTTTCACCATGTTGGCCA
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138114	136201	CTTGGTAGAGATAGGGTTTC
138115	136202	CTTTGGTAGAGATAGGGTTT
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138117	136204	TGCTTTGGTAGAGATAGGGT
138118	136205	ATGCTTTGGTAGAGATAGGG

39825	37912	AGAATTGCTTGAACTCAGGA
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39827	37914	CAAGAATTGCTTGAACTCAG
39828	37915	ACAAGAATTGCTTGAACTCA
39829	37916	CACAAGAATTGCTTGAACTC
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39837	37924	GGCTGAGGCACAAGAATTGC
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39843	37930	TTGGGAGGCTGAGGCACAAG
39844	37931	CTTGGGAGGCTGAGGCACAA
39845	37932	ACTTGGGAGGCTGAGGCACA
39846	37933	TACTTGGGAGGCTGAGGCAC
39847	37934	CTACTTGGGAGGCTGAGGCA
39848	37935	GCTACTTGGGAGGCTGAGGC
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39856	37943	TAATCCCAGCTACTTGGGAG
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39874	37961	TGTGGTGGCACATGTCTGTA
39875	37962	GTGTGGTGGCACATGTCTGT
39876	37963	CGTGTGGTGGCACATGTCTG
39877	37964	ACGTGTGGTGGCACATGTCT
39878	37965	CACGTGTGGTGGCACATGTC
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88972	87059	AGGCACCCGCCACCATGCCC
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88975	87062	TACAGGCACCCGCCACCATG
88976	87063	CTACAGGCACCCGCCACCAT
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88978	87065	GACTACAGGCACCCGCCACC
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88980	87067	GGGACTACAGGCACCCGCCA
88981	87068	TGGGACTACAGGCACCCGCC
88982	87069	CTGGGACTACAGGCACCCGC
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88984	87071	AGCTGGGACTACAGGCACCC
88985	87072	TAGCTGGGACTACAGGCACC
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88987	87074	AGTAGCTGGGACTACAGGCA
88988	87075	AAGTAGCTGGGACTACAGGC
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88991	87078	CCCAAGTAGCTGGGACTACA
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88994	87081	CCTCCCAAGTAGCTGGGACT
88995	87082	GCCTCCCAAGTAGCTGGGAC
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88997	87084	CAGCCTCCCAAGTAGCTGGG
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89010	87097	CATTCTCCTGCCTCAGCCTC
89011	87098	CCATTCTCCTGCCTCAGCCT
89012	87099	GCCATTCTCCTGCCTCAGCC
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89014	87101	ATGCCATTCTCCTGCCTCAG
89015	87102	CATGCCATTCTCCTGCCTCA
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89018	87105	GTTCATGCCATTCTCCTGCC
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89023	87110	CCCGAGTTCATGCCATTCTC
89024	87111	TCCCGAGTTCATGCCATTCT
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89026	87113	CTTCCCGAGTTCATGCCATT
89027	87114	GCTTCCCGAGTTCATGCCAT
89028	87115	CGCTTCCCGAGTTCATGCCA
89029	87116	CCGCTTCCCGAGTTCATGCC
89030	87117	TCCGCTTCCCGAGTTCATGC
89031	87118	CTCCGCTTCCCGAGTTCATG
89032	87119	GCTCCGCTTCCCGAGTTCAT
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89034	87121	AAGCTCCGCTTCCCGAGTTC
89035	87122	CAAGCTCCGCTTCCCGAGTT
89036	87123	GCAAGCTCCGCTTCCCGAGT
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89038	87125	CTGCAAGCTCCGCTTCCCGA
89039	87126	ACTGCAAGCTCCGCTTCCCG
89040	87127	AACTGCAAGCTCCGCTTCCC
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138119	136206	CATGCTTTGGTAGAGATAGG
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138121	136208	ACCATGCTTTGGTAGAGATA
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138127	136214	CGTGCCACCATGCTTTGGTA
138128	136215	GCGTGCCACCATGCTTTGGT
138129	136216	TGCGTGCCACCATGCTTTGG
138130	136217	GTGCGTGCCACCATGCTTTG
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138132	136219	AGGTGCGTGCCACCATGCTT
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138134	136221	ACAGGTGCGTGCCACCATGC
138135	136222	TACAGGTGCGTGCCACCATG
138136	136223	CTACAGGTGCGTGCCACCAT
138137	136224	ACTACAGGTGCGTGCCACCA
138138	136225	GACTACAGGTGCGTGCCACC
138139	136226	GGACTACAGGTGCGTGCCAC
138140	136227	GGGACTACAGGTGCGTGCCA
138141	136228	TGGGACTACAGGTGCGTGCC
138142	136229	CTGGGACTACAGGTGCGTGC
138143	136230	GCTGGGACTACAGGTGCGTG
138144	136231	AGCTGGGACTACAGGTGCGT
138145	136232	TAGCTGGGACTACAGGTGCG
138146	136233	GTAGCTGGGACTACAGGTGC
138147	136234	AGTAGCTGGGACTACAGGTG
138148	136235	AAGTAGCTGGGACTACAGGT
138149	136236	CAAGTAGCTGGGACTACAGG
138150	136237	CCAAGTAGCTGGGACTACAG
138151	136238	CCCAAGTAGCTGGGACTACA
138152	136239	TCCCAAGTAGCTGGGACTAC
138153	136240	CTCCCAAGTAGCTGGGACTA
138154	136241	CCTCCCAAGTAGCTGGGACT
138155	136242	GCCTCCCAAGTAGCTGGGAC
138156	136243	CGCCTCCCAAGTAGCTGGGA
138157	136244	CCGCCTCCCAAGTAGCTGGG
138158	136245	TCCGCCTCCCAAGTAGCTGG
138159	136246	CTCCGCCTCCCAAGTAGCTG
138160	136247	CCTCCGCCTCCCAAGTAGCT
138161	136248	GCCTCCGCCTCCCAAGTAGC
138162	136249	TGCCTCCGCCTCCCAAGTAG
138163	136250	GTGCCTCCGCCTCCCAAGTA
138164	136251	TGTGCCTCCGCCTCCCAAGT
138165	136252	TTGTGCCTCCGCCTCCCAAG
138166	136253	CTTGTGCCTCCGCCTCCCAA
138167	136254	TCTTGTGCCTCCGCCTCCCA
138168	136255	CTCTTGTGCCTCCGCCTCCC
138169	136256	ACTCTTGTGCCTCCGCCTCC
138170	136257	AACTCTTGTGCCTCCGCCTC
138171	136258	GAACTCTTGTGCCTCCGCCT
138172	136259	GGAACTCTTGTGCCTCCGCC
138173	136260	TGGAACTCTTGTGCCTCCGC
138174	136261	ATGGAACTCTTGTGCCTCCG
138175	136262	CATGGAACTCTTGTGCCTCC
138176	136263	TCATGGAACTCTTGTGCCTC
138177	136264	TTCATGGAACTCTTGTGCCT
138178	136265	GTTCATGGAACTCTTGTGCC
138179	136266	GGTTCATGGAACTCTTGTGC
138180	136267	GGGTTCATGGAACTCTTGTG
138181	136268	AGGGTTCATGGAACTCTTGT
138182	136269	CAGGGTTCATGGAACTCTTG
138183	136270	CCAGGGTTCATGGAACTCTT
138184	136271	TCCAGGGTTCATGGAACTCT
138185	136272	CTCCAGGGTTCATGGAACTC
138186	136273	CCTCCAGGGTTCATGGAACT
138187	136274	ACCTCCAGGGTTCATGGAAC
138188	136275	CACCTCCAGGGTTCATGGAA
138189	136276	CCACCTCCAGGGTTCATGGA

39896	37983	AAAACTATAAAAATTAGCCA
39897	37984	TAAAACTATAAAAATTAGCC
39898	37985	CTAAAACTATAAAAATTAGC
39899	37986	ACTAAAACTATAAAAATTAG
39900	37987	TACTAAAACTATAAAAATTA
39901	37988	CTACTAAAACTATAAAAATT
39902	37989	TCTACTAAAACTATAAAAAT
39903	37990	CTCTACTAAAACTATAAAAA
39904	37991	CCTCTACTAAAACTATAAAA
39905	37992	ACCTCTACTAAAACTATAAA
39906	37993	CACCTCTACTAAAACTATAA
39907	37994	CCACCTCTACTAAAACTATA
39908	37995	TCCACCTCTACTAAAACTAT
39909	37996	CTCCACCTCTACTAAAACTA
39910	37997	ACTCCACCTCTACTAAAACT
39911	37998	AACTCCACCTCTACTAAAAC
39912	37999	AAACTCCACCTCTACTAAAA
39913	38000	GAAACTCCACCTCTACTAAA
39914	38001	TGAAACTCCACCTCTACTAA
39915	38002	GTGAAACTCCACCTCTACTA
39916	38003	GGTGAAACTCCACCTCTACT
39917	38004	TGGTGAAACTCCACCTCTAC
39918	38005	ATGGTGAAACTCCACCTCTA
39919	38006	CATGGTGAAACTCCACCTCT
39920	38007	ACATGGTGAAACTCCACCTC
39921	38008	AACATGGTGAAACTCCACCT
39922	38009	CAACATGGTGAAACTCCACC
39923	38010	CCAACATGGTGAAACTCCAC
39924	38011	GCCAACATGGTGAAACTCCA
39925	38012	AGCCAACATGGTGAAACTCC
39926	38013	TAGCCAACATGGTGAAACTC
39927	38014	CTAGCCAACATGGTGAAACT
39928	38015	CCTAGCCAACATGGTGAAAC
39929	38016	GCCTAGCCAACATGGTGAAA
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39931	38018	CAGCCTAGCCAACATGGTGA
39932	38019	CCAGCCTAGCCAACATGGTG
39933	38020	ACCAGCCTAGCCAACATGGT
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39935	38022	AGACCAGCCTAGCCAACATG
39936	38023	AAGACCAGCCTAGCCAACAT
39937	38024	CAAGACCAGCCTAGCCAACA
39938	38025	TCAAGACCAGCCTAGCCAAC
39939	38026	TTCAAGACCAGCCTAGCCAA
39940	38027	GTTCAAGACCAGCCTAGCCA
39941	38028	AGTTCAAGACCAGCCTAGCC
39942	38029	GAGTTCAAGACCAGCCTAGC
39943	38030	GGAGTTCAAGACCAGCCTAG
39944	38031	AGGAGTTCAAGACCAGCCTA
39945	38032	CAGGAGTTCAAGACCAGCCT
39946	38033	TCAGGAGTTCAAGACCAGCC
39947	38034	GTCAGGAGTTCAAGACCAGC
39948	38035	AGTCAGGAGTTCAAGACCAG
39949	38036	AAGTCAGGAGTTCAAGACCA
39950	38037	GAAGTCAGGAGTTCAAGACC
39951	38038	TGAAGTCAGGAGTTCAAGAC
39952	38039	CTGAAGTCAGGAGTTCAAGA
39953	38040	CCTGAAGTCAGGAGTTCAAG
39954	38041	ACCTGAAGTCAGGAGTTCAA
39955	38042	CACCTGAAGTCAGGAGTTCA
39956	38043	TCACCTGAAGTCAGGAGTTC
39957	38044	ATCACCTGAAGTCAGGAGTT
39958	38045	GATCACCTGAAGTCAGGAGT
39959	38046	GGATCACCTGAAGTCAGGAG
39960	38047	TGGATCACCTGAAGTCAGGA
39961	38048	GTGGATCACCTGAAGTCAGG
39962	38049	GGTGGATCACCTGAAGTCAG
39963	38050	GGGTGGATCACCTGAAGTCA
39964	38051	CGGGTGGATCACCTGAAGTC
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39966	38053	GGCGGGTGGATCACCTGAAG

89043	87130	GCTAACTGCAAGCTCCGCTT
89044	87131	AGCTAACTGCAAGCTCCGCT
89045	87132	CAGCTAACTGCAAGCTCCGC
89046	87133	TCAGCTAACTGCAAGCTCCG
89047	87134	CTCAGCTAACTGCAAGCTCC
89048	87135	TCTCAGCTAACTGCAAGCTC
89049	87136	ATCTCAGCTAACTGCAAGCT
89050	87137	GATCTCAGCTAACTGCAAGC
89051	87138	TGATCTCAGCTAACTGCAAG
89052	87139	GTGATCTCAGCTAACTGCAA
89053	87140	CGTGATCTCAGCTAACTGCA
89054	87141	GCGTGATCTCAGCTAACTGC
89055	87142	GGCGTGATCTCAGCTAACTG
89056	87143	TGGCGTGATCTCAGCTAACT
89057	87144	ATGGCGTGATCTCAGCTAAC
89058	87145	AATGGCGTGATCTCAGCTAA
89059	87146	CAATGGCGTGATCTCAGCTA
89060	87147	GCAATGGCGTGATCTCAGCT
89061	87148	TGCAATGGCGTGATCTCAGC
89062	87149	GTGCAATGGCGTGATCTCAG
89063	87150	AGTGCAATGGCGTGATCTCA
89064	87151	GAGTGCAATGGCGTGATCTC
89065	87152	GGAGTGCAATGGCGTGATCT
89066	87153	TGGAGTGCAATGGCGTGATC
89067	87154	CTGGAGTGCAATGGCGTGAT
89068	87155	GCTGGAGTGCAATGGCGTGA
89069	87156	TGCTGGAGTGCAATGGCGTG
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89074	87161	GCCCATGCTGGAGTGCAATG
89075	87162	TGCCCATGCTGGAGTGCAAT
89076	87163	TTGCCCATGCTGGAGTGCAA
89077	87164	GTTGCCCATGCTGGAGTGCA
89078	87165	TGTTGCCCATGCTGGAGTGC
89079	87166	CTGTTGCCCATGCTGGAGTG
89080	87167	TCTGTTGCCCATGCTGGAGT
89081	87168	CTCTGTTGCCCATGCTGGAG
89082	87169	GCTCTGTTGCCCATGCTGGA
89083	87170	TGCTCTGTTGCCCATGCTGG
89084	87171	TTGCTCTGTTGCCCATGCTG
89085	87172	CTTGCTCTGTTGCCCATGCT
89086	87173	TCTTGCTCTGTTGCCCATGC
89087	87174	GTCTTGCTCTGTTGCCCATG
89088	87175	AGTCTTGCTCTGTTGCCCAT
89089	87176	GAGTCTTGCTCTGTTGCCCA
89090	87177	AGAGTCTTGCTCTGTTGCCC
89091	87178	CAGAGTCTTGCTCTGTTGCC
89092	87179	ACAGAGTCTTGCTCTGTTGC
89093	87180	GACAGAGTCTTGCTCTGTTG
89094	87181	AGACAGAGTCTTGCTCTGTT
89095	87182	GAGACAGAGTCTTGCTCTGT
89096	87183	TGAGACAGAGTCTTGCTCTG
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89098	87185	TTTGAGACAGAGTCTTGCTC
89099	87186	TTTTGAGACAGAGTCTTGCT
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89103	87190	TTTTTTTTGAGACAGAGTCT
89104	87191	TTTTTTTTTGAGACAGAGTC
89105	87192	TTTTTTTTTTGAGACAGAGT
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89107	87194	TTTTTTTTTTTTGAGACAGA
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89109	87196	TTTTTTTTTTTTTTGAGACA
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89111	87198	TTTTTTTTTTTTTTTTGAGA
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89113	87200	TTTTTTTTTTTTTTTTTTGA

138190	136277	TCCACCTCCAGGGTTCATGG
138191	136278	CTCCACCTCCAGGGTTCATG
138192	136279	CCTCCACCTCCAGGGTTCAT
138193	136280	ACCTCCACCTCCAGGGTTCA
138194	136281	AACCTCCACCTCCAGGGTTC
138195	136282	CAACCTCCACCTCCAGGGTT
138196	136283	GCAACCTCCACCTCCAGGGT
138197	136284	TGCAACCTCCACCTCCAGGG
138198	136285	CTGCAACCTCCACCTCCAGG
138199	136286	ACTGCAACCTCCACCTCCAG
138200	136287	CACTGCAACCTCCACCTCCA
138201	136288	TCACTGCAACCTCCACCTCC
138202	136289	CTCACTGCAACCTCCACCTC
138203	136290	GCTCACTGCAACCTCCACCT
138204	136291	AGCTCACTGCAACCTCCACC
138205	136292	CAGCTCACTGCAACCTCCAC
138206	136293	TCAGCTCACTGCAACCTCCA
138207	136294	CTCAGCTCACTGCAACCTCC
138208	136295	TCTCAGCTCACTGCAACCTC
138209	136296	ATCTCAGCTCACTGCAACCT
138210	136297	AATCTCAGCTCACTGCAACC
138211	136298	CAATCTCAGCTCACTGCAAC
138212	136299	ACAATCTCAGCTCACTGCAA
138213	136300	TACAATCTCAGCTCACTGCA
138214	136301	GTACAATCTCAGCTCACTGC
138215	136302	GGTACAATCTCAGCTCACTG
138216	136303	TGGTACAATCTCAGCTCACT
138217	136304	GTGGTACAATCTCAGCTCAC
138218	136305	AGTGGTACAATCTCAGCTCA
138219	136306	CAGTGGTACAATCTCAGCTC
138220	136307	GCAGTGGTACAATCTCAGCT
138221	136308	TGCAGTGGTACAATCTCAGC
138222	136309	GTGCAGTGGTACAATCTCAG
138223	136310	AGTGCAGTGGTACAATCTCA
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138225	136312	TGAGTGCAGTGGTACAATCT
138226	136313	CTGAGTGCAGTGGTACAATC
138227	136314	CCTGAGTGCAGTGGTACAAT
138228	136315	GCCTGAGTGCAGTGGTACAA
138229	136316	GGCCTGAGTGCAGTGGTACA
138230	136317	AGGCCTGAGTGCAGTGGTAC
138231	136318	CAGGCCTGAGTGCAGTGGTA
138232	136319	CCAGGCCTGAGTGCAGTGGT
138233	136320	CCCAGGCCTGAGTGCAGTGG
138234	136321	GCCCAGGCCTGAGTGCAGTG
138235	136322	TGCCCAGGCCTGAGTGCAGT
138236	136323	TTGCCCAGGCCTGAGTGCAG
138237	136324	GTTGCCCAGGCCTGAGTGCA
138238	136325	TGTTGCCCAGGCCTGAGTGC
138239	136326	CTGTTGCCCAGGCCTGAGTG
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138241	136328	CTCTGTTGCCCAGGCCTGAG
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138243	136330	CTCTCTGTTGCCCAGGCCTG
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138245	136332	CTCTCTCTGTTGCCCAGGCC
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138253	136340	GACAGAGTCTCTCTCTGTTG
138254	136341	AGACAGAGTCTCTCTCTGTT
138255	136342	GAGACAGAGTCTCTCTCTGT
138256	136343	TGAGACAGAGTCTCTCTCTG
138257	136344	TTGAGACAGAGTCTCTCTCT
138258	136345	TTTGAGACAGAGTCTCTCTC
138259	136346	TTTTGAGACAGAGTCTCTCT
138260	136347	ATTTTGAGACAGAGTCTCTC

39967	38054	AGGCGGGTGGATCACCTGAA
39968	38055	AAGGCGGGTGGATCACCTGA
39969	38056	CAAGGCGGGTGGATCACCTG
39970	38057	CCAAGGCGGGTGGATCACCT
39971	38058	GCCAAGGCGGGTGGATCACC
39972	38059	GGCCAAGGCGGGTGGATCAC
39973	38060	AGGCCAAGGCGGGTGGATCA
39974	38061	GAGGCCAAGGCGGGTGGATC
39975	38062	AGAGGCCAAGGCGGGTGGAT
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39977	38064	CAAGAGGCCAAGGCGGGTGG
39978	38065	TCAAGAGGCCAAGGCGGGTG
39979	38066	TTCAAGAGGCCAAGGCGGGT
39980	38067	CTTCAAGAGGCCAAGGCGGG
39981	38068	ACTTCAAGAGGCCAAGGCGG
39982	38069	CACTTCAAGAGGCCAAGGCG
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39985	38072	CACCACTTCAAGAGGCCAAG
39986	38073	CCACCACTTCAAGAGGCCAA
39987	38074	CCCACCACTTCAAGAGGCCA
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39989	38076	ATCCCACCACTTCAAGAGGC
39990	38077	AATCCCACCACTTCAAGAGG
39991	38078	TAATCCCACCACTTCAAGAG
39992	38079	ATAATCCCACCACTTCAAGA
39993	38080	CATAATCCCACCACTTCAAG
39994	38081	TCATAATCCCACCACTTCAA
39995	38082	CTCATAATCCCACCACTTCA
39996	38083	ACTCATAATCCCACCACTTC
39997	38084	CACTCATAATCCCACCACTT
39998	38085	ACACTCATAATCCCACCACT
39999	38086	CACACTCATAATCCCACCAC
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40001	38088	CTCACACTCATAATCCCACC
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40012	38099	GGGCACAGTGGCTCACACTC
40013	38100	TGGGCACAGTGGCTCACACT
40014	38101	CTGGGCACAGTGGCTCACAC
40015	38102	GCTGGGCACAGTGGCTCACA
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40017	38104	TGGCTGGGCACAGTGGCTCA
40018	38105	TTGGCTGGGCACAGTGGCTC
40019	38106	CTTGGCTGGGCACAGTGGCT
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40026	38113	ATACTCACTTGGCTGGGCAC
40027	38114	AATACTCACTTGGCTGGGCA
40028	38115	AAATACTCACTTGGCTGGGC
40029	38116	CAAATACTCACTTGGCTGGG
40030	38117	GCAAATACTCACTTGGCTGG
40031	38118	AGCAAATACTCACTTGGCTG
40032	38119	AAGCAAATACTCACTTGGCT
40033	38120	TAAGCAAATACTCACTTGGC
40034	38121	ATAAGCAAATACTCACTTGG
40035	38122	CATAAGCAAATACTCACTTG
40036	38123	ACATAAGCAAATACTCACTT
40037	38124	TACATAAGCAAATACTCACT

89114	87201	TTTTTTTTTTTTTTTTTTG
89115	87202	TTTTTTTTTTTTTTTTTT
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89118	87205	ACTTTTTTTTTTTTTTTTT
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89127	87214	AGTTTTTAAACTTTTTTTT
89128	87215	TAGTTTTTAAACTTTTTTT
89129	87216	CTAGTTTTTAAACTTTTTT
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89131	87218	GTCTAGTTTTTAAACTTTT
89132	87219	CGTCTAGTTTTTAAACTTT
89133	87220	ACGTCTAGTTTTTAAACTT
89134	87221	AACGTCTAGTTTTTAAACTT
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89137	87224	GTCAACGTCTAGTTTTTAAA
89138	87225	TGTCAACGTCTAGTTTTTAA
89139	87226	ATGTCAACGTCTAGTTTTTA
89140	87227	CATGTCAACGTCTAGTTTTT
89141	87228	TCATGTCAACGTCTAGTTTT
89142	87229	ATCATGTCAACGTCTAGTTT
89143	87230	AATCATGTCAACGTCTAGTT
89144	87231	AAATCATGTCAACGTCTAGT
89145	87232	AAAATCATGTCAACGTCTAG
89146	87233	TAAAATCATGTCAACGTCTA
89147	87234	GTAAAATCATGTCAACGTCT
89148	87235	TGTAAAATCATGTCAACGTC
89149	87236	TTGTAAAATCATGTCAACGT
89150	87237	ATTGTAAAATCATGTCAACG
89151	87238	TATTGTAAAATCATGTCAAC
89152	87239	TTATTGTAAAATCATGTCAA
89153	87240	CTTATTGTAAAATCATGTCA
89154	87241	CCTTATTGTAAAATCATGTC
89155	87242	GCCTTATTGTAAAATCATGT
89156	87243	AGCCTTATTGTAAAATCATG
89157	87244	CAGCCTTATTGTAAAATCAT
89158	87245	TCAGCCTTATTGTAAAATCA
89159	87246	GTCAGCCTTATTGTAAAATC
89160	87247	AGTCAGCCTTATTGTAAAAT
89161	87248	CAGTCAGCCTTATTGTAAAA
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89164	87251	AAGCAGTCAGCCTTATTGTA
89165	87252	AAAGCAGTCAGCCTTATTGT
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89170	87257	TAGCAAAAGCAGTCAGCCTT
89171	87258	GTAGCAAAAGCAGTCAGCCT
89172	87259	AGTAGCAAAAGCAGTCAGCC
89173	87260	AAGTAGCAAAAGCAGTCAGC
89174	87261	AAAGTAGCAAAAGCAGTCAG
89175	87262	CAAAGTAGCAAAAGCAGTCA
89176	87263	GCAAAGTAGCAAAAGCAGTC
89177	87264	GGCAAAGTAGCAAAAGCAGT
89178	87265	TGGCAAAGTAGCAAAAGCAG
89179	87266	TTGGCAAAGTAGCAAAAGCA
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89181	87268	GATTGGCAAAGTAGCAAAAG
89182	87269	TGATTGGCAAAGTAGCAAAA
89183	87270	CTGATTGGCAAAGTAGCAAA
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138261	136348	TATTTTGAGACAGAGTCTCT
138262	136349	TTATTTTGAGACAGAGTCTC
138263	136350	TTTATTTTGAGACAGAGTCT
138264	136351	TTTTATTTTGAGACAGAGTC
138265	136352	TTTTTATTTTGAGACAGAGT
138266	136353	TTTTTTATTTTGAGACAGAG
138267	136354	ATTTTTTATTTTGAGACAGA
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138269	136356	TTATTTTTTATTTTGAGACA
138270	136357	TTTATTTTTTATTTTGAGAC
138271	136358	TTTTATTTTTTATTTTGAGA
138272	136359	TTTTTATTTTTTATTTTGAG
138273	136360	ATTTTTATTTTTTATTTTGA
138274	136361	TATTTTTATTTTTTATTTTG
138275	136362	TTATTTTTATTTTTTATTTT
138276	136363	CTTATTTTTATTTTTTATTT
138277	136364	CCTTATTTTTATTTTTTATT
138278	136365	GCCTTATTTTTATTTTTTAT
138279	136366	AGCCTTATTTTTATTTTTTA
138280	136367	TAGCCTTATTTTTATTTTTT
138281	136368	CTAGCCTTATTTTTATTTTT
138282	136369	ACTAGCCTTATTTTTATTTT
138283	136370	GACTAGCCTTATTTTTATTT
138284	136371	AGACTAGCCTTATTTTTATT
138285	136372	AAGACTAGCCTTATTTTTAT
138286	136373	CAAGACTAGCCTTATTTTTA
138287	136374	CCAAGACTAGCCTTATTTTT
138288	136375	TCCAAGACTAGCCTTATTTT
138289	136376	GTCCAAGACTAGCCTTATTT
138290	136377	AGTCCAAGACTAGCCTTATT
138291	136378	AAGTCCAAGACTAGCCTTAT
138292	136379	AAAGTCCAAGACTAGCCTTA
138293	136380	CAAAGTCCAAGACTAGCCTT
138294	136381	CCAAAGTCCAAGACTAGCCT
138295	136382	ACCAAAGTCCAAGACTAGCC
138296	136383	TACCAAAGTCCAAGACTAGC
138297	136384	ATACCAAAGTCCAAGACTAG
138298	136385	AATACCAAAGTCCAAGACTA
138299	136386	AAATACCAAAGTCCAAGACT
138300	136387	TAAATACCAAAGTCCAAGAC
138301	136388	TTAAATACCAAAGTCCAAGA
138302	136389	TTTAAATACCAAAGTCCAAG
138303	136390	ATTTAAATACCAAAGTCCAA
138304	136391	TATTTAAATACCAAAGTCCA
138305	136392	CTATTTAAATACCAAAGTCC
138306	136393	CCTATTTAAATACCAAAGTC
138307	136394	TCCTATTTAAATACCAAAGT
138308	136395	TTCCTATTTAAATACCAAAG
138309	136396	CTTCCTATTTAAATACCAAA
138310	136397	CCTTCCTATTTAAATACCAA
138311	136398	TCCTTCCTATTTAAATACCA
138312	136399	CTCCTTCCTATTTAAATACC
138313	136400	ACTCCTTCCTATTTAAATAC
138314	136401	TACTCCTTCCTATTTAAATA
138315	136402	GTACTCCTTCCTATTTAAAT
138316	136403	AGTACTCCTTCCTATTTAAA
138317	136404	TAGTACTCCTTCCTATTTAA
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138319	136406	ATTAGTACTCCTTCCTATTT
138320	136407	TATTAGTACTCCTTCCTATT
138321	136408	ATATTAGTACTCCTTCCTAT
138322	136409	AATATTAGTACTCCTTCCTA
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138324	136411	CAAATATTAGTACTCCTTCC
138325	136412	ACAAATATTAGTACTCCTTC
138326	136413	TACAAATATTAGTACTCCTT
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138328	136415	TCTACAAATATTAGTACTCC
138329	136416	TTCTACAAATATTAGTACTC
138330	136417	TTTCTACAAATATTAGTACT
138331	136418	ATTTCTACAAATATTAGTAC

40038	38125	CTACATAAGCAAATACTCAC
40039	38126	ACTACATAAGCAAATACTCA
40040	38127	TACTACATAAGCAAATACTC
40041	38128	ATACTACATAAGCAAATACT
40042	38129	AATACTACATAAGCAAATAC
40043	38130	AAATACTACATAAGCAAATA
40044	38131	AAAATACTACATAAGCAAAT
40045	38132	TAAAATACTACATAAGCAAA
40046	38133	TTAAAATACTACATAAGCAA
40047	38134	ATTAAAATACTACATAAGCA
40048	38135	AATTAAAATACTACATAAGC
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40050	38137	AAAATTAAAATACTACATAA
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40052	38139	ATAAAATTAAAATACTACAT
40053	38140	CATAAAATTAAAATACTACA
40054	38141	TCATAAAATTAAAATACTAC
40055	38142	ATCATAAAATTAAAATACTA
40056	38143	AATCATAAAATTAAAATACT
40057	38144	AAATCATAAAATTAAAATAC
40058	38145	AAAATCATAAAATTAAAATA
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40060	38147	AAAAAATCATAAAATTAAAA
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40062	38149	AAAAAAAATCATAAAATTAA
40063	38150	AAAAAAAAATCATAAAATTA
40064	38151	GAAAAAAAAATCATAAAATT
40065	38152	AGAAAAAAAAATCATAAAAT
40066	38153	AAGAAAAAAAAATCATAAAA
40067	38154	AAAGAAAAAAAAATCATAAA
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40069	38156	TCAAAGAAAAAAAAATCATA
40070	38157	CTCAAAGAAAAAAAAATCAT
40071	38158	TCTCAAAGAAAAAAAAATCA
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40074	38161	CCGTCTCAAAGAAAAAAAA
40075	38162	TCCGTCTCAAAGAAAAAAA
40076	38163	CTCCGTCTCAAAGAAAAAA
40077	38164	CCTCCGTCTCAAAGAAAAA
40078	38165	ACCTCCGTCTCAAAGAAAA
40079	38166	AACCTCCGTCTCAAAGAAA
40080	38167	AAACCTCCGTCTCAAAGAA
40081	38168	CAAACCTCCGTCTCAAAGAA
40082	38169	GCAAACCTCCGTCTCAAAGA
40083	38170	AGCAAACCTCCGTCTCAAAG
40084	38171	GAGCAAACCTCCGTCTCAAA
40085	38172	AGAGCAAACCTCCGTCTCAA
40086	38173	AAGAGCAAACCTCCGTCTCA
40087	38174	CAAGAGCAAACCTCCGTCTC
40088	38175	ACAAGAGCAAACCTCCGTCT
40089	38176	AACAAGAGCAAACCTCCGTC
40090	38177	CAACAAGAGCAAACCTCCGT
40091	38178	GCAACAAGAGCAAACCTCCG
40092	38179	GGCAACAAGAGCAAACCTCC
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40095	38182	TTGGGCAACAAGAGCAAACC
40096	38183	CTTGGGCAACAAGAGCAAAC
40097	38184	GCTTGGGCAACAAGAGCAAA
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40099	38186	CAGCTTGGGCAACAAGAGCA
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40103	38190	ACTCCAGCTTGGGCAACAAG
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40105	38192	GTACTCCAGCTTGGGCAACA
40106	38193	TGTACTCCAGCTTGGGCAAC
40107	38194	CTGTACTCCAGCTTGGGCAA
40108	38195	ACTGTACTCCAGCTTGGGCA

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89187	87274	AGGACTGATTGGCAAAGTAG
89188	87275	AAGGACTGATTGGCAAAGTA
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89191	87278	ACTAAGGACTGATTGGCAAA
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89193	87280	GCACTAAGGACTGATTGGCA
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89201	87288	GGAACAAAGCACTAAGGACT
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89207	87294	GTTATGGGAACAAAGCACTA
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89213	87300	ACCACAGTTATGGGAACAAA
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89215	87302	TTACCACAGTTATGGGAACA
89216	87303	CTTACCACAGTTATGGGAAC
89217	87304	GCTTACCACAGTTATGGGAA
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89225	87312	AAGCTCTTGCTTACCACAGT
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89235	87322	TATTCTTTGTAAGCTCTTGC
89236	87323	GTATTCTTTGTAAGCTCTTG
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138332	136419	GATTTCTACAAATATTAGTA
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138334	136421	AGGATTTCTACAAATATTAG
138335	136422	AAGGATTTCTACAAATATTA
138336	136423	AAAGGATTTCTACAAATATT
138337	136424	TAAAGGATTTCTACAAATAT
138338	136425	CTAAAGGATTTCTACAAATA
138339	136426	TCTAAAGGATTTCTACAAAT
138340	136427	TTCTAAAGGATTTCTACAAA
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138343	136430	AATTTCTAAAGGATTTCTAC
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138347	136434	CACAAATTTCTAAAGGATTT
138348	136435	GCACAAATTTCTAAAGGATT
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138350	136437	TGGCACAAATTTCTAAAGGA
138351	136438	ATGGCACAAATTTCTAAAGG
138352	136439	AATGGCACAAATTTCTAAAG
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138361	136448	GACAATATTAATGGCACAAA
138362	136449	TGACAATATTAATGGCACAA
138363	136450	GTGACAATATTAATGGCACA
138364	136451	GGTGACAATATTAATGGCAC
138365	136452	AGGTGACAATATTAATGGCA
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138377	136464	ACATTTCATACAAGGTGACA
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138379	136466	CAACATTTCATACAAGGTGA
138380	136467	ACAACATTTCATACAAGGTG
138381	136468	CACAACATTTCATACAAGGT
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138383	136470	AACACAACATTTCATACAAG
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138385	136472	AGAACACAACATTTCATACA
138386	136473	TAGAACACAACATTTCATAC
138387	136474	CTAGAACACAACATTTCATA
138388	136475	TCTAGAACACAACATTTCAT
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138399	136486	CCTTAATATCCTCTAGAACA
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138401	136488	ATCCTTAATATCCTCTAGAA
138402	136489	AATCCTTAATATCCTCTAGA

40109	38196	CACTGTACTCCAGCTTGGGC
40110	38197	CCACTGTACTCCAGCTTGGG
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40112	38199	CACCACTGTACTCCAGCTTG
40113	38200	GCACCACTGTACTCCAGCTT
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40115	38202	TGGCACCACTGTACTCCAGC
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40117	38204	GATGGCACCACTGTACTCCA
40118	38205	AGATGGCACCACTGTACTCC
40119	38206	GAGATGGCACCACTGTACTC
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40122	38209	GCCGAGATGGCACCACTGTA
40123	38210	AGCCGAGATGGCACCACTGT
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40125	38212	TGAGCCGAGATGGCACCACT
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40127	38214	AGTGAGCCGAGATGGCACCA
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40136	38223	GGAGGCTGCAGTGAGCCGAG
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40146	38233	CCCAGGAGGTGGAGGCTGCA
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40148	38235	AACCCAGGAGGTGGAGGCTG
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40150	38237	TGAACCCAGGAGGTGGAGGC
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40159	38246	AGAACGGCTTGAACCCAGGA
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40168	38255	TGAGGGAGGAGAACGGCTTG
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40170	38257	GCTGAGGGAGGAGAACGGCT
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40176	38263	GAGGTGGCTGAGGGAGGAGA
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89256	87343	TGTTTGTTTGTTTGTTTTAA
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89317	87404	GATCTTGTTTCTTTTAAAGG
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89321	87408	GGCCGATCTTGTTTCTTTTA
89322	87409	TGGCCGATCTTGTTTCTTTT
89323	87410	CTGGCCGATCTTGTTTCTTT
89324	87411	ACTGGCCGATCTTGTTTCTT
89325	87412	AACTGGCCGATCTTGTTTCT
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138403	136490	GAATCCTTAATATCCTCTAG
138404	136491	TGAATCCTTAATATCCTCTA
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138406	136493	TTTGAATCCTTAATATCCTC
138407	136494	ATTTGAATCCTTAATATCCT
138408	136495	AATTTGAATCCTTAATATCC
138409	136496	AAATTTGAATCCTTAATATC
138410	136497	AAAATTTGAATCCTTAATAT
138411	136498	TAAAATTTGAATCCTTAATA
138412	136499	ATAAAATTTGAATCCTTAAT
138413	136500	CATAAAATTTGAATCCTTAA
138414	136501	ACATAAAATTTGAATCCTTA
138415	136502	AACATAAAATTTGAATCCTT
138416	136503	TAACATAAAATTTGAATCCT
138417	136504	CTAACATAAAATTTGAATCC
138418	136505	CCTAACATAAAATTTGAATC
138419	136506	GCCTAACATAAAATTTGAAT
138420	136507	TGCCTAACATAAAATTTGAA
138421	136508	GTGCCTAACATAAAATTTGA
138422	136509	TGTGCCTAACATAAAATTTG
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138425	136512	AAATGTGCCTAACATAAAAT
138426	136513	AAAATGTGCCTAACATAAAA
138427	136514	CAAAATGTGCCTAACATAAA
138428	136515	TCAAAATGTGCCTAACATAA
138429	136516	CTCAAAATGTGCCTAACATA
138430	136517	ACTCAAAATGTGCCTAACAT
138431	136518	AACTCAAAATGTGCCTAACA
138432	136519	TAACTCAAAATGTGCCTAAC
138433	136520	ATAACTCAAAATGTGCCTAA
138434	136521	AATAACTCAAAATGTGCCTA
138435	136522	AAATAACTCAAAATGTGCCT
138436	136523	AAAATAACTCAAAATGTGCC
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138444	136531	GTCACCCCAAAATAACTCAA
138445	136532	AGTCACCCCAAAATAACTCA
138446	136533	GAGTCACCCCAAAATAACTC
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138450	136537	CATTGAGTCACCCCAAAATA
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138452	136539	GACATTGAGTCACCCCAAAA
138453	136540	AGACATTGAGTCACCCCAAA
138454	136541	CAGACATTGAGTCACCCCAA
138455	136542	TCAGACATTGAGTCACCCCA
138456	136543	GTCAGACATTGAGTCACCCC
138457	136544	AGTCAGACATTGAGTCACCC
138458	136545	GAGTCAGACATTGAGTCACC
138459	136546	AGAGTCAGACATTGAGTCAC
138460	136547	TAGAGTCAGACATTGAGTCA
138461	136548	GTAGAGTCAGACATTGAGTC
138462	136549	AGTAGAGTCAGACATTGAGT
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138464	136551	TTAGTAGAGTCAGACATTGA
138465	136552	TTTAGTAGAGTCAGACATTG
138466	136553	ATTTAGTAGAGTCAGACATT
138467	136554	CATTTAGTAGAGTCAGACAT
138468	136555	GCATTTAGTAGAGTCAGACA
138469	136556	GGCATTTAGTAGAGTCAGAC
138470	136557	TGGCATTTAGTAGAGTCAGA
138471	136558	ATGGCATTTAGTAGAGTCAG
138472	136559	TATGGCATTTAGTAGAGTCA
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40180	38267	GGAGGAGGTGGCTGAGGGAG
40181	38268	AGGAGGAGGTGGCTGAGGGA
40182	38269	CAGGAGGAGGTGGCTGAGGG
40183	38270	TCAGGAGGAGGTGGCTGAGG
40184	38271	TTCAGGAGGAGGTGGCTGAG
40185	38272	ATTCAGGAGGAGGTGGCTGA
40186	38273	TATTCAGGAGGAGGTGGCTG
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40189	38276	AACTATTCAGGAGGAGGTGG
40190	38277	CAACTATTCAGGAGGAGGTG
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40198	38285	TATAATCCCAACTATTCAGG
40199	38286	CTATAATCCCAACTATTCAG
40200	38287	CCTATAATCCCAACTATTCA
40201	38288	GCCTATAATCCCAACTATTC
40202	38289	CGCCTATAATCCCAACTATT
40203	38290	GCGCCTATAATCCCAACTAT
40204	38291	GGCGCCTATAATCCCAACTA
40205	38292	AGGCGCCTATAATCCCAACT
40206	38293	CAGGCGCCTATAATCCCAAC
40207	38294	GCAGGCGCCTATAATCCCAA
40208	38295	GGCAGGCGCCTATAATCCCA
40209	38296	TGGCAGGCGCCTATAATCCC
40210	38297	GTGGCAGGCGCCTATAATCC
40211	38298	GGTGGCAGGCGCCTATAATC
40212	38299	TGGTGGCAGGCGCCTATAAT
40213	38300	ATGGTGGCAGGCGCCTATAA
40214	38301	CATGGTGGCAGGCGCCTATA
40215	38302	GCATGGTGGCAGGCGCCTAT
40216	38303	GGCATGGTGGCAGGCGCCTA
40217	38304	AGGCATGGTGGCAGGCGCCT
40218	38305	CAGGCATGGTGGCAGGCGCC
40219	38306	CCAGGCATGGTGGCAGGCGC
40220	38307	GCCAGGCATGGTGGCAGGCG
40221	38308	AGCCAGGCATGGTGGCAGGC
40222	38309	TAGCCAGGCATGGTGGCAGG
40223	38310	TTAGCCAGGCATGGTGGCAG
40224	38311	ATTAGCCAGGCATGGTGGCA
40225	38312	AATTAGCCAGGCATGGTGGC
40226	38313	AAATTAGCCAGGCATGGTGG
40227	38314	AAAATTAGCCAGGCATGGTG
40228	38315	AAAAATTAGCCAGGCATGGT
40229	38316	AAAAAATTAGCCAGGCATGG
40230	38317	CAAAAAATTAGCCAGGCATG
40231	38318	ACAAAAAATTAGCCAGGCAT
40232	38319	TACAAAAAATTAGCCAGGCA
40233	38320	ATACAAAAAATTAGCCAGGC
40234	38321	TATACAAAAAATTAGCCAGG
40235	38322	ATATACAAAAAATTAGCCAG
40236	38323	GATATACAAAAAATTAGCCA
40237	38324	AGATATACAAAAAATTAGCC
40238	38325	TAGATATACAAAAAATTAGC
40239	38326	CTAGATATACAAAAAATTAG
40240	38327	ACTAGATATACAAAAAATTA
40241	38328	TACTAGATATACAAAAAATT
40242	38329	CTACTAGATATACAAAAAAT
40243	38330	ACTACTAGATATACAAAAAA
40244	38331	CACTACTAGATATACAAAAA
40245	38332	TCACTACTAGATATACAAAA
40246	38333	ATCACTACTAGATATACAAA
40247	38334	CATCACTACTAGATATACAA
40248	38335	CCATCACTACTAGATATACA
40249	38336	TCCATCACTACTAGATATAC
40250	38337	CTCCATCACTACTAGATATA

89327	87414	GCAACTGGCCGATCTTGTTT
89328	87415	AGCAACTGGCCGATCTTGTT
89329	87416	CAGCAACTGGCCGATCTTGT
89330	87417	ACAGCAACTGGCCGATCTTG
89331	87418	CACAGCAACTGGCCGATCTT
89332	87419	CCACAGCAACTGGCCGATCT
89333	87420	GCCACAGCAACTGGCCGATC
89334	87421	AGCCACAGCAACTGGCCGAT
89335	87422	GAGCCACAGCAACTGGCCGA
89336	87423	TGAGCCACAGCAACTGGCCG
89337	87424	ATGAGCCACAGCAACTGGCC
89338	87425	CATGAGCCACAGCAACTGGC
89339	87426	GCATGAGCCACAGCAACTGG
89340	87427	GGCATGAGCCACAGCAACTG
89341	87428	AGGCATGAGCCACAGCAACT
89342	87429	CAGGCATGAGCCACAGCAAC
89343	87430	ACAGGCATGAGCCACAGCAA
89344	87431	TACAGGCATGAGCCACAGCA
89345	87432	TTACAGGCATGAGCCACAGC
89346	87433	ATTACAGGCATGAGCCACAG
89347	87434	GATTACAGGCATGAGCCACA
89348	87435	GGATTACAGGCATGAGCCAC
89349	87436	GGGATTACAGGCATGAGCCA
89350	87437	TGGGATTACAGGCATGAGCC
89351	87438	CTGGGATTACAGGCATGAGC
89352	87439	GCTGGGATTACAGGCATGAG
89353	87440	TGCTGGGATTACAGGCATGA
89354	87441	GTGCTGGGATTACAGGCATG
89355	87442	AGTGCTGGGATTACAGGCAT
89356	87443	AAGTGCTGGGATTACAGGCA
89357	87444	AAAGTGCTGGGATTACAGGC
89358	87445	CAAAGTGCTGGGATTACAGG
89359	87446	CCAAAGTGCTGGGATTACAG
89360	87447	CCCAAAGTGCTGGGATTACA
89361	87448	TCCCAAAGTGCTGGGATTAC
89362	87449	CTCCCAAAGTGCTGGGATTA
89363	87450	CCTCCCAAAGTGCTGGGATT
89364	87451	GCCTCCCAAAGTGCTGGGAT
89365	87452	AGCCTCCCAAAGTGCTGGGA
89366	87453	CAGCCTCCCAAAGTGCTGGG
89367	87454	TCAGCCTCCCAAAGTGCTGG
89368	87455	CTCAGCCTCCCAAAGTGCTG
89369	87456	CCTCAGCCTCCCAAAGTGCT
89370	87457	ACCTCAGCCTCCCAAAGTGC
89371	87458	CACCTCAGCCTCCCAAAGTG
89372	87459	CCACCTCAGCCTCCCAAAGT
89373	87460	CCCACCTCAGCCTCCCAAAG
89374	87461	ACCCACCTCAGCCTCCCAAA
89375	87462	CACCCACCTCAGCCTCCCAA
89376	87463	CCACCCACCTCAGCCTCCCA
89377	87464	TCCACCCACCTCAGCCTCCC
89378	87465	ATCCACCCACCTCAGCCTCC
89379	87466	GATCCACCCACCTCAGCCTC
89380	87467	TGATCCACCCACCTCAGCCT
89381	87468	GTGATCCACCCACCTCAGCC
89382	87469	AGTGATCCACCCACCTCAGC
89383	87470	AAGTGATCCACCCACCTCAG
89384	87471	CAAGTGATCCACCCACCTCA
89385	87472	TCAAGTGATCCACCCACCTC
89386	87473	CTCAAGTGATCCACCCACCT
89387	87474	CCTCAAGTGATCCACCCACC
89388	87475	ACCTCAAGTGATCCACCCAC
89389	87476	GACCTCAAGTGATCCACCCA
89390	87477	TGACCTCAAGTGATCCACCC
89391	87478	CTGACCTCAAGTGATCCACC
89392	87479	CCTGACCTCAAGTGATCCAC
89393	87480	TCCTGACCTCAAGTGATCCA
89394	87481	CTCCTGACCTCAAGTGATCC
89395	87482	ACTCCTGACCTCAAGTGATC
89396	87483	AACTCCTGACCTCAAGTGAT
89397	87484	GAACTCCTGACCTCAAGTGA

138474	136561	AATATGGCATTTAGTAGAGT
138475	136562	TAATATGGCATTTAGTAGAG
138476	136563	CTAATATGGCATTTAGTAGA
138477	136564	GCTAATATGGCATTTAGTAG
138478	136565	TGCTAATATGGCATTTAGTA
138479	136566	ATGCTAATATGGCATTTAGT
138480	136567	AATGCTAATATGGCATTTAG
138481	136568	AAATGCTAATATGGCATTTA
138482	136569	TAAATGCTAATATGGCATTT
138483	136570	TTAAATGCTAATATGGCATT
138484	136571	TTTAAATGCTAATATGGCAT
138485	136572	TTTTAAATGCTAATATGGCA
138486	136573	ATTTTAAATGCTAATATGGC
138487	136574	CATTTTAAATGCTAATATGG
138488	136575	GCATTTTAAATGCTAATATG
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138491	136578	AATGCATTTTAAATGCTAAT
138492	136579	AAATGCATTTTAAATGCTAA
138493	136580	CAAATGCATTTTAAATGCTA
138494	136581	TCAAATGCATTTTAAATGCT
138495	136582	GTCAAATGCATTTTAAATGC
138496	136583	GGTCAAATGCATTTTAAATG
138497	136584	AGGTCAAATGCATTTTAAAT
138498	136585	AAGGTCAAATGCATTTTAAA
138499	136586	TAAGGTCAAATGCATTTTAA
138500	136587	TTAAGGTCAAATGCATTTTA
138501	136588	TTTAAGGTCAAATGCATTTT
138502	136589	ATTTAAGGTCAAATGCATTT
138503	136590	GATTTAAGGTCAAATGCATT
138504	136591	AGATTTAAGGTCAAATGCAT
138505	136592	AAGATTTAAGGTCAAATGCA
138506	136593	AAAGATTTAAGGTCAAATGC
138507	136594	CAAAGATTTAAGGTCAAATG
138508	136595	ACAAAGATTTAAGGTCAAAT
138509	136596	AACAAAGATTTAAGGTCAAA
138510	136597	TAACAAAGATTTAAGGTCAA
138511	136598	TTAACAAAGATTTAAGGTCA
138512	136599	ATTAACAAAGATTTAAGGTC
138513	136600	AATTAACAAAGATTTAAGGT
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138515	136602	ATAATTAACAAAGATTTAAG
138516	136603	CATAATTAACAAAGATTTAA
138517	136604	GCATAATTAACAAAGATTTA
138518	136605	GGCATAATTAACAAAGATTT
138519	136606	TGGCATAATTAACAAAGATT
138520	136607	ATGGCATAATTAACAAAGAT
138521	136608	CATGGCATAATTAACAAAGA
138522	136609	TCATGGCATAATTAACAAAG
138523	136610	GTCATGGCATAATTAACAAA
138524	136611	AGTCATGGCATAATTAACAA
138525	136612	AAGTCATGGCATAATTAACA
138526	136613	CAAGTCATGGCATAATTAAC
138527	136614	CCAAGTCATGGCATAATTAA
138528	136615	ACCAAGTCATGGCATAATTA
138529	136616	TACCAAGTCATGGCATAATT
138530	136617	ATACCAAGTCATGGCATAAT
138531	136618	GATACCAAGTCATGGCATAA
138532	136619	GGATACCAAGTCATGGCATA
138533	136620	TGGATACCAAGTCATGGCAT
138534	136621	TTGGATACCAAGTCATGGCA
138535	136622	TTTGGATACCAAGTCATGGC
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138539	136626	TATTTTTGGATACCAAGTCA
138540	136627	TTATTTTTGGATACCAAGTC
138541	136628	CTTATTTTTGGATACCAAGT
138542	136629	GCTTATTTTTGGATACCAAG
138543	136630	AGCTTATTTTTGGATACCAA
138544	136631	CAGCTTATTTTTGGATACCA

40251	38338	ACTCCATCACTACTAGATAT
40252	38339	AACTCCATCACTACTAGATA
40253	38340	AAACTCCATCACTACTAGAT
40254	38341	CAAACTCCATCACTACTAGA
40255	38342	TCAAACTCCATCACTACTAG
40256	38343	CTCAAACTCCATCACTACTA
40257	38344	GCTCAAACTCCATCACTACT
40258	38345	TGCTCAAACTCCATCACTAC
40259	38346	ATGCTCAAACTCCATCACTA
40260	38347	CATGCTCAAACTCCATCACT
40261	38348	ACATGCTCAAACTCCATCAC
40262	38349	AACATGCTCAAACTCCATCA
40263	38350	CAACATGCTCAAACTCCATC
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40265	38352	GGCAACATGCTCAAACTCCA
40266	38353	TGGCAACATGCTCAAACTCC
40267	38354	CTGGCAACATGCTCAAACTC
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40269	38356	GCCTGGCAACATGCTCAAAC
40270	38357	AGCCTGGCAACATGCTCAAA
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40272	38359	CCAGCCTGGCAACATGCTCA
40273	38360	ACCAGCCTGGCAACATGCTC
40274	38361	GACCAGCCTGGCAACATGCT
40275	38362	AGACCAGCCTGGCAACATGC
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40277	38364	CAAGACCAGCCTGGCAACAT
40278	38365	TCAAGACCAGCCTGGCAACA
40279	38366	TTCAAGACCAGCCTGGCAAC
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40285	38372	CAGAGGTTCAAGACCAGCCT
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40287	38374	GTCAGAGGTTCAAGACCAGC
40288	38375	GGTCAGAGGTTCAAGACCAG
40289	38376	AGGTCAGAGGTTCAAGACCA
40290	38377	GAGGTCAGAGGTTCAAGACC
40291	38378	TGAGGTCAGAGGTTCAAGAC
40292	38379	CTGAGGTCAGAGGTTCAAGA
40293	38380	CCTGAGGTCAGAGGTTCAAG
40294	38381	ACCTGAGGTCAGAGGTTCAA
40295	38382	CACCTGAGGTCAGAGGTTCA
40296	38383	TCACCTGAGGTCAGAGGTTC
40297	38384	ATCACCTGAGGTCAGAGGTT
40298	38385	GATCACCTGAGGTCAGAGGT
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40301	38388	GTGGATCACCTGAGGTCAGA
40302	38389	GGTGGATCACCTGAGGTCAG
40303	38390	AGGTGGATCACCTGAGGTCA
40304	38391	CAGGTGGATCACCTGAGGTC
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40306	38393	GGCAGGTGGATCACCTGAGG
40307	38394	AGGCAGGTGGATCACCTGAG
40308	38395	AAGGCAGGTGGATCACCTGA
40309	38396	CAAGGCAGGTGGATCACCTG
40310	38397	CCAAGGCAGGTGGATCACCT
40311	38398	GCCAAGGCAGGTGGATCACC
40312	38399	GGCCAAGGCAGGTGGATCAC
40313	38400	AGGCCAAGGCAGGTGGATCA
40314	38401	GAGGCCAAGGCAGGTGGATC
40315	38402	GGAGGCCAAGGCAGGTGGAT
40316	38403	GGGAGGCCAAGGCAGGTGGA
40317	38404	TGGGAGGCCAAGGCAGGTGG
40318	38405	TTGGGAGGCCAAGGCAGGTG
40319	38406	TTTGGGAGGCCAAGGCAGGT
40320	38407	CTTTGGGAGGCCAAGGCAGG
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89398	87485	TGAACTCCTGACCTCAAGTG
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89401	87488	TCTTGAACTCCTGACCTCAA
89402	87489	GTCTTGAACTCCTGACCTCA
89403	87490	AGTCTTGAACTCCTGACCTC
89404	87491	CAGTCTTGAACTCCTGACCT
89405	87492	CCAGTCTTGAACTCCTGACC
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89407	87494	GGCCAGTCTTGAACTCCTGA
89408	87495	AGGCCAGTCTTGAACTCCTG
89409	87496	CAGGCCAGTCTTGAACTCCT
89410	87497	TCAGGCCAGTCTTGAACTCC
89411	87498	GTCAGGCCAGTCTTGAACTC
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89413	87500	TGGTCAGGCCAGTCTTGAAC
89414	87501	TTGGTCAGGCCAGTCTTGAA
89415	87502	GTTGGTCAGGCCAGTCTTGA
89416	87503	TGTTGGTCAGGCCAGTCTTG
89417	87504	ATGTTGGTCAGGCCAGTCTT
89418	87505	CATGTTGGTCAGGCCAGTCT
89419	87506	TCATGTTGGTCAGGCCAGTC
89420	87507	ATCATGTTGGTCAGGCCAGT
89421	87508	CATCATGTTGGTCAGGCCAG
89422	87509	TCATCATGTTGGTCAGGCCA
89423	87510	TTCATCATGTTGGTCAGGCC
89424	87511	TTTCATCATGTTGGTCAGGC
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89426	87513	GGTTTCATCATGTTGGTCAG
89427	87514	GGGTTTCATCATGTTGGTCA
89428	87515	GGGGTTTCATCATGTTGGTC
89429	87516	TGGGGTTTCATCATGTTGGT
89430	87517	ATGGGGTTTCATCATGTTGG
89431	87518	GATGGGGTTTCATCATGTTG
89432	87519	AGATGGGGTTTCATCATGTT
89433	87520	GAGATGGGGTTTCATCATGT
89434	87521	AGAGATGGGGTTTCATCATG
89435	87522	TAGAGATGGGGTTTCATCAT
89436	87523	GTAGAGATGGGGTTTCATCA
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89438	87525	TAGTAGAGATGGGGTTTCAT
89439	87526	TTAGTAGAGATGGGGTTTCA
89440	87527	TTTAGTAGAGATGGGGTTTC
89441	87528	TTTTAGTAGAGATGGGGTTT
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89443	87530	ATTTTTAGTAGAGATGGGGT
89444	87531	TATTTTTAGTAGAGATGGGG
89445	87532	GTATTTTTAGTAGAGATGGG
89446	87533	TGTATTTTTAGTAGAGATGG
89447	87534	TTGTATTTTTAGTAGAGATG
89448	87535	TTTGTATTTTTAGTAGAGAT
89449	87536	TTTTGTATTTTTAGTAGAGA
89450	87537	ATTTTGTATTTTTAGTAGAG
89451	87538	AATTTTGTATTTTTAGTAGA
89452	87539	TAATTTTGTATTTTTAGTAG
89453	87540	CTAATTTTGTATTTTTAGTA
89454	87541	GCTAATTTTGTATTTTTAGT
89455	87542	AGCTAATTTTGTATTTTTAG
89456	87543	CAGCTAATTTTGTATTTTTA
89457	87544	TCAGCTAATTTTGTATTTTT
89458	87545	CTCAGCTAATTTTGTATTTT
89459	87546	ACTCAGCTAATTTTGTATTT
89460	87547	CACTCAGCTAATTTTGTATT
89461	87548	ACACTCAGCTAATTTTGTAT
89462	87549	CACACTCAGCTAATTTTGTA
89463	87550	CCACACTCAGCTAATTTTGT
89464	87551	ACCACACTCAGCTAATTTTG
89465	87552	CACCACACTCAGCTAATTTT
89466	87553	CCACCACACTCAGCTAATTT
89467	87554	GCCACCACACTCAGCTAATT
89468	87555	AGCCACCACACTCAGCTAAT

138545	136632	TCAGCTTATTTTTGGATACC
138546	136633	ATCAGCTTATTTTTGGATAC
138547	136634	TATCAGCTTATTTTTGGATA
138548	136635	GTATCAGCTTATTTTTGGAT
138549	136636	TGTATCAGCTTATTTTTGGA
138550	136637	ATGTATCAGCTTATTTTTGG
138551	136638	TATGTATCAGCTTATTTTTG
138552	136639	GTATGTATCAGCTTATTTTT
138553	136640	TGTATGTATCAGCTTATTTT
138554	136641	ATGTATGTATCAGCTTATTT
138555	136642	TATGTATGTATCAGCTTATT
138556	136643	GTATGTATGTATCAGCTTAT
138557	136644	TGTATGTATGTATCAGCTTA
138558	136645	ATGTATGTATGTATCAGCTT
138559	136646	TATGTATGTATGTATCAGCT
138560	136647	GTATGTATGTATGTATCAGC
138561	136648	TGTATGTATGTATGTATCAG
138562	136649	ATGTATGTATGTATGTATCA
138563	136650	TATGTATGTATGTATGTATC
138564	136651	ATATGTATGTATGTATGTAT
138565	136652	TATATGTATGTATGTATGTA
138566	136653	ATATATGTATGTATGTATGT
138567	136654	CATATATGTATGTATGTATG
138568	136655	ACATATATGTATGTATGTAT
138569	136656	CACATATATGTATGTATGTA
138570	136657	ACACATATATGTATGTATGT
138571	136658	CACACATATATGTATGTATG
138572	136659	ACACACATATATGTATGTAT
138573	136660	CACACACATATATGTATGTA
138574	136661	ACACACACATATATGTATGT
138575	136662	CACACACACATATATGTATG
138576	136663	ACACACACACATATATGTAT
138577	136664	CACACACACACATATATGTA
138578	136665	ACACACACACACATATATGT
138579	136666	CACACACACACACATATATG
138580	136667	ACACACACACACACATATAT
138581	136668	CACACACACACACACATATA
138582	136669	ACACACACACACACACATAT
138583	136670	CACACACACACACACACATA
138584	136671	ACACACACACACACACACAT
138585	136672	CACACACACACACACACACA
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138587	136674	CACACACACACACACACACA
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138589	136676	CACACACACACACACACACA
138590	136677	ACACACACACACACACACAC
138591	136678	TACACACACACACACACACA
138592	136679	ATACACACACACACACACAC
138593	136680	TATACACACACACACACACA
138594	136681	ATATACACACACACACACAC
138595	136682	TATATACACACACACACACA
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138597	136684	TATATATACACACACACACA
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138599	136686	TATATATATACACACACACA
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138601	136688	TATATATATATACACACACA
138602	136689	ATATATATATATACACACAC
138603	136690	TATATATATATATACACACA
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138605	136692	CATATATATATATATACACA
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138607	136694	TACATATATATATATATACA
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138611	136698	CACATACATATATATATATA
138612	136699	ACACATACATATATATATAT
138613	136700	CACACATACATATATATATA
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138615	136702	TACACACATACATATATATA

40322	38409	CACTTTGGGAGGCCAAGGCA
40323	38410	GCACTTTGGGAGGCCAAGGC
40324	38411	AGCACTTTGGGAGGCCAAGG
40325	38412	CAGCACTTTGGGAGGCCAAG
40326	38413	CCAGCACTTTGGGAGGCCAA
40327	38414	CCCAGCACTTTGGGAGGCCA
40328	38415	TCCCAGCACTTTGGGAGGCC
40329	38416	ATCCCAGCACTTTGGGAGGC
40330	38417	AATCCCAGCACTTTGGGAGG
40331	38418	TAATCCCAGCACTTTGGGAG
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40342	38429	GGCTCATGCCTTAATCCCAG
40343	38430	TGGCTCATGCCTTAATCCCA
40344	38431	GTGGCTCATGCCTTAATCCC
40345	38432	GGTGGCTCATGCCTTAATCC
40346	38433	TGGTGGCTCATGCCTTAATC
40347	38434	ATGGTGGCTCATGCCTTAAT
40348	38435	CATGGTGGCTCATGCCTTAA
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40350	38437	GGCATGGTGGCTCATGCCTT
40351	38438	GGGCATGGTGGCTCATGCCT
40352	38439	CGGGCATGGTGGCTCATGCC
40353	38440	CCGGGCATGGTGGCTCATGC
40354	38441	GCCGGGCATGGTGGCTCATG
40355	38442	GGCCGGGCATGGTGGCTCAT
40356	38443	TGGCCGGGCATGGTGGCTCA
40357	38444	CTGGCCGGGCATGGTGGCTC
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40366	38453	GAACAGTCTCTGGCCGGGCA
40367	38454	TGAACAGTCTCTGGCCGGGC
40368	38455	ATGAACAGTCTCTGGCCGGG
40369	38456	AATGAACAGTCTCTGGCCGG
40370	38457	AAATGAACAGTCTCTGGCCG
40371	38458	TAAATGAACAGTCTCTGGCC
40372	38459	ATAAATGAACAGTCTCTGGC
40373	38460	AATAAATGAACAGTCTCTGG
40374	38461	AAATAAATGAACAGTCTCTG
40375	38462	AAAATAAATGAACAGTCTCT
40376	38463	AAAAATAAATGAACAGTCTC
40377	38464	AAAAAATAAATGAACAGTCT
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40379	38466	AAAAAAAATAAATGAACAGT
40380	38467	AAAAAAAAATAAATGAACAG
40381	38468	AAAAAAAAAATAAATGAACA
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40383	38470	AAAAAAAAAAAATAAATGAA
40384	38471	CAAAAAAAAAAAATAAATGA
40385	38472	TCAAAAAAAAAAAATAAATG
40386	38473	CTCAAAAAAAAAAAATAAAT
40387	38474	CCTCAAAAAAAAAAAATAAA
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40389	38476	CGCCTCAAAAAAAAAAAATA
40390	38477	CCGCCTCAAAAAAAAAAAAT
40391	38478	TCCGCCTCAAAAAAAAAAAA
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89470	87557	ATAGCCACCACACTCAGCTA
89471	87558	AATAGCCACCACACTCAGCT
89472	87559	AAATAGCCACCACACTCAGC
89473	87560	CAAATAGCCACCACACTCAG
89474	87561	TCAAATAGCCACCACACTCA
89475	87562	CTCAAATAGCCACCACACTC
89476	87563	TCTCAAATAGCCACCACACT
89477	87564	CTCTCAAATAGCCACCACAC
89478	87565	CCTCTCAAATAGCCACCACA
89479	87566	GCCTCTCAAATAGCCACCAC
89480	87567	AGCCTCTCAAATAGCCACCA
89481	87568	CAGCCTCTCAAATAGCCACC
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89488	87575	CCTGCCTCAGCCTCTCAAAT
89489	87576	TCCTGCCTCAGCCTCTCAAA
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89492	87579	TTCTCCTGCCTCAGCCTCTC
89493	87580	ATTCTCCTGCCTCAGCCTCT
89494	87581	GATTCTCCTGCCTCAGCCTC
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89500	87587	TCAAATGATTCTCCTGCCTC
89501	87588	TTCAAATGATTCTCCTGCCT
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89507	87594	CCTGGGTTCAAATGATTCTC
89508	87595	TCCTGGGTTCAAATGATTCT
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89512	87599	CACCTCCTGGGTTCAAATGA
89513	87600	TCACCTCCTGGGTTCAAATG
89514	87601	TTCACCTCCTGGGTTCAAAT
89515	87602	CTTCACCTCCTGGGTTCAAA
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89517	87604	ACCTTCACCTCCTGGGTTCA
89518	87605	AACCTTCACCTCCTGGGTTC
89519	87606	CAACCTTCACCTCCTGGGTT
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89521	87608	TGCAACCTTCACCTCCTGGG
89522	87609	CTGCAACCTTCACCTCCTGG
89523	87610	ACTGCAACCTTCACCTCCTG
89524	87611	CACTGCAACCTTCACCTCCT
89525	87612	TCACTGCAACCTTCACCTCC
89526	87613	CTCACTGCAACCTTCACCTC
89527	87614	GCTCACTGCAACCTTCACCT
89528	87615	GGCTCACTGCAACCTTCACC
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89530	87617	TTGGCTCACTGCAACCTTCA
89531	87618	CTTGGCTCACTGCAACCTTC
89532	87619	TCTTGGCTCACTGCAACCTT
89533	87620	ATCTTGGCTCACTGCAACCT
89534	87621	GATCTTGGCTCACTGCAACC
89535	87622	TGATCTTGGCTCACTGCAAC
89536	87623	GTGATCTTGGCTCACTGCAA
89537	87624	TGTGATCTTGGCTCACTGCA
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89539	87626	GGTGTGATCTTGGCTCACTG

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138619	136706	TATATACACACATACATATA
138620	136707	ATATATACACACATACATAT
138621	136708	TATATATACACACATACATA
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138623	136710	ATTATATATACACACATACA
138624	136711	AATTATATATACACACATAC
138625	136712	AAATTATATATACACACATA
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138627	136714	ATAAATTATATATACACACA
138628	136715	AATAAATTATATATACACAC
138629	136716	AAATAAATTATATATACACA
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138631	136718	CCAAATAAATTATATATACA
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138635	136722	AGCACCAAATAAATTATATA
138636	136723	TAGCACCAAATAAATTATAT
138637	136724	CTAGCACCAAATAAATTATA
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138660	136747	TAAAGGATTAAATTTAACAT
138661	136748	TTAAAGGATTAAATTTAACA
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138664	136751	CTATTAAAGGATTAAATTTA
138665	136752	TCTATTAAAGGATTAAATTT
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138667	136754	CATCTATTAAAGGATTAAAT
138668	136755	GCATCTATTAAAGGATTAAA
138669	136756	AGCATCTATTAAAGGATTAA
138670	136757	GAGCATCTATTAAAGGATTA
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138673	136760	AAAGAGCATCTATTAAAGGA
138674	136761	TAAAGAGCATCTATTAAAGG
138675	136762	TTAAAGAGCATCTATTAAAG
138676	136763	TTTAAAGAGCATCTATTAAA
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138678	136765	TTTTTAAAGAGCATCTATTA
138679	136766	CTTTTTAAAGAGCATCTATT
138680	136767	CCTTTTTAAAGAGCATCTAT
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138682	136769	CTCCTTTTTAAAGAGCATCT
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138684	136771	GACTCCTTTTTAAAGAGCAT
138685	136772	AGACTCCTTTTTAAAGAGCA
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40400	38487	CAGCGAGACTCCGCCTCAA
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40402	38489	TACAGCGAGACTCCGCCTC
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40444	38531	GCAGTGAGCCGAGATTGTGC
40445	38532	TGCAGTGAGCCGAGATTGTG
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40454	38541	GGCGGAGCTTGCAGTGAGCC
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89542	87629	AATGGTGTGATCTTGGCTCA
89543	87630	CAATGGTGTGATCTTGGCTC
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89574	87661	GAGTTTCGCTCTTGTCACCC
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89587	87674	TTTTTTTGAGATAGAGTTTC
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89594	87681	TTTTTCTTTTTTTTGAGATA
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138705	136792	AATAGTATATACATACAGCA
138706	136793	TAATAGTATATACATACAGC
138707	136794	TTAATAGTATATACATACAG
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138723	136810	AGACATAGTTTCCCCTTTAA
138724	136811	CAGACATAGTTTCCCCTTTA
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138732	136819	TACAATCACAGACATAGTTT
138733	136820	CTACAATCACAGACATAGTT
138734	136821	ACTACAATCACAGACATAGT
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138736	136823	ACACTACAATCACAGACATA
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138738	136825	ACACACTACAATCACAGACA
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138745	136832	ATCTTTTACACACTACAATC
138746	136833	TATCTTTTACACACTACAAT
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40464	38551	GAACTTGGGAGGCGGAGCTT
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40467	38554	TGTGAACTTGGGAGGCGGAG
40468	38555	GTGTGAACTTGGGAGGCGGA
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40470	38557	TGGTGTGAACTTGGGAGGCG
40471	38558	ATGGTGTGAACTTGGGAGGC
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40473	38560	CAATGGTGTGAACTTGGGAG
40474	38561	ACAATGGTGTGAACTTGGGA
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40481	38568	AGGCAGGACAATGGTGTGAA
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40513	38600	GGCACCTGTAGTCCCAGCTA
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40521	38608	TGGTGGCAGGCACCTGTAGT
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89612	87699	CTTGAAGATCTTGTTTCTTT
89613	87700	GCTTGAAGATCTTGTTTCTT
89614	87701	AGCTTGAAGATCTTGTTTCT
89615	87702	AAGCTTGAAGATCTTGTTTC
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89618	87705	CTTAAGCTTGAAGATCTTGT
89619	87706	CCTTAAGCTTGAAGATCTTG
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89621	87708	TTCCTTAAGCTTGAAGATCT
89622	87709	TTTCCTTAAGCTTGAAGATC
89623	87710	GTTTCCTTAAGCTTGAAGAT
89624	87711	TGTTTCCTTAAGCTTGAAGA
89625	87712	TTGTTTCCTTAAGCTTGAAG
89626	87713	TTTGTTTCCTTAAGCTTGAA
89627	87714	TTTTGTTTCCTTAAGCTTGA
89628	87715	TTTTTGTTTCCTTAAGCTTG
89629	87716	GTTTTTGTTTCCTTAAGCTT
89630	87717	TGTTTTTGTTTCCTTAAGCT
89631	87718	TTGTTTTTGTTTCCTTAAGC
89632	87719	TTTGTTTTTGTTTCCTTAAG
89633	87720	TTTTGTTTTTGTTTCCTTAA
89634	87721	GTTTTGTTTTTGTTTCCTTA
89635	87722	AGTTTTGTTTTTGTTTCCTT
89636	87723	GAGTTTTGTTTTTGTTTCCT
89637	87724	TGAGTTTTGTTTTTGTTTCC
89638	87725	CTGAGTTTTGTTTTTGTTTC
89639	87726	GCTGAGTTTTGTTTTTGTTT
89640	87727	AGCTGAGTTTTGTTTTTGTT
89641	87728	CAGCTGAGTTTTGTTTTTGT
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89643	87730	CACAGCTGAGTTTTGTTTTT
89644	87731	ACACAGCTGAGTTTTGTTTT
89645	87732	AACACAGCTGAGTTTTGTTT
89646	87733	TAACACAGCTGAGTTTTGTT
89647	87734	TTAACACAGCTGAGTTTTGT
89648	87735	TTTAACACAGCTGAGTTTTG
89649	87736	ATTTAACACAGCTGAGTTTT
89650	87737	GATTTAACACAGCTGAGTTT
89651	87738	AGATTTAACACAGCTGAGTT
89652	87739	CAGATTTAACACAGCTGAGT
89653	87740	ACAGATTTAACACAGCTGAG
89654	87741	AACAGATTTAACACAGCTGA
89655	87742	AAACAGATTTAACACAGCTG
89656	87743	AAAACAGATTTAACACAGCT
89657	87744	AAAAACAGATTTAACACAGC
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89659	87746	CTAAAAACAGATTTAACACA
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89661	87748	AACTAAAAACAGATTTAACA
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89663	87750	GCAACTAAAAACAGATTTAA
89664	87751	AGCAACTAAAAACAGATTTA
89665	87752	TAGCAACTAAAAACAGATTT
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89667	87754	TATAGCAACTAAAAACAGAT
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89669	87756	TGTATAGCAACTAAAAACAG
89670	87757	ATGTATAGCAACTAAAAACA
89671	87758	AATGTATAGCAACTAAAAAC
89672	87759	AAATGTATAGCAACTAAAAA
89673	87760	GAAATGTATAGCAACTAAAA
89674	87761	AGAAATGTATAGCAACTAAA
89675	87762	CAGAAATGTATAGCAACTAA
89676	87763	GCAGAAATGTATAGCAACTA
89677	87764	AGCAGAAATGTATAGCAACT
89678	87765	GAGCAGAAATGTATAGCAAC
89679	87766	TGAGCAGAAATGTATAGCAA
89680	87767	CTGAGCAGAAATGTATAGCA
89681	87768	GCTGAGCAGAAATGTATAGC

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138759	136846	TAAAATCACCTACTATCTTT
138760	136847	ATAAAATCACCTACTATCTT
138761	136848	AATAAAATCACCTACTATCT
138762	136849	TAATAAAATCACCTACTATC
138763	136850	ATAATAAAATCACCTACTAT
138764	136851	CATAATAAAATCACCTACTA
138765	136852	ACATAATAAAATCACCTACT
138766	136853	TACATAATAAAATCACCTAC
138767	136854	GTACATAATAAAATCACCTA
138768	136855	AGTACATAATAAAATCACCT
138769	136856	GAGTACATAATAAAATCACC
138770	136857	TGAGTACATAATAAAATCAC
138771	136858	TTGAGTACATAATAAAATCA
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138775	136862	CAAATTGAGTACATAATAAA
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138779	136866	ACCTCAAATTGAGTACATAA
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138781	136868	AGACCTCAAATTGAGTACAT
138782	136869	GAGACCTCAAATTGAGTACA
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138784	136871	TTGAGACCTCAAATTGAGTA
138785	136872	TTTGAGACCTCAAATTGAGT
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138789	136876	TACATTTGAGACCTCAAATT
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138791	136878	ACTACATTTGAGACCTCAAA
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138793	136880	TAACTACATTTGAGACCTCA
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138795	136882	GATAACTACATTTGAGACCT
138796	136883	GGATAACTACATTTGAGACC
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138798	136885	GAGGATAACTACATTTGAGA
138799	136886	TGAGGATAACTACATTTGAG
138800	136887	GTGAGGATAACTACATTTGA
138801	136888	GGTGAGGATAACTACATTTG
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138803	136890	ATGGTGAGGATAACTACATT
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138809	136896	AGTAAGATGGTGAGGATAAC
138810	136897	CAGTAAGATGGTGAGGATAA
138811	136898	ACAGTAAGATGGTGAGGATA
138812	136899	GACAGTAAGATGGTGAGGAT
138813	136900	AGACAGTAAGATGGTGAGGA
138814	136901	GAGACAGTAAGATGGTGAGG
138815	136902	AGAGACAGTAAGATGGTGAG
138816	136903	CAGAGACAGTAAGATGGTGA
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138821	136908	ACTAACAGAGACAGTAAGAT
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138823	136910	CTACTAACAGAGACAGTAAG
138824	136911	ACTACTAACAGAGACAGTAA
138825	136912	AACTACTAACAGAGACAGTA
138826	136913	AAACTACTAACAGAGACAGT
138827	136914	CAAACTACTAACAGAGACAG
138828	136915	CCAAACTACTAACAGAGACA

40535	38622	AAATTAGCCAGGCGTGGTGG
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40537	38624	CAAAATTAGCCAGGCGTGGT
40538	38625	ACAAAATTAGCCAGGCGTGG
40539	38626	AACAAAATTAGCCAGGCGTG
40540	38627	AAACAAAATTAGCCAGGCGT
40541	38628	AAAACAAAATTAGCCAGGCG
40542	38629	AAAAACAAAATTAGCCAGGC
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40544	38631	ACAAAAACAAAATTAGCCAG
40545	38632	TACAAAAACAAAATTAGCCA
40546	38633	ATACAAAAACAAAATTAGCC
40547	38634	AATACAAAAACAAAATTAGC
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40549	38636	AAAATACAAAAACAAAATTA
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40551	38638	TAAAAATACAAAAACAAAAT
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40564	38651	ACCCCATCTCTACTAAAAAT
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40571	38658	GGCTGAAACCCCATCTCTAC
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40579	38666	CCAAGGCGGGCTGAAACCCC
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40581	38668	GGCCAAGGCGGGCTGAAACC
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40595	38682	CCAGCACTCCAGGAGGCCAA
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40598	38685	ATCCCAGCACTCCAGGAGGC
40599	38686	AATCCCAGCACTCCAGGAGG
40600	38687	TAATCCCAGCACTCCAGGAG
40601	38688	GTAATCCCAGCACTCCAGGA
40602	38689	TGTAATCCCAGCACTCCAGG
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89682	87769	AGCTGAGCAGAAATGTATAG
89683	87770	AAGCTGAGCAGAAATGTATA
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89685	87772	TGAAGCTGAGCAGAAATGTA
89686	87773	ATGAAGCTGAGCAGAAATGT
89687	87774	CATGAAGCTGAGCAGAAATG
89688	87775	ACATGAAGCTGAGCAGAAAT
89689	87776	CACATGAAGCTGAGCAGAAA
89690	87777	TCACATGAAGCTGAGCAGAA
89691	87778	ATCACATGAAGCTGAGCAGA
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89693	87780	GCATCACATGAAGCTGAGCA
89694	87781	TGCATCACATGAAGCTGAGC
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89722	87809	AGGAATTTAGGATACAATTA
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89724	87811	AAAGGAATTTAGGATACAAT
89725	87812	CAAAGGAATTTAGGATACAA
89726	87813	ACAAAGGAATTTAGGATACA
89727	87814	TACAAAGGAATTTAGGATAC
89728	87815	GTACAAAGGAATTTAGGATA
89729	87816	AGTACAAAGGAATTTAGGAT
89730	87817	AAGTACAAAGGAATTTAGGA
89731	87818	AAAGTACAAAGGAATTTAGG
89732	87819	AAAAGTACAAAGGAATTTAG
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89735	87822	ATAAAAAGTACAAAGGAATT
89736	87823	AATAAAAAGTACAAAGGAAT
89737	87824	AAATAAAAAGTACAAAGGAA
89738	87825	AAAATAAAAAGTACAAAGGA
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89745	87832	AAGGAAGAAAATAAAAAGTA
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89749	87836	GACCAAGGAAGAAAATAAAA
89750	87837	AGACCAAGGAAGAAAATAAA
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89752	87839	GAAGACCAAGGAAGAAAATA

138829	136916	ACCAAACTACTAACAGAGAC
138830	136917	CACCAAACTACTAACAGAGA
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138832	136919	AACACCAAACTACTAACAGA
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138835	136922	AACAACACCAAACTACTAAC
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138837	136924	AAAACAACACCAAACTACTA
138838	136925	GAAAACAACACCAAACTACT
138839	136926	GGAAAACAACACCAAACTAC
138840	136927	AGGAAAACAACACCAAACTA
138841	136928	CAGGAAAACAACACCAAACT
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138843	136930	ACCAGGAAAACAACACCAAA
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138845	136932	TTACCAGGAAAACAACACCA
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138850	136937	GCTACTTACCAGGAAAACAA
138851	136938	AGCTACTTACCAGGAAAACA
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138854	136941	CTTAGCTACTTACCAGGAAA
138855	136942	CCTTAGCTACTTACCAGGAA
138856	136943	ACCTTAGCTACTTACCAGGA
138857	136944	GACCTTAGCTACTTACCAGG
138858	136945	GGACCTTAGCTACTTACCAG
138859	136946	AGGACCTTAGCTACTTACCA
138860	136947	AAGGACCTTAGCTACTTACC
138861	136948	TAAGGACCTTAGCTACTTAC
138862	136949	TTAAGGACCTTAGCTACTTA
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138869	136956	TTAATGATTAAGGACCTTAG
138870	136957	GTTAATGATTAAGGACCTTA
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138873	136960	GGTGTTAATGATTAAGGACC
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138875	136962	TAGGTGTTAATGATTAAGGA
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138877	136964	CTTAGGTGTTAATGATTAAG
138878	136965	GCTTAGGTGTTAATGATTAA
138879	136966	GGCTTAGGTGTTAATGATTA
138880	136967	AGGCTTAGGTGTTAATGATT
138881	136968	AAGGCTTAGGTGTTAATGAT
138882	136969	TAAGGCTTAGGTGTTAATGA
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138894	136981	TGCTAAGGCAATTAAGGCTT
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40608	38695	CACGCCTGTAATCCCAGCAC
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40612	38699	GACTCACGCCTGTAATCCCA
40613	38700	TGACTCACGCCTGTAATCCC
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40615	38702	CCTGACTCACGCCTGTAATC
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89753	87840	TGAAGACCAAGGAAGAAAAT
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89760	87847	AGATAATTGAAGACCAAGGA
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89762	87849	TAAGATAATTGAAGACCAAG
89763	87850	TTAAGATAATTGAAGACCAA
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89794	87881	GATTTTTAAAATTTTTGTTT
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89799	87886	AAGAAGATTTTTAAAATTTT
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89801	87888	TGAAGAAGATTTTTAAAATT
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89808	87895	GACCGGCTGAAGAAGATTTT
89809	87896	TGACCGGCTGAAGAAGATTT
89810	87897	CTGACCGGCTGAAGAAGATT
89811	87898	CCTGACCGGCTGAAGAAGAT
89812	87899	GCCTGACCGGCTGAAGAAGA
89813	87900	CGCCTGACCGGCTGAAGAAG
89814	87901	GCGCCTGACCGGCTGAAGAA
89815	87902	TGCGCCTGACCGGCTGAAGA
89816	87903	CTGCGCCTGACCGGCTGAAG
89817	87904	ACTGCGCCTGACCGGCTGAA
89818	87905	CACTGCGCCTGACCGGCTGA
89819	87906	CCACTGCGCCTGACCGGCTG
89820	87907	GCCACTGCGCCTGACCGGCT
89821	87908	AGCCACTGCGCCTGACCGGC
89822	87909	GAGCCACTGCGCCTGACCGG
89823	87910	TGAGCCACTGCGCCTGACCG

138900	136987	AAGTTGTGCTAAGGCAATTA
138901	136988	GAAGTTGTGCTAAGGCAATT
138902	136989	GGAAGTTGTGCTAAGGCAAT
138903	136990	GGGAAGTTGTGCTAAGGCAA
138904	136991	GGGGAAGTTGTGCTAAGGCA
138905	136992	AGGGGAAGTTGTGCTAAGGC
138906	136993	TAGGGGAAGTTGTGCTAAGG
138907	136994	TTAGGGGAAGTTGTGCTAAG
138908	136995	TTTAGGGGAAGTTGTGCTAA
138909	136996	TTTTAGGGGAAGTTGTGCTA
138910	136997	CTTTTAGGGGAAGTTGTGCT
138911	136998	CCTTTTAGGGGAAGTTGTGC
138912	136999	CCCTTTTAGGGGAAGTTGTG
138913	137000	TCCCTTTTAGGGGAAGTTGT
138914	137001	CTCCCTTTTAGGGGAAGTTG
138915	137002	ACTCCCTTTTAGGGGAAGTT
138916	137003	TACTCCCTTTTAGGGGAAGT
138917	137004	ATACTCCCTTTTAGGGGAAG
138918	137005	GATACTCCCTTTTAGGGGAA
138919	137006	TGATACTCCCTTTTAGGGGA
138920	137007	CTGATACTCCCTTTTAGGGG
138921	137008	ACTGATACTCCCTTTTAGGG
138922	137009	TACTGATACTCCCTTTTAGG
138923	137010	GTACTGATACTCCCTTTTAG
138924	137011	AGTACTGATACTCCCTTTTA
138925	137012	AAGTACTGATACTCCCTTTT
138926	137013	AAAGTACTGATACTCCCTTT
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138928	137015	AAAAAGTACTGATACTCCCT
138929	137016	TAAAAAGTACTGATACTCCC
138930	137017	TTAAAAAGTACTGATACTCC
138931	137018	TTTAAAAAGTACTGATACTC
138932	137019	TTTTAAAAAGTACTGATACT
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138934	137021	TCTTTTAAAAAGTACTGATA
138935	137022	TTCTTTTAAAAAGTACTGAT
138936	137023	TTTCTTTTAAAAAGTACTGA
138937	137024	GTTTCTTTTAAAAAGTACTG
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138939	137026	TAGTTTCTTTTAAAAAGTAC
138940	137027	TTAGTTTCTTTTAAAAAGTA
138941	137028	GTTAGTTTCTTTTAAAAAGT
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138943	137030	CTGTTAGTTTCTTTTAAAAA
138944	137031	ACTGTTAGTTTCTTTTAAAA
138945	137032	AACTGTTAGTTTCTTTTAAA
138946	137033	CAACTGTTAGTTTCTTTTAA
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138948	137035	CCCAACTGTTAGTTTCTTTT
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138960	137047	TTAAATTAGCAGCCCAACTG
138961	137048	ATTAAATTAGCAGCCCAACT
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138963	137050	AGATTAAATTAGCAGCCCAA
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138968	137055	GCAGCAGATTAAATTAGCAG
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40681	38768	ACATGTTTTAAGAACGAAAG
40682	38769	AACATGTTTTAAGAACGAAA
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40686	38773	TATAAACATGTTTTAAGAAC
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40743	38830	TAGAAATTGCTTGTATAACC
40744	38831	ATAGAAATTGCTTGTATAAC
40745	38832	AATAGAAATTGCTTGTATAA
40746	38833	CAATAGAAATTGCTTGTATA
40747	38834	GCAATAGAAATTGCTTGTAT

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89826	87913	CCGTGAGCCACTGCGCCTGA
89827	87914	GCCGTGAGCCACTGCGCCTG
89828	87915	AGCCGTGAGCCACTGCGCCT
89829	87916	CAGCCGTGAGCCACTGCGCC
89830	87917	ACAGCCGTGAGCCACTGCGC
89831	87918	TACAGCCGTGAGCCACTGCG
89832	87919	TTACAGCCGTGAGCCACTGC
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89835	87922	GGATTACAGCCGTGAGCCAC
89836	87923	GGGATTACAGCCGTGAGCCA
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89839	87926	GCTGGGATTACAGCCGTGAG
89840	87927	TGCTGGGATTACAGCCGTGA
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89845	87932	CCAAGTGCTGGGATTACAGC
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89891	87978	GCTGGTGTTGAACTCCTGAC
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138974	137061	AATGAAGCAGCAGATTAAAT
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138977	137064	GGAAATGAAGCAGCAGATTA
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138980	137067	GGGGGAAATGAAGCAGCAGA
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138982	137069	CAGGGGGAAATGAAGCAGCA
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138984	137071	AACAGGGGGAAATGAAGCAG
138985	137072	GAACAGGGGGAAATGAAGCA
138986	137073	AGAACAGGGGGAAATGAAGC
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138996	137083	AAAATGGCTTAGAACAGGGG
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40769	38856	CACCCACTGGAAAAAGAAGT
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89903	87990	CATGTTGGCCAGGCTGGTGT
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89934	88021	TTTTGTATTTTTAGTAGAGA
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89936	88023	ATTTTTGTATTTTTAGTAGA
89937	88024	AATTTTTGTATTTTTAGTAG
89938	88025	TAATTTTTGTATTTTTAGTA
89939	88026	CTAATTTTTGTATTTTTAGT
89940	88027	GCTAATTTTTGTATTTTTAG
89941	88028	AGCTAATTTTTGTATTTTTA
89942	88029	CAGCTAATTTTTGTATTTTT
89943	88030	CCAGCTAATTTTTGTATTTT
89944	88031	CCCAGCTAATTTTTGTATTT
89945	88032	GCCCAGCTAATTTTTGTATT
89946	88033	TGCCCAGCTAATTTTTGTAT
89947	88034	ATGCCCAGCTAATTTTTGTA
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89949	88036	CAATGCCCAGCTAATTTTTG
89950	88037	ACAATGCCCAGCTAATTTTT
89951	88038	CACAATGCCCAGCTAATTTT
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89954	88041	CGCCACAATGCCCAGCTAAT
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89956	88043	CGCGCCACAATGCCCAGCTA
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89959	88046	GAACGCGCCACAATGCCCAG
89960	88047	AGAACGCGCCACAATGCCCA
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89962	88049	CAAGAACGCGCCACAATGCC
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139057	137144	AAGTGAAGGAAAGTTGAAAA
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139060	137147	GGGAAGTGAAGGAAAGTTGA
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139062	137149	AAGGGAAGTGAAGGAAAGTT
139063	137150	AAAGGGAAGTGAAGGAAAGT
139064	137151	AAAAGGGAAGTGAAGGAAAG
139065	137152	AAAAAGGGAAGTGAAGGAAA
139066	137153	GAAAAAGGGAAGTGAAGGAA
139067	137154	AGAAAAAGGGAAGTGAAGGA
139068	137155	CAGAAAAAGGGAAGTGAAGG
139069	137156	TCAGAAAAAGGGAAGTGAAG
139070	137157	TTCAGAAAAAGGGAAGTGAA
139071	137158	ATTCAGAAAAAGGGAAGTGA
139072	137159	AATTCAGAAAAAGGGAAGTG
139073	137160	AAATTCAGAAAAAGGGAAGT
139074	137161	TAAATTCAGAAAAAGGGAAG
139075	137162	TTAAATTCAGAAAAAGGGAA
139076	137163	GTTAAATTCAGAAAAAGGGA
139077	137164	TGTTAAATTCAGAAAAAGGG
139078	137165	ATGTTAAATTCAGAAAAAGG
139079	137166	GATGTTAAATTCAGAAAAAG
139080	137167	TGATGTTAAATTCAGAAAAA
139081	137168	CTGATGTTAAATTCAGAAAA
139082	137169	TCTGATGTTAAATTCAGAAA
139083	137170	ATCTGATGTTAAATTCAGAA
139084	137171	AATCTGATGTTAAATTCAGA
139085	137172	AAATCTGATGTTAAATTCAG
139086	137173	TAAATCTGATGTTAAATTCA
139087	137174	GTAAATCTGATGTTAAATTC
139088	137175	TGTAAATCTGATGTTAAATT
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139090	137177	CTTGTAAATCTGATGTTAAA
139091	137178	ACTTGTAAATCTGATGTTAA
139092	137179	AACTTGTAAATCTGATGTTA
139093	137180	CAACTTGTAAATCTGATGTT
139094	137181	CCAACTTGTAAATCTGATGT
139095	137182	TCCAACTTGTAAATCTGATG
139096	137183	TTCCAACTTGTAAATCTGAT
139097	137184	CTTCCAACTTGTAAATCTGA
139098	137185	TCTTCCAACTTGTAAATCTG
139099	137186	ATCTTCCAACTTGTAAATCT
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139105	137192	AACAAAATCTTCCAACTTGT
139106	137193	AAACAAAATCTTCCAACTTG
139107	137194	AAAACAAAATCTTCCAACTT
139108	137195	CAAAACAAAATCTTCCAACT
139109	137196	ACAAAACAAAATCTTCCAAC
139110	137197	AACAAAACAAAATCTTCCAA
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139112	137199	AAAACAAAACAAAATCTTCC

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40820	38907	TTCAACAACAAAAAAAAAAA
40821	38908	TTTCAACAACAAAAAAAAAA
40822	38909	TTTTCAACAACAAAAAAAAA
40823	38910	GTTTTCAACAACAAAAAAAA
40824	38911	AGTTTTCAACAACAAAAAAA
40825	38912	CAGTTTTCAACAACAAAAAA
40826	38913	CCAGTTTTCAACAACAAAAA
40827	38914	TCCAGTTTTCAACAACAAAA
40828	38915	GTCCAGTTTTCAACAACAAA
40829	38916	TGTCCAGTTTTCAACAACAA
40830	38917	ATGTCCAGTTTTCAACAACA
40831	38918	AATGTCCAGTTTTCAACAAC
40832	38919	AAATGTCCAGTTTTCAACAA
40833	38920	AAAATGTCCAGTTTTCAACA
40834	38921	TAAAATGTCCAGTTTTCAAC
40835	38922	TTAAAATGTCCAGTTTTCAA
40836	38923	CTTAAAATGTCCAGTTTTCA
40837	38924	ACTTAAAATGTCCAGTTTTC
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40839	38926	TTACTTAAAATGTCCAGTTT
40840	38927	ATTACTTAAAATGTCCAGTT
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40843	38930	TACATTACTTAAAATGTCCA
40844	38931	CTACATTACTTAAAATGTCC
40845	38932	ACTACATTACTTAAAATGTC
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40847	38934	TTACTACATTACTTAAAATG
40848	38935	GTTACTACATTACTTAAAAT
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40850	38937	GAGTTACTACATTACTTAAA
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40855	38942	ATCCAGAGTTACTACATTAC
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40859	38946	AGGTATCCAGAGTTACTACA
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40864	38951	TAATGAGGTATCCAGAGTTA
40865	38952	CTAATGAGGTATCCAGAGTT
40866	38953	GCTAATGAGGTATCCAGAGT
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40868	38955	AGGCTAATGAGGTATCCAGA
40869	38956	TAGGCTAATGAGGTATCCAG
40870	38957	ATAGGCTAATGAGGTATCCA
40871	38958	CATAGGCTAATGAGGTATCC
40872	38959	CCATAGGCTAATGAGGTATC
40873	38960	ACCATAGGCTAATGAGGTAT
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40875	38962	CAACCATAGGCTAATGAGGT
40876	38963	CCAACCATAGGCTAATGAGG
40877	38964	CCCAACCATAGGCTAATGAG
40878	38965	CCCCAACCATAGGCTAATGA
40879	38966	CCCCCAACCATAGGCTAATG
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89966	88053	ATTACAAGAACGCGCCACAA
89967	88054	GATTACAAGAACGCGCCACA
89968	88055	GGATTACAAGAACGCGCCAC
89969	88056	GGGATTACAAGAACGCGCCA
89970	88057	TGGGATTACAAGAACGCGCC
89971	88058	CTGGGATTACAAGAACGCGC
89972	88059	GCTGGGATTACAAGAACGCG
89973	88060	AGCTGGGATTACAAGAACGC
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89975	88062	GCAGCTGGGATTACAAGAAC
89976	88063	AGCAGCTGGGATTACAAGAA
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89979	88066	CTGAGCAGCTGGGATTACAA
89980	88067	CCTGAGCAGCTGGGATTACA
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89982	88069	CTCCTGAGCAGCTGGGATTA
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89984	88071	GCCTCCTGAGCAGCTGGGAT
89985	88072	AGCCTCCTGAGCAGCTGGGA
89986	88073	CAGCCTCCTGAGCAGCTGGG
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89988	88075	CTCAGCCTCCTGAGCAGCTG
89989	88076	CCTCAGCCTCCTGAGCAGCT
89990	88077	GCCTCAGCCTCCTGAGCAGC
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90012	88099	TCCTGGTTCAAGCAATTCTC
90013	88100	GTCCTGGTTCAAGCAATTCT
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90021	88108	CCTCCCGGGTCCTGGTTCAA
90022	88109	ACCTCCCGGGTCCTGGTTCA
90023	88110	CACCTCCCGGGTCCTGGTTC
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90033	88120	CCGCAACCTACACCTCCCGG
90034	88121	ACCGCAACCTACACCTCCCG
90035	88122	CACCGCAACCTACACCTCCC
90036	88123	TCACCGCAACCTACACCTCC

139113	137200	TAAAACAAAACAAAATCTTC
139114	137201	ATAAAACAAAACAAAATCTT
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139116	137203	TTATAAAACAAAACAAAATC
139117	137204	CTTATAAAACAAAACAAAAT
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139119	137206	AACTTATAAAACAAAACAAA
139120	137207	AAACTTATAAAACAAAACAA
139121	137208	AAAACTTATAAAACAAAACA
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139123	137210	GCAAAACTTATAAAACAAAA
139124	137211	TGCAAAACTTATAAAACAAA
139125	137212	TTGCAAAACTTATAAAACAA
139126	137213	ATTGCAAAACTTATAAAACA
139127	137214	CATTGCAAAACTTATAAAAC
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139133	137220	CACCAGCATTGCAAAACTTA
139134	137221	TCACCAGCATTGCAAAACTT
139135	137222	ATCACCAGCATTGCAAAACT
139136	137223	GATCACCAGCATTGCAAAAC
139137	137224	AGATCACCAGCATTGCAAAA
139138	137225	GAGATCACCAGCATTGCAAA
139139	137226	AGAGATCACCAGCATTGCAA
139140	137227	AAGAGATCACCAGCATTGCA
139141	137228	TAAGAGATCACCAGCATTGC
139142	137229	ATAAGAGATCACCAGCATTG
139143	137230	CATAAGAGATCACCAGCATT
139144	137231	TCATAAGAGATCACCAGCAT
139145	137232	GTCATAAGAGATCACCAGCA
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139147	137234	AAGTCATAAGAGATCACCAG
139148	137235	CAAGTCATAAGAGATCACCA
139149	137236	ACAAGTCATAAGAGATCACC
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139151	137238	GCACAAGTCATAAGAGATCA
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139154	137241	GATGCACAAGTCATAAGAGA
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139157	137244	TTGGATGCACAAGTCATAAG
139158	137245	TTTGGATGCACAAGTCATAA
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139162	137249	TGACTTTGGATGCACAAGTC
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139165	137252	TTTTGACTTTGGATGCACAA
139166	137253	ATTTTGACTTTGGATGCACA
139167	137254	CATTTTGACTTTGGATGCAC
139168	137255	TCATTTTGACTTTGGATGCA
139169	137256	GTCATTTTGACTTTGGATGC
139170	137257	TGTCATTTTGACTTTGGATG
139171	137258	TTGTCATTTTGACTTTGGAT
139172	137259	TTTGTCATTTTGACTTTGGA
139173	137260	TTTTGTCATTTTGACTTTGG
139174	137261	GTTTTGTCATTTTGACTTTG
139175	137262	GGTTTTGTCATTTTGACTTT
139176	137263	AGGTTTTGTCATTTTGACTT
139177	137264	TAGGTTTTGTCATTTTGACT
139178	137265	CTAGGTTTTGTCATTTTGAC
139179	137266	ACTAGGTTTTGTCATTTTGA
139180	137267	AACTAGGTTTTGTCATTTTG
139181	137268	TAACTAGGTTTTGTCATTTT
139182	137269	GTAACTAGGTTTTGTCATTT
139183	137270	TGTAACTAGGTTTTGTCATT

40890	38977	AACAACCACCACCCCCAACC
40891	38978	TAACAACCACCACCCCCAAC
40892	38979	GTAACAACCACCACCCCCAA
40893	38980	AGTAACAACCACCACCCCCA
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40902	38989	GCAAATAACAGTAACAACCA
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40912	38999	AGACAAATAAGCAAATAACA
40913	39000	TAGACAAATAAGCAAATAAC
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40927	39014	ATTCAGCCAGTCATTAGACA
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40932	39019	AAATCATTCAGCCAGTCATT
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40935	39022	CTAAAATCATTCAGCCAGTC
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40938	39025	ACACTAAAATCATTCAGCCA
40939	39026	AACACTAAAATCATTCAGCC
40940	39027	GAACACTAAAATCATTCAGC
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40942	39029	TAGAACACTAAAATCATTCA
40943	39030	ATAGAACACTAAAATCATTC
40944	39031	GATAGAACACTAAAATCATT
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40947	39034	AAGGATAGAACACTAAAATC
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40950	39037	AAGAAGGATAGAACACTAAA
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40960	39047	ACAGGGAGGGAAGAAGGATA

90037	88124	CTCACCGCAACCTACACCTC
90038	88125	GCTCACCGCAACCTACACCT
90039	88126	CGCTCACCGCAACCTACACC
90040	88127	CCGCTCACCGCAACCTACAC
90041	88128	TCCGCTCACCGCAACCTACA
90042	88129	CTCCGCTCACCGCAACCTAC
90043	88130	TCTCCGCTCACCGCAACCTA
90044	88131	ATCTCCGCTCACCGCAACCT
90045	88132	GATCTCCGCTCACCGCAACC
90046	88133	CGATCTCCGCTCACCGCAAC
90047	88134	GCGATCTCCGCTCACCGCAA
90048	88135	CGCGATCTCCGCTCACCGCA
90049	88136	GCGCGATCTCCGCTCACCGC
90050	88137	GGCGCGATCTCCGCTCACCG
90051	88138	TGGCGCGATCTCCGCTCACC
90052	88139	GTGGCGCGATCTCCGCTCAC
90053	88140	AGTGGCGCGATCTCCGCTCA
90054	88141	CAGTGGCGCGATCTCCGCTC
90055	88142	GCAGTGGCGCGATCTCCGCT
90056	88143	TGCAGTGGCGCGATCTCCGC
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90058	88145	AGTGCAGTGGCGCGATCTCC
90059	88146	GAGTGCAGTGGCGCGATCTC
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90063	88150	GCTGGAGTGCAGTGGCGCGA
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90068	88155	CCCAGGCTGGAGTGCAGTGG
90069	88156	GCCCAGGCTGGAGTGCAGTG
90070	88157	AGCCCAGGCTGGAGTGCAGT
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90073	88160	TATAGCCCAGGCTGGAGTGC
90074	88161	CTATAGCCCAGGCTGGAGTG
90075	88162	TCTATAGCCCAGGCTGGAGT
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90077	88164	ACTCTATAGCCCAGGCTGGA
90078	88165	CACTCTATAGCCCAGGCTGG
90079	88166	TCACTCTATAGCCCAGGCTG
90080	88167	CTCACTCTATAGCCCAGGCT
90081	88168	TCTCACTCTATAGCCCAGGC
90082	88169	GTCTCACTCTATAGCCCAGG
90083	88170	AGTCTCACTCTATAGCCCAG
90084	88171	GAGTCTCACTCTATAGCCCA
90085	88172	GGAGTCTCACTCTATAGCCC
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90087	88174	ATGGAGTCTCACTCTATAGC
90088	88175	AATGGAGTCTCACTCTATAG
90089	88176	AAATGGAGTCTCACTCTATA
90090	88177	GAAATGGAGTCTCACTCTAT
90091	88178	TGAAATGGAGTCTCACTCTA
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90093	88180	TTTGAAATGGAGTCTCACTC
90094	88181	TTTTGAAATGGAGTCTCACT
90095	88182	TTTTTGAAATGGAGTCTCAC
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90105	88192	TTTTTTTTTTTTTTTGAAAT
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139184	137271	TTGTAACTAGGTTTTGTCAT
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139186	137273	ATTTGTAACTAGGTTTTGTC
139187	137274	AATTTGTAACTAGGTTTTGT
139188	137275	TAATTTGTAACTAGGTTTTG
139189	137276	TTAATTTGTAACTAGGTTTT
139190	137277	TTTAATTTGTAACTAGGTTT
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139192	137279	TGTTTAATTTGTAACTAGGT
139193	137280	GTGTTTAATTTGTAACTAGG
139194	137281	TGTGTTTAATTTGTAACTAG
139195	137282	GTGTGTTTAATTTGTAACTA
139196	137283	TGTGTGTTTAATTTGTAACT
139197	137284	CTGTGTGTTTAATTTGTAAC
139198	137285	GCTGTGTGTTTAATTTGTAA
139199	137286	AGCTGTGTGTTTAATTTGTA
139200	137287	AAGCTGTGTGTTTAATTTGT
139201	137288	AAAGCTGTGTGTTTAATTTG
139202	137289	GAAAGCTGTGTGTTTAATTT
139203	137290	AGAAAGCTGTGTGTTTAATT
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139205	137292	ACAGAAAGCTGTGTGTTTAA
139206	137293	TACAGAAAGCTGTGTGTTTA
139207	137294	GTACAGAAAGCTGTGTGTTT
139208	137295	AGTACAGAAAGCTGTGTGTT
139209	137296	AAGTACAGAAAGCTGTGTGT
139210	137297	TAAGTACAGAAAGCTGTGTG
139211	137298	TTAAGTACAGAAAGCTGTGT
139212	137299	ATTAAGTACAGAAAGCTGTG
139213	137300	AATTAAGTACAGAAAGCTGT
139214	137301	AAATTAAGTACAGAAAGCTG
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139216	137303	GCAAATTAAGTACAGAAAGC
139217	137304	AGCAAATTAAGTACAGAAAG
139218	137305	AAGCAAATTAAGTACAGAAA
139219	137306	GAAGCAAATTAAGTACAGAA
139220	137307	TGAAGCAAATTAAGTACAGA
139221	137308	CTGAAGCAAATTAAGTACAG
139222	137309	ACTGAAGCAAATTAAGTACA
139223	137310	CACTGAAGCAAATTAAGTAC
139224	137311	TCACTGAAGCAAATTAAGTA
139225	137312	CTCACTGAAGCAAATTAAGT
139226	137313	TCTCACTGAAGCAAATTAAG
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139230	137317	GTGATCTCACTGAAGCAAAT
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139232	137319	CTGTGATCTCACTGAAGCAA
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139234	137321	AGCTGTGATCTCACTGAAGC
139235	137322	CAGCTGTGATCTCACTGAAG
139236	137323	TCAGCTGTGATCTCACTGAA
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139238	137325	CCTCAGCTGTGATCTCACTG
139239	137326	TCCTCAGCTGTGATCTCACT
139240	137327	TTCCTCAGCTGTGATCTCAC
139241	137328	TTTCCTCAGCTGTGATCTCA
139242	137329	GTTTCCTCAGCTGTGATCTC
139243	137330	AGTTTCCTCAGCTGTGATCT
139244	137331	TAGTTTCCTCAGCTGTGATC
139245	137332	CTAGTTTCCTCAGCTGTGAT
139246	137333	ACTAGTTTCCTCAGCTGTGA
139247	137334	AACTAGTTTCCTCAGCTGTG
139248	137335	GAACTAGTTTCCTCAGCTGT
139249	137336	AGAACTAGTTTCCTCAGCTG
139250	137337	CAGAACTAGTTTCCTCAGCT
139251	137338	CCAGAACTAGTTTCCTCAGC
139252	137339	TCCAGAACTAGTTTCCTCAG
139253	137340	TTCCAGAACTAGTTTCCTCA
139254	137341	ATTCCAGAACTAGTTTCCTC

40961	39048	TACAGGGAGGGAAGAAGGAT
40962	39049	GTACAGGGAGGGAAGAAGGA
40963	39050	TGTACAGGGAGGGAAGAAGG
40964	39051	CTGTACAGGGAGGGAAGAAG
40965	39052	ACTGTACAGGGAGGGAAGAA
40966	39053	CACTGTACAGGGAGGGAAGA
40967	39054	ACACTGTACAGGGAGGGAAG
40968	39055	CACACTGTACAGGGAGGGAA
40969	39056	TCACACTGTACAGGGAGGGA
40970	39057	GTCACACTGTACAGGGAGGG
40971	39058	TGTCACACTGTACAGGGAGG
40972	39059	GTGTCACACTGTACAGGGAG
40973	39060	CGTGTCACACTGTACAGGGA
40974	39061	ACGTGTCACACTGTACAGGG
40975	39062	GACGTGTCACACTGTACAGG
40976	39063	AGACGTGTCACACTGTACAG
40977	39064	CAGACGTGTCACACTGTACA
40978	39065	TCAGACGTGTCACACTGTAC
40979	39066	ATCAGACGTGTCACACTGTA
40980	39067	CATCAGACGTGTCACACTGT
40981	39068	GCATCAGACGTGTCACACTG
40982	39069	AGCATCAGACGTGTCACACT
40983	39070	TAGCATCAGACGTGTCACAC
40984	39071	CTAGCATCAGACGTGTCACA
40985	39072	ACTAGCATCAGACGTGTCAC
40986	39073	AACTAGCATCAGACGTGTCA
40987	39074	AAACTAGCATCAGACGTGTC
40988	39075	AAAACTAGCATCAGACGTGT
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40991	39078	AAGAAAACTAGCATCAGACG
40992	39079	CAAGAAAACTAGCATCAGAC
40993	39080	CCAAGAAAACTAGCATCAGA
40994	39081	CCCAAGAAAACTAGCATCAG
40995	39082	TCCCAAGAAAACTAGCATCA
40996	39083	ATCCCAAGAAAACTAGCATC
40997	39084	CATCCCAAGAAAACTAGCAT
40998	39085	GCATCCCAAGAAAACTAGCA
40999	39086	TGCATCCCAAGAAAACTAGC
41000	39087	CTGCATCCCAAGAAAACTAG
41001	39088	GCTGCATCCCAAGAAAACTA
41002	39089	GGCTGCATCCCAAGAAAACT
41003	39090	AGGCTGCATCCCAAGAAAAC
41004	39091	AAGGCTGCATCCCAAGAAAA
41005	39092	CAAGGCTGCATCCCAAGAAA
41006	39093	CCAAGGCTGCATCCCAAGAA
41007	39094	CCCAAGGCTGCATCCCAAGA
41008	39095	ACCCAAGGCTGCATCCCAAG
41009	39096	TACCCAAGGCTGCATCCCAA
41010	39097	ATACCCAAGGCTGCATCCCA
41011	39098	CATACCCAAGGCTGCATCCC
41012	39099	GCATACCCAAGGCTGCATCC
41013	39100	GGCATACCCAAGGCTGCATC
41014	39101	AGGCATACCCAAGGCTGCAT
41015	39102	TAGGCATACCCAAGGCTGCA
41016	39103	GTAGGCATACCCAAGGCTGC
41017	39104	GGTAGGCATACCCAAGGCTG
41018	39105	TGGTAGGCATACCCAAGGCT
41019	39106	ATGGTAGGCATACCCAAGGC
41020	39107	GATGGTAGGCATACCCAAGG
41021	39108	TGATGGTAGGCATACCCAAG
41022	39109	GTGATGGTAGGCATACCCAA
41023	39110	AGTGATGGTAGGCATACCCA
41024	39111	GAGTGATGGTAGGCATACCC
41025	39112	AGAGTGATGGTAGGCATACC
41026	39113	TAGAGTGATGGTAGGCATAC
41027	39114	CTAGAGTGATGGTAGGCATA
41028	39115	TCTAGAGTGATGGTAGGCAT
41029	39116	TTCTAGAGTGATGGTAGGCA
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41031	39118	GATTCTAGAGTGATGGTAGG

90108	88195	ATTTTTTTTTTTTTTTTGA
90109	88196	GATTTTTTTTTTTTTTTTG
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90111	88198	CAGATTTTTTTTTTTTTTT
90112	88199	GCAGATTTTTTTTTTTTTT
90113	88200	AGCAGATTTTTTTTTTTTT
90114	88201	AAGCAGATTTTTTTTTTTT
90115	88202	GAAGCAGATTTTTTTTTTT
90116	88203	TGAAGCAGATTTTTTTTTT
90117	88204	CTGAAGCAGATTTTTTTTT
90118	88205	GCTGAAGCAGATTTTTTTT
90119	88206	AGCTGAAGCAGATTTTTTT
90120	88207	TAGCTGAAGCAGATTTTTT
90121	88208	ATAGCTGAAGCAGATTTTT
90122	88209	AATAGCTGAAGCAGATTTT
90123	88210	GAATAGCTGAAGCAGATTT
90124	88211	AGAATAGCTGAAGCAGATT
90125	88212	CAGAATAGCTGAAGCAGAT
90126	88213	ACAGAATAGCTGAAGCAGAT
90127	88214	AACAGAATAGCTGAAGCAGA
90128	88215	TAACAGAATAGCTGAAGCAG
90129	88216	TTAACAGAATAGCTGAAGCA
90130	88217	ATTAACAGAATAGCTGAAGC
90131	88218	GATTAACAGAATAGCTGAAG
90132	88219	AGATTAACAGAATAGCTGAA
90133	88220	AAGATTAACAGAATAGCTGA
90134	88221	AAAGATTAACAGAATAGCTG
90135	88222	AAAAGATTAACAGAATAGCT
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90138	88225	GTCAAAAGATTAACAGAATA
90139	88226	TGTCAAAAGATTAACAGAAT
90140	88227	ATGTCAAAAGATTAACAGAA
90141	88228	AATGTCAAAAGATTAACAGA
90142	88229	TAATGTCAAAAGATTAACAG
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90145	88232	AAGTAATGTCAAAAGATTAA
90146	88233	TAAGTAATGTCAAAAGATTA
90147	88234	CTAAGTAATGTCAAAAGATT
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90162	88249	TTATTTCCAGACCATCTAAG
90163	88250	TTTATTTCCAGACCATCTAA
90164	88251	ATTTATTTCCAGACCATCTA
90165	88252	AATTTATTTCCAGACCATCT
90166	88253	AAATTTATTTCCAGACCATC
90167	88254	AAAATTTATTTCCAGACCAT
90168	88255	CAAAATTTATTTCCAGACCA
90169	88256	TCAAAATTTATTTCCAGACC
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90175	88262	TTATTCTCAAAATTTATTTC
90176	88263	GTTATTCTCAAAATTTATTT
90177	88264	TGTTATTCTCAAAATTTATT
90178	88265	ATGTTATTCTCAAAATTTAT

139255	137342	CATTCCAGAACTAGTTTCCT
139256	137343	ACATTCCAGAACTAGTTTCC
139257	137344	CACATTCCAGAACTAGTTTC
139258	137345	CCACATTCCAGAACTAGTTT
139259	137346	ACCACATTCCAGAACTAGTT
139260	137347	AACCACATTCCAGAACTAGT
139261	137348	TAACCACATTCCAGAACTAG
139262	137349	CTAACCACATTCCAGAACTA
139263	137350	ACTAACCACATTCCAGAACT
139264	137351	CACTAACCACATTCCAGAAC
139265	137352	ACACTAACCACATTCCAGAA
139266	137353	AACACTAACCACATTCCAGA
139267	137354	TAACACTAACCACATTCCAG
139268	137355	ATAACACTAACCACATTCCA
139269	137356	AATAACACTAACCACATTCC
139270	137357	TAATAACACTAACCACATTC
139271	137358	TTAATAACACTAACCACATT
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139273	137360	CCTTAATAACACTAACCACA
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139275	137362	ATCCTTAATAACACTAACCA
139276	137363	AATCCTTAATAACACTAACC
139277	137364	AAATCCTTAATAACACTAAC
139278	137365	AAAATCCTTAATAACACTAA
139279	137366	AAAAATCCTTAATAACACTA
139280	137367	CAAAAATCCTTAATAACACT
139281	137368	TCAAAAATCCTTAATAACAC
139282	137369	GTCAAAAATCCTTAATAACA
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139291	137378	ATATGATCAGTCAAAAATCC
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139293	137380	ACATATGATCAGTCAAAAAT
139294	137381	AACATATGATCAGTCAAAAA
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139296	137383	TAAACATATGATCAGTCAAA
139297	137384	CTAAACATATGATCAGTCAA
139298	137385	TCTAAACATATGATCAGTCA
139299	137386	TTCTAAACATATGATCAGTC
139300	137387	ATTCTAAACATATGATCAGT
139301	137388	GATTCTAAACATATGATCAG
139302	137389	AGATTCTAAACATATGATCA
139303	137390	AAGATTCTAAACATATGATC
139304	137391	TAAGATTCTAAACATATGAT
139305	137392	TTAAGATTCTAAACATATGA
139306	137393	TTTAAGATTCTAAACATATG
139307	137394	ATTTAAGATTCTAAACATAT
139308	137395	TATTTAAGATTCTAAACATA
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139310	137397	AATATTTAAGATTCTAAACA
139311	137398	AAATATTTAAGATTCTAAAC
139312	137399	TAAATATTTAAGATTCTAAA
139313	137400	ATAAATATTTAAGATTCTAA
139314	137401	CATAAATATTTAAGATTCTA
139315	137402	ACATAAATATTTAAGATTCT
139316	137403	GACATAAATATTTAAGATTC
139317	137404	TGACATAAATATTTAAGATT
139318	137405	TTGACATAAATATTTAAGAT
139319	137406	CTTGACATAAATATTTAAGA
139320	137407	CCTTGACATAAATATTTAAG
139321	137408	TCCTTGACATAAATATTTAA
139322	137409	TTCCTTGACATAAATATTTA
139323	137410	GTTCCTTGACATAAATATTT
139324	137411	TGTTCCTTGACATAAATATT
139325	137412	GTGTTCCTTGACATAAATAT

41032	39119	TGATTCTAGAGTGATGGTAG
41033	39120	GTGATTCTAGAGTGATGGTA
41034	39121	TGTGATTCTAGAGTGATGGT
41035	39122	CTGTGATTCTAGAGTGATGG
41036	39123	ACTGTGATTCTAGAGTGATG
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41038	39125	TCACTGTGATTCTAGAGTGA
41039	39126	ATCACTGTGATTCTAGAGTG
41040	39127	AATCACTGTGATTCTAGAGT
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41042	39129	AAAATCACTGTGATTCTAGA
41043	39130	CAAAATCACTGTGATTCTAG
41044	39131	CCAAAATCACTGTGATTCTA
41045	39132	GCCAAAATCACTGTGATTCT
41046	39133	TGCCAAAATCACTGTGATTC
41047	39134	ATGCCAAAATCACTGTGATT
41048	39135	CATGCCAAAATCACTGTGAT
41049	39136	CCATGCCAAAATCACTGTGA
41050	39137	GCCATGCCAAAATCACTGTG
41051	39138	AGCCATGCCAAAATCACTGT
41052	39139	AAGCCATGCCAAAATCACTG
41053	39140	AAAGCCATGCCAAAATCACT
41054	39141	CAAAGCCATGCCAAAATCAC
41055	39142	ACAAAGCCATGCCAAAATCA
41056	39143	GACAAAGCCATGCCAAAATC
41057	39144	AGACAAAGCCATGCCAAAAT
41058	39145	GAGACAAAGCCATGCCAAAA
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41060	39147	AAGAGACAAAGCCATGCCAA
41061	39148	AAAGAGACAAAGCCATGCCA
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41063	39150	GAAAAGAGACAAAGCCATGC
41064	39151	GGAAAAGAGACAAAGCCATG
41065	39152	AGGAAAAGAGACAAAGCCAT
41066	39153	CAGGAAAAGAGACAAAGCCA
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41072	39159	TACAGTCAGGAAAAGAGACA
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41074	39161	GGTACAGTCAGGAAAAGAGA
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41078	39165	GCTGGGTACAGTCAGGAAAA
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41083	39170	TAACAGCTGGGTACAGTCAG
41084	39171	TTAACAGCTGGGTACAGTCA
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41088	39175	TAGCTTAACAGCTGGGTACA
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41093	39180	TAGTGTAGCTTAACAGCTGG
41094	39181	TTAGTGTAGCTTAACAGCTG
41095	39182	ATTAGTGTAGCTTAACAGCT
41096	39183	AATTAGTGTAGCTTAACAGC
41097	39184	TAATTAGTGTAGCTTAACAG
41098	39185	GTAATTAGTGTAGCTTAACA
41099	39186	AGTAATTAGTGTAGCTTAAC
41100	39187	TAGTAATTAGTGTAGCTTAA
41101	39188	CTAGTAATTAGTGTAGCTTA
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90179	88266	CATGTTATTCTCAAAATTTA
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90181	88268	ATCATGTTATTCTCAAAATT
90182	88269	AATCATGTTATTCTCAAAAT
90183	88270	TAATCATGTTATTCTCAAAA
90184	88271	CTAATCATGTTATTCTCAAA
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90199	88286	TATACTCTCTCACTTCTAAT
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90208	88295	AACTATGCTTATACTCTCTC
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90218	88305	GTATCTCCAAAACTATGCTT
90219	88306	TGTATCTCCAAAACTATGCT
90220	88307	GTGTATCTCCAAAACTATGC
90221	88308	AGTGTATCTCCAAAACTATG
90222	88309	GAGTGTATCTCCAAAACTAT
90223	88310	TGAGTGTATCTCCAAAACTA
90224	88311	CTGAGTGTATCTCCAAAACT
90225	88312	TCTGAGTGTATCTCCAAAAC
90226	88313	TTCTGAGTGTATCTCCAAAA
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90228	88315	TATTCTGAGTGTATCTCCAA
90229	88316	CTATTCTGAGTGTATCTCCA
90230	88317	GCTATTCTGAGTGTATCTCC
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90246	88333	AGAGAAAATCTATAATGCTA
90247	88334	AAGAGAAAATCTATAATGCT
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139326	137413	AGTGTTCCTTGACATAAATA
139327	137414	CAGTGTTCCTTGACATAAAT
139328	137415	TCAGTGTTCCTTGACATAAA
139329	137416	CTCAGTGTTCCTTGACATAA
139330	137417	ACTCAGTGTTCCTTGACATA
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139335	137422	TTCCCACTCAGTGTTCCTTG
139336	137423	TTTCCCACTCAGTGTTCCTT
139337	137424	GTTTCCCACTCAGTGTTCCT
139338	137425	AGTTTCCCACTCAGTGTTCC
139339	137426	AAGTTTCCCACTCAGTGTTC
139340	137427	GAAGTTTCCCACTCAGTGTT
139341	137428	AGAAGTTTCCCACTCAGTGT
139342	137429	CAGAAGTTTCCCACTCAGTG
139343	137430	CCAGAAGTTTCCCACTCAGT
139344	137431	TCCAGAAGTTTCCCACTCAG
139345	137432	GTCCAGAAGTTTCCCACTCA
139346	137433	AGTCCAGAAGTTTCCCACTC
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139348	137435	CTAGTCCAGAAGTTTCCCAC
139349	137436	CCTAGTCCAGAAGTTTCCCA
139350	137437	ACCTAGTCCAGAAGTTTCCC
139351	137438	GACCTAGTCCAGAAGTTTCC
139352	137439	AGACCTAGTCCAGAAGTTTC
139353	137440	CAGACCTAGTCCAGAAGTTT
139354	137441	CCAGACCTAGTCCAGAAGTT
139355	137442	TCCAGACCTAGTCCAGAAGT
139356	137443	GTCCAGACCTAGTCCAGAAG
139357	137444	GGTCCAGACCTAGTCCAGAA
139358	137445	TGGTCCAGACCTAGTCCAGA
139359	137446	TTGGTCCAGACCTAGTCCAG
139360	137447	TTTGGTCCAGACCTAGTCCA
139361	137448	CTTTGGTCCAGACCTAGTCC
139362	137449	TCTTTGGTCCAGACCTAGTC
139363	137450	TTCTTTGGTCCAGACCTAGT
139364	137451	CTTCTTTGGTCCAGACCTAG
139365	137452	GCTTCTTTGGTCCAGACCTA
139366	137453	TGCTTCTTTGGTCCAGACCT
139367	137454	ATGCTTCTTTGGTCCAGACC
139368	137455	TATGCTTCTTTGGTCCAGAC
139369	137456	ATATGCTTCTTTGGTCCAGA
139370	137457	CATATGCTTCTTTGGTCCAG
139371	137458	ACATATGCTTCTTTGGTCCA
139372	137459	GACATATGCTTCTTTGGTCC
139373	137460	AGACATATGCTTCTTTGGTC
139374	137461	AAGACATATGCTTCTTTGGT
139375	137462	AAAGACATATGCTTCTTTGG
139376	137463	CAAAGACATATGCTTCTTTG
139377	137464	TCAAAGACATATGCTTCTTT
139378	137465	ATCAAAGACATATGCTTCTT
139379	137466	AATCAAAGACATATGCTTCT
139380	137467	TAATCAAAGACATATGCTTC
139381	137468	ATAATCAAAGACATATGCTT
139382	137469	GATAATCAAAGACATATGCT
139383	137470	AGATAATCAAAGACATATGC
139384	137471	AAGATAATCAAAGACATATG
139385	137472	AAAGATAATCAAAGACATAT
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139388	137475	ATTAAAGATAATCAAAGACA
139389	137476	GATTAAAGATAATCAAAGAC
139390	137477	AGATTAAAGATAATCAAAGA
139391	137478	TAGATTAAAGATAATCAAAG
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139393	137480	TTTAGATTAAAGATAATCAA
139394	137481	TTTTAGATTAAAGATAATCA
139395	137482	CTTTTAGATTAAAGATAATC
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41103	39190	ACCTAGTAATTAGTGTAGCT
41104	39191	CACCTAGTAATTAGTGTAGC
41105	39192	TCACCTAGTAATTAGTGTAG
41106	39193	ATCACCTAGTAATTAGTGTA
41107	39194	CATCACCTAGTAATTAGTGT
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41109	39196	AGCATCACCTAGTAATTAGT
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41111	39198	ACAGCATCACCTAGTAATTA
41112	39199	CACAGCATCACCTAGTAATT
41113	39200	ACACAGCATCACCTAGTAAT
41114	39201	TACACAGCATCACCTAGTAA
41115	39202	CTACACAGCATCACCTAGTA
41116	39203	ACTACACAGCATCACCTAGT
41117	39204	GACTACACAGCATCACCTAG
41118	39205	TGACTACACAGCATCACCTA
41119	39206	ATGACTACACAGCATCACCT
41120	39207	AATGACTACACAGCATCACC
41121	39208	AAATGACTACACAGCATCAC
41122	39209	GAAATGACTACACAGCATCA
41123	39210	AGAAATGACTACACAGCATC
41124	39211	AAGAAATGACTACACAGCAT
41125	39212	CAAGAAATGACTACACAGCA
41126	39213	CCAAGAAATGACTACACAGC
41127	39214	ACCAAGAAATGACTACACAG
41128	39215	CACCAAGAAATGACTACACA
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41130	39217	GACACCAAGAAATGACTACA
41131	39218	GGACACCAAGAAATGACTAC
41132	39219	AGGACACCAAGAAATGACTA
41133	39220	AAGGACACCAAGAAATGACT
41134	39221	CAAGGACACCAAGAAATGAC
41135	39222	CCAAGGACACCAAGAAATGA
41136	39223	CCCAAGGACACCAAGAAATG
41137	39224	CCCCAAGGACACCAAGAAAT
41138	39225	CCCCCAAGGACACCAAGAAA
41139	39226	TCCCCCAAGGACACCAAGAA
41140	39227	ATCCCCCAAGGACACCAAGA
41141	39228	AATCCCCCAAGGACACCAAG
41142	39229	CAATCCCCCAAGGACACCAA
41143	39230	CCAATCCCCCAAGGACACCA
41144	39231	ACCAATCCCCCAAGGACACC
41145	39232	GACCAATCCCCCAAGGACAC
41146	39233	GGACCAATCCCCCAAGGACA
41147	39234	GGGACCAATCCCCCAAGGAC
41148	39235	TGGGACCAATCCCCCAAGGA
41149	39236	CTGGGACCAATCCCCCAAGG
41150	39237	CCTGGGACCAATCCCCCAAG
41151	39238	TCCTGGGACCAATCCCCCAA
41152	39239	GTCCTGGGACCAATCCCCCA
41153	39240	GGTCCTGGGACCAATCCCCC
41154	39241	GGGTCCTGGGACCAATCCCC
41155	39242	GGGGTCCTGGGACCAATCCC
41156	39243	GGGGGTCCTGGGACCAATCC
41157	39244	GGGGGGTCCTGGGACCAATC
41158	39245	GGGGGGGTCCTGGGACCAAT
41159	39246	CGGGGGGGTCCTGGGACCAA
41160	39247	ACGGGGGGGTCCTGGGACCA
41161	39248	AACGGGGGGGTCCTGGGACC
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41163	39250	CCAACGGGGGGGTCCTGGGA
41164	39251	TCCAACGGGGGGGTCCTGGG
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41167	39254	ATATCCAACGGGGGGGTCCT
41168	39255	TATATCCAACGGGGGGGTCC
41169	39256	TTATATCCAACGGGGGGGTC
41170	39257	TTTATATCCAACGGGGGGGT
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90250	88337	AAAAAGAGAAAATCTATAAT
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90253	88340	AGTAAAAAGAGAAAATCTAT
90254	88341	TAGTAAAAAGAGAAAATCTA
90255	88342	TTAGTAAAAAGAGAAAATCT
90256	88343	ATTAGTAAAAAGAGAAAATC
90257	88344	AATTAGTAAAAAGAGAAAAT
90258	88345	CAATTAGTAAAAAGAGAAAA
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90262	88349	TTTCCAATTAGTAAAAAGAG
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90268	88355	GCCATTTTTCCAATTAGTAA
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90272	88359	AACTGCCATTTTTCCAATTA
90273	88360	CAACTGCCATTTTTCCAATT
90274	88361	ACAACTGCCATTTTTCCAAT
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90276	88363	CAACAACTGCCATTTTTCCA
90277	88364	TCAACAACTGCCATTTTTCC
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90283	88370	TATTATTCAACAACTGCCAT
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90293	88380	GGAAGAAAACTATTATTCAA
90294	88381	CGGAAGAAAACTATTATTCA
90295	88382	ACGGAAGAAAACTATTATTC
90296	88383	CACGGAAGAAAACTATTATT
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90298	88385	GTCACGGAAGAAAACTATTA
90299	88386	GGTCACGGAAGAAAACTATT
90300	88387	GGGTCACGGAAGAAAACTAT
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90307	88394	GTCACAAGGGTCACGGAAGA
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139397	137484	ATCTTTTAGATTAAAGATAA
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139400	137487	AAAATCTTTTAGATTAAAGA
139401	137488	TAAAATCTTTTAGATTAAAG
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139403	137490	CATAAAATCTTTTAGATTAA
139404	137491	TCATAAAATCTTTTAGATTA
139405	137492	TTCATAAAATCTTTTAGATT
139406	137493	CTTCATAAAATCTTTTAGAT
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139408	137495	GTCTTCATAAAATCTTTTAG
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139410	137497	TAGTCTTCATAAAATCTTTT
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139412	137499	TTTAGTCTTCATAAAATCTT
139413	137500	CTTTAGTCTTCATAAAATCT
139414	137501	ACTTTAGTCTTCATAAAATC
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139417	137504	AAAACTTTAGTCTTCATAAA
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139419	137506	ATAAAACTTTAGTCTTCATA
139420	137507	TATAAAACTTTAGTCTTCAT
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139422	137509	TTTATAAAACTTTAGTCTTC
139423	137510	ATTTATAAAACTTTAGTCTT
139424	137511	TATTTATAAAACTTTAGTCT
139425	137512	CTATTTATAAAACTTTAGTC
139426	137513	TCTATTTATAAAACTTTAGT
139427	137514	TTCTATTTATAAAACTTTAG
139428	137515	CTTCTATTTATAAAACTTTA
139429	137516	ACTTCTATTTATAAAACTTT
139430	137517	AACTTCTATTTATAAAACTT
139431	137518	AAACTTCTATTTATAAAACT
139432	137519	TAAACTTCTATTTATAAAAC
139433	137520	TTAAACTTCTATTTATAAAA
139434	137521	GTTAAACTTCTATTTATAAA
139435	137522	AGTTAAACTTCTATTTATAA
139436	137523	CAGTTAAACTTCTATTTATA
139437	137524	TCAGTTAAACTTCTATTTAT
139438	137525	ATCAGTTAAACTTCTATTTA
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139440	137527	TCATCAGTTAAACTTCTATT
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139442	137529	ATTCATCAGTTAAACTTCTA
139443	137530	TATTCATCAGTTAAACTTCT
139444	137531	TTATTCATCAGTTAAACTTC
139445	137532	TTTATTCATCAGTTAAACTT
139446	137533	ATTTATTCATCAGTTAAACT
139447	137534	GATTTATTCATCAGTTAAAC
139448	137535	TGATTTATTCATCAGTTAAA
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139450	137537	ACTGATTTATTCATCAGTTA
139451	137538	TACTGATTTATTCATCAGTT
139452	137539	ATACTGATTTATTCATCAGT
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139461	137548	TTATTTGTAATACTGATTTA
139462	137549	TTTATTTGTAATACTGATTT
139463	137550	TTTTATTTGTAATACTGATT
139464	137551	ATTTTATTTGTAATACTGAT
139465	137552	AATTTTATTTGTAATACTGA
139466	137553	TAATTTTATTTGTAATACTG
139467	137554	TTAATTTTATTTGTAATACT

41174	39261	AATTTTTATATCCAACGGGG
41175	39262	AAATTTTTATATCCAACGGG
41176	39263	TAAATTTTTATATCCAACGG
41177	39264	ATAAATTTTTATATCCAACG
41178	39265	CATAAATTTTTATATCCAAC
41179	39266	CCATAAATTTTTATATCCAA
41180	39267	TCCATAAATTTTTATATCCA
41181	39268	ATCCATAAATTTTTATATCC
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41184	39271	AGCATCCATAAATTTTTATA
41185	39272	GAGCATCCATAAATTTTTAT
41186	39273	AGAGCATCCATAAATTTTTA
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41188	39275	CTAGAGCATCCATAAATTTT
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41194	39281	GAGGGACTAGAGCATCCATA
41195	39282	TGAGGGACTAGAGCATCCAT
41196	39283	ATGAGGGACTAGAGCATCCA
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41227	39314	GCACCGGTATATGCAAATAC
41228	39315	TGCACCGGTATATGCAAATA
41229	39316	GTGCACCGGTATATGCAAAT
41230	39317	TGTGCACCGGTATATGCAAA
41231	39318	ATGTGCACCGGTATATGCAA
41232	39319	GATGTGCACCGGTATATGCA
41233	39320	GGATGTGCACCGGTATATGC
41234	39321	AGGATGTGCACCGGTATATG
41235	39322	GAGGATGTGCACCGGTATAT
41236	39323	GGAGGATGTGCACCGGTATA
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41238	39325	CAGGAGGATGTGCACCGGTA
41239	39326	ACAGGAGGATGTGCACCGGT
41240	39327	TACAGGAGGATGTGCACCGG
41241	39328	ATACAGGAGGATGTGCACCG
41242	39329	CATACAGGAGGATGTGCACC
41243	39330	GCATACAGGAGGATGTGCAC
41244	39331	AGCATACAGGAGGATGTGCA

90321	88408	TTTTTTTTTTTTAAGTCACA
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90323	88410	GTTTTTTTTTTTTAAGTCA
90324	88411	TGTTTTTTTTTTTTAAGTC
90325	88412	GTGTTTTTTTTTTTTAAGT
90326	88413	AGTGTTTTTTTTTTTTAAG
90327	88414	CAGTGTTTTTTTTTTTTAA
90328	88415	TCAGTGTTTTTTTTTTTTA
90329	88416	TTCAGTGTTTTTTTTTTTT
90330	88417	TTTCAGTGTTTTTTTTTTT
90331	88418	ATTTCAGTGTTTTTTTTTT
90332	88419	CATTTCAGTGTTTTTTTTT
90333	88420	TCATTTCAGTGTTTTTTTT
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90337	88424	TATTTCATTTCAGTGTTTT
90338	88425	TTATTTCATTTCAGTGTTT
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90341	88428	CGATTATTTCATTTCAGTG
90342	88429	TCGATTATTTCATTTCAGTG
90343	88430	TTCGATTATTTCATTTCAGT
90344	88431	GTTCGATTATTTCATTTCAG
90345	88432	GGTTCGATTATTTCATTTCA
90346	88433	TGGTTCGATTATTTCATTTC
90347	88434	ATGGTTCGATTATTTCATTT
90348	88435	AATGGTTCGATTATTTCATT
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90351	88438	GAAAATGGTTCGATTATTTC
90352	88439	AGAAAATGGTTCGATTATTT
90353	88440	GAGAAAATGGTTCGATTATT
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90357	88444	TTTAGAGAAAATGGTTCGAT
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90359	88446	GGTTTAGAGAAAATGGTTCG
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90362	88449	AAAGGTTTAGAGAAAATGGT
90363	88450	CAAAGGTTTAGAGAAAATGG
90364	88451	TCAAAGGTTTAGAGAAAATG
90365	88452	TTCAAAGGTTTAGAGAAAAT
90366	88453	ATTCAAAGGTTTAGAGAAAA
90367	88454	GATTCAAAGGTTTAGAGAAA
90368	88455	AGATTCAAAGGTTTAGAGAA
90369	88456	CAGATTCAAAGGTTTAGAGA
90370	88457	TCAGATTCAAAGGTTTAGAG
90371	88458	CTCAGATTCAAAGGTTTAGA
90372	88459	GCTCAGATTCAAAGGTTTAG
90373	88460	AGCTCAGATTCAAAGGTTTA
90374	88461	GAGCTCAGATTCAAAGGTTT
90375	88462	AGAGCTCAGATTCAAAGGTT
90376	88463	CAGAGCTCAGATTCAAAGGT
90377	88464	GCAGAGCTCAGATTCAAAGG
90378	88465	TGCAGAGCTCAGATTCAAAG
90379	88466	CTGCAGAGCTCAGATTCAAA
90380	88467	ACTGCAGAGCTCAGATTCAA
90381	88468	AACTGCAGAGCTCAGATTCA
90382	88469	TAACTGCAGAGCTCAGATTC
90383	88470	CTAACTGCAGAGCTCAGATT
90384	88471	CCTAACTGCAGAGCTCAGAT
90385	88472	ACCTAACTGCAGAGCTCAGA
90386	88473	AACCTAACTGCAGAGCTCAG
90387	88474	AAACCTAACTGCAGAGCTCA
90388	88475	TAAACCTAACTGCAGAGCTC
90389	88476	ATAAACCTAACTGCAGAGCT
90390	88477	TATAAACCTAACTGCAGAGC
90391	88478	TTATAAACCTAACTGCAGAG

139468	137555	GTTAATTTTATTTGTAATAC
139469	137556	AGTTAATTTTATTTGTAATA
139470	137557	AAGTTAATTTTATTTGTAAT
139471	137558	AAAGTTAATTTTATTTGTAA
139472	137559	TAAAGTTAATTTTATTTGTA
139473	137560	ATAAAGTTAATTTTATTTGT
139474	137561	AATAAAGTTAATTTTATTTG
139475	137562	AAATAAAGTTAATTTTATTT
139476	137563	AAAATAAAGTTAATTTTATT
139477	137564	AAAAATAAAGTTAATTTTAT
139478	137565	TAAAAATAAAGTTAATTTTA
139479	137566	TTAAAAATAAAGTTAATTTT
139480	137567	GTTAAAAATAAAGTTAATTT
139481	137568	GGTTAAAAATAAAGTTAATT
139482	137569	AGGTTAAAAATAAAGTTAAT
139483	137570	GAGGTTAAAAATAAAGTTAA
139484	137571	AGAGGTTAAAAATAAAGTTA
139485	137572	GAGAGGTTAAAAATAAAGTT
139486	137573	AGAGAGGTTAAAAATAAAGT
139487	137574	CAGAGAGGTTAAAAATAAAG
139488	137575	CCAGAGAGGTTAAAAATAAA
139489	137576	CCCAGAGAGGTTAAAAATAA
139490	137577	TCCCAGAGAGGTTAAAAATA
139491	137578	ATCCCAGAGAGGTTAAAAAT
139492	137579	GATCCCAGAGAGGTTAAAAA
139493	137580	AGATCCCAGAGAGGTTAAAA
139494	137581	AAGATCCCAGAGAGGTTAAA
139495	137582	AAAGATCCCAGAGAGGTTAA
139496	137583	TAAAGATCCCAGAGAGGTTA
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139498	137585	GCTAAAGATCCCAGAGAGGT
139499	137586	GGCTAAAGATCCCAGAGAGG
139500	137587	TGGCTAAAGATCCCAGAGAG
139501	137588	CTGGCTAAAGATCCCAGAGA
139502	137589	TCTGGCTAAAGATCCCAGAG
139503	137590	TTCTGGCTAAAGATCCCAGA
139504	137591	ATTCTGGCTAAAGATCCCAG
139505	137592	CATTCTGGCTAAAGATCCCA
139506	137593	TCATTCTGGCTAAAGATCCC
139507	137594	CTCATTCTGGCTAAAGATCC
139508	137595	GCTCATTCTGGCTAAAGATC
139509	137596	TGCTCATTCTGGCTAAAGAT
139510	137597	ATGCTCATTCTGGCTAAAGA
139511	137598	TATGCTCATTCTGGCTAAAG
139512	137599	ATATGCTCATTCTGGCTAAA
139513	137600	TATATGCTCATTCTGGCTAA
139514	137601	ATATATGCTCATTCTGGCTA
139515	137602	TATATATGCTCATTCTGGCT
139516	137603	TTATATATGCTCATTCTGGC
139517	137604	GTTATATATGCTCATTCTGG
139518	137605	TGTTATATATGCTCATTCTG
139519	137606	TTGTTATATATGCTCATTCT
139520	137607	TTTGTTATATATGCTCATTC
139521	137608	TTTTGTTATATATGCTCATT
139522	137609	CTTTTGTTATATATGCTCAT
139523	137610	GCTTTTGTTATATATGCTCA
139524	137611	TGCTTTTGTTATATATGCTC
139525	137612	CTGCTTTTGTTATATATGCT
139526	137613	ACTGCTTTTGTTATATATGC
139527	137614	CACTGCTTTTGTTATATATG
139528	137615	TCACTGCTTTTGTTATATAT
139529	137616	TTCACTGCTTTTGTTATATA
139530	137617	TTTCACTGCTTTTGTTATAT
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139535	137622	TATTATTTCACTGCTTTTGT
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41245	39332	AAGCATACAGGAGGATGTGC
41246	39333	AAAGCATACAGGAGGATGTG
41247	39334	CAAAGCATACAGGAGGATGT
41248	39335	ACAAAGCATACAGGAGGATG
41249	39336	GACAAAGCATACAGGAGGAT
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41251	39338	ATGACAAAGCATACAGGAGG
41252	39339	AATGACAAAGCATACAGGAG
41253	39340	AAATGACAAAGCATACAGGA
41254	39341	GAAATGACAAAGCATACAGG
41255	39342	AGAAATGACAAAGCATACAG
41256	39343	TAGAAATGACAAAGCATACA
41257	39344	CTAGAAATGACAAAGCATAC
41258	39345	TCTAGAAATGACAAAGCATA
41259	39346	ATCTAGAAATGACAAAGCAT
41260	39347	AATCTAGAAATGACAAAGCA
41261	39348	TAATCTAGAAATGACAAAGC
41262	39349	GTAATCTAGAAATGACAAAG
41263	39350	AGTAATCTAGAAATGACAAA
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41265	39352	TAAGTAATCTAGAAATGACA
41266	39353	ATAAGTAATCTAGAAATGAC
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41276	39363	ATTAGGTATTATAAGTAATC
41277	39364	TATTAGGTATTATAAGTAAT
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41279	39366	CATATTAGGTATTATAAGTA
41280	39367	CCATATTAGGTATTATAAGT
41281	39368	ACCATATTAGGTATTATAAG
41282	39369	CACCATATTAGGTATTATAA
41283	39370	ACACCATATTAGGTATTATA
41284	39371	TACACCATATTAGGTATTAT
41285	39372	TTACACCATATTAGGTATTA
41286	39373	TTTACACCATATTAGGTATT
41287	39374	GTTTACACCATATTAGGTAT
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41296	39383	TTACCTAGTGTTTACACCAT
41297	39384	TTTACCTAGTGTTTACACCA
41298	39385	ATTTACCTAGTGTTTACACC
41299	39386	TATTTACCTAGTGTTTACAC
41300	39387	CTATTTACCTAGTGTTTACA
41301	39388	ACTATTTACCTAGTGTTTAC
41302	39389	AACTATTTACCTAGTGTTTA
41303	39390	CAACTATTTACCTAGTGTTT
41304	39391	ACAACTATTTACCTAGTGTT
41305	39392	AACAACTATTTACCTAGTGT
41306	39393	TAACAACTATTTACCTAGTG
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41310	39397	TATATAACAACTATTTACCT
41311	39398	ATATATAACAACTATTTACC
41312	39399	AATATATAACAACTATTTAC
41313	39400	AAATATATAACAACTATTTA
41314	39401	AAAATATATAACAACTATTT
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90392	88479	ATTATAAACCTAACTGCAGA
90393	88480	CATTATAAACCTAACTGCAG
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90398	88485	TATACCATTATAAACCTAAC
90399	88486	ATATACCATTATAAACCTAA
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90401	88488	TCATATACCATTATAAACCT
90402	88489	TTCATATACCATTATAAACC
90403	88490	TTTCATATACCATTATAAAC
90404	88491	GTTTCATATACCATTATAAA
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90406	88493	AGGTTTCATATACCATTATA
90407	88494	TAGGTTTCATATACCATTAT
90408	88495	ATAGGTTTCATATACCATTA
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90412	88499	TCTAATAGGTTTCATATACC
90413	88500	ATCTAATAGGTTTCATATAC
90414	88501	TATCTAATAGGTTTCATATA
90415	88502	ATATCTAATAGGTTTCATAT
90416	88503	TATATCTAATAGGTTTCATA
90417	88504	ATATATCTAATAGGTTTCAT
90418	88505	TATATATCTAATAGGTTTCA
90419	88506	GTATATATCTAATAGGTTTC
90420	88507	AGTATATATCTAATAGGTTT
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90422	88509	CAAGTATATATCTAATAGGT
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90424	88511	TCCAAGTATATATCTAATAG
90425	88512	TTCCAAGTATATATCTAATA
90426	88513	CTTCCAAGTATATATCTAAT
90427	88514	ACTTCCAAGTATATATCTAA
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90430	88517	ATGACTTCCAAGTATATATC
90431	88518	TATGACTTCCAAGTATATAT
90432	88519	ATATGACTTCCAAGTATATA
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90435	88522	CCCATATGACTTCCAAGTAT
90436	88523	TCCCATATGACTTCCAAGTA
90437	88524	ATCCCATATGACTTCCAAGT
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90450	88537	AAGCAGGGTTTGTATCCCAT
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139541	137628	CACACATATTATTTCACTGC
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139543	137630	CCCACACATATTATTTCACT
139544	137631	ACCCACACATATTATTTCAC
139545	137632	GACCCACACATATTATTTCA
139546	137633	TGACCCACACATATTATTTC
139547	137634	CTGACCCACACATATTATTT
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139550	137637	GTTCTGACCCACACATATTA
139551	137638	GGTTCTGACCCACACATATT
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139556	137643	CAGTGGGTTCTGACCCACAC
139557	137644	GCAGTGGGTTCTGACCCACA
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139559	137646	GGGCAGTGGGTTCTGACCCA
139560	137647	AGGGCAGTGGGTTCTGACCC
139561	137648	AAGGGCAGTGGGTTCTGACC
139562	137649	GAAGGGCAGTGGGTTCTGAC
139563	137650	GGAAGGGCAGTGGGTTCTGA
139564	137651	GGGAAGGGCAGTGGGTTCTG
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139573	137660	GAGTGGAGTGGGAAGGGCAG
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139581	137668	GAAAAGGAGAGTGGAGTGGG
139582	137669	GGAAAAGGAGAGTGGAGTGG
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139586	137673	TCAGGGAAAAGGAGAGTGGA
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139588	137675	AATCAGGGAAAAGGAGAGTG
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139591	137678	GAGAATCAGGGAAAAGGAGA
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139593	137680	AGGAGAATCAGGGAAAAGGA
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139595	137682	ACAGGAGAATCAGGGAAAAG
139596	137683	CACAGGAGAATCAGGGAAAA
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139598	137685	AACACAGGAGAATCAGGGAA
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41339	39426	AATACAATAAAAATAAGACA
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41383	39470	CATCCTCAGATTCAATCACT
41384	39471	ACATCCTCAGATTCAATCAC
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90470	88557	TCAAAAGGGGAAGATAATAA
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90478	88565	CAAGTTAGTCAAAAGGGGAA
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90487	88574	CTTGAGACCCAAGTTAGTCA
90488	88575	ACTTGAGACCCAAGTTAGTC
90489	88576	AACTTGAGACCCAAGTTAGT
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90521	88608	AACATCAAGGTCCACTGTGC
90522	88609	CAACATCAAGGTCCACTGTG
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90525	88612	TAGCAACATCAAGGTCCACT
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90527	88614	TATAGCAACATCAAGGTCCA
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90529	88616	TTTATAGCAACATCAAGGTC
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90531	88618	TCTTTATAGCAACATCAAGG
90532	88619	TTCTTTATAGCAACATCAAG
90533	88620	ATTCTTTATAGCAACATCAA

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139611	137698	TAAAGAAGGAAAAAACACAG
139612	137699	GTAAAGAAGGAAAAAACACA
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139614	137701	AGGTAAAGAAGGAAAAAACA
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139616	137703	TAAGGTAAAGAAGGAAAAAA
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139618	137705	GATAAGGTAAAGAAGGAAAA
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139621	137708	CAAGATAAGGTAAAGAAGGA
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139626	137713	GGAACCAAGATAAGGTAAAG
139627	137714	AGGAACCAAGATAAGGTAAA
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139667	137754	GACAGAGTGAGACTCCATCT
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41391	39478	AGATTTCACATCCTCAGATT
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41395	39482	CTGCAGATTTCACATCCTCA
41396	39483	TCTGCAGATTTCACATCCTC
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41399	39486	ATATCTGCAGATTTCACATC
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41408	39495	AGGCCCTCCATATCTGCAGA
41409	39496	CAGGCCCTCCATATCTGCAG
41410	39497	GCAGGCCCTCCATATCTGCA
41411	39498	TGCAGGCCCTCCATATCTGC
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41443	39530	GCAGTTTAGGCCCAAAGCTC
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41445	39532	GAGCAGTTTAGGCCCAAAGC
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90534	88621	CATTCTTTATAGCAACATCA
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90543	88630	AGCCCTACACATTCTTTATA
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90545	88632	CCAGCCCTACACATTCTTTA
90546	88633	CCCAGCCCTACACATTCTTT
90547	88634	GCCCAGCCCTACACATTCTT
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90577	88664	AGTGCTGGGATTACAGGCAT
90578	88665	AAGTGCTGGGATTACAGGCA
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90583	88670	TCCCAAAGTGCTGGGATTAC
90584	88671	CTCCCAAAGTGCTGGGATTA
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90586	88673	GCCTCCCAAAGTGCTGGGAT
90587	88674	GGCCTCCCAAAGTGCTGGGA
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139685	137772	CTGCACTCCAGCCTGGACGA
139686	137773	ACTGCACTCCAGCCTGGACG
139687	137774	CACTGCACTCCAGCCTGGAC
139688	137775	CCACTGCACTCCAGCCTGGA
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139827	137914	GAAACCCTGTCTCTACTAAA
139828	137915	TGAAACCCTGTCTCTACTAA
139829	137916	GTGAAACCCTGTCTCTACTA
139830	137917	GGTGAAACCCTGTCTCTACT
139831	137918	TGGTGAAACCCTGTCTCTAC
139832	137919	ATGGTGAAACCCTGTCTCTA
139833	137920	GATGGTGAAACCCTGTCTCT
139834	137921	AGATGGTGAAACCCTGTCTC
139835	137922	AAGATGGTGAAACCCTGTCT
139836	137923	CAAGATGGTGAAACCCTGTC
139837	137924	CCAAGATGGTGAAACCCTGT
139838	137925	GCCAAGATGGTGAAACCCTG
139839	137926	GGCCAAGATGGTGAAACCCT
139840	137927	TGGCCAAGATGGTGAAACCC
139841	137928	CTGGCCAAGATGGTGAAACC
139842	137929	CCTGGCCAAGATGGTGAAAC
139843	137930	GCCTGGCCAAGATGGTGAAA
139844	137931	AGCCTGGCCAAGATGGTGAA
139845	137932	CAGCCTGGCCAAGATGGTGA
139846	137933	CCAGCCTGGCCAAGATGGTG
139847	137934	ACCAGCCTGGCCAAGATGGT
139848	137935	GACCAGCCTGGCCAAGATGG
139849	137936	AGACCAGCCTGGCCAAGATG
139850	137937	AAGACCAGCCTGGCCAAGAT
139851	137938	CAAGACCAGCCTGGCCAAGA
139852	137939	TCAAGACCAGCCTGGCCAAG
139853	137940	TTCAAGACCAGCCTGGCCAA
139854	137941	GTTCAAGACCAGCCTGGCCA
139855	137942	AGTTCAAGACCAGCCTGGCC
139856	137943	GAGTTCAAGACCAGCCTGGC
139857	137944	GGAGTTCAAGACCAGCCTGG
139858	137945	AGGAGTTCAAGACCAGCCTG
139859	137946	CAGGAGTTCAAGACCAGCCT
139860	137947	TCAGGAGTTCAAGACCAGCC
139861	137948	GTCAGGAGTTCAAGACCAGC
139862	137949	GGTCAGGAGTTCAAGACCAG
139863	137950	AGGTCAGGAGTTCAAGACCA
139864	137951	GAGGTCAGGAGTTCAAGACC
139865	137952	CGAGGTCAGGAGTTCAAGAC
139866	137953	ACGAGGTCAGGAGTTCAAGA
139867	137954	CACGAGGTCAGGAGTTCAAG
139868	137955	TCACGAGGTCAGGAGTTCAA
139869	137956	ATCACGAGGTCAGGAGTTCA
139870	137957	GATCACGAGGTCAGGAGTTC
139871	137958	TGATCACGAGGTCAGGAGTT
139872	137959	GTGATCACGAGGTCAGGAGT
139873	137960	GGTGATCACGAGGTCAGGAG
139874	137961	AGGTGATCACGAGGTCAGGA
139875	137962	TAGGTGATCACGAGGTCAGG
139876	137963	GTAGGTGATCACGAGGTCAG
139877	137964	GGTAGGTGATCACGAGGTCA
139878	137965	AGGTAGGTGATCACGAGGTC
139879	137966	GAGGTAGGTGATCACGAGGT
139880	137967	CGAGGTAGGTGATCACGAGG
139881	137968	CCGAGGTAGGTGATCACGAG
139882	137969	GCCGAGGTAGGTGATCACGA
139883	137970	GGCCGAGGTAGGTGATCACG
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139885	137972	GGGGCCGAGGTAGGTGATCA
139886	137973	AGGGGCCGAGGTAGGTGATC
139887	137974	CAGGGGCCGAGGTAGGTGAT
139888	137975	CCAGGGGCCGAGGTAGGTGA
139889	137976	ACCAGGGGCCGAGGTAGGTG
139890	137977	AACCAGGGGCCGAGGTAGGT
139891	137978	GAACCAGGGGCCGAGGTAGG
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41603	39690	CATTGGAGATAAGTGCTAAA
41604	39691	TCATTGGAGATAAGTGCTAA
41605	39692	ATCATTGGAGATAAGTGCTA
41606	39693	AATCATTGGAGATAAGTGCT
41607	39694	GAATCATTGGAGATAAGTGC
41608	39695	AGAATCATTGGAGATAAGTG
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41610	39697	GGAGAATCATTGGAGATAAG
41611	39698	AGGAGAATCATTGGAGATAA
41612	39699	GAGGAGAATCATTGGAGATA
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41615	39702	TAGGAGGAGAATCATTGGAG
41616	39703	GTAGGAGGAGAATCATTGGA
41617	39704	GGTAGGAGGAGAATCATTGG
41618	39705	TGGTAGGAGGAGAATCATTG
41619	39706	TTGGTAGGAGGAGAATCATT
41620	39707	CTTGGTAGGAGGAGAATCAT
41621	39708	ACTTGGTAGGAGGAGAATCA
41622	39709	CACTTGGTAGGAGGAGAATC
41623	39710	GCACTTGGTAGGAGGAGAAT
41624	39711	GGCACTTGGTAGGAGGAGAA
41625	39712	AGGCACTTGGTAGGAGGAGA
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41627	39714	AAAGGCACTTGGTAGGAGGA
41628	39715	CAAAGGCACTTGGTAGGAGG
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41630	39717	TTCAAAGGCACTTGGTAGGA
41631	39718	TTTCAAAGGCACTTGGTAGG
41632	39719	CTTTCAAAGGCACTTGGTAG
41633	39720	GCTTTCAAAGGCACTTGGTA
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41639	39726	AATGATGCTTTCAAAGGCAC
41640	39727	TAATGATGCTTTCAAAGGCA
41641	39728	TTAATGATGCTTTCAAAGGC
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41643	39730	AGTTAATGATGCTTTCAAAG
41644	39731	GAGTTAATGATGCTTTCAAA
41645	39732	AGAGTTAATGATGCTTTCAA
41646	39733	AAGAGTTAATGATGCTTTCA
41647	39734	AAAGAGTTAATGATGCTTTC
41648	39735	GAAAGAGTTAATGATGCTTT
41649	39736	TGAAAGAGTTAATGATGCTT
41650	39737	ATGAAAGAGTTAATGATGCT
41651	39738	TATGAAAGAGTTAATGATGC
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41653	39740	GGTATGAAAGAGTTAATGAT
41654	39741	AGGTATGAAAGAGTTAATGA
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41656	39743	CAAGGTATGAAAGAGTTAAT
41657	39744	ACAAGGTATGAAAGAGTTAA
41658	39745	AACAAGGTATGAAAGAGTTA
41659	39746	CAACAAGGTATGAAAGAGTT
41660	39747	GCAACAAGGTATGAAAGAGT
41661	39748	TGCAACAAGGTATGAAAGAG
41662	39749	TTGCAACAAGGTATGAAAGA
41663	39750	TTTGCAACAAGGTATGAAAG
41664	39751	ATTTGCAACAAGGTATGAAA
41665	39752	CATTTGCAACAAGGTATGAA
41666	39753	TCATTTGCAACAAGGTATGA
41667	39754	TTCATTTGCAACAAGGTATG
41668	39755	TTTCATTTGCAACAAGGTAT
41669	39756	ATTTCATTTGCAACAAGGTA
41670	39757	AATTTCATTTGCAACAAGGT

90747	88834	GTATCAAGTGATTCTCCTGC
90748	88835	TGTATCAAGTGATTCTCCTG
90749	88836	ATGTATCAAGTGATTCTCCT
90750	88837	AATGTATCAAGTGATTCTCC
90751	88838	AAATGTATCAAGTGATTCTC
90752	88839	TAAATGTATCAAGTGATTCT
90753	88840	CTAAATGTATCAAGTGATTC
90754	88841	ACTAAATGTATCAAGTGATT
90755	88842	AACTAAATGTATCAAGTGAT
90756	88843	TAACTAAATGTATCAAGTGA
90757	88844	CTAACTAAATGTATCAAGTG
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90759	88846	TCCTAACTAAATGTATCAAG
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90761	88848	TCTCCTAACTAAATGTATCA
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90769	88856	TGATTTTCTCTCCTAACTAA
90770	88857	ATGATTTTCTCTCCTAACTA
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90782	88869	ACTAACATAAGTATGATTTT
90783	88870	TACTAACATAAGTATGATTT
90784	88871	TTACTAACATAAGTATGATT
90785	88872	ATTACTAACATAAGTATGAT
90786	88873	AATTACTAACATAAGTATGA
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90789	88876	AGCAATTACTAACATAAGTA
90790	88877	CAGCAATTACTAACATAAGT
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90793	88880	CAGCAGCAATTACTAACATA
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90797	88884	AGAACAGCAGCAATTACTAA
90798	88885	AAGAACAGCAGCAATTACTA
90799	88886	GAAGAACAGCAGCAATTACT
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90802	88889	TATGAAGAACAGCAGCAATT
90803	88890	ATATGAAGAACAGCAGCAAT
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90805	88892	GTATATGAAGAACAGCAGCA
90806	88893	AGTATATGAAGAACAGCAGC
90807	88894	AAGTATATGAAGAACAGCAG
90808	88895	CAAGTATATGAAGAACAGCA
90809	88896	ACAAGTATATGAAGAACAGC
90810	88897	CACAAGTATATGAAGAACAG
90811	88898	CCACAAGTATATGAAGAACA
90812	88899	ACCACAAGTATATGAAGAAC
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90814	88901	AAACCACAAGTATATGAAGA
90815	88902	AAAACCACAAGTATATGAAG
90816	88903	CAAAACCACAAGTATATGAA
90817	88904	TCAAAACCACAAGTATATGA

139894	137981	AAGGAACCAGGGGCCGAGGT
139895	137982	AAAGGAACCAGGGGCCGAGG
139896	137983	AAAAGGAACCAGGGGCCGAG
139897	137984	AAAAAGGAACCAGGGGCCGA
139898	137985	AAAAAAGGAACCAGGGGCCG
139899	137986	CAAAAAAGGAACCAGGGGCC
139900	137987	ACAAAAAAGGAACCAGGGGC
139901	137988	GACAAAAAAGGAACCAGGGG
139902	137989	AGACAAAAAAGGAACCAGGG
139903	137990	GAGACAAAAAAGGAACCAGG
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139905	137992	GAGAGACAAAAAAGGAACCA
139906	137993	AGAGAGACAAAAAAGGAACC
139907	137994	AAGAGAGACAAAAAAGGAAC
139908	137995	CAAGAGAGACAAAAAAGGAA
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139911	137998	AGACAAGAGAGACAAAAAAG
139912	137999	AAGACAAGAGAGACAAAAAA
139913	138000	GAAGACAAGAGAGACAAAAA
139914	138001	GGAAGACAAGAGAGACAAAA
139915	138002	TGGAAGACAAGAGAGACAAA
139916	138003	TTGGAAGACAAGAGAGACAA
139917	138004	CTTGGAAGACAAGAGAGACA
139918	138005	GCTTGGAAGACAAGAGAGAC
139919	138006	AGCTTGGAAGACAAGAGAGA
139920	138007	TAGCTTGGAAGACAAGAGAG
139921	138008	ATAGCTTGGAAGACAAGAGA
139922	138009	AATAGCTTGGAAGACAAGAG
139923	138010	AAATAGCTTGGAAGACAAGA
139924	138011	AAAATAGCTTGGAAGACAAG
139925	138012	AAAAATAGCTTGGAAGACAA
139926	138013	AAAAAATAGCTTGGAAGACA
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139928	138015	GAAAAAAATAGCTTGGAAGA
139929	138016	GGAAAAAAATAGCTTGGAAG
139930	138017	AGGAAAAAAATAGCTTGGAA
139931	138018	AAGGAAAAAAATAGCTTGGA
139932	138019	CAAGGAAAAAAATAGCTTGG
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139934	138021	GCCAAGGAAAAAAATAGCTT
139935	138022	AGCCAAGGAAAAAAATAGCT
139936	138023	AAGCCAAGGAAAAAAATAGC
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139957	138044	CAGGGTAGGAAGAAAATTTA
139958	138045	GCAGGGTAGGAAGAAAATTT
139959	138046	AGCAGGGTAGGAAGAAAATT
139960	138047	AAGCAGGGTAGGAAGAAAAT
139961	138048	AAAGCAGGGTAGGAAGAAAA
139962	138049	CAAAGCAGGGTAGGAAGAAA
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139964	138051	CACAAAGCAGGGTAGGAAGA

41671	39758	AAATTTCATTTGCAACAAGG
41672	39759	GAAATTTCATTTGCAACAAG
41673	39760	AGAAATTTCATTTGCAACAA
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41676	39763	CAAAGAAATTTCATTTGCAA
41677	39764	CCAAAGAAATTTCATTTGCA
41678	39765	CCCAAAGAAATTTCATTTGC
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41680	39767	TTCCCAAAGAAATTTCATTT
41681	39768	CTTCCCAAAGAAATTTCATT
41682	39769	TCTTCCCAAAGAAATTTCAT
41683	39770	CTCTTCCCAAAGAAATTTCA
41684	39771	TCTCTTCCCAAAGAAATTTC
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41686	39773	AATCTCTTCCCAAAGAAATT
41687	39774	CAATCTCTTCCCAAAGAAAT
41688	39775	ACAATCTCTTCCCAAAGAAA
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41690	39777	TCACAATCTCTTCCCAAAGA
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41692	39779	ACTCACAATCTCTTCCCAAA
41693	39780	AACTCACAATCTCTTCCCAA
41694	39781	AAACTCACAATCTCTTCCCA
41695	39782	AAAACTCACAATCTCTTCCC
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41697	39784	AAAAAACTCACAATCTCTTC
41698	39785	AAAAAAACTCACAATCTCTT
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41702	39789	GAGAAAAAAAACTCACAATC
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41708	39795	ATTTAGGAGAAAAAAAACTC
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41710	39797	TAATTTAGGAGAAAAAAAAC
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41714	39801	ACCATAATTTAGGAGAAAAA
41715	39802	CACCATAATTTAGGAGAAAA
41716	39803	GCACCATAATTTAGGAGAAA
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41718	39805	TTGCACCATAATTTAGGAGA
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41722	39809	TATATTGCACCATAATTTAG
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41724	39811	CTTATATTGCACCATAATTT
41725	39812	ACTTATATTGCACCATAATT
41726	39813	TACTTATATTGCACCATAAT
41727	39814	TTACTTATATTGCACCATAA
41728	39815	ATTACTTATATTGCACCATA
41729	39816	TATTACTTATATTGCACCAT
41730	39817	ATATTACTTATATTGCACCA
41731	39818	TATATTACTTATATTGCACC
41732	39819	GTATATTACTTATATTGCAC
41733	39820	GGTATATTACTTATATTGCA
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41737	39824	AAATGGTATATTACTTATAT
41738	39825	AAAATGGTATATTACTTATA
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90818	88905	ATCAAAACCACAAGTATATG
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90823	88910	TGGCAATCAAAACCACAAGT
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90825	88912	GCTGGCAATCAAAACCACAA
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90835	88922	TTAGGAATTTGCTGGCAATC
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90839	88926	AATGTTAGGAATTTGCTGGC
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90844	88931	TCCAAAATGTTAGGAATTTG
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90846	88933	TTTCCAAAATGTTAGGAATT
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90860	88947	CATTACTGTTTTCTTTTCCA
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90875	88962	CCTTACCCTTTATCCCATTA
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90877	88964	GCCCTTACCCTTTATCCCAT
90878	88965	AGCCCTTACCCTTTATCCCA
90879	88966	TAGCCCTTACCCTTTATCCC
90880	88967	CTAGCCCTTACCCTTTATCC
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90885	88972	CCTCTCTAGCCCTTACCCTT
90886	88973	TCCTCTCTAGCCCTTACCCT
90887	88974	GTCCTCTCTAGCCCTTACCC
90888	88975	TGTCCTCTCTAGCCCTTACC

139965	138052	ACACAAAGCAGGGTAGGAAG
139966	138053	GACACAAAGCAGGGTAGGAA
139967	138054	TGACACAAAGCAGGGTAGGA
139968	138055	GTGACACAAAGCAGGGTAGG
139969	138056	AGTGACACAAAGCAGGGTAG
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139971	138058	ACAGTGACACAAAGCAGGGT
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139973	138060	TGACAGTGACACAAAGCAGG
139974	138061	GTGACAGTGACACAAAGCAG
139975	138062	AGTGACAGTGACACAAAGCA
139976	138063	AAGTGACAGTGACACAAAGC
139977	138064	TAAGTGACAGTGACACAAAG
139978	138065	TTAAGTGACAGTGACACAAA
139979	138066	GTTAAGTGACAGTGACACAA
139980	138067	AGTTAAGTGACAGTGACACA
139981	138068	CAGTTAAGTGACAGTGACAC
139982	138069	CCAGTTAAGTGACAGTGACA
139983	138070	GCCAGTTAAGTGACAGTGAC
139984	138071	GGCCAGTTAAGTGACAGTGA
139985	138072	AGGCCAGTTAAGTGACAGTG
139986	138073	TAGGCCAGTTAAGTGACAGT
139987	138074	ATAGGCCAGTTAAGTGACAG
139988	138075	GATAGGCCAGTTAAGTGACA
139989	138076	TGATAGGCCAGTTAAGTGAC
139990	138077	TTGATAGGCCAGTTAAGTGA
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139992	138079	CCTTGATAGGCCAGTTAAGT
139993	138080	TCCTTGATAGGCCAGTTAAG
139994	138081	TTCCTTGATAGGCCAGTTAA
139995	138082	GTTCCTTGATAGGCCAGTTA
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139997	138084	CGGTTCCTTGATAGGCCAGT
139998	138085	TCGGTTCCTTGATAGGCCAG
139999	138086	TTCGGTTCCTTGATAGGCCA
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140002	138089	CAGTTCGGTTCCTTGATAGG
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140006	138093	AATACAGTTCGGTTCCTTGA
140007	138094	AAATACAGTTCGGTTCCTTG
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140010	138097	CAAAAATACAGTTCGGTTCC
140011	138098	ACAAAAATACAGTTCGGTTC
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140020	138107	ATACTAGTAACAAAAATACA
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140032	138119	TACTTTAAATCAATACTAGT
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140035	138122	TTATACTTTAAATCAATACT

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41743	39830	TTGTTAAAATGGTATATTAC
41744	39831	ATTGTTAAAATGGTATATTA
41745	39832	AATTGTTAAAATGGTATATT
41746	39833	AAATTGTTAAAATGGTATAT
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41748	39835	TAAAATTGTTAAAATGGTAT
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41750	39837	CTTAAAATTGTTAAAATGGT
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41753	39840	ACACTTAAAATTGTTAAAAT
41754	39841	TACACTTAAAATTGTTAAAA
41755	39842	ATACACTTAAAATTGTTAAA
41756	39843	AATACACTTAAAATTGTTAA
41757	39844	TAATACACTTAAAATTGTTA
41758	39845	TTAATACACTTAAAATTGTT
41759	39846	CTTAATACACTTAAAATTGT
41760	39847	ACTTAATACACTTAAAATTG
41761	39848	CACTTAATACACTTAAAATT
41762	39849	ACACTTAATACACTTAAAAT
41763	39850	AACACTTAATACACTTAAAA
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41765	39852	AAAACACTTAATACACTTAA
41766	39853	AAAAACACTTAATACACTTA
41767	39854	AAAAAACACTTAATACACTT
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90895	88982	ATAAAACTGTCCTCTCTAGC
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90904	88991	TCTAGGTAAATAAAACTGTC
90905	88992	ATCTAGGTAAATAAAACTGT
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90908	88995	AAGATCTAGGTAAATAAAAC
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90911	88998	CTGAAGATCTAGGTAAATAA
90912	88999	TCTGAAGATCTAGGTAAATA
90913	89000	CTCTGAAGATCTAGGTAAAT
90914	89001	TCTCTGAAGATCTAGGTAAA
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140042	138129	GTGAAACTTATACTTTAAAT
140043	138130	TGTGAAACTTATACTTTAAA
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41815	39902	ACAGAGCAAGACTATCTCAA
41816	39903	GACAGAGCAAGACTATCTCA
41817	39904	CGACAGAGCAAGACTATCTC
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90985	89072	CTAGAAGAAAGGGAAAATGT
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90988	89075	GAACTAGAAGAAAGGGAAAA
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91016	89103	GGTCTATGAGTTTTAGGGGA
91017	89104	GGGTCTATGAGTTTTAGGGG
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140116	138203	AAGAGCGAAACTCCGTCTCA
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140126	138213	CTTGGGCAACAAGAGCGAAA
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140137	138224	TTGCACTCCAGCTTGGGCAA
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140139	138226	CATTGCACTCCAGCTTGGGC
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140141	138228	ACCATTGCACTCCAGCTTGG
140142	138229	CACCATTGCACTCCAGCTTG
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41896	39983	CTGAGACCAGAGAATCACTT
41897	39984	GCTGAGACCAGAGAATCACT
41898	39985	GGCTGAGACCAGAGAATCAC
41899	39986	AGGCTGAGACCAGAGAATCA
41900	39987	GAGGCTGAGACCAGAGAATC
41901	39988	GGAGGCTGAGACCAGAGAAT
41902	39989	GGGAGGCTGAGACCAGAGAA
41903	39990	GGGGAGGCTGAGACCAGAGA
41904	39991	TGGGGAGGCTGAGACCAGAG
41905	39992	TTGGGGAGGCTGAGACCAGA
41906	39993	TTTGGGGAGGCTGAGACCAG
41907	39994	ATTTGGGGAGGCTGAGACCA
41908	39995	TATTTGGGGAGGCTGAGACC
41909	39996	ATATTTGGGGAGGCTGAGAC
41910	39997	GATATTTGGGGAGGCTGAGA
41911	39998	AGATATTTGGGGAGGCTGAG
41912	39999	CAGATATTTGGGGAGGCTGA
41913	40000	CCAGATATTTGGGGAGGCTG
41914	40001	CCCAGATATTTGGGGAGGCT
41915	40002	TCCCAGATATTTGGGGAGGC
41916	40003	ATCCCAGATATTTGGGGAGG
41917	40004	AATCCCAGATATTTGGGGAG
41918	40005	TAATCCCAGATATTTGGGGA
41919	40006	GTAATCCCAGATATTTGGGG
41920	40007	TGTAATCCCAGATATTTGGG
41921	40008	CTGTAATCCCAGATATTTGG
41922	40009	CCTGTAATCCCAGATATTTG
41923	40010	ACCTGTAATCCCAGATATTT
41924	40011	CACCTGTAATCCCAGATATT
41925	40012	ACACCTGTAATCCCAGATAT
41926	40013	CACACCTGTAATCCCAGATA
41927	40014	GCACACCTGTAATCCCAGAT
41928	40015	TGCACACCTGTAATCCCAGA
41929	40016	GTGCACACCTGTAATCCCAG
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41931	40018	TGGTGCACACCTGTAATCCC
41932	40019	GTGGTGCACACCTGTAATCC
41933	40020	GGTGGTGCACACCTGTAATC
41934	40021	TGGTGGTGCACACCTGTAAT
41935	40022	GTGGTGGTGCACACCTGTAA
41936	40023	CGTGGTGGTGCACACCTGTA
41937	40024	GCGTGGTGGTGCACACCTGT
41938	40025	GGCGTGGTGGTGCACACCTG
41939	40026	AGGCGTGGTGGTGCACACCT
41940	40027	CAGGCGTGGTGGTGCACACC
41941	40028	CCAGGCGTGGTGGTGCACAC
41942	40029	GCCAGGCGTGGTGGTGCACA
41943	40030	AGCCAGGCGTGGTGGTGCAC
41944	40031	TAGCCAGGCGTGGTGGTGCA
41945	40032	TTAGCCAGGCGTGGTGGTGC
41946	40033	ATTAGCCAGGCGTGGTGGTG
41947	40034	AATTAGCCAGGCGTGGTGGT
41948	40035	AAATTAGCCAGGCGTGGTGG
41949	40036	AAAATTAGCCAGGCGTGGTG
41950	40037	AAAAATTAGCCAGGCGTGGT
41951	40038	GAAAAATTAGCCAGGCGTGG
41952	40039	AGAAAAATTAGCCAGGCGTG
41953	40040	TAGAAAAATTAGCCAGGCGT
41954	40041	ATAGAAAAATTAGCCAGGCG

91031	89118	TGTCTGGGAGACCTGGGTCT
91032	89119	CTGTCTGGGAGACCTGGGTC
91033	89120	TCTGTCTGGGAGACCTGGGT
91034	89121	TTCTGTCTGGGAGACCTGGG
91035	89122	GTTCTGTCTGGGAGACCTGG
91036	89123	TGTTCTGTCTGGGAGACCTG
91037	89124	CTGTTCTGTCTGGGAGACCT
91038	89125	ACTGTTCTGTCTGGGAGACC
91039	89126	TACTGTTCTGTCTGGGAGAC
91040	89127	ATACTGTTCTGTCTGGGAGA
91041	89128	AATACTGTTCTGTCTGGGAG
91042	89129	CAATACTGTTCTGTCTGGGA
91043	89130	CCAATACTGTTCTGTCTGGG
91044	89131	TCCAATACTGTTCTGTCTGG
91045	89132	TTCCAATACTGTTCTGTCTG
91046	89133	TTTCCAATACTGTTCTGTCT
91047	89134	ATTTCCAATACTGTTCTGTC
91048	89135	TATTTCCAATACTGTTCTGT
91049	89136	GTATTTCCAATACTGTTCTG
91050	89137	GGTATTTCCAATACTGTTCT
91051	89138	GGGTATTTCCAATACTGTTC
91052	89139	GGGGTATTTCCAATACTGTT
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91055	89142	CTGGGGGTATTTCCAATACT
91056	89143	ACTGGGGGTATTTCCAATAC
91057	89144	CACTGGGGGTATTTCCAATA
91058	89145	CCACTGGGGGTATTTCCAAT
91059	89146	CCCACTGGGGGTATTTCCAA
91060	89147	GCCCACTGGGGGTATTTCCA
91061	89148	GGCCCACTGGGGGTATTTCC
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91063	89150	CTGGCCCACTGGGGGTATTT
91064	89151	ACTGGCCCACTGGGGGTATT
91065	89152	AACTGGCCCACTGGGGGTAT
91066	89153	GAACTGGCCCACTGGGGGTA
91067	89154	AGAACTGGCCCACTGGGGGT
91068	89155	AAGAACTGGCCCACTGGGGG
91069	89156	CAAGAACTGGCCCACTGGGG
91070	89157	GCAAGAACTGGCCCACTGGG
91071	89158	AGCAAGAACTGGCCCACTGG
91072	89159	AAGCAAGAACTGGCCCACTG
91073	89160	GAAGCAAGAACTGGCCCACT
91074	89161	AGAAGCAAGAACTGGCCCAC
91075	89162	GAGAAGCAAGAACTGGCCCA
91076	89163	GGAGAAGCAAGAACTGGCCC
91077	89164	GGGAGAAGCAAGAACTGGCC
91078	89165	GGGGAGAAGCAAGAACTGGC
91079	89166	TGGGGAGAAGCAAGAACTGG
91080	89167	TTGGGGAGAAGCAAGAACTG
91081	89168	CTTGGGGAGAAGCAAGAACT
91082	89169	GCTTGGGGAGAAGCAAGAAC
91083	89170	AGCTTGGGGAGAAGCAAGAA
91084	89171	CAGCTTGGGGAGAAGCAAGA
91085	89172	CCAGCTTGGGGAGAAGCAAG
91086	89173	ACCAGCTTGGGGAGAAGCAA
91087	89174	TACCAGCTTGGGGAGAAGCA
91088	89175	ATACCAGCTTGGGGAGAAGC
91089	89176	AATACCAGCTTGGGGAGAAG
91090	89177	TAATACCAGCTTGGGGAGAA
91091	89178	ATAATACCAGCTTGGGGAGA
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91093	89180	GAATAATACCAGCTTGGGGA
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91095	89182	TGGAATAATACCAGCTTGGG
91096	89183	TTGGAATAATACCAGCTTGG
91097	89184	GTTGGAATAATACCAGCTTG
91098	89185	AGTTGGAATAATACCAGCTT
91099	89186	CAGTTGGAATAATACCAGCT
91100	89187	TCAGTTGGAATAATACCAGC
91101	89188	TTCAGTTGGAATAATACCAG

140178	138265	AACCCGGGAGGTGGAGGTTG
140179	138266	GAACCCGGGAGGTGGAGGTT
140180	138267	TGAACCCGGGAGGTGGAGGT
140181	138268	TTGAACCCGGGAGGTGGAGG
140182	138269	CTTGAACCCGGGAGGTGGAG
140183	138270	GCTTGAACCCGGGAGGTGGA
140184	138271	AGCTTGAACCCGGGAGGTGG
140185	138272	TAGCTTGAACCCGGGAGGTG
140186	138273	ATAGCTTGAACCCGGGAGGT
140187	138274	AATAGCTTGAACCCGGGAGG
140188	138275	GAATAGCTTGAACCCGGGAG
140189	138276	AGAATAGCTTGAACCCGGGA
140190	138277	GAGAATAGCTTGAACCCGGG
140191	138278	GGAGAATAGCTTGAACCCGG
140192	138279	AGGAGAATAGCTTGAACCCG
140193	138280	AAGGAGAATAGCTTGAACCC
140194	138281	GAAGGAGAATAGCTTGAACC
140195	138282	GGAAGGAGAATAGCTTGAAC
140196	138283	GGGAAGGAGAATAGCTTGAA
140197	138284	GGGGAAGGAGAATAGCTTGA
140198	138285	TGGGGAAGGAGAATAGCTTG
140199	138286	GTGGGGAAGGAGAATAGCTT
140200	138287	AGTGGGGAAGGAGAATAGCT
140201	138288	GAGTGGGGAAGGAGAATAGC
140202	138289	AGAGTGGGGAAGGAGAATAG
140203	138290	GAGAGTGGGGAAGGAGAATA
140204	138291	GGAGAGTGGGGAAGGAGAAT
140205	138292	GGGAGAGTGGGGAAGGAGAA
140206	138293	AGGGAGAGTGGGGAAGGAGA
140207	138294	TAGGGAGAGTGGGGAAGGAG
140208	138295	CTAGGGAGAGTGGGGAAGGA
140209	138296	ACTAGGGAGAGTGGGGAAGG
140210	138297	TACTAGGGAGAGTGGGGAAG
140211	138298	CTACTAGGGAGAGTGGGGAA
140212	138299	GCTACTAGGGAGAGTGGGGA
140213	138300	AGCTACTAGGGAGAGTGGGG
140214	138301	CAGCTACTAGGGAGAGTGGG
140215	138302	ACAGCTACTAGGGAGAGTGG
140216	138303	CACAGCTACTAGGGAGAGTG
140217	138304	TCACAGCTACTAGGGAGAGT
140218	138305	ATCACAGCTACTAGGGAGAG
140219	138306	AATCACAGCTACTAGGGAGA
140220	138307	TAATCACAGCTACTAGGGAG
140221	138308	GTAATCACAGCTACTAGGGA
140222	138309	TGTAATCACAGCTACTAGGG
140223	138310	CTGTAATCACAGCTACTAGG
140224	138311	CCTGTAATCACAGCTACTAG
140225	138312	ACCTGTAATCACAGCTACTA
140226	138313	CACCTGTAATCACAGCTACT
140227	138314	GCACCTGTAATCACAGCTAC
140228	138315	GGCACCTGTAATCACAGCTA
140229	138316	AGGCACCTGTAATCACAGCT
140230	138317	CAGGCACCTGTAATCACAGC
140231	138318	GCAGGCACCTGTAATCACAG
140232	138319	GGCAGGCACCTGTAATCACA
140233	138320	TGGCAGGCACCTGTAATCAC
140234	138321	GTGGCAGGCACCTGTAATCA
140235	138322	GGTGGCAGGCACCTGTAATC
140236	138323	TGGTGGCAGGCACCTGTAAT
140237	138324	GTGGTGGCAGGCACCTGTAA
140238	138325	CGTGGTGGCAGGCACCTGTA
140239	138326	GCGTGGTGGCAGGCACCTGT
140240	138327	GGCGTGGTGGCAGGCACCTG
140241	138328	GGGCGTGGTGGCAGGCACCT
140242	138329	TGGGCGTGGTGGCAGGCACC
140243	138330	CTGGGCGTGGTGGCAGGCAC
140244	138331	GCTGGGCGTGGTGGCAGGCA
140245	138332	AGCTGGGCGTGGTGGCAGGC
140246	138333	TAGCTGGGCGTGGTGGCAGG
140247	138334	TTAGCTGGGCGTGGTGGCAG
140248	138335	ATTAGCTGGGCGTGGTGGCA

41955	40042	AATAGAAAAATTAGCCAGGC
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41958	40045	AAAAATAGAAAAATTAGCCA
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41973	40060	AACCCCGTTTCTACTAAAAA
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41975	40062	GAAACCCCGTTTCTACTAAA
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41977	40064	GTGAAACCCCGTTTCTACTA
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42006	40093	AGAAGTTCAAGACCAGCCTG
42007	40094	CAGAAGTTCAAGACCAGCCT
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42017	40104	ATCACGAGCTCAGAAGTTCA
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42022	40109	GGTGGATCACGAGCTCAGAA
42023	40110	GGGTGGATCACGAGCTCAGA
42024	40111	TGGGTGGATCACGAGCTCAG
42025	40112	GTGGGTGGATCACGAGCTCA

91102	89189	CTTCAGTTGGAATAATACCA
91103	89190	GCTTCAGTTGGAATAATACC
91104	89191	AGCTTCAGTTGGAATAATAC
91105	89192	CAGCTTCAGTTGGAATAATA
91106	89193	ACAGCTTCAGTTGGAATAAT
91107	89194	AACAGCTTCAGTTGGAATAA
91108	89195	CAACAGCTTCAGTTGGAATA
91109	89196	GCAACAGCTTCAGTTGGAAT
91110	89197	GGCAACAGCTTCAGTTGGAA
91111	89198	TGGCAACAGCTTCAGTTGGA
91112	89199	ATGGCAACAGCTTCAGTTGG
91113	89200	CATGGCAACAGCTTCAGTTG
91114	89201	GCATGGCAACAGCTTCAGTT
91115	89202	GGCATGGCAACAGCTTCAGT
91116	89203	AGGCATGGCAACAGCTTCAG
91117	89204	TAGGCATGGCAACAGCTTCA
91118	89205	ATAGGCATGGCAACAGCTTC
91119	89206	AATAGGCATGGCAACAGCTT
91120	89207	GAATAGGCATGGCAACAGCT
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91123	89210	CTGGAATAGGCATGGCAACA
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91125	89212	AGCTGGAATAGGCATGGCAA
91126	89213	CAGCTGGAATAGGCATGGCA
91127	89214	GCAGCTGGAATAGGCATGGC
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91130	89217	GATGCAGCTGGAATAGGCAT
91131	89218	AGATGCAGCTGGAATAGGCA
91132	89219	GAGATGCAGCTGGAATAGGC
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91134	89221	AGGAGATGCAGCTGGAATAG
91135	89222	TAGGAGATGCAGCTGGAATA
91136	89223	GTAGGAGATGCAGCTGGAAT
91137	89224	CGTAGGAGATGCAGCTGGAA
91138	89225	GCGTAGGAGATGCAGCTGGA
91139	89226	GGCGTAGGAGATGCAGCTGG
91140	89227	AGGCGTAGGAGATGCAGCTG
91141	89228	CAGGCGTAGGAGATGCAGCT
91142	89229	GCAGGCGTAGGAGATGCAGC
91143	89230	AGCAGGCGTAGGAGATGCAG
91144	89231	TAGCAGGCGTAGGAGATGCA
91145	89232	CTAGCAGGCGTAGGAGATGC
91146	89233	ACTAGCAGGCGTAGGAGATG
91147	89234	GACTAGCAGGCGTAGGAGAT
91148	89235	GGACTAGCAGGCGTAGGAGA
91149	89236	AGGACTAGCAGGCGTAGGAG
91150	89237	CAGGACTAGCAGGCGTAGGA
91151	89238	GCAGGACTAGCAGGCGTAGG
91152	89239	TGCAGGACTAGCAGGCGTAG
91153	89240	ATGCAGGACTAGCAGGCGTA
91154	89241	GATGCAGGACTAGCAGGCGT
91155	89242	CGATGCAGGACTAGCAGGCG
91156	89243	TCGATGCAGGACTAGCAGGC
91157	89244	TTCGATGCAGGACTAGCAGG
91158	89245	GTTCGATGCAGGACTAGCAG
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91160	89247	CTGTTCGATGCAGGACTAGC
91161	89248	TCTGTTCGATGCAGGACTAG
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91164	89251	AGCTCTGTTCGATGCAGGAC
91165	89252	CAGCTCTGTTCGATGCAGGA
91166	89253	ACAGCTCTGTTCGATGCAGG
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91168	89255	TAACAGCTCTGTTCGATGCA
91169	89256	GTAACAGCTCTGTTCGATGC
91170	89257	GGTAACAGCTCTGTTCGATG
91171	89258	GGGTAACAGCTCTGTTCGAT
91172	89259	GGGGTAACAGCTCTGTTCGA

140249	138336	AATTAGCTGGGCGTGGTGGC
140250	138337	AAATTAGCTGGGCGTGGTGG
140251	138338	AAAATTAGCTGGGCGTGGTG
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140253	138340	CAAAAATTAGCTGGGCGTGG
140254	138341	ACAAAAATTAGCTGGGCGTG
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140257	138344	AATACAAAAATTAGCTGGGC
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140260	138347	AAAAATACAAAAATTAGCTG
140261	138348	TAAAAATACAAAAATTAGCT
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140271	138358	CTGTCTCTACTAAAAATACA
140272	138359	CCTGTCTCTACTAAAAATAC
140273	138360	CCCTGTCTCTACTAAAAATA
140274	138361	ACCCTGTCTCTACTAAAAAT
140275	138362	AACCCTGTCTCTACTAAAAA
140276	138363	AAACCCTGTCTCTACTAAAA
140277	138364	GAAACCCTGTCTCTACTAAA
140278	138365	CGAAACCCTGTCTCTACTAA
140279	138366	GCGAAACCCTGTCTCTACTA
140280	138367	GGCGAAACCCTGTCTCTACT
140281	138368	CGGCGAAACCCTGTCTCTAC
140282	138369	ACGGCGAAACCCTGTCTCTA
140283	138370	CACGGCGAAACCCTGTCTCT
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140285	138372	AACACGGCGAAACCCTGTCT
140286	138373	CAACACGGCGAAACCCTGTC
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140289	138376	GGCCAACACGGCGAAACCCT
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140291	138378	TTGGCCAACACGGCGAAACC
140292	138379	CTTGGCCAACACGGCGAAAC
140293	138380	GCTTGGCCAACACGGCGAAA
140294	138381	AGCTTGGCCAACACGGCGAA
140295	138382	CAGCTTGGCCAACACGGCGA
140296	138383	CCAGCTTGGCCAACACGGCG
140297	138384	ACCAGCTTGGCCAACACGGC
140298	138385	GACCAGCTTGGCCAACACGG
140299	138386	AGACCAGCTTGGCCAACACG
140300	138387	GAGACCAGCTTGGCCAACAC
140301	138388	CGAGACCAGCTTGGCCAACA
140302	138389	TCGAGACCAGCTTGGCCAAC
140303	138390	TTCGAGACCAGCTTGGCCAA
140304	138391	GTTCGAGACCAGCTTGGCCA
140305	138392	AGTTCGAGACCAGCTTGGCC
140306	138393	GAGTTCGAGACCAGCTTGGC
140307	138394	GGAGTTCGAGACCAGCTTGG
140308	138395	AGGAGTTCGAGACCAGCTTG
140309	138396	TAGGAGTTCGAGACCAGCTT
140310	138397	TTAGGAGTTCGAGACCAGCT
140311	138398	GTTAGGAGTTCGAGACCAGC
140312	138399	GGTTAGGAGTTCGAGACCAG
140313	138400	AGGTTAGGAGTTCGAGACCA
140314	138401	GAGGTTAGGAGTTCGAGACC
140315	138402	TGAGGTTAGGAGTTCGAGAC
140316	138403	CTGAGGTTAGGAGTTCGAGA
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42026	40113	GGTGGGTGGATCACGAGCTC
42027	40114	AGGTGGGTGGATCACGAGCT
42028	40115	GAGGTGGGTGGATCACGAGC
42029	40116	CGAGGTGGGTGGATCACGAG
42030	40117	CCGAGGTGGGTGGATCACGA
42031	40118	GCCGAGGTGGGTGGATCACG
42032	40119	GGCCGAGGTGGGTGGATCAC
42033	40120	AGGCCGAGGTGGGTGGATCA
42034	40121	GAGGCCGAGGTGGGTGGATC
42035	40122	GGAGGCCGAGGTGGGTGGAT
42036	40123	GGGAGGCCGAGGTGGGTGGA
42037	40124	TGGGAGGCCGAGGTGGGTGG
42038	40125	TTGGGAGGCCGAGGTGGGTG
42039	40126	TTTGGGAGGCCGAGGTGGGT
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42051	40138	TAATCCCAGCACTTTGGGAG
42052	40139	GTAATCCCAGCACTTTGGGA
42053	40140	TGTAATCCCAGCACTTTGGG
42054	40141	CTGTAATCCCAGCACTTTGG
42055	40142	CCTGTAATCCCAGCACTTTG
42056	40143	GCCTGTAATCCCAGCACTTT
42057	40144	GGCCTGTAATCCCAGCACTT
42058	40145	AGGCCTGTAATCCCAGCACT
42059	40146	AAGGCCTGTAATCCCAGCAC
42060	40147	TAAGGCCTGTAATCCCAGCA
42061	40148	CTAAGGCCTGTAATCCCAGC
42062	40149	GCTAAGGCCTGTAATCCCAG
42063	40150	GGCTAAGGCCTGTAATCCCA
42064	40151	TGGCTAAGGCCTGTAATCCC
42065	40152	GTGGCTAAGGCCTGTAATCC
42066	40153	GGTGGCTAAGGCCTGTAATC
42067	40154	TGGTGGCTAAGGCCTGTAAT
42068	40155	GTGGTGGCTAAGGCCTGTAA
42069	40156	TGTGGTGGCTAAGGCCTGTA
42070	40157	GTGTGGTGGCTAAGGCCTGT
42071	40158	GGTGTGGTGGCTAAGGCCTG
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42073	40160	CAGGTGTGGTGGCTAAGGCC
42074	40161	CCAGGTGTGGTGGCTAAGGC
42075	40162	GCCAGGTGTGGTGGCTAAGG
42076	40163	GGCCAGGTGTGGTGGCTAAG
42077	40164	AGGCCAGGTGTGGTGGCTAA
42078	40165	TAGGCCAGGTGTGGTGGCTA
42079	40166	ATAGGCCAGGTGTGGTGGCT
42080	40167	CATAGGCCAGGTGTGGTGGC
42081	40168	GCATAGGCCAGGTGTGGTGG
42082	40169	TGCATAGGCCAGGTGTGGTG
42083	40170	ATGCATAGGCCAGGTGTGGT
42084	40171	AATGCATAGGCCAGGTGTGG
42085	40172	CAATGCATAGGCCAGGTGTG
42086	40173	GCAATGCATAGGCCAGGTGT
42087	40174	AGCAATGCATAGGCCAGGTG
42088	40175	AAGCAATGCATAGGCCAGGT
42089	40176	AAAGCAATGCATAGGCCAGG
42090	40177	AAAAGCAATGCATAGGCCAG
42091	40178	TAAAAGCAATGCATAGGCCA
42092	40179	ATAAAAGCAATGCATAGGCC
42093	40180	TATAAAAGCAATGCATAGGC
42094	40181	ATATAAAAGCAATGCATAGG
42095	40182	CATATAAAAGCAATGCATAG
42096	40183	ACATATAAAAGCAATGCATA

91173	89260	AGGGGTAACAGCTCTGTTCG
91174	89261	AAGGGGTAACAGCTCTGTTC
91175	89262	GAAGGGGTAACAGCTCTGTT
91176	89263	AGAAGGGGTAACAGCTCTGT
91177	89264	TAGAAGGGGTAACAGCTCTG
91178	89265	CTAGAAGGGGTAACAGCTCT
91179	89266	ACTAGAAGGGGTAACAGCTC
91180	89267	CACTAGAAGGGGTAACAGCT
91181	89268	TCACTAGAAGGGGTAACAGC
91182	89269	CTCACTAGAAGGGGTAACAG
91183	89270	CCTCACTAGAAGGGGTAACA
91184	89271	CCCTCACTAGAAGGGGTAAC
91185	89272	ACCCTCACTAGAAGGGGTAA
91186	89273	TACCCTCACTAGAAGGGGTA
91187	89274	ATACCCTCACTAGAAGGGGT
91188	89275	CATACCCTCACTAGAAGGGG
91189	89276	ACATACCCTCACTAGAAGGG
91190	89277	TACATACCCTCACTAGAAGG
91191	89278	TTACATACCCTCACTAGAAG
91192	89279	GTTACATACCCTCACTAGAA
91193	89280	TGTTACATACCCTCACTAGA
91194	89281	TTGTTACATACCCTCACTAG
91195	89282	TTTGTTACATACCCTCACTA
91196	89283	CTTTGTTACATACCCTCACT
91197	89284	CCTTTGTTACATACCCTCAC
91198	89285	CCCTTTGTTACATACCCTCA
91199	89286	GCCCTTTGTTACATACCCTC
91200	89287	AGCCCTTTGTTACATACCCT
91201	89288	AAGCCCTTTGTTACATACCC
91202	89289	GAAGCCCTTTGTTACATACC
91203	89290	AGAAGCCCTTTGTTACATAC
91204	89291	CAGAAGCCCTTTGTTACATA
91205	89292	CCAGAAGCCCTTTGTTACAT
91206	89293	TCCAGAAGCCCTTTGTTACA
91207	89294	ATCCAGAAGCCCTTTGTTAC
91208	89295	GATCCAGAAGCCCTTTGTTA
91209	89296	GGATCCAGAAGCCCTTTGTT
91210	89297	TGGATCCAGAAGCCCTTTGT
91211	89298	ATGGATCCAGAAGCCCTTTG
91212	89299	TATGGATCCAGAAGCCCTTT
91213	89300	TTATGGATCCAGAAGCCCTT
91214	89301	ATTATGGATCCAGAAGCCCT
91215	89302	GATTATGGATCCAGAAGCCC
91216	89303	AGATTATGGATCCAGAAGCC
91217	89304	GAGATTATGGATCCAGAAGC
91218	89305	TGAGATTATGGATCCAGAAG
91219	89306	CTGAGATTATGGATCCAGAA
91220	89307	GCTGAGATTATGGATCCAGA
91221	89308	AGCTGAGATTATGGATCCAG
91222	89309	CAGCTGAGATTATGGATCCA
91223	89310	ACAGCTGAGATTATGGATCC
91224	89311	CACAGCTGAGATTATGGATC
91225	89312	TCACAGCTGAGATTATGGAT
91226	89313	TTCACAGCTGAGATTATGGA
91227	89314	TTTCACAGCTGAGATTATGG
91228	89315	ATTTCACAGCTGAGATTATG
91229	89316	AATTTCACAGCTGAGATTAT
91230	89317	CAATTTCACAGCTGAGATTA
91231	89318	TCAATTTCACAGCTGAGATT
91232	89319	TTCAATTTCACAGCTGAGAT
91233	89320	ATTCAATTTCACAGCTGAGA
91234	89321	CATTCAATTTCACAGCTGAG
91235	89322	ACATTCAATTTCACAGCTGA
91236	89323	AACATTCAATTTCACAGCTG
91237	89324	TAACATTCAATTTCACAGCT
91238	89325	CTAACATTCAATTTCACAGC
91239	89326	TCTAACATTCAATTTCACAG
91240	89327	CTCTAACATTCAATTTCACA
91241	89328	CCTCTAACATTCAATTTCAC
91242	89329	CCCTCTAACATTCAATTTCA
91243	89330	ACCCTCTAACATTCAATTTC

140320	138407	TCACCTGAGGTTAGGAGTTC
140321	138408	ATCACCTGAGGTTAGGAGTT
140322	138409	GATCACCTGAGGTTAGGAGT
140323	138410	GGATCACCTGAGGTTAGGAG
140324	138411	CGGATCACCTGAGGTTAGGA
140325	138412	GCGGATCACCTGAGGTTAGG
140326	138413	GGCGGATCACCTGAGGTTAG
140327	138414	GGGCGGATCACCTGAGGTTA
140328	138415	CGGGCGGATCACCTGAGGTT
140329	138416	GCGGGCGGATCACCTGAGGT
140330	138417	GGCGGGCGGATCACCTGAGG
140331	138418	AGGCGGGCGGATCACCTGAG
140332	138419	GAGGCGGGCGGATCACCTGA
140333	138420	CGAGGCGGGCGGATCACCTG
140334	138421	CCGAGGCGGGCGGATCACCT
140335	138422	GCCGAGGCGGGCGGATCACC
140336	138423	GGCCGAGGCGGGCGGATCAC
140337	138424	AGGCCGAGGCGGGCGGATCA
140338	138425	GAGGCCGAGGCGGGCGGATC
140339	138426	GGAGGCCGAGGCGGGCGGAT
140340	138427	GGGAGGCCGAGGCGGGCGGA
140341	138428	TGGGAGGCCGAGGCGGGCGG
140342	138429	TTGGGAGGCCGAGGCGGGCG
140343	138430	TTTGGGAGGCCGAGGCGGGC
140344	138431	TTTTGGGAGGCCGAGGCGGG
140345	138432	ATTTTGGGAGGCCGAGGCGG
140346	138433	CATTTTGGGAGGCCGAGGCG
140347	138434	GCATTTTGGGAGGCCGAGGC
140348	138435	AGCATTTTGGGAGGCCGAGG
140349	138436	CAGCATTTTGGGAGGCCGAG
140350	138437	CCAGCATTTTGGGAGGCCGA
140351	138438	CCCAGCATTTTGGGAGGCCG
140352	138439	TCCCAGCATTTTGGGAGGCC
140353	138440	ATCCCAGCATTTTGGGAGGC
140354	138441	AATCCCAGCATTTTGGGAGG
140355	138442	TAATCCCAGCATTTTGGGAG
140356	138443	GTAATCCCAGCATTTTGGGA
140357	138444	TGTAATCCCAGCATTTTGGG
140358	138445	TTGTAATCCCAGCATTTTGG
140359	138446	CTTGTAATCCCAGCATTTTG
140360	138447	GCTTGTAATCCCAGCATTTT
140361	138448	CGCTTGTAATCCCAGCATTT
140362	138449	ACGCTTGTAATCCCAGCATT
140363	138450	CACGCTTGTAATCCCAGCAT
140364	138451	TCACGCTTGTAATCCCAGCA
140365	138452	CTCACGCTTGTAATCCCAGC
140366	138453	GCTCACGCTTGTAATCCCAG
140367	138454	GGCTCACGCTTGTAATCCCA
140368	138455	TGGCTCACGCTTGTAATCCC
140369	138456	GTGGCTCACGCTTGTAATCC
140370	138457	GGTGGCTCACGCTTGTAATC
140371	138458	CGGTGGCTCACGCTTGTAAT
140372	138459	ACGGTGGCTCACGCTTGTAA
140373	138460	CACGGTGGCTCACGCTTGTA
140374	138461	GCACGGTGGCTCACGCTTGT
140375	138462	GGCACGGTGGCTCACGCTTG
140376	138463	GGGCACGGTGGCTCACGCTT
140377	138464	CGGGCACGGTGGCTCACGCT
140378	138465	CCGGGCACGGTGGCTCACGC
140379	138466	GCCGGGCACGGTGGCTCACG
140380	138467	AGCCGGGCACGGTGGCTCAC
140381	138468	GAGCCGGGCACGGTGGCTCA
140382	138469	GGAGCCGGGCACGGTGGCTC
140383	138470	TGGAGCCGGGCACGGTGGCT
140384	138471	ATGGAGCCGGGCACGGTGGC
140385	138472	AATGGAGCCGGGCACGGTGG
140386	138473	AAATGGAGCCGGGCACGGTG
140387	138474	GAAATGGAGCCGGGCACGGT
140388	138475	AGAAATGGAGCCGGGCACGG
140389	138476	GAGAAATGGAGCCGGGCACG
140390	138477	GGAGAAATGGAGCCGGGCAC

42097	40184	TACATATAAAAGCAATGCAT
42098	40185	ATACATATAAAAGCAATGCA
42099	40186	AATACATATAAAAGCAATGC
42100	40187	AAATACATATAAAAGCAATG
42101	40188	AAAATACATATAAAAGCAAT
42102	40189	TAAAATACATATAAAAGCAA
42103	40190	TTAAAATACATATAAAAGCA
42104	40191	TTTAAAATACATATAAAAGC
42105	40192	TTTTAAAATACATATAAAAG
42106	40193	ATTTTAAAATACATATAAAA
42107	40194	AATTTTAAAATACATATAAA
42108	40195	GAATTTTAAAATACATATAA
42109	40196	TGAATTTTAAAATACATATA
42110	40197	ATGAATTTTAAAATACATAT
42111	40198	TATGAATTTTAAAATACATA
42112	40199	TTATGAATTTTAAAATACAT
42113	40200	CTTATGAATTTTAAAATACA
42114	40201	ACTTATGAATTTTAAAATAC
42115	40202	AACTTATGAATTTTAAAATA
42116	40203	GAACTTATGAATTTTAAAAT
42117	40204	AGAACTTATGAATTTTAAAA
42118	40205	GAGAACTTATGAATTTTAAA
42119	40206	GGAGAACTTATGAATTTTAA
42120	40207	AGGAGAACTTATGAATTTTA
42121	40208	GAGGAGAACTTATGAATTTT
42122	40209	GGAGGAGAACTTATGAATTT
42123	40210	AGGAGGAGAACTTATGAATT
42124	40211	TAGGAGGAGAACTTATGAAT
42125	40212	ATAGGAGGAGAACTTATGAA
42126	40213	CATAGGAGGAGAACTTATGA
42127	40214	TCATAGGAGGAGAACTTATG
42128	40215	ATCATAGGAGGAGAACTTAT
42129	40216	CATCATAGGAGGAGAACTTA
42130	40217	ACATCATAGGAGGAGAACTT
42131	40218	AACATCATAGGAGGAGAACT
42132	40219	AAACATCATAGGAGGAGAAC
42133	40220	AAAACATCATAGGAGGAGAA
42134	40221	AAAAACATCATAGGAGGAGA
42135	40222	CAAAAACATCATAGGAGGAG
42136	40223	ACAAAAACATCATAGGAGGA
42137	40224	GACAAAAACATCATAGGAGG
42138	40225	GGACAAAAACATCATAGGAG
42139	40226	GGGACAAAAACATCATAGGA
42140	40227	TGGGACAAAAACATCATAGG
42141	40228	ATGGGACAAAAACATCATAG
42142	40229	CATGGGACAAAAACATCATA
42143	40230	ACATGGGACAAAAACATCAT
42144	40231	CACATGGGACAAAAACATCA
42145	40232	TCACATGGGACAAAAACATC
42146	40233	ATCACATGGGACAAAAACAT
42147	40234	AATCACATGGGACAAAAACA
42148	40235	AAATCACATGGGACAAAAAC
42149	40236	TAAATCACATGGGACAAAAA
42150	40237	ATAAATCACATGGGACAAAA
42151	40238	AATAAATCACATGGGACAAA
42152	40239	AAATAAATCACATGGGACAA
42153	40240	CAAATAAATCACATGGGACA
42154	40241	ACAAATAAATCACATGGGAC
42155	40242	AACAAATAAATCACATGGGA
42156	40243	TAACAAATAAATCACATGGG
42157	40244	TTAACAAATAAATCACATGG
42158	40245	TTTAACAAATAAATCACATG
42159	40246	GTTTAACAAATAAATCACAT
42160	40247	GGTTTAACAAATAAATCACA
42161	40248	CGGTTTAACAAATAAATCAC
42162	40249	ACGGTTTAACAAATAAATCA
42163	40250	GACGGTTTAACAAATAAATC
42164	40251	TGACGGTTTAACAAATAAAT
42165	40252	ATGACGGTTTAACAAATAAA
42166	40253	GATGACGGTTTAACAAATAA
42167	40254	AGATGACGGTTTAACAAATA

91244	89331	CACCCTCTAACATTCAATTT
91245	89332	TCACCCTCTAACATTCAATT
91246	89333	ATCACCCTCTAACATTCAAT
91247	89334	TATCACCCTCTAACATTCAA
91248	89335	ATATCACCCTCTAACATTCA
91249	89336	AATATCACCCTCTAACATTC
91250	89337	TAATATCACCCTCTAACATT
91251	89338	ATAATATCACCCTCTAACAT
91252	89339	TATAATATCACCCTCTAACA
91253	89340	ATATAATATCACCCTCTAAC
91254	89341	CATATAATATCACCCTCTAA
91255	89342	TCATATAATATCACCCTCTA
91256	89343	TTCATATAATATCACCCTCT
91257	89344	TTTCATATAATATCACCCTC
91258	89345	TTTTCATATAATATCACCCT
91259	89346	TTTTTCATATAATATCACCC
91260	89347	TTTTTTCATATAATATCACC
91261	89348	ATTTTTTCATATAATATCAC
91262	89349	AATTTTTTCATATAATATCA
91263	89350	GAATTTTTTCATATAATATC
91264	89351	AGAATTTTTTCATATAATAT
91265	89352	TAGAATTTTTTCATATAATA
91266	89353	CTAGAATTTTTTCATATAAT
91267	89354	CCTAGAATTTTTTCATATAA
91268	89355	ACCTAGAATTTTTTCATATA
91269	89356	AACCTAGAATTTTTTCATAT
91270	89357	TAACCTAGAATTTTTTCATA
91271	89358	ATAACCTAGAATTTTTTCAT
91272	89359	AATAACCTAGAATTTTTTCA
91273	89360	AAATAACCTAGAATTTTTTC
91274	89361	AAAATAACCTAGAATTTTTT
91275	89362	AAAAATAACCTAGAATTTTT
91276	89363	TAAAAATAACCTAGAATTTT
91277	89364	ATAAAAATAACCTAGAATTT
91278	89365	AATAAAAATAACCTAGAATT
91279	89366	GAATAAAAATAACCTAGAAT
91280	89367	TGAATAAAAATAACCTAGAA
91281	89368	ATGAATAAAAATAACCTAGA
91282	89369	TATGAATAAAAATAACCTAG
91283	89370	CTATGAATAAAAATAACCTA
91284	89371	TCTATGAATAAAAATAACCT
91285	89372	GTCTATGAATAAAAATAACC
91286	89373	TGTCTATGAATAAAAATAAC
91287	89374	TTGTCTATGAATAAAAATAA
91288	89375	CTTGTCTATGAATAAAAATA
91289	89376	ACTTGTCTATGAATAAAAAT
91290	89377	TACTTGTCTATGAATAAAAA
91291	89378	ATACTTGTCTATGAATAAAA
91292	89379	AATACTTGTCTATGAATAAA
91293	89380	AAATACTTGTCTATGAATAA
91294	89381	AAAATACTTGTCTATGAATA
91295	89382	AAAAATACTTGTCTATGAAT
91296	89383	TAAAAATACTTGTCTATGAA
91297	89384	CTAAAAATACTTGTCTATGA
91298	89385	ACTAAAAATACTTGTCTATG
91299	89386	CACTAAAAATACTTGTCTAT
91300	89387	GCACTAAAAATACTTGTCTA
91301	89388	TGCACTAAAAATACTTGTCT
91302	89389	GTGCACTAAAAATACTTGTC
91303	89390	TGTGCACTAAAAATACTTGT
91304	89391	ATGTGCACTAAAAATACTTG
91305	89392	AATGTGCACTAAAAATACTT
91306	89393	AAATGTGCACTAAAAATACT
91307	89394	TAAATGTGCACTAAAAATAC
91308	89395	TTAAATGTGCACTAAAAATA
91309	89396	TTTAAATGTGCACTAAAAAT
91310	89397	TTTTAAATGTGCACTAAAAA
91311	89398	CTTTTAAATGTGCACTAAAA
91312	89399	ACTTTTAAATGTGCACTAAA
91313	89400	AACTTTTAAATGTGCACTAA
91314	89401	AAACTTTTAAATGTGCACTA

140391	138478	GGGAGAAATGGAGCCGGGCA
140392	138479	TGGGAGAAATGGAGCCGGGC
140393	138480	TTGGGAGAAATGGAGCCGGG
140394	138481	ATTGGGAGAAATGGAGCCGG
140395	138482	AATTGGGAGAAATGGAGCCG
140396	138483	AAATTGGGAGAAATGGAGCC
140397	138484	GAAATTGGGAGAAATGGAGC
140398	138485	TGAAATTGGGAGAAATGGAG
140399	138486	TTGAAATTGGGAGAAATGGA
140400	138487	TTTGAAATTGGGAGAAATGG
140401	138488	ATTTGAAATTGGGAGAAATG
140402	138489	AATTTGAAATTGGGAGAAAT
140403	138490	GAATTTGAAATTGGGAGAAA
140404	138491	TGAATTTGAAATTGGGAGAA
140405	138492	TTGAATTTGAAATTGGGAGA
140406	138493	CTTGAATTTGAAATTGGGAG
140407	138494	CCTTGAATTTGAAATTGGGA
140408	138495	TCCTTGAATTTGAAATTGGG
140409	138496	CTCCTTGAATTTGAAATTGG
140410	138497	CCTCCTTGAATTTGAAATTG
140411	138498	TCCTCCTTGAATTTGAAATT
140412	138499	TTCCTCCTTGAATTTGAAAT
140413	138500	TTTCCTCCTTGAATTTGAAA
140414	138501	TTTTCCTCCTTGAATTTGAA
140415	138502	CTTTTCCTCCTTGAATTTGA
140416	138503	TCTTTTCCTCCTTGAATTTG
140417	138504	TTCTTTTCCTCCTTGAATTT
140418	138505	ATTCTTTTCCTCCTTGAATT
140419	138506	AATTCTTTTCCTCCTTGAAT
140420	138507	GAATTCTTTTCCTCCTTGAA
140421	138508	GGAATTCTTTTCCTCCTTGA
140422	138509	AGGAATTCTTTTCCTCCTTG
140423	138510	CAGGAATTCTTTTCCTCCTT
140424	138511	TCAGGAATTCTTTTCCTCCT
140425	138512	ATCAGGAATTCTTTTCCTCC
140426	138513	AATCAGGAATTCTTTTCCTC
140427	138514	TAATCAGGAATTCTTTTCCT
140428	138515	TTAATCAGGAATTCTTTTCC
140429	138516	CTTAATCAGGAATTCTTTTC
140430	138517	CCTTAATCAGGAATTCTTTT
140431	138518	ACCTTAATCAGGAATTCTTT
140432	138519	TACCTTAATCAGGAATTCTT
140433	138520	GTACCTTAATCAGGAATTCT
140434	138521	AGTACCTTAATCAGGAATTC
140435	138522	AAGTACCTTAATCAGGAATT
140436	138523	GAAGTACCTTAATCAGGAAT
140437	138524	AGAAGTACCTTAATCAGGAA
140438	138525	AAGAAGTACCTTAATCAGGA
140439	138526	AAAGAAGTACCTTAATCAGG
140440	138527	GAAAGAAGTACCTTAATCAG
140441	138528	TGAAAGAAGTACCTTAATCA
140442	138529	CTGAAAGAAGTACCTTAATC
140443	138530	TCTGAAAGAAGTACCTTAAT
140444	138531	ATCTGAAAGAAGTACCTTAA
140445	138532	GATCTGAAAGAAGTACCTTA
140446	138533	AGATCTGAAAGAAGTACCTT
140447	138534	AAGATCTGAAAGAAGTACCT
140448	138535	AAAGATCTGAAAGAAGTACC
140449	138536	AAAAGATCTGAAAGAAGTAC
140450	138537	CAAAAGATCTGAAAGAAGTA
140451	138538	TCAAAAGATCTGAAAGAAGT
140452	138539	CTCAAAAGATCTGAAAGAAG
140453	138540	GCTCAAAAGATCTGAAAGAA
140454	138541	AGCTCAAAAGATCTGAAAGA
140455	138542	TAGCTCAAAAGATCTGAAAG
140456	138543	CTAGCTCAAAAGATCTGAAA
140457	138544	TCTAGCTCAAAAGATCTGAA
140458	138545	TTCTAGCTCAAAAGATCTGA
140459	138546	GTTCTAGCTCAAAAGATCTG
140460	138547	TGTTCTAGCTCAAAAGATCT
140461	138548	TTGTTCTAGCTCAAAAGATC

42168	40255	AAGATGACGGTTTAACAAAT
42169	40256	AAAGATGACGGTTTAACAAA
42170	40257	CAAAGATGACGGTTTAACAA
42171	40258	CCAAAGATGACGGTTTAACA
42172	40259	GCCAAAGATGACGGTTTAAC
42173	40260	GGCCAAAGATGACGGTTTAA
42174	40261	CGGCCAAAGATGACGGTTTA
42175	40262	CCGGCCAAAGATGACGGTTT
42176	40263	CCCGGCCAAAGATGACGGTT
42177	40264	GCCCGGCCAAAGATGACGGT
42178	40265	CGCCCGGCCAAAGATGACGG
42179	40266	ACGCCCGGCCAAAGATGACG
42180	40267	CACGCCCGGCCAAAGATGAC
42181	40268	CCACGCCCGGCCAAAGATGA
42182	40269	ACCACGCCCGGCCAAAGATG
42183	40270	TACCACGCCCGGCCAAAGAT
42184	40271	CTACCACGCCCGGCCAAAGA
42185	40272	GCTACCACGCCCGGCCAAAG
42186	40273	AGCTACCACGCCCGGCCAAA
42187	40274	GAGCTACCACGCCCGGCCAA
42188	40275	TGAGCTACCACGCCCGGCCA
42189	40276	GTGAGCTACCACGCCCGGCC
42190	40277	CGTGAGCTACCACGCCCGGC
42191	40278	GCGTGAGCTACCACGCCCGG
42192	40279	GGCGTGAGCTACCACGCCCG
42193	40280	AGGCGTGAGCTACCACGCCC
42194	40281	CAGGCGTGAGCTACCACGCC
42195	40282	ACAGGCGTGAGCTACCACGC
42196	40283	TACAGGCGTGAGCTACCACG
42197	40284	TTACAGGCGTGAGCTACCAC
42198	40285	ATTACAGGCGTGAGCTACCA
42199	40286	GATTACAGGCGTGAGCTACC
42200	40287	GGATTACAGGCGTGAGCTAC
42201	40288	GGGATTACAGGCGTGAGCTA
42202	40289	TGGGATTACAGGCGTGAGCT
42203	40290	CTGGGATTACAGGCGTGAGC
42204	40291	GCTGGGATTACAGGCGTGAG
42205	40292	TGCTGGGATTACAGGCGTGA
42206	40293	GTGCTGGGATTACAGGCGTG
42207	40294	AGTGCTGGGATTACAGGCGT
42208	40295	AAGTGCTGGGATTACAGGCG
42209	40296	AAAGTGCTGGGATTACAGGC
42210	40297	CAAAGTGCTGGGATTACAGG
42211	40298	CCAAAGTGCTGGGATTACAG
42212	40299	CCCAAAGTGCTGGGATTACA
42213	40300	TCCCAAAGTGCTGGGATTAC
42214	40301	CTCCCAAAGTGCTGGGATTA
42215	40302	CCTCCCAAAGTGCTGGGATT
42216	40303	GCCTCCCAAAGTGCTGGGAT
42217	40304	AGCCTCCCAAAGTGCTGGGA
42218	40305	CAGCCTCCCAAAGTGCTGGG
42219	40306	TCAGCCTCCCAAAGTGCTGG
42220	40307	CTCAGCCTCCCAAAGTGCTG
42221	40308	CCTCAGCCTCCCAAAGTGCT
42222	40309	ACCTCAGCCTCCCAAAGTGC
42223	40310	CACCTCAGCCTCCCAAAGTG
42224	40311	CCACCTCAGCCTCCCAAAGT
42225	40312	CCCACCTCAGCCTCCCAAAG
42226	40313	ACCCACCTCAGCCTCCCAAA
42227	40314	CACCCACCTCAGCCTCCCAA
42228	40315	CCACCCACCTCAGCCTCCCA
42229	40316	TCCACCCACCTCAGCCTCCC
42230	40317	ATCCACCCACCTCAGCCTCC
42231	40318	GATCCACCCACCTCAGCCTC
42232	40319	TGATCCACCCACCTCAGCCT
42233	40320	GTGATCCACCCACCTCAGCC
42234	40321	TGTGATCCACCCACCTCAGC
42235	40322	TTGTGATCCACCCACCTCAG
42236	40323	CTTGTGATCCACCCACCTCA
42237	40324	CCTTGTGATCCACCCACCTC
42238	40325	ACCTTGTGATCCACCCACCT

91315	89402	TAAACTTTTAAATGTGCACT
91316	89403	ATAAACTTTTAAATGTGCAC
91317	89404	CATAAACTTTTAAATGTGCA
91318	89405	ACATAAACTTTTAAATGTGC
91319	89406	TACATAAACTTTTAAATGTG
91320	89407	TTACATAAACTTTTAAATGT
91321	89408	TTTACATAAACTTTTAAATG
91322	89409	ATTTACATAAACTTTTAAAT
91323	89410	AATTTACATAAACTTTTAAA
91324	89411	AAATTTACATAAACTTTTAA
91325	89412	AAAATTTACATAAACTTTTA
91326	89413	CAAAATTTACATAAACTTTT
91327	89414	TCAAAATTTACATAAACTTT
91328	89415	ATCAAAATTTACATAAACTT
91329	89416	CATCAAAATTTACATAAACT
91330	89417	ACATCAAAATTTACATAAAC
91331	89418	AACATCAAAATTTACATAAA
91332	89419	CAACATCAAAATTTACATAA
91333	89420	ACAACATCAAAATTTACATA
91334	89421	AACAACATCAAAATTTACAT
91335	89422	AAACAACATCAAAATTTACA
91336	89423	TAAACAACATCAAAATTTAC
91337	89424	TTAAACAACATCAAAATTTA
91338	89425	ATTAAACAACATCAAAATTT
91339	89426	TATTAAACAACATCAAAATT
91340	89427	GTATTAAACAACATCAAAAT
91341	89428	AGTATTAAACAACATCAAAA
91342	89429	TAGTATTAAACAACATCAAA
91343	89430	GTAGTATTAAACAACATCAA
91344	89431	AGTAGTATTAAACAACATCA
91345	89432	TAGTAGTATTAAACAACATC
91346	89433	TTAGTAGTATTAAACAACAT
91347	89434	ATTAGTAGTATTAAACAACA
91348	89435	AATTAGTAGTATTAAACAAC
91349	89436	AAATTAGTAGTATTAAACAA
91350	89437	TAAATTAGTAGTATTAAACA
91351	89438	TTAAATTAGTAGTATTAAAC
91352	89439	ATTAAATTAGTAGTATTAAA
91353	89440	TATTAAATTAGTAGTATTAA
91354	89441	ATATTAAATTAGTAGTATTA
91355	89442	TATATTAAATTAGTAGTATT
91356	89443	CTATATTAAATTAGTAGTAT
91357	89444	ACTATATTAAATTAGTAGTA
91358	89445	CACTATATTAAATTAGTAGT
91359	89446	ACACTATATTAAATTAGTAG
91360	89447	GACACTATATTAAATTAGTA
91361	89448	AGACACTATATTAAATTAGT
91362	89449	CAGACACTATATTAAATTAG
91363	89450	ACAGACACTATATTAAATTA
91364	89451	CACAGACACTATATTAAATT
91365	89452	ACACAGACACTATATTAAAT
91366	89453	AACACAGACACTATATTAAA
91367	89454	TAACACAGACACTATATTAA
91368	89455	GTAACACAGACACTATATTA
91369	89456	TGTAACACAGACACTATATT
91370	89457	TTGTAACACAGACACTATAT
91371	89458	TTTGTAACACAGACACTATA
91372	89459	CTTTGTAACACAGACACTAT
91373	89460	CCTTTGTAACACAGACACTA
91374	89461	ACCTTTGTAACACAGACACT
91375	89462	AACCTTTGTAACACAGACAC
91376	89463	TAACCTTTGTAACACAGACA
91377	89464	TTAACCTTTGTAACACAGAC
91378	89465	GTTAACCTTTGTAACACAGA
91379	89466	TGTTAACCTTTGTAACACAG
91380	89467	ATGTTAACCTTTGTAACACA
91381	89468	AATGTTAACCTTTGTAACAC
91382	89469	GAATGTTAACCTTTGTAACA
91383	89470	GGAATGTTAACCTTTGTAAC
91384	89471	AGGAATGTTAACCTTTGTAA
91385	89472	CAGGAATGTTAACCTTTGTA

140462	138549	TTTGTTCTAGCTCAAAAGAT
140463	138550	TTTTGTTCTAGCTCAAAAGA
140464	138551	TTTTTGTTCTAGCTCAAAAG
140465	138552	TTTTTTGTTCTAGCTCAAAA
140466	138553	TTTTTTTGTTCTAGCTCAAA
140467	138554	GTTTTTTTGTTCTAGCTCAA
140468	138555	TGTTTTTTTGTTCTAGCTCA
140469	138556	TTGTTTTTTTGTTCTAGCTC
140470	138557	TTTGTTTTTTTGTTCTAGCT
140471	138558	CTTTGTTTTTTTGTTCTAGC
140472	138559	CCTTTGTTTTTTTGTTCTAG
140473	138560	CCCTTTGTTTTTTTGTTCTA
140474	138561	TCCCTTTGTTTTTTTGTTCT
140475	138562	TTCCCTTTGTTTTTTTGTTC
140476	138563	TTTCCCTTTGTTTTTTTGTT
140477	138564	ATTTCCCTTTGTTTTTTTGT
140478	138565	TATTTCCCTTTGTTTTTTTG
140479	138566	ATATTTCCCTTTGTTTTTTT
140480	138567	AATATTTCCCTTTGTTTTTT
140481	138568	AAATATTTCCCTTTGTTTTT
140482	138569	GAAATATTTCCCTTTGTTTT
140483	138570	AGAAATATTTCCCTTTGTTT
140484	138571	TAGAAATATTTCCCTTTGTT
140485	138572	TTAGAAATATTTCCCTTTGT
140486	138573	ATTAGAAATATTTCCCTTTG
140487	138574	AATTAGAAATATTTCCCTTT
140488	138575	TAATTAGAAATATTTCCCTT
140489	138576	TTAATTAGAAATATTTCCCT
140490	138577	GTTAATTAGAAATATTTCCC
140491	138578	AGTTAATTAGAAATATTTCC
140492	138579	GAGTTAATTAGAAATATTTC
140493	138580	AGAGTTAATTAGAAATATTT
140494	138581	AAGAGTTAATTAGAAATATT
140495	138582	AAAGAGTTAATTAGAAATAT
140496	138583	AAAAGAGTTAATTAGAAATA
140497	138584	AAAAAGAGTTAATTAGAAAT
140498	138585	TAAAAAGAGTTAATTAGAAA
140499	138586	TTAAAAAGAGTTAATTAGAA
140500	138587	TTTAAAAAGAGTTAATTAGA
140501	138588	ATTTAAAAAGAGTTAATTAG
140502	138589	AATTTAAAAAGAGTTAATTA
140503	138590	AAATTTAAAAAGAGTTAATT
140504	138591	AAAATTTAAAAAGAGTTAAT
140505	138592	CAAAATTTAAAAAGAGTTAA
140506	138593	ACAAAATTTAAAAAGAGTTA
140507	138594	AACAAAATTTAAAAAGAGTT
140508	138595	AAACAAAATTTAAAAAGAGT
140509	138596	TAAACAAAATTTAAAAAGAG
140510	138597	GTAAACAAAATTTAAAAAGA
140511	138598	TGTAAACAAAATTTAAAAAG
140512	138599	TTGTAAACAAAATTTAAAAA
140513	138600	GTTGTAAACAAAATTTAAAA
140514	138601	CGTTGTAAACAAAATTTAAA
140515	138602	ACGTTGTAAACAAAATTTAA
140516	138603	TACGTTGTAAACAAAATTTA
140517	138604	ATACGTTGTAAACAAAATTT
140518	138605	CATACGTTGTAAACAAAATT
140519	138606	TCATACGTTGTAAACAAAAT
140520	138607	ATCATACGTTGTAAACAAAA
140521	138608	TATCATACGTTGTAAACAAA
140522	138609	GTATCATACGTTGTAAACAA
140523	138610	TGTATCATACGTTGTAAACA
140524	138611	ATGTATCATACGTTGTAAAC
140525	138612	TATGTATCATACGTTGTAAA
140526	138613	ATATGTATCATACGTTGTAA
140527	138614	AATATGTATCATACGTTGTA
140528	138615	AAATATGTATCATACGTTGT
140529	138616	AAAATATGTATCATACGTTG
140530	138617	TAAAATATGTATCATACGTT
140531	138618	GTAAAATATGTATCATACGT
140532	138619	TGTAAAATATGTATCATACG

42239	40326	AACCTTGTGATCCACCCACC
42240	40327	TAACCTTGTGATCCACCCAC
42241	40328	TTAACCTTGTGATCCACCCA
42242	40329	CTTAACCTTGTGATCCACCC
42243	40330	TCTTAACCTTGTGATCCACC
42244	40331	CTCTTAACCTTGTGATCCAC
42245	40332	TCTCTTAACCTTGTGATCCA
42246	40333	ATCTCTTAACCTTGTGATCC
42247	40334	GATCTCTTAACCTTGTGATC
42248	40335	TGATCTCTTAACCTTGTGAT
42249	40336	TTGATCTCTTAACCTTGTGA
42250	40337	CTTGATCTCTTAACCTTGTG
42251	40338	TCTTGATCTCTTAACCTTGT
42252	40339	GTCTTGATCTCTTAACCTTG
42253	40340	GGTCTTGATCTCTTAACCTT
42254	40341	TGGTCTTGATCTCTTAACCT
42255	40342	ATGGTCTTGATCTCTTAACC
42256	40343	GATGGTCTTGATCTCTTAAC
42257	40344	GGATGGTCTTGATCTCTTAA
42258	40345	AGGATGGTCTTGATCTCTTA
42259	40346	CAGGATGGTCTTGATCTCTT
42260	40347	CCAGGATGGTCTTGATCTCT
42261	40348	GCCAGGATGGTCTTGATCTC
42262	40349	GGCCAGGATGGTCTTGATCT
42263	40350	TGGCCAGGATGGTCTTGATC
42264	40351	TTGGCCAGGATGGTCTTGAT
42265	40352	GTTGGCCAGGATGGTCTTGA
42266	40353	TGTTGGCCAGGATGGTCTTG
42267	40354	ATGTTGGCCAGGATGGTCTT
42268	40355	CATGTTGGCCAGGATGGTCT
42269	40356	CCATGTTGGCCAGGATGGTC
42270	40357	ACCATGTTGGCCAGGATGGT
42271	40358	CACCATGTTGGCCAGGATGG
42272	40359	TCACCATGTTGGCCAGGATG
42273	40360	TTCACCATGTTGGCCAGGAT
42274	40361	TTTCACCATGTTGGCCAGGA
42275	40362	GTTTCACCATGTTGGCCAGG
42276	40363	GGTTTCACCATGTTGGCCAG
42277	40364	GGGTTTCACCATGTTGGCCA
42278	40365	GGGGTTTCACCATGTTGGCC
42279	40366	CGGGGTTTCACCATGTTGGC
42280	40367	ACGGGGTTTCACCATGTTGG
42281	40368	GACGGGGTTTCACCATGTTG
42282	40369	AGACGGGGTTTCACCATGTT
42283	40370	GAGACGGGGTTTCACCATGT
42284	40371	AGAGACGGGGTTTCACCATG
42285	40372	TAGAGACGGGGTTTCACCAT
42286	40373	GTAGAGACGGGGTTTCACCA
42287	40374	AGTAGAGACGGGGTTTCACC
42288	40375	TAGTAGAGACGGGGTTTCAC
42289	40376	TTAGTAGAGACGGGGTTTCA
42290	40377	CTTAGTAGAGACGGGGTTTC
42291	40378	TCTTAGTAGAGACGGGGTTT
42292	40379	TTCTTAGTAGAGACGGGGTT
42293	40380	ATTCTTAGTAGAGACGGGGT
42294	40381	TATTCTTAGTAGAGACGGGG
42295	40382	GTATTCTTAGTAGAGACGGG
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42297	40384	TTGTATTCTTAGTAGAGACG
42298	40385	TTTGTATTCTTAGTAGAGAC
42299	40386	TTTTGTATTCTTAGTAGAGA
42300	40387	TTTTTGTATTCTTAGTAGAG
42301	40388	ATTTTTGTATTCTTAGTAGA
42302	40389	AATTTTTGTATTCTTAGTAG
42303	40390	TAATTTTTGTATTCTTAGTA
42304	40391	ATAATTTTTGTATTCTTAGT
42305	40392	GATAATTTTTGTATTCTTAG
42306	40393	AGATAATTTTTGTATTCTTA
42307	40394	CAGATAATTTTTGTATTCTT
42308	40395	CCAGATAATTTTTGTATTCT
42309	40396	CCCAGATAATTTTTGTATTC

91386	89473	CCAGGAATGTTAACCTTTGT
91387	89474	CCCAGGAATGTTAACCTTTG
91388	89475	ACCCAGGAATGTTAACCTTT
91389	89476	CACCCAGGAATGTTAACCTT
91390	89477	ACACCCAGGAATGTTAACCT
91391	89478	GACACCCAGGAATGTTAACC
91392	89479	TGACACCCAGGAATGTTAAC
91393	89480	TTGACACCCAGGAATGTTAA
91394	89481	TTTGACACCCAGGAATGTTA
91395	89482	ATTTGACACCCAGGAATGTT
91396	89483	TATTTGACACCCAGGAATGT
91397	89484	GTATTTGACACCCAGGAATG
91398	89485	GGTATTTGACACCCAGGAAT
91399	89486	AGGTATTTGACACCCAGGAA
91400	89487	TAGGTATTTGACACCCAGGA
91401	89488	GTAGGTATTTGACACCCAGG
91402	89489	TGTAGGTATTTGACACCCAG
91403	89490	ATGTAGGTATTTGACACCCA
91404	89491	TATGTAGGTATTTGACACCC
91405	89492	TTATGTAGGTATTTGACACC
91406	89493	TTTATGTAGGTATTTGACAC
91407	89494	ATTTATGTAGGTATTTGACA
91408	89495	TATTTATGTAGGTATTTGAC
91409	89496	TTATTTATGTAGGTATTTGA
91410	89497	TTTATTTATGTAGGTATTTG
91411	89498	TTTTATTTATGTAGGTATTT
91412	89499	ATTTTATTTATGTAGGTATT
91413	89500	AATTTTATTTATGTAGGTAT
91414	89501	TAATTTTATTTATGTAGGTA
91415	89502	ATAATTTTATTTATGTAGGT
91416	89503	AATAATTTTATTTATGTAGG
91417	89504	CAATAATTTTATTTATGTAG
91418	89505	CCAATAATTTTATTTATGTA
91419	89506	ACCAATAATTTTATTTATGT
91420	89507	CACCAATAATTTTATTTATG
91421	89508	ACACCAATAATTTTATTTAT
91422	89509	AACACCAATAATTTTATTTA
91423	89510	AAACACCAATAATTTTATTT
91424	89511	GAAACACCAATAATTTTATT
91425	89512	TGAAACACCAATAATTTTAT
91426	89513	ATGAAACACCAATAATTTTA
91427	89514	TATGAAACACCAATAATTTT
91428	89515	ATATGAAACACCAATAATTT
91429	89516	CATATGAAACACCAATAATT
91430	89517	TCATATGAAACACCAATAAT
91431	89518	GTCATATGAAACACCAATAA
91432	89519	TGTCATATGAAACACCAATA
91433	89520	ATGTCATATGAAACACCAAT
91434	89521	GATGTCATATGAAACACCAA
91435	89522	AGATGTCATATGAAACACCA
91436	89523	CAGATGTCATATGAAACACC
91437	89524	GCAGATGTCATATGAAACAC
91438	89525	TGCAGATGTCATATGAAACA
91439	89526	TTGCAGATGTCATATGAAAC
91440	89527	TTTGCAGATGTCATATGAAA
91441	89528	CTTTGCAGATGTCATATGAA
91442	89529	CCTTTGCAGATGTCATATGA
91443	89530	TCCTTTGCAGATGTCATATG
91444	89531	TTCCTTTGCAGATGTCATAT
91445	89532	TTTCCTTTGCAGATGTCATA
91446	89533	TTTTCCTTTGCAGATGTCAT
91447	89534	TTTTTCCTTTGCAGATGTCA
91448	89535	TTTTTTCCTTTGCAGATGTC
91449	89536	TTTTTTTCCTTTGCAGATGT
91450	89537	CTTTTTTTCCTTTGCAGATG
91451	89538	GCTTTTTTTCCTTTGCAGAT
91452	89539	GGCTTTTTTTCCTTTGCAGA
91453	89540	AGGCTTTTTTTCCTTTGCAG
91454	89541	GAGGCTTTTTTTCCTTTGCA
91455	89542	AGAGGCTTTTTTTCCTTTGC
91456	89543	CAGAGGCTTTTTTTCCTTTG

140533	138620	GTGTAAAATATGTATCATAC
140534	138621	TGTGTAAAATATGTATCATA
140535	138622	ATGTGTAAAATATGTATCAT
140536	138623	GATGTGTAAAATATGTATCA
140537	138624	GGATGTGTAAAATATGTATC
140538	138625	AGGATGTGTAAAATATGTAT
140539	138626	AAGGATGTGTAAAATATGTA
140540	138627	AAAGGATGTGTAAAATATGT
140541	138628	CAAAGGATGTGTAAAATATG
140542	138629	ACAAAGGATGTGTAAAATAT
140543	138630	CACAAAGGATGTGTAAAATA
140544	138631	CCACAAAGGATGTGTAAAAT
140545	138632	ACCACAAAGGATGTGTAAAA
140546	138633	AACCACAAAGGATGTGTAAA
140547	138634	AAACCACAAAGGATGTGTAA
140548	138635	AAAACCACAAAGGATGTGTA
140549	138636	AAAAACCACAAAGGATGTGT
140550	138637	CAAAAACCACAAAGGATGTG
140551	138638	ACAAAAACCACAAAGGATGT
140552	138639	AACAAAAACCACAAAGGATG
140553	138640	GAACAAAAACCACAAAGGAT
140554	138641	CGAACAAAAACCACAAAGGA
140555	138642	ACGAACAAAAACCACAAAGG
140556	138643	GACGAACAAAAACCACAAAG
140557	138644	AGACGAACAAAAACCACAAA
140558	138645	AAGACGAACAAAAACCACAA
140559	138646	CAAGACGAACAAAAACCACA
140560	138647	ACAAGACGAACAAAAACCAC
140561	138648	AACAAGACGAACAAAAACCA
140562	138649	AAACAAGACGAACAAAAACC
140563	138650	AAAACAAGACGAACAAAAAC
140564	138651	AAAAACAAGACGAACAAAAA
140565	138652	TAAAAACAAGACGAACAAAA
140566	138653	TTAAAAACAAGACGAACAAA
140567	138654	ATTAAAAACAAGACGAACAA
140568	138655	GATTAAAAACAAGACGAACA
140569	138656	TGATTAAAAACAAGACGAAC
140570	138657	TTGATTAAAAACAAGACGAA
140571	138658	ATTGATTAAAAACAAGACGA
140572	138659	CATTGATTAAAAACAAGACG
140573	138660	GCATTGATTAAAAACAAGAC
140574	138661	GGCATTGATTAAAAACAAGA
140575	138662	AGGCATTGATTAAAAACAAG
140576	138663	AAGGCATTGATTAAAAACAA
140577	138664	CAAGGCATTGATTAAAAACA
140578	138665	GCAAGGCATTGATTAAAAAC
140579	138666	TGCAAGGCATTGATTAAAAA
140580	138667	TTGCAAGGCATTGATTAAAA
140581	138668	CTTGCAAGGCATTGATTAAA
140582	138669	ACTTGCAAGGCATTGATTAA
140583	138670	AACTTGCAAGGCATTGATTA
140584	138671	AAACTTGCAAGGCATTGATT
140585	138672	TAAACTTGCAAGGCATTGAT
140586	138673	GTAAACTTGCAAGGCATTGA
140587	138674	GGTAAACTTGCAAGGCATTG
140588	138675	CGGTAAACTTGCAAGGCATT
140589	138676	CCGGTAAACTTGCAAGGCAT
140590	138677	ACCGGTAAACTTGCAAGGCA
140591	138678	TACCGGTAAACTTGCAAGGC
140592	138679	ATACCGGTAAACTTGCAAGG
140593	138680	AATACCGGTAAACTTGCAAG
140594	138681	AAATACCGGTAAACTTGCAA
140595	138682	TAAATACCGGTAAACTTGCA
140596	138683	CTAAATACCGGTAAACTTGC
140597	138684	CCTAAATACCGGTAAACTTG
140598	138685	ACCTAAATACCGGTAAACTT
140599	138686	TACCTAAATACCGGTAAACT
140600	138687	CTACCTAAATACCGGTAAAC
140601	138688	CCTACCTAAATACCGGTAAA
140602	138689	CCCTACCTAAATACCGGTAA
140603	138690	TCCCTACCTAAATACCGGTA

42310	40397	GCCCAGATAATTTTTGTATT
42311	40398	TGCCCAGATAATTTTTGTAT
42312	40399	ATGCCCAGATAATTTTTGTA
42313	40400	CATGCCCAGATAATTTTTGT
42314	40401	CCATGCCCAGATAATTTTTG
42315	40402	ACCATGCCCAGATAATTTTT
42316	40403	CACCATGCCCAGATAATTTT
42317	40404	TCACCATGCCCAGATAATTT
42318	40405	GTCACCATGCCCAGATAATT
42319	40406	CGTCACCATGCCCAGATAAT
42320	40407	GCGTCACCATGCCCAGATAA
42321	40408	CGCGTCACCATGCCCAGATA
42322	40409	ACGCGTCACCATGCCCAGAT
42323	40410	TACGCGTCACCATGCCCAGA
42324	40411	GTACGCGTCACCATGCCCAG
42325	40412	GGTACGCGTCACCATGCCCA
42326	40413	AGGTACGCGTCACCATGCCC
42327	40414	CAGGTACGCGTCACCATGCC
42328	40415	ACAGGTACGCGTCACCATGC
42329	40416	TACAGGTACGCGTCACCATG
42330	40417	CTACAGGTACGCGTCACCAT
42331	40418	ACTACAGGTACGCGTCACCA
42332	40419	GACTACAGGTACGCGTCACC
42333	40420	GGACTACAGGTACGCGTCAC
42334	40421	AGGACTACAGGTACGCGTCA
42335	40422	TAGGACTACAGGTACGCGTC
42336	40423	CTAGGACTACAGGTACGCGT
42337	40424	GCTAGGACTACAGGTACGCG
42338	40425	AGCTAGGACTACAGGTACGC
42339	40426	TAGCTAGGACTACAGGTACG
42340	40427	GTAGCTAGGACTACAGGTAC
42341	40428	GGTAGCTAGGACTACAGGTA
42342	40429	AGGTAGCTAGGACTACAGGT
42343	40430	CAGGTAGCTAGGACTACAGG
42344	40431	CCAGGTAGCTAGGACTACAG
42345	40432	CCCAGGTAGCTAGGACTACA
42346	40433	TCCCAGGTAGCTAGGACTAC
42347	40434	CTCCCAGGTAGCTAGGACTA
42348	40435	CCTCCCAGGTAGCTAGGACT
42349	40436	GCCTCCCAGGTAGCTAGGAC
42350	40437	CGCCTCCCAGGTAGCTAGGA
42351	40438	CCGCCTCCCAGGTAGCTAGG
42352	40439	TCCGCCTCCCAGGTAGCTAG
42353	40440	CTCCGCCTCCCAGGTAGCTA
42354	40441	CCTCCGCCTCCCAGGTAGCT
42355	40442	ACCTCCGCCTCCCAGGTAGC
42356	40443	AACCTCCGCCTCCCAGGTAG
42357	40444	CAACCTCCGCCTCCCAGGTA
42358	40445	GCAACCTCCGCCTCCCAGGT
42359	40446	TGCAACCTCCGCCTCCCAGG
42360	40447	CTGCAACCTCCGCCTCCCAG
42361	40448	ACTGCAACCTCCGCCTCCCA
42362	40449	CACTGCAACCTCCGCCTCCC
42363	40450	TCACTGCAACCTCCGCCTCC
42364	40451	CTCACTGCAACCTCCGCCTC
42365	40452	GCTCACTGCAACCTCCGCCT
42366	40453	GGCTCACTGCAACCTCCGCC
42367	40454	TGGCTCACTGCAACCTCCGC
42368	40455	TTGGCTCACTGCAACCTCCG
42369	40456	CTTGGCTCACTGCAACCTCC
42370	40457	TCTTGGCTCACTGCAACCTC
42371	40458	ATCTTGGCTCACTGCAACCT
42372	40459	GATCTTGGCTCACTGCAACC
42373	40460	CGATCTTGGCTCACTGCAAC
42374	40461	ACGATCTTGGCTCACTGCAA
42375	40462	CACGATCTTGGCTCACTGCA
42376	40463	GCACGATCTTGGCTCACTGC
42377	40464	GGCACGATCTTGGCTCACTG
42378	40465	TGGCACGATCTTGGCTCACT
42379	40466	GTGGCACGATCTTGGCTCAC
42380	40467	AGTGGCACGATCTTGGCTCA

91457	89544	ACAGAGGCTTTTTTTCCTTT
91458	89545	AACAGAGGCTTTTTTTCCTT
91459	89546	AAACAGAGGCTTTTTTTCCT
91460	89547	TAAACAGAGGCTTTTTTTCC
91461	89548	TTAAACAGAGGCTTTTTTTC
91462	89549	TTTAAACAGAGGCTTTTTTT
91463	89550	ATTTAAACAGAGGCTTTTTT
91464	89551	CATTTAAACAGAGGCTTTTT
91465	89552	TCATTTAAACAGAGGCTTTT
91466	89553	TTCATTTAAACAGAGGCTTT
91467	89554	TTTCATTTAAACAGAGGCTT
91468	89555	CTTTCATTTAAACAGAGGCT
91469	89556	GCTTTCATTTAAACAGAGGC
91470	89557	TGCTTTCATTTAAACAGAGG
91471	89558	ATGCTTTCATTTAAACAGAG
91472	89559	AATGCTTTCATTTAAACAGA
91473	89560	TAATGCTTTCATTTAAACAG
91474	89561	ATAATGCTTTCATTTAAACA
91475	89562	AATAATGCTTTCATTTAAAC
91476	89563	AAATAATGCTTTCATTTAAA
91477	89564	AAAATAATGCTTTCATTTAA
91478	89565	GAAAATAATGCTTTCATTTA
91479	89566	GGAAAATAATGCTTTCATTT
91480	89567	TGGAAAATAATGCTTTCATT
91481	89568	TTGGAAAATAATGCTTTCAT
91482	89569	TTTGGAAAATAATGCTTTCA
91483	89570	TTTTGGAAAATAATGCTTTC
91484	89571	TTTTTGGAAAATAATGCTTT
91485	89572	GTTTTTGGAAAATAATGCTT
91486	89573	TGTTTTTGGAAAATAATGCT
91487	89574	ATGTTTTTGGAAAATAATGC
91488	89575	TATGTTTTTGGAAAATAATG
91489	89576	CTATGTTTTTGGAAAATAAT
91490	89577	CCTATGTTTTTGGAAAATAA
91491	89578	TCCTATGTTTTTGGAAAATA
91492	89579	TTCCTATGTTTTTGGAAAAT
91493	89580	TTTCCTATGTTTTTGGAAAA
91494	89581	ATTTCCTATGTTTTTGGAAA
91495	89582	GATTTCCTATGTTTTTGGAA
91496	89583	TGATTTCCTATGTTTTTGGA
91497	89584	TTGATTTCCTATGTTTTTGG
91498	89585	TTTGATTTCCTATGTTTTTG
91499	89586	TTTTGATTTCCTATGTTTTT
91500	89587	ATTTTGATTTCCTATGTTTT
91501	89588	AATTTTGATTTCCTATGTTT
91502	89589	TAATTTTGATTTCCTATGTT
91503	89590	ATAATTTTGATTTCCTATGT
91504	89591	AATAATTTTGATTTCCTATG
91505	89592	CAATAATTTTGATTTCCTAT
91506	89593	ACAATAATTTTGATTTCCTA
91507	89594	AACAATAATTTTGATTTCCT
91508	89595	GAACAATAATTTTGATTTCC
91509	89596	TGAACAATAATTTTGATTTC
91510	89597	CTGAACAATAATTTTGATTT
91511	89598	ACTGAACAATAATTTTGATT
91512	89599	CACTGAACAATAATTTTGAT
91513	89600	ACACTGAACAATAATTTTGA
91514	89601	AACACTGAACAATAATTTTG
91515	89602	AAACACTGAACAATAATTTT
91516	89603	AAAACACTGAACAATAATTT
91517	89604	GAAAACACTGAACAATAATT
91518	89605	AGAAAACACTGAACAATAAT
91519	89606	AAGAAAACACTGAACAATAA
91520	89607	CAAGAAAACACTGAACAATA
91521	89608	ACAAGAAAACACTGAACAAT
91522	89609	AACAAGAAAACACTGAACAA
91523	89610	AAACAAGAAAACACTGAACA
91524	89611	AAAACAAGAAAACACTGAAC
91525	89612	CAAAACAAGAAAACACTGAA
91526	89613	GCAAAACAAGAAAACACTGA
91527	89614	AGCAAAACAAGAAAACACTG

140604	138691	TTCCCTACCTAAATACCGGT
140605	138692	TTTCCCTACCTAAATACCGG
140606	138693	CTTTCCCTACCTAAATACCG
140607	138694	CCTTTCCCTACCTAAATACC
140608	138695	TCCTTTCCCTACCTAAATAC
140609	138696	ATCCTTTCCCTACCTAAATA
140610	138697	AATCCTTTCCCTACCTAAAT
140611	138698	AAATCCTTTCCCTACCTAAA
140612	138699	AAAATCCTTTCCCTACCTAA
140613	138700	CAAAATCCTTTCCCTACCTA
140614	138701	ACAAAATCCTTTCCCTACCT
140615	138702	AACAAAATCCTTTCCCTACC
140616	138703	AAACAAAATCCTTTCCCTAC
140617	138704	AAAACAAAATCCTTTCCCTA
140618	138705	AAAAACAAAATCCTTTCCCT
140619	138706	CAAAAACAAAATCCTTTCCC
140620	138707	ACAAAAACAAAATCCTTTCC
140621	138708	AACAAAAACAAAATCCTTTC
140622	138709	AAACAAAAACAAAATCCTTT
140623	138710	AAAACAAAAACAAAATCCTT
140624	138711	AAAAACAAAAACAAAATCCT
140625	138712	AAAAAACAAAAACAAAATCC
140626	138713	AAAAAAACAAAAACAAAATC
140627	138714	TAAAAAAACAAAAACAAAAT
140628	138715	TTAAAAAAACAAAAACAAAA
140629	138716	TTTAAAAAAACAAAAACAAA
140630	138717	GTTTAAAAAAACAAAAACAA
140631	138718	TGTTTAAAAAAACAAAAACA
140632	138719	TTGTTTAAAAAAACAAAAAC
140633	138720	TTTGTTTAAAAAAACAAAAA
140634	138721	CTTTGTTTAAAAAAACAAAA
140635	138722	GCTTTGTTTAAAAAAACAAA
140636	138723	GGCTTTGTTTAAAAAAACAA
140637	138724	AGGCTTTGTTTAAAAAAACA
140638	138725	TAGGCTTTGTTTAAAAAAAC
140639	138726	ATAGGCTTTGTTTAAAAAAA
140640	138727	CATAGGCTTTGTTTAAAAAA
140641	138728	ACATAGGCTTTGTTTAAAAA
140642	138729	TACATAGGCTTTGTTTAAAA
140643	138730	GTACATAGGCTTTGTTTAAA
140644	138731	TGTACATAGGCTTTGTTTAA
140645	138732	ATGTACATAGGCTTTGTTTA
140646	138733	AATGTACATAGGCTTTGTTT
140647	138734	GAATGTACATAGGCTTTGTT
140648	138735	TGAATGTACATAGGCTTTGT
140649	138736	GTGAATGTACATAGGCTTTG
140650	138737	AGTGAATGTACATAGGCTTT
140651	138738	GAGTGAATGTACATAGGCTT
140652	138739	TGAGTGAATGTACATAGGCT
140653	138740	CTGAGTGAATGTACATAGGC
140654	138741	GCTGAGTGAATGTACATAGG
140655	138742	AGCTGAGTGAATGTACATAG
140656	138743	AAGCTGAGTGAATGTACATA
140657	138744	CAAGCTGAGTGAATGTACAT
140658	138745	CCAAGCTGAGTGAATGTACA
140659	138746	CCCAAGCTGAGTGAATGTAC
140660	138747	ACCCAAGCTGAGTGAATGTA
140661	138748	TACCCAAGCTGAGTGAATGT
140662	138749	ATACCCAAGCTGAGTGAATG
140663	138750	AATACCCAAGCTGAGTGAAT
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140665	138752	CAAATACCCAAGCTGAGTGA
140666	138753	ACAAATACCCAAGCTGAGTG
140667	138754	CACAAATACCCAAGCTGAGT
140668	138755	GCACAAATACCCAAGCTGAG
140669	138756	AGCACAAATACCCAAGCTGA
140670	138757	TAGCACAAATACCCAAGCTG
140671	138758	ATAGCACAAATACCCAAGCT
140672	138759	CATAGCACAAATACCCAAGC
140673	138760	GCATAGCACAAATACCCAAG
140674	138761	TGCATAGCACAAATACCCAA

42381	40468	CAGTGGCACGATCTTGGCTC
42382	40469	GCAGTGGCACGATCTTGGCT
42383	40470	TGCAGTGGCACGATCTTGGC
42384	40471	GTGCAGTGGCACGATCTTGG
42385	40472	AGTGCAGTGGCACGATCTTG
42386	40473	GAGTGCAGTGGCACGATCTT
42387	40474	GGAGTGCAGTGGCACGATCT
42388	40475	TGGAGTGCAGTGGCACGATC
42389	40476	CTGGAGTGCAGTGGCACGAT
42390	40477	GCTGGAGTGCAGTGGCACGA
42391	40478	GGCTGGAGTGCAGTGGCACG
42392	40479	AGGCTGGAGTGCAGTGGCAC
42393	40480	CAGGCTGGAGTGCAGTGGCA
42394	40481	CCAGGCTGGAGTGCAGTGGC
42395	40482	GCCAGGCTGGAGTGCAGTGG
42396	40483	CGCCAGGCTGGAGTGCAGTG
42397	40484	TCGCCAGGCTGGAGTGCAGT
42398	40485	GTCGCCAGGCTGGAGTGCAG
42399	40486	TGTCGCCAGGCTGGAGTGCA
42400	40487	CTGTCGCCAGGCTGGAGTGC
42401	40488	TCTGTCGCCAGGCTGGAGTG
42402	40489	CTCTGTCGCCAGGCTGGAGT
42403	40490	ACTCTGTCGCCAGGCTGGAG
42404	40491	CACTCTGTCGCCAGGCTGGA
42405	40492	TCACTCTGTCGCCAGGCTGG
42406	40493	CTCACTCTGTCGCCAGGCTG
42407	40494	TCTCACTCTGTCGCCAGGCT
42408	40495	GTCTCACTCTGTCGCCAGGC
42409	40496	AGTCTCACTCTGTCGCCAGG
42410	40497	GAGTCTCACTCTGTCGCCAG
42411	40498	AGAGTCTCACTCTGTCGCCA
42412	40499	CAGAGTCTCACTCTGTCGCC
42413	40500	ACAGAGTCTCACTCTGTCGC
42414	40501	GACAGAGTCTCACTCTGTCG
42415	40502	AGACAGAGTCTCACTCTGTC
42416	40503	GAGACAGAGTCTCACTCTGT
42417	40504	TGAGACAGAGTCTCACTCTG
42418	40505	CTGAGACAGAGTCTCACTCT
42419	40506	TCTGAGACAGAGTCTCACTC
42420	40507	TTCTGAGACAGAGTCTCACT
42421	40508	TTTCTGAGACAGAGTCTCAC
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42423	40510	TTTTTCTGAGACAGAGTCTC
42424	40511	TTTTTTCTGAGACAGAGTCT
42425	40512	TTTTTTTCTGAGACAGAGTC
42426	40513	TTTTTTTTCTGAGACAGAGT
42427	40514	TTTTTTTTTCTGAGACAGAG
42428	40515	TTTTTTTTTTCTGAGACAGA
42429	40516	TTTTTTTTTTTCTGAGACAG
42430	40517	TTTTTTTTTTTTCTGAGACA
42431	40518	TTTTTTTTTTTTTCTGAGAC
42432	40519	GTTTTTTTTTTTTTCTGAGA
42433	40520	TGTTTTTTTTTTTTTCTGAG
42434	40521	TTGTTTTTTTTTTTTTCTGA
42435	40522	TTTGTTTTTTTTTTTTTCTG
42436	40523	TTTTGTTTTTTTTTTTTCT
42437	40524	TTTTTGTTTTTTTTTTTTC
42438	40525	TTTTTTGTTTTTTTTTTTT
42439	40526	GTTTTTTGTTTTTTTTTTT
42440	40527	AGTTTTTTGTTTTTTTTTT
42441	40528	CAGTTTTTTGTTTTTTTTT
42442	40529	ACAGTTTTTTGTTTTTTTT
42443	40530	GACAGTTTTTTGTTTTTTT
42444	40531	TGACAGTTTTTTGTTTTTT
42445	40532	ATGACAGTTTTTTGTTTTT
42446	40533	AATGACAGTTTTTTGTTTT
42447	40534	AAATGACAGTTTTTTGTTT
42448	40535	AAAATGACAGTTTTTTGTT
42449	40536	AAAAATGACAGTTTTTTGT
42450	40537	AAAAAATGACAGTTTTTTG
42451	40538	TAAAAAATGACAGTTTTTTG

91528	89615	AAGCAAAACAAGAAAACACT
91529	89616	AAAGCAAAACAAGAAAACAC
91530	89617	AAAAGCAAAACAAGAAAACA
91531	89618	GAAAAGCAAAACAAGAAAAC
91532	89619	AGAAAAGCAAAACAAGAAAA
91533	89620	TAGAAAAGCAAAACAAGAAA
91534	89621	TTAGAAAAGCAAAACAAGAA
91535	89622	GTTAGAAAAGCAAAACAAGA
91536	89623	AGTTAGAAAAGCAAAACAAG
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91544	89631	TTCAGATAAGTTAGAAAAGC
91545	89632	ATTCAGATAAGTTAGAAAAG
91546	89633	AATTCAGATAAGTTAGAAAA
91547	89634	AAATTCAGATAAGTTAGAAA
91548	89635	AAAATTCAGATAAGTTAGAA
91549	89636	AAAAATTCAGATAAGTTAGA
91550	89637	AAAAAATTCAGATAAGTTAG
91551	89638	AAAAAAATTCAGATAAGTTA
91552	89639	AAAAAAAATTCAGATAAGTT
91553	89640	TAAAAAAAATTCAGATAAGT
91554	89641	TTAAAAAAAATTCAGATAAG
91555	89642	TTTAAAAAAAATTCAGATAA
91556	89643	TTTTAAAAAAAATTCAGATA
91557	89644	TTTTTAAAAAAAATTCAGAT
91558	89645	TTTTTTAAAAAAAATTCAGA
91559	89646	ATTTTTTAAAAAAAATTCAG
91560	89647	AATTTTTTAAAAAAAATTCA
91561	89648	CAATTTTTTAAAAAAAATTC
91562	89649	ACAATTTTTTAAAAAAAATT
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91566	89653	GAAAACAATTTTTTAAAAAA
91567	89654	AGAAAACAATTTTTTAAAAA
91568	89655	TAGAAAACAATTTTTTAAAA
91569	89656	CTAGAAAACAATTTTTTAAA
91570	89657	GCTAGAAAACAATTTTTTAA
91571	89658	AGCTAGAAAACAATTTTTTA
91572	89659	TAGCTAGAAAACAATTTTTT
91573	89660	TTAGCTAGAAAACAATTTTT
91574	89661	TTTAGCTAGAAAACAATTTT
91575	89662	CTTTAGCTAGAAAACAATTT
91576	89663	TCTTTAGCTAGAAAACAATT
91577	89664	ATCTTTAGCTAGAAAACAAT
91578	89665	AATCTTTAGCTAGAAAACAA
91579	89666	GAATCTTTAGCTAGAAAACA
91580	89667	GGAATCTTTAGCTAGAAAAC
91581	89668	TGGAATCTTTAGCTAGAAAA
91582	89669	CTGGAATCTTTAGCTAGAAA
91583	89670	CCTGGAATCTTTAGCTAGAA
91584	89671	GCCTGGAATCTTTAGCTAGA
91585	89672	AGCCTGGAATCTTTAGCTAG
91586	89673	AAGCCTGGAATCTTTAGCTA
91587	89674	GAAGCCTGGAATCTTTAGCT
91588	89675	TGAAGCCTGGAATCTTTAGC
91589	89676	TTGAAGCCTGGAATCTTTAG
91590	89677	CTTGAAGCCTGGAATCTTTA
91591	89678	TCTTGAAGCCTGGAATCTTT
91592	89679	ATCTTGAAGCCTGGAATCTT
91593	89680	GATCTTGAAGCCTGGAATCT
91594	89681	TGATCTTGAAGCCTGGAATC
91595	89682	CTGATCTTGAAGCCTGGAAT
91596	89683	TCTGATCTTGAAGCCTGGAA
91597	89684	CTCTGATCTTGAAGCCTGGA
91598	89685	CCTCTGATCTTGAAGCCTGG

140675	138762	ATGCATAGCACAAATACCCA
140676	138763	CATGCATAGCACAAATACCC
140677	138764	GCATGCATAGCACAAATACC
140678	138765	TGCATGCATAGCACAAATAC
140679	138766	TTGCATGCATAGCACAAATA
140680	138767	TTTGCATGCATAGCACAAAT
140681	138768	ATTTGCATGCATAGCACAAA
140682	138769	AATTTGCATGCATAGCACAA
140683	138770	TAATTTGCATGCATAGCACA
140684	138771	CTAATTTGCATGCATAGCAC
140685	138772	GCTAATTTGCATGCATAGCA
140686	138773	AGCTAATTTGCATGCATAGC
140687	138774	TAGCTAATTTGCATGCATAG
140688	138775	ATAGCTAATTTGCATGCATA
140689	138776	TATAGCTAATTTGCATGCAT
140690	138777	CTATAGCTAATTTGCATGCA
140691	138778	TCTATAGCTAATTTGCATGC
140692	138779	ATCTATAGCTAATTTGCATG
140693	138780	AATCTATAGCTAATTTGCAT
140694	138781	TAATCTATAGCTAATTTGCA
140695	138782	CTAATCTATAGCTAATTTGC
140696	138783	TCTAATCTATAGCTAATTTG
140697	138784	TTCTAATCTATAGCTAATTT
140698	138785	TTTCTAATCTATAGCTAATT
140699	138786	TTTTCTAATCTATAGCTAAT
140700	138787	GTTTTCTAATCTATAGCTAA
140701	138788	GGTTTTCTAATCTATAGCTA
140702	138789	CGGTTTTCTAATCTATAGCT
140703	138790	ACGGTTTTCTAATCTATAGC
140704	138791	TACGGTTTTCTAATCTATAG
140705	138792	ATACGGTTTTCTAATCTATA
140706	138793	AATACGGTTTTCTAATCTAT
140707	138794	TAATACGGTTTTCTAATCTA
140708	138795	ATAATACGGTTTTCTAATCT
140709	138796	TATAATACGGTTTTCTAATC
140710	138797	CTATAATACGGTTTTCTAAT
140711	138798	ACTATAATACGGTTTTCTAA
140712	138799	GACTATAATACGGTTTTCTA
140713	138800	AGACTATAATACGGTTTTCT
140714	138801	AAGACTATAATACGGTTTTC
140715	138802	AAAGACTATAATACGGTTTT
140716	138803	TAAAGACTATAATACGGTTT
140717	138804	TTAAAGACTATAATACGGTT
140718	138805	TTTAAAGACTATAATACGGT
140719	138806	ATTTAAAGACTATAATACGG
140720	138807	TATTTAAAGACTATAATACG
140721	138808	GTATTTAAAGACTATAATAC
140722	138809	AGTATTTAAAGACTATAATA
140723	138810	CAGTATTTAAAGACTATAAT
140724	138811	CCAGTATTTAAAGACTATAA
140725	138812	ACCAGTATTTAAAGACTATA
140726	138813	TACCAGTATTTAAAGACTAT
140727	138814	TTACCAGTATTTAAAGACTA
140728	138815	TTTACCAGTATTTAAAGACT
140729	138816	GTTTACCAGTATTTAAAGAC
140730	138817	AGTTTACCAGTATTTAAAGA
140731	138818	AAGTTTACCAGTATTTAAAG
140732	138819	TAAGTTTACCAGTATTTAAA
140733	138820	TTAAGTTTACCAGTATTTAA
140734	138821	TTTAAGTTTACCAGTATTTA
140735	138822	ATTTAAGTTTACCAGTATTT
140736	138823	AATTTAAGTTTACCAGTATT
140737	138824	CAATTTAAGTTTACCAGTAT
140738	138825	GCAATTTAAGTTTACCAGTA
140739	138826	TGCAATTTAAGTTTACCAGT
140740	138827	CTGCAATTTAAGTTTACCAG
140741	138828	TCTGCAATTTAAGTTTACCA
140742	138829	CTCTGCAATTTAAGTTTACC
140743	138830	TCTCTGCAATTTAAGTTTAC
140744	138831	ATCTCTGCAATTTAAGTTTA
140745	138832	CATCTCTGCAATTTAAGTTT

42452	40539	ATAAAAAATGACAGTTTTTT
42453	40540	CATAAAAAATGACAGTTTTT
42454	40541	ACATAAAAAATGACAGTTTT
42455	40542	AACATAAAAAATGACAGTTT
42456	40543	CAACATAAAAAATGACAGTT
42457	40544	GCAACATAAAAAATGACAGT
42458	40545	TGCAACATAAAAAATGACAG
42459	40546	ATGCAACATAAAAAATGACA
42460	40547	AATGCAACATAAAAAATGAC
42461	40548	AAATGCAACATAAAAAATGA
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42463	40550	GTAAATGCAACATAAAAAAT
42464	40551	AGTAAATGCAACATAAAAAA
42465	40552	CAGTAAATGCAACATAAAAA
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42467	40554	TGCAGTAAATGCAACATAAA
42468	40555	ATGCAGTAAATGCAACATAA
42469	40556	AATGCAGTAAATGCAACATA
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42473	40560	CCAGAATGCAGTAAATGCAA
42474	40561	TCCAGAATGCAGTAAATGCA
42475	40562	ATCCAGAATGCAGTAAATGC
42476	40563	AATCCAGAATGCAGTAAATG
42477	40564	AAATCCAGAATGCAGTAAAT
42478	40565	TAAATCCAGAATGCAGTAAA
42479	40566	TTAAATCCAGAATGCAGTAA
42480	40567	TTTAAATCCAGAATGCAGTA
42481	40568	GTTTAAATCCAGAATGCAGT
42482	40569	AGTTTAAATCCAGAATGCAG
42483	40570	CAGTTTAAATCCAGAATGCA
42484	40571	ACAGTTTAAATCCAGAATGC
42485	40572	CACAGTTTAAATCCAGAATG
42486	40573	TCACAGTTTAAATCCAGAAT
42487	40574	CTCACAGTTTAAATCCAGAA
42488	40575	CCTCACAGTTTAAATCCAGA
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42492	40579	GGTTCCTCACAGTTTAAATC
42493	40580	AGGTTCCTCACAGTTTAAAT
42494	40581	GAGGTTCCTCACAGTTTAAA
42495	40582	TGAGGTTCCTCACAGTTTAA
42496	40583	ATGAGGTTCCTCACAGTTTA
42497	40584	CATGAGGTTCCTCACAGTTT
42498	40585	CCATGAGGTTCCTCACAGTT
42499	40586	ACCATGAGGTTCCTCACAGT
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42501	40588	ATACCATGAGGTTCCTCACA
42502	40589	GATACCATGAGGTTCCTCAC
42503	40590	TGATACCATGAGGTTCCTCA
42504	40591	CTGATACCATGAGGTTCCTC
42505	40592	ACTGATACCATGAGGTTCCT
42506	40593	AACTGATACCATGAGGTTCC
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42512	40599	TATATTAACTGATACCATGA
42513	40600	ATATATTAACTGATACCATG
42514	40601	AATATATTAACTGATACCAT
42515	40602	GAATATATTAACTGATACCA
42516	40603	AGAATATATTAACTGATACC
42517	40604	AAGAATATATTAACTGATAC
42518	40605	GAAGAATATATTAACTGATA
42519	40606	GGAAGAATATATTAACTGAT
42520	40607	TGGAAGAATATATTAACTGA
42521	40608	ATGGAAGAATATATTAACTG
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91599	89686	GCCTCTGATCTTGAAGCCTG
91600	89687	TGCCTCTGATCTTGAAGCCT
91601	89688	CTGCCTCTGATCTTGAAGCC
91602	89689	TCTGCCTCTGATCTTGAAGC
91603	89690	TTCTGCCTCTGATCTTGAAG
91604	89691	GTTCTGCCTCTGATCTTGAA
91605	89692	AGTTCTGCCTCTGATCTTGA
91606	89693	GAGTTCTGCCTCTGATCTTG
91607	89694	AGAGTTCTGCCTCTGATCTT
91608	89695	GAGAGTTCTGCCTCTGATCT
91609	89696	GGAGAGTTCTGCCTCTGATC
91610	89697	AGGAGAGTTCTGCCTCTGAT
91611	89698	CAGGAGAGTTCTGCCTCTGA
91612	89699	GCAGGAGAGTTCTGCCTCTG
91613	89700	TGCAGGAGAGTTCTGCCTCT
91614	89701	CTGCAGGAGAGTTCTGCCTC
91615	89702	CCTGCAGGAGAGTTCTGCCT
91616	89703	CCCTGCAGGAGAGTTCTGCC
91617	89704	TCCCTGCAGGAGAGTTCTGC
91618	89705	TTCCCTGCAGGAGAGTTCTG
91619	89706	ATTCCCTGCAGGAGAGTTCT
91620	89707	TATTCCCTGCAGGAGAGTTC
91621	89708	TTATTCCCTGCAGGAGAGTT
91622	89709	TTTATTCCCTGCAGGAGAGT
91623	89710	CTTTATTCCCTGCAGGAGAG
91624	89711	TCTTTATTCCCTGCAGGAGA
91625	89712	TTCTTTATTCCCTGCAGGAG
91626	89713	TTTCTTTATTCCCTGCAGGA
91627	89714	TTTTCTTTATTCCCTGCAGG
91628	89715	ATTTTCTTTATTCCCTGCAG
91629	89716	TATTTTCTTTATTCCCTGCA
91630	89717	ATATTTTCTTTATTCCCTGC
91631	89718	AATATTTTCTTTATTCCCTG
91632	89719	TAATATTTTCTTTATTCCCT
91633	89720	TTAATATTTTCTTTATTCCC
91634	89721	TTTAATATTTTCTTTATTCC
91635	89722	GTTTAATATTTTCTTTATTC
91636	89723	GGTTTAATATTTTCTTTATT
91637	89724	GGGTTTAATATTTTCTTTAT
91638	89725	TGGGTTTAATATTTTCTTTA
91639	89726	TTGGGTTTAATATTTTCTTT
91640	89727	ATTGGGTTTAATATTTTCTT
91641	89728	CATTGGGTTTAATATTTTCT
91642	89729	TCATTGGGTTTAATATTTTC
91643	89730	TTCATTGGGTTTAATATTTT
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91645	89732	GTTTCATTGGGTTTAATATT
91646	89733	TGTTTCATTGGGTTTAATAT
91647	89734	ATGTTTCATTGGGTTTAATA
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91649	89736	TGATGTTTCATTGGGTTTAA
91650	89737	GTGATGTTTCATTGGGTTTA
91651	89738	GGTGATGTTTCATTGGGTTT
91652	89739	AGGTGATGTTTCATTGGGTT
91653	89740	TAGGTGATGTTTCATTGGGT
91654	89741	CTAGGTGATGTTTCATTGGG
91655	89742	GCTAGGTGATGTTTCATTGG
91656	89743	AGCTAGGTGATGTTTCATTG
91657	89744	AAGCTAGGTGATGTTTCATT
91658	89745	GAAGCTAGGTGATGTTTCAT
91659	89746	AGAAGCTAGGTGATGTTTCA
91660	89747	GAGAAGCTAGGTGATGTTTC
91661	89748	TGAGAAGCTAGGTGATGTTT
91662	89749	TTGAGAAGCTAGGTGATGTT
91663	89750	TTTGAGAAGCTAGGTGATGT
91664	89751	TTTTGAGAAGCTAGGTGATG
91665	89752	CTTTTGAGAAGCTAGGTGAT
91666	89753	GCTTTTGAGAAGCTAGGTGA
91667	89754	AGCTTTTGAGAAGCTAGGTG
91668	89755	CAGCTTTTGAGAAGCTAGGT
91669	89756	TCAGCTTTTGAGAAGCTAGG

140746	138833	GCATCTCTGCAATTTAAGTT
140747	138834	GGCATCTCTGCAATTTAAGT
140748	138835	AGGCATCTCTGCAATTTAAG
140749	138836	AAGGCATCTCTGCAATTTAA
140750	138837	AAAGGCATCTCTGCAATTTA
140751	138838	AAAAGGCATCTCTGCAATTT
140752	138839	TAAAAGGCATCTCTGCAATT
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140754	138841	TTTAAAAGGCATCTCTGCAA
140755	138842	TTTTAAAAGGCATCTCTGCA
140756	138843	TTTTTAAAAGGCATCTCTGC
140757	138844	ATTTTTAAAAGGCATCTCTG
140758	138845	CATTTTTAAAAGGCATCTCT
140759	138846	GCATTTTTAAAAGGCATCTC
140760	138847	TGCATTTTTAAAAGGCATCT
140761	138848	ATGCATTTTTAAAAGGCATC
140762	138849	TATGCATTTTTAAAAGGCAT
140763	138850	CTATGCATTTTTAAAAGGCA
140764	138851	ACTATGCATTTTTAAAAGGC
140765	138852	TACTATGCATTTTTAAAAGG
140766	138853	TTACTATGCATTTTTAAAAG
140767	138854	TTTACTATGCATTTTTAAAA
140768	138855	TTTTACTATGCATTTTTAAA
140769	138856	TTTTTACTATGCATTTTTAA
140770	138857	ATTTTTACTATGCATTTTTA
140771	138858	TATTTTTACTATGCATTTTT
140772	138859	ATATTTTTACTATGCATTTT
140773	138860	AATATTTTTACTATGCATTT
140774	138861	AAATATTTTTACTATGCATT
140775	138862	GAAATATTTTTACTATGCAT
140776	138863	TGAAATATTTTTACTATGCA
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140778	138865	GATGAAATATTTTTACTATG
140779	138866	AGATGAAATATTTTTACTAT
140780	138867	AAGATGAAATATTTTTACTA
140781	138868	AAAGATGAAATATTTTTACT
140782	138869	TAAAGATGAAATATTTTTAC
140783	138870	GTAAAGATGAAATATTTTTA
140784	138871	AGTAAAGATGAAATATTTTT
140785	138872	AAGTAAAGATGAAATATTTT
140786	138873	AAAGTAAAGATGAAATATTT
140787	138874	AAAAGTAAAGATGAAATATT
140788	138875	GAAAAGTAAAGATGAAATAT
140789	138876	AGAAAAGTAAAGATGAAATA
140790	138877	GAGAAAAGTAAAGATGAAAT
140791	138878	AGAGAAAAGTAAAGATGAAA
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140793	138880	GAAGAGAAAAGTAAAGATGA
140794	138881	TGAAGAGAAAAGTAAAGATG
140795	138882	TTGAAGAGAAAAGTAAAGAT
140796	138883	TTTGAAGAGAAAAGTAAAGA
140797	138884	ATTTGAAGAGAAAAGTAAAG
140798	138885	CATTTGAAGAGAAAAGTAAA
140799	138886	TCATTTGAAGAGAAAAGTAA
140800	138887	ATCATTTGAAGAGAAAAGTA
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140809	138896	AATCTTAAAATCATTTGAAG
140810	138897	AAATCTTAAAATCATTTGAA
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140812	138899	AAAAATCTTAAAATCATTTG
140813	138900	TAAAAATCTTAAAATCATTT
140814	138901	GTAAAAATCTTAAAATCATT
140815	138902	TGTAAAAATCTTAAAATCAT
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42523	40610	AGATGGAAGAATATATTAAC
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42527	40614	ATTAAGATGGAAGAATATAT
42528	40615	CATTAAGATGGAAGAATATA
42529	40616	ACATTAAGATGGAAGAATAT
42530	40617	AACATTAAGATGGAAGAATA
42531	40618	AAACATTAAGATGGAAGAAT
42532	40619	GAAACATTAAGATGGAAGAA
42533	40620	AGAAACATTAAGATGGAAGA
42534	40621	GAGAAACATTAAGATGGAAG
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42536	40623	ACGAGAAACATTAAGATGGA
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42538	40625	TTACGAGAAACATTAAGATG
42539	40626	TTTACGAGAAACATTAAGAT
42540	40627	GTTTACGAGAAACATTAAGA
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42545	40632	TACCAGTTTACGAGAAACAT
42546	40633	CTACCAGTTTACGAGAAACA
42547	40634	TCTACCAGTTTACGAGAAAC
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42550	40637	AGATCTACCAGTTTACGAGA
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42552	40639	ACAGATCTACCAGTTTACGA
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42560	40647	TCAAGTTTACAGATCTACCA
42561	40648	ATCAAGTTTACAGATCTACC
42562	40649	AATCAAGTTTACAGATCTAC
42563	40650	TAATCAAGTTTACAGATCTA
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42565	40652	CCTAATCAAGTTTACAGATC
42566	40653	ACCTAATCAAGTTTACAGAT
42567	40654	GACCTAATCAAGTTTACAGA
42568	40655	AGACCTAATCAAGTTTACAG
42569	40656	TAGACCTAATCAAGTTTACA
42570	40657	ATAGACCTAATCAAGTTTAC
42571	40658	GATAGACCTAATCAAGTTTA
42572	40659	GGATAGACCTAATCAAGTTT
42573	40660	AGGATAGACCTAATCAAGTT
42574	40661	TAGGATAGACCTAATCAAGT
42575	40662	ATAGGATAGACCTAATCAAG
42576	40663	AATAGGATAGACCTAATCAA
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42579	40666	TACAATAGGATAGACCTAAT
42580	40667	ATACAATAGGATAGACCTAA
42581	40668	GATACAATAGGATAGACCTA
42582	40669	TGATACAATAGGATAGACCT
42583	40670	GTGATACAATAGGATAGACC
42584	40671	TGTGATACAATAGGATAGAC
42585	40672	ATGTGATACAATAGGATAGA
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42587	40674	TGATGTGATACAATAGGATA
42588	40675	CTGATGTGATACAATAGGAT
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42590	40677	TTCTGATGTGATACAATAGG
42591	40678	CTTCTGATGTGATACAATAG
42592	40679	GCTTCTGATGTGATACAATA
42593	40680	TGCTTCTGATGTGATACAAT

91670	89757	TTCAGCTTTTGAGAAGCTAG
91671	89758	TTTCAGCTTTTGAGAAGCTA
91672	89759	TTTTCAGCTTTTGAGAAGCT
91673	89760	GTTTTCAGCTTTTGAGAAGC
91674	89761	TGTTTTCAGCTTTTGAGAAG
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91678	89765	CCTTTGTTTTCAGCTTTTGA
91679	89766	ACCTTTGTTTTCAGCTTTTG
91680	89767	AACCTTTGTTTTCAGCTTTT
91681	89768	TAACCTTTGTTTTCAGCTTT
91682	89769	CTAACCTTTGTTTTCAGCTT
91683	89770	TCTAACCTTTGTTTTCAGCT
91684	89771	CTCTAACCTTTGTTTTCAGC
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91687	89774	AAACTCTAACCTTTGTTTTC
91688	89775	TAAACTCTAACCTTTGTTTT
91689	89776	TTAAACTCTAACCTTTGTTT
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91691	89778	CTTTAAACTCTAACCTTTGT
91692	89779	TCTTTAAACTCTAACCTTTG
91693	89780	CTCTTTAAACTCTAACCTTT
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91696	89783	TGACTCTTTAAACTCTAACC
91697	89784	ATGACTCTTTAAACTCTAAC
91698	89785	AATGACTCTTTAAACTCTAA
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91700	89787	TTAATGACTCTTTAAACTCT
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91702	89789	GCTTAATGACTCTTTAAACT
91703	89790	AGCTTAATGACTCTTTAAAC
91704	89791	AAGCTTAATGACTCTTTAAA
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91706	89793	TTAAGCTTAATGACTCTTTA
91707	89794	GTTAAGCTTAATGACTCTTT
91708	89795	AGTTAAGCTTAATGACTCTT
91709	89796	CAGTTAAGCTTAATGACTCT
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91711	89798	TACAGTTAAGCTTAATGACT
91712	89799	CTACAGTTAAGCTTAATGAC
91713	89800	CCTACAGTTAAGCTTAATGA
91714	89801	TCCTACAGTTAAGCTTAATG
91715	89802	TTCCTACAGTTAAGCTTAAT
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91717	89804	TATTCCTACAGTTAAGCTTA
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91722	89809	CTTCCTATTCCTACAGTTAA
91723	89810	TCTTCCTATTCCTACAGTTA
91724	89811	TTCTTCCTATTCCTACAGTT
91725	89812	CTTCTTCCTATTCCTACAGT
91726	89813	ACTTCTTCCTATTCCTACAG
91727	89814	TACTTCTTCCTATTCCTACA
91728	89815	ATACTTCTTCCTATTCCTAC
91729	89816	CATACTTCTTCCTATTCCTA
91730	89817	ACATACTTCTTCCTATTCCT
91731	89818	GACATACTTCTTCCTATTCC
91732	89819	AGACATACTTCTTCCTATTC
91733	89820	TAGACATACTTCTTCCTATT
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91736	89823	AATTAGACATACTTCTTCCT
91737	89824	AAATTAGACATACTTCTTCC
91738	89825	GAAATTAGACATACTTCTTC
91739	89826	TGAAATTAGACATACTTCTT
91740	89827	ATGAAATTAGACATACTTCT

140817	138904	AATGTAAAAATCTTAAAATC
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140819	138906	AAAATGTAAAAATCTTAAAA
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140821	138908	GAAAAATGTAAAAATCTTAA
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140826	138913	AACTGGAAAAATGTAAAAAT
140827	138914	CAACTGGAAAAATGTAAAAA
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140837	138924	AGTTATTCATCAACTGGAAA
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140839	138926	TAAGTTATTCATCAACTGGA
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140844	138931	TAATTTAAGTTATTCATCAA
140845	138932	ATAATTTAAGTTATTCATCA
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140859	138946	GCCCATGAAATCTCATAATT
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140861	138948	ATGCCCATGAAATCTCATAA
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140870	138957	AAAATAATTATGCCCATGAA
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140875	138962	TATAGAAAATAATTATGCCC
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140880	138967	ATAAATATAGAAAATAATTA
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140882	138969	CAATAAATATAGAAAATAAT
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140884	138971	AACAATAAATATAGAAAATA
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42594	40681	CTGCTTCTGATGTGATACAA
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42661	40748	CAGGGGTTCACTTTACCATT
42662	40749	GCAGGGGTTCACTTTACCAT
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91741	89828	CATGAAATTAGACATACTTC
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91744	89831	GGGCATGAAATTAGACATAC
91745	89832	TGGGCATGAAATTAGACATA
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91748	89835	GTATGGGCATGAAATTAGAC
91749	89836	TGTATGGGCATGAAATTAGA
91750	89837	CTGTATGGGCATGAAATTAG
91751	89838	TCTGTATGGGCATGAAATTA
91752	89839	TTCTGTATGGGCATGAAATT
91753	89840	ATTCTGTATGGGCATGAAAT
91754	89841	TATTCTGTATGGGCATGAAA
91755	89842	ATATTCTGTATGGGCATGAA
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91778	89865	GTAAGAAGAAATGTTGAACA
91779	89866	AGTAAGAAGAAATGTTGAAC
91780	89867	TAGTAAGAAGAAATGTTGAA
91781	89868	ATAGTAAGAAGAAATGTTGA
91782	89869	AATAGTAAGAAGAAATGTTG
91783	89870	CAATAGTAAGAAGAAATGTT
91784	89871	ACAATAGTAAGAAGAAATGT
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91786	89873	TCACAATAGTAAGAAGAAAT
91787	89874	ATCACAATAGTAAGAAGAAA
91788	89875	TATCACAATAGTAAGAAGAA
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91793	89880	TTATCTATCACAATAGTAAG
91794	89881	TTTATCTATCACAATAGTAA
91795	89882	ATTTATCTATCACAATAGTA
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91798	89885	TACATTTATCTATCACAATA
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91800	89887	AATACATTTATCTATCACAA
91801	89888	CAATACATTTATCTATCACA
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91803	89890	AGCAATACATTTATCTATCA
91804	89891	AAGCAATACATTTATCTATC
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91808	89895	TGTCAAGCAATACATTTATC
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140888	138975	AAGTAACAATAAATATAGAA
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140915	139002	TCTAAGCAAAGTATTAAGAA
140916	139003	TTCTAAGCAAAGTATTAAGA
140917	139004	CTTCTAAGCAAAGTATTAAG
140918	139005	CCTTCTAAGCAAAGTATTAA
140919	139006	ACCTTCTAAGCAAAGTATTA
140920	139007	TACCTTCTAAGCAAAGTATT
140921	139008	ATACCTTCTAAGCAAAGTAT
140922	139009	AATACCTTCTAAGCAAAGTA
140923	139010	AAATACCTTCTAAGCAAAGT
140924	139011	TAAATACCTTCTAAGCAAAG
140925	139012	TTAAATACCTTCTAAGCAAA
140926	139013	TTTAAATACCTTCTAAGCAA
140927	139014	TTTTAAATACCTTCTAAGCA
140928	139015	CTTTTAAATACCTTCTAAGC
140929	139016	ACTTTTAAATACCTTCTAAG
140930	139017	CACTTTTAAATACCTTCTAA
140931	139018	TCACTTTTAAATACCTTCTA
140932	139019	TTCACTTTTAAATACCTTCT
140933	139020	TTTCACTTTTAAATACCTTC
140934	139021	ATTTCACTTTTAAATACCTT
140935	139022	AATTTCACTTTTAAATACCT
140936	139023	AAATTTCACTTTTAAATACC
140937	139024	GAAATTTCACTTTTAAATAC
140938	139025	TGAAATTTCACTTTTAAATA
140939	139026	TTGAAATTTCACTTTTAAAT
140940	139027	TTTGAAATTTCACTTTTAAA
140941	139028	GTTTGAAATTTCACTTTTAA
140942	139029	AGTTTGAAATTTCACTTTTA
140943	139030	AAGTTTGAAATTTCACTTTT
140944	139031	AAAGTTTGAAATTTCACTTT
140945	139032	AAAAGTTTGAAATTTCACTT
140946	139033	AAAAAGTTTGAAATTTCACT
140947	139034	TAAAAAGTTTGAAATTTCAC
140948	139035	CTAAAAAGTTTGAAATTTCA
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140950	139037	TACTAAAAAGTTTGAAATTT
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140952	139039	TGTACTAAAAAGTTTGAAAT
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140955	139042	TTTTGTACTAAAAAGTTTGA
140956	139043	ATTTTGTACTAAAAAGTTTG
140957	139044	AATTTTGTACTAAAAAGTTT
140958	139045	AAATTTTGTACTAAAAAGTT

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42666	40753	GTGTGCAGGGGTTCACTTTA
42667	40754	GGTGTGCAGGGGTTCACTTT
42668	40755	AGGTGTGCAGGGGTTCACTT
42669	40756	TAGGTGTGCAGGGGTTCACT
42670	40757	ATAGGTGTGCAGGGGTTCAC
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42681	40768	AAAGCTGGGTGATAGGTGTG
42682	40769	TAAAGCTGGGTGATAGGTGT
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42685	40772	TATTAAAGCTGGGTGATAGG
42686	40773	CTATTAAAGCTGGGTGATAG
42687	40774	ACTATTAAAGCTGGGTGATA
42688	40775	AACTATTAAAGCTGGGTGAT
42689	40776	TAACTATTAAAGCTGGGTGA
42690	40777	ATAACTATTAAAGCTGGGTG
42691	40778	GATAACTATTAAAGCTGGGT
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42696	40783	GAGCTGATAACTATTAAAGC
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42698	40785	ATGAGCTGATAACTATTAAA
42699	40786	TATGAGCTGATAACTATTAA
42700	40787	GTATGAGCTGATAACTATTA
42701	40788	GGTATGAGCTGATAACTATT
42702	40789	TGGTATGAGCTGATAACTAT
42703	40790	ATGGTATGAGCTGATAACTA
42704	40791	AATGGTATGAGCTGATAACT
42705	40792	GAATGGTATGAGCTGATAAC
42706	40793	AGAATGGTATGAGCTGATAA
42707	40794	AAGAATGGTATGAGCTGATA
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42709	40796	ACAAGAATGGTATGAGCTGA
42710	40797	AACAAGAATGGTATGAGCTG
42711	40798	AAACAAGAATGGTATGAGCT
42712	40799	CAAACAAGAATGGTATGAGC
42713	40800	TCAAACAAGAATGGTATGAG
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42716	40803	AAATCAAACAAGAATGGTAT
42717	40804	TAAATCAAACAAGAATGGTA
42718	40805	GTAAATCAAACAAGAATGGT
42719	40806	TGTAAATCAAACAAGAATGG
42720	40807	TTGTAAATCAAACAAGAATG
42721	40808	GTTGTAAATCAAACAAGAAT
42722	40809	GGTTGTAAATCAAACAAGAA
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42724	40811	GGGGTTGTAAATCAAACAAG
42725	40812	TGGGGTTGTAAATCAAACAA
42726	40813	ATGGGGTTGTAAATCAAACA
42727	40814	AATGGGGTTGTAAATCAAAC
42728	40815	GAATGGGGTTGTAAATCAAA
42729	40816	TGAATGGGGTTGTAAATCAA
42730	40817	ATGAATGGGGTTGTAAATCA
42731	40818	AATGAATGGGGTTGTAAATC
42732	40819	AAATGAATGGGGTTGTAAAT
42733	40820	GAAATGAATGGGGTTGTAAA
42734	40821	AGAAATGAATGGGGTTGTAA
42735	40822	GAGAAATGAATGGGGTTGTA

91812	89899	AATTTGTCAAGCAATACATT
91813	89900	GAATTTGTCAAGCAATACAT
91814	89901	GGAATTTGTCAAGCAATACA
91815	89902	TGGAATTTGTCAAGCAATAC
91816	89903	TTGGAATTTGTCAAGCAATA
91817	89904	TTTGGAATTTGTCAAGCAAT
91818	89905	TTTTGGAATTTGTCAAGCAA
91819	89906	ATTTTGGAATTTGTCAAGCA
91820	89907	GATTTTGGAATTTGTCAAGC
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91822	89909	TGGATTTTGGAATTTGTCAA
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91825	89912	ATTTGGATTTTGGAATTTGT
91826	89913	AATTTGGATTTTGGAATTTG
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91828	89915	TAAATTTGGATTTTGGAATT
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91830	89917	ATTAAATTTGGATTTTGGAA
91831	89918	TATTAAATTTGGATTTTGGA
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91833	89920	AATATTAAATTTGGATTTTG
91834	89921	AAATATTAAATTTGGATTTT
91835	89922	CAAATATTAAATTTGGATTT
91836	89923	TCAAATATTAAATTTGGATT
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91838	89925	TTTCAAATATTAAATTTGGA
91839	89926	ATTTCAAATATTAAATTTGG
91840	89927	AATTTCAAATATTAAATTTG
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91842	89929	ATAATTTCAAATATTAAATT
91843	89930	AATAATTTCAAATATTAAAT
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91845	89932	AAAATAATTTCAAATATTAA
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91849	89936	TCAGAAAATAATTTCAAATA
91850	89937	ATCAGAAAATAATTTCAAAT
91851	89938	GATCAGAAAATAATTTCAAA
91852	89939	AGATCAGAAAATAATTTCAA
91853	89940	AAGATCAGAAAATAATTTCA
91854	89941	TAAGATCAGAAAATAATTTC
91855	89942	ATAAGATCAGAAAATAATTT
91856	89943	TATAAGATCAGAAAATAATT
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91872	89959	AGAAATTAGAATAAGATATA
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91874	89961	ATAGAAATTAGAATAAGATA
91875	89962	GATAGAAATTAGAATAAGAT
91876	89963	TGATAGAAATTAGAATAAGA
91877	89964	ATGATAGAAATTAGAATAAG
91878	89965	GATGATAGAAATTAGAATAA
91879	89966	AGATGATAGAAATTAGAATA
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91881	89968	TGAGATGATAGAAATTAGAA
91882	89969	ATGAGATGATAGAAATTAGA

140959	139046	GAAATTTTGTACTAAAAAGT
140960	139047	AGAAATTTTGTACTAAAAAG
140961	139048	AAGAAATTTTGTACTAAAAA
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140965	139052	ATTCAAGAAATTTTGTACTA
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140967	139054	TTATTCAAGAAATTTTGTAC
140968	139055	TTTATTCAAGAAATTTTGTA
140969	139056	ATTTATTCAAGAAATTTTGT
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140976	139063	TAACTTTATTTATTCAAGAA
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140998	139085	AGAGGTTTTTGTTTTTTTTT
140999	139086	CAGAGGTTTTTGTTTTTTTT
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141003	139090	ATCTCAGAGGTTTTTGTTTT
141004	139091	AATCTCAGAGGTTTTTGTTT
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141006	139093	GGAATCTCAGAGGTTTTTGT
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141008	139095	ACGGAATCTCAGAGGTTTTT
141009	139096	TACGGAATCTCAGAGGTTTT
141010	139097	GTACGGAATCTCAGAGGTTT
141011	139098	AGTACGGAATCTCAGAGGTT
141012	139099	CAGTACGGAATCTCAGAGGT
141013	139100	ACAGTACGGAATCTCAGAGG
141014	139101	TACAGTACGGAATCTCAGAG
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141017	139104	AGATACAGTACGGAATCTCA
141018	139105	AAGATACAGTACGGAATCTC
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141020	139107	TAAAGATACAGTACGGAATC
141021	139108	ATAAAGATACAGTACGGAAT
141022	139109	CATAAAGATACAGTACGGAA
141023	139110	TCATAAAGATACAGTACGGA
141024	139111	TTCATAAAGATACAGTACGG
141025	139112	GTTCATAAAGATACAGTACG
141026	139113	GGTTCATAAAGATACAGTAC
141027	139114	AGGTTCATAAAGATACAGTA
141028	139115	GAGGTTCATAAAGATACAGT
141029	139116	GGAGGTTCATAAAGATACAG

42736	40823	GGAGAAATGAATGGGGTTGT
42737	40824	GGGAGAAATGAATGGGGTTG
42738	40825	AGGGAGAAATGAATGGGGTT
42739	40826	AAGGGAGAAATGAATGGGGT
42740	40827	GAAGGGAGAAATGAATGGGG
42741	40828	AGAAGGGAGAAATGAATGGG
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42743	40830	ACAGAAGGGAGAAATGAATG
42744	40831	TACAGAAGGGAGAAATGAAT
42745	40832	ATACAGAAGGGAGAAATGAA
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42747	40834	TAATACAGAAGGGAGAAATG
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42753	40840	TAATAATAATACAGAAGGGA
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42757	40844	TAAATAATAATAATACAGAA
42758	40845	CTAAATAATAATAATACAGA
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42760	40847	AACTAAATAATAATAATACA
42761	40848	TAACTAAATAATAATAATAC
42762	40849	TTAACTAAATAATAATAATA
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42783	40870	AAACCCTGTCTCAAAAAATA
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42788	40875	GAGCAAAACCCTGTCTCAAA
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42797	40884	TTGGTGACAGAGCAAAACCC
42798	40885	ATTGGTGACAGAGCAAAACC
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42800	40887	GCATTGGTGACAGAGCAAAA
42801	40888	AGCATTGGTGACAGAGCAAA
42802	40889	CAGCATTGGTGACAGAGCAA
42803	40890	CCAGCATTGGTGACAGAGCA
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91883	89970	TATGAGATGATAGAAATTAG
91884	89971	GTATGAGATGATAGAAATTA
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91886	89973	TAGTATGAGATGATAGAAAT
91887	89974	TTAGTATGAGATGATAGAAA
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91889	89976	TTTTAGTATGAGATGATAGA
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91898	89985	TCACATTCTTTTTAGTATGA
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91906	89993	CTTTAACATCACATTCTTTT
91907	89994	ACTTTAACATCACATTCTTT
91908	89995	AACTTTAACATCACATTCTT
91909	89996	AAACTTTAACATCACATTCT
91910	89997	TAAACTTTAACATCACATTC
91911	89998	TTAAACTTTAACATCACATT
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91913	90000	TTTTAAACTTTAACATCACA
91914	90001	TTTTTAAACTTTAACATCAC
91915	90002	ATTTTTAAACTTTAACATCA
91916	90003	TATTTTTAAACTTTAACATC
91917	90004	TTATTTTTAAACTTTAACAT
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91920	90007	GGTTTATTTTTAAACTTTAA
91921	90008	AGGTTTATTTTTAAACTTTA
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91923	90010	ACAGGTTTATTTTTAAACTT
91924	90011	CACAGGTTTATTTTTAAACT
91925	90012	ACACAGGTTTATTTTTAAAC
91926	90013	GACACAGGTTTATTTTTAAA
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91929	90016	TAAGACACAGGTTTATTTTT
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91932	90019	TGTTAAGACACAGGTTTATT
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91935	90022	AACTGTTAAGACACAGGTTT
91936	90023	GAACTGTTAAGACACAGGTT
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141030	139117	TGGAGGTTCATAAAGATACA
141031	139118	ATGGAGGTTCATAAAGATAC
141032	139119	CATGGAGGTTCATAAAGATA
141033	139120	TCATGGAGGTTCATAAAGAT
141034	139121	TTCATGGAGGTTCATAAAGA
141035	139122	GTTCATGGAGGTTCATAAAG
141036	139123	TGTTCATGGAGGTTCATAAA
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141040	139127	ATTCTGTTCATGGAGGTTCA
141041	139128	AATTCTGTTCATGGAGGTTC
141042	139129	AAATTCTGTTCATGGAGGTT
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141044	139131	CCAAATTCTGTTCATGGAGG
141045	139132	CCCAAATTCTGTTCATGGAG
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141061	139148	AAAGCAATTCCCAAATCCCA
141062	139149	AAAAGCAATTCCCAAATCCC
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141064	139151	GGAAAAGCAATTCCCAAATC
141065	139152	AGGAAAAGCAATTCCCAAAT
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141068	139155	CTAAGGAAAAGCAATTCCCA
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141074	139161	ATCTGTCTAAGGAAAAGCAA
141075	139162	AATCTGTCTAAGGAAAAGCA
141076	139163	AAATCTGTCTAAGGAAAAGC
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141078	139165	CTAAATCTGTCTAAGGAAAA
141079	139166	TCTAAATCTGTCTAAGGAAA
141080	139167	ATCTAAATCTGTCTAAGGAA
141081	139168	AATCTAAATCTGTCTAAGGA
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141083	139170	ACAATCTAAATCTGTCTAAG
141084	139171	AACAATCTAAATCTGTCTAA
141085	139172	TAACAATCTAAATCTGTCTA
141086	139173	GTAACAATCTAAATCTGTCT
141087	139174	TGTAACAATCTAAATCTGTC
141088	139175	TTGTAACAATCTAAATCTGT
141089	139176	TTTGTAACAATCTAAATCTG
141090	139177	ATTTGTAACAATCTAAATCT
141091	139178	CATTTGTAACAATCTAAATC
141092	139179	TCATTTGTAACAATCTAAAT
141093	139180	GTCATTTGTAACAATCTAAA
141094	139181	TGTCATTTGTAACAATCTAA
141095	139182	ATGTCATTTGTAACAATCTA
141096	139183	AATGTCATTTGTAACAATCT
141097	139184	AAATGTCATTTGTAACAATC
141098	139185	AAAATGTCATTTGTAACAAT
141099	139186	AAAAATGTCATTTGTAACAA
141100	139187	TAAAAATGTCATTTGTAACA

42807	40894	CACTCCAGCATTGGTGACAG
42808	40895	GCACTCCAGCATTGGTGACA
42809	40896	TGCACTCCAGCATTGGTGAC
42810	40897	CTGCACTCCAGCATTGGTGA
42811	40898	ACTGCACTCCAGCATTGGTG
42812	40899	CACTGCACTCCAGCATTGGT
42813	40900	CCACTGCACTCCAGCATTGG
42814	40901	GCCACTGCACTCCAGCATTG
42815	40902	TGCCACTGCACTCCAGCATT
42816	40903	ATGCCACTGCACTCCAGCAT
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42818	40905	TTATGCCACTGCACTCCAGC
42819	40906	ATTATGCCACTGCACTCCAG
42820	40907	GATTATGCCACTGCACTCCA
42821	40908	TGATTATGCCACTGCACTCC
42822	40909	GTGATTATGCCACTGCACTC
42823	40910	TGTGATTATGCCACTGCACT
42824	40911	CTGTGATTATGCCACTGCAC
42825	40912	GCTGTGATTATGCCACTGCA
42826	40913	AGCTGTGATTATGCCACTGC
42827	40914	GAGCTGTGATTATGCCACTG
42828	40915	TGAGCTGTGATTATGCCACT
42829	40916	GTGAGCTGTGATTATGCCAC
42830	40917	AGTGAGCTGTGATTATGCCA
42831	40918	CAGTGAGCTGTGATTATGCC
42832	40919	GCAGTGAGCTGTGATTATGC
42833	40920	AGCAGTGAGCTGTGATTATG
42834	40921	CAGCAGTGAGCTGTGATTAT
42835	40922	ACAGCAGTGAGCTGTGATTA
42836	40923	GACAGCAGTGAGCTGTGATT
42837	40924	AGACAGCAGTGAGCTGTGAT
42838	40925	AAGACAGCAGTGAGCTGTGA
42839	40926	CAAGACAGCAGTGAGCTGTG
42840	40927	TCAAGACAGCAGTGAGCTGT
42841	40928	GTCAAGACAGCAGTGAGCTG
42842	40929	GGTCAAGACAGCAGTGAGCT
42843	40930	AGGTCAAGACAGCAGTGAGC
42844	40931	GAGGTCAAGACAGCAGTGAG
42845	40932	GGAGGTCAAGACAGCAGTGA
42846	40933	AGGAGGTCAAGACAGCAGTG
42847	40934	CAGGAGGTCAAGACAGCAGT
42848	40935	CCAGGAGGTCAAGACAGCAG
42849	40936	CCCAGGAGGTCAAGACAGCA
42850	40937	GCCCAGGAGGTCAAGACAGC
42851	40938	AGCCCAGGAGGTCAAGACAG
42852	40939	GAGCCCAGGAGGTCAAGACA
42853	40940	TGAGCCCAGGAGGTCAAGAC
42854	40941	TTGAGCCCAGGAGGTCAAGA
42855	40942	CTTGAGCCCAGGAGGTCAAG
42856	40943	ACTTGAGCCCAGGAGGTCAA
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42858	40945	TCACTTGAGCCCAGGAGGTC
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42860	40947	GATCACTTGAGCCCAGGAGG
42861	40948	GGATCACTTGAGCCCAGGAG
42862	40949	AGGATCACTTGAGCCCAGGA
42863	40950	GAGGATCACTTGAGCCCAGG
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42865	40952	GGGAGGATCACTTGAGCCCA
42866	40953	TGGGAGGATCACTTGAGCCC
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42868	40955	GGTGGGAGGATCACTTGAGC
42869	40956	AGGTGGGAGGATCACTTGAG
42870	40957	GAGGTGGGAGGATCACTTGA
42871	40958	TGAGGTGGGAGGATCACTTG
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42873	40960	GGTGAGGTGGGAGGATCACT
42874	40961	GGGTGAGGTGGGAGGATCAC
42875	40962	AGGGTGAGGTGGGAGGATCA
42876	40963	TAGGGTGAGGTGGGAGGATC
42877	40964	GTAGGGTGAGGTGGGAGGAT

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91956	90043	TGATATACCTGTAAAATTAA
91957	90044	GTGATATACCTGTAAAATTA
91958	90045	GGTGATATACCTGTAAAATT
91959	90046	TGGTGATATACCTGTAAAAT
91960	90047	CTGGTGATATACCTGTAAAA
91961	90048	ACTGGTGATATACCTGTAAA
91962	90049	AACTGGTGATATACCTGTAA
91963	90050	CAACTGGTGATATACCTGTA
91964	90051	ACAACTGGTGATATACCTGT
91965	90052	AACAACTGGTGATATACCTG
91966	90053	AAACAACTGGTGATATACCT
91967	90054	GAAACAACTGGTGATATACC
91968	90055	AGAAACAACTGGTGATATAC
91969	90056	CAGAAACAACTGGTGATATA
91970	90057	TCAGAAACAACTGGTGATAT
91971	90058	TTCAGAAACAACTGGTGATA
91972	90059	GTTCAGAAACAACTGGTGAT
91973	90060	TGTTCAGAAACAACTGGTGA
91974	90061	ATGTTCAGAAACAACTGGTG
91975	90062	TATGTTCAGAAACAACTGGT
91976	90063	CTATGTTCAGAAACAACTGG
91977	90064	TCTATGTTCAGAAACAACTG
91978	90065	TTCTATGTTCAGAAACAACT
91979	90066	TTTCTATGTTCAGAAACAAC
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91981	90068	GTTTTCTATGTTCAGAAACA
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91988	90075	TCAATCTGTTTTCTATGTTC
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91991	90078	TCATCAATCTGTTTTCTATG
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91995	90082	TAAATCATCAATCTGTTTTC
91996	90083	TTAAATCATCAATCTGTTTT
91997	90084	TTTAAATCATCAATCTGTTT
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91999	90086	TCTTTAAATCATCAATCTGT
92000	90087	TTCTTTAAATCATCAATCTG
92001	90088	TTTCTTTAAATCATCAATCT
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92005	90092	TAAATTTCTTTAAATCATCA
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92007	90094	CTTAAATTTCTTTAAATCAT
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92012	90099	TCATTCTTAAATTTCTTTAA
92013	90100	ATCATTCTTAAATTTCTTTA
92014	90101	AATCATTCTTAAATTTCTTT
92015	90102	AAATCATTCTTAAATTTCTT
92016	90103	AAAATCATTCTTAAATTTCT
92017	90104	TAAAATCATTCTTAAATTTC
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92019	90106	CCTAAAATCATTCTTAAATT
92020	90107	CCCTAAAATCATTCTTAAAT
92021	90108	ACCCTAAAATCATTCTTAAA
92022	90109	TACCCTAAAATCATTCTTAA
92023	90110	TTACCCTAAAATCATTCTTA
92024	90111	CTTACCCTAAAATCATTCTT

141101	139188	TTAAAAATGTCATTTGTAAC
141102	139189	CTTAAAAATGTCATTTGTAA
141103	139190	TCTTAAAAATGTCATTTGTA
141104	139191	CTCTTAAAAATGTCATTTGT
141105	139192	CCTCTTAAAAATGTCATTTG
141106	139193	GCCTCTTAAAAATGTCATTT
141107	139194	AGCCTCTTAAAAATGTCATT
141108	139195	CAGCCTCTTAAAAATGTCAT
141109	139196	CCAGCCTCTTAAAAATGTCA
141110	139197	CCCAGCCTCTTAAAAATGTC
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141113	139200	CACCCCAGCCTCTTAAAAAT
141114	139201	CCACCCCAGCCTCTTAAAAA
141115	139202	GCCACCCCAGCCTCTTAAAA
141116	139203	CGCCACCCCAGCCTCTTAAA
141117	139204	CCGCCACCCCAGCCTCTTAA
141118	139205	ACCGCCACCCCAGCCTCTTA
141119	139206	TACCGCCACCCCAGCCTCTT
141120	139207	CTACCGCCACCCCAGCCTCT
141121	139208	CCTACCGCCACCCCAGCCTC
141122	139209	CCCTACCGCCACCCCAGCCT
141123	139210	CCCCTACCGCCACCCCAGCC
141124	139211	ACCCCTACCGCCACCCCAGC
141125	139212	AACCCCTACCGCCACCCCAG
141126	139213	TAACCCCTACCGCCACCCCA
141127	139214	CTAACCCCTACCGCCACCCC
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141129	139216	CACTAACCCCTACCGCCACC
141130	139217	GCACTAACCCCTACCGCCAC
141131	139218	AGCACTAACCCCTACCGCCA
141132	139219	TAGCACTAACCCCTACCGCC
141133	139220	TTAGCACTAACCCCTACCGC
141134	139221	ATTAGCACTAACCCCTACCG
141135	139222	CATTAGCACTAACCCCTACC
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141137	139224	ACCATTAGCACTAACCCCTA
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141139	139226	AAACCATTAGCACTAACCCC
141140	139227	TAAACCATTAGCACTAACCC
141141	139228	TTAAACCATTAGCACTAACC
141142	139229	GTTAAACCATTAGCACTAAC
141143	139230	TGTTAAACCATTAGCACTAA
141144	139231	CTGTTAAACCATTAGCACTA
141145	139232	ACTGTTAAACCATTAGCACT
141146	139233	TACTGTTAAACCATTAGCAC
141147	139234	CTACTGTTAAACCATTAGCA
141148	139235	CCTACTGTTAAACCATTAGC
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141151	139238	TCCCCTACTGTTAAACCATT
141152	139239	GTCCCCTACTGTTAAACCAT
141153	139240	GGTCCCCTACTGTTAAACCA
141154	139241	TGGTCCCCTACTGTTAAACC
141155	139242	ATGGTCCCCTACTGTTAAAC
141156	139243	CATGGTCCCCTACTGTTAAA
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141158	139245	TCCATGGTCCCCTACTGTTA
141159	139246	GTCCATGGTCCCCTACTGTT
141160	139247	TGTCCATGGTCCCCTACTGT
141161	139248	TTGTCCATGGTCCCCTACTG
141162	139249	GTTGTCCATGGTCCCCTACT
141163	139250	AGTTGTCCATGGTCCCCTAC
141164	139251	CAGTTGTCCATGGTCCCCTA
141165	139252	ACAGTTGTCCATGGTCCCCT
141166	139253	TACAGTTGTCCATGGTCCCC
141167	139254	CTACAGTTGTCCATGGTCCC
141168	139255	TCTACAGTTGTCCATGGTCC
141169	139256	GTCTACAGTTGTCCATGGTC
141170	139257	TGTCTACAGTTGTCCATGGT
141171	139258	ATGTCTACAGTTGTCCATGG

42878	40965	GGTAGGGTGAGGTGGGAGGA
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42880	40967	TTGGTAGGGTGAGGTGGGAG
42881	40968	CTTGGTAGGGTGAGGTGGGA
42882	40969	ACTTGGTAGGGTGAGGTGGG
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42884	40971	CTACTTGGTAGGGTGAGGTG
42885	40972	GCTACTTGGTAGGGTGAGGT
42886	40973	CGCTACTTGGTAGGGTGAGG
42887	40974	CCGCTACTTGGTAGGGTGAG
42888	40975	CCCGCTACTTGGTAGGGTGA
42889	40976	CCCCGCTACTTGGTAGGGTG
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42898	40985	GCCTGTGGTCCCCGCTACTT
42899	40986	CGCCTGTGGTCCCCGCTACT
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42901	40988	CACGCCTGTGGTCCCCGCTA
42902	40989	ACACGCCTGTGGTCCCCGCT
42903	40990	CACACGCCTGTGGTCCCCGC
42904	40991	GCACACGCCTGTGGTCCCCG
42905	40992	GGCACACGCCTGTGGTCCCC
42906	40993	TGGCACACGCCTGTGGTCCC
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42909	40996	TGGTGGCACACGCCTGTGGT
42910	40997	ATGGTGGCACACGCCTGTGG
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42912	40999	GCATGGTGGCACACGCCTGT
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42914	41001	AGGCATGGTGGCACACGCCT
42915	41002	CAGGCATGGTGGCACACGCC
42916	41003	CCAGGCATGGTGGCACACGC
42917	41004	GCCAGGCATGGTGGCACACG
42918	41005	AGCCAGGCATGGTGGCACAC
42919	41006	TAGCCAGGCATGGTGGCACA
42920	41007	CTAGCCAGGCATGGTGGCAC
42921	41008	ACTAGCCAGGCATGGTGGCA
42922	41009	AACTAGCCAGGCATGGTGGC
42923	41010	AAACTAGCCAGGCATGGTGG
42924	41011	AAAACTAGCCAGGCATGGTG
42925	41012	AAAAACTAGCCAGGCATGGT
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42927	41014	TAAAAAACTAGCCAGGCATG
42928	41015	ATAAAAAACTAGCCAGGCAT
42929	41016	AATAAAAAACTAGCCAGGCA
42930	41017	AAATAAAAAACTAGCCAGGC
42931	41018	AAAATAAAAAACTAGCCAGG
42932	41019	AAAAATAAAAAACTAGCCAG
42933	41020	AAAAAATAAAAAACTAGCCA
42934	41021	CAAAAAATAAAAAACTAGCC
42935	41022	ACAAAAAATAAAAAACTAGC
42936	41023	TACAAAAAATAAAAAACTAG
42937	41024	CTACAAAAAATAAAAAACTA
42938	41025	TCTACAAAAAATAAAAAACT
42939	41026	TTCTACAAAAAATAAAAAAC
42940	41027	TTTCTACAAAAAATAAAAAA
42941	41028	GTTTCTACAAAAAATAAAAA
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42943	41030	CTGTTTCTACAAAAAATAAA
42944	41031	CCTGTTTCTACAAAAAATAA
42945	41032	CCCTGTTTCTACAAAAAATA
42946	41033	ACCCTGTTTCTACAAAAAAT
42947	41034	AACCCTGTTTCTACAAAAAA
42948	41035	AAACCCTGTTTCTACAAAAA

92025	90112	ACTTACCCTAAAATCATTCT
92026	90113	TACTTACCCTAAAATCATTC
92027	90114	ATACTTACCCTAAAATCATT
92028	90115	AATACTTACCCTAAAATCAT
92029	90116	CAATACTTACCCTAAAATCA
92030	90117	ACAATACTTACCCTAAAATC
92031	90118	TACAATACTTACCCTAAAAT
92032	90119	GTACAATACTTACCCTAAAA
92033	90120	AGTACAATACTTACCCTAAA
92034	90121	TAGTACAATACTTACCCTAA
92035	90122	TTAGTACAATACTTACCCTA
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92037	90124	AGTTAGTACAATACTTACCC
92038	90125	CAGTTAGTACAATACTTACC
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92040	90127	ATCAGTTAGTACAATACTTA
92041	90128	CATCAGTTAGTACAATACTT
92042	90129	TCATCAGTTAGTACAATACT
92043	90130	TTCATCAGTTAGTACAATAC
92044	90131	ATTCATCAGTTAGTACAATA
92045	90132	AATTCATCAGTTAGTACAAT
92046	90133	AAATTCATCAGTTAGTACAA
92047	90134	CAAATTCATCAGTTAGTACA
92048	90135	TCAAATTCATCAGTTAGTAC
92049	90136	CTCAAATTCATCAGTTAGTA
92050	90137	ACTCAAATTCATCAGTTAGT
92051	90138	AACTCAAATTCATCAGTTAG
92052	90139	AAACTCAAATTCATCAGTTA
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92054	90141	TAAAACTCAAATTCATCAGT
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92056	90143	TCTAAAACTCAAATTCATCA
92057	90144	TTCTAAAACTCAAATTCATC
92058	90145	TTTCTAAAACTCAAATTCAT
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92060	90147	ATTTTCTAAAACTCAAATTC
92061	90148	TATTTTCTAAAACTCAAATT
92062	90149	TTATTTTCTAAAACTCAAAT
92063	90150	CTTATTTTCTAAAACTCAAA
92064	90151	GCTTATTTTCTAAAACTCAA
92065	90152	TGCTTATTTTCTAAAACTCA
92066	90153	ATGCTTATTTTCTAAAACTC
92067	90154	AATGCTTATTTTCTAAAACT
92068	90155	TAATGCTTATTTTCTAAAAC
92069	90156	GTAATGCTTATTTTCTAAAA
92070	90157	AGTAATGCTTATTTTCTAAA
92071	90158	TAGTAATGCTTATTTTCTAA
92072	90159	TTAGTAATGCTTATTTTCTA
92073	90160	TTTAGTAATGCTTATTTTCT
92074	90161	CTTTAGTAATGCTTATTTTC
92075	90162	TCTTTAGTAATGCTTATTTT
92076	90163	ATCTTTAGTAATGCTTATTT
92077	90164	AATCTTTAGTAATGCTTATT
92078	90165	AAATCTTTAGTAATGCTTAT
92079	90166	TAAATCTTTAGTAATGCTTA
92080	90167	ATAAATCTTTAGTAATGCTT
92081	90168	GATAAATCTTTAGTAATGCT
92082	90169	AGATAAATCTTTAGTAATGC
92083	90170	TAGATAAATCTTTAGTAATG
92084	90171	ATAGATAAATCTTTAGTAAT
92085	90172	AATAGATAAATCTTTAGTAA
92086	90173	AAATAGATAAATCTTTAGTA
92087	90174	TAAATAGATAAATCTTTAGT
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92089	90176	TATAAATAGATAAATCTTTA
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92091	90178	TTTATAAATAGATAAATCTT
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92094	90181	ATTTTTATAAATAGATAAAT
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141172	139259	GATGTCTACAGTTGTCCATG
141173	139260	TGATGTCTACAGTTGTCCAT
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141175	139262	AGTGATGTCTACAGTTGTCC
141176	139263	TAGTGATGTCTACAGTTGTC
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141178	139265	GATAGTGATGTCTACAGTTG
141179	139266	GGATAGTGATGTCTACAGTT
141180	139267	TGGATAGTGATGTCTACAGT
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141182	139269	ACTGGATAGTGATGTCTACA
141183	139270	TACTGGATAGTGATGTCTAC
141184	139271	CTACTGGATAGTGATGTCTA
141185	139272	TCTACTGGATAGTGATGTCT
141186	139273	TTCTACTGGATAGTGATGTC
141187	139274	GTTCTACTGGATAGTGATGT
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141189	139276	ATGTTCTACTGGATAGTGAT
141190	139277	AATGTTCTACTGGATAGTGA
141191	139278	AAATGTTCTACTGGATAGTG
141192	139279	AAAATGTTCTACTGGATAGT
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141194	139281	ACAAAATGTTCTACTGGATA
141195	139282	CACAAAATGTTCTACTGGAT
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141197	139284	GCCACAAAATGTTCTACTGG
141198	139285	AGCCACAAAATGTTCTACTG
141199	139286	CAGCCACAAAATGTTCTACT
141200	139287	CCAGCCACAAAATGTTCTAC
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141204	139291	GCGCCCAGCCACAAAATGTT
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141207	139294	ACCGCGCCCAGCCACAAAAT
141208	139295	CACCGCGCCCAGCCACAAAA
141209	139296	CCACCGCGCCCAGCCACAAA
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141211	139298	AGCCACCGCGCCCAGCCACA
141212	139299	GAGCCACCGCGCCCAGCCAC
141213	139300	TGAGCCACCGCGCCCAGCCA
141214	139301	GTGAGCCACCGCGCCCAGCC
141215	139302	CGTGAGCCACCGCGCCCAGC
141216	139303	GCGTGAGCCACCGCGCCCAG
141217	139304	GGCGTGAGCCACCGCGCCCA
141218	139305	AGGCGTGAGCCACCGCGCCC
141219	139306	CAGGCGTGAGCCACCGCGCC
141220	139307	ACAGGCGTGAGCCACCGCGC
141221	139308	TACAGGCGTGAGCCACCGCG
141222	139309	CTACAGGCGTGAGCCACCGC
141223	139310	ACTACAGGCGTGAGCCACCG
141224	139311	GACTACAGGCGTGAGCCACC
141225	139312	GGACTACAGGCGTGAGCCAC
141226	139313	GGGACTACAGGCGTGAGCCA
141227	139314	TGGGACTACAGGCGTGAGCC
141228	139315	CTGGGACTACAGGCGTGAGC
141229	139316	GCTGGGACTACAGGCGTGAG
141230	139317	TGCTGGGACTACAGGCGTGA
141231	139318	GTGCTGGGACTACAGGCGTG
141232	139319	AGTGCTGGGACTACAGGCGT
141233	139320	AAGTGCTGGGACTACAGGCG
141234	139321	AAAGTGCTGGGACTACAGGC
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141236	139323	CCAAAGTGCTGGGACTACAG
141237	139324	CCCAAAGTGCTGGGACTACA
141238	139325	TCCCAAAGTGCTGGGACTAC
141239	139326	CTCCCAAAGTGCTGGGACTA
141240	139327	CCTCCCAAAGTGCTGGGACT
141241	139328	GCCTCCCAAAGTGCTGGGAC
141242	139329	GGCCTCCCAAAGTGCTGGGA

42949	41036	AAAACCCTGTTTCTACAAAA
42950	41037	CAAAACCCTGTTTCTACAAA
42951	41038	GCAAAACCCTGTTTCTACAA
42952	41039	AGCAAAACCCTGTTTCTACA
42953	41040	AAGCAAAACCCTGTTTCTAC
42954	41041	AAAGCAAAACCCTGTTTCTA
42955	41042	CAAAGCAAAACCCTGTTTCT
42956	41043	ACAAAGCAAAACCCTGTTTC
42957	41044	AACAAAGCAAAACCCTGTTT
42958	41045	CAACAAAGCAAAACCCTGTT
42959	41046	GCAACAAAGCAAAACCCTGT
42960	41047	GGCAACAAAGCAAAACCCTG
42961	41048	GGGCAACAAAGCAAAACCCT
42962	41049	TGGGCAACAAAGCAAAACCC
42963	41050	CTGGGCAACAAAGCAAAACC
42964	41051	TCTGGGCAACAAAGCAAAAC
42965	41052	GTCTGGGCAACAAAGCAAAA
42966	41053	AGTCTGGGCAACAAAGCAAA
42967	41054	CAGTCTGGGCAACAAAGCAA
42968	41055	TCAGTCTGGGCAACAAAGCA
42969	41056	ATCAGTCTGGGCAACAAAGC
42970	41057	GATCAGTCTGGGCAACAAAG
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42972	41059	GAGATCAGTCTGGGCAACAA
42973	41060	TGAGATCAGTCTGGGCAACA
42974	41061	TTGAGATCAGTCTGGGCAAC
42975	41062	TTTGAGATCAGTCTGGGCAA
42976	41063	GTTTGAGATCAGTCTGGGCA
42977	41064	AGTTTGAGATCAGTCTGGGC
42978	41065	GAGTTTGAGATCAGTCTGGG
42979	41066	GGAGTTTGAGATCAGTCTGG
42980	41067	CGGAGTTTGAGATCAGTCTG
42981	41068	CCGGAGTTTGAGATCAGTCT
42982	41069	GCCGGAGTTTGAGATCAGTC
42983	41070	TGCCGGAGTTTGAGATCAGT
42984	41071	GTGCCGGAGTTTGAGATCAG
42985	41072	AGTGCCGGAGTTTGAGATCA
42986	41073	GAGTGCCGGAGTTTGAGATC
42987	41074	TGAGTGCCGGAGTTTGAGAT
42988	41075	TTGAGTGCCGGAGTTTGAGA
42989	41076	CTTGAGTGCCGGAGTTTGAG
42990	41077	ACTTGAGTGCCGGAGTTTGA
42991	41078	CACTTGAGTGCCGGAGTTTG
42992	41079	TCACTTGAGTGCCGGAGTTT
42993	41080	ATCACTTGAGTGCCGGAGTT
42994	41081	GATCACTTGAGTGCCGGAGT
42995	41082	GGATCACTTGAGTGCCGGAG
42996	41083	AGGATCACTTGAGTGCCGGA
42997	41084	GAGGATCACTTGAGTGCCGG
42998	41085	GGAGGATCACTTGAGTGCCG
42999	41086	AGGAGGATCACTTGAGTGCC
43000	41087	CAGGAGGATCACTTGAGTGC
43001	41088	GCAGGAGGATCACTTGAGTG
43002	41089	GGCAGGAGGATCACTTGAGT
43003	41090	AGGCAGGAGGATCACTTGAG
43004	41091	GAGGCAGGAGGATCACTTGA
43005	41092	TGAGGCAGGAGGATCACTTG
43006	41093	CTGAGGCAGGAGGATCACTT
43007	41094	GCTGAGGCAGGAGGATCACT
43008	41095	GGCTGAGGCAGGAGGATCAC
43009	41096	AGGCTGAGGCAGGAGGATCA
43010	41097	GAGGCTGAGGCAGGAGGATC
43011	41098	GGAGGCTGAGGCAGGAGGAT
43012	41099	AGGAGGCTGAGGCAGGAGGA
43013	41100	TAGGAGGCTGAGGCAGGAGG
43014	41101	TTAGGAGGCTGAGGCAGGAG
43015	41102	TTTAGGAGGCTGAGGCAGGA
43016	41103	CTTTAGGAGGCTGAGGCAGG
43017	41104	ACTTTAGGAGGCTGAGGCAG
43018	41105	CACTTTAGGAGGCTGAGGCA
43019	41106	GCACTTTAGGAGGCTGAGGC

92096	90183	GCATTTTTATAAATAGATAA
92097	90184	CGCATTTTTATAAATAGATA
92098	90185	ACGCATTTTTATAAATAGAT
92099	90186	AACGCATTTTTATAAATAGA
92100	90187	TAACGCATTTTTATAAATAG
92101	90188	ATAACGCATTTTTATAAATA
92102	90189	CATAACGCATTTTTATAAAT
92103	90190	ACATAACGCATTTTTATAAA
92104	90191	TACATAACGCATTTTTATAA
92105	90192	ATACATAACGCATTTTTATA
92106	90193	TATACATAACGCATTTTTAT
92107	90194	GTATACATAACGCATTTTTA
92108	90195	TGTATACATAACGCATTTTT
92109	90196	CTGTATACATAACGCATTTT
92110	90197	ACTGTATACATAACGCATTT
92111	90198	GACTGTATACATAACGCATT
92112	90199	TGACTGTATACATAACGCAT
92113	90200	CTGACTGTATACATAACGCA
92114	90201	TCTGACTGTATACATAACGC
92115	90202	TTCTGACTGTATACATAACG
92116	90203	TTTCTGACTGTATACATAAC
92117	90204	GTTTCTGACTGTATACATAA
92118	90205	TGTTTCTGACTGTATACATA
92119	90206	ATGTTTCTGACTGTATACAT
92120	90207	GATGTTTCTGACTGTATACA
92121	90208	TGATGTTTCTGACTGTATAC
92122	90209	TTGATGTTTCTGACTGTATA
92123	90210	TTTGATGTTTCTGACTGTAT
92124	90211	GTTTGATGTTTCTGACTGTA
92125	90212	GGTTTGATGTTTCTGACTGT
92126	90213	TGGTTTGATGTTTCTGACTG
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92128	90215	TATGGTTTGATGTTTCTGAC
92129	90216	ATATGGTTTGATGTTTCTGA
92130	90217	TATATGGTTTGATGTTTCTG
92131	90218	ATATATGGTTTGATGTTTCT
92132	90219	CATATATGGTTTGATGTTTC
92133	90220	ACATATATGGTTTGATGTTT
92134	90221	TACATATATGGTTTGATGTT
92135	90222	CTACATATATGGTTTGATGT
92136	90223	TCTACATATATGGTTTGATG
92137	90224	TTCTACATATATGGTTTGAT
92138	90225	TTTCTACATATATGGTTTGA
92139	90226	CTTTCTACATATATGGTTTG
92140	90227	GCTTTCTACATATATGGTTT
92141	90228	TGCTTTCTACATATATGGTT
92142	90229	CTGCTTTCTACATATATGGT
92143	90230	TCTGCTTTCTACATATATGG
92144	90231	TTCTGCTTTCTACATATATG
92145	90232	GTTCTGCTTTCTACATATAT
92146	90233	TGTTCTGCTTTCTACATATA
92147	90234	ATGTTCTGCTTTCTACATAT
92148	90235	AATGTTCTGCTTTCTACATA
92149	90236	AAATGTTCTGCTTTCTACAT
92150	90237	AAAATGTTCTGCTTTCTACA
92151	90238	AAAAATGTTCTGCTTTCTAC
92152	90239	TAAAAATGTTCTGCTTTCTA
92153	90240	TTAAAAATGTTCTGCTTTCT
92154	90241	TTTAAAAATGTTCTGCTTTC
92155	90242	CTTTAAAAATGTTCTGCTTT
92156	90243	ACTTTAAAAATGTTCTGCTT
92157	90244	CACTTTAAAAATGTTCTGCT
92158	90245	CCACTTTAAAAATGTTCTGC
92159	90246	ACCACTTTAAAAATGTTCTG
92160	90247	GACCACTTTAAAAATGTTCT
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92162	90249	AAGACCACTTTAAAAATGTT
92163	90250	AAAGACCACTTTAAAAATGT
92164	90251	CAAAGACCACTTTAAAAATG
92165	90252	GCAAAGACCACTTTAAAAAT
92166	90253	GGCAAAGACCACTTTAAAAA

141243	139330	TGGCCTCCCAAAGTGCTGGG
141244	139331	TTGGCCTCCCAAAGTGCTGG
141245	139332	CTTGGCCTCCCAAAGTGCTG
141246	139333	TCTTGGCCTCCCAAAGTGCT
141247	139334	GTCTTGGCCTCCCAAAGTGC
141248	139335	TGTCTTGGCCTCCCAAAGTG
141249	139336	TTGTCTTGGCCTCCCAAAGT
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141251	139338	ACTTGTCTTGGCCTCCCAAA
141252	139339	CACTTGTCTTGGCCTCCCAA
141253	139340	CCACTTGTCTTGGCCTCCCA
141254	139341	TCCACTTGTCTTGGCCTCCC
141255	139342	ATCCACTTGTCTTGGCCTCC
141256	139343	GATCCACTTGTCTTGGCCTC
141257	139344	TGATCCACTTGTCTTGGCCT
141258	139345	GTGATCCACTTGTCTTGGCC
141259	139346	GGTGATCCACTTGTCTTGGC
141260	139347	AGGTGATCCACTTGTCTTGG
141261	139348	CAGGTGATCCACTTGTCTTG
141262	139349	TCAGGTGATCCACTTGTCTT
141263	139350	CTCAGGTGATCCACTTGTCT
141264	139351	CCTCAGGTGATCCACTTGTC
141265	139352	ACCTCAGGTGATCCACTTGT
141266	139353	GACCTCAGGTGATCCACTTG
141267	139354	TGACCTCAGGTGATCCACTT
141268	139355	CTGACCTCAGGTGATCCACT
141269	139356	CCTGACCTCAGGTGATCCAC
141270	139357	TCCTGACCTCAGGTGATCCA
141271	139358	CTCCTGACCTCAGGTGATCC
141272	139359	ACTCCTGACCTCAGGTGATC
141273	139360	AACTCCTGACCTCAGGTGAT
141274	139361	GAACTCCTGACCTCAGGTGA
141275	139362	TGAACTCCTGACCTCAGGTG
141276	139363	TTGAACTCCTGACCTCAGGT
141277	139364	CTTGAACTCCTGACCTCAGG
141278	139365	TCTTGAACTCCTGACCTCAG
141279	139366	GTCTTGAACTCCTGACCTCA
141280	139367	GGTCTTGAACTCCTGACCTC
141281	139368	TGGTCTTGAACTCCTGACCT
141282	139369	CTGGTCTTGAACTCCTGACC
141283	139370	GCTGGTCTTGAACTCCTGAC
141284	139371	GGCTGGTCTTGAACTCCTGA
141285	139372	TGGCTGGTCTTGAACTCCTG
141286	139373	CTGGCTGGTCTTGAACTCCT
141287	139374	TCTGGCTGGTCTTGAACTCC
141288	139375	GTCTGGCTGGTCTTGAACTC
141289	139376	GGTCTGGCTGGTCTTGAACT
141290	139377	TGGTCTGGCTGGTCTTGAAC
141291	139378	TTGGTCTGGCTGGTCTTGAA
141292	139379	GTTGGTCTGGCTGGTCTTGA
141293	139380	TGTTGGTCTGGCTGGTCTTG
141294	139381	ATGTTGGTCTGGCTGGTCTT
141295	139382	CATGTTGGTCTGGCTGGTCT
141296	139383	CCATGTTGGTCTGGCTGGTC
141297	139384	ACCATGTTGGTCTGGCTGGT
141298	139385	CACCATGTTGGTCTGGCTGG
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141301	139388	TTTCACCATGTTGGTCTGGC
141302	139389	GTTTCACCATGTTGGTCTGG
141303	139390	GGTTTCACCATGTTGGTCTG
141304	139391	GGGTTTCACCATGTTGGTCT
141305	139392	AGGGTTTCACCATGTTGGTC
141306	139393	CAGGGTTTCACCATGTTGGT
141307	139394	ACAGGGTTTCACCATGTTGG
141308	139395	GACAGGGTTTCACCATGTTG
141309	139396	AGACAGGGTTTCACCATGTT
141310	139397	GAGACAGGGTTTCACCATGT
141311	139398	AGAGACAGGGTTTCACCATG
141312	139399	TAGAGACAGGGTTTCACCAT
141313	139400	GTAGAGACAGGGTTTCACCA

43020	41107	AGCACTTTAGGAGGCTGAGG
43021	41108	CAGCACTTTAGGAGGCTGAG
43022	41109	CCAGCACTTTAGGAGGCTGA
43023	41110	CCCAGCACTTTAGGAGGCTG
43024	41111	TCCCAGCACTTTAGGAGGCT
43025	41112	ATCCCAGCACTTTAGGAGGC
43026	41113	AATCCCAGCACTTTAGGAGG
43027	41114	TAATCCCAGCACTTTAGGAG
43028	41115	GTAATCCCAGCACTTTAGGA
43029	41116	TGTAATCCCAGCACTTTAGG
43030	41117	TTGTAATCCCAGCACTTTAG
43031	41118	CTTGTAATCCCAGCACTTTA
43032	41119	GCTTGTAATCCCAGCACTTT
43033	41120	TGCTTGTAATCCCAGCACTT
43034	41121	ATGCTTGTAATCCCAGCACT
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43036	41123	TCATGCTTGTAATCCCAGCA
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43039	41126	AGCTCATGCTTGTAATCCCA
43040	41127	TAGCTCATGCTTGTAATCCC
43041	41128	GTAGCTCATGCTTGTAATCC
43042	41129	GGTAGCTCATGCTTGTAATC
43043	41130	TGGTAGCTCATGCTTGTAAT
43044	41131	GTGGTAGCTCATGCTTGTAA
43045	41132	TGTGGTAGCTCATGCTTGTA
43046	41133	ATGTGGTAGCTCATGCTTGT
43047	41134	AATGTGGTAGCTCATGCTTG
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43049	41136	TGAATGTGGTAGCTCATGCT
43050	41137	CTGAATGTGGTAGCTCATGC
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43052	41139	TGCTGAATGTGGTAGCTCAT
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43054	41141	CATGCTGAATGTGGTAGCTC
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43056	41143	TACATGCTGAATGTGGTAGC
43057	41144	TTACATGCTGAATGTGGTAG
43058	41145	TTTACATGCTGAATGTGGTA
43059	41146	ATTTACATGCTGAATGTGGT
43060	41147	AATTTACATGCTGAATGTGG
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43072	41159	TTAATATAAAGAAATTTACA
43073	41160	ATTAATATAAAGAAATTTAC
43074	41161	AATTAATATAAAGAAATTTA
43075	41162	AAATTAATATAAAGAAATTT
43076	41163	CAAATTAATATAAAGAAATT
43077	41164	TCAAATTAATATAAAGAAAT
43078	41165	GTCAAATTAATATAAAGAAA
43079	41166	AGTCAAATTAATATAAAGAA
43080	41167	CAGTCAAATTAATATAAAGA
43081	41168	CCAGTCAAATTAATATAAAG
43082	41169	GCCAGTCAAATTAATATAAA
43083	41170	TGCCAGTCAAATTAATATAA
43084	41171	ATGCCAGTCAAATTAATATA
43085	41172	AATGCCAGTCAAATTAATAT
43086	41173	AAATGCCAGTCAAATTAATA
43087	41174	AAAATGCCAGTCAAATTAAT
43088	41175	TAAAATGCCAGTCAAATTAA
43089	41176	TTAAAATGCCAGTCAAATTA
43090	41177	CTTAAAATGCCAGTCAAATT

92167	90254	AGGCAAAGACCACTTTAAAA
92168	90255	TAGGCAAAGACCACTTTAAA
92169	90256	ATAGGCAAAGACCACTTTAA
92170	90257	GATAGGCAAAGACCACTTTA
92171	90258	GGATAGGCAAAGACCACTTT
92172	90259	AGGATAGGCAAAGACCACTT
92173	90260	AAGGATAGGCAAAGACCACT
92174	90261	AAAGGATAGGCAAAGACCAC
92175	90262	TAAAGGATAGGCAAAGACCA
92176	90263	TTAAAGGATAGGCAAAGACC
92177	90264	CTTAAAGGATAGGCAAAGAC
92178	90265	ACTTAAAGGATAGGCAAAGA
92179	90266	CACTTAAAGGATAGGCAAAG
92180	90267	CCACTTAAAGGATAGGCAAA
92181	90268	CCCACTTAAAGGATAGGCAA
92182	90269	TCCCACTTAAAGGATAGGCA
92183	90270	ATCCCACTTAAAGGATAGGC
92184	90271	TATCCCACTTAAAGGATAGG
92185	90272	TTATCCCACTTAAAGGATAG
92186	90273	GTTATCCCACTTAAAGGATA
92187	90274	AGTTATCCCACTTAAAGGAT
92188	90275	TAGTTATCCCACTTAAAGGA
92189	90276	TTAGTTATCCCACTTAAAGG
92190	90277	TTTAGTTATCCCACTTAAAG
92191	90278	TTTTAGTTATCCCACTTAAA
92192	90279	ATTTTAGTTATCCCACTTAA
92193	90280	GATTTTAGTTATCCCACTTA
92194	90281	TGATTTTAGTTATCCCACTT
92195	90282	ATGATTTTAGTTATCCCACT
92196	90283	CATGATTTTAGTTATCCCAC
92197	90284	TCATGATTTTAGTTATCCCA
92198	90285	CTCATGATTTTAGTTATCCC
92199	90286	TCTCATGATTTTAGTTATCC
92200	90287	ATCTCATGATTTTAGTTATC
92201	90288	AATCTCATGATTTTAGTTAT
92202	90289	AAATCTCATGATTTTAGTTA
92203	90290	CAAATCTCATGATTTTAGTT
92204	90291	CCAAATCTCATGATTTTAGT
92205	90292	ACCAAATCTCATGATTTTAG
92206	90293	TACCAAATCTCATGATTTTA
92207	90294	TTACCAAATCTCATGATTTT
92208	90295	GTTACCAAATCTCATGATTT
92209	90296	TGTTACCAAATCTCATGATT
92210	90297	TTGTTACCAAATCTCATGAT
92211	90298	GTTGTTACCAAATCTCATGA
92212	90299	TGTTGTTACCAAATCTCATG
92213	90300	TTGTTGTTACCAAATCTCAT
92214	90301	ATTGTTGTTACCAAATCTCA
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92217	90304	CATATTGTTGTTACCAAATC
92218	90305	ACATATTGTTGTTACCAAAT
92219	90306	TACATATTGTTGTTACCAAA
92220	90307	CTACATATTGTTGTTACCAA
92221	90308	CCTACATATTGTTGTTACCA
92222	90309	ACCTACATATTGTTGTTACC
92223	90310	TACCTACATATTGTTGTTAC
92224	90311	ATACCTACATATTGTTGTTA
92225	90312	GATACCTACATATTGTTGTT
92226	90313	TGATACCTACATATTGTTGT
92227	90314	TTGATACCTACATATTGTTG
92228	90315	TTTGATACCTACATATTGTT
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92233	90320	TCTCATTTGATACCTACATA
92234	90321	CTCTCATTTGATACCTACAT
92235	90322	ACTCTCATTTGATACCTACA
92236	90323	TACTCTCATTTGATACCTAC
92237	90324	ATACTCTCATTTGATACCTA

141314	139401	AGTAGAGACAGGGTTTCACC
141315	139402	TAGTAGAGACAGGGTTTCAC
141316	139403	TTAGTAGAGACAGGGTTTCA
141317	139404	TTTAGTAGAGACAGGGTTTC
141318	139405	TTTTAGTAGAGACAGGGTTT
141319	139406	TTTTTAGTAGAGACAGGGTT
141320	139407	ATTTTTAGTAGAGACAGGGT
141321	139408	TATTTTTAGTAGAGACAGGG
141322	139409	GTATTTTTAGTAGAGACAGG
141323	139410	TGTATTTTTAGTAGAGACAG
141324	139411	TTGTATTTTTAGTAGAGACA
141325	139412	TTTGTATTTTTAGTAGAGAC
141326	139413	TTTTGTATTTTTAGTAGAGA
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141329	139416	CTTTTTTGTATTTTTAGTAG
141330	139417	ACTTTTTTGTATTTTTAGTA
141331	139418	AACTTTTTTGTATTTTTAGT
141332	139419	TAACTTTTTTGTATTTTTAG
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141335	139422	GGCTAACTTTTTTGTATTTT
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141337	139424	CTGGCTAACTTTTTTGTATT
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141339	139426	GCCTGGCTAACTTTTTTGTA
141340	139427	CGCCTGGCTAACTTTTTTGT
141341	139428	GCGCCTGGCTAACTTTTTTG
141342	139429	CGCGCCTGGCTAACTTTTTT
141343	139430	GCGCGCCTGGCTAACTTTTT
141344	139431	GGCGCGCCTGGCTAACTTTT
141345	139432	AGGCGCGCCTGGCTAACTTT
141346	139433	CAGGCGCGCCTGGCTAACTT
141347	139434	ACAGGCGCGCCTGGCTAACT
141348	139435	TACAGGCGCGCCTGGCTAAC
141349	139436	CTACAGGCGCGCCTGGCTAA
141350	139437	ACTACAGGCGCGCCTGGCTA
141351	139438	GACTACAGGCGCGCCTGGCT
141352	139439	GGACTACAGGCGCGCCTGGC
141353	139440	AGGACTACAGGCGCGCCTGG
141354	139441	TAGGACTACAGGCGCGCCTG
141355	139442	CTAGGACTACAGGCGCGCCT
141356	139443	GCTAGGACTACAGGCGCGCC
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141358	139445	TAGCTAGGACTACAGGCGCG
141359	139446	GTAGCTAGGACTACAGGCGC
141360	139447	AGTAGCTAGGACTACAGGCG
141361	139448	GAGTAGCTAGGACTACAGGC
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141363	139450	CTGAGTAGCTAGGACTACAG
141364	139451	CCTGAGTAGCTAGGACTACA
141365	139452	TCCTGAGTAGCTAGGACTAC
141366	139453	CTCCTGAGTAGCTAGGACTA
141367	139454	CCTCCTGAGTAGCTAGGACT
141368	139455	GCCTCCTGAGTAGCTAGGAC
141369	139456	AGCCTCCTGAGTAGCTAGGA
141370	139457	CAGCCTCCTGAGTAGCTAGG
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141372	139459	GTCAGCCTCCTGAGTAGCTA
141373	139460	TGTCAGCCTCCTGAGTAGCT
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141381	139468	TTCTCCTGTGTCAGCCTCCT
141382	139469	ATTCTCCTGTGTCAGCCTCC
141383	139470	GATTCTCCTGTGTCAGCCTC
141384	139471	CGATTCTCCTGTGTCAGCCT

43091	41178	ACTTAAAATGCCAGTCAAAT
43092	41179	GACTTAAAATGCCAGTCAAA
43093	41180	TGACTTAAAATGCCAGTCAA
43094	41181	GTGACTTAAAATGCCAGTCA
43095	41182	TGTGACTTAAAATGCCAGTC
43096	41183	GTGTGACTTAAAATGCCAGT
43097	41184	AGTGTGACTTAAAATGCCAG
43098	41185	AAGTGTGACTTAAAATGCCA
43099	41186	CAAGTGTGACTTAAAATGCC
43100	41187	TCAAGTGTGACTTAAAATGC
43101	41188	TTCAAGTGTGACTTAAAATG
43102	41189	ATTCAAGTGTGACTTAAAAT
43103	41190	AATTCAAGTGTGACTTAAAA
43104	41191	AAATTCAAGTGTGACTTAAA
43105	41192	GAAATTCAAGTGTGACTTAA
43106	41193	TGAAATTCAAGTGTGACTTA
43107	41194	ATGAAATTCAAGTGTGACTT
43108	41195	TATGAAATTCAAGTGTGACT
43109	41196	ATATGAAATTCAAGTGTGAC
43110	41197	AATATGAAATTCAAGTGTGA
43111	41198	AAATATGAAATTCAAGTGTG
43112	41199	CAAATATGAAATTCAAGTGT
43113	41200	CCAAATATGAAATTCAAGTG
43114	41201	GCCAAATATGAAATTCAAGT
43115	41202	TGCCAAATATGAAATTCAAG
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43119	41206	TAGTTGCCAAATATGAAATT
43120	41207	ATAGTTGCCAAATATGAAAT
43121	41208	AATAGTTGCCAAATATGAAA
43122	41209	TAATAGTTGCCAAATATGAA
43123	41210	TTAATAGTTGCCAAATATGA
43124	41211	TTTAATAGTTGCCAAATATG
43125	41212	TTTTAATAGTTGCCAAATAT
43126	41213	CTTTTAATAGTTGCCAAATA
43127	41214	GCTTTTAATAGTTGCCAAAT
43128	41215	TGCTTTTAATAGTTGCCAAA
43129	41216	ATGCTTTTAATAGTTGCCAA
43130	41217	TATGCTTTTAATAGTTGCCA
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43132	41219	TCTATGCTTTTAATAGTTGC
43133	41220	CTCTATGCTTTTAATAGTTG
43134	41221	ACTCTATGCTTTTAATAGTT
43135	41222	GACTCTATGCTTTTAATAGT
43136	41223	GGACTCTATGCTTTTAATAG
43137	41224	AGGACTCTATGCTTTTAATA
43138	41225	CAGGACTCTATGCTTTTAAT
43139	41226	CCAGGACTCTATGCTTTTAA
43140	41227	TCCAGGACTCTATGCTTTTA
43141	41228	ATCCAGGACTCTATGCTTTT
43142	41229	TATCCAGGACTCTATGCTTT
43143	41230	ATATCCAGGACTCTATGCTT
43144	41231	AATATCCAGGACTCTATGCT
43145	41232	TAATATCCAGGACTCTATGC
43146	41233	CTAATATCCAGGACTCTATG
43147	41234	ACTAATATCCAGGACTCTAT
43148	41235	CACTAATATCCAGGACTCTA
43149	41236	ACACTAATATCCAGGACTCT
43150	41237	AACACTAATATCCAGGACTC
43151	41238	AAACACTAATATCCAGGACT
43152	41239	AAAACACTAATATCCAGGAC
43153	41240	CAAAACACTAATATCCAGGA
43154	41241	ACAAAACACTAATATCCAGG
43155	41242	AACAAAACACTAATATCCAG
43156	41243	TAACAAAACACTAATATCCA
43157	41244	TTAACAAAACACTAATATCC
43158	41245	TTTAACAAAACACTAATATC
43159	41246	GTTTAACAAAACACTAATAT
43160	41247	GGTTTAACAAAACACTAATA
43161	41248	AGGTTTAACAAAACACTAAT

92238	90325	TATACTCTCATTTGATACCT
92239	90326	CTATACTCTCATTTGATACC
92240	90327	GCTATACTCTCATTTGATAC
92241	90328	GGCTATACTCTCATTTGATA
92242	90329	GGGCTATACTCTCATTTGAT
92243	90330	AGGGCTATACTCTCATTTGA
92244	90331	CAGGGCTATACTCTCATTTG
92245	90332	TCAGGGCTATACTCTCATTT
92246	90333	GTCAGGGCTATACTCTCATT
92247	90334	TGTCAGGGCTATACTCTCAT
92248	90335	ATGTCAGGGCTATACTCTCA
92249	90336	AATGTCAGGGCTATACTCTC
92250	90337	AAATGTCAGGGCTATACTCT
92251	90338	CAAATGTCAGGGCTATACTC
92252	90339	TCAAATGTCAGGGCTATACT
92253	90340	TTCAAATGTCAGGGCTATAC
92254	90341	TTTCAAATGTCAGGGCTATA
92255	90342	GTTTCAAATGTCAGGGCTAT
92256	90343	GGTTTCAAATGTCAGGGCTA
92257	90344	TGGTTTCAAATGTCAGGGCT
92258	90345	GTGGTTTCAAATGTCAGGGC
92259	90346	GGTGGTTTCAAATGTCAGGG
92260	90347	TGGTGGTTTCAAATGTCAGG
92261	90348	ATGGTGGTTTCAAATGTCAG
92262	90349	TATGGTGGTTTCAAATGTCA
92263	90350	CTATGGTGGTTTCAAATGTC
92264	90351	GCTATGGTGGTTTCAAATGT
92265	90352	TGCTATGGTGGTTTCAAATG
92266	90353	GTGCTATGGTGGTTTCAAAT
92267	90354	TGTGCTATGGTGGTTTCAAA
92268	90355	CTGTGCTATGGTGGTTTCAA
92269	90356	GCTGTGCTATGGTGGTTTCA
92270	90357	AGCTGTGCTATGGTGGTTTC
92271	90358	AAGCTGTGCTATGGTGGTTT
92272	90359	TAAGCTGTGCTATGGTGGTT
92273	90360	GTAAGCTGTGCTATGGTGGT
92274	90361	AGTAAGCTGTGCTATGGTGG
92275	90362	TAGTAAGCTGTGCTATGGTG
92276	90363	ATAGTAAGCTGTGCTATGGT
92277	90364	AATAGTAAGCTGTGCTATGG
92278	90365	AAATAGTAAGCTGTGCTATG
92279	90366	CAAATAGTAAGCTGTGCTAT
92280	90367	TCAAATAGTAAGCTGTGCTA
92281	90368	ATCAAATAGTAAGCTGTGCT
92282	90369	CATCAAATAGTAAGCTGTGC
92283	90370	CCATCAAATAGTAAGCTGTG
92284	90371	ACCATCAAATAGTAAGCTGT
92285	90372	GACCATCAAATAGTAAGCTG
92286	90373	TGACCATCAAATAGTAAGCT
92287	90374	ATGACCATCAAATAGTAAGC
92288	90375	AATGACCATCAAATAGTAAG
92289	90376	AAATGACCATCAAATAGTAA
92290	90377	CAAATGACCATCAAATAGTA
92291	90378	ACAAATGACCATCAAATAGT
92292	90379	TACAAATGACCATCAAATAG
92293	90380	GTACAAATGACCATCAAATA
92294	90381	AGTACAAATGACCATCAAAT
92295	90382	AAGTACAAATGACCATCAAA
92296	90383	AAAGTACAAATGACCATCAA
92297	90384	CAAAGTACAAATGACCATCA
92298	90385	ACAAAGTACAAATGACCATC
92299	90386	AACAAAGTACAAATGACCAT
92300	90387	GAACAAAGTACAAATGACCA
92301	90388	TGAACAAAGTACAAATGACC
92302	90389	CTGAACAAAGTACAAATGAC
92303	90390	ACTGAACAAAGTACAAATGA
92304	90391	CACTGAACAAAGTACAAATG
92305	90392	TCACTGAACAAAGTACAAAT
92306	90393	TTCACTGAACAAAGTACAAA
92307	90394	CTTCACTGAACAAAGTACAA
92308	90395	GCTTCACTGAACAAAGTACA

141385	139472	GCGATTCTCCTGTGTCAGCC
141386	139473	AGCGATTCTCCTGTGTCAGC
141387	139474	AAGCGATTCTCCTGTGTCAG
141388	139475	CAAGCGATTCTCCTGTGTCA
141389	139476	TCAAGCGATTCTCCTGTGTC
141390	139477	TTCAAGCGATTCTCCTGTGT
141391	139478	GTTCAAGCGATTCTCCTGTG
141392	139479	GGTTCAAGCGATTCTCCTGT
141393	139480	GGGTTCAAGCGATTCTCCTG
141394	139481	CGGGTTCAAGCGATTCTCCT
141395	139482	CCGGGTTCAAGCGATTCTCC
141396	139483	CCCGGGTTCAAGCGATTCTC
141397	139484	TCCCGGGTTCAAGCGATTCT
141398	139485	CTCCCGGGTTCAAGCGATTC
141399	139486	CCTCCCGGGTTCAAGCGATT
141400	139487	GCCTCCCGGGTTCAAGCGAT
141401	139488	TGCCTCCCGGGTTCAAGCGA
141402	139489	CTGCCTCCCGGGTTCAAGCG
141403	139490	TCTGCCTCCCGGGTTCAAGC
141404	139491	CTCTGCCTCCCGGGTTCAAG
141405	139492	CCTCTGCCTCCCGGGTTCAA
141406	139493	ACCTCTGCCTCCCGGGTTCA
141407	139494	AACCTCTGCCTCCCGGGTTC
141408	139495	CAACCTCTGCCTCCCGGGTT
141409	139496	GCAACCTCTGCCTCCCGGGT
141410	139497	CGCAACCTCTGCCTCCCGGG
141411	139498	CCGCAACCTCTGCCTCCCGG
141412	139499	ACCGCAACCTCTGCCTCCCG
141413	139500	CACCGCAACCTCTGCCTCCC
141414	139501	TCACCGCAACCTCTGCCTCC
141415	139502	CTCACCGCAACCTCTGCCTC
141416	139503	GCTCACCGCAACCTCTGCCT
141417	139504	AGCTCACCGCAACCTCTGCC
141418	139505	CAGCTCACCGCAACCTCTGC
141419	139506	TCAGCTCACCGCAACCTCTG
141420	139507	ATCAGCTCACCGCAACCTCT
141421	139508	TATCAGCTCACCGCAACCTC
141422	139509	ATATCAGCTCACCGCAACCT
141423	139510	GATATCAGCTCACCGCAACC
141424	139511	TGATATCAGCTCACCGCAAC
141425	139512	GTGATATCAGCTCACCGCAA
141426	139513	CGTGATATCAGCTCACCGCA
141427	139514	GCGTGATATCAGCTCACCGC
141428	139515	GGCGTGATATCAGCTCACCG
141429	139516	TGGCGTGATATCAGCTCACC
141430	139517	GTGGCGTGATATCAGCTCAC
141431	139518	AGTGGCGTGATATCAGCTCA
141432	139519	CAGTGGCGTGATATCAGCTC
141433	139520	GCAGTGGCGTGATATCAGCT
141434	139521	TGCAGTGGCGTGATATCAGC
141435	139522	GTGCAGTGGCGTGATATCAG
141436	139523	AGTGCAGTGGCGTGATATCA
141437	139524	GAGTGCAGTGGCGTGATATC
141438	139525	GGAGTGCAGTGGCGTGATAT
141439	139526	TGGAGTGCAGTGGCGTGATA
141440	139527	GTGGAGTGCAGTGGCGTGAT
141441	139528	GGTGGAGTGCAGTGGCGTGA
141442	139529	GGGTGGAGTGCAGTGGCGTG
141443	139530	AGGGTGGAGTGCAGTGGCGT
141444	139531	CAGGGTGGAGTGCAGTGGCG
141445	139532	CCAGGGTGGAGTGCAGTGGC
141446	139533	CCCAGGGTGGAGTGCAGTGG
141447	139534	GCCCAGGGTGGAGTGCAGTG
141448	139535	TGCCCAGGGTGGAGTGCAGT
141449	139536	TTGCCCAGGGTGGAGTGCAG
141450	139537	GTTGCCCAGGGTGGAGTGCA
141451	139538	TGTTGCCCAGGGTGGAGTGC
141452	139539	CTGTTGCCCAGGGTGGAGTG
141453	139540	TCTGTTGCCCAGGGTGGAGT
141454	139541	CTCTGTTGCCCAGGGTGGAG
141455	139542	GCTCTGTTGCCCAGGGTGGA

43162	41249	CAGGTTTAACAAAACACTAA
43163	41250	TCAGGTTTAACAAAACACTA
43164	41251	ATCAGGTTTAACAAAACACT
43165	41252	GATCAGGTTTAACAAAACAC
43166	41253	AGATCAGGTTTAACAAAACA
43167	41254	TAGATCAGGTTTAACAAAAC
43168	41255	ATAGATCAGGTTTAACAAAA
43169	41256	GATAGATCAGGTTTAACAAA
43170	41257	AGATAGATCAGGTTTAACAA
43171	41258	TAGATAGATCAGGTTTAACA
43172	41259	TTAGATAGATCAGGTTTAAC
43173	41260	ATTAGATAGATCAGGTTTAA
43174	41261	GATTAGATAGATCAGGTTTA
43175	41262	TGATTAGATAGATCAGGTTT
43176	41263	ATGATTAGATAGATCAGGTT
43177	41264	TATGATTAGATAGATCAGGT
43178	41265	TTATGATTAGATAGATCAGG
43179	41266	TTTATGATTAGATAGATCAG
43180	41267	ATTTATGATTAGATAGATCA
43181	41268	TATTTATGATTAGATAGATC
43182	41269	ATATTTATGATTAGATAGAT
43183	41270	TATATTTATGATTAGATAGA
43184	41271	GTATATTTATGATTAGATAG
43185	41272	AGTATATTTATGATTAGATA
43186	41273	AAGTATATTTATGATTAGAT
43187	41274	TAAGTATATTTATGATTAGA
43188	41275	CTAAGTATATTTATGATTAG
43189	41276	CCTAAGTATATTTATGATTA
43190	41277	ACCTAAGTATATTTATGATT
43191	41278	GACCTAAGTATATTTATGAT
43192	41279	AGACCTAAGTATATTTATGA
43193	41280	TAGACCTAAGTATATTTATG
43194	41281	TTAGACCTAAGTATATTTAT
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43198	41285	TATTTTAGACCTAAGTATAT
43199	41286	ATATTTTAGACCTAAGTATA
43200	41287	CATATTTTAGACCTAAGTAT
43201	41288	GCATATTTTAGACCTAAGTA
43202	41289	AGCATATTTTAGACCTAAGT
43203	41290	GAGCATATTTTAGACCTAAG
43204	41291	AGAGCATATTTTAGACCTAA
43205	41292	AAGAGCATATTTTAGACCTA
43206	41293	CAAGAGCATATTTTAGACCT
43207	41294	CCAAGAGCATATTTTAGACC
43208	41295	GCCAAGAGCATATTTTAGAC
43209	41296	GGCCAAGAGCATATTTTAGA
43210	41297	AGGCCAAGAGCATATTTTAG
43211	41298	AAGGCCAAGAGCATATTTTA
43212	41299	AAAGGCCAAGAGCATATTTT
43213	41300	CAAAGGCCAAGAGCATATTT
43214	41301	ACAAAGGCCAAGAGCATATT
43215	41302	AACAAAGGCCAAGAGCATAT
43216	41303	AAACAAAGGCCAAGAGCATA
43217	41304	TAAACAAAGGCCAAGAGCAT
43218	41305	ATAAACAAAGGCCAAGAGCA
43219	41306	AATAAACAAAGGCCAAGAGC
43220	41307	CAATAAACAAAGGCCAAGAG
43221	41308	GCAATAAACAAAGGCCAAGA
43222	41309	CGCAATAAACAAAGGCCAAG
43223	41310	CCGCAATAAACAAAGGCCAA
43224	41311	ACCGCAATAAACAAAGGCCA
43225	41312	AACCGCAATAAACAAAGGCC
43226	41313	GAACCGCAATAAACAAAGGC
43227	41314	TGAACCGCAATAAACAAAGG
43228	41315	CTGAACCGCAATAAACAAAG
43229	41316	ACTGAACCGCAATAAACAAA
43230	41317	TACTGAACCGCAATAAACAA
43231	41318	ATACTGAACCGCAATAAACA
43232	41319	AATACTGAACCGCAATAAAC

92309	90396	AGCTTCACTGAACAAAGTAC
92310	90397	TAGCTTCACTGAACAAAGTA
92311	90398	CTAGCTTCACTGAACAAAGT
92312	90399	TCTAGCTTCACTGAACAAAG
92313	90400	ATCTAGCTTCACTGAACAAA
92314	90401	TATCTAGCTTCACTGAACAA
92315	90402	ATATCTAGCTTCACTGAACA
92316	90403	AATATCTAGCTTCACTGAAC
92317	90404	TAATATCTAGCTTCACTGAA
92318	90405	CTAATATCTAGCTTCACTGA
92319	90406	ACTAATATCTAGCTTCACTG
92320	90407	TACTAATATCTAGCTTCACT
92321	90408	CTACTAATATCTAGCTTCAC
92322	90409	TCTACTAATATCTAGCTTCA
92323	90410	CTCTACTAATATCTAGCTTC
92324	90411	GCTCTACTAATATCTAGCTT
92325	90412	TGCTCTACTAATATCTAGCT
92326	90413	TTGCTCTACTAATATCTAGC
92327	90414	CTTGCTCTACTAATATCTAG
92328	90415	CCTTGCTCTACTAATATCTA
92329	90416	GCCTTGCTCTACTAATATCT
92330	90417	GGCCTTGCTCTACTAATATC
92331	90418	TGGCCTTGCTCTACTAATAT
92332	90419	TTGGCCTTGCTCTACTAATA
92333	90420	CTTGGCCTTGCTCTACTAAT
92334	90421	ACTTGGCCTTGCTCTACTAA
92335	90422	GACTTGGCCTTGCTCTACTA
92336	90423	TGACTTGGCCTTGCTCTACT
92337	90424	ATGACTTGGCCTTGCTCTAC
92338	90425	AATGACTTGGCCTTGCTCTA
92339	90426	TAATGACTTGGCCTTGCTCT
92340	90427	TTAATGACTTGGCCTTGCTC
92341	90428	ATTAATGACTTGGCCTTGCT
92342	90429	TATTAATGACTTGGCCTTGC
92343	90430	TTATTAATGACTTGGCCTTG
92344	90431	ATTATTAATGACTTGGCCTT
92345	90432	GATTATTAATGACTTGGCCT
92346	90433	AGATTATTAATGACTTGGCC
92347	90434	TAGATTATTAATGACTTGGC
92348	90435	CTAGATTATTAATGACTTGG
92349	90436	ACTAGATTATTAATGACTTG
92350	90437	CACTAGATTATTAATGACTT
92351	90438	ACACTAGATTATTAATGACT
92352	90439	CACACTAGATTATTAATGAC
92353	90440	CCACACTAGATTATTAATGA
92354	90441	GCCACACTAGATTATTAATG
92355	90442	TGCCACACTAGATTATTAAT
92356	90443	TTGCCACACTAGATTATTAA
92357	90444	TTTGCCACACTAGATTATTA
92358	90445	ATTTGCCACACTAGATTATT
92359	90446	CATTTGCCACACTAGATTAT
92360	90447	CCATTTGCCACACTAGATTA
92361	90448	TCCATTTGCCACACTAGATT
92362	90449	TTCCATTTGCCACACTAGAT
92363	90450	CTTCCATTTGCCACACTAGA
92364	90451	TCTTCCATTTGCCACACTAG
92365	90452	ATCTTCCATTTGCCACACTA
92366	90453	CATCTTCCATTTGCCACACT
92367	90454	ACATCTTCCATTTGCCACAC
92368	90455	TACATCTTCCATTTGCCACA
92369	90456	GTACATCTTCCATTTGCCAC
92370	90457	AGTACATCTTCCATTTGCCA
92371	90458	CAGTACATCTTCCATTTGCC
92372	90459	CCAGTACATCTTCCATTTGC
92373	90460	TCCAGTACATCTTCCATTTG
92374	90461	GTCCAGTACATCTTCCATTT
92375	90462	AGTCCAGTACATCTTCCATT
92376	90463	GAGTCCAGTACATCTTCCAT
92377	90464	AGAGTCCAGTACATCTTCCA
92378	90465	CAGAGTCCAGTACATCTTCC
92379	90466	CCAGAGTCCAGTACATCTTC

141456	139543	CGCTCTGTTGCCCAGGGTGG
141457	139544	TCGCTCTGTTGCCCAGGGTG
141458	139545	CTCGCTCTGTTGCCCAGGGT
141459	139546	TCTCGCTCTGTTGCCCAGGG
141460	139547	GTCTCGCTCTGTTGCCCAGG
141461	139548	AGTCTCGCTCTGTTGCCCAG
141462	139549	GAGTCTCGCTCTGTTGCCCA
141463	139550	GGAGTCTCGCTCTGTTGCCC
141464	139551	CGGAGTCTCGCTCTGTTGCC
141465	139552	ACGGAGTCTCGCTCTGTTGC
141466	139553	GACGGAGTCTCGCTCTGTTG
141467	139554	AGACGGAGTCTCGCTCTGTT
141468	139555	GAGACGGAGTCTCGCTCTGT
141469	139556	TGAGACGGAGTCTCGCTCTG
141470	139557	TTGAGACGGAGTCTCGCTCT
141471	139558	TTTGAGACGGAGTCTCGCTC
141472	139559	TTTTGAGACGGAGTCTCGCT
141473	139560	GTTTTGAGACGGAGTCTCGC
141474	139561	TGTTTTGAGACGGAGTCTCG
141475	139562	TTGTTTTGAGACGGAGTCTC
141476	139563	GTTGTTTTGAGACGGAGTCT
141477	139564	TGTTGTTTTGAGACGGAGTC
141478	139565	TTGTTGTTTTGAGACGGAGT
141479	139566	GTTGTTGTTTTGAGACGGAG
141480	139567	TGTTGTTGTTTTGAGACGGA
141481	139568	TTGTTGTTGTTTTGAGACGG
141482	139569	TTTGTTGTTGTTTTGAGACG
141483	139570	TTTTGTTGTTGTTTTGAGAC
141484	139571	GTTTTGTTGTTGTTTTGAGA
141485	139572	AGTTTTGTTGTTGTTTTGAG
141486	139573	CAGTTTTGTTGTTGTTTTGA
141487	139574	GCAGTTTTGTTGTTGTTTTG
141488	139575	TGCAGTTTTGTTGTTGTTTT
141489	139576	GTGCAGTTTTGTTGTTGTTT
141490	139577	AGTGCAGTTTTGTTGTTGTT
141491	139578	CAGTGCAGTTTTGTTGTTGT
141492	139579	ACAGTGCAGTTTTGTTGTTG
141493	139580	GACAGTGCAGTTTTGTTGTT
141494	139581	GGACAGTGCAGTTTTGTTGT
141495	139582	TGGACAGTGCAGTTTTGTTG
141496	139583	GTGGACAGTGCAGTTTTGTT
141497	139584	GGTGGACAGTGCAGTTTTGT
141498	139585	CGGTGGACAGTGCAGTTTTG
141499	139586	ACGGTGGACAGTGCAGTTTT
141500	139587	TACGGTGGACAGTGCAGTTT
141501	139588	ATACGGTGGACAGTGCAGTT
141502	139589	AATACGGTGGACAGTGCAGT
141503	139590	TAATACGGTGGACAGTGCAG
141504	139591	CTAATACGGTGGACAGTGCA
141505	139592	GCTAATACGGTGGACAGTGC
141506	139593	AGCTAATACGGTGGACAGTG
141507	139594	TAGCTAATACGGTGGACAGT
141508	139595	GTAGCTAATACGGTGGACAG
141509	139596	AGTAGCTAATACGGTGGACA
141510	139597	AAGTAGCTAATACGGTGGAC
141511	139598	TAAGTAGCTAATACGGTGGA
141512	139599	CTAAGTAGCTAATACGGTGG
141513	139600	GCTAAGTAGCTAATACGGTG
141514	139601	AGCTAAGTAGCTAATACGGT
141515	139602	TAGCTAAGTAGCTAATACGG
141516	139603	GTAGCTAAGTAGCTAATACG
141517	139604	TGTAGCTAAGTAGCTAATAC
141518	139605	ATGTAGCTAAGTAGCTAATA
141519	139606	CATGTAGCTAAGTAGCTAAT
141520	139607	ACATGTAGCTAAGTAGCTAA
141521	139608	CACATGTAGCTAAGTAGCTA
141522	139609	CCACATGTAGCTAAGTAGCT
141523	139610	GCCACATGTAGCTAAGTAGC
141524	139611	AGCCACATGTAGCTAAGTAG
141525	139612	AAGCCACATGTAGCTAAGTA
141526	139613	AAAGCCACATGTAGCTAAGT

43233	41320	AAATACTGAACCGCAATAAA
43234	41321	CAAATACTGAACCGCAATAA
43235	41322	ACAAATACTGAACCGCAATA
43236	41323	AACAAATACTGAACCGCAAT
43237	41324	TAACAAATACTGAACCGCAA
43238	41325	GTAACAAATACTGAACCGCA
43239	41326	AGTAACAAATACTGAACCGC
43240	41327	TAGTAACAAATACTGAACCG
43241	41328	ATAGTAACAAATACTGAACC
43242	41329	TATAGTAACAAATACTGAAC
43243	41330	ATATAGTAACAAATACTGAA
43244	41331	AATATAGTAACAAATACTGA
43245	41332	TAATATAGTAACAAATACTG
43246	41333	TTAATATAGTAACAAATACT
43247	41334	TTTAATATAGTAACAAATAC
43248	41335	ATTTAATATAGTAACAAATA
43249	41336	TATTTAATATAGTAACAAAT
43250	41337	CTATTTAATATAGTAACAAA
43251	41338	ACTATTTAATATAGTAACAA
43252	41339	TACTATTTAATATAGTAACA
43253	41340	TTACTATTTAATATAGTAAC
43254	41341	TTTACTATTTAATATAGTAA
43255	41342	TTTTACTATTTAATATAGTA
43256	41343	ATTTTACTATTTAATATAGT
43257	41344	TATTTTACTATTTAATATAG
43258	41345	ATATTTTACTATTTAATATA
43259	41346	AATATTTTACTATTTAATAT
43260	41347	AAATATTTTACTATTTAATA
43261	41348	CAAATATTTTACTATTTAAT
43262	41349	CCAAATATTTTACTATTTAA
43263	41350	ACCAAATATTTTACTATTTA
43264	41351	AACCAAATATTTTACTATTT
43265	41352	AAACCAAATATTTTACTATT
43266	41353	CAAACCAAATATTTTACTAT
43267	41354	TCAAACCAAATATTTTACTA
43268	41355	CTCAAACCAAATATTTTACT
43269	41356	TCTCAAACCAAATATTTTAC
43270	41357	ATCTCAAACCAAATATTTTA
43271	41358	TATCTCAAACCAAATATTTT
43272	41359	GTATCTCAAACCAAATATTT
43273	41360	AGTATCTCAAACCAAATATT
43274	41361	TAGTATCTCAAACCAAATAT
43275	41362	TTAGTATCTCAAACCAAATA
43276	41363	ATTAGTATCTCAAACCAAAT
43277	41364	CATTAGTATCTCAAACCAAA
43278	41365	TCATTAGTATCTCAAACCAA
43279	41366	TTCATTAGTATCTCAAACCA
43280	41367	TTTCATTAGTATCTCAAACC
43281	41368	TTTTCATTAGTATCTCAAAC
43282	41369	CTTTTCATTAGTATCTCAAA
43283	41370	TCTTTTCATTAGTATCTCAA
43284	41371	ATCTTTTCATTAGTATCTCA
43285	41372	AATCTTTTCATTAGTATCTC
43286	41373	TAATCTTTTCATTAGTATCT
43287	41374	TTAATCTTTTCATTAGTATC
43288	41375	TTTAATCTTTTCATTAGTAT
43289	41376	TTTTAATCTTTTCATTAGTA
43290	41377	CTTTTAATCTTTTCATTAGT
43291	41378	ACTTTTAATCTTTTCATTAG
43292	41379	TACTTTTAATCTTTTCATTA
43293	41380	TTACTTTTAATCTTTTCATT
43294	41381	TTTACTTTTAATCTTTTCAT
43295	41382	CTTTACTTTTAATCTTTTCA
43296	41383	GCTTTACTTTTAATCTTTTC
43297	41384	TGCTTTACTTTTAATCTTTT
43298	41385	ATGCTTTACTTTTAATCTTT
43299	41386	TATGCTTTACTTTTAATCTT
43300	41387	TTATGCTTTACTTTTAATCT
43301	41388	GTTATGCTTTACTTTTAATC
43302	41389	AGTTATGCTTTACTTTTAAT
43303	41390	AAGTTATGCTTTACTTTTAA

92380	90467	ACCAGAGTCCAGTACATCTT
92381	90468	CACCAGAGTCCAGTACATCT
92382	90469	ACACCAGAGTCCAGTACATC
92383	90470	AACACCAGAGTCCAGTACAT
92384	90471	GAACACCAGAGTCCAGTACA
92385	90472	AGAACACCAGAGTCCAGTAC
92386	90473	CAGAACACCAGAGTCCAGTA
92387	90474	TCAGAACACCAGAGTCCAGT
92388	90475	CTCAGAACACCAGAGTCCAG
92389	90476	CCTCAGAACACCAGAGTCCA
92390	90477	ACCTCAGAACACCAGAGTCC
92391	90478	TACCTCAGAACACCAGAGTC
92392	90479	CTACCTCAGAACACCAGAGT
92393	90480	ACTACCTCAGAACACCAGAG
92394	90481	AACTACCTCAGAACACCAGA
92395	90482	CAACTACCTCAGAACACCAG
92396	90483	CCAACTACCTCAGAACACCA
92397	90484	TCCAACTACCTCAGAACACC
92398	90485	CTCCAACTACCTCAGAACAC
92399	90486	TCTCCAACTACCTCAGAACA
92400	90487	ATCTCCAACTACCTCAGAAC
92401	90488	AATCTCCAACTACCTCAGAA
92402	90489	AAATCTCCAACTACCTCAGA
92403	90490	TAAATCTCCAACTACCTCAG
92404	90491	ATAAATCTCCAACTACCTCA
92405	90492	TATAAATCTCCAACTACCTC
92406	90493	GTATAAATCTCCAACTACCT
92407	90494	AGTATAAATCTCCAACTACC
92408	90495	AAGTATAAATCTCCAACTAC
92409	90496	AAAGTATAAATCTCCAACTA
92410	90497	CAAAGTATAAATCTCCAACT
92411	90498	ACAAAGTATAAATCTCCAAC
92412	90499	TACAAAGTATAAATCTCCAA
92413	90500	GTACAAAGTATAAATCTCCA
92414	90501	TGTACAAAGTATAAATCTCC
92415	90502	GTGTACAAAGTATAAATCTC
92416	90503	TGTGTACAAAGTATAAATCT
92417	90504	TTGTGTACAAAGTATAAATC
92418	90505	TTTGTGTACAAAGTATAAAT
92419	90506	ATTTGTGTACAAAGTATAAA
92420	90507	TATTTGTGTACAAAGTATAA
92421	90508	ATATTTGTGTACAAAGTATA
92422	90509	TATATTTGTGTACAAAGTAT
92423	90510	ATATATTTGTGTACAAAGTA
92424	90511	AATATATTTGTGTACAAAGT
92425	90512	CAATATATTTGTGTACAAAG
92426	90513	ACAATATATTTGTGTACAAA
92427	90514	CACAATATATTTGTGTACAA
92428	90515	CCACAATATATTTGTGTACA
92429	90516	ACCACAATATATTTGTGTAC
92430	90517	GACCACAATATATTTGTGTA
92431	90518	TGACCACAATATATTTGTGT
92432	90519	TTGACCACAATATATTTGTG
92433	90520	TTTGACCACAATATATTTGT
92434	90521	TTTTGACCACAATATATTTG
92435	90522	ATTTTGACCACAATATATTT
92436	90523	GATTTTGACCACAATATATT
92437	90524	AGATTTTGACCACAATATAT
92438	90525	AAGATTTTGACCACAATATA
92439	90526	AAAGATTTTGACCACAATAT
92440	90527	GAAAGATTTTGACCACAATA
92441	90528	AGAAAGATTTTGACCACAAT
92442	90529	CAGAAAGATTTTGACCACAA
92443	90530	ACAGAAAGATTTTGACCACA
92444	90531	TACAGAAAGATTTTGACCAC
92445	90532	TTACAGAAAGATTTTGACCA
92446	90533	GTTACAGAAAGATTTTGACC
92447	90534	TGTTACAGAAAGATTTTGAC
92448	90535	ATGTTACAGAAAGATTTTGA
92449	90536	AATGTTACAGAAAGATTTTG
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141527	139614	AAAAGCCACATGTAGCTAAG
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141545	139632	TTTATTTTTGAATAATAAAA
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141547	139634	AATTTATTTTTGAATAATAA
141548	139635	AAATTTATTTTTGAATAATA
141549	139636	AAAATTTATTTTTGAATAAT
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141556	139643	CGGCCTAAAAATTTATTTTT
141557	139644	CCGGCCTAAAAATTTATTTT
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141567	139654	GCAACTGCACCCGGCCTAAA
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141569	139656	GAGCAACTGCACCCGGCCTA
141570	139657	TGAGCAACTGCACCCGGCCT
141571	139658	GTGAGCAACTGCACCCGGCC
141572	139659	TGTGAGCAACTGCACCCGGC
141573	139660	GTGTGAGCAACTGCACCCGG
141574	139661	GGTGTGAGCAACTGCACCCG
141575	139662	AGGTGTGAGCAACTGCACCC
141576	139663	CAGGTGTGAGCAACTGCACC
141577	139664	ACAGGTGTGAGCAACTGCAC
141578	139665	TACAGGTGTGAGCAACTGCA
141579	139666	TTACAGGTGTGAGCAACTGC
141580	139667	ATTACAGGTGTGAGCAACTG
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141592	139679	CAAAGTGTTGGGATTACAGG
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141594	139681	CCCAAAGTGTTGGGATTACA
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43304	41391	CAAGTTATGCTTTACTTTTA
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43306	41393	TTCAAGTTATGCTTTACTTT
43307	41394	ATTCAAGTTATGCTTTACTT
43308	41395	CATTCAAGTTATGCTTTACT
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43312	41399	TATCCATTCAAGTTATGCTT
43313	41400	GTATCCATTCAAGTTATGCT
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43315	41402	TTGTATCCATTCAAGTTATG
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43319	41406	CTTTTTGTATCCATTCAAGT
43320	41407	TCTTTTTGTATCCATTCAAG
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43323	41410	GTTTCTTTTTGTATCCATTC
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43326	41413	CTTGTTTCTTTTTGTATCCA
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43359	41446	CAGTATTCTCTGAAATCCAC
43360	41447	GCAGTATTCTCTGAAATCCA
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43362	41449	AAGCAGTATTCTCTGAAATC
43363	41450	GAAGCAGTATTCTCTGAAAT
43364	41451	CGAAGCAGTATTCTCTGAAA
43365	41452	TCGAAGCAGTATTCTCTGAA
43366	41453	ATCGAAGCAGTATTCTCTGA
43367	41454	TATCGAAGCAGTATTCTCTG
43368	41455	ATATCGAAGCAGTATTCTCT
43369	41456	CATATCGAAGCAGTATTCTC
43370	41457	GCATATCGAAGCAGTATTCT
43371	41458	AGCATATCGAAGCAGTATTC
43372	41459	TAGCATATCGAAGCAGTATT
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92451	90538	ATAATGTTACAGAAAGATTT
92452	90539	AATAATGTTACAGAAAGATT
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92462	90549	AAGACAGAGAAATAATGTTA
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92464	90551	CTAAGACAGAGAAATAATGT
92465	90552	GCTAAGACAGAGAAATAATG
92466	90553	TGCTAAGACAGAGAAATAAT
92467	90554	GTGCTAAGACAGAGAAATAA
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92471	90558	GCCTGTGCTAAGACAGAGAA
92472	90559	AGCCTGTGCTAAGACAGAGA
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92474	90561	AAAGCCTGTGCTAAGACAGA
92475	90562	TAAAGCCTGTGCTAAGACAG
92476	90563	GTAAAGCCTGTGCTAAGACA
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92480	90567	TTAAGTAAAGCCTGTGCTAA
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92491	90578	AAGGAGAGATGTTAAGTAAA
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92495	90582	AATCAAGGAGAGATGTTAAG
92496	90583	CAATCAAGGAGAGATGTTAA
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92502	90589	AAATGACAATCAAGGAGAGA
92503	90590	GAAATGACAATCAAGGAGAG
92504	90591	TGAAATGACAATCAAGGAGA
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92506	90593	AATGAAATGACAATCAAGGA
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92508	90595	AGAATGAAATGACAATCAAG
92509	90596	AAGAATGAAATGACAATCAA
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141598	139685	GCCTCCCAAAGTGTTGGGAT
141599	139686	GGCCTCCCAAAGTGTTGGGA
141600	139687	CGGCCTCCCAAAGTGTTGGG
141601	139688	TCGGCCTCCCAAAGTGTTGG
141602	139689	CTCGGCCTCCCAAAGTGTTG
141603	139690	TCTCGGCCTCCCAAAGTGTT
141604	139691	ATCTCGGCCTCCCAAAGTGT
141605	139692	CATCTCGGCCTCCCAAAGTG
141606	139693	CCATCTCGGCCTCCCAAAGT
141607	139694	TCCATCTCGGCCTCCCAAAG
141608	139695	GTCCATCTCGGCCTCCCAAA
141609	139696	CGTCCATCTCGGCCTCCCAA
141610	139697	CCGTCCATCTCGGCCTCCCA
141611	139698	TCCGTCCATCTCGGCCTCCC
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141613	139700	GATCCGTCCATCTCGGCCTC
141614	139701	TGATCCGTCCATCTCGGCCT
141615	139702	GTGATCCGTCCATCTCGGCC
141616	139703	AGTGATCCGTCCATCTCGGC
141617	139704	AAGTGATCCGTCCATCTCGG
141618	139705	CAAGTGATCCGTCCATCTCG
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141620	139707	CTCAAGTGATCCGTCCATCT
141621	139708	CCTCAAGTGATCCGTCCATC
141622	139709	GCCTCAAGTGATCCGTCCAT
141623	139710	GGCCTCAAGTGATCCGTCCA
141624	139711	TGGCCTCAAGTGATCCGTCC
141625	139712	CTGGCCTCAAGTGATCCGTC
141626	139713	CCTGGCCTCAAGTGATCCGT
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141628	139715	CTCCTGGCCTCAAGTGATCC
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141632	139719	CAAACTCCTGGCCTCAAGTG
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141635	139722	TCTCAAACTCCTGGCCTCAA
141636	139723	GTCTCAAACTCCTGGCCTCA
141637	139724	GGTCTCAAACTCCTGGCCTC
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141639	139726	CTGGTCTCAAACTCCTGGCC
141640	139727	GCTGGTCTCAAACTCCTGGC
141641	139728	GGCTGGTCTCAAACTCCTGG
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141646	139733	GGCCAGGCTGGTCTCAAACT
141647	139734	TGGCCAGGCTGGTCTCAAAC
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141650	139737	TGTTGGCCAGGCTGGTCTCA
141651	139738	ATGTTGGCCAGGCTGGTCTC
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141656	139743	TCACCATGTTGGCCAGGCTG
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141660	139747	GGTTTCACCATGTTGGCCAG
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141664	139751	ACGGGGTTTCACCATGTTGG
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141667	139754	GAGACGGGGTTTCACCATGT
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43375	41462	TGTTAGCATATCGAAGCAGT
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43379	41466	GGAATGTTAGCATATCGAAG
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43387	41474	ACCCAACAGGAATGTTAGCA
43388	41475	CACCCAACAGGAATGTTAGC
43389	41476	ACACCCAACAGGAATGTTAG
43390	41477	GACACCCAACAGGAATGTTA
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43394	41481	GTTGGACACCCAACAGGAAT
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43412	41499	CCACTGATCTATGACACGGT
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43415	41502	TTTCCACTGATCTATGACAC
43416	41503	ATTTCCACTGATCTATGACA
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43425	41512	AAACCACTAATTTCCACTGA
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43434	41521	AAAGTGCAGAAACCACTAAT
43435	41522	TAAAGTGCAGAAACCACTAA
43436	41523	GTAAAGTGCAGAAACCACTA
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43438	41525	CAGTAAAGTGCAGAAACCAC
43439	41526	ACAGTAAAGTGCAGAAACCA
43440	41527	TACAGTAAAGTGCAGAAACC
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92522	90609	AAATAACATGCAAAAGAATG
92523	90610	TAAATAACATGCAAAAGAAT
92524	90611	GTAAATAACATGCAAAAGAA
92525	90612	AGTAAATAACATGCAAAAGA
92526	90613	TAGTAAATAACATGCAAAAG
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92529	90616	CTATAGTAAATAACATGCAA
92530	90617	CCTATAGTAAATAACATGCA
92531	90618	ACCTATAGTAAATAACATGC
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92533	90620	ATACCTATAGTAAATAACAT
92534	90621	GATACCTATAGTAAATAACA
92535	90622	CGATACCTATAGTAAATAAC
92536	90623	TCGATACCTATAGTAAATAA
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92538	90625	CCTCGATACCTATAGTAAAT
92539	90626	ACCTCGATACCTATAGTAAA
92540	90627	TACCTCGATACCTATAGTAA
92541	90628	CTACCTCGATACCTATAGTA
92542	90629	TCTACCTCGATACCTATAGT
92543	90630	ATCTACCTCGATACCTATAG
92544	90631	AATCTACCTCGATACCTATA
92545	90632	AAATCTACCTCGATACCTAT
92546	90633	AAAATCTACCTCGATACCTA
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92548	90635	TCAAAATCTACCTCGATACC
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92552	90639	GGTCTCAAAATCTACCTCGA
92553	90640	TGGTCTCAAAATCTACCTCG
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92556	90643	GGTTGGTCTCAAAATCTACC
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92561	90648	TTATTGGTTGGTCTCAAAAT
92562	90649	TTTATTGGTTGGTCTCAAAA
92563	90650	ATTTATTGGTTGGTCTCAAA
92564	90651	GATTTATTGGTTGGTCTCAA
92565	90652	AGATTTATTGGTTGGTCTCA
92566	90653	AAGATTTATTGGTTGGTCTC
92567	90654	GAAGATTTATTGGTTGGTCT
92568	90655	AGAAGATTTATTGGTTGGTC
92569	90656	AAGAAGATTTATTGGTTGGT
92570	90657	CAAGAAGATTTATTGGTTGG
92571	90658	TCAAGAAGATTTATTGGTTG
92572	90659	TTCAAGAAGATTTATTGGTT
92573	90660	TTTCAAGAAGATTTATTGGT
92574	90661	GTTTCAAGAAGATTTATTGG
92575	90662	AGTTTCAAGAAGATTTATTG
92576	90663	AAGTTTCAAGAAGATTTATT
92577	90664	TAAGTTTCAAGAAGATTTAT
92578	90665	CTAAGTTTCAAGAAGATTTA
92579	90666	GCTAAGTTTCAAGAAGATTT
92580	90667	AGCTAAGTTTCAAGAAGATT
92581	90668	AAGCTAAGTTTCAAGAAGAT
92582	90669	GAAGCTAAGTTTCAAGAAGA
92583	90670	AGAAGCTAAGTTTCAAGAAG
92584	90671	AAGAAGCTAAGTTTCAAGAA
92585	90672	TAAGAAGCTAAGTTTCAAGA
92586	90673	CTAAGAAGCTAAGTTTCAAG
92587	90674	TCTAAGAAGCTAAGTTTCAA
92588	90675	TTCTAAGAAGCTAAGTTTCA
92589	90676	TTTCTAAGAAGCTAAGTTTC
92590	90677	CTTTCTAAGAAGCTAAGTTT
92591	90678	CCTTTCTAAGAAGCTAAGTT
92592	90679	TCCTTTCTAAGAAGCTAAGT

141669	139756	TAGAGACGGGGTTTCACCAT
141670	139757	GTAGAGACGGGGTTTCACCA
141671	139758	AGTAGAGACGGGGTTTCACC
141672	139759	TAGTAGAGACGGGGTTTCAC
141673	139760	TTAGTAGAGACGGGGTTTCA
141674	139761	TTTAGTAGAGACGGGGTTTC
141675	139762	TTTTAGTAGAGACGGGGTTT
141676	139763	TTTTTAGTAGAGACGGGGTT
141677	139764	ATTTTTAGTAGAGACGGGGT
141678	139765	TATTTTTAGTAGAGACGGGG
141679	139766	GTATTTTTAGTAGAGACGGG
141680	139767	TGTATTTTTAGTAGAGACGG
141681	139768	TTGTATTTTTAGTAGAGACG
141682	139769	TTTGTATTTTTAGTAGAGAC
141683	139770	TTTTGTATTTTTAGTAGAGA
141684	139771	TTTTTGTATTTTTAGTAGAG
141685	139772	ATTTTTGTATTTTTAGTAGA
141686	139773	AATTTTTGTATTTTTAGTAG
141687	139774	TAATTTTTGTATTTTTAGTA
141688	139775	CTAATTTTTGTATTTTTAGT
141689	139776	GCTAATTTTTGTATTTTTAG
141690	139777	GGCTAATTTTTGTATTTTTA
141691	139778	TGGCTAATTTTTGTATTTTT
141692	139779	CTGGCTAATTTTTGTATTTT
141693	139780	CCTGGCTAATTTTTGTATTT
141694	139781	ACCTGGCTAATTTTTGTATT
141695	139782	TACCTGGCTAATTTTTGTAT
141696	139783	TTACCTGGCTAATTTTTGTA
141697	139784	ATTACCTGGCTAATTTTTGT
141698	139785	GATTACCTGGCTAATTTTTG
141699	139786	GGATTACCTGGCTAATTTTT
141700	139787	GGGATTACCTGGCTAATTTT
141701	139788	TGGGATTACCTGGCTAATTT
141702	139789	CTGGGATTACCTGGCTAATT
141703	139790	GCTGGGATTACCTGGCTAAT
141704	139791	AGCTGGGATTACCTGGCTAA
141705	139792	TAGCTGGGATTACCTGGCTA
141706	139793	GTAGCTGGGATTACCTGGCT
141707	139794	AGTAGCTGGGATTACCTGGC
141708	139795	GAGTAGCTGGGATTACCTGG
141709	139796	TGAGTAGCTGGGATTACCTG
141710	139797	CTGAGTAGCTGGGATTACCT
141711	139798	TCTGAGTAGCTGGGATTACC
141712	139799	CTCTGAGTAGCTGGGATTAC
141713	139800	CCTCTGAGTAGCTGGGATTA
141714	139801	GCCTCTGAGTAGCTGGGATT
141715	139802	AGCCTCTGAGTAGCTGGGAT
141716	139803	CAGCCTCTGAGTAGCTGGGA
141717	139804	TCAGCCTCTGAGTAGCTGGG
141718	139805	TTCAGCCTCTGAGTAGCTGG
141719	139806	CTTCAGCCTCTGAGTAGCTG
141720	139807	GCTTCAGCCTCTGAGTAGCT
141721	139808	TGCTTCAGCCTCTGAGTAGC
141722	139809	CTGCTTCAGCCTCTGAGTAG
141723	139810	CCTGCTTCAGCCTCTGAGTA
141724	139811	TCCTGCTTCAGCCTCTGAGT
141725	139812	CTCCTGCTTCAGCCTCTGAG
141726	139813	ACTCCTGCTTCAGCCTCTGA
141727	139814	TACTCCTGCTTCAGCCTCTG
141728	139815	ATACTCCTGCTTCAGCCTCT
141729	139816	GATACTCCTGCTTCAGCCTC
141730	139817	TGATACTCCTGCTTCAGCCT
141731	139818	GTGATACTCCTGCTTCAGCC
141732	139819	AGTGATACTCCTGCTTCAGC
141733	139820	AAGTGATACTCCTGCTTCAG
141734	139821	AAAGTGATACTCCTGCTTCA
141735	139822	TAAAGTGATACTCCTGCTTC
141736	139823	TTAAAGTGATACTCCTGCTT
141737	139824	GTTAAAGTGATACTCCTGCT
141738	139825	GGTTAAAGTGATACTCCTGC
141739	139826	GGGTTAAAGTGATACTCCTG

43446	41533	AAACAGTACAGTAAAGTGCA
43447	41534	AAAACAGTACAGTAAAGTGC
43448	41535	AAAAACAGTACAGTAAAGTG
43449	41536	AAAAAACAGTACAGTAAAGT
43450	41537	AAAAAAACAGTACAGTAAAG
43451	41538	TAAAAAAACAGTACAGTAAA
43452	41539	ATAAAAAAACAGTACAGTAA
43453	41540	TATAAAAAAACAGTACAGTA
43454	41541	ATATAAAAAAACAGTACAGT
43455	41542	CATATAAAAAAACAGTACAG
43456	41543	TCATATAAAAAAACAGTACA
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43458	41545	TATCATATAAAAAAACAGTA
43459	41546	TTATCATATAAAAAAACAGT
43460	41547	ATTATCATATAAAAAAACAG
43461	41548	TATTATCATATAAAAAAACA
43462	41549	ATATTATCATATAAAAAAAC
43463	41550	AATATTATCATATAAAAAAA
43464	41551	AAATATTATCATATAAAAAA
43465	41552	AAAATATTATCATATAAAAA
43466	41553	GAAAATATTATCATATAAAA
43467	41554	GGAAAATATTATCATATAAA
43468	41555	AGGAAAATATTATCATATAA
43469	41556	CAGGAAAATATTATCATATA
43470	41557	CCAGGAAAATATTATCATAT
43471	41558	ACCAGGAAAATATTATCATA
43472	41559	AACCAGGAAAATATTATCAT
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43482	41569	CGAATCATTCAACCAGGAAA
43483	41570	ACGAATCATTCAACCAGGAA
43484	41571	AACGAATCATTCAACCAGGA
43485	41572	GAACGAATCATTCAACCAGG
43486	41573	AGAACGAATCATTCAACCAG
43487	41574	AAGAACGAATCATTCAACCA
43488	41575	AAAGAACGAATCATTCAACC
43489	41576	AAAAGAACGAATCATTCAAC
43490	41577	CAAAAGAACGAATCATTCAA
43491	41578	TCAAAAGAACGAATCATTCA
43492	41579	CTCAAAAGAACGAATCATTC
43493	41580	ACTCAAAAGAACGAATCATT
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43495	41582	TTACTCAAAAGAACGAATCA
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43497	41584	GTTTACTCAAAAGAACGAAT
43498	41585	AGTTTACTCAAAAGAACGAA
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43500	41587	GGAGTTTACTCAAAAGAACG
43501	41588	TGGAGTTTACTCAAAAGAAC
43502	41589	ATGGAGTTTACTCAAAAGAA
43503	41590	CATGGAGTTTACTCAAAAGA
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43505	41592	ACCATGGAGTTTACTCAAAA
43506	41593	GACCATGGAGTTTACTCAAA
43507	41594	TGACCATGGAGTTTACTCAA
43508	41595	TTGACCATGGAGTTTACTCA
43509	41596	TTTGACCATGGAGTTTACTC
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43511	41598	TGTTTGACCATGGAGTTTAC
43512	41599	TTGTTTGACCATGGAGTTTA
43513	41600	ATTGTTTGACCATGGAGTTT
43514	41601	AATTGTTTGACCATGGAGTT
43515	41602	TAATTGTTTGACCATGGAGT
43516	41603	GTAATTGTTTGACCATGGAG

92593	90680	TTCCTTTCTAAGAAGCTAAG
92594	90681	TTTCCTTTCTAAGAAGCTAA
92595	90682	TTTTCCTTTCTAAGAAGCTA
92596	90683	ATTTTCCTTTCTAAGAAGCT
92597	90684	GATTTTCCTTTCTAAGAAGC
92598	90685	AGATTTTCCTTTCTAAGAAG
92599	90686	TAGATTTTCCTTTCTAAGAA
92600	90687	TTAGATTTTCCTTTCTAAGA
92601	90688	TTTAGATTTTCCTTTCTAAG
92602	90689	ATTTAGATTTTCCTTTCTAA
92603	90690	TATTTAGATTTTCCTTTCTA
92604	90691	GTATTTAGATTTTCCTTTCT
92605	90692	GGTATTTAGATTTTCCTTTC
92606	90693	TGGTATTTAGATTTTCCTTT
92607	90694	CTGGTATTTAGATTTTCCTT
92608	90695	GCTGGTATTTAGATTTTCCT
92609	90696	GGCTGGTATTTAGATTTTCC
92610	90697	AGGCTGGTATTTAGATTTTC
92611	90698	AAGGCTGGTATTTAGATTTT
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92613	90700	AAAAGGCTGGTATTTAGATT
92614	90701	TAAAAGGCTGGTATTTAGAT
92615	90702	TTAAAAGGCTGGTATTTAGA
92616	90703	TTTAAAAGGCTGGTATTTAG
92617	90704	TTTTAAAAGGCTGGTATTTA
92618	90705	TTTTTAAAAGGCTGGTATTT
92619	90706	TTTTTTAAAAGGCTGGTATT
92620	90707	TTTTTTTAAAAGGCTGGTAT
92621	90708	CTTTTTTTAAAAGGCTGGTA
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92629	90716	TTCAGCTACTTTTTTTAAAA
92630	90717	ATTCAGCTACTTTTTTTAAA
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92632	90719	TAATTCAGCTACTTTTTTTA
92633	90720	TTAATTCAGCTACTTTTTTT
92634	90721	TTTAATTCAGCTACTTTTTT
92635	90722	CTTTAATTCAGCTACTTTTT
92636	90723	CCTTTAATTCAGCTACTTTT
92637	90724	TCCTTTAATTCAGCTACTTT
92638	90725	ATCCTTTAATTCAGCTACTT
92639	90726	CATCCTTTAATTCAGCTACT
92640	90727	TCATCCTTTAATTCAGCTAC
92641	90728	CTCATCCTTTAATTCAGCTA
92642	90729	ACTCATCCTTTAATTCAGCT
92643	90730	CACTCATCCTTTAATTCAGC
92644	90731	TCACTCATCCTTTAATTCAG
92645	90732	TTCACTCATCCTTTAATTCA
92646	90733	GTTCACTCATCCTTTAATTC
92647	90734	GGTTCACTCATCCTTTAATT
92648	90735	TGGTTCACTCATCCTTTAAT
92649	90736	TTGGTTCACTCATCCTTTAA
92650	90737	TTTGGTTCACTCATCCTTTA
92651	90738	CTTTGGTTCACTCATCCTTT
92652	90739	CCTTTGGTTCACTCATCCTT
92653	90740	GCCTTTGGTTCACTCATCCT
92654	90741	TGCCTTTGGTTCACTCATCC
92655	90742	TTGCCTTTGGTTCACTCATC
92656	90743	TTTGCCTTTGGTTCACTCAT
92657	90744	CTTTGCCTTTGGTTCACTCA
92658	90745	CCTTTGCCTTTGGTTCACTC
92659	90746	ACCTTTGCCTTTGGTTCACT
92660	90747	TACCTTTGCCTTTGGTTCAC
92661	90748	CTACCTTTGCCTTTGGTTCA
92662	90749	GCTACCTTTGCCTTTGGTTC
92663	90750	GGCTACCTTTGCCTTTGGTT

141740	139827	TGGGTTAAAGTGATACTCCT
141741	139828	CTGGGTTAAAGTGATACTCC
141742	139829	CCTGGGTTAAAGTGATACTC
141743	139830	TCCTGGGTTAAAGTGATACT
141744	139831	CTCCTGGGTTAAAGTGATAC
141745	139832	CCTCCTGGGTTAAAGTGATA
141746	139833	GCCTCCTGGGTTAAAGTGAT
141747	139834	CGCCTCCTGGGTTAAAGTGA
141748	139835	CCGCCTCCTGGGTTAAAGTG
141749	139836	TCCGCCTCCTGGGTTAAAGT
141750	139837	CTCCGCCTCCTGGGTTAAAG
141751	139838	CCTCCGCCTCCTGGGTTAAA
141752	139839	GCCTCCGCCTCCTGGGTTAA
141753	139840	AGCCTCCGCCTCCTGGGTTA
141754	139841	CAGCCTCCGCCTCCTGGGTT
141755	139842	GCAGCCTCCGCCTCCTGGGT
141756	139843	TGCAGCCTCCGCCTCCTGGG
141757	139844	CTGCAGCCTCCGCCTCCTGG
141758	139845	ACTGCAGCCTCCGCCTCCTG
141759	139846	CACTGCAGCCTCCGCCTCCT
141760	139847	TCACTGCAGCCTCCGCCTCC
141761	139848	CTCACTGCAGCCTCCGCCTC
141762	139849	GCTCACTGCAGCCTCCGCCT
141763	139850	GGCTCACTGCAGCCTCCGCC
141764	139851	CGGCTCACTGCAGCCTCCGC
141765	139852	TCGGCTCACTGCAGCCTCCG
141766	139853	CTCGGCTCACTGCAGCCTCC
141767	139854	TCTCGGCTCACTGCAGCCTC
141768	139855	ATCTCGGCTCACTGCAGCCT
141769	139856	GATCTCGGCTCACTGCAGCC
141770	139857	CGATCTCGGCTCACTGCAGC
141771	139858	GCGATCTCGGCTCACTGCAG
141772	139859	AGCGATCTCGGCTCACTGCA
141773	139860	GAGCGATCTCGGCTCACTGC
141774	139861	GGAGCGATCTCGGCTCACTG
141775	139862	TGGAGCGATCTCGGCTCACT
141776	139863	GTGGAGCGATCTCGGCTCAC
141777	139864	AGTGGAGCGATCTCGGCTCA
141778	139865	CAGTGGAGCGATCTCGGCTC
141779	139866	GCAGTGGAGCGATCTCGGCT
141780	139867	TGCAGTGGAGCGATCTCGGC
141781	139868	GTGCAGTGGAGCGATCTCGG
141782	139869	AGTGCAGTGGAGCGATCTCG
141783	139870	GAGTGCAGTGGAGCGATCTC
141784	139871	GGAGTGCAGTGGAGCGATCT
141785	139872	TGGAGTGCAGTGGAGCGATC
141786	139873	CTGGAGTGCAGTGGAGCGAT
141787	139874	GCTGGAGTGCAGTGGAGCGA
141788	139875	GGCTGGAGTGCAGTGGAGCG
141789	139876	AGGCTGGAGTGCAGTGGAGC
141790	139877	CAGGCTGGAGTGCAGTGGAG
141791	139878	CCAGGCTGGAGTGCAGTGGA
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141793	139880	ACCCAGGCTGGAGTGCAGTG
141794	139881	CACCCAGGCTGGAGTGCAGT
141795	139882	TCACCCAGGCTGGAGTGCAG
141796	139883	GTCACCCAGGCTGGAGTGCA
141797	139884	TGTCACCCAGGCTGGAGTGC
141798	139885	CTGTCACCCAGGCTGGAGTG
141799	139886	GCTGTCACCCAGGCTGGAGT
141800	139887	TGCTGTCACCCAGGCTGGAG
141801	139888	TTGCTGTCACCCAGGCTGGA
141802	139889	CTTGCTGTCACCCAGGCTGG
141803	139890	TCTTGCTGTCACCCAGGCTG
141804	139891	GTCTTGCTGTCACCCAGGCT
141805	139892	AGTCTTGCTGTCACCCAGGC
141806	139893	CAGTCTTGCTGTCACCCAGG
141807	139894	CCAGTCTTGCTGTCACCCAG
141808	139895	CCCAGTCTTGCTGTCACCCA
141809	139896	ACCCAGTCTTGCTGTCACCC
141810	139897	GACCCAGTCTTGCTGTCACC

43517	41604	AGTAATTGTTTGACCATGGA
43518	41605	AAGTAATTGTTTGACCATGG
43519	41606	AAAGTAATTGTTTGACCATG
43520	41607	AAAAGTAATTGTTTGACCAT
43521	41608	AAAAAGTAATTGTTTGACCA
43522	41609	TAAAAAGTAATTGTTTGACC
43523	41610	ATAAAAAGTAATTGTTTGAC
43524	41611	AATAAAAAGTAATTGTTTGA
43525	41612	TAATAAAAAGTAATTGTTTG
43526	41613	CTAATAAAAAGTAATTGTTT
43527	41614	ACTAATAAAAAGTAATTGTT
43528	41615	GACTAATAAAAAGTAATTGT
43529	41616	TGACTAATAAAAAGTAATTG
43530	41617	TTGACTAATAAAAAGTAATT
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43532	41619	CTTTGACTAATAAAAAGTAA
43533	41620	TCTTTGACTAATAAAAAGTA
43534	41621	ATCTTTGACTAATAAAAAGT
43535	41622	CATCTTTGACTAATAAAAAG
43536	41623	ACATCTTTGACTAATAAAAA
43537	41624	TACATCTTTGACTAATAAAA
43538	41625	TTACATCTTTGACTAATAAA
43539	41626	GTTACATCTTTGACTAATAA
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43541	41628	TGGTTACATCTTTGACTAAT
43542	41629	GTGGTTACATCTTTGACTAA
43543	41630	TGTGGTTACATCTTTGACTA
43544	41631	ATGTGGTTACATCTTTGACT
43545	41632	TATGTGGTTACATCTTTGAC
43546	41633	TTATGTGGTTACATCTTTGA
43547	41634	ATTATGTGGTTACATCTTTG
43548	41635	GATTATGTGGTTACATCTTT
43549	41636	TGATTATGTGGTTACATCTT
43550	41637	GTGATTATGTGGTTACATCT
43551	41638	AGTGATTATGTGGTTACATC
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43553	41640	TTAGTGATTATGTGGTTACA
43554	41641	TTTAGTGATTATGTGGTTAC
43555	41642	TTTTAGTGATTATGTGGTTA
43556	41643	TTTTTAGTGATTATGTGGTT
43557	41644	CTTTTTAGTGATTATGTGGT
43558	41645	TCTTTTTAGTGATTATGTGG
43559	41646	TTCTTTTTAGTGATTATGTG
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43566	41653	CACACTGTTCTTTTTAGTGA
43567	41654	TCACACTGTTCTTTTTAGTG
43568	41655	GTCACACTGTTCTTTTTAGT
43569	41656	AGTCACACTGTTCTTTTTAG
43570	41657	AAGTCACACTGTTCTTTTTA
43571	41658	TAAGTCACACTGTTCTTTTT
43572	41659	ATAAGTCACACTGTTCTTTT
43573	41660	AATAAGTCACACTGTTCTTT
43574	41661	AAATAAGTCACACTGTTCTT
43575	41662	TAAATAAGTCACACTGTTCT
43576	41663	TTAAATAAGTCACACTGTTC
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43583	41670	ATCCCCTTTAAATAAGTCAC
43584	41671	AATCCCCTTTAAATAAGTCA
43585	41672	TAATCCCCTTTAAATAAGTC
43586	41673	ATAATCCCCTTTAAATAAGT
43587	41674	CATAATCCCCTTTAAATAAG

92664	90751	AGGCTACCTTTGCCTTTGGT
92665	90752	AAGGCTACCTTTGCCTTTGG
92666	90753	AAAGGCTACCTTTGCCTTTG
92667	90754	GAAAGGCTACCTTTGCCTTT
92668	90755	GGAAAGGCTACCTTTGCCTT
92669	90756	AGGAAAGGCTACCTTTGCCT
92670	90757	GAGGAAAGGCTACCTTTGCC
92671	90758	TGAGGAAAGGCTACCTTTGC
92672	90759	CTGAGGAAAGGCTACCTTTG
92673	90760	GCTGAGGAAAGGCTACCTTT
92674	90761	GGCTGAGGAAAGGCTACCTT
92675	90762	AGGCTGAGGAAAGGCTACCT
92676	90763	CAGGCTGAGGAAAGGCTACC
92677	90764	ACAGGCTGAGGAAAGGCTAC
92678	90765	CACAGGCTGAGGAAAGGCTA
92679	90766	ACACAGGCTGAGGAAAGGCT
92680	90767	AACACAGGCTGAGGAAAGGC
92681	90768	AAACACAGGCTGAGGAAAGG
92682	90769	AAAACACAGGCTGAGGAAAG
92683	90770	TAAAACACAGGCTGAGGAAA
92684	90771	CTAAAACACAGGCTGAGGAA
92685	90772	GCTAAAACACAGGCTGAGGA
92686	90773	AGCTAAAACACAGGCTGAGG
92687	90774	AAGCTAAAACACAGGCTGAG
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92689	90776	GAAAGCTAAAACACAGGCTG
92690	90777	AGAAAGCTAAAACACAGGCT
92691	90778	TAGAAAGCTAAAACACAGGC
92692	90779	TTAGAAAGCTAAAACACAGG
92693	90780	TTTAGAAAGCTAAAACACAG
92694	90781	ATTTAGAAAGCTAAAACACA
92695	90782	CATTTAGAAAGCTAAAACAC
92696	90783	ACATTTAGAAAGCTAAAACA
92697	90784	AACATTTAGAAAGCTAAAAC
92698	90785	TAACATTTAGAAAGCTAAAA
92699	90786	TTAACATTTAGAAAGCTAAA
92700	90787	GTTAACATTTAGAAAGCTAA
92701	90788	TGTTAACATTTAGAAAGCTA
92702	90789	TTGTTAACATTTAGAAAGCT
92703	90790	ATTGTTAACATTTAGAAAGC
92704	90791	TATTGTTAACATTTAGAAAG
92705	90792	CTATTGTTAACATTTAGAAA
92706	90793	GCTATTGTTAACATTTAGAA
92707	90794	AGCTATTGTTAACATTTAGA
92708	90795	AAGCTATTGTTAACATTTAG
92709	90796	GAAGCTATTGTTAACATTTA
92710	90797	TGAAGCTATTGTTAACATTT
92711	90798	ATGAAGCTATTGTTAACATT
92712	90799	AATGAAGCTATTGTTAACAT
92713	90800	GAATGAAGCTATTGTTAACA
92714	90801	AGAATGAAGCTATTGTTAAC
92715	90802	AAGAATGAAGCTATTGTTAA
92716	90803	CAAGAATGAAGCTATTGTTA
92717	90804	TCAAGAATGAAGCTATTGTT
92718	90805	GTCAAGAATGAAGCTATTGT
92719	90806	AGTCAAGAATGAAGCTATTG
92720	90807	AAGTCAAGAATGAAGCTATT
92721	90808	TAAGTCAAGAATGAAGCTAT
92722	90809	ATAAGTCAAGAATGAAGCTA
92723	90810	AATAAGTCAAGAATGAAGCT
92724	90811	CAATAAGTCAAGAATGAAGC
92725	90812	CCAATAAGTCAAGAATGAAG
92726	90813	ACCAATAAGTCAAGAATGAA
92727	90814	TACCAATAAGTCAAGAATGA
92728	90815	TTACCAATAAGTCAAGAATG
92729	90816	GTTACCAATAAGTCAAGAAT
92730	90817	TGTTACCAATAAGTCAAGAA
92731	90818	ATGTTACCAATAAGTCAAGA
92732	90819	AATGTTACCAATAAGTCAAG
92733	90820	GAATGTTACCAATAAGTCAA
92734	90821	TGAATGTTACCAATAAGTCA

141811	139898	AGACCCAGTCTTGCTGTCAC
141812	139899	GAGACCCAGTCTTGCTGTCA
141813	139900	TGAGACCCAGTCTTGCTGTC
141814	139901	TTGAGACCCAGTCTTGCTGT
141815	139902	TTTGAGACCCAGTCTTGCTG
141816	139903	TTTTGAGACCCAGTCTTGCT
141817	139904	TTTTTGAGACCCAGTCTTGC
141818	139905	ATTTTTGAGACCCAGTCTTG
141819	139906	TATTTTTGAGACCCAGTCTT
141820	139907	TTATTTTTGAGACCCAGTCT
141821	139908	TTTATTTTTGAGACCCAGTC
141822	139909	GTTTATTTTTGAGACCCAGT
141823	139910	TGTTTATTTTTGAGACCCAG
141824	139911	TTGTTTATTTTTGAGACCCA
141825	139912	TTTGTTTATTTTTGAGACCC
141826	139913	GTTTGTTTATTTTTGAGACC
141827	139914	TGTTTGTTTATTTTTGAGAC
141828	139915	ATGTTTGTTTATTTTTGAGA
141829	139916	CATGTTTGTTTATTTTTGAG
141830	139917	CCATGTTTGTTTATTTTTGA
141831	139918	GCCATGTTTGTTTATTTTTG
141832	139919	GGCCATGTTTGTTTATTTTT
141833	139920	CGGCCATGTTTGTTTATTTT
141834	139921	CCGGCCATGTTTGTTTATTT
141835	139922	CCCGGCCATGTTTGTTTATT
141836	139923	GCCCGGCCATGTTTGTTTAT
141837	139924	CGCCCGGCCATGTTTGTTTA
141838	139925	GCGCCCGGCCATGTTTGTTT
141839	139926	TGCGCCCGGCCATGTTTGTT
141840	139927	CTGCGCCCGGCCATGTTTGT
141841	139928	ACTGCGCCCGGCCATGTTTG
141842	139929	CACTGCGCCCGGCCATGTTT
141843	139930	CCACTGCGCCCGGCCATGTT
141844	139931	GCCACTGCGCCCGGCCATGT
141845	139932	AGCCACTGCGCCCGGCCATG
141846	139933	GAGCCACTGCGCCCGGCCAT
141847	139934	TGAGCCACTGCGCCCGGCCA
141848	139935	ATGAGCCACTGCGCCCGGCC
141849	139936	CATGAGCCACTGCGCCCGGC
141850	139937	GCATGAGCCACTGCGCCCGG
141851	139938	GGCATGAGCCACTGCGCCCG
141852	139939	AGGCATGAGCCACTGCGCCC
141853	139940	CAGGCATGAGCCACTGCGCC
141854	139941	ACAGGCATGAGCCACTGCGC
141855	139942	TACAGGCATGAGCCACTGCG
141856	139943	TTACAGGCATGAGCCACTGC
141857	139944	ATTACAGGCATGAGCCACTG
141858	139945	GATTACAGGCATGAGCCACT
141859	139946	GGATTACAGGCATGAGCCAC
141860	139947	GGGATTACAGGCATGAGCCA
141861	139948	TGGGATTACAGGCATGAGCC
141862	139949	CTGGGATTACAGGCATGAGC
141863	139950	GCTGGGATTACAGGCATGAG
141864	139951	TGCTGGGATTACAGGCATGA
141865	139952	GTGCTGGGATTACAGGCATG
141866	139953	AGTGCTGGGATTACAGGCAT
141867	139954	AAGTGCTGGGATTACAGGCA
141868	139955	AAAGTGCTGGGATTACAGGC
141869	139956	CAAAGTGCTGGGATTACAGG
141870	139957	CCAAAGTGCTGGGATTACAG
141871	139958	CCCAAAGTGCTGGGATTACA
141872	139959	TCCCAAAGTGCTGGGATTAC
141873	139960	CTCCCAAAGTGCTGGGATTA
141874	139961	CCTCCCAAAGTGCTGGGATT
141875	139962	GCCTCCCAAAGTGCTGGGAT
141876	139963	GGCCTCCCAAAGTGCTGGGA
141877	139964	CGGCCTCCCAAAGTGCTGGG
141878	139965	TCGGCCTCCCAAAGTGCTGG
141879	139966	CTCGGCCTCCCAAAGTGCTG
141880	139967	CCTCGGCCTCCCAAAGTGCT
141881	139968	GCCTCGGCCTCCCAAAGTGC

43588	41675	ACATAATCCCCTTTAAATAA
43589	41676	AACATAATCCCCTTTAAATA
43590	41677	AAACATAATCCCCTTTAAAT
43591	41678	AAAACATAATCCCCTTTAAA
43592	41679	AAAAACATAATCCCCTTTAA
43593	41680	TAAAAACATAATCCCCTTTA
43594	41681	TTAAAAACATAATCCCCTTT
43595	41682	CTTAAAAACATAATCCCCTT
43596	41683	ACTTAAAAACATAATCCCCT
43597	41684	GACTTAAAAACATAATCCCC
43598	41685	AGACTTAAAAACATAATCCC
43599	41686	AAGACTTAAAAACATAATCC
43600	41687	AAAGACTTAAAAACATAATC
43601	41688	AAAAGACTTAAAAACATAAT
43602	41689	TAAAAGACTTAAAAACATAA
43603	41690	ATAAAAGACTTAAAAACATA
43604	41691	TATAAAAGACTTAAAAACAT
43605	41692	ATATAAAAGACTTAAAAACA
43606	41693	TATATAAAAGACTTAAAAAC
43607	41694	CTATATAAAAGACTTAAAAA
43608	41695	GCTATATAAAAGACTTAAAA
43609	41696	AGCTATATAAAAGACTTAAA
43610	41697	AAGCTATATAAAAGACTTAA
43611	41698	AAAGCTATATAAAAGACTTA
43612	41699	CAAAGCTATATAAAAGACTT
43613	41700	ACAAAGCTATATAAAAGACT
43614	41701	TACAAAGCTATATAAAAGAC
43615	41702	CTACAAAGCTATATAAAAGA
43616	41703	CCTACAAAGCTATATAAAAG
43617	41704	CCCTACAAAGCTATATAAAA
43618	41705	TCCCTACAAAGCTATATAAA
43619	41706	CTCCCTACAAAGCTATATAA
43620	41707	CCTCCCTACAAAGCTATATA
43621	41708	GCCTCCCTACAAAGCTATAT
43622	41709	GGCCTCCCTACAAAGCTATA
43623	41710	TGGCCTCCCTACAAAGCTAT
43624	41711	ATGGCCTCCCTACAAAGCTA
43625	41712	TATGGCCTCCCTACAAAGCT
43626	41713	ATATGGCCTCCCTACAAAGC
43627	41714	CATATGGCCTCCCTACAAAG
43628	41715	TCATATGGCCTCCCTACAAA
43629	41716	CTCATATGGCCTCCCTACAA
43630	41717	ACTCATATGGCCTCCCTACA
43631	41718	AACTCATATGGCCTCCCTAC
43632	41719	AAACTCATATGGCCTCCCTA
43633	41720	TAAACTCATATGGCCTCCCT
43634	41721	TTAAACTCATATGGCCTCCC
43635	41722	CTTAAACTCATATGGCCTCC
43636	41723	CCTTAAACTCATATGGCCTC
43637	41724	TCCTTAAACTCATATGGCCT
43638	41725	GTCCTTAAACTCATATGGCC
43639	41726	TGTCCTTAAACTCATATGGC
43640	41727	CTGTCCTTAAACTCATATGG
43641	41728	ACTGTCCTTAAACTCATATG
43642	41729	AACTGTCCTTAAACTCATAT
43643	41730	GAACTGTCCTTAAACTCATA
43644	41731	CGAACTGTCCTTAAACTCAT
43645	41732	ACGAACTGTCCTTAAACTCA
43646	41733	CACGAACTGTCCTTAAACTC
43647	41734	CCACGAACTGTCCTTAAACT
43648	41735	GCCACGAACTGTCCTTAAAC
43649	41736	TGCCACGAACTGTCCTTAAA
43650	41737	ATGCCACGAACTGTCCTTAA
43651	41738	AATGCCACGAACTGTCCTTA
43652	41739	AAATGCCACGAACTGTCCTT
43653	41740	CAAATGCCACGAACTGTCCT
43654	41741	ACAAATGCCACGAACTGTCC
43655	41742	AACAAATGCCACGAACTGTC
43656	41743	GAACAAATGCCACGAACTGT
43657	41744	TGAACAAATGCCACGAACTG
43658	41745	TTGAACAAATGCCACGAACT

92735	90822	TTGAATGTTACCAATAAGTC
92736	90823	TTTGAATGTTACCAATAAGT
92737	90824	TTTTGAATGTTACCAATAAG
92738	90825	ATTTTGAATGTTACCAATAA
92739	90826	TATTTTGAATGTTACCAATA
92740	90827	GTATTTTGAATGTTACCAAT
92741	90828	AGTATTTTGAATGTTACCAA
92742	90829	TAGTATTTTGAATGTTACCA
92743	90830	GTAGTATTTTGAATGTTACC
92744	90831	AGTAGTATTTTGAATGTTAC
92745	90832	AAGTAGTATTTTGAATGTTA
92746	90833	TAAGTAGTATTTTGAATGTT
92747	90834	ATAAGTAGTATTTTGAATGT
92748	90835	AATAAGTAGTATTTTGAATG
92749	90836	TAATAAGTAGTATTTTGAAT
92750	90837	ATAATAAGTAGTATTTTGAA
92751	90838	AATAATAAGTAGTATTTTGA
92752	90839	AAATAATAAGTAGTATTTTG
92753	90840	GAAATAATAAGTAGTATTTT
92754	90841	TGAAATAATAAGTAGTATTT
92755	90842	ATGAAATAATAAGTAGTATT
92756	90843	TATGAAATAATAAGTAGTAT
92757	90844	GTATGAAATAATAAGTAGTA
92758	90845	AGTATGAAATAATAAGTAGT
92759	90846	AAGTATGAAATAATAAGTAG
92760	90847	AAAGTATGAAATAATAAGTA
92761	90848	TAAAGTATGAAATAATAAGT
92762	90849	CTAAAGTATGAAATAATAAG
92763	90850	GCTAAAGTATGAAATAATAA
92764	90851	TGCTAAAGTATGAAATAATA
92765	90852	GTGCTAAAGTATGAAATAAT
92766	90853	TGTGCTAAAGTATGAAATAA
92767	90854	ATGTGCTAAAGTATGAAATA
92768	90855	CATGTGCTAAAGTATGAAAT
92769	90856	ACATGTGCTAAAGTATGAAA
92770	90857	TACATGTGCTAAAGTATGAA
92771	90858	ATACATGTGCTAAAGTATGA
92772	90859	GATACATGTGCTAAAGTATG
92773	90860	AGATACATGTGCTAAAGTAT
92774	90861	TAGATACATGTGCTAAAGTA
92775	90862	ATAGATACATGTGCTAAAGT
92776	90863	AATAGATACATGTGCTAAAG
92777	90864	GAATAGATACATGTGCTAAA
92778	90865	TGAATAGATACATGTGCTAA
92779	90866	CTGAATAGATACATGTGCTA
92780	90867	GCTGAATAGATACATGTGCT
92781	90868	AGCTGAATAGATACATGTGC
92782	90869	AAGCTGAATAGATACATGTG
92783	90870	AAAGCTGAATAGATACATGT
92784	90871	TAAAGCTGAATAGATACATG
92785	90872	TTAAAGCTGAATAGATACAT
92786	90873	ATTAAAGCTGAATAGATACA
92787	90874	CATTAAAGCTGAATAGATAC
92788	90875	GCATTAAAGCTGAATAGATA
92789	90876	AGCATTAAAGCTGAATAGAT
92790	90877	TAGCATTAAAGCTGAATAGA
92791	90878	ATAGCATTAAAGCTGAATAG
92792	90879	AATAGCATTAAAGCTGAATA
92793	90880	TAATAGCATTAAAGCTGAAT
92794	90881	TTAATAGCATTAAAGCTGAA
92795	90882	GTTAATAGCATTAAAGCTGA
92796	90883	TGTTAATAGCATTAAAGCTG
92797	90884	CTGTTAATAGCATTAAAGCT
92798	90885	ACTGTTAATAGCATTAAAGC
92799	90886	AACTGTTAATAGCATTAAAG
92800	90887	CAACTGTTAATAGCATTAAA
92801	90888	ACAACTGTTAATAGCATTAA
92802	90889	AACAACTGTTAATAGCATTA
92803	90890	TAACAACTGTTAATAGCATT
92804	90891	TTAACAACTGTTAATAGCAT
92805	90892	GTTAACAACTGTTAATAGCA

141882	139969	CGCCTCGGCCTCCCAAAGTG
141883	139970	CCGCCTCGGCCTCCCAAAGT
141884	139971	TCCGCCTCGGCCTCCCAAAG
141885	139972	ATCCGCCTCGGCCTCCCAAA
141886	139973	CATCCGCCTCGGCCTCCCAA
141887	139974	CCATCCGCCTCGGCCTCCCA
141888	139975	TCCATCCGCCTCGGCCTCCC
141889	139976	ATCCATCCGCCTCGGCCTCC
141890	139977	GATCCATCCGCCTCGGCCTC
141891	139978	TGATCCATCCGCCTCGGCCT
141892	139979	GTGATCCATCCGCCTCGGCC
141893	139980	AGTGATCCATCCGCCTCGGC
141894	139981	AAGTGATCCATCCGCCTCGG
141895	139982	CAAGTGATCCATCCGCCTCG
141896	139983	TCAAGTGATCCATCCGCCTC
141897	139984	CTCAAGTGATCCATCCGCCT
141898	139985	CCTCAAGTGATCCATCCGCC
141899	139986	GCCTCAAGTGATCCATCCGC
141900	139987	GGCCTCAAGTGATCCATCCG
141901	139988	TGGCCTCAAGTGATCCATCC
141902	139989	CTGGCCTCAAGTGATCCATC
141903	139990	ACTGGCCTCAAGTGATCCAT
141904	139991	TACTGGCCTCAAGTGATCCA
141905	139992	CTACTGGCCTCAAGTGATCC
141906	139993	ACTACTGGCCTCAAGTGATC
141907	139994	AACTACTGGCCTCAAGTGAT
141908	139995	GAACTACTGGCCTCAAGTGA
141909	139996	CGAACTACTGGCCTCAAGTG
141910	139997	TCGAACTACTGGCCTCAAGT
141911	139998	CTCGAACTACTGGCCTCAAG
141912	139999	TCTCGAACTACTGGCCTCAA
141913	140000	GTCTCGAACTACTGGCCTCA
141914	140001	GGTCTCGAACTACTGGCCTC
141915	140002	TGGTCTCGAACTACTGGCCT
141916	140003	CTGGTCTCGAACTACTGGCC
141917	140004	GCTGGTCTCGAACTACTGGC
141918	140005	GGCTGGTCTCGAACTACTGG
141919	140006	AGGCTGGTCTCGAACTACTG
141920	140007	CAGGCTGGTCTCGAACTACT
141921	140008	CCAGGCTGGTCTCGAACTAC
141922	140009	GCCAGGCTGGTCTCGAACTA
141923	140010	GGCCAGGCTGGTCTCGAACT
141924	140011	TGGCCAGGCTGGTCTCGAAC
141925	140012	TTGGCCAGGCTGGTCTCGAA
141926	140013	GTTGGCCAGGCTGGTCTCGA
141927	140014	TGTTGGCCAGGCTGGTCTCG
141928	140015	ATGTTGGCCAGGCTGGTCTC
141929	140016	CATGTTGGCCAGGCTGGTCT
141930	140017	CCATGTTGGCCAGGCTGGTC
141931	140018	ACCATGTTGGCCAGGCTGGT
141932	140019	CACCATGTTGGCCAGGCTGG
141933	140020	TCACCATGTTGGCCAGGCTG
141934	140021	TTCACCATGTTGGCCAGGCT
141935	140022	TTTCACCATGTTGGCCAGGC
141936	140023	GTTTCACCATGTTGGCCAGG
141937	140024	GGTTTCACCATGTTGGCCAG
141938	140025	GGGTTTCACCATGTTGGCCA
141939	140026	CGGGTTTCACCATGTTGGCC
141940	140027	ACGGGTTTCACCATGTTGGC
141941	140028	GACGGGTTTCACCATGTTGG
141942	140029	AGACGGGTTTCACCATGTTG
141943	140030	GAGACGGGTTTCACCATGTT
141944	140031	AGAGACGGGTTTCACCATGT
141945	140032	TAGAGACGGGTTTCACCATG
141946	140033	GTAGAGACGGGTTTCACCAT
141947	140034	AGTAGAGACGGGTTTCACCA
141948	140035	TAGTAGAGACGGGTTTCACC
141949	140036	TTAGTAGAGACGGGTTTCAC
141950	140037	TTTAGTAGAGACGGGTTTCA
141951	140038	TTTTAGTAGAGACGGGTTTC
141952	140039	TTTTTAGTAGAGACGGGTTT

43659	41746	CTTGAACAAATGCCACGAAC
43660	41747	CCTTGAACAAATGCCACGAA
43661	41748	ACCTTGAACAAATGCCACGA
43662	41749	AACCTTGAACAAATGCCACG
43663	41750	AAACCTTGAACAAATGCCAC
43664	41751	AAAACCTTGAACAAATGCCA
43665	41752	CAAAACCTTGAACAAATGCC
43666	41753	ACAAAACCTTGAACAAATGC
43667	41754	TACAAAACCTTGAACAAATG
43668	41755	TTACAAAACCTTGAACAAAT
43669	41756	GTTACAAAACCTTGAACAAA
43670	41757	AGTTACAAAACCTTGAACAA
43671	41758	AAGTTACAAAACCTTGAACA
43672	41759	CAAGTTACAAAACCTTGAAC
43673	41760	CCAAGTTACAAAACCTTGAA
43674	41761	GCCAAGTTACAAAACCTTGA
43675	41762	TGCCAAGTTACAAAACCTTG
43676	41763	ATGCCAAGTTACAAAACCTT
43677	41764	GATGCCAAGTTACAAAACCT
43678	41765	AGATGCCAAGTTACAAAACC
43679	41766	GAGATGCCAAGTTACAAAAC
43680	41767	TGAGATGCCAAGTTACAAAA
43681	41768	CTGAGATGCCAAGTTACAAA
43682	41769	GCTGAGATGCCAAGTTACAA
43683	41770	TGCTGAGATGCCAAGTTACA
43684	41771	CTGCTGAGATGCCAAGTTAC
43685	41772	GCTGCTGAGATGCCAAGTTA
43686	41773	GGCTGCTGAGATGCCAAGTT
43687	41774	TGGCTGCTGAGATGCCAAGT
43688	41775	GTGGCTGCTGAGATGCCAAG
43689	41776	GGTGGCTGCTGAGATGCCAA
43690	41777	TGGTGGCTGCTGAGATGCCA
43691	41778	CTGGTGGCTGCTGAGATGCC
43692	41779	CCTGGTGGCTGCTGAGATGC
43693	41780	TCCTGGTGGCTGCTGAGATG
43694	41781	ATCCTGGTGGCTGCTGAGAT
43695	41782	TATCCTGGTGGCTGCTGAGA
43696	41783	GTATCCTGGTGGCTGCTGAG
43697	41784	GGTATCCTGGTGGCTGCTGA
43698	41785	TGGTATCCTGGTGGCTGCTG
43699	41786	CTGGTATCCTGGTGGCTGCT
43700	41787	TCTGGTATCCTGGTGGCTGC
43701	41788	ATCTGGTATCCTGGTGGCTG
43702	41789	GATCTGGTATCCTGGTGGCT
43703	41790	TGATCTGGTATCCTGGTGGC
43704	41791	ATGATCTGGTATCCTGGTGG
43705	41792	GATGATCTGGTATCCTGGTG
43706	41793	CGATGATCTGGTATCCTGGT
43707	41794	ACGATGATCTGGTATCCTGG
43708	41795	AACGATGATCTGGTATCCTG
43709	41796	GAACGATGATCTGGTATCCT
43710	41797	AGAACGATGATCTGGTATCC
43711	41798	TAGAACGATGATCTGGTATC
43712	41799	TTAGAACGATGATCTGGTAT
43713	41800	CTTAGAACGATGATCTGGTA
43714	41801	ACTTAGAACGATGATCTGGT
43715	41802	TACTTAGAACGATGATCTGG
43716	41803	TTACTTAGAACGATGATCTG
43717	41804	CTTACTTAGAACGATGATCT
43718	41805	TCTTACTTAGAACGATGATC
43719	41806	ATCTTACTTAGAACGATGAT
43720	41807	AATCTTACTTAGAACGATGA
43721	41808	AAATCTTACTTAGAACGATG
43722	41809	TAAATCTTACTTAGAACGAT
43723	41810	CTAAATCTTACTTAGAACGA
43724	41811	CCTAAATCTTACTTAGAACG
43725	41812	GCCTAAATCTTACTTAGAAC
43726	41813	TGCCTAAATCTTACTTAGAA
43727	41814	ATGCCTAAATCTTACTTAGA
43728	41815	AATGCCTAAATCTTACTTAG
43729	41816	AAATGCCTAAATCTTACTTA

92806	90893	GGTTAACAACTGTTAATAGC
92807	90894	AGGTTAACAACTGTTAATAG
92808	90895	TAGGTTAACAACTGTTAATA
92809	90896	TTAGGTTAACAACTGTTAAT
92810	90897	CTTAGGTTAACAACTGTTAA
92811	90898	ACTTAGGTTAACAACTGTTA
92812	90899	AACTTAGGTTAACAACTGTT
92813	90900	AAACTTAGGTTAACAACTGT
92814	90901	AAAACTTAGGTTAACAACTG
92815	90902	GAAAACTTAGGTTAACAACT
92816	90903	TGAAAACTTAGGTTAACAAC
92817	90904	ATGAAAACTTAGGTTAACAA
92818	90905	AATGAAAACTTAGGTTAACA
92819	90906	AAATGAAAACTTAGGTTAAC
92820	90907	CAAATGAAAACTTAGGTTAA
92821	90908	ACAAATGAAAACTTAGGTTA
92822	90909	AACAAATGAAAACTTAGGTT
92823	90910	CAACAAATGAAAACTTAGGT
92824	90911	CCAACAAATGAAAACTTAGG
92825	90912	GCCAACAAATGAAAACTTAG
92826	90913	CGCCAACAAATGAAAACTTA
92827	90914	CCGCCAACAAATGAAAACTT
92828	90915	CCCGCCAACAAATGAAAACT
92829	90916	GCCCGCCAACAAATGAAAAC
92830	90917	TGCCCGCCAACAAATGAAAA
92831	90918	GTGCCCGCCAACAAATGAAA
92832	90919	CGTGCCCGCCAACAAATGAA
92833	90920	CCGTGCCCGCCAACAAATGA
92834	90921	ACCGTGCCCGCCAACAAATG
92835	90922	CACCGTGCCCGCCAACAAAT
92836	90923	CCACCGTGCCCGCCAACAAA
92837	90924	GCCACCGTGCCCGCCAACAA
92838	90925	AGCCACCGTGCCCGCCAACA
92839	90926	GAGCCACCGTGCCCGCCAAC
92840	90927	TGAGCCACCGTGCCCGCCAA
92841	90928	GTGAGCCACCGTGCCCGCCA
92842	90929	TGTGAGCCACCGTGCCCGCC
92843	90930	GTGTGAGCCACCGTGCCCGC
92844	90931	GGTGTGAGCCACCGTGCCCG
92845	90932	AGGTGTGAGCCACCGTGCCC
92846	90933	CAGGTGTGAGCCACCGTGCC
92847	90934	ACAGGTGTGAGCCACCGTGC
92848	90935	TACAGGTGTGAGCCACCGTG
92849	90936	TTACAGGTGTGAGCCACCGT
92850	90937	ATTACAGGTGTGAGCCACCG
92851	90938	GATTACAGGTGTGAGCCACC
92852	90939	GGATTACAGGTGTGAGCCAC
92853	90940	AGGATTACAGGTGTGAGCCA
92854	90941	TAGGATTACAGGTGTGAGCC
92855	90942	CTAGGATTACAGGTGTGAGC
92856	90943	GCTAGGATTACAGGTGTGAG
92857	90944	TGCTAGGATTACAGGTGTGA
92858	90945	GTGCTAGGATTACAGGTGTG
92859	90946	AGTGCTAGGATTACAGGTGT
92860	90947	AAGTGCTAGGATTACAGGTG
92861	90948	AAAGTGCTAGGATTACAGGT
92862	90949	CAAAGTGCTAGGATTACAGG
92863	90950	CCAAAGTGCTAGGATTACAG
92864	90951	CCCAAAGTGCTAGGATTACA
92865	90952	TCCCAAAGTGCTAGGATTAC
92866	90953	CTCCCAAAGTGCTAGGATTA
92867	90954	CCTCCCAAAGTGCTAGGATT
92868	90955	GCCTCCCAAAGTGCTAGGAT
92869	90956	GGCCTCCCAAAGTGCTAGGA
92870	90957	CGGCCTCCCAAAGTGCTAGG
92871	90958	TCGGCCTCCCAAAGTGCTAG
92872	90959	CTCGGCCTCCCAAAGTGCTA
92873	90960	CCTCGGCCTCCCAAAGTGCT
92874	90961	ACCTCGGCCTCCCAAAGTGC
92875	90962	CACCTCGGCCTCCCAAAGTG
92876	90963	CCACCTCGGCCTCCCAAAGT

141953	140040	ATTTTTAGTAGAGACGGGTT
141954	140041	TATTTTTAGTAGAGACGGGT
141955	140042	GTATTTTTAGTAGAGACGGG
141956	140043	TGTATTTTTAGTAGAGACGG
141957	140044	TTGTATTTTTAGTAGAGACG
141958	140045	TTTGTATTTTTAGTAGAGAC
141959	140046	TTTTGTATTTTTAGTAGAGA
141960	140047	TTTTTGTATTTTTAGTAGAG
141961	140048	ATTTTTGTATTTTTAGTAGA
141962	140049	GATTTTTGTATTTTTAGTAG
141963	140050	TGATTTTTGTATTTTTAGTA
141964	140051	CTGATTTTTGTATTTTTAGT
141965	140052	GCTGATTTTTGTATTTTTAG
141966	140053	GGCTGATTTTTGTATTTTTA
141967	140054	TGGCTGATTTTTGTATTTTT
141968	140055	CTGGCTGATTTTTGTATTTT
141969	140056	CCTGGCTGATTTTTGTATTT
141970	140057	GCCTGGCTGATTTTTGTATT
141971	140058	TGCCTGGCTGATTTTTGTAT
141972	140059	ATGCCTGGCTGATTTTTGTA
141973	140060	CATGCCTGGCTGATTTTTGT
141974	140061	CCATGCCTGGCTGATTTTTG
141975	140062	ACCATGCCTGGCTGATTTTT
141976	140063	CACCATGCCTGGCTGATTTT
141977	140064	TCACCATGCCTGGCTGATTT
141978	140065	ATCACCATGCCTGGCTGATT
141979	140066	CATCACCATGCCTGGCTGAT
141980	140067	GCATCACCATGCCTGGCTGA
141981	140068	AGCATCACCATGCCTGGCTG
141982	140069	AAGCATCACCATGCCTGGCT
141983	140070	CAAGCATCACCATGCCTGGC
141984	140071	GCAAGCATCACCATGCCTGG
141985	140072	GGCAAGCATCACCATGCCTG
141986	140073	AGGCAAGCATCACCATGCCT
141987	140074	TAGGCAAGCATCACCATGCC
141988	140075	ATAGGCAAGCATCACCATGC
141989	140076	TATAGGCAAGCATCACCATG
141990	140077	CTATAGGCAAGCATCACCAT
141991	140078	ACTATAGGCAAGCATCACCA
141992	140079	AACTATAGGCAAGCATCACC
141993	140080	GAACTATAGGCAAGCATCAC
141994	140081	GGAACTATAGGCAAGCATCA
141995	140082	TGGAACTATAGGCAAGCATC
141996	140083	CTGGAACTATAGGCAAGCAT
141997	140084	GCTGGAACTATAGGCAAGCA
141998	140085	AGCTGGAACTATAGGCAAGC
141999	140086	TAGCTGGAACTATAGGCAAG
142000	140087	GTAGCTGGAACTATAGGCAA
142001	140088	AGTAGCTGGAACTATAGGCA
142002	140089	GAGTAGCTGGAACTATAGGC
142003	140090	CGAGTAGCTGGAACTATAGG
142004	140091	CCGAGTAGCTGGAACTATAG
142005	140092	GCCGAGTAGCTGGAACTATA
142006	140093	TGCCGAGTAGCTGGAACTAT
142007	140094	CTGCCGAGTAGCTGGAACTA
142008	140095	CCTGCCGAGTAGCTGGAACT
142009	140096	GCCTGCCGAGTAGCTGGAAC
142010	140097	AGCCTGCCGAGTAGCTGGAA
142011	140098	CAGCCTGCCGAGTAGCTGGA
142012	140099	TCAGCCTGCCGAGTAGCTGG
142013	140100	CTCAGCCTGCCGAGTAGCTG
142014	140101	CCTCAGCCTGCCGAGTAGCT
142015	140102	GCCTCAGCCTGCCGAGTAGC
142016	140103	TGCCTCAGCCTGCCGAGTAG
142017	140104	CTGCCTCAGCCTGCCGAGTA
142018	140105	CCTGCCTCAGCCTGCCGAGT
142019	140106	TCCTGCCTCAGCCTGCCGAG
142020	140107	CTCCTGCCTCAGCCTGCCGA
142021	140108	TCTCCTGCCTCAGCCTGCCG
142022	140109	TTCTCCTGCCTCAGCCTGCC
142023	140110	ATTCTCCTGCCTCAGCCTGC

43730	41817	AAAATGCCTAAATCTTACTT
43731	41818	TAAAATGCCTAAATCTTACT
43732	41819	CTAAAATGCCTAAATCTTAC
43733	41820	GCTAAAATGCCTAAATCTTA
43734	41821	GGCTAAAATGCCTAAATCTT
43735	41822	AGGCTAAAATGCCTAAATCT
43736	41823	AAGGCTAAAATGCCTAAATC
43737	41824	GAAGGCTAAAATGCCTAAAT
43738	41825	TGAAGGCTAAAATGCCTAAA
43739	41826	ATGAAGGCTAAAATGCCTAA
43740	41827	CATGAAGGCTAAAATGCCTA
43741	41828	ACATGAAGGCTAAAATGCCT
43742	41829	TACATGAAGGCTAAAATGCC
43743	41830	GTACATGAAGGCTAAAATGC
43744	41831	TGTACATGAAGGCTAAAATG
43745	41832	CTGTACATGAAGGCTAAAAT
43746	41833	TCTGTACATGAAGGCTAAAA
43747	41834	GTCTGTACATGAAGGCTAAA
43748	41835	AGTCTGTACATGAAGGCTAA
43749	41836	TAGTCTGTACATGAAGGCTA
43750	41837	ATAGTCTGTACATGAAGGCT
43751	41838	TATAGTCTGTACATGAAGGC
43752	41839	TTATAGTCTGTACATGAAGG
43753	41840	CTTATAGTCTGTACATGAAG
43754	41841	ACTTATAGTCTGTACATGAA
43755	41842	TACTTATAGTCTGTACATGA
43756	41843	GTACTTATAGTCTGTACATG
43757	41844	TGTACTTATAGTCTGTACAT
43758	41845	GTGTACTTATAGTCTGTACA
43759	41846	GGTGTACTTATAGTCTGTAC
43760	41847	GGGTGTACTTATAGTCTGTA
43761	41848	GGGGTGTACTTATAGTCTGT
43762	41849	GGGGGTGTACTTATAGTCTG
43763	41850	GGGGGGTGTACTTATAGTCT
43764	41851	GGGGGGGTGTACTTATAGTC
43765	41852	TGGGGGGGTGTACTTATAGT
43766	41853	GTGGGGGGGTGTACTTATAG
43767	41854	TGTGGGGGGGTGTACTTATA
43768	41855	GTGTGGGGGGGTGTACTTAT
43769	41856	GGTGTGGGGGGGTGTACTTA
43770	41857	GGGTGTGGGGGGGTGTACTT
43771	41858	GGGGTGTGGGGGGGTGTACT
43772	41859	AGGGGTGTGGGGGGGTGTAC
43773	41860	TAGGGGTGTGGGGGGGTGTA
43774	41861	GTAGGGGTGTGGGGGGGTGT
43775	41862	GGTAGGGGTGTGGGGGGGTG
43776	41863	TGGTAGGGGTGTGGGGGGGT
43777	41864	TTGGTAGGGGTGTGGGGGGG
43778	41865	TTTGGTAGGGGTGTGGGGGG
43779	41866	TTTTGGTAGGGGTGTGGGGG
43780	41867	GTTTTGGTAGGGGTGTGGGG
43781	41868	AGTTTTGGTAGGGGTGTGGG
43782	41869	CAGTTTTGGTAGGGGTGTGG
43783	41870	ACAGTTTTGGTAGGGGTGTG
43784	41871	TACAGTTTTGGTAGGGGTGT
43785	41872	TTACAGTTTTGGTAGGGGTG
43786	41873	TTTACAGTTTTGGTAGGGGT
43787	41874	ATTTACAGTTTTGGTAGGGG
43788	41875	AATTTACAGTTTTGGTAGGG
43789	41876	GAATTTACAGTTTTGGTAGG
43790	41877	TGAATTTACAGTTTTGGTAG
43791	41878	TTGAATTTACAGTTTTGGTA
43792	41879	TTTGAATTTACAGTTTTGGT
43793	41880	ATTTGAATTTACAGTTTTGG
43794	41881	CATTTGAATTTACAGTTTTG
43795	41882	TCATTTGAATTTACAGTTTT
43796	41883	ATCATTTGAATTTACAGTTT
43797	41884	CATCATTTGAATTTACAGTT
43798	41885	ACATCATTTGAATTTACAGT
43799	41886	AACATCATTTGAATTTACAG
43800	41887	AAACATCATTTGAATTTACA

92877	90964	CCCACCTCGGCCTCCCAAAG
92878	90965	GCCCACCTCGGCCTCCCAAA
92879	90966	TGCCCACCTCGGCCTCCCAA
92880	90967	CTGCCCACCTCGGCCTCCCA
92881	90968	TCTGCCCACCTCGGCCTCCC
92882	90969	ATCTGCCCACCTCGGCCTCC
92883	90970	GATCTGCCCACCTCGGCCTC
92884	90971	TGATCTGCCCACCTCGGCCT
92885	90972	GTGATCTGCCCACCTCGGCC
92886	90973	GGTGATCTGCCCACCTCGGC
92887	90974	AGGTGATCTGCCCACCTCGG
92888	90975	TAGGTGATCTGCCCACCTCG
92889	90976	TTAGGTGATCTGCCCACCTC
92890	90977	CTTAGGTGATCTGCCCACCT
92891	90978	CCTTAGGTGATCTGCCCACC
92892	90979	ACCTTAGGTGATCTGCCCAC
92893	90980	GACCTTAGGTGATCTGCCCA
92894	90981	TGACCTTAGGTGATCTGCCC
92895	90982	CTGACCTTAGGTGATCTGCC
92896	90983	CCTGACCTTAGGTGATCTGC
92897	90984	TCCTGACCTTAGGTGATCTG
92898	90985	CTCCTGACCTTAGGTGATCT
92899	90986	ACTCCTGACCTTAGGTGATC
92900	90987	AACTCCTGACCTTAGGTGAT
92901	90988	GAACTCCTGACCTTAGGTGA
92902	90989	CGAACTCCTGACCTTAGGTG
92903	90990	TCGAACTCCTGACCTTAGGT
92904	90991	CTCGAACTCCTGACCTTAGG
92905	90992	TCTCGAACTCCTGACCTTAG
92906	90993	GTCTCGAACTCCTGACCTTA
92907	90994	GGTCTCGAACTCCTGACCTT
92908	90995	TGGTCTCGAACTCCTGACCT
92909	90996	CTGGTCTCGAACTCCTGACC
92910	90997	GCTGGTCTCGAACTCCTGAC
92911	90998	GGCTGGTCTCGAACTCCTGA
92912	90999	AGGCTGGTCTCGAACTCCTG
92913	91000	CAGGCTGGTCTCGAACTCCT
92914	91001	CCAGGCTGGTCTCGAACTCC
92915	91002	ACCAGGCTGGTCTCGAACTC
92916	91003	GACCAGGCTGGTCTCGAACT
92917	91004	TGACCAGGCTGGTCTCGAAC
92918	91005	TTGACCAGGCTGGTCTCGAA
92919	91006	GTTGACCAGGCTGGTCTCGA
92920	91007	TGTTGACCAGGCTGGTCTCG
92921	91008	ATGTTGACCAGGCTGGTCTC
92922	91009	CATGTTGACCAGGCTGGTCT
92923	91010	CCATGTTGACCAGGCTGGTC
92924	91011	ACCATGTTGACCAGGCTGGT
92925	91012	CACCATGTTGACCAGGCTGG
92926	91013	TCACCATGTTGACCAGGCTG
92927	91014	TTCACCATGTTGACCAGGCT
92928	91015	TTTCACCATGTTGACCAGGC
92929	91016	GTTTCACCATGTTGACCAGG
92930	91017	GGTTTCACCATGTTGACCAG
92931	91018	GGGTTTCACCATGTTGACCA
92932	91019	AGGGTTTCACCATGTTGACC
92933	91020	CAGGGTTTCACCATGTTGAC
92934	91021	ACAGGGTTTCACCATGTTGA
92935	91022	GACAGGGTTTCACCATGTTG
92936	91023	AGACAGGGTTTCACCATGTT
92937	91024	AAGACAGGGTTTCACCATGT
92938	91025	CAAGACAGGGTTTCACCATG
92939	91026	TCAAGACAGGGTTTCACCAT
92940	91027	GTCAAGACAGGGTTTCACCA
92941	91028	GGTCAAGACAGGGTTTCACC
92942	91029	TGGTCAAGACAGGGTTTCAC
92943	91030	TTGGTCAAGACAGGGTTTCA
92944	91031	TTTGGTCAAGACAGGGTTTC
92945	91032	TTTTGGTCAAGACAGGGTTT
92946	91033	TTTTTGGTCAAGACAGGGTT
92947	91034	ATTTTTGGTCAAGACAGGGT

142024	140111	GATTCTCCTGCCTCAGCCTG
142025	140112	CGATTCTCCTGCCTCAGCCT
142026	140113	GCGATTCTCCTGCCTCAGCC
142027	140114	AGCGATTCTCCTGCCTCAGC
142028	140115	AAGCGATTCTCCTGCCTCAG
142029	140116	CAAGCGATTCTCCTGCCTCA
142030	140117	TCAAGCGATTCTCCTGCCTC
142031	140118	TTCAAGCGATTCTCCTGCCT
142032	140119	GTTCAAGCGATTCTCCTGCC
142033	140120	GGTTCAAGCGATTCTCCTGC
142034	140121	GGGTTCAAGCGATTCTCCTG
142035	140122	CGGGTTCAAGCGATTCTCCT
142036	140123	CCGGGTTCAAGCGATTCTCC
142037	140124	CCCGGGTTCAAGCGATTCTC
142038	140125	TCCCGGGTTCAAGCGATTCT
142039	140126	CTCCCGGGTTCAAGCGATTC
142040	140127	CCTCCCGGGTTCAAGCGATT
142041	140128	GCCTCCCGGGTTCAAGCGAT
142042	140129	CGCCTCCCGGGTTCAAGCGA
142043	140130	CCGCCTCCCGGGTTCAAGCG
142044	140131	TCCGCCTCCCGGGTTCAAGC
142045	140132	CTCCGCCTCCCGGGTTCAAG
142046	140133	CCTCCGCCTCCCGGGTTCAA
142047	140134	ACCTCCGCCTCCCGGGTTCA
142048	140135	AACCTCCGCCTCCCGGGTTC
142049	140136	CAACCTCCGCCTCCCGGGTT
142050	140137	GCAACCTCCGCCTCCCGGGT
142051	140138	TGCAACCTCCGCCTCCCGGG
142052	140139	CTGCAACCTCCGCCTCCCGG
142053	140140	ACTGCAACCTCCGCCTCCCG
142054	140141	CACTGCAACCTCCGCCTCCC
142055	140142	TCACTGCAACCTCCGCCTCC
142056	140143	CTCACTGCAACCTCCGCCTC
142057	140144	GCTCACTGCAACCTCCGCCT
142058	140145	GGCTCACTGCAACCTCCGCC
142059	140146	CGGCTCACTGCAACCTCCGC
142060	140147	TCGGCTCACTGCAACCTCCG
142061	140148	CTCGGCTCACTGCAACCTCC
142062	140149	TCTCGGCTCACTGCAACCTC
142063	140150	ATCTCGGCTCACTGCAACCT
142064	140151	CATCTCGGCTCACTGCAACC
142065	140152	CCATCTCGGCTCACTGCAAC
142066	140153	ACCATCTCGGCTCACTGCAA
142067	140154	CACCATCTCGGCTCACTGCA
142068	140155	GCACCATCTCGGCTCACTGC
142069	140156	GGCACCATCTCGGCTCACTG
142070	140157	GGGCACCATCTCGGCTCACT
142071	140158	GGGGCACCATCTCGGCTCAC
142072	140159	AGGGGCACCATCTCGGCTCA
142073	140160	CAGGGGCACCATCTCGGCTC
142074	140161	GCAGGGGCACCATCTCGGCT
142075	140162	TGCAGGGGCACCATCTCGGC
142076	140163	GTGCAGGGGCACCATCTCGG
142077	140164	AGTGCAGGGGCACCATCTCG
142078	140165	GAGTGCAGGGGCACCATCTC
142079	140166	GGAGTGCAGGGGCACCATCT
142080	140167	TGGAGTGCAGGGGCACCATC
142081	140168	CTGGAGTGCAGGGGCACCAT
142082	140169	GCTGGAGTGCAGGGGCACCA
142083	140170	GGCTGGAGTGCAGGGGCACC
142084	140171	AGGCTGGAGTGCAGGGGCAC
142085	140172	CAGGCTGGAGTGCAGGGGCA
142086	140173	CCAGGCTGGAGTGCAGGGGC
142087	140174	CCCAGGCTGGAGTGCAGGGG
142088	140175	GCCCAGGCTGGAGTGCAGGG
142089	140176	TGCCCAGGCTGGAGTGCAGG
142090	140177	TTGCCCAGGCTGGAGTGCAG
142091	140178	GTTGCCCAGGCTGGAGTGCA
142092	140179	TGTTGCCCAGGCTGGAGTGC
142093	140180	CTGTTGCCCAGGCTGGAGTG
142094	140181	TCTGTTGCCCAGGCTGGAGT

43801	41888	CAAACATCATTTGAATTTAC
43802	41889	TCAAACATCATTTGAATTTA
43803	41890	TTCAAACATCATTTGAATTT
43804	41891	TTTCAAACATCATTTGAATT
43805	41892	TTTTCAAACATCATTTGAAT
43806	41893	TTTTTCAAACATCATTTGAA
43807	41894	CTTTTTCAAACATCATTTGA
43808	41895	GCTTTTTCAAACATCATTTG
43809	41896	TGCTTTTTCAAACATCATTT
43810	41897	ATGCTTTTTCAAACATCATT
43811	41898	TATGCTTTTTCAAACATCAT
43812	41899	CTATGCTTTTTCAAACATCA
43813	41900	TCTATGCTTTTTCAAACATC
43814	41901	TTCTATGCTTTTTCAAACAT
43815	41902	ATTCTATGCTTTTTCAAACA
43816	41903	AATTCTATGCTTTTTCAAAC
43817	41904	AAATTCTATGCTTTTTCAAA
43818	41905	AAAATTCTATGCTTTTTCAA
43819	41906	AAAAATTCTATGCTTTTTCA
43820	41907	CAAAAATTCTATGCTTTTTC
43821	41908	ACAAAAATTCTATGCTTTTT
43822	41909	AACAAAAATTCTATGCTTTT
43823	41910	TAACAAAAATTCTATGCTTT
43824	41911	CTAACAAAAATTCTATGCTT
43825	41912	CCTAACAAAAATTCTATGCT
43826	41913	GCCTAACAAAAATTCTATGC
43827	41914	CGCCTAACAAAAATTCTATG
43828	41915	TCGCCTAACAAAAATTCTAT
43829	41916	CTCGCCTAACAAAAATTCTA
43830	41917	CCTCGCCTAACAAAAATTCT
43831	41918	ACCTCGCCTAACAAAAATTC
43832	41919	TACCTCGCCTAACAAAAATT
43833	41920	CTACCTCGCCTAACAAAAAT
43834	41921	ACTACCTCGCCTAACAAAAA
43835	41922	AACTACCTCGCCTAACAAAA
43836	41923	AAACTACCTCGCCTAACAAA
43837	41924	TAAACTACCTCGCCTAACAA
43838	41925	ATAAACTACCTCGCCTAACA
43839	41926	AATAAACTACCTCGCCTAAC
43840	41927	GAATAAACTACCTCGCCTAA
43841	41928	GGAATAAACTACCTCGCCTA
43842	41929	AGGAATAAACTACCTCGCCT
43843	41930	AAGGAATAAACTACCTCGCC
43844	41931	CAAGGAATAAACTACCTCGC
43845	41932	ACAAGGAATAAACTACCTCG
43846	41933	CACAAGGAATAAACTACCTC
43847	41934	TCACAAGGAATAAACTACCT
43848	41935	ATCACAAGGAATAAACTACC
43849	41936	TATCACAAGGAATAAACTAC
43850	41937	GTATCACAAGGAATAAACTA
43851	41938	TGTATCACAAGGAATAAACT
43852	41939	CTGTATCACAAGGAATAAAC
43853	41940	ACTGTATCACAAGGAATAAA
43854	41941	AACTGTATCACAAGGAATAA
43855	41942	GAACTGTATCACAAGGAATA
43856	41943	GGAACTGTATCACAAGGAAT
43857	41944	TGGAACTGTATCACAAGGAA
43858	41945	CTGGAACTGTATCACAAGGA
43859	41946	TCTGGAACTGTATCACAAGG
43860	41947	CTCTGGAACTGTATCACAAG
43861	41948	TCTCTGGAACTGTATCACAA
43862	41949	CTCTCTGGAACTGTATCACA
43863	41950	CCTCTCTGGAACTGTATCAC
43864	41951	GCCTCTCTGGAACTGTATCA
43865	41952	TGCCTCTCTGGAACTGTATC
43866	41953	CTGCCTCTCTGGAACTGTAT
43867	41954	GCTGCCTCTCTGGAACTGTA
43868	41955	TGCTGCCTCTCTGGAACTGT
43869	41956	ATGCTGCCTCTCTGGAACTG
43870	41957	TATGCTGCCTCTCTGGAACT
43871	41958	TTATGCTGCCTCTCTGGAAC

92948	91035	TATTTTTGGTCAAGACAGGG
92949	91036	CTATTTTTGGTCAAGACAGG
92950	91037	TCTATTTTTGGTCAAGACAG
92951	91038	TTCTATTTTTGGTCAAGACA
92952	91039	TTTCTATTTTTGGTCAAGAC
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92957	91044	TAATTTTTCTATTTTTGGTC
92958	91045	CTAATTTTTCTATTTTTGGT
92959	91046	GCTAATTTTTCTATTTTTGG
92960	91047	AGCTAATTTTTCTATTTTTG
92961	91048	TAGCTAATTTTTCTATTTTT
92962	91049	CTAGCTAATTTTTCTATTTT
92963	91050	CCTAGCTAATTTTTCTATTT
92964	91051	GCCTAGCTAATTTTTCTATT
92965	91052	TGCCTAGCTAATTTTTCTAT
92966	91053	ATGCCTAGCTAATTTTTCTA
92967	91054	CATGCCTAGCTAATTTTTCT
92968	91055	CCATGCCTAGCTAATTTTTC
92969	91056	ACCATGCCTAGCTAATTTTT
92970	91057	CACCATGCCTAGCTAATTTT
92971	91058	CCACCATGCCTAGCTAATTT
92972	91059	GCCACCATGCCTAGCTAATT
92973	91060	CGCCACCATGCCTAGCTAAT
92974	91061	GCGCCACCATGCCTAGCTAA
92975	91062	TGCGCCACCATGCCTAGCTA
92976	91063	GTGCGCCACCATGCCTAGCT
92977	91064	TGTGCGCCACCATGCCTAGC
92978	91065	GTGTGCGCCACCATGCCTAG
92979	91066	AGTGTGCGCCACCATGCCTA
92980	91067	AAGTGTGCGCCACCATGCCT
92981	91068	CAAGTGTGCGCCACCATGCC
92982	91069	ACAAGTGTGCGCCACCATGC
92983	91070	TACAAGTGTGCGCCACCATG
92984	91071	TTACAAGTGTGCGCCACCAT
92985	91072	ATTACAAGTGTGCGCCACCA
92986	91073	GATTACAAGTGTGCGCCACC
92987	91074	GGATTACAAGTGTGCGCCAC
92988	91075	GGGATTACAAGTGTGCGCCA
92989	91076	TGGGATTACAAGTGTGCGCC
92990	91077	CTGGGATTACAAGTGTGCGC
92991	91078	GCTGGGATTACAAGTGTGCG
92992	91079	AGCTGGGATTACAAGTGTGC
92993	91080	TAGCTGGGATTACAAGTGTG
92994	91081	GTAGCTGGGATTACAAGTGT
92995	91082	AGTAGCTGGGATTACAAGTG
92996	91083	AAGTAGCTGGGATTACAAGT
92997	91084	CAAGTAGCTGGGATTACAAG
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93000	91087	TGCCAAGTAGCTGGGATTAC
93001	91088	CTGCCAAGTAGCTGGGATTA
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93003	91090	GCCTGCCAAGTAGCTGGGAT
93004	91091	AGCCTGCCAAGTAGCTGGGA
93005	91092	CAGCCTGCCAAGTAGCTGGG
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93007	91094	CTCAGCCTGCCAAGTAGCTG
93008	91095	CCTCAGCCTGCCAAGTAGCT
93009	91096	GCCTCAGCCTGCCAAGTAGC
93010	91097	TGCCTCAGCCTGCCAAGTAG
93011	91098	CTGCCTCAGCCTGCCAAGTA
93012	91099	CCTGCCTCAGCCTGCCAAGT
93013	91100	TCCTGCCTCAGCCTGCCAAG
93014	91101	ATCCTGCCTCAGCCTGCCAA
93015	91102	TATCCTGCCTCAGCCTGCCA
93016	91103	TTATCCTGCCTCAGCCTGCC
93017	91104	ATTATCCTGCCTCAGCCTGC
93018	91105	GATTATCCTGCCTCAGCCTG

142095	140182	CTCTGTTGCCCAGGCTGGAG
142096	140183	GCTCTGTTGCCCAGGCTGGA
142097	140184	CGCTCTGTTGCCCAGGCTGG
142098	140185	TCGCTCTGTTGCCCAGGCTG
142099	140186	CTCGCTCTGTTGCCCAGGCT
142100	140187	TCTCGCTCTGTTGCCCAGGC
142101	140188	GTCTCGCTCTGTTGCCCAGG
142102	140189	AGTCTCGCTCTGTTGCCCAG
142103	140190	GAGTCTCGCTCTGTTGCCCA
142104	140191	AGAGTCTCGCTCTGTTGCCC
142105	140192	CAGAGTCTCGCTCTGTTGCC
142106	140193	ACAGAGTCTCGCTCTGTTGC
142107	140194	GACAGAGTCTCGCTCTGTTG
142108	140195	TGACAGAGTCTCGCTCTGTT
142109	140196	TTGACAGAGTCTCGCTCTGT
142110	140197	TTTGACAGAGTCTCGCTCTG
142111	140198	TTTTGACAGAGTCTCGCTCT
142112	140199	TTTTTGACAGAGTCTCGCTC
142113	140200	ATTTTTGACAGAGTCTCGCT
142114	140201	AATTTTTGACAGAGTCTCGC
142115	140202	TAATTTTTGACAGAGTCTCG
142116	140203	TTAATTTTTGACAGAGTCTC
142117	140204	TTTAATTTTTGACAGAGTCT
142118	140205	GTTTAATTTTTGACAGAGTC
142119	140206	TGTTTAATTTTTGACAGAGT
142120	140207	TTGTTTAATTTTTGACAGAG
142121	140208	TTTGTTTAATTTTTGACAGA
142122	140209	ATTTGTTTAATTTTTGACAG
142123	140210	TATTTGTTTAATTTTTGACA
142124	140211	TTATTTGTTTAATTTTTGAC
142125	140212	TTTATTTGTTTAATTTTTGA
142126	140213	ATTTATTTGTTTAATTTTTG
142127	140214	TATTTATTTGTTTAATTTTT
142128	140215	GTATTTATTTGTTTAATTTT
142129	140216	TGTATTTATTTGTTTAATTT
142130	140217	ATGTATTTATTTGTTTAATT
142131	140218	AATGTATTTATTTGTTTAAT
142132	140219	AAATGTATTTATTTGTTTAA
142133	140220	AAAATGTATTTATTTGTTTA
142134	140221	AAAAATGTATTTATTTGTTT
142135	140222	TAAAAATGTATTTATTTGTT
142136	140223	TTAAAAATGTATTTATTTGT
142137	140224	TTTAAAAATGTATTTATTTG
142138	140225	TTTTAAAAATGTATTTATTT
142139	140226	ATTTTAAAAATGTATTTATT
142140	140227	CATTTTAAAAATGTATTTAT
142141	140228	TCATTTTAAAAATGTATTTA
142142	140229	TTCATTTTAAAAATGTATTT
142143	140230	GTTCATTTTAAAAATGTATT
142144	140231	CGTTCATTTTAAAAATGTAT
142145	140232	ACGTTCATTTTAAAAATGTA
142146	140233	TACGTTCATTTTAAAAATGT
142147	140234	TTACGTTCATTTTAAAAATG
142148	140235	CTTACGTTCATTTTAAAAAT
142149	140236	TCTTACGTTCATTTTAAAAA
142150	140237	ATCTTACGTTCATTTTAAAA
142151	140238	AATCTTACGTTCATTTTAAA
142152	140239	AAATCTTACGTTCATTTTAA
142153	140240	AAAATCTTACGTTCATTTTA
142154	140241	AAAAATCTTACGTTCATTTT
142155	140242	TAAAAATCTTACGTTCATTT
142156	140243	GTAAAAATCTTACGTTCATT
142157	140244	TGTAAAAATCTTACGTTCAT
142158	140245	TTGTAAAAATCTTACGTTCA
142159	140246	CTTGTAAAAATCTTACGTTC
142160	140247	ACTTGTAAAAATCTTACGTT
142161	140248	TACTTGTAAAAATCTTACGT
142162	140249	GTACTTGTAAAAATCTTACG
142163	140250	TGTACTTGTAAAAATCTTAC
142164	140251	TTGTACTTGTAAAAATCTTA
142165	140252	GTTGTACTTGTAAAAATCTT

43872	41959	GTTATGCTGCCTCTCTGGAA
43873	41960	GGTTATGCTGCCTCTCTGGA
43874	41961	AGGTTATGCTGCCTCTCTGG
43875	41962	TAGGTTATGCTGCCTCTCTG
43876	41963	CTAGGTTATGCTGCCTCTCT
43877	41964	CCTAGGTTATGCTGCCTCTC
43878	41965	TCCTAGGTTATGCTGCCTCT
43879	41966	TTCCTAGGTTATGCTGCCTC
43880	41967	ATTCCTAGGTTATGCTGCCT
43881	41968	CATTCCTAGGTTATGCTGCC
43882	41969	TCATTCCTAGGTTATGCTGC
43883	41970	TTCATTCCTAGGTTATGCTG
43884	41971	TTTCATTCCTAGGTTATGCT
43885	41972	TTTTCATTCCTAGGTTATGC
43886	41973	TTTTTCATTCCTAGGTTATG
43887	41974	GTTTTTCATTCCTAGGTTAT
43888	41975	AGTTTTTCATTCCTAGGTTA
43889	41976	AAGTTTTTCATTCCTAGGTT
43890	41977	TAAGTTTTTCATTCCTAGGT
43891	41978	CTAAGTTTTTCATTCCTAGG
43892	41979	TCTAAGTTTTTCATTCCTAG
43893	41980	GTCTAAGTTTTTCATTCCTA
43894	41981	CGTCTAAGTTTTTCATTCCT
43895	41982	ACGTCTAAGTTTTTCATTCC
43896	41983	CACGTCTAAGTTTTTCATTC
43897	41984	CCACGTCTAAGTTTTTCATT
43898	41985	TCCACGTCTAAGTTTTTCAT
43899	41986	TTCCACGTCTAAGTTTTTCA
43900	41987	ATTCCACGTCTAAGTTTTTC
43901	41988	GATTCCACGTCTAAGTTTTT
43902	41989	TGATTCCACGTCTAAGTTTT
43903	41990	CTGATTCCACGTCTAAGTTT
43904	41991	TCTGATTCCACGTCTAAGTT
43905	41992	ATCTGATTCCACGTCTAAGT
43906	41993	TATCTGATTCCACGTCTAAG
43907	41994	GTATCTGATTCCACGTCTAA
43908	41995	TGTATCTGATTCCACGTCTA
43909	41996	GTGTATCTGATTCCACGTCT
43910	41997	GGTGTATCTGATTCCACGTC
43911	41998	AGGTGTATCTGATTCCACGT
43912	41999	CAGGTGTATCTGATTCCACG
43913	42000	CCAGGTGTATCTGATTCCAC
43914	42001	ACCAGGTGTATCTGATTCCA
43915	42002	AACCAGGTGTATCTGATTCC
43916	42003	AAACCAGGTGTATCTGATTC
43917	42004	TAAACCAGGTGTATCTGATT
43918	42005	TTAAACCAGGTGTATCTGAT
43919	42006	TTTAAACCAGGTGTATCTGA
43920	42007	ATTTAAACCAGGTGTATCTG
43921	42008	TATTTAAACCAGGTGTATCT
43922	42009	GTATTTAAACCAGGTGTATC
43923	42010	GGTATTTAAACCAGGTGTAT
43924	42011	TGGTATTTAAACCAGGTGTA
43925	42012	CTGGTATTTAAACCAGGTGT
43926	42013	GCTGGTATTTAAACCAGGTG
43927	42014	AGCTGGTATTTAAACCAGGT
43928	42015	GAGCTGGTATTTAAACCAGG
43929	42016	AGAGCTGGTATTTAAACCAG
43930	42017	TAGAGCTGGTATTTAAACCA
43931	42018	GTAGAGCTGGTATTTAAACC
43932	42019	AGTAGAGCTGGTATTTAAAC
43933	42020	CAGTAGAGCTGGTATTTAAA
43934	42021	GCAGTAGAGCTGGTATTTAA
43935	42022	AGCAGTAGAGCTGGTATTTA
43936	42023	GAGCAGTAGAGCTGGTATTT
43937	42024	TGAGCAGTAGAGCTGGTATT
43938	42025	ATGAGCAGTAGAGCTGGTAT
43939	42026	CATGAGCAGTAGAGCTGGTA
43940	42027	TCATGAGCAGTAGAGCTGGT
43941	42028	TTCATGAGCAGTAGAGCTGG
43942	42029	GTTCATGAGCAGTAGAGCTG

93019	91106	CGATTATCCTGCCTCAGCCT
93020	91107	GCGATTATCCTGCCTCAGCC
93021	91108	AGCGATTATCCTGCCTCAGC
93022	91109	AAGCGATTATCCTGCCTCAG
93023	91110	CAAGCGATTATCCTGCCTCA
93024	91111	TCAAGCGATTATCCTGCCTC
93025	91112	TTCAAGCGATTATCCTGCCT
93026	91113	GTTCAAGCGATTATCCTGCC
93027	91114	GGTTCAAGCGATTATCCTGC
93028	91115	GGGTTCAAGCGATTATCCTG
93029	91116	TGGGTTCAAGCGATTATCCT
93030	91117	CTGGGTTCAAGCGATTATCC
93031	91118	CCTGGGTTCAAGCGATTATC
93032	91119	TCCTGGGTTCAAGCGATTAT
93033	91120	CTCCTGGGTTCAAGCGATTA
93034	91121	TCTCCTGGGTTCAAGCGATT
93035	91122	GTCTCCTGGGTTCAAGCGAT
93036	91123	TGTCTCCTGGGTTCAAGCGA
93037	91124	CTGTCTCCTGGGTTCAAGCG
93038	91125	TCTGTCTCCTGGGTTCAAGC
93039	91126	CTCTGTCTCCTGGGTTCAAG
93040	91127	CCTCTGTCTCCTGGGTTCAA
93041	91128	ACCTCTGTCTCCTGGGTTCA
93042	91129	AACCTCTGTCTCCTGGGTTC
93043	91130	CAACCTCTGTCTCCTGGGTT
93044	91131	GCAACCTCTGTCTCCTGGGT
93045	91132	TGCAACCTCTGTCTCCTGGG
93046	91133	CTGCAACCTCTGTCTCCTGG
93047	91134	ACTGCAACCTCTGTCTCCTG
93048	91135	CACTGCAACCTCTGTCTCCT
93049	91136	TCACTGCAACCTCTGTCTCC
93050	91137	CTCACTGCAACCTCTGTCTC
93051	91138	GCTCACTGCAACCTCTGTCT
93052	91139	GGCTCACTGCAACCTCTGTC
93053	91140	CGGCTCACTGCAACCTCTGT
93054	91141	TCGGCTCACTGCAACCTCTG
93055	91142	CTCGGCTCACTGCAACCTCT
93056	91143	TCTCGGCTCACTGCAACCTC
93057	91144	ATCTCGGCTCACTGCAACCT
93058	91145	GATCTCGGCTCACTGCAACC
93059	91146	TGATCTCGGCTCACTGCAAC
93060	91147	GTGATCTCGGCTCACTGCAA
93061	91148	TGTGATCTCGGCTCACTGCA
93062	91149	GTGTGATCTCGGCTCACTGC
93063	91150	GGTGTGATCTCGGCTCACTG
93064	91151	TGGTGTGATCTCGGCTCACT
93065	91152	GTGGTGTGATCTCGGCTCAC
93066	91153	AGTGGTGTGATCTCGGCTCA
93067	91154	GAGTGGTGTGATCTCGGCTC
93068	91155	GGAGTGGTGTGATCTCGGCT
93069	91156	TGGAGTGGTGTGATCTCGGC
93070	91157	GTGGAGTGGTGTGATCTCGG
93071	91158	AGTGGAGTGGTGTGATCTCG
93072	91159	GAGTGGAGTGGTGTGATCTC
93073	91160	GGAGTGGAGTGGTGTGATCT
93074	91161	TGGAGTGGAGTGGTGTGATC
93075	91162	ATGGAGTGGAGTGGTGTGAT
93076	91163	GATGGAGTGGAGTGGTGTGA
93077	91164	GGATGGAGTGGAGTGGTGTG
93078	91165	AGGATGGAGTGGAGTGGTGT
93079	91166	CAGGATGGAGTGGAGTGGTG
93080	91167	CCAGGATGGAGTGGAGTGGT
93081	91168	CCCAGGATGGAGTGGAGTGG
93082	91169	GCCCAGGATGGAGTGGAGTG
93083	91170	CGCCCAGGATGGAGTGGAGT
93084	91171	TCGCCCAGGATGGAGTGGAG
93085	91172	GTCGCCCAGGATGGAGTGGA
93086	91173	TGTCGCCCAGGATGGAGTGG
93087	91174	CTGTCGCCCAGGATGGAGTG
93088	91175	TCTGTCGCCCAGGATGGAGT
93089	91176	CTCTGTCGCCCAGGATGGAG

142166	140253	TGTTGTACTTGTAAAAATCT
142167	140254	TTGTTGTACTTGTAAAAATC
142168	140255	TTTGTTGTACTTGTAAAAAT
142169	140256	GTTTGTTGTACTTGTAAAAA
142170	140257	AGTTTGTTGTACTTGTAAAA
142171	140258	GAGTTTGTTGTACTTGTAAA
142172	140259	TGAGTTTGTTGTACTTGTAA
142173	140260	CTGAGTTTGTTGTACTTGTA
142174	140261	CCTGAGTTTGTTGTACTTGT
142175	140262	ACCTGAGTTTGTTGTACTTG
142176	140263	AACCTGAGTTTGTTGTACTT
142177	140264	GAACCTGAGTTTGTTGTACT
142178	140265	CGAACCTGAGTTTGTTGTAC
142179	140266	TCGAACCTGAGTTTGTTGTA
142180	140267	TTCGAACCTGAGTTTGTTGT
142181	140268	TTTCGAACCTGAGTTTGTTG
142182	140269	ATTTCGAACCTGAGTTTGTT
142183	140270	AATTTCGAACCTGAGTTTGT
142184	140271	AAATTTCGAACCTGAGTTTG
142185	140272	TAAATTTCGAACCTGAGTTT
142186	140273	GTAAATTTCGAACCTGAGTT
142187	140274	TGTAAATTTCGAACCTGAGT
142188	140275	ATGTAAATTTCGAACCTGAG
142189	140276	GATGTAAATTTCGAACCTGA
142190	140277	TGATGTAAATTTCGAACCTG
142191	140278	TTGATGTAAATTTCGAACCT
142192	140279	TTTGATGTAAATTTCGAACC
142193	140280	ATTTGATGTAAATTTCGAAC
142194	140281	GATTTGATGTAAATTTCGAA
142195	140282	AGATTTGATGTAAATTTCGA
142196	140283	AAGATTTGATGTAAATTTCG
142197	140284	AAAGATTTGATGTAAATTTC
142198	140285	AAAAGATTTGATGTAAATTT
142199	140286	TAAAAGATTTGATGTAAATT
142200	140287	CTAAAAGATTTGATGTAAAT
142201	140288	TCTAAAAGATTTGATGTAAA
142202	140289	GTCTAAAAGATTTGATGTAA
142203	140290	GGTCTAAAAGATTTGATGTA
142204	140291	TGGTCTAAAAGATTTGATGT
142205	140292	TTGGTCTAAAAGATTTGATG
142206	140293	CTTGGTCTAAAAGATTTGAT
142207	140294	ACTTGGTCTAAAAGATTTGA
142208	140295	GACTTGGTCTAAAAGATTTG
142209	140296	TGACTTGGTCTAAAAGATTT
142210	140297	CTGACTTGGTCTAAAAGATT
142211	140298	ACTGACTTGGTCTAAAAGAT
142212	140299	CACTGACTTGGTCTAAAAGA
142213	140300	GCACTGACTTGGTCTAAAAG
142214	140301	GGCACTGACTTGGTCTAAAA
142215	140302	AGGCACTGACTTGGTCTAAA
142216	140303	TAGGCACTGACTTGGTCTAA
142217	140304	ATAGGCACTGACTTGGTCTA
142218	140305	TATAGGCACTGACTTGGTCT
142219	140306	GTATAGGCACTGACTTGGTC
142220	140307	TGTATAGGCACTGACTTGGT
142221	140308	TTGTATAGGCACTGACTTGG
142222	140309	GTTGTATAGGCACTGACTTG
142223	140310	AGTTGTATAGGCACTGACTT
142224	140311	AAGTTGTATAGGCACTGACT
142225	140312	CAAGTTGTATAGGCACTGAC
142226	140313	CCAAGTTGTATAGGCACTGA
142227	140314	TCCAAGTTGTATAGGCACTG
142228	140315	CTCCAAGTTGTATAGGCACT
142229	140316	CCTCCAAGTTGTATAGGCAC
142230	140317	TCCTCCAAGTTGTATAGGCA
142231	140318	CTCCTCCAAGTTGTATAGGC
142232	140319	GCTCCTCCAAGTTGTATAGG
142233	140320	AGCTCCTCCAAGTTGTATAG
142234	140321	CAGCTCCTCCAAGTTGTATA
142235	140322	CCAGCTCCTCCAAGTTGTAT
142236	140323	TCCAGCTCCTCCAAGTTGTA

43943	42030	AGTTCATGAGCAGTAGAGCT
43944	42031	CAGTTCATGAGCAGTAGAGC
43945	42032	CCAGTTCATGAGCAGTAGAG
43946	42033	TCCAGTTCATGAGCAGTAGA
43947	42034	ATCCAGTTCATGAGCAGTAG
43948	42035	CATCCAGTTCATGAGCAGTA
43949	42036	TCATCCAGTTCATGAGCAGT
43950	42037	ATCATCCAGTTCATGAGCAG
43951	42038	AATCATCCAGTTCATGAGCA
43952	42039	AAATCATCCAGTTCATGAGC
43953	42040	AAAATCATCCAGTTCATGAG
43954	42041	CAAAATCATCCAGTTCATGA
43955	42042	CCAAAATCATCCAGTTCATG
43956	42043	ACCAAAATCATCCAGTTCAT
43957	42044	GACCAAAATCATCCAGTTCA
43958	42045	TGACCAAAATCATCCAGTTC
43959	42046	TTGACCAAAATCATCCAGTT
43960	42047	CTTGACCAAAATCATCCAGT
43961	42048	TCTTGACCAAAATCATCCAG
43962	42049	ATCTTGACCAAAATCATCCA
43963	42050	TATCTTGACCAAAATCATCC
43964	42051	GTATCTTGACCAAAATCATC
43965	42052	AGTATCTTGACCAAAATCAT
43966	42053	AAGTATCTTGACCAAAATCA
43967	42054	CAAGTATCTTGACCAAAATC
43968	42055	TCAAGTATCTTGACCAAAAT
43969	42056	GTCAAGTATCTTGACCAAAA
43970	42057	AGTCAAGTATCTTGACCAAA
43971	42058	CAGTCAAGTATCTTGACCAA
43972	42059	GCAGTCAAGTATCTTGACCA
43973	42060	AGCAGTCAAGTATCTTGACC
43974	42061	CAGCAGTCAAGTATCTTGAC
43975	42062	TCAGCAGTCAAGTATCTTGA
43976	42063	CTCAGCAGTCAAGTATCTTG
43977	42064	CCTCAGCAGTCAAGTATCTT
43978	42065	ACCTCAGCAGTCAAGTATCT
43979	42066	AACCTCAGCAGTCAAGTATC
43980	42067	GAACCTCAGCAGTCAAGTAT
43981	42068	TGAACCTCAGCAGTCAAGTA
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43983	42070	ACTGAACCTCAGCAGTCAAG
43984	42071	AACTGAACCTCAGCAGTCAA
43985	42072	AAACTGAACCTCAGCAGTCA
43986	42073	GAAACTGAACCTCAGCAGTC
43987	42074	GGAAACTGAACCTCAGCAGT
43988	42075	AGGAAACTGAACCTCAGCAG
43989	42076	GAGGAAACTGAACCTCAGCA
43990	42077	TGAGGAAACTGAACCTCAGC
43991	42078	GTGAGGAAACTGAACCTCAG
43992	42079	GGTGAGGAAACTGAACCTCA
43993	42080	AGGTGAGGAAACTGAACCTC
43994	42081	CAGGTGAGGAAACTGAACCT
43995	42082	ACAGGTGAGGAAACTGAACC
43996	42083	TACAGGTGAGGAAACTGAAC
43997	42084	TTACAGGTGAGGAAACTGAA
43998	42085	TTTACAGGTGAGGAAACTGA
43999	42086	CTTTACAGGTGAGGAAACTG
44000	42087	ACTTTACAGGTGAGGAAACT
44001	42088	TACTTTACAGGTGAGGAAAC
44002	42089	CTACTTTACAGGTGAGGAAA
44003	42090	TCTACTTTACAGGTGAGGAA
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44005	42092	CCTCTACTTTACAGGTGAGG
44006	42093	ACCTCTACTTTACAGGTGAG
44007	42094	CACCTCTACTTTACAGGTGA
44008	42095	TCACCTCTACTTTACAGGTG
44009	42096	ATCACCTCTACTTTACAGGT
44010	42097	TATCACCTCTACTTTACAGG
44011	42098	CTATCACCTCTACTTTACAG
44012	42099	TCTATCACCTCTACTTTACA
44013	42100	ATCTATCACCTCTACTTTAC

93090	91177	GCTCTGTCGCCCAGGATGGA
93091	91178	TGCTCTGTCGCCCAGGATGG
93092	91179	TTGCTCTGTCGCCCAGGATG
93093	91180	CTTGCTCTGTCGCCCAGGAT
93094	91181	TCTTGCTCTGTCGCCCAGGA
93095	91182	GTCTTGCTCTGTCGCCCAGG
93096	91183	AGTCTTGCTCTGTCGCCCAG
93097	91184	CAGTCTTGCTCTGTCGCCCA
93098	91185	GCAGTCTTGCTCTGTCGCCC
93099	91186	TGCAGTCTTGCTCTGTCGCC
93100	91187	ATGCAGTCTTGCTCTGTCGC
93101	91188	GATGCAGTCTTGCTCTGTCG
93102	91189	AGATGCAGTCTTGCTCTGTC
93103	91190	GAGATGCAGTCTTGCTCTGT
93104	91191	TGAGATGCAGTCTTGCTCTG
93105	91192	TTGAGATGCAGTCTTGCTCT
93106	91193	TTTGAGATGCAGTCTTGCTC
93107	91194	TTTTGAGATGCAGTCTTGCT
93108	91195	TTTTTGAGATGCAGTCTTGC
93109	91196	TTTTTTGAGATGCAGTCTTG
93110	91197	TTTTTTTGAGATGCAGTCTT
93111	91198	TTTTTTTTGAGATGCAGTCT
93112	91199	TTTTTTTTTGAGATGCAGTC
93113	91200	TTTTTTTTTTGAGATGCAGT
93114	91201	TTTTTTTTTTTGAGATGCAG
93115	91202	TTTTTTTTTTTTGAGATGCA
93116	91203	TTTTTTTTTTTTTGAGATGC
93117	91204	TTTTTTTTTTTTTTGAGATG
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93122	91209	TTTTTTTTTTTTTTTTTTTG
93123	91210	TTTTTTTTTTTTTTTTTTTT
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93125	91212	TTTTTTTTTTTTTTTTTTTT
93126	91213	TTTTTTTTTTTTTTTTTTTT
93127	91214	CTTTTTTTTTTTTTTTTTTT
93128	91215	ACTTTTTTTTTTTTTTTTTT
93129	91216	AACTTTTTTTTTTTTTTTTT
93130	91217	AAACTTTTTTTTTTTTTTTT
93131	91218	AAAACTTTTTTTTTTTTTTT
93132	91219	AAAAACTTTTTTTTTTTTT
93133	91220	GAAAAACTTTTTTTTTTTT
93134	91221	TGAAAAACTTTTTTTTTTT
93135	91222	TTGAAAAACTTTTTTTTTT
93136	91223	ATTGAAAAACTTTTTTTTT
93137	91224	AATTGAAAAACTTTTTTTT
93138	91225	AAATTGAAAAACTTTTTTT
93139	91226	CAAATTGAAAAACTTTTTT
93140	91227	ACAAATTGAAAAACTTTTT
93141	91228	AACAAATTGAAAAACTTTT
93142	91229	TAACAAATTGAAAAACTTT
93143	91230	TTAACAAATTGAAAAACTT
93144	91231	TTTAACAAATTGAAAAACT
93145	91232	GTTTAACAAATTGAAAAAC
93146	91233	TGTTTAACAAATTGAAAAA
93147	91234	TTGTTTAACAAATTGAAAA
93148	91235	ATTGTTTAACAAATTGAAA
93149	91236	TATTGTTTAACAAATTGAA
93150	91237	CTATTGTTTAACAAATTGA
93151	91238	ACTATTGTTTAACAAATTG
93152	91239	AACTATTGTTTAACAAATT
93153	91240	TAACTATTGTTTAACAAAT
93154	91241	TTAACTATTGTTTAACAAA
93155	91242	GTTAACTATTGTTTAACAA
93156	91243	TGTTAACTATTGTTTAACA
93157	91244	GTGTTAACTATTGTTTAAC
93158	91245	TGTGTTAACTATTGTTTAA
93159	91246	ATGTGTTAACTATTGTTTA
93160	91247	TATGTGTTAACTATTGTTT

142237	140324	TTCCAGCTCCTCCAAGTTGT
142238	140325	CTTCCAGCTCCTCCAAGTTG
142239	140326	ACTTCCAGCTCCTCCAAGTT
142240	140327	TACTTCCAGCTCCTCCAAGT
142241	140328	TTACTTCCAGCTCCTCCAAG
142242	140329	TTTACTTCCAGCTCCTCCAA
142243	140330	GTTTACTTCCAGCTCCTCCA
142244	140331	AGTTTACTTCCAGCTCCTCC
142245	140332	AAGTTTACTTCCAGCTCCTC
142246	140333	TAAGTTTACTTCCAGCTCCT
142247	140334	TTAAGTTTACTTCCAGCTCC
142248	140335	ATTAAGTTTACTTCCAGCTC
142249	140336	CATTAAGTTTACTTCCAGCT
142250	140337	TCATTAAGTTTACTTCCAGC
142251	140338	CTCATTAAGTTTACTTCCAG
142252	140339	ACTCATTAAGTTTACTTCCA
142253	140340	TACTCATTAAGTTTACTTCC
142254	140341	ATACTCATTAAGTTTACTTC
142255	140342	CATACTCATTAAGTTTACTT
142256	140343	TCATACTCATTAAGTTTACT
142257	140344	ATCATACTCATTAAGTTTAC
142258	140345	CATCATACTCATTAAGTTTA
142259	140346	TCATCATACTCATTAAGTTT
142260	140347	ATCATCATACTCATTAAGTT
142261	140348	CATCATCATACTCATTAAGT
142262	140349	TCATCATCATACTCATTAAG
142263	140350	ATCATCATCATACTCATTAA
142264	140351	CATCATCATCATACTCATTA
142265	140352	CCATCATCATCATACTCATT
142266	140353	TCCATCATCATCATACTCAT
142267	140354	CTCCATCATCATCATACTCA
142268	140355	CCTCCATCATCATCATACTC
142269	140356	CCCTCCATCATCATCATACT
142270	140357	GCCCTCCATCATCATCATAC
142271	140358	GGCCCTCCATCATCATCATA
142272	140359	AGGCCCTCCATCATCATCAT
142273	140360	CAGGCCCTCCATCATCATCA
142274	140361	ACAGGCCCTCCATCATCATC
142275	140362	AACAGGCCCTCCATCATCAT
142276	140363	TAACAGGCCCTCCATCATCA
142277	140364	TTAACAGGCCCTCCATCATC
142278	140365	ATTAACAGGCCCTCCATCAT
142279	140366	TATTAACAGGCCCTCCATCA
142280	140367	TTATTAACAGGCCCTCCATC
142281	140368	CTTATTAACAGGCCCTCCAT
142282	140369	GCTTATTAACAGGCCCTCCA
142283	140370	GGCTTATTAACAGGCCCTCC
142284	140371	TGGCTTATTAACAGGCCCTC
142285	140372	GTGGCTTATTAACAGGCCCT
142286	140373	GGTGGCTTATTAACAGGCCC
142287	140374	TGGTGGCTTATTAACAGGCC
142288	140375	TTGGTGGCTTATTAACAGGC
142289	140376	CTTGGTGGCTTATTAACAGG
142290	140377	ACTTGGTGGCTTATTAACAG
142291	140378	AACTTGGTGGCTTATTAACA
142292	140379	TAACTTGGTGGCTTATTAAC
142293	140380	CTAACTTGGTGGCTTATTAA
142294	140381	TCTAACTTGGTGGCTTATTA
142295	140382	TTCTAACTTGGTGGCTTATT
142296	140383	TTTCTAACTTGGTGGCTTAT
142297	140384	TTTTCTAACTTGGTGGCTTA
142298	140385	TTTTTCTAACTTGGTGGCTT
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142300	140387	TTTTTTTCTAACTTGGTGGC
142301	140388	CTTTTTTTCTAACTTGGTGG
142302	140389	CCTTTTTTTCTAACTTGGTG
142303	140390	TCCTTTTTTTCTAACTTGGT
142304	140391	GTCCTTTTTTTCTAACTTGG
142305	140392	AGTCCTTTTTTTCTAACTTG
142306	140393	CAGTCCTTTTTTTCTAACTT
142307	140394	ACAGTCCTTTTTTTCTAACT

44014	42101	AATCTATCACCTCTACTTTA
44015	42102	TAATCTATCACCTCTACTTT
44016	42103	CTAATCTATCACCTCTACTT
44017	42104	TCTAATCTATCACCTCTACT
44018	42105	GTCTAATCTATCACCTCTAC
44019	42106	TGTCTAATCTATCACCTCTA
44020	42107	ATGTCTAATCTATCACCTCT
44021	42108	CATGTCTAATCTATCACCTC
44022	42109	ACATGTCTAATCTATCACCT
44023	42110	AACATGTCTAATCTATCACC
44024	42111	CAACATGTCTAATCTATCAC
44025	42112	GCAACATGTCTAATCTATCA
44026	42113	TGCAACATGTCTAATCTATC
44027	42114	ATGCAACATGTCTAATCTAT
44028	42115	CATGCAACATGTCTAATCTA
44029	42116	ACATGCAACATGTCTAATCT
44030	42117	CACATGCAACATGTCTAATC
44031	42118	TCACATGCAACATGTCTAAT
44032	42119	TTCACATGCAACATGTCTAA
44033	42120	CTTCACATGCAACATGTCTA
44034	42121	ACTTCACATGCAACATGTCT
44035	42122	TACTTCACATGCAACATGTC
44036	42123	GTACTTCACATGCAACATGT
44037	42124	AGTACTTCACATGCAACATG
44038	42125	AAGTACTTCACATGCAACAT
44039	42126	TAAGTACTTCACATGCAACA
44040	42127	CTAAGTACTTCACATGCAAC
44041	42128	ACTAAGTACTTCACATGCAA
44042	42129	TACTAAGTACTTCACATGCA
44043	42130	ATACTAAGTACTTCACATGC
44044	42131	CATACTAAGTACTTCACATG
44045	42132	CCATACTAAGTACTTCACAT
44046	42133	ACCATACTAAGTACTTCACA
44047	42134	CACCATACTAAGTACTTCAC
44048	42135	ACACCATACTAAGTACTTCA
44049	42136	GACACCATACTAAGTACTTC
44050	42137	AGACACCATACTAAGTACTT
44051	42138	CAGACACCATACTAAGTACT
44052	42139	CCAGACACCATACTAAGTAC
44053	42140	ACCAGACACCATACTAAGTA
44054	42141	AACCAGACACCATACTAAGT
44055	42142	AAACCAGACACCATACTAAG
44056	42143	AAAACCAGACACCATACTAA
44057	42144	CAAAACCAGACACCATACTA
44058	42145	ACAAAACCAGACACCATACT
44059	42146	TACAAAACCAGACACCATAC
44060	42147	CTACAAAACCAGACACCATA
44061	42148	ACTACAAAACCAGACACCAT
44062	42149	TACTACAAAACCAGACACCA
44063	42150	TTACTACAAAACCAGACACC
44064	42151	CTTACTACAAAACCAGACAC
44065	42152	TCTTACTACAAAACCAGACA
44066	42153	ATCTTACTACAAAACCAGAC
44067	42154	GATCTTACTACAAAACCAGA
44068	42155	AGATCTTACTACAAAACCAG
44069	42156	TAGATCTTACTACAAAACCA
44070	42157	ATAGATCTTACTACAAAACC
44071	42158	TATAGATCTTACTACAAAAC
44072	42159	TTATAGATCTTACTACAAAA
44073	42160	TTTATAGATCTTACTACAAA
44074	42161	TTTTATAGATCTTACTACAA
44075	42162	CTTTTATAGATCTTACTACA
44076	42163	TCTTTTATAGATCTTACTAC
44077	42164	ATCTTTTATAGATCTTACTA
44078	42165	TATCTTTTATAGATCTTACT
44079	42166	TTATCTTTTATAGATCTTAC
44080	42167	TTTATCTTTTATAGATCTTA
44081	42168	ATTTATCTTTTATAGATCTT
44082	42169	AATTTATCTTTTATAGATCT
44083	42170	TAATTTATCTTTTATAGATC
44084	42171	ATAATTTATCTTTTATAGAT

93161	91248	GTATGTGTTAACTATTGTTT
93162	91249	TGTATGTGTTAACTATTGTT
93163	91250	TTGTATGTGTTAACTATTGT
93164	91251	TTTGTATGTGTTAACTATTG
93165	91252	ATTTGTATGTGTTAACTATT
93166	91253	CATTTGTATGTGTTAACTAT
93167	91254	TCATTTGTATGTGTTAACTA
93168	91255	ATCATTTGTATGTGTTAACT
93169	91256	TATCATTTGTATGTGTTAAC
93170	91257	GTATCATTTGTATGTGTTAA
93171	91258	TGTATCATTTGTATGTGTTA
93172	91259	TTGTATCATTTGTATGTGTT
93173	91260	TTTGTATCATTTGTATGTGT
93174	91261	CTTTGTATCATTTGTATGTG
93175	91262	TCTTTGTATCATTTGTATGT
93176	91263	TTCTTTGTATCATTTGTATG
93177	91264	ATTCTTTGTATCATTTGTAT
93178	91265	TATTCTTTGTATCATTTGTA
93179	91266	ATATTCTTTGTATCATTTGT
93180	91267	AATATTCTTTGTATCATTTG
93181	91268	CAATATTCTTTGTATCATTT
93182	91269	TCAATATTCTTTGTATCATT
93183	91270	TTCAATATTCTTTGTATCAT
93184	91271	ATTCAATATTCTTTGTATCA
93185	91272	TATTCAATATTCTTTGTATC
93186	91273	ATATTCAATATTCTTTGTAT
93187	91274	CATATTCAATATTCTTTGTA
93188	91275	TCATATTCAATATTCTTTGT
93189	91276	ATCATATTCAATATTCTTTG
93190	91277	GATCATATTCAATATTCTTT
93191	91278	TGATCATATTCAATATTCTT
93192	91279	ATGATCATATTCAATATTCT
93193	91280	CATGATCATATTCAATATTC
93194	91281	ACATGATCATATTCAATATT
93195	91282	CACATGATCATATTCAATAT
93196	91283	GCACATGATCATATTCAATA
93197	91284	GGCACATGATCATATTCAAT
93198	91285	GGGCACATGATCATATTCAA
93199	91286	TGGGCACATGATCATATTCA
93200	91287	GTGGGCACATGATCATATTC
93201	91288	AGTGGGCACATGATCATATT
93202	91289	TAGTGGGCACATGATCATAT
93203	91290	GTAGTGGGCACATGATCATA
93204	91291	GGTAGTGGGCACATGATCAT
93205	91292	GGGTAGTGGGCACATGATCA
93206	91293	TGGGTAGTGGGCACATGATC
93207	91294	CTGGGTAGTGGGCACATGAT
93208	91295	GCTGGGTAGTGGGCACATGA
93209	91296	AGCTGGGTAGTGGGCACATG
93210	91297	AAGCTGGGTAGTGGGCACAT
93211	91298	TAAGCTGGGTAGTGGGCACA
93212	91299	CTAAGCTGGGTAGTGGGCAC
93213	91300	ACTAAGCTGGGTAGTGGGCA
93214	91301	TACTAAGCTGGGTAGTGGGC
93215	91302	TTACTAAGCTGGGTAGTGGG
93216	91303	TTTACTAAGCTGGGTAGTGG
93217	91304	ATTTACTAAGCTGGGTAGTG
93218	91305	TATTTACTAAGCTGGGTAGT
93219	91306	TTATTTACTAAGCTGGGTAG
93220	91307	TTTATTTACTAAGCTGGGTA
93221	91308	CTTTATTTACTAAGCTGGGT
93222	91309	GCTTTATTTACTAAGCTGGG
93223	91310	TGCTTTATTTACTAAGCTGG
93224	91311	ATGCTTTATTTACTAAGCTG
93225	91312	AATGCTTTATTTACTAAGCT
93226	91313	GAATGCTTTATTTACTAAGC
93227	91314	AGAATGCTTTATTTACTAAG
93228	91315	TAGAATGCTTTATTTACTAA
93229	91316	TTAGAATGCTTTATTTACTA
93230	91317	GTTAGAATGCTTTATTTACT
93231	91318	TGTTAGAATGCTTTATTTAC

142308	140395	GACAGTCCTTTTTTTCTAAC
142309	140396	AGACAGTCCTTTTTTTCTAA
142310	140397	AAGACAGTCCTTTTTTTCTA
142311	140398	TAAGACAGTCCTTTTTTTCT
142312	140399	ATAAGACAGTCCTTTTTTTC
142313	140400	TATAAGACAGTCCTTTTTTT
142314	140401	CTATAAGACAGTCCTTTTTT
142315	140402	TCTATAAGACAGTCCTTTTT
142316	140403	GTCTATAAGACAGTCCTTTT
142317	140404	AGTCTATAAGACAGTCCTTT
142318	140405	AAGTCTATAAGACAGTCCTT
142319	140406	TAAGTCTATAAGACAGTCCT
142320	140407	ATAAGTCTATAAGACAGTCC
142321	140408	CATAAGTCTATAAGACAGTC
142322	140409	CCATAAGTCTATAAGACAGT
142323	140410	CCCATAAGTCTATAAGACAG
142324	140411	TCCCATAAGTCTATAAGACA
142325	140412	GTCCCATAAGTCTATAAGAC
142326	140413	AGTCCCATAAGTCTATAAGA
142327	140414	CAGTCCCATAAGTCTATAAG
142328	140415	ACAGTCCCATAAGTCTATAA
142329	140416	CACAGTCCCATAAGTCTATA
142330	140417	TCACAGTCCCATAAGTCTAT
142331	140418	TTCACAGTCCCATAAGTCTA
142332	140419	CTTCACAGTCCCATAAGTCT
142333	140420	GCTTCACAGTCCCATAAGTC
142334	140421	AGCTTCACAGTCCCATAAGT
142335	140422	GAGCTTCACAGTCCCATAAG
142336	140423	TGAGCTTCACAGTCCCATAA
142337	140424	CTGAGCTTCACAGTCCCATA
142338	140425	CCTGAGCTTCACAGTCCCAT
142339	140426	TCCTGAGCTTCACAGTCCCA
142340	140427	TTCCTGAGCTTCACAGTCCC
142341	140428	CTTCCTGAGCTTCACAGTCC
142342	140429	CCTTCCTGAGCTTCACAGTC
142343	140430	GCCTTCCTGAGCTTCACAGT
142344	140431	AGCCTTCCTGAGCTTCACAG
142345	140432	AAGCCTTCCTGAGCTTCACA
142346	140433	GAAGCCTTCCTGAGCTTCAC
142347	140434	TGAAGCCTTCCTGAGCTTCA
142348	140435	ATGAAGCCTTCCTGAGCTTC
142349	140436	GATGAAGCCTTCCTGAGCTT
142350	140437	CGATGAAGCCTTCCTGAGCT
142351	140438	ACGATGAAGCCTTCCTGAGC
142352	140439	AACGATGAAGCCTTCCTGAG
142353	140440	AAACGATGAAGCCTTCCTGA
142354	140441	CAAACGATGAAGCCTTCCTG
142355	140442	ACAAACGATGAAGCCTTCCT
142356	140443	TACAAACGATGAAGCCTTCC
142357	140444	GTACAAACGATGAAGCCTTC
142358	140445	TGTACAAACGATGAAGCCTT
142359	140446	ATGTACAAACGATGAAGCCT
142360	140447	GATGTACAAACGATGAAGCC
142361	140448	TGATGTACAAACGATGAAGC
142362	140449	ATGATGTACAAACGATGAAG
142363	140450	AATGATGTACAAACGATGAA
142364	140451	AAATGATGTACAAACGATGA
142365	140452	CAAATGATGTACAAACGATG
142366	140453	ACAAATGATGTACAAACGAT
142367	140454	AACAAATGATGTACAAACGA
142368	140455	GAACAAATGATGTACAAACG
142369	140456	AGAACAAATGATGTACAAAC
142370	140457	TAGAACAAATGATGTACAAA
142371	140458	CTAGAACAAATGATGTACAA
142372	140459	GCTAGAACAAATGATGTACA
142373	140460	AGCTAGAACAAATGATGTAC
142374	140461	GAGCTAGAACAAATGATGTA
142375	140462	GGAGCTAGAACAAATGATGT
142376	140463	GGGAGCTAGAACAAATGATG
142377	140464	TGGGAGCTAGAACAAATGAT
142378	140465	CTGGGAGCTAGAACAAATGA

44085	42172	AATAATTTATCTTTTATAGA
44086	42173	TAATAATTTATCTTTTATAG
44087	42174	CTAATAATTTATCTTTTATA
44088	42175	ACTAATAATTTATCTTTTAT
44089	42176	GACTAATAATTTATCTTTTA
44090	42177	TGACTAATAATTTATCTTTT
44091	42178	ATGACTAATAATTTATCTTT
44092	42179	TATGACTAATAATTTATCTT
44093	42180	ATATGACTAATAATTTATCT
44094	42181	AATATGACTAATAATTTATC
44095	42182	GAATATGACTAATAATTTAT
44096	42183	GGAATATGACTAATAATTTA
44097	42184	AGGAATATGACTAATAATTT
44098	42185	AAGGAATATGACTAATAATT
44099	42186	TAAGGAATATGACTAATAAT
44100	42187	CTAAGGAATATGACTAATAA
44101	42188	TCTAAGGAATATGACTAATA
44102	42189	GTCTAAGGAATATGACTAAT
44103	42190	AGTCTAAGGAATATGACTAA
44104	42191	AAGTCTAAGGAATATGACTA
44105	42192	GAAGTCTAAGGAATATGACT
44106	42193	TGAAGTCTAAGGAATATGAC
44107	42194	CTGAAGTCTAAGGAATATGA
44108	42195	CCTGAAGTCTAAGGAATATG
44109	42196	TCCTGAAGTCTAAGGAATAT
44110	42197	TTCCTGAAGTCTAAGGAATA
44111	42198	ATTCCTGAAGTCTAAGGAAT
44112	42199	AATTCCTGAAGTCTAAGGAA
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44115	42202	ATAAATTCCTGAAGTCTAAG
44116	42203	GATAAATTCCTGAAGTCTAA
44117	42204	AGATAAATTCCTGAAGTCTA
44118	42205	GAGATAAATTCCTGAAGTCT
44119	42206	AGAGATAAATTCCTGAAGTC
44120	42207	CAGAGATAAATTCCTGAAGT
44121	42208	ACAGAGATAAATTCCTGAAG
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44123	42210	GCACAGAGATAAATTCCTGA
44124	42211	GGCACAGAGATAAATTCCTG
44125	42212	TGGCACAGAGATAAATTCCT
44126	42213	ATGGCACAGAGATAAATTCC
44127	42214	CATGGCACAGAGATAAATTC
44128	42215	ACATGGCACAGAGATAAATT
44129	42216	AACATGGCACAGAGATAAAT
44130	42217	AAACATGGCACAGAGATAAA
44131	42218	CAAACATGGCACAGAGATAA
44132	42219	TCAAACATGGCACAGAGATA
44133	42220	CTCAAACATGGCACAGAGAT
44134	42221	CCTCAAACATGGCACAGAGA
44135	42222	GCCTCAAACATGGCACAGAG
44136	42223	TGCCTCAAACATGGCACAGA
44137	42224	TTGCCTCAAACATGGCACAG
44138	42225	TTTGCCTCAAACATGGCACA
44139	42226	GTTTGCCTCAAACATGGCAC
44140	42227	TGTTTGCCTCAAACATGGCA
44141	42228	CTGTTTGCCTCAAACATGGC
44142	42229	ACTGTTTGCCTCAAACATGG
44143	42230	AACTGTTTGCCTCAAACATG
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44145	42232	GTAACTGTTTGCCTCAAACA
44146	42233	TGTAACTGTTTGCCTCAAAC
44147	42234	CTGTAACTGTTTGCCTCAAA
44148	42235	TCTGTAACTGTTTGCCTCAA
44149	42236	TTCTGTAACTGTTTGCCTCA
44150	42237	ATTCTGTAACTGTTTGCCTC
44151	42238	AATTCTGTAACTGTTTGCCT
44152	42239	TAATTCTGTAACTGTTTGCC
44153	42240	CTAATTCTGTAACTGTTTGC
44154	42241	TCTAATTCTGTAACTGTTTG
44155	42242	TTCTAATTCTGTAACTGTTT

93232	91319	GTGTTAGAATGCTTTATTTA
93233	91320	TGTGTTAGAATGCTTTATTT
93234	91321	CTGTGTTAGAATGCTTTATT
93235	91322	ACTGTGTTAGAATGCTTTAT
93236	91323	AACTGTGTTAGAATGCTTTA
93237	91324	TAACTGTGTTAGAATGCTTT
93238	91325	TTAACTGTGTTAGAATGCTT
93239	91326	TTTAACTGTGTTAGAATGCT
93240	91327	GTTTAACTGTGTTAGAATGC
93241	91328	AGTTTAACTGTGTTAGAATG
93242	91329	GAGTTTAACTGTGTTAGAAT
93243	91330	GGAGTTTAACTGTGTTAGAA
93244	91331	AGGAGTTTAACTGTGTTAGA
93245	91332	GAGGAGTTTAACTGTGTTAG
93246	91333	AGAGGAGTTTAACTGTGTTA
93247	91334	AAGAGGAGTTTAACTGTGTT
93248	91335	TAAGAGGAGTTTAACTGTGT
93249	91336	ATAAGAGGAGTTTAACTGTG
93250	91337	CATAAGAGGAGTTTAACTGT
93251	91338	ACATAAGAGGAGTTTAACTG
93252	91339	TACATAAGAGGAGTTTAACT
93253	91340	ATACATAAGAGGAGTTTAAC
93254	91341	GATACATAAGAGGAGTTTAA
93255	91342	AGATACATAAGAGGAGTTTA
93256	91343	CAGATACATAAGAGGAGTTT
93257	91344	GCAGATACATAAGAGGAGTT
93258	91345	GGCAGATACATAAGAGGAGT
93259	91346	GGGCAGATACATAAGAGGAG
93260	91347	GGGGCAGATACATAAGAGGA
93261	91348	AGGGGCAGATACATAAGAGG
93262	91349	GAGGGGCAGATACATAAGAG
93263	91350	GGAGGGGCAGATACATAAGA
93264	91351	AGGAGGGGCAGATACATAAG
93265	91352	GAGGAGGGGCAGATACATAA
93266	91353	TGAGGAGGGGCAGATACATA
93267	91354	CTGAGGAGGGGCAGATACAT
93268	91355	GCTGAGGAGGGGCAGATACA
93269	91356	AGCTGAGGAGGGGCAGATAC
93270	91357	CAGCTGAGGAGGGGCAGATA
93271	91358	GCAGCTGAGGAGGGGCAGAT
93272	91359	AGCAGCTGAGGAGGGGCAGA
93273	91360	AAGCAGCTGAGGAGGGGCAG
93274	91361	GAAGCAGCTGAGGAGGGGCA
93275	91362	GGAAGCAGCTGAGGAGGGGC
93276	91363	GGGAAGCAGCTGAGGAGGGG
93277	91364	GGGGAAGCAGCTGAGGAGGG
93278	91365	GGGGGAAGCAGCTGAGGAGG
93279	91366	AGGGGGAAGCAGCTGAGGAG
93280	91367	CAGGGGGAAGCAGCTGAGGA
93281	91368	ACAGGGGGAAGCAGCTGAGG
93282	91369	AACAGGGGGAAGCAGCTGAG
93283	91370	AAACAGGGGGAAGCAGCTGA
93284	91371	GAAACAGGGGGAAGCAGCTG
93285	91372	GGAAACAGGGGGAAGCAGCT
93286	91373	AGGAAACAGGGGGAAGCAGC
93287	91374	AAGGAAACAGGGGGAAGCAG
93288	91375	GAAGGAAACAGGGGGAAGCA
93289	91376	GGAAGGAAACAGGGGGAAGC
93290	91377	TGGAAGGAAACAGGGGGAAG
93291	91378	TTGGAAGGAAACAGGGGGAA
93292	91379	TTTGGAAGGAAACAGGGGGA
93293	91380	TTTTGGAAGGAAACAGGGGG
93294	91381	CTTTTGGAAGGAAACAGGGG
93295	91382	CCTTTTGGAAGGAAACAGGG
93296	91383	TCCTTTTGGAAGGAAACAGG
93297	91384	TTCCTTTTGGAAGGAAACAG
93298	91385	CTTCCTTTTGGAAGGAAACA
93299	91386	CCTTCCTTTTGGAAGGAAAC
93300	91387	CCCTTCCTTTTGGAAGGAAA
93301	91388	ACCCTTCCTTTTGGAAGGAA
93302	91389	AACCCTTCCTTTTGGAAGGA

142379	140466	TCTGGGAGCTAGAACAAATG
142380	140467	TTCTGGGAGCTAGAACAAAT
142381	140468	CTTCTGGGAGCTAGAACAAA
142382	140469	TCTTCTGGGAGCTAGAACAA
142383	140470	GTCTTCTGGGAGCTAGAACA
142384	140471	CGTCTTCTGGGAGCTAGAAC
142385	140472	ACGTCTTCTGGGAGCTAGAA
142386	140473	AACGTCTTCTGGGAGCTAGA
142387	140474	GAACGTCTTCTGGGAGCTAG
142388	140475	TGAACGTCTTCTGGGAGCTA
142389	140476	GTGAACGTCTTCTGGGAGCT
142390	140477	AGTGAACGTCTTCTGGGAGC
142391	140478	TAGTGAACGTCTTCTGGGAG
142392	140479	GTAGTGAACGTCTTCTGGGA
142393	140480	AGTAGTGAACGTCTTCTGGG
142394	140481	GAGTAGTGAACGTCTTCTGG
142395	140482	AGAGTAGTGAACGTCTTCTG
142396	140483	AAGAGTAGTGAACGTCTTCT
142397	140484	TAAGAGTAGTGAACGTCTTC
142398	140485	TTAAGAGTAGTGAACGTCTT
142399	140486	TTTAAGAGTAGTGAACGTCT
142400	140487	TTTTAAGAGTAGTGAACGTC
142401	140488	TTTTTAAGAGTAGTGAACGT
142402	140489	GTTTTTAAGAGTAGTGAACG
142403	140490	TGTTTTTAAGAGTAGTGAAC
142404	140491	ATGTTTTTAAGAGTAGTGAA
142405	140492	AATGTTTTTAAGAGTAGTGA
142406	140493	GAATGTTTTTAAGAGTAGTG
142407	140494	TGAATGTTTTTAAGAGTAGT
142408	140495	CTGAATGTTTTTAAGAGTAG
142409	140496	TCTGAATGTTTTTAAGAGTA
142410	140497	CTCTGAATGTTTTTAAGAGT
142411	140498	TCTCTGAATGTTTTTAAGAG
142412	140499	GTCTCTGAATGTTTTTAAGA
142413	140500	AGTCTCTGAATGTTTTTAAG
142414	140501	TAGTCTCTGAATGTTTTTAA
142415	140502	ATAGTCTCTGAATGTTTTTA
142416	140503	CATAGTCTCTGAATGTTTTT
142417	140504	ACATAGTCTCTGAATGTTTT
142418	140505	AACATAGTCTCTGAATGTTT
142419	140506	CAACATAGTCTCTGAATGTT
142420	140507	GCAACATAGTCTCTGAATGT
142421	140508	GGCAACATAGTCTCTGAATG
142422	140509	TGGCAACATAGTCTCTGAAT
142423	140510	GTGGCAACATAGTCTCTGAA
142424	140511	TGTGGCAACATAGTCTCTGA
142425	140512	CTGTGGCAACATAGTCTCTG
142426	140513	ACTGTGGCAACATAGTCTCT
142427	140514	AACTGTGGCAACATAGTCTC
142428	140515	AAACTGTGGCAACATAGTCT
142429	140516	AAAACTGTGGCAACATAGTC
142430	140517	GAAAACTGTGGCAACATAGT
142431	140518	AGAAAACTGTGGCAACATAG
142432	140519	AAGAAAACTGTGGCAACATA
142433	140520	CAAGAAAACTGTGGCAACAT
142434	140521	ACAAGAAAACTGTGGCAACA
142435	140522	AACAAGAAAACTGTGGCAAC
142436	140523	TAACAAGAAAACTGTGGCAA
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142443	140530	AATATTTTAACAAGAAAACT
142444	140531	GAATATTTTAACAAGAAAAC
142445	140532	AGAATATTTTAACAAGAAAA
142446	140533	CAGAATATTTTAACAAGAAA
142447	140534	CCAGAATATTTTAACAAGAA
142448	140535	GCCAGAATATTTTAACAAGA
142449	140536	TGCCAGAATATTTTAACAAG

44156	42243	ATTCTAATTCTGTAACTGTT
44157	42244	CATTCTAATTCTGTAACTGT
44158	42245	ACATTCTAATTCTGTAACTG
44159	42246	AACATTCTAATTCTGTAACT
44160	42247	TAACATTCTAATTCTGTAAC
44161	42248	CTAACATTCTAATTCTGTAA
44162	42249	TCTAACATTCTAATTCTGTA
44163	42250	TTCTAACATTCTAATTCTGT
44164	42251	TTTCTAACATTCTAATTCTG
44165	42252	ATTTCTAACATTCTAATTCT
44166	42253	CATTTCTAACATTCTAATTC
44167	42254	TCATTTCTAACATTCTAATT
44168	42255	TTCATTTCTAACATTCTAAT
44169	42256	TTTCATTTCTAACATTCTAA
44170	42257	CTTTCATTTCTAACATTCTA
44171	42258	CCTTTCATTTCTAACATTCT
44172	42259	TCCTTTCATTTCTAACATTC
44173	42260	TTCCTTTCATTTCTAACATT
44174	42261	ATTCCTTTCATTTCTAACAT
44175	42262	GATTCCTTTCATTTCTAACA
44176	42263	GGATTCCTTTCATTTCTAAC
44177	42264	AGGATTCCTTTCATTTCTAA
44178	42265	TAGGATTCCTTTCATTTCTA
44179	42266	CTAGGATTCCTTTCATTTCT
44180	42267	TCTAGGATTCCTTTCATTTC
44181	42268	ATCTAGGATTCCTTTCATTT
44182	42269	CATCTAGGATTCCTTTCATT
44183	42270	ACATCTAGGATTCCTTTCAT
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44185	42272	TGACATCTAGGATTCCTTTC
44186	42273	ATGACATCTAGGATTCCTTT
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44188	42275	AAATGACATCTAGGATTCCT
44189	42276	TAAATGACATCTAGGATTCC
44190	42277	TTAAATGACATCTAGGATTC
44191	42278	ATTAAATGACATCTAGGATT
44192	42279	AATTAAATGACATCTAGGAT
44193	42280	GAATTAAATGACATCTAGGA
44194	42281	TGAATTAAATGACATCTAGG
44195	42282	TTGAATTAAATGACATCTAG
44196	42283	CTTGAATTAAATGACATCTA
44197	42284	ACTTGAATTAAATGACATCT
44198	42285	GACTTGAATTAAATGACATC
44199	42286	GGACTTGAATTAAATGACAT
44200	42287	TGGACTTGAATTAAATGACA
44201	42288	ATGGACTTGAATTAAATGAC
44202	42289	AATGGACTTGAATTAAATGA
44203	42290	CAATGGACTTGAATTAAATG
44204	42291	ACAATGGACTTGAATTAAAT
44205	42292	AACAATGGACTTGAATTAAA
44206	42293	AAACAATGGACTTGAATTAA
44207	42294	AAAACAATGGACTTGAATTA
44208	42295	GAAAACAATGGACTTGAATT
44209	42296	AGAAAACAATGGACTTGAAT
44210	42297	CAGAAAACAATGGACTTGAA
44211	42298	CCAGAAAACAATGGACTTGA
44212	42299	TCCAGAAAACAATGGACTTG
44213	42300	ATCCAGAAAACAATGGACTT
44214	42301	CATCCAGAAAACAATGGACT
44215	42302	TCATCCAGAAAACAATGGAC
44216	42303	CTCATCCAGAAAACAATGGA
44217	42304	TCTCATCCAGAAAACAATGG
44218	42305	CTCTCATCCAGAAAACAATG
44219	42306	TCTCTCATCCAGAAAACAAT
44220	42307	TTCTCTCATCCAGAAAACAA
44221	42308	CTTCTCTCATCCAGAAAACA
44222	42309	TCTTCTCTCATCCAGAAAAC
44223	42310	TTCTTCTCTCATCCAGAAAA
44224	42311	TTTCTTCTCTCATCCAGAAA
44225	42312	CTTTCTTCTCTCATCCAGAA
44226	42313	ACTTTCTTCTCTCATCCAGA

93303	91390	AAACCCTTCCTTTTGGAAGG
93304	91391	GAAACCCTTCCTTTTGGAAG
93305	91392	AGAAACCCTTCCTTTTGGAA
93306	91393	AAGAAACCCTTCCTTTTGGA
93307	91394	AAAGAAACCCTTCCTTTTGG
93308	91395	AAAAGAAACCCTTCCTTTTG
93309	91396	GAAAAGAAACCCTTCCTTTT
93310	91397	AGAAAAGAAACCCTTCCTTT
93311	91398	CAGAAAAGAAACCCTTCCTT
93312	91399	ACAGAAAAGAAACCCTTCCT
93313	91400	CACAGAAAAGAAACCCTTCC
93314	91401	GCACAGAAAAGAAACCCTTC
93315	91402	TGCACAGAAAAGAAACCCTT
93316	91403	CTGCACAGAAAAGAAACCCT
93317	91404	ACTGCACAGAAAAGAAACCC
93318	91405	AACTGCACAGAAAAGAAACC
93319	91406	GAACTGCACAGAAAAGAAAC
93320	91407	AGAACTGCACAGAAAAGAAA
93321	91408	AAGAACTGCACAGAAAAGAA
93322	91409	AAAGAACTGCACAGAAAAGA
93323	91410	TAAAGAACTGCACAGAAAAG
93324	91411	ATAAAGAACTGCACAGAAAA
93325	91412	TATAAAGAACTGCACAGAAA
93326	91413	ATATAAAGAACTGCACAGAA
93327	91414	AATATAAAGAACTGCACAGA
93328	91415	AAATATAAAGAACTGCACAG
93329	91416	TAAATATAAAGAACTGCACA
93330	91417	ATAAATATAAAGAACTGCAC
93331	91418	TATAAATATAAAGAACTGCA
93332	91419	GTATAAATATAAAGAACTGC
93333	91420	AGTATAAATATAAAGAACTG
93334	91421	CAGTATAAATATAAAGAACT
93335	91422	GCAGTATAAATATAAAGAAC
93336	91423	TGCAGTATAAATATAAAGAA
93337	91424	ATGCAGTATAAATATAAAGA
93338	91425	TATGCAGTATAAATATAAAG
93339	91426	ATATGCAGTATAAATATAAA
93340	91427	CATATGCAGTATAAATATAA
93341	91428	TCATATGCAGTATAAATATA
93342	91429	TTCATATGCAGTATAAATAT
93343	91430	ATTCATATGCAGTATAAATA
93344	91431	TATTCATATGCAGTATAAAT
93345	91432	ATATTCATATGCAGTATAAA
93346	91433	TATATTCATATGCAGTATAA
93347	91434	ATATATTCATATGCAGTATA
93348	91435	GATATATTCATATGCAGTAT
93349	91436	AGATATATTCATATGCAGTA
93350	91437	CAGATATATTCATATGCAGT
93351	91438	ACAGATATATTCATATGCAG
93352	91439	CACAGATATATTCATATGCA
93353	91440	TCACAGATATATTCATATGC
93354	91441	CTCACAGATATATTCATATG
93355	91442	GCTCACAGATATATTCATAT
93356	91443	TGCTCACAGATATATTCATA
93357	91444	TTGCTCACAGATATATTCAT
93358	91445	ATTGCTCACAGATATATTCA
93359	91446	TATTGCTCACAGATATATTC
93360	91447	CTATTGCTCACAGATATATT
93361	91448	TCTATTGCTCACAGATATAT
93362	91449	ATCTATTGCTCACAGATATA
93363	91450	CATCTATTGCTCACAGATAT
93364	91451	TCATCTATTGCTCACAGATA
93365	91452	ATCATCTATTGCTCACAGAT
93366	91453	TATCATCTATTGCTCACAGA
93367	91454	ATATCATCTATTGCTCACAG
93368	91455	AATATCATCTATTGCTCACA
93369	91456	AAATATCATCTATTGCTCAC
93370	91457	AAAATATCATCTATTGCTCA
93371	91458	CAAAATATCATCTATTGCTC
93372	91459	GCAAAATATCATCTATTGCT
93373	91460	TGCAAAATATCATCTATTGC

142450	140537	ATGCCAGAATATTTTAACAA
142451	140538	TATGCCAGAATATTTTAACA
142452	140539	ATATGCCAGAATATTTTAAC
142453	140540	CATATGCCAGAATATTTTAA
142454	140541	ACATATGCCAGAATATTTTA
142455	140542	AACATATGCCAGAATATTTT
142456	140543	TAACATATGCCAGAATATTT
142457	140544	TTAACATATGCCAGAATATT
142458	140545	ATTAACATATGCCAGAATAT
142459	140546	AATTAACATATGCCAGAATA
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142461	140548	GGAATTAACATATGCCAGAA
142462	140549	AGGAATTAACATATGCCAGA
142463	140550	TAGGAATTAACATATGCCAG
142464	140551	GTAGGAATTAACATATGCCA
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142466	140553	CTGTAGGAATTAACATATGC
142467	140554	ACTGTAGGAATTAACATATG
142468	140555	GACTGTAGGAATTAACATAT
142469	140556	AGACTGTAGGAATTAACATA
142470	140557	CAGACTGTAGGAATTAACAT
142471	140558	CCAGACTGTAGGAATTAACA
142472	140559	TCCAGACTGTAGGAATTAAC
142473	140560	TTCCAGACTGTAGGAATTAA
142474	140561	TTTCCAGACTGTAGGAATTA
142475	140562	TTTTCCAGACTGTAGGAATT
142476	140563	ATTTTCCAGACTGTAGGAAT
142477	140564	AATTTTCCAGACTGTAGGAA
142478	140565	AAATTTTCCAGACTGTAGGA
142479	140566	AAAATTTTCCAGACTGTAGG
142480	140567	GAAAATTTTCCAGACTGTAG
142481	140568	GGAAAATTTTCCAGACTGTA
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142484	140571	CTGGGAAAATTTTCCAGACT
142485	140572	ACTGGGAAAATTTTCCAGAC
142486	140573	CACTGGGAAAATTTTCCAGA
142487	140574	ACACTGGGAAAATTTTCCAG
142488	140575	TACACTGGGAAAATTTTCCA
142489	140576	ATACACTGGGAAAATTTTCC
142490	140577	TATACACTGGGAAAATTTTC
142491	140578	TTATACACTGGGAAAATTTT
142492	140579	TTTATACACTGGGAAAATTT
142493	140580	GTTTATACACTGGGAAAATT
142494	140581	TGTTTATACACTGGGAAAAT
142495	140582	TTGTTTATACACTGGGAAAA
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142502	140589	AGCAGCTTTGTTTATACACT
142503	140590	CAGCAGCTTTGTTTATACAC
142504	140591	ACAGCAGCTTTGTTTATACA
142505	140592	TACAGCAGCTTTGTTTATAC
142506	140593	ATACAGCAGCTTTGTTTATA
142507	140594	GATACAGCAGCTTTGTTTAT
142508	140595	GGATACAGCAGCTTTGTTTA
142509	140596	TGGATACAGCAGCTTTGTTT
142510	140597	CTGGATACAGCAGCTTTGTT
142511	140598	ACTGGATACAGCAGCTTTGT
142512	140599	GACTGGATACAGCAGCTTTG
142513	140600	AGACTGGATACAGCAGCTTT
142514	140601	TAGACTGGATACAGCAGCTT
142515	140602	TTAGACTGGATACAGCAGCT
142516	140603	TTTAGACTGGATACAGCAGC
142517	140604	GTTTAGACTGGATACAGCAG
142518	140605	AGTTTAGACTGGATACAGCA
142519	140606	CAGTTTAGACTGGATACAGC
142520	140607	CCAGTTTAGACTGGATACAG

44227	42314	CACTTTCTTCTCTCATCCAG
44228	42315	TCACTTTCTTCTCTCATCCA
44229	42316	CTCACTTTCTTCTCTCATCC
44230	42317	CCTCACTTTCTTCTCTCATC
44231	42318	TCCTCACTTTCTTCTCTCAT
44232	42319	TTCCTCACTTTCTTCTCTCA
44233	42320	TTTCCTCACTTTCTTCTCTC
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44235	42322	CTTTTCCTCACTTTCTTCTC
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44245	42332	AACTCTGTCACTTTTCCTCA
44246	42333	CAACTCTGTCACTTTTCCTC
44247	42334	CCAACTCTGTCACTTTTCCT
44248	42335	TCCAACTCTGTCACTTTTCC
44249	42336	CTCCAACTCTGTCACTTTTC
44250	42337	TCTCCAACTCTGTCACTTTT
44251	42338	GTCTCCAACTCTGTCACTTT
44252	42339	GGTCTCCAACTCTGTCACTT
44253	42340	TGGTCTCCAACTCTGTCACT
44254	42341	TTGGTCTCCAACTCTGTCAC
44255	42342	CTTGGTCTCCAACTCTGTCA
44256	42343	GCTTGGTCTCCAACTCTGTC
44257	42344	AGCTTGGTCTCCAACTCTGT
44258	42345	TAGCTTGGTCTCCAACTCTG
44259	42346	CTAGCTTGGTCTCCAACTCT
44260	42347	CCTAGCTTGGTCTCCAACTC
44261	42348	TCCTAGCTTGGTCTCCAACT
44262	42349	GTCCTAGCTTGGTCTCCAAC
44263	42350	AGTCCTAGCTTGGTCTCCAA
44264	42351	CAGTCCTAGCTTGGTCTCCA
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44266	42353	GCCAGTCCTAGCTTGGTCTC
44267	42354	GGCCAGTCCTAGCTTGGTCT
44268	42355	AGGCCAGTCCTAGCTTGGTC
44269	42356	GAGGCCAGTCCTAGCTTGGT
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44271	42358	CTGAGGCCAGTCCTAGCTTG
44272	42359	TCTGAGGCCAGTCCTAGCTT
44273	42360	TTCTGAGGCCAGTCCTAGCT
44274	42361	ATTCTGAGGCCAGTCCTAGC
44275	42362	CATTCTGAGGCCAGTCCTAG
44276	42363	ACATTCTGAGGCCAGTCCTA
44277	42364	AACATTCTGAGGCCAGTCCT
44278	42365	TAACATTCTGAGGCCAGTCC
44279	42366	TTAACATTCTGAGGCCAGTC
44280	42367	CTTAACATTCTGAGGCCAGT
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44282	42369	CTCTTAACATTCTGAGGCCA
44283	42370	ACTCTTAACATTCTGAGGCC
44284	42371	TACTCTTAACATTCTGAGGC
44285	42372	GTACTCTTAACATTCTGAGG
44286	42373	AGTACTCTTAACATTCTGAG
44287	42374	GAGTACTCTTAACATTCTGA
44288	42375	AGAGTACTCTTAACATTCTG
44289	42376	AAGAGTACTCTTAACATTCT
44290	42377	GAAGAGTACTCTTAACATTC
44291	42378	AGAAGAGTACTCTTAACATT
44292	42379	TAGAAGAGTACTCTTAACAT
44293	42380	CTAGAAGAGTACTCTTAACA
44294	42381	CCTAGAAGAGTACTCTTAAC
44295	42382	CCCTAGAAGAGTACTCTTAA
44296	42383	TCCCTAGAAGAGTACTCTTA
44297	42384	ATCCCTAGAAGAGTACTCTT

93374	91461	ATGCAAAATATCATCTATTG
93375	91462	TATGCAAAATATCATCTATT
93376	91463	TTATGCAAAATATCATCTAT
93377	91464	ATTATGCAAAATATCATCTA
93378	91465	GATTATGCAAAATATCATCT
93379	91466	AGATTATGCAAAATATCATC
93380	91467	AAGATTATGCAAAATATCAT
93381	91468	TAAGATTATGCAAAATATCA
93382	91469	TTAAGATTATGCAAAATATC
93383	91470	TTTAAGATTATGCAAAATAT
93384	91471	ATTTAAGATTATGCAAAATA
93385	91472	AATTTAAGATTATGCAAAAT
93386	91473	AAATTTAAGATTATGCAAAA
93387	91474	CAAATTTAAGATTATGCAAA
93388	91475	GCAAATTTAAGATTATGCAA
93389	91476	AGCAAATTTAAGATTATGCA
93390	91477	TAGCAAATTTAAGATTATGC
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93392	91479	TATAGCAAATTTAAGATTAT
93393	91480	TTATAGCAAATTTAAGATTA
93394	91481	TTTATAGCAAATTTAAGATT
93395	91482	CTTTATAGCAAATTTAAGAT
93396	91483	ACTTTATAGCAAATTTAAGA
93397	91484	GACTTTATAGCAAATTTAAG
93398	91485	AGACTTTATAGCAAATTTAA
93399	91486	AAGACTTTATAGCAAATTTA
93400	91487	AAAGACTTTATAGCAAATTT
93401	91488	AAAAGACTTTATAGCAAATT
93402	91489	AAAAAGACTTTATAGCAAAT
93403	91490	AAAAAAGACTTTATAGCAAA
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93407	91494	AAAAAAAAAAGACTTTATAG
93408	91495	AAAAAAAAAAAGACTTTATA
93409	91496	AAAAAAAAAAAAGACTTTAT
93410	91497	AAAAAAAAAAAAAGACTTTA
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93412	91499	TAAAAAAAAAAAAAAGACTT
93413	91500	TTAAAAAAAAAAAAAAAGACT
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93416	91503	CAATTAAAAAAAAAAAAAAG
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93418	91505	ATCAATTAAAAAAAAAAAAA
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93420	91507	TGATCAATTAAAAAAAAAAA
93421	91508	ATGATCAATTAAAAAAAAAA
93422	91509	AATGATCAATTAAAAAAAAA
93423	91510	GAATGATCAATTAAAAAAAA
93424	91511	AGAATGATCAATTAAAAAAA
93425	91512	AAGAATGATCAATTAAAAAA
93426	91513	CAAGAATGATCAATTAAAAA
93427	91514	CCAAGAATGATCAATTAAAA
93428	91515	CCCAAGAATGATCAATTAAA
93429	91516	ACCCAAGAATGATCAATTAA
93430	91517	CACCCAAGAATGATCAATTA
93431	91518	ACACCCAAGAATGATCAATT
93432	91519	AACACCCAAGAATGATCAAT
93433	91520	AAACACCCAAGAATGATCAA
93434	91521	GAAACACCCAAGAATGATCA
93435	91522	AGAAACACCCAAGAATGATC
93436	91523	GAGAAACACCCAAGAATGAT
93437	91524	CGAGAAACACCCAAGAATGA
93438	91525	GCGAGAAACACCCAAGAATG
93439	91526	TGCGAGAAACACCCAAGAAT
93440	91527	CTGCGAGAAACACCCAAGAA
93441	91528	TCTGCGAGAAACACCCAAGA
93442	91529	CTCTGCGAGAAACACCCAAG
93443	91530	CCTCTGCGAGAAACACCCAA
93444	91531	CCCTCTGCGAGAAACACCCA

142521	140608	TCCAGTTTAGACTGGATACA
142522	140609	ATCCAGTTTAGACTGGATAC
142523	140610	TATCCAGTTTAGACTGGATA
142524	140611	ATATCCAGTTTAGACTGGAT
142525	140612	CATATCCAGTTTAGACTGGA
142526	140613	TCATATCCAGTTTAGACTGG
142527	140614	TTCATATCCAGTTTAGACTG
142528	140615	CTTCATATCCAGTTTAGACT
142529	140616	CCTTCATATCCAGTTTAGAC
142530	140617	TCCTTCATATCCAGTTTAGA
142531	140618	TTCCTTCATATCCAGTTTAG
142532	140619	ATTCCTTCATATCCAGTTTA
142533	140620	TATTCCTTCATATCCAGTTT
142534	140621	ATATTCCTTCATATCCAGTT
142535	140622	AATATTCCTTCATATCCAGT
142536	140623	TAATATTCCTTCATATCCAG
142537	140624	TTAATATTCCTTCATATCCA
142538	140625	ATTAATATTCCTTCATATCC
142539	140626	CATTAATATTCCTTCATATC
142540	140627	GCATTAATATTCCTTCATAT
142541	140628	GGCATTAATATTCCTTCATA
142542	140629	TGGCATTAATATTCCTTCAT
142543	140630	CTGGCATTAATATTCCTTCA
142544	140631	GCTGGCATTAATATTCCTTC
142545	140632	AGCTGGCATTAATATTCCTT
142546	140633	CAGCTGGCATTAATATTCCT
142547	140634	ACAGCTGGCATTAATATTCC
142548	140635	CACAGCTGGCATTAATATTC
142549	140636	CCACAGCTGGCATTAATATT
142550	140637	GCCACAGCTGGCATTAATAT
142551	140638	TGCCACAGCTGGCATTAATA
142552	140639	ATGCCACAGCTGGCATTAAT
142553	140640	AATGCCACAGCTGGCATTAA
142554	140641	CAATGCCACAGCTGGCATTA
142555	140642	CCAATGCCACAGCTGGCATT
142556	140643	GCCAATGCCACAGCTGGCAT
142557	140644	TGCCAATGCCACAGCTGGCA
142558	140645	CTGCCAATGCCACAGCTGGC
142559	140646	ACTGCCAATGCCACAGCTGG
142560	140647	CACTGCCAATGCCACAGCTG
142561	140648	CCACTGCCAATGCCACAGCT
142562	140649	TCCACTGCCAATGCCACAGC
142563	140650	ATCCACTGCCAATGCCACAG
142564	140651	CATCCACTGCCAATGCCACA
142565	140652	GCATCCACTGCCAATGCCAC
142566	140653	TGCATCCACTGCCAATGCCA
142567	140654	GTGCATCCACTGCCAATGCC
142568	140655	TGTGCATCCACTGCCAATGC
142569	140656	CTGTGCATCCACTGCCAATG
142570	140657	CCTGTGCATCCACTGCCAAT
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142576	140663	GGATCACCTGTGCATCCACT
142577	140664	AGGATCACCTGTGCATCCAC
142578	140665	TAGGATCACCTGTGCATCCA
142579	140666	CTAGGATCACCTGTGCATCC
142580	140667	TCTAGGATCACCTGTGCATC
142581	140668	TTCTAGGATCACCTGTGCAT
142582	140669	GTTCTAGGATCACCTGTGCA
142583	140670	AGTTCTAGGATCACCTGTGC
142584	140671	CAGTTCTAGGATCACCTGTG
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142586	140673	GCCAGTTCTAGGATCACCTG
142587	140674	AGCCAGTTCTAGGATCACCT
142588	140675	GAGCCAGTTCTAGGATCACC
142589	140676	AGAGCCAGTTCTAGGATCAC
142590	140677	AAGAGCCAGTTCTAGGATCA
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44298	42385	GATCCCTAGAAGAGTACTCT
44299	42386	CGATCCCTAGAAGAGTACTC
44300	42387	TCGATCCCTAGAAGAGTACT
44301	42388	GTCGATCCCTAGAAGAGTAC
44302	42389	GGTCGATCCCTAGAAGAGTA
44303	42390	TGGTCGATCCCTAGAAGAGT
44304	42391	CTGGTCGATCCCTAGAAGAG
44305	42392	ACTGGTCGATCCCTAGAAGA
44306	42393	GACTGGTCGATCCCTAGAAG
44307	42394	CGACTGGTCGATCCCTAGAA
44308	42395	ACGACTGGTCGATCCCTAGA
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44310	42397	ACACGACTGGTCGATCCCTA
44311	42398	AACACGACTGGTCGATCCCT
44312	42399	TAACACGACTGGTCGATCCC
44313	42400	GTAACACGACTGGTCGATCC
44314	42401	AGTAACACGACTGGTCGATC
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44317	42404	TCTAGTAACACGACTGGTCG
44318	42405	GTCTAGTAACACGACTGGTC
44319	42406	AGTCTAGTAACACGACTGGT
44320	42407	AAGTCTAGTAACACGACTGG
44321	42408	AAAGTCTAGTAACACGACTG
44322	42409	AAAAGTCTAGTAACACGACT
44323	42410	AAAAAGTCTAGTAACACGAC
44324	42411	CAAAAAGTCTAGTAACACGA
44325	42412	CCAAAAAGTCTAGTAACACG
44326	42413	TCCAAAAAGTCTAGTAACAC
44327	42414	ATCCAAAAAGTCTAGTAACA
44328	42415	GATCCAAAAAGTCTAGTAAC
44329	42416	AGATCCAAAAAGTCTAGTAA
44330	42417	CAGATCCAAAAAGTCTAGTA
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44332	42419	TTCAGATCCAAAAAGTCTAG
44333	42420	ATTCAGATCCAAAAAGTCTA
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44335	42422	CAATTCAGATCCAAAAAGTC
44336	42423	ACAATTCAGATCCAAAAAGT
44337	42424	CACAATTCAGATCCAAAAAG
44338	42425	GCACAATTCAGATCCAAAAA
44339	42426	AGCACAATTCAGATCCAAAA
44340	42427	AAGCACAATTCAGATCCAAA
44341	42428	AAAGCACAATTCAGATCCAA
44342	42429	AAAAGCACAATTCAGATCCA
44343	42430	GAAAAGCACAATTCAGATCC
44344	42431	GGAAAAGCACAATTCAGATC
44345	42432	AGGAAAAGCACAATTCAGAT
44346	42433	AAGGAAAAGCACAATTCAGA
44347	42434	CAAGGAAAAGCACAATTCAG
44348	42435	TCAAGGAAAAGCACAATTCA
44349	42436	TTCAAGGAAAAGCACAATTC
44350	42437	ATTCAAGGAAAAGCACAATT
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44359	42446	ATTCAAAACATTCAAGGAAA
44360	42447	AATTCAAAACATTCAAGGAA
44361	42448	AAATTCAAAACATTCAAGGA
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44363	42450	CAAAATTCAAAACATTCAAG
44364	42451	CCAAAATTCAAAACATTCAA
44365	42452	GCCAAAATTCAAAACATTCA
44366	42453	AGCCAAAATTCAAAACATTC
44367	42454	AAGCCAAAATTCAAAACATT
44368	42455	CAAGCCAAAATTCAAAACAT

93445	91532	CCCCTCTGCGAGAAACACCC
93446	91533	CCCCCTCTGCGAGAAACACC
93447	91534	TCCCCCTCTGCGAGAAACAC
93448	91535	ATCCCCCTCTGCGAGAAACA
93449	91536	AATCCCCCTCTGCGAGAAAC
93450	91537	AAATCCCCCTCTGCGAGAAA
93451	91538	CAAATCCCCCTCTGCGAGAA
93452	91539	CCAAATCCCCCTCTGCGAGA
93453	91540	GCCAAATCCCCCTCTGCGAG
93454	91541	TGCCAAATCCCCCTCTGCGA
93455	91542	CTGCCAAATCCCCCTCTGCG
93456	91543	CCTGCCAAATCCCCCTCTGC
93457	91544	CCCTGCCAAATCCCCCTCTG
93458	91545	ACCCTGCCAAATCCCCCTCT
93459	91546	GACCCTGCCAAATCCCCCTC
93460	91547	TGACCCTGCCAAATCCCCCT
93461	91548	ATGACCCTGCCAAATCCCCC
93462	91549	TATGACCCTGCCAAATCCCC
93463	91550	CTATGACCCTGCCAAATCCC
93464	91551	CCTATGACCCTGCCAAATCC
93465	91552	TCCTATGACCCTGCCAAATC
93466	91553	GTCCTATGACCCTGCCAAAT
93467	91554	TGTCCTATGACCCTGCCAAA
93468	91555	TTGTCCTATGACCCTGCCAA
93469	91556	ATTGTCCTATGACCCTGCCA
93470	91557	TATTGTCCTATGACCCTGCC
93471	91558	CTATTGTCCTATGACCCTGC
93472	91559	ACTATTGTCCTATGACCCTG
93473	91560	CACTATTGTCCTATGACCCT
93474	91561	CCACTATTGTCCTATGACCC
93475	91562	TCCACTATTGTCCTATGACC
93476	91563	CTCCACTATTGTCCTATGAC
93477	91564	CCTCCACTATTGTCCTATGA
93478	91565	CCCTCCACTATTGTCCTATG
93479	91566	TCCCTCCACTATTGTCCTAT
93480	91567	TTCCCTCCACTATTGTCCTA
93481	91568	CTTCCCTCCACTATTGTCCT
93482	91569	CCTTCCCTCCACTATTGTCC
93483	91570	ACCTTCCCTCCACTATTGTC
93484	91571	GACCTTCCCTCCACTATTGT
93485	91572	TGACCTTCCCTCCACTATTG
93486	91573	CTGACCTTCCCTCCACTATT
93487	91574	GCTGACCTTCCCTCCACTAT
93488	91575	TGCTGACCTTCCCTCCACTA
93489	91576	CTGCTGACCTTCCCTCCACT
93490	91577	TCTGCTGACCTTCCCTCCAC
93491	91578	ATCTGCTGACCTTCCCTCCA
93492	91579	TATCTGCTGACCTTCCCTCC
93493	91580	TTATCTGCTGACCTTCCCTC
93494	91581	TTTATCTGCTGACCTTCCCT
93495	91582	TTTTATCTGCTGACCTTCCC
93496	91583	TTTTTATCTGCTGACCTTCC
93497	91584	CTTTTTATCTGCTGACCTTC
93498	91585	ACTTTTTATCTGCTGACCTT
93499	91586	CACTTTTTATCTGCTGACCT
93500	91587	TCACTTTTTATCTGCTGACC
93501	91588	TTCACTTTTTATCTGCTGAC
93502	91589	GTTCACTTTTTATCTGCTGA
93503	91590	TGTTCACTTTTTATCTGCTG
93504	91591	TTGTTCACTTTTTATCTGCT
93505	91592	TTTGTTCACTTTTTATCTGC
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93507	91594	CCTTTGTTCACTTTTTATCT
93508	91595	ACCTTTGTTCACTTTTTATC
93509	91596	GACCTTTGTTCACTTTTTAT
93510	91597	AGACCTTTGTTCACTTTTTA
93511	91598	GAGACCTTTGTTCACTTTTT
93512	91599	AGAGACCTTTGTTCACTTTT
93513	91600	CAGAGACCTTTGTTCACTTT
93514	91601	CCAGAGACCTTTGTTCACTT
93515	91602	ACCAGAGACCTTTGTTCACT

142592	140679	CAAAGAGCCAGTTCTAGGAT
142593	140680	GCAAAGAGCCAGTTCTAGGA
142594	140681	GGCAAAGAGCCAGTTCTAGG
142595	140682	AGGCAAAGAGCCAGTTCTAG
142596	140683	AAGGCAAAGAGCCAGTTCTA
142597	140684	CAAGGCAAAGAGCCAGTTCT
142598	140685	GCAAGGCAAAGAGCCAGTTC
142599	140686	GGCAAGGCAAAGAGCCAGTT
142600	140687	GGGCAAGGCAAAGAGCCAGT
142601	140688	AGGGCAAGGCAAAGAGCCAG
142602	140689	AAGGGCAAGGCAAAGAGCCA
142603	140690	AAAGGGCAAGGCAAAGAGCC
142604	140691	GAAAGGGCAAGGCAAAGAGC
142605	140692	GGAAAGGGCAAGGCAAAGAG
142606	140693	GGGAAAGGGCAAGGCAAAGA
142607	140694	GGGGAAAGGGCAAGGCAAAG
142608	140695	AGGGGAAAGGGCAAGGCAAA
142609	140696	CAGGGGAAAGGGCAAGGCAA
142610	140697	GCAGGGGAAAGGGCAAGGCA
142611	140698	AGCAGGGGAAAGGGCAAGGC
142612	140699	TAGCAGGGGAAAGGGCAAGG
142613	140700	TTAGCAGGGGAAAGGGCAAG
142614	140701	CTTAGCAGGGGAAAGGGCAA
142615	140702	TCTTAGCAGGGGAAAGGGCA
142616	140703	CTCTTAGCAGGGGAAAGGGC
142617	140704	TCTCTTAGCAGGGGAAAGGG
142618	140705	ATCTCTTAGCAGGGGAAAGG
142619	140706	TATCTCTTAGCAGGGGAAAG
142620	140707	CTATCTCTTAGCAGGGGAAA
142621	140708	GCTATCTCTTAGCAGGGGAA
142622	140709	AGCTATCTCTTAGCAGGGGA
142623	140710	AAGCTATCTCTTAGCAGGGG
142624	140711	AAAGCTATCTCTTAGCAGGG
142625	140712	CAAAGCTATCTCTTAGCAGG
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142629	140716	GCTGCAAAGCTATCTCTTAG
142630	140717	AGCTGCAAAGCTATCTCTTA
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142635	140722	TCTCCAGCTGCAAAGCTATC
142636	140723	GTCTCCAGCTGCAAAGCTAT
142637	140724	CGTCTCCAGCTGCAAAGCTA
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142639	140726	TACGTCTCCAGCTGCAAAGC
142640	140727	TTACGTCTCCAGCTGCAAAG
142641	140728	GTTACGTCTCCAGCTGCAAA
142642	140729	AGTTACGTCTCCAGCTGCAA
142643	140730	CAGTTACGTCTCCAGCTGCA
142644	140731	ACAGTTACGTCTCCAGCTGC
142645	140732	AACAGTTACGTCTCCAGCTG
142646	140733	TAACAGTTACGTCTCCAGCT
142647	140734	CTAACAGTTACGTCTCCAGC
142648	140735	CCTAACAGTTACGTCTCCAG
142649	140736	CCCTAACAGTTACGTCTCCA
142650	140737	GCCCTAACAGTTACGTCTCC
142651	140738	AGCCCTAACAGTTACGTCTC
142652	140739	CAGCCCTAACAGTTACGTCT
142653	140740	CCAGCCCTAACAGTTACGTC
142654	140741	TCCAGCCCTAACAGTTACGT
142655	140742	CTCCAGCCCTAACAGTTACG
142656	140743	TCTCCAGCCCTAACAGTTAC
142657	140744	CTCTCCAGCCCTAACAGTTA
142658	140745	ACTCTCCAGCCCTAACAGTT
142659	140746	AACTCTCCAGCCCTAACAGT
142660	140747	CAACTCTCCAGCCCTAACAG
142661	140748	CCAACTCTCCAGCCCTAACA
142662	140749	ACCAACTCTCCAGCCCTAAC

44369	42456	TCAAGCCAAAATTCAAAACA
44370	42457	CTCAAGCCAAAATTCAAAAC
44371	42458	ACTCAAGCCAAAATTCAAAA
44372	42459	CACTCAAGCCAAAATTCAAA
44373	42460	ACACTCAAGCCAAAATTCAA
44374	42461	AACACTCAAGCCAAAATTCA
44375	42462	CAACACTCAAGCCAAAATTC
44376	42463	ACAACACTCAAGCCAAAATT
44377	42464	CACAACACTCAAGCCAAAAT
44378	42465	TCACAACACTCAAGCCAAAA
44379	42466	ATCACAACACTCAAGCCAAA
44380	42467	AATCACAACACTCAAGCCAA
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44384	42471	AAATAATCACAACACTCAAG
44385	42472	AAAATAATCACAACACTCAA
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44387	42474	ATAAAATAATCACAACACTC
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44390	42477	TTAATAAAATAATCACAACA
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44392	42479	TTTTAATAAAATAATCACAA
44393	42480	ATTTTAATAAAATAATCACA
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44397	42484	TCTCATTTTAATAAAATAAT
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44410	42497	AATAGGACTGGAATCTCATT
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44416	42503	CATGACAATAGGACTGGAAT
44417	42504	TCATGACAATAGGACTGGAA
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44419	42506	AGTCATGACAATAGGACTGG
44420	42507	TAGTCATGACAATAGGACTG
44421	42508	TTAGTCATGACAATAGGACT
44422	42509	ATTAGTCATGACAATAGGAC
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44426	42513	AAACATTAGTCATGACAATA
44427	42514	TAAACATTAGTCATGACAAT
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44434	42521	TTTCTCATAAACATTAGTCA
44435	42522	ATTTCTCATAAACATTAGTC
44436	42523	TATTTCTCATAAACATTAGT
44437	42524	ATATTTCTCATAAACATTAG
44438	42525	TATATTTCTCATAAACATTA
44439	42526	TTATATTTCTCATAAACATT

93516	91603	AACCAGAGACCTTTGTTCAC
93517	91604	AAACCAGAGACCTTTGTTCA
93518	91605	AAAACCAGAGACCTTTGTTC
93519	91606	GAAAACCAGAGACCTTTGTT
93520	91607	GGAAAACCAGAGACCTTTGT
93521	91608	AGGAAAACCAGAGACCTTTG
93522	91609	TAGGAAAACCAGAGACCTTT
93523	91610	CTAGGAAAACCAGAGACCTT
93524	91611	CCTAGGAAAACCAGAGACCT
93525	91612	GCCTAGGAAAACCAGAGACC
93526	91613	TGCCTAGGAAAACCAGAGAC
93527	91614	CTGCCTAGGAAAACCAGAGA
93528	91615	TCTGCCTAGGAAAACCAGAG
93529	91616	CTCTGCCTAGGAAAACCAGA
93530	91617	CCTCTGCCTAGGAAAACCAG
93531	91618	TCCTCTGCCTAGGAAAACCA
93532	91619	GTCCTCTGCCTAGGAAAACC
93533	91620	GGTCCTCTGCCTAGGAAAAC
93534	91621	GGGTCCTCTGCCTAGGAAAA
93535	91622	AGGGTCCTCTGCCTAGGAAA
93536	91623	CAGGGTCCTCTGCCTAGGAA
93537	91624	GCAGGGTCCTCTGCCTAGGA
93538	91625	CGCAGGGTCCTCTGCCTAGG
93539	91626	CCGCAGGGTCCTCTGCCTAG
93540	91627	GCCGCAGGGTCCTCTGCCTA
93541	91628	GGCCGCAGGGTCCTCTGCCT
93542	91629	AGGCCGCAGGGTCCTCTGCC
93543	91630	AAGGCCGCAGGGTCCTCTGC
93544	91631	GAAGGCCGCAGGGTCCTCTG
93545	91632	GGAAGGCCGCAGGGTCCTCT
93546	91633	CGGAAGGCCGCAGGGTCCTC
93547	91634	GCGGAAGGCCGCAGGGTCCT
93548	91635	TGCGGAAGGCCGCAGGGTCC
93549	91636	CTGCGGAAGGCCGCAGGGTC
93550	91637	ACTGCGGAAGGCCGCAGGGT
93551	91638	CACTGCGGAAGGCCGCAGGG
93552	91639	ACACTGCGGAAGGCCGCAGG
93553	91640	AACACTGCGGAAGGCCGCAG
93554	91641	AAACACTGCGGAAGGCCGCA
93555	91642	CAAACACTGCGGAAGGCCGC
93556	91643	ACAAACACTGCGGAAGGCCG
93557	91644	CACAAACACTGCGGAAGGCC
93558	91645	ACACAAACACTGCGGAAGGC
93559	91646	GACACAAACACTGCGGAAGG
93560	91647	GGACACAAACACTGCGGAAG
93561	91648	GGGACACAAACACTGCGGAA
93562	91649	AGGGACACAAACACTGCGGA
93563	91650	CAGGGACACAAACACTGCGG
93564	91651	CCAGGGACACAAACACTGCG
93565	91652	CCCAGGGACACAAACACTGC
93566	91653	ACCCAGGGACACAAACACTG
93567	91654	TACCCAGGGACACAAACACT
93568	91655	GTACCCAGGGACACAAACAC
93569	91656	AGTACCCAGGGACACAAACA
93570	91657	AAGTACCCAGGGACACAAAC
93571	91658	CAAGTACCCAGGGACACAAA
93572	91659	TCAAGTACCCAGGGACACAA
93573	91660	CTCAAGTACCCAGGGACACA
93574	91661	TCTCAAGTACCCAGGGACAC
93575	91662	ATCTCAAGTACCCAGGGACA
93576	91663	AATCTCAAGTACCCAGGGAC
93577	91664	TAATCTCAAGTACCCAGGGA
93578	91665	CTAATCTCAAGTACCCAGGG
93579	91666	CCTAATCTCAAGTACCCAGG
93580	91667	CCCTAATCTCAAGTACCCAG
93581	91668	TCCCTAATCTCAAGTACCCA
93582	91669	CTCCCTAATCTCAAGTACCC
93583	91670	ACTCCCTAATCTCAAGTACC
93584	91671	CACTCCCTAATCTCAAGTAC
93585	91672	CCACTCCCTAATCTCAAGTA
93586	91673	ACCACTCCCTAATCTCAAGT

142663	140750	CACCAACTCTCCAGCCCTAA
142664	140751	CCACCAACTCTCCAGCCCTA
142665	140752	GCCACCAACTCTCCAGCCCT
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142667	140754	GGGCCACCAACTCTCCAGCC
142668	140755	AGGGCCACCAACTCTCCAGC
142669	140756	AAGGGCCACCAACTCTCCAG
142670	140757	TAAGGGCCACCAACTCTCCA
142671	140758	CTAAGGGCCACCAACTCTCC
142672	140759	GCTAAGGGCCACCAACTCTC
142673	140760	GGCTAAGGGCCACCAACTCT
142674	140761	GGGCTAAGGGCCACCAACTC
142675	140762	AGGGCTAAGGGCCACCAACT
142676	140763	TAGGGCTAAGGGCCACCAAC
142677	140764	GTAGGGCTAAGGGCCACCAA
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142679	140766	TTGTAGGGCTAAGGGCCACC
142680	140767	GTTGTAGGGCTAAGGGCCAC
142681	140768	TGTTGTAGGGCTAAGGGCCA
142682	140769	GTGTTGTAGGGCTAAGGGCC
142683	140770	GGTGTTGTAGGGCTAAGGGC
142684	140771	AGGTGTTGTAGGGCTAAGGG
142685	140772	TAGGTGTTGTAGGGCTAAGG
142686	140773	CTAGGTGTTGTAGGGCTAAG
142687	140774	CCTAGGTGTTGTAGGGCTAA
142688	140775	TCCTAGGTGTTGTAGGGCTA
142689	140776	ATCCTAGGTGTTGTAGGGCT
142690	140777	AATCCTAGGTGTTGTAGGGC
142691	140778	TAATCCTAGGTGTTGTAGGG
142692	140779	ATAATCCTAGGTGTTGTAGG
142693	140780	TATAATCCTAGGTGTTGTAG
142694	140781	CTATAATCCTAGGTGTTGTA
142695	140782	TCTATAATCCTAGGTGTTGT
142696	140783	TTCTATAATCCTAGGTGTTG
142697	140784	GTTCTATAATCCTAGGTGTT
142698	140785	AGTTCTATAATCCTAGGTGT
142699	140786	CAGTTCTATAATCCTAGGTG
142700	140787	GCAGTTCTATAATCCTAGGT
142701	140788	AGCAGTTCTATAATCCTAGG
142702	140789	GAGCAGTTCTATAATCCTAG
142703	140790	GGAGCAGTTCTATAATCCTA
142704	140791	TGGAGCAGTTCTATAATCCT
142705	140792	ATGGAGCAGTTCTATAATCC
142706	140793	CATGGAGCAGTTCTATAATC
142707	140794	ACATGGAGCAGTTCTATAAT
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142709	140796	GCACATGGAGCAGTTCTATA
142710	140797	GGCACATGGAGCAGTTCTAT
142711	140798	AGGCACATGGAGCAGTTCTA
142712	140799	TAGGCACATGGAGCAGTTCT
142713	140800	CTAGGCACATGGAGCAGTTC
142714	140801	GCTAGGCACATGGAGCAGTT
142715	140802	GGCTAGGCACATGGAGCAGT
142716	140803	AGGCTAGGCACATGGAGCAG
142717	140804	TAGGCTAGGCACATGGAGCA
142718	140805	TTAGGCTAGGCACATGGAGC
142719	140806	GTTAGGCTAGGCACATGGAG
142720	140807	GGTTAGGCTAGGCACATGGA
142721	140808	GGGTTAGGCTAGGCACATGG
142722	140809	AGGGTTAGGCTAGGCACATG
142723	140810	GAGGGTTAGGCTAGGCACAT
142724	140811	AGAGGGTTAGGCTAGGCACA
142725	140812	CAGAGGGTTAGGCTAGGCAC
142726	140813	GCAGAGGGTTAGGCTAGGCA
142727	140814	TGCAGAGGGTTAGGCTAGGC
142728	140815	GTGCAGAGGGTTAGGCTAGG
142729	140816	TGTGCAGAGGGTTAGGCTAG
142730	140817	GTGTGCAGAGGGTTAGGCTA
142731	140818	GGTGTGCAGAGGGTTAGGCT
142732	140819	TGGTGTGCAGAGGGTTAGGC
142733	140820	ATGGTGTGCAGAGGGTTAGG

44440	42527	GTTATATTTCTCATAAACAT
44441	42528	TGTTATATTTCTCATAAACA
44442	42529	ATGTTATATTTCTCATAAAC
44443	42530	AATGTTATATTTCTCATAAA
44444	42531	AAATGTTATATTTCTCATAA
44445	42532	GAAATGTTATATTTCTCATA
44446	42533	TGAAATGTTATATTTCTCAT
44447	42534	GTGAAATGTTATATTTCTCA
44448	42535	AGTGAAATGTTATATTTCTC
44449	42536	AAGTGAAATGTTATATTTCT
44450	42537	AAAGTGAAATGTTATATTTC
44451	42538	TAAAGTGAAATGTTATATTT
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44458	42545	ACATCATTAAAGTGAAATGT
44459	42546	AACATCATTAAAGTGAAATG
44460	42547	AAACATCATTAAAGTGAAAT
44461	42548	AAAACATCATTAAAGTGAAA
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44463	42550	AAAAAACATCATTAAAGTGA
44464	42551	TAAAAAACATCATTAAAGTG
44465	42552	TTAAAAAACATCATTAAAGT
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44467	42554	AATTAAAAAACATCATTAAA
44468	42555	TAATTAAAAAACATCATTAA
44469	42556	ATAATTAAAAAACATCATTA
44470	42557	AATAATTAAAAAACATCATT
44471	42558	GAATAATTAAAAAACATCAT
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44473	42560	TAGAATAATTAAAAAACATC
44474	42561	TTAGAATAATTAAAAAACAT
44475	42562	CTTAGAATAATTAAAAAACA
44476	42563	CCTTAGAATAATTAAAAAAC
44477	42564	CCCTTAGAATAATTAAAAAA
44478	42565	CCCCTTAGAATAATTAAAAA
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44480	42567	GGCCCCTTAGAATAATTAAA
44481	42568	AGGCCCCTTAGAATAATTAA
44482	42569	TAGGCCCCTTAGAATAATTA
44483	42570	TTAGGCCCCTTAGAATAATT
44484	42571	ATTAGGCCCCTTAGAATAAT
44485	42572	GATTAGGCCCCTTAGAATAA
44486	42573	AGATTAGGCCCCTTAGAATA
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93587	91674	CACCACTCCCTAATCTCAAG
93588	91675	TCACCACTCCCTAATCTCAA
93589	91676	ATCACCACTCCCTAATCTCA
93590	91677	CATCACCACTCCCTAATCTC
93591	91678	TCATCACCACTCCCTAATCT
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93595	91682	AGAGTCATCACCACTCCCTA
93596	91683	AAGAGTCATCACCACTCCCT
93597	91684	TAAGAGTCATCACCACTCCC
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93599	91686	GTTAAGAGTCATCACCACTC
93600	91687	CGTTAAGAGTCATCACCACT
93601	91688	TCGTTAAGAGTCATCACCAC
93602	91689	CTCGTTAAGAGTCATCACCA
93603	91690	GCTCGTTAAGAGTCATCACC
93604	91691	TGCTCGTTAAGAGTCATCAC
93605	91692	ATGCTCGTTAAGAGTCATCA
93606	91693	CATGCTCGTTAAGAGTCATC
93607	91694	GCATGCTCGTTAAGAGTCAT
93608	91695	AGCATGCTCGTTAAGAGTCA
93609	91696	CAGCATGCTCGTTAAGAGTC
93610	91697	GCAGCATGCTCGTTAAGAGT
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93612	91699	AGGCAGCATGCTCGTTAAGA
93613	91700	AAGGCAGCATGCTCGTTAAG
93614	91701	GAAGGCAGCATGCTCGTTAA
93615	91702	TGAAGGCAGCATGCTCGTTA
93616	91703	TTGAAGGCAGCATGCTCGTT
93617	91704	CTTGAAGGCAGCATGCTCGT
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93619	91706	TGCTTGAAGGCAGCATGCTC
93620	91707	ATGCTTGAAGGCAGCATGCT
93621	91708	GATGCTTGAAGGCAGCATGC
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93623	91710	CAGATGCTTGAAGGCAGCAT
93624	91711	ACAGATGCTTGAAGGCAGCA
93625	91712	AACAGATGCTTGAAGGCAGC
93626	91713	AAACAGATGCTTGAAGGCAG
93627	91714	TAAACAGATGCTTGAAGGCA
93628	91715	TTAAACAGATGCTTGAAGGC
93629	91716	GTTAAACAGATGCTTGAAGG
93630	91717	TGTTAAACAGATGCTTGAAG
93631	91718	TTGTTAAACAGATGCTTGAA
93632	91719	TTTGTTAAACAGATGCTTGA
93633	91720	CTTTGTTAAACAGATGCTTG
93634	91721	GCTTTGTTAAACAGATGCTT
93635	91722	TGCTTTGTTAAACAGATGCT
93636	91723	GTGCTTTGTTAAACAGATGC
93637	91724	TGTGCTTTGTTAAACAGATG
93638	91725	ATGTGCTTTGTTAAACAGAT
93639	91726	GATGTGCTTTGTTAAACAGA
93640	91727	AGATGTGCTTTGTTAAACAG
93641	91728	AAGATGTGCTTTGTTAAACA
93642	91729	CAAGATGTGCTTTGTTAAAC
93643	91730	GCAAGATGTGCTTTGTTAAA
93644	91731	TGCAAGATGTGCTTTGTTAA
93645	91732	GTGCAAGATGTGCTTTGTTA
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93647	91734	CGGTGCAAGATGTGCTTTGT
93648	91735	GCGGTGCAAGATGTGCTTTG
93649	91736	GGCGGTGCAAGATGTGCTTT
93650	91737	GGGCGGTGCAAGATGTGCTT
93651	91738	AGGGCGGTGCAAGATGTGCT
93652	91739	AAGGGCGGTGCAAGATGTGC
93653	91740	TAAGGGCGGTGCAAGATGTG
93654	91741	TTAAGGGCGGTGCAAGATGT
93655	91742	ATTAAGGGCGGTGCAAGATG
93656	91743	GATTAAGGGCGGTGCAAGAT
93657	91744	GGATTAAGGGCGGTGCAAGA

142734	140821	AATGGTGTGCAGAGGGTTAG
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142737	140824	GTAAATGGTGTGCAGAGGGT
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142739	140826	ACGTAAATGGTGTGCAGAGG
142740	140827	CACGTAAATGGTGTGCAGAG
142741	140828	CCACGTAAATGGTGTGCAGA
142742	140829	TCCACGTAAATGGTGTGCAG
142743	140830	TTCCACGTAAATGGTGTGCA
142744	140831	ATTCCACGTAAATGGTGTGC
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142746	140833	ATATTCCACGTAAATGGTGT
142747	140834	TATATTCCACGTAAATGGTG
142748	140835	GTATATTCCACGTAAATGGT
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142752	140839	CTGGGTATATTCCACGTAAA
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142754	140841	CTCTGGGTATATTCCACGTA
142755	140842	GCTCTGGGTATATTCCACGT
142756	140843	GGCTCTGGGTATATTCCACG
142757	140844	CGGCTCTGGGTATATTCCAC
142758	140845	ACGGCTCTGGGTATATTCCA
142759	140846	GACGGCTCTGGGTATATTCC
142760	140847	AGACGGCTCTGGGTATATTC
142761	140848	TAGACGGCTCTGGGTATATT
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142763	140850	CATAGACGGCTCTGGGTATA
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142765	140852	AGCATAGACGGCTCTGGGTA
142766	140853	CAGCATAGACGGCTCTGGGT
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142768	140855	ACCAGCATAGACGGCTCTGG
142769	140856	CACCAGCATAGACGGCTCTG
142770	140857	TCACCAGCATAGACGGCTCT
142771	140858	GTCACCAGCATAGACGGCTC
142772	140859	AGTCACCAGCATAGACGGCT
142773	140860	GAGTCACCAGCATAGACGGC
142774	140861	CGAGTCACCAGCATAGACGG
142775	140862	CCGAGTCACCAGCATAGACG
142776	140863	GCCGAGTCACCAGCATAGAC
142777	140864	TGCCGAGTCACCAGCATAGA
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142780	140867	GGCTGCCGAGTCACCAGCAT
142781	140868	AGGCTGCCGAGTCACCAGCA
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142784	140871	GCAAGGCTGCCGAGTCACCA
142785	140872	GGCAAGGCTGCCGAGTCACC
142786	140873	AGGCAAGGCTGCCGAGTCAC
142787	140874	TAGGCAAGGCTGCCGAGTCA
142788	140875	GTAGGCAAGGCTGCCGAGTC
142789	140876	GGTAGGCAAGGCTGCCGAGT
142790	140877	TGGTAGGCAAGGCTGCCGAG
142791	140878	CTGGTAGGCAAGGCTGCCGA
142792	140879	TCTGGTAGGCAAGGCTGCCG
142793	140880	GTCTGGTAGGCAAGGCTGCC
142794	140881	AGTCTGGTAGGCAAGGCTGC
142795	140882	CAGTCTGGTAGGCAAGGCTG
142796	140883	GCAGTCTGGTAGGCAAGGCT
142797	140884	AGCAGTCTGGTAGGCAAGGC
142798	140885	CAGCAGTCTGGTAGGCAAGG
142799	140886	CCAGCAGTCTGGTAGGCAAG
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142801	140888	TTCCAGCAGTCTGGTAGGCA
142802	140889	GTTCCAGCAGTCTGGTAGGC
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142804	140891	TAGTTCCAGCAGTCTGGTAG

44511	42598	AACCTAAAGCTTATTCCACT
44512	42599	CAACCTAAAGCTTATTCCAC
44513	42600	ACAACCTAAAGCTTATTCCA
44514	42601	TACAACCTAAAGCTTATTCC
44515	42602	ATACAACCTAAAGCTTATTC
44516	42603	AATACAACCTAAAGCTTATT
44517	42604	TAATACAACCTAAAGCTTAT
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44519	42606	TATAATACAACCTAAAGCTT
44520	42607	ATATAATACAACCTAAAGCT
44521	42608	AATATAATACAACCTAAAGC
44522	42609	GAATATAATACAACCTAAAG
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44525	42612	ATAGAATATAATACAACCTA
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44527	42614	TTATAGAATATAATACAACC
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44535	42622	CAAGTGAATTATAGAATATA
44536	42623	TCAAGTGAATTATAGAATAT
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44553	42640	AAAGATGAATTCTATTTTCA
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44557	42644	AAGTAAAGATGAATTCTATT
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44559	42646	TCAAGTAAAGATGAATTCTA
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44561	42648	TGTCAAGTAAAGATGAATTC
44562	42649	CTGTCAAGTAAAGATGAATT
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44570	42657	AAATTTGGCTGTCAAGTAAA
44571	42658	AAAATTTGGCTGTCAAGTAA
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44576	42663	TACACAAAATTTGGCTGTCA
44577	42664	GTACACAAAATTTGGCTGTC
44578	42665	AGTACACAAAATTTGGCTGT
44579	42666	CAGTACACAAAATTTGGCTG
44580	42667	GCAGTACACAAAATTTGGCT
44581	42668	TGCAGTACACAAAATTTGGC

93658	91745	TGGATTAAGGGCGGTGCAAG
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93660	91747	AATGGATTAAGGGCGGTGCA
93661	91748	AAATGGATTAAGGGCGGTGC
93662	91749	TAAATGGATTAAGGGCGGTG
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93674	91761	GTCACTCAGGGTTAAATGGA
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93682	91769	TGTGCTGTGTCACTCAGGGT
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93684	91771	CATGTGCTGTGTCACTCAGG
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93686	91773	AACATGTGCTGTGTCACTCA
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93700	91787	CCTGTGCTCTCTGAAACATG
93701	91788	CCCTGTGCTCTCTGAAACAT
93702	91789	ACCCTGTGCTCTCTGAAACA
93703	91790	AACCCTGTGCTCTCTGAAAC
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93707	91794	CCCCAACCCTGTGCTCTCTG
93708	91795	CCCCCAACCCTGTGCTCTCT
93709	91796	ACCCCCAACCCTGTGCTCTC
93710	91797	TACCCCCAACCCTGTGCTCT
93711	91798	TTACCCCCAACCCTGTGCTC
93712	91799	CTTACCCCCAACCCTGTGCT
93713	91800	CCTTACCCCCAACCCTGTGC
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93726	91813	TGTTGATCTATGACCTTACC
93727	91814	CTGTTGATCTATGACCTTAC
93728	91815	CCTGTTGATCTATGACCTTA

142805	140892	CTAGTTCCAGCAGTCTGGTA
142806	140893	CCTAGTTCCAGCAGTCTGGT
142807	140894	CCCTAGTTCCAGCAGTCTGG
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142809	140896	CACCCTAGTTCCAGCAGTCT
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142811	140898	GGCACCCTAGTTCCAGCAGT
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142815	140902	AAGAGGCACCCTAGTTCCAG
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142839	140926	GAGAGAAGCAAGCACAGCTT
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142846	140933	GATTGGTGAGAGAAGCAAGC
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142875	140962	TGTTAGCAAACACAGACATA

44582	42669	ATGCAGTACACAAAATTTGG
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44592	42679	CTCAGAAAAGATGCAGTACA
44593	42680	CCTCAGAAAAGATGCAGTAC
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44598	42685	CTCTCCCTCAGAAAAGATGC
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44603	42690	CAACTCTCTCCCTCAGAAAA
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44606	42693	TGCCAACTCTCTCCCTCAGA
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44625	42712	TGTAACAAGTGCCTTTCCTT
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44627	42714	GTTGTAACAAGTGCCTTTCC
44628	42715	CGTTGTAACAAGTGCCTTTC
44629	42716	TCGTTGTAACAAGTGCCTTT
44630	42717	ATCGTTGTAACAAGTGCCTT
44631	42718	GATCGTTGTAACAAGTGCCT
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44640	42727	ATATGTGTGGATCGTTGTAA
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44642	42729	CTATATGTGTGGATCGTTGT
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44644	42731	GTCTATATGTGTGGATCGTT
44645	42732	CGTCTATATGTGTGGATCGT
44646	42733	GCGTCTATATGTGTGGATCG
44647	42734	TGCGTCTATATGTGTGGATC
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44650	42737	ATATGCGTCTATATGTGTGG
44651	42738	AATATGCGTCTATATGTGTG
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93729	91816	TCCTGTTGATCTATGACCTT
93730	91817	ATCCTGTTGATCTATGACCT
93731	91818	GATCCTGTTGATCTATGACC
93732	91819	GGATCCTGTTGATCTATGAC
93733	91820	GGGATCCTGTTGATCTATGA
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93756	91843	ACTAAGAAAGATTCTTCTGC
93757	91844	TACTAAGAAAGATTCTTCTG
93758	91845	GTACTAAGAAAGATTCTTCT
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93760	91847	CTGTACTAAGAAAGATTCTT
93761	91848	TCTGTACTAAGAAAGATTCT
93762	91849	TTCTGTACTAAGAAAGATTC
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93765	91852	TTGTTCTGTACTAAGAAAGA
93766	91853	TTTGTTCTGTACTAAGAAAG
93767	91854	TTTTGTTCTGTACTAAGAAA
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93770	91857	TCATTTTGTTCTGTACTAAG
93771	91858	TTCATTTTGTTCTGTACTAA
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93775	91862	ACTTTTCATTTTGTTCTGTA
93776	91863	GACTTTTCATTTTGTTCTGT
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93778	91865	TAGACTTTTCATTTTGTTCT
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93796	91883	AGAAAGAAGTAGACATGGTA
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142881	140968	ATAACGTGTTAGCAAACACA
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93867	91954	GGCTTTGTGGAATAGAAAAG
93868	91955	CGGCTTTGTGGAATAGAAAA
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93923	92010	CCCGTCTGGGAGGTGTACCC
93924	92011	CCCCGTCTGGGAGGTGTACC
93925	92012	ACCCCGTCTGGGAGGTGTAC
93926	92013	CACCCCGTCTGGGAGGTGTA
93927	92014	CCACCCCGTCTGGGAGGTGT
93928	92015	ACCACCCCGTCTGGGAGGTG
93929	92016	CACCACCCCGTCTGGGAGGT
93930	92017	CCACCACCCCGTCTGGGAGG
93931	92018	GCCACCACCCCGTCTGGGAG
93932	92019	GGCCACCACCCCGTCTGGGA
93933	92020	CGGCCACCACCCCGTCTGGG
93934	92021	CCGGCCACCACCCCGTCTGG
93935	92022	CCCGGCCACCACCCCGTCTG
93936	92023	GCCCGGCCACCACCCCGTCT
93937	92024	TGCCCGGCCACCACCCCGTC
93938	92025	CTGCCCGGCCACCACCCCGT
93939	92026	TCTGCCCGGCCACCACCCCG
93940	92027	CTCTGCCCGGCCACCACCCC
93941	92028	CCTCTGCCCGGCCACCACCC

143018	141105	TGAGAATAGAGCGTTCTCAA
143019	141106	CTGAGAATAGAGCGTTCTCA
143020	141107	GCTGAGAATAGAGCGTTCTC
143021	141108	AGCTGAGAATAGAGCGTTCT
143022	141109	GAGCTGAGAATAGAGCGTTC
143023	141110	TGAGCTGAGAATAGAGCGTT
143024	141111	ATGAGCTGAGAATAGAGCGT
143025	141112	AATGAGCTGAGAATAGAGCG
143026	141113	CAATGAGCTGAGAATAGAGC
143027	141114	GCAATGAGCTGAGAATAGAG
143028	141115	GGCAATGAGCTGAGAATAGA
143029	141116	AGGCAATGAGCTGAGAATAG
143030	141117	GAGGCAATGAGCTGAGAATA
143031	141118	CGAGGCAATGAGCTGAGAAT
143032	141119	ACGAGGCAATGAGCTGAGAA
143033	141120	CACGAGGCAATGAGCTGAGA
143034	141121	CCACGAGGCAATGAGCTGAG
143035	141122	TCCACGAGGCAATGAGCTGA
143036	141123	CTCCACGAGGCAATGAGCTG
143037	141124	CCTCCACGAGGCAATGAGCT
143038	141125	ACCTCCACGAGGCAATGAGC
143039	141126	AACCTCCACGAGGCAATGAG
143040	141127	TAACCTCCACGAGGCAATGA
143041	141128	CTAACCTCCACGAGGCAATG
143042	141129	ACTAACCTCCACGAGGCAAT
143043	141130	AACTAACCTCCACGAGGCAA
143044	141131	AAACTAACCTCCACGAGGCA
143045	141132	AAAACTAACCTCCACGAGGC
143046	141133	AAAAACTAACCTCCACGAGG
143047	141134	AAAAAACTAACCTCCACGAG
143048	141135	TAAAAAACTAACCTCCACGA
143049	141136	ATAAAAAACTAACCTCCACG
143050	141137	GATAAAAAACTAACCTCCAC
143051	141138	TGATAAAAAACTAACCTCCA
143052	141139	ATGATAAAAAACTAACCTCC
143053	141140	GATGATAAAAAACTAACCTC
143054	141141	CGATGATAAAAAACTAACCT
143055	141142	CCGATGATAAAAAACTAACC
143056	141143	ACCGATGATAAAAAACTAAC
143057	141144	CACCGATGATAAAAAACTAA
143058	141145	ACACCGATGATAAAAAACTA
143059	141146	CACACCGATGATAAAAAACT
143060	141147	GCACACCGATGATAAAAAAC
143061	141148	AGCACACCGATGATAAAAAA
143062	141149	CAGCACACCGATGATAAAAA
143063	141150	ACAGCACACCGATGATAAAA
143064	141151	GACAGCACACCGATGATAAA
143065	141152	GGACAGCACACCGATGATAA
143066	141153	TGGACAGCACACCGATGATA
143067	141154	ATGGACAGCACACCGATGAT
143068	141155	TATGGACAGCACACCGATGA
143069	141156	CTATGGACAGCACACCGATG
143070	141157	ACTATGGACAGCACACCGAT
143071	141158	GACTATGGACAGCACACCGA
143072	141159	TGACTATGGACAGCACACCG
143073	141160	GTGACTATGGACAGCACACC
143074	141161	AGTGACTATGGACAGCACAC
143075	141162	CAGTGACTATGGACAGCACA
143076	141163	CCAGTGACTATGGACAGCAC
143077	141164	TCCAGTGACTATGGACAGCA
143078	141165	TTCCAGTGACTATGGACAGC
143079	141166	CTTCCAGTGACTATGGACAG
143080	141167	GCTTCCAGTGACTATGGACA
143081	141168	TGCTTCCAGTGACTATGGAC
143082	141169	CTGCTTCCAGTGACTATGGA
143083	141170	ACTGCTTCCAGTGACTATGG
143084	141171	CACTGCTTCCAGTGACTATG
143085	141172	TCACTGCTTCCAGTGACTAT
143086	141173	TTCACTGCTTCCAGTGACTA
143087	141174	GTTCACTGCTTCCAGTGACT
143088	141175	TGTTCACTGCTTCCAGTGAC

44795	42882	CCCATTGTACTCCAGCCGGG
44796	42883	CCCCATTGTACTCCAGCCGG
44797	42884	GCCCCATTGTACTCCAGCCG
44798	42885	CGCCCCATTGTACTCCAGCC
44799	42886	CCGCCCCATTGTACTCCAGC
44800	42887	ACCGCCCCATTGTACTCCAG
44801	42888	GACCGCCCCATTGTACTCCA
44802	42889	AGACCGCCCCATTGTACTCC
44803	42890	GAGACCGCCCCATTGTACTC
44804	42891	TGAGACCGCCCCATTGTACT
44805	42892	CTGAGACCGCCCCATTGTAC
44806	42893	GCTGAGACCGCCCCATTGTA
44807	42894	AGCTGAGACCGCCCCATTGT
44808	42895	GAGCTGAGACCGCCCCATTG
44809	42896	TGAGCTGAGACCGCCCCATT
44810	42897	GTGAGCTGAGACCGCCCCAT
44811	42898	AGTGAGCTGAGACCGCCCCA
44812	42899	CAGTGAGCTGAGACCGCCCC
44813	42900	GCAGTGAGCTGAGACCGCCC
44814	42901	TGCAGTGAGCTGAGACCGCC
44815	42902	TTGCAGTGAGCTGAGACCGC
44816	42903	GTTGCAGTGAGCTGAGACCG
44817	42904	GGTTGCAGTGAGCTGAGACC
44818	42905	AGGTTGCAGTGAGCTGAGAC
44819	42906	GAGGTTGCAGTGAGCTGAGA
44820	42907	GGAGGTTGCAGTGAGCTGAG
44821	42908	TGGAGGTTGCAGTGAGCTGA
44822	42909	GTGGAGGTTGCAGTGAGCTG
44823	42910	GGTGGAGGTTGCAGTGAGCT
44824	42911	AGGTGGAGGTTGCAGTGAGC
44825	42912	GAGGTGGAGGTTGCAGTGAG
44826	42913	GGAGGTGGAGGTTGCAGTGA
44827	42914	GGGAGGTGGAGGTTGCAGTG
44828	42915	TGGGAGGTGGAGGTTGCAGT
44829	42916	CTGGGAGGTGGAGGTTGCAG
44830	42917	CCTGGGAGGTGGAGGTTGCA
44831	42918	ACCTGGGAGGTGGAGGTTGC
44832	42919	AACCTGGGAGGTGGAGGTTG
44833	42920	GAACCTGGGAGGTGGAGGTT
44834	42921	TGAACCTGGGAGGTGGAGGT
44835	42922	CTGAACCTGGGAGGTGGAGG
44836	42923	CCTGAACCTGGGAGGTGGAG
44837	42924	GCCTGAACCTGGGAGGTGGA
44838	42925	CGCCTGAACCTGGGAGGTGG
44839	42926	TCGCCTGAACCTGGGAGGTG
44840	42927	ATCGCCTGAACCTGGGAGGT
44841	42928	AATCGCCTGAACCTGGGAGG
44842	42929	GAATCGCCTGAACCTGGGAG
44843	42930	AGAATCGCCTGAACCTGGGA
44844	42931	AAGAATCGCCTGAACCTGGG
44845	42932	GAAGAATCGCCTGAACCTGG
44846	42933	AGAAGAATCGCCTGAACCTG
44847	42934	CAGAAGAATCGCCTGAACCT
44848	42935	GCAGAAGAATCGCCTGAACC
44849	42936	GGCAGAAGAATCGCCTGAAC
44850	42937	AGGCAGAAGAATCGCCTGAA
44851	42938	GAGGCAGAAGAATCGCCTGA
44852	42939	TGAGGCAGAAGAATCGCCTG
44853	42940	CTGAGGCAGAAGAATCGCCT
44854	42941	GCTGAGGCAGAAGAATCGCC
44855	42942	GGCTGAGGCAGAAGAATCGC
44856	42943	AGGCTGAGGCAGAAGAATCG
44857	42944	GAGGCTGAGGCAGAAGAATC
44858	42945	GGAGGCTGAGGCAGAAGAAT
44859	42946	GGGAGGCTGAGGCAGAAGAA
44860	42947	AGGGAGGCTGAGGCAGAAGA
44861	42948	TAGGGAGGCTGAGGCAGAAG
44862	42949	CTAGGGAGGCTGAGGCAGAA
44863	42950	ACTAGGGAGGCTGAGGCAGA
44864	42951	TACTAGGGAGGCTGAGGCAG
44865	42952	CTACTAGGGAGGCTGAGGCA

93942	92029	CCCTCTGCCCGGCCACCACC
93943	92030	CCCCTCTGCCCGGCCACCAC
93944	92031	GCCCCTCTGCCCGGCCACCA
93945	92032	AGCCCCTCTGCCCGGCCACC
93946	92033	GAGCCCCTCTGCCCGGCCAC
93947	92034	GGAGCCCCTCTGCCCGGCCA
93948	92035	AGGAGCCCCTCTGCCCGGCC
93949	92036	GAGGAGCCCCTCTGCCCGGC
93950	92037	TGAGGAGCCCCTCTGCCCGG
93951	92038	GTGAGGAGCCCCTCTGCCCG
93952	92039	AGTGAGGAGCCCCTCTGCCC
93953	92040	AAGTGAGGAGCCCCTCTGCC
93954	92041	GAAGTGAGGAGCCCCTCTGC
93955	92042	GGAAGTGAGGAGCCCCTCTG
93956	92043	GGGAAGTGAGGAGCCCCTCT
93957	92044	TGGGAAGTGAGGAGCCCCTC
93958	92045	CTGGGAAGTGAGGAGCCCCT
93959	92046	TCTGGGAAGTGAGGAGCCCC
93960	92047	TTCTGGGAAGTGAGGAGCCC
93961	92048	CTTCTGGGAAGTGAGGAGCC
93962	92049	CCTTCTGGGAAGTGAGGAGC
93963	92050	CCCTTCTGGGAAGTGAGGAG
93964	92051	CCCCTTCTGGGAAGTGAGGA
93965	92052	GCCCCTTCTGGGAAGTGAGG
93966	92053	CGCCCCTTCTGGGAAGTGAG
93967	92054	CCGCCCCTTCTGGGAAGTGA
93968	92055	GCCGCCCCTTCTGGGAAGTG
93969	92056	GGCCGCCCCTTCTGGGAAGT
93970	92057	CGGCCGCCCCTTCTGGGAAG
93971	92058	CCGGCCGCCCCTTCTGGGAA
93972	92059	CCCGGCCGCCCCTTCTGGGA
93973	92060	GCCCGGCCGCCCCTTCTGGG
93974	92061	TGCCCGGCCGCCCCTTCTGG
93975	92062	CTGCCCGGCCGCCCCTTCTG
93976	92063	TCTGCCCGGCCGCCCCTTCT
93977	92064	CTCTGCCCGGCCGCCCCTTC
93978	92065	CCTCTGCCCGGCCGCCCCTT
93979	92066	ACCTCTGCCCGGCCGCCCCT
93980	92067	CACCTCTGCCCGGCCGCCCC
93981	92068	GCACCTCTGCCCGGCCGCCC
93982	92069	GGCACCTCTGCCCGGCCGCC
93983	92070	GGGCACCTCTGCCCGGCCGC
93984	92071	GGGGCACCTCTGCCCGGCCG
93985	92072	GGGGGCACCTCTGCCCGGCC
93986	92073	GGGGGGCACCTCTGCCCGGC
93987	92074	TGGGGGGCACCTCTGCCCGG
93988	92075	GTGGGGGGCACCTCTGCCCG
93989	92076	GGTGGGGGGCACCTCTGCCC
93990	92077	AGGTGGGGGGCACCTCTGCC
93991	92078	GAGGTGGGGGGCACCTCTGC
93992	92079	GGAGGTGGGGGGCACCTCTG
93993	92080	GGGAGGTGGGGGGCACCTCT
93994	92081	CGGGAGGTGGGGGGCACCTC
93995	92082	CCGGGAGGTGGGGGGCACCT
93996	92083	TCCGGGAGGTGGGGGGCACC
93997	92084	GTCCGGGAGGTGGGGGGCAC
93998	92085	CGTCCGGGAGGTGGGGGGCA
93999	92086	CCGTCCGGGAGGTGGGGGGC
94000	92087	CCCGTCCGGGAGGTGGGGGG
94001	92088	CCCCGTCCGGGAGGTGGGGG
94002	92089	GCCCCGTCCGGGAGGTGGGG
94003	92090	CGCCCCGTCCGGGAGGTGGG
94004	92091	CCGCCCCGTCCGGGAGGTGG
94005	92092	GCCGCCCCGTCCGGGAGGTG
94006	92093	AGCCGCCCCGTCCGGGAGGT
94007	92094	CAGCCGCCCCGTCCGGGAGG
94008	92095	CCAGCCGCCCCGTCCGGGAG
94009	92096	GCCAGCCGCCCCGTCCGGGA
94010	92097	AGCCAGCCGCCCCGTCCGGG
94011	92098	CAGCCAGCCGCCCCGTCCGG
94012	92099	CCAGCCAGCCGCCCCGTCCG

143089	141176	GTGTTCACTGCTTCCAGTGA
143090	141177	TGTGTTCACTGCTTCCAGTG
143091	141178	ATGTGTTCACTGCTTCCAGT
143092	141179	GATGTGTTCACTGCTTCCAG
143093	141180	GGATGTGTTCACTGCTTCCA
143094	141181	AGGATGTGTTCACTGCTTCC
143095	141182	TAGGATGTGTTCACTGCTTC
143096	141183	GTAGGATGTGTTCACTGCTT
143097	141184	AGTAGGATGTGTTCACTGCT
143098	141185	GAGTAGGATGTGTTCACTGC
143099	141186	AGAGTAGGATGTGTTCACTG
143100	141187	CAGAGTAGGATGTGTTCACT
143101	141188	GCAGAGTAGGATGTGTTCAC
143102	141189	AGCAGAGTAGGATGTGTTCA
143103	141190	AAGCAGAGTAGGATGTGTTC
143104	141191	GAAGCAGAGTAGGATGTGTT
143105	141192	AGAAGCAGAGTAGGATGTGT
143106	141193	CAGAAGCAGAGTAGGATGTG
143107	141194	TCAGAAGCAGAGTAGGATGT
143108	141195	ATCAGAAGCAGAGTAGGATG
143109	141196	AATCAGAAGCAGAGTAGGAT
143110	141197	GAATCAGAAGCAGAGTAGGA
143111	141198	AGAATCAGAAGCAGAGTAGG
143112	141199	GAGAATCAGAAGCAGAGTAG
143113	141200	TGAGAATCAGAAGCAGAGTA
143114	141201	TTGAGAATCAGAAGCAGAGT
143115	141202	GTTGAGAATCAGAAGCAGAG
143116	141203	AGTTGAGAATCAGAAGCAGA
143117	141204	AAGTTGAGAATCAGAAGCAG
143118	141205	TAAGTTGAGAATCAGAAGCA
143119	141206	GTAAGTTGAGAATCAGAAGC
143120	141207	AGTAAGTTGAGAATCAGAAG
143121	141208	CAGTAAGTTGAGAATCAGAA
143122	141209	ACAGTAAGTTGAGAATCAGA
143123	141210	AACAGTAAGTTGAGAATCAG
143124	141211	AAACAGTAAGTTGAGAATCA
143125	141212	AAAACAGTAAGTTGAGAATC
143126	141213	AAAAACAGTAAGTTGAGAAT
143127	141214	CAAAAACAGTAAGTTGAGAA
143128	141215	TCAAAAACAGTAAGTTGAGA
143129	141216	TTCAAAAACAGTAAGTTGAG
143130	141217	CTTCAAAAACAGTAAGTTGA
143131	141218	GCTTCAAAAACAGTAAGTTG
143132	141219	TGCTTCAAAAACAGTAAGTT
143133	141220	GTGCTTCAAAAACAGTAAGT
143134	141221	TGTGCTTCAAAAACAGTAAG
143135	141222	ATGTGCTTCAAAAACAGTAA
143136	141223	CATGTGCTTCAAAAACAGTA
143137	141224	TCATGTGCTTCAAAAACAGT
143138	141225	TTCATGTGCTTCAAAAACAG
143139	141226	GTTCATGTGCTTCAAAAACA
143140	141227	TGTTCATGTGCTTCAAAAAC
143141	141228	CTGTTCATGTGCTTCAAAAA
143142	141229	CCTGTTCATGTGCTTCAAAA
143143	141230	GCCTGTTCATGTGCTTCAAA
143144	141231	GGCCTGTTCATGTGCTTCAA
143145	141232	TGGCCTGTTCATGTGCTTCA
143146	141233	CTGGCCTGTTCATGTGCTTC
143147	141234	CCTGGCCTGTTCATGTGCTT
143148	141235	GCCTGGCCTGTTCATGTGCT
143149	141236	TGCCTGGCCTGTTCATGTGC
143150	141237	GTGCCTGGCCTGTTCATGTG
143151	141238	CGTGCCTGGCCTGTTCATGT
143152	141239	CCGTGCCTGGCCTGTTCATG
143153	141240	ACCGTGCCTGGCCTGTTCAT
143154	141241	CACCGTGCCTGGCCTGTTCA
143155	141242	CCACCGTGCCTGGCCTGTTC
143156	141243	GCCACCGTGCCTGGCCTGTT
143157	141244	AGCCACCGTGCCTGGCCTGT
143158	141245	GAGCCACCGTGCCTGGCCTG
143159	141246	TGAGCCACCGTGCCTGGCCT

44866	42953	GCTACTAGGGAGGCTGAGGC
44867	42954	AGCTACTAGGGAGGCTGAGG
44868	42955	CAGCTACTAGGGAGGCTGAG
44869	42956	CCAGCTACTAGGGAGGCTGA
44870	42957	CCCAGCTACTAGGGAGGCTG
44871	42958	TCCCAGCTACTAGGGAGGCT
44872	42959	GTCCCAGCTACTAGGGAGGC
44873	42960	AGTCCCAGCTACTAGGGAGG
44874	42961	TAGTCCCAGCTACTAGGGAG
44875	42962	GTAGTCCCAGCTACTAGGGA
44876	42963	TGTAGTCCCAGCTACTAGGG
44877	42964	CTGTAGTCCCAGCTACTAGG
44878	42965	CCTGTAGTCCCAGCTACTAG
44879	42966	GCCTGTAGTCCCAGCTACTA
44880	42967	CGCCTGTAGTCCCAGCTACT
44881	42968	GCGCCTGTAGTCCCAGCTAC
44882	42969	TGCGCCTGTAGTCCCAGCTA
44883	42970	ATGCGCCTGTAGTCCCAGCT
44884	42971	CATGCGCCTGTAGTCCCAGC
44885	42972	GCATGCGCCTGTAGTCCCAG
44886	42973	GGCATGCGCCTGTAGTCCCA
44887	42974	TGGCATGCGCCTGTAGTCCC
44888	42975	GTGGCATGCGCCTGTAGTCC
44889	42976	GGTGGCATGCGCCTGTAGTC
44890	42977	TGGTGGCATGCGCCTGTAGT
44891	42978	GTGGTGGCATGCGCCTGTAG
44892	42979	TGTGGTGGCATGCGCCTGTA
44893	42980	GTGTGGTGGCATGCGCCTGT
44894	42981	GGTGTGGTGGCATGCGCCTG
44895	42982	AGGTGTGGTGGCATGCGCCT
44896	42983	CAGGTGTGGTGGCATGCGCC
44897	42984	CCAGGTGTGGTGGCATGCGC
44898	42985	GCCAGGTGTGGTGGCATGCG
44899	42986	AGCCAGGTGTGGTGGCATGC
44900	42987	TAGCCAGGTGTGGTGGCATG
44901	42988	TTAGCCAGGTGTGGTGGCAT
44902	42989	ATTAGCCAGGTGTGGTGGCA
44903	42990	AATTAGCCAGGTGTGGTGGC
44904	42991	AAATTAGCCAGGTGTGGTGG
44905	42992	AAAATTAGCCAGGTGTGGTG
44906	42993	AAAAATTAGCCAGGTGTGGT
44907	42994	AAAAAATTAGCCAGGTGTGG
44908	42995	AAAAAAATTAGCCAGGTGTG
44909	42996	TAAAAAAATTAGCCAGGTGT
44910	42997	ATAAAAAAATTAGCCAGGTG
44911	42998	AATAAAAAAATTAGCCAGGT
44912	42999	GAATAAAAAAATTAGCCAGG
44913	43000	AGAATAAAAAAATTAGCCAG
44914	43001	AAGAATAAAAAAATTAGCCA
44915	43002	TAAGAATAAAAAAATTAGCC
44916	43003	CTAAGAATAAAAAAATTAGC
44917	43004	ACTAAGAATAAAAAAATTAG
44918	43005	TACTAAGAATAAAAAAATTA
44919	43006	CTACTAAGAATAAAAAAATT
44920	43007	TCTACTAAGAATAAAAAAAT
44921	43008	CTCTACTAAGAATAAAAAAA
44922	43009	TCTCTACTAAGAATAAAAAA
44923	43010	ATCTCTACTAAGAATAAAAA
44924	43011	CATCTCTACTAAGAATAAAA
44925	43012	CCATCTCTACTAAGAATAAA
44926	43013	CCCATCTCTACTAAGAATAA
44927	43014	CCCCATCTCTACTAAGAATA
44928	43015	ACCCCATCTCTACTAAGAAT
44929	43016	AACCCCATCTCTACTAAGAA
44930	43017	AAACCCCATCTCTACTAAGA
44931	43018	GAAACCCCATCTCTACTAAG
44932	43019	TGAAACCCCATCTCTACTAA
44933	43020	GTGAAACCCCATCTCTACTA
44934	43021	AGTGAAACCCCATCTCTACT
44935	43022	CAGTGAAACCCCATCTCTAC
44936	43023	ACAGTGAAACCCCATCTCTA

94013	92100	CCCAGCCAGCCGCCCCGTCC
94014	92101	GCCCAGCCAGCCGCCCCGTC
94015	92102	CGCCCAGCCAGCCGCCCCGT
94016	92103	CCGCCCAGCCAGCCGCCCCG
94017	92104	CCCGCCCAGCCAGCCGCCCC
94018	92105	CCCCGCCCAGCCAGCCGCCC
94019	92106	CCCCCGCCCAGCCAGCCGCC
94020	92107	GCCCCCGCCCAGCCAGCCGC
94021	92108	AGCCCCCGCCCAGCCAGCCG
94022	92109	CAGCCCCCGCCCAGCCAGCC
94023	92110	TCAGCCCCCGCCCAGCCAGC
94024	92111	GTCAGCCCCCGCCCAGCCAG
94025	92112	GGTCAGCCCCCGCCCAGCCA
94026	92113	GGGTCAGCCCCCGCCCAGCC
94027	92114	GGGGTCAGCCCCCGCCCAGC
94028	92115	GGGGGTCAGCCCCCGCCCAG
94029	92116	GGGGGGTCAGCCCCCGCCCA
94030	92117	TGGGGGGTCAGCCCCCGCCC
94031	92118	GTGGGGGGTCAGCCCCCGCC
94032	92119	GGTGGGGGGTCAGCCCCCGC
94033	92120	AGGTGGGGGGTCAGCCCCCG
94034	92121	GAGGTGGGGGGTCAGCCCCC
94035	92122	GGAGGTGGGGGGTCAGCCCC
94036	92123	GGGAGGTGGGGGGTCAGCCC
94037	92124	AGGGAGGTGGGGGGTCAGCC
94038	92125	GAGGGAGGTGGGGGGTCAGC
94039	92126	GGAGGGAGGTGGGGGGTCAG
94040	92127	GGGAGGGAGGTGGGGGGTCA
94041	92128	CGGGAGGGAGGTGGGGGGTC
94042	92129	CCGGGAGGGAGGTGGGGGGT
94043	92130	TCCGGGAGGGAGGTGGGGGG
94044	92131	ATCCGGGAGGGAGGTGGGGG
94045	92132	CATCCGGGAGGGAGGTGGGG
94046	92133	CCATCCGGGAGGGAGGTGGG
94047	92134	CCCATCCGGGAGGGAGGTGG
94048	92135	CCCCATCCGGGAGGGAGGTG
94049	92136	GCCCCATCCGGGAGGGAGGT
94050	92137	CGCCCCATCCGGGAGGGAGG
94051	92138	CCGCCCCATCCGGGAGGGAG
94052	92139	GCCGCCCCATCCGGGAGGGA
94053	92140	AGCCGCCCCATCCGGGAGGG
94054	92141	CAGCCGCCCCATCCGGGAGG
94055	92142	CCAGCCGCCCCATCCGGGAG
94056	92143	GCCAGCCGCCCCATCCGGGA
94057	92144	GGCCAGCCGCCCCATCCGGG
94058	92145	CGGCCAGCCGCCCCATCCGG
94059	92146	CCGGCCAGCCGCCCCATCCG
94060	92147	CCCGGCCAGCCGCCCCATCC
94061	92148	GCCCGGCCAGCCGCCCCATC
94062	92149	CGCCCGGCCAGCCGCCCCAT
94063	92150	CCGCCCGGCCAGCCGCCCCA
94064	92151	CCCGCCCGGCCAGCCGCCCC
94065	92152	CCCCGCCCGGCCAGCCGCCC
94066	92153	CCCCCGCCCGGCCAGCCGCC
94067	92154	GCCCCCGCCCGGCCAGCCGC
94068	92155	AGCCCCCGCCCGGCCAGCCG
94069	92156	CAGCCCCCGCCCGGCCAGCC
94070	92157	TCAGCCCCCGCCCGGCCAGC
94071	92158	GTCAGCCCCCGCCCGGCCAG
94072	92159	GGTCAGCCCCCGCCCGGCCA
94073	92160	GGGTCAGCCCCCGCCCGGCC
94074	92161	GGGGTCAGCCCCCGCCCGGC
94075	92162	GGGGGTCAGCCCCCGCCCGG
94076	92163	TGGGGGTCAGCCCCCGCCCG
94077	92164	GTGGGGGTCAGCCCCCGCCC
94078	92165	GGTGGGGGTCAGCCCCCGCC
94079	92166	AGGTGGGGGTCAGCCCCCGC
94080	92167	GAGGTGGGGGTCAGCCCCCG
94081	92168	GGAGGTGGGGGTCAGCCCCC
94082	92169	GGGAGGTGGGGGTCAGCCCC
94083	92170	AGGGAGGTGGGGGTCAGCCC

143160	141247	GTGAGCCACCGTGCCTGGCC
143161	141248	CGTGAGCCACCGTGCCTGGC
143162	141249	ACGTGAGCCACCGTGCCTGG
143163	141250	GACGTGAGCCACCGTGCCTG
143164	141251	AGACGTGAGCCACCGTGCCT
143165	141252	CAGACGTGAGCCACCGTGCC
143166	141253	ACAGACGTGAGCCACCGTGC
143167	141254	TACAGACGTGAGCCACCGTG
143168	141255	TTACAGACGTGAGCCACCGT
143169	141256	ATTACAGACGTGAGCCACCG
143170	141257	GATTACAGACGTGAGCCACC
143171	141258	GGATTACAGACGTGAGCCAC
143172	141259	GGGATTACAGACGTGAGCCA
143173	141260	TGGGATTACAGACGTGAGCC
143174	141261	CTGGGATTACAGACGTGAGC
143175	141262	GCTGGGATTACAGACGTGAG
143176	141263	TGCTGGGATTACAGACGTGA
143177	141264	GTGCTGGGATTACAGACGTG
143178	141265	AGTGCTGGGATTACAGACGT
143179	141266	AAGTGCTGGGATTACAGACG
143180	141267	AAAGTGCTGGGATTACAGAC
143181	141268	CAAAGTGCTGGGATTACAGA
143182	141269	CCAAAGTGCTGGGATTACAG
143183	141270	CCCAAAGTGCTGGGATTACA
143184	141271	TCCCAAAGTGCTGGGATTAC
143185	141272	CTCCCAAAGTGCTGGGATTA
143186	141273	CCTCCCAAAGTGCTGGGATT
143187	141274	GCCTCCCAAAGTGCTGGGAT
143188	141275	AGCCTCCCAAAGTGCTGGGA
143189	141276	CAGCCTCCCAAAGTGCTGGG
143190	141277	TCAGCCTCCCAAAGTGCTGG
143191	141278	TTCAGCCTCCCAAAGTGCTG
143192	141279	CTTCAGCCTCCCAAAGTGCT
143193	141280	ACTTCAGCCTCCCAAAGTGC
143194	141281	CACTTCAGCCTCCCAAAGTG
143195	141282	CCACTTCAGCCTCCCAAAGT
143196	141283	CCCACTTCAGCCTCCCAAAG
143197	141284	GCCCACTTCAGCCTCCCAAA
143198	141285	CGCCCACTTCAGCCTCCCAA
143199	141286	CCGCCCACTTCAGCCTCCCA
143200	141287	TCCGCCCACTTCAGCCTCCC
143201	141288	ATCCGCCCACTTCAGCCTCC
143202	141289	GATCCGCCCACTTCAGCCTC
143203	141290	TGATCCGCCCACTTCAGCCT
143204	141291	ATGATCCGCCCACTTCAGCC
143205	141292	AATGATCCGCCCACTTCAGC
143206	141293	AAATGATCCGCCCACTTCAG
143207	141294	CAAATGATCCGCCCACTTCA
143208	141295	TCAAATGATCCGCCCACTTC
143209	141296	CTCAAATGATCCGCCCACTT
143210	141297	CCTCAAATGATCCGCCCACT
143211	141298	ACCTCAAATGATCCGCCCAC
143212	141299	GACCTCAAATGATCCGCCCA
143213	141300	TGACCTCAAATGATCCGCCC
143214	141301	CTGACCTCAAATGATCCGCC
143215	141302	CCTGACCTCAAATGATCCGC
143216	141303	TCCTGACCTCAAATGATCCG
143217	141304	CTCCTGACCTCAAATGATCC
143218	141305	ACTCCTGACCTCAAATGATC
143219	141306	AACTCCTGACCTCAAATGAT
143220	141307	AAACTCCTGACCTCAAATGA
143221	141308	CAAACTCCTGACCTCAAATG
143222	141309	TCAAACTCCTGACCTCAAAT
143223	141310	CTCAAACTCCTGACCTCAAA
143224	141311	TCTCAAACTCCTGACCTCAA
143225	141312	ATCTCAAACTCCTGACCTCA
143226	141313	GATCTCAAACTCCTGACCTC
143227	141314	TGATCTCAAACTCCTGACCT
143228	141315	CTGATCTCAAACTCCTGACC
143229	141316	GCTGATCTCAAACTCCTGAC
143230	141317	GGCTGATCTCAAACTCCTGA

44937	43024	CACAGTGAAACCCCATCTCT
44938	43025	ACACAGTGAAACCCCATCTC
44939	43026	AACACAGTGAAACCCCATCT
44940	43027	TAACACAGTGAAACCCCATC
44941	43028	CTAACACAGTGAAACCCCAT
44942	43029	GCTAACACAGTGAAACCCCA
44943	43030	GGCTAACACAGTGAAACCCC
44944	43031	TGGCTAACACAGTGAAACCC
44945	43032	CTGGCTAACACAGTGAAACC
44946	43033	CCTGGCTAACACAGTGAAAC
44947	43034	TCCTGGCTAACACAGTGAAA
44948	43035	ATCCTGGCTAACACAGTGAA
44949	43036	CATCCTGGCTAACACAGTGA
44950	43037	CCATCCTGGCTAACACAGTG
44951	43038	ACCATCCTGGCTAACACAGT
44952	43039	GACCATCCTGGCTAACACAG
44953	43040	AGACCATCCTGGCTAACACA
44954	43041	GAGACCATCCTGGCTAACAC
44955	43042	CGAGACCATCCTGGCTAACA
44956	43043	TCGAGACCATCCTGGCTAAC
44957	43044	TTCGAGACCATCCTGGCTAA
44958	43045	GTTCGAGACCATCCTGGCTA
44959	43046	AGTTCGAGACCATCCTGGCT
44960	43047	GAGTTCGAGACCATCCTGGC
44961	43048	GGAGTTCGAGACCATCCTGG
44962	43049	AGGAGTTCGAGACCATCCTG
44963	43050	CAGGAGTTCGAGACCATCCT
44964	43051	TCAGGAGTTCGAGACCATCC
44965	43052	GTCAGGAGTTCGAGACCATC
44966	43053	GGTCAGGAGTTCGAGACCAT
44967	43054	AGGTCAGGAGTTCGAGACCA
44968	43055	AAGGTCAGGAGTTCGAGACC
44969	43056	CAAGGTCAGGAGTTCGAGAC
44970	43057	ACAAGGTCAGGAGTTCGAGA
44971	43058	CACAAGGTCAGGAGTTCGAG
44972	43059	TCACAAGGTCAGGAGTTCGA
44973	43060	ATCACAAGGTCAGGAGTTCG
44974	43061	GATCACAAGGTCAGGAGTTC
44975	43062	AGATCACAAGGTCAGGAGTT
44976	43063	CAGATCACAAGGTCAGGAGT
44977	43064	GCAGATCACAAGGTCAGGAG
44978	43065	GGCAGATCACAAGGTCAGGA
44979	43066	GGGCAGATCACAAGGTCAGG
44980	43067	TGGGCAGATCACAAGGTCAG
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44985	43072	AGAGGTGGGCAGATCACAAG
44986	43073	CAGAGGTGGGCAGATCACAA
44987	43074	GCAGAGGTGGGCAGATCACA
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44989	43076	AGGCAGAGGTGGGCAGATCA
44990	43077	GAGGCAGAGGTGGGCAGATC
44991	43078	GGAGGCAGAGGTGGGCAGAT
44992	43079	GGGAGGCAGAGGTGGGCAGA
44993	43080	TGGGAGGCAGAGGTGGGCAG
44994	43081	TTGGGAGGCAGAGGTGGGCA
44995	43082	TTTGGGAGGCAGAGGTGGGC
44996	43083	CTTTGGGAGGCAGAGGTGGG
44997	43084	ACTTTGGGAGGCAGAGGTGG
44998	43085	CACTTTGGGAGGCAGAGGTG
44999	43086	GCACTTTGGGAGGCAGAGGT
45000	43087	AGCACTTTGGGAGGCAGAGG
45001	43088	CAGCACTTTGGGAGGCAGAG
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45005	43092	ATCCCAGCACTTTGGGAGGC
45006	43093	AATCCCAGCACTTTGGGAGG
45007	43094	TAATCCCAGCACTTTGGGAG

94084	92171	GAGGGAGGTGGGGGTCAGCC
94085	92172	GGAGGGAGGTGGGGGTCAGC
94086	92173	GGGAGGGAGGTGGGGGTCAG
94087	92174	CGGGAGGGAGGTGGGGGTCA
94088	92175	CCGGGAGGGAGGTGGGGGTC
94089	92176	TCCGGGAGGGAGGTGGGGGT
94090	92177	GTCCGGGAGGGAGGTGGGGG
94091	92178	CGTCCGGGAGGGAGGTGGGG
94092	92179	CCGTCCGGGAGGGAGGTGGG
94093	92180	CCCGTCCGGGAGGGAGGTGG
94094	92181	ACCCGTCCGGGAGGGAGGTG
94095	92182	AACCCGTCCGGGAGGGAGGT
94096	92183	CAACCCGTCCGGGAGGGAGG
94097	92184	CCAACCCGTCCGGGAGGGAG
94098	92185	GCCAACCCGTCCGGGAGGGA
94099	92186	AGCCAACCCGTCCGGGAGGG
94100	92187	CAGCCAACCCGTCCGGGAGG
94101	92188	GCAGCCAACCCGTCCGGGAG
94102	92189	GGCAGCCAACCCGTCCGGGA
94103	92190	CGGCAGCCAACCCGTCCGGG
94104	92191	CCGGCAGCCAACCCGTCCGG
94105	92192	CCCGGCAGCCAACCCGTCCG
94106	92193	ACCCGGCAGCCAACCCGTCC
94107	92194	CACCCGGCAGCCAACCCGTC
94108	92195	CCACCCGGCAGCCAACCCGT
94109	92196	TCCACCCGGCAGCCAACCCG
94110	92197	CTCCACCCGGCAGCCAACCC
94111	92198	TCTCCACCCGGCAGCCAACC
94112	92199	ATCTCCACCCGGCAGCCAAC
94113	92200	CATCTCCACCCGGCAGCCAA
94114	92201	GCATCTCCACCCGGCAGCCA
94115	92202	AGCATCTCCACCCGGCAGCC
94116	92203	GAGCATCTCCACCCGGCAGC
94117	92204	GGAGCATCTCCACCCGGCAG
94118	92205	AGGAGCATCTCCACCCGGCA
94119	92206	GAGGAGCATCTCCACCCGGC
94120	92207	TGAGGAGCATCTCCACCCGG
94121	92208	GTGAGGAGCATCTCCACCCG
94122	92209	AGTGAGGAGCATCTCCACCC
94123	92210	AAGTGAGGAGCATCTCCACC
94124	92211	GAAGTGAGGAGCATCTCCAC
94125	92212	GGAAGTGAGGAGCATCTCCA
94126	92213	GGGAAGTGAGGAGCATCTCC
94127	92214	TGGGAAGTGAGGAGCATCTC
94128	92215	CTGGGAAGTGAGGAGCATCT
94129	92216	TCTGGGAAGTGAGGAGCATC
94130	92217	GTCTGGGAAGTGAGGAGCAT
94131	92218	CGTCTGGGAAGTGAGGAGCA
94132	92219	CCGTCTGGGAAGTGAGGAGC
94133	92220	CCCGTCTGGGAAGTGAGGAG
94134	92221	CCCCGTCTGGGAAGTGAGGA
94135	92222	ACCCCGTCTGGGAAGTGAGG
94136	92223	CACCCCGTCTGGGAAGTGAG
94137	92224	CCACCCCGTCTGGGAAGTGA
94138	92225	GCCACCCCGTCTGGGAAGTG
94139	92226	AGCCACCCCGTCTGGGAAGT
94140	92227	CAGCCACCCCGTCTGGGAAG
94141	92228	GCAGCCACCCCGTCTGGGAA
94142	92229	GGCAGCCACCCCGTCTGGGA
94143	92230	TGGCAGCCACCCCGTCTGGG
94144	92231	CTGGCAGCCACCCCGTCTGG
94145	92232	CCTGGCAGCCACCCCGTCTG
94146	92233	GCCTGGCAGCCACCCCGTCT
94147	92234	CGCCTGGCAGCCACCCCGTC
94148	92235	CCGCCTGGCAGCCACCCCGT
94149	92236	TCCGCCTGGCAGCCACCCCG
94150	92237	CTCCGCCTGGCAGCCACCCC
94151	92238	CCTCCGCCTGGCAGCCACCC
94152	92239	CCCTCCGCCTGGCAGCCACC
94153	92240	CCCCTCCGCCTGGCAGCCAC
94154	92241	GCCCCTCCGCCTGGCAGCCA

143231	141318	AGGCTGATCTCAAACTCCTG
143232	141319	CAGGCTGATCTCAAACTCCT
143233	141320	CCAGGCTGATCTCAAACTCC
143234	141321	GCCAGGCTGATCTCAAACTC
143235	141322	GGCCAGGCTGATCTCAAACT
143236	141323	TGGCCAGGCTGATCTCAAAC
143237	141324	CTGGCCAGGCTGATCTCAAA
143238	141325	GCTGGCCAGGCTGATCTCAA
143239	141326	TGCTGGCCAGGCTGATCTCA
143240	141327	ATGCTGGCCAGGCTGATCTC
143241	141328	CATGCTGGCCAGGCTGATCT
143242	141329	CCATGCTGGCCAGGCTGATC
143243	141330	GCCATGCTGGCCAGGCTGAT
143244	141331	CGCCATGCTGGCCAGGCTGA
143245	141332	TCGCCATGCTGGCCAGGCTG
143246	141333	TTCGCCATGCTGGCCAGGCT
143247	141334	TTTCGCCATGCTGGCCAGGC
143248	141335	GTTTCGCCATGCTGGCCAGG
143249	141336	GGTTTCGCCATGCTGGCCAG
143250	141337	GGGTTTCGCCATGCTGGCCA
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143252	141339	TGGGGTTTCGCCATGCTGGC
143253	141340	ATGGGGTTTCGCCATGCTGG
143254	141341	GATGGGGTTTCGCCATGCTG
143255	141342	AGATGGGGTTTCGCCATGCT
143256	141343	GAGATGGGGTTTCGCCATGC
143257	141344	AGAGATGGGGTTTCGCCATG
143258	141345	TAGAGATGGGGTTTCGCCAT
143259	141346	GTAGAGATGGGGTTTCGCCA
143260	141347	AGTAGAGATGGGGTTTCGCC
143261	141348	TAGTAGAGATGGGGTTTCGC
143262	141349	TTAGTAGAGATGGGGTTTCG
143263	141350	TTTAGTAGAGATGGGGTTTC
143264	141351	TTTTAGTAGAGATGGGGTTT
143265	141352	TTTTTAGTAGAGATGGGGTT
143266	141353	ATTTTTAGTAGAGATGGGGT
143267	141354	TATTTTTAGTAGAGATGGGG
143268	141355	GTATTTTTAGTAGAGATGGG
143269	141356	TGTATTTTTAGTAGAGATGG
143270	141357	TTGTATTTTTAGTAGAGATG
143271	141358	TTTGTATTTTTAGTAGAGAT
143272	141359	TTTTGTATTTTTAGTAGAGA
143273	141360	TTTTTGTATTTTTAGTAGAG
143274	141361	ATTTTTGTATTTTTAGTAGA
143275	141362	AATTTTTGTATTTTTAGTAG
143276	141363	TAATTTTTGTATTTTTAGTA
143277	141364	CTAATTTTTGTATTTTTAGT
143278	141365	GCTAATTTTTGTATTTTTAG
143279	141366	AGCTAATTTTTGTATTTTTA
143280	141367	CAGCTAATTTTTGTATTTTT
143281	141368	CCAGCTAATTTTTGTATTTT
143282	141369	CCCAGCTAATTTTTGTATTT
143283	141370	GCCCAGCTAATTTTTGTATT
143284	141371	CGCCCAGCTAATTTTTGTAT
143285	141372	ACGCCCAGCTAATTTTTGTA
143286	141373	CACGCCCAGCTAATTTTTGT
143287	141374	CCACGCCCAGCTAATTTTTG
143288	141375	ACCACGCCCAGCTAATTTTT
143289	141376	CACCACGCCCAGCTAATTTT
143290	141377	CCACCACGCCCAGCTAATTT
143291	141378	GCCACCACGCCCAGCTAATT
143292	141379	TGCCACCACGCCCAGCTAAT
143293	141380	GTGCCACCACGCCCAGCTAA
143294	141381	TGTGCCACCACGCCCAGCTA
143295	141382	ATGTGCCACCACGCCCAGCT
143296	141383	CATGTGCCACCACGCCCAGC
143297	141384	GCATGTGCCACCACGCCCAG
143298	141385	GGCATGTGCCACCACGCCCA
143299	141386	AGGCATGTGCCACCACGCCC
143300	141387	CAGGCATGTGCCACCACGCC
143301	141388	ACAGGCATGTGCCACCACGC

45008	43095	GTAATCCCAGCACTTTGGGA
45009	43096	TGTAATCCCAGCACTTTGGG
45010	43097	CTGTAATCCCAGCACTTTGG
45011	43098	CCTGTAATCCCAGCACTTTG
45012	43099	GCCTGTAATCCCAGCACTTT
45013	43100	TGCCTGTAATCCCAGCACTT
45014	43101	ATGCCTGTAATCCCAGCACT
45015	43102	CATGCCTGTAATCCCAGCAC
45016	43103	TCATGCCTGTAATCCCAGCA
45017	43104	CTCATGCCTGTAATCCCAGC
45018	43105	GCTCATGCCTGTAATCCCAG
45019	43106	GGCTCATGCCTGTAATCCCA
45020	43107	TGGCTCATGCCTGTAATCCC
45021	43108	GTGGCTCATGCCTGTAATCC
45022	43109	AGTGGCTCATGCCTGTAATC
45023	43110	CAGTGGCTCATGCCTGTAAT
45024	43111	GCAGTGGCTCATGCCTGTAA
45025	43112	CGCAGTGGCTCATGCCTGTA
45026	43113	GCGCAGTGGCTCATGCCTGT
45027	43114	GGCGCAGTGGCTCATGCCTG
45028	43115	GGGCGCAGTGGCTCATGCCT
45029	43116	CGGGCGCAGTGGCTCATGCC
45030	43117	CCGGGCGCAGTGGCTCATGC
45031	43118	GCCGGGCGCAGTGGCTCATG
45032	43119	GGCCGGGCGCAGTGGCTCAT
45033	43120	GGGCCGGGCGCAGTGGCTCA
45034	43121	TGGGCCGGGCGCAGTGGCTC
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45036	43123	TATGGGCCGGGCGCAGTGGC
45037	43124	ATATGGGCCGGGCGCAGTGG
45038	43125	CATATGGGCCGGGCGCAGTG
45039	43126	TCATATGGGCCGGGCGCAGT
45040	43127	GTCATATGGGCCGGGCGCAG
45041	43128	GGTCATATGGGCCGGGCGCA
45042	43129	AGGTCATATGGGCCGGGCGC
45043	43130	CAGGTCATATGGGCCGGGCG
45044	43131	ACAGGTCATATGGGCCGGGC
45045	43132	AACAGGTCATATGGGCCGGG
45046	43133	AAACAGGTCATATGGGCCGG
45047	43134	AAAACAGGTCATATGGGCCG
45048	43135	AAAAACAGGTCATATGGGCC
45049	43136	GAAAAACAGGTCATATGGGC
45050	43137	AGAAAAACAGGTCATATGGG
45051	43138	AAGAAAAACAGGTCATATGG
45052	43139	AAAGAAAAACAGGTCATATG
45053	43140	AAAAGAAAAACAGGTCATAT
45054	43141	TAAAAGAAAAACAGGTCATA
45055	43142	ATAAAAGAAAAACAGGTCAT
45056	43143	TATAAAAGAAAAACAGGTCA
45057	43144	CTATAAAAGAAAAACAGGTC
45058	43145	TCTATAAAAGAAAAACAGGT
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45060	43147	CATCTATAAAAGAAAAACAG
45061	43148	CCATCTATAAAAGAAAAACA
45062	43149	CCCATCTATAAAAGAAAAAC
45063	43150	CCCCATCTATAAAAGAAAAA
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45065	43152	TCCCCCATCTATAAAAGAAA
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45068	43155	TTCTCCCCCATCTATAAAAG
45069	43156	TTTCTCCCCCATCTATAAAA
45070	43157	ATTTCTCCCCCATCTATAAA
45071	43158	TATTTCTCCCCCATCTATAA
45072	43159	ATATTTCTCCCCCATCTATA
45073	43160	CATATTTCTCCCCCATCTAT
45074	43161	CCATATTTCTCCCCCATCTA
45075	43162	CCCATATTTCTCCCCCATCT
45076	43163	TCCCATATTTCTCCCCCATC
45077	43164	TTCCCATATTTCTCCCCCAT
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94155	92242	AGCCCCTCCGCCTGGCAGCC
94156	92243	AAGCCCCTCCGCCTGGCAGC
94157	92244	GAAGCCCCTCCGCCTGGCAG
94158	92245	AGAAGCCCCTCCGCCTGGCA
94159	92246	GAGAAGCCCCTCCGCCTGGC
94160	92247	TGAGAAGCCCCTCCGCCTGG
94161	92248	GTGAGAAGCCCCTCCGCCTG
94162	92249	AGTGAGAAGCCCCTCCGCCT
94163	92250	AAGTGAGAAGCCCCTCCGCC
94164	92251	GAAGTGAGAAGCCCCTCCGC
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94166	92253	GAGAAGTGAGAAGCCCCTCC
94167	92254	TGAGAAGTGAGAAGCCCCTC
94168	92255	CTGAGAAGTGAGAAGCCCCT
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94170	92257	GTCTGAGAAGTGAGAAGCCC
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94172	92259	CCGTCTGAGAAGTGAGAAGC
94173	92260	CCCGTCTGAGAAGTGAGAAG
94174	92261	CCCCGTCTGAGAAGTGAGAA
94175	92262	GCCCCGTCTGAGAAGTGAGA
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94177	92264	CCGCCCCGTCTGAGAAGTGA
94178	92265	GCCGCCCCGTCTGAGAAGTG
94179	92266	AGCCGCCCCGTCTGAGAAGT
94180	92267	CAGCCGCCCCGTCTGAGAAG
94181	92268	GCAGCCGCCCCGTCTGAGAA
94182	92269	GGCAGCCGCCCCGTCTGAGA
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94184	92271	CCGGCAGCCGCCCCGTCTGA
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94186	92273	GCCCGGCAGCCGCCCCGTCT
94187	92274	TGCCCGGCAGCCGCCCCGTC
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94189	92276	TCTGCCCGGCAGCCGCCCCG
94190	92277	CTCTGCCCGGCAGCCGCCCC
94191	92278	CCTCTGCCCGGCAGCCGCCC
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94195	92282	AGCCCCTCTGCCCGGCAGCC
94196	92283	GAGCCCCTCTGCCCGGCAGC
94197	92284	GGAGCCCCTCTGCCCGGCAG
94198	92285	AGGAGCCCCTCTGCCCGGCA
94199	92286	GAGGAGCCCCTCTGCCCGGC
94200	92287	TGAGGAGCCCCTCTGCCCGG
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94203	92290	AAGTGAGGAGCCCCTCTGCC
94204	92291	GAAGTGAGGAGCCCCTCTGC
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94206	92293	GAGAAGTGAGGAGCCCCTCT
94207	92294	TGAGAAGTGAGGAGCCCCTC
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94209	92296	TCTGAGAAGTGAGGAGCCCC
94210	92297	GTCTGAGAAGTGAGGAGCCC
94211	92298	CGTCTGAGAAGTGAGGAGCC
94212	92299	CCGTCTGAGAAGTGAGGAGC
94213	92300	CCCGTCTGAGAAGTGAGGAG
94214	92301	CCCCGTCTGAGAAGTGAGGA
94215	92302	GCCCCGTCTGAGAAGTGAGG
94216	92303	CGCCCCGTCTGAGAAGTGAG
94217	92304	CCGCCCCGTCTGAGAAGTGA
94218	92305	GCCGCCCCGTCTGAGAAGTG
94219	92306	GGCCGCCCCGTCTGAGAAGT
94220	92307	TGGCCGCCCCGTCTGAGAAG
94221	92308	CTGGCCGCCCCGTCTGAGAA
94222	92309	CCTGGCCGCCCCGTCTGAGA
94223	92310	GCCTGGCCGCCCCGTCTGAG
94224	92311	TGCCTGGCCGCCCCGTCTGA
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143302	141389	TACAGGCATGTGCCACCACG
143303	141390	TTACAGGCATGTGCCACCAC
143304	141391	ATTACAGGCATGTGCCACCA
143305	141392	GATTACAGGCATGTGCCACC
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143307	141394	GAGATTACAGGCATGTGCCA
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143309	141396	CTGAGATTACAGGCATGTGC
143310	141397	GCTGAGATTACAGGCATGTG
143311	141398	AGCTGAGATTACAGGCATGT
143312	141399	TAGCTGAGATTACAGGCATG
143313	141400	GTAGCTGAGATTACAGGCAT
143314	141401	AGTAGCTGAGATTACAGGCA
143315	141402	GAGTAGCTGAGATTACAGGC
143316	141403	CGAGTAGCTGAGATTACAGG
143317	141404	CCGAGTAGCTGAGATTACAG
143318	141405	CCCGAGTAGCTGAGATTACA
143319	141406	TCCCGAGTAGCTGAGATTAC
143320	141407	CTCCCGAGTAGCTGAGATTA
143321	141408	CCTCCCGAGTAGCTGAGATT
143322	141409	GCCTCCCGAGTAGCTGAGAT
143323	141410	AGCCTCCCGAGTAGCTGAGA
143324	141411	CAGCCTCCCGAGTAGCTGAG
143325	141412	TCAGCCTCCCGAGTAGCTGA
143326	141413	CTCAGCCTCCCGAGTAGCTG
143327	141414	CCTCAGCCTCCCGAGTAGCT
143328	141415	GCCTCAGCCTCCCGAGTAGC
143329	141416	TGCCTCAGCCTCCCGAGTAG
143330	141417	CTGCCTCAGCCTCCCGAGTA
143331	141418	CCTGCCTCAGCCTCCCGAGT
143332	141419	TCCTGCCTCAGCCTCCCGAG
143333	141420	CTCCTGCCTCAGCCTCCCGA
143334	141421	TCTCCTGCCTCAGCCTCCCG
143335	141422	TTCTCCTGCCTCAGCCTCCC
143336	141423	ATTCTCCTGCCTCAGCCTCC
143337	141424	AATTCTCCTGCCTCAGCCTC
143338	141425	CAATTCTCCTGCCTCAGCCT
143339	141426	GCAATTCTCCTGCCTCAGCC
143340	141427	AGCAATTCTCCTGCCTCAGC
143341	141428	AAGCAATTCTCCTGCCTCAG
143342	141429	CAAGCAATTCTCCTGCCTCA
143343	141430	TCAAGCAATTCTCCTGCCTC
143344	141431	TTCAAGCAATTCTCCTGCCT
143345	141432	GTTCAAGCAATTCTCCTGCC
143346	141433	GGTTCAAGCAATTCTCCTGC
143347	141434	AGGTTCAAGCAATTCTCCTG
143348	141435	CAGGTTCAAGCAATTCTCCT
143349	141436	CCAGGTTCAAGCAATTCTCC
143350	141437	CCCAGGTTCAAGCAATTCTC
143351	141438	TCCCAGGTTCAAGCAATTCT
143352	141439	CTCCCAGGTTCAAGCAATTC
143353	141440	CCTCCCAGGTTCAAGCAATT
143354	141441	GCCTCCCAGGTTCAAGCAAT
143355	141442	TGCCTCCCAGGTTCAAGCAA
143356	141443	CTGCCTCCCAGGTTCAAGCA
143357	141444	TCTGCCTCCCAGGTTCAAGC
143358	141445	CTCTGCCTCCCAGGTTCAAG
143359	141446	CCTCTGCCTCCCAGGTTCAA
143360	141447	ACCTCTGCCTCCCAGGTTCA
143361	141448	AACCTCTGCCTCCCAGGTTC
143362	141449	CAACCTCTGCCTCCCAGGTT
143363	141450	GCAACCTCTGCCTCCCAGGT
143364	141451	TGCAACCTCTGCCTCCCAGG
143365	141452	CTGCAACCTCTGCCTCCCAG
143366	141453	ACTGCAACCTCTGCCTCCCA
143367	141454	CACTGCAACCTCTGCCTCCC
143368	141455	TCACTGCAACCTCTGCCTCC
143369	141456	CTCACTGCAACCTCTGCCTC
143370	141457	GCTCACTGCAACCTCTGCCT
143371	141458	GGCTCACTGCAACCTCTGCC
143372	141459	AGGCTCACTGCAACCTCTGC

45079	43166	ACTTCCCATATTTCTCCCCC
45080	43167	CACTTCCCATATTTCTCCCC
45081	43168	TCACTTCCCATATTTCTCCC
45082	43169	GTCACTTCCCATATTTCTCC
45083	43170	AGTCACTTCCCATATTTCTC
45084	43171	AAGTCACTTCCCATATTTCT
45085	43172	CAAGTCACTTCCCATATTTC
45086	43173	CCAAGTCACTTCCCATATTT
45087	43174	ACCAAGTCACTTCCCATATT
45088	43175	CACCAAGTCACTTCCCATAT
45089	43176	ACACCAAGTCACTTCCCATA
45090	43177	GACACCAAGTCACTTCCCAT
45091	43178	TGACACCAAGTCACTTCCCA
45092	43179	CTGACACCAAGTCACTTCCC
45093	43180	ACTGACACCAAGTCACTTCC
45094	43181	GACTGACACCAAGTCACTTC
45095	43182	TGACTGACACCAAGTCACTT
45096	43183	ATGACTGACACCAAGTCACT
45097	43184	GATGACTGACACCAAGTCAC
45098	43185	AGATGACTGACACCAAGTCA
45099	43186	CAGATGACTGACACCAAGTC
45100	43187	ACAGATGACTGACACCAAGT
45101	43188	CACAGATGACTGACACCAAG
45102	43189	ACACAGATGACTGACACCAA
45103	43190	AACACAGATGACTGACACCA
45104	43191	CAACACAGATGACTGACACC
45105	43192	CCAACACAGATGACTGACAC
45106	43193	ACCAACACAGATGACTGACA
45107	43194	AACCAACACAGATGACTGAC
45108	43195	TAACCAACACAGATGACTGA
45109	43196	TTAACCAACACAGATGACTG
45110	43197	TTTAACCAACACAGATGACT
45111	43198	ATTTAACCAACACAGATGAC
45112	43199	GATTTAACCAACACAGATGA
45113	43200	TGATTTAACCAACACAGATG
45114	43201	TTGATTTAACCAACACAGAT
45115	43202	CTTGATTTAACCAACACAGA
45116	43203	TCTTGATTTAACCAACACAG
45117	43204	TTCTTGATTTAACCAACACA
45118	43205	ATTCTTGATTTAACCAACAC
45119	43206	TATTCTTGATTTAACCAACA
45120	43207	ATATTCTTGATTTAACCAAC
45121	43208	TATATTCTTGATTTAACCAA
45122	43209	TTATATTCTTGATTTAACCA
45123	43210	ATTATATTCTTGATTTAACC
45124	43211	GATTATATTCTTGATTTAAC
45125	43212	GGATTATATTCTTGATTTAA
45126	43213	CGGATTATATTCTTGATTTA
45127	43214	ACGGATTATATTCTTGATTT
45128	43215	CACGGATTATATTCTTGATT
45129	43216	ACACGGATTATATTCTTGAT
45130	43217	AACACGGATTATATTCTTGA
45131	43218	AAACACGGATTATATTCTTG
45132	43219	AAAACACGGATTATATTCTT
45133	43220	CAAAACACGGATTATATTCT
45134	43221	GCAAAACACGGATTATATTC
45135	43222	AGCAAAACACGGATTATATT
45136	43223	AAGCAAAACACGGATTATAT
45137	43224	GAAGCAAAACACGGATTATA
45138	43225	AGAAGCAAAACACGGATTAT
45139	43226	CAGAAGCAAAACACGGATTA
45140	43227	TCAGAAGCAAAACACGGATT
45141	43228	TTCAGAAGCAAAACACGGAT
45142	43229	ATTCAGAAGCAAAACACGGA
45143	43230	TATTCAGAAGCAAAACACGG
45144	43231	CTATTCAGAAGCAAAACACG
45145	43232	GCTATTCAGAAGCAAAACAC
45146	43233	AGCTATTCAGAAGCAAAACA
45147	43234	GAGCTATTCAGAAGCAAAAC
45148	43235	AGAGCTATTCAGAAGCAAAA
45149	43236	AAGAGCTATTCAGAAGCAAA

94226	92313	TCTGCCTGGCCGCCCCGTCT
94227	92314	CTCTGCCTGGCCGCCCCGTC
94228	92315	TCTCTGCCTGGCCGCCCCGT
94229	92316	GTCTCTGCCTGGCCGCCCCG
94230	92317	CGTCTCTGCCTGGCCGCCCC
94231	92318	GCGTCTCTGCCTGGCCGCCC
94232	92319	AGCGTCTCTGCCTGGCCGCC
94233	92320	GAGCGTCTCTGCCTGGCCGC
94234	92321	GGAGCGTCTCTGCCTGGCCG
94235	92322	AGGAGCGTCTCTGCCTGGCC
94236	92323	GAGGAGCGTCTCTGCCTGGC
94237	92324	TGAGGAGCGTCTCTGCCTGG
94238	92325	GTGAGGAGCGTCTCTGCCTG
94239	92326	GGTGAGGAGCGTCTCTGCCT
94240	92327	AGGTGAGGAGCGTCTCTGCC
94241	92328	GAGGTGAGGAGCGTCTCTGC
94242	92329	GGAGGTGAGGAGCGTCTCTG
94243	92330	GGGAGGTGAGGAGCGTCTCT
94244	92331	TGGGAGGTGAGGAGCGTCTC
94245	92332	CTGGGAGGTGAGGAGCGTCT
94246	92333	TCTGGGAGGTGAGGAGCGTC
94247	92334	GTCTGGGAGGTGAGGAGCGT
94248	92335	CGTCTGGGAGGTGAGGAGCG
94249	92336	CCGTCTGGGAGGTGAGGAGC
94250	92337	CCCGTCTGGGAGGTGAGGAG
94251	92338	CCCCGTCTGGGAGGTGAGGA
94252	92339	ACCCCGTCTGGGAGGTGAGG
94253	92340	GACCCCGTCTGGGAGGTGAG
94254	92341	CGACCCCGTCTGGGAGGTGA
94255	92342	GCGACCCCGTCTGGGAGGTG
94256	92343	CGCGACCCCGTCTGGGAGGT
94257	92344	CCGCGACCCCGTCTGGGAGG
94258	92345	GCCGCGACCCCGTCTGGGAG
94259	92346	GGCCGCGACCCCGTCTGGGA
94260	92347	CGGCCGCGACCCCGTCTGGG
94261	92348	CCGGCCGCGACCCCGTCTGG
94262	92349	CCCGGCCGCGACCCCGTCTG
94263	92350	GCCCGGCCGCGACCCCGTCT
94264	92351	TGCCCGGCCGCGACCCCGTC
94265	92352	CTGCCCGGCCGCGACCCCGT
94266	92353	TCTGCCCGGCCGCGACCCCG
94267	92354	CTCTGCCCGGCCGCGACCCC
94268	92355	CCTCTGCCCGGCCGCGACCC
94269	92356	GCCTCTGCCCGGCCGCGACC
94270	92357	CGCCTCTGCCCGGCCGCGAC
94271	92358	GCGCCTCTGCCCGGCCGCGA
94272	92359	AGCGCCTCTGCCCGGCCGCG
94273	92360	GAGCGCCTCTGCCCGGCCGC
94274	92361	GGAGCGCCTCTGCCCGGCCG
94275	92362	AGGAGCGCCTCTGCCCGGCC
94276	92363	GAGGAGCGCCTCTGCCCGGC
94277	92364	TGAGGAGCGCCTCTGCCCGG
94278	92365	GTGAGGAGCGCCTCTGCCCG
94279	92366	TGTGAGGAGCGCCTCTGCCC
94280	92367	ATGTGAGGAGCGCCTCTGCC
94281	92368	GATGTGAGGAGCGCCTCTGC
94282	92369	GGATGTGAGGAGCGCCTCTG
94283	92370	GGGATGTGAGGAGCGCCTCT
94284	92371	TGGGATGTGAGGAGCGCCTC
94285	92372	CTGGGATGTGAGGAGCGCCT
94286	92373	TCTGGGATGTGAGGAGCGCC
94287	92374	GTCTGGGATGTGAGGAGCGC
94288	92375	CGTCTGGGATGTGAGGAGCG
94289	92376	CCGTCTGGGATGTGAGGAGC
94290	92377	CCCGTCTGGGATGTGAGGAG
94291	92378	CCCCGTCTGGGATGTGAGGA
94292	92379	GCCCCGTCTGGGATGTGAGG
94293	92380	TGCCCCGTCTGGGATGTGAG
94294	92381	CTGCCCCGTCTGGGATGTGA
94295	92382	GCTGCCCCGTCTGGGATGTG
94296	92383	CGCTGCCCCGTCTGGGATGT

143373	141460	CAGGCTCACTGCAACCTCTG
143374	141461	CCAGGCTCACTGCAACCTCT
143375	141462	CCCAGGCTCACTGCAACCTC
143376	141463	GCCCAGGCTCACTGCAACCT
143377	141464	TGCCCAGGCTCACTGCAACC
143378	141465	TTGCCCAGGCTCACTGCAAC
143379	141466	GTTGCCCAGGCTCACTGCAA
143380	141467	TGTTGCCCAGGCTCACTGCA
143381	141468	CTGTTGCCCAGGCTCACTGC
143382	141469	TCTGTTGCCCAGGCTCACTG
143383	141470	CTCTGTTGCCCAGGCTCACT
143384	141471	ACTCTGTTGCCCAGGCTCAC
143385	141472	CACTCTGTTGCCCAGGCTCA
143386	141473	TCACTCTGTTGCCCAGGCTC
143387	141474	CTCACTCTGTTGCCCAGGCT
143388	141475	ACTCACTCTGTTGCCCAGGC
143389	141476	CACTCACTCTGTTGCCCAGG
143390	141477	TCACTCACTCTGTTGCCCAG
143391	141478	CTCACTCACTCTGTTGCCCA
143392	141479	TCTCACTCACTCTGTTGCCC
143393	141480	GTCTCACTCACTCTGTTGCC
143394	141481	AGTCTCACTCACTCTGTTGC
143395	141482	AAGTCTCACTCACTCTGTTG
143396	141483	TAAGTCTCACTCACTCTGTT
143397	141484	ATAAGTCTCACTCACTCTGT
143398	141485	TATAAGTCTCACTCACTCTG
143399	141486	ATATAAGTCTCACTCACTCT
143400	141487	GATATAAGTCTCACTCACTC
143401	141488	AGATATAAGTCTCACTCACT
143402	141489	GAGATATAAGTCTCACTCAC
143403	141490	TGAGATATAAGTCTCACTCA
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143405	141492	TTTGAGATATAAGTCTCACT
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143407	141494	TTTTTGAGATATAAGTCTCA
143408	141495	TTTTTTGAGATATAAGTCTC
143409	141496	TTTTTTTGAGATATAAGTCT
143410	141497	TTTTTTTTGAGATATAAGTC
143411	141498	TTTTTTTTTGAGATATAAGT
143412	141499	GTTTTTTTTTTGAGATATAAG
143413	141500	TGTTTTTTTTTGAGATATAA
143414	141501	TTGTTTTTTTTTGAGATATA
143415	141502	TTTGTTTTTTTTTGAGATAT
143416	141503	TTTTGTTTTTTTTTGAGATA
143417	141504	TTTTTGTTTTTTTTTGAGAT
143418	141505	TTTTTTGTTTTTTTTTGAGA
143419	141506	GTTTTTTGTTTTTTTTTGAG
143420	141507	TGTTTTTTGTTTTTTTTTGA
143421	141508	TTGTTTTTTGTTTTTTTTTG
143422	141509	TTTGTTTTTTGTTTTTTTTT
143423	141510	TTTTGTTTTTTGTTTTTTTT
143424	141511	TTTTTGTTTTTTGTTTTTTT
143425	141512	TTTTTTGTTTTTTGTTTTTT
143426	141513	GTTTTTTGTTTTTTGTTTTT
143427	141514	AGTTTTTTGTTTTTTGTTTT
143428	141515	CAGTTTTTTGTTTTTTGTTT
143429	141516	TCAGTTTTTTGTTTTTTGTT
143430	141517	TTCAGTTTTTTGTTTTTTGT
143431	141518	TTTCAGTTTTTTGTTTTTTG
143432	141519	CTTTCAGTTTTTTGTTTTTT
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143434	141521	GTCTTTCAGTTTTTTGTTTT
143435	141522	TGTCTTTCAGTTTTTTGTTT
143436	141523	ATGTCTTTCAGTTTTTTGTT
143437	141524	CATGTCTTTCAGTTTTTTGT
143438	141525	TCATGTCTTTCAGTTTTTTG
143439	141526	TTCATGTCTTTCAGTTTTTT
143440	141527	CTTCATGTCTTTCAGTTTTT
143441	141528	TCTTCATGTCTTTCAGTTTT
143442	141529	TTCTTCATGTCTTTCAGTTT
143443	141530	TTTCTTCATGTCTTTCAGTT

45150	43237	AAAGAGCTATTCAGAAGCAA
45151	43238	TAAAGAGCTATTCAGAAGCA
45152	43239	ATAAAGAGCTATTCAGAAGC
45153	43240	TATAAAGAGCTATTCAGAAG
45154	43241	TTATAAAGAGCTATTCAGAA
45155	43242	GTTATAAAGAGCTATTCAGA
45156	43243	TGTTATAAAGAGCTATTCAG
45157	43244	CTGTTATAAAGAGCTATTCA
45158	43245	ACTGTTATAAAGAGCTATTC
45159	43246	CACTGTTATAAAGAGCTATT
45160	43247	TCACTGTTATAAAGAGCTAT
45161	43248	ATCACTGTTATAAAGAGCTA
45162	43249	AATCACTGTTATAAAGAGCT
45163	43250	CAATCACTGTTATAAAGAGC
45164	43251	CCAATCACTGTTATAAAGAG
45165	43252	ACCAATCACTGTTATAAAGA
45166	43253	AACCAATCACTGTTATAAAG
45167	43254	TAACCAATCACTGTTATAAA
45168	43255	GTAACCAATCACTGTTATAA
45169	43256	AGTAACCAATCACTGTTATA
45170	43257	AAGTAACCAATCACTGTTAT
45171	43258	AAAGTAACCAATCACTGTTA
45172	43259	CAAAGTAACCAATCACTGTT
45173	43260	CCAAAGTAACCAATCACTGT
45174	43261	CCCAAAGTAACCAATCACTG
45175	43262	TCCCAAAGTAACCAATCACT
45176	43263	CTCCCAAAGTAACCAATCAC
45177	43264	ACTCCCAAAGTAACCAATCA
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45180	43267	TTTACTCCCAAAGTAACCAA
45181	43268	CTTTACTCCCAAAGTAACCA
45182	43269	TCTTTACTCCCAAAGTAACC
45183	43270	ATCTTTACTCCCAAAGTAAC
45184	43271	AATCTTTACTCCCAAAGTAA
45185	43272	TAATCTTTACTCCCAAAGTA
45186	43273	ATAATCTTTACTCCCAAAGT
45187	43274	AATAATCTTTACTCCCAAAG
45188	43275	TAATAATCTTTACTCCCAAA
45189	43276	ATAATAATCTTTACTCCCAA
45190	43277	AATAATAATCTTTACTCCCA
45191	43278	AAATAATAATCTTTACTCCC
45192	43279	TAAATAATAATCTTTACTCC
45193	43280	CTAAATAATAATCTTTACTC
45194	43281	TCTAAATAATAATCTTTACT
45195	43282	CTCTAAATAATAATCTTTAC
45196	43283	TCTCTAAATAATAATCTTTA
45197	43284	GTCTCTAAATAATAATCTTT
45198	43285	TGTCTCTAAATAATAATCTT
45199	43286	CTGTCTCTAAATAATAATCT
45200	43287	TCTGTCTCTAAATAATAATC
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45207	43294	GCAAGACTCTGTCTCTAAAT
45208	43295	AGCAAGACTCTGTCTCTAAA
45209	43296	AAGCAAGACTCTGTCTCTAA
45210	43297	AAAGCAAGACTCTGTCTCTA
45211	43298	CAAAGCAAGACTCTGTCTCT
45212	43299	ACAAAGCAAGACTCTGTCTC
45213	43300	GACAAAGCAAGACTCTGTCT
45214	43301	CGACAAAGCAAGACTCTGTC
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45216	43303	GGCGACAAAGCAAGACTCTG
45217	43304	GGGCGACAAAGCAAGACTCT
45218	43305	TGGGCGACAAAGCAAGACTC
45219	43306	CTGGGCGACAAAGCAAGACT
45220	43307	CCTGGGCGACAAAGCAAGAC

94297	92384	CCGCTGCCCCGTCTGGGATG
94298	92385	CCCGCTGCCCCGTCTGGGAT
94299	92386	CCCCGCTGCCCCGTCTGGGA
94300	92387	GCCCCGCTGCCCCGTCTGGG
94301	92388	TGCCCCGCTGCCCCGTCTGG
94302	92389	CTGCCCCGCTGCCCCGTCTG
94303	92390	TCTGCCCCGCTGCCCCGTCT
94304	92391	CTCTGCCCCGCTGCCCCGTC
94305	92392	CCTCTGCCCCGCTGCCCCGT
94306	92393	GCCTCTGCCCCGCTGCCCCG
94307	92394	CGCCTCTGCCCCGCTGCCCC
94308	92395	GCGCCTCTGCCCCGCTGCCC
94309	92396	AGCGCCTCTGCCCCGCTGCC
94310	92397	GAGCGCCTCTGCCCCGCTGC
94311	92398	GGAGCGCCTCTGCCCCGCTG
94312	92399	GGGAGCGCCTCTGCCCCGCT
94313	92400	GGGGAGCGCCTCTGCCCCGC
94314	92401	TGGGGAGCGCCTCTGCCCCG
94315	92402	GTGGGGAGCGCCTCTGCCCC
94316	92403	TGTGGGGAGCGCCTCTGCCC
94317	92404	ATGTGGGGAGCGCCTCTGCC
94318	92405	GATGTGGGGAGCGCCTCTGC
94319	92406	AGATGTGGGGAGCGCCTCTG
94320	92407	GAGATGTGGGGAGCGCCTCT
94321	92408	TGAGATGTGGGGAGCGCCTC
94322	92409	CTGAGATGTGGGGAGCGCCT
94323	92410	TCTGAGATGTGGGGAGCGCC
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94325	92412	CGTCTGAGATGTGGGGAGCG
94326	92413	TCGTCTGAGATGTGGGGAGC
94327	92414	GTCGTCTGAGATGTGGGGAG
94328	92415	CGTCGTCTGAGATGTGGGGA
94329	92416	CCGTCGTCTGAGATGTGGGG
94330	92417	CCCGTCGTCTGAGATGTGGG
94331	92418	ACCCGTCGTCTGAGATGTGG
94332	92419	CACCCGTCGTCTGAGATGTG
94333	92420	CCACCCGTCGTCTGAGATGT
94334	92421	GCCACCCGTCGTCTGAGATG
94335	92422	GGCCACCCGTCGTCTGAGAT
94336	92423	CGGCCACCCGTCGTCTGAGA
94337	92424	CCGGCCACCCGTCGTCTGAG
94338	92425	CCCGGCCACCCGTCGTCTGA
94339	92426	GCCCGGCCACCCGTCGTCTG
94340	92427	TGCCCGGCCACCCGTCGTCT
94341	92428	CTGCCCGGCCACCCGTCGTC
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94343	92430	CTCTGCCCGGCCACCCGTCG
94344	92431	TCTCTGCCCGGCCACCCGTC
94345	92432	GTCTCTGCCCGGCCACCCGT
94346	92433	CGTCTCTGCCCGGCCACCCG
94347	92434	GCGTCTCTGCCCGGCCACCC
94348	92435	AGCGTCTCTGCCCGGCCACC
94349	92436	GAGCGTCTCTGCCCGGCCAC
94350	92437	GGAGCGTCTCTGCCCGGCCA
94351	92438	AGGAGCGTCTCTGCCCGGCC
94352	92439	GAGGAGCGTCTCTGCCCGGC
94353	92440	TGAGGAGCGTCTCTGCCCGG
94354	92441	GTGAGGAGCGTCTCTGCCCG
94355	92442	AGTGAGGAGCGTCTCTGCCC
94356	92443	AAGTGAGGAGCGTCTCTGCC
94357	92444	GAAGTGAGGAGCGTCTCTGC
94358	92445	GGAAGTGAGGAGCGTCTCTG
94359	92446	AGGAAGTGAGGAGCGTCTCT
94360	92447	TAGGAAGTGAGGAGCGTCTC
94361	92448	CTAGGAAGTGAGGAGCGTCT
94362	92449	TCTAGGAAGTGAGGAGCGTC
94363	92450	GTCTAGGAAGTGAGGAGCGT
94364	92451	CGTCTAGGAAGTGAGGAGCG
94365	92452	CCGTCTAGGAAGTGAGGAGC
94366	92453	CCCGTCTAGGAAGTGAGGAG
94367	92454	TCCCGTCTAGGAAGTGAGGA

143444	141531	ATTTCTTCATGTCTTTCAGT
143445	141532	CATTTCTTCATGTCTTTCAG
143446	141533	CCATTTCTTCATGTCTTTCA
143447	141534	ACCATTTCTTCATGTCTTTC
143448	141535	AACCATTTCTTCATGTCTTT
143449	141536	AAACCATTTCTTCATGTCTT
143450	141537	AAAACCATTTCTTCATGTCT
143451	141538	AAAAACCATTTCTTCATGTC
143452	141539	CAAAAACCATTTCTTCATGT
143453	141540	ACAAAAACCATTTCTTCATG
143454	141541	TACAAAAACCATTTCTTCAT
143455	141542	GTACAAAAACCATTTCTTCA
143456	141543	GGTACAAAAACCATTTCTTC
143457	141544	TGGTACAAAAACCATTTCTT
143458	141545	TTGGTACAAAAACCATTTCT
143459	141546	CTTGGTACAAAAACCATTTC
143460	141547	CCTTGGTACAAAAACCATTT
143461	141548	ACCTTGGTACAAAAACCATT
143462	141549	AACCTTGGTACAAAAACCAT
143463	141550	AAACCTTGGTACAAAAACCA
143464	141551	CAAACCTTGGTACAAAAACC
143465	141552	CCAAACCTTGGTACAAAAAC
143466	141553	GCCAAACCTTGGTACAAAAA
143467	141554	GGCCAAACCTTGGTACAAAA
143468	141555	GGGCCAAACCTTGGTACAAA
143469	141556	TGGGCCAAACCTTGGTACAA
143470	141557	GTGGGCCAAACCTTGGTACA
143471	141558	CGTGGGCCAAACCTTGGTAC
143472	141559	GCGTGGGCCAAACCTTGGTA
143473	141560	AGCGTGGGCCAAACCTTGGT
143474	141561	CAGCGTGGGCCAAACCTTGG
143475	141562	TCAGCGTGGGCCAAACCTTG
143476	141563	CTCAGCGTGGGCCAAACCTT
143477	141564	TCTCAGCGTGGGCCAAACCT
143478	141565	ATCTCAGCGTGGGCCAAACC
143479	141566	AATCTCAGCGTGGGCCAAAC
143480	141567	GAATCTCAGCGTGGGCCAAA
143481	141568	TGAATCTCAGCGTGGGCCAA
143482	141569	GTGAATCTCAGCGTGGGCCA
143483	141570	TGTGAATCTCAGCGTGGGCC
143484	141571	TTGTGAATCTCAGCGTGGGC
143485	141572	TTTGTGAATCTCAGCGTGGG
143486	141573	CTTTGTGAATCTCAGCGTGG
143487	141574	TCTTTGTGAATCTCAGCGTG
143488	141575	TTCTTTGTGAATCTCAGCGT
143489	141576	GTTCTTTGTGAATCTCAGCG
143490	141577	AGTTCTTTGTGAATCTCAGC
143491	141578	CAGTTCTTTGTGAATCTCAG
143492	141579	CCAGTTCTTTGTGAATCTCA
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143495	141582	AAGCCAGTTCTTTGTGAATC
143496	141583	AAAGCCAGTTCTTTGTGAAT
143497	141584	GAAAGCCAGTTCTTTGTGAA
143498	141585	TGAAAGCCAGTTCTTTGTGA
143499	141586	CTGAAAGCCAGTTCTTTGTG
143500	141587	ACTGAAAGCCAGTTCTTTGT
143501	141588	AACTGAAAGCCAGTTCTTTG
143502	141589	GAACTGAAAGCCAGTTCTTT
143503	141590	AGAACTGAAAGCCAGTTCTT
143504	141591	AAGAACTGAAAGCCAGTTCT
143505	141592	TAAGAACTGAAAGCCAGTTC
143506	141593	ATAAGAACTGAAAGCCAGTT
143507	141594	GATAAGAACTGAAAGCCAGT
143508	141595	AGATAAGAACTGAAAGCCAG
143509	141596	AAGATAAGAACTGAAAGCCA
143510	141597	AAAGATAAGAACTGAAAGCC
143511	141598	TAAAGATAAGAACTGAAAGC
143512	141599	ATAAAGATAAGAACTGAAAG
143513	141600	AATAAAGATAAGAACTGAAA
143514	141601	AAATAAAGATAAGAACTGAA

45221	43308	GCCTGGGCGACAAAGCAAGA
45222	43309	AGCCTGGGCGACAAAGCAAG
45223	43310	TAGCCTGGGCGACAAAGCAA
45224	43311	CTAGCCTGGGCGACAAAGCA
45225	43312	TCTAGCCTGGGCGACAAAGC
45226	43313	GTCTAGCCTGGGCGACAAAG
45227	43314	AGTCTAGCCTGGGCGACAAA
45228	43315	CAGTCTAGCCTGGGCGACAA
45229	43316	GCAGTCTAGCCTGGGCGACA
45230	43317	TGCAGTCTAGCCTGGGCGAC
45231	43318	CTGCAGTCTAGCCTGGGCGA
45232	43319	ACTGCAGTCTAGCCTGGGCG
45233	43320	CACTGCAGTCTAGCCTGGGC
45234	43321	CCACTGCAGTCTAGCCTGGG
45235	43322	TCCACTGCAGTCTAGCCTGG
45236	43323	TTCCACTGCAGTCTAGCCTG
45237	43324	ATTCCACTGCAGTCTAGCCT
45238	43325	CATTCCACTGCAGTCTAGCC
45239	43326	TCATTCCACTGCAGTCTAGC
45240	43327	ATCATTCCACTGCAGTCTAG
45241	43328	GATCATTCCACTGCAGTCTA
45242	43329	CGATCATTCCACTGCAGTCT
45243	43330	ACGATCATTCCACTGCAGTC
45244	43331	TACGATCATTCCACTGCAGT
45245	43332	CTACGATCATTCCACTGCAG
45246	43333	GCTACGATCATTCCACTGCA
45247	43334	GGCTACGATCATTCCACTGC
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45249	43336	TAGGCTACGATCATTCCACT
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45251	43338	AGTAGGCTACGATCATTCCA
45252	43339	CAGTAGGCTACGATCATTCC
45253	43340	GCAGTAGGCTACGATCATTC
45254	43341	TGCAGTAGGCTACGATCATT
45255	43342	CTGCAGTAGGCTACGATCAT
45256	43343	GCTGCAGTAGGCTACGATCA
45257	43344	GGCTGCAGTAGGCTACGATC
45258	43345	AGGCTGCAGTAGGCTACGAT
45259	43346	GAGGCTGCAGTAGGCTACGA
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45261	43348	CTGAGGCTGCAGTAGGCTAC
45262	43349	TCTGAGGCTGCAGTAGGCTA
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45264	43351	AGTCTGAGGCTGCAGTAGGC
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45266	43353	GGAGTCTGAGGCTGCAGTAG
45267	43354	AGGAGTCTGAGGCTGCAGTA
45268	43355	CAGGAGTCTGAGGCTGCAGT
45269	43356	CCAGGAGTCTGAGGCTGCAG
45270	43357	TCCAGGAGTCTGAGGCTGCA
45271	43358	GTCCAGGAGTCTGAGGCTGC
45272	43359	AGTCCAGGAGTCTGAGGCTG
45273	43360	GAGTCCAGGAGTCTGAGGCT
45274	43361	AGAGTCCAGGAGTCTGAGGC
45275	43362	CAGAGTCCAGGAGTCTGAGG
45276	43363	CCAGAGTCCAGGAGTCTGAG
45277	43364	ACCAGAGTCCAGGAGTCTGA
45278	43365	CACCAGAGTCCAGGAGTCTG
45279	43366	TCACCAGAGTCCAGGAGTCT
45280	43367	ATCACCAGAGTCCAGGAGTC
45281	43368	GATCACCAGAGTCCAGGAGT
45282	43369	GGATCACCAGAGTCCAGGAG
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45284	43371	CAGGATCACCAGAGTCCAGG
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45287	43374	AGGCAGGATCACCAGAGTCC
45288	43375	GAGGCAGGATCACCAGAGTC
45289	43376	TGAGGCAGGATCACCAGAGT
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94371	92458	GCCATCCCGTCTAGGAAGTG
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94373	92460	CCGCCATCCCGTCTAGGAAG
94374	92461	GCCGCCATCCCGTCTAGGAA
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94376	92463	CGGCCGCCATCCCGTCTAGG
94377	92464	CCGGCCGCCATCCCGTCTAG
94378	92465	CCCGGCCGCCATCCCGTCTA
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94380	92467	TTCCCGGCCGCCATCCCGTC
94381	92468	CTTCCCGGCCGCCATCCCGT
94382	92469	TCTTCCCGGCCGCCATCCCG
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94384	92471	CCTCTTCCCGGCCGCCATCC
94385	92472	ACCTCTTCCCGGCCGCCATC
94386	92473	CACCTCTTCCCGGCCGCCAT
94387	92474	GCACCTCTTCCCGGCCGCCA
94388	92475	AGCACCTCTTCCCGGCCGCC
94389	92476	GAGCACCTCTTCCCGGCCGC
94390	92477	GGAGCACCTCTTCCCGGCCG
94391	92478	AGGAGCACCTCTTCCCGGCC
94392	92479	GAGGAGCACCTCTTCCCGGC
94393	92480	TGAGGAGCACCTCTTCCCGG
94394	92481	GTGAGGAGCACCTCTTCCCG
94395	92482	AGTGAGGAGCACCTCTTCCC
94396	92483	AAGTGAGGAGCACCTCTTCC
94397	92484	GAAGTGAGGAGCACCTCTTC
94398	92485	GGAAGTGAGGAGCACCTCTT
94399	92486	GGGAAGTGAGGAGCACCTCT
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94405	92492	CAGTCTGGGAAGTGAGGAGC
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94407	92494	CCCAGTCTGGGAAGTGAGGA
94408	92495	GCCCAGTCTGGGAAGTGAGG
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94414	92501	CCGGCTGCCCAGTCTGGGAA
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94416	92503	GCCCGGCTGCCCAGTCTGGG
94417	92504	TGCCCGGCTGCCCAGTCTGG
94418	92505	CTGCCCGGCTGCCCAGTCTG
94419	92506	TCTGCCCGGCTGCCCAGTCT
94420	92507	CTCTGCCCGGCTGCCCAGTC
94421	92508	CCTCTGCCCGGCTGCCCAGT
94422	92509	CCCTCTGCCCGGCTGCCCAG
94423	92510	CCCCTCTGCCCGGCTGCCCA
94424	92511	GCCCCTCTGCCCGGCTGCCC
94425	92512	AGCCCCTCTGCCCGGCTGCC
94426	92513	GAGCCCCTCTGCCCGGCTGC
94427	92514	GGAGCCCCTCTGCCCGGCTG
94428	92515	AGGAGCCCCTCTGCCCGGCT
94429	92516	GAGGAGCCCCTCTGCCCGGC
94430	92517	TGAGGAGCCCCTCTGCCCGG
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94435	92522	GGATGTGAGGAGCCCCTCTG
94436	92523	GGGATGTGAGGAGCCCCTCT
94437	92524	TGGGATGTGAGGAGCCCCTC
94438	92525	CTGGGATGTGAGGAGCCCCT

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143516	141603	CAAAATAAAGATAAGAACTG
143517	141604	TCAAAATAAAGATAAGAACT
143518	141605	ATCAAAATAAAGATAAGAAC
143519	141606	AATCAAAATAAAGATAAGAA
143520	141607	AAATCAAAATAAAGATAAGA
143521	141608	TAAATCAAAATAAAGATAAG
143522	141609	TTAAATCAAAATAAAGATAA
143523	141610	TTTAAATCAAAATAAAGATA
143524	141611	GTTTAAATCAAAATAAAGAT
143525	141612	AGTTTAAATCAAAATAAAGA
143526	141613	CAGTTTAAATCAAAATAAAG
143527	141614	CCAGTTTAAATCAAAATAAA
143528	141615	GCCAGTTTAAATCAAAATAA
143529	141616	GGCCAGTTTAAATCAAAATA
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143533	141620	GATGGGCCAGTTTAAATCAA
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143535	141622	ATGATGGGCCAGTTTAAATC
143536	141623	CATGATGGGCCAGTTTAAAT
143537	141624	ACATGATGGGCCAGTTTAAA
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143539	141626	CAACATGATGGGCCAGTTTA
143540	141627	ACAACATGATGGGCCAGTTT
143541	141628	GACAACATGATGGGCCAGTT
143542	141629	GGACAACATGATGGGCCAGT
143543	141630	AGGACAACATGATGGGCCAG
143544	141631	AAGGACAACATGATGGGCCA
143545	141632	AAAGGACAACATGATGGGCC
143546	141633	CAAAGGACAACATGATGGGC
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143549	141636	CTTCAAAGGACAACATGATG
143550	141637	ACTTCAAAGGACAACATGAT
143551	141638	AACTTCAAAGGACAACATGA
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143555	141642	GACTAACTTCAAAGGACAAC
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143559	141646	ACTAGACTAACTTCAAAGGA
143560	141647	TACTAGACTAACTTCAAAGG
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143564	141651	AATTTACTAGACTAACTTCA
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143569	141656	AAAGAAATTTACTAGACTAA
143570	141657	GAAAGAAATTTACTAGACTA
143571	141658	GGAAAGAAATTTACTAGACT
143572	141659	TGGAAAGAAATTTACTAGAC
143573	141660	TTGGAAAGAAATTTACTAGA
143574	141661	TTTGGAAAGAAATTTACTAG
143575	141662	CTTTGGAAAGAAATTTACTA
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143578	141665	GCCCTTTGGAAAGAAATTTA
143579	141666	AGCCCTTTGGAAAGAAATTT
143580	141667	CAGCCCTTTGGAAAGAAATT
143581	141668	CCAGCCCTTTGGAAAGAAAT
143582	141669	CCCAGCCCTTTGGAAAGAAA
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45321	43408	CATGCACCTCTAGTCCTAGC
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45323	43410	GGCATGCACCTCTAGTCCTA
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45331	43418	AGGCATGTGGCATGCACCTC
45332	43419	CAGGCATGTGGCATGCACCT
45333	43420	CCAGGCATGTGGCATGCACC
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45349	43436	TTAATAATAATTATAGCCAG
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45356	43443	ACGTAAATTAATAATAATTA
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94439	92526	TCTGGGATGTGAGGAGCCCC
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94442	92529	TCGTCTGGGATGTGAGGAGC
94443	92530	ATCGTCTGGGATGTGAGGAG
94444	92531	CATCGTCTGGGATGTGAGGA
94445	92532	CCATCGTCTGGGATGTGAGG
94446	92533	CCCATCGTCTGGGATGTGAG
94447	92534	ACCCATCGTCTGGGATGTGA
94448	92535	CACCCATCGTCTGGGATGTG
94449	92536	CCACCCATCGTCTGGGATGT
94450	92537	GCCACCCATCGTCTGGGATG
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94456	92543	TGCCTGGCCACCCATCGTCT
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94460	92547	TCTCTGCCTGGCCACCCATC
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94462	92549	CGTCTCTGCCTGGCCACCCA
94463	92550	GCGTCTCTGCCTGGCCACCC
94464	92551	AGCGTCTCTGCCTGGCCACC
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94466	92553	GGAGCGTCTCTGCCTGGCCA
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94468	92555	GAGGAGCGTCTCTGCCTGGC
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94470	92557	GTGAGGAGCGTCTCTGCCTG
94471	92558	AGTGAGGAGCGTCTCTGCCT
94472	92559	AAGTGAGGAGCGTCTCTGCC
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94475	92562	GGGAAGTGAGGAGCGTCTCT
94476	92563	TGGGAAGTGAGGAGCGTCTC
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94481	92568	CCGTCTGGGAAGTGAGGAGC
94482	92569	CCCGTCTGGGAAGTGAGGAG
94483	92570	CCCCGTCTGGGAAGTGAGGA
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94485	92572	CACCCCGTCTGGGAAGTGAG
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94494	92581	CCCGGCCGCCACCCCGTCTG
94495	92582	GCCCGGCCGCCACCCCGTCT
94496	92583	TGCCCGGCCGCCACCCCGTC
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143587	141674	AGTGCCCCAGCCCTTTGGAA
143588	141675	GAGTGCCCCAGCCCTTTGGA
143589	141676	TGAGTGCCCCAGCCCTTTGG
143590	141677	CTGAGTGCCCCAGCCCTTTG
143591	141678	TCTGAGTGCCCCAGCCCTTT
143592	141679	TTCTGAGTGCCCCAGCCCTT
143593	141680	CTTCTGAGTGCCCCAGCCCT
143594	141681	CCTTCTGAGTGCCCCAGCCC
143595	141682	CCCTTCTGAGTGCCCCAGCC
143596	141683	TCCCTTCTGAGTGCCCCAGC
143597	141684	CTCCCTTCTGAGTGCCCCAG
143598	141685	ACTCCCTTCTGAGTGCCCCA
143599	141686	AACTCCCTTCTGAGTGCCCC
143600	141687	AAACTCCCTTCTGAGTGCCC
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143602	141689	GTAAACTCCCTTCTGAGTGC
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143606	141693	AAAAGTAAACTCCCTTCTGA
143607	141694	GAAAAGTAAACTCCCTTCTG
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143610	141697	ATAGAAAAGTAAACTCCCTT
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143615	141702	TAAATATAGAAAAGTAAACT
143616	141703	ATAAATATAGAAAAGTAAAC
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143619	141706	GAAATAAATATAGAAAAGTA
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143622	141709	TATGAAATAAATATAGAAAA
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143631	141718	TCTTTGCTTTATGAAATAAA
143632	141719	ATCTTTGCTTTATGAAATAA
143633	141720	CATCTTTGCTTTATGAAATA
143634	141721	CCATCTTTGCTTTATGAAAT
143635	141722	CCCATCTTTGCTTTATGAAA
143636	141723	TCCCATCTTTGCTTTATGAA
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143638	141725	TCTCCCATCTTTGCTTTATG
143639	141726	ATCTCCCATCTTTGCTTTAT
143640	141727	GATCTCCCATCTTTGCTTTA
143641	141728	GGATCTCCCATCTTTGCTTT
143642	141729	AGGATCTCCCATCTTTGCTT
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143644	141731	GGAGGATCTCCCATCTTTGC
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143646	141733	ATGGAGGATCTCCCATCTTT
143647	141734	AATGGAGGATCTCCCATCTT
143648	141735	TAATGGAGGATCTCCCATCT
143649	141736	CTAATGGAGGATCTCCCATC
143650	141737	CCTAATGGAGGATCTCCCAT
143651	141738	CCCTAATGGAGGATCTCCCA
143652	141739	GCCCTAATGGAGGATCTCCC
143653	141740	AGCCCTAATGGAGGATCTCC
143654	141741	AAGCCCTAATGGAGGATCTC
143655	141742	CAAGCCCTAATGGAGGATCT
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45363	43450	ATGCTAAACGTAAATTAATA
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45366	43453	CTAATGCTAAACGTAAATTA
45367	43454	ACTAATGCTAAACGTAAATT
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45391	43478	AAAATAGCCTACTGGAAGAA
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45393	43480	GTAAAATAGCCTACTGGAAG
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45398	43485	ATAAAGTAAAATAGCCTACT
45399	43486	AATAAAGTAAAATAGCCTAC
45400	43487	AAATAAAGTAAAATAGCCTA
45401	43488	TAAATAAAGTAAAATAGCCT
45402	43489	ATAAATAAAGTAAAATAGCC
45403	43490	AATAAATAAAGTAAAATAGC
45404	43491	AAATAAATAAAGTAAAATAG
45405	43492	CAAATAAATAAAGTAAAATA
45406	43493	TCAAATAAATAAAGTAAAAT
45407	43494	ATCAAATAAATAAAGTAAAA
45408	43495	AATCAAATAAATAAAGTAAA
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45411	43498	CAAAATCAAATAAATAAAGT
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45414	43501	CATCAAAATCAAATAAATAA
45415	43502	TCATCAAAATCAAATAAATA
45416	43503	TTCATCAAAATCAAATAAAT
45417	43504	CTTCATCAAAATCAAATAAA
45418	43505	ACTTCATCAAAATCAAATAA
45419	43506	AACTTCATCAAAATCAAATA
45420	43507	AAACTTCATCAAAATCAAAT
45421	43508	CAAACTTCATCAAAATCAAA
45422	43509	TCAAACTTCATCAAAATCAA
45423	43510	ATCAAACTTCATCAAAATCA
45424	43511	AATCAAACTTCATCAAAATC
45425	43512	TAATCAAACTTCATCAAAAT
45426	43513	ATAATCAAACTTCATCAAAA
45427	43514	AATAATCAAACTTCATCAAA
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45429	43516	GAAATAATCAAACTTCATCA
45430	43517	AGAAATAATCAAACTTCATC
45431	43518	TAGAAATAATCAAACTTCAT
45432	43519	CTAGAAATAATCAAACTTCA
45433	43520	ACTAGAAATAATCAAACTTC

94510	92597	GAGATTGCAGCCTCTGCCCG
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94512	92599	CCGAGATTGCAGCCTCTGCC
94513	92600	GCCGAGATTGCAGCCTCTGC
94514	92601	TGCCGAGATTGCAGCCTCTG
94515	92602	GTGCCGAGATTGCAGCCTCT
94516	92603	AGTGCCGAGATTGCAGCCTC
94517	92604	AAGTGCCGAGATTGCAGCCT
94518	92605	AAAGTGCCGAGATTGCAGCC
94519	92606	CAAAGTGCCGAGATTGCAGC
94520	92607	CCAAAGTGCCGAGATTGCAG
94521	92608	CCCAAAGTGCCGAGATTGCA
94522	92609	TCCCAAAGTGCCGAGATTGC
94523	92610	CTCCCAAAGTGCCGAGATTG
94524	92611	CCTCCCAAAGTGCCGAGATT
94525	92612	GCCTCCCAAAGTGCCGAGAT
94526	92613	GGCCTCCCAAAGTGCCGAGA
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94528	92615	TTGGCCTCCCAAAGTGCCGA
94529	92616	CTTGGCCTCCCAAAGTGCCG
94530	92617	CCTTGGCCTCCCAAAGTGCC
94531	92618	GCCTTGGCCTCCCAAAGTGC
94532	92619	TGCCTTGGCCTCCCAAAGTG
94533	92620	CTGCCTTGGCCTCCCAAAGT
94534	92621	CCTGCCTTGGCCTCCCAAAG
94535	92622	ACCTGCCTTGGCCTCCCAAA
94536	92623	CACCTGCCTTGGCCTCCCAA
94537	92624	CCACCTGCCTTGGCCTCCCA
94538	92625	GCCACCTGCCTTGGCCTCCC
94539	92626	AGCCACCTGCCTTGGCCTCC
94540	92627	CAGCCACCTGCCTTGGCCTC
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94542	92629	CCCAGCCACCTGCCTTGGCC
94543	92630	TCCCAGCCACCTGCCTTGGC
94544	92631	CTCCCAGCCACCTGCCTTGG
94545	92632	CCTCCCAGCCACCTGCCTTG
94546	92633	ACCTCCCAGCCACCTGCCTT
94547	92634	CACCTCCCAGCCACCTGCCT
94548	92635	CCACCTCCCAGCCACCTGCC
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94550	92637	CTCCACCTCCCAGCCACCTG
94551	92638	CCTCCACCTCCCAGCCACCT
94552	92639	ACCTCCACCTCCCAGCCACC
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94554	92641	CAACCTCCACCTCCCAGCCA
94555	92642	ACAACCTCCACCTCCCAGCC
94556	92643	TACAACCTCCACCTCCCAGC
94557	92644	CTACAACCTCCACCTCCCAG
94558	92645	GCTACAACCTCCACCTCCCA
94559	92646	CGCTACAACCTCCACCTCCC
94560	92647	TCGCTACAACCTCCACCTCC
94561	92648	CTCGCTACAACCTCCACCTC
94562	92649	GCTCGCTACAACCTCCACCT
94563	92650	GGCTCGCTACAACCTCCACC
94564	92651	CGGCTCGCTACAACCTCCAC
94565	92652	TCGGCTCGCTACAACCTCCA
94566	92653	CTCGGCTCGCTACAACCTCC
94567	92654	TCTCGGCTCGCTACAACCTC
94568	92655	ATCTCGGCTCGCTACAACCT
94569	92656	GATCTCGGCTCGCTACAACC
94570	92657	TGATCTCGGCTCGCTACAAC
94571	92658	GTGATCTCGGCTCGCTACAA
94572	92659	CGTGATCTCGGCTCGCTACA
94573	92660	GCGTGATCTCGGCTCGCTAC
94574	92661	GGCGTGATCTCGGCTCGCTA
94575	92662	TGGCGTGATCTCGGCTCGCT
94576	92663	GTGGCGTGATCTCGGCTCGC
94577	92664	AGTGGCGTGATCTCGGCTCG
94578	92665	CAGTGGCGTGATCTCGGCTC
94579	92666	GCAGTGGCGTGATCTCGGCT
94580	92667	TGCAGTGGCGTGATCTCGGC

143657	141744	CCCAAGCCCTAATGGAGGAT
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143659	141746	TTCCCAAGCCCTAATGGAGG
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143661	141748	CTTTCCCAAGCCCTAATGGA
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143663	141750	TACTTTCCCAAGCCCTAATG
143664	141751	TTACTTTCCCAAGCCCTAAT
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143668	141755	CAGTTTACTTTCCCAAGCCC
143669	141756	TCAGTTTACTTTCCCAAGCC
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143672	141759	CACTCAGTTTACTTTCCCAA
143673	141760	CCACTCAGTTTACTTTCCCA
143674	141761	GCCACTCAGTTTACTTTCCC
143675	141762	TGCCACTCAGTTTACTTTCC
143676	141763	CTGCCACTCAGTTTACTTTC
143677	141764	TCTGCCACTCAGTTTACTTT
143678	141765	TTCTGCCACTCAGTTTACTT
143679	141766	CTTCTGCCACTCAGTTTACT
143680	141767	CCTTCTGCCACTCAGTTTAC
143681	141768	CCCTTCTGCCACTCAGTTTA
143682	141769	GCCCTTCTGCCACTCAGTTT
143683	141770	AGCCCTTCTGCCACTCAGTT
143684	141771	GAGCCCTTCTGCCACTCAGT
143685	141772	GGAGCCCTTCTGCCACTCAG
143686	141773	AGGAGCCCTTCTGCCACTCA
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143688	141775	ACAGGAGCCCTTCTGCCACT
143689	141776	CACAGGAGCCCTTCTGCCAC
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143691	141778	ATCACAGGAGCCCTTCTGCC
143692	141779	AATCACAGGAGCCCTTCTGC
143693	141780	TAATCACAGGAGCCCTTCTG
143694	141781	CTAATCACAGGAGCCCTTCT
143695	141782	GCTAATCACAGGAGCCCTTC
143696	141783	AGCTAATCACAGGAGCCCTT
143697	141784	CAGCTAATCACAGGAGCCCT
143698	141785	TCAGCTAATCACAGGAGCCC
143699	141786	CTCAGCTAATCACAGGAGCC
143700	141787	TCTCAGCTAATCACAGGAGC
143701	141788	CTCTCAGCTAATCACAGGAG
143702	141789	TCTCTCAGCTAATCACAGGA
143703	141790	CTCTCTCAGCTAATCACAGG
143704	141791	TCTCTCTCAGCTAATCACAG
143705	141792	GTCTCTCTCAGCTAATCACA
143706	141793	AGTCTCTCTCAGCTAATCAC
143707	141794	CAGTCTCTCTCAGCTAATCA
143708	141795	ACAGTCTCTCTCAGCTAATC
143709	141796	CACAGTCTCTCTCAGCTAAT
143710	141797	CCACAGTCTCTCTCAGCTAA
143711	141798	ACCACAGTCTCTCTCAGCTA
143712	141799	GACCACAGTCTCTCTCAGCT
143713	141800	GGACCACAGTCTCTCTCAGC
143714	141801	AGGACCACAGTCTCTCTCAG
143715	141802	AAGGACCACAGTCTCTCTCA
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143720	141807	GGCCGAAGGACCACAGTCTC
143721	141808	GGGCCGAAGGACCACAGTCT
143722	141809	AGGGCCGAAGGACCACAGTC
143723	141810	CAGGGCCGAAGGACCACAGT
143724	141811	TCAGGGCCGAAGGACCACAG
143725	141812	ATCAGGGCCGAAGGACCACA
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143727	141814	TCATCAGGGCCGAAGGACCA

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45435	43522	AAACTAGAAATAATCAAACT
45436	43523	CAAACTAGAAATAATCAAAC
45437	43524	GCAAACTAGAAATAATCAAA
45438	43525	AGCAAACTAGAAATAATCAA
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45447	43534	ATAGAAGGAAGCAAACTAGA
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45458	43545	AGGTAGGGGTCATAGAAGGA
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45466	43553	CCCACAACAGGTAGGGGTCA
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45495	43582	GCTCTACCTATGCACTGCTT
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45497	43584	TGGCTCTACCTATGCACTGC
45498	43585	ATGGCTCTACCTATGCACTG
45499	43586	GATGGCTCTACCTATGCACT
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45501	43588	AGGATGGCTCTACCTATGCA
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94581	92668	GTGCAGTGGCGTGATCTCGG
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94596	92683	GGTGCCCAGGCTGGAGTGCA
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94599	92686	AATGGTGCCCAGGCTGGAGT
94600	92687	CAATGGTGCCCAGGCTGGAG
94601	92688	TCAATGGTGCCCAGGCTGGA
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94607	92694	CAGTGCTCAATGGTGCCCAG
94608	92695	TCAGTGCTCAATGGTGCCCA
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94611	92698	CACTCAGTGCTCAATGGTGC
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94629	92716	TGCAGACGGAGTCTCGTTCA
94630	92717	TTGCAGACGGAGTCTCGTTC
94631	92718	ATTGCAGACGGAGTCTCGTT
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94634	92721	GGGATTGCAGACGGAGTCTC
94635	92722	CGGGATTGCAGACGGAGTCT
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94637	92724	GCCGGGATTGCAGACGGAGT
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94639	92726	GTGCCGGGATTGCAGACGGA
94640	92727	GGTGCCGGGATTGCAGACGG
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94643	92730	CGAGGTGCCGGGATTGCAGA
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94647	92734	CTCCCGAGGTGCCGGGATTG
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143728	141815	ATCATCAGGGCCGAAGGACC
143729	141816	TATCATCAGGGCCGAAGGAC
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143731	141818	TCTATCATCAGGGCCGAAGG
143732	141819	ATCTATCATCAGGGCCGAAG
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143734	141821	GGATCTATCATCAGGGCCGA
143735	141822	GGGATCTATCATCAGGGCCG
143736	141823	AGGGATCTATCATCAGGGCC
143737	141824	CAGGGATCTATCATCAGGGC
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143739	141826	GCCAGGGATCTATCATCAGG
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143745	141832	GGCAAGGCCAGGGATCTATC
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143748	141835	TGTGGCAAGGCCAGGGATCT
143749	141836	ATGTGGCAAGGCCAGGGATC
143750	141837	TATGTGGCAAGGCCAGGGAT
143751	141838	GTATGTGGCAAGGCCAGGGA
143752	141839	GGTATGTGGCAAGGCCAGGG
143753	141840	TGGTATGTGGCAAGGCCAGG
143754	141841	ATGGTATGTGGCAAGGCCAG
143755	141842	TATGGTATGTGGCAAGGCCA
143756	141843	GTATGGTATGTGGCAAGGCC
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143759	141846	TGTGTATGGTATGTGGCAAG
143760	141847	CTGTGTATGGTATGTGGCAA
143761	141848	ACTGTGTATGGTATGTGGCA
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143776	141863	GATGGGGGTGCGGGCACTGT
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143779	141866	GGGGATGGGGGTGCGGGCAC
143780	141867	GGGGGATGGGGGTGCGGGCA
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45506	43593	ACCTAAGGATGGCTCTACCT
45507	43594	TACCTAAGGATGGCTCTACC
45508	43595	CTACCTAAGGATGGCTCTAC
45509	43596	GCTACCTAAGGATGGCTCTA
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45511	43598	AGGCTACCTAAGGATGGCTC
45512	43599	AAGGCTACCTAAGGATGGCT
45513	43600	AAAGGCTACCTAAGGATGGC
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45515	43602	CTAAAGGCTACCTAAGGATG
45516	43603	TCTAAAGGCTACCTAAGGAT
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45519	43606	AAGTCTAAAGGCTACCTAAG
45520	43607	TAAGTCTAAAGGCTACCTAA
45521	43608	TTAAGTCTAAAGGCTACCTA
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45523	43610	TATTAAGTCTAAAGGCTACC
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45525	43612	AATATTAAGTCTAAAGGCTA
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45527	43614	CTAATATTAAGTCTAAAGGC
45528	43615	CCTAATATTAAGTCTAAAGG
45529	43616	ACCTAATATTAAGTCTAAAG
45530	43617	CACCTAATATTAAGTCTAAA
45531	43618	TCACCTAATATTAAGTCTAA
45532	43619	CTCACCTAATATTAAGTCTA
45533	43620	GCTCACCTAATATTAAGTCT
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45536	43623	AGAGCTCACCTAATATTAAG
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45543	43630	TGTGGGGAGAGCTCACCTAA
45544	43631	CTGTGGGGAGAGCTCACCTA
45545	43632	TCTGTGGGGAGAGCTCACCT
45546	43633	ATCTGTGGGGAGAGCTCACC
45547	43634	TATCTGTGGGGAGAGCTCAC
45548	43635	CTATCTGTGGGGAGAGCTCA
45549	43636	GCTATCTGTGGGGAGAGCTC
45550	43637	GGCTATCTGTGGGGAGAGCT
45551	43638	AGGCTATCTGTGGGGAGAGC
45552	43639	GAGGCTATCTGTGGGGAGAG
45553	43640	AGAGGCTATCTGTGGGGAGA
45554	43641	GAGAGGCTATCTGTGGGGAG
45555	43642	GGAGAGGCTATCTGTGGGGA
45556	43643	AGGAGAGGCTATCTGTGGGG
45557	43644	AAGGAGAGGCTATCTGTGGG
45558	43645	AAAGGAGAGGCTATCTGTGG
45559	43646	TAAAGGAGAGGCTATCTGTG
45560	43647	ATAAAGGAGAGGCTATCTGT
45561	43648	AATAAAGGAGAGGCTATCTG
45562	43649	AAATAAAGGAGAGGCTATCT
45563	43650	CAAATAAAGGAGAGGCTATC
45564	43651	TCAAATAAAGGAGAGGCTAT
45565	43652	TTCAAATAAAGGAGAGGCTA
45566	43653	ATTCAAATAAAGGAGAGGCT
45567	43654	CATTCAAATAAAGGAGAGGC
45568	43655	CCATTCAAATAAAGGAGAGG
45569	43656	TCCATTCAAATAAAGGAGAG
45570	43657	TTCCATTCAAATAAAGGAGA
45571	43658	ATTCCATTCAAATAAAGGAG
45572	43659	AATTCCATTCAAATAAAGGA
45573	43660	TAATTCCATTCAAATAAAGG
45574	43661	ATAATTCCATTCAAATAAAG
45575	43662	TATAATTCCATTCAAATAAA

94652	92739	TCGGCCTCCCGAGGTGCCGG
94653	92740	CTCGGCCTCCCGAGGTGCCG
94654	92741	CCTCGGCCTCCCGAGGTGCC
94655	92742	GCCTCGGCCTCCCGAGGTGC
94656	92743	AGCCTCGGCCTCCCGAGGTG
94657	92744	CAGCCTCGGCCTCCCGAGGT
94658	92745	CCAGCCTCGGCCTCCCGAGG
94659	92746	GCCAGCCTCGGCCTCCCGAG
94660	92747	TGCCAGCCTCGGCCTCCCGA
94661	92748	CTGCCAGCCTCGGCCTCCCG
94662	92749	TCTGCCAGCCTCGGCCTCCC
94663	92750	ATCTGCCAGCCTCGGCCTCC
94664	92751	GATCTGCCAGCCTCGGCCTC
94665	92752	TGATCTGCCAGCCTCGGCCT
94666	92753	GTGATCTGCCAGCCTCGGCC
94667	92754	AGTGATCTGCCAGCCTCGGC
94668	92755	GAGTGATCTGCCAGCCTCGG
94669	92756	CGAGTGATCTGCCAGCCTCG
94670	92757	GCGAGTGATCTGCCAGCCTC
94671	92758	CGCGAGTGATCTGCCAGCCT
94672	92759	CCGCGAGTGATCTGCCAGCC
94673	92760	ACCGCGAGTGATCTGCCAGC
94674	92761	AACCGCGAGTGATCTGCCAG
94675	92762	TAACCGCGAGTGATCTGCCA
94676	92763	CTAACCGCGAGTGATCTGCC
94677	92764	CCTAACCGCGAGTGATCTGC
94678	92765	TCCTAACCGCGAGTGATCTG
94679	92766	CTCCTAACCGCGAGTGATCT
94680	92767	GCTCCTAACCGCGAGTGATC
94681	92768	AGCTCCTAACCGCGAGTGAT
94682	92769	CAGCTCCTAACCGCGAGTGA
94683	92770	CCAGCTCCTAACCGCGAGTG
94684	92771	TCCAGCTCCTAACCGCGAGT
94685	92772	CTCCAGCTCCTAACCGCGAG
94686	92773	TCTCCAGCTCCTAACCGCGA
94687	92774	GTCTCCAGCTCCTAACCGCG
94688	92775	GGTCTCCAGCTCCTAACCGC
94689	92776	TGGTCTCCAGCTCCTAACCG
94690	92777	CTGGTCTCCAGCTCCTAACC
94691	92778	GCTGGTCTCCAGCTCCTAAC
94692	92779	GGCTGGTCTCCAGCTCCTAA
94693	92780	GGGCTGGTCTCCAGCTCCTA
94694	92781	CGGGCTGGTCTCCAGCTCCT
94695	92782	CCGGGCTGGTCTCCAGCTCC
94696	92783	GCCGGGCTGGTCTCCAGCTC
94697	92784	GGCCGGGCTGGTCTCCAGCT
94698	92785	TGGCCGGGCTGGTCTCCAGC
94699	92786	TTGGCCGGGCTGGTCTCCAG
94700	92787	GTTGGCCGGGCTGGTCTCCA
94701	92788	TGTTGGCCGGGCTGGTCTCC
94702	92789	GTGTTGGCCGGGCTGGTCTC
94703	92790	TGTGTTGGCCGGGCTGGTCT
94704	92791	CTGTGTTGGCCGGGCTGGTC
94705	92792	GCTGTGTTGGCCGGGCTGGT
94706	92793	CGCTGTGTTGGCCGGGCTGG
94707	92794	TCGCTGTGTTGGCCGGGCTG
94708	92795	TTCGCTGTGTTGGCCGGGCT
94709	92796	TTTCGCTGTGTTGGCCGGGC
94710	92797	GTTTCGCTGTGTTGGCCGGG
94711	92798	GGTTTCGCTGTGTTGGCCGG
94712	92799	GGGTTTCGCTGTGTTGGCCG
94713	92800	GGGGTTTCGCTGTGTTGGCC
94714	92801	CGGGGTTTCGCTGTGTTGGC
94715	92802	ACGGGGTTTCGCTGTGTTGG
94716	92803	GACGGGGTTTCGCTGTGTTG
94717	92804	AGACGGGGTTTCGCTGTGTT
94718	92805	GAGACGGGGTTTCGCTGTGT
94719	92806	GGAGACGGGGTTTCGCTGTG
94720	92807	TGGAGACGGGGTTTCGCTGT
94721	92808	GTGGAGACGGGGTTTCGCTG
94722	92809	GGTGGAGACGGGGTTTCGCT

143799	141886	AGACTATATTGGGTGTGGTG
143800	141887	CAGACTATATTGGGTGTGGT
143801	141888	ACAGACTATATTGGGTGTGG
143802	141889	CACAGACTATATTGGGTGTG
143803	141890	GCACAGACTATATTGGGTGT
143804	141891	GGCACAGACTATATTGGGTG
143805	141892	GGGCACAGACTATATTGGGT
143806	141893	AGGGCACAGACTATATTGGG
143807	141894	GAGGGCACAGACTATATTGG
143808	141895	TGAGGGCACAGACTATATTG
143809	141896	CTGAGGGCACAGACTATATT
143810	141897	CCTGAGGGCACAGACTATAT
143811	141898	TCCTGAGGGCACAGACTATA
143812	141899	GTCCTGAGGGCACAGACTAT
143813	141900	TGTCCTGAGGGCACAGACTA
143814	141901	ATGTCCTGAGGGCACAGACT
143815	141902	AATGTCCTGAGGGCACAGAC
143816	141903	CAATGTCCTGAGGGCACAGA
143817	141904	GCAATGTCCTGAGGGCACAG
143818	141905	AGCAATGTCCTGAGGGCACA
143819	141906	GAGCAATGTCCTGAGGGCAC
143820	141907	GGAGCAATGTCCTGAGGGCA
143821	141908	TGGAGCAATGTCCTGAGGGC
143822	141909	CTGGAGCAATGTCCTGAGGG
143823	141910	CCTGGAGCAATGTCCTGAGG
143824	141911	CCCTGGAGCAATGTCCTGAG
143825	141912	GCCCTGGAGCAATGTCCTGA
143826	141913	TGCCCTGGAGCAATGTCCTG
143827	141914	CTGCCCTGGAGCAATGTCCT
143828	141915	ACTGCCCTGGAGCAATGTCC
143829	141916	TACTGCCCTGGAGCAATGTC
143830	141917	CTACTGCCCTGGAGCAATGT
143831	141918	GCTACTGCCCTGGAGCAATG
143832	141919	TGCTACTGCCCTGGAGCAAT
143833	141920	ATGCTACTGCCCTGGAGCAA
143834	141921	CATGCTACTGCCCTGGAGCA
143835	141922	CCATGCTACTGCCCTGGAGC
143836	141923	ACCATGCTACTGCCCTGGAG
143837	141924	CACCATGCTACTGCCCTGGA
143838	141925	TCACCATGCTACTGCCCTGG
143839	141926	CTCACCATGCTACTGCCCTG
143840	141927	CCTCACCATGCTACTGCCCT
143841	141928	ACCTCACCATGCTACTGCCC
143842	141929	AACCTCACCATGCTACTGCC
143843	141930	TAACCTCACCATGCTACTGC
143844	141931	CTAACCTCACCATGCTACTG
143845	141932	GCTAACCTCACCATGCTACT
143846	141933	GGCTAACCTCACCATGCTAC
143847	141934	AGGCTAACCTCACCATGCTA
143848	141935	CAGGCTAACCTCACCATGCT
143849	141936	TCAGGCTAACCTCACCATGC
143850	141937	ATCAGGCTAACCTCACCATG
143851	141938	CATCAGGCTAACCTCACCAT
143852	141939	TCATCAGGCTAACCTCACCA
143853	141940	ATCATCAGGCTAACCTCACC
143854	141941	CATCATCAGGCTAACCTCAC
143855	141942	CCATCATCAGGCTAACCTCA
143856	141943	GCCATCATCAGGCTAACCTC
143857	141944	GGCCATCATCAGGCTAACCT
143858	141945	AGGCCATCATCAGGCTAACC
143859	141946	AAGGCCATCATCAGGCTAAC
143860	141947	CAAGGCCATCATCAGGCTAA
143861	141948	TCAAGGCCATCATCAGGCTA
143862	141949	CTCAAGGCCATCATCAGGCT
143863	141950	GCTCAAGGCCATCATCAGGC
143864	141951	AGCTCAAGGCCATCATCAGG
143865	141952	TAGCTCAAGGCCATCATCAG
143866	141953	TTAGCTCAAGGCCATCATCA
143867	141954	TTTAGCTCAAGGCCATCATC
143868	141955	CTTTAGCTCAAGGCCATCAT
143869	141956	TCTTTAGCTCAAGGCCATCA

45576	43663	ATATAATTCCATTCAAATAA
45577	43664	AATATAATTCCATTCAAATA
45578	43665	AAATATAATTCCATTCAAAT
45579	43666	AAAATATAATTCCATTCAAA
45580	43667	TAAAATATAATTCCATTCAA
45581	43668	TTAAAATATAATTCCATTCA
45582	43669	CTTAAAATATAATTCCATTC
45583	43670	ACTTAAAATATAATTCCATT
45584	43671	AACTTAAAATATAATTCCAT
45585	43672	AAACTTAAAATATAATTCCA
45586	43673	CAAACTTAAAATATAATTCC
45587	43674	CCAAACTTAAAATATAATTC
45588	43675	TCCAAACTTAAAATATAATT
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45590	43677	TTTCCAAACTTAAAATATAA
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45598	43685	GAAAAATATTTCCAAACTTA
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45600	43687	CTGAAAAATATTTCCAAACT
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45614	43701	ACAGGCTAAATAAGCTGAAA
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45618	43705	TTCAACAGGCTAAATAAGCT
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45624	43711	ATTAAATTCAACAGGCTAAA
45625	43712	TATTAAATTCAACAGGCTAA
45626	43713	TTATTAAATTCAACAGGCTA
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45628	43715	TTTTATTAAATTCAACAGGC
45629	43716	TTTTTATTAAATTCAACAGG
45630	43717	ATTTTTATTAAATTCAACAG
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45634	43721	TATTATTTTTATTAAATTCA
45635	43722	ATATTATTTTTATTAAATTC
45636	43723	AATATTATTTTTATTAAATT
45637	43724	AAATATTATTTTTTATTAAAT
45638	43725	TAAATATTATTTTTTATTAAA
45639	43726	TTAAATATTATTTTTTATTAA
45640	43727	ATTAAATATTATTTTTTATTA
45641	43728	GATTAAATATTATTTTTTATT
45642	43729	AGATTAAATATTATTTTTTAT
45643	43730	AAGATTAAATATTATTTTTTA
45644	43731	AAAGATTAAATATTATTTTTT
45645	43732	AAAAGATTAAATATTATTTTT
45646	43733	GAAAAGATTAAATATTATTTT

94723	92810	TGGTGGAGACGGGGTTTCGC
94724	92811	TTGGTGGAGACGGGGTTTCG
94725	92812	TTTGGTGGAGACGGGGTTTC
94726	92813	TTTTGGTGGAGACGGGGTTT
94727	92814	TTTTTGGTGGAGACGGGGTT
94728	92815	TTTTTTGGTGGAGACGGGGT
94729	92816	TTTTTTTGGTGGAGACGGGG
94730	92817	ATTTTTTTGGTGGAGACGGG
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94732	92819	GTATTTTTTTGGTGGAGACG
94733	92820	CGTATTTTTTTGGTGGAGAC
94734	92821	TCGTATTTTTTTGGTGGAGA
94735	92822	TTCGTATTTTTTTGGTGGAG
94736	92823	TTTCGTATTTTTTTGGTGGA
94737	92824	TTTTCGTATTTTTTTGGTGG
94738	92825	GTTTTCGTATTTTTTTGGTG
94739	92826	GGTTTTCGTATTTTTTTGGT
94740	92827	TGGTTTTCGTATTTTTTTGG
94741	92828	CTGGTTTTCGTATTTTTTTG
94742	92829	ACTGGTTTTCGTATTTTTTT
94743	92830	GACTGGTTTTCGTATTTTTT
94744	92831	TGACTGGTTTTCGTATTTTT
94745	92832	CTGACTGGTTTTCGTATTTT
94746	92833	CCTGACTGGTTTTCGTATTT
94747	92834	GCCTGACTGGTTTTCGTATT
94748	92835	CGCCTGACTGGTTTTCGTAT
94749	92836	ACGCCTGACTGGTTTTCGTA
94750	92837	CACGCCTGACTGGTTTTCGT
94751	92838	CCACGCCTGACTGGTTTTCG
94752	92839	GCCACGCCTGACTGGTTTTC
94753	92840	CGCCACGCCTGACTGGTTTT
94754	92841	CCGCCACGCCTGACTGGTTT
94755	92842	GCCGCCACGCCTGACTGGTT
94756	92843	CGCCGCCACGCCTGACTGGT
94757	92844	GCGCCGCCACGCCTGACTGG
94758	92845	CGCGCCGCCACGCCTGACTG
94759	92846	CCGCGCCGCCACGCCTGACT
94760	92847	CCCGCGCCGCCACGCCTGAC
94761	92848	GCCCGCGCCGCCACGCCTGA
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94763	92850	AGGCCCGCGCCGCCACGCCT
94764	92851	CAGGCCCGCGCCGCCACGCC
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94766	92853	TGCAGGCCCGCGCCGCCACG
94767	92854	TTGCAGGCCCGCGCCGCCAC
94768	92855	ATTGCAGGCCCGCGCCGCCA
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94770	92857	TGATTGCAGGCCCGCGCCGC
94771	92858	GTGATTGCAGGCCCGCGCCG
94772	92859	TGTGATTGCAGGCCCGCGCC
94773	92860	CTGTGATTGCAGGCCCGCGC
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94775	92862	GCCTGTGATTGCAGGCCCGC
94776	92863	TGCCTGTGATTGCAGGCCCG
94777	92864	GTGCCTGTGATTGCAGGCCC
94778	92865	AGTGCCTGTGATTGCAGGCC
94779	92866	TAGTGCCTGTGATTGCAGGC
94780	92867	CTAGTGCCTGTGATTGCAGG
94781	92868	CCTAGTGCCTGTGATTGCAG
94782	92869	GCCTAGTGCCTGTGATTGCA
94783	92870	TGCCTAGTGCCTGTGATTGC
94784	92871	CTGCCTAGTGCCTGTGATTG
94785	92872	CCTGCCTAGTGCCTGTGATT
94786	92873	GCCTGCCTAGTGCCTGTGAT
94787	92874	AGCCTGCCTAGTGCCTGTGA
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94789	92876	TCAGCCTGCCTAGTGCCTGT
94790	92877	CTCAGCCTGCCTAGTGCCTG
94791	92878	CCTCAGCCTGCCTAGTGCCT
94792	92879	GCCTCAGCCTGCCTAGTGCC
94793	92880	TGCCTCAGCCTGCCTAGTGC

143870	141957	CTCTTTAGCTCAAGGCCATC
143871	141958	ACTCTTTAGCTCAAGGCCAT
143872	141959	CACTCTTTAGCTCAAGGCCA
143873	141960	ACACTCTTTAGCTCAAGGCC
143874	141961	CACACTCTTTAGCTCAAGGC
143875	141962	GCACACTCTTTAGCTCAAGG
143876	141963	TGCACACTCTTTAGCTCAAG
143877	141964	GTGCACACTCTTTAGCTCAA
143878	141965	GGTGCACACTCTTTAGCTCA
143879	141966	AGGTGCACACTCTTTAGCTC
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143882	141969	TTTAGGTGCACACTCTTTAG
143883	141970	TTTTAGGTGCACACTCTTTA
143884	141971	ATTTTAGGTGCACACTCTTT
143885	141972	CATTTTAGGTGCACACTCTT
143886	141973	GCATTTTAGGTGCACACTCT
143887	141974	TGCATTTTAGGTGCACACTC
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143889	141976	AGTGCATTTTAGGTGCACAC
143890	141977	AAGTGCATTTTAGGTGCACA
143891	141978	CAAGTGCATTTTAGGTGCAC
143892	141979	ACAAGTGCATTTTAGGTGCA
143893	141980	AACAAGTGCATTTTAGGTGC
143894	141981	AAACAAGTGCATTTTAGGTG
143895	141982	CAAACAAGTGCATTTTAGGT
143896	141983	TCAAACAAGTGCATTTTAGG
143897	141984	CTCAAACAAGTGCATTTTAG
143898	141985	ACTCAAACAAGTGCATTTTA
143899	141986	TACTCAAACAAGTGCATTTT
143900	141987	CTACTCAAACAAGTGCATTT
143901	141988	ACTACTCAAACAAGTGCATT
143902	141989	AACTACTCAAACAAGTGCAT
143903	141990	AAACTACTCAAACAAGTGCA
143904	141991	GAAACTACTCAAACAAGTGC
143905	141992	AGAAACTACTCAAACAAGTG
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143909	141996	AGGCAGAAACTACTCAAACA
143910	141997	TAGGCAGAAACTACTCAAAC
143911	141998	ATAGGCAGAAACTACTCAAA
143912	141999	CATAGGCAGAAACTACTCAA
143913	142000	GCATAGGCAGAAACTACTCA
143914	142001	GGCATAGGCAGAAACTACTC
143915	142002	AGGCATAGGCAGAAACTACT
143916	142003	AAGGCATAGGCAGAAACTAC
143917	142004	GAAGGCATAGGCAGAAACTA
143918	142005	TGAAGGCATAGGCAGAAACT
143919	142006	TTGAAGGCATAGGCAGAAAC
143920	142007	CTTGAAGGCATAGGCAGAAA
143921	142008	ACTTGAAGGCATAGGCAGAA
143922	142009	AACTTGAAGGCATAGGCAGA
143923	142010	CAACTTGAAGGCATAGGCAG
143924	142011	GCAACTTGAAGGCATAGGCA
143925	142012	GGCAACTTGAAGGCATAGGC
143926	142013	AGGCAACTTGAAGGCATAGG
143927	142014	AAGGCAACTTGAAGGCATAG
143928	142015	AAAGGCAACTTGAAGGCATA
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143930	142017	AAAAAGGCAACTTGAAGGCA
143931	142018	CAAAAAGGCAACTTGAAGGC
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143933	142020	CCCAAAAAGGCAACTTGAAG
143934	142021	TCCCAAAAAGGCAACTTGAA
143935	142022	TTCCCAAAAAGGCAACTTGA
143936	142023	TTTCCCAAAAAGGCAACTTG
143937	142024	TTTTCCCAAAAAGGCAACTT
143938	142025	GTTTTCCCAAAAAGGCAACT
143939	142026	GGTTTTCCCAAAAAGGCAAC
143940	142027	AGGTTTTCCCAAAAAGGCAA

45647	43734	TGAAAAGATTAAATATTATT
45648	43735	CTGAAAAGATTAAATATTAT
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45650	43737	CTCTGAAAAGATTAAATATT
45651	43738	CCTCTGAAAAGATTAAATAT
45652	43739	ACCTCTGAAAAGATTAAATA
45653	43740	GACCTCTGAAAAGATTAAAT
45654	43741	CGACCTCTGAAAAGATTAAA
45655	43742	TCGACCTCTGAAAAGATTAA
45656	43743	TTCGACCTCTGAAAAGATTA
45657	43744	TTTCGACCTCTGAAAAGATT
45658	43745	GTTTCGACCTCTGAAAAGAT
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45660	43747	CTGTTTCGACCTCTGAAAAG
45661	43748	ACTGTTTCGACCTCTGAAAA
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45663	43750	TTACTGTTTCGACCTCTGAA
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45665	43752	TGTTACTGTTTCGACCTCTG
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45678	43765	TGAGGCAGTCCTTTGTTACT
45679	43766	CTGAGGCAGTCCTTTGTTAC
45680	43767	ACTGAGGCAGTCCTTTGTTA
45681	43768	GACTGAGGCAGTCCTTTGTT
45682	43769	AGACTGAGGCAGTCCTTTGT
45683	43770	TAGACTGAGGCAGTCCTTTG
45684	43771	GTAGACTGAGGCAGTCCTTT
45685	43772	CGTAGACTGAGGCAGTCCTT
45686	43773	CCGTAGACTGAGGCAGTCCT
45687	43774	ACCGTAGACTGAGGCAGTCC
45688	43775	CACCGTAGACTGAGGCAGTC
45689	43776	TCACCGTAGACTGAGGCAGT
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45691	43778	ACTCACCGTAGACTGAGGCA
45692	43779	TACTCACCGTAGACTGAGGC
45693	43780	TTACTCACCGTAGACTGAGG
45694	43781	GTTACTCACCGTAGACTGAG
45695	43782	AGTTACTCACCGTAGACTGA
45696	43783	AAGTTACTCACCGTAGACTG
45697	43784	AAAGTTACTCACCGTAGACT
45698	43785	TAAAGTTACTCACCGTAGAC
45699	43786	TTAAAGTTACTCACCGTAGA
45700	43787	ATTAAAGTTACTCACCGTAG
45701	43788	CATTAAAGTTACTCACCGTA
45702	43789	ACATTAAAGTTACTCACCGT
45703	43790	AACATTAAAGTTACTCACCG
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45706	43793	AGTAACATTAAAGTTACTCA
45707	43794	AAGTAACATTAAAGTTACTC
45708	43795	TAAGTAACATTAAAGTTACT
45709	43796	ATAAGTAACATTAAAGTTAC
45710	43797	AATAAGTAACATTAAAGTTA
45711	43798	CAATAAGTAACATTAAAGTT
45712	43799	CCAATAAGTAACATTAAAGT
45713	43800	CCCAATAAGTAACATTAAAG
45714	43801	CCCCAATAAGTAACATTAAA
45715	43802	TCCCCAATAAGTAACATTAA
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45717	43804	TTTCCCCAATAAGTAACATT

94794	92881	CTGCCTCAGCCTGCCTAGTG
94795	92882	CCTGCCTCAGCCTGCCTAGT
94796	92883	TCCTGCCTCAGCCTGCCTAG
94797	92884	CTCCTGCCTCAGCCTGCCTA
94798	92885	TCTCCTGCCTCAGCCTGCCT
94799	92886	TTCTCCTGCCTCAGCCTGCC
94800	92887	ATTCTCCTGCCTCAGCCTGC
94801	92888	GATTCTCCTGCCTCAGCCTG
94802	92889	TGATTCTCCTGCCTCAGCCT
94803	92890	CTGATTCTCCTGCCTCAGCC
94804	92891	CCTGATTCTCCTGCCTCAGC
94805	92892	GCCTGATTCTCCTGCCTCAG
94806	92893	TGCCTGATTCTCCTGCCTCA
94807	92894	CTGCCTGATTCTCCTGCCTC
94808	92895	CCTGCCTGATTCTCCTGCCT
94809	92896	CCCTGCCTGATTCTCCTGCC
94810	92897	TCCCTGCCTGATTCTCCTGC
94811	92898	CTCCCTGCCTGATTCTCCTG
94812	92899	CCTCCCTGCCTGATTCTCCT
94813	92900	ACCTCCCTGCCTGATTCTCC
94814	92901	AACCTCCCTGCCTGATTCTC
94815	92902	CAACCTCCCTGCCTGATTCT
94816	92903	GCAACCTCCCTGCCTGATTC
94817	92904	TGCAACCTCCCTGCCTGATT
94818	92905	CTGCAACCTCCCTGCCTGAT
94819	92906	ACTGCAACCTCCCTGCCTGA
94820	92907	CACTGCAACCTCCCTGCCTG
94821	92908	TCACTGCAACCTCCCTGCCT
94822	92909	CTCACTGCAACCTCCCTGCC
94823	92910	GCTCACTGCAACCTCCCTGC
94824	92911	GGCTCACTGCAACCTCCCTG
94825	92912	CGGCTCACTGCAACCTCCCT
94826	92913	TCGGCTCACTGCAACCTCCC
94827	92914	CTCGGCTCACTGCAACCTCC
94828	92915	TCTCGGCTCACTGCAACCTC
94829	92916	ATCTCGGCTCACTGCAACCT
94830	92917	CATCTCGGCTCACTGCAACC
94831	92918	CCATCTCGGCTCACTGCAAC
94832	92919	GCCATCTCGGCTCACTGCAA
94833	92920	TGCCATCTCGGCTCACTGCA
94834	92921	CTGCCATCTCGGCTCACTGC
94835	92922	GCTGCCATCTCGGCTCACTG
94836	92923	TGCTGCCATCTCGGCTCACT
94837	92924	CTGCTGCCATCTCGGCTCAC
94838	92925	ACTGCTGCCATCTCGGCTCA
94839	92926	TACTGCTGCCATCTCGGCTC
94840	92927	GTACTGCTGCCATCTCGGCT
94841	92928	TGTACTGCTGCCATCTCGGC
94842	92929	CTGTACTGCTGCCATCTCGG
94843	92930	ACTGTACTGCTGCCATCTCG
94844	92931	GACTGTACTGCTGCCATCTC
94845	92932	AGACTGTACTGCTGCCATCT
94846	92933	TAGACTGTACTGCTGCCATC
94847	92934	CTAGACTGTACTGCTGCCAT
94848	92935	GCTAGACTGTACTGCTGCCA
94849	92936	AGCTAGACTGTACTGCTGCC
94850	92937	AAGCTAGACTGTACTGCTGC
94851	92938	GAAGCTAGACTGTACTGCTG
94852	92939	CGAAGCTAGACTGTACTGCT
94853	92940	CCGAAGCTAGACTGTACTGC
94854	92941	GCCGAAGCTAGACTGTACTG
94855	92942	AGCCGAAGCTAGACTGTACT
94856	92943	GAGCCGAAGCTAGACTGTAC
94857	92944	CGAGCCGAAGCTAGACTGTA
94858	92945	CCGAGCCGAAGCTAGACTGT
94859	92946	GCCGAGCCGAAGCTAGACTG
94860	92947	TGCCGAGCCGAAGCTAGACT
94861	92948	ATGCCGAGCCGAAGCTAGAC
94862	92949	GATGCCGAGCCGAAGCTAGA
94863	92950	TGATGCCGAGCCGAAGCTAG
94864	92951	CTGATGCCGAGCCGAAGCTA

143941	142028	TAGGTTTTCCCAAAAAGGCA
143942	142029	CTAGGTTTTCCCAAAAAGGC
143943	142030	ACTAGGTTTTCCCAAAAAGG
143944	142031	CACTAGGTTTTCCCAAAAAG
143945	142032	TCACTAGGTTTTCCCAAAAA
143946	142033	GTCACTAGGTTTTCCCAAAA
143947	142034	GGTCACTAGGTTTTCCCAAA
143948	142035	CGGTCACTAGGTTTTCCCAA
143949	142036	ACGGTCACTAGGTTTTCCCA
143950	142037	AACGGTCACTAGGTTTTCCC
143951	142038	TAACGGTCACTAGGTTTTCC
143952	142039	TTAACGGTCACTAGGTTTTC
143953	142040	CTTAACGGTCACTAGGTTTT
143954	142041	TCTTAACGGTCACTAGGTTT
143955	142042	CTCTTAACGGTCACTAGGTT
143956	142043	ACTCTTAACGGTCACTAGGT
143957	142044	TACTCTTAACGGTCACTAGG
143958	142045	TTACTCTTAACGGTCACTAG
143959	142046	TTTACTCTTAACGGTCACTA
143960	142047	ATTTACTCTTAACGGTCACT
143961	142048	CATTTACTCTTAACGGTCAC
143962	142049	GCATTTACTCTTAACGGTCA
143963	142050	TGCATTTACTCTTAACGGTC
143964	142051	TTGCATTTACTCTTAACGGT
143965	142052	TTTGCATTTACTCTTAACGG
143966	142053	GTTTGCATTTACTCTTAACG
143967	142054	AGTTTGCATTTACTCTTAAC
143968	142055	TAGTTTGCATTTACTCTTAA
143969	142056	TTAGTTTGCATTTACTCTTA
143970	142057	ATTAGTTTGCATTTACTCTT
143971	142058	AATTAGTTTGCATTTACTCT
143972	142059	AAATTAGTTTGCATTTACTC
143973	142060	CAAATTAGTTTGCATTTACT
143974	142061	TCAAATTAGTTTGCATTTAC
143975	142062	ATCAAATTAGTTTGCATTTA
143976	142063	AATCAAATTAGTTTGCATTT
143977	142064	AAATCAAATTAGTTTGCATT
143978	142065	AAAATCAAATTAGTTTGCAT
143979	142066	TAAAATCAAATTAGTTTGCA
143980	142067	TTAAAATCAAATTAGTTTGC
143981	142068	ATTAAAATCAAATTAGTTTG
143982	142069	TATTAAAATCAAATTAGTTT
143983	142070	ATATTAAAATCAAATTAGTT
143984	142071	GATATTAAAATCAAATTAGT
143985	142072	TGATATTAAAATCAAATTAG
143986	142073	ATGATATTAAAATCAAATTA
143987	142074	TATGATATTAAAATCAAATT
143988	142075	ATATGATATTAAAATCAAAT
143989	142076	CATATGATATTAAAATCAAA
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143996	142083	AGCTCTACATATGATATTAA
143997	142084	CAGCTCTACATATGATATTA
143998	142085	ACAGCTCTACATATGATATT
143999	142086	TACAGCTCTACATATGATAT
144000	142087	ATACAGCTCTACATATGATA
144001	142088	AATACAGCTCTACATATGAT
144002	142089	TAATACAGCTCTACATATGA
144003	142090	ATAATACAGCTCTACATATG
144004	142091	TATAATACAGCTCTACATAT
144005	142092	ATATAATACAGCTCTACATA
144006	142093	CATATAATACAGCTCTACAT
144007	142094	TCATATAATACAGCTCTACA
144008	142095	TTCATATAATACAGCTCTAC
144009	142096	GTTCATATAATACAGCTCTA
144010	142097	GGTTCATATAATACAGCTCT
144011	142098	TGGTTCATATAATACAGCTC

45718	43805	TTTTCCCCAATAAGTAACAT
45719	43806	ATTTTCCCCAATAAGTAACA
45720	43807	AATTTTCCCCAATAAGTAAC
45721	43808	TAATTTTCCCCAATAAGTAA
45722	43809	CTAATTTTCCCCAATAAGTA
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45729	43816	TTAGCTACTAATTTTCCCCA
45730	43817	TTTAGCTACTAATTTTCCCC
45731	43818	TTTTAGCTACTAATTTTCCC
45732	43819	GTTTTAGCTACTAATTTTCC
45733	43820	TGTTTTAGCTACTAATTTTC
45734	43821	ATGTTTTAGCTACTAATTTT
45735	43822	CATGTTTTAGCTACTAATTT
45736	43823	TCATGTTTTAGCTACTAATT
45737	43824	ATCATGTTTTAGCTACTAAT
45738	43825	GATCATGTTTTAGCTACTAA
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45740	43827	GAGATCATGTTTTAGCTACT
45741	43828	AGAGATCATGTTTTAGCTAC
45742	43829	TAGAGATCATGTTTTAGCTA
45743	43830	TTAGAGATCATGTTTTAGCT
45744	43831	GTTAGAGATCATGTTTTAGC
45745	43832	GGTTAGAGATCATGTTTTAG
45746	43833	TGGTTAGAGATCATGTTTTA
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45763	43850	CCTTGGCATTTGGTCTGTGG
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45769	43856	CTTTTGCCTTGGCATTTGGT
45770	43857	TCTTTTGCCTTGGCATTTGG
45771	43858	ATCTTTTGCCTTGGCATTTG
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45773	43860	GAATCTTTTGCCTTGGCATT
45774	43861	GGAATCTTTTGCCTTGGCAT
45775	43862	GGGAATCTTTTGCCTTGGCA
45776	43863	AGGGAATCTTTTGCCTTGGC
45777	43864	AAGGGAATCTTTTGCCTTGG
45778	43865	GAAGGGAATCTTTTGCCTTG
45779	43866	AGAAGGGAATCTTTTGCCTT
45780	43867	AAGAAGGGAATCTTTTGCCT
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45784	43871	TCAAAAGAAGGGAATCTTTT
45785	43872	TTCAAAAGAAGGGAATCTTT
45786	43873	ATTCAAAAGAAGGGAATCTT
45787	43874	AATTCAAAAGAAGGGAATCT
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94865	92952	TCTGATGCCGAGCCGAAGCT
94866	92953	CTCTGATGCCGAGCCGAAGC
94867	92954	CCTCTGATGCCGAGCCGAAG
94868	92955	CCCTCTGATGCCGAGCCGAA
94869	92956	TCCCTCTGATGCCGAGCCGA
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94873	92960	GGTCTCCCTCTGATGCCGAG
94874	92961	CGGTCTCCCTCTGATGCCGA
94875	92962	ACGGTCTCCCTCTGATGCCG
94876	92963	CACGGTCTCCCTCTGATGCC
94877	92964	CCACGGTCTCCCTCTGATGC
94878	92965	TCCACGGTCTCCCTCTGATG
94879	92966	TTCCACGGTCTCCCTCTGAT
94880	92967	TTTCCACGGTCTCCCTCTGA
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94882	92969	TCTTTCCACGGTCTCCCTCT
94883	92970	CTCTTTCCACGGTCTCCCTC
94884	92971	TCTCTTTCCACGGTCTCCCT
94885	92972	CTCTCTTTCCACGGTCTCCC
94886	92973	CCTCTCTTTCCACGGTCTCC
94887	92974	CCCTCTCTTTCCACGGTCTC
94888	92975	TCCCTCTCTTTCCACGGTCT
94889	92976	CTCCCTCTCTTTCCACGGTC
94890	92977	TCTCCCTCTCTTTCCACGGT
94891	92978	CTCTCCCTCTCTTTCCACGG
94892	92979	CCTCTCCCTCTCTTTCCACG
94893	92980	CCCTCTCCCTCTCTTTCCAC
94894	92981	TCCCTCTCCCTCTCTTTCCA
94895	92982	CTCCCTCTCCCTCTCTTTCC
94896	92983	TCTCCCTCTCCCTCTCTTTC
94897	92984	GTCTCCCTCTCCCTCTCTTT
94898	92985	GGTCTCCCTCTCCCTCTCTT
94899	92986	CGGTCTCCCTCTCCCTCTCT
94900	92987	ACGGTCTCCCTCTCCCTCTC
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94902	92989	CCACGGTCTCCCTCTCCCTC
94903	92990	CCCACGGTCTCCCTCTCCCT
94904	92991	CCCCACGGTCTCCCTCTCCC
94905	92992	TCCCCACGGTCTCCCTCTCC
94906	92993	CTCCCCACGGTCTCCCTCTC
94907	92994	TCTCCCCACGGTCTCCCTCT
94908	92995	TTCTCCCCACGGTCTCCCTC
94909	92996	CTTCTCCCCACGGTCTCCCT
94910	92997	CCTTCTCCCCACGGTCTCCC
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94912	92999	CTCCTTCTCCCCACGGTCTC
94913	93000	TCTCCTTCTCCCCACGGTCT
94914	93001	TTCTCCTTCTCCCCACGGTC
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94919	93006	CCTCCTTCTCCTTCTCCCCA
94920	93007	CCCTCCTTCTCCTTCTCCCC
94921	93008	CCCCTCCTTCTCCTTCTCCC
94922	93009	CCCCCTCCTTCTCCTTCTCC
94923	93010	TCCCCCTCCTTCTCCTTCTC
94924	93011	CTCCCCCTCCTTCTCCTTCT
94925	93012	CCTCCCCCTCCTTCTCCTTC
94926	93013	CCCTCCCCCTCCTTCTCCTT
94927	93014	CCCCTCCCCCTCCTTCTCCT
94928	93015	CCCCCTCCCCCTCCTTCTCC
94929	93016	TCCCCCTCCCCCTCCTTCTC
94930	93017	CTCCCCCTCCCCCTCCTTCT
94931	93018	CCTCCCCCTCCCCCTCCTTC
94932	93019	CCCTCCCCCTCCCCCTCCTT
94933	93020	CCCCTCCCCCTCCCCCTCCT
94934	93021	CCCCCTCCCCCTCCCCCTCC
94935	93022	CCCCCCTCCCCCTCCCCCTC

144012	142099	TTGGTTCATATAATACAGCT
144013	142100	TTTGGTTCATATAATACAGC
144014	142101	ATTTGGTTCATATAATACAG
144015	142102	CATTTGGTTCATATAATACA
144016	142103	GCATTTGGTTCATATAATAC
144017	142104	AGCATTTGGTTCATATAATA
144018	142105	TAGCATTTGGTTCATATAAT
144019	142106	CTAGCATTTGGTTCATATAA
144020	142107	ACTAGCATTTGGTTCATATA
144021	142108	GACTAGCATTTGGTTCATAT
144022	142109	AGACTAGCATTTGGTTCATA
144023	142110	CAGACTAGCATTTGGTTCAT
144024	142111	ACAGACTAGCATTTGGTTCA
144025	142112	AACAGACTAGCATTTGGTTC
144026	142113	TAACAGACTAGCATTTGGTT
144027	142114	TTAACAGACTAGCATTTGGT
144028	142115	CTTAACAGACTAGCATTTGG
144029	142116	GCTTAACAGACTAGCATTTG
144030	142117	TGCTTAACAGACTAGCATTT
144031	142118	TTGCTTAACAGACTAGCATT
144032	142119	ATTGCTTAACAGACTAGCAT
144033	142120	TATTGCTTAACAGACTAGCA
144034	142121	CTATTGCTTAACAGACTAGC
144035	142122	GCTATTGCTTAACAGACTAG
144036	142123	AGCTATTGCTTAACAGACTA
144037	142124	TAGCTATTGCTTAACAGACT
144038	142125	GTAGCTATTGCTTAACAGAC
144039	142126	TGTAGCTATTGCTTAACAGA
144040	142127	GTGTAGCTATTGCTTAACAG
144041	142128	AGTGTAGCTATTGCTTAACA
144042	142129	AAGTGTAGCTATTGCTTAAC
144043	142130	TAAGTGTAGCTATTGCTTAA
144044	142131	ATAAGTGTAGCTATTGCTTA
144045	142132	AATAAGTGTAGCTATTGCTT
144046	142133	AAATAAGTGTAGCTATTGCT
144047	142134	AAAATAAGTGTAGCTATTGC
144048	142135	AAAAATAAGTGTAGCTATTG
144049	142136	AAAAAATAAGTGTAGCTATT
144050	142137	GAAAAAATAAGTGTAGCTAT
144051	142138	TGAAAAAATAAGTGTAGCTA
144052	142139	TTGAAAAAATAAGTGTAGCT
144053	142140	CTTGAAAAAATAAGTGTAGC
144054	142141	TCTTGAAAAAATAAGTGTAG
144055	142142	GTCTTGAAAAAATAAGTGTA
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144059	142146	CATTGTCTTGAAAAAATAAG
144060	142147	CCATTGTCTTGAAAAAATAA
144061	142148	TCCATTGTCTTGAAAAAATA
144062	142149	ATCCATTGTCTTGAAAAAAT
144063	142150	CATCCATTGTCTTGAAAAAA
144064	142151	CCATCCATTGTCTTGAAAAA
144065	142152	ACCATCCATTGTCTTGAAAA
144066	142153	AACCATCCATTGTCTTGAAA
144067	142154	AAACCATCCATTGTCTTGAA
144068	142155	TAAACCATCCATTGTCTTGA
144069	142156	TTAAACCATCCATTGTCTTG
144070	142157	TTTAAACCATCCATTGTCTT
144071	142158	ATTTAAACCATCCATTGTCT
144072	142159	CATTTAAACCATCCATTGTC
144073	142160	CCATTTAAACCATCCATTGT
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144077	142164	GACTCCATTTAAACCATCCA
144078	142165	TGACTCCATTTAAACCATCC
144079	142166	ATGACTCCATTTAAACCATC
144080	142167	GATGACTCCATTTAAACCAT
144081	142168	AGATGACTCCATTTAAACCA
144082	142169	TAGATGACTCCATTTAAACC

45789	43876	AAAATTCAAAAGAAGGGAAT
45790	43877	CAAAATTCAAAAGAAGGGAA
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45792	43879	GACAAAATTCAAAAGAAGGG
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45794	43881	ATGACAAAATTCAAAAGAAG
45795	43882	TATGACAAAATTCAAAAGAA
45796	43883	CTATGACAAAATTCAAAAGA
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45808	43895	CAGTCAAGTTATCTATGACA
45809	43896	ACAGTCAAGTTATCTATGAC
45810	43897	AACAGTCAAGTTATCTATGA
45811	43898	AAACAGTCAAGTTATCTATG
45812	43899	TAAACAGTCAAGTTATCTAT
45813	43900	TTAAACAGTCAAGTTATCTA
45814	43901	CTTAAACAGTCAAGTTATCT
45815	43902	ACTTAAACAGTCAAGTTATC
45816	43903	TACTTAAACAGTCAAGTTAT
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45822	43909	ATAACATACTTAAACAGTCA
45823	43910	AATAACATACTTAAACAGTC
45824	43911	TAATAACATACTTAAACAGT
45825	43912	CTAATAACATACTTAAACAG
45826	43913	GCTAATAACATACTTAAACA
45827	43914	GGCTAATAACATACTTAAAC
45828	43915	AGGCTAATAACATACTTAAA
45829	43916	TAGGCTAATAACATACTTAA
45830	43917	ATAGGCTAATAACATACTTA
45831	43918	TATAGGCTAATAACATACTT
45832	43919	ATATAGGCTAATAACATACT
45833	43920	CATATAGGCTAATAACATAC
45834	43921	ACATATAGGCTAATAACATA
45835	43922	CACATATAGGCTAATAACAT
45836	43923	ACACATATAGGCTAATAACA
45837	43924	AACACATATAGGCTAATAAC
45838	43925	AAACACATATAGGCTAATAA
45839	43926	AAAACACATATAGGCTAATA
45840	43927	AAAAACACATATAGGCTAAT
45841	43928	AAAAAACACATATAGGCTAA
45842	43929	AAAAAAACACATATAGGCTA
45843	43930	TAAAAAAACACATATAGGCT
45844	43931	TTAAAAAAACACATATAGGC
45845	43932	ATTAAAAAAACACATATAGG
45846	43933	CATTAAAAAAACACATATAG
45847	43934	TCATTAAAAAAACACATATA
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45858	43945	TTTATACAGAGTCATTAAAA
45859	43946	TTTTATACAGAGTCATTAAA

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94937	93024	TCCCCCCCTCCCCCTCCCCC
94938	93025	CTCCCCCCCTCCCCCTCCCC
94939	93026	TCTCCCCCCCCTCCCCCTCC
94940	93027	CTCTCCCCCCCCTCCCCCTC
94941	93028	CCTCTCCCCCCCCTCCCCCTC
94942	93029	CCCTCTCCCCCCCCTCCCCCT
94943	93030	TCCCTCTCCCCCCCCTCCCCC
94944	93031	CTCCCTCTCCCCCCCCTCCCC
94945	93032	TCTCCCTCTCCCCCCCCTCCC
94946	93033	CTCTCCCTCTCCCCCCCCTCC
94947	93034	CCTCTCCCTCTCCCCCCCTC
94948	93035	CCCTCTCCCTCTCCCCCCCT
94949	93036	TCCCTCTCCCTCTCCCCCCC
94950	93037	GTCCCTCTCCCTCTCCCCCC
94951	93038	TGTCCCTCTCCCTCTCCCCC
94952	93039	TTGTCCCTCTCCCTCTCCCC
94953	93040	ATTGTCCCTCTCCCTCTCCC
94954	93041	CATTGTCCCTCTCCCTCTCC
94955	93042	TCATTGTCCCTCTCCCTCTC
94956	93043	ATCATTGTCCCTCTCCCTCT
94957	93044	CATCATTGTCCCTCTCCCTC
94958	93045	ACATCATTGTCCCTCTCCCT
94959	93046	GACATCATTGTCCCTCTCCC
94960	93047	AGACATCATTGTCCCTCTCC
94961	93048	AAGACATCATTGTCCCTCTC
94962	93049	CAAGACATCATTGTCCCTCT
94963	93050	GCAAGACATCATTGTCCCTC
94964	93051	AGCAAGACATCATTGTCCCT
94965	93052	CAGCAAGACATCATTGTCCC
94966	93053	ACAGCAAGACATCATTGTCC
94967	93054	TACAGCAAGACATCATTGTC
94968	93055	CTACAGCAAGACATCATTGT
94969	93056	CCTACAGCAAGACATCATTG
94970	93057	ACCTACAGCAAGACATCATT
94971	93058	TACCTACAGCAAGACATCAT
94972	93059	ATACCTACAGCAAGACATCA
94973	93060	AATACCTACAGCAAGACATC
94974	93061	GAATACCTACAGCAAGACAT
94975	93062	AGAATACCTACAGCAAGACA
94976	93063	AAGAATACCTACAGCAAGAC
94977	93064	GAAGAATACCTACAGCAAGA
94978	93065	GGAAGAATACCTACAGCAAG
94979	93066	GGGAAGAATACCTACAGCAA
94980	93067	GGGGAAGAATACCTACAGCA
94981	93068	TGGGGAAGAATACCTACAGC
94982	93069	ATGGGGAAGAATACCTACAG
94983	93070	AATGGGGAAGAATACCTACA
94984	93071	AAATGGGGAAGAATACCTAC
94985	93072	CAAATGGGGAAGAATACCTA
94986	93073	TCAAATGGGGAAGAATACCT
94987	93074	TTCAAATGGGGAAGAATACC
94988	93075	ATTCAAATGGGGAAGAATAC
94989	93076	AATTCAAATGGGGAAGAATA
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94991	93078	AAAATTCAAATGGGGAAGAA
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94997	93084	GAGGAAAAAATTCAAATGGG
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94999	93086	CTGAGGAAAAAATTCAAATG
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95001	93088	TGCTGAGGAAAAAATTCAAA
95002	93089	ATGCTGAGGAAAAAATTCAA
95003	93090	AATGCTGAGGAAAAAATTCA
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95005	93092	ATAATGCTGAGGAAAAAATT
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144086	142173	TCTATAGATGACTCCATTTA
144087	142174	TTCTATAGATGACTCCATTT
144088	142175	TTTCTATAGATGACTCCATT
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144090	142177	AATTTCTATAGATGACTCCA
144091	142178	CAATTTCTATAGATGACTCC
144092	142179	CCAATTTCTATAGATGACTC
144093	142180	ACCAATTTCTATAGATGACT
144094	142181	TACCAATTTCTATAGATGAC
144095	142182	CTACCAATTTCTATAGATGA
144096	142183	ACTACCAATTTCTATAGATG
144097	142184	CACTACCAATTTCTATAGAT
144098	142185	CCACTACCAATTTCTATAGA
144099	142186	GCCACTACCAATTTCTATAG
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144101	142188	ACGCCACTACCAATTTCTAT
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144177	142264	ACCGATGTCTGACAACCTCC
144178	142265	AACCGATGTCTGACAACCTC
144179	142266	CAACCGATGTCTGACAACCT
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144181	142268	CACAACCGATGTCTGACAAC
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95088	93175	CAAAGTAGAAATGTTTTTTC
95089	93176	TCAAAGTAGAAATGTTTTTT
95090	93177	TTCAAAGTAGAAATGTTTTT
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95092	93179	GCTTCAAAGTAGAAATGTTT
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95141	93228	TGTAAATTATATCTCAATAA
95142	93229	ATGTAAATTATATCTCAATA
95143	93230	TATGTAAATTATATCTCAAT
95144	93231	ATATGTAAATTATATCTCAA
95145	93232	TATATGTAAATTATATCTCA
95146	93233	ATATATGTAAATTATATCTC
95147	93234	TATATATGTAAATTATATCT
95148	93235	TTATATATGTAAATTATATC

144225	142312	AAGGGAGCCCGTGGAAACTA
144226	142313	CAAGGGAGCCCGTGGAAACT
144227	142314	GCAAGGGAGCCCGTGGAAAC
144228	142315	AGCAAGGGAGCCCGTGGAAA
144229	142316	GAGCAAGGGAGCCCGTGGAA
144230	142317	TGAGCAAGGGAGCCCGTGGA
144231	142318	CTGAGCAAGGGAGCCCGTGG
144232	142319	GCTGAGCAAGGGAGCCCGTG
144233	142320	TGCTGAGCAAGGGAGCCCGT
144234	142321	CTGCTGAGCAAGGGAGCCCG
144235	142322	ACTGCTGAGCAAGGGAGCCC
144236	142323	TACTGCTGAGCAAGGGAGCC
144237	142324	ATACTGCTGAGCAAGGGAGC
144238	142325	CATACTGCTGAGCAAGGGAG
144239	142326	GCATACTGCTGAGCAAGGGA
144240	142327	CGCATACTGCTGAGCAAGGG
144241	142328	GCGCATACTGCTGAGCAAGG
144242	142329	TGCGCATACTGCTGAGCAAG
144243	142330	GTGCGCATACTGCTGAGCAA
144244	142331	GGTGCGCATACTGCTGAGCA
144245	142332	GGGTGCGCATACTGCTGAGC
144246	142333	AGGGTGCGCATACTGCTGAG
144247	142334	TAGGGTGCGCATACTGCTGA
144248	142335	TTAGGGTGCGCATACTGCTG
144249	142336	GTTAGGGTGCGCATACTGCT
144250	142337	CGTTAGGGTGCGCATACTGC
144251	142338	GCGTTAGGGTGCGCATACTG
144252	142339	AGCGTTAGGGTGCGCATACT
144253	142340	TAGCGTTAGGGTGCGCATAC
144254	142341	GTAGCGTTAGGGTGCGCATA
144255	142342	GGTAGCGTTAGGGTGCGCAT
144256	142343	GGGTAGCGTTAGGGTGCGCA
144257	142344	AGGGTAGCGTTAGGGTGCGC
144258	142345	CAGGGTAGCGTTAGGGTGCG
144259	142346	GCAGGGTAGCGTTAGGGTGC
144260	142347	TGCAGGGTAGCGTTAGGGTG
144261	142348	GTGCAGGGTAGCGTTAGGGT
144262	142349	GGTGCAGGGTAGCGTTAGGG
144263	142350	GGGTGCAGGGTAGCGTTAGG
144264	142351	TGGGTGCAGGGTAGCGTTAG
144265	142352	GTGGGTGCAGGGTAGCGTTA
144266	142353	TGTGGGTGCAGGGTAGCGTT
144267	142354	ATGTGGGTGCAGGGTAGCGT
144268	142355	TATGTGGGTGCAGGGTAGCG
144269	142356	GTATGTGGGTGCAGGGTAGC
144270	142357	AGTATGTGGGTGCAGGGTAG
144271	142358	GAGTATGTGGGTGCAGGGTA
144272	142359	GGAGTATGTGGGTGCAGGGT
144273	142360	TGGAGTATGTGGGTGCAGGG
144274	142361	GTGGAGTATGTGGGTGCAGG
144275	142362	TGTGGAGTATGTGGGTGCAG
144276	142363	GTGTGGAGTATGTGGGTGCA
144277	142364	GGTGTGGAGTATGTGGGTGC
144278	142365	GGGTGTGGAGTATGTGGGTG
144279	142366	AGGGTGTGGAGTATGTGGGT
144280	142367	GAGGGTGTGGAGTATGTGGG
144281	142368	TGAGGGTGTGGAGTATGTGG
144282	142369	CTGAGGGTGTGGAGTATGTG
144283	142370	GCTGAGGGTGTGGAGTATGT
144284	142371	GGCTGAGGGTGTGGAGTATG
144285	142372	AGGCTGAGGGTGTGGAGTAT
144286	142373	AAGGCTGAGGGTGTGGAGTA
144287	142374	GAAGGCTGAGGGTGTGGAGT
144288	142375	TGAAGGCTGAGGGTGTGGAG
144289	142376	CTGAAGGCTGAGGGTGTGGA
144290	142377	GCTGAAGGCTGAGGGTGTGG
144291	142378	AGCTGAAGGCTGAGGGTGTG
144292	142379	TAGCTGAAGGCTGAGGGTGT
144293	142380	GTAGCTGAAGGCTGAGGGTG
144294	142381	GGTAGCTGAAGGCTGAGGGT
144295	142382	GGGTAGCTGAAGGCTGAGGG

46002	44089	CACCATGATTGTAAGTTTCC
46003	44090	CCACCATGATTGTAAGTTTC
46004	44091	TCCACCATGATTGTAAGTTT
46005	44092	TTCCACCATGATTGTAAGTT
46006	44093	CTTCCACCATGATTGTAAGT
46007	44094	CCTTCCACCATGATTGTAAG
46008	44095	CCCTTCCACCATGATTGTAA
46009	44096	CCCCTTCCACCATGATTGTA
46010	44097	TCCCCTTCCACCATGATTGT
46011	44098	TTCCCCTTCCACCATGATTG
46012	44099	CTTCCCCTTCCACCATGATT
46013	44100	GCTTCCCCTTCCACCATGAT
46014	44101	TGCTTCCCCTTCCACCATGA
46015	44102	TTGCTTCCCCTTCCACCATG
46016	44103	TTTGCTTCCCCTTCCACCAT
46017	44104	GTTTGCTTCCCCTTCCACCA
46018	44105	TGTTTGCTTCCCCTTCCACC
46019	44106	GTGTTTGCTTCCCCTTCCAC
46020	44107	TGTGTTTGCTTCCCCTTCCA
46021	44108	ATGTGTTTGCTTCCCCTTCC
46022	44109	GATGTGTTTGCTTCCCCTTC
46023	44110	GGATGTGTTTGCTTCCCCTT
46024	44111	AGGATGTGTTTGCTTCCCCT
46025	44112	AAGGATGTGTTTGCTTCCCC
46026	44113	GAAGGATGTGTTTGCTTCCC
46027	44114	AGAAGGATGTGTTTGCTTCC
46028	44115	AAGAAGGATGTGTTTGCTTC
46029	44116	GAAGAAGGATGTGTTTGCTT
46030	44117	TGAAGAAGGATGTGTTTGCT
46031	44118	GTGAAGAAGGATGTGTTTGC
46032	44119	TGTGAAGAAGGATGTGTTTG
46033	44120	ATGTGAAGAAGGATGTGTTT
46034	44121	TATGTGAAGAAGGATGTGTT
46035	44122	CTATGTGAAGAAGGATGTGT
46036	44123	GCTATGTGAAGAAGGATGTG
46037	44124	CGCTATGTGAAGAAGGATGT
46038	44125	TCGCTATGTGAAGAAGGATG
46039	44126	GTCGCTATGTGAAGAAGGAT
46040	44127	TGTCGCTATGTGAAGAAGGA
46041	44128	CTGTCGCTATGTGAAGAAGG
46042	44129	CCTGTCGCTATGTGAAGAAG
46043	44130	TCCTGTCGCTATGTGAAGAA
46044	44131	CTCCTGTCGCTATGTGAAGA
46045	44132	TCTCCTGTCGCTATGTGAAG
46046	44133	CTCTCCTGTCGCTATGTGAA
46047	44134	TCTCTCCTGTCGCTATGTGA
46048	44135	CTCTCTCCTGTCGCTATGTG
46049	44136	TCTCTCTCCTGTCGCTATGT
46050	44137	TTCTCTCTCCTGTCGCTATG
46051	44138	CTTCTCTCTCCTGTCGCTAT
46052	44139	ACTTCTCTCTCCTGTCGCTA
46053	44140	CACTTCTCTCTCCTGTCGCT
46054	44141	GCACTTCTCTCTCCTGTCGC
46055	44142	AGCACTTCTCTCTCCTGTCG
46056	44143	CAGCACTTCTCTCTCCTGTC
46057	44144	TCAGCACTTCTCTCTCCTGT
46058	44145	CTCAGCACTTCTCTCTCCTG
46059	44146	GCTCAGCACTTCTCTCTCCT
46060	44147	TGCTCAGCACTTCTCTCTCC
46061	44148	TTGCTCAGCACTTCTCTCTC
46062	44149	TTTGCTCAGCACTTCTCTCT
46063	44150	CTTTGCTCAGCACTTCTCTC
46064	44151	GCTTTGCTCAGCACTTCTCT
46065	44152	TGCTTTGCTCAGCACTTCTC
46066	44153	CTGCTTTGCTCAGCACTTCT
46067	44154	CCTGCTTTGCTCAGCACTTC
46068	44155	CCCTGCTTTGCTCAGCACTT
46069	44156	TCCCTGCTTTGCTCAGCACT
46070	44157	TTCCCTGCTTTGCTCAGCAC
46071	44158	TTTCCCTGCTTTGCTCAGCA
46072	44159	CTTTCCCTGCTTTGCTCAGC

95149	93236	TTTATATATGTAAATTATAT
95150	93237	ATTTATATATGTAAATTATA
95151	93238	TATTTATATATGTAAATTAT
95152	93239	TTATTTATATATGTAAATTA
95153	93240	TTTATTTATATATGTAAATT
95154	93241	GTTTATTTATATATGTAAAT
95155	93242	GGTTTATTTATATATGTAAA
95156	93243	CGGTTTATTTATATATGTAA
95157	93244	ACGGTTTATTTATATATGTA
95158	93245	AACGGTTTATTTATATATGT
95159	93246	AAACGGTTTATTTATATATG
95160	93247	TAAACGGTTTATTTATATAT
95161	93248	TTAAACGGTTTATTTATATA
95162	93249	TTTAAACGGTTTATTTATAT
95163	93250	CTTTAAACGGTTTATTTATA
95164	93251	ACTTTAAACGGTTTATTTAT
95165	93252	CACTTTAAACGGTTTATTTA
95166	93253	ACACTTTAAACGGTTTATTT
95167	93254	TACACTTTAAACGGTTTATT
95168	93255	ATACACTTTAAACGGTTTAT
95169	93256	TATACACTTTAAACGGTTTA
95170	93257	TTATACACTTTAAACGGTTT
95171	93258	TTTATACACTTTAAACGGTT
95172	93259	ATTTATACACTTTAAACGGT
95173	93260	GATTTATACACTTTAAACGG
95174	93261	TGATTTATACACTTTAAACG
95175	93262	CTGATTTATACACTTTAAAC
95176	93263	ACTGATTTATACACTTTAAA
95177	93264	CACTGATTTATACACTTTAA
95178	93265	CCACTGATTTATACACTTTA
95179	93266	ACCACTGATTTATACACTTT
95180	93267	AACCACTGATTTATACACTT
95181	93268	AAACCACTGATTTATACACT
95182	93269	AAAACCACTGATTTATACAC
95183	93270	AAAAACCACTGATTTATACA
95184	93271	TAAAAACCACTGATTTATAC
95185	93272	TTAAAAACCACTGATTTATA
95186	93273	ATTAAAAACCACTGATTTAT
95187	93274	CATTAAAAACCACTGATTTA
95188	93275	TCATTAAAAACCACTGATTT
95189	93276	CTCATTAAAAACCACTGATT
95190	93277	TCTCATTAAAAACCACTGAT
95191	93278	ATCTCATTAAAAACCACTGA
95192	93279	TATCTCATTAAAAACCACTG
95193	93280	ATATCTCATTAAAAACCACT
95194	93281	TATATCTCATTAAAAACCAC
95195	93282	TTATATCTCATTAAAAACCA
95196	93283	ATTATATCTCATTAAAAACC
95197	93284	AATTATATCTCATTAAAAAC
95198	93285	AAATTATATCTCATTAAAAA
95199	93286	TAAATTATATCTCATTAAAA
95200	93287	GTAAATTATATCTCATTAAA
95201	93288	TGTAAATTATATCTCATTAA
95202	93289	ATGTAAATTATATCTCATTA
95203	93290	TATGTAAATTATATCTCATT
95204	93291	ATATGTAAATTATATCTCAT
95205	93292	TATATGTAAATTATATCTCA
95206	93293	ATATATGTAAATTATATCTC
95207	93294	TATATATGTAAATTATATCT
95208	93295	TTATATATGTAAATTATATC
95209	93296	TTTATATATGTAAATTATAT
95210	93297	ATTTATATATGTAAATTATA
95211	93298	GATTTATATATGTAAATTAT
95212	93299	TGATTTATATATGTAAATTA
95213	93300	TTGATTTATATATGTAAATT
95214	93301	GTTGATTTATATATGTAAAT
95215	93302	GGTTGATTTATATATGTAAA
95216	93303	TGGTTGATTTATATATGTAA
95217	93304	ATGGTTGATTTATATATGTA
95218	93305	AATGGTTGATTTATATATGT
95219	93306	AAATGGTTGATTTATATATG

144296	142383	GGGGTAGCTGAAGGCTGAGG
144297	142384	GGGGGTAGCTGAAGGCTGAG
144298	142385	TGGGGGTAGCTGAAGGCTGA
144299	142386	GTGGGGGTAGCTGAAGGCTG
144300	142387	AGTGGGGGTAGCTGAAGGCT
144301	142388	CAGTGGGGGTAGCTGAAGGC
144302	142389	CCAGTGGGGGTAGCTGAAGG
144303	142390	TCCAGTGGGGGTAGCTGAAG
144304	142391	GTCCAGTGGGGGTAGCTGAA
144305	142392	TGTCCAGTGGGGGTAGCTGA
144306	142393	CTGTCCAGTGGGGGTAGCTG
144307	142394	GCTGTCCAGTGGGGGTAGCT
144308	142395	TGCTGTCCAGTGGGGGTAGC
144309	142396	CTGCTGTCCAGTGGGGGTAG
144310	142397	GCTGCTGTCCAGTGGGGGTA
144311	142398	TGCTGCTGTCCAGTGGGGGT
144312	142399	TTGCTGCTGTCCAGTGGGGG
144313	142400	TTTGCTGCTGTCCAGTGGGG
144314	142401	CTTTGCTGCTGTCCAGTGGG
144315	142402	GCTTTGCTGCTGTCCAGTGG
144316	142403	GGCTTTGCTGCTGTCCAGTG
144317	142404	TGGCTTTGCTGCTGTCCAGT
144318	142405	TTGGCTTTGCTGCTGTCCAG
144319	142406	GTTGGCTTTGCTGCTGTCCA
144320	142407	TGTTGGCTTTGCTGCTGTCC
144321	142408	ATGTTGGCTTTGCTGCTGTC
144322	142409	CATGTTGGCTTTGCTGCTGT
144323	142410	CCATGTTGGCTTTGCTGCTG
144324	142411	ACCATGTTGGCTTTGCTGCT
144325	142412	CACCATGTTGGCTTTGCTGC
144326	142413	CCACCATGTTGGCTTTGCTG
144327	142414	TCCACCATGTTGGCTTTGCT
144328	142415	TTCCACCATGTTGGCTTTGC
144329	142416	CTTCCACCATGTTGGCTTTG
144330	142417	ACTTCCACCATGTTGGCTTT
144331	142418	GACTTCCACCATGTTGGCTT
144332	142419	TGACTTCCACCATGTTGGCT
144333	142420	ATGACTTCCACCATGTTGGC
144334	142421	GATGACTTCCACCATGTTGG
144335	142422	GGATGACTTCCACCATGTTG
144336	142423	AGGATGACTTCCACCATGTT
144337	142424	CAGGATGACTTCCACCATGT
144338	142425	GCAGGATGACTTCCACCATG
144339	142426	TGCAGGATGACTTCCACCAT
144340	142427	GTGCAGGATGACTTCCACCA
144341	142428	GGTGCAGGATGACTTCCACC
144342	142429	GGGTGCAGGATGACTTCCAC
144343	142430	TGGGTGCAGGATGACTTCCA
144344	142431	CTGGGTGCAGGATGACTTCC
144345	142432	ACTGGGTGCAGGATGACTTC
144346	142433	GACTGGGTGCAGGATGACTT
144347	142434	GGACTGGGTGCAGGATGACT
144348	142435	AGGACTGGGTGCAGGATGAC
144349	142436	CAGGACTGGGTGCAGGATGA
144350	142437	ACAGGACTGGGTGCAGGATG
144351	142438	AACAGGACTGGGTGCAGGAT
144352	142439	GAACAGGACTGGGTGCAGGA
144353	142440	TGAACAGGACTGGGTGCAGG
144354	142441	CTGAACAGGACTGGGTGCAG
144355	142442	CCTGAACAGGACTGGGTGCA
144356	142443	ACCTGAACAGGACTGGGTGC
144357	142444	TACCTGAACAGGACTGGGTG
144358	142445	TTACCTGAACAGGACTGGGT
144359	142446	CTTACCTGAACAGGACTGGG
144360	142447	CCTTACCTGAACAGGACTGG
144361	142448	CCCTTACCTGAACAGGACTG
144362	142449	GCCCTTACCTGAACAGGACT
144363	142450	TGCCCTTACCTGAACAGGAC
144364	142451	TTGCCCTTACCTGAACAGGA
144365	142452	GTTGCCCTTACCTGAACAGG
144366	142453	AGTTGCCCTTACCTGAACAG

46073	44160	GCTTTCCCTGCTTTGCTCAG
46074	44161	GGCTTTCCCTGCTTTGCTCA
46075	44162	GGGCTTTCCCTGCTTTGCTC
46076	44163	GGGGCTTTCCCTGCTTTGCT
46077	44164	AGGGGCTTTCCCTGCTTTGC
46078	44165	AAGGGGCTTTCCCTGCTTTG
46079	44166	TAAGGGGCTTTCCCTGCTTT
46080	44167	ATAAGGGGCTTTCCCTGCTT
46081	44168	TATAAGGGGCTTTCCCTGCT
46082	44169	TTATAAGGGGCTTTCCCTGC
46083	44170	TTTATAAGGGGCTTTCCCTG
46084	44171	TTTTATAAGGGGCTTTCCCT
46085	44172	GTTTTATAAGGGGCTTTCCC
46086	44173	GGTTTTATAAGGGGCTTTCC
46087	44174	TGGTTTTATAAGGGGCTTTC
46088	44175	ATGGTTTTATAAGGGGCTTT
46089	44176	GATGGTTTTATAAGGGGCTT
46090	44177	TGATGGTTTTATAAGGGGCT
46091	44178	CTGATGGTTTTATAAGGGGC
46092	44179	TCTGATGGTTTTATAAGGGG
46093	44180	ATCTGATGGTTTTATAAGGG
46094	44181	GATCTGATGGTTTTATAAGG
46095	44182	AGATCTGATGGTTTTATAAG
46096	44183	GAGATCTGATGGTTTTATAA
46097	44184	GGAGATCTGATGGTTTTATA
46098	44185	AGGAGATCTGATGGTTTTAT
46099	44186	CAGGAGATCTGATGGTTTTA
46100	44187	TCAGGAGATCTGATGGTTTT
46101	44188	CTCAGGAGATCTGATGGTTT
46102	44189	TCTCAGGAGATCTGATGGTT
46103	44190	TTCTCAGGAGATCTGATGGT
46104	44191	GTTCTCAGGAGATCTGATGG
46105	44192	AGTTCTCAGGAGATCTGATG
46106	44193	GAGTTCTCAGGAGATCTGAT
46107	44194	TGAGTTCTCAGGAGATCTGA
46108	44195	GTGAGTTCTCAGGAGATCTG
46109	44196	AGTGAGTTCTCAGGAGATCT
46110	44197	GAGTGAGTTCTCAGGAGATC
46111	44198	TGAGTGAGTTCTCAGGAGAT
46112	44199	GTGAGTGAGTTCTCAGGAGA
46113	44200	AGTGAGTGAGTTCTCAGGAG
46114	44201	TAGTGAGTGAGTTCTCAGGA
46115	44202	ATAGTGAGTGAGTTCTCAGG
46116	44203	GATAGTGAGTGAGTTCTCAG
46117	44204	TGATAGTGAGTGAGTTCTCA
46118	44205	ATGATAGTGAGTGAGTTCTC
46119	44206	CATGATAGTGAGTGAGTTCT
46120	44207	TCATGATAGTGAGTGAGTTC
46121	44208	CTCATGATAGTGAGTGAGTT
46122	44209	TCTCATGATAGTGAGTGAGT
46123	44210	CTCTCATGATAGTGAGTGAG
46124	44211	GCTCTCATGATAGTGAGTGA
46125	44212	TGCTCTCATGATAGTGAGTG
46126	44213	CTGCTCTCATGATAGTGAGT
46127	44214	GCTGCTCTCATGATAGTGAG
46128	44215	CGCTGCTCTCATGATAGTGA
46129	44216	ACGCTGCTCTCATGATAGTG
46130	44217	TACGCTGCTCTCATGATAGT
46131	44218	CTACGCTGCTCTCATGATAG
46132	44219	CCTACGCTGCTCTCATGATA
46133	44220	CCCTACGCTGCTCTCATGAT
46134	44221	CCCCTACGCTGCTCTCATGA
46135	44222	TCCCCTACGCTGCTCTCATG
46136	44223	TTCCCCTACGCTGCTCTCAT
46137	44224	TTTCCCCTACGCTGCTCTCA
46138	44225	GTTTCCCCTACGCTGCTCTC
46139	44226	AGTTTCCCCTACGCTGCTCT
46140	44227	CAGTTTCCCCTACGCTGCTC
46141	44228	GCAGTTTCCCCTACGCTGCT
46142	44229	GGCAGTTTCCCCTACGCTGC
46143	44230	GGGCAGTTTCCCCTACGCTG

95220	93307	TAAATGGTTGATTTATATAT
95221	93308	TTAAATGGTTGATTTATATA
95222	93309	TTTAAATGGTTGATTTATAT
95223	93310	CTTTAAATGGTTGATTTATA
95224	93311	ACTTTAAATGGTTGATTTAT
95225	93312	CACTTTAAATGGTTGATTTA
95226	93313	ACACTTTAAATGGTTGATTT
95227	93314	TACACTTTAAATGGTTGATT
95228	93315	ATACACTTTAAATGGTTGAT
95229	93316	TATACACTTTAAATGGTTGA
95230	93317	TTATACACTTTAAATGGTTG
95231	93318	TTTATACACTTTAAATGGTT
95232	93319	ATTTATACACTTTAAATGGT
95233	93320	GATTTATACACTTTAAATGG
95234	93321	TGATTTATACACTTTAAATG
95235	93322	CTGATTTATACACTTTAAAT
95236	93323	ACTGATTTATACACTTTAAA
95237	93324	CACTGATTTATACACTTTAA
95238	93325	CCACTGATTTATACACTTTA
95239	93326	ACCACTGATTTATACACTTT
95240	93327	AACCACTGATTTATACACTT
95241	93328	AAACCACTGATTTATACACT
95242	93329	AAAACCACTGATTTATACAC
95243	93330	AAAAACCACTGATTTATACA
95244	93331	TAAAAACCACTGATTTATAC
95245	93332	TTAAAAACCACTGATTTATA
95246	93333	TTTAAAAACCACTGATTTAT
95247	93334	TTTTAAAAACCACTGATTTA
95248	93335	ATTTTAAAAACCACTGATTT
95249	93336	TATTTTAAAAACCACTGATT
95250	93337	ATATTTTAAAAACCACTGAT
95251	93338	AATATTTTAAAAACCACTGA
95252	93339	GAATATTTTAAAAACCACTG
95253	93340	TGAATATTTTAAAAACCACT
95254	93341	GTGAATATTTTAAAAACCAC
95255	93342	TGTGAATATTTTAAAAACCA
95256	93343	TTGTGAATATTTTAAAAACC
95257	93344	ATTGTGAATATTTTAAAAAC
95258	93345	CATTGTGAATATTTTAAAAA
95259	93346	ACATTGTGAATATTTTAAAA
95260	93347	AACATTGTGAATATTTTAAA
95261	93348	CAACATTGTGAATATTTTAA
95262	93349	ACAACATTGTGAATATTTTA
95263	93350	TACAACATTGTGAATATTTT
95264	93351	GTACAACATTGTGAATATTT
95265	93352	TGTACAACATTGTGAATATT
95266	93353	TTGTACAACATTGTGAATAT
95267	93354	GTTGTACAACATTGTGAATA
95268	93355	GGTTGTACAACATTGTGAAT
95269	93356	CGGTTGTACAACATTGTGAA
95270	93357	ACGGTTGTACAACATTGTGA
95271	93358	GACGGTTGTACAACATTGTG
95272	93359	AGACGGTTGTACAACATTGT
95273	93360	AAGACGGTTGTACAACATTG
95274	93361	GAAGACGGTTGTACAACATT
95275	93362	AGAAGACGGTTGTACAACAT
95276	93363	GAGAAGACGGTTGTACAACA
95277	93364	TGAGAAGACGGTTGTACAAC
95278	93365	CTGAGAAGACGGTTGTACAA
95279	93366	ACTGAGAAGACGGTTGTACA
95280	93367	AACTGAGAAGACGGTTGTAC
95281	93368	CAACTGAGAAGACGGTTGTA
95282	93369	TCAACTGAGAAGACGGTTGT
95283	93370	ATCAACTGAGAAGACGGTTG
95284	93371	AATCAACTGAGAAGACGGTT
95285	93372	AAATCAACTGAGAAGACGGT
95286	93373	AAAATCAACTGAGAAGACGG
95287	93374	TAAAATCAACTGAGAAGACG
95288	93375	TTAAAATCAACTGAGAAGAC
95289	93376	TTTAAAATCAACTGAGAAGA
95290	93377	TTTTAAAATCAACTGAGAAG

144367	142454	GAGTTGCCCTTACCTGAACA
144368	142455	TGAGTTGCCCTTACCTGAAC
144369	142456	CTGAGTTGCCCTTACCTGAA
144370	142457	TCTGAGTTGCCCTTACCTGA
144371	142458	CTCTGAGTTGCCCTTACCTG
144372	142459	CCTCTGAGTTGCCCTTACCT
144373	142460	ACCTCTGAGTTGCCCTTACC
144374	142461	GACCTCTGAGTTGCCCTTAC
144375	142462	AGACCTCTGAGTTGCCCTTA
144376	142463	CAGACCTCTGAGTTGCCCTT
144377	142464	GCAGACCTCTGAGTTGCCCT
144378	142465	TGCAGACCTCTGAGTTGCCC
144379	142466	ATGCAGACCTCTGAGTTGCC
144380	142467	CATGCAGACCTCTGAGTTGC
144381	142468	CCATGCAGACCTCTGAGTTG
144382	142469	TCCATGCAGACCTCTGAGTT
144383	142470	CTCCATGCAGACCTCTGAGT
144384	142471	ACTCCATGCAGACCTCTGAG
144385	142472	CACTCCATGCAGACCTCTGA
144386	142473	CCACTCCATGCAGACCTCTG
144387	142474	GCCACTCCATGCAGACCTCT
144388	142475	AGCCACTCCATGCAGACCTC
144389	142476	AAGCCACTCCATGCAGACCT
144390	142477	GAAGCCACTCCATGCAGACC
144391	142478	AGAAGCCACTCCATGCAGAC
144392	142479	AAGAAGCCACTCCATGCAGA
144393	142480	AAAGAAGCCACTCCATGCAG
144394	142481	TAAAGAAGCCACTCCATGCA
144395	142482	ATAAAGAAGCCACTCCATGC
144396	142483	GATAAAGAAGCCACTCCATG
144397	142484	GGATAAAGAAGCCACTCCAT
144398	142485	AGGATAAAGAAGCCACTCCA
144399	142486	TAGGATAAAGAAGCCACTCC
144400	142487	CTAGGATAAAGAAGCCACTC
144401	142488	ACTAGGATAAAGAAGCCACT
144402	142489	TACTAGGATAAAGAAGCCAC
144403	142490	ATACTAGGATAAAGAAGCCA
144404	142491	GATACTAGGATAAAGAAGCC
144405	142492	AGATACTAGGATAAAGAAGC
144406	142493	CAGATACTAGGATAAAGAAG
144407	142494	TCAGATACTAGGATAAAGAA
144408	142495	CTCAGATACTAGGATAAAGA
144409	142496	ACTCAGATACTAGGATAAAG
144410	142497	CACTCAGATACTAGGATAAA
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144412	142499	AGCACTCAGATACTAGGATA
144413	142500	AAGCACTCAGATACTAGGAT
144414	142501	AAAGCACTCAGATACTAGGA
144415	142502	GAAAGCACTCAGATACTAGG
144416	142503	AGAAAGCACTCAGATACTAG
144417	142504	AAGAAAGCACTCAGATACTA
144418	142505	GAAGAAAGCACTCAGATACT
144419	142506	TGAAGAAAGCACTCAGATAC
144420	142507	CTGAAGAAAGCACTCAGATA
144421	142508	CCTGAAGAAAGCACTCAGAT
144422	142509	ACCTGAAGAAAGCACTCAGA
144423	142510	CACCTGAAGAAAGCACTCAG
144424	142511	GCACCTGAAGAAAGCACTCA
144425	142512	GGCACCTGAAGAAAGCACTC
144426	142513	TGGCACCTGAAGAAAGCACT
144427	142514	CTGGCACCTGAAGAAAGCAC
144428	142515	CCTGGCACCTGAAGAAAGCA
144429	142516	ACCTGGCACCTGAAGAAAGC
144430	142517	TACCTGGCACCTGAAGAAAG
144431	142518	ATACCTGGCACCTGAAGAAA
144432	142519	GATACCTGGCACCTGAAGAA
144433	142520	CGATACCTGGCACCTGAAGA
144434	142521	GCGATACCTGGCACCTGAAG
144435	142522	TGCGATACCTGGCACCTGAA
144436	142523	ATGCGATACCTGGCACCTGA
144437	142524	GATGCGATACCTGGCACCTG

46144	44231	GGGGCAGTTTCCCCTACGCT
46145	44232	GGGGGCAGTTTCCCCTACGC
46146	44233	TGGGGGCAGTTTCCCCTACG
46147	44234	ATGGGGGCAGTTTCCCCTAC
46148	44235	CATGGGGGCAGTTTCCCCTA
46149	44236	TCATGGGGGCAGTTTCCCCT
46150	44237	ATCATGGGGGCAGTTTCCCC
46151	44238	AATCATGGGGGCAGTTTCCC
46152	44239	GAATCATGGGGGCAGTTTCC
46153	44240	TGAATCATGGGGGCAGTTTC
46154	44241	CTGAATCATGGGGGCAGTTT
46155	44242	ACTGAATCATGGGGGCAGTT
46156	44243	AACTGAATCATGGGGGCAGT
46157	44244	TAACTGAATCATGGGGGCAG
46158	44245	ATAACTGAATCATGGGGGCA
46159	44246	GATAACTGAATCATGGGGGC
46160	44247	AGATAACTGAATCATGGGGG
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46162	44249	GGAGATAACTGAATCATGGG
46163	44250	TGGAGATAACTGAATCATGG
46164	44251	GTGGAGATAACTGAATCATG
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46166	44253	AGGTGGAGATAACTGAATCA
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46175	44262	GGCAAGACCAGGTGGAGATA
46176	44263	GGGCAAGACCAGGTGGAGAT
46177	44264	AGGGCAAGACCAGGTGGAGA
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46179	44266	CAAGGGCAAGACCAGGTGGA
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95296	93383	AGTATGTTTTAAAATCAACT
95297	93384	GAGTATGTTTTAAAATCAAC
95298	93385	AGAGTATGTTTTAAAATCAA
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95300	93387	GAAGAGTATGTTTTAAAATC
95301	93388	TGAAGAGTATGTTTTAAAAT
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95309	93396	TTTGGGGGTGAAGAGTATGT
95310	93397	TTTTGGGGGTGAAGAGTATG
95311	93398	CTTTTGGGGGTGAAGAGTAT
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95315	93402	GTTTCTTTTGGGGGTGAAGA
95316	93403	GGTTTCTTTTGGGGGTGAAG
95317	93404	GGGTTTCTTTTGGGGGTGAA
95318	93405	GGGGTTTCTTTTGGGGGTGA
95319	93406	CGGGGTTTCTTTTGGGGGTG
95320	93407	ACGGGGTTTCTTTTGGGGGT
95321	93408	CACGGGGTTTCTTTTGGGGG
95322	93409	GCACGGGGTTTCTTTTGGGG
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95324	93411	GGGCACGGGGTTTCTTTTGG
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95327	93414	ACTGGGCACGGGGTTTCTTT
95328	93415	AACTGGGCACGGGGTTTCTT
95329	93416	AAACTGGGCACGGGGTTTCT
95330	93417	TAAACTGGGCACGGGGTTTC
95331	93418	CTAAACTGGGCACGGGGTTT
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95337	93424	CGACTGCTAAACTGGGCACG
95338	93425	ACGACTGCTAAACTGGGCAC
95339	93426	AACGACTGCTAAACTGGGCA
95340	93427	GAACGACTGCTAAACTGGGC
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95342	93429	TGGAACGACTGCTAAACTGG
95343	93430	GTGGAACGACTGCTAAACTG
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95346	93433	AATGTGGAACGACTGCTAAA
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95349	93436	GCAAATGTGGAACGACTGCT
95350	93437	GGCAAATGTGGAACGACTGC
95351	93438	AGGCAAATGTGGAACGACTG
95352	93439	GAGGCAAATGTGGAACGACT
95353	93440	GGAGGCAAATGTGGAACGAC
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95355	93442	CTGGAGGCAAATGTGGAACG
95356	93443	GCTGGAGGCAAATGTGGAAC
95357	93444	GGCTGGAGGCAAATGTGGAA
95358	93445	GGGCTGGAGGCAAATGTGGA
95359	93446	AGGGCTGGAGGCAAATGTGG
95360	93447	AAGGGCTGGAGGCAAATGTG
95361	93448	GAAGGGCTGGAGGCAAATGT

144438	142525	CGATGCGATACCTGGCACCT
144439	142526	ACGATGCGATACCTGGCACC
144440	142527	GACGATGCGATACCTGGCAC
144441	142528	TGACGATGCGATACCTGGCA
144442	142529	CTGACGATGCGATACCTGGC
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144446	142533	TGTTCTGACGATGCGATACC
144447	142534	GTGTTCTGACGATGCGATAC
144448	142535	TGTGTTCTGACGATGCGATA
144449	142536	ATGTGTTCTGACGATGCGAT
144450	142537	CATGTGTTCTGACGATGCGA
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144452	142539	GCCATGTGTTCTGACGATGC
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144455	142542	CATGCCATGTGTTCTGACGA
144456	142543	ACATGCCATGTGTTCTGACG
144457	142544	GACATGCCATGTGTTCTGAC
144458	142545	GGACATGCCATGTGTTCTGA
144459	142546	TGGACATGCCATGTGTTCTG
144460	142547	GTGGACATGCCATGTGTTCT
144461	142548	GGTGGACATGCCATGTGTTC
144462	142549	GGGTGGACATGCCATGTGTT
144463	142550	AGGGTGGACATGCCATGTGT
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144466	142553	ACGAGGGTGGACATGCCATG
144467	142554	CACGAGGGTGGACATGCCAT
144468	142555	TCACGAGGGTGGACATGCCA
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144472	142559	ATCTTCACGAGGGTGGACAT
144473	142560	CATCTTCACGAGGGTGGACA
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144475	142562	TCCATCTTCACGAGGGTGGA
144476	142563	ATCCATCTTCACGAGGGTGG
144477	142564	TATCCATCTTCACGAGGGTG
144478	142565	GTATCCATCTTCACGAGGGT
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144480	142567	CTGTATCCATCTTCACGAGG
144481	142568	GCTGTATCCATCTTCACGAG
144482	142569	AGCTGTATCCATCTTCACGA
144483	142570	CAGCTGTATCCATCTTCACG
144484	142571	ACAGCTGTATCCATCTTCAC
144485	142572	CACAGCTGTATCCATCTTCA
144486	142573	GCACAGCTGTATCCATCTTC
144487	142574	GGCACAGCTGTATCCATCTT
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144489	142576	GGGGCACAGCTGTATCCATC
144490	142577	AGGGGCACAGCTGTATCCAT
144491	142578	CAGGGGCACAGCTGTATCCA
144492	142579	CCAGGGGCACAGCTGTATCC
144493	142580	CCCAGGGGCACAGCTGTATC
144494	142581	CCCCAGGGGCACAGCTGTAT
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144498	142585	ACCACCCCAGGGGCACAGCT
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46222	44309	CCCCACCCAAATCTTATCTT
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46224	44311	GTCCCCACCCAAATCTTATC
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46271	44358	TACACGTGACAAAAATACTA
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46276	44363	GTTATTACACGTGACAAAAA
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95407	93494	CAGAAAGTAGATTAACGGTT
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95410	93497	AGACAGAAAGTAGATTAACG
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95413	93500	TAGAGACAGAAAGTAGATTA
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95416	93503	CCATAGAGACAGAAAGTAGA
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95419	93506	CATCCATAGAGACAGAAAGT
95420	93507	CCATCCATAGAGACAGAAAG
95421	93508	CCCATCCATAGAGACAGAAA
95422	93509	GCCCATCCATAGAGACAGAA
95423	93510	AGCCCATCCATAGAGACAGA
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95425	93512	TAAGCCCATCCATAGAGACA
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95427	93514	AATAAGCCCATCCATAGAGA
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144512	142599	TGATTCTTAAAACCACCACC
144513	142600	GTGATTCTTAAAACCACCAC
144514	142601	TGTGATTCTTAAAACCACCA
144515	142602	ATGTGATTCTTAAAACCACC
144516	142603	AATGTGATTCTTAAAACCAC
144517	142604	AAATGTGATTCTTAAAACCA
144518	142605	TAAATGTGATTCTTAAAACC
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144520	142607	TTTAAATGTGATTCTTAAAA
144521	142608	CTTTAAATGTGATTCTTAAA
144522	142609	CCTTTAAATGTGATTCTTAA
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144524	142611	AGCCTTTAAATGTGATTCTT
144525	142612	CAGCCTTTAAATGTGATTCT
144526	142613	CCAGCCTTTAAATGTGATTC
144527	142614	CCCAGCCTTTAAATGTGATT
144528	142615	GCCCAGCCTTTAAATGTGAT
144529	142616	CGCCCAGCCTTTAAATGTGA
144530	142617	GCGCCCAGCCTTTAAATGTG
144531	142618	TGCGCCCAGCCTTTAAATGT
144532	142619	CTGCGCCCAGCCTTTAAATG
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144534	142621	CACTGCGCCCAGCCTTTAAA
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144538	142625	GAGCCACTGCGCCCAGCCTT
144539	142626	TGAGCCACTGCGCCCAGCCT
144540	142627	GTGAGCCACTGCGCCCAGCC
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144543	142630	GGCGTGAGCCACTGCGCCCA
144544	142631	AGGCGTGAGCCACTGCGCCC
144545	142632	CAGGCGTGAGCCACTGCGCC
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144547	142634	TACAGGCGTGAGCCACTGCG
144548	142635	TTACAGGCGTGAGCCACTGC
144549	142636	ATTACAGGCGTGAGCCACTG
144550	142637	GATTACAGGCGTGAGCCACT
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144553	142640	TGGGATTACAGGCGTGAGCC
144554	142641	GTGGGATTACAGGCGTGAGC
144555	142642	GGTGGGATTACAGGCGTGAG
144556	142643	TGGTGGGATTACAGGCGTGA
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144558	142645	AGTGGTGGGATTACAGGCGT
144559	142646	AAGTGGTGGGATTACAGGCG
144560	142647	AAAGTGGTGGGATTACAGGC
144561	142648	CAAAGTGGTGGGATTACAGG
144562	142649	CCAAAGTGGTGGGATTACAG
144563	142650	CCCAAAGTGGTGGGATTACA
144564	142651	TCCCAAAGTGGTGGGATTAC
144565	142652	CTCCCAAAGTGGTGGGATTA
144566	142653	CCTCCCAAAGTGGTGGGATT
144567	142654	GCCTCCCAAAGTGGTGGGAT
144568	142655	GGCCTCCCAAAGTGGTGGGA
144569	142656	CGGCCTCCCAAAGTGGTGGG
144570	142657	TCGGCCTCCCAAAGTGGTGG
144571	142658	CTCGGCCTCCCAAAGTGGTG
144572	142659	CCTCGGCCTCCCAAAGTGGT
144573	142660	GCCTCGGCCTCCCAAAGTGG
144574	142661	CGCCTCGGCCTCCCAAAGTG
144575	142662	CCGCCTCGGCCTCCCAAAGT
144576	142663	CCCGCCTCGGCCTCCCAAAG
144577	142664	ACCCGCCTCGGCCTCCCAAA
144578	142665	CACCCGCCTCGGCCTCCCAA
144579	142666	CCACCCGCCTCGGCCTCCCA

46286	44373	ACTTGTTCTTGTTATTACAC
46287	44374	GACTTGTTCTTGTTATTACA
46288	44375	CGACTTGTTCTTGTTATTAC
46289	44376	GCGACTTGTTCTTGTTATTA
46290	44377	AGCGACTTGTTCTTGTTATT
46291	44378	AAGCGACTTGTTCTTGTTAT
46292	44379	CAAGCGACTTGTTCTTGTTA
46293	44380	ACAAGCGACTTGTTCTTGTT
46294	44381	AACAAGCGACTTGTTCTTGT
46295	44382	GAACAAGCGACTTGTTCTTG
46296	44383	AGAACAAGCGACTTGTTCTT
46297	44384	AAGAACAAGCGACTTGTTCT
46298	44385	AAAGAACAAGCGACTTGTTC
46299	44386	AAAAGAACAAGCGACTTGTT
46300	44387	GAAAAGAACAAGCGACTTGT
46301	44388	AGAAAAGAACAAGCGACTTG
46302	44389	TAGAAAAGAACAAGCGACTT
46303	44390	TTAGAAAAGAACAAGCGACT
46304	44391	TTTAGAAAAGAACAAGCGAC
46305	44392	ATTTAGAAAAGAACAAGCGA
46306	44393	CATTTAGAAAAGAACAAGCG
46307	44394	TCATTTAGAAAAGAACAAGC
46308	44395	GTCATTTAGAAAAGAACAAG
46309	44396	AGTCATTTAGAAAAGAACAA
46310	44397	TAGTCATTTAGAAAAGAACA
46311	44398	TTAGTCATTTAGAAAAGAAC
46312	44399	CTTAGTCATTTAGAAAAGAA
46313	44400	ACTTAGTCATTTAGAAAAGA
46314	44401	CACTTAGTCATTTAGAAAAG
46315	44402	GCACTTAGTCATTTAGAAAA
46316	44403	TGCACTTAGTCATTTAGAAA
46317	44404	TTGCACTTAGTCATTTAGAA
46318	44405	TTTGCACTTAGTCATTTAGA
46319	44406	ATTTGCACTTAGTCATTTAG
46320	44407	GATTTGCACTTAGTCATTTA
46321	44408	AGATTTGCACTTAGTCATTT
46322	44409	TAGATTTGCACTTAGTCATT
46323	44410	TTAGATTTGCACTTAGTCAT
46324	44411	CTTAGATTTGCACTTAGTCA
46325	44412	ACTTAGATTTGCACTTAGTC
46326	44413	CACTTAGATTTGCACTTAGT
46327	44414	TCACTTAGATTTGCACTTAG
46328	44415	TTCACTTAGATTTGCACTTA
46329	44416	TTTCACTTAGATTTGCACTT
46330	44417	TTTTCACTTAGATTTGCACT
46331	44418	TTTTTCACTTAGATTTGCAC
46332	44419	GTTTTTCACTTAGATTTGCA
46333	44420	GGTTTTTCACTTAGATTTGC
46334	44421	AGGTTTTTCACTTAGATTTG
46335	44422	GAGGTTTTTCACTTAGATTT
46336	44423	GGAGGTTTTTCACTTAGATT
46337	44424	TGGAGGTTTTTCACTTAGAT
46338	44425	TTGGAGGTTTTTCACTTAGA
46339	44426	TTTGGAGGTTTTTCACTTAG
46340	44427	TTTTGGAGGTTTTTCACTTA
46341	44428	CTTTTGGAGGTTTTTCACTT
46342	44429	TCTTTTGGAGGTTTTTCACT
46343	44430	ATCTTTTGGAGGTTTTTCAC
46344	44431	TATCTTTTGGAGGTTTTTCA
46345	44432	GTATCTTTTGGAGGTTTTTC
46346	44433	CGTATCTTTTGGAGGTTTTT
46347	44434	ACGTATCTTTTGGAGGTTTT
46348	44435	TACGTATCTTTTGGAGGTTT
46349	44436	CTACGTATCTTTTGGAGGTT
46350	44437	TCTACGTATCTTTTGGAGGT
46351	44438	TTCTACGTATCTTTTGGAGG
46352	44439	GTTCTACGTATCTTTTGGAG
46353	44440	TGTTCTACGTATCTTTTGGA
46354	44441	GTGTTCTACGTATCTTTTGG
46355	44442	GGTGTTCTACGTATCTTTTG
46356	44443	TGGTGTTCTACGTATCTTTT

95433	93520	GCCCCAAATAAGCCCATCCA
95434	93521	TGCCCCAAATAAGCCCATCC
95435	93522	TTGCCCCAAATAAGCCCATC
95436	93523	TTTGCCCCAAATAAGCCCAT
95437	93524	ATTTGCCCCAAATAAGCCCA
95438	93525	AATTTGCCCCAAATAAGCCC
95439	93526	GAATTTGCCCCAAATAAGCC
95440	93527	GGAATTTGCCCCAAATAAGC
95441	93528	TGGAATTTGCCCCAAATAAG
95442	93529	ATGGAATTTGCCCCAAATAA
95443	93530	AATGGAATTTGCCCCAAATA
95444	93531	AAATGGAATTTGCCCCAAAT
95445	93532	GAAATGGAATTTGCCCCAAA
95446	93533	TGAAATGGAATTTGCCCCAA
95447	93534	ATGAAATGGAATTTGCCCCA
95448	93535	TATGAAATGGAATTTGCCCC
95449	93536	GTATGAAATGGAATTTGCCC
95450	93537	TGTATGAAATGGAATTTGCC
95451	93538	TTGTATGAAATGGAATTTGC
95452	93539	TTTGTATGAAATGGAATTTG
95453	93540	ATTTGTATGAAATGGAATTT
95454	93541	CATTTGTATGAAATGGAATT
95455	93542	CCATTTGTATGAAATGGAAT
95456	93543	TCCATTTGTATGAAATGGAA
95457	93544	TTCCATTTGTATGAAATGGA
95458	93545	ATTCCATTTGTATGAAATGG
95459	93546	TATTCCATTTGTATGAAATG
95460	93547	TTATTCCATTTGTATGAAAT
95461	93548	ATTATTCCATTTGTATGAAA
95462	93549	TATTATTCCATTTGTATGAA
95463	93550	TTATTATTCCATTTGTATGA
95464	93551	TTTATTATTCCATTTGTATG
95465	93552	TTTTATTATTCCATTTGTAT
95466	93553	ATTTTATTATTCCATTTGTA
95467	93554	TATTTTATTATTCCATTTGT
95468	93555	ATATTTTATTATTCCATTTG
95469	93556	CATATTTTATTATTCCATTT
95470	93557	ACATATTTTATTATTCCATT
95471	93558	CACATATTTTATTATTCCAT
95472	93559	CCACATATTTTATTATTCCA
95473	93560	GCCACATATTTTATTATTCC
95474	93561	AGCCACATATTTTATTATTC
95475	93562	AAGCCACATATTTTATTATT
95476	93563	AAAGCCACATATTTTATTAT
95477	93564	AAAAGCCACATATTTTATTA
95478	93565	TAAAAGCCACATATTTTATT
95479	93566	ATAAAAGCCACATATTTTAT
95480	93567	CATAAAAGCCACATATTTTA
95481	93568	TCATAAAAGCCACATATTTT
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95483	93570	AGTCATAAAAGCCACATATT
95484	93571	CAGTCATAAAAGCCACATAT
95485	93572	CCAGTCATAAAAGCCACATA
95486	93573	GCCAGTCATAAAAGCCACAT
95487	93574	AGCCAGTCATAAAAGCCACA
95488	93575	AAGCCAGTCATAAAAGCCAC
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95491	93578	AAGAAGCCAGTCATAAAAGC
95492	93579	AAAGAAGCCAGTCATAAAAG
95493	93580	GAAAGAAGCCAGTCATAAAA
95494	93581	TGAAAGAAGCCAGTCATAAA
95495	93582	GTGAAAGAAGCCAGTCATAA
95496	93583	AGTGAAAGAAGCCAGTCATA
95497	93584	GAGTGAAAGAAGCCAGTCAT
95498	93585	TGAGTGAAAGAAGCCAGTCA
95499	93586	CTGAGTGAAAGAAGCCAGTC
95500	93587	TCTGAGTGAAAGAAGCCAGT
95501	93588	CTCTGAGTGAAAGAAGCCAG
95502	93589	ACTCTGAGTGAAAGAAGCCA
95503	93590	TACTCTGAGTGAAAGAAGCC

144580	142667	TCCACCCGCCTCGGCCTCCC
144581	142668	ATCCACCCGCCTCGGCCTCC
144582	142669	GATCCACCCGCCTCGGCCTC
144583	142670	TGATCCACCCGCCTCGGCCT
144584	142671	GTGATCCACCCGCCTCGGCC
144585	142672	CGTGATCCACCCGCCTCGGC
144586	142673	TCGTGATCCACCCGCCTCGG
144587	142674	CTCGTGATCCACCCGCCTCG
144588	142675	CCTCGTGATCCACCCGCCTC
144589	142676	ACCTCGTGATCCACCCGCCT
144590	142677	GACCTCGTGATCCACCCGCC
144591	142678	TGACCTCGTGATCCACCCGC
144592	142679	CTGACCTCGTGATCCACCCG
144593	142680	CCTGACCTCGTGATCCACCC
144594	142681	TCCTGACCTCGTGATCCACC
144595	142682	CTCCTGACCTCGTGATCCAC
144596	142683	TCTCCTGACCTCGTGATCCA
144597	142684	ATCTCCTGACCTCGTGATCC
144598	142685	AATCTCCTGACCTCGTGATC
144599	142686	CAATCTCCTGACCTCGTGAT
144600	142687	TCAATCTCCTGACCTCGTGA
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144606	142693	ATGGTCTCAATCTCCTGACC
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144609	142696	AGGATGGTCTCAATCTCCTG
144610	142697	CAGGATGGTCTCAATCTCCT
144611	142698	CCAGGATGGTCTCAATCTCC
144612	142699	GCCAGGATGGTCTCAATCTC
144613	142700	CGCCAGGATGGTCTCAATCT
144614	142701	TCGCCAGGATGGTCTCAATC
144615	142702	TTCGCCAGGATGGTCTCAAT
144616	142703	GTTCGCCAGGATGGTCTCAA
144617	142704	TGTTCGCCAGGATGGTCTCA
144618	142705	GTGTTCGCCAGGATGGTCTC
144619	142706	AGTGTTCGCCAGGATGGTCT
144620	142707	CAGTGTTCGCCAGGATGGTC
144621	142708	ACAGTGTTCGCCAGGATGGT
144622	142709	CACAGTGTTCGCCAGGATGG
144623	142710	TCACAGTGTTCGCCAGGATG
144624	142711	TTCACAGTGTTCGCCAGGAT
144625	142712	TTTCACAGTGTTCGCCAGGA
144626	142713	GTTTCACAGTGTTCGCCAGG
144627	142714	AGTTTCACAGTGTTCGCCAG
144628	142715	GAGTTTCACAGTGTTCGCCA
144629	142716	GGAGTTTCACAGTGTTCGCC
144630	142717	CGGAGTTTCACAGTGTTCGC
144631	142718	ACGGAGTTTCACAGTGTTCG
144632	142719	GACGGAGTTTCACAGTGTTC
144633	142720	AGACGGAGTTTCACAGTGTT
144634	142721	GAGACGGAGTTTCACAGTGT
144635	142722	AGAGACGGAGTTTCACAGTG
144636	142723	TAGAGACGGAGTTTCACAGT
144637	142724	TTAGAGACGGAGTTTCACAG
144638	142725	ATTAGAGACGGAGTTTCACA
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144640	142727	TTATTAGAGACGGAGTTTCA
144641	142728	TTTATTAGAGACGGAGTTTC
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144644	142731	ATTTTTATTAGAGACGGAGT
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144646	142733	GTATTTTTATTAGAGACGGA
144647	142734	TGTATTTTTATTAGAGACGG
144648	142735	TTGTATTTTTATTAGAGACG
144649	142736	TTTGTATTTTTATTAGAGAC
144650	142737	TTTTGTATTTTTATTAGAGA

46357	44444	TTGGTGTTCTACGTATCTTT
46358	44445	CTTGGTGTTCTACGTATCTT
46359	44446	TCTTGGTGTTCTACGTATCT
46360	44447	CTCTTGGTGTTCTACGTATC
46361	44448	ACTCTTGGTGTTCTACGTAT
46362	44449	CACTCTTGGTGTTCTACGTA
46363	44450	CCACTCTTGGTGTTCTACGT
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46365	44452	CTCCACTCTTGGTGTTCTAC
46366	44453	ACTCCACTCTTGGTGTTCTA
46367	44454	GACTCCACTCTTGGTGTTCT
46368	44455	AGACTCCACTCTTGGTGTTC
46369	44456	CAGACTCCACTCTTGGTGTT
46370	44457	GCAGACTCCACTCTTGGTGT
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46372	44459	CTGCAGACTCCACTCTTGGT
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46374	44461	CTCTGCAGACTCCACTCTTG
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46381	44468	TAAAGAACTCTGCAGACTCC
46382	44469	ATAAAGAACTCTGCAGACTC
46383	44470	CATAAAGAACTCTGCAGACT
46384	44471	GCATAAAGAACTCTGCAGAC
46385	44472	AGCATAAAGAACTCTGCAGA
46386	44473	AAGCATAAAGAACTCTGCAG
46387	44474	AAAGCATAAAGAACTCTGCA
46388	44475	AAAAGCATAAAGAACTCTGC
46389	44476	AAAAAGCATAAAGAACTCTG
46390	44477	TAAAAAGCATAAAGAACTCT
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46395	44482	CAAAATAAAAAGCATAAAGA
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46397	44484	TTCAAAATAAAAAGCATAAA
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46399	44486	AATTCAAAATAAAAAGCATA
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46402	44489	ATTAATTCAAAATAAAAAGC
46403	44490	CATTAATTCAAAATAAAAAG
46404	44491	ACATTAATTCAAAATAAAAA
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46406	44493	GCACATTAATTCAAAATAAA
46407	44494	AGCACATTAATTCAAAATAA
46408	44495	AAGCACATTAATTCAAAATA
46409	44496	AAAGCACATTAATTCAAAAT
46410	44497	AAAAGCACATTAATTCAAAA
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46412	44499	AAAAAAGCACATTAATTCAA
46413	44500	AAAAAAAGCACATTAATTCA
46414	44501	GAAAAAAAGCACATTAATTC
46415	44502	AGAAAAAAAGCACATTAATT
46416	44503	CAGAAAAAAAGCACATTAAT
46417	44504	GCAGAAAAAAAGCACATTAA
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46421	44508	AGCAGCAGAAAAAAAGCACA
46422	44509	AAGCAGCAGAAAAAAAGCAC
46423	44510	AAAGCAGCAGAAAAAAAGCA
46424	44511	GAAAGCAGCAGAAAAAAAGC
46425	44512	TGAAAGCAGCAGAAAAAAAG
46426	44513	ATGAAAGCAGCAGAAAAAAA
46427	44514	AATGAAAGCAGCAGAAAAAA

95504	93591	CTACTCTGAGTGAAAGAAGC
95505	93592	ACTACTCTGAGTGAAAGAAG
95506	93593	CACTACTCTGAGTGAAAGAA
95507	93594	ACACTACTCTGAGTGAAAGA
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95511	93598	TATAACACTACTCTGAGTGA
95512	93599	TTATAACACTACTCTGAGTG
95513	93600	TTTATAACACTACTCTGAGT
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95518	93605	GAACTTTTATAACACTACTC
95519	93606	TGAACTTTTATAACACTACT
95520	93607	ATGAACTTTTATAACACTAC
95521	93608	GATGAACTTTTATAACACTA
95522	93609	GGATGAACTTTTATAACACT
95523	93610	TGGATGAACTTTTATAACAC
95524	93611	ATGGATGAACTTTTATAACA
95525	93612	CATGGATGAACTTTTATAAC
95526	93613	ACATGGATGAACTTTTATAA
95527	93614	AACATGGATGAACTTTTATA
95528	93615	CAACATGGATGAACTTTTAT
95529	93616	CCAACATGGATGAACTTTTA
95530	93617	TCCAACATGGATGAACTTTT
95531	93618	CTCCAACATGGATGAACTTT
95532	93619	GCTCCAACATGGATGAACTT
95533	93620	TGCTCCAACATGGATGAACT
95534	93621	ATGCTCCAACATGGATGAAC
95535	93622	CATGCTCCAACATGGATGAA
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95537	93624	AACATGCTCCAACATGGATG
95538	93625	AAACATGCTCCAACATGGAT
95539	93626	GAAACATGCTCCAACATGGA
95540	93627	TGAAACATGCTCCAACATGG
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95547	93634	GAAGTACTGAAACATGCTCC
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95551	93638	AAATGAAGTACTGAAACATG
95552	93639	GAAATGAAGTACTGAAACAT
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95554	93641	AAGAAATGAAGTACTGAAAC
95555	93642	AAAGAAATGAAGTACTGAAA
95556	93643	AAAAGAAATGAAGTACTGAA
95557	93644	AAAAAGAAATGAAGTACTGA
95558	93645	CAAAAAGAAATGAAGTACTG
95559	93646	ACAAAAAGAAATGAAGTACT
95560	93647	CACAAAAAGAAATGAAGTAC
95561	93648	TCACAAAAAGAAATGAAGTA
95562	93649	GTCACAAAAAGAAATGAAGT
95563	93650	AGTCACAAAAAGAAATGAAG
95564	93651	CAGTCACAAAAAGAAATGAA
95565	93652	TCAGTCACAAAAAGAAATGA
95566	93653	GTCAGTCACAAAAAGAAATG
95567	93654	AGTCAGTCACAAAAAGAAAT
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95570	93657	ATTAGTCAGTCACAAAAAGA
95571	93658	TATTAGTCAGTCACAAAAAG
95572	93659	ATATTAGTCAGTCACAAAAA
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144651	142738	TTTTTGTATTTTTATTAGAG
144652	142739	TTTTTTGTATTTTTATTAGA
144653	142740	TTTTTTTGTATTTTTATTAG
144654	142741	ATTTTTTTGTATTTTTATTA
144655	142742	AATTTTTTTGTATTTTTATT
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144657	142744	CTAATTTTTTTGTATTTTTA
144658	142745	GCTAATTTTTTTGTATTTTT
144659	142746	GGCTAATTTTTTTGTATTTT
144660	142747	CGGCTAATTTTTTTGTATTT
144661	142748	CCGGCTAATTTTTTTGTATT
144662	142749	CCCGGCTAATTTTTTTGTAT
144663	142750	GCCCGGCTAATTTTTTTGTA
144664	142751	CGCCCGGCTAATTTTTTTGT
144665	142752	ACGCCCGGCTAATTTTTTTG
144666	142753	CACGCCCGGCTAATTTTTTT
144667	142754	CCACGCCCGGCTAATTTTTT
144668	142755	ACCACGCCCGGCTAATTTTT
144669	142756	CACCACGCCCGGCTAATTTT
144670	142757	CCACCACGCCCGGCTAATTT
144671	142758	ACCACCACGCCCGGCTAATT
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144673	142760	CCACCACCACGCCCGGCTAA
144674	142761	CCCACCACCACGCCCGGCTA
144675	142762	GCCCACCACCACGCCCGGCT
144676	142763	CGCCCACCACCACGCCCGGC
144677	142764	GCGCCCACCACCACGCCCGG
144678	142765	GGCGCCCACCACCACGCCCG
144679	142766	AGGCGCCCACCACCACGCCC
144680	142767	CAGGCGCCCACCACCACGCC
144681	142768	ACAGGCGCCCACCACCACGC
144682	142769	TACAGGCGCCCACCACCACG
144683	142770	CTACAGGCGCCCACCACCAC
144684	142771	ACTACAGGCGCCCACCACCA
144685	142772	GACTACAGGCGCCCACCACC
144686	142773	GGACTACAGGCGCCCACCAC
144687	142774	GGGACTACAGGCGCCCACCA
144688	142775	TGGGACTACAGGCGCCCACC
144689	142776	CTGGGACTACAGGCGCCCAC
144690	142777	GCTGGGACTACAGGCGCCCA
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144692	142779	AAGCTGGGACTACAGGCGCC
144693	142780	GAAGCTGGGACTACAGGCGC
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144695	142782	GAGAAGCTGGGACTACAGGC
144696	142783	CGAGAAGCTGGGACTACAGG
144697	142784	CCGAGAAGCTGGGACTACAG
144698	142785	CCCGAGAAGCTGGGACTACA
144699	142786	TCCCGAGAAGCTGGGACTAC
144700	142787	CTCCCGAGAAGCTGGGACTA
144701	142788	CCTCCCGAGAAGCTGGGACT
144702	142789	GCCTCCCGAGAAGCTGGGAC
144703	142790	AGCCTCCCGAGAAGCTGGGA
144704	142791	CAGCCTCCCGAGAAGCTGGG
144705	142792	TCAGCCTCCCGAGAAGCTGG
144706	142793	CTCAGCCTCCCGAGAAGCTG
144707	142794	CCTCAGCCTCCCGAGAAGCT
144708	142795	TCCTCAGCCTCCCGAGAAGC
144709	142796	TTCCTCAGCCTCCCGAGAAG
144710	142797	CTTCCTCAGCCTCCCGAGAA
144711	142798	CCTTCCTCAGCCTCCCGAGA
144712	142799	TCCTTCCTCAGCCTCCCGAG
144713	142800	CTCCTTCCTCAGCCTCCCGA
144714	142801	TCTCCTTCCTCAGCCTCCCG
144715	142802	TTCTCCTTCCTCAGCCTCCC
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144717	142804	CATTCTCCTTCCTCAGCCTC
144718	142805	CCATTCTCCTTCCTCAGCCT
144719	142806	GCCATTCTCCTTCCTCAGCC
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46428	44515	AAATGAAAGCAGCAGAAAAA
46429	44516	AAAATGAAAGCAGCAGAAAA
46430	44517	AAAAATGAAAGCAGCAGAAA
46431	44518	GAAAAATGAAAGCAGCAGAA
46432	44519	AGAAAAATGAAAGCAGCAGA
46433	44520	GAGAAAAATGAAAGCAGCAG
46434	44521	GGAGAAAAATGAAAGCAGCA
46435	44522	AGGAGAAAAATGAAAGCAGC
46436	44523	AAGGAGAAAAATGAAAGCAG
46437	44524	AAAGGAGAAAAATGAAAGCA
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46439	44526	CCAAAGGAGAAAAATGAAAG
46440	44527	GCCAAAGGAGAAAAATGAAA
46441	44528	AGCCAAAGGAGAAAAATGAA
46442	44529	AAGCCAAAGGAGAAAAATGA
46443	44530	AAAGCCAAAGGAGAAAAATG
46444	44531	GAAAGCCAAAGGAGAAAAAT
46445	44532	AGAAAGCCAAAGGAGAAAAA
46446	44533	CAGAAAGCCAAAGGAGAAAA
46447	44534	CCAGAAAGCCAAAGGAGAAA
46448	44535	ACCAGAAAGCCAAAGGAGAA
46449	44536	GACCAGAAAGCCAAAGGAGA
46450	44537	AGACCAGAAAGCCAAAGGAG
46451	44538	AAGACCAGAAAGCCAAAGGA
46452	44539	TAAGACCAGAAAGCCAAAGG
46453	44540	TTAAGACCAGAAAGCCAAAG
46454	44541	TTTAAGACCAGAAAGCCAAA
46455	44542	ATTTAAGACCAGAAAGCCAA
46456	44543	AATTTAAGACCAGAAAGCCA
46457	44544	AAATTTAAGACCAGAAAGCC
46458	44545	AAAATTTAAGACCAGAAAGC
46459	44546	CAAAATTTAAGACCAGAAAG
46460	44547	CCAAAATTTAAGACCAGAAA
46461	44548	TCCAAAATTTAAGACCAGAA
46462	44549	TTCCAAAATTTAAGACCAGA
46463	44550	ATTCCAAAATTTAAGACCAG
46464	44551	CATTCCAAAATTTAAGACCA
46465	44552	ACATTCCAAAATTTAAGACC
46466	44553	AACATTCCAAAATTTAAGAC
46467	44554	TAACATTCCAAAATTTAAGA
46468	44555	ATAACATTCCAAAATTTAAG
46469	44556	GATAACATTCCAAAATTTAA
46470	44557	TGATAACATTCCAAAATTTA
46471	44558	TTGATAACATTCCAAAATTT
46472	44559	ATTGATAACATTCCAAAATT
46473	44560	CATTGATAACATTCCAAAAT
46474	44561	TCATTGATAACATTCCAAAA
46475	44562	TTCATTGATAACATTCCAAA
46476	44563	TTTCATTGATAACATTCCAA
46477	44564	ATTTCATTGATAACATTCCA
46478	44565	AATTTCATTGATAACATTCC
46479	44566	CAATTTCATTGATAACATTC
46480	44567	TCAATTTCATTGATAACATT
46481	44568	TTCAATTTCATTGATAACAT
46482	44569	GTTCAATTTCATTGATAACA
46483	44570	GGTTCAATTTCATTGATAAC
46484	44571	CGGTTCAATTTCATTGATAA
46485	44572	CCGGTTCAATTTCATTGATA
46486	44573	TCCGGTTCAATTTCATTGAT
46487	44574	GTCCGGTTCAATTTCATTGA
46488	44575	TGTCCGGTTCAATTTCATTG
46489	44576	ATGTCCGGTTCAATTTCATT
46490	44577	CATGTCCGGTTCAATTTCAT
46491	44578	TCATGTCCGGTTCAATTTCA
46492	44579	TTCATGTCCGGTTCAATTTC
46493	44580	CTTCATGTCCGGTTCAATTT
46494	44581	CCTTCATGTCCGGTTCAATT
46495	44582	CCCTTCATGTCCGGTTCAAT
46496	44583	GCCCTTCATGTCCGGTTCAA
46497	44584	TGCCCTTCATGTCCGGTTCA
46498	44585	CTGCCCTTCATGTCCGGTTC

95575	93662	GGAATATTAGTCAGTCACAA
95576	93663	AGGAATATTAGTCAGTCACA
95577	93664	AAGGAATATTAGTCAGTCAC
95578	93665	CAAGGAATATTAGTCAGTCA
95579	93666	TCAAGGAATATTAGTCAGTC
95580	93667	ATCAAGGAATATTAGTCAGT
95581	93668	CATCAAGGAATATTAGTCAG
95582	93669	ACATCAAGGAATATTAGTCA
95583	93670	CACATCAAGGAATATTAGTC
95584	93671	CCACATCAAGGAATATTAGT
95585	93672	TCCACATCAAGGAATATTAG
95586	93673	ATCCACATCAAGGAATATTA
95587	93674	TATCCACATCAAGGAATATT
95588	93675	TTATCCACATCAAGGAATAT
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95590	93677	TATTATCCACATCAAGGAAT
95591	93678	GTATTATCCACATCAAGGAA
95592	93679	GGTATTATCCACATCAAGGA
95593	93680	TGGTATTATCCACATCAAGG
95594	93681	GTGGTATTATCCACATCAAG
95595	93682	TGTGGTATTATCCACATCAA
95596	93683	ATGTGGTATTATCCACATCA
95597	93684	AATGTGGTATTATCCACATC
95598	93685	AAATGTGGTATTATCCACAT
95599	93686	AAAATGTGGTATTATCCACA
95600	93687	CAAAATGTGGTATTATCCAC
95601	93688	ACAAAATGTGGTATTATCCA
95602	93689	AACAAAATGTGGTATTATCC
95603	93690	AAACAAAATGTGGTATTATC
95604	93691	TAAACAAAATGTGGTATTAT
95605	93692	ATAAACAAAATGTGGTATTA
95606	93693	GATAAACAAAATGTGGTATT
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95608	93695	TGGATAAACAAAATGTGGTA
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95611	93698	TAATGGATAAACAAAATGTG
95612	93699	TTAATGGATAAACAAAATGT
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95614	93701	GATTAATGGATAAACAAAAT
95615	93702	TGATTAATGGATAAACAAAA
95616	93703	CTGATTAATGGATAAACAAA
95617	93704	ACTGATTAATGGATAAACAA
95618	93705	AACTGATTAATGGATAAACA
95619	93706	AAACTGATTAATGGATAAAC
95620	93707	CAAACTGATTAATGGATAAA
95621	93708	ACAAACTGATTAATGGATAA
95622	93709	TACAAACTGATTAATGGATA
95623	93710	CTACAAACTGATTAATGGAT
95624	93711	GCTACAAACTGATTAATGGA
95625	93712	AGCTACAAACTGATTAATGG
95626	93713	TAGCTACAAACTGATTAATG
95627	93714	ATAGCTACAAACTGATTAAT
95628	93715	AATAGCTACAAACTGATTAA
95629	93716	AAATAGCTACAAACTGATTA
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95632	93719	CACAAATAGCTACAAACTGA
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95634	93721	ACCACAAATAGCTACAAACT
95635	93722	CACCACAAATAGCTACAAAC
95636	93723	ACACCACAAATAGCTACAAA
95637	93724	AACACCACAAATAGCTACAA
95638	93725	GAACACCACAAATAGCTACA
95639	93726	AGAACACCACAAATAGCTAC
95640	93727	GAGAACACCACAAATAGCTA
95641	93728	TGAGAACACCACAAATAGCT
95642	93729	GTGAGAACACCACAAATAGC
95643	93730	AGTGAGAACACCACAAATAG
95644	93731	CAGTGAGAACACCACAAATA
95645	93732	ACAGTGAGAACACCACAAAT

144722	142809	CACGCCATTCTCCTTCCTCA
144723	142810	TCACGCCATTCTCCTTCCTC
144724	142811	TTCACGCCATTCTCCTTCCT
144725	142812	GTTCACGCCATTCTCCTTCC
144726	142813	GGTTCACGCCATTCTCCTTC
144727	142814	GGGTTCACGCCATTCTCCTT
144728	142815	CGGGTTCACGCCATTCTCCT
144729	142816	CCGGGTTCACGCCATTCTCC
144730	142817	CCCGGGTTCACGCCATTCTC
144731	142818	TCCCGGGTTCACGCCATTCT
144732	142819	CTCCCGGGTTCACGCCATTC
144733	142820	CCTCCCGGGTTCACGCCATT
144734	142821	GCCTCCCGGGTTCACGCCAT
144735	142822	CGCCTCCCGGGTTCACGCCA
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144741	142828	AAGCTCCGCCTCCCGGGTTC
144742	142829	CAAGCTCCGCCTCCCGGGTT
144743	142830	GCAAGCTCCGCCTCCCGGGT
144744	142831	TGCAAGCTCCGCCTCCCGGG
144745	142832	CTGCAAGCTCCGCCTCCCGG
144746	142833	ACTGCAAGCTCCGCCTCCCG
144747	142834	CACTGCAAGCTCCGCCTCCC
144748	142835	TCACTGCAAGCTCCGCCTCC
144749	142836	CTCACTGCAAGCTCCGCCTC
144750	142837	GCTCACTGCAAGCTCCGCCT
144751	142838	TGCTCACTGCAAGCTCCGCC
144752	142839	CTGCTCACTGCAAGCTCCGC
144753	142840	TCTGCTCACTGCAAGCTCCG
144754	142841	CTCTGCTCACTGCAAGCTCC
144755	142842	TCTCTGCTCACTGCAAGCTC
144756	142843	ATCTCTGCTCACTGCAAGCT
144757	142844	GATCTCTGCTCACTGCAAGC
144758	142845	CGATCTCTGCTCACTGCAAG
144759	142846	GCGATCTCTGCTCACTGCAA
144760	142847	CGCGATCTCTGCTCACTGCA
144761	142848	GCGCGATCTCTGCTCACTGC
144762	142849	GGCGCGATCTCTGCTCACTG
144763	142850	TGGCGCGATCTCTGCTCACT
144764	142851	GTGGCGCGATCTCTGCTCAC
144765	142852	AGTGGCGCGATCTCTGCTCA
144766	142853	CAGTGGCGCGATCTCTGCTC
144767	142854	GCAGTGGCGCGATCTCTGCT
144768	142855	TGCAGTGGCGCGATCTCTGC
144769	142856	GTGCAGTGGCGCGATCTCTG
144770	142857	AGTGCAGTGGCGCGATCTCT
144771	142858	GAGTGCAGTGGCGCGATCTC
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144774	142861	CTGGAGTGCAGTGGCGCGAT
144775	142862	GCTGGAGTGCAGTGGCGCGA
144776	142863	AGCTGGAGTGCAGTGGCGCG
144777	142864	AAGCTGGAGTGCAGTGGCGC
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144779	142866	CCAAGCTGGAGTGCAGTGGC
144780	142867	TCCAAGCTGGAGTGCAGTGG
144781	142868	GTCCAAGCTGGAGTGCAGTG
144782	142869	TGTCCAAGCTGGAGTGCAGT
144783	142870	TTGTCCAAGCTGGAGTGCAG
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144785	142872	TGTTGTCCAAGCTGGAGTGC
144786	142873	CTGTTGTCCAAGCTGGAGTG
144787	142874	GCTGTTGTCCAAGCTGGAGT
144788	142875	CGCTGTTGTCCAAGCTGGAG
144789	142876	TCGCTGTTGTCCAAGCTGGA
144790	142877	CTCGCTGTTGTCCAAGCTGG
144791	142878	TCTCGCTGTTGTCCAAGCTG
144792	142879	GTCTCGCTGTTGTCCAAGCT

46499	44586	TCTGCCCTTCATGTCCGGTT
46500	44587	TTCTGCCCTTCATGTCCGGT
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46502	44589	GTTTCTGCCCTTCATGTCCG
46503	44590	AGTTTCTGCCCTTCATGTCC
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46507	44594	TTATAGTTTCTGCCCTTCAT
46508	44595	CTTATAGTTTCTGCCCTTCA
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46516	44603	ATGTGGGACTTATAGTTTCT
46517	44604	CATGTGGGACTTATAGTTTC
46518	44605	TCATGTGGGACTTATAGTTT
46519	44606	ATCATGTGGGACTTATAGTT
46520	44607	CATCATGTGGGACTTATAGT
46521	44608	CCATCATGTGGGACTTATAG
46522	44609	TCCATCATGTGGGACTTATA
46523	44610	TTCCATCATGTGGGACTTAT
46524	44611	CTTCCATCATGTGGGACTTA
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46527	44614	TTTCTTCCATCATGTGGGAC
46528	44615	ATTTCTTCCATCATGTGGGA
46529	44616	TATTTCTTCCATCATGTGGG
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46531	44618	TTTATTTCTTCCATCATGTG
46532	44619	ATTTATTTCTTCCATCATGT
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46539	44626	GCTTCTCATTTATTTCTTCC
46540	44627	AGCTTCTCATTTATTTCTTC
46541	44628	TAGCTTCTCATTTATTTCTT
46542	44629	ATAGCTTCTCATTTATTTCT
46543	44630	GATAGCTTCTCATTTATTTC
46544	44631	TGATAGCTTCTCATTTATTT
46545	44632	GTGATAGCTTCTCATTTATT
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46548	44635	TTTGTGATAGCTTCTCATTT
46549	44636	ATTTGTGATAGCTTCTCATT
46550	44637	AATTTGTGATAGCTTCTCAT
46551	44638	AAATTTGTGATAGCTTCTCA
46552	44639	AAAATTTGTGATAGCTTCTC
46553	44640	AAAAATTTGTGATAGCTTCT
46554	44641	CAAAAATTTGTGATAGCTTC
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46558	44645	GTCTCAAAAATTTGTGATAG
46559	44646	AGTCTCAAAAATTTGTGATA
46560	44647	AAGTCTCAAAAATTTGTGAT
46561	44648	AAAGTCTCAAAAATTTGTGA
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46563	44650	GCAAAGTCTCAAAAATTTGT
46564	44651	GGCAAAGTCTCAAAAATTTG
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46566	44653	AAGGCAAAGTCTCAAAAATT
46567	44654	AAAGGCAAAGTCTCAAAAAT
46568	44655	TAAAGGCAAAGTCTCAAAAA
46569	44656	ATAAAGGCAAAGTCTCAAAA

95646	93733	AACAGTGAGAACACCACAAA
95647	93734	AAACAGTGAGAACACCACAA
95648	93735	CAAACAGTGAGAACACCACA
95649	93736	TCAAACAGTGAGAACACCAC
95650	93737	GTCAAACAGTGAGAACACCA
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95652	93739	TAGTCAAACAGTGAGAACAC
95653	93740	ATAGTCAAACAGTGAGAACA
95654	93741	AATAGTCAAACAGTGAGAAC
95655	93742	GAATAGTCAAACAGTGAGAA
95656	93743	AGAATAGTCAAACAGTGAGA
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95658	93745	TCAGAATAGTCAAACAGTGA
95659	93746	TTCAGAATAGTCAAACAGTG
95660	93747	ATTCAGAATAGTCAAACAGT
95661	93748	TATTCAGAATAGTCAAACAG
95662	93749	TTATTCAGAATAGTCAAACA
95663	93750	GTTATTCAGAATAGTCAAAC
95664	93751	TGTTATTCAGAATAGTCAAA
95665	93752	GTGTTATTCAGAATAGTCAA
95666	93753	AGTGTTATTCAGAATAGTCA
95667	93754	CAGTGTTATTCAGAATAGTC
95668	93755	GCAGTGTTATTCAGAATAGT
95669	93756	GGCAGTGTTATTCAGAATAG
95670	93757	TGGCAGTGTTATTCAGAATA
95671	93758	GTGGCAGTGTTATTCAGAAT
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95674	93761	TTTGTGGCAGTGTTATTCAG
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95676	93763	TGTTTGTGGCAGTGTTATTC
95677	93764	ATGTTTGTGGCAGTGTTATT
95678	93765	CATGTTTGTGGCAGTGTTAT
95679	93766	TCATGTTTGTGGCAGTGTTA
95680	93767	CTCATGTTTGTGGCAGTGTT
95681	93768	ACTCATGTTTGTGGCAGTGT
95682	93769	CACTCATGTTTGTGGCAGTG
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95684	93771	CACACTCATGTTTGTGGCAG
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95693	93780	AAAAAACTGCACACTCATGT
95694	93781	AAAAAAACTGCACACTCATG
95695	93782	GAAAAAAACTGCACACTCAT
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95701	93788	GGACGAGAAAAAAACTGCAC
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144793	142880	AGTCTCGCTGTTGTCCAAGC
144794	142881	GAGTCTCGCTGTTGTCCAAG
144795	142882	AGAGTCTCGCTGTTGTCCAA
144796	142883	CAGAGTCTCGCTGTTGTCCA
144797	142884	ACAGAGTCTCGCTGTTGTCC
144798	142885	GACAGAGTCTCGCTGTTGTC
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144800	142887	GAGACAGAGTCTCGCTGTTG
144801	142888	TGAGACAGAGTCTCGCTGTT
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144812	142899	TTTTATTTTTTTGAGACAGA
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144814	142901	TTTTTTATTTTTTTGAGACA
144815	142902	ATTTTTTATTTTTTTGAGAC
144816	142903	AATTTTTTATTTTTTTGAGA
144817	142904	TAATTTTTTATTTTTTTGAG
144818	142905	TTAATTTTTTATTTTTTTGA
144819	142906	TTTAATTTTTTATTTTTTTG
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144822	142909	TTTTTTAATTTTTTATTTTT
144823	142910	TTTTTTTAATTTTTTATTTT
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144825	142912	ATTTTTTTTAATTTTTTATT
144826	142913	GATTTTTTTTAATTTTTTAT
144827	142914	TGATTTTTTTTAATTTTTTA
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144829	142916	TGTGATTTTTTTTAATTTTT
144830	142917	ATGTGATTTTTTTTAATTTT
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144832	142919	AAATGTGATTTTTTTTAATT
144833	142920	TAAATGTGATTTTTTTTAAT
144834	142921	TTAAATGTGATTTTTTTTAA
144835	142922	CTTAAATGTGATTTTTTTTA
144836	142923	TCTTAAATGTGATTTTTTTT
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144838	142925	TATCTTAAATGTGATTTTTT
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144840	142927	TGTATCTTAAATGTGATTTT
144841	142928	ATGTATCTTAAATGTGATTT
144842	142929	CATGTATCTTAAATGTGATT
144843	142930	ACATGTATCTTAAATGTGAT
144844	142931	AACATGTATCTTAAATGTGA
144845	142932	CAACATGTATCTTAAATGTG
144846	142933	TCAACATGTATCTTAAATGT
144847	142934	ATCAACATGTATCTTAAATG
144848	142935	TATCAACATGTATCTTAAAT
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144859	142946	AATCACCTTATTATCAACAT
144860	142947	CAATCACCTTATTATCAACA
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46570	44657	AATAAAGGCAAAGTCTCAAA
46571	44658	TAATAAAGGCAAAGTCTCAA
46572	44659	CTAATAAAGGCAAAGTCTCA
46573	44660	TCTAATAAAGGCAAAGTCTC
46574	44661	ATCTAATAAAGGCAAAGTCT
46575	44662	AATCTAATAAAGGCAAAGTC
46576	44663	CAATCTAATAAAGGCAAAGT
46577	44664	ACAATCTAATAAAGGCAAAG
46578	44665	AACAATCTAATAAAGGCAAA
46579	44666	AAACAATCTAATAAAGGCAA
46580	44667	AAAACAATCTAATAAAGGCA
46581	44668	TAAAACAATCTAATAAAGGC
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46584	44671	TTGTAAAACAATCTAATAAA
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46586	44673	TCTTGTAAAACAATCTAATA
46587	44674	TTCTTGTAAAACAATCTAAT
46588	44675	ATTCTTGTAAAACAATCTAA
46589	44676	GATTCTTGTAAAACAATCTA
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46591	44678	CTGATTCTTGTAAAACAATC
46592	44679	CCTGATTCTTGTAAAACAAT
46593	44680	TCCTGATTCTTGTAAAACAA
46594	44681	TTCCTGATTCTTGTAAAACA
46595	44682	CTTCCTGATTCTTGTAAAAC
46596	44683	TCTTCCTGATTCTTGTAAAA
46597	44684	ATCTTCCTGATTCTTGTAAA
46598	44685	TATCTTCCTGATTCTTGTAA
46599	44686	ATATCTTCCTGATTCTTGTA
46600	44687	TATATCTTCCTGATTCTTGT
46601	44688	GTATATCTTCCTGATTCTTG
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46603	44690	GTGTATATCTTCCTGATTCT
46604	44691	CGTGTATATCTTCCTGATTC
46605	44692	ACGTGTATATCTTCCTGATT
46606	44693	TACGTGTATATCTTCCTGAT
46607	44694	ATACGTGTATATCTTCCTGA
46608	44695	TATACGTGTATATCTTCCTG
46609	44696	ATATACGTGTATATCTTCCT
46610	44697	CATATACGTGTATATCTTCC
46611	44698	CCATATACGTGTATATCTTC
46612	44699	ACCATATACGTGTATATCTT
46613	44700	TACCATATACGTGTATATCT
46614	44701	CTACCATATACGTGTATATC
46615	44702	ACTACCATATACGTGTATAT
46616	44703	TACTACCATATACGTGTATA
46617	44704	TTACTACCATATACGTGTAT
46618	44705	ATTACTACCATATACGTGTA
46619	44706	TATTACTACCATATACGTGT
46620	44707	ATATTACTACCATATACGTG
46621	44708	CATATTACTACCATATACGT
46622	44709	CCATATTACTACCATATACG
46623	44710	TCCATATTACTACCATATAC
46624	44711	CTCCATATTACTACCATATA
46625	44712	ACTCCATATTACTACCATAT
46626	44713	TACTCCATATTACTACCATA
46627	44714	CTACTCCATATTACTACCAT
46628	44715	ACTACTCCATATTACTACCA
46629	44716	CACTACTCCATATTACTACC
46630	44717	ACACTACTCCATATTACTAC
46631	44718	CACACTACTCCATATTACTA
46632	44719	CCACACTACTCCATATTACT
46633	44720	ACCACACTACTCCATATTAC
46634	44721	AACCACACTACTCCATATTA
46635	44722	CAACCACACTACTCCATATT
46636	44723	TCAACCACACTACTCCATAT
46637	44724	ATCAACCACACTACTCCATA
46638	44725	GATCAACCACACTACTCCAT
46639	44726	TGATCAACCACACTACTCCA
46640	44727	CTGATCAACCACACTACTCC

95717	93804	AAGAAATGAAAAGATAGGAC
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95719	93806	AAAAGAAATGAAAAGATAGG
95720	93807	CAAAAGAAATGAAAAGATAG
95721	93808	ACAAAAGAAATGAAAAGATA
95722	93809	CACAAAAGAAATGAAAAGAT
95723	93810	ACACAAAAGAAATGAAAAGA
95724	93811	TACACAAAAGAAATGAAAAG
95725	93812	GTACACAAAAGAAATGAAAA
95726	93813	GGTACACAAAAGAAATGAAA
95727	93814	AGGTACACAAAAGAAATGAA
95728	93815	TAGGTACACAAAAGAAATGA
95729	93816	GTAGGTACACAAAAGAAATG
95730	93817	GGTAGGTACACAAAAGAAAT
95731	93818	AGGTAGGTACACAAAAGAAA
95732	93819	TAGGTAGGTACACAAAAGAA
95733	93820	CTAGGTAGGTACACAAAAGA
95734	93821	CCTAGGTAGGTACACAAAAG
95735	93822	TCCTAGGTAGGTACACAAAA
95736	93823	CTCCTAGGTAGGTACACAAA
95737	93824	ACTCCTAGGTAGGTACACAA
95738	93825	AACTCCTAGGTAGGTACACA
95739	93826	CAACTCCTAGGTAGGTACAC
95740	93827	TCAACTCCTAGGTAGGTACA
95741	93828	TTCAACTCCTAGGTAGGTAC
95742	93829	ATTCAACTCCTAGGTAGGTA
95743	93830	AATTCAACTCCTAGGTAGGT
95744	93831	CAATTCAACTCCTAGGTAGG
95745	93832	GCAATTCAACTCCTAGGTAG
95746	93833	AGCAATTCAACTCCTAGGTA
95747	93834	CAGCAATTCAACTCCTAGGT
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95749	93836	CCCAGCAATTCAACTCCTAG
95750	93837	ACCCAGCAATTCAACTCCTA
95751	93838	GACCCAGCAATTCAACTCCT
95752	93839	TGACCCAGCAATTCAACTCC
95753	93840	ATGACCCAGCAATTCAACTC
95754	93841	TATGACCCAGCAATTCAACT
95755	93842	ATATGACCCAGCAATTCAAC
95756	93843	CATATGACCCAGCAATTCAA
95757	93844	CCATATGACCCAGCAATTCA
95758	93845	GCCATATGACCCAGCAATTC
95759	93846	TGCCATATGACCCAGCAATT
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95761	93848	GTTGCCATATGACCCAGCAA
95762	93849	AGTTGCCATATGACCCAGCA
95763	93850	CAGTTGCCATATGACCCAGC
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95765	93852	CACAGTTGCCATATGACCCA
95766	93853	ACACAGTTGCCATATGACCC
95767	93854	AACACAGTTGCCATATGACC
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95769	93856	TAAACACAGTTGCCATATGA
95770	93857	TTAAACACAGTTGCCATATG
95771	93858	GTTAAACACAGTTGCCATAT
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95776	93863	AAAAGGTTAAACACAGTTGC
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95782	93869	TTCCTCAAAAGGTTAAACAC
95783	93870	GTTCCTCAAAAGGTTAAACA
95784	93871	AGTTCCTCAAAAGGTTAAAC
95785	93872	TAGTTCCTCAAAAGGTTAAA
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95787	93874	GGTAGTTCCTCAAAAGGTTA

144864	142951	TATCCAATCACCTTATTATC
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144867	142954	GCTTATCCAATCACCTTATT
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144870	142957	AGAGCTTATCCAATCACCTT
144871	142958	CAGAGCTTATCCAATCACCT
144872	142959	CCAGAGCTTATCCAATCACC
144873	142960	TCCAGAGCTTATCCAATCAC
144874	142961	TTCCAGAGCTTATCCAATCA
144875	142962	TTTCCAGAGCTTATCCAATC
144876	142963	GTTTCCAGAGCTTATCCAAT
144877	142964	AGTTTCCAGAGCTTATCCAA
144878	142965	AAGTTTCCAGAGCTTATCCA
144879	142966	CAAGTTTCCAGAGCTTATCC
144880	142967	GCAAGTTTCCAGAGCTTATC
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144882	142969	CTGCAAGTTTCCAGAGCTTA
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144890	142977	TTTCATTACTGCAAGTTTCC
144891	142978	TTTTCATTACTGCAAGTTTC
144892	142979	TTTTTCATTACTGCAAGTTT
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144896	142983	TTGATTTTTCATTACTGCAA
144897	142984	TTTGATTTTTCATTACTGCA
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144900	142987	AAATTTGATTTTTCATTACT
144901	142988	TAAATTTGATTTTTCATTAC
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144906	142993	TATGTTAAATTTGATTTTTC
144907	142994	TTATGTTAAATTTGATTTTT
144908	142995	TTTATGTTAAATTTGATTTT
144909	142996	CTTTATGTTAAATTTGATTT
144910	142997	ACTTTATGTTAAATTTGATT
144911	142998	AACTTTATGTTAAATTTGAT
144912	142999	GAACTTTATGTTAAATTTGA
144913	143000	TGAACTTTATGTTAAATTTG
144914	143001	ATGAACTTTATGTTAAATTT
144915	143002	TATGAACTTTATGTTAAATT
144916	143003	TTATGAACTTTATGTTAAAT
144917	143004	CTTATGAACTTTATGTTAAA
144918	143005	CCTTATGAACTTTATGTTAA
144919	143006	GCCTTATGAACTTTATGTTA
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144923	143010	ATTTGCCTTATGAACTTTAT
144924	143011	AATTTGCCTTATGAACTTTA
144925	143012	GAATTTGCCTTATGAACTTT
144926	143013	GGAATTTGCCTTATGAACTT
144927	143014	AGGAATTTGCCTTATGAACT
144928	143015	TAGGAATTTGCCTTATGAAC
144929	143016	ATAGGAATTTGCCTTATGAA
144930	143017	AATAGGAATTTGCCTTATGA
144931	143018	AAATAGGAATTTGCCTTATG
144932	143019	CAAATAGGAATTTGCCTTAT
144933	143020	GCAAATAGGAATTTGCCTTA
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46641	44728	TCTGATCAACCACACTACTC
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46644	44731	AAGTCTGATCAACCACACTA
46645	44732	TAAGTCTGATCAACCACACT
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46649	44736	TGCTTAAGTCTGATCAACCA
46650	44737	GTGCTTAAGTCTGATCAACC
46651	44738	AGTGCTTAAGTCTGATCAAC
46652	44739	CAGTGCTTAAGTCTGATCAA
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46686	44773	TGACTAGGTTCTCCCAGCAT
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46693	44780	AGAACCCTGACTAGGTTCTC
46694	44781	AAGAACCCTGACTAGGTTCT
46695	44782	GAAGAACCCTGACTAGGTTC
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46698	44785	ATAGAAGAACCCTGACTAGG
46699	44786	CATAGAAGAACCCTGACTAG
46700	44787	TCATAGAAGAACCCTGACTA
46701	44788	TTCATAGAAGAACCCTGACT
46702	44789	CTTCATAGAAGAACCCTGAC
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46707	44794	CATACCTTCATAGAAGAACC
46708	44795	TCATACCTTCATAGAAGAAC
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95788	93875	TGGTAGTTCCTCAAAAGGTT
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95794	93881	ATAGCTTGGTAGTTCCTCAA
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95798	93885	GCAAATAGCTTGGTAGTTCC
95799	93886	GGCAAATAGCTTGGTAGTTC
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95801	93888	TTGGCAAATAGCTTGGTAGT
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95806	93893	ATATCTTGGCAAATAGCTTG
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95810	93897	GTAGATATCTTGGCAAATAG
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95813	93900	AGTGTAGATATCTTGGCAAA
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95815	93902	ATAGTGTAGATATCTTGGCA
95816	93903	AATAGTGTAGATATCTTGGC
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95818	93905	AAAATAGTGTAGATATCTTG
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95853	93940	AAACAGAAACCCTCATACCC
95854	93941	GAAACAGAAACCCTCATACC
95855	93942	AGAAACAGAAACCCTCATAC
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144935	143022	AAGCAAATAGGAATTTGCCT
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144939	143026	TCCCAAGCAAATAGGAATTT
144940	143027	GTCCCAAGCAAATAGGAATT
144941	143028	AGTCCCAAGCAAATAGGAAT
144942	143029	AAGTCCCAAGCAAATAGGAA
144943	143030	AAAGTCCCAAGCAAATAGGA
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144948	143035	ATTAAAAAGTCCCAAGCAAA
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144959	143046	AAACCTTAGAAATTAAAAAG
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144961	143048	ATAAACCTTAGAAATTAAAA
144962	143049	CATAAACCTTAGAAATTAAA
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144964	143051	CACATAAACCTTAGAAATTA
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144969	143056	CTCATCACATAAACCTTAGA
144970	143057	CCTCATCACATAAACCTTAG
144971	143058	ACCTCATCACATAAACCTTA
144972	143059	AACCTCATCACATAAACCTT
144973	143060	TAACCTCATCACATAAACCT
144974	143061	ATAACCTCATCACATAAACC
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144976	143063	AAATAACCTCATCACATAAA
144977	143064	AAAATAACCTCATCACATAA
144978	143065	GAAAATAACCTCATCACATA
144979	143066	GGAAAATAACCTCATCACAT
144980	143067	AGGAAAATAACCTCATCACA
144981	143068	TAGGAAAATAACCTCATCAC
144982	143069	ATAGGAAAATAACCTCATCA
144983	143070	CATAGGAAAATAACCTCATC
144984	143071	TCATAGGAAAATAACCTCAT
144985	143072	CTCATAGGAAAATAACCTCA
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145001	143088	AACATAATTCAAGAAGCTCA
145002	143089	AAACATAATTCAAGAAGCTC
145003	143090	CAAACATAATTCAAGAAGCT
145004	143091	GCAAACATAATTCAAGAAGC
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46712	44799	CAGGTCATACCTTCATAGAA
46713	44800	CCAGGTCATACCTTCATAGA
46714	44801	GCCAGGTCATACCTTCATAG
46715	44802	AGCCAGGTCATACCTTCATA
46716	44803	AAGCCAGGTCATACCTTCAT
46717	44804	GAAGCCAGGTCATACCTTCA
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46720	44807	TAGGAAGCCAGGTCATACCT
46721	44808	GTAGGAAGCCAGGTCATACC
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46723	44810	GGGTAGGAAGCCAGGTCATA
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46725	44812	TGGGGTAGGAAGCCAGGTCA
46726	44813	ATGGGGTAGGAAGCCAGGTC
46727	44814	AATGGGGTAGGAAGCCAGGT
46728	44815	AAATGGGGTAGGAAGCCAGG
46729	44816	TAAATGGGGTAGGAAGCCAG
46730	44817	ATAAATGGGGTAGGAAGCCA
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46732	44819	AAATAAATGGGGTAGGAAGC
46733	44820	TAAATAAATGGGGTAGGAAG
46734	44821	ATAAATAAATGGGGTAGGAA
46735	44822	TATAAATAAATGGGGTAGGA
46736	44823	GTATAAATAAATGGGGTAGG
46737	44824	AGTATAAATAAATGGGGTAG
46738	44825	AAGTATAAATAAATGGGGTA
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46755	44842	GTACCCTAAGAAGGGTGAAG
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46758	44845	AATGTACCCTAAGAAGGGTG
46759	44846	AAATGTACCCTAAGAAGGGT
46760	44847	GAAATGTACCCTAAGAAGGG
46761	44848	AGAAATGTACCCTAAGAAGG
46762	44849	CAGAAATGTACCCTAAGAAG
46763	44850	ACAGAAATGTACCCTAAGAA
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46765	44852	TCACAGAAATGTACCCTAAG
46766	44853	CTCACAGAAATGTACCCTAA
46767	44854	ACTCACAGAAATGTACCCTA
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46769	44856	AAACTCACAGAAATGTACCC
46770	44857	AAAACTCACAGAAATGTACC
46771	44858	TAAAACTCACAGAAATGTAC
46772	44859	TTAAAACTCACAGAAATGTA
46773	44860	GTTAAAACTCACAGAAATGT
46774	44861	TGTTAAAACTCACAGAAATG
46775	44862	TTGTTAAAACTCACAGAAAT
46776	44863	ATTGTTAAAACTCACAGAAA
46777	44864	AATTGTTAAAACTCACAGAA
46778	44865	CAATTGTTAAAACTCACAGA
46779	44866	GCAATTGTTAAAACTCACAG
46780	44867	TGCAATTGTTAAAACTCACA
46781	44868	ATGCAATTGTTAAAACTCAC
46782	44869	TATGCAATTGTTAAAACTCA

95859	93946	GTGGAGAAACAGAAACCCTC
95860	93947	TGTGGAGAAACAGAAACCCT
95861	93948	ATGTGGAGAAACAGAAACCC
95862	93949	GATGTGGAGAAACAGAAACC
95863	93950	GGATGTGGAGAAACAGAAAC
95864	93951	AGGATGTGGAGAAACAGAAA
95865	93952	AAGGATGTGGAGAAACAGAA
95866	93953	CAAGGATGTGGAGAAACAGA
95867	93954	GCAAGGATGTGGAGAAACAG
95868	93955	AGCAAGGATGTGGAGAAACA
95869	93956	TAGCAAGGATGTGGAGAAAC
95870	93957	TTAGCAAGGATGTGGAGAAA
95871	93958	GTTAGCAAGGATGTGGAGAA
95872	93959	TGTTAGCAAGGATGTGGAGA
95873	93960	GTGTTAGCAAGGATGTGGAG
95874	93961	AGTGTTAGCAAGGATGTGGA
95875	93962	AAGTGTTAGCAAGGATGTGG
95876	93963	TAAGTGTTAGCAAGGATGTG
95877	93964	ATAAGTGTTAGCAAGGATGT
95878	93965	AATAAGTGTTAGCAAGGATG
95879	93966	CAATAAGTGTTAGCAAGGAT
95880	93967	ACAATAAGTGTTAGCAAGGA
95881	93968	GACAATAAGTGTTAGCAAGG
95882	93969	AGACAATAAGTGTTAGCAAG
95883	93970	AAGACAATAAGTGTTAGCAA
95884	93971	CAAGACAATAAGTGTTAGCA
95885	93972	ACAAGACAATAAGTGTTAGC
95886	93973	GACAAGACAATAAGTGTTAG
95887	93974	AGACAAGACAATAAGTGTTA
95888	93975	AAGACAAGACAATAAGTGTT
95889	93976	AAAGACAAGACAATAAGTGT
95890	93977	AAAAGACAAGACAATAAGTG
95891	93978	AAAAAGACAAGACAATAAGT
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95893	93980	CAAAAAAGACAAGACAATAA
95894	93981	TCAAAAAAGACAAGACAATA
95895	93982	ATCAAAAAAGACAAGACAAT
95896	93983	AATCAAAAAAGACAAGACAA
95897	93984	TAATCAAAAAAGACAAGACA
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95899	93986	TATAATCAAAAAAGACAAGA
95900	93987	CTATAATCAAAAAAGACAAG
95901	93988	ACTATAATCAAAAAAGACAA
95902	93989	GACTATAATCAAAAAAGACA
95903	93990	TGACTATAATCAAAAAAGAC
95904	93991	ATGACTATAATCAAAAAAGA
95905	93992	GATGACTATAATCAAAAAAG
95906	93993	GGATGACTATAATCAAAAAA
95907	93994	AGGATGACTATAATCAAAAA
95908	93995	AAGGATGACTATAATCAAAA
95909	93996	CAAGGATGACTATAATCAAA
95910	93997	ACAAGGATGACTATAATCAA
95911	93998	CACAAGGATGACTATAATCA
95912	93999	CCACAAGGATGACTATAATC
95913	94000	CCCACAAGGATGACTATAAT
95914	94001	ACCCACAAGGATGACTATAA
95915	94002	CACCCACAAGGATGACTATA
95916	94003	ACACCCACAAGGATGACTAT
95917	94004	CACACCCACAAGGATGACTA
95918	94005	TCACACCCACAAGGATGACT
95919	94006	TTCACACCCACAAGGATGAC
95920	94007	CTTCACACCCACAAGGATGA
95921	94008	ACTTCACACCCACAAGGATG
95922	94009	CACTTCACACCCACAAGGAT
95923	94010	ACACTTCACACCCACAAGGA
95924	94011	AACACTTCACACCCACAAGG
95925	94012	TAACACTTCACACCCACAAG
95926	94013	TTAACACTTCACACCCACAA
95927	94014	GTTAACACTTCACACCCACA
95928	94015	GGTTAACACTTCACACCCAC
95929	94016	AGGTTAACACTTCACACCCA

145006	143093	TAGCAAACATAATTCAAGAA
145007	143094	TTAGCAAACATAATTCAAGA
145008	143095	ATTAGCAAACATAATTCAAG
145009	143096	CATTAGCAAACATAATTCAA
145010	143097	CCATTAGCAAACATAATTCA
145011	143098	TCCATTAGCAAACATAATTC
145012	143099	CTCCATTAGCAAACATAATT
145013	143100	CCTCCATTAGCAAACATAAT
145014	143101	GCCTCCATTAGCAAACATAA
145015	143102	TGCCTCCATTAGCAAACATA
145016	143103	CTGCCTCCATTAGCAAACAT
145017	143104	ACTGCCTCCATTAGCAAACA
145018	143105	AACTGCCTCCATTAGCAAAC
145019	143106	TAACTGCCTCCATTAGCAAA
145020	143107	TTAACTGCCTCCATTAGCAA
145021	143108	TTTAACTGCCTCCATTAGCA
145022	143109	CTTTAACTGCCTCCATTAGC
145023	143110	TCTTTAACTGCCTCCATTAG
145024	143111	ATCTTTAACTGCCTCCATTA
145025	143112	CATCTTTAACTGCCTCCATT
145026	143113	ACATCTTTAACTGCCTCCAT
145027	143114	GACATCTTTAACTGCCTCCA
145028	143115	AGACATCTTTAACTGCCTCC
145029	143116	AAGACATCTTTAACTGCCTC
145030	143117	AAAGACATCTTTAACTGCCT
145031	143118	CAAAGACATCTTTAACTGCC
145032	143119	TCAAAGACATCTTTAACTGC
145033	143120	ATCAAAGACATCTTTAACTG
145034	143121	TATCAAAGACATCTTTAACT
145035	143122	ATATCAAAGACATCTTTAAC
145036	143123	GATATCAAAGACATCTTTAA
145037	143124	AGATATCAAAGACATCTTTA
145038	143125	TAGATATCAAAGACATCTTT
145039	143126	ATAGATATCAAAGACATCTT
145040	143127	GATAGATATCAAAGACATCT
145041	143128	TGATAGATATCAAAGACATC
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145043	143130	ACTGATAGATATCAAAGACA
145044	143131	AACTGATAGATATCAAAGAC
145045	143132	GAACTGATAGATATCAAAGA
145046	143133	GGAACTGATAGATATCAAAG
145047	143134	GGGAACTGATAGATATCAAA
145048	143135	AGGGAACTGATAGATATCAA
145049	143136	CAGGGAACTGATAGATATCA
145050	143137	CCAGGGAACTGATAGATATC
145051	143138	CCCAGGGAACTGATAGATAT
145052	143139	CCCCAGGGAACTGATAGATA
145053	143140	GCCCCAGGGAACTGATAGAT
145054	143141	TGCCCCAGGGAACTGATAGA
145055	143142	CTGCCCCAGGGAACTGATAG
145056	143143	ACTGCCCCAGGGAACTGATA
145057	143144	TACTGCCCCAGGGAACTGAT
145058	143145	CTACTGCCCCAGGGAACTGA
145059	143146	ACTACTGCCCCAGGGAACTG
145060	143147	GACTACTGCCCCAGGGAACT
145061	143148	AGACTACTGCCCCAGGGAAC
145062	143149	AAGACTACTGCCCCAGGGAA
145063	143150	AAAGACTACTGCCCCAGGGA
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145065	143152	AAAAAGACTACTGCCCCAGG
145066	143153	AAAAAAGACTACTGCCCCAG
145067	143154	CAAAAAAGACTACTGCCCCA
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145070	143157	AGTCAAAAAAGACTACTGCC
145071	143158	AAGTCAAAAAAGACTACTGC
145072	143159	AAAGTCAAAAAAGACTACTG
145073	143160	TAAAGTCAAAAAAGACTACT
145074	143161	CTAAAGTCAAAAAAGACTAC
145075	143162	ACTAAAGTCAAAAAAGACTA
145076	143163	TACTAAAGTCAAAAAAGACT

46783	44870	GTATGCAATTGTTAAAACTC
46784	44871	TGTATGCAATTGTTAAAACT
46785	44872	TTGTATGCAATTGTTAAAAC
46786	44873	ATTGTATGCAATTGTTAAAA
46787	44874	GATTGTATGCAATTGTTAAA
46788	44875	TGATTGTATGCAATTGTTAA
46789	44876	CTGATTGTATGCAATTGTTA
46790	44877	ACTGATTGTATGCAATTGTT
46791	44878	CACTGATTGTATGCAATTGT
46792	44879	ACACTGATTGTATGCAATTG
46793	44880	TACACTGATTGTATGCAATT
46794	44881	TTACACTGATTGTATGCAAT
46795	44882	GTTACACTGATTGTATGCAA
46796	44883	AGTTACACTGATTGTATGCA
46797	44884	TAGTTACACTGATTGTATGC
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46799	44886	GGTAGTTACACTGATTGTAT
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46802	44889	GGTGGTAGTTACACTGATTG
46803	44890	TGGTGGTAGTTACACTGATT
46804	44891	GTGGTGGTAGTTACACTGAT
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46808	44895	GATTGTGGTGGTAGTTACAC
46809	44896	TGATTGTGGTGGTAGTTACA
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46812	44899	ACTTGATTGTGGTGGTAGTT
46813	44900	AACTTGATTGTGGTGGTAGT
46814	44901	TAACTTGATTGTGGTGGTAG
46815	44902	TTAACTTGATTGTGGTGGTA
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46828	44915	TGAAACTGTTCTATTAACTT
46829	44916	ATGAAACTGTTCTATTAACT
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46835	44922	TGGGCAATGAAACTGTTCTA
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46841	44928	TTTTGGTGGGCAATGAAACT
46842	44929	ATTTTGGTGGGCAATGAAAC
46843	44930	GATTTTGGTGGGCAATGAAA
46844	44931	GGATTTTGGTGGGCAATGAA
46845	44932	GGGATTTTGGTGGGCAATGA
46846	44933	AGGGATTTTGGTGGGCAATG
46847	44934	GAGGGATTTTGGTGGGCAAT
46848	44935	TGAGGGATTTTGGTGGGCAA
46849	44936	TTGAGGGATTTTGGTGGGCA
46850	44937	TTTGAGGGATTTTGGTGGGC
46851	44938	ATTTGAGGGATTTTGGTGGG
46852	44939	GATTTGAGGGATTTTGGTGG
46853	44940	TGATTTGAGGGATTTTGGTG

95930	94017	GAGGTTAACACTTCACACCC
95931	94018	TGAGGTTAACACTTCACACC
95932	94019	ATGAGGTTAACACTTCACAC
95933	94020	AATGAGGTTAACACTTCACA
95934	94021	CAATGAGGTTAACACTTCAC
95935	94022	ACAATGAGGTTAACACTTCA
95936	94023	CACAATGAGGTTAACACTTC
95937	94024	CCACAATGAGGTTAACACTT
95938	94025	GCCACAATGAGGTTAACACT
95939	94026	AGCCACAATGAGGTTAACAC
95940	94027	AAGCCACAATGAGGTTAACA
95941	94028	AAAGCCACAATGAGGTTAAC
95942	94029	TAAAGCCACAATGAGGTTAA
95943	94030	TTAAAGCCACAATGAGGTTA
95944	94031	ATTAAAGCCACAATGAGGTT
95945	94032	CATTAAAGCCACAATGAGGT
95946	94033	ACATTAAAGCCACAATGAGG
95947	94034	CACATTAAAGCCACAATGAG
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95952	94039	AACTGCACATTAAAGCCACA
95953	94040	GAACTGCACATTAAAGCCAC
95954	94041	AGAACTGCACATTAAAGCCA
95955	94042	AAGAACTGCACATTAAAGCC
95956	94043	AAAGAACTGCACATTAAAGC
95957	94044	GAAAGAACTGCACATTAAAG
95958	94045	TGAAAGAACTGCACATTAAA
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95960	94047	CATGAAAGAACTGCACATTA
95961	94048	CCATGAAAGAACTGCACATT
95962	94049	GCCATGAAAGAACTGCACAT
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95969	94056	ATCATTAGCCATGAAAGAAC
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95971	94058	ACATCATTAGCCATGAAAGA
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95973	94060	CAACATCATTAGCCATGAAA
95974	94061	TCAACATCATTAGCCATGAA
95975	94062	TTCAACATCATTAGCCATGA
95976	94063	GTTCAACATCATTAGCCATG
95977	94064	TGTTCAACATCATTAGCCAT
95978	94065	ATGTTCAACATCATTAGCCA
95979	94066	GATGTTCAACATCATTAGCC
95980	94067	AGATGTTCAACATCATTAGC
95981	94068	AAGATGTTCAACATCATTAG
95982	94069	AAAGATGTTCAACATCATTA
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95987	94074	ACACAAAAGATGTTCAACAT
95988	94075	AACACAAAAGATGTTCAACA
95989	94076	AAACACAAAAGATGTTCAAC
95990	94077	TAAACACAAAAGATGTTCAA
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95992	94079	AATAAACACAAAAGATGTTC
95993	94080	CAATAAACACAAAAGATGTT
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95996	94083	GGCCAATAAACACAAAAGAT
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95998	94085	ATGGCCAATAAACACAAAAG
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96000	94087	AAATGGCCAATAAACACAAA

145077	143164	ATACTAAAGTCAAAAAAGAC
145078	143165	CATACTAAAGTCAAAAAAGA
145079	143166	ACATACTAAAGTCAAAAAAG
145080	143167	TACATACTAAAGTCAAAAAA
145081	143168	ATACATACTAAAGTCAAAAA
145082	143169	CATACATACTAAAGTCAAAA
145083	143170	GCATACATACTAAAGTCAAA
145084	143171	AGCATACATACTAAAGTCAA
145085	143172	GAGCATACATACTAAAGTCA
145086	143173	TGAGCATACATACTAAAGTC
145087	143174	CTGAGCATACATACTAAAGT
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145091	143178	ACTTCTGAGCATACATACTA
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145093	143180	AAACTTCTGAGCATACATAC
145094	143181	GAAACTTCTGAGCATACATA
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145098	143185	GTTAGAAACTTCTGAGCATA
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145100	143187	CAGTTAGAAACTTCTGAGCA
145101	143188	GCAGTTAGAAACTTCTGAGC
145102	143189	GGCAGTTAGAAACTTCTGAG
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145107	143194	AGTCTGGCAGTTAGAAACTT
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145118	143205	GCCTGATTCTCAGTCTGGCA
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145123	143210	CAGAAGCCTGATTCTCAGTC
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145126	143213	GTACAGAAGCCTGATTCTCA
145127	143214	GGTACAGAAGCCTGATTCTC
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145130	143217	TAGGGTACAGAAGCCTGATT
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145132	143219	TCTAGGGTACAGAAGCCTGA
145133	143220	TTCTAGGGTACAGAAGCCTG
145134	143221	TTTCTAGGGTACAGAAGCCT
145135	143222	CTTTCTAGGGTACAGAAGCC
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46854	44941	GTGATTTGAGGGATTTTGGT
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46859	44946	GAAAAGTGATTTGAGGGATT
46860	44947	TGAAAAGTGATTTGAGGGAT
46861	44948	CTGAAAAGTGATTTGAGGGA
46862	44949	ACTGAAAAGTGATTTGAGGG
46863	44950	CACTGAAAAGTGATTTGAGG
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46870	44957	GAGGGTTCACTGAAAAGTGA
46871	44958	GGAGGGTTCACTGAAAAGTG
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46880	44967	GGAGAGAGAGGAGGGTTCAC
46881	44968	TGGAGAGAGAGGAGGGTTCA
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46884	44971	GGTTGGAGAGAGAGGAGGGT
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46890	44977	ATCAATGGTTGGAGAGAGAG
46891	44978	AATCAATGGTTGGAGAGAGA
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46893	44980	CAAATCAATGGTTGGAGAGA
46894	44981	ACAAATCAATGGTTGGAGAG
46895	44982	GACAAATCAATGGTTGGAGA
46896	44983	AGACAAATCAATGGTTGGAG
46897	44984	AAGACAAATCAATGGTTGGA
46898	44985	GAAGACAAATCAATGGTTGG
46899	44986	GGAAGACAAATCAATGGTTG
46900	44987	TGGAAGACAAATCAATGGTT
46901	44988	ATGGAAGACAAATCAATGGT
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46906	44993	TAAGGATGGAAGACAAATCA
46907	44994	GTAAGGATGGAAGACAAATC
46908	44995	CGTAAGGATGGAAGACAAAT
46909	44996	CCGTAAGGATGGAAGACAAA
46910	44997	ACCGTAAGGATGGAAGACAA
46911	44998	AACCGTAAGGATGGAAGACA
46912	44999	AAACCGTAAGGATGGAAGAC
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46914	45001	ACAAACCGTAAGGATGGAAG
46915	45002	CACAAACCGTAAGGATGGAA
46916	45003	ACACAAACCGTAAGGATGGA
46917	45004	GACACAAACCGTAAGGATGG
46918	45005	GGACACAAACCGTAAGGATG
46919	45006	AGGACACAAACCGTAAGGAT
46920	45007	AAGGACACAAACCGTAAGGA
46921	45008	GAAGGACACAAACCGTAAGG
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46923	45010	AGGAAGGACACAAACCGTAA
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96001	94088	TAAATGGCCAATAAACACAA
96002	94089	ATAAATGGCCAATAAACACA
96003	94090	TATAAATGGCCAATAAACAC
96004	94091	ATATAAATGGCCAATAAACA
96005	94092	TATATAAATGGCCAATAAAC
96006	94093	ATATATAAATGGCCAATAAA
96007	94094	GATATATAAATGGCCAATAA
96008	94095	AGATATATAAATGGCCAATA
96009	94096	AAGATATATAAATGGCCAAT
96010	94097	GAAGATATATAAATGGCCAA
96011	94098	AGAAGATATATAAATGGCCA
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96015	94102	CCAAAGAAGATATATAAATG
96016	94103	TCCAAAGAAGATATATAAAT
96017	94104	ATCCAAAGAAGATATATAAA
96018	94105	AATCCAAAGAAGATATATAA
96019	94106	CAATCCAAAGAAGATATATA
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96021	94108	ATCAATCCAAAGAAGATATA
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96025	94112	AGACATCAATCCAAAGAAGA
96026	94113	CAGACATCAATCCAAAGAAG
96027	94114	ACAGACATCAATCCAAAGAA
96028	94115	AACAGACATCAATCCAAAGA
96029	94116	GAACAGACATCAATCCAAAG
96030	94117	TGAACAGACATCAATCCAAA
96031	94118	TTGAACAGACATCAATCCAA
96032	94119	TTTGAACAGACATCAATCCA
96033	94120	ATTTGAACAGACATCAATCC
96034	94121	GATTTGAACAGACATCAATC
96035	94122	AGATTTGAACAGACATCAAT
96036	94123	AAGATTTGAACAGACATCAA
96037	94124	AAAGATTTGAACAGACATCA
96038	94125	TAAAGATTTGAACAGACATC
96039	94126	GTAAAGATTTGAACAGACAT
96040	94127	GGTAAAGATTTGAACAGACA
96041	94128	GGGTAAAGATTTGAACAGAC
96042	94129	TGGGTAAAGATTTGAACAGA
96043	94130	ATGGGTAAAGATTTGAACAG
96044	94131	AATGGGTAAAGATTTGAACA
96045	94132	AAATGGGTAAAGATTTGAAC
96046	94133	AAAATGGGTAAAGATTTGAA
96047	94134	TAAAATGGGTAAAGATTTGA
96048	94135	TTAAAATGGGTAAAGATTTG
96049	94136	TTTAAAATGGGTAAAGATTT
96050	94137	TTTTAAAATGGGTAAAGATT
96051	94138	TTTTTAAAATGGGTAAAGAT
96052	94139	ATTTTTAAAATGGGTAAAGA
96053	94140	AATTTTTAAAATGGGTAAAG
96054	94141	CAATTTTTAAAATGGGTAAA
96055	94142	TCAATTTTTAAAATGGGTAA
96056	94143	CTCAATTTTTAAAATGGGTA
96057	94144	ACTCAATTTTTAAAATGGGT
96058	94145	AACTCAATTTTTAAAATGGG
96059	94146	CAACTCAATTTTTAAAATGG
96060	94147	ACAACTCAATTTTTAAAATG
96061	94148	GACAACTCAATTTTTAAAAT
96062	94149	AGACAACTCAATTTTTAAAA
96063	94150	AAGACAACTCAATTTTTAAA
96064	94151	AAAGACAACTCAATTTTTAA
96065	94152	AAAAGACAACTCAATTTTTA
96066	94153	AAAAAGACAACTCAATTTTT
96067	94154	TAAAAAGACAACTCAATTTT
96068	94155	ATAAAAAGACAACTCAATTT
96069	94156	AATAAAAAGACAACTCAATT
96070	94157	TAATAAAAAGACAACTCAAT
96071	94158	ATAATAAAAAGACAACTCAA

145148	143235	ATCTGGACAACTCCTTTCTA
145149	143236	CATCTGGACAACTCCTTTCT
145150	143237	CCATCTGGACAACTCCTTTC
145151	143238	CCCATCTGGACAACTCCTTT
145152	143239	TCCCATCTGGACAACTCCTT
145153	143240	CTCCCATCTGGACAACTCCT
145154	143241	CCTCCCATCTGGACAACTCC
145155	143242	GCCTCCCATCTGGACAACTC
145156	143243	TGCCTCCCATCTGGACAACT
145157	143244	GTGCCTCCCATCTGGACAAC
145158	143245	GGTGCCTCCCATCTGGACAA
145159	143246	AGGTGCCTCCCATCTGGACA
145160	143247	GAGGTGCCTCCCATCTGGAC
145161	143248	GGAGGTGCCTCCCATCTGGA
145162	143249	TGGAGGTGCCTCCCATCTGG
145163	143250	CTGGAGGTGCCTCCCATCTG
145164	143251	GCTGGAGGTGCCTCCCATCT
145165	143252	GGCTGGAGGTGCCTCCCATC
145166	143253	AGGCTGGAGGTGCCTCCCAT
145167	143254	AAGGCTGGAGGTGCCTCCCA
145168	143255	CAAGGCTGGAGGTGCCTCCC
145169	143256	GCAAGGCTGGAGGTGCCTCC
145170	143257	AGCAAGGCTGGAGGTGCCTC
145171	143258	GAGCAAGGCTGGAGGTGCCT
145172	143259	AGAGCAAGGCTGGAGGTGCC
145173	143260	AAGAGCAAGGCTGGAGGTGC
145174	143261	TAAGAGCAAGGCTGGAGGTG
145175	143262	GTAAGAGCAAGGCTGGAGGT
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145177	143264	TGGTAAGAGCAAGGCTGGAG
145178	143265	GTGGTAAGAGCAAGGCTGGA
145179	143266	GGTGGTAAGAGCAAGGCTGG
145180	143267	GGGTGGTAAGAGCAAGGCTG
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145182	143269	CAGGGTGGTAAGAGCAAGGC
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145184	143271	TACAGGGTGGTAAGAGCAAG
145185	143272	GTACAGGGTGGTAAGAGCAA
145186	143273	TGTACAGGGTGGTAAGAGCA
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145190	143277	AGAATGTACAGGGTGGTAAG
145191	143278	GAGAATGTACAGGGTGGTAA
145192	143279	GGAGAATGTACAGGGTGGTA
145193	143280	AGGAGAATGTACAGGGTGGT
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145209	143296	GGTCACTGGAAAGTACAGGA
145210	143297	GGGTCACTGGAAAGTACAGG
145211	143298	AGGGTCACTGGAAAGTACAG
145212	143299	GAGGGTCACTGGAAAGTACA
145213	143300	TGAGGGTCACTGGAAAGTAC
145214	143301	ATGAGGGTCACTGGAAAGTA
145215	143302	GATGAGGGTCACTGGAAAGT
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145217	143304	ATGATGAGGGTCACTGGAAA
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46925	45012	GGAGGAAGGACACAAACCGT
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46927	45014	GAGGAGGAAGGACACAAACC
46928	45015	AGAGGAGGAAGGACACAAAC
46929	45016	TAGAGGAGGAAGGACACAAA
46930	45017	ATAGAGGAGGAAGGACACAA
46931	45018	CATAGAGGAGGAAGGACACA
46932	45019	CCATAGAGGAGGAAGGACAC
46933	45020	TCCATAGAGGAGGAAGGACA
46934	45021	TTCCATAGAGGAGGAAGGAC
46935	45022	CTTCCATAGAGGAGGAAGGA
46936	45023	ACTTCCATAGAGGAGGAAGG
46937	45024	AACTTCCATAGAGGAGGAAG
46938	45025	AAACTTCCATAGAGGAGGAA
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46945	45032	CAAGAGTAAACTTCCATAGA
46946	45033	GCAAGAGTAAACTTCCATAG
46947	45034	AGCAAGAGTAAACTTCCATA
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46979	45066	TAATGGTGTTTTGACTAAAC
46980	45067	CTAATGGTGTTTTGACTAAA
46981	45068	ACTAATGGTGTTTTGACTAA
46982	45069	AACTAATGGTGTTTTGACTA
46983	45070	CAACTAATGGTGTTTTGACT
46984	45071	CCAACTAATGGTGTTTTGAC
46985	45072	ACCAACTAATGGTGTTTTGA
46986	45073	AACCAACTAATGGTGTTTTG
46987	45074	AAACCAACTAATGGTGTTTT
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46989	45076	TCAAACCAACTAATGGTGTT
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46995	45082	TATCAGTCAAACCAACTAAT

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96075	94162	CCCAATAATAAAAAGACAAC
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96079	94166	ACAACCCAATAATAAAAAGA
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96081	94168	CCACAACCCAATAATAAAAA
96082	94169	CCCACAACCCAATAATAAAA
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96085	94172	ACTCCCACAACCCAATAATA
96086	94173	AACTCCCACAACCCAATAAT
96087	94174	GAACTCCCACAACCCAATAA
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96089	94176	AAGAACTCCCACAACCCAAT
96090	94177	AAAGAACTCCCACAACCCAA
96091	94178	TAAAGAACTCCCACAACCCA
96092	94179	ATAAAGAACTCCCACAACCC
96093	94180	TATAAAGAACTCCCACAACC
96094	94181	ATATAAAGAACTCCCACAAC
96095	94182	TATATAAAGAACTCCCACAA
96096	94183	ATATATAAAGAACTCCCACA
96097	94184	AATATATAAAGAACTCCCAC
96098	94185	CAATATATAAAGAACTCCCA
96099	94186	ACAATATATAAAGAACTCCC
96100	94187	CACAATATATAAAGAACTCC
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96102	94189	CACACAATATATAAAGAACT
96103	94190	ACACACAATATATAAAGAAC
96104	94191	TACACACAATATATAAAGAA
96105	94192	GTACACACAATATATAAAGA
96106	94193	TGTACACACAATATATAAAG
96107	94194	TTGTACACACAATATATAAA
96108	94195	CTTGTACACACAATATATAA
96109	94196	ACTTGTACACACAATATATA
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96111	94198	GGACTTGTACACACAATATA
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96115	94202	ACAGGGACTTGTACACACAA
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96117	94204	TAACAGGGACTTGTACACAC
96118	94205	CTAACAGGGACTTGTACACA
96119	94206	TCTAACAGGGACTTGTACAC
96120	94207	ATCTAACAGGGACTTGTACA
96121	94208	TATCTAACAGGGACTTGTAC
96122	94209	GTATCTAACAGGGACTTGTA
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96126	94213	CCATGTATCTAACAGGGACT
96127	94214	ACCATGTATCTAACAGGGAC
96128	94215	AACCATGTATCTAACAGGGA
96129	94216	AAACCATGTATCTAACAGGG
96130	94217	CAAACCATGTATCTAACAGG
96131	94218	GCAAACCATGTATCTAACAG
96132	94219	TGCAAACCATGTATCTAACA
96133	94220	TTGCAAACCATGTATCTAAC
96134	94221	TTTGCAAACCATGTATCTAA
96135	94222	ATTTGCAAACCATGTATCTA
96136	94223	CATTTGCAAACCATGTATCT
96137	94224	ACATTTGCAAACCATGTATC
96138	94225	AACATTTGCAAACCATGTAT
96139	94226	AAACATTTGCAAACCATGTA
96140	94227	AAAACATTTGCAAACCATGT
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145219	143306	CTATGATGAGGGTCACTGGA
145220	143307	CCTATGATGAGGGTCACTGG
145221	143308	GCCTATGATGAGGGTCACTG
145222	143309	GGCCTATGATGAGGGTCACT
145223	143310	GGGCCTATGATGAGGGTCAC
145224	143311	TGGGCCTATGATGAGGGTCA
145225	143312	TTGGGCCTATGATGAGGGTC
145226	143313	CTTGGGCCTATGATGAGGGT
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145229	143316	ACACTTGGGCCTATGATGAG
145230	143317	CACACTTGGGCCTATGATGA
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145234	143321	TTTGCACACTTGGGCCTATG
145235	143322	CTTTGCACACTTGGGCCTAT
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145238	143325	AAGCTTTGCACACTTGGGCC
145239	143326	TAAGCTTTGCACACTTGGGC
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145245	143332	CAAAGCTAAGCTTTGCACAC
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145251	143338	TACCCACAAAGCTAAGCTTT
145252	143339	ATACCCACAAAGCTAAGCTT
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145254	143341	GGATACCCACAAAGCTAAGC
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145260	143347	GCCAAGGGATACCCACAAAG
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145267	143354	AAAAGCAGCCAAGGGATACC
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47000	45087	AGTGTTATCAGTCAAACCAA
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47002	45089	CAAGTGTTATCAGTCAAACC
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47004	45091	TTCAAGTGTTATCAGTCAAA
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47007	45094	GTTTTCAAGTGTTATCAGTC
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47010	45097	CAGGTTTTCAAGTGTTATCA
47011	45098	TCAGGTTTTCAAGTGTTATC
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47015	45102	AAGGTCAGGTTTTCAAGTGT
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47021	45108	GAACAGAAGGTCAGGTTTTC
47022	45109	GGAACAGAAGGTCAGGTTTT
47023	45110	AGGAACAGAAGGTCAGGTTT
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47032	45119	GAGAACAGAAGGAACAGAAG
47033	45120	AGAGAACAGAAGGAACAGAA
47034	45121	TAGAGAACAGAAGGAACAGA
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47036	45123	CATAGAGAACAGAAGGAACA
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47038	45125	TCCATAGAGAACAGAAGGAA
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47041	45128	GCTTCCATAGAGAACAGAAG
47042	45129	TGCTTCCATAGAGAACAGAA
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47046	45133	ATTTTGCTTCCATAGAGAAC
47047	45134	TATTTTGCTTCCATAGAGAA
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47059	45146	TTGTTTATTTAATATTTTGC
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47063	45150	GATTTTGTTTATTTAATATT
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96143	94230	GAGAAAACATTTGCAAACCA
96144	94231	GGAGAAAACATTTGCAAACC
96145	94232	AGGAGAAAACATTTGCAAAC
96146	94233	CAGGAGAAAACATTTGCAAA
96147	94234	ACAGGAGAAAACATTTGCAA
96148	94235	AACAGGAGAAAACATTTGCA
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96153	94240	AACAGAACAGGAGAAAACAT
96154	94241	CAACAGAACAGGAGAAAACA
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96156	94243	ACCAACAGAACAGGAGAAAA
96157	94244	AACCAACAGAACAGGAGAAA
96158	94245	CAACCAACAGAACAGGAGAA
96159	94246	ACAACCAACAGAACAGGAGA
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96167	94254	GTAAAAAGACAACCAACAGA
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96201	94288	AATTAAAAATTTTTGTGCTT
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96206	94293	ATCAAAATTAAAAATTTTTG
96207	94294	CATCAAAATTAAAAATTTTT
96208	94295	TCATCAAAATTAAAAATTTT
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96210	94297	CTTCATCAAAATTAAAAATT
96211	94298	ACTTCATCAAAATTAAAAAT
96212	94299	GACTTCATCAAAATTAAAAA
96213	94300	GGACTTCATCAAAATTAAAA

145290	143377	TTGAGAGGAAAACTTCTTTA
145291	143378	ATTGAGAGGAAAACTTCTTT
145292	143379	AATTGAGAGGAAAACTTCTT
145293	143380	GAATTGAGAGGAAAACTTCT
145294	143381	AGAATTGAGAGGAAAACTTC
145295	143382	AAGAATTGAGAGGAAAACTT
145296	143383	AAAGAATTGAGAGGAAAACT
145297	143384	GAAAGAATTGAGAGGAAAAC
145298	143385	GGAAAGAATTGAGAGGAAAA
145299	143386	AGGAAAGAATTGAGAGGAAA
145300	143387	CAGGAAAGAATTGAGAGGAA
145301	143388	ACAGGAAAGAATTGAGAGGA
145302	143389	GACAGGAAAGAATTGAGAGG
145303	143390	CGACAGGAAAGAATTGAGAG
145304	143391	GCGACAGGAAAGAATTGAGA
145305	143392	AGCGACAGGAAAGAATTGAG
145306	143393	AAGCGACAGGAAAGAATTGA
145307	143394	AAAGCGACAGGAAAGAATTG
145308	143395	CAAAGCGACAGGAAAGAATT
145309	143396	GCAAAGCGACAGGAAAGAAT
145310	143397	TGCAAAGCGACAGGAAAGAA
145311	143398	CTGCAAAGCGACAGGAAAGA
145312	143399	GCTGCAAAGCGACAGGAAAG
145313	143400	TGCTGCAAAGCGACAGGAAA
145314	143401	GTGCTGCAAAGCGACAGGAA
145315	143402	GGTGCTGCAAAGCGACAGGA
145316	143403	TGGTGCTGCAAAGCGACAGG
145317	143404	ATGGTGCTGCAAAGCGACAG
145318	143405	GATGGTGCTGCAAAGCGACA
145319	143406	TGATGGTGCTGCAAAGCGAC
145320	143407	CTGATGGTGCTGCAAAGCGA
145321	143408	GCTGATGGTGCTGCAAAGCG
145322	143409	TGCTGATGGTGCTGCAAAGC
145323	143410	GTGCTGATGGTGCTGCAAAG
145324	143411	GGTGCTGATGGTGCTGCAAA
145325	143412	TGGTGCTGATGGTGCTGCAA
145326	143413	CTGGTGCTGATGGTGCTGCA
145327	143414	CCTGGTGCTGATGGTGCTGC
145328	143415	GCCTGGTGCTGATGGTGCTG
145329	143416	GGCCTGGTGCTGATGGTGCT
145330	143417	CGGCCTGGTGCTGATGGTGC
145331	143418	GCGGCCTGGTGCTGATGGTG
145332	143419	GGCGGCCTGGTGCTGATGGT
145333	143420	GGGCGGCCTGGTGCTGATGG
145334	143421	TGGGCGGCCTGGTGCTGATG
145335	143422	CTGGGCGGCCTGGTGCTGAT
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145337	143424	GCCTGGGCGGCCTGGTGCTG
145338	143425	AGCCTGGGCGGCCTGGTGCT
145339	143426	GAGCCTGGGCGGCCTGGTGC
145340	143427	AGAGCCTGGGCGGCCTGGTG
145341	143428	GAGAGCCTGGGCGGCCTGGT
145342	143429	GGAGAGCCTGGGCGGCCTGG
145343	143430	TGGAGAGCCTGGGCGGCCTG
145344	143431	ATGGAGAGCCTGGGCGGCCT
145345	143432	GATGGAGAGCCTGGGCGGCC
145346	143433	AGATGGAGAGCCTGGGCGGC
145347	143434	CAGATGGAGAGCCTGGGCGG
145348	143435	CCAGATGGAGAGCCTGGGCG
145349	143436	GCCAGATGGAGAGCCTGGGC
145350	143437	GGCCAGATGGAGAGCCTGGG
145351	143438	TGGCCAGATGGAGAGCCTGG
145352	143439	CTGGCCAGATGGAGAGCCTG
145353	143440	ACTGGCCAGATGGAGAGCCT
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145355	143442	GGACTGGCCAGATGGAGAGC
145356	143443	TGGACTGGCCAGATGGAGAG
145357	143444	GTGGACTGGCCAGATGGAGA
145358	143445	TGTGGACTGGCCAGATGGAG
145359	143446	CTGTGGACTGGCCAGATGGA
145360	143447	GCTGTGGACTGGCCAGATGG

47067	45154	GGAAGATTTTGTTTATTTAA
47068	45155	GGGAAGATTTTGTTTATTTA
47069	45156	AGGGAAGATTTTGTTTATTT
47070	45157	AAGGGAAGATTTTGTTTATT
47071	45158	TAAGGGAAGATTTTGTTTAT
47072	45159	TTAAGGGAAGATTTTGTTTA
47073	45160	ATTAAGGGAAGATTTTGTTT
47074	45161	TATTAAGGGAAGATTTTGTT
47075	45162	GTATTAAGGGAAGATTTTGT
47076	45163	TGTATTAAGGGAAGATTTTG
47077	45164	ATGTATTAAGGGAAGATTTT
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47081	45168	TTACATGTATTAAGGGAAGA
47082	45169	CTTACATGTATTAAGGGAAG
47083	45170	TCTTACATGTATTAAGGGAA
47084	45171	ATCTTACATGTATTAAGGGA
47085	45172	TATCTTACATGTATTAAGGG
47086	45173	ATATCTTACATGTATTAAGG
47087	45174	GATATCTTACATGTATTAAG
47088	45175	TGATATCTTACATGTATTAA
47089	45176	ATGATATCTTACATGTATTA
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47094	45181	GGTTTATGATATCTTACATG
47095	45182	AGGTTTATGATATCTTACAT
47096	45183	TAGGTTTATGATATCTTACA
47097	45184	TTAGGTTTATGATATCTTAC
47098	45185	GTTAGGTTTATGATATCTTA
47099	45186	AGTTAGGTTTATGATATCTT
47100	45187	TAGTTAGGTTTATGATATCT
47101	45188	TTAGTTAGGTTTATGATATC
47102	45189	TTTAGTTAGGTTTATGATAT
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47104	45191	TGTTTAGTTAGGTTTATGAT
47105	45192	ATGTTTAGTTAGGTTTATGA
47106	45193	AATGTTTAGTTAGGTTTATG
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47108	45195	AAAATGTTTAGTTAGGTTTA
47109	45196	CAAAATGTTTAGTTAGGTTT
47110	45197	GCAAAATGTTTAGTTAGGTT
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47112	45199	TTGCAAAATGTTTAGTTAGG
47113	45200	GTTGCAAAATGTTTAGTTAG
47114	45201	TGTTGCAAAATGTTTAGTTA
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47116	45203	TTTGTTGCAAAATGTTTAGT
47117	45204	ATTTGTTGCAAAATGTTTAG
47118	45205	TATTTGTTGCAAAATGTTTA
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47130	45217	GCTAACGTTTATTATTTGTT
47131	45218	AGCTAACGTTTATTATTTGT
47132	45219	AAGCTAACGTTTATTATTTG
47133	45220	AAAGCTAACGTTTATTATTT
47134	45221	TAAAGCTAACGTTTATTATT
47135	45222	ATAAAGCTAACGTTTATTAT
47136	45223	TATAAAGCTAACGTTTATTA
47137	45224	ATATAAAGCTAACGTTTATT

96214	94301	TGGACTTCATCAAAATTAAA
96215	94302	TTGGACTTCATCAAAATTAA
96216	94303	ATTGGACTTCATCAAAATTA
96217	94304	AATTGGACTTCATCAAAATT
96218	94305	AAATTGGACTTCATCAAAAT
96219	94306	TAAATTGGACTTCATCAAAA
96220	94307	ATAAATTGGACTTCATCAAA
96221	94308	GATAAATTGGACTTCATCAA
96222	94309	AGATAAATTGGACTTCATCA
96223	94310	CAGATAAATTGGACTTCATC
96224	94311	TCAGATAAATTGGACTTCAT
96225	94312	ATCAGATAAATTGGACTTCA
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96227	94314	AAATCAGATAAATTGGACTT
96228	94315	AAAATCAGATAAATTGGACT
96229	94316	CAAAATCAGATAAATTGGAC
96230	94317	TCAAAATCAGATAAATTGGA
96231	94318	TTCAAAATCAGATAAATTGG
96232	94319	CTTCAAAATCAGATAAATTG
96233	94320	ACTTCAAAATCAGATAAATT
96234	94321	TACTTCAAAATCAGATAAAT
96235	94322	TTACTTCAAAATCAGATAAA
96236	94323	CTTACTTCAAAATCAGATAA
96237	94324	GCTTACTTCAAAATCAGATA
96238	94325	AGCTTACTTCAAAATCAGAT
96239	94326	AAGCTTACTTCAAAATCAGA
96240	94327	AAAGCTTACTTCAAAATCAG
96241	94328	AAAAGCTTACTTCAAAATCA
96242	94329	CAAAAGCTTACTTCAAAATC
96243	94330	CCAAAAGCTTACTTCAAAAT
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96250	94337	TACGACACCAAAAGCTTACT
96251	94338	ATACGACACCAAAAGCTTAC
96252	94339	GATACGACACCAAAAGCTTA
96253	94340	AGATACGACACCAAAAGCTT
96254	94341	TAGATACGACACCAAAAGCT
96255	94342	TTAGATACGACACCAAAAGC
96256	94343	CTTAGATACGACACCAAAAG
96257	94344	TCTTAGATACGACACCAAAA
96258	94345	TTCTTAGATACGACACCAAA
96259	94346	TTTCTTAGATACGACACCAA
96260	94347	TTTTCTTAGATACGACACCA
96261	94348	ATTTTCTTAGATACGACACC
96262	94349	TATTTTCTTAGATACGACAC
96263	94350	GTATTTTCTTAGATACGACA
96264	94351	AGTATTTTCTTAGATACGAC
96265	94352	CAGTATTTTCTTAGATACGA
96266	94353	ACAGTATTTTCTTAGATACG
96267	94354	AACAGTATTTTCTTAGATAC
96268	94355	AAACAGTATTTTCTTAGATA
96269	94356	GAAACAGTATTTTCTTAGAT
96270	94357	TGAAACAGTATTTTCTTAGA
96271	94358	ATGAAACAGTATTTTCTTAG
96272	94359	GATGAAACAGTATTTTCTTA
96273	94360	TGATGAAACAGTATTTTCTT
96274	94361	TTGATGAAACAGTATTTTCT
96275	94362	ATTGATGAAACAGTATTTTC
96276	94363	GATTGATGAAACAGTATTTT
96277	94364	TGATTGATGAAACAGTATTT
96278	94365	ATGATTGATGAAACAGTATT
96279	94366	AATGATTGATGAAACAGTAT
96280	94367	TAATGATTGATGAAACAGTA
96281	94368	TTAATGATTGATGAAACAGT
96282	94369	CTTAATGATTGATGAAACAG
96283	94370	CCTTAATGATTGATGAAACA
96284	94371	ACCTTAATGATTGATGAAAC

145361	143448	TGCTGTGGACTGGCCAGATG
145362	143449	CTGCTGTGGACTGGCCAGAT
145363	143450	GCTGCTGTGGACTGGCCAGA
145364	143451	TGCTGCTGTGGACTGGCCAG
145365	143452	CTGCTGCTGTGGACTGGCCA
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145367	143454	GACTGCTGCTGTGGACTGGC
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145371	143458	GGCTGACTGCTGCTGTGGAC
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145374	143461	AATGGCTGACTGCTGCTGTG
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145376	143463	TAAATGGCTGACTGCTGCTG
145377	143464	GTAAATGGCTGACTGCTGCT
145378	143465	GGTAAATGGCTGACTGCTGC
145379	143466	TGGTAAATGGCTGACTGCTG
145380	143467	GTGGTAAATGGCTGACTGCT
145381	143468	CGTGGTAAATGGCTGACTGC
145382	143469	GCGTGGTAAATGGCTGACTG
145383	143470	CGCGTGGTAAATGGCTGACT
145384	143471	CCGCGTGGTAAATGGCTGAC
145385	143472	CCCGCGTGGTAAATGGCTGA
145386	143473	CCCCGCGTGGTAAATGGCTG
145387	143474	GCCCCGCGTGGTAAATGGCT
145388	143475	AGCCCCGCGTGGTAAATGGC
145389	143476	AAGCCCCGCGTGGTAAATGG
145390	143477	CAAGCCCCGCGTGGTAAATG
145391	143478	GCAAGCCCCGCGTGGTAAAT
145392	143479	CGCAAGCCCCGCGTGGTAAA
145393	143480	GCGCAAGCCCCGCGTGGTAA
145394	143481	GGCGCAAGCCCCGCGTGGTA
145395	143482	TGGCGCAAGCCCCGCGTGGT
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145397	143484	GTTGGCGCAAGCCCCGCGTG
145398	143485	AGTTGGCGCAAGCCCCGCGT
145399	143486	GAGTTGGCGCAAGCCCCGCG
145400	143487	GGAGTTGGCGCAAGCCCCGC
145401	143488	TGGAGTTGGCGCAAGCCCCG
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145407	143494	GGAGGGTGGAGTTGGCGCAA
145408	143495	TGGAGGGTGGAGTTGGCGCA
145409	143496	ATGGAGGGTGGAGTTGGCGC
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145412	143499	GTCATGGAGGGTGGAGTTGG
145413	143500	TGTCATGGAGGGTGGAGTTG
145414	143501	GTGTCATGGAGGGTGGAGTT
145415	143502	GGTGTCATGGAGGGTGGAGT
145416	143503	AGGTGTCATGGAGGGTGGAG
145417	143504	CAGGTGTCATGGAGGGTGGA
145418	143505	GCAGGTGTCATGGAGGGTGG
145419	143506	GGCAGGTGTCATGGAGGGTG
145420	143507	AGGCAGGTGTCATGGAGGGT
145421	143508	GAGGCAGGTGTCATGGAGGG
145422	143509	GGAGGCAGGTGTCATGGAGG
145423	143510	TGGAGGCAGGTGTCATGGAG
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145425	143512	GTTGGAGGCAGGTGTCATGG
145426	143513	TGTTGGAGGCAGGTGTCATG
145427	143514	GTGTTGGAGGCAGGTGTCAT
145428	143515	CGTGTTGGAGGCAGGTGTCA
145429	143516	GCGTGTTGGAGGCAGGTGTC
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47138	45225	CATATAAAGCTAACGTTTAT
47139	45226	GCATATAAAGCTAACGTTTA
47140	45227	TGCATATAAAGCTAACGTTT
47141	45228	TTGCATATAAAGCTAACGTT
47142	45229	TTTGCATATAAAGCTAACGT
47143	45230	ATTTGCATATAAAGCTAACG
47144	45231	CATTTGCATATAAAGCTAAC
47145	45232	ACATTTGCATATAAAGCTAA
47146	45233	TACATTTGCATATAAAGCTA
47147	45234	TTACATTTGCATATAAAGCT
47148	45235	TTTACATTTGCATATAAAGC
47149	45236	ATTTACATTTGCATATAAAG
47150	45237	TATTTACATTTGCATATAAA
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47152	45239	TGTATTTACATTTGCATATA
47153	45240	CTGTATTTACATTTGCATAT
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47155	45242	GCCTGTATTTACATTTGCAT
47156	45243	AGCCTGTATTTACATTTGCA
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47159	45246	CTCAGCCTGTATTTACATTT
47160	45247	GCTCAGCCTGTATTTACATT
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47171	45258	CGATTAGGGATGCTCAGCCT
47172	45259	CCGATTAGGGATGCTCAGCC
47173	45260	TCCGATTAGGGATGCTCAGC
47174	45261	TTCCGATTAGGGATGCTCAG
47175	45262	TTTCCGATTAGGGATGCTCA
47176	45263	ATTTCCGATTAGGGATGCTC
47177	45264	CATTTCCGATTAGGGATGCT
47178	45265	GCATTTCCGATTAGGGATGC
47179	45266	AGCATTTCCGATTAGGGATG
47180	45267	GAGCATTTCCGATTAGGGAT
47181	45268	GGAGCATTTCCGATTAGGGA
47182	45269	TGGAGCATTTCCGATTAGGG
47183	45270	TTGGAGCATTTCCGATTAGG
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47186	45273	ATTTTGGAGCATTTCCGATT
47187	45274	AATTTTGGAGCATTTCCGAT
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47189	45276	GAAATTTTGGAGCATTTCCG
47190	45277	TGAAATTTTGGAGCATTTCC
47191	45278	ATGAAATTTTGGAGCATTTC
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47205	45292	CCCTAATTCAAAATATGAAA
47206	45293	TCCCTAATTCAAAATATGAA
47207	45294	ATCCCTAATTCAAAATATGA
47208	45295	CATCCCTAATTCAAAATATG

96285	94372	AACCTTAATGATTGATGAAA
96286	94373	AAACCTTAATGATTGATGAA
96287	94374	TAAACCTTAATGATTGATGA
96288	94375	ATAAACCTTAATGATTGATG
96289	94376	AATAAACCTTAATGATTGAT
96290	94377	TAATAAACCTTAATGATTGA
96291	94378	GTAATAAACCTTAATGATTG
96292	94379	AGTAATAAACCTTAATGATT
96293	94380	GAGTAATAAACCTTAATGAT
96294	94381	AGAGTAATAAACCTTAATGA
96295	94382	AAGAGTAATAAACCTTAATG
96296	94383	GAAGAGTAATAAACCTTAAT
96297	94384	AGAAGAGTAATAAACCTTAA
96298	94385	CAGAAGAGTAATAAACCTTA
96299	94386	CCAGAAGAGTAATAAACCTT
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96301	94388	ACCCAGAAGAGTAATAAACC
96302	94389	AACCCAGAAGAGTAATAAAC
96303	94390	AAACCCAGAAGAGTAATAAA
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96305	94392	AAAAACCCAGAAGAGTAATA
96306	94393	AAAAAACCCAGAAGAGTAAT
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96308	94395	TAAAAAAACCCAGAAGAGTA
96309	94396	TTAAAAAAACCCAGAAGAGT
96310	94397	CTTAAAAAAAACCCAGAAGAG
96311	94398	TCTTAAAAAAAACCCAGAAGA
96312	94399	TTCTTAAAAAAAACCCAGAAG
96313	94400	ATTCTTAAAAAAACCCAGAA
96314	94401	AATTCTTAAAAAAACCCAGA
96315	94402	TAATTCTTAAAAAAACCCAG
96316	94403	GTAATTCTTAAAAAAACCCA
96317	94404	TGTAATTCTTAAAAAAACCC
96318	94405	ATGTAATTCTTAAAAAAACC
96319	94406	AATGTAATTCTTAAAAAAAC
96320	94407	AAATGTAATTCTTAAAAAAA
96321	94408	TAAATGTAATTCTTAAAAAA
96322	94409	CTAAATGTAATTCTTAAAAA
96323	94410	TCTAAATGTAATTCTTAAAA
96324	94411	CTCTAAATGTAATTCTTAAA
96325	94412	CCTCTAAATGTAATTCTTAA
96326	94413	ACCTCTAAATGTAATTCTTA
96327	94414	CACCTCTAAATGTAATTCTT
96328	94415	ACACCTCTAAATGTAATTCT
96329	94416	CACACCTCTAAATGTAATTC
96330	94417	TCACACCTCTAAATGTAATT
96331	94418	ATCACACCTCTAAATGTAAT
96332	94419	GATCACACCTCTAAATGTAA
96333	94420	GGATCACACCTCTAAATGTA
96334	94421	TGGATCACACCTCTAAATGT
96335	94422	ATGGATCACACCTCTAAATG
96336	94423	AATGGATCACACCTCTAAAT
96337	94424	AAATGGATCACACCTCTAAA
96338	94425	CAAATGGATCACACCTCTAA
96339	94426	CCAAATGGATCACACCTCTA
96340	94427	TCCAAATGGATCACACCTCT
96341	94428	CTCCAAATGGATCACACCTC
96342	94429	GCTCCAAATGGATCACACCT
96343	94430	TGCTCCAAATGGATCACACC
96344	94431	TTGCTCCAAATGGATCACAC
96345	94432	GTTGCTCCAAATGGATCACA
96346	94433	AGTTGCTCCAAATGGATCAC
96347	94434	AAGTTGCTCCAAATGGATCA
96348	94435	AAAGTTGCTCCAAATGGATC
96349	94436	AAAAGTTGCTCCAAATGGAT
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96351	94438	AAAAAAGTTGCTCCAAATGG
96352	94439	AAAAAAAGTTGCTCCAAATG
96353	94440	AAAAAAAAGTTGCTCCAAAT
96354	94441	AAAAAAAAAGTTGCTCCAAA
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145432	143519	ACTGCGTGTTGGAGGCAGGT
145433	143520	GACTGCGTGTTGGAGGCAGG
145434	143521	CGACTGCGTGTTGGAGGCAG
145435	143522	GCGACTGCGTGTTGGAGGCA
145436	143523	GGCGACTGCGTGTTGGAGGC
145437	143524	TGGCGACTGCGTGTTGGAGG
145438	143525	GTGGCGACTGCGTGTTGGAG
145439	143526	TGTGGCGACTGCGTGTTGGA
145440	143527	CTGTGGCGACTGCGTGTTGG
145441	143528	TCTGTGGCGACTGCGTGTTG
145442	143529	TTCTGTGGCGACTGCGTGTT
145443	143530	ATTCTGTGGCGACTGCGTGT
145444	143531	TATTCTGTGGCGACTGCGTG
145445	143532	CTATTCTGTGGCGACTGCGT
145446	143533	ACTATTCTGTGGCGACTGCG
145447	143534	AACTATTCTGTGGCGACTGC
145448	143535	AAACTATTCTGTGGCGACTG
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145450	143537	GGAAACTATTCTGTGGCGAC
145451	143538	GGGAAACTATTCTGTGGCGA
145452	143539	TGGGAAACTATTCTGTGGCG
145453	143540	CTGGGAAACTATTCTGTGGC
145454	143541	GCTGGGAAACTATTCTGTGG
145455	143542	TGCTGGGAAACTATTCTGTG
145456	143543	CTGCTGGGAAACTATTCTGT
145457	143544	GCTGCTGGGAAACTATTCTG
145458	143545	TGCTGCTGGGAAACTATTCT
145459	143546	GTGCTGCTGGGAAACTATTC
145460	143547	TGTGCTGCTGGGAAACTATT
145461	143548	TTGTGCTGCTGGGAAACTAT
145462	143549	GTTGTGCTGCTGGGAAACTA
145463	143550	TGTTGTGCTGCTGGGAAACT
145464	143551	CTGTTGTGCTGCTGGGAAAC
145465	143552	TCTGTTGTGCTGCTGGGAAA
145466	143553	GTCTGTTGTGCTGCTGGGAA
145467	143554	AGTCTGTTGTGCTGCTGGGA
145468	143555	CAGTCTGTTGTGCTGCTGGG
145469	143556	ACAGTCTGTTGTGCTGCTGG
145470	143557	GACAGTCTGTTGTGCTGCTG
145471	143558	AGACAGTCTGTTGTGCTGCT
145472	143559	AAGACAGTCTGTTGTGCTGC
145473	143560	AAAGACAGTCTGTTGTGCTG
145474	143561	TAAAGACAGTCTGTTGTGCT
145475	143562	GTAAAGACAGTCTGTTGTGC
145476	143563	CGTAAAGACAGTCTGTTGTG
145477	143564	TCGTAAAGACAGTCTGTTGT
145478	143565	ATCGTAAAGACAGTCTGTTG
145479	143566	GATCGTAAAGACAGTCTGTT
145480	143567	GGATCGTAAAGACAGTCTGT
145481	143568	TGGATCGTAAAGACAGTCTG
145482	143569	ATGGATCGTAAAGACAGTCT
145483	143570	GATGGATCGTAAAGACAGTC
145484	143571	GGATGGATCGTAAAGACAGT
145485	143572	AGGATGGATCGTAAAGACAG
145486	143573	AAGGATGGATCGTAAAGACA
145487	143574	GAAGGATGGATCGTAAAGAC
145488	143575	AGAAGGATGGATCGTAAAGA
145489	143576	GAGAAGGATGGATCGTAAAG
145490	143577	TGAGAAGGATGGATCGTAAA
145491	143578	GTGAGAAGGATGGATCGTAA
145492	143579	CGTGAGAAGGATGGATCGTA
145493	143580	ACGTGAGAAGGATGGATCGT
145494	143581	AACGTGAGAAGGATGGATCG
145495	143582	GAACGTGAGAAGGATGGATC
145496	143583	TGAACGTGAGAAGGATGGAT
145497	143584	CTGAACGTGAGAAGGATGGA
145498	143585	GCTGAACGTGAGAAGGATGG
145499	143586	GGCTGAACGTGAGAAGGATG
145500	143587	CGGCTGAACGTGAGAAGGAT
145501	143588	CCGGCTGAACGTGAGAAGGA
145502	143589	GCCGGCTGAACGTGAGAAGG

47209	45296	ACATCCCTAATTCAAAATAT
47210	45297	AACATCCCTAATTCAAAATA
47211	45298	GAACATCCCTAATTCAAAAT
47212	45299	TGAACATCCCTAATTCAAAA
47213	45300	TTGAACATCCCTAATTCAAA
47214	45301	CTTGAACATCCCTAATTCAA
47215	45302	GCTTGAACATCCCTAATTCA
47216	45303	TGCTTGAACATCCCTAATTC
47217	45304	GTGCTTGAACATCCCTAATT
47218	45305	AGTGCTTGAACATCCCTAAT
47219	45306	TAGTGCTTGAACATCCCTAA
47220	45307	TTAGTGCTTGAACATCCCTA
47221	45308	CTTAGTGCTTGAACATCCCT
47222	45309	ACTTAGTGCTTGAACATCCC
47223	45310	TACTTAGTGCTTGAACATCC
47224	45311	ATACTTAGTGCTTGAACATC
47225	45312	TATACTTAGTGCTTGAACAT
47226	45313	TTATACTTAGTGCTTGAACA
47227	45314	ATTATACTTAGTGCTTGAAC
47228	45315	CATTATACTTAGTGCTTGAA
47229	45316	GCATTATACTTAGTGCTTGA
47230	45317	TGCATTATACTTAGTGCTTG
47231	45318	TTGCATTATACTTAGTGCTT
47232	45319	TTTGCATTATACTTAGTGCT
47233	45320	ATTTGCATTATACTTAGTGC
47234	45321	TATTTGCATTATACTTAGTG
47235	45322	ATATTTGCATTATACTTAGT
47236	45323	GATATTTGCATTATACTTAG
47237	45324	GGATATTTGCATTATACTTA
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47239	45326	GGGGATATTTGCATTATACT
47240	45327	TGGGGATATTTGCATTATAC
47241	45328	TTGGGGATATTTGCATTATA
47242	45329	TTTGGGGATATTTGCATTAT
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47244	45331	GATTTGGGGATATTTGCATT
47245	45332	GGATTTGGGGATATTTGCAT
47246	45333	CGGATTTGGGGATATTTGCA
47247	45334	TCGGATTTGGGGATATTTGC
47248	45335	TTCGGATTTGGGGATATTTG
47249	45336	TTTCGGATTTGGGGATATTT
47250	45337	TTTTCGGATTTGGGGATATT
47251	45338	TTTTTCGGATTTGGGGATAT
47252	45339	TTTTTTCGGATTTGGGGATA
47253	45340	TTTTTTTCGGATTTGGGGAT
47254	45341	ATTTTTTTCGGATTTGGGGA
47255	45342	GATTTTTTTCGGATTTGGGG
47256	45343	GGATTTTTTTCGGATTTGGG
47257	45344	CGGATTTTTTTCGGATTTGG
47258	45345	GCGGATTTTTTTCGGATTTG
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47260	45347	CTGCGGATTTTTTTCGGATT
47261	45348	ACTGCGGATTTTTTTCGGAT
47262	45349	GACTGCGGATTTTTTTCGGA
47263	45350	AGACTGCGGATTTTTTTCGG
47264	45351	TAGACTGCGGATTTTTTTCG
47265	45352	TTAGACTGCGGATTTTTTTC
47266	45353	TTTAGACTGCGGATTTTTTT
47267	45354	TTTTAGACTGCGGATTTTTT
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47269	45356	TATTTTAGACTGCGGATTTT
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47271	45358	AGTATTTTAGACTGCGGATT
47272	45359	AAGTATTTTAGACTGCGGAT
47273	45360	GAAGTATTTTAGACTGCGGA
47274	45361	AGAAGTATTTTAGACTGCGG
47275	45362	CAGAAGTATTTTAGACTGCG
47276	45363	CCAGAAGTATTTTAGACTGC
47277	45364	ACCAGAAGTATTTTAGACTG
47278	45365	GACCAGAAGTATTTTAGACT
47279	45366	GGACCAGAAGTATTTTAGAC

96356	94443	AGAAAAAAAAAGTTGCTCCA
96357	94444	AAGAAAAAAAAAGTTGCTCC
96358	94445	AAAGAAAAAAAAAGTTGCTC
96359	94446	AAAAGAAAAAAAAAGTTGCT
96360	94447	CAAAAGAAAAAAAAAGTTGC
96361	94448	TCAAAAGAAAAAAAAAGTTG
96362	94449	GTCAAAAGAAAAAAAAAGTT
96363	94450	TGTCAAAAGAAAAAAAAAGT
96364	94451	GTGTCAAAAGAAAAAAAAAG
96365	94452	TGTGTCAAAAGAAAAAAAAA
96366	94453	CTGTGTCAAAAGAAAAAAAA
96367	94454	TCTGTGTCAAAAGAAAAAAA
96368	94455	TTCTGTGTCAAAAGAAAAAA
96369	94456	ATTCTGTGTCAAAAGAAAAA
96370	94457	GATTCTGTGTCAAAAGAAAA
96371	94458	AGATTCTGTGTCAAAAGAAA
96372	94459	GAGATTCTGTGTCAAAAGAA
96373	94460	CGAGATTCTGTGTCAAAAGA
96374	94461	GCGAGATTCTGTGTCAAAAG
96375	94462	AGCGAGATTCTGTGTCAAAA
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96378	94465	AAGAGCGAGATTCTGTGTCA
96379	94466	AAAGAGCGAGATTCTGTGTC
96380	94467	AAAAGAGCGAGATTCTGTGT
96381	94468	CAAAAGAGCGAGATTCTGTG
96382	94469	GCAAAAGAGCGAGATTCTGT
96383	94470	AGCAAAAGAGCGAGATTCTG
96384	94471	AAGCAAAAGAGCGAGATTCT
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96386	94473	CTAAGCAAAAGAGCGAGATT
96387	94474	CCTAAGCAAAAGAGCGAGAT
96388	94475	GCCTAAGCAAAAGAGCGAGA
96389	94476	AGCCTAAGCAAAAGAGCGAG
96390	94477	CAGCCTAAGCAAAAGAGCGA
96391	94478	CCAGCCTAAGCAAAAGAGCG
96392	94479	TCCAGCCTAAGCAAAAGAGC
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96397	94484	TGCCCTCCAGCCTAAGCAAA
96398	94485	CTGCCCTCCAGCCTAAGCAA
96399	94486	ACTGCCCTCCAGCCTAAGCA
96400	94487	CACTGCCCTCCAGCCTAAGC
96401	94488	CCACTGCCCTCCAGCCTAAG
96402	94489	ACCACTGCCCTCCAGCCTAA
96403	94490	CACCACTGCCCTCCAGCCTA
96404	94491	GCACCACTGCCCTCCAGCCT
96405	94492	TGCACCACTGCCCTCCAGCC
96406	94493	TTGCACCACTGCCCTCCAGC
96407	94494	ATTGCACCACTGCCCTCCAG
96408	94495	GATTGCACCACTGCCCTCCA
96409	94496	AGATTGCACCACTGCCCTCC
96410	94497	AAGATTGCACCACTGCCCTC
96411	94498	CAAGATTGCACCACTGCCCT
96412	94499	CCAAGATTGCACCACTGCCC
96413	94500	GCCAAGATTGCACCACTGCC
96414	94501	AGCCAAGATTGCACCACTGC
96415	94502	GAGCCAAGATTGCACCACTG
96416	94503	TGAGCCAAGATTGCACCACT
96417	94504	GTGAGCCAAGATTGCACCAC
96418	94505	TGTGAGCCAAGATTGCACCA
96419	94506	CTGTGAGCCAAGATTGCACC
96420	94507	GCTGTGAGCCAAGATTGCAC
96421	94508	TGCTGTGAGCCAAGATTGCA
96422	94509	CTGCTGTGAGCCAAGATTGC
96423	94510	GCTGCTGTGAGCCAAGATTG
96424	94511	GGCTGCTGTGAGCCAAGATT
96425	94512	AGGCTGCTGTGAGCCAAGAT
96426	94513	GAGGCTGCTGTGAGCCAAGA

145503	143590	CGCCGGCTGAACGTGAGAAG
145504	143591	ACGCCGGCTGAACGTGAGAA
145505	143592	TACGCCGGCTGAACGTGAGA
145506	143593	ATACGCCGGCTGAACGTGAG
145507	143594	TATACGCCGGCTGAACGTGA
145508	143595	GTATACGCCGGCTGAACGTG
145509	143596	GGTATACGCCGGCTGAACGT
145510	143597	TGGTATACGCCGGCTGAACG
145511	143598	TTGGTATACGCCGGCTGAAC
145512	143599	GTTGGTATACGCCGGCTGAA
145513	143600	GGTTGGTATACGCCGGCTGA
145514	143601	GGGTTGGTATACGCCGGCTG
145515	143602	TGGGTTGGTATACGCCGGCT
145516	143603	GTGGGTTGGTATACGCCGGC
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145518	143605	GGGTGGGTTGGTATACGCCG
145519	143606	GGGGTGGGTTGGTATACGCC
145520	143607	TGGGGTGGGTTGGTATACGC
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145522	143609	TGTGGGGTGGGTTGGTATAC
145523	143610	ATGTGGGGTGGGTTGGTATA
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145525	143612	CCATGTGGGGTGGGTTGGTA
145526	143613	GCCATGTGGGGTGGGTTGGT
145527	143614	GGCCATGTGGGGTGGGTTGG
145528	143615	GGGCCATGTGGGGTGGGTTG
145529	143616	TGGGCCATGTGGGGTGGGTT
145530	143617	GTGGGCCATGTGGGGTGGGT
145531	143618	CGTGGGCCATGTGGGGTGGG
145532	143619	ACGTGGGCCATGTGGGGTGG
145533	143620	TACGTGGGCCATGTGGGGTG
145534	143621	GTACGTGGGCCATGTGGGGT
145535	143622	GGTACGTGGGCCATGTGGGG
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145540	143627	CCTGAGGTACGTGGGCCATG
145541	143628	ACCTGAGGTACGTGGGCCAT
145542	143629	TACCTGAGGTACGTGGGCCA
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145544	143631	ATTACCTGAGGTACGTGGGC
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145546	143633	GTATTACCTGAGGTACGTGG
145547	143634	GGTATTACCTGAGGTACGTG
145548	143635	TGGTATTACCTGAGGTACGT
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145550	143637	GCTGGTATTACCTGAGGTAC
145551	143638	AGCTGGTATTACCTGAGGTA
145552	143639	AAGCTGGTATTACCTGAGGT
145553	143640	AAAGCTGGTATTACCTGAGG
145554	143641	TAAAGCTGGTATTACCTGAG
145555	143642	CTAAAGCTGGTATTACCTGA
145556	143643	GCTAAAGCTGGTATTACCTG
145557	143644	GGCTAAAGCTGGTATTACCT
145558	143645	TGGCTAAAGCTGGTATTACC
145559	143646	TTGGCTAAAGCTGGTATTAC
145560	143647	GTTGGCTAAAGCTGGTATTA
145561	143648	AGTTGGCTAAAGCTGGTATT
145562	143649	AAGTTGGCTAAAGCTGGTAT
145563	143650	AAAGTTGGCTAAAGCTGGTA
145564	143651	GAAAGTTGGCTAAAGCTGGT
145565	143652	AGAAAGTTGGCTAAAGCTGG
145566	143653	CAGAAAGTTGGCTAAAGCTG
145567	143654	ACAGAAAGTTGGCTAAAGCT
145568	143655	CACAGAAAGTTGGCTAAAGC
145569	143656	TCACAGAAAGTTGGCTAAAG
145570	143657	TTCACAGAAAGTTGGCTAAA
145571	143658	CTTCACAGAAAGTTGGCTAA
145572	143659	CCTTCACAGAAAGTTGGCTA
145573	143660	GCCTTCACAGAAAGTTGGCT

47280	45367	GGGACCAGAAGTATTTTAGA
47281	45368	TGGGACCAGAAGTATTTTAG
47282	45369	TTGGGACCAGAAGTATTTTA
47283	45370	CTTGGGACCAGAAGTATTTT
47284	45371	GCTTGGGACCAGAAGTATTT
47285	45372	TGCTTGGGACCAGAAGTATT
47286	45373	ATGCTTGGGACCAGAAGTAT
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47289	45376	AAAATGCTTGGGACCAGAAG
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47291	45378	CTAAAATGCTTGGGACCAGA
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47293	45380	ATCTAAAATGCTTGGGACCA
47294	45381	CATCTAAAATGCTTGGGACC
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47296	45383	CTCATCTAAAATGCTTGGGA
47297	45384	CCTCATCTAAAATGCTTGGG
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47299	45386	TTCCTCATCTAAAATGCTTG
47300	45387	CTTCCTCATCTAAAATGCTT
47301	45388	TCTTCCTCATCTAAAATGCT
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47305	45392	TGAATCTTCCTCATCTAAAA
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47316	45403	TTAGTACAAACTGAATCTTC
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47319	45406	AAATTAGTACAAACTGAATC
47320	45407	GAAATTAGTACAAACTGAAT
47321	45408	AGAAATTAGTACAAACTGAA
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47325	45412	TATTAGAAATTAGTACAAAC
47326	45413	CTATTAGAAATTAGTACAAA
47327	45414	ACTATTAGAAATTAGTACAA
47328	45415	AACTATTAGAAATTAGTACA
47329	45416	AAACTATTAGAAATTAGTAC
47330	45417	AAAACTATTAGAAATTAGTA
47331	45418	AAAAACTATTAGAAATTAGT
47332	45419	AAAAAACTATTAGAAATTAG
47333	45420	AAAAAAACTATTAGAAATTA
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47336	45423	AAAAAAAAAACTATTAGAAA
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47338	45425	AAAAAAAAAAAACTATTAGA
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47341	45428	TAAAAAAAAAAAAAACTATT
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47345	45432	ATATTAAAAAAAAAAAAAAC
47346	45433	AATATTAAAAAAAAAAAAAA
47347	45434	GAATATTAAAAAAAAAAAAA
47348	45435	GGAATATTAAAAAAAAAAAA
47349	45436	TGGAATATTAAAAAAAAAAA
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96427	94514	TGAGGCTGCTGTGAGCCAAG
96428	94515	CTGAGGCTGCTGTGAGCCAA
96429	94516	GCTGAGGCTGCTGTGAGCCA
96430	94517	GGCTGAGGCTGCTGTGAGCC
96431	94518	AGGCTGAGGCTGCTGTGAGC
96432	94519	GAGGCTGAGGCTGCTGTGAG
96433	94520	GGAGGCTGAGGCTGCTGTGA
96434	94521	AGGAGGCTGAGGCTGCTGTG
96435	94522	CAGGAGGCTGAGGCTGCTGT
96436	94523	CCAGGAGGCTGAGGCTGCTG
96437	94524	CCCAGGAGGCTGAGGCTGCT
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96441	94528	TGAGCCCAGGAGGCTGAGGC
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96447	94534	CTCATTTGAGCCCAGGAGGC
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96452	94539	AGCTACTCATTTGAGCCCAG
96453	94540	CAGCTACTCATTTGAGCCCA
96454	94541	CCAGCTACTCATTTGAGCCC
96455	94542	ACCAGCTACTCATTTGAGCC
96456	94543	TACCAGCTACTCATTTGAGC
96457	94544	GTACCAGCTACTCATTTGAG
96458	94545	AGTACCAGCTACTCATTTGA
96459	94546	TAGTACCAGCTACTCATTTG
96460	94547	GTAGTACCAGCTACTCATTT
96461	94548	TGTAGTACCAGCTACTCATT
96462	94549	CTGTAGTACCAGCTACTCAT
96463	94550	CCTGTAGTACCAGCTACTCA
96464	94551	ACCTGTAGTACCAGCTACTC
96465	94552	CACCTGTAGTACCAGCTACT
96466	94553	ACACCTGTAGTACCAGCTAC
96467	94554	CACACCTGTAGTACCAGCTA
96468	94555	GCACACCTGTAGTACCAGCT
96469	94556	TGCACACCTGTAGTACCAGC
96470	94557	GTGCACACCTGTAGTACCAG
96471	94558	GGTGCACACCTGTAGTACCA
96472	94559	TGGTGCACACCTGTAGTACC
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96474	94561	GGTGGTGCACACCTGTAGTA
96475	94562	TGGTGGTGCACACCTGTAGT
96476	94563	GTGGTGGTGCACACCTGTAG
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96478	94565	GTGTGGTGGTGCACACCTGT
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96480	94567	AGGTGTGGTGGTGCACACCT
96481	94568	AAGGTGTGGTGGTGCACACC
96482	94569	CAAGGTGTGGTGGTGCACAC
96483	94570	GCAAGGTGTGGTGGTGCACA
96484	94571	AGCAAGGTGTGGTGGTGCAC
96485	94572	TAGCAAGGTGTGGTGGTGCA
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96487	94574	AATAGCAAGGTGTGGTGGTG
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96494	94581	AGTTATTAATAGCAAGGTGT
96495	94582	AAGTTATTAATAGCAAGGTG
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145574	143661	GGCCTTCACAGAAAGTTGGC
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145576	143663	TTGGCCTTCACAGAAAGTTG
145577	143664	CTTGGCCTTCACAGAAAGTT
145578	143665	ACTTGGCCTTCACAGAAAGT
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145580	143667	CTACTTGGCCTTCACAGAAA
145581	143668	TCTACTTGGCCTTCACAGAA
145582	143669	TTCTACTTGGCCTTCACAGA
145583	143670	ATTCTACTTGGCCTTCACAG
145584	143671	CATTCTACTTGGCCTTCACA
145585	143672	ACATTCTACTTGGCCTTCAC
145586	143673	CACATTCTACTTGGCCTTCA
145587	143674	TCACATTCTACTTGGCCTTC
145588	143675	TTCACATTCTACTTGGCCTT
145589	143676	CTTCACATTCTACTTGGCCT
145590	143677	CCTTCACATTCTACTTGGCC
145591	143678	ACCTTCACATTCTACTTGGC
145592	143679	AACCTTCACATTCTACTTGG
145593	143680	TAACCTTCACATTCTACTTG
145594	143681	ATAACCTTCACATTCTACTT
145595	143682	GATAACCTTCACATTCTACT
145596	143683	TGATAACCTTCACATTCTAC
145597	143684	CTGATAACCTTCACATTCTA
145598	143685	ACTGATAACCTTCACATTCT
145599	143686	TACTGATAACCTTCACATTC
145600	143687	TTACTGATAACCTTCACATT
145601	143688	CTTACTGATAACCTTCACAT
145602	143689	GCTTACTGATAACCTTCACA
145603	143690	TGCTTACTGATAACCTTCAC
145604	143691	CTGCTTACTGATAACCTTCA
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145606	143693	AGCTGCTTACTGATAACCTT
145607	143694	TAGCTGCTTACTGATAACCT
145608	143695	CTAGCTGCTTACTGATAACC
145609	143696	TCTAGCTGCTTACTGATAAC
145610	143697	CTCTAGCTGCTTACTGATAA
145611	143698	CCTCTAGCTGCTTACTGATA
145612	143699	GCCTCTAGCTGCTTACTGAT
145613	143700	AGCCTCTAGCTGCTTACTGA
145614	143701	GAGCCTCTAGCTGCTTACTG
145615	143702	AGAGCCTCTAGCTGCTTACT
145616	143703	GAGAGCCTCTAGCTGCTTAC
145617	143704	GGAGAGCCTCTAGCTGCTTA
145618	143705	GGGAGAGCCTCTAGCTGCTT
145619	143706	TGGGAGAGCCTCTAGCTGCT
145620	143707	CTGGGAGAGCCTCTAGCTGC
145621	143708	GCTGGGAGAGCCTCTAGCTG
145622	143709	AGCTGGGAGAGCCTCTAGCT
145623	143710	TAGCTGGGAGAGCCTCTAGC
145624	143711	CTAGCTGGGAGAGCCTCTAG
145625	143712	CCTAGCTGGGAGAGCCTCTA
145626	143713	TCCTAGCTGGGAGAGCCTCT
145627	143714	TTCCTAGCTGGGAGAGCCTC
145628	143715	TTTCCTAGCTGGGAGAGCCT
145629	143716	GTTTCCTAGCTGGGAGAGCC
145630	143717	GGTTTCCTAGCTGGGAGAGC
145631	143718	GGGTTTCCTAGCTGGGAGAG
145632	143719	AGGGTTTCCTAGCTGGGAGA
145633	143720	CAGGGTTTCCTAGCTGGGAG
145634	143721	ACAGGGTTTCCTAGCTGGGA
145635	143722	CACAGGGTTTCCTAGCTGGG
145636	143723	ACACAGGGTTTCCTAGCTGG
145637	143724	CACACAGGGTTTCCTAGCTG
145638	143725	ACACACAGGGTTTCCTAGCT
145639	143726	GACACACAGGGTTTCCTAGC
145640	143727	TGACACACAGGGTTTCCTAG
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47353	45440	AATCTGGAATATTAAAAAAA
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47355	45442	GAAATCTGGAATATTAAAAA
47356	45443	AGAAATCTGGAATATTAAAA
47357	45444	AAGAAATCTGGAATATTAAA
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47371	45458	ATAGATTCCATCAAAAGAAA
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47373	45460	GCATAGATTCCATCAAAAGA
47374	45461	TGCATAGATTCCATCAAAAG
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47376	45463	TTTGCATAGATTCCATCAAA
47377	45464	ATTTGCATAGATTCCATCAA
47378	45465	TATTTGCATAGATTCCATCA
47379	45466	ATATTTGCATAGATTCCATC
47380	45467	CATATTTGCATAGATTCCAT
47381	45468	TCATATTTGCATAGATTCCA
47382	45469	CTCATATTTGCATAGATTCC
47383	45470	CCTCATATTTGCATAGATTC
47384	45471	TCCTCATATTTGCATAGATT
47385	45472	ATCCTCATATTTGCATAGAT
47386	45473	CATCCTCATATTTGCATAGA
47387	45474	CCATCCTCATATTTGCATAG
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47395	45482	TATATGAACCATCCTCATAT
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47398	45485	AAGTATATGAACCATCCTCA
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47401	45488	TGTAAGTATATGAACCATCC
47402	45489	ATGTAAGTATATGAACCATC
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47405	45492	CTGATGTAAGTATATGAACC
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96546	94633	GAGACCAGCCTGGGCAACAT
96547	94634	TGAGACCAGCCTGGGCAACA
96548	94635	TTGAGACCAGCCTGGGCAAC
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96552	94639	GTGTTTGAGACCAGCCTGGG
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96558	94645	GTCCAAGTGTTTGAGACCAG
96559	94646	AGTCCAAGTGTTTGAGACCA
96560	94647	GAGTCCAAGTGTTTGAGACC
96561	94648	TGAGTCCAAGTGTTTGAGAC
96562	94649	TTGAGTCCAAGTGTTTGAGA
96563	94650	CTTGAGTCCAAGTGTTTGAG
96564	94651	ACTTGAGTCCAAGTGTTTGA
96565	94652	CACTTGAGTCCAAGTGTTTG
96566	94653	TCACTTGAGTCCAAGTGTTT
96567	94654	GTCACTTGAGTCCAAGTGTT
96568	94655	TGTCACTTGAGTCCAAGTGT

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145650	143737	GCAAATGGCATGACACACAG
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145665	143752	GGGAAAGGGAGACAGGCAAA
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145667	143754	GAGGGAAAGGGAGACAGGCA
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145670	143757	TGAGAGGGAAAGGGAGACAG
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145675	143762	GTATTTGAGAGGGAAAGGGA
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145688	143775	GGCCAGATCACGTGTATTTG
145689	143776	GGGCCAGATCACGTGTATTT
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145705	143792	CACAAACATTCCCTTAGGGC
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145710	143797	AACCACACAAACATTCCCTT
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145712	143799	AAAACCACACAAACATTCCC
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47426	45513	TAATCTAATAACTTACAACA
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47428	45515	AATAATCTAATAACTTACAA
47429	45516	CAATAATCTAATAACTTACA
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47467	45554	TGGAATTACTTTATTCTACC
47468	45555	ATGGAATTACTTTATTCTAC
47469	45556	CATGGAATTACTTTATTCTA
47470	45557	TCATGGAATTACTTTATTCT
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47473	45560	ACTTCATGGAATTACTTTAT
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47477	45564	TTTAACTTCATGGAATTACT
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47482	45569	CACATTTTAACTTCATGGAA
47483	45570	CCACATTTTAACTTCATGGA
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96569	94656	GTGTCACTTGAGTCCAAGTG
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96571	94658	GCGTGTCACTTGAGTCCAAG
96572	94659	GGCGTGTCACTTGAGTCCAA
96573	94660	GGGCGTGTCACTTGAGTCCA
96574	94661	TGGGCGTGTCACTTGAGTCC
96575	94662	GTGGGCGTGTCACTTGAGTC
96576	94663	GGTGGGCGTGTCACTTGAGT
96577	94664	AGGTGGGCGTGTCACTTGAG
96578	94665	GAGGTGGGCGTGTCACTTGA
96579	94666	TGAGGTGGGCGTGTCACTTG
96580	94667	CTGAGGTGGGCGTGTCACTT
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96582	94669	GGCTGAGGTGGGCGTGTCAC
96583	94670	AGGCTGAGGTGGGCGTGTCA
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96620	94707	TCCGCAGTGCAAGGTGAAAG
96621	94708	GTCCGCAGTGCAAGGTGAAA
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96623	94710	GAGTCCGCAGTGCAAGGTGA
96624	94711	CGAGTCCGCAGTGCAAGGTG
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96630	94717	TCAGGGCGAGTCCGCAGTGC
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96632	94719	ATTCAGGGCGAGTCCGCAGT
96633	94720	AATTCAGGGCGAGTCCGCAG
96634	94721	GAATTCAGGGCGAGTCCGCA
96635	94722	AGAATTCAGGGCGAGTCCGC
96636	94723	AAGAATTCAGGGCGAGTCCG
96637	94724	AAAGAATTCAGGGCGAGTCC
96638	94725	GAAAGAATTCAGGGCGAGTC
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145717	143804	ATGACAAAACCACACAAACA
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145719	143806	CCATGACAAAACCACACAAA
145720	143807	CCCATGACAAAACCACACAA
145721	143808	TCCCATGACAAAACCACACA
145722	143809	ATCCCATGACAAAACCACAC
145723	143810	GATCCCATGACAAAACCACA
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145725	143812	CTGATCCCATGACAAAACCA
145726	143813	ACTGATCCCATGACAAAACC
145727	143814	CACTGATCCCATGACAAAAC
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145737	143824	TCAGCACCTTCACTGATCCC
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145739	143826	AATCAGCACCTTCACTGATC
145740	143827	CAATCAGCACCTTCACTGAT
145741	143828	CCAATCAGCACCTTCACTGA
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145744	143831	TGACCAATCAGCACCTTCAC
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145746	143833	ACTGACCAATCAGCACCTTC
145747	143834	GACTGACCAATCAGCACCTT
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145749	143836	AGGACTGACCAATCAGCACC
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145759	143846	GGAAAACTAAAGGACTGACC
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145763	143850	AGTTGGAAAACTAAAGGACT
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145770	143857	AGGTCTCAGTTGGAAAACTA
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145784	143871	CAAAGATATTTTTAAGGTCT
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47495	45582	ACAATCATTTATCCACATTT
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47501	45588	ACTTTGACAATCATTTATCC
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47503	45590	TTACTTTGACAATCATTTAT
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47506	45593	ATGTTACTTTGACAATCATT
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47516	45603	GATCTAAGCAATGTTACTTT
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47520	45607	ACATGATCTAAGCAATGTTA
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47544	45631	ATTTCTCTAAATCATCCTGA
47545	45632	TATTTCTCTAAATCATCCTG
47546	45633	CTATTTCTCTAAATCATCCT
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47548	45635	ATCTATTTCTCTAAATCATC
47549	45636	AATCTATTTCTCTAAATCAT
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47553	45640	TTCTAATCTATTTCTCTAAA
47554	45641	GTTCTAATCTATTTCTCTAA
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96661	94748	GAGGGCTCTTGGATCTTGCA
96662	94749	AGAGGGCTCTTGGATCTTGC
96663	94750	GAGAGGGCTCTTGGATCTTG
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96691	94778	AGGAAAGGGGTCCCGATCCA
96692	94779	TAGGAAAGGGGTCCCGATCC
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145811	143898	AAGAAGGACTGGGTTGCATT
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47664	45751	TTAACAAATATTTTTGATCC
47665	45752	TTTAACAAATATTTTTGATC
47666	45753	TTTTAACAAATATTTTTGAT
47667	45754	TTTTTAACAAATATTTTTGA
47668	45755	CTTTTTAACAAATATTTTTG
47669	45756	CCTTTTTAACAAATATTTTT
47670	45757	GCCTTTTTAACAAATATTTT
47671	45758	GGCCTTTTTAACAAATATTT
47672	45759	TGGCCTTTTTAACAAATATT
47673	45760	CTGGCCTTTTTAACAAATAT
47674	45761	CCTGGCCTTTTTAACAAATA
47675	45762	GCCTGGCCTTTTTAACAAAT
47676	45763	TGCCTGGCCTTTTTAACAAA
47677	45764	GTGCCTGGCCTTTTTAACAA
47678	45765	TGTGCCTGGCCTTTTTAACA
47679	45766	CTGTGCCTGGCCTTTTTAAC
47680	45767	ACTGTGCCTGGCCTTTTTAA
47681	45768	CACTGTGCCTGGCCTTTTTA
47682	45769	TCACTGTGCCTGGCCTTTTT
47683	45770	GTCACTGTGCCTGGCCTTTT
47684	45771	AGTCACTGTGCCTGGCCTTT
47685	45772	GAGTCACTGTGCCTGGCCTT
47686	45773	TGAGTCACTGTGCCTGGCCT
47687	45774	GTGAGTCACTGTGCCTGGCC
47688	45775	CGTGAGTCACTGTGCCTGGC
47689	45776	GCGTGAGTCACTGTGCCTGG
47690	45777	GGCGTGAGTCACTGTGCCTG
47691	45778	AGGCGTGAGTCACTGTGCCT
47692	45779	CAGGCGTGAGTCACTGTGCC
47693	45780	ACAGGCGTGAGTCACTGTGC
47694	45781	TACAGGCGTGAGTCACTGTG
47695	45782	TTACAGGCGTGAGTCACTGT
47696	45783	ATTACAGGCGTGAGTCACTG
47697	45784	GATTACAGGCGTGAGTCACT
47698	45785	GGATTACAGGCGTGAGTCAC
47699	45786	GGGATTACAGGCGTGAGTCA
47700	45787	TGGGATTACAGGCGTGAGTC
47701	45788	CTGGGATTACAGGCGTGAGT
47702	45789	GCTGGGATTACAGGCGTGAG
47703	45790	TGCTGGGATTACAGGCGTGA
47704	45791	GTGCTGGGATTACAGGCGTG
47705	45792	AGTGCTGGGATTACAGGCGT

96782	94869	CCAAGTCACTCTCCTATGAC
96783	94870	ACCAAGTCACTCTCCTATGA
96784	94871	CACCAAGTCACTCTCCTATG
96785	94872	GCACCAAGTCACTCTCCTAT
96786	94873	AGCACCAAGTCACTCTCCTA
96787	94874	GAGCACCAAGTCACTCTCCT
96788	94875	TGAGCACCAAGTCACTCTCC
96789	94876	CTGAGCACCAAGTCACTCTC
96790	94877	GCTGAGCACCAAGTCACTCT
96791	94878	GGCTGAGCACCAAGTCACTC
96792	94879	GGGCTGAGCACCAAGTCACT
96793	94880	TGGGCTGAGCACCAAGTCAC
96794	94881	ATGGGCTGAGCACCAAGTCA
96795	94882	AATGGGCTGAGCACCAAGTC
96796	94883	AAATGGGCTGAGCACCAAGT
96797	94884	AAAATGGGCTGAGCACCAAG
96798	94885	CAAAATGGGCTGAGCACCAA
96799	94886	TCAAAATGGGCTGAGCACCA
96800	94887	CTCAAAATGGGCTGAGCACC
96801	94888	GCTCAAAATGGGCTGAGCAC
96802	94889	TGCTCAAAATGGGCTGAGCA
96803	94890	CTGCTCAAAATGGGCTGAGC
96804	94891	ACTGCTCAAAATGGGCTGAG
96805	94892	AACTGCTCAAAATGGGCTGA
96806	94893	TAACTGCTCAAAATGGGCTG
96807	94894	ATAACTGCTCAAAATGGGCT
96808	94895	AATAACTGCTCAAAATGGGC
96809	94896	AAATAACTGCTCAAAATGGG
96810	94897	TAAATAACTGCTCAAAATGG
96811	94898	TTAAATAACTGCTCAAAATG
96812	94899	ATTAAATAACTGCTCAAAAT
96813	94900	TATTAAATAACTGCTCAAAA
96814	94901	ATATTAAATAACTGCTCAAA
96815	94902	TATATTAAATAACTGCTCAA
96816	94903	CTATATTAAATAACTGCTCA
96817	94904	GCTATATTAAATAACTGCTC
96818	94905	TGCTATATTAAATAACTGCT
96819	94906	ATGCTATATTAAATAACTGC
96820	94907	TATGCTATATTAAATAACTG
96821	94908	TTATGCTATATTAAATAACT
96822	94909	CTTATGCTATATTAAATAAC
96823	94910	CCTTATGCTATATTAAATAA
96824	94911	ACCTTATGCTATATTAAATA
96825	94912	CACCTTATGCTATATTAAAT
96826	94913	CCACCTTATGCTATATTAAA
96827	94914	CCCACCTTATGCTATATTAA
96828	94915	CCCCACCTTATGCTATATTA
96829	94916	ACCCCACCTTATGCTATATT
96830	94917	AACCCCACCTTATGCTATAT
96831	94918	GAACCCCACCTTATGCTATA
96832	94919	TGAACCCCACCTTATGCTAT
96833	94920	TTGAACCCCACCTTATGCTA
96834	94921	TTTGAACCCCACCTTATGCT
96835	94922	ATTTGAACCCCACCTTATGC
96836	94923	AATTTGAACCCCACCTTATG
96837	94924	GAATTTGAACCCCACCTTAT
96838	94925	TGAATTTGAACCCCACCTTA
96839	94926	ATGAATTTGAACCCCACCTT
96840	94927	AATGAATTTGAACCCCACCT
96841	94928	GAATGAATTTGAACCCCACC
96842	94929	AGAATGAATTTGAACCCCAC
96843	94930	AAGAATGAATTTGAACCCCA
96844	94931	AAAGAATGAATTTGAACCCC
96845	94932	TAAAGAATGAATTTGAACCC
96846	94933	ATAAAGAATGAATTTGAACC
96847	94934	TATAAAGAATGAATTTGAAC
96848	94935	ATATAAAGAATGAATTTGAA
96849	94936	AATATAAAGAATGAATTTGA
96850	94937	TAATATAAAGAATGAATTTG
96851	94938	TTAATATAAAGAATGAATTT
96852	94939	ATTAATATAAAGAATGAATT

145929	144016	CTCTGTGAAGGCCATCATCC
145930	144017	ACTCTGTGAAGGCCATCATC
145931	144018	GACTCTGTGAAGGCCATCAT
145932	144019	AGACTCTGTGAAGGCCATCA
145933	144020	GAGACTCTGTGAAGGCCATC
145934	144021	TGAGACTCTGTGAAGGCCAT
145935	144022	CTGAGACTCTGTGAAGGCCA
145936	144023	GCTGAGACTCTGTGAAGGCC
145937	144024	AGCTGAGACTCTGTGAAGGC
145938	144025	GAGCTGAGACTCTGTGAAGG
145939	144026	AGAGCTGAGACTCTGTGAAG
145940	144027	GAGAGCTGAGACTCTGTGAA
145941	144028	GGAGAGCTGAGACTCTGTGA
145942	144029	CGGAGAGCTGAGACTCTGTG
145943	144030	TCGGAGAGCTGAGACTCTGT
145944	144031	TTCGGAGAGCTGAGACTCTG
145945	144032	CTTCGGAGAGCTGAGACTCT
145946	144033	ACTTCGGAGAGCTGAGACTC
145947	144034	CACTTCGGAGAGCTGAGACT
145948	144035	TCACTTCGGAGAGCTGAGAC
145949	144036	GTCACTTCGGAGAGCTGAGA
145950	144037	AGTCACTTCGGAGAGCTGAG
145951	144038	TAGTCACTTCGGAGAGCTGA
145952	144039	GTAGTCACTTCGGAGAGCTG
145953	144040	GGTAGTCACTTCGGAGAGCT
145954	144041	CGGTAGTCACTTCGGAGAGC
145955	144042	CCGGTAGTCACTTCGGAGAG
145956	144043	CCCGGTAGTCACTTCGGAGA
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145958	144045	GCCCCGGTAGTCACTTCGGA
145959	144046	GGCCCCGGTAGTCACTTCGG
145960	144047	AGGCCCCGGTAGTCACTTCG
145961	144048	CAGGCCCCGGTAGTCACTTC
145962	144049	ACAGGCCCCGGTAGTCACTT
145963	144050	GACAGGCCCCGGTAGTCACT
145964	144051	TGACAGGCCCCGGTAGTCAC
145965	144052	TTGACAGGCCCCGGTAGTCA
145966	144053	GTTGACAGGCCCCGGTAGTC
145967	144054	AGTTGACAGGCCCCGGTAGT
145968	144055	AAGTTGACAGGCCCCGGTAG
145969	144056	CAAGTTGACAGGCCCCGGTA
145970	144057	TCAAGTTGACAGGCCCCGGT
145971	144058	ATCAAGTTGACAGGCCCCGG
145972	144059	AATCAAGTTGACAGGCCCCG
145973	144060	CAATCAAGTTGACAGGCCCC
145974	144061	ACAATCAAGTTGACAGGCCC
145975	144062	AACAATCAAGTTGACAGGCC
145976	144063	TAACAATCAAGTTGACAGGC
145977	144064	GTAACAATCAAGTTGACAGG
145978	144065	AGTAACAATCAAGTTGACAG
145979	144066	GAGTAACAATCAAGTTGACA
145980	144067	TGAGTAACAATCAAGTTGAC
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145985	144072	TCATGTGAGTAACAATCAAG
145986	144073	CTCATGTGAGTAACAATCAA
145987	144074	ACTCATGTGAGTAACAATCA
145988	144075	AACTCATGTGAGTAACAATC
145989	144076	GAACTCATGTGAGTAACAAT
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145996	144083	GTGTCTGGAACTCATGTGAG
145997	144084	TGTGTCTGGAACTCATGTGA
145998	144085	ATGTGTCTGGAACTCATGTG
145999	144086	GATGTGTCTGGAACTCATGT

47706	45793	AAGTGCTGGGATTACAGGCG
47707	45794	AAAGTGCTGGGATTACAGGC
47708	45795	CAAAGTGCTGGGATTACAGG
47709	45796	CCAAAGTGCTGGGATTACAG
47710	45797	CCCAAAGTGCTGGGATTACA
47711	45798	TCCCAAAGTGCTGGGATTAC
47712	45799	CTCCCAAAGTGCTGGGATTA
47713	45800	ACTCCCAAAGTGCTGGGATT
47714	45801	AACTCCCAAAGTGCTGGGAT
47715	45802	AAACTCCCAAAGTGCTGGGA
47716	45803	CAAACTCCCAAAGTGCTGGG
47717	45804	TCAAACTCCCAAAGTGCTGG
47718	45805	CTCAAACTCCCAAAGTGCTG
47719	45806	CCTCAAACTCCCAAAGTGCT
47720	45807	ACCTCAAACTCCCAAAGTGC
47721	45808	CACCTCAAACTCCCAAAGTG
47722	45809	CCACCTCAAACTCCCAAAGT
47723	45810	CCCACCTCAAACTCCCAAAG
47724	45811	GCCCACCTCAAACTCCCAAA
47725	45812	TGCCCACCTCAAACTCCCAA
47726	45813	CTGCCCACCTCAAACTCCCA
47727	45814	TCTGCCCACCTCAAACTCCC
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47729	45816	CATCTGCCCACCTCAAACTC
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47732	45819	AGCCATCTGCCCACCTCAAA
47733	45820	AAGCCATCTGCCCACCTCAA
47734	45821	CAAGCCATCTGCCCACCTCA
47735	45822	TCAAGCCATCTGCCCACCTC
47736	45823	CTCAAGCCATCTGCCCACCT
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47739	45826	GAGCTCAAGCCATCTGCCCA
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47744	45831	CTTGTGAGCTCAAGCCATCT
47745	45832	ACTTGTGAGCTCAAGCCATC
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47749	45836	TTAAACTTGTGAGCTCAAGC
47750	45837	CTTAAACTTGTGAGCTCAAG
47751	45838	TCTTAAACTTGTGAGCTCAA
47752	45839	GTCTTAAACTTGTGAGCTCA
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47754	45841	TGGTCTTAAACTTGTGAGCT
47755	45842	CTGGTCTTAAACTTGTGAGC
47756	45843	GCTGGTCTTAAACTTGTGAG
47757	45844	GGCTGGTCTTAAACTTGTGA
47758	45845	AGGCTGGTCTTAAACTTGTG
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47760	45847	CCAGGCTGGTCTTAAACTTG
47761	45848	CCCAGGCTGGTCTTAAACTT
47762	45849	GCCCAGGCTGGTCTTAAACT
47763	45850	TGCCCAGGCTGGTCTTAAAC
47764	45851	TTGCCCAGGCTGGTCTTAAA
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47766	45853	TGTTGCCCAGGCTGGTCTTA
47767	45854	ATGTTGCCCAGGCTGGTCTT
47768	45855	CATGTTGCCCAGGCTGGTCT
47769	45856	CCATGTTGCCCAGGCTGGTC
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47771	45858	TGCCATGTTGCCCAGGCTGG
47772	45859	CTGCCATGTTGCCCAGGCTG
47773	45860	TCTGCCATGTTGCCCAGGCT
47774	45861	TTCTGCCATGTTGCCCAGGC
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47776	45863	AGTTCTGCCATGTTGCCCAG

96853	94940	AATTAATATAAAGAATGAAT
96854	94941	AAATTAATATAAAGAATGAA
96855	94942	AAAATTAATATAAAGAATGA
96856	94943	AAAAATTAATATAAAGAATG
96857	94944	AAAAAATTAATATAAAGAAT
96858	94945	TAAAAAATTAATATAAAGAA
96859	94946	ATAAAAAATTAATATAAAGA
96860	94947	AATAAAAAATTAATATAAAG
96861	94948	AAATAAAAAATTAATATAAA
96862	94949	GAAATAAAAAATTAATATAA
96863	94950	AGAAATAAAAAATTAATATA
96864	94951	TAGAAATAAAAAATTAATAT
96865	94952	TTAGAAATAAAAAATTAATA
96866	94953	ATTAGAAATAAAAAATTAAT
96867	94954	AATTAGAAATAAAAAATTAA
96868	94955	CAATTAGAAATAAAAAATTA
96869	94956	TCAATTAGAAATAAAAAATT
96870	94957	GTCAATTAGAAATAAAAAAT
96871	94958	TGTCAATTAGAAATAAAAAA
96872	94959	GTGTCAATTAGAAATAAAAA
96873	94960	TGTGTCAATTAGAAATAAAA
96874	94961	ATGTGTCAATTAGAAATAAA
96875	94962	TATGTGTCAATTAGAAATAA
96876	94963	TTATGTGTCAATTAGAAATA
96877	94964	GTTATGTGTCAATTAGAAAT
96878	94965	GGTTATGTGTCAATTAGAAA
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96880	94967	ATGGTTATGTGTCAATTAGA
96881	94968	TATGGTTATGTGTCAATTAG
96882	94969	GTATGGTTATGTGTCAATTA
96883	94970	TGTATGGTTATGTGTCAATT
96884	94971	GTGTATGGTTATGTGTCAAT
96885	94972	AGTGTATGGTTATGTGTCAA
96886	94973	AAGTGTATGGTTATGTGTCA
96887	94974	TAAGTGTATGGTTATGTGTC
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96893	94980	TGGTTATAAGTGTATGGTTA
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96895	94982	AATGGTTATAAGTGTATGGT
96896	94983	AAATGGTTATAAGTGTATGG
96897	94984	AAAATGGTTATAAGTGTATG
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96901	94988	AGTAAAAATGGTTATAAGTG
96902	94989	CAGTAAAAATGGTTATAAGT
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96904	94991	CACAGTAAAAATGGTTATAA
96905	94992	ACACAGTAAAAATGGTTATA
96906	94993	TACACAGTAAAAATGGTTAT
96907	94994	TTACACAGTAAAAATGGTTA
96908	94995	CTTACACAGTAAAAATGGTT
96909	94996	ACTTACACAGTAAAAATGGT
96910	94997	AACTTACACAGTAAAAATGG
96911	94998	GAACTTACACAGTAAAAATG
96912	94999	TGAACTTACACAGTAAAAAT
96913	95000	CTGAACTTACACAGTAAAAA
96914	95001	TCTGAACTTACACAGTAAAA
96915	95002	ATCTGAACTTACACAGTAAA
96916	95003	AATCTGAACTTACACAGTAA
96917	95004	GAATCTGAACTTACACAGTA
96918	95005	TGAATCTGAACTTACACAGT
96919	95006	ATGAATCTGAACTTACACAG
96920	95007	AATGAATCTGAACTTACACA
96921	95008	GAATGAATCTGAACTTACAC
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96923	95010	AAGAATGAATCTGAACTTAC

146000	144087	AGATGTGTCTGGAACTCATG
146001	144088	GAGATGTGTCTGGAACTCAT
146002	144089	AGAGATGTGTCTGGAACTCA
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146004	144091	GGAGAGATGTGTCTGGAACT
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146006	144093	TTGGAGAGATGTGTCTGGAA
146007	144094	ATTGGAGAGATGTGTCTGGA
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146010	144097	ACAATTGGAGAGATGTGTCT
146011	144098	AACAATTGGAGAGATGTGTC
146012	144099	AAACAATTGGAGAGATGTGT
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146014	144101	GAAAACAATTGGAGAGATGT
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146016	144103	GGGAAAACAATTGGAGAGAT
146017	144104	AGGGAAAACAATTGGAGAGA
146018	144105	CAGGGAAAACAATTGGAGAG
146019	144106	CCAGGGAAAACAATTGGAGA
146020	144107	ACCAGGGAAAACAATTGGAG
146021	144108	AACCAGGGAAAACAATTGGA
146022	144109	TAACCAGGGAAAACAATTGG
146023	144110	ATAACCAGGGAAAACAATTG
146024	144111	GATAACCAGGGAAAACAATT
146025	144112	GGATAACCAGGGAAAACAAT
146026	144113	TGGATAACCAGGGAAAACAA
146027	144114	ATGGATAACCAGGGAAAACA
146028	144115	TATGGATAACCAGGGAAAAC
146029	144116	ATATGGATAACCAGGGAAAA
146030	144117	TATATGGATAACCAGGGAAA
146031	144118	ATATATGGATAACCAGGGAA
146032	144119	GATATATGGATAACCAGGGA
146033	144120	AGATATATGGATAACCAGGG
146034	144121	CAGATATATGGATAACCAGG
146035	144122	GCAGATATATGGATAACCAG
146036	144123	AGCAGATATATGGATAACCA
146037	144124	AAGCAGATATATGGATAACC
146038	144125	AAAGCAGATATATGGATAAC
146039	144126	CAAAGCAGATATATGGATAA
146040	144127	TCAAAGCAGATATATGGATA
146041	144128	GTCAAAGCAGATATATGGAT
146042	144129	GGTCAAAGCAGATATATGGA
146043	144130	TGGTCAAAGCAGATATATGG
146044	144131	ATGGTCAAAGCAGATATATG
146045	144132	TATGGTCAAAGCAGATATAT
146046	144133	TTATGGTCAAAGCAGATATA
146047	144134	CTTATGGTCAAAGCAGATAT
146048	144135	ACTTATGGTCAAAGCAGATA
146049	144136	AACTTATGGTCAAAGCAGAT
146050	144137	CAACTTATGGTCAAAGCAGA
146051	144138	ACAACTTATGGTCAAAGCAG
146052	144139	TACAACTTATGGTCAAAGCA
146053	144140	GTACAACTTATGGTCAAAGC
146054	144141	AGTACAACTTATGGTCAAAG
146055	144142	GAGTACAACTTATGGTCAAA
146056	144143	AGAGTACAACTTATGGTCAA
146057	144144	AAGAGTACAACTTATGGTCA
146058	144145	CAAGAGTACAACTTATGGTC
146059	144146	TCAAGAGTACAACTTATGGT
146060	144147	CTCAAGAGTACAACTTATGG
146061	144148	TCTCAAGAGTACAACTTATG
146062	144149	CTCTCAAGAGTACAACTTAT
146063	144150	CCTCTCAAGAGTACAACTTA
146064	144151	CCCTCTCAAGAGTACAACTT
146065	144152	GCCCTCTCAAGAGTACAACT
146066	144153	AGCCCTCTCAAGAGTACAAC
146067	144154	AAGCCCTCTCAAGAGTACAA
146068	144155	CAAGCCCTCTCAAGAGTACA
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47777	45864	GAGTTCTGCCATGTTGCCCA
47778	45865	GGAGTTCTGCCATGTTGCCC
47779	45866	CGGAGTTCTGCCATGTTGCC
47780	45867	ACGGAGTTCTGCCATGTTGC
47781	45868	GACGGAGTTCTGCCATGTTG
47782	45869	AGACGGAGTTCTGCCATGTT
47783	45870	GAGACGGAGTTCTGCCATGT
47784	45871	AGAGACGGAGTTCTGCCATG
47785	45872	TAGAGACGGAGTTCTGCCAT
47786	45873	GTAGAGACGGAGTTCTGCCA
47787	45874	TGTAGAGACGGAGTTCTGCC
47788	45875	TTGTAGAGACGGAGTTCTGC
47789	45876	TTTGTAGAGACGGAGTTCTG
47790	45877	TTTTGTAGAGACGGAGTTCT
47791	45878	TTTTTGTAGAGACGGAGTTC
47792	45879	CTTTTTGTAGAGACGGAGTT
47793	45880	ACTTTTTGTAGAGACGGAGT
47794	45881	TACTTTTTGTAGAGACGGAG
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47799	45886	TTTTTTACTTTTTGTAGAGA
47800	45887	TTTTTTTACTTTTTGTAGAG
47801	45888	GTTTTTTTACTTTTTGTAGA
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47803	45890	TAGTTTTTTTACTTTTTGTA
47804	45891	CTAGTTTTTTTACTTTTTGT
47805	45892	GCTAGTTTTTTTACTTTTTG
47806	45893	GGCTAGTTTTTTTACTTTTT
47807	45894	CGGCTAGTTTTTTTACTTTT
47808	45895	TCGGCTAGTTTTTTTACTTT
47809	45896	TTCGGCTAGTTTTTTTACTT
47810	45897	GTTCGGCTAGTTTTTTTACT
47811	45898	CGTTCGGCTAGTTTTTTTAC
47812	45899	ACGTTCGGCTAGTTTTTTTA
47813	45900	CACGTTCGGCTAGTTTTTTT
47814	45901	CCACGTTCGGCTAGTTTTTT
47815	45902	ACCACGTTCGGCTAGTTTTT
47816	45903	CACCACGTTCGGCTAGTTTT
47817	45904	CCACCACGTTCGGCTAGTTT
47818	45905	ACCACCACGTTCGGCTAGTT
47819	45906	TACCACCACGTTCGGCTAGT
47820	45907	GTACCACCACGTTCGGCTAG
47821	45908	CGTACCACCACGTTCGGCTA
47822	45909	ACGTACCACCACGTTCGGCT
47823	45910	CACGTACCACCACGTTCGGC
47824	45911	GCACGTACCACCACGTTCGG
47825	45912	GGCACGTACCACCACGTTCG
47826	45913	AGGCACGTACCACCACGTTC
47827	45914	CAGGCACGTACCACCACGTT
47828	45915	ACAGGCACGTACCACCACGT
47829	45916	TACAGGCACGTACCACCACG
47830	45917	CTACAGGCACGTACCACCAC
47831	45918	ACTACAGGCACGTACCACCA
47832	45919	GACTACAGGCACGTACCACC
47833	45920	GGACTACAGGCACGTACCAC
47834	45921	AGGACTACAGGCACGTACCA
47835	45922	TAGGACTACAGGCACGTACC
47836	45923	CTAGGACTACAGGCACGTAC
47837	45924	ACTAGGACTACAGGCACGTA
47838	45925	CACTAGGACTACAGGCACGT
47839	45926	TCACTAGGACTACAGGCACG
47840	45927	GTCACTAGGACTACAGGCAC
47841	45928	AGTCACTAGGACTACAGGCA
47842	45929	AAGTCACTAGGACTACAGGC
47843	45930	CAAGTCACTAGGACTACAGG
47844	45931	CCAAGTCACTAGGACTACAG
47845	45932	CCCAAGTCACTAGGACTACA
47846	45933	TCCCAAGTCACTAGGACTAC
47847	45934	CTCCCAAGTCACTAGGACTA

96924	95011	GAAGAATGAATCTGAACTTA
96925	95012	GGAAGAATGAATCTGAACTT
96926	95013	CGGAAGAATGAATCTGAACT
96927	95014	ACGGAAGAATGAATCTGAAC
96928	95015	TACGGAAGAATGAATCTGAA
96929	95016	ATACGGAAGAATGAATCTGA
96930	95017	CATACGGAAGAATGAATCTG
96931	95018	ACATACGGAAGAATGAATCT
96932	95019	TACATACGGAAGAATGAATC
96933	95020	CTACATACGGAAGAATGAAT
96934	95021	CCTACATACGGAAGAATGAA
96935	95022	ACCTACATACGGAAGAATGA
96936	95023	TACCTACATACGGAAGAATG
96937	95024	ATACCTACATACGGAAGAAT
96938	95025	AATACCTACATACGGAAGAA
96939	95026	TAATACCTACATACGGAAGA
96940	95027	CTAATACCTACATACGGAAG
96941	95028	ACTAATACCTACATACGGAA
96942	95029	AACTAATACCTACATACGGA
96943	95030	CAACTAATACCTACATACGG
96944	95031	ACAACTAATACCTACATACG
96945	95032	GACAACTAATACCTACATAC
96946	95033	GGACAACTAATACCTACATA
96947	95034	GGGACAACTAATACCTACAT
96948	95035	TGGGACAACTAATACCTACA
96949	95036	CTGGGACAACTAATACCTAC
96950	95037	GCTGGGACAACTAATACCTA
96951	95038	TGCTGGGACAACTAATACCT
96952	95039	GTGCTGGGACAACTAATACC
96953	95040	GGTGCTGGGACAACTAATAC
96954	95041	TGGTGCTGGGACAACTAATA
96955	95042	ATGGTGCTGGGACAACTAAT
96956	95043	GATGGTGCTGGGACAACTAA
96957	95044	AGATGGTGCTGGGACAACTA
96958	95045	CAGATGGTGCTGGGACAACT
96959	95046	ACAGATGGTGCTGGGACAAC
96960	95047	AACAGATGGTGCTGGGACAA
96961	95048	TAACAGATGGTGCTGGGACA
96962	95049	TTAACAGATGGTGCTGGGAC
96963	95050	TTTAACAGATGGTGCTGGGA
96964	95051	TTTTAACAGATGGTGCTGGG
96965	95052	TTTTTAACAGATGGTGCTGG
96966	95053	CTTTTTAACAGATGGTGCTG
96967	95054	TCTTTTTAACAGATGGTGCT
96968	95055	GTCTTTTTAACAGATGGTGC
96969	95056	AGTCTTTTTAACAGATGGTG
96970	95057	TAGTCTTTTTAACAGATGGT
96971	95058	ATAGTCTTTTTAACAGATGG
96972	95059	AATAGTCTTTTTAACAGATG
96973	95060	GAATAGTCTTTTTAACAGAT
96974	95061	AGAATAGTCTTTTTAACAGA
96975	95062	AAGAATAGTCTTTTTAACAG
96976	95063	CAAGAATAGTCTTTTTAACA
96977	95064	CCAAGAATAGTCTTTTTAAC
96978	95065	GCCAAGAATAGTCTTTTTAA
96979	95066	GGCCAAGAATAGTCTTTTTA
96980	95067	TGGCCAAGAATAGTCTTTTT
96981	95068	CTGGCCAAGAATAGTCTTTT
96982	95069	CCTGGCCAAGAATAGTCTTT
96983	95070	GCCTGGCCAAGAATAGTCTT
96984	95071	TGCCTGGCCAAGAATAGTCT
96985	95072	GTGCCTGGCCAAGAATAGTC
96986	95073	TGTGCCTGGCCAAGAATAGT
96987	95074	CTGTGCCTGGCCAAGAATAG
96988	95075	ACTGTGCCTGGCCAAGAATA
96989	95076	CACTGTGCCTGGCCAAGAAT
96990	95077	CCACTGTGCCTGGCCAAGAA
96991	95078	GCCACTGTGCCTGGCCAAGA
96992	95079	AGCCACTGTGCCTGGCCAAG
96993	95080	GAGCCACTGTGCCTGGCCAA
96994	95081	AGAGCCACTGTGCCTGGCCA

146071	144158	GGCCAAGCCCTCTCAAGAGT
146072	144159	AGGCCAAGCCCTCTCAAGAG
146073	144160	AAGGCCAAGCCCTCTCAAGA
146074	144161	CAAGGCCAAGCCCTCTCAAG
146075	144162	CCAAGGCCAAGCCCTCTCAA
146076	144163	TCCAAGGCCAAGCCCTCTCA
146077	144164	GTCCAAGGCCAAGCCCTCTC
146078	144165	TGTCCAAGGCCAAGCCCTCT
146079	144166	ATGTCCAAGGCCAAGCCCTC
146080	144167	AATGTCCAAGGCCAAGCCCT
146081	144168	CAATGTCCAAGGCCAAGCCC
146082	144169	CCAATGTCCAAGGCCAAGCC
146083	144170	ACCAATGTCCAAGGCCAAGC
146084	144171	CACCAATGTCCAAGGCCAAG
146085	144172	GCACCAATGTCCAAGGCCAA
146086	144173	TGCACCAATGTCCAAGGCCA
146087	144174	CTGCACCAATGTCCAAGGCC
146088	144175	ACTGCACCAATGTCCAAGGC
146089	144176	CACTGCACCAATGTCCAAGG
146090	144177	ACACTGCACCAATGTCCAAG
146091	144178	TACACTGCACCAATGTCCAA
146092	144179	TTACACTGCACCAATGTCCA
146093	144180	GTTACACTGCACCAATGTCC
146094	144181	AGTTACACTGCACCAATGTC
146095	144182	TAGTTACACTGCACCAATGT
146096	144183	CTAGTTACACTGCACCAATG
146097	144184	TCTAGTTACACTGCACCAAT
146098	144185	TTCTAGTTACACTGCACCAA
146099	144186	CTTCTAGTTACACTGCACCA
146100	144187	GCTTCTAGTTACACTGCACC
146101	144188	AGCTTCTAGTTACACTGCAC
146102	144189	CAGCTTCTAGTTACACTGCA
146103	144190	CCAGCTTCTAGTTACACTGC
146104	144191	TCCAGCTTCTAGTTACACTG
146105	144192	TTCCAGCTTCTAGTTACACT
146106	144193	CTTCCAGCTTCTAGTTACAC
146107	144194	GCTTCCAGCTTCTAGTTACA
146108	144195	TGCTTCCAGCTTCTAGTTAC
146109	144196	GTGCTTCCAGCTTCTAGTTA
146110	144197	GGTGCTTCCAGCTTCTAGTT
146111	144198	GGGTGCTTCCAGCTTCTAGT
146112	144199	TGGGTGCTTCCAGCTTCTAG
146113	144200	CTGGGTGCTTCCAGCTTCTA
146114	144201	CCTGGGTGCTTCCAGCTTCT
146115	144202	ACCTGGGTGCTTCCAGCTTC
146116	144203	CACCTGGGTGCTTCCAGCTT
146117	144204	CCACCTGGGTGCTTCCAGCT
146118	144205	ACCACCTGGGTGCTTCCAGC
146119	144206	GACCACCTGGGTGCTTCCAG
146120	144207	GGACCACCTGGGTGCTTCCA
146121	144208	GGGACCACCTGGGTGCTTCC
146122	144209	TGGGACCACCTGGGTGCTTC
146123	144210	ATGGGACCACCTGGGTGCTT
146124	144211	AATGGGACCACCTGGGTGCT
146125	144212	AAATGGGACCACCTGGGTGC
146126	144213	AAAATGGGACCACCTGGGTG
146127	144214	AAAAATGGGACCACCTGGGT
146128	144215	GAAAAATGGGACCACCTGGG
146129	144216	AGAAAAATGGGACCACCTGG
146130	144217	AAGAAAAATGGGACCACCTG
146131	144218	AAAGAAAAATGGGACCACCT
146132	144219	TAAAGAAAAATGGGACCACC
146133	144220	TTAAAGAAAAATGGGACCAC
146134	144221	CTTAAAGAAAAATGGGACCA
146135	144222	TCTTAAAGAAAAATGGGACC
146136	144223	CTCTTAAAGAAAAATGGGAC
146137	144224	GCTCTTAAAGAAAAATGGGA
146138	144225	TGCTCTTAAAGAAAAATGGG
146139	144226	CTGCTCTTAAAGAAAAATGG
146140	144227	GCTGCTCTTAAAGAAAAATG
146141	144228	GGCTGCTCTTAAAGAAAAAT

47848	45935	CCTCCCAAGTCACTAGGACT
47849	45936	GCCTCCCAAGTCACTAGGAC
47850	45937	AGCCTCCCAAGTCACTAGGA
47851	45938	CAGCCTCCCAAGTCACTAGG
47852	45939	TCAGCCTCCCAAGTCACTAG
47853	45940	GTCAGCCTCCCAAGTCACTA
47854	45941	CGTCAGCCTCCCAAGTCACT
47855	45942	ACGTCAGCCTCCCAAGTCAC
47856	45943	CACGTCAGCCTCCCAAGTCA
47857	45944	CCACGTCAGCCTCCCAAGTC
47858	45945	CCCACGTCAGCCTCCCAAGT
47859	45946	TCCCACGTCAGCCTCCCAAG
47860	45947	CTCCCACGTCAGCCTCCCAA
47861	45948	CCTCCCACGTCAGCCTCCCA
47862	45949	TCCTCCCACGTCAGCCTCCC
47863	45950	ATCCTCCCACGTCAGCCTCC
47864	45951	AATCCTCCCACGTCAGCCTC
47865	45952	CAATCCTCCCACGTCAGCCT
47866	45953	ACAATCCTCCCACGTCAGCC
47867	45954	AACAATCCTCCCACGTCAGC
47868	45955	AAACAATCCTCCCACGTCAG
47869	45956	CAAACAATCCTCCCACGTCA
47870	45957	TCAAACAATCCTCCCACGTC
47871	45958	CTCAAACAATCCTCCCACGT
47872	45959	GCTCAAACAATCCTCCCACG
47873	45960	GGCTCAAACAATCCTCCCAC
47874	45961	AGGCTCAAACAATCCTCCCA
47875	45962	CAGGCTCAAACAATCCTCCC
47876	45963	CCAGGCTCAAACAATCCTCC
47877	45964	CCCAGGCTCAAACAATCCTC
47878	45965	TCCCAGGCTCAAACAATCCT
47879	45966	CTCCCAGGCTCAAACAATCC
47880	45967	CCTCCCAGGCTCAAACAATC
47881	45968	ACCTCCCAGGCTCAAACAAT
47882	45969	CACCTCCCAGGCTCAAACAA
47883	45970	CCACCTCCCAGGCTCAAACA
47884	45971	TCCACCTCCCAGGCTCAAAC
47885	45972	CTCCACCTCCCAGGCTCAAA
47886	45973	CCTCCACCTCCCAGGCTCAA
47887	45974	ACCTCCACCTCCCAGGCTCA
47888	45975	AACCTCCACCTCCCAGGCTC
47889	45976	AAACCTCCACCTCCCAGGCT
47890	45977	GAAACCTCCACCTCCCAGGC
47891	45978	TGAAACCTCCACCTCCCAGG
47892	45979	GTGAAACCTCCACCTCCCAG
47893	45980	AGTGAAACCTCCACCTCCCA
47894	45981	CAGTGAAACCTCCACCTCCC
47895	45982	TCAGTGAAACCTCCACCTCC
47896	45983	CTCAGTGAAACCTCCACCTC
47897	45984	GCTCAGTGAAACCTCCACCT
47898	45985	AGCTCAGTGAAACCTCCACC
47899	45986	CAGCTCAGTGAAACCTCCAC
47900	45987	TCAGCTCAGTGAAACCTCCA
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47904	45991	TATCTCAGCTCAGTGAAACC
47905	45992	TTATCTCAGCTCAGTGAAAC
47906	45993	ATTATCTCAGCTCAGTGAAA
47907	45994	CATTATCTCAGCTCAGTGAA
47908	45995	GCATTATCTCAGCTCAGTGA
47909	45996	GGCATTATCTCAGCTCAGTG
47910	45997	GGGCATTATCTCAGCTCAGT
47911	45998	GGGGCATTATCTCAGCTCAG
47912	45999	AGGGGCATTATCTCAGCTCA
47913	46000	CAGGGGCATTATCTCAGCTC
47914	46001	GCAGGGGCATTATCTCAGCT
47915	46002	TGCAGGGGCATTATCTCAGC
47916	46003	GTGCAGGGGCATTATCTCAG
47917	46004	AGTGCAGGGGCATTATCTCA
47918	46005	GAGTGCAGGGGCATTATCTC

96995	95082	GAGAGCCACTGTGCCTGGCC
96996	95083	TGAGAGCCACTGTGCCTGGC
96997	95084	TTGAGAGCCACTGTGCCTGG
96998	95085	GTTGAGAGCCACTGTGCCTG
96999	95086	CGTTGAGAGCCACTGTGCCT
97000	95087	GCGTTGAGAGCCACTGTGCC
97001	95088	GGCGTTGAGAGCCACTGTGC
97002	95089	AGGCGTTGAGAGCCACTGTG
97003	95090	CAGGCGTTGAGAGCCACTGT
97004	95091	ACAGGCGTTGAGAGCCACTG
97005	95092	TACAGGCGTTGAGAGCCACT
97006	95093	TTACAGGCGTTGAGAGCCAC
97007	95094	ATTACAGGCGTTGAGAGCCA
97008	95095	GATTACAGGCGTTGAGAGCC
97009	95096	GGATTACAGGCGTTGAGAGC
97010	95097	GGGATTACAGGCGTTGAGAG
97011	95098	TGGGATTACAGGCGTTGAGA
97012	95099	CTGGGATTACAGGCGTTGAG
97013	95100	GCTGGGATTACAGGCGTTGA
97014	95101	TGCTGGGATTACAGGCGTTG
97015	95102	GTGCTGGGATTACAGGCGTT
97016	95103	AGTGCTGGGATTACAGGCGT
97017	95104	AAGTGCTGGGATTACAGGCG
97018	95105	AAAGTGCTGGGATTACAGGC
97019	95106	CAAAGTGCTGGGATTACAGG
97020	95107	CCAAAGTGCTGGGATTACAG
97021	95108	CCCAAAGTGCTGGGATTACA
97022	95109	TCCCAAAGTGCTGGGATTAC
97023	95110	CTCCCAAAGTGCTGGGATTA
97024	95111	ACTCCCAAAGTGCTGGGATT
97025	95112	GACTCCCAAAGTGCTGGGAT
97026	95113	GGACTCCCAAAGTGCTGGGA
97027	95114	GGGACTCCCAAAGTGCTGGG
97028	95115	TGGGACTCCCAAAGTGCTGG
97029	95116	TTGGGACTCCCAAAGTGCTG
97030	95117	CTTGGGACTCCCAAAGTGCT
97031	95118	GCTTGGGACTCCCAAAGTGC
97032	95119	TGCTTGGGACTCCCAAAGTG
97033	95120	CTGCTTGGGACTCCCAAAGT
97034	95121	CCTGCTTGGGACTCCCAAAG
97035	95122	GCCTGCTTGGGACTCCCAAA
97036	95123	TGCCTGCTTGGGACTCCCAA
97037	95124	CTGCCTGCTTGGGACTCCCA
97038	95125	TCTGCCTGCTTGGGACTCCC
97039	95126	ATCTGCCTGCTTGGGACTCC
97040	95127	GATCTGCCTGCTTGGGACTC
97041	95128	TGATCTGCCTGCTTGGGACT
97042	95129	GTGATCTGCCTGCTTGGGAC
97043	95130	TGTGATCTGCCTGCTTGGGA
97044	95131	ATGTGATCTGCCTGCTTGGG
97045	95132	CATGTGATCTGCCTGCTTGG
97046	95133	TCATGTGATCTGCCTGCTTG
97047	95134	CTCATGTGATCTGCCTGCTT
97048	95135	CCTCATGTGATCTGCCTGCT
97049	95136	ACCTCATGTGATCTGCCTGC
97050	95137	GACCTCATGTGATCTGCCTG
97051	95138	TGACCTCATGTGATCTGCCT
97052	95139	CTGACCTCATGTGATCTGCC
97053	95140	CCTGACCTCATGTGATCTGC
97054	95141	TCCTGACCTCATGTGATCTG
97055	95142	CTCCTGACCTCATGTGATCT
97056	95143	ACTCCTGACCTCATGTGATC
97057	95144	AACTCCTGACCTCATGTGAT
97058	95145	GAACTCCTGACCTCATGTGA
97059	95146	CGAACTCCTGACCTCATGTG
97060	95147	TCGAACTCCTGACCTCATGT
97061	95148	TTCGAACTCCTGACCTCATG
97062	95149	TTTCGAACTCCTGACCTCAT
97063	95150	GTTTCGAACTCCTGACCTCA
97064	95151	GGTTTCGAACTCCTGACCTC
97065	95152	TGGTTTCGAACTCCTGACCT

146142	144229	GGGCTGCTCTTAAAGAAAAA
146143	144230	AGGGCTGCTCTTAAAGAAAA
146144	144231	CAGGGCTGCTCTTAAAGAAA
146145	144232	CCAGGGCTGCTCTTAAAGAA
146146	144233	TCCAGGGCTGCTCTTAAAGA
146147	144234	TTCCAGGGCTGCTCTTAAAG
146148	144235	CTTCCAGGGCTGCTCTTAAA
146149	144236	GCTTCCAGGGCTGCTCTTAA
146150	144237	TGCTTCCAGGGCTGCTCTTA
146151	144238	GTGCTTCCAGGGCTGCTCTT
146152	144239	AGTGCTTCCAGGGCTGCTCT
146153	144240	AAGTGCTTCCAGGGCTGCTC
146154	144241	AAAGTGCTTCCAGGGCTGCT
146155	144242	CAAAGTGCTTCCAGGGCTGC
146156	144243	CCAAAGTGCTTCCAGGGCTG
146157	144244	TCCAAAGTGCTTCCAGGGCT
146158	144245	CTCCAAAGTGCTTCCAGGGC
146159	144246	GCTCCAAAGTGCTTCCAGGG
146160	144247	AGCTCCAAAGTGCTTCCAGG
146161	144248	GAGCTCCAAAGTGCTTCCAG
146162	144249	TGAGCTCCAAAGTGCTTCCA
146163	144250	GTGAGCTCCAAAGTGCTTCC
146164	144251	GGTGAGCTCCAAAGTGCTTC
146165	144252	AGGTGAGCTCCAAAGTGCTT
146166	144253	GAGGTGAGCTCCAAAGTGCT
146167	144254	GGAGGTGAGCTCCAAAGTGC
146168	144255	TGGAGGTGAGCTCCAAAGTG
146169	144256	CTGGAGGTGAGCTCCAAAGT
146170	144257	ACTGGAGGTGAGCTCCAAAG
146171	144258	CACTGGAGGTGAGCTCCAAA
146172	144259	ACACTGGAGGTGAGCTCCAA
146173	144260	TACACTGGAGGTGAGCTCCA
146174	144261	TTACACTGGAGGTGAGCTCC
146175	144262	CTTACACTGGAGGTGAGCTC
146176	144263	GCTTACACTGGAGGTGAGCT
146177	144264	AGCTTACACTGGAGGTGAGC
146178	144265	CAGCTTACACTGGAGGTGAG
146179	144266	GCAGCTTACACTGGAGGTGA
146180	144267	AGCAGCTTACACTGGAGGTG
146181	144268	TAGCAGCTTACACTGGAGGT
146182	144269	GTAGCAGCTTACACTGGAGG
146183	144270	TGTAGCAGCTTACACTGGAG
146184	144271	CTGTAGCAGCTTACACTGGA
146185	144272	CCTGTAGCAGCTTACACTGG
146186	144273	ACCTGTAGCAGCTTACACTG
146187	144274	CACCTGTAGCAGCTTACACT
146188	144275	TCACCTGTAGCAGCTTACAC
146189	144276	TTCACCTGTAGCAGCTTACA
146190	144277	TTTCACCTGTAGCAGCTTAC
146191	144278	CTTTCACCTGTAGCAGCTTA
146192	144279	CCTTTCACCTGTAGCAGCTT
146193	144280	ACCTTTCACCTGTAGCAGCT
146194	144281	CACCTTTCACCTGTAGCAGC
146195	144282	ACACCTTTCACCTGTAGCAG
146196	144283	CACACCTTTCACCTGTAGCA
146197	144284	GCACACCTTTCACCTGTAGC
146198	144285	AGCACACCTTTCACCTGTAG
146199	144286	AAGCACACCTTTCACCTGTA
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146201	144288	GCAAGCACACCTTTCACCTG
146202	144289	GGCAAGCACACCTTTCACCT
146203	144290	TGGCAAGCACACCTTTCACC
146204	144291	ATGGCAAGCACACCTTTCAC
146205	144292	GATGGCAAGCACACCTTTCA
146206	144293	AGATGGCAAGCACACCTTTC
146207	144294	GAGATGGCAAGCACACCTTT
146208	144295	TGAGATGGCAAGCACACCTT
146209	144296	CTGAGATGGCAAGCACACCT
146210	144297	ACTGAGATGGCAAGCACACC
146211	144298	CACTGAGATGGCAAGCACAC
146212	144299	CCACTGAGATGGCAAGCACA

47919	46006	TGAGTGCAGGGGCATTATCT
47920	46007	CTGAGTGCAGGGGCATTATC
47921	46008	GCTGAGTGCAGGGGCATTAT
47922	46009	GGCTGAGTGCAGGGGCATTA
47923	46010	AGGCTGAGTGCAGGGGCATT
47924	46011	CAGGCTGAGTGCAGGGGCAT
47925	46012	CCAGGCTGAGTGCAGGGGCA
47926	46013	ACCAGGCTGAGTGCAGGGGC
47927	46014	GACCAGGCTGAGTGCAGGGG
47928	46015	TGACCAGGCTGAGTGCAGGG
47929	46016	TTGACCAGGCTGAGTGCAGG
47930	46017	GTTGACCAGGCTGAGTGCAG
47931	46018	TGTTGACCAGGCTGAGTGCA
47932	46019	CTGTTGACCAGGCTGAGTGC
47933	46020	ACTGTTGACCAGGCTGAGTG
47934	46021	CACTGTTGACCAGGCTGAGT
47935	46022	GCACTGTTGACCAGGCTGAG
47936	46023	GGCACTGTTGACCAGGCTGA
47937	46024	TGGCACTGTTGACCAGGCTG
47938	46025	CTGGCACTGTTGACCAGGCT
47939	46026	TCTGGCACTGTTGACCAGGC
47940	46027	GTCTGGCACTGTTGACCAGG
47941	46028	TGTCTGGCACTGTTGACCAG
47942	46029	CTGTCTGGCACTGTTGACCA
47943	46030	TCTGTCTGGCACTGTTGACC
47944	46031	GTCTGTCTGGCACTGTTGAC
47945	46032	GGTCTGTCTGGCACTGTTGA
47946	46033	GGGTCTGTCTGGCACTGTTG
47947	46034	GGGGTCTGTCTGGCACTGTT
47948	46035	AGGGGTCTGTCTGGCACTGT
47949	46036	AAGGGGTCTGTCTGGCACTG
47950	46037	GAAGGGGTCTGTCTGGCACT
47951	46038	AGAAGGGGTCTGTCTGGCAC
47952	46039	GAGAAGGGGTCTGTCTGGCA
47953	46040	TGAGAAGGGGTCTGTCTGGC
47954	46041	TTGAGAAGGGGTCTGTCTGG
47955	46042	TTTGAGAAGGGGTCTGTCTG
47956	46043	TTTTGAGAAGGGGTCTGTCT
47957	46044	TTTTTGAGAAGGGGTCTGTC
47958	46045	TTTTTTGAGAAGGGGTCTGT
47959	46046	TTTTTTTGAGAAGGGGTCTG
47960	46047	TTTTTTTTGAGAAGGGGTCT
47961	46048	TTTTTTTTTGAGAAGGGGTC
47962	46049	TTTTTTTTTTGAGAAGGGGT
47963	46050	TTTTTTTTTTTGAGAAGGGG
47964	46051	ATTTTTTTTTTTGAGAAGGG
47965	46052	AATTTTTTTTTTTGAGAAGG
47966	46053	AAATTTTTTTTTTTGAGAAG
47967	46054	AAAATTTTTTTTTTTGAGAA
47968	46055	AAAAATTTTTTTTTTTGAGA
47969	46056	AAAAAATTTTTTTTTTTGAG
47970	46057	AAAAAAATTTTTTTTTTTGA
47971	46058	AAAAAAAATTTTTTTTTTTG
47972	46059	AAAAAAAAATTTTTTTTTTT
47973	46060	AAAAAAAAAATTTTTTTTTT
47974	46061	AAAAAAAAAAATTTTTTTTT
47975	46062	AAAAAAAAAAAATTTTTTTT
47976	46063	AAAAAAAAAAAAATTTTTTT
47977	46064	AAAAAAAAAAAAAATTTTTT
47978	46065	AAAAAAAAAAAAAAATTTTT
47979	46066	AAAAAAAAAAAAAAAATTTT
47980	46067	AAAAAAAAAAAAAAAAATTT
47981	46068	AAAAAAAAAAAAAAAAAATT
47982	46069	AAAAAAAAAAAAAAAAAAAT
47983	46070	AAAAAAAAAAAAAAAAAAAA
47984	46071	AAAAAAAAAAAAAAAAAAAA
47985	46072	AAAAAAAAAAAAAAAAAAAA
47986	46073	AAAAAAAAAAAAAAAAAAAA
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97066	95153	CTGGTTTCGAACTCCTGACC
97067	95154	ACTGGTTTCGAACTCCTGAC
97068	95155	GACTGGTTTCGAACTCCTGA
97069	95156	AGACTGGTTTCGAACTCCTG
97070	95157	CAGACTGGTTTCGAACTCCT
97071	95158	TCAGACTGGTTTCGAACTCC
97072	95159	GTCAGACTGGTTTCGAACTC
97073	95160	GGTCAGACTGGTTTCGAACT
97074	95161	TGGTCAGACTGGTTTCGAAC
97075	95162	TTGGTCAGACTGGTTTCGAA
97076	95163	TTTGGTCAGACTGGTTTCGA
97077	95164	ATTTGGTCAGACTGGTTTCG
97078	95165	CATTTGGTCAGACTGGTTTC
97079	95166	CCATTTGGTCAGACTGGTTT
97080	95167	ACCATTTGGTCAGACTGGTT
97081	95168	CACCATTTGGTCAGACTGGT
97082	95169	TCACCATTTGGTCAGACTGG
97083	95170	TTCACCATTTGGTCAGACTG
97084	95171	TTTCACCATTTGGTCAGACT
97085	95172	GTTTCACCATTTGGTCAGAC
97086	95173	GGTTTCACCATTTGGTCAGA
97087	95174	CGGTTTCACCATTTGGTCAG
97088	95175	GCGGTTTCACCATTTGGTCA
97089	95176	TGCGGTTTCACCATTTGGTC
97090	95177	ATGCGGTTTCACCATTTGGT
97091	95178	CATGCGGTTTCACCATTTGG
97092	95179	ACATGCGGTTTCACCATTTG
97093	95180	GACATGCGGTTTCACCATTT
97094	95181	AGACATGCGGTTTCACCATT
97095	95182	TAGACATGCGGTTTCACCAT
97096	95183	GTAGACATGCGGTTTCACCA
97097	95184	AGTAGACATGCGGTTTCACC
97098	95185	TAGTAGACATGCGGTTTCAC
97099	95186	TTAGTAGACATGCGGTTTCA
97100	95187	TTTAGTAGACATGCGGTTTC
97101	95188	TTTTAGTAGACATGCGGTTT
97102	95189	TTTTTAGTAGACATGCGGTT
97103	95190	ATTTTTAGTAGACATGCGGT
97104	95191	TATTTTTAGTAGACATGCGG
97105	95192	GTATTTTTAGTAGACATGCG
97106	95193	TGTATTTTTAGTAGACATGC
97107	95194	TTGTATTTTTAGTAGACATG
97108	95195	TTTGTATTTTTAGTAGACAT
97109	95196	TTTTGTATTTTTAGTAGACA
97110	95197	TTTTTGTATTTTTAGTAGAC
97111	95198	ATTTTTGTATTTTTAGTAGA
97112	95199	AATTTTTGTATTTTTAGTAG
97113	95200	TAATTTTTGTATTTTTAGTA
97114	95201	GTAATTTTTGTATTTTTAGT
97115	95202	GGTAATTTTTGTATTTTTAG
97116	95203	AGGTAATTTTTGTATTTTTA
97117	95204	CAGGTAATTTTTGTATTTTT
97118	95205	CCAGGTAATTTTTGTATTTT
97119	95206	CCCAGGTAATTTTTGTATTT
97120	95207	ACCCAGGTAATTTTTGTATT
97121	95208	CACCCAGGTAATTTTTGTAT
97122	95209	ACACCCAGGTAATTTTTGTA
97123	95210	CACACCCAGGTAATTTTTGT
97124	95211	CCACACCCAGGTAATTTTTG
97125	95212	ACCACACCCAGGTAATTTTT
97126	95213	CACCACACCCAGGTAATTTT
97127	95214	CCACCACACCCAGGTAATTT
97128	95215	GCCACCACACCCAGGTAATT
97129	95216	CGCCACCACACCCAGGTAAT
97130	95217	GCGCCACCACACCCAGGTAA
97131	95218	TGCGCCACCACACCCAGGTA
97132	95219	GTGCGCCACCACACCCAGGT
97133	95220	TGTGCGCCACCACACCCAGG
97134	95221	GTGTGCGCCACCACACCCAG
97135	95222	GGTGTGCGCCACCACACCCA
97136	95223	AGGTGTGCGCCACCACACCC

146213	144300	ACCACTGAGATGGCAAGCAC
146214	144301	AACCACTGAGATGGCAAGCA
146215	144302	CAACCACTGAGATGGCAAGC
146216	144303	GCAACCACTGAGATGGCAAG
146217	144304	AGCAACCACTGAGATGGCAA
146218	144305	CAGCAACCACTGAGATGGCA
146219	144306	ACAGCAACCACTGAGATGGC
146220	144307	GACAGCAACCACTGAGATGG
146221	144308	AGACAGCAACCACTGAGATG
146222	144309	CAGACAGCAACCACTGAGAT
146223	144310	GCAGACAGCAACCACTGAGA
146224	144311	TGCAGACAGCAACCACTGAG
146225	144312	ATGCAGACAGCAACCACTGA
146226	144313	GATGCAGACAGCAACCACTG
146227	144314	TGATGCAGACAGCAACCACT
146228	144315	CTGATGCAGACAGCAACCAC
146229	144316	GCTGATGCAGACAGCAACCA
146230	144317	AGCTGATGCAGACAGCAACC
146231	144318	CAGCTGATGCAGACAGCAAC
146232	144319	GCAGCTGATGCAGACAGCAA
146233	144320	AGCAGCTGATGCAGACAGCA
146234	144321	CAGCAGCTGATGCAGACAGC
146235	144322	TCAGCAGCTGATGCAGACAG
146236	144323	GTCAGCAGCTGATGCAGACA
146237	144324	TGTCAGCAGCTGATGCAGAC
146238	144325	TTGTCAGCAGCTGATGCAGA
146239	144326	TTTGTCAGCAGCTGATGCAG
146240	144327	CTTTGTCAGCAGCTGATGCA
146241	144328	CCTTTGTCAGCAGCTGATGC
146242	144329	ACCTTTGTCAGCAGCTGATG
146243	144330	GACCTTTGTCAGCAGCTGAT
146244	144331	GGACCTTTGTCAGCAGCTGA
146245	144332	GGGACCTTTGTCAGCAGCTG
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146247	144334	CAGGGACCTTTGTCAGCAGC
146248	144335	GCAGGGACCTTTGTCAGCAG
146249	144336	TGCAGGGACCTTTGTCAGCA
146250	144337	GTGCAGGGACCTTTGTCAGC
146251	144338	AGTGCAGGGACCTTTGTCAG
146252	144339	GAGTGCAGGGACCTTTGTCA
146253	144340	GGAGTGCAGGGACCTTTGTC
146254	144341	TGGAGTGCAGGGACCTTTGT
146255	144342	CTGGAGTGCAGGGACCTTTG
146256	144343	CCTGGAGTGCAGGGACCTTT
146257	144344	CCCTGGAGTGCAGGGACCTT
146258	144345	GCCCTGGAGTGCAGGGACCT
146259	144346	GGCCCTGGAGTGCAGGGACC
146260	144347	GGGCCCTGGAGTGCAGGGAC
146261	144348	TGGGCCCTGGAGTGCAGGGA
146262	144349	CTGGGCCCTGGAGTGCAGGG
146263	144350	CCTGGGCCCTGGAGTGCAGG
146264	144351	CCCTGGGCCCTGGAGTGCAG
146265	144352	CCCCTGGGCCCTGGAGTGCA
146266	144353	TCCCCTGGGCCCTGGAGTGC
146267	144354	ATCCCCTGGGCCCTGGAGTG
146268	144355	AATCCCCTGGGCCCTGGAGT
146269	144356	CAATCCCCTGGGCCCTGGAG
146270	144357	ACAATCCCCTGGGCCCTGGA
146271	144358	GACAATCCCCTGGGCCCTGG
146272	144359	AGACAATCCCCTGGGCCCTG
146273	144360	AAGACAATCCCCTGGGCCCT
146274	144361	TAAGACAATCCCCTGGGCCC
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146276	144363	ATTAAGACAATCCCCTGGGC
146277	144364	CATTAAGACAATCCCCTGGG
146278	144365	TCATTAAGACAATCCCCTGG
146279	144366	CTCATTAAGACAATCCCCTG
146280	144367	CCTCATTAAGACAATCCCCT
146281	144368	TCCTCATTAAGACAATCCCC
146282	144369	CTCCTCATTAAGACAATCCC
146283	144370	TCTCCTCATTAAGACAATCC

47990	46077	AAAAAAAAAAAAAAAAAAA
47991	46078	AAAAAAAAAAAAAAAAAAA
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47993	46080	AAAAAAAAAAAAAAAAAAA
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47996	46083	CAAAAAAAAAAAAAAAAAA
47997	46084	TCAAAAAAAAAAAAAAAAA
47998	46085	CTCAAAAAAAAAAAAAAAA
47999	46086	TCTCAAAAAAAAAAAAAAA
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48001	46088	TTTCTCAAAAAAAAAAAAA
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48003	46090	TTTTTCTCAAAAAAAAAAA
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48006	46093	TCTTTTTTCTCAAAAAAAA
48007	46094	CTCTTTTTTCTCAAAAAAA
48008	46095	CCTCTTTTTTCTCAAAAAA
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48010	46097	TGCCTCTTTTTTCTCAAAA
48011	46098	ATGCCTCTTTTTTCTCAAA
48012	46099	CATGCCTCTTTTTTCTCAA
48013	46100	CCATGCCTCTTTTTTCTCA
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48016	46103	CAACCATGCCTCTTTTTTCT
48017	46104	GCAACCATGCCTCTTTTTTC
48018	46105	CGCAACCATGCCTCTTTTTT
48019	46106	ACGCAACCATGCCTCTTTTT
48020	46107	GACGCAACCATGCCTCTTTT
48021	46108	AGACGCAACCATGCCTCTTT
48022	46109	CAGACGCAACCATGCCTCTT
48023	46110	TCAGACGCAACCATGCCTCT
48024	46111	TTCAGACGCAACCATGCCTC
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48033	46120	CATCTTTGGTTCAGACGCAA
48034	46121	ACATCTTTGGTTCAGACGCA
48035	46122	TACATCTTTGGTTCAGACGC
48036	46123	GTACATCTTTGGTTCAGACG
48037	46124	CGTACATCTTTGGTTCAGAC
48038	46125	CCGTACATCTTTGGTTCAGA
48039	46126	TCCGTACATCTTTGGTTCAG
48040	46127	GTCCGTACATCTTTGGTTCA
48041	46128	CGTCCGTACATCTTTGGTTC
48042	46129	ACGTCCGTACATCTTTGGTT
48043	46130	AACGTCCGTACATCTTTGGT
48044	46131	AAACGTCCGTACATCTTTGG
48045	46132	AAAACGTCCGTACATCTTTG
48046	46133	AAAAACGTCCGTACATCTTT
48047	46134	GAAAAACGTCCGTACATCTT
48048	46135	AGAAAAACGTCCGTACATCT
48049	46136	AAGAAAAACGTCCGTACATC
48050	46137	CAAGAAAAACGTCCGTACAT
48051	46138	ACAAGAAAAACGTCCGTACA
48052	46139	GACAAGAAAAACGTCCGTAC
48053	46140	TGACAAGAAAAACGTCCGTA
48054	46141	ATGACAAGAAAAACGTCCGT
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48056	46143	TAATGACAAGAAAAACGTCC
48057	46144	ATAATGACAAGAAAAACGTC
48058	46145	AATAATGACAAGAAAAACGT
48059	46146	GAATAATGACAAGAAAAACG
48060	46147	GGAATAATGACAAGAAAAAC

97137	95224	CAGGTGTGCGCCACCACACC
97138	95225	ACAGGTGTGCGCCACCACAC
97139	95226	TACAGGTGTGCGCCACCACA
97140	95227	CTACAGGTGTGCGCCACCAC
97141	95228	ACTACAGGTGTGCGCCACCA
97142	95229	GACTACAGGTGTGCGCCACC
97143	95230	AGACTACAGGTGTGCGCCAC
97144	95231	TAGACTACAGGTGTGCGCCA
97145	95232	CTAGACTACAGGTGTGCGCC
97146	95233	ACTAGACTACAGGTGTGCGC
97147	95234	GACTAGACTACAGGTGTGCG
97148	95235	GGACTAGACTACAGGTGTGC
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97155	95242	AGTAGTGGGACTAGACTACA
97156	95243	CAGTAGTGGGACTAGACTAC
97157	95244	ACAGTAGTGGGACTAGACTA
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97159	95246	CTACAGTAGTGGGACTAGAC
97160	95247	ACTACAGTAGTGGGACTAGA
97161	95248	CACTACAGTAGTGGGACTAG
97162	95249	CCACTACAGTAGTGGGACTA
97163	95250	GCCACTACAGTAGTGGGACT
97164	95251	AGCCACTACAGTAGTGGGAC
97165	95252	CAGCCACTACAGTAGTGGGA
97166	95253	TCAGCCACTACAGTAGTGGG
97167	95254	CTCAGCCACTACAGTAGTGG
97168	95255	CCTCAGCCACTACAGTAGTG
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97170	95257	TGCCTCAGCCACTACAGTAG
97171	95258	CTGCCTCAGCCACTACAGTA
97172	95259	CCTGCCTCAGCCACTACAGT
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97174	95261	CTCCTGCCTCAGCCACTACA
97175	95262	TCTCCTGCCTCAGCCACTAC
97176	95263	ATCTCCTGCCTCAGCCACTA
97177	95264	AATCTCCTGCCTCAGCCACT
97178	95265	GAATCTCCTGCCTCAGCCAC
97179	95266	CGAATCTCCTGCCTCAGCCA
97180	95267	GCGAATCTCCTGCCTCAGCC
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97185	95272	TTCAAGCGAATCTCCTGCCT
97186	95273	GTTCAAGCGAATCTCCTGCC
97187	95274	GGTTCAAGCGAATCTCCTGC
97188	95275	GGGTTCAAGCGAATCTCCTG
97189	95276	TGGGTTCAAGCGAATCTCCT
97190	95277	CTGGGTTCAAGCGAATCTCC
97191	95278	CCTGGGTTCAAGCGAATCTC
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97196	95283	TACCTCCTGGGTTCAAGCGA
97197	95284	CTACCTCCTGGGTTCAAGCG
97198	95285	TCTACCTCCTGGGTTCAAGC
97199	95286	CTCTACCTCCTGGGTTCAAG
97200	95287	CCTCTACCTCCTGGGTTCAA
97201	95288	ACCTCTACCTCCTGGGTTCA
97202	95289	AACCTCTACCTCCTGGGTTC
97203	95290	CAACCTCTACCTCCTGGGTT
97204	95291	GCAACCTCTACCTCCTGGGT
97205	95292	TGCAACCTCTACCTCCTGGG
97206	95293	CTGCAACCTCTACCTCCTGG
97207	95294	ACTGCAACCTCTACCTCCTG

146284	144371	TTCTCCTCATTAAGACAATC
146285	144372	CTTCTCCTCATTAAGACAAT
146286	144373	CCTTCTCCTCATTAAGACAA
146287	144374	TCCTTCTCCTCATTAAGACA
146288	144375	CTCCTTCTCCTCATTAAGAC
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146291	144378	CAGCTCCTTCTCCTCATTAA
146292	144379	GCAGCTCCTTCTCCTCATTA
146293	144380	TGCAGCTCCTTCTCCTCATT
146294	144381	GTGCAGCTCCTTCTCCTCAT
146295	144382	AGTGCAGCTCCTTCTCCTCA
146296	144383	CAGTGCAGCTCCTTCTCCTC
146297	144384	TCAGTGCAGCTCCTTCTCCT
146298	144385	TTCAGTGCAGCTCCTTCTCC
146299	144386	CTTCAGTGCAGCTCCTTCTC
146300	144387	ACTTCAGTGCAGCTCCTTCT
146301	144388	AACTTCAGTGCAGCTCCTTC
146302	144389	CAACTTCAGTGCAGCTCCTT
146303	144390	CCAACTTCAGTGCAGCTCCT
146304	144391	CCCAACTTCAGTGCAGCTCC
146305	144392	GCCCAACTTCAGTGCAGCTC
146306	144393	AGCCCAACTTCAGTGCAGCT
146307	144394	GAGCCCAACTTCAGTGCAGC
146308	144395	AGAGCCCAACTTCAGTGCAG
146309	144396	TAGAGCCCAACTTCAGTGCA
146310	144397	TTAGAGCCCAACTTCAGTGC
146311	144398	GTTAGAGCCCAACTTCAGTG
146312	144399	CGTTAGAGCCCAACTTCAGT
146313	144400	GCGTTAGAGCCCAACTTCAG
146314	144401	AGCGTTAGAGCCCAACTTCA
146315	144402	CAGCGTTAGAGCCCAACTTC
146316	144403	CCAGCGTTAGAGCCCAACTT
146317	144404	GCCAGCGTTAGAGCCCAACT
146318	144405	GGCCAGCGTTAGAGCCCAAC
146319	144406	AGGCCAGCGTTAGAGCCCAA
146320	144407	AAGGCCAGCGTTAGAGCCCA
146321	144408	CAAGGCCAGCGTTAGAGCCC
146322	144409	TCAAGGCCAGCGTTAGAGCC
146323	144410	CTCAAGGCCAGCGTTAGAGC
146324	144411	CCTCAAGGCCAGCGTTAGAG
146325	144412	GCCTCAAGGCCAGCGTTAGA
146326	144413	GGCCTCAAGGCCAGCGTTAG
146327	144414	GGGCCTCAAGGCCAGCGTTA
146328	144415	AGGGCCTCAAGGCCAGCGTT
146329	144416	GAGGGCCTCAAGGCCAGCGT
146330	144417	GGAGGGCCTCAAGGCCAGCG
146331	144418	GGGAGGGCCTCAAGGCCAGC
146332	144419	AGGGAGGGCCTCAAGGCCAG
146333	144420	CAGGGAGGGCCTCAAGGCCA
146334	144421	CCAGGGAGGGCCTCAAGGCC
146335	144422	CCCAGGGAGGGCCTCAAGGC
146336	144423	CCCCAGGGAGGGCCTCAAGG
146337	144424	GCCCCAGGGAGGGCCTCAAG
146338	144425	AGCCCCAGGGAGGGCCTCAA
146339	144426	CAGCCCCAGGGAGGGCCTCA
146340	144427	ACAGCCCCAGGGAGGGCCTC
146341	144428	AACAGCCCCAGGGAGGGCCT
146342	144429	TAACAGCCCCAGGGAGGGCC
146343	144430	GTAACAGCCCCAGGGAGGGC
146344	144431	CGTAACAGCCCCAGGGAGGG
146345	144432	CCGTAACAGCCCCAGGGAGG
146346	144433	CCCGTAACAGCCCCAGGGAG
146347	144434	ACCCGTAACAGCCCCAGGGA
146348	144435	CACCCGTAACAGCCCCAGGG
146349	144436	TCACCCGTAACAGCCCCAGG
146350	144437	TTCACCCGTAACAGCCCCAG
146351	144438	ATTCACCCGTAACAGCCCCA
146352	144439	AATTCACCCGTAACAGCCCC
146353	144440	CAATTCACCCGTAACAGCCC
146354	144441	CCAATTCACCCGTAACAGCC

48061	46148	AGGAATAATGACAAGAAAAA
48062	46149	TAGGAATAATGACAAGAAAA
48063	46150	TTAGGAATAATGACAAGAAA
48064	46151	TTTAGGAATAATGACAAGAA
48065	46152	TTTTAGGAATAATGACAAGA
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48072	46159	TGTATTGTTTTAGGAATAAT
48073	46160	CTGTATTGTTTTAGGAATAA
48074	46161	ACTGTATTGTTTTAGGAATA
48075	46162	TACTGTATTGTTTTAGGAAT
48076	46163	ATACTGTATTGTTTTAGGAA
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48079	46166	GTCATACTGTATTGTTTTAG
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48082	46169	ATTGTCATACTGTATTGTTT
48083	46170	AATTGTCATACTGTATTGTT
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48091	46178	GCTATGTAAATTGTCATACT
48092	46179	TGCTATGTAAATTGTCATAC
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48095	46182	AAATGCTATGTAAATTGTCA
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48111	46198	ATACCTAATATAATGTAAAT
48112	46199	AATACCTAATATAATGTAAA
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48114	46201	GTAATACCTAATATAATGTA
48115	46202	TGTAATACCTAATATAATGT
48116	46203	TTGTAATACCTAATATAATG
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48119	46206	TACTTGTAATACCTAATATA
48120	46207	TTACTTGTAATACCTAATAT
48121	46208	ATTACTTGTAATACCTAATA
48122	46209	AATTACTTGTAATACCTAAT
48123	46210	AAATTACTTGTAATACCTAA
48124	46211	TAAATTACTTGTAATACCTA
48125	46212	CTAAATTACTTGTAATACCT
48126	46213	CCTAAATTACTTGTAATACC
48127	46214	CCCTAAATTACTTGTAATAC
48128	46215	TCCCTAAATTACTTGTAATA
48129	46216	ATCCCTAAATTACTTGTAAT
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48131	46218	CTATCCCTAAATTACTTGTA

97208	95295	CACTGCAACCTCTACCTCCT
97209	95296	TCACTGCAACCTCTACCTCC
97210	95297	CTCACTGCAACCTCTACCTC
97211	95298	GCTCACTGCAACCTCTACCT
97212	95299	AGCTCACTGCAACCTCTACC
97213	95300	CAGCTCACTGCAACCTCTAC
97214	95301	TCAGCTCACTGCAACCTCTA
97215	95302	CTCAGCTCACTGCAACCTCT
97216	95303	TCTCAGCTCACTGCAACCTC
97217	95304	ATCTCAGCTCACTGCAACCT
97218	95305	GATCTCAGCTCACTGCAACC
97219	95306	TGATCTCAGCTCACTGCAAC
97220	95307	ATGATCTCAGCTCACTGCAA
97221	95308	CATGATCTCAGCTCACTGCA
97222	95309	GCATGATCTCAGCTCACTGC
97223	95310	TGCATGATCTCAGCTCACTG
97224	95311	GTGCATGATCTCAGCTCACT
97225	95312	AGTGCATGATCTCAGCTCAC
97226	95313	GAGTGCATGATCTCAGCTCA
97227	95314	GGAGTGCATGATCTCAGCTC
97228	95315	TGGAGTGCATGATCTCAGCT
97229	95316	CTGGAGTGCATGATCTCAGC
97230	95317	ACTGGAGTGCATGATCTCAG
97231	95318	CACTGGAGTGCATGATCTCA
97232	95319	ACACTGGAGTGCATGATCTC
97233	95320	CACACTGGAGTGCATGATCT
97234	95321	CCACACTGGAGTGCATGATC
97235	95322	CCCACACTGGAGTGCATGAT
97236	95323	GCCCACACTGGAGTGCATGA
97237	95324	CGCCCACACTGGAGTGCATG
97238	95325	TCGCCCACACTGGAGTGCAT
97239	95326	GTCGCCCACACTGGAGTGCA
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97241	95328	CTGTCGCCCACACTGGAGTG
97242	95329	TCTGTCGCCCACACTGGAGT
97243	95330	CTCTGTCGCCCACACTGGAG
97244	95331	ACTCTGTCGCCCACACTGGA
97245	95332	CACTCTGTCGCCCACACTGG
97246	95333	TCACTCTGTCGCCCACACTG
97247	95334	CTCACTCTGTCGCCCACACT
97248	95335	TCTCACTCTGTCGCCCACAC
97249	95336	GTCTCACTCTGTCGCCCACA
97250	95337	AGTCTCACTCTGTCGCCCAC
97251	95338	GAGTCTCACTCTGTCGCCCA
97252	95339	GGAGTCTCACTCTGTCGCCC
97253	95340	TGGAGTCTCACTCTGTCGCC
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97265	95352	TTTTTTTTGAGATGGAGTCT
97266	95353	CTTTTTTTTGAGATGGAGTC
97267	95354	TCTTTTTTTTGAGATGGAGT
97268	95355	GTCTTTTTTTTTGAGATGGAG
97269	95356	AGTCTTTTTTTTTGAGATGGA
97270	95357	TAGTCTTTTTTTTTGAGATGG
97271	95358	ATAGTCTTTTTTTTTGAGATG
97272	95359	AATAGTCTTTTTTTTTGAGAT
97273	95360	GAATAGTCTTTTTTTTTGAGA
97274	95361	AGAATAGTCTTTTTTTTTGAG
97275	95362	AAGAATAGTCTTTTTTTTTGA
97276	95363	AAAGAATAGTCTTTTTTTTTG
97277	95364	GAAAGAATAGTCTTTTTTTT
97278	95365	GGAAAGAATAGTCTTTTTTT

146355	144442	GCCAATTCACCCGTAACAGC
146356	144443	AGCCAATTCACCCGTAACAG
146357	144444	CAGCCAATTCACCCGTAACA
146358	144445	ACAGCCAATTCACCCGTAAC
146359	144446	TACAGCCAATTCACCCGTAA
146360	144447	ATACAGCCAATTCACCCGTA
146361	144448	AATACAGCCAATTCACCCGT
146362	144449	TAATACAGCCAATTCACCCG
146363	144450	CTAATACAGCCAATTCACCC
146364	144451	TCTAATACAGCCAATTCACC
146365	144452	ATCTAATACAGCCAATTCAC
146366	144453	CATCTAATACAGCCAATTCA
146367	144454	ACATCTAATACAGCCAATTC
146368	144455	GACATCTAATACAGCCAATT
146369	144456	AGACATCTAATACAGCCAAT
146370	144457	GAGACATCTAATACAGCCAA
146371	144458	AGAGACATCTAATACAGCCA
146372	144459	CAGAGACATCTAATACAGCC
146373	144460	GCAGAGACATCTAATACAGC
146374	144461	AGCAGAGACATCTAATACAG
146375	144462	TAGCAGAGACATCTAATACA
146376	144463	GTAGCAGAGACATCTAATAC
146377	144464	AGTAGCAGAGACATCTAATA
146378	144465	AAGTAGCAGAGACATCTAAT
146379	144466	AAAGTAGCAGAGACATCTAA
146380	144467	GAAAGTAGCAGAGACATCTA
146381	144468	TGAAAGTAGCAGAGACATCT
146382	144469	ATGAAAGTAGCAGAGACATC
146383	144470	TATGAAAGTAGCAGAGACAT
146384	144471	TTATGAAAGTAGCAGAGACA
146385	144472	GTTATGAAAGTAGCAGAGAC
146386	144473	TGTTATGAAAGTAGCAGAGA
146387	144474	CTGTTATGAAAGTAGCAGAG
146388	144475	TCTGTTATGAAAGTAGCAGA
146389	144476	TTCTGTTATGAAAGTAGCAG
146390	144477	GTTCTGTTATGAAAGTAGCA
146391	144478	AGTTCTGTTATGAAAGTAGC
146392	144479	GAGTTCTGTTATGAAAGTAG
146393	144480	AGAGTTCTGTTATGAAAGTA
146394	144481	GAGAGTTCTGTTATGAAAGT
146395	144482	AGAGAGTTCTGTTATGAAAG
146396	144483	CAGAGAGTTCTGTTATGAAA
146397	144484	TCAGAGAGTTCTGTTATGAA
146398	144485	CTCAGAGAGTTCTGTTATGA
146399	144486	CCTCAGAGAGTTCTGTTATG
146400	144487	GCCTCAGAGAGTTCTGTTAT
146401	144488	CGCCTCAGAGAGTTCTGTTA
146402	144489	CCGCCTCAGAGAGTTCTGTT
146403	144490	CCCGCCTCAGAGAGTTCTGT
146404	144491	ACCCGCCTCAGAGAGTTCTG
146405	144492	GACCCGCCTCAGAGAGTTCT
146406	144493	AGACCCGCCTCAGAGAGTTC
146407	144494	TAGACCCGCCTCAGAGAGTT
146408	144495	TTAGACCCGCCTCAGAGAGT
146409	144496	CTTAGACCCGCCTCAGAGAG
146410	144497	ACTTAGACCCGCCTCAGAGA
146411	144498	CACTTAGACCCGCCTCAGAG
146412	144499	TCACTTAGACCCGCCTCAGA
146413	144500	CTCACTTAGACCCGCCTCAG
146414	144501	TCTCACTTAGACCCGCCTCA
146415	144502	GTCTCACTTAGACCCGCCTC
146416	144503	GGTCTCACTTAGACCCGCCT
146417	144504	AGGTCTCACTTAGACCCGCC
146418	144505	CAGGTCTCACTTAGACCCGC
146419	144506	GCAGGTCTCACTTAGACCCG
146420	144507	GGCAGGTCTCACTTAGACCC
146421	144508	TGGCAGGTCTCACTTAGACC
146422	144509	GTGGCAGGTCTCACTTAGAC
146423	144510	TGTGGCAGGTCTCACTTAGA
146424	144511	TTGTGGCAGGTCTCACTTAG
146425	144512	ATTGTGGCAGGTCTCACTTA

48132	46219	ACTATCCCTAAATTACTTGT
48133	46220	AACTATCCCTAAATTACTTG
48134	46221	AAACTATCCCTAAATTACTT
48135	46222	TAAACTATCCCTAAATTACT
48136	46223	TTAAACTATCCCTAAATTAC
48137	46224	TTTAAACTATCCCTAAATTA
48138	46225	CTTTAAACTATCCCTAAATT
48139	46226	ACTTTAAACTATCCCTAAAT
48140	46227	TACTTTAAACTATCCCTAAA
48141	46228	ATACTTTAAACTATCCCTAA
48142	46229	AATACTTTAAACTATCCCTA
48143	46230	AAATACTTTAAACTATCCCT
48144	46231	CAAATACTTTAAACTATCCC
48145	46232	CCAAATACTTTAAACTATCC
48146	46233	CCCAAATACTTTAAACTATC
48147	46234	TCCCAAATACTTTAAACTAT
48148	46235	CTCCCAAATACTTTAAACTA
48149	46236	TCTCCCAAATACTTTAAACT
48150	46237	TTCTCCCAAATACTTTAAAC
48151	46238	ATTCTCCCAAATACTTTAAA
48152	46239	CATTCTCCCAAATACTTTAA
48153	46240	ACATTCTCCCAAATACTTTA
48154	46241	CACATTCTCCCAAATACTTT
48155	46242	GCACATTCTCCCAAATACTT
48156	46243	AGCACATTCTCCCAAATACT
48157	46244	AAGCACATTCTCCCAAATAC
48158	46245	TAAGCACATTCTCCCAAATA
48159	46246	CTAAGCACATTCTCCCAAAT
48160	46247	ACTAAGCACATTCTCCCAAA
48161	46248	AACTAAGCACATTCTCCCAA
48162	46249	TAACTAAGCACATTCTCCCA
48163	46250	ATAACTAAGCACATTCTCCC
48164	46251	TATAACTAAGCACATTCTCC
48165	46252	ATATAACTAAGCACATTCTC
48166	46253	CATATAACTAAGCACATTCT
48167	46254	GCATATAACTAAGCACATTC
48168	46255	TGCATATAACTAAGCACATT
48169	46256	TTGCATATAACTAAGCACAT
48170	46257	TTTGCATATAACTAAGCACA
48171	46258	ATTTGCATATAACTAAGCAC
48172	46259	TATTTGCATATAACTAAGCA
48173	46260	GTATTTGCATATAACTAAGC
48174	46261	AGTATTTGCATATAACTAAG
48175	46262	TAGTATTTGCATATAACTAA
48176	46263	ATAGTATTTGCATATAACTA
48177	46264	AATAGTATTTGCATATAACT
48178	46265	TAATAGTATTTGCATATAAC
48179	46266	GTAATAGTATTTGCATATAA
48180	46267	TGTAATAGTATTTGCATATA
48181	46268	ATGTAATAGTATTTGCATAT
48182	46269	AATGTAATAGTATTTGCATA
48183	46270	AAATGTAATAGTATTTGCAT
48184	46271	AAAATGTAATAGTATTTGCA
48185	46272	TAAAATGTAATAGTATTTGC
48186	46273	ATAAAATGTAATAGTATTTG
48187	46274	CATAAAATGTAATAGTATTT
48188	46275	ACATAAAATGTAATAGTATT
48189	46276	TACATAAAATGTAATAGTAT
48190	46277	TTACATAAAATGTAATAGTA
48191	46278	CTTACATAAAATGTAATAGT
48192	46279	ACTTACATAAAATGTAATAG
48193	46280	CACTTACATAAAATGTAATA
48194	46281	TCACTTACATAAAATGTAAT
48195	46282	GTCACTTACATAAAATGTAA
48196	46283	AGTCACTTACATAAAATGTA
48197	46284	AAGTCACTTACATAAAATGT
48198	46285	TAAGTCACTTACATAAAATG
48199	46286	TTAAGTCACTTACATAAAAT
48200	46287	CTTAAGTCACTTACATAAAA
48201	46288	ACTTAAGTCACTTACATAAA
48202	46289	TACTTAAGTCACTTACATAA

97279	95366	AGGAAAGAATAGTCTTTTTT
97280	95367	GAGGAAAGAATAGTCTTTTT
97281	95368	GGAGGAAAGAATAGTCTTTT
97282	95369	TGGAGGAAAGAATAGTCTTT
97283	95370	ATGGAGGAAAGAATAGTCTT
97284	95371	AATGGAGGAAAGAATAGTCT
97285	95372	CAATGGAGGAAAGAATAGTC
97286	95373	TCAATGGAGGAAAGAATAGT
97287	95374	TTCAATGGAGGAAAGAATAG
97288	95375	ATTCAATGGAGGAAAGAATA
97289	95376	AATTCAATGGAGGAAAGAAT
97290	95377	TAATTCAATGGAGGAAAGAA
97291	95378	ATAATTCAATGGAGGAAAGA
97292	95379	GATAATTCAATGGAGGAAAG
97293	95380	AGATAATTCAATGGAGGAAA
97294	95381	AAGATAATTCAATGGAGGAA
97295	95382	GAAGATAATTCAATGGAGGA
97296	95383	TGAAGATAATTCAATGGAGG
97297	95384	GTGAAGATAATTCAATGGAG
97298	95385	TGTGAAGATAATTCAATGGA
97299	95386	ATGTGAAGATAATTCAATGG
97300	95387	CATGTGAAGATAATTCAATG
97301	95388	GCATGTGAAGATAATTCAAT
97302	95389	AGCATGTGAAGATAATTCAA
97303	95390	AAGCATGTGAAGATAATTCA
97304	95391	CAAGCATGTGAAGATAATTC
97305	95392	ACAAGCATGTGAAGATAATT
97306	95393	AACAAGCATGTGAAGATAAT
97307	95394	CAACAAGCATGTGAAGATAA
97308	95395	CCAACAAGCATGTGAAGATA
97309	95396	TCCAACAAGCATGTGAAGAT
97310	95397	TTCCAACAAGCATGTGAAGA
97311	95398	CTTCCAACAAGCATGTGAAG
97312	95399	ACTTCCAACAAGCATGTGAA
97313	95400	GACTTCCAACAAGCATGTGA
97314	95401	AGACTTCCAACAAGCATGTG
97315	95402	CAGACTTCCAACAAGCATGT
97316	95403	ACAGACTTCCAACAAGCATG
97317	95404	AACAGACTTCCAACAAGCAT
97318	95405	CAACAGACTTCCAACAAGCA
97319	95406	TCAACAGACTTCCAACAAGC
97320	95407	GTCAACAGACTTCCAACAAG
97321	95408	AGTCAACAGACTTCCAACAA
97322	95409	TAGTCAACAGACTTCCAACA
97323	95410	GTAGTCAACAGACTTCCAAC
97324	95411	TGTAGTCAACAGACTTCCAA
97325	95412	TTGTAGTCAACAGACTTCCA
97326	95413	TTTGTAGTCAACAGACTTCC
97327	95414	ATTTGTAGTCAACAGACTTC
97328	95415	CATTTGTAGTCAACAGACTT
97329	95416	ACATTTGTAGTCAACAGACT
97330	95417	CACATTTGTAGTCAACAGAC
97331	95418	TCACATTTGTAGTCAACAGA
97332	95419	TTCACATTTGTAGTCAACAG
97333	95420	TTTCACATTTGTAGTCAACA
97334	95421	CTTTCACATTTGTAGTCAAC
97335	95422	ACTTTCACATTTGTAGTCAA
97336	95423	AACTTTCACATTTGTAGTCA
97337	95424	AAACTTTCACATTTGTAGTC
97338	95425	TAAACTTTCACATTTGTAGT
97339	95426	ATAAACTTTCACATTTGTAG
97340	95427	AATAAACTTTCACATTTGTA
97341	95428	TAATAAACTTTCACATTTGT
97342	95429	GTAATAAACTTTCACATTTG
97343	95430	AGTAATAAACTTTCACATTT
97344	95431	CAGTAATAAACTTTCACATT
97345	95432	CCAGTAATAAACTTTCACAT
97346	95433	TCCAGTAATAAACTTTCACA
97347	95434	GTCCAGTAATAAACTTTCAC
97348	95435	AGTCCAGTAATAAACTTTCA
97349	95436	GAGTCCAGTAATAAACTTTC

146426	144513	CATTGTGGCAGGTCTCACTT
146427	144514	TCATTGTGGCAGGTCTCACT
146428	144515	TTCATTGTGGCAGGTCTCAC
146429	144516	ATTCATTGTGGCAGGTCTCA
146430	144517	AATTCATTGTGGCAGGTCTC
146431	144518	GAATTCATTGTGGCAGGTCT
146432	144519	GGAATTCATTGTGGCAGGTC
146433	144520	TGGAATTCATTGTGGCAGGT
146434	144521	ATGGAATTCATTGTGGCAGG
146435	144522	AATGGAATTCATTGTGGCAG
146436	144523	AAATGGAATTCATTGTGGCA
146437	144524	GAAATGGAATTCATTGTGGC
146438	144525	GGAAATGGAATTCATTGTGG
146439	144526	AGGAAATGGAATTCATTGTG
146440	144527	CAGGAAATGGAATTCATTGT
146441	144528	ACAGGAAATGGAATTCATTG
146442	144529	AACAGGAAATGGAATTCATT
146443	144530	TAACAGGAAATGGAATTCAT
146444	144531	TTAACAGGAAATGGAATTCA
146445	144532	TTTAACAGGAAATGGAATTC
146446	144533	ATTTAACAGGAAATGGAATT
146447	144534	TATTTAACAGGAAATGGAAT
146448	144535	CTATTTAACAGGAAATGGAA
146449	144536	ACTATTTAACAGGAAATGGA
146450	144537	CACTATTTAACAGGAAATGG
146451	144538	GCACTATTTAACAGGAAATG
146452	144539	CGCACTATTTAACAGGAAAT
146453	144540	GCGCACTATTTAACAGGAAA
146454	144541	GGCGCACTATTTAACAGGAA
146455	144542	TGGCGCACTATTTAACAGGA
146456	144543	CTGGCGCACTATTTAACAGG
146457	144544	ACTGGCGCACTATTTAACAG
146458	144545	CACTGGCGCACTATTTAACA
146459	144546	TCACTGGCGCACTATTTAAC
146460	144547	CTCACTGGCGCACTATTTAA
146461	144548	CCTCACTGGCGCACTATTTA
146462	144549	GCCTCACTGGCGCACTATTT
146463	144550	AGCCTCACTGGCGCACTATT
146464	144551	GAGCCTCACTGGCGCACTAT
146465	144552	AGAGCCTCACTGGCGCACTA
146466	144553	CAGAGCCTCACTGGCGCACT
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146470	144557	TTGCCAGAGCCTCACTGGCG
146471	144558	CTTGCCAGAGCCTCACTGGC
146472	144559	CCTTGCCAGAGCCTCACTGG
146473	144560	ACCTTGCCAGAGCCTCACTG
146474	144561	CACCTTGCCAGAGCCTCACT
146475	144562	ACACCTTGCCAGAGCCTCAC
146476	144563	CACACCTTGCCAGAGCCTCA
146477	144564	CCACACCTTGCCAGAGCCTC
146478	144565	CCCACACCTTGCCAGAGCCT
146479	144566	GCCCACACCTTGCCAGAGCC
146480	144567	AGCCCACACCTTGCCAGAGC
146481	144568	TAGCCCACACCTTGCCAGAG
146482	144569	CTAGCCCACACCTTGCCAGA
146483	144570	TCTAGCCCACACCTTGCCAG
146484	144571	CTCTAGCCCACACCTTGCCA
146485	144572	TCTCTAGCCCACACCTTGCC
146486	144573	ATCTCTAGCCCACACCTTGC
146487	144574	CATCTCTAGCCCACACCTTG
146488	144575	GCATCTCTAGCCCACACCTT
146489	144576	CGCATCTCTAGCCCACACCT
146490	144577	TCGCATCTCTAGCCCACACC
146491	144578	GTCGCATCTCTAGCCCACAC
146492	144579	AGTCGCATCTCTAGCCCACA
146493	144580	GAGTCGCATCTCTAGCCCAC
146494	144581	TGAGTCGCATCTCTAGCCCA
146495	144582	CTGAGTCGCATCTCTAGCCC
146496	144583	ACTGAGTCGCATCTCTAGCC

48203	46290	ATACTTAAGTCACTTACATA
48204	46291	AATACTTAAGTCACTTACAT
48205	46292	TAATACTTAAGTCACTTACA
48206	46293	ATAATACTTAAGTCACTTAC
48207	46294	CATAATACTTAAGTCACTTA
48208	46295	ACATAATACTTAAGTCACTT
48209	46296	TACATAATACTTAAGTCACT
48210	46297	TTACATAATACTTAAGTCAC
48211	46298	ATTACATAATACTTAAGTCA
48212	46299	AATTACATAATACTTAAGTC
48213	46300	GAATTACATAATACTTAAGT
48214	46301	CGAATTACATAATACTTAAG
48215	46302	CCGAATTACATAATACTTAA
48216	46303	ACCGAATTACATAATACTTA
48217	46304	TACCGAATTACATAATACTT
48218	46305	ATACCGAATTACATAATACT
48219	46306	GATACCGAATTACATAATAC
48220	46307	AGATACCGAATTACATAATA
48221	46308	CAGATACCGAATTACATAAT
48222	46309	TCAGATACCGAATTACATAA
48223	46310	TTCAGATACCGAATTACATA
48224	46311	CTTCAGATACCGAATTACAT
48225	46312	CCTTCAGATACCGAATTACA
48226	46313	TCCTTCAGATACCGAATTAC
48227	46314	CTCCTTCAGATACCGAATTA
48228	46315	CCTCCTTCAGATACCGAATT
48229	46316	ACCTCCTTCAGATACCGAAT
48230	46317	GACCTCCTTCAGATACCGAA
48231	46318	GGACCTCCTTCAGATACCGA
48232	46319	AGGACCTCCTTCAGATACCG
48233	46320	CAGGACCTCCTTCAGATACC
48234	46321	CCAGGACCTCCTTCAGATAC
48235	46322	TCCAGGACCTCCTTCAGATA
48236	46323	TTCCAGGACCTCCTTCAGAT
48237	46324	GTTCCAGGACCTCCTTCAGA
48238	46325	GGTTCCAGGACCTCCTTCAG
48239	46326	TGGTTCCAGGACCTCCTTCA
48240	46327	CTGGTTCCAGGACCTCCTTC
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48244	46331	GGGACTGGTTCCAGGACCTC
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48247	46334	TAGGGGACTGGTTCCAGGAC
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48251	46338	TTGGTAGGGGACTGGTTCCA
48252	46339	ATTGGTAGGGGACTGGTTCC
48253	46340	TATTGGTAGGGGACTGGTTC
48254	46341	TTATTGGTAGGGGACTGGTT
48255	46342	GTTATTGGTAGGGGACTGGT
48256	46343	TGTTATTGGTAGGGGACTGG
48257	46344	TTGTTATTGGTAGGGGACTG
48258	46345	GTTGTTATTGGTAGGGGACT
48259	46346	TGTTGTTATTGGTAGGGGAC
48260	46347	CTGTTGTTATTGGTAGGGGA
48261	46348	TCTGTTGTTATTGGTAGGGG
48262	46349	ATCTGTTGTTATTGGTAGGG
48263	46350	TATCTGTTGTTATTGGTAGG
48264	46351	CTATCTGTTGTTATTGGTAG
48265	46352	GCTATCTGTTGTTATTGGTA
48266	46353	AGCTATCTGTTGTTATTGGT
48267	46354	CAGCTATCTGTTGTTATTGG
48268	46355	ACAGCTATCTGTTGTTATTG
48269	46356	TACAGCTATCTGTTGTTATT
48270	46357	ATACAGCTATCTGTTGTTAT
48271	46358	AATACAGCTATCTGTTGTTA
48272	46359	GAATACAGCTATCTGTTGTT
48273	46360	AGAATACAGCTATCTGTTGT

97350	95437	AGAGTCCAGTAATAAACTTT
97351	95438	CAGAGTCCAGTAATAAACTT
97352	95439	TCAGAGTCCAGTAATAAACT
97353	95440	TTCAGAGTCCAGTAATAAAC
97354	95441	ATTCAGAGTCCAGTAATAAA
97355	95442	AATTCAGAGTCCAGTAATAA
97356	95443	CAATTCAGAGTCCAGTAATA
97357	95444	ACAATTCAGAGTCCAGTAAT
97358	95445	GACAATTCAGAGTCCAGTAA
97359	95446	GGACAATTCAGAGTCCAGTA
97360	95447	AGGACAATTCAGAGTCCAGT
97361	95448	GAGGACAATTCAGAGTCCAG
97362	95449	GGAGGACAATTCAGAGTCCA
97363	95450	TGGAGGACAATTCAGAGTCC
97364	95451	GTGGAGGACAATTCAGAGTC
97365	95452	AGTGGAGGACAATTCAGAGT
97366	95453	CAGTGGAGGACAATTCAGAG
97367	95454	TCAGTGGAGGACAATTCAGA
97368	95455	TTCAGTGGAGGACAATTCAG
97369	95456	ATTCAGTGGAGGACAATTCA
97370	95457	GATTCAGTGGAGGACAATTC
97371	95458	AGATTCAGTGGAGGACAATT
97372	95459	GAGATTCAGTGGAGGACAAT
97373	95460	AGAGATTCAGTGGAGGACAA
97374	95461	TAGAGATTCAGTGGAGGACA
97375	95462	ATAGAGATTCAGTGGAGGAC
97376	95463	CATAGAGATTCAGTGGAGGA
97377	95464	ACATAGAGATTCAGTGGAGG
97378	95465	GACATAGAGATTCAGTGGAG
97379	95466	AGACATAGAGATTCAGTGGA
97380	95467	AAGACATAGAGATTCAGTGG
97381	95468	TAAGACATAGAGATTCAGTG
97382	95469	ATAAGACATAGAGATTCAGT
97383	95470	GATAAGACATAGAGATTCAG
97384	95471	GGATAAGACATAGAGATTCA
97385	95472	AGGATAAGACATAGAGATTC
97386	95473	AAGGATAAGACATAGAGATT
97387	95474	TAAGGATAAGACATAGAGAT
97388	95475	ATAAGGATAAGACATAGAGA
97389	95476	CATAAGGATAAGACATAGAG
97390	95477	CCATAAGGATAAGACATAGA
97391	95478	GCCATAAGGATAAGACATAG
97392	95479	TGCCATAAGGATAAGACATA
97393	95480	CTGCCATAAGGATAAGACAT
97394	95481	ACTGCCATAAGGATAAGACA
97395	95482	TACTGCCATAAGGATAAGAC
97396	95483	GTACTGCCATAAGGATAAGA
97397	95484	GGTACTGCCATAAGGATAAG
97398	95485	TGGTACTGCCATAAGGATAA
97399	95486	ATGGTACTGCCATAAGGATA
97400	95487	TATGGTACTGCCATAAGGAT
97401	95488	GTATGGTACTGCCATAAGGA
97402	95489	AGTATGGTACTGCCATAAGG
97403	95490	CAGTATGGTACTGCCATAAG
97404	95491	ACAGTATGGTACTGCCATAA
97405	95492	GACAGTATGGTACTGCCATA
97406	95493	AGACAGTATGGTACTGCCAT
97407	95494	AAGACAGTATGGTACTGCCA
97408	95495	CAAGACAGTATGGTACTGCC
97409	95496	TCAAGACAGTATGGTACTGC
97410	95497	ATCAAGACAGTATGGTACTG
97411	95498	AATCAAGACAGTATGGTACT
97412	95499	TAATCAAGACAGTATGGTAC
97413	95500	CTAATCAAGACAGTATGGTA
97414	95501	TCTAATCAAGACAGTATGGT
97415	95502	CTCTAATCAAGACAGTATGG
97416	95503	ACTCTAATCAAGACAGTATG
97417	95504	AACTCTAATCAAGACAGTAT
97418	95505	TAACTCTAATCAAGACAGTA
97419	95506	GTAACTCTAATCAAGACAGT
97420	95507	AGTAACTCTAATCAAGACAG

146497	144584	AACTGAGTCGCATCTCTAGC
146498	144585	CAACTGAGTCGCATCTCTAG
146499	144586	CCAACTGAGTCGCATCTCTA
146500	144587	TCCAACTGAGTCGCATCTCT
146501	144588	ATCCAACTGAGTCGCATCTC
146502	144589	GATCCAACTGAGTCGCATCT
146503	144590	AGATCCAACTGAGTCGCATC
146504	144591	TAGATCCAACTGAGTCGCAT
146505	144592	ATAGATCCAACTGAGTCGCA
146506	144593	GATAGATCCAACTGAGTCGC
146507	144594	AGATAGATCCAACTGAGTCG
146508	144595	GAGATAGATCCAACTGAGTC
146509	144596	AGAGATAGATCCAACTGAGT
146510	144597	GAGAGATAGATCCAACTGAG
146511	144598	TGAGAGATAGATCCAACTGA
146512	144599	CTGAGAGATAGATCCAACTG
146513	144600	TCTGAGAGATAGATCCAACT
146514	144601	TTCTGAGAGATAGATCCAAC
146515	144602	CTTCTGAGAGATAGATCCAA
146516	144603	CCTTCTGAGAGATAGATCCA
146517	144604	GCCTTCTGAGAGATAGATCC
146518	144605	AGCCTTCTGAGAGATAGATC
146519	144606	TAGCCTTCTGAGAGATAGAT
146520	144607	GTAGCCTTCTGAGAGATAGA
146521	144608	GGTAGCCTTCTGAGAGATAG
146522	144609	AGGTAGCCTTCTGAGAGATA
146523	144610	AAGGTAGCCTTCTGAGAGAT
146524	144611	CAAGGTAGCCTTCTGAGAGA
146525	144612	ACAAGGTAGCCTTCTGAGAG
146526	144613	TACAAGGTAGCCTTCTGAGA
146527	144614	TTACAAGGTAGCCTTCTGAG
146528	144615	CTTACAAGGTAGCCTTCTGA
146529	144616	ACTTACAAGGTAGCCTTCTG
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146531	144618	CTACTTACAAGGTAGCCTTC
146532	144619	TCTACTTACAAGGTAGCCTT
146533	144620	CTCTACTTACAAGGTAGCCT
146534	144621	ACTCTACTTACAAGGTAGCC
146535	144622	AACTCTACTTACAAGGTAGC
146536	144623	GAACTCTACTTACAAGGTAG
146537	144624	GGAACTCTACTTACAAGGTA
146538	144625	TGGAACTCTACTTACAAGGT
146539	144626	GTGGAACTCTACTTACAAGG
146540	144627	TGTGGAACTCTACTTACAAG
146541	144628	CTGTGGAACTCTACTTACAA
146542	144629	GCTGTGGAACTCTACTTACA
146543	144630	AGCTGTGGAACTCTACTTAC
146544	144631	GAGCTGTGGAACTCTACTTA
146545	144632	AGAGCTGTGGAACTCTACTT
146546	144633	CAGAGCTGTGGAACTCTACT
146547	144634	CCAGAGCTGTGGAACTCTAC
146548	144635	CCCAGAGCTGTGGAACTCTA
146549	144636	TCCCAGAGCTGTGGAACTCT
146550	144637	TTCCCAGAGCTGTGGAACTC
146551	144638	CTTCCCAGAGCTGTGGAACT
146552	144639	ACTTCCCAGAGCTGTGGAAC
146553	144640	AACTTCCCAGAGCTGTGGAA
146554	144641	AAACTTCCCAGAGCTGTGGA
146555	144642	CAAACTTCCCAGAGCTGTGG
146556	144643	CCAAACTTCCCAGAGCTGTG
146557	144644	CCCAAACTTCCCAGAGCTGT
146558	144645	GCCCAAACTTCCCAGAGCTG
146559	144646	CGCCCAAACTTCCCAGAGCT
146560	144647	ACGCCCAAACTTCCCAGAGC
146561	144648	GACGCCCAAACTTCCCAGAG
146562	144649	GGACGCCCAAACTTCCCAGA
146563	144650	AGGACGCCCAAACTTCCCAG
146564	144651	GAGGACGCCCAAACTTCCCA
146565	144652	TGAGGACGCCCAAACTTCCC
146566	144653	GTGAGGACGCCCAAACTTCC
146567	144654	GGTGAGGACGCCCAAACTTC

48274	46361	AAGAATACAGCTATCTGTTG
48275	46362	CAAGAATACAGCTATCTGTT
48276	46363	ACAAGAATACAGCTATCTGT
48277	46364	AACAAGAATACAGCTATCTG
48278	46365	TAACAAGAATACAGCTATCT
48279	46366	TTAACAAGAATACAGCTATC
48280	46367	GTTAACAAGAATACAGCTAT
48281	46368	GGTTAACAAGAATACAGCTA
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48283	46370	AGGGTTAACAAGAATACAGC
48284	46371	CAGGGTTAACAAGAATACAG
48285	46372	GCAGGGTTAACAAGAATACA
48286	46373	AGCAGGGTTAACAAGAATAC
48287	46374	CAGCAGGGTTAACAAGAATA
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48289	46376	CACAGCAGGGTTAACAAGAA
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48295	46382	TACACACACAGCAGGGTTAA
48296	46383	TTACACACACAGCAGGGTTA
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48298	46385	TTTTACACACACAGCAGGGT
48299	46386	ATTTTACACACACAGCAGGG
48300	46387	TATTTTACACACACAGCAGG
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48307	46394	CTAACATTATTTTACACACA
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48309	46396	TACTAACATTATTTTACACA
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48314	46401	TCAACTACTAACATTATTTT
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48316	46403	AATCAACTACTAACATTATT
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48330	46417	AATGTACAAAAGACAATCAA
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48341	46428	AGTGACAAAATAATGTACAA
48342	46429	AAGTGACAAAATAATGTACA
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48344	46431	TTAAGTGACAAAATAATGTA

97421	95508	CAGTAACTCTAATCAAGACA
97422	95509	ACAGTAACTCTAATCAAGAC
97423	95510	TACAGTAACTCTAATCAAGA
97424	95511	ATACAGTAACTCTAATCAAG
97425	95512	AATACAGTAACTCTAATCAA
97426	95513	AAATACAGTAACTCTAATCA
97427	95514	AAAATACAGTAACTCTAATC
97428	95515	TAAAATACAGTAACTCTAAT
97429	95516	TTAAAATACAGTAACTCTAA
97430	95517	TTTAAAATACAGTAACTCTA
97431	95518	TTTTAAAATACAGTAACTCT
97432	95519	CTTTTAAAATACAGTAACTC
97433	95520	CCTTTTAAAATACAGTAACT
97434	95521	GCCTTTTAAAATACAGTAAC
97435	95522	AGCCTTTTAAAATACAGTAA
97436	95523	CAGCCTTTTAAAATACAGTA
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97438	95525	TACAGCCTTTTAAAATACAG
97439	95526	GTACAGCCTTTTAAAATACA
97440	95527	AGTACAGCCTTTTAAAATAC
97441	95528	AAGTACAGCCTTTTAAAATA
97442	95529	AAAGTACAGCCTTTTAAAAT
97443	95530	AAAAGTACAGCCTTTTAAAA
97444	95531	AAAAAGTACAGCCTTTTAAA
97445	95532	GAAAAAGTACAGCCTTTTAA
97446	95533	TGAAAAAGTACAGCCTTTTA
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97449	95536	AACTGAAAAAGTACAGCCTT
97450	95537	TAACTGAAAAAGTACAGCCT
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97460	95547	TGTTTTCTGCTAACTGAAAA
97461	95548	ATGTTTTCTGCTAACTGAAA
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97464	95551	AAAATGTTTTCTGCTAACTG
97465	95552	TAAAATGTTTTCTGCTAACT
97466	95553	CTAAAATGTTTTCTGCTAAC
97467	95554	GCTAAAATGTTTTCTGCTAA
97468	95555	AGCTAAAATGTTTTCTGCTA
97469	95556	TAGCTAAAATGTTTTCTGCT
97470	95557	ATAGCTAAAATGTTTTCTGC
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97473	95560	CTGATAGCTAAAATGTTTTC
97474	95561	GCTGATAGCTAAAATGTTTT
97475	95562	TGCTGATAGCTAAAATGTTT
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97477	95564	TGTGCTGATAGCTAAAATGT
97478	95565	TTGTGCTGATAGCTAAAATG
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97481	95568	AAGTTGTGCTGATAGCTAAA
97482	95569	AAAGTTGTGCTGATAGCTAA
97483	95570	GAAAGTTGTGCTGATAGCTA
97484	95571	AGAAAGTTGTGCTGATAGCT
97485	95572	CAGAAAGTTGTGCTGATAGC
97486	95573	ACAGAAAGTTGTGCTGATAG
97487	95574	TACAGAAAGTTGTGCTGATA
97488	95575	TTACAGAAAGTTGTGCTGAT
97489	95576	TTTACAGAAAGTTGTGCTGA
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146568	144655	GGGTGAGGACGCCCAAACTT
146569	144656	AGGGTGAGGACGCCCAAACT
146570	144657	CAGGGTGAGGACGCCCAAAC
146571	144658	GCAGGGTGAGGACGCCCAAA
146572	144659	TGCAGGGTGAGGACGCCCAA
146573	144660	TTGCAGGGTGAGGACGCCCA
146574	144661	TTTGCAGGGTGAGGACGCCC
146575	144662	CTTTGCAGGGTGAGGACGCC
146576	144663	ACTTTGCAGGGTGAGGACGC
146577	144664	AACTTTGCAGGGTGAGGACG
146578	144665	AAACTTTGCAGGGTGAGGAC
146579	144666	TAAACTTTGCAGGGTGAGGA
146580	144667	CTAAACTTTGCAGGGTGAGG
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146585	144672	AGAACCTAAACTTTGCAGGG
146586	144673	CAGAACCTAAACTTTGCAGG
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146588	144675	CACAGAACCTAAACTTTGCA
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146590	144677	ACCACAGAACCTAAACTTTG
146591	144678	CACCACAGAACCTAAACTTT
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146593	144680	TACACCACAGAACCTAAACT
146594	144681	CTACACCACAGAACCTAAAC
146595	144682	GCTACACCACAGAACCTAAA
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146597	144684	GCGCTACACCACAGAACCTA
146598	144685	TGCGCTACACCACAGAACCT
146599	144686	GTGCGCTACACCACAGAACC
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146601	144688	CAGTGCGCTACACCACAGAA
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146609	144696	ATCAACTGCAGTGCGCTACA
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146612	144699	CAAATCAACTGCAGTGCGCT
146613	144700	GCAAATCAACTGCAGTGCGC
146614	144701	AGCAAATCAACTGCAGTGCG
146615	144702	AAGCAAATCAACTGCAGTGC
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48345	46432	TTTAAGTGACAAAATAATGT
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48386	46473	GAATTTTAATACTGAAGTCA
48387	46474	CGAATTTTAATACTGAAGTC
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48410	46497	GGCTCTACTCAGAGTTTGCA
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48412	46499	GAGGCTCTACTCAGAGTTTG
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97492	95579	AGGTTTACAGAAAGTTGTGC
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97495	95582	TGAAGGTTTACAGAAAGTTG
97496	95583	ATGAAGGTTTACAGAAAGTT
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97501	95588	CATTAATGAAGGTTTACAGA
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97514	95601	AATTTAAGTCAAGCATTAAT
97515	95602	GAATTTAAGTCAAGCATTAA
97516	95603	GGAATTTAAGTCAAGCATTA
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97524	95611	TCCTTCTTGGAATTTAAGTC
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97526	95613	GCTCCTTCTTGGAATTTAAG
97527	95614	TGCTCCTTCTTGGAATTTAA
97528	95615	TTGCTCCTTCTTGGAATTTA
97529	95616	GTTGCTCCTTCTTGGAATTT
97530	95617	TGTTGCTCCTTCTTGGAATT
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97544	95631	GATAAGACTTTTTATGTTGC
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146639	144726	CCGGCTTCCCTCCCCACTAT
146640	144727	ACCGGCTTCCCTCCCCACTA
146641	144728	AACCGGCTTCCCTCCCCACT
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146647	144734	GGACCAAACCGGCTTCCCTC
146648	144735	CGGACCAAACCGGCTTCCCT
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146651	144738	ACACGGACCAAACCGGCTTC
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146661	144748	ACGCTGGCCCACACGGACCA
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146667	144754	CAAACCACGCTGGCCCACAC
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146670	144757	CACCAAACCACGCTGGCCCA
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146674	144761	ACTCCACCAAACCACGCTGG
146675	144762	GACTCCACCAAACCACGCTG
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146686	144773	CTTATGAAGCTGACTCCACC
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146697	144784	GGACCCCAGCTCTTATGAAG
146698	144785	AGGACCCCAGCTCTTATGAA
146699	144786	CAGGACCCCAGCTCTTATGA
146700	144787	ACAGGACCCCAGCTCTTATG
146701	144788	TACAGGACCCCAGCTCTTAT
146702	144789	CTACAGGACCCCAGCTCTTA
146703	144790	CCTACAGGACCCCAGCTCTT
146704	144791	ACCTACAGGACCCCAGCTCT
146705	144792	CACCTACAGGACCCCAGCTC
146706	144793	ACACCTACAGGACCCCAGCT
146707	144794	GACACCTACAGGACCCCAGC
146708	144795	AGACACCTACAGGACCCCAG
146709	144796	TAGACACCTACAGGACCCCA

48416	46503	TCAGGAGGCTCTACTCAGAG
48417	46504	TTCAGGAGGCTCTACTCAGA
48418	46505	CTTCAGGAGGCTCTACTCAG
48419	46506	TCTTCAGGAGGCTCTACTCA
48420	46507	TTCTTCAGGAGGCTCTACTC
48421	46508	ATTCTTCAGGAGGCTCTACT
48422	46509	AATTCTTCAGGAGGCTCTAC
48423	46510	AAATTCTTCAGGAGGCTCTA
48424	46511	GAAATTCTTCAGGAGGCTCT
48425	46512	TGAAATTCTTCAGGAGGCTC
48426	46513	TTGAAATTCTTCAGGAGGCT
48427	46514	CTTGAAATTCTTCAGGAGGC
48428	46515	TCTTGAAATTCTTCAGGAGG
48429	46516	CTCTTGAAATTCTTCAGGAG
48430	46517	ACTCTTGAAATTCTTCAGGA
48431	46518	AACTCTTGAAATTCTTCAGG
48432	46519	GAACTCTTGAAATTCTTCAG
48433	46520	TGAACTCTTGAAATTCTTCA
48434	46521	CTGAACTCTTGAAATTCTTC
48435	46522	ACTGAACTCTTGAAATTCTT
48436	46523	CACTGAACTCTTGAAATTCT
48437	46524	ACACTGAACTCTTGAAATTC
48438	46525	TACACTGAACTCTTGAAATT
48439	46526	ATACACTGAACTCTTGAAAT
48440	46527	AATACACTGAACTCTTGAAA
48441	46528	CAATACACTGAACTCTTGAA
48442	46529	ACAATACACTGAACTCTTGA
48443	46530	AACAATACACTGAACTCTTG
48444	46531	TAACAATACACTGAACTCTT
48445	46532	TTAACAATACACTGAACTCT
48446	46533	ATTAACAATACACTGAACTC
48447	46534	CATTAACAATACACTGAACT
48448	46535	ACATTAACAATACACTGAAC
48449	46536	AACATTAACAATACACTGAA
48450	46537	AAACATTAACAATACACTGA
48451	46538	AAAACATTAACAATACACTG
48452	46539	CAAAACATTAACAATACACT
48453	46540	TCAAAACATTAACAATACAC
48454	46541	TTCAAAACATTAACAATACA
48455	46542	TTTCAAAACATTAACAATAC
48456	46543	ATTTCAAAACATTAACAATA
48457	46544	AATTTCAAAACATTAACAAT
48458	46545	AAATTTCAAAACATTAACAA
48459	46546	AAAATTTCAAAACATTAACA
48460	46547	AAAAATTTCAAAACATTAAC
48461	46548	AAAAAATTTCAAAACATTAA
48462	46549	AAAAAAATTTCAAAACATTA
48463	46550	TAAAAAAATTTCAAAACATT
48464	46551	ATAAAAAAATTTCAAAACAT
48465	46552	AATAAAAAAATTTCAAAACA
48466	46553	CAATAAAAAAATTTCAAAAC
48467	46554	ACAATAAAAAAATTTCAAAA
48468	46555	AACAATAAAAAAATTTCAAA
48469	46556	AAACAATAAAAAAATTTCAA
48470	46557	AAAACAATAAAAAAATTTCA
48471	46558	CAAAACAATAAAAAAATTTC
48472	46559	ACAAAACAATAAAAAAATTT
48473	46560	AACAAAACAATAAAAAAATT
48474	46561	TAACAAAACAATAAAAAAAT
48475	46562	CTAACAAAACAATAAAAAAA
48476	46563	ACTAACAAAACAATAAAAAA
48477	46564	CACTAACAAAACAATAAAAA
48478	46565	TCACTAACAAAACAATAAAA
48479	46566	TTCACTAACAAAACAATAAA
48480	46567	ATTCACTAACAAAACAATAA
48481	46568	TATTCACTAACAAAACAATA
48482	46569	GTATTCACTAACAAAACAAT
48483	46570	GGTATTCACTAACAAAACAA
48484	46571	AGGTATTCACTAACAAAACA
48485	46572	TAGGTATTCACTAACAAAAC
48486	46573	TTAGGTATTCACTAACAAAA

97563	95650	AGACTAAAACTCCTAAAGAG
97564	95651	AAGACTAAAACTCCTAAAGA
97565	95652	TAAGACTAAAACTCCTAAAG
97566	95653	GTAAGACTAAAACTCCTAAA
97567	95654	AGTAAGACTAAAACTCCTAA
97568	95655	TAGTAAGACTAAAACTCCTA
97569	95656	GTAGTAAGACTAAAACTCCT
97570	95657	AGTAGTAAGACTAAAACTCC
97571	95658	AAGTAGTAAGACTAAAACTC
97572	95659	AAAGTAGTAAGACTAAAACT
97573	95660	AAAAGTAGTAAGACTAAAAC
97574	95661	TAAAAGTAGTAAGACTAAAA
97575	95662	CTAAAAGTAGTAAGACTAAA
97576	95663	CCTAAAAGTAGTAAGACTAA
97577	95664	ACCTAAAAGTAGTAAGACTA
97578	95665	CACCTAAAAGTAGTAAGACT
97579	95666	GCACCTAAAAGTAGTAAGAC
97580	95667	GGCACCTAAAAGTAGTAAGA
97581	95668	AGGCACCTAAAAGTAGTAAG
97582	95669	CAGGCACCTAAAAGTAGTAA
97583	95670	TCAGGCACCTAAAAGTAGTA
97584	95671	TTCAGGCACCTAAAAGTAGT
97585	95672	ATTCAGGCACCTAAAAGTAG
97586	95673	TATTCAGGCACCTAAAAGTA
97587	95674	TTATTCAGGCACCTAAAAGT
97588	95675	GTTATTCAGGCACCTAAAAG
97589	95676	GGTTATTCAGGCACCTAAAA
97590	95677	TGGTTATTCAGGCACCTAAA
97591	95678	TTGGTTATTCAGGCACCTAA
97592	95679	TTTGGTTATTCAGGCACCTA
97593	95680	ATTTGGTTATTCAGGCACCT
97594	95681	CATTTGGTTATTCAGGCACC
97595	95682	ACATTTGGTTATTCAGGCAC
97596	95683	TACATTTGGTTATTCAGGCA
97597	95684	ATACATTTGGTTATTCAGGC
97598	95685	AATACATTTGGTTATTCAGG
97599	95686	TAATACATTTGGTTATTCAG
97600	95687	ATAATACATTTGGTTATTCA
97601	95688	AATAATACATTTGGTTATTC
97602	95689	AAATAATACATTTGGTTATT
97603	95690	TAAATAATACATTTGGTTAT
97604	95691	CTAAATAATACATTTGGTTA
97605	95692	GCTAAATAATACATTTGGTT
97606	95693	GGCTAAATAATACATTTGGT
97607	95694	AGGCTAAATAATACATTTGG
97608	95695	GAGGCTAAATAATACATTTG
97609	95696	AGAGGCTAAATAATACATTT
97610	95697	AAGAGGCTAAATAATACATT
97611	95698	TAAGAGGCTAAATAATACAT
97612	95699	GTAAGAGGCTAAATAATACA
97613	95700	AGTAAGAGGCTAAATAATAC
97614	95701	TAGTAAGAGGCTAAATAATA
97615	95702	TTAGTAAGAGGCTAAATAAT
97616	95703	ATTAGTAAGAGGCTAAATAA
97617	95704	TATTAGTAAGAGGCTAAATA
97618	95705	TTATTAGTAAGAGGCTAAAT
97619	95706	GTTATTAGTAAGAGGCTAAA
97620	95707	AGTTATTAGTAAGAGGCTAA
97621	95708	GAGTTATTAGTAAGAGGCTA
97622	95709	GGAGTTATTAGTAAGAGGCT
97623	95710	AGGAGTTATTAGTAAGAGGC
97624	95711	AAGGAGTTATTAGTAAGAGG
97625	95712	CAAGGAGTTATTAGTAAGAG
97626	95713	TCAAGGAGTTATTAGTAAGA
97627	95714	ATCAAGGAGTTATTAGTAAG
97628	95715	GATCAAGGAGTTATTAGTAA
97629	95716	GGATCAAGGAGTTATTAGTA
97630	95717	TGGATCAAGGAGTTATTAGT
97631	95718	ATGGATCAAGGAGTTATTAG
97632	95719	TATGGATCAAGGAGTTATTA
97633	95720	CTATGGATCAAGGAGTTATT

146710	144797	GTAGACACCTACAGGACCCC
146711	144798	GGTAGACACCTACAGGACCC
146712	144799	TGGTAGACACCTACAGGACC
146713	144800	CTGGTAGACACCTACAGGAC
146714	144801	TCTGGTAGACACCTACAGGA
146715	144802	CTCTGGTAGACACCTACAGG
146716	144803	CCTCTGGTAGACACCTACAG
146717	144804	GCCTCTGGTAGACACCTACA
146718	144805	AGCCTCTGGTAGACACCTAC
146719	144806	CAGCCTCTGGTAGACACCTA
146720	144807	CCAGCCTCTGGTAGACACCT
146721	144808	ACCAGCCTCTGGTAGACACC
146722	144809	CACCAGCCTCTGGTAGACAC
146723	144810	CCACCAGCCTCTGGTAGACA
146724	144811	GCCACCAGCCTCTGGTAGAC
146725	144812	AGCCACCAGCCTCTGGTAGA
146726	144813	TAGCCACCAGCCTCTGGTAG
146727	144814	TTAGCCACCAGCCTCTGGTA
146728	144815	CTTAGCCACCAGCCTCTGGT
146729	144816	ACTTAGCCACCAGCCTCTGG
146730	144817	TACTTAGCCACCAGCCTCTG
146731	144818	CTACTTAGCCACCAGCCTCT
146732	144819	CCTACTTAGCCACCAGCCTC
146733	144820	GCCTACTTAGCCACCAGCCT
146734	144821	TGCCTACTTAGCCACCAGCC
146735	144822	ATGCCTACTTAGCCACCAGC
146736	144823	CATGCCTACTTAGCCACCAG
146737	144824	ACATGCCTACTTAGCCACCA
146738	144825	CACATGCCTACTTAGCCACC
146739	144826	TCACATGCCTACTTAGCCAC
146740	144827	TTCACATGCCTACTTAGCCA
146741	144828	GTTCACATGCCTACTTAGCC
146742	144829	AGTTCACATGCCTACTTAGC
146743	144830	AAGTTCACATGCCTACTTAG
146744	144831	TAAGTTCACATGCCTACTTA
146745	144832	GTAAGTTCACATGCCTACTT
146746	144833	TGTAAGTTCACATGCCTACT
146747	144834	ATGTAAGTTCACATGCCTAC
146748	144835	CATGTAAGTTCACATGCCTA
146749	144836	ACATGTAAGTTCACATGCCT
146750	144837	TACATGTAAGTTCACATGCC
146751	144838	TTACATGTAAGTTCACATGC
146752	144839	CTTACATGTAAGTTCACATG
146753	144840	ACTTACATGTAAGTTCACAT
146754	144841	GACTTACATGTAAGTTCACA
146755	144842	TGACTTACATGTAAGTTCAC
146756	144843	CTGACTTACATGTAAGTTCA
146757	144844	CCTGACTTACATGTAAGTTC
146758	144845	CCCTGACTTACATGTAAGTT
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146760	144847	ATCCCTGACTTACATGTAAG
146761	144848	GATCCCTGACTTACATGTAA
146762	144849	GGATCCCTGACTTACATGTA
146763	144850	GGGATCCCTGACTTACATGT
146764	144851	AGGGATCCCTGACTTACATG
146765	144852	TAGGGATCCCTGACTTACAT
146766	144853	TTAGGGATCCCTGACTTACA
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146768	144855	TTTTAGGGATCCCTGACTTA
146769	144856	GTTTTAGGGATCCCTGACTT
146770	144857	GGTTTTAGGGATCCCTGACT
146771	144858	AGGTTTTAGGGATCCCTGAC
146772	144859	GAGGTTTTAGGGATCCCTGA
146773	144860	TGAGGTTTTAGGGATCCCTG
146774	144861	GTGAGGTTTTAGGGATCCCT
146775	144862	AGTGAGGTTTTAGGGATCCC
146776	144863	GAGTGAGGTTTTAGGGATCC
146777	144864	AGAGTGAGGTTTTAGGGATC
146778	144865	CAGAGTGAGGTTTTAGGGAT
146779	144866	ACAGAGTGAGGTTTTAGGGA
146780	144867	AACAGAGTGAGGTTTTAGGG

48487	46574	ATTAGGTATTCACTAACAAA
48488	46575	TATTAGGTATTCACTAACAA
48489	46576	ATATTAGGTATTCACTAACA
48490	46577	AATATTAGGTATTCACTAAC
48491	46578	CAATATTAGGTATTCACTAA
48492	46579	TCAATATTAGGTATTCACTA
48493	46580	TTCAATATTAGGTATTCACT
48494	46581	ATTCAATATTAGGTATTCAC
48495	46582	CATTCAATATTAGGTATTCA
48496	46583	TCATTCAATATTAGGTATTC
48497	46584	TTCATTCAATATTAGGTATT
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48499	46586	GCTTCATTCAATATTAGGTA
48500	46587	GGCTTCATTCAATATTAGGT
48501	46588	AGGCTTCATTCAATATTAGG
48502	46589	CAGGCTTCATTCAATATTAG
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48507	46594	CTCATCAGGCTTCATTCAAT
48508	46595	CCTCATCAGGCTTCATTCAA
48509	46596	ACCTCATCAGGCTTCATTCA
48510	46597	TACCTCATCAGGCTTCATTC
48511	46598	ATACCTCATCAGGCTTCATT
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48513	46600	TTATACCTCATCAGGCTTCA
48514	46601	TTTATACCTCATCAGGCTTC
48515	46602	TTTTATACCTCATCAGGCTT
48516	46603	TTTTTATACCTCATCAGGCT
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48518	46605	ACTTTTTATACCTCATCAGG
48519	46606	TACTTTTTATACCTCATCAG
48520	46607	TTACTTTTTATACCTCATCA
48521	46608	TTTACTTTTTATACCTCATC
48522	46609	TTTTACTTTTTATACCTCAT
48523	46610	ATTTTACTTTTTATACCTCA
48524	46611	CATTTTACTTTTTATACCTC
48525	46612	TCATTTTACTTTTTATACCT
48526	46613	TTCATTTTACTTTTTATACC
48527	46614	TTTCATTTTACTTTTTATAC
48528	46615	TTTTCATTTTACTTTTTATA
48529	46616	GTTTTCATTTTACTTTTTAT
48530	46617	TGTTTTCATTTTACTTTTTA
48531	46618	TTGTTTTCATTTTACTTTTT
48532	46619	TTTGTTTTCATTTTACTTTT
48533	46620	ATTTGTTTTCATTTTACTTT
48534	46621	TATTTGTTTTCATTTTACTT
48535	46622	ATATTTGTTTTCATTTTACT
48536	46623	GATATTTGTTTTCATTTTAC
48537	46624	GGATATTTGTTTTCATTTTA
48538	46625	GGGATATTTGTTTTCATTTT
48539	46626	AGGGATATTTGTTTTCATTT
48540	46627	CAGGGATATTTGTTTTCATT
48541	46628	CCAGGGATATTTGTTTTCAT
48542	46629	ACCAGGGATATTTGTTTTCA
48543	46630	CACCAGGGATATTTGTTTTC
48544	46631	TCACCAGGGATATTTGTTTT
48545	46632	GTCACCAGGGATATTTGTTT
48546	46633	GGTCACCAGGGATATTTGTT
48547	46634	CGGTCACCAGGGATATTTGT
48548	46635	CCGGTCACCAGGGATATTTG
48549	46636	CCCGGTCACCAGGGATATTT
48550	46637	ACCCGGTCACCAGGGATATT
48551	46638	TACCCGGTCACCAGGGATAT
48552	46639	CTACCCGGTCACCAGGGATA
48553	46640	ACTACCCGGTCACCAGGGAT
48554	46641	TACTACCCGGTCACCAGGGA
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48556	46643	TATACTACCCGGTCACCAGG
48557	46644	GTATACTACCCGGTCACCAG

97634	95721	CCTATGGATCAAGGAGTTAT
97635	95722	CCCTATGGATCAAGGAGTTA
97636	95723	CCCCTATGGATCAAGGAGTT
97637	95724	GCCCCTATGGATCAAGGAGT
97638	95725	TGCCCCTATGGATCAAGGAG
97639	95726	ATGCCCCTATGGATCAAGGA
97640	95727	TATGCCCCTATGGATCAAGG
97641	95728	GTATGCCCCTATGGATCAAG
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97644	95731	CTGGTATGCCCCTATGGATC
97645	95732	CCTGGTATGCCCCTATGGAT
97646	95733	TCCTGGTATGCCCCTATGGA
97647	95734	TTCCTGGTATGCCCCTATGG
97648	95735	CTTCCTGGTATGCCCCTATG
97649	95736	TCTTCCTGGTATGCCCCTAT
97650	95737	TTCTTCCTGGTATGCCCCTA
97651	95738	TTTCTTCCTGGTATGCCCCT
97652	95739	TTTTCTTCCTGGTATGCCCC
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97655	95742	TTCTTTTCTTCCTGGTATGC
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97657	95744	ACTTCTTTTCTTCCTGGTAT
97658	95745	CACTTCTTTTCTTCCTGGTA
97659	95746	CCACTTCTTTTCTTCCTGGT
97660	95747	ACCACTTCTTTTCTTCCTGG
97661	95748	AACCACTTCTTTTCTTCCTG
97662	95749	AAACCACTTCTTTTCTTCCT
97663	95750	AAAACCACTTCTTTTCTTCC
97664	95751	AAAAACCACTTCTTTTCTTC
97665	95752	TAAAAACCACTTCTTTTCTT
97666	95753	TTAAAAACCACTTCTTTTCT
97667	95754	TTTAAAAACCACTTCTTTTC
97668	95755	TTTTAAAAACCACTTCTTTT
97669	95756	TTTTTAAAAACCACTTCTTT
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97674	95761	CTCATTTTTTAAAAACCACT
97675	95762	TCTCATTTTTTAAAAACCAC
97676	95763	CTCTCATTTTTTAAAAACCA
97677	95764	ACTCTCATTTTTTAAAAACC
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97683	95770	CGGCCCACTCTCATTTTTTA
97684	95771	CCGGCCCACTCTCATTTTTT
97685	95772	CCCGGCCCACTCTCATTTTT
97686	95773	GCCCGGCCCACTCTCATTTT
97687	95774	TGCCCGGCCCACTCTCATTT
97688	95775	GTGCCCGGCCCACTCTCATT
97689	95776	CGTGCCCGGCCCACTCTCAT
97690	95777	CCGTGCCCGGCCCACTCTCA
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97695	95782	AGCCACCGTGCCCGGCCCAC
97696	95783	CAGCCACCGTGCCCGGCCCA
97697	95784	TCAGCCACCGTGCCCGGCCC
97698	95785	ATCAGCCACCGTGCCCGGCC
97699	95786	TATCAGCCACCGTGCCCGGC
97700	95787	GTATCAGCCACCGTGCCCGG
97701	95788	GGTATCAGCCACCGTGCCCG
97702	95789	AGGTATCAGCCACCGTGCCC
97703	95790	TAGGTATCAGCCACCGTGCC
97704	95791	ATAGGTATCAGCCACCGTGC

146781	144868	AAACAGAGTGAGGTTTTAGG
146782	144869	AAAACAGAGTGAGGTTTTAG
146783	144870	AAAAACAGAGTGAGGTTTTA
146784	144871	CAAAAACAGAGTGAGGTTTT
146785	144872	ACAAAAACAGAGTGAGGTTT
146786	144873	CACAAAAACAGAGTGAGGTT
146787	144874	GCACAAAAACAGAGTGAGGT
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146790	144877	TCAGCACAAAAACAGAGTGA
146791	144878	TTCAGCACAAAAACAGAGTG
146792	144879	TTTCAGCACAAAAACAGAGT
146793	144880	CTTTCAGCACAAAAACAGAG
146794	144881	CCTTTCAGCACAAAAACAGA
146795	144882	CCCTTTCAGCACAAAAACAG
146796	144883	GCCCTTTCAGCACAAAAACA
146797	144884	TGCCCTTTCAGCACAAAAAC
146798	144885	TTGCCCTTTCAGCACAAAAA
146799	144886	TTTGCCCTTTCAGCACAAAA
146800	144887	TTTTGCCCTTTCAGCACAAA
146801	144888	TTTTTGCCCTTTCAGCACAA
146802	144889	CTTTTTGCCCTTTCAGCACA
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146808	144895	GTTAACCTTTTTGCCCTTTC
146809	144896	TGTTAACCTTTTTGCCCTTT
146810	144897	GTGTTAACCTTTTTGCCCTT
146811	144898	TGTGTTAACCTTTTTGCCCT
146812	144899	CTGTGTTAACCTTTTTGCCC
146813	144900	CCTGTGTTAACCTTTTTGCC
146814	144901	CCCTGTGTTAACCTTTTTGC
146815	144902	TCCCTGTGTTAACCTTTTTG
146816	144903	TTCCCTGTGTTAACCTTTTT
146817	144904	CTTCCCTGTGTTAACCTTTT
146818	144905	GCTTCCCTGTGTTAACCTTT
146819	144906	AGCTTCCCTGTGTTAACCTT
146820	144907	GAGCTTCCCTGTGTTAACCT
146821	144908	TGAGCTTCCCTGTGTTAACC
146822	144909	TTGAGCTTCCCTGTGTTAAC
146823	144910	TTTGAGCTTCCCTGTGTTAA
146824	144911	ATTTGAGCTTCCCTGTGTTA
146825	144912	AATTTGAGCTTCCCTGTGTT
146826	144913	AAATTTGAGCTTCCCTGTGT
146827	144914	CAAATTTGAGCTTCCCTGTG
146828	144915	GCAAATTTGAGCTTCCCTGT
146829	144916	GGCAAATTTGAGCTTCCCTG
146830	144917	TGGCAAATTTGAGCTTCCCT
146831	144918	ATGGCAAATTTGAGCTTCCC
146832	144919	CATGGCAAATTTGAGCTTCC
146833	144920	ACATGGCAAATTTGAGCTTC
146834	144921	CACATGGCAAATTTGAGCTT
146835	144922	GCACATGGCAAATTTGAGCT
146836	144923	GGCACATGGCAAATTTGAGC
146837	144924	GGGCACATGGCAAATTTGAG
146838	144925	CGGGCACATGGCAAATTTGA
146839	144926	ACGGGCACATGGCAAATTTG
146840	144927	AACGGGCACATGGCAAATTT
146841	144928	AAACGGGCACATGGCAAATT
146842	144929	CAAACGGGCACATGGCAAAT
146843	144930	TCAAACGGGCACATGGCAAA
146844	144931	TTCAAACGGGCACATGGCAA
146845	144932	ATTCAAACGGGCACATGGCA
146846	144933	TATTCAAACGGGCACATGGC
146847	144934	ATATTCAAACGGGCACATGG
146848	144935	CATATTCAAACGGGCACATG
146849	144936	ACATATTCAAACGGGCACAT
146850	144937	CACATATTCAAACGGGCACA
146851	144938	TCACATATTCAAACGGGCAC

48558	46645	AGTATACTACCCGGTCACCA
48559	46646	CAGTATACTACCCGGTCACC
48560	46647	ACAGTATACTACCCGGTCAC
48561	46648	AACAGTATACTACCCGGTCA
48562	46649	AAACAGTATACTACCCGGTC
48563	46650	GAAACAGTATACTACCCGGT
48564	46651	AGAAACAGTATACTACCCGG
48565	46652	AAGAAACAGTATACTACCCG
48566	46653	AAAGAAACAGTATACTACCC
48567	46654	CAAAGAAACAGTATACTACC
48568	46655	TCAAAGAAACAGTATACTAC
48569	46656	ATCAAAGAAACAGTATACTA
48570	46657	TATCAAAGAAACAGTATACT
48571	46658	TTATCAAAGAAACAGTATAC
48572	46659	TTTATCAAAGAAACAGTATA
48573	46660	ATTTATCAAAGAAACAGTAT
48574	46661	TATTTATCAAAGAAACAGTA
48575	46662	TTATTTATCAAAGAAACAGT
48576	46663	TTTATTTATCAAAGAAACAG
48577	46664	ATTTATTTATCAAAGAAACA
48578	46665	AATTTATTTATCAAAGAAAC
48579	46666	TAATTTATTTATCAAAGAAA
48580	46667	ATAATTTATTTATCAAAGAA
48581	46668	TATAATTTATTTATCAAAGA
48582	46669	ATATAATTTATTTATCAAAG
48583	46670	CATATAATTTATTTATCAAA
48584	46671	ACATATAATTTATTTATCAA
48585	46672	AACATATAATTTATTTATCA
48586	46673	AAACATATAATTTATTTATC
48587	46674	AAAACATATAATTTATTTAT
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48592	46679	CCCTAAAAACATATAATTTA
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48599	46686	TTTGGAGCCCTAAAAACATA
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48607	46694	ACTTCACATTTGGAGCCCTA
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48613	46700	ACTTGTACTTCACATTTGGA
48614	46701	CACTTGTACTTCACATTTGG
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48625	46712	CCTCCATTTTTCACTTGTAC
48626	46713	ACCTCCATTTTTCACTTGTA
48627	46714	TACCTCCATTTTTCACTTGT
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97705	95792	TATAGGTATCAGCCACCGTG
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97708	95795	GATTATAGGTATCAGCCACC
97709	95796	GGATTATAGGTATCAGCCAC
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97711	95798	TAGGATTATAGGTATCAGCC
97712	95799	TTAGGATTATAGGTATCAGC
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97714	95801	TGTTAGGATTATAGGTATCA
97715	95802	GTGTTAGGATTATAGGTATC
97716	95803	AGTGTTAGGATTATAGGTAT
97717	95804	AAGTGTTAGGATTATAGGTA
97718	95805	AAAGTGTTAGGATTATAGGT
97719	95806	CAAAGTGTTAGGATTATAGG
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97731	95818	GCCTCAGCCTCCCAAAGTGT
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97737	95824	CCACCCGCCTCAGCCTCCCA
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97746	95833	TCAAGTGATCCACCCGCCTC
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97752	95839	CTGACCTCAAGTGATCCACC
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146858	144945	TTTACTCTCACATATTCAAA
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146868	144955	AAATGCCGTTTTTACTCTCA
146869	144956	GAAATGCCGTTTTTACTCTC
146870	144957	TGAAATGCCGTTTTTACTCT
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146874	144961	TGGATGAAATGCCGTTTTTA
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146877	144964	CCTTGGATGAAATGCCGTTT
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146879	144966	AGCCTTGGATGAAATGCCGT
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97784	95871	TTCGCCATGTTATCCAGGCT
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97788	95875	GGGTTTCGCCATGTTATCCA
97789	95876	AGGGTTTCGCCATGTTATCC
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97797	95884	ATAAAGATAGGGTTTCGCCA
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97800	95887	TTAATAAAGATAGGGTTTCG
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146929	145016	GAGCCCTTGTTTCCTTTTTC
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146931	145018	AAGAGCCCTTGTTTCCTTTT
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146936	145023	CCAGGAAGAGCCCTTGTTTC
146937	145024	GCCAGGAAGAGCCCTTGTTT
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146939	145026	GGGCCAGGAAGAGCCCTTGT
146940	145027	AGGGCCAGGAAGAGCCCTTG
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48700	46787	TTTTACTTTGTAAGAAAAAG
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48738	46825	TTTAAAAACTAGGTAAAACA
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48749	46836	TTCAAAGTGGCTTTAAAAAC
48750	46837	ATTCAAAGTGGCTTTAAAAA
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48752	46839	TCATTCAAAGTGGCTTTAAA
48753	46840	ATCATTCAAAGTGGCTTTAA
48754	46841	AATCATTCAAAGTGGCTTTA
48755	46842	AAATCATTCAAAGTGGCTTT
48756	46843	AAAATCATTCAAAGTGGCTT
48757	46844	TAAAATCATTCAAAGTGGCT
48758	46845	GTAAAATCATTCAAAGTGGC
48759	46846	AGTAAAATCATTCAAAGTGG
48760	46847	AAGTAAAATCATTCAAAGTG
48761	46848	GAAGTAAAATCATTCAAAGT
48762	46849	AGAAGTAAAATCATTCAAAG
48763	46850	GAGAAGTAAAATCATTCAAA
48764	46851	TGAGAAGTAAAATCATTCAA
48765	46852	CTGAGAAGTAAAATCATTCA
48766	46853	ACTGAGAAGTAAAATCATTC
48767	46854	AACTGAGAAGTAAAATCATT
48768	46855	AAACTGAGAAGTAAAATCAT
48769	46856	GAAACTGAGAAGTAAAATCA
48770	46857	TGAAACTGAGAAGTAAAATC

97847	95934	CTGGGATTACAGGCATGTGC
97848	95935	GCTGGGATTACAGGCATGTG
97849	95936	AGCTGGGATTACAGGCATGT
97850	95937	TAGCTGGGATTACAGGCATG
97851	95938	GTAGCTGGGATTACAGGCAT
97852	95939	AGTAGCTGGGATTACAGGCA
97853	95940	GAGTAGCTGGGATTACAGGC
97854	95941	TGAGTAGCTGGGATTACAGG
97855	95942	CTGAGTAGCTGGGATTACAG
97856	95943	CCTGAGTAGCTGGGATTACA
97857	95944	TCCTGAGTAGCTGGGATTAC
97858	95945	CTCCTGAGTAGCTGGGATTA
97859	95946	CCTCCTGAGTAGCTGGGATT
97860	95947	GCCTCCTGAGTAGCTGGGAT
97861	95948	AGCCTCCTGAGTAGCTGGGA
97862	95949	CAGCCTCCTGAGTAGCTGGG
97863	95950	TCAGCCTCCTGAGTAGCTGG
97864	95951	CTCAGCCTCCTGAGTAGCTG
97865	95952	CCTCAGCCTCCTGAGTAGCT
97866	95953	GCCTCAGCCTCCTGAGTAGC
97867	95954	TGCCTCAGCCTCCTGAGTAG
97868	95955	CTGCCTCAGCCTCCTGAGTA
97869	95956	CCTGCCTCAGCCTCCTGAGT
97870	95957	TCCTGCCTCAGCCTCCTGAG
97871	95958	CTCCTGCCTCAGCCTCCTGA
97872	95959	TCTCCTGCCTCAGCCTCCTG
97873	95960	TTCTCCTGCCTCAGCCTCCT
97874	95961	ATTCTCCTGCCTCAGCCTCC
97875	95962	GATTCTCCTGCCTCAGCCTC
97876	95963	TGATTCTCCTGCCTCAGCCT
97877	95964	GTGATTCTCCTGCCTCAGCC
97878	95965	AGTGATTCTCCTGCCTCAGC
97879	95966	AAGTGATTCTCCTGCCTCAG
97880	95967	CAAGTGATTCTCCTGCCTCA
97881	95968	TCAAGTGATTCTCCTGCCTC
97882	95969	TTCAAGTGATTCTCCTGCCT
97883	95970	ATTCAAGTGATTCTCCTGCC
97884	95971	GATTCAAGTGATTCTCCTGC
97885	95972	GGATTCAAGTGATTCTCCTG
97886	95973	TGGATTCAAGTGATTCTCCT
97887	95974	CTGGATTCAAGTGATTCTCC
97888	95975	CCTGGATTCAAGTGATTCTC
97889	95976	TCCTGGATTCAAGTGATTCT
97890	95977	CTCCTGGATTCAAGTGATTC
97891	95978	CCTCCTGGATTCAAGTGATT
97892	95979	ACCTCCTGGATTCAAGTGAT
97893	95980	CACCTCCTGGATTCAAGTGA
97894	95981	CCACCTCCTGGATTCAAGTG
97895	95982	TCCACCTCCTGGATTCAAGT
97896	95983	CTCCACCTCCTGGATTCAAG
97897	95984	CCTCCACCTCCTGGATTCAA
97898	95985	ACCTCCACCTCCTGGATTCA
97899	95986	AACCTCCACCTCCTGGATTC
97900	95987	CAACCTCCACCTCCTGGATT
97901	95988	GCAACCTCCACCTCCTGGAT
97902	95989	TGCAACCTCCACCTCCTGGA
97903	95990	CTGCAACCTCCACCTCCTGG
97904	95991	ACTGCAACCTCCACCTCCTG
97905	95992	CACTGCAACCTCCACCTCCT
97906	95993	TCACTGCAACCTCCACCTCC
97907	95994	ATCACTGCAACCTCCACCTC
97908	95995	GATCACTGCAACCTCCACCT
97909	95996	GGATCACTGCAACCTCCACC
97910	95997	CGGATCACTGCAACCTCCAC
97911	95998	TCGGATCACTGCAACCTCCA
97912	95999	CTCGGATCACTGCAACCTCC
97913	96000	TCTCGGATCACTGCAACCTC
97914	96001	ATCTCGGATCACTGCAACCT
97915	96002	AATCTCGGATCACTGCAACC
97916	96003	CAATCTCGGATCACTGCAAC
97917	96004	GCAATCTCGGATCACTGCAA

146994	145081	AAGGTGATTTTAGTCAGCCC
146995	145082	AAAGGTGATTTTAGTCAGCC
146996	145083	GAAAGGTGATTTTAGTCAGC
146997	145084	GGAAAGGTGATTTTAGTCAG
146998	145085	TGGAAAGGTGATTTTAGTCA
146999	145086	TTGGAAAGGTGATTTTAGTC
147000	145087	GTTGGAAAGGTGATTTTAGT
147001	145088	AGTTGGAAAGGTGATTTTAG
147002	145089	AAGTTGGAAAGGTGATTTTA
147003	145090	CAAGTTGGAAAGGTGATTTT
147004	145091	TCAAGTTGGAAAGGTGATTT
147005	145092	GTCAAGTTGGAAAGGTGATT
147006	145093	TGTCAAGTTGGAAAGGTGAT
147007	145094	CTGTCAAGTTGGAAAGGTGA
147008	145095	ACTGTCAAGTTGGAAAGGTG
147009	145096	CACTGTCAAGTTGGAAAGGT
147010	145097	TCACTGTCAAGTTGGAAAGG
147011	145098	CTCACTGTCAAGTTGGAAAG
147012	145099	ACTCACTGTCAAGTTGGAAA
147013	145100	CACTCACTGTCAAGTTGGAA
147014	145101	TCACTCACTGTCAAGTTGGA
147015	145102	CTCACTCACTGTCAAGTTGG
147016	145103	TCTCACTCACTGTCAAGTTG
147017	145104	GTCTCACTCACTGTCAAGTT
147018	145105	GGTCTCACTCACTGTCAAGT
147019	145106	TGGTCTCACTCACTGTCAAG
147020	145107	CTGGTCTCACTCACTGTCAA
147021	145108	CCTGGTCTCACTCACTGTCA
147022	145109	ACCTGGTCTCACTCACTGTC
147023	145110	AACCTGGTCTCACTCACTGT
147024	145111	CAACCTGGTCTCACTCACTG
147025	145112	TCAACCTGGTCTCACTCACT
147026	145113	TTCAACCTGGTCTCACTCAC
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147031	145118	CCAAGTTCAACCTGGTCTCA
147032	145119	ACCAAGTTCAACCTGGTCTC
147033	145120	TACCAAGTTCAACCTGGTCT
147034	145121	GTACCAAGTTCAACCTGGTC
147035	145122	TGTACCAAGTTCAACCTGGT
147036	145123	CTGTACCAAGTTCAACCTGG
147037	145124	TCTGTACCAAGTTCAACCTG
147038	145125	CTCTGTACCAAGTTCAACCT
147039	145126	TCTCTGTACCAAGTTCAACC
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147042	145129	GCGTCTCTGTACCAAGTTCA
147043	145130	AGCGTCTCTGTACCAAGTTC
147044	145131	CAGCGTCTCTGTACCAAGTT
147045	145132	CCAGCGTCTCTGTACCAAGT
147046	145133	CCCAGCGTCTCTGTACCAAG
147047	145134	GCCCAGCGTCTCTGTACCAA
147048	145135	AGCCCAGCGTCTCTGTACCA
147049	145136	CAGCCCAGCGTCTCTGTACC
147050	145137	CCAGCCCAGCGTCTCTGTAC
147051	145138	GCCAGCCCAGCGTCTCTGTA
147052	145139	GGCCAGCCCAGCGTCTCTGT
147053	145140	GGGCCAGCCCAGCGTCTCTG
147054	145141	TGGGCCAGCCCAGCGTCTCT
147055	145142	CTGGGCCAGCCCAGCGTCTC
147056	145143	TCTGGGCCAGCCCAGCGTCT
147057	145144	ATCTGGGCCAGCCCAGCGTC
147058	145145	CATCTGGGCCAGCCCAGCGT
147059	145146	TCATCTGGGCCAGCCCAGCG
147060	145147	GTCATCTGGGCCAGCCCAGC
147061	145148	AGTCATCTGGGCCAGCCCAG
147062	145149	AAGTCATCTGGGCCAGCCCA
147063	145150	GAAGTCATCTGGGCCAGCCC
147064	145151	TGAAGTCATCTGGGCCAGCC

48771	46858	TTGAAACTGAGAAGTAAAAT
48772	46859	TTTGAAACTGAGAAGTAAAA
48773	46860	ATTTGAAACTGAGAAGTAAA
48774	46861	TATTTGAAACTGAGAAGTAA
48775	46862	GTATTTGAAACTGAGAAGTA
48776	46863	AGTATTTGAAACTGAGAAGT
48777	46864	CAGTATTTGAAACTGAGAAG
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48783	46870	AATAATCAGTATTTGAAACT
48784	46871	AAATAATCAGTATTTGAAAC
48785	46872	AAAATAATCAGTATTTGAAA
48786	46873	TAAAATAATCAGTATTTGAA
48787	46874	ATAAAATAATCAGTATTTGA
48788	46875	TATAAAATAATCAGTATTTG
48789	46876	CTATAAAATAATCAGTATTT
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48799	46886	ACAAACCAGTCTATAAAATA
48800	46887	CACAAACCAGTCTATAAAAT
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48806	46893	TGATTACACAAACCAGTCTA
48807	46894	CTGATTACACAAACCAGTCT
48808	46895	TCTGATTACACAAACCAGTC
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48812	46899	CCTCTCTGATTACACAAACC
48813	46900	GCCTCTCTGATTACACAAAC
48814	46901	AGCCTCTCTGATTACACAAA
48815	46902	AAGCCTCTCTGATTACACAA
48816	46903	GAAGCCTCTCTGATTACACA
48817	46904	AGAAGCCTCTCTGATTACAC
48818	46905	AAGAAGCCTCTCTGATTACA
48819	46906	CAAGAAGCCTCTCTGATTAC
48820	46907	TCAAGAAGCCTCTCTGATTA
48821	46908	ATCAAGAAGCCTCTCTGATT
48822	46909	CATCAAGAAGCCTCTCTGAT
48823	46910	ACATCAAGAAGCCTCTCTGA
48824	46911	CACATCAAGAAGCCTCTCTG
48825	46912	ACACATCAAGAAGCCTCTCT
48826	46913	CACACATCAAGAAGCCTCTC
48827	46914	ACACACATCAAGAAGCCTCT
48828	46915	CACACACATCAAGAAGCCTC
48829	46916	GCACACACATCAAGAAGCCT
48830	46917	AGCACACACATCAAGAAGCC
48831	46918	AAGCACACACATCAAGAAGC
48832	46919	TAAGCACACACATCAAGAAG
48833	46920	ATAAGCACACACATCAAGAA
48834	46921	AATAAGCACACACATCAAGA
48835	46922	TAATAAGCACACACATCAAG
48836	46923	TTAATAAGCACACACATCAA
48837	46924	TTTAATAAGCACACACATCA
48838	46925	TTTTAATAAGCACACACATC
48839	46926	ATTTTAATAAGCACACACAT
48840	46927	TATTTTAATAAGCACACACA
48841	46928	ATATTTTAATAAGCACACAC

97918	96005	TGCAATCTCGGATCACTGCA
97919	96006	ATGCAATCTCGGATCACTGC
97920	96007	GATGCAATCTCGGATCACTG
97921	96008	TGATGCAATCTCGGATCACT
97922	96009	CTGATGCAATCTCGGATCAC
97923	96010	ACTGATGCAATCTCGGATCA
97924	96011	CACTGATGCAATCTCGGATC
97925	96012	CCACTGATGCAATCTCGGAT
97926	96013	CCCACTGATGCAATCTCGGA
97927	96014	GCCCACTGATGCAATCTCGG
97928	96015	CGCCCACTGATGCAATCTCG
97929	96016	TCGCCCACTGATGCAATCTC
97930	96017	GTCGCCCACTGATGCAATCT
97931	96018	TGTCGCCCACTGATGCAATC
97932	96019	CTGTCGCCCACTGATGCAAT
97933	96020	TCTGTCGCCCACTGATGCAA
97934	96021	CTCTGTCGCCCACTGATGCA
97935	96022	GCTCTGTCGCCCACTGATGC
97936	96023	CGCTCTGTCGCCCACTGATG
97937	96024	TCGCTCTGTCGCCCACTGAT
97938	96025	CTCGCTCTGTCGCCCACTGA
97939	96026	TCTCGCTCTGTCGCCCACTG
97940	96027	TTCTCGCTCTGTCGCCCACT
97941	96028	ATTCTCGCTCTGTCGCCCAC
97942	96029	GATTCTCGCTCTGTCGCCCA
97943	96030	AGATTCTCGCTCTGTCGCCC
97944	96031	CAGATTCTCGCTCTGTCGCC
97945	96032	ACAGATTCTCGCTCTGTCGC
97946	96033	GACAGATTCTCGCTCTGTCG
97947	96034	AGACAGATTCTCGCTCTGTC
97948	96035	GAGACAGATTCTCGCTCTGT
97949	96036	TGAGACAGATTCTCGCTCTG
97950	96037	TTGAGACAGATTCTCGCTCT
97951	96038	TTTGAGACAGATTCTCGCTC
97952	96039	CTTTGAGACAGATTCTCGCT
97953	96040	TCTTTGAGACAGATTCTCGC
97954	96041	TTCTTTGAGACAGATTCTCG
97955	96042	TTTCTTTGAGACAGATTCTC
97956	96043	TTTTCTTTGAGACAGATTCT
97957	96044	TTTTTCTTTGAGACAGATTC
97958	96045	TTTTTTCTTTGAGACAGATT
97959	96046	TTTTTTTCTTTGAGACAGAT
97960	96047	TTTTTTTTCTTTGAGACAGA
97961	96048	TTTTTTTTTCTTTGAGACAG
97962	96049	CTTTTTTTTTCTTTGAGACA
97963	96050	TCTTTTTTTTTCTTTGAGAC
97964	96051	CTCTTTTTTTTTCTTTGAGA
97965	96052	TCTCTTTTTTTTTCTTTGAG
97966	96053	CTCTCTTTTTTTTTCTTTGA
97967	96054	ACTCTCTTTTTTTTTCTTTG
97968	96055	CACTCTCTTTTTTTTTCTTT
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97971	96058	TTCCACTCTCTTTTTTTTTC
97972	96059	TTTCCACTCTCTTTTTTTTT
97973	96060	TTTTCCACTCTCTTTTTTTT
97974	96061	TTTTTCCACTCTCTTTTTTT
97975	96062	TTTTTTCCACTCTCTTTTTT
97976	96063	TTTTTTTCCACTCTCTTTTT
97977	96064	TTTTTTTTCCACTCTCTTTT
97978	96065	TTTTTTTTTCCACTCTCTTT
97979	96066	TTTTTTTTTTCCACTCTCTT
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97984	96071	ACATATTTTTTTTTTCCACT
97985	96072	CACATATTTTTTTTTTCCAC
97986	96073	ACACATATTTTTTTTTTCCA
97987	96074	GACACATATTTTTTTTTTCC
97988	96075	GGACACATATTTTTTTTTTC

147065	145152	CTGAAGTCATCTGGGCCAGC
147066	145153	CCTGAAGTCATCTGGGCCAG
147067	145154	ACCTGAAGTCATCTGGGCCA
147068	145155	AACCTGAAGTCATCTGGGCC
147069	145156	TAACCTGAAGTCATCTGGGC
147070	145157	GTAACCTGAAGTCATCTGGG
147071	145158	AGTAACCTGAAGTCATCTGG
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147078	145165	GGAAAGGAGTAACCTGAAGT
147079	145166	TGGAAAGGAGTAACCTGAAG
147080	145167	ATGGAAAGGAGTAACCTGAA
147081	145168	GATGGAAAGGAGTAACCTGA
147082	145169	AGATGGAAAGGAGTAACCTG
147083	145170	GAGATGGAAAGGAGTAACCT
147084	145171	TGAGATGGAAAGGAGTAACC
147085	145172	GTGAGATGGAAAGGAGTAAC
147086	145173	AGTGAGATGGAAAGGAGTAA
147087	145174	CAGTGAGATGGAAAGGAGTA
147088	145175	CCAGTGAGATGGAAAGGAGT
147089	145176	TCCAGTGAGATGGAAAGGAG
147090	145177	CTCCAGTGAGATGGAAAGGA
147091	145178	GCTCCAGTGAGATGGAAAGG
147092	145179	GGCTCCAGTGAGATGGAAAG
147093	145180	TGGCTCCAGTGAGATGGAAA
147094	145181	ATGGCTCCAGTGAGATGGAA
147095	145182	AATGGCTCCAGTGAGATGGA
147096	145183	TAATGGCTCCAGTGAGATGG
147097	145184	TTAATGGCTCCAGTGAGATG
147098	145185	TTTAATGGCTCCAGTGAGAT
147099	145186	TTTTAATGGCTCCAGTGAGA
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147104	145191	GGAGTTTTTAATGGCTCCAG
147105	145192	TGGAGTTTTTAATGGCTCCA
147106	145193	TTGGAGTTTTTAATGGCTCC
147107	145194	GTTGGAGTTTTTAATGGCTC
147108	145195	AGTTGGAGTTTTTAATGGCT
147109	145196	GAGTTGGAGTTTTTAATGGC
147110	145197	GGAGTTGGAGTTTTTAATGG
147111	145198	AGGAGTTGGAGTTTTTAATG
147112	145199	GAGGAGTTGGAGTTTTTAAT
147113	145200	GGAGGAGTTGGAGTTTTTAA
147114	145201	AGGAGGAGTTGGAGTTTTTA
147115	145202	GAGGAGGAGTTGGAGTTTTT
147116	145203	GGAGGAGGAGTTGGAGTTTT
147117	145204	AGGAGGAGGAGTTGGAGTTT
147118	145205	GAGGAGGAGGAGTTGGAGTT
147119	145206	GGAGGAGGAGGAGTTGGAGT
147120	145207	AGGAGGAGGAGGAGTTGGAG
147121	145208	GAGGAGGAGGAGGAGTTGGA
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147123	145210	AGGAGGAGGAGGAGGAGTTG
147124	145211	CAGGAGGAGGAGGAGGAGTT
147125	145212	GCAGGAGGAGGAGGAGGAGT
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147127	145214	GAGCAGGAGGAGGAGGAGGA
147128	145215	GGAGCAGGAGGAGGAGGAGG
147129	145216	TGGAGCAGGAGGAGGAGGAG
147130	145217	ATGGAGCAGGAGGAGGAGGA
147131	145218	GATGGAGCAGGAGGAGGAGG
147132	145219	TGATGGAGCAGGAGGAGGAG
147133	145220	CTGATGGAGCAGGAGGAGGA
147134	145221	GCTGATGGAGCAGGAGGAGG
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48842	46929	AATATTTTAATAAGCACACA
48843	46930	AAATATTTTAATAAGCACAC
48844	46931	GAAATATTTTAATAAGCACA
48845	46932	TGAAATATTTTAATAAGCAC
48846	46933	TTGAAATATTTTAATAAGCA
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48849	46936	TGGTTGAAATATTTTAATAA
48850	46937	ATGGTTGAAATATTTTAATA
48851	46938	AATGGTTGAAATATTTTAAT
48852	46939	AAATGGTTGAAATATTTTAA
48853	46940	AAAATGGTTGAAATATTTTA
48854	46941	AAAAATGGTTGAAATATTTT
48855	46942	TAAAAATGGTTGAAATATTT
48856	46943	TTAAAAATGGTTGAAATATT
48857	46944	CTTAAAAATGGTTGAAATAT
48858	46945	GCTTAAAAATGGTTGAAATA
48859	46946	TGCTTAAAAATGGTTGAAAT
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48861	46948	AATGCTTAAAAATGGTTGAA
48862	46949	CAATGCTTAAAAATGGTTGA
48863	46950	ACAATGCTTAAAAATGGTTG
48864	46951	CACAATGCTTAAAAATGGTT
48865	46952	TCACAATGCTTAAAAATGGT
48866	46953	CTCACAATGCTTAAAAATGG
48867	46954	GCTCACAATGCTTAAAAATG
48868	46955	AGCTCACAATGCTTAAAAAT
48869	46956	TAGCTCACAATGCTTAAAAA
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48874	46961	TCTATTAGCTCACAATGCTT
48875	46962	CTCTATTAGCTCACAATGCT
48876	46963	CCTCTATTAGCTCACAATGC
48877	46964	CCCTCTATTAGCTCACAATG
48878	46965	TCCCTCTATTAGCTCACAAT
48879	46966	ATCCCTCTATTAGCTCACAA
48880	46967	CATCCCTCTATTAGCTCACA
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48885	46972	CACCACATCCCTCTATTAGC
48886	46973	CCACCACATCCCTCTATTAG
48887	46974	ACCACCACATCCCTCTATTA
48888	46975	AACCACCACATCCCTCTATT
48889	46976	AAACCACCACATCCCTCTAT
48890	46977	CAAACCACCACATCCCTCTA
48891	46978	ACAAACCACCACATCCCTCT
48892	46979	AACAAACCACCACATCCCTC
48893	46980	AAACAAACCACCACATCCCT
48894	46981	AAAACAAACCACCACATCCC
48895	46982	AAAAACAAACCACCACATCC
48896	46983	AAAAAACAAACCACCACATC
48897	46984	GAAAAAACAAACCACCACAT
48898	46985	GGAAAAAACAAACCACCACA
48899	46986	AGGAAAAAACAAACCACCAC
48900	46987	GAGGAAAAAACAAACCACCA
48901	46988	AGAGGAAAAAACAAACCACC
48902	46989	AAGAGGAAAAAACAAACCAC
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48909	46996	AATTTTTAAGAGGAAAAAAC
48910	46997	TAATTTTTAAGAGGAAAAAA
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97989	96076	GGGACACATATTTTTTTTTT
97990	96077	TGGGACACATATTTTTTTTT
97991	96078	CTGGGACACATATTTTTTTT
97992	96079	TCTGGGACACATATTTTTTT
97993	96080	TTCTGGGACACATATTTTTT
97994	96081	GTTCTGGGACACATATTTTT
97995	96082	AGTTCTGGGACACATATTTT
97996	96083	AAGTTCTGGGACACATATTT
97997	96084	TAAGTTCTGGGACACATATT
97998	96085	TTAAGTTCTGGGACACATAT
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98003	96090	AAAATTTAAGTTCTGGGACA
98004	96091	TAAAATTTAAGTTCTGGGAC
98005	96092	TTAAAATTTAAGTTCTGGGA
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98007	96094	AATTAAAATTTAAGTTCTGG
98008	96095	TAATTAAAATTTAAGTTCTG
98009	96096	TTAATTAAAATTTAAGTTCT
98010	96097	TTTAATTAAAATTTAAGTTC
98011	96098	TTTTAATTAAAATTTAAGTT
98012	96099	TTTTTAATTAAAATTTAAGT
98013	96100	TTTTTTAATTAAAATTTAAG
98014	96101	TTTTTTTAATTAAAATTTAA
98015	96102	TTTTTTTTAATTAAAATTTA
98016	96103	TTTTTTTTTAATTAAAATTT
98017	96104	ATTTTTTTTTAATTAAAATT
98018	96105	TATTTTTTTTTAATTAAAAT
98019	96106	TTATTTTTTTTTAATTAAAA
98020	96107	TTTATTTTTTTTTAATTAAA
98021	96108	TTTTATTTTTTTTTAATTAA
98022	96109	CTTTTATTTTTTTTTAATTA
98023	96110	TCTTTTATTTTTTTTTAATT
98024	96111	CTCTTTTATTTTTTTTTAAT
98025	96112	ACTCTTTTATTTTTTTTTAA
98026	96113	CACTCTTTTATTTTTTTTTA
98027	96114	TCACTCTTTTATTTTTTTTT
98028	96115	TTCACTCTTTTATTTTTTTT
98029	96116	GTTCACTCTTTTATTTTTTT
98030	96117	AGTTCACTCTTTTATTTTTT
98031	96118	AAGTTCACTCTTTTATTTTT
98032	96119	AAAGTTCACTCTTTTATTTT
98033	96120	GAAAGTTCACTCTTTTATTT
98034	96121	AGAAAGTTCACTCTTTTATT
98035	96122	TAGAAAGTTCACTCTTTTAT
98036	96123	TTAGAAAGTTCACTCTTTTA
98037	96124	ATTAGAAAGTTCACTCTTTT
98038	96125	AATTAGAAAGTTCACTCTTT
98039	96126	CAATTAGAAAGTTCACTCTT
98040	96127	ACAATTAGAAAGTTCACTCT
98041	96128	AACAATTAGAAAGTTCACTC
98042	96129	GAACAATTAGAAAGTTCACT
98043	96130	AGAACAATTAGAAAGTTCAC
98044	96131	GAGAACAATTAGAAAGTTCA
98045	96132	AGAGAACAATTAGAAAGTTC
98046	96133	AAGAGAACAATTAGAAAGTT
98047	96134	GAAGAGAACAATTAGAAAGT
98048	96135	TGAAGAGAACAATTAGAAAG
98049	96136	CTGAAGAGAACAATTAGAAA
98050	96137	TCTGAAGAGAACAATTAGAA
98051	96138	ATCTGAAGAGAACAATTAGA
98052	96139	TATCTGAAGAGAACAATTAG
98053	96140	TTATCTGAAGAGAACAATTA
98054	96141	ATTATCTGAAGAGAACAATT
98055	96142	TATTATCTGAAGAGAACAAT
98056	96143	ATATTATCTGAAGAGAACAA
98057	96144	TATATTATCTGAAGAGAACA
98058	96145	TTATATTATCTGAAGAGAAC
98059	96146	ATTATATTATCTGAAGAGAA

147136	145223	ATGCTGATGGAGCAGGAGGA
147137	145224	TATGCTGATGGAGCAGGAGG
147138	145225	ATATGCTGATGGAGCAGGAG
147139	145226	GATATGCTGATGGAGCAGGA
147140	145227	AGATATGCTGATGGAGCAGG
147141	145228	GAGATATGCTGATGGAGCAG
147142	145229	AGAGATATGCTGATGGAGCA
147143	145230	CAGAGATATGCTGATGGAGC
147144	145231	TCAGAGATATGCTGATGGAG
147145	145232	CTCAGAGATATGCTGATGGA
147146	145233	TCTCAGAGATATGCTGATGG
147147	145234	CTCTCAGAGATATGCTGATG
147148	145235	TCTCTCAGAGATATGCTGAT
147149	145236	CTCTCTCAGAGATATGCTGA
147150	145237	ACTCTCTCAGAGATATGCTG
147151	145238	GACTCTCTCAGAGATATGCT
147152	145239	TGACTCTCTCAGAGATATGC
147153	145240	GTGACTCTCTCAGAGATATG
147154	145241	CGTGACTCTCTCAGAGATAT
147155	145242	CCGTGACTCTCTCAGAGATA
147156	145243	CCCGTGACTCTCTCAGAGAT
147157	145244	CCCCGTGACTCTCTCAGAGA
147158	145245	CCCCCGTGACTCTCTCAGAG
147159	145246	GCCCCCGTGACTCTCTCAGA
147160	145247	GGCCCCCGTGACTCTCTCAG
147161	145248	AGGCCCCCGTGACTCTCTCA
147162	145249	TAGGCCCCCGTGACTCTCTC
147163	145250	TTAGGCCCCCGTGACTCTCT
147164	145251	CTTAGGCCCCCGTGACTCTC
147165	145252	TCTTAGGCCCCCGTGACTCT
147166	145253	CTCTTAGGCCCCCGTGACTC
147167	145254	ACTCTTAGGCCCCCGTGACT
147168	145255	GACTCTTAGGCCCCCGTGAC
147169	145256	AGACTCTTAGGCCCCCGTGA
147170	145257	GAGACTCTTAGGCCCCCGTG
147171	145258	AGAGACTCTTAGGCCCCCGT
147172	145259	AAGAGACTCTTAGGCCCCCG
147173	145260	AAAGAGACTCTTAGGCCCCC
147174	145261	AAAAGAGACTCTTAGGCCCC
147175	145262	GAAAAGAGACTCTTAGGCCC
147176	145263	TGAAAAGAGACTCTTAGGCC
147177	145264	GTGAAAAGAGACTCTTAGGC
147178	145265	AGTGAAAAGAGACTCTTAGG
147179	145266	CAGTGAAAAGAGACTCTTAG
147180	145267	GCAGTGAAAAGAGACTCTTA
147181	145268	GGCAGTGAAAAGAGACTCTT
147182	145269	AGGCAGTGAAAAGAGACTCT
147183	145270	CAGGCAGTGAAAAGAGACTC
147184	145271	CCAGGCAGTGAAAAGAGACT
147185	145272	ACCAGGCAGTGAAAAGAGAC
147186	145273	CACCAGGCAGTGAAAAGAGA
147187	145274	TCACCAGGCAGTGAAAAGAG
147188	145275	CTCACCAGGCAGTGAAAAGA
147189	145276	GCTCACCAGGCAGTGAAAAG
147190	145277	TGCTCACCAGGCAGTGAAAA
147191	145278	CTGCTCACCAGGCAGTGAAA
147192	145279	TCTGCTCACCAGGCAGTGAA
147193	145280	GTCTGCTCACCAGGCAGTGA
147194	145281	GGTCTGCTCACCAGGCAGTG
147195	145282	TGGTCTGCTCACCAGGCAGT
147196	145283	CTGGTCTGCTCACCAGGCAG
147197	145284	TCTGGTCTGCTCACCAGGCA
147198	145285	TTCTGGTCTGCTCACCAGGC
147199	145286	CTTCTGGTCTGCTCACCAGG
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147201	145288	TGCTTCTGGTCTGCTCACCA
147202	145289	CTGCTTCTGGTCTGCTCACC
147203	145290	TCTGCTTCTGGTCTGCTCAC
147204	145291	CTCTGCTTCTGGTCTGCTCA
147205	145292	CCTCTGCTTCTGGTCTGCTC
147206	145293	CCCTCTGCTTCTGGTCTGCT

48913	47000	TAATAATTTTTAAGAGGAAA
48914	47001	ATAATAATTTTTAAGAGGAA
48915	47002	AATAATAATTTTTAAGAGGA
48916	47003	TAATAATAATTTTTAAGAGG
48917	47004	TTAATAATAATTTTTAAGAG
48918	47005	ATTAATAATAATTTTTAAGA
48919	47006	CATTAATAATAATTTTTAAG
48920	47007	ACATTAATAATAATTTTTAA
48921	47008	TACATTAATAATAATTTTTA
48922	47009	GTACATTAATAATAATTTTT
48923	47010	AGTACATTAATAATAATTTT
48924	47011	AAGTACATTAATAATAATTT
48925	47012	TAAGTACATTAATAATAATT
48926	47013	TTAAGTACATTAATAATAAT
48927	47014	CTTAAGTACATTAATAATAA
48928	47015	TCTTAAGTACATTAATAATA
48929	47016	GTCTTAAGTACATTAATAAT
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48931	47018	TTGTCTTAAGTACATTAATA
48932	47019	TTTGTCTTAAGTACATTAAT
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48947	47034	TTTTTGTTTCTATGGTTTGT
48948	47035	TTTTTTGTTTCTATGGTTTG
48949	47036	GTTTTTTGTTTCTATGGTTT
48950	47037	TGTTTTTTGTTTCTATGGTT
48951	47038	ATGTTTTTTGTTTCTATGGT
48952	47039	AATGTTTTTTGTTTCTATGG
48953	47040	AAATGTTTTTTGTTTCTATG
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48956	47043	TCTAAATGTTTTTTGTTTCT
48957	47044	ATCTAAATGTTTTTTGTTTC
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48960	47047	CATATCTAAATGTTTTTTGT
48961	47048	TCATATCTAAATGTTTTTTG
48962	47049	CTCATATCTAAATGTTTTTT
48963	47050	CCTCATATCTAAATGTTTTT
48964	47051	TCCTCATATCTAAATGTTTT
48965	47052	ATCCTCATATCTAAATGTTT
48966	47053	AATCCTCATATCTAAATGTT
48967	47054	AAATCCTCATATCTAAATGT
48968	47055	AAAATCCTCATATCTAAATG
48969	47056	AAAAATCCTCATATCTAAAT
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48978	47065	CCATCATTTAAAAATCCTCA
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48981	47068	ATTCCATCATTTAAAAATCC
48982	47069	CATTCCATCATTTAAAAATC
48983	47070	CCATTCCATCATTTAAAAAT

98060	96147	CATTATATTATCTGAAGAGA
98061	96148	ACATTATATTATCTGAAGAG
98062	96149	AACATTATATTATCTGAAGA
98063	96150	TAACATTATATTATCTGAAG
98064	96151	ATAACATTATATTATCTGAA
98065	96152	AATAACATTATATTATCTGA
98066	96153	GAATAACATTATATTATCTG
98067	96154	AGAATAACATTATATTATCT
98068	96155	GAGAATAACATTATATTATC
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98071	96158	TAAGAGAATAACATTATATT
98072	96159	ATAAGAGAATAACATTATAT
98073	96160	CATAAGAGAATAACATTATA
98074	96161	ACATAAGAGAATAACATTAT
98075	96162	AACATAAGAGAATAACATTA
98076	96163	AAACATAAGAGAATAACATT
98077	96164	AAAACATAAGAGAATAACAT
98078	96165	TAAAACATAAGAGAATAACA
98079	96166	ATAAAACATAAGAGAATAAC
98080	96167	AATAAAACATAAGAGAATAA
98081	96168	CAATAAAACATAAGAGAATA
98082	96169	GCAATAAAACATAAGAGAAT
98083	96170	CGCAATAAAACATAAGAGAA
98084	96171	ACGCAATAAAACATAAGAGA
98085	96172	TACGCAATAAAACATAAGAG
98086	96173	ATACGCAATAAAACATAAGA
98087	96174	AATACGCAATAAAACATAAG
98088	96175	AAATACGCAATAAAACATAA
98089	96176	GAAATACGCAATAAAACATA
98090	96177	GGAAATACGCAATAAAACAT
98091	96178	AGGAAATACGCAATAAAACA
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98093	96180	ACAGGAAATACGCAATAAAA
98094	96181	CACAGGAAATACGCAATAAA
98095	96182	ACACAGGAAATACGCAATAA
98096	96183	TACACAGGAAATACGCAATA
98097	96184	GTACACAGGAAATACGCAAT
98098	96185	GGTACACAGGAAATACGCAA
98099	96186	TGGTACACAGGAAATACGCA
98100	96187	CTGGTACACAGGAAATACGC
98101	96188	TCTGGTACACAGGAAATACG
98102	96189	ATCTGGTACACAGGAAATAC
98103	96190	CATCTGGTACACAGGAAATA
98104	96191	GCATCTGGTACACAGGAAAT
98105	96192	AGCATCTGGTACACAGGAAA
98106	96193	CAGCATCTGGTACACAGGAA
98107	96194	ACAGCATCTGGTACACAGGA
98108	96195	AACAGCATCTGGTACACAGG
98109	96196	GAACAGCATCTGGTACACAG
98110	96197	AGAACAGCATCTGGTACACA
98111	96198	AAGAACAGCATCTGGTACAC
98112	96199	GAAGAACAGCATCTGGTACA
98113	96200	TGAAGAACAGCATCTGGTAC
98114	96201	ATGAAGAACAGCATCTGGTA
98115	96202	CATGAAGAACAGCATCTGGT
98116	96203	GCATGAAGAACAGCATCTGG
98117	96204	AGCATGAAGAACAGCATCTG
98118	96205	AAGCATGAAGAACAGCATCT
98119	96206	CAAGCATGAAGAACAGCATC
98120	96207	ACAAGCATGAAGAACAGCAT
98121	96208	TACAAGCATGAAGAACAGCA
98122	96209	ATACAAGCATGAAGAACAGC
98123	96210	CATACAAGCATGAAGAACAG
98124	96211	ACATACAAGCATGAAGAACA
98125	96212	AACATACAAGCATGAAGAAC
98126	96213	TAACATACAAGCATGAAGAA
98127	96214	TTAACATACAAGCATGAAGA
98128	96215	TTTAACATACAAGCATGAAG
98129	96216	ATTTAACATACAAGCATGAA
98130	96217	GATTTAACATACAAGCATGA

147207	145294	TCCCTCTGCTTCTGGTCTGC
147208	145295	CTCCCTCTGCTTCTGGTCTG
147209	145296	TCTCCCTCTGCTTCTGGTCT
147210	145297	CTCTCCCTCTGCTTCTGGTC
147211	145298	TCTCTCCCTCTGCTTCTGGT
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147213	145300	CCTCTCTCCCTCTGCTTCTG
147214	145301	GCCTCTCTCCCTCTGCTTCT
147215	145302	TGCCTCTCTCCCTCTGCTTC
147216	145303	TTGCCTCTCTCCCTCTGCTT
147217	145304	TTTGCCTCTCTCCCTCTGCT
147218	145305	ATTTGCCTCTCTCCCTCTGC
147219	145306	CATTTGCCTCTCTCCCTCTG
147220	145307	TCATTTGCCTCTCTCCCTCT
147221	145308	TTCATTTGCCTCTCTCCCTC
147222	145309	GTTCATTTGCCTCTCTCCCT
147223	145310	TGTTCATTTGCCTCTCTCCC
147224	145311	CTGTTCATTTGCCTCTCTCC
147225	145312	TCTGTTCATTTGCCTCTCTC
147226	145313	CTCTGTTCATTTGCCTCTCT
147227	145314	CCTCTGTTCATTTGCCTCTC
147228	145315	ACCTCTGTTCATTTGCCTCT
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147230	145317	GGACCTCTGTTCATTTGCCT
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147232	145319	TTGGACCTCTGTTCATTTGC
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147235	145322	TACTTGGACCTCTGTTCATT
147236	145323	TTACTTGGACCTCTGTTCAT
147237	145324	ATTACTTGGACCTCTGTTCA
147238	145325	AATTACTTGGACCTCTGTTC
147239	145326	GAATTACTTGGACCTCTGTT
147240	145327	TGAATTACTTGGACCTCTGT
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147243	145330	ATGTGAATTACTTGGACCTC
147244	145331	TATGTGAATTACTTGGACCT
147245	145332	GTATGTGAATTACTTGGACC
147246	145333	AGTATGTGAATTACTTGGAC
147247	145334	AAGTATGTGAATTACTTGGA
147248	145335	CAAGTATGTGAATTACTTGG
147249	145336	TCAAGTATGTGAATTACTTG
147250	145337	GTCAAGTATGTGAATTACTT
147251	145338	AGTCAAGTATGTGAATTACT
147252	145339	CAGTCAAGTATGTGAATTAC
147253	145340	ACAGTCAAGTATGTGAATTA
147254	145341	CACAGTCAAGTATGTGAATT
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147256	145343	GTCACAGTCAAGTATGTGAA
147257	145344	TGTCACAGTCAAGTATGTGA
147258	145345	CTGTCACAGTCAAGTATGTG
147259	145346	ACTGTCACAGTCAAGTATGT
147260	145347	GACTGTCACAGTCAAGTATG
147261	145348	AGACTGTCACAGTCAAGTAT
147262	145349	GAGACTGTCACAGTCAAGTA
147263	145350	AGAGACTGTCACAGTCAAGT
147264	145351	CAGAGACTGTCACAGTCAAG
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147266	145353	AGCAGAGACTGTCACAGTCA
147267	145354	AAGCAGAGACTGTCACAGTC
147268	145355	TAAGCAGAGACTGTCACAGT
147269	145356	ATAAGCAGAGACTGTCACAG
147270	145357	AATAAGCAGAGACTGTCACA
147271	145358	TAATAAGCAGAGACTGTCAC
147272	145359	TTAATAAGCAGAGACTGTCA
147273	145360	ATTAATAAGCAGAGACTGTC
147274	145361	CATTAATAAGCAGAGACTGT
147275	145362	ACATTAATAAGCAGAGACTG
147276	145363	TACATTAATAAGCAGAGACT
147277	145364	TTACATTAATAAGCAGAGAC

48984	47071	TCCATTCCATCATTTAAAAA
48985	47072	ATCCATTCCATCATTTAAAA
48986	47073	TATCCATTCCATCATTTAAA
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48988	47075	ATTATCCATTCCATCATTTA
48989	47076	TATTATCCATTCCATCATTT
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48999	47086	GCATATGATCTATTATCCAT
49000	47087	GGCATATGATCTATTATCCA
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49005	47092	TCCCAGGCATATGATCTATT
49006	47093	TTCCCAGGCATATGATCTAT
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49019	47106	AATCATACCCTTTTTCCCAG
49020	47107	GAATCATACCCTTTTTCCCA
49021	47108	AGAATCATACCCTTTTTCCC
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49023	47110	AGAGAATCATACCCTTTTTC
49024	47111	AAGAGAATCATACCCTTTTT
49025	47112	CAAGAGAATCATACCCTTTT
49026	47113	TCAAGAGAATCATACCCTTT
49027	47114	CTCAAGAGAATCATACCCTT
49028	47115	TCTCAAGAGAATCATACCCT
49029	47116	ATCTCAAGAGAATCATACCC
49030	47117	AATCTCAAGAGAATCATACC
49031	47118	TAATCTCAAGAGAATCATAC
49032	47119	ATAATCTCAAGAGAATCATA
49033	47120	AATAATCTCAAGAGAATCAT
49034	47121	AAATAATCTCAAGAGAATCA
49035	47122	AAAATAATCTCAAGAGAATC
49036	47123	AAAAATAATCTCAAGAGAAT
49037	47124	CAAAAATAATCTCAAGAGAA
49038	47125	ACAAAAATAATCTCAAGAGA
49039	47126	GACAAAAATAATCTCAAGAG
49040	47127	TGACAAAAATAATCTCAAGA
49041	47128	TTGACAAAAATAATCTCAAG
49042	47129	TTTGACAAAAATAATCTCAA
49043	47130	CTTTGACAAAAATAATCTCA
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49050	47137	TATATGCCTTTGACAAAAAT
49051	47138	TTATATGCCTTTGACAAAAA
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98131	96218	AGATTTAACATACAAGCATG
98132	96219	AAGATTTAACATACAAGCAT
98133	96220	CAAGATTTAACATACAAGCA
98134	96221	ACAAGATTTAACATACAAGC
98135	96222	GACAAGATTTAACATACAAG
98136	96223	AGACAAGATTTAACATACAA
98137	96224	TAGACAAGATTTAACATACA
98138	96225	TTAGACAAGATTTAACATAC
98139	96226	GTTAGACAAGATTTAACATA
98140	96227	TGTTAGACAAGATTTAACAT
98141	96228	ATGTTAGACAAGATTTAACA
98142	96229	GATGTTAGACAAGATTTAAC
98143	96230	AGATGTTAGACAAGATTTAA
98144	96231	GAGATGTTAGACAAGATTTA
98145	96232	AGAGATGTTAGACAAGATTT
98146	96233	CAGAGATGTTAGACAAGATT
98147	96234	ACAGAGATGTTAGACAAGAT
98148	96235	GACAGAGATGTTAGACAAGA
98149	96236	TGACAGAGATGTTAGACAAG
98150	96237	TTGACAGAGATGTTAGACAA
98151	96238	CTTGACAGAGATGTTAGACA
98152	96239	GCTTGACAGAGATGTTAGAC
98153	96240	TGCTTGACAGAGATGTTAGA
98154	96241	TTGCTTGACAGAGATGTTAG
98155	96242	CTTGCTTGACAGAGATGTTA
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98157	96244	AACTTGCTTGACAGAGATGT
98158	96245	GAACTTGCTTGACAGAGATG
98159	96246	AGAACTTGCTTGACAGAGAT
98160	96247	CAGAACTTGCTTGACAGAGA
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98163	96250	AAACAGAACTTGCTTGACAG
98164	96251	CAAACAGAACTTGCTTGACA
98165	96252	ACAAACAGAACTTGCTTGAC
98166	96253	TACAAACAGAACTTGCTTGA
98167	96254	ATACAAACAGAACTTGCTTG
98168	96255	GATACAAACAGAACTTGCTT
98169	96256	AGATACAAACAGAACTTGCT
98170	96257	CAGATACAAACAGAACTTGC
98171	96258	GCAGATACAAACAGAACTTG
98172	96259	TGCAGATACAAACAGAACTT
98173	96260	GTGCAGATACAAACAGAACT
98174	96261	AGTGCAGATACAAACAGAAC
98175	96262	CAGTGCAGATACAAACAGAA
98176	96263	ACAGTGCAGATACAAACAGA
98177	96264	CACAGTGCAGATACAAACAG
98178	96265	ACACAGTGCAGATACAAACA
98179	96266	TACACAGTGCAGATACAAAC
98180	96267	ATACACAGTGCAGATACAAA
98181	96268	TATACACAGTGCAGATACAA
98182	96269	ATATACACAGTGCAGATACA
98183	96270	AATATACACAGTGCAGATAC
98184	96271	TAATATACACAGTGCAGATA
98185	96272	CTAATATACACAGTGCAGAT
98186	96273	CCTAATATACACAGTGCAGA
98187	96274	GCCTAATATACACAGTGCAG
98188	96275	TGCCTAATATACACAGTGCA
98189	96276	CTGCCTAATATACACAGTGC
98190	96277	GCTGCCTAATATACACAGTG
98191	96278	AGCTGCCTAATATACACAGT
98192	96279	AAGCTGCCTAATATACACAG
98193	96280	CAAGCTGCCTAATATACACA
98194	96281	CCAAGCTGCCTAATATACAC
98195	96282	CCCAAGCTGCCTAATATACA
98196	96283	GCCCAAGCTGCCTAATATAC
98197	96284	TGCCCAAGCTGCCTAATATA
98198	96285	TTGCCCAAGCTGCCTAATAT
98199	96286	TTTGCCCAAGCTGCCTAATA
98200	96287	CTTTGCCCAAGCTGCCTAAT
98201	96288	TCTTTGCCCAAGCTGCCTAA

147278	145365	ATTACATTAATAAGCAGAGA
147279	145366	GATTACATTAATAAGCAGAG
147280	145367	AGATTACATTAATAAGCAGA
147281	145368	CAGATTACATTAATAAGCAG
147282	145369	ACAGATTACATTAATAAGCA
147283	145370	AACAGATTACATTAATAAGC
147284	145371	AAACAGATTACATTAATAAG
147285	145372	AAAACAGATTACATTAATAA
147286	145373	GAAAACAGATTACATTAATA
147287	145374	GGAAAACAGATTACATTAAT
147288	145375	AGGAAAACAGATTACATTAA
147289	145376	TAGGAAAACAGATTACATTA
147290	145377	ATAGGAAAACAGATTACATT
147291	145378	AATAGGAAAACAGATTACAT
147292	145379	AAATAGGAAAACAGATTACA
147293	145380	CAAATAGGAAAACAGATTAC
147294	145381	TCAAATAGGAAAACAGATTA
147295	145382	TTCAAATAGGAAAACAGATT
147296	145383	TTTCAAATAGGAAAACAGAT
147297	145384	CTTTCAAATAGGAAAACAGA
147298	145385	CCTTTCAAATAGGAAAACAG
147299	145386	CCCTTTCAAATAGGAAAACA
147300	145387	TCCCTTTCAAATAGGAAAAC
147301	145388	ATCCCTTTCAAATAGGAAAA
147302	145389	CATCCCTTTCAAATAGGAAA
147303	145390	ACATCCCTTTCAAATAGGAA
147304	145391	AACATCCCTTTCAAATAGGA
147305	145392	TAACATCCCTTTCAAATAGG
147306	145393	ATAACATCCCTTTCAAATAG
147307	145394	GATAACATCCCTTTCAAATA
147308	145395	AGATAACATCCCTTTCAAAT
147309	145396	CAGATAACATCCCTTTCAAA
147310	145397	GCAGATAACATCCCTTTCAA
147311	145398	TGCAGATAACATCCCTTTCA
147312	145399	TTGCAGATAACATCCCTTTC
147313	145400	TTTGCAGATAACATCCCTTT
147314	145401	TTTTGCAGATAACATCCCTT
147315	145402	GTTTTGCAGATAACATCCCT
147316	145403	AGTTTTGCAGATAACATCCC
147317	145404	TAGTTTTGCAGATAACATCC
147318	145405	GTAGTTTTGCAGATAACATC
147319	145406	GGTAGTTTTGCAGATAACAT
147320	145407	AGGTAGTTTTGCAGATAACA
147321	145408	GAGGTAGTTTTGCAGATAAC
147322	145409	TGAGGTAGTTTTGCAGATAA
147323	145410	CTGAGGTAGTTTTGCAGATA
147324	145411	CCTGAGGTAGTTTTGCAGAT
147325	145412	GCCTGAGGTAGTTTTGCAGA
147326	145413	GGCCTGAGGTAGTTTTGCAG
147327	145414	GGGCCTGAGGTAGTTTTGCA
147328	145415	GGGGCCTGAGGTAGTTTTGC
147329	145416	TGGGGCCTGAGGTAGTTTTG
147330	145417	GTGGGGCCTGAGGTAGTTTT
147331	145418	TGTGGGGCCTGAGGTAGTTT
147332	145419	ATGTGGGGCCTGAGGTAGTT
147333	145420	CATGTGGGGCCTGAGGTAGT
147334	145421	CCATGTGGGGCCTGAGGTAG
147335	145422	GCCATGTGGGGCCTGAGGTA
147336	145423	TGCCATGTGGGGCCTGAGGT
147337	145424	CTGCCATGTGGGGCCTGAGG
147338	145425	GCTGCCATGTGGGGCCTGAG
147339	145426	GGCTGCCATGTGGGGCCTGA
147340	145427	AGGCTGCCATGTGGGGCCTG
147341	145428	CAGGCTGCCATGTGGGGCCT
147342	145429	TCAGGCTGCCATGTGGGGCC
147343	145430	ATCAGGCTGCCATGTGGGGC
147344	145431	AATCAGGCTGCCATGTGGGG
147345	145432	GAATCAGGCTGCCATGTGGG
147346	145433	AGAATCAGGCTGCCATGTGG
147347	145434	CAGAATCAGGCTGCCATGTG
147348	145435	TCAGAATCAGGCTGCCATGT

49055	47142	GTTCTTATATGCCTTTGACA
49056	47143	AGTTCTTATATGCCTTTGAC
49057	47144	CAGTTCTTATATGCCTTTGA
49058	47145	CCAGTTCTTATATGCCTTTG
49059	47146	ACCAGTTCTTATATGCCTTT
49060	47147	TACCAGTTCTTATATGCCTT
49061	47148	GTACCAGTTCTTATATGCCT
49062	47149	GGTACCAGTTCTTATATGCC
49063	47150	AGGTACCAGTTCTTATATGC
49064	47151	AAGGTACCAGTTCTTATATG
49065	47152	CAAGGTACCAGTTCTTATAT
49066	47153	TCAAGGTACCAGTTCTTATA
49067	47154	ATCAAGGTACCAGTTCTTAT
49068	47155	CATCAAGGTACCAGTTCTTA
49069	47156	TCATCAAGGTACCAGTTCTT
49070	47157	CTCATCAAGGTACCAGTTCT
49071	47158	GCTCATCAAGGTACCAGTTC
49072	47159	AGCTCATCAAGGTACCAGTT
49073	47160	TAGCTCATCAAGGTACCAGT
49074	47161	TTAGCTCATCAAGGTACCAG
49075	47162	TTTAGCTCATCAAGGTACCA
49076	47163	CTTTAGCTCATCAAGGTACC
49077	47164	TCTTTAGCTCATCAAGGTAC
49078	47165	TTCTTTAGCTCATCAAGGTA
49079	47166	ATTCTTTAGCTCATCAAGGT
49080	47167	AATTCTTTAGCTCATCAAGG
49081	47168	GAATTCTTTAGCTCATCAAG
49082	47169	GGAATTCTTTAGCTCATCAA
49083	47170	AGGAATTCTTTAGCTCATCA
49084	47171	TAGGAATTCTTTAGCTCATC
49085	47172	TTAGGAATTCTTTAGCTCAT
49086	47173	GTTAGGAATTCTTTAGCTCA
49087	47174	TGTTAGGAATTCTTTAGCTC
49088	47175	TTGTTAGGAATTCTTTAGCT
49089	47176	TTTGTTAGGAATTCTTTAGC
49090	47177	ATTTGTTAGGAATTCTTTAG
49091	47178	AATTTGTTAGGAATTCTTTA
49092	47179	AAATTTGTTAGGAATTCTTT
49093	47180	AAAATTTGTTAGGAATTCTT
49094	47181	TAAAATTTGTTAGGAATTCT
49095	47182	ATAAAATTTGTTAGGAATTC
49096	47183	AATAAAATTTGTTAGGAATT
49097	47184	AAATAAAATTTGTTAGGAAT
49098	47185	AAAATAAAATTTGTTAGGAA
49099	47186	CAAAATAAAATTTGTTAGGA
49100	47187	ACAAAATAAAATTTGTTAGG
49101	47188	TACAAAATAAAATTTGTTAG
49102	47189	TTACAAAATAAAATTTGTTA
49103	47190	TTTACAAAATAAAATTTGTT
49104	47191	CTTTACAAAATAAAATTTGT
49105	47192	CCTTTACAAAATAAAATTTG
49106	47193	ACCTTTACAAAATAAAATTT
49107	47194	AACCTTTACAAAATAAAATT
49108	47195	AAACCTTTACAAAATAAAAT
49109	47196	CAAACCTTTACAAAATAAAA
49110	47197	CCAAACCTTTACAAAATAAA
49111	47198	TCCAAACCTTTACAAAATAA
49112	47199	CTCCAAACCTTTACAAAATA
49113	47200	ACTCCAAACCTTTACAAAAT
49114	47201	TACTCCAAACCTTTACAAAA
49115	47202	GTACTCCAAACCTTTACAAA
49116	47203	AGTACTCCAAACCTTTACAA
49117	47204	AAGTACTCCAAACCTTTACA
49118	47205	TAAGTACTCCAAACCTTTAC
49119	47206	GTAAGTACTCCAAACCTTTA
49120	47207	AGTAAGTACTCCAAACCTTT
49121	47208	AAGTAAGTACTCCAAACCTT
49122	47209	CAAGTAAGTACTCCAAACCT
49123	47210	ACAAGTAAGTACTCCAAACC
49124	47211	CACAAGTAAGTACTCCAAAC
49125	47212	ACACAAGTAAGTACTCCAAA

98202	96289	CTCTTTGCCCAAGCTGCCTA
98203	96290	TCTCTTTGCCCAAGCTGCCT
98204	96291	TTCTCTTTGCCCAAGCTGCC
98205	96292	CTTCTCTTTGCCCAAGCTGC
98206	96293	ACTTCTCTTTGCCCAAGCTG
98207	96294	AACTTCTCTTTGCCCAAGCT
98208	96295	TAACTTCTCTTTGCCCAAGC
98209	96296	TTAACTTCTCTTTGCCCAAG
98210	96297	CTTAACTTCTCTTTGCCCAA
98211	96298	ACTTAACTTCTCTTTGCCCA
98212	96299	TACTTAACTTCTCTTTGCCC
98213	96300	TTACTTAACTTCTCTTTGCC
98214	96301	ATTACTTAACTTCTCTTTGC
98215	96302	GATTACTTAACTTCTCTTTG
98216	96303	AGATTACTTAACTTCTCTTT
98217	96304	CAGATTACTTAACTTCTCTT
98218	96305	GCAGATTACTTAACTTCTCT
98219	96306	GGCAGATTACTTAACTTCTC
98220	96307	GGGCAGATTACTTAACTTCT
98221	96308	TGGGCAGATTACTTAACTTC
98222	96309	TTGGGCAGATTACTTAACTT
98223	96310	TTTGGGCAGATTACTTAACT
98224	96311	GTTTGGGCAGATTACTTAAC
98225	96312	AGTTTGGGCAGATTACTTAA
98226	96313	GAGTTTGGGCAGATTACTTA
98227	96314	TGAGTTTGGGCAGATTACTT
98228	96315	GTGAGTTTGGGCAGATTACT
98229	96316	TGTGAGTTTGGGCAGATTAC
98230	96317	ATGTGAGTTTGGGCAGATTA
98231	96318	CATGTGAGTTTGGGCAGATT
98232	96319	CCATGTGAGTTTGGGCAGAT
98233	96320	GCCATGTGAGTTTGGGCAGA
98234	96321	AGCCATGTGAGTTTGGGCAG
98235	96322	TAGCCATGTGAGTTTGGGCA
98236	96323	CTAGCCATGTGAGTTTGGGC
98237	96324	ACTAGCCATGTGAGTTTGGG
98238	96325	TACTAGCCATGTGAGTTTGG
98239	96326	TTACTAGCCATGTGAGTTTG
98240	96327	CTTACTAGCCATGTGAGTTT
98241	96328	ACTTACTAGCCATGTGAGTT
98242	96329	TACTTACTAGCCATGTGAGT
98243	96330	TTACTTACTAGCCATGTGAG
98244	96331	CTTACTTACTAGCCATGTGA
98245	96332	TCTTACTTACTAGCCATGTG
98246	96333	CTCTTACTTACTAGCCATGT
98247	96334	CCTCTTACTTACTAGCCATG
98248	96335	CCCTCTTACTTACTAGCCAT
98249	96336	GCCCTCTTACTTACTAGCCA
98250	96337	AGCCCTCTTACTTACTAGCC
98251	96338	CAGCCCTCTTACTTACTAGC
98252	96339	TCAGCCCTCTTACTTACTAG
98253	96340	GTCAGCCCTCTTACTTACTA
98254	96341	GGTCAGCCCTCTTACTTACT
98255	96342	TGGTCAGCCCTCTTACTTAC
98256	96343	ATGGTCAGCCCTCTTACTTA
98257	96344	GATGGTCAGCCCTCTTACTT
98258	96345	AGATGGTCAGCCCTCTTACT
98259	96346	CAGATGGTCAGCCCTCTTAC
98260	96347	CCAGATGGTCAGCCCTCTTA
98261	96348	ACCAGATGGTCAGCCCTCTT
98262	96349	CACCAGATGGTCAGCCCTCT
98263	96350	ACACCAGATGGTCAGCCCTC
98264	96351	AACACCAGATGGTCAGCCCT
98265	96352	AAACACCAGATGGTCAGCCC
98266	96353	TAAACACCAGATGGTCAGCC
98267	96354	TTAAACACCAGATGGTCAGC
98268	96355	CTTAAACACCAGATGGTCAG
98269	96356	GCTTAAACACCAGATGGTCA
98270	96357	AGCTTAAACACCAGATGGTC
98271	96358	AAGCTTAAACACCAGATGGT
98272	96359	GAAGCTTAAACACCAGATGG

147349	145436	TTCAGAATCAGGCTGCCATG
147350	145437	CTTCAGAATCAGGCTGCCAT
147351	145438	GCTTCAGAATCAGGCTGCCA
147352	145439	TGCTTCAGAATCAGGCTGCC
147353	145440	ATGCTTCAGAATCAGGCTGC
147354	145441	GATGCTTCAGAATCAGGCTG
147355	145442	TGATGCTTCAGAATCAGGCT
147356	145443	ATGATGCTTCAGAATCAGGC
147357	145444	AATGATGCTTCAGAATCAGG
147358	145445	CAATGATGCTTCAGAATCAG
147359	145446	TCAATGATGCTTCAGAATCA
147360	145447	TTCAATGATGCTTCAGAATC
147361	145448	ATTCAATGATGCTTCAGAAT
147362	145449	GATTCAATGATGCTTCAGAA
147363	145450	AGATTCAATGATGCTTCAGA
147364	145451	AAGATTCAATGATGCTTCAG
147365	145452	CAAGATTCAATGATGCTTCA
147366	145453	ACAAGATTCAATGATGCTTC
147367	145454	TACAAGATTCAATGATGCTT
147368	145455	ATACAAGATTCAATGATGCT
147369	145456	CATACAAGATTCAATGATGC
147370	145457	TCATACAAGATTCAATGATG
147371	145458	ATCATACAAGATTCAATGAT
147372	145459	TATCATACAAGATTCAATGA
147373	145460	ATATCATACAAGATTCAATG
147374	145461	AATATCATACAAGATTCAAT
147375	145462	TAATATCATACAAGATTCAA
147376	145463	TTAATATCATACAAGATTCA
147377	145464	CTTAATATCATACAAGATTC
147378	145465	ACTTAATATCATACAAGATT
147379	145466	AACTTAATATCATACAAGAT
147380	145467	CAACTTAATATCATACAAGA
147381	145468	TCAACTTAATATCATACAAG
147382	145469	CTCAACTTAATATCATACAA
147383	145470	TCTCAACTTAATATCATACA
147384	145471	TTCTCAACTTAATATCATAC
147385	145472	TTTCTCAACTTAATATCATA
147386	145473	CTTTCTCAACTTAATATCAT
147387	145474	GCTTTCTCAACTTAATATCA
147388	145475	AGCTTTCTCAACTTAATATC
147389	145476	CAGCTTTCTCAACTTAATAT
147390	145477	GCAGCTTTCTCAACTTAATA
147391	145478	GGCAGCTTTCTCAACTTAAT
147392	145479	GGGCAGCTTTCTCAACTTAA
147393	145480	AGGGCAGCTTTCTCAACTTA
147394	145481	AAGGGCAGCTTTCTCAACTT
147395	145482	CAAGGGCAGCTTTCTCAACT
147396	145483	CCAAGGGCAGCTTTCTCAAC
147397	145484	TCCAAGGGCAGCTTTCTCAA
147398	145485	ATCCAAGGGCAGCTTTCTCA
147399	145486	GATCCAAGGGCAGCTTTCTC
147400	145487	GGATCCAAGGGCAGCTTTCT
147401	145488	TGGATCCAAGGGCAGCTTTC
147402	145489	CTGGATCCAAGGGCAGCTTT
147403	145490	ACTGGATCCAAGGGCAGCTT
147404	145491	CACTGGATCCAAGGGCAGCT
147405	145492	ACACTGGATCCAAGGGCAGC
147406	145493	GACACTGGATCCAAGGGCAG
147407	145494	AGACACTGGATCCAAGGGCA
147408	145495	TAGACACTGGATCCAAGGGC
147409	145496	TTAGACACTGGATCCAAGGG
147410	145497	ATTAGACACTGGATCCAAGG
147411	145498	GATTAGACACTGGATCCAAG
147412	145499	AGATTAGACACTGGATCCAA
147413	145500	AAGATTAGACACTGGATCCA
147414	145501	AAAGATTAGACACTGGATCC
147415	145502	CAAAGATTAGACACTGGATC
147416	145503	ACAAAGATTAGACACTGGAT
147417	145504	CACAAAGATTAGACACTGGA
147418	145505	TCACAAAGATTAGACACTGG
147419	145506	TTCACAAAGATTAGACACTG

49126	47213	AACACAAGTAAGTACTCCAA
49127	47214	AAACACAAGTAAGTACTCCA
49128	47215	AAAACACAAGTAAGTACTCC
49129	47216	AAAAACACAAGTAAGTACTC
49130	47217	GAAAAACACAAGTAAGTACT
49131	47218	TGAAAAACACAAGTAAGTAC
49132	47219	ATGAAAAACACAAGTAAGTA
49133	47220	AATGAAAAACACAAGTAAGT
49134	47221	AAATGAAAAACACAAGTAAG
49135	47222	AAAATGAAAAACACAAGTAA
49136	47223	TAAAATGAAAAACACAAGTA
49137	47224	CTAAAATGAAAAACACAAGT
49138	47225	ACTAAAATGAAAAACACAAG
49139	47226	CACTAAAATGAAAAACACAA
49140	47227	ACACTAAAATGAAAAACACA
49141	47228	CACACTAAAATGAAAAACAC
49142	47229	TCACACTAAAATGAAAAACA
49143	47230	ATCACACTAAAATGAAAAAC
49144	47231	AATCACACTAAAATGAAAAA
49145	47232	AAATCACACTAAAATGAAAA
49146	47233	CAAATCACACTAAAATGAAA
49147	47234	CCAAATCACACTAAAATGAA
49148	47235	ACCAAATCACACTAAAATGA
49149	47236	TACCAAATCACACTAAAATG
49150	47237	GTACCAAATCACACTAAAAT
49151	47238	AGTACCAAATCACACTAAAA
49152	47239	AAGTACCAAATCACACTAAA
49153	47240	CAAGTACCAAATCACACTAA
49154	47241	TCAAGTACCAAATCACACTA
49155	47242	ATCAAGTACCAAATCACACT
49156	47243	CATCAAGTACCAAATCACAC
49157	47244	GCATCAAGTACCAAATCACA
49158	47245	GGCATCAAGTACCAAATCAC
49159	47246	CGGCATCAAGTACCAAATCA
49160	47247	GCGGCATCAAGTACCAAATC
49161	47248	TGCGGCATCAAGTACCAAAT
49162	47249	GTGCGGCATCAAGTACCAAA
49163	47250	TGTGCGGCATCAAGTACCAA
49164	47251	ATGTGCGGCATCAAGTACCA
49165	47252	CATGTGCGGCATCAAGTACC
49166	47253	TCATGTGCGGCATCAAGTAC
49167	47254	CTCATGTGCGGCATCAAGTA
49168	47255	TCTCATGTGCGGCATCAAGT
49169	47256	TTCTCATGTGCGGCATCAAG
49170	47257	TTTCTCATGTGCGGCATCAA
49171	47258	TTTTCTCATGTGCGGCATCA
49172	47259	CTTTTCTCATGTGCGGCATC
49173	47260	ACTTTTCTCATGTGCGGCAT
49174	47261	TACTTTTCTCATGTGCGGCA
49175	47262	GTACTTTTCTCATGTGCGGC
49176	47263	TGTACTTTTCTCATGTGCGG
49177	47264	CTGTACTTTTCTCATGTGCG
49178	47265	TCTGTACTTTTCTCATGTGC
49179	47266	TTCTGTACTTTTCTCATGTG
49180	47267	ATTCTGTACTTTTCTCATGT
49181	47268	GATTCTGTACTTTTCTCATG
49182	47269	GGATTCTGTACTTTTCTCAT
49183	47270	TGGATTCTGTACTTTTCTCA
49184	47271	CTGGATTCTGTACTTTTCTC
49185	47272	ACTGGATTCTGTACTTTTCT
49186	47273	AACTGGATTCTGTACTTTTC
49187	47274	GAACTGGATTCTGTACTTTT
49188	47275	CGAACTGGATTCTGTACTTT
49189	47276	CCGAACTGGATTCTGTACTT
49190	47277	CCCGAACTGGATTCTGTACT
49191	47278	CCCCGAACTGGATTCTGTAC
49192	47279	GCCCCGAACTGGATTCTGTA
49193	47280	GGCCCCGAACTGGATTCTGT
49194	47281	CGGCCCCGAACTGGATTCTG
49195	47282	TCGGCCCCGAACTGGATTCT
49196	47283	TTCGGCCCCGAACTGGATTC

98273	96360	AGAAGCTTAAACACCAGATG
98274	96361	TAGAAGCTTAAACACCAGAT
98275	96362	CTAGAAGCTTAAACACCAGA
98276	96363	GCTAGAAGCTTAAACACCAG
98277	96364	TGCTAGAAGCTTAAACACCA
98278	96365	CTGCTAGAAGCTTAAACACC
98279	96366	ACTGCTAGAAGCTTAAACAC
98280	96367	CACTGCTAGAAGCTTAAACA
98281	96368	GCACTGCTAGAAGCTTAAAC
98282	96369	AGCACTGCTAGAAGCTTAAA
98283	96370	AAGCACTGCTAGAAGCTTAA
98284	96371	AAAGCACTGCTAGAAGCTTA
98285	96372	CAAAGCACTGCTAGAAGCTT
98286	96373	TCAAAGCACTGCTAGAAGCT
98287	96374	TTCAAAGCACTGCTAGAAGC
98288	96375	ATTCAAAGCACTGCTAGAAG
98289	96376	TATTCAAAGCACTGCTAGAA
98290	96377	CTATTCAAAGCACTGCTAGA
98291	96378	ACTATTCAAAGCACTGCTAG
98292	96379	TACTATTCAAAGCACTGCTA
98293	96380	TTACTATTCAAAGCACTGCT
98294	96381	GTTACTATTCAAAGCACTGC
98295	96382	AGTTACTATTCAAAGCACTG
98296	96383	TAGTTACTATTCAAAGCACT
98297	96384	TTAGTTACTATTCAAAGCAC
98298	96385	ATTAGTTACTATTCAAAGCA
98299	96386	CATTAGTTACTATTCAAAGC
98300	96387	GCATTAGTTACTATTCAAAG
98301	96388	TGCATTAGTTACTATTCAAA
98302	96389	ATGCATTAGTTACTATTCAA
98303	96390	TATGCATTAGTTACTATTCA
98304	96391	CTATGCATTAGTTACTATTC
98305	96392	ACTATGCATTAGTTACTATT
98306	96393	CACTATGCATTAGTTACTAT
98307	96394	GCACTATGCATTAGTTACTA
98308	96395	TGCACTATGCATTAGTTACT
98309	96396	ATGCACTATGCATTAGTTAC
98310	96397	CATGCACTATGCATTAGTTA
98311	96398	GCATGCACTATGCATTAGTT
98312	96399	AGCATGCACTATGCATTAGT
98313	96400	CAGCATGCACTATGCATTAG
98314	96401	GCAGCATGCACTATGCATTA
98315	96402	TGCAGCATGCACTATGCATT
98316	96403	GTGCAGCATGCACTATGCAT
98317	96404	AGTGCAGCATGCACTATGCA
98318	96405	CAGTGCAGCATGCACTATGC
98319	96406	ACAGTGCAGCATGCACTATG
98320	96407	GACAGTGCAGCATGCACTAT
98321	96408	TGACAGTGCAGCATGCACTA
98322	96409	CTGACAGTGCAGCATGCACT
98323	96410	ACTGACAGTGCAGCATGCAC
98324	96411	GACTGACAGTGCAGCATGCA
98325	96412	TGACTGACAGTGCAGCATGC
98326	96413	CTGACTGACAGTGCAGCATG
98327	96414	ACTGACTGACAGTGCAGCAT
98328	96415	CACTGACTGACAGTGCAGCA
98329	96416	TCACTGACTGACAGTGCAGC
98330	96417	ATCACTGACTGACAGTGCAG
98331	96418	AATCACTGACTGACAGTGCA
98332	96419	GAATCACTGACTGACAGTGC
98333	96420	TGAATCACTGACTGACAGTG
98334	96421	ATGAATCACTGACTGACAGT
98335	96422	AATGAATCACTGACTGACAG
98336	96423	TAATGAATCACTGACTGACA
98337	96424	CTAATGAATCACTGACTGAC
98338	96425	TCTAATGAATCACTGACTGA
98339	96426	CTCTAATGAATCACTGACTG
98340	96427	GCTCTAATGAATCACTGACT
98341	96428	AGCTCTAATGAATCACTGAC
98342	96429	TAGCTCTAATGAATCACTGA
98343	96430	TTAGCTCTAATGAATCACTG

147420	145507	CTTCACAAAGATTAGACACT
147421	145508	TCTTCACAAAGATTAGACAC
147422	145509	ATCTTCACAAAGATTAGACA
147423	145510	GATCTTCACAAAGATTAGAC
147424	145511	AGATCTTCACAAAGATTAGA
147425	145512	AAGATCTTCACAAAGATTAG
147426	145513	TAAGATCTTCACAAAGATTA
147427	145514	GTAAGATCTTCACAAAGATT
147428	145515	GGTAAGATCTTCACAAAGAT
147429	145516	GGGTAAGATCTTCACAAAGA
147430	145517	GGGGTAAGATCTTCACAAAG
147431	145518	TGGGGTAAGATCTTCACAAA
147432	145519	ATGGGGTAAGATCTTCACAA
147433	145520	TATGGGGTAAGATCTTCACA
147434	145521	GTATGGGGTAAGATCTTCAC
147435	145522	TGTATGGGGTAAGATCTTCA
147436	145523	ATGTATGGGGTAAGATCTTC
147437	145524	TATGTATGGGGTAAGATCTT
147438	145525	CTATGTATGGGGTAAGATCT
147439	145526	TCTATGTATGGGGTAAGATC
147440	145527	TTCTATGTATGGGGTAAGAT
147441	145528	ATTCTATGTATGGGGTAAGA
147442	145529	TATTCTATGTATGGGGTAAG
147443	145530	GTATTCTATGTATGGGGTAA
147444	145531	TGTATTCTATGTATGGGGTA
147445	145532	TTGTATTCTATGTATGGGGT
147446	145533	ATTGTATTCTATGTATGGGG
147447	145534	CATTGTATTCTATGTATGGG
147448	145535	TCATTGTATTCTATGTATGG
147449	145536	ATCATTGTATTCTATGTATG
147450	145537	GATCATTGTATTCTATGTAT
147451	145538	TGATCATTGTATTCTATGTA
147452	145539	CTGATCATTGTATTCTATGT
147453	145540	TCTGATCATTGTATTCTATG
147454	145541	TTCTGATCATTGTATTCTAT
147455	145542	TTTCTGATCATTGTATTCTA
147456	145543	ATTTCTGATCATTGTATTCT
147457	145544	CATTTCTGATCATTGTATTC
147458	145545	ACATTTCTGATCATTGTATT
147459	145546	GACATTTCTGATCATTGTAT
147460	145547	TGACATTTCTGATCATTGTA
147461	145548	TTGACATTTCTGATCATTGT
147462	145549	CTTGACATTTCTGATCATTG
147463	145550	CCTTGACATTTCTGATCATT
147464	145551	CCCTTGACATTTCTGATCAT
147465	145552	ACCCTTGACATTTCTGATCA
147466	145553	AACCCTTGACATTTCTGATC
147467	145554	TAACCCTTGACATTTCTGAT
147468	145555	CTAACCCTTGACATTTCTGA
147469	145556	CCTAACCCTTGACATTTCTG
147470	145557	TCCTAACCCTTGACATTTCT
147471	145558	GTCCTAACCCTTGACATTTC
147472	145559	TGTCCTAACCCTTGACATTT
147473	145560	CTGTCCTAACCCTTGACATT
147474	145561	GCTGTCCTAACCCTTGACAT
147475	145562	TGCTGTCCTAACCCTTGACA
147476	145563	GTGCTGTCCTAACCCTTGAC
147477	145564	TGTGCTGTCCTAACCCTTGA
147478	145565	CTGTGCTGTCCTAACCCTTG
147479	145566	GCTGTGCTGTCCTAACCCTT
147480	145567	GGCTGTGCTGTCCTAACCCT
147481	145568	GGGCTGTGCTGTCCTAACCC
147482	145569	AGGGCTGTGCTGTCCTAACC
147483	145570	CAGGGCTGTGCTGTCCTAAC
147484	145571	TCAGGGCTGTGCTGTCCTAA
147485	145572	GTCAGGGCTGTGCTGTCCTA
147486	145573	AGTCAGGGCTGTGCTGTCCT
147487	145574	AAGTCAGGGCTGTGCTGTCC
147488	145575	GAAGTCAGGGCTGTGCTGTC
147489	145576	AGAAGTCAGGGCTGTGCTGT
147490	145577	TAGAAGTCAGGGCTGTGCTG

49197	47284	TTTCGGCCCCGAACTGGATT
49198	47285	GTTTCGGCCCCGAACTGGAT
49199	47286	CGTTTCGGCCCCGAACTGGA
49200	47287	ACGTTTCGGCCCCGAACTGG
49201	47288	CACGTTTCGGCCCCGAACTG
49202	47289	TCACGTTTCGGCCCCGAACT
49203	47290	TTCACGTTTCGGCCCCGAAC
49204	47291	CTTCACGTTTCGGCCCCGAA
49205	47292	TCTTCACGTTTCGGCCCCGA
49206	47293	TTCTTCACGTTTCGGCCCCG
49207	47294	TTTCTTCACGTTTCGGCCCC
49208	47295	ATTTCTTCACGTTTCGGCCC
49209	47296	TATTTCTTCACGTTTCGGCC
49210	47297	TTATTTCTTCACGTTTCGGC
49211	47298	ATTATTTCTTCACGTTTCGG
49212	47299	CATTATTTCTTCACGTTTCG
49213	47300	CCATTATTTCTTCACGTTTC
49214	47301	TCCATTATTTCTTCACGTTT
49215	47302	CTCCATTATTTCTTCACGTT
49216	47303	TCTCCATTATTTCTTCACGT
49217	47304	CTCTCCATTATTTCTTCACG
49218	47305	ACTCTCCATTATTTCTTCAC
49219	47306	TACTCTCCATTATTTCTTCA
49220	47307	ATACTCTCCATTATTTCTTC
49221	47308	AATACTCTCCATTATTTCTT
49222	47309	AAATACTCTCCATTATTTCT
49223	47310	AAAATACTCTCCATTATTTC
49224	47311	CAAAATACTCTCCATTATTT
49225	47312	ACAAAATACTCTCCATTATT
49226	47313	AACAAAATACTCTCCATTAT
49227	47314	GAACAAAATACTCTCCATTA
49228	47315	TGAACAAAATACTCTCCATT
49229	47316	TTGAACAAAATACTCTCCAT
49230	47317	TTTGAACAAAATACTCTCCA
49231	47318	ATTTGAACAAAATACTCTCC
49232	47319	CATTTGAACAAAATACTCTC
49233	47320	ACATTTGAACAAAATACTCT
49234	47321	AACATTTGAACAAAATACTC
49235	47322	GAACATTTGAACAAAATACT
49236	47323	TGAACATTTGAACAAAATAC
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49242	47329	AAAGTCTGAACATTTGAACA
49243	47330	CAAAGTCTGAACATTTGAAC
49244	47331	ACAAAGTCTGAACATTTGAA
49245	47332	AACAAAGTCTGAACATTTGA
49246	47333	CAACAAAGTCTGAACATTTG
49247	47334	ACAACAAAGTCTGAACATTT
49248	47335	CACAACAAAGTCTGAACATT
49249	47336	CCACAACAAAGTCTGAACAT
49250	47337	ACCACAACAAAGTCTGAACA
49251	47338	TACCACAACAAAGTCTGAAC
49252	47339	GTACCACAACAAAGTCTGAA
49253	47340	TGTACCACAACAAAGTCTGA
49254	47341	CTGTACCACAACAAAGTCTG
49255	47342	ACTGTACCACAACAAAGTCT
49256	47343	AACTGTACCACAACAAAGTC
49257	47344	AAACTGTACCACAACAAAGT
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49259	47346	TTAAACTGTACCACAACAAA
49260	47347	TTTAAACTGTACCACAACAA
49261	47348	CTTTAAACTGTACCACAACA
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49264	47351	TATCTTTAAACTGTACCACA
49265	47352	ATATCTTTAAACTGTACCAC
49266	47353	CATATCTTTAAACTGTACCA
49267	47354	CCATATCTTTAAACTGTACC

98344	96431	GTTAGCTCTAATGAATCACT
98345	96432	AGTTAGCTCTAATGAATCAC
98346	96433	AAGTTAGCTCTAATGAATCA
98347	96434	GAAGTTAGCTCTAATGAATC
98348	96435	TGAAGTTAGCTCTAATGAAT
98349	96436	ATGAAGTTAGCTCTAATGAA
98350	96437	CATGAAGTTAGCTCTAATGA
98351	96438	TCATGAAGTTAGCTCTAATG
98352	96439	GTCATGAAGTTAGCTCTAAT
98353	96440	TGTCATGAAGTTAGCTCTAA
98354	96441	ATGTCATGAAGTTAGCTCTA
98355	96442	CATGTCATGAAGTTAGCTCT
98356	96443	GCATGTCATGAAGTTAGCTC
98357	96444	AGCATGTCATGAAGTTAGCT
98358	96445	GAGCATGTCATGAAGTTAGC
98359	96446	TGAGCATGTCATGAAGTTAG
98360	96447	ATGAGCATGTCATGAAGTTA
98361	96448	TATGAGCATGTCATGAAGTT
98362	96449	CTATGAGCATGTCATGAAGT
98363	96450	GCTATGAGCATGTCATGAAG
98364	96451	GGCTATGAGCATGTCATGAA
98365	96452	GGGCTATGAGCATGTCATGA
98366	96453	GGGGCTATGAGCATGTCATG
98367	96454	TGGGGCTATGAGCATGTCAT
98368	96455	TTGGGGCTATGAGCATGTCA
98369	96456	TTTGGGGCTATGAGCATGTC
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98374	96461	TGCAGTTTGGGGCTATGAGC
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98377	96464	AAATGCAGTTTGGGGCTATG
98378	96465	CAAATGCAGTTTGGGGCTAT
98379	96466	ACAAATGCAGTTTGGGGCTA
98380	96467	AACAAATGCAGTTTGGGGCT
98381	96468	GAACAAATGCAGTTTGGGGC
98382	96469	TGAACAAATGCAGTTTGGGG
98383	96470	GTGAACAAATGCAGTTTGGG
98384	96471	TGTGAACAAATGCAGTTTGG
98385	96472	TTGTGAACAAATGCAGTTTG
98386	96473	TTTGTGAACAAATGCAGTTT
98387	96474	ATTTGTGAACAAATGCAGTT
98388	96475	TATTTGTGAACAAATGCAGT
98389	96476	ATATTTGTGAACAAATGCAG
98390	96477	GATATTTGTGAACAAATGCA
98391	96478	AGATATTTGTGAACAAATGC
98392	96479	CAGATATTTGTGAACAAATG
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98396	96483	ACTACAGATATTTGTGAACA
98397	96484	GACTACAGATATTTGTGAAC
98398	96485	GGACTACAGATATTTGTGAA
98399	96486	AGGACTACAGATATTTGTGA
98400	96487	AAGGACTACAGATATTTGTG
98401	96488	GAAGGACTACAGATATTTGT
98402	96489	TGAAGGACTACAGATATTTG
98403	96490	ATGAAGGACTACAGATATTT
98404	96491	AATGAAGGACTACAGATATT
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98406	96493	TAAATGAAGGACTACAGATA
98407	96494	CTAAATGAAGGACTACAGAT
98408	96495	CCTAAATGAAGGACTACAGA
98409	96496	GCCTAAATGAAGGACTACAG
98410	96497	TGCCTAAATGAAGGACTACA
98411	96498	CTGCCTAAATGAAGGACTAC
98412	96499	TCTGCCTAAATGAAGGACTA
98413	96500	TTCTGCCTAAATGAAGGACT
98414	96501	TTTCTGCCTAAATGAAGGAC

147491	145578	GTAGAAGTCAGGGCTGTGCT
147492	145579	GGTAGAAGTCAGGGCTGTGC
147493	145580	GGGTAGAAGTCAGGGCTGTG
147494	145581	TGGGTAGAAGTCAGGGCTGT
147495	145582	CTGGGTAGAAGTCAGGGCTG
147496	145583	CCTGGGTAGAAGTCAGGGCT
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147499	145586	GAGCCTGGGTAGAAGTCAGG
147500	145587	TGAGCCTGGGTAGAAGTCAG
147501	145588	GTGAGCCTGGGTAGAAGTCA
147502	145589	AGTGAGCCTGGGTAGAAGTC
147503	145590	AAGTGAGCCTGGGTAGAAGT
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147505	145592	ACAAGTGAGCCTGGGTAGAA
147506	145593	AACAAGTGAGCCTGGGTAGA
147507	145594	CAACAAGTGAGCCTGGGTAG
147508	145595	GCAACAAGTGAGCCTGGGTA
147509	145596	GGCAACAAGTGAGCCTGGGT
147510	145597	AGGCAACAAGTGAGCCTGGG
147511	145598	CAGGCAACAAGTGAGCCTGG
147512	145599	GCAGGCAACAAGTGAGCCTG
147513	145600	AGCAGGCAACAAGTGAGCCT
147514	145601	GAGCAGGCAACAAGTGAGCC
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147516	145603	GGGAGCAGGCAACAAGTGAG
147517	145604	AGGGAGCAGGCAACAAGTGA
147518	145605	CAGGGAGCAGGCAACAAGTG
147519	145606	TCAGGGAGCAGGCAACAAGT
147520	145607	GTCAGGGAGCAGGCAACAAG
147521	145608	GGTCAGGGAGCAGGCAACAA
147522	145609	GGGTCAGGGAGCAGGCAACA
147523	145610	AGGGTCAGGGAGCAGGCAAC
147524	145611	AAGGGTCAGGGAGCAGGCAA
147525	145612	CAAGGGTCAGGGAGCAGGCA
147526	145613	GCAAGGGTCAGGGAGCAGGC
147527	145614	TGCAAGGGTCAGGGAGCAGG
147528	145615	CTGCAAGGGTCAGGGAGCAG
147529	145616	CCTGCAAGGGTCAGGGAGCA
147530	145617	TCCTGCAAGGGTCAGGGAGC
147531	145618	ATCCTGCAAGGGTCAGGGAG
147532	145619	GATCCTGCAAGGGTCAGGGA
147533	145620	AGATCCTGCAAGGGTCAGGG
147534	145621	CAGATCCTGCAAGGGTCAGG
147535	145622	GCAGATCCTGCAAGGGTCAG
147536	145623	GGCAGATCCTGCAAGGGTCA
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147542	145629	CCTTTGGGCAGATCCTGCAA
147543	145630	ACCTTTGGGCAGATCCTGCA
147544	145631	CACCTTTGGGCAGATCCTGC
147545	145632	TCACCTTTGGGCAGATCCTG
147546	145633	TTCACCTTTGGGCAGATCCT
147547	145634	CTTCACCTTTGGGCAGATCC
147548	145635	GCTTCACCTTTGGGCAGATC
147549	145636	CGCTTCACCTTTGGGCAGAT
147550	145637	GCGCTTCACCTTTGGGCAGA
147551	145638	CGCGCTTCACCTTTGGGCAG
147552	145639	ACGCGCTTCACCTTTGGGCA
147553	145640	GACGCGCTTCACCTTTGGGC
147554	145641	AGACGCGCTTCACCTTTGGG
147555	145642	AAGACGCGCTTCACCTTTGG
147556	145643	GAAGACGCGCTTCACCTTTG
147557	145644	TGAAGACGCGCTTCACCTTT
147558	145645	CTGAAGACGCGCTTCACCTT
147559	145646	CCTGAAGACGCGCTTCACCT
147560	145647	ACCTGAAGACGCGCTTCACC
147561	145648	GACCTGAAGACGCGCTTCAC

49268	47355	TCCATATCTTTAAACTGTAC
49269	47356	GTCCATATCTTTAAACTGTA
49270	47357	AGTCCATATCTTTAAACTGT
49271	47358	GAGTCCATATCTTTAAACTG
49272	47359	GGAGTCCATATCTTTAAACT
49273	47360	TGGAGTCCATATCTTTAAAC
49274	47361	CTGGAGTCCATATCTTTAAA
49275	47362	ACTGGAGTCCATATCTTTAA
49276	47363	AACTGGAGTCCATATCTTTA
49277	47364	TAACTGGAGTCCATATCTTT
49278	47365	ATAACTGGAGTCCATATCTT
49279	47366	CATAACTGGAGTCCATATCT
49280	47367	GCATAACTGGAGTCCATATC
49281	47368	TGCATAACTGGAGTCCATAT
49282	47369	TTGCATAACTGGAGTCCATA
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49286	47373	CTTTTTGCATAACTGGAGTC
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49291	47378	CACCTCTTTTTGCATAACTG
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49300	47387	ATCAAAACCCACCTCTTTTT
49301	47388	AATCAAAACCCACCTCTTTT
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49303	47390	GAAATCAAAACCCACCTCTT
49304	47391	GGAAATCAAAACCCACCTCT
49305	47392	AGGAAATCAAAACCCACCTC
49306	47393	TAGGAAATCAAAACCCACCT
49307	47394	TTAGGAAATCAAAACCCACC
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49311	47398	ATATTTAGGAAATCAAAACC
49312	47399	CATATTTAGGAAATCAAAAC
49313	47400	GCATATTTAGGAAATCAAAA
49314	47401	GGCATATTTAGGAAATCAAA
49315	47402	AGGCATATTTAGGAAATCAA
49316	47403	GAGGCATATTTAGGAAATCA
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49323	47410	AAACCATGAGGCATATTTAG
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49326	47413	AATAAACCATGAGGCATATT
49327	47414	TAATAAACCATGAGGCATAT
49328	47415	CTAATAAACCATGAGGCATA
49329	47416	TCTAATAAACCATGAGGCAT
49330	47417	ATCTAATAAACCATGAGGCA
49331	47418	AATCTAATAAACCATGAGGC
49332	47419	AAATCTAATAAACCATGAGG
49333	47420	TAAATCTAATAAACCATGAG
49334	47421	ATAAATCTAATAAACCATGA
49335	47422	AATAAATCTAATAAACCATG
49336	47423	GAATAAATCTAATAAACCAT
49337	47424	TGAATAAATCTAATAAACCA
49338	47425	TTGAATAAATCTAATAAACC

98415	96502	ATTTCTGCCTAAATGAAGGA
98416	96503	TATTTCTGCCTAAATGAAGG
98417	96504	CTATTTCTGCCTAAATGAAG
98418	96505	TCTATTTCTGCCTAAATGAA
98419	96506	TTCTATTTCTGCCTAAATGA
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98423	96510	GTATTTCTATTTCTGCCTAA
98424	96511	GGTATTTCTATTTCTGCCTA
98425	96512	AGGTATTTCTATTTCTGCCT
98426	96513	AAGGTATTTCTATTTCTGCC
98427	96514	CAAGGTATTTCTATTTCTGC
98428	96515	ACAAGGTATTTCTATTTCTG
98429	96516	CACAAGGTATTTCTATTTCT
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98431	96518	CACACAAGGTATTTCTATTT
98432	96519	ACACACAAGGTATTTCTATT
98433	96520	AACACACAAGGTATTTCTAT
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98437	96524	AACAAACACACAAGGTATTT
98438	96525	CAACAAACACACAAGGTATT
98439	96526	ACAACAAACACACAAGGTAT
98440	96527	AACAACAAACACACAAGGTA
98441	96528	GAACAACAAACACACAAGGT
98442	96529	GGAACAACAAACACACAAGG
98443	96530	AGGAACAACAAACACACAAG
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98445	96532	GAAGGAACAACAAACACACA
98446	96533	GGAAGGAACAACAAACACAC
98447	96534	GGGAAGGAACAACAAACACA
98448	96535	AGGGAAGGAACAACAAACAC
98449	96536	AAGGGAAGGAACAACAAACA
98450	96537	AAAGGGAAGGAACAACAAAC
98451	96538	AAAAGGGAAGGAACAACAAA
98452	96539	CAAAAGGGAAGGAACAACAA
98453	96540	TCAAAAGGGAAGGAACAACA
98454	96541	CTCAAAAGGGAAGGAACAAC
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98459	96546	TATGGCTCAAAAGGGAAGGA
98460	96547	ATATGGCTCAAAAGGGAAGG
98461	96548	CATATGGCTCAAAAGGGAAG
98462	96549	GCATATGGCTCAAAAGGGAA
98463	96550	TGCATATGGCTCAAAAGGGA
98464	96551	CTGCATATGGCTCAAAAGGG
98465	96552	TCTGCATATGGCTCAAAAGG
98466	96553	CTCTGCATATGGCTCAAAAG
98467	96554	ACTCTGCATATGGCTCAAAA
98468	96555	CACTCTGCATATGGCTCAAA
98469	96556	GCACTCTGCATATGGCTCAA
98470	96557	AGCACTCTGCATATGGCTCA
98471	96558	CAGCACTCTGCATATGGCTC
98472	96559	TCAGCACTCTGCATATGGCT
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98476	96563	GCTATCAGCACTCTGCATAT
98477	96564	AGCTATCAGCACTCTGCATA
98478	96565	AAGCTATCAGCACTCTGCAT
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98480	96567	TAAAGCTATCAGCACTCTGC
98481	96568	ATAAAGCTATCAGCACTCTG
98482	96569	AATAAAGCTATCAGCACTCT
98483	96570	AAATAAAGCTATCAGCACTC
98484	96571	CAAATAAAGCTATCAGCACT
98485	96572	ACAAATAAAGCTATCAGCAC

147562	145649	TGACCTGAAGACGCGCTTCA
147563	145650	TTGACCTGAAGACGCGCTTC
147564	145651	ATTGACCTGAAGACGCGCTT
147565	145652	TATTGACCTGAAGACGCGCT
147566	145653	CTATTGACCTGAAGACGCGC
147567	145654	TCTATTGACCTGAAGACGCG
147568	145655	ATCTATTGACCTGAAGACGC
147569	145656	TATCTATTGACCTGAAGACG
147570	145657	TTATCTATTGACCTGAAGAC
147571	145658	ATTATCTATTGACCTGAAGA
147572	145659	GATTATCTATTGACCTGAAG
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147574	145661	TAGATTATCTATTGACCTGA
147575	145662	GTAGATTATCTATTGACCTG
147576	145663	AGTAGATTATCTATTGACCT
147577	145664	TAGTAGATTATCTATTGACC
147578	145665	CTAGTAGATTATCTATTGAC
147579	145666	TCTAGTAGATTATCTATTGA
147580	145667	CTCTAGTAGATTATCTATTG
147581	145668	TCTCTAGTAGATTATCTATT
147582	145669	ATCTCTAGTAGATTATCTAT
147583	145670	AATCTCTAGTAGATTATCTA
147584	145671	CAATCTCTAGTAGATTATCT
147585	145672	ACAATCTCTAGTAGATTATC
147586	145673	GACAATCTCTAGTAGATTAT
147587	145674	GGACAATCTCTAGTAGATTA
147588	145675	GGGACAATCTCTAGTAGATT
147589	145676	GGGGACAATCTCTAGTAGAT
147590	145677	TGGGGACAATCTCTAGTAGA
147591	145678	CTGGGGACAATCTCTAGTAG
147592	145679	TCTGGGGACAATCTCTAGTA
147593	145680	CTCTGGGGACAATCTCTAGT
147594	145681	TCTCTGGGGACAATCTCTAG
147595	145682	TTCTCTGGGGACAATCTCTA
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147597	145684	TGTTCTCTGGGGACAATCTC
147598	145685	CTGTTCTCTGGGGACAATCT
147599	145686	TCTGTTCTCTGGGGACAATC
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147601	145688	GTTCTGTTCTCTGGGGACAA
147602	145689	AGTTCTGTTCTCTGGGGACA
147603	145690	CAGTTCTGTTCTCTGGGGAC
147604	145691	CCAGTTCTGTTCTCTGGGGA
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147606	145693	GCCCAGTTCTGTTCTCTGGG
147607	145694	GGCCCAGTTCTGTTCTCTGG
147608	145695	GGGCCCAGTTCTGTTCTCTG
147609	145696	AGGGCCCAGTTCTGTTCTCT
147610	145697	CAGGGCCCAGTTCTGTTCTC
147611	145698	TCAGGGCCCAGTTCTGTTCT
147612	145699	CTCAGGGCCCAGTTCTGTTC
147613	145700	CCTCAGGGCCCAGTTCTGTT
147614	145701	GCCTCAGGGCCCAGTTCTGT
147615	145702	GGCCTCAGGGCCCAGTTCTG
147616	145703	GGGCCTCAGGGCCCAGTTCT
147617	145704	TGGGCCTCAGGGCCCAGTTC
147618	145705	GTGGGCCTCAGGGCCCAGTT
147619	145706	GGTGGGCCTCAGGGCCCAGT
147620	145707	CGGTGGGCCTCAGGGCCCAG
147621	145708	ACGGTGGGCCTCAGGGCCCA
147622	145709	AACGGTGGGCCTCAGGGCCC
147623	145710	CAACGGTGGGCCTCAGGGCC
147624	145711	GCAACGGTGGGCCTCAGGGC
147625	145712	GGCAACGGTGGGCCTCAGGG
147626	145713	GGGCAACGGTGGGCCTCAGG
147627	145714	AGGGCAACGGTGGGCCTCAG
147628	145715	AAGGGCAACGGTGGGCCTCA
147629	145716	AAAGGGCAACGGTGGGCCTC
147630	145717	GAAAGGGCAACGGTGGGCCT
147631	145718	GGAAAGGGCAACGGTGGGCC
147632	145719	AGGAAAGGGCAACGGTGGGC

49339	47426	CTTGAATAAATCTAATAAAC
49340	47427	GCTTGAATAAATCTAATAAA
49341	47428	TGCTTGAATAAATCTAATAA
49342	47429	TTGCTTGAATAAATCTAATA
49343	47430	TTTGCTTGAATAAATCTAAT
49344	47431	CTTTGCTTGAATAAATCTAA
49345	47432	TCTTTGCTTGAATAAATCTA
49346	47433	ATCTTTGCTTGAATAAATCT
49347	47434	AATCTTTGCTTGAATAAATC
49348	47435	AAATCTTTGCTTGAATAAAT
49349	47436	AAAATCTTTGCTTGAATAAA
49350	47437	GAAAATCTTTGCTTGAATAA
49351	47438	TGAAAATCTTTGCTTGAATA
49352	47439	GTGAAAATCTTTGCTTGAAT
49353	47440	TGTGAAAATCTTTGCTTGAA
49354	47441	CTGTGAAAATCTTTGCTTGA
49355	47442	ACTGTGAAAATCTTTGCTTG
49356	47443	CACTGTGAAAATCTTTGCTT
49357	47444	TCACTGTGAAAATCTTTGCT
49358	47445	ATCACTGTGAAAATCTTTGC
49359	47446	GATCACTGTGAAAATCTTTG
49360	47447	AGATCACTGTGAAAATCTTT
49361	47448	AAGATCACTGTGAAAATCTT
49362	47449	TAAGATCACTGTGAAAATCT
49363	47450	GTAAGATCACTGTGAAAATC
49364	47451	TGTAAGATCACTGTGAAAAT
49365	47452	TTGTAAGATCACTGTGAAAA
49366	47453	TTTGTAAGATCACTGTGAAA
49367	47454	GTTTGTAAGATCACTGTGAA
49368	47455	AGTTTGTAAGATCACTGTGA
49369	47456	AAGTTTGTAAGATCACTGTG
49370	47457	AAAGTTTGTAAGATCACTGT
49371	47458	AAAAGTTTGTAAGATCACTG
49372	47459	AAAAAGTTTGTAAGATCACT
49373	47460	AAAAAAGTTTGTAAGATCAC
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49383	47470	TATTTCTTTAAAAAAAGTTT
49384	47471	ATATTTCTTTAAAAAAAGTT
49385	47472	GATATTTCTTTAAAAAAAGT
49386	47473	AGATATTTCTTTAAAAAAAG
49387	47474	CAGATATTTCTTTAAAAAAA
49388	47475	CCAGATATTTCTTTAAAAAA
49389	47476	CCCAGATATTTCTTTAAAAA
49390	47477	GCCCAGATATTTCTTTAAAA
49391	47478	AGCCCAGATATTTCTTTAAA
49392	47479	CAGCCCAGATATTTCTTTAA
49393	47480	CCAGCCCAGATATTTCTTTA
49394	47481	CCCAGCCCAGATATTTCTTT
49395	47482	ACCCAGCCCAGATATTTCTT
49396	47483	TACCCAGCCCAGATATTTCT
49397	47484	ATACCCAGCCCAGATATTTC
49398	47485	CATACCCAGCCCAGATATTT
49399	47486	CCATACCCAGCCCAGATATT
49400	47487	GCCATACCCAGCCCAGATAT
49401	47488	CGCCATACCCAGCCCAGATA
49402	47489	CCGCCATACCCAGCCCAGAT
49403	47490	GCCGCCATACCCAGCCCAGA
49404	47491	AGCCGCCATACCCAGCCCAG
49405	47492	GAGCCGCCATACCCAGCCCA
49406	47493	TGAGCCGCCATACCCAGCCC
49407	47494	ATGAGCCGCCATACCCAGCC
49408	47495	AATGAGCCGCCATACCCAGC
49409	47496	GAATGAGCCGCCATACCCAG

98486	96573	CACAAATAAAGCTATCAGCA
98487	96574	ACACAAATAAAGCTATCAGC
98488	96575	TACACAAATAAAGCTATCAG
98489	96576	TTACACAAATAAAGCTATCA
98490	96577	CTTACACAAATAAAGCTATC
98491	96578	TCTTACACAAATAAAGCTAT
98492	96579	TTCTTACACAAATAAAGCTA
98493	96580	ATTCTTACACAAATAAAGCT
98494	96581	AATTCTTACACAAATAAAGC
98495	96582	CAATTCTTACACAAATAAAG
98496	96583	GCAATTCTTACACAAATAAA
98497	96584	AGCAATTCTTACACAAATAA
98498	96585	TAGCAATTCTTACACAAATA
98499	96586	CTAGCAATTCTTACACAAAT
98500	96587	ACTAGCAATTCTTACACAAA
98501	96588	TACTAGCAATTCTTACACAA
98502	96589	TTACTAGCAATTCTTACACA
98503	96590	ATTACTAGCAATTCTTACAC
98504	96591	AATTACTAGCAATTCTTACA
98505	96592	AAATTACTAGCAATTCTTAC
98506	96593	CAAATTACTAGCAATTCTTA
98507	96594	TCAAATTACTAGCAATTCTT
98508	96595	ATCAAATTACTAGCAATTCT
98509	96596	GATCAAATTACTAGCAATTC
98510	96597	AGATCAAATTACTAGCAATT
98511	96598	CAGATCAAATTACTAGCAAT
98512	96599	ACAGATCAAATTACTAGCAA
98513	96600	AACAGATCAAATTACTAGCA
98514	96601	AAACAGATCAAATTACTAGC
98515	96602	AAAACAGATCAAATTACTAG
98516	96603	CAAAACAGATCAAATTACTA
98517	96604	CCAAAACAGATCAAATTACT
98518	96605	CCCAAAACAGATCAAATTAC
98519	96606	ACCCAAAACAGATCAAATTA
98520	96607	AACCCAAAACAGATCAAATT
98521	96608	TAACCCAAAACAGATCAAAT
98522	96609	TTAACCCAAAACAGATCAAA
98523	96610	ATTAACCCAAAACAGATCAA
98524	96611	TATTAACCCAAAACAGATCA
98525	96612	TTATTAACCCAAAACAGATC
98526	96613	ATTATTAACCCAAAACAGAT
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98529	96616	CACATTATTAACCCAAAACA
98530	96617	CCACATTATTAACCCAAAAC
98531	96618	CCCACATTATTAACCCAAAA
98532	96619	ACCCACATTATTAACCCAAA
98533	96620	AACCCACATTATTAACCCAA
98534	96621	AAACCCACATTATTAACCCA
98535	96622	AAAACCCACATTATTAACCC
98536	96623	TAAAACCCACATTATTAACC
98537	96624	CTAAAACCCACATTATTAAC
98538	96625	TCTAAAACCCACATTATTAA
98539	96626	CTCTAAAACCCACATTATTA
98540	96627	CCTCTAAAACCCACATTATT
98541	96628	ACCTCTAAAACCCACATTAT
98542	96629	TACCTCTAAAACCCACATTA
98543	96630	TTACCTCTAAAACCCACATT
98544	96631	TTTACCTCTAAAACCCACAT
98545	96632	ATTTACCTCTAAAACCCACA
98546	96633	CATTTACCTCTAAAACCCAC
98547	96634	CCATTTACCTCTAAAACCCA
98548	96635	TCCATTTACCTCTAAAACCC
98549	96636	GTCCATTTACCTCTAAAACC
98550	96637	GGTCCATTTACCTCTAAAAC
98551	96638	AGGTCCATTTACCTCTAAAA
98552	96639	TAGGTCCATTTACCTCTAAA
98553	96640	CTAGGTCCATTTACCTCTAA
98554	96641	CCTAGGTCCATTTACCTCTA
98555	96642	ACCTAGGTCCATTTACCTCT
98556	96643	AACCTAGGTCCATTTACCTC

147633	145720	CAGGAAAGGGCAACGGTGGG
147634	145721	TCAGGAAAGGGCAACGGTGG
147635	145722	CTCAGGAAAGGGCAACGGTG
147636	145723	TCTCAGGAAAGGGCAACGGT
147637	145724	CTCTCAGGAAAGGGCAACGG
147638	145725	ACTCTCAGGAAAGGGCAACG
147639	145726	GACTCTCAGGAAAGGGCAAC
147640	145727	GGACTCTCAGGAAAGGGCAA
147641	145728	GGGACTCTCAGGAAAGGGCA
147642	145729	TGGGACTCTCAGGAAAGGGC
147643	145730	CTGGGACTCTCAGGAAAGGG
147644	145731	GCTGGGACTCTCAGGAAAGG
147645	145732	GGCTGGGACTCTCAGGAAAG
147646	145733	GGGCTGGGACTCTCAGGAAA
147647	145734	TGGGCTGGGACTCTCAGGAA
147648	145735	CTGGGCTGGGACTCTCAGGA
147649	145736	ACTGGGCTGGGACTCTCAGG
147650	145737	CACTGGGCTGGGACTCTCAG
147651	145738	TCACTGGGCTGGGACTCTCA
147652	145739	TTCACTGGGCTGGGACTCTC
147653	145740	TTTCACTGGGCTGGGACTCT
147654	145741	CTTTCACTGGGCTGGGACTC
147655	145742	CCTTTCACTGGGCTGGGACT
147656	145743	TCCTTTCACTGGGCTGGGAC
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147658	145745	GTTCCTTTCACTGGGCTGGG
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147660	145747	GTGTTCCTTTCACTGGGCTG
147661	145748	TGTGTTCCTTTCACTGGGCT
147662	145749	CTGTGTTCCTTTCACTGGGC
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147668	145755	TGTCAACTGTGTTCCTTTCA
147669	145756	ATGTCAACTGTGTTCCTTTC
147670	145757	CATGTCAACTGTGTTCCTTT
147671	145758	ACATGTCAACTGTGTTCCTT
147672	145759	AACATGTCAACTGTGTTCCT
147673	145760	CAACATGTCAACTGTGTTCC
147674	145761	ACAACATGTCAACTGTGTTC
147675	145762	AACAACATGTCAACTGTGTT
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147677	145764	TCAACAACATGTCAACTGTG
147678	145765	TTCAACAACATGTCAACTGT
147679	145766	CTTCAACAACATGTCAACTG
147680	145767	GCTTCAACAACATGTCAACT
147681	145768	GGCTTCAACAACATGTCAAC
147682	145769	CGGCTTCAACAACATGTCAA
147683	145770	CCGGCTTCAACAACATGTCA
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147685	145772	CTCCGGCTTCAACAACATGT
147686	145773	TCTCCGGCTTCAACAACATG
147687	145774	ATCTCCGGCTTCAACAACAT
147688	145775	CATCTCCGGCTTCAACAACA
147689	145776	ACATCTCCGGCTTCAACAAC
147690	145777	AACATCTCCGGCTTCAACAA
147691	145778	CAACATCTCCGGCTTCAACA
147692	145779	GCAACATCTCCGGCTTCAAC
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147698	145785	ATACAGGCAACATCTCCGGC
147699	145786	CATACAGGCAACATCTCCGG
147700	145787	GCATACAGGCAACATCTCCG
147701	145788	CGCATACAGGCAACATCTCC
147702	145789	ACGCATACAGGCAACATCTC
147703	145790	TACGCATACAGGCAACATCT

49410	47497	GGAATGAGCCGCCATACCCA
49411	47498	AGGAATGAGCCGCCATACCC
49412	47499	CAGGAATGAGCCGCCATACC
49413	47500	ACAGGAATGAGCCGCCATAC
49414	47501	TACAGGAATGAGCCGCCATA
49415	47502	TTACAGGAATGAGCCGCCAT
49416	47503	ATTACAGGAATGAGCCGCCA
49417	47504	GATTACAGGAATGAGCCGCC
49418	47505	AGATTACAGGAATGAGCCGC
49419	47506	AAGATTACAGGAATGAGCCG
49420	47507	TAAGATTACAGGAATGAGCC
49421	47508	CTAAGATTACAGGAATGAGC
49422	47509	GCTAAGATTACAGGAATGAG
49423	47510	TGCTAAGATTACAGGAATGA
49424	47511	GTGCTAAGATTACAGGAATG
49425	47512	AGTGCTAAGATTACAGGAAT
49426	47513	AAGTGCTAAGATTACAGGAA
49427	47514	TAAGTGCTAAGATTACAGGA
49428	47515	CTAAGTGCTAAGATTACAGG
49429	47516	CCTAAGTGCTAAGATTACAG
49430	47517	CCCTAAGTGCTAAGATTACA
49431	47518	TCCCTAAGTGCTAAGATTAC
49432	47519	CTCCCTAAGTGCTAAGATTA
49433	47520	CCTCCCTAAGTGCTAAGATT
49434	47521	GCCTCCCTAAGTGCTAAGAT
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49436	47523	CAGCCTCCCTAAGTGCTAAG
49437	47524	TCAGCCTCCCTAAGTGCTAA
49438	47525	CTCAGCCTCCCTAAGTGCTA
49439	47526	CCTCAGCCTCCCTAAGTGCT
49440	47527	GCCTCAGCCTCCCTAAGTGC
49441	47528	CGCCTCAGCCTCCCTAAGTG
49442	47529	CCGCCTCAGCCTCCCTAAGT
49443	47530	CCCGCCTCAGCCTCCCTAAG
49444	47531	ACCCGCCTCAGCCTCCCTAA
49445	47532	CACCCGCCTCAGCCTCCCTA
49446	47533	CCACCCGCCTCAGCCTCCCT
49447	47534	TCCACCCGCCTCAGCCTCCC
49448	47535	ATCCACCCGCCTCAGCCTCC
49449	47536	GATCCACCCGCCTCAGCCTC
49450	47537	TGATCCACCCGCCTCAGCCT
49451	47538	GTGATCCACCCGCCTCAGCC
49452	47539	GGTGATCCACCCGCCTCAGC
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49460	47547	TGACCTCAGGTGATCCACCC
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49467	47554	GAACTCCTGACCTCAGGTGA
49468	47555	CGAACTCCTGACCTCAGGTG
49469	47556	TCGAACTCCTGACCTCAGGT
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49476	47563	GCTGGTCTCGAACTCCTGAC
49477	47564	GGCTGGTCTCGAACTCCTGA
49478	47565	AGGCTGGTCTCGAACTCCTG
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98557	96644	AAACCTAGGTCCATTTACCT
98558	96645	CAAACCTAGGTCCATTTACC
98559	96646	TCAAACCTAGGTCCATTTAC
98560	96647	TTCAAACCTAGGTCCATTTA
98561	96648	ATTCAAACCTAGGTCCATTT
98562	96649	CATTCAAACCTAGGTCCATT
98563	96650	ACATTCAAACCTAGGTCCAT
98564	96651	AACATTCAAACCTAGGTCCA
98565	96652	CAACATTCAAACCTAGGTCC
98566	96653	CCAACATTCAAACCTAGGTC
98567	96654	GCCAACATTCAAACCTAGGT
98568	96655	GGCCAACATTCAAACCTAGG
98569	96656	AGGCCAACATTCAAACCTAG
98570	96657	GAGGCCAACATTCAAACCTA
98571	96658	AGAGGCCAACATTCAAACCT
98572	96659	TAGAGGCCAACATTCAAACC
98573	96660	ATAGAGGCCAACATTCAAAC
98574	96661	TATAGAGGCCAACATTCAAA
98575	96662	GTATAGAGGCCAACATTCAA
98576	96663	TGTATAGAGGCCAACATTCA
98577	96664	ATGTATAGAGGCCAACATTC
98578	96665	GATGTATAGAGGCCAACATT
98579	96666	TGATGTATAGAGGCCAACAT
98580	96667	ATGATGTATAGAGGCCAACA
98581	96668	CATGATGTATAGAGGCCAAC
98582	96669	ACATGATGTATAGAGGCCAA
98583	96670	CACATGATGTATAGAGGCCA
98584	96671	GCACATGATGTATAGAGGCC
98585	96672	CGCACATGATGTATAGAGGC
98586	96673	ACGCACATGATGTATAGAGG
98587	96674	TACGCACATGATGTATAGAG
98588	96675	TTACGCACATGATGTATAGA
98589	96676	GTTACGCACATGATGTATAG
98590	96677	TGTTACGCACATGATGTATA
98591	96678	ATGTTACGCACATGATGTAT
98592	96679	AATGTTACGCACATGATGTA
98593	96680	CAATGTTACGCACATGATGT
98594	96681	ACAATGTTACGCACATGATG
98595	96682	CACAATGTTACGCACATGAT
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98597	96684	GCCACAATGTTACGCACATG
98598	96685	TGCCACAATGTTACGCACAT
98599	96686	ATGCCACAATGTTACGCACA
98600	96687	CATGCCACAATGTTACGCAC
98601	96688	GCATGCCACAATGTTACGCA
98602	96689	AGCATGCCACAATGTTACGC
98603	96690	TAGCATGCCACAATGTTACG
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98607	96694	TAGATAGCATGCCACAATGT
98608	96695	GTAGATAGCATGCCACAATG
98609	96696	AGTAGATAGCATGCCACAAT
98610	96697	AAGTAGATAGCATGCCACAA
98611	96698	GAAGTAGATAGCATGCCACA
98612	96699	GGAAGTAGATAGCATGCCAC
98613	96700	GGGAAGTAGATAGCATGCCA
98614	96701	GGGGAAGTAGATAGCATGCC
98615	96702	GGGGGAAGTAGATAGCATGC
98616	96703	TGGGGGAAGTAGATAGCATG
98617	96704	TTGGGGGAAGTAGATAGCAT
98618	96705	CTTGGGGGAAGTAGATAGCA
98619	96706	GCTTGGGGGAAGTAGATAGC
98620	96707	GGCTTGGGGGAAGTAGATAG
98621	96708	TGGCTTGGGGGAAGTAGATA
98622	96709	TTGGCTTGGGGGAAGTAGAT
98623	96710	TTTGGCTTGGGGGAAGTAGA
98624	96711	TTTTGGCTTGGGGGAAGTAG
98625	96712	ATTTTGGCTTGGGGGAAGTA
98626	96713	CATTTTGGCTTGGGGGAAGT
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147704	145791	TTACGCATACAGGCAACATC
147705	145792	TTTACGCATACAGGCAACAT
147706	145793	TTTTACGCATACAGGCAACA
147707	145794	CTTTTACGCATACAGGCAAC
147708	145795	TCTTTTACGCATACAGGCAA
147709	145796	CTCTTTTACGCATACAGGCA
147710	145797	GCTCTTTTACGCATACAGGC
147711	145798	AGCTCTTTTACGCATACAGG
147712	145799	GAGCTCTTTTACGCATACAG
147713	145800	AGAGCTCTTTTACGCATACA
147714	145801	GAGAGCTCTTTTACGCATAC
147715	145802	AGAGAGCTCTTTTACGCATA
147716	145803	CAGAGAGCTCTTTTACGCAT
147717	145804	ACAGAGAGCTCTTTTACGCA
147718	145805	AACAGAGAGCTCTTTTACGC
147719	145806	AAACAGAGAGCTCTTTTACG
147720	145807	GAAACAGAGAGCTCTTTTAC
147721	145808	TGAAACAGAGAGCTCTTTTA
147722	145809	CTGAAACAGAGAGCTCTTTT
147723	145810	CCTGAAACAGAGAGCTCTTT
147724	145811	GCCTGAAACAGAGAGCTCTT
147725	145812	AGCCTGAAACAGAGAGCTCT
147726	145813	GAGCCTGAAACAGAGAGCTC
147727	145814	TGAGCCTGAAACAGAGAGCT
147728	145815	ATGAGCCTGAAACAGAGAGC
147729	145816	CATGAGCCTGAAACAGAGAG
147730	145817	ACATGAGCCTGAAACAGAGA
147731	145818	TACATGAGCCTGAAACAGAG
147732	145819	GTACATGAGCCTGAAACAGA
147733	145820	TGTACATGAGCCTGAAACAG
147734	145821	CTGTACATGAGCCTGAAACA
147735	145822	ACTGTACATGAGCCTGAAAC
147736	145823	GACTGTACATGAGCCTGAAA
147737	145824	TGACTGTACATGAGCCTGAA
147738	145825	CTGACTGTACATGAGCCTGA
147739	145826	CCTGACTGTACATGAGCCTG
147740	145827	TCCTGACTGTACATGAGCCT
147741	145828	TTCCTGACTGTACATGAGCC
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147743	145830	CATTCCTGACTGTACATGAG
147744	145831	CCATTCCTGACTGTACATGA
147745	145832	ACCATTCCTGACTGTACATG
147746	145833	AACCATTCCTGACTGTACAT
147747	145834	GAACCATTCCTGACTGTACA
147748	145835	GGAACCATTCCTGACTGTAC
147749	145836	AGGAACCATTCCTGACTGTA
147750	145837	AAGGAACCATTCCTGACTGT
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147752	145839	AGAAGGAACCATTCCTGACT
147753	145840	GAGAAGGAACCATTCCTGAC
147754	145841	TGAGAAGGAACCATTCCTGA
147755	145842	ATGAGAAGGAACCATTCCTG
147756	145843	GATGAGAAGGAACCATTCCT
147757	145844	GGATGAGAAGGAACCATTCC
147758	145845	TGGATGAGAAGGAACCATTC
147759	145846	TTGGATGAGAAGGAACCATT
147760	145847	GTTGGATGAGAAGGAACCAT
147761	145848	AGTTGGATGAGAAGGAACCA
147762	145849	CAGTTGGATGAGAAGGAACC
147763	145850	GCAGTTGGATGAGAAGGAAC
147764	145851	GGCAGTTGGATGAGAAGGAA
147765	145852	GGGCAGTTGGATGAGAAGGA
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147768	145855	CATGGGCAGTTGGATGAGAA
147769	145856	GCATGGGCAGTTGGATGAGA
147770	145857	CGCATGGGCAGTTGGATGAG
147771	145858	GCGCATGGGCAGTTGGATGA
147772	145859	GGCGCATGGGCAGTTGGATG
147773	145860	TGGCGCATGGGCAGTTGGAT
147774	145861	TTGGCGCATGGGCAGTTGGA

49481	47568	GCCAGGCTGGTCTCGAACTC
49482	47569	GGCCAGGCTGGTCTCGAACT
49483	47570	TGGCCAGGCTGGTCTCGAAC
49484	47571	TTGGCCAGGCTGGTCTCGAA
49485	47572	GTTGGCCAGGCTGGTCTCGA
49486	47573	TGTTGGCCAGGCTGGTCTCG
49487	47574	ATGTTGGCCAGGCTGGTCTC
49488	47575	CATGTTGGCCAGGCTGGTCT
49489	47576	CCATGTTGGCCAGGCTGGTC
49490	47577	GCCATGTTGGCCAGGCTGGT
49491	47578	CGCCATGTTGGCCAGGCTGG
49492	47579	TCGCCATGTTGGCCAGGCTG
49493	47580	TTCGCCATGTTGGCCAGGCT
49494	47581	TTTCGCCATGTTGGCCAGGC
49495	47582	GTTTCGCCATGTTGGCCAGG
49496	47583	GGTTTCGCCATGTTGGCCAG
49497	47584	GGGGTTTCGCCATGTTGGCCA
49498	47585	GGGGTTTCGCCATGTTGGCC
49499	47586	CGGGGTTTCGCCATGTTGGC
49500	47587	ACGGGGTTTCGCCATGTTGG
49501	47588	GACGGGGTTTCGCCATGTTG
49502	47589	AGACGGGGTTTCGCCATGTT
49503	47590	GAGACGGGGTTTCGCCATGT
49504	47591	AGAGACGGGGTTTCGCCATG
49505	47592	TAGAGACGGGGTTTCGCCAT
49506	47593	GTAGAGACGGGGTTTCGCCA
49507	47594	AGTAGAGACGGGGTTTCGCC
49508	47595	TAGTAGAGACGGGGTTTCGC
49509	47596	TTAGTAGAGACGGGGTTTCG
49510	47597	TTTAGTAGAGACGGGGTTTC
49511	47598	TTTTAGTAGAGACGGGGTTT
49512	47599	TTTTTAGTAGAGACGGGGTT
49513	47600	ATTTTTAGTAGAGACGGGGT
49514	47601	TATTTTTAGTAGAGACGGGG
49515	47602	GTATTTTTAGTAGAGACGGG
49516	47603	TGTATTTTTAGTAGAGACGG
49517	47604	TTGTATTTTTAGTAGAGACG
49518	47605	TTTGTATTTTTAGTAGAGAC
49519	47606	TTTTGTATTTTTAGTAGAGA
49520	47607	TTTTTGTATTTTTAGTAGAG
49521	47608	ATTTTTGTATTTTTAGTAGA
49522	47609	AATTTTTGTATTTTTAGTAG
49523	47610	AAATTTTTGTATTTTTAGTA
49524	47611	TAAATTTTTGTATTTTTAGT
49525	47612	ATAAATTTTTGTATTTTTAG
49526	47613	AATAAATTTTTGTATTTTTA
49527	47614	AAATAAATTTTTGTATTTTT
49528	47615	AAAATAAATTTTTGTATTTT
49529	47616	AAAAATAAATTTTTGTATTT
49530	47617	CAAAAATAAATTTTTGTATT
49531	47618	ACAAAAATAAATTTTTGTAT
49532	47619	CACAAAAATAAATTTTTGTA
49533	47620	ACACAAAAATAAATTTTTGT
49534	47621	CACACAAAAATAAATTTTTG
49535	47622	ACACACAAAAATAAATTTTT
49536	47623	CACACACAAAAATAAATTTT
49537	47624	CCACACACAAAAATAAATTT
49538	47625	ACCACACACAAAAATAAATT
49539	47626	CACCACACACAAAAATAAAT
49540	47627	CCACCACACACAAAAATAAA
49541	47628	GCCACCACACACAAAAATAA
49542	47629	CGCCACCACACACAAAAATA
49543	47630	ACGCCACCACACACAAAAAT
49544	47631	CACGCCACCACACACAAAAA
49545	47632	GCACGCCACCACACACAAAA
49546	47633	CGCACGCCACCACACACAAA
49547	47634	GCGCACGCCACCACACACAA
49548	47635	GGCGCACGCCACCACACACA
49549	47636	AGGCGCACGCCACCACACAC
49550	47637	TAGGCGCACGCCACCACACA
49551	47638	ATAGGCGCACGCCACCACAC

98628	96715	CCCATTTTGGCTTGGGGGAA
98629	96716	ACCCATTTTGGCTTGGGGGA
98630	96717	AACCCATTTTGGCTTGGGGG
98631	96718	TAACCCATTTTGGCTTGGGG
98632	96719	TTAACCCATTTTGGCTTGGG
98633	96720	ATTAACCCATTTTGGCTTGG
98634	96721	AATTAACCCATTTTGGCTTG
98635	96722	AAATTAACCCATTTTGGCTT
98636	96723	AAAATTAACCCATTTTGGCT
98637	96724	TAAAATTAACCCATTTTGGC
98638	96725	CTAAAATTAACCCATTTTGG
98639	96726	TCTAAAATTAACCCATTTTG
98640	96727	TTCTAAAATTAACCCATTTT
98641	96728	GTTCTAAAATTAACCCATTT
98642	96729	GGTTCTAAAATTAACCCATT
98643	96730	AGGTTCTAAAATTAACCCAT
98644	96731	CAGGTTCTAAAATTAACCCA
98645	96732	GCAGGTTCTAAAATTAACCC
98646	96733	AGCAGGTTCTAAAATTAACC
98647	96734	AAGCAGGTTCTAAAATTAAC
98648	96735	GAAGCAGGTTCTAAAATTAA
98649	96736	TGAAGCAGGTTCTAAAATTA
98650	96737	ATGAAGCAGGTTCTAAAATT
98651	96738	TATGAAGCAGGTTCTAAAAT
98652	96739	CTATGAAGCAGGTTCTAAAA
98653	96740	ACTATGAAGCAGGTTCTAAA
98654	96741	CACTATGAAGCAGGTTCTAA
98655	96742	ACACTATGAAGCAGGTTCTA
98656	96743	AACACTATGAAGCAGGTTCT
98657	96744	GAACACTATGAAGCAGGTTC
98658	96745	GGAACACTATGAAGCAGGTT
98659	96746	AGGAACACTATGAAGCAGGT
98660	96747	CAGGAACACTATGAAGCAGG
98661	96748	ACAGGAACACTATGAAGCAG
98662	96749	CACAGGAACACTATGAAGCA
98663	96750	TCACAGGAACACTATGAAGC
98664	96751	CTCACAGGAACACTATGAAG
98665	96752	TCTCACAGGAACACTATGAA
98666	96753	CTCTCACAGGAACACTATGA
98667	96754	GCTCTCACAGGAACACTATG
98668	96755	AGCTCTCACAGGAACACTAT
98669	96756	GAGCTCTCACAGGAACACTA
98670	96757	CGAGCTCTCACAGGAACACT
98671	96758	TCGAGCTCTCACAGGAACAC
98672	96759	ATCGAGCTCTCACAGGAACA
98673	96760	CATCGAGCTCTCACAGGAAC
98674	96761	TCATCGAGCTCTCACAGGAA
98675	96762	CTCATCGAGCTCTCACAGGA
98676	96763	TCTCATCGAGCTCTCACAGG
98677	96764	ATCTCATCGAGCTCTCACAG
98678	96765	TATCTCATCGAGCTCTCACA
98679	96766	ATATCTCATCGAGCTCTCAC
98680	96767	AATATCTCATCGAGCTCTCA
98681	96768	CAATATCTCATCGAGCTCTC
98682	96769	GCAATATCTCATCGAGCTCT
98683	96770	GGCAATATCTCATCGAGCTC
98684	96771	AGGCAATATCTCATCGAGCT
98685	96772	TAGGCAATATCTCATCGAGC
98686	96773	ATAGGCAATATCTCATCGAG
98687	96774	TATAGGCAATATCTCATCGA
98688	96775	TTATAGGCAATATCTCATCG
98689	96776	TTTATAGGCAATATCTCATC
98690	96777	CTTTATAGGCAATATCTCAT
98691	96778	ACTTTATAGGCAATATCTCA
98692	96779	CACTTTATAGGCAATATCTC
98693	96780	ACACTTTATAGGCAATATCT
98694	96781	AACACTTTATAGGCAATATC
98695	96782	AAACACTTTATAGGCAATAT
98696	96783	TAAACACTTTATAGGCAATA
98697	96784	CTAAACACTTTATAGGCAAT
98698	96785	GCTAAACACTTTATAGGCAA

147775	145862	ATTGGCGCATGGGCAGTTGG
147776	145863	CATTGGCGCATGGGCAGTTG
147777	145864	TCATTGGCGCATGGGCAGTT
147778	145865	ATCATTGGCGCATGGGCAGT
147779	145866	CATCATTGGCGCATGGGCAG
147780	145867	GCATCATTGGCGCATGGGCA
147781	145868	AGCATCATTGGCGCATGGGC
147782	145869	TAGCATCATTGGCGCATGGG
147783	145870	TTAGCATCATTGGCGCATGG
147784	145871	ATTAGCATCATTGGCGCATG
147785	145872	CATTAGCATCATTGGCGCAT
147786	145873	TCATTAGCATCATTGGCGCA
147787	145874	GTCATTAGCATCATTGGCGC
147788	145875	CGTCATTAGCATCATTGGCG
147789	145876	TCGTCATTAGCATCATTGGC
147790	145877	GTCGTCATTAGCATCATTGG
147791	145878	TGTCGTCATTAGCATCATTG
147792	145879	GTGTCGTCATTAGCATCATT
147793	145880	TGTGTCGTCATTAGCATCAT
147794	145881	CTGTGTCGTCATTAGCATCA
147795	145882	GCTGTGTCGTCATTAGCATC
147796	145883	GGCTGTGTCGTCATTAGCAT
147797	145884	TGGCTGTGTCGTCATTAGCA
147798	145885	GTGGCTGTGTCGTCATTAGC
147799	145886	GGTGGCTGTGTCGTCATTAG
147800	145887	GGGTGGCTGTGTCGTCATTA
147801	145888	CGGGTGGCTGTGTCGTCATT
147802	145889	CCGGGTGGCTGTGTCGTCAT
147803	145890	GCCGGGTGGCTGTGTCGTCA
147804	145891	CGCCGGGTGGCTGTGTCGTC
147805	145892	CCGCCGGGTGGCTGTGTCGT
147806	145893	ACCGCCGGGTGGCTGTGTCG
147807	145894	GACCGCCGGGTGGCTGTGTC
147808	145895	GGACCGCCGGGTGGCTGTGT
147809	145896	GGGACCGCCGGGTGGCTGTG
147810	145897	GGGGACCGCCGGGTGGCTGT
147811	145898	TGGGGACCGCCGGGTGGCTG
147812	145899	CTGGGGACCGCCGGGTGGCT
147813	145900	CCTGGGGACCGCCGGGTGGC
147814	145901	GCCTGGGGACCGCCGGGTGG
147815	145902	GGCCTGGGGACCGCCGGGTG
147816	145903	CGGCCTGGGGACCGCCGGGT
147817	145904	GCGGCCTGGGGACCGCCGGG
147818	145905	GGCGGCCTGGGGACCGCCGG
147819	145906	GGGCGGCCTGGGGACCGCCG
147820	145907	AGGGCGGCCTGGGGACCGCC
147821	145908	GAGGGCGGCCTGGGGACCGC
147822	145909	CGAGGGCGGCCTGGGGACCG
147823	145910	GCGAGGGCGGCCTGGGGACC
147824	145911	AGCGAGGGCGGCCTGGGGAC
147825	145912	GAGCGAGGGCGGCCTGGGGA
147826	145913	TGAGCGAGGGCGGCCTGGGG
147827	145914	TTGAGCGAGGGCGGCCTGGG
147828	145915	TTTGAGCGAGGGCGGCCTGG
147829	145916	CTTTGAGCGAGGGCGGCCTG
147830	145917	ACTTTGAGCGAGGGCGGCCT
147831	145918	CACTTTGAGCGAGGGCGGCC
147832	145919	GCACTTTGAGCGAGGGCGGC
147833	145920	TGCACTTTGAGCGAGGGCGG
147834	145921	GTGCACTTTGAGCGAGGGCG
147835	145922	AGTGCACTTTGAGCGAGGGC
147836	145923	TAGTGCACTTTGAGCGAGGG
147837	145924	GTAGTGCACTTTGAGCGAGG
147838	145925	TGTAGTGCACTTTGAGCGAG
147839	145926	CTGTAGTGCACTTTGAGCGA
147840	145927	GCTGTAGTGCACTTTGAGCG
147841	145928	GGCTGTAGTGCACTTTGAGC
147842	145929	GGGCTGTAGTGCACTTTGAG
147843	145930	TGGGCTGTAGTGCACTTTGA
147844	145931	ATGGGCTGTAGTGCACTTTG
147845	145932	AATGGGCTGTAGTGCACTTT

49552	47639	TATAGGCGCACGCCACCACA
49553	47640	CTATAGGCGCACGCCACCAC
49554	47641	ACTATAGGCGCACGCCACCA
49555	47642	GACTATAGGCGCACGCCACC
49556	47643	GGACTATAGGCGCACGCCAC
49557	47644	AGGACTATAGGCGCACGCCA
49558	47645	TAGGACTATAGGCGCACGCC
49559	47646	CTAGGACTATAGGCGCACGC
49560	47647	GCTAGGACTATAGGCGCACG
49561	47648	AGCTAGGACTATAGGCGCAC
49562	47649	TAGCTAGGACTATAGGCGCA
49563	47650	GTAGCTAGGACTATAGGCGC
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49565	47652	TAGTAGCTAGGACTATAGGC
49566	47653	CTAGTAGCTAGGACTATAGG
49567	47654	CCTAGTAGCTAGGACTATAG
49568	47655	CCCTAGTAGCTAGGACTATA
49569	47656	TCCCTAGTAGCTAGGACTAT
49570	47657	CTCCCTAGTAGCTAGGACTA
49571	47658	CCTCCCTAGTAGCTAGGACT
49572	47659	GCCTCCCTAGTAGCTAGGAC
49573	47660	AGCCTCCCTAGTAGCTAGGA
49574	47661	CAGCCTCCCTAGTAGCTAGG
49575	47662	TCAGCCTCCCTAGTAGCTAG
49576	47663	CTCAGCCTCCCTAGTAGCTA
49577	47664	TCTCAGCCTCCCTAGTAGCT
49578	47665	GTCTCAGCCTCCCTAGTAGC
49579	47666	TGTCTCAGCCTCCCTAGTAG
49580	47667	CTGTCTCAGCCTCCCTAGTA
49581	47668	TCTGTCTCAGCCTCCCTAGT
49582	47669	TTCTGTCTCAGCCTCCCTAG
49583	47670	ATTCTGTCTCAGCCTCCCTA
49584	47671	AATTCTGTCTCAGCCTCCCT
49585	47672	CAATTCTGTCTCAGCCTCCC
49586	47673	GCAATTCTGTCTCAGCCTCC
49587	47674	AGCAATTCTGTCTCAGCCTC
49588	47675	AAGCAATTCTGTCTCAGCCT
49589	47676	CAAGCAATTCTGTCTCAGCC
49590	47677	TCAAGCAATTCTGTCTCAGC
49591	47678	TTCAAGCAATTCTGTCTCAG
49592	47679	GTTCAAGCAATTCTGTCTCA
49593	47680	GGTTCAAGCAATTCTGTCTC
49594	47681	GGGTTCAAGCAATTCTGTCT
49595	47682	TGGGTTCAAGCAATTCTGTC
49596	47683	CTGGGTTCAAGCAATTCTGT
49597	47684	CCTGGGTTCAAGCAATTCTG
49598	47685	TCCTGGGTTCAAGCAATTCT
49599	47686	CTCCTGGGTTCAAGCAATTC
49600	47687	CCTCCTGGGTTCAAGCAATT
49601	47688	GCCTCCTGGGTTCAAGCAAT
49602	47689	TGCCTCCTGGGTTCAAGCAA
49603	47690	CTGCCTCCTGGGTTCAAGCA
49604	47691	TCTGCCTCCTGGGTTCAAGC
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49606	47693	CCTCTGCCTCCTGGGTTCAA
49607	47694	ACCTCTGCCTCCTGGGTTCA
49608	47695	AACCTCTGCCTCCTGGGTTC
49609	47696	CAACCTCTGCCTCCTGGGTT
49610	47697	GCAACCTCTGCCTCCTGGGT
49611	47698	TGCAACCTCTGCCTCCTGGG
49612	47699	CTGCAACCTCTGCCTCCTGG
49613	47700	ACTGCAACCTCTGCCTCCTG
49614	47701	CACTGCAACCTCTGCCTCCT
49615	47702	TCACTGCAACCTCTGCCTCC
49616	47703	CTCACTGCAACCTCTGCCTC
49617	47704	GCTCACTGCAACCTCTGCCT
49618	47705	AGCTCACTGCAACCTCTGCC
49619	47706	CAGCTCACTGCAACCTCTGC
49620	47707	TCAGCTCACTGCAACCTCTG
49621	47708	ATCAGCTCACTGCAACCTCT
49622	47709	TATCAGCTCACTGCAACCTC

98699	96786	TGCTAAACACTTTATAGGCA
98700	96787	ATGCTAAACACTTTATAGGC
98701	96788	TATGCTAAACACTTTATAGG
98702	96789	CTATGCTAAACACTTTATAG
98703	96790	ACTATGCTAAACACTTTATA
98704	96791	CACTATGCTAAACACTTTAT
98705	96792	GCACTATGCTAAACACTTTA
98706	96793	GGCACTATGCTAAACACTTT
98707	96794	AGGCACTATGCTAAACACTT
98708	96795	TAGGCACTATGCTAAACACT
98709	96796	CTAGGCACTATGCTAAACAC
98710	96797	GCTAGGCACTATGCTAAACA
98711	96798	TGCTAGGCACTATGCTAAAC
98712	96799	GTGCTAGGCACTATGCTAAA
98713	96800	TGTGCTAGGCACTATGCTAA
98714	96801	ATGTGCTAGGCACTATGCTA
98715	96802	CATGTGCTAGGCACTATGCT
98716	96803	CCATGTGCTAGGCACTATGC
98717	96804	ACCATGTGCTAGGCACTATG
98718	96805	TACCATGTGCTAGGCACTAT
98719	96806	ATACCATGTGCTAGGCACTA
98720	96807	CATACCATGTGCTAGGCACT
98721	96808	ACATACCATGTGCTAGGCAC
98722	96809	TACATACCATGTGCTAGGCA
98723	96810	ATACATACCATGTGCTAGGC
98724	96811	AATACATACCATGTGCTAGG
98725	96812	GAATACATACCATGTGCTAG
98726	96813	TGAATACATACCATGTGCTA
98727	96814	TTGAATACATACCATGTGCT
98728	96815	ATTGAATACATACCATGTGC
98729	96816	TATTGAATACATACCATGTG
98730	96817	GTATTGAATACATACCATGT
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98734	96821	ACATGTATTGAATACATACC
98735	96822	AACATGTATTGAATACATAC
98736	96823	GAACATGTATTGAATACATA
98737	96824	TGAACATGTATTGAATACAT
98738	96825	ATGAACATGTATTGAATACA
98739	96826	AATGAACATGTATTGAATAC
98740	96827	GAATGAACATGTATTGAATA
98741	96828	AGAATGAACATGTATTGAAT
98742	96829	AAGAATGAACATGTATTGAA
98743	96830	TAAGAATGAACATGTATTGA
98744	96831	GTAAGAATGAACATGTATTG
98745	96832	AGTAAGAATGAACATGTATT
98746	96833	TAGTAAGAATGAACATGTAT
98747	96834	CTAGTAAGAATGAACATGTA
98748	96835	GCTAGTAAGAATGAACATGT
98749	96836	TGCTAGTAAGAATGAACATG
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98751	96838	TTTGCTAGTAAGAATGAACA
98752	96839	TTTTGCTAGTAAGAATGAAC
98753	96840	ATTTTGCTAGTAAGAATGAA
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98755	96842	ATATTTTGCTAGTAAGAATG
98756	96843	TATATTTTGCTAGTAAGAAT
98757	96844	CTATATTTTGCTAGTAAGAA
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98762	96849	GTCATCTATATTTTGCTAGT
98763	96850	GGTCATCTATATTTTGCTAG
98764	96851	GGGTCATCTATATTTTGCTA
98765	96852	TGGGTCATCTATATTTTGCT
98766	96853	CTGGGTCATCTATATTTTGC
98767	96854	ACTGGGTCATCTATATTTTG
98768	96855	TACTGGGTCATCTATATTTT
98769	96856	ATACTGGGTCATCTATATTT

147846	145933	GAATGGGCTGTAGTGCACTT
147847	145934	GGAATGGGCTGTAGTGCACT
147848	145935	TGGAATGGGCTGTAGTGCAC
147849	145936	CTGGAATGGGCTGTAGTGCA
147850	145937	ACTGGAATGGGCTGTAGTGC
147851	145938	GACTGGAATGGGCTGTAGTG
147852	145939	AGACTGGAATGGGCTGTAGT
147853	145940	GAGACTGGAATGGGCTGTAG
147854	145941	CGAGACTGGAATGGGCTGTA
147855	145942	TCGAGACTGGAATGGGCTGT
147856	145943	GTCGAGACTGGAATGGGCTG
147857	145944	TGTCGAGACTGGAATGGGCT
147858	145945	TTGTCGAGACTGGAATGGGC
147859	145946	GTTGTCGAGACTGGAATGGG
147860	145947	TGTTGTCGAGACTGGAATGG
147861	145948	CTGTTGTCGAGACTGGAATG
147862	145949	GCTGTTGTCGAGACTGGAAT
147863	145950	CGCTGTTGTCGAGACTGGAA
147864	145951	GCGCTGTTGTCGAGACTGGA
147865	145952	TGCGCTGTTGTCGAGACTGG
147866	145953	ATGCGCTGTTGTCGAGACTG
147867	145954	AATGCGCTGTTGTCGAGACT
147868	145955	AAATGCGCTGTTGTCGAGAC
147869	145956	GAAATGCGCTGTTGTCGAGA
147870	145957	GGAAATGCGCTGTTGTCGAG
147871	145958	GGGAAATGCGCTGTTGTCGA
147872	145959	GGGGAAATGCGCTGTTGTCG
147873	145960	AGGGGAAATGCGCTGTTGTC
147874	145961	TAGGGGAAATGCGCTGTTGT
147875	145962	ATAGGGGAAATGCGCTGTTG
147876	145963	TATAGGGGAAATGCGCTGTT
147877	145964	ATATAGGGGAAATGCGCTGT
147878	145965	CATATAGGGGAAATGCGCTG
147879	145966	TCATATAGGGGAAATGCGCT
147880	145967	GTCATATAGGGGAAATGCGC
147881	145968	CGTCATATAGGGGAAATGCG
147882	145969	GCGTCATATAGGGGAAATGC
147883	145970	TGCGTCATATAGGGGAAATG
147884	145971	GTGCGTCATATAGGGGAAAT
147885	145972	GGTGCGTCATATAGGGGAAA
147886	145973	GGGTGCGTCATATAGGGGAA
147887	145974	AGGGTGCGTCATATAGGGGA
147888	145975	AAGGGTGCGTCATATAGGGG
147889	145976	GAAGGGTGCGTCATATAGGG
147890	145977	TGAAGGGTGCGTCATATAGG
147891	145978	CTGAAGGGTGCGTCATATAG
147892	145979	CCTGAAGGGTGCGTCATATA
147893	145980	ACCTGAAGGGTGCGTCATAT
147894	145981	CACCTGAAGGGTGCGTCATA
147895	145982	TCACCTGAAGGGTGCGTCAT
147896	145983	CTCACCTGAAGGGTGCGTCA
147897	145984	CCTCACCTGAAGGGTGCGTC
147898	145985	GCCTCACCTGAAGGGTGCGT
147899	145986	CGCCTCACCTGAAGGGTGCG
147900	145987	ACGCCTCACCTGAAGGGTGC
147901	145988	CACGCCTCACCTGAAGGGTG
147902	145989	ACACGCCTCACCTGAAGGGT
147903	145990	CACACGCCTCACCTGAAGGG
147904	145991	ACACACGCCTCACCTGAAGG
147905	145992	CACACACGCCTCACCTGAAG
147906	145993	ACACACACGCCTCACCTGAA
147907	145994	CACACACACGCCTCACCTGA
147908	145995	GCACACACACGCCTCACCTG
147909	145996	TGCACACACACGCCTCACCT
147910	145997	CTGCACACACACGCCTCACC
147911	145998	CCTGCACACACACGCCTCAC
147912	145999	CCCTGCACACACACGCCTCA
147913	146000	CCCCTGCACACACACGCCTC
147914	146001	GCCCCTGCACACACACGCCT
147915	146002	GGCCCCTGCACACACACGCC
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49623	47710	GTATCAGCTCACTGCAACCT
49624	47711	GGTATCAGCTCACTGCAACC
49625	47712	CGGTATCAGCTCACTGCAAC
49626	47713	GCGGTATCAGCTCACTGCAA
49627	47714	TGCGGTATCAGCTCACTGCA
49628	47715	GTGCGGTATCAGCTCACTGC
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49630	47717	TGGTGCGGTATCAGCTCACT
49631	47718	GTGGTGCGGTATCAGCTCAC
49632	47719	AGTGGTGCGGTATCAGCTCA
49633	47720	CAGTGGTGCGGTATCAGCTC
49634	47721	GCAGTGGTGCGGTATCAGCT
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49636	47723	GTGCAGTGGTGCGGTATCAG
49637	47724	AGTGCAGTGGTGCGGTATCA
49638	47725	GAGTGCAGTGGTGCGGTATC
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49641	47728	CTGGAGTGCAGTGGTGCGGT
49642	47729	GCTGGAGTGCAGTGGTGCGG
49643	47730	GGCTGGAGTGCAGTGGTGCG
49644	47731	AGGCTGGAGTGCAGTGGTGC
49645	47732	CAGGCTGGAGTGCAGTGGTG
49646	47733	CCAGGCTGGAGTGCAGTGGT
49647	47734	CCCAGGCTGGAGTGCAGTGG
49648	47735	ACCCAGGCTGGAGTGCAGTG
49649	47736	CACCCAGGCTGGAGTGCAGT
49650	47737	TCACCCAGGCTGGAGTGCAG
49651	47738	GTCACCCAGGCTGGAGTGCA
49652	47739	TGTCACCCAGGCTGGAGTGC
49653	47740	CTGTCACCCAGGCTGGAGTG
49654	47741	TCTGTCACCCAGGCTGGAGT
49655	47742	CTCTGTCACCCAGGCTGGAG
49656	47743	GCTCTGTCACCCAGGCTGGA
49657	47744	TGCTCTGTCACCCAGGCTGG
49658	47745	TTGCTCTGTCACCCAGGCTG
49659	47746	CTTGCTCTGTCACCCAGGCT
49660	47747	TCTTGCTCTGTCACCCAGGC
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49662	47749	AGTCTTGCTCTGTCACCCAG
49663	47750	GAGTCTTGCTCTGTCACCCA
49664	47751	GGAGTCTTGCTCTGTCACCC
49665	47752	CGGAGTCTTGCTCTGTCACC
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49669	47756	GAAACGGAGTCTTGCTCTGT
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49676	47763	TTTTTTTGAAACGGAGTCTT
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49684	47771	TTTCTTTTTTTTTTTGAAAC
49685	47772	CTTTCTTTTTTTTTTTGAAA
49686	47773	TCTTTCTTTTTTTTTTTGAA
49687	47774	TTCTTTCTTTTTTTTTTTGA
49688	47775	TTTCTTTCTTTTTTTTTTTG
49689	47776	TTTTCTTTCTTTTTTTTTTT
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98774	96861	GTACAATACTGGGTCATCTA
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98785	96872	GTACATACTCTGTACAATAC
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98788	96875	ATTGTACATACTCTGTACAA
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98790	96877	CCATTGTACATACTCTGTAC
98791	96878	ACCATTGTACATACTCTGTA
98792	96879	CACCATTGTACATACTCTGT
98793	96880	ACACCATTGTACATACTCTG
98794	96881	GACACCATTGTACATACTCT
98795	96882	TGACACCATTGTACATACTC
98796	96883	ATGACACCATTGTACATACT
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98820	96907	TGTGACTCCACATGAAATGG
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98822	96909	TATGTGACTCCACATGAAAT
98823	96910	TTATGTGACTCCACATGAAA
98824	96911	CTTATGTGACTCCACATGAA
98825	96912	TCTTATGTGACTCCACATGA
98826	96913	TTCTTATGTGACTCCACATG
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98828	96915	AATTCTTATGTGACTCCACA
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147919	146006	CGGCGGCCCCTGCACACACA
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147923	146010	GCCCCGGCGGCCCCTGCACA
147924	146011	TGCCCCGGCGGCCCCTGCAC
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147928	146015	GGGGTGCCCCGGCGGCCCCT
147929	146016	TGGGGTGCCCCGGCGGCCCC
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147932	146019	CTTTGGGGTGCCCCGGCGGC
147933	146020	GCTTTGGGGTGCCCCGGCGG
147934	146021	TGCTTTGGGGTGCCCCGGCG
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147941	146028	AGCAGAATGCTTTGGGGTGC
147942	146029	GAGCAGAATGCTTTGGGGTG
147943	146030	CGAGCAGAATGCTTTGGGGT
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147960	146047	CTGCCATTCCACCTGTGCGA
147961	146048	CCTGCCATTCCACCTGTGCG
147962	146049	GCCTGCCATTCCACCTGTGC
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147964	146051	CTGCCTGCCATTCCACCTGT
147965	146052	CCTGCCTGCCATTCCACCTG
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147970	146057	CTGGCCCTGCCTGCCATTCC
147971	146058	ACTGGCCCTGCCTGCCATTC
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147979	146066	CTTGAAGCACTGGCCCTGCC
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147982	146069	GGGCTTGAAGCACTGGCCCT
147983	146070	GGGGCTTGAAGCACTGGCCC
147984	146071	CGGGGCTTGAAGCACTGGCC
147985	146072	GCGGGGCTTGAAGCACTGGC
147986	146073	TGCGGGGCTTGAAGCACTGG
147987	146074	ATGCGGGGCTTGAAGCACTG

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49725	47812	CCTTACTTGGGCTATTCTAG
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49747	47834	TTCTCATTTTTCTAAAAAAT
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49756	47843	GCATTAACATTCTCATTTTT
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98841	96928	AGCAGAAAACTGAAATTCTT
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98843	96930	CCAGCAGAAAACTGAAATTC
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98845	96932	GCCCAGCAGAAAACTGAAAT
98846	96933	TGCCCAGCAGAAAACTGAAA
98847	96934	ATGCCCAGCAGAAAACTGAA
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98865	96952	TTACAGGAGTGAGCCATCAT
98866	96953	ATTACAGGAGTGAGCCATCA
98867	96954	GATTACAGGAGTGAGCCATC
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98891	96978	CACCTCAGCCTCCCAAAGTG
98892	96979	CCACCTCAGCCTCCCAAAGT
98893	96980	TCCACCTCAGCCTCCCAAAG
98894	96981	ATCCACCTCAGCCTCCCAAA
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98896	96983	CCATCCACCTCAGCCTCCCA
98897	96984	TCCATCCACCTCAGCCTCCC
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98908	96995	ACCTCAGCTGATCCATCCAC
98909	96996	GACCTCAGCTGATCCATCCA
98910	96997	TGACCTCAGCTGATCCATCC
98911	96998	CTGACCTCAGCTGATCCATC

147988	146075	AATGCGGGGCTTGAAGCACT
147989	146076	AAATGCGGGGCTTGAAGCAC
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147991	146078	TCAAATGCGGGGCTTGAAGC
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148029	146116	CCCTCCTGTGCACACTCCTG
148030	146117	TCCCTCCTGTGCACACTCCT
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148032	146119	AGTCCCTCCTGTGCACACTC
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148038	146125	CGTCACAGTCCCTCCTGTGC
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148040	146127	ATCGTCACAGTCCCTCCTGT
148041	146128	GATCGTCACAGTCCCTCCTG
148042	146129	TGATCGTCACAGTCCCTCCT
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148045	146132	AACTGATCGTCACAGTCCCT
148046	146133	GAACTGATCGTCACAGTCCC
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49787	47874	TCTAAAGTTCTAATTGTTTT
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49823	47910	TTTTTAAGAGATCACAAAAA
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49825	47912	ATTTTTTAAGAGATCACAAA
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49827	47914	TAATTTTTTAAGAGATCACA
49828	47915	CTAATTTTTTAAGAGATCAC
49829	47916	ACTAATTTTTTAAGAGATCA
49830	47917	AACTAATTTTTTAAGAGATC
49831	47918	AAACTAATTTTTTAAGAGAT
49832	47919	CAAACTAATTTTTTAAGAGA
49833	47920	ACAAACTAATTTTTTAAGAG
49834	47921	TACAAACTAATTTTTTAAGA
49835	47922	TTACAAACTAATTTTTTAAG

98912	96999	CCTGACCTCAGCTGATCCAT
98913	97000	TCCTGACCTCAGCTGATCCA
98914	97001	CTCCTGACCTCAGCTGATCC
98915	97002	ACTCCTGACCTCAGCTGATC
98916	97003	AACTCCTGACCTCAGCTGAT
98917	97004	GAACTCCTGACCTCAGCTGA
98918	97005	GGAACTCCTGACCTCAGCTG
98919	97006	TGGAACTCCTGACCTCAGCT
98920	97007	CTGGAACTCCTGACCTCAGC
98921	97008	TCTGGAACTCCTGACCTCAG
98922	97009	GTCTGGAACTCCTGACCTCA
98923	97010	GGTCTGGAACTCCTGACCTC
98924	97011	TGGTCTGGAACTCCTGACCT
98925	97012	CTGGTCTGGAACTCCTGACC
98926	97013	GCTGGTCTGGAACTCCTGAC
98927	97014	GGCTGGTCTGGAACTCCTGA
98928	97015	AGGCTGGTCTGGAACTCCTG
98929	97016	CAGGCTGGTCTGGAACTCCT
98930	97017	CCAGGCTGGTCTGGAACTCC
98931	97018	GCCAGGCTGGTCTGGAACTC
98932	97019	GGCCAGGCTGGTCTGGAACT
98933	97020	CGGCCAGGCTGGTCTGGAAC
98934	97021	TCGGCCAGGCTGGTCTGGAA
98935	97022	GTCGGCCAGGCTGGTCTGGA
98936	97023	TGTCGGCCAGGCTGGTCTGG
98937	97024	ATGTCGGCCAGGCTGGTCTG
98938	97025	CATGTCGGCCAGGCTGGTCT
98939	97026	TCATGTCGGCCAGGCTGGTC
98940	97027	ATCATGTCGGCCAGGCTGGT
98941	97028	CATCATGTCGGCCAGGCTGG
98942	97029	TCATCATGTCGGCCAGGCTG
98943	97030	TTCATCATGTCGGCCAGGCT
98944	97031	TTTCATCATGTCGGCCAGGC
98945	97032	GTTTCATCATGTCGGCCAGG
98946	97033	GGTTTCATCATGTCGGCCAG
98947	97034	GGGTTTCATCATGTCGGCCA
98948	97035	GGGGTTTCATCATGTCGGCC
98949	97036	TGGGGTTTCATCATGTCGGC
98950	97037	ATGGGGTTTCATCATGTCGG
98951	97038	GATGGGGTTTCATCATGTCG
98952	97039	AGATGGGGTTTCATCATGTC
98953	97040	GAGATGGGGTTTCATCATGT
98954	97041	AGAGATGGGGTTTCATCATG
98955	97042	TAGAGATGGGGTTTCATCAT
98956	97043	GTAGAGATGGGGTTTCATCA
98957	97044	AGTAGAGATGGGGTTTCATC
98958	97045	TAGTAGAGATGGGGTTTCAT
98959	97046	TTAGTAGAGATGGGGTTTCA
98960	97047	TTTAGTAGAGATGGGGTTTC
98961	97048	TTTTAGTAGAGATGGGGTTT
98962	97049	TTTTTAGTAGAGATGGGGTT
98963	97050	ATTTTTAGTAGAGATGGGGT
98964	97051	TATTTTTAGTAGAGATGGGG
98965	97052	GTATTTTTAGTAGAGATGGG
98966	97053	TGTATTTTTAGTAGAGATGG
98967	97054	TTGTATTTTTAGTAGAGATG
98968	97055	TTTGTATTTTTAGTAGAGAT
98969	97056	TTTTGTATTTTTAGTAGAGA
98970	97057	TTTTTGTATTTTTAGTAGAG
98971	97058	TTTTTTGTATTTTTAGTAGA
98972	97059	ATTTTTTGTATTTTTAGTAG
98973	97060	AATTTTTTGTATTTTTAGTA
98974	97061	TAATTTTTTGTATTTTTAGT
98975	97062	CTAATTTTTTGTATTTTTAG
98976	97063	GCTAATTTTTTGTATTTTTA
98977	97064	GGCTAATTTTTTGTATTTTT
98978	97065	TGGCTAATTTTTTGTATTTT
98979	97066	CTGGCTAATTTTTTGTATTT
98980	97067	CCTGGCTAATTTTTTGTATT
98981	97068	GCCTGGCTAATTTTTTGTAT
98982	97069	CGCCTGGCTAATTTTTTGTA

148059	146146	AGGCCCTGATGCTGAACTGA
148060	146147	CAGGCCCTGATGCTGAACTG
148061	146148	TCAGGCCCTGATGCTGAACT
148062	146149	CTCAGGCCCTGATGCTGAAC
148063	146150	CCTCAGGCCCTGATGCTGAA
148064	146151	GCCTCAGGCCCTGATGCTGA
148065	146152	AGCCTCAGGCCCTGATGCTG
148066	146153	AAGCCTCAGGCCCTGATGCT
148067	146154	GAAGCCTCAGGCCCTGATGC
148068	146155	GGAAGCCTCAGGCCCTGATG
148069	146156	CGGAAGCCTCAGGCCCTGAT
148070	146157	CCGGAAGCCTCAGGCCCTGA
148071	146158	CCCGGAAGCCTCAGGCCCTG
148072	146159	TCCCGGAAGCCTCAGGCCCT
148073	146160	CTCCCGGAAGCCTCAGGCCC
148074	146161	GCTCCCGGAAGCCTCAGGCC
148075	146162	GGCTCCCGGAAGCCTCAGGC
148076	146163	CGGCTCCCGGAAGCCTCAGG
148077	146164	TCGGCTCCCGGAAGCCTCAG
148078	146165	CTCGGCTCCCGGAAGCCTCA
148079	146166	ACTCGGCTCCCGGAAGCCTC
148080	146167	GACTCGGCTCCCGGAAGCCT
148081	146168	AGACTCGGCTCCCGGAAGCC
148082	146169	CAGACTCGGCTCCCGGAAGC
148083	146170	ACAGACTCGGCTCCCGGAAG
148084	146171	CACAGACTCGGCTCCCGGAA
148085	146172	ACACAGACTCGGCTCCCGGA
148086	146173	CACACAGACTCGGCTCCCGG
148087	146174	ACACACAGACTCGGCTCCCG
148088	146175	CACACACAGACTCGGCTCCC
148089	146176	ACACACACAGACTCGGCTCC
148090	146177	AACACACACAGACTCGGCTC
148091	146178	GAACACACACAGACTCGGCT
148092	146179	AGAACACACACAGACTCGGC
148093	146180	CAGAACACACACAGACTCGG
148094	146181	TCAGAACACACACAGACTCG
148095	146182	ATCAGAACACACACAGACTC
148096	146183	CATCAGAACACACACAGACT
148097	146184	CCATCAGAACACACACAGAC
148098	146185	ACCATCAGAACACACACAGA
148099	146186	TACCATCAGAACACACACAG
148100	146187	ATACCATCAGAACACACACA
148101	146188	TATACCATCAGAACACACAC
148102	146189	GTATACCATCAGAACACACA
148103	146190	TGTATACCATCAGAACACAC
148104	146191	CTGTATACCATCAGAACACA
148105	146192	CCTGTATACCATCAGAACAC
148106	146193	TCCTGTATACCATCAGAACA
148107	146194	ATCCTGTATACCATCAGAAC
148108	146195	AATCCTGTATACCATCAGAA
148109	146196	AAATCCTGTATACCATCAGA
148110	146197	CAAATCCTGTATACCATCAG
148111	146198	CCAAATCCTGTATACCATCA
148112	146199	GCCAAATCCTGTATACCATC
148113	146200	AGCCAAATCCTGTATACCAT
148114	146201	AAGCCAAATCCTGTATACCA
148115	146202	CAAGCCAAATCCTGTATACC
148116	146203	TCAAGCCAAATCCTGTATAC
148117	146204	ATCAAGCCAAATCCTGTATA
148118	146205	CATCAAGCCAAATCCTGTAT
148119	146206	TCATCAAGCCAAATCCTGTA
148120	146207	CTCATCAAGCCAAATCCTGT
148121	146208	TCTCATCAAGCCAAATCCTG
148122	146209	TTCTCATCAAGCCAAATCCT
148123	146210	CTTCTCATCAAGCCAAATCC
148124	146211	GCTTCTCATCAAGCCAAATC
148125	146212	TGCTTCTCATCAAGCCAAAT
148126	146213	CTGCTTCTCATCAAGCCAAA
148127	146214	GCTGCTTCTCATCAAGCCAA
148128	146215	TGCTGCTTCTCATCAAGCCA
148129	146216	CTGCTGCTTCTCATCAAGCC

49836	47923	TTTACAAACTAATTTTTTAA
49837	47924	CTTTACAAACTAATTTTTTA
49838	47925	GCTTTACAAACTAATTTTTT
49839	47926	TGCTTTACAAACTAATTTTT
49840	47927	ATGCTTTACAAACTAATTTT
49841	47928	AATGCTTTACAAACTAATTT
49842	47929	AAATGCTTTACAAACTAATT
49843	47930	AAAATGCTTTACAAACTAAT
49844	47931	GAAAATGCTTTACAAACTAA
49845	47932	AGAAAATGCTTTACAAACTA
49846	47933	TAGAAAATGCTTTACAAACT
49847	47934	GTAGAAAATGCTTTACAAAC
49848	47935	TGTAGAAAATGCTTTACAAA
49849	47936	CTGTAGAAAATGCTTTACAA
49850	47937	ACTGTAGAAAATGCTTTACA
49851	47938	AACTGTAGAAAATGCTTTAC
49852	47939	AAACTGTAGAAAATGCTTTA
49853	47940	AAAACTGTAGAAAATGCTTT
49854	47941	CAAAACTGTAGAAAATGCTT
49855	47942	ACAAAACTGTAGAAAATGCT
49856	47943	CACAAAACTGTAGAAAATGC
49857	47944	CCACAAAACTGTAGAAAATG
49858	47945	ACCACAAAACTGTAGAAAAT
49859	47946	GACCACAAAACTGTAGAAAA
49860	47947	TGACCACAAAACTGTAGAAA
49861	47948	TTGACCACAAAACTGTAGAA
49862	47949	CTTGACCACAAAACTGTAGA
49863	47950	TCTTGACCACAAAACTGTAG
49864	47951	TTCTTGACCACAAAACTGTA
49865	47952	ATTCTTGACCACAAAACTGT
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49868	47955	AGCATTCTTGACCACAAAAC
49869	47956	TAGCATTCTTGACCACAAAA
49870	47957	GTAGCATTCTTGACCACAAA
49871	47958	AGTAGCATTCTTGACCACAA
49872	47959	CAGTAGCATTCTTGACCACA
49873	47960	TCAGTAGCATTCTTGACCAC
49874	47961	ATCAGTAGCATTCTTGACCA
49875	47962	AATCAGTAGCATTCTTGACC
49876	47963	TAATCAGTAGCATTCTTGAC
49877	47964	ATAATCAGTAGCATTCTTGA
49878	47965	TATAATCAGTAGCATTCTTG
49879	47966	ATATAATCAGTAGCATTCTT
49880	47967	AATATAATCAGTAGCATTCT
49881	47968	GAATATAATCAGTAGCATTC
49882	47969	TGAATATAATCAGTAGCATT
49883	47970	TTGAATATAATCAGTAGCAT
49884	47971	GTTGAATATAATCAGTAGCA
49885	47972	AGTTGAATATAATCAGTAGC
49886	47973	CAGTTGAATATAATCAGTAG
49887	47974	TCAGTTGAATATAATCAGTA
49888	47975	TTCAGTTGAATATAATCAGT
49889	47976	TTTCAGTTGAATATAATCAG
49890	47977	TTTTCAGTTGAATATAATCA
49891	47978	ATTTTCAGTTGAATATAATC
49892	47979	AATTTTCAGTTGAATATAAT
49893	47980	AAATTTTCAGTTGAATATAA
49894	47981	GAAATTTTCAGTTGAATATA
49895	47982	AGAAATTTTCAGTTGAATAT
49896	47983	AAGAAATTTTCAGTTGAATA
49897	47984	CAAGAAATTTTCAGTTGAAT
49898	47985	ACAAGAAATTTTCAGTTGAA
49899	47986	GACAAGAAATTTTCAGTTGA
49900	47987	GGACAAGAAATTTTCAGTTG
49901	47988	GGGACAAGAAATTTTCAGTT
49902	47989	TGGGACAAGAAATTTTCAGT
49903	47990	ATGGGACAAGAAATTTTCAG
49904	47991	AATGGGACAAGAAATTTTCA
49905	47992	AAATGGGACAAGAAATTTTC
49906	47993	CAAATGGGACAAGAAATTTT

98983	97070	ACGCCTGGCTAATTTTTTGT
98984	97071	CACGCCTGGCTAATTTTTTG
98985	97072	CCACGCCTGGCTAATTTTTT
98986	97073	ACCACGCCTGGCTAATTTTT
98987	97074	CACCACGCCTGGCTAATTTT
98988	97075	CCACCACGCCTGGCTAATTT
98989	97076	GCCACCACGCCTGGCTAATT
98990	97077	TGCCACCACGCCTGGCTAAT
98991	97078	CTGCCACCACGCCTGGCTAA
98992	97079	CCTGCCACCACGCCTGGCTA
98993	97080	ACCTGCCACCACGCCTGGCT
98994	97081	CACCTGCCACCACGCCTGGC
98995	97082	GCACCTGCCACCACGCCTGG
98996	97083	GGCACCTGCCACCACGCCTG
98997	97084	AGGCACCTGCCACCACGCCT
98998	97085	CAGGCACCTGCCACCACGCC
98999	97086	ACAGGCACCTGCCACCACGC
99000	97087	TACAGGCACCTGCCACCACG
99001	97088	TTACAGGCACCTGCCACCAC
99002	97089	ATTACAGGCACCTGCCACCA
99003	97090	GATTACAGGCACCTGCCACC
99004	97091	GGATTACAGGCACCTGCCAC
99005	97092	GGGATTACAGGCACCTGCCA
99006	97093	TGGGATTACAGGCACCTGCC
99007	97094	CTGGGATTACAGGCACCTGC
99008	97095	GCTGGGATTACAGGCACCTG
99009	97096	AGCTGGGATTACAGGCACCT
99010	97097	TAGCTGGGATTACAGGCACC
99011	97098	GTAGCTGGGATTACAGGCAC
99012	97099	AGTAGCTGGGATTACAGGCA
99013	97100	GAGTAGCTGGGATTACAGGC
99014	97101	CGAGTAGCTGGGATTACAGG
99015	97102	GCGAGTAGCTGGGATTACAG
99016	97103	TGCGAGTAGCTGGGATTACA
99017	97104	TTGCGAGTAGCTGGGATTAC
99018	97105	CTTGCGAGTAGCTGGGATTA
99019	97106	TCTTGCGAGTAGCTGGGATT
99020	97107	GTCTTGCGAGTAGCTGGGAT
99021	97108	AGTCTTGCGAGTAGCTGGGA
99022	97109	CAGTCTTGCGAGTAGCTGGG
99023	97110	TCAGTCTTGCGAGTAGCTGG
99024	97111	CTCAGTCTTGCGAGTAGCTG
99025	97112	CCTCAGTCTTGCGAGTAGCT
99026	97113	GCCTCAGTCTTGCGAGTAGC
99027	97114	TGCCTCAGTCTTGCGAGTAG
99028	97115	CTGCCTCAGTCTTGCGAGTA
99029	97116	CCTGCCTCAGTCTTGCGAGT
99030	97117	TCCTGCCTCAGTCTTGCGAG
99031	97118	CTCCTGCCTCAGTCTTGCGA
99032	97119	TCTCCTGCCTCAGTCTTGCG
99033	97120	TTCTCCTGCCTCAGTCTTGC
99034	97121	TTTCTCCTGCCTCAGTCTTG
99035	97122	ATTTCTCCTGCCTCAGTCTT
99036	97123	CATTTCTCCTGCCTCAGTCT
99037	97124	GCATTTCTCCTGCCTCAGTC
99038	97125	AGCATTTCTCCTGCCTCAGT
99039	97126	AAGCATTTCTCCTGCCTCAG
99040	97127	CAAGCATTTCTCCTGCCTCA
99041	97128	TCAAGCATTTCTCCTGCCTC
99042	97129	TTCAAGCATTTCTCCTGCCT
99043	97130	GTTCAAGCATTTCTCCTGCC
99044	97131	GGTTCAAGCATTTCTCCTGC
99045	97132	GGGTTCAAGCATTTCTCCTG
99046	97133	CGGGTTCAAGCATTTCTCCT
99047	97134	CCGGGTTCAAGCATTTCTCC
99048	97135	CCCGGGTTCAAGCATTTCTC
99049	97136	TCCCGGGTTCAAGCATTTCT
99050	97137	CTCCCGGGTTCAAGCATTTC
99051	97138	CCTCCCGGGTTCAAGCATTT
99052	97139	GCCTCCCGGGTTCAAGCATT
99053	97140	CGCCTCCCGGGTTCAAGCAT

148130	146217	GCTGCTGCTTCTCATCAAGC
148131	146218	TGCTGCTGCTTCTCATCAAG
148132	146219	CTGCTGCTGCTTCTCATCAA
148133	146220	GCTGCTGCTGCTTCTCATCA
148134	146221	TGCTGCTGCTGCTTCTCATC
148135	146222	CTGCTGCTGCTGCTTCTCAT
148136	146223	GCTGCTGCTGCTGCTTCTCA
148137	146224	TGCTGCTGCTGCTGCTTCTC
148138	146225	TTGCTGCTGCTGCTGCTTCT
148139	146226	GTTGCTGCTGCTGCTGCTTC
148140	146227	TGTTGCTGCTGCTGCTGCTT
148141	146228	CTGTTGCTGCTGCTGCTGCT
148142	146229	GCTGTTGCTGCTGCTGCTGC
148143	146230	TGCTGTTGCTGCTGCTGCTG
148144	146231	CTGCTGTTGCTGCTGCTGCT
148145	146232	GCTGCTGTTGCTGCTGCTGC
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148147	146234	AGGCTGCTGTTGCTGCTGCT
148148	146235	CAGGCTGCTGTTGCTGCTGC
148149	146236	TCAGGCTGCTGTTGCTGCTG
148150	146237	ATCAGGCTGCTGTTGCTGCT
148151	146238	CATCAGGCTGCTGTTGCTGC
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148153	146240	TGCATCAGGCTGCTGTTGCT
148154	146241	ATGCATCAGGCTGCTGTTGC
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148156	146243	GCATGCATCAGGCTGCTGTT
148157	146244	GGCATGCATCAGGCTGCTGT
148158	146245	AGGCATGCATCAGGCTGCTG
148159	146246	TAGGCATGCATCAGGCTGCT
148160	146247	CTAGGCATGCATCAGGCTGC
148161	146248	CCTAGGCATGCATCAGGCTG
148162	146249	TCCTAGGCATGCATCAGGCT
148163	146250	GTCCTAGGCATGCATCAGGC
148164	146251	AGTCCTAGGCATGCATCAGG
148165	146252	GAGTCCTAGGCATGCATCAG
148166	146253	TGAGTCCTAGGCATGCATCA
148167	146254	CTGAGTCCTAGGCATGCATC
148168	146255	ACTGAGTCCTAGGCATGCAT
148169	146256	AACTGAGTCCTAGGCATGCA
148170	146257	CAACTGAGTCCTAGGCATGC
148171	146258	CCAACTGAGTCCTAGGCATG
148172	146259	GCCAACTGAGTCCTAGGCAT
148173	146260	GGCCAACTGAGTCCTAGGCA
148174	146261	AGGCCAACTGAGTCCTAGGC
148175	146262	AAGGCCAACTGAGTCCTAGG
148176	146263	GAAGGCCAACTGAGTCCTAG
148177	146264	GGAAGGCCAACTGAGTCCTA
148178	146265	AGGAAGGCCAACTGAGTCCT
148179	146266	AAGGAAGGCCAACTGAGTCC
148180	146267	CAAGGAAGGCCAACTGAGTC
148181	146268	ACAAGGAAGGCCAACTGAGT
148182	146269	AACAAGGAAGGCCAACTGAG
148183	146270	TAACAAGGAAGGCCAACTGA
148184	146271	ATAACAAGGAAGGCCAACTG
148185	146272	CATAACAAGGAAGGCCAACT
148186	146273	TCATAACAAGGAAGGCCAAC
148187	146274	GTCATAACAAGGAAGGCCAA
148188	146275	TGTCATAACAAGGAAGGCCA
148189	146276	CTGTCATAACAAGGAAGGCC
148190	146277	CCTGTCATAACAAGGAAGGC
148191	146278	GCCTGTCATAACAAGGAAGG
148192	146279	AGCCTGTCATAACAAGGAAG
148193	146280	CAGCCTGTCATAACAAGGAA
148194	146281	CCAGCCTGTCATAACAAGGA
148195	146282	TCCAGCCTGTCATAACAAGG
148196	146283	GTCCAGCCTGTCATAACAAG
148197	146284	TGTCCAGCCTGTCATAACAA
148198	146285	CTGTCCAGCCTGTCATAACA
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49907	47994	CCAAATGGGACAAGAAATTT
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49910	47997	AGGCCAAATGGGACAAGAAA
49911	47998	TAGGCCAAATGGGACAAGAA
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49913	48000	TGTAGGCCAAATGGGACAAG
49914	48001	TTGTAGGCCAAATGGGACAA
49915	48002	ATTGTAGGCCAAATGGGACA
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49917	48004	GCATTGTAGGCCAAATGGGA
49918	48005	AGCATTGTAGGCCAAATGGG
49919	48006	AAGCATTGTAGGCCAAATGG
49920	48007	AAAGCATTGTAGGCCAAATG
49921	48008	TAAAGCATTGTAGGCCAAAT
49922	48009	CTAAAGCATTGTAGGCCAAA
49923	48010	ACTAAAGCATTGTAGGCCAA
49924	48011	AACTAAAGCATTGTAGGCCA
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49926	48013	TAAACTAAAGCATTGTAGGC
49927	48014	ATAAACTAAAGCATTGTAGG
49928	48015	TATAAACTAAAGCATTGTAG
49929	48016	TTATAAACTAAAGCATTGTA
49930	48017	CTTATAAACTAAAGCATTGT
49931	48018	ACTTATAAACTAAAGCATTG
49932	48019	CACTTATAAACTAAAGCATT
49933	48020	CCACTTATAAACTAAAGCAT
49934	48021	CCCACTTATAAACTAAAGCA
49935	48022	GCCCACTTATAAACTAAAGC
49936	48023	TGCCCACTTATAAACTAAAG
49937	48024	ATGCCCACTTATAAACTAAA
49938	48025	CATGCCCACTTATAAACTAA
49939	48026	ACATGCCCACTTATAAACTA
49940	48027	CACATGCCCACTTATAAACT
49941	48028	CCACATGCCCACTTATAAAC
49942	48029	GCCACATGCCCACTTATAAA
49943	48030	TGCCACATGCCCACTTATAA
49944	48031	TTGCCACATGCCCACTTATA
49945	48032	TTTGCCACATGCCCACTTAT
49946	48033	ATTTGCCACATGCCCACTTA
49947	48034	GATTTGCCACATGCCCACTT
49948	48035	AGATTTGCCACATGCCCACT
49949	48036	CAGATTTGCCACATGCCCAC
49950	48037	CCAGATTTGCCACATGCCCA
49951	48038	TCCAGATTTGCCACATGCCC
49952	48039	TTCCAGATTTGCCACATGCC
49953	48040	TTTCCAGATTTGCCACATGC
49954	48041	CTTTCCAGATTTGCCACATG
49955	48042	TCTTTCCAGATTTGCCACAT
49956	48043	TTCTTTCCAGATTTGCCACA
49957	48044	TTTCTTTCCAGATTTGCCAC
49958	48045	ATTTCTTTCCAGATTTGCCA
49959	48046	GATTTCTTTCCAGATTTGCC
49960	48047	TGATTTCTTTCCAGATTTGC
49961	48048	TTGATTTCTTTCCAGATTTG
49962	48049	TTTGATTTCTTTCCAGATTT
49963	48050	CTTTGATTTCTTTCCAGATT
49964	48051	ACTTTGATTTCTTTCCAGAT
49965	48052	TACTTTGATTTCTTTCCAGA
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49967	48054	TATACTTTGATTTCTTTCCA
49968	48055	TTATACTTTGATTTCTTTCC
49969	48056	CTTATACTTTGATTTCTTTC
49970	48057	CCTTATACTTTGATTTCTTT
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49972	48059	AGCCTTATACTTTGATTTCT
49973	48060	TAGCCTTATACTTTGATTTC
49974	48061	TTAGCCTTATACTTTGATTT
49975	48062	CTTAGCCTTATACTTTGATT
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99054	97141	CCGCCTCCCGGGTTCAAGCA
99055	97142	ACCGCCTCCCGGGTTCAAGC
99056	97143	CACCGCCTCCCGGGTTCAAG
99057	97144	CCACCGCCTCCCGGGTTCAA
99058	97145	ACCACCGCCTCCCGGGTTCA
99059	97146	AACCACCGCCTCCCGGGTTC
99060	97147	CAACCACCGCCTCCCGGGTT
99061	97148	GCAACCACCGCCTCCCGGGT
99062	97149	GGCAACCACCGCCTCCCGGG
99063	97150	TGGCAACCACCGCCTCCCGG
99064	97151	ATGGCAACCACCGCCTCCCG
99065	97152	CATGGCAACCACCGCCTCCC
99066	97153	TCATGGCAACCACCGCCTCC
99067	97154	CTCATGGCAACCACCGCCTC
99068	97155	ACTCATGGCAACCACCGCCT
99069	97156	AACTCATGGCAACCACCGCC
99070	97157	TAACTCATGGCAACCACCGC
99071	97158	TTAACTCATGGCAACCACCG
99072	97159	CTTAACTCATGGCAACCACC
99073	97160	TCTTAACTCATGGCAACCAC
99074	97161	ATCTTAACTCATGGCAACCA
99075	97162	GATCTTAACTCATGGCAACC
99076	97163	CGATCTTAACTCATGGCAAC
99077	97164	ACGATCTTAACTCATGGCAA
99078	97165	CACGATCTTAACTCATGGCA
99079	97166	GCACGATCTTAACTCATGGC
99080	97167	GGCACGATCTTAACTCATGG
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99082	97169	GCGGCACGATCTTAACTCAT
99083	97170	AGCGGCACGATCTTAACTCA
99084	97171	CAGCGGCACGATCTTAACTC
99085	97172	GCAGCGGCACGATCTTAACT
99086	97173	TGCAGCGGCACGATCTTAAC
99087	97174	GTGCAGCGGCACGATCTTAA
99088	97175	AGTGCAGCGGCACGATCTTA
99089	97176	GAGTGCAGCGGCACGATCTT
99090	97177	GGAGTGCAGCGGCACGATCT
99091	97178	TGGAGTGCAGCGGCACGATC
99092	97179	CTGGAGTGCAGCGGCACGAT
99093	97180	GCTGGAGTGCAGCGGCACGA
99094	97181	GGCTGGAGTGCAGCGGCACG
99095	97182	AGGCTGGAGTGCAGCGGCAC
99096	97183	CAGGCTGGAGTGCAGCGGCA
99097	97184	CCAGGCTGGAGTGCAGCGGC
99098	97185	CCCAGGCTGGAGTGCAGCGG
99099	97186	GCCCAGGCTGGAGTGCAGCG
99100	97187	TGCCCAGGCTGGAGTGCAGC
99101	97188	TTGCCCAGGCTGGAGTGCAG
99102	97189	ATTGCCCAGGCTGGAGTGCA
99103	97190	TATTGCCCAGGCTGGAGTGC
99104	97191	TTATTGCCCAGGCTGGAGTG
99105	97192	CTTATTGCCCAGGCTGGAGT
99106	97193	TCTTATTGCCCAGGCTGGAG
99107	97194	CTCTTATTGCCCAGGCTGGA
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99109	97196	CGCTCTTATTGCCCAGGCTG
99110	97197	TCGCTCTTATTGCCCAGGCT
99111	97198	TTCGCTCTTATTGCCCAGGC
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99113	97200	GTTTCGCTCTTATTGCCCAG
99114	97201	AGTTTCGCTCTTATTGCCCA
99115	97202	GAGTTTCGCTCTTATTGCCC
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99117	97204	CGGAGTTTCGCTCTTATTGC
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99119	97206	GACGGAGTTTCGCTCTTATT
99120	97207	AGACGGAGTTTCGCTCTTAT
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99122	97209	GGAGACGGAGTTTCGCTCTT
99123	97210	TGGAGACGGAGTTTCGCTCT
99124	97211	TTGGAGACGGAGTTTCGCTC

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148202	146289	TGCCCTGTCCAGCCTGTCAT
148203	146290	CTGCCCTGTCCAGCCTGTCA
148204	146291	ACTGCCCTGTCCAGCCTGTC
148205	146292	CACTGCCCTGTCCAGCCTGT
148206	146293	ACACTGCCCTGTCCAGCCTG
148207	146294	AACACTGCCCTGTCCAGCCT
148208	146295	AAACACTGCCCTGTCCAGCC
148209	146296	AAAACACTGCCCTGTCCAGC
148210	146297	GAAAACACTGCCCTGTCCAG
148211	146298	GGAAAACACTGCCCTGTCCA
148212	146299	AGGAAAACACTGCCCTGTCC
148213	146300	AAGGAAAACACTGCCCTGTC
148214	146301	GAAGGAAAACACTGCCCTGT
148215	146302	GGAAGGAAAACACTGCCCTG
148216	146303	AGGAAGGAAAACACTGCCCT
148217	146304	CAGGAAGGAAAACACTGCCC
148218	146305	TCAGGAAGGAAAACACTGCC
148219	146306	CTCAGGAAGGAAAACACTGC
148220	146307	ACTCAGGAAGGAAAACACTG
148221	146308	GACTCAGGAAGGAAAACACT
148222	146309	GGACTCAGGAAGGAAAACAC
148223	146310	GGGACTCAGGAAGGAAAACA
148224	146311	TGGGACTCAGGAAGGAAAAC
148225	146312	TTGGGACTCAGGAAGGAAAA
148226	146313	TTTGGGACTCAGGAAGGAAA
148227	146314	TTTTGGGACTCAGGAAGGAA
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148229	146316	ACTTTTGGGACTCAGGAAGG
148230	146317	GACTTTTGGGACTCAGGAAG
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148233	146320	TCAGACTTTTGGGACTCAGG
148234	146321	GTCAGACTTTTGGGACTCAG
148235	146322	TGTCAGACTTTTGGGACTCA
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148240	146327	CCACATGTCAGACTTTTGGG
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148243	146330	CCCCCACATGTCAGACTTTT
148244	146331	CCCCCCACATGTCAGACTTT
148245	146332	ACCCCCCACATGTCAGACTT
148246	146333	AACCCCCCACATGTCAGACT
148247	146334	TAACCCCCCACATGTCAGAC
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148253	146340	TGGTAATAACCCCCCACATG
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148257	146344	GCCATGGTAATAACCCCCCA
148258	146345	TGCCATGGTAATAACCCCCC
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148262	146349	ACTCTGCCATGGTAATAACC
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148264	146351	AAACTCTGCCATGGTAATAA
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49981	48068	TTCTTCCTTAGCCTTATACT
49982	48069	TTTCTTCCTTAGCCTTATAC
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49999	48086	ACCAACCGTTCTCTACCTTT
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50039	48126	TTCTTCACCCTTTTTCATTT
50040	48127	CTTCTTCACCCTTTTTCATT
50041	48128	ACTTCTTCACCCTTTTTCAT
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50044	48131	TCTACTTCTTCACCCTTTTT
50045	48132	TTCTACTTCTTCACCCTTTT
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50047	48134	TGTTCTACTTCTTCACCCTT
50048	48135	ATGTTCTACTTCTTCACCCT

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99150	97237	ACTTAAGTTCTTTTTTTTTC
99151	97238	AACTTAAGTTCTTTTTTTTT
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99170	97257	TATACTAAATCTAATGGAAA
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99172	97259	ACTATACTAAATCTAATGGA
99173	97260	CACTATACTAAATCTAATGG
99174	97261	GCACTATACTAAATCTAATG
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99176	97263	CTGCACTATACTAAATCTAA
99177	97264	TCTGCACTATACTAAATCTA
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99180	97267	CTCTCTGCACTATACTAAAT
99181	97268	CCTCTCTGCACTATACTAAA
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99185	97272	ATTTCCTCTCTGCACTATAC
99186	97273	TATTTCCTCTCTGCACTATA
99187	97274	GTATTTCCTCTCTGCACTAT
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99190	97277	GCTGTATTTCCTCTCTGCAC
99191	97278	TGCTGTATTTCCTCTCTGCA
99192	97279	CTGCTGTATTTCCTCTCTGC
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148272	146359	CTACAATCAAACTCTGCCAT
148273	146360	GCTACAATCAAACTCTGCCA
148274	146361	AGCTACAATCAAACTCTGCC
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148277	146364	CAGAGCTACAATCAAACTCT
148278	146365	CCAGAGCTACAATCAAACTC
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148280	146367	CTCCAGAGCTACAATCAAAC
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148296	146383	TTCTCAGCAGTATCTTCTCC
148297	146384	TTTCTCAGCAGTATCTTCTC
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148307	146394	TCCACAGCGCTTTCTCAGCA
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148310	146397	CCATCCACAGCGCTTTCTCA
148311	146398	TCCATCCACAGCGCTTTCTC
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148313	146400	AGTCCATCCACAGCGCTTTC
148314	146401	CAGTCCATCCACAGCGCTTT
148315	146402	CCAGTCCATCCACAGCGCTT
148316	146403	GCCAGTCCATCCACAGCGCT
148317	146404	AGCCAGTCCATCCACAGCGC
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148320	146407	CAAAGCCAGTCCATCCACAG
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148324	146411	CACTCAAAGCCAGTCCATCC
148325	146412	ACACTCAAAGCCAGTCCATC
148326	146413	TACACTCAAAGCCAGTCCAT
148327	146414	CTACACTCAAAGCCAGTCCA
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148330	146417	ACGCTACACTCAAAGCCAGT
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148335	146422	GGCTAACGCTACACTCAAAG
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148339	146426	CTGGGGCTAACGCTACACTC
148340	146427	GCTGGGGCTAACGCTACACT
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148342	146429	GGGCTGGGGCTAACGCTACA

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99214	97301	GCTATATATGGAATATAGCA
99215	97302	TGCTATATATGGAATATAGC
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99217	97304	ATTGCTATATATGGAATATA
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99240	97327	GGAATATATTGTTCTAATGC
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99259	97346	TATAGCACTCTGCTGTATTG
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148343	146430	GGGGCTGGGGCTAACGCTAC
148344	146431	AGGGGCTGGGGCTAACGCTA
148345	146432	CAGGGGCTGGGGCTAACGCT
148346	146433	TCAGGGGCTGGGGCTAACGC
148347	146434	TTCAGGGGCTGGGGCTAACG
148348	146435	GTTCAGGGGCTGGGGCTAAC
148349	146436	TGTTCAGGGGCTGGGGCTAA
148350	146437	CTGTTCAGGGGCTGGGGCTA
148351	146438	CCTGTTCAGGGGCTGGGGCT
148352	146439	CCCTGTTCAGGGGCTGGGGC
148353	146440	CCCCTGTTCAGGGGCTGGGG
148354	146441	TCCCCTGTTCAGGGGCTGGG
148355	146442	CTCCCCTGTTCAGGGGCTGG
148356	146443	TCTCCCCTGTTCAGGGGCTG
148357	146444	CTCTCCCCTGTTCAGGGGCT
148358	146445	GCTCTCCCCTGTTCAGGGGC
148359	146446	CGCTCTCCCCTGTTCAGGGG
148360	146447	GCGCTCTCCCCTGTTCAGGG
148361	146448	GGCGCTCTCCCCTGTTCAGG
148362	146449	GGGCGCTCTCCCCTGTTCAG
148363	146450	AGGGCGCTCTCCCCTGTTCA
148364	146451	CAGGGCGCTCTCCCCTGTTC
148365	146452	ACAGGGCGCTCTCCCCTGTT
148366	146453	CACAGGGCGCTCTCCCCTGT
148367	146454	TCACAGGGCGCTCTCCCCTG
148368	146455	ATCACAGGGCGCTCTCCCCT
148369	146456	AATCACAGGGCGCTCTCCCC
148370	146457	CAATCACAGGGCGCTCTCCC
148371	146458	ACAATCACAGGGCGCTCTCC
148372	146459	CACAATCACAGGGCGCTCTC
148373	146460	GCACAATCACAGGGCGCTCT
148374	146461	AGCACAATCACAGGGCGCTC
148375	146462	GAGCACAATCACAGGGCGCT
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148377	146464	TAGAGCACAATCACAGGGCG
148378	146465	GTAGAGCACAATCACAGGGC
148379	146466	AGTAGAGCACAATCACAGGG
148380	146467	TAGTAGAGCACAATCACAGG
148381	146468	GTAGTAGAGCACAATCACAG
148382	146469	AGTAGTAGAGCACAATCACA
148383	146470	AAGTAGTAGAGCACAATCAC
148384	146471	CAAGTAGTAGAGCACAATCA
148385	146472	TCAAGTAGTAGAGCACAATC
148386	146473	ATCAAGTAGTAGAGCACAAT
148387	146474	CATCAAGTAGTAGAGCACAA
148388	146475	CCATCAAGTAGTAGAGCACA
148389	146476	GCCATCAAGTAGTAGAGCAC
148390	146477	AGCCATCAAGTAGTAGAGCA
148391	146478	CAGCCATCAAGTAGTAGAGC
148392	146479	GCAGCCATCAAGTAGTAGAG
148393	146480	GGCAGCCATCAAGTAGTAGA
148394	146481	TGGCAGCCATCAAGTAGTAG
148395	146482	ATGGCAGCCATCAAGTAGTA
148396	146483	CATGGCAGCCATCAAGTAGT
148397	146484	CCATGGCAGCCATCAAGTAG
148398	146485	GCCATGGCAGCCATCAAGTA
148399	146486	CGCCATGGCAGCCATCAAGT
148400	146487	TCGCCATGGCAGCCATCAAG
148401	146488	ATCGCCATGGCAGCCATCAA
148402	146489	TATCGCCATGGCAGCCATCA
148403	146490	GTATCGCCATGGCAGCCATC
148404	146491	AGTATCGCCATGGCAGCCAT
148405	146492	AAGTATCGCCATGGCAGCCA
148406	146493	GAAGTATCGCCATGGCAGCC
148407	146494	TGAAGTATCGCCATGGCAGC
148408	146495	GTGAAGTATCGCCATGGCAG
148409	146496	TGTGAAGTATCGCCATGGCA
148410	146497	CTGTGAAGTATCGCCATGGC
148411	146498	ACTGTGAAGTATCGCCATGG
148412	146499	GACTGTGAAGTATCGCCATG
148413	146500	AGACTGTGAAGTATCGCCAT

50120	48207	TTAATATAACTACATAATCG
50121	48208	TTTAATATAACTACATAATC
50122	48209	TTTTAATATAACTACATAAT
50123	48210	TTTTTAATATAACTACATAA
50124	48211	ATTTTTAATATAACTACATA
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50126	48213	AAATTTTTAATATAACTACA
50127	48214	TAAATTTTTAATATAACTAC
50128	48215	CTAAATTTTTAATATAACTA
50129	48216	ACTAAATTTTTAATATAACT
50130	48217	GACTAAATTTTTAATATAAC
50131	48218	AGACTAAATTTTTAATATAA
50132	48219	GAGACTAAATTTTTAATATA
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50135	48222	AAAGAGACTAAATTTTTAAT
50136	48223	AAAAGAGACTAAATTTTTAA
50137	48224	AAAAAGAGACTAAATTTTTA
50138	48225	TAAAAAGAGACTAAATTTTT
50139	48226	TTAAAAAGAGACTAAATTTT
50140	48227	CTTAAAAAGAGACTAAATTT
50141	48228	ACTTAAAAAGAGACTAAATT
50142	48229	CACTTAAAAAGAGACTAAAT
50143	48230	ACACTTAAAAAGAGACTAAA
50144	48231	GACACTTAAAAAGAGACTAA
50145	48232	GGACACTTAAAAAGAGACTA
50146	48233	TGGACACTTAAAAAGAGACT
50147	48234	ATGGACACTTAAAAAGAGAC
50148	48235	AATGGACACTTAAAAAGAGA
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50153	48240	TCATCAATGGACACTTAAAA
50154	48241	TTCATCAATGGACACTTAAA
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50161	48248	CACTTTGTTCATCAATGGAC
50162	48249	CCACTTTGTTCATCAATGGA
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50164	48251	TCCCACTTTGTTCATCAATG
50165	48252	TTCCCACTTTGTTCATCAAT
50166	48253	ATTCCCACTTTGTTCATCAA
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50178	48265	TGAGTAACAGGAATTCCCAC
50179	48266	ATGAGTAACAGGAATTCCCA
50180	48267	AATGAGTAACAGGAATTCCC
50181	48268	AAATGAGTAACAGGAATTCC
50182	48269	CAAATGAGTAACAGGAATTC
50183	48270	GCAAATGAGTAACAGGAATT
50184	48271	TGCAAATGAGTAACAGGAAT
50185	48272	TTGCAAATGAGTAACAGGAA
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50187	48274	CCTTGCAAATGAGTAACAGG
50188	48275	GCCTTGCAAATGAGTAACAG
50189	48276	TGCCTTGCAAATGAGTAACA
50190	48277	ATGCCTTGCAAATGAGTAAC

99267	97354	TATCTGAATATAGCACTCTG
99268	97355	GTATCTGAATATAGCACTCT
99269	97356	GGTATCTGAATATAGCACTC
99270	97357	TGGTATCTGAATATAGCACT
99271	97358	TTGGTATCTGAATATAGCAC
99272	97359	GTTGGTATCTGAATATAGCA
99273	97360	AGTTGGTATCTGAATATAGC
99274	97361	TAGTTGGTATCTGAATATAG
99275	97362	CTAGTTGGTATCTGAATATA
99276	97363	ACTAGTTGGTATCTGAATAT
99277	97364	CACTAGTTGGTATCTGAATA
99278	97365	CCACTAGTTGGTATCTGAAT
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99281	97368	AGTCCACTAGTTGGTATCTG
99282	97369	AAGTCCACTAGTTGGTATCT
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99287	97374	ATAGCAAGTCCACTAGTTGG
99288	97375	AATAGCAAGTCCACTAGTTG
99289	97376	AAATAGCAAGTCCACTAGTT
99290	97377	CAAATAGCAAGTCCACTAGT
99291	97378	ACAAATAGCAAGTCCACTAG
99292	97379	TACAAATAGCAAGTCCACTA
99293	97380	TTACAAATAGCAAGTCCACT
99294	97381	CTTACAAATAGCAAGTCCAC
99295	97382	TCTTACAAATAGCAAGTCCA
99296	97383	ATCTTACAAATAGCAAGTCC
99297	97384	CATCTTACAAATAGCAAGTC
99298	97385	CCATCTTACAAATAGCAAGT
99299	97386	GCCATCTTACAAATAGCAAG
99300	97387	TGCCATCTTACAAATAGCAA
99301	97388	TTGCCATCTTACAAATAGCA
99302	97389	ATTGCCATCTTACAAATAGC
99303	97390	TATTGCCATCTTACAAATAG
99304	97391	TTATTGCCATCTTACAAATA
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99306	97393	TATTATTGCCATCTTACAAA
99307	97394	CTATTATTGCCATCTTACAA
99308	97395	ACTATTATTGCCATCTTACA
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99310	97397	ATACTATTATTGCCATCTTA
99311	97398	GATACTATTATTGCCATCTT
99312	97399	AGATACTATTATTGCCATCT
99313	97400	TAGATACTATTATTGCCATC
99314	97401	GTAGATACTATTATTGCCAT
99315	97402	TGTAGATACTATTATTGCCA
99316	97403	ATGTAGATACTATTATTGCC
99317	97404	GATGTAGATACTATTATTGC
99318	97405	TGATGTAGATACTATTATTG
99319	97406	TTGATGTAGATACTATTATT
99320	97407	TTTGATGTAGATACTATTAT
99321	97408	ATTTGATGTAGATACTATTA
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99323	97410	CTATTTGATGTAGATACTAT
99324	97411	CCTATTTGATGTAGATACTA
99325	97412	CCCTATTTGATGTAGATACT
99326	97413	GCCCTATTTGATGTAGATAC
99327	97414	AGCCCTATTTGATGTAGATA
99328	97415	CAGCCCTATTTGATGTAGAT
99329	97416	ACAGCCCTATTTGATGTAGA
99330	97417	AACAGCCCTATTTGATGTAG
99331	97418	CAACAGCCCTATTTGATGTA
99332	97419	ACAACAGCCCTATTTGATGT
99333	97420	CACAACAGCCCTATTTGATG
99334	97421	TCACAACAGCCCTATTTGAT
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99336	97423	CTTCACAACAGCCCTATTTG
99337	97424	TCTTCACAACAGCCCTATTT

148414	146501	CAGACTGTGAAGTATCGCCA
148415	146502	TCAGACTGTGAAGTATCGCC
148416	146503	GTCAGACTGTGAAGTATCGC
148417	146504	GGTCAGACTGTGAAGTATCG
148418	146505	AGGTCAGACTGTGAAGTATC
148419	146506	CAGGTCAGACTGTGAAGTAT
148420	146507	ACAGGTCAGACTGTGAAGTA
148421	146508	AACAGGTCAGACTGTGAAGT
148422	146509	TAACAGGTCAGACTGTGAAG
148423	146510	ATAACAGGTCAGACTGTGAA
148424	146511	AATAACAGGTCAGACTGTGA
148425	146512	GAATAACAGGTCAGACTGTG
148426	146513	AGAATAACAGGTCAGACTGT
148427	146514	CAGAATAACAGGTCAGACTG
148428	146515	TCAGAATAACAGGTCAGACT
148429	146516	TTCAGAATAACAGGTCAGAC
148430	146517	TTTCAGAATAACAGGTCAGA
148431	146518	CTTTCAGAATAACAGGTCAG
148432	146519	GCTTTCAGAATAACAGGTCA
148433	146520	TGCTTTCAGAATAACAGGTC
148434	146521	TTGCTTTCAGAATAACAGGT
148435	146522	ATTGCTTTCAGAATAACAGG
148436	146523	TATTGCTTTCAGAATAACAG
148437	146524	GTATTGCTTTCAGAATAACA
148438	146525	AGTATTGCTTTCAGAATAAC
148439	146526	CAGTATTGCTTTCAGAATAA
148440	146527	CCAGTATTGCTTTCAGAATA
148441	146528	ACCAGTATTGCTTTCAGAAT
148442	146529	CACCAGTATTGCTTTCAGAA
148443	146530	GCACCAGTATTGCTTTCAGA
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148445	146532	AAGCACCAGTATTGCTTTCA
148446	146533	CAAGCACCAGTATTGCTTTC
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148449	146536	AGCCAAGCACCAGTATTGCT
148450	146537	TAGCCAAGCACCAGTATTGC
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148455	146542	AATATTAGCCAAGCACCAGT
148456	146543	AAATATTAGCCAAGCACCAG
148457	146544	CAAATATTAGCCAAGCACCA
148458	146545	CCAAATATTAGCCAAGCACC
148459	146546	CCCAAATATTAGCCAAGCAC
148460	146547	CCCCAAATATTAGCCAAGCA
148461	146548	TCCCCAAATATTAGCCAAGC
148462	146549	CTCCCCAAATATTAGCCAAG
148463	146550	CCTCCCCAAATATTAGCCAA
148464	146551	CCCTCCCCAAATATTAGCCA
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148466	146553	CCCCCTCCCCAAATATTAGC
148467	146554	ACCCCCTCCCCAAATATTAG
148468	146555	AACCCCCTCCCCAAATATTA
148469	146556	AAACCCCCTCCCCAAATATT
148470	146557	CAAACCCCCTCCCCAAATAT
148471	146558	ACAAACCCCCTCCCCAAATA
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148474	146561	TTAACAAACCCCCTCCCCAA
148475	146562	CTTAACAAACCCCCTCCCCA
148476	146563	CCTTAACAAACCCCCTCCCC
148477	146564	GCCTTAACAAACCCCCTCCC
148478	146565	GGCCTTAACAAACCCCCTCC
148479	146566	AGGCCTTAACAAACCCCCTC
148480	146567	AAGGCCTTAACAAACCCCCT
148481	146568	AAAGGCCTTAACAAACCCCC
148482	146569	AAAAGGCCTTAACAAACCCC
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148484	146571	AAAAAAGGCCTTAACAAACC

50191	48278	AATGCCTTGCAAATGAGTAA
50192	48279	TAATGCCTTGCAAATGAGTA
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50195	48282	CAATAATGCCTTGCAAATGA
50196	48283	TCAATAATGCCTTGCAAATG
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50201	48288	AACACTCAATAATGCCTTGC
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50203	48290	TGAACACTCAATAATGCCTT
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50243	48330	CAAGTTCAGGATTGCCCAGA
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99338	97425	GTCTTCACAACAGCCCTATT
99339	97426	AGTCTTCACAACAGCCCTAT
99340	97427	TAGTCTTCACAACAGCCCTA
99341	97428	TTAGTCTTCACAACAGCCCT
99342	97429	TTTAGTCTTCACAACAGCCC
99343	97430	ATTTAGTCTTCACAACAGCC
99344	97431	CATTTAGTCTTCACAACAGC
99345	97432	TCATTTAGTCTTCACAACAG
99346	97433	TTCATTTAGTCTTCACAACA
99347	97434	ATTCATTTAGTCTTCACAAC
99348	97435	TATTCATTTAGTCTTCACAA
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99351	97438	ACTTATTCATTTAGTCTTCA
99352	97439	GACTTATTCATTTAGTCTTC
99353	97440	AGACTTATTCATTTAGTCTT
99354	97441	TAGACTTATTCATTTAGTCT
99355	97442	ATAGACTTATTCATTTAGTC
99356	97443	TATAGACTTATTCATTTAGT
99357	97444	TTATAGACTTATTCATTTAG
99358	97445	TTTATAGACTTATTCATTTA
99359	97446	ATTTATAGACTTATTCATTT
99360	97447	TATTTATAGACTTATTCATT
99361	97448	CTATTTATAGACTTATTCAT
99362	97449	ACTATTTATAGACTTATTCA
99363	97450	AACTATTTATAGACTTATTC
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99369	97456	GTTCTAAACTATTTATAGAC
99370	97457	TGTTCTAAACTATTTATAGA
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99372	97459	ACTGTTCTAAACTATTTATA
99373	97460	CACTGTTCTAAACTATTTAT
99374	97461	ACACTGTTCTAAACTATTTA
99375	97462	GACACTGTTCTAAACTATTT
99376	97463	AGACACTGTTCTAAACTATT
99377	97464	CAGACACTGTTCTAAACTAT
99378	97465	CCAGACACTGTTCTAAACTA
99379	97466	TCCAGACACTGTTCTAAACT
99380	97467	GTCCAGACACTGTTCTAAAC
99381	97468	TGTCCAGACACTGTTCTAAA
99382	97469	CTGTCCAGACACTGTTCTAA
99383	97470	CCTGTCCAGACACTGTTCTA
99384	97471	ACCTGTCCAGACACTGTTCT
99385	97472	TACCTGTCCAGACACTGTTC
99386	97473	GTACCTGTCCAGACACTGTT
99387	97474	TGTACCTGTCCAGACACTGT
99388	97475	CTGTACCTGTCCAGACACTG
99389	97476	ACTGTACCTGTCCAGACACT
99390	97477	CACTGTACCTGTCCAGACAC
99391	97478	CCACTGTACCTGTCCAGACA
99392	97479	GCCACTGTACCTGTCCAGAC
99393	97480	AGCCACTGTACCTGTCCAGA
99394	97481	GAGCCACTGTACCTGTCCAG
99395	97482	TGAGCCACTGTACCTGTCCA
99396	97483	ATGAGCCACTGTACCTGTCC
99397	97484	CATGAGCCACTGTACCTGTC
99398	97485	GCATGAGCCACTGTACCTGT
99399	97486	GGCATGAGCCACTGTACCTG
99400	97487	AGGCATGAGCCACTGTACCT
99401	97488	CAGGCATGAGCCACTGTACC
99402	97489	TCAGGCATGAGCCACTGTAC
99403	97490	TTCAGGCATGAGCCACTGTA
99404	97491	ATTCAGGCATGAGCCACTGT
99405	97492	GATTCAGGCATGAGCCACTG
99406	97493	AGATTCAGGCATGAGCCACT
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99408	97495	TAAGATTCAGGCATGAGCCA

148485	146572	AAAAAAAGGCCTTAACAAAC
148486	146573	GAAAAAAAGGCCTTAACAAA
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148488	146575	TAGAAAAAAAGGCCTTAACA
148489	146576	GTAGAAAAAAAGGCCTTAAC
148490	146577	GGTAGAAAAAAAGGCCTTAA
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148493	146580	TGGGGTAGAAAAAAAGGCCT
148494	146581	ATGGGGTAGAAAAAAAGGCC
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148496	146583	TCATGGGGTAGAAAAAAAGG
148497	146584	TTCATGGGGTAGAAAAAAAG
148498	146585	GTTCATGGGGTAGAAAAAAA
148499	146586	TGTTCATGGGGTAGAAAAAA
148500	146587	TTGTTCATGGGGTAGAAAAA
148501	146588	CTTGTTCATGGGGTAGAAAA
148502	146589	ACTTGTTCATGGGGTAGAAA
148503	146590	GACTTGTTCATGGGGTAGAA
148504	146591	AGACTTGTTCATGGGGTAGA
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148506	146593	GAAGACTTGTTCATGGGGTA
148507	146594	AGAAGACTTGTTCATGGGGT
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148509	146596	CCAGAAGACTTGTTCATGGG
148510	146597	CCCAGAAGACTTGTTCATGG
148511	146598	TCCCAGAAGACTTGTTCATG
148512	146599	CTCCCAGAAGACTTGTTCAT
148513	146600	ACTCCCAGAAGACTTGTTCA
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148515	146602	AAACTCCCAGAAGACTTGTT
148516	146603	AAAACTCCCAGAAGACTTGT
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148518	146605	ATAAAACTCCCAGAAGACTT
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148520	146607	AGATAAAACTCCCAGAAGAC
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148524	146611	CTTCAGATAAAACTCCCAGA
148525	146612	ACTTCAGATAAAACTCCCAG
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148527	146614	CCACTTCAGATAAAACTCCC
148528	146615	ACCACTTCAGATAAAACTCC
148529	146616	AACCACTTCAGATAAAACTC
148530	146617	AAACCACTTCAGATAAAACT
148531	146618	AAAACCACTTCAGATAAAAC
148532	146619	TAAAACCACTTCAGATAAAA
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148537	146624	AGACGTAAAACCACTTCAGA
148538	146625	CAGACGTAAAACCACTTCAG
148539	146626	TCAGACGTAAAACCACTTCA
148540	146627	GTCAGACGTAAAACCACTTC
148541	146628	AGTCAGACGTAAAACCACTT
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148543	146630	CCAGTCAGACGTAAAACCAC
148544	146631	ACCAGTCAGACGTAAAACCA
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148547	146634	CAAACCAGTCAGACGTAAAA
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148551	146638	GAAACAAACCAGTCAGACGT
148552	146639	AGAAACAAACCAGTCAGACG
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99428	97515	GTCTCAGCCTCCCAAAGTGC
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50404	48491	GCACACGCCTGTAGTCCCAG
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50406	48493	TGGCACACGCCTGTAGTCCC
50407	48494	GTGGCACACGCCTGTAGTCC
50408	48495	GGTGGCACACGCCTGTAGTC
50409	48496	TGGTGGCACACGCCTGTAGT
50410	48497	GTGGTGGCACACGCCTGTAG
50411	48498	TGTGGTGGCACACGCCTGTA
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50413	48500	GGTGTGGTGGCACACGCCTG
50414	48501	TGGTGTGGTGGCACACGCCT
50415	48502	TTGGTGTGGTGGCACACGCC
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50417	48504	GCTTGGTGTGGTGGCACACG
50418	48505	AGCTTGGTGTGGTGGCACAC
50419	48506	TAGCTTGGTGTGGTGGCACA
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50440	48527	CTCTACAAAAAATACAAAAA
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50442	48529	GTCTCTACAAAAAATACAAA
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50444	48531	CTGTCTCTACAAAAAATACA
50445	48532	CCTGTCTCTACAAAAAATAC
50446	48533	CCCTGTCTCTACAAAAAATA
50447	48534	ACCCTGTCTCTACAAAAAAT
50448	48535	AACCCTGTCTCTACAAAAAA
50449	48536	AAACCCTGTCTCTACAAAAA
50450	48537	GAAACCCTGTCTCTACAAAA
50451	48538	TGAAACCCTGTCTCTACAAA
50452	48539	GTGAAACCCTGTCTCTACAA
50453	48540	GGTGAAACCCTGTCTCTACA
50454	48541	TGGTGAAACCCTGTCTCTAC
50455	48542	ATGGTGAAACCCTGTCTCTA
50456	48543	CATGGTGAAACCCTGTCTCT
50457	48544	ACATGGTGAAACCCTGTCTC
50458	48545	AACATGGTGAAACCCTGTCT
50459	48546	CAACATGGTGAAACCCTGTC
50460	48547	CCAACATGGTGAAACCCTGT
50461	48548	GCCAACATGGTGAAACCCTG
50462	48549	GGCCAACATGGTGAAACCCT
50463	48550	TGGCCAACATGGTGAAACCC
50464	48551	CTGGCCAACATGGTGAAACC
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50466	48553	TCCTGGCCAACATGGTGAAA
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50473	48560	GAGACCATCCTGGCCAACAT
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99552	97639	TGAGTAGCTGGTACTATTAG
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99558	97645	GCCTCCTGAGTAGCTGGTAC
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99563	97650	CCTCAGCCTCCTGAGTAGCT
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99568	97655	TCCCACCTCAGCCTCCTGAG
99569	97656	CTCCCACCTCAGCCTCCTGA
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99571	97658	TTCTCCCACCTCAGCCTCCT
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99574	97661	TGATTCTCCCACCTCAGCCT
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99576	97663	AGTGATTCTCCCACCTCAGC
99577	97664	AAGTGATTCTCCCACCTCAG
99578	97665	CAAGTGATTCTCCCACCTCA
99579	97666	TCAAGTGATTCTCCCACCTC
99580	97667	CTCAAGTGATTCTCCCACCT
99581	97668	GCTCAAGTGATTCTCCCACC
99582	97669	GGCTCAAGTGATTCTCCCAC
99583	97670	AGGCTCAAGTGATTCTCCCA
99584	97671	CAGGCTCAAGTGATTCTCCC
99585	97672	CCAGGCTCAAGTGATTCTCC
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99587	97674	TCCCAGGCTCAAGTGATTCT
99588	97675	CTCCCAGGCTCAAGTGATTC
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99597	97684	AACCTCCATCTCCCAGGCTC
99598	97685	CAACCTCCATCTCCCAGGCT
99599	97686	GCAACCTCCATCTCCCAGGC
99600	97687	TGCAACCTCCATCTCCCAGG
99601	97688	CTGCAACCTCCATCTCCCAG
99602	97689	ACTGCAACCTCCATCTCCCA
99603	97690	CACTGCAACCTCCATCTCCC
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99605	97692	CTCACTGCAACCTCCATCTC
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99607	97694	ACCTCACTGCAACCTCCATC
99608	97695	CACCTCACTGCAACCTCCAT
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99611	97698	GCTCACCTCACTGCAACCTC
99612	97699	AGCTCACCTCACTGCAACCT
99613	97700	AAGCTCACCTCACTGCAACC
99614	97701	CAAGCTCACCTCACTGCAAC
99615	97702	GCAAGCTCACCTCACTGCAA
99616	97703	TGCAAGCTCACCTCACTGCA
99617	97704	GTGCAAGCTCACCTCACTGC
99618	97705	GGTGCAAGCTCACCTCACTG
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99620	97707	GTGGTGCAAGCTCACCTCAC
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148698	146785	GAAAACTGGCAACACCACAC
148699	146786	AGAAAACTGGCAACACCACA
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148701	146788	ACAGAAAACTGGCAACACCA
148702	146789	AACAGAAAACTGGCAACACC
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148711	146798	GAACATTGAAACAGAAAACT
148712	146799	CGAACATTGAAACAGAAAAC
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148716	146803	AAAGCGAACATTGAAACAGA
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148718	146805	GAAAAGCGAACATTGAAACA
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148720	146807	AAGAAAAGCGAACATTGAAA
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148722	146809	AAAAGAAAAGCGAACATTGA
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148746	146833	TGTTGGTGGTGGGCTTGTAC
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148749	146836	TGCTGTTGGTGGTGGGCTTG
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148766	146853	CAGGGCAGCCTTACAACTGC
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50475	48562	TCGAGACCATCCTGGCCAAC
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50478	48565	CAATCGAGACCATCCTGGCC
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50487	48574	GAGGTCAAACAATCGAGACC
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50541	48628	AGTGGCTCATGCCTGTAATT
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99622	97709	CAGTGGTGCAAGCTCACCTC
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99626	97713	AGCGCAGTGGTGCAAGCTCA
99627	97714	GAGCGCAGTGGTGCAAGCTC
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99629	97716	TGGAGCGCAGTGGTGCAAGC
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148769	146856	CTCCAGGGCAGCCTTACAAC
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148774	146861	GGTTCCTCCAGGGCAGCCTT
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148780	146867	CCTTTCGGTTCCTCCAGGGC
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148782	146869	GGCCTTTCGGTTCCTCCAGG
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148800	146887	GAAGGGAGGAGGGAATTTGG
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148824	146911	TGCTTCCAGTTGGTAGAAGC
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50546	48633	GGTGCAGTGGCTCATGCCTG
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50548	48635	TGGGTGCAGTGGCTCATGCC
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50567	48654	AAAGAATTTTAGAACCGGCT
50568	48655	AAAAGAATTTTAGAACCGGC
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50570	48657	ATAAAAGAATTTTAGAACCG
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50574	48661	ATAAATAAAAGAATTTTAGA
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50577	48664	CAAATAAATAAAAGAATTTT
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50582	48669	ATATACAAATAAATAAAAGA
50583	48670	CATATACAAATAAATAAAAG
50584	48671	GCATATACAAATAAATAAAA
50585	48672	GGCATATACAAATAAATAAA
50586	48673	TGGCATATACAAATAAATAA
50587	48674	TTGGCATATACAAATAAATA
50588	48675	TTTGGCATATACAAATAAAT
50589	48676	ATTTGGCATATACAAATAAA
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50611	48698	GAATTACGTATTTCACTACA
50612	48699	AGAATTACGTATTTCACTAC
50613	48700	CAGAATTACGTATTTCACTA
50614	48701	ACAGAATTACGTATTTCACT
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99696	97783	ATTTCTTACTATGGGTTGGA
99697	97784	CATTTCTTACTATGGGTTGG
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99703	97790	CATCTGCATTTCTTACTATG
99704	97791	ACATCTGCATTTCTTACTAT
99705	97792	CACATCTGCATTTCTTACTA
99706	97793	ACACATCTGCATTTCTTACT
99707	97794	AACACATCTGCATTTCTTAC
99708	97795	AAACACATCTGCATTTCTTA
99709	97796	CAAACACATCTGCATTTCTT
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99784	97871	CGGAGTTTAATTATCATAAG
99785	97872	TCGGAGTTTAATTATCATAA
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99831	97918	AGAGGCGATCCACATAACAG
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148942	147029	GCCTCTACTCGGTCCAAGTA
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148946	147033	AAATGCCTCTACTCGGTCCA
148947	147034	TAAATGCCTCTACTCGGTCC
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50699	48786	GTAGAAGAATCAGCCCAACA
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50737	48824	GAAAGAATCCTGGTATATTA
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50743	48830	CTAAGAGAAAGAATCCTGGT
50744	48831	TCTAAGAGAAAGAATCCTGG
50745	48832	GTCTAAGAGAAAGAATCCTG
50746	48833	AGTCTAAGAGAAAGAATCCT
50747	48834	AAGTCTAAGAGAAAGAATCC
50748	48835	TAAGTCTAAGAGAAAGAATC
50749	48836	CTAAGTCTAAGAGAAAGAAT
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50754	48841	GACTCCTAAGTCTAAGAGAA
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99837	97924	TTTAGTAGAGGCGATCCACA
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99839	97926	TCTTTAGTAGAGGCGATCCA
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99845	97932	CAAAAATCTTTAGTAGAGGC
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148986	147073	GAAACAGCATATGGAATTAT
148987	147074	TGAAACAGCATATGGAATTA
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149025	147112	CAGTTTCGGCAAGCAGAGCT
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100002	98089	CATTATGCAACTCTGGCGCA
100003	98090	GCATTATGCAACTCTGGCGC
100004	98091	AGCATTATGCAACTCTGGCG
100005	98092	CAGCATTATGCAACTCTGGC
100006	98093	ACAGCATTATGCAACTCTGG
100007	98094	AACAGCATTATGCAACTCTG
100008	98095	AAACAGCATTATGCAACTCT
100009	98096	CAAACAGCATTATGCAACTC
100010	98097	GCAAACAGCATTATGCAACT
100011	98098	GGCAAACAGCATTATGCAAC
100012	98099	TGGCAAACAGCATTATGCAA
100013	98100	ATGGCAAACAGCATTATGCA
100014	98101	CATGGCAAACAGCATTATGC
100015	98102	TCATGGCAAACAGCATTATG
100016	98103	GTCATGGCAAACAGCATTAT
100017	98104	TGTCATGGCAAACAGCATTA
100018	98105	GTGTCATGGCAAACAGCATT
100019	98106	GGTGTCATGGCAAACAGCAT
100020	98107	TGGTGTCATGGCAAACAGCA
100021	98108	TTGGTGTCATGGCAAACAGC
100022	98109	CTTGGTGTCATGGCAAACAG
100023	98110	TCTTGGTGTCATGGCAAACA
100024	98111	CTCTTGGTGTCATGGCAAAC
100025	98112	GCTCTTGGTGTCATGGCAAA
100026	98113	GGCTCTTGGTGTCATGGCAA
100027	98114	AGGCTCTTGGTGTCATGGCA
100028	98115	AAGGCTCTTGGTGTCATGGC
100029	98116	CAAGGCTCTTGGTGTCATGG
100030	98117	CCAAGGCTCTTGGTGTCATG
100031	98118	ACCAAGGCTCTTGGTGTCAT
100032	98119	TACCAAGGCTCTTGGTGTCA
100033	98120	TTACCAAGGCTCTTGGTGTC
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100036	98123	TCATTACCAAGGCTCTTGGT
100037	98124	TTCATTACCAAGGCTCTTGG
100038	98125	TTTCATTACCAAGGCTCTTG
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100043	98130	AATGGTTTCATTACCAAGGC
100044	98131	CAATGGTTTCATTACCAAGG
100045	98132	TCAATGGTTTCATTACCAAG
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100047	98134	TTTCAATGGTTTCATTACCA

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149125	147212	TTTTTTTAGCAGTAATAGC
149126	147213	TTTTTTTTAGCAGTAATAG
149127	147214	TTTTTTTTTAGCAGTAATA
149128	147215	TTTTTTTTTTAGCAGTAAT
149129	147216	TTTTTTTTTTTAGCAGTAA
149130	147217	TTTTTTTTTTTTAGCAGTA
149131	147218	TTTTTTTTTTTTTAGCAGT
149132	147219	TTTTTTTTTTTTTTAGCAG
149133	147220	TTTTTTTTTTTTTTTAGCA
149134	147221	TTTTTTTTTTTTTTTTAGC
149135	147222	TTTTTTTTTTTTTTTTTAG
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149141	147228	TGATTTTTTTTTTTTTTTT
149142	147229	TTGATTTTTTTTTTTTTTT
149143	147230	CTTGATTTTTTTTTTTTTT
149144	147231	TCTTGATTTTTTTTTTTTT
149145	147232	GTCTTGATTTTTTTTTTTT
149146	147233	AGTCTTGATTTTTTTTTTT
149147	147234	AAGTCTTGATTTTTTTTTT
149148	147235	CAAGTCTTGATTTTTTTTT
149149	147236	CCAAGTCTTGATTTTTTTT
149150	147237	TCCAAGTCTTGATTTTTTT
149151	147238	TTCCAAGTCTTGATTTTTT
149152	147239	GTTCCAAGTCTTGATTTTT
149153	147240	CGTTCCAAGTCTTGATTTT
149154	147241	GCGTTCCAAGTCTTGATTT
149155	147242	GGCGTTCCAAGTCTTGATT
149156	147243	GGGCGTTCCAAGTCTTGATT
149157	147244	AGGGCGTTCCAAGTCTTGAT
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149160	147247	AAAAGGGCGTTCCAAGTCTT
149161	147248	TAAAAGGGCGTTCCAAGTCT
149162	147249	GTAAAAGGGCGTTCCAAGTC
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149164	147251	TAGTAAAAGGGCGTTCCAAG
149165	147252	TTAGTAAAAGGGCGTTCCAA
149166	147253	TTTAGTAAAAGGGCGTTCCA
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149170	147257	CAAGTTTAGTAAAAGGGCGT
149171	147258	TCAAGTTTAGTAAAAGGGCG
149172	147259	GTCAAGTTTAGTAAAAGGGC
149173	147260	TGTCAAGTTTAGTAAAAGGG
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149175	147262	TTTGTCAAGTTTAGTAAAAG
149176	147263	CTTTGTCAAGTTTAGTAAAA
149177	147264	ACTTTGTCAAGTTTAGTAAA
149178	147265	AACTTTGTCAAGTTTAGTAA
149179	147266	AAACTTTGTCAAGTTTAGTA
149180	147267	GAAACTTTGTCAAGTTTAGT
149181	147268	TGAAACTTTGTCAAGTTTAG
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149185	147272	TTACTGAAACTTTGTCAAGT
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149187	147274	ATTTACTGAAACTTTGTCAA
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149191	147278	AAGAATTTACTGAAACTTTG
149192	147279	TAAGAATTTACTGAAACTTT
149193	147280	GTAAGAATTTACTGAAACTT
149194	147281	GGTAAGAATTTACTGAAACT

50901	48988	GAAGGCCTCTTAAGACAAAA
50902	48989	TGAAGGCCTCTTAAGACAAA
50903	48990	CTGAAGGCCTCTTAAGACAA
50904	48991	GCTGAAGGCCTCTTAAGACA
50905	48992	TGCTGAAGGCCTCTTAAGAC
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50910	48997	TGGGATGCTGAAGGCCTCTT
50911	48998	ATGGGATGCTGAAGGCCTCT
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50935	49022	CTAAAAAAAGACTTGTTTCC
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50939	49026	GCAGCTAAAAAAAGACTTGT
50940	49027	AGCAGCTAAAAAAAGACTTG
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50945	49032	AAGGTAGCAGCTAAAAAAAG
50946	49033	AAAGGTAGCAGCTAAAAAAA
50947	49034	CAAAGGTAGCAGCTAAAAAA
50948	49035	CCAAAGGTAGCAGCTAAAAA
50949	49036	TCCAAAGGTAGCAGCTAAAA
50950	49037	CTCCAAAGGTAGCAGCTAAA
50951	49038	ACTCCAAAGGTAGCAGCTAA
50952	49039	AACTCCAAAGGTAGCAGCTA
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50954	49041	TCAACTCCAAAGGTAGCAGC
50955	49042	ATCAACTCCAAAGGTAGCAG
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50962	49049	AAACAAAATCAACTCCAAAG
50963	49050	TAAACAAAATCAACTCCAAA
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50965	49052	CATAAACAAAATCAACTCCA
50966	49053	ACATAAACAAAATCAACTCC
50967	49054	GACATAAACAAAATCAACTC
50968	49055	AGACATAAACAAAATCAACT
50969	49056	TAGACATAAACAAAATCAAC
50970	49057	CTAGACATAAACAAAATCAA
50971	49058	CCTAGACATAAACAAAATCA

100048	98135	ATTTCAATGGTTTCATTACC
100049	98136	AATTTCAATGGTTTCATTAC
100050	98137	CAATTTCAATGGTTTCATTA
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100053	98140	AACCAATTTCAATGGTTTCA
100054	98141	AAACCAATTTCAATGGTTTC
100055	98142	CAAACCAATTTCAATGGTTT
100056	98143	GCAAACCAATTTCAATGGTT
100057	98144	GGCAAACCAATTTCAATGGT
100058	98145	AGGCAAACCAATTTCAATGG
100059	98146	TAGGCAAACCAATTTCAATG
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100061	98148	TATAGGCAAACCAATTTCAA
100062	98149	GTATAGGCAAACCAATTTCA
100063	98150	AGTATAGGCAAACCAATTTC
100064	98151	CAGTATAGGCAAACCAATTT
100065	98152	TCAGTATAGGCAAACCAATT
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100067	98154	CCTCAGTATAGGCAAACCAA
100068	98155	GCCTCAGTATAGGCAAACCA
100069	98156	AGCCTCAGTATAGGCAAACC
100070	98157	CAGCCTCAGTATAGGCAAAC
100071	98158	TCAGCCTCAGTATAGGCAAA
100072	98159	TTCAGCCTCAGTATAGGCAA
100073	98160	CTTCAGCCTCAGTATAGGCA
100074	98161	TCTTCAGCCTCAGTATAGGC
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100076	98163	CCTCTTCAGCCTCAGTATAG
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100083	98170	CAAGATACCTCTTCAGCCTC
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100096	98183	AAAATTAGAGAGCCAAGATA
100097	98184	TAAAATTAGAGAGCCAAGAT
100098	98185	TTAAAATTAGAGAGCCAAGA
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100101	98188	GCCTTAAAATTAGAGAGCCA
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100105	98192	GGTTGCCTTAAAATTAGAGA
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100114	98201	AGCCAAAAAGGTTGCCTTAA
100115	98202	CAGCCAAAAAGGTTGCCTTA
100116	98203	ACAGCCAAAAAGGTTGCCTT
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149195	147282	CGGTAAGAATTTACTGAAAC
149196	147283	ACGGTAAGAATTTACTGAAA
149197	147284	GACGGTAAGAATTTACTGAA
149198	147285	TGACGGTAAGAATTTACTGA
149199	147286	TTGACGGTAAGAATTTACTG
149200	147287	TTTGACGGTAAGAATTTACT
149201	147288	GTTTGACGGTAAGAATTTAC
149202	147289	AGTTTGACGGTAAGAATTTA
149203	147290	CAGTTTGACGGTAAGAATTT
149204	147291	TCAGTTTGACGGTAAGAATT
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149206	147293	CGTCAGTTTGACGGTAAGAA
149207	147294	CCGTCAGTTTGACGGTAAGA
149208	147295	TCCGTCAGTTTGACGGTAAG
149209	147296	ATCCGTCAGTTTGACGGTAA
149210	147297	AATCCGTCAGTTTGACGGTA
149211	147298	TAATCCGTCAGTTTGACGGT
149212	147299	ATAATCCGTCAGTTTGACGG
149213	147300	AATAATCCGTCAGTTTGACG
149214	147301	TAATAATCCGTCAGTTTGAC
149215	147302	ATAATAATCCGTCAGTTTGA
149216	147303	AATAATAATCCGTCAGTTTG
149217	147304	AAATAATAATCCGTCAGTTT
149218	147305	TAAATAATAATCCGTCAGTT
149219	147306	ATAAATAATAATCCGTCAGT
149220	147307	TATAAATAATAATCCGTCAG
149221	147308	TTATAAATAATAATCCGTCA
149222	147309	TTTATAAATAATAATCCGTC
149223	147310	ATTTATAAATAATAATCCGT
149224	147311	GATTTATAAATAATAATCCG
149225	147312	TGATTTATAAATAATAATCC
149226	147313	TTGATTTATAAATAATAATC
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149231	147318	CAAACTTGATTTATAAATAA
149232	147319	TCAAACTTGATTTATAAATA
149233	147320	ATCAAACTTGATTTATAAAT
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149235	147322	TCATCAAACTTGATTTATAA
149236	147323	CTCATCAAACTTGATTTATA
149237	147324	CCTCATCAAACTTGATTTAT
149238	147325	ACCTCATCAAACTTGATTTA
149239	147326	CACCTCATCAAACTTGATTT
149240	147327	TCACCTCATCAAACTTGATT
149241	147328	ATCACCTCATCAAACTTGAT
149242	147329	GATCACCTCATCAAACTTGA
149243	147330	TGATCACCTCATCAAACTTG
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149245	147332	AGTGATCACCTCATCAAACT
149246	147333	CAGTGATCACCTCATCAAAC
149247	147334	ACAGTGATCACCTCATCAAA
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149249	147336	AGACAGTGATCACCTCATCA
149250	147337	TAGACAGTGATCACCTCATC
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149252	147339	TGTAGACAGTGATCACCTCA
149253	147340	CTGTAGACAGTGATCACCTC
149254	147341	ACTGTAGACAGTGATCACCT
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149257	147344	ACCACTGTAGACAGTGATCA
149258	147345	AACCACTGTAGACAGTGATC
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149260	147347	TGAACCACTGTAGACAGTGA
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50972	49059	TCCTAGACATAAACAAAATC
50973	49060	CTCCTAGACATAAACAAAAT
50974	49061	GCTCCTAGACATAAACAAAA
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50979	49066	TTAGTGCTCCTAGACATAAA
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51018	49105	ATAACAGAGGAATATTTCAA
51019	49106	TATAACAGAGGAATATTTCA
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51032	49119	CAATTTTTGAATTTATAACA
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51034	49121	GTCAATTTTTGAATTTATAA
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51039	49126	CCAAAGTCAATTTTTGAATT
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100119	98206	TACACAGCCAAAAAGGTTGC
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100121	98208	CCTACACAGCCAAAAAGGTT
100122	98209	ACCTACACAGCCAAAAAGGT
100123	98210	AACCTACACAGCCAAAAAGG
100124	98211	AAACCTACACAGCCAAAAAG
100125	98212	GAAACCTACACAGCCAAAAA
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100127	98214	GAGAAACCTACACAGCCAAA
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100129	98216	AAGAGAAACCTACACAGCCA
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100131	98218	TAAAGAGAAACCTACACAGC
100132	98219	CTAAAGAGAAACCTACACAG
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100136	98223	CAAGCTAAAGAGAAACCTAC
100137	98224	ACAAGCTAAAGAGAAACCTA
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100139	98226	AAACAAGCTAAAGAGAAACC
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100143	98230	TGAGAAACAAGCTAAAGAGA
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100145	98232	GGTGAGAAACAAGCTAAAGA
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100149	98236	AGGTGGTGAGAAACAAGCTA
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100153	98240	CCCCAGGTGGTGAGAAACAA
100154	98241	GCCCCAGGTGGTGAGAAACA
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100156	98243	CAGCCCCAGGTGGTGAGAAA
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100158	98245	CACAGCCCCAGGTGGTGAGA
100159	98246	CCACAGCCCCAGGTGGTGAG
100160	98247	GCCACAGCCCCAGGTGGTGA
100161	98248	AGCCACAGCCCCAGGTGGTG
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100186	98273	GCCACAGGTTAGGACAACGG
100187	98274	AGCCACAGGTTAGGACAACG
100188	98275	AAGCCACAGGTTAGGACAAC
100189	98276	TAAGCCACAGGTTAGGACAA

149266	147353	AAAAGTTGAACCACTGTAGA
149267	147354	TAAAAGTTGAACCACTGTAG
149268	147355	TTAAAAGTTGAACCACTGTA
149269	147356	CTTAAAAGTTGAACCACTGT
149270	147357	ACTTAAAAGTTGAACCACTG
149271	147358	AACTTAAAAGTTGAACCACT
149272	147359	TAACTTAAAAGTTGAACCAC
149273	147360	TTAACTTAAAAGTTGAACCA
149274	147361	CTTAACTTAAAAGTTGAACC
149275	147362	CCTTAACTTAAAAGTTGAAC
149276	147363	CCCTTAACTTAAAAGTTGAA
149277	147364	TCCCTTAACTTAAAAGTTGA
149278	147365	TTCCCTTAACTTAAAAGTTG
149279	147366	TTTCCCTTAACTTAAAAGTT
149280	147367	TTTTCCCTTAACTTAAAAGT
149281	147368	TTTTTCCCTTAACTTAAAAG
149282	147369	GTTTTTCCCTTAACTTAAAA
149283	147370	AGTTTTTCCCTTAACTTAAA
149284	147371	AAGTTTTTCCCTTAACTTAA
149285	147372	AAAGTTTTTCCCTTAACTTA
149286	147373	AAAAGTTTTTCCCTTAACTT
149287	147374	TAAAAGTTTTTCCCTTAACT
149288	147375	GTAAAAGTTTTTCCCTTAAC
149289	147376	AGTAAAAGTTTTTCCCTTAA
149290	147377	AAGTAAAAGTTTTTCCCTTA
149291	147378	AAAGTAAAAGTTTTTCCCTT
149292	147379	CAAAGTAAAAGTTTTTCCCT
149293	147380	ACAAAGTAAAAGTTTTTCCC
149294	147381	TACAAAGTAAAAGTTTTTCC
149295	147382	CTACAAAGTAAAAGTTTTTC
149296	147383	TCTACAAAGTAAAAGTTTTT
149297	147384	ATCTACAAAGTAAAAGTTTT
149298	147385	TATCTACAAAGTAAAAGTTT
149299	147386	TTATCTACAAAGTAAAAGTT
149300	147387	ATTATCTACAAAGTAAAAGT
149301	147388	TATTATCTACAAAGTAAAAG
149302	147389	ATATTATCTACAAAGTAAAA
149303	147390	TATATTATCTACAAAGTAAA
149304	147391	TTATATTATCTACAAAGTAA
149305	147392	TTTATATTATCTACAAAGTA
149306	147393	TTTTATATTATCTACAAAGT
149307	147394	ATTTTATATTATCTACAAAG
149308	147395	TATTTTATATTATCTACAAA
149309	147396	TTATTTTATATTATCTACAA
149310	147397	TTTATTTTATATTATCTACA
149311	147398	TTTTATTTTATATTATCTAC
149312	147399	TTTTTATTTTATATTATCTA
149313	147400	GTTTTTATTTTATATTATCT
149314	147401	AGTTTTTATTTTATATTATC
149315	147402	AAGTTTTTATTTTATATTAT
149316	147403	TAAGTTTTTATTTTATATTA
149317	147404	TTAAGTTTTTATTTTATATT
149318	147405	TTTAAGTTTTTATTTTATAT
149319	147406	TTTTAAGTTTTTATTTTATA
149320	147407	TTTTTAAGTTTTTATTTTAT
149321	147408	TTTTTTAAGTTTTTATTTTA
149322	147409	TTTTTTTAAGTTTTTATTTT
149323	147410	TTTTTTTTAAGTTTTTATTT
149324	147411	ATTTTTTTTAAGTTTTTATT
149325	147412	AATTTTTTTTAAGTTTTTAT
149326	147413	AAATTTTTTTTAAGTTTTTA
149327	147414	TAAATTTTTTTTAAGTTTTT
149328	147415	TTAAATTTTTTTTAAGTTTT
149329	147416	TTTAAATTTTTTTTAAGTTT
149330	147417	TTTTAAATTTTTTTTAAGTT
149331	147418	TTTTTAAATTTTTTTTAAGT
149332	147419	TTTTTTAAATTTTTTTTAAG
149333	147420	ATTTTTTAAATTTTTTTTAA
149334	147421	TATTTTTTAAATTTTTTTTA
149335	147422	TTATTTTTTAAATTTTTTTT
149336	147423	TTTATTTTTTAAATTTTTTT

51043	49130	TCTTCCAAAGTCAATTTTTG
51044	49131	ATCTTCCAAAGTCAATTTTT
51045	49132	TATCTTCCAAAGTCAATTTT
51046	49133	TTATCTTCCAAAGTCAATTT
51047	49134	TTTATCTTCCAAAGTCAATT
51048	49135	TTTTATCTTCCAAAGTCAAT
51049	49136	ATTTTATCTTCCAAAGTCAA
51050	49137	AATTTTATCTTCCAAAGTCA
51051	49138	AAATTTTATCTTCCAAAGTC
51052	49139	AAAATTTTATCTTCCAAAGT
51053	49140	TAAAATTTTATCTTCCAAAG
51054	49141	CTAAAATTTTATCTTCCAAA
51055	49142	ACTAAAATTTTATCTTCCAA
51056	49143	AACTAAAATTTTATCTTCCA
51057	49144	CAACTAAAATTTTATCTTCC
51058	49145	TCAACTAAAATTTTATCTTC
51059	49146	TTCAACTAAAATTTTATCTT
51060	49147	ATTCAACTAAAATTTTATCT

100190	98277	CTAAGCCACAGGTTAGGACA
100191	98278	CCTAAGCCACAGGTTAGGAC
100192	98279	ACCTAAGCCACAGGTTAGGA
100193	98280	AACCTAAGCCACAGGTTAGG
100194	98281	GAACCTAAGCCACAGGTTAG
100195	98282	AGAACCTAAGCCACAGGTTA
100196	98283	CAGAACCTAAGCCACAGGTT
100197	98284	ACAGAACCTAAGCCACAGGT
100198	98285	AACAGAACCTAAGCCACAGG
100199	98286	AAACAGAACCTAAGCCACAG
100200	98287	AAAACAGAACCTAAGCCACA
100201	98288	AAAAACAGAACCTAAGCCAC
100202	98289	CAAAAACAGAACCTAAGCCA
100203	98290	ACAAAAACAGAACCTAAGCC
100204	98291	AACAAAAACAGAACCTAAGC
100205	98292	CAACAAAAACAGAACCTAAG
100206	98293	GCAACAAAAACAGAACCTAA
100207	98294	AGCAACAAAAACAGAACCTA

149337	147424	TTTTATTTTTTAAATTTTTT
149338	147425	TTTTTATTTTTTAAATTTTT
149339	147426	TTTTTTATTTTTTAAATTTT
149340	147427	TTTTTTTATTTTTTAAATTT
149341	147428	CTTTTTTTATTTTTTAAATT
149342	147429	ACTTTTTTTATTTTTTAAAT
149343	147430	AACTTTTTTTATTTTTTAAA
149344	147431	AAACTTTTTTTATTTTTTAA
149345	147432	AAAACTTTTTTTATTTTTTA
149346	147433	TAAAACTTTTTTTATTTTTT
149347	147434	TTAAAACTTTTTTTATTTTT
149348	147435	TTTAAAACTTTTTTTATTTT
149349	147436	TTTTAAAACTTTTTTTATTT
149350	147437	TTTTTAAAACTTTTTTTATT
149351	147438	GTTTTTAAAACTTTTTTTAT
149352	147439	AGTTTTTAAAACTTTTTTTA
149353	147440	CAGTTTTTAAAACTTTTTTT
149354	147441	TCAGTTTTTAAAACTTTTTT

Table 1C: Example SOD1 AON sequences and Corresponding Target Sequences

SEQ ID NO:	OligoStart	ASOSequence 5' to 3'	SEQ ID NO:	TargetSequence
149362	1	GCTGCAGGAGACTACGACGC	158582	GCGTCGTAGTCTCCTGCAGC
149363	2	CGCTGCAGGAGACTACGACG	158583	CGTCGTAGTCTCCTGCAGCG
149364	3	ACGCTGCAGGAGACTACGAC	158584	GTCGTAGTCTCCTGCAGCGT
149365	4	GACGCTGCAGGAGACTACGA	158585	TCGTAGTCTCCTGCAGCGTC
149366	5	AGACGCTGCAGGAGACTACG	158586	CGTAGTCTCCTGCAGCGTCT
149367	6	CAGACGCTGCAGGAGACTAC	158587	GTAGTCTCCTGCAGCGTCTG
149368	7	CCAGACGCTGCAGGAGACTA	158588	TAGTCTCCTGCAGCGTCTGG
149369	8	CCCAGACGCTGCAGGAGACT	158589	AGTCTCCTGCAGCGTCTGGG
149370	9	CCCCAGACGCTGCAGGAGAC	158590	GTCTCCTGCAGCGTCTGGGG
149371	10	ACCCCAGACGCTGCAGGAGA	158591	TCTCCTGCAGCGTCTGGGGT
149372	11	AACCCCAGACGCTGCAGGAG	158592	CTCCTGCAGCGTCTGGGGTT
149373	12	AAACCCCAGACGCTGCAGGA	158593	TCCTGCAGCGTCTGGGGTTT
149374	13	GAAACCCCAGACGCTGCAGG	158594	CCTGCAGCGTCTGGGGTTTC
149375	14	GGAAACCCCAGACGCTGCAG	158595	CTGCAGCGTCTGGGGTTTCC
149376	15	CGGAAACCCCAGACGCTGCA	158596	TGCAGCGTCTGGGGTTTCCG
149377	16	ACGGAAACCCCAGACGCTGC	158597	GCAGCGTCTGGGGTTTCCGT
149378	17	AACGGAAACCCCAGACGCTG	158598	CAGCGTCTGGGGTTTCCGTT
149379	18	CAACGGAAACCCCAGACGCT	158599	AGCGTCTGGGGTTTCCGTTG
149380	19	GCAACGGAAACCCCAGACGC	158600	GCGTCTGGGGTTTCCGTTGC
149381	20	TGCAACGGAAACCCCAGACG	158601	CGTCTGGGGTTTCCGTTGCA
149382	21	CTGCAACGGAAACCCCAGAC	158602	GTCTGGGGTTTCCGTTGCAG
149383	22	ACTGCAACGGAAACCCCAGA	158603	TCTGGGGTTTCCGTTGCAGT
149384	23	GACTGCAACGGAAACCCCAG	158604	CTGGGGTTTCCGTTGCAGTC
149385	24	GGACTGCAACGGAAACCCCA	158605	TGGGGTTTCCGTTGCAGTCC
149386	25	AGGACTGCAACGGAAACCCC	158606	GGGGTTTCCGTTGCAGTCCT
149387	26	GAGGACTGCAACGGAAACCC	158607	GGGTTTCCGTTGCAGTCCTC
149388	27	CGAGGACTGCAACGGAAACC	158608	GGTTTCCGTTGCAGTCCTCG
149389	28	CCGAGGACTGCAACGGAAAC	158609	GTTTCCGTTGCAGTCCTCGG
149390	29	TCCGAGGACTGCAACGGAAA	158610	TTTCCGTTGCAGTCCTCGGA
149391	30	TTCCGAGGACTGCAACGGAA	158611	TTCCGTTGCAGTCCTCGGAA
149392	31	GTTCCGAGGACTGCAACGGA	158612	TCCGTTGCAGTCCTCGGAAC
149393	32	GGTTCCGAGGACTGCAACGG	158613	CCGTTGCAGTCCTCGGAACC
149394	33	TGGTTCCGAGGACTGCAACG	158614	CGTTGCAGTCCTCGGAACCA
149395	34	CTGGTTCCGAGGACTGCAAC	158615	GTTGCAGTCCTCGGAACCAG
149396	35	CCTGGTTCCGAGGACTGCAA	158616	TTGCAGTCCTCGGAACCAGG
149397	36	TCCTGGTTCCGAGGACTGCA	158617	TGCAGTCCTCGGAACCAGGA
149398	37	GTCCTGGTTCCGAGGACTGC	158618	GCAGTCCTCGGAACCAGGAC
149399	38	GGTCCTGGTTCCGAGGACTG	158619	CAGTCCTCGGAACCAGGACC
149400	39	AGGTCCTGGTTCCGAGGACT	158620	AGTCCTCGGAACCAGGACCT
149401	40	GAGGTCCTGGTTCCGAGGAC	158621	GTCCTCGGAACCAGGACCTC
149402	41	CGAGGTCCTGGTTCCGAGGA	158622	TCCTCGGAACCAGGACCTCG
149403	42	CCGAGGTCCTGGTTCCGAGG	158623	CCTCGGAACCAGGACCTCGG
149404	43	GCCGAGGTCCTGGTTCCGAG	158624	CTCGGAACCAGGACCTCGGC
149405	44	CGCCGAGGTCCTGGTTCCGA	158625	TCGGAACCAGGACCTCGGCG
149406	45	ACGCCGAGGTCCTGGTTCCG	158626	CGGAACCAGGACCTCGGCGT
149407	46	CACGCCGAGGTCCTGGTTCC	158627	GGAACCAGGACCTCGGCGTG
149408	47	CCACGCCGAGGTCCTGGTTC	158628	GAACCAGGACCTCGGCGTGG
149409	48	GCCACGCCGAGGTCCTGGTT	158629	AACCAGGACCTCGGCGTGGC
149410	49	GGCCACGCCGAGGTCCTGGT	158630	ACCAGGACCTCGGCGTGGCC
149411	50	AGGCCACGCCGAGGTCCTGG	158631	CCAGGACCTCGGCGTGGCCT
149412	51	TAGGCCACGCCGAGGTCCTG	158632	CAGGACCTCGGCGTGGCCTA
149413	52	CTAGGCCACGCCGAGGTCCT	158633	AGGACCTCGGCGTGGCCTAG
149414	53	GCTAGGCCACGCCGAGGTCC	158634	GGACCTCGGCGTGGCCTAGC
149415	54	CGCTAGGCCACGCCGAGGTC	158635	GACCTCGGCGTGGCCTAGCG
149416	55	TCGCTAGGCCACGCCGAGGT	158636	ACCTCGGCGTGGCCTAGCGA
149417	56	CTCGCTAGGCCACGCCGAGG	158637	CCTCGGCGTGGCCTAGCGAG
149418	57	ACTCGCTAGGCCACGCCGAG	158638	CTCGGCGTGGCCTAGCGAGT
149419	58	AACTCGCTAGGCCACGCCGA	158639	TCGGCGTGGCCTAGCGAGTT
149420	59	TAACTCGCTAGGCCACGCCG	158640	CGGCGTGGCCTAGCGAGTTA
149421	60	ATAACTCGCTAGGCCACGCC	158641	GGCGTGGCCTAGCGAGTTAT
149422	61	CATAACTCGCTAGGCCACGC	158642	GCGTGGCCTAGCGAGTTATG
149423	62	CCATAACTCGCTAGGCCACG	158643	CGTGGCCTAGCGAGTTATGG
149424	63	GCCATAACTCGCTAGGCCAC	158644	GTGGCCTAGCGAGTTATGGC
149425	64	CGCCATAACTCGCTAGGCCA	158645	TGGCCTAGCGAGTTATGGCG
149426	65	TCGCCATAACTCGCTAGGCC	158646	GGCCTAGCGAGTTATGGCGA
149427	66	GTCGCCATAACTCGCTAGGC	158647	GCCTAGCGAGTTATGGCGAC
149428	67	CGTCGCCATAACTCGCTAGG	158648	CCTAGCGAGTTATGGCGACG
149429	68	TCGTCGCCATAACTCGCTAG	158649	CTAGCGAGTTATGGCGACGA
149430	69	TTCGTCGCCATAACTCGCTA	158650	TAGCGAGTTATGGCGACGAA
149431	70	CTTCGTCGCCATAACTCGCT	158651	AGCGAGTTATGGCGACGAAG

149432	71	CCTTCGTCGCCATAACTCGC	158652	GCGAGTTATGGCGACGAAGG
149433	72	GCCTTCGTCGCCATAACTCG	158653	CGAGTTATGGCGACGAAGGC
149434	73	GGCCTTCGTCGCCATAACTC	158654	GAGTTATGGCGACGAAGGCC
149435	74	CGGCCTTCGTCGCCATAACT	158655	AGTTATGGCGACGAAGGCCG
149436	75	ACGGCCTTCGTCGCCATAAC	158656	GTTATGGCGACGAAGGCCGT
149437	76	CACGGCCTTCGTCGCCATAA	158657	TTATGGCGACGAAGGCCGTG
149438	77	ACACGGCCTTCGTCGCCATA	158658	TATGGCGACGAAGGCCGTGT
149439	78	CACACGGCCTTCGTCGCCAT	158659	ATGGCGACGAAGGCCGTGTG
149440	79	GCACACGGCCTTCGTCGCCA	158660	TGGCGACGAAGGCCGTGTGC
149441	80	CGCACACGGCCTTCGTCGCC	158661	GGCGACGAAGGCCGTGTGCG
149442	81	ACGCACACGGCCTTCGTCGC	158662	GCGACGAAGGCCGTGTGCGT
149443	82	CACGCACACGGCCTTCGTCG	158663	CGACGAAGGCCGTGTGCGTG
149444	83	GCACGCACACGGCCTTCGTC	158664	GACGAAGGCCGTGTGCGTGC
149445	84	AGCACGCACACGGCCTTCGT	158665	ACGAAGGCCGTGTGCGTGCT
149446	85	CAGCACGCACACGGCCTTCG	158666	CGAAGGCCGTGTGCGTGCTG
149447	86	TCAGCACGCACACGGCCTTC	158667	GAAGGCCGTGTGCGTGCTGA
149448	87	TTCAGCACGCACACGGCCTT	158668	AAGGCCGTGTGCGTGCTGAA
149449	88	CTTCAGCACGCACACGGCCT	158669	AGGCCGTGTGCGTGCTGAAG
149450	89	CCTTCAGCACGCACACGGCC	158670	GGCCGTGTGCGTGCTGAAGG
149451	90	CCCTTCAGCACGCACACGGC	158671	GCCGTGTGCGTGCTGAAGGG
149452	91	GCCCTTCAGCACGCACACGG	158672	CCGTGTGCGTGCTGAAGGGC
149453	92	CGCCCTTCAGCACGCACACG	158673	CGTGTGCGTGCTGAAGGGCG
149454	93	TCGCCCTTCAGCACGCACAC	158674	GTGTGCGTGCTGAAGGGCGA
149455	94	GTCGCCCTTCAGCACGCACA	158675	TGTGCGTGCTGAAGGGCGAC
149456	95	CGTCGCCCTTCAGCACGCAC	158676	GTGCGTGCTGAAGGGCGACG
149457	96	CCGTCGCCCTTCAGCACGCA	158677	TGCGTGCTGAAGGGCGACGG
149458	97	GCCGTCGCCCTTCAGCACGC	158678	GCGTGCTGAAGGGCGACGGC
149459	98	GGCCGTCGCCCTTCAGCACG	158679	CGTGCTGAAGGGCGACGGCC
149460	99	GGGCCGTCGCCCTTCAGCAC	158680	GTGCTGAAGGGCGACGGCCC
149461	100	TGGGCCGTCGCCCTTCAGCA	158681	TGCTGAAGGGCGACGGCCCA
149462	101	CTGGGCCGTCGCCCTTCAGC	158682	GCTGAAGGGCGACGGCCCAG
149463	102	ACTGGGCCGTCGCCCTTCAG	158683	CTGAAGGGCGACGGCCCAGT
149464	103	CACTGGGCCGTCGCCCTTCA	158684	TGAAGGGCGACGGCCCAGTG
149465	104	GCACTGGGCCGTCGCCCTTC	158685	GAAGGGCGACGGCCCAGTGC
149466	105	TGCACTGGGCCGTCGCCCTT	158686	AAGGGCGACGGCCCAGTGCA
149467	106	CTGCACTGGGCCGTCGCCCT	158687	AGGGCGACGGCCCAGTGCAG
149468	107	CCTGCACTGGGCCGTCGCCC	158688	GGGCGACGGCCCAGTGCAGG
149469	108	CCCTGCACTGGGCCGTCGCC	158689	GGCGACGGCCCAGTGCAGGG
149470	109	GCCCTGCACTGGGCCGTCGC	158690	GCGACGGCCCAGTGCAGGGC
149471	110	TGCCCTGCACTGGGCCGTCG	158691	CGACGGCCCAGTGCAGGGCA
149472	111	ATGCCCTGCACTGGGCCGTC	158692	GACGGCCCAGTGCAGGGCAT
149473	112	GATGCCCTGCACTGGGCCGT	158693	ACGGCCCAGTGCAGGGCATC
149474	113	TGATGCCCTGCACTGGGCCG	158694	CGGCCCAGTGCAGGGCATCA
149475	114	ATGATGCCCTGCACTGGGCC	158695	GGCCCAGTGCAGGGCATCAT
149476	115	GATGATGCCCTGCACTGGGC	158696	GCCCAGTGCAGGGCATCATC
149477	116	TGATGATGCCCTGCACTGGG	158697	CCCAGTGCAGGGCATCATCA
149478	117	TTGATGATGCCCTGCACTGG	158698	CCAGTGCAGGGCATCATCAA
149479	118	ATTGATGATGCCCTGCACTG	158699	CAGTGCAGGGCATCATCAAT
149480	119	AATTGATGATGCCCTGCACT	158700	AGTGCAGGGCATCATCAATT
149481	120	AAATTGATGATGCCCTGCAC	158701	GTGCAGGGCATCATCAATTT
149482	121	GAAATTGATGATGCCCTGCA	158702	TGCAGGGCATCATCAATTTC
149483	122	CGAAATTGATGATGCCCTGC	158703	GCAGGGCATCATCAATTTCG
149484	123	TCGAAATTGATGATGCCCTG	158704	CAGGGCATCATCAATTTCGA
149485	124	CTCGAAATTGATGATGCCCT	158705	AGGGCATCATCAATTTCGAG
149486	125	GCTCGAAATTGATGATGCCC	158706	GGGCATCATCAATTTCGAGC
149487	126	TGCTCGAAATTGATGATGCC	158707	GGCATCATCAATTTCGAGCA
149488	127	CTGCTCGAAATTGATGATGC	158708	GCATCATCAATTTCGAGCAG
149489	128	TCTGCTCGAAATTGATGATG	158709	CATCATCAATTTCGAGCAGA
149490	129	TTCTGCTCGAAATTGATGAT	158710	ATCATCAATTTCGAGCAGAA
149491	130	CTTCTGCTCGAAATTGATGA	158711	TCATCAATTTCGAGCAGAAG
149492	131	CCTTCTGCTCGAAATTGATG	158712	CATCAATTTCGAGCAGAAGG
149493	132	GCCTTCTGCTCGAAATTGAT	158713	ATCAATTTCGAGCAGAAGGC
149494	133	TGCCTTCTGCTCGAAATTGA	158714	TCAATTTCGAGCAGAAGGCA
149495	134	TTGCCTTCTGCTCGAAATTG	158715	CAATTTCGAGCAGAAGGCAA
149496	135	CTTGCCTTCTGCTCGAAATT	158716	AATTTCGAGCAGAAGGCAAG
149497	136	CCTTGCCTTCTGCTCGAAAT	158717	ATTTCGAGCAGAAGGCAAGG
149498	137	CCCTTGCCTTCTGCTCGAAA	158718	TTTCGAGCAGAAGGCAAGGG
149499	138	GCCCTTGCCTTCTGCTCGAA	158719	TTCGAGCAGAAGGCAAGGGC
149500	139	AGCCCTTGCCTTCTGCTCGA	158720	TCGAGCAGAAGGCAAGGGCT
149501	140	CAGCCCTTGCCTTCTGCTCG	158721	CGAGCAGAAGGCAAGGGCTG
149502	141	CCAGCCCTTGCCTTCTGCTC	158722	GAGCAGAAGGCAAGGGCTGG
149503	142	CCCAGCCCTTGCCTTCTGCT	158723	AGCAGAAGGCAAGGGCTGGG

149504	143	TCCCAGCCCTTGCCTTCTGC	158724	GCAGAAGGCAAGGGCTGGGA
149505	144	GTCCCAGCCCTTGCCTTCTG	158725	CAGAAGGCAAGGGCTGGGAC
149506	145	CGTCCCAGCCCTTGCCTTCT	158726	AGAAGGCAAGGGCTGGGACG
149507	146	CCGTCCCAGCCCTTGCCTTC	158727	GAAGGCAAGGGCTGGGACGG
149508	147	TCCGTCCCAGCCCTTGCCTT	158728	AAGGCAAGGGCTGGGACGGA
149509	148	CTCCGTCCCAGCCCTTGCCT	158729	AGGCAAGGGCTGGGACGGAG
149510	149	CCTCCGTCCCAGCCCTTGCC	158730	GGCAAGGGCTGGGACGGAGG
149511	150	GCCTCCGTCCCAGCCCTTGC	158731	GCAAGGGCTGGGACGGAGGC
149512	151	AGCCTCCGTCCCAGCCCTTG	158732	CAAGGGCTGGGACGGAGGCT
149513	152	AAGCCTCCGTCCCAGCCCTT	158733	AAGGGCTGGGACGGAGGCTT
149514	153	CAAGCCTCCGTCCCAGCCCT	158734	AGGGCTGGGACGGAGGCTTG
149515	154	ACAAGCCTCCGTCCCAGCCC	158735	GGGCTGGGACGGAGGCTTGT
149516	155	AACAAGCCTCCGTCCCAGCC	158736	GGCTGGGACGGAGGCTTGTT
149517	156	AAACAAGCCTCCGTCCCAGC	158737	GCTGGGACGGAGGCTTGTTT
149518	157	CAAACAAGCCTCCGTCCCAG	158738	CTGGGACGGAGGCTTGTTTG
149519	158	GCAAACAAGCCTCCGTCCCA	158739	TGGGACGGAGGCTTGTTTGC
149520	159	CGCAAACAAGCCTCCGTCCC	158740	GGGACGGAGGCTTGTTTGCG
149521	160	TCGCAAACAAGCCTCCGTCC	158741	GGACGGAGGCTTGTTTGCGA
149522	161	CTCGCAAACAAGCCTCCGTC	158742	GACGGAGGCTTGTTTGCGAG
149523	162	CCTCGCAAACAAGCCTCCGT	158743	ACGGAGGCTTGTTTGCGAGG
149524	163	GCCTCGCAAACAAGCCTCCG	158744	CGGAGGCTTGTTTGCGAGGC
149525	164	GGCCTCGCAAACAAGCCTCC	158745	GGAGGCTTGTTTGCGAGGCC
149526	165	CGGCCTCGCAAACAAGCCTC	158746	GAGGCTTGTTTGCGAGGCCG
149527	166	GCGGCCTCGCAAACAAGCCT	158747	AGGCTTGTTTGCGAGGCCGC
149528	167	AGCGGCCTCGCAAACAAGCC	158748	GGCTTGTTTGCGAGGCCGCT
149529	168	GAGCGGCCTCGCAAACAAGC	158749	GCTTGTTTGCGAGGCCGCTC
149530	169	GGAGCGGCCTCGCAAACAAG	158750	CTTGTTTGCGAGGCCGCTCC
149531	170	GGGAGCGGCCTCGCAAACAA	158751	TTGTTTGCGAGGCCGCTCCC
149532	171	TGGGAGCGGCCTCGCAAACA	158752	TGTTTGCGAGGCCGCTCCCA
149533	172	GTGGGAGCGGCCTCGCAAAC	158753	GTTTGCGAGGCCGCTCCCAC
149534	173	GGTGGGAGCGGCCTCGCAAA	158754	TTTGCGAGGCCGCTCCCACC
149535	174	GGGTGGGAGCGGCCTCGCAA	158755	TTGCGAGGCCGCTCCCACCC
149536	175	CGGGTGGGAGCGGCCTCGCA	158756	TGCGAGGCCGCTCCCACCCG
149537	176	GCGGGTGGGAGCGGCCTCGC	158757	GCGAGGCCGCTCCCACCCGC
149538	177	AGCGGGTGGGAGCGGCCTCG	158758	CGAGGCCGCTCCCACCCGCT
149539	178	GAGCGGGTGGGAGCGGCCTC	158759	GAGGCCGCTCCCACCCGCTC
149540	179	CGAGCGGGTGGGAGCGGCCT	158760	AGGCCGCTCCCACCCGCTCG
149541	180	ACGAGCGGGTGGGAGCGGCC	158761	GGCCGCTCCCACCCGCTCGT
149542	181	GACGAGCGGGTGGGAGCGGC	158762	GCCGCTCCCACCCGCTCGTC
149543	182	GGACGAGCGGGTGGGAGCGG	158763	CCGCTCCCACCCGCTCGTCC
149544	183	GGGACGAGCGGGTGGGAGCG	158764	CGCTCCCACCCGCTCGTCCC
149545	184	GGGGACGAGCGGGTGGGAGC	158765	GCTCCCACCCGCTCGTCCCC
149546	185	GGGGGACGAGCGGGTGGGAG	158766	CTCCCACCCGCTCGTCCCCC
149547	186	GGGGGGACGAGCGGGTGGGA	158767	TCCCACCCGCTCGTCCCCCC
149548	187	CGGGGGGACGAGCGGGTGGG	158768	CCCACCCGCTCGTCCCCCCG
149549	188	GCGGGGGGACGAGCGGGTGG	158769	CCACCCGCTCGTCCCCCCGC
149550	189	CGCGGGGGGACGAGCGGGTG	158770	CACCCGCTCGTCCCCCCGCG
149551	190	GCGCGGGGGGACGAGCGGGT	158771	ACCCGCTCGTCCCCCCGCGC
149552	191	TGCGCGGGGGGACGAGCGGG	158772	CCCGCTCGTCCCCCCGCGCA
149553	192	GTGCGCGGGGGGACGAGCGG	158773	CCGCTCGTCCCCCCGCGCAC
149554	193	GGTGCGCGGGGGGACGAGCG	158774	CGCTCGTCCCCCCGCGCACC
149555	194	AGGTGCGCGGGGGGACGAGC	158775	GCTCGTCCCCCCGCGCACCT
149556	195	AAGGTGCGCGGGGGGACGAG	158776	CTCGTCCCCCCGCGCACCTT
149557	196	AAAGGTGCGCGGGGGGACGA	158777	TCGTCCCCCCGCGCACCTTT
149558	197	CAAAGGTGCGCGGGGGGACG	158778	CGTCCCCCCGCGCACCTTTG
149559	198	GCAAAGGTGCGCGGGGGGAC	158779	GTCCCCCCGCGCACCTTTGC
149560	199	AGCAAAGGTGCGCGGGGGGA	158780	TCCCCCCGCGCACCTTTGCT
149561	200	TAGCAAAGGTGCGCGGGGGG	158781	CCCCCCGCGCACCTTTGCTA
149562	201	CTAGCAAAGGTGCGCGGGGG	158782	CCCCCGCGCACCTTTGCTAG
149563	202	CCTAGCAAAGGTGCGCGGGG	158783	CCCCGCGCACCTTTGCTAGG
149564	203	TCCTAGCAAAGGTGCGCGGG	158784	CCCGCGCACCTTTGCTAGGA
149565	204	CTCCTAGCAAAGGTGCGCGG	158785	CCGCGCACCTTTGCTAGGAG
149566	205	GCTCCTAGCAAAGGTGCGCG	158786	CGCGCACCTTTGCTAGGAGC
149567	206	CGCTCCTAGCAAAGGTGCGC	158787	GCGCACCTTTGCTAGGAGCG
149568	207	CCGCTCCTAGCAAAGGTGCG	158788	CGCACCTTTGCTAGGAGCGG
149569	208	CCCGCTCCTAGCAAAGGTGC	158789	GCACCTTTGCTAGGAGCGGG
149570	209	ACCCGCTCCTAGCAAAGGTG	158790	CACCTTTGCTAGGAGCGGGT
149571	210	GACCCGCTCCTAGCAAAGGT	158791	ACCTTTGCTAGGAGCGGGTC
149572	211	CGACCCGCTCCTAGCAAAGG	158792	CCTTTGCTAGGAGCGGGTCG
149573	212	GCGACCCGCTCCTAGCAAAG	158793	CTTTGCTAGGAGCGGGTCGC
149574	213	GGCGACCCGCTCCTAGCAAA	158794	TTTGCTAGGAGCGGGTCGCC
149575	214	GGGCGACCCGCTCCTAGCAA	158795	TTGCTAGGAGCGGGTCGCCC

149576	215	CGGGCGACCCGCTCCTAGCA	158796	TGCTAGGAGCGGGTCGCCCG
149577	216	GCGGGCGACCCGCTCCTAGC	158797	GCTAGGAGCGGGTCGCCCGC
149578	217	GGCGGGCGACCCGCTCCTAG	158798	CTAGGAGCGGGTCGCCCGCC
149579	218	TGGCGGGCGACCCGCTCCTA	158799	TAGGAGCGGGTCGCCCGCCA
149580	219	CTGGCGGGCGACCCGCTCCT	158800	AGGAGCGGGTCGCCCGCCAG
149581	220	CCTGGCGGGCGACCCGCTCC	158801	GGAGCGGGTCGCCCGCCAGG
149582	221	GCCTGGCGGGCGACCCGCTC	158802	GAGCGGGTCGCCCGCCAGGC
149583	222	GGCCTGGCGGGCGACCCGCT	158803	AGCGGGTCGCCCGCCAGGCC
149584	223	AGGCCTGGCGGGCGACCCGC	158804	GCGGGTCGCCCGCCAGGCCT
149585	224	GAGGCCTGGCGGGCGACCCG	158805	CGGGTCGCCCGCCAGGCCTC
149586	225	CGAGGCCTGGCGGGCGACCC	158806	GGGTCGCCCGCCAGGCCTCG
149587	226	CCGAGGCCTGGCGGGCGACC	158807	GGTCGCCCGCCAGGCCTCGG
149588	227	CCCGAGGCCTGGCGGGCGAC	158808	GTCGCCCGCCAGGCCTCGGG
149589	228	CCCCGAGGCCTGGCGGGCGA	158809	TCGCCCGCCAGGCCTCGGGG
149590	229	GCCCCGAGGCCTGGCGGGCG	158810	CGCCCGCCAGGCCTCGGGGC
149591	230	GGCCCCGAGGCCTGGCGGGC	158811	GCCCGCCAGGCCTCGGGGCC
149592	231	CGGCCCCGAGGCCTGGCGGG	158812	CCCGCCAGGCCTCGGGGCCG
149593	232	GCGGCCCCGAGGCCTGGCGG	158813	CCGCCAGGCCTCGGGGCCGC
149594	233	GGCGGCCCCGAGGCCTGGCG	158814	CGCCAGGCCTCGGGGCCGCC
149595	234	GGGCGGCCCCGAGGCCTGGC	158815	GCCAGGCCTCGGGGCCGCCC
149596	235	AGGGCGGCCCCGAGGCCTGG	158816	CCAGGCCTCGGGGCCGCCCT
149597	236	CAGGGCGGCCCCGAGGCCTG	158817	CAGGCCTCGGGGCCGCCCTG
149598	237	CCAGGGCGGCCCCGAGGCCT	158818	AGGCCTCGGGGCCGCCCTGG
149599	238	ACCAGGGCGGCCCCGAGGCC	158819	GGCCTCGGGGCCGCCCTGGT
149600	239	GACCAGGGCGGCCCCGAGGC	158820	GCCTCGGGGCCGCCCTGGTC
149601	240	GGACCAGGGCGGCCCCGAGG	158821	CCTCGGGGCCGCCCTGGTCC
149602	241	TGGACCAGGGCGGCCCCGAG	158822	CTCGGGGCCGCCCTGGTCCA
149603	242	CTGGACCAGGGCGGCCCCGA	158823	TCGGGGCCGCCCTGGTCCAG
149604	243	GCTGGACCAGGGCGGCCCCG	158824	CGGGGCCGCCCTGGTCCAGC
149605	244	CGCTGGACCAGGGCGGCCCC	158825	GGGGCCGCCCTGGTCCAGCG
149606	245	GCGCTGGACCAGGGCGGCCC	158826	GGGCCGCCCTGGTCCAGCGC
149607	246	GGCGCTGGACCAGGGCGGCC	158827	GGCCGCCCTGGTCCAGCGCC
149608	247	GGGCGCTGGACCAGGGCGGC	158828	GCCGCCCTGGTCCAGCGCCC
149609	248	CGGGCGCTGGACCAGGGCGG	158829	CCGCCCTGGTCCAGCGCCCG
149610	249	CCGGGCGCTGGACCAGGGCG	158830	CGCCCTGGTCCAGCGCCCGG
149611	250	ACCGGGCGCTGGACCAGGGC	158831	GCCCTGGTCCAGCGCCCGGT
149612	251	GACCGGGCGCTGGACCAGGG	158832	CCCTGGTCCAGCGCCCGGTC
149613	252	GGACCGGGCGCTGGACCAGG	158833	CCTGGTCCAGCGCCCGGTCC
149614	253	GGGACCGGGCGCTGGACCAG	158834	CTGGTCCAGCGCCCGGTCCC
149615	254	CGGGACCGGGCGCTGGACCA	158835	TGGTCCAGCGCCCGGTCCCG
149616	255	CCGGGACCGGGCGCTGGACC	158836	GGTCCAGCGCCCGGTCCCGG
149617	256	GCCGGGACCGGGCGCTGGAC	158837	GTCCAGCGCCCGGTCCCGGC
149618	257	GGCCGGGACCGGGCGCTGGA	158838	TCCAGCGCCCGGTCCCGGCC
149619	258	GGGCCGGGACCGGGCGCTGG	158839	CCAGCGCCCGGTCCCGGCCC
149620	259	CGGGCCGGGACCGGGCGCTG	158840	CAGCGCCCGGTCCCGGCCCG
149621	260	ACGGGCCGGGACCGGGCGCT	158841	AGCGCCCGGTCCCGGCCCGT
149622	261	CACGGGCCGGGACCGGGCGC	158842	GCGCCCGGTCCCGGCCCGTG
149623	262	GCACGGGCCGGGACCGGGCG	158843	CGCCCGGTCCCGGCCCGTGC
149624	263	GGCACGGGCCGGGACCGGGC	158844	GCCCGGTCCCGGCCCGTGCC
149625	264	CGGCACGGGCCGGGACCGGG	158845	CCCGGTCCCGGCCCGTGCCG
149626	265	GCGGCACGGGCCGGGACCGG	158846	CCGGTCCCGGCCCGTGCCGC
149627	266	GGCGGCACGGGCCGGGACCG	158847	CGGTCCCGGCCCGTGCCGCC
149628	267	GGGCGGCACGGGCCGGGACC	158848	GGTCCCGGCCCGTGCCGCCC
149629	268	CGGGCGGCACGGGCCGGGAC	158849	GTCCCGGCCCGTGCCGCCCG
149630	269	CCGGGCGGCACGGGCCGGGA	158850	TCCCGGCCCGTGCCGCCCGG
149631	270	ACCGGGCGGCACGGGCCGGG	158851	CCCGGCCCGTGCCGCCCGGT
149632	271	GACCGGGCGGCACGGGCCGG	158852	CCGGCCCGTGCCGCCCGGTC
149633	272	CGACCGGGCGGCACGGGCCG	158853	CGGCCCGTGCCGCCCGGTCG
149634	273	CCGACCGGGCGGCACGGGCC	158854	GGCCCGTGCCGCCCGGTCGG
149635	274	ACCGACCGGGCGGCACGGGC	158855	GCCCGTGCCGCCCGGTCGGT
149636	275	CACCGACCGGGCGGCACGGG	158856	CCCGTGCCGCCCGGTCGGTG
149637	276	GCACCGACCGGGCGGCACGG	158857	CCGTGCCGCCCGGTCGGTGC
149638	277	GGCACCGACCGGGCGGCACG	158858	CGTGCCGCCCGGTCGGTGCC
149639	278	AGGCACCGACCGGGCGGCAC	158859	GTGCCGCCCGGTCGGTGCCT
149640	279	AAGGCACCGACCGGGCGGCA	158860	TGCCGCCCGGTCGGTGCCTT
149641	280	GAAGGCACCGACCGGGCGGC	158861	GCCGCCCGGTCGGTGCCTTC
149642	281	CGAAGGCACCGACCGGGCGG	158862	CCGCCCGGTCGGTGCCTTCG
149643	282	GCGAAGGCACCGACCGGGCG	158863	CGCCCGGTCGGTGCCTTCGC
149644	283	GGCGAAGGCACCGACCGGGC	158864	GCCCGGTCGGTGCCTTCGCC
149645	284	GGGCGAAGGCACCGACCGGG	158865	CCCGGTCGGTGCCTTCGCCC
149646	285	GGGGCGAAGGCACCGACCGG	158866	CCGGTCGGTGCCTTCGCCCC
149647	286	GGGGGCGAAGGCACCGACCG	158867	CGGTCGGTGCCTTCGCCCCC

149648	287	TGGGGGCGAAGGCACCGACC	158868	GGTCGGTGCCTTCGCCCCCA
149649	288	CTGGGGGCGAAGGCACCGAC	158869	GTCGGTGCCTTCGCCCCCAG
149650	289	GCTGGGGGCGAAGGCACCGA	158870	TCGGTGCCTTCGCCCCCAGC
149651	290	CGCTGGGGGCGAAGGCACCG	158871	CGGTGCCTTCGCCCCCAGCG
149652	291	CCGCTGGGGGCGAAGGCACC	158872	GGTGCCTTCGCCCCCAGCGG
149653	292	ACCGCTGGGGGCGAAGGCAC	158873	GTGCCTTCGCCCCCAGCGGT
149654	293	CACCGCTGGGGGCGAAGGCA	158874	TGCCTTCGCCCCCAGCGGTG
149655	294	GCACCGCTGGGGGCGAAGGC	158875	GCCTTCGCCCCCAGCGGTGC
149656	295	CGCACCGCTGGGGGCGAAGG	158876	CCTTCGCCCCCAGCGGTGCG
149657	296	CCGCACCGCTGGGGGCGAAG	158877	CTTCGCCCCCAGCGGTGCGG
149658	297	ACCGCACCGCTGGGGGCGAA	158878	TTCGCCCCCAGCGGTGCGGT
149659	298	CACCGCACCGCTGGGGGCGA	158879	TCGCCCCCAGCGGTGCGGTG
149660	299	GCACCGCACCGCTGGGGGCG	158880	CGCCCCCAGCGGTGCGGTGC
149661	300	GGCACCGCACCGCTGGGGGC	158881	GCCCCCAGCGGTGCGGTGCC
149662	301	GGGCACCGCACCGCTGGGGG	158882	CCCCCAGCGGTGCGGTGCCC
149663	302	TGGGCACCGCACCGCTGGGG	158883	CCCCAGCGGTGCGGTGCCCA
149664	303	TTGGGCACCGCACCGCTGGG	158884	CCCAGCGGTGCGGTGCCCAA
149665	304	CTTGGGCACCGCACCGCTGG	158885	CCAGCGGTGCGGTGCCCAAG
149666	305	ACTTGGGCACCGCACCGCTG	158886	CAGCGGTGCGGTGCCCAAGT
149667	306	CACTTGGGCACCGCACCGCT	158887	AGCGGTGCGGTGCCCAAGTG
149668	307	GCACTTGGGCACCGCACCGC	158888	GCGGTGCGGTGCCCAAGTGC
149669	308	AGCACTTGGGCACCGCACCG	158889	CGGTGCGGTGCCCAAGTGCT
149670	309	CAGCACTTGGGCACCGCACC	158890	GGTGCGGTGCCCAAGTGCTG
149671	310	TCAGCACTTGGGCACCGCAC	158891	GTGCGGTGCCCAAGTGCTGA
149672	311	CTCAGCACTTGGGCACCGCA	158892	TGCGGTGCCCAAGTGCTGAG
149673	312	ACTCAGCACTTGGGCACCGC	158893	GCGGTGCCCAAGTGCTGAGT
149674	313	GACTCAGCACTTGGGCACCG	158894	CGGTGCCCAAGTGCTGAGTC
149675	314	TGACTCAGCACTTGGGCACC	158895	GGTGCCCAAGTGCTGAGTCA
149676	315	GTGACTCAGCACTTGGGCAC	158896	GTGCCCAAGTGCTGAGTCAC
149677	316	GGTGACTCAGCACTTGGGCA	158897	TGCCCAAGTGCTGAGTCACC
149678	317	CGGTGACTCAGCACTTGGGC	158898	GCCCAAGTGCTGAGTCACCG
149679	318	CCGGTGACTCAGCACTTGGG	158899	CCCAAGTGCTGAGTCACCGG
149680	319	CCCGGTGACTCAGCACTTGG	158900	CCAAGTGCTGAGTCACCGGG
149681	320	GCCCGGTGACTCAGCACTTG	158901	CAAGTGCTGAGTCACCGGGC
149682	321	CGCCCGGTGACTCAGCACTT	158902	AAGTGCTGAGTCACCGGGCG
149683	322	CCGCCCGGTGACTCAGCACT	158903	AGTGCTGAGTCACCGGGCGG
149684	323	CCCGCCCGGTGACTCAGCAC	158904	GTGCTGAGTCACCGGGCGGG
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149686	325	GGCCCGCCCGGTGACTCAGC	158906	GCTGAGTCACCGGGCGGGCC
149687	326	GGGCCCGCCCGGTGACTCAG	158907	CTGAGTCACCGGGCGGGCCC
149688	327	CGGGCCCGCCCGGTGACTCA	158908	TGAGTCACCGGGCGGGCCCG
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149690	329	CCCGGGCCCGCCCGGTGACT	158910	AGTCACCGGGCGGGCCCGGG
149691	330	GCCCGGGCCCGCCCGGTGAC	158911	GTCACCGGGCGGGCCCGGGC
149692	331	CGCCCGGGCCCGCCCGGTGA	158912	TCACCGGGCGGGCCCGGGCG
149693	332	GCGCCCGGGCCCGCCCGGTG	158913	CACCGGGCGGGCCCGGGCGC
149694	333	CGCGCCCGGGCCCGCCCGGT	158914	ACCGGGCGGGCCCGGGCGCG
149695	334	CCGCGCCCGGGCCCGCCCGG	158915	CCGGGCGGGCCCGGGCGCGG
149696	335	CCCGCGCCCGGGCCCGCCCG	158916	CGGGCGGGCCCGGGCGCGGG
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149698	337	GCCCCGCGCCCGGGCCCGCC	158918	GGCGGGCCCGGGCGCGGGGC
149699	338	CGCCCCGCGCCCGGGCCCGC	158919	GCGGGCCCGGGCGCGGGGCG
149700	339	ACGCCCCGCGCCCGGGCCCG	158920	CGGGCCCGGGCGCGGGGCGT
149701	340	CACGCCCCGCGCCCGGGCCC	158921	GGGCCCGGGCGCGGGGCGTG
149702	341	CCACGCCCCGCGCCCGGGCC	158922	GGCCCGGGCGCGGGGCGTGG
149703	342	CCCACGCCCCGCGCCCGGGC	158923	GCCCGGGCGCGGGGCGTGGG
149704	343	TCCCACGCCCCGCGCCCGGG	158924	CCCGGGCGCGGGGCGTGGGA
149705	344	GTCCCACGCCCCGCGCCCGG	158925	CCGGGCGCGGGGCGTGGGAC
149706	345	GGTCCCACGCCCCGCGCCCG	158926	CGGGCGCGGGGCGTGGGACC
149707	346	CGGTCCCACGCCCCGCGCCC	158927	GGGCGCGGGGCGTGGGACCG
149708	347	TCGGTCCCACGCCCCGCGCC	158928	GGCGCGGGGCGTGGGACCGA
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149710	349	CCTCGGTCCCACGCCCCGCG	158930	CGCGGGGCGTGGGACCGAGG
149711	350	GCCTCGGTCCCACGCCCCGC	158931	GCGGGGCGTGGGACCGAGGC
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149717	356	GCGGCGGCCTCGGTCCCACG	158937	CGTGGGACCGAGGCCGCCGC
149718	357	CGCGGCGGCCTCGGTCCCAC	158938	GTGGGACCGAGGCCGCCGCG
149719	358	CCGCGGCGGCCTCGGTCCCA	158939	TGGGACCGAGGCCGCCGCGG

149720	359	CCCGCGGCGGCCTCGGTCCC	158940	GGGACCGAGGCCGCCGCGGG
149721	360	CCCCGCGGCGGCCTCGGTCC	158941	GGACCGAGGCCGCCGCGGGG
149722	361	GCCCCGCGGCGGCCTCGGTC	158942	GACCGAGGCCGCCGCGGGGC
149723	362	AGCCCCGCGGCGGCCTCGGT	158943	ACCGAGGCCGCCGCGGGGCT
149724	363	CAGCCCCGCGGCGGCCTCGG	158944	CCGAGGCCGCCGCGGGGCTG
149725	364	CCAGCCCCGCGGCGGCCTCG	158945	CGAGGCCGCCGCGGGGCTGG
149726	365	CCCAGCCCCGCGGCGGCCTC	158946	GAGGCCGCCGCGGGGCTGGG
149727	366	GCCCAGCCCCGCGGCGGCCT	158947	AGGCCGCCGCGGGGCTGGGC
149728	367	GGCCCAGCCCCGCGGCGGCC	158948	GGCCGCCGCGGGGCTGGGCC
149729	368	AGGCCCAGCCCCGCGGCGGC	158949	GCCGCCGCGGGGCTGGGCCT
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149734	373	CGCGCAGGCCCAGCCCCGCG	158954	CGCGGGGCTGGGCCTGCGCG
149735	374	ACGCGCAGGCCCAGCCCCGC	158955	GCGGGGCTGGGCCTGCGCGT
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149741	380	CCCGCCACGCGCAGGCCCAG	158961	CTGGGCCTGCGCGTGGCGGG
149742	381	TCCCGCCACGCGCAGGCCCA	158962	TGGGCCTGCGCGTGGCGGGA
149743	382	CTCCCGCCACGCGCAGGCCC	158963	GGGCCTGCGCGTGGCGGGAG
149744	383	GCTCCCGCCACGCGCAGGCC	158964	GGCCTGCGCGTGGCGGGAGC
149745	384	CGCTCCCGCCACGCGCAGGC	158965	GCCTGCGCGTGGCGGGAGCG
149746	385	GCGCTCCCGCCACGCGCAGG	158966	CCTGCGCGTGGCGGGAGCGC
149747	386	CGCGCTCCCGCCACGCGCAG	158967	CTGCGCGTGGCGGGAGCGCG
149748	387	CCGCGCTCCCGCCACGCGCA	158968	TGCGCGTGGCGGGAGCGCGG
149749	388	CCCGCGCTCCCGCCACGCGC	158969	GCGCGTGGCGGGAGCGCGGG
149750	389	CCCCGCGCTCCCGCCACGCG	158970	CGCGTGGCGGGAGCGCGGGG
149751	390	TCCCCGCGCTCCCGCCACGC	158971	GCGTGGCGGGAGCGCGGGGA
149752	391	CTCCCCGCGCTCCCGCCACG	158972	CGTGGCGGGAGCGCGGGGAG
149753	392	CCTCCCCGCGCTCCCGCCAC	158973	GTGGCGGGAGCGCGGGGAGG
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149755	394	TCCCTCCCCGCGCTCCCGCC	158975	GGCGGGAGCGCGGGGAGGGA
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149758	397	CAATCCCTCCCCGCGCTCCC	158978	GGGAGCGCGGGGAGGGATTG
149759	398	GCAATCCCTCCCCGCGCTCC	158979	GGAGCGCGGGGAGGGATTGC
149760	399	GGCAATCCCTCCCCGCGCTC	158980	GAGCGCGGGGAGGGATTGCC
149761	400	CGGCAATCCCTCCCCGCGCT	158981	AGCGCGGGGAGGGATTGCCG
149762	401	GCGGCAATCCCTCCCCGCGC	158982	GCGCGGGGAGGGATTGCCGC
149763	402	CGCGGCAATCCCTCCCCGCG	158983	CGCGGGGAGGGATTGCCGCG
149764	403	CCGCGGCAATCCCTCCCCGC	158984	GCGGGGAGGGATTGCCGCGG
149765	404	CCCGCGGCAATCCCTCCCCG	158985	CGGGGAGGGATTGCCGCGGG
149766	405	GCCCGCGGCAATCCCTCCCC	158986	GGGGAGGGATTGCCGCGGGC
149767	406	GGCCCGCGGCAATCCCTCCC	158987	GGGAGGGATTGCCGCGGGCC
149768	407	CGGCCCGCGGCAATCCCTCC	158988	GGAGGGATTGCCGCGGGCCG
149769	408	CCGGCCCGCGGCAATCCCTC	158989	GAGGGATTGCCGCGGGCCGG
149770	409	CCCGGCCCGCGGCAATCCCT	158990	AGGGATTGCCGCGGGCCGGG
149771	410	CCCCGGCCCGCGGCAATCCC	158991	GGGATTGCCGCGGGCCGGGG
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149773	412	CTCCCCGGCCCGCGGCAATC	158993	GATTGCCGCGGGCCGGGGAG
149774	413	CCTCCCCGGCCCGCGGCAAT	158994	ATTGCCGCGGGCCGGGGAGG
149775	414	CCCTCCCCGGCCCGCGGCAA	158995	TTGCCGCGGGCCGGGGAGGG
149776	415	CCCCTCCCCGGCCCGCGGCA	158996	TGCCGCGGGCCGGGGAGGGG
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149779	418	CCGCCCCTCCCCGGCCCGCG	158999	CGCGGGCCGGGGAGGGGCGG
149780	419	CCCGCCCCTCCCCGGCCCGC	159000	GCGGGCCGGGGAGGGGCGGG
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149783	422	GCCCCCGCCCCTCCCCGGCC	159003	GGCCGGGGAGGGGCGGGGGC
149784	423	CGCCCCCGCCCCTCCCCGGC	159004	GCCGGGGAGGGGCGGGGGCG
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149786	425	CCCGCCCCCGCCCCTCCCCG	159006	CGGGGAGGGGCGGGGGCGGG
149787	426	GCCCGCCCCCGCCCCTCCCC	159007	GGGGAGGGGCGGGGGCGGGC
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149789	428	ACGCCCGCCCCCGCCCCTCC	159009	GGAGGGGCGGGGGCGGGCGT
149790	429	CACGCCCGCCCCCGCCCCTC	159010	GAGGGGCGGGGGCGGGCGTG
149791	430	GCACGCCCGCCCCCGCCCCT	159011	AGGGGCGGGGGCGGGCGTGC

149792	431	AGCACGCCCGCCCCCGCCCC	159012	GGGGCGGGGGCGGGCGTGCT
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149794	433	GCAGCACGCCCGCCCCCGCC	159014	GGCGGGGGCGGGCGTGCTGC
149795	434	GGCAGCACGCCCGCCCCCGC	159015	GCGGGGGCGGGCGTGCTGCC
149796	435	GGGCAGCACGCCCGCCCCCG	159016	CGGGGGCGGGCGTGCTGCCC
149797	436	AGGGCAGCACGCCCGCCCCC	159017	GGGGGCGGGCGTGCTGCCCT
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149799	438	AGAGGGCAGCACGCCCGCCC	159019	GGGCGGGCGTGCTGCCCTCT
149800	439	CAGAGGGCAGCACGCCCGCC	159020	GGCGGGCGTGCTGCCCTCTG
149801	440	ACAGAGGGCAGCACGCCCGC	159021	GCGGGCGTGCTGCCCTCTGT
149802	441	CACAGAGGGCAGCACGCCCG	159022	CGGGCGTGCTGCCCTCTGTG
149803	442	CCACAGAGGGCAGCACGCCC	159023	GGGCGTGCTGCCCTCTGTGG
149804	443	ACCACAGAGGGCAGCACGCC	159024	GGCGTGCTGCCCTCTGTGGT
149805	444	GACCACAGAGGGCAGCACGC	159025	GCGTGCTGCCCTCTGTGGTC
149806	445	GGACCACAGAGGGCAGCACG	159026	CGTGCTGCCCTCTGTGGTCC
149807	446	AGGACCACAGAGGGCAGCAC	159027	GTGCTGCCCTCTGTGGTCCT
149808	447	AAGGACCACAGAGGGCAGCA	159028	TGCTGCCCTCTGTGGTCCTT
149809	448	CAAGGACCACAGAGGGCAGC	159029	GCTGCCCTCTGTGGTCCTTG
149810	449	CCAAGGACCACAGAGGGCAG	159030	CTGCCCTCTGTGGTCCTTGG
149811	450	CCCAAGGACCACAGAGGGCA	159031	TGCCCTCTGTGGTCCTTGGG
149812	451	GCCCAAGGACCACAGAGGGC	159032	GCCCTCTGTGGTCCTTGGGC
149813	452	GGCCCAAGGACCACAGAGGG	159033	CCCTCTGTGGTCCTTGGGCC
149814	453	CGGCCCAAGGACCACAGAGG	159034	CCTCTGTGGTCCTTGGGCCG
149815	454	GCGGCCCAAGGACCACAGAG	159035	CTCTGTGGTCCTTGGGCCGC
149816	455	GGCGGCCCAAGGACCACAGA	159036	TCTGTGGTCCTTGGGCCGCC
149817	456	CGGCGGCCCAAGGACCACAG	159037	CTGTGGTCCTTGGGCCGCCG
149818	457	GCGGCGGCCCAAGGACCACA	159038	TGTGGTCCTTGGGCCGCCGC
149819	458	GGCGGCGGCCCAAGGACCAC	159039	GTGGTCCTTGGGCCGCCGCC
149820	459	CGGCGGCGGCCCAAGGACCA	159040	TGGTCCTTGGGCCGCCGCCG
149821	460	GCGGCGGCGGCCCAAGGACC	159041	GGTCCTTGGGCCGCCGCCGC
149822	461	CGCGGCGGCGGCCCAAGGAC	159042	GTCCTTGGGCCGCCGCCGCG
149823	462	CCGCGGCGGCGGCCCAAGGA	159043	TCCTTGGGCCGCCGCCGCGG
149824	463	CCCGCGGCGGCGGCCCAAGG	159044	CCTTGGGCCGCCGCCGCGGG
149825	464	ACCCGCGGCGGCGGCCCAAG	159045	CTTGGGCCGCCGCCGCGGGT
149826	465	GACCCGCGGCGGCGGCCCAA	159046	TTGGGCCGCCGCCGCGGGTC
149827	466	AGACCCGCGGCGGCGGCCCA	159047	TGGGCCGCCGCCGCGGGTCT
149828	467	CAGACCCGCGGCGGCGGCCC	159048	GGGCCGCCGCCGCGGGTCTG
149829	468	ACAGACCCGCGGCGGCGGCC	159049	GGCCGCCGCCGCGGGTCTGT
149830	469	GACAGACCCGCGGCGGCGGC	159050	GCCGCCGCCGCGGGTCTGTC
149831	470	CGACAGACCCGCGGCGGCGG	159051	CCGCCGCCGCGGGTCTGTCG
149832	471	ACGACAGACCCGCGGCGGCG	159052	CGCCGCCGCGGGTCTGTCGT
149833	472	CACGACAGACCCGCGGCGGC	159053	GCCGCCGCGGGTCTGTCGTG
149834	473	CCACGACAGACCCGCGGCGG	159054	CCGCCGCGGGTCTGTCGTGG
149835	474	ACCACGACAGACCCGCGGCG	159055	CGCCGCGGGTCTGTCGTGGT
149836	475	CACCACGACAGACCCGCGGC	159056	GCCGCGGGTCTGTCGTGGTG
149837	476	GCACCACGACAGACCCGCGG	159057	CCGCGGGTCTGTCGTGGTGC
149838	477	GGCACCACGACAGACCCGCG	159058	CGCGGGTCTGTCGTGGTGCC
149839	478	AGGCACCACGACAGACCCGC	159059	GCGGGTCTGTCGTGGTGCCT
149840	479	CAGGCACCACGACAGACCCG	159060	CGGGTCTGTCGTGGTGCCTG
149841	480	CCAGGCACCACGACAGACCC	159061	GGGTCTGTCGTGGTGCCTGG
149842	481	TCCAGGCACCACGACAGACC	159062	GGTCTGTCGTGGTGCCTGGA
149843	482	CTCCAGGCACCACGACAGAC	159063	GTCTGTCGTGGTGCCTGGAG
149844	483	GCTCCAGGCACCACGACAGA	159064	TCTGTCGTGGTGCCTGGAGC
149845	484	CGCTCCAGGCACCACGACAG	159065	CTGTCGTGGTGCCTGGAGCG
149846	485	CCGCTCCAGGCACCACGACA	159066	TGTCGTGGTGCCTGGAGCGG
149847	486	GCCGCTCCAGGCACCACGAC	159067	GTCGTGGTGCCTGGAGCGGC
149848	487	AGCCGCTCCAGGCACCACGA	159068	TCGTGGTGCCTGGAGCGGCT
149849	488	CAGCCGCTCCAGGCACCACG	159069	CGTGGTGCCTGGAGCGGCTG
149850	489	ACAGCCGCTCCAGGCACCAC	159070	GTGGTGCCTGGAGCGGCTGT
149851	490	CACAGCCGCTCCAGGCACCA	159071	TGGTGCCTGGAGCGGCTGTG
149852	491	GCACAGCCGCTCCAGGCACC	159072	GGTGCCTGGAGCGGCTGTGC
149853	492	AGCACAGCCGCTCCAGGCAC	159073	GTGCCTGGAGCGGCTGTGCT
149854	493	GAGCACAGCCGCTCCAGGCA	159074	TGCCTGGAGCGGCTGTGCTC
149855	494	CGAGCACAGCCGCTCCAGGC	159075	GCCTGGAGCGGCTGTGCTCG
149856	495	ACGAGCACAGCCGCTCCAGG	159076	CCTGGAGCGGCTGTGCTCGT
149857	496	GACGAGCACAGCCGCTCCAG	159077	CTGGAGCGGCTGTGCTCGTC
149858	497	GGACGAGCACAGCCGCTCCA	159078	TGGAGCGGCTGTGCTCGTCC
149859	498	GGGACGAGCACAGCCGCTCC	159079	GGAGCGGCTGTGCTCGTCCC
149860	499	AGGGACGAGCACAGCCGCTC	159080	GAGCGGCTGTGCTCGTCCCT
149861	500	AAGGGACGAGCACAGCCGCT	159081	AGCGGCTGTGCTCGTCCCTT
149862	501	CAAGGGACGAGCACAGCCGC	159082	GCGGCTGTGCTCGTCCCTTG
149863	502	GCAAGGGACGAGCACAGCCG	159083	CGGCTGTGCTCGTCCCTTGC

149864	503	AGCAAGGGACGAGCACAGCC	159084	GGCTGTGCTCGTCCCTTGCT
149865	504	AAGCAAGGGACGAGCACAGC	159085	GCTGTGCTCGTCCCTTGCTT
149866	505	CAAGCAAGGGACGAGCACAG	159086	CTGTGCTCGTCCCTTGCTTG
149867	506	CCAAGCAAGGGACGAGCACA	159087	TGTGCTCGTCCCTTGCTTGG
149868	507	GCCAAGCAAGGGACGAGCAC	159088	GTGCTCGTCCCTTGCTTGGC
149869	508	GGCCAAGCAAGGGACGAGCA	159089	TGCTCGTCCCTTGCTTGGCC
149870	509	CGGCCAAGCAAGGGACGAGC	159090	GCTCGTCCCTTGCTTGGCCG
149871	510	ACGGCCAAGCAAGGGACGAG	159091	CTCGTCCCTTGCTTGGCCGT
149872	511	CACGGCCAAGCAAGGGACGA	159092	TCGTCCCTTGCTTGGCCGTG
149873	512	ACACGGCCAAGCAAGGGACG	159093	CGTCCCTTGCTTGGCCGTGT
149874	513	AACACGGCCAAGCAAGGGAC	159094	GTCCCTTGCTTGGCCGTGTT
149875	514	GAACACGGCCAAGCAAGGGA	159095	TCCCTTGCTTGGCCGTGTTC
149876	515	AGAACACGGCCAAGCAAGGG	159096	CCCTTGCTTGGCCGTGTTCT
149877	516	GAGAACACGGCCAAGCAAGG	159097	CCTTGCTTGGCCGTGTTCTC
149878	517	CGAGAACACGGCCAAGCAAG	159098	CTTGCTTGGCCGTGTTCTCG
149879	518	ACGAGAACACGGCCAAGCAA	159099	TTGCTTGGCCGTGTTCTCGT
149880	519	AACGAGAACACGGCCAAGCA	159100	TGCTTGGCCGTGTTCTCGTT
149881	520	GAACGAGAACACGGCCAAGC	159101	GCTTGGCCGTGTTCTCGTTC
149882	521	GGAACGAGAACACGGCCAAG	159102	CTTGGCCGTGTTCTCGTTCC
149883	522	AGGAACGAGAACACGGCCAA	159103	TTGGCCGTGTTCTCGTTCCT
149884	523	CAGGAACGAGAACACGGCCA	159104	TGGCCGTGTTCTCGTTCCTG
149885	524	TCAGGAACGAGAACACGGCC	159105	GGCCGTGTTCTCGTTCCTGA
149886	525	CTCAGGAACGAGAACACGGC	159106	GCCGTGTTCTCGTTCCTGAG
149887	526	CCTCAGGAACGAGAACACGG	159107	CCGTGTTCTCGTTCCTGAGG
149888	527	CCCTCAGGAACGAGAACACG	159108	CGTGTTCTCGTTCCTGAGGG
149889	528	ACCCTCAGGAACGAGAACAC	159109	GTGTTCTCGTTCCTGAGGGT
149890	529	GACCCTCAGGAACGAGAACA	159110	TGTTCTCGTTCCTGAGGGTC
149891	530	GGACCCTCAGGAACGAGAAC	159111	GTTCTCGTTCCTGAGGGTCC
149892	531	GGGACCCTCAGGAACGAGAA	159112	TTCTCGTTCCTGAGGGTCCC
149893	532	CGGGACCCTCAGGAACGAGA	159113	TCTCGTTCCTGAGGGTCCCG
149894	533	GCGGGACCCTCAGGAACGAG	159114	CTCGTTCCTGAGGGTCCCGC
149895	534	CGCGGGACCCTCAGGAACGA	159115	TCGTTCCTGAGGGTCCCGCG
149896	535	CCGCGGGACCCTCAGGAACG	159116	CGTTCCTGAGGGTCCCGCGG
149897	536	TCCGCGGGACCCTCAGGAAC	159117	GTTCCTGAGGGTCCCGCGGA
149898	537	GTCCGCGGGACCCTCAGGAA	159118	TTCCTGAGGGTCCCGCGGAC
149899	538	TGTCCGCGGGACCCTCAGGA	159119	TCCTGAGGGTCCCGCGGACA
149900	539	GTGTCCGCGGGACCCTCAGG	159120	CCTGAGGGTCCCGCGGACAC
149901	540	GGTGTCCGCGGGACCCTCAG	159121	CTGAGGGTCCCGCGGACACC
149902	541	CGGTGTCCGCGGGACCCTCA	159122	TGAGGGTCCCGCGGACACCG
149903	542	TCGGTGTCCGCGGGACCCTC	159123	GAGGGTCCCGCGGACACCGA
149904	543	CTCGGTGTCCGCGGGACCCT	159124	AGGGTCCCGCGGACACCGAG
149905	544	ACTCGGTGTCCGCGGGACCC	159125	GGGTCCCGCGGACACCGAGT
149906	545	CACTCGGTGTCCGCGGGACC	159126	GGTCCCGCGGACACCGAGTG
149907	546	CCACTCGGTGTCCGCGGGAC	159127	GTCCCGCGGACACCGAGTGG
149908	547	GCCACTCGGTGTCCGCGGGA	159128	TCCCGCGGACACCGAGTGGC
149909	548	CGCCACTCGGTGTCCGCGGG	159129	CCCGCGGACACCGAGTGGCG
149910	549	GCGCCACTCGGTGTCCGCGG	159130	CCGCGGACACCGAGTGGCGC
149911	550	TGCGCCACTCGGTGTCCGCG	159131	CGCGGACACCGAGTGGCGCA
149912	551	CTGCGCCACTCGGTGTCCGC	159132	GCGGACACCGAGTGGCGCAG
149913	552	ACTGCGCCACTCGGTGTCCG	159133	CGGACACCGAGTGGCGCAGT
149914	553	CACTGCGCCACTCGGTGTCC	159134	GGACACCGAGTGGCGCAGTG
149915	554	GCACTGCGCCACTCGGTGTC	159135	GACACCGAGTGGCGCAGTGC
149916	555	GGCACTGCGCCACTCGGTGT	159136	ACACCGAGTGGCGCAGTGCC
149917	556	TGGCACTGCGCCACTCGGTG	159137	CACCGAGTGGCGCAGTGCCA
149918	557	CTGGCACTGCGCCACTCGGT	159138	ACCGAGTGGCGCAGTGCCAG
149919	558	CCTGGCACTGCGCCACTCGG	159139	CCGAGTGGCGCAGTGCCAGG
149920	559	GCCTGGCACTGCGCCACTCG	159140	CGAGTGGCGCAGTGCCAGGC
149921	560	GGCCTGGCACTGCGCCACTC	159141	GAGTGGCGCAGTGCCAGGCC
149922	561	GGGCCTGGCACTGCGCCACT	159142	AGTGGCGCAGTGCCAGGCCC
149923	562	TGGGCCTGGCACTGCGCCAC	159143	GTGGCGCAGTGCCAGGCCCA
149924	563	CTGGGCCTGGCACTGCGCCA	159144	TGGCGCAGTGCCAGGCCCAG
149925	564	GCTGGGCCTGGCACTGCGCC	159145	GGCGCAGTGCCAGGCCCAGC
149926	565	GGCTGGGCCTGGCACTGCGC	159146	GCGCAGTGCCAGGCCCAGCC
149927	566	GGGCTGGGCCTGGCACTGCG	159147	CGCAGTGCCAGGCCCAGCCC
149928	567	CGGGCTGGGCCTGGCACTGC	159148	GCAGTGCCAGGCCCAGCCCG
149929	568	CCGGGCTGGGCCTGGCACTG	159149	CAGTGCCAGGCCCAGCCCGG
149930	569	CCCGGGCTGGGCCTGGCACT	159150	AGTGCCAGGCCCAGCCCGGG
149931	570	CCCCGGGCTGGGCCTGGCAC	159151	GTGCCAGGCCCAGCCCGGGG
149932	571	TCCCCGGGCTGGGCCTGGCA	159152	TGCCAGGCCCAGCCCGGGGA
149933	572	ATCCCCGGGCTGGGCCTGGC	159153	GCCAGGCCCAGCCCGGGGAT
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149935	574	CCATCCCCGGGCTGGGCCTG	159155	CAGGCCCAGCCCGGGGATGG

149936	575	GCCATCCCCGGGCTGGGCCT	159156	AGGCCCAGCCCGGGGATGGC
149937	576	CGCCATCCCCGGGCTGGGCC	159157	GGCCCAGCCCGGGGATGGCG
149938	577	TCGCCATCCCCGGGCTGGGC	159158	GCCCAGCCCGGGGATGGCGA
149939	578	GTCGCCATCCCCGGGCTGGG	159159	CCCAGCCCGGGGATGGCGAC
149940	579	AGTCGCCATCCCCGGGCTGG	159160	CCAGCCCGGGGATGGCGACT
149941	580	CAGTCGCCATCCCCGGGCTG	159161	CAGCCCGGGGATGGCGACTG
149942	581	GCAGTCGCCATCCCCGGGCT	159162	AGCCCGGGGATGGCGACTGC
149943	582	CGCAGTCGCCATCCCCGGGC	159163	GCCCGGGGATGGCGACTGCG
149944	583	GCGCAGTCGCCATCCCCGGG	159164	CCCGGGGATGGCGACTGCGC
149945	584	GGCGCAGTCGCCATCCCCGG	159165	CCGGGGATGGCGACTGCGCC
149946	585	AGGCGCAGTCGCCATCCCCG	159166	CGGGGATGGCGACTGCGCCT
149947	586	CAGGCGCAGTCGCCATCCCC	159167	GGGGATGGCGACTGCGCCTG
149948	587	CCAGGCGCAGTCGCCATCCC	159168	GGGATGGCGACTGCGCCTGG
149949	588	CCCAGGCGCAGTCGCCATCC	159169	GGATGGCGACTGCGCCTGGG
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149951	590	GGCCCAGGCGCAGTCGCCAT	159171	ATGGCGACTGCGCCTGGGCC
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149953	592	CGGGCCCAGGCGCAGTCGCC	159173	GGCGACTGCGCCTGGGCCCG
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149955	594	GGCGGGCCCAGGCGCAGTCG	159175	CGACTGCGCCTGGGCCCGCC
149956	595	AGGCGGGCCCAGGCGCAGTC	159176	GACTGCGCCTGGGCCCGCCT
149957	596	CAGGCGGGCCCAGGCGCAGT	159177	ACTGCGCCTGGGCCCGCCTG
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149959	598	ACCAGGCGGGCCCAGGCGCA	159179	TGCGCCTGGGCCCGCCTGGT
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149963	602	AGACACCAGGCGGGCCCAGG	159183	CCTGGGCCCGCCTGGTGTCT
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149965	604	GAAGACACCAGGCGGGCCCA	159185	TGGGCCCGCCTGGTGTCTTC
149966	605	CGAAGACACCAGGCGGGCCC	159186	GGGCCCGCCTGGTGTCTTCG
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149968	607	TGCGAAGACACCAGGCGGGC	159188	GCCCGCCTGGTGTCTTCGCA
149969	608	ATGCGAAGACACCAGGCGGG	159189	CCCGCCTGGTGTCTTCGCAT
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149972	611	GGGATGCGAAGACACCAGGC	159192	GCCTGGTGTCTTCGCATCCC
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149977	616	GGAGAGGGATGCGAAGACAC	159197	GTGTCTTCGCATCCCTCTCC
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149980	619	AGCGGAGAGGGATGCGAAGA	159200	TCTTCGCATCCCTCTCCGCT
149981	620	AAGCGGAGAGGGATGCGAAG	159201	CTTCGCATCCCTCTCCGCTT
149982	621	AAAGCGGAGAGGGATGCGAA	159202	TTCGCATCCCTCTCCGCTTT
149983	622	GAAAGCGGAGAGGGATGCGA	159203	TCGCATCCCTCTCCGCTTTC
149984	623	GGAAAGCGGAGAGGGATGCG	159204	CGCATCCCTCTCCGCTTTCC
149985	624	CGGAAAGCGGAGAGGGATGC	159205	GCATCCCTCTCCGCTTTCCG
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149987	626	GCCGGAAAGCGGAGAGGGAT	159207	ATCCCTCTCCGCTTTCCGGC
149988	627	AGCCGGAAAGCGGAGAGGGA	159208	TCCCTCTCCGCTTTCCGGCT
149989	628	AAGCCGGAAAGCGGAGAGGG	159209	CCCTCTCCGCTTTCCGGCTT
149990	629	GAAGCCGGAAAGCGGAGAGG	159210	CCTCTCCGCTTTCCGGCTTC
149991	630	TGAAGCCGGAAAGCGGAGAG	159211	CTCTCCGCTTTCCGGCTTCA
149992	631	CTGAAGCCGGAAAGCGGAGA	159212	TCTCCGCTTTCCGGCTTCAG
149993	632	GCTGAAGCCGGAAAGCGGAG	159213	CTCCGCTTTCCGGCTTCAGC
149994	633	CGCTGAAGCCGGAAAGCGGA	159214	TCCGCTTTCCGGCTTCAGCG
149995	634	GCGCTGAAGCCGGAAAGCGG	159215	CCGCTTTCCGGCTTCAGCGC
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149997	636	GAGCGCTGAAGCCGGAAAGC	159217	GCTTTCCGGCTTCAGCGCTC
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150058	697	TAAAAATATAAAAACCATTC	159278	GAATGGTTTTTATATTTTTA
150059	698	TTAAAAATATAAAAACCATT	159279	AATGGTTTTTATATTTTTAA
150060	699	TTTAAAAATATAAAAACCAT	159280	ATGGTTTTTATATTTTTAAA
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150062	701	CTTTTAAAAATATAAAAACC	159282	GGTTTTTATATTTTTAAAAG
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150064	703	GCCTTTTAAAAATATAAAAA	159284	TTTTTATATTTTTAAAAGGC
150065	704	AGCCTTTTAAAAATATAAAA	159285	TTTTATATTTTTAAAAGGCT
150066	705	AAGCCTTTTAAAAATATAAA	159286	TTTATATTTTTAAAAGGCTT
150067	706	AAAGCCTTTTAAAAATATAA	159287	TTATATTTTTAAAAGGCTTT
150068	707	CAAAGCCTTTTAAAAATATA	159288	TATATTTTTAAAAGGCTTTG
150069	708	CCAAAGCCTTTTAAAAATAT	159289	ATATTTTTAAAAGGCTTTGG
150070	709	TCCAAAGCCTTTTAAAAATA	159290	TATTTTTAAAAGGCTTTGGA
150071	710	TTCCAAAGCCTTTTAAAAAT	159291	ATTTTTAAAAGGCTTTGGAA
150072	711	TTTCCAAAGCCTTTTAAAAA	159292	TTTTTAAAAGGCTTTGGAAA
150073	712	TTTTCCAAAGCCTTTTAAAA	159293	TTTTAAAAGGCTTTGGAAAA
150074	713	GTTTTCCAAAGCCTTTTAAA	159294	TTTAAAAGGCTTTGGAAAAC
150075	714	TGTTTTCCAAAGCCTTTTAA	159295	TTAAAAGGCTTTGGAAAACA
150076	715	TTGTTTTCCAAAGCCTTTTA	159296	TAAAAGGCTTTGGAAAACAA
150077	716	TTTGTTTTCCAAAGCCTTTT	159297	AAAAGGCTTTGGAAAACAAA
150078	717	TTTTGTTTTCCAAAGCCTTT	159298	AAAGGCTTTGGAAAACAAAA
150079	718	TTTTTGTTTTCCAAAGCCTT	159299	AAGGCTTTGGAAAACAAAAA

150080	719	ATTTTTGTTTTCCAAAGCCT	159300	AGGCTTTGGAAAACAAAAAT
150081	720	TATTTTTGTTTTCCAAAGCC	159301	GGCTTTGGAAAACAAAAATA
150082	721	GTATTTTTGTTTTCCAAAGC	159302	GCTTTGGAAAACAAAAATAC
150083	722	CGTATTTTTGTTTTCCAAAG	159303	CTTTGGAAAACAAAAATACG
150084	723	GCGTATTTTTGTTTTCCAAA	159304	TTTGGAAAACAAAAATACGC
150085	724	TGCGTATTTTTGTTTTCCAA	159305	TTGGAAAACAAAAATACGCA
150086	725	TTGCGTATTTTTGTTTTCCA	159306	TGGAAAACAAAAATACGCAA
150087	726	GTTGCGTATTTTTGTTTTCC	159307	GGAAAACAAAAATACGCAAC
150088	727	TGTTGCGTATTTTTGTTTTC	159308	GAAAACAAAAATACGCAACA
150089	728	CTGTTGCGTATTTTTGTTTT	159309	AAAACAAAAATACGCAACAG
150090	729	TCTGTTGCGTATTTTTGTTT	159310	AAACAAAAATACGCAACAGA
150091	730	CTCTGTTGCGTATTTTTGTT	159311	AACAAAAATACGCAACAGAG
150092	731	TCTCTGTTGCGTATTTTTGT	159312	ACAAAAATACGCAACAGAGA
150093	732	GTCTCTGTTGCGTATTTTTG	159313	CAAAAATACGCAACAGAGAC
150094	733	GGTCTCTGTTGCGTATTTTT	159314	AAAAATACGCAACAGAGACC
150095	734	CGGTCTCTGTTGCGTATTTT	159315	AAAATACGCAACAGAGACCG
150096	735	ACGGTCTCTGTTGCGTATTT	159316	AAATACGCAACAGAGACCGT
150097	736	AACGGTCTCTGTTGCGTATT	159317	AATACGCAACAGAGACCGTT
150098	737	AAACGGTCTCTGTTGCGTAT	159318	ATACGCAACAGAGACCGTTT
150099	738	CAAACGGTCTCTGTTGCGTA	159319	TACGCAACAGAGACCGTTTG
150100	739	ACAAACGGTCTCTGTTGCGT	159320	ACGCAACAGAGACCGTTTGT
150101	740	CACAAACGGTCTCTGTTGCG	159321	CGCAACAGAGACCGTTTGTG
150102	741	ACACAAACGGTCTCTGTTGC	159322	GCAACAGAGACCGTTTGTGT
150103	742	CACACAAACGGTCTCTGTTG	159323	CAACAGAGACCGTTTGTGTG
150104	743	TCACACAAACGGTCTCTGTT	159324	AACAGAGACCGTTTGTGTGA
150105	744	GTCACACAAACGGTCTCTGT	159325	ACAGAGACCGTTTGTGTGAC
150106	745	TGTCACACAAACGGTCTCTG	159326	CAGAGACCGTTTGTGTGACA
150107	746	GTGTCACACAAACGGTCTCT	159327	AGAGACCGTTTGTGTGACAC
150108	747	AGTGTCACACAAACGGTCTC	159328	GAGACCGTTTGTGTGACACT
150109	748	AAGTGTCACACAAACGGTCT	159329	AGACCGTTTGTGTGACACTT
150110	749	AAAGTGTCACACAAACGGTC	159330	GACCGTTTGTGTGACACTTT
150111	750	CAAAGTGTCACACAAACGGT	159331	ACCGTTTGTGTGACACTTTG
150112	751	GCAAAGTGTCACACAAACGG	159332	CCGTTTGTGTGACACTTTGC
150113	752	TGCAAAGTGTCACACAAACG	159333	CGTTTGTGTGACACTTTGCA
150114	753	CTGCAAAGTGTCACACAAAC	159334	GTTTGTGTGACACTTTGCAG
150115	754	CCTGCAAAGTGTCACACAAA	159335	TTTGTGTGACACTTTGCAGG
150116	755	CCCTGCAAAGTGTCACACAA	159336	TTGTGTGACACTTTGCAGGG
150117	756	TCCCTGCAAAGTGTCACACA	159337	TGTGTGACACTTTGCAGGGA
150118	757	TTCCCTGCAAAGTGTCACAC	159338	GTGTGACACTTTGCAGGGAA
150119	758	CTTCCCTGCAAAGTGTCACA	159339	TGTGACACTTTGCAGGGAAG
150120	759	ACTTCCCTGCAAAGTGTCAC	159340	GTGACACTTTGCAGGGAAGT
150121	760	AACTTCCCTGCAAAGTGTCA	159341	TGACACTTTGCAGGGAAGTT
150122	761	AAACTTCCCTGCAAAGTGTC	159342	GACACTTTGCAGGGAAGTTT
150123	762	CAAACTTCCCTGCAAAGTGT	159343	ACACTTTGCAGGGAAGTTTG
150124	763	GCAAACTTCCCTGCAAAGTG	159344	CACTTTGCAGGGAAGTTTGC
150125	764	AGCAAACTTCCCTGCAAAGT	159345	ACTTTGCAGGGAAGTTTGCT
150126	765	CAGCAAACTTCCCTGCAAAG	159346	CTTTGCAGGGAAGTTTGCTG
150127	766	CCAGCAAACTTCCCTGCAAA	159347	TTTGCAGGGAAGTTTGCTGG
150128	767	GCCAGCAAACTTCCCTGCAA	159348	TTGCAGGGAAGTTTGCTGGC
150129	768	GGCCAGCAAACTTCCCTGCA	159349	TGCAGGGAAGTTTGCTGGCC
150130	769	AGGCCAGCAAACTTCCCTGC	159350	GCAGGGAAGTTTGCTGGCCT
150131	770	GAGGCCAGCAAACTTCCCTG	159351	CAGGGAAGTTTGCTGGCCTC
150132	771	AGAGGCCAGCAAACTTCCCT	159352	AGGGAAGTTTGCTGGCCTCT
150133	772	CAGAGGCCAGCAAACTTCCC	159353	GGGAAGTTTGCTGGCCTCTG
150134	773	ACAGAGGCCAGCAAACTTCC	159354	GGAAGTTTGCTGGCCTCTGT
150135	774	AACAGAGGCCAGCAAACTTC	159355	GAAGTTTGCTGGCCTCTGTT
150136	775	GAACAGAGGCCAGCAAACTT	159356	AAGTTTGCTGGCCTCTGTTC
150137	776	AGAACAGAGGCCAGCAAACT	159357	AGTTTGCTGGCCTCTGTTCT
150138	777	TAGAACAGAGGCCAGCAAAC	159358	GTTTGCTGGCCTCTGTTCTA
150139	778	CTAGAACAGAGGCCAGCAAA	159359	TTTGCTGGCCTCTGTTCTAG
150140	779	CCTAGAACAGAGGCCAGCAA	159360	TTGCTGGCCTCTGTTCTAGG
150141	780	ACCTAGAACAGAGGCCAGCA	159361	TGCTGGCCTCTGTTCTAGGT
150142	781	GACCTAGAACAGAGGCCAGC	159362	GCTGGCCTCTGTTCTAGGTC
150143	782	TGACCTAGAACAGAGGCCAG	159363	CTGGCCTCTGTTCTAGGTCA
150144	783	ATGACCTAGAACAGAGGCCA	159364	TGGCCTCTGTTCTAGGTCAT
150145	784	CATGACCTAGAACAGAGGCC	159365	GGCCTCTGTTCTAGGTCATG
150146	785	TCATGACCTAGAACAGAGGC	159366	GCCTCTGTTCTAGGTCATGA
150147	786	ATCATGACCTAGAACAGAGG	159367	CCTCTGTTCTAGGTCATGAT
150148	787	AATCATGACCTAGAACAGAG	159368	CTCTGTTCTAGGTCATGATT
150149	788	CAATCATGACCTAGAACAGA	159369	TCTGTTCTAGGTCATGATTG
150150	789	CCAATCATGACCTAGAACAG	159370	CTGTTCTAGGTCATGATTGG
150151	790	CCCAATCATGACCTAGAACA	159371	TGTTCTAGGTCATGATTGGG

150152	791	GCCCAATCATGACCTAGAAC	159372	GTTCTAGGTCATGATTGGGC
150153	792	AGCCCAATCATGACCTAGAA	159373	TTCTAGGTCATGATTGGGCT
150154	793	CAGCCCAATCATGACCTAGA	159374	TCTAGGTCATGATTGGGCTG
150155	794	GCAGCCCAATCATGACCTAG	159375	CTAGGTCATGATTGGGCTGC
150156	795	TGCAGCCCAATCATGACCTA	159376	TAGGTCATGATTGGGCTGCA
150157	796	TTGCAGCCCAATCATGACCT	159377	AGGTCATGATTGGGCTGCAA
150158	797	CTTGCAGCCCAATCATGACC	159378	GGTCATGATTGGGCTGCAAG
150159	798	CCTTGCAGCCCAATCATGAC	159379	GTCATGATTGGGCTGCAAGG
150160	799	CCCTTGCAGCCCAATCATGA	159380	TCATGATTGGGCTGCAAGGG
150161	800	GCCCTTGCAGCCCAATCATG	159381	CATGATTGGGCTGCAAGGGC
150162	801	TGCCCTTGCAGCCCAATCAT	159382	ATGATTGGGCTGCAAGGGCA
150163	802	CTGCCCTTGCAGCCCAATCA	159383	TGATTGGGCTGCAAGGGCAG
150164	803	TCTGCCCTTGCAGCCCAATC	159384	GATTGGGCTGCAAGGGCAGA
150165	804	CTCTGCCCTTGCAGCCCAAT	159385	ATTGGGCTGCAAGGGCAGAG
150166	805	TCTCTGCCCTTGCAGCCCAA	159386	TTGGGCTGCAAGGGCAGAGA
150167	806	TTCTCTGCCCTTGCAGCCCA	159387	TGGGCTGCAAGGGCAGAGAA
150168	807	CTTCTCTGCCCTTGCAGCCC	159388	GGGCTGCAAGGGCAGAGAAG
150169	808	CCTTCTCTGCCCTTGCAGCC	159389	GGCTGCAAGGGCAGAGAAGG
150170	809	ACCTTCTCTGCCCTTGCAGC	159390	GCTGCAAGGGCAGAGAAGGT
150171	810	TACCTTCTCTGCCCTTGCAG	159391	CTGCAAGGGCAGAGAAGGTA
150172	811	CTACCTTCTCTGCCCTTGCA	159392	TGCAAGGGCAGAGAAGGTAG
150173	812	GCTACCTTCTCTGCCCTTGC	159393	GCAAGGGCAGAGAAGGTAGC
150174	813	GGCTACCTTCTCTGCCCTTG	159394	CAAGGGCAGAGAAGGTAGCC
150175	814	AGGCTACCTTCTCTGCCCTT	159395	AAGGGCAGAGAAGGTAGCCT
150176	815	AAGGCTACCTTCTCTGCCCT	159396	AGGGCAGAGAAGGTAGCCTT
150177	816	CAAGGCTACCTTCTCTGCCC	159397	GGGCAGAGAAGGTAGCCTTG
150178	817	TCAAGGCTACCTTCTCTGCC	159398	GGCAGAGAAGGTAGCCTTGA
150179	818	TTCAAGGCTACCTTCTCTGC	159399	GCAGAGAAGGTAGCCTTGAA
150180	819	GTTCAAGGCTACCTTCTCTG	159400	CAGAGAAGGTAGCCTTGAAC
150181	820	TGTTCAAGGCTACCTTCTCT	159401	AGAGAAGGTAGCCTTGAACA
150182	821	CTGTTCAAGGCTACCTTCTC	159402	GAGAAGGTAGCCTTGAACAG
150183	822	TCTGTTCAAGGCTACCTTCT	159403	AGAAGGTAGCCTTGAACAGA
150184	823	CTCTGTTCAAGGCTACCTTC	159404	GAAGGTAGCCTTGAACAGAG
150185	824	CCTCTGTTCAAGGCTACCTT	159405	AAGGTAGCCTTGAACAGAGG
150186	825	ACCTCTGTTCAAGGCTACCT	159406	AGGTAGCCTTGAACAGAGGT
150187	826	GACCTCTGTTCAAGGCTACC	159407	GGTAGCCTTGAACAGAGGTC
150188	827	GGACCTCTGTTCAAGGCTAC	159408	GTAGCCTTGAACAGAGGTCC
150189	828	AGGACCTCTGTTCAAGGCTA	159409	TAGCCTTGAACAGAGGTCCT
150190	829	AAGGACCTCTGTTCAAGGCT	159410	AGCCTTGAACAGAGGTCCTT
150191	830	AAAGGACCTCTGTTCAAGGC	159411	GCCTTGAACAGAGGTCCTTT
150192	831	AAAAGGACCTCTGTTCAAGG	159412	CCTTGAACAGAGGTCCTTTT
150193	832	GAAAAGGACCTCTGTTCAAG	159413	CTTGAACAGAGGTCCTTTTC
150194	833	GGAAAAGGACCTCTGTTCAA	159414	TTGAACAGAGGTCCTTTTCC
150195	834	AGGAAAAGGACCTCTGTTCA	159415	TGAACAGAGGTCCTTTTCCT
150196	835	GAGGAAAAGGACCTCTGTTC	159416	GAACAGAGGTCCTTTTCCTC
150197	836	GGAGGAAAAGGACCTCTGTT	159417	AACAGAGGTCCTTTTCCTCC
150198	837	AGGAGGAAAAGGACCTCTGT	159418	ACAGAGGTCCTTTTCCTCCT
150199	838	GAGGAGGAAAAGGACCTCTG	159419	CAGAGGTCCTTTTCCTCCTC
150200	839	GGAGGAGGAAAAGGACCTCT	159420	AGAGGTCCTTTTCCTCCTCC
150201	840	AGGAGGAGGAAAAGGACCTC	159421	GAGGTCCTTTTCCTCCTCCT
150202	841	TAGGAGGAGGAAAAGGACCT	159422	AGGTCCTTTTCCTCCTCCTA
150203	842	TTAGGAGGAGGAAAAGGACC	159423	GGTCCTTTTCCTCCTCCTAA
150204	843	CTTAGGAGGAGGAAAAGGAC	159424	GTCCTTTTCCTCCTCCTAAG
150205	844	GCTTAGGAGGAGGAAAAGGA	159425	TCCTTTTCCTCCTCCTAAGC
150206	845	AGCTTAGGAGGAGGAAAAGG	159426	CCTTTTCCTCCTCCTAAGCT
150207	846	GAGCTTAGGAGGAGGAAAAG	159427	CTTTTCCTCCTCCTAAGCTC
150208	847	GGAGCTTAGGAGGAGGAAAA	159428	TTTTCCTCCTCCTAAGCTCC
150209	848	CGGAGCTTAGGAGGAGGAAA	159429	TTTCCTCCTCCTAAGCTCCG
150210	849	CCGGAGCTTAGGAGGAGGAA	159430	TTCCTCCTCCTAAGCTCCGG
150211	850	CCCGGAGCTTAGGAGGAGGA	159431	TCCTCCTCCTAAGCTCCGGG
150212	851	TCCCGGAGCTTAGGAGGAGG	159432	CCTCCTCCTAAGCTCCGGGA
150213	852	CTCCCGGAGCTTAGGAGGAG	159433	CTCCTCCTAAGCTCCGGGAG
150214	853	GCTCCCGGAGCTTAGGAGGA	159434	TCCTCCTAAGCTCCGGGAGC
150215	854	GGCTCCCGGAGCTTAGGAGG	159435	CCTCCTAAGCTCCGGGAGCC
150216	855	TGGCTCCCGGAGCTTAGGAG	159436	CTCCTAAGCTCCGGGAGCCA
150217	856	CTGGCTCCCGGAGCTTAGGA	159437	TCCTAAGCTCCGGGAGCCAG
150218	857	TCTGGCTCCCGGAGCTTAGG	159438	CCTAAGCTCCGGGAGCCAGA
150219	858	CTCTGGCTCCCGGAGCTTAG	159439	CTAAGCTCCGGGAGCCAGAG
150220	859	CCTCTGGCTCCCGGAGCTTA	159440	TAAGCTCCGGGAGCCAGAGG
150221	860	ACCTCTGGCTCCCGGAGCTT	159441	AAGCTCCGGGAGCCAGAGGT
150222	861	AACCTCTGGCTCCCGGAGCT	159442	AGCTCCGGGAGCCAGAGGTT
150223	862	AAACCTCTGGCTCCCGGAGC	159443	GCTCCGGGAGCCAGAGGTTT

150224	863	TAAACCTCTGGCTCCCGGAG	159444	CTCCGGGAGCCAGAGGTTTA
150225	864	TTAAACCTCTGGCTCCCGGA	159445	TCCGGGAGCCAGAGGTTTAA
150226	865	GTTAAACCTCTGGCTCCCGG	159446	CCGGGAGCCAGAGGTTTAAC
150227	866	AGTTAAACCTCTGGCTCCCG	159447	CGGGAGCCAGAGGTTTAACT
150228	867	CAGTTAAACCTCTGGCTCCC	159448	GGGAGCCAGAGGTTTAACTG
150229	868	TCAGTTAAACCTCTGGCTCC	159449	GGAGCCAGAGGTTTAACTGA
150230	869	GTCAGTTAAACCTCTGGCTC	159450	GAGCCAGAGGTTTAACTGAC
150231	870	GGTCAGTTAAACCTCTGGCT	159451	AGCCAGAGGTTTAACTGACC
150232	871	GGGTCAGTTAAACCTCTGGC	159452	GCCAGAGGTTTAACTGACCC
150233	872	AGGGTCAGTTAAACCTCTGG	159453	CCAGAGGTTTAACTGACCCT
150234	873	AAGGGTCAGTTAAACCTCTG	159454	CAGAGGTTTAACTGACCCTT
150235	874	AAAGGGTCAGTTAAACCTCT	159455	AGAGGTTTAACTGACCCTTT
150236	875	AAAAGGGTCAGTTAAACCTC	159456	GAGGTTTAACTGACCCTTTT
150237	876	CAAAAGGGTCAGTTAAACCT	159457	AGGTTTAACTGACCCTTTTG
150238	877	CCAAAAGGGTCAGTTAAACC	159458	GGTTTAACTGACCCTTTTGG
150239	878	CCCAAAAGGGTCAGTTAAAC	159459	GTTTAACTGACCCTTTTGGG
150240	879	CCCCAAAAGGGTCAGTTAAA	159460	TTTAACTGACCCTTTTGGGG
150241	880	TCCCCAAAAGGGTCAGTTAA	159461	TTAACTGACCCTTTTGGGGA
150242	881	ATCCCCAAAAGGGTCAGTTA	159462	TAACTGACCCTTTTGGGGAT
150243	882	AATCCCCAAAAGGGTCAGTT	159463	AACTGACCCTTTTGGGGATT
150244	883	AAATCCCCAAAAGGGTCAGT	159464	ACTGACCCTTTTGGGGATTT
150245	884	AAAATCCCCAAAAGGGTCAG	159465	CTGACCCTTTTGGGGATTTT
150246	885	AAAAATCCCCAAAAGGGTCA	159466	TGACCCTTTTGGGGATTTTT
150247	886	CAAAAATCCCCAAAAGGGTC	159467	GACCCTTTTGGGGATTTTTG
150248	887	TCAAAAATCCCCAAAAGGGT	159468	ACCCTTTTGGGGATTTTTGA
150249	888	CTCAAAAATCCCCAAAAGGG	159469	CCCTTTTGGGGATTTTTGAG
150250	889	CCTCAAAAATCCCCAAAAGG	159470	CCTTTTGGGGATTTTTGAGG
150251	890	CCCTCAAAAATCCCCAAAAG	159471	CTTTTGGGGATTTTTGAGGG
150252	891	GCCCTCAAAAATCCCCAAAA	159472	TTTTGGGGATTTTTGAGGGC
150253	892	TGCCCTCAAAAATCCCCAAA	159473	TTTGGGGATTTTTGAGGGCA
150254	893	CTGCCCTCAAAAATCCCCAA	159474	TTGGGGATTTTTGAGGGCAG
150255	894	ACTGCCCTCAAAAATCCCCA	159475	TGGGGATTTTTGAGGGCAGT
150256	895	CACTGCCCTCAAAAATCCCC	159476	GGGGATTTTTGAGGGCAGTG
150257	896	TCACTGCCCTCAAAAATCCC	159477	GGGATTTTTGAGGGCAGTGA
150258	897	ATCACTGCCCTCAAAAATCC	159478	GGATTTTTGAGGGCAGTGAT
150259	898	GATCACTGCCCTCAAAAATC	159479	GATTTTTGAGGGCAGTGATC
150260	899	AGATCACTGCCCTCAAAAAT	159480	ATTTTTGAGGGCAGTGATCT
150261	900	AAGATCACTGCCCTCAAAAA	159481	TTTTTGAGGGCAGTGATCTT
150262	901	TAAGATCACTGCCCTCAAAA	159482	TTTTGAGGGCAGTGATCTTA
150263	902	TTAAGATCACTGCCCTCAAA	159483	TTTGAGGGCAGTGATCTTAA
150264	903	GTTAAGATCACTGCCCTCAA	159484	TTGAGGGCAGTGATCTTAAC
150265	904	AGTTAAGATCACTGCCCTCA	159485	TGAGGGCAGTGATCTTAACT
150266	905	AAGTTAAGATCACTGCCCTC	159486	GAGGGCAGTGATCTTAACTT
150267	906	AAAGTTAAGATCACTGCCCT	159487	AGGGCAGTGATCTTAACTTT
150268	907	CAAAGTTAAGATCACTGCCC	159488	GGGCAGTGATCTTAACTTTG
150269	908	CCAAAGTTAAGATCACTGCC	159489	GGCAGTGATCTTAACTTTGG
150270	909	CCCAAAGTTAAGATCACTGC	159490	GCAGTGATCTTAACTTTGGG
150271	910	ACCCAAAGTTAAGATCACTG	159491	CAGTGATCTTAACTTTGGGT
150272	911	CACCCAAAGTTAAGATCACT	159492	AGTGATCTTAACTTTGGGTG
150273	912	GCACCCAAAGTTAAGATCAC	159493	GTGATCTTAACTTTGGGTGC
150274	913	TGCACCCAAAGTTAAGATCA	159494	TGATCTTAACTTTGGGTGCA
150275	914	GTGCACCCAAAGTTAAGATC	159495	GATCTTAACTTTGGGTGCAC
150276	915	TGTGCACCCAAAGTTAAGAT	159496	ATCTTAACTTTGGGTGCACA
150277	916	CTGTGCACCCAAAGTTAAGA	159497	TCTTAACTTTGGGTGCACAG
150278	917	ACTGTGCACCCAAAGTTAAG	159498	CTTAACTTTGGGTGCACAGT
150279	918	AACTGTGCACCCAAAGTTAA	159499	TTAACTTTGGGTGCACAGTT
150280	919	TAACTGTGCACCCAAAGTTA	159500	TAACTTTGGGTGCACAGTTA
150281	920	CTAACTGTGCACCCAAAGTT	159501	AACTTTGGGTGCACAGTTAG
150282	921	GCTAACTGTGCACCCAAAGT	159502	ACTTTGGGTGCACAGTTAGC
150283	922	AGCTAACTGTGCACCCAAAG	159503	CTTTGGGTGCACAGTTAGCT
150284	923	AAGCTAACTGTGCACCCAAA	159504	TTTGGGTGCACAGTTAGCTT
150285	924	TAAGCTAACTGTGCACCCAA	159505	TTGGGTGCACAGTTAGCTTA
150286	925	ATAAGCTAACTGTGCACCCA	159506	TGGGTGCACAGTTAGCTTAT
150287	926	AATAAGCTAACTGTGCACCC	159507	GGGTGCACAGTTAGCTTATT
150288	927	AAATAAGCTAACTGTGCACC	159508	GGTGCACAGTTAGCTTATTT
150289	928	CAAATAAGCTAACTGTGCAC	159509	GTGCACAGTTAGCTTATTTG
150290	929	TCAAATAAGCTAACTGTGCA	159510	TGCACAGTTAGCTTATTTGA
150291	930	TTCAAATAAGCTAACTGTGC	159511	GCACAGTTAGCTTATTTGAA
150292	931	CTTCAAATAAGCTAACTGTG	159512	CACAGTTAGCTTATTTGAAG
150293	932	TCTTCAAATAAGCTAACTGT	159513	ACAGTTAGCTTATTTGAAGA
150294	933	ATCTTCAAATAAGCTAACTG	159514	CAGTTAGCTTATTTGAAGAT
150295	934	GATCTTCAAATAAGCTAACT	159515	AGTTAGCTTATTTGAAGATC

150296	935	AGATCTTCAAATAAGCTAAC	159516	GTTAGCTTATTTGAAGATCT
150297	936	AAGATCTTCAAATAAGCTAA	159517	TTAGCTTATTTGAAGATCTT
150298	937	TAAGATCTTCAAATAAGCTA	159518	TAGCTTATTTGAAGATCTTA
150299	938	GTAAGATCTTCAAATAAGCT	159519	AGCTTATTTGAAGATCTTAC
150300	939	AGTAAGATCTTCAAATAAGC	159520	GCTTATTTGAAGATCTTACT
150301	940	TAGTAAGATCTTCAAATAAG	159521	CTTATTTGAAGATCTTACTA
150302	941	TTAGTAAGATCTTCAAATAA	159522	TTATTTGAAGATCTTACTAA
150303	942	TTTAGTAAGATCTTCAAATA	159523	TATTTGAAGATCTTACTAAA
150304	943	TTTTAGTAAGATCTTCAAAT	159524	ATTTGAAGATCTTACTAAAA
150305	944	TTTTTAGTAAGATCTTCAAA	159525	TTTGAAGATCTTACTAAAAA
150306	945	ATTTTTAGTAAGATCTTCAA	159526	TTGAAGATCTTACTAAAAAT
150307	946	TATTTTTAGTAAGATCTTCA	159527	TGAAGATCTTACTAAAAATA
150308	947	GTATTTTTAGTAAGATCTTC	159528	GAAGATCTTACTAAAAATAC
150309	948	TGTATTTTTAGTAAGATCTT	159529	AAGATCTTACTAAAAATACA
150310	949	GTGTATTTTTAGTAAGATCT	159530	AGATCTTACTAAAAATACAC
150311	950	GGTGTATTTTTAGTAAGATC	159531	GATCTTACTAAAAATACACC
150312	951	TGGTGTATTTTTAGTAAGAT	159532	ATCTTACTAAAAATACACCA
150313	952	CTGGTGTATTTTTAGTAAGA	159533	TCTTACTAAAAATACACCAG
150314	953	TCTGGTGTATTTTTAGTAAG	159534	CTTACTAAAAATACACCAGA
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150316	955	GCTCTGGTGTATTTTTAGTA	159536	TACTAAAAATACACCAGAGC
150317	956	GGCTCTGGTGTATTTTTAGT	159537	ACTAAAAATACACCAGAGCC
150318	957	GGGCTCTGGTGTATTTTTAG	159538	CTAAAAATACACCAGAGCCC
150319	958	TGGGCTCTGGTGTATTTTTA	159539	TAAAAATACACCAGAGCCCA
150320	959	TTGGGCTCTGGTGTATTTTT	159540	AAAAATACACCAGAGCCCAA
150321	960	GTTGGGCTCTGGTGTATTTT	159541	AAAATACACCAGAGCCCAAC
150322	961	GGTTGGGCTCTGGTGTATTT	159542	AAATACACCAGAGCCCAACC
150323	962	AGGTTGGGCTCTGGTGTATT	159543	AATACACCAGAGCCCAACCT
150324	963	GAGGTTGGGCTCTGGTGTAT	159544	ATACACCAGAGCCCAACCTC
150325	964	GGAGGTTGGGCTCTGGTGTA	159545	TACACCAGAGCCCAACCTCC
150326	965	CGGAGGTTGGGCTCTGGTGT	159546	ACACCAGAGCCCAACCTCCG
150327	966	TCGGAGGTTGGGCTCTGGTG	159547	CACCAGAGCCCAACCTCCGA
150328	967	GTCGGAGGTTGGGCTCTGGT	159548	ACCAGAGCCCAACCTCCGAC
150329	968	GGTCGGAGGTTGGGCTCTGG	159549	CCAGAGCCCAACCTCCGACC
150330	969	TGGTCGGAGGTTGGGCTCTG	159550	CAGAGCCCAACCTCCGACCA
150331	970	TTGGTCGGAGGTTGGGCTCT	159551	AGAGCCCAACCTCCGACCAA
150332	971	ATTGGTCGGAGGTTGGGCTC	159552	GAGCCCAACCTCCGACCAAT
150333	972	AATTGGTCGGAGGTTGGGCT	159553	AGCCCAACCTCCGACCAATT
150334	973	TAATTGGTCGGAGGTTGGGC	159554	GCCCAACCTCCGACCAATTA
150335	974	GTAATTGGTCGGAGGTTGGG	159555	CCCAACCTCCGACCAATTAC
150336	975	TGTAATTGGTCGGAGGTTGG	159556	CCAACCTCCGACCAATTACA
150337	976	ATGTAATTGGTCGGAGGTTG	159557	CAACCTCCGACCAATTACAT
150338	977	GATGTAATTGGTCGGAGGTT	159558	AACCTCCGACCAATTACATC
150339	978	TGATGTAATTGGTCGGAGGT	159559	ACCTCCGACCAATTACATCA
150340	979	TTGATGTAATTGGTCGGAGG	159560	CCTCCGACCAATTACATCAA
150341	980	TTTGATGTAATTGGTCGGAG	159561	CTCCGACCAATTACATCAAA
150342	981	TTTTGATGTAATTGGTCGGA	159562	TCCGACCAATTACATCAAAA
150343	982	GTTTTGATGTAATTGGTCGG	159563	CCGACCAATTACATCAAAAC
150344	983	GGTTTTGATGTAATTGGTCG	159564	CGACCAATTACATCAAAACC
150345	984	AGGTTTTGATGTAATTGGTC	159565	GACCAATTACATCAAAACCT
150346	985	CAGGTTTTGATGTAATTGGT	159566	ACCAATTACATCAAAACCTG
150347	986	ACAGGTTTTGATGTAATTGG	159567	CCAATTACATCAAAACCTGT
150348	987	GACAGGTTTTGATGTAATTG	159568	CAATTACATCAAAACCTGTC
150349	988	GGACAGGTTTTGATGTAATT	159569	AATTACATCAAAACCTGTCC
150350	989	AGGACAGGTTTTGATGTAAT	159570	ATTACATCAAAACCTGTCCT
150351	990	TAGGACAGGTTTTGATGTAA	159571	TTACATCAAAACCTGTCCTA
150352	991	CTAGGACAGGTTTTGATGTA	159572	TACATCAAAACCTGTCCTAG
150353	992	ACTAGGACAGGTTTTGATGT	159573	ACATCAAAACCTGTCCTAGT
150354	993	CACTAGGACAGGTTTTGATG	159574	CATCAAAACCTGTCCTAGTG
150355	994	GCACTAGGACAGGTTTTGAT	159575	ATCAAAACCTGTCCTAGTGC
150356	995	TGCACTAGGACAGGTTTTGA	159576	TCAAAACCTGTCCTAGTGCA
150357	996	CTGCACTAGGACAGGTTTTG	159577	CAAAACCTGTCCTAGTGCAG
150358	997	CCTGCACTAGGACAGGTTTT	159578	AAAACCTGTCCTAGTGCAGG
150359	998	CCCTGCACTAGGACAGGTTT	159579	AAACCTGTCCTAGTGCAGGG
150360	999	ACCCTGCACTAGGACAGGTT	159580	AACCTGTCCTAGTGCAGGGT
150361	1000	CACCCTGCACTAGGACAGGT	159581	ACCTGTCCTAGTGCAGGGTG
150362	1001	TCACCCTGCACTAGGACAGG	159582	CCTGTCCTAGTGCAGGGTGA
150363	1002	CTCACCCTGCACTAGGACAG	159583	CTGTCCTAGTGCAGGGTGAG
150364	1003	ACTCACCCTGCACTAGGACA	159584	TGTCCTAGTGCAGGGTGAGT
150365	1004	TACTCACCCTGCACTAGGAC	159585	GTCCTAGTGCAGGGTGAGTA
150366	1005	ATACTCACCCTGCACTAGGA	159586	TCCTAGTGCAGGGTGAGTAT
150367	1006	AATACTCACCCTGCACTAGG	159587	CCTAGTGCAGGGTGAGTATT

150368	1007	CAATACTCACCCTGCACTAG	159588	CTAGTGCAGGGTGAGTATTG
150369	1008	GCAATACTCACCCTGCACTA	159589	TAGTGCAGGGTGAGTATTGC
150370	1009	AGCAATACTCACCCTGCACT	159590	AGTGCAGGGTGAGTATTGCT
150371	1010	CAGCAATACTCACCCTGCAC	159591	GTGCAGGGTGAGTATTGCTG
150372	1011	ACAGCAATACTCACCCTGCA	159592	TGCAGGGTGAGTATTGCTGT
150373	1012	AACAGCAATACTCACCCTGC	159593	GCAGGGTGAGTATTGCTGTT
150374	1013	AAACAGCAATACTCACCCTG	159594	CAGGGTGAGTATTGCTGTTT
150375	1014	AAAACAGCAATACTCACCCT	159595	AGGGTGAGTATTGCTGTTTT
150376	1015	AAAAACAGCAATACTCACCC	159596	GGGTGAGTATTGCTGTTTTT
150377	1016	AAAAAACAGCAATACTCACC	159597	GGTGAGTATTGCTGTTTTTT
150378	1017	CAAAAAACAGCAATACTCAC	159598	GTGAGTATTGCTGTTTTTTG
150379	1018	TCAAAAAACAGCAATACTCA	159599	TGAGTATTGCTGTTTTTTGA
150380	1019	TTCAAAAAACAGCAATACTC	159600	GAGTATTGCTGTTTTTTGAA
150381	1020	TTTCAAAAAACAGCAATACT	159601	AGTATTGCTGTTTTTTGAAA
150382	1021	CTTTCAAAAAACAGCAATAC	159602	GTATTGCTGTTTTTTGAAAG
150383	1022	ACTTTCAAAAAACAGCAATA	159603	TATTGCTGTTTTTTGAAAGT
150384	1023	AACTTTCAAAAAACAGCAAT	159604	ATTGCTGTTTTTTGAAAGTT
150385	1024	AAACTTTCAAAAAACAGCAA	159605	TTGCTGTTTTTTGAAAGTTT
150386	1025	GAAACTTTCAAAAAACAGCA	159606	TGCTGTTTTTTGAAAGTTTC
150387	1026	GGAAACTTTCAAAAAACAGC	159607	GCTGTTTTTTGAAAGTTTCC
150388	1027	TGGAAACTTTCAAAAAACAG	159608	CTGTTTTTTGAAAGTTTCCA
150389	1028	TTGGAAACTTTCAAAAAACA	159609	TGTTTTTTGAAAGTTTCCAA
150390	1029	TTTGGAAACTTTCAAAAAAC	159610	GTTTTTTGAAAGTTTCCAAA
150391	1030	TTTTGGAAACTTTCAAAAAA	159611	TTTTTTGAAAGTTTCCAAAA
150392	1031	CTTTTGGAAACTTTCAAAAA	159612	TTTTTGAAAGTTTCCAAAAG
150393	1032	ACTTTTGGAAACTTTCAAAA	159613	TTTTGAAAGTTTCCAAAAGT
150394	1033	CACTTTTGGAAACTTTCAAA	159614	TTTGAAAGTTTCCAAAAGTG
150395	1034	TCACTTTTGGAAACTTTCAA	159615	TTGAAAGTTTCCAAAAGTGA
150396	1035	ATCACTTTTGGAAACTTTCA	159616	TGAAAGTTTCCAAAAGTGAT
150397	1036	AATCACTTTTGGAAACTTTC	159617	GAAAGTTTCCAAAAGTGATT
150398	1037	AAATCACTTTTGGAAACTTT	159618	AAAGTTTCCAAAAGTGATTT
150399	1038	AAAATCACTTTTGGAAACTT	159619	AAGTTTCCAAAAGTGATTTT
150400	1039	CAAAATCACTTTTGGAAACT	159620	AGTTTCCAAAAGTGATTTTG
150401	1040	TCAAAATCACTTTTGGAAAC	159621	GTTTCCAAAAGTGATTTTGA
150402	1041	ATCAAAATCACTTTTGGAAA	159622	TTTCCAAAAGTGATTTTGAT
150403	1042	CATCAAAATCACTTTTGGAA	159623	TTCCAAAAGTGATTTTGATG
150404	1043	ACATCAAAATCACTTTTGGA	159624	TCCAAAAGTGATTTTGATGT
150405	1044	CACATCAAAATCACTTTTGG	159625	CCAAAAGTGATTTTGATGTG
150406	1045	GCACATCAAAATCACTTTTG	159626	CAAAAGTGATTTTGATGTGC
150407	1046	TGCACATCAAAATCACTTTT	159627	AAAAGTGATTTTGATGTGCA
150408	1047	GTGCACATCAAAATCACTTT	159628	AAAGTGATTTTGATGTGCAC
150409	1048	GGTGCACATCAAAATCACTT	159629	AAGTGATTTTGATGTGCACC
150410	1049	AGGTGCACATCAAAATCACT	159630	AGTGATTTTGATGTGCACCT
150411	1050	TAGGTGCACATCAAAATCAC	159631	GTGATTTTGATGTGCACCTA
150412	1051	GTAGGTGCACATCAAAATCA	159632	TGATTTTGATGTGCACCTAC
150413	1052	CGTAGGTGCACATCAAAATC	159633	GATTTTGATGTGCACCTACG
150414	1053	TCGTAGGTGCACATCAAAAT	159634	ATTTTGATGTGCACCTACGA
150415	1054	ATCGTAGGTGCACATCAAAA	159635	TTTTGATGTGCACCTACGAT
150416	1055	AATCGTAGGTGCACATCAAA	159636	TTTGATGTGCACCTACGATT
150417	1056	CAATCGTAGGTGCACATCAA	159637	TTGATGTGCACCTACGATTG
150418	1057	TCAATCGTAGGTGCACATCA	159638	TGATGTGCACCTACGATTGA
150419	1058	CTCAATCGTAGGTGCACATC	159639	GATGTGCACCTACGATTGAG
150420	1059	TCTCAATCGTAGGTGCACAT	159640	ATGTGCACCTACGATTGAGA
150421	1060	TTCTCAATCGTAGGTGCACA	159641	TGTGCACCTACGATTGAGAA
150422	1061	GTTCTCAATCGTAGGTGCAC	159642	GTGCACCTACGATTGAGAAC
150423	1062	AGTTCTCAATCGTAGGTGCA	159643	TGCACCTACGATTGAGAACT
150424	1063	CAGTTCTCAATCGTAGGTGC	159644	GCACCTACGATTGAGAACTG
150425	1064	ACAGTTCTCAATCGTAGGTG	159645	CACCTACGATTGAGAACTGT
150426	1065	GACAGTTCTCAATCGTAGGT	159646	ACCTACGATTGAGAACTGTC
150427	1066	CGACAGTTCTCAATCGTAGG	159647	CCTACGATTGAGAACTGTCG
150428	1067	ACGACAGTTCTCAATCGTAG	159648	CTACGATTGAGAACTGTCGT
150429	1068	AACGACAGTTCTCAATCGTA	159649	TACGATTGAGAACTGTCGTT
150430	1069	AAACGACAGTTCTCAATCGT	159650	ACGATTGAGAACTGTCGTTT
150431	1070	CAAACGACAGTTCTCAATCG	159651	CGATTGAGAACTGTCGTTTG
150432	1071	TCAAACGACAGTTCTCAATC	159652	GATTGAGAACTGTCGTTTGA
150433	1072	CTCAAACGACAGTTCTCAAT	159653	ATTGAGAACTGTCGTTTGAG
150434	1073	CCTCAAACGACAGTTCTCAA	159654	TTGAGAACTGTCGTTTGAGG
150435	1074	TCCTCAAACGACAGTTCTCA	159655	TGAGAACTGTCGTTTGAGGA
150436	1075	GTCCTCAAACGACAGTTCTC	159656	GAGAACTGTCGTTTGAGGAC
150437	1076	TGTCCTCAAACGACAGTTCT	159657	AGAACTGTCGTTTGAGGACA
150438	1077	CTGTCCTCAAACGACAGTTC	159658	GAACTGTCGTTTGAGGACAG
150439	1078	ACTGTCCTCAAACGACAGTT	159659	AACTGTCGTTTGAGGACAGT

150440	1079	CACTGTCCTCAAACGACAGT	159660	ACTGTCGTTTGAGGACAGTG
150441	1080	CCACTGTCCTCAAACGACAG	159661	CTGTCGTTTGAGGACAGTGG
150442	1081	CCCACTGTCCTCAAACGACA	159662	TGTCGTTTGAGGACAGTGGG
150443	1082	ACCCACTGTCCTCAAACGAC	159663	GTCGTTTGAGGACAGTGGGT
150444	1083	CACCCACTGTCCTCAAACGA	159664	TCGTTTGAGGACAGTGGGTG
150445	1084	CCACCCACTGTCCTCAAACG	159665	CGTTTGAGGACAGTGGGTGG
150446	1085	TCCACCCACTGTCCTCAAAC	159666	GTTTGAGGACAGTGGGTGGA
150447	1086	CTCCACCCACTGTCCTCAAA	159667	TTTGAGGACAGTGGGTGGAG
150448	1087	ACTCCACCCACTGTCCTCAA	159668	TTGAGGACAGTGGGTGGAGT
150449	1088	AACTCCACCCACTGTCCTCA	159669	TGAGGACAGTGGGTGGAGTT
150450	1089	AAACTCCACCCACTGTCCTC	159670	GAGGACAGTGGGTGGAGTTT
150451	1090	GAAACTCCACCCACTGTCCT	159671	AGGACAGTGGGTGGAGTTTC
150452	1091	CGAAACTCCACCCACTGTCC	159672	GGACAGTGGGTGGAGTTTCG
150453	1092	ACGAAACTCCACCCACTGTC	159673	GACAGTGGGTGGAGTTTCGT
150454	1093	TACGAAACTCCACCCACTGT	159674	ACAGTGGGTGGAGTTTCGTA
150455	1094	ATACGAAACTCCACCCACTG	159675	CAGTGGGTGGAGTTTCGTAT
150456	1095	AATACGAAACTCCACCCACT	159676	AGTGGGTGGAGTTTCGTATT
150457	1096	AAATACGAAACTCCACCCAC	159677	GTGGGTGGAGTTTCGTATTT
150458	1097	CAAATACGAAACTCCACCCA	159678	TGGGTGGAGTTTCGTATTTG
150459	1098	CCAAATACGAAACTCCACCC	159679	GGGTGGAGTTTCGTATTTGG
150460	1099	TCCAAATACGAAACTCCACC	159680	GGTGGAGTTTCGTATTTGGA
150461	1100	TTCCAAATACGAAACTCCAC	159681	GTGGAGTTTCGTATTTGGAA
150462	1101	TTTCCAAATACGAAACTCCA	159682	TGGAGTTTCGTATTTGGAAA
150463	1102	ATTTCCAAATACGAAACTCC	159683	GGAGTTTCGTATTTGGAAAT
150464	1103	AATTTCCAAATACGAAACTC	159684	GAGTTTCGTATTTGGAAATT
150465	1104	TAATTTCCAAATACGAAACT	159685	AGTTTCGTATTTGGAAATTA
150466	1105	CTAATTTCCAAATACGAAAC	159686	GTTTCGTATTTGGAAATTAG
150467	1106	TCTAATTTCCAAATACGAAA	159687	TTTCGTATTTGGAAATTAGA
150468	1107	TTCTAATTTCCAAATACGAA	159688	TTCGTATTTGGAAATTAGAA
150469	1108	CTTCTAATTTCCAAATACGA	159689	TCGTATTTGGAAATTAGAAG
150470	1109	TCTTCTAATTTCCAAATACG	159690	CGTATTTGGAAATTAGAAGA
150471	1110	GTCTTCTAATTTCCAAATAC	159691	GTATTTGGAAATTAGAAGAC
150472	1111	GGTCTTCTAATTTCCAAATA	159692	TATTTGGAAATTAGAAGACC
150473	1112	AGGTCTTCTAATTTCCAAAT	159693	ATTTGGAAATTAGAAGACCT
150474	1113	CAGGTCTTCTAATTTCCAAA	159694	TTTGGAAATTAGAAGACCTG
150475	1114	CCAGGTCTTCTAATTTCCAA	159695	TTGGAAATTAGAAGACCTGG
150476	1115	TCCAGGTCTTCTAATTTCCA	159696	TGGAAATTAGAAGACCTGGA
150477	1116	CTCCAGGTCTTCTAATTTCC	159697	GGAAATTAGAAGACCTGGAG
150478	1117	ACTCCAGGTCTTCTAATTTC	159698	GAAATTAGAAGACCTGGAGT
150479	1118	AACTCCAGGTCTTCTAATTT	159699	AAATTAGAAGACCTGGAGTT
150480	1119	AAACTCCAGGTCTTCTAATT	159700	AATTAGAAGACCTGGAGTTT
150481	1120	GAAACTCCAGGTCTTCTAAT	159701	ATTAGAAGACCTGGAGTTTC
150482	1121	GGAAACTCCAGGTCTTCTAA	159702	TTAGAAGACCTGGAGTTTCC
150483	1122	TGGAAACTCCAGGTCTTCTA	159703	TAGAAGACCTGGAGTTTCCA
150484	1123	ATGGAAACTCCAGGTCTTCT	159704	AGAAGACCTGGAGTTTCCAT
150485	1124	AATGGAAACTCCAGGTCTTC	159705	GAAGACCTGGAGTTTCCATT
150486	1125	TAATGGAAACTCCAGGTCTT	159706	AAGACCTGGAGTTTCCATTA
150487	1126	GTAATGGAAACTCCAGGTCT	159707	AGACCTGGAGTTTCCATTAC
150488	1127	TGTAATGGAAACTCCAGGTC	159708	GACCTGGAGTTTCCATTACA
150489	1128	GTGTAATGGAAACTCCAGGT	159709	ACCTGGAGTTTCCATTACAC
150490	1129	GGTGTAATGGAAACTCCAGG	159710	CCTGGAGTTTCCATTACACC
150491	1130	CGGTGTAATGGAAACTCCAG	159711	CTGGAGTTTCCATTACACCG
150492	1131	TCGGTGTAATGGAAACTCCA	159712	TGGAGTTTCCATTACACCGA
150493	1132	TTCGGTGTAATGGAAACTCC	159713	GGAGTTTCCATTACACCGAA
150494	1133	ATTCGGTGTAATGGAAACTC	159714	GAGTTTCCATTACACCGAAT
150495	1134	AATTCGGTGTAATGGAAACT	159715	AGTTTCCATTACACCGAATT
150496	1135	CAATTCGGTGTAATGGAAAC	159716	GTTTCCATTACACCGAATTG
150497	1136	CCAATTCGGTGTAATGGAAA	159717	TTTCCATTACACCGAATTGG
150498	1137	GCCAATTCGGTGTAATGGAA	159718	TTCCATTACACCGAATTGGC
150499	1138	TGCCAATTCGGTGTAATGGA	159719	TCCATTACACCGAATTGGCA
150500	1139	GTGCCAATTCGGTGTAATGG	159720	CCATTACACCGAATTGGCAC
150501	1140	AGTGCCAATTCGGTGTAATG	159721	CATTACACCGAATTGGCACT
150502	1141	AAGTGCCAATTCGGTGTAAT	159722	ATTACACCGAATTGGCACTT
150503	1142	TAAGTGCCAATTCGGTGTAA	159723	TTACACCGAATTGGCACTTA
150504	1143	TTAAGTGCCAATTCGGTGTA	159724	TACACCGAATTGGCACTTAA
150505	1144	ATTAAGTGCCAATTCGGTGT	159725	ACACCGAATTGGCACTTAAT
150506	1145	TATTAAGTGCCAATTCGGTG	159726	CACCGAATTGGCACTTAATA
150507	1146	TTATTAAGTGCCAATTCGGT	159727	ACCGAATTGGCACTTAATAA
150508	1147	GTTATTAAGTGCCAATTCGG	159728	CCGAATTGGCACTTAATAAC
150509	1148	AGTTATTAAGTGCCAATTCG	159729	CGAATTGGCACTTAATAACT
150510	1149	CAGTTATTAAGTGCCAATTC	159730	GAATTGGCACTTAATAACTG
150511	1150	ACAGTTATTAAGTGCCAATT	159731	AATTGGCACTTAATAACTGT

150512	1151	AACAGTTATTAAGTGCCAAT	159732	ATTGGCACTTAATAACTGTT
150513	1152	CAACAGTTATTAAGTGCCAA	159733	TTGGCACTTAATAACTGTTG
150514	1153	ACAACAGTTATTAAGTGCCA	159734	TGGCACTTAATAACTGTTGT
150515	1154	GACAACAGTTATTAAGTGCC	159735	GGCACTTAATAACTGTTGTC
150516	1155	CGACAACAGTTATTAAGTGC	159736	GCACTTAATAACTGTTGTCG
150517	1156	CCGACAACAGTTATTAAGTG	159737	CACTTAATAACTGTTGTCGG
150518	1157	TCCGACAACAGTTATTAAGT	159738	ACTTAATAACTGTTGTCGGA
150519	1158	CTCCGACAACAGTTATTAAG	159739	CTTAATAACTGTTGTCGGAG
150520	1159	GCTCCGACAACAGTTATTAA	159740	TTAATAACTGTTGTCGGAGC
150521	1160	TGCTCCGACAACAGTTATTA	159741	TAATAACTGTTGTCGGAGCA
150522	1161	ATGCTCCGACAACAGTTATT	159742	AATAACTGTTGTCGGAGCAT
150523	1162	AATGCTCCGACAACAGTTAT	159743	ATAACTGTTGTCGGAGCATT
150524	1163	AAATGCTCCGACAACAGTTA	159744	TAACTGTTGTCGGAGCATTT
150525	1164	GAAATGCTCCGACAACAGTT	159745	AACTGTTGTCGGAGCATTTC
150526	1165	AGAAATGCTCCGACAACAGT	159746	ACTGTTGTCGGAGCATTTCT
150527	1166	AAGAAATGCTCCGACAACAG	159747	CTGTTGTCGGAGCATTTCTT
150528	1167	TAAGAAATGCTCCGACAACA	159748	TGTTGTCGGAGCATTTCTTA
150529	1168	TTAAGAAATGCTCCGACAAC	159749	GTTGTCGGAGCATTTCTTAA
150530	1169	CTTAAGAAATGCTCCGACAA	159750	TTGTCGGAGCATTTCTTAAG
150531	1170	GCTTAAGAAATGCTCCGACA	159751	TGTCGGAGCATTTCTTAAGC
150532	1171	GGCTTAAGAAATGCTCCGAC	159752	GTCGGAGCATTTCTTAAGCC
150533	1172	TGGCTTAAGAAATGCTCCGA	159753	TCGGAGCATTTCTTAAGCCA
150534	1173	GTGGCTTAAGAAATGCTCCG	159754	CGGAGCATTTCTTAAGCCAC
150535	1174	TGTGGCTTAAGAAATGCTCC	159755	GGAGCATTTCTTAAGCCACA
150536	1175	ATGTGGCTTAAGAAATGCTC	159756	GAGCATTTCTTAAGCCACAT
150537	1176	AATGTGGCTTAAGAAATGCT	159757	AGCATTTCTTAAGCCACATT
150538	1177	AAATGTGGCTTAAGAAATGC	159758	GCATTTCTTAAGCCACATTT
150539	1178	AAAATGTGGCTTAAGAAATG	159759	CATTTCTTAAGCCACATTTT
150540	1179	GAAAATGTGGCTTAAGAAAT	159760	ATTTCTTAAGCCACATTTTC
150541	1180	CGAAAATGTGGCTTAAGAAA	159761	TTTCTTAAGCCACATTTTCG
150542	1181	ACGAAAATGTGGCTTAAGAA	159762	TTCTTAAGCCACATTTTCGT
150543	1182	TACGAAAATGTGGCTTAAGA	159763	TCTTAAGCCACATTTTCGTA
150544	1183	TTACGAAAATGTGGCTTAAG	159764	CTTAAGCCACATTTTCGTAA
150545	1184	TTTACGAAAATGTGGCTTAA	159765	TTAAGCCACATTTTCGTAAA
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150547	1186	ACTTTACGAAAATGTGGCTT	159767	AAGCCACATTTTCGTAAAGT
150548	1187	CACTTTACGAAAATGTGGCT	159768	AGCCACATTTTCGTAAAGTG
150549	1188	CCACTTTACGAAAATGTGGC	159769	GCCACATTTTCGTAAAGTGG
150550	1189	GCCACTTTACGAAAATGTGG	159770	CCACATTTTCGTAAAGTGGC
150551	1190	AGCCACTTTACGAAAATGTG	159771	CACATTTTCGTAAAGTGGCT
150552	1191	AAGCCACTTTACGAAAATGT	159772	ACATTTTCGTAAAGTGGCTT
150553	1192	AAAGCCACTTTACGAAAATG	159773	CATTTTCGTAAAGTGGCTTT
150554	1193	TAAAGCCACTTTACGAAAAT	159774	ATTTTCGTAAAGTGGCTTTA
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150556	1195	TTTAAAGCCACTTTACGAAA	159776	TTTCGTAAAGTGGCTTTAAA
150557	1196	TTTTAAAGCCACTTTACGAA	159777	TTCGTAAAGTGGCTTTAAAA
150558	1197	ATTTTAAAGCCACTTTACGA	159778	TCGTAAAGTGGCTTTAAAAT
150559	1198	AATTTTAAAGCCACTTTACG	159779	CGTAAAGTGGCTTTAAAATT
150560	1199	CAATTTTAAAGCCACTTTAC	159780	GTAAAGTGGCTTTAAAATTG
150561	1200	GCAATTTTAAAGCCACTTTA	159781	TAAAGTGGCTTTAAAATTGC
150562	1201	AGCAATTTTAAAGCCACTTT	159782	AAAGTGGCTTTAAAATTGCT
150563	1202	GAGCAATTTTAAAGCCACTT	159783	AAGTGGCTTTAAAATTGCTC
150564	1203	AGAGCAATTTTAAAGCCACT	159784	AGTGGCTTTAAAATTGCTCT
150565	1204	CAGAGCAATTTTAAAGCCAC	159785	GTGGCTTTAAAATTGCTCTG
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150568	1207	TGGCAGAGCAATTTTAAAGC	159788	GCTTTAAAATTGCTCTGCCA
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150574	1213	GCCTACTGGCAGAGCAATTT	159794	AAATTGCTCTGCCAGTAGGC
150575	1214	TGCCTACTGGCAGAGCAATT	159795	AATTGCTCTGCCAGTAGGCA
150576	1215	CTGCCTACTGGCAGAGCAAT	159796	ATTGCTCTGCCAGTAGGCAG
150577	1216	CCTGCCTACTGGCAGAGCAA	159797	TTGCTCTGCCAGTAGGCAGG
150578	1217	ACCTGCCTACTGGCAGAGCA	159798	TGCTCTGCCAGTAGGCAGGT
150579	1218	AACCTGCCTACTGGCAGAGC	159799	GCTCTGCCAGTAGGCAGGTT
150580	1219	CAACCTGCCTACTGGCAGAG	159800	CTCTGCCAGTAGGCAGGTTG
150581	1220	GCAACCTGCCTACTGGCAGA	159801	TCTGCCAGTAGGCAGGTTGC
150582	1221	AGCAACCTGCCTACTGGCAG	159802	CTGCCAGTAGGCAGGTTGCT
150583	1222	TAGCAACCTGCCTACTGGCA	159803	TGCCAGTAGGCAGGTTGCTA

150584	1223	TTAGCAACCTGCCTACTGGC	159804	GCCAGTAGGCAGGTTGCTAA
150585	1224	CTTAGCAACCTGCCTACTGG	159805	CCAGTAGGCAGGTTGCTAAG
150586	1225	TCTTAGCAACCTGCCTACTG	159806	CAGTAGGCAGGTTGCTAAGA
150587	1226	ATCTTAGCAACCTGCCTACT	159807	AGTAGGCAGGTTGCTAAGAT
150588	1227	CATCTTAGCAACCTGCCTAC	159808	GTAGGCAGGTTGCTAAGATG
150589	1228	CCATCTTAGCAACCTGCCTA	159809	TAGGCAGGTTGCTAAGATGG
150590	1229	ACCATCTTAGCAACCTGCCT	159810	AGGCAGGTTGCTAAGATGGT
150591	1230	GACCATCTTAGCAACCTGCC	159811	GGCAGGTTGCTAAGATGGTC
150592	1231	TGACCATCTTAGCAACCTGC	159812	GCAGGTTGCTAAGATGGTCA
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150594	1233	TCTGACCATCTTAGCAACCT	159814	AGGTTGCTAAGATGGTCAGA
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150596	1235	TCTCTGACCATCTTAGCAAC	159816	GTTGCTAAGATGGTCAGAGA
150597	1236	GTCTCTGACCATCTTAGCAA	159817	TTGCTAAGATGGTCAGAGAC
150598	1237	TGTCTCTGACCATCTTAGCA	159818	TGCTAAGATGGTCAGAGACA
150599	1238	TTGTCTCTGACCATCTTAGC	159819	GCTAAGATGGTCAGAGACAA
150600	1239	TTTGTCTCTGACCATCTTAG	159820	CTAAGATGGTCAGAGACAAA
150601	1240	GTTTGTCTCTGACCATCTTA	159821	TAAGATGGTCAGAGACAAAC
150602	1241	AGTTTGTCTCTGACCATCTT	159822	AAGATGGTCAGAGACAAACT
150603	1242	AAGTTTGTCTCTGACCATCT	159823	AGATGGTCAGAGACAAACTT
150604	1243	GAAGTTTGTCTCTGACCATC	159824	GATGGTCAGAGACAAACTTC
150605	1244	AGAAGTTTGTCTCTGACCAT	159825	ATGGTCAGAGACAAACTTCT
150606	1245	CAGAAGTTTGTCTCTGACCA	159826	TGGTCAGAGACAAACTTCTG
150607	1246	TCAGAAGTTTGTCTCTGACC	159827	GGTCAGAGACAAACTTCTGA
150608	1247	TTCAGAAGTTTGTCTCTGAC	159828	GTCAGAGACAAACTTCTGAA
150609	1248	GTTCAGAAGTTTGTCTCTGA	159829	TCAGAGACAAACTTCTGAAC
150610	1249	CGTTCAGAAGTTTGTCTCTG	159830	CAGAGACAAACTTCTGAACG
150611	1250	TCGTTCAGAAGTTTGTCTCT	159831	AGAGACAAACTTCTGAACGA
150612	1251	GTCGTTCAGAAGTTTGTCTC	159832	GAGACAAACTTCTGAACGAC
150613	1252	AGTCGTTCAGAAGTTTGTCT	159833	AGACAAACTTCTGAACGACT
150614	1253	GAGTCGTTCAGAAGTTTGTC	159834	GACAAACTTCTGAACGACTC
150615	1254	AGAGTCGTTCAGAAGTTTGT	159835	ACAAACTTCTGAACGACTCT
150616	1255	AAGAGTCGTTCAGAAGTTTG	159836	CAAACTTCTGAACGACTCTT
150617	1256	CAAGAGTCGTTCAGAAGTTT	159837	AAACTTCTGAACGACTCTTG
150618	1257	ACAAGAGTCGTTCAGAAGTT	159838	AACTTCTGAACGACTCTTGT
150619	1258	TACAAGAGTCGTTCAGAAGT	159839	ACTTCTGAACGACTCTTGTA
150620	1259	TTACAAGAGTCGTTCAGAAG	159840	CTTCTGAACGACTCTTGTAA
150621	1260	TTTACAAGAGTCGTTCAGAA	159841	TTCTGAACGACTCTTGTAAA
150622	1261	TTTTACAAGAGTCGTTCAGA	159842	TCTGAACGACTCTTGTAAAA
150623	1262	ATTTTACAAGAGTCGTTCAG	159843	CTGAACGACTCTTGTAAAAT
150624	1263	TATTTTACAAGAGTCGTTCA	159844	TGAACGACTCTTGTAAAATA
150625	1264	ATATTTTACAAGAGTCGTTC	159845	GAACGACTCTTGTAAAATAT
150626	1265	TATATTTTACAAGAGTCGTT	159846	AACGACTCTTGTAAAATATA
150627	1266	GTATATTTTACAAGAGTCGT	159847	ACGACTCTTGTAAAATATAC
150628	1267	TGTATATTTTACAAGAGTCG	159848	CGACTCTTGTAAAATATACA
150629	1268	CTGTATATTTTACAAGAGTC	159849	GACTCTTGTAAAATATACAG
150630	1269	TCTGTATATTTTACAAGAGT	159850	ACTCTTGTAAAATATACAGA
150631	1270	TTCTGTATATTTTACAAGAG	159851	CTCTTGTAAAATATACAGAA
150632	1271	TTTCTGTATATTTTACAAGA	159852	TCTTGTAAAATATACAGAAA
150633	1272	ATTTCTGTATATTTTACAAG	159853	CTTGTAAAATATACAGAAAT
150634	1273	TATTTCTGTATATTTTACAA	159854	TTGTAAAATATACAGAAATA
150635	1274	ATATTTCTGTATATTTTACA	159855	TGTAAAATATACAGAAATAT
150636	1275	AATATTTCTGTATATTTTAC	159856	GTAAAATATACAGAAATATT
150637	1276	AAATATTTCTGTATATTTTA	159857	TAAAATATACAGAAATATTT
150638	1277	AAAATATTTCTGTATATTTT	159858	AAAATATACAGAAATATTTT
150639	1278	GAAAATATTTCTGTATATTT	159859	AAATATACAGAAATATTTTC
150640	1279	TGAAAATATTTCTGTATATT	159860	AATATACAGAAATATTTTCA
150641	1280	CTGAAAATATTTCTGTATAT	159861	ATATACAGAAATATTTTCAG
150642	1281	TCTGAAAATATTTCTGTATA	159862	TATACAGAAATATTTTCAGA
150643	1282	TTCTGAAAATATTTCTGTAT	159863	ATACAGAAATATTTTCAGAA
150644	1283	GTTCTGAAAATATTTCTGTA	159864	TACAGAAATATTTTCAGAAC
150645	1284	AGTTCTGAAAATATTTCTGT	159865	ACAGAAATATTTTCAGAACT
150646	1285	AAGTTCTGAAAATATTTCTG	159866	CAGAAATATTTTCAGAACTT
150647	1286	AAAGTTCTGAAAATATTTCT	159867	AGAAATATTTTCAGAACTTT
150648	1287	AAAAGTTCTGAAAATATTTC	159868	GAAATATTTTCAGAACTTTT
150649	1288	TAAAAGTTCTGAAAATATTT	159869	AAATATTTTCAGAACTTTTA
150650	1289	ATAAAAGTTCTGAAAATATT	159870	AATATTTTCAGAACTTTTAT
150651	1290	GATAAAAGTTCTGAAAATAT	159871	ATATTTTCAGAACTTTTATC
150652	1291	TGATAAAAGTTCTGAAAATA	159872	TATTTTCAGAACTTTTATCA
150653	1292	CTGATAAAAGTTCTGAAAAT	159873	ATTTTCAGAACTTTTATCAG
150654	1293	ACTGATAAAAGTTCTGAAAA	159874	TTTTCAGAACTTTTATCAGT
150655	1294	TACTGATAAAAGTTCTGAAA	159875	TTTCAGAACTTTTATCAGTA

150656	1295	TTACTGATAAAAGTTCTGAA	159876	TTCAGAACTTTTATCAGTAA
150657	1296	TTTACTGATAAAAGTTCTGA	159877	TCAGAACTTTTATCAGTAAA
150658	1297	TTTTACTGATAAAAGTTCTG	159878	CAGAACTTTTATCAGTAAAA
150659	1298	ATTTTACTGATAAAAGTTCT	159879	AGAACTTTTATCAGTAAAAT
150660	1299	AATTTTACTGATAAAAGTTC	159880	GAACTTTTATCAGTAAAATT
150661	1300	TAATTTTACTGATAAAAGTT	159881	AACTTTTATCAGTAAAATTA
150662	1301	GTAATTTTACTGATAAAAGT	159882	ACTTTTATCAGTAAAATTAC
150663	1302	TGTAATTTTACTGATAAAAG	159883	CTTTTATCAGTAAAATTACA
150664	1303	TTGTAATTTTACTGATAAAA	159884	TTTTATCAGTAAAATTACAA
150665	1304	TTTGTAATTTTACTGATAAA	159885	TTTATCAGTAAAATTACAAA
150666	1305	TTTTGTAATTTTACTGATAA	159886	TTATCAGTAAAATTACAAAA
150667	1306	GTTTTGTAATTTTACTGATA	159887	TATCAGTAAAATTACAAAAC
150668	1307	CGTTTTGTAATTTTACTGAT	159888	ATCAGTAAAATTACAAAACG
150669	1308	ACGTTTTGTAATTTTACTGA	159889	TCAGTAAAATTACAAAACGT
150670	1309	CACGTTTTGTAATTTTACTG	159890	CAGTAAAATTACAAAACGTG
150671	1310	ACACGTTTTGTAATTTTACT	159891	AGTAAAATTACAAAACGTGT
150672	1311	AACACGTTTTGTAATTTTAC	159892	GTAAAATTACAAAACGTGTT
150673	1312	CAACACGTTTTGTAATTTTA	159893	TAAAATTACAAAACGTGTTG
150674	1313	GCAACACGTTTTGTAATTTT	159894	AAAATTACAAAACGTGTTGC
150675	1314	TGCAACACGTTTTGTAATTT	159895	AAATTACAAAACGTGTTGCA
150676	1315	TTGCAACACGTTTTGTAATT	159896	AATTACAAAACGTGTTGCAA
150677	1316	CTTGCAACACGTTTTGTAAT	159897	ATTACAAAACGTGTTGCAAG
150678	1317	CCTTGCAACACGTTTTGTAA	159898	TTACAAAACGTGTTGCAAGG
150679	1318	TCCTTGCAACACGTTTTGTA	159899	TACAAAACGTGTTGCAAGGA
150680	1319	TTCCTTGCAACACGTTTTGT	159900	ACAAAACGTGTTGCAAGGAA
150681	1320	CTTCCTTGCAACACGTTTTG	159901	CAAAACGTGTTGCAAGGAAG
150682	1321	CCTTCCTTGCAACACGTTTT	159902	AAAACGTGTTGCAAGGAAGG
150683	1322	ACCTTCCTTGCAACACGTTT	159903	AAACGTGTTGCAAGGAAGGT
150684	1323	CACCTTCCTTGCAACACGTT	159904	AACGTGTTGCAAGGAAGGTG
150685	1324	GCACCTTCCTTGCAACACGT	159905	ACGTGTTGCAAGGAAGGTGC
150686	1325	AGCACCTTCCTTGCAACACG	159906	CGTGTTGCAAGGAAGGTGCT
150687	1326	AAGCACCTTCCTTGCAACAC	159907	GTGTTGCAAGGAAGGTGCTT
150688	1327	CAAGCACCTTCCTTGCAACA	159908	TGTTGCAAGGAAGGTGCTTG
150689	1328	ACAAGCACCTTCCTTGCAAC	159909	GTTGCAAGGAAGGTGCTTGT
150690	1329	CACAAGCACCTTCCTTGCAA	159910	TTGCAAGGAAGGTGCTTGTG
150691	1330	TCACAAGCACCTTCCTTGCA	159911	TGCAAGGAAGGTGCTTGTGA
150692	1331	ATCACAAGCACCTTCCTTGC	159912	GCAAGGAAGGTGCTTGTGAT
150693	1332	TATCACAAGCACCTTCCTTG	159913	CAAGGAAGGTGCTTGTGATA
150694	1333	TTATCACAAGCACCTTCCTT	159914	AAGGAAGGTGCTTGTGATAA
150695	1334	GTTATCACAAGCACCTTCCT	159915	AGGAAGGTGCTTGTGATAAC
150696	1335	TGTTATCACAAGCACCTTCC	159916	GGAAGGTGCTTGTGATAACA
150697	1336	GTGTTATCACAAGCACCTTC	159917	GAAGGTGCTTGTGATAACAC
150698	1337	AGTGTTATCACAAGCACCTT	159918	AAGGTGCTTGTGATAACACT
150699	1338	CAGTGTTATCACAAGCACCT	159919	AGGTGCTTGTGATAACACTG
150700	1339	ACAGTGTTATCACAAGCACC	159920	GGTGCTTGTGATAACACTGT
150701	1340	GACAGTGTTATCACAAGCAC	159921	GTGCTTGTGATAACACTGTC
150702	1341	GGACAGTGTTATCACAAGCA	159922	TGCTTGTGATAACACTGTCC
150703	1342	GGGACAGTGTTATCACAAGC	159923	GCTTGTGATAACACTGTCCC
150704	1343	GGGGACAGTGTTATCACAAG	159924	CTTGTGATAACACTGTCCCC
150705	1344	TGGGGACAGTGTTATCACAA	159925	TTGTGATAACACTGTCCCCA
150706	1345	CTGGGGACAGTGTTATCACA	159926	TGTGATAACACTGTCCCCAG
150707	1346	TCTGGGGACAGTGTTATCAC	159927	GTGATAACACTGTCCCCAGA
150708	1347	TTCTGGGGACAGTGTTATCA	159928	TGATAACACTGTCCCCAGAA
150709	1348	GTTCTGGGGACAGTGTTATC	159929	GATAACACTGTCCCCAGAAC
150710	1349	GGTTCTGGGGACAGTGTTAT	159930	ATAACACTGTCCCCAGAACC
150711	1350	AGGTTCTGGGGACAGTGTTA	159931	TAACACTGTCCCCAGAACCT
150712	1351	AAGGTTCTGGGGACAGTGTT	159932	AACACTGTCCCCAGAACCTT
150713	1352	TAAGGTTCTGGGGACAGTGT	159933	ACACTGTCCCCAGAACCTTA
150714	1353	CTAAGGTTCTGGGGACAGTG	159934	CACTGTCCCCAGAACCTTAG
150715	1354	ACTAAGGTTCTGGGGACAGT	159935	ACTGTCCCCAGAACCTTAGT
150716	1355	CACTAAGGTTCTGGGGACAG	159936	CTGTCCCCAGAACCTTAGTG
150717	1356	TCACTAAGGTTCTGGGGACA	159937	TGTCCCCAGAACCTTAGTGA
150718	1357	TTCACTAAGGTTCTGGGGAC	159938	GTCCCCAGAACCTTAGTGAA
150719	1358	CTTCACTAAGGTTCTGGGGA	159939	TCCCCAGAACCTTAGTGAAG
150720	1359	ACTTCACTAAGGTTCTGGGG	159940	CCCCAGAACCTTAGTGAAGT
150721	1360	AACTTCACTAAGGTTCTGGG	159941	CCCAGAACCTTAGTGAAGTT
150722	1361	TAACTTCACTAAGGTTCTGG	159942	CCAGAACCTTAGTGAAGTTA
150723	1362	GTAACTTCACTAAGGTTCTG	159943	CAGAACCTTAGTGAAGTTAC
150724	1363	GGTAACTTCACTAAGGTTCT	159944	AGAACCTTAGTGAAGTTACC
150725	1364	TGGTAACTTCACTAAGGTTC	159945	GAACCTTAGTGAAGTTACCA
150726	1365	TTGGTAACTTCACTAAGGTT	159946	AACCTTAGTGAAGTTACCAA
150727	1366	GTTGGTAACTTCACTAAGGT	159947	ACCTTAGTGAAGTTACCAAC

150728	1367	AGTTGGTAACTTCACTAAGG	159948	CCTTAGTGAAGTTACCAACT
150729	1368	CAGTTGGTAACTTCACTAAG	159949	CTTAGTGAAGTTACCAACTG
150730	1369	CCAGTTGGTAACTTCACTAA	159950	TTAGTGAAGTTACCAACTGG
150731	1370	ACCAGTTGGTAACTTCACTA	159951	TAGTGAAGTTACCAACTGGT
150732	1371	CACCAGTTGGTAACTTCACT	159952	AGTGAAGTTACCAACTGGTG
150733	1372	CCACCAGTTGGTAACTTCAC	159953	GTGAAGTTACCAACTGGTGG
150734	1373	TCCACCAGTTGGTAACTTCA	159954	TGAAGTTACCAACTGGTGGA
150735	1374	TTCCACCAGTTGGTAACTTC	159955	GAAGTTACCAACTGGTGGAA
150736	1375	TTTCCACCAGTTGGTAACTT	159956	AAGTTACCAACTGGTGGAAA
150737	1376	TTTTCCACCAGTTGGTAACT	159957	AGTTACCAACTGGTGGAAAA
150738	1377	ATTTTCCACCAGTTGGTAAC	159958	GTTACCAACTGGTGGAAAAT
150739	1378	AATTTTCCACCAGTTGGTAA	159959	TTACCAACTGGTGGAAAATT
150740	1379	AAATTTTCCACCAGTTGGTA	159960	TACCAACTGGTGGAAAATTT
150741	1380	AAAATTTTCCACCAGTTGGT	159961	ACCAACTGGTGGAAAATTTT
150742	1381	GAAAATTTTCCACCAGTTGG	159962	CCAACTGGTGGAAAATTTTC
150743	1382	AGAAAATTTTCCACCAGTTG	159963	CAACTGGTGGAAAATTTTCT
150744	1383	GAGAAAATTTTCCACCAGTT	159964	AACTGGTGGAAAATTTTCTC
150745	1384	AGAGAAAATTTTCCACCAGT	159965	ACTGGTGGAAAATTTTCTCT
150746	1385	AAGAGAAAATTTTCCACCAG	159966	CTGGTGGAAAATTTTCTCTT
150747	1386	CAAGAGAAAATTTTCCACCA	159967	TGGTGGAAAATTTTCTCTTG
150748	1387	GCAAGAGAAAATTTTCCACC	159968	GGTGGAAAATTTTCTCTTGC
150749	1388	TGCAAGAGAAAATTTTCCAC	159969	GTGGAAAATTTTCTCTTGCA
150750	1389	GTGCAAGAGAAAATTTTCCA	159970	TGGAAAATTTTCTCTTGCAC
150751	1390	AGTGCAAGAGAAAATTTTCC	159971	GGAAAATTTTCTCTTGCACT
150752	1391	GAGTGCAAGAGAAAATTTTC	159972	GAAAATTTTCTCTTGCACTC
150753	1392	CGAGTGCAAGAGAAAATTTT	159973	AAAATTTTCTCTTGCACTCG
150754	1393	CCGAGTGCAAGAGAAAATTT	159974	AAATTTTCTCTTGCACTCGG
150755	1394	GCCGAGTGCAAGAGAAAATT	159975	AATTTTCTCTTGCACTCGGC
150756	1395	AGCCGAGTGCAAGAGAAAAT	159976	ATTTTCTCTTGCACTCGGCT
150757	1396	AAGCCGAGTGCAAGAGAAAA	159977	TTTTCTCTTGCACTCGGCTT
150758	1397	TAAGCCGAGTGCAAGAGAAA	159978	TTTCTCTTGCACTCGGCTTA
150759	1398	TTAAGCCGAGTGCAAGAGAA	159979	TTCTCTTGCACTCGGCTTAA
150760	1399	TTTAAGCCGAGTGCAAGAGA	159980	TCTCTTGCACTCGGCTTAAA
150761	1400	TTTTAAGCCGAGTGCAAGAG	159981	CTCTTGCACTCGGCTTAAAA
150762	1401	TTTTTAAGCCGAGTGCAAGA	159982	TCTTGCACTCGGCTTAAAAA
150763	1402	ATTTTTAAGCCGAGTGCAAG	159983	CTTGCACTCGGCTTAAAAAT
150764	1403	GATTTTTAAGCCGAGTGCAA	159984	TTGCACTCGGCTTAAAAATC
150765	1404	TGATTTTTAAGCCGAGTGCA	159985	TGCACTCGGCTTAAAAATCA
150766	1405	ATGATTTTTAAGCCGAGTGC	159986	GCACTCGGCTTAAAAATCAT
150767	1406	CATGATTTTTAAGCCGAGTG	159987	CACTCGGCTTAAAAATCATG
150768	1407	TCATGATTTTTAAGCCGAGT	159988	ACTCGGCTTAAAAATCATGA
150769	1408	CTCATGATTTTTAAGCCGAG	159989	CTCGGCTTAAAAATCATGAG
150770	1409	CCTCATGATTTTTAAGCCGA	159990	TCGGCTTAAAAATCATGAGG
150771	1410	CCCTCATGATTTTTAAGCCG	159991	CGGCTTAAAAATCATGAGGG
150772	1411	TCCCTCATGATTTTTAAGCC	159992	GGCTTAAAAATCATGAGGGA
150773	1412	TTCCCTCATGATTTTTAAGC	159993	GCTTAAAAATCATGAGGGAA
150774	1413	ATTCCCTCATGATTTTTAAG	159994	CTTAAAAATCATGAGGGAAT
150775	1414	TATTCCCTCATGATTTTTAA	159995	TTAAAAATCATGAGGGAATA
150776	1415	ATATTCCCTCATGATTTTTA	159996	TAAAAATCATGAGGGAATAT
150777	1416	AATATTCCCTCATGATTTTT	159997	AAAAATCATGAGGGAATATT
150778	1417	AAATATTCCCTCATGATTTT	159998	AAAATCATGAGGGAATATTT
150779	1418	TAAATATTCCCTCATGATTT	159999	AAATCATGAGGGAATATTTA
150780	1419	GTAAATATTCCCTCATGATT	160000	AATCATGAGGGAATATTTAC
150781	1420	AGTAAATATTCCCTCATGAT	160001	ATCATGAGGGAATATTTACT
150782	1421	TAGTAAATATTCCCTCATGA	160002	TCATGAGGGAATATTTACTA
150783	1422	ATAGTAAATATTCCCTCATG	160003	CATGAGGGAATATTTACTAT
150784	1423	TATAGTAAATATTCCCTCAT	160004	ATGAGGGAATATTTACTATA
150785	1424	GTATAGTAAATATTCCCTCA	160005	TGAGGGAATATTTACTATAC
150786	1425	CGTATAGTAAATATTCCCTC	160006	GAGGGAATATTTACTATACG
150787	1426	TCGTATAGTAAATATTCCCT	160007	AGGGAATATTTACTATACGA
150788	1427	TTCGTATAGTAAATATTCCC	160008	GGGAATATTTACTATACGAA
150789	1428	ATTCGTATAGTAAATATTCC	160009	GGAATATTTACTATACGAAT
150790	1429	CATTCGTATAGTAAATATTC	160010	GAATATTTACTATACGAATG
150791	1430	TCATTCGTATAGTAAATATT	160011	AATATTTACTATACGAATGA
150792	1431	CTCATTCGTATAGTAAATAT	160012	ATATTTACTATACGAATGAG
150793	1432	TCTCATTCGTATAGTAAATA	160013	TATTTACTATACGAATGAGA
150794	1433	ATCTCATTCGTATAGTAAAT	160014	ATTTACTATACGAATGAGAT
150795	1434	AATCTCATTCGTATAGTAAA	160015	TTTACTATACGAATGAGATT
150796	1435	GAATCTCATTCGTATAGTAA	160016	TTACTATACGAATGAGATTC
150797	1436	TGAATCTCATTCGTATAGTA	160017	TACTATACGAATGAGATTCA
150798	1437	CTGAATCTCATTCGTATAGT	160018	ACTATACGAATGAGATTCAG
150799	1438	ACTGAATCTCATTCGTATAG	160019	CTATACGAATGAGATTCAGT

150800	1439	GACTGAATCTCATTCGTATA	160020	TATACGAATGAGATTCAGTC
150801	1440	AGACTGAATCTCATTCGTAT	160021	ATACGAATGAGATTCAGTCT
150802	1441	AAGACTGAATCTCATTCGTA	160022	TACGAATGAGATTCAGTCTT
150803	1442	AAAGACTGAATCTCATTCGT	160023	ACGAATGAGATTCAGTCTTT
150804	1443	TAAAGACTGAATCTCATTCG	160024	CGAATGAGATTCAGTCTTTA
150805	1444	TTAAAGACTGAATCTCATTC	160025	GAATGAGATTCAGTCTTTAA
150806	1445	TTTAAAGACTGAATCTCATT	160026	AATGAGATTCAGTCTTTAAA
150807	1446	CTTTAAAGACTGAATCTCAT	160027	ATGAGATTCAGTCTTTAAAG
150808	1447	CCTTTAAAGACTGAATCTCA	160028	TGAGATTCAGTCTTTAAAGG
150809	1448	CCCTTTAAAGACTGAATCTC	160029	GAGATTCAGTCTTTAAAGGG
150810	1449	CCCCTTTAAAGACTGAATCT	160030	AGATTCAGTCTTTAAAGGGG
150811	1450	ACCCCTTTAAAGACTGAATC	160031	GATTCAGTCTTTAAAGGGGT
150812	1451	AACCCCTTTAAAGACTGAAT	160032	ATTCAGTCTTTAAAGGGGTT
150813	1452	AAACCCCTTTAAAGACTGAA	160033	TTCAGTCTTTAAAGGGGTTT
150814	1453	TAAACCCCTTTAAAGACTGA	160034	TCAGTCTTTAAAGGGGTTTA
150815	1454	GTAAACCCCTTTAAAGACTG	160035	CAGTCTTTAAAGGGGTTTAC
150816	1455	TGTAAACCCCTTTAAAGACT	160036	AGTCTTTAAAGGGGTTTACA
150817	1456	CTGTAAACCCCTTTAAAGAC	160037	GTCTTTAAAGGGGTTTACAG
150818	1457	TCTGTAAACCCCTTTAAAGA	160038	TCTTTAAAGGGGTTTACAGA
150819	1458	TTCTGTAAACCCCTTTAAAG	160039	CTTTAAAGGGGTTTACAGAA
150820	1459	TTTCTGTAAACCCCTTTAAA	160040	TTTAAAGGGGTTTACAGAAA
150821	1460	GTTTCTGTAAACCCCTTTAA	160041	TTAAAGGGGTTTACAGAAAC
150822	1461	CGTTTCTGTAAACCCCTTTA	160042	TAAAGGGGTTTACAGAAACG
150823	1462	ACGTTTCTGTAAACCCCTTT	160043	AAAGGGGTTTACAGAAACGT
150824	1463	CACGTTTCTGTAAACCCCTT	160044	AAGGGGTTTACAGAAACGTG
150825	1464	TCACGTTTCTGTAAACCCCT	160045	AGGGGTTTACAGAAACGTGA
150826	1465	CTCACGTTTCTGTAAACCCC	160046	GGGGTTTACAGAAACGTGAG
150827	1466	TCTCACGTTTCTGTAAACCC	160047	GGGTTTACAGAAACGTGAGA
150828	1467	CTCTCACGTTTCTGTAAACC	160048	GGTTTACAGAAACGTGAGAG
150829	1468	CCTCTCACGTTTCTGTAAAC	160049	GTTTACAGAAACGTGAGAGG
150830	1469	TCCTCTCACGTTTCTGTAAA	160050	TTTACAGAAACGTGAGAGGA
150831	1470	GTCCTCTCACGTTTCTGTAA	160051	TTACAGAAACGTGAGAGGAC
150832	1471	TGTCCTCTCACGTTTCTGTA	160052	TACAGAAACGTGAGAGGACA
150833	1472	CTGTCCTCTCACGTTTCTGT	160053	ACAGAAACGTGAGAGGACAG
150834	1473	CCTGTCCTCTCACGTTTCTG	160054	CAGAAACGTGAGAGGACAGG
150835	1474	TCCTGTCCTCTCACGTTTCT	160055	AGAAACGTGAGAGGACAGGA
150836	1475	TTCCTGTCCTCTCACGTTTC	160056	GAAACGTGAGAGGACAGGAA
150837	1476	GTTCCTGTCCTCTCACGTTT	160057	AAACGTGAGAGGACAGGAAC
150838	1477	TGTTCCTGTCCTCTCACGTT	160058	AACGTGAGAGGACAGGAACA
150839	1478	CTGTTCCTGTCCTCTCACGT	160059	ACGTGAGAGGACAGGAACAG
150840	1479	ACTGTTCCTGTCCTCTCACG	160060	CGTGAGAGGACAGGAACAGT
150841	1480	AACTGTTCCTGTCCTCTCAC	160061	GTGAGAGGACAGGAACAGTT
150842	1481	TAACTGTTCCTGTCCTCTCA	160062	TGAGAGGACAGGAACAGTTA
150843	1482	CTAACTGTTCCTGTCCTCTC	160063	GAGAGGACAGGAACAGTTAG
150844	1483	ACTAACTGTTCCTGTCCTCT	160064	AGAGGACAGGAACAGTTAGT
150845	1484	GACTAACTGTTCCTGTCCTC	160065	GAGGACAGGAACAGTTAGTC
150846	1485	AGACTAACTGTTCCTGTCCT	160066	AGGACAGGAACAGTTAGTCT
150847	1486	CAGACTAACTGTTCCTGTCC	160067	GGACAGGAACAGTTAGTCTG
150848	1487	ACAGACTAACTGTTCCTGTC	160068	GACAGGAACAGTTAGTCTGT
150849	1488	CACAGACTAACTGTTCCTGT	160069	ACAGGAACAGTTAGTCTGTG
150850	1489	ACACAGACTAACTGTTCCTG	160070	CAGGAACAGTTAGTCTGTGT
150851	1490	TACACAGACTAACTGTTCCT	160071	AGGAACAGTTAGTCTGTGTA
150852	1491	TTACACAGACTAACTGTTCC	160072	GGAACAGTTAGTCTGTGTAA
150853	1492	TTTACACAGACTAACTGTTC	160073	GAACAGTTAGTCTGTGTAAA
150854	1493	ATTTACACAGACTAACTGTT	160074	AACAGTTAGTCTGTGTAAAT
150855	1494	CATTTACACAGACTAACTGT	160075	ACAGTTAGTCTGTGTAAATG
150856	1495	ACATTTACACAGACTAACTG	160076	CAGTTAGTCTGTGTAAATGT
150857	1496	GACATTTACACAGACTAACT	160077	AGTTAGTCTGTGTAAATGTC
150858	1497	AGACATTTACACAGACTAAC	160078	GTTAGTCTGTGTAAATGTCT
150859	1498	CAGACATTTACACAGACTAA	160079	TTAGTCTGTGTAAATGTCTG
150860	1499	TCAGACATTTACACAGACTA	160080	TAGTCTGTGTAAATGTCTGA
150861	1500	TTCAGACATTTACACAGACT	160081	AGTCTGTGTAAATGTCTGAA
150862	1501	TTTCAGACATTTACACAGAC	160082	GTCTGTGTAAATGTCTGAAA
150863	1502	ATTTCAGACATTTACACAGA	160083	TCTGTGTAAATGTCTGAAAT
150864	1503	TATTTCAGACATTTACACAG	160084	CTGTGTAAATGTCTGAAATA
150865	1504	ATATTTCAGACATTTACACA	160085	TGTGTAAATGTCTGAAATAT
150866	1505	TATATTTCAGACATTTACAC	160086	GTGTAAATGTCTGAAATATA
150867	1506	ATATATTTCAGACATTTACA	160087	TGTAAATGTCTGAAATATAT
150868	1507	CATATATTTCAGACATTTAC	160088	GTAAATGTCTGAAATATATG
150869	1508	ACATATATTTCAGACATTTA	160089	TAAATGTCTGAAATATATGT
150870	1509	CACATATATTTCAGACATTT	160090	AAATGTCTGAAATATATGTG
150871	1510	TCACATATATTTCAGACATT	160091	AATGTCTGAAATATATGTGA

150872	1511	CTCACATATATTTCAGACAT	160092	ATGTCTGAAATATATGTGAG
150873	1512	CCTCACATATATTTCAGACA	160093	TGTCTGAAATATATGTGAGG
150874	1513	CCCTCACATATATTTCAGAC	160094	GTCTGAAATATATGTGAGGG
150875	1514	TCCCTCACATATATTTCAGA	160095	TCTGAAATATATGTGAGGGA
150876	1515	CTCCCTCACATATATTTCAG	160096	CTGAAATATATGTGAGGGAG
150877	1516	TCTCCCTCACATATATTTCA	160097	TGAAATATATGTGAGGGAGA
150878	1517	ATCTCCCTCACATATATTTC	160098	GAAATATATGTGAGGGAGAT
150879	1518	TATCTCCCTCACATATATTT	160099	AAATATATGTGAGGGAGATA
150880	1519	TTATCTCCCTCACATATATT	160100	AATATATGTGAGGGAGATAA
150881	1520	ATTATCTCCCTCACATATAT	160101	ATATATGTGAGGGAGATAAT
150882	1521	CATTATCTCCCTCACATATA	160102	TATATGTGAGGGAGATAATG
150883	1522	TCATTATCTCCCTCACATAT	160103	ATATGTGAGGGAGATAATGA
150884	1523	CTCATTATCTCCCTCACATA	160104	TATGTGAGGGAGATAATGAG
150885	1524	ACTCATTATCTCCCTCACAT	160105	ATGTGAGGGAGATAATGAGT
150886	1525	AACTCATTATCTCCCTCACA	160106	TGTGAGGGAGATAATGAGTT
150887	1526	AAACTCATTATCTCCCTCAC	160107	GTGAGGGAGATAATGAGTTT
150888	1527	TAAACTCATTATCTCCCTCA	160108	TGAGGGAGATAATGAGTTTA
150889	1528	CTAAACTCATTATCTCCCTC	160109	GAGGGAGATAATGAGTTTAG
150890	1529	GCTAAACTCATTATCTCCCT	160110	AGGGAGATAATGAGTTTAGC
150891	1530	GGCTAAACTCATTATCTCCC	160111	GGGAGATAATGAGTTTAGCC
150892	1531	AGGCTAAACTCATTATCTCC	160112	GGAGATAATGAGTTTAGCCT
150893	1532	AAGGCTAAACTCATTATCTC	160113	GAGATAATGAGTTTAGCCTT
150894	1533	AAAGGCTAAACTCATTATCT	160114	AGATAATGAGTTTAGCCTTT
150895	1534	AAAAGGCTAAACTCATTATC	160115	GATAATGAGTTTAGCCTTTT
150896	1535	AAAAAGGCTAAACTCATTAT	160116	ATAATGAGTTTAGCCTTTTT
150897	1536	GAAAAAGGCTAAACTCATTA	160117	TAATGAGTTTAGCCTTTTTC
150898	1537	AGAAAAAGGCTAAACTCATT	160118	AATGAGTTTAGCCTTTTTCT
150899	1538	AAGAAAAAGGCTAAACTCAT	160119	ATGAGTTTAGCCTTTTTCTT
150900	1539	AAAGAAAAAGGCTAAACTCA	160120	TGAGTTTAGCCTTTTTCTTT
150901	1540	TAAAGAAAAAGGCTAAACTC	160121	GAGTTTAGCCTTTTTCTTTA
150902	1541	TTAAAGAAAAAGGCTAAACT	160122	AGTTTAGCCTTTTTCTTTAA
150903	1542	ATTAAAGAAAAAGGCTAAAC	160123	GTTTAGCCTTTTTCTTTAAT
150904	1543	TATTAAAGAAAAAGGCTAAA	160124	TTTAGCCTTTTTCTTTAATA
150905	1544	CTATTAAAGAAAAAGGCTAA	160125	TTAGCCTTTTTCTTTAATAG
150906	1545	CCTATTAAAGAAAAAGGCTA	160126	TAGCCTTTTTCTTTAATAGG
150907	1546	ACCTATTAAAGAAAAAGGCT	160127	AGCCTTTTTCTTTAATAGGT
150908	1547	GACCTATTAAAGAAAAAGGC	160128	GCCTTTTTCTTTAATAGGTC
150909	1548	AGACCTATTAAAGAAAAAGG	160129	CCTTTTTCTTTAATAGGTCT
150910	1549	GAGACCTATTAAAGAAAAAG	160130	CTTTTTCTTTAATAGGTCTC
150911	1550	GGAGACCTATTAAAGAAAAA	160131	TTTTTCTTTAATAGGTCTCC
150912	1551	TGGAGACCTATTAAAGAAAA	160132	TTTTCTTTAATAGGTCTCCA
150913	1552	CTGGAGACCTATTAAAGAAA	160133	TTTCTTTAATAGGTCTCCAG
150914	1553	TCTGGAGACCTATTAAAGAA	160134	TTCTTTAATAGGTCTCCAGA
150915	1554	ATCTGGAGACCTATTAAAGA	160135	TCTTTAATAGGTCTCCAGAT
150916	1555	AATCTGGAGACCTATTAAAG	160136	CTTTAATAGGTCTCCAGATT
150917	1556	AAATCTGGAGACCTATTAAA	160137	TTTAATAGGTCTCCAGATTT
150918	1557	AAAATCTGGAGACCTATTAA	160138	TTAATAGGTCTCCAGATTTT
150919	1558	GAAAATCTGGAGACCTATTA	160139	TAATAGGTCTCCAGATTTTC
150920	1559	AGAAAATCTGGAGACCTATT	160140	AATAGGTCTCCAGATTTTCT
150921	1560	CAGAAAATCTGGAGACCTAT	160141	ATAGGTCTCCAGATTTTCTG
150922	1561	CCAGAAAATCTGGAGACCTA	160142	TAGGTCTCCAGATTTTCTGG
150923	1562	TCCAGAAAATCTGGAGACCT	160143	AGGTCTCCAGATTTTCTGGA
150924	1563	TTCCAGAAAATCTGGAGACC	160144	GGTCTCCAGATTTTCTGGAA
150925	1564	TTTCCAGAAAATCTGGAGAC	160145	GTCTCCAGATTTTCTGGAAA
150926	1565	TTTTCCAGAAAATCTGGAGA	160146	TCTCCAGATTTTCTGGAAAA
150927	1566	CTTTTCCAGAAAATCTGGAG	160147	CTCCAGATTTTCTGGAAAAG
150928	1567	CCTTTTCCAGAAAATCTGGA	160148	TCCAGATTTTCTGGAAAAGG
150929	1568	ACCTTTTCCAGAAAATCTGG	160149	CCAGATTTTCTGGAAAAGGT
150930	1569	AACCTTTTCCAGAAAATCTG	160150	CAGATTTTCTGGAAAAGGTT
150931	1570	GAACCTTTTCCAGAAAATCT	160151	AGATTTTCTGGAAAAGGTTC
150932	1571	AGAACCTTTTCCAGAAAATC	160152	GATTTTCTGGAAAAGGTTCT
150933	1572	AAGAACCTTTTCCAGAAAAT	160153	ATTTTCTGGAAAAGGTTCTT
150934	1573	AAAGAACCTTTTCCAGAAAA	160154	TTTTCTGGAAAAGGTTCTTT
150935	1574	CAAAGAACCTTTTCCAGAAA	160155	TTTCTGGAAAAGGTTCTTTG
150936	1575	CCAAAGAACCTTTTCCAGAA	160156	TTCTGGAAAAGGTTCTTTGG
150937	1576	GCCAAAGAACCTTTTCCAGA	160157	TCTGGAAAAGGTTCTTTGGC
150938	1577	TGCCAAAGAACCTTTTCCAG	160158	CTGGAAAAGGTTCTTTGGCA
150939	1578	ATGCCAAAGAACCTTTTCCA	160159	TGGAAAAGGTTCTTTGGCAT
150940	1579	AATGCCAAAGAACCTTTTCC	160160	GGAAAAGGTTCTTTGGCATT
150941	1580	AAATGCCAAAGAACCTTTTC	160161	GAAAAGGTTCTTTGGCATTT
150942	1581	CAAATGCCAAAGAACCTTTT	160162	AAAAGGTTCTTTGGCATTTG
150943	1582	TCAAATGCCAAAGAACCTTT	160163	AAAGGTTCTTTGGCATTTGA

150944	1583	GTCAAATGCCAAAGAACCTT	160164	AAGGTTCTTTGGCATTTGAC
150945	1584	AGTCAAATGCCAAAGAACCT	160165	AGGTTCTTTGGCATTTGACT
150946	1585	GAGTCAAATGCCAAAGAACC	160166	GGTTCTTTGGCATTTGACTC
150947	1586	GGAGTCAAATGCCAAAGAAC	160167	GTTCTTTGGCATTTGACTCC
150948	1587	TGGAGTCAAATGCCAAAGAA	160168	TTCTTTGGCATTTGACTCCA
150949	1588	ATGGAGTCAAATGCCAAAGA	160169	TCTTTGGCATTTGACTCCAT
150950	1589	AATGGAGTCAAATGCCAAAG	160170	CTTTGGCATTTGACTCCATT
150951	1590	AAATGGAGTCAAATGCCAAA	160171	TTTGGCATTTGACTCCATTT
150952	1591	AAAATGGAGTCAAATGCCAA	160172	TTGGCATTTGACTCCATTTT
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150954	1593	GCAAAATGGAGTCAAATGCC	160174	GGCATTTGACTCCATTTTGC
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150959	1598	AAACAGCAAAATGGAGTCAA	160179	TTGACTCCATTTTGCTGTTT
150960	1599	GAAACAGCAAAATGGAGTCA	160180	TGACTCCATTTTGCTGTTTC
150961	1600	TGAAACAGCAAAATGGAGTC	160181	GACTCCATTTTGCTGTTTCA
150962	1601	ATGAAACAGCAAAATGGAGT	160182	ACTCCATTTTGCTGTTTCAT
150963	1602	AATGAAACAGCAAAATGGAG	160183	CTCCATTTTGCTGTTTCATT
150964	1603	AAATGAAACAGCAAAATGGA	160184	TCCATTTTGCTGTTTCATTT
150965	1604	CAAATGAAACAGCAAAATGG	160185	CCATTTTGCTGTTTCATTTG
150966	1605	ACAAATGAAACAGCAAAATG	160186	CATTTTGCTGTTTCATTTGT
150967	1606	GACAAATGAAACAGCAAAAT	160187	ATTTTGCTGTTTCATTTGTC
150968	1607	TGACAAATGAAACAGCAAAA	160188	TTTTGCTGTTTCATTTGTCA
150969	1608	CTGACAAATGAAACAGCAAA	160189	TTTGCTGTTTCATTTGTCAG
150970	1609	TCTGACAAATGAAACAGCAA	160190	TTGCTGTTTCATTTGTCAGA
150971	1610	GTCTGACAAATGAAACAGCA	160191	TGCTGTTTCATTTGTCAGAC
150972	1611	AGTCTGACAAATGAAACAGC	160192	GCTGTTTCATTTGTCAGACT
150973	1612	AAGTCTGACAAATGAAACAG	160193	CTGTTTCATTTGTCAGACTT
150974	1613	GAAGTCTGACAAATGAAACA	160194	TGTTTCATTTGTCAGACTTC
150975	1614	AGAAGTCTGACAAATGAAAC	160195	GTTTCATTTGTCAGACTTCT
150976	1615	AAGAAGTCTGACAAATGAAA	160196	TTTCATTTGTCAGACTTCTT
150977	1616	AAAGAAGTCTGACAAATGAA	160197	TTCATTTGTCAGACTTCTTT
150978	1617	AAAAGAAGTCTGACAAATGA	160198	TCATTTGTCAGACTTCTTTT
150979	1618	AAAAAGAAGTCTGACAAATG	160199	CATTTGTCAGACTTCTTTTT
150980	1619	CAAAAAGAAGTCTGACAAAT	160200	ATTTGTCAGACTTCTTTTTG
150981	1620	ACAAAAAGAAGTCTGACAAA	160201	TTTGTCAGACTTCTTTTTGT
150982	1621	GACAAAAAGAAGTCTGACAA	160202	TTGTCAGACTTCTTTTTGTC
150983	1622	GGACAAAAAGAAGTCTGACA	160203	TGTCAGACTTCTTTTTGTCC
150984	1623	GGGACAAAAAGAAGTCTGAC	160204	GTCAGACTTCTTTTTGTCCC
150985	1624	AGGGACAAAAAGAAGTCTGA	160205	TCAGACTTCTTTTTGTCCCT
150986	1625	GAGGGACAAAAAGAAGTCTG	160206	CAGACTTCTTTTTGTCCCTC
150987	1626	AGAGGGACAAAAAGAAGTCT	160207	AGACTTCTTTTTGTCCCTCT
150988	1627	AAGAGGGACAAAAAGAAGTC	160208	GACTTCTTTTTGTCCCTCTT
150989	1628	AAAGAGGGACAAAAAGAAGT	160209	ACTTCTTTTTGTCCCTCTTT
150990	1629	TAAAGAGGGACAAAAAGAAG	160210	CTTCTTTTTGTCCCTCTTTA
150991	1630	GTAAAGAGGGACAAAAAGAA	160211	TTCTTTTTGTCCCTCTTTAC
150992	1631	AGTAAAGAGGGACAAAAAGA	160212	TCTTTTTGTCCCTCTTTACT
150993	1632	AAGTAAAGAGGGACAAAAAG	160213	CTTTTTGTCCCTCTTTACTT
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150995	1634	AGAAGTAAAGAGGGACAAAA	160215	TTTTGTCCCTCTTTACTTCT
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150997	1636	GGAGAAGTAAAGAGGGACAA	160217	TTGTCCCTCTTTACTTCTCC
150998	1637	GGGAGAAGTAAAGAGGGACA	160218	TGTCCCTCTTTACTTCTCCC
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151002	1641	TGTGGGGAGAAGTAAAGAGG	160222	CCTCTTTACTTCTCCCCACA
151003	1642	ATGTGGGGAGAAGTAAAGAG	160223	CTCTTTACTTCTCCCCACAT
151004	1643	TATGTGGGGAGAAGTAAAGA	160224	TCTTTACTTCTCCCCACATA
151005	1644	TTATGTGGGGAGAAGTAAAG	160225	CTTTACTTCTCCCCACATAA
151006	1645	ATTATGTGGGGAGAAGTAAA	160226	TTTACTTCTCCCCACATAAT
151007	1646	AATTATGTGGGGAGAAGTAA	160227	TTACTTCTCCCCACATAATT
151008	1647	GAATTATGTGGGGAGAAGTA	160228	TACTTCTCCCCACATAATTC
151009	1648	TGAATTATGTGGGGAGAAGT	160229	ACTTCTCCCCACATAATTCA
151010	1649	GTGAATTATGTGGGGAGAAG	160230	CTTCTCCCCACATAATTCAC
151011	1650	GGTGAATTATGTGGGGAGAA	160231	TTCTCCCCACATAATTCACC
151012	1651	TGGTGAATTATGTGGGGAGA	160232	TCTCCCCACATAATTCACCA
151013	1652	CTGGTGAATTATGTGGGGAG	160233	CTCCCCACATAATTCACCAG
151014	1653	ACTGGTGAATTATGTGGGGA	160234	TCCCCACATAATTCACCAGT
151015	1654	TACTGGTGAATTATGTGGGG	160235	CCCCACATAATTCACCAGTA

151016	1655	GTACTGGTGAATTATGTGGG	160236	CCCACATAATTCACCAGTAC
151017	1656	AGTACTGGTGAATTATGTGG	160237	CCACATAATTCACCAGTACT
151018	1657	TAGTACTGGTGAATTATGTG	160238	CACATAATTCACCAGTACTA
151019	1658	CTAGTACTGGTGAATTATGT	160239	ACATAATTCACCAGTACTAG
151020	1659	ACTAGTACTGGTGAATTATG	160240	CATAATTCACCAGTACTAGT
151021	1660	CACTAGTACTGGTGAATTAT	160241	ATAATTCACCAGTACTAGTG
151022	1661	ACACTAGTACTGGTGAATTA	160242	TAATTCACCAGTACTAGTGT
151023	1662	AACACTAGTACTGGTGAATT	160243	AATTCACCAGTACTAGTGTT
151024	1663	AAACACTAGTACTGGTGAAT	160244	ATTCACCAGTACTAGTGTTT
151025	1664	AAAACACTAGTACTGGTGAA	160245	TTCACCAGTACTAGTGTTTT
151026	1665	CAAAACACTAGTACTGGTGA	160246	TCACCAGTACTAGTGTTTTG
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151028	1667	AACAAAACACTAGTACTGGT	160248	ACCAGTACTAGTGTTTTGTT
151029	1668	AAACAAAACACTAGTACTGG	160249	CCAGTACTAGTGTTTTGTTT
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151031	1670	AAAAACAAAACACTAGTACT	160251	AGTACTAGTGTTTTGTTTTT
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151033	1672	TGAAAAACAAAACACTAGTA	160253	TACTAGTGTTTTGTTTTTCA
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151036	1675	GTCTGAAAAACAAAACACTA	160256	TAGTGTTTTGTTTTTCAGAC
151037	1676	GGTCTGAAAAACAAAACACT	160257	AGTGTTTTGTTTTTCAGACC
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151039	1678	TTGGTCTGAAAAACAAAACA	160259	TGTTTTGTTTTTCAGACCAA
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151043	1682	AGACTTGGTCTGAAAAACAA	160263	TTGTTTTTCAGACCAAGTCT
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151048	1687	GAGCGAGACTTGGTCTGAAA	160268	TTTCAGACCAAGTCTCGCTC
151049	1688	AGAGCGAGACTTGGTCTGAA	160269	TTCAGACCAAGTCTCGCTCT
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151054	1693	GCGACAGAGCGAGACTTGGT	160274	ACCAAGTCTCGCTCTGTCGC
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151056	1695	GGGCGACAGAGCGAGACTTG	160276	CAAGTCTCGCTCTGTCGCCC
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151058	1697	CTGGGCGACAGAGCGAGACT	160278	AGTCTCGCTCTGTCGCCCAG
151059	1698	CCTGGGCGACAGAGCGAGAC	160279	GTCTCGCTCTGTCGCCCAGG
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151062	1701	CAGCCTGGGCGACAGAGCGA	160282	TCGCTCTGTCGCCCAGGCTG
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151068	1707	GCACTCCAGCCTGGGCGACA	160288	TGTCGCCCAGGCTGGAGTGC
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151070	1709	CTGCACTCCAGCCTGGGCGA	160290	TCGCCCAGGCTGGAGTGCAG
151071	1710	ACTGCACTCCAGCCTGGGCG	160291	CGCCCAGGCTGGAGTGCAGT
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151074	1713	GCCACTGCACTCCAGCCTGG	160294	CCAGGCTGGAGTGCAGTGGC
151075	1714	CGCCACTGCACTCCAGCCTG	160295	CAGGCTGGAGTGCAGTGGCG
151076	1715	GCGCCACTGCACTCCAGCCT	160296	AGGCTGGAGTGCAGTGGCGC
151077	1716	CGCGCCACTGCACTCCAGCC	160297	GGCTGGAGTGCAGTGGCGCG
151078	1717	TCGCGCCACTGCACTCCAGC	160298	GCTGGAGTGCAGTGGCGCGA
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151080	1719	GATCGCGCCACTGCACTCCA	160300	TGGAGTGCAGTGGCGCGATC
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151083	1722	TGAGATCGCGCCACTGCACT	160303	AGTGCAGTGGCGCGATCTCA
151084	1723	CTGAGATCGCGCCACTGCAC	160304	GTGCAGTGGCGCGATCTCAG
151085	1724	GCTGAGATCGCGCCACTGCA	160305	TGCAGTGGCGCGATCTCAGC
151086	1725	AGCTGAGATCGCGCCACTGC	160306	GCAGTGGCGCGATCTCAGCT
151087	1726	GAGCTGAGATCGCGCCACTG	160307	CAGTGGCGCGATCTCAGCTC

151088	1727	TGAGCTGAGATCGCGCCACT	160308	AGTGGCGCGATCTCAGCTCA
151089	1728	GTGAGCTGAGATCGCGCCAC	160309	GTGGCGCGATCTCAGCTCAC
151090	1729	AGTGAGCTGAGATCGCGCCA	160310	TGGCGCGATCTCAGCTCACT
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151092	1731	GCAGTGAGCTGAGATCGCGC	160312	GCGCGATCTCAGCTCACTGC
151093	1732	TGCAGTGAGCTGAGATCGCG	160313	CGCGATCTCAGCTCACTGCA
151094	1733	TTGCAGTGAGCTGAGATCGC	160314	GCGATCTCAGCTCACTGCAA
151095	1734	GTTGCAGTGAGCTGAGATCG	160315	CGATCTCAGCTCACTGCAAC
151096	1735	GGTTGCAGTGAGCTGAGATC	160316	GATCTCAGCTCACTGCAACC
151097	1736	AGGTTGCAGTGAGCTGAGAT	160317	ATCTCAGCTCACTGCAACCT
151098	1737	GAGGTTGCAGTGAGCTGAGA	160318	TCTCAGCTCACTGCAACCTC
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151100	1739	CGGAGGTTGCAGTGAGCTGA	160320	TCAGCTCACTGCAACCTCCG
151101	1740	GCGGAGGTTGCAGTGAGCTG	160321	CAGCTCACTGCAACCTCCGC
151102	1741	GGCGGAGGTTGCAGTGAGCT	160322	AGCTCACTGCAACCTCCGCC
151103	1742	AGGCGGAGGTTGCAGTGAGC	160323	GCTCACTGCAACCTCCGCCT
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151106	1745	GGGAGGCGGAGGTTGCAGTG	160326	CACTGCAACCTCCGCCTCCC
151107	1746	TGGGAGGCGGAGGTTGCAGT	160327	ACTGCAACCTCCGCCTCCCA
151108	1747	CTGGGAGGCGGAGGTTGCAG	160328	CTGCAACCTCCGCCTCCCAG
151109	1748	CCTGGGAGGCGGAGGTTGCA	160329	TGCAACCTCCGCCTCCCAGG
151110	1749	ACCTGGGAGGCGGAGGTTGC	160330	GCAACCTCCGCCTCCCAGGT
151111	1750	AACCTGGGAGGCGGAGGTTG	160331	CAACCTCCGCCTCCCAGGTT
151112	1751	GAACCTGGGAGGCGGAGGTT	160332	AACCTCCGCCTCCCAGGTTC
151113	1752	TGAACCTGGGAGGCGGAGGT	160333	ACCTCCGCCTCCCAGGTTCA
151114	1753	TTGAACCTGGGAGGCGGAGG	160334	CCTCCGCCTCCCAGGTTCAA
151115	1754	CTTGAACCTGGGAGGCGGAG	160335	CTCCGCCTCCCAGGTTCAAG
151116	1755	GCTTGAACCTGGGAGGCGGA	160336	TCCGCCTCCCAGGTTCAAGC
151117	1756	TGCTTGAACCTGGGAGGCGG	160337	CCGCCTCCCAGGTTCAAGCA
151118	1757	TTGCTTGAACCTGGGAGGCG	160338	CGCCTCCCAGGTTCAAGCAA
151119	1758	ATTGCTTGAACCTGGGAGGC	160339	GCCTCCCAGGTTCAAGCAAT
151120	1759	AATTGCTTGAACCTGGGAGG	160340	CCTCCCAGGTTCAAGCAATT
151121	1760	GAATTGCTTGAACCTGGGAG	160341	CTCCCAGGTTCAAGCAATTC
151122	1761	AGAATTGCTTGAACCTGGGA	160342	TCCCAGGTTCAAGCAATTCT
151123	1762	GAGAATTGCTTGAACCTGGG	160343	CCCAGGTTCAAGCAATTCTC
151124	1763	GGAGAATTGCTTGAACCTGG	160344	CCAGGTTCAAGCAATTCTCC
151125	1764	AGGAGAATTGCTTGAACCTG	160345	CAGGTTCAAGCAATTCTCCT
151126	1765	CAGGAGAATTGCTTGAACCT	160346	AGGTTCAAGCAATTCTCCTG
151127	1766	GCAGGAGAATTGCTTGAACC	160347	GGTTCAAGCAATTCTCCTGC
151128	1767	GGCAGGAGAATTGCTTGAAC	160348	GTTCAAGCAATTCTCCTGCC
151129	1768	AGGCAGGAGAATTGCTTGAA	160349	TTCAAGCAATTCTCCTGCCT
151130	1769	GAGGCAGGAGAATTGCTTGA	160350	TCAAGCAATTCTCCTGCCTC
151131	1770	TGAGGCAGGAGAATTGCTTG	160351	CAAGCAATTCTCCTGCCTCA
151132	1771	CTGAGGCAGGAGAATTGCTT	160352	AAGCAATTCTCCTGCCTCAG
151133	1772	GCTGAGGCAGGAGAATTGCT	160353	AGCAATTCTCCTGCCTCAGC
151134	1773	GGCTGAGGCAGGAGAATTGC	160354	GCAATTCTCCTGCCTCAGCC
151135	1774	AGGCTGAGGCAGGAGAATTG	160355	CAATTCTCCTGCCTCAGCCT
151136	1775	GAGGCTGAGGCAGGAGAATT	160356	AATTCTCCTGCCTCAGCCTC
151137	1776	GGAGGCTGAGGCAGGAGAAT	160357	ATTCTCCTGCCTCAGCCTCC
151138	1777	GGGAGGCTGAGGCAGGAGAA	160358	TTCTCCTGCCTCAGCCTCCC
151139	1778	CGGGAGGCTGAGGCAGGAGA	160359	TCTCCTGCCTCAGCCTCCCG
151140	1779	CCGGGAGGCTGAGGCAGGAG	160360	CTCCTGCCTCAGCCTCCCGG
151141	1780	CCCGGGAGGCTGAGGCAGGA	160361	TCCTGCCTCAGCCTCCCGGG
151142	1781	ACCCGGGAGGCTGAGGCAGG	160362	CCTGCCTCAGCCTCCCGGGT
151143	1782	TACCCGGGAGGCTGAGGCAG	160363	CTGCCTCAGCCTCCCGGGTA
151144	1783	CTACCCGGGAGGCTGAGGCA	160364	TGCCTCAGCCTCCCGGGTAG
151145	1784	GCTACCCGGGAGGCTGAGGC	160365	GCCTCAGCCTCCCGGGTAGC
151146	1785	AGCTACCCGGGAGGCTGAGG	160366	CCTCAGCCTCCCGGGTAGCT
151147	1786	CAGCTACCCGGGAGGCTGAG	160367	CTCAGCCTCCCGGGTAGCTG
151148	1787	CCAGCTACCCGGGAGGCTGA	160368	TCAGCCTCCCGGGTAGCTGG
151149	1788	CCCAGCTACCCGGGAGGCTG	160369	CAGCCTCCCGGGTAGCTGGG
151150	1789	TCCCAGCTACCCGGGAGGCT	160370	AGCCTCCCGGGTAGCTGGGA
151151	1790	GTCCCAGCTACCCGGGAGGC	160371	GCCTCCCGGGTAGCTGGGAC
151152	1791	AGTCCCAGCTACCCGGGAGG	160372	CCTCCCGGGTAGCTGGGACT
151153	1792	TAGTCCCAGCTACCCGGGAG	160373	CTCCCGGGTAGCTGGGACTA
151154	1793	GTAGTCCCAGCTACCCGGGA	160374	TCCCGGGTAGCTGGGACTAC
151155	1794	TGTAGTCCCAGCTACCCGGG	160375	CCCGGGTAGCTGGGACTACA
151156	1795	CTGTAGTCCCAGCTACCCGG	160376	CCGGGTAGCTGGGACTACAG
151157	1796	CCTGTAGTCCCAGCTACCCG	160377	CGGGTAGCTGGGACTACAGG
151158	1797	GCCTGTAGTCCCAGCTACCC	160378	GGGTAGCTGGGACTACAGGC
151159	1798	CGCCTGTAGTCCCAGCTACC	160379	GGTAGCTGGGACTACAGGCG

151160	1799	GCGCCTGTAGTCCCAGCTAC	160380	GTAGCTGGGACTACAGGCGC
151161	1800	CGCGCCTGTAGTCCCAGCTA	160381	TAGCTGGGACTACAGGCGCG
151162	1801	GCGCGCCTGTAGTCCCAGCT	160382	AGCTGGGACTACAGGCGCGC
151163	1802	CGCGCGCCTGTAGTCCCAGC	160383	GCTGGGACTACAGGCGCGCG
151164	1803	GCGCGCGCCTGTAGTCCCAG	160384	CTGGGACTACAGGCGCGCGC
151165	1804	GGCGCGCGCCTGTAGTCCCA	160385	TGGGACTACAGGCGCGCGCC
151166	1805	CGGCGCGCGCCTGTAGTCCC	160386	GGGACTACAGGCGCGCGCCG
151167	1806	GCGGCGCGCGCCTGTAGTCC	160387	GGACTACAGGCGCGCGCCGC
151168	1807	GGCGGCGCGCGCCTGTAGTC	160388	GACTACAGGCGCGCGCCGCC
151169	1808	TGGCGGCGCGCGCCTGTAGT	160389	ACTACAGGCGCGCGCCGCCA
151170	1809	GTGGCGGCGCGCGCCTGTAG	160390	CTACAGGCGCGCGCCGCCAC
151171	1810	CGTGGCGGCGCGCGCCTGTA	160391	TACAGGCGCGCGCCGCCACG
151172	1811	GCGTGGCGGCGCGCGCCTGT	160392	ACAGGCGCGCGCCGCCACGC
151173	1812	GGCGTGGCGGCGCGCGCCTG	160393	CAGGCGCGCGCCGCCACGCC
151174	1813	AGGCGTGGCGGCGCGCGCCT	160394	AGGCGCGCGCCGCCACGCCT
151175	1814	CAGGCGTGGCGGCGCGCGCC	160395	GGCGCGCGCCGCCACGCCTG
151176	1815	CCAGGCGTGGCGGCGCGCGC	160396	GCGCGCGCCGCCACGCCTGG
151177	1816	GCCAGGCGTGGCGGCGCGCG	160397	CGCGCGCCGCCACGCCTGGC
151178	1817	AGCCAGGCGTGGCGGCGCGC	160398	GCGCGCCGCCACGCCTGGCT
151179	1818	TAGCCAGGCGTGGCGGCGCG	160399	CGCGCCGCCACGCCTGGCTA
151180	1819	TTAGCCAGGCGTGGCGGCGC	160400	GCGCCGCCACGCCTGGCTAA
151181	1820	ATTAGCCAGGCGTGGCGGCG	160401	CGCCGCCACGCCTGGCTAAT
151182	1821	AATTAGCCAGGCGTGGCGGC	160402	GCCGCCACGCCTGGCTAATT
151183	1822	AAATTAGCCAGGCGTGGCGG	160403	CCGCCACGCCTGGCTAATTT
151184	1823	AAAATTAGCCAGGCGTGGCG	160404	CGCCACGCCTGGCTAATTTT
151185	1824	AAAAATTAGCCAGGCGTGGC	160405	GCCACGCCTGGCTAATTTTT
151186	1825	AAAAAATTAGCCAGGCGTGG	160406	CCACGCCTGGCTAATTTTTT
151187	1826	TAAAAAATTAGCCAGGCGTG	160407	CACGCCTGGCTAATTTTTTA
151188	1827	ATAAAAAATTAGCCAGGCGT	160408	ACGCCTGGCTAATTTTTTAT
151189	1828	TATAAAAAATTAGCCAGGCG	160409	CGCCTGGCTAATTTTTTATA
151190	1829	ATATAAAAAATTAGCCAGGC	160410	GCCTGGCTAATTTTTTATAT
151191	1830	AATATAAAAAATTAGCCAGG	160411	CCTGGCTAATTTTTTATATT
151192	1831	AAATATAAAAAATTAGCCAG	160412	CTGGCTAATTTTTTATATTT
151193	1832	AAAATATAAAAAATTAGCCA	160413	TGGCTAATTTTTTATATTTT
151194	1833	TAAAATATAAAAAATTAGCC	160414	GGCTAATTTTTTATATTTTA
151195	1834	CTAAAATATAAAAAATTAGC	160415	GCTAATTTTTTATATTTTAG
151196	1835	ACTAAAATATAAAAAATTAG	160416	CTAATTTTTTATATTTTAGT
151197	1836	TACTAAAATATAAAAAATTA	160417	TAATTTTTTATATTTTAGTA
151198	1837	CTACTAAAATATAAAAAATT	160418	AATTTTTTATATTTTAGTAG
151199	1838	TCTACTAAAATATAAAAAAT	160419	ATTTTTTATATTTTAGTAGA
151200	1839	CTCTACTAAAATATAAAAAA	160420	TTTTTTATATTTTAGTAGAG
151201	1840	TCTCTACTAAAATATAAAAA	160421	TTTTTATATTTTAGTAGAGA
151202	1841	GTCTCTACTAAAATATAAAA	160422	TTTTATATTTTAGTAGAGAC
151203	1842	CGTCTCTACTAAAATATAAA	160423	TTTATATTTTAGTAGAGACG
151204	1843	CCGTCTCTACTAAAATATAA	160424	TTATATTTTAGTAGAGACGG
151205	1844	GCCGTCTCTACTAAAATATA	160425	TATATTTTAGTAGAGACGGC
151206	1845	CGCCGTCTCTACTAAAATAT	160426	ATATTTTAGTAGAGACGGCG
151207	1846	ACGCCGTCTCTACTAAAATA	160427	TATTTTAGTAGAGACGGCGT
151208	1847	AACGCCGTCTCTACTAAAAT	160428	ATTTTAGTAGAGACGGCGTT
151209	1848	AAACGCCGTCTCTACTAAAA	160429	TTTTAGTAGAGACGGCGTTT
151210	1849	GAAACGCCGTCTCTACTAAA	160430	TTTAGTAGAGACGGCGTTTC
151211	1850	TGAAACGCCGTCTCTACTAA	160431	TTAGTAGAGACGGCGTTTCA
151212	1851	GTGAAACGCCGTCTCTACTA	160432	TAGTAGAGACGGCGTTTCAC
151213	1852	GGTGAAACGCCGTCTCTACT	160433	AGTAGAGACGGCGTTTCACC
151214	1853	TGGTGAAACGCCGTCTCTAC	160434	GTAGAGACGGCGTTTCACCA
151215	1854	ATGGTGAAACGCCGTCTCTA	160435	TAGAGACGGCGTTTCACCAT
151216	1855	CATGGTGAAACGCCGTCTCT	160436	AGAGACGGCGTTTCACCATG
151217	1856	ACATGGTGAAACGCCGTCTC	160437	GAGACGGCGTTTCACCATGT
151218	1857	AACATGGTGAAACGCCGTCT	160438	AGACGGCGTTTCACCATGTT
151219	1858	CAACATGGTGAAACGCCGTC	160439	GACGGCGTTTCACCATGTTG
151220	1859	CCAACATGGTGAAACGCCGT	160440	ACGGCGTTTCACCATGTTGG
151221	1860	GCCAACATGGTGAAACGCCG	160441	CGGCGTTTCACCATGTTGGC
151222	1861	GGCCAACATGGTGAAACGCC	160442	GGCGTTTCACCATGTTGGCC
151223	1862	TGGCCAACATGGTGAAACGC	160443	GCGTTTCACCATGTTGGCCA
151224	1863	CTGGCCAACATGGTGAAACG	160444	CGTTTCACCATGTTGGCCAG
151225	1864	CCTGGCCAACATGGTGAAAC	160445	GTTTCACCATGTTGGCCAGG
151226	1865	TCCTGGCCAACATGGTGAAA	160446	TTTCACCATGTTGGCCAGGA
151227	1866	ATCCTGGCCAACATGGTGAA	160447	TTCACCATGTTGGCCAGGAT
151228	1867	CATCCTGGCCAACATGGTGA	160448	TCACCATGTTGGCCAGGATG
151229	1868	CCATCCTGGCCAACATGGTG	160449	CACCATGTTGGCCAGGATGG
151230	1869	ACCATCCTGGCCAACATGGT	160450	ACCATGTTGGCCAGGATGGT
151231	1870	GACCATCCTGGCCAACATGG	160451	CCATGTTGGCCAGGATGGTC

151232	1871	AGACCATCCTGGCCAACATG	160452	CATGTTGGCCAGGATGGTCT
151233	1872	GAGACCATCCTGGCCAACAT	160453	ATGTTGGCCAGGATGGTCTC
151234	1873	CGAGACCATCCTGGCCAACA	160454	TGTTGGCCAGGATGGTCTCG
151235	1874	TCGAGACCATCCTGGCCAAC	160455	GTTGGCCAGGATGGTCTCGA
151236	1875	ATCGAGACCATCCTGGCCAA	160456	TTGGCCAGGATGGTCTCGAT
151237	1876	GATCGAGACCATCCTGGCCA	160457	TGGCCAGGATGGTCTCGATC
151238	1877	AGATCGAGACCATCCTGGCC	160458	GGCCAGGATGGTCTCGATCT
151239	1878	CAGATCGAGACCATCCTGGC	160459	GCCAGGATGGTCTCGATCTG
151240	1879	ACAGATCGAGACCATCCTGG	160460	CCAGGATGGTCTCGATCTGT
151241	1880	AACAGATCGAGACCATCCTG	160461	CAGGATGGTCTCGATCTGTT
151242	1881	CAACAGATCGAGACCATCCT	160462	AGGATGGTCTCGATCTGTTG
151243	1882	TCAACAGATCGAGACCATCC	160463	GGATGGTCTCGATCTGTTGA
151244	1883	GTCAACAGATCGAGACCATC	160464	GATGGTCTCGATCTGTTGAC
151245	1884	CGTCAACAGATCGAGACCAT	160465	ATGGTCTCGATCTGTTGACG
151246	1885	ACGTCAACAGATCGAGACCA	160466	TGGTCTCGATCTGTTGACGT
151247	1886	GACGTCAACAGATCGAGACC	160467	GGTCTCGATCTGTTGACGTC
151248	1887	CGACGTCAACAGATCGAGAC	160468	GTCTCGATCTGTTGACGTCG
151249	1888	ACGACGTCAACAGATCGAGA	160469	TCTCGATCTGTTGACGTCGT
151250	1889	CACGACGTCAACAGATCGAG	160470	CTCGATCTGTTGACGTCGTG
151251	1890	TCACGACGTCAACAGATCGA	160471	TCGATCTGTTGACGTCGTGA
151252	1891	ATCACGACGTCAACAGATCG	160472	CGATCTGTTGACGTCGTGAT
151253	1892	GATCACGACGTCAACAGATC	160473	GATCTGTTGACGTCGTGATC
151254	1893	GGATCACGACGTCAACAGAT	160474	ATCTGTTGACGTCGTGATCC
151255	1894	TGGATCACGACGTCAACAGA	160475	TCTGTTGACGTCGTGATCCA
151256	1895	GTGGATCACGACGTCAACAG	160476	CTGTTGACGTCGTGATCCAC
151257	1896	GGTGGATCACGACGTCAACA	160477	TGTTGACGTCGTGATCCACC
151258	1897	GGGTGGATCACGACGTCAAC	160478	GTTGACGTCGTGATCCACCC
151259	1898	CGGGTGGATCACGACGTCAA	160479	TTGACGTCGTGATCCACCCG
151260	1899	GCGGGTGGATCACGACGTCA	160480	TGACGTCGTGATCCACCCGC
151261	1900	GGCGGGTGGATCACGACGTC	160481	GACGTCGTGATCCACCCGCC
151262	1901	AGGCGGGTGGATCACGACGT	160482	ACGTCGTGATCCACCCGCCT
151263	1902	GAGGCGGGTGGATCACGACG	160483	CGTCGTGATCCACCCGCCTC
151264	1903	CGAGGCGGGTGGATCACGAC	160484	GTCGTGATCCACCCGCCTCG
151265	1904	CCGAGGCGGGTGGATCACGA	160485	TCGTGATCCACCCGCCTCGG
151266	1905	GCCGAGGCGGGTGGATCACG	160486	CGTGATCCACCCGCCTCGGC
151267	1906	GGCCGAGGCGGGTGGATCAC	160487	GTGATCCACCCGCCTCGGCC
151268	1907	AGGCCGAGGCGGGTGGATCA	160488	TGATCCACCCGCCTCGGCCT
151269	1908	GAGGCCGAGGCGGGTGGATC	160489	GATCCACCCGCCTCGGCCTC
151270	1909	GGAGGCCGAGGCGGGTGGAT	160490	ATCCACCCGCCTCGGCCTCC
151271	1910	GGGAGGCCGAGGCGGGTGGA	160491	TCCACCCGCCTCGGCCTCCC
151272	1911	TGGGAGGCCGAGGCGGGTGG	160492	CCACCCGCCTCGGCCTCCCA
151273	1912	TTGGGAGGCCGAGGCGGGTG	160493	CACCCGCCTCGGCCTCCCAA
151274	1913	TTTGGGAGGCCGAGGCGGGT	160494	ACCCGCCTCGGCCTCCCAAA
151275	1914	CTTTGGGAGGCCGAGGCGGG	160495	CCCGCCTCGGCCTCCCAAAG
151276	1915	ACTTTGGGAGGCCGAGGCGG	160496	CCGCCTCGGCCTCCCAAAGT
151277	1916	CACTTTGGGAGGCCGAGGCG	160497	CGCCTCGGCCTCCCAAAGTG
151278	1917	GCACTTTGGGAGGCCGAGGC	160498	GCCTCGGCCTCCCAAAGTGC
151279	1918	AGCACTTTGGGAGGCCGAGG	160499	CCTCGGCCTCCCAAAGTGCT
151280	1919	CAGCACTTTGGGAGGCCGAG	160500	CTCGGCCTCCCAAAGTGCTG
151281	1920	CCAGCACTTTGGGAGGCCGA	160501	TCGGCCTCCCAAAGTGCTGG
151282	1921	CCCAGCACTTTGGGAGGCCG	160502	CGGCCTCCCAAAGTGCTGGG
151283	1922	TCCCAGCACTTTGGGAGGCC	160503	GGCCTCCCAAAGTGCTGGGA
151284	1923	ATCCCAGCACTTTGGGAGGC	160504	GCCTCCCAAAGTGCTGGGAT
151285	1924	AATCCCAGCACTTTGGGAGG	160505	CCTCCCAAAGTGCTGGGATT
151286	1925	TAATCCCAGCACTTTGGGAG	160506	CTCCCAAAGTGCTGGGATTA
151287	1926	GTAATCCCAGCACTTTGGGA	160507	TCCCAAAGTGCTGGGATTAC
151288	1927	TGTAATCCCAGCACTTTGGG	160508	CCCAAAGTGCTGGGATTACA
151289	1928	CTGTAATCCCAGCACTTTGG	160509	CCAAAGTGCTGGGATTACAG
151290	1929	CCTGTAATCCCAGCACTTTG	160510	CAAAGTGCTGGGATTACAGG
151291	1930	GCCTGTAATCCCAGCACTTT	160511	AAAGTGCTGGGATTACAGGC
151292	1931	CGCCTGTAATCCCAGCACTT	160512	AAGTGCTGGGATTACAGGCG
151293	1932	ACGCCTGTAATCCCAGCACT	160513	AGTGCTGGGATTACAGGCGT
151294	1933	CACGCCTGTAATCCCAGCAC	160514	GTGCTGGGATTACAGGCGTG
151295	1934	TCACGCCTGTAATCCCAGCA	160515	TGCTGGGATTACAGGCGTGA
151296	1935	CTCACGCCTGTAATCCCAGC	160516	GCTGGGATTACAGGCGTGAG
151297	1936	GCTCACGCCTGTAATCCCAG	160517	CTGGGATTACAGGCGTGAGC
151298	1937	GGCTCACGCCTGTAATCCCA	160518	TGGGATTACAGGCGTGAGCC
151299	1938	TGGCTCACGCCTGTAATCCC	160519	GGGATTACAGGCGTGAGCCA
151300	1939	GTGGCTCACGCCTGTAATCC	160520	GGATTACAGGCGTGAGCCAC
151301	1940	GGTGGCTCACGCCTGTAATC	160521	GATTACAGGCGTGAGCCACC
151302	1941	GGGTGGCTCACGCCTGTAAT	160522	ATTACAGGCGTGAGCCACCC
151303	1942	GGGGTGGCTCACGCCTGTAA	160523	TTACAGGCGTGAGCCACCCC

151304	1943	CGGGGTGGCTCACGCCTGTA	160524	TACAGGCGTGAGCCACCCCG
151305	1944	GCGGGGTGGCTCACGCCTGT	160525	ACAGGCGTGAGCCACCCCGC
151306	1945	GGCGGGGTGGCTCACGCCTG	160526	CAGGCGTGAGCCACCCCGCC
151307	1946	GGGCGGGGTGGCTCACGCCT	160527	AGGCGTGAGCCACCCCGCCC
151308	1947	CGGGCGGGGTGGCTCACGCC	160528	GGCGTGAGCCACCCCGCCCG
151309	1948	CCGGGCGGGGTGGCTCACGC	160529	GCGTGAGCCACCCCGCCCGG
151310	1949	GCCGGGCGGGGTGGCTCACG	160530	CGTGAGCCACCCCGCCCGGC
151311	1950	GGCCGGGCGGGGTGGCTCAC	160531	GTGAGCCACCCCGCCCGGCC
151312	1951	TGGCCGGGCGGGGTGGCTCA	160532	TGAGCCACCCCGCCCGGCCA
151313	1952	GTGGCCGGGCGGGGTGGCTC	160533	GAGCCACCCCGCCCGGCCAC
151314	1953	GGTGGCCGGGCGGGGTGGCT	160534	AGCCACCCCGCCCGGCCACC
151315	1954	TGGTGGCCGGGCGGGGTGGC	160535	GCCACCCCGCCCGGCCACCA
151316	1955	CTGGTGGCCGGGCGGGGTGG	160536	CCACCCCGCCCGGCCACCAG
151317	1956	ACTGGTGGCCGGGCGGGGTG	160537	CACCCCGCCCGGCCACCAGT
151318	1957	CACTGGTGGCCGGGCGGGGT	160538	ACCCCGCCCGGCCACCAGTG
151319	1958	GCACTGGTGGCCGGGCGGGG	160539	CCCCGCCCGGCCACCAGTGC
151320	1959	AGCACTGGTGGCCGGGCGGG	160540	CCCGCCCGGCCACCAGTGCT
151321	1960	TAGCACTGGTGGCCGGGCGG	160541	CCGCCCGGCCACCAGTGCTA
151322	1961	ATAGCACTGGTGGCCGGGCG	160542	CGCCCGGCCACCAGTGCTAT
151323	1962	AATAGCACTGGTGGCCGGGC	160543	GCCCGGCCACCAGTGCTATT
151324	1963	GAATAGCACTGGTGGCCGGG	160544	CCCGGCCACCAGTGCTATTC
151325	1964	AGAATAGCACTGGTGGCCGG	160545	CCGGCCACCAGTGCTATTCT
151326	1965	AAGAATAGCACTGGTGGCCG	160546	CGGCCACCAGTGCTATTCTT
151327	1966	TAAGAATAGCACTGGTGGCC	160547	GGCCACCAGTGCTATTCTTA
151328	1967	TTAAGAATAGCACTGGTGGC	160548	GCCACCAGTGCTATTCTTAA
151329	1968	CTTAAGAATAGCACTGGTGG	160549	CCACCAGTGCTATTCTTAAG
151330	1969	TCTTAAGAATAGCACTGGTG	160550	CACCAGTGCTATTCTTAAGA
151331	1970	GTCTTAAGAATAGCACTGGT	160551	ACCAGTGCTATTCTTAAGAC
151332	1971	CGTCTTAAGAATAGCACTGG	160552	CCAGTGCTATTCTTAAGACG
151333	1972	GCGTCTTAAGAATAGCACTG	160553	CAGTGCTATTCTTAAGACGC
151334	1973	GGCGTCTTAAGAATAGCACT	160554	AGTGCTATTCTTAAGACGCC
151335	1974	AGGCGTCTTAAGAATAGCAC	160555	GTGCTATTCTTAAGACGCCT
151336	1975	GAGGCGTCTTAAGAATAGCA	160556	TGCTATTCTTAAGACGCCTC
151337	1976	AGAGGCGTCTTAAGAATAGC	160557	GCTATTCTTAAGACGCCTCT
151338	1977	CAGAGGCGTCTTAAGAATAG	160558	CTATTCTTAAGACGCCTCTG
151339	1978	TCAGAGGCGTCTTAAGAATA	160559	TATTCTTAAGACGCCTCTGA
151340	1979	CTCAGAGGCGTCTTAAGAAT	160560	ATTCTTAAGACGCCTCTGAG
151341	1980	CCTCAGAGGCGTCTTAAGAA	160561	TTCTTAAGACGCCTCTGAGG
151342	1981	TCCTCAGAGGCGTCTTAAGA	160562	TCTTAAGACGCCTCTGAGGA
151343	1982	TTCCTCAGAGGCGTCTTAAG	160563	CTTAAGACGCCTCTGAGGAA
151344	1983	ATTCCTCAGAGGCGTCTTAA	160564	TTAAGACGCCTCTGAGGAAT
151345	1984	GATTCCTCAGAGGCGTCTTA	160565	TAAGACGCCTCTGAGGAATC
151346	1985	GGATTCCTCAGAGGCGTCTT	160566	AAGACGCCTCTGAGGAATCC
151347	1986	GGGATTCCTCAGAGGCGTCT	160567	AGACGCCTCTGAGGAATCCC
151348	1987	AGGGATTCCTCAGAGGCGTC	160568	GACGCCTCTGAGGAATCCCT
151349	1988	AAGGGATTCCTCAGAGGCGT	160569	ACGCCTCTGAGGAATCCCTT
151350	1989	GAAGGGATTCCTCAGAGGCG	160570	CGCCTCTGAGGAATCCCTTC
151351	1990	AGAAGGGATTCCTCAGAGGC	160571	GCCTCTGAGGAATCCCTTCT
151352	1991	GAGAAGGGATTCCTCAGAGG	160572	CCTCTGAGGAATCCCTTCTC
151353	1992	GGAGAAGGGATTCCTCAGAG	160573	CTCTGAGGAATCCCTTCTCC
151354	1993	GGGAGAAGGGATTCCTCAGA	160574	TCTGAGGAATCCCTTCTCCC
151355	1994	AGGGAGAAGGGATTCCTCAG	160575	CTGAGGAATCCCTTCTCCCT
151356	1995	CAGGGAGAAGGGATTCCTCA	160576	TGAGGAATCCCTTCTCCCTG
151357	1996	CCAGGGAGAAGGGATTCCTC	160577	GAGGAATCCCTTCTCCCTGG
151358	1997	GCCAGGGAGAAGGGATTCCT	160578	AGGAATCCCTTCTCCCTGGC
151359	1998	GGCCAGGGAGAAGGGATTCC	160579	GGAATCCCTTCTCCCTGGCC
151360	1999	TGGCCAGGGAGAAGGGATTC	160580	GAATCCCTTCTCCCTGGCCA
151361	2000	ATGGCCAGGGAGAAGGGATT	160581	AATCCCTTCTCCCTGGCCAT
151362	2001	AATGGCCAGGGAGAAGGGAT	160582	ATCCCTTCTCCCTGGCCATT
151363	2002	CAATGGCCAGGGAGAAGGGA	160583	TCCCTTCTCCCTGGCCATTG
151364	2003	TCAATGGCCAGGGAGAAGGG	160584	CCCTTCTCCCTGGCCATTGA
151365	2004	CTCAATGGCCAGGGAGAAGG	160585	CCTTCTCCCTGGCCATTGAG
151366	2005	TCTCAATGGCCAGGGAGAAG	160586	CTTCTCCCTGGCCATTGAGA
151367	2006	TTCTCAATGGCCAGGGAGAA	160587	TTCTCCCTGGCCATTGAGAA
151368	2007	ATTCTCAATGGCCAGGGAGA	160588	TCTCCCTGGCCATTGAGAAT
151369	2008	GATTCTCAATGGCCAGGGAG	160589	CTCCCTGGCCATTGAGAATC
151370	2009	GGATTCTCAATGGCCAGGGA	160590	TCCCTGGCCATTGAGAATCC
151371	2010	TGGATTCTCAATGGCCAGGG	160591	CCCTGGCCATTGAGAATCCA
151372	2011	ATGGATTCTCAATGGCCAGG	160592	CCTGGCCATTGAGAATCCAT
151373	2012	CATGGATTCTCAATGGCCAG	160593	CTGGCCATTGAGAATCCATG
151374	2013	GCATGGATTCTCAATGGCCA	160594	TGGCCATTGAGAATCCATGC
151375	2014	TGCATGGATTCTCAATGGCC	160595	GGCCATTGAGAATCCATGCA

151376	2015	ATGCATGGATTCTCAATGGC	160596	GCCATTGAGAATCCATGCAT
151377	2016	CATGCATGGATTCTCAATGG	160597	CCATTGAGAATCCATGCATG
151378	2017	TCATGCATGGATTCTCAATG	160598	CATTGAGAATCCATGCATGA
151379	2018	TTCATGCATGGATTCTCAAT	160599	ATTGAGAATCCATGCATGAA
151380	2019	GTTCATGCATGGATTCTCAA	160600	TTGAGAATCCATGCATGAAC
151381	2020	GGTTCATGCATGGATTCTCA	160601	TGAGAATCCATGCATGAACC
151382	2021	GGGTTCATGCATGGATTCTC	160602	GAGAATCCATGCATGAACCC
151383	2022	TGGGTTCATGCATGGATTCT	160603	AGAATCCATGCATGAACCCA
151384	2023	CTGGGTTCATGCATGGATTC	160604	GAATCCATGCATGAACCCAG
151385	2024	CCTGGGTTCATGCATGGATT	160605	AATCCATGCATGAACCCAGG
151386	2025	ACCTGGGTTCATGCATGGAT	160606	ATCCATGCATGAACCCAGGT
151387	2026	AACCTGGGTTCATGCATGGA	160607	TCCATGCATGAACCCAGGTT
151388	2027	AAACCTGGGTTCATGCATGG	160608	CCATGCATGAACCCAGGTTT
151389	2028	AAAACCTGGGTTCATGCATG	160609	CATGCATGAACCCAGGTTTT
151390	2029	GAAAACCTGGGTTCATGCAT	160610	ATGCATGAACCCAGGTTTTC
151391	2030	GGAAAACCTGGGTTCATGCA	160611	TGCATGAACCCAGGTTTTCC
151392	2031	TGGAAAACCTGGGTTCATGC	160612	GCATGAACCCAGGTTTTCCA
151393	2032	GTGGAAAACCTGGGTTCATG	160613	CATGAACCCAGGTTTTCCAC
151394	2033	GGTGGAAAACCTGGGTTCAT	160614	ATGAACCCAGGTTTTCCACC
151395	2034	AGGTGGAAAACCTGGGTTCA	160615	TGAACCCAGGTTTTCCACCT
151396	2035	AAGGTGGAAAACCTGGGTTC	160616	GAACCCAGGTTTTCCACCTT
151397	2036	GAAGGTGGAAAACCTGGGTT	160617	AACCCAGGTTTTCCACCTTC
151398	2037	GGAAGGTGGAAAACCTGGGT	160618	ACCCAGGTTTTCCACCTTCC
151399	2038	GGGAAGGTGGAAAACCTGGG	160619	CCCAGGTTTTCCACCTTCCC
151400	2039	AGGGAAGGTGGAAAACCTGG	160620	CCAGGTTTTCCACCTTCCCT
151401	2040	CAGGGAAGGTGGAAAACCTG	160621	CAGGTTTTCCACCTTCCCTG
151402	2041	TCAGGGAAGGTGGAAAACCT	160622	AGGTTTTCCACCTTCCCTGA
151403	2042	CTCAGGGAAGGTGGAAAACC	160623	GGTTTTCCACCTTCCCTGAG
151404	2043	GCTCAGGGAAGGTGGAAAAC	160624	GTTTTCCACCTTCCCTGAGC
151405	2044	TGCTCAGGGAAGGTGGAAAA	160625	TTTTCCACCTTCCCTGAGCA
151406	2045	CTGCTCAGGGAAGGTGGAAA	160626	TTTCCACCTTCCCTGAGCAG
151407	2046	GCTGCTCAGGGAAGGTGGAA	160627	TTCCACCTTCCCTGAGCAGC
151408	2047	AGCTGCTCAGGGAAGGTGGA	160628	TCCACCTTCCCTGAGCAGCT
151409	2048	AAGCTGCTCAGGGAAGGTGG	160629	CCACCTTCCCTGAGCAGCTT
151410	2049	CAAGCTGCTCAGGGAAGGTG	160630	CACCTTCCCTGAGCAGCTTG
151411	2050	GCAAGCTGCTCAGGGAAGGT	160631	ACCTTCCCTGAGCAGCTTGC
151412	2051	TGCAAGCTGCTCAGGGAAGG	160632	CCTTCCCTGAGCAGCTTGCA
151413	2052	ATGCAAGCTGCTCAGGGAAG	160633	CTTCCCTGAGCAGCTTGCAT
151414	2053	TATGCAAGCTGCTCAGGGAA	160634	TTCCCTGAGCAGCTTGCATA
151415	2054	CTATGCAAGCTGCTCAGGGA	160635	TCCCTGAGCAGCTTGCATAG
151416	2055	ACTATGCAAGCTGCTCAGGG	160636	CCCTGAGCAGCTTGCATAGT
151417	2056	AACTATGCAAGCTGCTCAGG	160637	CCTGAGCAGCTTGCATAGTT
151418	2057	GAACTATGCAAGCTGCTCAG	160638	CTGAGCAGCTTGCATAGTTC
151419	2058	GGAACTATGCAAGCTGCTCA	160639	TGAGCAGCTTGCATAGTTCC
151420	2059	AGGAACTATGCAAGCTGCTC	160640	GAGCAGCTTGCATAGTTCCT
151421	2060	AAGGAACTATGCAAGCTGCT	160641	AGCAGCTTGCATAGTTCCTT
151422	2061	GAAGGAACTATGCAAGCTGC	160642	GCAGCTTGCATAGTTCCTTC
151423	2062	AGAAGGAACTATGCAAGCTG	160643	CAGCTTGCATAGTTCCTTCT
151424	2063	AAGAAGGAACTATGCAAGCT	160644	AGCTTGCATAGTTCCTTCTT
151425	2064	AAAGAAGGAACTATGCAAGC	160645	GCTTGCATAGTTCCTTCTTT
151426	2065	AAAAGAAGGAACTATGCAAG	160646	CTTGCATAGTTCCTTCTTTT
151427	2066	TAAAAGAAGGAACTATGCAA	160647	TTGCATAGTTCCTTCTTTTA
151428	2067	TTAAAAGAAGGAACTATGCA	160648	TGCATAGTTCCTTCTTTTAA
151429	2068	CTTAAAAGAAGGAACTATGC	160649	GCATAGTTCCTTCTTTTAAG
151430	2069	GCTTAAAAGAAGGAACTATG	160650	CATAGTTCCTTCTTTTAAGC
151431	2070	CGCTTAAAAGAAGGAACTAT	160651	ATAGTTCCTTCTTTTAAGCG
151432	2071	GCGCTTAAAAGAAGGAACTA	160652	TAGTTCCTTCTTTTAAGCGC
151433	2072	GGCGCTTAAAAGAAGGAACT	160653	AGTTCCTTCTTTTAAGCGCC
151434	2073	AGGCGCTTAAAAGAAGGAAC	160654	GTTCCTTCTTTTAAGCGCCT
151435	2074	CAGGCGCTTAAAAGAAGGAA	160655	TTCCTTCTTTTAAGCGCCTG
151436	2075	TCAGGCGCTTAAAAGAAGGA	160656	TCCTTCTTTTAAGCGCCTGA
151437	2076	GTCAGGCGCTTAAAAGAAGG	160657	CCTTCTTTTAAGCGCCTGAC
151438	2077	AGTCAGGCGCTTAAAAGAAG	160658	CTTCTTTTAAGCGCCTGACT
151439	2078	AAGTCAGGCGCTTAAAAGAA	160659	TTCTTTTAAGCGCCTGACTT
151440	2079	GAAGTCAGGCGCTTAAAAGA	160660	TCTTTTAAGCGCCTGACTTC
151441	2080	CGAAGTCAGGCGCTTAAAAG	160661	CTTTTAAGCGCCTGACTTCG
151442	2081	ACGAAGTCAGGCGCTTAAAA	160662	TTTTAAGCGCCTGACTTCGT
151443	2082	AACGAAGTCAGGCGCTTAAA	160663	TTTAAGCGCCTGACTTCGTT
151444	2083	AAACGAAGTCAGGCGCTTAA	160664	TTAAGCGCCTGACTTCGTTT
151445	2084	AAAACGAAGTCAGGCGCTTA	160665	TAAGCGCCTGACTTCGTTTT
151446	2085	CAAAACGAAGTCAGGCGCTT	160666	AAGCGCCTGACTTCGTTTTG
151447	2086	ACAAAACGAAGTCAGGCGCT	160667	AGCGCCTGACTTCGTTTTGT

151448	2087	AACAAAACGAAGTCAGGCGC	160668	GCGCCTGACTTCGTTTTGTT
151449	2088	AAACAAAACGAAGTCAGGCG	160669	CGCCTGACTTCGTTTTGTTT
151450	2089	CAAACAAAACGAAGTCAGGC	160670	GCCTGACTTCGTTTTGTTTG
151451	2090	CCAAACAAAACGAAGTCAGG	160671	CCTGACTTCGTTTTGTTTGG
151452	2091	ACCAAACAAAACGAAGTCAG	160672	CTGACTTCGTTTTGTTTGGT
151453	2092	CACCAAACAAAACGAAGTCA	160673	TGACTTCGTTTTGTTTGGTG
151454	2093	GCACCAAACAAAACGAAGTC	160674	GACTTCGTTTTGTTTGGTGC
151455	2094	GGCACCAAACAAAACGAAGT	160675	ACTTCGTTTTGTTTGGTGCC
151456	2095	GGGCACCAAACAAAACGAAG	160676	CTTCGTTTTGTTTGGTGCCC
151457	2096	CGGGCACCAAACAAAACGAA	160677	TTCGTTTTGTTTGGTGCCCG
151458	2097	ACGGGCACCAAACAAAACGA	160678	TCGTTTTGTTTGGTGCCCGT
151459	2098	AACGGGCACCAAACAAAACG	160679	CGTTTTGTTTGGTGCCCGTT
151460	2099	CAACGGGCACCAAACAAAAC	160680	GTTTTGTTTGGTGCCCGTTG
151461	2100	ACAACGGGCACCAAACAAAA	160681	TTTTGTTTGGTGCCCGTTGT
151462	2101	TACAACGGGCACCAAACAAA	160682	TTTGTTTGGTGCCCGTTGTA
151463	2102	GTACAACGGGCACCAAACAA	160683	TTGTTTGGTGCCCGTTGTAC
151464	2103	GGTACAACGGGCACCAAACA	160684	TGTTTGGTGCCCGTTGTACC
151465	2104	AGGTACAACGGGCACCAAAC	160685	GTTTGGTGCCCGTTGTACCT
151466	2105	CAGGTACAACGGGCACCAAA	160686	TTTGGTGCCCGTTGTACCTG
151467	2106	TCAGGTACAACGGGCACCAA	160687	TTGGTGCCCGTTGTACCTGA
151468	2107	CTCAGGTACAACGGGCACCA	160688	TGGTGCCCGTTGTACCTGAG
151469	2108	TCTCAGGTACAACGGGCACC	160689	GGTGCCCGTTGTACCTGAGA
151470	2109	TTCTCAGGTACAACGGGCAC	160690	GTGCCCGTTGTACCTGAGAA
151471	2110	ATTCTCAGGTACAACGGGCA	160691	TGCCCGTTGTACCTGAGAAT
151472	2111	CATTCTCAGGTACAACGGGC	160692	GCCCGTTGTACCTGAGAATG
151473	2112	TCATTCTCAGGTACAACGGG	160693	CCCGTTGTACCTGAGAATGA
151474	2113	CTCATTCTCAGGTACAACGG	160694	CCGTTGTACCTGAGAATGAG
151475	2114	GCTCATTCTCAGGTACAACG	160695	CGTTGTACCTGAGAATGAGC
151476	2115	GGCTCATTCTCAGGTACAAC	160696	GTTGTACCTGAGAATGAGCC
151477	2116	AGGCTCATTCTCAGGTACAA	160697	TTGTACCTGAGAATGAGCCT
151478	2117	AAGGCTCATTCTCAGGTACA	160698	TGTACCTGAGAATGAGCCTT
151479	2118	CAAGGCTCATTCTCAGGTAC	160699	GTACCTGAGAATGAGCCTTG
151480	2119	CCAAGGCTCATTCTCAGGTA	160700	TACCTGAGAATGAGCCTTGG
151481	2120	TCCAAGGCTCATTCTCAGGT	160701	ACCTGAGAATGAGCCTTGGA
151482	2121	ATCCAAGGCTCATTCTCAGG	160702	CCTGAGAATGAGCCTTGGAT
151483	2122	TATCCAAGGCTCATTCTCAG	160703	CTGAGAATGAGCCTTGGATA
151484	2123	CTATCCAAGGCTCATTCTCA	160704	TGAGAATGAGCCTTGGATAG
151485	2124	ACTATCCAAGGCTCATTCTC	160705	GAGAATGAGCCTTGGATAGT
151486	2125	CACTATCCAAGGCTCATTCT	160706	AGAATGAGCCTTGGATAGTG
151487	2126	CCACTATCCAAGGCTCATTC	160707	GAATGAGCCTTGGATAGTGG
151488	2127	TCCACTATCCAAGGCTCATT	160708	AATGAGCCTTGGATAGTGGA
151489	2128	CTCCACTATCCAAGGCTCAT	160709	ATGAGCCTTGGATAGTGGAG
151490	2129	GCTCCACTATCCAAGGCTCA	160710	TGAGCCTTGGATAGTGGAGC
151491	2130	TGCTCCACTATCCAAGGCTC	160711	GAGCCTTGGATAGTGGAGCA
151492	2131	ATGCTCCACTATCCAAGGCT	160712	AGCCTTGGATAGTGGAGCAT
151493	2132	AATGCTCCACTATCCAAGGC	160713	GCCTTGGATAGTGGAGCATT
151494	2133	GAATGCTCCACTATCCAAGG	160714	CCTTGGATAGTGGAGCATTC
151495	2134	GGAATGCTCCACTATCCAAG	160715	CTTGGATAGTGGAGCATTCC
151496	2135	TGGAATGCTCCACTATCCAA	160716	TTGGATAGTGGAGCATTCCA
151497	2136	CTGGAATGCTCCACTATCCA	160717	TGGATAGTGGAGCATTCCAG
151498	2137	GCTGGAATGCTCCACTATCC	160718	GGATAGTGGAGCATTCCAGC
151499	2138	AGCTGGAATGCTCCACTATC	160719	GATAGTGGAGCATTCCAGCT
151500	2139	AAGCTGGAATGCTCCACTAT	160720	ATAGTGGAGCATTCCAGCTT
151501	2140	AAAGCTGGAATGCTCCACTA	160721	TAGTGGAGCATTCCAGCTTT
151502	2141	GAAAGCTGGAATGCTCCACT	160722	AGTGGAGCATTCCAGCTTTC
151503	2142	GGAAAGCTGGAATGCTCCAC	160723	GTGGAGCATTCCAGCTTTCC
151504	2143	TGGAAAGCTGGAATGCTCCA	160724	TGGAGCATTCCAGCTTTCCA
151505	2144	CTGGAAAGCTGGAATGCTCC	160725	GGAGCATTCCAGCTTTCCAG
151506	2145	TCTGGAAAGCTGGAATGCTC	160726	GAGCATTCCAGCTTTCCAGA
151507	2146	ATCTGGAAAGCTGGAATGCT	160727	AGCATTCCAGCTTTCCAGAT
151508	2147	TATCTGGAAAGCTGGAATGC	160728	GCATTCCAGCTTTCCAGATA
151509	2148	ATATCTGGAAAGCTGGAATG	160729	CATTCCAGCTTTCCAGATAT
151510	2149	CATATCTGGAAAGCTGGAAT	160730	ATTCCAGCTTTCCAGATATG
151511	2150	GCATATCTGGAAAGCTGGAA	160731	TTCCAGCTTTCCAGATATGC
151512	2151	TGCATATCTGGAAAGCTGGA	160732	TCCAGCTTTCCAGATATGCA
151513	2152	CTGCATATCTGGAAAGCTGG	160733	CCAGCTTTCCAGATATGCAG
151514	2153	TCTGCATATCTGGAAAGCTG	160734	CAGCTTTCCAGATATGCAGA
151515	2154	CTCTGCATATCTGGAAAGCT	160735	AGCTTTCCAGATATGCAGAG
151516	2155	TCTCTGCATATCTGGAAAGC	160736	GCTTTCCAGATATGCAGAGA
151517	2156	ATCTCTGCATATCTGGAAAG	160737	CTTTCCAGATATGCAGAGAT
151518	2157	TATCTCTGCATATCTGGAAA	160738	TTTCCAGATATGCAGAGATA
151519	2158	TTATCTCTGCATATCTGGAA	160739	TTCCAGATATGCAGAGATAA

151520	2159	ATTATCTCTGCATATCTGGA	160740	TCCAGATATGCAGAGATAAT
151521	2160	TATTATCTCTGCATATCTGG	160741	CCAGATATGCAGAGATAATA
151522	2161	GTATTATCTCTGCATATCTG	160742	CAGATATGCAGAGATAATAC
151523	2162	TGTATTATCTCTGCATATCT	160743	AGATATGCAGAGATAATACA
151524	2163	ATGTATTATCTCTGCATATC	160744	GATATGCAGAGATAATACAT
151525	2164	AATGTATTATCTCTGCATAT	160745	ATATGCAGAGATAATACATT
151526	2165	CAATGTATTATCTCTGCATA	160746	TATGCAGAGATAATACATTG
151527	2166	CCAATGTATTATCTCTGCAT	160747	ATGCAGAGATAATACATTGG
151528	2167	GCCAATGTATTATCTCTGCA	160748	TGCAGAGATAATACATTGGC
151529	2168	AGCCAATGTATTATCTCTGC	160749	GCAGAGATAATACATTGGCT
151530	2169	TAGCCAATGTATTATCTCTG	160750	CAGAGATAATACATTGGCTA
151531	2170	ATAGCCAATGTATTATCTCT	160751	AGAGATAATACATTGGCTAT
151532	2171	GATAGCCAATGTATTATCTC	160752	GAGATAATACATTGGCTATC
151533	2172	TGATAGCCAATGTATTATCT	160753	AGATAATACATTGGCTATCA
151534	2173	CTGATAGCCAATGTATTATC	160754	GATAATACATTGGCTATCAG
151535	2174	GCTGATAGCCAATGTATTAT	160755	ATAATACATTGGCTATCAGC
151536	2175	AGCTGATAGCCAATGTATTA	160756	TAATACATTGGCTATCAGCT
151537	2176	TAGCTGATAGCCAATGTATT	160757	AATACATTGGCTATCAGCTA
151538	2177	GTAGCTGATAGCCAATGTAT	160758	ATACATTGGCTATCAGCTAC
151539	2178	AGTAGCTGATAGCCAATGTA	160759	TACATTGGCTATCAGCTACT
151540	2179	AAGTAGCTGATAGCCAATGT	160760	ACATTGGCTATCAGCTACTT
151541	2180	CAAGTAGCTGATAGCCAATG	160761	CATTGGCTATCAGCTACTTG
151542	2181	CCAAGTAGCTGATAGCCAAT	160762	ATTGGCTATCAGCTACTTGG
151543	2182	GCCAAGTAGCTGATAGCCAA	160763	TTGGCTATCAGCTACTTGGC
151544	2183	AGCCAAGTAGCTGATAGCCA	160764	TGGCTATCAGCTACTTGGCT
151545	2184	AAGCCAAGTAGCTGATAGCC	160765	GGCTATCAGCTACTTGGCTT
151546	2185	CAAGCCAAGTAGCTGATAGC	160766	GCTATCAGCTACTTGGCTTG
151547	2186	CCAAGCCAAGTAGCTGATAG	160767	CTATCAGCTACTTGGCTTGG
151548	2187	GCCAAGCCAAGTAGCTGATA	160768	TATCAGCTACTTGGCTTGGC
151549	2188	GGCCAAGCCAAGTAGCTGAT	160769	ATCAGCTACTTGGCTTGGCC
151550	2189	AGGCCAAGCCAAGTAGCTGA	160770	TCAGCTACTTGGCTTGGCCT
151551	2190	TAGGCCAAGCCAAGTAGCTG	160771	CAGCTACTTGGCTTGGCCTA
151552	2191	ATAGGCCAAGCCAAGTAGCT	160772	AGCTACTTGGCTTGGCCTAT
151553	2192	AATAGGCCAAGCCAAGTAGC	160773	GCTACTTGGCTTGGCCTATT
151554	2193	GAATAGGCCAAGCCAAGTAG	160774	CTACTTGGCTTGGCCTATTC
151555	2194	GGAATAGGCCAAGCCAAGTA	160775	TACTTGGCTTGGCCTATTCC
151556	2195	CGGAATAGGCCAAGCCAAGT	160776	ACTTGGCTTGGCCTATTCCG
151557	2196	ACGGAATAGGCCAAGCCAAG	160777	CTTGGCTTGGCCTATTCCGT
151558	2197	CACGGAATAGGCCAAGCCAA	160778	TTGGCTTGGCCTATTCCGTG
151559	2198	ACACGGAATAGGCCAAGCCA	160779	TGGCTTGGCCTATTCCGTGT
151560	2199	AACACGGAATAGGCCAAGCC	160780	GGCTTGGCCTATTCCGTGTT
151561	2200	AAACACGGAATAGGCCAAGC	160781	GCTTGGCCTATTCCGTGTTT
151562	2201	TAAACACGGAATAGGCCAAG	160782	CTTGGCCTATTCCGTGTTTA
151563	2202	TTAAACACGGAATAGGCCAA	160783	TTGGCCTATTCCGTGTTTAA
151564	2203	TTTAAACACGGAATAGGCCA	160784	TGGCCTATTCCGTGTTTAAA
151565	2204	TTTTAAACACGGAATAGGCC	160785	GGCCTATTCCGTGTTTAAAA
151566	2205	ATTTTAAACACGGAATAGGC	160786	GCCTATTCCGTGTTTAAAAT
151567	2206	GATTTTAAACACGGAATAGG	160787	CCTATTCCGTGTTTAAAATC
151568	2207	AGATTTTAAACACGGAATAG	160788	CTATTCCGTGTTTAAAATCT
151569	2208	AAGATTTTAAACACGGAATA	160789	TATTCCGTGTTTAAAATCTT
151570	2209	CAAGATTTTAAACACGGAAT	160790	ATTCCGTGTTTAAAATCTTG
151571	2210	CCAAGATTTTAAACACGGAA	160791	TTCCGTGTTTAAAATCTTGG
151572	2211	TCCAAGATTTTAAACACGGA	160792	TCCGTGTTTAAAATCTTGGA
151573	2212	GTCCAAGATTTTAAACACGG	160793	CCGTGTTTAAAATCTTGGAC
151574	2213	AGTCCAAGATTTTAAACACG	160794	CGTGTTTAAAATCTTGGACT
151575	2214	GAGTCCAAGATTTTAAACAC	160795	GTGTTTAAAATCTTGGACTC
151576	2215	AGAGTCCAAGATTTTAAACA	160796	TGTTTAAAATCTTGGACTCT
151577	2216	AAGAGTCCAAGATTTTAAAC	160797	GTTTAAAATCTTGGACTCTT
151578	2217	AAAGAGTCCAAGATTTTAAA	160798	TTTAAAATCTTGGACTCTTT
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151580	2219	GCAAAGAGTCCAAGATTTTA	160800	TAAAATCTTGGACTCTTTGC
151581	2220	AGCAAAGAGTCCAAGATTTT	160801	AAAATCTTGGACTCTTTGCT
151582	2221	TAGCAAAGAGTCCAAGATTT	160802	AAATCTTGGACTCTTTGCTA
151583	2222	CTAGCAAAGAGTCCAAGATT	160803	AATCTTGGACTCTTTGCTAG
151584	2223	ACTAGCAAAGAGTCCAAGAT	160804	ATCTTGGACTCTTTGCTAGT
151585	2224	AACTAGCAAAGAGTCCAAGA	160805	TCTTGGACTCTTTGCTAGTT
151586	2225	AAACTAGCAAAGAGTCCAAG	160806	CTTGGACTCTTTGCTAGTTT
151587	2226	AAAACTAGCAAAGAGTCCAA	160807	TTGGACTCTTTGCTAGTTTT
151588	2227	AAAAACTAGCAAAGAGTCCA	160808	TGGACTCTTTGCTAGTTTTT
151589	2228	TAAAAACTAGCAAAGAGTCC	160809	GGACTCTTTGCTAGTTTTTA
151590	2229	GTAAAAACTAGCAAAGAGTC	160810	GACTCTTTGCTAGTTTTTAC
151591	2230	TGTAAAAACTAGCAAAGAGT	160811	ACTCTTTGCTAGTTTTTACA

151592	2231	CTGTAAAAACTAGCAAAGAG	160812	CTCTTTGCTAGTTTTTACAG
151593	2232	TCTGTAAAAACTAGCAAAGA	160813	TCTTTGCTAGTTTTTACAGA
151594	2233	ATCTGTAAAAACTAGCAAAG	160814	CTTTGCTAGTTTTTACAGAT
151595	2234	GATCTGTAAAAACTAGCAAA	160815	TTTGCTAGTTTTTACAGATC
151596	2235	TGATCTGTAAAAACTAGCAA	160816	TTGCTAGTTTTTACAGATCA
151597	2236	CTGATCTGTAAAAACTAGCA	160817	TGCTAGTTTTTACAGATCAG
151598	2237	TCTGATCTGTAAAAACTAGC	160818	GCTAGTTTTTACAGATCAGA
151599	2238	TTCTGATCTGTAAAAACTAG	160819	CTAGTTTTTACAGATCAGAA
151600	2239	ATTCTGATCTGTAAAAACTA	160820	TAGTTTTTACAGATCAGAAT
151601	2240	AATTCTGATCTGTAAAAACT	160821	AGTTTTTACAGATCAGAATT
151602	2241	AAATTCTGATCTGTAAAAAC	160822	GTTTTTACAGATCAGAATTT
151603	2242	AAAATTCTGATCTGTAAAAA	160823	TTTTTACAGATCAGAATTTT
151604	2243	AAAAATTCTGATCTGTAAAA	160824	TTTTACAGATCAGAATTTTT
151605	2244	GAAAAATTCTGATCTGTAAA	160825	TTTACAGATCAGAATTTTTC
151606	2245	TGAAAAATTCTGATCTGTAA	160826	TTACAGATCAGAATTTTTCA
151607	2246	GTGAAAAATTCTGATCTGTA	160827	TACAGATCAGAATTTTTCAC
151608	2247	CGTGAAAAATTCTGATCTGT	160828	ACAGATCAGAATTTTTCACG
151609	2248	ACGTGAAAAATTCTGATCTG	160829	CAGATCAGAATTTTTCACGT
151610	2249	TACGTGAAAAATTCTGATCT	160830	AGATCAGAATTTTTCACGTA
151611	2250	ATACGTGAAAAATTCTGATC	160831	GATCAGAATTTTTCACGTAT
151612	2251	AATACGTGAAAAATTCTGAT	160832	ATCAGAATTTTTCACGTATT
151613	2252	TAATACGTGAAAAATTCTGA	160833	TCAGAATTTTTCACGTATTA
151614	2253	TTAATACGTGAAAAATTCTG	160834	CAGAATTTTTCACGTATTAA
151615	2254	ATTAATACGTGAAAAATTCT	160835	AGAATTTTTCACGTATTAAT
151616	2255	GATTAATACGTGAAAAATTC	160836	GAATTTTTCACGTATTAATC
151617	2256	GGATTAATACGTGAAAAATT	160837	AATTTTTCACGTATTAATCC
151618	2257	TGGATTAATACGTGAAAAAT	160838	ATTTTTCACGTATTAATCCA
151619	2258	CTGGATTAATACGTGAAAAA	160839	TTTTTCACGTATTAATCCAG
151620	2259	ACTGGATTAATACGTGAAAA	160840	TTTTCACGTATTAATCCAGT
151621	2260	AACTGGATTAATACGTGAAA	160841	TTTCACGTATTAATCCAGTT
151622	2261	AAACTGGATTAATACGTGAA	160842	TTCACGTATTAATCCAGTTT
151623	2262	AAAACTGGATTAATACGTGA	160843	TCACGTATTAATCCAGTTTT
151624	2263	GAAAACTGGATTAATACGTG	160844	CACGTATTAATCCAGTTTTC
151625	2264	GGAAAACTGGATTAATACGT	160845	ACGTATTAATCCAGTTTTCC
151626	2265	AGGAAAACTGGATTAATACG	160846	CGTATTAATCCAGTTTTCCT
151627	2266	TAGGAAAACTGGATTAATAC	160847	GTATTAATCCAGTTTTCCTA
151628	2267	CTAGGAAAACTGGATTAATA	160848	TATTAATCCAGTTTTCCTAG
151629	2268	GCTAGGAAAACTGGATTAAT	160849	ATTAATCCAGTTTTCCTAGC
151630	2269	AGCTAGGAAAACTGGATTAA	160850	TTAATCCAGTTTTCCTAGCT
151631	2270	AAGCTAGGAAAACTGGATTA	160851	TAATCCAGTTTTCCTAGCTT
151632	2271	GAAGCTAGGAAAACTGGATT	160852	AATCCAGTTTTCCTAGCTTC
151633	2272	AGAAGCTAGGAAAACTGGAT	160853	ATCCAGTTTTCCTAGCTTCT
151634	2273	GAGAAGCTAGGAAAACTGGA	160854	TCCAGTTTTCCTAGCTTCTC
151635	2274	AGAGAAGCTAGGAAAACTGG	160855	CCAGTTTTCCTAGCTTCTCT
151636	2275	AAGAGAAGCTAGGAAAACTG	160856	CAGTTTTCCTAGCTTCTCTT
151637	2276	CAAGAGAAGCTAGGAAAACT	160857	AGTTTTCCTAGCTTCTCTTG
151638	2277	TCAAGAGAAGCTAGGAAAAC	160858	GTTTTCCTAGCTTCTCTTGA
151639	2278	TTCAAGAGAAGCTAGGAAAA	160859	TTTTCCTAGCTTCTCTTGAA
151640	2279	CTTCAAGAGAAGCTAGGAAA	160860	TTTCCTAGCTTCTCTTGAAG
151641	2280	TCTTCAAGAGAAGCTAGGAA	160861	TTCCTAGCTTCTCTTGAAGA
151642	2281	TTCTTCAAGAGAAGCTAGGA	160862	TCCTAGCTTCTCTTGAAGAA
151643	2282	ATTCTTCAAGAGAAGCTAGG	160863	CCTAGCTTCTCTTGAAGAAT
151644	2283	AATTCTTCAAGAGAAGCTAG	160864	CTAGCTTCTCTTGAAGAATT
151645	2284	AAATTCTTCAAGAGAAGCTA	160865	TAGCTTCTCTTGAAGAATTT
151646	2285	AAAATTCTTCAAGAGAAGCT	160866	AGCTTCTCTTGAAGAATTTT
151647	2286	AAAAATTCTTCAAGAGAAGC	160867	GCTTCTCTTGAAGAATTTTT
151648	2287	CAAAAATTCTTCAAGAGAAG	160868	CTTCTCTTGAAGAATTTTTG
151649	2288	CCAAAAATTCTTCAAGAGAA	160869	TTCTCTTGAAGAATTTTTGG
151650	2289	TCCAAAAATTCTTCAAGAGA	160870	TCTCTTGAAGAATTTTTGGA
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151652	2291	TCTCCAAAAATTCTTCAAGA	160872	TCTTGAAGAATTTTTGGAGA
151653	2292	ATCTCCAAAAATTCTTCAAG	160873	CTTGAAGAATTTTTGGAGAT
151654	2293	GATCTCCAAAAATTCTTCAA	160874	TTGAAGAATTTTTGGAGATC
151655	2294	AGATCTCCAAAAATTCTTCA	160875	TGAAGAATTTTTGGAGATCT
151656	2295	GAGATCTCCAAAAATTCTTC	160876	GAAGAATTTTTGGAGATCTC
151657	2296	AGAGATCTCCAAAAATTCTT	160877	AAGAATTTTTGGAGATCTCT
151658	2297	AAGAGATCTCCAAAAATTCT	160878	AGAATTTTTGGAGATCTCTT
151659	2298	GAAGAGATCTCCAAAAATTC	160879	GAATTTTTGGAGATCTCTTC
151660	2299	TGAAGAGATCTCCAAAAATT	160880	AATTTTTGGAGATCTCTTCA
151661	2300	ATGAAGAGATCTCCAAAAAT	160881	ATTTTTGGAGATCTCTTCAT
151662	2301	TATGAAGAGATCTCCAAAAA	160882	TTTTTGGAGATCTCTTCATA
151663	2302	GTATGAAGAGATCTCCAAAA	160883	TTTTGGAGATCTCTTCATAC

151664	2303	AGTATGAAGAGATCTCCAAA	160884	TTTGGAGATCTCTTCATACT
151665	2304	CAGTATGAAGAGATCTCCAA	160885	TTGGAGATCTCTTCATACTG
151666	2305	TCAGTATGAAGAGATCTCCA	160886	TGGAGATCTCTTCATACTGA
151667	2306	CTCAGTATGAAGAGATCTCC	160887	GGAGATCTCTTCATACTGAG
151668	2307	GCTCAGTATGAAGAGATCTC	160888	GAGATCTCTTCATACTGAGC
151669	2308	GGCTCAGTATGAAGAGATCT	160889	AGATCTCTTCATACTGAGCC
151670	2309	AGGCTCAGTATGAAGAGATC	160890	GATCTCTTCATACTGAGCCT
151671	2310	AAGGCTCAGTATGAAGAGAT	160891	ATCTCTTCATACTGAGCCTT
151672	2311	GAAGGCTCAGTATGAAGAGA	160892	TCTCTTCATACTGAGCCTTC
151673	2312	TGAAGGCTCAGTATGAAGAG	160893	CTCTTCATACTGAGCCTTCA
151674	2313	ATGAAGGCTCAGTATGAAGA	160894	TCTTCATACTGAGCCTTCAT
151675	2314	AATGAAGGCTCAGTATGAAG	160895	CTTCATACTGAGCCTTCATT
151676	2315	TAATGAAGGCTCAGTATGAA	160896	TTCATACTGAGCCTTCATTA
151677	2316	CTAATGAAGGCTCAGTATGA	160897	TCATACTGAGCCTTCATTAG
151678	2317	GCTAATGAAGGCTCAGTATG	160898	CATACTGAGCCTTCATTAGC
151679	2318	GGCTAATGAAGGCTCAGTAT	160899	ATACTGAGCCTTCATTAGCC
151680	2319	GGGCTAATGAAGGCTCAGTA	160900	TACTGAGCCTTCATTAGCCC
151681	2320	TGGGCTAATGAAGGCTCAGT	160901	ACTGAGCCTTCATTAGCCCA
151682	2321	CTGGGCTAATGAAGGCTCAG	160902	CTGAGCCTTCATTAGCCCAG
151683	2322	CCTGGGCTAATGAAGGCTCA	160903	TGAGCCTTCATTAGCCCAGG
151684	2323	TCCTGGGCTAATGAAGGCTC	160904	GAGCCTTCATTAGCCCAGGA
151685	2324	GTCCTGGGCTAATGAAGGCT	160905	AGCCTTCATTAGCCCAGGAC
151686	2325	TGTCCTGGGCTAATGAAGGC	160906	GCCTTCATTAGCCCAGGACA
151687	2326	CTGTCCTGGGCTAATGAAGG	160907	CCTTCATTAGCCCAGGACAG
151688	2327	ACTGTCCTGGGCTAATGAAG	160908	CTTCATTAGCCCAGGACAGT
151689	2328	TACTGTCCTGGGCTAATGAA	160909	TTCATTAGCCCAGGACAGTA
151690	2329	GTACTGTCCTGGGCTAATGA	160910	TCATTAGCCCAGGACAGTAC
151691	2330	AGTACTGTCCTGGGCTAATG	160911	CATTAGCCCAGGACAGTACT
151692	2331	CAGTACTGTCCTGGGCTAAT	160912	ATTAGCCCAGGACAGTACTG
151693	2332	GCAGTACTGTCCTGGGCTAA	160913	TTAGCCCAGGACAGTACTGC
151694	2333	AGCAGTACTGTCCTGGGCTA	160914	TAGCCCAGGACAGTACTGCT
151695	2334	CAGCAGTACTGTCCTGGGCT	160915	AGCCCAGGACAGTACTGCTG
151696	2335	ACAGCAGTACTGTCCTGGGC	160916	GCCCAGGACAGTACTGCTGT
151697	2336	TACAGCAGTACTGTCCTGGG	160917	CCCAGGACAGTACTGCTGTA
151698	2337	CTACAGCAGTACTGTCCTGG	160918	CCAGGACAGTACTGCTGTAG
151699	2338	GCTACAGCAGTACTGTCCTG	160919	CAGGACAGTACTGCTGTAGC
151700	2339	TGCTACAGCAGTACTGTCCT	160920	AGGACAGTACTGCTGTAGCA
151701	2340	CTGCTACAGCAGTACTGTCC	160921	GGACAGTACTGCTGTAGCAG
151702	2341	ACTGCTACAGCAGTACTGTC	160922	GACAGTACTGCTGTAGCAGT
151703	2342	AACTGCTACAGCAGTACTGT	160923	ACAGTACTGCTGTAGCAGTT
151704	2343	GAACTGCTACAGCAGTACTG	160924	CAGTACTGCTGTAGCAGTTC
151705	2344	TGAACTGCTACAGCAGTACT	160925	AGTACTGCTGTAGCAGTTCA
151706	2345	ATGAACTGCTACAGCAGTAC	160926	GTACTGCTGTAGCAGTTCAT
151707	2346	TATGAACTGCTACAGCAGTA	160927	TACTGCTGTAGCAGTTCATA
151708	2347	ATATGAACTGCTACAGCAGT	160928	ACTGCTGTAGCAGTTCATAT
151709	2348	TATATGAACTGCTACAGCAG	160929	CTGCTGTAGCAGTTCATATA
151710	2349	ATATATGAACTGCTACAGCA	160930	TGCTGTAGCAGTTCATATAT
151711	2350	AATATATGAACTGCTACAGC	160931	GCTGTAGCAGTTCATATATT
151712	2351	AAATATATGAACTGCTACAG	160932	CTGTAGCAGTTCATATATTT
151713	2352	AAAATATATGAACTGCTACA	160933	TGTAGCAGTTCATATATTTT
151714	2353	AAAAATATATGAACTGCTAC	160934	GTAGCAGTTCATATATTTTT
151715	2354	AAAAAATATATGAACTGCTA	160935	TAGCAGTTCATATATTTTTT
151716	2355	GAAAAAATATATGAACTGCT	160936	AGCAGTTCATATATTTTTTC
151717	2356	CGAAAAAATATATGAACTGC	160937	GCAGTTCATATATTTTTTCG
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151719	2358	AGCGAAAAAATATATGAACT	160939	AGTTCATATATTTTTTCGCT
151720	2359	AAGCGAAAAAATATATGAAC	160940	GTTCATATATTTTTTCGCTT
151721	2360	GAAGCGAAAAAATATATGAA	160941	TTCATATATTTTTTCGCTTC
151722	2361	GGAAGCGAAAAAATATATGA	160942	TCATATATTTTTTCGCTTCC
151723	2362	GGGAAGCGAAAAAATATATG	160943	CATATATTTTTTCGCTTCCC
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151725	2364	CTGGGAAGCGAAAAAATATA	160945	TATATTTTTTCGCTTCCCAG
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151727	2366	GCCTGGGAAGCGAAAAAATA	160947	TATTTTTTCGCTTCCCAGGC
151728	2367	GGCCTGGGAAGCGAAAAAAT	160948	ATTTTTTCGCTTCCCAGGCC
151729	2368	AGGCCTGGGAAGCGAAAAAA	160949	TTTTTTCGCTTCCCAGGCCT
151730	2369	CAGGCCTGGGAAGCGAAAAA	160950	TTTTTCGCTTCCCAGGCCTG
151731	2370	ACAGGCCTGGGAAGCGAAAA	160951	TTTTCGCTTCCCAGGCCTGT
151732	2371	CACAGGCCTGGGAAGCGAAA	160952	TTTCGCTTCCCAGGCCTGTG
151733	2372	ACACAGGCCTGGGAAGCGAA	160953	TTCGCTTCCCAGGCCTGTGT
151734	2373	AACACAGGCCTGGGAAGCGA	160954	TCGCTTCCCAGGCCTGTGTT
151735	2374	TAACACAGGCCTGGGAAGCG	160955	CGCTTCCCAGGCCTGTGTTA

151736	2375	ATAACACAGGCCTGGGAAGC	160956	GCTTCCCAGGCCTGTGTTAT
151737	2376	AATAACACAGGCCTGGGAAG	160957	CTTCCCAGGCCTGTGTTATT
151738	2377	GAATAACACAGGCCTGGGAA	160958	TTCCCAGGCCTGTGTTATTC
151739	2378	TGAATAACACAGGCCTGGGA	160959	TCCCAGGCCTGTGTTATTCA
151740	2379	GTGAATAACACAGGCCTGGG	160960	CCCAGGCCTGTGTTATTCAC
151741	2380	AGTGAATAACACAGGCCTGG	160961	CCAGGCCTGTGTTATTCACT
151742	2381	AAGTGAATAACACAGGCCTG	160962	CAGGCCTGTGTTATTCACTT
151743	2382	TAAGTGAATAACACAGGCCT	160963	AGGCCTGTGTTATTCACTTA
151744	2383	TTAAGTGAATAACACAGGCC	160964	GGCCTGTGTTATTCACTTAA
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151746	2385	ACTTAAGTGAATAACACAGG	160966	CCTGTGTTATTCACTTAAGT
151747	2386	AACTTAAGTGAATAACACAG	160967	CTGTGTTATTCACTTAAGTT
151748	2387	GAACTTAAGTGAATAACACA	160968	TGTGTTATTCACTTAAGTTC
151749	2388	TGAACTTAAGTGAATAACAC	160969	GTGTTATTCACTTAAGTTCA
151750	2389	ATGAACTTAAGTGAATAACA	160970	TGTTATTCACTTAAGTTCAT
151751	2390	TATGAACTTAAGTGAATAAC	160971	GTTATTCACTTAAGTTCATA
151752	2391	CTATGAACTTAAGTGAATAA	160972	TTATTCACTTAAGTTCATAG
151753	2392	GCTATGAACTTAAGTGAATA	160973	TATTCACTTAAGTTCATAGC
151754	2393	GGCTATGAACTTAAGTGAAT	160974	ATTCACTTAAGTTCATAGCC
151755	2394	AGGCTATGAACTTAAGTGAA	160975	TTCACTTAAGTTCATAGCCT
151756	2395	CAGGCTATGAACTTAAGTGA	160976	TCACTTAAGTTCATAGCCTG
151757	2396	CCAGGCTATGAACTTAAGTG	160977	CACTTAAGTTCATAGCCTGG
151758	2397	ACCAGGCTATGAACTTAAGT	160978	ACTTAAGTTCATAGCCTGGT
151759	2398	GACCAGGCTATGAACTTAAG	160979	CTTAAGTTCATAGCCTGGTC
151760	2399	GGACCAGGCTATGAACTTAA	160980	TTAAGTTCATAGCCTGGTCC
151761	2400	GGGACCAGGCTATGAACTTA	160981	TAAGTTCATAGCCTGGTCCC
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151763	2402	CAGGGACCAGGCTATGAACT	160983	AGTTCATAGCCTGGTCCCTG
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151766	2405	CTGCAGGGACCAGGCTATGA	160986	TCATAGCCTGGTCCCTGCAG
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151768	2407	CCCTGCAGGGACCAGGCTAT	160988	ATAGCCTGGTCCCTGCAGGG
151769	2408	ACCCTGCAGGGACCAGGCTA	160989	TAGCCTGGTCCCTGCAGGGT
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151773	2412	TACAACCCTGCAGGGACCAG	160993	CTGGTCCCTGCAGGGTTGTA
151774	2413	GTACAACCCTGCAGGGACCA	160994	TGGTCCCTGCAGGGTTGTAC
151775	2414	GGTACAACCCTGCAGGGACC	160995	GGTCCCTGCAGGGTTGTACC
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151777	2416	CGGGTACAACCCTGCAGGGA	160997	TCCCTGCAGGGTTGTACCCG
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151780	2419	GCTCGGGTACAACCCTGCAG	161000	CTGCAGGGTTGTACCCGAGC
151781	2420	TGCTCGGGTACAACCCTGCA	161001	TGCAGGGTTGTACCCGAGCA
151782	2421	GTGCTCGGGTACAACCCTGC	161002	GCAGGGTTGTACCCGAGCAC
151783	2422	TGTGCTCGGGTACAACCCTG	161003	CAGGGTTGTACCCGAGCACA
151784	2423	CTGTGCTCGGGTACAACCCT	161004	AGGGTTGTACCCGAGCACAG
151785	2424	GCTGTGCTCGGGTACAACCC	161005	GGGTTGTACCCGAGCACAGC
151786	2425	AGCTGTGCTCGGGTACAACC	161006	GGTTGTACCCGAGCACAGCT
151787	2426	TAGCTGTGCTCGGGTACAAC	161007	GTTGTACCCGAGCACAGCTA
151788	2427	GTAGCTGTGCTCGGGTACAA	161008	TTGTACCCGAGCACAGCTAC
151789	2428	AGTAGCTGTGCTCGGGTACA	161009	TGTACCCGAGCACAGCTACT
151790	2429	AAGTAGCTGTGCTCGGGTAC	161010	GTACCCGAGCACAGCTACTT
151791	2430	TAAGTAGCTGTGCTCGGGTA	161011	TACCCGAGCACAGCTACTTA
151792	2431	CTAAGTAGCTGTGCTCGGGT	161012	ACCCGAGCACAGCTACTTAG
151793	2432	TCTAAGTAGCTGTGCTCGGG	161013	CCCGAGCACAGCTACTTAGA
151794	2433	ATCTAAGTAGCTGTGCTCGG	161014	CCGAGCACAGCTACTTAGAT
151795	2434	CATCTAAGTAGCTGTGCTCG	161015	CGAGCACAGCTACTTAGATG
151796	2435	ACATCTAAGTAGCTGTGCTC	161016	GAGCACAGCTACTTAGATGT
151797	2436	GACATCTAAGTAGCTGTGCT	161017	AGCACAGCTACTTAGATGTC
151798	2437	GGACATCTAAGTAGCTGTGC	161018	GCACAGCTACTTAGATGTCC
151799	2438	AGGACATCTAAGTAGCTGTG	161019	CACAGCTACTTAGATGTCCT
151800	2439	CAGGACATCTAAGTAGCTGT	161020	ACAGCTACTTAGATGTCCTG
151801	2440	TCAGGACATCTAAGTAGCTG	161021	CAGCTACTTAGATGTCCTGA
151802	2441	TTCAGGACATCTAAGTAGCT	161022	AGCTACTTAGATGTCCTGAA
151803	2442	ATTCAGGACATCTAAGTAGC	161023	GCTACTTAGATGTCCTGAAT
151804	2443	CATTCAGGACATCTAAGTAG	161024	CTACTTAGATGTCCTGAATG
151805	2444	ACATTCAGGACATCTAAGTA	161025	TACTTAGATGTCCTGAATGT
151806	2445	TACATTCAGGACATCTAAGT	161026	ACTTAGATGTCCTGAATGTA
151807	2446	ATACATTCAGGACATCTAAG	161027	CTTAGATGTCCTGAATGTAT

151808	2447	AATACATTCAGGACATCTAA	161028	TTAGATGTCCTGAATGTATT
151809	2448	TAATACATTCAGGACATCTA	161029	TAGATGTCCTGAATGTATTA
151810	2449	GTAATACATTCAGGACATCT	161030	AGATGTCCTGAATGTATTAC
151811	2450	GGTAATACATTCAGGACATC	161031	GATGTCCTGAATGTATTACC
151812	2451	CGGTAATACATTCAGGACAT	161032	ATGTCCTGAATGTATTACCG
151813	2452	CCGGTAATACATTCAGGACA	161033	TGTCCTGAATGTATTACCGG
151814	2453	ACCGGTAATACATTCAGGAC	161034	GTCCTGAATGTATTACCGGT
151815	2454	AACCGGTAATACATTCAGGA	161035	TCCTGAATGTATTACCGGTT
151816	2455	TAACCGGTAATACATTCAGG	161036	CCTGAATGTATTACCGGTTA
151817	2456	TTAACCGGTAATACATTCAG	161037	CTGAATGTATTACCGGTTAA
151818	2457	TTTAACCGGTAATACATTCA	161038	TGAATGTATTACCGGTTAAA
151819	2458	ATTTAACCGGTAATACATTC	161039	GAATGTATTACCGGTTAAAT
151820	2459	CATTTAACCGGTAATACATT	161040	AATGTATTACCGGTTAAATG
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151822	2461	TCCATTTAACCGGTAATACA	161042	TGTATTACCGGTTAAATGGA
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151824	2463	CCTCCATTTAACCGGTAATA	161044	TATTACCGGTTAAATGGAGG
151825	2464	ACCTCCATTTAACCGGTAAT	161045	ATTACCGGTTAAATGGAGGT
151826	2465	AACCTCCATTTAACCGGTAA	161046	TTACCGGTTAAATGGAGGTT
151827	2466	AAACCTCCATTTAACCGGTA	161047	TACCGGTTAAATGGAGGTTT
151828	2467	GAAACCTCCATTTAACCGGT	161048	ACCGGTTAAATGGAGGTTTC
151829	2468	TGAAACCTCCATTTAACCGG	161049	CCGGTTAAATGGAGGTTTCA
151830	2469	TTGAAACCTCCATTTAACCG	161050	CGGTTAAATGGAGGTTTCAA
151831	2470	TTTGAAACCTCCATTTAACC	161051	GGTTAAATGGAGGTTTCAAA
151832	2471	CTTTGAAACCTCCATTTAAC	161052	GTTAAATGGAGGTTTCAAAG
151833	2472	TCTTTGAAACCTCCATTTAA	161053	TTAAATGGAGGTTTCAAAGA
151834	2473	TTCTTTGAAACCTCCATTTA	161054	TAAATGGAGGTTTCAAAGAA
151835	2474	GTTCTTTGAAACCTCCATTT	161055	AAATGGAGGTTTCAAAGAAC
151836	2475	GGTTCTTTGAAACCTCCATT	161056	AATGGAGGTTTCAAAGAACC
151837	2476	AGGTTCTTTGAAACCTCCAT	161057	ATGGAGGTTTCAAAGAACCT
151838	2477	CAGGTTCTTTGAAACCTCCA	161058	TGGAGGTTTCAAAGAACCTG
151839	2478	GCAGGTTCTTTGAAACCTCC	161059	GGAGGTTTCAAAGAACCTGC
151840	2479	AGCAGGTTCTTTGAAACCTC	161060	GAGGTTTCAAAGAACCTGCT
151841	2480	CAGCAGGTTCTTTGAAACCT	161061	AGGTTTCAAAGAACCTGCTG
151842	2481	ACAGCAGGTTCTTTGAAACC	161062	GGTTTCAAAGAACCTGCTGT
151843	2482	AACAGCAGGTTCTTTGAAAC	161063	GTTTCAAAGAACCTGCTGTT
151844	2483	AAACAGCAGGTTCTTTGAAA	161064	TTTCAAAGAACCTGCTGTTT
151845	2484	AAAACAGCAGGTTCTTTGAA	161065	TTCAAAGAACCTGCTGTTTT
151846	2485	AAAAACAGCAGGTTCTTTGA	161066	TCAAAGAACCTGCTGTTTTT
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151850	2489	GGCCAAAAACAGCAGGTTCT	161070	AGAACCTGCTGTTTTTGGCC
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151853	2492	CAGGGCCAAAAACAGCAGGT	161073	ACCTGCTGTTTTTGGCCCTG
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151858	2497	GAGCACAGGGCCAAAAACAG	161078	CTGTTTTTGGCCCTGTGCTC
151859	2498	AGAGCACAGGGCCAAAAACA	161079	TGTTTTTGGCCCTGTGCTCT
151860	2499	AAGAGCACAGGGCCAAAAAC	161080	GTTTTTGGCCCTGTGCTCTT
151861	2500	CAAGAGCACAGGGCCAAAAA	161081	TTTTTGGCCCTGTGCTCTTG
151862	2501	TCAAGAGCACAGGGCCAAAA	161082	TTTTGGCCCTGTGCTCTTGA
151863	2502	ATCAAGAGCACAGGGCCAAA	161083	TTTGGCCCTGTGCTCTTGAT
151864	2503	TATCAAGAGCACAGGGCCAA	161084	TTGGCCCTGTGCTCTTGATA
151865	2504	TTATCAAGAGCACAGGGCCA	161085	TGGCCCTGTGCTCTTGATAA
151866	2505	GTTATCAAGAGCACAGGGCC	161086	GGCCCTGTGCTCTTGATAAC
151867	2506	TGTTATCAAGAGCACAGGGC	161087	GCCCTGTGCTCTTGATAACA
151868	2507	CTGTTATCAAGAGCACAGGG	161088	CCCTGTGCTCTTGATAACAG
151869	2508	TCTGTTATCAAGAGCACAGG	161089	CCTGTGCTCTTGATAACAGA
151870	2509	CTCTGTTATCAAGAGCACAG	161090	CTGTGCTCTTGATAACAGAG
151871	2510	ACTCTGTTATCAAGAGCACA	161091	TGTGCTCTTGATAACAGAGT
151872	2511	CACTCTGTTATCAAGAGCAC	161092	GTGCTCTTGATAACAGAGTG
151873	2512	ACACTCTGTTATCAAGAGCA	161093	TGCTCTTGATAACAGAGTGT
151874	2513	AACACTCTGTTATCAAGAGC	161094	GCTCTTGATAACAGAGTGTT
151875	2514	AAACACTCTGTTATCAAGAG	161095	CTCTTGATAACAGAGTGTTT
151876	2515	CAAACACTCTGTTATCAAGA	161096	TCTTGATAACAGAGTGTTTG
151877	2516	TCAAACACTCTGTTATCAAG	161097	CTTGATAACAGAGTGTTTGA
151878	2517	CTCAAACACTCTGTTATCAA	161098	TTGATAACAGAGTGTTTGAG
151879	2518	CCTCAAACACTCTGTTATCA	161099	TGATAACAGAGTGTTTGAGG

151880	2519	CCCTCAAACACTCTGTTATC	161100	GATAACAGAGTGTTTGAGGG
151881	2520	TCCCTCAAACACTCTGTTAT	161101	ATAACAGAGTGTTTGAGGGA
151882	2521	GTCCCTCAAACACTCTGTTA	161102	TAACAGAGTGTTTGAGGGAC
151883	2522	TGTCCCTCAAACACTCTGTT	161103	AACAGAGTGTTTGAGGGACA
151884	2523	TTGTCCCTCAAACACTCTGT	161104	ACAGAGTGTTTGAGGGACAA
151885	2524	GTTGTCCCTCAAACACTCTG	161105	CAGAGTGTTTGAGGGACAAC
151886	2525	AGTTGTCCCTCAAACACTCT	161106	AGAGTGTTTGAGGGACAACT
151887	2526	AAGTTGTCCCTCAAACACTC	161107	GAGTGTTTGAGGGACAACTT
151888	2527	AAAGTTGTCCCTCAAACACT	161108	AGTGTTTGAGGGACAACTTT
151889	2528	GAAAGTTGTCCCTCAAACAC	161109	GTGTTTGAGGGACAACTTTC
151890	2529	TGAAAGTTGTCCCTCAAACA	161110	TGTTTGAGGGACAACTTTCA
151891	2530	GTGAAAGTTGTCCCTCAAAC	161111	GTTTGAGGGACAACTTTCAC
151892	2531	TGTGAAAGTTGTCCCTCAAA	161112	TTTGAGGGACAACTTTCACA
151893	2532	ATGTGAAAGTTGTCCCTCAA	161113	TTGAGGGACAACTTTCACAT
151894	2533	AATGTGAAAGTTGTCCCTCA	161114	TGAGGGACAACTTTCACATT
151895	2534	AAATGTGAAAGTTGTCCCTC	161115	GAGGGACAACTTTCACATTT
151896	2535	CAAATGTGAAAGTTGTCCCT	161116	AGGGACAACTTTCACATTTG
151897	2536	TCAAATGTGAAAGTTGTCCC	161117	GGGACAACTTTCACATTTGA
151898	2537	CTCAAATGTGAAAGTTGTCC	161118	GGACAACTTTCACATTTGAG
151899	2538	ACTCAAATGTGAAAGTTGTC	161119	GACAACTTTCACATTTGAGT
151900	2539	AACTCAAATGTGAAAGTTGT	161120	ACAACTTTCACATTTGAGTT
151901	2540	AAACTCAAATGTGAAAGTTG	161121	CAACTTTCACATTTGAGTTT
151902	2541	AAAACTCAAATGTGAAAGTT	161122	AACTTTCACATTTGAGTTTT
151903	2542	AAAAACTCAAATGTGAAAGT	161123	ACTTTCACATTTGAGTTTTT
151904	2543	GAAAAACTCAAATGTGAAAG	161124	CTTTCACATTTGAGTTTTTC
151905	2544	GGAAAAACTCAAATGTGAAA	161125	TTTCACATTTGAGTTTTTCC
151906	2545	TGGAAAAACTCAAATGTGAA	161126	TTCACATTTGAGTTTTTCCA
151907	2546	TTGGAAAAACTCAAATGTGA	161127	TCACATTTGAGTTTTTCCAA
151908	2547	TTTGGAAAAACTCAAATGTG	161128	CACATTTGAGTTTTTCCAAA
151909	2548	TTTTGGAAAAACTCAAATGT	161129	ACATTTGAGTTTTTCCAAAA
151910	2549	ATTTTGGAAAAACTCAAATG	161130	CATTTGAGTTTTTCCAAAAT
151911	2550	AATTTTGGAAAAACTCAAAT	161131	ATTTGAGTTTTTCCAAAATT
151912	2551	TAATTTTGGAAAAACTCAAA	161132	TTTGAGTTTTTCCAAAATTA
151913	2552	TTAATTTTGGAAAAACTCAA	161133	TTGAGTTTTTCCAAAATTAA
151914	2553	TTTAATTTTGGAAAAACTCA	161134	TGAGTTTTTCCAAAATTAAA
151915	2554	CTTTAATTTTGGAAAAACTC	161135	GAGTTTTTCCAAAATTAAAG
151916	2555	CCTTTAATTTTGGAAAAACT	161136	AGTTTTTCCAAAATTAAAGG
151917	2556	ACCTTTAATTTTGGAAAAAC	161137	GTTTTTCCAAAATTAAAGGT
151918	2557	AACCTTTAATTTTGGAAAAA	161138	TTTTTCCAAAATTAAAGGTT
151919	2558	CAACCTTTAATTTTGGAAAA	161139	TTTTCCAAAATTAAAGGTTG
151920	2559	ACAACCTTTAATTTTGGAAA	161140	TTTCCAAAATTAAAGGTTGT
151921	2560	TACAACCTTTAATTTTGGAA	161141	TTCCAAAATTAAAGGTTGTA
151922	2561	CTACAACCTTTAATTTTGGA	161142	TCCAAAATTAAAGGTTGTAG
151923	2562	TCTACAACCTTTAATTTTGG	161143	CCAAAATTAAAGGTTGTAGA
151924	2563	TTCTACAACCTTTAATTTTG	161144	CAAAATTAAAGGTTGTAGAA
151925	2564	CTTCTACAACCTTTAATTTT	161145	AAAATTAAAGGTTGTAGAAG
151926	2565	TCTTCTACAACCTTTAATTT	161146	AAATTAAAGGTTGTAGAAGA
151927	2566	CTCTTCTACAACCTTTAATT	161147	AATTAAAGGTTGTAGAAGAG
151928	2567	ACTCTTCTACAACCTTTAAT	161148	ATTAAAGGTTGTAGAAGAGT
151929	2568	GACTCTTCTACAACCTTTAA	161149	TTAAAGGTTGTAGAAGAGTC
151930	2569	TGACTCTTCTACAACCTTTA	161150	TAAAGGTTGTAGAAGAGTCA
151931	2570	GTGACTCTTCTACAACCTTT	161151	AAAGGTTGTAGAAGAGTCAC
151932	2571	TGTGACTCTTCTACAACCTT	161152	AAGGTTGTAGAAGAGTCACA
151933	2572	CTGTGACTCTTCTACAACCT	161153	AGGTTGTAGAAGAGTCACAG
151934	2573	ACTGTGACTCTTCTACAACC	161154	GGTTGTAGAAGAGTCACAGT
151935	2574	TACTGTGACTCTTCTACAAC	161155	GTTGTAGAAGAGTCACAGTA
151936	2575	ATACTGTGACTCTTCTACAA	161156	TTGTAGAAGAGTCACAGTAT
151937	2576	GATACTGTGACTCTTCTACA	161157	TGTAGAAGAGTCACAGTATC
151938	2577	AGATACTGTGACTCTTCTAC	161158	GTAGAAGAGTCACAGTATCT
151939	2578	TAGATACTGTGACTCTTCTA	161159	TAGAAGAGTCACAGTATCTA
151940	2579	ATAGATACTGTGACTCTTCT	161160	AGAAGAGTCACAGTATCTAT
151941	2580	AATAGATACTGTGACTCTTC	161161	GAAGAGTCACAGTATCTATT
151942	2581	CAATAGATACTGTGACTCTT	161162	AAGAGTCACAGTATCTATTG
151943	2582	ACAATAGATACTGTGACTCT	161163	AGAGTCACAGTATCTATTGT
151944	2583	GACAATAGATACTGTGACTC	161164	GAGTCACAGTATCTATTGTC
151945	2584	TGACAATAGATACTGTGACT	161165	AGTCACAGTATCTATTGTCA
151946	2585	TTGACAATAGATACTGTGAC	161166	GTCACAGTATCTATTGTCAA
151947	2586	TTTGACAATAGATACTGTGA	161167	TCACAGTATCTATTGTCAAA
151948	2587	TTTTGACAATAGATACTGTG	161168	CACAGTATCTATTGTCAAAA
151949	2588	TTTTTGACAATAGATACTGT	161169	ACAGTATCTATTGTCAAAAA
151950	2589	CTTTTTGACAATAGATACTG	161170	CAGTATCTATTGTCAAAAAG
151951	2590	TCTTTTTGACAATAGATACT	161171	AGTATCTATTGTCAAAAAGA

151952	2591	TTCTTTTTGACAATAGATAC	161172	GTATCTATTGTCAAAAAGAA
151953	2592	TTTCTTTTTGACAATAGATA	161173	TATCTATTGTCAAAAAGAAA
151954	2593	TTTTCTTTTTGACAATAGAT	161174	ATCTATTGTCAAAAAGAAAA
151955	2594	CTTTTCTTTTTGACAATAGA	161175	TCTATTGTCAAAAAGAAAAG
151956	2595	TCTTTTCTTTTTGACAATAG	161176	CTATTGTCAAAAAGAAAAGA
151957	2596	TTCTTTTCTTTTTGACAATA	161177	TATTGTCAAAAAGAAAAGAA
151958	2597	ATTCTTTTCTTTTTGACAAT	161178	ATTGTCAAAAAGAAAAGAAT
151959	2598	AATTCTTTTCTTTTTGACAA	161179	TTGTCAAAAAGAAAAGAATT
151960	2599	AAATTCTTTTCTTTTTGACA	161180	TGTCAAAAAGAAAAGAATTT
151961	2600	TAAATTCTTTTCTTTTTGAC	161181	GTCAAAAAGAAAAGAATTTA
151962	2601	TTAAATTCTTTTCTTTTTGA	161182	TCAAAAAGAAAAGAATTTAA
151963	2602	TTTAAATTCTTTTCTTTTTG	161183	CAAAAAGAAAAGAATTTAAA
151964	2603	TTTTAAATTCTTTTCTTTTT	161184	AAAAAGAAAAGAATTTAAAA
151965	2604	TTTTTAAATTCTTTTCTTTT	161185	AAAAGAAAAGAATTTAAAAA
151966	2605	CTTTTTAAATTCTTTTCTTT	161186	AAAGAAAAGAATTTAAAAAG
151967	2606	CCTTTTTAAATTCTTTTCTT	161187	AAGAAAAGAATTTAAAAAGG
151968	2607	GCCTTTTTAAATTCTTTTCT	161188	AGAAAAGAATTTAAAAAGGC
151969	2608	TGCCTTTTTAAATTCTTTTC	161189	GAAAAGAATTTAAAAAGGCA
151970	2609	CTGCCTTTTTAAATTCTTTT	161190	AAAAGAATTTAAAAAGGCAG
151971	2610	GCTGCCTTTTTAAATTCTTT	161191	AAAGAATTTAAAAAGGCAGC
151972	2611	TGCTGCCTTTTTAAATTCTT	161192	AAGAATTTAAAAAGGCAGCA
151973	2612	TTGCTGCCTTTTTAAATTCT	161193	AGAATTTAAAAAGGCAGCAA
151974	2613	ATTGCTGCCTTTTTAAATTC	161194	GAATTTAAAAAGGCAGCAAT
151975	2614	AATTGCTGCCTTTTTAAATT	161195	AATTTAAAAAGGCAGCAATT
151976	2615	CAATTGCTGCCTTTTTAAAT	161196	ATTTAAAAAGGCAGCAATTG
151977	2616	GCAATTGCTGCCTTTTTAAA	161197	TTTAAAAAGGCAGCAATTGC
151978	2617	GGCAATTGCTGCCTTTTTAA	161198	TTAAAAAGGCAGCAATTGCC
151979	2618	TGGCAATTGCTGCCTTTTTA	161199	TAAAAAGGCAGCAATTGCCA
151980	2619	CTGGCAATTGCTGCCTTTTT	161200	AAAAAGGCAGCAATTGCCAG
151981	2620	CCTGGCAATTGCTGCCTTTT	161201	AAAAGGCAGCAATTGCCAGG
151982	2621	TCCTGGCAATTGCTGCCTTT	161202	AAAGGCAGCAATTGCCAGGA
151983	2622	ATCCTGGCAATTGCTGCCTT	161203	AAGGCAGCAATTGCCAGGAT
151984	2623	TATCCTGGCAATTGCTGCCT	161204	AGGCAGCAATTGCCAGGATA
151985	2624	GTATCCTGGCAATTGCTGCC	161205	GGCAGCAATTGCCAGGATAC
151986	2625	AGTATCCTGGCAATTGCTGC	161206	GCAGCAATTGCCAGGATACT
151987	2626	AAGTATCCTGGCAATTGCTG	161207	CAGCAATTGCCAGGATACTT
151988	2627	GAAGTATCCTGGCAATTGCT	161208	AGCAATTGCCAGGATACTTC
151989	2628	TGAAGTATCCTGGCAATTGC	161209	GCAATTGCCAGGATACTTCA
151990	2629	ATGAAGTATCCTGGCAATTG	161210	CAATTGCCAGGATACTTCAT
151991	2630	AATGAAGTATCCTGGCAATT	161211	AATTGCCAGGATACTTCATT
151992	2631	AAATGAAGTATCCTGGCAAT	161212	ATTGCCAGGATACTTCATTT
151993	2632	CAAATGAAGTATCCTGGCAA	161213	TTGCCAGGATACTTCATTTG
151994	2633	TCAAATGAAGTATCCTGGCA	161214	TGCCAGGATACTTCATTTGA
151995	2634	CTCAAATGAAGTATCCTGGC	161215	GCCAGGATACTTCATTTGAG
151996	2635	GCTCAAATGAAGTATCCTGG	161216	CCAGGATACTTCATTTGAGC
151997	2636	TGCTCAAATGAAGTATCCTG	161217	CAGGATACTTCATTTGAGCA
151998	2637	TTGCTCAAATGAAGTATCCT	161218	AGGATACTTCATTTGAGCAA
151999	2638	ATTGCTCAAATGAAGTATCC	161219	GGATACTTCATTTGAGCAAT
152000	2639	CATTGCTCAAATGAAGTATC	161220	GATACTTCATTTGAGCAATG
152001	2640	TCATTGCTCAAATGAAGTAT	161221	ATACTTCATTTGAGCAATGA
152002	2641	ATCATTGCTCAAATGAAGTA	161222	TACTTCATTTGAGCAATGAT
152003	2642	TATCATTGCTCAAATGAAGT	161223	ACTTCATTTGAGCAATGATA
152004	2643	ATATCATTGCTCAAATGAAG	161224	CTTCATTTGAGCAATGATAT
152005	2644	AATATCATTGCTCAAATGAA	161225	TTCATTTGAGCAATGATATT
152006	2645	AAATATCATTGCTCAAATGA	161226	TCATTTGAGCAATGATATTT
152007	2646	AAAATATCATTGCTCAAATG	161227	CATTTGAGCAATGATATTTT
152008	2647	GAAAATATCATTGCTCAAAT	161228	ATTTGAGCAATGATATTTTC
152009	2648	GGAAAATATCATTGCTCAAA	161229	TTTGAGCAATGATATTTTCC
152010	2649	TGGAAAATATCATTGCTCAA	161230	TTGAGCAATGATATTTTCCA
152011	2650	CTGGAAAATATCATTGCTCA	161231	TGAGCAATGATATTTTCCAG
152012	2651	ACTGGAAAATATCATTGCTC	161232	GAGCAATGATATTTTCCAGT
152013	2652	CACTGGAAAATATCATTGCT	161233	AGCAATGATATTTTCCAGTG
152014	2653	CCACTGGAAAATATCATTGC	161234	GCAATGATATTTTCCAGTGG
152015	2654	TCCACTGGAAAATATCATTG	161235	CAATGATATTTTCCAGTGGA
152016	2655	TTCCACTGGAAAATATCATT	161236	AATGATATTTTCCAGTGGAA
152017	2656	TTTCCACTGGAAAATATCAT	161237	ATGATATTTTCCAGTGGAAA
152018	2657	CTTTCCACTGGAAAATATCA	161238	TGATATTTTCCAGTGGAAAG
152019	2658	ACTTTCCACTGGAAAATATC	161239	GATATTTTCCAGTGGAAAGT
152020	2659	GACTTTCCACTGGAAAATAT	161240	ATATTTTCCAGTGGAAAGTC
152021	2660	TGACTTTCCACTGGAAAATA	161241	TATTTTCCAGTGGAAAGTCA
152022	2661	GTGACTTTCCACTGGAAAAT	161242	ATTTTCCAGTGGAAAGTCAC
152023	2662	TGTGACTTTCCACTGGAAAA	161243	TTTTCCAGTGGAAAGTCACA

152024	2663	ATGTGACTTTCCACTGGAAA	161244	TTTCCAGTGGAAAGTCACAT
152025	2664	GATGTGACTTTCCACTGGAA	161245	TTCCAGTGGAAAGTCACATC
152026	2665	AGATGTGACTTTCCACTGGA	161246	TCCAGTGGAAAGTCACATCT
152027	2666	AAGATGTGACTTTCCACTGG	161247	CCAGTGGAAAGTCACATCTT
152028	2667	TAAGATGTGACTTTCCACTG	161248	CAGTGGAAAGTCACATCTTA
152029	2668	TTAAGATGTGACTTTCCACT	161249	AGTGGAAAGTCACATCTTAA
152030	2669	CTTAAGATGTGACTTTCCAC	161250	GTGGAAAGTCACATCTTAAG
152031	2670	CCTTAAGATGTGACTTTCCA	161251	TGGAAAGTCACATCTTAAGG
152032	2671	CCCTTAAGATGTGACTTTCC	161252	GGAAAGTCACATCTTAAGGG
152033	2672	ACCCTTAAGATGTGACTTTC	161253	GAAAGTCACATCTTAAGGGT
152034	2673	AACCCTTAAGATGTGACTTT	161254	AAAGTCACATCTTAAGGGTT
152035	2674	TAACCCTTAAGATGTGACTT	161255	AAGTCACATCTTAAGGGTTA
152036	2675	TTAACCCTTAAGATGTGACT	161256	AGTCACATCTTAAGGGTTAA
152037	2676	ATTAACCCTTAAGATGTGAC	161257	GTCACATCTTAAGGGTTAAT
152038	2677	CATTAACCCTTAAGATGTGA	161258	TCACATCTTAAGGGTTAATG
152039	2678	GCATTAACCCTTAAGATGTG	161259	CACATCTTAAGGGTTAATGC
152040	2679	GGCATTAACCCTTAAGATGT	161260	ACATCTTAAGGGTTAATGCC
152041	2680	GGGCATTAACCCTTAAGATG	161261	CATCTTAAGGGTTAATGCCC
152042	2681	GGGGCATTAACCCTTAAGAT	161262	ATCTTAAGGGTTAATGCCCC
152043	2682	AGGGGCATTAACCCTTAAGA	161263	TCTTAAGGGTTAATGCCCCT
152044	2683	AAGGGGCATTAACCCTTAAG	161264	CTTAAGGGTTAATGCCCCTT
152045	2684	TAAGGGGCATTAACCCTTAA	161265	TTAAGGGTTAATGCCCCTTA
152046	2685	TTAAGGGGCATTAACCCTTA	161266	TAAGGGTTAATGCCCCTTAA
152047	2686	GTTAAGGGGCATTAACCCTT	161267	AAGGGTTAATGCCCCTTAAC
152048	2687	AGTTAAGGGGCATTAACCCT	161268	AGGGTTAATGCCCCTTAACT
152049	2688	CAGTTAAGGGGCATTAACCC	161269	GGGTTAATGCCCCTTAACTG
152050	2689	ACAGTTAAGGGGCATTAACC	161270	GGTTAATGCCCCTTAACTGT
152051	2690	AACAGTTAAGGGGCATTAAC	161271	GTTAATGCCCCTTAACTGTT
152052	2691	CAACAGTTAAGGGGCATTAA	161272	TTAATGCCCCTTAACTGTTG
152053	2692	CCAACAGTTAAGGGGCATTA	161273	TAATGCCCCTTAACTGTTGG
152054	2693	GCCAACAGTTAAGGGGCATT	161274	AATGCCCCTTAACTGTTGGC
152055	2694	GGCCAACAGTTAAGGGGCAT	161275	ATGCCCCTTAACTGTTGGCC
152056	2695	CGGCCAACAGTTAAGGGGCA	161276	TGCCCCTTAACTGTTGGCCG
152057	2696	ACGGCCAACAGTTAAGGGGC	161277	GCCCCTTAACTGTTGGCCGT
152058	2697	TACGGCCAACAGTTAAGGGG	161278	CCCCTTAACTGTTGGCCGTA
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152060	2699	AATACGGCCAACAGTTAAGG	161280	CCTTAACTGTTGGCCGTATT
152061	2700	AAATACGGCCAACAGTTAAG	161281	CTTAACTGTTGGCCGTATTT
152062	2701	CAAATACGGCCAACAGTTAA	161282	TTAACTGTTGGCCGTATTTG
152063	2702	TCAAATACGGCCAACAGTTA	161283	TAACTGTTGGCCGTATTTGA
152064	2703	TTCAAATACGGCCAACAGTT	161284	AACTGTTGGCCGTATTTGAA
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152066	2705	TTTTCAAATACGGCCAACAG	161286	CTGTTGGCCGTATTTGAAAA
152067	2706	GTTTTCAAATACGGCCAACA	161287	TGTTGGCCGTATTTGAAAAC
152068	2707	TGTTTTCAAATACGGCCAAC	161288	GTTGGCCGTATTTGAAAACA
152069	2708	TTGTTTTCAAATACGGCCAA	161289	TTGGCCGTATTTGAAAACAA
152070	2709	TTTGTTTTCAAATACGGCCA	161290	TGGCCGTATTTGAAAACAAA
152071	2710	GTTTGTTTTCAAATACGGCC	161291	GGCCGTATTTGAAAACAAAC
152072	2711	GGTTTGTTTTCAAATACGGC	161292	GCCGTATTTGAAAACAAACC
152073	2712	TGGTTTGTTTTCAAATACGG	161293	CCGTATTTGAAAACAAACCA
152074	2713	TTGGTTTGTTTTCAAATACG	161294	CGTATTTGAAAACAAACCAA
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152076	2715	GCTTGGTTTGTTTTCAAATA	161296	TATTTGAAAACAAACCAAGC
152077	2716	AGCTTGGTTTGTTTTCAAAT	161297	ATTTGAAAACAAACCAAGCT
152078	2717	TAGCTTGGTTTGTTTTCAAA	161298	TTTGAAAACAAACCAAGCTA
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152080	2719	TTTAGCTTGGTTTGTTTTCA	161300	TGAAAACAAACCAAGCTAAA
152081	2720	TTTTAGCTTGGTTTGTTTTC	161301	GAAAACAAACCAAGCTAAAA
152082	2721	TTTTTAGCTTGGTTTGTTTT	161302	AAAACAAACCAAGCTAAAAA
152083	2722	GTTTTTAGCTTGGTTTGTTT	161303	AAACAAACCAAGCTAAAAAC
152084	2723	TGTTTTTAGCTTGGTTTGTT	161304	AACAAACCAAGCTAAAAACA
152085	2724	TTGTTTTTAGCTTGGTTTGT	161305	ACAAACCAAGCTAAAAACAA
152086	2725	CTTGTTTTTAGCTTGGTTTG	161306	CAAACCAAGCTAAAAACAAG
152087	2726	TCTTGTTTTTAGCTTGGTTT	161307	AAACCAAGCTAAAAACAAGA
152088	2727	CTCTTGTTTTTAGCTTGGTT	161308	AACCAAGCTAAAAACAAGAG
152089	2728	TCTCTTGTTTTTAGCTTGGT	161309	ACCAAGCTAAAAACAAGAGA
152090	2729	GTCTCTTGTTTTTAGCTTGG	161310	CCAAGCTAAAAACAAGAGAC
152091	2730	TGTCTCTTGTTTTTAGCTTG	161311	CAAGCTAAAAACAAGAGACA
152092	2731	GTGTCTCTTGTTTTTAGCTT	161312	AAGCTAAAAACAAGAGACAC
152093	2732	AGTGTCTCTTGTTTTTAGCT	161313	AGCTAAAAACAAGAGACACT
152094	2733	CAGTGTCTCTTGTTTTTAGC	161314	GCTAAAAACAAGAGACACTG
152095	2734	TCAGTGTCTCTTGTTTTTAG	161315	CTAAAAACAAGAGACACTGA

152096	2735	GTCAGTGTCTCTTGTTTTTA	161316	TAAAAACAAGAGACACTGAC
152097	2736	TGTCAGTGTCTCTTGTTTTT	161317	AAAAACAAGAGACACTGACA
152098	2737	ATGTCAGTGTCTCTTGTTTT	161318	AAAACAAGAGACACTGACAT
152099	2738	CATGTCAGTGTCTCTTGTTT	161319	AAACAAGAGACACTGACATG
152100	2739	ACATGTCAGTGTCTCTTGTT	161320	AACAAGAGACACTGACATGT
152101	2740	AACATGTCAGTGTCTCTTGT	161321	ACAAGAGACACTGACATGTT
152102	2741	CAACATGTCAGTGTCTCTTG	161322	CAAGAGACACTGACATGTTG
152103	2742	ACAACATGTCAGTGTCTCTT	161323	AAGAGACACTGACATGTTGT
152104	2743	TACAACATGTCAGTGTCTCT	161324	AGAGACACTGACATGTTGTA
152105	2744	ATACAACATGTCAGTGTCTC	161325	GAGACACTGACATGTTGTAT
152106	2745	CATACAACATGTCAGTGTCT	161326	AGACACTGACATGTTGTATG
152107	2746	TCATACAACATGTCAGTGTC	161327	GACACTGACATGTTGTATGA
152108	2747	GTCATACAACATGTCAGTGT	161328	ACACTGACATGTTGTATGAC
152109	2748	CGTCATACAACATGTCAGTG	161329	CACTGACATGTTGTATGACG
152110	2749	CCGTCATACAACATGTCAGT	161330	ACTGACATGTTGTATGACGG
152111	2750	ACCGTCATACAACATGTCAG	161331	CTGACATGTTGTATGACGGT
152112	2751	CACCGTCATACAACATGTCA	161332	TGACATGTTGTATGACGGTG
152113	2752	ACACCGTCATACAACATGTC	161333	GACATGTTGTATGACGGTGT
152114	2753	CACACCGTCATACAACATGT	161334	ACATGTTGTATGACGGTGTG
152115	2754	CCACACCGTCATACAACATG	161335	CATGTTGTATGACGGTGTGG
152116	2755	ACCACACCGTCATACAACAT	161336	ATGTTGTATGACGGTGTGGT
152117	2756	CACCACACCGTCATACAACA	161337	TGTTGTATGACGGTGTGGTG
152118	2757	ACACCACACCGTCATACAAC	161338	GTTGTATGACGGTGTGGTGT
152119	2758	CACACCACACCGTCATACAA	161339	TTGTATGACGGTGTGGTGTG
152120	2759	CCACACCACACCGTCATACA	161340	TGTATGACGGTGTGGTGTGG
152121	2760	TCCACACCACACCGTCATAC	161341	GTATGACGGTGTGGTGTGGA
152122	2761	ATCCACACCACACCGTCATA	161342	TATGACGGTGTGGTGTGGAT
152123	2762	CATCCACACCACACCGTCAT	161343	ATGACGGTGTGGTGTGGATG
152124	2763	ACATCCACACCACACCGTCA	161344	TGACGGTGTGGTGTGGATGT
152125	2764	AACATCCACACCACACCGTC	161345	GACGGTGTGGTGTGGATGTT
152126	2765	CAACATCCACACCACACCGT	161346	ACGGTGTGGTGTGGATGTTG
152127	2766	ACAACATCCACACCACACCG	161347	CGGTGTGGTGTGGATGTTGT
152128	2767	CACAACATCCACACCACACC	161348	GGTGTGGTGTGGATGTTGTG
152129	2768	ACACAACATCCACACCACAC	161349	GTGTGGTGTGGATGTTGTGT
152130	2769	AACACAACATCCACACCACA	161350	TGTGGTGTGGATGTTGTGTT
152131	2770	AAACACAACATCCACACCAC	161351	GTGGTGTGGATGTTGTGTTT
152132	2771	TAAACACAACATCCACACCA	161352	TGGTGTGGATGTTGTGTTTA
152133	2772	ATAAACACAACATCCACACC	161353	GGTGTGGATGTTGTGTTTAT
152134	2773	AATAAACACAACATCCACAC	161354	GTGTGGATGTTGTGTTTATT
152135	2774	AAATAAACACAACATCCACA	161355	TGTGGATGTTGTGTTTATTT
152136	2775	AAAATAAACACAACATCCAC	161356	GTGGATGTTGTGTTTATTTT
152137	2776	TAAAATAAACACAACATCCA	161357	TGGATGTTGTGTTTATTTTA
152138	2777	CTAAAATAAACACAACATCC	161358	GGATGTTGTGTTTATTTTAG
152139	2778	ACTAAAATAAACACAACATC	161359	GATGTTGTGTTTATTTTAGT
152140	2779	GACTAAAATAAACACAACAT	161360	ATGTTGTGTTTATTTTAGTC
152141	2780	GGACTAAAATAAACACAACA	161361	TGTTGTGTTTATTTTAGTCC
152142	2781	AGGACTAAAATAAACACAAC	161362	GTTGTGTTTATTTTAGTCCT
152143	2782	CAGGACTAAAATAAACACAA	161363	TTGTGTTTATTTTAGTCCTG
152144	2783	TCAGGACTAAAATAAACACA	161364	TGTGTTTATTTTAGTCCTGA
152145	2784	CTCAGGACTAAAATAAACAC	161365	GTGTTTATTTTAGTCCTGAG
152146	2785	TCTCAGGACTAAAATAAACA	161366	TGTTTATTTTAGTCCTGAGA
152147	2786	ATCTCAGGACTAAAATAAAC	161367	GTTTATTTTAGTCCTGAGAT
152148	2787	GATCTCAGGACTAAAATAAA	161368	TTTATTTTAGTCCTGAGATC
152149	2788	AGATCTCAGGACTAAAATAA	161369	TTATTTTAGTCCTGAGATCT
152150	2789	TAGATCTCAGGACTAAAATA	161370	TATTTTAGTCCTGAGATCTA
152151	2790	CTAGATCTCAGGACTAAAAT	161371	ATTTTAGTCCTGAGATCTAG
152152	2791	ACTAGATCTCAGGACTAAAA	161372	TTTTAGTCCTGAGATCTAGT
152153	2792	AACTAGATCTCAGGACTAAA	161373	TTTAGTCCTGAGATCTAGTT
152154	2793	CAACTAGATCTCAGGACTAA	161374	TTAGTCCTGAGATCTAGTTG
152155	2794	ACAACTAGATCTCAGGACTA	161375	TAGTCCTGAGATCTAGTTGT
152156	2795	TACAACTAGATCTCAGGACT	161376	AGTCCTGAGATCTAGTTGTA
152157	2796	TTACAACTAGATCTCAGGAC	161377	GTCCTGAGATCTAGTTGTAA
152158	2797	GTTACAACTAGATCTCAGGA	161378	TCCTGAGATCTAGTTGTAAC
152159	2798	AGTTACAACTAGATCTCAGG	161379	CCTGAGATCTAGTTGTAACT
152160	2799	AAGTTACAACTAGATCTCAG	161380	CTGAGATCTAGTTGTAACTT
152161	2800	GAAGTTACAACTAGATCTCA	161381	TGAGATCTAGTTGTAACTTC
152162	2801	GGAAGTTACAACTAGATCTC	161382	GAGATCTAGTTGTAACTTCC
152163	2802	AGGAAGTTACAACTAGATCT	161383	AGATCTAGTTGTAACTTCCT
152164	2803	AAGGAAGTTACAACTAGATC	161384	GATCTAGTTGTAACTTCCTT
152165	2804	CAAGGAAGTTACAACTAGAT	161385	ATCTAGTTGTAACTTCCTTG
152166	2805	TCAAGGAAGTTACAACTAGA	161386	TCTAGTTGTAACTTCCTTGA
152167	2806	ATCAAGGAAGTTACAACTAG	161387	CTAGTTGTAACTTCCTTGAT

152168	2807	AATCAAGGAAGTTACAACTA	161388	TAGTTGTAACTTCCTTGATT
152169	2808	AAATCAAGGAAGTTACAACT	161389	AGTTGTAACTTCCTTGATTT
152170	2809	GAAATCAAGGAAGTTACAAC	161390	GTTGTAACTTCCTTGATTTC
152171	2810	AGAAATCAAGGAAGTTACAA	161391	TTGTAACTTCCTTGATTTCT
152172	2811	CAGAAATCAAGGAAGTTACA	161392	TGTAACTTCCTTGATTTCTG
152173	2812	ACAGAAATCAAGGAAGTTAC	161393	GTAACTTCCTTGATTTCTGT
152174	2813	TACAGAAATCAAGGAAGTTA	161394	TAACTTCCTTGATTTCTGTA
152175	2814	ATACAGAAATCAAGGAAGTT	161395	AACTTCCTTGATTTCTGTAT
152176	2815	CATACAGAAATCAAGGAAGT	161396	ACTTCCTTGATTTCTGTATG
152177	2816	ACATACAGAAATCAAGGAAG	161397	CTTCCTTGATTTCTGTATGT
152178	2817	TACATACAGAAATCAAGGAA	161398	TTCCTTGATTTCTGTATGTA
152179	2818	CTACATACAGAAATCAAGGA	161399	TCCTTGATTTCTGTATGTAG
152180	2819	GCTACATACAGAAATCAAGG	161400	CCTTGATTTCTGTATGTAGC
152181	2820	GGCTACATACAGAAATCAAG	161401	CTTGATTTCTGTATGTAGCC
152182	2821	TGGCTACATACAGAAATCAA	161402	TTGATTTCTGTATGTAGCCA
152183	2822	GTGGCTACATACAGAAATCA	161403	TGATTTCTGTATGTAGCCAC
152184	2823	CGTGGCTACATACAGAAATC	161404	GATTTCTGTATGTAGCCACG
152185	2824	CCGTGGCTACATACAGAAAT	161405	ATTTCTGTATGTAGCCACGG
152186	2825	TCCGTGGCTACATACAGAAA	161406	TTTCTGTATGTAGCCACGGA
152187	2826	CTCCGTGGCTACATACAGAA	161407	TTCTGTATGTAGCCACGGAG
152188	2827	GCTCCGTGGCTACATACAGA	161408	TCTGTATGTAGCCACGGAGC
152189	2828	TGCTCCGTGGCTACATACAG	161409	CTGTATGTAGCCACGGAGCA
152190	2829	GTGCTCCGTGGCTACATACA	161410	TGTATGTAGCCACGGAGCAC
152191	2830	GGTGCTCCGTGGCTACATAC	161411	GTATGTAGCCACGGAGCACC
152192	2831	TGGTGCTCCGTGGCTACATA	161412	TATGTAGCCACGGAGCACCA
152193	2832	ATGGTGCTCCGTGGCTACAT	161413	ATGTAGCCACGGAGCACCAT
152194	2833	AATGGTGCTCCGTGGCTACA	161414	TGTAGCCACGGAGCACCATT
152195	2834	TAATGGTGCTCCGTGGCTAC	161415	GTAGCCACGGAGCACCATTA
152196	2835	GTAATGGTGCTCCGTGGCTA	161416	TAGCCACGGAGCACCATTAC
152197	2836	GGTAATGGTGCTCCGTGGCT	161417	AGCCACGGAGCACCATTACC
152198	2837	AGGTAATGGTGCTCCGTGGC	161418	GCCACGGAGCACCATTACCT
152199	2838	CAGGTAATGGTGCTCCGTGG	161419	CCACGGAGCACCATTACCTG
152200	2839	ACAGGTAATGGTGCTCCGTG	161420	CACGGAGCACCATTACCTGT
152201	2840	GACAGGTAATGGTGCTCCGT	161421	ACGGAGCACCATTACCTGTC
152202	2841	TGACAGGTAATGGTGCTCCG	161422	CGGAGCACCATTACCTGTCA
152203	2842	GTGACAGGTAATGGTGCTCC	161423	GGAGCACCATTACCTGTCAC
152204	2843	GGTGACAGGTAATGGTGCTC	161424	GAGCACCATTACCTGTCACC
152205	2844	TGGTGACAGGTAATGGTGCT	161425	AGCACCATTACCTGTCACCA
152206	2845	ATGGTGACAGGTAATGGTGC	161426	GCACCATTACCTGTCACCAT
152207	2846	AATGGTGACAGGTAATGGTG	161427	CACCATTACCTGTCACCATT
152208	2847	TAATGGTGACAGGTAATGGT	161428	ACCATTACCTGTCACCATTA
152209	2848	GTAATGGTGACAGGTAATGG	161429	CCATTACCTGTCACCATTAC
152210	2849	GGTAATGGTGACAGGTAATG	161430	CATTACCTGTCACCATTACC
152211	2850	AGGTAATGGTGACAGGTAAT	161431	ATTACCTGTCACCATTACCT
152212	2851	CAGGTAATGGTGACAGGTAA	161432	TTACCTGTCACCATTACCTG
152213	2852	TCAGGTAATGGTGACAGGTA	161433	TACCTGTCACCATTACCTGA
152214	2853	TTCAGGTAATGGTGACAGGT	161434	ACCTGTCACCATTACCTGAA
152215	2854	ATTCAGGTAATGGTGACAGG	161435	CCTGTCACCATTACCTGAAT
152216	2855	CATTCAGGTAATGGTGACAG	161436	CTGTCACCATTACCTGAATG
152217	2856	CCATTCAGGTAATGGTGACA	161437	TGTCACCATTACCTGAATGG
152218	2857	GCCATTCAGGTAATGGTGAC	161438	GTCACCATTACCTGAATGGC
152219	2858	AGCCATTCAGGTAATGGTGA	161439	TCACCATTACCTGAATGGCT
152220	2859	TAGCCATTCAGGTAATGGTG	161440	CACCATTACCTGAATGGCTA
152221	2860	ATAGCCATTCAGGTAATGGT	161441	ACCATTACCTGAATGGCTAT
152222	2861	TATAGCCATTCAGGTAATGG	161442	CCATTACCTGAATGGCTATA
152223	2862	GTATAGCCATTCAGGTAATG	161443	CATTACCTGAATGGCTATAC
152224	2863	AGTATAGCCATTCAGGTAAT	161444	ATTACCTGAATGGCTATACT
152225	2864	CAGTATAGCCATTCAGGTAA	161445	TTACCTGAATGGCTATACTG
152226	2865	GCAGTATAGCCATTCAGGTA	161446	TACCTGAATGGCTATACTGC
152227	2866	AGCAGTATAGCCATTCAGGT	161447	ACCTGAATGGCTATACTGCT
152228	2867	AAGCAGTATAGCCATTCAGG	161448	CCTGAATGGCTATACTGCTT
152229	2868	CAAGCAGTATAGCCATTCAG	161449	CTGAATGGCTATACTGCTTG
152230	2869	GCAAGCAGTATAGCCATTCA	161450	TGAATGGCTATACTGCTTGC
152231	2870	AGCAAGCAGTATAGCCATTC	161451	GAATGGCTATACTGCTTGCT
152232	2871	AAGCAAGCAGTATAGCCATT	161452	AATGGCTATACTGCTTGCTT
152233	2872	AAAGCAAGCAGTATAGCCAT	161453	ATGGCTATACTGCTTGCTTT
152234	2873	GAAAGCAAGCAGTATAGCCA	161454	TGGCTATACTGCTTGCTTTC
152235	2874	TGAAAGCAAGCAGTATAGCC	161455	GGCTATACTGCTTGCTTTCA
152236	2875	ATGAAAGCAAGCAGTATAGC	161456	GCTATACTGCTTGCTTTCAT
152237	2876	AATGAAAGCAAGCAGTATAG	161457	CTATACTGCTTGCTTTCATT
152238	2877	AAATGAAAGCAAGCAGTATA	161458	TATACTGCTTGCTTTCATTT
152239	2878	AAAATGAAAGCAAGCAGTAT	161459	ATACTGCTTGCTTTCATTTT

152240	2879	CAAAATGAAAGCAAGCAGTA	161460	TACTGCTTGCTTTCATTTTG
152241	2880	CCAAAATGAAAGCAAGCAGT	161461	ACTGCTTGCTTTCATTTTGG
152242	2881	ACCAAAATGAAAGCAAGCAG	161462	CTGCTTGCTTTCATTTTGGT
152243	2882	TACCAAAATGAAAGCAAGCA	161463	TGCTTGCTTTCATTTTGGTA
152244	2883	CTACCAAAATGAAAGCAAGC	161464	GCTTGCTTTCATTTTGGTAG
152245	2884	TCTACCAAAATGAAAGCAAG	161465	CTTGCTTTCATTTTGGTAGA
152246	2885	CTCTACCAAAATGAAAGCAA	161466	TTGCTTTCATTTTGGTAGAG
152247	2886	ACTCTACCAAAATGAAAGCA	161467	TGCTTTCATTTTGGTAGAGT
152248	2887	CACTCTACCAAAATGAAAGC	161468	GCTTTCATTTTGGTAGAGTG
152249	2888	CCACTCTACCAAAATGAAAG	161469	CTTTCATTTTGGTAGAGTGG
152250	2889	TCCACTCTACCAAAATGAAA	161470	TTTCATTTTGGTAGAGTGGA
152251	2890	TTCCACTCTACCAAAATGAA	161471	TTCATTTTGGTAGAGTGGAA
152252	2891	TTTCCACTCTACCAAAATGA	161472	TCATTTTGGTAGAGTGGAAA
152253	2892	CTTTCCACTCTACCAAAATG	161473	CATTTTGGTAGAGTGGAAAG
152254	2893	CCTTTCCACTCTACCAAAAT	161474	ATTTTGGTAGAGTGGAAAGG
152255	2894	ACCTTTCCACTCTACCAAAA	161475	TTTTGGTAGAGTGGAAAGGT
152256	2895	AACCTTTCCACTCTACCAAA	161476	TTTGGTAGAGTGGAAAGGTT
152257	2896	TAACCTTTCCACTCTACCAA	161477	TTGGTAGAGTGGAAAGGTTA
152258	2897	GTAACCTTTCCACTCTACCA	161478	TGGTAGAGTGGAAAGGTTAC
152259	2898	GGTAACCTTTCCACTCTACC	161479	GGTAGAGTGGAAAGGTTACC
152260	2899	AGGTAACCTTTCCACTCTAC	161480	GTAGAGTGGAAAGGTTACCT
152261	2900	TAGGTAACCTTTCCACTCTA	161481	TAGAGTGGAAAGGTTACCTA
152262	2901	CTAGGTAACCTTTCCACTCT	161482	AGAGTGGAAAGGTTACCTAG
152263	2902	CCTAGGTAACCTTTCCACTC	161483	GAGTGGAAAGGTTACCTAGG
152264	2903	ACCTAGGTAACCTTTCCACT	161484	AGTGGAAAGGTTACCTAGGT
152265	2904	AACCTAGGTAACCTTTCCAC	161485	GTGGAAAGGTTACCTAGGTT
152266	2905	AAACCTAGGTAACCTTTCCA	161486	TGGAAAGGTTACCTAGGTTT
152267	2906	GAAACCTAGGTAACCTTTCC	161487	GGAAAGGTTACCTAGGTTTC
152268	2907	TGAAACCTAGGTAACCTTTC	161488	GAAAGGTTACCTAGGTTTCA
152269	2908	CTGAAACCTAGGTAACCTTT	161489	AAAGGTTACCTAGGTTTCAG
152270	2909	ACTGAAACCTAGGTAACCTT	161490	AAGGTTACCTAGGTTTCAGT
152271	2910	CACTGAAACCTAGGTAACCT	161491	AGGTTACCTAGGTTTCAGTG
152272	2911	GCACTGAAACCTAGGTAACC	161492	GGTTACCTAGGTTTCAGTGC
152273	2912	AGCACTGAAACCTAGGTAAC	161493	GTTACCTAGGTTTCAGTGCT
152274	2913	AAGCACTGAAACCTAGGTAA	161494	TTACCTAGGTTTCAGTGCTT
152275	2914	CAAGCACTGAAACCTAGGTA	161495	TACCTAGGTTTCAGTGCTTG
152276	2915	TCAAGCACTGAAACCTAGGT	161496	ACCTAGGTTTCAGTGCTTGA
152277	2916	TTCAAGCACTGAAACCTAGG	161497	CCTAGGTTTCAGTGCTTGAA
152278	2917	TTTCAAGCACTGAAACCTAG	161498	CTAGGTTTCAGTGCTTGAAA
152279	2918	TTTTCAAGCACTGAAACCTA	161499	TAGGTTTCAGTGCTTGAAAA
152280	2919	CTTTTCAAGCACTGAAACCT	161500	AGGTTTCAGTGCTTGAAAAG
152281	2920	TCTTTTCAAGCACTGAAACC	161501	GGTTTCAGTGCTTGAAAAGA
152282	2921	ATCTTTTCAAGCACTGAAAC	161502	GTTTCAGTGCTTGAAAAGAT
152283	2922	AATCTTTTCAAGCACTGAAA	161503	TTTCAGTGCTTGAAAAGATT
152284	2923	AAATCTTTTCAAGCACTGAA	161504	TTCAGTGCTTGAAAAGATTT
152285	2924	GAAATCTTTTCAAGCACTGA	161505	TCAGTGCTTGAAAAGATTTC
152286	2925	TGAAATCTTTTCAAGCACTG	161506	CAGTGCTTGAAAAGATTTCA
152287	2926	CTGAAATCTTTTCAAGCACT	161507	AGTGCTTGAAAAGATTTCAG
152288	2927	TCTGAAATCTTTTCAAGCAC	161508	GTGCTTGAAAAGATTTCAGA
152289	2928	TTCTGAAATCTTTTCAAGCA	161509	TGCTTGAAAAGATTTCAGAA
152290	2929	TTTCTGAAATCTTTTCAAGC	161510	GCTTGAAAAGATTTCAGAAA
152291	2930	CTTTCTGAAATCTTTTCAAG	161511	CTTGAAAAGATTTCAGAAAG
152292	2931	GCTTTCTGAAATCTTTTCAA	161512	TTGAAAAGATTTCAGAAAGC
152293	2932	TGCTTTCTGAAATCTTTTCA	161513	TGAAAAGATTTCAGAAAGCA
152294	2933	CTGCTTTCTGAAATCTTTTC	161514	GAAAAGATTTCAGAAAGCAG
152295	2934	ACTGCTTTCTGAAATCTTTT	161515	AAAAGATTTCAGAAAGCAGT
152296	2935	TACTGCTTTCTGAAATCTTT	161516	AAAGATTTCAGAAAGCAGTA
152297	2936	CTACTGCTTTCTGAAATCTT	161517	AAGATTTCAGAAAGCAGTAG
152298	2937	ACTACTGCTTTCTGAAATCT	161518	AGATTTCAGAAAGCAGTAGT
152299	2938	TACTACTGCTTTCTGAAATC	161519	GATTTCAGAAAGCAGTAGTA
152300	2939	GTACTACTGCTTTCTGAAAT	161520	ATTTCAGAAAGCAGTAGTAC
152301	2940	CGTACTACTGCTTTCTGAAA	161521	TTTCAGAAAGCAGTAGTACG
152302	2941	ACGTACTACTGCTTTCTGAA	161522	TTCAGAAAGCAGTAGTACGT
152303	2942	GACGTACTACTGCTTTCTGA	161523	TCAGAAAGCAGTAGTACGTC
152304	2943	AGACGTACTACTGCTTTCTG	161524	CAGAAAGCAGTAGTACGTCT
152305	2944	CAGACGTACTACTGCTTTCT	161525	AGAAAGCAGTAGTACGTCTG
152306	2945	CCAGACGTACTACTGCTTTC	161526	GAAAGCAGTAGTACGTCTGG
152307	2946	ACCAGACGTACTACTGCTTT	161527	AAAGCAGTAGTACGTCTGGT
152308	2947	AACCAGACGTACTACTGCTT	161528	AAGCAGTAGTACGTCTGGTT
152309	2948	TAACCAGACGTACTACTGCT	161529	AGCAGTAGTACGTCTGGTTA
152310	2949	CTAACCAGACGTACTACTGC	161530	GCAGTAGTACGTCTGGTTAG
152311	2950	TCTAACCAGACGTACTACTG	161531	CAGTAGTACGTCTGGTTAGA

152312	2951	GTCTAACCAGACGTACTACT	161532	AGTAGTACGTCTGGTTAGAC
152313	2952	AGTCTAACCAGACGTACTAC	161533	GTAGTACGTCTGGTTAGACT
152314	2953	TAGTCTAACCAGACGTACTA	161534	TAGTACGTCTGGTTAGACTA
152315	2954	CTAGTCTAACCAGACGTACT	161535	AGTACGTCTGGTTAGACTAG
152316	2955	TCTAGTCTAACCAGACGTAC	161536	GTACGTCTGGTTAGACTAGA
152317	2956	TTCTAGTCTAACCAGACGTA	161537	TACGTCTGGTTAGACTAGAA
152318	2957	ATTCTAGTCTAACCAGACGT	161538	ACGTCTGGTTAGACTAGAAT
152319	2958	GATTCTAGTCTAACCAGACG	161539	CGTCTGGTTAGACTAGAATC
152320	2959	TGATTCTAGTCTAACCAGAC	161540	GTCTGGTTAGACTAGAATCA
152321	2960	CTGATTCTAGTCTAACCAGA	161541	TCTGGTTAGACTAGAATCAG
152322	2961	ACTGATTCTAGTCTAACCAG	161542	CTGGTTAGACTAGAATCAGT
152323	2962	GACTGATTCTAGTCTAACCA	161543	TGGTTAGACTAGAATCAGTC
152324	2963	GGACTGATTCTAGTCTAACC	161544	GGTTAGACTAGAATCAGTCC
152325	2964	AGGACTGATTCTAGTCTAAC	161545	GTTAGACTAGAATCAGTCCT
152326	2965	GAGGACTGATTCTAGTCTAA	161546	TTAGACTAGAATCAGTCCTC
152327	2966	AGAGGACTGATTCTAGTCTA	161547	TAGACTAGAATCAGTCCTCT
152328	2967	GAGAGGACTGATTCTAGTCT	161548	AGACTAGAATCAGTCCTCTC
152329	2968	GGAGAGGACTGATTCTAGTC	161549	GACTAGAATCAGTCCTCTCC
152330	2969	AGGAGAGGACTGATTCTAGT	161550	ACTAGAATCAGTCCTCTCCT
152331	2970	CAGGAGAGGACTGATTCTAG	161551	CTAGAATCAGTCCTCTCCTG
152332	2971	CCAGGAGAGGACTGATTCTA	161552	TAGAATCAGTCCTCTCCTGG
152333	2972	CCCAGGAGAGGACTGATTCT	161553	AGAATCAGTCCTCTCCTGGG
152334	2973	CCCCAGGAGAGGACTGATTC	161554	GAATCAGTCCTCTCCTGGGG
152335	2974	CCCCCAGGAGAGGACTGATT	161555	AATCAGTCCTCTCCTGGGGG
152336	2975	GCCCCCAGGAGAGGACTGAT	161556	ATCAGTCCTCTCCTGGGGGC
152337	2976	TGCCCCCAGGAGAGGACTGA	161557	TCAGTCCTCTCCTGGGGGCA
152338	2977	CTGCCCCCAGGAGAGGACTG	161558	CAGTCCTCTCCTGGGGGCAG
152339	2978	ACTGCCCCCAGGAGAGGACT	161559	AGTCCTCTCCTGGGGGCAGT
152340	2979	CACTGCCCCCAGGAGAGGAC	161560	GTCCTCTCCTGGGGGCAGTG
152341	2980	CCACTGCCCCCAGGAGAGGA	161561	TCCTCTCCTGGGGGCAGTGG
152342	2981	TCCACTGCCCCCAGGAGAGG	161562	CCTCTCCTGGGGGCAGTGGA
152343	2982	TTCCACTGCCCCCAGGAGAG	161563	CTCTCCTGGGGGCAGTGGAA
152344	2983	ATTCCACTGCCCCCAGGAGA	161564	TCTCCTGGGGGCAGTGGAAT
152345	2984	TATTCCACTGCCCCCAGGAG	161565	CTCCTGGGGGCAGTGGAATA
152346	2985	ATATTCCACTGCCCCCAGGA	161566	TCCTGGGGGCAGTGGAATAT
152347	2986	TATATTCCACTGCCCCCAGG	161567	CCTGGGGGCAGTGGAATATA
152348	2987	TTATATTCCACTGCCCCCAG	161568	CTGGGGGCAGTGGAATATAA
152349	2988	ATTATATTCCACTGCCCCCA	161569	TGGGGGCAGTGGAATATAAT
152350	2989	TATTATATTCCACTGCCCCC	161570	GGGGGCAGTGGAATATAATA
152351	2990	ATATTATATTCCACTGCCCC	161571	GGGGCAGTGGAATATAATAT
152352	2991	AATATTATATTCCACTGCCC	161572	GGGCAGTGGAATATAATATT
152353	2992	AAATATTATATTCCACTGCC	161573	GGCAGTGGAATATAATATTT
152354	2993	AAAATATTATATTCCACTGC	161574	GCAGTGGAATATAATATTTT
152355	2994	GAAAATATTATATTCCACTG	161575	CAGTGGAATATAATATTTTC
152356	2995	AGAAAATATTATATTCCACT	161576	AGTGGAATATAATATTTTCT
152357	2996	CAGAAAATATTATATTCCAC	161577	GTGGAATATAATATTTTCTG
152358	2997	TCAGAAAATATTATATTCCA	161578	TGGAATATAATATTTTCTGA
152359	2998	GTCAGAAAATATTATATTCC	161579	GGAATATAATATTTTCTGAC
152360	2999	AGTCAGAAAATATTATATTC	161580	GAATATAATATTTTCTGACT
152361	3000	CAGTCAGAAAATATTATATT	161581	AATATAATATTTTCTGACTG
152362	3001	GCAGTCAGAAAATATTATAT	161582	ATATAATATTTTCTGACTGC
152363	3002	AGCAGTCAGAAAATATTATA	161583	TATAATATTTTCTGACTGCT
152364	3003	TAGCAGTCAGAAAATATTAT	161584	ATAATATTTTCTGACTGCTA
152365	3004	TTAGCAGTCAGAAAATATTA	161585	TAATATTTTCTGACTGCTAA
152366	3005	ATTAGCAGTCAGAAAATATT	161586	AATATTTTCTGACTGCTAAT
152367	3006	AATTAGCAGTCAGAAAATAT	161587	ATATTTTCTGACTGCTAATT
152368	3007	TAATTAGCAGTCAGAAAATA	161588	TATTTTCTGACTGCTAATTA
152369	3008	TTAATTAGCAGTCAGAAAAT	161589	ATTTTCTGACTGCTAATTAA
152370	3009	TTTAATTAGCAGTCAGAAAA	161590	TTTTCTGACTGCTAATTAAA
152371	3010	TTTTAATTAGCAGTCAGAAA	161591	TTTCTGACTGCTAATTAAAA
152372	3011	TTTTTAATTAGCAGTCAGAA	161592	TTCTGACTGCTAATTAAAAA
152373	3012	ATTTTTAATTAGCAGTCAGA	161593	TCTGACTGCTAATTAAAAAT
152374	3013	TATTTTTAATTAGCAGTCAG	161594	CTGACTGCTAATTAAAAATA
152375	3014	GTATTTTTAATTAGCAGTCA	161595	TGACTGCTAATTAAAAATAC
152376	3015	GGTATTTTTAATTAGCAGTC	161596	GACTGCTAATTAAAAATACC
152377	3016	AGGTATTTTTAATTAGCAGT	161597	ACTGCTAATTAAAAATACCT
152378	3017	CAGGTATTTTTAATTAGCAG	161598	CTGCTAATTAAAAATACCTG
152379	3018	ACAGGTATTTTTAATTAGCA	161599	TGCTAATTAAAAATACCTGT
152380	3019	CACAGGTATTTTTAATTAGC	161600	GCTAATTAAAAATACCTGTG
152381	3020	TCACAGGTATTTTTAATTAG	161601	CTAATTAAAAATACCTGTGA
152382	3021	ATCACAGGTATTTTTAATTA	161602	TAATTAAAAATACCTGTGAT
152383	3022	TATCACAGGTATTTTTAATT	161603	AATTAAAAATACCTGTGATA

152384	3023	CTATCACAGGTATTTTTAAT	161604	ATTAAAAATACCTGTGATAG
152385	3024	GCTATCACAGGTATTTTTAA	161605	TTAAAAATACCTGTGATAGC
152386	3025	GGCTATCACAGGTATTTTTA	161606	TAAAAATACCTGTGATAGCC
152387	3026	CGGCTATCACAGGTATTTTT	161607	AAAAATACCTGTGATAGCCG
152388	3027	CCGGCTATCACAGGTATTTT	161608	AAAATACCTGTGATAGCCGG
152389	3028	CCCGGCTATCACAGGTATTT	161609	AAATACCTGTGATAGCCGGG
152390	3029	GCCCGGCTATCACAGGTATT	161610	AATACCTGTGATAGCCGGGC
152391	3030	CGCCCGGCTATCACAGGTAT	161611	ATACCTGTGATAGCCGGGCG
152392	3031	ACGCCCGGCTATCACAGGTA	161612	TACCTGTGATAGCCGGGCGT
152393	3032	CACGCCCGGCTATCACAGGT	161613	ACCTGTGATAGCCGGGCGTG
152394	3033	CCACGCCCGGCTATCACAGG	161614	CCTGTGATAGCCGGGCGTGG
152395	3034	ACCACGCCCGGCTATCACAG	161615	CTGTGATAGCCGGGCGTGGT
152396	3035	CACCACGCCCGGCTATCACA	161616	TGTGATAGCCGGGCGTGGTG
152397	3036	CCACCACGCCCGGCTATCAC	161617	GTGATAGCCGGGCGTGGTGG
152398	3037	GCCACCACGCCCGGCTATCA	161618	TGATAGCCGGGCGTGGTGGC
152399	3038	AGCCACCACGCCCGGCTATC	161619	GATAGCCGGGCGTGGTGGCT
152400	3039	AAGCCACCACGCCCGGCTAT	161620	ATAGCCGGGCGTGGTGGCTT
152401	3040	TAAGCCACCACGCCCGGCTA	161621	TAGCCGGGCGTGGTGGCTTA
152402	3041	GTAAGCCACCACGCCCGGCT	161622	AGCCGGGCGTGGTGGCTTAC
152403	3042	CGTAAGCCACCACGCCCGGC	161623	GCCGGGCGTGGTGGCTTACG
152404	3043	GCGTAAGCCACCACGCCCGG	161624	CCGGGCGTGGTGGCTTACGC
152405	3044	GGCGTAAGCCACCACGCCCG	161625	CGGGCGTGGTGGCTTACGCC
152406	3045	AGGCGTAAGCCACCACGCCC	161626	GGGCGTGGTGGCTTACGCCT
152407	3046	CAGGCGTAAGCCACCACGCC	161627	GGCGTGGTGGCTTACGCCTG
152408	3047	ACAGGCGTAAGCCACCACGC	161628	GCGTGGTGGCTTACGCCTGT
152409	3048	TACAGGCGTAAGCCACCACG	161629	CGTGGTGGCTTACGCCTGTA
152410	3049	TTACAGGCGTAAGCCACCAC	161630	GTGGTGGCTTACGCCTGTAA
152411	3050	ATTACAGGCGTAAGCCACCA	161631	TGGTGGCTTACGCCTGTAAT
152412	3051	GATTACAGGCGTAAGCCACC	161632	GGTGGCTTACGCCTGTAATC
152413	3052	GGATTACAGGCGTAAGCCAC	161633	GTGGCTTACGCCTGTAATCC
152414	3053	GGGATTACAGGCGTAAGCCA	161634	TGGCTTACGCCTGTAATCCC
152415	3054	TGGGATTACAGGCGTAAGCC	161635	GGCTTACGCCTGTAATCCCA
152416	3055	CTGGGATTACAGGCGTAAGC	161636	GCTTACGCCTGTAATCCCAG
152417	3056	GCTGGGATTACAGGCGTAAG	161637	CTTACGCCTGTAATCCCAGC
152418	3057	TGCTGGGATTACAGGCGTAA	161638	TTACGCCTGTAATCCCAGCA
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152420	3059	AGTGCTGGGATTACAGGCGT	161640	ACGCCTGTAATCCCAGCACT
152421	3060	AAGTGCTGGGATTACAGGCG	161641	CGCCTGTAATCCCAGCACTT
152422	3061	AAAGTGCTGGGATTACAGGC	161642	GCCTGTAATCCCAGCACTTT
152423	3062	CAAAGTGCTGGGATTACAGG	161643	CCTGTAATCCCAGCACTTTG
152424	3063	CCAAAGTGCTGGGATTACAG	161644	CTGTAATCCCAGCACTTTGG
152425	3064	CCCAAAGTGCTGGGATTACA	161645	TGTAATCCCAGCACTTTGGG
152426	3065	TCCCAAAGTGCTGGGATTAC	161646	GTAATCCCAGCACTTTGGGA
152427	3066	CTCCCAAAGTGCTGGGATTA	161647	TAATCCCAGCACTTTGGGAG
152428	3067	CCTCCCAAAGTGCTGGGATT	161648	AATCCCAGCACTTTGGGAGG
152429	3068	GCCTCCCAAAGTGCTGGGAT	161649	ATCCCAGCACTTTGGGAGGC
152430	3069	GGCCTCCCAAAGTGCTGGGA	161650	TCCCAGCACTTTGGGAGGCC
152431	3070	CGGCCTCCCAAAGTGCTGGG	161651	CCCAGCACTTTGGGAGGCCG
152432	3071	TCGGCCTCCCAAAGTGCTGG	161652	CCAGCACTTTGGGAGGCCGA
152433	3072	CTCGGCCTCCCAAAGTGCTG	161653	CAGCACTTTGGGAGGCCGAG
152434	3073	TCTCGGCCTCCCAAAGTGCT	161654	AGCACTTTGGGAGGCCGAGA
152435	3074	GTCTCGGCCTCCCAAAGTGC	161655	GCACTTTGGGAGGCCGAGAC
152436	3075	CGTCTCGGCCTCCCAAAGTG	161656	CACTTTGGGAGGCCGAGACG
152437	3076	CCGTCTCGGCCTCCCAAAGT	161657	ACTTTGGGAGGCCGAGACGG
152438	3077	CCCGTCTCGGCCTCCCAAAG	161658	CTTTGGGAGGCCGAGACGGG
152439	3078	ACCCGTCTCGGCCTCCCAAA	161659	TTTGGGAGGCCGAGACGGGT
152440	3079	CACCCGTCTCGGCCTCCCAA	161660	TTGGGAGGCCGAGACGGGTG
152441	3080	CCACCCGTCTCGGCCTCCCA	161661	TGGGAGGCCGAGACGGGTGG
152442	3081	TCCACCCGTCTCGGCCTCCC	161662	GGGAGGCCGAGACGGGTGGA
152443	3082	ATCCACCCGTCTCGGCCTCC	161663	GGAGGCCGAGACGGGTGGAT
152444	3083	GATCCACCCGTCTCGGCCTC	161664	GAGGCCGAGACGGGTGGATC
152445	3084	TGATCCACCCGTCTCGGCCT	161665	AGGCCGAGACGGGTGGATCA
152446	3085	GTGATCCACCCGTCTCGGCC	161666	GGCCGAGACGGGTGGATCAC
152447	3086	CGTGATCCACCCGTCTCGGC	161667	GCCGAGACGGGTGGATCACG
152448	3087	TCGTGATCCACCCGTCTCGG	161668	CCGAGACGGGTGGATCACGA
152449	3088	CTCGTGATCCACCCGTCTCG	161669	CGAGACGGGTGGATCACGAG
152450	3089	CCTCGTGATCCACCCGTCTC	161670	GAGACGGGTGGATCACGAGG
152451	3090	ACCTCGTGATCCACCCGTCT	161671	AGACGGGTGGATCACGAGGT
152452	3091	GACCTCGTGATCCACCCGTC	161672	GACGGGTGGATCACGAGGTC
152453	3092	TGACCTCGTGATCCACCCGT	161673	ACGGGTGGATCACGAGGTCA
152454	3093	CTGACCTCGTGATCCACCCG	161674	CGGGTGGATCACGAGGTCAG
152455	3094	GCTGACCTCGTGATCCACCC	161675	GGGTGGATCACGAGGTCAGC

152456	3095	TGCTGACCTCGTGATCCACC	161676	GGTGGATCACGAGGTCAGCA
152457	3096	CTGCTGACCTCGTGATCCAC	161677	GTGGATCACGAGGTCAGCAG
152458	3097	TCTGCTGACCTCGTGATCCA	161678	TGGATCACGAGGTCAGCAGA
152459	3098	ATCTGCTGACCTCGTGATCC	161679	GGATCACGAGGTCAGCAGAT
152460	3099	CATCTGCTGACCTCGTGATC	161680	GATCACGAGGTCAGCAGATG
152461	3100	CCATCTGCTGACCTCGTGAT	161681	ATCACGAGGTCAGCAGATGG
152462	3101	TCCATCTGCTGACCTCGTGA	161682	TCACGAGGTCAGCAGATGGA
152463	3102	CTCCATCTGCTGACCTCGTG	161683	CACGAGGTCAGCAGATGGAG
152464	3103	TCTCCATCTGCTGACCTCGT	161684	ACGAGGTCAGCAGATGGAGA
152465	3104	GTCTCCATCTGCTGACCTCG	161685	CGAGGTCAGCAGATGGAGAC
152466	3105	GGTCTCCATCTGCTGACCTC	161686	GAGGTCAGCAGATGGAGACC
152467	3106	TGGTCTCCATCTGCTGACCT	161687	AGGTCAGCAGATGGAGACCA
152468	3107	ATGGTCTCCATCTGCTGACC	161688	GGTCAGCAGATGGAGACCAT
152469	3108	GATGGTCTCCATCTGCTGAC	161689	GTCAGCAGATGGAGACCATC
152470	3109	GGATGGTCTCCATCTGCTGA	161690	TCAGCAGATGGAGACCATCC
152471	3110	AGGATGGTCTCCATCTGCTG	161691	CAGCAGATGGAGACCATCCT
152472	3111	CAGGATGGTCTCCATCTGCT	161692	AGCAGATGGAGACCATCCTG
152473	3112	CCAGGATGGTCTCCATCTGC	161693	GCAGATGGAGACCATCCTGG
152474	3113	GCCAGGATGGTCTCCATCTG	161694	CAGATGGAGACCATCCTGGC
152475	3114	AGCCAGGATGGTCTCCATCT	161695	AGATGGAGACCATCCTGGCT
152476	3115	TAGCCAGGATGGTCTCCATC	161696	GATGGAGACCATCCTGGCTA
152477	3116	TTAGCCAGGATGGTCTCCAT	161697	ATGGAGACCATCCTGGCTAA
152478	3117	GTTAGCCAGGATGGTCTCCA	161698	TGGAGACCATCCTGGCTAAC
152479	3118	TGTTAGCCAGGATGGTCTCC	161699	GGAGACCATCCTGGCTAACA
152480	3119	GTGTTAGCCAGGATGGTCTC	161700	GAGACCATCCTGGCTAACAC
152481	3120	CGTGTTAGCCAGGATGGTCT	161701	AGACCATCCTGGCTAACACG
152482	3121	CCGTGTTAGCCAGGATGGTC	161702	GACCATCCTGGCTAACACGG
152483	3122	ACCGTGTTAGCCAGGATGGT	161703	ACCATCCTGGCTAACACGGT
152484	3123	CACCGTGTTAGCCAGGATGG	161704	CCATCCTGGCTAACACGGTG
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152486	3125	TTCACCGTGTTAGCCAGGAT	161706	ATCCTGGCTAACACGGTGAA
152487	3126	TTTCACCGTGTTAGCCAGGA	161707	TCCTGGCTAACACGGTGAAA
152488	3127	GTTTCACCGTGTTAGCCAGG	161708	CCTGGCTAACACGGTGAAAC
152489	3128	GGTTTCACCGTGTTAGCCAG	161709	CTGGCTAACACGGTGAAACC
152490	3129	GGGTTTCACCGTGTTAGCCA	161710	TGGCTAACACGGTGAAACCC
152491	3130	GGGGTTTCACCGTGTTAGCC	161711	GGCTAACACGGTGAAACCCC
152492	3131	CGGGGTTTCACCGTGTTAGC	161712	GCTAACACGGTGAAACCCCG
152493	3132	ACGGGGTTTCACCGTGTTAG	161713	CTAACACGGTGAAACCCCGT
152494	3133	GACGGGGTTTCACCGTGTTA	161714	TAACACGGTGAAACCCCGTC
152495	3134	AGACGGGGTTTCACCGTGTT	161715	AACACGGTGAAACCCCGTCT
152496	3135	GAGACGGGGTTTCACCGTGT	161716	ACACGGTGAAACCCCGTCTC
152497	3136	AGAGACGGGGTTTCACCGTG	161717	CACGGTGAAACCCCGTCTCT
152498	3137	TAGAGACGGGGTTTCACCGT	161718	ACGGTGAAACCCCGTCTCTA
152499	3138	GTAGAGACGGGGTTTCACCG	161719	CGGTGAAACCCCGTCTCTAC
152500	3139	AGTAGAGACGGGGTTTCACC	161720	GGTGAAACCCCGTCTCTACT
152501	3140	TAGTAGAGACGGGGTTTCAC	161721	GTGAAACCCCGTCTCTACTA
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152504	3143	TTTTAGTAGAGACGGGGTTT	161724	AAACCCCGTCTCTACTAAAA
152505	3144	TTTTTAGTAGAGACGGGGTT	161725	AACCCCGTCTCTACTAAAAA
152506	3145	ATTTTTAGTAGAGACGGGGT	161726	ACCCCGTCTCTACTAAAAAT
152507	3146	CATTTTTAGTAGAGACGGGG	161727	CCCCGTCTCTACTAAAAATG
152508	3147	GCATTTTTAGTAGAGACGGG	161728	CCCGTCTCTACTAAAAATGC
152509	3148	TGCATTTTTAGTAGAGACGG	161729	CCGTCTCTACTAAAAATGCA
152510	3149	TTGCATTTTTAGTAGAGACG	161730	CGTCTCTACTAAAAATGCAA
152511	3150	TTTGCATTTTTAGTAGAGAC	161731	GTCTCTACTAAAAATGCAAA
152512	3151	TTTTGCATTTTTAGTAGAGA	161732	TCTCTACTAAAAATGCAAAA
152513	3152	TTTTTGCATTTTTAGTAGAG	161733	CTCTACTAAAAATGCAAAAA
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152515	3154	TTTTTTTGCATTTTTAGTAG	161735	CTACTAAAAATGCAAAAAAA
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152517	3156	AATTTTTTTGCATTTTTAGT	161737	ACTAAAAATGCAAAAAAATT
152518	3157	TAATTTTTTTGCATTTTTAG	161738	CTAAAAATGCAAAAAAATTA
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152520	3159	GCTAATTTTTTTGCATTTTT	161740	AAAAATGCAAAAAAATTAGC
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152522	3161	CGGCTAATTTTTTTGCATTT	161742	AAATGCAAAAAAATTAGCCG
152523	3162	CCGGCTAATTTTTTTGCATT	161743	AATGCAAAAAAATTAGCCGG
152524	3163	CCCGGCTAATTTTTTTGCAT	161744	ATGCAAAAAAATTAGCCGGG
152525	3164	ACCCGGCTAATTTTTTTGCA	161745	TGCAAAAAAATTAGCCGGGT
152526	3165	CACCCGGCTAATTTTTTTGC	161746	GCAAAAAAATTAGCCGGGTG
152527	3166	ACACCCGGCTAATTTTTTTG	161747	CAAAAAAATTAGCCGGGTGT

152528	3167	CACACCCGGCTAATTTTTTT	161748	AAAAAAATTAGCCGGGTGTG
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152530	3169	ACCACACCCGGCTAATTTTT	161750	AAAAATTAGCCGGGTGTGGT
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152542	3181	CAGGCGCCCACCACCACACC	161762	GGTGTGGTGGTGGGCGCCTG
152543	3182	ACAGGCGCCCACCACCACAC	161763	GTGTGGTGGTGGGCGCCTGT
152544	3183	TACAGGCGCCCACCACCACA	161764	TGTGGTGGTGGGCGCCTGTA
152545	3184	CTACAGGCGCCCACCACCAC	161765	GTGGTGGTGGGCGCCTGTAG
152546	3185	ACTACAGGCGCCCACCACCA	161766	TGGTGGTGGGCGCCTGTAGT
152547	3186	GACTACAGGCGCCCACCACC	161767	GGTGGTGGGCGCCTGTAGTC
152548	3187	GGACTACAGGCGCCCACCAC	161768	GTGGTGGGCGCCTGTAGTCC
152549	3188	GGGACTACAGGCGCCCACCA	161769	TGGTGGGCGCCTGTAGTCCC
152550	3189	TGGGACTACAGGCGCCCACC	161770	GGTGGGCGCCTGTAGTCCCA
152551	3190	CTGGGACTACAGGCGCCCAC	161771	GTGGGCGCCTGTAGTCCCAG
152552	3191	GCTGGGACTACAGGCGCCCA	161772	TGGGCGCCTGTAGTCCCAGC
152553	3192	AGCTGGGACTACAGGCGCCC	161773	GGGCGCCTGTAGTCCCAGCT
152554	3193	TAGCTGGGACTACAGGCGCC	161774	GGCGCCTGTAGTCCCAGCTA
152555	3194	GTAGCTGGGACTACAGGCGC	161775	GCGCCTGTAGTCCCAGCTAC
152556	3195	AGTAGCTGGGACTACAGGCG	161776	CGCCTGTAGTCCCAGCTACT
152557	3196	GAGTAGCTGGGACTACAGGC	161777	GCCTGTAGTCCCAGCTACTC
152558	3197	TGAGTAGCTGGGACTACAGG	161778	CCTGTAGTCCCAGCTACTCA
152559	3198	CTGAGTAGCTGGGACTACAG	161779	CTGTAGTCCCAGCTACTCAG
152560	3199	CCTGAGTAGCTGGGACTACA	161780	TGTAGTCCCAGCTACTCAGG
152561	3200	TCCTGAGTAGCTGGGACTAC	161781	GTAGTCCCAGCTACTCAGGA
152562	3201	CTCCTGAGTAGCTGGGACTA	161782	TAGTCCCAGCTACTCAGGAG
152563	3202	CCTCCTGAGTAGCTGGGACT	161783	AGTCCCAGCTACTCAGGAGG
152564	3203	GCCTCCTGAGTAGCTGGGAC	161784	GTCCCAGCTACTCAGGAGGC
152565	3204	AGCCTCCTGAGTAGCTGGGA	161785	TCCCAGCTACTCAGGAGGCT
152566	3205	CAGCCTCCTGAGTAGCTGGG	161786	CCCAGCTACTCAGGAGGCTG
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152568	3207	CTCAGCCTCCTGAGTAGCTG	161788	CAGCTACTCAGGAGGCTGAG
152569	3208	CCTCAGCCTCCTGAGTAGCT	161789	AGCTACTCAGGAGGCTGAGG
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152572	3211	CTGCCTCAGCCTCCTGAGTA	161792	TACTCAGGAGGCTGAGGCAG
152573	3212	CCTGCCTCAGCCTCCTGAGT	161793	ACTCAGGAGGCTGAGGCAGG
152574	3213	TCCTGCCTCAGCCTCCTGAG	161794	CTCAGGAGGCTGAGGCAGGA
152575	3214	CTCCTGCCTCAGCCTCCTGA	161795	TCAGGAGGCTGAGGCAGGAG
152576	3215	TCTCCTGCCTCAGCCTCCTG	161796	CAGGAGGCTGAGGCAGGAGA
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152578	3217	ATTCTCCTGCCTCAGCCTCC	161798	GGAGGCTGAGGCAGGAGAAT
152579	3218	CATTCTCCTGCCTCAGCCTC	161799	GAGGCTGAGGCAGGAGAATG
152580	3219	CCATTCTCCTGCCTCAGCCT	161800	AGGCTGAGGCAGGAGAATGG
152581	3220	GCCATTCTCCTGCCTCAGCC	161801	GGCTGAGGCAGGAGAATGGC
152582	3221	TGCCATTCTCCTGCCTCAGC	161802	GCTGAGGCAGGAGAATGGCA
152583	3222	ATGCCATTCTCCTGCCTCAG	161803	CTGAGGCAGGAGAATGGCAT
152584	3223	CATGCCATTCTCCTGCCTCA	161804	TGAGGCAGGAGAATGGCATG
152585	3224	TCATGCCATTCTCCTGCCTC	161805	GAGGCAGGAGAATGGCATGA
152586	3225	TTCATGCCATTCTCCTGCCT	161806	AGGCAGGAGAATGGCATGAA
152587	3226	GTTCATGCCATTCTCCTGCC	161807	GGCAGGAGAATGGCATGAAC
152588	3227	GGTTCATGCCATTCTCCTGC	161808	GCAGGAGAATGGCATGAACC
152589	3228	AGGTTCATGCCATTCTCCTG	161809	CAGGAGAATGGCATGAACCT
152590	3229	CAGGTTCATGCCATTCTCCT	161810	AGGAGAATGGCATGAACCTG
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152593	3232	TCCCAGGTTCATGCCATTCT	161813	AGAATGGCATGAACCTGGGA
152594	3233	CTCCCAGGTTCATGCCATTC	161814	GAATGGCATGAACCTGGGAG
152595	3234	CCTCCCAGGTTCATGCCATT	161815	AATGGCATGAACCTGGGAGG
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152597	3236	CGCCTCCCAGGTTCATGCCA	161817	TGGCATGAACCTGGGAGGCG
152598	3237	CCGCCTCCCAGGTTCATGCC	161818	GGCATGAACCTGGGAGGCGG
152599	3238	TCCGCCTCCCAGGTTCATGC	161819	GCATGAACCTGGGAGGCGGA

152600	3239	CTCCGCCTCCCAGGTTCATG	161820	CATGAACCTGGGAGGCGGAG
152601	3240	GCTCCGCCTCCCAGGTTCAT	161821	ATGAACCTGGGAGGCGGAGC
152602	3241	AGCTCCGCCTCCCAGGTTCA	161822	TGAACCTGGGAGGCGGAGCT
152603	3242	AAGCTCCGCCTCCCAGGTTC	161823	GAACCTGGGAGGCGGAGCTT
152604	3243	CAAGCTCCGCCTCCCAGGTT	161824	AACCTGGGAGGCGGAGCTTG
152605	3244	GCAAGCTCCGCCTCCCAGGT	161825	ACCTGGGAGGCGGAGCTTGC
152606	3245	TGCAAGCTCCGCCTCCCAGG	161826	CCTGGGAGGCGGAGCTTGCA
152607	3246	CTGCAAGCTCCGCCTCCCAG	161827	CTGGGAGGCGGAGCTTGCAG
152608	3247	ACTGCAAGCTCCGCCTCCCA	161828	TGGGAGGCGGAGCTTGCAGT
152609	3248	CACTGCAAGCTCCGCCTCCC	161829	GGGAGGCGGAGCTTGCAGTG
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152612	3251	GCTCACTGCAAGCTCCGCCT	161832	AGGCGGAGCTTGCAGTGAGC
152613	3252	GGCTCACTGCAAGCTCCGCC	161833	GGCGGAGCTTGCAGTGAGCC
152614	3253	CGGCTCACTGCAAGCTCCGC	161834	GCGGAGCTTGCAGTGAGCCG
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152616	3255	CTCGGCTCACTGCAAGCTCC	161836	GGAGCTTGCAGTGAGCCGAG
152617	3256	TCTCGGCTCACTGCAAGCTC	161837	GAGCTTGCAGTGAGCCGAGA
152618	3257	ATCTCGGCTCACTGCAAGCT	161838	AGCTTGCAGTGAGCCGAGAT
152619	3258	GATCTCGGCTCACTGCAAGC	161839	GCTTGCAGTGAGCCGAGATC
152620	3259	TGATCTCGGCTCACTGCAAG	161840	CTTGCAGTGAGCCGAGATCA
152621	3260	ATGATCTCGGCTCACTGCAA	161841	TTGCAGTGAGCCGAGATCAT
152622	3261	CATGATCTCGGCTCACTGCA	161842	TGCAGTGAGCCGAGATCATG
152623	3262	ACATGATCTCGGCTCACTGC	161843	GCAGTGAGCCGAGATCATGT
152624	3263	GACATGATCTCGGCTCACTG	161844	CAGTGAGCCGAGATCATGTC
152625	3264	TGACATGATCTCGGCTCACT	161845	AGTGAGCCGAGATCATGTCA
152626	3265	GTGACATGATCTCGGCTCAC	161846	GTGAGCCGAGATCATGTCAC
152627	3266	AGTGACATGATCTCGGCTCA	161847	TGAGCCGAGATCATGTCACT
152628	3267	CAGTGACATGATCTCGGCTC	161848	GAGCCGAGATCATGTCACTG
152629	3268	GCAGTGACATGATCTCGGCT	161849	AGCCGAGATCATGTCACTGC
152630	3269	TGCAGTGACATGATCTCGGC	161850	GCCGAGATCATGTCACTGCA
152631	3270	GTGCAGTGACATGATCTCGG	161851	CCGAGATCATGTCACTGCAC
152632	3271	AGTGCAGTGACATGATCTCG	161852	CGAGATCATGTCACTGCACT
152633	3272	GAGTGCAGTGACATGATCTC	161853	GAGATCATGTCACTGCACTC
152634	3273	GGAGTGCAGTGACATGATCT	161854	AGATCATGTCACTGCACTCC
152635	3274	TGGAGTGCAGTGACATGATC	161855	GATCATGTCACTGCACTCCA
152636	3275	CTGGAGTGCAGTGACATGAT	161856	ATCATGTCACTGCACTCCAG
152637	3276	GCTGGAGTGCAGTGACATGA	161857	TCATGTCACTGCACTCCAGC
152638	3277	GGCTGGAGTGCAGTGACATG	161858	CATGTCACTGCACTCCAGCC
152639	3278	AGGCTGGAGTGCAGTGACAT	161859	ATGTCACTGCACTCCAGCCT
152640	3279	CAGGCTGGAGTGCAGTGACA	161860	TGTCACTGCACTCCAGCCTG
152641	3280	CCAGGCTGGAGTGCAGTGAC	161861	GTCACTGCACTCCAGCCTGG
152642	3281	CCCAGGCTGGAGTGCAGTGA	161862	TCACTGCACTCCAGCCTGGG
152643	3282	GCCCAGGCTGGAGTGCAGTG	161863	CACTGCACTCCAGCCTGGGC
152644	3283	CGCCCAGGCTGGAGTGCAGT	161864	ACTGCACTCCAGCCTGGGCG
152645	3284	TCGCCCAGGCTGGAGTGCAG	161865	CTGCACTCCAGCCTGGGCGA
152646	3285	GTCGCCCAGGCTGGAGTGCA	161866	TGCACTCCAGCCTGGGCGAC
152647	3286	TGTCGCCCAGGCTGGAGTGC	161867	GCACTCCAGCCTGGGCGACA
152648	3287	CTGTCGCCCAGGCTGGAGTG	161868	CACTCCAGCCTGGGCGACAG
152649	3288	TCTGTCGCCCAGGCTGGAGT	161869	ACTCCAGCCTGGGCGACAGA
152650	3289	CTCTGTCGCCCAGGCTGGAG	161870	CTCCAGCCTGGGCGACAGAG
152651	3290	GCTCTGTCGCCCAGGCTGGA	161871	TCCAGCCTGGGCGACAGAGC
152652	3291	CGCTCTGTCGCCCAGGCTGG	161872	CCAGCCTGGGCGACAGAGCG
152653	3292	TCGCTCTGTCGCCCAGGCTG	161873	CAGCCTGGGCGACAGAGCGA
152654	3293	CTCGCTCTGTCGCCCAGGCT	161874	AGCCTGGGCGACAGAGCGAG
152655	3294	TCTCGCTCTGTCGCCCAGGC	161875	GCCTGGGCGACAGAGCGAGA
152656	3295	GTCTCGCTCTGTCGCCCAGG	161876	CCTGGGCGACAGAGCGAGAC
152657	3296	AGTCTCGCTCTGTCGCCCAG	161877	CTGGGCGACAGAGCGAGACT
152658	3297	GAGTCTCGCTCTGTCGCCCA	161878	TGGGCGACAGAGCGAGACTC
152659	3298	CGAGTCTCGCTCTGTCGCCC	161879	GGGCGACAGAGCGAGACTCG
152660	3299	ACGAGTCTCGCTCTGTCGCC	161880	GGCGACAGAGCGAGACTCGT
152661	3300	GACGAGTCTCGCTCTGTCGC	161881	GCGACAGAGCGAGACTCGTC
152662	3301	AGACGAGTCTCGCTCTGTCG	161882	CGACAGAGCGAGACTCGTCT
152663	3302	GAGACGAGTCTCGCTCTGTC	161883	GACAGAGCGAGACTCGTCTC
152664	3303	TGAGACGAGTCTCGCTCTGT	161884	ACAGAGCGAGACTCGTCTCA
152665	3304	TTGAGACGAGTCTCGCTCTG	161885	CAGAGCGAGACTCGTCTCAA
152666	3305	TTTGAGACGAGTCTCGCTCT	161886	AGAGCGAGACTCGTCTCAAA
152667	3306	TTTTGAGACGAGTCTCGCTC	161887	GAGCGAGACTCGTCTCAAAA
152668	3307	TTTTTGAGACGAGTCTCGCT	161888	AGCGAGACTCGTCTCAAAAA
152669	3308	TTTTTTGAGACGAGTCTCGC	161889	GCGAGACTCGTCTCAAAAAA
152670	3309	TTTTTTTGAGACGAGTCTCG	161890	CGAGACTCGTCTCAAAAAAA
152671	3310	TTTTTTTTGAGACGAGTCTC	161891	GAGACTCGTCTCAAAAAAAA

152672	3311	TTTTTTTTTGAGACGAGTCT	161892	AGACTCGTCTCAAAAAAAAA
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152675	3314	CTTTTTTTTTTGAGACGAG	161895	CTCGTCTCAAAAAAAAAAG
152676	3315	TCTTTTTTTTTTGAGACGA	161896	TCGTCTCAAAAAAAAAAGA
152677	3316	TTCTTTTTTTTTTGAGACG	161897	CGTCTCAAAAAAAAAAGAA
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152679	3318	TTTTCTTTTTTTTTTGAGA	161899	TCTCAAAAAAAAAAGAAAA
152680	3319	TTTTTCTTTTTTTTTTGAG	161900	CTCAAAAAAAAAAGAAAAA
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152682	3321	TTTTTTTCTTTTTTTTTTG	161902	CAAAAAAAAAAGAAAAAAA
152683	3322	GTTTTTTTCTTTTTTTTTT	161903	AAAAAAAAAAGAAAAAAAC
152684	3323	AGTTTTTTTCTTTTTTTTT	161904	AAAAAAAAAGAAAAAAACT
152685	3324	AAGTTTTTTTCTTTTTTTT	161905	AAAAAAAAGAAAAAAACTT
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152690	3329	ATCATAAGTTTTTTTCTTTT	161910	AAAAGAAAAAAACTTATGAT
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152692	3331	CCATCATAAGTTTTTTTCTT	161912	AAGAAAAAAACTTATGATGG
152693	3332	TCCATCATAAGTTTTTTTCT	161913	AGAAAAAAACTTATGATGGA
152694	3333	GTCCATCATAAGTTTTTTTC	161914	GAAAAAAACTTATGATGGAC
152695	3334	TGTCCATCATAAGTTTTTTT	161915	AAAAAAACTTATGATGGACA
152696	3335	GTGTCCATCATAAGTTTTTT	161916	AAAAAACTTATGATGGACAC
152697	3336	AGTGTCCATCATAAGTTTTT	161917	AAAAACTTATGATGGACACT
152698	3337	AAGTGTCCATCATAAGTTTT	161918	AAAACTTATGATGGACACTT
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152700	3339	TTAAGTGTCCATCATAAGTT	161920	AACTTATGATGGACACTTAA
152701	3340	TTTAAGTGTCCATCATAAGT	161921	ACTTATGATGGACACTTAAA
152702	3341	TTTTAAGTGTCCATCATAAG	161922	CTTATGATGGACACTTAAAA
152703	3342	TTTTTAAGTGTCCATCATAA	161923	TTATGATGGACACTTAAAAA
152704	3343	GTTTTTAAGTGTCCATCATA	161924	TATGATGGACACTTAAAAAC
152705	3344	TGTTTTTAAGTGTCCATCAT	161925	ATGATGGACACTTAAAAACA
152706	3345	GTGTTTTTAAGTGTCCATCA	161926	TGATGGACACTTAAAAACAC
152707	3346	AGTGTTTTTAAGTGTCCATC	161927	GATGGACACTTAAAAACACT
152708	3347	GAGTGTTTTTAAGTGTCCAT	161928	ATGGACACTTAAAAACACTC
152709	3348	TGAGTGTTTTTAAGTGTCCA	161929	TGGACACTTAAAAACACTCA
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152711	3350	AGTGAGTGTTTTTAAGTGTC	161931	GACACTTAAAAACACTCACT
152712	3351	CAGTGAGTGTTTTTAAGTGT	161932	ACACTTAAAAACACTCACTG
152713	3352	TCAGTGAGTGTTTTTAAGTG	161933	CACTTAAAAACACTCACTGA
152714	3353	CTCAGTGAGTGTTTTTAAGT	161934	ACTTAAAAACACTCACTGAG
152715	3354	ACTCAGTGAGTGTTTTTAAG	161935	CTTAAAAACACTCACTGAGT
152716	3355	CACTCAGTGAGTGTTTTTAA	161936	TTAAAAACACTCACTGAGTG
152717	3356	CCACTCAGTGAGTGTTTTTA	161937	TAAAAACACTCACTGAGTGG
152718	3357	CCCACTCAGTGAGTGTTTTT	161938	AAAAACACTCACTGAGTGGG
152719	3358	CCCCACTCAGTGAGTGTTTT	161939	AAAACACTCACTGAGTGGGG
152720	3359	TCCCCACTCAGTGAGTGTTT	161940	AAACACTCACTGAGTGGGGA
152721	3360	CTCCCCACTCAGTGAGTGTT	161941	AACACTCACTGAGTGGGGAG
152722	3361	ACTCCCCACTCAGTGAGTGT	161942	ACACTCACTGAGTGGGGAGT
152723	3362	CACTCCCCACTCAGTGAGTG	161943	CACTCACTGAGTGGGGAGTG
152724	3363	CCACTCCCCACTCAGTGAGT	161944	ACTCACTGAGTGGGGAGTGG
152725	3364	TCCACTCCCCACTCAGTGAG	161945	CTCACTGAGTGGGGAGTGGA
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152727	3366	TCTCCACTCCCCACTCAGTG	161947	CACTGAGTGGGGAGTGGAGA
152728	3367	CTCTCCACTCCCCACTCAGT	161948	ACTGAGTGGGGAGTGGAGAG
152729	3368	GCTCTCCACTCCCCACTCAG	161949	CTGAGTGGGGAGTGGAGAGC
152730	3369	TGCTCTCCACTCCCCACTCA	161950	TGAGTGGGGAGTGGAGAGCA
152731	3370	CTGCTCTCCACTCCCCACTC	161951	GAGTGGGGAGTGGAGAGCAG
152732	3371	CCTGCTCTCCACTCCCCACT	161952	AGTGGGGAGTGGAGAGCAGG
152733	3372	CCCTGCTCTCCACTCCCCAC	161953	GTGGGGAGTGGAGAGCAGGG
152734	3373	CCCCTGCTCTCCACTCCCCA	161954	TGGGGAGTGGAGAGCAGGGG
152735	3374	ACCCCTGCTCTCCACTCCCC	161955	GGGGAGTGGAGAGCAGGGGT
152736	3375	GACCCCTGCTCTCCACTCCC	161956	GGGAGTGGAGAGCAGGGGTC
152737	3376	GGACCCCTGCTCTCCACTCC	161957	GGAGTGGAGAGCAGGGGTCC
152738	3377	GGGACCCCTGCTCTCCACTC	161958	GAGTGGAGAGCAGGGGTCCC
152739	3378	TGGGACCCCTGCTCTCCACT	161959	AGTGGAGAGCAGGGGTCCCA
152740	3379	CTGGGACCCCTGCTCTCCAC	161960	GTGGAGAGCAGGGGTCCCAG
152741	3380	CCTGGGACCCCTGCTCTCCA	161961	TGGAGAGCAGGGGTCCCAGG
152742	3381	CCCTGGGACCCCTGCTCTCC	161962	GGAGAGCAGGGGTCCCAGGG
152743	3382	ACCCTGGGACCCCTGCTCTC	161963	GAGAGCAGGGGTCCCAGGGT

152744	3383	TACCCTGGGACCCCTGCTCT	161964	AGAGCAGGGGTCCCAGGGTA
152745	3384	CTACCCTGGGACCCCTGCTC	161965	GAGCAGGGGTCCCAGGGTAG
152746	3385	GCTACCCTGGGACCCCTGCT	161966	AGCAGGGGTCCCAGGGTAGC
152747	3386	GGCTACCCTGGGACCCCTGC	161967	GCAGGGGTCCCAGGGTAGCC
152748	3387	AGGCTACCCTGGGACCCCTG	161968	CAGGGGTCCCAGGGTAGCCT
152749	3388	CAGGCTACCCTGGGACCCCT	161969	AGGGGTCCCAGGGTAGCCTG
152750	3389	ACAGGCTACCCTGGGACCCC	161970	GGGGTCCCAGGGTAGCCTGT
152751	3390	AACAGGCTACCCTGGGACCC	161971	GGGTCCCAGGGTAGCCTGTT
152752	3391	CAACAGGCTACCCTGGGACC	161972	GGTCCCAGGGTAGCCTGTTG
152753	3392	CCAACAGGCTACCCTGGGAC	161973	GTCCCAGGGTAGCCTGTTGG
152754	3393	TCCAACAGGCTACCCTGGGA	161974	TCCCAGGGTAGCCTGTTGGA
152755	3394	GTCCAACAGGCTACCCTGGG	161975	CCCAGGGTAGCCTGTTGGAC
152756	3395	TGTCCAACAGGCTACCCTGG	161976	CCAGGGTAGCCTGTTGGACA
152757	3396	ATGTCCAACAGGCTACCCTG	161977	CAGGGTAGCCTGTTGGACAT
152758	3397	AATGTCCAACAGGCTACCCT	161978	AGGGTAGCCTGTTGGACATT
152759	3398	AAATGTCCAACAGGCTACCC	161979	GGGTAGCCTGTTGGACATTT
152760	3399	GAAATGTCCAACAGGCTACC	161980	GGTAGCCTGTTGGACATTTC
152761	3400	GGAAATGTCCAACAGGCTAC	161981	GTAGCCTGTTGGACATTTCC
152762	3401	TGGAAATGTCCAACAGGCTA	161982	TAGCCTGTTGGACATTTCCA
152763	3402	CTGGAAATGTCCAACAGGCT	161983	AGCCTGTTGGACATTTCCAG
152764	3403	CCTGGAAATGTCCAACAGGC	161984	GCCTGTTGGACATTTCCAGG
152765	3404	CCCTGGAAATGTCCAACAGG	161985	CCTGTTGGACATTTCCAGGG
152766	3405	GCCCTGGAAATGTCCAACAG	161986	CTGTTGGACATTTCCAGGGC
152767	3406	CGCCCTGGAAATGTCCAACA	161987	TGTTGGACATTTCCAGGGCG
152768	3407	TCGCCCTGGAAATGTCCAAC	161988	GTTGGACATTTCCAGGGCGA
152769	3408	GTCGCCCTGGAAATGTCCAA	161989	TTGGACATTTCCAGGGCGAC
152770	3409	AGTCGCCCTGGAAATGTCCA	161990	TGGACATTTCCAGGGCGACT
152771	3410	AAGTCGCCCTGGAAATGTCC	161991	GGACATTTCCAGGGCGACTT
152772	3411	AAAGTCGCCCTGGAAATGTC	161992	GACATTTCCAGGGCGACTTT
152773	3412	AAAAGTCGCCCTGGAAATGT	161993	ACATTTCCAGGGCGACTTTT
152774	3413	AAAAAGTCGCCCTGGAAATG	161994	CATTTCCAGGGCGACTTTTT
152775	3414	GAAAAAGTCGCCCTGGAAAT	161995	ATTTCCAGGGCGACTTTTTC
152776	3415	AGAAAAAGTCGCCCTGGAAA	161996	TTTCCAGGGCGACTTTTTCT
152777	3416	AAGAAAAAGTCGCCCTGGAA	161997	TTCCAGGGCGACTTTTTCTT
152778	3417	AAAGAAAAAGTCGCCCTGGA	161998	TCCAGGGCGACTTTTTCTTT
152779	3418	AAAAGAAAAAGTCGCCCTGG	161999	CCAGGGCGACTTTTTCTTTT
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152781	3420	AAAAAAGAAAAAGTCGCCCT	162001	AGGGCGACTTTTTCTTTTTT
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152787	3426	AAAAAAAAAAAAGAAAAAGT	162007	ACTTTTTCTTTTTTTTTTTT
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152789	3428	TAAAAAAAAAAAAAGAAAAA	162009	TTTTTCTTTTTTTTTTTTA
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152791	3430	TTTAAAAAAAAAAAAAGAAA	162011	TTTCTTTTTTTTTTTTAAA
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152793	3432	ACTTTAAAAAAAAAAAAAGA	162013	TCTTTTTTTTTTTTAAAGT
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152803	3442	TACTCACTTGACTTTAAAAA	162023	TTTTAAAGTCAAGTGAGTA
152804	3443	ATACTCACTTGACTTTAAAA	162024	TTTAAAGTCAAGTGAGTAT
152805	3444	CATACTCACTTGACTTTAAA	162025	TTAAAGTCAAGTGAGTATG
152806	3445	GCATACTCACTTGACTTTAA	162026	TAAAGTCAAGTGAGTATGC
152807	3446	GGCATACTCACTTGACTTTA	162027	TAAAGTCAAGTGAGTATGCC
152808	3447	TGGCATACTCACTTGACTTT	162028	AAAGTCAAGTGAGTATGCCA
152809	3448	ATGGCATACTCACTTGACTT	162029	AAGTCAAGTGAGTATGCCAT
152810	3449	TATGGCATACTCACTTGACT	162030	AGTCAAGTGAGTATGCCATA
152811	3450	ATATGGCATACTCACTTGAC	162031	GTCAAGTGAGTATGCCATAT
152812	3451	CATATGGCATACTCACTTGA	162032	TCAAGTGAGTATGCCATATG
152813	3452	CCATATGGCATACTCACTTG	162033	CAAGTGAGTATGCCATATGG
152814	3453	TCCATATGGCATACTCACTT	162034	AAGTGAGTATGCCATATGGA
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152816	3455	TTTCCATATGGCATACTCAC	162036	GTGAGTATGCCATATGGAAA
152817	3456	TTTTCCATATGGCATACTCA	162037	TGAGTATGCCATATGGAAAA
152818	3457	CTTTTCCATATGGCATACTC	162038	GAGTATGCCATATGGAAAAG
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152820	3459	CCCTTTTCCATATGGCATAC	162040	GTATGCCATATGGAAAAGGG
152821	3460	ACCCTTTTCCATATGGCATA	162041	TATGCCATATGGAAAAGGGT
152822	3461	CACCCTTTTCCATATGGCAT	162042	ATGCCATATGGAAAAGGGTG
152823	3462	ACACCCTTTTCCATATGGCA	162043	TGCCATATGGAAAAGGGTGT
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152827	3466	ACGCACACCCTTTTCCATAT	162047	ATATGGAAAAGGGTGTGCGT
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152829	3468	CCACGCACACCCTTTTCCAT	162049	ATGGAAAAGGGTGTGCGTGG
152830	3469	TCCACGCACACCCTTTTCCA	162050	TGGAAAAGGGTGTGCGTGGA
152831	3470	CTCCACGCACACCCTTTTCC	162051	GGAAAAGGGTGTGCGTGGAG
152832	3471	TCTCCACGCACACCCTTTTC	162052	GAAAAGGGTGTGCGTGGAGA
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152836	3475	TTTTTCTCCACGCACACCCT	162056	AGGGTGTGCGTGGAGAAAAA
152837	3476	CTTTTTCTCCACGCACACCC	162057	GGGTGTGCGTGGAGAAAAAG
152838	3477	GCTTTTTCTCCACGCACACC	162058	GGTGTGCGTGGAGAAAAAGC
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152842	3481	CCTTGCTTTTTCTCCACGCA	162062	TGCGTGGAGAAAAAGCAAGG
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152845	3484	GCCCCTTGCTTTTTCTCCAC	162065	GTGGAGAAAAAGCAAGGGGC
152846	3485	AGCCCCTTGCTTTTTCTCCA	162066	TGGAGAAAAAGCAAGGGGCT
152847	3486	GAGCCCCTTGCTTTTTCTCC	162067	GGAGAAAAAGCAAGGGGCTC
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152851	3490	TCTGGAGCCCCTTGCTTTTT	162071	AAAAAGCAAGGGGCTCCAGA
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152853	3492	ACTCTGGAGCCCCTTGCTTT	162073	AAAGCAAGGGGCTCCAGAGT
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152857	3496	CTACACTCTGGAGCCCCTTG	162077	CAAGGGGCTCCAGAGTGTAG
152858	3497	CCTACACTCTGGAGCCCCTT	162078	AAGGGGCTCCAGAGTGTAGG
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152860	3499	ATCCTACACTCTGGAGCCCC	162080	GGGGCTCCAGAGTGTAGGAT
152861	3500	CATCCTACACTCTGGAGCCC	162081	GGGCTCCAGAGTGTAGGATG
152862	3501	TCATCCTACACTCTGGAGCC	162082	GGCTCCAGAGTGTAGGATGA
152863	3502	CTCATCCTACACTCTGGAGC	162083	GCTCCAGAGTGTAGGATGAG
152864	3503	TCTCATCCTACACTCTGGAG	162084	CTCCAGAGTGTAGGATGAGA
152865	3504	GTCTCATCCTACACTCTGGA	162085	TCCAGAGTGTAGGATGAGAC
152866	3505	TGTCTCATCCTACACTCTGG	162086	CCAGAGTGTAGGATGAGACA
152867	3506	ATGTCTCATCCTACACTCTG	162087	CAGAGTGTAGGATGAGACAT
152868	3507	TATGTCTCATCCTACACTCT	162088	AGAGTGTAGGATGAGACATA
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152870	3509	TGTATGTCTCATCCTACACT	162090	AGTGTAGGATGAGACATACA
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152874	3513	AAGGTGTATGTCTCATCCTA	162094	TAGGATGAGACATACACCTT
152875	3514	AAAGGTGTATGTCTCATCCT	162095	AGGATGAGACATACACCTTT
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152881	3520	AACCCAAAAGGTGTATGTCT	162101	AGACATACACCTTTTGGGTT
152882	3521	TAACCCAAAAGGTGTATGTC	162102	GACATACACCTTTTGGGTTA
152883	3522	TTAACCCAAAAGGTGTATGT	162103	ACATACACCTTTTGGGTTAA
152884	3523	TTTAACCCAAAAGGTGTATG	162104	CATACACCTTTTGGGTTAAA
152885	3524	TTTTAACCCAAAAGGTGTAT	162105	ATACACCTTTTGGGTTAAAA
152886	3525	TTTTTAACCCAAAAGGTGTA	162106	TACACCTTTTGGGTTAAAAA
152887	3526	CTTTTTAACCCAAAAGGTGT	162107	ACACCTTTTGGGTTAAAAAG

152888	3527	CCTTTTTAACCCAAAAGGTG	162108	CACCTTTTGGGTTAAAAAGG
152889	3528	GCCTTTTTAACCCAAAAGGT	162109	ACCTTTTGGGTTAAAAAGGC
152890	3529	AGCCTTTTTAACCCAAAAGG	162110	CCTTTTGGGTTAAAAAGGCT
152891	3530	CAGCCTTTTTAACCCAAAAG	162111	CTTTTGGGTTAAAAAGGCTG
152892	3531	TCAGCCTTTTTAACCCAAAA	162112	TTTTGGGTTAAAAAGGCTGA
152893	3532	CTCAGCCTTTTTAACCCAAA	162113	TTTGGGTTAAAAAGGCTGAG
152894	3533	CCTCAGCCTTTTTAACCCAA	162114	TTGGGTTAAAAAGGCTGAGG
152895	3534	GCCTCAGCCTTTTTAACCCA	162115	TGGGTTAAAAAGGCTGAGGC
152896	3535	TGCCTCAGCCTTTTTAACCC	162116	GGGTTAAAAAGGCTGAGGCA
152897	3536	CTGCCTCAGCCTTTTTAACC	162117	GGTTAAAAAGGCTGAGGCAG
152898	3537	CCTGCCTCAGCCTTTTTAAC	162118	GTTAAAAAGGCTGAGGCAGG
152899	3538	TCCTGCCTCAGCCTTTTTAA	162119	TTAAAAAGGCTGAGGCAGGA
152900	3539	CTCCTGCCTCAGCCTTTTTA	162120	TAAAAAGGCTGAGGCAGGAG
152901	3540	TCTCCTGCCTCAGCCTTTTT	162121	AAAAAGGCTGAGGCAGGAGA
152902	3541	TTCTCCTGCCTCAGCCTTTT	162122	AAAAGGCTGAGGCAGGAGAA
152903	3542	ATTCTCCTGCCTCAGCCTTT	162123	AAAGGCTGAGGCAGGAGAAT
152904	3543	CATTCTCCTGCCTCAGCCTT	162124	AAGGCTGAGGCAGGAGAATG
152905	3544	CCATTCTCCTGCCTCAGCCT	162125	AGGCTGAGGCAGGAGAATGG
152906	3545	GCCATTCTCCTGCCTCAGCC	162126	GGCTGAGGCAGGAGAATGGC
152907	3546	CGCCATTCTCCTGCCTCAGC	162127	GCTGAGGCAGGAGAATGGCG
152908	3547	ACGCCATTCTCCTGCCTCAG	162128	CTGAGGCAGGAGAATGGCGT
152909	3548	CACGCCATTCTCCTGCCTCA	162129	TGAGGCAGGAGAATGGCGTG
152910	3549	TCACGCCATTCTCCTGCCTC	162130	GAGGCAGGAGAATGGCGTGA
152911	3550	TTCACGCCATTCTCCTGCCT	162131	AGGCAGGAGAATGGCGTGAA
152912	3551	GTTCACGCCATTCTCCTGCC	162132	GGCAGGAGAATGGCGTGAAC
152913	3552	GGTTCACGCCATTCTCCTGC	162133	GCAGGAGAATGGCGTGAACC
152914	3553	GGGTTCACGCCATTCTCCTG	162134	CAGGAGAATGGCGTGAACCC
152915	3554	CGGGTTCACGCCATTCTCCT	162135	AGGAGAATGGCGTGAACCCG
152916	3555	CCGGGTTCACGCCATTCTCC	162136	GGAGAATGGCGTGAACCCGG
152917	3556	CCCGGGTTCACGCCATTCTC	162137	GAGAATGGCGTGAACCCGGG
152918	3557	TCCCGGGTTCACGCCATTCT	162138	AGAATGGCGTGAACCCGGGA
152919	3558	CTCCCGGGTTCACGCCATTC	162139	GAATGGCGTGAACCCGGGAG
152920	3559	CCTCCCGGGTTCACGCCATT	162140	AATGGCGTGAACCCGGGAGG
152921	3560	GCCTCCCGGGTTCACGCCAT	162141	ATGGCGTGAACCCGGGAGGC
152922	3561	CGCCTCCCGGGTTCACGCCA	162142	TGGCGTGAACCCGGGAGGCG
152923	3562	CCGCCTCCCGGGTTCACGCC	162143	GGCGTGAACCCGGGAGGCGG
152924	3563	TCCGCCTCCCGGGTTCACGC	162144	GCGTGAACCCGGGAGGCGGA
152925	3564	CTCCGCCTCCCGGGTTCACG	162145	CGTGAACCCGGGAGGCGGAG
152926	3565	GCTCCGCCTCCCGGGTTCAC	162146	GTGAACCCGGGAGGCGGAGC
152927	3566	AGCTCCGCCTCCCGGGTTCA	162147	TGAACCCGGGAGGCGGAGCT
152928	3567	AAGCTCCGCCTCCCGGGTTC	162148	GAACCCGGGAGGCGGAGCTT
152929	3568	CAAGCTCCGCCTCCCGGGTT	162149	AACCCGGGAGGCGGAGCTTG
152930	3569	GCAAGCTCCGCCTCCCGGGT	162150	ACCCGGGAGGCGGAGCTTGC
152931	3570	TGCAAGCTCCGCCTCCCGGG	162151	CCCGGGAGGCGGAGCTTGCA
152932	3571	CTGCAAGCTCCGCCTCCCGG	162152	CCGGGAGGCGGAGCTTGCAG
152933	3572	ACTGCAAGCTCCGCCTCCCG	162153	CGGGAGGCGGAGCTTGCAGT
152934	3573	CACTGCAAGCTCCGCCTCCC	162154	GGGAGGCGGAGCTTGCAGTG
152935	3574	TCACTGCAAGCTCCGCCTCC	162155	GGAGGCGGAGCTTGCAGTGA
152936	3575	CTCACTGCAAGCTCCGCCTC	162156	GAGGCGGAGCTTGCAGTGAG
152937	3576	GCTCACTGCAAGCTCCGCCT	162157	AGGCGGAGCTTGCAGTGAGC
152938	3577	AGCTCACTGCAAGCTCCGCC	162158	GGCGGAGCTTGCAGTGAGCT
152939	3578	CAGCTCACTGCAAGCTCCGC	162159	GCGGAGCTTGCAGTGAGCTG
152940	3579	TCAGCTCACTGCAAGCTCCG	162160	CGGAGCTTGCAGTGAGCTGA
152941	3580	CTCAGCTCACTGCAAGCTCC	162161	GGAGCTTGCAGTGAGCTGAG
152942	3581	TCTCAGCTCACTGCAAGCTC	162162	GAGCTTGCAGTGAGCTGAGA
152943	3582	ATCTCAGCTCACTGCAAGCT	162163	AGCTTGCAGTGAGCTGAGAT
152944	3583	GATCTCAGCTCACTGCAAGC	162164	GCTTGCAGTGAGCTGAGATC
152945	3584	TGATCTCAGCTCACTGCAAG	162165	CTTGCAGTGAGCTGAGATCA
152946	3585	ATGATCTCAGCTCACTGCAA	162166	TTGCAGTGAGCTGAGATCAT
152947	3586	CATGATCTCAGCTCACTGCA	162167	TGCAGTGAGCTGAGATCATG
152948	3587	GCATGATCTCAGCTCACTGC	162168	GCAGTGAGCTGAGATCATGC
152949	3588	GGCATGATCTCAGCTCACTG	162169	CAGTGAGCTGAGATCATGCC
152950	3589	TGGCATGATCTCAGCTCACT	162170	AGTGAGCTGAGATCATGCCA
152951	3590	GTGGCATGATCTCAGCTCAC	162171	GTGAGCTGAGATCATGCCAC
152952	3591	AGTGGCATGATCTCAGCTCA	162172	TGAGCTGAGATCATGCCACT
152953	3592	CAGTGGCATGATCTCAGCTC	162173	GAGCTGAGATCATGCCACTG
152954	3593	GCAGTGGCATGATCTCAGCT	162174	AGCTGAGATCATGCCACTGC
152955	3594	TGCAGTGGCATGATCTCAGC	162175	GCTGAGATCATGCCACTGCA
152956	3595	GTGCAGTGGCATGATCTCAG	162176	CTGAGATCATGCCACTGCAC
152957	3596	AGTGCAGTGGCATGATCTCA	162177	TGAGATCATGCCACTGCACT
152958	3597	GAGTGCAGTGGCATGATCTC	162178	GAGATCATGCCACTGCACTC
152959	3598	GGAGTGCAGTGGCATGATCT	162179	AGATCATGCCACTGCACTCC

152960	3599	TGGAGTGCAGTGGCATGATC	162180	GATCATGCCACTGCACTCCA
152961	3600	CTGGAGTGCAGTGGCATGAT	162181	ATCATGCCACTGCACTCCAG
152962	3601	GCTGGAGTGCAGTGGCATGA	162182	TCATGCCACTGCACTCCAGC
152963	3602	GGCTGGAGTGCAGTGGCATG	162183	CATGCCACTGCACTCCAGCC
152964	3603	AGGCTGGAGTGCAGTGGCAT	162184	ATGCCACTGCACTCCAGCCT
152965	3604	CAGGCTGGAGTGCAGTGGCA	162185	TGCCACTGCACTCCAGCCTG
152966	3605	CCAGGCTGGAGTGCAGTGGC	162186	GCCACTGCACTCCAGCCTGG
152967	3606	CCCAGGCTGGAGTGCAGTGG	162187	CCACTGCACTCCAGCCTGGG
152968	3607	GCCCAGGCTGGAGTGCAGTG	162188	CACTGCACTCCAGCCTGGGC
152969	3608	CGCCCAGGCTGGAGTGCAGT	162189	ACTGCACTCCAGCCTGGGCG
152970	3609	TCGCCCAGGCTGGAGTGCAG	162190	CTGCACTCCAGCCTGGGCGA
152971	3610	GTCGCCCAGGCTGGAGTGCA	162191	TGCACTCCAGCCTGGGCGAC
152972	3611	TGTCGCCCAGGCTGGAGTGC	162192	GCACTCCAGCCTGGGCGACA
152973	3612	CTGTCGCCCAGGCTGGAGTG	162193	CACTCCAGCCTGGGCGACAG
152974	3613	TCTGTCGCCCAGGCTGGAGT	162194	ACTCCAGCCTGGGCGACAGA
152975	3614	CTCTGTCGCCCAGGCTGGAG	162195	CTCCAGCCTGGGCGACAGAG
152976	3615	GCTCTGTCGCCCAGGCTGGA	162196	TCCAGCCTGGGCGACAGAGC
152977	3616	CGCTCTGTCGCCCAGGCTGG	162197	CCAGCCTGGGCGACAGAGCG
152978	3617	TCGCTCTGTCGCCCAGGCTG	162198	CAGCCTGGGCGACAGAGCGA
152979	3618	CTCGCTCTGTCGCCCAGGCT	162199	AGCCTGGGCGACAGAGCGAG
152980	3619	TCTCGCTCTGTCGCCCAGGC	162200	GCCTGGGCGACAGAGCGAGA
152981	3620	GTCTCGCTCTGTCGCCCAGG	162201	CCTGGGCGACAGAGCGAGAC
152982	3621	AGTCTCGCTCTGTCGCCCAG	162202	CTGGGCGACAGAGCGAGACT
152983	3622	GAGTCTCGCTCTGTCGCCCA	162203	TGGGCGACAGAGCGAGACTC
152984	3623	AGAGTCTCGCTCTGTCGCCC	162204	GGGCGACAGAGCGAGACTCT
152985	3624	AAGAGTCTCGCTCTGTCGCC	162205	GGCGACAGAGCGAGACTCTT
152986	3625	CAAGAGTCTCGCTCTGTCGC	162206	GCGACAGAGCGAGACTCTTG
152987	3626	ACAAGAGTCTCGCTCTGTCG	162207	CGACAGAGCGAGACTCTTGT
152988	3627	GACAAGAGTCTCGCTCTGTC	162208	GACAGAGCGAGACTCTTGTC
152989	3628	AGACAAGAGTCTCGCTCTGT	162209	ACAGAGCGAGACTCTTGTCT
152990	3629	GAGACAAGAGTCTCGCTCTG	162210	CAGAGCGAGACTCTTGTCTC
152991	3630	TGAGACAAGAGTCTCGCTCT	162211	AGAGCGAGACTCTTGTCTCA
152992	3631	TTGAGACAAGAGTCTCGCTC	162212	GAGCGAGACTCTTGTCTCAA
152993	3632	TTTGAGACAAGAGTCTCGCT	162213	AGCGAGACTCTTGTCTCAAA
152994	3633	TTTTGAGACAAGAGTCTCGC	162214	GCGAGACTCTTGTCTCAAAA
152995	3634	ATTTTGAGACAAGAGTCTCG	162215	CGAGACTCTTGTCTCAAAAT
152996	3635	TATTTTGAGACAAGAGTCTC	162216	GAGACTCTTGTCTCAAAATA
152997	3636	TTATTTTGAGACAAGAGTCT	162217	AGACTCTTGTCTCAAAATAA
152998	3637	TTTATTTTGAGACAAGAGTC	162218	GACTCTTGTCTCAAAATAAA
152999	3638	TTTTATTTTGAGACAAGAGT	162219	ACTCTTGTCTCAAAATAAAA
153000	3639	TTTTTATTTTGAGACAAGAG	162220	CTCTTGTCTCAAAATAAAAA
153001	3640	TTTTTTATTTTGAGACAAGA	162221	TCTTGTCTCAAAATAAAAAA
153002	3641	GTTTTTTATTTTGAGACAAG	162222	CTTGTCTCAAAATAAAAAAC
153003	3642	CGTTTTTTATTTTGAGACAA	162223	TTGTCTCAAAATAAAAAACG
153004	3643	ACGTTTTTTATTTTGAGACA	162224	TGTCTCAAAATAAAAAACGT
153005	3644	AACGTTTTTTATTTTGAGAC	162225	GTCTCAAAATAAAAAACGTT
153006	3645	AAACGTTTTTTATTTTGAGA	162226	TCTCAAAATAAAAAACGTTT
153007	3646	TAAACGTTTTTTATTTTGAG	162227	CTCAAAATAAAAAACGTTTA
153008	3647	GTAAACGTTTTTTATTTTGA	162228	TCAAAATAAAAAACGTTTAC
153009	3648	TGTAAACGTTTTTTATTTTG	162229	CAAAATAAAAAACGTTTACA
153010	3649	ATGTAAACGTTTTTTATTTT	162230	AAAATAAAAAACGTTTACAT
153011	3650	CATGTAAACGTTTTTTATTT	162231	AAATAAAAAACGTTTACATG
153012	3651	ACATGTAAACGTTTTTTATT	162232	AATAAAAAACGTTTACATGT
153013	3652	TACATGTAAACGTTTTTTAT	162233	ATAAAAAACGTTTACATGTA
153014	3653	GTACATGTAAACGTTTTTTA	162234	TAAAAAACGTTTACATGTAC
153015	3654	TGTACATGTAAACGTTTTTT	162235	AAAAAACGTTTACATGTACA
153016	3655	ATGTACATGTAAACGTTTTT	162236	AAAAACGTTTACATGTACAT
153017	3656	CATGTACATGTAAACGTTTT	162237	AAAACGTTTACATGTACATG
153018	3657	ACATGTACATGTAAACGTTT	162238	AAACGTTTACATGTACATGT
153019	3658	TACATGTACATGTAAACGTT	162239	AACGTTTACATGTACATGTA
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153021	3660	TATACATGTACATGTAAACG	162241	CGTTTACATGTACATGTATA
153022	3661	ATATACATGTACATGTAAAC	162242	GTTTACATGTACATGTATAT
153023	3662	AATATACATGTACATGTAAA	162243	TTTACATGTACATGTATATT
153024	3663	GAATATACATGTACATGTAA	162244	TTACATGTACATGTATATTC
153025	3664	TGAATATACATGTACATGTA	162245	TACATGTACATGTATATTCA
153026	3665	TTGAATATACATGTACATGT	162246	ACATGTACATGTATATTCAA
153027	3666	GTTGAATATACATGTACATG	162247	CATGTACATGTATATTCAAC
153028	3667	TGTTGAATATACATGTACAT	162248	ATGTACATGTATATTCAACA
153029	3668	ATGTTGAATATACATGTACA	162249	TGTACATGTATATTCAACAT
153030	3669	CATGTTGAATATACATGTAC	162250	GTACATGTATATTCAACATG
153031	3670	ACATGTTGAATATACATGTA	162251	TACATGTATATTCAACATGT

153032	3671	TACATGTTGAATATACATGT	162252	ACATGTATATTCAACATGTA
153033	3672	GTACATGTTGAATATACATG	162253	CATGTATATTCAACATGTAC
153034	3673	TGTACATGTTGAATATACAT	162254	ATGTATATTCAACATGTACA
153035	3674	TTGTACATGTTGAATATACA	162255	TGTATATTCAACATGTACAA
153036	3675	TTTGTACATGTTGAATATAC	162256	GTATATTCAACATGTACAAA
153037	3676	ATTTGTACATGTTGAATATA	162257	TATATTCAACATGTACAAAT
153038	3677	TATTTGTACATGTTGAATAT	162258	ATATTCAACATGTACAAATA
153039	3678	ATATTTGTACATGTTGAATA	162259	TATTCAACATGTACAAATAT
153040	3679	TATATTTGTACATGTTGAAT	162260	ATTCAACATGTACAAATATA
153041	3680	TTATATTTGTACATGTTGAA	162261	TTCAACATGTACAAATATAA
153042	3681	GTTATATTTGTACATGTTGA	162262	TCAACATGTACAAATATAAC
153043	3682	GGTTATATTTGTACATGTTG	162263	CAACATGTACAAATATAACC
153044	3683	AGGTTATATTTGTACATGTT	162264	AACATGTACAAATATAACCT
153045	3684	TAGGTTATATTTGTACATGT	162265	ACATGTACAAATATAACCTA
153046	3685	ATAGGTTATATTTGTACATG	162266	CATGTACAAATATAACCTAT
153047	3686	AATAGGTTATATTTGTACAT	162267	ATGTACAAATATAACCTATT
153048	3687	GAATAGGTTATATTTGTACA	162268	TGTACAAATATAACCTATTC
153049	3688	TGAATAGGTTATATTTGTAC	162269	GTACAAATATAACCTATTCA
153050	3689	TTGAATAGGTTATATTTGTA	162270	TACAAATATAACCTATTCAA
153051	3690	TTTGAATAGGTTATATTTGT	162271	ACAAATATAACCTATTCAAA
153052	3691	TTTTGAATAGGTTATATTTG	162272	CAAATATAACCTATTCAAAA
153053	3692	CTTTTGAATAGGTTATATTT	162273	AAATATAACCTATTCAAAAG
153054	3693	ACTTTTGAATAGGTTATATT	162274	AATATAACCTATTCAAAAGT
153055	3694	TACTTTTGAATAGGTTATAT	162275	ATATAACCTATTCAAAAGTA
153056	3695	ATACTTTTGAATAGGTTATA	162276	TATAACCTATTCAAAAGTAT
153057	3696	AATACTTTTGAATAGGTTAT	162277	ATAACCTATTCAAAAGTATT
153058	3697	AAATACTTTTGAATAGGTTA	162278	TAACCTATTCAAAAGTATTT
153059	3698	TAAATACTTTTGAATAGGTT	162279	AACCTATTCAAAAGTATTTA
153060	3699	GTAAATACTTTTGAATAGGT	162280	ACCTATTCAAAAGTATTTAC
153061	3700	AGTAAATACTTTTGAATAGG	162281	CCTATTCAAAAGTATTTACT
153062	3701	TAGTAAATACTTTTGAATAG	162282	CTATTCAAAAGTATTTACTA
153063	3702	GTAGTAAATACTTTTGAATA	162283	TATTCAAAAGTATTTACTAC
153064	3703	TGTAGTAAATACTTTTGAAT	162284	ATTCAAAAGTATTTACTACA
153065	3704	ATGTAGTAAATACTTTTGAA	162285	TTCAAAAGTATTTACTACAT
153066	3705	TATGTAGTAAATACTTTTGA	162286	TCAAAAGTATTTACTACATA
153067	3706	TTATGTAGTAAATACTTTTG	162287	CAAAAGTATTTACTACATAA
153068	3707	TTTATGTAGTAAATACTTTT	162288	AAAAGTATTTACTACATAAA
153069	3708	ATTTATGTAGTAAATACTTT	162289	AAAGTATTTACTACATAAAT
153070	3709	TATTTATGTAGTAAATACTT	162290	AAGTATTTACTACATAAATA
153071	3710	CTATTTATGTAGTAAATACT	162291	AGTATTTACTACATAAATAG
153072	3711	CCTATTTATGTAGTAAATAC	162292	GTATTTACTACATAAATAGG
153073	3712	ACCTATTTATGTAGTAAATA	162293	TATTTACTACATAAATAGGT
153074	3713	TACCTATTTATGTAGTAAAT	162294	ATTTACTACATAAATAGGTA
153075	3714	GTACCTATTTATGTAGTAAA	162295	TTTACTACATAAATAGGTAC
153076	3715	AGTACCTATTTATGTAGTAA	162296	TTACTACATAAATAGGTACT
153077	3716	AAGTACCTATTTATGTAGTA	162297	TACTACATAAATAGGTACTT
153078	3717	TAAGTACCTATTTATGTAGT	162298	ACTACATAAATAGGTACTTA
153079	3718	GTAAGTACCTATTTATGTAG	162299	CTACATAAATAGGTACTTAC
153080	3719	TGTAAGTACCTATTTATGTA	162300	TACATAAATAGGTACTTACA
153081	3720	ATGTAAGTACCTATTTATGT	162301	ACATAAATAGGTACTTACAT
153082	3721	AATGTAAGTACCTATTTATG	162302	CATAAATAGGTACTTACATT
153083	3722	TAATGTAAGTACCTATTTAT	162303	ATAAATAGGTACTTACATTA
153084	3723	GTAATGTAAGTACCTATTTA	162304	TAAATAGGTACTTACATTAC
153085	3724	GGTAATGTAAGTACCTATTT	162305	AAATAGGTACTTACATTACC
153086	3725	AGGTAATGTAAGTACCTATT	162306	AATAGGTACTTACATTACCT
153087	3726	TAGGTAATGTAAGTACCTAT	162307	ATAGGTACTTACATTACCTA
153088	3727	ATAGGTAATGTAAGTACCTA	162308	TAGGTACTTACATTACCTAT
153089	3728	AATAGGTAATGTAAGTACCT	162309	AGGTACTTACATTACCTATT
153090	3729	AAATAGGTAATGTAAGTACC	162310	GGTACTTACATTACCTATTT
153091	3730	TAAATAGGTAATGTAAGTAC	162311	GTACTTACATTACCTATTTA
153092	3731	GTAAATAGGTAATGTAAGTA	162312	TACTTACATTACCTATTTAC
153093	3732	AGTAAATAGGTAATGTAAGT	162313	ACTTACATTACCTATTTACT
153094	3733	CAGTAAATAGGTAATGTAAG	162314	CTTACATTACCTATTTACTG
153095	3734	ACAGTAAATAGGTAATGTAA	162315	TTACATTACCTATTTACTGT
153096	3735	TACAGTAAATAGGTAATGTA	162316	TACATTACCTATTTACTGTA
153097	3736	TTACAGTAAATAGGTAATGT	162317	ACATTACCTATTTACTGTAA
153098	3737	ATTACAGTAAATAGGTAATG	162318	CATTACCTATTTACTGTAAT
153099	3738	TATTACAGTAAATAGGTAAT	162319	ATTACCTATTTACTGTAATA
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153101	3740	ACTATTACAGTAAATAGGTA	162321	TACCTATTTACTGTAATAGT
153102	3741	GACTATTACAGTAAATAGGT	162322	ACCTATTTACTGTAATAGTC
153103	3742	TGACTATTACAGTAAATAGG	162323	CCTATTTACTGTAATAGTCA

153104	3743	TTGACTATTACAGTAAATAG	162324	CTATTTACTGTAATAGTCAA
153105	3744	TTTGACTATTACAGTAAATA	162325	TATTTACTGTAATAGTCAAA
153106	3745	CTTTGACTATTACAGTAAAT	162326	ATTTACTGTAATAGTCAAAG
153107	3746	GCTTTGACTATTACAGTAAA	162327	TTTACTGTAATAGTCAAAGC
153108	3747	GGCTTTGACTATTACAGTAA	162328	TTACTGTAATAGTCAAAGCC
153109	3748	AGGCTTTGACTATTACAGTA	162329	TACTGTAATAGTCAAAGCCT
153110	3749	TAGGCTTTGACTATTACAGT	162330	ACTGTAATAGTCAAAGCCTA
153111	3750	ATAGGCTTTGACTATTACAG	162331	CTGTAATAGTCAAAGCCTAT
153112	3751	CATAGGCTTTGACTATTACA	162332	TGTAATAGTCAAAGCCTATG
153113	3752	TCATAGGCTTTGACTATTAC	162333	GTAATAGTCAAAGCCTATGA
153114	3753	TTCATAGGCTTTGACTATTA	162334	TAATAGTCAAAGCCTATGAA
153115	3754	CTTCATAGGCTTTGACTATT	162335	AATAGTCAAAGCCTATGAAG
153116	3755	ACTTCATAGGCTTTGACTAT	162336	ATAGTCAAAGCCTATGAAGT
153117	3756	TACTTCATAGGCTTTGACTA	162337	TAGTCAAAGCCTATGAAGTA
153118	3757	ATACTTCATAGGCTTTGACT	162338	AGTCAAAGCCTATGAAGTAT
153119	3758	GATACTTCATAGGCTTTGAC	162339	GTCAAAGCCTATGAAGTATC
153120	3759	AGATACTTCATAGGCTTTGA	162340	TCAAAGCCTATGAAGTATCT
153121	3760	TAGATACTTCATAGGCTTTG	162341	CAAAGCCTATGAAGTATCTA
153122	3761	TTAGATACTTCATAGGCTTT	162342	AAAGCCTATGAAGTATCTAA
153123	3762	GTTAGATACTTCATAGGCTT	162343	AAGCCTATGAAGTATCTAAC
153124	3763	TGTTAGATACTTCATAGGCT	162344	AGCCTATGAAGTATCTAACA
153125	3764	GTGTTAGATACTTCATAGGC	162345	GCCTATGAAGTATCTAACAC
153126	3765	AGTGTTAGATACTTCATAGG	162346	CCTATGAAGTATCTAACACT
153127	3766	CAGTGTTAGATACTTCATAG	162347	CTATGAAGTATCTAACACTG
153128	3767	TCAGTGTTAGATACTTCATA	162348	TATGAAGTATCTAACACTGA
153129	3768	ATCAGTGTTAGATACTTCAT	162349	ATGAAGTATCTAACACTGAT
153130	3769	CATCAGTGTTAGATACTTCA	162350	TGAAGTATCTAACACTGATG
153131	3770	ACATCAGTGTTAGATACTTC	162351	GAAGTATCTAACACTGATGT
153132	3771	CACATCAGTGTTAGATACTT	162352	AAGTATCTAACACTGATGTG
153133	3772	ACACATCAGTGTTAGATACT	162353	AGTATCTAACACTGATGTGT
153134	3773	TACACATCAGTGTTAGATAC	162354	GTATCTAACACTGATGTGTA
153135	3774	CTACACATCAGTGTTAGATA	162355	TATCTAACACTGATGTGTAG
153136	3775	CCTACACATCAGTGTTAGAT	162356	ATCTAACACTGATGTGTAGG
153137	3776	ACCTACACATCAGTGTTAGA	162357	TCTAACACTGATGTGTAGGT
153138	3777	TACCTACACATCAGTGTTAG	162358	CTAACACTGATGTGTAGGTA
153139	3778	GTACCTACACATCAGTGTTA	162359	TAACACTGATGTGTAGGTAC
153140	3779	AGTACCTACACATCAGTGTT	162360	AACACTGATGTGTAGGTACT
153141	3780	GAGTACCTACACATCAGTGT	162361	ACACTGATGTGTAGGTACTC
153142	3781	TGAGTACCTACACATCAGTG	162362	CACTGATGTGTAGGTACTCA
153143	3782	GTGAGTACCTACACATCAGT	162363	ACTGATGTGTAGGTACTCAC
153144	3783	AGTGAGTACCTACACATCAG	162364	CTGATGTGTAGGTACTCACT
153145	3784	AAGTGAGTACCTACACATCA	162365	TGATGTGTAGGTACTCACTT
153146	3785	AAAGTGAGTACCTACACATC	162366	GATGTGTAGGTACTCACTTT
153147	3786	CAAAGTGAGTACCTACACAT	162367	ATGTGTAGGTACTCACTTTG
153148	3787	GCAAAGTGAGTACCTACACA	162368	TGTGTAGGTACTCACTTTGC
153149	3788	AGCAAAGTGAGTACCTACAC	162369	GTGTAGGTACTCACTTTGCT
153150	3789	AAGCAAAGTGAGTACCTACA	162370	TGTAGGTACTCACTTTGCTT
153151	3790	CAAGCAAAGTGAGTACCTAC	162371	GTAGGTACTCACTTTGCTTG
153152	3791	GCAAGCAAAGTGAGTACCTA	162372	TAGGTACTCACTTTGCTTGC
153153	3792	GGCAAGCAAAGTGAGTACCT	162373	AGGTACTCACTTTGCTTGCC
153154	3793	TGGCAAGCAAAGTGAGTACC	162374	GGTACTCACTTTGCTTGCCA
153155	3794	GTGGCAAGCAAAGTGAGTAC	162375	GTACTCACTTTGCTTGCCAC
153156	3795	AGTGGCAAGCAAAGTGAGTA	162376	TACTCACTTTGCTTGCCACT
153157	3796	GAGTGGCAAGCAAAGTGAGT	162377	ACTCACTTTGCTTGCCACTC
153158	3797	AGAGTGGCAAGCAAAGTGAG	162378	CTCACTTTGCTTGCCACTCT
153159	3798	TAGAGTGGCAAGCAAAGTGA	162379	TCACTTTGCTTGCCACTCTA
153160	3799	ATAGAGTGGCAAGCAAAGTG	162380	CACTTTGCTTGCCACTCTAT
153161	3800	AATAGAGTGGCAAGCAAAGT	162381	ACTTTGCTTGCCACTCTATT
153162	3801	TAATAGAGTGGCAAGCAAAG	162382	CTTTGCTTGCCACTCTATTA
153163	3802	CTAATAGAGTGGCAAGCAAA	162383	TTTGCTTGCCACTCTATTAG
153164	3803	CCTAATAGAGTGGCAAGCAA	162384	TTGCTTGCCACTCTATTAGG
153165	3804	ACCTAATAGAGTGGCAAGCA	162385	TGCTTGCCACTCTATTAGGT
153166	3805	CACCTAATAGAGTGGCAAGC	162386	GCTTGCCACTCTATTAGGTG
153167	3806	GCACCTAATAGAGTGGCAAG	162387	CTTGCCACTCTATTAGGTGC
153168	3807	AGCACCTAATAGAGTGGCAA	162388	TTGCCACTCTATTAGGTGCT
153169	3808	AAGCACCTAATAGAGTGGCA	162389	TGCCACTCTATTAGGTGCTT
153170	3809	AAAGCACCTAATAGAGTGGC	162390	GCCACTCTATTAGGTGCTTT
153171	3810	AAAAGCACCTAATAGAGTGG	162391	CCACTCTATTAGGTGCTTTT
153172	3811	AAAAAGCACCTAATAGAGTG	162392	CACTCTATTAGGTGCTTTTT
153173	3812	TAAAAAGCACCTAATAGAGT	162393	ACTCTATTAGGTGCTTTTTA
153174	3813	ATAAAAAGCACCTAATAGAG	162394	CTCTATTAGGTGCTTTTTAT
153175	3814	CATAAAAAGCACCTAATAGA	162395	TCTATTAGGTGCTTTTTATG

153176	3815	ACATAAAAAGCACCTAATAG	162396	CTATTAGGTGCTTTTTATGT
153177	3816	AACATAAAAAGCACCTAATA	162397	TATTAGGTGCTTTTTATGTT
153178	3817	TAACATAAAAAGCACCTAAT	162398	ATTAGGTGCTTTTTATGTTA
153179	3818	ATAACATAAAAAGCACCTAA	162399	TTAGGTGCTTTTTATGTTAT
153180	3819	AATAACATAAAAAGCACCTA	162400	TAGGTGCTTTTTATGTTATT
153181	3820	AAATAACATAAAAAGCACCT	162401	AGGTGCTTTTTATGTTATTT
153182	3821	TAAATAACATAAAAAGCACC	162402	GGTGCTTTTTATGTTATTTA
153183	3822	TTAAATAACATAAAAAGCAC	162403	GTGCTTTTTATGTTATTTAA
153184	3823	ATTAAATAACATAAAAAGCA	162404	TGCTTTTTATGTTATTTAAT
153185	3824	GATTAAATAACATAAAAAGC	162405	GCTTTTTATGTTATTTAATC
153186	3825	TGATTAAATAACATAAAAAG	162406	CTTTTTATGTTATTTAATCA
153187	3826	ATGATTAAATAACATAAAAA	162407	TTTTTATGTTATTTAATCAT
153188	3827	CATGATTAAATAACATAAAA	162408	TTTTATGTTATTTAATCATG
153189	3828	TCATGATTAAATAACATAAA	162409	TTTATGTTATTTAATCATGA
153190	3829	TTCATGATTAAATAACATAA	162410	TTATGTTATTTAATCATGAA
153191	3830	CTTCATGATTAAATAACATA	162411	TATGTTATTTAATCATGAAG
153192	3831	GCTTCATGATTAAATAACAT	162412	ATGTTATTTAATCATGAAGC
153193	3832	GGCTTCATGATTAAATAACA	162413	TGTTATTTAATCATGAAGCC
153194	3833	AGGCTTCATGATTAAATAAC	162414	GTTATTTAATCATGAAGCCT
153195	3834	CAGGCTTCATGATTAAATAA	162415	TTATTTAATCATGAAGCCTG
153196	3835	CCAGGCTTCATGATTAAATA	162416	TATTTAATCATGAAGCCTGG
153197	3836	GCCAGGCTTCATGATTAAAT	162417	ATTTAATCATGAAGCCTGGC
153198	3837	GGCCAGGCTTCATGATTAAA	162418	TTTAATCATGAAGCCTGGCC
153199	3838	TGGCCAGGCTTCATGATTAA	162419	TTAATCATGAAGCCTGGCCA
153200	3839	GTGGCCAGGCTTCATGATTA	162420	TAATCATGAAGCCTGGCCAC
153201	3840	TGTGGCCAGGCTTCATGATT	162421	AATCATGAAGCCTGGCCACA
153202	3841	CTGTGGCCAGGCTTCATGAT	162422	ATCATGAAGCCTGGCCACAG
153203	3842	CCTGTGGCCAGGCTTCATGA	162423	TCATGAAGCCTGGCCACAGG
153204	3843	CCCTGTGGCCAGGCTTCATG	162424	CATGAAGCCTGGCCACAGGG
153205	3844	ACCCTGTGGCCAGGCTTCAT	162425	ATGAAGCCTGGCCACAGGGT
153206	3845	CACCCTGTGGCCAGGCTTCA	162426	TGAAGCCTGGCCACAGGGTG
153207	3846	GCACCCTGTGGCCAGGCTTC	162427	GAAGCCTGGCCACAGGGTGC
153208	3847	AGCACCCTGTGGCCAGGCTT	162428	AAGCCTGGCCACAGGGTGCT
153209	3848	AAGCACCCTGTGGCCAGGCT	162429	AGCCTGGCCACAGGGTGCTT
153210	3849	CAAGCACCCTGTGGCCAGGC	162430	GCCTGGCCACAGGGTGCTTG
153211	3850	ACAAGCACCCTGTGGCCAGG	162431	CCTGGCCACAGGGTGCTTGT
153212	3851	CACAAGCACCCTGTGGCCAG	162432	CTGGCCACAGGGTGCTTGTG
153213	3852	GCACAAGCACCCTGTGGCCA	162433	TGGCCACAGGGTGCTTGTGC
153214	3853	TGCACAAGCACCCTGTGGCC	162434	GGCCACAGGGTGCTTGTGCA
153215	3854	ATGCACAAGCACCCTGTGGC	162435	GCCACAGGGTGCTTGTGCAT
153216	3855	AATGCACAAGCACCCTGTGG	162436	CCACAGGGTGCTTGTGCATT
153217	3856	CAATGCACAAGCACCCTGTG	162437	CACAGGGTGCTTGTGCATTG
153218	3857	TCAATGCACAAGCACCCTGT	162438	ACAGGGTGCTTGTGCATTGA
153219	3858	CTCAATGCACAAGCACCCTG	162439	CAGGGTGCTTGTGCATTGAG
153220	3859	ACTCAATGCACAAGCACCCT	162440	AGGGTGCTTGTGCATTGAGT
153221	3860	CACTCAATGCACAAGCACCC	162441	GGGTGCTTGTGCATTGAGTG
153222	3861	ACACTCAATGCACAAGCACC	162442	GGTGCTTGTGCATTGAGTGT
153223	3862	CACACTCAATGCACAAGCAC	162443	GTGCTTGTGCATTGAGTGTG
153224	3863	CCACACTCAATGCACAAGCA	162444	TGCTTGTGCATTGAGTGTGG
153225	3864	CCCACACTCAATGCACAAGC	162445	GCTTGTGCATTGAGTGTGGG
153226	3865	TCCCACACTCAATGCACAAG	162446	CTTGTGCATTGAGTGTGGGA
153227	3866	TTCCCACACTCAATGCACAA	162447	TTGTGCATTGAGTGTGGGAA
153228	3867	GTTCCCACACTCAATGCACA	162448	TGTGCATTGAGTGTGGGAAC
153229	3868	TGTTCCCACACTCAATGCAC	162449	GTGCATTGAGTGTGGGAACA
153230	3869	TTGTTCCCACACTCAATGCA	162450	TGCATTGAGTGTGGGAACAA
153231	3870	CTTGTTCCCACACTCAATGC	162451	GCATTGAGTGTGGGAACAAG
153232	3871	TCTTGTTCCCACACTCAATG	162452	CATTGAGTGTGGGAACAAGA
153233	3872	ATCTTGTTCCCACACTCAAT	162453	ATTGAGTGTGGGAACAAGAT
153234	3873	AATCTTGTTCCCACACTCAA	162454	TTGAGTGTGGGAACAAGATT
153235	3874	TAATCTTGTTCCCACACTCA	162455	TGAGTGTGGGAACAAGATTA
153236	3875	GTAATCTTGTTCCCACACTC	162456	GAGTGTGGGAACAAGATTAC
153237	3876	GGTAATCTTGTTCCCACACT	162457	AGTGTGGGAACAAGATTACC
153238	3877	TGGTAATCTTGTTCCCACAC	162458	GTGTGGGAACAAGATTACCA
153239	3878	ATGGTAATCTTGTTCCCACA	162459	TGTGGGAACAAGATTACCAT
153240	3879	GATGGTAATCTTGTTCCCAC	162460	GTGGGAACAAGATTACCATC
153241	3880	AGATGGTAATCTTGTTCCCA	162461	TGGGAACAAGATTACCATCT
153242	3881	GAGATGGTAATCTTGTTCCC	162462	GGGAACAAGATTACCATCTC
153243	3882	GGAGATGGTAATCTTGTTCC	162463	GGAACAAGATTACCATCTCC
153244	3883	GGGAGATGGTAATCTTGTTC	162464	GAACAAGATTACCATCTCCC
153245	3884	AGGGAGATGGTAATCTTGTT	162465	AACAAGATTACCATCTCCCT
153246	3885	AAGGGAGATGGTAATCTTGT	162466	ACAAGATTACCATCTCCCTT
153247	3886	AAAGGGAGATGGTAATCTTG	162467	CAAGATTACCATCTCCCTTT

153248	3887	AAAAGGGAGATGGTAATCTT	162468	AAGATTACCATCTCCCTTTT
153249	3888	CAAAAGGGAGATGGTAATCT	162469	AGATTACCATCTCCCTTTTG
153250	3889	TCAAAAGGGAGATGGTAATC	162470	GATTACCATCTCCCTTTTGA
153251	3890	CTCAAAAGGGAGATGGTAAT	162471	ATTACCATCTCCCTTTTGAG
153252	3891	CCTCAAAAGGGAGATGGTAA	162472	TTACCATCTCCCTTTTGAGG
153253	3892	TCCTCAAAAGGGAGATGGTA	162473	TACCATCTCCCTTTTGAGGA
153254	3893	GTCCTCAAAAGGGAGATGGT	162474	ACCATCTCCCTTTTGAGGAC
153255	3894	TGTCCTCAAAAGGGAGATGG	162475	CCATCTCCCTTTTGAGGACA
153256	3895	GTGTCCTCAAAAGGGAGATG	162476	CATCTCCCTTTTGAGGACAC
153257	3896	TGTGTCCTCAAAAGGGAGAT	162477	ATCTCCCTTTTGAGGACACA
153258	3897	CTGTGTCCTCAAAAGGGAGA	162478	TCTCCCTTTTGAGGACACAG
153259	3898	CCTGTGTCCTCAAAAGGGAG	162479	CTCCCTTTTGAGGACACAGG
153260	3899	GCCTGTGTCCTCAAAAGGGA	162480	TCCCTTTTGAGGACACAGGC
153261	3900	GGCCTGTGTCCTCAAAAGGG	162481	CCCTTTTGAGGACACAGGCC
153262	3901	AGGCCTGTGTCCTCAAAAGG	162482	CCTTTTGAGGACACAGGCCT
153263	3902	TAGGCCTGTGTCCTCAAAAG	162483	CTTTTGAGGACACAGGCCTA
153264	3903	CTAGGCCTGTGTCCTCAAAA	162484	TTTTGAGGACACAGGCCTAG
153265	3904	TCTAGGCCTGTGTCCTCAAA	162485	TTTGAGGACACAGGCCTAGA
153266	3905	CTCTAGGCCTGTGTCCTCAA	162486	TTGAGGACACAGGCCTAGAG
153267	3906	GCTCTAGGCCTGTGTCCTCA	162487	TGAGGACACAGGCCTAGAGC
153268	3907	TGCTCTAGGCCTGTGTCCTC	162488	GAGGACACAGGCCTAGAGCA
153269	3908	CTGCTCTAGGCCTGTGTCCT	162489	AGGACACAGGCCTAGAGCAG
153270	3909	ACTGCTCTAGGCCTGTGTCC	162490	GGACACAGGCCTAGAGCAGT
153271	3910	AACTGCTCTAGGCCTGTGTC	162491	GACACAGGCCTAGAGCAGTT
153272	3911	TAACTGCTCTAGGCCTGTGT	162492	ACACAGGCCTAGAGCAGTTA
153273	3912	TTAACTGCTCTAGGCCTGTG	162493	CACAGGCCTAGAGCAGTTAA
153274	3913	CTTAACTGCTCTAGGCCTGT	162494	ACAGGCCTAGAGCAGTTAAG
153275	3914	GCTTAACTGCTCTAGGCCTG	162495	CAGGCCTAGAGCAGTTAAGC
153276	3915	TGCTTAACTGCTCTAGGCCT	162496	AGGCCTAGAGCAGTTAAGCA
153277	3916	CTGCTTAACTGCTCTAGGCC	162497	GGCCTAGAGCAGTTAAGCAG
153278	3917	GCTGCTTAACTGCTCTAGGC	162498	GCCTAGAGCAGTTAAGCAGC
153279	3918	AGCTGCTTAACTGCTCTAGG	162499	CCTAGAGCAGTTAAGCAGCT
153280	3919	AAGCTGCTTAACTGCTCTAG	162500	CTAGAGCAGTTAAGCAGCTT
153281	3920	CAAGCTGCTTAACTGCTCTA	162501	TAGAGCAGTTAAGCAGCTTG
153282	3921	GCAAGCTGCTTAACTGCTCT	162502	AGAGCAGTTAAGCAGCTTGC
153283	3922	AGCAAGCTGCTTAACTGCTC	162503	GAGCAGTTAAGCAGCTTGCT
153284	3923	CAGCAAGCTGCTTAACTGCT	162504	AGCAGTTAAGCAGCTTGCTG
153285	3924	CCAGCAAGCTGCTTAACTGC	162505	GCAGTTAAGCAGCTTGCTGG
153286	3925	TCCAGCAAGCTGCTTAACTG	162506	CAGTTAAGCAGCTTGCTGGA
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153288	3927	CCTCCAGCAAGCTGCTTAAC	162508	GTTAAGCAGCTTGCTGGAGG
153289	3928	ACCTCCAGCAAGCTGCTTAA	162509	TTAAGCAGCTTGCTGGAGGT
153290	3929	AACCTCCAGCAAGCTGCTTA	162510	TAAGCAGCTTGCTGGAGGTT
153291	3930	GAACCTCCAGCAAGCTGCTT	162511	AAGCAGCTTGCTGGAGGTTC
153292	3931	TGAACCTCCAGCAAGCTGCT	162512	AGCAGCTTGCTGGAGGTTCA
153293	3932	GTGAACCTCCAGCAAGCTGC	162513	GCAGCTTGCTGGAGGTTCAC
153294	3933	AGTGAACCTCCAGCAAGCTG	162514	CAGCTTGCTGGAGGTTCACT
153295	3934	CAGTGAACCTCCAGCAAGCT	162515	AGCTTGCTGGAGGTTCACTG
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153297	3936	GCCAGTGAACCTCCAGCAAG	162517	CTTGCTGGAGGTTCACTGGC
153298	3937	AGCCAGTGAACCTCCAGCAA	162518	TTGCTGGAGGTTCACTGGCT
153299	3938	TAGCCAGTGAACCTCCAGCA	162519	TGCTGGAGGTTCACTGGCTA
153300	3939	CTAGCCAGTGAACCTCCAGC	162520	GCTGGAGGTTCACTGGCTAG
153301	3940	TCTAGCCAGTGAACCTCCAG	162521	CTGGAGGTTCACTGGCTAGA
153302	3941	TTCTAGCCAGTGAACCTCCA	162522	TGGAGGTTCACTGGCTAGAA
153303	3942	TTTCTAGCCAGTGAACCTCC	162523	GGAGGTTCACTGGCTAGAAA
153304	3943	CTTTCTAGCCAGTGAACCTC	162524	GAGGTTCACTGGCTAGAAAG
153305	3944	ACTTTCTAGCCAGTGAACCT	162525	AGGTTCACTGGCTAGAAAGT
153306	3945	CACTTTCTAGCCAGTGAACC	162526	GGTTCACTGGCTAGAAAGTG
153307	3946	CCACTTTCTAGCCAGTGAAC	162527	GTTCACTGGCTAGAAAGTGG
153308	3947	ACCACTTTCTAGCCAGTGAA	162528	TTCACTGGCTAGAAAGTGGT
153309	3948	GACCACTTTCTAGCCAGTGA	162529	TCACTGGCTAGAAAGTGGTC
153310	3949	TGACCACTTTCTAGCCAGTG	162530	CACTGGCTAGAAAGTGGTCA
153311	3950	CTGACCACTTTCTAGCCAGT	162531	ACTGGCTAGAAAGTGGTCAG
153312	3951	GCTGACCACTTTCTAGCCAG	162532	CTGGCTAGAAAGTGGTCAGC
153313	3952	GGCTGACCACTTTCTAGCCA	162533	TGGCTAGAAAGTGGTCAGCC
153314	3953	AGGCTGACCACTTTCTAGCC	162534	GGCTAGAAAGTGGTCAGCCT
153315	3954	CAGGCTGACCACTTTCTAGC	162535	GCTAGAAAGTGGTCAGCCTG
153316	3955	CCAGGCTGACCACTTTCTAG	162536	CTAGAAAGTGGTCAGCCTGG
153317	3956	CCCAGGCTGACCACTTTCTA	162537	TAGAAAGTGGTCAGCCTGGG
153318	3957	TCCCAGGCTGACCACTTTCT	162538	AGAAAGTGGTCAGCCTGGGA
153319	3958	ATCCCAGGCTGACCACTTTC	162539	GAAAGTGGTCAGCCTGGGAT

153320	3959	AATCCCAGGCTGACCACTTT	162540	AAAGTGGTCAGCCTGGGATT
153321	3960	AAATCCCAGGCTGACCACTT	162541	AAGTGGTCAGCCTGGGATTT
153322	3961	CAAATCCCAGGCTGACCACT	162542	AGTGGTCAGCCTGGGATTTG
153323	3962	CCAAATCCCAGGCTGACCAC	162543	GTGGTCAGCCTGGGATTTGG
153324	3963	TCCAAATCCCAGGCTGACCA	162544	TGGTCAGCCTGGGATTTGGA
153325	3964	GTCCAAATCCCAGGCTGACC	162545	GGTCAGCCTGGGATTTGGAC
153326	3965	TGTCCAAATCCCAGGCTGAC	162546	GTCAGCCTGGGATTTGGACA
153327	3966	GTGTCCAAATCCCAGGCTGA	162547	TCAGCCTGGGATTTGGACAC
153328	3967	TGTGTCCAAATCCCAGGCTG	162548	CAGCCTGGGATTTGGACACA
153329	3968	CTGTGTCCAAATCCCAGGCT	162549	AGCCTGGGATTTGGACACAG
153330	3969	TCTGTGTCCAAATCCCAGGC	162550	GCCTGGGATTTGGACACAGA
153331	3970	ATCTGTGTCCAAATCCCAGG	162551	CCTGGGATTTGGACACAGAT
153332	3971	AATCTGTGTCCAAATCCCAG	162552	CTGGGATTTGGACACAGATT
153333	3972	AAATCTGTGTCCAAATCCCA	162553	TGGGATTTGGACACAGATTT
153334	3973	AAAATCTGTGTCCAAATCCC	162554	GGGATTTGGACACAGATTTT
153335	3974	AAAAATCTGTGTCCAAATCC	162555	GGATTTGGACACAGATTTTT
153336	3975	GAAAAATCTGTGTCCAAATC	162556	GATTTGGACACAGATTTTTC
153337	3976	GGAAAAATCTGTGTCCAAAT	162557	ATTTGGACACAGATTTTTCC
153338	3977	TGGAAAAATCTGTGTCCAAA	162558	TTTGGACACAGATTTTTCCA
153339	3978	GTGGAAAAATCTGTGTCCAA	162559	TTGGACACAGATTTTTCCAC
153340	3979	AGTGGAAAAATCTGTGTCCA	162560	TGGACACAGATTTTTCCACT
153341	3980	GAGTGGAAAAATCTGTGTCC	162561	GGACACAGATTTTTCCACTC
153342	3981	GGAGTGGAAAAATCTGTGTC	162562	GACACAGATTTTTCCACTCC
153343	3982	GGGAGTGGAAAAATCTGTGT	162563	ACACAGATTTTTCCACTCCC
153344	3983	TGGGAGTGGAAAAATCTGTG	162564	CACAGATTTTTCCACTCCCA
153345	3984	TTGGGAGTGGAAAAATCTGT	162565	ACAGATTTTTCCACTCCCAA
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153347	3986	ACTTGGGAGTGGAAAAATCT	162567	AGATTTTTCCACTCCCAAGT
153348	3987	GACTTGGGAGTGGAAAAATC	162568	GATTTTTCCACTCCCAAGTC
153349	3988	AGACTTGGGAGTGGAAAAAT	162569	ATTTTTCCACTCCCAAGTCT
153350	3989	CAGACTTGGGAGTGGAAAAA	162570	TTTTTCCACTCCCAAGTCTG
153351	3990	CCAGACTTGGGAGTGGAAAA	162571	TTTTCCACTCCCAAGTCTGG
153352	3991	GCCAGACTTGGGAGTGGAAA	162572	TTTCCACTCCCAAGTCTGGC
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153354	3993	CAGCCAGACTTGGGAGTGGA	162574	TCCACTCCCAAGTCTGGCTG
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153356	3995	AGCAGCCAGACTTGGGAGTG	162576	CACTCCCAAGTCTGGCTGCT
153357	3996	AAGCAGCCAGACTTGGGAGT	162577	ACTCCCAAGTCTGGCTGCTT
153358	3997	AAAGCAGCCAGACTTGGGAG	162578	CTCCCAAGTCTGGCTGCTTT
153359	3998	AAAAGCAGCCAGACTTGGGA	162579	TCCCAAGTCTGGCTGCTTTT
153360	3999	AAAAAGCAGCCAGACTTGGG	162580	CCCAAGTCTGGCTGCTTTTT
153361	4000	TAAAAAGCAGCCAGACTTGG	162581	CCAAGTCTGGCTGCTTTTTA
153362	4001	GTAAAAAGCAGCCAGACTTG	162582	CAAGTCTGGCTGCTTTTTAC
153363	4002	AGTAAAAAGCAGCCAGACTT	162583	AAGTCTGGCTGCTTTTTACT
153364	4003	AAGTAAAAAGCAGCCAGACT	162584	AGTCTGGCTGCTTTTTACTT
153365	4004	GAAGTAAAAAGCAGCCAGAC	162585	GTCTGGCTGCTTTTTACTTC
153366	4005	TGAAGTAAAAAGCAGCCAGA	162586	TCTGGCTGCTTTTTACTTCA
153367	4006	GTGAAGTAAAAAGCAGCCAG	162587	CTGGCTGCTTTTTACTTCAC
153368	4007	AGTGAAGTAAAAAGCAGCCA	162588	TGGCTGCTTTTTACTTCACT
153369	4008	CAGTGAAGTAAAAAGCAGCC	162589	GGCTGCTTTTTACTTCACTG
153370	4009	ACAGTGAAGTAAAAAGCAGC	162590	GCTGCTTTTTACTTCACTGT
153371	4010	CACAGTGAAGTAAAAAGCAG	162591	CTGCTTTTTACTTCACTGTG
153372	4011	TCACAGTGAAGTAAAAAGCA	162592	TGCTTTTTACTTCACTGTGA
153373	4012	CTCACAGTGAAGTAAAAAGC	162593	GCTTTTTACTTCACTGTGAG
153374	4013	CCTCACAGTGAAGTAAAAAG	162594	CTTTTTACTTCACTGTGAGG
153375	4014	CCCTCACAGTGAAGTAAAAA	162595	TTTTTACTTCACTGTGAGGG
153376	4015	CCCCTCACAGTGAAGTAAAA	162596	TTTTACTTCACTGTGAGGGG
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153380	4019	TTTACCCCTCACAGTGAAGT	162600	ACTTCACTGTGAGGGGTAAA
153381	4020	CTTTACCCCTCACAGTGAAG	162601	CTTCACTGTGAGGGGTAAAG
153382	4021	CCTTTACCCCTCACAGTGAA	162602	TTCACTGTGAGGGGTAAAGG
153383	4022	ACCTTTACCCCTCACAGTGA	162603	TCACTGTGAGGGGTAAAGGT
153384	4023	TACCTTTACCCCTCACAGTG	162604	CACTGTGAGGGGTAAAGGTA
153385	4024	TTACCTTTACCCCTCACAGT	162605	ACTGTGAGGGGTAAAGGTAA
153386	4025	TTTACCTTTACCCCTCACAG	162606	CTGTGAGGGGTAAAGGTAAA
153387	4026	ATTTACCTTTACCCCTCACA	162607	TGTGAGGGGTAAAGGTAAAT
153388	4027	GATTTACCTTTACCCCTCAC	162608	GTGAGGGGTAAAGGTAAATC
153389	4028	TGATTTACCTTTACCCCTCA	162609	TGAGGGGTAAAGGTAAATCA
153390	4029	CTGATTTACCTTTACCCCTC	162610	GAGGGGTAAAGGTAAATCAG
153391	4030	GCTGATTTACCTTTACCCCT	162611	AGGGGTAAAGGTAAATCAGC

153392	4031	AGCTGATTTACCTTTACCCC	162612	GGGGTAAAGGTAAATCAGCT
153393	4032	CAGCTGATTTACCTTTACCC	162613	GGGTAAAGGTAAATCAGCTG
153394	4033	ACAGCTGATTTACCTTTACC	162614	GGTAAAGGTAAATCAGCTGT
153395	4034	AACAGCTGATTTACCTTTAC	162615	GTAAAGGTAAATCAGCTGTT
153396	4035	AAACAGCTGATTTACCTTTA	162616	TAAAGGTAAATCAGCTGTTT
153397	4036	AAAACAGCTGATTTACCTTT	162617	AAAGGTAAATCAGCTGTTTT
153398	4037	GAAAACAGCTGATTTACCTT	162618	AAGGTAAATCAGCTGTTTTC
153399	4038	AGAAAACAGCTGATTTACCT	162619	AGGTAAATCAGCTGTTTTCT
153400	4039	AAGAAAACAGCTGATTTACC	162620	GGTAAATCAGCTGTTTTCTT
153401	4040	AAAGAAAACAGCTGATTTAC	162621	GTAAATCAGCTGTTTTCTTT
153402	4041	CAAAGAAAACAGCTGATTTA	162622	TAAATCAGCTGTTTTCTTTG
153403	4042	ACAAAGAAAACAGCTGATTT	162623	AAATCAGCTGTTTTCTTTGT
153404	4043	AACAAAGAAAACAGCTGATT	162624	AATCAGCTGTTTTCTTTGTT
153405	4044	GAACAAAGAAAACAGCTGAT	162625	ATCAGCTGTTTTCTTTGTTC
153406	4045	TGAACAAAGAAAACAGCTGA	162626	TCAGCTGTTTTCTTTGTTCA
153407	4046	CTGAACAAAGAAAACAGCTG	162627	CAGCTGTTTTCTTTGTTCAG
153408	4047	TCTGAACAAAGAAAACAGCT	162628	AGCTGTTTTCTTTGTTCAGA
153409	4048	TTCTGAACAAAGAAAACAGC	162629	GCTGTTTTCTTTGTTCAGAA
153410	4049	TTTCTGAACAAAGAAAACAG	162630	CTGTTTTCTTTGTTCAGAAA
153411	4050	GTTTCTGAACAAAGAAAACA	162631	TGTTTTCTTTGTTCAGAAAC
153412	4051	AGTTTCTGAACAAAGAAAAC	162632	GTTTTCTTTGTTCAGAAACT
153413	4052	GAGTTTCTGAACAAAGAAAA	162633	TTTTCTTTGTTCAGAAACTC
153414	4053	AGAGTTTCTGAACAAAGAAA	162634	TTTCTTTGTTCAGAAACTCT
153415	4054	GAGAGTTTCTGAACAAAGAA	162635	TTCTTTGTTCAGAAACTCTC
153416	4055	AGAGAGTTTCTGAACAAAGA	162636	TCTTTGTTCAGAAACTCTCT
153417	4056	GAGAGAGTTTCTGAACAAAG	162637	CTTTGTTCAGAAACTCTCTC
153418	4057	GGAGAGAGTTTCTGAACAAA	162638	TTTGTTCAGAAACTCTCTCC
153419	4058	TGGAGAGAGTTTCTGAACAA	162639	TTGTTCAGAAACTCTCTCCA
153420	4059	TTGGAGAGAGTTTCTGAACA	162640	TGTTCAGAAACTCTCTCCAA
153421	4060	GTTGGAGAGAGTTTCTGAAC	162641	GTTCAGAAACTCTCTCCAAC
153422	4061	AGTTGGAGAGAGTTTCTGAA	162642	TTCAGAAACTCTCTCCAACT
153423	4062	AAGTTGGAGAGAGTTTCTGA	162643	TCAGAAACTCTCTCCAACTT
153424	4063	AAAGTTGGAGAGAGTTTCTG	162644	CAGAAACTCTCTCCAACTTT
153425	4064	CAAAGTTGGAGAGAGTTTCT	162645	AGAAACTCTCTCCAACTTTG
153426	4065	GCAAAGTTGGAGAGAGTTTC	162646	GAAACTCTCTCCAACTTTGC
153427	4066	TGCAAAGTTGGAGAGAGTTT	162647	AAACTCTCTCCAACTTTGCA
153428	4067	GTGCAAAGTTGGAGAGAGTT	162648	AACTCTCTCCAACTTTGCAC
153429	4068	AGTGCAAAGTTGGAGAGAGT	162649	ACTCTCTCCAACTTTGCACT
153430	4069	AAGTGCAAAGTTGGAGAGAG	162650	CTCTCTCCAACTTTGCACTT
153431	4070	AAAGTGCAAAGTTGGAGAGA	162651	TCTCTCCAACTTTGCACTTT
153432	4071	AAAAGTGCAAAGTTGGAGAG	162652	CTCTCCAACTTTGCACTTTT
153433	4072	GAAAAGTGCAAAGTTGGAGA	162653	TCTCCAACTTTGCACTTTTC
153434	4073	AGAAAAGTGCAAAGTTGGAG	162654	CTCCAACTTTGCACTTTTCT
153435	4074	AAGAAAAGTGCAAAGTTGGA	162655	TCCAACTTTGCACTTTTCTT
153436	4075	TAAGAAAAGTGCAAAGTTGG	162656	CCAACTTTGCACTTTTCTTA
153437	4076	TTAAGAAAAGTGCAAAGTTG	162657	CAACTTTGCACTTTTCTTAA
153438	4077	TTTAAGAAAAGTGCAAAGTT	162658	AACTTTGCACTTTTCTTAAA
153439	4078	CTTTAAGAAAAGTGCAAAGT	162659	ACTTTGCACTTTTCTTAAAG
153440	4079	CCTTTAAGAAAAGTGCAAAG	162660	CTTTGCACTTTTCTTAAAGG
153441	4080	TCCTTTAAGAAAAGTGCAAA	162661	TTTGCACTTTTCTTAAAGGA
153442	4081	TTCCTTTAAGAAAAGTGCAA	162662	TTGCACTTTTCTTAAAGGAA
153443	4082	TTTCCTTTAAGAAAAGTGCA	162663	TGCACTTTTCTTAAAGGAAA
153444	4083	CTTTCCTTTAAGAAAAGTGC	162664	GCACTTTTCTTAAAGGAAAG
153445	4084	ACTTTCCTTTAAGAAAAGTG	162665	CACTTTTCTTAAAGGAAAGT
153446	4085	TACTTTCCTTTAAGAAAAGT	162666	ACTTTTCTTAAAGGAAAGTA
153447	4086	TTACTTTCCTTTAAGAAAAG	162667	CTTTTCTTAAAGGAAAGTAA
153448	4087	ATTACTTTCCTTTAAGAAAA	162668	TTTTCTTAAAGGAAAGTAAT
153449	4088	CATTACTTTCCTTTAAGAAA	162669	TTTCTTAAAGGAAAGTAATG
153450	4089	CCATTACTTTCCTTTAAGAA	162670	TTCTTAAAGGAAAGTAATGG
153451	4090	TCCATTACTTTCCTTTAAGA	162671	TCTTAAAGGAAAGTAATGGA
153452	4091	GTCCATTACTTTCCTTTAAG	162672	CTTAAAGGAAAGTAATGGAC
153453	4092	GGTCCATTACTTTCCTTTAA	162673	TTAAAGGAAAGTAATGGACC
153454	4093	TGGTCCATTACTTTCCTTTA	162674	TAAAGGAAAGTAATGGACCA
153455	4094	CTGGTCCATTACTTTCCTTT	162675	AAAGGAAAGTAATGGACCAG
153456	4095	ACTGGTCCATTACTTTCCTT	162676	AAGGAAAGTAATGGACCAGT
153457	4096	CACTGGTCCATTACTTTCCT	162677	AGGAAAGTAATGGACCAGTG
153458	4097	TCACTGGTCCATTACTTTCC	162678	GGAAAGTAATGGACCAGTGA
153459	4098	TTCACTGGTCCATTACTTTC	162679	GAAAGTAATGGACCAGTGAA
153460	4099	CTTCACTGGTCCATTACTTT	162680	AAAGTAATGGACCAGTGAAG
153461	4100	CCTTCACTGGTCCATTACTT	162681	AAGTAATGGACCAGTGAAGG
153462	4101	ACCTTCACTGGTCCATTACT	162682	AGTAATGGACCAGTGAAGGT
153463	4102	CACCTTCACTGGTCCATTAC	162683	GTAATGGACCAGTGAAGGTG

153464	4103	ACACCTTCACTGGTCCATTA	162684	TAATGGACCAGTGAAGGTGT
153465	4104	CACACCTTCACTGGTCCATT	162685	AATGGACCAGTGAAGGTGTG
153466	4105	CCACACCTTCACTGGTCCAT	162686	ATGGACCAGTGAAGGTGTGG
153467	4106	CCCACACCTTCACTGGTCCA	162687	TGGACCAGTGAAGGTGTGGG
153468	4107	CCCCACACCTTCACTGGTCC	162688	GGACCAGTGAAGGTGTGGGG
153469	4108	TCCCCACACCTTCACTGGTC	162689	GACCAGTGAAGGTGTGGGGA
153470	4109	TTCCCCACACCTTCACTGGT	162690	ACCAGTGAAGGTGTGGGGAA
153471	4110	CTTCCCCACACCTTCACTGG	162691	CCAGTGAAGGTGTGGGGAAG
153472	4111	GCTTCCCCACACCTTCACTG	162692	CAGTGAAGGTGTGGGGAAGC
153473	4112	TGCTTCCCCACACCTTCACT	162693	AGTGAAGGTGTGGGGAAGCA
153474	4113	ATGCTTCCCCACACCTTCAC	162694	GTGAAGGTGTGGGGAAGCAT
153475	4114	AATGCTTCCCCACACCTTCA	162695	TGAAGGTGTGGGGAAGCATT
153476	4115	TAATGCTTCCCCACACCTTC	162696	GAAGGTGTGGGGAAGCATTA
153477	4116	TTAATGCTTCCCCACACCTT	162697	AAGGTGTGGGGAAGCATTAA
153478	4117	TTTAATGCTTCCCCACACCT	162698	AGGTGTGGGGAAGCATTAAA
153479	4118	CTTTAATGCTTCCCCACACC	162699	GGTGTGGGGAAGCATTAAAG
153480	4119	CCTTTAATGCTTCCCCACAC	162700	GTGTGGGGAAGCATTAAAGG
153481	4120	TCCTTTAATGCTTCCCCACA	162701	TGTGGGGAAGCATTAAAGGA
153482	4121	GTCCTTTAATGCTTCCCCAC	162702	GTGGGGAAGCATTAAAGGAC
153483	4122	AGTCCTTTAATGCTTCCCCA	162703	TGGGGAAGCATTAAAGGACT
153484	4123	CAGTCCTTTAATGCTTCCCC	162704	GGGGAAGCATTAAAGGACTG
153485	4124	TCAGTCCTTTAATGCTTCCC	162705	GGGAAGCATTAAAGGACTGA
153486	4125	GTCAGTCCTTTAATGCTTCC	162706	GGAAGCATTAAAGGACTGAC
153487	4126	AGTCAGTCCTTTAATGCTTC	162707	GAAGCATTAAAGGACTGACT
153488	4127	CAGTCAGTCCTTTAATGCTT	162708	AAGCATTAAAGGACTGACTG
153489	4128	TCAGTCAGTCCTTTAATGCT	162709	AGCATTAAAGGACTGACTGA
153490	4129	TTCAGTCAGTCCTTTAATGC	162710	GCATTAAAGGACTGACTGAA
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153493	4132	GCCTTCAGTCAGTCCTTTAA	162713	TTAAAGGACTGACTGAAGGC
153494	4133	GGCCTTCAGTCAGTCCTTTA	162714	TAAAGGACTGACTGAAGGCC
153495	4134	AGGCCTTCAGTCAGTCCTTT	162715	AAAGGACTGACTGAAGGCCT
153496	4135	CAGGCCTTCAGTCAGTCCTT	162716	AAGGACTGACTGAAGGCCTG
153497	4136	GCAGGCCTTCAGTCAGTCCT	162717	AGGACTGACTGAAGGCCTGC
153498	4137	TGCAGGCCTTCAGTCAGTCC	162718	GGACTGACTGAAGGCCTGCA
153499	4138	ATGCAGGCCTTCAGTCAGTC	162719	GACTGACTGAAGGCCTGCAT
153500	4139	CATGCAGGCCTTCAGTCAGT	162720	ACTGACTGAAGGCCTGCATG
153501	4140	CCATGCAGGCCTTCAGTCAG	162721	CTGACTGAAGGCCTGCATGG
153502	4141	TCCATGCAGGCCTTCAGTCA	162722	TGACTGAAGGCCTGCATGGA
153503	4142	ATCCATGCAGGCCTTCAGTC	162723	GACTGAAGGCCTGCATGGAT
153504	4143	AATCCATGCAGGCCTTCAGT	162724	ACTGAAGGCCTGCATGGATT
153505	4144	GAATCCATGCAGGCCTTCAG	162725	CTGAAGGCCTGCATGGATTC
153506	4145	GGAATCCATGCAGGCCTTCA	162726	TGAAGGCCTGCATGGATTCC
153507	4146	TGGAATCCATGCAGGCCTTC	162727	GAAGGCCTGCATGGATTCCA
153508	4147	ATGGAATCCATGCAGGCCTT	162728	AAGGCCTGCATGGATTCCAT
153509	4148	CATGGAATCCATGCAGGCCT	162729	AGGCCTGCATGGATTCCATG
153510	4149	ACATGGAATCCATGCAGGCC	162730	GGCCTGCATGGATTCCATGT
153511	4150	AACATGGAATCCATGCAGGC	162731	GCCTGCATGGATTCCATGTT
153512	4151	GAACATGGAATCCATGCAGG	162732	CCTGCATGGATTCCATGTTC
153513	4152	TGAACATGGAATCCATGCAG	162733	CTGCATGGATTCCATGTTCA
153514	4153	ATGAACATGGAATCCATGCA	162734	TGCATGGATTCCATGTTCAT
153515	4154	CATGAACATGGAATCCATGC	162735	GCATGGATTCCATGTTCATG
153516	4155	TCATGAACATGGAATCCATG	162736	CATGGATTCCATGTTCATGA
153517	4156	CTCATGAACATGGAATCCAT	162737	ATGGATTCCATGTTCATGAG
153518	4157	ACTCATGAACATGGAATCCA	162738	TGGATTCCATGTTCATGAGT
153519	4158	AACTCATGAACATGGAATCC	162739	GGATTCCATGTTCATGAGTT
153520	4159	AAACTCATGAACATGGAATC	162740	GATTCCATGTTCATGAGTTT
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153523	4162	TCCAAACTCATGAACATGGA	162743	TCCATGTTCATGAGTTTGGA
153524	4163	CTCCAAACTCATGAACATGG	162744	CCATGTTCATGAGTTTGGAG
153525	4164	TCTCCAAACTCATGAACATG	162745	CATGTTCATGAGTTTGGAGA
153526	4165	ATCTCCAAACTCATGAACAT	162746	ATGTTCATGAGTTTGGAGAT
153527	4166	TATCTCCAAACTCATGAACA	162747	TGTTCATGAGTTTGGAGATA
153528	4167	TTATCTCCAAACTCATGAAC	162748	GTTCATGAGTTTGGAGATAA
153529	4168	ATTATCTCCAAACTCATGAA	162749	TTCATGAGTTTGGAGATAAT
153530	4169	TATTATCTCCAAACTCATGA	162750	TCATGAGTTTGGAGATAATA
153531	4170	GTATTATCTCCAAACTCATG	162751	CATGAGTTTGGAGATAATAC
153532	4171	TGTATTATCTCCAAACTCAT	162752	ATGAGTTTGGAGATAATACA
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153534	4173	GCTGTATTATCTCCAAACTC	162754	GAGTTTGGAGATAATACAGC
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153536	4175	CTGCTGTATTATCTCCAAAC	162756	GTTTGGAGATAATACAGCAG
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153538	4177	ACCTGCTGTATTATCTCCAA	162758	TTGGAGATAATACAGCAGGT
153539	4178	CACCTGCTGTATTATCTCCA	162759	TGGAGATAATACAGCAGGTG
153540	4179	CCACCTGCTGTATTATCTCC	162760	GGAGATAATACAGCAGGTGG
153541	4180	CCCACCTGCTGTATTATCTC	162761	GAGATAATACAGCAGGTGGG
153542	4181	ACCCACCTGCTGTATTATCT	162762	AGATAATACAGCAGGTGGGT
153543	4182	CACCCACCTGCTGTATTATC	162763	GATAATACAGCAGGTGGGTG
153544	4183	ACACCCACCTGCTGTATTAT	162764	ATAATACAGCAGGTGGGTGT
153545	4184	AACACCCACCTGCTGTATTA	162765	TAATACAGCAGGTGGGTGTT
153546	4185	CAACACCCACCTGCTGTATT	162766	AATACAGCAGGTGGGTGTTG
153547	4186	ACAACACCCACCTGCTGTAT	162767	ATACAGCAGGTGGGTGTTGT
153548	4187	CACAACACCCACCTGCTGTA	162768	TACAGCAGGTGGGTGTTGTG
153549	4188	GCACAACACCCACCTGCTGT	162769	ACAGCAGGTGGGTGTTGTGC
153550	4189	AGCACAACACCCACCTGCTG	162770	CAGCAGGTGGGTGTTGTGCT
153551	4190	CAGCACAACACCCACCTGCT	162771	AGCAGGTGGGTGTTGTGCTG
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153556	4195	CAGCACAGCACAACACCCAC	162776	GTGGGTGTTGTGCTGTGCTG
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153558	4197	ACCAGCACAGCACAACACCC	162778	GGGTGTTGTGCTGTGCTGGT
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153562	4201	GGTCACCAGCACAGCACAAC	162782	GTTGTGCTGTGCTGGTGACC
153563	4202	GGGTCACCAGCACAGCACAA	162783	TTGTGCTGTGCTGGTGACCC
153564	4203	TGGGTCACCAGCACAGCACA	162784	TGTGCTGTGCTGGTGACCCA
153565	4204	ATGGGTCACCAGCACAGCAC	162785	GTGCTGTGCTGGTGACCCAT
153566	4205	TATGGGTCACCAGCACAGCA	162786	TGCTGTGCTGGTGACCCATA
153567	4206	GTATGGGTCACCAGCACAGC	162787	GCTGTGCTGGTGACCCATAC
153568	4207	AGTATGGGTCACCAGCACAG	162788	CTGTGCTGGTGACCCATACT
153569	4208	AAGTATGGGTCACCAGCACA	162789	TGTGCTGGTGACCCATACTT
153570	4209	CAAGTATGGGTCACCAGCAC	162790	GTGCTGGTGACCCATACTTG
153571	4210	ACAAGTATGGGTCACCAGCA	162791	TGCTGGTGACCCATACTTGT
153572	4211	AACAAGTATGGGTCACCAGC	162792	GCTGGTGACCCATACTTGTT
153573	4212	GAACAAGTATGGGTCACCAG	162793	CTGGTGACCCATACTTGTTC
153574	4213	TGAACAAGTATGGGTCACCA	162794	TGGTGACCCATACTTGTTCA
153575	4214	GTGAACAAGTATGGGTCACC	162795	GGTGACCCATACTTGTTCAC
153576	4215	GGTGAACAAGTATGGGTCAC	162796	GTGACCCATACTTGTTCACC
153577	4216	GGGTGAACAAGTATGGGTCA	162797	TGACCCATACTTGTTCACCC
153578	4217	AGGGTGAACAAGTATGGGTC	162798	GACCCATACTTGTTCACCCT
153579	4218	TAGGGTGAACAAGTATGGGT	162799	ACCCATACTTGTTCACCCTA
153580	4219	CTAGGGTGAACAAGTATGGG	162800	CCCATACTTGTTCACCCTAG
153581	4220	ACTAGGGTGAACAAGTATGG	162801	CCATACTTGTTCACCCTAGT
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153583	4222	TAACTAGGGTGAACAAGTAT	162803	ATACTTGTTCACCCTAGTTA
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153585	4224	TCTAACTAGGGTGAACAAGT	162805	ACTTGTTCACCCTAGTTAGA
153586	4225	ATCTAACTAGGGTGAACAAG	162806	CTTGTTCACCCTAGTTAGAT
153587	4226	TATCTAACTAGGGTGAACAA	162807	TTGTTCACCCTAGTTAGATA
153588	4227	TTATCTAACTAGGGTGAACA	162808	TGTTCACCCTAGTTAGATAA
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153590	4229	GTTTATCTAACTAGGGTGAA	162810	TTCACCCTAGTTAGATAAAC
153591	4230	TGTTTATCTAACTAGGGTGA	162811	TCACCCTAGTTAGATAAACA
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153596	4235	TCTACTGTTTATCTAACTAG	162816	CTAGTTAGATAAACAGTAGA
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153598	4237	ACTCTACTGTTTATCTAACT	162818	AGTTAGATAAACAGTAGAGT
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153600	4239	CTACTCTACTGTTTATCTAA	162820	TTAGATAAACAGTAGAGTAG
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153602	4241	GGCTACTCTACTGTTTATCT	162822	AGATAAACAGTAGAGTAGCC
153603	4242	GGGCTACTCTACTGTTTATC	162823	GATAAACAGTAGAGTAGCCC
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153606	4245	TAGGGGCTACTCTACTGTTT	162826	AAACAGTAGAGTAGCCCCTA
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153608	4247	TTTAGGGGCTACTCTACTGT	162828	ACAGTAGAGTAGCCCCTAAA
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153612	4251	AACGTTTAGGGGCTACTCTA	162832	TAGAGTAGCCCCTAAACGTT
153613	4252	TAACGTTTAGGGGCTACTCT	162833	AGAGTAGCCCCTAAACGTTA
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153615	4254	TTTAACGTTTAGGGGCTACT	162835	AGTAGCCCCTAAACGTTAAA
153616	4255	TTTTAACGTTTAGGGGCTAC	162836	GTAGCCCCTAAACGTTAAAA
153617	4256	GTTTTAACGTTTAGGGGCTA	162837	TAGCCCCTAAACGTTAAAAC
153618	4257	GGTTTTAACGTTTAGGGGCT	162838	AGCCCCTAAACGTTAAAACC
153619	4258	GGGTTTTAACGTTTAGGGGC	162839	GCCCCTAAACGTTAAAACCC
153620	4259	GGGGTTTTAACGTTTAGGGG	162840	CCCCTAAACGTTAAAACCCC
153621	4260	AGGGGTTTTAACGTTTAGGG	162841	CCCTAAACGTTAAAACCCCT
153622	4261	GAGGGGTTTTAACGTTTAGG	162842	CCTAAACGTTAAAACCCCTC
153623	4262	TGAGGGGTTTTAACGTTTAG	162843	CTAAACGTTAAAACCCCTCA
153624	4263	TTGAGGGGTTTTAACGTTTA	162844	TAAACGTTAAAACCCCTCAA
153625	4264	GTTGAGGGGTTTTAACGTTT	162845	AAACGTTAAAACCCCTCAAC
153626	4265	AGTTGAGGGGTTTTAACGTT	162846	AACGTTAAAACCCCTCAACT
153627	4266	AAGTTGAGGGGTTTTAACGT	162847	ACGTTAAAACCCCTCAACTT
153628	4267	CAAGTTGAGGGGTTTTAACG	162848	CGTTAAAACCCCTCAACTTG
153629	4268	ACAAGTTGAGGGGTTTTAAC	162849	GTTAAAACCCCTCAACTTGT
153630	4269	AACAAGTTGAGGGGTTTTAA	162850	TTAAAACCCCTCAACTTGTT
153631	4270	AAACAAGTTGAGGGGTTTTA	162851	TAAAACCCCTCAACTTGTTT
153632	4271	AAAACAAGTTGAGGGGTTTT	162852	AAAACCCCTCAACTTGTTTT
153633	4272	AAAAACAAGTTGAGGGGTTT	162853	AAACCCCTCAACTTGTTTTT
153634	4273	CAAAAACAAGTTGAGGGGTT	162854	AACCCCTCAACTTGTTTTTG
153635	4274	ACAAAAACAAGTTGAGGGGT	162855	ACCCCTCAACTTGTTTTTGT
153636	4275	AACAAAAACAAGTTGAGGGG	162856	CCCCTCAACTTGTTTTTGTT
153637	4276	AAACAAAAACAAGTTGAGGG	162857	CCCTCAACTTGTTTTTGTTT
153638	4277	AAAACAAAAACAAGTTGAGG	162858	CCTCAACTTGTTTTTGTTTT
153639	4278	AAAAACAAAAACAAGTTGAG	162859	CTCAACTTGTTTTTGTTTTT
153640	4279	CAAAAACAAAAACAAGTTGA	162860	TCAACTTGTTTTTGTTTTTG
153641	4280	TCAAAAACAAAAACAAGTTG	162861	CAACTTGTTTTTGTTTTTGA
153642	4281	CTCAAAAACAAAAACAAGTT	162862	AACTTGTTTTTGTTTTTGAG
153643	4282	TCTCAAAAACAAAAACAAGT	162863	ACTTGTTTTTGTTTTTGAGA
153644	4283	TTCTCAAAAACAAAAACAAG	162864	CTTGTTTTTGTTTTTGAGAA
153645	4284	TTTCTCAAAAACAAAAACAA	162865	TTGTTTTTGTTTTTGAGAAA
153646	4285	CTTTCTCAAAAACAAAAACA	162866	TGTTTTTGTTTTTGAGAAAG
153647	4286	CCTTTCTCAAAAACAAAAAC	162867	GTTTTTGTTTTTGAGAAAGG
153648	4287	CCCTTTCTCAAAAACAAAAA	162868	TTTTTGTTTTTGAGAAAGGG
153649	4288	ACCCTTTCTCAAAAACAAAA	162869	TTTTGTTTTTGAGAAAGGGT
153650	4289	GACCCTTTCTCAAAAACAAA	162870	TTTGTTTTTGAGAAAGGGTC
153651	4290	AGACCCTTTCTCAAAAACAA	162871	TTGTTTTTGAGAAAGGGTCT
153652	4291	AAGACCCTTTCTCAAAAACA	162872	TGTTTTTGAGAAAGGGTCTT
153653	4292	CAAGACCCTTTCTCAAAAAC	162873	GTTTTTGAGAAAGGGTCTTG
153654	4293	GCAAGACCCTTTCTCAAAAA	162874	TTTTTGAGAAAGGGTCTTGC
153655	4294	AGCAAGACCCTTTCTCAAAA	162875	TTTTGAGAAAGGGTCTTGCT
153656	4295	GAGCAAGACCCTTTCTCAAA	162876	TTTGAGAAAGGGTCTTGCTC
153657	4296	AGAGCAAGACCCTTTCTCAA	162877	TTGAGAAAGGGTCTTGCTCT
153658	4297	CAGAGCAAGACCCTTTCTCA	162878	TGAGAAAGGGTCTTGCTCTG
153659	4298	ACAGAGCAAGACCCTTTCTC	162879	GAGAAAGGGTCTTGCTCTGT
153660	4299	GACAGAGCAAGACCCTTTCT	162880	AGAAAGGGTCTTGCTCTGTC
153661	4300	CGACAGAGCAAGACCCTTTC	162881	GAAAGGGTCTTGCTCTGTCG
153662	4301	GCGACAGAGCAAGACCCTTT	162882	AAAGGGTCTTGCTCTGTCGC
153663	4302	AGCGACAGAGCAAGACCCTT	162883	AAGGGTCTTGCTCTGTCGCT
153664	4303	GAGCGACAGAGCAAGACCCT	162884	AGGGTCTTGCTCTGTCGCTC
153665	4304	TGAGCGACAGAGCAAGACCC	162885	GGGTCTTGCTCTGTCGCTCA
153666	4305	CTGAGCGACAGAGCAAGACC	162886	GGTCTTGCTCTGTCGCTCAG
153667	4306	CCTGAGCGACAGAGCAAGAC	162887	GTCTTGCTCTGTCGCTCAGG
153668	4307	GCCTGAGCGACAGAGCAAGA	162888	TCTTGCTCTGTCGCTCAGGC
153669	4308	AGCCTGAGCGACAGAGCAAG	162889	CTTGCTCTGTCGCTCAGGCT
153670	4309	CAGCCTGAGCGACAGAGCAA	162890	TTGCTCTGTCGCTCAGGCTG
153671	4310	CCAGCCTGAGCGACAGAGCA	162891	TGCTCTGTCGCTCAGGCTGG
153672	4311	TCCAGCCTGAGCGACAGAGC	162892	GCTCTGTCGCTCAGGCTGGA
153673	4312	CTCCAGCCTGAGCGACAGAG	162893	CTCTGTCGCTCAGGCTGGAG
153674	4313	ACTCCAGCCTGAGCGACAGA	162894	TCTGTCGCTCAGGCTGGAGT
153675	4314	CACTCCAGCCTGAGCGACAG	162895	CTGTCGCTCAGGCTGGAGTG
153676	4315	GCACTCCAGCCTGAGCGACA	162896	TGTCGCTCAGGCTGGAGTGC
153677	4316	TGCACTCCAGCCTGAGCGAC	162897	GTCGCTCAGGCTGGAGTGCA
153678	4317	CTGCACTCCAGCCTGAGCGA	162898	TCGCTCAGGCTGGAGTGCAG
153679	4318	ACTGCACTCCAGCCTGAGCG	162899	CGCTCAGGCTGGAGTGCAGT

153680	4319	CACTGCACTCCAGCCTGAGC	162900	GCTCAGGCTGGAGTGCAGTG
153681	4320	CCACTGCACTCCAGCCTGAG	162901	CTCAGGCTGGAGTGCAGTGG
153682	4321	GCCACTGCACTCCAGCCTGA	162902	TCAGGCTGGAGTGCAGTGGC
153683	4322	CGCCACTGCACTCCAGCCTG	162903	CAGGCTGGAGTGCAGTGGCG
153684	4323	GCGCCACTGCACTCCAGCCT	162904	AGGCTGGAGTGCAGTGGCGC
153685	4324	AGCGCCACTGCACTCCAGCC	162905	GGCTGGAGTGCAGTGGCGCT
153686	4325	CAGCGCCACTGCACTCCAGC	162906	GCTGGAGTGCAGTGGCGCTG
153687	4326	ACAGCGCCACTGCACTCCAG	162907	CTGGAGTGCAGTGGCGCTGT
153688	4327	CACAGCGCCACTGCACTCCA	162908	TGGAGTGCAGTGGCGCTGTG
153689	4328	GCACAGCGCCACTGCACTCC	162909	GGAGTGCAGTGGCGCTGTGC
153690	4329	CGCACAGCGCCACTGCACTC	162910	GAGTGCAGTGGCGCTGTGCG
153691	4330	TCGCACAGCGCCACTGCACT	162911	AGTGCAGTGGCGCTGTGCGA
153692	4331	ATCGCACAGCGCCACTGCAC	162912	GTGCAGTGGCGCTGTGCGAT
153693	4332	GATCGCACAGCGCCACTGCA	162913	TGCAGTGGCGCTGTGCGATC
153694	4333	TGATCGCACAGCGCCACTGC	162914	GCAGTGGCGCTGTGCGATCA
153695	4334	ATGATCGCACAGCGCCACTG	162915	CAGTGGCGCTGTGCGATCAT
153696	4335	CATGATCGCACAGCGCCACT	162916	AGTGGCGCTGTGCGATCATG
153697	4336	CCATGATCGCACAGCGCCAC	162917	GTGGCGCTGTGCGATCATGG
153698	4337	GCCATGATCGCACAGCGCCA	162918	TGGCGCTGTGCGATCATGGC
153699	4338	AGCCATGATCGCACAGCGCC	162919	GGCGCTGTGCGATCATGGCT
153700	4339	CAGCCATGATCGCACAGCGC	162920	GCGCTGTGCGATCATGGCTG
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153702	4341	GTCAGCCATGATCGCACAGC	162922	GCTGTGCGATCATGGCTGAC
153703	4342	GGTCAGCCATGATCGCACAG	162923	CTGTGCGATCATGGCTGACC
153704	4343	AGGTCAGCCATGATCGCACA	162924	TGTGCGATCATGGCTGACCT
153705	4344	AAGGTCAGCCATGATCGCAC	162925	GTGCGATCATGGCTGACCTT
153706	4345	TAAGGTCAGCCATGATCGCA	162926	TGCGATCATGGCTGACCTTA
153707	4346	CTAAGGTCAGCCATGATCGC	162927	GCGATCATGGCTGACCTTAG
153708	4347	GCTAAGGTCAGCCATGATCG	162928	CGATCATGGCTGACCTTAGC
153709	4348	GGCTAAGGTCAGCCATGATC	162929	GATCATGGCTGACCTTAGCC
153710	4349	AGGCTAAGGTCAGCCATGAT	162930	ATCATGGCTGACCTTAGCCT
153711	4350	AAGGCTAAGGTCAGCCATGA	162931	TCATGGCTGACCTTAGCCTT
153712	4351	CAAGGCTAAGGTCAGCCATG	162932	CATGGCTGACCTTAGCCTTG
153713	4352	TCAAGGCTAAGGTCAGCCAT	162933	ATGGCTGACCTTAGCCTTGA
153714	4353	GTCAAGGCTAAGGTCAGCCA	162934	TGGCTGACCTTAGCCTTGAC
153715	4354	GGTCAAGGCTAAGGTCAGCC	162935	GGCTGACCTTAGCCTTGACC
153716	4355	AGGTCAAGGCTAAGGTCAGC	162936	GCTGACCTTAGCCTTGACCT
153717	4356	GAGGTCAAGGCTAAGGTCAG	162937	CTGACCTTAGCCTTGACCTC
153718	4357	GGAGGTCAAGGCTAAGGTCA	162938	TGACCTTAGCCTTGACCTCC
153719	4358	GGGAGGTCAAGGCTAAGGTC	162939	GACCTTAGCCTTGACCTCCC
153720	4359	TGGGAGGTCAAGGCTAAGGT	162940	ACCTTAGCCTTGACCTCCCA
153721	4360	CTGGGAGGTCAAGGCTAAGG	162941	CCTTAGCCTTGACCTCCCAG
153722	4361	CCTGGGAGGTCAAGGCTAAG	162942	CTTAGCCTTGACCTCCCAGG
153723	4362	GCCTGGGAGGTCAAGGCTAA	162943	TTAGCCTTGACCTCCCAGGC
153724	4363	AGCCTGGGAGGTCAAGGCTA	162944	TAGCCTTGACCTCCCAGGCT
153725	4364	GAGCCTGGGAGGTCAAGGCT	162945	AGCCTTGACCTCCCAGGCTC
153726	4365	GGAGCCTGGGAGGTCAAGGC	162946	GCCTTGACCTCCCAGGCTCC
153727	4366	TGGAGCCTGGGAGGTCAAGG	162947	CCTTGACCTCCCAGGCTCCA
153728	4367	ATGGAGCCTGGGAGGTCAAG	162948	CTTGACCTCCCAGGCTCCAT
153729	4368	AATGGAGCCTGGGAGGTCAA	162949	TTGACCTCCCAGGCTCCATT
153730	4369	CAATGGAGCCTGGGAGGTCA	162950	TGACCTCCCAGGCTCCATTG
153731	4370	TCAATGGAGCCTGGGAGGTC	162951	GACCTCCCAGGCTCCATTGA
153732	4371	ATCAATGGAGCCTGGGAGGT	162952	ACCTCCCAGGCTCCATTGAT
153733	4372	GATCAATGGAGCCTGGGAGG	162953	CCTCCCAGGCTCCATTGATC
153734	4373	GGATCAATGGAGCCTGGGAG	162954	CTCCCAGGCTCCATTGATCC
153735	4374	AGGATCAATGGAGCCTGGGA	162955	TCCCAGGCTCCATTGATCCT
153736	4375	GAGGATCAATGGAGCCTGGG	162956	CCCAGGCTCCATTGATCCTC
153737	4376	TGAGGATCAATGGAGCCTGG	162957	CCAGGCTCCATTGATCCTCA
153738	4377	ATGAGGATCAATGGAGCCTG	162958	CAGGCTCCATTGATCCTCAT
153739	4378	CATGAGGATCAATGGAGCCT	162959	AGGCTCCATTGATCCTCATG
153740	4379	GCATGAGGATCAATGGAGCC	162960	GGCTCCATTGATCCTCATGC
153741	4380	GGCATGAGGATCAATGGAGC	162961	GCTCCATTGATCCTCATGCC
153742	4381	AGGCATGAGGATCAATGGAG	162962	CTCCATTGATCCTCATGCCT
153743	4382	AAGGCATGAGGATCAATGGA	162963	TCCATTGATCCTCATGCCTT
153744	4383	CAAGGCATGAGGATCAATGG	162964	CCATTGATCCTCATGCCTTG
153745	4384	CCAAGGCATGAGGATCAATG	162965	CATTGATCCTCATGCCTTGG
153746	4385	GCCAAGGCATGAGGATCAAT	162966	ATTGATCCTCATGCCTTGGC
153747	4386	GGCCAAGGCATGAGGATCAA	162967	TTGATCCTCATGCCTTGGCC
153748	4387	GGGCCAAGGCATGAGGATCA	162968	TGATCCTCATGCCTTGGCCC
153749	4388	CGGGCCAAGGCATGAGGATC	162969	GATCCTCATGCCTTGGCCCG
153750	4389	ACGGGCCAAGGCATGAGGAT	162970	ATCCTCATGCCTTGGCCCGT
153751	4390	TACGGGCCAAGGCATGAGGA	162971	TCCTCATGCCTTGGCCCGTA

153752	4391	CTACGGGCCAAGGCATGAGG	162972	CCTCATGCCTTGGCCCGTAG
153753	4392	GCTACGGGCCAAGGCATGAG	162973	CTCATGCCTTGGCCCGTAGC
153754	4393	AGCTACGGGCCAAGGCATGA	162974	TCATGCCTTGGCCCGTAGCT
153755	4394	CAGCTACGGGCCAAGGCATG	162975	CATGCCTTGGCCCGTAGCTG
153756	4395	CCAGCTACGGGCCAAGGCAT	162976	ATGCCTTGGCCCGTAGCTGG
153757	4396	CCCAGCTACGGGCCAAGGCA	162977	TGCCTTGGCCCGTAGCTGGG
153758	4397	TCCCAGCTACGGGCCAAGGC	162978	GCCTTGGCCCGTAGCTGGGA
153759	4398	GTCCCAGCTACGGGCCAAGG	162979	CCTTGGCCCGTAGCTGGGAC
153760	4399	AGTCCCAGCTACGGGCCAAG	162980	CTTGGCCCGTAGCTGGGACT
153761	4400	TAGTCCCAGCTACGGGCCAA	162981	TTGGCCCGTAGCTGGGACTA
153762	4401	GTAGTCCCAGCTACGGGCCA	162982	TGGCCCGTAGCTGGGACTAC
153763	4402	TGTAGTCCCAGCTACGGGCC	162983	GGCCCGTAGCTGGGACTACA
153764	4403	CTGTAGTCCCAGCTACGGGC	162984	GCCCGTAGCTGGGACTACAG
153765	4404	CCTGTAGTCCCAGCTACGGG	162985	CCCGTAGCTGGGACTACAGG
153766	4405	ACCTGTAGTCCCAGCTACGG	162986	CCGTAGCTGGGACTACAGGT
153767	4406	TACCTGTAGTCCCAGCTACG	162987	CGTAGCTGGGACTACAGGTA
153768	4407	GTACCTGTAGTCCCAGCTAC	162988	GTAGCTGGGACTACAGGTAC
153769	4408	TGTACCTGTAGTCCCAGCTA	162989	TAGCTGGGACTACAGGTACA
153770	4409	GTGTACCTGTAGTCCCAGCT	162990	AGCTGGGACTACAGGTACAC
153771	4410	TGTGTACCTGTAGTCCCAGC	162991	GCTGGGACTACAGGTACACA
153772	4411	GTGTGTACCTGTAGTCCCAG	162992	CTGGGACTACAGGTACACAC
153773	4412	GGTGTGTACCTGTAGTCCCA	162993	TGGGACTACAGGTACACACC
153774	4413	TGGTGTGTACCTGTAGTCCC	162994	GGGACTACAGGTACACACCA
153775	4414	GTGGTGTGTACCTGTAGTCC	162995	GGACTACAGGTACACACCAC
153776	4415	GGTGGTGTGTACCTGTAGTC	162996	GACTACAGGTACACACCACC
153777	4416	TGGTGGTGTGTACCTGTAGT	162997	ACTACAGGTACACACCACCA
153778	4417	GTGGTGGTGTGTACCTGTAG	162998	CTACAGGTACACACCACCAC
153779	4418	CGTGGTGGTGTGTACCTGTA	162999	TACAGGTACACACCACCACG
153780	4419	GCGTGGTGGTGTGTACCTGT	163000	ACAGGTACACACCACCACGC
153781	4420	GGCGTGGTGGTGTGTACCTG	163001	CAGGTACACACCACCACGCC
153782	4421	AGGCGTGGTGGTGTGTACCT	163002	AGGTACACACCACCACGCCT
153783	4422	CAGGCGTGGTGGTGTGTACC	163003	GGTACACACCACCACGCCTG
153784	4423	CCAGGCGTGGTGGTGTGTAC	163004	GTACACACCACCACGCCTGG
153785	4424	GCCAGGCGTGGTGGTGTGTA	163005	TACACACCACCACGCCTGGC
153786	4425	AGCCAGGCGTGGTGGTGTGT	163006	ACACACCACCACGCCTGGCT
153787	4426	TAGCCAGGCGTGGTGGTGTG	163007	CACACCACCACGCCTGGCTA
153788	4427	TTAGCCAGGCGTGGTGGTGT	163008	ACACCACCACGCCTGGCTAA
153789	4428	ATTAGCCAGGCGTGGTGGTG	163009	CACCACCACGCCTGGCTAAT
153790	4429	AATTAGCCAGGCGTGGTGGT	163010	ACCACCACGCCTGGCTAATT
153791	4430	AAATTAGCCAGGCGTGGTGG	163011	CCACCACGCCTGGCTAATTT
153792	4431	AAAATTAGCCAGGCGTGGTG	163012	CACCACGCCTGGCTAATTTT
153793	4432	AAAAATTAGCCAGGCGTGGT	163013	ACCACGCCTGGCTAATTTTT
153794	4433	CAAAAATTAGCCAGGCGTGG	163014	CCACGCCTGGCTAATTTTTG
153795	4434	ACAAAAATTAGCCAGGCGTG	163015	CACGCCTGGCTAATTTTTGT
153796	4435	TACAAAAATTAGCCAGGCGT	163016	ACGCCTGGCTAATTTTTGTA
153797	4436	ATACAAAAATTAGCCAGGCG	163017	CGCCTGGCTAATTTTTGTAT
153798	4437	AATACAAAAATTAGCCAGGC	163018	GCCTGGCTAATTTTTGTATT
153799	4438	AAATACAAAAATTAGCCAGG	163019	CCTGGCTAATTTTTGTATTT
153800	4439	AAAATACAAAAATTAGCCAG	163020	CTGGCTAATTTTTGTATTTT
153801	4440	AAAAATACAAAAATTAGCCA	163021	TGGCTAATTTTTGTATTTTT
153802	4441	AAAAAATACAAAAATTAGCC	163022	GGCTAATTTTTGTATTTTTT
153803	4442	AAAAAAATACAAAAATTAGC	163023	GCTAATTTTTGTATTTTTTT
153804	4443	GAAAAAAATACAAAAATTAG	163024	CTAATTTTTGTATTTTTTTC
153805	4444	AGAAAAAAATACAAAAATTA	163025	TAATTTTTGTATTTTTTTCT
153806	4445	TAGAAAAAAATACAAAAATT	163026	AATTTTTGTATTTTTTTCTA
153807	4446	CTAGAAAAAAATACAAAAAT	163027	ATTTTTGTATTTTTTTCTAG
153808	4447	TCTAGAAAAAAATACAAAAA	163028	TTTTTGTATTTTTTTCTAGA
153809	4448	CTCTAGAAAAAAATACAAAA	163029	TTTTGTATTTTTTTCTAGAG
153810	4449	CCTCTAGAAAAAAATACAAA	163030	TTTGTATTTTTTTCTAGAGG
153811	4450	ACCTCTAGAAAAAAATACAA	163031	TTGTATTTTTTTCTAGAGGT
153812	4451	CACCTCTAGAAAAAAATACA	163032	TGTATTTTTTTCTAGAGGTG
153813	4452	CCACCTCTAGAAAAAAATAC	163033	GTATTTTTTTCTAGAGGTGG
153814	4453	CCCACCTCTAGAAAAAAATA	163034	TATTTTTTTCTAGAGGTGGG
153815	4454	CCCCACCTCTAGAAAAAAAT	163035	ATTTTTTTCTAGAGGTGGGG
153816	4455	ACCCCACCTCTAGAAAAAAA	163036	TTTTTTTCTAGAGGTGGGGT
153817	4456	AACCCCACCTCTAGAAAAAA	163037	TTTTTTCTAGAGGTGGGGTT
153818	4457	AAACCCCACCTCTAGAAAAA	163038	TTTTTCTAGAGGTGGGGTTT
153819	4458	GAAACCCCACCTCTAGAAAA	163039	TTTTCTAGAGGTGGGGTTTC
153820	4459	TGAAACCCCACCTCTAGAAA	163040	TTTCTAGAGGTGGGGTTTCA
153821	4460	ATGAAACCCCACCTCTAGAA	163041	TTCTAGAGGTGGGGTTTCAT
153822	4461	GATGAAACCCCACCTCTAGA	163042	TCTAGAGGTGGGGTTTCATC
153823	4462	TGATGAAACCCCACCTCTAG	163043	CTAGAGGTGGGGTTTCATCA

153824	4463	ATGATGAAACCCCACCTCTA	163044	TAGAGGTGGGGTTTCATCAT
153825	4464	CATGATGAAACCCCACCTCT	163045	AGAGGTGGGGTTTCATCATG
153826	4465	ACATGATGAAACCCCACCTC	163046	GAGGTGGGGTTTCATCATGT
153827	4466	AACATGATGAAACCCCACCT	163047	AGGTGGGGTTTCATCATGTT
153828	4467	CAACATGATGAAACCCCACC	163048	GGTGGGGTTTCATCATGTTG
153829	4468	GCAACATGATGAAACCCCAC	163049	GTGGGGTTTCATCATGTTGC
153830	4469	GGCAACATGATGAAACCCCA	163050	TGGGGTTTCATCATGTTGCC
153831	4470	GGGCAACATGATGAAACCCC	163051	GGGGTTTCATCATGTTGCCC
153832	4471	TGGGCAACATGATGAAACCC	163052	GGGTTTCATCATGTTGCCCA
153833	4472	CTGGGCAACATGATGAAACC	163053	GGTTTCATCATGTTGCCCAG
153834	4473	CCTGGGCAACATGATGAAAC	163054	GTTTCATCATGTTGCCCAGG
153835	4474	GCCTGGGCAACATGATGAAA	163055	TTTCATCATGTTGCCCAGGC
153836	4475	AGCCTGGGCAACATGATGAA	163056	TTCATCATGTTGCCCAGGCT
153837	4476	CAGCCTGGGCAACATGATGA	163057	TCATCATGTTGCCCAGGCTG
153838	4477	CCAGCCTGGGCAACATGATG	163058	CATCATGTTGCCCAGGCTGG
153839	4478	ACCAGCCTGGGCAACATGAT	163059	ATCATGTTGCCCAGGCTGGT
153840	4479	GACCAGCCTGGGCAACATGA	163060	TCATGTTGCCCAGGCTGGTC
153841	4480	AGACCAGCCTGGGCAACATG	163061	CATGTTGCCCAGGCTGGTCT
153842	4481	AAGACCAGCCTGGGCAACAT	163062	ATGTTGCCCAGGCTGGTCTT
153843	4482	CAAGACCAGCCTGGGCAACA	163063	TGTTGCCCAGGCTGGTCTTG
153844	4483	TCAAGACCAGCCTGGGCAAC	163064	GTTGCCCAGGCTGGTCTTGA
153845	4484	TTCAAGACCAGCCTGGGCAA	163065	TTGCCCAGGCTGGTCTTGAA
153846	4485	GTTCAAGACCAGCCTGGGCA	163066	TGCCCAGGCTGGTCTTGAAC
153847	4486	AGTTCAAGACCAGCCTGGGC	163067	GCCCAGGCTGGTCTTGAACT
153848	4487	CAGTTCAAGACCAGCCTGGG	163068	CCCAGGCTGGTCTTGAACTG
153849	4488	GCAGTTCAAGACCAGCCTGG	163069	CCAGGCTGGTCTTGAACTGC
153850	4489	AGCAGTTCAAGACCAGCCTG	163070	CAGGCTGGTCTTGAACTGCT
153851	4490	CAGCAGTTCAAGACCAGCCT	163071	AGGCTGGTCTTGAACTGCTG
153852	4491	CCAGCAGTTCAAGACCAGCC	163072	GGCTGGTCTTGAACTGCTGG
153853	4492	CCCAGCAGTTCAAGACCAGC	163073	GCTGGTCTTGAACTGCTGGG
153854	4493	GCCCAGCAGTTCAAGACCAG	163074	CTGGTCTTGAACTGCTGGGC
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153856	4495	GAGCCCAGCAGTTCAAGACC	163076	GGTCTTGAACTGCTGGGCTC
153857	4496	TGAGCCCAGCAGTTCAAGAC	163077	GTCTTGAACTGCTGGGCTCA
153858	4497	TTGAGCCCAGCAGTTCAAGA	163078	TCTTGAACTGCTGGGCTCAA
153859	4498	CTTGAGCCCAGCAGTTCAAG	163079	CTTGAACTGCTGGGCTCAAG
153860	4499	ACTTGAGCCCAGCAGTTCAA	163080	TTGAACTGCTGGGCTCAAGT
153861	4500	CACTTGAGCCCAGCAGTTCA	163081	TGAACTGCTGGGCTCAAGTG
153862	4501	CCACTTGAGCCCAGCAGTTC	163082	GAACTGCTGGGCTCAAGTGG
153863	4502	ACCACTTGAGCCCAGCAGTT	163083	AACTGCTGGGCTCAAGTGGT
153864	4503	GACCACTTGAGCCCAGCAGT	163084	ACTGCTGGGCTCAAGTGGTC
153865	4504	AGACCACTTGAGCCCAGCAG	163085	CTGCTGGGCTCAAGTGGTCT
153866	4505	TAGACCACTTGAGCCCAGCA	163086	TGCTGGGCTCAAGTGGTCTA
153867	4506	ATAGACCACTTGAGCCCAGC	163087	GCTGGGCTCAAGTGGTCTAT
153868	4507	GATAGACCACTTGAGCCCAG	163088	CTGGGCTCAAGTGGTCTATC
153869	4508	GGATAGACCACTTGAGCCCA	163089	TGGGCTCAAGTGGTCTATCC
153870	4509	AGGATAGACCACTTGAGCCC	163090	GGGCTCAAGTGGTCTATCCT
153871	4510	GAGGATAGACCACTTGAGCC	163091	GGCTCAAGTGGTCTATCCTC
153872	4511	GGAGGATAGACCACTTGAGC	163092	GCTCAAGTGGTCTATCCTCC
153873	4512	AGGAGGATAGACCACTTGAG	163093	CTCAAGTGGTCTATCCTCCT
153874	4513	GAGGAGGATAGACCACTTGA	163094	TCAAGTGGTCTATCCTCCTC
153875	4514	CGAGGAGGATAGACCACTTG	163095	CAAGTGGTCTATCCTCCTCG
153876	4515	TCGAGGAGGATAGACCACTT	163096	AAGTGGTCTATCCTCCTCGA
153877	4516	GTCGAGGAGGATAGACCACT	163097	AGTGGTCTATCCTCCTCGAC
153878	4517	GGTCGAGGAGGATAGACCAC	163098	GTGGTCTATCCTCCTCGACC
153879	4518	AGGTCGAGGAGGATAGACCA	163099	TGGTCTATCCTCCTCGACCT
153880	4519	GAGGTCGAGGAGGATAGACC	163100	GGTCTATCCTCCTCGACCTC
153881	4520	GGAGGTCGAGGAGGATAGAC	163101	GTCTATCCTCCTCGACCTCC
153882	4521	GGGAGGTCGAGGAGGATAGA	163102	TCTATCCTCCTCGACCTCCC
153883	4522	TGGGAGGTCGAGGAGGATAG	163103	CTATCCTCCTCGACCTCCCA
153884	4523	TTGGGAGGTCGAGGAGGATA	163104	TATCCTCCTCGACCTCCCAA
153885	4524	TTTGGGAGGTCGAGGAGGAT	163105	ATCCTCCTCGACCTCCCAAA
153886	4525	CTTTGGGAGGTCGAGGAGGA	163106	TCCTCCTCGACCTCCCAAAG
153887	4526	ACTTTGGGAGGTCGAGGAGG	163107	CCTCCTCGACCTCCCAAAGT
153888	4527	CACTTTGGGAGGTCGAGGAG	163108	CTCCTCGACCTCCCAAAGTG
153889	4528	GCACTTTGGGAGGTCGAGGA	163109	TCCTCGACCTCCCAAAGTGC
153890	4529	AGCACTTTGGGAGGTCGAGG	163110	CCTCGACCTCCCAAAGTGCT
153891	4530	CAGCACTTTGGGAGGTCGAG	163111	CTCGACCTCCCAAAGTGCTG
153892	4531	CCAGCACTTTGGGAGGTCGA	163112	TCGACCTCCCAAAGTGCTGG
153893	4532	CCCAGCACTTTGGGAGGTCG	163113	CGACCTCCCAAAGTGCTGGG
153894	4533	TCCCAGCACTTTGGGAGGTC	163114	GACCTCCCAAAGTGCTGGGA
153895	4534	ATCCCAGCACTTTGGGAGGT	163115	ACCTCCCAAAGTGCTGGGAT

153896	4535	AATCCCAGCACTTTGGGAGG	163116	CCTCCCAAAGTGCTGGGATT
153897	4536	TAATCCCAGCACTTTGGGAG	163117	CTCCCAAAGTGCTGGGATTA
153898	4537	GTAATCCCAGCACTTTGGGA	163118	TCCCAAAGTGCTGGGATTAC
153899	4538	TGTAATCCCAGCACTTTGGG	163119	CCCAAAGTGCTGGGATTACA
153900	4539	ATGTAATCCCAGCACTTTGG	163120	CCAAAGTGCTGGGATTACAT
153901	4540	CATGTAATCCCAGCACTTTG	163121	CAAAGTGCTGGGATTACATG
153902	4541	ACATGTAATCCCAGCACTTT	163122	AAAGTGCTGGGATTACATGT
153903	4542	CACATGTAATCCCAGCACTT	163123	AAGTGCTGGGATTACATGTG
153904	4543	ACACATGTAATCCCAGCACT	163124	AGTGCTGGGATTACATGTGT
153905	4544	CACACATGTAATCCCAGCAC	163125	GTGCTGGGATTACATGTGTG
153906	4545	TCACACATGTAATCCCAGCA	163126	TGCTGGGATTACATGTGTGA
153907	4546	CTCACACATGTAATCCCAGC	163127	GCTGGGATTACATGTGTGAG
153908	4547	GCTCACACATGTAATCCCAG	163128	CTGGGATTACATGTGTGAGC
153909	4548	GGCTCACACATGTAATCCCA	163129	TGGGATTACATGTGTGAGCC
153910	4549	TGGCTCACACATGTAATCCC	163130	GGGATTACATGTGTGAGCCA
153911	4550	GTGGCTCACACATGTAATCC	163131	GGATTACATGTGTGAGCCAC
153912	4551	AGTGGCTCACACATGTAATC	163132	GATTACATGTGTGAGCCACT
153913	4552	CAGTGGCTCACACATGTAAT	163133	ATTACATGTGTGAGCCACTG
153914	4553	ACAGTGGCTCACACATGTAA	163134	TTACATGTGTGAGCCACTGT
153915	4554	CACAGTGGCTCACACATGTA	163135	TACATGTGTGAGCCACTGTG
153916	4555	GCACAGTGGCTCACACATGT	163136	ACATGTGTGAGCCACTGTGC
153917	4556	GGCACAGTGGCTCACACATG	163137	CATGTGTGAGCCACTGTGCC
153918	4557	AGGCACAGTGGCTCACACAT	163138	ATGTGTGAGCCACTGTGCCT
153919	4558	CAGGCACAGTGGCTCACACA	163139	TGTGTGAGCCACTGTGCCTG
153920	4559	CCAGGCACAGTGGCTCACAC	163140	GTGTGAGCCACTGTGCCTGG
153921	4560	CCCAGGCACAGTGGCTCACA	163141	TGTGAGCCACTGTGCCTGGG
153922	4561	TCCCAGGCACAGTGGCTCAC	163142	GTGAGCCACTGTGCCTGGGA
153923	4562	TTCCCAGGCACAGTGGCTCA	163143	TGAGCCACTGTGCCTGGGAA
153924	4563	TTTCCCAGGCACAGTGGCTC	163144	GAGCCACTGTGCCTGGGAAA
153925	4564	TTTTCCCAGGCACAGTGGCT	163145	AGCCACTGTGCCTGGGAAAA
153926	4565	GTTTTCCCAGGCACAGTGGC	163146	GCCACTGTGCCTGGGAAAAC
153927	4566	GGTTTTCCCAGGCACAGTGG	163147	CCACTGTGCCTGGGAAAACC
153928	4567	GGGTTTTCCCAGGCACAGTG	163148	CACTGTGCCTGGGAAAACCC
153929	4568	AGGGTTTTCCCAGGCACAGT	163149	ACTGTGCCTGGGAAAACCCT
153930	4569	GAGGGTTTTCCCAGGCACAG	163150	CTGTGCCTGGGAAAACCCTC
153931	4570	TGAGGGTTTTCCCAGGCACA	163151	TGTGCCTGGGAAAACCCTCA
153932	4571	TTGAGGGTTTTCCCAGGCAC	163152	GTGCCTGGGAAAACCCTCAA
153933	4572	GTTGAGGGTTTTCCCAGGCA	163153	TGCCTGGGAAAACCCTCAAC
153934	4573	AGTTGAGGGTTTTCCCAGGC	163154	GCCTGGGAAAACCCTCAACT
153935	4574	AAGTTGAGGGTTTTCCCAGG	163155	CCTGGGAAAACCCTCAACTT
153936	4575	AAAGTTGAGGGTTTTCCCAG	163156	CTGGGAAAACCCTCAACTTT
153937	4576	AAAAGTTGAGGGTTTTCCCA	163157	TGGGAAAACCCTCAACTTTT
153938	4577	GAAAAGTTGAGGGTTTTCCC	163158	GGGAAAACCCTCAACTTTTC
153939	4578	AGAAAAGTTGAGGGTTTTCC	163159	GGAAAACCCTCAACTTTTCT
153940	4579	AAGAAAAGTTGAGGGTTTTC	163160	GAAAACCCTCAACTTTTCTT
153941	4580	AAAGAAAAGTTGAGGGTTTT	163161	AAAACCCTCAACTTTTCTTT
153942	4581	AAAAGAAAAGTTGAGGGTTT	163162	AAACCCTCAACTTTTCTTTT
153943	4582	TAAAAGAAAAGTTGAGGGTT	163163	AACCCTCAACTTTTCTTTTA
153944	4583	TTAAAAGAAAAGTTGAGGGT	163164	ACCCTCAACTTTTCTTTTAA
153945	4584	TTTAAAAGAAAAGTTGAGGG	163165	CCCTCAACTTTTCTTTTAAA
153946	4585	TTTTAAAAGAAAAGTTGAGG	163166	CCTCAACTTTTCTTTTAAAA
153947	4586	TTTTTAAAAGAAAAGTTGAG	163167	CTCAACTTTTCTTTTAAAAA
153948	4587	TTTTTTAAAAGAAAAGTTGA	163168	TCAACTTTTCTTTTAAAAAA
153949	4588	CTTTTTTAAAAGAAAAGTTG	163169	CAACTTTTCTTTTAAAAAAG
153950	4589	TCTTTTTTAAAAGAAAAGTT	163170	AACTTTTCTTTTAAAAAAGA
153951	4590	CTCTTTTTTAAAAGAAAAGT	163171	ACTTTTCTTTTAAAAAAGAG
153952	4591	CCTCTTTTTTAAAAGAAAAG	163172	CTTTTCTTTTAAAAAAGAGG
153953	4592	ACCTCTTTTTTAAAAGAAAA	163173	TTTTCTTTTAAAAAAGAGGT
153954	4593	GACCTCTTTTTTAAAAGAAA	163174	TTTCTTTTAAAAAAGAGGTC
153955	4594	TGACCTCTTTTTTAAAAGAA	163175	TTCTTTTAAAAAAGAGGTCA
153956	4595	TTGACCTCTTTTTTAAAAGA	163176	TCTTTTAAAAAAGAGGTCAA
153957	4596	GTTGACCTCTTTTTTAAAAG	163177	CTTTTAAAAAAGAGGTCAAC
153958	4597	AGTTGACCTCTTTTTTAAAA	163178	TTTTAAAAAAGAGGTCAACT
153959	4598	AAGTTGACCTCTTTTTTAAA	163179	TTTAAAAAAGAGGTCAACTT
153960	4599	AAAGTTGACCTCTTTTTTAA	163180	TTAAAAAAGAGGTCAACTTT
153961	4600	TAAAGTTGACCTCTTTTTTA	163181	TAAAAAAGAGGTCAACTTTA
153962	4601	ATAAAGTTGACCTCTTTTTT	163182	AAAAAAGAGGTCAACTTTAT
153963	4602	AATAAAGTTGACCTCTTTTT	163183	AAAAAGAGGTCAACTTTATT
153964	4603	CAATAAAGTTGACCTCTTTT	163184	AAAAGAGGTCAACTTTATTG
153965	4604	ACAATAAAGTTGACCTCTTT	163185	AAAGAGGTCAACTTTATTGT
153966	4605	TACAATAAAGTTGACCTCTT	163186	AAGAGGTCAACTTTATTGTA
153967	4606	ATACAATAAAGTTGACCTCT	163187	AGAGGTCAACTTTATTGTAT

153968	4607	TATACAATAAAGTTGACCTC	163188	GAGGTCAACTTTATTGTATA
153969	4608	ATATACAATAAAGTTGACCT	163189	AGGTCAACTTTATTGTATAT
153970	4609	TATATACAATAAAGTTGACC	163190	GGTCAACTTTATTGTATATA
153971	4610	TTATATACAATAAAGTTGAC	163191	GTCAACTTTATTGTATATAA
153972	4611	CTTATATACAATAAAGTTGA	163192	TCAACTTTATTGTATATAAG
153973	4612	GCTTATATACAATAAAGTTG	163193	CAACTTTATTGTATATAAGC
153974	4613	TGCTTATATACAATAAAGTT	163194	AACTTTATTGTATATAAGCA
153975	4614	GTGCTTATATACAATAAAGT	163195	ACTTTATTGTATATAAGCAC
153976	4615	AGTGCTTATATACAATAAAG	163196	CTTTATTGTATATAAGCACT
153977	4616	CAGTGCTTATATACAATAAA	163197	TTTATTGTATATAAGCACTG
153978	4617	ACAGTGCTTATATACAATAA	163198	TTATTGTATATAAGCACTGT
153979	4618	CACAGTGCTTATATACAATA	163199	TATTGTATATAAGCACTGTG
153980	4619	GCACAGTGCTTATATACAAT	163200	ATTGTATATAAGCACTGTGC
153981	4620	AGCACAGTGCTTATATACAA	163201	TTGTATATAAGCACTGTGCT
153982	4621	TAGCACAGTGCTTATATACA	163202	TGTATATAAGCACTGTGCTA
153983	4622	TTAGCACAGTGCTTATATAC	163203	GTATATAAGCACTGTGCTAA
153984	4623	TTTAGCACAGTGCTTATATA	163204	TATATAAGCACTGTGCTAAA
153985	4624	TTTTAGCACAGTGCTTATAT	163205	ATATAAGCACTGTGCTAAAA
153986	4625	ATTTTAGCACAGTGCTTATA	163206	TATAAGCACTGTGCTAAAAT
153987	4626	AATTTTAGCACAGTGCTTAT	163207	ATAAGCACTGTGCTAAAATT
153988	4627	CAATTTTAGCACAGTGCTTA	163208	TAAGCACTGTGCTAAAATTG
153989	4628	GCAATTTTAGCACAGTGCTT	163209	AAGCACTGTGCTAAAATTGC
153990	4629	TGCAATTTTAGCACAGTGCT	163210	AGCACTGTGCTAAAATTGCA
153991	4630	CTGCAATTTTAGCACAGTGC	163211	GCACTGTGCTAAAATTGCAG
153992	4631	CCTGCAATTTTAGCACAGTG	163212	CACTGTGCTAAAATTGCAGG
153993	4632	TCCTGCAATTTTAGCACAGT	163213	ACTGTGCTAAAATTGCAGGA
153994	4633	TTCCTGCAATTTTAGCACAG	163214	CTGTGCTAAAATTGCAGGAA
153995	4634	GTTCCTGCAATTTTAGCACA	163215	TGTGCTAAAATTGCAGGAAC
153996	4635	AGTTCCTGCAATTTTAGCAC	163216	GTGCTAAAATTGCAGGAACT
153997	4636	CAGTTCCTGCAATTTTAGCA	163217	TGCTAAAATTGCAGGAACTG
153998	4637	CCAGTTCCTGCAATTTTAGC	163218	GCTAAAATTGCAGGAACTGG
153999	4638	CCCAGTTCCTGCAATTTTAG	163219	CTAAAATTGCAGGAACTGGG
154000	4639	TCCCAGTTCCTGCAATTTTA	163220	TAAAATTGCAGGAACTGGGA
154001	4640	GTCCCAGTTCCTGCAATTTT	163221	AAAATTGCAGGAACTGGGAC
154002	4641	GGTCCCAGTTCCTGCAATTT	163222	AAATTGCAGGAACTGGGACC
154003	4642	TGGTCCCAGTTCCTGCAATT	163223	AATTGCAGGAACTGGGACCA
154004	4643	ATGGTCCCAGTTCCTGCAAT	163224	ATTGCAGGAACTGGGACCAT
154005	4644	TATGGTCCCAGTTCCTGCAA	163225	TTGCAGGAACTGGGACCATA
154006	4645	ATATGGTCCCAGTTCCTGCA	163226	TGCAGGAACTGGGACCATAT
154007	4646	GATATGGTCCCAGTTCCTGC	163227	GCAGGAACTGGGACCATATC
154008	4647	GGATATGGTCCCAGTTCCTG	163228	CAGGAACTGGGACCATATCC
154009	4648	AGGATATGGTCCCAGTTCCT	163229	AGGAACTGGGACCATATCCT
154010	4649	CAGGATATGGTCCCAGTTCC	163230	GGAACTGGGACCATATCCTG
154011	4650	TCAGGATATGGTCCCAGTTC	163231	GAACTGGGACCATATCCTGA
154012	4651	ATCAGGATATGGTCCCAGTT	163232	AACTGGGACCATATCCTGAT
154013	4652	AATCAGGATATGGTCCCAGT	163233	ACTGGGACCATATCCTGATT
154014	4653	AAATCAGGATATGGTCCCAG	163234	CTGGGACCATATCCTGATTT
154015	4654	AAAATCAGGATATGGTCCCA	163235	TGGGACCATATCCTGATTTT
154016	4655	AAAAATCAGGATATGGTCCC	163236	GGGACCATATCCTGATTTTT
154017	4656	CAAAAATCAGGATATGGTCC	163237	GGACCATATCCTGATTTTTG
154018	4657	ACAAAAATCAGGATATGGTC	163238	GACCATATCCTGATTTTTGT
154019	4658	TACAAAAATCAGGATATGGT	163239	ACCATATCCTGATTTTTGTA
154020	4659	TTACAAAAATCAGGATATGG	163240	CCATATCCTGATTTTTGTAA
154021	4660	ATTACAAAAATCAGGATATG	163241	CATATCCTGATTTTTGTAAT
154022	4661	TATTACAAAAATCAGGATAT	163242	ATATCCTGATTTTTGTAATA
154023	4662	TTATTACAAAAATCAGGATA	163243	TATCCTGATTTTTGTAATAA
154024	4663	ATTATTACAAAAATCAGGAT	163244	ATCCTGATTTTTGTAATAAT
154025	4664	CATTATTACAAAAATCAGGA	163245	TCCTGATTTTTGTAATAATG
154026	4665	GCATTATTACAAAAATCAGG	163246	CCTGATTTTTGTAATAATGC
154027	4666	GGCATTATTACAAAAATCAG	163247	CTGATTTTTGTAATAATGCC
154028	4667	TGGCATTATTACAAAAATCA	163248	TGATTTTTGTAATAATGCCA
154029	4668	CTGGCATTATTACAAAAATC	163249	GATTTTTGTAATAATGCCAG
154030	4669	GCTGGCATTATTACAAAAAT	163250	ATTTTTGTAATAATGCCAGC
154031	4670	TGCTGGCATTATTACAAAAA	163251	TTTTTGTAATAATGCCAGCA
154032	4671	CTGCTGGCATTATTACAAAA	163252	TTTTGTAATAATGCCAGCAG
154033	4672	TCTGCTGGCATTATTACAAA	163253	TTTGTAATAATGCCAGCAGA
154034	4673	CTCTGCTGGCATTATTACAA	163254	TTGTAATAATGCCAGCAGAG
154035	4674	ACTCTGCTGGCATTATTACA	163255	TGTAATAATGCCAGCAGAGT
154036	4675	TACTCTGCTGGCATTATTAC	163256	GTAATAATGCCAGCAGAGTA
154037	4676	GTACTCTGCTGGCATTATTA	163257	TAATAATGCCAGCAGAGTAC
154038	4677	TGTACTCTGCTGGCATTATT	163258	AATAATGCCAGCAGAGTACA
154039	4678	GTGTACTCTGCTGGCATTAT	163259	ATAATGCCAGCAGAGTACAC

154040	4679	TGTGTACTCTGCTGGCATTA	163260	TAATGCCAGCAGAGTACACA
154041	4680	GTGTGTACTCTGCTGGCATT	163261	AATGCCAGCAGAGTACACAC
154042	4681	TGTGTGTACTCTGCTGGCAT	163262	ATGCCAGCAGAGTACACACA
154043	4682	TTGTGTGTACTCTGCTGGCA	163263	TGCCAGCAGAGTACACACAA
154044	4683	CTTGTGTGTACTCTGCTGGC	163264	GCCAGCAGAGTACACACAAG
154045	4684	TCTTGTGTGTACTCTGCTGG	163265	CCAGCAGAGTACACACAAGA
154046	4685	TTCTTGTGTGTACTCTGCTG	163266	CAGCAGAGTACACACAAGAA
154047	4686	TTTCTTGTGTGTACTCTGCT	163267	AGCAGAGTACACACAAGAAA
154048	4687	TTTTCTTGTGTGTACTCTGC	163268	GCAGAGTACACACAAGAAAA
154049	4688	CTTTTCTTGTGTGTACTCTG	163269	CAGAGTACACACAAGAAAAG
154050	4689	ACTTTTCTTGTGTGTACTCT	163270	AGAGTACACACAAGAAAAGT
154051	4690	TACTTTTCTTGTGTGTACTC	163271	GAGTACACACAAGAAAAGTA
154052	4691	TTACTTTTCTTGTGTGTACT	163272	AGTACACACAAGAAAAGTAA
154053	4692	GTTACTTTTCTTGTGTGTAC	163273	GTACACACAAGAAAAGTAAC
154054	4693	AGTTACTTTTCTTGTGTGTA	163274	TACACACAAGAAAAGTAACT
154055	4694	CAGTTACTTTTCTTGTGTGT	163275	ACACACAAGAAAAGTAACTG
154056	4695	GCAGTTACTTTTCTTGTGTG	163276	CACACAAGAAAAGTAACTGC
154057	4696	TGCAGTTACTTTTCTTGTGT	163277	ACACAAGAAAAGTAACTGCA
154058	4697	GTGCAGTTACTTTTCTTGTG	163278	CACAAGAAAAGTAACTGCAC
154059	4698	AGTGCAGTTACTTTTCTTGT	163279	ACAAGAAAAGTAACTGCACT
154060	4699	TAGTGCAGTTACTTTTCTTG	163280	CAAGAAAAGTAACTGCACTA
154061	4700	CTAGTGCAGTTACTTTTCTT	163281	AAGAAAAGTAACTGCACTAG
154062	4701	TCTAGTGCAGTTACTTTTCT	163282	AGAAAAGTAACTGCACTAGA
154063	4702	ATCTAGTGCAGTTACTTTTC	163283	GAAAAGTAACTGCACTAGAT
154064	4703	AATCTAGTGCAGTTACTTTT	163284	AAAAGTAACTGCACTAGATT
154065	4704	CAATCTAGTGCAGTTACTTT	163285	AAAGTAACTGCACTAGATTG
154066	4705	ACAATCTAGTGCAGTTACTT	163286	AAGTAACTGCACTAGATTGT
154067	4706	CACAATCTAGTGCAGTTACT	163287	AGTAACTGCACTAGATTGTG
154068	4707	TCACAATCTAGTGCAGTTAC	163288	GTAACTGCACTAGATTGTGA
154069	4708	TTCACAATCTAGTGCAGTTA	163289	TAACTGCACTAGATTGTGAA
154070	4709	CTTCACAATCTAGTGCAGTT	163290	AACTGCACTAGATTGTGAAG
154071	4710	TCTTCACAATCTAGTGCAGT	163291	ACTGCACTAGATTGTGAAGA
154072	4711	GTCTTCACAATCTAGTGCAG	163292	CTGCACTAGATTGTGAAGAC
154073	4712	AGTCTTCACAATCTAGTGCA	163293	TGCACTAGATTGTGAAGACT
154074	4713	CAGTCTTCACAATCTAGTGC	163294	GCACTAGATTGTGAAGACTG
154075	4714	CCAGTCTTCACAATCTAGTG	163295	CACTAGATTGTGAAGACTGG
154076	4715	CCCAGTCTTCACAATCTAGT	163296	ACTAGATTGTGAAGACTGGG
154077	4716	CCCCAGTCTTCACAATCTAG	163297	CTAGATTGTGAAGACTGGGG
154078	4717	ACCCCAGTCTTCACAATCTA	163298	TAGATTGTGAAGACTGGGGT
154079	4718	CACCCCAGTCTTCACAATCT	163299	AGATTGTGAAGACTGGGGTG
154080	4719	CCACCCCAGTCTTCACAATC	163300	GATTGTGAAGACTGGGGTGG
154081	4720	TCCACCCCAGTCTTCACAAT	163301	ATTGTGAAGACTGGGGTGGA
154082	4721	GTCCACCCCAGTCTTCACAA	163302	TTGTGAAGACTGGGGTGGAC
154083	4722	GGTCCACCCCAGTCTTCACA	163303	TGTGAAGACTGGGGTGGACC
154084	4723	AGGTCCACCCCAGTCTTCAC	163304	GTGAAGACTGGGGTGGACCT
154085	4724	CAGGTCCACCCCAGTCTTCA	163305	TGAAGACTGGGGTGGACCTG
154086	4725	GCAGGTCCACCCCAGTCTTC	163306	GAAGACTGGGGTGGACCTGC
154087	4726	AGCAGGTCCACCCCAGTCTT	163307	AAGACTGGGGTGGACCTGCT
154088	4727	AAGCAGGTCCACCCCAGTCT	163308	AGACTGGGGTGGACCTGCTT
154089	4728	GAAGCAGGTCCACCCCAGTC	163309	GACTGGGGTGGACCTGCTTC
154090	4729	AGAAGCAGGTCCACCCCAGT	163310	ACTGGGGTGGACCTGCTTCT
154091	4730	CAGAAGCAGGTCCACCCCAG	163311	CTGGGGTGGACCTGCTTCTG
154092	4731	TCAGAAGCAGGTCCACCCCA	163312	TGGGGTGGACCTGCTTCTGA
154093	4732	TTCAGAAGCAGGTCCACCCC	163313	GGGGTGGACCTGCTTCTGAA
154094	4733	CTTCAGAAGCAGGTCCACCC	163314	GGGTGGACCTGCTTCTGAAG
154095	4734	CCTTCAGAAGCAGGTCCACC	163315	GGTGGACCTGCTTCTGAAGG
154096	4735	ACCTTCAGAAGCAGGTCCAC	163316	GTGGACCTGCTTCTGAAGGT
154097	4736	GACCTTCAGAAGCAGGTCCA	163317	TGGACCTGCTTCTGAAGGTC
154098	4737	GGACCTTCAGAAGCAGGTCC	163318	GGACCTGCTTCTGAAGGTCC
154099	4738	TGGACCTTCAGAAGCAGGTC	163319	GACCTGCTTCTGAAGGTCCA
154100	4739	CTGGACCTTCAGAAGCAGGT	163320	ACCTGCTTCTGAAGGTCCAG
154101	4740	ACTGGACCTTCAGAAGCAGG	163321	CCTGCTTCTGAAGGTCCAGT
154102	4741	CACTGGACCTTCAGAAGCAG	163322	CTGCTTCTGAAGGTCCAGTG
154103	4742	GCACTGGACCTTCAGAAGCA	163323	TGCTTCTGAAGGTCCAGTGC
154104	4743	GGCACTGGACCTTCAGAAGC	163324	GCTTCTGAAGGTCCAGTGCC
154105	4744	GGGCACTGGACCTTCAGAAG	163325	CTTCTGAAGGTCCAGTGCCC
154106	4745	AGGGCACTGGACCTTCAGAA	163326	TTCTGAAGGTCCAGTGCCCT
154107	4746	AAGGGCACTGGACCTTCAGA	163327	TCTGAAGGTCCAGTGCCCTT
154108	4747	AAAGGGCACTGGACCTTCAG	163328	CTGAAGGTCCAGTGCCCTTT
154109	4748	CAAAGGGCACTGGACCTTCA	163329	TGAAGGTCCAGTGCCCTTTG
154110	4749	ACAAAGGGCACTGGACCTTC	163330	GAAGGTCCAGTGCCCTTTGT
154111	4750	GACAAAGGGCACTGGACCTT	163331	AAGGTCCAGTGCCCTTTGTC

154112	4751	AGACAAAGGGCACTGGACCT	163332	AGGTCCAGTGCCCTTTGTCT
154113	4752	AAGACAAAGGGCACTGGACC	163333	GGTCCAGTGCCCTTTGTCTT
154114	4753	TAAGACAAAGGGCACTGGAC	163334	GTCCAGTGCCCTTTGTCTTA
154115	4754	TTAAGACAAAGGGCACTGGA	163335	TCCAGTGCCCTTTGTCTTAA
154116	4755	CTTAAGACAAAGGGCACTGG	163336	CCAGTGCCCTTTGTCTTAAG
154117	4756	TCTTAAGACAAAGGGCACTG	163337	CAGTGCCCTTTGTCTTAAGA
154118	4757	ATCTTAAGACAAAGGGCACT	163338	AGTGCCCTTTGTCTTAAGAT
154119	4758	AATCTTAAGACAAAGGGCAC	163339	GTGCCCTTTGTCTTAAGATT
154120	4759	AAATCTTAAGACAAAGGGCA	163340	TGCCCTTTGTCTTAAGATTT
154121	4760	CAAATCTTAAGACAAAGGGC	163341	GCCCTTTGTCTTAAGATTTG
154122	4761	CCAAATCTTAAGACAAAGGG	163342	CCCTTTGTCTTAAGATTTGG
154123	4762	ACCAAATCTTAAGACAAAGG	163343	CCTTTGTCTTAAGATTTGGT
154124	4763	CACCAAATCTTAAGACAAAG	163344	CTTTGTCTTAAGATTTGGTG
154125	4764	ACACCAAATCTTAAGACAAA	163345	TTTGTCTTAAGATTTGGTGT
154126	4765	TACACCAAATCTTAAGACAA	163346	TTGTCTTAAGATTTGGTGTA
154127	4766	CTACACCAAATCTTAAGACA	163347	TGTCTTAAGATTTGGTGTAG
154128	4767	ACTACACCAAATCTTAAGAC	163348	GTCTTAAGATTTGGTGTAGT
154129	4768	CACTACACCAAATCTTAAGA	163349	TCTTAAGATTTGGTGTAGTG
154130	4769	ACACTACACCAAATCTTAAG	163350	CTTAAGATTTGGTGTAGTGT
154131	4770	CACACTACACCAAATCTTAA	163351	TTAAGATTTGGTGTAGTGTG
154132	4771	ACACACTACACCAAATCTTA	163352	TAAGATTTGGTGTAGTGTGT
154133	4772	GACACACTACACCAAATCTT	163353	AAGATTTGGTGTAGTGTGTC
154134	4773	AGACACACTACACCAAATCT	163354	AGATTTGGTGTAGTGTGTCT
154135	4774	AAGACACACTACACCAAATC	163355	GATTTGGTGTAGTGTGTCTT
154136	4775	AAAGACACACTACACCAAAT	163356	ATTTGGTGTAGTGTGTCTTT
154137	4776	TAAAGACACACTACACCAAA	163357	TTTGGTGTAGTGTGTCTTTA
154138	4777	CTAAAGACACACTACACCAA	163358	TTGGTGTAGTGTGTCTTTAG
154139	4778	TCTAAAGACACACTACACCA	163359	TGGTGTAGTGTGTCTTTAGA
154140	4779	TTCTAAAGACACACTACACC	163360	GGTGTAGTGTGTCTTTAGAA
154141	4780	TTTCTAAAGACACACTACAC	163361	GTGTAGTGTGTCTTTAGAAA
154142	4781	GTTTCTAAAGACACACTACA	163362	TGTAGTGTGTCTTTAGAAAC
154143	4782	GGTTTCTAAAGACACACTAC	163363	GTAGTGTGTCTTTAGAAACC
154144	4783	TGGTTTCTAAAGACACACTA	163364	TAGTGTGTCTTTAGAAACCA
154145	4784	TTGGTTTCTAAAGACACACT	163365	AGTGTGTCTTTAGAAACCAA
154146	4785	TTTGGTTTCTAAAGACACAC	163366	GTGTGTCTTTAGAAACCAAA
154147	4786	TTTTGGTTTCTAAAGACACA	163367	TGTGTCTTTAGAAACCAAAA
154148	4787	TTTTTGGTTTCTAAAGACAC	163368	GTGTCTTTAGAAACCAAAAA
154149	4788	TTTTTTGGTTTCTAAAGACA	163369	TGTCTTTAGAAACCAAAAAA
154150	4789	TTTTTTTGGTTTCTAAAGAC	163370	GTCTTTAGAAACCAAAAAAA
154151	4790	CTTTTTTTGGTTTCTAAAGA	163371	TCTTTAGAAACCAAAAAAAG
154152	4791	TCTTTTTTTGGTTTCTAAAG	163372	CTTTAGAAACCAAAAAAAGA
154153	4792	CTCTTTTTTTGGTTTCTAAA	163373	TTTAGAAACCAAAAAAAGAG
154154	4793	TCTCTTTTTTTGGTTTCTAA	163374	TTAGAAACCAAAAAAAGAGA
154155	4794	TTCTCTTTTTTTGGTTTCTA	163375	TAGAAACCAAAAAAAGAGAA
154156	4795	CTTCTCTTTTTTTGGTTTCT	163376	AGAAACCAAAAAAAGAGAAG
154157	4796	TCTTCTCTTTTTTTGGTTTC	163377	GAAACCAAAAAAAGAGAAGA
154158	4797	TTCTTCTCTTTTTTTGGTTT	163378	AAACCAAAAAAAGAGAAGAA
154159	4798	CTTCTTCTCTTTTTTTGGTT	163379	AACCAAAAAAAGAGAAGAAG
154160	4799	TCTTCTTCTCTTTTTTTGGT	163380	ACCAAAAAAAGAGAAGAAGA
154161	4800	ATCTTCTTCTCTTTTTTTGG	163381	CCAAAAAAAGAGAAGAAGAT
154162	4801	GATCTTCTTCTCTTTTTTTG	163382	CAAAAAAAGAGAAGAAGATC
154163	4802	TGATCTTCTTCTCTTTTTTT	163383	AAAAAAAGAGAAGAAGATCA
154164	4803	TTGATCTTCTTCTCTTTTTT	163384	AAAAAAGAGAAGAAGATCAA
154165	4804	GTTGATCTTCTTCTCTTTTT	163385	AAAAAGAGAAGAAGATCAAC
154166	4805	GGTTGATCTTCTTCTCTTTT	163386	AAAAGAGAAGAAGATCAACC
154167	4806	AGGTTGATCTTCTTCTCTTT	163387	AAAGAGAAGAAGATCAACCT
154168	4807	AAGGTTGATCTTCTTCTCTT	163388	AAGAGAAGAAGATCAACCTT
154169	4808	TAAGGTTGATCTTCTTCTCT	163389	AGAGAAGAAGATCAACCTTA
154170	4809	TTAAGGTTGATCTTCTTCTC	163390	GAGAAGAAGATCAACCTTAA
154171	4810	CTTAAGGTTGATCTTCTTCT	163391	AGAAGAAGATCAACCTTAAG
154172	4811	TCTTAAGGTTGATCTTCTTC	163392	GAAGAAGATCAACCTTAAGA
154173	4812	ATCTTAAGGTTGATCTTCTT	163393	AAGAAGATCAACCTTAAGAT
154174	4813	AATCTTAAGGTTGATCTTCT	163394	AGAAGATCAACCTTAAGATT
154175	4814	TAATCTTAAGGTTGATCTTC	163395	GAAGATCAACCTTAAGATTA
154176	4815	CTAATCTTAAGGTTGATCTT	163396	AAGATCAACCTTAAGATTAG
154177	4816	GCTAATCTTAAGGTTGATCT	163397	AGATCAACCTTAAGATTAGC
154178	4817	GGCTAATCTTAAGGTTGATC	163398	GATCAACCTTAAGATTAGCC
154179	4818	TGGCTAATCTTAAGGTTGAT	163399	ATCAACCTTAAGATTAGCCA
154180	4819	GTGGCTAATCTTAAGGTTGA	163400	TCAACCTTAAGATTAGCCAC
154181	4820	TGTGGCTAATCTTAAGGTTG	163401	CAACCTTAAGATTAGCCACA
154182	4821	TTGTGGCTAATCTTAAGGTT	163402	AACCTTAAGATTAGCCACAA
154183	4822	TTTGTGGCTAATCTTAAGGT	163403	ACCTTAAGATTAGCCACAAA

154184	4823	TTTTGTGGCTAATCTTAAGG	163404	CCTTAAGATTAGCCACAAAA
154185	4824	GTTTTGTGGCTAATCTTAAG	163405	CTTAAGATTAGCCACAAAAC
154186	4825	AGTTTTGTGGCTAATCTTAA	163406	TTAAGATTAGCCACAAAACT
154187	4826	CAGTTTTGTGGCTAATCTTA	163407	TAAGATTAGCCACAAAACTG
154188	4827	CCAGTTTTGTGGCTAATCTT	163408	AAGATTAGCCACAAAACTGG
154189	4828	CCCAGTTTTGTGGCTAATCT	163409	AGATTAGCCACAAAACTGGG
154190	4829	GCCCAGTTTTGTGGCTAATC	163410	GATTAGCCACAAAACTGGGC
154191	4830	AGCCCAGTTTTGTGGCTAAT	163411	ATTAGCCACAAAACTGGGCT
154192	4831	AAGCCCAGTTTTGTGGCTAA	163412	TTAGCCACAAAACTGGGCTT
154193	4832	AAAGCCCAGTTTTGTGGCTA	163413	TAGCCACAAAACTGGGCTTT
154194	4833	CAAAGCCCAGTTTTGTGGCT	163414	AGCCACAAAACTGGGCTTTG
154195	4834	TCAAAGCCCAGTTTTGTGGC	163415	GCCACAAAACTGGGCTTTGA
154196	4835	ATCAAAGCCCAGTTTTGTGG	163416	CCACAAAACTGGGCTTTGAT
154197	4836	TATCAAAGCCCAGTTTTGTG	163417	CACAAAACTGGGCTTTGATA
154198	4837	GTATCAAAGCCCAGTTTTGT	163418	ACAAAACTGGGCTTTGATAC
154199	4838	GGTATCAAAGCCCAGTTTTG	163419	CAAAACTGGGCTTTGATACC
154200	4839	AGGTATCAAAGCCCAGTTTT	163420	AAAACTGGGCTTTGATACCT
154201	4840	TAGGTATCAAAGCCCAGTTT	163421	AAACTGGGCTTTGATACCTA
154202	4841	CTAGGTATCAAAGCCCAGTT	163422	AACTGGGCTTTGATACCTAG
154203	4842	CCTAGGTATCAAAGCCCAGT	163423	ACTGGGCTTTGATACCTAGG
154204	4843	ACCTAGGTATCAAAGCCCAG	163424	CTGGGCTTTGATACCTAGGT
154205	4844	CACCTAGGTATCAAAGCCCA	163425	TGGGCTTTGATACCTAGGTG
154206	4845	ACACCTAGGTATCAAAGCCC	163426	GGGCTTTGATACCTAGGTGT
154207	4846	CACACCTAGGTATCAAAGCC	163427	GGCTTTGATACCTAGGTGTG
154208	4847	CCACACCTAGGTATCAAAGC	163428	GCTTTGATACCTAGGTGTGG
154209	4848	TCCACACCTAGGTATCAAAG	163429	CTTTGATACCTAGGTGTGGA
154210	4849	TTCCACACCTAGGTATCAAA	163430	TTTGATACCTAGGTGTGGAA
154211	4850	TTTCCACACCTAGGTATCAA	163431	TTGATACCTAGGTGTGGAAA
154212	4851	TTTTCCACACCTAGGTATCA	163432	TGATACCTAGGTGTGGAAAA
154213	4852	CTTTTCCACACCTAGGTATC	163433	GATACCTAGGTGTGGAAAAG
154214	4853	TCTTTTCCACACCTAGGTAT	163434	ATACCTAGGTGTGGAAAAGA
154215	4854	TTCTTTTCCACACCTAGGTA	163435	TACCTAGGTGTGGAAAAGAA
154216	4855	TTTCTTTTCCACACCTAGGT	163436	ACCTAGGTGTGGAAAAGAAA
154217	4856	CTTTCTTTTCCACACCTAGG	163437	CCTAGGTGTGGAAAAGAAAG
154218	4857	CCTTTCTTTTCCACACCTAG	163438	CTAGGTGTGGAAAAGAAAGG
154219	4858	CCCTTTCTTTTCCACACCTA	163439	TAGGTGTGGAAAAGAAAGGG
154220	4859	TCCCTTTCTTTTCCACACCT	163440	AGGTGTGGAAAAGAAAGGGA
154221	4860	TTCCCTTTCTTTTCCACACC	163441	GGTGTGGAAAAGAAAGGGAA
154222	4861	TTTCCCTTTCTTTTCCACAC	163442	GTGTGGAAAAGAAAGGGAAA
154223	4862	CTTTCCCTTTCTTTTCCACA	163443	TGTGGAAAAGAAAGGGAAAG
154224	4863	TCTTTCCCTTTCTTTTCCAC	163444	GTGGAAAAGAAAGGGAAAGA
154225	4864	CTCTTTCCCTTTCTTTTCCA	163445	TGGAAAAGAAAGGGAAAGAG
154226	4865	ACTCTTTCCCTTTCTTTTCC	163446	GGAAAAGAAAGGGAAAGAGT
154227	4866	AACTCTTTCCCTTTCTTTTC	163447	GAAAAGAAAGGGAAAGAGTT
154228	4867	CAACTCTTTCCCTTTCTTTT	163448	AAAAGAAAGGGAAAGAGTTG
154229	4868	TCAACTCTTTCCCTTTCTTT	163449	AAAGAAAGGGAAAGAGTTGA
154230	4869	ATCAACTCTTTCCCTTTCTT	163450	AAGAAAGGGAAAGAGTTGAT
154231	4870	CATCAACTCTTTCCCTTTCT	163451	AGAAAGGGAAAGAGTTGATG
154232	4871	ACATCAACTCTTTCCCTTTC	163452	GAAAGGGAAAGAGTTGATGT
154233	4872	AACATCAACTCTTTCCCTTT	163453	AAAGGGAAAGAGTTGATGTT
154234	4873	AAACATCAACTCTTTCCCTT	163454	AAGGGAAAGAGTTGATGTTT
154235	4874	AAAACATCAACTCTTTCCCT	163455	AGGGAAAGAGTTGATGTTTT
154236	4875	CAAAACATCAACTCTTTCCC	163456	GGGAAAGAGTTGATGTTTTG
154237	4876	ACAAAACATCAACTCTTTCC	163457	GGAAAGAGTTGATGTTTTGT
154238	4877	GACAAAACATCAACTCTTTC	163458	GAAAGAGTTGATGTTTTGTC
154239	4878	AGACAAAACATCAACTCTTT	163459	AAAGAGTTGATGTTTTGTCT
154240	4879	AAGACAAAACATCAACTCTT	163460	AAGAGTTGATGTTTTGTCTT
154241	4880	TAAGACAAAACATCAACTCT	163461	AGAGTTGATGTTTTGTCTTA
154242	4881	GTAAGACAAAACATCAACTC	163462	GAGTTGATGTTTTGTCTTAC
154243	4882	TGTAAGACAAAACATCAACT	163463	AGTTGATGTTTTGTCTTACA
154244	4883	CTGTAAGACAAAACATCAAC	163464	GTTGATGTTTTGTCTTACAG
154245	4884	GCTGTAAGACAAAACATCAA	163465	TTGATGTTTTGTCTTACAGC
154246	4885	TGCTGTAAGACAAAACATCA	163466	TGATGTTTTGTCTTACAGCA
154247	4886	ATGCTGTAAGACAAAACATC	163467	GATGTTTTGTCTTACAGCAT
154248	4887	GATGCTGTAAGACAAAACAT	163468	ATGTTTTGTCTTACAGCATC
154249	4888	TGATGCTGTAAGACAAAACA	163469	TGTTTTGTCTTACAGCATCA
154250	4889	ATGATGCTGTAAGACAAAAC	163470	GTTTTGTCTTACAGCATCAT
154251	4890	AATGATGCTGTAAGACAAAA	163471	TTTTGTCTTACAGCATCATT
154252	4891	CAATGATGCTGTAAGACAAA	163472	TTTGTCTTACAGCATCATTG
154253	4892	ACAATGATGCTGTAAGACAA	163473	TTGTCTTACAGCATCATTGT
154254	4893	TACAATGATGCTGTAAGACA	163474	TGTCTTACAGCATCATTGTA
154255	4894	CTACAATGATGCTGTAAGAC	163475	GTCTTACAGCATCATTGTAG

154256	4895	TCTACAATGATGCTGTAAGA	163476	TCTTACAGCATCATTGTAGA
154257	4896	TTCTACAATGATGCTGTAAG	163477	CTTACAGCATCATTGTAGAA
154258	4897	CTTCTACAATGATGCTGTAA	163478	TTACAGCATCATTGTAGAAG
154259	4898	TCTTCTACAATGATGCTGTA	163479	TACAGCATCATTGTAGAAGA
154260	4899	CTCTTCTACAATGATGCTGT	163480	ACAGCATCATTGTAGAAGAG
154261	4900	CCTCTTCTACAATGATGCTG	163481	CAGCATCATTGTAGAAGAGG
154262	4901	CCCTCTTCTACAATGATGCT	163482	AGCATCATTGTAGAAGAGGG
154263	4902	ACCCTCTTCTACAATGATGC	163483	GCATCATTGTAGAAGAGGGT
154264	4903	CACCCTCTTCTACAATGATG	163484	CATCATTGTAGAAGAGGGTG
154265	4904	ACACCCTCTTCTACAATGAT	163485	ATCATTGTAGAAGAGGGTGT
154266	4905	AACACCCTCTTCTACAATGA	163486	TCATTGTAGAAGAGGGTGTT
154267	4906	AAACACCCTCTTCTACAATG	163487	CATTGTAGAAGAGGGTGTTT
154268	4907	AAAACACCCTCTTCTACAAT	163488	ATTGTAGAAGAGGGTGTTTT
154269	4908	AAAAACACCCTCTTCTACAA	163489	TTGTAGAAGAGGGTGTTTTT
154270	4909	AAAAAACACCCTCTTCTACA	163490	TGTAGAAGAGGGTGTTTTTT
154271	4910	AAAAAAACACCCTCTTCTAC	163491	GTAGAAGAGGGTGTTTTTTT
154272	4911	CAAAAAAACACCCTCTTCTA	163492	TAGAAGAGGGTGTTTTTTTG
154273	4912	ACAAAAAAACACCCTCTTCT	163493	AGAAGAGGGTGTTTTTTTGT
154274	4913	AACAAAAAAACACCCTCTTC	163494	GAAGAGGGTGTTTTTTTGTT
154275	4914	AAACAAAAAAACACCCTCTT	163495	AAGAGGGTGTTTTTTTGTTT
154276	4915	CAAACAAAAAAACACCCTCT	163496	AGAGGGTGTTTTTTTGTTTG
154277	4916	ACAAACAAAAAAACACCCTC	163497	GAGGGTGTTTTTTTGTTTGT
154278	4917	AACAAACAAAAAAACACCCT	163498	AGGGTGTTTTTTTGTTTGTT
154279	4918	AAACAAACAAAAAAACACCC	163499	GGGTGTTTTTTTGTTTGTTT
154280	4919	CAAACAAACAAAAAAACACC	163500	GGTGTTTTTTTGTTTGTTTG
154281	4920	ACAAACAAACAAAAAAACAC	163501	GTGTTTTTTTGTTTGTTTGT
154282	4921	AACAAACAAACAAAAAAACA	163502	TGTTTTTTTGTTTGTTTGTT
154283	4922	AAACAAACAAACAAAAAAAC	163503	GTTTTTTTGTTTGTTTGTTT
154284	4923	AAAACAAACAAACAAAAAAA	163504	TTTTTTTGTTTGTTTGTTTT
154285	4924	AAAAACAAACAAACAAAAAA	163505	TTTTTTGTTTGTTTGTTTTT
154286	4925	AAAAAACAAACAAACAAAAA	163506	TTTTTGTTTGTTTGTTTTTT
154287	4926	CAAAAAACAAACAAACAAAA	163507	TTTTGTTTGTTTGTTTTTTG
154288	4927	TCAAAAAACAAACAAACAAA	163508	TTTGTTTGTTTGTTTTTTGA
154289	4928	CTCAAAAAACAAACAAACAA	163509	TTGTTTGTTTGTTTTTTGAG
154290	4929	TCTCAAAAAACAAACAAACA	163510	TGTTTGTTTGTTTTTTGAGA
154291	4930	GTCTCAAAAAACAAACAAAC	163511	GTTTGTTTGTTTTTTGAGAC
154292	4931	CGTCTCAAAAAACAAACAAA	163512	TTTGTTTGTTTTTTGAGACG
154293	4932	CCGTCTCAAAAAACAAACAA	163513	TTGTTTGTTTTTTGAGACGG
154294	4933	TCCGTCTCAAAAAACAAACA	163514	TGTTTGTTTTTTGAGACGGA
154295	4934	CTCCGTCTCAAAAAACAAAC	163515	GTTTGTTTTTTGAGACGGAG
154296	4935	ACTCCGTCTCAAAAAACAAA	163516	TTTGTTTTTTGAGACGGAGT
154297	4936	GACTCCGTCTCAAAAAACAA	163517	TTGTTTTTTGAGACGGAGTC
154298	4937	AGACTCCGTCTCAAAAAACA	163518	TGTTTTTTGAGACGGAGTCT
154299	4938	AAGACTCCGTCTCAAAAAAC	163519	GTTTTTTGAGACGGAGTCTT
154300	4939	TAAGACTCCGTCTCAAAAAA	163520	TTTTTTGAGACGGAGTCTTA
154301	4940	GTAAGACTCCGTCTCAAAAA	163521	TTTTTGAGACGGAGTCTTAC
154302	4941	AGTAAGACTCCGTCTCAAAA	163522	TTTTGAGACGGAGTCTTACT
154303	4942	GAGTAAGACTCCGTCTCAAA	163523	TTTGAGACGGAGTCTTACTC
154304	4943	AGAGTAAGACTCCGTCTCAA	163524	TTGAGACGGAGTCTTACTCT
154305	4944	CAGAGTAAGACTCCGTCTCA	163525	TGAGACGGAGTCTTACTCTG
154306	4945	ACAGAGTAAGACTCCGTCTC	163526	GAGACGGAGTCTTACTCTGT
154307	4946	CACAGAGTAAGACTCCGTCT	163527	AGACGGAGTCTTACTCTGTG
154308	4947	CCACAGAGTAAGACTCCGTC	163528	GACGGAGTCTTACTCTGTGG
154309	4948	GCCACAGAGTAAGACTCCGT	163529	ACGGAGTCTTACTCTGTGGC
154310	4949	GGCCACAGAGTAAGACTCCG	163530	CGGAGTCTTACTCTGTGGCC
154311	4950	GGGCCACAGAGTAAGACTCC	163531	GGAGTCTTACTCTGTGGCCC
154312	4951	TGGGCCACAGAGTAAGACTC	163532	GAGTCTTACTCTGTGGCCCA
154313	4952	CTGGGCCACAGAGTAAGACT	163533	AGTCTTACTCTGTGGCCCAG
154314	4953	CCTGGGCCACAGAGTAAGAC	163534	GTCTTACTCTGTGGCCCAGG
154315	4954	GCCTGGGCCACAGAGTAAGA	163535	TCTTACTCTGTGGCCCAGGC
154316	4955	AGCCTGGGCCACAGAGTAAG	163536	CTTACTCTGTGGCCCAGGCT
154317	4956	CAGCCTGGGCCACAGAGTAA	163537	TTACTCTGTGGCCCAGGCTG
154318	4957	CCAGCCTGGGCCACAGAGTA	163538	TACTCTGTGGCCCAGGCTGG
154319	4958	TCCAGCCTGGGCCACAGAGT	163539	ACTCTGTGGCCCAGGCTGGA
154320	4959	CTCCAGCCTGGGCCACAGAG	163540	CTCTGTGGCCCAGGCTGGAG
154321	4960	ACTCCAGCCTGGGCCACAGA	163541	TCTGTGGCCCAGGCTGGAGT
154322	4961	CACTCCAGCCTGGGCCACAG	163542	CTGTGGCCCAGGCTGGAGTG
154323	4962	GCACTCCAGCCTGGGCCACA	163543	TGTGGCCCAGGCTGGAGTGC
154324	4963	TGCACTCCAGCCTGGGCCAC	163544	GTGGCCCAGGCTGGAGTGCA
154325	4964	CTGCACTCCAGCCTGGGCCA	163545	TGGCCCAGGCTGGAGTGCAG
154326	4965	ACTGCACTCCAGCCTGGGCC	163546	GGCCCAGGCTGGAGTGCAGT
154327	4966	CACTGCACTCCAGCCTGGGC	163547	GCCCAGGCTGGAGTGCAGTG

154328	4967	CCACTGCACTCCAGCCTGGG	163548	CCCAGGCTGGAGTGCAGTGG
154329	4968	GCCACTGCACTCCAGCCTGG	163549	CCAGGCTGGAGTGCAGTGGC
154330	4969	CGCCACTGCACTCCAGCCTG	163550	CAGGCTGGAGTGCAGTGGCG
154331	4970	GCGCCACTGCACTCCAGCCT	163551	AGGCTGGAGTGCAGTGGCGC
154332	4971	CGCGCCACTGCACTCCAGCC	163552	GGCTGGAGTGCAGTGGCGCG
154333	4972	TCGCGCCACTGCACTCCAGC	163553	GCTGGAGTGCAGTGGCGCGA
154334	4973	ATCGCGCCACTGCACTCCAG	163554	CTGGAGTGCAGTGGCGCGAT
154335	4974	GATCGCGCCACTGCACTCCA	163555	TGGAGTGCAGTGGCGCGATC
154336	4975	AGATCGCGCCACTGCACTCC	163556	GGAGTGCAGTGGCGCGATCT
154337	4976	GAGATCGCGCCACTGCACTC	163557	GAGTGCAGTGGCGCGATCTC
154338	4977	CGAGATCGCGCCACTGCACT	163558	AGTGCAGTGGCGCGATCTCG
154339	4978	CCGAGATCGCGCCACTGCAC	163559	GTGCAGTGGCGCGATCTCGG
154340	4979	GCCGAGATCGCGCCACTGCA	163560	TGCAGTGGCGCGATCTCGGC
154341	4980	AGCCGAGATCGCGCCACTGC	163561	GCAGTGGCGCGATCTCGGCT
154342	4981	GAGCCGAGATCGCGCCACTG	163562	CAGTGGCGCGATCTCGGCTC
154343	4982	TGAGCCGAGATCGCGCCACT	163563	AGTGGCGCGATCTCGGCTCA
154344	4983	GTGAGCCGAGATCGCGCCAC	163564	GTGGCGCGATCTCGGCTCAC
154345	4984	AGTGAGCCGAGATCGCGCCA	163565	TGGCGCGATCTCGGCTCACT
154346	4985	CAGTGAGCCGAGATCGCGCC	163566	GGCGCGATCTCGGCTCACTG
154347	4986	GCAGTGAGCCGAGATCGCGC	163567	GCGCGATCTCGGCTCACTGC
154348	4987	TGCAGTGAGCCGAGATCGCG	163568	CGCGATCTCGGCTCACTGCA
154349	4988	TTGCAGTGAGCCGAGATCGC	163569	GCGATCTCGGCTCACTGCAA
154350	4989	CTTGCAGTGAGCCGAGATCG	163570	CGATCTCGGCTCACTGCAAG
154351	4990	GCTTGCAGTGAGCCGAGATC	163571	GATCTCGGCTCACTGCAAGC
154352	4991	AGCTTGCAGTGAGCCGAGAT	163572	ATCTCGGCTCACTGCAAGCT
154353	4992	GAGCTTGCAGTGAGCCGAGA	163573	TCTCGGCTCACTGCAAGCTC
154354	4993	GGAGCTTGCAGTGAGCCGAG	163574	CTCGGCTCACTGCAAGCTCC
154355	4994	CGGAGCTTGCAGTGAGCCGA	163575	TCGGCTCACTGCAAGCTCCG
154356	4995	GCGGAGCTTGCAGTGAGCCG	163576	CGGCTCACTGCAAGCTCCGC
154357	4996	GGCGGAGCTTGCAGTGAGCC	163577	GGCTCACTGCAAGCTCCGCC
154358	4997	AGGCGGAGCTTGCAGTGAGC	163578	GCTCACTGCAAGCTCCGCCT
154359	4998	GAGGCGGAGCTTGCAGTGAG	163579	CTCACTGCAAGCTCCGCCTC
154360	4999	GGAGGCGGAGCTTGCAGTGA	163580	TCACTGCAAGCTCCGCCTCC
154361	5000	GGGAGGCGGAGCTTGCAGTG	163581	CACTGCAAGCTCCGCCTCCC
154362	5001	CGGGAGGCGGAGCTTGCAGT	163582	ACTGCAAGCTCCGCCTCCCG
154363	5002	CCGGGAGGCGGAGCTTGCAG	163583	CTGCAAGCTCCGCCTCCCGG
154364	5003	CCCGGGAGGCGGAGCTTGCA	163584	TGCAAGCTCCGCCTCCCGGG
154365	5004	ACCCGGGAGGCGGAGCTTGC	163585	GCAAGCTCCGCCTCCCGGGT
154366	5005	AACCCGGGAGGCGGAGCTTG	163586	CAAGCTCCGCCTCCCGGGTT
154367	5006	GAACCCGGGAGGCGGAGCTT	163587	AAGCTCCGCCTCCCGGGTTC
154368	5007	TGAACCCGGGAGGCGGAGCT	163588	AGCTCCGCCTCCCGGGTTCA
154369	5008	ATGAACCCGGGAGGCGGAGC	163589	GCTCCGCCTCCCGGGTTCAT
154370	5009	CATGAACCCGGGAGGCGGAG	163590	CTCCGCCTCCCGGGTTCATG
154371	5010	GCATGAACCCGGGAGGCGGA	163591	TCCGCCTCCCGGGTTCATGC
154372	5011	GGCATGAACCCGGGAGGCGG	163592	CCGCCTCCCGGGTTCATGCC
154373	5012	TGGCATGAACCCGGGAGGCG	163593	CGCCTCCCGGGTTCATGCCA
154374	5013	ATGGCATGAACCCGGGAGGC	163594	GCCTCCCGGGTTCATGCCAT
154375	5014	AATGGCATGAACCCGGGAGG	163595	CCTCCCGGGTTCATGCCATT
154376	5015	GAATGGCATGAACCCGGGAG	163596	CTCCCGGGTTCATGCCATTC
154377	5016	AGAATGGCATGAACCCGGGA	163597	TCCCGGGTTCATGCCATTCT
154378	5017	GAGAATGGCATGAACCCGGG	163598	CCCGGGTTCATGCCATTCTC
154379	5018	GGAGAATGGCATGAACCCGG	163599	CCGGGTTCATGCCATTCTCC
154380	5019	AGGAGAATGGCATGAACCCG	163600	CGGGTTCATGCCATTCTCCT
154381	5020	CAGGAGAATGGCATGAACCC	163601	GGGTTCATGCCATTCTCCTG
154382	5021	GCAGGAGAATGGCATGAACC	163602	GGTTCATGCCATTCTCCTGC
154383	5022	GGCAGGAGAATGGCATGAAC	163603	GTTCATGCCATTCTCCTGCC
154384	5023	AGGCAGGAGAATGGCATGAA	163604	TTCATGCCATTCTCCTGCCT
154385	5024	GAGGCAGGAGAATGGCATGA	163605	TCATGCCATTCTCCTGCCTC
154386	5025	TGAGGCAGGAGAATGGCATG	163606	CATGCCATTCTCCTGCCTCA
154387	5026	CTGAGGCAGGAGAATGGCAT	163607	ATGCCATTCTCCTGCCTCAG
154388	5027	GCTGAGGCAGGAGAATGGCA	163608	TGCCATTCTCCTGCCTCAGC
154389	5028	GGCTGAGGCAGGAGAATGGC	163609	GCCATTCTCCTGCCTCAGCC
154390	5029	GGGCTGAGGCAGGAGAATGG	163610	CCATTCTCCTGCCTCAGCCC
154391	5030	GGGGCTGAGGCAGGAGAATG	163611	CATTCTCCTGCCTCAGCCCC
154392	5031	GGGGGCTGAGGCAGGAGAAT	163612	ATTCTCCTGCCTCAGCCCCC
154393	5032	AGGGGGCTGAGGCAGGAGAA	163613	TTCTCCTGCCTCAGCCCCCT
154394	5033	CAGGGGGCTGAGGCAGGAGA	163614	TCTCCTGCCTCAGCCCCCTG
154395	5034	TCAGGGGGCTGAGGCAGGAG	163615	CTCCTGCCTCAGCCCCCTGA
154396	5035	CTCAGGGGGCTGAGGCAGGA	163616	TCCTGCCTCAGCCCCCTGAG
154397	5036	ACTCAGGGGGCTGAGGCAGG	163617	CCTGCCTCAGCCCCCTGAGT
154398	5037	TACTCAGGGGGCTGAGGCAG	163618	CTGCCTCAGCCCCCTGAGTA
154399	5038	CTACTCAGGGGGCTGAGGCA	163619	TGCCTCAGCCCCCTGAGTAG

154400	5039	GCTACTCAGGGGGCTGAGGC	163620	GCCTCAGCCCCCTGAGTAGC
154401	5040	AGCTACTCAGGGGGCTGAGG	163621	CCTCAGCCCCCTGAGTAGCT
154402	5041	CAGCTACTCAGGGGGCTGAG	163622	CTCAGCCCCCTGAGTAGCTG
154403	5042	CCAGCTACTCAGGGGGCTGA	163623	TCAGCCCCCTGAGTAGCTGG
154404	5043	CCCAGCTACTCAGGGGGCTG	163624	CAGCCCCCTGAGTAGCTGGG
154405	5044	TCCCAGCTACTCAGGGGGCT	163625	AGCCCCCTGAGTAGCTGGGA
154406	5045	GTCCCAGCTACTCAGGGGGC	163626	GCCCCCTGAGTAGCTGGGAC
154407	5046	AGTCCCAGCTACTCAGGGGG	163627	CCCCCTGAGTAGCTGGGACT
154408	5047	TAGTCCCAGCTACTCAGGGG	163628	CCCCTGAGTAGCTGGGACTA
154409	5048	GTAGTCCCAGCTACTCAGGG	163629	CCCTGAGTAGCTGGGACTAC
154410	5049	TGTAGTCCCAGCTACTCAGG	163630	CCTGAGTAGCTGGGACTACA
154411	5050	CTGTAGTCCCAGCTACTCAG	163631	CTGAGTAGCTGGGACTACAG
154412	5051	CCTGTAGTCCCAGCTACTCA	163632	TGAGTAGCTGGGACTACAGG
154413	5052	ACCTGTAGTCCCAGCTACTC	163633	GAGTAGCTGGGACTACAGGT
154414	5053	CACCTGTAGTCCCAGCTACT	163634	AGTAGCTGGGACTACAGGTG
154415	5054	GCACCTGTAGTCCCAGCTAC	163635	GTAGCTGGGACTACAGGTGC
154416	5055	GGCACCTGTAGTCCCAGCTA	163636	TAGCTGGGACTACAGGTGCC
154417	5056	GGGCACCTGTAGTCCCAGCT	163637	AGCTGGGACTACAGGTGCCC
154418	5057	CGGGCACCTGTAGTCCCAGC	163638	GCTGGGACTACAGGTGCCCG
154419	5058	GCGGGCACCTGTAGTCCCAG	163639	CTGGGACTACAGGTGCCCGC
154420	5059	GGCGGGCACCTGTAGTCCCA	163640	TGGGACTACAGGTGCCCGCC
154421	5060	TGGCGGGCACCTGTAGTCCC	163641	GGGACTACAGGTGCCCGCCA
154422	5061	GTGGCGGGCACCTGTAGTCC	163642	GGACTACAGGTGCCCGCCAC
154423	5062	GGTGGCGGGCACCTGTAGTC	163643	GACTACAGGTGCCCGCCACC
154424	5063	GGGTGGCGGGCACCTGTAGT	163644	ACTACAGGTGCCCGCCACCC
154425	5064	GGGGTGGCGGGCACCTGTAG	163645	CTACAGGTGCCCGCCACCCC
154426	5065	CGGGGTGGCGGGCACCTGTA	163646	TACAGGTGCCCGCCACCCCG
154427	5066	GCGGGGTGGCGGGCACCTGT	163647	ACAGGTGCCCGCCACCCCGC
154428	5067	GGCGGGGTGGCGGGCACCTG	163648	CAGGTGCCCGCCACCCCGCC
154429	5068	AGGCGGGGTGGCGGGCACCT	163649	AGGTGCCCGCCACCCCGCCT
154430	5069	CAGGCGGGGTGGCGGGCACC	163650	GGTGCCCGCCACCCCGCCTG
154431	5070	CCAGGCGGGGTGGCGGGCAC	163651	GTGCCCGCCACCCCGCCTGG
154432	5071	GCCAGGCGGGGTGGCGGGCA	163652	TGCCCGCCACCCCGCCTGGC
154433	5072	AGCCAGGCGGGGTGGCGGGC	163653	GCCCGCCACCCCGCCTGGCT
154434	5073	TAGCCAGGCGGGGTGGCGGG	163654	CCCGCCACCCCGCCTGGCTA
154435	5074	TTAGCCAGGCGGGGTGGCGG	163655	CCGCCACCCCGCCTGGCTAA
154436	5075	ATTAGCCAGGCGGGGTGGCG	163656	CGCCACCCCGCCTGGCTAAT
154437	5076	AATTAGCCAGGCGGGGTGGC	163657	GCCACCCCGCCTGGCTAATT
154438	5077	AAATTAGCCAGGCGGGGTGG	163658	CCACCCCGCCTGGCTAATTT
154439	5078	AAAATTAGCCAGGCGGGGTG	163659	CACCCCGCCTGGCTAATTTT
154440	5079	AAAAATTAGCCAGGCGGGGT	163660	ACCCCGCCTGGCTAATTTTT
154441	5080	AAAAAATTAGCCAGGCGGGG	163661	CCCCGCCTGGCTAATTTTTT
154442	5081	CAAAAAATTAGCCAGGCGGG	163662	CCCGCCTGGCTAATTTTTTG
154443	5082	ACAAAAAATTAGCCAGGCGG	163663	CCGCCTGGCTAATTTTTTGT
154444	5083	TACAAAAAATTAGCCAGGCG	163664	CGCCTGGCTAATTTTTTGTA
154445	5084	ATACAAAAAATTAGCCAGGC	163665	GCCTGGCTAATTTTTTGTAT
154446	5085	AATACAAAAAATTAGCCAGG	163666	CCTGGCTAATTTTTTGTATT
154447	5086	AAATACAAAAAATTAGCCAG	163667	CTGGCTAATTTTTTGTATTT
154448	5087	AAAATACAAAAAATTAGCCA	163668	TGGCTAATTTTTTGTATTTT
154449	5088	AAAAATACAAAAAATTAGCC	163669	GGCTAATTTTTTGTATTTTT
154450	5089	TAAAAATACAAAAAATTAGC	163670	GCTAATTTTTTGTATTTTTA
154451	5090	CTAAAAATACAAAAAATTAG	163671	CTAATTTTTTGTATTTTTAG
154452	5091	ACTAAAAATACAAAAAATTA	163672	TAATTTTTTGTATTTTTAGT
154453	5092	TACTAAAAATACAAAAAATT	163673	AATTTTTTGTATTTTTAGTA
154454	5093	CTACTAAAAATACAAAAAAT	163674	ATTTTTTGTATTTTTAGTAG
154455	5094	TCTACTAAAAATACAAAAAA	163675	TTTTTTGTATTTTTAGTAGA
154456	5095	CTCTACTAAAAATACAAAAA	163676	TTTTTGTATTTTTAGTAGAG
154457	5096	TCTCTACTAAAAATACAAAA	163677	TTTTGTATTTTTAGTAGAGA
154458	5097	GTCTCTACTAAAAATACAAA	163678	TTTGTATTTTTAGTAGAGAC
154459	5098	CGTCTCTACTAAAAATACAA	163679	TTGTATTTTTAGTAGAGACG
154460	5099	CCGTCTCTACTAAAAATACA	163680	TGTATTTTTAGTAGAGACGG
154461	5100	CCCGTCTCTACTAAAAATAC	163681	GTATTTTTAGTAGAGACGGG
154462	5101	CCCCGTCTCTACTAAAAATA	163682	TATTTTTAGTAGAGACGGGG
154463	5102	ACCCCGTCTCTACTAAAAAT	163683	ATTTTTAGTAGAGACGGGGT
154464	5103	AACCCCGTCTCTACTAAAAA	163684	TTTTTAGTAGAGACGGGGTT
154465	5104	AAACCCCGTCTCTACTAAAA	163685	TTTTAGTAGAGACGGGGTTT
154466	5105	GAAACCCCGTCTCTACTAAA	163686	TTTAGTAGAGACGGGGTTTC
154467	5106	TGAAACCCCGTCTCTACTAA	163687	TTAGTAGAGACGGGGTTTCA
154468	5107	GTGAAACCCCGTCTCTACTA	163688	TAGTAGAGACGGGGTTTCAC
154469	5108	AGTGAAACCCCGTCTCTACT	163689	AGTAGAGACGGGGTTTCACT
154470	5109	CAGTGAAACCCCGTCTCTAC	163690	GTAGAGACGGGGTTTCACTG
154471	5110	ACAGTGAAACCCCGTCTCTA	163691	TAGAGACGGGGTTTCACTGT

154472	5111	CACAGTGAAACCCCGTCTCT	163692	AGAGACGGGGTTTCACTGTG
154473	5112	ACACAGTGAAACCCCGTCTC	163693	GAGACGGGGTTTCACTGTGT
154474	5113	AACACAGTGAAACCCCGTCT	163694	AGACGGGGTTTCACTGTGTT
154475	5114	TAACACAGTGAAACCCCGTC	163695	GACGGGGTTTCACTGTGTTA
154476	5115	CTAACACAGTGAAACCCCGT	163696	ACGGGGTTTCACTGTGTTAG
154477	5116	GCTAACACAGTGAAACCCCG	163697	CGGGGTTTCACTGTGTTAGC
154478	5117	GGCTAACACAGTGAAACCCC	163698	GGGGTTTCACTGTGTTAGCC
154479	5118	TGGCTAACACAGTGAAACCC	163699	GGGTTTCACTGTGTTAGCCA
154480	5119	TTGGCTAACACAGTGAAACC	163700	GGTTTCACTGTGTTAGCCAA
154481	5120	CTTGGCTAACACAGTGAAAC	163701	GTTTCACTGTGTTAGCCAAG
154482	5121	TCTTGGCTAACACAGTGAAA	163702	TTTCACTGTGTTAGCCAAGA
154483	5122	ATCTTGGCTAACACAGTGAA	163703	TTCACTGTGTTAGCCAAGAT
154484	5123	CATCTTGGCTAACACAGTGA	163704	TCACTGTGTTAGCCAAGATG
154485	5124	CCATCTTGGCTAACACAGTG	163705	CACTGTGTTAGCCAAGATGG
154486	5125	ACCATCTTGGCTAACACAGT	163706	ACTGTGTTAGCCAAGATGGT
154487	5126	GACCATCTTGGCTAACACAG	163707	CTGTGTTAGCCAAGATGGTC
154488	5127	AGACCATCTTGGCTAACACA	163708	TGTGTTAGCCAAGATGGTCT
154489	5128	GAGACCATCTTGGCTAACAC	163709	GTGTTAGCCAAGATGGTCTC
154490	5129	AGAGACCATCTTGGCTAACA	163710	TGTTAGCCAAGATGGTCTCT
154491	5130	GAGAGACCATCTTGGCTAAC	163711	GTTAGCCAAGATGGTCTCTC
154492	5131	AGAGAGACCATCTTGGCTAA	163712	TTAGCCAAGATGGTCTCTCT
154493	5132	GAGAGAGACCATCTTGGCTA	163713	TAGCCAAGATGGTCTCTCTC
154494	5133	GGAGAGAGACCATCTTGGCT	163714	AGCCAAGATGGTCTCTCTCC
154495	5134	AGGAGAGAGACCATCTTGGC	163715	GCCAAGATGGTCTCTCTCCT
154496	5135	CAGGAGAGAGACCATCTTGG	163716	CCAAGATGGTCTCTCTCCTG
154497	5136	TCAGGAGAGAGACCATCTTG	163717	CAAGATGGTCTCTCTCCTGA
154498	5137	GTCAGGAGAGAGACCATCTT	163718	AAGATGGTCTCTCTCCTGAC
154499	5138	GGTCAGGAGAGAGACCATCT	163719	AGATGGTCTCTCTCCTGACC
154500	5139	AGGTCAGGAGAGAGACCATC	163720	GATGGTCTCTCTCCTGACCT
154501	5140	GAGGTCAGGAGAGAGACCAT	163721	ATGGTCTCTCTCCTGACCTC
154502	5141	CGAGGTCAGGAGAGAGACCA	163722	TGGTCTCTCTCCTGACCTCG
154503	5142	ACGAGGTCAGGAGAGAGACC	163723	GGTCTCTCTCCTGACCTCGT
154504	5143	CACGAGGTCAGGAGAGAGAC	163724	GTCTCTCTCCTGACCTCGTG
154505	5144	TCACGAGGTCAGGAGAGAGA	163725	TCTCTCTCCTGACCTCGTGA
154506	5145	ATCACGAGGTCAGGAGAGAG	163726	CTCTCTCCTGACCTCGTGAT
154507	5146	GATCACGAGGTCAGGAGAGA	163727	TCTCTCCTGACCTCGTGATC
154508	5147	GGATCACGAGGTCAGGAGAG	163728	CTCTCCTGACCTCGTGATCC
154509	5148	CGGATCACGAGGTCAGGAGA	163729	TCTCCTGACCTCGTGATCCG
154510	5149	GCGGATCACGAGGTCAGGAG	163730	CTCCTGACCTCGTGATCCGC
154511	5150	GGCGGATCACGAGGTCAGGA	163731	TCCTGACCTCGTGATCCGCC
154512	5151	AGGCGGATCACGAGGTCAGG	163732	CCTGACCTCGTGATCCGCCT
154513	5152	CAGGCGGATCACGAGGTCAG	163733	CTGACCTCGTGATCCGCCTG
154514	5153	ACAGGCGGATCACGAGGTCA	163734	TGACCTCGTGATCCGCCTGT
154515	5154	GACAGGCGGATCACGAGGTC	163735	GACCTCGTGATCCGCCTGTC
154516	5155	AGACAGGCGGATCACGAGGT	163736	ACCTCGTGATCCGCCTGTCT
154517	5156	GAGACAGGCGGATCACGAGG	163737	CCTCGTGATCCGCCTGTCTC
154518	5157	TGAGACAGGCGGATCACGAG	163738	CTCGTGATCCGCCTGTCTCA
154519	5158	CTGAGACAGGCGGATCACGA	163739	TCGTGATCCGCCTGTCTCAG
154520	5159	GCTGAGACAGGCGGATCACG	163740	CGTGATCCGCCTGTCTCAGC
154521	5160	GGCTGAGACAGGCGGATCAC	163741	GTGATCCGCCTGTCTCAGCC
154522	5161	AGGCTGAGACAGGCGGATCA	163742	TGATCCGCCTGTCTCAGCCT
154523	5162	GAGGCTGAGACAGGCGGATC	163743	GATCCGCCTGTCTCAGCCTC
154524	5163	GGAGGCTGAGACAGGCGGAT	163744	ATCCGCCTGTCTCAGCCTCC
154525	5164	GGGAGGCTGAGACAGGCGGA	163745	TCCGCCTGTCTCAGCCTCCC
154526	5165	TGGGAGGCTGAGACAGGCGG	163746	CCGCCTGTCTCAGCCTCCCA
154527	5166	TTGGGAGGCTGAGACAGGCG	163747	CGCCTGTCTCAGCCTCCCAA
154528	5167	TTTGGGAGGCTGAGACAGGC	163748	GCCTGTCTCAGCCTCCCAAA
154529	5168	CTTTGGGAGGCTGAGACAGG	163749	CCTGTCTCAGCCTCCCAAAG
154530	5169	ACTTTGGGAGGCTGAGACAG	163750	CTGTCTCAGCCTCCCAAAGT
154531	5170	CACTTTGGGAGGCTGAGACA	163751	TGTCTCAGCCTCCCAAAGTG
154532	5171	GCACTTTGGGAGGCTGAGAC	163752	GTCTCAGCCTCCCAAAGTGC
154533	5172	AGCACTTTGGGAGGCTGAGA	163753	TCTCAGCCTCCCAAAGTGCT
154534	5173	CAGCACTTTGGGAGGCTGAG	163754	CTCAGCCTCCCAAAGTGCTG
154535	5174	CCAGCACTTTGGGAGGCTGA	163755	TCAGCCTCCCAAAGTGCTGG
154536	5175	CCCAGCACTTTGGGAGGCTG	163756	CAGCCTCCCAAAGTGCTGGG
154537	5176	TCCCAGCACTTTGGGAGGCT	163757	AGCCTCCCAAAGTGCTGGGA
154538	5177	ATCCCAGCACTTTGGGAGGC	163758	GCCTCCCAAAGTGCTGGGAT
154539	5178	AATCCCAGCACTTTGGGAGG	163759	CCTCCCAAAGTGCTGGGATT
154540	5179	TAATCCCAGCACTTTGGGAG	163760	CTCCCAAAGTGCTGGGATTA
154541	5180	GTAATCCCAGCACTTTGGGA	163761	TCCCAAAGTGCTGGGATTAC
154542	5181	TGTAATCCCAGCACTTTGGG	163762	CCCAAAGTGCTGGGATTACA
154543	5182	CTGTAATCCCAGCACTTTGG	163763	CCAAAGTGCTGGGATTACAG

154544	5183	CCTGTAATCCCAGCACTTTG	163764	CAAAGTGCTGGGATTACAGG
154545	5184	GCCTGTAATCCCAGCACTTT	163765	AAAGTGCTGGGATTACAGGC
154546	5185	TGCCTGTAATCCCAGCACTT	163766	AAGTGCTGGGATTACAGGCA
154547	5186	ATGCCTGTAATCCCAGCACT	163767	AGTGCTGGGATTACAGGCAT
154548	5187	CATGCCTGTAATCCCAGCAC	163768	GTGCTGGGATTACAGGCATG
154549	5188	TCATGCCTGTAATCCCAGCA	163769	TGCTGGGATTACAGGCATGA
154550	5189	CTCATGCCTGTAATCCCAGC	163770	GCTGGGATTACAGGCATGAG
154551	5190	GCTCATGCCTGTAATCCCAG	163771	CTGGGATTACAGGCATGAGC
154552	5191	GGCTCATGCCTGTAATCCCA	163772	TGGGATTACAGGCATGAGCC
154553	5192	TGGCTCATGCCTGTAATCCC	163773	GGGATTACAGGCATGAGCCA
154554	5193	GTGGCTCATGCCTGTAATCC	163774	GGATTACAGGCATGAGCCAC
154555	5194	GGTGGCTCATGCCTGTAATC	163775	GATTACAGGCATGAGCCACC
154556	5195	CGGTGGCTCATGCCTGTAAT	163776	ATTACAGGCATGAGCCACCG
154557	5196	GCGGTGGCTCATGCCTGTAA	163777	TTACAGGCATGAGCCACCGC
154558	5197	TGCGGTGGCTCATGCCTGTA	163778	TACAGGCATGAGCCACCGCA
154559	5198	GTGCGGTGGCTCATGCCTGT	163779	ACAGGCATGAGCCACCGCAC
154560	5199	GGTGCGGTGGCTCATGCCTG	163780	CAGGCATGAGCCACCGCACC
154561	5200	GGGTGCGGTGGCTCATGCCT	163781	AGGCATGAGCCACCGCACCC
154562	5201	TGGGTGCGGTGGCTCATGCC	163782	GGCATGAGCCACCGCACCCA
154563	5202	CTGGGTGCGGTGGCTCATGC	163783	GCATGAGCCACCGCACCCAG
154564	5203	GCTGGGTGCGGTGGCTCATG	163784	CATGAGCCACCGCACCCAGC
154565	5204	GGCTGGGTGCGGTGGCTCAT	163785	ATGAGCCACCGCACCCAGCC
154566	5205	TGGCTGGGTGCGGTGGCTCA	163786	TGAGCCACCGCACCCAGCCA
154567	5206	CTGGCTGGGTGCGGTGGCTC	163787	GAGCCACCGCACCCAGCCAG
154568	5207	TCTGGCTGGGTGCGGTGGCT	163788	AGCCACCGCACCCAGCCAGA
154569	5208	TTCTGGCTGGGTGCGGTGGC	163789	GCCACCGCACCCAGCCAGAA
154570	5209	CTTCTGGCTGGGTGCGGTGG	163790	CCACCGCACCCAGCCAGAAG
154571	5210	TCTTCTGGCTGGGTGCGGTG	163791	CACCGCACCCAGCCAGAAGA
154572	5211	CTCTTCTGGCTGGGTGCGGT	163792	ACCGCACCCAGCCAGAAGAG
154573	5212	CCTCTTCTGGCTGGGTGCGG	163793	CCGCACCCAGCCAGAAGAGG
154574	5213	CCCTCTTCTGGCTGGGTGCG	163794	CGCACCCAGCCAGAAGAGGG
154575	5214	ACCCTCTTCTGGCTGGGTGC	163795	GCACCCAGCCAGAAGAGGGT
154576	5215	CACCCTCTTCTGGCTGGGTG	163796	CACCCAGCCAGAAGAGGGTG
154577	5216	ACACCCTCTTCTGGCTGGGT	163797	ACCCAGCCAGAAGAGGGTGT
154578	5217	AACACCCTCTTCTGGCTGGG	163798	CCCAGCCAGAAGAGGGTGTT
154579	5218	AAACACCCTCTTCTGGCTGG	163799	CCAGCCAGAAGAGGGTGTTT
154580	5219	AAAACACCCTCTTCTGGCTG	163800	CAGCCAGAAGAGGGTGTTTT
154581	5220	AAAAACACCCTCTTCTGGCT	163801	AGCCAGAAGAGGGTGTTTTT
154582	5221	AAAAAACACCCTCTTCTGGC	163802	GCCAGAAGAGGGTGTTTTTT
154583	5222	TAAAAAACACCCTCTTCTGG	163803	CCAGAAGAGGGTGTTTTTTA
154584	5223	TTAAAAAACACCCTCTTCTG	163804	CAGAAGAGGGTGTTTTTTAA
154585	5224	TTTAAAAAACACCCTCTTCT	163805	AGAAGAGGGTGTTTTTTAAA
154586	5225	CTTTAAAAAACACCCTCTTC	163806	GAAGAGGGTGTTTTTTAAAG
154587	5226	TCTTTAAAAAACACCCTCTT	163807	AAGAGGGTGTTTTTTAAAGA
154588	5227	TTCTTTAAAAAACACCCTCT	163808	AGAGGGTGTTTTTTAAAGAA
154589	5228	CTTCTTTAAAAAACACCCTC	163809	GAGGGTGTTTTTTAAAGAAG
154590	5229	CCTTCTTTAAAAAACACCCT	163810	AGGGTGTTTTTTAAAGAAGG
154591	5230	GCCTTCTTTAAAAAACACCC	163811	GGGTGTTTTTTAAAGAAGGC
154592	5231	TGCCTTCTTTAAAAAACACC	163812	GGTGTTTTTTAAAGAAGGCA
154593	5232	TTGCCTTCTTTAAAAAACAC	163813	GTGTTTTTTAAAGAAGGCAA
154594	5233	TTTGCCTTCTTTAAAAAACA	163814	TGTTTTTTAAAGAAGGCAAA
154595	5234	ATTTGCCTTCTTTAAAAAAC	163815	GTTTTTTAAAGAAGGCAAAT
154596	5235	TATTTGCCTTCTTTAAAAAA	163816	TTTTTTAAAGAAGGCAAATA
154597	5236	CTATTTGCCTTCTTTAAAAA	163817	TTTTTAAAGAAGGCAAATAG
154598	5237	CCTATTTGCCTTCTTTAAAA	163818	TTTTAAAGAAGGCAAATAGG
154599	5238	TCCTATTTGCCTTCTTTAAA	163819	TTTAAAGAAGGCAAATAGGA
154600	5239	TTCCTATTTGCCTTCTTTAA	163820	TTAAAGAAGGCAAATAGGAA
154601	5240	TTTCCTATTTGCCTTCTTTA	163821	TAAAGAAGGCAAATAGGAAA
154602	5241	ATTTCCTATTTGCCTTCTTT	163822	AAAGAAGGCAAATAGGAAAT
154603	5242	TATTTCCTATTTGCCTTCTT	163823	AAGAAGGCAAATAGGAAATA
154604	5243	TTATTTCCTATTTGCCTTCT	163824	AGAAGGCAAATAGGAAATAA
154605	5244	TTTATTTCCTATTTGCCTTC	163825	GAAGGCAAATAGGAAATAAA
154606	5245	TTTTATTTCCTATTTGCCTT	163826	AAGGCAAATAGGAAATAAAA
154607	5246	TTTTTATTTCCTATTTGCCT	163827	AGGCAAATAGGAAATAAAAA
154608	5247	GTTTTTATTTCCTATTTGCC	163828	GGCAAATAGGAAATAAAAAC
154609	5248	AGTTTTTATTTCCTATTTGC	163829	GCAAATAGGAAATAAAAACT
154610	5249	AAGTTTTTATTTCCTATTTG	163830	CAAATAGGAAATAAAAACTT
154611	5250	CAAGTTTTTATTTCCTATTT	163831	AAATAGGAAATAAAAACTTG
154612	5251	CCAAGTTTTTATTTCCTATT	163832	AATAGGAAATAAAAACTTGG
154613	5252	CCCAAGTTTTTATTTCCTAT	163833	ATAGGAAATAAAAACTTGGG
154614	5253	GCCCAAGTTTTTATTTCCTA	163834	TAGGAAATAAAAACTTGGGC
154615	5254	AGCCCAAGTTTTTATTTCCT	163835	AGGAAATAAAAACTTGGGCT

154616	5255	GAGCCCAAGTTTTTATTTCC	163836	GGAAATAAAAACTTGGGCTC
154617	5256	AGAGCCCAAGTTTTTATTTC	163837	GAAATAAAAACTTGGGCTCT
154618	5257	AAGAGCCCAAGTTTTTATTT	163838	AAATAAAAACTTGGGCTCTT
154619	5258	TAAGAGCCCAAGTTTTTATT	163839	AATAAAAACTTGGGCTCTTA
154620	5259	TTAAGAGCCCAAGTTTTTAT	163840	ATAAAAACTTGGGCTCTTAA
154621	5260	GTTAAGAGCCCAAGTTTTTA	163841	TAAAAACTTGGGCTCTTAAC
154622	5261	AGTTAAGAGCCCAAGTTTTT	163842	AAAAACTTGGGCTCTTAACT
154623	5262	AAGTTAAGAGCCCAAGTTTT	163843	AAAACTTGGGCTCTTAACTT
154624	5263	AAAGTTAAGAGCCCAAGTTT	163844	AAACTTGGGCTCTTAACTTT
154625	5264	AAAAGTTAAGAGCCCAAGTT	163845	AACTTGGGCTCTTAACTTTT
154626	5265	CAAAAGTTAAGAGCCCAAGT	163846	ACTTGGGCTCTTAACTTTTG
154627	5266	ACAAAAGTTAAGAGCCCAAG	163847	CTTGGGCTCTTAACTTTTGT
154628	5267	TACAAAAGTTAAGAGCCCAA	163848	TTGGGCTCTTAACTTTTGTA
154629	5268	TTACAAAAGTTAAGAGCCCA	163849	TGGGCTCTTAACTTTTGTAA
154630	5269	ATTACAAAAGTTAAGAGCCC	163850	GGGCTCTTAACTTTTGTAAT
154631	5270	CATTACAAAAGTTAAGAGCC	163851	GGCTCTTAACTTTTGTAATG
154632	5271	TCATTACAAAAGTTAAGAGC	163852	GCTCTTAACTTTTGTAATGA
154633	5272	ATCATTACAAAAGTTAAGAG	163853	CTCTTAACTTTTGTAATGAT
154634	5273	GATCATTACAAAAGTTAAGA	163854	TCTTAACTTTTGTAATGATC
154635	5274	GGATCATTACAAAAGTTAAG	163855	CTTAACTTTTGTAATGATCC
154636	5275	GGGATCATTACAAAAGTTAA	163856	TTAACTTTTGTAATGATCCC
154637	5276	TGGGATCATTACAAAAGTTA	163857	TAACTTTTGTAATGATCCCA
154638	5277	CTGGGATCATTACAAAAGTT	163858	AACTTTTGTAATGATCCCAG
154639	5278	CCTGGGATCATTACAAAAGT	163859	ACTTTTGTAATGATCCCAGG
154640	5279	ACCTGGGATCATTACAAAAG	163860	CTTTTGTAATGATCCCAGGT
154641	5280	CACCTGGGATCATTACAAAA	163861	TTTTGTAATGATCCCAGGTG
154642	5281	ACACCTGGGATCATTACAAA	163862	TTTGTAATGATCCCAGGTGT
154643	5282	AACACCTGGGATCATTACAA	163863	TTGTAATGATCCCAGGTGTT
154644	5283	AAACACCTGGGATCATTACA	163864	TGTAATGATCCCAGGTGTTT
154645	5284	CAAACACCTGGGATCATTAC	163865	GTAATGATCCCAGGTGTTTG
154646	5285	TCAAACACCTGGGATCATTA	163866	TAATGATCCCAGGTGTTTGA
154647	5286	CTCAAACACCTGGGATCATT	163867	AATGATCCCAGGTGTTTGAG
154648	5287	GCTCAAACACCTGGGATCAT	163868	ATGATCCCAGGTGTTTGAGC
154649	5288	AGCTCAAACACCTGGGATCA	163869	TGATCCCAGGTGTTTGAGCT
154650	5289	CAGCTCAAACACCTGGGATC	163870	GATCCCAGGTGTTTGAGCTG
154651	5290	CCAGCTCAAACACCTGGGAT	163871	ATCCCAGGTGTTTGAGCTGG
154652	5291	CCCAGCTCAAACACCTGGGA	163872	TCCCAGGTGTTTGAGCTGGG
154653	5292	CCCCAGCTCAAACACCTGGG	163873	CCCAGGTGTTTGAGCTGGGG
154654	5293	CCCCCAGCTCAAACACCTGG	163874	CCAGGTGTTTGAGCTGGGGG
154655	5294	ACCCCCAGCTCAAACACCTG	163875	CAGGTGTTTGAGCTGGGGGT
154656	5295	AACCCCCAGCTCAAACACCT	163876	AGGTGTTTGAGCTGGGGGTT
154657	5296	CAACCCCCAGCTCAAACACC	163877	GGTGTTTGAGCTGGGGGTTG
154658	5297	TCAACCCCCAGCTCAAACAC	163878	GTGTTTGAGCTGGGGGTTGA
154659	5298	CTCAACCCCCAGCTCAAACA	163879	TGTTTGAGCTGGGGGTTGAG
154660	5299	CCTCAACCCCCAGCTCAAAC	163880	GTTTGAGCTGGGGGTTGAGG
154661	5300	CCCTCAACCCCCAGCTCAAA	163881	TTTGAGCTGGGGGTTGAGGG
154662	5301	ACCCTCAACCCCCAGCTCAA	163882	TTGAGCTGGGGGTTGAGGGT
154663	5302	CACCCTCAACCCCCAGCTCA	163883	TGAGCTGGGGGTTGAGGGTG
154664	5303	CCACCCTCAACCCCCAGCTC	163884	GAGCTGGGGGTTGAGGGTGG
154665	5304	CCCACCCTCAACCCCCAGCT	163885	AGCTGGGGGTTGAGGGTGGG
154666	5305	ACCCACCCTCAACCCCCAGC	163886	GCTGGGGGTTGAGGGTGGGT
154667	5306	CACCCACCCTCAACCCCCAG	163887	CTGGGGGTTGAGGGTGGGTG
154668	5307	GCACCCACCCTCAACCCCCA	163888	TGGGGGTTGAGGGTGGGTGC
154669	5308	GGCACCCACCCTCAACCCCC	163889	GGGGGTTGAGGGTGGGTGCC
154670	5309	AGGCACCCACCCTCAACCCC	163890	GGGGTTGAGGGTGGGTGCCT
154671	5310	GAGGCACCCACCCTCAACCC	163891	GGGTTGAGGGTGGGTGCCTC
154672	5311	CGAGGCACCCACCCTCAACC	163892	GGTTGAGGGTGGGTGCCTCG
154673	5312	TCGAGGCACCCACCCTCAAC	163893	GTTGAGGGTGGGTGCCTCGA
154674	5313	CTCGAGGCACCCACCCTCAA	163894	TTGAGGGTGGGTGCCTCGAG
154675	5314	GCTCGAGGCACCCACCCTCA	163895	TGAGGGTGGGTGCCTCGAGC
154676	5315	TGCTCGAGGCACCCACCCTC	163896	GAGGGTGGGTGCCTCGAGCA
154677	5316	TTGCTCGAGGCACCCACCCT	163897	AGGGTGGGTGCCTCGAGCAA
154678	5317	TTTGCTCGAGGCACCCACCC	163898	GGGTGGGTGCCTCGAGCAAA
154679	5318	CTTTGCTCGAGGCACCCACC	163899	GGTGGGTGCCTCGAGCAAAG
154680	5319	CCTTTGCTCGAGGCACCCAC	163900	GTGGGTGCCTCGAGCAAAGG
154681	5320	CCCTTTGCTCGAGGCACCCA	163901	TGGGTGCCTCGAGCAAAGGG
154682	5321	CCCCTTTGCTCGAGGCACCC	163902	GGGTGCCTCGAGCAAAGGGG
154683	5322	GCCCCTTTGCTCGAGGCACC	163903	GGTGCCTCGAGCAAAGGGGC
154684	5323	AGCCCCTTTGCTCGAGGCAC	163904	GTGCCTCGAGCAAAGGGGCT
154685	5324	CAGCCCCTTTGCTCGAGGCA	163905	TGCCTCGAGCAAAGGGGCTG
154686	5325	GCAGCCCCTTTGCTCGAGGC	163906	GCCTCGAGCAAAGGGGCTGC
154687	5326	TGCAGCCCCTTTGCTCGAGG	163907	CCTCGAGCAAAGGGGCTGCA

154688	5327	ATGCAGCCCCTTTGCTCGAG	163908	CTCGAGCAAAGGGGCTGCAT
154689	5328	AATGCAGCCCCTTTGCTCGA	163909	TCGAGCAAAGGGGCTGCATT
154690	5329	AAATGCAGCCCCTTTGCTCG	163910	CGAGCAAAGGGGCTGCATTT
154691	5330	TAAATGCAGCCCCTTTGCTC	163911	GAGCAAAGGGGCTGCATTTA
154692	5331	ATAAATGCAGCCCCTTTGCT	163912	AGCAAAGGGGCTGCATTTAT
154693	5332	AATAAATGCAGCCCCTTTGC	163913	GCAAAGGGGCTGCATTTATT
154694	5333	AAATAAATGCAGCCCCTTTG	163914	CAAAGGGGCTGCATTTATTT
154695	5334	CAAATAAATGCAGCCCCTTT	163915	AAAGGGGCTGCATTTATTTG
154696	5335	GCAAATAAATGCAGCCCCTT	163916	AAGGGGCTGCATTTATTTGC
154697	5336	TGCAAATAAATGCAGCCCCT	163917	AGGGGCTGCATTTATTTGCA
154698	5337	ATGCAAATAAATGCAGCCCC	163918	GGGGCTGCATTTATTTGCAT
154699	5338	TATGCAAATAAATGCAGCCC	163919	GGGCTGCATTTATTTGCATA
154700	5339	TTATGCAAATAAATGCAGCC	163920	GGCTGCATTTATTTGCATAA
154701	5340	ATTATGCAAATAAATGCAGC	163921	GCTGCATTTATTTGCATAAT
154702	5341	CATTATGCAAATAAATGCAG	163922	CTGCATTTATTTGCATAATG
154703	5342	GCATTATGCAAATAAATGCA	163923	TGCATTTATTTGCATAATGC
154704	5343	GGCATTATGCAAATAAATGC	163924	GCATTTATTTGCATAATGCC
154705	5344	TGGCATTATGCAAATAAATG	163925	CATTTATTTGCATAATGCCA
154706	5345	ATGGCATTATGCAAATAAAT	163926	ATTTATTTGCATAATGCCAT
154707	5346	CATGGCATTATGCAAATAAA	163927	TTTATTTGCATAATGCCATG
154708	5347	ACATGGCATTATGCAAATAA	163928	TTATTTGCATAATGCCATGT
154709	5348	TACATGGCATTATGCAAATA	163929	TATTTGCATAATGCCATGTA
154710	5349	TTACATGGCATTATGCAAAT	163930	ATTTGCATAATGCCATGTAA
154711	5350	CTTACATGGCATTATGCAAA	163931	TTTGCATAATGCCATGTAAG
154712	5351	TCTTACATGGCATTATGCAA	163932	TTGCATAATGCCATGTAAGA
154713	5352	CTCTTACATGGCATTATGCA	163933	TGCATAATGCCATGTAAGAG
154714	5353	ACTCTTACATGGCATTATGC	163934	GCATAATGCCATGTAAGAGT
154715	5354	TACTCTTACATGGCATTATG	163935	CATAATGCCATGTAAGAGTA
154716	5355	CTACTCTTACATGGCATTAT	163936	ATAATGCCATGTAAGAGTAG
154717	5356	GCTACTCTTACATGGCATTA	163937	TAATGCCATGTAAGAGTAGC
154718	5357	AGCTACTCTTACATGGCATT	163938	AATGCCATGTAAGAGTAGCT
154719	5358	GAGCTACTCTTACATGGCAT	163939	ATGCCATGTAAGAGTAGCTC
154720	5359	AGAGCTACTCTTACATGGCA	163940	TGCCATGTAAGAGTAGCTCT
154721	5360	TAGAGCTACTCTTACATGGC	163941	GCCATGTAAGAGTAGCTCTA
154722	5361	GTAGAGCTACTCTTACATGG	163942	CCATGTAAGAGTAGCTCTAC
154723	5362	TGTAGAGCTACTCTTACATG	163943	CATGTAAGAGTAGCTCTACA
154724	5363	GTGTAGAGCTACTCTTACAT	163944	ATGTAAGAGTAGCTCTACAC
154725	5364	GGTGTAGAGCTACTCTTACA	163945	TGTAAGAGTAGCTCTACACC
154726	5365	GGGTGTAGAGCTACTCTTAC	163946	GTAAGAGTAGCTCTACACCC
154727	5366	GGGGTGTAGAGCTACTCTTA	163947	TAAGAGTAGCTCTACACCCC
154728	5367	TGGGGTGTAGAGCTACTCTT	163948	AAGAGTAGCTCTACACCCCA
154729	5368	TTGGGGTGTAGAGCTACTCT	163949	AGAGTAGCTCTACACCCCAA
154730	5369	TTTGGGGTGTAGAGCTACTC	163950	GAGTAGCTCTACACCCCAAA
154731	5370	GTTTGGGGTGTAGAGCTACT	163951	AGTAGCTCTACACCCCAAAC
154732	5371	TGTTTGGGGTGTAGAGCTAC	163952	GTAGCTCTACACCCCAAACA
154733	5372	GTGTTTGGGGTGTAGAGCTA	163953	TAGCTCTACACCCCAAACAC
154734	5373	TGTGTTTGGGGTGTAGAGCT	163954	AGCTCTACACCCCAAACACA
154735	5374	CTGTGTTTGGGGTGTAGAGC	163955	GCTCTACACCCCAAACACAG
154736	5375	CCTGTGTTTGGGGTGTAGAG	163956	CTCTACACCCCAAACACAGG
154737	5376	GCCTGTGTTTGGGGTGTAGA	163957	TCTACACCCCAAACACAGGC
154738	5377	AGCCTGTGTTTGGGGTGTAG	163958	CTACACCCCAAACACAGGCT
154739	5378	AAGCCTGTGTTTGGGGTGTA	163959	TACACCCCAAACACAGGCTT
154740	5379	GAAGCCTGTGTTTGGGGTGT	163960	ACACCCCAAACACAGGCTTC
154741	5380	AGAAGCCTGTGTTTGGGGTG	163961	CACCCCAAACACAGGCTTCT
154742	5381	AAGAAGCCTGTGTTTGGGGT	163962	ACCCCAAACACAGGCTTCTT
154743	5382	TAAGAAGCCTGTGTTTGGGG	163963	CCCCAAACACAGGCTTCTTA
154744	5383	CTAAGAAGCCTGTGTTTGGG	163964	CCCAAACACAGGCTTCTTAG
154745	5384	ACTAAGAAGCCTGTGTTTGG	163965	CCAAACACAGGCTTCTTAGT
154746	5385	CACTAAGAAGCCTGTGTTTG	163966	CAAACACAGGCTTCTTAGTG
154747	5386	CCACTAAGAAGCCTGTGTTT	163967	AAACACAGGCTTCTTAGTGG
154748	5387	CCCACTAAGAAGCCTGTGTT	163968	AACACAGGCTTCTTAGTGGG
154749	5388	TCCCACTAAGAAGCCTGTGT	163969	ACACAGGCTTCTTAGTGGGA
154750	5389	GTCCCACTAAGAAGCCTGTG	163970	CACAGGCTTCTTAGTGGGAC
154751	5390	GGTCCCACTAAGAAGCCTGT	163971	ACAGGCTTCTTAGTGGGACC
154752	5391	TGGTCCCACTAAGAAGCCTG	163972	CAGGCTTCTTAGTGGGACCA
154753	5392	TTGGTCCCACTAAGAAGCCT	163973	AGGCTTCTTAGTGGGACCAA
154754	5393	TTTGGTCCCACTAAGAAGCC	163974	GGCTTCTTAGTGGGACCAAA
154755	5394	CTTTGGTCCCACTAAGAAGC	163975	GCTTCTTAGTGGGACCAAAG
154756	5395	ACTTTGGTCCCACTAAGAAG	163976	CTTCTTAGTGGGACCAAAGT
154757	5396	TACTTTGGTCCCACTAAGAA	163977	TTCTTAGTGGGACCAAAGTA
154758	5397	ATACTTTGGTCCCACTAAGA	163978	TCTTAGTGGGACCAAAGTAT
154759	5398	CATACTTTGGTCCCACTAAG	163979	CTTAGTGGGACCAAAGTATG

154760	5399	TCATACTTTGGTCCCACTAA	163980	TTAGTGGGACCAAAGTATGA
154761	5400	ATCATACTTTGGTCCCACTA	163981	TAGTGGGACCAAAGTATGAT
154762	5401	TATCATACTTTGGTCCCACT	163982	AGTGGGACCAAAGTATGATA
154763	5402	GTATCATACTTTGGTCCCAC	163983	GTGGGACCAAAGTATGATAC
154764	5403	TGTATCATACTTTGGTCCCA	163984	TGGGACCAAAGTATGATACA
154765	5404	TTGTATCATACTTTGGTCCC	163985	GGGACCAAAGTATGATACAA
154766	5405	TTTGTATCATACTTTGGTCC	163986	GGACCAAAGTATGATACAAA
154767	5406	GTTTGTATCATACTTTGGTC	163987	GACCAAAGTATGATACAAAC
154768	5407	AGTTTGTATCATACTTTGGT	163988	ACCAAAGTATGATACAAACT
154769	5408	CAGTTTGTATCATACTTTGG	163989	CCAAAGTATGATACAAACTG
154770	5409	TCAGTTTGTATCATACTTTG	163990	CAAAGTATGATACAAACTGA
154771	5410	TTCAGTTTGTATCATACTTT	163991	AAAGTATGATACAAACTGAA
154772	5411	CTTCAGTTTGTATCATACTT	163992	AAGTATGATACAAACTGAAG
154773	5412	TCTTCAGTTTGTATCATACT	163993	AGTATGATACAAACTGAAGA
154774	5413	ATCTTCAGTTTGTATCATAC	163994	GTATGATACAAACTGAAGAT
154775	5414	CATCTTCAGTTTGTATCATA	163995	TATGATACAAACTGAAGATG
154776	5415	CCATCTTCAGTTTGTATCAT	163996	ATGATACAAACTGAAGATGG
154777	5416	TCCATCTTCAGTTTGTATCA	163997	TGATACAAACTGAAGATGGA
154778	5417	TTCCATCTTCAGTTTGTATC	163998	GATACAAACTGAAGATGGAA
154779	5418	ATTCCATCTTCAGTTTGTAT	163999	ATACAAACTGAAGATGGAAT
154780	5419	CATTCCATCTTCAGTTTGTA	164000	TACAAACTGAAGATGGAATG
154781	5420	GCATTCCATCTTCAGTTTGT	164001	ACAAACTGAAGATGGAATGC
154782	5421	TGCATTCCATCTTCAGTTTG	164002	CAAACTGAAGATGGAATGCA
154783	5422	CTGCATTCCATCTTCAGTTT	164003	AAACTGAAGATGGAATGCAG
154784	5423	TCTGCATTCCATCTTCAGTT	164004	AACTGAAGATGGAATGCAGA
154785	5424	CTCTGCATTCCATCTTCAGT	164005	ACTGAAGATGGAATGCAGAG
154786	5425	CCTCTGCATTCCATCTTCAG	164006	CTGAAGATGGAATGCAGAGG
154787	5426	TCCTCTGCATTCCATCTTCA	164007	TGAAGATGGAATGCAGAGGA
154788	5427	ATCCTCTGCATTCCATCTTC	164008	GAAGATGGAATGCAGAGGAT
154789	5428	AATCCTCTGCATTCCATCTT	164009	AAGATGGAATGCAGAGGATT
154790	5429	TAATCCTCTGCATTCCATCT	164010	AGATGGAATGCAGAGGATTA
154791	5430	ATAATCCTCTGCATTCCATC	164011	GATGGAATGCAGAGGATTAT
154792	5431	AATAATCCTCTGCATTCCAT	164012	ATGGAATGCAGAGGATTATT
154793	5432	CAATAATCCTCTGCATTCCA	164013	TGGAATGCAGAGGATTATTG
154794	5433	CCAATAATCCTCTGCATTCC	164014	GGAATGCAGAGGATTATTGG
154795	5434	ACCAATAATCCTCTGCATTC	164015	GAATGCAGAGGATTATTGGT
154796	5435	TACCAATAATCCTCTGCATT	164016	AATGCAGAGGATTATTGGTA
154797	5436	GTACCAATAATCCTCTGCAT	164017	ATGCAGAGGATTATTGGTAC
154798	5437	AGTACCAATAATCCTCTGCA	164018	TGCAGAGGATTATTGGTACT
154799	5438	AAGTACCAATAATCCTCTGC	164019	GCAGAGGATTATTGGTACTT
154800	5439	AAAGTACCAATAATCCTCTG	164020	CAGAGGATTATTGGTACTTT
154801	5440	CAAAGTACCAATAATCCTCT	164021	AGAGGATTATTGGTACTTTG
154802	5441	CCAAAGTACCAATAATCCTC	164022	GAGGATTATTGGTACTTTGG
154803	5442	TCCAAAGTACCAATAATCCT	164023	AGGATTATTGGTACTTTGGA
154804	5443	TTCCAAAGTACCAATAATCC	164024	GGATTATTGGTACTTTGGAA
154805	5444	ATTCCAAAGTACCAATAATC	164025	GATTATTGGTACTTTGGAAT
154806	5445	TATTCCAAAGTACCAATAAT	164026	ATTATTGGTACTTTGGAATA
154807	5446	ATATTCCAAAGTACCAATAA	164027	TTATTGGTACTTTGGAATAT
154808	5447	CATATTCCAAAGTACCAATA	164028	TATTGGTACTTTGGAATATG
154809	5448	GCATATTCCAAAGTACCAAT	164029	ATTGGTACTTTGGAATATGC
154810	5449	AGCATATTCCAAAGTACCAA	164030	TTGGTACTTTGGAATATGCT
154811	5450	AAGCATATTCCAAAGTACCA	164031	TGGTACTTTGGAATATGCTT
154812	5451	TAAGCATATTCCAAAGTACC	164032	GGTACTTTGGAATATGCTTA
154813	5452	TTAAGCATATTCCAAAGTAC	164033	GTACTTTGGAATATGCTTAA
154814	5453	TTTAAGCATATTCCAAAGTA	164034	TACTTTGGAATATGCTTAAA
154815	5454	TTTTAAGCATATTCCAAAGT	164035	ACTTTGGAATATGCTTAAAA
154816	5455	TTTTTAAGCATATTCCAAAG	164036	CTTTGGAATATGCTTAAAAA
154817	5456	TTTTTTAAGCATATTCCAAA	164037	TTTGGAATATGCTTAAAAAA
154818	5457	TTTTTTTAAGCATATTCCAA	164038	TTGGAATATGCTTAAAAAAA
154819	5458	TTTTTTTTAAGCATATTCCA	164039	TGGAATATGCTTAAAAAAAA
154820	5459	ATTTTTTTTAAGCATATTCC	164040	GGAATATGCTTAAAAAAAAT
154821	5460	AATTTTTTTTAAGCATATTC	164041	GAATATGCTTAAAAAAAATT
154822	5461	AAATTTTTTTTAAGCATATT	164042	AATATGCTTAAAAAAAATTT
154823	5462	AAAATTTTTTTTAAGCATAT	164043	ATATGCTTAAAAAAAATTTT
154824	5463	AAAAATTTTTTTTAAGCATA	164044	TATGCTTAAAAAAAATTTTT
154825	5464	AAAAAATTTTTTTTAAGCAT	164045	ATGCTTAAAAAAAATTTTTT
154826	5465	AAAAAAATTTTTTTTAAGCA	164046	TGCTTAAAAAAAATTTTTTT
154827	5466	TAAAAAAATTTTTTTTAAGC	164047	GCTTAAAAAAAATTTTTTTA
154828	5467	TTAAAAAAATTTTTTTTAAG	164048	CTTAAAAAAAATTTTTTTAA
154829	5468	TTTAAAAAAATTTTTTTTAA	164049	TTAAAAAAAATTTTTTTAAA
154830	5469	CTTTAAAAAAATTTTTTTTA	164050	TAAAAAAAATTTTTTTAAAG
154831	5470	ACTTTAAAAAAATTTTTTTT	164051	AAAAAAAATTTTTTTAAAGT

154832	5471	TACTTTAAAAAAATTTTTTT	164052	AAAAAAATTTTTTTAAAGTA
154833	5472	ATACTTTAAAAAAATTTTTT	164053	AAAAAATTTTTTTAAAGTAT
154834	5473	AATACTTTAAAAAAATTTTT	164054	AAAAATTTTTTTAAAGTATT
154835	5474	AAATACTTTAAAAAAATTTT	164055	AAAATTTTTTTAAAGTATTT
154836	5475	AAAATACTTTAAAAAAATTT	164056	AAATTTTTTTAAAGTATTTT
154837	5476	AAAAATACTTTAAAAAAATT	164057	AATTTTTTTAAAGTATTTTT
154838	5477	TAAAAATACTTTAAAAAAAT	164058	ATTTTTTTAAAGTATTTTTA
154839	5478	TTAAAAATACTTTAAAAAAA	164059	TTTTTTTAAAGTATTTTTAA
154840	5479	TTTAAAAATACTTTAAAAAA	164060	TTTTTTAAAGTATTTTTAAA
154841	5480	TTTTAAAAATACTTTAAAAA	164061	TTTTTAAAGTATTTTTAAAA
154842	5481	TTTTTAAAAATACTTTAAAA	164062	TTTTAAAGTATTTTTAAAAA
154843	5482	TTTTTTAAAAATACTTTAAA	164063	TTTAAAGTATTTTTAAAAAA
154844	5483	ATTTTTTAAAAATACTTTAA	164064	TTAAAGTATTTTTAAAAAAT
154845	5484	GATTTTTTAAAAATACTTTA	164065	TAAAGTATTTTTAAAAAATC
154846	5485	TGATTTTTTAAAAATACTTT	164066	AAAGTATTTTTAAAAAATCA
154847	5486	CTGATTTTTTAAAAATACTT	164067	AAGTATTTTTAAAAAATCAG
154848	5487	CCTGATTTTTTAAAAATACT	164068	AGTATTTTTAAAAAATCAGG
154849	5488	GCCTGATTTTTTAAAAATAC	164069	GTATTTTTAAAAAATCAGGC
154850	5489	TGCCTGATTTTTTAAAAATA	164070	TATTTTTAAAAAATCAGGCA
154851	5490	TTGCCTGATTTTTTAAAAAT	164071	ATTTTTAAAAAATCAGGCAA
154852	5491	GTTGCCTGATTTTTTAAAAA	164072	TTTTTAAAAAATCAGGCAAC
154853	5492	GGTTGCCTGATTTTTTAAAA	164073	TTTTAAAAAATCAGGCAACC
154854	5493	GGGTTGCCTGATTTTTTAAA	164074	TTTAAAAAATCAGGCAACCC
154855	5494	GGGGTTGCCTGATTTTTTAA	164075	TTAAAAAATCAGGCAACCCC
154856	5495	AGGGGTTGCCTGATTTTTTA	164076	TAAAAAATCAGGCAACCCCT
154857	5496	CAGGGGTTGCCTGATTTTTT	164077	AAAAAATCAGGCAACCCCTG
154858	5497	TCAGGGGTTGCCTGATTTTT	164078	AAAAATCAGGCAACCCCTGA
154859	5498	TTCAGGGGTTGCCTGATTTT	164079	AAAATCAGGCAACCCCTGAA
154860	5499	GTTCAGGGGTTGCCTGATTT	164080	AAATCAGGCAACCCCTGAAC
154861	5500	GGTTCAGGGGTTGCCTGATT	164081	AATCAGGCAACCCCTGAACC
154862	5501	TGGTTCAGGGGTTGCCTGAT	164082	ATCAGGCAACCCCTGAACCA
154863	5502	CTGGTTCAGGGGTTGCCTGA	164083	TCAGGCAACCCCTGAACCAG
154864	5503	TCTGGTTCAGGGGTTGCCTG	164084	CAGGCAACCCCTGAACCAGA
154865	5504	CTCTGGTTCAGGGGTTGCCT	164085	AGGCAACCCCTGAACCAGAG
154866	5505	ACTCTGGTTCAGGGGTTGCC	164086	GGCAACCCCTGAACCAGAGT
154867	5506	TACTCTGGTTCAGGGGTTGC	164087	GCAACCCCTGAACCAGAGTA
154868	5507	CTACTCTGGTTCAGGGGTTG	164088	CAACCCCTGAACCAGAGTAG
154869	5508	CCTACTCTGGTTCAGGGGTT	164089	AACCCCTGAACCAGAGTAGG
154870	5509	ACCTACTCTGGTTCAGGGGT	164090	ACCCCTGAACCAGAGTAGGT
154871	5510	AACCTACTCTGGTTCAGGGG	164091	CCCCTGAACCAGAGTAGGTT
154872	5511	GAACCTACTCTGGTTCAGGG	164092	CCCTGAACCAGAGTAGGTTC
154873	5512	TGAACCTACTCTGGTTCAGG	164093	CCTGAACCAGAGTAGGTTCA
154874	5513	CTGAACCTACTCTGGTTCAG	164094	CTGAACCAGAGTAGGTTCAG
154875	5514	TCTGAACCTACTCTGGTTCA	164095	TGAACCAGAGTAGGTTCAGA
154876	5515	CTCTGAACCTACTCTGGTTC	164096	GAACCAGAGTAGGTTCAGAG
154877	5516	TCTCTGAACCTACTCTGGTT	164097	AACCAGAGTAGGTTCAGAGA
154878	5517	TTCTCTGAACCTACTCTGGT	164098	ACCAGAGTAGGTTCAGAGAA
154879	5518	TTTCTCTGAACCTACTCTGG	164099	CCAGAGTAGGTTCAGAGAAA
154880	5519	GTTTCTCTGAACCTACTCTG	164100	CAGAGTAGGTTCAGAGAAAC
154881	5520	AGTTTCTCTGAACCTACTCT	164101	AGAGTAGGTTCAGAGAAACT
154882	5521	CAGTTTCTCTGAACCTACTC	164102	GAGTAGGTTCAGAGAAACTG
154883	5522	GCAGTTTCTCTGAACCTACT	164103	AGTAGGTTCAGAGAAACTGC
154884	5523	GGCAGTTTCTCTGAACCTAC	164104	GTAGGTTCAGAGAAACTGCC
154885	5524	TGGCAGTTTCTCTGAACCTA	164105	TAGGTTCAGAGAAACTGCCA
154886	5525	TTGGCAGTTTCTCTGAACCT	164106	AGGTTCAGAGAAACTGCCAA
154887	5526	TTTGGCAGTTTCTCTGAACC	164107	GGTTCAGAGAAACTGCCAAA
154888	5527	ATTTGGCAGTTTCTCTGAAC	164108	GTTCAGAGAAACTGCCAAAT
154889	5528	AATTTGGCAGTTTCTCTGAA	164109	TTCAGAGAAACTGCCAAATT
154890	5529	AAATTTGGCAGTTTCTCTGA	164110	TCAGAGAAACTGCCAAATTT
154891	5530	AAAATTTGGCAGTTTCTCTG	164111	CAGAGAAACTGCCAAATTTT
154892	5531	TAAAATTTGGCAGTTTCTCT	164112	AGAGAAACTGCCAAATTTTA
154893	5532	ATAAAATTTGGCAGTTTCTC	164113	GAGAAACTGCCAAATTTTAT
154894	5533	AATAAAATTTGGCAGTTTCT	164114	AGAAACTGCCAAATTTTATT
154895	5534	AAATAAAATTTGGCAGTTTC	164115	GAAACTGCCAAATTTTATTT
154896	5535	AAAATAAAATTTGGCAGTTT	164116	AAACTGCCAAATTTTATTTT
154897	5536	GAAAATAAAATTTGGCAGTT	164117	AACTGCCAAATTTTATTTTC
154898	5537	AGAAAATAAAATTTGGCAGT	164118	ACTGCCAAATTTTATTTTCT
154899	5538	AAGAAAATAAAATTTGGCAG	164119	CTGCCAAATTTTATTTTCTT
154900	5539	TAAGAAAATAAAATTTGGCA	164120	TGCCAAATTTTATTTTCTTA
154901	5540	TTAAGAAAATAAAATTTGGC	164121	GCCAAATTTTATTTTCTTAA
154902	5541	ATTAAGAAAATAAAATTTGG	164122	CCAAATTTTATTTTCTTAAT
154903	5542	AATTAAGAAAATAAAATTTG	164123	CAAATTTTATTTTCTTAATT

154904	5543	AAATTAAGAAAATAAAATTT	164124	AAATTTTATTTTCTTAATTT
154905	5544	CAAATTAAGAAAATAAAATT	164125	AATTTTATTTTCTTAATTTG
154906	5545	CCAAATTAAGAAAATAAAAT	164126	ATTTTATTTTCTTAATTTGG
154907	5546	CCCAAATTAAGAAAATAAAA	164127	TTTTATTTTCTTAATTTGGG
154908	5547	TCCCAAATTAAGAAAATAAA	164128	TTTATTTTCTTAATTTGGGA
154909	5548	ATCCCAAATTAAGAAAATAA	164129	TTATTTTCTTAATTTGGGAT
154910	5549	AATCCCAAATTAAGAAAATA	164130	TATTTTCTTAATTTGGGATT
154911	5550	CAATCCCAAATTAAGAAAAT	164131	ATTTTCTTAATTTGGGATTG
154912	5551	CCAATCCCAAATTAAGAAAA	164132	TTTTCTTAATTTGGGATTGG
154913	5552	TCCAATCCCAAATTAAGAAA	164133	TTTCTTAATTTGGGATTGGA
154914	5553	TTCCAATCCCAAATTAAGAA	164134	TTCTTAATTTGGGATTGGAA
154915	5554	CTTCCAATCCCAAATTAAGA	164135	TCTTAATTTGGGATTGGAAG
154916	5555	GCTTCCAATCCCAAATTAAG	164136	CTTAATTTGGGATTGGAAGC
154917	5556	TGCTTCCAATCCCAAATTAA	164137	TTAATTTGGGATTGGAAGCA
154918	5557	TTGCTTCCAATCCCAAATTA	164138	TAATTTGGGATTGGAAGCAA
154919	5558	CTTGCTTCCAATCCCAAATT	164139	AATTTGGGATTGGAAGCAAG
154920	5559	ACTTGCTTCCAATCCCAAAT	164140	ATTTGGGATTGGAAGCAAGT
154921	5560	AACTTGCTTCCAATCCCAAA	164141	TTTGGGATTGGAAGCAAGTT
154922	5561	TAACTTGCTTCCAATCCCAA	164142	TTGGGATTGGAAGCAAGTTA
154923	5562	TTAACTTGCTTCCAATCCCA	164143	TGGGATTGGAAGCAAGTTAA
154924	5563	GTTAACTTGCTTCCAATCCC	164144	GGGATTGGAAGCAAGTTAAC
154925	5564	TGTTAACTTGCTTCCAATCC	164145	GGATTGGAAGCAAGTTAACA
154926	5565	CTGTTAACTTGCTTCCAATC	164146	GATTGGAAGCAAGTTAACAG
154927	5566	TCTGTTAACTTGCTTCCAAT	164147	ATTGGAAGCAAGTTAACAGA
154928	5567	TTCTGTTAACTTGCTTCCAA	164148	TTGGAAGCAAGTTAACAGAA
154929	5568	CTTCTGTTAACTTGCTTCCA	164149	TGGAAGCAAGTTAACAGAAG
154930	5569	ACTTCTGTTAACTTGCTTCC	164150	GGAAGCAAGTTAACAGAAGT
154931	5570	AACTTCTGTTAACTTGCTTC	164151	GAAGCAAGTTAACAGAAGTT
154932	5571	AAACTTCTGTTAACTTGCTT	164152	AAGCAAGTTAACAGAAGTTT
154933	5572	TAAACTTCTGTTAACTTGCT	164153	AGCAAGTTAACAGAAGTTTA
154934	5573	ATAAACTTCTGTTAACTTGC	164154	GCAAGTTAACAGAAGTTTAT
154935	5574	CATAAACTTCTGTTAACTTG	164155	CAAGTTAACAGAAGTTTATG
154936	5575	TCATAAACTTCTGTTAACTT	164156	AAGTTAACAGAAGTTTATGA
154937	5576	CTCATAAACTTCTGTTAACT	164157	AGTTAACAGAAGTTTATGAG
154938	5577	ACTCATAAACTTCTGTTAAC	164158	GTTAACAGAAGTTTATGAGT
154939	5578	AACTCATAAACTTCTGTTAA	164159	TTAACAGAAGTTTATGAGTT
154940	5579	TAACTCATAAACTTCTGTTA	164160	TAACAGAAGTTTATGAGTTA
154941	5580	TTAACTCATAAACTTCTGTT	164161	AACAGAAGTTTATGAGTTAA
154942	5581	CTTAACTCATAAACTTCTGT	164162	ACAGAAGTTTATGAGTTAAG
154943	5582	ACTTAACTCATAAACTTCTG	164163	CAGAAGTTTATGAGTTAAGT
154944	5583	AACTTAACTCATAAACTTCT	164164	AGAAGTTTATGAGTTAAGTT
154945	5584	CAACTTAACTCATAAACTTC	164165	GAAGTTTATGAGTTAAGTTG
154946	5585	GCAACTTAACTCATAAACTT	164166	AAGTTTATGAGTTAAGTTGC
154947	5586	TGCAACTTAACTCATAAACT	164167	AGTTTATGAGTTAAGTTGCA
154948	5587	ATGCAACTTAACTCATAAAC	164168	GTTTATGAGTTAAGTTGCAT
154949	5588	AATGCAACTTAACTCATAAA	164169	TTTATGAGTTAAGTTGCATT
154950	5589	AAATGCAACTTAACTCATAA	164170	TTATGAGTTAAGTTGCATTT
154951	5590	TAAATGCAACTTAACTCATA	164171	TATGAGTTAAGTTGCATTTA
154952	5591	CTAAATGCAACTTAACTCAT	164172	ATGAGTTAAGTTGCATTTAG
154953	5592	ACTAAATGCAACTTAACTCA	164173	TGAGTTAAGTTGCATTTAGT
154954	5593	CACTAAATGCAACTTAACTC	164174	GAGTTAAGTTGCATTTAGTG
154955	5594	TCACTAAATGCAACTTAACT	164175	AGTTAAGTTGCATTTAGTGA
154956	5595	ATCACTAAATGCAACTTAAC	164176	GTTAAGTTGCATTTAGTGAT
154957	5596	GATCACTAAATGCAACTTAA	164177	TTAAGTTGCATTTAGTGATC
154958	5597	AGATCACTAAATGCAACTTA	164178	TAAGTTGCATTTAGTGATCT
154959	5598	AAGATCACTAAATGCAACTT	164179	AAGTTGCATTTAGTGATCTT
154960	5599	AAAGATCACTAAATGCAACT	164180	AGTTGCATTTAGTGATCTTT
154961	5600	AAAAGATCACTAAATGCAAC	164181	GTTGCATTTAGTGATCTTTT
154962	5601	CAAAAGATCACTAAATGCAA	164182	TTGCATTTAGTGATCTTTTG
154963	5602	GCAAAAGATCACTAAATGCA	164183	TGCATTTAGTGATCTTTTGC
154964	5603	GGCAAAAGATCACTAAATGC	164184	GCATTTAGTGATCTTTTGCC
154965	5604	TGGCAAAAGATCACTAAATG	164185	CATTTAGTGATCTTTTGCCA
154966	5605	ATGGCAAAAGATCACTAAAT	164186	ATTTAGTGATCTTTTGCCAT
154967	5606	TATGGCAAAAGATCACTAAA	164187	TTTAGTGATCTTTTGCCATA
154968	5607	ATATGGCAAAAGATCACTAA	164188	TTAGTGATCTTTTGCCATAT
154969	5608	AATATGGCAAAAGATCACTA	164189	TAGTGATCTTTTGCCATATT
154970	5609	AAATATGGCAAAAGATCACT	164190	AGTGATCTTTTGCCATATTT
154971	5610	CAAATATGGCAAAAGATCAC	164191	GTGATCTTTTGCCATATTTG
154972	5611	TCAAATATGGCAAAAGATCA	164192	TGATCTTTTGCCATATTTGA
154973	5612	CTCAAATATGGCAAAAGATC	164193	GATCTTTTGCCATATTTGAG
154974	5613	ACTCAAATATGGCAAAAGAT	164194	ATCTTTTGCCATATTTGAGT
154975	5614	TACTCAAATATGGCAAAAGA	164195	TCTTTTGCCATATTTGAGTA

154976	5615	TTACTCAAATATGGCAAAAG	164196	CTTTTGCCATATTTGAGTAA
154977	5616	ATTACTCAAATATGGCAAAA	164197	TTTTGCCATATTTGAGTAAT
154978	5617	TATTACTCAAATATGGCAAA	164198	TTTGCCATATTTGAGTAATA
154979	5618	TTATTACTCAAATATGGCAA	164199	TTGCCATATTTGAGTAATAA
154980	5619	ATTATTACTCAAATATGGCA	164200	TGCCATATTTGAGTAATAAT
154981	5620	GATTATTACTCAAATATGGC	164201	GCCATATTTGAGTAATAATC
154982	5621	AGATTATTACTCAAATATGG	164202	CCATATTTGAGTAATAATCT
154983	5622	CAGATTATTACTCAAATATG	164203	CATATTTGAGTAATAATCTG
154984	5623	TCAGATTATTACTCAAATAT	164204	ATATTTGAGTAATAATCTGA
154985	5624	ATCAGATTATTACTCAAATA	164205	TATTTGAGTAATAATCTGAT
154986	5625	AATCAGATTATTACTCAAAT	164206	ATTTGAGTAATAATCTGATT
154987	5626	AAATCAGATTATTACTCAAA	164207	TTTGAGTAATAATCTGATTT
154988	5627	AAAATCAGATTATTACTCAA	164208	TTGAGTAATAATCTGATTTT
154989	5628	AAAAATCAGATTATTACTCA	164209	TGAGTAATAATCTGATTTTT
154990	5629	AAAAAATCAGATTATTACTC	164210	GAGTAATAATCTGATTTTTT
154991	5630	AAAAAAATCAGATTATTACT	164211	AGTAATAATCTGATTTTTTT
154992	5631	CAAAAAAATCAGATTATTAC	164212	GTAATAATCTGATTTTTTTG
154993	5632	ACAAAAAAATCAGATTATTA	164213	TAATAATCTGATTTTTTTGT
154994	5633	AACAAAAAAATCAGATTATT	164214	AATAATCTGATTTTTTTGTT
154995	5634	AAACAAAAAAATCAGATTAT	164215	ATAATCTGATTTTTTTGTTT
154996	5635	TAAACAAAAAAATCAGATTA	164216	TAATCTGATTTTTTTGTTTA
154997	5636	ATAAACAAAAAAATCAGATT	164217	AATCTGATTTTTTTGTTTAT
154998	5637	TATAAACAAAAAAATCAGAT	164218	ATCTGATTTTTTTGTTTATA
154999	5638	CTATAAACAAAAAAATCAGA	164219	TCTGATTTTTTTGTTTATAG
155000	5639	TCTATAAACAAAAAAATCAG	164220	CTGATTTTTTTGTTTATAGA
155001	5640	ATCTATAAACAAAAAAATCA	164221	TGATTTTTTTGTTTATAGAT
155002	5641	AATCTATAAACAAAAAAATC	164222	GATTTTTTTGTTTATAGATT
155003	5642	AAATCTATAAACAAAAAAAT	164223	ATTTTTTTGTTTATAGATTT
155004	5643	GAAATCTATAAACAAAAAAA	164224	TTTTTTTGTTTATAGATTTC
155005	5644	AGAAATCTATAAACAAAAAA	164225	TTTTTTGTTTATAGATTTCT
155006	5645	AAGAAATCTATAAACAAAAA	164226	TTTTTGTTTATAGATTTCTT
155007	5646	GAAGAAATCTATAAACAAAA	164227	TTTTGTTTATAGATTTCTTC
155008	5647	AGAAGAAATCTATAAACAAA	164228	TTTGTTTATAGATTTCTTCT
155009	5648	AAGAAGAAATCTATAAACAA	164229	TTGTTTATAGATTTCTTCTT
155010	5649	TAAGAAGAAATCTATAAACA	164230	TGTTTATAGATTTCTTCTTA
155011	5650	TTAAGAAGAAATCTATAAAC	164231	GTTTATAGATTTCTTCTTAA
155012	5651	TTTAAGAAGAAATCTATAAA	164232	TTTATAGATTTCTTCTTAAA
155013	5652	ATTTAAGAAGAAATCTATAA	164233	TTATAGATTTCTTCTTAAAT
155014	5653	AATTTAAGAAGAAATCTATA	164234	TATAGATTTCTTCTTAAATT
155015	5654	TAATTTAAGAAGAAATCTAT	164235	ATAGATTTCTTCTTAAATTA
155016	5655	TTAATTTAAGAAGAAATCTA	164236	TAGATTTCTTCTTAAATTAA
155017	5656	GTTAATTTAAGAAGAAATCT	164237	AGATTTCTTCTTAAATTAAC
155018	5657	AGTTAATTTAAGAAGAAATC	164238	GATTTCTTCTTAAATTAACT
155019	5658	AAGTTAATTTAAGAAGAAAT	164239	ATTTCTTCTTAAATTAACTT
155020	5659	AAAGTTAATTTAAGAAGAAA	164240	TTTCTTCTTAAATTAACTTT
155021	5660	TAAAGTTAATTTAAGAAGAA	164241	TTCTTCTTAAATTAACTTTA
155022	5661	ATAAAGTTAATTTAAGAAGA	164242	TCTTCTTAAATTAACTTTAT
155023	5662	AATAAAGTTAATTTAAGAAG	164243	CTTCTTAAATTAACTTTATT
155024	5663	GAATAAAGTTAATTTAAGAA	164244	TTCTTAAATTAACTTTATTC
155025	5664	TGAATAAAGTTAATTTAAGA	164245	TCTTAAATTAACTTTATTCA
155026	5665	ATGAATAAAGTTAATTTAAG	164246	CTTAAATTAACTTTATTCAT
155027	5666	GATGAATAAAGTTAATTTAA	164247	TTAAATTAACTTTATTCATC
155028	5667	AGATGAATAAAGTTAATTTA	164248	TAAATTAACTTTATTCATCT
155029	5668	AAGATGAATAAAGTTAATTT	164249	AAATTAACTTTATTCATCTT
155030	5669	CAAGATGAATAAAGTTAATT	164250	AATTAACTTTATTCATCTTG
155031	5670	GCAAGATGAATAAAGTTAAT	164251	ATTAACTTTATTCATCTTGC
155032	5671	AGCAAGATGAATAAAGTTAA	164252	TTAACTTTATTCATCTTGCT
155033	5672	TAGCAAGATGAATAAAGTTA	164253	TAACTTTATTCATCTTGCTA
155034	5673	TTAGCAAGATGAATAAAGTT	164254	AACTTTATTCATCTTGCTAA
155035	5674	ATTAGCAAGATGAATAAAGT	164255	ACTTTATTCATCTTGCTAAT
155036	5675	AATTAGCAAGATGAATAAAG	164256	CTTTATTCATCTTGCTAATT
155037	5676	AAATTAGCAAGATGAATAAA	164257	TTTATTCATCTTGCTAATTT
155038	5677	TAAATTAGCAAGATGAATAA	164258	TTATTCATCTTGCTAATTTA
155039	5678	CTAAATTAGCAAGATGAATA	164259	TATTCATCTTGCTAATTTAG
155040	5679	ACTAAATTAGCAAGATGAAT	164260	ATTCATCTTGCTAATTTAGT
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155042	5681	AAACTAAATTAGCAAGATGA	164262	TCATCTTGCTAATTTAGTTT
155043	5682	GAAACTAAATTAGCAAGATG	164263	CATCTTGCTAATTTAGTTTC
155044	5683	TGAAACTAAATTAGCAAGAT	164264	ATCTTGCTAATTTAGTTTCA
155045	5684	TTGAAACTAAATTAGCAAGA	164265	TCTTGCTAATTTAGTTTCAA
155046	5685	TTTGAAACTAAATTAGCAAG	164266	CTTGCTAATTTAGTTTCAAA
155047	5686	ATTTGAAACTAAATTAGCAA	164267	TTGCTAATTTAGTTTCAAAT

155048	5687	TATTTGAAACTAAATTAGCA	164268	TGCTAATTTAGTTTCAAATA
155049	5688	CTATTTGAAACTAAATTAGC	164269	GCTAATTTAGTTTCAAATAG
155050	5689	ACTATTTGAAACTAAATTAG	164270	CTAATTTAGTTTCAAATAGT
155051	5690	CACTATTTGAAACTAAATTA	164271	TAATTTAGTTTCAAATAGTG
155052	5691	TCACTATTTGAAACTAAATT	164272	AATTTAGTTTCAAATAGTGA
155053	5692	ATCACTATTTGAAACTAAAT	164273	ATTTAGTTTCAAATAGTGAT
155054	5693	AATCACTATTTGAAACTAAA	164274	TTTAGTTTCAAATAGTGATT
155055	5694	AAATCACTATTTGAAACTAA	164275	TTAGTTTCAAATAGTGATTT
155056	5695	CAAATCACTATTTGAAACTA	164276	TAGTTTCAAATAGTGATTTG
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155058	5697	TACAAATCACTATTTGAAAC	164278	GTTTCAAATAGTGATTTGTA
155059	5698	TTACAAATCACTATTTGAAA	164279	TTTCAAATAGTGATTTGTAA
155060	5699	ATTACAAATCACTATTTGAA	164280	TTCAAATAGTGATTTGTAAT
155061	5700	CATTACAAATCACTATTTGA	164281	TCAAATAGTGATTTGTAATG
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155063	5702	ATCATTACAAATCACTATTT	164283	AAATAGTGATTTGTAATGAT
155064	5703	GATCATTACAAATCACTATT	164284	AATAGTGATTTGTAATGATC
155065	5704	TGATCATTACAAATCACTAT	164285	ATAGTGATTTGTAATGATCA
155066	5705	CTGATCATTACAAATCACTA	164286	TAGTGATTTGTAATGATCAG
155067	5706	TCTGATCATTACAAATCACT	164287	AGTGATTTGTAATGATCAGA
155068	5707	ATCTGATCATTACAAATCAC	164288	GTGATTTGTAATGATCAGAT
155069	5708	AATCTGATCATTACAAATCA	164289	TGATTTGTAATGATCAGATT
155070	5709	AAATCTGATCATTACAAATC	164290	GATTTGTAATGATCAGATTT
155071	5710	CAAATCTGATCATTACAAAT	164291	ATTTGTAATGATCAGATTTG
155072	5711	TCAAATCTGATCATTACAAA	164292	TTTGTAATGATCAGATTTGA
155073	5712	ATCAAATCTGATCATTACAA	164293	TTGTAATGATCAGATTTGAT
155074	5713	GATCAAATCTGATCATTACA	164294	TGTAATGATCAGATTTGATC
155075	5714	GGATCAAATCTGATCATTAC	164295	GTAATGATCAGATTTGATCC
155076	5715	TGGATCAAATCTGATCATTA	164296	TAATGATCAGATTTGATCCA
155077	5716	ATGGATCAAATCTGATCATT	164297	AATGATCAGATTTGATCCAT
155078	5717	AATGGATCAAATCTGATCAT	164298	ATGATCAGATTTGATCCATT
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155080	5719	GAAATGGATCAAATCTGATC	164300	GATCAGATTTGATCCATTTC
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155083	5722	ACAGAAATGGATCAAATCTG	164303	CAGATTTGATCCATTTCTGT
155084	5723	TACAGAAATGGATCAAATCT	164304	AGATTTGATCCATTTCTGTA
155085	5724	TTACAGAAATGGATCAAATC	164305	GATTTGATCCATTTCTGTAA
155086	5725	ATTACAGAAATGGATCAAAT	164306	ATTTGATCCATTTCTGTAAT
155087	5726	AATTACAGAAATGGATCAAA	164307	TTTGATCCATTTCTGTAATT
155088	5727	CAATTACAGAAATGGATCAA	164308	TTGATCCATTTCTGTAATTG
155089	5728	GCAATTACAGAAATGGATCA	164309	TGATCCATTTCTGTAATTGC
155090	5729	AGCAATTACAGAAATGGATC	164310	GATCCATTTCTGTAATTGCT
155091	5730	CAGCAATTACAGAAATGGAT	164311	ATCCATTTCTGTAATTGCTG
155092	5731	TCAGCAATTACAGAAATGGA	164312	TCCATTTCTGTAATTGCTGA
155093	5732	TTCAGCAATTACAGAAATGG	164313	CCATTTCTGTAATTGCTGAA
155094	5733	TTTCAGCAATTACAGAAATG	164314	CATTTCTGTAATTGCTGAAA
155095	5734	ATTTCAGCAATTACAGAAAT	164315	ATTTCTGTAATTGCTGAAAT
155096	5735	AATTTCAGCAATTACAGAAA	164316	TTTCTGTAATTGCTGAAATT
155097	5736	GAATTTCAGCAATTACAGAA	164317	TTCTGTAATTGCTGAAATTC
155098	5737	GGAATTTCAGCAATTACAGA	164318	TCTGTAATTGCTGAAATTCC
155099	5738	GGGAATTTCAGCAATTACAG	164319	CTGTAATTGCTGAAATTCCC
155100	5739	GGGGAATTTCAGCAATTACA	164320	TGTAATTGCTGAAATTCCCC
155101	5740	GGGGGAATTTCAGCAATTAC	164321	GTAATTGCTGAAATTCCCCC
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155103	5742	TCGGGGGAATTTCAGCAATT	164323	AATTGCTGAAATTCCCCCGA
155104	5743	CTCGGGGGAATTTCAGCAAT	164324	ATTGCTGAAATTCCCCCGAG
155105	5744	ACTCGGGGGAATTTCAGCAA	164325	TTGCTGAAATTCCCCCGAGT
155106	5745	AACTCGGGGGAATTTCAGCA	164326	TGCTGAAATTCCCCCGAGTT
155107	5746	CAACTCGGGGGAATTTCAGC	164327	GCTGAAATTCCCCCGAGTTG
155108	5747	GCAACTCGGGGGAATTTCAG	164328	CTGAAATTCCCCCGAGTTGC
155109	5748	AGCAACTCGGGGGAATTTCA	164329	TGAAATTCCCCCGAGTTGCT
155110	5749	AAGCAACTCGGGGGAATTTC	164330	GAAATTCCCCCGAGTTGCTT
155111	5750	AAAGCAACTCGGGGGAATTT	164331	AAATTCCCCCGAGTTGCTTT
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155113	5752	AAAAAGCAACTCGGGGGAAT	164333	ATTCCCCCGAGTTGCTTTTT
155114	5753	CAAAAAGCAACTCGGGGGAA	164334	TTCCCCCGAGTTGCTTTTTG
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155117	5756	AGCCAAAAAGCAACTCGGGG	164337	CCCCGAGTTGCTTTTTGGCT
155118	5757	AAGCCAAAAAGCAACTCGGG	164338	CCCGAGTTGCTTTTTGGCTT
155119	5758	AAAGCCAAAAAGCAACTCGG	164339	CCGAGTTGCTTTTTGGCTTT

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155122	5761	GGTAAAGCCAAAAAGCAACT	164342	AGTTGCTTTTTGGCTTTACC
155123	5762	CGGTAAAGCCAAAAAGCAAC	164343	GTTGCTTTTTGGCTTTACCG
155124	5763	GCGGTAAAGCCAAAAAGCAA	164344	TTGCTTTTTGGCTTTACCGC
155125	5764	GGCGGTAAAGCCAAAAAGCA	164345	TGCTTTTTGGCTTTACCGCC
155126	5765	AGGCGGTAAAGCCAAAAAGC	164346	GCTTTTTGGCTTTACCGCCT
155127	5766	GAGGCGGTAAAGCCAAAAAG	164347	CTTTTTGGCTTTACCGCCTC
155128	5767	AGAGGCGGTAAAGCCAAAAA	164348	TTTTTGGCTTTACCGCCTCT
155129	5768	CAGAGGCGGTAAAGCCAAAA	164349	TTTTGGCTTTACCGCCTCTG
155130	5769	CCAGAGGCGGTAAAGCCAAA	164350	TTTGGCTTTACCGCCTCTGG
155131	5770	ACCAGAGGCGGTAAAGCCAA	164351	TTGGCTTTACCGCCTCTGGT
155132	5771	GACCAGAGGCGGTAAAGCCA	164352	TGGCTTTACCGCCTCTGGTC
155133	5772	AGACCAGAGGCGGTAAAGCC	164353	GGCTTTACCGCCTCTGGTCT
155134	5773	CAGACCAGAGGCGGTAAAGC	164354	GCTTTACCGCCTCTGGTCTG
155135	5774	CCAGACCAGAGGCGGTAAAG	164355	CTTTACCGCCTCTGGTCTGG
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155139	5778	CCTCCCAGACCAGAGGCGGT	164359	ACCGCCTCTGGTCTGGGAGG
155140	5779	ACCTCCCAGACCAGAGGCGG	164360	CCGCCTCTGGTCTGGGAGGT
155141	5780	CACCTCCCAGACCAGAGGCG	164361	CGCCTCTGGTCTGGGAGGTG
155142	5781	TCACCTCCCAGACCAGAGGC	164362	GCCTCTGGTCTGGGAGGTGA
155143	5782	ATCACCTCCCAGACCAGAGG	164363	CCTCTGGTCTGGGAGGTGAT
155144	5783	AATCACCTCCCAGACCAGAG	164364	CTCTGGTCTGGGAGGTGATT
155145	5784	CAATCACCTCCCAGACCAGA	164365	TCTGGTCTGGGAGGTGATTG
155146	5785	GCAATCACCTCCCAGACCAG	164366	CTGGTCTGGGAGGTGATTGC
155147	5786	AGCAATCACCTCCCAGACCA	164367	TGGTCTGGGAGGTGATTGCT
155148	5787	GAGCAATCACCTCCCAGACC	164368	GGTCTGGGAGGTGATTGCTC
155149	5788	AGAGCAATCACCTCCCAGAC	164369	GTCTGGGAGGTGATTGCTCT
155150	5789	CAGAGCAATCACCTCCCAGA	164370	TCTGGGAGGTGATTGCTCTG
155151	5790	GCAGAGCAATCACCTCCCAG	164371	CTGGGAGGTGATTGCTCTGC
155152	5791	AGCAGAGCAATCACCTCCCA	164372	TGGGAGGTGATTGCTCTGCT
155153	5792	CAGCAGAGCAATCACCTCCC	164373	GGGAGGTGATTGCTCTGCTG
155154	5793	GCAGCAGAGCAATCACCTCC	164374	GGAGGTGATTGCTCTGCTGC
155155	5794	AGCAGCAGAGCAATCACCTC	164375	GAGGTGATTGCTCTGCTGCT
155156	5795	AAGCAGCAGAGCAATCACCT	164376	AGGTGATTGCTCTGCTGCTT
155157	5796	GAAGCAGCAGAGCAATCACC	164377	GGTGATTGCTCTGCTGCTTC
155158	5797	GGAAGCAGCAGAGCAATCAC	164378	GTGATTGCTCTGCTGCTTCC
155159	5798	AGGAAGCAGCAGAGCAATCA	164379	TGATTGCTCTGCTGCTTCCT
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155161	5800	ACAGGAAGCAGCAGAGCAAT	164381	ATTGCTCTGCTGCTTCCTGT
155162	5801	TACAGGAAGCAGCAGAGCAA	164382	TTGCTCTGCTGCTTCCTGTA
155163	5802	TTACAGGAAGCAGCAGAGCA	164383	TGCTCTGCTGCTTCCTGTAA
155164	5803	GTTACAGGAAGCAGCAGAGC	164384	GCTCTGCTGCTTCCTGTAAC
155165	5804	AGTTACAGGAAGCAGCAGAG	164385	CTCTGCTGCTTCCTGTAACT
155166	5805	AAGTTACAGGAAGCAGCAGA	164386	TCTGCTGCTTCCTGTAACTT
155167	5806	CAAGTTACAGGAAGCAGCAG	164387	CTGCTGCTTCCTGTAACTTG
155168	5807	GCAAGTTACAGGAAGCAGCA	164388	TGCTGCTTCCTGTAACTTGC
155169	5808	GGCAAGTTACAGGAAGCAGC	164389	GCTGCTTCCTGTAACTTGCC
155170	5809	AGGCAAGTTACAGGAAGCAG	164390	CTGCTTCCTGTAACTTGCCT
155171	5810	CAGGCAAGTTACAGGAAGCA	164391	TGCTTCCTGTAACTTGCCTG
155172	5811	GCAGGCAAGTTACAGGAAGC	164392	GCTTCCTGTAACTTGCCTGC
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155175	5814	AAGGCAGGCAAGTTACAGGA	164395	TCCTGTAACTTGCCTGCCTT
155176	5815	AAAGGCAGGCAAGTTACAGG	164396	CCTGTAACTTGCCTGCCTTT
155177	5816	GAAAGGCAGGCAAGTTACAG	164397	CTGTAACTTGCCTGCCTTTC
155178	5817	AGAAAGGCAGGCAAGTTACA	164398	TGTAACTTGCCTGCCTTTCT
155179	5818	GAGAAAGGCAGGCAAGTTAC	164399	GTAACTTGCCTGCCTTTCTC
155180	5819	GGAGAAAGGCAGGCAAGTTA	164400	TAACTTGCCTGCCTTTCTCC
155181	5820	GGGAGAAAGGCAGGCAAGTT	164401	AACTTGCCTGCCTTTCTCCC
155182	5821	AGGGAGAAAGGCAGGCAAGT	164402	ACTTGCCTGCCTTTCTCCCT
155183	5822	CAGGGAGAAAGGCAGGCAAG	164403	CTTGCCTGCCTTTCTCCCTG
155184	5823	ACAGGGAGAAAGGCAGGCAA	164404	TTGCCTGCCTTTCTCCCTGT
155185	5824	CACAGGGAGAAAGGCAGGCA	164405	TGCCTGCCTTTCTCCCTGTG
155186	5825	ACACAGGGAGAAAGGCAGGC	164406	GCCTGCCTTTCTCCCTGTGT
155187	5826	CACACAGGGAGAAAGGCAGG	164407	CCTGCCTTTCTCCCTGTGTG
155188	5827	CCACACAGGGAGAAAGGCAG	164408	CTGCCTTTCTCCCTGTGTGG
155189	5828	CCCACACAGGGAGAAAGGCA	164409	TGCCTTTCTCCCTGTGTGGG
155190	5829	TCCCACACAGGGAGAAAGGC	164410	GCCTTTCTCCCTGTGTGGGA
155191	5830	GTCCCACACAGGGAGAAAGG	164411	CCTTTCTCCCTGTGTGGGAC

155192	5831	AGTCCCACACAGGGAGAAAG	164412	CTTTCTCCCTGTGTGGGACT
155193	5832	GAGTCCCACACAGGGAGAAA	164413	TTTCTCCCTGTGTGGGACTC
155194	5833	GGAGTCCCACACAGGGAGAA	164414	TTCTCCCTGTGTGGGACTCC
155195	5834	AGGAGTCCCACACAGGGAGA	164415	TCTCCCTGTGTGGGACTCCT
155196	5835	CAGGAGTCCCACACAGGGAG	164416	CTCCCTGTGTGGGACTCCTG
155197	5836	GCAGGAGTCCCACACAGGGA	164417	TCCCTGTGTGGGACTCCTGC
155198	5837	CGCAGGAGTCCCACACAGGG	164418	CCCTGTGTGGGACTCCTGCG
155199	5838	CCGCAGGAGTCCCACACAGG	164419	CCTGTGTGGGACTCCTGCGG
155200	5839	CCCGCAGGAGTCCCACACAG	164420	CTGTGTGGGACTCCTGCGGG
155201	5840	ACCCGCAGGAGTCCCACACA	164421	TGTGTGGGACTCCTGCGGGT
155202	5841	CACCCGCAGGAGTCCCACAC	164422	GTGTGGGACTCCTGCGGGTG
155203	5842	TCACCCGCAGGAGTCCCACA	164423	TGTGGGACTCCTGCGGGTGA
155204	5843	CTCACCCGCAGGAGTCCCAC	164424	GTGGGACTCCTGCGGGTGAG
155205	5844	TCTCACCCGCAGGAGTCCCA	164425	TGGGACTCCTGCGGGTGAGA
155206	5845	CTCTCACCCGCAGGAGTCCC	164426	GGGACTCCTGCGGGTGAGAG
155207	5846	GCTCTCACCCGCAGGAGTCC	164427	GGACTCCTGCGGGTGAGAGC
155208	5847	CGCTCTCACCCGCAGGAGTC	164428	GACTCCTGCGGGTGAGAGCG
155209	5848	ACGCTCTCACCCGCAGGAGT	164429	ACTCCTGCGGGTGAGAGCGT
155210	5849	CACGCTCTCACCCGCAGGAG	164430	CTCCTGCGGGTGAGAGCGTG
155211	5850	CCACGCTCTCACCCGCAGGA	164431	TCCTGCGGGTGAGAGCGTGG
155212	5851	GCCACGCTCTCACCCGCAGG	164432	CCTGCGGGTGAGAGCGTGGC
155213	5852	AGCCACGCTCTCACCCGCAG	164433	CTGCGGGTGAGAGCGTGGCT
155214	5853	CAGCCACGCTCTCACCCGCA	164434	TGCGGGTGAGAGCGTGGCTG
155215	5854	TCAGCCACGCTCTCACCCGC	164435	GCGGGTGAGAGCGTGGCTGA
155216	5855	TTCAGCCACGCTCTCACCCG	164436	CGGGTGAGAGCGTGGCTGAA
155217	5856	CTTCAGCCACGCTCTCACCC	164437	GGGTGAGAGCGTGGCTGAAG
155218	5857	TCTTCAGCCACGCTCTCACC	164438	GGTGAGAGCGTGGCTGAAGA
155219	5858	GTCTTCAGCCACGCTCTCAC	164439	GTGAGAGCGTGGCTGAAGAC
155220	5859	TGTCTTCAGCCACGCTCTCA	164440	TGAGAGCGTGGCTGAAGACA
155221	5860	CTGTCTTCAGCCACGCTCTC	164441	GAGAGCGTGGCTGAAGACAG
155222	5861	GCTGTCTTCAGCCACGCTCT	164442	AGAGCGTGGCTGAAGACAGC
155223	5862	GGCTGTCTTCAGCCACGCTC	164443	GAGCGTGGCTGAAGACAGCC
155224	5863	CGGCTGTCTTCAGCCACGCT	164444	AGCGTGGCTGAAGACAGCCG
155225	5864	ACGGCTGTCTTCAGCCACGC	164445	GCGTGGCTGAAGACAGCCGT
155226	5865	CACGGCTGTCTTCAGCCACG	164446	CGTGGCTGAAGACAGCCGTG
155227	5866	ACACGGCTGTCTTCAGCCAC	164447	GTGGCTGAAGACAGCCGTGT
155228	5867	AACACGGCTGTCTTCAGCCA	164448	TGGCTGAAGACAGCCGTGTT
155229	5868	TAACACGGCTGTCTTCAGCC	164449	GGCTGAAGACAGCCGTGTTA
155230	5869	ATAACACGGCTGTCTTCAGC	164450	GCTGAAGACAGCCGTGTTAT
155231	5870	CATAACACGGCTGTCTTCAG	164451	CTGAAGACAGCCGTGTTATG
155232	5871	TCATAACACGGCTGTCTTCA	164452	TGAAGACAGCCGTGTTATGA
155233	5872	TTCATAACACGGCTGTCTTC	164453	GAAGACAGCCGTGTTATGAA
155234	5873	TTTCATAACACGGCTGTCTT	164454	AAGACAGCCGTGTTATGAAA
155235	5874	CTTTCATAACACGGCTGTCT	164455	AGACAGCCGTGTTATGAAAG
155236	5875	CCTTTCATAACACGGCTGTC	164456	GACAGCCGTGTTATGAAAGG
155237	5876	CCCTTTCATAACACGGCTGT	164457	ACAGCCGTGTTATGAAAGGG
155238	5877	GCCCTTTCATAACACGGCTG	164458	CAGCCGTGTTATGAAAGGGC
155239	5878	GGCCCTTTCATAACACGGCT	164459	AGCCGTGTTATGAAAGGGCC
155240	5879	AGGCCCTTTCATAACACGGC	164460	GCCGTGTTATGAAAGGGCCT
155241	5880	GAGGCCCTTTCATAACACGG	164461	CCGTGTTATGAAAGGGCCTC
155242	5881	GGAGGCCCTTTCATAACACG	164462	CGTGTTATGAAAGGGCCTCC
155243	5882	AGGAGGCCCTTTCATAACAC	164463	GTGTTATGAAAGGGCCTCCT
155244	5883	CAGGAGGCCCTTTCATAACA	164464	TGTTATGAAAGGGCCTCCTG
155245	5884	ACAGGAGGCCCTTTCATAAC	164465	GTTATGAAAGGGCCTCCTGT
155246	5885	CACAGGAGGCCCTTTCATAA	164466	TTATGAAAGGGCCTCCTGTG
155247	5886	GCACAGGAGGCCCTTTCATA	164467	TATGAAAGGGCCTCCTGTGC
155248	5887	AGCACAGGAGGCCCTTTCAT	164468	ATGAAAGGGCCTCCTGTGCT
155249	5888	CAGCACAGGAGGCCCTTTCA	164469	TGAAAGGGCCTCCTGTGCTG
155250	5889	ACAGCACAGGAGGCCCTTTC	164470	GAAAGGGCCTCCTGTGCTGT
155251	5890	GACAGCACAGGAGGCCCTTT	164471	AAAGGGCCTCCTGTGCTGTC
155252	5891	CGACAGCACAGGAGGCCCTT	164472	AAGGGCCTCCTGTGCTGTCG
155253	5892	TCGACAGCACAGGAGGCCCT	164473	AGGGCCTCCTGTGCTGTCGA
155254	5893	CTCGACAGCACAGGAGGCCC	164474	GGGCCTCCTGTGCTGTCGAG
155255	5894	CCTCGACAGCACAGGAGGCC	164475	GGCCTCCTGTGCTGTCGAGG
155256	5895	ACCTCGACAGCACAGGAGGC	164476	GCCTCCTGTGCTGTCGAGGT
155257	5896	AACCTCGACAGCACAGGAGG	164477	CCTCCTGTGCTGTCGAGGTT
155258	5897	CAACCTCGACAGCACAGGAG	164478	CTCCTGTGCTGTCGAGGTTG
155259	5898	ACAACCTCGACAGCACAGGA	164479	TCCTGTGCTGTCGAGGTTGT
155260	5899	CACAACCTCGACAGCACAGG	164480	CCTGTGCTGTCGAGGTTGTG
155261	5900	GCACAACCTCGACAGCACAG	164481	CTGTGCTGTCGAGGTTGTGC
155262	5901	AGCACAACCTCGACAGCACA	164482	TGTGCTGTCGAGGTTGTGCT
155263	5902	GAGCACAACCTCGACAGCAC	164483	GTGCTGTCGAGGTTGTGCTC

155264	5903	AGAGCACAACCTCGACAGCA	164484	TGCTGTCGAGGTTGTGCTCT
155265	5904	CAGAGCACAACCTCGACAGC	164485	GCTGTCGAGGTTGTGCTCTG
155266	5905	ACAGAGCACAACCTCGACAG	164486	CTGTCGAGGTTGTGCTCTGT
155267	5906	CACAGAGCACAACCTCGACA	164487	TGTCGAGGTTGTGCTCTGTG
155268	5907	TCACAGAGCACAACCTCGAC	164488	GTCGAGGTTGTGCTCTGTGA
155269	5908	TTCACAGAGCACAACCTCGA	164489	TCGAGGTTGTGCTCTGTGAA
155270	5909	ATTCACAGAGCACAACCTCG	164490	CGAGGTTGTGCTCTGTGAAT
155271	5910	CATTCACAGAGCACAACCTC	164491	GAGGTTGTGCTCTGTGAATG
155272	5911	ACATTCACAGAGCACAACCT	164492	AGGTTGTGCTCTGTGAATGT
155273	5912	GACATTCACAGAGCACAACC	164493	GGTTGTGCTCTGTGAATGTC
155274	5913	TGACATTCACAGAGCACAAC	164494	GTTGTGCTCTGTGAATGTCA
155275	5914	ATGACATTCACAGAGCACAA	164495	TTGTGCTCTGTGAATGTCAT
155276	5915	GATGACATTCACAGAGCACA	164496	TGTGCTCTGTGAATGTCATC
155277	5916	GGATGACATTCACAGAGCAC	164497	GTGCTCTGTGAATGTCATCC
155278	5917	GGGATGACATTCACAGAGCA	164498	TGCTCTGTGAATGTCATCCC
155279	5918	GGGGATGACATTCACAGAGC	164499	GCTCTGTGAATGTCATCCCC
155280	5919	AGGGGATGACATTCACAGAG	164500	CTCTGTGAATGTCATCCCCT
155281	5920	CAGGGGATGACATTCACAGA	164501	TCTGTGAATGTCATCCCCTG
155282	5921	CCAGGGGATGACATTCACAG	164502	CTGTGAATGTCATCCCCTGG
155283	5922	ACCAGGGGATGACATTCACA	164503	TGTGAATGTCATCCCCTGGT
155284	5923	CACCAGGGGATGACATTCAC	164504	GTGAATGTCATCCCCTGGTG
155285	5924	GCACCAGGGGATGACATTCA	164505	TGAATGTCATCCCCTGGTGC
155286	5925	TGCACCAGGGGATGACATTC	164506	GAATGTCATCCCCTGGTGCA
155287	5926	GTGCACCAGGGGATGACATT	164507	AATGTCATCCCCTGGTGCAC
155288	5927	TGTGCACCAGGGGATGACAT	164508	ATGTCATCCCCTGGTGCACA
155289	5928	CTGTGCACCAGGGGATGACA	164509	TGTCATCCCCTGGTGCACAG
155290	5929	GCTGTGCACCAGGGGATGAC	164510	GTCATCCCCTGGTGCACAGC
155291	5930	TGCTGTGCACCAGGGGATGA	164511	TCATCCCCTGGTGCACAGCA
155292	5931	CTGCTGTGCACCAGGGGATG	164512	CATCCCCTGGTGCACAGCAG
155293	5932	GCTGCTGTGCACCAGGGGAT	164513	ATCCCCTGGTGCACAGCAGC
155294	5933	TGCTGCTGTGCACCAGGGGA	164514	TCCCCTGGTGCACAGCAGCA
155295	5934	GTGCTGCTGTGCACCAGGGG	164515	CCCCTGGTGCACAGCAGCAC
155296	5935	GGTGCTGCTGTGCACCAGGG	164516	CCCTGGTGCACAGCAGCACC
155297	5936	AGGTGCTGCTGTGCACCAGG	164517	CCTGGTGCACAGCAGCACCT
155298	5937	AAGGTGCTGCTGTGCACCAG	164518	CTGGTGCACAGCAGCACCTT
155299	5938	GAAGGTGCTGCTGTGCACCA	164519	TGGTGCACAGCAGCACCTTC
155300	5939	AGAAGGTGCTGCTGTGCACC	164520	GGTGCACAGCAGCACCTTCT
155301	5940	TAGAAGGTGCTGCTGTGCAC	164521	GTGCACAGCAGCACCTTCTA
155302	5941	GTAGAAGGTGCTGCTGTGCA	164522	TGCACAGCAGCACCTTCTAC
155303	5942	TGTAGAAGGTGCTGCTGTGC	164523	GCACAGCAGCACCTTCTACA
155304	5943	GTGTAGAAGGTGCTGCTGTG	164524	CACAGCAGCACCTTCTACAC
155305	5944	TGTGTAGAAGGTGCTGCTGT	164525	ACAGCAGCACCTTCTACACA
155306	5945	CTGTGTAGAAGGTGCTGCTG	164526	CAGCAGCACCTTCTACACAG
155307	5946	CCTGTGTAGAAGGTGCTGCT	164527	AGCAGCACCTTCTACACAGG
155308	5947	TCCTGTGTAGAAGGTGCTGC	164528	GCAGCACCTTCTACACAGGA
155309	5948	ATCCTGTGTAGAAGGTGCTG	164529	CAGCACCTTCTACACAGGAT
155310	5949	TATCCTGTGTAGAAGGTGCT	164530	AGCACCTTCTACACAGGATA
155311	5950	GTATCCTGTGTAGAAGGTGC	164531	GCACCTTCTACACAGGATAC
155312	5951	TGTATCCTGTGTAGAAGGTG	164532	CACCTTCTACACAGGATACA
155313	5952	CTGTATCCTGTGTAGAAGGT	164533	ACCTTCTACACAGGATACAG
155314	5953	ACTGTATCCTGTGTAGAAGG	164534	CCTTCTACACAGGATACAGT
155315	5954	AACTGTATCCTGTGTAGAAG	164535	CTTCTACACAGGATACAGTT
155316	5955	CAACTGTATCCTGTGTAGAA	164536	TTCTACACAGGATACAGTTG
155317	5956	CCAACTGTATCCTGTGTAGA	164537	TCTACACAGGATACAGTTGG
155318	5957	TCCAACTGTATCCTGTGTAG	164538	CTACACAGGATACAGTTGGA
155319	5958	TTCCAACTGTATCCTGTGTA	164539	TACACAGGATACAGTTGGAA
155320	5959	ATTCCAACTGTATCCTGTGT	164540	ACACAGGATACAGTTGGAAT
155321	5960	CATTCCAACTGTATCCTGTG	164541	CACAGGATACAGTTGGAATG
155322	5961	GCATTCCAACTGTATCCTGT	164542	ACAGGATACAGTTGGAATGC
155323	5962	GGCATTCCAACTGTATCCTG	164543	CAGGATACAGTTGGAATGCC
155324	5963	CGGCATTCCAACTGTATCCT	164544	AGGATACAGTTGGAATGCCG
155325	5964	GCGGCATTCCAACTGTATCC	164545	GGATACAGTTGGAATGCCGC
155326	5965	GGCGGCATTCCAACTGTATC	164546	GATACAGTTGGAATGCCGCC
155327	5966	GGGCGGCATTCCAACTGTAT	164547	ATACAGTTGGAATGCCGCCC
155328	5967	GGGGCGGCATTCCAACTGTA	164548	TACAGTTGGAATGCCGCCCC
155329	5968	GGGGGCGGCATTCCAACTGT	164549	ACAGTTGGAATGCCGCCCCC
155330	5969	AGGGGGCGGCATTCCAACTG	164550	CAGTTGGAATGCCGCCCCCT
155331	5970	GAGGGGGCGGCATTCCAACT	164551	AGTTGGAATGCCGCCCCCTC
155332	5971	CGAGGGGGCGGCATTCCAAC	164552	GTTGGAATGCCGCCCCCTCG
155333	5972	TCGAGGGGGCGGCATTCCAA	164553	TTGGAATGCCGCCCCCTCGA
155334	5973	CTCGAGGGGGCGGCATTCCA	164554	TGGAATGCCGCCCCCTCGAG
155335	5974	ACTCGAGGGGGCGGCATTCC	164555	GGAATGCCGCCCCCTCGAGT

155336	5975	AACTCGAGGGGGCGGCATTC	164556	GAATGCCGCCCCCTCGAGTT
155337	5976	CAACTCGAGGGGGCGGCATT	164557	AATGCCGCCCCCTCGAGTTG
155338	5977	ACAACTCGAGGGGGCGGCAT	164558	ATGCCGCCCCCTCGAGTTGT
155339	5978	CACAACTCGAGGGGGCGGCA	164559	TGCCGCCCCCTCGAGTTGTG
155340	5979	ACACAACTCGAGGGGGCGGC	164560	GCCGCCCCCTCGAGTTGTGT
155341	5980	TACACAACTCGAGGGGGCGG	164561	CCGCCCCCTCGAGTTGTGTA
155342	5981	TTACACAACTCGAGGGGGCG	164562	CGCCCCCTCGAGTTGTGTAA
155343	5982	CTTACACAACTCGAGGGGGC	164563	GCCCCCTCGAGTTGTGTAAG
155344	5983	CCTTACACAACTCGAGGGGG	164564	CCCCCTCGAGTTGTGTAAGG
155345	5984	GCCTTACACAACTCGAGGGG	164565	CCCCTCGAGTTGTGTAAGGC
155346	5985	TGCCTTACACAACTCGAGGG	164566	CCCTCGAGTTGTGTAAGGCA
155347	5986	CTGCCTTACACAACTCGAGG	164567	CCTCGAGTTGTGTAAGGCAG
155348	5987	GCTGCCTTACACAACTCGAG	164568	CTCGAGTTGTGTAAGGCAGC
155349	5988	TGCTGCCTTACACAACTCGA	164569	TCGAGTTGTGTAAGGCAGCA
155350	5989	CTGCTGCCTTACACAACTCG	164570	CGAGTTGTGTAAGGCAGCAG
155351	5990	GCTGCTGCCTTACACAACTC	164571	GAGTTGTGTAAGGCAGCAGC
155352	5991	GGCTGCTGCCTTACACAACT	164572	AGTTGTGTAAGGCAGCAGCC
155353	5992	AGGCTGCTGCCTTACACAAC	164573	GTTGTGTAAGGCAGCAGCCT
155354	5993	AAGGCTGCTGCCTTACACAA	164574	TTGTGTAAGGCAGCAGCCTT
155355	5994	CAAGGCTGCTGCCTTACACA	164575	TGTGTAAGGCAGCAGCCTTG
155356	5995	CCAAGGCTGCTGCCTTACAC	164576	GTGTAAGGCAGCAGCCTTGG
155357	5996	GCCAAGGCTGCTGCCTTACA	164577	TGTAAGGCAGCAGCCTTGGC
155358	5997	GGCCAAGGCTGCTGCCTTAC	164578	GTAAGGCAGCAGCCTTGGCC
155359	5998	GGGCCAAGGCTGCTGCCTTA	164579	TAAGGCAGCAGCCTTGGCCC
155360	5999	AGGGCCAAGGCTGCTGCCTT	164580	AAGGCAGCAGCCTTGGCCCT
155361	6000	AAGGGCCAAGGCTGCTGCCT	164581	AGGCAGCAGCCTTGGCCCTT
155362	6001	CAAGGGCCAAGGCTGCTGCC	164582	GGCAGCAGCCTTGGCCCTTG
155363	6002	GCAAGGGCCAAGGCTGCTGC	164583	GCAGCAGCCTTGGCCCTTGC
155364	6003	TGCAAGGGCCAAGGCTGCTG	164584	CAGCAGCCTTGGCCCTTGCA
155365	6004	GTGCAAGGGCCAAGGCTGCT	164585	AGCAGCCTTGGCCCTTGCAC
155366	6005	TGTGCAAGGGCCAAGGCTGC	164586	GCAGCCTTGGCCCTTGCACA
155367	6006	ATGTGCAAGGGCCAAGGCTG	164587	CAGCCTTGGCCCTTGCACAT
155368	6007	TATGTGCAAGGGCCAAGGCT	164588	AGCCTTGGCCCTTGCACATA
155369	6008	TTATGTGCAAGGGCCAAGGC	164589	GCCTTGGCCCTTGCACATAA
155370	6009	CTTATGTGCAAGGGCCAAGG	164590	CCTTGGCCCTTGCACATAAG
155371	6010	TCTTATGTGCAAGGGCCAAG	164591	CTTGGCCCTTGCACATAAGA
155372	6011	ATCTTATGTGCAAGGGCCAA	164592	TTGGCCCTTGCACATAAGAT
155373	6012	CATCTTATGTGCAAGGGCCA	164593	TGGCCCTTGCACATAAGATG
155374	6013	GCATCTTATGTGCAAGGGCC	164594	GGCCCTTGCACATAAGATGC
155375	6014	AGCATCTTATGTGCAAGGGC	164595	GCCCTTGCACATAAGATGCT
155376	6015	CAGCATCTTATGTGCAAGGG	164596	CCCTTGCACATAAGATGCTG
155377	6016	ACAGCATCTTATGTGCAAGG	164597	CCTTGCACATAAGATGCTGT
155378	6017	AACAGCATCTTATGTGCAAG	164598	CTTGCACATAAGATGCTGTT
155379	6018	CAACAGCATCTTATGTGCAA	164599	TTGCACATAAGATGCTGTTG
155380	6019	TCAACAGCATCTTATGTGCA	164600	TGCACATAAGATGCTGTTGA
155381	6020	TTCAACAGCATCTTATGTGC	164601	GCACATAAGATGCTGTTGAA
155382	6021	ATTCAACAGCATCTTATGTG	164602	CACATAAGATGCTGTTGAAT
155383	6022	TATTCAACAGCATCTTATGT	164603	ACATAAGATGCTGTTGAATA
155384	6023	ATATTCAACAGCATCTTATG	164604	CATAAGATGCTGTTGAATAT
155385	6024	AATATTCAACAGCATCTTAT	164605	ATAAGATGCTGTTGAATATT
155386	6025	GAATATTCAACAGCATCTTA	164606	TAAGATGCTGTTGAATATTC
155387	6026	AGAATATTCAACAGCATCTT	164607	AAGATGCTGTTGAATATTCT
155388	6027	CAGAATATTCAACAGCATCT	164608	AGATGCTGTTGAATATTCTG
155389	6028	GCAGAATATTCAACAGCATC	164609	GATGCTGTTGAATATTCTGC
155390	6029	GGCAGAATATTCAACAGCAT	164610	ATGCTGTTGAATATTCTGCC
155391	6030	AGGCAGAATATTCAACAGCA	164611	TGCTGTTGAATATTCTGCCT
155392	6031	CAGGCAGAATATTCAACAGC	164612	GCTGTTGAATATTCTGCCTG
155393	6032	GCAGGCAGAATATTCAACAG	164613	CTGTTGAATATTCTGCCTGC
155394	6033	TGCAGGCAGAATATTCAACA	164614	TGTTGAATATTCTGCCTGCA
155395	6034	GTGCAGGCAGAATATTCAAC	164615	GTTGAATATTCTGCCTGCAC
155396	6035	GGTGCAGGCAGAATATTCAA	164616	TTGAATATTCTGCCTGCACC
155397	6036	TGGTGCAGGCAGAATATTCA	164617	TGAATATTCTGCCTGCACCA
155398	6037	TTGGTGCAGGCAGAATATTC	164618	GAATATTCTGCCTGCACCAA
155399	6038	CTTGGTGCAGGCAGAATATT	164619	AATATTCTGCCTGCACCAAG
155400	6039	ACTTGGTGCAGGCAGAATAT	164620	ATATTCTGCCTGCACCAAGT
155401	6040	TACTTGGTGCAGGCAGAATA	164621	TATTCTGCCTGCACCAAGTA
155402	6041	TTACTTGGTGCAGGCAGAAT	164622	ATTCTGCCTGCACCAAGTAA
155403	6042	TTTACTTGGTGCAGGCAGAA	164623	TTCTGCCTGCACCAAGTAAA
155404	6043	CTTTACTTGGTGCAGGCAGA	164624	TCTGCCTGCACCAAGTAAAG
155405	6044	CCTTTACTTGGTGCAGGCAG	164625	CTGCCTGCACCAAGTAAAGG
155406	6045	CCCTTTACTTGGTGCAGGCA	164626	TGCCTGCACCAAGTAAAGGG
155407	6046	GCCCTTTACTTGGTGCAGGC	164627	GCCTGCACCAAGTAAAGGGC

155408	6047	TGCCCTTTACTTGGTGCAGG	164628	CCTGCACCAAGTAAAGGGCA
155409	6048	GTGCCCTTTACTTGGTGCAG	164629	CTGCACCAAGTAAAGGGCAC
155410	6049	TGTGCCCTTTACTTGGTGCA	164630	TGCACCAAGTAAAGGGCACA
155411	6050	CTGTGCCCTTTACTTGGTGC	164631	GCACCAAGTAAAGGGCACAG
155412	6051	TCTGTGCCCTTTACTTGGTG	164632	CACCAAGTAAAGGGCACAGA
155413	6052	ATCTGTGCCCTTTACTTGGT	164633	ACCAAGTAAAGGGCACAGAT
155414	6053	TATCTGTGCCCTTTACTTGG	164634	CCAAGTAAAGGGCACAGATA
155415	6054	CTATCTGTGCCCTTTACTTG	164635	CAAGTAAAGGGCACAGATAG
155416	6055	TCTATCTGTGCCCTTTACTT	164636	AAGTAAAGGGCACAGATAGA
155417	6056	TTCTATCTGTGCCCTTTACT	164637	AGTAAAGGGCACAGATAGAA
155418	6057	GTTCTATCTGTGCCCTTTAC	164638	GTAAAGGGCACAGATAGAAC
155419	6058	AGTTCTATCTGTGCCCTTTA	164639	TAAAGGGCACAGATAGAACT
155420	6059	CAGTTCTATCTGTGCCCTTT	164640	AAAGGGCACAGATAGAACTG
155421	6060	GCAGTTCTATCTGTGCCCTT	164641	AAGGGCACAGATAGAACTGC
155422	6061	AGCAGTTCTATCTGTGCCCT	164642	AGGGCACAGATAGAACTGCT
155423	6062	AAGCAGTTCTATCTGTGCCC	164643	GGGCACAGATAGAACTGCTT
155424	6063	CAAGCAGTTCTATCTGTGCC	164644	GGCACAGATAGAACTGCTTG
155425	6064	CCAAGCAGTTCTATCTGTGC	164645	GCACAGATAGAACTGCTTGG
155426	6065	GCCAAGCAGTTCTATCTGTG	164646	CACAGATAGAACTGCTTGGC
155427	6066	TGCCAAGCAGTTCTATCTGT	164647	ACAGATAGAACTGCTTGGCA
155428	6067	ATGCCAAGCAGTTCTATCTG	164648	CAGATAGAACTGCTTGGCAT
155429	6068	TATGCCAAGCAGTTCTATCT	164649	AGATAGAACTGCTTGGCATA
155430	6069	ATATGCCAAGCAGTTCTATC	164650	GATAGAACTGCTTGGCATAT
155431	6070	CATATGCCAAGCAGTTCTAT	164651	ATAGAACTGCTTGGCATATG
155432	6071	ACATATGCCAAGCAGTTCTA	164652	TAGAACTGCTTGGCATATGT
155433	6072	AACATATGCCAAGCAGTTCT	164653	AGAACTGCTTGGCATATGTT
155434	6073	CAACATATGCCAAGCAGTTC	164654	GAACTGCTTGGCATATGTTG
155435	6074	GCAACATATGCCAAGCAGTT	164655	AACTGCTTGGCATATGTTGC
155436	6075	AGCAACATATGCCAAGCAGT	164656	ACTGCTTGGCATATGTTGCT
155437	6076	CAGCAACATATGCCAAGCAG	164657	CTGCTTGGCATATGTTGCTG
155438	6077	CCAGCAACATATGCCAAGCA	164658	TGCTTGGCATATGTTGCTGG
155439	6078	CCCAGCAACATATGCCAAGC	164659	GCTTGGCATATGTTGCTGGG
155440	6079	CCCCAGCAACATATGCCAAG	164660	CTTGGCATATGTTGCTGGGG
155441	6080	TCCCCAGCAACATATGCCAA	164661	TTGGCATATGTTGCTGGGGA
155442	6081	CTCCCCAGCAACATATGCCA	164662	TGGCATATGTTGCTGGGGAG
155443	6082	TCTCCCCAGCAACATATGCC	164663	GGCATATGTTGCTGGGGAGA
155444	6083	ATCTCCCCAGCAACATATGC	164664	GCATATGTTGCTGGGGAGAT
155445	6084	CATCTCCCCAGCAACATATG	164665	CATATGTTGCTGGGGAGATG
155446	6085	TCATCTCCCCAGCAACATAT	164666	ATATGTTGCTGGGGAGATGA
155447	6086	CTCATCTCCCCAGCAACATA	164667	TATGTTGCTGGGGAGATGAG
155448	6087	ACTCATCTCCCCAGCAACAT	164668	ATGTTGCTGGGGAGATGAGT
155449	6088	AACTCATCTCCCCAGCAACA	164669	TGTTGCTGGGGAGATGAGTT
155450	6089	AAACTCATCTCCCCAGCAAC	164670	GTTGCTGGGGAGATGAGTTT
155451	6090	AAAACTCATCTCCCCAGCAA	164671	TTGCTGGGGAGATGAGTTTT
155452	6091	AAAAACTCATCTCCCCAGCA	164672	TGCTGGGGAGATGAGTTTTT
155453	6092	AAAAAACTCATCTCCCCAGC	164673	GCTGGGGAGATGAGTTTTTT
155454	6093	CAAAAAACTCATCTCCCCAG	164674	CTGGGGAGATGAGTTTTTTG
155455	6094	ACAAAAAACTCATCTCCCCA	164675	TGGGGAGATGAGTTTTTTGT
155456	6095	TACAAAAAACTCATCTCCCC	164676	GGGGAGATGAGTTTTTTGTA
155457	6096	TTACAAAAAACTCATCTCCC	164677	GGGAGATGAGTTTTTTGTAA
155458	6097	TTTACAAAAAACTCATCTCC	164678	GGAGATGAGTTTTTTGTAAA
155459	6098	CTTTACAAAAAACTCATCTC	164679	GAGATGAGTTTTTTGTAAAG
155460	6099	ACTTTACAAAAAACTCATCT	164680	AGATGAGTTTTTTGTAAAGT
155461	6100	TACTTTACAAAAAACTCATC	164681	GATGAGTTTTTTGTAAAGTA
155462	6101	ATACTTTACAAAAAACTCAT	164682	ATGAGTTTTTTGTAAAGTAT
155463	6102	TATACTTTACAAAAAACTCA	164683	TGAGTTTTTTGTAAAGTATA
155464	6103	GTATACTTTACAAAAAACTC	164684	GAGTTTTTTGTAAAGTATAC
155465	6104	AGTATACTTTACAAAAAACT	164685	AGTTTTTTGTAAAGTATACT
155466	6105	TAGTATACTTTACAAAAAAC	164686	GTTTTTTGTAAAGTATACTA
155467	6106	GTAGTATACTTTACAAAAAA	164687	TTTTTTGTAAAGTATACTAC
155468	6107	CGTAGTATACTTTACAAAAA	164688	TTTTTGTAAAGTATACTACG
155469	6108	ACGTAGTATACTTTACAAAA	164689	TTTTGTAAAGTATACTACGT
155470	6109	AACGTAGTATACTTTACAAA	164690	TTTGTAAAGTATACTACGTT
155471	6110	GAACGTAGTATACTTTACAA	164691	TTGTAAAGTATACTACGTTC
155472	6111	AGAACGTAGTATACTTTACA	164692	TGTAAAGTATACTACGTTCT
155473	6112	AAGAACGTAGTATACTTTAC	164693	GTAAAGTATACTACGTTCTT
155474	6113	TAAGAACGTAGTATACTTTA	164694	TAAAGTATACTACGTTCTTA
155475	6114	TTAAGAACGTAGTATACTTT	164695	AAAGTATACTACGTTCTTAA
155476	6115	CTTAAGAACGTAGTATACTT	164696	AAGTATACTACGTTCTTAAG
155477	6116	TCTTAAGAACGTAGTATACT	164697	AGTATACTACGTTCTTAAGA
155478	6117	TTCTTAAGAACGTAGTATAC	164698	GTATACTACGTTCTTAAGAA
155479	6118	ATTCTTAAGAACGTAGTATA	164699	TATACTACGTTCTTAAGAAT

155480	6119	AATTCTTAAGAACGTAGTAT	164700	ATACTACGTTCTTAAGAATT
155481	6120	AAATTCTTAAGAACGTAGTA	164701	TACTACGTTCTTAAGAATTT
155482	6121	CAAATTCTTAAGAACGTAGT	164702	ACTACGTTCTTAAGAATTTG
155483	6122	CCAAATTCTTAAGAACGTAG	164703	CTACGTTCTTAAGAATTTGG
155484	6123	TCCAAATTCTTAAGAACGTA	164704	TACGTTCTTAAGAATTTGGA
155485	6124	ATCCAAATTCTTAAGAACGT	164705	ACGTTCTTAAGAATTTGGAT
155486	6125	GATCCAAATTCTTAAGAACG	164706	CGTTCTTAAGAATTTGGATC
155487	6126	TGATCCAAATTCTTAAGAAC	164707	GTTCTTAAGAATTTGGATCA
155488	6127	ATGATCCAAATTCTTAAGAA	164708	TTCTTAAGAATTTGGATCAT
155489	6128	TATGATCCAAATTCTTAAGA	164709	TCTTAAGAATTTGGATCATA
155490	6129	TTATGATCCAAATTCTTAAG	164710	CTTAAGAATTTGGATCATAA
155491	6130	GTTATGATCCAAATTCTTAA	164711	TTAAGAATTTGGATCATAAC
155492	6131	GGTTATGATCCAAATTCTTA	164712	TAAGAATTTGGATCATAACC
155493	6132	TGGTTATGATCCAAATTCTT	164713	AAGAATTTGGATCATAACCA
155494	6133	ATGGTTATGATCCAAATTCT	164714	AGAATTTGGATCATAACCAT
155495	6134	CATGGTTATGATCCAAATTC	164715	GAATTTGGATCATAACCATG
155496	6135	CCATGGTTATGATCCAAATT	164716	AATTTGGATCATAACCATGG
155497	6136	CCCATGGTTATGATCCAAAT	164717	ATTTGGATCATAACCATGGG
155498	6137	TCCCATGGTTATGATCCAAA	164718	TTTGGATCATAACCATGGGA
155499	6138	ATCCCATGGTTATGATCCAA	164719	TTGGATCATAACCATGGGAT
155500	6139	AATCCCATGGTTATGATCCA	164720	TGGATCATAACCATGGGATT
155501	6140	AAATCCCATGGTTATGATCC	164721	GGATCATAACCATGGGATTT
155502	6141	AAAATCCCATGGTTATGATC	164722	GATCATAACCATGGGATTTT
155503	6142	TAAAATCCCATGGTTATGAT	164723	ATCATAACCATGGGATTTTA
155504	6143	TTAAAATCCCATGGTTATGA	164724	TCATAACCATGGGATTTTAA
155505	6144	ATTAAAATCCCATGGTTATG	164725	CATAACCATGGGATTTTAAT
155506	6145	TATTAAAATCCCATGGTTAT	164726	ATAACCATGGGATTTTAATA
155507	6146	TTATTAAAATCCCATGGTTA	164727	TAACCATGGGATTTTAATAA
155508	6147	ATTATTAAAATCCCATGGTT	164728	AACCATGGGATTTTAATAAT
155509	6148	TATTATTAAAATCCCATGGT	164729	ACCATGGGATTTTAATAATA
155510	6149	CTATTATTAAAATCCCATGG	164730	CCATGGGATTTTAATAATAG
155511	6150	TCTATTATTAAAATCCCATG	164731	CATGGGATTTTAATAATAGA
155512	6151	TTCTATTATTAAAATCCCAT	164732	ATGGGATTTTAATAATAGAA
155513	6152	TTTCTATTATTAAAATCCCA	164733	TGGGATTTTAATAATAGAAA
155514	6153	TTTTCTATTATTAAAATCCC	164734	GGGATTTTAATAATAGAAAA
155515	6154	TTTTTCTATTATTAAAATCC	164735	GGATTTTAATAATAGAAAAA
155516	6155	GTTTTTCTATTATTAAAATC	164736	GATTTTAATAATAGAAAAAC
155517	6156	AGTTTTTCTATTATTAAAAT	164737	ATTTTAATAATAGAAAAACT
155518	6157	CAGTTTTTCTATTATTAAAA	164738	TTTTAATAATAGAAAAACTG
155519	6158	ACAGTTTTTCTATTATTAAA	164739	TTTAATAATAGAAAAACTGT
155520	6159	AACAGTTTTTCTATTATTAA	164740	TTAATAATAGAAAAACTGTT
155521	6160	CAACAGTTTTTCTATTATTA	164741	TAATAATAGAAAAACTGTTG
155522	6161	TCAACAGTTTTTCTATTATT	164742	AATAATAGAAAAACTGTTGA
155523	6162	TTCAACAGTTTTTCTATTAT	164743	ATAATAGAAAAACTGTTGAA
155524	6163	CTTCAACAGTTTTTCTATTA	164744	TAATAGAAAAACTGTTGAAG
155525	6164	TCTTCAACAGTTTTTCTATT	164745	AATAGAAAAACTGTTGAAGA
155526	6165	ATCTTCAACAGTTTTTCTAT	164746	ATAGAAAAACTGTTGAAGAT
155527	6166	GATCTTCAACAGTTTTTCTA	164747	TAGAAAAACTGTTGAAGATC
155528	6167	TGATCTTCAACAGTTTTTCT	164748	AGAAAAACTGTTGAAGATCA
155529	6168	CTGATCTTCAACAGTTTTTC	164749	GAAAAACTGTTGAAGATCAG
155530	6169	ACTGATCTTCAACAGTTTTT	164750	AAAAACTGTTGAAGATCAGT
155531	6170	GACTGATCTTCAACAGTTTT	164751	AAAACTGTTGAAGATCAGTC
155532	6171	AGACTGATCTTCAACAGTTT	164752	AAACTGTTGAAGATCAGTCT
155533	6172	CAGACTGATCTTCAACAGTT	164753	AACTGTTGAAGATCAGTCTG
155534	6173	CCAGACTGATCTTCAACAGT	164754	ACTGTTGAAGATCAGTCTGG
155535	6174	ACCAGACTGATCTTCAACAG	164755	CTGTTGAAGATCAGTCTGGT
155536	6175	GACCAGACTGATCTTCAACA	164756	TGTTGAAGATCAGTCTGGTC
155537	6176	GGACCAGACTGATCTTCAAC	164757	GTTGAAGATCAGTCTGGTCC
155538	6177	GGGACCAGACTGATCTTCAA	164758	TTGAAGATCAGTCTGGTCCC
155539	6178	AGGGACCAGACTGATCTTCA	164759	TGAAGATCAGTCTGGTCCCT
155540	6179	AAGGGACCAGACTGATCTTC	164760	GAAGATCAGTCTGGTCCCTT
155541	6180	TAAGGGACCAGACTGATCTT	164761	AAGATCAGTCTGGTCCCTTA
155542	6181	ATAAGGGACCAGACTGATCT	164762	AGATCAGTCTGGTCCCTTAT
155543	6182	AATAAGGGACCAGACTGATC	164763	GATCAGTCTGGTCCCTTATT
155544	6183	AAATAAGGGACCAGACTGAT	164764	ATCAGTCTGGTCCCTTATTT
155545	6184	AAAATAAGGGACCAGACTGA	164765	TCAGTCTGGTCCCTTATTTT
155546	6185	AAAAATAAGGGACCAGACTG	164766	CAGTCTGGTCCCTTATTTTT
155547	6186	TAAAAATAAGGGACCAGACT	164767	AGTCTGGTCCCTTATTTTTA
155548	6187	GTAAAAATAAGGGACCAGAC	164768	GTCTGGTCCCTTATTTTTAC
155549	6188	TGTAAAAATAAGGGACCAGA	164769	TCTGGTCCCTTATTTTTACA
155550	6189	CTGTAAAAATAAGGGACCAG	164770	CTGGTCCCTTATTTTTACAG
155551	6190	ACTGTAAAAATAAGGGACCA	164771	TGGTCCCTTATTTTTACAGT

155552	6191	CACTGTAAAAATAAGGGACC	164772	GGTCCCTTATTTTTACAGTG
155553	6192	TCACTGTAAAAATAAGGGAC	164773	GTCCCTTATTTTTACAGTGA
155554	6193	TTCACTGTAAAAATAAGGGA	164774	TCCCTTATTTTTACAGTGAA
155555	6194	CTTCACTGTAAAAATAAGGG	164775	CCCTTATTTTTACAGTGAAG
155556	6195	TCTTCACTGTAAAAATAAGG	164776	CCTTATTTTTACAGTGAAGA
155557	6196	TTCTTCACTGTAAAAATAAG	164777	CTTATTTTTACAGTGAAGAA
155558	6197	CTTCTTCACTGTAAAAATAA	164778	TTATTTTTACAGTGAAGAAG
155559	6198	GCTTCTTCACTGTAAAAATA	164779	TATTTTTACAGTGAAGAAGC
155560	6199	GGCTTCTTCACTGTAAAAAT	164780	ATTTTTACAGTGAAGAAGCC
155561	6200	TGGCTTCTTCACTGTAAAAA	164781	TTTTTACAGTGAAGAAGCCA
155562	6201	TTGGCTTCTTCACTGTAAAA	164782	TTTTACAGTGAAGAAGCCAA
155563	6202	TTTGGCTTCTTCACTGTAAA	164783	TTTACAGTGAAGAAGCCAAA
155564	6203	CTTTGGCTTCTTCACTGTAA	164784	TTACAGTGAAGAAGCCAAAG
155565	6204	GCTTTGGCTTCTTCACTGTA	164785	TACAGTGAAGAAGCCAAAGC
155566	6205	GGCTTTGGCTTCTTCACTGT	164786	ACAGTGAAGAAGCCAAAGCC
155567	6206	GGGCTTTGGCTTCTTCACTG	164787	CAGTGAAGAAGCCAAAGCCC
155568	6207	TGGGCTTTGGCTTCTTCACT	164788	AGTGAAGAAGCCAAAGCCCA
155569	6208	CTGGGCTTTGGCTTCTTCAC	164789	GTGAAGAAGCCAAAGCCCAG
155570	6209	TCTGGGCTTTGGCTTCTTCA	164790	TGAAGAAGCCAAAGCCCAGA
155571	6210	CTCTGGGCTTTGGCTTCTTC	164791	GAAGAAGCCAAAGCCCAGAG
155572	6211	TCTCTGGGCTTTGGCTTCTT	164792	AAGAAGCCAAAGCCCAGAGA
155573	6212	TTCTCTGGGCTTTGGCTTCT	164793	AGAAGCCAAAGCCCAGAGAA
155574	6213	CTTCTCTGGGCTTTGGCTTC	164794	GAAGCCAAAGCCCAGAGAAG
155575	6214	CCTTCTCTGGGCTTTGGCTT	164795	AAGCCAAAGCCCAGAGAAGG
155576	6215	CCCTTCTCTGGGCTTTGGCT	164796	AGCCAAAGCCCAGAGAAGGG
155577	6216	ACCCTTCTCTGGGCTTTGGC	164797	GCCAAAGCCCAGAGAAGGGT
155578	6217	CACCCTTCTCTGGGCTTTGG	164798	CCAAAGCCCAGAGAAGGGTG
155579	6218	ACACCCTTCTCTGGGCTTTG	164799	CAAAGCCCAGAGAAGGGTGT
155580	6219	AACACCCTTCTCTGGGCTTT	164800	AAAGCCCAGAGAAGGGTGTT
155581	6220	TAACACCCTTCTCTGGGCTT	164801	AAGCCCAGAGAAGGGTGTTA
155582	6221	TTAACACCCTTCTCTGGGCT	164802	AGCCCAGAGAAGGGTGTTAA
155583	6222	GTTAACACCCTTCTCTGGGC	164803	GCCCAGAGAAGGGTGTTAAC
155584	6223	AGTTAACACCCTTCTCTGGG	164804	CCCAGAGAAGGGTGTTAACT
155585	6224	AAGTTAACACCCTTCTCTGG	164805	CCAGAGAAGGGTGTTAACTT
155586	6225	AAAGTTAACACCCTTCTCTG	164806	CAGAGAAGGGTGTTAACTTT
155587	6226	TAAAGTTAACACCCTTCTCT	164807	AGAGAAGGGTGTTAACTTTA
155588	6227	GTAAAGTTAACACCCTTCTC	164808	GAGAAGGGTGTTAACTTTAC
155589	6228	TGTAAAGTTAACACCCTTCT	164809	AGAAGGGTGTTAACTTTACA
155590	6229	TTGTAAAGTTAACACCCTTC	164810	GAAGGGTGTTAACTTTACAA
155591	6230	CTTGTAAAGTTAACACCCTT	164811	AAGGGTGTTAACTTTACAAG
155592	6231	ACTTGTAAAGTTAACACCCT	164812	AGGGTGTTAACTTTACAAGT
155593	6232	CACTTGTAAAGTTAACACCC	164813	GGGTGTTAACTTTACAAGTG
155594	6233	ACACTTGTAAAGTTAACACC	164814	GGTGTTAACTTTACAAGTGT
155595	6234	GACACTTGTAAAGTTAACAC	164815	GTGTTAACTTTACAAGTGTC
155596	6235	TGACACTTGTAAAGTTAACA	164816	TGTTAACTTTACAAGTGTCA
155597	6236	CTGACACTTGTAAAGTTAAC	164817	GTTAACTTTACAAGTGTCAG
155598	6237	TCTGACACTTGTAAAGTTAA	164818	TTAACTTTACAAGTGTCAGA
155599	6238	GTCTGACACTTGTAAAGTTA	164819	TAACTTTACAAGTGTCAGAC
155600	6239	TGTCTGACACTTGTAAAGTT	164820	AACTTTACAAGTGTCAGACA
155601	6240	CTGTCTGACACTTGTAAAGT	164821	ACTTTACAAGTGTCAGACAG
155602	6241	ACTGTCTGACACTTGTAAAG	164822	CTTTACAAGTGTCAGACAGT
155603	6242	TACTGTCTGACACTTGTAAA	164823	TTTACAAGTGTCAGACAGTA
155604	6243	CTACTGTCTGACACTTGTAA	164824	TTACAAGTGTCAGACAGTAG
155605	6244	ACTACTGTCTGACACTTGTA	164825	TACAAGTGTCAGACAGTAGT
155606	6245	AACTACTGTCTGACACTTGT	164826	ACAAGTGTCAGACAGTAGTT
155607	6246	TAACTACTGTCTGACACTTG	164827	CAAGTGTCAGACAGTAGTTA
155608	6247	CTAACTACTGTCTGACACTT	164828	AAGTGTCAGACAGTAGTTAG
155609	6248	TCTAACTACTGTCTGACACT	164829	AGTGTCAGACAGTAGTTAGA
155610	6249	TTCTAACTACTGTCTGACAC	164830	GTGTCAGACAGTAGTTAGAA
155611	6250	GTTCTAACTACTGTCTGACA	164831	TGTCAGACAGTAGTTAGAAC
155612	6251	AGTTCTAACTACTGTCTGAC	164832	GTCAGACAGTAGTTAGAACT
155613	6252	AAGTTCTAACTACTGTCTGA	164833	TCAGACAGTAGTTAGAACTT
155614	6253	CAAGTTCTAACTACTGTCTG	164834	CAGACAGTAGTTAGAACTTG
155615	6254	CCAAGTTCTAACTACTGTCT	164835	AGACAGTAGTTAGAACTTGG
155616	6255	ACCAAGTTCTAACTACTGTC	164836	GACAGTAGTTAGAACTTGGT
155617	6256	CACCAAGTTCTAACTACTGT	164837	ACAGTAGTTAGAACTTGGTG
155618	6257	CCACCAAGTTCTAACTACTG	164838	CAGTAGTTAGAACTTGGTGG
155619	6258	CCCACCAAGTTCTAACTACT	164839	AGTAGTTAGAACTTGGTGGG
155620	6259	CCCCACCAAGTTCTAACTAC	164840	GTAGTTAGAACTTGGTGGGG
155621	6260	ACCCCACCAAGTTCTAACTA	164841	TAGTTAGAACTTGGTGGGGT
155622	6261	AACCCCACCAAGTTCTAACT	164842	AGTTAGAACTTGGTGGGGTT
155623	6262	AAACCCCACCAAGTTCTAAC	164843	GTTAGAACTTGGTGGGGTTT

155624	6263	AAAACCCCACCAAGTTCTAA	164844	TTAGAACTTGGTGGGGTTTT
155625	6264	AAAAACCCCACCAAGTTCTA	164845	TAGAACTTGGTGGGGTTTTT
155626	6265	AAAAAACCCCACCAAGTTCT	164846	AGAACTTGGTGGGGTTTTTT
155627	6266	AAAAAAACCCCACCAAGTTC	164847	GAACTTGGTGGGGTTTTTTT
155628	6267	AAAAAAAACCCCACCAAGTT	164848	AACTTGGTGGGGTTTTTTTT
155629	6268	AAAAAAAAACCCCACCAAGT	164849	ACTTGGTGGGGTTTTTTTTT
155630	6269	AAAAAAAAAACCCCACCAAG	164850	CTTGGTGGGGTTTTTTTTTT
155631	6270	AAAAAAAAAAACCCCACCAA	164851	TTGGTGGGGTTTTTTTTTTT
155632	6271	AAAAAAAAAAAACCCCACCA	164852	TGGTGGGGTTTTTTTTTTTT
155633	6272	AAAAAAAAAAAAACCCCACC	164853	GGTGGGGTTTTTTTTTTTTT
155634	6273	AAAAAAAAAAAAAACCCCAC	164854	GTGGGGTTTTTTTTTTTTTT
155635	6274	AAAAAAAAAAAAAAACCCCA	164855	TGGGGTTTTTTTTTTTTTTT
155636	6275	AAAAAAAAAAAAAAAACCCC	164856	GGGGTTTTTTTTTTTTTTTT
155637	6276	AAAAAAAAAAAAAAAAACCC	164857	GGGTTTTTTTTTTTTTTTTT
155638	6277	AAAAAAAAAAAAAAAAAACC	164858	GGTTTTTTTTTTTTTTTTTT
155639	6278	AAAAAAAAAAAAAAAAAAAC	164859	GTTTTTTTTTTTTTTTTTTT
155640	6279	CAAAAAAAAAAAAAAAAAAA	164860	TTTTTTTTTTTTTTTTTTTG
155641	6280	TCAAAAAAAAAAAAAAAAAA	164861	TTTTTTTTTTTTTTTTTTGA
155642	6281	CTCAAAAAAAAAAAAAAAAA	164862	TTTTTTTTTTTTTTTTTGAG
155643	6282	TCTCAAAAAAAAAAAAAAAA	164863	TTTTTTTTTTTTTTTTGAGA
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155646	6285	CCATCTCAAAAAAAAAAAAA	164866	TTTTTTTTTTTTTGAGATGG
155647	6286	TCCATCTCAAAAAAAAAAAA	164867	TTTTTTTTTTTTGAGATGGA
155648	6287	CTCCATCTCAAAAAAAAAAA	164868	TTTTTTTTTTGAGATGGAG
155649	6288	ACTCCATCTCAAAAAAAAAA	164869	TTTTTTTTTGAGATGGAGT
155650	6289	GACTCCATCTCAAAAAAAAA	164870	TTTTTTTTTGAGATGGAGTC
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155652	6291	AAGACTCCATCTCAAAAAAA	164872	TTTTTTGAGATGGAGTCTT
155653	6292	CAAGACTCCATCTCAAAAAA	164873	TTTTTGAGATGGAGTCTTG
155654	6293	GCAAGACTCCATCTCAAAAA	164874	TTTTTGAGATGGAGTCTTGC
155655	6294	AGCAAGACTCCATCTCAAAA	164875	TTTTGAGATGGAGTCTTGCT
155656	6295	GAGCAAGACTCCATCTCAAA	164876	TTTGAGATGGAGTCTTGCTC
155657	6296	AGAGCAAGACTCCATCTCAA	164877	TTGAGATGGAGTCTTGCTCT
155658	6297	CAGAGCAAGACTCCATCTCA	164878	TGAGATGGAGTCTTGCTCTG
155659	6298	ACAGAGCAAGACTCCATCTC	164879	GAGATGGAGTCTTGCTCTGT
155660	6299	AACAGAGCAAGACTCCATCT	164880	AGATGGAGTCTTGCTCTGTT
155661	6300	CAACAGAGCAAGACTCCATC	164881	GATGGAGTCTTGCTCTGTTG
155662	6301	GCAACAGAGCAAGACTCCAT	164882	ATGGAGTCTTGCTCTGTTGC
155663	6302	GGCAACAGAGCAAGACTCCA	164883	TGGAGTCTTGCTCTGTTGCC
155664	6303	GGGCAACAGAGCAAGACTCC	164884	GGAGTCTTGCTCTGTTGCCC
155665	6304	TGGGCAACAGAGCAAGACTC	164885	GAGTCTTGCTCTGTTGCCCA
155666	6305	CTGGGCAACAGAGCAAGACT	164886	AGTCTTGCTCTGTTGCCCAG
155667	6306	CCTGGGCAACAGAGCAAGAC	164887	GTCTTGCTCTGTTGCCCAGG
155668	6307	GCCTGGGCAACAGAGCAAGA	164888	TCTTGCTCTGTTGCCCAGGC
155669	6308	AGCCTGGGCAACAGAGCAAG	164889	CTTGCTCTGTTGCCCAGGCT
155670	6309	CAGCCTGGGCAACAGAGCAA	164890	TTGCTCTGTTGCCCAGGCTG
155671	6310	CCAGCCTGGGCAACAGAGCA	164891	TGCTCTGTTGCCCAGGCTGG
155672	6311	TCCAGCCTGGGCAACAGAGC	164892	GCTCTGTTGCCCAGGCTGGA
155673	6312	CTCCAGCCTGGGCAACAGAG	164893	CTCTGTTGCCCAGGCTGGAG
155674	6313	ACTCCAGCCTGGGCAACAGA	164894	TCTGTTGCCCAGGCTGGAGT
155675	6314	CACTCCAGCCTGGGCAACAG	164895	CTGTTGCCCAGGCTGGAGTG
155676	6315	GCACTCCAGCCTGGGCAACA	164896	TGTTGCCCAGGCTGGAGTGC
155677	6316	TGCACTCCAGCCTGGGCAAC	164897	GTTGCCCAGGCTGGAGTGCA
155678	6317	CTGCACTCCAGCCTGGGCAA	164898	TTGCCCAGGCTGGAGTGCAG
155679	6318	ACTGCACTCCAGCCTGGGCA	164899	TGCCCAGGCTGGAGTGCAGT
155680	6319	CACTGCACTCCAGCCTGGGC	164900	GCCCAGGCTGGAGTGCAGTG
155681	6320	CCACTGCACTCCAGCCTGGG	164901	CCCAGGCTGGAGTGCAGTGG
155682	6321	ACCACTGCACTCCAGCCTGG	164902	CCAGGCTGGAGTGCAGTGGT
155683	6322	CACCACTGCACTCCAGCCTG	164903	CAGGCTGGAGTGCAGTGGTG
155684	6323	GCACCACTGCACTCCAGCCT	164904	AGGCTGGAGTGCAGTGGTGC
155685	6324	CGCACCACTGCACTCCAGCC	164905	GGCTGGAGTGCAGTGGTGCG
155686	6325	TCGCACCACTGCACTCCAGC	164906	GCTGGAGTGCAGTGGTGCGA
155687	6326	ATCGCACCACTGCACTCCAG	164907	CTGGAGTGCAGTGGTGCGAT
155688	6327	GATCGCACCACTGCACTCCA	164908	TGGAGTGCAGTGGTGCGATC
155689	6328	AGATCGCACCACTGCACTCC	164909	GGAGTGCAGTGGTGCGATCT
155690	6329	GAGATCGCACCACTGCACTC	164910	GAGTGCAGTGGTGCGATCTC
155691	6330	TGAGATCGCACCACTGCACT	164911	AGTGCAGTGGTGCGATCTCA
155692	6331	CTGAGATCGCACCACTGCAC	164912	GTGCAGTGGTGCGATCTCAG
155693	6332	GCTGAGATCGCACCACTGCA	164913	TGCAGTGGTGCGATCTCAGC
155694	6333	AGCTGAGATCGCACCACTGC	164914	GCAGTGGTGCGATCTCAGCT
155695	6334	GAGCTGAGATCGCACCACTG	164915	CAGTGGTGCGATCTCAGCTC

155696	6335	TGAGCTGAGATCGCACCACT	164916	AGTGGTGCGATCTCAGCTCA
155697	6336	GTGAGCTGAGATCGCACCAC	164917	GTGGTGCGATCTCAGCTCAC
155698	6337	AGTGAGCTGAGATCGCACCA	164918	TGGTGCGATCTCAGCTCACT
155699	6338	CAGTGAGCTGAGATCGCACC	164919	GGTGCGATCTCAGCTCACTG
155700	6339	GCAGTGAGCTGAGATCGCAC	164920	GTGCGATCTCAGCTCACTGC
155701	6340	TGCAGTGAGCTGAGATCGCA	164921	TGCGATCTCAGCTCACTGCA
155702	6341	TTGCAGTGAGCTGAGATCGC	164922	GCGATCTCAGCTCACTGCAA
155703	6342	GTTGCAGTGAGCTGAGATCG	164923	CGATCTCAGCTCACTGCAAC
155704	6343	GGTTGCAGTGAGCTGAGATC	164924	GATCTCAGCTCACTGCAACC
155705	6344	AGGTTGCAGTGAGCTGAGAT	164925	ATCTCAGCTCACTGCAACCT
155706	6345	GAGGTTGCAGTGAGCTGAGA	164926	TCTCAGCTCACTGCAACCTC
155707	6346	AGAGGTTGCAGTGAGCTGAG	164927	CTCAGCTCACTGCAACCTCT
155708	6347	CAGAGGTTGCAGTGAGCTGA	164928	TCAGCTCACTGCAACCTCTG
155709	6348	GCAGAGGTTGCAGTGAGCTG	164929	CAGCTCACTGCAACCTCTGC
155710	6349	GGCAGAGGTTGCAGTGAGCT	164930	AGCTCACTGCAACCTCTGCC
155711	6350	AGGCAGAGGTTGCAGTGAGC	164931	GCTCACTGCAACCTCTGCCT
155712	6351	GAGGCAGAGGTTGCAGTGAG	164932	CTCACTGCAACCTCTGCCTC
155713	6352	GGAGGCAGAGGTTGCAGTGA	164933	TCACTGCAACCTCTGCCTCC
155714	6353	GGGAGGCAGAGGTTGCAGTG	164934	CACTGCAACCTCTGCCTCCC
155715	6354	TGGGAGGCAGAGGTTGCAGT	164935	ACTGCAACCTCTGCCTCCCA
155716	6355	CTGGGAGGCAGAGGTTGCAG	164936	CTGCAACCTCTGCCTCCCAG
155717	6356	CCTGGGAGGCAGAGGTTGCA	164937	TGCAACCTCTGCCTCCCAGG
155718	6357	ACCTGGGAGGCAGAGGTTGC	164938	GCAACCTCTGCCTCCCAGGT
155719	6358	AACCTGGGAGGCAGAGGTTG	164939	CAACCTCTGCCTCCCAGGTT
155720	6359	GAACCTGGGAGGCAGAGGTT	164940	AACCTCTGCCTCCCAGGTTC
155721	6360	TGAACCTGGGAGGCAGAGGT	164941	ACCTCTGCCTCCCAGGTTCA
155722	6361	TTGAACCTGGGAGGCAGAGG	164942	CCTCTGCCTCCCAGGTTCAA
155723	6362	CTTGAACCTGGGAGGCAGAG	164943	CTCTGCCTCCCAGGTTCAAG
155724	6363	GCTTGAACCTGGGAGGCAGA	164944	TCTGCCTCCCAGGTTCAAGC
155725	6364	CGCTTGAACCTGGGAGGCAG	164945	CTGCCTCCCAGGTTCAAGCG
155726	6365	TCGCTTGAACCTGGGAGGCA	164946	TGCCTCCCAGGTTCAAGCGA
155727	6366	ATCGCTTGAACCTGGGAGGC	164947	GCCTCCCAGGTTCAAGCGAT
155728	6367	AATCGCTTGAACCTGGGAGG	164948	CCTCCCAGGTTCAAGCGATT
155729	6368	GAATCGCTTGAACCTGGGAG	164949	CTCCCAGGTTCAAGCGATTC
155730	6369	AGAATCGCTTGAACCTGGGA	164950	TCCCAGGTTCAAGCGATTCT
155731	6370	GAGAATCGCTTGAACCTGGG	164951	CCCAGGTTCAAGCGATTCTC
155732	6371	GGAGAATCGCTTGAACCTGG	164952	CCAGGTTCAAGCGATTCTCC
155733	6372	AGGAGAATCGCTTGAACCTG	164953	CAGGTTCAAGCGATTCTCCT
155734	6373	CAGGAGAATCGCTTGAACCT	164954	AGGTTCAAGCGATTCTCCTG
155735	6374	GCAGGAGAATCGCTTGAACC	164955	GGTTCAAGCGATTCTCCTGC
155736	6375	GGCAGGAGAATCGCTTGAAC	164956	GTTCAAGCGATTCTCCTGCC
155737	6376	AGGCAGGAGAATCGCTTGAA	164957	TTCAAGCGATTCTCCTGCCT
155738	6377	GAGGCAGGAGAATCGCTTGA	164958	TCAAGCGATTCTCCTGCCTC
155739	6378	TGAGGCAGGAGAATCGCTTG	164959	CAAGCGATTCTCCTGCCTCA
155740	6379	CTGAGGCAGGAGAATCGCTT	164960	AAGCGATTCTCCTGCCTCAG
155741	6380	GCTGAGGCAGGAGAATCGCT	164961	AGCGATTCTCCTGCCTCAGC
155742	6381	GGCTGAGGCAGGAGAATCGC	164962	GCGATTCTCCTGCCTCAGCC
155743	6382	AGGCTGAGGCAGGAGAATCG	164963	CGATTCTCCTGCCTCAGCCT
155744	6383	TAGGCTGAGGCAGGAGAATC	164964	GATTCTCCTGCCTCAGCCTA
155745	6384	GTAGGCTGAGGCAGGAGAAT	164965	ATTCTCCTGCCTCAGCCTAC
155746	6385	AGTAGGCTGAGGCAGGAGAA	164966	TTCTCCTGCCTCAGCCTACT
155747	6386	TAGTAGGCTGAGGCAGGAGA	164967	TCTCCTGCCTCAGCCTACTA
155748	6387	TTAGTAGGCTGAGGCAGGAG	164968	CTCCTGCCTCAGCCTACTAA
155749	6388	CTTAGTAGGCTGAGGCAGGA	164969	TCCTGCCTCAGCCTACTAAG
155750	6389	ACTTAGTAGGCTGAGGCAGG	164970	CCTGCCTCAGCCTACTAAGT
155751	6390	TACTTAGTAGGCTGAGGCAG	164971	CTGCCTCAGCCTACTAAGTA
155752	6391	CTACTTAGTAGGCTGAGGCA	164972	TGCCTCAGCCTACTAAGTAG
155753	6392	GCTACTTAGTAGGCTGAGGC	164973	GCCTCAGCCTACTAAGTAGC
155754	6393	AGCTACTTAGTAGGCTGAGG	164974	CCTCAGCCTACTAAGTAGCT
155755	6394	CAGCTACTTAGTAGGCTGAG	164975	CTCAGCCTACTAAGTAGCTG
155756	6395	CCAGCTACTTAGTAGGCTGA	164976	TCAGCCTACTAAGTAGCTGG
155757	6396	CCCAGCTACTTAGTAGGCTG	164977	CAGCCTACTAAGTAGCTGGG
155758	6397	TCCCAGCTACTTAGTAGGCT	164978	AGCCTACTAAGTAGCTGGGA
155759	6398	GTCCCAGCTACTTAGTAGGC	164979	GCCTACTAAGTAGCTGGGAC
155760	6399	AGTCCCAGCTACTTAGTAGG	164980	CCTACTAAGTAGCTGGGACT
155761	6400	TAGTCCCAGCTACTTAGTAG	164981	CTACTAAGTAGCTGGGACTA
155762	6401	ATAGTCCCAGCTACTTAGTA	164982	TACTAAGTAGCTGGGACTAT
155763	6402	TATAGTCCCAGCTACTTAGT	164983	ACTAAGTAGCTGGGACTATA
155764	6403	CTATAGTCCCAGCTACTTAG	164984	CTAAGTAGCTGGGACTATAG
155765	6404	CCTATAGTCCCAGCTACTTA	164985	TAAGTAGCTGGGACTATAGG
155766	6405	ACCTATAGTCCCAGCTACTT	164986	AAGTAGCTGGGACTATAGGT
155767	6406	CACCTATAGTCCCAGCTACT	164987	AGTAGCTGGGACTATAGGTG

155768	6407	GCACCTATAGTCCCAGCTAC	164988	GTAGCTGGGACTATAGGTGC
155769	6408	CGCACCTATAGTCCCAGCTA	164989	TAGCTGGGACTATAGGTGCG
155770	6409	GCGCACCTATAGTCCCAGCT	164990	AGCTGGGACTATAGGTGCGC
155771	6410	TGCGCACCTATAGTCCCAGC	164991	GCTGGGACTATAGGTGCGCA
155772	6411	GTGCGCACCTATAGTCCCAG	164992	CTGGGACTATAGGTGCGCAC
155773	6412	GGTGCGCACCTATAGTCCCA	164993	TGGGACTATAGGTGCGCACC
155774	6413	TGGTGCGCACCTATAGTCCC	164994	GGGACTATAGGTGCGCACCA
155775	6414	GTGGTGCGCACCTATAGTCC	164995	GGACTATAGGTGCGCACCAC
155776	6415	GGTGGTGCGCACCTATAGTC	164996	GACTATAGGTGCGCACCACC
155777	6416	TGGTGGTGCGCACCTATAGT	164997	ACTATAGGTGCGCACCACCA
155778	6417	GTGGTGGTGCGCACCTATAG	164998	CTATAGGTGCGCACCACCAC
155779	6418	CGTGGTGGTGCGCACCTATA	164999	TATAGGTGCGCACCACCACG
155780	6419	GCGTGGTGGTGCGCACCTAT	165000	ATAGGTGCGCACCACCACGC
155781	6420	GGCGTGGTGGTGCGCACCTA	165001	TAGGTGCGCACCACCACGCC
155782	6421	AGGCGTGGTGGTGCGCACCT	165002	AGGTGCGCACCACCACGCCT
155783	6422	TAGGCGTGGTGGTGCGCACC	165003	GGTGCGCACCACCACGCCTA
155784	6423	CTAGGCGTGGTGGTGCGCAC	165004	GTGCGCACCACCACGCCTAG
155785	6424	GCTAGGCGTGGTGGTGCGCA	165005	TGCGCACCACCACGCCTAGC
155786	6425	AGCTAGGCGTGGTGGTGCGC	165006	GCGCACCACCACGCCTAGCT
155787	6426	TAGCTAGGCGTGGTGGTGCG	165007	CGCACCACCACGCCTAGCTA
155788	6427	TTAGCTAGGCGTGGTGGTGC	165008	GCACCACCACGCCTAGCTAA
155789	6428	ATTAGCTAGGCGTGGTGGTG	165009	CACCACCACGCCTAGCTAAT
155790	6429	AATTAGCTAGGCGTGGTGGT	165010	ACCACCACGCCTAGCTAATT
155791	6430	AAATTAGCTAGGCGTGGTGG	165011	CCACCACGCCTAGCTAATTT
155792	6431	AAAATTAGCTAGGCGTGGTG	165012	CACCACGCCTAGCTAATTTT
155793	6432	AAAAATTAGCTAGGCGTGGT	165013	ACCACGCCTAGCTAATTTTT
155794	6433	CAAAAATTAGCTAGGCGTGG	165014	CCACGCCTAGCTAATTTTTG
155795	6434	ACAAAAATTAGCTAGGCGTG	165015	CACGCCTAGCTAATTTTTGT
155796	6435	TACAAAAATTAGCTAGGCGT	165016	ACGCCTAGCTAATTTTTGTA
155797	6436	ATACAAAAATTAGCTAGGCG	165017	CGCCTAGCTAATTTTTGTAT
155798	6437	AATACAAAAATTAGCTAGGC	165018	GCCTAGCTAATTTTTGTATT
155799	6438	AAATACAAAAATTAGCTAGG	165019	CCTAGCTAATTTTTGTATTT
155800	6439	AAAATACAAAAATTAGCTAG	165020	CTAGCTAATTTTTGTATTTT
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155802	6441	AAAAAATACAAAAATTAGCT	165022	AGCTAATTTTTGTATTTTTT
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155804	6443	TGAAAAAATACAAAAATTAG	165024	CTAATTTTTGTATTTTTTCA
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155807	6446	TACTGAAAAAATACAAAAAT	165027	ATTTTTGTATTTTTTCAGTA
155808	6447	CTACTGAAAAAATACAAAAA	165028	TTTTTGTATTTTTTCAGTAG
155809	6448	TCTACTGAAAAAATACAAAA	165029	TTTTGTATTTTTTCAGTAGA
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155811	6450	TCTCTACTGAAAAAATACAA	165031	TTGTATTTTTTCAGTAGAGA
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155815	6454	CCTGTCTCTACTGAAAAAAT	165035	ATTTTTTCAGTAGAGACAGG
155816	6455	CCCTGTCTCTACTGAAAAAA	165036	TTTTTTCAGTAGAGACAGGG
155817	6456	ACCCTGTCTCTACTGAAAAA	165037	TTTTTCAGTAGAGACAGGGT
155818	6457	AACCCTGTCTCTACTGAAAA	165038	TTTTCAGTAGAGACAGGGTT
155819	6458	AAACCCTGTCTCTACTGAAA	165039	TTTCAGTAGAGACAGGGTTT
155820	6459	AAAACCCTGTCTCTACTGAA	165040	TTCAGTAGAGACAGGGTTTT
155821	6460	CAAAACCCTGTCTCTACTGA	165041	TCAGTAGAGACAGGGTTTTG
155822	6461	GCAAAACCCTGTCTCTACTG	165042	CAGTAGAGACAGGGTTTTGC
155823	6462	AGCAAAACCCTGTCTCTACT	165043	AGTAGAGACAGGGTTTTGCT
155824	6463	TAGCAAAACCCTGTCTCTAC	165044	GTAGAGACAGGGTTTTGCTA
155825	6464	ATAGCAAAACCCTGTCTCTA	165045	TAGAGACAGGGTTTTGCTAT
155826	6465	CATAGCAAAACCCTGTCTCT	165046	AGAGACAGGGTTTTGCTATG
155827	6466	GCATAGCAAAACCCTGTCTC	165047	GAGACAGGGTTTTGCTATGC
155828	6467	AGCATAGCAAAACCCTGTCT	165048	AGACAGGGTTTTGCTATGCT
155829	6468	CAGCATAGCAAAACCCTGTC	165049	GACAGGGTTTTGCTATGCTG
155830	6469	CCAGCATAGCAAAACCCTGT	165050	ACAGGGTTTTGCTATGCTGG
155831	6470	GCCAGCATAGCAAAACCCTG	165051	CAGGGTTTTGCTATGCTGGC
155832	6471	GGCCAGCATAGCAAAACCCT	165052	AGGGTTTTGCTATGCTGGCC
155833	6472	TGGCCAGCATAGCAAAACCC	165053	GGGTTTTGCTATGCTGGCCA
155834	6473	CTGGCCAGCATAGCAAAACC	165054	GGTTTTGCTATGCTGGCCAG
155835	6474	CCTGGCCAGCATAGCAAAAC	165055	GTTTTGCTATGCTGGCCAGG
155836	6475	GCCTGGCCAGCATAGCAAAA	165056	TTTTGCTATGCTGGCCAGGC
155837	6476	AGCCTGGCCAGCATAGCAAA	165057	TTTGCTATGCTGGCCAGGCT
155838	6477	CAGCCTGGCCAGCATAGCAA	165058	TTGCTATGCTGGCCAGGCTG
155839	6478	CCAGCCTGGCCAGCATAGCA	165059	TGCTATGCTGGCCAGGCTGG

155840	6479	ACCAGCCTGGCCAGCATAGC	165060	GCTATGCTGGCCAGGCTGGT
155841	6480	GACCAGCCTGGCCAGCATAG	165061	CTATGCTGGCCAGGCTGGTC
155842	6481	AGACCAGCCTGGCCAGCATA	165062	TATGCTGGCCAGGCTGGTCT
155843	6482	GAGACCAGCCTGGCCAGCAT	165063	ATGCTGGCCAGGCTGGTCTC
155844	6483	TGAGACCAGCCTGGCCAGCA	165064	TGCTGGCCAGGCTGGTCTCA
155845	6484	TTGAGACCAGCCTGGCCAGC	165065	GCTGGCCAGGCTGGTCTCAA
155846	6485	TTTGAGACCAGCCTGGCCAG	165066	CTGGCCAGGCTGGTCTCAAA
155847	6486	GTTTGAGACCAGCCTGGCCA	165067	TGGCCAGGCTGGTCTCAAAC
155848	6487	AGTTTGAGACCAGCCTGGCC	165068	GGCCAGGCTGGTCTCAAACT
155849	6488	GAGTTTGAGACCAGCCTGGC	165069	GCCAGGCTGGTCTCAAACTC
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155851	6490	AGGAGTTTGAGACCAGCCTG	165071	CAGGCTGGTCTCAAACTCCT
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155853	6492	TCAGGAGTTTGAGACCAGCC	165073	GGCTGGTCTCAAACTCCTGA
155854	6493	GTCAGGAGTTTGAGACCAGC	165074	GCTGGTCTCAAACTCCTGAC
155855	6494	GGTCAGGAGTTTGAGACCAG	165075	CTGGTCTCAAACTCCTGACC
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155858	6497	TGAGGTCAGGAGTTTGAGAC	165078	GTCTCAAACTCCTGACCTCA
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155860	6499	TCTGAGGTCAGGAGTTTGAG	165080	CTCAAACTCCTGACCTCAGA
155861	6500	ATCTGAGGTCAGGAGTTTGA	165081	TCAAACTCCTGACCTCAGAT
155862	6501	CATCTGAGGTCAGGAGTTTG	165082	CAAACTCCTGACCTCAGATG
155863	6502	TCATCTGAGGTCAGGAGTTT	165083	AAACTCCTGACCTCAGATGA
155864	6503	ATCATCTGAGGTCAGGAGTT	165084	AACTCCTGACCTCAGATGAT
155865	6504	GATCATCTGAGGTCAGGAGT	165085	ACTCCTGACCTCAGATGATC
155866	6505	GGATCATCTGAGGTCAGGAG	165086	CTCCTGACCTCAGATGATCC
155867	6506	TGGATCATCTGAGGTCAGGA	165087	TCCTGACCTCAGATGATCCA
155868	6507	CTGGATCATCTGAGGTCAGG	165088	CCTGACCTCAGATGATCCAG
155869	6508	GCTGGATCATCTGAGGTCAG	165089	CTGACCTCAGATGATCCAGC
155870	6509	GGCTGGATCATCTGAGGTCA	165090	TGACCTCAGATGATCCAGCC
155871	6510	TGGCTGGATCATCTGAGGTC	165091	GACCTCAGATGATCCAGCCA
155872	6511	GTGGCTGGATCATCTGAGGT	165092	ACCTCAGATGATCCAGCCAC
155873	6512	GGTGGCTGGATCATCTGAGG	165093	CCTCAGATGATCCAGCCACC
155874	6513	AGGTGGCTGGATCATCTGAG	165094	CTCAGATGATCCAGCCACCT
155875	6514	GAGGTGGCTGGATCATCTGA	165095	TCAGATGATCCAGCCACCTC
155876	6515	TGAGGTGGCTGGATCATCTG	165096	CAGATGATCCAGCCACCTCA
155877	6516	CTGAGGTGGCTGGATCATCT	165097	AGATGATCCAGCCACCTCAG
155878	6517	GCTGAGGTGGCTGGATCATC	165098	GATGATCCAGCCACCTCAGC
155879	6518	AGCTGAGGTGGCTGGATCAT	165099	ATGATCCAGCCACCTCAGCT
155880	6519	AAGCTGAGGTGGCTGGATCA	165100	TGATCCAGCCACCTCAGCTT
155881	6520	GAAGCTGAGGTGGCTGGATC	165101	GATCCAGCCACCTCAGCTTC
155882	6521	GGAAGCTGAGGTGGCTGGAT	165102	ATCCAGCCACCTCAGCTTCC
155883	6522	GGGAAGCTGAGGTGGCTGGA	165103	TCCAGCCACCTCAGCTTCCC
155884	6523	TGGGAAGCTGAGGTGGCTGG	165104	CCAGCCACCTCAGCTTCCCA
155885	6524	TTGGGAAGCTGAGGTGGCTG	165105	CAGCCACCTCAGCTTCCCAA
155886	6525	TTTGGGAAGCTGAGGTGGCT	165106	AGCCACCTCAGCTTCCCAAA
155887	6526	CTTTGGGAAGCTGAGGTGGC	165107	GCCACCTCAGCTTCCCAAAG
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155889	6528	CACTTTGGGAAGCTGAGGTG	165109	CACCTCAGCTTCCCAAAGTG
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155891	6530	AGCACTTTGGGAAGCTGAGG	165111	CCTCAGCTTCCCAAAGTGCT
155892	6531	CAGCACTTTGGGAAGCTGAG	165112	CTCAGCTTCCCAAAGTGCTG
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155896	6535	ACCCCAGCACTTTGGGAAGC	165116	GCTTCCCAAAGTGCTGGGGT
155897	6536	AACCCCAGCACTTTGGGAAG	165117	CTTCCCAAAGTGCTGGGGTT
155898	6537	GAACCCCAGCACTTTGGGAA	165118	TTCCCAAAGTGCTGGGGTTC
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155902	6541	CCTGGAACCCCAGCACTTTG	165122	CAAAGTGCTGGGGTTCCAGG
155903	6542	ACCTGGAACCCCAGCACTTT	165123	AAAGTGCTGGGGTTCCAGGT
155904	6543	CACCTGGAACCCCAGCACTT	165124	AAGTGCTGGGGTTCCAGGTG
155905	6544	ACACCTGGAACCCCAGCACT	165125	AGTGCTGGGGTTCCAGGTGT
155906	6545	AACACCTGGAACCCCAGCAC	165126	GTGCTGGGGTTCCAGGTGTT
155907	6546	TAACACCTGGAACCCCAGCA	165127	TGCTGGGGTTCCAGGTGTTA
155908	6547	CTAACACCTGGAACCCCAGC	165128	GCTGGGGTTCCAGGTGTTAG
155909	6548	GCTAACACCTGGAACCCCAG	165129	CTGGGGTTCCAGGTGTTAGC
155910	6549	GGCTAACACCTGGAACCCCA	165130	TGGGGTTCCAGGTGTTAGCC
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155912	6551	GTGGCTAACACCTGGAACCC	165132	GGGTTCCAGGTGTTAGCCAC
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155914	6553	TGGTGGCTAACACCTGGAAC	165134	GTTCCAGGTGTTAGCCACCA
155915	6554	ATGGTGGCTAACACCTGGAA	165135	TTCCAGGTGTTAGCCACCAT
155916	6555	CATGGTGGCTAACACCTGGA	165136	TCCAGGTGTTAGCCACCATG
155917	6556	GCATGGTGGCTAACACCTGG	165137	CCAGGTGTTAGCCACCATGC
155918	6557	GGCATGGTGGCTAACACCTG	165138	CAGGTGTTAGCCACCATGCC
155919	6558	AGGCATGGTGGCTAACACCT	165139	AGGTGTTAGCCACCATGCCT
155920	6559	CAGGCATGGTGGCTAACACC	165140	GGTGTTAGCCACCATGCCTG
155921	6560	CCAGGCATGGTGGCTAACAC	165141	GTGTTAGCCACCATGCCTGG
155922	6561	GCCAGGCATGGTGGCTAACA	165142	TGTTAGCCACCATGCCTGGC
155923	6562	GGCCAGGCATGGTGGCTAAC	165143	GTTAGCCACCATGCCTGGCC
155924	6563	TGGCCAGGCATGGTGGCTAA	165144	TTAGCCACCATGCCTGGCCA
155925	6564	ATGGCCAGGCATGGTGGCTA	165145	TAGCCACCATGCCTGGCCAT
155926	6565	TATGGCCAGGCATGGTGGCT	165146	AGCCACCATGCCTGGCCATA
155927	6566	CTATGGCCAGGCATGGTGGC	165147	GCCACCATGCCTGGCCATAG
155928	6567	TCTATGGCCAGGCATGGTGG	165148	CCACCATGCCTGGCCATAGA
155929	6568	GTCTATGGCCAGGCATGGTG	165149	CACCATGCCTGGCCATAGAC
155930	6569	AGTCTATGGCCAGGCATGGT	165150	ACCATGCCTGGCCATAGACT
155931	6570	AAGTCTATGGCCAGGCATGG	165151	CCATGCCTGGCCATAGACTT
155932	6571	CAAGTCTATGGCCAGGCATG	165152	CATGCCTGGCCATAGACTTG
155933	6572	ACAAGTCTATGGCCAGGCAT	165153	ATGCCTGGCCATAGACTTGT
155934	6573	AACAAGTCTATGGCCAGGCA	165154	TGCCTGGCCATAGACTTGTT
155935	6574	AAACAAGTCTATGGCCAGGC	165155	GCCTGGCCATAGACTTGTTT
155936	6575	GAAACAAGTCTATGGCCAGG	165156	CCTGGCCATAGACTTGTTTC
155937	6576	AGAAACAAGTCTATGGCCAG	165157	CTGGCCATAGACTTGTTTCT
155938	6577	CAGAAACAAGTCTATGGCCA	165158	TGGCCATAGACTTGTTTCTG
155939	6578	ACAGAAACAAGTCTATGGCC	165159	GGCCATAGACTTGTTTCTGT
155940	6579	AACAGAAACAAGTCTATGGC	165160	GCCATAGACTTGTTTCTGTT
155941	6580	GAACAGAAACAAGTCTATGG	165161	CCATAGACTTGTTTCTGTTC
155942	6581	GGAACAGAAACAAGTCTATG	165162	CATAGACTTGTTTCTGTTCC
155943	6582	GGGAACAGAAACAAGTCTAT	165163	ATAGACTTGTTTCTGTTCCC
155944	6583	AGGGAACAGAAACAAGTCTA	165164	TAGACTTGTTTCTGTTCCCT
155945	6584	AAGGGAACAGAAACAAGTCT	165165	AGACTTGTTTCTGTTCCCTT
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155947	6586	AGAAGGGAACAGAAACAAGT	165167	ACTTGTTTCTGTTCCCTTCT
155948	6587	GAGAAGGGAACAGAAACAAG	165168	CTTGTTTCTGTTCCCTTCTC
155949	6588	TGAGAAGGGAACAGAAACAA	165169	TTGTTTCTGTTCCCTTCTCA
155950	6589	GTGAGAAGGGAACAGAAACA	165170	TGTTTCTGTTCCCTTCTCAC
155951	6590	AGTGAGAAGGGAACAGAAAC	165171	GTTTCTGTTCCCTTCTCACT
155952	6591	CAGTGAGAAGGGAACAGAAA	165172	TTTCTGTTCCCTTCTCACTG
155953	6592	ACAGTGAGAAGGGAACAGAA	165173	TTCTGTTCCCTTCTCACTGT
155954	6593	CACAGTGAGAAGGGAACAGA	165174	TCTGTTCCCTTCTCACTGTG
155955	6594	CCACAGTGAGAAGGGAACAG	165175	CTGTTCCCTTCTCACTGTGG
155956	6595	GCCACAGTGAGAAGGGAACA	165176	TGTTCCCTTCTCACTGTGGC
155957	6596	AGCCACAGTGAGAAGGGAAC	165177	GTTCCCTTCTCACTGTGGCT
155958	6597	CAGCCACAGTGAGAAGGGAA	165178	TTCCCTTCTCACTGTGGCTG
155959	6598	ACAGCCACAGTGAGAAGGGA	165179	TCCCTTCTCACTGTGGCTGT
155960	6599	TACAGCCACAGTGAGAAGGG	165180	CCCTTCTCACTGTGGCTGTA
155961	6600	GTACAGCCACAGTGAGAAGG	165181	CCTTCTCACTGTGGCTGTAC
155962	6601	GGTACAGCCACAGTGAGAAG	165182	CTTCTCACTGTGGCTGTACC
155963	6602	TGGTACAGCCACAGTGAGAA	165183	TTCTCACTGTGGCTGTACCA
155964	6603	TTGGTACAGCCACAGTGAGA	165184	TCTCACTGTGGCTGTACCAA
155965	6604	CTTGGTACAGCCACAGTGAG	165185	CTCACTGTGGCTGTACCAAG
155966	6605	CCTTGGTACAGCCACAGTGA	165186	TCACTGTGGCTGTACCAAGG
155967	6606	ACCTTGGTACAGCCACAGTG	165187	CACTGTGGCTGTACCAAGGT
155968	6607	CACCTTGGTACAGCCACAGT	165188	ACTGTGGCTGTACCAAGGTG
155969	6608	ACACCTTGGTACAGCCACAG	165189	CTGTGGCTGTACCAAGGTGT
155970	6609	AACACCTTGGTACAGCCACA	165190	TGTGGCTGTACCAAGGTGTT
155971	6610	CAACACCTTGGTACAGCCAC	165191	GTGGCTGTACCAAGGTGTTG
155972	6611	GCAACACCTTGGTACAGCCA	165192	TGGCTGTACCAAGGTGTTGC
155973	6612	AGCAACACCTTGGTACAGCC	165193	GGCTGTACCAAGGTGTTGCT
155974	6613	AAGCAACACCTTGGTACAGC	165194	GCTGTACCAAGGTGTTGCTT
155975	6614	TAAGCAACACCTTGGTACAG	165195	CTGTACCAAGGTGTTGCTTA
155976	6615	ATAAGCAACACCTTGGTACA	165196	TGTACCAAGGTGTTGCTTAT
155977	6616	GATAAGCAACACCTTGGTAC	165197	GTACCAAGGTGTTGCTTATC
155978	6617	GGATAAGCAACACCTTGGTA	165198	TACCAAGGTGTTGCTTATCC
155979	6618	GGGATAAGCAACACCTTGGT	165199	ACCAAGGTGTTGCTTATCCC
155980	6619	TGGGATAAGCAACACCTTGG	165200	CCAAGGTGTTGCTTATCCCA
155981	6620	CTGGGATAAGCAACACCTTG	165201	CAAGGTGTTGCTTATCCCAG
155982	6621	TCTGGGATAAGCAACACCTT	165202	AAGGTGTTGCTTATCCCAGA
155983	6622	TTCTGGGATAAGCAACACCT	165203	AGGTGTTGCTTATCCCAGAA

155984	6623	CTTCTGGGATAAGCAACACC	165204	GGTGTTGCTTATCCCAGAAG
155985	6624	ACTTCTGGGATAAGCAACAC	165205	GTGTTGCTTATCCCAGAAGT
155986	6625	GACTTCTGGGATAAGCAACA	165206	TGTTGCTTATCCCAGAAGTC
155987	6626	CGACTTCTGGGATAAGCAAC	165207	GTTGCTTATCCCAGAAGTCG
155988	6627	ACGACTTCTGGGATAAGCAA	165208	TTGCTTATCCCAGAAGTCGT
155989	6628	CACGACTTCTGGGATAAGCA	165209	TGCTTATCCCAGAAGTCGTG
155990	6629	TCACGACTTCTGGGATAAGC	165210	GCTTATCCCAGAAGTCGTGA
155991	6630	ATCACGACTTCTGGGATAAG	165211	CTTATCCCAGAAGTCGTGAT
155992	6631	CATCACGACTTCTGGGATAA	165212	TTATCCCAGAAGTCGTGATG
155993	6632	GCATCACGACTTCTGGGATA	165213	TATCCCAGAAGTCGTGATGC
155994	6633	TGCATCACGACTTCTGGGAT	165214	ATCCCAGAAGTCGTGATGCA
155995	6634	CTGCATCACGACTTCTGGGA	165215	TCCCAGAAGTCGTGATGCAG
155996	6635	CCTGCATCACGACTTCTGGG	165216	CCCAGAAGTCGTGATGCAGG
155997	6636	ACCTGCATCACGACTTCTGG	165217	CCAGAAGTCGTGATGCAGGT
155998	6637	GACCTGCATCACGACTTCTG	165218	CAGAAGTCGTGATGCAGGTC
155999	6638	TGACCTGCATCACGACTTCT	165219	AGAAGTCGTGATGCAGGTCA
156000	6639	CTGACCTGCATCACGACTTC	165220	GAAGTCGTGATGCAGGTCAG
156001	6640	GCTGACCTGCATCACGACTT	165221	AAGTCGTGATGCAGGTCAGC
156002	6641	TGCTGACCTGCATCACGACT	165222	AGTCGTGATGCAGGTCAGCA
156003	6642	GTGCTGACCTGCATCACGAC	165223	GTCGTGATGCAGGTCAGCAC
156004	6643	AGTGCTGACCTGCATCACGA	165224	TCGTGATGCAGGTCAGCACT
156005	6644	AAGTGCTGACCTGCATCACG	165225	CGTGATGCAGGTCAGCACTT
156006	6645	AAAGTGCTGACCTGCATCAC	165226	GTGATGCAGGTCAGCACTTT
156007	6646	GAAAGTGCTGACCTGCATCA	165227	TGATGCAGGTCAGCACTTTC
156008	6647	AGAAAGTGCTGACCTGCATC	165228	GATGCAGGTCAGCACTTTCT
156009	6648	GAGAAAGTGCTGACCTGCAT	165229	ATGCAGGTCAGCACTTTCTC
156010	6649	GGAGAAAGTGCTGACCTGCA	165230	TGCAGGTCAGCACTTTCTCC
156011	6650	TGGAGAAAGTGCTGACCTGC	165231	GCAGGTCAGCACTTTCTCCA
156012	6651	ATGGAGAAAGTGCTGACCTG	165232	CAGGTCAGCACTTTCTCCAT
156013	6652	CATGGAGAAAGTGCTGACCT	165233	AGGTCAGCACTTTCTCCATG
156014	6653	CCATGGAGAAAGTGCTGACC	165234	GGTCAGCACTTTCTCCATGG
156015	6654	CCCATGGAGAAAGTGCTGAC	165235	GTCAGCACTTTCTCCATGGG
156016	6655	TCCCATGGAGAAAGTGCTGA	165236	TCAGCACTTTCTCCATGGGA
156017	6656	TTCCCATGGAGAAAGTGCTG	165237	CAGCACTTTCTCCATGGGAA
156018	6657	CTTCCCATGGAGAAAGTGCT	165238	AGCACTTTCTCCATGGGAAG
156019	6658	ACTTCCCATGGAGAAAGTGC	165239	GCACTTTCTCCATGGGAAGT
156020	6659	AACTTCCCATGGAGAAAGTG	165240	CACTTTCTCCATGGGAAGTT
156021	6660	AAACTTCCCATGGAGAAAGT	165241	ACTTTCTCCATGGGAAGTTT
156022	6661	AAAACTTCCCATGGAGAAAG	165242	CTTTCTCCATGGGAAGTTTT
156023	6662	TAAAACTTCCCATGGAGAAA	165243	TTTCTCCATGGGAAGTTTTA
156024	6663	CTAAAACTTCCCATGGAGAA	165244	TTCTCCATGGGAAGTTTTAG
156025	6664	GCTAAAACTTCCCATGGAGA	165245	TCTCCATGGGAAGTTTTAGC
156026	6665	TGCTAAAACTTCCCATGGAG	165246	CTCCATGGGAAGTTTTAGCA
156027	6666	CTGCTAAAACTTCCCATGGA	165247	TCCATGGGAAGTTTTAGCAG
156028	6667	ACTGCTAAAACTTCCCATGG	165248	CCATGGGAAGTTTTAGCAGT
156029	6668	CACTGCTAAAACTTCCCATG	165249	CATGGGAAGTTTTAGCAGTG
156030	6669	ACACTGCTAAAACTTCCCAT	165250	ATGGGAAGTTTTAGCAGTGT
156031	6670	AACACTGCTAAAACTTCCCA	165251	TGGGAAGTTTTAGCAGTGTT
156032	6671	AAACACTGCTAAAACTTCCC	165252	GGGAAGTTTTAGCAGTGTTT
156033	6672	GAAACACTGCTAAAACTTCC	165253	GGAAGTTTTAGCAGTGTTTC
156034	6673	AGAAACACTGCTAAAACTTC	165254	GAAGTTTTAGCAGTGTTTCT
156035	6674	AAGAAACACTGCTAAAACTT	165255	AAGTTTTAGCAGTGTTTCTT
156036	6675	AAAGAAACACTGCTAAAACT	165256	AGTTTTAGCAGTGTTTCTTT
156037	6676	AAAAGAAACACTGCTAAAAC	165257	GTTTTAGCAGTGTTTCTTTT
156038	6677	AAAAAGAAACACTGCTAAAA	165258	TTTTAGCAGTGTTTCTTTTT
156039	6678	TAAAAAGAAACACTGCTAAA	165259	TTTAGCAGTGTTTCTTTTTA
156040	6679	CTAAAAAGAAACACTGCTAA	165260	TTAGCAGTGTTTCTTTTTAG
156041	6680	TCTAAAAAGAAACACTGCTA	165261	TAGCAGTGTTTCTTTTTAGA
156042	6681	TTCTAAAAAGAAACACTGCT	165262	AGCAGTGTTTCTTTTTAGAA
156043	6682	ATTCTAAAAAGAAACACTGC	165263	GCAGTGTTTCTTTTTAGAAT
156044	6683	CATTCTAAAAAGAAACACTG	165264	CAGTGTTTCTTTTTAGAATG
156045	6684	ACATTCTAAAAAGAAACACT	165265	AGTGTTTCTTTTTAGAATGT
156046	6685	TACATTCTAAAAAGAAACAC	165266	GTGTTTCTTTTTAGAATGTA
156047	6686	ATACATTCTAAAAAGAAACA	165267	TGTTTCTTTTTAGAATGTAT
156048	6687	AATACATTCTAAAAAGAAAC	165268	GTTTCTTTTTAGAATGTATT
156049	6688	AAATACATTCTAAAAAGAAA	165269	TTTCTTTTTAGAATGTATTT
156050	6689	CAAATACATTCTAAAAAGAA	165270	TTCTTTTTAGAATGTATTTG
156051	6690	CCAAATACATTCTAAAAAGA	165271	TCTTTTTAGAATGTATTTGG
156052	6691	CCCAAATACATTCTAAAAAG	165272	CTTTTTAGAATGTATTTGGG
156053	6692	TCCCAAATACATTCTAAAAA	165273	TTTTTAGAATGTATTTGGGA
156054	6693	TTCCCAAATACATTCTAAAA	165274	TTTTAGAATGTATTTGGGAA
156055	6694	GTTCCCAAATACATTCTAAA	165275	TTTAGAATGTATTTGGGAAC

156056	6695	AGTTCCCAAATACATTCTAA	165276	TTAGAATGTATTTGGGAACT
156057	6696	AAGTTCCCAAATACATTCTA	165277	TAGAATGTATTTGGGAACTT
156058	6697	AAAGTTCCCAAATACATTCT	165278	AGAATGTATTTGGGAACTTT
156059	6698	TAAAGTTCCCAAATACATTC	165279	GAATGTATTTGGGAACTTTA
156060	6699	TTAAAGTTCCCAAATACATT	165280	AATGTATTTGGGAACTTTAA
156061	6700	ATTAAAGTTCCCAAATACAT	165281	ATGTATTTGGGAACTTTAAT
156062	6701	AATTAAAGTTCCCAAATACA	165282	TGTATTTGGGAACTTTAATT
156063	6702	GAATTAAAGTTCCCAAATAC	165283	GTATTTGGGAACTTTAATTC
156064	6703	TGAATTAAAGTTCCCAAATA	165284	TATTTGGGAACTTTAATTCA
156065	6704	ATGAATTAAAGTTCCCAAAT	165285	ATTTGGGAACTTTAATTCAT
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156067	6706	TTATGAATTAAAGTTCCCAA	165287	TTGGGAACTTTAATTCATAA
156068	6707	ATTATGAATTAAAGTTCCCA	165288	TGGGAACTTTAATTCATAAT
156069	6708	AATTATGAATTAAAGTTCCC	165289	GGGAACTTTAATTCATAATT
156070	6709	AAATTATGAATTAAAGTTCC	165290	GGAACTTTAATTCATAATTT
156071	6710	TAAATTATGAATTAAAGTTC	165291	GAACTTTAATTCATAATTTA
156072	6711	CTAAATTATGAATTAAAGTT	165292	AACTTTAATTCATAATTTAG
156073	6712	GCTAAATTATGAATTAAAGT	165293	ACTTTAATTCATAATTTAGC
156074	6713	AGCTAAATTATGAATTAAAG	165294	CTTTAATTCATAATTTAGCT
156075	6714	AAGCTAAATTATGAATTAAA	165295	TTTAATTCATAATTTAGCTT
156076	6715	AAAGCTAAATTATGAATTAA	165296	TTAATTCATAATTTAGCTTT
156077	6716	AAAAGCTAAATTATGAATTA	165297	TAATTCATAATTTAGCTTTT
156078	6717	AAAAAGCTAAATTATGAATT	165298	AATTCATAATTTAGCTTTTT
156079	6718	AAAAAAGCTAAATTATGAAT	165299	ATTCATAATTTAGCTTTTTT
156080	6719	AAAAAAAGCTAAATTATGAA	165300	TTCATAATTTAGCTTTTTTT
156081	6720	AAAAAAAAGCTAAATTATGA	165301	TCATAATTTAGCTTTTTTTT
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156083	6722	AGAAAAAAAAGCTAAATTAT	165303	ATAATTTAGCTTTTTTTTCT
156084	6723	AAGAAAAAAAAGCTAAATTA	165304	TAATTTAGCTTTTTTTTCTT
156085	6724	GAAGAAAAAAAAGCTAAATT	165305	AATTTAGCTTTTTTTTCTTC
156086	6725	AGAAGAAAAAAAAGCTAAAT	165306	ATTTAGCTTTTTTTTCTTCT
156087	6726	AAGAAGAAAAAAAAGCTAAA	165307	TTTAGCTTTTTTTTCTTCTT
156088	6727	GAAGAAGAAAAAAAAGCTAA	165308	TTAGCTTTTTTTTCTTCTTC
156089	6728	AGAAGAAGAAAAAAAAGCTA	165309	TAGCTTTTTTTTCTTCTTCT
156090	6729	AAGAAGAAGAAAAAAAAGCT	165310	AGCTTTTTTTTCTTCTTCTT
156091	6730	TAAGAAGAAGAAAAAAAAGC	165311	GCTTTTTTTTCTTCTTCTTA
156092	6731	ATAAGAAGAAGAAAAAAAAG	165312	CTTTTTTTTCTTCTTCTTAT
156093	6732	TATAAGAAGAAGAAAAAAAA	165313	TTTTTTTTCTTCTTCTTATA
156094	6733	TTATAAGAAGAAGAAAAAAA	165314	TTTTTTTCTTCTTCTTATAA
156095	6734	TTTATAAGAAGAAGAAAAAA	165315	TTTTTTCTTCTTCTTATAAA
156096	6735	ATTTATAAGAAGAAGAAAAA	165316	TTTTTCTTCTTCTTATAAAT
156097	6736	TATTTATAAGAAGAAGAAAA	165317	TTTTCTTCTTCTTATAAATA
156098	6737	CTATTTATAAGAAGAAGAAA	165318	TTTCTTCTTCTTATAAATAG
156099	6738	CCTATTTATAAGAAGAAGAA	165319	TTCTTCTTCTTATAAATAGG
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156101	6740	AGCCTATTTATAAGAAGAAG	165321	CTTCTTCTTATAAATAGGCT
156102	6741	CAGCCTATTTATAAGAAGAA	165322	TTCTTCTTATAAATAGGCTG
156103	6742	ACAGCCTATTTATAAGAAGA	165323	TCTTCTTATAAATAGGCTGT
156104	6743	TACAGCCTATTTATAAGAAG	165324	CTTCTTATAAATAGGCTGTA
156105	6744	GTACAGCCTATTTATAAGAA	165325	TTCTTATAAATAGGCTGTAC
156106	6745	GGTACAGCCTATTTATAAGA	165326	TCTTATAAATAGGCTGTACC
156107	6746	TGGTACAGCCTATTTATAAG	165327	CTTATAAATAGGCTGTACCA
156108	6747	CTGGTACAGCCTATTTATAA	165328	TTATAAATAGGCTGTACCAG
156109	6748	ACTGGTACAGCCTATTTATA	165329	TATAAATAGGCTGTACCAGT
156110	6749	CACTGGTACAGCCTATTTAT	165330	ATAAATAGGCTGTACCAGTG
156111	6750	GCACTGGTACAGCCTATTTA	165331	TAAATAGGCTGTACCAGTGC
156112	6751	TGCACTGGTACAGCCTATTT	165332	AAATAGGCTGTACCAGTGCA
156113	6752	CTGCACTGGTACAGCCTATT	165333	AATAGGCTGTACCAGTGCAG
156114	6753	CCTGCACTGGTACAGCCTAT	165334	ATAGGCTGTACCAGTGCAGG
156115	6754	ACCTGCACTGGTACAGCCTA	165335	TAGGCTGTACCAGTGCAGGT
156116	6755	GACCTGCACTGGTACAGCCT	165336	AGGCTGTACCAGTGCAGGTC
156117	6756	GGACCTGCACTGGTACAGCC	165337	GGCTGTACCAGTGCAGGTCC
156118	6757	AGGACCTGCACTGGTACAGC	165338	GCTGTACCAGTGCAGGTCCT
156119	6758	GAGGACCTGCACTGGTACAG	165339	CTGTACCAGTGCAGGTCCTC
156120	6759	TGAGGACCTGCACTGGTACA	165340	TGTACCAGTGCAGGTCCTCA
156121	6760	GTGAGGACCTGCACTGGTAC	165341	GTACCAGTGCAGGTCCTCAC
156122	6761	AGTGAGGACCTGCACTGGTA	165342	TACCAGTGCAGGTCCTCACT
156123	6762	AAGTGAGGACCTGCACTGGT	165343	ACCAGTGCAGGTCCTCACTT
156124	6763	AAAGTGAGGACCTGCACTGG	165344	CCAGTGCAGGTCCTCACTTT
156125	6764	TAAAGTGAGGACCTGCACTG	165345	CAGTGCAGGTCCTCACTTTA
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156127	6766	ATTAAAGTGAGGACCTGCAC	165347	GTGCAGGTCCTCACTTTAAT

156128	6767	GATTAAAGTGAGGACCTGCA	165348	TGCAGGTCCTCACTTTAATC
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156131	6770	GAGGATTAAAGTGAGGACCT	165351	AGGTCCTCACTTTAATCCTC
156132	6771	AGAGGATTAAAGTGAGGACC	165352	GGTCCTCACTTTAATCCTCT
156133	6772	TAGAGGATTAAAGTGAGGAC	165353	GTCCTCACTTTAATCCTCTA
156134	6773	ATAGAGGATTAAAGTGAGGA	165354	TCCTCACTTTAATCCTCTAT
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156136	6775	GGATAGAGGATTAAAGTGAG	165356	CTCACTTTAATCCTCTATCC
156137	6776	TGGATAGAGGATTAAAGTGA	165357	TCACTTTAATCCTCTATCCA
156138	6777	CTGGATAGAGGATTAAAGTG	165358	CACTTTAATCCTCTATCCAG
156139	6778	TCTGGATAGAGGATTAAAGT	165359	ACTTTAATCCTCTATCCAGA
156140	6779	TTCTGGATAGAGGATTAAAG	165360	CTTTAATCCTCTATCCAGAA
156141	6780	TTTCTGGATAGAGGATTAAA	165361	TTTAATCCTCTATCCAGAAA
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156143	6782	GTTTTCTGGATAGAGGATTA	165363	TAATCCTCTATCCAGAAAAC
156144	6783	TGTTTTCTGGATAGAGGATT	165364	AATCCTCTATCCAGAAAACA
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156146	6785	CGTGTTTTCTGGATAGAGGA	165366	TCCTCTATCCAGAAAACACG
156147	6786	CCGTGTTTTCTGGATAGAGG	165367	CCTCTATCCAGAAAACACGG
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156152	6791	GCCCACCGTGTTTTCTGGAT	165372	ATCCAGAAAACACGGTGGGC
156153	6792	GGCCCACCGTGTTTTCTGGA	165373	TCCAGAAAACACGGTGGGCC
156154	6793	TGGCCCACCGTGTTTTCTGG	165374	CCAGAAAACACGGTGGGCCA
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156156	6795	TTTGGCCCACCGTGTTTTCT	165376	AGAAAACACGGTGGGCCAAA
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156159	6798	TCCTTTGGCCCACCGTGTTT	165379	AAACACGGTGGGCCAAAGGA
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156166	6805	CTCTTCATCCTTTGGCCCAC	165386	GTGGGCCAAAGGATGAAGAG
156167	6806	TCTCTTCATCCTTTGGCCCA	165387	TGGGCCAAAGGATGAAGAGA
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156169	6808	CCTCTCTTCATCCTTTGGCC	165389	GGCCAAAGGATGAAGAGAGG
156170	6809	ACCTCTCTTCATCCTTTGGC	165390	GCCAAAGGATGAAGAGAGGT
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156172	6811	TTACCTCTCTTCATCCTTTG	165392	CAAAGGATGAAGAGAGGTAA
156173	6812	GTTACCTCTCTTCATCCTTT	165393	AAAGGATGAAGAGAGGTAAC
156174	6813	TGTTACCTCTCTTCATCCTT	165394	AAGGATGAAGAGAGGTAACA
156175	6814	TTGTTACCTCTCTTCATCCT	165395	AGGATGAAGAGAGGTAACAA
156176	6815	CTTGTTACCTCTCTTCATCC	165396	GGATGAAGAGAGGTAACAAG
156177	6816	TCTTGTTACCTCTCTTCATC	165397	GATGAAGAGAGGTAACAAGA
156178	6817	ATCTTGTTACCTCTCTTCAT	165398	ATGAAGAGAGGTAACAAGAT
156179	6818	CATCTTGTTACCTCTCTTCA	165399	TGAAGAGAGGTAACAAGATG
156180	6819	GCATCTTGTTACCTCTCTTC	165400	GAAGAGAGGTAACAAGATGC
156181	6820	AGCATCTTGTTACCTCTCTT	165401	AAGAGAGGTAACAAGATGCT
156182	6821	AAGCATCTTGTTACCTCTCT	165402	AGAGAGGTAACAAGATGCTT
156183	6822	TAAGCATCTTGTTACCTCTC	165403	GAGAGGTAACAAGATGCTTA
156184	6823	TTAAGCATCTTGTTACCTCT	165404	AGAGGTAACAAGATGCTTAA
156185	6824	GTTAAGCATCTTGTTACCTC	165405	GAGGTAACAAGATGCTTAAC
156186	6825	AGTTAAGCATCTTGTTACCT	165406	AGGTAACAAGATGCTTAACT
156187	6826	GAGTTAAGCATCTTGTTACC	165407	GGTAACAAGATGCTTAACTC
156188	6827	AGAGTTAAGCATCTTGTTAC	165408	GTAACAAGATGCTTAACTCT
156189	6828	AAGAGTTAAGCATCTTGTTA	165409	TAACAAGATGCTTAACTCTT
156190	6829	CAAGAGTTAAGCATCTTGTT	165410	AACAAGATGCTTAACTCTTG
156191	6830	ACAAGAGTTAAGCATCTTGT	165411	ACAAGATGCTTAACTCTTGT
156192	6831	TACAAGAGTTAAGCATCTTG	165412	CAAGATGCTTAACTCTTGTA
156193	6832	TTACAAGAGTTAAGCATCTT	165413	AAGATGCTTAACTCTTGTAA
156194	6833	ATTACAAGAGTTAAGCATCT	165414	AGATGCTTAACTCTTGTAAT
156195	6834	TATTACAAGAGTTAAGCATC	165415	GATGCTTAACTCTTGTAATA
156196	6835	TTATTACAAGAGTTAAGCAT	165416	ATGCTTAACTCTTGTAATAA
156197	6836	ATTATTACAAGAGTTAAGCA	165417	TGCTTAACTCTTGTAATAAT
156198	6837	CATTATTACAAGAGTTAAGC	165418	GCTTAACTCTTGTAATAATG
156199	6838	CCATTATTACAAGAGTTAAG	165419	CTTAACTCTTGTAATAATGG

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156201	6840	CGCCATTATTACAAGAGTTA	165421	TAACTCTTGTAATAATGGCG
156202	6841	TCGCCATTATTACAAGAGTT	165422	AACTCTTGTAATAATGGCGA
156203	6842	ATCGCCATTATTACAAGAGT	165423	ACTCTTGTAATAATGGCGAT
156204	6843	TATCGCCATTATTACAAGAG	165424	CTCTTGTAATAATGGCGATA
156205	6844	CTATCGCCATTATTACAAGA	165425	TCTTGTAATAATGGCGATAG
156206	6845	GCTATCGCCATTATTACAAG	165426	CTTGTAATAATGGCGATAGC
156207	6846	AGCTATCGCCATTATTACAA	165427	TTGTAATAATGGCGATAGCT
156208	6847	AAGCTATCGCCATTATTACA	165428	TGTAATAATGGCGATAGCTT
156209	6848	AAAGCTATCGCCATTATTAC	165429	GTAATAATGGCGATAGCTTT
156210	6849	GAAAGCTATCGCCATTATTA	165430	TAATAATGGCGATAGCTTTC
156211	6850	AGAAAGCTATCGCCATTATT	165431	AATAATGGCGATAGCTTTCT
156212	6851	CAGAAAGCTATCGCCATTAT	165432	ATAATGGCGATAGCTTTCTG
156213	6852	CCAGAAAGCTATCGCCATTA	165433	TAATGGCGATAGCTTTCTGG
156214	6853	TCCAGAAAGCTATCGCCATT	165434	AATGGCGATAGCTTTCTGGA
156215	6854	CTCCAGAAAGCTATCGCCAT	165435	ATGGCGATAGCTTTCTGGAG
156216	6855	ACTCCAGAAAGCTATCGCCA	165436	TGGCGATAGCTTTCTGGAGT
156217	6856	AACTCCAGAAAGCTATCGCC	165437	GGCGATAGCTTTCTGGAGTT
156218	6857	GAACTCCAGAAAGCTATCGC	165438	GCGATAGCTTTCTGGAGTTC
156219	6858	TGAACTCCAGAAAGCTATCG	165439	CGATAGCTTTCTGGAGTTCA
156220	6859	ATGAACTCCAGAAAGCTATC	165440	GATAGCTTTCTGGAGTTCAT
156221	6860	TATGAACTCCAGAAAGCTAT	165441	ATAGCTTTCTGGAGTTCATA
156222	6861	ATATGAACTCCAGAAAGCTA	165442	TAGCTTTCTGGAGTTCATAT
156223	6862	CATATGAACTCCAGAAAGCT	165443	AGCTTTCTGGAGTTCATATG
156224	6863	CCATATGAACTCCAGAAAGC	165444	GCTTTCTGGAGTTCATATGG
156225	6864	ACCATATGAACTCCAGAAAG	165445	CTTTCTGGAGTTCATATGGT
156226	6865	TACCATATGAACTCCAGAAA	165446	TTTCTGGAGTTCATATGGTA
156227	6866	ATACCATATGAACTCCAGAA	165447	TTCTGGAGTTCATATGGTAT
156228	6867	TATACCATATGAACTCCAGA	165448	TCTGGAGTTCATATGGTATA
156229	6868	GTATACCATATGAACTCCAG	165449	CTGGAGTTCATATGGTATAC
156230	6869	AGTATACCATATGAACTCCA	165450	TGGAGTTCATATGGTATACT
156231	6870	TAGTATACCATATGAACTCC	165451	GGAGTTCATATGGTATACTA
156232	6871	GTAGTATACCATATGAACTC	165452	GAGTTCATATGGTATACTAC
156233	6872	AGTAGTATACCATATGAACT	165453	AGTTCATATGGTATACTACT
156234	6873	AAGTAGTATACCATATGAAC	165454	GTTCATATGGTATACTACTT
156235	6874	CAAGTAGTATACCATATGAA	165455	TTCATATGGTATACTACTTG
156236	6875	ACAAGTAGTATACCATATGA	165456	TCATATGGTATACTACTTGT
156237	6876	TACAAGTAGTATACCATATG	165457	CATATGGTATACTACTTGTA
156238	6877	TTACAAGTAGTATACCATAT	165458	ATATGGTATACTACTTGTAA
156239	6878	TTTACAAGTAGTATACCATA	165459	TATGGTATACTACTTGTAAA
156240	6879	ATTTACAAGTAGTATACCAT	165460	ATGGTATACTACTTGTAAAT
156241	6880	TATTTACAAGTAGTATACCA	165461	TGGTATACTACTTGTAAATA
156242	6881	ATATTTACAAGTAGTATACC	165462	GGTATACTACTTGTAAATAT
156243	6882	CATATTTACAAGTAGTATAC	165463	GTATACTACTTGTAAATATG
156244	6883	ACATATTTACAAGTAGTATA	165464	TATACTACTTGTAAATATGT
156245	6884	CACATATTTACAAGTAGTAT	165465	ATACTACTTGTAAATATGTG
156246	6885	GCACATATTTACAAGTAGTA	165466	TACTACTTGTAAATATGTGC
156247	6886	AGCACATATTTACAAGTAGT	165467	ACTACTTGTAAATATGTGCT
156248	6887	TAGCACATATTTACAAGTAG	165468	CTACTTGTAAATATGTGCTA
156249	6888	TTAGCACATATTTACAAGTA	165469	TACTTGTAAATATGTGCTAA
156250	6889	CTTAGCACATATTTACAAGT	165470	ACTTGTAAATATGTGCTAAG
156251	6890	TCTTAGCACATATTTACAAG	165471	CTTGTAAATATGTGCTAAGA
156252	6891	ATCTTAGCACATATTTACAA	165472	TTGTAAATATGTGCTAAGAT
156253	6892	TATCTTAGCACATATTTACA	165473	TGTAAATATGTGCTAAGATA
156254	6893	TTATCTTAGCACATATTTAC	165474	GTAAATATGTGCTAAGATAA
156255	6894	ATTATCTTAGCACATATTTA	165475	TAAATATGTGCTAAGATAAT
156256	6895	AATTATCTTAGCACATATTT	165476	AAATATGTGCTAAGATAATT
156257	6896	GAATTATCTTAGCACATATT	165477	AATATGTGCTAAGATAATTC
156258	6897	GGAATTATCTTAGCACATAT	165478	ATATGTGCTAAGATAATTCC
156259	6898	CGGAATTATCTTAGCACATA	165479	TATGTGCTAAGATAATTCCG
156260	6899	ACGGAATTATCTTAGCACAT	165480	ATGTGCTAAGATAATTCCGT
156261	6900	CACGGAATTATCTTAGCACA	165481	TGTGCTAAGATAATTCCGTG
156262	6901	ACACGGAATTATCTTAGCAC	165482	GTGCTAAGATAATTCCGTGT
156263	6902	AACACGGAATTATCTTAGCA	165483	TGCTAAGATAATTCCGTGTT
156264	6903	AAACACGGAATTATCTTAGC	165484	GCTAAGATAATTCCGTGTTT
156265	6904	GAAACACGGAATTATCTTAG	165485	CTAAGATAATTCCGTGTTTC
156266	6905	GGAAACACGGAATTATCTTA	165486	TAAGATAATTCCGTGTTTCC
156267	6906	GGGAAACACGGAATTATCTT	165487	AAGATAATTCCGTGTTTCCC
156268	6907	GGGGAAACACGGAATTATCT	165488	AGATAATTCCGTGTTTCCCC
156269	6908	GGGGGAAACACGGAATTATC	165489	GATAATTCCGTGTTTCCCCC
156270	6909	TGGGGGAAACACGGAATTAT	165490	ATAATTCCGTGTTTCCCCCA
156271	6910	GTGGGGGAAACACGGAATTA	165491	TAATTCCGTGTTTCCCCCAC

156272	6911	GGTGGGGGAAACACGGAATT	165492	AATTCCGTGTTTCCCCCACC
156273	6912	AGGTGGGGGAAACACGGAAT	165493	ATTCCGTGTTTCCCCCACCT
156274	6913	AAGGTGGGGGAAACACGGAA	165494	TTCCGTGTTTCCCCCACCTT
156275	6914	AAAGGTGGGGGAAACACGGA	165495	TCCGTGTTTCCCCCACCTTT
156276	6915	CAAAGGTGGGGGAAACACGG	165496	CCGTGTTTCCCCCACCTTTG
156277	6916	GCAAAGGTGGGGGAAACACG	165497	CGTGTTTCCCCCACCTTTGC
156278	6917	AGCAAAGGTGGGGGAAACAC	165498	GTGTTTCCCCCACCTTTGCT
156279	6918	AAGCAAAGGTGGGGGAAACA	165499	TGTTTCCCCCACCTTTGCTT
156280	6919	AAAGCAAAGGTGGGGGAAAC	165500	GTTTCCCCCACCTTTGCTTT
156281	6920	AAAAGCAAAGGTGGGGGAAA	165501	TTTCCCCCACCTTTGCTTTT
156282	6921	CAAAAGCAAAGGTGGGGGAA	165502	TTCCCCCACCTTTGCTTTTG
156283	6922	TCAAAAGCAAAGGTGGGGGA	165503	TCCCCCACCTTTGCTTTTGA
156284	6923	TTCAAAAGCAAAGGTGGGGG	165504	CCCCCACCTTTGCTTTTGAA
156285	6924	GTTCAAAAGCAAAGGTGGGG	165505	CCCCACCTTTGCTTTTGAAC
156286	6925	AGTTCAAAAGCAAAGGTGGG	165506	CCCACCTTTGCTTTTGAACT
156287	6926	AAGTTCAAAAGCAAAGGTGG	165507	CCACCTTTGCTTTTGAACTT
156288	6927	CAAGTTCAAAAGCAAAGGTG	165508	CACCTTTGCTTTTGAACTTG
156289	6928	GCAAGTTCAAAAGCAAAGGT	165509	ACCTTTGCTTTTGAACTTGC
156290	6929	AGCAAGTTCAAAAGCAAAGG	165510	CCTTTGCTTTTGAACTTGCT
156291	6930	CAGCAAGTTCAAAAGCAAAG	165511	CTTTGCTTTTGAACTTGCTG
156292	6931	TCAGCAAGTTCAAAAGCAAA	165512	TTTGCTTTTGAACTTGCTGA
156293	6932	GTCAGCAAGTTCAAAAGCAA	165513	TTGCTTTTGAACTTGCTGAC
156294	6933	AGTCAGCAAGTTCAAAAGCA	165514	TGCTTTTGAACTTGCTGACT
156295	6934	GAGTCAGCAAGTTCAAAAGC	165515	GCTTTTGAACTTGCTGACTC
156296	6935	TGAGTCAGCAAGTTCAAAAG	165516	CTTTTGAACTTGCTGACTCA
156297	6936	ATGAGTCAGCAAGTTCAAAA	165517	TTTTGAACTTGCTGACTCAT
156298	6937	GATGAGTCAGCAAGTTCAAA	165518	TTTGAACTTGCTGACTCATC
156299	6938	AGATGAGTCAGCAAGTTCAA	165519	TTGAACTTGCTGACTCATCT
156300	6939	TAGATGAGTCAGCAAGTTCA	165520	TGAACTTGCTGACTCATCTA
156301	6940	TTAGATGAGTCAGCAAGTTC	165521	GAACTTGCTGACTCATCTAA
156302	6941	TTTAGATGAGTCAGCAAGTT	165522	AACTTGCTGACTCATCTAAA
156303	6942	GTTTAGATGAGTCAGCAAGT	165523	ACTTGCTGACTCATCTAAAC
156304	6943	GGTTTAGATGAGTCAGCAAG	165524	CTTGCTGACTCATCTAAACC
156305	6944	GGGTTTAGATGAGTCAGCAA	165525	TTGCTGACTCATCTAAACCC
156306	6945	GGGGTTTAGATGAGTCAGCA	165526	TGCTGACTCATCTAAACCCC
156307	6946	AGGGGTTTAGATGAGTCAGC	165527	GCTGACTCATCTAAACCCCT
156308	6947	CAGGGGTTTAGATGAGTCAG	165528	CTGACTCATCTAAACCCCTG
156309	6948	GCAGGGGTTTAGATGAGTCA	165529	TGACTCATCTAAACCCCTGC
156310	6949	AGCAGGGGTTTAGATGAGTC	165530	GACTCATCTAAACCCCTGCT
156311	6950	GAGCAGGGGTTTAGATGAGT	165531	ACTCATCTAAACCCCTGCTC
156312	6951	GGAGCAGGGGTTTAGATGAG	165532	CTCATCTAAACCCCTGCTCC
156313	6952	GGGAGCAGGGGTTTAGATGA	165533	TCATCTAAACCCCTGCTCCC
156314	6953	TGGGAGCAGGGGTTTAGATG	165534	CATCTAAACCCCTGCTCCCA
156315	6954	TTGGGAGCAGGGGTTTAGAT	165535	ATCTAAACCCCTGCTCCCAA
156316	6955	TTTGGGAGCAGGGGTTTAGA	165536	TCTAAACCCCTGCTCCCAAA
156317	6956	ATTTGGGAGCAGGGGTTTAG	165537	CTAAACCCCTGCTCCCAAAT
156318	6957	CATTTGGGAGCAGGGGTTTA	165538	TAAACCCCTGCTCCCAAATG
156319	6958	GCATTTGGGAGCAGGGGTTT	165539	AAACCCCTGCTCCCAAATGC
156320	6959	AGCATTTGGGAGCAGGGGTT	165540	AACCCCTGCTCCCAAATGCT
156321	6960	CAGCATTTGGGAGCAGGGGT	165541	ACCCCTGCTCCCAAATGCTG
156322	6961	CCAGCATTTGGGAGCAGGGG	165542	CCCCTGCTCCCAAATGCTGG
156323	6962	TCCAGCATTTGGGAGCAGGG	165543	CCCTGCTCCCAAATGCTGGA
156324	6963	TTCCAGCATTTGGGAGCAGG	165544	CCTGCTCCCAAATGCTGGAA
156325	6964	ATTCCAGCATTTGGGAGCAG	165545	CTGCTCCCAAATGCTGGAAT
156326	6965	CATTCCAGCATTTGGGAGCA	165546	TGCTCCCAAATGCTGGAATG
156327	6966	GCATTCCAGCATTTGGGAGC	165547	GCTCCCAAATGCTGGAATGC
156328	6967	AGCATTCCAGCATTTGGGAG	165548	CTCCCAAATGCTGGAATGCT
156329	6968	AAGCATTCCAGCATTTGGGA	165549	TCCCAAATGCTGGAATGCTT
156330	6969	AAAGCATTCCAGCATTTGGG	165550	CCCAAATGCTGGAATGCTTT
156331	6970	AAAAGCATTCCAGCATTTGG	165551	CCAAATGCTGGAATGCTTTT
156332	6971	TAAAAGCATTCCAGCATTTG	165552	CAAATGCTGGAATGCTTTTA
156333	6972	GTAAAAGCATTCCAGCATTT	165553	AAATGCTGGAATGCTTTTAC
156334	6973	AGTAAAAGCATTCCAGCATT	165554	AATGCTGGAATGCTTTTACT
156335	6974	AAGTAAAAGCATTCCAGCAT	165555	ATGCTGGAATGCTTTTACTT
156336	6975	GAAGTAAAAGCATTCCAGCA	165556	TGCTGGAATGCTTTTACTTC
156337	6976	GGAAGTAAAAGCATTCCAGC	165557	GCTGGAATGCTTTTACTTCC
156338	6977	AGGAAGTAAAAGCATTCCAG	165558	CTGGAATGCTTTTACTTCCT
156339	6978	CAGGAAGTAAAAGCATTCCA	165559	TGGAATGCTTTTACTTCCTG
156340	6979	CCAGGAAGTAAAAGCATTCC	165560	GGAATGCTTTTACTTCCTGG
156341	6980	CCCAGGAAGTAAAAGCATTC	165561	GAATGCTTTTACTTCCTGGG
156342	6981	GCCCAGGAAGTAAAAGCATT	165562	AATGCTTTTACTTCCTGGGC
156343	6982	AGCCCAGGAAGTAAAAGCAT	165563	ATGCTTTTACTTCCTGGGCT

156344	6983	AAGCCCAGGAAGTAAAAGCA	165564	TGCTTTTACTTCCTGGGCTT
156345	6984	TAAGCCCAGGAAGTAAAAGC	165565	GCTTTTACTTCCTGGGCTTA
156346	6985	TTAAGCCCAGGAAGTAAAAG	165566	CTTTTACTTCCTGGGCTTAA
156347	6986	TTTAAGCCCAGGAAGTAAAA	165567	TTTTACTTCCTGGGCTTAAA
156348	6987	CTTTAAGCCCAGGAAGTAAA	165568	TTTACTTCCTGGGCTTAAAG
156349	6988	CCTTTAAGCCCAGGAAGTAA	165569	TTACTTCCTGGGCTTAAAGG
156350	6989	TCCTTTAAGCCCAGGAAGTA	165570	TACTTCCTGGGCTTAAAGGA
156351	6990	TTCCTTTAAGCCCAGGAAGT	165571	ACTTCCTGGGCTTAAAGGAA
156352	6991	ATTCCTTTAAGCCCAGGAAG	165572	CTTCCTGGGCTTAAAGGAAT
156353	6992	AATTCCTTTAAGCCCAGGAA	165573	TTCCTGGGCTTAAAGGAATT
156354	6993	CAATTCCTTTAAGCCCAGGA	165574	TCCTGGGCTTAAAGGAATTG
156355	6994	TCAATTCCTTTAAGCCCAGG	165575	CCTGGGCTTAAAGGAATTGA
156356	6995	GTCAATTCCTTTAAGCCCAG	165576	CTGGGCTTAAAGGAATTGAC
156357	6996	TGTCAATTCCTTTAAGCCCA	165577	TGGGCTTAAAGGAATTGACA
156358	6997	TTGTCAATTCCTTTAAGCCC	165578	GGGCTTAAAGGAATTGACAA
156359	6998	TTTGTCAATTCCTTTAAGCC	165579	GGCTTAAAGGAATTGACAAA
156360	6999	ATTTGTCAATTCCTTTAAGC	165580	GCTTAAAGGAATTGACAAAT
156361	7000	CATTTGTCAATTCCTTTAAG	165581	CTTAAAGGAATTGACAAATG
156362	7001	CCATTTGTCAATTCCTTTAA	165582	TTAAAGGAATTGACAAATGG
156363	7002	CCCATTTGTCAATTCCTTTA	165583	TAAAGGAATTGACAAATGGG
156364	7003	CCCCATTTGTCAATTCCTTT	165584	AAAGGAATTGACAAATGGGG
156365	7004	TCCCCATTTGTCAATTCCTT	165585	AAGGAATTGACAAATGGGGA
156366	7005	GTCCCCATTTGTCAATTCCT	165586	AGGAATTGACAAATGGGGAC
156367	7006	TGTCCCCATTTGTCAATTCC	165587	GGAATTGACAAATGGGGACA
156368	7007	GTGTCCCCATTTGTCAATTC	165588	GAATTGACAAATGGGGACAC
156369	7008	AGTGTCCCCATTTGTCAATT	165589	AATTGACAAATGGGGACACT
156370	7009	AAGTGTCCCCATTTGTCAAT	165590	ATTGACAAATGGGGACACTT
156371	7010	TAAGTGTCCCCATTTGTCAA	165591	TTGACAAATGGGGACACTTA
156372	7011	TTAAGTGTCCCCATTTGTCA	165592	TGACAAATGGGGACACTTAA
156373	7012	TTTAAGTGTCCCCATTTGTC	165593	GACAAATGGGGACACTTAAA
156374	7013	TTTTAAGTGTCCCCATTTGT	165594	ACAAATGGGGACACTTAAAA
156375	7014	GTTTTAAGTGTCCCCATTTG	165595	CAAATGGGGACACTTAAAAC
156376	7015	CGTTTTAAGTGTCCCCATTT	165596	AAATGGGGACACTTAAAACG
156377	7016	TCGTTTTAAGTGTCCCCATT	165597	AATGGGGACACTTAAAACGA
156378	7017	ATCGTTTTAAGTGTCCCCAT	165598	ATGGGGACACTTAAAACGAT
156379	7018	AATCGTTTTAAGTGTCCCCA	165599	TGGGGACACTTAAAACGATT
156380	7019	AAATCGTTTTAAGTGTCCCC	165600	GGGGACACTTAAAACGATTT
156381	7020	CAAATCGTTTTAAGTGTCCC	165601	GGGACACTTAAAACGATTTG
156382	7021	CCAAATCGTTTTAAGTGTCC	165602	GGACACTTAAAACGATTTGG
156383	7022	ACCAAATCGTTTTAAGTGTC	165603	GACACTTAAAACGATTTGGT
156384	7023	AACCAAATCGTTTTAAGTGT	165604	ACACTTAAAACGATTTGGTT
156385	7024	AAACCAAATCGTTTTAAGTG	165605	CACTTAAAACGATTTGGTTT
156386	7025	AAAACCAAATCGTTTTAAGT	165606	ACTTAAAACGATTTGGTTTT
156387	7026	CAAAACCAAATCGTTTTAAG	165607	CTTAAAACGATTTGGTTTTG
156388	7027	ACAAAACCAAATCGTTTTAA	165608	TTAAAACGATTTGGTTTTGT
156389	7028	TACAAAACCAAATCGTTTTA	165609	TAAAACGATTTGGTTTTGTA
156390	7029	CTACAAAACCAAATCGTTTT	165610	AAAACGATTTGGTTTTGTAG
156391	7030	GCTACAAAACCAAATCGTTT	165611	AAACGATTTGGTTTTGTAGC
156392	7031	TGCTACAAAACCAAATCGTT	165612	AACGATTTGGTTTTGTAGCA
156393	7032	ATGCTACAAAACCAAATCGT	165613	ACGATTTGGTTTTGTAGCAT
156394	7033	AATGCTACAAAACCAAATCG	165614	CGATTTGGTTTTGTAGCATT
156395	7034	AAATGCTACAAAACCAAATC	165615	GATTTGGTTTTGTAGCATTT
156396	7035	TAAATGCTACAAAACCAAAT	165616	ATTTGGTTTTGTAGCATTTA
156397	7036	ATAAATGCTACAAAACCAAA	165617	TTTGGTTTTGTAGCATTTAT
156398	7037	AATAAATGCTACAAAACCAA	165618	TTGGTTTTGTAGCATTTATT
156399	7038	CAATAAATGCTACAAAACCA	165619	TGGTTTTGTAGCATTTATTG
156400	7039	TCAATAAATGCTACAAAACC	165620	GGTTTTGTAGCATTTATTGA
156401	7040	TTCAATAAATGCTACAAAAC	165621	GTTTTGTAGCATTTATTGAA
156402	7041	ATTCAATAAATGCTACAAAA	165622	TTTTGTAGCATTTATTGAAT
156403	7042	TATTCAATAAATGCTACAAA	165623	TTTGTAGCATTTATTGAATA
156404	7043	ATATTCAATAAATGCTACAA	165624	TTGTAGCATTTATTGAATAT
156405	7044	TATATTCAATAAATGCTACA	165625	TGTAGCATTTATTGAATATA
156406	7045	CTATATTCAATAAATGCTAC	165626	GTAGCATTTATTGAATATAG
156407	7046	TCTATATTCAATAAATGCTA	165627	TAGCATTTATTGAATATAGA
156408	7047	TTCTATATTCAATAAATGCT	165628	AGCATTTATTGAATATAGAA
156409	7048	GTTCTATATTCAATAAATGC	165629	GCATTTATTGAATATAGAAC
156410	7049	AGTTCTATATTCAATAAATG	165630	CATTTATTGAATATAGAACT
156411	7050	TAGTTCTATATTCAATAAAT	165631	ATTTATTGAATATAGAACTA
156412	7051	TTAGTTCTATATTCAATAAA	165632	TTTATTGAATATAGAACTAA
156413	7052	ATTAGTTCTATATTCAATAA	165633	TTATTGAATATAGAACTAAT
156414	7053	TATTAGTTCTATATTCAATA	165634	TATTGAATATAGAACTAATA
156415	7054	GTATTAGTTCTATATTCAAT	165635	ATTGAATATAGAACTAATAC

156416	7055	TGTATTAGTTCTATATTCAA	165636	TTGAATATAGAACTAATACA
156417	7056	TTGTATTAGTTCTATATTCA	165637	TGAATATAGAACTAATACAA
156418	7057	CTTGTATTAGTTCTATATTC	165638	GAATATAGAACTAATACAAG
156419	7058	ACTTGTATTAGTTCTATATT	165639	AATATAGAACTAATACAAGT
156420	7059	CACTTGTATTAGTTCTATAT	165640	ATATAGAACTAATACAAGTG
156421	7060	GCACTTGTATTAGTTCTATA	165641	TATAGAACTAATACAAGTGC
156422	7061	GGCACTTGTATTAGTTCTAT	165642	ATAGAACTAATACAAGTGCC
156423	7062	TGGCACTTGTATTAGTTCTA	165643	TAGAACTAATACAAGTGCCA
156424	7063	TTGGCACTTGTATTAGTTCT	165644	AGAACTAATACAAGTGCCAA
156425	7064	TTTGGCACTTGTATTAGTTC	165645	GAACTAATACAAGTGCCAAA
156426	7065	CTTTGGCACTTGTATTAGTT	165646	AACTAATACAAGTGCCAAAG
156427	7066	CCTTTGGCACTTGTATTAGT	165647	ACTAATACAAGTGCCAAAGG
156428	7067	CCCTTTGGCACTTGTATTAG	165648	CTAATACAAGTGCCAAAGGG
156429	7068	CCCCTTTGGCACTTGTATTA	165649	TAATACAAGTGCCAAAGGGG
156430	7069	TCCCCTTTGGCACTTGTATT	165650	AATACAAGTGCCAAAGGGGA
156431	7070	TTCCCCTTTGGCACTTGTAT	165651	ATACAAGTGCCAAAGGGGAA
156432	7071	GTTCCCCTTTGGCACTTGTA	165652	TACAAGTGCCAAAGGGGAAC
156433	7072	AGTTCCCCTTTGGCACTTGT	165653	ACAAGTGCCAAAGGGGAACT
156434	7073	TAGTTCCCCTTTGGCACTTG	165654	CAAGTGCCAAAGGGGAACTA
156435	7074	TTAGTTCCCCTTTGGCACTT	165655	AAGTGCCAAAGGGGAACTAA
156436	7075	ATTAGTTCCCCTTTGGCACT	165656	AGTGCCAAAGGGGAACTAAT
156437	7076	TATTAGTTCCCCTTTGGCAC	165657	GTGCCAAAGGGGAACTAATA
156438	7077	GTATTAGTTCCCCTTTGGCA	165658	TGCCAAAGGGGAACTAATAC
156439	7078	TGTATTAGTTCCCCTTTGGC	165659	GCCAAAGGGGAACTAATACA
156440	7079	CTGTATTAGTTCCCCTTTGG	165660	CCAAAGGGGAACTAATACAG
156441	7080	CCTGTATTAGTTCCCCTTTG	165661	CAAAGGGGAACTAATACAGG
156442	7081	TCCTGTATTAGTTCCCCTTT	165662	AAAGGGGAACTAATACAGGA
156443	7082	TTCCTGTATTAGTTCCCCTT	165663	AAGGGGAACTAATACAGGAA
156444	7083	TTTCCTGTATTAGTTCCCCT	165664	AGGGGAACTAATACAGGAAA
156445	7084	ATTTCCTGTATTAGTTCCCC	165665	GGGGAACTAATACAGGAAAT
156446	7085	CATTTCCTGTATTAGTTCCC	165666	GGGAACTAATACAGGAAATG
156447	7086	ACATTTCCTGTATTAGTTCC	165667	GGAACTAATACAGGAAATGT
156448	7087	GACATTTCCTGTATTAGTTC	165668	GAACTAATACAGGAAATGTC
156449	7088	TGACATTTCCTGTATTAGTT	165669	AACTAATACAGGAAATGTCA
156450	7089	ATGACATTTCCTGTATTAGT	165670	ACTAATACAGGAAATGTCAT
156451	7090	CATGACATTTCCTGTATTAG	165671	CTAATACAGGAAATGTCATG
156452	7091	TCATGACATTTCCTGTATTA	165672	TAATACAGGAAATGTCATGA
156453	7092	TTCATGACATTTCCTGTATT	165673	AATACAGGAAATGTCATGAA
156454	7093	GTTCATGACATTTCCTGTAT	165674	ATACAGGAAATGTCATGAAC
156455	7094	TGTTCATGACATTTCCTGTA	165675	TACAGGAAATGTCATGAACA
156456	7095	CTGTTCATGACATTTCCTGT	165676	ACAGGAAATGTCATGAACAG
156457	7096	ACTGTTCATGACATTTCCTG	165677	CAGGAAATGTCATGAACAGT
156458	7097	TACTGTTCATGACATTTCCT	165678	AGGAAATGTCATGAACAGTA
156459	7098	GTACTGTTCATGACATTTCC	165679	GGAAATGTCATGAACAGTAC
156460	7099	AGTACTGTTCATGACATTTC	165680	GAAATGTCATGAACAGTACT
156461	7100	CAGTACTGTTCATGACATTT	165681	AAATGTCATGAACAGTACTG
156462	7101	ACAGTACTGTTCATGACATT	165682	AATGTCATGAACAGTACTGT
156463	7102	GACAGTACTGTTCATGACAT	165683	ATGTCATGAACAGTACTGTC
156464	7103	TGACAGTACTGTTCATGACA	165684	TGTCATGAACAGTACTGTCA
156465	7104	TTGACAGTACTGTTCATGAC	165685	GTCATGAACAGTACTGTCAA
156466	7105	GTTGACAGTACTGTTCATGA	165686	TCATGAACAGTACTGTCAAC
156467	7106	GGTTGACAGTACTGTTCATG	165687	CATGAACAGTACTGTCAACC
156468	7107	TGGTTGACAGTACTGTTCAT	165688	ATGAACAGTACTGTCAACCA
156469	7108	GTGGTTGACAGTACTGTTCA	165689	TGAACAGTACTGTCAACCAC
156470	7109	AGTGGTTGACAGTACTGTTC	165690	GAACAGTACTGTCAACCACT
156471	7110	TAGTGGTTGACAGTACTGTT	165691	AACAGTACTGTCAACCACTA
156472	7111	CTAGTGGTTGACAGTACTGT	165692	ACAGTACTGTCAACCACTAG
156473	7112	GCTAGTGGTTGACAGTACTG	165693	CAGTACTGTCAACCACTAGC
156474	7113	TGCTAGTGGTTGACAGTACT	165694	AGTACTGTCAACCACTAGCA
156475	7114	TTGCTAGTGGTTGACAGTAC	165695	GTACTGTCAACCACTAGCAA
156476	7115	TTTGCTAGTGGTTGACAGTA	165696	TACTGTCAACCACTAGCAAA
156477	7116	TTTTGCTAGTGGTTGACAGT	165697	ACTGTCAACCACTAGCAAAA
156478	7117	ATTTTGCTAGTGGTTGACAG	165698	CTGTCAACCACTAGCAAAAT
156479	7118	GATTTTGCTAGTGGTTGACA	165699	TGTCAACCACTAGCAAAATC
156480	7119	TGATTTTGCTAGTGGTTGAC	165700	GTCAACCACTAGCAAAATCA
156481	7120	TTGATTTTGCTAGTGGTTGA	165701	TCAACCACTAGCAAAATCAA
156482	7121	ATTGATTTTGCTAGTGGTTG	165702	CAACCACTAGCAAAATCAAT
156483	7122	GATTGATTTTGCTAGTGGTT	165703	AACCACTAGCAAAATCAATC
156484	7123	TGATTGATTTTGCTAGTGGT	165704	ACCACTAGCAAAATCAATCA
156485	7124	ATGATTGATTTTGCTAGTGG	165705	CCACTAGCAAAATCAATCAT
156486	7125	GATGATTGATTTTGCTAGTG	165706	CACTAGCAAAATCAATCATC
156487	7126	TGATGATTGATTTTGCTAGT	165707	ACTAGCAAAATCAATCATCA

156488	7127	ATGATGATTGATTTTGCTAG	165708	CTAGCAAAATCAATCATCAT
156489	7128	AATGATGATTGATTTTGCTA	165709	TAGCAAAATCAATCATCATT
156490	7129	CAATGATGATTGATTTTGCT	165710	AGCAAAATCAATCATCATTG
156491	7130	ACAATGATGATTGATTTTGC	165711	GCAAAATCAATCATCATTGT
156492	7131	CACAATGATGATTGATTTTG	165712	CAAAATCAATCATCATTGTG
156493	7132	TCACAATGATGATTGATTTT	165713	AAAATCAATCATCATTGTGA
156494	7133	TTCACAATGATGATTGATTT	165714	AAATCAATCATCATTGTGAA
156495	7134	TTTCACAATGATGATTGATT	165715	AATCAATCATCATTGTGAAA
156496	7135	GTTTCACAATGATGATTGAT	165716	ATCAATCATCATTGTGAAAC
156497	7136	TGTTTCACAATGATGATTGA	165717	TCAATCATCATTGTGAAACA
156498	7137	ATGTTTCACAATGATGATTG	165718	CAATCATCATTGTGAAACAT
156499	7138	TATGTTTCACAATGATGATT	165719	AATCATCATTGTGAAACATA
156500	7139	CTATGTTTCACAATGATGAT	165720	ATCATCATTGTGAAACATAG
156501	7140	CCTATGTTTCACAATGATGA	165721	TCATCATTGTGAAACATAGG
156502	7141	TCCTATGTTTCACAATGATG	165722	CATCATTGTGAAACATAGGA
156503	7142	TTCCTATGTTTCACAATGAT	165723	ATCATTGTGAAACATAGGAA
156504	7143	CTTCCTATGTTTCACAATGA	165724	TCATTGTGAAACATAGGAAG
156505	7144	GCTTCCTATGTTTCACAATG	165725	CATTGTGAAACATAGGAAGC
156506	7145	AGCTTCCTATGTTTCACAAT	165726	ATTGTGAAACATAGGAAGCT
156507	7146	AAGCTTCCTATGTTTCACAA	165727	TTGTGAAACATAGGAAGCTT
156508	7147	GAAGCTTCCTATGTTTCACA	165728	TGTGAAACATAGGAAGCTTC
156509	7148	AGAAGCTTCCTATGTTTCAC	165729	GTGAAACATAGGAAGCTTCT
156510	7149	CAGAAGCTTCCTATGTTTCA	165730	TGAAACATAGGAAGCTTCTG
156511	7150	ACAGAAGCTTCCTATGTTTC	165731	GAAACATAGGAAGCTTCTGT
156512	7151	TACAGAAGCTTCCTATGTTT	165732	AAACATAGGAAGCTTCTGTA
156513	7152	CTACAGAAGCTTCCTATGTT	165733	AACATAGGAAGCTTCTGTAG
156514	7153	TCTACAGAAGCTTCCTATGT	165734	ACATAGGAAGCTTCTGTAGA
156515	7154	ATCTACAGAAGCTTCCTATG	165735	CATAGGAAGCTTCTGTAGAT
156516	7155	TATCTACAGAAGCTTCCTAT	165736	ATAGGAAGCTTCTGTAGATA
156517	7156	TTATCTACAGAAGCTTCCTA	165737	TAGGAAGCTTCTGTAGATAA
156518	7157	TTTATCTACAGAAGCTTCCT	165738	AGGAAGCTTCTGTAGATAAA
156519	7158	TTTTATCTACAGAAGCTTCC	165739	GGAAGCTTCTGTAGATAAAA
156520	7159	TTTTTATCTACAGAAGCTTC	165740	GAAGCTTCTGTAGATAAAAA
156521	7160	TTTTTTATCTACAGAAGCTT	165741	AAGCTTCTGTAGATAAAAAA
156522	7161	TTTTTTTATCTACAGAAGCT	165742	AGCTTCTGTAGATAAAAAAA
156523	7162	TTTTTTTTATCTACAGAAGC	165743	GCTTCTGTAGATAAAAAAAA
156524	7163	TTTTTTTTTATCTACAGAAG	165744	CTTCTGTAGATAAAAAAAAA
156525	7164	TTTTTTTTTTATCTACAGAA	165745	TTCTGTAGATAAAAAAAAAA
156526	7165	TTTTTTTTTTTATCTACAGA	165746	TCTGTAGATAAAAAAAAAAA
156527	7166	ATTTTTTTTTTTATCTACAG	165747	CTGTAGATAAAAAAAAAAAT
156528	7167	AATTTTTTTTTTTATCTACA	165748	TGTAGATAAAAAAAAAAATT
156529	7168	CAATTTTTTTTTTTATCTAC	165749	GTAGATAAAAAAAAAAATTG
156530	7169	TCAATTTTTTTTTTTATCTA	165750	TAGATAAAAAAAAAAATTGA
156531	7170	ATCAATTTTTTTTTTTATCT	165751	AGATAAAAAAAAAAATTGAT
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156533	7172	GTATCAATTTTTTTTTTTAT	165753	ATAAAAAAAAAAATTGATAC
156534	7173	AGTATCAATTTTTTTTTTTA	165754	TAAAAAAAAAAATTGATACT
156535	7174	CAGTATCAATTTTTTTTTTT	165755	AAAAAAAAAAATTGATACTG
156536	7175	TCAGTATCAATTTTTTTTTT	165756	AAAAAAAAAATTGATACTGA
156537	7176	TTCAGTATCAATTTTTTTTT	165757	AAAAAAAAATTGATACTGAA
156538	7177	TTTCAGTATCAATTTTTTTT	165758	AAAAAAAATTGATACTGAAA
156539	7178	TTTTCAGTATCAATTTTTTT	165759	AAAAAAATTGATACTGAAAA
156540	7179	GTTTTCAGTATCAATTTTTT	165760	AAAAAATTGATACTGAAAAC
156541	7180	AGTTTTCAGTATCAATTTTT	165761	AAAAATTGATACTGAAAACT
156542	7181	TAGTTTTCAGTATCAATTTT	165762	AAAATTGATACTGAAAACTA
156543	7182	CTAGTTTTCAGTATCAATTT	165763	AAATTGATACTGAAAACTAG
156544	7183	ACTAGTTTTCAGTATCAATT	165764	AATTGATACTGAAAACTAGT
156545	7184	GACTAGTTTTCAGTATCAAT	165765	ATTGATACTGAAAACTAGTC
156546	7185	CGACTAGTTTTCAGTATCAA	165766	TTGATACTGAAAACTAGTCG
156547	7186	TCGACTAGTTTTCAGTATCA	165767	TGATACTGAAAACTAGTCGA
156548	7187	CTCGACTAGTTTTCAGTATC	165768	GATACTGAAAACTAGTCGAG
156549	7188	TCTCGACTAGTTTTCAGTAT	165769	ATACTGAAAACTAGTCGAGA
156550	7189	GTCTCGACTAGTTTTCAGTA	165770	TACTGAAAACTAGTCGAGAC
156551	7190	AGTCTCGACTAGTTTTCAGT	165771	ACTGAAAACTAGTCGAGACT
156552	7191	GAGTCTCGACTAGTTTTCAG	165772	CTGAAAACTAGTCGAGACTC
156553	7192	GGAGTCTCGACTAGTTTTCA	165773	TGAAAACTAGTCGAGACTCC
156554	7193	TGGAGTCTCGACTAGTTTTC	165774	GAAAACTAGTCGAGACTCCA
156555	7194	ATGGAGTCTCGACTAGTTTT	165775	AAAACTAGTCGAGACTCCAT
156556	7195	AATGGAGTCTCGACTAGTTT	165776	AAACTAGTCGAGACTCCATT
156557	7196	AAATGGAGTCTCGACTAGTT	165777	AACTAGTCGAGACTCCATTT
156558	7197	TAAATGGAGTCTCGACTAGT	165778	ACTAGTCGAGACTCCATTTA
156559	7198	ATAAATGGAGTCTCGACTAG	165779	CTAGTCGAGACTCCATTTAT

156560	7199	TATAAATGGAGTCTCGACTA	165780	TAGTCGAGACTCCATTTATA
156561	7200	ATATAAATGGAGTCTCGACT	165781	AGTCGAGACTCCATTTATAT
156562	7201	CATATAAATGGAGTCTCGAC	165782	GTCGAGACTCCATTTATATG
156563	7202	ACATATAAATGGAGTCTCGA	165783	TCGAGACTCCATTTATATGT
156564	7203	CACATATAAATGGAGTCTCG	165784	CGAGACTCCATTTATATGTG
156565	7204	ACACATATAAATGGAGTCTC	165785	GAGACTCCATTTATATGTGT
156566	7205	TACACATATAAATGGAGTCT	165786	AGACTCCATTTATATGTGTA
156567	7206	ATACACATATAAATGGAGTC	165787	GACTCCATTTATATGTGTAT
156568	7207	CATACACATATAAATGGAGT	165788	ACTCCATTTATATGTGTATG
156569	7208	ACATACACATATAAATGGAG	165789	CTCCATTTATATGTGTATGT
156570	7209	AACATACACATATAAATGGA	165790	TCCATTTATATGTGTATGTT
156571	7210	AAACATACACATATAAATGG	165791	CCATTTATATGTGTATGTTT
156572	7211	AAAACATACACATATAAATG	165792	CATTTATATGTGTATGTTTT
156573	7212	GAAAACATACACATATAAAT	165793	ATTTATATGTGTATGTTTTC
156574	7213	AGAAAACATACACATATAAA	165794	TTTATATGTGTATGTTTTCT
156575	7214	CAGAAAACATACACATATAA	165795	TTATATGTGTATGTTTTCTG
156576	7215	TCAGAAAACATACACATATA	165796	TATATGTGTATGTTTTCTGA
156577	7216	TTCAGAAAACATACACATAT	165797	ATATGTGTATGTTTTCTGAA
156578	7217	TTTCAGAAAACATACACATA	165798	TATGTGTATGTTTTCTGAAA
156579	7218	CTTTCAGAAAACATACACAT	165799	ATGTGTATGTTTTCTGAAAG
156580	7219	GCTTTCAGAAAACATACACA	165800	TGTGTATGTTTTCTGAAAGC
156581	7220	GGCTTTCAGAAAACATACAC	165801	GTGTATGTTTTCTGAAAGCC
156582	7221	AGGCTTTCAGAAAACATACA	165802	TGTATGTTTTCTGAAAGCCT
156583	7222	AAGGCTTTCAGAAAACATAC	165803	GTATGTTTTCTGAAAGCCTT
156584	7223	AAAGGCTTTCAGAAAACATA	165804	TATGTTTTCTGAAAGCCTTT
156585	7224	GAAAGGCTTTCAGAAAACAT	165805	ATGTTTTCTGAAAGCCTTTC
156586	7225	TGAAAGGCTTTCAGAAAACA	165806	TGTTTTCTGAAAGCCTTTCA
156587	7226	CTGAAAGGCTTTCAGAAAAC	165807	GTTTTCTGAAAGCCTTTCAG
156588	7227	TCTGAAAGGCTTTCAGAAAA	165808	TTTTCTGAAAGCCTTTCAGA
156589	7228	TTCTGAAAGGCTTTCAGAAA	165809	TTTCTGAAAGCCTTTCAGAA
156590	7229	TTTCTGAAAGGCTTTCAGAA	165810	TTCTGAAAGCCTTTCAGAAA
156591	7230	TTTTCTGAAAGGCTTTCAGA	165811	TCTGAAAGCCTTTCAGAAAA
156592	7231	TTTTTCTGAAAGGCTTTCAG	165812	CTGAAAGCCTTTCAGAAAAA
156593	7232	ATTTTTCTGAAAGGCTTTCA	165813	TGAAAGCCTTTCAGAAAAAT
156594	7233	TATTTTTCTGAAAGGCTTTC	165814	GAAAGCCTTTCAGAAAAATA
156595	7234	ATATTTTTCTGAAAGGCTTT	165815	AAAGCCTTTCAGAAAAATAT
156596	7235	AATATTTTTCTGAAAGGCTT	165816	AAGCCTTTCAGAAAAATATT
156597	7236	TAATATTTTTCTGAAAGGCT	165817	AGCCTTTCAGAAAAATATTA
156598	7237	TTAATATTTTTCTGAAAGGC	165818	GCCTTTCAGAAAAATATTAA
156599	7238	TTTAATATTTTTCTGAAAGG	165819	CCTTTCAGAAAAATATTAAA
156600	7239	ATTTAATATTTTTCTGAAAG	165820	CTTTCAGAAAAATATTAAAT
156601	7240	AATTTAATATTTTTCTGAAA	165821	TTTCAGAAAAATATTAAATT
156602	7241	AAATTTAATATTTTTCTGAA	165822	TTCAGAAAAATATTAAATTT
156603	7242	TAAATTTAATATTTTTCTGA	165823	TCAGAAAAATATTAAATTTA
156604	7243	TTAAATTTAATATTTTTCTG	165824	CAGAAAAATATTAAATTTAA
156605	7244	CTTAAATTTAATATTTTTCT	165825	AGAAAAATATTAAATTTAAG
156606	7245	CCTTAAATTTAATATTTTTC	165826	GAAAAATATTAAATTTAAGG
156607	7246	TCCTTAAATTTAATATTTTT	165827	AAAAATATTAAATTTAAGGA
156608	7247	GTCCTTAAATTTAATATTTT	165828	AAAATATTAAATTTAAGGAC
156609	7248	TGTCCTTAAATTTAATATTT	165829	AAATATTAAATTTAAGGACA
156610	7249	TTGTCCTTAAATTTAATATT	165830	AATATTAAATTTAAGGACAA
156611	7250	CTTGTCCTTAAATTTAATAT	165831	ATATTAAATTTAAGGACAAG
156612	7251	TCTTGTCCTTAAATTTAATA	165832	TATTAAATTTAAGGACAAGA
156613	7252	ATCTTGTCCTTAAATTTAAT	165833	ATTAAATTTAAGGACAAGAT
156614	7253	AATCTTGTCCTTAAATTTAA	165834	TTAAATTTAAGGACAAGATT
156615	7254	AAATCTTGTCCTTAAATTTA	165835	TAAATTTAAGGACAAGATTT
156616	7255	AAAATCTTGTCCTTAAATTT	165836	AAATTTAAGGACAAGATTTT
156617	7256	AAAAATCTTGTCCTTAAATT	165837	AATTTAAGGACAAGATTTTT
156618	7257	TAAAAATCTTGTCCTTAAAT	165838	ATTTAAGGACAAGATTTTTA
156619	7258	ATAAAAATCTTGTCCTTAAA	165839	TTTAAGGACAAGATTTTTAT
156620	7259	TATAAAAATCTTGTCCTTAA	165840	TTAAGGACAAGATTTTTATA
156621	7260	ATATAAAAATCTTGTCCTTA	165841	TAAGGACAAGATTTTTATAT
156622	7261	GATATAAAAATCTTGTCCTT	165842	AAGGACAAGATTTTTATATC
156623	7262	TGATATAAAAATCTTGTCCT	165843	AGGACAAGATTTTTATATCA
156624	7263	CTGATATAAAAATCTTGTCC	165844	GGACAAGATTTTTATATCAG
156625	7264	TCTGATATAAAAATCTTGTC	165845	GACAAGATTTTTATATCAGA
156626	7265	CTCTGATATAAAAATCTTGT	165846	ACAAGATTTTTATATCAGAG
156627	7266	CCTCTGATATAAAAATCTTG	165847	CAAGATTTTTATATCAGAGG
156628	7267	GCCTCTGATATAAAAATCTT	165848	AAGATTTTTATATCAGAGGC
156629	7268	GGCCTCTGATATAAAAATCT	165849	AGATTTTTATATCAGAGGCC
156630	7269	AGGCCTCTGATATAAAAATC	165850	GATTTTTATATCAGAGGCCT
156631	7270	AAGGCCTCTGATATAAAAAT	165851	ATTTTTATATCAGAGGCCTT

156632	7271	CAAGGCCTCTGATATAAAAA	165852	TTTTTATATCAGAGGCCTTG
156633	7272	CCAAGGCCTCTGATATAAAA	165853	TTTTATATCAGAGGCCTTGG
156634	7273	CCCAAGGCCTCTGATATAAA	165854	TTTATATCAGAGGCCTTGGG
156635	7274	TCCCAAGGCCTCTGATATAA	165855	TTATATCAGAGGCCTTGGGA
156636	7275	GTCCCAAGGCCTCTGATATA	165856	TATATCAGAGGCCTTGGGAC
156637	7276	TGTCCCAAGGCCTCTGATAT	165857	ATATCAGAGGCCTTGGGACA
156638	7277	ATGTCCCAAGGCCTCTGATA	165858	TATCAGAGGCCTTGGGACAT
156639	7278	TATGTCCCAAGGCCTCTGAT	165859	ATCAGAGGCCTTGGGACATA
156640	7279	CTATGTCCCAAGGCCTCTGA	165860	TCAGAGGCCTTGGGACATAG
156641	7280	GCTATGTCCCAAGGCCTCTG	165861	CAGAGGCCTTGGGACATAGC
156642	7281	AGCTATGTCCCAAGGCCTCT	165862	AGAGGCCTTGGGACATAGCT
156643	7282	AAGCTATGTCCCAAGGCCTC	165863	GAGGCCTTGGGACATAGCTT
156644	7283	AAAGCTATGTCCCAAGGCCT	165864	AGGCCTTGGGACATAGCTTT
156645	7284	CAAAGCTATGTCCCAAGGCC	165865	GGCCTTGGGACATAGCTTTG
156646	7285	ACAAAGCTATGTCCCAAGGC	165866	GCCTTGGGACATAGCTTTGT
156647	7286	AACAAAGCTATGTCCCAAGG	165867	CCTTGGGACATAGCTTTGTT
156648	7287	TAACAAAGCTATGTCCCAAG	165868	CTTGGGACATAGCTTTGTTA
156649	7288	CTAACAAAGCTATGTCCCAA	165869	TTGGGACATAGCTTTGTTAG
156650	7289	GCTAACAAAGCTATGTCCCA	165870	TGGGACATAGCTTTGTTAGC
156651	7290	AGCTAACAAAGCTATGTCCC	165871	GGGACATAGCTTTGTTAGCT
156652	7291	TAGCTAACAAAGCTATGTCC	165872	GGACATAGCTTTGTTAGCTA
156653	7292	ATAGCTAACAAAGCTATGTC	165873	GACATAGCTTTGTTAGCTAT
156654	7293	CATAGCTAACAAAGCTATGT	165874	ACATAGCTTTGTTAGCTATG
156655	7294	GCATAGCTAACAAAGCTATG	165875	CATAGCTTTGTTAGCTATGC
156656	7295	GGCATAGCTAACAAAGCTAT	165876	ATAGCTTTGTTAGCTATGCC
156657	7296	TGGCATAGCTAACAAAGCTA	165877	TAGCTTTGTTAGCTATGCCA
156658	7297	CTGGCATAGCTAACAAAGCT	165878	AGCTTTGTTAGCTATGCCAG
156659	7298	ACTGGCATAGCTAACAAAGC	165879	GCTTTGTTAGCTATGCCAGT
156660	7299	TACTGGCATAGCTAACAAAG	165880	CTTTGTTAGCTATGCCAGTA
156661	7300	TTACTGGCATAGCTAACAAA	165881	TTTGTTAGCTATGCCAGTAA
156662	7301	ATTACTGGCATAGCTAACAA	165882	TTGTTAGCTATGCCAGTAAT
156663	7302	AATTACTGGCATAGCTAACA	165883	TGTTAGCTATGCCAGTAATT
156664	7303	TAATTACTGGCATAGCTAAC	165884	GTTAGCTATGCCAGTAATTA
156665	7304	TTAATTACTGGCATAGCTAA	165885	TTAGCTATGCCAGTAATTAA
156666	7305	GTTAATTACTGGCATAGCTA	165886	TAGCTATGCCAGTAATTAAC
156667	7306	TGTTAATTACTGGCATAGCT	165887	AGCTATGCCAGTAATTAACA
156668	7307	CTGTTAATTACTGGCATAGC	165888	GCTATGCCAGTAATTAACAG
156669	7308	CCTGTTAATTACTGGCATAG	165889	CTATGCCAGTAATTAACAGG
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156671	7310	TGCCTGTTAATTACTGGCAT	165891	ATGCCAGTAATTAACAGGCA
156672	7311	ATGCCTGTTAATTACTGGCA	165892	TGCCAGTAATTAACAGGCAT
156673	7312	TATGCCTGTTAATTACTGGC	165893	GCCAGTAATTAACAGGCATA
156674	7313	TTATGCCTGTTAATTACTGG	165894	CCAGTAATTAACAGGCATAA
156675	7314	GTTATGCCTGTTAATTACTG	165895	CAGTAATTAACAGGCATAAC
156676	7315	AGTTATGCCTGTTAATTACT	165896	AGTAATTAACAGGCATAACT
156677	7316	GAGTTATGCCTGTTAATTAC	165897	GTAATTAACAGGCATAACTC
156678	7317	TGAGTTATGCCTGTTAATTA	165898	TAATTAACAGGCATAACTCA
156679	7318	CTGAGTTATGCCTGTTAATT	165899	AATTAACAGGCATAACTCAG
156680	7319	ACTGAGTTATGCCTGTTAAT	165900	ATTAACAGGCATAACTCAGT
156681	7320	TACTGAGTTATGCCTGTTAA	165901	TTAACAGGCATAACTCAGTA
156682	7321	TTACTGAGTTATGCCTGTTA	165902	TAACAGGCATAACTCAGTAA
156683	7322	GTTACTGAGTTATGCCTGTT	165903	AACAGGCATAACTCAGTAAC
156684	7323	AGTTACTGAGTTATGCCTGT	165904	ACAGGCATAACTCAGTAACT
156685	7324	CAGTTACTGAGTTATGCCTG	165905	CAGGCATAACTCAGTAACTG
156686	7325	TCAGTTACTGAGTTATGCCT	165906	AGGCATAACTCAGTAACTGA
156687	7326	CTCAGTTACTGAGTTATGCC	165907	GGCATAACTCAGTAACTGAG
156688	7327	TCTCAGTTACTGAGTTATGC	165908	GCATAACTCAGTAACTGAGA
156689	7328	CTCTCAGTTACTGAGTTATG	165909	CATAACTCAGTAACTGAGAG
156690	7329	ACTCTCAGTTACTGAGTTAT	165910	ATAACTCAGTAACTGAGAGT
156691	7330	AACTCTCAGTTACTGAGTTA	165911	TAACTCAGTAACTGAGAGTT
156692	7331	AAACTCTCAGTTACTGAGTT	165912	AACTCAGTAACTGAGAGTTT
156693	7332	TAAACTCTCAGTTACTGAGT	165913	ACTCAGTAACTGAGAGTTTA
156694	7333	GTAAACTCTCAGTTACTGAG	165914	CTCAGTAACTGAGAGTTTAC
156695	7334	GGTAAACTCTCAGTTACTGA	165915	TCAGTAACTGAGAGTTTACC
156696	7335	GGGTAAACTCTCAGTTACTG	165916	CAGTAACTGAGAGTTTACCC
156697	7336	AGGGTAAACTCTCAGTTACT	165917	AGTAACTGAGAGTTTACCCT
156698	7337	AAGGGTAAACTCTCAGTTAC	165918	GTAACTGAGAGTTTACCCTT
156699	7338	AAAGGGTAAACTCTCAGTTA	165919	TAACTGAGAGTTTACCCTTT
156700	7339	CAAAGGGTAAACTCTCAGTT	165920	AACTGAGAGTTTACCCTTTG
156701	7340	CCAAAGGGTAAACTCTCAGT	165921	ACTGAGAGTTTACCCTTTGG
156702	7341	ACCAAAGGGTAAACTCTCAG	165922	CTGAGAGTTTACCCTTTGGT
156703	7342	TACCAAAGGGTAAACTCTCA	165923	TGAGAGTTTACCCTTTGGTA

156704	7343	GTACCAAAGGGTAAACTCTC	165924	GAGAGTTTACCCTTTGGTAC
156705	7344	AGTACCAAAGGGTAAACTCT	165925	AGAGTTTACCCTTTGGTACT
156706	7345	AAGTACCAAAGGGTAAACTC	165926	GAGTTTACCCTTTGGTACTT
156707	7346	GAAGTACCAAAGGGTAAACT	165927	AGTTTACCCTTTGGTACTTC
156708	7347	AGAAGTACCAAAGGGTAAAC	165928	GTTTACCCTTTGGTACTTCT
156709	7348	CAGAAGTACCAAAGGGTAAA	165929	TTTACCCTTTGGTACTTCTG
156710	7349	TCAGAAGTACCAAAGGGTAA	165930	TTACCCTTTGGTACTTCTGA
156711	7350	TTCAGAAGTACCAAAGGGTA	165931	TACCCTTTGGTACTTCTGAA
156712	7351	TTTCAGAAGTACCAAAGGGT	165932	ACCCTTTGGTACTTCTGAAA
156713	7352	ATTTCAGAAGTACCAAAGGG	165933	CCCTTTGGTACTTCTGAAAT
156714	7353	GATTTCAGAAGTACCAAAGG	165934	CCTTTGGTACTTCTGAAATC
156715	7354	TGATTTCAGAAGTACCAAAG	165935	CTTTGGTACTTCTGAAATCA
156716	7355	CTGATTTCAGAAGTACCAAA	165936	TTTGGTACTTCTGAAATCAG
156717	7356	CCTGATTTCAGAAGTACCAA	165937	TTGGTACTTCTGAAATCAGG
156718	7357	ACCTGATTTCAGAAGTACCA	165938	TGGTACTTCTGAAATCAGGT
156719	7358	CACCTGATTTCAGAAGTACC	165939	GGTACTTCTGAAATCAGGTG
156720	7359	GCACCTGATTTCAGAAGTAC	165940	GTACTTCTGAAATCAGGTGC
156721	7360	TGCACCTGATTTCAGAAGTA	165941	TACTTCTGAAATCAGGTGCA
156722	7361	CTGCACCTGATTTCAGAAGT	165942	ACTTCTGAAATCAGGTGCAG
156723	7362	GCTGCACCTGATTTCAGAAG	165943	CTTCTGAAATCAGGTGCAGC
156724	7363	GGCTGCACCTGATTTCAGAA	165944	TTCTGAAATCAGGTGCAGCC
156725	7364	GGGCTGCACCTGATTTCAGA	165945	TCTGAAATCAGGTGCAGCCC
156726	7365	GGGGCTGCACCTGATTTCAG	165946	CTGAAATCAGGTGCAGCCCC
156727	7366	TGGGGCTGCACCTGATTTCA	165947	TGAAATCAGGTGCAGCCCCA
156728	7367	ATGGGGCTGCACCTGATTTC	165948	GAAATCAGGTGCAGCCCCAT
156729	7368	GATGGGGCTGCACCTGATTT	165949	AAATCAGGTGCAGCCCCATC
156730	7369	AGATGGGGCTGCACCTGATT	165950	AATCAGGTGCAGCCCCATCT
156731	7370	AAGATGGGGCTGCACCTGAT	165951	ATCAGGTGCAGCCCCATCTT
156732	7371	AAAGATGGGGCTGCACCTGA	165952	TCAGGTGCAGCCCCATCTTT
156733	7372	GAAAGATGGGGCTGCACCTG	165953	CAGGTGCAGCCCCATCTTTC
156734	7373	AGAAAGATGGGGCTGCACCT	165954	AGGTGCAGCCCCATCTTTCT
156735	7374	AAGAAAGATGGGGCTGCACC	165955	GGTGCAGCCCCATCTTTCTT
156736	7375	GAAGAAAGATGGGGCTGCAC	165956	GTGCAGCCCCATCTTTCTTC
156737	7376	GGAAGAAAGATGGGGCTGCA	165957	TGCAGCCCCATCTTTCTTCC
156738	7377	GGGAAGAAAGATGGGGCTGC	165958	GCAGCCCCATCTTTCTTCCC
156739	7378	TGGGAAGAAAGATGGGGCTG	165959	CAGCCCCATCTTTCTTCCCA
156740	7379	CTGGGAAGAAAGATGGGGCT	165960	AGCCCCATCTTTCTTCCCAG
156741	7380	TCTGGGAAGAAAGATGGGGC	165961	GCCCCATCTTTCTTCCCAGA
156742	7381	CTCTGGGAAGAAAGATGGGG	165962	CCCCATCTTTCTTCCCAGAG
156743	7382	GCTCTGGGAAGAAAGATGGG	165963	CCCATCTTTCTTCCCAGAGC
156744	7383	TGCTCTGGGAAGAAAGATGG	165964	CCATCTTTCTTCCCAGAGCA
156745	7384	ATGCTCTGGGAAGAAAGATG	165965	CATCTTTCTTCCCAGAGCAT
156746	7385	AATGCTCTGGGAAGAAAGAT	165966	ATCTTTCTTCCCAGAGCATT
156747	7386	TAATGCTCTGGGAAGAAAGA	165967	TCTTTCTTCCCAGAGCATTA
156748	7387	CTAATGCTCTGGGAAGAAAG	165968	CTTTCTTCCCAGAGCATTAG
156749	7388	ACTAATGCTCTGGGAAGAAA	165969	TTTCTTCCCAGAGCATTAGT
156750	7389	CACTAATGCTCTGGGAAGAA	165970	TTCTTCCCAGAGCATTAGTG
156751	7390	ACACTAATGCTCTGGGAAGA	165971	TCTTCCCAGAGCATTAGTGT
156752	7391	CACACTAATGCTCTGGGAAG	165972	CTTCCCAGAGCATTAGTGTG
156753	7392	ACACACTAATGCTCTGGGAA	165973	TTCCCAGAGCATTAGTGTGT
156754	7393	TACACACTAATGCTCTGGGA	165974	TCCCAGAGCATTAGTGTGTA
156755	7394	CTACACACTAATGCTCTGGG	165975	CCCAGAGCATTAGTGTGTAG
156756	7395	TCTACACACTAATGCTCTGG	165976	CCAGAGCATTAGTGTGTAGA
156757	7396	GTCTACACACTAATGCTCTG	165977	CAGAGCATTAGTGTGTAGAC
156758	7397	CGTCTACACACTAATGCTCT	165978	AGAGCATTAGTGTGTAGACG
156759	7398	ACGTCTACACACTAATGCTC	165979	GAGCATTAGTGTGTAGACGT
156760	7399	CACGTCTACACACTAATGCT	165980	AGCATTAGTGTGTAGACGTG
156761	7400	TCACGTCTACACACTAATGC	165981	GCATTAGTGTGTAGACGTGA
156762	7401	TTCACGTCTACACACTAATG	165982	CATTAGTGTGTAGACGTGAA
156763	7402	CTTCACGTCTACACACTAAT	165983	ATTAGTGTGTAGACGTGAAG
156764	7403	GCTTCACGTCTACACACTAA	165984	TTAGTGTGTAGACGTGAAGC
156765	7404	GGCTTCACGTCTACACACTA	165985	TAGTGTGTAGACGTGAAGCC
156766	7405	AGGCTTCACGTCTACACACT	165986	AGTGTGTAGACGTGAAGCCT
156767	7406	AAGGCTTCACGTCTACACAC	165987	GTGTGTAGACGTGAAGCCTT
156768	7407	CAAGGCTTCACGTCTACACA	165988	TGTGTAGACGTGAAGCCTTG
156769	7408	ACAAGGCTTCACGTCTACAC	165989	GTGTAGACGTGAAGCCTTGT
156770	7409	AACAAGGCTTCACGTCTACA	165990	TGTAGACGTGAAGCCTTGTT
156771	7410	AAACAAGGCTTCACGTCTAC	165991	GTAGACGTGAAGCCTTGTTT
156772	7411	CAAACAAGGCTTCACGTCTA	165992	TAGACGTGAAGCCTTGTTTG
156773	7412	TCAAACAAGGCTTCACGTCT	165993	AGACGTGAAGCCTTGTTTGA
156774	7413	TTCAAACAAGGCTTCACGTC	165994	GACGTGAAGCCTTGTTTGAA
156775	7414	CTTCAAACAAGGCTTCACGT	165995	ACGTGAAGCCTTGTTTGAAG

156776	7415	TCTTCAAACAAGGCTTCACG	165996	CGTGAAGCCTTGTTTGAAGA
156777	7416	CTCTTCAAACAAGGCTTCAC	165997	GTGAAGCCTTGTTTGAAGAG
156778	7417	GCTCTTCAAACAAGGCTTCA	165998	TGAAGCCTTGTTTGAAGAGC
156779	7418	AGCTCTTCAAACAAGGCTTC	165999	GAAGCCTTGTTTGAAGAGCT
156780	7419	CAGCTCTTCAAACAAGGCTT	166000	AAGCCTTGTTTGAAGAGCTG
156781	7420	ACAGCTCTTCAAACAAGGCT	166001	AGCCTTGTTTGAAGAGCTGT
156782	7421	TACAGCTCTTCAAACAAGGC	166002	GCCTTGTTTGAAGAGCTGTA
156783	7422	ATACAGCTCTTCAAACAAGG	166003	CCTTGTTTGAAGAGCTGTAT
156784	7423	AATACAGCTCTTCAAACAAG	166004	CTTGTTTGAAGAGCTGTATT
156785	7424	AAATACAGCTCTTCAAACAA	166005	TTGTTTGAAGAGCTGTATTT
156786	7425	TAAATACAGCTCTTCAAACA	166006	TGTTTGAAGAGCTGTATTTA
156787	7426	CTAAATACAGCTCTTCAAAC	166007	GTTTGAAGAGCTGTATTTAG
156788	7427	TCTAAATACAGCTCTTCAAA	166008	TTTGAAGAGCTGTATTTAGA
156789	7428	TTCTAAATACAGCTCTTCAA	166009	TTGAAGAGCTGTATTTAGAA
156790	7429	ATTCTAAATACAGCTCTTCA	166010	TGAAGAGCTGTATTTAGAAT
156791	7430	CATTCTAAATACAGCTCTTC	166011	GAAGAGCTGTATTTAGAATG
156792	7431	GCATTCTAAATACAGCTCTT	166012	AAGAGCTGTATTTAGAATGC
156793	7432	GGCATTCTAAATACAGCTCT	166013	AGAGCTGTATTTAGAATGCC
156794	7433	AGGCATTCTAAATACAGCTC	166014	GAGCTGTATTTAGAATGCCT
156795	7434	TAGGCATTCTAAATACAGCT	166015	AGCTGTATTTAGAATGCCTA
156796	7435	CTAGGCATTCTAAATACAGC	166016	GCTGTATTTAGAATGCCTAG
156797	7436	GCTAGGCATTCTAAATACAG	166017	CTGTATTTAGAATGCCTAGC
156798	7437	AGCTAGGCATTCTAAATACA	166018	TGTATTTAGAATGCCTAGCT
156799	7438	TAGCTAGGCATTCTAAATAC	166019	GTATTTAGAATGCCTAGCTA
156800	7439	GTAGCTAGGCATTCTAAATA	166020	TATTTAGAATGCCTAGCTAC
156801	7440	AGTAGCTAGGCATTCTAAAT	166021	ATTTAGAATGCCTAGCTACT
156802	7441	AAGTAGCTAGGCATTCTAAA	166022	TTTAGAATGCCTAGCTACTT
156803	7442	CAAGTAGCTAGGCATTCTAA	166023	TTAGAATGCCTAGCTACTTG
156804	7443	ACAAGTAGCTAGGCATTCTA	166024	TAGAATGCCTAGCTACTTGT
156805	7444	AACAAGTAGCTAGGCATTCT	166025	AGAATGCCTAGCTACTTGTT
156806	7445	AAACAAGTAGCTAGGCATTC	166026	GAATGCCTAGCTACTTGTTT
156807	7446	CAAACAAGTAGCTAGGCATT	166027	AATGCCTAGCTACTTGTTTG
156808	7447	GCAAACAAGTAGCTAGGCAT	166028	ATGCCTAGCTACTTGTTTGC
156809	7448	TGCAAACAAGTAGCTAGGCA	166029	TGCCTAGCTACTTGTTTGCA
156810	7449	TTGCAAACAAGTAGCTAGGC	166030	GCCTAGCTACTTGTTTGCAA
156811	7450	TTTGCAAACAAGTAGCTAGG	166031	CCTAGCTACTTGTTTGCAAA
156812	7451	ATTTGCAAACAAGTAGCTAG	166032	CTAGCTACTTGTTTGCAAAT
156813	7452	AATTTGCAAACAAGTAGCTA	166033	TAGCTACTTGTTTGCAAATT
156814	7453	AAATTTGCAAACAAGTAGCT	166034	AGCTACTTGTTTGCAAATTT
156815	7454	CAAATTTGCAAACAAGTAGC	166035	GCTACTTGTTTGCAAATTTG
156816	7455	ACAAATTTGCAAACAAGTAG	166036	CTACTTGTTTGCAAATTTGT
156817	7456	CACAAATTTGCAAACAAGTA	166037	TACTTGTTTGCAAATTTGTG
156818	7457	ACACAAATTTGCAAACAAGT	166038	ACTTGTTTGCAAATTTGTGT
156819	7458	GACACAAATTTGCAAACAAG	166039	CTTGTTTGCAAATTTGTGTC
156820	7459	AGACACAAATTTGCAAACAA	166040	TTGTTTGCAAATTTGTGTCT
156821	7460	TAGACACAAATTTGCAAACA	166041	TGTTTGCAAATTTGTGTCTA
156822	7461	GTAGACACAAATTTGCAAAC	166042	GTTTGCAAATTTGTGTCTAC
156823	7462	AGTAGACACAAATTTGCAAA	166043	TTTGCAAATTTGTGTCTACT
156824	7463	GAGTAGACACAAATTTGCAA	166044	TTGCAAATTTGTGTCTACTC
156825	7464	TGAGTAGACACAAATTTGCA	166045	TGCAAATTTGTGTCTACTCA
156826	7465	CTGAGTAGACACAAATTTGC	166046	GCAAATTTGTGTCTACTCAG
156827	7466	ACTGAGTAGACACAAATTTG	166047	CAAATTTGTGTCTACTCAGT
156828	7467	GACTGAGTAGACACAAATTT	166048	AAATTTGTGTCTACTCAGTC
156829	7468	TGACTGAGTAGACACAAATT	166049	AATTTGTGTCTACTCAGTCA
156830	7469	TTGACTGAGTAGACACAAAT	166050	ATTTGTGTCTACTCAGTCAA
156831	7470	CTTGACTGAGTAGACACAAA	166051	TTTGTGTCTACTCAGTCAAG
156832	7471	ACTTGACTGAGTAGACACAA	166052	TTGTGTCTACTCAGTCAAGT
156833	7472	AACTTGACTGAGTAGACACA	166053	TGTGTCTACTCAGTCAAGTT
156834	7473	AAACTTGACTGAGTAGACAC	166054	GTGTCTACTCAGTCAAGTTT
156835	7474	AAAACTTGACTGAGTAGACA	166055	TGTCTACTCAGTCAAGTTTT
156836	7475	TAAAACTTGACTGAGTAGAC	166056	GTCTACTCAGTCAAGTTTTA
156837	7476	TTAAAACTTGACTGAGTAGA	166057	TCTACTCAGTCAAGTTTTAA
156838	7477	ATTAAAACTTGACTGAGTAG	166058	CTACTCAGTCAAGTTTTAAT
156839	7478	AATTAAAACTTGACTGAGTA	166059	TACTCAGTCAAGTTTTAATT
156840	7479	AAATTAAAACTTGACTGAGT	166060	ACTCAGTCAAGTTTTAATTT
156841	7480	TAAATTAAAACTTGACTGAG	166061	CTCAGTCAAGTTTTAATTTA
156842	7481	CTAAATTAAAACTTGACTGA	166062	TCAGTCAAGTTTTAATTTAG
156843	7482	GCTAAATTAAAACTTGACTG	166063	CAGTCAAGTTTTAATTTAGC
156844	7483	AGCTAAATTAAAACTTGACT	166064	AGTCAAGTTTTAATTTAGCT
156845	7484	GAGCTAAATTAAAACTTGAC	166065	GTCAAGTTTTAATTTAGCTC
156846	7485	TGAGCTAAATTAAAACTTGA	166066	TCAAGTTTTAATTTAGCTCA
156847	7486	ATGAGCTAAATTAAAACTTG	166067	CAAGTTTTAATTTAGCTCAT

156848	7487	CATGAGCTAAATTAAAACTT	166068	AAGTTTTAATTTAGCTCATG
156849	7488	TCATGAGCTAAATTAAAACT	166069	AGTTTTAATTTAGCTCATGA
156850	7489	TTCATGAGCTAAATTAAAAC	166070	GTTTTAATTTAGCTCATGAA
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156852	7491	AGTTCATGAGCTAAATTAAA	166072	TTTAATTTAGCTCATGAACT
156853	7492	TAGTTCATGAGCTAAATTAA	166073	TTAATTTAGCTCATGAACTA
156854	7493	GTAGTTCATGAGCTAAATTA	166074	TAATTTAGCTCATGAACTAC
156855	7494	GGTAGTTCATGAGCTAAATT	166075	AATTTAGCTCATGAACTACC
156856	7495	AGGTAGTTCATGAGCTAAAT	166076	ATTTAGCTCATGAACTACCT
156857	7496	AAGGTAGTTCATGAGCTAAA	166077	TTTAGCTCATGAACTACCTT
156858	7497	CAAGGTAGTTCATGAGCTAA	166078	TTAGCTCATGAACTACCTTG
156859	7498	TCAAGGTAGTTCATGAGCTA	166079	TAGCTCATGAACTACCTTGA
156860	7499	ATCAAGGTAGTTCATGAGCT	166080	AGCTCATGAACTACCTTGAT
156861	7500	CATCAAGGTAGTTCATGAGC	166081	GCTCATGAACTACCTTGATG
156862	7501	ACATCAAGGTAGTTCATGAG	166082	CTCATGAACTACCTTGATGT
156863	7502	AACATCAAGGTAGTTCATGA	166083	TCATGAACTACCTTGATGTT
156864	7503	AAACATCAAGGTAGTTCATG	166084	CATGAACTACCTTGATGTTT
156865	7504	TAAACATCAAGGTAGTTCAT	166085	ATGAACTACCTTGATGTTTA
156866	7505	CTAAACATCAAGGTAGTTCA	166086	TGAACTACCTTGATGTTTAG
156867	7506	ACTAAACATCAAGGTAGTTC	166087	GAACTACCTTGATGTTTAGT
156868	7507	CACTAAACATCAAGGTAGTT	166088	AACTACCTTGATGTTTAGTG
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156872	7511	ATGCCACTAAACATCAAGGT	166092	ACCTTGATGTTTAGTGGCAT
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156875	7514	CTGATGCCACTAAACATCAA	166095	TTGATGTTTAGTGGCATCAG
156876	7515	GCTGATGCCACTAAACATCA	166096	TGATGTTTAGTGGCATCAGC
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156878	7517	GGGCTGATGCCACTAAACAT	166098	ATGTTTAGTGGCATCAGCCC
156879	7518	AGGGCTGATGCCACTAAACA	166099	TGTTTAGTGGCATCAGCCCT
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156882	7521	ATTAGGGCTGATGCCACTAA	166102	TTAGTGGCATCAGCCCTAAT
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156884	7523	GGATTAGGGCTGATGCCACT	166104	AGTGGCATCAGCCCTAATCC
156885	7524	TGGATTAGGGCTGATGCCAC	166105	GTGGCATCAGCCCTAATCCA
156886	7525	ATGGATTAGGGCTGATGCCA	166106	TGGCATCAGCCCTAATCCAT
156887	7526	GATGGATTAGGGCTGATGCC	166107	GGCATCAGCCCTAATCCATC
156888	7527	AGATGGATTAGGGCTGATGC	166108	GCATCAGCCCTAATCCATCT
156889	7528	CAGATGGATTAGGGCTGATG	166109	CATCAGCCCTAATCCATCTG
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156891	7530	ATCAGATGGATTAGGGCTGA	166111	TCAGCCCTAATCCATCTGAT
156892	7531	CATCAGATGGATTAGGGCTG	166112	CAGCCCTAATCCATCTGATG
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156894	7533	AGCATCAGATGGATTAGGGC	166114	GCCCTAATCCATCTGATGCT
156895	7534	AAGCATCAGATGGATTAGGG	166115	CCCTAATCCATCTGATGCTT
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156897	7536	AAAAGCATCAGATGGATTAG	166117	CTAATCCATCTGATGCTTTT
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156906	7545	TAATAATGAAAAAGCATCAG	166126	CTGATGCTTTTTCATTATTA
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156908	7547	CCTAATAATGAAAAAGCATC	166128	GATGCTTTTTCATTATTAGG
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156910	7549	TGCCTAATAATGAAAAAGCA	166130	TGCTTTTTCATTATTAGGCA
156911	7550	ATGCCTAATAATGAAAAAGC	166131	GCTTTTTCATTATTAGGCAT
156912	7551	CATGCCTAATAATGAAAAAG	166132	CTTTTTCATTATTAGGCATG
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156914	7553	AACATGCCTAATAATGAAAA	166134	TTTTCATTATTAGGCATGTT
156915	7554	CAACATGCCTAATAATGAAA	166135	TTTCATTATTAGGCATGTTG
156916	7555	CCAACATGCCTAATAATGAA	166136	TTCATTATTAGGCATGTTGG
156917	7556	TCCAACATGCCTAATAATGA	166137	TCATTATTAGGCATGTTGGA
156918	7557	CTCCAACATGCCTAATAATG	166138	CATTATTAGGCATGTTGGAG
156919	7558	TCTCCAACATGCCTAATAAT	166139	ATTATTAGGCATGTTGGAGA

156920	7559	GTCTCCAACATGCCTAATAA	166140	TTATTAGGCATGTTGGAGAC
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156922	7561	AAGTCTCCAACATGCCTAAT	166142	ATTAGGCATGTTGGAGACTT
156923	7562	CAAGTCTCCAACATGCCTAA	166143	TTAGGCATGTTGGAGACTTG
156924	7563	CCAAGTCTCCAACATGCCTA	166144	TAGGCATGTTGGAGACTTGG
156925	7564	CCCAAGTCTCCAACATGCCT	166145	AGGCATGTTGGAGACTTGGG
156926	7565	GCCCAAGTCTCCAACATGCC	166146	GGCATGTTGGAGACTTGGGC
156927	7566	TGCCCAAGTCTCCAACATGC	166147	GCATGTTGGAGACTTGGGCA
156928	7567	TTGCCCAAGTCTCCAACATG	166148	CATGTTGGAGACTTGGGCAA
156929	7568	ATTGCCCAAGTCTCCAACAT	166149	ATGTTGGAGACTTGGGCAAT
156930	7569	CATTGCCCAAGTCTCCAACA	166150	TGTTGGAGACTTGGGCAATG
156931	7570	ACATTGCCCAAGTCTCCAAC	166151	GTTGGAGACTTGGGCAATGT
156932	7571	CACATTGCCCAAGTCTCCAA	166152	TTGGAGACTTGGGCAATGTG
156933	7572	TCACATTGCCCAAGTCTCCA	166153	TGGAGACTTGGGCAATGTGA
156934	7573	GTCACATTGCCCAAGTCTCC	166154	GGAGACTTGGGCAATGTGAC
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156936	7575	CAGTCACATTGCCCAAGTCT	166156	AGACTTGGGCAATGTGACTG
156937	7576	GCAGTCACATTGCCCAAGTC	166157	GACTTGGGCAATGTGACTGC
156938	7577	AGCAGTCACATTGCCCAAGT	166158	ACTTGGGCAATGTGACTGCT
156939	7578	CAGCAGTCACATTGCCCAAG	166159	CTTGGGCAATGTGACTGCTG
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156941	7580	GTCAGCAGTCACATTGCCCA	166161	TGGGCAATGTGACTGCTGAC
156942	7581	TGTCAGCAGTCACATTGCCC	166162	GGGCAATGTGACTGCTGACA
156943	7582	TTGTCAGCAGTCACATTGCC	166163	GGCAATGTGACTGCTGACAA
156944	7583	TTTGTCAGCAGTCACATTGC	166164	GCAATGTGACTGCTGACAAA
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156948	7587	CATCTTTGTCAGCAGTCACA	166168	TGTGACTGCTGACAAAGATG
156949	7588	CCATCTTTGTCAGCAGTCAC	166169	GTGACTGCTGACAAAGATGG
156950	7589	ACCATCTTTGTCAGCAGTCA	166170	TGACTGCTGACAAAGATGGT
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156952	7591	ACACCATCTTTGTCAGCAGT	166172	ACTGCTGACAAAGATGGTGT
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156954	7593	CCACACCATCTTTGTCAGCA	166174	TGCTGACAAAGATGGTGTGG
156955	7594	GCCACACCATCTTTGTCAGC	166175	GCTGACAAAGATGGTGTGGC
156956	7595	GGCCACACCATCTTTGTCAG	166176	CTGACAAAGATGGTGTGGCC
156957	7596	CGGCCACACCATCTTTGTCA	166177	TGACAAAGATGGTGTGGCCG
156958	7597	TCGGCCACACCATCTTTGTC	166178	GACAAAGATGGTGTGGCCGA
156959	7598	ATCGGCCACACCATCTTTGT	166179	ACAAAGATGGTGTGGCCGAT
156960	7599	CATCGGCCACACCATCTTTG	166180	CAAAGATGGTGTGGCCGATG
156961	7600	ACATCGGCCACACCATCTTT	166181	AAAGATGGTGTGGCCGATGT
156962	7601	CACATCGGCCACACCATCTT	166182	AAGATGGTGTGGCCGATGTG
156963	7602	ACACATCGGCCACACCATCT	166183	AGATGGTGTGGCCGATGTGT
156964	7603	GACACATCGGCCACACCATC	166184	GATGGTGTGGCCGATGTGTC
156965	7604	AGACACATCGGCCACACCAT	166185	ATGGTGTGGCCGATGTGTCT
156966	7605	TAGACACATCGGCCACACCA	166186	TGGTGTGGCCGATGTGTCTA
156967	7606	ATAGACACATCGGCCACACC	166187	GGTGTGGCCGATGTGTCTAT
156968	7607	AATAGACACATCGGCCACAC	166188	GTGTGGCCGATGTGTCTATT
156969	7608	CAATAGACACATCGGCCACA	166189	TGTGGCCGATGTGTCTATTG
156970	7609	TCAATAGACACATCGGCCAC	166190	GTGGCCGATGTGTCTATTGA
156971	7610	TTCAATAGACACATCGGCCA	166191	TGGCCGATGTGTCTATTGAA
156972	7611	CTTCAATAGACACATCGGCC	166192	GGCCGATGTGTCTATTGAAG
156973	7612	TCTTCAATAGACACATCGGC	166193	GCCGATGTGTCTATTGAAGA
156974	7613	ATCTTCAATAGACACATCGG	166194	CCGATGTGTCTATTGAAGAT
156975	7614	AATCTTCAATAGACACATCG	166195	CGATGTGTCTATTGAAGATT
156976	7615	GAATCTTCAATAGACACATC	166196	GATGTGTCTATTGAAGATTC
156977	7616	AGAATCTTCAATAGACACAT	166197	ATGTGTCTATTGAAGATTCT
156978	7617	CAGAATCTTCAATAGACACA	166198	TGTGTCTATTGAAGATTCTG
156979	7618	ACAGAATCTTCAATAGACAC	166199	GTGTCTATTGAAGATTCTGT
156980	7619	CACAGAATCTTCAATAGACA	166200	TGTCTATTGAAGATTCTGTG
156981	7620	TCACAGAATCTTCAATAGAC	166201	GTCTATTGAAGATTCTGTGA
156982	7621	ATCACAGAATCTTCAATAGA	166202	TCTATTGAAGATTCTGTGAT
156983	7622	GATCACAGAATCTTCAATAG	166203	CTATTGAAGATTCTGTGATC
156984	7623	AGATCACAGAATCTTCAATA	166204	TATTGAAGATTCTGTGATCT
156985	7624	GAGATCACAGAATCTTCAAT	166205	ATTGAAGATTCTGTGATCTC
156986	7625	TGAGATCACAGAATCTTCAA	166206	TTGAAGATTCTGTGATCTCA
156987	7626	GTGAGATCACAGAATCTTCA	166207	TGAAGATTCTGTGATCTCAC
156988	7627	AGTGAGATCACAGAATCTTC	166208	GAAGATTCTGTGATCTCACT
156989	7628	GAGTGAGATCACAGAATCTT	166209	AAGATTCTGTGATCTCACTC
156990	7629	AGAGTGAGATCACAGAATCT	166210	AGATTCTGTGATCTCACTCT
156991	7630	GAGAGTGAGATCACAGAATC	166211	GATTCTGTGATCTCACTCTC

156992	7631	TGAGAGTGAGATCACAGAAT	166212	ATTCTGTGATCTCACTCTCA
156993	7632	CTGAGAGTGAGATCACAGAA	166213	TTCTGTGATCTCACTCTCAG
156994	7633	CCTGAGAGTGAGATCACAGA	166214	TCTGTGATCTCACTCTCAGG
156995	7634	TCCTGAGAGTGAGATCACAG	166215	CTGTGATCTCACTCTCAGGA
156996	7635	CTCCTGAGAGTGAGATCACA	166216	TGTGATCTCACTCTCAGGAG
156997	7636	TCTCCTGAGAGTGAGATCAC	166217	GTGATCTCACTCTCAGGAGA
156998	7637	GTCTCCTGAGAGTGAGATCA	166218	TGATCTCACTCTCAGGAGAC
156999	7638	GGTCTCCTGAGAGTGAGATC	166219	GATCTCACTCTCAGGAGACC
157000	7639	TGGTCTCCTGAGAGTGAGAT	166220	ATCTCACTCTCAGGAGACCA
157001	7640	ATGGTCTCCTGAGAGTGAGA	166221	TCTCACTCTCAGGAGACCAT
157002	7641	AATGGTCTCCTGAGAGTGAG	166222	CTCACTCTCAGGAGACCATT
157003	7642	CAATGGTCTCCTGAGAGTGA	166223	TCACTCTCAGGAGACCATTG
157004	7643	GCAATGGTCTCCTGAGAGTG	166224	CACTCTCAGGAGACCATTGC
157005	7644	TGCAATGGTCTCCTGAGAGT	166225	ACTCTCAGGAGACCATTGCA
157006	7645	ATGCAATGGTCTCCTGAGAG	166226	CTCTCAGGAGACCATTGCAT
157007	7646	GATGCAATGGTCTCCTGAGA	166227	TCTCAGGAGACCATTGCATC
157008	7647	TGATGCAATGGTCTCCTGAG	166228	CTCAGGAGACCATTGCATCA
157009	7648	ATGATGCAATGGTCTCCTGA	166229	TCAGGAGACCATTGCATCAT
157010	7649	AATGATGCAATGGTCTCCTG	166230	CAGGAGACCATTGCATCATT
157011	7650	CAATGATGCAATGGTCTCCT	166231	AGGAGACCATTGCATCATTG
157012	7651	CCAATGATGCAATGGTCTCC	166232	GGAGACCATTGCATCATTGG
157013	7652	GCCAATGATGCAATGGTCTC	166233	GAGACCATTGCATCATTGGC
157014	7653	GGCCAATGATGCAATGGTCT	166234	AGACCATTGCATCATTGGCC
157015	7654	CGGCCAATGATGCAATGGTC	166235	GACCATTGCATCATTGGCCG
157016	7655	GCGGCCAATGATGCAATGGT	166236	ACCATTGCATCATTGGCCGC
157017	7656	TGCGGCCAATGATGCAATGG	166237	CCATTGCATCATTGGCCGCA
157018	7657	GTGCGGCCAATGATGCAATG	166238	CATTGCATCATTGGCCGCAC
157019	7658	TGTGCGGCCAATGATGCAAT	166239	ATTGCATCATTGGCCGCACA
157020	7659	GTGTGCGGCCAATGATGCAA	166240	TTGCATCATTGGCCGCACAC
157021	7660	AGTGTGCGGCCAATGATGCA	166241	TGCATCATTGGCCGCACACT
157022	7661	CAGTGTGCGGCCAATGATGC	166242	GCATCATTGGCCGCACACTG
157023	7662	CCAGTGTGCGGCCAATGATG	166243	CATCATTGGCCGCACACTGG
157024	7663	ACCAGTGTGCGGCCAATGAT	166244	ATCATTGGCCGCACACTGGT
157025	7664	CACCAGTGTGCGGCCAATGA	166245	TCATTGGCCGCACACTGGTG
157026	7665	CCACCAGTGTGCGGCCAATG	166246	CATTGGCCGCACACTGGTGG
157027	7666	ACCACCAGTGTGCGGCCAAT	166247	ATTGGCCGCACACTGGTGGT
157028	7667	TACCACCAGTGTGCGGCCAA	166248	TTGGCCGCACACTGGTGGTA
157029	7668	TTACCACCAGTGTGCGGCCA	166249	TGGCCGCACACTGGTGGTAA
157030	7669	CTTACCACCAGTGTGCGGCC	166250	GGCCGCACACTGGTGGTAAG
157031	7670	ACTTACCACCAGTGTGCGGC	166251	GCCGCACACTGGTGGTAAGT
157032	7671	AACTTACCACCAGTGTGCGG	166252	CCGCACACTGGTGGTAAGTT
157033	7672	AAACTTACCACCAGTGTGCG	166253	CGCACACTGGTGGTAAGTTT
157034	7673	AAAACTTACCACCAGTGTGC	166254	GCACACTGGTGGTAAGTTTT
157035	7674	GAAAACTTACCACCAGTGTG	166255	CACACTGGTGGTAAGTTTTC
157036	7675	TGAAAACTTACCACCAGTGT	166256	ACACTGGTGGTAAGTTTTCA
157037	7676	ATGAAAACTTACCACCAGTG	166257	CACTGGTGGTAAGTTTTCAT
157038	7677	TATGAAAACTTACCACCAGT	166258	ACTGGTGGTAAGTTTTCATA
157039	7678	TTATGAAAACTTACCACCAG	166259	CTGGTGGTAAGTTTTCATAA
157040	7679	TTTATGAAAACTTACCACCA	166260	TGGTGGTAAGTTTTCATAAA
157041	7680	TTTTATGAAAACTTACCACC	166261	GGTGGTAAGTTTTCATAAAA
157042	7681	CTTTTATGAAAACTTACCAC	166262	GTGGTAAGTTTTCATAAAAG
157043	7682	CCTTTTATGAAAACTTACCA	166263	TGGTAAGTTTTCATAAAAGG
157044	7683	TCCTTTTATGAAAACTTACC	166264	GGTAAGTTTTCATAAAAGGA
157045	7684	ATCCTTTTATGAAAACTTAC	166265	GTAAGTTTTCATAAAAGGAT
157046	7685	TATCCTTTTATGAAAACTTA	166266	TAAGTTTTCATAAAAGGATA
157047	7686	ATATCCTTTTATGAAAACTT	166267	AAGTTTTCATAAAAGGATAT
157048	7687	CATATCCTTTTATGAAAACT	166268	AGTTTTCATAAAAGGATATG
157049	7688	GCATATCCTTTTATGAAAAC	166269	GTTTTCATAAAAGGATATGC
157050	7689	TGCATATCCTTTTATGAAAA	166270	TTTTCATAAAAGGATATGCA
157051	7690	ATGCATATCCTTTTATGAAA	166271	TTTCATAAAAGGATATGCAT
157052	7691	TATGCATATCCTTTTATGAA	166272	TTCATAAAAGGATATGCATA
157053	7692	TTATGCATATCCTTTTATGA	166273	TCATAAAAGGATATGCATAA
157054	7693	TTTATGCATATCCTTTTATG	166274	CATAAAAGGATATGCATAAA
157055	7694	TTTTATGCATATCCTTTTAT	166275	ATAAAAGGATATGCATAAAA
157056	7695	GTTTTATGCATATCCTTTTA	166276	TAAAAGGATATGCATAAAAC
157057	7696	AGTTTTATGCATATCCTTTT	166277	AAAAGGATATGCATAAAACT
157058	7697	AAGTTTTATGCATATCCTTT	166278	AAAGGATATGCATAAAACTT
157059	7698	GAAGTTTTATGCATATCCTT	166279	AAGGATATGCATAAAACTTC
157060	7699	AGAAGTTTTATGCATATCCT	166280	AGGATATGCATAAAACTTCT
157061	7700	AAGAAGTTTTATGCATATCC	166281	GGATATGCATAAAACTTCTT
157062	7701	GAAGAAGTTTTATGCATATC	166282	GATATGCATAAAACTTCTTC
157063	7702	AGAAGAAGTTTTATGCATAT	166283	ATATGCATAAAACTTCTTCT

157064	7703	TAGAAGAAGTTTTATGCATA	166284	TATGCATAAAACTTCTTCTA
157065	7704	TTAGAAGAAGTTTTATGCAT	166285	ATGCATAAAACTTCTTCTAA
157066	7705	GTTAGAAGAAGTTTTATGCA	166286	TGCATAAAACTTCTTCTAAC
157067	7706	TGTTAGAAGAAGTTTTATGC	166287	GCATAAAACTTCTTCTAACA
157068	7707	ATGTTAGAAGAAGTTTTATG	166288	CATAAAACTTCTTCTAACAT
157069	7708	TATGTTAGAAGAAGTTTTAT	166289	ATAAAACTTCTTCTAACATA
157070	7709	GTATGTTAGAAGAAGTTTTA	166290	TAAAACTTCTTCTAACATAC
157071	7710	TGTATGTTAGAAGAAGTTTT	166291	AAAACTTCTTCTAACATACA
157072	7711	CTGTATGTTAGAAGAAGTTT	166292	AAACTTCTTCTAACATACAG
157073	7712	ACTGTATGTTAGAAGAAGTT	166293	AACTTCTTCTAACATACAGT
157074	7713	GACTGTATGTTAGAAGAAGT	166294	ACTTCTTCTAACATACAGTC
157075	7714	TGACTGTATGTTAGAAGAAG	166295	CTTCTTCTAACATACAGTCA
157076	7715	ATGACTGTATGTTAGAAGAA	166296	TTCTTCTAACATACAGTCAT
157077	7716	CATGACTGTATGTTAGAAGA	166297	TCTTCTAACATACAGTCATG
157078	7717	ACATGACTGTATGTTAGAAG	166298	CTTCTAACATACAGTCATGT
157079	7718	TACATGACTGTATGTTAGAA	166299	TTCTAACATACAGTCATGTA
157080	7719	ATACATGACTGTATGTTAGA	166300	TCTAACATACAGTCATGTAT
157081	7720	GATACATGACTGTATGTTAG	166301	CTAACATACAGTCATGTATC
157082	7721	AGATACATGACTGTATGTTA	166302	TAACATACAGTCATGTATCT
157083	7722	AAGATACATGACTGTATGTT	166303	AACATACAGTCATGTATCTT
157084	7723	AAAGATACATGACTGTATGT	166304	ACATACAGTCATGTATCTTT
157085	7724	AAAAGATACATGACTGTATG	166305	CATACAGTCATGTATCTTTT
157086	7725	GAAAAGATACATGACTGTAT	166306	ATACAGTCATGTATCTTTTC
157087	7726	TGAAAAGATACATGACTGTA	166307	TACAGTCATGTATCTTTTCA
157088	7727	GTGAAAAGATACATGACTGT	166308	ACAGTCATGTATCTTTTCAC
157089	7728	AGTGAAAAGATACATGACTG	166309	CAGTCATGTATCTTTTCACT
157090	7729	AAGTGAAAAGATACATGACT	166310	AGTCATGTATCTTTTCACTT
157091	7730	AAAGTGAAAAGATACATGAC	166311	GTCATGTATCTTTTCACTTT
157092	7731	CAAAGTGAAAAGATACATGA	166312	TCATGTATCTTTTCACTTTG
157093	7732	TCAAAGTGAAAAGATACATG	166313	CATGTATCTTTTCACTTTGA
157094	7733	ATCAAAGTGAAAAGATACAT	166314	ATGTATCTTTTCACTTTGAT
157095	7734	AATCAAAGTGAAAAGATACA	166315	TGTATCTTTTCACTTTGATT
157096	7735	CAATCAAAGTGAAAAGATAC	166316	GTATCTTTTCACTTTGATTG
157097	7736	ACAATCAAAGTGAAAAGATA	166317	TATCTTTTCACTTTGATTGT
157098	7737	AACAATCAAAGTGAAAAGAT	166318	ATCTTTTCACTTTGATTGTT
157099	7738	TAACAATCAAAGTGAAAAGA	166319	TCTTTTCACTTTGATTGTTA
157100	7739	CTAACAATCAAAGTGAAAAG	166320	CTTTTCACTTTGATTGTTAG
157101	7740	ACTAACAATCAAAGTGAAAA	166321	TTTTCACTTTGATTGTTAGT
157102	7741	GACTAACAATCAAAGTGAAA	166322	TTTCACTTTGATTGTTAGTC
157103	7742	CGACTAACAATCAAAGTGAA	166323	TTCACTTTGATTGTTAGTCG
157104	7743	GCGACTAACAATCAAAGTGA	166324	TCACTTTGATTGTTAGTCGC
157105	7744	CGCGACTAACAATCAAAGTG	166325	CACTTTGATTGTTAGTCGCG
157106	7745	CCGCGACTAACAATCAAAGT	166326	ACTTTGATTGTTAGTCGCGG
157107	7746	ACCGCGACTAACAATCAAAG	166327	CTTTGATTGTTAGTCGCGGT
157108	7747	AACCGCGACTAACAATCAAA	166328	TTTGATTGTTAGTCGCGGTT
157109	7748	AAACCGCGACTAACAATCAA	166329	TTGATTGTTAGTCGCGGTTT
157110	7749	GAAACCGCGACTAACAATCA	166330	TGATTGTTAGTCGCGGTTTC
157111	7750	AGAAACCGCGACTAACAATC	166331	GATTGTTAGTCGCGGTTTCT
157112	7751	TAGAAACCGCGACTAACAAT	166332	ATTGTTAGTCGCGGTTTCTA
157113	7752	TTAGAAACCGCGACTAACAA	166333	TTGTTAGTCGCGGTTTCTAA
157114	7753	TTTAGAAACCGCGACTAACA	166334	TGTTAGTCGCGGTTTCTAAA
157115	7754	CTTTAGAAACCGCGACTAAC	166335	GTTAGTCGCGGTTTCTAAAG
157116	7755	TCTTTAGAAACCGCGACTAA	166336	TTAGTCGCGGTTTCTAAAGA
157117	7756	ATCTTTAGAAACCGCGACTA	166337	TAGTCGCGGTTTCTAAAGAT
157118	7757	GATCTTTAGAAACCGCGACT	166338	AGTCGCGGTTTCTAAAGATC
157119	7758	GGATCTTTAGAAACCGCGAC	166339	GTCGCGGTTTCTAAAGATCC
157120	7759	TGGATCTTTAGAAACCGCGA	166340	TCGCGGTTTCTAAAGATCCA
157121	7760	CTGGATCTTTAGAAACCGCG	166341	CGCGGTTTCTAAAGATCCAG
157122	7761	TCTGGATCTTTAGAAACCGC	166342	GCGGTTTCTAAAGATCCAGA
157123	7762	ATCTGGATCTTTAGAAACCG	166343	CGGTTTCTAAAGATCCAGAT
157124	7763	TATCTGGATCTTTAGAAACC	166344	GGTTTCTAAAGATCCAGATA
157125	7764	TTATCTGGATCTTTAGAAAC	166345	GTTTCTAAAGATCCAGATAA
157126	7765	TTTATCTGGATCTTTAGAAA	166346	TTTCTAAAGATCCAGATAAA
157127	7766	GTTTATCTGGATCTTTAGAA	166347	TTCTAAAGATCCAGATAAAC
157128	7767	AGTTTATCTGGATCTTTAGA	166348	TCTAAAGATCCAGATAAACT
157129	7768	CAGTTTATCTGGATCTTTAG	166349	CTAAAGATCCAGATAAACTG
157130	7769	ACAGTTTATCTGGATCTTTA	166350	TAAAGATCCAGATAAACTGT
157131	7770	TACAGTTTATCTGGATCTTT	166351	AAAGATCCAGATAAACTGTA
157132	7771	GTACAGTTTATCTGGATCTT	166352	AAGATCCAGATAAACTGTAC
157133	7772	AGTACAGTTTATCTGGATCT	166353	AGATCCAGATAAACTGTACT
157134	7773	AAGTACAGTTTATCTGGATC	166354	GATCCAGATAAACTGTACTT
157135	7774	CAAGTACAGTTTATCTGGAT	166355	ATCCAGATAAACTGTACTTG

157136	7775	GCAAGTACAGTTTATCTGGA	166356	TCCAGATAAACTGTACTTGC
157137	7776	TGCAAGTACAGTTTATCTGG	166357	CCAGATAAACTGTACTTGCA
157138	7777	CTGCAAGTACAGTTTATCTG	166358	CAGATAAACTGTACTTGCAG
157139	7778	ACTGCAAGTACAGTTTATCT	166359	AGATAAACTGTACTTGCAGT
157140	7779	AACTGCAAGTACAGTTTATC	166360	GATAAACTGTACTTGCAGTT
157141	7780	GAACTGCAAGTACAGTTTAT	166361	ATAAACTGTACTTGCAGTTC
157142	7781	TGAACTGCAAGTACAGTTTA	166362	TAAACTGTACTTGCAGTTCA
157143	7782	TTGAACTGCAAGTACAGTTT	166363	AAACTGTACTTGCAGTTCAA
157144	7783	TTTGAACTGCAAGTACAGTT	166364	AACTGTACTTGCAGTTCAAA
157145	7784	ATTTGAACTGCAAGTACAGT	166365	ACTGTACTTGCAGTTCAAAT
157146	7785	AATTTGAACTGCAAGTACAG	166366	CTGTACTTGCAGTTCAAATT
157147	7786	TAATTTGAACTGCAAGTACA	166367	TGTACTTGCAGTTCAAATTA
157148	7787	CTAATTTGAACTGCAAGTAC	166368	GTACTTGCAGTTCAAATTAG
157149	7788	CCTAATTTGAACTGCAAGTA	166369	TACTTGCAGTTCAAATTAGG
157150	7789	TCCTAATTTGAACTGCAAGT	166370	ACTTGCAGTTCAAATTAGGA
157151	7790	TTCCTAATTTGAACTGCAAG	166371	CTTGCAGTTCAAATTAGGAA
157152	7791	TTTCCTAATTTGAACTGCAA	166372	TTGCAGTTCAAATTAGGAAA
157153	7792	TTTTCCTAATTTGAACTGCA	166373	TGCAGTTCAAATTAGGAAAA
157154	7793	CTTTTCCTAATTTGAACTGC	166374	GCAGTTCAAATTAGGAAAAG
157155	7794	GCTTTTCCTAATTTGAACTG	166375	CAGTTCAAATTAGGAAAAGC
157156	7795	TGCTTTTCCTAATTTGAACT	166376	AGTTCAAATTAGGAAAAGCA
157157	7796	TTGCTTTTCCTAATTTGAAC	166377	GTTCAAATTAGGAAAAGCAA
157158	7797	ATTGCTTTTCCTAATTTGAA	166378	TTCAAATTAGGAAAAGCAAT
157159	7798	AATTGCTTTTCCTAATTTGA	166379	TCAAATTAGGAAAAGCAATT
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157161	7800	AAAATTGCTTTTCCTAATTT	166381	AAATTAGGAAAAGCAATTTT
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157166	7805	CCAATAAAATTGCTTTTCCT	166386	AGGAAAAGCAATTTTATTGG
157167	7806	TCCAATAAAATTGCTTTTCC	166387	GGAAAAGCAATTTTATTGGA
157168	7807	GTCCAATAAAATTGCTTTTC	166388	GAAAAGCAATTTTATTGGAC
157169	7808	TGTCCAATAAAATTGCTTTT	166389	AAAAGCAATTTTATTGGACA
157170	7809	TTGTCCAATAAAATTGCTTT	166390	AAAGCAATTTTATTGGACAA
157171	7810	ATTGTCCAATAAAATTGCTT	166391	AAGCAATTTTATTGGACAAT
157172	7811	AATTGTCCAATAAAATTGCT	166392	AGCAATTTTATTGGACAATT
157173	7812	TAATTGTCCAATAAAATTGC	166393	GCAATTTTATTGGACAATTA
157174	7813	GTAATTGTCCAATAAAATTG	166394	CAATTTTATTGGACAATTAC
157175	7814	CGTAATTGTCCAATAAAATT	166395	AATTTTATTGGACAATTACG
157176	7815	CCGTAATTGTCCAATAAAAT	166396	ATTTTATTGGACAATTACGG
157177	7816	ACCGTAATTGTCCAATAAAA	166397	TTTTATTGGACAATTACGGT
157178	7817	CACCGTAATTGTCCAATAAA	166398	TTTATTGGACAATTACGGTG
157179	7818	TCACCGTAATTGTCCAATAA	166399	TTATTGGACAATTACGGTGA
157180	7819	TTCACCGTAATTGTCCAATA	166400	TATTGGACAATTACGGTGAA
157181	7820	TTTCACCGTAATTGTCCAAT	166401	ATTGGACAATTACGGTGAAA
157182	7821	TTTTCACCGTAATTGTCCAA	166402	TTGGACAATTACGGTGAAAA
157183	7822	ATTTTCACCGTAATTGTCCA	166403	TGGACAATTACGGTGAAAAT
157184	7823	CATTTTCACCGTAATTGTCC	166404	GGACAATTACGGTGAAAATG
157185	7824	TCATTTTCACCGTAATTGTC	166405	GACAATTACGGTGAAAATGA
157186	7825	TTCATTTTCACCGTAATTGT	166406	ACAATTACGGTGAAAATGAA
157187	7826	ATTCATTTTCACCGTAATTG	166407	CAATTACGGTGAAAATGAAT
157188	7827	AATTCATTTTCACCGTAATT	166408	AATTACGGTGAAAATGAATT
157189	7828	TAATTCATTTTCACCGTAAT	166409	ATTACGGTGAAAATGAATTA
157190	7829	ATAATTCATTTTCACCGTAA	166410	TTACGGTGAAAATGAATTAT
157191	7830	AATAATTCATTTTCACCGTA	166411	TACGGTGAAAATGAATTATT
157192	7831	AAATAATTCATTTTCACCGT	166412	ACGGTGAAAATGAATTATTT
157193	7832	AAAATAATTCATTTTCACCG	166413	CGGTGAAAATGAATTATTTT
157194	7833	TAAAATAATTCATTTTCACC	166414	GGTGAAAATGAATTATTTTA
157195	7834	ATAAAATAATTCATTTTCAC	166415	GTGAAAATGAATTATTTTAT
157196	7835	GATAAAATAATTCATTTTCA	166416	TGAAAATGAATTATTTTATC
157197	7836	AGATAAAATAATTCATTTTC	166417	GAAAATGAATTATTTTATCT
157198	7837	TAGATAAAATAATTCATTTT	166418	AAAATGAATTATTTTATCTA
157199	7838	CTAGATAAAATAATTCATTT	166419	AAATGAATTATTTTATCTAG
157200	7839	CCTAGATAAAATAATTCATT	166420	AATGAATTATTTTATCTAGG
157201	7840	ACCTAGATAAAATAATTCAT	166421	ATGAATTATTTTATCTAGGT
157202	7841	GACCTAGATAAAATAATTCA	166422	TGAATTATTTTATCTAGGTC
157203	7842	TGACCTAGATAAAATAATTC	166423	GAATTATTTTATCTAGGTCA
157204	7843	CTGACCTAGATAAAATAATT	166424	AATTATTTTATCTAGGTCAG
157205	7844	ACTGACCTAGATAAAATAAT	166425	ATTATTTTATCTAGGTCAGT
157206	7845	AACTGACCTAGATAAAATAA	166426	TTATTTTATCTAGGTCAGTT
157207	7846	TAACTGACCTAGATAAAATA	166427	TATTTTATCTAGGTCAGTTA

157208	7847	TTAACTGACCTAGATAAAAT	166428	ATTTTATCTAGGTCAGTTAA
157209	7848	CTTAACTGACCTAGATAAAA	166429	TTTTATCTAGGTCAGTTAAG
157210	7849	TCTTAACTGACCTAGATAAA	166430	TTTATCTAGGTCAGTTAAGA
157211	7850	TTCTTAACTGACCTAGATAA	166431	TTATCTAGGTCAGTTAAGAA
157212	7851	GTTCTTAACTGACCTAGATA	166432	TATCTAGGTCAGTTAAGAAC
157213	7852	TGTTCTTAACTGACCTAGAT	166433	ATCTAGGTCAGTTAAGAACA
157214	7853	GTGTTCTTAACTGACCTAGA	166434	TCTAGGTCAGTTAAGAACAC
157215	7854	AGTGTTCTTAACTGACCTAG	166435	CTAGGTCAGTTAAGAACACT
157216	7855	CAGTGTTCTTAACTGACCTA	166436	TAGGTCAGTTAAGAACACTG
157217	7856	ACAGTGTTCTTAACTGACCT	166437	AGGTCAGTTAAGAACACTGT
157218	7857	AACAGTGTTCTTAACTGACC	166438	GGTCAGTTAAGAACACTGTT
157219	7858	GAACAGTGTTCTTAACTGAC	166439	GTCAGTTAAGAACACTGTTC
157220	7859	AGAACAGTGTTCTTAACTGA	166440	TCAGTTAAGAACACTGTTCT
157221	7860	CAGAACAGTGTTCTTAACTG	166441	CAGTTAAGAACACTGTTCTG
157222	7861	GCAGAACAGTGTTCTTAACT	166442	AGTTAAGAACACTGTTCTGC
157223	7862	AGCAGAACAGTGTTCTTAAC	166443	GTTAAGAACACTGTTCTGCT
157224	7863	TAGCAGAACAGTGTTCTTAA	166444	TTAAGAACACTGTTCTGCTA
157225	7864	TTAGCAGAACAGTGTTCTTA	166445	TAAGAACACTGTTCTGCTAA
157226	7865	CTTAGCAGAACAGTGTTCTT	166446	AAGAACACTGTTCTGCTAAG
157227	7866	TCTTAGCAGAACAGTGTTCT	166447	AGAACACTGTTCTGCTAAGA
157228	7867	ATCTTAGCAGAACAGTGTTC	166448	GAACACTGTTCTGCTAAGAT
157229	7868	CATCTTAGCAGAACAGTGTT	166449	AACACTGTTCTGCTAAGATG
157230	7869	GCATCTTAGCAGAACAGTGT	166450	ACACTGTTCTGCTAAGATGC
157231	7870	TGCATCTTAGCAGAACAGTG	166451	CACTGTTCTGCTAAGATGCA
157232	7871	CTGCATCTTAGCAGAACAGT	166452	ACTGTTCTGCTAAGATGCAG
157233	7872	ACTGCATCTTAGCAGAACAG	166453	CTGTTCTGCTAAGATGCAGT
157234	7873	TACTGCATCTTAGCAGAACA	166454	TGTTCTGCTAAGATGCAGTA
157235	7874	TTACTGCATCTTAGCAGAAC	166455	GTTCTGCTAAGATGCAGTAA
157236	7875	TTTACTGCATCTTAGCAGAA	166456	TTCTGCTAAGATGCAGTAAA
157237	7876	TTTTACTGCATCTTAGCAGA	166457	TCTGCTAAGATGCAGTAAAA
157238	7877	TTTTTACTGCATCTTAGCAG	166458	CTGCTAAGATGCAGTAAAAA
157239	7878	CTTTTTACTGCATCTTAGCA	166459	TGCTAAGATGCAGTAAAAAG
157240	7879	GCTTTTTACTGCATCTTAGC	166460	GCTAAGATGCAGTAAAAAGC
157241	7880	TGCTTTTTACTGCATCTTAG	166461	CTAAGATGCAGTAAAAAGCA
157242	7881	CTGCTTTTTACTGCATCTTA	166462	TAAGATGCAGTAAAAAGCAG
157243	7882	CCTGCTTTTTACTGCATCTT	166463	AAGATGCAGTAAAAAGCAGG
157244	7883	ACCTGCTTTTTACTGCATCT	166464	AGATGCAGTAAAAAGCAGGT
157245	7884	AACCTGCTTTTTACTGCATC	166465	GATGCAGTAAAAAGCAGGTT
157246	7885	TAACCTGCTTTTTACTGCAT	166466	ATGCAGTAAAAAGCAGGTTA
157247	7886	GTAACCTGCTTTTTACTGCA	166467	TGCAGTAAAAAGCAGGTTAC
157248	7887	TGTAACCTGCTTTTTACTGC	166468	GCAGTAAAAAGCAGGTTACA
157249	7888	ATGTAACCTGCTTTTTACTG	166469	CAGTAAAAAGCAGGTTACAT
157250	7889	AATGTAACCTGCTTTTTACT	166470	AGTAAAAAGCAGGTTACATT
157251	7890	AAATGTAACCTGCTTTTTAC	166471	GTAAAAAGCAGGTTACATTT
157252	7891	CAAATGTAACCTGCTTTTTA	166472	TAAAAAGCAGGTTACATTTG
157253	7892	TCAAATGTAACCTGCTTTTT	166473	AAAAAGCAGGTTACATTTGA
157254	7893	GTCAAATGTAACCTGCTTTT	166474	AAAAGCAGGTTACATTTGAC
157255	7894	GGTCAAATGTAACCTGCTTT	166475	AAAGCAGGTTACATTTGACC
157256	7895	TGGTCAAATGTAACCTGCTT	166476	AAGCAGGTTACATTTGACCA
157257	7896	ATGGTCAAATGTAACCTGCT	166477	AGCAGGTTACATTTGACCAT
157258	7897	TATGGTCAAATGTAACCTGC	166478	GCAGGTTACATTTGACCATA
157259	7898	ATATGGTCAAATGTAACCTG	166479	CAGGTTACATTTGACCATAT
157260	7899	AATATGGTCAAATGTAACCT	166480	AGGTTACATTTGACCATATT
157261	7900	TAATATGGTCAAATGTAACC	166481	GGTTACATTTGACCATATTA
157262	7901	CTAATATGGTCAAATGTAAC	166482	GTTACATTTGACCATATTAG
157263	7902	TCTAATATGGTCAAATGTAA	166483	TTACATTTGACCATATTAGA
157264	7903	ATCTAATATGGTCAAATGTA	166484	TACATTTGACCATATTAGAT
157265	7904	GATCTAATATGGTCAAATGT	166485	ACATTTGACCATATTAGATC
157266	7905	AGATCTAATATGGTCAAATG	166486	CATTTGACCATATTAGATCT
157267	7906	CAGATCTAATATGGTCAAAT	166487	ATTTGACCATATTAGATCTG
157268	7907	TCAGATCTAATATGGTCAAA	166488	TTTGACCATATTAGATCTGA
157269	7908	CTCAGATCTAATATGGTCAA	166489	TTGACCATATTAGATCTGAG
157270	7909	ACTCAGATCTAATATGGTCA	166490	TGACCATATTAGATCTGAGT
157271	7910	AACTCAGATCTAATATGGTC	166491	GACCATATTAGATCTGAGTT
157272	7911	AAACTCAGATCTAATATGGT	166492	ACCATATTAGATCTGAGTTT
157273	7912	CAAACTCAGATCTAATATGG	166493	CCATATTAGATCTGAGTTTG
157274	7913	CCAAACTCAGATCTAATATG	166494	CATATTAGATCTGAGTTTGG
157275	7914	TCCAAACTCAGATCTAATAT	166495	ATATTAGATCTGAGTTTGGA
157276	7915	TTCCAAACTCAGATCTAATA	166496	TATTAGATCTGAGTTTGGAA
157277	7916	TTTCCAAACTCAGATCTAAT	166497	ATTAGATCTGAGTTTGGAAA
157278	7917	TTTTCCAAACTCAGATCTAA	166498	TTAGATCTGAGTTTGGAAAA
157279	7918	GTTTTCCAAACTCAGATCTA	166499	TAGATCTGAGTTTGGAAAAC

157280	7919	TGTTTTCCAAACTCAGATCT	166500	AGATCTGAGTTTGGAAAACA
157281	7920	CTGTTTTCCAAACTCAGATC	166501	GATCTGAGTTTGGAAAACAG
157282	7921	TCTGTTTTCCAAACTCAGAT	166502	ATCTGAGTTTGGAAAACAGA
157283	7922	TTCTGTTTTCCAAACTCAGA	166503	TCTGAGTTTGGAAAACAGAA
157284	7923	CTTCTGTTTTCCAAACTCAG	166504	CTGAGTTTGGAAAACAGAAG
157285	7924	ACTTCTGTTTTCCAAACTCA	166505	TGAGTTTGGAAAACAGAAGT
157286	7925	TACTTCTGTTTTCCAAACTC	166506	GAGTTTGGAAAACAGAAGTA
157287	7926	CTACTTCTGTTTTCCAAACT	166507	AGTTTGGAAAACAGAAGTAG
157288	7927	ACTACTTCTGTTTTCCAAAC	166508	GTTTGGAAAACAGAAGTAGT
157289	7928	GACTACTTCTGTTTTCCAAA	166509	TTTGGAAAACAGAAGTAGTC
157290	7929	AGACTACTTCTGTTTTCCAA	166510	TTGGAAAACAGAAGTAGTCT
157291	7930	AAGACTACTTCTGTTTTCCA	166511	TGGAAAACAGAAGTAGTCTT
157292	7931	AAAGACTACTTCTGTTTTCC	166512	GGAAAACAGAAGTAGTCTTT
157293	7932	TAAAGACTACTTCTGTTTTC	166513	GAAAACAGAAGTAGTCTTTA
157294	7933	CTAAAGACTACTTCTGTTTT	166514	AAAACAGAAGTAGTCTTTAG
157295	7934	ACTAAAGACTACTTCTGTTT	166515	AAACAGAAGTAGTCTTTAGT
157296	7935	AACTAAAGACTACTTCTGTT	166516	AACAGAAGTAGTCTTTAGTT
157297	7936	AAACTAAAGACTACTTCTGT	166517	ACAGAAGTAGTCTTTAGTTT
157298	7937	AAAACTAAAGACTACTTCTG	166518	CAGAAGTAGTCTTTAGTTTT
157299	7938	TAAAACTAAAGACTACTTCT	166519	AGAAGTAGTCTTTAGTTTTA
157300	7939	TTAAAACTAAAGACTACTTC	166520	GAAGTAGTCTTTAGTTTTAA
157301	7940	TTTAAAACTAAAGACTACTT	166521	AAGTAGTCTTTAGTTTTAAA
157302	7941	TTTTAAAACTAAAGACTACT	166522	AGTAGTCTTTAGTTTTAAAA
157303	7942	ATTTTAAAACTAAAGACTAC	166523	GTAGTCTTTAGTTTTAAAAT
157304	7943	CATTTTAAAACTAAAGACTA	166524	TAGTCTTTAGTTTTAAAATG
157305	7944	CCATTTTAAAACTAAAGACT	166525	AGTCTTTAGTTTTAAAATGG
157306	7945	GCCATTTTAAAACTAAAGAC	166526	GTCTTTAGTTTTAAAATGGC
157307	7946	GGCCATTTTAAAACTAAAGA	166527	TCTTTAGTTTTAAAATGGCC
157308	7947	TGGCCATTTTAAAACTAAAG	166528	CTTTAGTTTTAAAATGGCCA
157309	7948	CTGGCCATTTTAAAACTAAA	166529	TTTAGTTTTAAAATGGCCAG
157310	7949	TCTGGCCATTTTAAAACTAA	166530	TTAGTTTTAAAATGGCCAGA
157311	7950	ATCTGGCCATTTTAAAACTA	166531	TAGTTTTAAAATGGCCAGAT
157312	7951	AATCTGGCCATTTTAAAACT	166532	AGTTTTAAAATGGCCAGATT
157313	7952	AAATCTGGCCATTTTAAAAC	166533	GTTTTAAAATGGCCAGATTT
157314	7953	AAAATCTGGCCATTTTAAAA	166534	TTTTAAAATGGCCAGATTTT
157315	7954	GAAAATCTGGCCATTTTAAA	166535	TTTAAAATGGCCAGATTTTC
157316	7955	AGAAAATCTGGCCATTTTAA	166536	TTAAAATGGCCAGATTTTCT
157317	7956	AAGAAAATCTGGCCATTTTA	166537	TAAAATGGCCAGATTTTCTT
157318	7957	CAAGAAAATCTGGCCATTTT	166538	AAAATGGCCAGATTTTCTTG
157319	7958	GCAAGAAAATCTGGCCATTT	166539	AAATGGCCAGATTTTCTTGC
157320	7959	GGCAAGAAAATCTGGCCATT	166540	AATGGCCAGATTTTCTTGCC
157321	7960	TGGCAAGAAAATCTGGCCAT	166541	ATGGCCAGATTTTCTTGCCA
157322	7961	CTGGCAAGAAAATCTGGCCA	166542	TGGCCAGATTTTCTTGCCAG
157323	7962	CCTGGCAAGAAAATCTGGCC	166543	GGCCAGATTTTCTTGCCAGG
157324	7963	TCCTGGCAAGAAAATCTGGC	166544	GCCAGATTTTCTTGCCAGGA
157325	7964	ATCCTGGCAAGAAAATCTGG	166545	CCAGATTTTCTTGCCAGGAT
157326	7965	AATCCTGGCAAGAAAATCTG	166546	CAGATTTTCTTGCCAGGATT
157327	7966	CAATCCTGGCAAGAAAATCT	166547	AGATTTTCTTGCCAGGATTG
157328	7967	CCAATCCTGGCAAGAAAATC	166548	GATTTTCTTGCCAGGATTGG
157329	7968	CCCAATCCTGGCAAGAAAAT	166549	ATTTTCTTGCCAGGATTGGG
157330	7969	ACCCAATCCTGGCAAGAAAA	166550	TTTTCTTGCCAGGATTGGGT
157331	7970	AACCCAATCCTGGCAAGAAA	166551	TTTCTTGCCAGGATTGGGTT
157332	7971	AAACCCAATCCTGGCAAGAA	166552	TTCTTGCCAGGATTGGGTTT
157333	7972	GAAACCCAATCCTGGCAAGA	166553	TCTTGCCAGGATTGGGTTTC
157334	7973	AGAAACCCAATCCTGGCAAG	166554	CTTGCCAGGATTGGGTTTCT
157335	7974	GAGAAACCCAATCCTGGCAA	166555	TTGCCAGGATTGGGTTTCTC
157336	7975	TGAGAAACCCAATCCTGGCA	166556	TGCCAGGATTGGGTTTCTCA
157337	7976	GTGAGAAACCCAATCCTGGC	166557	GCCAGGATTGGGTTTCTCAC
157338	7977	AGTGAGAAACCCAATCCTGG	166558	CCAGGATTGGGTTTCTCACT
157339	7978	AAGTGAGAAACCCAATCCTG	166559	CAGGATTGGGTTTCTCACTT
157340	7979	CAAGTGAGAAACCCAATCCT	166560	AGGATTGGGTTTCTCACTTG
157341	7980	ACAAGTGAGAAACCCAATCC	166561	GGATTGGGTTTCTCACTTGT
157342	7981	AACAAGTGAGAAACCCAATC	166562	GATTGGGTTTCTCACTTGTT
157343	7982	TAACAAGTGAGAAACCCAAT	166563	ATTGGGTTTCTCACTTGTTA
157344	7983	TTAACAAGTGAGAAACCCAA	166564	TTGGGTTTCTCACTTGTTAA
157345	7984	TTTAACAAGTGAGAAACCCA	166565	TGGGTTTCTCACTTGTTAAA
157346	7985	GTTTAACAAGTGAGAAACCC	166566	GGGTTTCTCACTTGTTAAAC
157347	7986	TGTTTAACAAGTGAGAAACC	166567	GGTTTCTCACTTGTTAAACA
157348	7987	CTGTTTAACAAGTGAGAAAC	166568	GTTTCTCACTTGTTAAACAG
157349	7988	TCTGTTTAACAAGTGAGAAA	166569	TTTCTCACTTGTTAAACAGA
157350	7989	TTCTGTTTAACAAGTGAGAA	166570	TTCTCACTTGTTAAACAGAA
157351	7990	GTTCTGTTTAACAAGTGAGA	166571	TCTCACTTGTTAAACAGAAC

157352	7991	TGTTCTGTTTAACAAGTGAG	166572	CTCACTTGTTAAACAGAACA
157353	7992	ATGTTCTGTTTAACAAGTGA	166573	TCACTTGTTAAACAGAACAT
157354	7993	AATGTTCTGTTTAACAAGTG	166574	CACTTGTTAAACAGAACATT
157355	7994	AAATGTTCTGTTTAACAAGT	166575	ACTTGTTAAACAGAACATTT
157356	7995	AAAATGTTCTGTTTAACAAG	166576	CTTGTTAAACAGAACATTTT
157357	7996	CAAAATGTTCTGTTTAACAA	166577	TTGTTAAACAGAACATTTTG
157358	7997	ACAAAATGTTCTGTTTAACA	166578	TGTTAAACAGAACATTTTGT
157359	7998	AACAAAATGTTCTGTTTAAC	166579	GTTAAACAGAACATTTTGTT
157360	7999	TAACAAAATGTTCTGTTTAA	166580	TTAAACAGAACATTTTGTTA
157361	8000	TTAACAAAATGTTCTGTTTA	166581	TAAACAGAACATTTTGTTAA
157362	8001	CTTAACAAAATGTTCTGTTT	166582	AAACAGAACATTTTGTTAAG
157363	8002	ACTTAACAAAATGTTCTGTT	166583	AACAGAACATTTTGTTAAGT
157364	8003	AACTTAACAAAATGTTCTGT	166584	ACAGAACATTTTGTTAAGTT
157365	8004	AAACTTAACAAAATGTTCTG	166585	CAGAACATTTTGTTAAGTTT
157366	8005	TAAACTTAACAAAATGTTCT	166586	AGAACATTTTGTTAAGTTTA
157367	8006	TTAAACTTAACAAAATGTTC	166587	GAACATTTTGTTAAGTTTAA
157368	8007	TTTAAACTTAACAAAATGTT	166588	AACATTTTGTTAAGTTTAAA
157369	8008	TTTTAAACTTAACAAAATGT	166589	ACATTTTGTTAAGTTTAAAA
157370	8009	GTTTTAAACTTAACAAAATG	166590	CATTTTGTTAAGTTTAAAAC
157371	8010	GGTTTTAAACTTAACAAAAT	166591	ATTTTGTTAAGTTTAAAACC
157372	8011	AGGTTTTAAACTTAACAAAA	166592	TTTTGTTAAGTTTAAAACCT
157373	8012	CAGGTTTTAAACTTAACAAA	166593	TTTGTTAAGTTTAAAACCTG
157374	8013	CCAGGTTTTAAACTTAACAA	166594	TTGTTAAGTTTAAAACCTGG
157375	8014	CCCAGGTTTTAAACTTAACA	166595	TGTTAAGTTTAAAACCTGGG
157376	8015	TCCCAGGTTTTAAACTTAAC	166596	GTTAAGTTTAAAACCTGGGA
157377	8016	ATCCCAGGTTTTAAACTTAA	166597	TTAAGTTTAAAACCTGGGAT
157378	8017	CATCCCAGGTTTTAAACTTA	166598	TAAGTTTAAAACCTGGGATG
157379	8018	CCATCCCAGGTTTTAAACTT	166599	AAGTTTAAAACCTGGGATGG
157380	8019	TCCATCCCAGGTTTTAAACT	166600	AGTTTAAAACCTGGGATGGA
157381	8020	GTCCATCCCAGGTTTTAAAC	166601	GTTTAAAACCTGGGATGGAC
157382	8021	AGTCCATCCCAGGTTTTAAA	166602	TTTAAAACCTGGGATGGACT
157383	8022	AAGTCCATCCCAGGTTTTAA	166603	TTAAAACCTGGGATGGACTT
157384	8023	TAAGTCCATCCCAGGTTTTA	166604	TAAAACCTGGGATGGACTTA
157385	8024	TTAAGTCCATCCCAGGTTTT	166605	AAAACCTGGGATGGACTTAA
157386	8025	CTTAAGTCCATCCCAGGTTT	166606	AAACCTGGGATGGACTTAAG
157387	8026	ACTTAAGTCCATCCCAGGTT	166607	AACCTGGGATGGACTTAAGT
157388	8027	TACTTAAGTCCATCCCAGGT	166608	ACCTGGGATGGACTTAAGTA
157389	8028	ATACTTAAGTCCATCCCAGG	166609	CCTGGGATGGACTTAAGTAT
157390	8029	AATACTTAAGTCCATCCCAG	166610	CTGGGATGGACTTAAGTATT
157391	8030	GAATACTTAAGTCCATCCCA	166611	TGGGATGGACTTAAGTATTC
157392	8031	TGAATACTTAAGTCCATCCC	166612	GGGATGGACTTAAGTATTCA
157393	8032	ATGAATACTTAAGTCCATCC	166613	GGATGGACTTAAGTATTCAT
157394	8033	CATGAATACTTAAGTCCATC	166614	GATGGACTTAAGTATTCATG
157395	8034	ACATGAATACTTAAGTCCAT	166615	ATGGACTTAAGTATTCATGT
157396	8035	AACATGAATACTTAAGTCCA	166616	TGGACTTAAGTATTCATGTT
157397	8036	GAACATGAATACTTAAGTCC	166617	GGACTTAAGTATTCATGTTC
157398	8037	TGAACATGAATACTTAAGTC	166618	GACTTAAGTATTCATGTTCA
157399	8038	ATGAACATGAATACTTAAGT	166619	ACTTAAGTATTCATGTTCAT
157400	8039	AATGAACATGAATACTTAAG	166620	CTTAAGTATTCATGTTCATT
157401	8040	GAATGAACATGAATACTTAA	166621	TTAAGTATTCATGTTCATTC
157402	8041	TGAATGAACATGAATACTTA	166622	TAAGTATTCATGTTCATTCA
157403	8042	ATGAATGAACATGAATACTT	166623	AAGTATTCATGTTCATTCAT
157404	8043	CATGAATGAACATGAATACT	166624	AGTATTCATGTTCATTCATG
157405	8044	ACATGAATGAACATGAATAC	166625	GTATTCATGTTCATTCATGT
157406	8045	AACATGAATGAACATGAATA	166626	TATTCATGTTCATTCATGTT
157407	8046	GAACATGAATGAACATGAAT	166627	ATTCATGTTCATTCATGTTC
157408	8047	TGAACATGAATGAACATGAA	166628	TTCATGTTCATTCATGTTCA
157409	8048	ATGAACATGAATGAACATGA	166629	TCATGTTCATTCATGTTCAT
157410	8049	AATGAACATGAATGAACATG	166630	CATGTTCATTCATGTTCATT
157411	8050	GAATGAACATGAATGAACAT	166631	ATGTTCATTCATGTTCATTC
157412	8051	TGAATGAACATGAATGAACA	166632	TGTTCATTCATGTTCATTCA
157413	8052	CTGAATGAACATGAATGAAC	166633	GTTCATTCATGTTCATTCAG
157414	8053	CCTGAATGAACATGAATGAA	166634	TTCATTCATGTTCATTCAGG
157415	8054	TCCTGAATGAACATGAATGA	166635	TCATTCATGTTCATTCAGGA
157416	8055	GTCCTGAATGAACATGAATG	166636	CATTCATGTTCATTCAGGAC
157417	8056	AGTCCTGAATGAACATGAAT	166637	ATTCATGTTCATTCAGGACT
157418	8057	CAGTCCTGAATGAACATGAA	166638	TTCATGTTCATTCAGGACTG
157419	8058	GCAGTCCTGAATGAACATGA	166639	TCATGTTCATTCAGGACTGC
157420	8059	TGCAGTCCTGAATGAACATG	166640	CATGTTCATTCAGGACTGCA
157421	8060	CTGCAGTCCTGAATGAACAT	166641	ATGTTCATTCAGGACTGCAG
157422	8061	CCTGCAGTCCTGAATGAACA	166642	TGTTCATTCAGGACTGCAGG
157423	8062	ACCTGCAGTCCTGAATGAAC	166643	GTTCATTCAGGACTGCAGGT

157424	8063	AACCTGCAGTCCTGAATGAA	166644	TTCATTCAGGACTGCAGGTT
157425	8064	TAACCTGCAGTCCTGAATGA	166645	TCATTCAGGACTGCAGGTTA
157426	8065	ATAACCTGCAGTCCTGAATG	166646	CATTCAGGACTGCAGGTTAT
157427	8066	GATAACCTGCAGTCCTGAAT	166647	ATTCAGGACTGCAGGTTATC
157428	8067	TGATAACCTGCAGTCCTGAA	166648	TTCAGGACTGCAGGTTATCA
157429	8068	ATGATAACCTGCAGTCCTGA	166649	TCAGGACTGCAGGTTATCAT
157430	8069	CATGATAACCTGCAGTCCTG	166650	CAGGACTGCAGGTTATCATG
157431	8070	TCATGATAACCTGCAGTCCT	166651	AGGACTGCAGGTTATCATGA
157432	8071	GTCATGATAACCTGCAGTCC	166652	GGACTGCAGGTTATCATGAC
157433	8072	AGTCATGATAACCTGCAGTC	166653	GACTGCAGGTTATCATGACT
157434	8073	AAGTCATGATAACCTGCAGT	166654	ACTGCAGGTTATCATGACTT
157435	8074	CAAGTCATGATAACCTGCAG	166655	CTGCAGGTTATCATGACTTG
157436	8075	ACAAGTCATGATAACCTGCA	166656	TGCAGGTTATCATGACTTGT
157437	8076	AACAAGTCATGATAACCTGC	166657	GCAGGTTATCATGACTTGTT
157438	8077	AAACAAGTCATGATAACCTG	166658	CAGGTTATCATGACTTGTTT
157439	8078	TAAACAAGTCATGATAACCT	166659	AGGTTATCATGACTTGTTTA
157440	8079	TTAAACAAGTCATGATAACC	166660	GGTTATCATGACTTGTTTAA
157441	8080	GTTAAACAAGTCATGATAAC	166661	GTTATCATGACTTGTTTAAC
157442	8081	AGTTAAACAAGTCATGATAA	166662	TTATCATGACTTGTTTAACT
157443	8082	AAGTTAAACAAGTCATGATA	166663	TATCATGACTTGTTTAACTT
157444	8083	CAAGTTAAACAAGTCATGAT	166664	ATCATGACTTGTTTAACTTG
157445	8084	ACAAGTTAAACAAGTCATGA	166665	TCATGACTTGTTTAACTTGT
157446	8085	CACAAGTTAAACAAGTCATG	166666	CATGACTTGTTTAACTTGTG
157447	8086	CCACAAGTTAAACAAGTCAT	166667	ATGACTTGTTTAACTTGTGG
157448	8087	CCCACAAGTTAAACAAGTCA	166668	TGACTTGTTTAACTTGTGGG
157449	8088	TCCCACAAGTTAAACAAGTC	166669	GACTTGTTTAACTTGTGGGA
157450	8089	TTCCCACAAGTTAAACAAGT	166670	ACTTGTTTAACTTGTGGGAA
157451	8090	CTTCCCACAAGTTAAACAAG	166671	CTTGTTTAACTTGTGGGAAG
157452	8091	GCTTCCCACAAGTTAAACAA	166672	TTGTTTAACTTGTGGGAAGC
157453	8092	AGCTTCCCACAAGTTAAACA	166673	TGTTTAACTTGTGGGAAGCT
157454	8093	CAGCTTCCCACAAGTTAAAC	166674	GTTTAACTTGTGGGAAGCTG
157455	8094	ACAGCTTCCCACAAGTTAAA	166675	TTTAACTTGTGGGAAGCTGT
157456	8095	AACAGCTTCCCACAAGTTAA	166676	TTAACTTGTGGGAAGCTGTT
157457	8096	CAACAGCTTCCCACAAGTTA	166677	TAACTTGTGGGAAGCTGTTG
157458	8097	ACAACAGCTTCCCACAAGTT	166678	AACTTGTGGGAAGCTGTTGT
157459	8098	GACAACAGCTTCCCACAAGT	166679	ACTTGTGGGAAGCTGTTGTC
157460	8099	GGACAACAGCTTCCCACAAG	166680	CTTGTGGGAAGCTGTTGTCC
157461	8100	GGGACAACAGCTTCCCACAA	166681	TTGTGGGAAGCTGTTGTCCC
157462	8101	TGGGACAACAGCTTCCCACA	166682	TGTGGGAAGCTGTTGTCCCA
157463	8102	TTGGGACAACAGCTTCCCAC	166683	GTGGGAAGCTGTTGTCCCAA
157464	8103	CTTGGGACAACAGCTTCCCA	166684	TGGGAAGCTGTTGTCCCAAG
157465	8104	ACTTGGGACAACAGCTTCCC	166685	GGGAAGCTGTTGTCCCAAGT
157466	8105	AACTTGGGACAACAGCTTCC	166686	GGAAGCTGTTGTCCCAAGTT
157467	8106	TAACTTGGGACAACAGCTTC	166687	GAAGCTGTTGTCCCAAGTTA
157468	8107	ATAACTTGGGACAACAGCTT	166688	AAGCTGTTGTCCCAAGTTAT
157469	8108	GATAACTTGGGACAACAGCT	166689	AGCTGTTGTCCCAAGTTATC
157470	8109	GGATAACTTGGGACAACAGC	166690	GCTGTTGTCCCAAGTTATCC
157471	8110	AGGATAACTTGGGACAACAG	166691	CTGTTGTCCCAAGTTATCCT
157472	8111	CAGGATAACTTGGGACAACA	166692	TGTTGTCCCAAGTTATCCTG
157473	8112	CCAGGATAACTTGGGACAAC	166693	GTTGTCCCAAGTTATCCTGG
157474	8113	CCCAGGATAACTTGGGACAA	166694	TTGTCCCAAGTTATCCTGGG
157475	8114	CCCCAGGATAACTTGGGACA	166695	TGTCCCAAGTTATCCTGGGG
157476	8115	TCCCCAGGATAACTTGGGAC	166696	GTCCCAAGTTATCCTGGGGA
157477	8116	TTCCCCAGGATAACTTGGGA	166697	TCCCAAGTTATCCTGGGGAA
157478	8117	GTTCCCCAGGATAACTTGGG	166698	CCCAAGTTATCCTGGGGAAC
157479	8118	AGTTCCCCAGGATAACTTGG	166699	CCAAGTTATCCTGGGGAACT
157480	8119	CAGTTCCCCAGGATAACTTG	166700	CAAGTTATCCTGGGGAACTG
157481	8120	GCAGTTCCCCAGGATAACTT	166701	AAGTTATCCTGGGGAACTGC
157482	8121	TGCAGTTCCCCAGGATAACT	166702	AGTTATCCTGGGGAACTGCA
157483	8122	ATGCAGTTCCCCAGGATAAC	166703	GTTATCCTGGGGAACTGCAT
157484	8123	GATGCAGTTCCCCAGGATAA	166704	TTATCCTGGGGAACTGCATC
157485	8124	AGATGCAGTTCCCCAGGATA	166705	TATCCTGGGGAACTGCATCT
157486	8125	CAGATGCAGTTCCCCAGGAT	166706	ATCCTGGGGAACTGCATCTG
157487	8126	CCAGATGCAGTTCCCCAGGA	166707	TCCTGGGGAACTGCATCTGG
157488	8127	ACCAGATGCAGTTCCCCAGG	166708	CCTGGGGAACTGCATCTGGT
157489	8128	AACCAGATGCAGTTCCCCAG	166709	CTGGGGAACTGCATCTGGTT
157490	8129	GAACCAGATGCAGTTCCCCA	166710	TGGGGAACTGCATCTGGTTC
157491	8130	AGAACCAGATGCAGTTCCCC	166711	GGGGAACTGCATCTGGTTCT
157492	8131	AAGAACCAGATGCAGTTCCC	166712	GGGAACTGCATCTGGTTCTT
157493	8132	CAAGAACCAGATGCAGTTCC	166713	GGAACTGCATCTGGTTCTTG
157494	8133	GCAAGAACCAGATGCAGTTC	166714	GAACTGCATCTGGTTCTTGC
157495	8134	TGCAAGAACCAGATGCAGTT	166715	AACTGCATCTGGTTCTTGCA

157496	8135	TTGCAAGAACCAGATGCAGT	166716	ACTGCATCTGGTTCTTGCAA
157497	8136	TTTGCAAGAACCAGATGCAG	166717	CTGCATCTGGTTCTTGCAAA
157498	8137	TTTTGCAAGAACCAGATGCA	166718	TGCATCTGGTTCTTGCAAAA
157499	8138	GTTTTGCAAGAACCAGATGC	166719	GCATCTGGTTCTTGCAAAAC
157500	8139	TGTTTTGCAAGAACCAGATG	166720	CATCTGGTTCTTGCAAAACA
157501	8140	GTGTTTTGCAAGAACCAGAT	166721	ATCTGGTTCTTGCAAAACAC
157502	8141	GGTGTTTTGCAAGAACCAGA	166722	TCTGGTTCTTGCAAAACACC
157503	8142	TGGTGTTTTGCAAGAACCAG	166723	CTGGTTCTTGCAAAACACCA
157504	8143	TTGGTGTTTTGCAAGAACCA	166724	TGGTTCTTGCAAAACACCAA
157505	8144	CTTGGTGTTTTGCAAGAACC	166725	GGTTCTTGCAAAACACCAAG
157506	8145	ACTTGGTGTTTTGCAAGAAC	166726	GTTCTTGCAAAACACCAAGT
157507	8146	TACTTGGTGTTTTGCAAGAA	166727	TTCTTGCAAAACACCAAGTA
157508	8147	CTACTTGGTGTTTTGCAAGA	166728	TCTTGCAAAACACCAAGTAG
157509	8148	TCTACTTGGTGTTTTGCAAG	166729	CTTGCAAAACACCAAGTAGA
157510	8149	GTCTACTTGGTGTTTTGCAA	166730	TTGCAAAACACCAAGTAGAC
157511	8150	TGTCTACTTGGTGTTTTGCA	166731	TGCAAAACACCAAGTAGACA
157512	8151	CTGTCTACTTGGTGTTTTGC	166732	GCAAAACACCAAGTAGACAG
157513	8152	CCTGTCTACTTGGTGTTTTG	166733	CAAAACACCAAGTAGACAGG
157514	8153	GCCTGTCTACTTGGTGTTTT	166734	AAAACACCAAGTAGACAGGC
157515	8154	AGCCTGTCTACTTGGTGTTT	166735	AAACACCAAGTAGACAGGCT
157516	8155	GAGCCTGTCTACTTGGTGTT	166736	AACACCAAGTAGACAGGCTC
157517	8156	AGAGCCTGTCTACTTGGTGT	166737	ACACCAAGTAGACAGGCTCT
157518	8157	GAGAGCCTGTCTACTTGGTG	166738	CACCAAGTAGACAGGCTCTC
157519	8158	AGAGAGCCTGTCTACTTGGT	166739	ACCAAGTAGACAGGCTCTCT
157520	8159	AAGAGAGCCTGTCTACTTGG	166740	CCAAGTAGACAGGCTCTCTT
157521	8160	AAAGAGAGCCTGTCTACTTG	166741	CAAGTAGACAGGCTCTCTTT
157522	8161	AAAAGAGAGCCTGTCTACTT	166742	AAGTAGACAGGCTCTCTTTT
157523	8162	TAAAAGAGAGCCTGTCTACT	166743	AGTAGACAGGCTCTCTTTTA
157524	8163	GTAAAAGAGAGCCTGTCTAC	166744	GTAGACAGGCTCTCTTTTAC
157525	8164	GGTAAAAGAGAGCCTGTCTA	166745	TAGACAGGCTCTCTTTTACC
157526	8165	AGGTAAAAGAGAGCCTGTCT	166746	AGACAGGCTCTCTTTTACCT
157527	8166	GAGGTAAAAGAGAGCCTGTC	166747	GACAGGCTCTCTTTTACCTC
157528	8167	GGAGGTAAAAGAGAGCCTGT	166748	ACAGGCTCTCTTTTACCTCC
157529	8168	GGGAGGTAAAAGAGAGCCTG	166749	CAGGCTCTCTTTTACCTCCC
157530	8169	GGGGAGGTAAAAGAGAGCCT	166750	AGGCTCTCTTTTACCTCCCC
157531	8170	AGGGGAGGTAAAAGAGAGCC	166751	GGCTCTCTTTTACCTCCCCT
157532	8171	AAGGGGAGGTAAAAGAGAGC	166752	GCTCTCTTTTACCTCCCCTT
157533	8172	CAAGGGGAGGTAAAAGAGAG	166753	CTCTCTTTTACCTCCCCTTG
157534	8173	TCAAGGGGAGGTAAAAGAGA	166754	TCTCTTTTACCTCCCCTTGA
157535	8174	CTCAAGGGGAGGTAAAAGAG	166755	CTCTTTTACCTCCCCTTGAG
157536	8175	CCTCAAGGGGAGGTAAAAGA	166756	TCTTTTACCTCCCCTTGAGG
157537	8176	CCCTCAAGGGGAGGTAAAAG	166757	CTTTTACCTCCCCTTGAGGG
157538	8177	GCCCTCAAGGGGAGGTAAAA	166758	TTTTACCTCCCCTTGAGGGC
157539	8178	TGCCCTCAAGGGGAGGTAAA	166759	TTTACCTCCCCTTGAGGGCA
157540	8179	ATGCCCTCAAGGGGAGGTAA	166760	TTACCTCCCCTTGAGGGCAT
157541	8180	AATGCCCTCAAGGGGAGGTA	166761	TACCTCCCCTTGAGGGCATT
157542	8181	TAATGCCCTCAAGGGGAGGT	166762	ACCTCCCCTTGAGGGCATTA
157543	8182	TTAATGCCCTCAAGGGGAGG	166763	CCTCCCCTTGAGGGCATTAA
157544	8183	GTTAATGCCCTCAAGGGGAG	166764	CTCCCCTTGAGGGCATTAAC
157545	8184	TGTTAATGCCCTCAAGGGGA	166765	TCCCCTTGAGGGCATTAACA
157546	8185	ATGTTAATGCCCTCAAGGGG	166766	CCCCTTGAGGGCATTAACAT
157547	8186	AATGTTAATGCCCTCAAGGG	166767	CCCTTGAGGGCATTAACATT
157548	8187	GAATGTTAATGCCCTCAAGG	166768	CCTTGAGGGCATTAACATTC
157549	8188	TGAATGTTAATGCCCTCAAG	166769	CTTGAGGGCATTAACATTCA
157550	8189	CTGAATGTTAATGCCCTCAA	166770	TTGAGGGCATTAACATTCAG
157551	8190	ACTGAATGTTAATGCCCTCA	166771	TGAGGGCATTAACATTCAGT
157552	8191	TACTGAATGTTAATGCCCTC	166772	GAGGGCATTAACATTCAGTA
157553	8192	CTACTGAATGTTAATGCCCT	166773	AGGGCATTAACATTCAGTAG
157554	8193	ACTACTGAATGTTAATGCCC	166774	GGGCATTAACATTCAGTAGT
157555	8194	GACTACTGAATGTTAATGCC	166775	GGCATTAACATTCAGTAGTC
157556	8195	TGACTACTGAATGTTAATGC	166776	GCATTAACATTCAGTAGTCA
157557	8196	GTGACTACTGAATGTTAATG	166777	CATTAACATTCAGTAGTCAC
157558	8197	AGTGACTACTGAATGTTAAT	166778	ATTAACATTCAGTAGTCACT
157559	8198	AAGTGACTACTGAATGTTAA	166779	TTAACATTCAGTAGTCACTT
157560	8199	GAAGTGACTACTGAATGTTA	166780	TAACATTCAGTAGTCACTTC
157561	8200	GGAAGTGACTACTGAATGTT	166781	AACATTCAGTAGTCACTTCC
157562	8201	TGGAAGTGACTACTGAATGT	166782	ACATTCAGTAGTCACTTCCA
157563	8202	ATGGAAGTGACTACTGAATG	166783	CATTCAGTAGTCACTTCCAT
157564	8203	AATGGAAGTGACTACTGAAT	166784	ATTCAGTAGTCACTTCCATT
157565	8204	GAATGGAAGTGACTACTGAA	166785	TTCAGTAGTCACTTCCATTC
157566	8205	TGAATGGAAGTGACTACTGA	166786	TCAGTAGTCACTTCCATTCA
157567	8206	CTGAATGGAAGTGACTACTG	166787	CAGTAGTCACTTCCATTCAG

157568	8207	ACTGAATGGAAGTGACTACT	166788	AGTAGTCACTTCCATTCAGT
157569	8208	AACTGAATGGAAGTGACTAC	166789	GTAGTCACTTCCATTCAGTT
157570	8209	TAACTGAATGGAAGTGACTA	166790	TAGTCACTTCCATTCAGTTA
157571	8210	TTAACTGAATGGAAGTGACT	166791	AGTCACTTCCATTCAGTTAA
157572	8211	GTTAACTGAATGGAAGTGAC	166792	GTCACTTCCATTCAGTTAAC
157573	8212	GGTTAACTGAATGGAAGTGA	166793	TCACTTCCATTCAGTTAACC
157574	8213	GGGTTAACTGAATGGAAGTG	166794	CACTTCCATTCAGTTAACCC
157575	8214	AGGGTTAACTGAATGGAAGT	166795	ACTTCCATTCAGTTAACCCT
157576	8215	AAGGGTTAACTGAATGGAAG	166796	CTTCCATTCAGTTAACCCTT
157577	8216	AAAGGGTTAACTGAATGGAA	166797	TTCCATTCAGTTAACCCTTT
157578	8217	TAAAGGGTTAACTGAATGGA	166798	TCCATTCAGTTAACCCTTTA
157579	8218	ATAAAGGGTTAACTGAATGG	166799	CCATTCAGTTAACCCTTTAT
157580	8219	AATAAAGGGTTAACTGAATG	166800	CATTCAGTTAACCCTTTATT
157581	8220	AAATAAAGGGTTAACTGAAT	166801	ATTCAGTTAACCCTTTATTT
157582	8221	AAAATAAAGGGTTAACTGAA	166802	TTCAGTTAACCCTTTATTTT
157583	8222	AAAAATAAAGGGTTAACTGA	166803	TCAGTTAACCCTTTATTTTT
157584	8223	TAAAAATAAAGGGTTAACTG	166804	CAGTTAACCCTTTATTTTTA
157585	8224	ATAAAAATAAAGGGTTAACT	166805	AGTTAACCCTTTATTTTTAT
157586	8225	CATAAAAATAAAGGGTTAAC	166806	GTTAACCCTTTATTTTTATG
157587	8226	CCATAAAAATAAAGGGTTAA	166807	TTAACCCTTTATTTTTATGG
157588	8227	ACCATAAAAATAAAGGGTTA	166808	TAACCCTTTATTTTTATGGT
157589	8228	AACCATAAAAATAAAGGGTT	166809	AACCCTTTATTTTTATGGTT
157590	8229	AAACCATAAAAATAAAGGGT	166810	ACCCTTTATTTTTATGGTTT
157591	8230	AAAACCATAAAAATAAAGGG	166811	CCCTTTATTTTTATGGTTTT
157592	8231	AAAAACCATAAAAATAAAGG	166812	CCTTTATTTTTATGGTTTTT
157593	8232	GAAAAACCATAAAAATAAAG	166813	CTTTATTTTTATGGTTTTTC
157594	8233	AGAAAAACCATAAAAATAAA	166814	TTTATTTTTATGGTTTTTCT
157595	8234	AAGAAAAACCATAAAAATAA	166815	TTATTTTTATGGTTTTTCTT
157596	8235	CAAGAAAAACCATAAAAATA	166816	TATTTTTATGGTTTTTCTTG
157597	8236	TCAAGAAAAACCATAAAAAT	166817	ATTTTTATGGTTTTTCTTGA
157598	8237	CTCAAGAAAAACCATAAAAA	166818	TTTTTATGGTTTTTCTTGAG
157599	8238	GCTCAAGAAAAACCATAAAA	166819	TTTTATGGTTTTTCTTGAGC
157600	8239	GGCTCAAGAAAAACCATAAA	166820	TTTATGGTTTTTCTTGAGCC
157601	8240	TGGCTCAAGAAAAACCATAA	166821	TTATGGTTTTTCTTGAGCCA
157602	8241	ATGGCTCAAGAAAAACCATA	166822	TATGGTTTTTCTTGAGCCAT
157603	8242	TATGGCTCAAGAAAAACCAT	166823	ATGGTTTTTCTTGAGCCATA
157604	8243	CTATGGCTCAAGAAAAACCA	166824	TGGTTTTTCTTGAGCCATAG
157605	8244	ACTATGGCTCAAGAAAAACC	166825	GGTTTTTCTTGAGCCATAGT
157606	8245	AACTATGGCTCAAGAAAAAC	166826	GTTTTTCTTGAGCCATAGTT
157607	8246	CAACTATGGCTCAAGAAAAA	166827	TTTTTCTTGAGCCATAGTTG
157608	8247	ACAACTATGGCTCAAGAAAA	166828	TTTTCTTGAGCCATAGTTGT
157609	8248	TACAACTATGGCTCAAGAAA	166829	TTTCTTGAGCCATAGTTGTA
157610	8249	TTACAACTATGGCTCAAGAA	166830	TTCTTGAGCCATAGTTGTAA
157611	8250	TTTACAACTATGGCTCAAGA	166831	TCTTGAGCCATAGTTGTAAA
157612	8251	CTTTACAACTATGGCTCAAG	166832	CTTGAGCCATAGTTGTAAAG
157613	8252	GCTTTACAACTATGGCTCAA	166833	TTGAGCCATAGTTGTAAAGC
157614	8253	TGCTTTACAACTATGGCTCA	166834	TGAGCCATAGTTGTAAAGCA
157615	8254	CTGCTTTACAACTATGGCTC	166835	GAGCCATAGTTGTAAAGCAG
157616	8255	TCTGCTTTACAACTATGGCT	166836	AGCCATAGTTGTAAAGCAGA
157617	8256	TTCTGCTTTACAACTATGGC	166837	GCCATAGTTGTAAAGCAGAA
157618	8257	TTTCTGCTTTACAACTATGG	166838	CCATAGTTGTAAAGCAGAAA
157619	8258	TTTTCTGCTTTACAACTATG	166839	CATAGTTGTAAAGCAGAAAA
157620	8259	TTTTTCTGCTTTACAACTAT	166840	ATAGTTGTAAAGCAGAAAAA
157621	8260	ATTTTTCTGCTTTACAACTA	166841	TAGTTGTAAAGCAGAAAAAT
157622	8261	GATTTTTCTGCTTTACAACT	166842	AGTTGTAAAGCAGAAAAATC
157623	8262	TGATTTTTCTGCTTTACAAC	166843	GTTGTAAAGCAGAAAAATCA
157624	8263	ATGATTTTTCTGCTTTACAA	166844	TTGTAAAGCAGAAAAATCAT
157625	8264	AATGATTTTTCTGCTTTACA	166845	TGTAAAGCAGAAAAATCATT
157626	8265	AAATGATTTTTCTGCTTTAC	166846	GTAAAGCAGAAAAATCATTT
157627	8266	TAAATGATTTTTCTGCTTTA	166847	TAAAGCAGAAAAATCATTTA
157628	8267	ATAAATGATTTTTCTGCTTT	166848	AAAGCAGAAAAATCATTTAT
157629	8268	TATAAATGATTTTTCTGCTT	166849	AAGCAGAAAAATCATTTATA
157630	8269	TTATAAATGATTTTTCTGCT	166850	AGCAGAAAAATCATTTATAA
157631	8270	TTTATAAATGATTTTTCTGC	166851	GCAGAAAAATCATTTATAAA
157632	8271	CTTTATAAATGATTTTTCTG	166852	CAGAAAAATCATTTATAAAG
157633	8272	CCTTTATAAATGATTTTTCT	166853	AGAAAAATCATTTATAAAGG
157634	8273	ACCTTTATAAATGATTTTTC	166854	GAAAAATCATTTATAAAGGT
157635	8274	AACCTTTATAAATGATTTTT	166855	AAAAATCATTTATAAAGGTT
157636	8275	AAACCTTTATAAATGATTTT	166856	AAAATCATTTATAAAGGTTT
157637	8276	CAAACCTTTATAAATGATTT	166857	AAATCATTTATAAAGGTTTG
157638	8277	ACAAACCTTTATAAATGATT	166858	AATCATTTATAAAGGTTTGT
157639	8278	AACAAACCTTTATAAATGAT	166859	ATCATTTATAAAGGTTTGTT

157640	8279	CAACAAACCTTTATAAATGA	166860	TCATTTATAAAGGTTTGTTG
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157642	8281	TTCAACAAACCTTTATAAAT	166862	ATTTATAAAGGTTTGTTGAA
157643	8282	GTTCAACAAACCTTTATAAA	166863	TTTATAAAGGTTTGTTGAAC
157644	8283	TGTTCAACAAACCTTTATAA	166864	TTATAAAGGTTTGTTGAACA
157645	8284	TTGTTCAACAAACCTTTATA	166865	TATAAAGGTTTGTTGAACAA
157646	8285	TTTGTTCAACAAACCTTTAT	166866	ATAAAGGTTTGTTGAACAAA
157647	8286	TTTTGTTCAACAAACCTTTA	166867	TAAAGGTTTGTTGAACAAAA
157648	8287	ATTTTGTTCAACAAACCTTT	166868	AAAGGTTTGTTGAACAAAAT
157649	8288	AATTTTGTTCAACAAACCTT	166869	AAGGTTTGTTGAACAAAATT
157650	8289	GAATTTTGTTCAACAAACCT	166870	AGGTTTGTTGAACAAAATTC
157651	8290	TGAATTTTGTTCAACAAACC	166871	GGTTTGTTGAACAAAATTCA
157652	8291	TTGAATTTTGTTCAACAAAC	166872	GTTTGTTGAACAAAATTCAA
157653	8292	TTTGAATTTTGTTCAACAAA	166873	TTTGTTGAACAAAATTCAAA
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157655	8294	ATTTTGAATTTTGTTCAACA	166875	TGTTGAACAAAATTCAAAAT
157656	8295	TATTTTGAATTTTGTTCAAC	166876	GTTGAACAAAATTCAAAATA
157657	8296	GTATTTTGAATTTTGTTCAA	166877	TTGAACAAAATTCAAAATAC
157658	8297	AGTATTTTGAATTTTGTTCA	166878	TGAACAAAATTCAAAATACT
157659	8298	CAGTATTTTGAATTTTGTTC	166879	GAACAAAATTCAAAATACTG
157660	8299	ACAGTATTTTGAATTTTGTT	166880	AACAAAATTCAAAATACTGT
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157662	8301	CAACAGTATTTTGAATTTTG	166882	CAAAATTCAAAATACTGTTG
157663	8302	GCAACAGTATTTTGAATTTT	166883	AAAATTCAAAATACTGTTGC
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157665	8304	AAGCAACAGTATTTTGAATT	166885	AATTCAAAATACTGTTGCTT
157666	8305	TAAGCAACAGTATTTTGAAT	166886	ATTCAAAATACTGTTGCTTA
157667	8306	TTAAGCAACAGTATTTTGAA	166887	TTCAAAATACTGTTGCTTAA
157668	8307	TTTAAGCAACAGTATTTTGA	166888	TCAAAATACTGTTGCTTAAA
157669	8308	CTTTAAGCAACAGTATTTTG	166889	CAAAATACTGTTGCTTAAAG
157670	8309	ACTTTAAGCAACAGTATTTT	166890	AAAATACTGTTGCTTAAAGT
157671	8310	TACTTTAAGCAACAGTATTT	166891	AAATACTGTTGCTTAAAGTA
157672	8311	ATACTTTAAGCAACAGTATT	166892	AATACTGTTGCTTAAAGTAT
157673	8312	AATACTTTAAGCAACAGTAT	166893	ATACTGTTGCTTAAAGTATT
157674	8313	TAATACTTTAAGCAACAGTA	166894	TACTGTTGCTTAAAGTATTA
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157677	8316	TCTTAATACTTTAAGCAACA	166897	TGTTGCTTAAAGTATTAAGA
157678	8317	ATCTTAATACTTTAAGCAAC	166898	GTTGCTTAAAGTATTAAGAT
157679	8318	AATCTTAATACTTTAAGCAA	166899	TTGCTTAAAGTATTAAGATT
157680	8319	AAATCTTAATACTTTAAGCA	166900	TGCTTAAAGTATTAAGATTT
157681	8320	AAAATCTTAATACTTTAAGC	166901	GCTTAAAGTATTAAGATTTT
157682	8321	AAAAATCTTAATACTTTAAG	166902	CTTAAAGTATTAAGATTTTT
157683	8322	AAAAAATCTTAATACTTTAA	166903	TTAAAGTATTAAGATTTTTT
157684	8323	TAAAAAATCTTAATACTTTA	166904	TAAAGTATTAAGATTTTTTA
157685	8324	CTAAAAAATCTTAATACTTT	166905	AAAGTATTAAGATTTTTTAG
157686	8325	CCTAAAAAATCTTAATACTT	166906	AAGTATTAAGATTTTTTAGG
157687	8326	TCCTAAAAAATCTTAATACT	166907	AGTATTAAGATTTTTTAGGA
157688	8327	ATCCTAAAAAATCTTAATAC	166908	GTATTAAGATTTTTTAGGAT
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157691	8330	ATAATCCTAAAAAATCTTAA	166911	TTAAGATTTTTTAGGATTAT
157692	8331	TATAATCCTAAAAAATCTTA	166912	TAAGATTTTTTAGGATTATA
157693	8332	GTATAATCCTAAAAAATCTT	166913	AAGATTTTTTAGGATTATAC
157694	8333	GGTATAATCCTAAAAAATCT	166914	AGATTTTTTAGGATTATACC
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157696	8335	AAGGTATAATCCTAAAAAAT	166916	ATTTTTTAGGATTATACCTT
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157698	8337	GTAAGGTATAATCCTAAAAA	166918	TTTTTAGGATTATACCTTAC
157699	8338	AGTAAGGTATAATCCTAAAA	166919	TTTTAGGATTATACCTTACT
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157702	8341	ATAAGTAAGGTATAATCCTA	166922	TAGGATTATACCTTACTTAT
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157704	8343	CTATAAGTAAGGTATAATCC	166924	GGATTATACCTTACTTATAG
157705	8344	CCTATAAGTAAGGTATAATC	166925	GATTATACCTTACTTATAGG
157706	8345	GCCTATAAGTAAGGTATAAT	166926	ATTATACCTTACTTATAGGC
157707	8346	GGCCTATAAGTAAGGTATAA	166927	TTATACCTTACTTATAGGCC
157708	8347	GGGCCTATAAGTAAGGTATA	166928	TATACCTTACTTATAGGCCC
157709	8348	CGGGCCTATAAGTAAGGTAT	166929	ATACCTTACTTATAGGCCCG
157710	8349	ACGGGCCTATAAGTAAGGTA	166930	TACCTTACTTATAGGCCCGT
157711	8350	GACGGGCCTATAAGTAAGGT	166931	ACCTTACTTATAGGCCCGTC

157712	8351	TGACGGGCCTATAAGTAAGG	166932	CCTTACTTATAGGCCCGTCA
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157714	8353	AATGACGGGCCTATAAGTAA	166934	TTACTTATAGGCCCGTCATT
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157716	8355	TGAATGACGGGCCTATAAGT	166936	ACTTATAGGCCCGTCATTCA
157717	8356	ATGAATGACGGGCCTATAAG	166937	CTTATAGGCCCGTCATTCAT
157718	8357	AATGAATGACGGGCCTATAA	166938	TTATAGGCCCGTCATTCATT
157719	8358	AAATGAATGACGGGCCTATA	166939	TATAGGCCCGTCATTCATTT
157720	8359	CAAATGAATGACGGGCCTAT	166940	ATAGGCCCGTCATTCATTTG
157721	8360	CCAAATGAATGACGGGCCTA	166941	TAGGCCCGTCATTCATTTGG
157722	8361	GCCAAATGAATGACGGGCCT	166942	AGGCCCGTCATTCATTTGGC
157723	8362	TGCCAAATGAATGACGGGCC	166943	GGCCCGTCATTCATTTGGCA
157724	8363	ATGCCAAATGAATGACGGGC	166944	GCCCGTCATTCATTTGGCAT
157725	8364	CATGCCAAATGAATGACGGG	166945	CCCGTCATTCATTTGGCATG
157726	8365	TCATGCCAAATGAATGACGG	166946	CCGTCATTCATTTGGCATGA
157727	8366	TTCATGCCAAATGAATGACG	166947	CGTCATTCATTTGGCATGAA
157728	8367	TTTCATGCCAAATGAATGAC	166948	GTCATTCATTTGGCATGAAA
157729	8368	ATTTCATGCCAAATGAATGA	166949	TCATTCATTTGGCATGAAAT
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157731	8370	AAATTTCATGCCAAATGAAT	166951	ATTCATTTGGCATGAAATTT
157732	8371	AAAATTTCATGCCAAATGAA	166952	TTCATTTGGCATGAAATTTT
157733	8372	CAAAATTTCATGCCAAATGA	166953	TCATTTGGCATGAAATTTTG
157734	8373	TCAAAATTTCATGCCAAATG	166954	CATTTGGCATGAAATTTTGA
157735	8374	CTCAAAATTTCATGCCAAAT	166955	ATTTGGCATGAAATTTTGAG
157736	8375	ACTCAAAATTTCATGCCAAA	166956	TTTGGCATGAAATTTTGAGT
157737	8376	AACTCAAAATTTCATGCCAA	166957	TTGGCATGAAATTTTGAGTT
157738	8377	AAACTCAAAATTTCATGCCA	166958	TGGCATGAAATTTTGAGTTT
157739	8378	AAAACTCAAAATTTCATGCC	166959	GGCATGAAATTTTGAGTTTT
157740	8379	TAAAACTCAAAATTTCATGC	166960	GCATGAAATTTTGAGTTTTA
157741	8380	ATAAAACTCAAAATTTCATG	166961	CATGAAATTTTGAGTTTTAT
157742	8381	AATAAAACTCAAAATTTCAT	166962	ATGAAATTTTGAGTTTTATT
157743	8382	GAATAAAACTCAAAATTTCA	166963	TGAAATTTTGAGTTTTATTC
157744	8383	TGAATAAAACTCAAAATTTC	166964	GAAATTTTGAGTTTTATTCA
157745	8384	GTGAATAAAACTCAAAATTT	166965	AAATTTTGAGTTTTATTCAC
157746	8385	AGTGAATAAAACTCAAAATT	166966	AATTTTGAGTTTTATTCACT
157747	8386	AAGTGAATAAAACTCAAAAT	166967	ATTTTGAGTTTTATTCACTT
157748	8387	AAAGTGAATAAAACTCAAAA	166968	TTTTGAGTTTTATTCACTTT
157749	8388	GAAAGTGAATAAAACTCAAA	166969	TTTGAGTTTTATTCACTTTC
157750	8389	TGAAAGTGAATAAAACTCAA	166970	TTGAGTTTTATTCACTTTCA
157751	8390	GTGAAAGTGAATAAAACTCA	166971	TGAGTTTTATTCACTTTCAC
157752	8391	AGTGAAAGTGAATAAAACTC	166972	GAGTTTTATTCACTTTCACT
157753	8392	AAGTGAAAGTGAATAAAACT	166973	AGTTTTATTCACTTTCACTT
157754	8393	AAAGTGAAAGTGAATAAAAC	166974	GTTTTATTCACTTTCACTTT
157755	8394	GAAAGTGAAAGTGAATAAAA	166975	TTTTATTCACTTTCACTTTC
157756	8395	GGAAAGTGAAAGTGAATAAA	166976	TTTATTCACTTTCACTTTCC
157757	8396	AGGAAAGTGAAAGTGAATAA	166977	TTATTCACTTTCACTTTCCT
157758	8397	AAGGAAAGTGAAAGTGAATA	166978	TATTCACTTTCACTTTCCTT
157759	8398	AAAGGAAAGTGAAAGTGAAT	166979	ATTCACTTTCACTTTCCTTT
157760	8399	AAAAGGAAAGTGAAAGTGAA	166980	TTCACTTTCACTTTCCTTTT
157761	8400	AAAAAGGAAAGTGAAAGTGA	166981	TCACTTTCACTTTCCTTTTT
157762	8401	AAAAAAGGAAAGTGAAAGTG	166982	CACTTTCACTTTCCTTTTTT
157763	8402	AAAAAAAGGAAAGTGAAAGT	166983	ACTTTCACTTTCCTTTTTTT
157764	8403	GAAAAAAAGGAAAGTGAAAG	166984	CTTTCACTTTCCTTTTTTTC
157765	8404	GGAAAAAAAGGAAAGTGAAA	166985	TTTCACTTTCCTTTTTTTCC
157766	8405	TGGAAAAAAAGGAAAGTGAA	166986	TTCACTTTCCTTTTTTTCCA
157767	8406	TTGGAAAAAAAGGAAAGTGA	166987	TCACTTTCCTTTTTTTCCAA
157768	8407	TTTGGAAAAAAAGGAAAGTG	166988	CACTTTCCTTTTTTTCCAAA
157769	8408	CTTTGGAAAAAAAGGAAAGT	166989	ACTTTCCTTTTTTTCCAAAG
157770	8409	GCTTTGGAAAAAAAGGAAAG	166990	CTTTCCTTTTTTTCCAAAGC
157771	8410	TGCTTTGGAAAAAAAGGAAA	166991	TTTCCTTTTTTTCCAAAGCA
157772	8411	TTGCTTTGGAAAAAAAGGAA	166992	TTCCTTTTTTTCCAAAGCAA
157773	8412	ATTGCTTTGGAAAAAAAGGA	166993	TCCTTTTTTTCCAAAGCAAT
157774	8413	AATTGCTTTGGAAAAAAAGG	166994	CCTTTTTTTCCAAAGCAATT
157775	8414	TAATTGCTTTGGAAAAAAAG	166995	CTTTTTTTCCAAAGCAATTA
157776	8415	TTAATTGCTTTGGAAAAAAA	166996	TTTTTTTCCAAAGCAATTAA
157777	8416	TTTAATTGCTTTGGAAAAAA	166997	TTTTTTCCAAAGCAATTAAA
157778	8417	TTTTAATTGCTTTGGAAAAA	166998	TTTTTCCAAAGCAATTAAAA
157779	8418	TTTTTAATTGCTTTGGAAAA	166999	TTTTCCAAAGCAATTAAAAA
157780	8419	TTTTTTAATTGCTTTGGAAA	167000	TTTCCAAAGCAATTAAAAAA
157781	8420	TTTTTTTAATTGCTTTGGAA	167001	TTCCAAAGCAATTAAAAAAA
157782	8421	GTTTTTTTAATTGCTTTGGA	167002	TCCAAAGCAATTAAAAAAAC
157783	8422	AGTTTTTTTAATTGCTTTGG	167003	CCAAAGCAATTAAAAAAACT

157784	8423	CAGTTTTTTTAATTGCTTTG	167004	CAAAGCAATTAAAAAAACTG
157785	8424	GCAGTTTTTTTAATTGCTTT	167005	AAAGCAATTAAAAAAACTGC
157786	8425	GGCAGTTTTTTTAATTGCTT	167006	AAGCAATTAAAAAAACTGCC
157787	8426	TGGCAGTTTTTTTAATTGCT	167007	AGCAATTAAAAAAACTGCCA
157788	8427	TTGGCAGTTTTTTTAATTGC	167008	GCAATTAAAAAAACTGCCAA
157789	8428	TTTGGCAGTTTTTTTAATTG	167009	CAATTAAAAAAACTGCCAAA
157790	8429	CTTTGGCAGTTTTTTTAATT	167010	AATTAAAAAAACTGCCAAAG
157791	8430	ACTTTGGCAGTTTTTTTAAT	167011	ATTAAAAAAACTGCCAAAGT
157792	8431	TACTTTGGCAGTTTTTTTAA	167012	TTAAAAAAACTGCCAAAGTA
157793	8432	TTACTTTGGCAGTTTTTTTA	167013	TAAAAAAACTGCCAAAGTAA
157794	8433	CTTACTTTGGCAGTTTTTTT	167014	AAAAAAACTGCCAAAGTAAG
157795	8434	TCTTACTTTGGCAGTTTTTT	167015	AAAAAACTGCCAAAGTAAGA
157796	8435	CTCTTACTTTGGCAGTTTTT	167016	AAAAACTGCCAAAGTAAGAG
157797	8436	ACTCTTACTTTGGCAGTTTT	167017	AAAACTGCCAAAGTAAGAGT
157798	8437	CACTCTTACTTTGGCAGTTT	167018	AAACTGCCAAAGTAAGAGTG
157799	8438	TCACTCTTACTTTGGCAGTT	167019	AACTGCCAAAGTAAGAGTGA
157800	8439	GTCACTCTTACTTTGGCAGT	167020	ACTGCCAAAGTAAGAGTGAC
157801	8440	AGTCACTCTTACTTTGGCAG	167021	CTGCCAAAGTAAGAGTGACT
157802	8441	CAGTCACTCTTACTTTGGCA	167022	TGCCAAAGTAAGAGTGACTG
157803	8442	GCAGTCACTCTTACTTTGGC	167023	GCCAAAGTAAGAGTGACTGC
157804	8443	CGCAGTCACTCTTACTTTGG	167024	CCAAAGTAAGAGTGACTGCG
157805	8444	CCGCAGTCACTCTTACTTTG	167025	CAAAGTAAGAGTGACTGCGG
157806	8445	TCCGCAGTCACTCTTACTTT	167026	AAAGTAAGAGTGACTGCGGA
157807	8446	TTCCGCAGTCACTCTTACTT	167027	AAGTAAGAGTGACTGCGGAA
157808	8447	GTTCCGCAGTCACTCTTACT	167028	AGTAAGAGTGACTGCGGAAC
157809	8448	AGTTCCGCAGTCACTCTTAC	167029	GTAAGAGTGACTGCGGAACT
157810	8449	TAGTTCCGCAGTCACTCTTA	167030	TAAGAGTGACTGCGGAACTA
157811	8450	TTAGTTCCGCAGTCACTCTT	167031	AAGAGTGACTGCGGAACTAA
157812	8451	CTTAGTTCCGCAGTCACTCT	167032	AGAGTGACTGCGGAACTAAG
157813	8452	CCTTAGTTCCGCAGTCACTC	167033	GAGTGACTGCGGAACTAAGG
157814	8453	ACCTTAGTTCCGCAGTCACT	167034	AGTGACTGCGGAACTAAGGT
157815	8454	AACCTTAGTTCCGCAGTCAC	167035	GTGACTGCGGAACTAAGGTT
157816	8455	TAACCTTAGTTCCGCAGTCA	167036	TGACTGCGGAACTAAGGTTA
157817	8456	GTAACCTTAGTTCCGCAGTC	167037	GACTGCGGAACTAAGGTTAC
157818	8457	AGTAACCTTAGTTCCGCAGT	167038	ACTGCGGAACTAAGGTTACT
157819	8458	CAGTAACCTTAGTTCCGCAG	167039	CTGCGGAACTAAGGTTACTG
157820	8459	ACAGTAACCTTAGTTCCGCA	167040	TGCGGAACTAAGGTTACTGT
157821	8460	TACAGTAACCTTAGTTCCGC	167041	GCGGAACTAAGGTTACTGTA
157822	8461	TTACAGTAACCTTAGTTCCG	167042	CGGAACTAAGGTTACTGTAA
157823	8462	GTTACAGTAACCTTAGTTCC	167043	GGAACTAAGGTTACTGTAAC
157824	8463	AGTTACAGTAACCTTAGTTC	167044	GAACTAAGGTTACTGTAACT
157825	8464	AAGTTACAGTAACCTTAGTT	167045	AACTAAGGTTACTGTAACTT
157826	8465	TAAGTTACAGTAACCTTAGT	167046	ACTAAGGTTACTGTAACTTA
157827	8466	GTAAGTTACAGTAACCTTAG	167047	CTAAGGTTACTGTAACTTAC
157828	8467	GGTAAGTTACAGTAACCTTA	167048	TAAGGTTACTGTAACTTACC
157829	8468	TGGTAAGTTACAGTAACCTT	167049	AAGGTTACTGTAACTTACCA
157830	8469	ATGGTAAGTTACAGTAACCT	167050	AGGTTACTGTAACTTACCAT
157831	8470	CATGGTAAGTTACAGTAACC	167051	GGTTACTGTAACTTACCATG
157832	8471	CCATGGTAAGTTACAGTAAC	167052	GTTACTGTAACTTACCATGG
157833	8472	TCCATGGTAAGTTACAGTAA	167053	TTACTGTAACTTACCATGGA
157834	8473	CTCCATGGTAAGTTACAGTA	167054	TACTGTAACTTACCATGGAG
157835	8474	CCTCCATGGTAAGTTACAGT	167055	ACTGTAACTTACCATGGAGG
157836	8475	TCCTCCATGGTAAGTTACAG	167056	CTGTAACTTACCATGGAGGA
157837	8476	ATCCTCCATGGTAAGTTACA	167057	TGTAACTTACCATGGAGGAT
157838	8477	AATCCTCCATGGTAAGTTAC	167058	GTAACTTACCATGGAGGATT
157839	8478	TAATCCTCCATGGTAAGTTA	167059	TAACTTACCATGGAGGATTA
157840	8479	TTAATCCTCCATGGTAAGTT	167060	AACTTACCATGGAGGATTAA
157841	8480	CTTAATCCTCCATGGTAAGT	167061	ACTTACCATGGAGGATTAAG
157842	8481	CCTTAATCCTCCATGGTAAG	167062	CTTACCATGGAGGATTAAGG
157843	8482	CCCTTAATCCTCCATGGTAA	167063	TTACCATGGAGGATTAAGGG
157844	8483	ACCCTTAATCCTCCATGGTA	167064	TACCATGGAGGATTAAGGGT
157845	8484	TACCCTTAATCCTCCATGGT	167065	ACCATGGAGGATTAAGGGTA
157846	8485	CTACCCTTAATCCTCCATGG	167066	CCATGGAGGATTAAGGGTAG
157847	8486	GCTACCCTTAATCCTCCATG	167067	CATGGAGGATTAAGGGTAGC
157848	8487	CGCTACCCTTAATCCTCCAT	167068	ATGGAGGATTAAGGGTAGCG
157849	8488	ACGCTACCCTTAATCCTCCA	167069	TGGAGGATTAAGGGTAGCGT
157850	8489	CACGCTACCCTTAATCCTCC	167070	GGAGGATTAAGGGTAGCGTG
157851	8490	ACACGCTACCCTTAATCCTC	167071	GAGGATTAAGGGTAGCGTGT
157852	8491	CACACGCTACCCTTAATCCT	167072	AGGATTAAGGGTAGCGTGTG
157853	8492	CCACACGCTACCCTTAATCC	167073	GGATTAAGGGTAGCGTGTGG
157854	8493	ACCACACGCTACCCTTAATC	167074	GATTAAGGGTAGCGTGTGGT
157855	8494	CACCACACGCTACCCTTAAT	167075	ATTAAGGGTAGCGTGTGGTG

157856	8495	CCACCACACGCTACCCTTAA	167076	TTAAGGGTAGCGTGTGGTGG
157857	8496	ACCACCACACGCTACCCTTA	167077	TAAGGGTAGCGTGTGGTGGT
157858	8497	GACCACCACACGCTACCCTT	167078	AAGGGTAGCGTGTGGTGGTC
157859	8498	AGACCACCACACGCTACCCT	167079	AGGGTAGCGTGTGGTGGTCT
157860	8499	TAGACCACCACACGCTACCC	167080	GGGTAGCGTGTGGTGGTCTA
157861	8500	GTAGACCACCACACGCTACC	167081	GGTAGCGTGTGGTGGTCTAC
157862	8501	TGTAGACCACCACACGCTAC	167082	GTAGCGTGTGGTGGTCTACA
157863	8502	TTGTAGACCACCACACGCTA	167083	TAGCGTGTGGTGGTCTACAA
157864	8503	GTTGTAGACCACCACACGCT	167084	AGCGTGTGGTGGTCTACAAC
157865	8504	TGTTGTAGACCACCACACGC	167085	GCGTGTGGTGGTCTACAACA
157866	8505	ATGTTGTAGACCACCACACG	167086	CGTGTGGTGGTCTACAACAT
157867	8506	TATGTTGTAGACCACCACAC	167087	GTGTGGTGGTCTACAACATA
157868	8507	CTATGTTGTAGACCACCACA	167088	TGTGGTGGTCTACAACATAG
157869	8508	ACTATGTTGTAGACCACCAC	167089	GTGGTGGTCTACAACATAGT
157870	8509	AACTATGTTGTAGACCACCA	167090	TGGTGGTCTACAACATAGTT
157871	8510	TAACTATGTTGTAGACCACC	167091	GGTGGTCTACAACATAGTTA
157872	8511	ATAACTATGTTGTAGACCAC	167092	GTGGTCTACAACATAGTTAT
157873	8512	AATAACTATGTTGTAGACCA	167093	TGGTCTACAACATAGTTATT
157874	8513	AAATAACTATGTTGTAGACC	167094	GGTCTACAACATAGTTATTT
157875	8514	CAAATAACTATGTTGTAGAC	167095	GTCTACAACATAGTTATTTG
157876	8515	CCAAATAACTATGTTGTAGA	167096	TCTACAACATAGTTATTTGG
157877	8516	CCCAAATAACTATGTTGTAG	167097	CTACAACATAGTTATTTGGG
157878	8517	ACCCAAATAACTATGTTGTA	167098	TACAACATAGTTATTTGGGT
157879	8518	AACCCAAATAACTATGTTGT	167099	ACAACATAGTTATTTGGGTT
157880	8519	AAACCCAAATAACTATGTTG	167100	CAACATAGTTATTTGGGTTT
157881	8520	AAAACCCAAATAACTATGTT	167101	AACATAGTTATTTGGGTTTT
157882	8521	TAAAACCCAAATAACTATGT	167102	ACATAGTTATTTGGGTTTTA
157883	8522	CTAAAACCCAAATAACTATG	167103	CATAGTTATTTGGGTTTTAG
157884	8523	ACTAAAACCCAAATAACTAT	167104	ATAGTTATTTGGGTTTTAGT
157885	8524	TACTAAAACCCAAATAACTA	167105	TAGTTATTTGGGTTTTAGTA
157886	8525	ATACTAAAACCCAAATAACT	167106	AGTTATTTGGGTTTTAGTAT
157887	8526	AATACTAAAACCCAAATAAC	167107	GTTATTTGGGTTTTAGTATT
157888	8527	AAATACTAAAACCCAAATAA	167108	TTATTTGGGTTTTAGTATTT
157889	8528	GAAATACTAAAACCCAAATA	167109	TATTTGGGTTTTAGTATTTC
157890	8529	TGAAATACTAAAACCCAAAT	167110	ATTTGGGTTTTAGTATTTCA
157891	8530	ATGAAATACTAAAACCCAAA	167111	TTTGGGTTTTAGTATTTCAT
157892	8531	AATGAAATACTAAAACCCAA	167112	TTGGGTTTTAGTATTTCATT
157893	8532	AAATGAAATACTAAAACCCA	167113	TGGGTTTTAGTATTTCATTT
157894	8533	TAAATGAAATACTAAAACCC	167114	GGGTTTTAGTATTTCATTTA
157895	8534	CTAAATGAAATACTAAAACC	167115	GGTTTTAGTATTTCATTTAG
157896	8535	TCTAAATGAAATACTAAAAC	167116	GTTTTAGTATTTCATTTAGA
157897	8536	GTCTAAATGAAATACTAAAA	167117	TTTTAGTATTTCATTTAGAC
157898	8537	TGTCTAAATGAAATACTAAA	167118	TTTAGTATTTCATTTAGACA
157899	8538	CTGTCTAAATGAAATACTAA	167119	TTAGTATTTCATTTAGACAG
157900	8539	GCTGTCTAAATGAAATACTA	167120	TAGTATTTCATTTAGACAGC
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157902	8541	TTGCTGTCTAAATGAAATAC	167122	GTATTTCATTTAGACAGCAA
157903	8542	GTTGCTGTCTAAATGAAATA	167123	TATTTCATTTAGACAGCAAC
157904	8543	TGTTGCTGTCTAAATGAAAT	167124	ATTTCATTTAGACAGCAACA
157905	8544	GTGTTGCTGTCTAAATGAAA	167125	TTTCATTTAGACAGCAACAC
157906	8545	AGTGTTGCTGTCTAAATGAA	167126	TTCATTTAGACAGCAACACT
157907	8546	AAGTGTTGCTGTCTAAATGA	167127	TCATTTAGACAGCAACACTT
157908	8547	TAAGTGTTGCTGTCTAAATG	167128	CATTTAGACAGCAACACTTA
157909	8548	GTAAGTGTTGCTGTCTAAAT	167129	ATTTAGACAGCAACACTTAC
157910	8549	GGTAAGTGTTGCTGTCTAAA	167130	TTTAGACAGCAACACTTACC
157911	8550	AGGTAAGTGTTGCTGTCTAA	167131	TTAGACAGCAACACTTACCT
157912	8551	TAGGTAAGTGTTGCTGTCTA	167132	TAGACAGCAACACTTACCTA
157913	8552	TTAGGTAAGTGTTGCTGTCT	167133	AGACAGCAACACTTACCTAA
157914	8553	ATTAGGTAAGTGTTGCTGTC	167134	GACAGCAACACTTACCTAAT
157915	8554	CATTAGGTAAGTGTTGCTGT	167135	ACAGCAACACTTACCTAATG
157916	8555	ACATTAGGTAAGTGTTGCTG	167136	CAGCAACACTTACCTAATGT
157917	8556	AACATTAGGTAAGTGTTGCT	167137	AGCAACACTTACCTAATGTT
157918	8557	AAACATTAGGTAAGTGTTGC	167138	GCAACACTTACCTAATGTTT
157919	8558	TAAACATTAGGTAAGTGTTG	167139	CAACACTTACCTAATGTTTA
157920	8559	TTAAACATTAGGTAAGTGTT	167140	AACACTTACCTAATGTTTAA
157921	8560	TTTAAACATTAGGTAAGTGT	167141	ACACTTACCTAATGTTTAAA
157922	8561	CTTTAAACATTAGGTAAGTG	167142	CACTTACCTAATGTTTAAAG
157923	8562	CCTTTAAACATTAGGTAAGT	167143	ACTTACCTAATGTTTAAAGG
157924	8563	ACCTTTAAACATTAGGTAAG	167144	CTTACCTAATGTTTAAAGGT
157925	8564	TACCTTTAAACATTAGGTAA	167145	TTACCTAATGTTTAAAGGTA
157926	8565	TTACCTTTAAACATTAGGTA	167146	TACCTAATGTTTAAAGGTAA
157927	8566	ATTACCTTTAAACATTAGGT	167147	ACCTAATGTTTAAAGGTAAT

157928	8567	CATTACCTTTAAACATTAGG	167148	CCTAATGTTTAAAGGTAATG
157929	8568	ACATTACCTTTAAACATTAG	167149	CTAATGTTTAAAGGTAATGT
157930	8569	GACATTACCTTTAAACATTA	167150	TAATGTTTAAAGGTAATGTC
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157932	8571	AAGACATTACCTTTAAACAT	167152	ATGTTTAAAGGTAATGTCTT
157933	8572	AAAGACATTACCTTTAAACA	167153	TGTTTAAAGGTAATGTCTTT
157934	8573	CAAAGACATTACCTTTAAAC	167154	GTTTAAAGGTAATGTCTTTG
157935	8574	GCAAAGACATTACCTTTAAA	167155	TTTAAAGGTAATGTCTTTGC
157936	8575	TGCAAAGACATTACCTTTAA	167156	TTAAAGGTAATGTCTTTGCA
157937	8576	TTGCAAAGACATTACCTTTA	167157	TAAAGGTAATGTCTTTGCAA
157938	8577	GTTGCAAAGACATTACCTTT	167158	AAAGGTAATGTCTTTGCAAC
157939	8578	TGTTGCAAAGACATTACCTT	167159	AAGGTAATGTCTTTGCAACA
157940	8579	GTGTTGCAAAGACATTACCT	167160	AGGTAATGTCTTTGCAACAC
157941	8580	GGTGTTGCAAAGACATTACC	167161	GGTAATGTCTTTGCAACACC
157942	8581	TGGTGTTGCAAAGACATTAC	167162	GTAATGTCTTTGCAACACCA
157943	8582	TTGGTGTTGCAAAGACATTA	167163	TAATGTCTTTGCAACACCAA
157944	8583	CTTGGTGTTGCAAAGACATT	167164	AATGTCTTTGCAACACCAAG
157945	8584	TCTTGGTGTTGCAAAGACAT	167165	ATGTCTTTGCAACACCAAGA
157946	8585	TTCTTGGTGTTGCAAAGACA	167166	TGTCTTTGCAACACCAAGAA
157947	8586	TTTCTTGGTGTTGCAAAGAC	167167	GTCTTTGCAACACCAAGAAA
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157949	8588	TTTTTCTTGGTGTTGCAAAG	167169	CTTTGCAACACCAAGAAAAA
157950	8589	CTTTTTCTTGGTGTTGCAAA	167170	TTTGCAACACCAAGAAAAAG
157951	8590	GCTTTTTCTTGGTGTTGCAA	167171	TTGCAACACCAAGAAAAAGC
157952	8591	AGCTTTTTCTTGGTGTTGCA	167172	TGCAACACCAAGAAAAAGCT
157953	8592	AAGCTTTTTCTTGGTGTTGC	167173	GCAACACCAAGAAAAAGCTT
157954	8593	AAAGCTTTTTCTTGGTGTTG	167174	CAACACCAAGAAAAAGCTTT
157955	8594	CAAAGCTTTTTCTTGGTGTT	167175	AACACCAAGAAAAAGCTTTG
157956	8595	TCAAAGCTTTTTCTTGGTGT	167176	ACACCAAGAAAAAGCTTTGA
157957	8596	CTCAAAGCTTTTTCTTGGTG	167177	CACCAAGAAAAAGCTTTGAG
157958	8597	ACTCAAAGCTTTTTCTTGGT	167178	ACCAAGAAAAAGCTTTGAGT
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157961	8600	ACTACTCAAAGCTTTTTCTT	167181	AAGAAAAAGCTTTGAGTAGT
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157963	8602	CTACTACTCAAAGCTTTTTC	167183	GAAAAAGCTTTGAGTAGTAG
157964	8603	ACTACTACTCAAAGCTTTTT	167184	AAAAAGCTTTGAGTAGTAGT
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157966	8605	AAACTACTACTCAAAGCTTT	167186	AAAGCTTTGAGTAGTAGTTT
157967	8606	GAAACTACTACTCAAAGCTT	167187	AAGCTTTGAGTAGTAGTTTC
157968	8607	AGAAACTACTACTCAAAGCT	167188	AGCTTTGAGTAGTAGTTTCT
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157973	8612	AAAGTAGAAACTACTACTCA	167193	TGAGTAGTAGTTTCTACTTT
157974	8613	AAAAGTAGAAACTACTACTC	167194	GAGTAGTAGTTTCTACTTTT
157975	8614	TAAAAGTAGAAACTACTACT	167195	AGTAGTAGTTTCTACTTTTA
157976	8615	TTAAAAGTAGAAACTACTAC	167196	GTAGTAGTTTCTACTTTTAA
157977	8616	TTTAAAAGTAGAAACTACTA	167197	TAGTAGTTTCTACTTTTAAA
157978	8617	GTTTAAAAGTAGAAACTACT	167198	AGTAGTTTCTACTTTTAAAC
157979	8618	AGTTTAAAAGTAGAAACTAC	167199	GTAGTTTCTACTTTTAAACT
157980	8619	TAGTTTAAAAGTAGAAACTA	167200	TAGTTTCTACTTTTAAACTA
157981	8620	GTAGTTTAAAAGTAGAAACT	167201	AGTTTCTACTTTTAAACTAC
157982	8621	AGTAGTTTAAAAGTAGAAAC	167202	GTTTCTACTTTTAAACTACT
157983	8622	TAGTAGTTTAAAAGTAGAAA	167203	TTTCTACTTTTAAACTACTA
157984	8623	TTAGTAGTTTAAAAGTAGAA	167204	TTCTACTTTTAAACTACTAA
157985	8624	TTTAGTAGTTTAAAAGTAGA	167205	TCTACTTTTAAACTACTAAA
157986	8625	ATTTAGTAGTTTAAAAGTAG	167206	CTACTTTTAAACTACTAAAT
157987	8626	TATTTAGTAGTTTAAAAGTA	167207	TACTTTTAAACTACTAAATA
157988	8627	ATATTTAGTAGTTTAAAAGT	167208	ACTTTTAAACTACTAAATAT
157989	8628	AATATTTAGTAGTTTAAAAG	167209	CTTTTAAACTACTAAATATT
157990	8629	TAATATTTAGTAGTTTAAAA	167210	TTTTAAACTACTAAATATTA
157991	8630	CTAATATTTAGTAGTTTAAA	167211	TTTAAACTACTAAATATTAG
157992	8631	ACTAATATTTAGTAGTTTAA	167212	TTAAACTACTAAATATTAGT
157993	8632	TACTAATATTTAGTAGTTTA	167213	TAAACTACTAAATATTAGTA
157994	8633	ATACTAATATTTAGTAGTTT	167214	AAACTACTAAATATTAGTAT
157995	8634	TATACTAATATTTAGTAGTT	167215	AACTACTAAATATTAGTATA
157996	8635	ATATACTAATATTTAGTAGT	167216	ACTACTAAATATTAGTATAT
157997	8636	GATATACTAATATTTAGTAG	167217	CTACTAAATATTAGTATATC
157998	8637	AGATATACTAATATTTAGTA	167218	TACTAAATATTAGTATATCT
157999	8638	GAGATATACTAATATTTAGT	167219	ACTAAATATTAGTATATCTC

158000	8639	AGAGATATACTAATATTTAG	167220	CTAAATATTAGTATATCTCT
158001	8640	GAGAGATATACTAATATTTA	167221	TAAATATTAGTATATCTCTC
158002	8641	AGAGAGATATACTAATATTT	167222	AAATATTAGTATATCTCTCT
158003	8642	TAGAGAGATATACTAATATT	167223	AATATTAGTATATCTCTCTA
158004	8643	GTAGAGAGATATACTAATAT	167224	ATATTAGTATATCTCTCTAC
158005	8644	AGTAGAGAGATATACTAATA	167225	TATTAGTATATCTCTCTACT
158006	8645	TAGTAGAGAGATATACTAAT	167226	ATTAGTATATCTCTCTACTA
158007	8646	CTAGTAGAGAGATATACTAA	167227	TTAGTATATCTCTCTACTAG
158008	8647	CCTAGTAGAGAGATATACTA	167228	TAGTATATCTCTCTACTAGG
158009	8648	TCCTAGTAGAGAGATATACT	167229	AGTATATCTCTCTACTAGGA
158010	8649	ATCCTAGTAGAGAGATATAC	167230	GTATATCTCTCTACTAGGAT
158011	8650	AATCCTAGTAGAGAGATATA	167231	TATATCTCTCTACTAGGATT
158012	8651	TAATCCTAGTAGAGAGATAT	167232	ATATCTCTCTACTAGGATTA
158013	8652	TTAATCCTAGTAGAGAGATA	167233	TATCTCTCTACTAGGATTAA
158014	8653	ATTAATCCTAGTAGAGAGAT	167234	ATCTCTCTACTAGGATTAAT
158015	8654	CATTAATCCTAGTAGAGAGA	167235	TCTCTCTACTAGGATTAATG
158016	8655	ACATTAATCCTAGTAGAGAG	167236	CTCTCTACTAGGATTAATGT
158017	8656	AACATTAATCCTAGTAGAGA	167237	TCTCTACTAGGATTAATGTT
158018	8657	TAACATTAATCCTAGTAGAG	167238	CTCTACTAGGATTAATGTTA
158019	8658	ATAACATTAATCCTAGTAGA	167239	TCTACTAGGATTAATGTTAT
158020	8659	AATAACATTAATCCTAGTAG	167240	CTACTAGGATTAATGTTATT
158021	8660	AAATAACATTAATCCTAGTA	167241	TACTAGGATTAATGTTATTT
158022	8661	AAAATAACATTAATCCTAGT	167242	ACTAGGATTAATGTTATTTT
158023	8662	AAAAATAACATTAATCCTAG	167243	CTAGGATTAATGTTATTTTT
158024	8663	GAAAAATAACATTAATCCTA	167244	TAGGATTAATGTTATTTTTC
158025	8664	AGAAAAATAACATTAATCCT	167245	AGGATTAATGTTATTTTTCT
158026	8665	TAGAAAAATAACATTAATCC	167246	GGATTAATGTTATTTTTCTA
158027	8666	TTAGAAAAATAACATTAATC	167247	GATTAATGTTATTTTTCTAA
158028	8667	ATTAGAAAAATAACATTAAT	167248	ATTAATGTTATTTTTCTAAT
158029	8668	TATTAGAAAAATAACATTAA	167249	TTAATGTTATTTTTCTAATA
158030	8669	ATATTAGAAAAATAACATTA	167250	TAATGTTATTTTTCTAATAT
158031	8670	AATATTAGAAAAATAACATT	167251	AATGTTATTTTTCTAATATT
158032	8671	TAATATTAGAAAAATAACAT	167252	ATGTTATTTTTCTAATATTA
158033	8672	ATAATATTAGAAAAATAACA	167253	TGTTATTTTTCTAATATTAT
158034	8673	CATAATATTAGAAAAATAAC	167254	GTTATTTTTCTAATATTATG
158035	8674	TCATAATATTAGAAAAATAA	167255	TTATTTTTCTAATATTATGA
158036	8675	CTCATAATATTAGAAAAATA	167256	TATTTTTCTAATATTATGAG
158037	8676	CCTCATAATATTAGAAAAAT	167257	ATTTTTCTAATATTATGAGG
158038	8677	ACCTCATAATATTAGAAAAA	167258	TTTTTCTAATATTATGAGGT
158039	8678	AACCTCATAATATTAGAAAA	167259	TTTTCTAATATTATGAGGTT
158040	8679	GAACCTCATAATATTAGAAA	167260	TTTCTAATATTATGAGGTTC
158041	8680	AGAACCTCATAATATTAGAA	167261	TTCTAATATTATGAGGTTCT
158042	8681	AAGAACCTCATAATATTAGA	167262	TCTAATATTATGAGGTTCTT
158043	8682	TAAGAACCTCATAATATTAG	167263	CTAATATTATGAGGTTCTTA
158044	8683	TTAAGAACCTCATAATATTA	167264	TAATATTATGAGGTTCTTAA
158045	8684	TTTAAGAACCTCATAATATT	167265	AATATTATGAGGTTCTTAAA
158046	8685	GTTTAAGAACCTCATAATAT	167266	ATATTATGAGGTTCTTAAAC
158047	8686	TGTTTAAGAACCTCATAATA	167267	TATTATGAGGTTCTTAAACA
158048	8687	ATGTTTAAGAACCTCATAAT	167268	ATTATGAGGTTCTTAAACAT
158049	8688	GATGTTTAAGAACCTCATAA	167269	TTATGAGGTTCTTAAACATC
158050	8689	AGATGTTTAAGAACCTCATA	167270	TATGAGGTTCTTAAACATCT
158051	8690	AAGATGTTTAAGAACCTCAT	167271	ATGAGGTTCTTAAACATCTT
158052	8691	AAAGATGTTTAAGAACCTCA	167272	TGAGGTTCTTAAACATCTTT
158053	8692	AAAAGATGTTTAAGAACCTC	167273	GAGGTTCTTAAACATCTTTT
158054	8693	CAAAAGATGTTTAAGAACCT	167274	AGGTTCTTAAACATCTTTTG
158055	8694	CCAAAAGATGTTTAAGAACC	167275	GGTTCTTAAACATCTTTTGG
158056	8695	CCCAAAAGATGTTTAAGAAC	167276	GTTCTTAAACATCTTTTGGG
158057	8696	ACCCAAAAGATGTTTAAGAA	167277	TTCTTAAACATCTTTTGGGT
158058	8697	TACCCAAAAGATGTTTAAGA	167278	TCTTAAACATCTTTTGGGTA
158059	8698	ATACCCAAAAGATGTTTAAG	167279	CTTAAACATCTTTTGGGTAT
158060	8699	AATACCCAAAAGATGTTTAA	167280	TTAAACATCTTTTGGGTATT
158061	8700	CAATACCCAAAAGATGTTTA	167281	TAAACATCTTTTGGGTATTG
158062	8701	ACAATACCCAAAAGATGTTT	167282	AAACATCTTTTGGGTATTGT
158063	8702	AACAATACCCAAAAGATGTT	167283	AACATCTTTTGGGTATTGTT
158064	8703	CAACAATACCCAAAAGATGT	167284	ACATCTTTTGGGTATTGTTG
158065	8704	CCAACAATACCCAAAAGATG	167285	CATCTTTTGGGTATTGTTGG
158066	8705	CCCAACAATACCCAAAAGAT	167286	ATCTTTTGGGTATTGTTGGG
158067	8706	TCCCAACAATACCCAAAAGA	167287	TCTTTTGGGTATTGTTGGGA
158068	8707	CTCCCAACAATACCCAAAAG	167288	CTTTTGGGTATTGTTGGGAG
158069	8708	CCTCCCAACAATACCCAAAA	167289	TTTTGGGTATTGTTGGGAGG
158070	8709	TCCTCCCAACAATACCCAAA	167290	TTTGGGTATTGTTGGGAGGA
158071	8710	CTCCTCCCAACAATACCCAA	167291	TTGGGTATTGTTGGGAGGAG

158072	8711	CCTCCTCCCAACAATACCCA	167292	TGGGTATTGTTGGGAGGAGG
158073	8712	ACCTCCTCCCAACAATACCC	167293	GGGTATTGTTGGGAGGAGGT
158074	8713	TACCTCCTCCCAACAATACC	167294	GGTATTGTTGGGAGGAGGTA
158075	8714	CTACCTCCTCCCAACAATAC	167295	GTATTGTTGGGAGGAGGTAG
158076	8715	ACTACCTCCTCCCAACAATA	167296	TATTGTTGGGAGGAGGTAGT
158077	8716	CACTACCTCCTCCCAACAAT	167297	ATTGTTGGGAGGAGGTAGTG
158078	8717	TCACTACCTCCTCCCAACAA	167298	TTGTTGGGAGGAGGTAGTGA
158079	8718	ATCACTACCTCCTCCCAACA	167299	TGTTGGGAGGAGGTAGTGAT
158080	8719	AATCACTACCTCCTCCCAAC	167300	GTTGGGAGGAGGTAGTGATT
158081	8720	TAATCACTACCTCCTCCCAA	167301	TTGGGAGGAGGTAGTGATTA
158082	8721	GTAATCACTACCTCCTCCCA	167302	TGGGAGGAGGTAGTGATTAC
158083	8722	AGTAATCACTACCTCCTCCC	167303	GGGAGGAGGTAGTGATTACT
158084	8723	AAGTAATCACTACCTCCTCC	167304	GGAGGAGGTAGTGATTACTT
158085	8724	CAAGTAATCACTACCTCCTC	167305	GAGGAGGTAGTGATTACTTG
158086	8725	TCAAGTAATCACTACCTCCT	167306	AGGAGGTAGTGATTACTTGA
158087	8726	GTCAAGTAATCACTACCTCC	167307	GGAGGTAGTGATTACTTGAC
158088	8727	TGTCAAGTAATCACTACCTC	167308	GAGGTAGTGATTACTTGACA
158089	8728	CTGTCAAGTAATCACTACCT	167309	AGGTAGTGATTACTTGACAG
158090	8729	GCTGTCAAGTAATCACTACC	167310	GGTAGTGATTACTTGACAGC
158091	8730	GGCTGTCAAGTAATCACTAC	167311	GTAGTGATTACTTGACAGCC
158092	8731	GGGCTGTCAAGTAATCACTA	167312	TAGTGATTACTTGACAGCCC
158093	8732	TGGGCTGTCAAGTAATCACT	167313	AGTGATTACTTGACAGCCCA
158094	8733	TTGGGCTGTCAAGTAATCAC	167314	GTGATTACTTGACAGCCCAA
158095	8734	TTTGGGCTGTCAAGTAATCA	167315	TGATTACTTGACAGCCCAAA
158096	8735	CTTTGGGCTGTCAAGTAATC	167316	GATTACTTGACAGCCCAAAG
158097	8736	ACTTTGGGCTGTCAAGTAAT	167317	ATTACTTGACAGCCCAAAGT
158098	8737	AACTTTGGGCTGTCAAGTAA	167318	TTACTTGACAGCCCAAAGTT
158099	8738	TAACTTTGGGCTGTCAAGTA	167319	TACTTGACAGCCCAAAGTTA
158100	8739	ATAACTTTGGGCTGTCAAGT	167320	ACTTGACAGCCCAAAGTTAT
158101	8740	GATAACTTTGGGCTGTCAAG	167321	CTTGACAGCCCAAAGTTATC
158102	8741	AGATAACTTTGGGCTGTCAA	167322	TTGACAGCCCAAAGTTATCT
158103	8742	AAGATAACTTTGGGCTGTCA	167323	TGACAGCCCAAAGTTATCTT
158104	8743	GAAGATAACTTTGGGCTGTC	167324	GACAGCCCAAAGTTATCTTC
158105	8744	AGAAGATAACTTTGGGCTGT	167325	ACAGCCCAAAGTTATCTTCT
158106	8745	AAGAAGATAACTTTGGGCTG	167326	CAGCCCAAAGTTATCTTCTT
158107	8746	TAAGAAGATAACTTTGGGCT	167327	AGCCCAAAGTTATCTTCTTA
158108	8747	TTAAGAAGATAACTTTGGGC	167328	GCCCAAAGTTATCTTCTTAA
158109	8748	TTTAAGAAGATAACTTTGGG	167329	CCCAAAGTTATCTTCTTAAA
158110	8749	TTTTAAGAAGATAACTTTGG	167330	CCAAAGTTATCTTCTTAAAA
158111	8750	ATTTTAAGAAGATAACTTTG	167331	CAAAGTTATCTTCTTAAAAT
158112	8751	AATTTTAAGAAGATAACTTT	167332	AAAGTTATCTTCTTAAAATT
158113	8752	AAATTTTAAGAAGATAACTT	167333	AAGTTATCTTCTTAAAATTT
158114	8753	AAAATTTTAAGAAGATAACT	167334	AGTTATCTTCTTAAAATTTT
158115	8754	AAAAATTTTAAGAAGATAAC	167335	GTTATCTTCTTAAAATTTTT
158116	8755	AAAAAATTTTAAGAAGATAA	167336	TTATCTTCTTAAAATTTTTT
158117	8756	TAAAAAATTTTAAGAAGATA	167337	TATCTTCTTAAAATTTTTTA
158118	8757	GTAAAAAATTTTAAGAAGAT	167338	ATCTTCTTAAAATTTTTTAC
158119	8758	TGTAAAAAATTTTAAGAAGA	167339	TCTTCTTAAAATTTTTTACA
158120	8759	CTGTAAAAAATTTTAAGAAG	167340	CTTCTTAAAATTTTTTACAG
158121	8760	CCTGTAAAAAATTTTAAGAA	167341	TTCTTAAAATTTTTTACAGG
158122	8761	ACCTGTAAAAAATTTTAAGA	167342	TCTTAAAATTTTTTACAGGT
158123	8762	GACCTGTAAAAAATTTTAAG	167343	CTTAAAATTTTTTACAGGTC
158124	8763	GGACCTGTAAAAAATTTTAA	167344	TTAAAATTTTTTACAGGTCC
158125	8764	TGGACCTGTAAAAAATTTTA	167345	TAAAATTTTTTACAGGTCCA
158126	8765	ATGGACCTGTAAAAAATTTT	167346	AAAATTTTTTACAGGTCCAT
158127	8766	CATGGACCTGTAAAAAATTT	167347	AAATTTTTTACAGGTCCATG
158128	8767	TCATGGACCTGTAAAAAATT	167348	AATTTTTTACAGGTCCATGA
158129	8768	TTCATGGACCTGTAAAAAAT	167349	ATTTTTTACAGGTCCATGAA
158130	8769	TTTCATGGACCTGTAAAAAA	167350	TTTTTTACAGGTCCATGAAA
158131	8770	TTTTCATGGACCTGTAAAAA	167351	TTTTTACAGGTCCATGAAAA
158132	8771	TTTTTCATGGACCTGTAAAA	167352	TTTTACAGGTCCATGAAAAA
158133	8772	CTTTTTCATGGACCTGTAAA	167353	TTTACAGGTCCATGAAAAAG
158134	8773	GCTTTTTCATGGACCTGTAA	167354	TTACAGGTCCATGAAAAAGC
158135	8774	TGCTTTTTCATGGACCTGTA	167355	TACAGGTCCATGAAAAAGCA
158136	8775	CTGCTTTTTCATGGACCTGT	167356	ACAGGTCCATGAAAAAGCAG
158137	8776	TCTGCTTTTTCATGGACCTG	167357	CAGGTCCATGAAAAAGCAGA
158138	8777	ATCTGCTTTTTCATGGACCT	167358	AGGTCCATGAAAAAGCAGAT
158139	8778	CATCTGCTTTTTCATGGACC	167359	GGTCCATGAAAAAGCAGATG
158140	8779	TCATCTGCTTTTTCATGGAC	167360	GTCCATGAAAAAGCAGATGA
158141	8780	GTCATCTGCTTTTTCATGGA	167361	TCCATGAAAAAGCAGATGAC
158142	8781	AGTCATCTGCTTTTTCATGG	167362	CCATGAAAAAGCAGATGACT
158143	8782	AAGTCATCTGCTTTTTCATG	167363	CATGAAAAAGCAGATGACTT

158144	8783	CAAGTCATCTGCTTTTTCAT	167364	ATGAAAAAGCAGATGACTTG
158145	8784	CCAAGTCATCTGCTTTTTCA	167365	TGAAAAAGCAGATGACTTGG
158146	8785	CCCAAGTCATCTGCTTTTTC	167366	GAAAAAGCAGATGACTTGGG
158147	8786	GCCCAAGTCATCTGCTTTTT	167367	AAAAAGCAGATGACTTGGGC
158148	8787	TGCCCAAGTCATCTGCTTTT	167368	AAAAGCAGATGACTTGGGCA
158149	8788	TTGCCCAAGTCATCTGCTTT	167369	AAAGCAGATGACTTGGGCAA
158150	8789	TTTGCCCAAGTCATCTGCTT	167370	AAGCAGATGACTTGGGCAAA
158151	8790	CTTTGCCCAAGTCATCTGCT	167371	AGCAGATGACTTGGGCAAAG
158152	8791	CCTTTGCCCAAGTCATCTGC	167372	GCAGATGACTTGGGCAAAGG
158153	8792	ACCTTTGCCCAAGTCATCTG	167373	CAGATGACTTGGGCAAAGGT
158154	8793	CACCTTTGCCCAAGTCATCT	167374	AGATGACTTGGGCAAAGGTG
158155	8794	CCACCTTTGCCCAAGTCATC	167375	GATGACTTGGGCAAAGGTGG
158156	8795	TCCACCTTTGCCCAAGTCAT	167376	ATGACTTGGGCAAAGGTGGA
158157	8796	TTCCACCTTTGCCCAAGTCA	167377	TGACTTGGGCAAAGGTGGAA
158158	8797	TTTCCACCTTTGCCCAAGTC	167378	GACTTGGGCAAAGGTGGAAA
158159	8798	ATTTCCACCTTTGCCCAAGT	167379	ACTTGGGCAAAGGTGGAAAT
158160	8799	CATTTCCACCTTTGCCCAAG	167380	CTTGGGCAAAGGTGGAAATG
158161	8800	TCATTTCCACCTTTGCCCAA	167381	TTGGGCAAAGGTGGAAATGA
158162	8801	TTCATTTCCACCTTTGCCCA	167382	TGGGCAAAGGTGGAAATGAA
158163	8802	CTTCATTTCCACCTTTGCCC	167383	GGGCAAAGGTGGAAATGAAG
158164	8803	TCTTCATTTCCACCTTTGCC	167384	GGCAAAGGTGGAAATGAAGA
158165	8804	TTCTTCATTTCCACCTTTGC	167385	GCAAAGGTGGAAATGAAGAA
158166	8805	TTTCTTCATTTCCACCTTTG	167386	CAAAGGTGGAAATGAAGAAA
158167	8806	CTTTCTTCATTTCCACCTTT	167387	AAAGGTGGAAATGAAGAAAG
158168	8807	ACTTTCTTCATTTCCACCTT	167388	AAGGTGGAAATGAAGAAAGT
158169	8808	TACTTTCTTCATTTCCACCT	167389	AGGTGGAAATGAAGAAAGTA
158170	8809	GTACTTTCTTCATTTCCACC	167390	GGTGGAAATGAAGAAAGTAC
158171	8810	TGTACTTTCTTCATTTCCAC	167391	GTGGAAATGAAGAAAGTACA
158172	8811	TTGTACTTTCTTCATTTCCA	167392	TGGAAATGAAGAAAGTACAA
158173	8812	TTTGTACTTTCTTCATTTCC	167393	GGAAATGAAGAAAGTACAAA
158174	8813	CTTTGTACTTTCTTCATTTC	167394	GAAATGAAGAAAGTACAAAG
158175	8814	TCTTTGTACTTTCTTCATTT	167395	AAATGAAGAAAGTACAAAGA
158176	8815	GTCTTTGTACTTTCTTCATT	167396	AATGAAGAAAGTACAAAGAC
158177	8816	TGTCTTTGTACTTTCTTCAT	167397	ATGAAGAAAGTACAAAGACA
158178	8817	CTGTCTTTGTACTTTCTTCA	167398	TGAAGAAAGTACAAAGACAG
158179	8818	CCTGTCTTTGTACTTTCTTC	167399	GAAGAAAGTACAAAGACAGG
158180	8819	TCCTGTCTTTGTACTTTCTT	167400	AAGAAAGTACAAAGACAGGA
158181	8820	TTCCTGTCTTTGTACTTTCT	167401	AGAAAGTACAAAGACAGGAA
158182	8821	TTTCCTGTCTTTGTACTTTC	167402	GAAAGTACAAAGACAGGAAA
158183	8822	GTTTCCTGTCTTTGTACTTT	167403	AAAGTACAAAGACAGGAAAC
158184	8823	CGTTTCCTGTCTTTGTACTT	167404	AAGTACAAAGACAGGAAACG
158185	8824	GCGTTTCCTGTCTTTGTACT	167405	AGTACAAAGACAGGAAACGC
158186	8825	AGCGTTTCCTGTCTTTGTAC	167406	GTACAAAGACAGGAAACGCT
158187	8826	CAGCGTTTCCTGTCTTTGTA	167407	TACAAAGACAGGAAACGCTG
158188	8827	CCAGCGTTTCCTGTCTTTGT	167408	ACAAAGACAGGAAACGCTGG
158189	8828	TCCAGCGTTTCCTGTCTTTG	167409	CAAAGACAGGAAACGCTGGA
158190	8829	TTCCAGCGTTTCCTGTCTTT	167410	AAAGACAGGAAACGCTGGAA
158191	8830	CTTCCAGCGTTTCCTGTCTT	167411	AAGACAGGAAACGCTGGAAG
158192	8831	ACTTCCAGCGTTTCCTGTCT	167412	AGACAGGAAACGCTGGAAGT
158193	8832	GACTTCCAGCGTTTCCTGTC	167413	GACAGGAAACGCTGGAAGTC
158194	8833	CGACTTCCAGCGTTTCCTGT	167414	ACAGGAAACGCTGGAAGTCG
158195	8834	ACGACTTCCAGCGTTTCCTG	167415	CAGGAAACGCTGGAAGTCGT
158196	8835	AACGACTTCCAGCGTTTCCT	167416	AGGAAACGCTGGAAGTCGTT
158197	8836	AAACGACTTCCAGCGTTTCC	167417	GGAAACGCTGGAAGTCGTTT
158198	8837	CAAACGACTTCCAGCGTTTC	167418	GAAACGCTGGAAGTCGTTTG
158199	8838	CCAAACGACTTCCAGCGTTT	167419	AAACGCTGGAAGTCGTTTGG
158200	8839	GCCAAACGACTTCCAGCGTT	167420	AACGCTGGAAGTCGTTTGGC
158201	8840	AGCCAAACGACTTCCAGCGT	167421	ACGCTGGAAGTCGTTTGGCT
158202	8841	AAGCCAAACGACTTCCAGCG	167422	CGCTGGAAGTCGTTTGGCTT
158203	8842	CAAGCCAAACGACTTCCAGC	167423	GCTGGAAGTCGTTTGGCTTG
158204	8843	ACAAGCCAAACGACTTCCAG	167424	CTGGAAGTCGTTTGGCTTGT
158205	8844	CACAAGCCAAACGACTTCCA	167425	TGGAAGTCGTTTGGCTTGTG
158206	8845	CCACAAGCCAAACGACTTCC	167426	GGAAGTCGTTTGGCTTGTGG
158207	8846	ACCACAAGCCAAACGACTTC	167427	GAAGTCGTTTGGCTTGTGGT
158208	8847	CACCACAAGCCAAACGACTT	167428	AAGTCGTTTGGCTTGTGGTG
158209	8848	ACACCACAAGCCAAACGACT	167429	AGTCGTTTGGCTTGTGGTGT
158210	8849	TACACCACAAGCCAAACGAC	167430	GTCGTTTGGCTTGTGGTGTA
158211	8850	TTACACCACAAGCCAAACGA	167431	TCGTTTGGCTTGTGGTGTAA
158212	8851	ATTACACCACAAGCCAAACG	167432	CGTTTGGCTTGTGGTGTAAT
158213	8852	AATTACACCACAAGCCAAAC	167433	GTTTGGCTTGTGGTGTAATT
158214	8853	CAATTACACCACAAGCCAAA	167434	TTTGGCTTGTGGTGTAATTG
158215	8854	CCAATTACACCACAAGCCAA	167435	TTGGCTTGTGGTGTAATTGG

158216	8855	CCCAATTACACCACAAGCCA	167436	TGGCTTGTGGTGTAATTGGG
158217	8856	TCCCAATTACACCACAAGCC	167437	GGCTTGTGGTGTAATTGGGA
158218	8857	ATCCCAATTACACCACAAGC	167438	GCTTGTGGTGTAATTGGGAT
158219	8858	GATCCCAATTACACCACAAG	167439	CTTGTGGTGTAATTGGGATC
158220	8859	CGATCCCAATTACACCACAA	167440	TTGTGGTGTAATTGGGATCG
158221	8860	GCGATCCCAATTACACCACA	167441	TGTGGTGTAATTGGGATCGC
158222	8861	GGCGATCCCAATTACACCAC	167442	GTGGTGTAATTGGGATCGCC
158223	8862	GGGCGATCCCAATTACACCA	167443	TGGTGTAATTGGGATCGCCC
158224	8863	TGGGCGATCCCAATTACACC	167444	GGTGTAATTGGGATCGCCCA
158225	8864	TTGGGCGATCCCAATTACAC	167445	GTGTAATTGGGATCGCCCAA
158226	8865	ATTGGGCGATCCCAATTACA	167446	TGTAATTGGGATCGCCCAAT
158227	8866	TATTGGGCGATCCCAATTAC	167447	GTAATTGGGATCGCCCAATA
158228	8867	TTATTGGGCGATCCCAATTA	167448	TAATTGGGATCGCCCAATAA
158229	8868	TTTATTGGGCGATCCCAATT	167449	AATTGGGATCGCCCAATAAA
158230	8869	GTTTATTGGGCGATCCCAAT	167450	ATTGGGATCGCCCAATAAAC
158231	8870	TGTTTATTGGGCGATCCCAA	167451	TTGGGATCGCCCAATAAACA
158232	8871	ATGTTTATTGGGCGATCCCA	167452	TGGGATCGCCCAATAAACAT
158233	8872	AATGTTTATTGGGCGATCCC	167453	GGGATCGCCCAATAAACATT
158234	8873	GAATGTTTATTGGGCGATCC	167454	GGATCGCCCAATAAACATTC
158235	8874	GGAATGTTTATTGGGCGATC	167455	GATCGCCCAATAAACATTCC
158236	8875	GGGAATGTTTATTGGGCGAT	167456	ATCGCCCAATAAACATTCCC
158237	8876	AGGGAATGTTTATTGGGCGA	167457	TCGCCCAATAAACATTCCCT
158238	8877	AAGGGAATGTTTATTGGGCG	167458	CGCCCAATAAACATTCCCTT
158239	8878	CAAGGGAATGTTTATTGGGC	167459	GCCCAATAAACATTCCCTTG
158240	8879	CCAAGGGAATGTTTATTGGG	167460	CCCAATAAACATTCCCTTGG
158241	8880	TCCAAGGGAATGTTTATTGG	167461	CCAATAAACATTCCCTTGGA
158242	8881	ATCCAAGGGAATGTTTATTG	167462	CAATAAACATTCCCTTGGAT
158243	8882	CATCCAAGGGAATGTTTATT	167463	AATAAACATTCCCTTGGATG
158244	8883	ACATCCAAGGGAATGTTTAT	167464	ATAAACATTCCCTTGGATGT
158245	8884	TACATCCAAGGGAATGTTTA	167465	TAAACATTCCCTTGGATGTA
158246	8885	CTACATCCAAGGGAATGTTT	167466	AAACATTCCCTTGGATGTAG
158247	8886	ACTACATCCAAGGGAATGTT	167467	AACATTCCCTTGGATGTAGT
158248	8887	GACTACATCCAAGGGAATGT	167468	ACATTCCCTTGGATGTAGTC
158249	8888	AGACTACATCCAAGGGAATG	167469	CATTCCCTTGGATGTAGTCT
158250	8889	CAGACTACATCCAAGGGAAT	167470	ATTCCCTTGGATGTAGTCTG
158251	8890	TCAGACTACATCCAAGGGAA	167471	TTCCCTTGGATGTAGTCTGA
158252	8891	CTCAGACTACATCCAAGGGA	167472	TCCCTTGGATGTAGTCTGAG
158253	8892	CCTCAGACTACATCCAAGGG	167473	CCCTTGGATGTAGTCTGAGG
158254	8893	GCCTCAGACTACATCCAAGG	167474	CCTTGGATGTAGTCTGAGGC
158255	8894	GGCCTCAGACTACATCCAAG	167475	CTTGGATGTAGTCTGAGGCC
158256	8895	GGGCCTCAGACTACATCCAA	167476	TTGGATGTAGTCTGAGGCCC
158257	8896	GGGGCCTCAGACTACATCCA	167477	TGGATGTAGTCTGAGGCCCC
158258	8897	AGGGGCCTCAGACTACATCC	167478	GGATGTAGTCTGAGGCCCCT
158259	8898	AAGGGGCCTCAGACTACATC	167479	GATGTAGTCTGAGGCCCCTT
158260	8899	TAAGGGGCCTCAGACTACAT	167480	ATGTAGTCTGAGGCCCCTTA
158261	8900	TTAAGGGGCCTCAGACTACA	167481	TGTAGTCTGAGGCCCCTTAA
158262	8901	GTTAAGGGGCCTCAGACTAC	167482	GTAGTCTGAGGCCCCTTAAC
158263	8902	AGTTAAGGGGCCTCAGACTA	167483	TAGTCTGAGGCCCCTTAACT
158264	8903	GAGTTAAGGGGCCTCAGACT	167484	AGTCTGAGGCCCCTTAACTC
158265	8904	TGAGTTAAGGGGCCTCAGAC	167485	GTCTGAGGCCCCTTAACTCA
158266	8905	ATGAGTTAAGGGGCCTCAGA	167486	TCTGAGGCCCCTTAACTCAT
158267	8906	GATGAGTTAAGGGGCCTCAG	167487	CTGAGGCCCCTTAACTCATC
158268	8907	AGATGAGTTAAGGGGCCTCA	167488	TGAGGCCCCTTAACTCATCT
158269	8908	CAGATGAGTTAAGGGGCCTC	167489	GAGGCCCCTTAACTCATCTG
158270	8909	ACAGATGAGTTAAGGGGCCT	167490	AGGCCCCTTAACTCATCTGT
158271	8910	AACAGATGAGTTAAGGGGCC	167491	GGCCCCTTAACTCATCTGTT
158272	8911	TAACAGATGAGTTAAGGGGC	167492	GCCCCTTAACTCATCTGTTA
158273	8912	ATAACAGATGAGTTAAGGGG	167493	CCCCTTAACTCATCTGTTAT
158274	8913	GATAACAGATGAGTTAAGGG	167494	CCCTTAACTCATCTGTTATC
158275	8914	GGATAACAGATGAGTTAAGG	167495	CCTTAACTCATCTGTTATCC
158276	8915	AGGATAACAGATGAGTTAAG	167496	CTTAACTCATCTGTTATCCT
158277	8916	CAGGATAACAGATGAGTTAA	167497	TTAACTCATCTGTTATCCTG
158278	8917	GCAGGATAACAGATGAGTTA	167498	TAACTCATCTGTTATCCTGC
158279	8918	AGCAGGATAACAGATGAGTT	167499	AACTCATCTGTTATCCTGCT
158280	8919	TAGCAGGATAACAGATGAGT	167500	ACTCATCTGTTATCCTGCTA
158281	8920	CTAGCAGGATAACAGATGAG	167501	CTCATCTGTTATCCTGCTAG
158282	8921	GCTAGCAGGATAACAGATGA	167502	TCATCTGTTATCCTGCTAGC
158283	8922	AGCTAGCAGGATAACAGATG	167503	CATCTGTTATCCTGCTAGCT
158284	8923	CAGCTAGCAGGATAACAGAT	167504	ATCTGTTATCCTGCTAGCTG
158285	8924	ACAGCTAGCAGGATAACAGA	167505	TCTGTTATCCTGCTAGCTGT
158286	8925	TACAGCTAGCAGGATAACAG	167506	CTGTTATCCTGCTAGCTGTA
158287	8926	CTACAGCTAGCAGGATAACA	167507	TGTTATCCTGCTAGCTGTAG

158288	8927	TCTACAGCTAGCAGGATAAC	167508	GTTATCCTGCTAGCTGTAGA
158289	8928	TTCTACAGCTAGCAGGATAA	167509	TTATCCTGCTAGCTGTAGAA
158290	8929	TTTCTACAGCTAGCAGGATA	167510	TATCCTGCTAGCTGTAGAAA
158291	8930	ATTTCTACAGCTAGCAGGAT	167511	ATCCTGCTAGCTGTAGAAAT
158292	8931	CATTTCTACAGCTAGCAGGA	167512	TCCTGCTAGCTGTAGAAATG
158293	8932	ACATTTCTACAGCTAGCAGG	167513	CCTGCTAGCTGTAGAAATGT
158294	8933	TACATTTCTACAGCTAGCAG	167514	CTGCTAGCTGTAGAAATGTA
158295	8934	ATACATTTCTACAGCTAGCA	167515	TGCTAGCTGTAGAAATGTAT
158296	8935	GATACATTTCTACAGCTAGC	167516	GCTAGCTGTAGAAATGTATC
158297	8936	GGATACATTTCTACAGCTAG	167517	CTAGCTGTAGAAATGTATCC
158298	8937	AGGATACATTTCTACAGCTA	167518	TAGCTGTAGAAATGTATCCT
158299	8938	CAGGATACATTTCTACAGCT	167519	AGCTGTAGAAATGTATCCTG
158300	8939	TCAGGATACATTTCTACAGC	167520	GCTGTAGAAATGTATCCTGA
158301	8940	ATCAGGATACATTTCTACAG	167521	CTGTAGAAATGTATCCTGAT
158302	8941	TATCAGGATACATTTCTACA	167522	TGTAGAAATGTATCCTGATA
158303	8942	TTATCAGGATACATTTCTAC	167523	GTAGAAATGTATCCTGATAA
158304	8943	TTTATCAGGATACATTTCTA	167524	TAGAAATGTATCCTGATAAA
158305	8944	GTTTATCAGGATACATTTCT	167525	AGAAATGTATCCTGATAAAC
158306	8945	TGTTTATCAGGATACATTTC	167526	GAAATGTATCCTGATAAACA
158307	8946	ATGTTTATCAGGATACATTT	167527	AAATGTATCCTGATAAACAT
158308	8947	AATGTTTATCAGGATACATT	167528	AATGTATCCTGATAAACATT
158309	8948	TAATGTTTATCAGGATACAT	167529	ATGTATCCTGATAAACATTA
158310	8949	TTAATGTTTATCAGGATACA	167530	TGTATCCTGATAAACATTAA
158311	8950	TTTAATGTTTATCAGGATAC	167531	GTATCCTGATAAACATTAAA
158312	8951	GTTTAATGTTTATCAGGATA	167532	TATCCTGATAAACATTAAAC
158313	8952	TGTTTAATGTTTATCAGGAT	167533	ATCCTGATAAACATTAAACA
158314	8953	GTGTTTAATGTTTATCAGGA	167534	TCCTGATAAACATTAAACAC
158315	8954	AGTGTTTAATGTTTATCAGG	167535	CCTGATAAACATTAAACACT
158316	8955	CAGTGTTTAATGTTTATCAG	167536	CTGATAAACATTAAACACTG
158317	8956	ACAGTGTTTAATGTTTATCA	167537	TGATAAACATTAAACACTGT
158318	8957	TACAGTGTTTAATGTTTATC	167538	GATAAACATTAAACACTGTA
158319	8958	TTACAGTGTTTAATGTTTAT	167539	ATAAACATTAAACACTGTAA
158320	8959	ATTACAGTGTTTAATGTTTA	167540	TAAACATTAAACACTGTAAT
158321	8960	GATTACAGTGTTTAATGTTT	167541	AAACATTAAACACTGTAATC
158322	8961	AGATTACAGTGTTTAATGTT	167542	AACATTAAACACTGTAATCT
158323	8962	AAGATTACAGTGTTTAATGT	167543	ACATTAAACACTGTAATCTT
158324	8963	TAAGATTACAGTGTTTAATG	167544	CATTAAACACTGTAATCTTA
158325	8964	TTAAGATTACAGTGTTTAAT	167545	ATTAAACACTGTAATCTTAA
158326	8965	TTTAAGATTACAGTGTTTAA	167546	TTAAACACTGTAATCTTAAA
158327	8966	TTTTAAGATTACAGTGTTTA	167547	TAAACACTGTAATCTTAAAA
158328	8967	CTTTTAAGATTACAGTGTTT	167548	AAACACTGTAATCTTAAAAG
158329	8968	ACTTTTAAGATTACAGTGTT	167549	AACACTGTAATCTTAAAAGT
158330	8969	CACTTTTAAGATTACAGTGT	167550	ACACTGTAATCTTAAAAGTG
158331	8970	ACACTTTTAAGATTACAGTG	167551	CACTGTAATCTTAAAAGTGT
158332	8971	TACACTTTTAAGATTACAGT	167552	ACTGTAATCTTAAAAGTGTA
158333	8972	TTACACTTTTAAGATTACAG	167553	CTGTAATCTTAAAAGTGTAA
158334	8973	ATTACACTTTTAAGATTACA	167554	TGTAATCTTAAAAGTGTAAT
158335	8974	AATTACACTTTTAAGATTAC	167555	GTAATCTTAAAAGTGTAATT
158336	8975	CAATTACACTTTTAAGATTA	167556	TAATCTTAAAAGTGTAATTG
158337	8976	ACAATTACACTTTTAAGATT	167557	AATCTTAAAAGTGTAATTGT
158338	8977	CACAATTACACTTTTAAGAT	167558	ATCTTAAAAGTGTAATTGTG
158339	8978	ACACAATTACACTTTTAAGA	167559	TCTTAAAAGTGTAATTGTGT
158340	8979	CACACAATTACACTTTTAAG	167560	CTTAAAAGTGTAATTGTGTG
158341	8980	TCACACAATTACACTTTTAA	167561	TTAAAAGTGTAATTGTGTGA
158342	8981	GTCACACAATTACACTTTTA	167562	TAAAAGTGTAATTGTGTGAC
158343	8982	AGTCACACAATTACACTTTT	167563	AAAAGTGTAATTGTGTGACT
158344	8983	AAGTCACACAATTACACTTT	167564	AAAGTGTAATTGTGTGACTT
158345	8984	AAAGTCACACAATTACACTT	167565	AAGTGTAATTGTGTGACTTT
158346	8985	AAAAGTCACACAATTACACT	167566	AGTGTAATTGTGTGACTTTT
158347	8986	AAAAAGTCACACAATTACAC	167567	GTGTAATTGTGTGACTTTTT
158348	8987	GAAAAAGTCACACAATTACA	167568	TGTAATTGTGTGACTTTTTC
158349	8988	TGAAAAAGTCACACAATTAC	167569	GTAATTGTGTGACTTTTTCA
158350	8989	CTGAAAAAGTCACACAATTA	167570	TAATTGTGTGACTTTTTCAG
158351	8990	TCTGAAAAAGTCACACAATT	167571	AATTGTGTGACTTTTTCAGA
158352	8991	CTCTGAAAAAGTCACACAAT	167572	ATTGTGTGACTTTTTCAGAG
158353	8992	ACTCTGAAAAAGTCACACAA	167573	TTGTGTGACTTTTTCAGAGT
158354	8993	AACTCTGAAAAAGTCACACA	167574	TGTGTGACTTTTTCAGAGTT
158355	8994	CAACTCTGAAAAAGTCACAC	167575	GTGTGACTTTTTCAGAGTTG
158356	8995	GCAACTCTGAAAAAGTCACA	167576	TGTGACTTTTTCAGAGTTGC
158357	8996	AGCAACTCTGAAAAAGTCAC	167577	GTGACTTTTTCAGAGTTGCT
158358	8997	AAGCAACTCTGAAAAAGTCA	167578	TGACTTTTTCAGAGTTGCTT
158359	8998	AAAGCAACTCTGAAAAAGTC	167579	GACTTTTTCAGAGTTGCTTT

158360	8999	TAAAGCAACTCTGAAAAAGT	167580	ACTTTTTCAGAGTTGCTTTA
158361	9000	TTAAAGCAACTCTGAAAAAG	167581	CTTTTTCAGAGTTGCTTTAA
158362	9001	TTTAAAGCAACTCTGAAAAA	167582	TTTTTCAGAGTTGCTTTAAA
158363	9002	CTTTAAAGCAACTCTGAAAA	167583	TTTTCAGAGTTGCTTTAAAG
158364	9003	ACTTTAAAGCAACTCTGAAA	167584	TTTCAGAGTTGCTTTAAAGT
158365	9004	TACTTTAAAGCAACTCTGAA	167585	TTCAGAGTTGCTTTAAAGTA
158366	9005	GTACTTTAAAGCAACTCTGA	167586	TCAGAGTTGCTTTAAAGTAC
158367	9006	GGTACTTTAAAGCAACTCTG	167587	CAGAGTTGCTTTAAAGTACC
158368	9007	AGGTACTTTAAAGCAACTCT	167588	AGAGTTGCTTTAAAGTACCT
158369	9008	CAGGTACTTTAAAGCAACTC	167589	GAGTTGCTTTAAAGTACCTG
158370	9009	ACAGGTACTTTAAAGCAACT	167590	AGTTGCTTTAAAGTACCTGT
158371	9010	TACAGGTACTTTAAAGCAAC	167591	GTTGCTTTAAAGTACCTGTA
158372	9011	CTACAGGTACTTTAAAGCAA	167592	TTGCTTTAAAGTACCTGTAG
158373	9012	ACTACAGGTACTTTAAAGCA	167593	TGCTTTAAAGTACCTGTAGT
158374	9013	CACTACAGGTACTTTAAAGC	167594	GCTTTAAAGTACCTGTAGTG
158375	9014	TCACTACAGGTACTTTAAAG	167595	CTTTAAAGTACCTGTAGTGA
158376	9015	CTCACTACAGGTACTTTAAA	167596	TTTAAAGTACCTGTAGTGAG
158377	9016	TCTCACTACAGGTACTTTAA	167597	TTAAAGTACCTGTAGTGAGA
158378	9017	TTCTCACTACAGGTACTTTA	167598	TAAAGTACCTGTAGTGAGAA
158379	9018	TTTCTCACTACAGGTACTTT	167599	AAAGTACCTGTAGTGAGAAA
158380	9019	GTTTCTCACTACAGGTACTT	167600	AAGTACCTGTAGTGAGAAAC
158381	9020	AGTTTCTCACTACAGGTACT	167601	AGTACCTGTAGTGAGAAACT
158382	9021	CAGTTTCTCACTACAGGTAC	167602	GTACCTGTAGTGAGAAACTG
158383	9022	TCAGTTTCTCACTACAGGTA	167603	TACCTGTAGTGAGAAACTGA
158384	9023	ATCAGTTTCTCACTACAGGT	167604	ACCTGTAGTGAGAAACTGAT
158385	9024	AATCAGTTTCTCACTACAGG	167605	CCTGTAGTGAGAAACTGATT
158386	9025	AAATCAGTTTCTCACTACAG	167606	CTGTAGTGAGAAACTGATTT
158387	9026	TAAATCAGTTTCTCACTACA	167607	TGTAGTGAGAAACTGATTTA
158388	9027	ATAAATCAGTTTCTCACTAC	167608	GTAGTGAGAAACTGATTTAT
158389	9028	CATAAATCAGTTTCTCACTA	167609	TAGTGAGAAACTGATTTATG
158390	9029	TCATAAATCAGTTTCTCACT	167610	AGTGAGAAACTGATTTATGA
158391	9030	ATCATAAATCAGTTTCTCAC	167611	GTGAGAAACTGATTTATGAT
158392	9031	GATCATAAATCAGTTTCTCA	167612	TGAGAAACTGATTTATGATC
158393	9032	TGATCATAAATCAGTTTCTC	167613	GAGAAACTGATTTATGATCA
158394	9033	GTGATCATAAATCAGTTTCT	167614	AGAAACTGATTTATGATCAC
158395	9034	AGTGATCATAAATCAGTTTC	167615	GAAACTGATTTATGATCACT
158396	9035	AAGTGATCATAAATCAGTTT	167616	AAACTGATTTATGATCACTT
158397	9036	CAAGTGATCATAAATCAGTT	167617	AACTGATTTATGATCACTTG
158398	9037	CCAAGTGATCATAAATCAGT	167618	ACTGATTTATGATCACTTGG
158399	9038	TCCAAGTGATCATAAATCAG	167619	CTGATTTATGATCACTTGGA
158400	9039	TTCCAAGTGATCATAAATCA	167620	TGATTTATGATCACTTGGAA
158401	9040	CTTCCAAGTGATCATAAATC	167621	GATTTATGATCACTTGGAAG
158402	9041	TCTTCCAAGTGATCATAAAT	167622	ATTTATGATCACTTGGAAGA
158403	9042	ATCTTCCAAGTGATCATAAA	167623	TTTATGATCACTTGGAAGAT
158404	9043	AATCTTCCAAGTGATCATAA	167624	TTATGATCACTTGGAAGATT
158405	9044	AAATCTTCCAAGTGATCATA	167625	TATGATCACTTGGAAGATTT
158406	9045	CAAATCTTCCAAGTGATCAT	167626	ATGATCACTTGGAAGATTTG
158407	9046	ACAAATCTTCCAAGTGATCA	167627	TGATCACTTGGAAGATTTGT
158408	9047	TACAAATCTTCCAAGTGATC	167628	GATCACTTGGAAGATTTGTA
158409	9048	ATACAAATCTTCCAAGTGAT	167629	ATCACTTGGAAGATTTGTAT
158410	9049	TATACAAATCTTCCAAGTGA	167630	TCACTTGGAAGATTTGTATA
158411	9050	CTATACAAATCTTCCAAGTG	167631	CACTTGGAAGATTTGTATAG
158412	9051	ACTATACAAATCTTCCAAGT	167632	ACTTGGAAGATTTGTATAGT
158413	9052	AACTATACAAATCTTCCAAG	167633	CTTGGAAGATTTGTATAGTT
158414	9053	AAACTATACAAATCTTCCAA	167634	TTGGAAGATTTGTATAGTTT
158415	9054	AAAACTATACAAATCTTCCA	167635	TGGAAGATTTGTATAGTTTT
158416	9055	TAAAACTATACAAATCTTCC	167636	GGAAGATTTGTATAGTTTTA
158417	9056	ATAAAACTATACAAATCTTC	167637	GAAGATTTGTATAGTTTTAT
158418	9057	TATAAAACTATACAAATCTT	167638	AAGATTTGTATAGTTTTATA
158419	9058	TTATAAAACTATACAAATCT	167639	AGATTTGTATAGTTTTATAA
158420	9059	TTTATAAAACTATACAAATC	167640	GATTTGTATAGTTTTATAAA
158421	9060	TTTTATAAAACTATACAAAT	167641	ATTTGTATAGTTTTATAAAA
158422	9061	GTTTTATAAAACTATACAAA	167642	TTTGTATAGTTTTATAAAAC
158423	9062	AGTTTTATAAAACTATACAA	167643	TTGTATAGTTTTATAAAACT
158424	9063	GAGTTTTATAAAACTATACA	167644	TGTATAGTTTTATAAAACTC
158425	9064	TGAGTTTTATAAAACTATAC	167645	GTATAGTTTTATAAAACTCA
158426	9065	CTGAGTTTTATAAAACTATA	167646	TATAGTTTTATAAAACTCAG
158427	9066	ACTGAGTTTTATAAAACTAT	167647	ATAGTTTTATAAAACTCAGT
158428	9067	AACTGAGTTTTATAAAACTA	167648	TAGTTTTATAAAACTCAGTT
158429	9068	TAACTGAGTTTTATAAAACT	167649	AGTTTTATAAAACTCAGTTA
158430	9069	TTAACTGAGTTTTATAAAAC	167650	GTTTTATAAAACTCAGTTAA
158431	9070	TTTAACTGAGTTTTATAAAA	167651	TTTTATAAAACTCAGTTAAA

158432	9071	TTTTAACTGAGTTTTATAAA	167652	TTTATAAAACTCAGTTAAAA
158433	9072	ATTTTAACTGAGTTTTATAA	167653	TTATAAAACTCAGTTAAAAT
158434	9073	CATTTTAACTGAGTTTTATA	167654	TATAAAACTCAGTTAAAATG
158435	9074	ACATTTTAACTGAGTTTTAT	167655	ATAAAACTCAGTTAAAATGT
158436	9075	GACATTTTAACTGAGTTTTA	167656	TAAAACTCAGTTAAAATGTC
158437	9076	AGACATTTTAACTGAGTTTT	167657	AAAACTCAGTTAAAATGTCT
158438	9077	CAGACATTTTAACTGAGTTT	167658	AAACTCAGTTAAAATGTCTG
158439	9078	ACAGACATTTTAACTGAGTT	167659	AACTCAGTTAAAATGTCTGT
158440	9079	AACAGACATTTTAACTGAGT	167660	ACTCAGTTAAAATGTCTGTT
158441	9080	AAACAGACATTTTAACTGAG	167661	CTCAGTTAAAATGTCTGTTT
158442	9081	GAAACAGACATTTTAACTGA	167662	TCAGTTAAAATGTCTGTTTC
158443	9082	TGAAACAGACATTTTAACTG	167663	CAGTTAAAATGTCTGTTTCA
158444	9083	TTGAAACAGACATTTTAACT	167664	AGTTAAAATGTCTGTTTCAA
158445	9084	ATTGAAACAGACATTTTAAC	167665	GTTAAAATGTCTGTTTCAAT
158446	9085	CATTGAAACAGACATTTTAA	167666	TTAAAATGTCTGTTTCAATG
158447	9086	TCATTGAAACAGACATTTTA	167667	TAAAATGTCTGTTTCAATGA
158448	9087	GTCATTGAAACAGACATTTT	167668	AAAATGTCTGTTTCAATGAC
158449	9088	GGTCATTGAAACAGACATTT	167669	AAATGTCTGTTTCAATGACC
158450	9089	AGGTCATTGAAACAGACATT	167670	AATGTCTGTTTCAATGACCT
158451	9090	CAGGTCATTGAAACAGACAT	167671	ATGTCTGTTTCAATGACCTG
158452	9091	ACAGGTCATTGAAACAGACA	167672	TGTCTGTTTCAATGACCTGT
158453	9092	TACAGGTCATTGAAACAGAC	167673	GTCTGTTTCAATGACCTGTA
158454	9093	ATACAGGTCATTGAAACAGA	167674	TCTGTTTCAATGACCTGTAT
158455	9094	AATACAGGTCATTGAAACAG	167675	CTGTTTCAATGACCTGTATT
158456	9095	AAATACAGGTCATTGAAACA	167676	TGTTTCAATGACCTGTATTT
158457	9096	AAAATACAGGTCATTGAAAC	167677	GTTTCAATGACCTGTATTTT
158458	9097	CAAAATACAGGTCATTGAAA	167678	TTTCAATGACCTGTATTTTG
158459	9098	GCAAAATACAGGTCATTGAA	167679	TTCAATGACCTGTATTTTGC
158460	9099	GGCAAAATACAGGTCATTGA	167680	TCAATGACCTGTATTTTGCC
158461	9100	TGGCAAAATACAGGTCATTG	167681	CAATGACCTGTATTTTGCCA
158462	9101	CTGGCAAAATACAGGTCATT	167682	AATGACCTGTATTTTGCCAG
158463	9102	TCTGGCAAAATACAGGTCAT	167683	ATGACCTGTATTTTGCCAGA
158464	9103	GTCTGGCAAAATACAGGTCA	167684	TGACCTGTATTTTGCCAGAC
158465	9104	AGTCTGGCAAAATACAGGTC	167685	GACCTGTATTTTGCCAGACT
158466	9105	AAGTCTGGCAAAATACAGGT	167686	ACCTGTATTTTGCCAGACTT
158467	9106	TAAGTCTGGCAAAATACAGG	167687	CCTGTATTTTGCCAGACTTA
158468	9107	TTAAGTCTGGCAAAATACAG	167688	CTGTATTTTGCCAGACTTAA
158469	9108	TTTAAGTCTGGCAAAATACA	167689	TGTATTTTGCCAGACTTAAA
158470	9109	ATTTAAGTCTGGCAAAATAC	167690	GTATTTTGCCAGACTTAAAT
158471	9110	GATTTAAGTCTGGCAAAATA	167691	TATTTTGCCAGACTTAAATC
158472	9111	TGATTTAAGTCTGGCAAAAT	167692	ATTTTGCCAGACTTAAATCA
158473	9112	GTGATTTAAGTCTGGCAAAA	167693	TTTTGCCAGACTTAAATCAC
158474	9113	TGTGATTTAAGTCTGGCAAA	167694	TTTGCCAGACTTAAATCACA
158475	9114	CTGTGATTTAAGTCTGGCAA	167695	TTGCCAGACTTAAATCACAG
158476	9115	TCTGTGATTTAAGTCTGGCA	167696	TGCCAGACTTAAATCACAGA
158477	9116	ATCTGTGATTTAAGTCTGGC	167697	GCCAGACTTAAATCACAGAT
158478	9117	CATCTGTGATTTAAGTCTGG	167698	CCAGACTTAAATCACAGATG
158479	9118	CCATCTGTGATTTAAGTCTG	167699	CAGACTTAAATCACAGATGG
158480	9119	CCCATCTGTGATTTAAGTCT	167700	AGACTTAAATCACAGATGGG
158481	9120	ACCCATCTGTGATTTAAGTC	167701	GACTTAAATCACAGATGGGT
158482	9121	TACCCATCTGTGATTTAAGT	167702	ACTTAAATCACAGATGGGTA
158483	9122	ATACCCATCTGTGATTTAAG	167703	CTTAAATCACAGATGGGTAT
158484	9123	AATACCCATCTGTGATTTAA	167704	TTAAATCACAGATGGGTATT
158485	9124	TAATACCCATCTGTGATTTA	167705	TAAATCACAGATGGGTATTA
158486	9125	TTAATACCCATCTGTGATTT	167706	AAATCACAGATGGGTATTAA
158487	9126	TTTAATACCCATCTGTGATT	167707	AATCACAGATGGGTATTAAA
158488	9127	GTTTAATACCCATCTGTGAT	167708	ATCACAGATGGGTATTAAAC
158489	9128	AGTTTAATACCCATCTGTGA	167709	TCACAGATGGGTATTAAACT
158490	9129	AAGTTTAATACCCATCTGTG	167710	CACAGATGGGTATTAAACTT
158491	9130	CAAGTTTAATACCCATCTGT	167711	ACAGATGGGTATTAAACTTG
158492	9131	ACAAGTTTAATACCCATCTG	167712	CAGATGGGTATTAAACTTGT
158493	9132	GACAAGTTTAATACCCATCT	167713	AGATGGGTATTAAACTTGTC
158494	9133	TGACAAGTTTAATACCCATC	167714	GATGGGTATTAAACTTGTCA
158495	9134	CTGACAAGTTTAATACCCAT	167715	ATGGGTATTAAACTTGTCAG
158496	9135	TCTGACAAGTTTAATACCCA	167716	TGGGTATTAAACTTGTCAGA
158497	9136	TTCTGACAAGTTTAATACCC	167717	GGGTATTAAACTTGTCAGAA
158498	9137	ATTCTGACAAGTTTAATACC	167718	GGTATTAAACTTGTCAGAAT
158499	9138	AATTCTGACAAGTTTAATAC	167719	GTATTAAACTTGTCAGAATT
158500	9139	AAATTCTGACAAGTTTAATA	167720	TATTAAACTTGTCAGAATTT
158501	9140	GAAATTCTGACAAGTTTAAT	167721	ATTAAACTTGTCAGAATTTC
158502	9141	AGAAATTCTGACAAGTTTAA	167722	TTAAACTTGTCAGAATTTCT
158503	9142	AAGAAATTCTGACAAGTTTA	167723	TAAACTTGTCAGAATTTCTT

158504	9143	AAAGAAATTCTGACAAGTTT	167724	AAACTTGTCAGAATTTCTTT
158505	9144	CAAAGAAATTCTGACAAGTT	167725	AACTTGTCAGAATTTCTTTG
158506	9145	ACAAAGAAATTCTGACAAGT	167726	ACTTGTCAGAATTTCTTTGT
158507	9146	GACAAAGAAATTCTGACAAG	167727	CTTGTCAGAATTTCTTTGTC
158508	9147	TGACAAAGAAATTCTGACAA	167728	TTGTCAGAATTTCTTTGTCA
158509	9148	ATGACAAAGAAATTCTGACA	167729	TGTCAGAATTTCTTTGTCAT
158510	9149	AATGACAAAGAAATTCTGAC	167730	GTCAGAATTTCTTTGTCATT
158511	9150	GAATGACAAAGAAATTCTGA	167731	TCAGAATTTCTTTGTCATTC
158512	9151	TGAATGACAAAGAAATTCTG	167732	CAGAATTTCTTTGTCATTCA
158513	9152	TTGAATGACAAAGAAATTCT	167733	AGAATTTCTTTGTCATTCAA
158514	9153	CTTGAATGACAAAGAAATTC	167734	GAATTTCTTTGTCATTCAAG
158515	9154	GCTTGAATGACAAAGAAATT	167735	AATTTCTTTGTCATTCAAGC
158516	9155	GGCTTGAATGACAAAGAAAT	167736	ATTTCTTTGTCATTCAAGCC
158517	9156	AGGCTTGAATGACAAAGAAA	167737	TTTCTTTGTCATTCAAGCCT
158518	9157	CAGGCTTGAATGACAAAGAA	167738	TTCTTTGTCATTCAAGCCTG
158519	9158	ACAGGCTTGAATGACAAAGA	167739	TCTTTGTCATTCAAGCCTGT
158520	9159	CACAGGCTTGAATGACAAAG	167740	CTTTGTCATTCAAGCCTGTG
158521	9160	TCACAGGCTTGAATGACAAA	167741	TTTGTCATTCAAGCCTGTGA
158522	9161	TTCACAGGCTTGAATGACAA	167742	TTGTCATTCAAGCCTGTGAA
158523	9162	ATTCACAGGCTTGAATGACA	167743	TGTCATTCAAGCCTGTGAAT
158524	9163	TATTCACAGGCTTGAATGAC	167744	GTCATTCAAGCCTGTGAATA
158525	9164	TTATTCACAGGCTTGAATGA	167745	TCATTCAAGCCTGTGAATAA
158526	9165	TTTATTCACAGGCTTGAATG	167746	CATTCAAGCCTGTGAATAAA
158527	9166	TTTTATTCACAGGCTTGAAT	167747	ATTCAAGCCTGTGAATAAAA
158528	9167	TTTTTATTCACAGGCTTGAA	167748	TTCAAGCCTGTGAATAAAAA
158529	9168	GTTTTTATTCACAGGCTTGA	167749	TCAAGCCTGTGAATAAAAAC
158530	9169	GGTTTTTATTCACAGGCTTG	167750	CAAGCCTGTGAATAAAAACC
158531	9170	GGGTTTTTATTCACAGGCTT	167751	AAGCCTGTGAATAAAAACCC
158532	9171	AGGGTTTTTATTCACAGGCT	167752	AGCCTGTGAATAAAAACCCT
158533	9172	CAGGGTTTTTATTCACAGGC	167753	GCCTGTGAATAAAAACCCTG
158534	9173	ACAGGGTTTTTATTCACAGG	167754	CCTGTGAATAAAAACCCTGT
158535	9174	TACAGGGTTTTTATTCACAG	167755	CTGTGAATAAAAACCCTGTA
158536	9175	ATACAGGGTTTTTATTCACA	167756	TGTGAATAAAAACCCTGTAT
158537	9176	CATACAGGGTTTTTATTCAC	167757	GTGAATAAAAACCCTGTATG
158538	9177	CCATACAGGGTTTTTATTCA	167758	TGAATAAAAACCCTGTATGG
158539	9178	GCCATACAGGGTTTTTATTC	167759	GAATAAAAACCCTGTATGGC
158540	9179	TGCCATACAGGGTTTTTATT	167760	AATAAAAACCCTGTATGGCA
158541	9180	GTGCCATACAGGGTTTTTAT	167761	ATAAAAACCCTGTATGGCAC
158542	9181	AGTGCCATACAGGGTTTTTA	167762	TAAAAACCCTGTATGGCACT
158543	9182	AAGTGCCATACAGGGTTTTT	167763	AAAAACCCTGTATGGCACTT
158544	9183	TAAGTGCCATACAGGGTTTT	167764	AAAACCCTGTATGGCACTTA
158545	9184	ATAAGTGCCATACAGGGTTT	167765	AAACCCTGTATGGCACTTAT
158546	9185	AATAAGTGCCATACAGGGTT	167766	AACCCTGTATGGCACTTATT
158547	9186	TAATAAGTGCCATACAGGGT	167767	ACCCTGTATGGCACTTATTA
158548	9187	ATAATAAGTGCCATACAGGG	167768	CCCTGTATGGCACTTATTAT
158549	9188	CATAATAAGTGCCATACAGG	167769	CCTGTATGGCACTTATTATG
158550	9189	TCATAATAAGTGCCATACAG	167770	CTGTATGGCACTTATTATGA
158551	9190	CTCATAATAAGTGCCATACA	167771	TGTATGGCACTTATTATGAG
158552	9191	CCTCATAATAAGTGCCATAC	167772	GTATGGCACTTATTATGAGG
158553	9192	GCCTCATAATAAGTGCCATA	167773	TATGGCACTTATTATGAGGC
158554	9193	AGCCTCATAATAAGTGCCAT	167774	ATGGCACTTATTATGAGGCT
158555	9194	TAGCCTCATAATAAGTGCCA	167775	TGGCACTTATTATGAGGCTA
158556	9195	ATAGCCTCATAATAAGTGCC	167776	GGCACTTATTATGAGGCTAT
158557	9196	AATAGCCTCATAATAAGTGC	167777	GCACTTATTATGAGGCTATT
158558	9197	TAATAGCCTCATAATAAGTG	167778	CACTTATTATGAGGCTATTA
158559	9198	TTAATAGCCTCATAATAAGT	167779	ACTTATTATGAGGCTATTAA
158560	9199	TTTAATAGCCTCATAATAAG	167780	CTTATTATGAGGCTATTAAA
158561	9200	TTTTAATAGCCTCATAATAA	167781	TTATTATGAGGCTATTAAAA
158562	9201	CTTTTAATAGCCTCATAATA	167782	TATTATGAGGCTATTAAAAG
158563	9202	TCTTTTAATAGCCTCATAAT	167783	ATTATGAGGCTATTAAAAGA
158564	9203	TTCTTTTAATAGCCTCATAA	167784	TTATGAGGCTATTAAAAGAA
158565	9204	ATTCTTTTAATAGCCTCATA	167785	TATGAGGCTATTAAAAGAAT
158566	9205	GATTCTTTTAATAGCCTCAT	167786	ATGAGGCTATTAAAAGAATC
158567	9206	GGATTCTTTTAATAGCCTCA	167787	TGAGGCTATTAAAAGAATCC
158568	9207	TGGATTCTTTTAATAGCCTC	167788	GAGGCTATTAAAAGAATCCA
158569	9208	TTGGATTCTTTTAATAGCCT	167789	AGGCTATTAAAAGAATCCAA
158570	9209	TTTGGATTCTTTTAATAGCC	167790	GGCTATTAAAAGAATCCAAA
158571	9210	ATTTGGATTCTTTTAATAGC	167791	GCTATTAAAAGAATCCAAAT
158572	9211	AATTTGGATTCTTTTAATAG	167792	CTATTAAAAGAATCCAAATT
158573	9212	GAATTTGGATTCTTTTAATA	167793	TATTAAAAGAATCCAAATTC
158574	9213	TGAATTTGGATTCTTTTAAT	167794	ATTAAAAGAATCCAAATTCA
158575	9214	TTGAATTTGGATTCTTTTAA	167795	TTAAAAGAATCCAAATTCAA

158576	9215	TTTGAATTTGGATTCTTTTA	167796	TAAAAGAATCCAAATTCAAA
158577	9216	GTTTGAATTTGGATTCTTTT	167797	AAAAGAATCCAAATTCAAAC
158578	9217	AGTTTGAATTTGGATTCTTT	167798	AAAGAATCCAAATTCAAACT
158579	9218	TAGTTTGAATTTGGATTCTT	167799	AAGAATCCAAATTCAAACTA
158580	9219	TTAGTTTGAATTTGGATTCT	167800	AGAATCCAAATTCAAACTAA
158581	9220	TTTAGTTTGAATTTGGATTC	167801	GAATCCAAATTCAAACTAAA

Table 1D: Example MAPT AON sequences

SEQ ID	Oligo	AON Sequence 5' to 3'	SEQ ID	Oligo	AON Sequence 5' to 3'	SEQ ID	Oligo	AON Sequence 5' to 3'
167805	1	TGGTGGGTGGCGGTGACTGC	212392	44588	ATGGTAAAACCCCATCTCTA	256979	89175	GCTCCTTCTGCACGTTGGGT
167806	2	CTGGTGGGTGGCGGTGACTG	212393	44589	AATGGTAAAACCCCATCTCT	256980	89176	TGCTCCTTCTGCACGTTGGG
167807	3	GCTGGTGGGTGGCGGTGACT	212394	44590	AAATGGTAAAACCCCATCTC	256981	89177	CTGCTCCTTCTGCACGTTGG
167808	4	AGCTGGTGGGTGGCGGTGAC	212395	44591	AAAATGGTAAAACCCCATCT	256982	89178	CCTGCTCCTTCTGCACGTTG
167809	5	GAGCTGGTGGGTGGCGGTGA	212396	44592	CAAAATGGTAAAACCCCATC	256983	89179	GCCTGCTCCTTCTGCACGTT
167810	6	GGAGCTGGTGGGTGGCGGTG	212397	44593	ACAAAATGGTAAAACCCCAT	256984	89180	CGCCTGCTCCTTCTGCACGT
167811	7	CGGAGCTGGTGGGTGGCGGT	212398	44594	GACAAAATGGTAAAACCCCA	256985	89181	GCGCCTGCTCCTTCTGCACG
167812	8	CCGGAGCTGGTGGGTGGCGG	212399	44595	AGACAAAATGGTAAAACCCC	256986	89182	TGCGCCTGCTCCTTCTGCAC
167813	9	GCCGGAGCTGGTGGGTGGCG	212400	44596	TAGACAAAATGGTAAAACCC	256987	89183	GTGCGCCTGCTCCTTCTGCA
167814	10	TGCCGGAGCTGGTGGGTGGC	212401	44597	CTAGACAAAATGGTAAAACC	256988	89184	AGTGCGCCTGCTCCTTCTGC
167815	11	GTGCCGGAGCTGGTGGGTGG	212402	44598	CCTAGACAAAATGGTAAAAC	256989	89185	GAGTGCGCCTGCTCCTTCTG
167816	12	GGTGCCGGAGCTGGTGGGTG	212403	44599	GCCTAGACAAAATGGTAAAA	256990	89186	CGAGTGCGCCTGCTCCTTCT
167817	13	TGGTGCCGGAGCTGGTGGGT	212404	44600	AGCCTAGACAAAATGGTAAA	256991	89187	CCGAGTGCGCCTGCTCCTTC
167818	14	TTGGTGCCGGAGCTGGTGGG	212405	44601	CAGCCTAGACAAAATGGTAA	256992	89188	TCCGAGTGCGCCTGCTCCTT
167819	15	GTTGGTGCCGGAGCTGGTGG	212406	44602	CCAGCCTAGACAAAATGGTA	256993	89189	CTCCGAGTGCGCCTGCTCCT
167820	16	TGTTGGTGCCGGAGCTGGTG	212407	44603	ACCAGCCTAGACAAAATGGT	256994	89190	CCTCCGAGTGCGCCTGCTCC
167821	17	CTGTTGGTGCCGGAGCTGGT	212408	44604	GACCAGCCTAGACAAAATGG	256995	89191	TCCTCCGAGTGCGCCTGCTC
167822	18	GCTGTTGGTGCCGGAGCTGG	212409	44605	AGACCAGCCTAGACAAAATG	256996	89192	CTCCTCCGAGTGCGCCTGCT
167823	19	TGCTGTTGGTGCCGGAGCTG	212410	44606	AAGACCAGCCTAGACAAAAT	256997	89193	GCTCCTCCGAGTGCGCCTGC
167824	20	CTGCTGTTGGTGCCGGAGCT	212411	44607	CAAGACCAGCCTAGACAAAA	256998	89194	TGCTCCTCCGAGTGCGCCTG
167825	21	GCTGCTGTTGGTGCCGGAGC	212412	44608	TCAAGACCAGCCTAGACAAA	256999	89195	ATGCTCCTCCGAGTGCGCCT
167826	22	CGCTGCTGTTGGTGCCGGAG	212413	44609	TTCAAGACCAGCCTAGACAA	257000	89196	AATGCTCCTCCGAGTGCGCC
167827	23	GCGCTGCTGTTGGTGCCGGA	212414	44610	GTTCAAGACCAGCCTAGACA	257001	89197	AAATGCTCCTCCGAGTGCGC
167828	24	GGCGCTGCTGTTGGTGCCGG	212415	44611	AGTTCAAGACCAGCCTAGAC	257002	89198	CAAATGCTCCTCCGAGTGCG
167829	25	CGGCGCTGCTGTTGGTGCCG	212416	44612	GAGTTCAAGACCAGCCTAGA	257003	89199	CCAAATGCTCCTCCGAGTGC
167830	26	GCGGCGCTGCTGTTGGTGCC	212417	44613	GGAGTTCAAGACCAGCCTAG	257004	89200	CCCAAATGCTCCTCCGAGTG
167831	27	AGCGGCGCTGCTGTTGGTGC	212418	44614	AGGAGTTCAAGACCAGCCTA	257005	89201	TCCCAAATGCTCCTCCGAGT
167832	28	CAGCGGCGCTGCTGTTGGTG	212419	44615	CAGGAGTTCAAGACCAGCCT	257006	89202	TTCCCAAATGCTCCTCCGAG
167833	29	GCAGCGGCGCTGCTGTTGGT	212420	44616	CCAGGAGTTCAAGACCAGCC	257007	89203	CTTCCCAAATGCTCCTCCGA
167834	30	GGCAGCGGCGCTGCTGTTGG	212421	44617	CCCAGGAGTTCAAGACCAGC	257008	89204	CCTTCCCAAATGCTCCTCCG
167835	31	TGGCAGCGGCGCTGCTGTTG	212422	44618	GCCCAGGAGTTCAAGACCAG	257009	89205	CCCTTCCCAAATGCTCCTCC
167836	32	GTGGCAGCGGCGCTGCTGTT	212423	44619	AGCCCAGGAGTTCAAGACCA	257010	89206	GCCCTTCCCAAATGCTCCTC
167837	33	GGTGGCAGCGGCGCTGCTGT	212424	44620	GAGCCCAGGAGTTCAAGACC	257011	89207	AGCCCTTCCCAAATGCTCCT
167838	34	CGGTGGCAGCGGCGCTGCTG	212425	44621	TGAGCCCAGGAGTTCAAGAC	257012	89208	CAGCCCTTCCCAAATGCTCC
167839	35	GCGGTGGCAGCGGCGCTGCT	212426	44622	TTGAGCCCAGGAGTTCAAGA	257013	89209	GCAGCCCTTCCCAAATGCTC
167840	36	GGCGGTGGCAGCGGCGCTGC	212427	44623	CTTGAGCCCAGGAGTTCAAG	257014	89210	TGCAGCCCTTCCCAAATGCT
167841	37	GGGCGGTGGCAGCGGCGCTG	212428	44624	GCTTGAGCCCAGGAGTTCAA	257015	89211	ATGCAGCCCTTCCCAAATGC
167842	38	TGGGCGGTGGCAGCGGCGCT	212429	44625	TGCTTGAGCCCAGGAGTTCA	257016	89212	AATGCAGCCCTTCCCAAATG
167843	39	GTGGGCGGTGGCAGCGGCGC	212430	44626	TTGCTTGAGCCCAGGAGTTC	257017	89213	AAATGCAGCCCTTCCCAAAT
167844	40	GGTGGGCGGTGGCAGCGGCG	212431	44627	TTTGCTTGAGCCCAGGAGTT	257018	89214	GAAATGCAGCCCTTCCCAAA
167845	41	AGGTGGGCGGTGGCAGCGGC	212432	44628	GTTTGCTTGAGCCCAGGAGT	257019	89215	GGAAATGCAGCCCTTCCCAA
167846	42	AAGGTGGGCGGTGGCAGCGG	212433	44629	GGTTTGCTTGAGCCCAGGAG	257020	89216	TGGAAATGCAGCCCTTCCCA
167847	43	GAAGGTGGGCGGTGGCAGCG	212434	44630	AGGTTTGCTTGAGCCCAGGA	257021	89217	CTGGAAATGCAGCCCTTCCC
167848	44	AGAAGGTGGGCGGTGGCAGC	212435	44631	GAGGTTTGCTTGAGCCCAGG	257022	89218	CCTGGAAATGCAGCCCTTCC
167849	45	CAGAAGGTGGGCGGTGGCAG	212436	44632	GGAGGTTTGCTTGAGCCCAG	257023	89219	CCCTGGAAATGCAGCCCTTC
167850	46	GCAGAAGGTGGGCGGTGGCA	212437	44633	GGGAGGTTTGCTTGAGCCCA	257024	89220	CCCCTGGAAATGCAGCCCTT
167851	47	GGCAGAAGGTGGGCGGTGGC	212438	44634	TGGGAGGTTTGCTTGAGCCC	257025	89221	GCCCCTGGAAATGCAGCCCT
167852	48	CGGCAGAAGGTGGGCGGTGG	212439	44635	GTGGGAGGTTTGCTTGAGCC	257026	89222	GGCCCCTGGAAATGCAGCCC
167853	49	GCGGCAGAAGGTGGGCGGTG	212440	44636	GGTGGGAGGTTTGCTTGAGC	257027	89223	GGGCCCCTGGAAATGCAGCC
167854	50	GGCGGCAGAAGGTGGGCGGT	212441	44637	AGGTGGGAGGTTTGCTTGAG	257028	89224	GGGGCCCCTGGAAATGCAGC
167855	51	CGGCGGCAGAAGGTGGGCGG	212442	44638	AAGGTGGGAGGTTTGCTTGA	257029	89225	AGGGGCCCCTGGAAATGCAG
167856	52	GCGGCGGCAGAAGGTGGGCG	212443	44639	CAAGGTGGGAGGTTTGCTTG	257030	89226	CAGGGGCCCCTGGAAATGCA
167857	53	GGCGGCGGCAGAAGGTGGGC	212444	44640	CCAAGGTGGGAGGTTTGCTT	257031	89227	CCAGGGGCCCCTGGAAATGC
167858	54	TGGCGGCGGCAGAAGGTGGG	212445	44641	ACCAAGGTGGGAGGTTTGCT	257032	89228	TCCAGGGGCCCCTGGAAATG
167859	55	GTGGCGGCGGCAGAAGGTGG	212446	44642	GACCAAGGTGGGAGGTTTGC	257033	89229	CTCCAGGGGCCCCTGGAAAT
167860	56	GGTGGCGGCGGCAGAAGGTG	212447	44643	AGACCAAGGTGGGAGGTTTG	257034	89230	TCTCCAGGGGCCCCTGGAAA
167861	57	TGGTGGCGGCGGCAGAAGGT	212448	44644	GAGACCAAGGTGGGAGGTTT	257035	89231	CTCTCCAGGGGCCCCTGGAA
167862	58	GTGGTGGCGGCGGCAGAAGG	212449	44645	GGAGACCAAGGTGGGAGGTT	257036	89232	CCTCTCCAGGGGCCCCTGGA
167863	59	TGTGGTGGCGGCGGCAGAAG	212450	44646	GGGAGACCAAGGTGGGAGGT	257037	89233	CCCTCTCCAGGGGCCCCTGG
167864	60	CTGTGGTGGCGGCGGCAGAA	212451	44647	TGGGAGACCAAGGTGGGAGG	257038	89234	CCCCTCTCCAGGGGCCCCTG
167865	61	GCTGTGGTGGCGGCGGCAGA	212452	44648	TTGGGAGACCAAGGTGGGAG	257039	89235	GCCCCTCTCCAGGGGCCCCT
167866	62	GGCTGTGGTGGCGGCGGCAG	212453	44649	TTTGGGAGACCAAGGTGGGA	257040	89236	GGCCCCTCTCCAGGGGCCCC
167867	63	TGGCTGTGGTGGCGGCGGCA	212454	44650	CTTTGGGAGACCAAGGTGGG	257041	89237	TGGCCCCTCTCCAGGGGCCC
167868	64	GTGGCTGTGGTGGCGGCGGC	212455	44651	ACTTTGGGAGACCAAGGTGG	257042	89238	CTGGCCCCTCTCCAGGGGCC
167869	65	GGTGGCTGTGGTGGCGGCGG	212456	44652	CACTTTGGGAGACCAAGGTG	257043	89239	TCTGGCCCCTCTCCAGGGGC
167870	66	AGGTGGCTGTGGTGGCGGCG	212457	44653	GCACTTTGGGAGACCAAGGT	257044	89240	CTCTGGCCCCTCTCCAGGGG
167871	67	AAGGTGGCTGTGGTGGCGGC	212458	44654	AGCACTTTGGGAGACCAAGG	257045	89241	CCTCTGGCCCCTCTCCAGGG
167872	68	GAAGGTGGCTGTGGTGGCGG	212459	44655	CAGCACTTTGGGAGACCAAG	257046	89242	GCCTCTGGCCCCTCTCCAGG
167873	69	AGAAGGTGGCTGTGGTGGCG	212460	44656	CCAGCACTTTGGGAGACCAA	257047	89243	GGCCTCTGGCCCCTCTCCAG
167874	70	GAGAAGGTGGCTGTGGTGGC	212461	44657	CCCAGCACTTTGGGAGACCA	257048	89244	GGGCCTCTGGCCCCTCTCCA

167875	71	GGAGAAGGTGGCTGTGGTGG	212462	44658	TCCCAGCACTTTGGGAGACC	257049	89245	CGGGCCTCTGGCCCCTCTCC
167876	72	AGGAGAAGGTGGCTGTGGTG	212463	44659	ATCCCAGCACTTTGGGAGAC	257050	89246	CCGGGCCTCTGGCCCCTCTC
167877	73	GAGGAGAAGGTGGCTGTGGT	212464	44660	AATCCCAGCACTTTGGGAGA	257051	89247	CCCGGGCCTCTGGCCCCTCT
167878	74	GGAGGAGAAGGTGGCTGTGG	212465	44661	TAATCCCAGCACTTTGGGAG	257052	89248	CCCCGGGCCTCTGGCCCCTC
167879	75	AGGAGGAGAAGGTGGCTGTG	212466	44662	GTAATCCCAGCACTTTGGGA	257053	89249	GCCCCGGGCCTCTGGCCCCT
167880	76	GAGGAGGAGAAGGTGGCTGT	212467	44663	TGTAATCCCAGCACTTTGGG	257054	89250	GGCCCCGGGCCTCTGGCCCC
167881	77	GGAGGAGGAGAAGGTGGCTG	212468	44664	CTGTAATCCCAGCACTTTGG	257055	89251	GGGCCCCGGGCCTCTGGCCC
167882	78	CGGAGGAGGAGAAGGTGGCT	212469	44665	GCTGTAATCCCAGCACTTTG	257056	89252	GGGGCCCCGGGCCTCTGGCC
167883	79	GCGGAGGAGGAGAAGGTGGC	212470	44666	TGCTGTAATCCCAGCACTTT	257057	89253	AGGGGCCCCGGGCCTCTGGC
167884	80	AGCGGAGGAGGAGAAGGTGG	212471	44667	ATGCTGTAATCCCAGCACTT	257058	89254	GAGGGGCCCCGGGCCTCTGG
167885	81	CAGCGGAGGAGGAGAAGGTG	212472	44668	CATGCTGTAATCCCAGCACT	257059	89255	AGAGGGGCCCCGGGCCTCTG
167886	82	ACAGCGGAGGAGGAGAAGGT	212473	44669	TCATGCTGTAATCCCAGCAC	257060	89256	AAGAGGGGCCCCGGGCCTCT
167887	83	GACAGCGGAGGAGGAGAAGG	212474	44670	CTCATGCTGTAATCCCAGCA	257061	89257	AAAGAGGGGCCCCGGGCCTC
167888	84	GGACAGCGGAGGAGGAGAAG	212475	44671	GCTCATGCTGTAATCCCAGC	257062	89258	CAAAGAGGGGCCCCGGGCCT
167889	85	AGGACAGCGGAGGAGGAGAA	212476	44672	GGCTCATGCTGTAATCCCAG	257063	89259	CCAAAGAGGGGCCCCGGGCC
167890	86	GAGGACAGCGGAGGAGGAGA	212477	44673	TGGCTCATGCTGTAATCCCA	257064	89260	CCCAAAGAGGGGCCCCGGGC
167891	87	AGAGGACAGCGGAGGAGGAG	212478	44674	GTGGCTCATGCTGTAATCCC	257065	89261	TCCCAAAGAGGGGCCCCGGG
167892	88	GAGAGGACAGCGGAGGAGGA	212479	44675	AGTGGCTCATGCTGTAATCC	257066	89262	CTCCCAAAGAGGGGCCCCGG
167893	89	GGAGAGGACAGCGGAGGAGG	212480	44676	CAGTGGCTCATGCTGTAATC	257067	89263	TCTCCCAAAGAGGGGCCCCG
167894	90	GGGAGAGGACAGCGGAGGAG	212481	44677	GCAGTGGCTCATGCTGTAAT	257068	89264	CTCTCCCAAAGAGGGGCCCC
167895	91	CGGGAGAGGACAGCGGAGGA	212482	44678	TGCAGTGGCTCATGCTGTAA	257069	89265	CCTCTCCCAAAGAGGGGCCC
167896	92	ACGGGAGAGGACAGCGGAGG	212483	44679	GTGCAGTGGCTCATGCTGTA	257070	89266	TCCTCTCCCAAAGAGGGGCC
167897	93	GACGGGAGAGGACAGCGGAG	212484	44680	AGTGCAGTGGCTCATGCTGT	257071	89267	GTCCTCTCCCAAAGAGGGGC
167898	94	GGACGGGAGAGGACAGCGGA	212485	44681	GAGTGCAGTGGCTCATGCTG	257072	89268	TGTCCTCTCCCAAAGAGGGG
167899	95	AGGACGGGAGAGGACAGCGG	212486	44682	CGAGTGCAGTGGCTCATGCT	257073	89269	GTGTCCTCTCCCAAAGAGGG
167900	96	GAGGACGGGAGAGGACAGCG	212487	44683	CCGAGTGCAGTGGCTCATGC	257074	89270	TGTGTCCTCTCCCAAAGAGG
167901	97	CGAGGACGGGAGAGGACAGC	212488	44684	GCCGAGTGCAGTGGCTCATG	257075	89271	TTGTGTCCTCTCCCAAAGAG
167902	98	GCGAGGACGGGAGAGGACAG	212489	44685	GGCCGAGTGCAGTGGCTCAT	257076	89272	TTTGTGTCCTCTCCCAAAGA
167903	99	GGCGAGGACGGGAGAGGACA	212490	44686	AGGCCGAGTGCAGTGGCTCA	257077	89273	TTTTGTGTCCTCTCCCAAAG
167904	100	AGGCGAGGACGGGAGAGGAC	212491	44687	AAGGCCGAGTGCAGTGGCTC	257078	89274	CTTTTGTGTCCTCTCCCAAA
167905	101	GAGGCGAGGACGGGAGAGGA	212492	44688	TAAGGCCGAGTGCAGTGGCT	257079	89275	TCTTTTGTGTCCTCTCCCAA
167906	102	AGAGGCGAGGACGGGAGAGG	212493	44689	TTAAGGCCGAGTGCAGTGGC	257080	89276	CTCTTTTGTGTCCTCTCCCA
167907	103	CAGAGGCGAGGACGGGAGAG	212494	44690	CTTAAGGCCGAGTGCAGTGG	257081	89277	CCTCTTTTGTGTCCTCTCCC
167908	104	ACAGAGGCGAGGACGGGAGA	212495	44691	TCTTAAGGCCGAGTGCAGTG	257082	89278	GCCTCTTTTGTGTCCTCTCC
167909	105	GACAGAGGCGAGGACGGGAG	212496	44692	CTCTTAAGGCCGAGTGCAGT	257083	89279	AGCCTCTTTTGTGTCCTCTC
167910	106	CGACAGAGGCGAGGACGGGA	212497	44693	TCTCTTAAGGCCGAGTGCAG	257084	89280	CAGCCTCTTTTGTGTCCTCT
167911	107	TCGACAGAGGCGAGGACGGG	212498	44694	TTCTCTTAAGGCCGAGTGCA	257085	89281	TCAGCCTCTTTTGTGTCCTC
167912	108	GTCGACAGAGGCGAGGACGG	212499	44695	CTTCTCTTAAGGCCGAGTGC	257086	89282	GTCAGCCTCTTTTGTGTCCT
167913	109	AGTCGACAGAGGCGAGGACG	212500	44696	TCTTCTCTTAAGGCCGAGTG	257087	89283	GGTCAGCCTCTTTTGTGTCC
167914	110	TAGTCGACAGAGGCGAGGAC	212501	44697	ATCTTCTCTTAAGGCCGAGT	257088	89284	AGGTCAGCCTCTTTTGTGTC
167915	111	ATAGTCGACAGAGGCGAGGA	212502	44698	AATCTTCTCTTAAGGCCGAG	257089	89285	AAGGTCAGCCTCTTTTGTGT
167916	112	GATAGTCGACAGAGGCGAGG	212503	44699	AAATCTTCTCTTAAGGCCGA	257090	89286	GAAGGTCAGCCTCTTTTGTG
167917	113	TGATAGTCGACAGAGGCGAG	212504	44700	TAAATCTTCTCTTAAGGCCG	257091	89287	GGAAGGTCAGCCTCTTTTGT
167918	114	CTGATAGTCGACAGAGGCGA	212505	44701	TTAAATCTTCTCTTAAGGCC	257092	89288	TGGAAGGTCAGCCTCTTTTG
167919	115	CCTGATAGTCGACAGAGGCG	212506	44702	ATTAAATCTTCTCTTAAGGC	257093	89289	CTGGAAGGTCAGCCTCTTTT
167920	116	ACCTGATAGTCGACAGAGGC	212507	44703	TATTAAATCTTCTCTTAAGG	257094	89290	TCTGGAAGGTCAGCCTCTTT
167921	117	TACCTGATAGTCGACAGAGG	212508	44704	TTATTAAATCTTCTCTTAAG	257095	89291	CTCTGGAAGGTCAGCCTCTT
167922	118	TTACCTGATAGTCGACAGAG	212509	44705	ATTATTAAATCTTCTCTTAA	257096	89292	GCTCTGGAAGGTCAGCCTCT
167923	119	CTTACCTGATAGTCGACAGA	212510	44706	AATTATTAAATCTTCTCTTA	257097	89293	GGCTCTGGAAGGTCAGCCTC
167924	120	GCTTACCTGATAGTCGACAG	212511	44707	TAATTATTAAATCTTCTCTT	257098	89294	GGGCTCTGGAAGGTCAGCCT
167925	121	CGCTTACCTGATAGTCGACA	212512	44708	TTAATTATTAAATCTTCTCT	257099	89295	AGGGCTCTGGAAGGTCAGCC
167926	122	GCGCTTACCTGATAGTCGAC	212513	44709	ATTAATTATTAAATCTTCTC	257100	89296	GAGGGCTCTGGAAGGTCAGC
167927	123	GGCGCTTACCTGATAGTCGA	212514	44710	TATTAATTATTAAATCTTCT	257101	89297	AGAGGGCTCTGGAAGGTCAG
167928	124	CGGCGCTTACCTGATAGTCG	212515	44711	GTATTAATTATTAAATCTTC	257102	89298	CAGAGGGCTCTGGAAGGTCA
167929	125	GCGGCGCTTACCTGATAGTC	212516	44712	AGTATTAATTATTAAATCTT	257103	89299	TCAGAGGGCTCTGGAAGGTC
167930	126	CGCGGCGCTTACCTGATAGT	212517	44713	AAGTATTAATTATTAAATCT	257104	89300	TTCAGAGGGCTCTGGAAGGT
167931	127	CCGCGGCGCTTACCTGATAG	212518	44714	AAAGTATTAATTATTAAATC	257105	89301	TTTCAGAGGGCTCTGGAAGG
167932	128	GCCGCGGCGCTTACCTGATA	212519	44715	TAAAGTATTAATTATTAAAT	257106	89302	TTTTCAGAGGGCTCTGGAAG
167933	129	AGCCGCGGCGCTTACCTGAT	212520	44716	GTAAAGTATTAATTATTAAA	257107	89303	CTTTTCAGAGGGCTCTGGAA
167934	130	GAGCCGCGGCGCTTACCTGA	212521	44717	TGTAAAGTATTAATTATTAA	257108	89304	GCTTTTCAGAGGGCTCTGGA
167935	131	GGAGCCGCGGCGCTTACCTG	212522	44718	TTGTAAAGTATTAATTATTA	257109	89305	TGCTTTTCAGAGGGCTCTGG
167936	132	CGGAGCCGCGGCGCTTACCT	212523	44719	GTTGTAAAGTATTAATTATT	257110	89306	CTGCTTTTCAGAGGGCTCTG
167937	133	TCGGAGCCGCGGCGCTTACC	212524	44720	TGTTGTAAAGTATTAATTAT	257111	89307	GCTGCTTTTCAGAGGGCTCT
167938	134	TTCGGAGCCGCGGCGCTTAC	212525	44721	TTGTTGTAAAGTATTAATTA	257112	89308	GGCTGCTTTTCAGAGGGCTC
167939	135	TTTCGGAGCCGCGGCGCTTA	212526	44722	CTTGTTGTAAAGTATTAATT	257113	89309	AGGCTGCTTTTCAGAGGGCT
167940	136	ATTTCGGAGCCGCGGCGCTT	212527	44723	TCTTGTTGTAAAGTATTAAT	257114	89310	CAGGCTGCTTTTCAGAGGGC
167941	137	GATTTCGGAGCCGCGGCGCT	212528	44724	ATCTTGTTGTAAAGTATTAA	257115	89311	GCAGGCTGCTTTTCAGAGGG
167942	138	AGATTTCGGAGCCGCGGCGC	212529	44725	GATCTTGTTGTAAAGTATTA	257116	89312	AGCAGGCTGCTTTTCAGAGG
167943	139	CAGATTTCGGAGCCGCGGCG	212530	44726	AGATCTTGTTGTAAAGTATT	257117	89313	CAGCAGGCTGCTTTTCAGAG
167944	140	GCAGATTTCGGAGCCGCGGC	212531	44727	CAGATCTTGTTGTAAAGTAT	257118	89314	GCAGCAGGCTGCTTTTCAGA
167945	141	GGCAGATTTCGGAGCCGCGG	212532	44728	CCAGATCTTGTTGTAAAGTA	257119	89315	AGCAGCAGGCTGCTTTTCAG
167946	142	AGGCAGATTTCGGAGCCGCG	212533	44729	TCCAGATCTTGTTGTAAAGT	257120	89316	CAGCAGCAGGCTGCTTTTCA

167947	143	GAGGCAGATTTCGGAGCCGC	212534	44730	TTCCAGATCTTGTTGTAAAG	257121	89317	GCAGCAGCAGGCTGCTTTTC
167948	144	CGAGGCAGATTTCGGAGCCG	212535	44731	CTTCCAGATCTTGTTGTAAA	257122	89318	AGCAGCAGCAGGCTGCTTTT
167949	145	GCGAGGCAGATTTCGGAGCC	212536	44732	TCTTCCAGATCTTGTTGTAA	257123	89319	GAGCAGCAGCAGGCTGCTTT
167950	146	GGCGAGGCAGATTTCGGAGC	212537	44733	CTCTTCCAGATCTTGTTGTA	257124	89320	GGAGCAGCAGCAGGCTGCTT
167951	147	CGGCGAGGCAGATTTCGGAG	212538	44734	CCTCTTCCAGATCTTGTTGT	257125	89321	CGGAGCAGCAGCAGGCTGCT
167952	148	ACGGCGAGGCAGATTTCGGA	212539	44735	ACCTCTTCCAGATCTTGTTG	257126	89322	GCGGAGCAGCAGCAGGCTGC
167953	149	GACGGCGAGGCAGATTTCGG	212540	44736	CACCTCTTCCAGATCTTGTT	257127	89323	CGCGGAGCAGCAGCAGGCTG
167954	150	GGACGGCGAGGCAGATTTCG	212541	44737	CCACCTCTTCCAGATCTTGT	257128	89324	CCGCGGAGCAGCAGCAGGCT
167955	151	CGGACGGCGAGGCAGATTTC	212542	44738	CCCACCTCTTCCAGATCTTG	257129	89325	CCCGCGGAGCAGCAGCAGGC
167956	152	GCGGACGGCGAGGCAGATTT	212543	44739	TCCCACCTCTTCCAGATCTT	257130	89326	CCCCGCGGAGCAGCAGCAGG
167957	153	GGCGGACGGCGAGGCAGATT	212544	44740	ATCCCACCTCTTCCAGATCT	257131	89327	CCCCCGCGGAGCAGCAGCAG
167958	154	AGGCGGACGGCGAGGCAGAT	212545	44741	CATCCCACCTCTTCCAGATC	257132	89328	TCCCCCGCGGAGCAGCAGCA
167959	155	GAGGCGGACGGCGAGGCAGA	212546	44742	TCATCCCACCTCTTCCAGAT	257133	89329	TTCCCCCGCGGAGCAGCAGC
167960	156	AGAGGCGGACGGCGAGGCAG	212547	44743	CTCATCCCACCTCTTCCAGA	257134	89330	CTTCCCCCGCGGAGCAGCAG
167961	157	CAGAGGCGGACGGCGAGGCA	212548	44744	ACTCATCCCACCTCTTCCAG	257135	89331	GCTTCCCCCGCGGAGCAGCA
167962	158	ACAGAGGCGGACGGCGAGGC	212549	44745	TACTCATCCCACCTCTTCCA	257136	89332	GGCTTCCCCCGCGGAGCAGC
167963	159	CACAGAGGCGGACGGCGAGG	212550	44746	TTACTCATCCCACCTCTTCC	257137	89333	GGGCTTCCCCCGCGGAGCAG
167964	160	GCACAGAGGCGGACGGCGAG	212551	44747	GTTACTCATCCCACCTCTTC	257138	89334	CGGGCTTCCCCCGCGGAGCA
167965	161	TGCACAGAGGCGGACGGCGA	212552	44748	AGTTACTCATCCCACCTCTT	257139	89335	ACGGGCTTCCCCCGCGGAGC
167966	162	GTGCACAGAGGCGGACGGCG	212553	44749	TAGTTACTCATCCCACCTCT	257140	89336	GACGGGCTTCCCCCGCGGAG
167967	163	GGTGCACAGAGGCGGACGGC	212554	44750	TTAGTTACTCATCCCACCTC	257141	89337	TGACGGGCTTCCCCCGCGGA
167968	164	GGGTGCACAGAGGCGGACGG	212555	44751	TTTAGTTACTCATCCCACCT	257142	89338	CTGACGGGCTTCCCCCGCGG
167969	165	GGGGTGCACAGAGGCGGACG	212556	44752	ATTTAGTTACTCATCCCACC	257143	89339	GCTGACGGGCTTCCCCCGCG
167970	166	AGGGGTGCACAGAGGCGGAC	212557	44753	CATTTAGTTACTCATCCCAC	257144	89340	GGCTGACGGGCTTCCCCCGC
167971	167	CAGGGGTGCACAGAGGCGGA	212558	44754	TCATTTAGTTACTCATCCCA	257145	89341	CGGCTGACGGGCTTCCCCCG
167972	168	GCAGGGGTGCACAGAGGCGG	212559	44755	CTCATTTAGTTACTCATCCC	257146	89342	CCGGCTGACGGGCTTCCCCC
167973	169	CGCAGGGGTGCACAGAGGCG	212560	44756	CCTCATTTAGTTACTCATCC	257147	89343	CCCGGCTGACGGGCTTCCCC
167974	170	GCGCAGGGGTGCACAGAGGC	212561	44757	TCCTCATTTAGTTACTCATC	257148	89344	ACCCGGCTGACGGGCTTCCC
167975	171	GGCGCAGGGGTGCACAGAGG	212562	44758	ATCCTCATTTAGTTACTCAT	257149	89345	GACCCGGCTGACGGGCTTCC
167976	172	CGGCGCAGGGGTGCACAGAG	212563	44759	TATCCTCATTTAGTTACTCA	257150	89346	GGACCCGGCTGACGGGCTTC
167977	173	GCGGCGCAGGGGTGCACAGA	212564	44760	GTATCCTCATTTAGTTACTC	257151	89347	GGGACCCGGCTGACGGGCTT
167978	174	GGCGGCGCAGGGGTGCACAG	212565	44761	TGTATCCTCATTTAGTTACT	257152	89348	AGGGACCCGGCTGACGGGCT
167979	175	CGGCGGCGCAGGGGTGCACA	212566	44762	TTGTATCCTCATTTAGTTAC	257153	89349	GAGGGACCCGGCTGACGGGC
167980	176	GCGGCGGCGCAGGGGTGCAC	212567	44763	CTTGTATCCTCATTTAGTTA	257154	89350	TGAGGGACCCGGCTGACGGG
167981	177	GGCGGCGGCGCAGGGGTGCA	212568	44764	ACTTGTATCCTCATTTAGTT	257155	89351	TTGAGGGACCCGGCTGACGG
167982	178	GGGCGGCGGCGCAGGGGTGC	212569	44765	TACTTGTATCCTCATTTAGT	257156	89352	GTTGAGGGACCCGGCTGACG
167983	179	GGGGCGGCGGCGCAGGGGTG	212570	44766	TTACTTGTATCCTCATTTAG	257157	89353	AGTTGAGGGACCCGGCTGAC
167984	180	AGGGGCGGCGGCGCAGGGGT	212571	44767	GTTACTTGTATCCTCATTTA	257158	89354	GAGTTGAGGGACCCGGCTGA
167985	181	GAGGGGCGGCGGCGCAGGGG	212572	44768	GGTTACTTGTATCCTCATTT	257159	89355	TGAGTTGAGGGACCCGGCTG
167986	182	CGAGGGGCGGCGGCGCAGGG	212573	44769	GGGTTACTTGTATCCTCATT	257160	89356	TTGAGTTGAGGGACCCGGCT
167987	183	GCGAGGGGCGGCGGCGCAGG	212574	44770	CGGGTTACTTGTATCCTCAT	257161	89357	TTTGAGTTGAGGGACCCGGC
167988	184	GGCGAGGGGCGGCGGCGCAG	212575	44771	CCGGGTTACTTGTATCCTCA	257162	89358	CTTTGAGTTGAGGGACCCGG
167989	185	GGGCGAGGGGCGGCGGCGCA	212576	44772	CCCGGGTTACTTGTATCCTC	257163	89359	CCTTTGAGTTGAGGGACCCG
167990	186	AGGGCGAGGGGCGGCGGCGC	212577	44773	ACCCGGGTTACTTGTATCCT	257164	89360	ACCTTTGAGTTGAGGGACCC
167991	187	GAGGGCGAGGGGCGGCGGCG	212578	44774	GACCCGGGTTACTTGTATCC	257165	89361	GACCTTTGAGTTGAGGGACC
167992	188	GGAGGGCGAGGGGCGGCGGC	212579	44775	TGACCCGGGTTACTTGTATC	257166	89362	AGACCTTTGAGTTGAGGGAC
167993	189	GGGAGGGCGAGGGGCGGCGG	212580	44776	ATGACCCGGGTTACTTGTAT	257167	89363	CAGACCTTTGAGTTGAGGGA
167994	190	AGGGAGGGCGAGGGGCGGCG	212581	44777	TATGACCCGGGTTACTTGTA	257168	89364	ACAGACCTTTGAGTTGAGGG
167995	191	GAGGGAGGGCGAGGGGCGGC	212582	44778	ATATGACCCGGGTTACTTGT	257169	89365	CACAGACCTTTGAGTTGAGG
167996	192	AGAGGGAGGGCGAGGGGCGG	212583	44779	AATATGACCCGGGTTACTTG	257170	89366	ACACAGACCTTTGAGTTGAG
167997	193	GAGAGGGAGGGCGAGGGGCG	212584	44780	AAATATGACCCGGGTTACTT	257171	89367	GACACAGACCTTTGAGTTGA
167998	194	GGAGAGGGAGGGCGAGGGGC	212585	44781	CAAATATGACCCGGGTTACT	257172	89368	AGACACAGACCTTTGAGTTG
167999	195	CGGAGAGGGAGGGCGAGGGG	212586	44782	GCAAATATGACCCGGGTTAC	257173	89369	AAGACACAGACCTTTGAGTT
168000	196	GCGGAGAGGGAGGGCGAGGG	212587	44783	AGCAAATATGACCCGGGTTA	257174	89370	CAAGACACAGACCTTTGAGT
168001	197	TGCGGAGAGGGAGGGCGAGG	212588	44784	TAGCAAATATGACCCGGGTT	257175	89371	TCAAGACACAGACCTTTGAG
168002	198	CTGCGGAGAGGGAGGGCGAG	212589	44785	TTAGCAAATATGACCCGGGT	257176	89372	CTCAAGACACAGACCTTTGA
168003	199	TCTGCGGAGAGGGAGGGCGA	212590	44786	ATTAGCAAATATGACCCGGG	257177	89373	GCTCAAGACACAGACCTTTG
168004	200	GTCTGCGGAGAGGGAGGGCG	212591	44787	TATTAGCAAATATGACCCGG	257178	89374	AGCTCAAGACACAGACCTTT
168005	201	AGTCTGCGGAGAGGGAGGGC	212592	44788	GTATTAGCAAATATGACCCG	257179	89375	AAGCTCAAGACACAGACCTT
168006	202	CAGTCTGCGGAGAGGGAGGG	212593	44789	GGTATTAGCAAATATGACCC	257180	89376	GAAGCTCAAGACACAGACCT
168007	203	CCAGTCTGCGGAGAGGGAGG	212594	44790	GGGTATTAGCAAATATGACC	257181	89377	AGAAGCTCAAGACACAGACC
168008	204	CCCAGTCTGCGGAGAGGGAG	212595	44791	AGGGTATTAGCAAATATGAC	257182	89378	AAGAAGCTCAAGACACAGAC
168009	205	CCCCAGTCTGCGGAGAGGGA	212596	44792	AAGGGTATTAGCAAATATGA	257183	89379	GAAGAAGCTCAAGACACAGA
168010	206	GCCCCAGTCTGCGGAGAGGG	212597	44793	CAAGGGTATTAGCAAATATG	257184	89380	CGAAGAAGCTCAAGACACAG
168011	207	AGCCCCAGTCTGCGGAGAGG	212598	44794	CCAAGGGTATTAGCAAATAT	257185	89381	GCGAAGAAGCTCAAGACACA
168012	208	AAGCCCCAGTCTGCGGAGAG	212599	44795	ACCAAGGGTATTAGCAAATA	257186	89382	AGCGAAGAAGCTCAAGACAC
168013	209	GAAGCCCCAGTCTGCGGAGA	212600	44796	GACCAAGGGTATTAGCAAAT	257187	89383	GAGCGAAGAAGCTCAAGACA
168014	210	CGAAGCCCCAGTCTGCGGAG	212601	44797	TGACCAAGGGTATTAGCAAA	257188	89384	GGAGCGAAGAAGCTCAAGAC
168015	211	ACGAAGCCCCAGTCTGCGGA	212602	44798	GTGACCAAGGGTATTAGCAA	257189	89385	AGGAGCGAAGAAGCTCAAGA
168016	212	CACGAAGCCCCAGTCTGCGG	212603	44799	TGTGACCAAGGGTATTAGCA	257190	89386	AAGGAGCGAAGAAGCTCAAG
168017	213	GCACGAAGCCCCAGTCTGCG	212604	44800	ATGTGACCAAGGGTATTAGC	257191	89387	GAAGGAGCGAAGAAGCTCAA
168018	214	CGCACGAAGCCCCAGTCTGC	212605	44801	AATGTGACCAAGGGTATTAG	257192	89388	GGAAGGAGCGAAGAAGCTCA

168019	215	GCGCACGAAGCCCCAGTCTG	212606	44802	CAATGTGACCAAGGGTATTA	257193	89389	GGGAAGGAGCGAAGAAGCTC
168020	216	GGCGCACGAAGCCCCAGTCT	212607	44803	TCAATGTGACCAAGGGTATT	257194	89390	AGGGAAGGAGCGAAGAAGCT
168021	217	CGGCGCACGAAGCCCCAGTC	212608	44804	TTCAATGTGACCAAGGGTAT	257195	89391	CAGGGAAGGAGCGAAGAAGC
168022	218	CCGGCGCACGAAGCCCCAGT	212609	44805	GTTCAATGTGACCAAGGGTA	257196	89392	CCAGGGAAGGAGCGAAGAAG
168023	219	CCCGGCGCACGAAGCCCCAG	212610	44806	AGTTCAATGTGACCAAGGGT	257197	89393	CCCAGGGAAGGAGCGAAGAA
168024	220	GCCCGGCGCACGAAGCCCCA	212611	44807	AAGTTCAATGTGACCAAGGG	257198	89394	CCCCAGGGAAGGAGCGAAGA
168025	221	TGCCCGGCGCACGAAGCCCC	212612	44808	CAAGTTCAATGTGACCAAGG	257199	89395	TCCCCAGGGAAGGAGCGAAG
168026	222	ATGCCCGGCGCACGAAGCCC	212613	44809	TCAAGTTCAATGTGACCAAG	257200	89396	GTCCCCAGGGAAGGAGCGAA
168027	223	GATGCCCGGCGCACGAAGCC	212614	44810	ATCAAGTTCAATGTGACCAA	257201	89397	GGTCCCCAGGGAAGGAGCGA
168028	224	CGATGCCCGGCGCACGAAGC	212615	44811	TATCAAGTTCAATGTGACCA	257202	89398	AGGTCCCCAGGGAAGGAGCG
168029	225	CCGATGCCCGGCGCACGAAG	212616	44812	ATATCAAGTTCAATGTGACC	257203	89399	GAGGTCCCCAGGGAAGGAGC
168030	226	ACCGATGCCCGGCGCACGAA	212617	44813	GATATCAAGTTCAATGTGAC	257204	89400	GGAGGTCCCCAGGGAAGGAG
168031	227	GACCGATGCCCGGCGCACGA	212618	44814	AGATATCAAGTTCAATGTGA	257205	89401	GGGAGGTCCCCAGGGAAGGA
168032	228	CGACCGATGCCCGGCGCACG	212619	44815	AAGATATCAAGTTCAATGTG	257206	89402	TGGGAGGTCCCCAGGGAAGG
168033	229	CCGACCGATGCCCGGCGCAC	212620	44816	TAAGATATCAAGTTCAATGT	257207	89403	CTGGGAGGTCCCCAGGGAAG
168034	230	CCCGACCGATGCCCGGCGCA	212621	44817	ATAAGATATCAAGTTCAATG	257208	89404	CCTGGGAGGTCCCCAGGGAA
168035	231	CCCCGACCGATGCCCGGCGC	212622	44818	GATAAGATATCAAGTTCAAT	257209	89405	GCCTGGGAGGTCCCCAGGGA
168036	232	GCCCCGACCGATGCCCGGCG	212623	44819	TGATAAGATATCAAGTTCAA	257210	89406	GGCCTGGGAGGTCCCCAGGG
168037	233	GGCCCCGACCGATGCCCGGC	212624	44820	CTGATAAGATATCAAGTTCA	257211	89407	AGGCCTGGGAGGTCCCCAGG
168038	234	TGGCCCCGACCGATGCCCGG	212625	44821	TCTGATAAGATATCAAGTTC	257212	89408	GAGGCCTGGGAGGTCCCCAG
168039	235	GTGGCCCCGACCGATGCCCG	212626	44822	ATCTGATAAGATATCAAGTT	257213	89409	GGAGGCCTGGGAGGTCCCCA
168040	236	GGTGGCCCCGACCGATGCCC	212627	44823	AATCTGATAAGATATCAAGT	257214	89410	GGGAGGCCTGGGAGGTCCCC
168041	237	CGGTGGCCCCGACCGATGCC	212628	44824	AAATCTGATAAGATATCAAG	257215	89411	TGGGAGGCCTGGGAGGTCCC
168042	238	GCGGTGGCCCCGACCGATGC	212629	44825	AAAATCTGATAAGATATCAA	257216	89412	CTGGGAGGCCTGGGAGGTCC
168043	239	TGCGGTGGCCCCGACCGATG	212630	44826	GAAAATCTGATAAGATATCA	257217	89413	CCTGGGAGGCCTGGGAGGTC
168044	240	CTGCGGTGGCCCCGACCGAT	212631	44827	GGAAAATCTGATAAGATATC	257218	89414	GCCTGGGAGGCCTGGGAGGT
168045	241	CCTGCGGTGGCCCCGACCGA	212632	44828	AGGAAAATCTGATAAGATAT	257219	89415	AGCCTGGGAGGCCTGGGAGG
168046	242	CCCTGCGGTGGCCCCGACCG	212633	44829	TAGGAAAATCTGATAAGATA	257220	89416	CAGCCTGGGAGGCCTGGGAG
168047	243	GCCCTGCGGTGGCCCCGACC	212634	44830	TTAGGAAAATCTGATAAGAT	257221	89417	GCAGCCTGGGAGGCCTGGGA
168048	244	GGCCCTGCGGTGGCCCCGAC	212635	44831	ATTAGGAAAATCTGATAAGA	257222	89418	CGCAGCCTGGGAGGCCTGGG
168049	245	GGGCCCTGCGGTGGCCCCGA	212636	44832	GATTAGGAAAATCTGATAAG	257223	89419	CCGCAGCCTGGGAGGCCTGG
168050	246	GGGGCCCTGCGGTGGCCCCG	212637	44833	TGATTAGGAAAATCTGATAA	257224	89420	CCCGCAGCCTGGGAGGCCTG
168051	247	AGGGGCCCTGCGGTGGCCCC	212638	44834	CTGATTAGGAAAATCTGATA	257225	89421	GCCCGCAGCCTGGGAGGCCT
168052	248	GAGGGGCCCTGCGGTGGCCC	212639	44835	GCTGATTAGGAAAATCTGAT	257226	89422	TGCCCGCAGCCTGGGAGGCC
168053	249	GGAGGGGCCCTGCGGTGGCC	212640	44836	AGCTGATTAGGAAAATCTGA	257227	89423	GTGCCCGCAGCCTGGGAGGC
168054	250	GGGAGGGGCCCTGCGGTGGC	212641	44837	GAGCTGATTAGGAAAATCTG	257228	89424	AGTGCCCGCAGCCTGGGAGG
168055	251	AGGGAGGGGCCCTGCGGTGG	212642	44838	GGAGCTGATTAGGAAAATCT	257229	89425	CAGTGCCCGCAGCCTGGGAG
168056	252	CAGGGAGGGGCCCTGCGGTG	212643	44839	AGGAGCTGATTAGGAAAATC	257230	89426	GCAGTGCCCGCAGCCTGGGA
168057	253	GCAGGGAGGGGCCCTGCGGT	212644	44840	AAGGAGCTGATTAGGAAAAT	257231	89427	GGCAGTGCCCGCAGCCTGGG
168058	254	GGCAGGGAGGGGCCCTGCGG	212645	44841	AAAGGAGCTGATTAGGAAAA	257232	89428	TGGCAGTGCCCGCAGCCTGG
168059	255	AGGCAGGGAGGGGCCCTGCG	212646	44842	TAAAGGAGCTGATTAGGAAA	257233	89429	GTGGCAGTGCCCGCAGCCTG
168060	256	GAGGCAGGGAGGGGCCCTGC	212647	44843	CTAAAGGAGCTGATTAGGAA	257234	89430	AGTGGCAGTGCCCGCAGCCT
168061	257	GGAGGCAGGGAGGGGCCCTG	212648	44844	GCTAAAGGAGCTGATTAGGA	257235	89431	CAGTGGCAGTGCCCGCAGCC
168062	258	GGGAGGCAGGGAGGGGCCCT	212649	44845	TGCTAAAGGAGCTGATTAGG	257236	89432	TCAGTGGCAGTGCCCGCAGC
168063	259	GGGGAGGCAGGGAGGGGCCC	212650	44846	CTGCTAAAGGAGCTGATTAG	257237	89433	CTCAGTGGCAGTGCCCGCAG
168064	260	AGGGGAGGCAGGGAGGGGCC	212651	44847	GCTGCTAAAGGAGCTGATTA	257238	89434	GCTCAGTGGCAGTGCCCGCA
168065	261	CAGGGGAGGCAGGGAGGGGC	212652	44848	TGCTGCTAAAGGAGCTGATT	257239	89435	AGCTCAGTGGCAGTGCCCGC
168066	262	GCAGGGGAGGCAGGGAGGGG	212653	44849	CTGCTGCTAAAGGAGCTGAT	257240	89436	AAGCTCAGTGGCAGTGCCCG
168067	263	AGCAGGGGAGGCAGGGAGGG	212654	44850	ACTGCTGCTAAAGGAGCTGA	257241	89437	GAAGCTCAGTGGCAGTGCCC
168068	264	GAGCAGGGGAGGCAGGGAGG	212655	44851	CACTGCTGCTAAAGGAGCTG	257242	89438	GGAAGCTCAGTGGCAGTGCC
168069	265	CGAGCAGGGGAGGCAGGGAG	212656	44852	ACACTGCTGCTAAAGGAGCT	257243	89439	TGGAAGCTCAGTGGCAGTGC
168070	266	CCGAGCAGGGGAGGCAGGGA	212657	44853	AACACTGCTGCTAAAGGAGC	257244	89440	CTGGAAGCTCAGTGGCAGTG
168071	267	CCCGAGCAGGGGAGGCAGGG	212658	44854	CAACACTGCTGCTAAAGGAG	257245	89441	CCTGGAAGCTCAGTGGCAGT
168072	268	CCCCGAGCAGGGGAGGCAGG	212659	44855	GCAACACTGCTGCTAAAGGA	257246	89442	GCCTGGAAGCTCAGTGGCAG
168073	269	CCCCCGAGCAGGGGAGGCAG	212660	44856	TGCAACACTGCTGCTAAAGG	257247	89443	GGCCTGGAAGCTCAGTGGCA
168074	270	GCCCCCGAGCAGGGGAGGCA	212661	44857	CTGCAACACTGCTGCTAAAG	257248	89444	AGGCCTGGAAGCTCAGTGGC
168075	271	AGCCCCCGAGCAGGGGAGGC	212662	44858	GCTGCAACACTGCTGCTAAA	257249	89445	GAGGCCTGGAAGCTCAGTGG
168076	272	CAGCCCCCGAGCAGGGGAGG	212663	44859	TGCTGCAACACTGCTGCTAA	257250	89446	GGAGGCCTGGAAGCTCAGTG
168077	273	CCAGCCCCCGAGCAGGGGAG	212664	44860	ATGCTGCAACACTGCTGCTA	257251	89447	GGGAGGCCTGGAAGCTCAGT
168078	274	CCCAGCCCCCGAGCAGGGGA	212665	44861	GATGCTGCAACACTGCTGCT	257252	89448	CGGGAGGCCTGGAAGCTCAG
168079	275	CCCCAGCCCCCGAGCAGGGG	212666	44862	AGATGCTGCAACACTGCTGC	257253	89449	TCGGGAGGCCTGGAAGCTCA
168080	276	GCCCCAGCCCCCGAGCAGGG	212667	44863	AAGATGCTGCAACACTGCTG	257254	89450	GTCGGGAGGCCTGGAAGCTC
168081	277	GGCCCCAGCCCCCGAGCAGG	212668	44864	TAAGATGCTGCAACACTGCT	257255	89451	AGTCGGGAGGCCTGGAAGCT
168082	278	TGGCCCCAGCCCCCGAGCAG	212669	44865	ATAAGATGCTGCAACACTGC	257256	89452	GAGTCGGGAGGCCTGGAAGC
168083	279	CTGGCCCCAGCCCCCGAGCA	212670	44866	GATAAGATGCTGCAACACTG	257257	89453	GGAGTCGGGAGGCCTGGAAG
168084	280	CCTGGCCCCAGCCCCCGAGC	212671	44867	AGATAAGATGCTGCAACACT	257258	89454	AGGAGTCGGGAGGCCTGGAA
168085	281	CCCTGGCCCCAGCCCCCGAG	212672	44868	GAGATAAGATGCTGCAACAC	257259	89455	CAGGAGTCGGGAGGCCTGGA
168086	282	GCCCTGGCCCCAGCCCCCGA	212673	44869	TGAGATAAGATGCTGCAACA	257260	89456	GCAGGAGTCGGGAGGCCTGG
168087	283	CGCCCTGGCCCCAGCCCCCG	212674	44870	ATGAGATAAGATGCTGCAAC	257261	89457	AGCAGGAGTCGGGAGGCCTG
168088	284	CCGCCCTGGCCCCAGCCCCC	212675	44871	AATGAGATAAGATGCTGCAA	257262	89458	CAGCAGGAGTCGGGAGGCCT
168089	285	GCCGCCCTGGCCCCAGCCCC	212676	44872	AAATGAGATAAGATGCTGCA	257263	89459	GCAGCAGGAGTCGGGAGGCC
168090	286	GGCCGCCCTGGCCCCAGCCC	212677	44873	AAAATGAGATAAGATGCTGC	257264	89460	AGCAGCAGGAGTCGGGAGGC

168091	287	AGGCCGCCCTGGCCCCAGCC	212678	44874	CAAAATGAGATAAGATGCTG	257265	89461	AAGCAGCAGGAGTCGGGAGG
168092	288	CAGGCCGCCCTGGCCCCAGC	212679	44875	ACAAAATGAGATAAGATGCT	257266	89462	GAAGCAGCAGGAGTCGGGAG
168093	289	CCAGGCCGCCCTGGCCCCAG	212680	44876	AACAAAATGAGATAAGATGC	257267	89463	AGAAGCAGCAGGAGTCGGGA
168094	290	TCCAGGCCGCCCTGGCCCCA	212681	44877	AAACAAAATGAGATAAGATG	257268	89464	CAGAAGCAGCAGGAGTCGGG
168095	291	TTCCAGGCCGCCCTGGCCCC	212682	44878	AAAACAAAATGAGATAAGAT	257269	89465	TCAGAAGCAGCAGGAGTCGG
168096	292	TTTCCAGGCCGCCCTGGCCC	212683	44879	AAAAACAAAATGAGATAAGA	257270	89466	GTCAGAAGCAGCAGGAGTCG
168097	293	CTTTCCAGGCCGCCCTGGCC	212684	44880	AAAAAACAAAATGAGATAAG	257271	89467	CGTCAGAAGCAGCAGGAGTC
168098	294	CCTTTCCAGGCCGCCCTGGC	212685	44881	CAAAAAACAAAATGAGATAA	257272	89468	ACGTCAGAAGCAGCAGGAGT
168099	295	CCCTTTCCAGGCCGCCCTGG	212686	44882	ACAAAAAACAAAATGAGATA	257273	89469	AACGTCAGAAGCAGCAGGAG
168100	296	TCCCTTTCCAGGCCGCCCTG	212687	44883	AACAAAAAACAAAATGAGAT	257274	89470	GAACGTCAGAAGCAGCAGGA
168101	297	GTCCCTTTCCAGGCCGCCCT	212688	44884	AAACAAAAAACAAAATGAGA	257275	89471	GGAACGTCAGAAGCAGCAGG
168102	298	GGTCCCTTTCCAGGCCGCCC	212689	44885	AAAACAAAAAACAAAATGAG	257276	89472	AGGAACGTCAGAAGCAGCAG
168103	299	AGGTCCCTTTCCAGGCCGCC	212690	44886	AAAAACAAAAAACAAAATGA	257277	89473	TAGGAACGTCAGAAGCAGCA
168104	300	CAGGTCCCTTTCCAGGCCGC	212691	44887	AAAAAACAAAAAACAAAATG	257278	89474	CTAGGAACGTCAGAAGCAGC
168105	301	TCAGGTCCCTTTCCAGGCCG	212692	44888	AAAAAAACAAAAAACAAAAT	257279	89475	CCTAGGAACGTCAGAAGCAG
168106	302	CTCAGGTCCCTTTCCAGGCC	212693	44889	CAAAAAAACAAAAAACAAAA	257280	89476	TCCTAGGAACGTCAGAAGCA
168107	303	GCTCAGGTCCCTTTCCAGGC	212694	44890	GCAAAAAAACAAAAAACAAA	257281	89477	GTCCTAGGAACGTCAGAAGC
168108	304	TGCTCAGGTCCCTTTCCAGG	212695	44891	GGCAAAAAAACAAAAAACAA	257282	89478	CGTCCTAGGAACGTCAGAAG
168109	305	TTGCTCAGGTCCCTTTCCAG	212696	44892	AGGCAAAAAAACAAAAAACA	257283	89479	GCGTCCTAGGAACGTCAGAA
168110	306	CTTGCTCAGGTCCCTTTCCA	212697	44893	TAGGCAAAAAAACAAAAAAC	257284	89480	GGCGTCCTAGGAACGTCAGA
168111	307	CCTTGCTCAGGTCCCTTTCC	212698	44894	CTAGGCAAAAAAACAAAAAA	257285	89481	TGGCGTCCTAGGAACGTCAG
168112	308	CCCTTGCTCAGGTCCCTTTC	212699	44895	GCTAGGCAAAAAAACAAAAA	257286	89482	GTGGCGTCCTAGGAACGTCA
168113	309	TCCCTTGCTCAGGTCCCTTT	212700	44896	TGCTAGGCAAAAAAACAAAA	257287	89483	AGTGGCGTCCTAGGAACGTC
168114	310	ATCCCTTGCTCAGGTCCCTT	212701	44897	GTGCTAGGCAAAAAAACAAA	257288	89484	TAGTGGCGTCCTAGGAACGT
168115	311	CATCCCTTGCTCAGGTCCCT	212702	44898	TGTGCTAGGCAAAAAAACAA	257289	89485	TTAGTGGCGTCCTAGGAACG
168116	312	GCATCCCTTGCTCAGGTCCC	212703	44899	ATGTGCTAGGCAAAAAAACA	257290	89486	TTTAGTGGCGTCCTAGGAAC
168117	313	TGCATCCCTTGCTCAGGTCC	212704	44900	CATGTGCTAGGCAAAAAAAC	257291	89487	ATTTAGTGGCGTCCTAGGAA
168118	314	GTGCATCCCTTGCTCAGGTC	212705	44901	GCATGTGCTAGGCAAAAAAA	257292	89488	GATTTAGTGGCGTCCTAGGA
168119	315	CGTGCATCCCTTGCTCAGGT	212706	44902	GGCATGTGCTAGGCAAAAAA	257293	89489	CGATTTAGTGGCGTCCTAGG
168120	316	GCGTGCATCCCTTGCTCAGG	212707	44903	AGGCATGTGCTAGGCAAAAA	257294	89490	TCGATTTAGTGGCGTCCTAG
168121	317	TGCGTGCATCCCTTGCTCAG	212708	44904	CAGGCATGTGCTAGGCAAAA	257295	89491	GTCGATTTAGTGGCGTCCTA
168122	318	GTGCGTGCATCCCTTGCTCA	212709	44905	ACAGGCATGTGCTAGGCAAA	257296	89492	TGTCGATTTAGTGGCGTCCT
168123	319	CGTGCGTGCATCCCTTGCTC	212710	44906	TACAGGCATGTGCTAGGCAA	257297	89493	GTGTCGATTTAGTGGCGTCC
168124	320	GCGTGCGTGCATCCCTTGCT	212711	44907	TTACAGGCATGTGCTAGGCA	257298	89494	GGTGTCGATTTAGTGGCGTC
168125	321	CGCGTGCGTGCATCCCTTGC	212712	44908	TTTACAGGCATGTGCTAGGC	257299	89495	AGGTGTCGATTTAGTGGCGT
168126	322	ACGCGTGCGTGCATCCCTTG	212713	44909	ATTTACAGGCATGTGCTAGG	257300	89496	CAGGTGTCGATTTAGTGGCG
168127	323	CACGCGTGCGTGCATCCCTT	212714	44910	GATTTACAGGCATGTGCTAG	257301	89497	CCAGGTGTCGATTTAGTGGC
168128	324	TCACGCGTGCGTGCATCCCT	212715	44911	TGATTTACAGGCATGTGCTA	257302	89498	CCCAGGTGTCGATTTAGTGG
168129	325	CTCACGCGTGCGTGCATCCC	212716	44912	GTGATTTACAGGCATGTGCT	257303	89499	ACCCAGGTGTCGATTTAGTG
168130	326	ACTCACGCGTGCGTGCATCC	212717	44913	AGTGATTTACAGGCATGTGC	257304	89500	CACCCAGGTGTCGATTTAGT
168131	327	CACTCACGCGTGCGTGCATC	212718	44914	CAGTGATTTACAGGCATGTG	257305	89501	GCACCCAGGTGTCGATTTAG
168132	328	GCACTCACGCGTGCGTGCAT	212719	44915	CCAGTGATTTACAGGCATGT	257306	89502	TGCACCCAGGTGTCGATTTA
168133	329	CGCACTCACGCGTGCGTGCA	212720	44916	TCCAGTGATTTACAGGCATG	257307	89503	CTGCACCCAGGTGTCGATTT
168134	330	GCGCACTCACGCGTGCGTGC	212721	44917	ATCCAGTGATTTACAGGCAT	257308	89504	GCTGCACCCAGGTGTCGATT
168135	331	CGCGCACTCACGCGTGCGTG	212722	44918	AATCCAGTGATTTACAGGCA	257309	89505	AGCTGCACCCAGGTGTCGAT
168136	332	GCGCGCACTCACGCGTGCGT	212723	44919	CAATCCAGTGATTTACAGGC	257310	89506	CAGCTGCACCCAGGTGTCGA
168137	333	CGCGCGCACTCACGCGTGCG	212724	44920	TCAATCCAGTGATTTACAGG	257311	89507	GCAGCTGCACCCAGGTGTCG
168138	334	ACGCGCGCACTCACGCGTGC	212725	44921	CTCAATCCAGTGATTTACAG	257312	89508	AGCAGCTGCACCCAGGTGTC
168139	335	CACGCGCGCACTCACGCGTG	212726	44922	CCTCAATCCAGTGATTTACA	257313	89509	GAGCAGCTGCACCCAGGTGT
168140	336	ACACGCGCGCACTCACGCGT	212727	44923	ACCTCAATCCAGTGATTTAC	257314	89510	GGAGCAGCTGCACCCAGGTG
168141	337	CACACGCGCGCACTCACGCG	212728	44924	CACCTCAATCCAGTGATTTA	257315	89511	TGGAGCAGCTGCACCCAGGT
168142	338	ACACACGCGCGCACTCACGC	212729	44925	ACACCTCAATCCAGTGATTT	257316	89512	GTGGAGCAGCTGCACCCAGG
168143	339	CACACACGCGCGCACTCACG	212730	44926	AACACCTCAATCCAGTGATT	257317	89513	AGTGGAGCAGCTGCACCCAG
168144	340	ACACACACGCGCGCACTCAC	212731	44927	AAACACCTCAATCCAGTGAT	257318	89514	GAGTGGAGCAGCTGCACCCA
168145	341	CACACACACGCGCGCACTCA	212732	44928	TAAACACCTCAATCCAGTGA	257319	89515	GGAGTGGAGCAGCTGCACCC
168146	342	ACACACACACGCGCGCACTC	212733	44929	CTAAACACCTCAATCCAGTG	257320	89516	GGGAGTGGAGCAGCTGCACC
168147	343	CACACACACACGCGCGCACT	212734	44930	TCTAAACACCTCAATCCAGT	257321	89517	AGGGAGTGGAGCAGCTGCAC
168148	344	GCACACACACACGCGCGCAC	212735	44931	ATCTAAACACCTCAATCCAG	257322	89518	GAGGGAGTGGAGCAGCTGCA
168149	345	AGCACACACACACGCGCGCA	212736	44932	CATCTAAACACCTCAATCCA	257323	89519	CGAGGGAGTGGAGCAGCTGC
168150	346	CAGCACACACACACGCGCGC	212737	44933	ACATCTAAACACCTCAATCC	257324	89520	CCGAGGGAGTGGAGCAGCTG
168151	347	CCAGCACACACACACGCGCG	212738	44934	AACATCTAAACACCTCAATC	257325	89521	GCCGAGGGAGTGGAGCAGCT
168152	348	TCCAGCACACACACACGCGC	212739	44935	AAACATCTAAACACCTCAAT	257326	89522	GGCCGAGGGAGTGGAGCAGC
168153	349	CTCCAGCACACACACACGCG	212740	44936	CAAACATCTAAACACCTCAA	257327	89523	AGGCCGAGGGAGTGGAGCAG
168154	350	CCTCCAGCACACACACACGC	212741	44937	ACAAACATCTAAACACCTCA	257328	89524	GAGGCCGAGGGAGTGGAGCA
168155	351	CCCTCCAGCACACACACACG	212742	44938	AACAAACATCTAAACACCTC	257329	89525	GGAGGCCGAGGGAGTGGAGC
168156	352	ACCCTCCAGCACACACACAC	212743	44939	CAACAAACATCTAAACACCT	257330	89526	AGGAGGCCGAGGGAGTGGAG
168157	353	GACCCTCCAGCACACACACA	212744	44940	ACAACAAACATCTAAACACC	257331	89527	GAGGAGGCCGAGGGAGTGGA
168158	354	AGACCCTCCAGCACACACAC	212745	44941	GACAACAAACATCTAAACAC	257332	89528	GGAGGAGGCCGAGGGAGTGG
168159	355	AAGACCCTCCAGCACACACA	212746	44942	GGACAACAAACATCTAAACA	257333	89529	GGGAGGAGGCCGAGGGAGTG
168160	356	GAAGACCCTCCAGCACACAC	212747	44943	AGGACAACAAACATCTAAAC	257334	89530	CGGGAGGAGGCCGAGGGAGT
168161	357	TGAAGACCCTCCAGCACACA	212748	44944	AAGGACAACAAACATCTAAA	257335	89531	ACGGGAGGAGGCCGAGGGAG
168162	358	GTGAAGACCCTCCAGCACAC	212749	44945	AAAGGACAACAAACATCTAA	257336	89532	CACGGGAGGAGGCCGAGGGA

168163	359	GGTGAAGACCCTCCAGCACA	212750	44946	CAAAGGACAACAAACATCTA	257337	89533	GCACGGGAGGAGGCCGAGGG
168164	360	TGGTGAAGACCCTCCAGCAC	212751	44947	CCAAAGGACAACAAACATCT	257338	89534	AGCACGGGAGGAGGCCGAGG
168165	361	GTGGTGAAGACCCTCCAGCA	212752	44948	TCCAAAGGACAACAAACATC	257339	89535	GAGCACGGGAGGAGGCCGAG
168166	362	GGTGGTGAAGACCCTCCAGC	212753	44949	ATCCAAAGGACAACAAACAT	257340	89536	TGAGCACGGGAGGAGGCCGA
168167	363	TGGTGGTGAAGACCCTCCAG	212754	44950	CATCCAAAGGACAACAAACA	257341	89537	CTGAGCACGGGAGGAGGCCG
168168	364	CTGGTGGTGAAGACCCTCCA	212755	44951	GCATCCAAAGGACAACAAAC	257342	89538	CCTGAGCACGGGAGGAGGCC
168169	365	TCTGGTGGTGAAGACCCTCC	212756	44952	AGCATCCAAAGGACAACAAA	257343	89539	GCCTGAGCACGGGAGGAGGC
168170	366	ATCTGGTGGTGAAGACCCTC	212757	44953	AAGCATCCAAAGGACAACAA	257344	89540	AGCCTGAGCACGGGAGGAGG
168171	367	AATCTGGTGGTGAAGACCCT	212758	44954	GAAGCATCCAAAGGACAACA	257345	89541	CAGCCTGAGCACGGGAGGAG
168172	368	GAATCTGGTGGTGAAGACCC	212759	44955	AGAAGCATCCAAAGGACAAC	257346	89542	ACAGCCTGAGCACGGGAGGA
168173	369	CGAATCTGGTGGTGAAGACC	212760	44956	AAGAAGCATCCAAAGGACAA	257347	89543	CACAGCCTGAGCACGGGAGG
168174	370	GCGAATCTGGTGGTGAAGAC	212761	44957	TAAGAAGCATCCAAAGGACA	257348	89544	CCACAGCCTGAGCACGGGAG
168175	371	CGCGAATCTGGTGGTGAAGA	212762	44958	ATAAGAAGCATCCAAAGGAC	257349	89545	GCCACAGCCTGAGCACGGGA
168176	372	GCGCGAATCTGGTGGTGAAG	212763	44959	TATAAGAAGCATCCAAAGGA	257350	89546	GGCCACAGCCTGAGCACGGG
168177	373	TGCGCGAATCTGGTGGTGAA	212764	44960	TTATAAGAAGCATCCAAAGG	257351	89547	CGGCCACAGCCTGAGCACGG
168178	374	CTGCGCGAATCTGGTGGTGA	212765	44961	TTTATAAGAAGCATCCAAAG	257352	89548	GCGGCCACAGCCTGAGCACG
168179	375	TCTGCGCGAATCTGGTGGTG	212766	44962	ATTTATAAGAAGCATCCAAA	257353	89549	TGCGGCCACAGCCTGAGCAC
168180	376	GTCTGCGCGAATCTGGTGGT	212767	44963	GATTTATAAGAAGCATCCAA	257354	89550	GTGCGGCCACAGCCTGAGCA
168181	377	GGTCTGCGCGAATCTGGTGG	212768	44964	GGATTTATAAGAAGCATCCA	257355	89551	CGTGCGGCCACAGCCTGAGC
168182	378	GGGTCTGCGCGAATCTGGTG	212769	44965	TGGATTTATAAGAAGCATCC	257356	89552	GCGTGCGGCCACAGCCTGAG
168183	379	GGGGTCTGCGCGAATCTGGT	212770	44966	ATGGATTTATAAGAAGCATC	257357	89553	CGCGTGCGGCCACAGCCTGA
168184	380	TGGGGTCTGCGCGAATCTGG	212771	44967	TATGGATTTATAAGAAGCAT	257358	89554	GCGCGTGCGGCCACAGCCTG
168185	381	CTGGGGTCTGCGCGAATCTG	212772	44968	ATATGGATTTATAAGAAGCA	257359	89555	GGCGCGTGCGGCCACAGCCT
168186	382	CCTGGGGTCTGCGCGAATCT	212773	44969	AATATGGATTTATAAGAAGC	257360	89556	GGGCGCGTGCGGCCACAGCC
168187	383	ACCTGGGGTCTGCGCGAATC	212774	44970	AAATATGGATTTATAAGAAG	257361	89557	GGGGCGCGTGCGGCCACAGC
168188	384	CACCTGGGGTCTGCGCGAAT	212775	44971	GAAATATGGATTTATAAGAA	257362	89558	AGGGGCGCGTGCGGCCACAG
168189	385	CCACCTGGGGTCTGCGCGAA	212776	44972	TGAAATATGGATTTATAAGA	257363	89559	GAGGGGCGCGTGCGGCCACA
168190	386	TCCACCTGGGGTCTGCGCGA	212777	44973	ATGAAATATGGATTTATAAG	257364	89560	TGAGGGGCGCGTGCGGCCAC
168191	387	CTCCACCTGGGGTCTGCGCG	212778	44974	CATGAAATATGGATTTATAA	257365	89561	GTGAGGGGCGCGTGCGGCCA
168192	388	CCTCCACCTGGGGTCTGCGC	212779	44975	CCATGAAATATGGATTTATA	257366	89562	CGTGAGGGGCGCGTGCGGCC
168193	389	GCCTCCACCTGGGGTCTGCG	212780	44976	GCCATGAAATATGGATTTAT	257367	89563	GCGTGAGGGGCGCGTGCGGC
168194	390	AGCCTCCACCTGGGGTCTGC	212781	44977	AGCCATGAAATATGGATTTA	257368	89564	AGCGTGAGGGGCGCGTGCGG
168195	391	CAGCCTCCACCTGGGGTCTG	212782	44978	GAGCCATGAAATATGGATTT	257369	89565	AAGCGTGAGGGGCGCGTGCG
168196	392	ACAGCCTCCACCTGGGGTCT	212783	44979	GGAGCCATGAAATATGGATT	257370	89566	CAAGCGTGAGGGGCGCGTGC
168197	393	CACAGCCTCCACCTGGGGTC	212784	44980	GGGAGCCATGAAATATGGAT	257371	89567	GCAAGCGTGAGGGGCGCGTG
168198	394	GCACAGCCTCCACCTGGGGT	212785	44981	AGGGAGCCATGAAATATGGA	257372	89568	GGCAAGCGTGAGGGGCGCGT
168199	395	GGCACAGCCTCCACCTGGGG	212786	44982	CAGGGAGCCATGAAATATGG	257373	89569	GGGCAAGCGTGAGGGGCGCG
168200	396	CGGCACAGCCTCCACCTGGG	212787	44983	CCAGGGAGCCATGAAATATG	257374	89570	CGGGCAAGCGTGAGGGGCGC
168201	397	CCGGCACAGCCTCCACCTGG	212788	44984	TCCAGGGAGCCATGAAATAT	257375	89571	GCGGGCAAGCGTGAGGGGCG
168202	398	GCCGGCACAGCCTCCACCTG	212789	44985	TTCCAGGGAGCCATGAAATA	257376	89572	GGCGGGCAAGCGTGAGGGGC
168203	399	TGCCGGCACAGCCTCCACCT	212790	44986	TTTCCAGGGAGCCATGAAAT	257377	89573	TGGCGGGCAAGCGTGAGGGG
168204	400	CTGCCGGCACAGCCTCCACC	212791	44987	CTTTCCAGGGAGCCATGAAA	257378	89574	GTGGCGGGCAAGCGTGAGGG
168205	401	CCTGCCGGCACAGCCTCCAC	212792	44988	ACTTTCCAGGGAGCCATGAA	257379	89575	AGTGGCGGGCAAGCGTGAGG
168206	402	CCCTGCCGGCACAGCCTCCA	212793	44989	CACTTTCCAGGGAGCCATGA	257380	89576	GAGTGGCGGGCAAGCGTGAG
168207	403	ACCCTGCCGGCACAGCCTCC	212794	44990	GCACTTTCCAGGGAGCCATG	257381	89577	AGAGTGGCGGGCAAGCGTGA
168208	404	CACCCTGCCGGCACAGCCTC	212795	44991	AGCACTTTCCAGGGAGCCAT	257382	89578	CAGAGTGGCGGGCAAGCGTG
168209	405	CCACCCTGCCGGCACAGCCT	212796	44992	TAGCACTTTCCAGGGAGCCA	257383	89579	GCAGAGTGGCGGGCAAGCGT
168210	406	CCCACCCTGCCGGCACAGCC	212797	44993	ATAGCACTTTCCAGGGAGCC	257384	89580	TGCAGAGTGGCGGGCAAGCG
168211	407	CCCCACCCTGCCGGCACAGC	212798	44994	CATAGCACTTTCCAGGGAGC	257385	89581	ATGCAGAGTGGCGGGCAAGC
168212	408	GCCCCACCCTGCCGGCACAG	212799	44995	GCATAGCACTTTCCAGGGAG	257386	89582	CATGCAGAGTGGCGGGCAAG
168213	409	CGCCCCACCCTGCCGGCACA	212800	44996	TGCATAGCACTTTCCAGGGA	257387	89583	ACATGCAGAGTGGCGGGCAA
168214	410	GCGCCCCACCCTGCCGGCAC	212801	44997	TTGCATAGCACTTTCCAGGG	257388	89584	GACATGCAGAGTGGCGGGCA
168215	411	CGCGCCCCACCCTGCCGGCA	212802	44998	TTTGCATAGCACTTTCCAGG	257389	89585	TGACATGCAGAGTGGCGGGC
168216	412	CCGCGCCCCACCCTGCCGGC	212803	44999	ATTTGCATAGCACTTTCCAG	257390	89586	GTGACATGCAGAGTGGCGGG
168217	413	GCCGCGCCCCACCCTGCCGG	212804	45000	CATTTGCATAGCACTTTCCA	257391	89587	GGTGACATGCAGAGTGGCGG
168218	414	CGCCGCGCCCCACCCTGCCG	212805	45001	TCATTTGCATAGCACTTTCC	257392	89588	TGGTGACATGCAGAGTGGCG
168219	415	CCGCCGCGCCCCACCCTGCC	212806	45002	ATCATTTGCATAGCACTTTC	257393	89589	CTGGTGACATGCAGAGTGGC
168220	416	GCCGCCGCGCCCCACCCTGC	212807	45003	TATCATTTGCATAGCACTTT	257394	89590	GCTGGTGACATGCAGAGTGG
168221	417	CGCCGCCGCGCCCCACCCTG	212808	45004	TTATCATTTGCATAGCACTT	257395	89591	TGCTGGTGACATGCAGAGTG
168222	418	CCGCCGCCGCGCCCCACCCT	212809	45005	CTTATCATTTGCATAGCACT	257396	89592	GTGCTGGTGACATGCAGAGT
168223	419	ACCGCCGCCGCGCCCCACCC	212810	45006	GCTTATCATTTGCATAGCAC	257397	89593	GGTGCTGGTGACATGCAGAG
168224	420	CACCGCCGCCGCGCCCCACC	212811	45007	AGCTTATCATTTGCATAGCA	257398	89594	GGGTGCTGGTGACATGCAGA
168225	421	TCACCGCCGCCGCGCCCCAC	212812	45008	CAGCTTATCATTTGCATAGC	257399	89595	GGGGTGCTGGTGACATGCAG
168226	422	GTCACCGCCGCCGCGCCCCA	212813	45009	GCAGCTTATCATTTGCATAG	257400	89596	GGGGGTGCTGGTGACATGCA
168227	423	AGTCACCGCCGCCGCGCCCC	212814	45010	TGCAGCTTATCATTTGCATA	257401	89597	CGGGGGTGCTGGTGACATGC
168228	424	AAGTCACCGCCGCCGCGCCC	212815	45011	TTGCAGCTTATCATTTGCAT	257402	89598	GCGGGGGTGCTGGTGACATG
168229	425	CAAGTCACCGCCGCCGCGCC	212816	45012	CTTGCAGCTTATCATTTGCA	257403	89599	AGCGGGGGTGCTGGTGACAT
168230	426	CCAAGTCACCGCCGCCGCGC	212817	45013	CCTTGCAGCTTATCATTTGC	257404	89600	GAGCGGGGGTGCTGGTGACA
168231	427	CCCAAGTCACCGCCGCCGCG	212818	45014	TCCTTGCAGCTTATCATTTG	257405	89601	GGAGCGGGGGTGCTGGTGAC
168232	428	CCCCAAGTCACCGCCGCCGC	212819	45015	ATCCTTGCAGCTTATCATTT	257406	89602	CGGAGCGGGGGTGCTGGTGA
168233	429	CCCCCAAGTCACCGCCGCCG	212820	45016	CATCCTTGCAGCTTATCATT	257407	89603	ACGGAGCGGGGGTGCTGGTG
168234	430	TCCCCCAAGTCACCGCCGCC	212821	45017	CCATCCTTGCAGCTTATCAT	257408	89604	CACGGAGCGGGGGTGCTGGT

168235	431	CTCCCCCAAGTCACCGCCGC	212822	45018	TCCATCCTTGCAGCTTATCA	257409	89605	GCACGGAGCGGGGGTGCTGG
168236	432	CCTCCCCCAAGTCACCGCCG	212823	45019	TTCCATCCTTGCAGCTTATC	257410	89606	AGCACGGAGCGGGGGTGCTG
168237	433	CCCTCCCCCAAGTCACCGCC	212824	45020	TTTCCATCCTTGCAGCTTAT	257411	89607	TAGCACGGAGCGGGGGTGCT
168238	434	CCCCTCCCCCAAGTCACCGC	212825	45021	CTTTCCATCCTTGCAGCTTA	257412	89608	GTAGCACGGAGCGGGGGTGC
168239	435	CCCCCTCCCCCAAGTCACCG	212826	45022	CCTTTCCATCCTTGCAGCTT	257413	89609	GGTAGCACGGAGCGGGGGTG
168240	436	GCCCCCTCCCCCAAGTCACC	212827	45023	TCCTTTCCATCCTTGCAGCT	257414	89610	GGGTAGCACGGAGCGGGGGT
168241	437	AGCCCCCTCCCCCAAGTCAC	212828	45024	TTCCTTTCCATCCTTGCAGC	257415	89611	TGGGTAGCACGGAGCGGGGG
168242	438	CAGCCCCCTCCCCCAAGTCA	212829	45025	TTTCCTTTCCATCCTTGCAG	257416	89612	GTGGGTAGCACGGAGCGGGG
168243	439	GCAGCCCCCTCCCCCAAGTC	212830	45026	ATTTCCTTTCCATCCTTGCA	257417	89613	GGTGGGTAGCACGGAGCGGG
168244	440	GGCAGCCCCCTCCCCCAAGT	212831	45027	AATTTCCTTTCCATCCTTGC	257418	89614	AGGTGGGTAGCACGGAGCGG
168245	441	GGGCAGCCCCCTCCCCCAAG	212832	45028	CAATTTCCTTTCCATCCTTG	257419	89615	AAGGTGGGTAGCACGGAGCG
168246	442	AGGGCAGCCCCCTCCCCCAA	212833	45029	GCAATTTCCTTTCCATCCTT	257420	89616	CAAGGTGGGTAGCACGGAGC
168247	443	AAGGGCAGCCCCCTCCCCCA	212834	45030	TGCAATTTCCTTTCCATCCT	257421	89617	ACAAGGTGGGTAGCACGGAG
168248	444	GAAGGGCAGCCCCCTCCCCC	212835	45031	CTGCAATTTCCTTTCCATCC	257422	89618	AACAAGGTGGGTAGCACGGA
168249	445	TGAAGGGCAGCCCCCTCCCC	212836	45032	ACTGCAATTTCCTTTCCATC	257423	89619	AAACAAGGTGGGTAGCACGG
168250	446	GTGAAGGGCAGCCCCCTCCC	212837	45033	CACTGCAATTTCCTTTCCAT	257424	89620	CAAACAAGGTGGGTAGCACG
168251	447	AGTGAAGGGCAGCCCCCTCC	212838	45034	GCACTGCAATTTCCTTTCCA	257425	89621	TCAAACAAGGTGGGTAGCAC
168252	448	GAGTGAAGGGCAGCCCCCTC	212839	45035	AGCACTGCAATTTCCTTTCC	257426	89622	GTCAAACAAGGTGGGTAGCA
168253	449	AGAGTGAAGGGCAGCCCCCT	212840	45036	GAGCACTGCAATTTCCTTTC	257427	89623	AGTCAAACAAGGTGGGTAGC
168254	450	GAGAGTGAAGGGCAGCCCCC	212841	45037	GGAGCACTGCAATTTCCTTT	257428	89624	GAGTCAAACAAGGTGGGTAG
168255	451	CGAGAGTGAAGGGCAGCCCC	212842	45038	AGGAGCACTGCAATTTCCTT	257429	89625	AGAGTCAAACAAGGTGGGTA
168256	452	TCGAGAGTGAAGGGCAGCCC	212843	45039	CAGGAGCACTGCAATTTCCT	257430	89626	GAGAGTCAAACAAGGTGGGT
168257	453	GTCGAGAGTGAAGGGCAGCC	212844	45040	TCAGGAGCACTGCAATTTCC	257431	89627	AGAGAGTCAAACAAGGTGGG
168258	454	AGTCGAGAGTGAAGGGCAGC	212845	45041	TTCAGGAGCACTGCAATTTC	257432	89628	CAGAGAGTCAAACAAGGTGG
168259	455	CAGTCGAGAGTGAAGGGCAG	212846	45042	ATTCAGGAGCACTGCAATTT	257433	89629	CCAGAGAGTCAAACAAGGTG
168260	456	GCAGTCGAGAGTGAAGGGCA	212847	45043	AATTCAGGAGCACTGCAATT	257434	89630	GCCAGAGAGTCAAACAAGGT
168261	457	TGCAGTCGAGAGTGAAGGGC	212848	45044	CAATTCAGGAGCACTGCAAT	257435	89631	GGCCAGAGAGTCAAACAAGG
168262	458	CTGCAGTCGAGAGTGAAGGG	212849	45045	ACAATTCAGGAGCACTGCAA	257436	89632	TGGCCAGAGAGTCAAACAAG
168263	459	GCTGCAGTCGAGAGTGAAGG	212850	45046	TACAATTCAGGAGCACTGCA	257437	89633	GTGGCCAGAGAGTCAAACAA
168264	460	GGCTGCAGTCGAGAGTGAAG	212851	45047	TTACAATTCAGGAGCACTGC	257438	89634	AGTGGCCAGAGAGTCAAACA
168265	461	AGGCTGCAGTCGAGAGTGAA	212852	45048	TTTACAATTCAGGAGCACTG	257439	89635	AAGTGGCCAGAGAGTCAAAC
168266	462	AAGGCTGCAGTCGAGAGTGA	212853	45049	ATTTACAATTCAGGAGCACT	257440	89636	CAAGTGGCCAGAGAGTCAAA
168267	463	AAAGGCTGCAGTCGAGAGTG	212854	45050	CATTTACAATTCAGGAGCAC	257441	89637	TCAAGTGGCCAGAGAGTCAA
168268	464	AAAAGGCTGCAGTCGAGAGT	212855	45051	CCATTTACAATTCAGGAGCA	257442	89638	ATCAAGTGGCCAGAGAGTCA
168269	465	CAAAAGGCTGCAGTCGAGAG	212856	45052	CCCATTTACAATTCAGGAGC	257443	89639	AATCAAGTGGCCAGAGAGTC
168270	466	GCAAAAGGCTGCAGTCGAGA	212857	45053	GCCCATTTACAATTCAGGAG	257444	89640	AAATCAAGTGGCCAGAGAGT
168271	467	GGCAAAAGGCTGCAGTCGAG	212858	45054	AGCCCATTTACAATTCAGGA	257445	89641	CAAATCAAGTGGCCAGAGAG
168272	468	CGGCAAAAGGCTGCAGTCGA	212859	45055	AAGCCCATTTACAATTCAGG	257446	89642	ACAAATCAAGTGGCCAGAGA
168273	469	GCGGCAAAAGGCTGCAGTCG	212860	45056	AAAGCCCATTTACAATTCAG	257447	89643	GACAAATCAAGTGGCCAGAG
168274	470	TGCGGCAAAAGGCTGCAGTC	212861	45057	AAAAGCCCATTTACAATTCA	257448	89644	GGACAAATCAAGTGGCCAGA
168275	471	TTGCGGCAAAAGGCTGCAGT	212862	45058	TAAAAGCCCATTTACAATTC	257449	89645	TGGACAAATCAAGTGGCCAG
168276	472	ATTGCGGCAAAAGGCTGCAG	212863	45059	GTAAAAGCCCATTTACAATT	257450	89646	GTGGACAAATCAAGTGGCCA
168277	473	CATTGCGGCAAAAGGCTGCA	212864	45060	CGTAAAAGCCCATTTACAAT	257451	89647	TGTGGACAAATCAAGTGGCC
168278	474	CCATTGCGGCAAAAGGCTGC	212865	45061	TCGTAAAAGCCCATTTACAA	257452	89648	TTGTGGACAAATCAAGTGGC
168279	475	CCCATTGCGGCAAAAGGCTG	212866	45062	CTCGTAAAAGCCCATTTACA	257453	89649	GTTGTGGACAAATCAAGTGG
168280	476	GCCCATTGCGGCAAAAGGCT	212867	45063	CCTCGTAAAAGCCCATTTAC	257454	89650	CGTTGTGGACAAATCAAGTG
168281	477	CGCCCATTGCGGCAAAAGGC	212868	45064	TCCTCGTAAAAGCCCATTTA	257455	89651	CCGTTGTGGACAAATCAAGT
168282	478	ACGCCCATTGCGGCAAAAGG	212869	45065	CTCCTCGTAAAAGCCCATTT	257456	89652	GCCGTTGTGGACAAATCAAG
168283	479	CACGCCCATTGCGGCAAAAG	212870	45066	CCTCCTCGTAAAAGCCCATT	257457	89653	GGCCGTTGTGGACAAATCAA
168284	480	ACACGCCCATTGCGGCAAAA	212871	45067	ACCTCCTCGTAAAAGCCCAT	257458	89654	GGGCCGTTGTGGACAAATCA
168285	481	CACACGCCCATTGCGGCAAA	212872	45068	AACCTCCTCGTAAAAGCCCA	257459	89655	TGGGCCGTTGTGGACAAATC
168286	482	ACACACGCCCATTGCGGCAA	212873	45069	AAACCTCCTCGTAAAAGCCC	257460	89656	ATGGGCCGTTGTGGACAAAT
168287	483	CACACACGCCCATTGCGGCA	212874	45070	GAAACCTCCTCGTAAAAGCC	257461	89657	GATGGGCCGTTGTGGACAAA
168288	484	ACACACACGCCCATTGCGGC	212875	45071	AGAAACCTCCTCGTAAAAGC	257462	89658	TGATGGGCCGTTGTGGACAA
168289	485	CACACACACGCCCATTGCGG	212876	45072	TAGAAACCTCCTCGTAAAAG	257463	89659	CTGATGGGCCGTTGTGGACA
168290	486	ACACACACACGCCCATTGCG	212877	45073	TTAGAAACCTCCTCGTAAAA	257464	89660	GCTGATGGGCCGTTGTGGAC
168291	487	CACACACACACGCCCATTGC	212878	45074	ATTAGAAACCTCCTCGTAAA	257465	89661	GGCTGATGGGCCGTTGTGGA
168292	488	ACACACACACACGCCCATTG	212879	45075	AATTAGAAACCTCCTCGTAA	257466	89662	GGGCTGATGGGCCGTTGTGG
168293	489	CACACACACACACGCCCATT	212880	45076	TAATTAGAAACCTCCTCGTA	257467	89663	TGGGCTGATGGGCCGTTGTG
168294	490	ACACACACACACACGCCCAT	212881	45077	GTAATTAGAAACCTCCTCGT	257468	89664	GTGGGCTGATGGGCCGTTGT
168295	491	CACACACACACACACGCCCA	212882	45078	AGTAATTAGAAACCTCCTCG	257469	89665	TGTGGGCTGATGGGCCGTTG
168296	492	ACACACACACACACACGCCC	212883	45079	GAGTAATTAGAAACCTCCTC	257470	89666	CTGTGGGCTGATGGGCCGTT
168297	493	CACACACACACACACACGCC	212884	45080	CGAGTAATTAGAAACCTCCT	257471	89667	CCTGTGGGCTGATGGGCCGT
168298	494	ACACACACACACACACACGC	212885	45081	GCGAGTAATTAGAAACCTCC	257472	89668	TCCTGTGGGCTGATGGGCCG
168299	495	CACACACACACACACACACG	212886	45082	AGCGAGTAATTAGAAACCTC	257473	89669	CTCCTGTGGGCTGATGGGCC
168300	496	ACACACACACACACACACAC	212887	45083	GAGCGAGTAATTAGAAACCT	257474	89670	CCTCCTGTGGGCTGATGGGC
168301	497	CACACACACACACACACACA	212888	45084	AGAGCGAGTAATTAGAAACC	257475	89671	ACCTCCTGTGGGCTGATGGG
168302	498	ACACACACACACACACACAC	212889	45085	AAGAGCGAGTAATTAGAAAC	257476	89672	AACCTCCTGTGGGCTGATGG
168303	499	CACACACACACACACACACA	212890	45086	AAAGAGCGAGTAATTAGAAA	257477	89673	AAACCTCCTGTGGGCTGATG
168304	500	ACACACACACACACACACAC	212891	45087	GAAAGAGCGAGTAATTAGAA	257478	89674	CAAACCTCCTGTGGGCTGAT
168305	501	CACACACACACACACACACA	212892	45088	AGAAAGAGCGAGTAATTAGA	257479	89675	CCAAACCTCCTGTGGGCTGA
168306	502	ACACACACACACACACACAC	212893	45089	GAGAAAGAGCGAGTAATTAG	257480	89676	ACCAAACCTCCTGTGGGCTG

168307	503	CACACACACACACACACA	212894	45090	AGAGAAAGAGCGAGTAATTA	257481	89677	CACCAAACCTCCTGTGGGCT
168308	504	ACACACACACACACACAC	212895	45091	AAGAGAAAGAGCGAGTAATT	257482	89678	CCACCAAACCTCCTGTGGGC
168309	505	CACACACACACACACACA	212896	45092	CAAGAGAAAGAGCGAGTAAT	257483	89679	CCCACCAAACCTCCTGTGGG
168310	506	ACACACACACACACACAC	212897	45093	TCAAGAGAAAGAGCGAGTAA	257484	89680	ACCCACCAAACCTCCTGTGG
168311	507	CACACACACACACACACA	212898	45094	TTCAAGAGAAAGAGCGAGTA	257485	89681	CACCCACCAAACCTCCTGTG
168312	508	ACACACACACACACACAC	212899	45095	GTTCAAGAGAAAGAGCGAGT	257486	89682	GCACCCACCAAACCTCCTGT
168313	509	CACACACACACACACACA	212900	45096	AGTTCAAGAGAAAGAGCGAG	257487	89683	GGCACCCACCAAACCTCCTG
168314	510	ACACACACACACACACAC	212901	45097	CAGTTCAAGAGAAAGAGCGA	257488	89684	AGGCACCCACCAAACCTCCT
168315	511	CACACACACACACACACA	212902	45098	TCAGTTCAAGAGAAAGAGCG	257489	89685	AAGGCACCCACCAAACCTCC
168316	512	ACACACACACACACACAC	212903	45099	CTCAGTTCAAGAGAAAGAGC	257490	89686	GAAGGCACCCACCAAACCTC
168317	513	CACACACACACACACACA	212904	45100	CCTCAGTTCAAGAGAAAGAG	257491	89687	GGAAGGCACCCACCAAACCT
168318	514	ACACACACACACACACAC	212905	45101	TCCTCAGTTCAAGAGAAAGA	257492	89688	TGGAAGGCACCCACCAAACC
168319	515	CACACACACACACACACA	212906	45102	CTCCTCAGTTCAAGAGAAAG	257493	89689	GTGGAAGGCACCCACCAAAC
168320	516	ACACACACACACACACAC	212907	45103	ACTCCTCAGTTCAAGAGAAA	257494	89690	GGTGGAAGGCACCCACCAAA
168321	517	CACACACACACACACACA	212908	45104	AACTCCTCAGTTCAAGAGAA	257495	89691	CGGTGGAAGGCACCCACCAA
168322	518	ACACACACACACACACAC	212909	45105	CAACTCCTCAGTTCAAGAGA	257496	89692	TCGGTGGAAGGCACCCACCA
168323	519	CACACACACACACACACA	212910	45106	TCAACTCCTCAGTTCAAGAG	257497	89693	GTCGGTGGAAGGCACCCACC
168324	520	CCACACACACACACACAC	212911	45107	TTCAACTCCTCAGTTCAAGA	257498	89694	TGTCGGTGGAAGGCACCCAC
168325	521	TCCACACACACACACACA	212912	45108	CTTCAACTCCTCAGTTCAAG	257499	89695	CTGTCGGTGGAAGGCACCCA
168326	522	CTCCACACACACACACAC	212913	45109	ACTTCAACTCCTCAGTTCAA	257500	89696	CCTGTCGGTGGAAGGCACCC
168327	523	CCTCCACACACACACACA	212914	45110	CACTTCAACTCCTCAGTTCA	257501	89697	TCCTGTCGGTGGAAGGCACC
168328	524	CCCTCCACACACACACAC	212915	45111	ACACTTCAACTCCTCAGTTC	257502	89698	ATCCTGTCGGTGGAAGGCAC
168329	525	CCCCTCCACACACACACA	212916	45112	TACACTTCAACTCCTCAGTT	257503	89699	CATCCTGTCGGTGGAAGGCA
168330	526	ACCCCTCCACACACACAC	212917	45113	CTACACTTCAACTCCTCAGT	257504	89700	TCATCCTGTCGGTGGAAGGC
168331	527	GACCCCTCCACACACACA	212918	45114	CCTACACTTCAACTCCTCAG	257505	89701	GTCATCCTGTCGGTGGAAGG
168332	528	GGACCCCTCCACACACAC	212919	45115	ACCTACACTTCAACTCCTCA	257506	89702	CGTCATCCTGTCGGTGGAAG
168333	529	CGGACCCCTCCACACACA	212920	45116	CACCTACACTTCAACTCCTC	257507	89703	CCGTCATCCTGTCGGTGGAA
168334	530	TCGGACCCCTCCACACAC	212921	45117	CCACCTACACTTCAACTCCT	257508	89704	CCCGTCATCCTGTCGGTGGA
168335	531	ATCGGACCCCTCCACACA	212922	45118	GCCACCTACACTTCAACTCC	257509	89705	ACCCGTCATCCTGTCGGTGG
168336	532	TATCGGACCCCTCCACACA	212923	45119	TGCCACCTACACTTCAACTC	257510	89706	CACCCGTCATCCTGTCGGTG
168337	533	TTATCGGACCCCTCCACACA	212924	45120	CTGCCACCTACACTTCAACT	257511	89707	GCACCCGTCATCCTGTCGGT
168338	534	GTTATCGGACCCCTCCACAC	212925	45121	TCTGCCACCTACACTTCAAC	257512	89708	GGCACCCGTCATCCTGTCGG
168339	535	CGTTATCGGACCCCTCCACA	212926	45122	ATCTGCCACCTACACTTCAA	257513	89709	GGGCACCCGTCATCCTGTCG
168340	536	TCGTTATCGGACCCCTCCAC	212927	45123	GATCTGCCACCTACACTTCA	257514	89710	AGGGCACCCGTCATCCTGTC
168341	537	GTCGTTATCGGACCCCTCCA	212928	45124	GGATCTGCCACCTACACTTC	257515	89711	GAGGGCACCCGTCATCCTGT
168342	538	GGTCGTTATCGGACCCCTCC	212929	45125	TGGATCTGCCACCTACACTT	257516	89712	TGAGGGCACCCGTCATCCTG
168343	539	GGGTCGTTATCGGACCCCTC	212930	45126	ATGGATCTGCCACCTACACT	257517	89713	ATGAGGGCACCCGTCATCCT
168344	540	GGGGTCGTTATCGGACCCCT	212931	45127	TATGGATCTGCCACCTACAC	257518	89714	CATGAGGGCACCCGTCATCC
168345	541	GGGGGTCGTTATCGGACCCC	212932	45128	TTATGGATCTGCCACCTACA	257519	89715	CCATGAGGGCACCCGTCATC
168346	542	CGGGGGTCGTTATCGGACCC	212933	45129	GTTATGGATCTGCCACCTAC	257520	89716	ACCATGAGGGCACCCGTCAT
168347	543	TCGGGGGTCGTTATCGGACC	212934	45130	TGTTATGGATCTGCCACCTA	257521	89717	CACCATGAGGGCACCCGTCA
168348	544	TTCGGGGGTCGTTATCGGAC	212935	45131	CTGTTATGGATCTGCCACCT	257522	89718	ACACCATGAGGGCACCCGTC
168349	545	TTTCGGGGGTCGTTATCGGA	212936	45132	TCTGTTATGGATCTGCCACC	257523	89719	GACACCATGAGGGCACCCGT
168350	546	GTTTCGGGGGTCGTTATCGG	212937	45133	ATCTGTTATGGATCTGCCAC	257524	89720	AGACACCATGAGGGCACCCG
168351	547	GGTTTCGGGGGTCGTTATCG	212938	45134	TATCTGTTATGGATCTGCCA	257525	89721	TAGACACCATGAGGGCACCC
168352	548	CGGTTTCGGGGGTCGTTATC	212939	45135	TTATCTGTTATGGATCTGCC	257526	89722	CTAGACACCATGAGGGCACC
168353	549	TCGGTTTCGGGGGTCGTTAT	212940	45136	ATTATCTGTTATGGATCTGC	257527	89723	TCTAGACACCATGAGGGCAC
168354	550	TTCGGTTTCGGGGGTCGTTA	212941	45137	GATTATCTGTTATGGATCTG	257528	89724	TTCTAGACACCATGAGGGCA
168355	551	ATTCGGTTTCGGGGGTCGTT	212942	45138	TGATTATCTGTTATGGATCT	257529	89725	GTTCTAGACACCATGAGGGC
168356	552	GATTCGGTTTCGGGGGTCGT	212943	45139	ATGATTATCTGTTATGGATC	257530	89726	AGTTCTAGACACCATGAGGG
168357	553	AGATTCGGTTTCGGGGGTCG	212944	45140	CATGATTATCTGTTATGGAT	257531	89727	GAGTTCTAGACACCATGAGG
168358	554	CAGATTCGGTTTCGGGGGTC	212945	45141	ACATGATTATCTGTTATGGA	257532	89728	AGAGTTCTAGACACCATGAG
168359	555	TCAGATTCGGTTTCGGGGGT	212946	45142	CACATGATTATCTGTTATGG	257533	89729	GAGAGTTCTAGACACCATGA
168360	556	TTCAGATTCGGTTTCGGGGG	212947	45143	ACACATGATTATCTGTTATG	257534	89730	GGAGAGTTCTAGACACCATG
168361	557	TTTCAGATTCGGTTTCGGGG	212948	45144	CACACATGATTATCTGTTAT	257535	89731	TGGAGAGTTCTAGACACCAT
168362	558	ATTTCAGATTCGGTTTCGGG	212949	45145	ACACACATGATTATCTGTTA	257536	89732	TTGGAGAGTTCTAGACACCA
168363	559	GATTTCAGATTCGGTTTCGG	212950	45146	CACACACATGATTATCTGTT	257537	89733	GTTGGAGAGTTCTAGACACC
168364	560	GGATTTCAGATTCGGTTTCG	212951	45147	TCACACACATGATTATCTGT	257538	89734	GGTTGGAGAGTTCTAGACAC
168365	561	CGGATTTCAGATTCGGTTTC	212952	45148	ATCACACACATGATTATCTG	257539	89735	GGGTTGGAGAGTTCTAGACA
168366	562	GCGGATTTCAGATTCGGTTT	212953	45149	CATCACACACATGATTATCT	257540	89736	AGGGTTGGAGAGTTCTAGAC
168367	563	AGCGGATTTCAGATTCGGTT	212954	45150	ACATCACACACATGATTATC	257541	89737	GAGGGTTGGAGAGTTCTAGA
168368	564	CAGCGGATTTCAGATTCGGT	212955	45151	CACATCACACACATGATTAT	257542	89738	GGAGGGTTGGAGAGTTCTAG
168369	565	ACAGCGGATTTCAGATTCGG	212956	45152	TCACATCACACACATGATTA	257543	89739	GGGAGGGTTGGAGAGTTCTA
168370	566	GACAGCGGATTTCAGATTCG	212957	45153	GTCACATCACACACATGATT	257544	89740	TGGGAGGGTTGGAGAGTTCT
168371	567	GGACAGCGGATTTCAGATTC	212958	45154	AGTCACATCACACACATGAT	257545	89741	ATGGGAGGGTTGGAGAGTTC
168372	568	GGGACAGCGGATTTCAGATT	212959	45155	AAGTCACATCACACACATGA	257546	89742	CATGGGAGGGTTGGAGAGTT
168373	569	AGGGACAGCGGATTTCAGAT	212960	45156	GAAGTCACATCACACACATG	257547	89743	ACATGGGAGGGTTGGAGAGT
168374	570	CAGGGACAGCGGATTTCAGA	212961	45157	TGAAGTCACATCACACACAT	257548	89744	TACATGGGAGGGTTGGAGAG
168375	571	GCAGGGACAGCGGATTTCAG	212962	45158	CTGAAGTCACATCACACACA	257549	89745	CTACATGGGAGGGTTGGAGA
168376	572	GGCAGGGACAGCGGATTTCA	212963	45159	GCTGAAGTCACATCACACAC	257550	89746	CCTACATGGGAGGGTTGGAG
168377	573	CGGCAGGGACAGCGGATTTC	212964	45160	GGCTGAAGTCACATCACACA	257551	89747	GCCTACATGGGAGGGTTGGA
168378	574	GCGGCAGGGACAGCGGATTT	212965	45161	AGGCTGAAGTCACATCACAC	257552	89748	TGCCTACATGGGAGGGTTGG

168379	575	AGCGGCAGGGACAGCGGATT	212966	45162	CAGGCTGAAGTCACATCACA	257553	89749	ATGCCTACATGGGAGGGTTG
168380	576	CAGCGGCAGGGACAGCGGAT	212967	45163	TCAGGCTGAAGTCACATCAC	257554	89750	TATGCCTACATGGGAGGGTT
168381	577	ACAGCGGCAGGGACAGCGGA	212968	45164	CTCAGGCTGAAGTCACATCA	257555	89751	TTATGCCTACATGGGAGGGT
168382	578	AACAGCGGCAGGGACAGCGG	212969	45165	GCTCAGGCTGAAGTCACATC	257556	89752	CTTATGCCTACATGGGAGGG
168383	579	GAACAGCGGCAGGGACAGCG	212970	45166	CGCTCAGGCTGAAGTCACAT	257557	89753	GCTTATGCCTACATGGGAGG
168384	580	CGAACAGCGGCAGGGACAGC	212971	45167	ACGCTCAGGCTGAAGTCACA	257558	89754	TGCTTATGCCTACATGGGAG
168385	581	GCGAACAGCGGCAGGGACAG	212972	45168	GACGCTCAGGCTGAAGTCAC	257559	89755	CTGCTTATGCCTACATGGGA
168386	582	GGCGAACAGCGGCAGGGACA	212973	45169	CGACGCTCAGGCTGAAGTCA	257560	89756	GCTGCTTATGCCTACATGGG
168387	583	TGGCGAACAGCGGCAGGGAC	212974	45170	TCGACGCTCAGGCTGAAGTC	257561	89757	GGCTGCTTATGCCTACATGG
168388	584	ATGGCGAACAGCGGCAGGGA	212975	45171	CTCGACGCTCAGGCTGAAGT	257562	89758	GGGCTGCTTATGCCTACATG
168389	585	GATGGCGAACAGCGGCAGGG	212976	45172	CCTCGACGCTCAGGCTGAAG	257563	89759	GGGGCTGCTTATGCCTACAT
168390	586	TGATGGCGAACAGCGGCAGG	212977	45173	TCCTCGACGCTCAGGCTGAA	257564	89760	TGGGGCTGCTTATGCCTACA
168391	587	CTGATGGCGAACAGCGGCAG	212978	45174	GTCCTCGACGCTCAGGCTGA	257565	89761	GTGGGGCTGCTTATGCCTAC
168392	588	GCTGATGGCGAACAGCGGCA	212979	45175	GGTCCTCGACGCTCAGGCTG	257566	89762	AGTGGGGCTGCTTATGCCTA
168393	589	AGCTGATGGCGAACAGCGGC	212980	45176	TGGTCCTCGACGCTCAGGCT	257567	89763	AAGTGGGGCTGCTTATGCCT
168394	590	GAGCTGATGGCGAACAGCGG	212981	45177	TTGGTCCTCGACGCTCAGGC	257568	89764	AAAGTGGGGCTGCTTATGCC
168395	591	AGAGCTGATGGCGAACAGCG	212982	45178	CTTGGTCCTCGACGCTCAGG	257569	89765	CAAAGTGGGGCTGCTTATGC
168396	592	TAGAGCTGATGGCGAACAGC	212983	45179	ACTTGGTCCTCGACGCTCAG	257570	89766	GCAAAGTGGGGCTGCTTATG
168397	593	TTAGAGCTGATGGCGAACAG	212984	45180	GACTTGGTCCTCGACGCTCA	257571	89767	TGCAAAGTGGGGCTGCTTAT
168398	594	CTTAGAGCTGATGGCGAACA	212985	45181	TGACTTGGTCCTCGACGCTC	257572	89768	CTGCAAAGTGGGGCTGCTTA
168399	595	TCTTAGAGCTGATGGCGAAC	212986	45182	GTGACTTGGTCCTCGACGCT	257573	89769	TCTGCAAAGTGGGGCTGCTT
168400	596	TTCTTAGAGCTGATGGCGAA	212987	45183	TGTGACTTGGTCCTCGACGC	257574	89770	ATCTGCAAAGTGGGGCTGCT
168401	597	TTTCTTAGAGCTGATGGCGA	212988	45184	CTGTGACTTGGTCCTCGACG	257575	89771	CATCTGCAAAGTGGGGCTGC
168402	598	CTTTCTTAGAGCTGATGGCG	212989	45185	TCTGTGACTTGGTCCTCGAC	257576	89772	TCATCTGCAAAGTGGGGCTG
168403	599	TCTTTCTTAGAGCTGATGGC	212990	45186	CTCTGTGACTTGGTCCTCGA	257577	89773	CTCATCTGCAAAGTGGGGCT
168404	600	GTCTTTCTTAGAGCTGATGG	212991	45187	GCTCTGTGACTTGGTCCTCG	257578	89774	CCTCATCTGCAAAGTGGGGC
168405	601	CGTCTTTCTTAGAGCTGATG	212992	45188	TGCTCTGTGACTTGGTCCTC	257579	89775	TCCTCATCTGCAAAGTGGGG
168406	602	ACGTCTTTCTTAGAGCTGAT	212993	45189	CTGCTCTGTGACTTGGTCCT	257580	89776	TTCCTCATCTGCAAAGTGGG
168407	603	CACGTCTTTCTTAGAGCTGA	212994	45190	CCTGCTCTGTGACTTGGTCC	257581	89777	TTTCCTCATCTGCAAAGTGG
168408	604	CCACGTCTTTCTTAGAGCTG	212995	45191	TCCTGCTCTGTGACTTGGTC	257582	89778	GTTTCCTCATCTGCAAAGTG
168409	605	TCCACGTCTTTCTTAGAGCT	212996	45192	TTCCTGCTCTGTGACTTGGT	257583	89779	CGTTTCCTCATCTGCAAAGT
168410	606	ATCCACGTCTTTCTTAGAGC	212997	45193	GTTCCTGCTCTGTGACTTGG	257584	89780	CCGTTTCCTCATCTGCAAAG
168411	607	GATCCACGTCTTTCTTAGAG	212998	45194	TGTTCCTGCTCTGTGACTTG	257585	89781	TCCGTTTCCTCATCTGCAAA
168412	608	CGATCCACGTCTTTCTTAGA	212999	45195	CTGTTCCTGCTCTGTGACTT	257586	89782	CTCCGTTTCCTCATCTGCAA
168413	609	CCGATCCACGTCTTTCTTAG	213000	45196	GCTGTTCCTGCTCTGTGACT	257587	89783	CCTCCGTTTCCTCATCTGCA
168414	610	CCCGATCCACGTCTTTCTTA	213001	45197	GGCTGTTCCTGCTCTGTGAC	257588	89784	GCCTCCGTTTCCTCATCTGC
168415	611	ACCCGATCCACGTCTTTCTT	213002	45198	TGGCTGTTCCTGCTCTGTGA	257589	89785	AGCCTCCGTTTCCTCATCTG
168416	612	AACCCGATCCACGTCTTTCT	213003	45199	GTGGCTGTTCCTGCTCTGTG	257590	89786	GAGCCTCCGTTTCCTCATCT
168417	613	GAACCCGATCCACGTCTTTC	213004	45200	AGTGGCTGTTCCTGCTCTGT	257591	89787	TGAGCCTCCGTTTCCTCATC
168418	614	AGAACCCGATCCACGTCTTT	213005	45201	GAGTGGCTGTTCCTGCTCTG	257592	89788	CTGAGCCTCCGTTTCCTCAT
168419	615	TAGAACCCGATCCACGTCTT	213006	45202	AGAGTGGCTGTTCCTGCTCT	257593	89789	TCTGAGCCTCCGTTTCCTCA
168420	616	CTAGAACCCGATCCACGTCT	213007	45203	GAGAGTGGCTGTTCCTGCTC	257594	89790	CTCTGAGCCTCCGTTTCCTC
168421	617	TCTAGAACCCGATCCACGTC	213008	45204	GGAGAGTGGCTGTTCCTGCT	257595	89791	TCTCTGAGCCTCCGTTTCCT
168422	618	TTCTAGAACCCGATCCACGT	213009	45205	TGGAGAGTGGCTGTTCCTGC	257596	89792	TTCTCTGAGCCTCCGTTTCC
168423	619	TTTCTAGAACCCGATCCACG	213010	45206	CTGGAGAGTGGCTGTTCCTG	257597	89793	CTTCTCTGAGCCTCCGTTTC
168424	620	TTTTCTAGAACCCGATCCAC	213011	45207	ACTGGAGAGTGGCTGTTCCT	257598	89794	ACTTCTCTGAGCCTCCGTTT
168425	621	CTTTTCTAGAACCCGATCCA	213012	45208	CACTGGAGAGTGGCTGTTCC	257599	89795	TACTTCTCTGAGCCTCCGTT
168426	622	TCTTTTCTAGAACCCGATCC	213013	45209	ACACTGGAGAGTGGCTGTTC	257600	89796	GTACTTCTCTGAGCCTCCGT
168427	623	ATCTTTTCTAGAACCCGATC	213014	45210	GACACTGGAGAGTGGCTGTT	257601	89797	TGTACTTCTCTGAGCCTCCG
168428	624	CATCTTTTCTAGAACCCGAT	213015	45211	GGACACTGGAGAGTGGCTGT	257602	89798	CTGTACTTCTCTGAGCCTCC
168429	625	TCATCTTTTCTAGAACCCGA	213016	45212	AGGACACTGGAGAGTGGCTG	257603	89799	ACTGTACTTCTCTGAGCCTC
168430	626	GTCATCTTTTCTAGAACCCG	213017	45213	AAGGACACTGGAGAGTGGCT	257604	89800	TACTGTACTTCTCTGAGCCT
168431	627	AGTCATCTTTTCTAGAACCC	213018	45214	CAAGGACACTGGAGAGTGGC	257605	89801	TTACTGTACTTCTCTGAGCC
168432	628	GAGTCATCTTTTCTAGAACC	213019	45215	CCAAGGACACTGGAGAGTGG	257606	89802	GTTACTGTACTTCTCTGAGC
168433	629	GGAGTCATCTTTTCTAGAAC	213020	45216	CCCAAGGACACTGGAGAGTG	257607	89803	AGTTACTGTACTTCTCTGAG
168434	630	GGGAGTCATCTTTTCTAGAA	213021	45217	CCCCAAGGACACTGGAGAGT	257608	89804	AAGTTACTGTACTTCTCTGA
168435	631	AGGGAGTCATCTTTTCTAGA	213022	45218	GCCCCAAGGACACTGGAGAG	257609	89805	CAAGTTACTGTACTTCTCTG
168436	632	CAGGGAGTCATCTTTTCTAG	213023	45219	AGCCCCAAGGACACTGGAGA	257610	89806	GCAAGTTACTGTACTTCTCT
168437	633	GCAGGGAGTCATCTTTTCTA	213024	45220	TAGCCCCAAGGACACTGGAG	257611	89807	GGCAAGTTACTGTACTTCTC
168438	634	TGCAGGGAGTCATCTTTTCT	213025	45221	GTAGCCCCAAGGACACTGGA	257612	89808	CGGCAAGTTACTGTACTTCT
168439	635	GTGCAGGGAGTCATCTTTTC	213026	45222	CGTAGCCCCAAGGACACTGG	257613	89809	TCGGCAAGTTACTGTACTTC
168440	636	CGTGCAGGGAGTCATCTTTT	213027	45223	ACGTAGCCCCAAGGACACTG	257614	89810	TTCGGCAAGTTACTGTACTT
168441	637	GCGTGCAGGGAGTCATCTTT	213028	45224	GACGTAGCCCCAAGGACACT	257615	89811	CTTCGGCAAGTTACTGTACT
168442	638	GGCGTGCAGGGAGTCATCTT	213029	45225	AGACGTAGCCCCAAGGACAC	257616	89812	CCTTCGGCAAGTTACTGTAC
168443	639	GGGCGTGCAGGGAGTCATCT	213030	45226	CAGACGTAGCCCCAAGGACA	257617	89813	GCCTTCGGCAAGTTACTGTA
168444	640	GGGGCGTGCAGGGAGTCATC	213031	45227	TCAGACGTAGCCCCAAGGAC	257618	89814	GGCCTTCGGCAAGTTACTGT
168445	641	AGGGGCGTGCAGGGAGTCAT	213032	45228	CTCAGACGTAGCCCCAAGGA	257619	89815	TGGCCTTCGGCAAGTTACTG
168446	642	GAGGGGCGTGCAGGGAGTCA	213033	45229	CCTCAGACGTAGCCCCAAGG	257620	89816	TTGGCCTTCGGCAAGTTACT
168447	643	GGAGGGGCGTGCAGGGAGTC	213034	45230	TCCTCAGACGTAGCCCCAAG	257621	89817	ATTGGCCTTCGGCAAGTTAC
168448	644	GGGAGGGGCGTGCAGGGAGT	213035	45231	CTCCTCAGACGTAGCCCCAA	257622	89818	CATTGGCCTTCGGCAAGTTA
168449	645	AGGGAGGGGCGTGCAGGGAG	213036	45232	TCTCCTCAGACGTAGCCCCA	257623	89819	TCATTGGCCTTCGGCAAGTT
168450	646	CAGGGAGGGGCGTGCAGGGA	213037	45233	TTCTCCTCAGACGTAGCCCC	257624	89820	CTCATTGGCCTTCGGCAAGT

168451	647	GCAGGGAGGGGCGTGCAGGG	213038	45234	GTTCTCCTCAGACGTAGCCC	257625	89821	ACTCATTGGCCTTCGGCAAG
168452	648	TGCAGGGAGGGGCGTGCAGG	213039	45235	GGTTCTCCTCAGACGTAGCC	257626	89822	TACTCATTGGCCTTCGGCAA
168453	649	GTGCAGGGAGGGGCGTGCAG	213040	45236	AGGTTCTCCTCAGACGTAGC	257627	89823	CTACTCATTGGCCTTCGGCA
168454	650	GGTGCAGGGAGGGGCGTGCA	213041	45237	CAGGTTCTCCTCAGACGTAG	257628	89824	ACTACTCATTGGCCTTCGGC
168455	651	AGGTGCAGGGAGGGGCGTGC	213042	45238	CCAGGTTCTCCTCAGACGTA	257629	89825	TACTACTCATTGGCCTTCGG
168456	652	GAGGTGCAGGGAGGGGCGTG	213043	45239	CCCAGGTTCTCCTCAGACGT	257630	89826	TTACTACTCATTGGCCTTCG
168457	653	GGAGGTGCAGGGAGGGGCGT	213044	45240	TCCCAGGTTCTCCTCAGACG	257631	89827	CTTACTACTCATTGGCCTTC
168458	654	GGGAGGTGCAGGGAGGGGCG	213045	45241	ATCCCAGGTTCTCCTCAGAC	257632	89828	ACTTACTACTCATTGGCCTT
168459	655	CGGGAGGTGCAGGGAGGGGC	213046	45242	AATCCCAGGTTCTCCTCAGA	257633	89829	CACTTACTACTCATTGGCCT
168460	656	TCGGGAGGTGCAGGGAGGGG	213047	45243	AAATCCCAGGTTCTCCTCAG	257634	89830	TCACTTACTACTCATTGGCC
168461	657	CTCGGGAGGTGCAGGGAGGG	213048	45244	GAAATCCCAGGTTCTCCTCA	257635	89831	GTCACTTACTACTCATTGGC
168462	658	GCTCGGGAGGTGCAGGGAGG	213049	45245	TGAAATCCCAGGTTCTCCTC	257636	89832	TGTCACTTACTACTCATTGG
168463	659	TGCTCGGGAGGTGCAGGGAG	213050	45246	ATGAAATCCCAGGTTCTCCT	257637	89833	CTGTCACTTACTACTCATTG
168464	660	CTGCTCGGGAGGTGCAGGGA	213051	45247	TATGAAATCCCAGGTTCTCC	257638	89834	TCTGTCACTTACTACTCATT
168465	661	ACTGCTCGGGAGGTGCAGGG	213052	45248	ATATGAAATCCCAGGTTCTC	257639	89835	CTCTGTCACTTACTACTCAT
168466	662	CACTGCTCGGGAGGTGCAGG	213053	45249	TATATGAAATCCCAGGTTCT	257640	89836	GCTCTGTCACTTACTACTCA
168467	663	TCACTGCTCGGGAGGTGCAG	213054	45250	ATATATGAAATCCCAGGTTC	257641	89837	GGCTCTGTCACTTACTACTC
168468	664	ATCACTGCTCGGGAGGTGCA	213055	45251	CATATATGAAATCCCAGGTT	257642	89838	TGGCTCTGTCACTTACTACT
168469	665	AATCACTGCTCGGGAGGTGC	213056	45252	TCATATATGAAATCCCAGGT	257643	89839	CTGGCTCTGTCACTTACTAC
168470	666	GAATCACTGCTCGGGAGGTG	213057	45253	GTCATATATGAAATCCCAGG	257644	89840	CCTGGCTCTGTCACTTACTA
168471	667	GGAATCACTGCTCGGGAGGT	213058	45254	GGTCATATATGAAATCCCAG	257645	89841	ACCTGGCTCTGTCACTTACT
168472	668	CGGAATCACTGCTCGGGAGG	213059	45255	AGGTCATATATGAAATCCCA	257646	89842	AACCTGGCTCTGTCACTTAC
168473	669	TCGGAATCACTGCTCGGGAG	213060	45256	CAGGTCATATATGAAATCCC	257647	89843	AAACCTGGCTCTGTCACTTA
168474	670	GTCGGAATCACTGCTCGGGA	213061	45257	GCAGGTCATATATGAAATCC	257648	89844	CAAACCTGGCTCTGTCACTT
168475	671	TGTCGGAATCACTGCTCGGG	213062	45258	TGCAGGTCATATATGAAATC	257649	89845	CCAAACCTGGCTCTGTCACT
168476	672	CTGTCGGAATCACTGCTCGG	213063	45259	GTGCAGGTCATATATGAAAT	257650	89846	CCCAAACCTGGCTCTGTCAC
168477	673	CCTGTCGGAATCACTGCTCG	213064	45260	AGTGCAGGTCATATATGAAA	257651	89847	TCCCAAACCTGGCTCTGTCA
168478	674	CCCTGTCGGAATCACTGCTC	213065	45261	CAGTGCAGGTCATATATGAA	257652	89848	ATCCCAAACCTGGCTCTGTC
168479	675	GCCCTGTCGGAATCACTGCT	213066	45262	CCAGTGCAGGTCATATATGA	257653	89849	GATCCCAAACCTGGCTCTGT
168480	676	GGCCCTGTCGGAATCACTGC	213067	45263	GCCAGTGCAGGTCATATATG	257654	89850	GGATCCCAAACCTGGCTCTG
168481	677	AGGCCCTGTCGGAATCACTG	213068	45264	AGCCAGTGCAGGTCATATAT	257655	89851	TGGATCCCAAACCTGGCTCT
168482	678	AAGGCCCTGTCGGAATCACT	213069	45265	CAGCCAGTGCAGGTCATATA	257656	89852	CTGGATCCCAAACCTGGCTC
168483	679	GAAGGCCCTGTCGGAATCAC	213070	45266	CCAGCCAGTGCAGGTCATAT	257657	89853	CCTGGATCCCAAACCTGGCT
168484	680	TGAAGGCCCTGTCGGAATCA	213071	45267	CCCAGCCAGTGCAGGTCATA	257658	89854	ACCTGGATCCCAAACCTGGC
168485	681	GTGAAGGCCCTGTCGGAATC	213072	45268	CCCCAGCCAGTGCAGGTCAT	257659	89855	TACCTGGATCCCAAACCTGG
168486	682	AGTGAAGGCCCTGTCGGAAT	213073	45269	CCCCCAGCCAGTGCAGGTCA	257660	89856	CTACCTGGATCCCAAACCTG
168487	683	CAGTGAAGGCCCTGTCGGAA	213074	45270	CCCCCCAGCCAGTGCAGGTC	257661	89857	CCTACCTGGATCCCAAACCT
168488	684	GCAGTGAAGGCCCTGTCGGA	213075	45271	GCCCCCCAGCCAGTGCAGGT	257662	89858	ACCTACCTGGATCCCAAACC
168489	685	GGCAGTGAAGGCCCTGTCGG	213076	45272	AGCCCCCCAGCCAGTGCAGG	257663	89859	AACCTACCTGGATCCCAAAC
168490	686	GGGCAGTGAAGGCCCTGTCG	213077	45273	GAGCCCCCCAGCCAGTGCAG	257664	89860	CAACCTACCTGGATCCCAAA
168491	687	GGGGCAGTGAAGGCCCTGTC	213078	45274	AGAGCCCCCCAGCCAGTGCA	257665	89861	ACAACCTACCTGGATCCCAA
168492	688	AGGGGCAGTGAAGGCCCTGT	213079	45275	GAGAGCCCCCCAGCCAGTGC	257666	89862	GACAACCTACCTGGATCCCA
168493	689	CAGGGGCAGTGAAGGCCCTG	213080	45276	AGAGAGCCCCCCAGCCAGTG	257667	89863	AGACAACCTACCTGGATCCC
168494	690	TCAGGGGCAGTGAAGGCCCT	213081	45277	AAGAGAGCCCCCCAGCCAGT	257668	89864	GAGACAACCTACCTGGATCC
168495	691	ATCAGGGGCAGTGAAGGCCC	213082	45278	CAAGAGAGCCCCCCAGCCAG	257669	89865	AGAGACAACCTACCTGGATC
168496	692	AATCAGGGGCAGTGAAGGCC	213083	45279	TCAAGAGAGCCCCCCAGCCA	257670	89866	CAGAGACAACCTACCTGGAT
168497	693	AAATCAGGGGCAGTGAAGGC	213084	45280	GTCAAGAGAGCCCCCCAGCC	257671	89867	TCAGAGACAACCTACCTGGA
168498	694	AAAATCAGGGGCAGTGAAGG	213085	45281	CGTCAAGAGAGCCCCCCAGC	257672	89868	TTCAGAGACAACCTACCTGG
168499	695	TAAAATCAGGGGCAGTGAAG	213086	45282	ACGTCAAGAGAGCCCCCCAG	257673	89869	TTTCAGAGACAACCTACCTG
168500	696	CTAAAATCAGGGGCAGTGAA	213087	45283	TACGTCAAGAGAGCCCCCCA	257674	89870	CTTTCAGAGACAACCTACCT
168501	697	CCTAAAATCAGGGGCAGTGA	213088	45284	TTACGTCAAGAGAGCCCCCC	257675	89871	TCTTTCAGAGACAACCTACC
168502	698	GCCTAAAATCAGGGGCAGTG	213089	45285	GTTACGTCAAGAGAGCCCCC	257676	89872	GTCTTTCAGAGACAACCTAC
168503	699	CGCCTAAAATCAGGGGCAGT	213090	45286	CGTTACGTCAAGAGAGCCCC	257677	89873	TGTCTTTCAGAGACAACCTA
168504	700	CCGCCTAAAATCAGGGGCAG	213091	45287	ACGTTACGTCAAGAGAGCCC	257678	89874	GTGTCTTTCAGAGACAACCT
168505	701	CCCGCCTAAAATCAGGGGCA	213092	45288	CACGTTACGTCAAGAGAGCC	257679	89875	CGTGTCTTTCAGAGACAACC
168506	702	CCCCGCCTAAAATCAGGGGC	213093	45289	ACACGTTACGTCAAGAGAGC	257680	89876	GCGTGTCTTTCAGAGACAAC
168507	703	CCCCCGCCTAAAATCAGGGG	213094	45290	AACACGTTACGTCAAGAGAG	257681	89877	GGCGTGTCTTTCAGAGACAA
168508	704	GCCCCCGCCTAAAATCAGGG	213095	45291	GAACACGTTACGTCAAGAGA	257682	89878	AGGCGTGTCTTTCAGAGACA
168509	705	GGCCCCCGCCTAAAATCAGG	213096	45292	GGAACACGTTACGTCAAGAG	257683	89879	CAGGCGTGTCTTTCAGAGAC
168510	706	CGGCCCCCGCCTAAAATCAG	213097	45293	GGGAACACGTTACGTCAAGA	257684	89880	ACAGGCGTGTCTTTCAGAGA
168511	707	CCGGCCCCCGCCTAAAATCA	213098	45294	AGGGAACACGTTACGTCAAG	257685	89881	GACAGGCGTGTCTTTCAGAG
168512	708	GCCGGCCCCCGCCTAAAATC	213099	45295	GAGGGAACACGTTACGTCAA	257686	89882	GGACAGGCGTGTCTTTCAGA
168513	709	GGCCGGCCCCCGCCTAAAAT	213100	45296	AGAGGGAACACGTTACGTCA	257687	89883	AGGACAGGCGTGTCTTTCAG
168514	710	GGGCCGGCCCCCGCCTAAAA	213101	45297	CAGAGGGAACACGTTACGTC	257688	89884	CAGGACAGGCGTGTCTTTCA
168515	711	GGGGCCGGCCCCCGCCTAAA	213102	45298	TCAGAGGGAACACGTTACGT	257689	89885	GCAGGACAGGCGTGTCTTTC
168516	712	GGGGGCCGGCCCCCGCCTAA	213103	45299	CTCAGAGGGAACACGTTACG	257690	89886	TGCAGGACAGGCGTGTCTTT
168517	713	AGGGGGCCGGCCCCCGCCTA	213104	45300	GCTCAGAGGGAACACGTTAC	257691	89887	ATGCAGGACAGGCGTGTCTT
168518	714	GAGGGGGCCGGCCCCCGCCT	213105	45301	TGCTCAGAGGGAACACGTTA	257692	89888	GATGCAGGACAGGCGTGTCT
168519	715	GGAGGGGGCCGGCCCCCGCC	213106	45302	ATGCTCAGAGGGAACACGTT	257693	89889	GGATGCAGGACAGGCGTGTC
168520	716	GGGAGGGGGCCGGCCCCCGC	213107	45303	CATGCTCAGAGGGAACACGT	257694	89890	GGGATGCAGGACAGGCGTGT
168521	717	GGGGAGGGGGCCGGCCCCCG	213108	45304	ACATGCTCAGAGGGAACACG	257695	89891	TGGGATGCAGGACAGGCGTG
168522	718	AGGGGAGGGGGCCGGCCCCC	213109	45305	AACATGCTCAGAGGGAACAC	257696	89892	GTGGGATGCAGGACAGGCGT

168523	719	AAGGGGAGGGGGCCGGCCCC	213110	45306	TAACATGCTCAGAGGGAACA	257697	89893	TGTGGGATGCAGGACAGGCG
168524	720	AAAGGGGAGGGGGCCGGCCC	213111	45307	GTAACATGCTCAGAGGGAAC	257698	89894	TTGTGGGATGCAGGACAGGC
168525	721	AAAAGGGGAGGGGGCCGGCC	213112	45308	TGTAACATGCTCAGAGGGAA	257699	89895	GTTGTGGGATGCAGGACAGG
168526	722	GAAAAGGGGAGGGGGCCGGC	213113	45309	CTGTAACATGCTCAGAGGGA	257700	89896	CGTTGTGGGATGCAGGACAG
168527	723	GGAAAAGGGGAGGGGGCCGG	213114	45310	TCTGTAACATGCTCAGAGGG	257701	89897	GCGTTGTGGGATGCAGGACA
168528	724	AGGAAAAGGGGAGGGGGCCG	213115	45311	ATCTGTAACATGCTCAGAGG	257702	89898	GGCGTTGTGGGATGCAGGAC
168529	725	GAGGAAAAGGGGAGGGGGCC	213116	45312	AATCTGTAACATGCTCAGAG	257703	89899	AGGCGTTGTGGGATGCAGGA
168530	726	GGAGGAAAAGGGGAGGGGGC	213117	45313	GAATCTGTAACATGCTCAGA	257704	89900	GAGGCGTTGTGGGATGCAGG
168531	727	AGGAGGAAAAGGGGAGGGGG	213118	45314	AGAATCTGTAACATGCTCAG	257705	89901	GGAGGCGTTGTGGGATGCAG
168532	728	AAGGAGGAAAAGGGGAGGGG	213119	45315	CAGAATCTGTAACATGCTCA	257706	89902	GGGAGGCGTTGTGGGATGCA
168533	729	GAAGGAGGAAAAGGGGAGGG	213120	45316	TCAGAATCTGTAACATGCTC	257707	89903	TGGGAGGCGTTGTGGGATGC
168534	730	TGAAGGAGGAAAAGGGGAGG	213121	45317	GTCAGAATCTGTAACATGCT	257708	89904	CTGGGAGGCGTTGTGGGATG
168535	731	CTGAAGGAGGAAAAGGGGAG	213122	45318	TGTCAGAATCTGTAACATGC	257709	89905	CCTGGGAGGCGTTGTGGGAT
168536	732	TCTGAAGGAGGAAAAGGGGA	213123	45319	ATGTCAGAATCTGTAACATG	257710	89906	TCCTGGGAGGCGTTGTGGGA
168537	733	TTCTGAAGGAGGAAAAGGGG	213124	45320	AATGTCAGAATCTGTAACAT	257711	89907	CTCCTGGGAGGCGTTGTGGG
168538	734	TTTCTGAAGGAGGAAAAGGG	213125	45321	GAATGTCAGAATCTGTAACA	257712	89908	CCTCCTGGGAGGCGTTGTGG
168539	735	GTTTCTGAAGGAGGAAAAGG	213126	45322	AGAATGTCAGAATCTGTAAC	257713	89909	ACCTCCTGGGAGGCGTTGTG
168540	736	GGTTTCTGAAGGAGGAAAAG	213127	45323	AAGAATGTCAGAATCTGTAA	257714	89910	CACCTCCTGGGAGGCGTTGT
168541	737	GGGTTTCTGAAGGAGGAAAA	213128	45324	TAAGAATGTCAGAATCTGTA	257715	89911	GCACCTCCTGGGAGGCGTTG
168542	738	CGGGTTTCTGAAGGAGGAAA	213129	45325	ATAAGAATGTCAGAATCTGT	257716	89912	AGCACCTCCTGGGAGGCGTT
168543	739	ACGGGTTTCTGAAGGAGGAA	213130	45326	CATAAGAATGTCAGAATCTG	257717	89913	CAGCACCTCCTGGGAGGCGT
168544	740	TACGGGTTTCTGAAGGAGGA	213131	45327	ACATAAGAATGTCAGAATCT	257718	89914	CCAGCACCTCCTGGGAGGCG
168545	741	CTACGGGTTTCTGAAGGAGG	213132	45328	AACATAAGAATGTCAGAATC	257719	89915	TCCAGCACCTCCTGGGAGGC
168546	742	CCTACGGGTTTCTGAAGGAG	213133	45329	GAACATAAGAATGTCAGAAT	257720	89916	CTCCAGCACCTCCTGGGAGG
168547	743	CCCTACGGGTTTCTGAAGGA	213134	45330	GGAACATAAGAATGTCAGAA	257721	89917	ACTCCAGCACCTCCTGGGAG
168548	744	CCCCTACGGGTTTCTGAAGG	213135	45331	AGGAACATAAGAATGTCAGA	257722	89918	CACTCCAGCACCTCCTGGGA
168549	745	TCCCCTACGGGTTTCTGAAG	213136	45332	AAGGAACATAAGAATGTCAG	257723	89919	ACACTCCAGCACCTCCTGGG
168550	746	GTCCCCTACGGGTTTCTGAA	213137	45333	GAAGGAACATAAGAATGTCA	257724	89920	CACACTCCAGCACCTCCTGG
168551	747	TGTCCCCTACGGGTTTCTGA	213138	45334	AGAAGGAACATAAGAATGTC	257725	89921	CCACACTCCAGCACCTCCTG
168552	748	ATGTCCCCTACGGGTTTCTG	213139	45335	CAGAAGGAACATAAGAATGT	257726	89922	TCCACACTCCAGCACCTCCT
168553	749	AATGTCCCCTACGGGTTTCT	213140	45336	ACAGAAGGAACATAAGAATG	257727	89923	GTCCACACTCCAGCACCTCC
168554	750	AAATGTCCCCTACGGGTTTC	213141	45337	CACAGAAGGAACATAAGAAT	257728	89924	CGTCCACACTCCAGCACCTC
168555	751	CAAATGTCCCCTACGGGTTT	213142	45338	CCACAGAAGGAACATAAGAA	257729	89925	GCGTCCACACTCCAGCACCT
168556	752	CCAAATGTCCCCTACGGGTT	213143	45339	TCCACAGAAGGAACATAAGA	257730	89926	GGCGTCCACACTCCAGCACC
168557	753	CCCAAATGTCCCCTACGGGT	213144	45340	CTCCACAGAAGGAACATAAG	257731	89927	AGGCGTCCACACTCCAGCAC
168558	754	CCCCAAATGTCCCCTACGGG	213145	45341	TCTCCACAGAAGGAACATAA	257732	89928	TAGGCGTCCACACTCCAGCA
168559	755	CCCCCAAATGTCCCCTACGG	213146	45342	CTCTCCACAGAAGGAACATA	257733	89929	TTAGGCGTCCACACTCCAGC
168560	756	GCCCCCAAATGTCCCCTACG	213147	45343	TCTCTCCACAGAAGGAACAT	257734	89930	GTTAGGCGTCCACACTCCAG
168561	757	AGCCCCCAAATGTCCCCTAC	213148	45344	GTCTCTCCACAGAAGGAACA	257735	89931	TGTTAGGCGTCCACACTCCA
168562	758	CAGCCCCCAAATGTCCCCTA	213149	45345	TGTCTCTCCACAGAAGGAAC	257736	89932	GTGTTAGGCGTCCACACTCC
168563	759	CCAGCCCCCAAATGTCCCCT	213150	45346	ATGTCTCTCCACAGAAGGAA	257737	89933	TGTGTTAGGCGTCCACACTC
168564	760	CCCAGCCCCCAAATGTCCCC	213151	45347	CATGTCTCTCCACAGAAGGA	257738	89934	CTGTGTTAGGCGTCCACACT
168565	761	TCCCAGCCCCCAAATGTCCC	213152	45348	ACATGTCTCTCCACAGAAGG	257739	89935	TCTGTGTTAGGCGTCCACAC
168566	762	CTCCCAGCCCCCAAATGTCC	213153	45349	TACATGTCTCTCCACAGAAG	257740	89936	CTCTGTGTTAGGCGTCCACA
168567	763	TCTCCCAGCCCCCAAATGTC	213154	45350	GTACATGTCTCTCCACAGAA	257741	89937	TCTCTGTGTTAGGCGTCCAC
168568	764	TTCTCCCAGCCCCCAAATGT	213155	45351	AGTACATGTCTCTCCACAGA	257742	89938	ATCTCTGTGTTAGGCGTCCA
168569	765	TTTCTCCCAGCCCCCAAATG	213156	45352	AAGTACATGTCTCTCCACAG	257743	89939	CATCTCTGTGTTAGGCGTCC
168570	766	ATTTCTCCCAGCCCCCAAAT	213157	45353	TAAGTACATGTCTCTCCACA	257744	89940	ACATCTCTGTGTTAGGCGTC
168571	767	GATTTCTCCCAGCCCCCAAA	213158	45354	CTAAGTACATGTCTCTCCAC	257745	89941	CACATCTCTGTGTTAGGCGT
168572	768	CGATTTCTCCCAGCCCCCAA	213159	45355	ACTAAGTACATGTCTCTCCA	257746	89942	GCACATCTCTGTGTTAGGCG
168573	769	TCGATTTCTCCCAGCCCCCA	213160	45356	CACTAAGTACATGTCTCTCC	257747	89943	TGCACATCTCTGTGTTAGGC
168574	770	CTCGATTTCTCCCAGCCCCC	213161	45357	TCACTAAGTACATGTCTCTC	257748	89944	CTGCACATCTCTGTGTTAGG
168575	771	CCTCGATTTCTCCCAGCCCC	213162	45358	GTCACTAAGTACATGTCTCT	257749	89945	CCTGCACATCTCTGTGTTAG
168576	772	TCCTCGATTTCTCCCAGCCC	213163	45359	GGTCACTAAGTACATGTCTC	257750	89946	CCCTGCACATCTCTGTGTTA
168577	773	CTCCTCGATTTCTCCCAGCC	213164	45360	AGGTCACTAAGTACATGTCT	257751	89947	GCCCTGCACATCTCTGTGTT
168578	774	TCTCCTCGATTTCTCCCAGC	213165	45361	TAGGTCACTAAGTACATGTC	257752	89948	TGCCCTGCACATCTCTGTGT
168579	775	ATCTCCTCGATTTCTCCCAG	213166	45362	TTAGGTCACTAAGTACATGT	257753	89949	GTGCCCTGCACATCTCTGTG
168580	776	CATCTCCTCGATTTCTCCCA	213167	45363	GTTAGGTCACTAAGTACATG	257754	89950	TGTGCCCTGCACATCTCTGT
168581	777	CCATCTCCTCGATTTCTCCC	213168	45364	AGTTAGGTCACTAAGTACAT	257755	89951	GTGTGCCCTGCACATCTCTG
168582	778	CCCATCTCCTCGATTTCTCC	213169	45365	GAGTTAGGTCACTAAGTACA	257756	89952	TGTGTGCCCTGCACATCTCT
168583	779	CCCCATCTCCTCGATTTCTC	213170	45366	TGAGTTAGGTCACTAAGTAC	257757	89953	GTGTGTGCCCTGCACATCTC
168584	780	TCCCCATCTCCTCGATTTCT	213171	45367	GTGAGTTAGGTCACTAAGTA	257758	89954	TGTGTGTGCCCTGCACATCT
168585	781	CTCCCCATCTCCTCGATTTC	213172	45368	AGTGAGTTAGGTCACTAAGT	257759	89955	CTGTGTGTGCCCTGCACATC
168586	782	CCTCCCCATCTCCTCGATTT	213173	45369	AAGTGAGTTAGGTCACTAAG	257760	89956	GCTGTGTGTGCCCTGCACAT
168587	783	CCCTCCCCATCTCCTCGATT	213174	45370	AAAGTGAGTTAGGTCACTAA	257761	89957	TGCTGTGTGTGCCCTGCACA
168588	784	CCCCTCCCCATCTCCTCGAT	213175	45371	TAAAGTGAGTTAGGTCACTA	257762	89958	CTGCTGTGTGTGCCCTGCAC
168589	785	ACCCCTCCCCATCTCCTCGA	213176	45372	CTAAAGTGAGTTAGGTCACT	257763	89959	CCTGCTGTGTGTGCCCTGCA
168590	786	GACCCCTCCCCATCTCCTCG	213177	45373	GCTAAAGTGAGTTAGGTCAC	257764	89960	ACCTGCTGTGTGTGCCCTGC
168591	787	GGACCCCTCCCCATCTCCTC	213178	45374	TGCTAAAGTGAGTTAGGTCA	257765	89961	CACCTGCTGTGTGTGCCCTG
168592	788	TGGACCCCTCCCCATCTCCT	213179	45375	ATGCTAAAGTGAGTTAGGTC	257766	89962	TCACCTGCTGTGTGTGCCCT
168593	789	GTGGACCCCTCCCCATCTCC	213180	45376	TATGCTAAAGTGAGTTAGGT	257767	89963	GTCACCTGCTGTGTGTGCCC
168594	790	CGTGGACCCCTCCCCATCTC	213181	45377	ATATGCTAAAGTGAGTTAGG	257768	89964	TGTCACCTGCTGTGTGTGCC

168595	791	GCGTGGACCCCTCCCCATCT	213182	45378	AATATGCTAAAGTGAGTTAG	257769	89965	GTGTCACCTGCTGTGTGTGC
168596	792	CGCGTGGACCCCTCCCCATC	213183	45379	AAATATGCTAAAGTGAGTTA	257770	89966	TGTGTCACCTGCTGTGTGTG
168597	793	GCGCGTGGACCCCTCCCCAT	213184	45380	AAAATATGCTAAAGTGAGTT	257771	89967	GTGTGTCACCTGCTGTGTGT
168598	794	AGCGCGTGGACCCCTCCCCA	213185	45381	AAAAATATGCTAAAGTGAGT	257772	89968	TGTGTGTCACCTGCTGTGTG
168599	795	CAGCGCGTGGACCCCTCCCC	213186	45382	CAAAAATATGCTAAAGTGAG	257773	89969	GTGTGTGTCACCTGCTGTGT
168600	796	ACAGCGCGTGGACCCCTCCC	213187	45383	GCAAAAATATGCTAAAGTGA	257774	89970	TGTGTGTGTCACCTGCTGTG
168601	797	GACAGCGCGTGGACCCCTCC	213188	45384	AGCAAAAATATGCTAAAGTG	257775	89971	CTGTGTGTGTCACCTGCTGT
168602	798	TGACAGCGCGTGGACCCCTC	213189	45385	GAGCAAAAATATGCTAAAGT	257776	89972	GCTGTGTGTGTCACCTGCTG
168603	799	GTGACAGCGCGTGGACCCCT	213190	45386	TGAGCAAAAATATGCTAAAG	257777	89973	TGCTGTGTGTGTCACCTGCT
168604	800	AGTGACAGCGCGTGGACCCC	213191	45387	ATGAGCAAAAATATGCTAAA	257778	89974	ATGCTGTGTGTGTCACCTGC
168605	801	AAGTGACAGCGCGTGGACCC	213192	45388	GATGAGCAAAAATATGCTAA	257779	89975	GATGCTGTGTGTGTCACCTG
168606	802	AAAGTGACAGCGCGTGGACC	213193	45389	CGATGAGCAAAAATATGCTA	257780	89976	GGATGCTGTGTGTGTCACCT
168607	803	TAAAGTGACAGCGCGTGGAC	213194	45390	ACGATGAGCAAAAATATGCT	257781	89977	TGGATGCTGTGTGTGTCACC
168608	804	CTAAAGTGACAGCGCGTGGA	213195	45391	AACGATGAGCAAAAATATGC	257782	89978	CTGGATGCTGTGTGTGTCAC
168609	805	ACTAAAGTGACAGCGCGTGG	213196	45392	AAACGATGAGCAAAAATATG	257783	89979	TCTGGATGCTGTGTGTGTCA
168610	806	AACTAAAGTGACAGCGCGTG	213197	45393	CAAACGATGAGCAAAAATAT	257784	89980	CTCTGGATGCTGTGTGTGTC
168611	807	CAACTAAAGTGACAGCGCGT	213198	45394	ACAAACGATGAGCAAAAATA	257785	89981	CCTCTGGATGCTGTGTGTGT
168612	808	GCAACTAAAGTGACAGCGCG	213199	45395	CACAAACGATGAGCAAAAAT	257786	89982	ACCTCTGGATGCTGTGTGTG
168613	809	GGCAACTAAAGTGACAGCGC	213200	45396	ACACAAACGATGAGCAAAAA	257787	89983	CACCTCTGGATGCTGTGTGT
168614	810	GGGCAACTAAAGTGACAGCG	213201	45397	TACACAAACGATGAGCAAAA	257788	89984	CCACCTCTGGATGCTGTGTG
168615	811	AGGGCAACTAAAGTGACAGC	213202	45398	CTACACAAACGATGAGCAAA	257789	89985	GCCACCTCTGGATGCTGTGT
168616	812	AAGGGCAACTAAAGTGACAG	213203	45399	GCTACACAAACGATGAGCAA	257790	89986	GGCCACCTCTGGATGCTGTG
168617	813	GAAGGGCAACTAAAGTGACA	213204	45400	AGCTACACAAACGATGAGCA	257791	89987	GGGCCACCTCTGGATGCTGT
168618	814	GGAAGGGCAACTAAAGTGAC	213205	45401	AAGCTACACAAACGATGAGC	257792	89988	TGGGCCACCTCTGGATGCTG
168619	815	GGGAAGGGCAACTAAAGTGA	213206	45402	TAAGCTACACAAACGATGAG	257793	89989	CTGGGCCACCTCTGGATGCT
168620	816	GGGGAAGGGCAACTAAAGTG	213207	45403	TTAAGCTACACAAACGATGA	257794	89990	TCTGGGCCACCTCTGGATGC
168621	817	GGGGGAAGGGCAACTAAAGT	213208	45404	TTTAAGCTACACAAACGATG	257795	89991	CTCTGGGCCACCTCTGGATG
168622	818	AGGGGGAAGGGCAACTAAAG	213209	45405	CTTTAAGCTACACAAACGAT	257796	89992	GCTCTGGGCCACCTCTGGAT
168623	819	CAGGGGGAAGGGCAACTAAA	213210	45406	CCTTTAAGCTACACAAACGA	257797	89993	AGCTCTGGGCCACCTCTGGA
168624	820	GCAGGGGGAAGGGCAACTAA	213211	45407	TCCTTTAAGCTACACAAACG	257798	89994	GAGCTCTGGGCCACCTCTGG
168625	821	CGCAGGGGGAAGGGCAACTA	213212	45408	TTCCTTTAAGCTACACAAAC	257799	89995	TGAGCTCTGGGCCACCTCTG
168626	822	GCGCAGGGGGAAGGGCAACT	213213	45409	ATTCCTTTAAGCTACACAAA	257800	89996	ATGAGCTCTGGGCCACCTCT
168627	823	TGCGCAGGGGGAAGGGCAAC	213214	45410	GATTCCTTTAAGCTACACAA	257801	89997	CATGAGCTCTGGGCCACCTC
168628	824	GTGCGCAGGGGGAAGGGCAA	213215	45411	TGATTCCTTTAAGCTACACA	257802	89998	GCATGAGCTCTGGGCCACCT
168629	825	CGTGCGCAGGGGGAAGGGCA	213216	45412	CTGATTCCTTTAAGCTACAC	257803	89999	AGCATGAGCTCTGGGCCACC
168630	826	GCGTGCGCAGGGGGAAGGGC	213217	45413	TCTGATTCCTTTAAGCTACA	257804	90000	CAGCATGAGCTCTGGGCCAC
168631	827	GGCGTGCGCAGGGGGAAGGG	213218	45414	ATCTGATTCCTTTAAGCTAC	257805	90001	ACAGCATGAGCTCTGGGCCA
168632	828	AGGCGTGCGCAGGGGGAAGG	213219	45415	TATCTGATTCCTTTAAGCTA	257806	90002	CACAGCATGAGCTCTGGGCC
168633	829	CAGGCGTGCGCAGGGGGAAG	213220	45416	TTATCTGATTCCTTTAAGCT	257807	90003	GCACAGCATGAGCTCTGGGC
168634	830	CCAGGCGTGCGCAGGGGGAA	213221	45417	ATTATCTGATTCCTTTAAGC	257808	90004	GGCACAGCATGAGCTCTGGG
168635	831	GCCAGGCGTGCGCAGGGGGA	213222	45418	AATTATCTGATTCCTTTAAG	257809	90005	AGGCACAGCATGAGCTCTGG
168636	832	TGCCAGGCGTGCGCAGGGGG	213223	45419	TAATTATCTGATTCCTTTAA	257810	90006	AAGGCACAGCATGAGCTCTG
168637	833	GTGCCAGGCGTGCGCAGGGG	213224	45420	GTAATTATCTGATTCCTTTA	257811	90007	AAAGGCACAGCATGAGCTCT
168638	834	TGTGCCAGGCGTGCGCAGGG	213225	45421	GGTAATTATCTGATTCCTTT	257812	90008	CAAAGGCACAGCATGAGCTC
168639	835	CTGTGCCAGGCGTGCGCAGG	213226	45422	GGGTAATTATCTGATTCCTT	257813	90009	CCAAAGGCACAGCATGAGCT
168640	836	TCTGTGCCAGGCGTGCGCAG	213227	45423	GGGGTAATTATCTGATTCCT	257814	90010	GCCAAAGGCACAGCATGAGC
168641	837	CTCTGTGCCAGGCGTGCGCA	213228	45424	GGGGGTAATTATCTGATTCC	257815	90011	GGCCAAAGGCACAGCATGAG
168642	838	TCTCTGTGCCAGGCGTGCGC	213229	45425	AGGGGGTAATTATCTGATTC	257816	90012	GGGCCAAAGGCACAGCATGA
168643	839	GTCTCTGTGCCAGGCGTGCG	213230	45426	GAGGGGGTAATTATCTGATT	257817	90013	TGGGCCAAAGGCACAGCATG
168644	840	CGTCTCTGTGCCAGGCGTGC	213231	45427	GGAGGGGGTAATTATCTGAT	257818	90014	CTGGGCCAAAGGCACAGCAT
168645	841	GCGTCTCTGTGCCAGGCGTG	213232	45428	GGGAGGGGGTAATTATCTGA	257819	90015	ACTGGGCCAAAGGCACAGCA
168646	842	CGCGTCTCTGTGCCAGGCGT	213233	45429	GGGGAGGGGGTAATTATCTG	257820	90016	CACTGGGCCAAAGGCACAGC
168647	843	TCGCGTCTCTGTGCCAGGCG	213234	45430	TGGGGAGGGGGTAATTATCT	257821	90017	GCACTGGGCCAAAGGCACAG
168648	844	CTCGCGTCTCTGTGCCAGGC	213235	45431	GTGGGGAGGGGGTAATTATC	257822	90018	GGCACTGGGCCAAAGGCACA
168649	845	GCTCGCGTCTCTGTGCCAGG	213236	45432	AGTGGGGAGGGGGTAATTAT	257823	90019	GGGCACTGGGCCAAAGGCAC
168650	846	TGCTCGCGTCTCTGTGCCAG	213237	45433	TAGTGGGGAGGGGGTAATTA	257824	90020	AGGGCACTGGGCCAAAGGCA
168651	847	CTGCTCGCGTCTCTGTGCCA	213238	45434	GTAGTGGGGAGGGGGTAATT	257825	90021	CAGGGCACTGGGCCAAAGGC
168652	848	GCTGCTCGCGTCTCTGTGCC	213239	45435	AGTAGTGGGGAGGGGGTAAT	257826	90022	GCAGGGCACTGGGCCAAAGG
168653	849	CGCTGCTCGCGTCTCTGTGC	213240	45436	AAGTAGTGGGGAGGGGGTAA	257827	90023	GGCAGGGCACTGGGCCAAAG
168654	850	GCGCTGCTCGCGTCTCTGTG	213241	45437	AAAGTAGTGGGGAGGGGGTA	257828	90024	GGGCAGGGCACTGGGCCAAA
168655	851	GGCGCTGCTCGCGTCTCTGT	213242	45438	GAAAGTAGTGGGGAGGGGGT	257829	90025	GGGGCAGGGCACTGGGCCAA
168656	852	CGGCGCTGCTCGCGTCTCTG	213243	45439	CGAAAGTAGTGGGGAGGGGG	257830	90026	GGGGGCAGGGCACTGGGCCA
168657	853	ACGGCGCTGCTCGCGTCTCT	213244	45440	CCGAAAGTAGTGGGGAGGGG	257831	90027	TGGGGGCAGGGCACTGGGCC
168658	854	CACGGCGCTGCTCGCGTCTC	213245	45441	TCCGAAAGTAGTGGGGAGGG	257832	90028	GTGGGGGCAGGGCACTGGGC
168659	855	GCACGGCGCTGCTCGCGTCT	213246	45442	TTCCGAAAGTAGTGGGGAGG	257833	90029	GGTGGGGGCAGGGCACTGGG
168660	856	GGCACGGCGCTGCTCGCGTC	213247	45443	CTTCCGAAAGTAGTGGGGAG	257834	90030	GGGTGGGGGCAGGGCACTGG
168661	857	AGGCACGGCGCTGCTCGCGT	213248	45444	GCTTCCGAAAGTAGTGGGGA	257835	90031	TGGGTGGGGGCAGGGCACTG
168662	858	CAGGCACGGCGCTGCTCGCG	213249	45445	TGCTTCCGAAAGTAGTGGGG	257836	90032	GTGGGTGGGGGCAGGGCACT
168663	859	TCAGGCACGGCGCTGCTCGC	213250	45446	GTGCTTCCGAAAGTAGTGGG	257837	90033	AGTGGGTGGGGGCAGGGCAC
168664	860	CTCAGGCACGGCGCTGCTCG	213251	45447	TGTGCTTCCGAAAGTAGTGG	257838	90034	GAGTGGGTGGGGGCAGGGCA
168665	861	TCTCAGGCACGGCGCTGCTC	213252	45448	TTGTGCTTCCGAAAGTAGTG	257839	90035	AGAGTGGGTGGGGGCAGGGC
168666	862	TTCTCAGGCACGGCGCTGCT	213253	45449	TTTGTGCTTCCGAAAGTAGT	257840	90036	CAGAGTGGGTGGGGGCAGGG

168667	863	GTTCTCAGGCACGGCGCTGC	213254	45450	ATTTGTGCTTCCGAAAGTAG	257841	90037	GCAGAGTGGGTGGGGGCAGG
168668	864	TGTTCTCAGGCACGGCGCTG	213255	45451	CATTTGTGCTTCCGAAAGTA	257842	90038	GGCAGAGTGGGTGGGGGCAG
168669	865	CTGTTCTCAGGCACGGCGCT	213256	45452	GCATTTGTGCTTCCGAAAGT	257843	90039	AGGCAGAGTGGGTGGGGGCA
168670	866	ACTGTTCTCAGGCACGGCGC	213257	45453	TGCATTTGTGCTTCCGAAAG	257844	90040	AAGGCAGAGTGGGTGGGGGC
168671	867	CACTGTTCTCAGGCACGGCG	213258	45454	TTGCATTTGTGCTTCCGAAA	257845	90041	CAAGGCAGAGTGGGTGGGGG
168672	868	GCACTGTTCTCAGGCACGGC	213259	45455	ATTGCATTTGTGCTTCCGAA	257846	90042	ACAAGGCAGAGTGGGTGGGG
168673	869	CGCACTGTTCTCAGGCACGG	213260	45456	CATTGCATTTGTGCTTCCGA	257847	90043	CACAAGGCAGAGTGGGTGGG
168674	870	GCGCACTGTTCTCAGGCACG	213261	45457	GCATTGCATTTGTGCTTCCG	257848	90044	CCACAAGGCAGAGTGGGTGG
168675	871	CGCGCACTGTTCTCAGGCAC	213262	45458	GGCATTGCATTTGTGCTTCC	257849	90045	GCCACAAGGCAGAGTGGGTG
168676	872	CCGCGCACTGTTCTCAGGCA	213263	45459	GGGCATTGCATTTGTGCTTC	257850	90046	TGCCACAAGGCAGAGTGGGT
168677	873	TCCGCGCACTGTTCTCAGGC	213264	45460	AGGGCATTGCATTTGTGCTT	257851	90047	CTGCCACAAGGCAGAGTGGG
168678	874	ATCCGCGCACTGTTCTCAGG	213265	45461	TAGGGCATTGCATTTGTGCT	257852	90048	CCTGCCACAAGGCAGAGTGG
168679	875	GATCCGCGCACTGTTCTCAG	213266	45462	CTAGGGCATTGCATTTGTGC	257853	90049	TCCTGCCACAAGGCAGAGTG
168680	876	GGATCCGCGCACTGTTCTCA	213267	45463	TCTAGGGCATTGCATTTGTG	257854	90050	TTCCTGCCACAAGGCAGAGT
168681	877	GGGATCCGCGCACTGTTCTC	213268	45464	TTCTAGGGCATTGCATTTGT	257855	90051	CTTCCTGCCACAAGGCAGAG
168682	878	TGGGATCCGCGCACTGTTCT	213269	45465	ATTCTAGGGCATTGCATTTG	257856	90052	TCTTCCTGCCACAAGGCAGA
168683	879	GTGGGATCCGCGCACTGTTC	213270	45466	AATTCTAGGGCATTGCATTT	257857	90053	GTCTTCCTGCCACAAGGCAG
168684	880	AGTGGGATCCGCGCACTGTT	213271	45467	CAATTCTAGGGCATTGCATT	257858	90054	TGTCTTCCTGCCACAAGGCA
168685	881	CAGTGGGATCCGCGCACTGT	213272	45468	ACAATTCTAGGGCATTGCAT	257859	90055	TTGTCTTCCTGCCACAAGGC
168686	882	ACAGTGGGATCCGCGCACTG	213273	45469	TACAATTCTAGGGCATTGCA	257860	90056	CTTGTCTTCCTGCCACAAGG
168687	883	CACAGTGGGATCCGCGCACT	213274	45470	GTACAATTCTAGGGCATTGC	257861	90057	CCTTGTCTTCCTGCCACAAG
168688	884	GCACAGTGGGATCCGCGCAC	213275	45471	AGTACAATTCTAGGGCATTG	257862	90058	TCCTTGTCTTCCTGCCACAA
168689	885	TGCACAGTGGGATCCGCGCA	213276	45472	CAGTACAATTCTAGGGCATT	257863	90059	CTCCTTGTCTTCCTGCCACA
168690	886	GTGCACAGTGGGATCCGCGC	213277	45473	CCAGTACAATTCTAGGGCAT	257864	90060	GCTCCTTGTCTTCCTGCCAC
168691	887	CGTGCACAGTGGGATCCGCG	213278	45474	CCCAGTACAATTCTAGGGCA	257865	90061	TGCTCCTTGTCTTCCTGCCA
168692	888	GCGTGCACAGTGGGATCCGC	213279	45475	CCCCAGTACAATTCTAGGGC	257866	90062	CTGCTCCTTGTCTTCCTGCC
168693	889	AGCGTGCACAGTGGGATCCG	213280	45476	TCCCCAGTACAATTCTAGGG	257867	90063	TCTGCTCCTTGTCTTCCTGC
168694	890	GAGCGTGCACAGTGGGATCC	213281	45477	GTCCCCAGTACAATTCTAGG	257868	90064	GTCTGCTCCTTGTCTTCCTG
168695	891	CGAGCGTGCACAGTGGGATC	213282	45478	AGTCCCCAGTACAATTCTAG	257869	90065	TGTCTGCTCCTTGTCTTCCT
168696	892	GCGAGCGTGCACAGTGGGAT	213283	45479	GAGTCCCCAGTACAATTCTA	257870	90066	GTGTCTGCTCCTTGTCTTCC
168697	893	TGCGAGCGTGCACAGTGGGA	213284	45480	TGAGTCCCCAGTACAATTCT	257871	90067	TGTGTCTGCTCCTTGTCTTC
168698	894	TTGCGAGCGTGCACAGTGGG	213285	45481	TTGAGTCCCCAGTACAATTC	257872	90068	TTGTGTCTGCTCCTTGTCTT
168699	895	TTTGCGAGCGTGCACAGTGG	213286	45482	TTTGAGTCCCCAGTACAATT	257873	90069	CTTGTGTCTGCTCCTTGTCT
168700	896	CTTTGCGAGCGTGCACAGTG	213287	45483	TTTTGAGTCCCCAGTACAAT	257874	90070	TCTTGTGTCTGCTCCTTGTC
168701	897	CCTTTGCGAGCGTGCACAGT	213288	45484	TTTTTGAGTCCCCAGTACAA	257875	90071	ATCTTGTGTCTGCTCCTTGT
168702	898	GCCTTTGCGAGCGTGCACAG	213289	45485	CTTTTTGAGTCCCCAGTACA	257876	90072	GATCTTGTGTCTGCTCCTTG
168703	899	TGCCTTTGCGAGCGTGCACA	213290	45486	TCTTTTTGAGTCCCCAGTAC	257877	90073	AGATCTTGTGTCTGCTCCTT
168704	900	CTGCCTTTGCGAGCGTGCAC	213291	45487	TTCTTTTTGAGTCCCCAGTA	257878	90074	GAGATCTTGTGTCTGCTCCT
168705	901	CCTGCCTTTGCGAGCGTGCA	213292	45488	TTTCTTTTTGAGTCCCCAGT	257879	90075	GGAGATCTTGTGTCTGCTCC
168706	902	CCCTGCCTTTGCGAGCGTGC	213293	45489	TTTTCTTTTTGAGTCCCCAG	257880	90076	GGGAGATCTTGTGTCTGCTC
168707	903	ACCCTGCCTTTGCGAGCGTG	213294	45490	CTTTTCTTTTTGAGTCCCCA	257881	90077	AGGGAGATCTTGTGTCTGCT
168708	904	AACCCTGCCTTTGCGAGCGT	213295	45491	TCTTTTCTTTTTGAGTCCCC	257882	90078	CAGGGAGATCTTGTGTCTGC
168709	905	GAACCCTGCCTTTGCGAGCG	213296	45492	CTCTTTTCTTTTTGAGTCCC	257883	90079	CCAGGGAGATCTTGTGTCTG
168710	906	TGAACCCTGCCTTTGCGAGC	213297	45493	TCTCTTTTCTTTTTGAGTCC	257884	90080	ACCAGGGAGATCTTGTGTCT
168711	907	GTGAACCCTGCCTTTGCGAG	213298	45494	CTCTCTTTTCTTTTTGAGTC	257885	90081	GACCAGGGAGATCTTGTGTC
168712	908	GGTGAACCCTGCCTTTGCGA	213299	45495	ACTCTCTTTTCTTTTTGAGT	257886	90082	GGACCAGGGAGATCTTGTGT
168713	909	AGGTGAACCCTGCCTTTGCG	213300	45496	TACTCTCTTTTCTTTTTGAG	257887	90083	TGGACCAGGGAGATCTTGTG
168714	910	CAGGTGAACCCTGCCTTTGC	213301	45497	CTACTCTCTTTTCTTTTTGA	257888	90084	GTGGACCAGGGAGATCTTGT
168715	911	CCAGGTGAACCCTGCCTTTG	213302	45498	ACTACTCTCTTTTCTTTTTG	257889	90085	TGTGGACCAGGGAGATCTTG
168716	912	GCCAGGTGAACCCTGCCTTT	213303	45499	TACTACTCTCTTTTCTTTTT	257890	90086	ATGTGGACCAGGGAGATCTT
168717	913	GGCCAGGTGAACCCTGCCTT	213304	45500	TTACTACTCTCTTTTCTTTT	257891	90087	CATGTGGACCAGGGAGATCT
168718	914	AGGCCAGGTGAACCCTGCCT	213305	45501	TTTACTACTCTCTTTTCTTT	257892	90088	GCATGTGGACCAGGGAGATC
168719	915	CAGGCCAGGTGAACCCTGCC	213306	45502	TTTTACTACTCTCTTTTCTT	257893	90089	GGCATGTGGACCAGGGAGAT
168720	916	CCAGGCCAGGTGAACCCTGC	213307	45503	ATTTTACTACTCTCTTTTCT	257894	90090	TGGCATGTGGACCAGGGAGA
168721	917	GCCAGGCCAGGTGAACCCTG	213308	45504	GATTTTACTACTCTCTTTTC	257895	90091	GTGGCATGTGGACCAGGGAG
168722	918	CGCCAGGCCAGGTGAACCCT	213309	45505	AGATTTTACTACTCTCTTTT	257896	90092	GGTGGCATGTGGACCAGGGA
168723	919	TCGCCAGGCCAGGTGAACCC	213310	45506	TAGATTTTACTACTCTCTTT	257897	90093	TGGTGGCATGTGGACCAGGG
168724	920	ATCGCCAGGCCAGGTGAACC	213311	45507	ATAGATTTTACTACTCTCTT	257898	90094	GTGGTGGCATGTGGACCAGG
168725	921	CATCGCCAGGCCAGGTGAAC	213312	45508	AATAGATTTTACTACTCTCT	257899	90095	GGTGGTGGCATGTGGACCAG
168726	922	ACATCGCCAGGCCAGGTGAA	213313	45509	TAATAGATTTTACTACTCTC	257900	90096	AGGTGGTGGCATGTGGACCA
168727	923	CACATCGCCAGGCCAGGTGA	213314	45510	TTAATAGATTTTACTACTCT	257901	90097	GAGGTGGTGGCATGTGGACC
168728	924	CCACATCGCCAGGCCAGGTG	213315	45511	TTTAATAGATTTTACTACTC	257902	90098	GGAGGTGGTGGCATGTGGAC
168729	925	TCCACATCGCCAGGCCAGGT	213316	45512	CTTTAATAGATTTTACTACT	257903	90099	GGGAGGTGGTGGCATGTGGA
168730	926	GTCCACATCGCCAGGCCAGG	213317	45513	CCTTTAATAGATTTTACTAC	257904	90100	AGGGAGGTGGTGGCATGTGG
168731	927	CGTCCACATCGCCAGGCCAG	213318	45514	CCCTTTAATAGATTTTACTA	257905	90101	GAGGGAGGTGGTGGCATGTG
168732	928	CCGTCCACATCGCCAGGCCA	213319	45515	CCCCTTTAATAGATTTTACT	257906	90102	AGAGGGAGGTGGTGGCATGT
168733	929	TCCGTCCACATCGCCAGGCC	213320	45516	TCCCCTTTAATAGATTTTAC	257907	90103	CAGAGGGAGGTGGTGGCATG
168734	930	GTCCGTCCACATCGCCAGGC	213321	45517	GTCCCCTTTAATAGATTTTA	257908	90104	GCAGAGGGAGGTGGTGGCAT
168735	931	AGTCCGTCCACATCGCCAGG	213322	45518	TGTCCCCTTTAATAGATTTT	257909	90105	TGCAGAGGGAGGTGGTGGCA
168736	932	GAGTCCGTCCACATCGCCAG	213323	45519	TTGTCCCCTTTAATAGATTT	257910	90106	CTGCAGAGGGAGGTGGTGGC
168737	933	CGAGTCCGTCCACATCGCCA	213324	45520	TTTGTCCCCTTTAATAGATT	257911	90107	TCTGCAGAGGGAGGTGGTGG
168738	934	CCGAGTCCGTCCACATCGCC	213325	45521	CTTTGTCCCCTTTAATAGAT	257912	90108	CTCTGCAGAGGGAGGTGGTG

168739	935	GCCGAGTCCGTCCACATCGC	213326	45522	TCTTTGTCCCCTTTAATAGA	257913	90109	CCTCTGCAGAGGGAGGTGGT
168740	936	CGCCGAGTCCGTCCACATCG	213327	45523	GTCTTTGTCCCCTTTAATAG	257914	90110	TCCTCTGCAGAGGGAGGTGG
168741	937	CCGCCGAGTCCGTCCACATC	213328	45524	TGTCTTTGTCCCCTTTAATA	257915	90111	GTCCTCTGCAGAGGGAGGTG
168742	938	GCCGCCGAGTCCGTCCACAT	213329	45525	CTGTCTTTGTCCCCTTTAAT	257916	90112	TGTCCTCTGCAGAGGGAGGT
168743	939	GGCCGCCGAGTCCGTCCACA	213330	45526	GCTGTCTTTGTCCCCTTTAA	257917	90113	TTGTCCTCTGCAGAGGGAGG
168744	940	CGGCCGCCGAGTCCGTCCAC	213331	45527	GGCTGTCTTTGTCCCCTTTA	257918	90114	CTTGTCCTCTGCAGAGGGAG
168745	941	GCGGCCGCCGAGTCCGTCCA	213332	45528	AGGCTGTCTTTGTCCCCTTT	257919	90115	CCTTGTCCTCTGCAGAGGGA
168746	942	AGCGGCCGCCGAGTCCGTCC	213333	45529	TAGGCTGTCTTTGTCCCCTT	257920	90116	CCCTTGTCCTCTGCAGAGGG
168747	943	CAGCGGCCGCCGAGTCCGTC	213334	45530	ATAGGCTGTCTTTGTCCCCT	257921	90117	CCCCTTGTCCTCTGCAGAGG
168748	944	CCAGCGGCCGCCGAGTCCGT	213335	45531	TATAGGCTGTCTTTGTCCCC	257922	90118	TCCCCTTGTCCTCTGCAGAG
168749	945	ACCAGCGGCCGCCGAGTCCG	213336	45532	ATATAGGCTGTCTTTGTCCC	257923	90119	ATCCCCTTGTCCTCTGCAGA
168750	946	GACCAGCGGCCGCCGAGTCC	213337	45533	TATATAGGCTGTCTTTGTCC	257924	90120	GATCCCCTTGTCCTCTGCAG
168751	947	GGACCAGCGGCCGCCGAGTC	213338	45534	GTATATAGGCTGTCTTTGTC	257925	90121	GGATCCCCTTGTCCTCTGCA
168752	948	GGGACCAGCGGCCGCCGAGT	213339	45535	AGTATATAGGCTGTCTTTGT	257926	90122	AGGATCCCCTTGTCCTCTGC
168753	949	GGGGACCAGCGGCCGCCGAG	213340	45536	TAGTATATAGGCTGTCTTTG	257927	90123	GAGGATCCCCTTGTCCTCTG
168754	950	CGGGGACCAGCGGCCGCCGA	213341	45537	GTAGTATATAGGCTGTCTTT	257928	90124	TGAGGATCCCCTTGTCCTCT
168755	951	ACGGGGACCAGCGGCCGCCG	213342	45538	TGTAGTATATAGGCTGTCTT	257929	90125	ATGAGGATCCCCTTGTCCTC
168756	952	AACGGGGACCAGCGGCCGCC	213343	45539	TTGTAGTATATAGGCTGTCT	257930	90126	CATGAGGATCCCCTTGTCCT
168757	953	GAACGGGGACCAGCGGCCGC	213344	45540	CTTGTAGTATATAGGCTGTC	257931	90127	GCATGAGGATCCCCTTGTCC
168758	954	CGAACGGGGACCAGCGGCCG	213345	45541	GCTTGTAGTATATAGGCTGT	257932	90128	AGCATGAGGATCCCCTTGTC
168759	955	GCGAACGGGGACCAGCGGCC	213346	45542	AGCTTGTAGTATATAGGCTG	257933	90129	CAGCATGAGGATCCCCTTGT
168760	956	CGCGAACGGGGACCAGCGGC	213347	45543	AAGCTTGTAGTATATAGGCT	257934	90130	CCAGCATGAGGATCCCCTTG
168761	957	CCGCGAACGGGGACCAGCGG	213348	45544	AAAGCTTGTAGTATATAGGC	257935	90131	GCCAGCATGAGGATCCCCTT
168762	958	CCCGCGAACGGGGACCAGCG	213349	45545	GAAAGCTTGTAGTATATAGG	257936	90132	TGCCAGCATGAGGATCCCCT
168763	959	GCCCGCGAACGGGGACCAGC	213350	45546	AGAAAGCTTGTAGTATATAG	257937	90133	ATGCCAGCATGAGGATCCCC
168764	960	TGCCCGCGAACGGGGACCAG	213351	45547	TAGAAAGCTTGTAGTATATA	257938	90134	AATGCCAGCATGAGGATCCC
168765	961	GTGCCCGCGAACGGGGACCA	213352	45548	ATAGAAAGCTTGTAGTATAT	257939	90135	CAATGCCAGCATGAGGATCC
168766	962	CGTGCCCGCGAACGGGGACC	213353	45549	AATAGAAAGCTTGTAGTATA	257940	90136	CCAATGCCAGCATGAGGATC
168767	963	GCGTGCCCGCGAACGGGGAC	213354	45550	AAATAGAAAGCTTGTAGTAT	257941	90137	TCCAATGCCAGCATGAGGAT
168768	964	TGCGTGCCCGCGAACGGGGA	213355	45551	AAAATAGAAAGCTTGTAGTA	257942	90138	CTCCAATGCCAGCATGAGGA
168769	965	GTGCGTGCCCGCGAACGGGG	213356	45552	AAAAATAGAAAGCTTGTAGT	257943	90139	CCTCCAATGCCAGCATGAGG
168770	966	TGTGCGTGCCCGCGAACGGG	213357	45553	TAAAAATAGAAAGCTTGTAG	257944	90140	CCCTCCAATGCCAGCATGAG
168771	967	CTGTGCGTGCCCGCGAACGG	213358	45554	ATAAAAATAGAAAGCTTGTA	257945	90141	CCCCTCCAATGCCAGCATGA
168772	968	GCTGTGCGTGCCCGCGAACG	213359	45555	CATAAAAATAGAAAGCTTGT	257946	90142	CCCCCTCCAATGCCAGCATG
168773	969	GGCTGTGCGTGCCCGCGAAC	213360	45556	CCATAAAAATAGAAAGCTTG	257947	90143	ACCCCCTCCAATGCCAGCAT
168774	970	CGGCTGTGCGTGCCCGCGAA	213361	45557	GCCATAAAAATAGAAAGCTT	257948	90144	AACCCCCTCCAATGCCAGCA
168775	971	GCGGCTGTGCGTGCCCGCGA	213362	45558	TGCCATAAAAATAGAAAGCT	257949	90145	CAACCCCCTCCAATGCCAGC
168776	972	TGCGGCTGTGCGTGCCCGCG	213363	45559	CTGCCATAAAAATAGAAAGC	257950	90146	TCAACCCCCTCCAATGCCAG
168777	973	CTGCGGCTGTGCGTGCCCGC	213364	45560	TCTGCCATAAAAATAGAAAG	257951	90147	CTCAACCCCCTCCAATGCCA
168778	974	GCTGCGGCTGTGCGTGCCCG	213365	45561	CTCTGCCATAAAAATAGAAA	257952	90148	GCTCAACCCCCTCCAATGCC
168779	975	GGCTGCGGCTGTGCGTGCCC	213366	45562	TCTCTGCCATAAAAATAGAA	257953	90149	TGCTCAACCCCCTCCAATGC
168780	976	TGGCTGCGGCTGTGCGTGCC	213367	45563	TTCTCTGCCATAAAAATAGA	257954	90150	CTGCTCAACCCCCTCCAATG
168781	977	GTGGCTGCGGCTGTGCGTGC	213368	45564	ATTCTCTGCCATAAAAATAG	257955	90151	CCTGCTCAACCCCCTCCAAT
168782	978	CGTGGCTGCGGCTGTGCGTG	213369	45565	CATTCTCTGCCATAAAAATA	257956	90152	CCCTGCTCAACCCCCTCCAA
168783	979	GCGTGGCTGCGGCTGTGCGT	213370	45566	GCATTCTCTGCCATAAAAAT	257957	90153	GCCCTGCTCAACCCCCTCCA
168784	980	TGCGTGGCTGCGGCTGTGCG	213371	45567	GGCATTCTCTGCCATAAAAA	257958	90154	GGCCCTGCTCAACCCCCTCC
168785	981	GTGCGTGGCTGCGGCTGTGC	213372	45568	TGGCATTCTCTGCCATAAAA	257959	90155	GGGCCCTGCTCAACCCCCTC
168786	982	CGTGCGTGGCTGCGGCTGTG	213373	45569	ATGGCATTCTCTGCCATAAA	257960	90156	TGGGCCCTGCTCAACCCCCT
168787	983	CCGTGCGTGGCTGCGGCTGT	213374	45570	AATGGCATTCTCTGCCATAA	257961	90157	GTGGGCCCTGCTCAACCCCC
168788	984	TCCGTGCGTGGCTGCGGCTG	213375	45571	AAATGGCATTCTCTGCCATA	257962	90158	GGTGGGCCCTGCTCAACCCC
168789	985	ATCCGTGCGTGGCTGCGGCT	213376	45572	AAAATGGCATTCTCTGCCAT	257963	90159	AGGTGGGCCCTGCTCAACCC
168790	986	CATCCGTGCGTGGCTGCGGC	213377	45573	GAAAATGGCATTCTCTGCCA	257964	90160	AAGGTGGGCCCTGCTCAACC
168791	987	CCATCCGTGCGTGGCTGCGG	213378	45574	AGAAAATGGCATTCTCTGCC	257965	90161	CAAGGTGGGCCCTGCTCAAC
168792	988	CCCATCCGTGCGTGGCTGCG	213379	45575	TAGAAAATGGCATTCTCTGC	257966	90162	TCAAGGTGGGCCCTGCTCAA
168793	989	GCCCATCCGTGCGTGGCTGC	213380	45576	TTAGAAAATGGCATTCTCTG	257967	90163	CTCAAGGTGGGCCCTGCTCA
168794	990	CGCCCATCCGTGCGTGGCTG	213381	45577	CTTAGAAAATGGCATTCTCT	257968	90164	GCTCAAGGTGGGCCCTGCTC
168795	991	GCGCCCATCCGTGCGTGGCT	213382	45578	ACTTAGAAAATGGCATTCTC	257969	90165	GGCTCAAGGTGGGCCCTGCT
168796	992	CGCGCCCATCCGTGCGTGGC	213383	45579	TACTTAGAAAATGGCATTCT	257970	90166	GGGCTCAAGGTGGGCCCTGC
168797	993	CCGCGCCCATCCGTGCGTGG	213384	45580	TTACTTAGAAAATGGCATTC	257971	90167	AGGGCTCAAGGTGGGCCCTG
168798	994	CCCGCGCCCATCCGTGCGTG	213385	45581	TTTACTTAGAAAATGGCATT	257972	90168	GAGGGCTCAAGGTGGGCCCT
168799	995	CCCCGCGCCCATCCGTGCGT	213386	45582	GTTTACTTAGAAAATGGCAT	257973	90169	TGAGGGCTCAAGGTGGGCCC
168800	996	GCCCCGCGCCCATCCGTGCG	213387	45583	TGTTTACTTAGAAAATGGCA	257974	90170	CTGAGGGCTCAAGGTGGGCC
168801	997	AGCCCCGCGCCCATCCGTGC	213388	45584	CTGTTTACTTAGAAAATGGC	257975	90171	CCTGAGGGCTCAAGGTGGGC
168802	998	CAGCCCCGCGCCCATCCGTG	213389	45585	TCTGTTTACTTAGAAAATGG	257976	90172	TCCTGAGGGCTCAAGGTGGG
168803	999	GCAGCCCCGCGCCCATCCGT	213390	45586	CTCTGTTTACTTAGAAAATG	257977	90173	CTCCTGAGGGCTCAAGGTGG
168804	1000	TGCAGCCCCGCGCCCATCCG	213391	45587	TCTCTGTTTACTTAGAAAAT	257978	90174	GCTCCTGAGGGCTCAAGGTG
168805	1001	CTGCAGCCCCGCGCCCATCC	213392	45588	TTCTCTGTTTACTTAGAAAA	257979	90175	TGCTCCTGAGGGCTCAAGGT
168806	1002	CCTGCAGCCCCGCGCCCATC	213393	45589	GTTCTCTGTTTACTTAGAAA	257980	90176	GTGCTCCTGAGGGCTCAAGG
168807	1003	ACCTGCAGCCCCGCGCCCAT	213394	45590	AGTTCTCTGTTTACTTAGAA	257981	90177	CGTGCTCCTGAGGGCTCAAG
168808	1004	CACCTGCAGCCCCGCGCCCA	213395	45591	CAGTTCTCTGTTTACTTAGA	257982	90178	TCGTGCTCCTGAGGGCTCAA
168809	1005	GCACCTGCAGCCCCGCGCCC	213396	45592	GCAGTTCTCTGTTTACTTAG	257983	90179	GTCGTGCTCCTGAGGGCTCA
168810	1006	TGCACCTGCAGCCCCGCGCC	213397	45593	TGCAGTTCTCTGTTTACTTA	257984	90180	GGTCGTGCTCCTGAGGGCTC

168811	1007	ATGCACCTGCAGCCCCGCGC	213398	45594	ATGCAGTTCTCTGTTTACTT	257985	90181	TGGTCGTGCTCCTGAGGGCT
168812	1008	GATGCACCTGCAGCCCCGCG	213399	45595	AATGCAGTTCTCTGTTTACT	257986	90182	GTGGTCGTGCTCCTGAGGGC
168813	1009	AGATGCACCTGCAGCCCCGC	213400	45596	AAATGCAGTTCTCTGTTTAC	257987	90183	TGTGGTCGTGCTCCTGAGGG
168814	1010	GAGATGCACCTGCAGCCCCG	213401	45597	CAAATGCAGTTCTCTGTTTA	257988	90184	CTGTGGTCGTGCTCCTGAGG
168815	1011	CGAGATGCACCTGCAGCCCC	213402	45598	TCAAATGCAGTTCTCTGTTT	257989	90185	GCTGTGGTCGTGCTCCTGAG
168816	1012	CCGAGATGCACCTGCAGCCC	213403	45599	GTCAAATGCAGTTCTCTGTT	257990	90186	TGCTGTGGTCGTGCTCCTGA
168817	1013	CCCGAGATGCACCTGCAGCC	213404	45600	GGTCAAATGCAGTTCTCTGT	257991	90187	CTGCTGTGGTCGTGCTCCTG
168818	1014	CCCCGAGATGCACCTGCAGC	213405	45601	AGGTCAAATGCAGTTCTCTG	257992	90188	GCTGCTGTGGTCGTGCTCCT
168819	1015	GCCCCGAGATGCACCTGCAG	213406	45602	CAGGTCAAATGCAGTTCTCT	257993	90189	GGCTGCTGTGGTCGTGCTCC
168820	1016	CGCCCCGAGATGCACCTGCA	213407	45603	GCAGGTCAAATGCAGTTCTC	257994	90190	GGGCTGCTGTGGTCGTGCTC
168821	1017	CCGCCCCGAGATGCACCTGC	213408	45604	TGCAGGTCAAATGCAGTTCT	257995	90191	AGGGCTGCTGTGGTCGTGCT
168822	1018	TCCGCCCCGAGATGCACCTG	213409	45605	TTGCAGGTCAAATGCAGTTC	257996	90192	CAGGGCTGCTGTGGTCGTGC
168823	1019	ATCCGCCCCGAGATGCACCT	213410	45606	ATTGCAGGTCAAATGCAGTT	257997	90193	GCAGGGCTGCTGTGGTCGTG
168824	1020	AATCCGCCCCGAGATGCACC	213411	45607	TATTGCAGGTCAAATGCAGT	257998	90194	TGCAGGGCTGCTGTGGTCGT
168825	1021	AAATCCGCCCCGAGATGCAC	213412	45608	ATATTGCAGGTCAAATGCAG	257999	90195	CTGCAGGGCTGCTGTGGTCG
168826	1022	GAAATCCGCCCCGAGATGCA	213413	45609	GATATTGCAGGTCAAATGCA	258000	90196	CCTGCAGGGCTGCTGTGGTC
168827	1023	AGAAATCCGCCCCGAGATGC	213414	45610	TGATATTGCAGGTCAAATGC	258001	90197	CCCTGCAGGGCTGCTGTGGT
168828	1024	AAGAAATCCGCCCCGAGATG	213415	45611	TTGATATTGCAGGTCAAATG	258002	90198	TCCCTGCAGGGCTGCTGTGG
168829	1025	AAAGAAATCCGCCCCGAGAT	213416	45612	TTTGATATTGCAGGTCAAAT	258003	90199	CTCCCTGCAGGGCTGCTGTG
168830	1026	GAAAGAAATCCGCCCCGAGA	213417	45613	ATTTGATATTGCAGGTCAAA	258004	90200	CCTCCCTGCAGGGCTGCTGT
168831	1027	AGAAAGAAATCCGCCCCGAG	213418	45614	CATTTGATATTGCAGGTCAA	258005	90201	CCCTCCCTGCAGGGCTGCTG
168832	1028	GAGAAAGAAATCCGCCCCGA	213419	45615	GCATTTGATATTGCAGGTCA	258006	90202	TCCCTCCCTGCAGGGCTGCT
168833	1029	TGAGAAAGAAATCCGCCCCG	213420	45616	TGCATTTGATATTGCAGGTC	258007	90203	ATCCCTCCCTGCAGGGCTGC
168834	1030	CTGAGAAAGAAATCCGCCCC	213421	45617	ATGCATTTGATATTGCAGGT	258008	90204	AATCCCTCCCTGCAGGGCTG
168835	1031	GCTGAGAAAGAAATCCGCCC	213422	45618	CATGCATTTGATATTGCAGG	258009	90205	CAATCCCTCCCTGCAGGGCT
168836	1032	CGCTGAGAAAGAAATCCGCC	213423	45619	CCATGCATTTGATATTGCAG	258010	90206	CCAATCCCTCCCTGCAGGGC
168837	1033	GCGCTGAGAAAGAAATCCGC	213424	45620	TCCATGCATTTGATATTGCA	258011	90207	ACCAATCCCTCCCTGCAGGG
168838	1034	AGCGCTGAGAAAGAAATCCG	213425	45621	ATCCATGCATTTGATATTGC	258012	90208	CACCAATCCCTCCCTGCAGG
168839	1035	GAGCGCTGAGAAAGAAATCC	213426	45622	AATCCATGCATTTGATATTG	258013	90209	CCACCAATCCCTCCCTGCAG
168840	1036	CGAGCGCTGAGAAAGAAATC	213427	45623	AAATCCATGCATTTGATATT	258014	90210	CCCACCAATCCCTCCCTGCA
168841	1037	CCGAGCGCTGAGAAAGAAAT	213428	45624	CAAATCCATGCATTTGATAT	258015	90211	TCCCACCAATCCCTCCCTGC
168842	1038	TCCGAGCGCTGAGAAAGAAA	213429	45625	TCAAATCCATGCATTTGATA	258016	90212	CTCCCACCAATCCCTCCCTG
168843	1039	CTCCGAGCGCTGAGAAAGAA	213430	45626	ATCAAATCCATGCATTTGAT	258017	90213	CCTCCCACCAATCCCTCCCT
168844	1040	GCTCCGAGCGCTGAGAAAGA	213431	45627	CATCAAATCCATGCATTTGA	258018	90214	TCCTCCCACCAATCCCTCCC
168845	1041	CGCTCCGAGCGCTGAGAAAG	213432	45628	GCATCAAATCCATGCATTTG	258019	90215	CTCCTCCCACCAATCCCTCC
168846	1042	GCGCTCCGAGCGCTGAGAAA	213433	45629	AGCATCAAATCCATGCATTT	258020	90216	TCTCCTCCCACCAATCCCTC
168847	1043	TGCGCTCCGAGCGCTGAGAA	213434	45630	AAGCATCAAATCCATGCATT	258021	90217	CTCTCCTCCCACCAATCCCT
168848	1044	CTGCGCTCCGAGCGCTGAGA	213435	45631	AAAGCATCAAATCCATGCAT	258022	90218	ACTCTCCTCCCACCAATCCC
168849	1045	CCTGCGCTCCGAGCGCTGAG	213436	45632	CAAAGCATCAAATCCATGCA	258023	90219	GACTCTCCTCCCACCAATCC
168850	1046	CCCTGCGCTCCGAGCGCTGA	213437	45633	CCAAAGCATCAAATCCATGC	258024	90220	GGACTCTCCTCCCACCAATC
168851	1047	GCCCTGCGCTCCGAGCGCTG	213438	45634	TCCAAAGCATCAAATCCATG	258025	90221	GGGACTCTCCTCCCACCAAT
168852	1048	CGCCCTGCGCTCCGAGCGCT	213439	45635	TTCCAAAGCATCAAATCCAT	258026	90222	TGGGACTCTCCTCCCACCAA
168853	1049	GCGCCCTGCGCTCCGAGCGC	213440	45636	TTTCCAAAGCATCAAATCCA	258027	90223	TTGGGACTCTCCTCCCACCA
168854	1050	GGCGCCCTGCGCTCCGAGCG	213441	45637	CTTTCCAAAGCATCAAATCC	258028	90224	CTTGGGACTCTCCTCCCACC
168855	1051	GGGCGCCCTGCGCTCCGAGC	213442	45638	GCTTTCCAAAGCATCAAATC	258029	90225	ACTTGGGACTCTCCTCCCAC
168856	1052	CGGGCGCCCTGCGCTCCGAG	213443	45639	TGCTTTCCAAAGCATCAAAT	258030	90226	TACTTGGGACTCTCCTCCCA
168857	1053	CCGGGCGCCCTGCGCTCCGA	213444	45640	TTGCTTTCCAAAGCATCAAA	258031	90227	ATACTTGGGACTCTCCTCCC
168858	1054	GCCGGGCGCCCTGCGCTCCG	213445	45641	GTTGCTTTCCAAAGCATCAA	258032	90228	GATACTTGGGACTCTCCTCC
168859	1055	CGCCGGGCGCCCTGCGCTCC	213446	45642	AGTTGCTTTCCAAAGCATCA	258033	90229	TGATACTTGGGACTCTCCTC
168860	1056	ACGCCGGGCGCCCTGCGCTC	213447	45643	CAGTTGCTTTCCAAAGCATC	258034	90230	CTGATACTTGGGACTCTCCT
168861	1057	CACGCCGGGCGCCCTGCGCT	213448	45644	ACAGTTGCTTTCCAAAGCAT	258035	90231	CCTGATACTTGGGACTCTCC
168862	1058	ACACGCCGGGCGCCCTGCGC	213449	45645	AACAGTTGCTTTCCAAAGCA	258036	90232	CCCTGATACTTGGGACTCTC
168863	1059	CACACGCCGGGCGCCCTGCG	213450	45646	AAACAGTTGCTTTCCAAAGC	258037	90233	TCCCTGATACTTGGGACTCT
168864	1060	GCACACGCCGGGCGCCCTGC	213451	45647	AAAACAGTTGCTTTCCAAAG	258038	90234	CTCCCTGATACTTGGGACTC
168865	1061	CGCACACGCCGGGCGCCCTG	213452	45648	GAAAACAGTTGCTTTCCAAA	258039	90235	TCTCCCTGATACTTGGGACT
168866	1062	GCGCACACGCCGGGCGCCCT	213453	45649	AGAAAACAGTTGCTTTCCAA	258040	90236	CTCTCCCTGATACTTGGGAC
168867	1063	AGCGCACACGCCGGGCGCCC	213454	45650	CAGAAAACAGTTGCTTTCCA	258041	90237	CCTCTCCCTGATACTTGGGA
168868	1064	GAGCGCACACGCCGGGCGCC	213455	45651	GCAGAAAACAGTTGCTTTCC	258042	90238	TCCTCTCCCTGATACTTGGG
168869	1065	GGAGCGCACACGCCGGGCGC	213456	45652	CGCAGAAAACAGTTGCTTTC	258043	90239	CTCCTCTCCCTGATACTTGG
168870	1066	GGGAGCGCACACGCCGGGCG	213457	45653	ACGCAGAAAACAGTTGCTTT	258044	90240	TCTCCTCTCCCTGATACTTG
168871	1067	AGGGAGCGCACACGCCGGGC	213458	45654	AACGCAGAAAACAGTTGCTT	258045	90241	CTCTCCTCTCCCTGATACTT
168872	1068	CAGGGAGCGCACACGCCGGG	213459	45655	TAACGCAGAAAACAGTTGCT	258046	90242	ACTCTCCTCTCCCTGATACT
168873	1069	GCAGGGAGCGCACACGCCGG	213460	45656	TTAACGCAGAAAACAGTTGC	258047	90243	AACTCTCCTCTCCCTGATAC
168874	1070	GGCAGGGAGCGCACACGCCG	213461	45657	ATTAACGCAGAAAACAGTTG	258048	90244	CAACTCTCCTCTCCCTGATA
168875	1071	CGGCAGGGAGCGCACACGCC	213462	45658	GATTAACGCAGAAAACAGTT	258049	90245	CCAACTCTCCTCTCCCTGAT
168876	1072	CCGGCAGGGAGCGCACACGC	213463	45659	AGATTAACGCAGAAAACAGT	258050	90246	ACCAACTCTCCTCTCCCTGA
168877	1073	TCCGGCAGGGAGCGCACACG	213464	45660	CAGATTAACGCAGAAAACAG	258051	90247	CACCAACTCTCCTCTCCCTG
168878	1074	CTCCGGCAGGGAGCGCACAC	213465	45661	CCAGATTAACGCAGAAAACA	258052	90248	ACACCAACTCTCCTCTCCCT
168879	1075	CCTCCGGCAGGGAGCGCACA	213466	45662	CCCAGATTAACGCAGAAAAC	258053	90249	GACACCAACTCTCCTCTCCC
168880	1076	GCCTCCGGCAGGGAGCGCAC	213467	45663	ACCCAGATTAACGCAGAAAA	258054	90250	GGACACCAACTCTCCTCTCC
168881	1077	CGCCTCCGGCAGGGAGCGCA	213468	45664	CACCCAGATTAACGCAGAAA	258055	90251	GGGACACCAACTCTCCTCTC
168882	1078	GCGCCTCCGGCAGGGAGCGC	213469	45665	ACACCCAGATTAACGCAGAA	258056	90252	TGGGACACCAACTCTCCTCT

168883	1079	CGCGCCTCCGGCAGGGAGCG	213470	45666	GACACCCAGATTAACGCAGA	258057	90253	GTGGGACACCAACTCTCCTC
168884	1080	CCGCGCCTCCGGCAGGGAGC	213471	45667	AGACACCCAGATTAACGCAG	258058	90254	TGTGGGACACCAACTCTCCT
168885	1081	CCCGCGCCTCCGGCAGGGAG	213472	45668	AAGACACCCAGATTAACGCA	258059	90255	CTGTGGGACACCAACTCTCC
168886	1082	CCCCGCGCCTCCGGCAGGGA	213473	45669	GAAGACACCCAGATTAACGC	258060	90256	CCTGTGGGACACCAACTCTC
168887	1083	GCCCCGCGCCTCCGGCAGGG	213474	45670	GGAAGACACCCAGATTAACG	258061	90257	TCCTGTGGGACACCAACTCT
168888	1084	AGCCCCGCGCCTCCGGCAGG	213475	45671	CGGAAGACACCCAGATTAAC	258062	90258	CTCCTGTGGGACACCAACTC
168889	1085	CAGCCCCGCGCCTCCGGCAG	213476	45672	ACGGAAGACACCCAGATTAA	258063	90259	TCTCCTGTGGGACACCAACT
168890	1086	CCAGCCCCGCGCCTCCGGCA	213477	45673	CACGGAAGACACCCAGATTA	258064	90260	GTCTCCTGTGGGACACCAAC
168891	1087	GCCAGCCCCGCGCCTCCGGC	213478	45674	TCACGGAAGACACCCAGATT	258065	90261	GGTCTCCTGTGGGACACCAA
168892	1088	CGCCAGCCCCGCGCCTCCGG	213479	45675	TTCACGGAAGACACCCAGAT	258066	90262	AGGTCTCCTGTGGGACACCA
168893	1089	GCGCCAGCCCCGCGCCTCCG	213480	45676	TTTCACGGAAGACACCCAGA	258067	90263	GAGGTCTCCTGTGGGACACC
168894	1090	CGCGCCAGCCCCGCGCCTCC	213481	45677	ATTTCACGGAAGACACCCAG	258068	90264	TGAGGTCTCCTGTGGGACAC
168895	1091	GCGCGCCAGCCCCGCGCCTC	213482	45678	CATTTCACGGAAGACACCCA	258069	90265	CTGAGGTCTCCTGTGGGACA
168896	1092	TGCGCGCCAGCCCCGCGCCT	213483	45679	ACATTTCACGGAAGACACCC	258070	90266	TCTGAGGTCTCCTGTGGGAC
168897	1093	CTGCGCGCCAGCCCCGCGCC	213484	45680	GACATTTCACGGAAGACACC	258071	90267	CTCTGAGGTCTCCTGTGGGA
168898	1094	CCTGCGCGCCAGCCCCGCGC	213485	45681	GGACATTTCACGGAAGACAC	258072	90268	GCTCTGAGGTCTCCTGTGGG
168899	1095	CCCTGCGCGCCAGCCCCGCG	213486	45682	AGGACATTTCACGGAAGACA	258073	90269	GGCTCTGAGGTCTCCTGTGG
168900	1096	GCCCTGCGCGCCAGCCCCGC	213487	45683	GAGGACATTTCACGGAAGAC	258074	90270	TGGCTCTGAGGTCTCCTGTG
168901	1097	AGCCCTGCGCGCCAGCCCCG	213488	45684	GGAGGACATTTCACGGAAGA	258075	90271	GTGGCTCTGAGGTCTCCTGT
168902	1098	GAGCCCTGCGCGCCAGCCCC	213489	45685	AGGAGGACATTTCACGGAAG	258076	90272	TGTGGCTCTGAGGTCTCCTG
168903	1099	CGAGCCCTGCGCGCCAGCCC	213490	45686	CAGGAGGACATTTCACGGAA	258077	90273	TTGTGGCTCTGAGGTCTCCT
168904	1100	GCGAGCCCTGCGCGCCAGCC	213491	45687	GCAGGAGGACATTTCACGGA	258078	90274	CTTGTGGCTCTGAGGTCTCC
168905	1101	GGCGAGCCCTGCGCGCCAGC	213492	45688	GGCAGGAGGACATTTCACGG	258079	90275	CCTTGTGGCTCTGAGGTCTC
168906	1102	GGGCGAGCCCTGCGCGCCAG	213493	45689	AGGCAGGAGGACATTTCACG	258080	90276	GCCTTGTGGCTCTGAGGTCT
168907	1103	GGGGCGAGCCCTGCGCGCCA	213494	45690	AAGGCAGGAGGACATTTCAC	258081	90277	CGCCTTGTGGCTCTGAGGTC
168908	1104	AGGGGCGAGCCCTGCGCGCC	213495	45691	AAAGGCAGGAGGACATTTCA	258082	90278	TCGCCTTGTGGCTCTGAGGT
168909	1105	GAGGGGCGAGCCCTGCGCGC	213496	45692	CAAAGGCAGGAGGACATTTC	258083	90279	CTCGCCTTGTGGCTCTGAGG
168910	1106	TGAGGGGCGAGCCCTGCGCG	213497	45693	CCAAAGGCAGGAGGACATTT	258084	90280	GCTCGCCTTGTGGCTCTGAG
168911	1107	GTGAGGGGCGAGCCCTGCGC	213498	45694	GCCAAAGGCAGGAGGACATT	258085	90281	AGCTCGCCTTGTGGCTCTGA
168912	1108	AGTGAGGGGCGAGCCCTGCG	213499	45695	AGCCAAAGGCAGGAGGACAT	258086	90282	AAGCTCGCCTTGTGGCTCTG
168913	1109	CAGTGAGGGGCGAGCCCTGC	213500	45696	AAGCCAAAGGCAGGAGGACA	258087	90283	CAAGCTCGCCTTGTGGCTCT
168914	1110	GCAGTGAGGGGCGAGCCCTG	213501	45697	TAAGCCAAAGGCAGGAGGAC	258088	90284	ACAAGCTCGCCTTGTGGCTC
168915	1111	CGCAGTGAGGGGCGAGCCCT	213502	45698	TTAAGCCAAAGGCAGGAGGA	258089	90285	AACAAGCTCGCCTTGTGGCT
168916	1112	CCGCAGTGAGGGGCGAGCCC	213503	45699	TTTAAGCCAAAGGCAGGAGG	258090	90286	GAACAAGCTCGCCTTGTGGC
168917	1113	GCCGCAGTGAGGGGCGAGCC	213504	45700	GTTTAAGCCAAAGGCAGGAG	258091	90287	TGAACAAGCTCGCCTTGTGG
168918	1114	TGCCGCAGTGAGGGGCGAGC	213505	45701	TGTTTAAGCCAAAGGCAGGA	258092	90288	ATGAACAAGCTCGCCTTGTG
168919	1115	CTGCCGCAGTGAGGGGCGAG	213506	45702	GTGTTTAAGCCAAAGGCAGG	258093	90289	TATGAACAAGCTCGCCTTGT
168920	1116	ACTGCCGCAGTGAGGGGCGA	213507	45703	AGTGTTTAAGCCAAAGGCAG	258094	90290	TTATGAACAAGCTCGCCTTG
168921	1117	CACTGCCGCAGTGAGGGGCG	213508	45704	TAGTGTTTAAGCCAAAGGCA	258095	90291	TTTATGAACAAGCTCGCCTT
168922	1118	CCACTGCCGCAGTGAGGGGC	213509	45705	CTAGTGTTTAAGCCAAAGGC	258096	90292	ATTTATGAACAAGCTCGCCT
168923	1119	CCCACTGCCGCAGTGAGGGG	213510	45706	GCTAGTGTTTAAGCCAAAGG	258097	90293	AATTTATGAACAAGCTCGCC
168924	1120	ACCCACTGCCGCAGTGAGGG	213511	45707	AGCTAGTGTTTAAGCCAAAG	258098	90294	AAATTTATGAACAAGCTCGC
168925	1121	CACCCACTGCCGCAGTGAGG	213512	45708	AAGCTAGTGTTTAAGCCAAA	258099	90295	CAAATTTATGAACAAGCTCG
168926	1122	ACACCCACTGCCGCAGTGAG	213513	45709	AAAGCTAGTGTTTAAGCCAA	258100	90296	CCAAATTTATGAACAAGCTC
168927	1123	CACACCCACTGCCGCAGTGA	213514	45710	CAAAGCTAGTGTTTAAGCCA	258101	90297	CCCAAATTTATGAACAAGCT
168928	1124	CCACACCCACTGCCGCAGTG	213515	45711	ACAAAGCTAGTGTTTAAGCC	258102	90298	TCCCAAATTTATGAACAAGC
168929	1125	TCCACACCCACTGCCGCAGT	213516	45712	GACAAAGCTAGTGTTTAAGC	258103	90299	GTCCCAAATTTATGAACAAG
168930	1126	GTCCACACCCACTGCCGCAG	213517	45713	AGACAAAGCTAGTGTTTAAG	258104	90300	GGTCCCAAATTTATGAACAA
168931	1127	GGTCCACACCCACTGCCGCA	213518	45714	TAGACAAAGCTAGTGTTTAA	258105	90301	GGGTCCCAAATTTATGAACA
168932	1128	GGGTCCACACCCACTGCCGC	213519	45715	GTAGACAAAGCTAGTGTTTA	258106	90302	AGGGTCCCAAATTTATGAAC
168933	1129	AGGGTCCACACCCACTGCCG	213520	45716	TGTAGACAAAGCTAGTGTTT	258107	90303	AAGGGTCCCAAATTTATGAA
168934	1130	CAGGGTCCACACCCACTGCC	213521	45717	CTGTAGACAAAGCTAGTGTT	258108	90304	TAAGGGTCCCAAATTTATGA
168935	1131	CCAGGGTCCACACCCACTGC	213522	45718	GCTGTAGACAAAGCTAGTGT	258109	90305	CTAAGGGTCCCAAATTTATG
168936	1132	ACCAGGGTCCACACCCACTG	213523	45719	GGCTGTAGACAAAGCTAGTG	258110	90306	GCTAAGGGTCCCAAATTTAT
168937	1133	CACCAGGGTCCACACCCACT	213524	45720	TGGCTGTAGACAAAGCTAGT	258111	90307	TGCTAAGGGTCCCAAATTTA
168938	1134	CCACCAGGGTCCACACCCAC	213525	45721	ATGGCTGTAGACAAAGCTAG	258112	90308	ATGCTAAGGGTCCCAAATTT
168939	1135	CCCACCAGGGTCCACACCCA	213526	45722	AATGGCTGTAGACAAAGCTA	258113	90309	AATGCTAAGGGTCCCAAATT
168940	1136	GCCCACCAGGGTCCACACCC	213527	45723	GAATGGCTGTAGACAAAGCT	258114	90310	AAATGCTAAGGGTCCCAAAT
168941	1137	CGCCCACCAGGGTCCACACC	213528	45724	GGAATGGCTGTAGACAAAGC	258115	90311	GAAATGCTAAGGGTCCCAAA
168942	1138	TCGCCCACCAGGGTCCACAC	213529	45725	TGGAATGGCTGTAGACAAAG	258116	90312	TGAAATGCTAAGGGTCCCAA
168943	1139	CTCGCCCACCAGGGTCCACA	213530	45726	ATGGAATGGCTGTAGACAAA	258117	90313	GTGAAATGCTAAGGGTCCCA
168944	1140	CCTCGCCCACCAGGGTCCAC	213531	45727	GATGGAATGGCTGTAGACAA	258118	90314	TGTGAAATGCTAAGGGTCCC
168945	1141	TCCTCGCCCACCAGGGTCCA	213532	45728	GGATGGAATGGCTGTAGACA	258119	90315	CTGTGAAATGCTAAGGGTCC
168946	1142	TTCCTCGCCCACCAGGGTCC	213533	45729	AGGATGGAATGGCTGTAGAC	258120	90316	ACTGTGAAATGCTAAGGGTC
168947	1143	CTTCCTCGCCCACCAGGGTC	213534	45730	CAGGATGGAATGGCTGTAGA	258121	90317	AACTGTGAAATGCTAAGGGT
168948	1144	CCTTCCTCGCCCACCAGGGT	213535	45731	TCAGGATGGAATGGCTGTAG	258122	90318	TAACTGTGAAATGCTAAGGG
168949	1145	CCCTTCCTCGCCCACCAGGG	213536	45732	TTCAGGATGGAATGGCTGTA	258123	90319	ATAACTGTGAAATGCTAAGG
168950	1146	CCCCTTCCTCGCCCACCAGG	213537	45733	GTTCAGGATGGAATGGCTGT	258124	90320	AATAACTGTGAAATGCTAAG
168951	1147	CCCCCTTCCTCGCCCACCAG	213538	45734	GGTTCAGGATGGAATGGCTG	258125	90321	AAATAACTGTGAAATGCTAA
168952	1148	TCCCCCTTCCTCGCCCACCA	213539	45735	AGGTTCAGGATGGAATGGCT	258126	90322	CAAATAACTGTGAAATGCTA
168953	1149	CTCCCCCTTCCTCGCCCACC	213540	45736	CAGGTTCAGGATGGAATGGC	258127	90323	GCAAATAACTGTGAAATGCT
168954	1150	CCTCCCCCTTCCTCGCCCAC	213541	45737	GCAGGTTCAGGATGGAATGG	258128	90324	TGCAAATAACTGTGAAATGC

168955	1151	TCCTCCCCCTTCCTCGCCCA	213542	45738	GGCAGGTTCAGGATGGAATG	258129	90325	CTGCAAATAACTGTGAAATG
168956	1152	ATCCTCCCCCTTCCTCGCCC	213543	45739	GGGCAGGTTCAGGATGGAAT	258130	90326	TCTGCAAATAACTGTGAAAT
168957	1153	TATCCTCCCCCTTCCTCGCC	213544	45740	TGGGCAGGTTCAGGATGGAA	258131	90327	CTCTGCAAATAACTGTGAAA
168958	1154	CTATCCTCCCCCTTCCTCGC	213545	45741	TTGGGCAGGTTCAGGATGGA	258132	90328	GCTCTGCAAATAACTGTGAA
168959	1155	CCTATCCTCCCCCTTCCTCG	213546	45742	ATTGGGCAGGTTCAGGATGG	258133	90329	GGCTCTGCAAATAACTGTGA
168960	1156	GCCTATCCTCCCCCTTCCTC	213547	45743	GATTGGGCAGGTTCAGGATG	258134	90330	GGGCTCTGCAAATAACTGTG
168961	1157	AGCCTATCCTCCCCCTTCCT	213548	45744	AGATTGGGCAGGTTCAGGAT	258135	90331	TGGGCTCTGCAAATAACTGT
168962	1158	CAGCCTATCCTCCCCCTTCC	213549	45745	AAGATTGGGCAGGTTCAGGA	258136	90332	CTGGGCTCTGCAAATAACTG
168963	1159	ACAGCCTATCCTCCCCCTTC	213550	45746	CAAGATTGGGCAGGTTCAGG	258137	90333	TCTGGGCTCTGCAAATAACT
168964	1160	CACAGCCTATCCTCCCCCTT	213551	45747	ACAAGATTGGGCAGGTTCAG	258138	90334	TTCTGGGCTCTGCAAATAAC
168965	1161	GCACAGCCTATCCTCCCCCT	213552	45748	GACAAGATTGGGCAGGTTCA	258139	90335	TTTCTGGGCTCTGCAAATAA
168966	1162	GGCACAGCCTATCCTCCCCC	213553	45749	AGACAAGATTGGGCAGGTTC	258140	90336	ATTTCTGGGCTCTGCAAATA
168967	1163	AGGCACAGCCTATCCTCCCC	213554	45750	CAGACAAGATTGGGCAGGTT	258141	90337	CATTTCTGGGCTCTGCAAAT
168968	1164	GAGGCACAGCCTATCCTCCC	213555	45751	TCAGACAAGATTGGGCAGGT	258142	90338	CCATTTCTGGGCTCTGCAAA
168969	1165	GGAGGCACAGCCTATCCTCC	213556	45752	TTCAGACAAGATTGGGCAGG	258143	90339	TCCATTTCTGGGCTCTGCAA
168970	1166	AGGAGGCACAGCCTATCCTC	213557	45753	ATTCAGACAAGATTGGGCAG	258144	90340	ATCCATTTCTGGGCTCTGCA
168971	1167	GAGGAGGCACAGCCTATCCT	213558	45754	GATTCAGACAAGATTGGGCA	258145	90341	CATCCATTTCTGGGCTCTGC
168972	1168	GGAGGAGGCACAGCCTATCC	213559	45755	GGATTCAGACAAGATTGGGC	258146	90342	ACATCCATTTCTGGGCTCTG
168973	1169	GGGAGGAGGCACAGCCTATC	213560	45756	AGGATTCAGACAAGATTGGG	258147	90343	AACATCCATTTCTGGGCTCT
168974	1170	TGGGAGGAGGCACAGCCTAT	213561	45757	CAGGATTCAGACAAGATTGG	258148	90344	TAACATCCATTTCTGGGCTC
168975	1171	GTGGGAGGAGGCACAGCCTA	213562	45758	CCAGGATTCAGACAAGATTG	258149	90345	GTAACATCCATTTCTGGGCT
168976	1172	AGTGGGAGGAGGCACAGCCT	213563	45759	ACCAGGATTCAGACAAGATT	258150	90346	AGTAACATCCATTTCTGGGC
168977	1173	GAGTGGGAGGAGGCACAGCC	213564	45760	AACCAGGATTCAGACAAGAT	258151	90347	CAGTAACATCCATTTCTGGG
168978	1174	GGAGTGGGAGGAGGCACAGC	213565	45761	AAACCAGGATTCAGACAAGA	258152	90348	TCAGTAACATCCATTTCTGG
168979	1175	GGGAGTGGGAGGAGGCACAG	213566	45762	GAAACCAGGATTCAGACAAG	258153	90349	TTCAGTAACATCCATTTCTG
168980	1176	CGGGAGTGGGAGGAGGCACA	213567	45763	TGAAACCAGGATTCAGACAA	258154	90350	CTTCAGTAACATCCATTTCT
168981	1177	GCGGGAGTGGGAGGAGGCAC	213568	45764	GTGAAACCAGGATTCAGACA	258155	90351	GCTTCAGTAACATCCATTTC
168982	1178	GGCGGGAGTGGGAGGAGGCA	213569	45765	GGTGAAACCAGGATTCAGAC	258156	90352	AGCTTCAGTAACATCCATTT
168983	1179	GGGCGGGAGTGGGAGGAGGC	213570	45766	TGGTGAAACCAGGATTCAGA	258157	90353	GAGCTTCAGTAACATCCATT
168984	1180	GGGGCGGGAGTGGGAGGAGG	213571	45767	GTGGTGAAACCAGGATTCAG	258158	90354	TGAGCTTCAGTAACATCCAT
168985	1181	GGGGGCGGGAGTGGGAGGAG	213572	45768	AGTGGTGAAACCAGGATTCA	258159	90355	GTGAGCTTCAGTAACATCCA
168986	1182	TGGGGGCGGGAGTGGGAGGA	213573	45769	CAGTGGTGAAACCAGGATTC	258160	90356	TGTGAGCTTCAGTAACATCC
168987	1183	CTGGGGGCGGGAGTGGGAGG	213574	45770	TCAGTGGTGAAACCAGGATT	258161	90357	CTGTGAGCTTCAGTAACATC
168988	1184	GCTGGGGGCGGGAGTGGGAG	213575	45771	GTCAGTGGTGAAACCAGGAT	258162	90358	ACTGTGAGCTTCAGTAACAT
168989	1185	GGCTGGGGGCGGGAGTGGGA	213576	45772	TGTCAGTGGTGAAACCAGGA	258163	90359	AACTGTGAGCTTCAGTAACA
168990	1186	GGGCTGGGGGCGGGAGTGGG	213577	45773	TTGTCAGTGGTGAAACCAGG	258164	90360	CAACTGTGAGCTTCAGTAAC
168991	1187	GGGGCTGGGGGCGGGAGTGG	213578	45774	CTTGTCAGTGGTGAAACCAG	258165	90361	GCAACTGTGAGCTTCAGTAA
168992	1188	GGGGGCTGGGGGCGGGAGTG	213579	45775	GCTTGTCAGTGGTGAAACCA	258166	90362	TGCAACTGTGAGCTTCAGTA
168993	1189	GGGGGGCTGGGGGCGGGAGT	213580	45776	AGCTTGTCAGTGGTGAAACC	258167	90363	TTGCAACTGTGAGCTTCAGT
168994	1190	AGGGGGGCTGGGGGCGGGAG	213581	45777	CAGCTTGTCAGTGGTGAAAC	258168	90364	CTTGCAACTGTGAGCTTCAG
168995	1191	AAGGGGGGCTGGGGGCGGGA	213582	45778	ACAGCTTGTCAGTGGTGAAA	258169	90365	GCTTGCAACTGTGAGCTTCA
168996	1192	AAAGGGGGGCTGGGGGCGGG	213583	45779	CACAGCTTGTCAGTGGTGAA	258170	90366	TGCTTGCAACTGTGAGCTTC
168997	1193	AAAAGGGGGGCTGGGGGCGG	213584	45780	ACACAGCTTGTCAGTGGTGA	258171	90367	ATGCTTGCAACTGTGAGCTT
168998	1194	AAAAAGGGGGGCTGGGGGCG	213585	45781	CACACAGCTTGTCAGTGGTG	258172	90368	GATGCTTGCAACTGTGAGCT
168999	1195	AAAAAAGGGGGGCTGGGGGC	213586	45782	ACACACAGCTTGTCAGTGGT	258173	90369	AGATGCTTGCAACTGTGAGC
169000	1196	AAAAAAAGGGGGGCTGGGGG	213587	45783	GACACACAGCTTGTCAGTGG	258174	90370	CAGATGCTTGCAACTGTGAG
169001	1197	GAAAAAAAGGGGGGCTGGGG	213588	45784	GGACACACAGCTTGTCAGTG	258175	90371	ACAGATGCTTGCAACTGTGA
169002	1198	GGAAAAAAAGGGGGGCTGGG	213589	45785	AGGACACACAGCTTGTCAGT	258176	90372	AACAGATGCTTGCAACTGTG
169003	1199	GGGAAAAAAAGGGGGGCTGG	213590	45786	AAGGACACACAGCTTGTCAG	258177	90373	TAACAGATGCTTGCAACTGT
169004	1200	GGGGAAAAAAAGGGGGGCTG	213591	45787	CAAGGACACACAGCTTGTCA	258178	90374	TTAACAGATGCTTGCAACTG
169005	1201	GGGGGAAAAAAAGGGGGGCT	213592	45788	CCAAGGACACACAGCTTGTC	258179	90375	TTTAACAGATGCTTGCAACT
169006	1202	AGGGGGAAAAAAAGGGGGGC	213593	45789	CCCAAGGACACACAGCTTGT	258180	90376	ATTTAACAGATGCTTGCAAC
169007	1203	GAGGGGGAAAAAAAGGGGGG	213594	45790	GCCCAAGGACACACAGCTTG	258181	90377	AATTTAACAGATGCTTGCAA
169008	1204	CGAGGGGGAAAAAAAGGGGG	213595	45791	TGCCCAAGGACACACAGCTT	258182	90378	AAATTTAACAGATGCTTGCA
169009	1205	CCGAGGGGGAAAAAAAGGGG	213596	45792	TTGCCCAAGGACACACAGCT	258183	90379	AAAATTTAACAGATGCTTGC
169010	1206	TCCGAGGGGGAAAAAAAGGG	213597	45793	CTTGCCCAAGGACACACAGC	258184	90380	AAAAATTTAACAGATGCTTG
169011	1207	TTCCGAGGGGGAAAAAAAGG	213598	45794	ACTTGCCCAAGGACACACAG	258185	90381	TAAAAATTTAACAGATGCTT
169012	1208	GTTCCGAGGGGGAAAAAAAG	213599	45795	AACTTGCCCAAGGACACACA	258186	90382	ATAAAAATTTAACAGATGCT
169013	1209	CGTTCCGAGGGGGAAAAAAA	213600	45796	TAACTTGCCCAAGGACACAC	258187	90383	AATAAAAATTTAACAGATGC
169014	1210	GCGTTCCGAGGGGGAAAAAA	213601	45797	GTAACTTGCCCAAGGACACA	258188	90384	TAATAAAAATTTAACAGATG
169015	1211	CGCGTTCCGAGGGGGAAAAA	213602	45798	AGTAACTTGCCCAAGGACAC	258189	90385	CTAATAAAAATTTAACAGAT
169016	1212	TCGCGTTCCGAGGGGGAAAA	213603	45799	AAGTAACTTGCCCAAGGACA	258190	90386	TCTAATAAAAATTTAACAGA
169017	1213	CTCGCGTTCCGAGGGGGAAA	213604	45800	GAAGTAACTTGCCCAAGGAC	258191	90387	ATCTAATAAAAATTTAACAG
169018	1214	CCTCGCGTTCCGAGGGGGAA	213605	45801	TGAAGTAACTTGCCCAAGGA	258192	90388	AATCTAATAAAAATTTAACA
169019	1215	ACCTCGCGTTCCGAGGGGGA	213606	45802	GTGAAGTAACTTGCCCAAGG	258193	90389	AAATCTAATAAAAATTTAAC
169020	1216	CACCTCGCGTTCCGAGGGGG	213607	45803	GGTGAAGTAACTTGCCCAAG	258194	90390	AAAATCTAATAAAAATTTAA
169021	1217	GCACCTCGCGTTCCGAGGGG	213608	45804	AGGTGAAGTAACTTGCCCAA	258195	90391	TAAAATCTAATAAAAATTTA
169022	1218	GGCACCTCGCGTTCCGAGGG	213609	45805	CAGGTGAAGTAACTTGCCCA	258196	90392	GTAAAATCTAATAAAAATTT
169023	1219	TGGCACCTCGCGTTCCGAGG	213610	45806	ACAGGTGAAGTAACTTGCCC	258197	90393	AGTAAAATCTAATAAAAATT
169024	1220	ATGGCACCTCGCGTTCCGAG	213611	45807	GACAGGTGAAGTAACTTGCC	258198	90394	AAGTAAAATCTAATAAAAAT
169025	1221	GATGGCACCTCGCGTTCCGA	213612	45808	AGACAGGTGAAGTAACTTGC	258199	90395	AAAGTAAAATCTAATAAAAA
169026	1222	AGATGGCACCTCGCGTTCCG	213613	45809	CAGACAGGTGAAGTAACTTG	258200	90396	AAAAGTAAAATCTAATAAAA

169027	1223	AAGATGGCACCTCGCGTTCC	213614	45810	ACAGACAGGTGAAGTAACTT	258201	90397	TAAAAGTAAAATCTAATAAA
169028	1224	AAAGATGGCACCTCGCGTTC	213615	45811	CACAGACAGGTGAAGTAACT	258202	90398	CTAAAAGTAAAATCTAATAA
169029	1225	AAAAGATGGCACCTCGCGTT	213616	45812	GCACAGACAGGTGAAGTAAC	258203	90399	CCTAAAAGTAAAATCTAATA
169030	1226	AAAAAGATGGCACCTCGCGT	213617	45813	AGCACAGACAGGTGAAGTAA	258204	90400	CCCTAAAAGTAAAATCTAAT
169031	1227	AAAAAAGATGGCACCTCGCG	213618	45814	AAGCACAGACAGGTGAAGTA	258205	90401	TCCCTAAAAGTAAAATCTAA
169032	1228	GAAAAAAGATGGCACCTCGC	213619	45815	GAAGCACAGACAGGTGAAGT	258206	90402	TTCCCTAAAAGTAAAATCTA
169033	1229	CGAAAAAAGATGGCACCTCG	213620	45816	TGAAGCACAGACAGGTGAAG	258207	90403	TTTCCCTAAAAGTAAAATCT
169034	1230	CCGAAAAAAGATGGCACCTC	213621	45817	CTGAAGCACAGACAGGTGAA	258208	90404	TTTTCCCTAAAAGTAAAATC
169035	1231	GCCGAAAAAAGATGGCACCT	213622	45818	TCTGAAGCACAGACAGGTGA	258209	90405	GTTTTCCCTAAAAGTAAAAT
169036	1232	CGCCGAAAAAAGATGGCACC	213623	45819	CTCTGAAGCACAGACAGGTG	258210	90406	AGTTTTCCCTAAAAGTAAAA
169037	1233	ACGCCGAAAAAAGATGGCAC	213624	45820	ACTCTGAAGCACAGACAGGT	258211	90407	AAGTTTTCCCTAAAAGTAAA
169038	1234	CACGCCGAAAAAAGATGGCA	213625	45821	GACTCTGAAGCACAGACAGG	258212	90408	AAAGTTTTCCCTAAAAGTAA
169039	1235	ACACGCCGAAAAAAGATGGC	213626	45822	GGACTCTGAAGCACAGACAG	258213	90409	CAAAGTTTTCCCTAAAAGTA
169040	1236	GACACGCCGAAAAAAGATGG	213627	45823	AGGACTCTGAAGCACAGACA	258214	90410	TCAAAGTTTTCCCTAAAAGT
169041	1237	TGACACGCCGAAAAAAGATG	213628	45824	GAGGACTCTGAAGCACAGAC	258215	90411	TTCAAAGTTTTCCCTAAAAG
169042	1238	GTGACACGCCGAAAAAAGAT	213629	45825	TGAGGACTCTGAAGCACAGA	258216	90412	TTTCAAAGTTTTCCCTAAAA
169043	1239	CGTGACACGCCGAAAAAAGA	213630	45826	ATGAGGACTCTGAAGCACAG	258217	90413	ATTTCAAAGTTTTCCCTAAA
169044	1240	ACGTGACACGCCGAAAAAAG	213631	45827	GATGAGGACTCTGAAGCACA	258218	90414	CATTTCAAAGTTTTCCCTAA
169045	1241	GACGTGACACGCCGAAAAAA	213632	45828	AGATGAGGACTCTGAAGCAC	258219	90415	GCATTTCAAAGTTTTCCCTA
169046	1242	AGACGTGACACGCCGAAAAA	213633	45829	CAGATGAGGACTCTGAAGCA	258220	90416	AGCATTTCAAAGTTTTCCCT
169047	1243	AAGACGTGACACGCCGAAAA	213634	45830	ACAGATGAGGACTCTGAAGC	258221	90417	TAGCATTTCAAAGTTTTCCC
169048	1244	AAAGACGTGACACGCCGAAA	213635	45831	CACAGATGAGGACTCTGAAG	258222	90418	ATAGCATTTCAAAGTTTTCC
169049	1245	TAAAGACGTGACACGCCGAA	213636	45832	TCACAGATGAGGACTCTGAA	258223	90419	TATAGCATTTCAAAGTTTTC
169050	1246	GTAAAGACGTGACACGCCGA	213637	45833	CTCACAGATGAGGACTCTGA	258224	90420	TTATAGCATTTCAAAGTTTT
169051	1247	CGTAAAGACGTGACACGCCG	213638	45834	ACTCACAGATGAGGACTCTG	258225	90421	TTTATAGCATTTCAAAGTTT
169052	1248	CCGTAAAGACGTGACACGCC	213639	45835	AACTCACAGATGAGGACTCT	258226	90422	CTTTATAGCATTTCAAAGTT
169053	1249	ACCGTAAAGACGTGACACGC	213640	45836	CAACTCACAGATGAGGACTC	258227	90423	TCTTTATAGCATTTCAAAGT
169054	1250	CACCGTAAAGACGTGACACG	213641	45837	CCAACTCACAGATGAGGACT	258228	90424	TTCTTTATAGCATTTCAAAG
169055	1251	GCACCGTAAAGACGTGACAC	213642	45838	CCCAACTCACAGATGAGGAC	258229	90425	CTTCTTTATAGCATTTCAAA
169056	1252	GGCACCGTAAAGACGTGACA	213643	45839	CCCCAACTCACAGATGAGGA	258230	90426	GCTTCTTTATAGCATTTCAA
169057	1253	TGGCACCGTAAAGACGTGAC	213644	45840	TCCCCAACTCACAGATGAGG	258231	90427	GGCTTCTTTATAGCATTTCA
169058	1254	ATGGCACCGTAAAGACGTGA	213645	45841	TTCCCCAACTCACAGATGAG	258232	90428	AGGCTTCTTTATAGCATTTC
169059	1255	CATGGCACCGTAAAGACGTG	213646	45842	ATTCCCCAACTCACAGATGA	258233	90429	CAGGCTTCTTTATAGCATTT
169060	1256	GCATGGCACCGTAAAGACGT	213647	45843	GATTCCCCAACTCACAGATG	258234	90430	ACAGGCTTCTTTATAGCATT
169061	1257	GGCATGGCACCGTAAAGACG	213648	45844	AGATTCCCCAACTCACAGAT	258235	90431	CACAGGCTTCTTTATAGCAT
169062	1258	TGGCATGGCACCGTAAAGAC	213649	45845	CAGATTCCCCAACTCACAGA	258236	90432	ACACAGGCTTCTTTATAGCA
169063	1259	TTGGCATGGCACCGTAAAGA	213650	45846	CCAGATTCCCCAACTCACAG	258237	90433	AACACAGGCTTCTTTATAGC
169064	1260	TTTGGCATGGCACCGTAAAG	213651	45847	TCCAGATTCCCCAACTCACA	258238	90434	AAACACAGGCTTCTTTATAG
169065	1261	GTTTGGCATGGCACCGTAAA	213652	45848	GTCCAGATTCCCCAACTCAC	258239	90435	TAAACACAGGCTTCTTTATA
169066	1262	GGTTTGGCATGGCACCGTAA	213653	45849	TGTCCAGATTCCCCAACTCA	258240	90436	TTAAACACAGGCTTCTTTAT
169067	1263	CGGTTTGGCATGGCACCGTA	213654	45850	CTGTCCAGATTCCCCAACTC	258241	90437	TTTAAACACAGGCTTCTTTA
169068	1264	CCGGTTTGGCATGGCACCGT	213655	45851	TCTGTCCAGATTCCCCAACT	258242	90438	TTTTAAACACAGGCTTCTTT
169069	1265	CCCGGTTTGGCATGGCACCG	213656	45852	TTCTGTCCAGATTCCCCAAC	258243	90439	CTTTTAAACACAGGCTTCTT
169070	1266	ACCCGGTTTGGCATGGCACC	213657	45853	ATTCTGTCCAGATTCCCCAA	258244	90440	ACTTTTAAACACAGGCTTCT
169071	1267	CACCCGGTTTGGCATGGCAC	213658	45854	GATTCTGTCCAGATTCCCCA	258245	90441	AACTTTTAAACACAGGCTTC
169072	1268	CCACCCGGTTTGGCATGGCA	213659	45855	AGATTCTGTCCAGATTCCCC	258246	90442	TAACTTTTAAACACAGGCTT
169073	1269	GCCACCCGGTTTGGCATGGC	213660	45856	TAGATTCTGTCCAGATTCCC	258247	90443	TTAACTTTTAAACACAGGCT
169074	1270	GGCCACCCGGTTTGGCATGG	213661	45857	GTAGATTCTGTCCAGATTCC	258248	90444	CTTAACTTTTAAACACAGGC
169075	1271	CGGCCACCCGGTTTGGCATG	213662	45858	GGTAGATTCTGTCCAGATTC	258249	90445	TCTTAACTTTTAAACACAGG
169076	1272	CCGGCCACCCGGTTTGGCAT	213663	45859	GGGTAGATTCTGTCCAGATT	258250	90446	GTCTTAACTTTTAAACACAG
169077	1273	CCCGGCCACCCGGTTTGGCA	213664	45860	GGGGTAGATTCTGTCCAGAT	258251	90447	TGTCTTAACTTTTAAACACA
169078	1274	GCCCGGCCACCCGGTTTGGC	213665	45861	TGGGGTAGATTCTGTCCAGA	258252	90448	CTGTCTTAACTTTTAAACAC
169079	1275	AGCCCGGCCACCCGGTTTGG	213666	45862	ATGGGGTAGATTCTGTCCAG	258253	90449	TCTGTCTTAACTTTTAAACA
169080	1276	AAGCCCGGCCACCCGGTTTG	213667	45863	TATGGGGTAGATTCTGTCCA	258254	90450	CTCTGTCTTAACTTTTAAAC
169081	1277	GAAGCCCGGCCACCCGGTTT	213668	45864	CTATGGGGTAGATTCTGTCC	258255	90451	CCTCTGTCTTAACTTTTAAA
169082	1278	TGAAGCCCGGCCACCCGGTT	213669	45865	CCTATGGGGTAGATTCTGTC	258256	90452	GCCTCTGTCTTAACTTTTAA
169083	1279	ATGAAGCCCGGCCACCCGGT	213670	45866	CCCTATGGGGTAGATTCTGT	258257	90453	AGCCTCTGTCTTAACTTTTA
169084	1280	TATGAAGCCCGGCCACCCGG	213671	45867	GCCCTATGGGGTAGATTCTG	258258	90454	CAGCCTCTGTCTTAACTTTT
169085	1281	CTATGAAGCCCGGCCACCCG	213672	45868	CGCCCTATGGGGTAGATTCT	258259	90455	CCAGCCTCTGTCTTAACTTT
169086	1282	CCTATGAAGCCCGGCCACCC	213673	45869	ACGCCCTATGGGGTAGATTC	258260	90456	CCCAGCCTCTGTCTTAACTT
169087	1283	TCCTATGAAGCCCGGCCACC	213674	45870	TACGCCCTATGGGGTAGATT	258261	90457	CCCCAGCCTCTGTCTTAACT
169088	1284	GTCCTATGAAGCCCGGCCAC	213675	45871	CTACGCCCTATGGGGTAGAT	258262	90458	CCCCCAGCCTCTGTCTTAAC
169089	1285	TGTCCTATGAAGCCCGGCCA	213676	45872	ACTACGCCCTATGGGGTAGA	258263	90459	GCCCCCAGCCTCTGTCTTAA
169090	1286	CTGTCCTATGAAGCCCGGCC	213677	45873	CACTACGCCCTATGGGGTAG	258264	90460	CGCCCCCAGCCTCTGTCTTA
169091	1287	CCTGTCCTATGAAGCCCGGC	213678	45874	TCACTACGCCCTATGGGGTA	258265	90461	TCGCCCCCAGCCTCTGTCTT
169092	1288	CCCTGTCCTATGAAGCCCGG	213679	45875	CTCACTACGCCCTATGGGGT	258266	90462	ATCGCCCCCAGCCTCTGTCT
169093	1289	GCCCTGTCCTATGAAGCCCG	213680	45876	CCTCACTACGCCCTATGGGG	258267	90463	CATCGCCCCCAGCCTCTGTC
169094	1290	CGCCCTGTCCTATGAAGCCC	213681	45877	TCCTCACTACGCCCTATGGG	258268	90464	CCATCGCCCCCAGCCTCTGT
169095	1291	CCGCCCTGTCCTATGAAGCC	213682	45878	ATCCTCACTACGCCCTATGG	258269	90465	GCCATCGCCCCCAGCCTCTG
169096	1292	CCCGCCCTGTCCTATGAAGC	213683	45879	CATCCTCACTACGCCCTATG	258270	90466	AGCCATCGCCCCCAGCCTCT
169097	1293	CCCCGCCCTGTCCTATGAAG	213684	45880	ACATCCTCACTACGCCCTAT	258271	90467	GAGCCATCGCCCCCAGCCTC
169098	1294	GCCCCGCCCTGTCCTATGAA	213685	45881	CACATCCTCACTACGCCCTA	258272	90468	TGAGCCATCGCCCCCAGCCT

169099	1295	GGCCCCGCCCTGTCCTATGA	213686	45882	ACACATCCTCACTACGCCCT	258273	90469	GTGAGCCATCGCCCCCAGCC
169100	1296	AGGCCCCGCCCTGTCCTATG	213687	45883	AACACATCCTCACTACGCCC	258274	90470	CGTGAGCCATCGCCCCCAGC
169101	1297	CAGGCCCCGCCCTGTCCTAT	213688	45884	CAACACATCCTCACTACGCC	258275	90471	GCGTGAGCCATCGCCCCCAG
169102	1298	CCAGGCCCCGCCCTGTCCTA	213689	45885	TCAACACATCCTCACTACGC	258276	90472	GGCGTGAGCCATCGCCCCCA
169103	1299	GCCAGGCCCCGCCCTGTCCT	213690	45886	TTCAACACATCCTCACTACG	258277	90473	AGGCGTGAGCCATCGCCCCC
169104	1300	TGCCAGGCCCCGCCCTGTCC	213691	45887	ATTCAACACATCCTCACTAC	258278	90474	CAGGCGTGAGCCATCGCCCC
169105	1301	ATGCCAGGCCCCGCCCTGTC	213692	45888	AATTCAACACATCCTCACTA	258279	90475	ACAGGCGTGAGCCATCGCCC
169106	1302	AATGCCAGGCCCCGCCCTGT	213693	45889	TAATTCAACACATCCTCACT	258280	90476	TACAGGCGTGAGCCATCGCC
169107	1303	TAATGCCAGGCCCCGCCCTG	213694	45890	ATAATTCAACACATCCTCAC	258281	90477	TTACAGGCGTGAGCCATCGC
169108	1304	TTAATGCCAGGCCCCGCCCT	213695	45891	GATAATTCAACACATCCTCA	258282	90478	ATTACAGGCGTGAGCCATCG
169109	1305	TTTAATGCCAGGCCCCGCCC	213696	45892	GGATAATTCAACACATCCTC	258283	90479	GATTACAGGCGTGAGCCATC
169110	1306	CTTTAATGCCAGGCCCCGCC	213697	45893	GGGATAATTCAACACATCCT	258284	90480	AGATTACAGGCGTGAGCCAT
169111	1307	CCTTTAATGCCAGGCCCCGC	213698	45894	TGGGATAATTCAACACATCC	258285	90481	GAGATTACAGGCGTGAGCCA
169112	1308	CCCTTTAATGCCAGGCCCCG	213699	45895	TTGGGATAATTCAACACATC	258286	90482	TGAGATTACAGGCGTGAGCC
169113	1309	TCCCTTTAATGCCAGGCCCC	213700	45896	CTTGGGATAATTCAACACAT	258287	90483	CTGAGATTACAGGCGTGAGC
169114	1310	CTCCCTTTAATGCCAGGCCC	213701	45897	ACTTGGGATAATTCAACACA	258288	90484	GCTGAGATTACAGGCGTGAG
169115	1311	CCTCCCTTTAATGCCAGGCC	213702	45898	CACTTGGGATAATTCAACAC	258289	90485	TGCTGAGATTACAGGCGTGA
169116	1312	CCCTCCCTTTAATGCCAGGC	213703	45899	CCACTTGGGATAATTCAACA	258290	90486	GTGCTGAGATTACAGGCGTG
169117	1313	CCCCTCCCTTTAATGCCAGG	213704	45900	GCCACTTGGGATAATTCAAC	258291	90487	AGTGCTGAGATTACAGGCGT
169118	1314	CCCCCTCCCTTTAATGCCAG	213705	45901	AGCCACTTGGGATAATTCAA	258292	90488	AAGTGCTGAGATTACAGGCG
169119	1315	TCCCCCTCCCTTTAATGCCA	213706	45902	TAGCCACTTGGGATAATTCA	258293	90489	AAAGTGCTGAGATTACAGGC
169120	1316	GTCCCCCTCCCTTTAATGCC	213707	45903	GTAGCCACTTGGGATAATTC	258294	90490	CAAAGTGCTGAGATTACAGG
169121	1317	TGTCCCCCTCCCTTTAATGC	213708	45904	TGTAGCCACTTGGGATAATT	258295	90491	CCAAAGTGCTGAGATTACAG
169122	1318	TTGTCCCCCTCCCTTTAATG	213709	45905	GTGTAGCCACTTGGGATAAT	258296	90492	CCCAAAGTGCTGAGATTACA
169123	1319	ATTGTCCCCCTCCCTTTAAT	213710	45906	TGTGTAGCCACTTGGGATAA	258297	90493	TCCCAAAGTGCTGAGATTAC
169124	1320	GATTGTCCCCCTCCCTTTAA	213711	45907	CTGTGTAGCCACTTGGGATA	258298	90494	CTCCCAAAGTGCTGAGATTA
169125	1321	TGATTGTCCCCCTCCCTTTA	213712	45908	TCTGTGTAGCCACTTGGGAT	258299	90495	CCTCCCAAAGTGCTGAGATT
169126	1322	CTGATTGTCCCCCTCCCTTT	213713	45909	CTCTGTGTAGCCACTTGGGA	258300	90496	GCCTCCCAAAGTGCTGAGAT
169127	1323	GCTGATTGTCCCCCTCCCTT	213714	45910	ACTCTGTGTAGCCACTTGGG	258301	90497	GGCCTCCCAAAGTGCTGAGA
169128	1324	CGCTGATTGTCCCCCTCCCT	213715	45911	TACTCTGTGTAGCCACTTGG	258302	90498	TGGCCTCCCAAAGTGCTGAG
169129	1325	GCGCTGATTGTCCCCCTCCC	213716	45912	TTACTCTGTGTAGCCACTTG	258303	90499	TTGGCCTCCCAAAGTGCTGA
169130	1326	AGCGCTGATTGTCCCCCTCC	213717	45913	CTTACTCTGTGTAGCCACTT	258304	90500	CTTGGCCTCCCAAAGTGCTG
169131	1327	CAGCGCTGATTGTCCCCCTC	213718	45914	GCTTACTCTGTGTAGCCACT	258305	90501	CCTTGGCCTCCCAAAGTGCT
169132	1328	TCAGCGCTGATTGTCCCCCT	213719	45915	TGCTTACTCTGTGTAGCCAC	258306	90502	GCCTTGGCCTCCCAAAGTGC
169133	1329	TTCAGCGCTGATTGTCCCCC	213720	45916	GTGCTTACTCTGTGTAGCCA	258307	90503	TGCCTTGGCCTCCCAAAGTG
169134	1330	TTTCAGCGCTGATTGTCCCC	213721	45917	AGTGCTTACTCTGTGTAGCC	258308	90504	CTGCCTTGGCCTCCCAAAGT
169135	1331	ATTTCAGCGCTGATTGTCCC	213722	45918	GAGTGCTTACTCTGTGTAGC	258309	90505	CCTGCCTTGGCCTCCCAAAG
169136	1332	GATTTCAGCGCTGATTGTCC	213723	45919	TGAGTGCTTACTCTGTGTAG	258310	90506	ACCTGCCTTGGCCTCCCAAA
169137	1333	AGATTTCAGCGCTGATTGTC	213724	45920	TTGAGTGCTTACTCTGTGTA	258311	90507	CACCTGCCTTGGCCTCCCAA
169138	1334	AAGATTTCAGCGCTGATTGT	213725	45921	TTTGAGTGCTTACTCTGTGT	258312	90508	CCACCTGCCTTGGCCTCCCA
169139	1335	CAAGATTTCAGCGCTGATTG	213726	45922	ATTTGAGTGCTTACTCTGTG	258313	90509	TCCACCTGCCTTGGCCTCCC
169140	1336	CCAAGATTTCAGCGCTGATT	213727	45923	CATTTGAGTGCTTACTCTGT	258314	90510	ATCCACCTGCCTTGGCCTCC
169141	1337	GCCAAGATTTCAGCGCTGAT	213728	45924	TCATTTGAGTGCTTACTCTG	258315	90511	GATCCACCTGCCTTGGCCTC
169142	1338	CGCCAAGATTTCAGCGCTGA	213729	45925	ATCATTTGAGTGCTTACTCT	258316	90512	TGATCCACCTGCCTTGGCCT
169143	1339	ACGCCAAGATTTCAGCGCTG	213730	45926	CATCATTTGAGTGCTTACTC	258317	90513	ATGATCCACCTGCCTTGGCC
169144	1340	AACGCCAAGATTTCAGCGCT	213731	45927	ACATCATTTGAGTGCTTACT	258318	90514	AATGATCCACCTGCCTTGGC
169145	1341	AAACGCCAAGATTTCAGCGC	213732	45928	GACATCATTTGAGTGCTTAC	258319	90515	AAATGATCCACCTGCCTTGG
169146	1342	AAAACGCCAAGATTTCAGCG	213733	45929	TGACATCATTTGAGTGCTTA	258320	90516	CAAATGATCCACCTGCCTTG
169147	1343	CAAAACGCCAAGATTTCAGC	213734	45930	ATGACATCATTTGAGTGCTT	258321	90517	TCAAATGATCCACCTGCCTT
169148	1344	GCAAAACGCCAAGATTTCAG	213735	45931	GATGACATCATTTGAGTGCT	258322	90518	CTCAAATGATCCACCTGCCT
169149	1345	AGCAAAACGCCAAGATTTCA	213736	45932	CGATGACATCATTTGAGTGC	258323	90519	CCTCAAATGATCCACCTGCC
169150	1346	CAGCAAAACGCCAAGATTTC	213737	45933	ACGATGACATCATTTGAGTG	258324	90520	ACCTCAAATGATCCACCTGC
169151	1347	GCAGCAAAACGCCAAGATTT	213738	45934	AACGATGACATCATTTGAGT	258325	90521	AACCTCAAATGATCCACCTG
169152	1348	AGCAGCAAAACGCCAAGATT	213739	45935	CAACGATGACATCATTTGAG	258326	90522	TAACCTCAAATGATCCACCT
169153	1349	CAGCAGCAAAACGCCAAGAT	213740	45936	ACAACGATGACATCATTTGA	258327	90523	CTAACCTCAAATGATCCACC
169154	1350	GCAGCAGCAAAACGCCAAGA	213741	45937	GACAACGATGACATCATTTG	258328	90524	CCTAACCTCAAATGATCCAC
169155	1351	CGCAGCAGCAAAACGCCAAG	213742	45938	TGACAACGATGACATCATTT	258329	90525	TCCTAACCTCAAATGATCCA
169156	1352	CCGCAGCAGCAAAACGCCAA	213743	45939	ATGACAACGATGACATCATT	258330	90526	CTCCTAACCTCAAATGATCC
169157	1353	CCCGCAGCAGCAAAACGCCA	213744	45940	CATGACAACGATGACATCAT	258331	90527	ACTCCTAACCTCAAATGATC
169158	1354	GCCCGCAGCAGCAAAACGCC	213745	45941	TCATGACAACGATGACATCA	258332	90528	AACTCCTAACCTCAAATGAT
169159	1355	CGCCCGCAGCAGCAAAACGC	213746	45942	ATCATGACAACGATGACATC	258333	90529	GAACTCCTAACCTCAAATGA
169160	1356	ACGCCCGCAGCAGCAAAACG	213747	45943	AATCATGACAACGATGACAT	258334	90530	CGAACTCCTAACCTCAAATG
169161	1357	CACGCCCGCAGCAGCAAAAC	213748	45944	CAATCATGACAACGATGACA	258335	90531	TCGAACTCCTAACCTCAAAT
169162	1358	TCACGCCCGCAGCAGCAAAA	213749	45945	GCAATCATGACAACGATGAC	258336	90532	CTCGAACTCCTAACCTCAAA
169163	1359	CTCACGCCCGCAGCAGCAAA	213750	45946	AGCAATCATGACAACGATGA	258337	90533	TCTCGAACTCCTAACCTCAA
169164	1360	GCTCACGCCCGCAGCAGCAA	213751	45947	CAGCAATCATGACAACGATG	258338	90534	GTCTCGAACTCCTAACCTCA
169165	1361	TGCTCACGCCCGCAGCAGCA	213752	45948	ACAGCAATCATGACAACGAT	258339	90535	GGTCTCGAACTCCTAACCTC
169166	1362	GTGCTCACGCCCGCAGCAGC	213753	45949	AACAGCAATCATGACAACGA	258340	90536	TGGTCTCGAACTCCTAACCT
169167	1363	AGTGCTCACGCCCGCAGCAG	213754	45950	TAACAGCAATCATGACAACG	258341	90537	CTGGTCTCGAACTCCTAACC
169168	1364	CAGTGCTCACGCCCGCAGCA	213755	45951	GTAACAGCAATCATGACAAC	258342	90538	GCTGGTCTCGAACTCCTAAC
169169	1365	CCAGTGCTCACGCCCGCAGC	213756	45952	GGTAACAGCAATCATGACAA	258343	90539	GGCTGGTCTCGAACTCCTAA
169170	1366	CCCAGTGCTCACGCCCGCAG	213757	45953	TGGTAACAGCAATCATGACA	258344	90540	AGGCTGGTCTCGAACTCCTA

169171	1367	CCCCAGTGCTCACGCCCGCA	213758	45954	CTGGTAACAGCAATCATGAC	258345	90541	CAGGCTGGTCTCGAACTCCT
169172	1368	CCCCCAGTGCTCACGCCCGC	213759	45955	TCTGGTAACAGCAATCATGA	258346	90542	CCAGGCTGGTCTCGAACTCC
169173	1369	GCCCCCAGTGCTCACGCCCG	213760	45956	CTCTGGTAACAGCAATCATG	258347	90543	GCCAGGCTGGTCTCGAACTC
169174	1370	CGCCCCCAGTGCTCACGCCC	213761	45957	GCTCTGGTAACAGCAATCAT	258348	90544	GGCCAGGCTGGTCTCGAACT
169175	1371	ACGCCCCCAGTGCTCACGCC	213762	45958	GGCTCTGGTAACAGCAATCA	258349	90545	TGGCCAGGCTGGTCTCGAAC
169176	1372	AACGCCCCCAGTGCTCACGC	213763	45959	AGGCTCTGGTAACAGCAATC	258350	90546	TTGGCCAGGCTGGTCTCGAA
169177	1373	GAACGCCCCCAGTGCTCACG	213764	45960	TAGGCTCTGGTAACAGCAAT	258351	90547	GTTGGCCAGGCTGGTCTCGA
169178	1374	CGAACGCCCCCAGTGCTCAC	213765	45961	CTAGGCTCTGGTAACAGCAA	258352	90548	TGTTGGCCAGGCTGGTCTCG
169179	1375	GCGAACGCCCCCAGTGCTCA	213766	45962	TCTAGGCTCTGGTAACAGCA	258353	90549	ATGTTGGCCAGGCTGGTCTC
169180	1376	GGCGAACGCCCCCAGTGCTC	213767	45963	CTCTAGGCTCTGGTAACAGC	258354	90550	CATGTTGGCCAGGCTGGTCT
169181	1377	GGGCGAACGCCCCCAGTGCT	213768	45964	ACTCTAGGCTCTGGTAACAG	258355	90551	CCATGTTGGCCAGGCTGGTC
169182	1378	TGGGCGAACGCCCCCAGTGC	213769	45965	AACTCTAGGCTCTGGTAACA	258356	90552	ACCATGTTGGCCAGGCTGGT
169183	1379	CTGGGCGAACGCCCCCAGTG	213770	45966	GAACTCTAGGCTCTGGTAAC	258357	90553	CACCATGTTGGCCAGGCTGG
169184	1380	GCTGGGCGAACGCCCCCAGT	213771	45967	TGAACTCTAGGCTCTGGTAA	258358	90554	TCACCATGTTGGCCAGGCTG
169185	1381	TGCTGGGCGAACGCCCCCAG	213772	45968	ATGAACTCTAGGCTCTGGTA	258359	90555	CTCACCATGTTGGCCAGGCT
169186	1382	GTGCTGGGCGAACGCCCCCA	213773	45969	AATGAACTCTAGGCTCTGGT	258360	90556	TCTCACCATGTTGGCCAGGC
169187	1383	GGTGCTGGGCGAACGCCCCC	213774	45970	GAATGAACTCTAGGCTCTGG	258361	90557	GTCTCACCATGTTGGCCAGG
169188	1384	AGGTGCTGGGCGAACGCCCC	213775	45971	AGAATGAACTCTAGGCTCTG	258362	90558	GGTCTCACCATGTTGGCCAG
169189	1385	AAGGTGCTGGGCGAACGCCC	213776	45972	CAGAATGAACTCTAGGCTCT	258363	90559	GGGTCTCACCATGTTGGCCA
169190	1386	GAAGGTGCTGGGCGAACGCC	213777	45973	TCAGAATGAACTCTAGGCTC	258364	90560	AGGGTCTCACCATGTTGGCC
169191	1387	AGAAGGTGCTGGGCGAACGC	213778	45974	ATCAGAATGAACTCTAGGCT	258365	90561	CAGGGTCTCACCATGTTGGC
169192	1388	AAGAAGGTGCTGGGCGAACG	213779	45975	TATCAGAATGAACTCTAGGC	258366	90562	ACAGGGTCTCACCATGTTGG
169193	1389	GAAGAAGGTGCTGGGCGAAC	213780	45976	GTATCAGAATGAACTCTAGG	258367	90563	GACAGGGTCTCACCATGTTG
169194	1390	CGAAGAAGGTGCTGGGCGAA	213781	45977	AGTATCAGAATGAACTCTAG	258368	90564	AGACAGGGTCTCACCATGTT
169195	1391	CCGAAGAAGGTGCTGGGCGA	213782	45978	GAGTATCAGAATGAACTCTA	258369	90565	GAGACAGGGTCTCACCATGT
169196	1392	CCCGAAGAAGGTGCTGGGCG	213783	45979	CGAGTATCAGAATGAACTCT	258370	90566	AGAGACAGGGTCTCACCATG
169197	1393	CCCCGAAGAAGGTGCTGGGC	213784	45980	TCGAGTATCAGAATGAACTC	258371	90567	TAGAGACAGGGTCTCACCAT
169198	1394	CCCCCGAAGAAGGTGCTGGG	213785	45981	CTCGAGTATCAGAATGAACT	258372	90568	GTAGAGACAGGGTCTCACCA
169199	1395	GCCCCCGAAGAAGGTGCTGG	213786	45982	ACTCGAGTATCAGAATGAAC	258373	90569	AGTAGAGACAGGGTCTCACC
169200	1396	AGCCCCCGAAGAAGGTGCTG	213787	45983	GACTCGAGTATCAGAATGAA	258374	90570	TAGTAGAGACAGGGTCTCAC
169201	1397	GAGCCCCCGAAGAAGGTGCT	213788	45984	AGACTCGAGTATCAGAATGA	258375	90571	TTAGTAGAGACAGGGTCTCA
169202	1398	AGAGCCCCCGAAGAAGGTGC	213789	45985	CAGACTCGAGTATCAGAATG	258376	90572	TTTAGTAGAGACAGGGTCTC
169203	1399	AAGAGCCCCCGAAGAAGGTG	213790	45986	ACAGACTCGAGTATCAGAAT	258377	90573	TTTTAGTAGAGACAGGGTCT
169204	1400	AAAGAGCCCCCGAAGAAGGT	213791	45987	CACAGACTCGAGTATCAGAA	258378	90574	ATTTTAGTAGAGACAGGGTC
169205	1401	CAAAGAGCCCCCGAAGAAGG	213792	45988	CCACAGACTCGAGTATCAGA	258379	90575	AATTTTAGTAGAGACAGGGT
169206	1402	GCAAAGAGCCCCCGAAGAAG	213793	45989	GCCACAGACTCGAGTATCAG	258380	90576	TAATTTTAGTAGAGACAGGG
169207	1403	AGCAAAGAGCCCCCGAAGAA	213794	45990	GGCCACAGACTCGAGTATCA	258381	90577	GTAATTTTAGTAGAGACAGG
169208	1404	AAGCAAAGAGCCCCCGAAGA	213795	45991	GGGCCACAGACTCGAGTATC	258382	90578	TGTAATTTTAGTAGAGACAG
169209	1405	AAAGCAAAGAGCCCCCGAAG	213796	45992	TGGGCCACAGACTCGAGTAT	258383	90579	TTGTAATTTTAGTAGAGACA
169210	1406	CAAAGCAAAGAGCCCCCGAA	213797	45993	ATGGGCCACAGACTCGAGTA	258384	90580	TTTGTAATTTTAGTAGAGAC
169211	1407	ACAAAGCAAAGAGCCCCCGA	213798	45994	GATGGGCCACAGACTCGAGT	258385	90581	TTTTGTAATTTTAGTAGAGA
169212	1408	GACAAAGCAAAGAGCCCCCG	213799	45995	GGATGGGCCACAGACTCGAG	258386	90582	TTTTTGTAATTTTAGTAGAG
169213	1409	AGACAAAGCAAAGAGCCCCC	213800	45996	TGGATGGGCCACAGACTCGA	258387	90583	TTTTTTGTAATTTTAGTAGA
169214	1410	CAGACAAAGCAAAGAGCCCC	213801	45997	CTGGATGGGCCACAGACTCG	258388	90584	ATTTTTTGTAATTTTAGTAG
169215	1411	ACAGACAAAGCAAAGAGCCC	213802	45998	GCTGGATGGGCCACAGACTC	258389	90585	AATTTTTTGTAATTTTAGTA
169216	1412	TACAGACAAAGCAAAGAGCC	213803	45999	GGCTGGATGGGCCACAGACT	258390	90586	TAATTTTTTGTAATTTTAGT
169217	1413	CTACAGACAAAGCAAAGAGC	213804	46000	GGGCTGGATGGGCCACAGAC	258391	90587	CTAATTTTTTGTAATTTTAG
169218	1414	TCTACAGACAAAGCAAAGAG	213805	46001	TGGGCTGGATGGGCCACAGA	258392	90588	GCTAATTTTTTGTAATTTTA
169219	1415	CTCTACAGACAAAGCAAAGA	213806	46002	CTGGGCTGGATGGGCCACAG	258393	90589	AGCTAATTTTTTGTAATTTT
169220	1416	CCTCTACAGACAAAGCAAAG	213807	46003	CCTGGGCTGGATGGGCCACA	258394	90590	CAGCTAATTTTTTGTAATTT
169221	1417	ACCTCTACAGACAAAGCAAA	213808	46004	ACCTGGGCTGGATGGGCCAC	258395	90591	CCAGCTAATTTTTTGTAATT
169222	1418	AACCTCTACAGACAAAGCAA	213809	46005	TACCTGGGCTGGATGGGCCA	258396	90592	CCCAGCTAATTTTTTGTAAT
169223	1419	TAACCTCTACAGACAAAGCA	213810	46006	TTACCTGGGCTGGATGGGCC	258397	90593	GCCCAGCTAATTTTTTGTAA
169224	1420	GTAACCTCTACAGACAAAGC	213811	46007	CTTACCTGGGCTGGATGGGC	258398	90594	CGCCCAGCTAATTTTTTGTA
169225	1421	CGTAACCTCTACAGACAAAG	213812	46008	CCTTACCTGGGCTGGATGGG	258399	90595	ACGCCCAGCTAATTTTTTGT
169226	1422	ACGTAACCTCTACAGACAAA	213813	46009	TCCTTACCTGGGCTGGATGG	258400	90596	CACGCCCAGCTAATTTTTTG
169227	1423	CACGTAACCTCTACAGACAA	213814	46010	TTCCTTACCTGGGCTGGATG	258401	90597	CCACGCCCAGCTAATTTTTT
169228	1424	TCACGTAACCTCTACAGACA	213815	46011	ATTCCTTACCTGGGCTGGAT	258402	90598	ACCACGCCCAGCTAATTTTT
169229	1425	ATCACGTAACCTCTACAGAC	213816	46012	TATTCCTTACCTGGGCTGGA	258403	90599	CACCACGCCCAGCTAATTTT
169230	1426	GATCACGTAACCTCTACAGA	213817	46013	CTATTCCTTACCTGGGCTGG	258404	90600	CCACCACGCCCAGCTAATTT
169231	1427	AGATCACGTAACCTCTACAG	213818	46014	ACTATTCCTTACCTGGGCTG	258405	90601	GCCACCACGCCCAGCTAATT
169232	1428	CAGATCACGTAACCTCTACA	213819	46015	AACTATTCCTTACCTGGGCT	258406	90602	CGCCACCACGCCCAGCTAAT
169233	1429	GCAGATCACGTAACCTCTAC	213820	46016	CAACTATTCCTTACCTGGGC	258407	90603	CCGCCACCACGCCCAGCTAA
169234	1430	CGCAGATCACGTAACCTCTA	213821	46017	CCAACTATTCCTTACCTGGG	258408	90604	CCCGCCACCACGCCCAGCTA
169235	1431	GCGCAGATCACGTAACCTCT	213822	46018	TCCAACTATTCCTTACCTGG	258409	90605	GCCCGCCACCACGCCCAGCT
169236	1432	AGCGCAGATCACGTAACCTC	213823	46019	CTCCAACTATTCCTTACCTG	258410	90606	TGCCCGCCACCACGCCCAGC
169237	1433	GAGCGCAGATCACGTAACCT	213824	46020	CCTCCAACTATTCCTTACCT	258411	90607	GTGCCCGCCACCACGCCCAG
169238	1434	GGAGCGCAGATCACGTAACC	213825	46021	TCCTCCAACTATTCCTTACC	258412	90608	GGTGCCCGCCACCACGCCCA
169239	1435	GGGAGCGCAGATCACGTAAC	213826	46022	CTCCTCCAACTATTCCTTAC	258413	90609	AGGTGCCCGCCACCACGCCC
169240	1436	TGGGAGCGCAGATCACGTAA	213827	46023	ACTCCTCCAACTATTCCTTA	258414	90610	CAGGTGCCCGCCACCACGCC
169241	1437	CTGGGAGCGCAGATCACGTA	213828	46024	AACTCCTCCAACTATTCCTT	258415	90611	ACAGGTGCCCGCCACCACGC
169242	1438	GCTGGGAGCGCAGATCACGT	213829	46025	CAACTCCTCCAACTATTCCT	258416	90612	TACAGGTGCCCGCCACCACG

169243	1439	GGCTGGGAGCGCAGATCACG	213830	46026	CCAACTCCTCCAACTATTCC	258417	90613	CTACAGGTGCCCGCCACCAC
169244	1440	GGGCTGGGAGCGCAGATCAC	213831	46027	CCCAACTCCTCCAACTATTC	258418	90614	ACTACAGGTGCCCGCCACCA
169245	1441	AGGGCTGGGAGCGCAGATCA	213832	46028	GCCCAACTCCTCCAACTATT	258419	90615	GACTACAGGTGCCCGCCACC
169246	1442	CAGGGCTGGGAGCGCAGATC	213833	46029	TGCCCAACTCCTCCAACTAT	258420	90616	GGACTACAGGTGCCCGCCAC
169247	1443	CCAGGGCTGGGAGCGCAGAT	213834	46030	ATGCCCAACTCCTCCAACTA	258421	90617	GGGACTACAGGTGCCCGCCA
169248	1444	ACCAGGGCTGGGAGCGCAGA	213835	46031	CATGCCCAACTCCTCCAACT	258422	90618	TGGGACTACAGGTGCCCGCC
169249	1445	AACCAGGGCTGGGAGCGCAG	213836	46032	ACATGCCCAACTCCTCCAAC	258423	90619	CTGGGACTACAGGTGCCCGC
169250	1446	AAACCAGGGCTGGGAGCGCA	213837	46033	AACATGCCCAACTCCTCCAA	258424	90620	GCTGGGACTACAGGTGCCCG
169251	1447	GAAACCAGGGCTGGGAGCGC	213838	46034	GAACATGCCCAACTCCTCCA	258425	90621	AGCTGGGACTACAGGTGCCC
169252	1448	AGAAACCAGGGCTGGGAGCG	213839	46035	TGAACATGCCCAACTCCTCC	258426	90622	TAGCTGGGACTACAGGTGCC
169253	1449	CAGAAACCAGGGCTGGGAGC	213840	46036	CTGAACATGCCCAACTCCTC	258427	90623	GTAGCTGGGACTACAGGTGC
169254	1450	CCAGAAACCAGGGCTGGGAG	213841	46037	GCTGAACATGCCCAACTCCT	258428	90624	AGTAGCTGGGACTACAGGTG
169255	1451	GCCAGAAACCAGGGCTGGGA	213842	46038	AGCTGAACATGCCCAACTCC	258429	90625	CAGTAGCTGGGACTACAGGT
169256	1452	AGCCAGAAACCAGGGCTGGG	213843	46039	AAGCTGAACATGCCCAACTC	258430	90626	CCAGTAGCTGGGACTACAGG
169257	1453	AAGCCAGAAACCAGGGCTGG	213844	46040	CAAGCTGAACATGCCCAACT	258431	90627	CCCAGTAGCTGGGACTACAG
169258	1454	AAAGCCAGAAACCAGGGCTG	213845	46041	TCAAGCTGAACATGCCCAAC	258432	90628	CCCCAGTAGCTGGGACTACA
169259	1455	AAAAGCCAGAAACCAGGGCT	213846	46042	TTCAAGCTGAACATGCCCAA	258433	90629	TCCCCAGTAGCTGGGACTAC
169260	1456	TAAAAGCCAGAAACCAGGGC	213847	46043	CTTCAAGCTGAACATGCCCA	258434	90630	CTCCCCAGTAGCTGGGACTA
169261	1457	ATAAAAGCCAGAAACCAGGG	213848	46044	TCTTCAAGCTGAACATGCCC	258435	90631	CCTCCCCAGTAGCTGGGACT
169262	1458	AATAAAAGCCAGAAACCAGG	213849	46045	CTCTTCAAGCTGAACATGCC	258436	90632	GCCTCCCCAGTAGCTGGGAC
169263	1459	GAATAAAAGCCAGAAACCAG	213850	46046	CCTCTTCAAGCTGAACATGC	258437	90633	AGCCTCCCCAGTAGCTGGGA
169264	1460	AGAATAAAAGCCAGAAACCA	213851	46047	TCCTCTTCAAGCTGAACATG	258438	90634	CAGCCTCCCCAGTAGCTGGG
169265	1461	CAGAATAAAAGCCAGAAACC	213852	46048	CTCCTCTTCAAGCTGAACAT	258439	90635	TCAGCCTCCCCAGTAGCTGG
169266	1462	TCAGAATAAAAGCCAGAAAC	213853	46049	TCTCCTCTTCAAGCTGAACA	258440	90636	TTCAGCCTCCCCAGTAGCTG
169267	1463	CTCAGAATAAAAGCCAGAAA	213854	46050	GTCTCCTCTTCAAGCTGAAC	258441	90637	CTTCAGCCTCCCCAGTAGCT
169268	1464	CCTCAGAATAAAAGCCAGAA	213855	46051	CGTCTCCTCTTCAAGCTGAA	258442	90638	GCTTCAGCCTCCCCAGTAGC
169269	1465	CCCTCAGAATAAAAGCCAGA	213856	46052	TCGTCTCCTCTTCAAGCTGA	258443	90639	TGCTTCAGCCTCCCCAGTAG
169270	1466	ACCCTCAGAATAAAAGCCAG	213857	46053	GTCGTCTCCTCTTCAAGCTG	258444	90640	CTGCTTCAGCCTCCCCAGTA
169271	1467	CACCCTCAGAATAAAAGCCA	213858	46054	TGTCGTCTCCTCTTCAAGCT	258445	90641	CCTGCTTCAGCCTCCCCAGT
169272	1468	ACACCCTCAGAATAAAAGCC	213859	46055	CTGTCGTCTCCTCTTCAAGC	258446	90642	TCCTGCTTCAGCCTCCCCAG
169273	1469	AACACCCTCAGAATAAAAGC	213860	46056	CCTGTCGTCTCCTCTTCAAG	258447	90643	ATCCTGCTTCAGCCTCCCCA
169274	1470	GAACACCCTCAGAATAAAAG	213861	46057	CCCTGTCGTCTCCTCTTCAA	258448	90644	TATCCTGCTTCAGCCTCCCC
169275	1471	TGAACACCCTCAGAATAAAA	213862	46058	CCCCTGTCGTCTCCTCTTCA	258449	90645	TTATCCTGCTTCAGCCTCCC
169276	1472	CTGAACACCCTCAGAATAAA	213863	46059	TCCCCTGTCGTCTCCTCTTC	258450	90646	CTTATCCTGCTTCAGCCTCC
169277	1473	ACTGAACACCCTCAGAATAA	213864	46060	ATCCCCTGTCGTCTCCTCTT	258451	90647	ACTTATCCTGCTTCAGCCTC
169278	1474	GACTGAACACCCTCAGAATA	213865	46061	TATCCCCTGTCGTCTCCTCT	258452	90648	CACTTATCCTGCTTCAGCCT
169279	1475	TGACTGAACACCCTCAGAAT	213866	46062	ATATCCCCTGTCGTCTCCTC	258453	90649	GCACTTATCCTGCTTCAGCC
169280	1476	TTGACTGAACACCCTCAGAA	213867	46063	CATATCCCCTGTCGTCTCCT	258454	90650	AGCACTTATCCTGCTTCAGC
169281	1477	GTTGACTGAACACCCTCAGA	213868	46064	CCATATCCCCTGTCGTCTCC	258455	90651	AAGCACTTATCCTGCTTCAG
169282	1478	GGTTGACTGAACACCCTCAG	213869	46065	CCCATATCCCCTGTCGTCTC	258456	90652	CAAGCACTTATCCTGCTTCA
169283	1479	AGGTTGACTGAACACCCTCA	213870	46066	TCCCATATCCCCTGTCGTCT	258457	90653	TCAAGCACTTATCCTGCTTC
169284	1480	GAGGTTGACTGAACACCCTC	213871	46067	ATCCCATATCCCCTGTCGTC	258458	90654	TTCAAGCACTTATCCTGCTT
169285	1481	GGAGGTTGACTGAACACCCT	213872	46068	TATCCCATATCCCCTGTCGT	258459	90655	GTTCAAGCACTTATCCTGCT
169286	1482	GGGAGGTTGACTGAACACCC	213873	46069	CTATCCCATATCCCCTGTCG	258460	90656	GGTTCAAGCACTTATCCTGC
169287	1483	GGGGAGGTTGACTGAACACC	213874	46070	ACTATCCCATATCCCCTGTC	258461	90657	GGGTTCAAGCACTTATCCTG
169288	1484	GGGGGAGGTTGACTGAACAC	213875	46071	AACTATCCCATATCCCCTGT	258462	90658	TGGGTTCAAGCACTTATCCT
169289	1485	GGGGGGAGGTTGACTGAACA	213876	46072	CAACTATCCCATATCCCCTG	258463	90659	CTGGGTTCAAGCACTTATCC
169290	1486	AGGGGGGAGGTTGACTGAAC	213877	46073	TCAACTATCCCATATCCCCT	258464	90660	CCTGGGTTCAAGCACTTATC
169291	1487	TAGGGGGGAGGTTGACTGAA	213878	46074	TTCAACTATCCCATATCCCC	258465	90661	TCCTGGGTTCAAGCACTTAT
169292	1488	GTAGGGGGGAGGTTGACTGA	213879	46075	ATTCAACTATCCCATATCCC	258466	90662	CTCCTGGGTTCAAGCACTTA
169293	1489	CGTAGGGGGGAGGTTGACTG	213880	46076	GATTCAACTATCCCATATCC	258467	90663	CCTCCTGGGTTCAAGCACTT
169294	1490	GCGTAGGGGGGAGGTTGACT	213881	46077	AGATTCAACTATCCCATATC	258468	90664	GCCTCCTGGGTTCAAGCACT
169295	1491	GGCGTAGGGGGGAGGTTGAC	213882	46078	CAGATTCAACTATCCCATAT	258469	90665	TGCCTCCTGGGTTCAAGCAC
169296	1492	GGGCGTAGGGGGGAGGTTGA	213883	46079	ACAGATTCAACTATCCCATA	258470	90666	CTGCCTCCTGGGTTCAAGCA
169297	1493	TGGGCGTAGGGGGGAGGTTG	213884	46080	CACAGATTCAACTATCCCAT	258471	90667	TCTGCCTCCTGGGTTCAAGC
169298	1494	ATGGGCGTAGGGGGGAGGTT	213885	46081	TCACAGATTCAACTATCCCA	258472	90668	CTCTGCCTCCTGGGTTCAAG
169299	1495	CATGGGCGTAGGGGGGAGGT	213886	46082	TTCACAGATTCAACTATCCC	258473	90669	CCTCTGCCTCCTGGGTTCAA
169300	1496	GCATGGGCGTAGGGGGGAGG	213887	46083	CTTCACAGATTCAACTATCC	258474	90670	ACCTCTGCCTCCTGGGTTCA
169301	1497	CGCATGGGCGTAGGGGGGAG	213888	46084	CCTTCACAGATTCAACTATC	258475	90671	AACCTCTGCCTCCTGGGTTC
169302	1498	GCGCATGGGCGTAGGGGGGA	213889	46085	CCCTTCACAGATTCAACTAT	258476	90672	TAACCTCTGCCTCCTGGGTT
169303	1499	GGCGCATGGGCGTAGGGGGG	213890	46086	GCCCTTCACAGATTCAACTA	258477	90673	GTAACCTCTGCCTCCTGGGT
169304	1500	AGGCGCATGGGCGTAGGGGG	213891	46087	GGCCCTTCACAGATTCAACT	258478	90674	TGTAACCTCTGCCTCCTGGG
169305	1501	GAGGCGCATGGGCGTAGGGG	213892	46088	GGGCCCTTCACAGATTCAAC	258479	90675	CTGTAACCTCTGCCTCCTGG
169306	1502	AGAGGCGCATGGGCGTAGGG	213893	46089	GGGGCCCTTCACAGATTCAA	258480	90676	ACTGTAACCTCTGCCTCCTG
169307	1503	GAGAGGCGCATGGGCGTAGG	213894	46090	GGGGGCCCTTCACAGATTCA	258481	90677	CACTGTAACCTCTGCCTCCT
169308	1504	AGAGAGGCGCATGGGCGTAG	213895	46091	AGGGGGCCCTTCACAGATTC	258482	90678	TCACTGTAACCTCTGCCTCC
169309	1505	AAGAGAGGCGCATGGGCGTA	213896	46092	CAGGGGGCCCTTCACAGATT	258483	90679	CTCACTGTAACCTCTGCCTC
169310	1506	AAAGAGAGGCGCATGGGCGT	213897	46093	CCAGGGGGCCCTTCACAGAT	258484	90680	GCTCACTGTAACCTCTGCCT
169311	1507	GAAAGAGAGGCGCATGGGCG	213898	46094	CCCAGGGGGCCCTTCACAGA	258485	90681	GGCTCACTGTAACCTCTGCC
169312	1508	GGAAAGAGAGGCGCATGGGC	213899	46095	TCCCAGGGGGCCCTTCACAG	258486	90682	TGGCTCACTGTAACCTCTGC
169313	1509	AGGAAAGAGAGGCGCATGGG	213900	46096	ATCCCAGGGGGCCCTTCACA	258487	90683	TTGGCTCACTGTAACCTCTG
169314	1510	AAGGAAAGAGAGGCGCATGG	213901	46097	CATCCCAGGGGGCCCTTCAC	258488	90684	CTTGGCTCACTGTAACCTCT

169315	1511	AAAGGAAAGAGAGGCGCATG	213902	46098	TCATCCCAGGGGGCCCTTCA	258489	90685	TCTTGGCTCACTGTAACCTC
169316	1512	AAAAGGAAAGAGAGGCGCAT	213903	46099	TTCATCCCAGGGGGCCCTTC	258490	90686	ATCTTGGCTCACTGTAACCT
169317	1513	AAAAAGGAAAGAGAGGCGCA	213904	46100	CTTCATCCCAGGGGGCCCTT	258491	90687	GATCTTGGCTCACTGTAACC
169318	1514	GAAAAAGGAAAGAGAGGCGC	213905	46101	TCTTCATCCCAGGGGGCCCT	258492	90688	TGATCTTGGCTCACTGTAAC
169319	1515	CGAAAAAGGAAAGAGAGGCG	213906	46102	TTCTTCATCCCAGGGGGCCC	258493	90689	GTGATCTTGGCTCACTGTAA
169320	1516	GCGAAAAAGGAAAGAGAGGC	213907	46103	GTTCTTCATCCCAGGGGGCC	258494	90690	TGTGATCTTGGCTCACTGTA
169321	1517	AGCGAAAAAGGAAAGAGAGG	213908	46104	AGTTCTTCATCCCAGGGGGC	258495	90691	GTGTGATCTTGGCTCACTGT
169322	1518	GAGCGAAAAAGGAAAGAGAG	213909	46105	CAGTTCTTCATCCCAGGGGG	258496	90692	GGTGTGATCTTGGCTCACTG
169323	1519	GGAGCGAAAAAGGAAAGAGA	213910	46106	CCAGTTCTTCATCCCAGGGG	258497	90693	TGGTGTGATCTTGGCTCACT
169324	1520	AGGAGCGAAAAAGGAAAGAG	213911	46107	GCCAGTTCTTCATCCCAGGG	258498	90694	GTGGTGTGATCTTGGCTCAC
169325	1521	GAGGAGCGAAAAAGGAAAGA	213912	46108	TGCCAGTTCTTCATCCCAGG	258499	90695	AGTGGTGTGATCTTGGCTCA
169326	1522	TGAGGAGCGAAAAAGGAAAG	213913	46109	ATGCCAGTTCTTCATCCCAG	258500	90696	CAGTGGTGTGATCTTGGCTC
169327	1523	ATGAGGAGCGAAAAAGGAAA	213914	46110	CATGCCAGTTCTTCATCCCA	258501	90697	ACAGTGGTGTGATCTTGGCT
169328	1524	AATGAGGAGCGAAAAAGGAA	213915	46111	ACATGCCAGTTCTTCATCCC	258502	90698	TACAGTGGTGTGATCTTGGC
169329	1525	AAATGAGGAGCGAAAAAGGA	213916	46112	AACATGCCAGTTCTTCATCC	258503	90699	GTACAGTGGTGTGATCTTGG
169330	1526	GAAATGAGGAGCGAAAAAGG	213917	46113	GAACATGCCAGTTCTTCATC	258504	90700	GGTACAGTGGTGTGATCTTG
169331	1527	GGAAATGAGGAGCGAAAAAG	213918	46114	AGAACATGCCAGTTCTTCAT	258505	90701	GGGTACAGTGGTGTGATCTT
169332	1528	CGGAAATGAGGAGCGAAAAA	213919	46115	CAGAACATGCCAGTTCTTCA	258506	90702	AGGGTACAGTGGTGTGATCT
169333	1529	TCGGAAATGAGGAGCGAAAA	213920	46116	ACAGAACATGCCAGTTCTTC	258507	90703	TAGGGTACAGTGGTGTGATC
169334	1530	CTCGGAAATGAGGAGCGAAA	213921	46117	CACAGAACATGCCAGTTCTT	258508	90704	TTAGGGTACAGTGGTGTGAT
169335	1531	GCTCGGAAATGAGGAGCGAA	213922	46118	ACACAGAACATGCCAGTTCT	258509	90705	CTTAGGGTACAGTGGTGTGA
169336	1532	GGCTCGGAAATGAGGAGCGA	213923	46119	CACACAGAACATGCCAGTTC	258510	90706	GCTTAGGGTACAGTGGTGTG
169337	1533	GGGCTCGGAAATGAGGAGCG	213924	46120	CCACACAGAACATGCCAGTT	258511	90707	GGCTTAGGGTACAGTGGTGT
169338	1534	TGGGCTCGGAAATGAGGAGC	213925	46121	GCCACACAGAACATGCCAGT	258512	90708	AGGCTTAGGGTACAGTGGTG
169339	1535	ATGGGCTCGGAAATGAGGAG	213926	46122	AGCCACACAGAACATGCCAG	258513	90709	CAGGCTTAGGGTACAGTGGT
169340	1536	AATGGGCTCGGAAATGAGGA	213927	46123	GAGCCACACAGAACATGCCA	258514	90710	CCAGGCTTAGGGTACAGTGG
169341	1537	CAATGGGCTCGGAAATGAGG	213928	46124	GGAGCCACACAGAACATGCC	258515	90711	CCCAGGCTTAGGGTACAGTG
169342	1538	ACAATGGGCTCGGAAATGAG	213929	46125	TGGAGCCACACAGAACATGC	258516	90712	GCCCAGGCTTAGGGTACAGT
169343	1539	AACAATGGGCTCGGAAATGA	213930	46126	CTGGAGCCACACAGAACATG	258517	90713	CGCCCAGGCTTAGGGTACAG
169344	1540	CAACAATGGGCTCGGAAATG	213931	46127	CCTGGAGCCACACAGAACAT	258518	90714	TCGCCCAGGCTTAGGGTACA
169345	1541	CCAACAATGGGCTCGGAAAT	213932	46128	CCCTGGAGCCACACAGAACA	258519	90715	GTCGCCCAGGCTTAGGGTAC
169346	1542	TCCAACAATGGGCTCGGAAA	213933	46129	GCCCTGGAGCCACACAGAAC	258520	90716	TGTCGCCCAGGCTTAGGGTA
169347	1543	ATCCAACAATGGGCTCGGAA	213934	46130	TGCCCTGGAGCCACACAGAA	258521	90717	CTGTCGCCCAGGCTTAGGGT
169348	1544	GATCCAACAATGGGCTCGGA	213935	46131	GTGCCCTGGAGCCACACAGA	258522	90718	TCTGTCGCCCAGGCTTAGGG
169349	1545	AGATCCAACAATGGGCTCGG	213936	46132	AGTGCCCTGGAGCCACACAG	258523	90719	CTCTGTCGCCCAGGCTTAGG
169350	1546	GAGATCCAACAATGGGCTCG	213937	46133	CAGTGCCCTGGAGCCACACA	258524	90720	ACTCTGTCGCCCAGGCTTAG
169351	1547	CGAGATCCAACAATGGGCTC	213938	46134	TCAGTGCCCTGGAGCCACAC	258525	90721	CACTCTGTCGCCCAGGCTTA
169352	1548	TCGAGATCCAACAATGGGCT	213939	46135	CTCAGTGCCCTGGAGCCACA	258526	90722	TCACTCTGTCGCCCAGGCTT
169353	1549	CTCGAGATCCAACAATGGGC	213940	46136	GCTCAGTGCCCTGGAGCCAC	258527	90723	CTCACTCTGTCGCCCAGGCT
169354	1550	CCTCGAGATCCAACAATGGG	213941	46137	TGCTCAGTGCCCTGGAGCCA	258528	90724	TCTCACTCTGTCGCCCAGGC
169355	1551	GCCTCGAGATCCAACAATGG	213942	46138	CTGCTCAGTGCCCTGGAGCC	258529	90725	GTCTCACTCTGTCGCCCAGG
169356	1552	AGCCTCGAGATCCAACAATG	213943	46139	CCTGCTCAGTGCCCTGGAGC	258530	90726	AGTCTCACTCTGTCGCCCAG
169357	1553	AAGCCTCGAGATCCAACAAT	213944	46140	TCCTGCTCAGTGCCCTGGAG	258531	90727	GAGTCTCACTCTGTCGCCCA
169358	1554	CAAGCCTCGAGATCCAACAA	213945	46141	GTCCTGCTCAGTGCCCTGGA	258532	90728	AGAGTCTCACTCTGTCGCCC
169359	1555	GCAAGCCTCGAGATCCAACA	213946	46142	GGTCCTGCTCAGTGCCCTGG	258533	90729	CAGAGTCTCACTCTGTCGCC
169360	1556	AGCAAGCCTCGAGATCCAAC	213947	46143	GGGTCCTGCTCAGTGCCCTG	258534	90730	ACAGAGTCTCACTCTGTCGC
169361	1557	CAGCAAGCCTCGAGATCCAA	213948	46144	TGGGTCCTGCTCAGTGCCCT	258535	90731	GACAGAGTCTCACTCTGTCG
169362	1558	CCAGCAAGCCTCGAGATCCA	213949	46145	ATGGGTCCTGCTCAGTGCCC	258536	90732	AGACAGAGTCTCACTCTGTC
169363	1559	CCCAGCAAGCCTCGAGATCC	213950	46146	AATGGGTCCTGCTCAGTGCC	258537	90733	GAGACAGAGTCTCACTCTGT
169364	1560	ACCCAGCAAGCCTCGAGATC	213951	46147	AAATGGGTCCTGCTCAGTGC	258538	90734	TGAGACAGAGTCTCACTCTG
169365	1561	AACCCAGCAAGCCTCGAGAT	213952	46148	CAAATGGGTCCTGCTCAGTG	258539	90735	TTGAGACAGAGTCTCACTCT
169366	1562	GAACCCAGCAAGCCTCGAGA	213953	46149	GCAAATGGGTCCTGCTCAGT	258540	90736	TTTGAGACAGAGTCTCACTC
169367	1563	CGAACCCAGCAAGCCTCGAG	213954	46150	GGCAAATGGGTCCTGCTCAG	258541	90737	TTTTGAGACAGAGTCTCACT
169368	1564	TCGAACCCAGCAAGCCTCGA	213955	46151	TGGCAAATGGGTCCTGCTCA	258542	90738	TTTTTGAGACAGAGTCTCAC
169369	1565	ATCGAACCCAGCAAGCCTCG	213956	46152	TTGGCAAATGGGTCCTGCTC	258543	90739	TTTTTTGAGACAGAGTCTCA
169370	1566	CATCGAACCCAGCAAGCCTC	213957	46153	TTTGGCAAATGGGTCCTGCT	258544	90740	ATTTTTTGAGACAGAGTCTC
169371	1567	TCATCGAACCCAGCAAGCCT	213958	46154	CTTTGGCAAATGGGTCCTGC	258545	90741	TATTTTTTGAGACAGAGTCT
169372	1568	TTCATCGAACCCAGCAAGCC	213959	46155	ACTTTGGCAAATGGGTCCTG	258546	90742	TTATTTTTTGAGACAGAGTC
169373	1569	GTTCATCGAACCCAGCAAGC	213960	46156	GACTTTGGCAAATGGGTCCT	258547	90743	TTTATTTTTTGAGACAGAGT
169374	1570	AGTTCATCGAACCCAGCAAG	213961	46157	AGACTTTGGCAAATGGGTCC	258548	90744	TTTTATTTTTTGAGACAGAG
169375	1571	GAGTTCATCGAACCCAGCAA	213962	46158	GAGACTTTGGCAAATGGGTC	258549	90745	ATTTTATTTTTTGAGACAGA
169376	1572	CGAGTTCATCGAACCCAGCA	213963	46159	TGAGACTTTGGCAAATGGGT	258550	90746	TATTTTATTTTTTGAGACAG
169377	1573	TCGAGTTCATCGAACCCAGC	213964	46160	CTGAGACTTTGGCAAATGGG	258551	90747	TTATTTTATTTTTTGAGACA
169378	1574	CTCGAGTTCATCGAACCCAG	213965	46161	CCTGAGACTTTGGCAAATGG	258552	90748	TTTATTTTATTTTTTGAGAC
169379	1575	ACTCGAGTTCATCGAACCCA	213966	46162	CCCTGAGACTTTGGCAAATG	258553	90749	TTTTATTTTATTTTTTGAGA
169380	1576	GACTCGAGTTCATCGAACCC	213967	46163	TCCCTGAGACTTTGGCAAAT	258554	90750	ATTTTATTTTATTTTTTGAG
169381	1577	TGACTCGAGTTCATCGAACC	213968	46164	GTCCCTGAGACTTTGGCAAA	258555	90751	TATTTTATTTTATTTTTTGA
169382	1578	TTGACTCGAGTTCATCGAAC	213969	46165	TGTCCCTGAGACTTTGGCAA	258556	90752	TTATTTTATTTTATTTTTTG
169383	1579	GTTGACTCGAGTTCATCGAA	213970	46166	GTGTCCCTGAGACTTTGGCA	258557	90753	TTTATTTTATTTTATTTTTT
169384	1580	GGTTGACTCGAGTTCATCGA	213971	46167	TGTGTCCCTGAGACTTTGGC	258558	90754	CTTTATTTTATTTTATTTTT
169385	1581	GGGTTGACTCGAGTTCATCG	213972	46168	CTGTGTCCCTGAGACTTTGG	258559	90755	ACTTTATTTTATTTTATTTT
169386	1582	GGGGTTGACTCGAGTTCATC	213973	46169	ACTGTGTCCCTGAGACTTTG	258560	90756	AACTTTATTTTATTTTATTT

169387	1583	GGGGGTTGACTCGAGTTCAT	213974	46170	AACTGTGTCCCTGAGACTTT	258561	90757	TAACTTTATTTTATTTTATT
169388	1584	GGGGGGTTGACTCGAGTTCA	213975	46171	AAACTGTGTCCCTGAGACTT	258562	90758	TTAACTTTATTTTATTTTAT
169389	1585	CGGGGGGTTGACTCGAGTTC	213976	46172	GAAACTGTGTCCCTGAGACT	258563	90759	CTTAACTTTATTTTATTTTA
169390	1586	TCGGGGGGTTGACTCGAGTT	213977	46173	AGAAACTGTGTCCCTGAGAC	258564	90760	TCTTAACTTTATTTTATTTT
169391	1587	GTCGGGGGGTTGACTCGAGT	213978	46174	TAGAAACTGTGTCCCTGAGA	258565	90761	CTCTTAACTTTATTTTATTT
169392	1588	GGTCGGGGGGTTGACTCGAG	213979	46175	CTAGAAACTGTGTCCCTGAG	258566	90762	TCTCTTAACTTTATTTTATT
169393	1589	GGGTCGGGGGGTTGACTCGA	213980	46176	GCTAGAAACTGTGTCCCTGA	258567	90763	CTCTCTTAACTTTATTTTAT
169394	1590	GGGGTCGGGGGGTTGACTCG	213981	46177	AGCTAGAAACTGTGTCCCTG	258568	90764	TCTCTCTTAACTTTATTTTA
169395	1591	GGGGGTCGGGGGGTTGACTC	213982	46178	TAGCTAGAAACTGTGTCCCT	258569	90765	TTCTCTCTTAACTTTATTTT
169396	1592	CGGGGGTCGGGGGGTTGACT	213983	46179	ATAGCTAGAAACTGTGTCCC	258570	90766	TTTCTCTCTTAACTTTATTT
169397	1593	CCGGGGGTCGGGGGGTTGAC	213984	46180	TATAGCTAGAAACTGTGTCC	258571	90767	TTTTCTCTCTTAACTTTATT
169398	1594	GCCGGGGGTCGGGGGGTTGA	213985	46181	CTATAGCTAGAAACTGTGTC	258572	90768	TTTTTCTCTCTTAACTTTAT
169399	1595	TGCCGGGGGTCGGGGGGTTG	213986	46182	TCTATAGCTAGAAACTGTGT	258573	90769	TTTTTTCTCTCTTAACTTTA
169400	1596	GTGCCGGGGGTCGGGGGGTT	213987	46183	GTCTATAGCTAGAAACTGTG	258574	90770	TTTTTTTCTCTCTTAACTTT
169401	1597	CGTGCCGGGGGTCGGGGGGT	213988	46184	TGTCTATAGCTAGAAACTGT	258575	90771	ATTTTTTTCTCTCTTAACTT
169402	1598	GCGTGCCGGGGGTCGGGGGG	213989	46185	CTGTCTATAGCTAGAAACTG	258576	90772	TATTTTTTTCTCTCTTAACT
169403	1599	TGCGTGCCGGGGGTCGGGGG	213990	46186	TCTGTCTATAGCTAGAAACT	258577	90773	ATATTTTTTTCTCTCTTAAC
169404	1600	ATGCGTGCCGGGGGTCGGGG	213991	46187	TTCTGTCTATAGCTAGAAAC	258578	90774	TATATTTTTTTCTCTCTTAA
169405	1601	CATGCGTGCCGGGGGTCGGG	213992	46188	TTTCTGTCTATAGCTAGAAA	258579	90775	ATATATTTTTTTCTCTCTTA
169406	1602	CCATGCGTGCCGGGGGTCGG	213993	46189	TTTTCTGTCTATAGCTAGAA	258580	90776	GATATATTTTTTTCTCTCTT
169407	1603	TCCATGCGTGCCGGGGGTCG	213994	46190	TTTTTCTGTCTATAGCTAGA	258581	90777	GGATATATTTTTTTCTCTCT
169408	1604	TTCCATGCGTGCCGGGGGTC	213995	46191	ATTTTTCTGTCTATAGCTAG	258582	90778	AGGATATATTTTTTTCTCTC
169409	1605	GTTCCATGCGTGCCGGGGGT	213996	46192	AATTTTTCTGTCTATAGCTA	258583	90779	TAGGATATATTTTTTTCTCT
169410	1606	CGTTCCATGCGTGCCGGGGG	213997	46193	AAATTTTTCTGTCTATAGCT	258584	90780	ATAGGATATATTTTTTTCTC
169411	1607	CCGTTCCATGCGTGCCGGGG	213998	46194	AAAATTTTTCTGTCTATAGC	258585	90781	TATAGGATATATTTTTTTCT
169412	1608	CCCGTTCCATGCGTGCCGGG	213999	46195	GAAAATTTTTCTGTCTATAG	258586	90782	ATATAGGATATATTTTTTTC
169413	1609	GCCCGTTCCATGCGTGCCGG	214000	46196	AGAAAATTTTTCTGTCTATA	258587	90783	GATATAGGATATATTTTTTT
169414	1610	CGCCCGTTCCATGCGTGCCG	214001	46197	CAGAAAATTTTTCTGTCTAT	258588	90784	GGATATAGGATATATTTTTT
169415	1611	ACGCCCGTTCCATGCGTGCC	214002	46198	ACAGAAAATTTTTCTGTCTA	258589	90785	AGGATATAGGATATATTTTT
169416	1612	CACGCCCGTTCCATGCGTGC	214003	46199	GACAGAAAATTTTTCTGTCT	258590	90786	AAGGATATAGGATATATTTT
169417	1613	TCACGCCCGTTCCATGCGTG	214004	46200	TGACAGAAAATTTTTCTGTC	258591	90787	AAAGGATATAGGATATATTT
169418	1614	GTCACGCCCGTTCCATGCGT	214005	46201	GTGACAGAAAATTTTTCTGT	258592	90788	CAAAGGATATAGGATATATT
169419	1615	GGTCACGCCCGTTCCATGCG	214006	46202	AGTGACAGAAAATTTTTCTG	258593	90789	ACAAAGGATATAGGATATAT
169420	1616	CGGTCACGCCCGTTCCATGC	214007	46203	GAGTGACAGAAAATTTTTCT	258594	90790	AACAAAGGATATAGGATATA
169421	1617	GCGGTCACGCCCGTTCCATG	214008	46204	TGAGTGACAGAAAATTTTTC	258595	90791	TAACAAAGGATATAGGATAT
169422	1618	CGCGGTCACGCCCGTTCCAT	214009	46205	CTGAGTGACAGAAAATTTTT	258596	90792	TTAACAAAGGATATAGGATA
169423	1619	GCGCGGTCACGCCCGTTCCA	214010	46206	TCTGAGTGACAGAAAATTTT	258597	90793	TTTAACAAAGGATATAGGAT
169424	1620	CGCGCGGTCACGCCCGTTCC	214011	46207	CTCTGAGTGACAGAAAATTT	258598	90794	ATTTAACAAAGGATATAGGA
169425	1621	GCGCGCGGTCACGCCCGTTC	214012	46208	CCTCTGAGTGACAGAAAATT	258599	90795	AATTTAACAAAGGATATAGG
169426	1622	TGCGCGCGGTCACGCCCGTT	214013	46209	TCCTCTGAGTGACAGAAAAT	258600	90796	GAATTTAACAAAGGATATAG
169427	1623	CTGCGCGCGGTCACGCCCGT	214014	46210	ATCCTCTGAGTGACAGAAAA	258601	90797	GGAATTTAACAAAGGATATA
169428	1624	GCTGCGCGCGGTCACGCCCG	214015	46211	CATCCTCTGAGTGACAGAAA	258602	90798	TGGAATTTAACAAAGGATAT
169429	1625	GGCTGCGCGCGGTCACGCCC	214016	46212	TCATCCTCTGAGTGACAGAA	258603	90799	TTGGAATTTAACAAAGGATA
169430	1626	AGGCTGCGCGCGGTCACGCC	214017	46213	TTCATCCTCTGAGTGACAGA	258604	90800	TTTGGAATTTAACAAAGGAT
169431	1627	GAGGCTGCGCGCGGTCACGC	214018	46214	TTTCATCCTCTGAGTGACAG	258605	90801	TTTTGGAATTTAACAAAGGA
169432	1628	CGAGGCTGCGCGCGGTCACG	214019	46215	TTTTCATCCTCTGAGTGACA	258606	90802	GTTTTGGAATTTAACAAAGG
169433	1629	ACGAGGCTGCGCGCGGTCAC	214020	46216	ATTTTCATCCTCTGAGTGAC	258607	90803	TGTTTTGGAATTTAACAAAG
169434	1630	GACGAGGCTGCGCGCGGTCA	214021	46217	TATTTTCATCCTCTGAGTGA	258608	90804	CTGTTTTGGAATTTAACAAA
169435	1631	AGACGAGGCTGCGCGCGGTC	214022	46218	CTATTTTCATCCTCTGAGTG	258609	90805	ACTGTTTTGGAATTTAACAA
169436	1632	GAGACGAGGCTGCGCGCGGT	214023	46219	TCTATTTTCATCCTCTGAGT	258610	90806	TACTGTTTTGGAATTTAACA
169437	1633	CGAGACGAGGCTGCGCGCGG	214024	46220	TTCTATTTTCATCCTCTGAG	258611	90807	CTACTGTTTTGGAATTTAAC
169438	1634	CCGAGACGAGGCTGCGCGCG	214025	46221	ATTCTATTTTCATCCTCTGA	258612	90808	CCTACTGTTTTGGAATTTAA
169439	1635	TCCGAGACGAGGCTGCGCGC	214026	46222	CATTCTATTTTCATCCTCTG	258613	90809	CCCTACTGTTTTGGAATTTA
169440	1636	CTCCGAGACGAGGCTGCGCG	214027	46223	TCATTCTATTTTCATCCTCT	258614	90810	CCCCTACTGTTTTGGAATTT
169441	1637	ACTCCGAGACGAGGCTGCGC	214028	46224	CTCATTCTATTTTCATCCTC	258615	90811	TCCCCTACTGTTTTGGAATT
169442	1638	GACTCCGAGACGAGGCTGCG	214029	46225	GCTCATTCTATTTTCATCCT	258616	90812	GTCCCCTACTGTTTTGGAAT
169443	1639	AGACTCCGAGACGAGGCTGC	214030	46226	GGCTCATTCTATTTTCATCC	258617	90813	TGTCCCCTACTGTTTTGGAA
169444	1640	CAGACTCCGAGACGAGGCTG	214031	46227	GGGCTCATTCTATTTTCATC	258618	90814	TTGTCCCCTACTGTTTTGGA
169445	1641	GCAGACTCCGAGACGAGGCT	214032	46228	GGGGCTCATTCTATTTTCAT	258619	90815	TTTGTCCCCTACTGTTTTGG
169446	1642	GGCAGACTCCGAGACGAGGC	214033	46229	GGGGGCTCATTCTATTTTCA	258620	90816	ATTTGTCCCCTACTGTTTTG
169447	1643	CGGCAGACTCCGAGACGAGG	214034	46230	AGGGGGCTCATTCTATTTTC	258621	90817	TATTTGTCCCCTACTGTTTT
169448	1644	CCGGCAGACTCCGAGACGAG	214035	46231	AAGGGGGCTCATTCTATTTT	258622	90818	TTATTTGTCCCCTACTGTTT
169449	1645	GCCGGCAGACTCCGAGACGA	214036	46232	TAAGGGGGCTCATTCTATTT	258623	90819	GTTATTTGTCCCCTACTGTT
169450	1646	CGCCGGCAGACTCCGAGACG	214037	46233	TTAAGGGGGCTCATTCTATT	258624	90820	AGTTATTTGTCCCCTACTGT
169451	1647	GCGCCGGCAGACTCCGAGAC	214038	46234	CTTAAGGGGGCTCATTCTAT	258625	90821	CAGTTATTTGTCCCCTACTG
169452	1648	GGCGCCGGCAGACTCCGAGA	214039	46235	TCTTAAGGGGGCTCATTCTA	258626	90822	TCAGTTATTTGTCCCCTACT
169453	1649	CGGCGCCGGCAGACTCCGAG	214040	46236	CTCTTAAGGGGGCTCATTCT	258627	90823	GTCAGTTATTTGTCCCCTAC
169454	1650	CCGGCGCCGGCAGACTCCGA	214041	46237	CCTCTTAAGGGGGCTCATTC	258628	90824	AGTCAGTTATTTGTCCCCTA
169455	1651	CCCGGCGCCGGCAGACTCCG	214042	46238	ACCTCTTAAGGGGGCTCATT	258629	90825	AAGTCAGTTATTTGTCCCCT
169456	1652	TCCCGGCGCCGGCAGACTCC	214043	46239	TACCTCTTAAGGGGGCTCAT	258630	90826	CAAGTCAGTTATTTGTCCCC
169457	1653	TTCCCGGCGCCGGCAGACTC	214044	46240	TTACCTCTTAAGGGGGCTCA	258631	90827	TCAAGTCAGTTATTTGTCCC
169458	1654	CTTCCCGGCGCCGGCAGACT	214045	46241	ATTACCTCTTAAGGGGGCTC	258632	90828	GTCAAGTCAGTTATTTGTCC

169459	1655	GCTTCCCGGCGCCGGCAGAC	214046	46242	CATTACCTCTTAAGGGGGCT	258633	90829	TGTCAAGTCAGTTATTTGTC
169460	1656	AGCTTCCCGGCGCCGGCAGA	214047	46243	TCATTACCTCTTAAGGGGGC	258634	90830	CTGTCAAGTCAGTTATTTGT
169461	1657	AAGCTTCCCGGCGCCGGCAG	214048	46244	CTCATTACCTCTTAAGGGGG	258635	90831	CCTGTCAAGTCAGTTATTTG
169462	1658	GAAGCTTCCCGGCGCCGGCA	214049	46245	GCTCATTACCTCTTAAGGGG	258636	90832	ACCTGTCAAGTCAGTTATTT
169463	1659	AGAAGCTTCCCGGCGCCGGC	214050	46246	AGCTCATTACCTCTTAAGGG	258637	90833	AACCTGTCAAGTCAGTTATT
169464	1660	CAGAAGCTTCCCGGCGCCGG	214051	46247	GAGCTCATTACCTCTTAAGG	258638	90834	TAACCTGTCAAGTCAGTTAT
169465	1661	TCAGAAGCTTCCCGGCGCCG	214052	46248	GGAGCTCATTACCTCTTAAG	258639	90835	GTAACCTGTCAAGTCAGTTA
169466	1662	TTCAGAAGCTTCCCGGCGCC	214053	46249	GGGAGCTCATTACCTCTTAA	258640	90836	AGTAACCTGTCAAGTCAGTT
169467	1663	CTTCAGAAGCTTCCCGGCGC	214054	46250	AGGGAGCTCATTACCTCTTA	258641	90837	TAGTAACCTGTCAAGTCAGT
169468	1664	CCTTCAGAAGCTTCCCGGCG	214055	46251	CAGGGAGCTCATTACCTCTT	258642	90838	GTAGTAACCTGTCAAGTCAG
169469	1665	CCCTTCAGAAGCTTCCCGGC	214056	46252	ACAGGGAGCTCATTACCTCT	258643	90839	TGTAGTAACCTGTCAAGTCA
169470	1666	TCCCTTCAGAAGCTTCCCGG	214057	46253	GACAGGGAGCTCATTACCTC	258644	90840	TTGTAGTAACCTGTCAAGTC
169471	1667	ATCCCTTCAGAAGCTTCCCG	214058	46254	TGACAGGGAGCTCATTACCT	258645	90841	ATTGTAGTAACCTGTCAAGT
169472	1668	CATCCCTTCAGAAGCTTCCC	214059	46255	ATGACAGGGAGCTCATTACC	258646	90842	TATTGTAGTAACCTGTCAAG
169473	1669	CCATCCCTTCAGAAGCTTCC	214060	46256	AATGACAGGGAGCTCATTAC	258647	90843	ATATTGTAGTAACCTGTCAA
169474	1670	CCCATCCCTTCAGAAGCTTC	214061	46257	CAATGACAGGGAGCTCATTA	258648	90844	AATATTGTAGTAACCTGTCA
169475	1671	TCCCATCCCTTCAGAAGCTT	214062	46258	CCAATGACAGGGAGCTCATT	258649	90845	AAATATTGTAGTAACCTGTC
169476	1672	ATCCCATCCCTTCAGAAGCT	214063	46259	TCCAATGACAGGGAGCTCAT	258650	90846	GAAATATTGTAGTAACCTGT
169477	1673	AATCCCATCCCTTCAGAAGC	214064	46260	TTCCAATGACAGGGAGCTCA	258651	90847	GGAAATATTGTAGTAACCTG
169478	1674	GAATCCCATCCCTTCAGAAG	214065	46261	CTTCCAATGACAGGGAGCTC	258652	90848	AGGAAATATTGTAGTAACCT
169479	1675	CGAATCCCATCCCTTCAGAA	214066	46262	CCTTCCAATGACAGGGAGCT	258653	90849	CAGGAAATATTGTAGTAACC
169480	1676	TCGAATCCCATCCCTTCAGA	214067	46263	TCCTTCCAATGACAGGGAGC	258654	90850	TCAGGAAATATTGTAGTAAC
169481	1677	CTCGAATCCCATCCCTTCAG	214068	46264	ATCCTTCCAATGACAGGGAG	258655	90851	TTCAGGAAATATTGTAGTAA
169482	1678	ACTCGAATCCCATCCCTTCA	214069	46265	AATCCTTCCAATGACAGGGA	258656	90852	TTTCAGGAAATATTGTAGTA
169483	1679	GACTCGAATCCCATCCCTTC	214070	46266	GAATCCTTCCAATGACAGGG	258657	90853	ATTTCAGGAAATATTGTAGT
169484	1680	AGACTCGAATCCCATCCCTT	214071	46267	GGAATCCTTCCAATGACAGG	258658	90854	CATTTCAGGAAATATTGTAG
169485	1681	GAGACTCGAATCCCATCCCT	214072	46268	TGGAATCCTTCCAATGACAG	258659	90855	TCATTTCAGGAAATATTGTA
169486	1682	GGAGACTCGAATCCCATCCC	214073	46269	CTGGAATCCTTCCAATGACA	258660	90856	ATCATTTCAGGAAATATTGT
169487	1683	CGGAGACTCGAATCCCATCC	214074	46270	TCTGGAATCCTTCCAATGAC	258661	90857	CATCATTTCAGGAAATATTG
169488	1684	ACGGAGACTCGAATCCCATC	214075	46271	TTCTGGAATCCTTCCAATGA	258662	90858	ACATCATTTCAGGAAATATT
169489	1685	CACGGAGACTCGAATCCCAT	214076	46272	CTTCTGGAATCCTTCCAATG	258663	90859	AACATCATTTCAGGAAATAT
169490	1686	GCACGGAGACTCGAATCCCA	214077	46273	TCTTCTGGAATCCTTCCAAT	258664	90860	AAACATCATTTCAGGAAATA
169491	1687	CGCACGGAGACTCGAATCCC	214078	46274	CTCTTCTGGAATCCTTCCAA	258665	90861	AAAACATCATTTCAGGAAAT
169492	1688	GCGCACGGAGACTCGAATCC	214079	46275	GCTCTTCTGGAATCCTTCCA	258666	90862	GAAAACATCATTTCAGGAAA
169493	1689	CGCGCACGGAGACTCGAATC	214080	46276	AGCTCTTCTGGAATCCTTCC	258667	90863	AGAAAACATCATTTCAGGAA
169494	1690	GCGCGCACGGAGACTCGAAT	214081	46277	TAGCTCTTCTGGAATCCTTC	258668	90864	AAGAAAACATCATTTCAGGA
169495	1691	AGCGCGCACGGAGACTCGAA	214082	46278	CTAGCTCTTCTGGAATCCTT	258669	90865	CAAGAAAACATCATTTCAGG
169496	1692	CAGCGCGCACGGAGACTCGA	214083	46279	CCTAGCTCTTCTGGAATCCT	258670	90866	TCAAGAAAACATCATTTCAG
169497	1693	GCAGCGCGCACGGAGACTCG	214084	46280	ACCTAGCTCTTCTGGAATCC	258671	90867	TTCAAGAAAACATCATTTCA
169498	1694	CGCAGCGCGCACGGAGACTC	214085	46281	TACCTAGCTCTTCTGGAATC	258672	90868	ATTCAAGAAAACATCATTTC
169499	1695	CCGCAGCGCGCACGGAGACT	214086	46282	TTACCTAGCTCTTCTGGAAT	258673	90869	TATTCAAGAAAACATCATTT
169500	1696	CCCGCAGCGCGCACGGAGAC	214087	46283	GTTACCTAGCTCTTCTGGAA	258674	90870	GTATTCAAGAAAACATCATT
169501	1697	GCCCGCAGCGCGCACGGAGA	214088	46284	GGTTACCTAGCTCTTCTGGA	258675	90871	AGTATTCAAGAAAACATCAT
169502	1698	CGCCCGCAGCGCGCACGGAG	214089	46285	TGGTTACCTAGCTCTTCTGG	258676	90872	CAGTATTCAAGAAAACATCA
169503	1699	CCGCCCGCAGCGCGCACGGA	214090	46286	GTGGTTACCTAGCTCTTCTG	258677	90873	CCAGTATTCAAGAAAACATC
169504	1700	GCCGCCCGCAGCGCGCACGG	214091	46287	AGTGGTTACCTAGCTCTTCT	258678	90874	GCCAGTATTCAAGAAAACAT
169505	1701	CGCCGCCCGCAGCGCGCACG	214092	46288	AAGTGGTTACCTAGCTCTTC	258679	90875	GGCCAGTATTCAAGAAAACA
169506	1702	CCGCCGCCCGCAGCGCGCAC	214093	46289	AAAGTGGTTACCTAGCTCTT	258680	90876	AGGCCAGTATTCAAGAAAAC
169507	1703	GCCGCCGCCCGCAGCGCGCA	214094	46290	TAAAGTGGTTACCTAGCTCT	258681	90877	TAGGCCAGTATTCAAGAAAA
169508	1704	TGCCGCCGCCCGCAGCGCGC	214095	46291	CTAAAGTGGTTACCTAGCTC	258682	90878	GTAGGCCAGTATTCAAGAAA
169509	1705	CTGCCGCCGCCCGCAGCGCG	214096	46292	CCTAAAGTGGTTACCTAGCT	258683	90879	AGTAGGCCAGTATTCAAGAA
169510	1706	TCTGCCGCCGCCCGCAGCGC	214097	46293	ACCTAAAGTGGTTACCTAGC	258684	90880	TAGTAGGCCAGTATTCAAGA
169511	1707	CTCTGCCGCCGCCCGCAGCG	214098	46294	CACCTAAAGTGGTTACCTAG	258685	90881	CTAGTAGGCCAGTATTCAAG
169512	1708	CCTCTGCCGCCGCCCGCAGC	214099	46295	GCACCTAAAGTGGTTACCTA	258686	90882	TCTAGTAGGCCAGTATTCAA
169513	1709	CCCTCTGCCGCCGCCCGCAG	214100	46296	AGCACCTAAAGTGGTTACCT	258687	90883	CTCTAGTAGGCCAGTATTCA
169514	1710	TCCCTCTGCCGCCGCCCGCA	214101	46297	TAGCACCTAAAGTGGTTACC	258688	90884	CCTCTAGTAGGCCAGTATTC
169515	1711	ATCCCTCTGCCGCCGCCCGC	214102	46298	ATAGCACCTAAAGTGGTTAC	258689	90885	ACCTCTAGTAGGCCAGTATT
169516	1712	GATCCCTCTGCCGCCGCCCG	214103	46299	GATAGCACCTAAAGTGGTTA	258690	90886	AACCTCTAGTAGGCCAGTAT
169517	1713	AGATCCCTCTGCCGCCGCCC	214104	46300	TGATAGCACCTAAAGTGGTT	258691	90887	GAACCTCTAGTAGGCCAGTA
169518	1714	GAGATCCCTCTGCCGCCGCC	214105	46301	TTGATAGCACCTAAAGTGGT	258692	90888	TGAACCTCTAGTAGGCCAGT
169519	1715	CGAGATCCCTCTGCCGCCGC	214106	46302	CTTGATAGCACCTAAAGTGG	258693	90889	ATGAACCTCTAGTAGGCCAG
169520	1716	GCGAGATCCCTCTGCCGCCG	214107	46303	CCTTGATAGCACCTAAAGTG	258694	90890	TATGAACCTCTAGTAGGCCA
169521	1717	GGCGAGATCCCTCTGCCGCC	214108	46304	CCCTTGATAGCACCTAAAGT	258695	90891	CTATGAACCTCTAGTAGGCC
169522	1718	GGGCGAGATCCCTCTGCCGC	214109	46305	CCCCTTGATAGCACCTAAAG	258696	90892	CCTATGAACCTCTAGTAGGC
169523	1719	GGGGCGAGATCCCTCTGCCG	214110	46306	GCCCCTTGATAGCACCTAAA	258697	90893	ACCTATGAACCTCTAGTAGG
169524	1720	AGGGGCGAGATCCCTCTGCC	214111	46307	AGCCCCTTGATAGCACCTAA	258698	90894	CACCTATGAACCTCTAGTAG
169525	1721	GAGGGGCGAGATCCCTCTGC	214112	46308	AAGCCCCTTGATAGCACCTA	258699	90895	ACACCTATGAACCTCTAGTA
169526	1722	GGAGGGGCGAGATCCCTCTG	214113	46309	AAAGCCCCTTGATAGCACCT	258700	90896	CACACCTATGAACCTCTAGT
169527	1723	GGGAGGGGCGAGATCCCTCT	214114	46310	AAAAGCCCCTTGATAGCACC	258701	90897	ACACACCTATGAACCTCTAG
169528	1724	AGGGAGGGGCGAGATCCCTC	214115	46311	AAAAAGCCCCTTGATAGCAC	258702	90898	AACACACCTATGAACCTCTA
169529	1725	TAGGGAGGGGCGAGATCCCT	214116	46312	AAAAAAGCCCCTTGATAGCA	258703	90899	AAACACACCTATGAACCTCT
169530	1726	GTAGGGAGGGGCGAGATCCC	214117	46313	GAAAAAAGCCCCTTGATAGC	258704	90900	CAAACACACCTATGAACCTC

169531	1727	TGTAGGGAGGGGCGAGATCC	214118	46314	AGAAAAAAGCCCCTTGATAG	258705	90901	CCAAACACACCTATGAACCT
169532	1728	GTGTAGGGAGGGGCGAGATC	214119	46315	AAGAAAAAAGCCCCTTGATA	258706	90902	TCCAAACACACCTATGAACC
169533	1729	GGTGTAGGGAGGGGCGAGAT	214120	46316	AAAGAAAAAAGCCCCTTGAT	258707	90903	ATCCAAACACACCTATGAAC
169534	1730	GGGTGTAGGGAGGGGCGAGA	214121	46317	TAAAGAAAAAAGCCCCTTGA	258708	90904	AATCCAAACACACCTATGAA
169535	1731	GGGGTGTAGGGAGGGGCGAG	214122	46318	TTAAAGAAAAAAGCCCCTTG	258709	90905	TAATCCAAACACACCTATGA
169536	1732	TGGGGTGTAGGGAGGGGCGA	214123	46319	TTTAAAGAAAAAAGCCCCTT	258710	90906	TTAATCCAAACACACCTATG
169537	1733	TTGGGGTGTAGGGAGGGGCG	214124	46320	CTTTAAAGAAAAAAGCCCCT	258711	90907	TTTAATCCAAACACACCTAT
169538	1734	CTTGGGGTGTAGGGAGGGGC	214125	46321	ACTTTAAAGAAAAAAGCCCC	258712	90908	TTTTAATCCAAACACACCTA
169539	1735	ACTTGGGGTGTAGGGAGGGG	214126	46322	GACTTTAAAGAAAAAAGCCC	258713	90909	TTTTTAATCCAAACACACCT
169540	1736	CACTTGGGGTGTAGGGAGGG	214127	46323	GGACTTTAAAGAAAAAAGCC	258714	90910	TTTTTTAATCCAAACACACC
169541	1737	ACACTTGGGGTGTAGGGAGG	214128	46324	AGGACTTTAAAGAAAAAAGC	258715	90911	CTTTTTTAATCCAAACACAC
169542	1738	GACACTTGGGGTGTAGGGAG	214129	46325	AAGGACTTTAAAGAAAAAAG	258716	90912	TCTTTTTTAATCCAAACACA
169543	1739	GGACACTTGGGGTGTAGGGA	214130	46326	AAAGGACTTTAAAGAAAAAA	258717	90913	CTCTTTTTTAATCCAAACAC
169544	1740	AGGACACTTGGGGTGTAGGG	214131	46327	GAAAGGACTTTAAAGAAAAA	258718	90914	ACTCTTTTTTAATCCAAACA
169545	1741	CAGGACACTTGGGGTGTAGG	214132	46328	GGAAAGGACTTTAAAGAAAA	258719	90915	AACTCTTTTTTAATCCAAAC
169546	1742	TCAGGACACTTGGGGTGTAG	214133	46329	TGGAAAGGACTTTAAAGAAA	258720	90916	GAACTCTTTTTTAATCCAAA
169547	1743	CTCAGGACACTTGGGGTGTA	214134	46330	TTGGAAAGGACTTTAAAGAA	258721	90917	GGAACTCTTTTTTAATCCAA
169548	1744	CCTCAGGACACTTGGGGTGT	214135	46331	TTTGGAAAGGACTTTAAAGA	258722	90918	TGGAACTCTTTTTTAATCCA
169549	1745	CCCTCAGGACACTTGGGGTG	214136	46332	TTTTGGAAAGGACTTTAAAG	258723	90919	ATGGAACTCTTTTTTAATCC
169550	1746	GCCCTCAGGACACTTGGGGT	214137	46333	CTTTTGGAAAGGACTTTAAA	258724	90920	CATGGAACTCTTTTTTAATC
169551	1747	GGCCCTCAGGACACTTGGGG	214138	46334	GCTTTTGGAAAGGACTTTAA	258725	90921	CCATGGAACTCTTTTTTAAT
169552	1748	TGGCCCTCAGGACACTTGGG	214139	46335	AGCTTTTGGAAAGGACTTTA	258726	90922	GCCATGGAACTCTTTTTTAA
169553	1749	GTGGCCCTCAGGACACTTGG	214140	46336	AAGCTTTTGGAAAGGACTTT	258727	90923	GGCCATGGAACTCTTTTTTA
169554	1750	CGTGGCCCTCAGGACACTTG	214141	46337	GAAGCTTTTGGAAAGGACTT	258728	90924	GGGCCATGGAACTCTTTTTT
169555	1751	GCGTGGCCCTCAGGACACTT	214142	46338	AGAAGCTTTTGGAAAGGACT	258729	90925	TGGGCCATGGAACTCTTTTT
169556	1752	GGCGTGGCCCTCAGGACACT	214143	46339	CAGAAGCTTTTGGAAAGGAC	258730	90926	CTGGGCCATGGAACTCTTTT
169557	1753	TGGCGTGGCCCTCAGGACAC	214144	46340	TCAGAAGCTTTTGGAAAGGA	258731	90927	ACTGGGCCATGGAACTCTTT
169558	1754	GTGGCGTGGCCCTCAGGACA	214145	46341	CTCAGAAGCTTTTGGAAAGG	258732	90928	CACTGGGCCATGGAACTCTT
169559	1755	TGTGGCGTGGCCCTCAGGAC	214146	46342	TCTCAGAAGCTTTTGGAAAG	258733	90929	TCACTGGGCCATGGAACTCT
169560	1756	GTGTGGCGTGGCCCTCAGGA	214147	46343	ATCTCAGAAGCTTTTGGAAA	258734	90930	GTCACTGGGCCATGGAACTC
169561	1757	GGTGTGGCGTGGCCCTCAGG	214148	46344	AATCTCAGAAGCTTTTGGAA	258735	90931	AGTCACTGGGCCATGGAACT
169562	1758	TGGTGTGGCGTGGCCCTCAG	214149	46345	CAATCTCAGAAGCTTTTGGA	258736	90932	CAGTCACTGGGCCATGGAAC
169563	1759	CTGGTGTGGCGTGGCCCTCA	214150	46346	GCAATCTCAGAAGCTTTTGG	258737	90933	CCAGTCACTGGGCCATGGAA
169564	1760	CCTGGTGTGGCGTGGCCCTC	214151	46347	TGCAATCTCAGAAGCTTTTG	258738	90934	CCCAGTCACTGGGCCATGGA
169565	1761	ACCTGGTGTGGCGTGGCCCT	214152	46348	ATGCAATCTCAGAAGCTTTT	258739	90935	CCCCAGTCACTGGGCCATGG
169566	1762	AACCTGGTGTGGCGTGGCCC	214153	46349	TATGCAATCTCAGAAGCTTT	258740	90936	CCCCCAGTCACTGGGCCATG
169567	1763	CAACCTGGTGTGGCGTGGCC	214154	46350	TTATGCAATCTCAGAAGCTT	258741	90937	TCCCCCAGTCACTGGGCCAT
169568	1764	GCAACCTGGTGTGGCGTGGC	214155	46351	TTTATGCAATCTCAGAAGCT	258742	90938	TTCCCCCAGTCACTGGGCCA
169569	1765	GGCAACCTGGTGTGGCGTGG	214156	46352	GTTTATGCAATCTCAGAAGC	258743	90939	TTTCCCCCAGTCACTGGGCC
169570	1766	GGGCAACCTGGTGTGGCGTG	214157	46353	TGTTTATGCAATCTCAGAAG	258744	90940	TTTTCCCCCAGTCACTGGGC
169571	1767	TGGGCAACCTGGTGTGGCGT	214158	46354	TTGTTTATGCAATCTCAGAA	258745	90941	TTTTTCCCCCAGTCACTGGG
169572	1768	CTGGGCAACCTGGTGTGGCG	214159	46355	ATTGTTTATGCAATCTCAGA	258746	90942	TTTTTTCCCCCAGTCACTGG
169573	1769	GCTGGGCAACCTGGTGTGGC	214160	46356	TATTGTTTATGCAATCTCAG	258747	90943	TTTTTTTCCCCCAGTCACTG
169574	1770	CGCTGGGCAACCTGGTGTGG	214161	46357	CTATTGTTTATGCAATCTCA	258748	90944	ATTTTTTTCCCCCAGTCACT
169575	1771	TCGCTGGGCAACCTGGTGTG	214162	46358	CCTATTGTTTATGCAATCTC	258749	90945	TATTTTTTTCCCCCAGTCAC
169576	1772	CTCGCTGGGCAACCTGGTGT	214163	46359	TCCTATTGTTTATGCAATCT	258750	90946	TTATTTTTTTCCCCCAGTCA
169577	1773	CCTCGCTGGGCAACCTGGTG	214164	46360	TTCCTATTGTTTATGCAATC	258751	90947	TTTATTTTTTTCCCCCAGTC
169578	1774	CCCTCGCTGGGCAACCTGGT	214165	46361	CTTCCTATTGTTTATGCAAT	258752	90948	TTTTATTTTTTTCCCCCAGT
169579	1775	TCCCTCGCTGGGCAACCTGG	214166	46362	GCTTCCTATTGTTTATGCAA	258753	90949	CTTTTATTTTTTTCCCCCAG
169580	1776	GTCCCTCGCTGGGCAACCTG	214167	46363	GGCTTCCTATTGTTTATGCA	258754	90950	TCTTTTATTTTTTTCCCCCA
169581	1777	CGTCCCTCGCTGGGCAACCT	214168	46364	TGGCTTCCTATTGTTTATGC	258755	90951	GTCTTTTATTTTTTTCCCCC
169582	1778	GCGTCCCTCGCTGGGCAACC	214169	46365	ATGGCTTCCTATTGTTTATG	258756	90952	AGTCTTTTATTTTTTTCCCC
169583	1779	AGCGTCCCTCGCTGGGCAAC	214170	46366	GATGGCTTCCTATTGTTTAT	258757	90953	TAGTCTTTTATTTTTTTCCC
169584	1780	CAGCGTCCCTCGCTGGGCAA	214171	46367	AGATGGCTTCCTATTGTTTA	258758	90954	TTAGTCTTTTATTTTTTTCC
169585	1781	CCAGCGTCCCTCGCTGGGCA	214172	46368	AAGATGGCTTCCTATTGTTT	258759	90955	TTTAGTCTTTTATTTTTTTC
169586	1782	GCCAGCGTCCCTCGCTGGGC	214173	46369	CAAGATGGCTTCCTATTGTT	258760	90956	CTTTAGTCTTTTATTTTTTT
169587	1783	AGCCAGCGTCCCTCGCTGGG	214174	46370	CCAAGATGGCTTCCTATTGT	258761	90957	ACTTTAGTCTTTTATTTTTT
169588	1784	TAGCCAGCGTCCCTCGCTGG	214175	46371	ACCAAGATGGCTTCCTATTG	258762	90958	TACTTTAGTCTTTTATTTTT
169589	1785	GTAGCCAGCGTCCCTCGCTG	214176	46372	CACCAAGATGGCTTCCTATT	258763	90959	TTACTTTAGTCTTTTATTTT
169590	1786	GGTAGCCAGCGTCCCTCGCT	214177	46373	GCACCAAGATGGCTTCCTAT	258764	90960	CTTACTTTAGTCTTTTATTT
169591	1787	GGGTAGCCAGCGTCCCTCGC	214178	46374	AGCACCAAGATGGCTTCCTA	258765	90961	ACTTACTTTAGTCTTTTATT
169592	1788	TGGGTAGCCAGCGTCCCTCG	214179	46375	AAGCACCAAGATGGCTTCCT	258766	90962	AACTTACTTTAGTCTTTTAT
169593	1789	ATGGGTAGCCAGCGTCCCTC	214180	46376	AAAGCACCAAGATGGCTTCC	258767	90963	TAACTTACTTTAGTCTTTTA
169594	1790	GATGGGTAGCCAGCGTCCCT	214181	46377	TAAAGCACCAAGATGGCTTC	258768	90964	TTAACTTACTTTAGTCTTTT
169595	1791	GGATGGGTAGCCAGCGTCCC	214182	46378	TTAAAGCACCAAGATGGCTT	258769	90965	TTTAACTTACTTTAGTCTTT
169596	1792	CGGATGGGTAGCCAGCGTCC	214183	46379	GTTAAAGCACCAAGATGGCT	258770	90966	GTTTAACTTACTTTAGTCTT
169597	1793	CCGGATGGGTAGCCAGCGTC	214184	46380	TGTTAAAGCACCAAGATGGC	258771	90967	TGTTTAACTTACTTTAGTCT
169598	1794	CCCGGATGGGTAGCCAGCGT	214185	46381	GTGTTAAAGCACCAAGATGG	258772	90968	CTGTTTAACTTACTTTAGTC
169599	1795	CCCCGGATGGGTAGCCAGCG	214186	46382	TGTGTTAAAGCACCAAGATG	258773	90969	CCTGTTTAACTTACTTTAGT
169600	1796	TCCCCGGATGGGTAGCCAGC	214187	46383	TTGTGTTAAAGCACCAAGAT	258774	90970	GCCTGTTTAACTTACTTTAG
169601	1797	ATCCCCGGATGGGTAGCCAG	214188	46384	TTTGTGTTAAAGCACCAAGA	258775	90971	AGCCTGTTTAACTTACTTTA
169602	1798	CATCCCCGGATGGGTAGCCA	214189	46385	GTTTGTGTTAAAGCACCAAG	258776	90972	AAGCCTGTTTAACTTACTTT

169603	1799	CCATCCCCGGATGGGTAGCC	214190	46386	AGTTTGTGTTAAAGCACCAA	258777	90973	AAAGCCTGTTTAACTTACTT
169604	1800	CCCATCCCCGGATGGGTAGC	214191	46387	GAGTTTGTGTTAAAGCACCA	258778	90974	AAAAGCCTGTTTAACTTACT
169605	1801	ACCCATCCCCGGATGGGTAG	214192	46388	AGAGTTTGTGTTAAAGCACC	258779	90975	GAAAAGCCTGTTTAACTTAC
169606	1802	CACCCATCCCCGGATGGGTA	214193	46389	GAGAGTTTGTGTTAAAGCAC	258780	90976	AGAAAAGCCTGTTTAACTTA
169607	1803	CCACCCATCCCCGGATGGGT	214194	46390	GGAGAGTTTGTGTTAAAGCA	258781	90977	CAGAAAAGCCTGTTTAACTT
169608	1804	CCCACCCATCCCCGGATGGG	214195	46391	GGGAGAGTTTGTGTTAAAGC	258782	90978	GCAGAAAAGCCTGTTTAACT
169609	1805	CCCCACCCATCCCCGGATGG	214196	46392	GGGGAGAGTTTGTGTTAAAG	258783	90979	AGCAGAAAAGCCTGTTTAAC
169610	1806	TCCCCACCCATCCCCGGATG	214197	46393	TGGGGAGAGTTTGTGTTAAA	258784	90980	CAGCAGAAAAGCCTGTTTAA
169611	1807	CTCCCCACCCATCCCCGGAT	214198	46394	CTGGGGAGAGTTTGTGTTAA	258785	90981	GCAGCAGAAAAGCCTGTTTA
169612	1808	GCTCCCCACCCATCCCCGGA	214199	46395	ACTGGGGAGAGTTTGTGTTA	258786	90982	TGCAGCAGAAAAGCCTGTTT
169613	1809	GGCTCCCCACCCATCCCCGG	214200	46396	CACTGGGGAGAGTTTGTGTT	258787	90983	CTGCAGCAGAAAAGCCTGTT
169614	1810	GGGCTCCCCACCCATCCCCG	214201	46397	TCACTGGGGAGAGTTTGTGT	258788	90984	CCTGCAGCAGAAAAGCCTGT
169615	1811	AGGGCTCCCCACCCATCCCC	214202	46398	ATCACTGGGGAGAGTTTGTG	258789	90985	TCCTGCAGCAGAAAAGCCTG
169616	1812	CAGGGCTCCCCACCCATCCC	214203	46399	CATCACTGGGGAGAGTTTGT	258790	90986	GTCCTGCAGCAGAAAAGCCT
169617	1813	CCAGGGCTCCCCACCCATCC	214204	46400	TCATCACTGGGGAGAGTTTG	258791	90987	AGTCCTGCAGCAGAAAAGCC
169618	1814	GCCAGGGCTCCCCACCCATC	214205	46401	CTCATCACTGGGGAGAGTTT	258792	90988	AAGTCCTGCAGCAGAAAAGC
169619	1815	CGCCAGGGCTCCCCACCCAT	214206	46402	CCTCATCACTGGGGAGAGTT	258793	90989	CAAGTCCTGCAGCAGAAAAG
169620	1816	CCGCCAGGGCTCCCCACCCA	214207	46403	CCCTCATCACTGGGGAGAGT	258794	90990	ACAAGTCCTGCAGCAGAAAA
169621	1817	CCCGCCAGGGCTCCCCACCC	214208	46404	ACCCTCATCACTGGGGAGAG	258795	90991	GACAAGTCCTGCAGCAGAAA
169622	1818	CCCCGCCAGGGCTCCCCACC	214209	46405	AACCCTCATCACTGGGGAGA	258796	90992	TGACAAGTCCTGCAGCAGAA
169623	1819	GCCCCGCCAGGGCTCCCCAC	214210	46406	CAACCCTCATCACTGGGGAG	258797	90993	CTGACAAGTCCTGCAGCAGA
169624	1820	GGCCCCGCCAGGGCTCCCCA	214211	46407	TCAACCCTCATCACTGGGGA	258798	90994	TCTGACAAGTCCTGCAGCAG
169625	1821	AGGCCCCGCCAGGGCTCCCC	214212	46408	CTCAACCCTCATCACTGGGG	258799	90995	CTCTGACAAGTCCTGCAGCA
169626	1822	GAGGCCCCGCCAGGGCTCCC	214213	46409	GCTCAACCCTCATCACTGGG	258800	90996	GCTCTGACAAGTCCTGCAGC
169627	1823	AGAGGCCCCGCCAGGGCTCC	214214	46410	GGCTCAACCCTCATCACTGG	258801	90997	GGCTCTGACAAGTCCTGCAG
169628	1824	GAGAGGCCCCGCCAGGGCTC	214215	46411	TGGCTCAACCCTCATCACTG	258802	90998	AGGCTCTGACAAGTCCTGCA
169629	1825	GGAGAGGCCCCGCCAGGGCT	214216	46412	TTGGCTCAACCCTCATCACT	258803	90999	AAGGCTCTGACAAGTCCTGC
169630	1826	CGGAGAGGCCCCGCCAGGGC	214217	46413	TTTGGCTCAACCCTCATCAC	258804	91000	AAAGGCTCTGACAAGTCCTG
169631	1827	CCGGAGAGGCCCCGCCAGGG	214218	46414	CTTTGGCTCAACCCTCATCA	258805	91001	TAAAGGCTCTGACAAGTCCT
169632	1828	GCCGGAGAGGCCCCGCCAGG	214219	46415	GCTTTGGCTCAACCCTCATC	258806	91002	TTAAAGGCTCTGACAAGTCC
169633	1829	AGCCGGAGAGGCCCCGCCAG	214220	46416	GGCTTTGGCTCAACCCTCAT	258807	91003	ATTAAAGGCTCTGACAAGTC
169634	1830	AAGCCGGAGAGGCCCCGCCA	214221	46417	TGGCTTTGGCTCAACCCTCA	258808	91004	CATTAAAGGCTCTGACAAGT
169635	1831	AAAGCCGGAGAGGCCCCGCC	214222	46418	CTGGCTTTGGCTCAACCCTC	258809	91005	ACATTAAAGGCTCTGACAAG
169636	1832	TAAAGCCGGAGAGGCCCCGC	214223	46419	TCTGGCTTTGGCTCAACCCT	258810	91006	TACATTAAAGGCTCTGACAA
169637	1833	GTAAAGCCGGAGAGGCCCCG	214224	46420	ATCTGGCTTTGGCTCAACCC	258811	91007	GTACATTAAAGGCTCTGACA
169638	1834	CGTAAAGCCGGAGAGGCCCC	214225	46421	AATCTGGCTTTGGCTCAACC	258812	91008	AGTACATTAAAGGCTCTGAC
169639	1835	GCGTAAAGCCGGAGAGGCCC	214226	46422	CAATCTGGCTTTGGCTCAAC	258813	91009	TAGTACATTAAAGGCTCTGA
169640	1836	GGCGTAAAGCCGGAGAGGCC	214227	46423	CCAATCTGGCTTTGGCTCAA	258814	91010	TTAGTACATTAAAGGCTCTG
169641	1837	GGGCGTAAAGCCGGAGAGGC	214228	46424	GCCAATCTGGCTTTGGCTCA	258815	91011	ATTAGTACATTAAAGGCTCT
169642	1838	AGGGCGTAAAGCCGGAGAGG	214229	46425	TGCCAATCTGGCTTTGGCTC	258816	91012	CATTAGTACATTAAAGGCTC
169643	1839	CAGGGCGTAAAGCCGGAGAG	214230	46426	TTGCCAATCTGGCTTTGGCT	258817	91013	CCATTAGTACATTAAAGGCT
169644	1840	ACAGGGCGTAAAGCCGGAGA	214231	46427	CTTGCCAATCTGGCTTTGGC	258818	91014	GCCATTAGTACATTAAAGGC
169645	1841	AACAGGGCGTAAAGCCGGAG	214232	46428	GCTTGCCAATCTGGCTTTGG	258819	91015	GGCCATTAGTACATTAAAGG
169646	1842	CAACAGGGCGTAAAGCCGGA	214233	46429	TGCTTGCCAATCTGGCTTTG	258820	91016	TGGCCATTAGTACATTAAAG
169647	1843	GCAACAGGGCGTAAAGCCGG	214234	46430	CTGCTTGCCAATCTGGCTTT	258821	91017	ATGGCCATTAGTACATTAAA
169648	1844	AGCAACAGGGCGTAAAGCCG	214235	46431	TCTGCTTGCCAATCTGGCTT	258822	91018	AATGGCCATTAGTACATTAA
169649	1845	AAGCAACAGGGCGTAAAGCC	214236	46432	CTCTGCTTGCCAATCTGGCT	258823	91019	CAATGGCCATTAGTACATTA
169650	1846	GAAGCAACAGGGCGTAAAGC	214237	46433	TCTCTGCTTGCCAATCTGGC	258824	91020	ACAATGGCCATTAGTACATT
169651	1847	CGAAGCAACAGGGCGTAAAG	214238	46434	CTCTCTGCTTGCCAATCTGG	258825	91021	CACAATGGCCATTAGTACAT
169652	1848	GCGAAGCAACAGGGCGTAAA	214239	46435	CCTCTCTGCTTGCCAATCTG	258826	91022	TCACAATGGCCATTAGTACA
169653	1849	GGCGAAGCAACAGGGCGTAA	214240	46436	TCCTCTCTGCTTGCCAATCT	258827	91023	GTCACAATGGCCATTAGTAC
169654	1850	AGGCGAAGCAACAGGGCGTA	214241	46437	CTCCTCTCTGCTTGCCAATC	258828	91024	GGTCACAATGGCCATTAGTA
169655	1851	CAGGCGAAGCAACAGGGCGT	214242	46438	TCTCCTCTCTGCTTGCCAAT	258829	91025	GGGTCACAATGGCCATTAGT
169656	1852	CCAGGCGAAGCAACAGGGCG	214243	46439	GTCTCCTCTCTGCTTGCCAA	258830	91026	AGGGTCACAATGGCCATTAG
169657	1853	GCCAGGCGAAGCAACAGGGC	214244	46440	AGTCTCCTCTCTGCTTGCCA	258831	91027	GAGGGTCACAATGGCCATTA
169658	1854	GGCCAGGCGAAGCAACAGGG	214245	46441	AAGTCTCCTCTCTGCTTGCC	258832	91028	AGAGGGTCACAATGGCCATT
169659	1855	CGGCCAGGCGAAGCAACAGG	214246	46442	CAAGTCTCCTCTCTGCTTGC	258833	91029	CAGAGGGTCACAATGGCCAT
169660	1856	CCGGCCAGGCGAAGCAACAG	214247	46443	ACAAGTCTCCTCTCTGCTTG	258834	91030	TCAGAGGGTCACAATGGCCA
169661	1857	TCCGGCCAGGCGAAGCAACA	214248	46444	CACAAGTCTCCTCTCTGCTT	258835	91031	CTCAGAGGGTCACAATGGCC
169662	1858	CTCCGGCCAGGCGAAGCAAC	214249	46445	ACACAAGTCTCCTCTCTGCT	258836	91032	TCTCAGAGGGTCACAATGGC
169663	1859	TCTCCGGCCAGGCGAAGCAA	214250	46446	TACACAAGTCTCCTCTCTGC	258837	91033	TTCTCAGAGGGTCACAATGG
169664	1860	TTCTCCGGCCAGGCGAAGCA	214251	46447	GTACACAAGTCTCCTCTCTG	258838	91034	CTTCTCAGAGGGTCACAATG
169665	1861	ATTCTCCGGCCAGGCGAAGC	214252	46448	TGTACACAAGTCTCCTCTCT	258839	91035	CCTTCTCAGAGGGTCACAAT
169666	1862	CATTCTCCGGCCAGGCGAAG	214253	46449	TTGTACACAAGTCTCCTCTC	258840	91036	ACCTTCTCAGAGGGTCACAA
169667	1863	ACATTCTCCGGCCAGGCGAA	214254	46450	CTTGTACACAAGTCTCCTCT	258841	91037	GACCTTCTCAGAGGGTCACA
169668	1864	CACATTCTCCGGCCAGGCGA	214255	46451	CCTTGTACACAAGTCTCCTC	258842	91038	TGACCTTCTCAGAGGGTCAC
169669	1865	TCACATTCTCCGGCCAGGCG	214256	46452	TCCTTGTACACAAGTCTCCT	258843	91039	GTGACCTTCTCAGAGGGTCA
169670	1866	CTCACATTCTCCGGCCAGGC	214257	46453	CTCCTTGTACACAAGTCTCC	258844	91040	TGTGACCTTCTCAGAGGGTC
169671	1867	CCTCACATTCTCCGGCCAGG	214258	46454	ACTCCTTGTACACAAGTCTC	258845	91041	CTGTGACCTTCTCAGAGGGT
169672	1868	TCCTCACATTCTCCGGCCAG	214259	46455	AACTCCTTGTACACAAGTCT	258846	91042	TCTGTGACCTTCTCAGAGGG
169673	1869	TTCCTCACATTCTCCGGCCA	214260	46456	GAACTCCTTGTACACAAGTC	258847	91043	CTCTGTGACCTTCTCAGAGG
169674	1870	CTTCCTCACATTCTCCGGCC	214261	46457	GGAACTCCTTGTACACAAGT	258848	91044	ACTCTGTGACCTTCTCAGAG

169675	1871	CCTTCCTCACATTCTCCGGC	214262	46458	AGGAACTCCTTGTACACAAG	258849	91045	CACTCTGTGACCTTCTCAGA
169676	1872	CCCTTCCTCACATTCTCCGG	214263	46459	GAGGAACTCCTTGTACACAA	258850	91046	CCACTCTGTGACCTTCTCAG
169677	1873	CCCCTTCCTCACATTCTCCG	214264	46460	CGAGGAACTCCTTGTACACA	258851	91047	CCCACTCTGTGACCTTCTCA
169678	1874	GCCCCTTCCTCACATTCTCC	214265	46461	TCGAGGAACTCCTTGTACAC	258852	91048	ACCCACTCTGTGACCTTCTC
169679	1875	TGCCCCTTCCTCACATTCTC	214266	46462	CTCGAGGAACTCCTTGTACA	258853	91049	AACCCACTCTGTGACCTTCT
169680	1876	ATGCCCCTTCCTCACATTCT	214267	46463	ACTCGAGGAACTCCTTGTAC	258854	91050	AAACCCACTCTGTGACCTTC
169681	1877	TATGCCCCTTCCTCACATTC	214268	46464	GACTCGAGGAACTCCTTGTA	258855	91051	GAAACCCACTCTGTGACCTT
169682	1878	TTATGCCCCTTCCTCACATT	214269	46465	TGACTCGAGGAACTCCTTGT	258856	91052	GGAAACCCACTCTGTGACCT
169683	1879	CTTATGCCCCTTCCTCACAT	214270	46466	TTGACTCGAGGAACTCCTTG	258857	91053	GGGAAACCCACTCTGTGACC
169684	1880	CCTTATGCCCCTTCCTCACA	214271	46467	ATTGACTCGAGGAACTCCTT	258858	91054	TGGGAAACCCACTCTGTGAC
169685	1881	ACCTTATGCCCCTTCCTCAC	214272	46468	AATTGACTCGAGGAACTCCT	258859	91055	TTGGGAAACCCACTCTGTGA
169686	1882	AACCTTATGCCCCTTCCTCA	214273	46469	CAATTGACTCGAGGAACTCC	258860	91056	TTTGGGAAACCCACTCTGTG
169687	1883	TAACCTTATGCCCCTTCCTC	214274	46470	GCAATTGACTCGAGGAACTC	258861	91057	GTTTGGGAAACCCACTCTGT
169688	1884	GTAACCTTATGCCCCTTCCT	214275	46471	AGCAATTGACTCGAGGAACT	258862	91058	AGTTTGGGAAACCCACTCTG
169689	1885	AGTAACCTTATGCCCCTTCC	214276	46472	AAGCAATTGACTCGAGGAAC	258863	91059	AAGTTTGGGAAACCCACTCT
169690	1886	CAGTAACCTTATGCCCCTTC	214277	46473	AAAGCAATTGACTCGAGGAA	258864	91060	TAAGTTTGGGAAACCCACTC
169691	1887	CCAGTAACCTTATGCCCCTT	214278	46474	AAAAGCAATTGACTCGAGGA	258865	91061	GTAAGTTTGGGAAACCCACT
169692	1888	ACCAGTAACCTTATGCCCCT	214279	46475	AAAAAGCAATTGACTCGAGG	258866	91062	AGTAAGTTTGGGAAACCCAC
169693	1889	CACCAGTAACCTTATGCCCC	214280	46476	GAAAAAGCAATTGACTCGAG	258867	91063	AAGTAAGTTTGGGAAACCCA
169694	1890	GCACCAGTAACCTTATGCCC	214281	46477	GGAAAAAGCAATTGACTCGA	258868	91064	CAAGTAAGTTTGGGAAACCC
169695	1891	AGCACCAGTAACCTTATGCC	214282	46478	AGGAAAAAGCAATTGACTCG	258869	91065	TCAAGTAAGTTTGGGAAACC
169696	1892	AAGCACCAGTAACCTTATGC	214283	46479	AAGGAAAAAGCAATTGACTC	258870	91066	ATCAAGTAAGTTTGGGAAAC
169697	1893	GAAGCACCAGTAACCTTATG	214284	46480	CAAGGAAAAAGCAATTGACT	258871	91067	AATCAAGTAAGTTTGGGAAA
169698	1894	CGAAGCACCAGTAACCTTAT	214285	46481	ACAAGGAAAAAGCAATTGAC	258872	91068	GAATCAAGTAAGTTTGGGAA
169699	1895	CCGAAGCACCAGTAACCTTA	214286	46482	AACAAGGAAAAAGCAATTGA	258873	91069	AGAATCAAGTAAGTTTGGGA
169700	1896	GCCGAAGCACCAGTAACCTT	214287	46483	GAACAAGGAAAAAGCAATTG	258874	91070	TAGAATCAAGTAAGTTTGGG
169701	1897	GGCCGAAGCACCAGTAACCT	214288	46484	AGAACAAGGAAAAAGCAATT	258875	91071	GTAGAATCAAGTAAGTTTGG
169702	1898	TGGCCGAAGCACCAGTAACC	214289	46485	TAGAACAAGGAAAAAGCAAT	258876	91072	GGTAGAATCAAGTAAGTTTG
169703	1899	GTGGCCGAAGCACCAGTAAC	214290	46486	CTAGAACAAGGAAAAAGCAA	258877	91073	AGGTAGAATCAAGTAAGTTT
169704	1900	TGTGGCCGAAGCACCAGTAA	214291	46487	GCTAGAACAAGGAAAAAGCA	258878	91074	CAGGTAGAATCAAGTAAGTT
169705	1901	GTGTGGCCGAAGCACCAGTA	214292	46488	GGCTAGAACAAGGAAAAAGC	258879	91075	GCAGGTAGAATCAAGTAAGT
169706	1902	GGTGTGGCCGAAGCACCAGT	214293	46489	TGGCTAGAACAAGGAAAAAG	258880	91076	AGCAGGTAGAATCAAGTAAG
169707	1903	GGGTGTGGCCGAAGCACCAG	214294	46490	CTGGCTAGAACAAGGAAAAA	258881	91077	TAGCAGGTAGAATCAAGTAA
169708	1904	TGGGTGTGGCCGAAGCACCA	214295	46491	GCTGGCTAGAACAAGGAAAA	258882	91078	TTAGCAGGTAGAATCAAGTA
169709	1905	ATGGGTGTGGCCGAAGCACC	214296	46492	GGCTGGCTAGAACAAGGAAA	258883	91079	GTTAGCAGGTAGAATCAAGT
169710	1906	GATGGGTGTGGCCGAAGCAC	214297	46493	TGGCTGGCTAGAACAAGGAA	258884	91080	TGTTAGCAGGTAGAATCAAG
169711	1907	AGATGGGTGTGGCCGAAGCA	214298	46494	CTGGCTGGCTAGAACAAGGA	258885	91081	ATGTTAGCAGGTAGAATCAA
169712	1908	AAGATGGGTGTGGCCGAAGC	214299	46495	TCTGGCTGGCTAGAACAAGG	258886	91082	AATGTTAGCAGGTAGAATCA
169713	1909	AAAGATGGGTGTGGCCGAAG	214300	46496	CTCTGGCTGGCTAGAACAAG	258887	91083	AAATGTTAGCAGGTAGAATC
169714	1910	GAAAGATGGGTGTGGCCGAA	214301	46497	CCTCTGGCTGGCTAGAACAA	258888	91084	GAAATGTTAGCAGGTAGAAT
169715	1911	AGAAAGATGGGTGTGGCCGA	214302	46498	CCCTCTGGCTGGCTAGAACA	258889	91085	GGAAATGTTAGCAGGTAGAA
169716	1912	CAGAAAGATGGGTGTGGCCG	214303	46499	GCCCTCTGGCTGGCTAGAAC	258890	91086	AGGAAATGTTAGCAGGTAGA
169717	1913	TCAGAAAGATGGGTGTGGCC	214304	46500	AGCCCTCTGGCTGGCTAGAA	258891	91087	CAGGAAATGTTAGCAGGTAG
169718	1914	CTCAGAAAGATGGGTGTGGC	214305	46501	GAGCCCTCTGGCTGGCTAGA	258892	91088	CCAGGAAATGTTAGCAGGTA
169719	1915	GCTCAGAAAGATGGGTGTGG	214306	46502	GGAGCCCTCTGGCTGGCTAG	258893	91089	TCCAGGAAATGTTAGCAGGT
169720	1916	GGCTCAGAAAGATGGGTGTG	214307	46503	AGGAGCCCTCTGGCTGGCTA	258894	91090	CTCCAGGAAATGTTAGCAGG
169721	1917	GGGCTCAGAAAGATGGGTGT	214308	46504	CAGGAGCCCTCTGGCTGGCT	258895	91091	CCTCCAGGAAATGTTAGCAG
169722	1918	TGGGCTCAGAAAGATGGGTG	214309	46505	ACAGGAGCCCTCTGGCTGGC	258896	91092	TCCTCCAGGAAATGTTAGCA
169723	1919	GTGGGCTCAGAAAGATGGGT	214310	46506	AACAGGAGCCCTCTGGCTGG	258897	91093	TTCCTCCAGGAAATGTTAGC
169724	1920	AGTGGGCTCAGAAAGATGGG	214311	46507	CAACAGGAGCCCTCTGGCTG	258898	91094	CTTCCTCCAGGAAATGTTAG
169725	1921	CAGTGGGCTCAGAAAGATGG	214312	46508	CCAACAGGAGCCCTCTGGCT	258899	91095	ACTTCCTCCAGGAAATGTTA
169726	1922	CCAGTGGGCTCAGAAAGATG	214313	46509	TCCAACAGGAGCCCTCTGGC	258900	91096	AACTTCCTCCAGGAAATGTT
169727	1923	TCCAGTGGGCTCAGAAAGAT	214314	46510	TTCCAACAGGAGCCCTCTGG	258901	91097	AAACTTCCTCCAGGAAATGT
169728	1924	GTCCAGTGGGCTCAGAAAGA	214315	46511	TTTCCAACAGGAGCCCTCTG	258902	91098	CAAACTTCCTCCAGGAAATG
169729	1925	AGTCCAGTGGGCTCAGAAAG	214316	46512	TTTTCCAACAGGAGCCCTCT	258903	91099	CCAAACTTCCTCCAGGAAAT
169730	1926	CAGTCCAGTGGGCTCAGAAA	214317	46513	GTTTTCCAACAGGAGCCCTC	258904	91100	CCCAAACTTCCTCCAGGAAA
169731	1927	CCAGTCCAGTGGGCTCAGAA	214318	46514	TGTTTTCCAACAGGAGCCCT	258905	91101	TCCCAAACTTCCTCCAGGAA
169732	1928	CCCAGTCCAGTGGGCTCAGA	214319	46515	CTGTTTTCCAACAGGAGCCC	258906	91102	TTCCCAAACTTCCTCCAGGA
169733	1929	GCCCAGTCCAGTGGGCTCAG	214320	46516	CCTGTTTTCCAACAGGAGCC	258907	91103	TTTCCCAAACTTCCTCCAGG
169734	1930	CGCCCAGTCCAGTGGGCTCA	214321	46517	TCCTGTTTTCCAACAGGAGC	258908	91104	ATTTCCCAAACTTCCTCCAG
169735	1931	GCGCCCAGTCCAGTGGGCTC	214322	46518	CTCCTGTTTTCCAACAGGAG	258909	91105	CATTTCCCAAACTTCCTCCA
169736	1932	TGCGCCCAGTCCAGTGGGCT	214323	46519	TCTCCTGTTTTCCAACAGGA	258910	91106	GCATTTCCCAAACTTCCTCC
169737	1933	CTGCGCCCAGTCCAGTGGGC	214324	46520	GTCTCCTGTTTTCCAACAGG	258911	91107	GGCATTTCCCAAACTTCCTC
169738	1934	TCTGCGCCCAGTCCAGTGGG	214325	46521	GGTCTCCTGTTTTCCAACAG	258912	91108	CGGCATTTCCCAAACTTCCT
169739	1935	CTCTGCGCCCAGTCCAGTGG	214326	46522	CGGTCTCCTGTTTTCCAACA	258913	91109	TCGGCATTTCCCAAACTTCC
169740	1936	CCTCTGCGCCCAGTCCAGTG	214327	46523	CCGGTCTCCTGTTTTCCAAC	258914	91110	ATCGGCATTTCCCAAACTTC
169741	1937	CCCTCTGCGCCCAGTCCAGT	214328	46524	TCCGGTCTCCTGTTTTCCAA	258915	91111	AATCGGCATTTCCCAAACTT
169742	1938	CCCCTCTGCGCCCAGTCCAG	214329	46525	CTCCGGTCTCCTGTTTTCCA	258916	91112	AAATCGGCATTTCCCAAACT
169743	1939	CCCCCTCTGCGCCCAGTCCA	214330	46526	TCTCCGGTCTCCTGTTTTCC	258917	91113	TAAATCGGCATTTCCCAAAC
169744	1940	CCCCCCTCTGCGCCCAGTCC	214331	46527	CTCTCCGGTCTCCTGTTTTC	258918	91114	CTAAATCGGCATTTCCCAAA
169745	1941	TCCCCCCTCTGCGCCCAGTC	214332	46528	CCTCTCCGGTCTCCTGTTTT	258919	91115	GCTAAATCGGCATTTCCCAA
169746	1942	ATCCCCCCTCTGCGCCCAGT	214333	46529	GCCTCTCCGGTCTCCTGTTT	258920	91116	TGCTAAATCGGCATTTCCCA

169747	1943	AATCCCCCCTCTGCGCCCAG	214334	46530	AGCCTCTCCGGTCTCCTGTT	258921	91117	CTGCTAAATCGGCATTTCCC
169748	1944	CAATCCCCCCTCTGCGCCCA	214335	46531	CAGCCTCTCCGGTCTCCTGT	258922	91118	TCTGCTAAATCGGCATTTCC
169749	1945	GCAATCCCCCCTCTGCGCCC	214336	46532	TCAGCCTCTCCGGTCTCCTG	258923	91119	ATCTGCTAAATCGGCATTTC
169750	1946	GGCAATCCCCCCTCTGCGCC	214337	46533	CTCAGCCTCTCCGGTCTCCT	258924	91120	AATCTGCTAAATCGGCATTT
169751	1947	TGGCAATCCCCCCTCTGCGC	214338	46534	CCTCAGCCTCTCCGGTCTCC	258925	91121	GAATCTGCTAAATCGGCATT
169752	1948	ATGGCAATCCCCCCTCTGCG	214339	46535	GCCTCAGCCTCTCCGGTCTC	258926	91122	AGAATCTGCTAAATCGGCAT
169753	1949	CATGGCAATCCCCCCTCTGC	214340	46536	GGCCTCAGCCTCTCCGGTCT	258927	91123	AAGAATCTGCTAAATCGGCA
169754	1950	CCATGGCAATCCCCCCTCTG	214341	46537	AGGCCTCAGCCTCTCCGGTC	258928	91124	AAAGAATCTGCTAAATCGGC
169755	1951	TCCATGGCAATCCCCCCTCT	214342	46538	CAGGCCTCAGCCTCTCCGGT	258929	91125	AAAAGAATCTGCTAAATCGG
169756	1952	TTCCATGGCAATCCCCCCTC	214343	46539	TCAGGCCTCAGCCTCTCCGG	258930	91126	CAAAAGAATCTGCTAAATCG
169757	1953	TTTCCATGGCAATCCCCCCT	214344	46540	GTCAGGCCTCAGCCTCTCCG	258931	91127	ACAAAAGAATCTGCTAAATC
169758	1954	GTTTCCATGGCAATCCCCCC	214345	46541	GGTCAGGCCTCAGCCTCTCC	258932	91128	AACAAAAGAATCTGCTAAAT
169759	1955	GGTTTCCATGGCAATCCCCC	214346	46542	TGGTCAGGCCTCAGCCTCTC	258933	91129	CAACAAAAGAATCTGCTAAA
169760	1956	TGGTTTCCATGGCAATCCCC	214347	46543	TTGGTCAGGCCTCAGCCTCT	258934	91130	ACAACAAAAGAATCTGCTAA
169761	1957	GTGGTTTCCATGGCAATCCC	214348	46544	TTTGGTCAGGCCTCAGCCTC	258935	91131	CACAACAAAAGAATCTGCTA
169762	1958	TGTGGTTTCCATGGCAATCC	214349	46545	GTTTGGTCAGGCCTCAGCCT	258936	91132	GCACAACAAAAGAATCTGCT
169763	1959	CTGTGGTTTCCATGGCAATC	214350	46546	GGTTTGGTCAGGCCTCAGCC	258937	91133	GGCACAACAAAAGAATCTGC
169764	1960	CCTGTGGTTTCCATGGCAAT	214351	46547	TGGTTTGGTCAGGCCTCAGC	258938	91134	CGGCACAACAAAAGAATCTG
169765	1961	ACCTGTGGTTTCCATGGCAA	214352	46548	CTGGTTTGGTCAGGCCTCAG	258939	91135	ACGGCACAACAAAAGAATCT
169766	1962	CACCTGTGGTTTCCATGGCA	214353	46549	GCTGGTTTGGTCAGGCCTCA	258940	91136	CACGGCACAACAAAAGAATC
169767	1963	ACACCTGTGGTTTCCATGGC	214354	46550	AGCTGGTTTGGTCAGGCCTC	258941	91137	CCACGGCACAACAAAAGAAT
169768	1964	GACACCTGTGGTTTCCATGG	214355	46551	AAGCTGGTTTGGTCAGGCCT	258942	91138	TCCACGGCACAACAAAAGAA
169769	1965	GGACACCTGTGGTTTCCATG	214356	46552	GAAGCTGGTTTGGTCAGGCC	258943	91139	ATCCACGGCACAACAAAAGA
169770	1966	CGGACACCTGTGGTTTCCAT	214357	46553	AGAAGCTGGTTTGGTCAGGC	258944	91140	CATCCACGGCACAACAAAAG
169771	1967	CCGGACACCTGTGGTTTCCA	214358	46554	CAGAAGCTGGTTTGGTCAGG	258945	91141	CCATCCACGGCACAACAAAA
169772	1968	TCCGGACACCTGTGGTTTCC	214359	46555	GCAGAAGCTGGTTTGGTCAG	258946	91142	ACCATCCACGGCACAACAAA
169773	1969	CTCCGGACACCTGTGGTTTC	214360	46556	TGCAGAAGCTGGTTTGGTCA	258947	91143	CACCATCCACGGCACAACAA
169774	1970	TCTCCGGACACCTGTGGTTT	214361	46557	CTGCAGAAGCTGGTTTGGTC	258948	91144	GCACCATCCACGGCACAACA
169775	1971	CTCTCCGGACACCTGTGGTT	214362	46558	CCTGCAGAAGCTGGTTTGGT	258949	91145	AGCACCATCCACGGCACAAC
169776	1972	CCTCTCCGGACACCTGTGGT	214363	46559	GCCTGCAGAAGCTGGTTTGG	258950	91146	CAGCACCATCCACGGCACAA
169777	1973	CCCTCTCCGGACACCTGTGG	214364	46560	GGCCTGCAGAAGCTGGTTTG	258951	91147	CCAGCACCATCCACGGCACA
169778	1974	CCCCTCTCCGGACACCTGTG	214365	46561	TGGCCTGCAGAAGCTGGTTT	258952	91148	ACCAGCACCATCCACGGCAC
169779	1975	TCCCCTCTCCGGACACCTGT	214366	46562	CTGGCCTGCAGAAGCTGGTT	258953	91149	AACCAGCACCATCCACGGCA
169780	1976	ATCCCCTCTCCGGACACCTG	214367	46563	GCTGGCCTGCAGAAGCTGGT	258954	91150	CAACCAGCACCATCCACGGC
169781	1977	GATCCCCTCTCCGGACACCT	214368	46564	AGCTGGCCTGCAGAAGCTGG	258955	91151	TCAACCAGCACCATCCACGG
169782	1978	AGATCCCCTCTCCGGACACC	214369	46565	CAGCTGGCCTGCAGAAGCTG	258956	91152	ATCAACCAGCACCATCCACG
169783	1979	AAGATCCCCTCTCCGGACAC	214370	46566	CCAGCTGGCCTGCAGAAGCT	258957	91153	CATCAACCAGCACCATCCAC
169784	1980	CAAGATCCCCTCTCCGGACA	214371	46567	CCCAGCTGGCCTGCAGAAGC	258958	91154	ACATCAACCAGCACCATCCA
169785	1981	CCAAGATCCCCTCTCCGGAC	214372	46568	TCCCAGCTGGCCTGCAGAAG	258959	91155	CACATCAACCAGCACCATCC
169786	1982	CCCAAGATCCCCTCTCCGGA	214373	46569	CTCCCAGCTGGCCTGCAGAA	258960	91156	CCACATCAACCAGCACCATC
169787	1983	CCCCAAGATCCCCTCTCCGG	214374	46570	CCTCCCAGCTGGCCTGCAGA	258961	91157	CCCACATCAACCAGCACCAT
169788	1984	GCCCCAAGATCCCCTCTCCG	214375	46571	GCCTCCCAGCTGGCCTGCAG	258962	91158	GCCCACATCAACCAGCACCA
169789	1985	AGCCCCAAGATCCCCTCTCC	214376	46572	GGCCTCCCAGCTGGCCTGCA	258963	91159	TGCCCACATCAACCAGCACC
169790	1986	CAGCCCCAAGATCCCCTCTC	214377	46573	TGGCCTCCCAGCTGGCCTGC	258964	91160	TTGCCCACATCAACCAGCAC
169791	1987	CCAGCCCCAAGATCCCCTCT	214378	46574	GTGGCCTCCCAGCTGGCCTG	258965	91161	TTTGCCCACATCAACCAGCA
169792	1988	GCCAGCCCCAAGATCCCCTC	214379	46575	TGTGGCCTCCCAGCTGGCCT	258966	91162	TTTTGCCCACATCAACCAGC
169793	1989	GGCCAGCCCCAAGATCCCCT	214380	46576	TTGTGGCCTCCCAGCTGGCC	258967	91163	GTTTTGCCCACATCAACCAG
169794	1990	AGGCCAGCCCCAAGATCCCC	214381	46577	GTTGTGGCCTCCCAGCTGGC	258968	91164	TGTTTTGCCCACATCAACCA
169795	1991	GAGGCCAGCCCCAAGATCCC	214382	46578	AGTTGTGGCCTCCCAGCTGG	258969	91165	TTGTTTTGCCCACATCAACC
169796	1992	TGAGGCCAGCCCCAAGATCC	214383	46579	GAGTTGTGGCCTCCCAGCTG	258970	91166	TTTGTTTTGCCCACATCAAC
169797	1993	GTGAGGCCAGCCCCAAGATC	214384	46580	GGAGTTGTGGCCTCCCAGCT	258971	91167	CTTTGTTTTGCCCACATCAA
169798	1994	GGTGAGGCCAGCCCCAAGAT	214385	46581	AGGAGTTGTGGCCTCCCAGC	258972	91168	TCTTTGTTTTGCCCACATCA
169799	1995	GGGTGAGGCCAGCCCCAAGA	214386	46582	TAGGAGTTGTGGCCTCCCAG	258973	91169	TTCTTTGTTTTGCCCACATC
169800	1996	GGGGTGAGGCCAGCCCCAAG	214387	46583	GTAGGAGTTGTGGCCTCCCA	258974	91170	GTTCTTTGTTTTGCCCACAT
169801	1997	AGGGGTGAGGCCAGCCCCAA	214388	46584	GGTAGGAGTTGTGGCCTCCC	258975	91171	TGTTCTTTGTTTTGCCCACA
169802	1998	AAGGGGTGAGGCCAGCCCCA	214389	46585	AGGTAGGAGTTGTGGCCTCC	258976	91172	GTGTTCTTTGTTTTGCCCAC
169803	1999	GAAGGGGTGAGGCCAGCCCC	214390	46586	TAGGTAGGAGTTGTGGCCTC	258977	91173	CGTGTTCTTTGTTTTGCCCA
169804	2000	GGAAGGGGTGAGGCCAGCCC	214391	46587	GTAGGTAGGAGTTGTGGCCT	258978	91174	ACGTGTTCTTTGTTTTGCCC
169805	2001	GGGAAGGGGTGAGGCCAGCC	214392	46588	CGTAGGTAGGAGTTGTGGCC	258979	91175	CACGTGTTCTTTGTTTTGCC
169806	2002	AGGGAAGGGGTGAGGCCAGC	214393	46589	CCGTAGGTAGGAGTTGTGGC	258980	91176	TCACGTGTTCTTTGTTTTGC
169807	2003	CAGGGAAGGGGTGAGGCCAG	214394	46590	CCCGTAGGTAGGAGTTGTGG	258981	91177	CTCACGTGTTCTTTGTTTTG
169808	2004	GCAGGGAAGGGGTGAGGCCA	214395	46591	TCCCGTAGGTAGGAGTTGTG	258982	91178	ACTCACGTGTTCTTTGTTTT
169809	2005	CGCAGGGAAGGGGTGAGGCC	214396	46592	TTCCCGTAGGTAGGAGTTGT	258983	91179	GACTCACGTGTTCTTTGTTT
169810	2006	CCGCAGGGAAGGGGTGAGGC	214397	46593	TTTCCCGTAGGTAGGAGTTG	258984	91180	TGACTCACGTGTTCTTTGTT
169811	2007	TCCGCAGGGAAGGGGTGAGG	214398	46594	TTTTCCCGTAGGTAGGAGTT	258985	91181	CTGACTCACGTGTTCTTTGT
169812	2008	CTCCGCAGGGAAGGGGTGAG	214399	46595	GTTTTCCCGTAGGTAGGAGT	258986	91182	TCTGACTCACGTGTTCTTTG
169813	2009	TCTCCGCAGGGAAGGGGTGA	214400	46596	AGTTTTCCCGTAGGTAGGAG	258987	91183	ATCTGACTCACGTGTTCTTT
169814	2010	ATCTCCGCAGGGAAGGGGTG	214401	46597	CAGTTTTCCCGTAGGTAGGA	258988	91184	GATCTGACTCACGTGTTCTT
169815	2011	AATCTCCGCAGGGAAGGGGT	214402	46598	TCAGTTTTCCCGTAGGTAGG	258989	91185	GGATCTGACTCACGTGTTCT
169816	2012	CAATCTCCGCAGGGAAGGGG	214403	46599	TTCAGTTTTCCCGTAGGTAG	258990	91186	CGGATCTGACTCACGTGTTC
169817	2013	CCAATCTCCGCAGGGAAGGG	214404	46600	CTTCAGTTTTCCCGTAGGTA	258991	91187	GCGGATCTGACTCACGTGTT
169818	2014	CCCAATCTCCGCAGGGAAGG	214405	46601	CCTTCAGTTTTCCCGTAGGT	258992	91188	GGCGGATCTGACTCACGTGT

169819	2015	CCCCAATCTCCGCAGGGAAG	214406	46602	CCCTTCAGTTTTCCCGTAGG	258993	91189	AGGCGGATCTGACTCACGTG
169820	2016	TCCCCAATCTCCGCAGGGAA	214407	46603	GCCCTTCAGTTTTCCCGTAG	258994	91190	CAGGCGGATCTGACTCACGT
169821	2017	GTCCCCAATCTCCGCAGGGA	214408	46604	TGCCCTTCAGTTTTCCCGTA	258995	91191	CCAGGCGGATCTGACTCACG
169822	2018	GGTCCCCAATCTCCGCAGGG	214409	46605	ATGCCCTTCAGTTTTCCCGT	258996	91192	CCCAGGCGGATCTGACTCAC
169823	2019	GGGTCCCCAATCTCCGCAGG	214410	46606	GATGCCCTTCAGTTTTCCCG	258997	91193	CCCCAGGCGGATCTGACTCA
169824	2020	AGGGTCCCCAATCTCCGCAG	214411	46607	AGATGCCCTTCAGTTTTCCC	258998	91194	GCCCCAGGCGGATCTGACTC
169825	2021	CAGGGTCCCCAATCTCCGCA	214412	46608	GAGATGCCCTTCAGTTTTCC	258999	91195	AGCCCCAGGCGGATCTGACT
169826	2022	CCAGGGTCCCCAATCTCCGC	214413	46609	AGAGATGCCCTTCAGTTTTC	259000	91196	GAGCCCCAGGCGGATCTGAC
169827	2023	CCCAGGGTCCCCAATCTCCG	214414	46610	TAGAGATGCCCTTCAGTTTT	259001	91197	AGAGCCCCAGGCGGATCTGA
169828	2024	CCCCAGGGTCCCCAATCTCC	214415	46611	ATAGAGATGCCCTTCAGTTT	259002	91198	AAGAGCCCCAGGCGGATCTG
169829	2025	ACCCCAGGGTCCCCAATCTC	214416	46612	AATAGAGATGCCCTTCAGTT	259003	91199	TAAGAGCCCCAGGCGGATCT
169830	2026	TACCCCAGGGTCCCCAATCT	214417	46613	AAATAGAGATGCCCTTCAGT	259004	91200	GTAAGAGCCCCAGGCGGATC
169831	2027	CTACCCCAGGGTCCCCAATC	214418	46614	AAAATAGAGATGCCCTTCAG	259005	91201	AGTAAGAGCCCCAGGCGGAT
169832	2028	CCTACCCCAGGGTCCCCAAT	214419	46615	AAAAATAGAGATGCCCTTCA	259006	91202	TAGTAAGAGCCCCAGGCGGA
169833	2029	CCCTACCCCAGGGTCCCCAA	214420	46616	TAAAAATAGAGATGCCCTTC	259007	91203	TTAGTAAGAGCCCCAGGCGG
169834	2030	CCCCTACCCCAGGGTCCCCA	214421	46617	CTAAAAATAGAGATGCCCTT	259008	91204	TTTAGTAAGAGCCCCAGGCG
169835	2031	CCCCCTACCCCAGGGTCCCC	214422	46618	TCTAAAAATAGAGATGCCCT	259009	91205	CTTTAGTAAGAGCCCCAGGC
169836	2032	TCCCCCTACCCCAGGGTCCC	214423	46619	ATCTAAAAATAGAGATGCCC	259010	91206	ACTTTAGTAAGAGCCCCAGG
169837	2033	CTCCCCCTACCCCAGGGTCC	214424	46620	AATCTAAAAATAGAGATGCC	259011	91207	CACTTTAGTAAGAGCCCCAG
169838	2034	GCTCCCCCTACCCCAGGGTC	214425	46621	TAATCTAAAAATAGAGATGC	259012	91208	GCACTTTAGTAAGAGCCCCA
169839	2035	GGCTCCCCCTACCCCAGGGT	214426	46622	CTAATCTAAAAATAGAGATG	259013	91209	TGCACTTTAGTAAGAGCCCC
169840	2036	CGGCTCCCCCTACCCCAGGG	214427	46623	GCTAATCTAAAAATAGAGAT	259014	91210	CTGCACTTTAGTAAGAGCCC
169841	2037	GCGGCTCCCCCTACCCCAGG	214428	46624	TGCTAATCTAAAAATAGAGA	259015	91211	CCTGCACTTTAGTAAGAGCC
169842	2038	CGCGGCTCCCCCTACCCCAG	214429	46625	TTGCTAATCTAAAAATAGAG	259016	91212	ACCTGCACTTTAGTAAGAGC
169843	2039	GCGCGGCTCCCCCTACCCCA	214430	46626	TTTGCTAATCTAAAAATAGA	259017	91213	AACCTGCACTTTAGTAAGAG
169844	2040	GGCGCGGCTCCCCCTACCCC	214431	46627	TTTTGCTAATCTAAAAATAG	259018	91214	GAACCTGCACTTTAGTAAGA
169845	2041	GGGCGCGGCTCCCCCTACCC	214432	46628	CTTTTGCTAATCTAAAAATA	259019	91215	GGAACCTGCACTTTAGTAAG
169846	2042	TGGGCGCGGCTCCCCCTACC	214433	46629	TCTTTTGCTAATCTAAAAAT	259020	91216	GGGAACCTGCACTTTAGTAA
169847	2043	CTGGGCGCGGCTCCCCCTAC	214434	46630	TTCTTTTGCTAATCTAAAAA	259021	91217	TGGGAACCTGCACTTTAGTA
169848	2044	ACTGGGCGCGGCTCCCCCTA	214435	46631	TTTCTTTTGCTAATCTAAAA	259022	91218	CTGGGAACCTGCACTTTAGT
169849	2045	GACTGGGCGCGGCTCCCCCT	214436	46632	TTTTCTTTTGCTAATCTAAA	259023	91219	CCTGGGAACCTGCACTTTAG
169850	2046	CGACTGGGCGCGGCTCCCCC	214437	46633	ATTTTCTTTTGCTAATCTAA	259024	91220	ACCTGGGAACCTGCACTTTA
169851	2047	CCGACTGGGCGCGGCTCCCC	214438	46634	TATTTTCTTTTGCTAATCTA	259025	91221	CACCTGGGAACCTGCACTTT
169852	2048	GCCGACTGGGCGCGGCTCCC	214439	46635	TTATTTTCTTTTGCTAATCT	259026	91222	GCACCTGGGAACCTGCACTT
169853	2049	GGCCGACTGGGCGCGGCTCC	214440	46636	TTTATTTTCTTTTGCTAATC	259027	91223	GGCACCTGGGAACCTGCACT
169854	2050	AGGCCGACTGGGCGCGGCTC	214441	46637	ATTTATTTTCTTTTGCTAAT	259028	91224	TGGCACCTGGGAACCTGCAC
169855	2051	GAGGCCGACTGGGCGCGGCT	214442	46638	AATTTATTTTCTTTTGCTAA	259029	91225	GTGGCACCTGGGAACCTGCA
169856	2052	GGAGGCCGACTGGGCGCGGC	214443	46639	AAATTTATTTTCTTTTGCTA	259030	91226	AGTGGCACCTGGGAACCTGC
169857	2053	AGGAGGCCGACTGGGCGCGG	214444	46640	TAAATTTATTTTCTTTTGCT	259031	91227	AAGTGGCACCTGGGAACCTG
169858	2054	CAGGAGGCCGACTGGGCGCG	214445	46641	TTAAATTTATTTTCTTTTGC	259032	91228	AAAGTGGCACCTGGGAACCT
169859	2055	CCAGGAGGCCGACTGGGCGC	214446	46642	CTTAAATTTATTTTCTTTTG	259033	91229	TAAAGTGGCACCTGGGAACC
169860	2056	TCCAGGAGGCCGACTGGGCG	214447	46643	ACTTAAATTTATTTTCTTTT	259034	91230	CTAAAGTGGCACCTGGGAAC
169861	2057	CTCCAGGAGGCCGACTGGGC	214448	46644	AACTTAAATTTATTTTCTTT	259035	91231	CCTAAAGTGGCACCTGGGAA
169862	2058	CCTCCAGGAGGCCGACTGGG	214449	46645	AAACTTAAATTTATTTTCTT	259036	91232	GCCTAAAGTGGCACCTGGGA
169863	2059	TCCTCCAGGAGGCCGACTGG	214450	46646	CAAACTTAAATTTATTTTCT	259037	91233	AGCCTAAAGTGGCACCTGGG
169864	2060	GTCCTCCAGGAGGCCGACTG	214451	46647	TCAAACTTAAATTTATTTTC	259038	91234	AAGCCTAAAGTGGCACCTGG
169865	2061	TGTCCTCCAGGAGGCCGACT	214452	46648	CTCAAACTTAAATTTATTTT	259039	91235	TAAGCCTAAAGTGGCACCTG
169866	2062	GTGTCCTCCAGGAGGCCGAC	214453	46649	ACTCAAACTTAAATTTATTT	259040	91236	GTAAGCCTAAAGTGGCACCT
169867	2063	CGTGTCCTCCAGGAGGCCGA	214454	46650	GACTCAAACTTAAATTTATT	259041	91237	TGTAAGCCTAAAGTGGCACC
169868	2064	CCGTGTCCTCCAGGAGGCCG	214455	46651	AGACTCAAACTTAAATTTAT	259042	91238	CTGTAAGCCTAAAGTGGCAC
169869	2065	CCCGTGTCCTCCAGGAGGCC	214456	46652	GAGACTCAAACTTAAATTTA	259043	91239	TCTGTAAGCCTAAAGTGGCA
169870	2066	TCCCGTGTCCTCCAGGAGGC	214457	46653	GGAGACTCAAACTTAAATTT	259044	91240	GTCTGTAAGCCTAAAGTGGC
169871	2067	CTCCCGTGTCCTCCAGGAGG	214458	46654	AGGAGACTCAAACTTAAATT	259045	91241	GGTCTGTAAGCCTAAAGTGG
169872	2068	CCTCCCGTGTCCTCCAGGAG	214459	46655	AAGGAGACTCAAACTTAAAT	259046	91242	GGGTCTGTAAGCCTAAAGTG
169873	2069	TCCTCCCGTGTCCTCCAGGA	214460	46656	AAAGGAGACTCAAACTTAAA	259047	91243	TGGGTCTGTAAGCCTAAAGT
169874	2070	TTCCTCCCGTGTCCTCCAGG	214461	46657	CAAAGGAGACTCAAACTTAA	259048	91244	CTGGGTCTGTAAGCCTAAAG
169875	2071	CTTCCTCCCGTGTCCTCCAG	214462	46658	GCAAAGGAGACTCAAACTTA	259049	91245	ACTGGGTCTGTAAGCCTAAA
169876	2072	GCTTCCTCCCGTGTCCTCCA	214463	46659	TGCAAAGGAGACTCAAACTT	259050	91246	AACTGGGTCTGTAAGCCTAA
169877	2073	GGCTTCCTCCCGTGTCCTCC	214464	46660	TTGCAAAGGAGACTCAAACT	259051	91247	CAACTGGGTCTGTAAGCCTA
169878	2074	GGGCTTCCTCCCGTGTCCTC	214465	46661	GTTGCAAAGGAGACTCAAAC	259052	91248	ACAACTGGGTCTGTAAGCCT
169879	2075	GGGGCTTCCTCCCGTGTCCT	214466	46662	AGTTGCAAAGGAGACTCAAA	259053	91249	CACAACTGGGTCTGTAAGCC
169880	2076	CGGGGCTTCCTCCCGTGTCC	214467	46663	AAGTTGCAAAGGAGACTCAA	259054	91250	CCACAACTGGGTCTGTAAGC
169881	2077	TCGGGGCTTCCTCCCGTGTC	214468	46664	AAAGTTGCAAAGGAGACTCA	259055	91251	CCCACAACTGGGTCTGTAAG
169882	2078	TTCGGGGCTTCCTCCCGTGT	214469	46665	AAAAGTTGCAAAGGAGACTC	259056	91252	CCCCACAACTGGGTCTGTAA
169883	2079	GTTCGGGGCTTCCTCCCGTG	214470	46666	TAAAAGTTGCAAAGGAGACT	259057	91253	ACCCCACAACTGGGTCTGTA
169884	2080	GGTTCGGGGCTTCCTCCCGT	214471	46667	TTAAAAGTTGCAAAGGAGAC	259058	91254	TACCCCACAACTGGGTCTGT
169885	2081	GGGTTCGGGGCTTCCTCCCG	214472	46668	TTTAAAAGTTGCAAAGGAGA	259059	91255	TTACCCCACAACTGGGTCTG
169886	2082	GGGGTTCGGGGCTTCCTCCC	214473	46669	TTTTAAAAGTTGCAAAGGAG	259060	91256	CTTACCCCACAACTGGGTCT
169887	2083	GGGGGTTCGGGGCTTCCTCC	214474	46670	CTTTTAAAAGTTGCAAAGGA	259061	91257	GCTTACCCCACAACTGGGTC
169888	2084	CGGGGGTTCGGGGCTTCCTC	214475	46671	TCTTTTAAAAGTTGCAAAGG	259062	91258	GGCTTACCCCACAACTGGGT
169889	2085	GCGGGGGTTCGGGGCTTCCT	214476	46672	GTCTTTTAAAAGTTGCAAAG	259063	91259	AGGCTTACCCCACAACTGGG
169890	2086	CGCGGGGGTTCGGGGCTTCC	214477	46673	TGTCTTTTAAAAGTTGCAAA	259064	91260	CAGGCTTACCCCACAACTGG

169891	2087	GCGCGGGGGTTCGGGGCTTC	214478	46674	ATGTCTTTTAAAAGTTGCAA	259065	91261	CCAGGCTTACCCCACAACTG
169892	2088	GGCGCGGGGGTTCGGGGCTT	214479	46675	GATGTCTTTTAAAAGTTGCA	259066	91262	CCCAGGCTTACCCCACAACT
169893	2089	AGGCGCGGGGGTTCGGGGCT	214480	46676	AGATGTCTTTTAAAAGTTGC	259067	91263	TCCCAGGCTTACCCCACAAC
169894	2090	CAGGCGCGGGGGTTCGGGGC	214481	46677	AAGATGTCTTTTAAAAGTTG	259068	91264	CTCCCAGGCTTACCCCACAA
169895	2091	TCAGGCGCGGGGGTTCGGGG	214482	46678	AAAGATGTCTTTTAAAAGTT	259069	91265	ACTCCCAGGCTTACCCCACA
169896	2092	CTCAGGCGCGGGGGTTCGGG	214483	46679	TAAAGATGTCTTTTAAAAGT	259070	91266	GACTCCCAGGCTTACCCCAC
169897	2093	CCTCAGGCGCGGGGGTTCGG	214484	46680	ATAAAGATGTCTTTTAAAAG	259071	91267	AGACTCCCAGGCTTACCCCA
169898	2094	GCCTCAGGCGCGGGGGTTCG	214485	46681	AATAAAGATGTCTTTTAAAA	259072	91268	AAGACTCCCAGGCTTACCCC
169899	2095	AGCCTCAGGCGCGGGGGTTC	214486	46682	CAATAAAGATGTCTTTTAAA	259073	91269	AAAGACTCCCAGGCTTACCC
169900	2096	CAGCCTCAGGCGCGGGGGTT	214487	46683	TCAATAAAGATGTCTTTTAA	259074	91270	AAAAGACTCCCAGGCTTACC
169901	2097	ACAGCCTCAGGCGCGGGGGT	214488	46684	CTCAATAAAGATGTCTTTTA	259075	91271	TAAAAGACTCCCAGGCTTAC
169902	2098	AACAGCCTCAGGCGCGGGGG	214489	46685	TCTCAATAAAGATGTCTTTT	259076	91272	CTAAAAGACTCCCAGGCTTA
169903	2099	AAACAGCCTCAGGCGCGGGG	214490	46686	ATCTCAATAAAGATGTCTTT	259077	91273	GCTAAAAGACTCCCAGGCTT
169904	2100	GAAACAGCCTCAGGCGCGGG	214491	46687	CATCTCAATAAAGATGTCTT	259078	91274	TGCTAAAAGACTCCCAGGCT
169905	2101	AGAAACAGCCTCAGGCGCGG	214492	46688	TCATCTCAATAAAGATGTCT	259079	91275	CTGCTAAAAGACTCCCAGGC
169906	2102	CAGAAACAGCCTCAGGCGCG	214493	46689	ATCATCTCAATAAAGATGTC	259080	91276	CCTGCTAAAAGACTCCCAGG
169907	2103	TCAGAAACAGCCTCAGGCGC	214494	46690	GATCATCTCAATAAAGATGT	259081	91277	ACCTGCTAAAAGACTCCCAG
169908	2104	ATCAGAAACAGCCTCAGGCG	214495	46691	TGATCATCTCAATAAAGATG	259082	91278	CACCTGCTAAAAGACTCCCA
169909	2105	AATCAGAAACAGCCTCAGGC	214496	46692	ATGATCATCTCAATAAAGAT	259083	91279	TCACCTGCTAAAAGACTCCC
169910	2106	CAATCAGAAACAGCCTCAGG	214497	46693	AATGATCATCTCAATAAAGA	259084	91280	ATCACCTGCTAAAAGACTCC
169911	2107	CCAATCAGAAACAGCCTCAG	214498	46694	GAATGATCATCTCAATAAAG	259085	91281	AATCACCTGCTAAAAGACTC
169912	2108	GCCAATCAGAAACAGCCTCA	214499	46695	TGAATGATCATCTCAATAAA	259086	91282	GAATCACCTGCTAAAAGACT
169913	2109	GGCCAATCAGAAACAGCCTC	214500	46696	GTGAATGATCATCTCAATAA	259087	91283	AGAATCACCTGCTAAAAGAC
169914	2110	GGGCCAATCAGAAACAGCCT	214501	46697	TGTGAATGATCATCTCAATA	259088	91284	CAGAATCACCTGCTAAAAGA
169915	2111	GGGGCCAATCAGAAACAGCC	214502	46698	ATGTGAATGATCATCTCAAT	259089	91285	GCAGAATCACCTGCTAAAAG
169916	2112	AGGGGCCAATCAGAAACAGC	214503	46699	AATGTGAATGATCATCTCAA	259090	91286	GGCAGAATCACCTGCTAAAA
169917	2113	CAGGGGCCAATCAGAAACAG	214504	46700	GAATGTGAATGATCATCTCA	259091	91287	TGGCAGAATCACCTGCTAAA
169918	2114	CCAGGGGCCAATCAGAAACA	214505	46701	AGAATGTGAATGATCATCTC	259092	91288	GTGGCAGAATCACCTGCTAA
169919	2115	TCCAGGGGCCAATCAGAAAC	214506	46702	TAGAATGTGAATGATCATCT	259093	91289	TGTGGCAGAATCACCTGCTA
169920	2116	CTCCAGGGGCCAATCAGAAA	214507	46703	ATAGAATGTGAATGATCATC	259094	91290	ATGTGGCAGAATCACCTGCT
169921	2117	CCTCCAGGGGCCAATCAGAA	214508	46704	TATAGAATGTGAATGATCAT	259095	91291	TATGTGGCAGAATCACCTGC
169922	2118	GCCTCCAGGGGCCAATCAGA	214509	46705	TTATAGAATGTGAATGATCA	259096	91292	CTATGTGGCAGAATCACCTG
169923	2119	GGCCTCCAGGGGCCAATCAG	214510	46706	TTTATAGAATGTGAATGATC	259097	91293	ACTATGTGGCAGAATCACCT
169924	2120	CGGCCTCCAGGGGCCAATCA	214511	46707	TTTTATAGAATGTGAATGAT	259098	91294	TACTATGTGGCAGAATCACC
169925	2121	GCGGCCTCCAGGGGCCAATC	214512	46708	ATTTTATAGAATGTGAATGA	259099	91295	ATACTATGTGGCAGAATCAC
169926	2122	TGCGGCCTCCAGGGGCCAAT	214513	46709	AATTTTATAGAATGTGAATG	259100	91296	TATACTATGTGGCAGAATCA
169927	2123	CTGCGGCCTCCAGGGGCCAA	214514	46710	GAATTTTATAGAATGTGAAT	259101	91297	CTATACTATGTGGCAGAATC
169928	2124	TCTGCGGCCTCCAGGGGCCA	214515	46711	GGAATTTTATAGAATGTGAA	259102	91298	ACTATACTATGTGGCAGAAT
169929	2125	GTCTGCGGCCTCCAGGGGCC	214516	46712	GGGAATTTTATAGAATGTGA	259103	91299	AACTATACTATGTGGCAGAA
169930	2126	TGTCTGCGGCCTCCAGGGGC	214517	46713	GGGGAATTTTATAGAATGTG	259104	91300	CAACTATACTATGTGGCAGA
169931	2127	GTGTCTGCGGCCTCCAGGGG	214518	46714	GGGGGAATTTTATAGAATGT	259105	91301	CCAACTATACTATGTGGCAG
169932	2128	CGTGTCTGCGGCCTCCAGGG	214519	46715	TGGGGGAATTTTATAGAATG	259106	91302	TCCAACTATACTATGTGGCA
169933	2129	GCGTGTCTGCGGCCTCCAGG	214520	46716	GTGGGGGAATTTTATAGAAT	259107	91303	TTCCAACTATACTATGTGGC
169934	2130	TGCGTGTCTGCGGCCTCCAG	214521	46717	AGTGGGGGAATTTTATAGAA	259108	91304	TTTCCAACTATACTATGTGG
169935	2131	CTGCGTGTCTGCGGCCTCCA	214522	46718	AAGTGGGGGAATTTTATAGA	259109	91305	TTTTCCAACTATACTATGTG
169936	2132	TCTGCGTGTCTGCGGCCTCC	214523	46719	AAAGTGGGGGAATTTTATAG	259110	91306	GTTTTCCAACTATACTATGT
169937	2133	ATCTGCGTGTCTGCGGCCTC	214524	46720	CAAAGTGGGGGAATTTTATA	259111	91307	GGTTTTCCAACTATACTATG
169938	2134	TATCTGCGTGTCTGCGGCCT	214525	46721	TCAAAGTGGGGGAATTTTAT	259112	91308	AGGTTTTCCAACTATACTAT
169939	2135	CTATCTGCGTGTCTGCGGCC	214526	46722	CTCAAAGTGGGGGAATTTTA	259113	91309	GAGGTTTTCCAACTATACTA
169940	2136	CCTATCTGCGTGTCTGCGGC	214527	46723	ACTCAAAGTGGGGGAATTTT	259114	91310	AGAGGTTTTCCAACTATACT
169941	2137	GCCTATCTGCGTGTCTGCGG	214528	46724	AACTCAAAGTGGGGGAATTT	259115	91311	CAGAGGTTTTCCAACTATAC
169942	2138	CGCCTATCTGCGTGTCTGCG	214529	46725	TAACTCAAAGTGGGGGAATT	259116	91312	CCAGAGGTTTTCCAACTATA
169943	2139	CCGCCTATCTGCGTGTCTGC	214530	46726	GTAACTCAAAGTGGGGGAAT	259117	91313	CCCAGAGGTTTTCCAACTAT
169944	2140	GCCGCCTATCTGCGTGTCTG	214531	46727	TGTAACTCAAAGTGGGGGAA	259118	91314	GCCCAGAGGTTTTCCAACTA
169945	2141	GGCCGCCTATCTGCGTGTCT	214532	46728	TTGTAACTCAAAGTGGGGGA	259119	91315	TGCCCAGAGGTTTTCCAACT
169946	2142	GGGCCGCCTATCTGCGTGTC	214533	46729	ATTGTAACTCAAAGTGGGGG	259120	91316	ATGCCCAGAGGTTTTCCAAC
169947	2143	AGGGCCGCCTATCTGCGTGT	214534	46730	AATTGTAACTCAAAGTGGGG	259121	91317	TATGCCCAGAGGTTTTCCAA
169948	2144	CAGGGCCGCCTATCTGCGTG	214535	46731	GAATTGTAACTCAAAGTGGG	259122	91318	GTATGCCCAGAGGTTTTCCA
169949	2145	CCAGGGCCGCCTATCTGCGT	214536	46732	TGAATTGTAACTCAAAGTGG	259123	91319	AGTATGCCCAGAGGTTTTCC
169950	2146	CCCAGGGCCGCCTATCTGCG	214537	46733	CTGAATTGTAACTCAAAGTG	259124	91320	GAGTATGCCCAGAGGTTTTC
169951	2147	ACCCAGGGCCGCCTATCTGC	214538	46734	ACTGAATTGTAACTCAAAGT	259125	91321	TGAGTATGCCCAGAGGTTTT
169952	2148	CACCCAGGGCCGCCTATCTG	214539	46735	CACTGAATTGTAACTCAAAG	259126	91322	ATGAGTATGCCCAGAGGTTT
169953	2149	ACACCCAGGGCCGCCTATCT	214540	46736	CCACTGAATTGTAACTCAAA	259127	91323	AATGAGTATGCCCAGAGGTT
169954	2150	TACACCCAGGGCCGCCTATC	214541	46737	ACCACTGAATTGTAACTCAA	259128	91324	CAATGAGTATGCCCAGAGGT
169955	2151	ATACACCCAGGGCCGCCTAT	214542	46738	AACCACTGAATTGTAACTCA	259129	91325	GCAATGAGTATGCCCAGAGG
169956	2152	AATACACCCAGGGCCGCCTA	214543	46739	AAACCACTGAATTGTAACTC	259130	91326	AGCAATGAGTATGCCCAGAG
169957	2153	AAATACACCCAGGGCCGCCT	214544	46740	AAAACCACTGAATTGTAACT	259131	91327	CAGCAATGAGTATGCCCAGA
169958	2154	AAAATACACCCAGGGCCGCC	214545	46741	TAAAACCACTGAATTGTAAC	259132	91328	CCAGCAATGAGTATGCCCAG
169959	2155	AAAAATACACCCAGGGCCGC	214546	46742	CTAAAACCACTGAATTGTAA	259133	91329	ACCAGCAATGAGTATGCCCA
169960	2156	TAAAAATACACCCAGGGCCG	214547	46743	ACTAAAACCACTGAATTGTA	259134	91330	GACCAGCAATGAGTATGCCC
169961	2157	ATAAAAATACACCCAGGGCC	214548	46744	GACTAAAACCACTGAATTGT	259135	91331	GGACCAGCAATGAGTATGCC
169962	2158	AATAAAAATACACCCAGGGC	214549	46745	AGACTAAAACCACTGAATTG	259136	91332	GGGACCAGCAATGAGTATGC

169963	2159	TAATAAAAATACACCCAGGG	214550	46746	AAGACTAAAACCACTGAATT	259137	91333	AGGGACCAGCAATGAGTATG
169964	2160	TTAATAAAAATACACCCAGG	214551	46747	GAAGACTAAAACCACTGAAT	259138	91334	GAGGGACCAGCAATGAGTAT
169965	2161	ATTAATAAAAATACACCCAG	214552	46748	GGAAGACTAAAACCACTGAA	259139	91335	AGAGGGACCAGCAATGAGTA
169966	2162	TATTAATAAAAATACACCCA	214553	46749	AGGAAGACTAAAACCACTGA	259140	91336	TAGAGGGACCAGCAATGAGT
169967	2163	ATATTAATAAAAATACACCC	214554	46750	AAGGAAGACTAAAACCACTG	259141	91337	CTAGAGGGACCAGCAATGAG
169968	2164	AATATTAATAAAAATACACC	214555	46751	CAAGGAAGACTAAAACCACT	259142	91338	TCTAGAGGGACCAGCAATGA
169969	2165	TAATATTAATAAAAATACAC	214556	46752	TCAAGGAAGACTAAAACCAC	259143	91339	TTCTAGAGGGACCAGCAATG
169970	2166	ATAATATTAATAAAAATACA	214557	46753	ATCAAGGAAGACTAAAACCA	259144	91340	TTTCTAGAGGGACCAGCAAT
169971	2167	CATAATATTAATAAAAATAC	214558	46754	CATCAAGGAAGACTAAAACC	259145	91341	ATTTCTAGAGGGACCAGCAA
169972	2168	ACATAATATTAATAAAAATA	214559	46755	TCATCAAGGAAGACTAAAAC	259146	91342	GATTTCTAGAGGGACCAGCA
169973	2169	GACATAATATTAATAAAAAT	214560	46756	ATCATCAAGGAAGACTAAAA	259147	91343	GGATTTCTAGAGGGACCAGC
169974	2170	GGACATAATATTAATAAAAA	214561	46757	AATCATCAAGGAAGACTAAA	259148	91344	TGGATTTCTAGAGGGACCAG
169975	2171	CGGACATAATATTAATAAAA	214562	46758	AAATCATCAAGGAAGACTAA	259149	91345	CTGGATTTCTAGAGGGACCA
169976	2172	ACGGACATAATATTAATAAA	214563	46759	AAAATCATCAAGGAAGACTA	259150	91346	CCTGGATTTCTAGAGGGACC
169977	2173	TACGGACATAATATTAATAA	214564	46760	CAAAATCATCAAGGAAGACT	259151	91347	ACCTGGATTTCTAGAGGGAC
169978	2174	GTACGGACATAATATTAATA	214565	46761	TCAAAATCATCAAGGAAGAC	259152	91348	CACCTGGATTTCTAGAGGGA
169979	2175	AGTACGGACATAATATTAAT	214566	46762	ATCAAAATCATCAAGGAAGA	259153	91349	TCACCTGGATTTCTAGAGGG
169980	2176	CAGTACGGACATAATATTAA	214567	46763	CATCAAAATCATCAAGGAAG	259154	91350	GTCACCTGGATTTCTAGAGG
169981	2177	TCAGTACGGACATAATATTA	214568	46764	CCATCAAAATCATCAAGGAA	259155	91351	TGTCACCTGGATTTCTAGAG
169982	2178	ATCAGTACGGACATAATATT	214569	46765	ACCATCAAAATCATCAAGGA	259156	91352	TTGTCACCTGGATTTCTAGA
169983	2179	AATCAGTACGGACATAATAT	214570	46766	GACCATCAAAATCATCAAGG	259157	91353	ATTGTCACCTGGATTTCTAG
169984	2180	TAATCAGTACGGACATAATA	214571	46767	AGACCATCAAAATCATCAAG	259158	91354	TATTGTCACCTGGATTTCTA
169985	2181	TTAATCAGTACGGACATAAT	214572	46768	AAGACCATCAAAATCATCAA	259159	91355	CTATTGTCACCTGGATTTCT
169986	2182	ATTAATCAGTACGGACATAA	214573	46769	AAAGACCATCAAAATCATCA	259160	91356	GCTATTGTCACCTGGATTTC
169987	2183	TATTAATCAGTACGGACATA	214574	46770	AAAAGACCATCAAAATCATC	259161	91357	GGCTATTGTCACCTGGATTT
169988	2184	ATATTAATCAGTACGGACAT	214575	46771	GAAAAGACCATCAAAATCAT	259162	91358	TGGCTATTGTCACCTGGATT
169989	2185	AATATTAATCAGTACGGACA	214576	46772	AGAAAAGACCATCAAAATCA	259163	91359	TTGGCTATTGTCACCTGGAT
169990	2186	TAATATTAATCAGTACGGAC	214577	46773	AAGAAAAGACCATCAAAATC	259164	91360	ATTGGCTATTGTCACCTGGA
169991	2187	ATAATATTAATCAGTACGGA	214578	46774	TAAGAAAAGACCATCAAAAT	259165	91361	CATTGGCTATTGTCACCTGG
169992	2188	AATAATATTAATCAGTACGG	214579	46775	TTAAGAAAAGACCATCAAAA	259166	91362	TCATTGGCTATTGTCACCTG
169993	2189	AAATAATATTAATCAGTACG	214580	46776	CTTAAGAAAAGACCATCAAA	259167	91363	CTCATTGGCTATTGTCACCT
169994	2190	TAAATAATATTAATCAGTAC	214581	46777	CCTTAAGAAAAGACCATCAA	259168	91364	TCTCATTGGCTATTGTCACC
169995	2191	ATAAATAATATTAATCAGTA	214582	46778	GCCTTAAGAAAAGACCATCA	259169	91365	TTCTCATTGGCTATTGTCAC
169996	2192	GATAAATAATATTAATCAGT	214583	46779	AGCCTTAAGAAAAGACCATC	259170	91366	CTTCTCATTGGCTATTGTCA
169997	2193	AGATAAATAATATTAATCAG	214584	46780	GAGCCTTAAGAAAAGACCAT	259171	91367	GCTTCTCATTGGCTATTGTC
169998	2194	AAGATAAATAATATTAATCA	214585	46781	AGAGCCTTAAGAAAAGACCA	259172	91368	AGCTTCTCATTGGCTATTGT
169999	2195	TAAGATAAATAATATTAATC	214586	46782	AAGAGCCTTAAGAAAAGACC	259173	91369	GAGCTTCTCATTGGCTATTG
170000	2196	TTAAGATAAATAATATTAAT	214587	46783	CAAGAGCCTTAAGAAAAGAC	259174	91370	GGAGCTTCTCATTGGCTATT
170001	2197	TTTAAGATAAATAATATTAA	214588	46784	CCAAGAGCCTTAAGAAAAGA	259175	91371	TGGAGCTTCTCATTGGCTAT
170002	2198	ATTTAAGATAAATAATATTA	214589	46785	TCCAAGAGCCTTAAGAAAAG	259176	91372	TTGGAGCTTCTCATTGGCTA
170003	2199	TATTTAAGATAAATAATATT	214590	46786	TTCCAAGAGCCTTAAGAAAA	259177	91373	CTTGGAGCTTCTCATTGGCT
170004	2200	TTATTTAAGATAAATAATAT	214591	46787	CTTCCAAGAGCCTTAAGAAA	259178	91374	TCTTGGAGCTTCTCATTGGC
170005	2201	TTTATTTAAGATAAATAATA	214592	46788	TCTTCCAAGAGCCTTAAGAA	259179	91375	CTCTTGGAGCTTCTCATTGG
170006	2202	ATTTATTTAAGATAAATAAT	214593	46789	GTCTTCCAAGAGCCTTAAGA	259180	91376	TCTCTTGGAGCTTCTCATTG
170007	2203	AATTTATTTAAGATAAATAA	214594	46790	GGTCTTCCAAGAGCCTTAAG	259181	91377	GTCTCTTGGAGCTTCTCATT
170008	2204	AAATTTATTTAAGATAAATA	214595	46791	GGGTCTTCCAAGAGCCTTAA	259182	91378	GGTCTCTTGGAGCTTCTCAT
170009	2205	GAAATTTATTTAAGATAAAT	214596	46792	TGGGTCTTCCAAGAGCCTTA	259183	91379	GGGTCTCTTGGAGCTTCTCA
170010	2206	TGAAATTTATTTAAGATAAA	214597	46793	CTGGGTCTTCCAAGAGCCTT	259184	91380	TGGGTCTCTTGGAGCTTCTC
170011	2207	GTGAAATTTATTTAAGATAA	214598	46794	TCTGGGTCTTCCAAGAGCCT	259185	91381	CTGGGTCTCTTGGAGCTTCT
170012	2208	GGTGAAATTTATTTAAGATA	214599	46795	TTCTGGGTCTTCCAAGAGCC	259186	91382	ACTGGGTCTCTTGGAGCTTC
170013	2209	GGGTGAAATTTATTTAAGAT	214600	46796	CTTCTGGGTCTTCCAAGAGC	259187	91383	AACTGGGTCTCTTGGAGCTT
170014	2210	CGGGTGAAATTTATTTAAGA	214601	46797	GCTTCTGGGTCTTCCAAGAG	259188	91384	CAACTGGGTCTCTTGGAGCT
170015	2211	ACGGGTGAAATTTATTTAAG	214602	46798	GGCTTCTGGGTCTTCCAAGA	259189	91385	ACAACTGGGTCTCTTGGAGC
170016	2212	CACGGGTGAAATTTATTTAA	214603	46799	AGGCTTCTGGGTCTTCCAAG	259190	91386	GACAACTGGGTCTCTTGGAG
170017	2213	ACACGGGTGAAATTTATTTA	214604	46800	GAGGCTTCTGGGTCTTCCAA	259191	91387	GGACAACTGGGTCTCTTGGA
170018	2214	GACACGGGTGAAATTTATTT	214605	46801	AGAGGCTTCTGGGTCTTCCA	259192	91388	TGGACAACTGGGTCTCTTGG
170019	2215	GGACACGGGTGAAATTTATT	214606	46802	GAGAGGCTTCTGGGTCTTCC	259193	91389	ATGGACAACTGGGTCTCTTG
170020	2216	TGGACACGGGTGAAATTTAT	214607	46803	TGAGAGGCTTCTGGGTCTTC	259194	91390	CATGGACAACTGGGTCTCTT
170021	2217	TTGGACACGGGTGAAATTTA	214608	46804	CTGAGAGGCTTCTGGGTCTT	259195	91391	CCATGGACAACTGGGTCTCT
170022	2218	CTTGGACACGGGTGAAATTT	214609	46805	TCTGAGAGGCTTCTGGGTCT	259196	91392	CCCATGGACAACTGGGTCTC
170023	2219	ACTTGGACACGGGTGAAATT	214610	46806	GTCTGAGAGGCTTCTGGGTC	259197	91393	CCCCATGGACAACTGGGTCT
170024	2220	AACTTGGACACGGGTGAAAT	214611	46807	TGTCTGAGAGGCTTCTGGGT	259198	91394	ACCCCATGGACAACTGGGTC
170025	2221	GAACTTGGACACGGGTGAAA	214612	46808	GTGTCTGAGAGGCTTCTGGG	259199	91395	TACCCCATGGACAACTGGGT
170026	2222	TGAACTTGGACACGGGTGAA	214613	46809	TGTGTCTGAGAGGCTTCTGG	259200	91396	CTACCCCATGGACAACTGGG
170027	2223	GTGAACTTGGACACGGGTGA	214614	46810	CTGTGTCTGAGAGGCTTCTG	259201	91397	TCTACCCCATGGACAACTGG
170028	2224	GGTGAACTTGGACACGGGTG	214615	46811	CCTGTGTCTGAGAGGCTTCT	259202	91398	CTCTACCCCATGGACAACTG
170029	2225	CGGTGAACTTGGACACGGGT	214616	46812	ACCTGTGTCTGAGAGGCTTC	259203	91399	CCTCTACCCCATGGACAACT
170030	2226	GCGGTGAACTTGGACACGGG	214617	46813	CACCTGTGTCTGAGAGGCTT	259204	91400	CCCTCTACCCCATGGACAAC
170031	2227	CGCGGTGAACTTGGACACGG	214618	46814	CCACCTGTGTCTGAGAGGCT	259205	91401	TCCCTCTACCCCATGGACAA
170032	2228	GCGCGGTGAACTTGGACACG	214619	46815	CCCACCTGTGTCTGAGAGGC	259206	91402	TTCCCTCTACCCCATGGACA
170033	2229	GGCGCGGTGAACTTGGACAC	214620	46816	ACCCACCTGTGTCTGAGAGG	259207	91403	ATTCCCTCTACCCCATGGAC
170034	2230	GGGCGCGGTGAACTTGGACA	214621	46817	CACCCACCTGTGTCTGAGAG	259208	91404	CATTCCCTCTACCCCATGGA

170035	2231	GGGGCGCGGTGAACTTGGAC	214622	46818	ACACCCACCTGTGTCTGAGA	259209	91405	ACATTCCCTCTACCCCATGG
170036	2232	GGGGGCGCGGTGAACTTGGA	214623	46819	CACACCCACCTGTGTCTGAG	259210	91406	CACATTCCCTCTACCCCATG
170037	2233	TGGGGGCGCGGTGAACTTGG	214624	46820	CCACACCCACCTGTGTCTGA	259211	91407	TCACATTCCCTCTACCCCAT
170038	2234	TTGGGGGCGCGGTGAACTTG	214625	46821	TCCACACCCACCTGTGTCTG	259212	91408	ATCACATTCCCTCTACCCCA
170039	2235	TTTGGGGGCGCGGTGAACTT	214626	46822	CTCCACACCCACCTGTGTCT	259213	91409	TATCACATTCCCTCTACCCC
170040	2236	TTTTGGGGGCGCGGTGAACT	214627	46823	CCTCCACACCCACCTGTGTC	259214	91410	ATATCACATTCCCTCTACCC
170041	2237	GTTTTGGGGGCGCGGTGAAC	214628	46824	CCCTCCACACCCACCTGTGT	259215	91411	AATATCACATTCCCTCTACC
170042	2238	GGTTTTGGGGGCGCGGTGAA	214629	46825	GCCCTCCACACCCACCTGTG	259216	91412	CAATATCACATTCCCTCTAC
170043	2239	CGGTTTTGGGGGCGCGGTGA	214630	46826	CGCCCTCCACACCCACCTGT	259217	91413	TCAATATCACATTCCCTCTA
170044	2240	TCGGTTTTGGGGGCGCGGTG	214631	46827	ACGCCCTCCACACCCACCTG	259218	91414	TTCAATATCACATTCCCTCT
170045	2241	CTCGGTTTTGGGGGCGCGGT	214632	46828	TACGCCCTCCACACCCACCT	259219	91415	TTTCAATATCACATTCCCTC
170046	2242	ACTCGGTTTTGGGGGCGCGG	214633	46829	CTACGCCCTCCACACCCACC	259220	91416	GTTTCAATATCACATTCCCT
170047	2243	GACTCGGTTTTGGGGGCGCG	214634	46830	GCTACGCCCTCCACACCCAC	259221	91417	GGTTTCAATATCACATTCCC
170048	2244	AGACTCGGTTTTGGGGGCGC	214635	46831	TGCTACGCCCTCCACACCCA	259222	91418	TGGTTTCAATATCACATTCC
170049	2245	CAGACTCGGTTTTGGGGGCG	214636	46832	GTGCTACGCCCTCCACACCC	259223	91419	TTGGTTTCAATATCACATTC
170050	2246	CCAGACTCGGTTTTGGGGGC	214637	46833	TGTGCTACGCCCTCCACACC	259224	91420	TTTGGTTTCAATATCACATT
170051	2247	CCCAGACTCGGTTTTGGGGG	214638	46834	CTGTGCTACGCCCTCCACAC	259225	91421	CTTTGGTTTCAATATCACAT
170052	2248	CCCCAGACTCGGTTTTGGGG	214639	46835	TCTGTGCTACGCCCTCCACA	259226	91422	TCTTTGGTTTCAATATCACA
170053	2249	GCCCCAGACTCGGTTTTGGG	214640	46836	CTCTGTGCTACGCCCTCCAC	259227	91423	TTCTTTGGTTTCAATATCAC
170054	2250	CGCCCCAGACTCGGTTTTGG	214641	46837	CCTCTGTGCTACGCCCTCCA	259228	91424	CTTCTTTGGTTTCAATATCA
170055	2251	CCGCCCCAGACTCGGTTTTG	214642	46838	GCCTCTGTGCTACGCCCTCC	259229	91425	TCTTCTTTGGTTTCAATATC
170056	2252	GCCGCCCCAGACTCGGTTTT	214643	46839	TGCCTCTGTGCTACGCCCTC	259230	91426	TTCTTCTTTGGTTTCAATAT
170057	2253	TGCCGCCCCAGACTCGGTTT	214644	46840	CTGCCTCTGTGCTACGCCCT	259231	91427	TTTCTTCTTTGGTTTCAATA
170058	2254	CTGCCGCCCCAGACTCGGTT	214645	46841	TCTGCCTCTGTGCTACGCCC	259232	91428	TTTTCTTCTTTGGTTTCAAT
170059	2255	CCTGCCGCCCCAGACTCGGT	214646	46842	GTCTGCCTCTGTGCTACGCC	259233	91429	ATTTTCTTCTTTGGTTTCAA
170060	2256	CCCTGCCGCCCCAGACTCGG	214647	46843	AGTCTGCCTCTGTGCTACGC	259234	91430	GATTTTCTTCTTTGGTTTCA
170061	2257	CCCCTGCCGCCCCAGACTCG	214648	46844	AAGTCTGCCTCTGTGCTACG	259235	91431	AGATTTTCTTCTTTGGTTTC
170062	2258	CCCCCTGCCGCCCCAGACTC	214649	46845	GAAGTCTGCCTCTGTGCTAC	259236	91432	TAGATTTTCTTCTTTGGTTT
170063	2259	TCCCCCTGCCGCCCCAGACT	214650	46846	AGAAGTCTGCCTCTGTGCTA	259237	91433	ATAGATTTTCTTCTTTGGTT
170064	2260	TTCCCCCTGCCGCCCCAGAC	214651	46847	GAGAAGTCTGCCTCTGTGCT	259238	91434	CATAGATTTTCTTCTTTGGT
170065	2261	GTTCCCCCTGCCGCCCCAGA	214652	46848	TGAGAAGTCTGCCTCTGTGC	259239	91435	TCATAGATTTTCTTCTTTGG
170066	2262	AGTTCCCCCTGCCGCCCCAG	214653	46849	ATGAGAAGTCTGCCTCTGTG	259240	91436	ATCATAGATTTTCTTCTTTG
170067	2263	GAGTTCCCCCTGCCGCCCCA	214654	46850	AATGAGAAGTCTGCCTCTGT	259241	91437	GATCATAGATTTTCTTCTTT
170068	2264	GGAGTTCCCCCTGCCGCCCC	214655	46851	AAATGAGAAGTCTGCCTCTG	259242	91438	TGATCATAGATTTTCTTCTT
170069	2265	AGGAGTTCCCCCTGCCGCCC	214656	46852	GAAATGAGAAGTCTGCCTCT	259243	91439	CTGATCATAGATTTTCTTCT
170070	2266	CAGGAGTTCCCCCTGCCGCC	214657	46853	GGAAATGAGAAGTCTGCCTC	259244	91440	ACTGATCATAGATTTTCTTC
170071	2267	CCAGGAGTTCCCCCTGCCGC	214658	46854	AGGAAATGAGAAGTCTGCCT	259245	91441	AACTGATCATAGATTTTCTT
170072	2268	GCCAGGAGTTCCCCCTGCCG	214659	46855	CAGGAAATGAGAAGTCTGCC	259246	91442	AAACTGATCATAGATTTTCT
170073	2269	GGCCAGGAGTTCCCCCTGCC	214660	46856	CCAGGAAATGAGAAGTCTGC	259247	91443	AAAACTGATCATAGATTTTC
170074	2270	TGGCCAGGAGTTCCCCCTGC	214661	46857	CCCAGGAAATGAGAAGTCTG	259248	91444	GAAAACTGATCATAGATTTT
170075	2271	TTGGCCAGGAGTTCCCCCTG	214662	46858	ACCCAGGAAATGAGAAGTCT	259249	91445	TGAAAACTGATCATAGATTT
170076	2272	GTTGGCCAGGAGTTCCCCCT	214663	46859	GACCCAGGAAATGAGAAGTC	259250	91446	CTGAAAACTGATCATAGATT
170077	2273	CGTTGGCCAGGAGTTCCCCC	214664	46860	AGACCCAGGAAATGAGAAGT	259251	91447	GCTGAAAACTGATCATAGAT
170078	2274	TCGTTGGCCAGGAGTTCCCC	214665	46861	GAGACCCAGGAAATGAGAAG	259252	91448	TGCTGAAAACTGATCATAGA
170079	2275	TTCGTTGGCCAGGAGTTCCC	214666	46862	GGAGACCCAGGAAATGAGAA	259253	91449	CTGCTGAAAACTGATCATAG
170080	2276	ATTCGTTGGCCAGGAGTTCC	214667	46863	GGGAGACCCAGGAAATGAGA	259254	91450	ACTGCTGAAAACTGATCATA
170081	2277	GATTCGTTGGCCAGGAGTTC	214668	46864	GGGGAGACCCAGGAAATGAG	259255	91451	CACTGCTGAAAACTGATCAT
170082	2278	GGATTCGTTGGCCAGGAGTT	214669	46865	AGGGGAGACCCAGGAAATGA	259256	91452	TCACTGCTGAAAACTGATCA
170083	2279	TGGATTCGTTGGCCAGGAGT	214670	46866	AAGGGGAGACCCAGGAAATG	259257	91453	GTCACTGCTGAAAACTGATC
170084	2280	ATGGATTCGTTGGCCAGGAG	214671	46867	AAAGGGGAGACCCAGGAAAT	259258	91454	AGTCACTGCTGAAAACTGAT
170085	2281	CATGGATTCGTTGGCCAGGA	214672	46868	TAAAGGGGAGACCCAGGAAA	259259	91455	CAGTCACTGCTGAAAACTGA
170086	2282	GCATGGATTCGTTGGCCAGG	214673	46869	TTAAAGGGGAGACCCAGGAA	259260	91456	ACAGTCACTGCTGAAAACTG
170087	2283	GGCATGGATTCGTTGGCCAG	214674	46870	ATTAAAGGGGAGACCCAGGA	259261	91457	GACAGTCACTGCTGAAAACT
170088	2284	AGGCATGGATTCGTTGGCCA	214675	46871	CATTAAAGGGGAGACCCAGG	259262	91458	TGACAGTCACTGCTGAAAAC
170089	2285	GAGGCATGGATTCGTTGGCC	214676	46872	TCATTAAAGGGGAGACCCAG	259263	91459	TTGACAGTCACTGCTGAAAA
170090	2286	CGAGGCATGGATTCGTTGGC	214677	46873	GTCATTAAAGGGGAGACCCA	259264	91460	CTTGACAGTCACTGCTGAAA
170091	2287	GCGAGGCATGGATTCGTTGG	214678	46874	AGTCATTAAAGGGGAGACCC	259265	91461	TCTTGACAGTCACTGCTGAA
170092	2288	GGCGAGGCATGGATTCGTTG	214679	46875	GAGTCATTAAAGGGGAGACC	259266	91462	CTCTTGACAGTCACTGCTGA
170093	2289	GGGCGAGGCATGGATTCGTT	214680	46876	AGAGTCATTAAAGGGGAGAC	259267	91463	TCTCTTGACAGTCACTGCTG
170094	2290	AGGGCGAGGCATGGATTCGT	214681	46877	GAGAGTCATTAAAGGGGAGA	259268	91464	TTCTCTTGACAGTCACTGCT
170095	2291	GAGGGCGAGGCATGGATTCG	214682	46878	TGAGAGTCATTAAAGGGGAG	259269	91465	CTTCTCTTGACAGTCACTGC
170096	2292	GGAGGGCGAGGCATGGATTC	214683	46879	CTGAGAGTCATTAAAGGGGA	259270	91466	CCTTCTCTTGACAGTCACTG
170097	2293	AGGAGGGCGAGGCATGGATT	214684	46880	TCTGAGAGTCATTAAAGGGG	259271	91467	TCCTTCTCTTGACAGTCACT
170098	2294	CAGGAGGGCGAGGCATGGAT	214685	46881	CTCTGAGAGTCATTAAAGGG	259272	91468	CTCCTTCTCTTGACAGTCAC
170099	2295	ACAGGAGGGCGAGGCATGGA	214686	46882	TCTCTGAGAGTCATTAAAGG	259273	91469	TCTCCTTCTCTTGACAGTCA
170100	2296	CACAGGAGGGCGAGGCATGG	214687	46883	GTCTCTGAGAGTCATTAAAG	259274	91470	TTCTCCTTCTCTTGACAGTC
170101	2297	TCACAGGAGGGCGAGGCATG	214688	46884	GGTCTCTGAGAGTCATTAAA	259275	91471	CTTCTCCTTCTCTTGACAGT
170102	2298	ATCACAGGAGGGCGAGGCAT	214689	46885	GGGTCTCTGAGAGTCATTAA	259276	91472	CCTTCTCCTTCTCTTGACAG
170103	2299	CATCACAGGAGGGCGAGGCA	214690	46886	GGGGTCTCTGAGAGTCATTA	259277	91473	CCCTTCTCCTTCTCTTGACA
170104	2300	TCATCACAGGAGGGCGAGGC	214691	46887	AGGGGTCTCTGAGAGTCATT	259278	91474	ACCCTTCTCCTTCTCTTGAC
170105	2301	TTCATCACAGGAGGGCGAGG	214692	46888	GAGGGGTCTCTGAGAGTCAT	259279	91475	CACCCTTCTCCTTCTCTTGA
170106	2302	GTTCATCACAGGAGGGCGAG	214693	46889	GGAGGGGTCTCTGAGAGTCA	259280	91476	TCACCCTTCTCCTTCTCTTG

170107	2303	GGTTCATCACAGGAGGGCGA	214694	46890	AGGAGGGGTCTCTGAGAGTC	259281	91477	CTCACCCTTCTCCTTCTCTT
170108	2304	AGGTTCATCACAGGAGGGCG	214695	46891	AAGGAGGGGTCTCTGAGAGT	259282	91478	ACTCACCCTTCTCCTTCTCT
170109	2305	CAGGTTCATCACAGGAGGGC	214696	46892	GAAGGAGGGGTCTCTGAGAG	259283	91479	AACTCACCCTTCTCCTTCTC
170110	2306	CCAGGTTCATCACAGGAGGG	214697	46893	GGAAGGAGGGGTCTCTGAGA	259284	91480	TAACTCACCCTTCTCCTTCT
170111	2307	ACCAGGTTCATCACAGGAGG	214698	46894	GGGAAGGAGGGGTCTCTGAG	259285	91481	CTAACTCACCCTTCTCCTTC
170112	2308	TACCAGGTTCATCACAGGAG	214699	46895	GGGGAAGGAGGGGTCTCTGA	259286	91482	GCTAACTCACCCTTCTCCTT
170113	2309	GTACCAGGTTCATCACAGGA	214700	46896	GGGGGAAGGAGGGGTCTCTG	259287	91483	CGCTAACTCACCCTTCTCCT
170114	2310	CGTACCAGGTTCATCACAGG	214701	46897	AGGGGGAAGGAGGGGTCTCT	259288	91484	GCGCTAACTCACCCTTCTCC
170115	2311	GCGTACCAGGTTCATCACAG	214702	46898	CAGGGGGAAGGAGGGGTCTC	259289	91485	AGCGCTAACTCACCCTTCTC
170116	2312	TGCGTACCAGGTTCATCACA	214703	46899	GCAGGGGGAAGGAGGGGTCT	259290	91486	CAGCGCTAACTCACCCTTCT
170117	2313	GTGCGTACCAGGTTCATCAC	214704	46900	GGCAGGGGGAAGGAGGGGTC	259291	91487	TCAGCGCTAACTCACCCTTC
170118	2314	CGTGCGTACCAGGTTCATCA	214705	46901	GGGCAGGGGGAAGGAGGGGT	259292	91488	ATCAGCGCTAACTCACCCTT
170119	2315	CCGTGCGTACCAGGTTCATC	214706	46902	GGGGCAGGGGGAAGGAGGGG	259293	91489	CATCAGCGCTAACTCACCCT
170120	2316	ACCGTGCGTACCAGGTTCAT	214707	46903	AGGGGCAGGGGGAAGGAGGG	259294	91490	GCATCAGCGCTAACTCACCC
170121	2317	AACCGTGCGTACCAGGTTCA	214708	46904	CAGGGGCAGGGGGAAGGAGG	259295	91491	AGCATCAGCGCTAACTCACC
170122	2318	AAACCGTGCGTACCAGGTTC	214709	46905	CCAGGGGCAGGGGGAAGGAG	259296	91492	CAGCATCAGCGCTAACTCAC
170123	2319	AAAACCGTGCGTACCAGGTT	214710	46906	GCCAGGGGCAGGGGGAAGGA	259297	91493	CCAGCATCAGCGCTAACTCA
170124	2320	GAAAACCGTGCGTACCAGGT	214711	46907	AGCCAGGGGCAGGGGGAAGG	259298	91494	GCCAGCATCAGCGCTAACTC
170125	2321	AGAAAACCGTGCGTACCAGG	214712	46908	AAGCCAGGGGCAGGGGGAAG	259299	91495	AGCCAGCATCAGCGCTAACT
170126	2322	CAGAAAACCGTGCGTACCAG	214713	46909	GAAGCCAGGGGCAGGGGGAA	259300	91496	CAGCCAGCATCAGCGCTAAC
170127	2323	CCAGAAAACCGTGCGTACCA	214714	46910	AGAAGCCAGGGGCAGGGGGA	259301	91497	TCAGCCAGCATCAGCGCTAA
170128	2324	ACCAGAAAACCGTGCGTACC	214715	46911	TAGAAGCCAGGGGCAGGGGG	259302	91498	GTCAGCCAGCATCAGCGCTA
170129	2325	AACCAGAAAACCGTGCGTAC	214716	46912	GTAGAAGCCAGGGGCAGGGG	259303	91499	TGTCAGCCAGCATCAGCGCT
170130	2326	TAACCAGAAAACCGTGCGTA	214717	46913	GGTAGAAGCCAGGGGCAGGG	259304	91500	CTGTCAGCCAGCATCAGCGC
170131	2327	TTAACCAGAAAACCGTGCGT	214718	46914	GGGTAGAAGCCAGGGGCAGG	259305	91501	CCTGTCAGCCAGCATCAGCG
170132	2328	ATTAACCAGAAAACCGTGCG	214719	46915	GGGGTAGAAGCCAGGGGCAG	259306	91502	ACCTGTCAGCCAGCATCAGC
170133	2329	AATTAACCAGAAAACCGTGC	214720	46916	TGGGGTAGAAGCCAGGGGCA	259307	91503	GACCTGTCAGCCAGCATCAG
170134	2330	GAATTAACCAGAAAACCGTG	214721	46917	CTGGGGTAGAAGCCAGGGGC	259308	91504	TGACCTGTCAGCCAGCATCA
170135	2331	AGAATTAACCAGAAAACCGT	214722	46918	CCTGGGGTAGAAGCCAGGGG	259309	91505	CTGACCTGTCAGCCAGCATC
170136	2332	TAGAATTAACCAGAAAACCG	214723	46919	CCCTGGGGTAGAAGCCAGGG	259310	91506	GCTGACCTGTCAGCCAGCAT
170137	2333	ATAGAATTAACCAGAAAACC	214724	46920	CCCCTGGGGTAGAAGCCAGG	259311	91507	CGCTGACCTGTCAGCCAGCA
170138	2334	GATAGAATTAACCAGAAAAC	214725	46921	ACCCCTGGGGTAGAAGCCAG	259312	91508	CCGCTGACCTGTCAGCCAGC
170139	2335	CGATAGAATTAACCAGAAAA	214726	46922	CACCCCTGGGGTAGAAGCCA	259313	91509	CCCGCTGACCTGTCAGCCAG
170140	2336	GCGATAGAATTAACCAGAAA	214727	46923	ACACCCCTGGGGTAGAAGCC	259314	91510	ACCCGCTGACCTGTCAGCCA
170141	2337	AGCGATAGAATTAACCAGAA	214728	46924	TACACCCCTGGGGTAGAAGC	259315	91511	AACCCGCTGACCTGTCAGCC
170142	2338	CAGCGATAGAATTAACCAGA	214729	46925	CTACACCCCTGGGGTAGAAG	259316	91512	CAACCCGCTGACCTGTCAGC
170143	2339	TCAGCGATAGAATTAACCAG	214730	46926	TCTACACCCCTGGGGTAGAA	259317	91513	CCAACCCGCTGACCTGTCAG
170144	2340	TTCAGCGATAGAATTAACCA	214731	46927	CTCTACACCCCTGGGGTAGA	259318	91514	ACCAACCCGCTGACCTGTCA
170145	2341	TTTCAGCGATAGAATTAACC	214732	46928	ACTCTACACCCCTGGGGTAG	259319	91515	AACCAACCCGCTGACCTGTC
170146	2342	TTTTCAGCGATAGAATTAAC	214733	46929	AACTCTACACCCCTGGGGTA	259320	91516	AAACCAACCCGCTGACCTGT
170147	2343	GTTTTCAGCGATAGAATTAA	214734	46930	AAACTCTACACCCCTGGGGT	259321	91517	GAAACCAACCCGCTGACCTG
170148	2344	AGTTTTCAGCGATAGAATTA	214735	46931	AAAACTCTACACCCCTGGGG	259322	91518	TGAAACCAACCCGCTGACCT
170149	2345	CAGTTTTCAGCGATAGAATT	214736	46932	CAAAACTCTACACCCCTGGG	259323	91519	GTGAAACCAACCCGCTGACC
170150	2346	CCAGTTTTCAGCGATAGAAT	214737	46933	GCAAAACTCTACACCCCTGG	259324	91520	GGTGAAACCAACCCGCTGAC
170151	2347	ACCAGTTTTCAGCGATAGAA	214738	46934	GGCAAAACTCTACACCCCTG	259325	91521	TGGTGAAACCAACCCGCTGA
170152	2348	CACCAGTTTTCAGCGATAGA	214739	46935	TGGCAAAACTCTACACCCCT	259326	91522	TTGGTGAAACCAACCCGCTG
170153	2349	GCACCAGTTTTCAGCGATAG	214740	46936	ATGGCAAAACTCTACACCCC	259327	91523	CTTGGTGAAACCAACCCGCT
170154	2350	CGCACCAGTTTTCAGCGATA	214741	46937	AATGGCAAAACTCTACACCC	259328	91524	CCTTGGTGAAACCAACCCGC
170155	2351	CCGCACCAGTTTTCAGCGAT	214742	46938	AAATGGCAAAACTCTACACC	259329	91525	TCCTTGGTGAAACCAACCCG
170156	2352	CCCGCACCAGTTTTCAGCGA	214743	46939	AAAATGGCAAAACTCTACAC	259330	91526	CTCCTTGGTGAAACCAACCC
170157	2353	CCCCGCACCAGTTTTCAGCG	214744	46940	GAAAATGGCAAAACTCTACA	259331	91527	ACTCCTTGGTGAAACCAACC
170158	2354	CCCCCGCACCAGTTTTCAGC	214745	46941	GGAAAATGGCAAAACTCTAC	259332	91528	CACTCCTTGGTGAAACCAAC
170159	2355	CCCCCCGCACCAGTTTTCAG	214746	46942	TGGAAAATGGCAAAACTCTA	259333	91529	ACACTCCTTGGTGAAACCAA
170160	2356	GCCCCCCGCACCAGTTTTCA	214747	46943	TTGGAAAATGGCAAAACTCT	259334	91530	CACACTCCTTGGTGAAACCA
170161	2357	CGCCCCCCGCACCAGTTTTC	214748	46944	CTTGGAAAATGGCAAAACTC	259335	91531	TCACACTCCTTGGTGAAACC
170162	2358	GCGCCCCCCGCACCAGTTTT	214749	46945	GCTTGGAAAATGGCAAAACT	259336	91532	ATCACACTCCTTGGTGAAAC
170163	2359	TGCGCCCCCCGCACCAGTTT	214750	46946	TGCTTGGAAAATGGCAAAAC	259337	91533	CATCACACTCCTTGGTGAAA
170164	2360	GTGCGCCCCCCGCACCAGTT	214751	46947	CTGCTTGGAAAATGGCAAAA	259338	91534	TCATCACACTCCTTGGTGAA
170165	2361	AGTGCGCCCCCCGCACCAGT	214752	46948	TCTGCTTGGAAAATGGCAAA	259339	91535	TTCATCACACTCCTTGGTGA
170166	2362	AAGTGCGCCCCCCGCACCAG	214753	46949	TTCTGCTTGGAAAATGGCAA	259340	91536	CTTCATCACACTCCTTGGTG
170167	2363	GAAGTGCGCCCCCCGCACCA	214754	46950	GTTCTGCTTGGAAAATGGCA	259341	91537	CCTTCATCACACTCCTTGGT
170168	2364	AGAAGTGCGCCCCCCGCACC	214755	46951	AGTTCTGCTTGGAAAATGGC	259342	91538	GCCTTCATCACACTCCTTGG
170169	2365	CAGAAGTGCGCCCCCCGCAC	214756	46952	AAGTTCTGCTTGGAAAATGG	259343	91539	AGCCTTCATCACACTCCTTG
170170	2366	TCAGAAGTGCGCCCCCCGCA	214757	46953	GAAGTTCTGCTTGGAAAATG	259344	91540	CAGCCTTCATCACACTCCTT
170171	2367	CTCAGAAGTGCGCCCCCCGC	214758	46954	TGAAGTTCTGCTTGGAAAAT	259345	91541	TCAGCCTTCATCACACTCCT
170172	2368	TCTCAGAAGTGCGCCCCCCG	214759	46955	ATGAAGTTCTGCTTGGAAAA	259346	91542	ATCAGCCTTCATCACACTCC
170173	2369	GTCTCAGAAGTGCGCCCCCC	214760	46956	AATGAAGTTCTGCTTGGAAA	259347	91543	CATCAGCCTTCATCACACTC
170174	2370	CGTCTCAGAAGTGCGCCCCC	214761	46957	AAATGAAGTTCTGCTTGGAA	259348	91544	ACATCAGCCTTCATCACACT
170175	2371	CCGTCTCAGAAGTGCGCCCC	214762	46958	GAAATGAAGTTCTGCTTGGA	259349	91545	AACATCAGCCTTCATCACAC
170176	2372	TCCGTCTCAGAAGTGCGCCC	214763	46959	GGAAATGAAGTTCTGCTTGG	259350	91546	CAACATCAGCCTTCATCACA
170177	2373	TTCCGTCTCAGAAGTGCGCC	214764	46960	AGGAAATGAAGTTCTGCTTG	259351	91547	ACAACATCAGCCTTCATCAC
170178	2374	CTTCCGTCTCAGAAGTGCGC	214765	46961	GAGGAAATGAAGTTCTGCTT	259352	91548	GACAACATCAGCCTTCATCA

170179	2375	TCTTCCGTCTCAGAAGTGCG	214766	46962	AGAGGAAATGAAGTTCTGCT	259353	91549	AGACAACATCAGCCTTCATC
170180	2376	CTCTTCCGTCTCAGAAGTGC	214767	46963	AAGAGGAAATGAAGTTCTGC	259354	91550	CAGACAACATCAGCCTTCAT
170181	2377	GCTCTTCCGTCTCAGAAGTG	214768	46964	GAAGAGGAAATGAAGTTCTG	259355	91551	ACAGACAACATCAGCCTTCA
170182	2378	TGCTCTTCCGTCTCAGAAGT	214769	46965	AGAAGAGGAAATGAAGTTCT	259356	91552	CACAGACAACATCAGCCTTC
170183	2379	ATGCTCTTCCGTCTCAGAAG	214770	46966	CAGAAGAGGAAATGAAGTTC	259357	91553	CCACAGACAACATCAGCCTT
170184	2380	GATGCTCTTCCGTCTCAGAA	214771	46967	ACAGAAGAGGAAATGAAGTT	259358	91554	CCCACAGACAACATCAGCCT
170185	2381	AGATGCTCTTCCGTCTCAGA	214772	46968	CACAGAAGAGGAAATGAAGT	259359	91555	TCCCACAGACAACATCAGCC
170186	2382	TAGATGCTCTTCCGTCTCAG	214773	46969	ACACAGAAGAGGAAATGAAG	259360	91556	TTCCCACAGACAACATCAGC
170187	2383	CTAGATGCTCTTCCGTCTCA	214774	46970	GACACAGAAGAGGAAATGAA	259361	91557	ATTCCCACAGACAACATCAG
170188	2384	CCTAGATGCTCTTCCGTCTC	214775	46971	AGACACAGAAGAGGAAATGA	259362	91558	CATTCCCACAGACAACATCA
170189	2385	TCCTAGATGCTCTTCCGTCT	214776	46972	TAGACACAGAAGAGGAAATG	259363	91559	ACATTCCCACAGACAACATC
170190	2386	CTCCTAGATGCTCTTCCGTC	214777	46973	GTAGACACAGAAGAGGAAAT	259364	91560	TACATTCCCACAGACAACAT
170191	2387	GCTCCTAGATGCTCTTCCGT	214778	46974	TGTAGACACAGAAGAGGAAA	259365	91561	ATACATTCCCACAGACAACA
170192	2388	AGCTCCTAGATGCTCTTCCG	214779	46975	GTGTAGACACAGAAGAGGAA	259366	91562	CATACATTCCCACAGACAAC
170193	2389	CAGCTCCTAGATGCTCTTCC	214780	46976	AGTGTAGACACAGAAGAGGA	259367	91563	TCATACATTCCCACAGACAA
170194	2390	TCAGCTCCTAGATGCTCTTC	214781	46977	GAGTGTAGACACAGAAGAGG	259368	91564	ATCATACATTCCCACAGACA
170195	2391	TTCAGCTCCTAGATGCTCTT	214782	46978	AGAGTGTAGACACAGAAGAG	259369	91565	CATCATACATTCCCACAGAC
170196	2392	ATTCAGCTCCTAGATGCTCT	214783	46979	AAGAGTGTAGACACAGAAGA	259370	91566	CCATCATACATTCCCACAGA
170197	2393	GATTCAGCTCCTAGATGCTC	214784	46980	AAAGAGTGTAGACACAGAAG	259371	91567	ACCATCATACATTCCCACAG
170198	2394	GGATTCAGCTCCTAGATGCT	214785	46981	CAAAGAGTGTAGACACAGAA	259372	91568	TACCATCATACATTCCCACA
170199	2395	AGGATTCAGCTCCTAGATGC	214786	46982	ACAAAGAGTGTAGACACAGA	259373	91569	TTACCATCATACATTCCCAC
170200	2396	GAGGATTCAGCTCCTAGATG	214787	46983	CACAAAGAGTGTAGACACAG	259374	91570	GTTACCATCATACATTCCCA
170201	2397	GGAGGATTCAGCTCCTAGAT	214788	46984	GCACAAAGAGTGTAGACACA	259375	91571	AGTTACCATCATACATTCCC
170202	2398	TGGAGGATTCAGCTCCTAGA	214789	46985	AGCACAAAGAGTGTAGACAC	259376	91572	CAGTTACCATCATACATTCC
170203	2399	GTGGAGGATTCAGCTCCTAG	214790	46986	AAGCACAAAGAGTGTAGACA	259377	91573	CCAGTTACCATCATACATTC
170204	2400	CGTGGAGGATTCAGCTCCTA	214791	46987	GAAGCACAAAGAGTGTAGAC	259378	91574	ACCAGTTACCATCATACATT
170205	2401	GCGTGGAGGATTCAGCTCCT	214792	46988	AGAAGCACAAAGAGTGTAGA	259379	91575	AACCAGTTACCATCATACAT
170206	2402	CGCGTGGAGGATTCAGCTCC	214793	46989	AAGAAGCACAAAGAGTGTAG	259380	91576	AAACCAGTTACCATCATACA
170207	2403	CCGCGTGGAGGATTCAGCTC	214794	46990	AAAGAAGCACAAAGAGTGTA	259381	91577	CAAACCAGTTACCATCATAC
170208	2404	CCCGCGTGGAGGATTCAGCT	214795	46991	GAAAGAAGCACAAAGAGTGT	259382	91578	ACAAACCAGTTACCATCATA
170209	2405	ACCCGCGTGGAGGATTCAGC	214796	46992	AGAAAGAAGCACAAAGAGTG	259383	91579	TACAAACCAGTTACCATCAT
170210	2406	GACCCGCGTGGAGGATTCAG	214797	46993	AAGAAAGAAGCACAAAGAGT	259384	91580	CTACAAACCAGTTACCATCA
170211	2407	CGACCCGCGTGGAGGATTCA	214798	46994	CAAGAAAGAAGCACAAAGAG	259385	91581	GCTACAAACCAGTTACCATC
170212	2408	GCGACCCGCGTGGAGGATTC	214799	46995	GCAAGAAAGAAGCACAAAGA	259386	91582	AGCTACAAACCAGTTACCAT
170213	2409	GGCGACCCGCGTGGAGGATT	214800	46996	GGCAAGAAAGAAGCACAAAG	259387	91583	TAGCTACAAACCAGTTACCA
170214	2410	GGGCGACCCGCGTGGAGGAT	214801	46997	TGGCAAGAAAGAAGCACAAA	259388	91584	TTAGCTACAAACCAGTTACC
170215	2411	TGGGCGACCCGCGTGGAGGA	214802	46998	CTGGCAAGAAAGAAGCACAA	259389	91585	ATTAGCTACAAACCAGTTAC
170216	2412	CTGGGCGACCCGCGTGGAGG	214803	46999	GCTGGCAAGAAAGAAGCACA	259390	91586	AATTAGCTACAAACCAGTTA
170217	2413	CCTGGGCGACCCGCGTGGAG	214804	47000	AGCTGGCAAGAAAGAAGCAC	259391	91587	AAATTAGCTACAAACCAGTT
170218	2414	ACCTGGGCGACCCGCGTGGA	214805	47001	AAGCTGGCAAGAAAGAAGCA	259392	91588	CAAATTAGCTACAAACCAGT
170219	2415	AACCTGGGCGACCCGCGTGG	214806	47002	AAAGCTGGCAAGAAAGAAGC	259393	91589	CCAAATTAGCTACAAACCAG
170220	2416	CAACCTGGGCGACCCGCGTG	214807	47003	AAAAGCTGGCAAGAAAGAAG	259394	91590	CCCAAATTAGCTACAAACCA
170221	2417	TCAACCTGGGCGACCCGCGT	214808	47004	AAAAAGCTGGCAAGAAAGAA	259395	91591	CCCCAAATTAGCTACAAACC
170222	2418	ATCAACCTGGGCGACCCGCG	214809	47005	GAAAAAGCTGGCAAGAAAGA	259396	91592	TCCCCAAATTAGCTACAAAC
170223	2419	GATCAACCTGGGCGACCCGC	214810	47006	AGAAAAAGCTGGCAAGAAAG	259397	91593	TTCCCCAAATTAGCTACAAA
170224	2420	AGATCAACCTGGGCGACCCG	214811	47007	GAGAAAAAGCTGGCAAGAAA	259398	91594	CTTCCCCAAATTAGCTACAA
170225	2421	CAGATCAACCTGGGCGACCC	214812	47008	GGAGAAAAAGCTGGCAAGAA	259399	91595	GCTTCCCCAAATTAGCTACA
170226	2422	TCAGATCAACCTGGGCGACC	214813	47009	AGGAGAAAAAGCTGGCAAGA	259400	91596	TGCTTCCCCAAATTAGCTAC
170227	2423	TTCAGATCAACCTGGGCGAC	214814	47010	AAGGAGAAAAAGCTGGCAAG	259401	91597	CTGCTTCCCCAAATTAGCTA
170228	2424	ATTCAGATCAACCTGGGCGA	214815	47011	AAAGGAGAAAAAGCTGGCAA	259402	91598	ACTGCTTCCCCAAATTAGCT
170229	2425	AATTCAGATCAACCTGGGCG	214816	47012	CAAAGGAGAAAAAGCTGGCA	259403	91599	CACTGCTTCCCCAAATTAGC
170230	2426	AAATTCAGATCAACCTGGGC	214817	47013	GCAAAGGAGAAAAAGCTGGC	259404	91600	TCACTGCTTCCCCAAATTAG
170231	2427	GAAATTCAGATCAACCTGGG	214818	47014	GGCAAAGGAGAAAAAGCTGG	259405	91601	CTCACTGCTTCCCCAAATTA
170232	2428	AGAAATTCAGATCAACCTGG	214819	47015	GGGCAAAGGAGAAAAAGCTG	259406	91602	TCTCACTGCTTCCCCAAATT
170233	2429	CAGAAATTCAGATCAACCTG	214820	47016	CGGGCAAAGGAGAAAAAGCT	259407	91603	TTCTCACTGCTTCCCCAAAT
170234	2430	CCAGAAATTCAGATCAACCT	214821	47017	GCGGGCAAAGGAGAAAAAGC	259408	91604	ATTCTCACTGCTTCCCCAAA
170235	2431	CCCAGAAATTCAGATCAACC	214822	47018	GGCGGGCAAAGGAGAAAAAG	259409	91605	AATTCTCACTGCTTCCCCAA
170236	2432	CCCCAGAAATTCAGATCAAC	214823	47019	GGGCGGGCAAAGGAGAAAAA	259410	91606	GAATTCTCACTGCTTCCCCA
170237	2433	TCCCCAGAAATTCAGATCAA	214824	47020	AGGGCGGGCAAAGGAGAAAA	259411	91607	CGAATTCTCACTGCTTCCCC
170238	2434	TTCCCCAGAAATTCAGATCA	214825	47021	AAGGGCGGGCAAAGGAGAAA	259412	91608	ACGAATTCTCACTGCTTCCC
170239	2435	ATTCCCCAGAAATTCAGATC	214826	47022	GAAGGGCGGGCAAAGGAGAA	259413	91609	CACGAATTCTCACTGCTTCC
170240	2436	CATTCCCCAGAAATTCAGAT	214827	47023	GGAAGGGCGGGCAAAGGAGA	259414	91610	GCACGAATTCTCACTGCTTC
170241	2437	CCATTCCCCAGAAATTCAGA	214828	47024	AGGAAGGGCGGGCAAAGGAG	259415	91611	GGCACGAATTCTCACTGCTT
170242	2438	GCCATTCCCCAGAAATTCAG	214829	47025	AAGGAAGGGCGGGCAAAGGA	259416	91612	GGGCACGAATTCTCACTGCT
170243	2439	AGCCATTCCCCAGAAATTCA	214830	47026	GAAGGAAGGGCGGGCAAAGG	259417	91613	AGGGCACGAATTCTCACTGC
170244	2440	AAGCCATTCCCCAGAAATTC	214831	47027	GGAAGGAAGGGCGGGCAAAG	259418	91614	AAGGGCACGAATTCTCACTG
170245	2441	CAAGCCATTCCCCAGAAATT	214832	47028	AGGAAGGAAGGGCGGGCAAA	259419	91615	AAAGGGCACGAATTCTCACT
170246	2442	CCAAGCCATTCCCCAGAAAT	214833	47029	AAGGAAGGAAGGGCGGGCAA	259420	91616	CAAAGGGCACGAATTCTCAC
170247	2443	GCCAAGCCATTCCCCAGAAA	214834	47030	GAAGGAAGGAAGGGCGGGCA	259421	91617	TCAAAGGGCACGAATTCTCA
170248	2444	AGCCAAGCCATTCCCCAGAA	214835	47031	GGAAGGAAGGAAGGGCGGGC	259422	91618	TTCAAAGGGCACGAATTCTC
170249	2445	CAGCCAAGCCATTCCCCAGA	214836	47032	AGGAAGGAAGGAAGGGCGGG	259423	91619	CTTCAAAGGGCACGAATTCT
170250	2446	GCAGCCAAGCCATTCCCCAG	214837	47033	AAGGAAGGAAGGAAGGGCGG	259424	91620	TCTTCAAAGGGCACGAATTC

170251	2447	GGCAGCCAAGCCATTCCCCA	214838	47034	GAAGGAAGGAAGGAAGGGCG	259425	91621	GTCTTCAAAGGGCACGAATT
170252	2448	GGGCAGCCAAGCCATTCCCC	214839	47035	GGAAGGAAGGAAGGAAGGGC	259426	91622	GGTCTTCAAAGGGCACGAAT
170253	2449	CGGGCAGCCAAGCCATTCCC	214840	47036	GGGAAGGAAGGAAGGAAGGG	259427	91623	TGGTCTTCAAAGGGCACGAA
170254	2450	GCGGGCAGCCAAGCCATTCC	214841	47037	AGGGAAGGAAGGAAGGAAGG	259428	91624	CTGGTCTTCAAAGGGCACGA
170255	2451	GGCGGGCAGCCAAGCCATTC	214842	47038	GAGGGAAGGAAGGAAGGAAG	259429	91625	ACTGGTCTTCAAAGGGCACG
170256	2452	GGGCGGGCAGCCAAGCCATT	214843	47039	GGAGGGAAGGAAGGAAGGAA	259430	91626	TACTGGTCTTCAAAGGGCAC
170257	2453	CGGGCGGGCAGCCAAGCCAT	214844	47040	GGGAGGGAAGGAAGGAAGGA	259431	91627	TTACTGGTCTTCAAAGGGCA
170258	2454	CCGGGCGGGCAGCCAAGCCA	214845	47041	AGGGAGGGAAGGAAGGAAGG	259432	91628	CTTACTGGTCTTCAAAGGGC
170259	2455	CCCGGGCGGGCAGCCAAGCC	214846	47042	GAGGGAGGGAAGGAAGGAAG	259433	91629	ACTTACTGGTCTTCAAAGGG
170260	2456	TCCCGGGCGGGCAGCCAAGC	214847	47043	GGAGGGAGGGAAGGAAGGAA	259434	91630	CACTTACTGGTCTTCAAAGG
170261	2457	GTCCCGGGCGGGCAGCCAAG	214848	47044	GGGAGGGAGGGAAGGAAGGA	259435	91631	CCACTTACTGGTCTTCAAAG
170262	2458	GGTCCCGGGCGGGCAGCCAA	214849	47045	GGGGAGGGAGGGAAGGAAGG	259436	91632	GCCACTTACTGGTCTTCAAA
170263	2459	TGGTCCCGGGCGGGCAGCCA	214850	47046	GGGGGAGGGAGGGAAGGAAG	259437	91633	TGCCACTTACTGGTCTTCAA
170264	2460	CTGGTCCCGGGCGGGCAGCC	214851	47047	GGGGGGAGGGAGGGAAGGAA	259438	91634	TTGCCACTTACTGGTCTTCA
170265	2461	CCTGGTCCCGGGCGGGCAGC	214852	47048	AGGGGGGAGGGAGGGAAGGA	259439	91635	CTTGCCACTTACTGGTCTTC
170266	2462	GCCTGGTCCCGGGCGGGCAG	214853	47049	AAGGGGGGAGGGAGGGAAGG	259440	91636	TCTTGCCACTTACTGGTCTT
170267	2463	GGCCTGGTCCCGGGCGGGCA	214854	47050	GAAGGGGGGAGGGAGGGAAG	259441	91637	TTCTTGCCACTTACTGGTCT
170268	2464	CGGCCTGGTCCCGGGCGGGC	214855	47051	GGAAGGGGGGAGGGAGGGAA	259442	91638	TTTCTTGCCACTTACTGGTC
170269	2465	TCGGCCTGGTCCCGGGCGGG	214856	47052	GGGAAGGGGGGAGGGAGGGA	259443	91639	GTTTCTTGCCACTTACTGGT
170270	2466	GTCGGCCTGGTCCCGGGCGG	214857	47053	AGGGAAGGGGGGAGGGAGGG	259444	91640	GGTTTCTTGCCACTTACTGG
170271	2467	GGTCGGCCTGGTCCCGGGCG	214858	47054	GAGGGAAGGGGGGAGGGAGG	259445	91641	GGGTTTCTTGCCACTTACTG
170272	2468	GGGTCGGCCTGGTCCCGGGC	214859	47055	GGAGGGAAGGGGGGAGGGAG	259446	91642	TGGGTTTCTTGCCACTTACT
170273	2469	AGGGTCGGCCTGGTCCCGGG	214860	47056	AGGAGGGAAGGGGGGAGGGA	259447	91643	GTGGGTTTCTTGCCACTTAC
170274	2470	GAGGGTCGGCCTGGTCCCGG	214861	47057	AAGGAGGGAAGGGGGGAGGG	259448	91644	GGTGGGTTTCTTGCCACTTA
170275	2471	GGAGGGTCGGCCTGGTCCCG	214862	47058	GAAGGAGGGAAGGGGGGAGG	259449	91645	TGGTGGGTTTCTTGCCACTT
170276	2472	AGGAGGGTCGGCCTGGTCCC	214863	47059	GGAAGGAGGGAAGGGGGGAG	259450	91646	CTGGTGGGTTTCTTGCCACT
170277	2473	AAGGAGGGTCGGCCTGGTCC	214864	47060	GGGAAGGAGGGAAGGGGGGA	259451	91647	CCTGGTGGGTTTCTTGCCAC
170278	2474	CAAGGAGGGTCGGCCTGGTC	214865	47061	AGGGAAGGAGGGAAGGGGGG	259452	91648	GCCTGGTGGGTTTCTTGCCA
170279	2475	TCAAGGAGGGTCGGCCTGGT	214866	47062	GAGGGAAGGAGGGAAGGGGG	259453	91649	GGCCTGGTGGGTTTCTTGCC
170280	2476	GTCAAGGAGGGTCGGCCTGG	214867	47063	AGAGGGAAGGAGGGAAGGGG	259454	91650	AGGCCTGGTGGGTTTCTTGC
170281	2477	CGTCAAGGAGGGTCGGCCTG	214868	47064	AAGAGGGAAGGAGGGAAGGG	259455	91651	CAGGCCTGGTGGGTTTCTTG
170282	2478	CCGTCAAGGAGGGTCGGCCT	214869	47065	AAAGAGGGAAGGAGGGAAGG	259456	91652	CCAGGCCTGGTGGGTTTCTT
170283	2479	ACCGTCAAGGAGGGTCGGCC	214870	47066	GAAAGAGGGAAGGAGGGAAG	259457	91653	GCCAGGCCTGGTGGGTTTCT
170284	2480	CACCGTCAAGGAGGGTCGGC	214871	47067	GGAAAGAGGGAAGGAGGGAA	259458	91654	AGCCAGGCCTGGTGGGTTTC
170285	2481	CCACCGTCAAGGAGGGTCGG	214872	47068	GGGAAAGAGGGAAGGAGGGA	259459	91655	GAGCCAGGCCTGGTGGGTTT
170286	2482	GCCACCGTCAAGGAGGGTCG	214873	47069	AGGGAAAGAGGGAAGGAGGG	259460	91656	TGAGCCAGGCCTGGTGGGTT
170287	2483	CGCCACCGTCAAGGAGGGTC	214874	47070	GAGGGAAAGAGGGAAGGAGG	259461	91657	CTGAGCCAGGCCTGGTGGGT
170288	2484	ACGCCACCGTCAAGGAGGGT	214875	47071	GGAGGGAAAGAGGGAAGGAG	259462	91658	CCTGAGCCAGGCCTGGTGGG
170289	2485	TACGCCACCGTCAAGGAGGG	214876	47072	AGGAGGGAAAGAGGGAAGGA	259463	91659	CCCTGAGCCAGGCCTGGTGG
170290	2486	CTACGCCACCGTCAAGGAGG	214877	47073	AAGGAGGGAAAGAGGGAAGG	259464	91660	GCCCTGAGCCAGGCCTGGTG
170291	2487	TCTACGCCACCGTCAAGGAG	214878	47074	GAAGGAGGGAAAGAGGGAAG	259465	91661	AGCCCTGAGCCAGGCCTGGT
170292	2488	CTCTACGCCACCGTCAAGGA	214879	47075	GGAAGGAGGGAAAGAGGGAA	259466	91662	CAGCCCTGAGCCAGGCCTGG
170293	2489	CCTCTACGCCACCGTCAAGG	214880	47076	GGGAAGGAGGGAAAGAGGGA	259467	91663	CCAGCCCTGAGCCAGGCCTG
170294	2490	CCCTCTACGCCACCGTCAAG	214881	47077	GGGGAAGGAGGGAAAGAGGG	259468	91664	CCCAGCCCTGAGCCAGGCCT
170295	2491	GCCCTCTACGCCACCGTCAA	214882	47078	GGGGGAAGGAGGGAAAGAGG	259469	91665	GCCCAGCCCTGAGCCAGGCC
170296	2492	AGCCCTCTACGCCACCGTCA	214883	47079	GGGGGGAAGGAGGGAAAGAG	259470	91666	AGCCCAGCCCTGAGCCAGGC
170297	2493	CAGCCCTCTACGCCACCGTC	214884	47080	AGGGGGGAAGGAGGGAAAGA	259471	91667	CAGCCCAGCCCTGAGCCAGG
170298	2494	CCAGCCCTCTACGCCACCGT	214885	47081	AAGGGGGGAAGGAGGGAAAG	259472	91668	CCAGCCCAGCCCTGAGCCAG
170299	2495	TCCAGCCCTCTACGCCACCG	214886	47082	GAAGGGGGGAAGGAGGGAAA	259473	91669	CCCAGCCCAGCCCTGAGCCA
170300	2496	CTCCAGCCCTCTACGCCACC	214887	47083	GGAAGGGGGGAAGGAGGGAA	259474	91670	GCCCAGCCCAGCCCTGAGCC
170301	2497	GCTCCAGCCCTCTACGCCAC	214888	47084	TGGAAGGGGGGAAGGAGGGA	259475	91671	AGCCCAGCCCAGCCCTGAGC
170302	2498	GGCTCCAGCCCTCTACGCCA	214889	47085	GTGGAAGGGGGGAAGGAGGG	259476	91672	AAGCCCAGCCCAGCCCTGAG
170303	2499	AGGCTCCAGCCCTCTACGCC	214890	47086	GGTGGAAGGGGGGAAGGAGG	259477	91673	CAAGCCCAGCCCAGCCCTGA
170304	2500	CAGGCTCCAGCCCTCTACGC	214891	47087	GGGTGGAAGGGGGGAAGGAG	259478	91674	CCAAGCCCAGCCCAGCCCTG
170305	2501	CCAGGCTCCAGCCCTCTACG	214892	47088	AGGGTGGAAGGGGGGAAGGA	259479	91675	GCCAAGCCCAGCCCAGCCCT
170306	2502	CCCAGGCTCCAGCCCTCTAC	214893	47089	AAGGGTGGAAGGGGGGAAGG	259480	91676	AGCCAAGCCCAGCCCAGCCC
170307	2503	ACCCAGGCTCCAGCCCTCTA	214894	47090	GAAGGGTGGAAGGGGGGAAG	259481	91677	GAGCCAAGCCCAGCCCAGCC
170308	2504	TACCCAGGCTCCAGCCCTCT	214895	47091	GGAAGGGTGGAAGGGGGGAA	259482	91678	CGAGCCAAGCCCAGCCCAGC
170309	2505	GTACCCAGGCTCCAGCCCTC	214896	47092	GGGAAGGGTGGAAGGGGGGA	259483	91679	ACGAGCCAAGCCCAGCCCAG
170310	2506	AGTACCCAGGCTCCAGCCCT	214897	47093	GGGGAAGGGTGGAAGGGGGG	259484	91680	GACGAGCCAAGCCCAGCCCA
170311	2507	CAGTACCCAGGCTCCAGCCC	214898	47094	GGGGGAAGGGTGGAAGGGGG	259485	91681	AGACGAGCCAAGCCCAGCCC
170312	2508	GCAGTACCCAGGCTCCAGCC	214899	47095	GGGGGGAAGGGTGGAAGGGG	259486	91682	GAGACGAGCCAAGCCCAGCC
170313	2509	CGCAGTACCCAGGCTCCAGC	214900	47096	AGGGGGGAAGGGTGGAAGGG	259487	91683	TGAGACGAGCCAAGCCCAGC
170314	2510	TCGCAGTACCCAGGCTCCAG	214901	47097	AAGGGGGGAAGGGTGGAAGG	259488	91684	CTGAGACGAGCCAAGCCCAG
170315	2511	CTCGCAGTACCCAGGCTCCA	214902	47098	GAAGGGGGGAAGGGTGGAAG	259489	91685	TCTGAGACGAGCCAAGCCCA
170316	2512	CCTCGCAGTACCCAGGCTCC	214903	47099	GGAAGGGGGGAAGGGTGGAA	259490	91686	CTCTGAGACGAGCCAAGCCC
170317	2513	GCCTCGCAGTACCCAGGCTC	214904	47100	GGGAAGGGGGGAAGGGTGGA	259491	91687	GCTCTGAGACGAGCCAAGCC
170318	2514	AGCCTCGCAGTACCCAGGCT	214905	47101	GGGGAAGGGGGGAAGGGTGG	259492	91688	TGCTCTGAGACGAGCCAAGC
170319	2515	GAGCCTCGCAGTACCCAGGC	214906	47102	GGGGGAAGGGGGGAAGGGTG	259493	91689	CTGCTCTGAGACGAGCCAAG
170320	2516	GGAGCCTCGCAGTACCCAGG	214907	47103	GGGGGGAAGGGGGGAAGGGT	259494	91690	GCTGCTCTGAGACGAGCCAA
170321	2517	AGGAGCCTCGCAGTACCCAG	214908	47104	AGGGGGGAAGGGGGGAAGGG	259495	91691	AGCTGCTCTGAGACGAGCCA
170322	2518	GAGGAGCCTCGCAGTACCCA	214909	47105	AAGGGGGGAAGGGGGGAAGG	259496	91692	CAGCTGCTCTGAGACGAGCC

170323	2519	CGAGGAGCCTCGCAGTACCC	214910	47106	GAAGGGGGGAAGGGGGGAAG	259497	91693	CCAGCTGCTCTGAGACGAGC
170324	2520	GCGAGGAGCCTCGCAGTACC	214911	47107	GGAAGGGGGGAAGGGGGGAA	259498	91694	CCCAGCTGCTCTGAGACGAG
170325	2521	TGCGAGGAGCCTCGCAGTAC	214912	47108	GGGAAGGGGGGGAAGGGGGGA	259499	91695	CCCCAGCTGCTCTGAGACGA
170326	2522	ATGCGAGGAGCCTCGCAGTA	214913	47109	AGGGAAGGGGGGGAAGGGGGG	259500	91696	GCCCCAGCTGCTCTGAGACG
170327	2523	CATGCGAGGAGCCTCGCAGT	214914	47110	GAGGGAAGGGGGGAAGGGGG	259501	91697	AGCCCCAGCTGCTCTGAGAC
170328	2524	CCATGCGAGGAGCCTCGCAG	214915	47111	GGAGGGAAGGGGGGAAGGGG	259502	91698	CAGCCCCAGCTGCTCTGAGA
170329	2525	GCCATGCGAGGAGCCTCGCA	214916	47112	AGGAGGGAAGGGGGGAAGGG	259503	91699	CCAGCCCCAGCTGCTCTGAG
170330	2526	AGCCATGCGAGGAGCCTCGC	214917	47113	AAGGAGGGAAGGGGGGAAGG	259504	91700	ACCAGCCCCAGCTGCTCTGA
170331	2527	CAGCCATGCGAGGAGCCTCG	214918	47114	GAAGGAGGGAAGGGGGGAAG	259505	91701	CACCAGCCCCAGCTGCTCTG
170332	2528	CCAGCCATGCGAGGAGCCTC	214919	47115	GGAAGGAGGGAAGGGGGGAA	259506	91702	CCACCAGCCCCAGCTGCTCT
170333	2529	CCCAGCCATGCGAGGAGCCT	214920	47116	AGGAAGGAGGGAAGGGGGGA	259507	91703	GCCACCAGCCCCAGCTGCTC
170334	2530	GCCCAGCCATGCGAGGAGCC	214921	47117	AAGGAAGGAGGGAAGGGGGG	259508	91704	GGCCACCAGCCCCAGCTGCT
170335	2531	GGCCCAGCCATGCGAGGAGC	214922	47118	GAAGGAAGGAGGGAAGGGGG	259509	91705	TGGCCACCAGCCCCAGCTGC
170336	2532	GGGCCCAGCCATGCGAGGAG	214923	47119	GGAAGGAAGGAGGGAAGGGG	259510	91706	TTGGCCACCAGCCCCAGCTG
170337	2533	CGGGCCCAGCCATGCGAGGA	214924	47120	AGGAAGGAAGGAGGGAAGGG	259511	91707	TTTGGCCACCAGCCCCAGCT
170338	2534	GCGGGCCCAGCCATGCGAGG	214925	47121	AAGGAAGGAAGGAGGGAAGG	259512	91708	CTTTGGCCACCAGCCCCAGC
170339	2535	GGCGGGCCCAGCCATGCGAG	214926	47122	GAAGGAAGGAAGGAGGGAAG	259513	91709	GCTTTGGCCACCAGCCCCAG
170340	2536	CGGCGGGCCCAGCCATGCGA	214927	47123	GGAAGGAAGGAAGGAGGGAA	259514	91710	GGCTTTGGCCACCAGCCCCA
170341	2537	GCGGCGGGCCCAGCCATGCG	214928	47124	AGGAAGGAAGGAAGGAGGGA	259515	91711	TGGCTTTGGCCACCAGCCCC
170342	2538	CGCGGCGGGCCCAGCCATGC	214929	47125	AAGGAAGGAAGGAAGGAGGG	259516	91712	GTGGCTTTGGCCACCAGCCC
170343	2539	TCGCGGCGGGCCCAGCCATG	214930	47126	GAAGGAAGGAAGGAAGGAGG	259517	91713	GGTGGCTTTGGCCACCAGCC
170344	2540	CTCGCGGCGGGCCCAGCCAT	214931	47127	GGAAGGAAGGAAGGAAGGAG	259518	91714	TGGTGGCTTTGGCCACCAGC
170345	2541	CCTCGCGGCGGGCCCAGCCA	214932	47128	AGGAAGGAAGGAAGGAAGGA	259519	91715	ATGGTGGCTTTGGCCACCAG
170346	2542	CCCTCGCGGCGGGCCCAGCC	214933	47129	CAGGAAGGAAGGAAGGAAGG	259520	91716	AATGGTGGCTTTGGCCACCA
170347	2543	CCCCTCGCGGCGGGCCCAGC	214934	47130	GCAGGAAGGAAGGAAGGAAG	259521	91717	TAATGGTGGCTTTGGCCACC
170348	2544	ACCCCTCGCGGCGGGCCCAG	214935	47131	GGCAGGAAGGAAGGAAGGAA	259522	91718	CTAATGGTGGCTTTGGCCAC
170349	2545	AACCCCTCGCGGCGGGCCCA	214936	47132	AGGCAGGAAGGAAGGAAGGA	259523	91719	ACTAATGGTGGCTTTGGCCA
170350	2546	CAACCCCTCGCGGCGGGCCC	214937	47133	CAGGCAGGAAGGAAGGAAGG	259524	91720	CACTAATGGTGGCTTTGGCC
170351	2547	GCAACCCCTCGCGGCGGGCC	214938	47134	GCAGGCAGGAAGGAAGGAAG	259525	91721	TCACTAATGGTGGCTTTGGC
170352	2548	TGCAACCCCTCGCGGCGGGC	214939	47135	GGCAGGCAGGAAGGAAGGAA	259526	91722	CTCACTAATGGTGGCTTTGG
170353	2549	CTGCAACCCCTCGCGGCGGG	214940	47136	AGGCAGGCAGGAAGGAAGGA	259527	91723	CCTCACTAATGGTGGCTTTG
170354	2550	TCTGCAACCCCTCGCGGCGG	214941	47137	AAGGCAGGCAGGAAGGAAGG	259528	91724	CCCTCACTAATGGTGGCTTT
170355	2551	CTCTGCAACCCCTCGCGGCG	214942	47138	GAAGGCAGGCAGGAAGGAAG	259529	91725	CCCCTCACTAATGGTGGCTT
170356	2552	GCTCTGCAACCCCTCGCGGC	214943	47139	GGAAGGCAGGCAGGAAGGAA	259530	91726	GCCCCTCACTAATGGTGGCT
170357	2553	CGCTCTGCAACCCCTCGCGG	214944	47140	AGGAAGGCAGGCAGGAAGGA	259531	91727	TGCCCCTCACTAATGGTGGC
170358	2554	CCGCTCTGCAACCCCTCGCG	214945	47141	AAGGAAGGCAGGCAGGAAGG	259532	91728	CTGCCCCTCACTAATGGTGG
170359	2555	GCCGCTCTGCAACCCCTCGC	214946	47142	GAAGGAAGGCAGGCAGGAAG	259533	91729	CCTGCCCCTCACTAATGGTG
170360	2556	AGCCGCTCTGCAACCCCTCG	214947	47143	GGAAGGAAGGCAGGCAGGAA	259534	91730	GCCTGCCCCTCACTAATGGT
170361	2557	GAGCCGCTCTGCAACCCCTC	214948	47144	AGGAAGGAAGGCAGGCAGGA	259535	91731	GGCCTGCCCCTCACTAATGG
170362	2558	TGAGCCGCTCTGCAACCCCT	214949	47145	AAGGAAGGAAGGCAGGCAGG	259536	91732	GGGCCTGCCCCTCACTAATG
170363	2559	CTGAGCCGCTCTGCAACCCC	214950	47146	GAAGGAAGGAAGGCAGGCAG	259537	91733	AGGGCCTGCCCCTCACTAAT
170364	2560	CCTGAGCCGCTCTGCAACCC	214951	47147	GGAAGGAAGGAAGGCAGGCA	259538	91734	CAGGGCCTGCCCCTCACTAA
170365	2561	CCCTGAGCCGCTCTGCAACC	214952	47148	AGGAAGGAAGGAAGGCAGGC	259539	91735	CCAGGGCCTGCCCCTCACTA
170366	2562	TCCCTGAGCCGCTCTGCAAC	214953	47149	AAGGAAGGAAGGAAGGCAGG	259540	91736	CCCAGGGCCTGCCCCTCACT
170367	2563	ATCCCTGAGCCGCTCTGCAA	214954	47150	GAAGGAAGGAAGGAAGGCAG	259541	91737	CCCCAGGGCCTGCCCCTCAC
170368	2564	GATCCCTGAGCCGCTCTGCA	214955	47151	GGAAGGAAGGAAGGAAGGCA	259542	91738	CCCCCAGGGCCTGCCCCTCA
170369	2565	CGATCCCTGAGCCGCTCTGC	214956	47152	AGGAAGGAAGGAAGGAAGGC	259543	91739	ACCCCCAGGGCCTGCCCCTC
170370	2566	TCGATCCCTGAGCCGCTCTG	214957	47153	AAGGAAGGAAGGAAGGAAGG	259544	91740	TACCCCCAGGGCCTGCCCCT
170371	2567	ATCGATCCCTGAGCCGCTCT	214958	47154	GAAGGAAGGAAGGAAGGAAG	259545	91741	GTACCCCCAGGGCCTGCCCC
170372	2568	AATCGATCCCTGAGCCGCTC	214959	47155	GGAAGGAAGGAAGGAAGGAA	259546	91742	TGTACCCCCAGGGCCTGCCC
170373	2569	GAATCGATCCCTGAGCCGCT	214960	47156	AGGAAGGAAGGAAGGAAGGA	259547	91743	TTGTACCCCCAGGGCCTGCC
170374	2570	TGAATCGATCCCTGAGCCGC	214961	47157	AAGGAAGGAAGGAAGGAAGG	259548	91744	GTTGTACCCCCAGGGCCTGC
170375	2571	TTGAATCGATCCCTGAGCCG	214962	47158	GAAGGAAGGAAGGAAGGAAG	259549	91745	GGTTGTACCCCCAGGGCCTG
170376	2572	CTTGAATCGATCCCTGAGCC	214963	47159	GGAAGGAAGGAAGGAAGGAA	259550	91746	TGGTTGTACCCCCAGGGCCT
170377	2573	GCTTGAATCGATCCCTGAGC	214964	47160	AGGAAGGAAGGAAGGAAGGA	259551	91747	CTGGTTGTACCCCCAGGGCC
170378	2574	TGCTTGAATCGATCCCTGAG	214965	47161	AAGGAAGGAAGGAAGGAAGG	259552	91748	GCTGGTTGTACCCCCAGGGC
170379	2575	ATGCTTGAATCGATCCCTGA	214966	47162	GAAGGAAGGAAGGAAGGAAG	259553	91749	TGCTGGTTGTACCCCCAGGG
170380	2576	GATGCTTGAATCGATCCCTG	214967	47163	GGAAGGAAGGAAGGAAGGAA	259554	91750	TTGCTGGTTGTACCCCCAGG
170381	2577	CGATGCTTGAATCGATCCCT	214968	47164	AGGAAGGAAGGAAGGAAGGA	259555	91751	GTTGCTGGTTGTACCCCCAG
170382	2578	ACGATGCTTGAATCGATCCC	214969	47165	AAGGAAGGAAGGAAGGAAGG	259556	91752	AGTTGCTGGTTGTACCCCCA
170383	2579	GACGATGCTTGAATCGATCC	214970	47166	GAAGGAAGGAAGGAAGGAAG	259557	91753	TAGTTGCTGGTTGTACCCCC
170384	2580	AGACGATGCTTGAATCGATC	214971	47167	GGAAGGAAGGAAGGAAGGAA	259558	91754	CTAGTTGCTGGTTGTACCCC
170385	2581	GAGACGATGCTTGAATCGAT	214972	47168	AGGAAGGAAGGAAGGAAGGA	259559	91755	CCTAGTTGCTGGTTGTACCC
170386	2582	AGAGACGATGCTTGAATCGA	214973	47169	AAGGAAGGAAGGAAGGAAGG	259560	91756	CCCTAGTTGCTGGTTGTACC
170387	2583	GAGAGACGATGCTTGAATCG	214974	47170	GAAGGAAGGAAGGAAGGAAG	259561	91757	CCCCTAGTTGCTGGTTGTAC
170388	2584	GGAGAGACGATGCTTGAATC	214975	47171	GGAAGGAAGGAAGGAAGGAA	259562	91758	TCCCCTAGTTGCTGGTTGTA
170389	2585	AGGAGAGACGATGCTTGAAT	214976	47172	AGGAAGGAAGGAAGGAAGGA	259563	91759	GTCCCCTAGTTGCTGGTTGT
170390	2586	GAGGAGAGACGATGCTTGAA	214977	47173	AAGGAAGGAAGGAAGGAAGG	259564	91760	TGTCCCCTAGTTGCTGGTTG
170391	2587	GGAGGAGAGACGATGCTTGA	214978	47174	GAAGGAAGGAAGGAAGGAAG	259565	91761	TTGTCCCCTAGTTGCTGGTT
170392	2588	GGGAGGAGAGACGATGCTTG	214979	47175	GGAAGGAAGGAAGGAAGGAA	259566	91762	TTTGTCCCCTAGTTGCTGGT
170393	2589	AGGGAGGAGAGACGATGCTT	214980	47176	AGGAAGGAAGGAAGGAAGGA	259567	91763	CTTTGTCCCCTAGTTGCTGG
170394	2590	GAGGGAGGAGAGACGATGCT	214981	47177	AAGGAAGGAAGGAAGGAAGG	259568	91764	TCTTTGTCCCCTAGTTGCTG

170395	2591	CGAGGGAGGAGAGACGATGC	214982	47178	GAAGGAAGGAAGGAAGGAAG	259569	91765	GTCTTTGTCCCCTAGTTGCT
170396	2592	GCGAGGGAGGAGAGACGATG	214983	47179	GGAAGGAAGGAAGGAAGGAA	259570	91766	TGTCTTTGTCCCCTAGTTGC
170397	2593	GGCGAGGGAGGAGAGACGAT	214984	47180	AGGAAGGAAGGAAGGAAGGA	259571	91767	TTGTCTTTGTCCCCTAGTTG
170398	2594	GGGCGAGGGAGGAGAGACGA	214985	47181	AAGGAAGGAAGGAAGGAAGG	259572	91768	GTTGTCTTTGTCCCCTAGTT
170399	2595	GGGGCGAGGGAGGAGAGACG	214986	47182	GAAGGAAGGAAGGAAGGAAG	259573	91769	GGTTGTCTTTGTCCCCTAGT
170400	2596	GGGGGCGAGGGAGGAGAGAC	214987	47183	GGAAGGAAGGAAGGAAGGAA	259574	91770	GGGTTGTCTTTGTCCCCTAG
170401	2597	TGGGGGCGAGGGAGGAGAGA	214988	47184	AGGAAGGAAGGAAGGAAGGA	259575	91771	AGGGTTGTCTTTGTCCCCTA
170402	2598	CTGGGGGCGAGGGAGGAGAG	214989	47185	CAGGAAGGAAGGAAGGAAGG	259576	91772	CAGGGTTGTCTTTGTCCCCT
170403	2599	TCTGGGGGCGAGGGAGGAGA	214990	47186	CCAGGAAGGAAGGAAGGAAG	259577	91773	GCAGGGTTGTCTTTGTCCCC
170404	2600	GTCTGGGGGCGAGGGAGGAG	214991	47187	ACCAGGAAGGAAGGAAGGAA	259578	91774	GGCAGGGTTGTCTTTGTCCC
170405	2601	TGTCTGGGGGCGAGGGAGGA	214992	47188	TACCAGGAAGGAAGGAAGGA	259579	91775	TGGCAGGGTTGTCTTTGTCC
170406	2602	CTGTCTGGGGGCGAGGGAGG	214993	47189	ATACCAGGAAGGAAGGAAGG	259580	91776	CTGGCAGGGTTGTCTTTGTC
170407	2603	TCTGTCTGGGGGCGAGGGAG	214994	47190	CATACCAGGAAGGAAGGAAG	259581	91777	GCTGGCAGGGTTGTCTTTGT
170408	2604	CTCTGTCTGGGGGCGAGGGA	214995	47191	ACATACCAGGAAGGAAGGAA	259582	91778	GGCTGGCAGGGTTGTCTTTG
170409	2605	GCTCTGTCTGGGGGCGAGGG	214996	47192	CACATACCAGGAAGGAAGGA	259583	91779	AGGCTGGCAGGGTTGTCTTT
170410	2606	AGCTCTGTCTGGGGGCGAGG	214997	47193	TCACATACCAGGAAGGAAGG	259584	91780	GAGGCTGGCAGGGTTGTCTT
170411	2607	CAGCTCTGTCTGGGGGCGAG	214998	47194	GTCACATACCAGGAAGGAAG	259585	91781	AGAGGCTGGCAGGGTTGTCT
170412	2608	CCAGCTCTGTCTGGGGGCGA	214999	47195	AGTCACATACCAGGAAGGAA	259586	91782	GAGAGGCTGGCAGGGTTGTC
170413	2609	CCCAGCTCTGTCTGGGGGCG	215000	47196	TAGTCACATACCAGGAAGGA	259587	91783	GGAGAGGCTGGCAGGGTTGT
170414	2610	GCCCAGCTCTGTCTGGGGGC	215001	47197	TTAGTCACATACCAGGAAGG	259588	91784	AGGAGAGGCTGGCAGGGTTG
170415	2611	CGCCCAGCTCTGTCTGGGGG	215002	47198	ATTAGTCACATACCAGGAAG	259589	91785	TAGGAGAGGCTGGCAGGGTT
170416	2612	GCGCCCAGCTCTGTCTGGGG	215003	47199	AATTAGTCACATACCAGGAA	259590	91786	ATAGGAGAGGCTGGCAGGGT
170417	2613	CGCGCCCAGCTCTGTCTGGG	215004	47200	AAATTAGTCACATACCAGGA	259591	91787	AATAGGAGAGGCTGGCAGGG
170418	2614	CCGCGCCCAGCTCTGTCTGG	215005	47201	GAAATTAGTCACATACCAGG	259592	91788	GAATAGGAGAGGCTGGCAGG
170419	2615	CCCGCGCCCAGCTCTGTCTG	215006	47202	AGAAATTAGTCACATACCAG	259593	91789	AGAATAGGAGAGGCTGGCAG
170420	2616	CCCCGCGCCCAGCTCTGTCT	215007	47203	CAGAAATTAGTCACATACCA	259594	91790	CAGAATAGGAGAGGCTGGCA
170421	2617	ACCCCGCGCCCAGCTCTGTC	215008	47204	ACAGAAATTAGTCACATACC	259595	91791	CCAGAATAGGAGAGGCTGGC
170422	2618	AACCCCGCGCCCAGCTCTGT	215009	47205	AACAGAAATTAGTCACATAC	259596	91792	TCCAGAATAGGAGAGGCTGG
170423	2619	GAACCCCGCGCCCAGCTCTG	215010	47206	AAACAGAAATTAGTCACATA	259597	91793	CTCCAGAATAGGAGAGGCTG
170424	2620	GGAACCCCGCGCCCAGCTCT	215011	47207	GAAACAGAAATTAGTCACAT	259598	91794	CCTCCAGAATAGGAGAGGCT
170425	2621	GGGAACCCCGCGCCCAGCTC	215012	47208	TGAAACAGAAATTAGTCACA	259599	91795	GCCTCCAGAATAGGAGAGGC
170426	2622	GGGGAACCCCGCGCCCAGCT	215013	47209	CTGAAACAGAAATTAGTCAC	259600	91796	CGCCTCCAGAATAGGAGAGG
170427	2623	AGGGGAACCCCGCGCCCAGC	215014	47210	CCTGAAACAGAAATTAGTCA	259601	91797	ACGCCTCCAGAATAGGAGAG
170428	2624	AAGGGGAACCCCGCGCCCAG	215015	47211	TCCTGAAACAGAAATTAGTC	259602	91798	CACGCCTCCAGAATAGGAGA
170429	2625	GAAGGGGAACCCCGCGCCCA	215016	47212	GTCCTGAAACAGAAATTAGT	259603	91799	ACACGCCTCCAGAATAGGAG
170430	2626	GGAAGGGGAACCCCGCGCCC	215017	47213	TGTCCTGAAACAGAAATTAG	259604	91800	CACACGCCTCCAGAATAGGA
170431	2627	TGGAAGGGGAACCCCGCGCC	215018	47214	ATGTCCTGAAACAGAAATTA	259605	91801	TCACACGCCTCCAGAATAGG
170432	2628	CTGGAAGGGGAACCCCGCGC	215019	47215	TATGTCCTGAAACAGAAATT	259606	91802	GTCACACGCCTCCAGAATAG
170433	2629	TCTGGAAGGGGAACCCCGCG	215020	47216	TTATGTCCTGAAACAGAAAT	259607	91803	GGTCACACGCCTCCAGAATA
170434	2630	ATCTGGAAGGGGAACCCCGC	215021	47217	TTTATGTCCTGAAACAGAAA	259608	91804	TGGTCACACGCCTCCAGAAT
170435	2631	CATCTGGAAGGGGAACCCCG	215022	47218	ATTTATGTCCTGAAACAGAA	259609	91805	CTGGTCACACGCCTCCAGAA
170436	2632	CCATCTGGAAGGGGAACCCC	215023	47219	CATTTATGTCCTGAAACAGA	259610	91806	TCTGGTCACACGCCTCCAGA
170437	2633	TCCATCTGGAAGGGGAACCC	215024	47220	ACATTTATGTCCTGAAACAG	259611	91807	TTCTGGTCACACGCCTCCAG
170438	2634	CTCCATCTGGAAGGGGAACC	215025	47221	AACATTTATGTCCTGAAACA	259612	91808	TTTCTGGTCACACGCCTCCA
170439	2635	GCTCCATCTGGAAGGGGAAC	215026	47222	CAACATTTATGTCCTGAAAC	259613	91809	ATTTCTGGTCACACGCCTCC
170440	2636	CGCTCCATCTGGAAGGGGAA	215027	47223	ACAACATTTATGTCCTGAAA	259614	91810	CATTTCTGGTCACACGCCTC
170441	2637	TCGCTCCATCTGGAAGGGGA	215028	47224	GACAACATTTATGTCCTGAA	259615	91811	CCATTTCTGGTCACACGCCT
170442	2638	CTCGCTCCATCTGGAAGGGG	215029	47225	GGACAACATTTATGTCCTGA	259616	91812	TCCATTTCTGGTCACACGCC
170443	2639	CCTCGCTCCATCTGGAAGGG	215030	47226	TGGACAACATTTATGTCCTG	259617	91813	CTCCATTTCTGGTCACACGC
170444	2640	CCCTCGCTCCATCTGGAAGG	215031	47227	CTGGACAACATTTATGTCCT	259618	91814	TCTCCATTTCTGGTCACACG
170445	2641	ACCCTCGCTCCATCTGGAAG	215032	47228	CCTGGACAACATTTATGTCC	259619	91815	ATCTCCATTTCTGGTCACAC
170446	2642	GACCCTCGCTCCATCTGGAA	215033	47229	GCCTGGACAACATTTATGTC	259620	91816	CATCTCCATTTCTGGTCACA
170447	2643	AGACCCTCGCTCCATCTGGA	215034	47230	AGCCTGGACAACATTTATGT	259621	91817	CCATCTCCATTTCTGGTCAC
170448	2644	GAGACCCTCGCTCCATCTGG	215035	47231	CAGCCTGGACAACATTTATG	259622	91818	CCCATCTCCATTTCTGGTCA
170449	2645	CGAGACCCTCGCTCCATCTG	215036	47232	ACAGCCTGGACAACATTTAT	259623	91819	ACCCATCTCCATTTCTGGTC
170450	2646	CCGAGACCCTCGCTCCATCT	215037	47233	AACAGCCTGGACAACATTTA	259624	91820	AACCCATCTCCATTTCTGGT
170451	2647	CCCGAGACCCTCGCTCCATC	215038	47234	GAACAGCCTGGACAACATTT	259625	91821	CAACCCATCTCCATTTCTGG
170452	2648	CCCCGAGACCCTCGCTCCAT	215039	47235	AGAACAGCCTGGACAACATT	259626	91822	CCAACCCATCTCCATTTCTG
170453	2649	ACCCCGAGACCCTCGCTCCA	215040	47236	AAGAACAGCCTGGACAACAT	259627	91823	ACCAACCCATCTCCATTTCT
170454	2650	CACCCCGAGACCCTCGCTCC	215041	47237	AAAGAACAGCCTGGACAACA	259628	91824	GACCAACCCATCTCCATTTC
170455	2651	CCACCCCGAGACCCTCGCTC	215042	47238	CAAAGAACAGCCTGGACAAC	259629	91825	TGACCAACCCATCTCCATTT
170456	2652	GCCACCCCGAGACCCTCGCT	215043	47239	CCAAAGAACAGCCTGGACAA	259630	91826	CTGACCAACCCATCTCCATT
170457	2653	GGCCACCCCGAGACCCTCGC	215044	47240	ACCAAAGAACAGCCTGGACA	259631	91827	GCTGACCAACCCATCTCCAT
170458	2654	GGGCCACCCCGAGACCCTCG	215045	47241	GACCAAAGAACAGCCTGGAC	259632	91828	TGCTGACCAACCCATCTCCA
170459	2655	GGGGCCACCCCGAGACCCTC	215046	47242	AGACCAAAGAACAGCCTGGA	259633	91829	ATGCTGACCAACCCATCTCC
170460	2656	CGGGGCCACCCCGAGACCCT	215047	47243	AAGACCAAAGAACAGCCTGG	259634	91830	TATGCTGACCAACCCATCTC
170461	2657	CCGGGGCCACCCCGAGACCC	215048	47244	AAAGACCAAAGAACAGCCTG	259635	91831	TTATGCTGACCAACCCATCT
170462	2658	TCCGGGGCCACCCCGAGACC	215049	47245	GAAAGACCAAAGAACAGCCT	259636	91832	CTTATGCTGACCAACCCATC
170463	2659	TTCCGGGGCCACCCCGAGAC	215050	47246	AGAAAGACCAAAGAACAGCC	259637	91833	TCTTATGCTGACCAACCCAT
170464	2660	TTTCCGGGGCCACCCCGAGA	215051	47247	CAGAAAGACCAAAGAACAGC	259638	91834	ATCTTATGCTGACCAACCCA
170465	2661	TTTTCCGGGGCCACCCCGAG	215052	47248	ACAGAAAGACCAAAGAACAG	259639	91835	CATCTTATGCTGACCAACCC
170466	2662	CTTTTCCGGGGCCACCCCGA	215053	47249	AACAGAAAGACCAAAGAACA	259640	91836	CCATCTTATGCTGACCAACC

170467	2663	CCTTTTCCGGGGCCACCCCG	215054	47250	CAACAGAAAGACCAAAGAAC	259641	91837	GCCATCTTATGCTGACCAAC
170468	2664	CCCTTTTCCGGGGCCACCCC	215055	47251	CCAACAGAAAGACCAAAGAA	259642	91838	GGCCATCTTATGCTGACCAA
170469	2665	CCCCTTTTCCGGGGCCACCC	215056	47252	TCCAACAGAAAGACCAAAGA	259643	91839	TGGCCATCTTATGCTGACCA
170470	2666	TCCCCTTTTCCGGGGCCACC	215057	47253	ATCCAACAGAAAGACCAAAG	259644	91840	CTGGCCATCTTATGCTGACC
170471	2667	CTCCCCTTTTCCGGGGCCAC	215058	47254	TATCCAACAGAAAGACCAAA	259645	91841	CCTGGCCATCTTATGCTGAC
170472	2668	GCTCCCCTTTTCCGGGGCCA	215059	47255	TTATCCAACAGAAAGACCAA	259646	91842	TCCTGGCCATCTTATGCTGA
170473	2669	GGCTCCCCTTTTCCGGGGCC	215060	47256	ATTATCCAACAGAAAGACCA	259647	91843	TTCCTGGCCATCTTATGCTG
170474	2670	GGGCTCCCCTTTTCCGGGGC	215061	47257	CATTATCCAACAGAAAGACC	259648	91844	CTTCCTGGCCATCTTATGCT
170475	2671	CGGGCTCCCCTTTTCCGGGG	215062	47258	CCATTATCCAACAGAAAGAC	259649	91845	CCTTCCTGGCCATCTTATGC
170476	2672	GCGGGCTCCCCTTTTCCGGG	215063	47259	TCCATTATCCAACAGAAAGA	259650	91846	ACCTTCCTGGCCATCTTATG
170477	2673	CGCGGGCTCCCCTTTTCCGG	215064	47260	GTCCATTATCCAACAGAAAG	259651	91847	CACCTTCCTGGCCATCTTAT
170478	2674	CCGCGGGCTCCCCTTTTCCG	215065	47261	TGTCCATTATCCAACAGAAA	259652	91848	CCACCTTCCTGGCCATCTTA
170479	2675	GCCGCGGGCTCCCCTTTTCC	215066	47262	ATGTCCATTATCCAACAGAA	259653	91849	TCCACCTTCCTGGCCATCTT
170480	2676	GGCCGCGGGCTCCCCTTTTC	215067	47263	AATGTCCATTATCCAACAGA	259654	91850	TTCCACCTTCCTGGCCATCT
170481	2677	TGGCCGCGGGCTCCCCTTTT	215068	47264	AAATGTCCATTATCCAACAG	259655	91851	TTTCCACCTTCCTGGCCATC
170482	2678	GTGGCCGCGGGCTCCCCTTT	215069	47265	CAAATGTCCATTATCCAACA	259656	91852	ATTTCCACCTTCCTGGCCAT
170483	2679	CGTGGCCGCGGGCTCCCCTT	215070	47266	CCAAATGTCCATTATCCAAC	259657	91853	GATTTCCACCTTCCTGGCCA
170484	2680	CCGTGGCCGCGGGCTCCCCT	215071	47267	GCCAAATGTCCATTATCCAA	259658	91854	TGATTTCCACCTTCCTGGCC
170485	2681	GCCGTGGCCGCGGGCTCCCC	215072	47268	TGCCAAATGTCCATTATCCA	259659	91855	CTGATTTCCACCTTCCTGGC
170486	2682	AGCCGTGGCCGCGGGCTCCC	215073	47269	ATGCCAAATGTCCATTATCC	259660	91856	CCTGATTTCCACCTTCCTGG
170487	2683	TAGCCGTGGCCGCGGGCTCC	215074	47270	AATGCCAAATGTCCATTATC	259661	91857	TCCTGATTTCCACCTTCCTG
170488	2684	GTAGCCGTGGCCGCGGGCTC	215075	47271	CAATGCCAAATGTCCATTAT	259662	91858	GTCCTGATTTCCACCTTCCT
170489	2685	CGTAGCCGTGGCCGCGGGCT	215076	47272	TCAATGCCAAATGTCCATTA	259663	91859	AGTCCTGATTTCCACCTTCC
170490	2686	ACGTAGCCGTGGCCGCGGGC	215077	47273	CTCAATGCCAAATGTCCATT	259664	91860	CAGTCCTGATTTCCACCTTC
170491	2687	TACGTAGCCGTGGCCGCGGG	215078	47274	TCTCAATGCCAAATGTCCAT	259665	91861	GCAGTCCTGATTTCCACCTT
170492	2688	ATACGTAGCCGTGGCCGCGG	215079	47275	CTCTCAATGCCAAATGTCCA	259666	91862	AGCAGTCCTGATTTCCACCT
170493	2689	AATACGTAGCCGTGGCCGCG	215080	47276	TCTCTCAATGCCAAATGTCC	259667	91863	CAGCAGTCCTGATTTCCACC
170494	2690	CAATACGTAGCCGTGGCCGC	215081	47277	CTCTCTCAATGCCAAATGTC	259668	91864	CCAGCAGTCCTGATTTCCAC
170495	2691	GCAATACGTAGCCGTGGCCG	215082	47278	CCTCTCTCAATGCCAAATGT	259669	91865	GCCAGCAGTCCTGATTTCCA
170496	2692	GGCAATACGTAGCCGTGGCC	215083	47279	GCCTCTCTCAATGCCAAATG	259670	91866	TGCCAGCAGTCCTGATTTCC
170497	2693	TGGCAATACGTAGCCGTGGC	215084	47280	AGCCTCTCTCAATGCCAAAT	259671	91867	TTGCCAGCAGTCCTGATTTC
170498	2694	ATGGCAATACGTAGCCGTGG	215085	47281	CAGCCTCTCTCAATGCCAAA	259672	91868	ATTGCCAGCAGTCCTGATTT
170499	2695	GATGGCAATACGTAGCCGTG	215086	47282	GCAGCCTCTCTCAATGCCAA	259673	91869	GATTGCCAGCAGTCCTGATT
170500	2696	AGATGGCAATACGTAGCCGT	215087	47283	AGCAGCCTCTCTCAATGCCA	259674	91870	AGATTGCCAGCAGTCCTGAT
170501	2697	GAGATGGCAATACGTAGCCG	215088	47284	AAGCAGCCTCTCTCAATGCC	259675	91871	TAGATTGCCAGCAGTCCTGA
170502	2698	CGAGATGGCAATACGTAGCC	215089	47285	AAAGCAGCCTCTCTCAATGC	259676	91872	CTAGATTGCCAGCAGTCCTG
170503	2699	GCGAGATGGCAATACGTAGC	215090	47286	AAAAGCAGCCTCTCTCAATG	259677	91873	GCTAGATTGCCAGCAGTCCT
170504	2700	CGCGAGATGGCAATACGTAG	215091	47287	AAAAAGCAGCCTCTCTCAAT	259678	91874	GGCTAGATTGCCAGCAGTCC
170505	2701	TCGCGAGATGGCAATACGTA	215092	47288	GAAAAAGCAGCCTCTCTCAA	259679	91875	TGGCTAGATTGCCAGCAGTC
170506	2702	CTCGCGAGATGGCAATACGT	215093	47289	AGAAAAAGCAGCCTCTCTCA	259680	91876	GTGGCTAGATTGCCAGCAGT
170507	2703	GCTCGCGAGATGGCAATACG	215094	47290	CAGAAAAAGCAGCCTCTCTC	259681	91877	TGTGGCTAGATTGCCAGCAG
170508	2704	TGCTCGCGAGATGGCAATAC	215095	47291	TCAGAAAAAGCAGCCTCTCT	259682	91878	ATGTGGCTAGATTGCCAGCA
170509	2705	CTGCTCGCGAGATGGCAATA	215096	47292	TTCAGAAAAAGCAGCCTCTC	259683	91879	CATGTGGCTAGATTGCCAGC
170510	2706	TCTGCTCGCGAGATGGCAAT	215097	47293	TTTCAGAAAAAGCAGCCTCT	259684	91880	CCATGTGGCTAGATTGCCAG
170511	2707	CTCTGCTCGCGAGATGGCAA	215098	47294	ATTTCAGAAAAAGCAGCCTC	259685	91881	CCCATGTGGCTAGATTGCCA
170512	2708	TCTCTGCTCGCGAGATGGCA	215099	47295	GATTTCAGAAAAAGCAGCCT	259686	91882	GCCCATGTGGCTAGATTGCC
170513	2709	ATCTCTGCTCGCGAGATGGC	215100	47296	TGATTTCAGAAAAAGCAGCC	259687	91883	TGCCCATGTGGCTAGATTGC
170514	2710	CATCTCTGCTCGCGAGATGG	215101	47297	ATGATTTCAGAAAAAGCAGC	259688	91884	CTGCCCATGTGGCTAGATTG
170515	2711	ACATCTCTGCTCGCGAGATG	215102	47298	CATGATTTCAGAAAAAGCAG	259689	91885	CCTGCCCATGTGGCTAGATT
170516	2712	GACATCTCTGCTCGCGAGAT	215103	47299	ACATGATTTCAGAAAAAGCA	259690	91886	CCCTGCCCATGTGGCTAGAT
170517	2713	TGACATCTCTGCTCGCGAGA	215104	47300	AACATGATTTCAGAAAAAGC	259691	91887	CCCCTGCCCATGTGGCTAGA
170518	2714	GTGACATCTCTGCTCGCGAG	215105	47301	GAACATGATTTCAGAAAAAG	259692	91888	TCCCCTGCCCATGTGGCTAG
170519	2715	GGTGACATCTCTGCTCGCGA	215106	47302	AGAACATGATTTCAGAAAAA	259693	91889	CTCCCCTGCCCATGTGGCTA
170520	2716	AGGTGACATCTCTGCTCGCG	215107	47303	AAGAACATGATTTCAGAAAA	259694	91890	GCTCCCCTGCCCATGTGGCT
170521	2717	GAGGTGACATCTCTGCTCGC	215108	47304	CAAGAACATGATTTCAGAAA	259695	91891	GGCTCCCCTGCCCATGTGGC
170522	2718	GGAGGTGACATCTCTGCTCG	215109	47305	CCAAGAACATGATTTCAGAA	259696	91892	CGGCTCCCCTGCCCATGTGG
170523	2719	AGGAGGTGACATCTCTGCTC	215110	47306	CCCAAGAACATGATTTCAGA	259697	91893	CCGGCTCCCCTGCCCATGTG
170524	2720	CAGGAGGTGACATCTCTGCT	215111	47307	CCCCAAGAACATGATTTCAG	259698	91894	CCCGGCTCCCCTGCCCATGT
170525	2721	GCAGGAGGTGACATCTCTGC	215112	47308	GCCCCAAGAACATGATTTCA	259699	91895	ACCCGGCTCCCCTGCCCATG
170526	2722	GGCAGGAGGTGACATCTCTG	215113	47309	GGCCCCAAGAACATGATTTC	259700	91896	CACCCGGCTCCCCTGCCCAT
170527	2723	AGGCAGGAGGTGACATCTCT	215114	47310	GGGCCCCAAGAACATGATTT	259701	91897	CCACCCGGCTCCCCTGCCCA
170528	2724	AAGGCAGGAGGTGACATCTC	215115	47311	TGGGCCCCAAGAACATGATT	259702	91898	ACCACCCGGCTCCCCTGCCC
170529	2725	AAAGGCAGGAGGTGACATCT	215116	47312	CTGGGCCCCAAGAACATGAT	259703	91899	AACCACCCGGCTCCCCTGCC
170530	2726	CAAAGGCAGGAGGTGACATC	215117	47313	TCTGGGCCCCAAGAACATGA	259704	91900	GAACCACCCGGCTCCCCTGC
170531	2727	CCAAAGGCAGGAGGTGACAT	215118	47314	TTCTGGGCCCCAAGAACATG	259705	91901	GGAACCACCCGGCTCCCCTG
170532	2728	TCCAAAGGCAGGAGGTGACA	215119	47315	GTTCTGGGCCCCAAGAACAT	259706	91902	TGGAACCACCCGGCTCCCCT
170533	2729	CTCCAAAGGCAGGAGGTGAC	215120	47316	GGTTCTGGGCCCCAAGAACA	259707	91903	CTGGAACCACCCGGCTCCCC
170534	2730	CCTCCAAAGGCAGGAGGTGA	215121	47317	AGGTTCTGGGCCCCAAGAAC	259708	91904	CCTGGAACCACCCGGCTCCC
170535	2731	TCCTCCAAAGGCAGGAGGTG	215122	47318	TAGGTTCTGGGCCCCAAGAA	259709	91905	GCCTGGAACCACCCGGCTCC
170536	2732	TTCCTCCAAAGGCAGGAGGT	215123	47319	CTAGGTTCTGGGCCCCAAGA	259710	91906	TGCCTGGAACCACCCGGCTC
170537	2733	TTTCCTCCAAAGGCAGGAGG	215124	47320	CCTAGGTTCTGGGCCCCAAG	259711	91907	CTGCCTGGAACCACCCGGCT
170538	2734	CTTTCCTCCAAAGGCAGGAG	215125	47321	ACCTAGGTTCTGGGCCCCAA	259712	91908	ACTGCCTGGAACCACCCGGC

170539	2735	CCTTTCCTCCAAAGGCAGGA	215126	47322	CACCTAGGTTCTGGGCCCCA	259713	91909	AACTGCCTGGAACCACCCGG
170540	2736	CCCTTTCCTCCAAAGGCAGG	215127	47323	ACACCTAGGTTCTGGGCCCC	259714	91910	AAACTGCCTGGAACCACCCG
170541	2737	TCCCTTTCCTCCAAAGGCAG	215128	47324	CACACCTAGGTTCTGGGCCC	259715	91911	GAAACTGCCTGGAACCACCC
170542	2738	CTCCCTTTCCTCCAAAGGCA	215129	47325	ACACACCTAGGTTCTGGGCC	259716	91912	GGAAACTGCCTGGAACCACC
170543	2739	GCTCCCTTTCCTCCAAAGGC	215130	47326	CACACACCTAGGTTCTGGGC	259717	91913	TGGAAACTGCCTGGAACCAC
170544	2740	GGCTCCCTTTCCTCCAAAGG	215131	47327	GCACACACCTAGGTTCTGGG	259718	91914	TTGGAAACTGCCTGGAACCA
170545	2741	GGGCTCCCTTTCCTCCAAAG	215132	47328	AGCACACACCTAGGTTCTGG	259719	91915	CTTGGAAACTGCCTGGAACC
170546	2742	CGGGCTCCCTTTCCTCCAAA	215133	47329	AAGCACACACCTAGGTTCTG	259720	91916	CCTTGGAAACTGCCTGGAAC
170547	2743	CCGGGCTCCCTTTCCTCCAA	215134	47330	GAAGCACACACCTAGGTTCT	259721	91917	GCCTTGGAAACTGCCTGGAA
170548	2744	ACCGGGCTCCCTTTCCTCCA	215135	47331	AGAAGCACACACCTAGGTTC	259722	91918	GGCCTTGGAAACTGCCTGGA
170549	2745	CACCGGGCTCCCTTTCCTCC	215136	47332	CAGAAGCACACACCTAGGTT	259723	91919	TGGCCTTGGAAACTGCCTGG
170550	2746	CCACCGGGCTCCCTTTCCTC	215137	47333	TCAGAAGCACACACCTAGGT	259724	91920	TTGGCCTTGGAAACTGCCTG
170551	2747	CCCACCGGGCTCCCTTTCCT	215138	47334	GTCAGAAGCACACACCTAGG	259725	91921	CTTGGCCTTGGAAACTGCCT
170552	2748	CCCCACCGGGCTCCCTTTCC	215139	47335	AGTCAGAAGCACACACCTAG	259726	91922	TCTTGGCCTTGGAAACTGCC
170553	2749	TCCCCACCGGGCTCCCTTTC	215140	47336	AAGTCAGAAGCACACACCTA	259727	91923	CTCTTGGCCTTGGAAACTGC
170554	2750	ATCCCCACCGGGCTCCCTTT	215141	47337	AAAGTCAGAAGCACACACCT	259728	91924	CCTCTTGGCCTTGGAAACTG
170555	2751	CATCCCCACCGGGCTCCCTT	215142	47338	CAAAGTCAGAAGCACACACC	259729	91925	CCCTCTTGGCCTTGGAAACT
170556	2752	TCATCCCCACCGGGCTCCCT	215143	47339	ACAAAGTCAGAAGCACACAC	259730	91926	ACCCTCTTGGCCTTGGAAAC
170557	2753	CTCATCCCCACCGGGCTCCC	215144	47340	AACAAAGTCAGAAGCACACA	259731	91927	CACCCTCTTGGCCTTGGAAA
170558	2754	GCTCATCCCCACCGGGCTCC	215145	47341	AAACAAAGTCAGAAGCACAC	259732	91928	TCACCCTCTTGGCCTTGGAA
170559	2755	CGCTCATCCCCACCGGGCTC	215146	47342	AAAACAAAGTCAGAAGCACA	259733	91929	CTCACCCTCTTGGCCTTGGA
170560	2756	GCGCTCATCCCCACCGGGCT	215147	47343	GAAAACAAAGTCAGAAGCAC	259734	91930	GCTCACCCTCTTGGCCTTGG
170561	2757	TGCGCTCATCCCCACCGGGC	215148	47344	AGAAAACAAAGTCAGAAGCA	259735	91931	TGCTCACCCTCTTGGCCTTG
170562	2758	ATGCGCTCATCCCCACCGGG	215149	47345	AAGAAAACAAAGTCAGAAGC	259736	91932	CTGCTCACCCTCTTGGCCTT
170563	2759	AATGCGCTCATCCCCACCGG	215150	47346	GAAGAAAACAAAGTCAGAAG	259737	91933	CCTGCTCACCCTCTTGGCCT
170564	2760	AAATGCGCTCATCCCCACCG	215151	47347	GGAAGAAAACAAAGTCAGAA	259738	91934	GCCTGCTCACCCTCTTGGCC
170565	2761	TAAATGCGCTCATCCCCACC	215152	47348	AGGAAGAAAACAAAGTCAGA	259739	91935	TGCCTGCTCACCCTCTTGGC
170566	2762	CTAAATGCGCTCATCCCCAC	215153	47349	CAGGAAGAAAACAAAGTCAG	259740	91936	GTGCCTGCTCACCCTCTTGG
170567	2763	GCTAAATGCGCTCATCCCCA	215154	47350	TCAGGAAGAAAACAAAGTCA	259741	91937	GGTGCCTGCTCACCCTCTTG
170568	2764	GGCTAAATGCGCTCATCCCC	215155	47351	ATCAGGAAGAAAACAAAGTC	259742	91938	AGGTGCCTGCTCACCCTCTT
170569	2765	GGGCTAAATGCGCTCATCCC	215156	47352	GATCAGGAAGAAAACAAAGT	259743	91939	GAGGTGCCTGCTCACCCTCT
170570	2766	TGGGCTAAATGCGCTCATCC	215157	47353	GGATCAGGAAGAAAACAAAG	259744	91940	TGAGGTGCCTGCTCACCCTC
170571	2767	TTGGGCTAAATGCGCTCATC	215158	47354	TGGATCAGGAAGAAAACAAA	259745	91941	GTGAGGTGCCTGCTCACCCT
170572	2768	ATTGGGCTAAATGCGCTCAT	215159	47355	TTGGATCAGGAAGAAAACAA	259746	91942	TGTGAGGTGCCTGCTCACCC
170573	2769	CATTGGGCTAAATGCGCTCA	215160	47356	TTTGGATCAGGAAGAAAACA	259747	91943	CTGTGAGGTGCCTGCTCACC
170574	2770	GCATTGGGCTAAATGCGCTC	215161	47357	ATTTGGATCAGGAAGAAAAC	259748	91944	CCTGTGAGGTGCCTGCTCAC
170575	2771	AGCATTGGGCTAAATGCGCT	215162	47358	AATTTGGATCAGGAAGAAAA	259749	91945	CCCTGTGAGGTGCCTGCTCA
170576	2772	CAGCATTGGGCTAAATGCGC	215163	47359	GAATTTGGATCAGGAAGAAA	259750	91946	TCCCTGTGAGGTGCCTGCTC
170577	2773	CCAGCATTGGGCTAAATGCG	215164	47360	AGAATTTGGATCAGGAAGAA	259751	91947	TTCCCTGTGAGGTGCCTGCT
170578	2774	CCCAGCATTGGGCTAAATGC	215165	47361	CAGAATTTGGATCAGGAAGA	259752	91948	ATTCCCTGTGAGGTGCCTGC
170579	2775	TCCCAGCATTGGGCTAAATG	215166	47362	TCAGAATTTGGATCAGGAAG	259753	91949	GATTCCCTGTGAGGTGCCTG
170580	2776	TTCCCAGCATTGGGCTAAAT	215167	47363	ATCAGAATTTGGATCAGGAA	259754	91950	TGATTCCCTGTGAGGTGCCT
170581	2777	GTTCCCAGCATTGGGCTAAA	215168	47364	TATCAGAATTTGGATCAGGA	259755	91951	CTGATTCCCTGTGAGGTGCC
170582	2778	TGTTCCCAGCATTGGGCTAA	215169	47365	ATATCAGAATTTGGATCAGG	259756	91952	CCTGATTCCCTGTGAGGTGC
170583	2779	TTGTTCCCAGCATTGGGCTA	215170	47366	CATATCAGAATTTGGATCAG	259757	91953	CCCTGATTCCCTGTGAGGTG
170584	2780	TTTGTTCCCAGCATTGGGCT	215171	47367	ACATATCAGAATTTGGATCA	259758	91954	GCCCTGATTCCCTGTGAGGT
170585	2781	CTTTGTTCCCAGCATTGGGC	215172	47368	GACATATCAGAATTTGGATC	259759	91955	GGCCCTGATTCCCTGTGAGG
170586	2782	GCTTTGTTCCCAGCATTGGG	215173	47369	GGACATATCAGAATTTGGAT	259760	91956	TGGCCCTGATTCCCTGTGAG
170587	2783	CGCTTTGTTCCCAGCATTGG	215174	47370	TGGACATATCAGAATTTGGA	259761	91957	TTGGCCCTGATTCCCTGTGA
170588	2784	GCGCTTTGTTCCCAGCATTG	215175	47371	ATGGACATATCAGAATTTGG	259762	91958	CTTGGCCCTGATTCCCTGTG
170589	2785	TGCGCTTTGTTCCCAGCATT	215176	47372	AATGGACATATCAGAATTTG	259763	91959	GCTTGGCCCTGATTCCCTGT
170590	2786	GTGCGCTTTGTTCCCAGCAT	215177	47373	AAATGGACATATCAGAATTT	259764	91960	GGCTTGGCCCTGATTCCCTG
170591	2787	AGTGCGCTTTGTTCCCAGCA	215178	47374	TAAATGGACATATCAGAATT	259765	91961	AGGCTTGGCCCTGATTCCCT
170592	2788	GAGTGCGCTTTGTTCCCAGC	215179	47375	TTAAATGGACATATCAGAAT	259766	91962	CAGGCTTGGCCCTGATTCCC
170593	2789	GGAGTGCGCTTTGTTCCCAG	215180	47376	TTTAAATGGACATATCAGAA	259767	91963	CCAGGCTTGGCCCTGATTCC
170594	2790	CGGAGTGCGCTTTGTTCCCA	215181	47377	ATTTAAATGGACATATCAGA	259768	91964	GCCAGGCTTGGCCCTGATTC
170595	2791	GCGGAGTGCGCTTTGTTCCC	215182	47378	AATTTAAATGGACATATCAG	259769	91965	AGCCAGGCTTGGCCCTGATT
170596	2792	CGCGGAGTGCGCTTTGTTCC	215183	47379	CAATTTAAATGGACATATCA	259770	91966	CAGCCAGGCTTGGCCCTGAT
170597	2793	GCGCGGAGTGCGCTTTGTTC	215184	47380	TCAATTTAAATGGACATATC	259771	91967	GCAGCCAGGCTTGGCCCTGA
170598	2794	AGCGCGGAGTGCGCTTTGTT	215185	47381	ATCAATTTAAATGGACATAT	259772	91968	TGCAGCCAGGCTTGGCCCTG
170599	2795	AAGCGCGGAGTGCGCTTTGT	215186	47382	GATCAATTTAAATGGACATA	259773	91969	CTGCAGCCAGGCTTGGCCCT
170600	2796	GAAGCGCGGAGTGCGCTTTG	215187	47383	AGATCAATTTAAATGGACAT	259774	91970	ACTGCAGCCAGGCTTGGCCC
170601	2797	AGAAGCGCGGAGTGCGCTTT	215188	47384	TAGATCAATTTAAATGGACA	259775	91971	CACTGCAGCCAGGCTTGGCC
170602	2798	CAGAAGCGCGGAGTGCGCTT	215189	47385	CTAGATCAATTTAAATGGAC	259776	91972	ACACTGCAGCCAGGCTTGGC
170603	2799	GCAGAAGCGCGGAGTGCGCT	215190	47386	TCTAGATCAATTTAAATGGA	259777	91973	CACACTGCAGCCAGGCTTGG
170604	2800	CGCAGAAGCGCGGAGTGCGC	215191	47387	GTCTAGATCAATTTAAATGG	259778	91974	CCACACTGCAGCCAGGCTTG
170605	2801	TCGCAGAAGCGCGGAGTGCG	215192	47388	GGTCTAGATCAATTTAAATG	259779	91975	TCCACACTGCAGCCAGGCTT
170606	2802	ATCGCAGAAGCGCGGAGTGC	215193	47389	GGGTCTAGATCAATTTAAAT	259780	91976	CTCCACACTGCAGCCAGGCT
170607	2803	AATCGCAGAAGCGCGGAGTG	215194	47390	TGGGTCTAGATCAATTTAAA	259781	91977	TCTCCACACTGCAGCCAGGC
170608	2804	AAATCGCAGAAGCGCGGAGT	215195	47391	GTGGGTCTAGATCAATTTAA	259782	91978	GTCTCCACACTGCAGCCAGG
170609	2805	GAAATCGCAGAAGCGCGGAG	215196	47392	TGTGGGTCTAGATCAATTTA	259783	91979	TGTCTCCACACTGCAGCCAG
170610	2806	CGAAATCGCAGAAGCGCGGA	215197	47393	CTGTGGGTCTAGATCAATTT	259784	91980	TTGTCTCCACACTGCAGCCA

170611	2807	GCGAAATCGCAGAAGCGCGG	215198	47394	CCTGTGGGTCTAGATCAATT	259785	91981	ATTGTCTCCACACTGCAGCC
170612	2808	AGCGAAATCGCAGAAGCGCG	215199	47395	CCCTGTGGGTCTAGATCAAT	259786	91982	CATTGTCTCCACACTGCAGC
170613	2809	GAGCGAAATCGCAGAAGCGC	215200	47396	GCCCTGTGGGTCTAGATCAA	259787	91983	GCATTGTCTCCACACTGCAG
170614	2810	GGAGCGAAATCGCAGAAGCG	215201	47397	TGCCCTGTGGGTCTAGATCA	259788	91984	TGCATTGTCTCCACACTGCA
170615	2811	TGGAGCGAAATCGCAGAAGC	215202	47398	GTGCCCTGTGGGTCTAGATC	259789	91985	GTGCATTGTCTCCACACTGC
170616	2812	ATGGAGCGAAATCGCAGAAG	215203	47399	AGTGCCCTGTGGGTCTAGAT	259790	91986	GGTGCATTGTCTCCACACTG
170617	2813	AATGGAGCGAAATCGCAGAA	215204	47400	CAGTGCCCTGTGGGTCTAGA	259791	91987	GGGTGCATTGTCTCCACACT
170618	2814	AAATGGAGCGAAATCGCAGA	215205	47401	ACAGTGCCCTGTGGGTCTAG	259792	91988	TGGGTGCATTGTCTCCACAC
170619	2815	AAAATGGAGCGAAATCGCAG	215206	47402	CACAGTGCCCTGTGGGTCTA	259793	91989	GTGGGTGCATTGTCTCCACA
170620	2816	CAAAATGGAGCGAAATCGCA	215207	47403	CCACAGTGCCCTGTGGGTCT	259794	91990	GGTGGGTGCATTGTCTCCAC
170621	2817	TCAAAATGGAGCGAAATCGC	215208	47404	CCCACAGTGCCCTGTGGGTC	259795	91991	GGGTGGGTGCATTGTCTCCA
170622	2818	TTCAAAATGGAGCGAAATCG	215209	47405	TCCCACAGTGCCCTGTGGGT	259796	91992	GGGGTGGGTGCATTGTCTCC
170623	2819	TTTCAAAATGGAGCGAAATC	215210	47406	GTCCCACAGTGCCCTGTGGG	259797	91993	GGGGGTGGGTGCATTGTCTC
170624	2820	ATTTCAAAATGGAGCGAAAT	215211	47407	TGTCCCACAGTGCCCTGTGG	259798	91994	TGGGGGTGGGTGCATTGTCT
170625	2821	CATTTCAAAATGGAGCGAAA	215212	47408	CTGTCCCACAGTGCCCTGTG	259799	91995	ATGGGGGTGGGTGCATTGTC
170626	2822	ACATTTCAAAATGGAGCGAA	215213	47409	TCTGTCCCACAGTGCCCTGT	259800	91996	GATGGGGGTGGGTGCATTGT
170627	2823	CACATTTCAAAATGGAGCGA	215214	47410	ATCTGTCCCACAGTGCCCTG	259801	91997	GGATGGGGGTGGGTGCATTG
170628	2824	ACACATTTCAAAATGGAGCG	215215	47411	GATCTGTCCCACAGTGCCCT	259802	91998	AGGATGGGGGTGGGTGCATT
170629	2825	AACACATTTCAAAATGGAGC	215216	47412	GGATCTGTCCCACAGTGCCC	259803	91999	AAGGATGGGGGTGGGTGCAT
170630	2826	CAACACATTTCAAAATGGAG	215217	47413	AGGATCTGTCCCACAGTGCC	259804	92000	CAAGGATGGGGGTGGGTGCA
170631	2827	CCAACACATTTCAAAATGGA	215218	47414	GAGGATCTGTCCCACAGTGC	259805	92001	CCAAGGATGGGGGTGGGTGC
170632	2828	GCCAACACATTTCAAAATGG	215219	47415	TGAGGATCTGTCCCACAGTG	259806	92002	TCCAAGGATGGGGGTGGGTG
170633	2829	CGCCAACACATTTCAAAATG	215220	47416	CTGAGGATCTGTCCCACAGT	259807	92003	ATCCAAGGATGGGGGTGGGT
170634	2830	GCGCCAACACATTTCAAAAT	215221	47417	ACTGAGGATCTGTCCCACAG	259808	92004	GATCCAAGGATGGGGGTGGG
170635	2831	AGCGCCAACACATTTCAAAA	215222	47418	CACTGAGGATCTGTCCCACA	259809	92005	AGATCCAAGGATGGGGGTGG
170636	2832	AAGCGCCAACACATTTCAAA	215223	47419	CCACTGAGGATCTGTCCCAC	259810	92006	AAGATCCAAGGATGGGGGTG
170637	2833	AAAGCGCCAACACATTTCAA	215224	47420	TCCACTGAGGATCTGTCCCA	259811	92007	CAAGATCCAAGGATGGGGGT
170638	2834	CAAAGCGCCAACACATTTCA	215225	47421	TTCCACTGAGGATCTGTCCC	259812	92008	GCAAGATCCAAGGATGGGGG
170639	2835	CCAAAGCGCCAACACATTTC	215226	47422	GTTCCACTGAGGATCTGTCC	259813	92009	TGCAAGATCCAAGGATGGGG
170640	2836	ACCAAAGCGCCAACACATTT	215227	47423	TGTTCCACTGAGGATCTGTC	259814	92010	CTGCAAGATCCAAGGATGGG
170641	2837	CACCAAAGCGCCAACACATT	215228	47424	ATGTTCCACTGAGGATCTGT	259815	92011	CCTGCAAGATCCAAGGATGG
170642	2838	CCACCAAAGCGCCAACACAT	215229	47425	CATGTTCCACTGAGGATCTG	259816	92012	TCCTGCAAGATCCAAGGATG
170643	2839	CCCACCAAAGCGCCAACACA	215230	47426	TCATGTTCCACTGAGGATCT	259817	92013	CTCCTGCAAGATCCAAGGAT
170644	2840	CCCCACCAAAGCGCCAACAC	215231	47427	GTCATGTTCCACTGAGGATC	259818	92014	CCTCCTGCAAGATCCAAGGA
170645	2841	GCCCCACCAAAGCGCCAACA	215232	47428	AGTCATGTTCCACTGAGGAT	259819	92015	GCCTCCTGCAAGATCCAAGG
170646	2842	GGCCCCACCAAAGCGCCAAC	215233	47429	GAGTCATGTTCCACTGAGGA	259820	92016	AGCCTCCTGCAAGATCCAAG
170647	2843	CGGCCCCACCAAAGCGCCAA	215234	47430	AGAGTCATGTTCCACTGAGG	259821	92017	CAGCCTCCTGCAAGATCCAA
170648	2844	GCGGCCCCACCAAAGCGCCA	215235	47431	CAGAGTCATGTTCCACTGAG	259822	92018	CCAGCCTCCTGCAAGATCCA
170649	2845	AGCGGCCCCACCAAAGCGCC	215236	47432	ACAGAGTCATGTTCCACTGA	259823	92019	CCCAGCCTCCTGCAAGATCC
170650	2846	CAGCGGCCCCACCAAAGCGC	215237	47433	TACAGAGTCATGTTCCACTG	259824	92020	ACCCAGCCTCCTGCAAGATC
170651	2847	GCAGCGGCCCCACCAAAGCG	215238	47434	TTACAGAGTCATGTTCCACT	259825	92021	GACCCAGCCTCCTGCAAGAT
170652	2848	CGCAGCGGCCCCACCAAAGC	215239	47435	GTTACAGAGTCATGTTCCAC	259826	92022	GGACCCAGCCTCCTGCAAGA
170653	2849	CCGCAGCGGCCCCACCAAAG	215240	47436	CGTTACAGAGTCATGTTCCA	259827	92023	AGGACCCAGCCTCCTGCAAG
170654	2850	ACCGCAGCGGCCCCACCAAA	215241	47437	TCGTTACAGAGTCATGTTCC	259828	92024	GAGGACCCAGCCTCCTGCAA
170655	2851	CACCGCAGCGGCCCCACCAA	215242	47438	CTCGTTACAGAGTCATGTTC	259829	92025	TGAGGACCCAGCCTCCTGCA
170656	2852	CCACCGCAGCGGCCCCACCA	215243	47439	TCTCGTTACAGAGTCATGTT	259830	92026	GTGAGGACCCAGCCTCCTGC
170657	2853	CCCACCGCAGCGGCCCCACC	215244	47440	CTCTCGTTACAGAGTCATGT	259831	92027	AGTGAGGACCCAGCCTCCTG
170658	2854	GCCCACCGCAGCGGCCCCAC	215245	47441	GCTCTCGTTACAGAGTCATG	259832	92028	CAGTGAGGACCCAGCCTCCT
170659	2855	TGCCCACCGCAGCGGCCCCA	215246	47442	TGCTCTCGTTACAGAGTCAT	259833	92029	TCAGTGAGGACCCAGCCTCC
170660	2856	TTGCCCACCGCAGCGGCCCC	215247	47443	ATGCTCTCGTTACAGAGTCA	259834	92030	CTCAGTGAGGACCCAGCCTC
170661	2857	CTTGCCCACCGCAGCGGCCC	215248	47444	AATGCTCTCGTTACAGAGTC	259835	92031	GCTCAGTGAGGACCCAGCCT
170662	2858	CCTTGCCCACCGCAGCGGCC	215249	47445	AAATGCTCTCGTTACAGAGT	259836	92032	AGCTCAGTGAGGACCCAGCC
170663	2859	GCCTTGCCCACCGCAGCGGC	215250	47446	AAAATGCTCTCGTTACAGAG	259837	92033	TAGCTCAGTGAGGACCCAGC
170664	2860	GGCCTTGCCCACCGCAGCGG	215251	47447	CAAAATGCTCTCGTTACAGA	259838	92034	GTAGCTCAGTGAGGACCCAG
170665	2861	CGGCCTTGCCCACCGCAGCG	215252	47448	ACAAAATGCTCTCGTTACAG	259839	92035	GGTAGCTCAGTGAGGACCCA
170666	2862	CCGGCCTTGCCCACCGCAGC	215253	47449	AACAAAATGCTCTCGTTACA	259840	92036	TGGTAGCTCAGTGAGGACCC
170667	2863	CCCGGCCTTGCCCACCGCAG	215254	47450	AAACAAAATGCTCTCGTTAC	259841	92037	TTGGTAGCTCAGTGAGGACC
170668	2864	CCCCGGCCTTGCCCACCGCA	215255	47451	AAAACAAAATGCTCTCGTTA	259842	92038	GTTGGTAGCTCAGTGAGGAC
170669	2865	CCCCCGGCCTTGCCCACCGC	215256	47452	CAAAACAAAATGCTCTCGTT	259843	92039	TGTTGGTAGCTCAGTGAGGA
170670	2866	GCCCCCGGCCTTGCCCACCG	215257	47453	ACAAAACAAAATGCTCTCGT	259844	92040	ATGTTGGTAGCTCAGTGAGG
170671	2867	CGCCCCCGGCCTTGCCCACC	215258	47454	GACAAAACAAAATGCTCTCG	259845	92041	GATGTTGGTAGCTCAGTGAG
170672	2868	GCGCCCCCGGCCTTGCCCAC	215259	47455	TGACAAAACAAAATGCTCTC	259846	92042	GGATGTTGGTAGCTCAGTGA
170673	2869	AGCGCCCCCGGCCTTGCCCA	215260	47456	TTGACAAAACAAAATGCTCT	259847	92043	TGGATGTTGGTAGCTCAGTG
170674	2870	CAGCGCCCCCGGCCTTGCCC	215261	47457	TTTGACAAAACAAAATGCTC	259848	92044	ATGGATGTTGGTAGCTCAGT
170675	2871	ACAGCGCCCCCGGCCTTGCC	215262	47458	TTTTGACAAAACAAAATGCT	259849	92045	CATGGATGTTGGTAGCTCAG
170676	2872	AACAGCGCCCCCGGCCTTGC	215263	47459	ATTTTGACAAAACAAAATGC	259850	92046	CCATGGATGTTGGTAGCTCA
170677	2873	TAACAGCGCCCCCGGCCTTG	215264	47460	CATTTTGACAAAACAAAATG	259851	92047	GCCATGGATGTTGGTAGCTC
170678	2874	TTAACAGCGCCCCCGGCCTT	215265	47461	TCATTTTGACAAAACAAAAT	259852	92048	GGCCATGGATGTTGGTAGCT
170679	2875	ATTAACAGCGCCCCCGGCCT	215266	47462	CTCATTTTGACAAAACAAAA	259853	92049	GGGCCATGGATGTTGGTAGC
170680	2876	CATTAACAGCGCCCCCGGCC	215267	47463	TCTCATTTTGACAAAACAAA	259854	92050	AGGGCCATGGATGTTGGTAG
170681	2877	CCATTAACAGCGCCCCCGGC	215268	47464	TTCTCATTTTGACAAAACAA	259855	92051	CAGGGCCATGGATGTTGGTA
170682	2878	TCCATTAACAGCGCCCCCGG	215269	47465	GTTCTCATTTTGACAAAACA	259856	92052	TCAGGGCCATGGATGTTGGT

170683	2879	CTCCATTAACAGCGCCCCCG	215270	47466	TGTTCTCATTTTGACAAAAC	259857	92053	CTCAGGGCCATGGATGTTGG
170684	2880	CCTCCATTAACAGCGCCCCC	215271	47467	ATGTTCTCATTTTGACAAAA	259858	92054	CCTCAGGGCCATGGATGTTG
170685	2881	TCCTCCATTAACAGCGCCCC	215272	47468	TATGTTCTCATTTTGACAAA	259859	92055	GCCTCAGGGCCATGGATGTT
170686	2882	TTCCTCCATTAACAGCGCCC	215273	47469	ATATGTTCTCATTTTGACAA	259860	92056	AGCCTCAGGGCCATGGATGT
170687	2883	GTTCCTCCATTAACAGCGCC	215274	47470	AATATGTTCTCATTTTGACA	259861	92057	AAGCCTCAGGGCCATGGATG
170688	2884	GGTTCCTCCATTAACAGCGC	215275	47471	TAATATGTTCTCATTTTGAC	259862	92058	AAAGCCTCAGGGCCATGGAT
170689	2885	AGGTTCCTCCATTAACAGCG	215276	47472	ATAATATGTTCTCATTTTGA	259863	92059	AAAAGCCTCAGGGCCATGGA
170690	2886	GAGGTTCCTCCATTAACAGC	215277	47473	AATAATATGTTCTCATTTTG	259864	92060	TAAAAGCCTCAGGGCCATGG
170691	2887	TGAGGTTCCTCCATTAACAG	215278	47474	CAATAATATGTTCTCATTTT	259865	92061	TTAAAAGCCTCAGGGCCATG
170692	2888	CTGAGGTTCCTCCATTAACA	215279	47475	GCAATAATATGTTCTCATTT	259866	92062	TTTAAAAGCCTCAGGGCCAT
170693	2889	CCTGAGGTTCCTCCATTAAC	215280	47476	GGCAATAATATGTTCTCATT	259867	92063	TTTTAAAAGCCTCAGGGCCA
170694	2890	CCCTGAGGTTCCTCCATTAA	215281	47477	AGGCAATAATATGTTCTCAT	259868	92064	GTTTTAAAAGCCTCAGGGCC
170695	2891	CCCCTGAGGTTCCTCCATTA	215282	47478	AAGGCAATAATATGTTCTCA	259869	92065	TGTTTTAAAAGCCTCAGGGC
170696	2892	CCCCCTGAGGTTCCTCCATT	215283	47479	AAAGGCAATAATATGTTCTC	259870	92066	GTGTTTTAAAAGCCTCAGGG
170697	2893	TCCCCCTGAGGTTCCTCCAT	215284	47480	GAAAGGCAATAATATGTTCT	259871	92067	GGTGTTTTAAAAGCCTCAGG
170698	2894	GTCCCCCTGAGGTTCCTCCA	215285	47481	TGAAAGGCAATAATATGTTC	259872	92068	GGGTGTTTTAAAAGCCTCAG
170699	2895	CGTCCCCCTGAGGTTCCTCC	215286	47482	ATGAAAGGCAATAATATGTT	259873	92069	TGGGTGTTTTAAAAGCCTCA
170700	2896	CCGTCCCCCTGAGGTTCCTC	215287	47483	GATGAAAGGCAATAATATGT	259874	92070	ATGGGTGTTTTAAAAGCCTC
170701	2897	ACCGTCCCCCTGAGGTTCCT	215288	47484	AGATGAAAGGCAATAATATG	259875	92071	GATGGGTGTTTTAAAAGCCT
170702	2898	GACCGTCCCCCTGAGGTTCC	215289	47485	CAGATGAAAGGCAATAATAT	259876	92072	GGATGGGTGTTTTAAAAGCC
170703	2899	GGACCGTCCCCCTGAGGTTC	215290	47486	TCAGATGAAAGGCAATAATA	259877	92073	TGGATGGGTGTTTTAAAAGC
170704	2900	AGGACCGTCCCCCTGAGGTT	215291	47487	ATCAGATGAAAGGCAATAAT	259878	92074	ATGGATGGGTGTTTTAAAAG
170705	2901	AAGGACCGTCCCCCTGAGGT	215292	47488	AATCAGATGAAAGGCAATAA	259879	92075	CATGGATGGGTGTTTTAAAA
170706	2902	GAAGGACCGTCCCCCTGAGG	215293	47489	CAATCAGATGAAAGGCAATA	259880	92076	CCATGGATGGGTGTTTTAAA
170707	2903	CGAAGGACCGTCCCCCTGAG	215294	47490	ACAATCAGATGAAAGGCAAT	259881	92077	TCCATGGATGGGTGTTTTAA
170708	2904	ACGAAGGACCGTCCCCCTGA	215295	47491	TACAATCAGATGAAAGGCAA	259882	92078	CTCCATGGATGGGTGTTTTA
170709	2905	TACGAAGGACCGTCCCCCTG	215296	47492	TTACAATCAGATGAAAGGCA	259883	92079	ACTCCATGGATGGGTGTTTT
170710	2906	CTACGAAGGACCGTCCCCCT	215297	47493	TTTACAATCAGATGAAAGGC	259884	92080	CACTCCATGGATGGGTGTTT
170711	2907	CCTACGAAGGACCGTCCCCC	215298	47494	GTTTACAATCAGATGAAAGG	259885	92081	CCACTCCATGGATGGGTGTT
170712	2908	TCCTACGAAGGACCGTCCCC	215299	47495	TGTTTACAATCAGATGAAAG	259886	92082	CCCACTCCATGGATGGGTGT
170713	2909	TTCCTACGAAGGACCGTCCC	215300	47496	ATGTTTACAATCAGATGAAA	259887	92083	CCCCACTCCATGGATGGGTG
170714	2910	TTTCCTACGAAGGACCGTCC	215301	47497	TATGTTTACAATCAGATGAA	259888	92084	GCCCCACTCCATGGATGGGT
170715	2911	GTTTCCTACGAAGGACCGTC	215302	47498	TTATGTTTACAATCAGATGA	259889	92085	AGCCCCACTCCATGGATGGG
170716	2912	AGTTTCCTACGAAGGACCGT	215303	47499	ATTATGTTTACAATCAGATG	259890	92086	CAGCCCCACTCCATGGATGG
170717	2913	GAGTTTCCTACGAAGGACCG	215304	47500	TATTATGTTTACAATCAGAT	259891	92087	CCAGCCCCACTCCATGGATG
170718	2914	AGAGTTTCCTACGAAGGACC	215305	47501	GTATTATGTTTACAATCAGA	259892	92088	ACCAGCCCCACTCCATGGAT
170719	2915	TAGAGTTTCCTACGAAGGAC	215306	47502	TGTATTATGTTTACAATCAG	259893	92089	GACCAGCCCCACTCCATGGA
170720	2916	ATAGAGTTTCCTACGAAGGA	215307	47503	ATGTATTATGTTTACAATCA	259894	92090	GGACCAGCCCCACTCCATGG
170721	2917	GATAGAGTTTCCTACGAAGG	215308	47504	CATGTATTATGTTTACAATC	259895	92091	GGGACCAGCCCCACTCCATG
170722	2918	GGATAGAGTTTCCTACGAAG	215309	47505	ACATGTATTATGTTTACAAT	259896	92092	TGGGACCAGCCCCACTCCAT
170723	2919	AGGATAGAGTTTCCTACGAA	215310	47506	AACATGTATTATGTTTACAA	259897	92093	CTGGGACCAGCCCCACTCCA
170724	2920	CAGGATAGAGTTTCCTACGA	215311	47507	AAACATGTATTATGTTTACA	259898	92094	ACTGGGACCAGCCCCACTCC
170725	2921	CCAGGATAGAGTTTCCTACG	215312	47508	TAAACATGTATTATGTTTAC	259899	92095	CACTGGGACCAGCCCCACTC
170726	2922	GCCAGGATAGAGTTTCCTAC	215313	47509	ATAAACATGTATTATGTTTA	259900	92096	CCACTGGGACCAGCCCCACT
170727	2923	AGCCAGGATAGAGTTTCCTA	215314	47510	TATAAACATGTATTATGTTT	259901	92097	CCCACTGGGACCAGCCCCAC
170728	2924	GAGCCAGGATAGAGTTTCCT	215315	47511	TTATAAACATGTATTATGTT	259902	92098	CCCCACTGGGACCAGCCCCA
170729	2925	AGAGCCAGGATAGAGTTTCC	215316	47512	TTTATAAACATGTATTATGT	259903	92099	ACCCCACTGGGACCAGCCCC
170730	2926	CAGAGCCAGGATAGAGTTTC	215317	47513	TTTTATAAACATGTATTATG	259904	92100	CACCCCACTGGGACCAGCCC
170731	2927	GCAGAGCCAGGATAGAGTTT	215318	47514	GTTTTATAAACATGTATTAT	259905	92101	TCACCCCACTGGGACCAGCC
170732	2928	CGCAGAGCCAGGATAGAGTT	215319	47515	TGTTTTATAAACATGTATTA	259906	92102	CTCACCCCACTGGGACCAGC
170733	2929	GCGCAGAGCCAGGATAGAGT	215320	47516	CTGTTTTATAAACATGTATT	259907	92103	CCTCACCCCACTGGGACCAG
170734	2930	CGCGCAGAGCCAGGATAGAG	215321	47517	ACTGTTTTATAAACATGTAT	259908	92104	GCCTCACCCCACTGGGACCA
170735	2931	GCGCGCAGAGCCAGGATAGA	215322	47518	TACTGTTTTATAAACATGTA	259909	92105	AGCCTCACCCCACTGGGACC
170736	2932	CGCGCGCAGAGCCAGGATAG	215323	47519	ATACTGTTTTATAAACATGT	259910	92106	CAGCCTCACCCCACTGGGAC
170737	2933	GCGCGCGCAGAGCCAGGATA	215324	47520	TATACTGTTTTATAAACATG	259911	92107	TCAGCCTCACCCCACTGGGA
170738	2934	AGCGCGCGCAGAGCCAGGAT	215325	47521	TTATACTGTTTTATAAACAT	259912	92108	GTCAGCCTCACCCCACTGGG
170739	2935	AAGCGCGCGCAGAGCCAGGA	215326	47522	ATTATACTGTTTTATAAACA	259913	92109	GGTCAGCCTCACCCCACTGG
170740	2936	AAAGCGCGCGCAGAGCCAGG	215327	47523	CATTATACTGTTTTATAAAC	259914	92110	GGGTCAGCCTCACCCCACTG
170741	2937	TAAAGCGCGCGCAGAGCCAG	215328	47524	TCATTATACTGTTTTATAAA	259915	92111	AGGGTCAGCCTCACCCCACT
170742	2938	TTAAAGCGCGCGCAGAGCCA	215329	47525	CTCATTATACTGTTTTATAA	259916	92112	CAGGGTCAGCCTCACCCCAC
170743	2939	CTTAAAGCGCGCGCAGAGCC	215330	47526	TCTCATTATACTGTTTTATA	259917	92113	CCAGGGTCAGCCTCACCCCA
170744	2940	CCTTAAAGCGCGCGCAGAGC	215331	47527	GTCTCATTATACTGTTTTAT	259918	92114	GCCAGGGTCAGCCTCACCCC
170745	2941	TCCTTAAAGCGCGCGCAGAG	215332	47528	TGTCTCATTATACTGTTTTA	259919	92115	TGCCAGGGTCAGCCTCACCC
170746	2942	TTCCTTAAAGCGCGCGCAGA	215333	47529	TTGTCTCATTATACTGTTTT	259920	92116	CTGCCAGGGTCAGCCTCACC
170747	2943	TTTCCTTAAAGCGCGCGCAG	215334	47530	TTTGTCTCATTATACTGTTT	259921	92117	TCTGCCAGGGTCAGCCTCAC
170748	2944	ATTTCCTTAAAGCGCGCGCA	215335	47531	TTTTGTCTCATTATACTGTT	259922	92118	TTCTGCCAGGGTCAGCCTCA
170749	2945	CATTTCCTTAAAGCGCGCGC	215336	47532	TTTTTGTCTCATTATACTGT	259923	92119	TTTCTGCCAGGGTCAGCCTC
170750	2946	CCATTTCCTTAAAGCGCGCG	215337	47533	ATTTTTGTCTCATTATACTG	259924	92120	GTTTCTGCCAGGGTCAGCCT
170751	2947	GCCATTTCCTTAAAGCGCGC	215338	47534	CATTTTTGTCTCATTATACT	259925	92121	TGTTTCTGCCAGGGTCAGCC
170752	2948	AGCCATTTCCTTAAAGCGCG	215339	47535	ACATTTTTGTCTCATTATAC	259926	92122	CTGTTTCTGCCAGGGTCAGC
170753	2949	AAGCCATTTCCTTAAAGCGC	215340	47536	TACATTTTTGTCTCATTATA	259927	92123	CCTGTTTCTGCCAGGGTCAG
170754	2950	GAAGCCATTTCCTTAAAGCG	215341	47537	CTACATTTTTGTCTCATTAT	259928	92124	CCCTGTTTCTGCCAGGGTCA

170755	2951	GGAAGCCATTTCCTTAAAGC	215342	47538	TCTACATTTTTGTCTCATTA	259929	92125	GCCCTGTTTCTGCCAGGGTC
170756	2952	GGGAAGCCATTTCCTTAAAG	215343	47539	GTCTACATTTTTGTCTCATT	259930	92126	TGCCCTGTTTCTGCCAGGGT
170757	2953	AGGGAAGCCATTTCCTTAAA	215344	47540	TGTCTACATTTTTGTCTCAT	259931	92127	CTGCCCTGTTTCTGCCAGGG
170758	2954	GAGGGAAGCCATTTCCTTAA	215345	47541	GTGTCTACATTTTTGTCTCA	259932	92128	CCTGCCCTGTTTCTGCCAGG
170759	2955	GGAGGGAAGCCATTTCCTTA	215346	47542	AGTGTCTACATTTTTGTCTC	259933	92129	TCCTGCCCTGTTTCTGCCAG
170760	2956	TGGAGGGAAGCCATTTCCTT	215347	47543	TAGTGTCTACATTTTTGTCT	259934	92130	CTCCTGCCCTGTTTCTGCCA
170761	2957	CTGGAGGGAAGCCATTTCCT	215348	47544	TTAGTGTCTACATTTTTGTC	259935	92131	GCTCCTGCCCTGTTTCTGCC
170762	2958	CCTGGAGGGAAGCCATTTCC	215349	47545	ATTAGTGTCTACATTTTTGT	259936	92132	GGCTCCTGCCCTGTTTCTGC
170763	2959	TCCTGGAGGGAAGCCATTTC	215350	47546	TATTAGTGTCTACATTTTTG	259937	92133	AGGCTCCTGCCCTGTTTCTG
170764	2960	GTCCTGGAGGGAAGCCATTT	215351	47547	TTATTAGTGTCTACATTTTT	259938	92134	CAGGCTCCTGCCCTGTTTCT
170765	2961	GGTCCTGGAGGGAAGCCATT	215352	47548	CTTATTAGTGTCTACATTTT	259939	92135	ACAGGCTCCTGCCCTGTTTC
170766	2962	AGGTCCTGGAGGGAAGCCAT	215353	47549	CCTTATTAGTGTCTACATTT	259940	92136	CACAGGCTCCTGCCCTGTTT
170767	2963	GAGGTCCTGGAGGGAAGCCA	215354	47550	CCCTTATTAGTGTCTACATT	259941	92137	CCACAGGCTCCTGCCCTGTT
170768	2964	CGAGGTCCTGGAGGGAAGCC	215355	47551	TCCCTTATTAGTGTCTACAT	259942	92138	CCCACAGGCTCCTGCCCTGT
170769	2965	TCGAGGTCCTGGAGGGAAGC	215356	47552	TTCCCTTATTAGTGTCTACA	259943	92139	ACCCACAGGCTCCTGCCCTG
170770	2966	CTCGAGGTCCTGGAGGGAAG	215357	47553	TTTCCCTTATTAGTGTCTAC	259944	92140	AACCCACAGGCTCCTGCCCT
170771	2967	CCTCGAGGTCCTGGAGGGAA	215358	47554	TTTTCCCTTATTAGTGTCTA	259945	92141	TAACCCACAGGCTCCTGCCC
170772	2968	CCCTCGAGGTCCTGGAGGGA	215359	47555	ATTTTCCCTTATTAGTGTCT	259946	92142	CTAACCCACAGGCTCCTGCC
170773	2969	TCCCTCGAGGTCCTGGAGGG	215360	47556	GATTTTCCCTTATTAGTGTC	259947	92143	CCTAACCCACAGGCTCCTGC
170774	2970	ATCCCTCGAGGTCCTGGAGG	215361	47557	AGATTTTCCCTTATTAGTGT	259948	92144	CCCTAACCCACAGGCTCCTG
170775	2971	CATCCCTCGAGGTCCTGGAG	215362	47558	GAGATTTTCCCTTATTAGTG	259949	92145	TCCCTAACCCACAGGCTCCT
170776	2972	GCATCCCTCGAGGTCCTGGA	215363	47559	GGAGATTTTCCCTTATTAGT	259950	92146	CTCCCTAACCCACAGGCTCC
170777	2973	TGCATCCCTCGAGGTCCTGG	215364	47560	GGGAGATTTTCCCTTATTAG	259951	92147	TCTCCCTAACCCACAGGCTC
170778	2974	CTGCATCCCTCGAGGTCCTG	215365	47561	AGGGAGATTTTCCCTTATTA	259952	92148	GTCTCCCTAACCCACAGGCT
170779	2975	GCTGCATCCCTCGAGGTCCT	215366	47562	TAGGGAGATTTTCCCTTATT	259953	92149	AGTCTCCCTAACCCACAGGC
170780	2976	AGCTGCATCCCTCGAGGTCC	215367	47563	TTAGGGAGATTTTCCCTTAT	259954	92150	CAGTCTCCCTAACCCACAGG
170781	2977	AAGCTGCATCCCTCGAGGTC	215368	47564	ATTAGGGAGATTTTCCCTTA	259955	92151	GCAGTCTCCCTAACCCACAG
170782	2978	AAAGCTGCATCCCTCGAGGT	215369	47565	AATTAGGGAGATTTTCCCTT	259956	92152	TGCAGTCTCCCTAACCCACA
170783	2979	AAAAGCTGCATCCCTCGAGG	215370	47566	CAATTAGGGAGATTTTCCCT	259957	92153	GTGCAGTCTCCCTAACCCAC
170784	2980	CAAAAGCTGCATCCCTCGAG	215371	47567	ACAATTAGGGAGATTTTCCC	259958	92154	GGTGCAGTCTCCCTAACCCA
170785	2981	GCAAAAGCTGCATCCCTCGA	215372	47568	TACAATTAGGGAGATTTTCC	259959	92155	AGGTGCAGTCTCCCTAACCC
170786	2982	CGCAAAAGCTGCATCCCTCG	215373	47569	ATACAATTAGGGAGATTTTC	259960	92156	AAGGTGCAGTCTCCCTAACC
170787	2983	GCGCAAAAGCTGCATCCCTC	215374	47570	AATACAATTAGGGAGATTTT	259961	92157	GAAGGTGCAGTCTCCCTAAC
170788	2984	CGCGCAAAAGCTGCATCCCT	215375	47571	AAATACAATTAGGGAGATTT	259962	92158	GGAAGGTGCAGTCTCCCTAA
170789	2985	CCGCGCAAAAGCTGCATCCC	215376	47572	GAAATACAATTAGGGAGATT	259963	92159	AGGAAGGTGCAGTCTCCCTA
170790	2986	TCCGCGCAAAAGCTGCATCC	215377	47573	AGAAATACAATTAGGGAGAT	259964	92160	AAGGAAGGTGCAGTCTCCCT
170791	2987	ATCCGCGCAAAAGCTGCATC	215378	47574	GAGAAATACAATTAGGGAGA	259965	92161	TAAGGAAGGTGCAGTCTCCC
170792	2988	CATCCGCGCAAAAGCTGCAT	215379	47575	AGAGAAATACAATTAGGGAG	259966	92162	CTAAGGAAGGTGCAGTCTCC
170793	2989	TCATCCGCGCAAAAGCTGCA	215380	47576	AAGAGAAATACAATTAGGGA	259967	92163	TCTAAGGAAGGTGCAGTCTC
170794	2990	GTCATCCGCGCAAAAGCTGC	215381	47577	GAAGAGAAATACAATTAGGG	259968	92164	ATCTAAGGAAGGTGCAGTCT
170795	2991	CGTCATCCGCGCAAAAGCTG	215382	47578	TGAAGAGAAATACAATTAGG	259969	92165	TATCTAAGGAAGGTGCAGTC
170796	2992	CCGTCATCCGCGCAAAAGCT	215383	47579	GTGAAGAGAAATACAATTAG	259970	92166	CTATCTAAGGAAGGTGCAGT
170797	2993	ACCGTCATCCGCGCAAAAGC	215384	47580	TGTGAAGAGAAATACAATTA	259971	92167	GCTATCTAAGGAAGGTGCAG
170798	2994	CACCGTCATCCGCGCAAAAG	215385	47581	CTGTGAAGAGAAATACAATT	259972	92168	GGCTATCTAAGGAAGGTGCA
170799	2995	CCACCGTCATCCGCGCAAAA	215386	47582	TCTGTGAAGAGAAATACAAT	259973	92169	AGGCTATCTAAGGAAGGTGC
170800	2996	CCCACCGTCATCCGCGCAAA	215387	47583	CTCTGTGAAGAGAAATACAA	259974	92170	GAGGCTATCTAAGGAAGGTG
170801	2997	CCCCACCGTCATCCGCGCAA	215388	47584	TCTCTGTGAAGAGAAATACA	259975	92171	GGAGGCTATCTAAGGAAGGT
170802	2998	ACCCCACCGTCATCCGCGCA	215389	47585	TTCTCTGTGAAGAGAAATAC	259976	92172	TGGAGGCTATCTAAGGAAGG
170803	2999	CACCCCACCGTCATCCGCGC	215390	47586	TTTCTCTGTGAAGAGAAATA	259977	92173	ATGGAGGCTATCTAAGGAAG
170804	3000	GCACCCCACCGTCATCCGCG	215391	47587	CTTTCTCTGTGAAGAGAAAT	259978	92174	CATGGAGGCTATCTAAGGAA
170805	3001	AGCACCCCACCGTCATCCGC	215392	47588	GCTTTCTCTGTGAAGAGAAA	259979	92175	GCATGGAGGCTATCTAAGGA
170806	3002	CAGCACCCCACCGTCATCCG	215393	47589	GGCTTTCTCTGTGAAGAGAA	259980	92176	GGCATGGAGGCTATCTAAGG
170807	3003	TCAGCACCCCACCGTCATCC	215394	47590	GGGCTTTCTCTGTGAAGAGA	259981	92177	TGGCATGGAGGCTATCTAAG
170808	3004	TTCAGCACCCCACCGTCATC	215395	47591	GGGGCTTTCTCTGTGAAGAG	259982	92178	ATGGCATGGAGGCTATCTAA
170809	3005	GTTCAGCACCCCACCGTCAT	215396	47592	AGGGGCTTTCTCTGTGAAGA	259983	92179	GATGGCATGGAGGCTATCTA
170810	3006	GGTTCAGCACCCCACCGTCA	215397	47593	CAGGGGCTTTCTCTGTGAAG	259984	92180	TGATGGCATGGAGGCTATCT
170811	3007	TGGTTCAGCACCCCACCGTC	215398	47594	ACAGGGGCTTTCTCTGTGAA	259985	92181	ATGATGGCATGGAGGCTATC
170812	3008	CTGGTTCAGCACCCCACCGT	215399	47595	AACAGGGGCTTTCTCTGTGA	259986	92182	CATGATGGCATGGAGGCTAT
170813	3009	GCTGGTTCAGCACCCCACCG	215400	47596	CAACAGGGGCTTTCTCTGTG	259987	92183	ACATGATGGCATGGAGGCTA
170814	3010	GGCTGGTTCAGCACCCCACC	215401	47597	CCAACAGGGGCTTTCTCTGT	259988	92184	GACATGATGGCATGGAGGCT
170815	3011	CGGCTGGTTCAGCACCCCAC	215402	47598	CCCAACAGGGGCTTTCTCTG	259989	92185	GGACATGATGGCATGGAGGC
170816	3012	CCGGCTGGTTCAGCACCCCA	215403	47599	GCCCAACAGGGGCTTTCTCT	259990	92186	GGGACATGATGGCATGGAGG
170817	3013	ACCGGCTGGTTCAGCACCCC	215404	47600	TGCCCAACAGGGGCTTTCTC	259991	92187	GGGGACATGATGGCATGGAG
170818	3014	CACCGGCTGGTTCAGCACCC	215405	47601	ATGCCCAACAGGGGCTTTCT	259992	92188	CGGGGACATGATGGCATGGA
170819	3015	GCACCGGCTGGTTCAGCACC	215406	47602	TATGCCCAACAGGGGCTTTC	259993	92189	ACGGGGACATGATGGCATGG
170820	3016	CGCACCGGCTGGTTCAGCAC	215407	47603	ATATGCCCAACAGGGGCTTT	259994	92190	CACGGGGACATGATGGCATG
170821	3017	GCGCACCGGCTGGTTCAGCA	215408	47604	TATATGCCCAACAGGGGCTT	259995	92191	TCACGGGGACATGATGGCAT
170822	3018	GGCGCACCGGCTGGTTCAGC	215409	47605	ATATATGCCCAACAGGGGCT	259996	92192	GTCACGGGGACATGATGGCA
170823	3019	AGGCGCACCGGCTGGTTCAG	215410	47606	TATATATGCCCAACAGGGGC	259997	92193	TGTCACGGGGACATGATGGC
170824	3020	GAGGCGCACCGGCTGGTTCA	215411	47607	GTATATATGCCCAACAGGGG	259998	92194	CTGTCACGGGGACATGATGG
170825	3021	AGAGGCGCACCGGCTGGTTC	215412	47608	AGTATATATGCCCAACAGGG	259999	92195	ACTGTCACGGGGACATGATG
170826	3022	CAGAGGCGCACCGGCTGGTT	215413	47609	GAGTATATATGCCCAACAGG	260000	92196	AACTGTCACGGGGACATGAT

170827	3023	CCAGAGGCGCACCGGCTGGT	215414	47610	AGAGTATATATGCCCAACAG	260001	92197	AAACTGTCACGGGGACATGA
170828	3024	TCCAGAGGCGCACCGGCTGG	215415	47611	TAGAGTATATATGCCCAACA	260002	92198	GAAACTGTCACGGGGACATG
170829	3025	TTCCAGAGGCGCACCGGCTG	215416	47612	CTAGAGTATATATGCCCAAC	260003	92199	AGAAACTGTCACGGGGACAT
170830	3026	TTTCCAGAGGCGCACCGGCT	215417	47613	ACTAGAGTATATATGCCCAA	260004	92200	CAGAAACTGTCACGGGGACA
170831	3027	ATTTCCAGAGGCGCACCGGC	215418	47614	AACTAGAGTATATATGCCCA	260005	92201	GCAGAAACTGTCACGGGGAC
170832	3028	CATTTCCAGAGGCGCACCGG	215419	47615	AAACTAGAGTATATATGCCC	260006	92202	AGCAGAAACTGTCACGGGGA
170833	3029	ACATTTCCAGAGGCGCACCG	215420	47616	CAAACTAGAGTATATATGCC	260007	92203	CAGCAGAAACTGTCACGGGG
170834	3030	GACATTTCCAGAGGCGCACC	215421	47617	ACAAACTAGAGTATATATGC	260008	92204	GCAGCAGAAACTGTCACGGG
170835	3031	AGACATTTCCAGAGGCGCAC	215422	47618	AACAAACTAGAGTATATATG	260009	92205	CGCAGCAGAAACTGTCACGG
170836	3032	CAGACATTTCCAGAGGCGCA	215423	47619	AAACAAACTAGAGTATATAT	260010	92206	ACGCAGCAGAAACTGTCACG
170837	3033	CCAGACATTTCCAGAGGCGC	215424	47620	TAAACAAACTAGAGTATATA	260011	92207	GACGCAGCAGAAACTGTCAC
170838	3034	CCCAGACATTTCCAGAGGCG	215425	47621	ATAAACAAACTAGAGTATAT	260012	92208	GGACGCAGCAGAAACTGTCA
170839	3035	GCCCAGACATTTCCAGAGGC	215426	47622	AATAAACAAACTAGAGTATA	260013	92209	GGGACGCAGCAGAAACTGTC
170840	3036	TGCCCAGACATTTCCAGAGG	215427	47623	AAATAAACAAACTAGAGTAT	260014	92210	GGGGACGCAGCAGAAACTGT
170841	3037	GTGCCCAGACATTTCCAGAG	215428	47624	CAAATAAACAAACTAGAGTA	260015	92211	AGGGGACGCAGCAGAAACTG
170842	3038	CGTGCCCAGACATTTCCAGA	215429	47625	ACAAATAAACAAACTAGAGT	260016	92212	GAGGGGACGCAGCAGAAACT
170843	3039	CCGTGCCCAGACATTTCCAG	215430	47626	AACAAATAAACAAACTAGAG	260017	92213	AGAGGGGACGCAGCAGAAAC
170844	3040	TCCGTGCCCAGACATTTCCA	215431	47627	AAACAAATAAACAAACTAGA	260018	92214	CAGAGGGGACGCAGCAGAAA
170845	3041	ATCCGTGCCCAGACATTTCC	215432	47628	CAAACAAATAAACAAACTAG	260019	92215	GCAGAGGGGACGCAGCAGAA
170846	3042	GATCCGTGCCCAGACATTTC	215433	47629	TCAAACAAATAAACAAACTA	260020	92216	TGCAGAGGGGACGCAGCAGA
170847	3043	GGATCCGTGCCCAGACATTT	215434	47630	GTCAAACAAATAAACAAACT	260021	92217	ATGCAGAGGGGACGCAGCAG
170848	3044	AGGATCCGTGCCCAGACATT	215435	47631	AGTCAAACAAATAAACAAAC	260022	92218	CATGCAGAGGGGACGCAGCA
170849	3045	CAGGATCCGTGCCCAGACAT	215436	47632	TAGTCAAACAAATAAACAAA	260023	92219	CCATGCAGAGGGGACGCAGC
170850	3046	CCAGGATCCGTGCCCAGACA	215437	47633	GTAGTCAAACAAATAAACAA	260024	92220	ACCATGCAGAGGGGACGCAG
170851	3047	CCCAGGATCCGTGCCCAGAC	215438	47634	TGTAGTCAAACAAATAAACA	260025	92221	GACCATGCAGAGGGGACGCA
170852	3048	CCCCAGGATCCGTGCCCAGA	215439	47635	GTGTAGTCAAACAAATAAAC	260026	92222	GGACCATGCAGAGGGGACGC
170853	3049	GCCCCAGGATCCGTGCCCAG	215440	47636	TGTGTAGTCAAACAAATAAA	260027	92223	GGGACCATGCAGAGGGGACG
170854	3050	GGCCCCAGGATCCGTGCCCA	215441	47637	ATGTGTAGTCAAACAAATAA	260028	92224	TGGGACCATGCAGAGGGGAC
170855	3051	TGGCCCCAGGATCCGTGCCC	215442	47638	TATGTGTAGTCAAACAAATA	260029	92225	GTGGGACCATGCAGAGGGGA
170856	3052	ATGGCCCCAGGATCCGTGCC	215443	47639	ATATGTGTAGTCAAACAAAT	260030	92226	GGTGGGACCATGCAGAGGGG
170857	3053	GATGGCCCCAGGATCCGTGC	215444	47640	TATATGTGTAGTCAAACAAA	260031	92227	GGGTGGGACCATGCAGAGGG
170858	3054	CGATGGCCCCAGGATCCGTG	215445	47641	ATATATGTGTAGTCAAACAA	260032	92228	AGGGTGGGACCATGCAGAGG
170859	3055	TCGATGGCCCCAGGATCCGT	215446	47642	CATATATGTGTAGTCAAACA	260033	92229	GAGGGTGGGACCATGCAGAG
170860	3056	GTCGATGGCCCCAGGATCCG	215447	47643	ACATATATGTGTAGTCAAAC	260034	92230	CGAGGGTGGGACCATGCAGA
170861	3057	CGTCGATGGCCCCAGGATCC	215448	47644	TACATATATGTGTAGTCAAA	260035	92231	CCGAGGGTGGGACCATGCAG
170862	3058	TCGTCGATGGCCCCAGGATC	215449	47645	ATACATATATGTGTAGTCAA	260036	92232	GCCGAGGGTGGGACCATGCA
170863	3059	GTCGTCGATGGCCCCAGGAT	215450	47646	AATACATATATGTGTAGTCA	260037	92233	GGCCGAGGGTGGGACCATGC
170864	3060	AGTCGTCGATGGCCCCAGGA	215451	47647	GAATACATATATGTGTAGTC	260038	92234	TGGCCGAGGGTGGGACCATG
170865	3061	GAGTCGTCGATGGCCCCAGG	215452	47648	AGAATACATATATGTGTAGT	260039	92235	CTGGCCGAGGGTGGGACCAT
170866	3062	GGAGTCGTCGATGGCCCCAG	215453	47649	AAGAATACATATATGTGTAG	260040	92236	GCTGGCCGAGGGTGGGACCA
170867	3063	AGGAGTCGTCGATGGCCCCA	215454	47650	AAAGAATACATATATGTGTA	260041	92237	GGCTGGCCGAGGGTGGGACC
170868	3064	GAGGAGTCGTCGATGGCCCC	215455	47651	AAAAGAATACATATATGTGT	260042	92238	AGGCTGGCCGAGGGTGGGAC
170869	3065	GGAGGAGTCGTCGATGGCCC	215456	47652	GAAAAGAATACATATATGTG	260043	92239	CAGGCTGGCCGAGGGTGGGA
170870	3066	GGGAGGAGTCGTCGATGGCC	215457	47653	AGAAAAGAATACATATATGT	260044	92240	GCAGGCTGGCCGAGGGTGGG
170871	3067	GGGGAGGAGTCGTCGATGGC	215458	47654	AAGAAAAGAATACATATATG	260045	92241	AGCAGGCTGGCCGAGGGTGG
170872	3068	TGGGGAGGAGTCGTCGATGG	215459	47655	TAAGAAAAGAATACATATAT	260046	92242	CAGCAGGCTGGCCGAGGGTG
170873	3069	ATGGGGAGGAGTCGTCGATG	215460	47656	ATAAGAAAAGAATACATATA	260047	92243	GCAGCAGGCTGGCCGAGGGT
170874	3070	AATGGGGAGGAGTCGTCGAT	215461	47657	CATAAGAAAAGAATACATAT	260048	92244	GGCAGCAGGCTGGCCGAGGG
170875	3071	GAATGGGGAGGAGTCGTCGA	215462	47658	ACATAAGAAAAGAATACATA	260049	92245	GGGCAGCAGGCTGGCCGAGG
170876	3072	GGAATGGGGAGGAGTCGTCG	215463	47659	TACATAAGAAAAGAATACAT	260050	92246	GGGGCAGCAGGCTGGCCGAG
170877	3073	GGGAATGGGGAGGAGTCGTC	215464	47660	ATACATAAGAAAAGAATACA	260051	92247	GGGGGCAGCAGGCTGGCCGA
170878	3074	TGGGAATGGGGAGGAGTCGT	215465	47661	TATACATAAGAAAAGAATAC	260052	92248	AGGGGGCAGCAGGCTGGCCG
170879	3075	CTGGGAATGGGGAGGAGTCG	215466	47662	TTATACATAAGAAAAGAATA	260053	92249	GAGGGGGCAGCAGGCTGGCC
170880	3076	GCTGGGAATGGGGAGGAGTC	215467	47663	TTTATACATAAGAAAAGAAT	260054	92250	AGAGGGGGCAGCAGGCTGGC
170881	3077	TGCTGGGAATGGGGAGGAGT	215468	47664	TTTTATACATAAGAAAAGAA	260055	92251	AAGAGGGGGCAGCAGGCTGG
170882	3078	CTGCTGGGAATGGGGAGGAG	215469	47665	TTTTTATACATAAGAAAAGA	260056	92252	CAAGAGGGGGCAGCAGGCTG
170883	3079	CCTGCTGGGAATGGGGAGGA	215470	47666	ATTTTTATACATAAGAAAAG	260057	92253	GCAAGAGGGGGCAGCAGGCT
170884	3080	GCCTGCTGGGAATGGGGAGG	215471	47667	AATTTTTATACATAAGAAAA	260058	92254	GGCAAGAGGGGGCAGCAGGC
170885	3081	CGCCTGCTGGGAATGGGGAG	215472	47668	GAATTTTTATACATAAGAAA	260059	92255	TGGCAAGAGGGGGCAGCAGG
170886	3082	CCGCCTGCTGGGAATGGGGA	215473	47669	AGAATTTTTATACATAAGAA	260060	92256	CTGGCAAGAGGGGGCAGCAG
170887	3083	CCCGCCTGCTGGGAATGGGG	215474	47670	CAGAATTTTTATACATAAGA	260061	92257	CCTGGCAAGAGGGGGCAGCA
170888	3084	TCCCGCCTGCTGGGAATGGG	215475	47671	TCAGAATTTTTATACATAAG	260062	92258	ACCTGGCAAGAGGGGGCAGC
170889	3085	CTCCCGCCTGCTGGGAATGG	215476	47672	TTCAGAATTTTTATACATAA	260063	92259	AACCTGGCAAGAGGGGGCAG
170890	3086	GCTCCCGCCTGCTGGGAATG	215477	47673	GTTCAGAATTTTTATACATA	260064	92260	CAACCTGGCAAGAGGGGGCA
170891	3087	AGCTCCCGCCTGCTGGGAAT	215478	47674	TGTTCAGAATTTTTATACAT	260065	92261	GCAACCTGGCAAGAGGGGGC
170892	3088	GAGCTCCCGCCTGCTGGGAA	215479	47675	ATGTTCAGAATTTTTATACA	260066	92262	CGCAACCTGGCAAGAGGGGG
170893	3089	AGAGCTCCCGCCTGCTGGGA	215480	47676	CATGTTCAGAATTTTTATAC	260067	92263	GCGCAACCTGGCAAGAGGGG
170894	3090	AAGAGCTCCCGCCTGCTGGG	215481	47677	GCATGTTCAGAATTTTTATA	260068	92264	AGCGCAACCTGGCAAGAGGG
170895	3091	TAAGAGCTCCCGCCTGCTGG	215482	47678	TGCATGTTCAGAATTTTTAT	260069	92265	TAGCGCAACCTGGCAAGAGG
170896	3092	GTAAGAGCTCCCGCCTGCTG	215483	47679	GTGCATGTTCAGAATTTTTA	260070	92266	TTAGCGCAACCTGGCAAGAG
170897	3093	TGTAAGAGCTCCCGCCTGCT	215484	47680	TGTGCATGTTCAGAATTTTT	260071	92267	ATTAGCGCAACCTGGCAAGA
170898	3094	ATGTAAGAGCTCCCGCCTGC	215485	47681	ATGTGCATGTTCAGAATTTT	260072	92268	GATTAGCGCAACCTGGCAAG

170899	3095	AATGTAAGAGCTCCCGCCTG	215486	47682	AATGTGCATGTTCAGAATTT	260073	92269	TGATTAGCGCAACCTGGCAA
170900	3096	GAATGTAAGAGCTCCCGCCT	215487	47683	AAATGTGCATGTTCAGAATT	260074	92270	CTGATTAGCGCAACCTGGCA
170901	3097	GGAATGTAAGAGCTCCCGCC	215488	47684	GAAATGTGCATGTTCAGAAT	260075	92271	ACTGATTAGCGCAACCTGGC
170902	3098	CGGAATGTAAGAGCTCCCGC	215489	47685	AGAAATGTGCATGTTCAGAA	260076	92272	CACTGATTAGCGCAACCTGG
170903	3099	TCGGAATGTAAGAGCTCCCG	215490	47686	CAGAAATGTGCATGTTCAGA	260077	92273	TCACTGATTAGCGCAACCTG
170904	3100	CTCGGAATGTAAGAGCTCCC	215491	47687	GCAGAAATGTGCATGTTCAG	260078	92274	GTCACTGATTAGCGCAACCT
170905	3101	GCTCGGAATGTAAGAGCTCC	215492	47688	TGCAGAAATGTGCATGTTCA	260079	92275	GGTCACTGATTAGCGCAACC
170906	3102	CGCTCGGAATGTAAGAGCTC	215493	47689	TTGCAGAAATGTGCATGTTC	260080	92276	GGGTCACTGATTAGCGCAAC
170907	3103	TCGCTCGGAATGTAAGAGCT	215494	47690	GTTGCAGAAATGTGCATGTT	260081	92277	GGGGTCACTGATTAGCGCAA
170908	3104	CTCGCTCGGAATGTAAGAGC	215495	47691	AGTTGCAGAAATGTGCATGT	260082	92278	TGGGGTCACTGATTAGCGCA
170909	3105	ACTCGCTCGGAATGTAAGAG	215496	47692	TAGTTGCAGAAATGTGCATG	260083	92279	CTGGGGTCACTGATTAGCGC
170910	3106	CACTCGCTCGGAATGTAAGA	215497	47693	GTAGTTGCAGAAATGTGCAT	260084	92280	ACTGGGGTCACTGATTAGCG
170911	3107	TCACTCGCTCGGAATGTAAG	215498	47694	AGTAGTTGCAGAAATGTGCA	260085	92281	CACTGGGGTCACTGATTAGC
170912	3108	GTCACTCGCTCGGAATGTAA	215499	47695	CAGTAGTTGCAGAAATGTGC	260086	92282	ACACTGGGGTCACTGATTAG
170913	3109	GGTCACTCGCTCGGAATGTA	215500	47696	ACAGTAGTTGCAGAAATGTG	260087	92283	CACACTGGGGTCACTGATTA
170914	3110	GGGTCACTCGCTCGGAATGT	215501	47697	AACAGTAGTTGCAGAAATGT	260088	92284	GCACACTGGGGTCACTGATT
170915	3111	GGGGTCACTCGCTCGGAATG	215502	47698	AAACAGTAGTTGCAGAAATG	260089	92285	AGCACACTGGGGTCACTGAT
170916	3112	AGGGGTCACTCGCTCGGAAT	215503	47699	AAAACAGTAGTTGCAGAAAT	260090	92286	CAGCACACTGGGGTCACTGA
170917	3113	GAGGGGTCACTCGCTCGGAA	215504	47700	GAAAACAGTAGTTGCAGAAA	260091	92287	ACAGCACACTGGGGTCACTG
170918	3114	AGAGGGGTCACTCGCTCGGA	215505	47701	TGAAAACAGTAGTTGCAGAA	260092	92288	CACAGCACACTGGGGTCACT
170919	3115	GAGAGGGGTCACTCGCTCGG	215506	47702	GTGAAAACAGTAGTTGCAGA	260093	92289	ACACAGCACACTGGGGTCAC
170920	3116	TGAGAGGGGTCACTCGCTCG	215507	47703	AGTGAAAACAGTAGTTGCAG	260094	92290	AACACAGCACACTGGGGTCA
170921	3117	GTGAGAGGGGTCACTCGCTC	215508	47704	AAGTGAAAACAGTAGTTGCA	260095	92291	CAACACAGCACACTGGGGTC
170922	3118	GGTGAGAGGGGTCACTCGCT	215509	47705	CAAGTGAAAACAGTAGTTGC	260096	92292	TCAACACAGCACACTGGGGT
170923	3119	GGGTGAGAGGGGTCACTCGC	215510	47706	TCAAGTGAAAACAGTAGTTG	260097	92293	ATCAACACAGCACACTGGGG
170924	3120	AGGGTGAGAGGGGTCACTCG	215511	47707	ATCAAGTGAAAACAGTAGTT	260098	92294	TATCAACACAGCACACTGGG
170925	3121	GAGGGTGAGAGGGGTCACTC	215512	47708	CATCAAGTGAAAACAGTAGT	260099	92295	GTATCAACACAGCACACTGG
170926	3122	AGAGGGTGAGAGGGGTCACT	215513	47709	TCATCAAGTGAAAACAGTAG	260100	92296	AGTATCAACACAGCACACTG
170927	3123	CAGAGGGTGAGAGGGGTCAC	215514	47710	ATCATCAAGTGAAAACAGTA	260101	92297	TAGTATCAACACAGCACACT
170928	3124	CCAGAGGGTGAGAGGGGTCA	215515	47711	CATCATCAAGTGAAAACAGT	260102	92298	TTAGTATCAACACAGCACAC
170929	3125	GCCAGAGGGTGAGAGGGGTC	215516	47712	GCATCATCAAGTGAAAACAG	260103	92299	GTTAGTATCAACACAGCACA
170930	3126	CGCCAGAGGGTGAGAGGGGT	215517	47713	TGCATCATCAAGTGAAAACA	260104	92300	TGTTAGTATCAACACAGCAC
170931	3127	GCGCCAGAGGGTGAGAGGGG	215518	47714	ATGCATCATCAAGTGAAAAC	260105	92301	TTGTTAGTATCAACACAGCA
170932	3128	AGCGCCAGAGGGTGAGAGGG	215519	47715	CATGCATCATCAAGTGAAAA	260106	92302	ATTGTTAGTATCAACACAGC
170933	3129	GAGCGCCAGAGGGTGAGAGG	215520	47716	CCATGCATCATCAAGTGAAA	260107	92303	CATTGTTAGTATCAACACAG
170934	3130	TGAGCGCCAGAGGGTGAGAG	215521	47717	TCCATGCATCATCAAGTGAA	260108	92304	GCATTGTTAGTATCAACACA
170935	3131	GTGAGCGCCAGAGGGTGAGA	215522	47718	GTCCATGCATCATCAAGTGA	260109	92305	CGCATTGTTAGTATCAACAC
170936	3132	TGTGAGCGCCAGAGGGTGAG	215523	47719	GGTCCATGCATCATCAAGTG	260110	92306	TCGCATTGTTAGTATCAACA
170937	3133	GTGTGAGCGCCAGAGGGTGA	215524	47720	AGGTCCATGCATCATCAAGT	260111	92307	CTCGCATTGTTAGTATCAAC
170938	3134	TGTGTGAGCGCCAGAGGGTG	215525	47721	GAGGTCCATGCATCATCAAG	260112	92308	CCTCGCATTGTTAGTATCAA
170939	3135	GTGTGTGAGCGCCAGAGGGT	215526	47722	AGAGGTCCATGCATCATCAA	260113	92309	GCCTCGCATTGTTAGTATCA
170940	3136	GGTGTGTGAGCGCCAGAGGG	215527	47723	GAGAGGTCCATGCATCATCA	260114	92310	GGCCTCGCATTGTTAGTATC
170941	3137	AGGTGTGTGAGCGCCAGAGG	215528	47724	AGAGAGGTCCATGCATCATC	260115	92311	AGGCCTCGCATTGTTAGTAT
170942	3138	CAGGTGTGTGAGCGCCAGAG	215529	47725	TAGAGAGGTCCATGCATCAT	260116	92312	TAGGCCTCGCATTGTTAGTA
170943	3139	ACAGGTGTGTGAGCGCCAGA	215530	47726	CTAGAGAGGTCCATGCATCA	260117	92313	CTAGGCCTCGCATTGTTAGT
170944	3140	TACAGGTGTGTGAGCGCCAG	215531	47727	TCTAGAGAGGTCCATGCATC	260118	92314	GCTAGGCCTCGCATTGTTAG
170945	3141	TTACAGGTGTGTGAGCGCCA	215532	47728	CTCTAGAGAGGTCCATGCAT	260119	92315	TGCTAGGCCTCGCATTGTTA
170946	3142	GTTACAGGTGTGTGAGCGCC	215533	47729	ACTCTAGAGAGGTCCATGCA	260120	92316	CTGCTAGGCCTCGCATTGTT
170947	3143	AGTTACAGGTGTGTGAGCGC	215534	47730	CACTCTAGAGAGGTCCATGC	260121	92317	TCTGCTAGGCCTCGCATTGT
170948	3144	GAGTTACAGGTGTGTGAGCG	215535	47731	ACACTCTAGAGAGGTCCATG	260122	92318	ATCTGCTAGGCCTCGCATTG
170949	3145	GGAGTTACAGGTGTGTGAGC	215536	47732	TACACTCTAGAGAGGTCCAT	260123	92319	AATCTGCTAGGCCTCGCATT
170950	3146	TGGAGTTACAGGTGTGTGAG	215537	47733	GTACACTCTAGAGAGGTCCA	260124	92320	GAATCTGCTAGGCCTCGCAT
170951	3147	TTGGAGTTACAGGTGTGTGA	215538	47734	CGTACACTCTAGAGAGGTCC	260125	92321	TGAATCTGCTAGGCCTCGCA
170952	3148	TTTGGAGTTACAGGTGTGTG	215539	47735	ACGTACACTCTAGAGAGGTC	260126	92322	TTGAATCTGCTAGGCCTCGC
170953	3149	GTTTGGAGTTACAGGTGTGT	215540	47736	AACGTACACTCTAGAGAGGT	260127	92323	CTTGAATCTGCTAGGCCTCG
170954	3150	GGTTTGGAGTTACAGGTGTG	215541	47737	AAACGTACACTCTAGAGAGG	260128	92324	CCTTGAATCTGCTAGGCCTC
170955	3151	AGGTTTGGAGTTACAGGTGT	215542	47738	GAAACGTACACTCTAGAGAG	260129	92325	CCCTTGAATCTGCTAGGCCT
170956	3152	GAGGTTTGGAGTTACAGGTG	215543	47739	AGAAACGTACACTCTAGAGA	260130	92326	TCCCTTGAATCTGCTAGGCC
170957	3153	GGAGGTTTGGAGTTACAGGT	215544	47740	AAGAAACGTACACTCTAGAG	260131	92327	TTCCCTTGAATCTGCTAGGC
170958	3154	CGGAGGTTTGGAGTTACAGG	215545	47741	GAAGAAACGTACACTCTAGA	260132	92328	TTTCCCTTGAATCTGCTAGG
170959	3155	ACGGAGGTTTGGAGTTACAG	215546	47742	AGAAGAAACGTACACTCTAG	260133	92329	TTTTCCCTTGAATCTGCTAG
170960	3156	GACGGAGGTTTGGAGTTACA	215547	47743	AAGAAGAAACGTACACTCTA	260134	92330	CTTTTCCCTTGAATCTGCTA
170961	3157	AGACGGAGGTTTGGAGTTAC	215548	47744	GAAGAAGAAACGTACACTCT	260135	92331	TCTTTTCCCTTGAATCTGCT
170962	3158	GAGACGGAGGTTTGGAGTTA	215549	47745	GGAAGAAGAAACGTACACTC	260136	92332	CTCTTTTCCCTTGAATCTGC
170963	3159	TGAGACGGAGGTTTGGAGTT	215550	47746	AGGAAGAAGAAACGTACACT	260137	92333	TCTCTTTTCCCTTGAATCTG
170964	3160	CTGAGACGGAGGTTTGGAGT	215551	47747	AAGGAAGAAGAAACGTACAC	260138	92334	TTCTCTTTTCCCTTGAATCT
170965	3161	TCTGAGACGGAGGTTTGGAG	215552	47748	TAAGGAAGAAGAAACGTACA	260139	92335	GTTCTCTTTTCCCTTGAATC
170966	3162	TTCTGAGACGGAGGTTTGGA	215553	47749	GTAAGGAAGAAGAAACGTAC	260140	92336	GGTTCTCTTTTCCCTTGAAT
170967	3163	ATTCTGAGACGGAGGTTTGG	215554	47750	TGTAAGGAAGAAGAAACGTA	260141	92337	TGGTTCTCTTTTCCCTTGAA
170968	3164	CATTCTGAGACGGAGGTTTG	215555	47751	TTGTAAGGAAGAAGAAACGT	260142	92338	TTGGTTCTCTTTTCCCTTGA
170969	3165	CCATTCTGAGACGGAGGTTT	215556	47752	TTTGTAAGGAAGAAGAAACG	260143	92339	GTTGGTTCTCTTTTCCCTTG
170970	3166	ACCATTCTGAGACGGAGGTT	215557	47753	CTTTGTAAGGAAGAAGAAAC	260144	92340	AGTTGGTTCTCTTTTCCCTT

170971	3167	GACCATTCTGAGACGGAGGT	215558	47754	GCTTTGTAAGGAAGAAGAAA	260145	92341	CAGTTGGTTCTCTTTTCCCT
170972	3168	GGACCATTCTGAGACGGAGG	215559	47755	TGCTTTGTAAGGAAGAAGAA	260146	92342	CCAGTTGGTTCTCTTTTCCC
170973	3169	TGGACCATTCTGAGACGGAG	215560	47756	CTGCTTTGTAAGGAAGAAGA	260147	92343	CCCAGTTGGTTCTCTTTTCC
170974	3170	CTGGACCATTCTGAGACGGA	215561	47757	ACTGCTTTGTAAGGAAGAAG	260148	92344	ACCCAGTTGGTTCTCTTTTC
170975	3171	CCTGGACCATTCTGAGACGG	215562	47758	AACTGCTTTGTAAGGAAGAA	260149	92345	AACCCAGTTGGTTCTCTTTT
170976	3172	GCCTGGACCATTCTGAGACG	215563	47759	CAACTGCTTTGTAAGGAAGA	260150	92346	AAACCCAGTTGGTTCTCTTT
170977	3173	AGCCTGGACCATTCTGAGAC	215564	47760	CCAACTGCTTTGTAAGGAAG	260151	92347	GAAACCCAGTTGGTTCTCTT
170978	3174	CAGCCTGGACCATTCTGAGA	215565	47761	GCCAACTGCTTTGTAAGGAA	260152	92348	GGAAACCCAGTTGGTTCTCT
170979	3175	CCAGCCTGGACCATTCTGAG	215566	47762	AGCCAACTGCTTTGTAAGGA	260153	92349	TGGAAACCCAGTTGGTTCTC
170980	3176	TCCAGCCTGGACCATTCTGA	215567	47763	AAGCCAACTGCTTTGTAAGG	260154	92350	GTGGAAACCCAGTTGGTTCT
170981	3177	TTCCAGCCTGGACCATTCTG	215568	47764	GAAGCCAACTGCTTTGTAAG	260155	92351	GGTGGAAACCCAGTTGGTTC
170982	3178	CTTCCAGCCTGGACCATTCT	215569	47765	CGAAGCCAACTGCTTTGTAA	260156	92352	TGGTGGAAACCCAGTTGGTT
170983	3179	CCTTCCAGCCTGGACCATTC	215570	47766	GCGAAGCCAACTGCTTTGTA	260157	92353	CTGGTGGAAACCCAGTTGGT
170984	3180	CCCTTCCAGCCTGGACCATT	215571	47767	GGCGAAGCCAACTGCTTTGT	260158	92354	TCTGGTGGAAACCCAGTTGG
170985	3181	TCCCTTCCAGCCTGGACCAT	215572	47768	GGGCGAAGCCAACTGCTTTG	260159	92355	GTCTGGTGGAAACCCAGTTG
170986	3182	ATCCCTTCCAGCCTGGACCA	215573	47769	TGGGCGAAGCCAACTGCTTT	260160	92356	GGTCTGGTGGAAACCCAGTT
170987	3183	CATCCCTTCCAGCCTGGACC	215574	47770	CTGGGCGAAGCCAACTGCTT	260161	92357	GGGTCTGGTGGAAACCCAGT
170988	3184	TCATCCCTTCCAGCCTGGAC	215575	47771	CCTGGGCGAAGCCAACTGCT	260162	92358	TGGGTCTGGTGGAAACCCAG
170989	3185	ATCATCCCTTCCAGCCTGGA	215576	47772	CCCTGGGCGAAGCCAACTGC	260163	92359	TTGGGTCTGGTGGAAACCCA
170990	3186	CATCATCCCTTCCAGCCTGG	215577	47773	ACCCTGGGCGAAGCCAACTG	260164	92360	GTTGGGTCTGGTGGAAACCC
170991	3187	CCATCATCCCTTCCAGCCTG	215578	47774	CACCCTGGGCGAAGCCAACT	260165	92361	AGTTGGGTCTGGTGGAAACC
170992	3188	CCCATCATCCCTTCCAGCCT	215579	47775	GCACCCTGGGCGAAGCCAAC	260166	92362	TAGTTGGGTCTGGTGGAAAC
170993	3189	CCCCATCATCCCTTCCAGCC	215580	47776	TGCACCCTGGGCGAAGCCAA	260167	92363	TTAGTTGGGTCTGGTGGAAA
170994	3190	CCCCCATCATCCCTTCCAGC	215581	47777	GTGCACCCTGGGCGAAGCCA	260168	92364	TTTAGTTGGGTCTGGTGGAA
170995	3191	GCCCCCATCATCCCTTCCAG	215582	47778	GGTGCACCCTGGGCGAAGCC	260169	92365	GTTTAGTTGGGTCTGGTGGA
170996	3192	AGCCCCCATCATCCCTTCCA	215583	47779	TGGTGCACCCTGGGCGAAGC	260170	92366	TGTTTAGTTGGGTCTGGTGG
170997	3193	GAGCCCCCATCATCCCTTCC	215584	47780	CTGGTGCACCCTGGGCGAAG	260171	92367	TTGTTTAGTTGGGTCTGGTG
170998	3194	GGAGCCCCCATCATCCCTTC	215585	47781	CCTGGTGCACCCTGGGCGAA	260172	92368	TTTGTTTAGTTGGGTCTGGT
170999	3195	CGGAGCCCCCATCATCCCTT	215586	47782	TCCTGGTGCACCCTGGGCGA	260173	92369	GTTTGTTTAGTTGGGTCTGG
171000	3196	TCGGAGCCCCCATCATCCCT	215587	47783	GTCCTGGTGCACCCTGGGCG	260174	92370	TGTTTGTTTAGTTGGGTCTG
171001	3197	GTCGGAGCCCCCATCATCCC	215588	47784	TGTCCTGGTGCACCCTGGGC	260175	92371	ATGTTTGTTTAGTTGGGTCT
171002	3198	TGTCGGAGCCCCCATCATCC	215589	47785	GTGTCCTGGTGCACCCTGGG	260176	92372	CATGTTTGTTTAGTTGGGTC
171003	3199	CTGTCGGAGCCCCCATCATC	215590	47786	CGTGTCCTGGTGCACCCTGG	260177	92373	CCATGTTTGTTTAGTTGGGT
171004	3200	GCTGTCGGAGCCCCCATCAT	215591	47787	CCGTGTCCTGGTGCACCCTG	260178	92374	TCCATGTTTGTTTAGTTGGG
171005	3201	CGCTGTCGGAGCCCCCATCA	215592	47788	ACCGTGTCCTGGTGCACCCT	260179	92375	GTCCATGTTTGTTTAGTTGG
171006	3202	TCGCTGTCGGAGCCCCCATC	215593	47789	AACCGTGTCCTGGTGCACCC	260180	92376	GGTCCATGTTTGTTTAGTTG
171007	3203	GTCGCTGTCGGAGCCCCCAT	215594	47790	AAACCGTGTCCTGGTGCACC	260181	92377	AGGTCCATGTTTGTTTAGTT
171008	3204	AGTCGCTGTCGGAGCCCCCA	215595	47791	AAAACCGTGTCCTGGTGCAC	260182	92378	TAGGTCCATGTTTGTTTAGT
171009	3205	CAGTCGCTGTCGGAGCCCCC	215596	47792	CAAAACCGTGTCCTGGTGCA	260183	92379	ATAGGTCCATGTTTGTTTAG
171010	3206	GCAGTCGCTGTCGGAGCCCC	215597	47793	CCAAAACCGTGTCCTGGTGC	260184	92380	GATAGGTCCATGTTTGTTTA
171011	3207	GGCAGTCGCTGTCGGAGCCC	215598	47794	GCCAAAACCGTGTCCTGGTG	260185	92381	GGATAGGTCCATGTTTGTTT
171012	3208	AGGCAGTCGCTGTCGGAGCC	215599	47795	AGCCAAAACCGTGTCCTGGT	260186	92382	GGGATAGGTCCATGTTTGTT
171013	3209	TAGGCAGTCGCTGTCGGAGC	215600	47796	GAGCCAAAACCGTGTCCTGG	260187	92383	TGGGATAGGTCCATGTTTGT
171014	3210	CTAGGCAGTCGCTGTCGGAG	215601	47797	AGAGCCAAAACCGTGTCCTG	260188	92384	CTGGGATAGGTCCATGTTTG
171015	3211	GCTAGGCAGTCGCTGTCGGA	215602	47798	CAGAGCCAAAACCGTGTCCT	260189	92385	TCTGGGATAGGTCCATGTTT
171016	3212	AGCTAGGCAGTCGCTGTCGG	215603	47799	ACAGAGCCAAAACCGTGTCC	260190	92386	CTCTGGGATAGGTCCATGTT
171017	3213	GAGCTAGGCAGTCGCTGTCG	215604	47800	GACAGAGCCAAAACCGTGTC	260191	92387	TCTCTGGGATAGGTCCATGT
171018	3214	TGAGCTAGGCAGTCGCTGTC	215605	47801	GGACAGAGCCAAAACCGTGT	260192	92388	TTCTCTGGGATAGGTCCATG
171019	3215	GTGAGCTAGGCAGTCGCTGT	215606	47802	GGGACAGAGCCAAAACCGTG	260193	92389	TTTCTCTGGGATAGGTCCAT
171020	3216	GGTGAGCTAGGCAGTCGCTG	215607	47803	GGGGACAGAGCCAAAACCGT	260194	92390	ATTTCTCTGGGATAGGTCCA
171021	3217	GGGTGAGCTAGGCAGTCGCT	215608	47804	TGGGGACAGAGCCAAAACCG	260195	92391	GATTTCTCTGGGATAGGTCC
171022	3218	GGGGTGAGCTAGGCAGTCGC	215609	47805	CTGGGGACAGAGCCAAAACC	260196	92392	GGATTTCTCTGGGATAGGTC
171023	3219	AGGGGTGAGCTAGGCAGTCG	215610	47806	CCTGGGGACAGAGCCAAAAC	260197	92393	TGGATTTCTCTGGGATAGGT
171024	3220	GAGGGGTGAGCTAGGCAGTC	215611	47807	CCCTGGGGACAGAGCCAAAA	260198	92394	CTGGATTTCTCTGGGATAGG
171025	3221	AGAGGGGTGAGCTAGGCAGT	215612	47808	ACCCTGGGGACAGAGCCAAA	260199	92395	GCTGGATTTCTCTGGGATAG
171026	3222	CAGAGGGGTGAGCTAGGCAG	215613	47809	CACCCTGGGGACAGAGCCAA	260200	92396	AGCTGGATTTCTCTGGGATA
171027	3223	GCAGAGGGGTGAGCTAGGCA	215614	47810	ACACCCTGGGGACAGAGCCA	260201	92397	AAGCTGGATTTCTCTGGGAT
171028	3224	CGCAGAGGGGTGAGCTAGGC	215615	47811	GACACCCTGGGGACAGAGCC	260202	92398	GAAGCTGGATTTCTCTGGGA
171029	3225	ACGCAGAGGGGTGAGCTAGG	215616	47812	TGACACCCTGGGGACAGAGC	260203	92399	TGAAGCTGGATTTCTCTGGG
171030	3226	CACGCAGAGGGGTGAGCTAG	215617	47813	GTGACACCCTGGGGACAGAG	260204	92400	GTGAAGCTGGATTTCTCTGG
171031	3227	GCACGCAGAGGGGTGAGCTA	215618	47814	CGTGACACCCTGGGGACAGA	260205	92401	GGTGAAGCTGGATTTCTCTG
171032	3228	AGCACGCAGAGGGGTGAGCT	215619	47815	CCGTGACACCCTGGGGACAG	260206	92402	TGGTGAAGCTGGATTTCTCT
171033	3229	GAGCACGCAGAGGGGTGAGC	215620	47816	CCCGTGACACCCTGGGGACA	260207	92403	GTGGTGAAGCTGGATTTCTC
171034	3230	TGAGCACGCAGAGGGGTGAG	215621	47817	TCCCGTGACACCCTGGGGAC	260208	92404	TGTGGTGAAGCTGGATTTCT
171035	3231	CTGAGCACGCAGAGGGGTGA	215622	47818	GTCCCGTGACACCCTGGGGA	260209	92405	CTGTGGTGAAGCTGGATTTC
171036	3232	CCTGAGCACGCAGAGGGGTG	215623	47819	GGTCCCGTGACACCCTGGGG	260210	92406	GCTGTGGTGAAGCTGGATTT
171037	3233	GCCTGAGCACGCAGAGGGGT	215624	47820	TGGTCCCGTGACACCCTGGG	260211	92407	AGCTGTGGTGAAGCTGGATT
171038	3234	AGCCTGAGCACGCAGAGGGG	215625	47821	CTGGTCCCGTGACACCCTGG	260212	92408	CAGCTGTGGTGAAGCTGGAT
171039	3235	GAGCCTGAGCACGCAGAGGG	215626	47822	CCTGGTCCCGTGACACCCTG	260213	92409	CCAGCTGTGGTGAAGCTGGA
171040	3236	GGAGCCTGAGCACGCAGAGG	215627	47823	CCCTGGTCCCGTGACACCCT	260214	92410	GCCAGCTGTGGTGAAGCTGG
171041	3237	TGGAGCCTGAGCACGCAGAG	215628	47824	CCCCTGGTCCCGTGACACCC	260215	92411	AGCCAGCTGTGGTGAAGCTG
171042	3238	CTGGAGCCTGAGCACGCAGA	215629	47825	TCCCCTGGTCCCGTGACACC	260216	92412	AAGCCAGCTGTGGTGAAGCT

171043	3239	CCTGGAGCCTGAGCACGCAG	215630	47826	ATCCCCTGGTCCCGTGACAC	260217	92413	AAAGCCAGCTGTGGTGAAGC
171044	3240	GCCTGGAGCCTGAGCACGCA	215631	47827	CATCCCCTGGTCCCGTGACA	260218	92414	GAAAGCCAGCTGTGGTGAAG
171045	3241	AGCCTGGAGCCTGAGCACGC	215632	47828	TCATCCCCTGGTCCCGTGAC	260219	92415	AGAAAGCCAGCTGTGGTGAA
171046	3242	GAGCCTGGAGCCTGAGCACG	215633	47829	ATCATCCCCTGGTCCCGTGA	260220	92416	CAGAAAGCCAGCTGTGGTGA
171047	3243	TGAGCCTGGAGCCTGAGCAC	215634	47830	GATCATCCCCTGGTCCCGTG	260221	92417	ACAGAAAGCCAGCTGTGGTG
171048	3244	CTGAGCCTGGAGCCTGAGCA	215635	47831	AGATCATCCCCTGGTCCCGT	260222	92418	CACAGAAAGCCAGCTGTGGT
171049	3245	GCTGAGCCTGGAGCCTGAGC	215636	47832	GAGATCATCCCCTGGTCCCG	260223	92419	TCACAGAAAGCCAGCTGTGG
171050	3246	TGCTGAGCCTGGAGCCTGAG	215637	47833	TGAGATCATCCCCTGGTCCC	260224	92420	TTCACAGAAAGCCAGCTGTG
171051	3247	CTGCTGAGCCTGGAGCCTGA	215638	47834	GTGAGATCATCCCCTGGTCC	260225	92421	GTTCACAGAAAGCCAGCTGT
171052	3248	CCTGCTGAGCCTGGAGCCTG	215639	47835	TGTGAGATCATCCCCTGGTC	260226	92422	TGTTCACAGAAAGCCAGCTG
171053	3249	TCCTGCTGAGCCTGGAGCCT	215640	47836	CTGTGAGATCATCCCCTGGT	260227	92423	CTGTTCACAGAAAGCCAGCT
171054	3250	GTCCTGCTGAGCCTGGAGCC	215641	47837	CCTGTGAGATCATCCCCTGG	260228	92424	ACTGTTCACAGAAAGCCAGC
171055	3251	GGTCCTGCTGAGCCTGGAGC	215642	47838	CCCTGTGAGATCATCCCCTG	260229	92425	CACTGTTCACAGAAAGCCAG
171056	3252	TGGTCCTGCTGAGCCTGGAG	215643	47839	ACCCTGTGAGATCATCCCCT	260230	92426	TCACTGTTCACAGAAAGCCA
171057	3253	TTGGTCCTGCTGAGCCTGGA	215644	47840	GACCCTGTGAGATCATCCCC	260231	92427	TTCACTGTTCACAGAAAGCC
171058	3254	ATTGGTCCTGCTGAGCCTGG	215645	47841	AGACCCTGTGAGATCATCCC	260232	92428	TTTCACTGTTCACAGAAAGC
171059	3255	AATTGGTCCTGCTGAGCCTG	215646	47842	CAGACCCTGTGAGATCATCC	260233	92429	TTTTCACTGTTCACAGAAAG
171060	3256	AAATTGGTCCTGCTGAGCCT	215647	47843	GCAGACCCTGTGAGATCATC	260234	92430	ATTTTCACTGTTCACAGAAA
171061	3257	CAAATTGGTCCTGCTGAGCC	215648	47844	GGCAGACCCTGTGAGATCAT	260235	92431	CATTTTCACTGTTCACAGAA
171062	3258	TCAAATTGGTCCTGCTGAGC	215649	47845	TGGCAGACCCTGTGAGATCA	260236	92432	CCATTTTCACTGTTCACAGA
171063	3259	CTCAAATTGGTCCTGCTGAG	215650	47846	ATGGCAGACCCTGTGAGATC	260237	92433	TCCATTTTCACTGTTCACAG
171064	3260	ACTCAAATTGGTCCTGCTGA	215651	47847	GATGGCAGACCCTGTGAGAT	260238	92434	CTCCATTTTCACTGTTCACA
171065	3261	AACTCAAATTGGTCCTGCTG	215652	47848	AGATGGCAGACCCTGTGAGA	260239	92435	ACTCCATTTTCACTGTTCAC
171066	3262	GAACTCAAATTGGTCCTGCT	215653	47849	CAGATGGCAGACCCTGTGAG	260240	92436	CACTCCATTTTCACTGTTCA
171067	3263	AGAACTCAAATTGGTCCTGC	215654	47850	GCAGATGGCAGACCCTGTGA	260241	92437	ACACTCCATTTTCACTGTTC
171068	3264	TAGAACTCAAATTGGTCCTG	215655	47851	GGCAGATGGCAGACCCTGTG	260242	92438	CACACTCCATTTTCACTGTT
171069	3265	ATAGAACTCAAATTGGTCCT	215656	47852	GGGCAGATGGCAGACCCTGT	260243	92439	TCACACTCCATTTTCACTGT
171070	3266	GATAGAACTCAAATTGGTCC	215657	47853	AGGGCAGATGGCAGACCCTG	260244	92440	GTCACACTCCATTTTCACTG
171071	3267	AGATAGAACTCAAATTGGTC	215658	47854	CAGGGCAGATGGCAGACCCT	260245	92441	TGTCACACTCCATTTTCACT
171072	3268	CAGATAGAACTCAAATTGGT	215659	47855	GCAGGGCAGATGGCAGACCC	260246	92442	TTGTCACACTCCATTTTCAC
171073	3269	TCAGATAGAACTCAAATTGG	215660	47856	GGCAGGGCAGATGGCAGACC	260247	92443	CTTGTCACACTCCATTTTCA
171074	3270	ATCAGATAGAACTCAAATTG	215661	47857	AGGCAGGGCAGATGGCAGAC	260248	92444	GCTTGTCACACTCCATTTTC
171075	3271	GATCAGATAGAACTCAAATT	215662	47858	CAGGCAGGGCAGATGGCAGA	260249	92445	TGCTTGTCACACTCCATTTT
171076	3272	GGATCAGATAGAACTCAAAT	215663	47859	CCAGGCAGGGCAGATGGCAG	260250	92446	ATGCTTGTCACACTCCATTT
171077	3273	GGGATCAGATAGAACTCAAA	215664	47860	GCCAGGCAGGGCAGATGGCA	260251	92447	AATGCTTGTCACACTCCATT
171078	3274	GGGGATCAGATAGAACTCAA	215665	47861	GGCCAGGCAGGGCAGATGGC	260252	92448	GAATGCTTGTCACACTCCAT
171079	3275	GGGGGATCAGATAGAACTCA	215666	47862	CGGCCAGGCAGGGCAGATGG	260253	92449	AGAATGCTTGTCACACTCCA
171080	3276	AGGGGGATCAGATAGAACTC	215667	47863	CCGGCCAGGCAGGGCAGATG	260254	92450	AAGAATGCTTGTCACACTCC
171081	3277	GAGGGGGATCAGATAGAACT	215668	47864	TCCGGCCAGGCAGGGCAGAT	260255	92451	TAAGAATGCTTGTCACACTC
171082	3278	CGAGGGGGATCAGATAGAAC	215669	47865	CTCCGGCCAGGCAGGGCAGA	260256	92452	ATAAGAATGCTTGTCACACT
171083	3279	CCGAGGGGGATCAGATAGAA	215670	47866	CCTCCGGCCAGGCAGGGCAG	260257	92453	AATAAGAATGCTTGTCACAC
171084	3280	GCCGAGGGGGATCAGATAGA	215671	47867	GCCTCCGGCCAGGCAGGGCA	260258	92454	AAATAAGAATGCTTGTCACA
171085	3281	GGCCGAGGGGGATCAGATAG	215672	47868	AGCCTCCGGCCAGGCAGGGC	260259	92455	AAAATAAGAATGCTTGTCAC
171086	3282	GGGCCGAGGGGGATCAGATA	215673	47869	CAGCCTCCGGCCAGGCAGGG	260260	92456	TAAAATAAGAATGCTTGTCA
171087	3283	GGGGCCGAGGGGGATCAGAT	215674	47870	GCAGCCTCCGGCCAGGCAGG	260261	92457	ATAAAATAAGAATGCTTGTC
171088	3284	AGGGGCCGAGGGGGATCAGA	215675	47871	TGCAGCCTCCGGCCAGGCAG	260262	92458	TATAAAATAAGAATGCTTGT
171089	3285	AAGGGGCCGAGGGGGATCAG	215676	47872	ATGCAGCCTCCGGCCAGGCA	260263	92459	ATATAAAATAAGAATGCTTG
171090	3286	TAAGGGGCCGAGGGGGATCA	215677	47873	GATGCAGCCTCCGGCCAGGC	260264	92460	AATATAAAATAAGAATGCTT
171091	3287	TTAAGGGGCCGAGGGGGATC	215678	47874	CGATGCAGCCTCCGGCCAGG	260265	92461	AAATATAAAATAAGAATGCT
171092	3288	GTTAAGGGGCCGAGGGGGAT	215679	47875	TCGATGCAGCCTCCGGCCAG	260266	92462	AAAATATAAAATAAGAATGC
171093	3289	AGTTAAGGGGCCGAGGGGGA	215680	47876	CTCGATGCAGCCTCCGGCCA	260267	92463	TAAAATATAAAATAAGAATG
171094	3290	CAGTTAAGGGGCCGAGGGGG	215681	47877	TCTCGATGCAGCCTCCGGCC	260268	92464	ATAAAATATAAAATAAGAAT
171095	3291	TCAGTTAAGGGGCCGAGGGG	215682	47878	CTCTCGATGCAGCCTCCGGC	260269	92465	GATAAAATATAAAATAAGAA
171096	3292	GTCAGTTAAGGGGCCGAGGG	215683	47879	CCTCTCGATGCAGCCTCCGG	260270	92466	TGATAAAATATAAAATAAGA
171097	3293	GGTCAGTTAAGGGGCCGAGG	215684	47880	CCCTCTCGATGCAGCCTCCG	260271	92467	CTGATAAAATATAAAATAAG
171098	3294	GGGTCAGTTAAGGGGCCGAG	215685	47881	GCCCTCTCGATGCAGCCTCC	260272	92468	GCTGATAAAATATAAAATAA
171099	3295	TGGGTCAGTTAAGGGGCCGA	215686	47882	GGCCCTCTCGATGCAGCCTC	260273	92469	AGCTGATAAAATATAAAATA
171100	3296	ATGGGTCAGTTAAGGGGCCG	215687	47883	TGGCCCTCTCGATGCAGCCT	260274	92470	GAGCTGATAAAATATAAAAT
171101	3297	GATGGGTCAGTTAAGGGGCC	215688	47884	TTGGCCCTCTCGATGCAGCC	260275	92471	CGAGCTGATAAAATATAAAA
171102	3298	GGATGGGTCAGTTAAGGGGC	215689	47885	CTTGGCCCTCTCGATGCAGC	260276	92472	GCGAGCTGATAAAATATAAA
171103	3299	AGGATGGGTCAGTTAAGGGG	215690	47886	CCTTGGCCCTCTCGATGCAG	260277	92473	TGCGAGCTGATAAAATATAA
171104	3300	TAGGATGGGTCAGTTAAGGG	215691	47887	CCCTTGGCCCTCTCGATGCA	260278	92474	ATGCGAGCTGATAAAATATA
171105	3301	GTAGGATGGGTCAGTTAAGG	215692	47888	CCCCTTGGCCCTCTCGATGC	260279	92475	CATGCGAGCTGATAAAATAT
171106	3302	TGTAGGATGGGTCAGTTAAG	215693	47889	GCCCCTTGGCCCTCTCGATG	260280	92476	CCATGCGAGCTGATAAAATA
171107	3303	CTGTAGGATGGGTCAGTTAA	215694	47890	TGCCCCTTGGCCCTCTCGAT	260281	92477	ACCATGCGAGCTGATAAAAT
171108	3304	CCTGTAGGATGGGTCAGTTA	215695	47891	GTGCCCCTTGGCCCTCTCGA	260282	92478	GACCATGCGAGCTGATAAAA
171109	3305	TCCTGTAGGATGGGTCAGTT	215696	47892	GGTGCCCCTTGGCCCTCTCG	260283	92479	TGACCATGCGAGCTGATAAA
171110	3306	CTCCTGTAGGATGGGTCAGT	215697	47893	TGGTGCCCCTTGGCCCTCTC	260284	92480	CTGACCATGCGAGCTGATAA
171111	3307	TCTCCTGTAGGATGGGTCAG	215698	47894	GTGGTGCCCCTTGGCCCTCT	260285	92481	ACTGACCATGCGAGCTGATA
171112	3308	GTCTCCTGTAGGATGGGTCA	215699	47895	CGTGGTGCCCCTTGGCCCTC	260286	92482	TACTGACCATGCGAGCTGAT
171113	3309	TGTCTCCTGTAGGATGGGTC	215700	47896	ACGTGGTGCCCCTTGGCCCT	260287	92483	TTACTGACCATGCGAGCTGA
171114	3310	CTGTCTCCTGTAGGATGGGT	215701	47897	CACGTGGTGCCCCTTGGCCC	260288	92484	TTTACTGACCATGCGAGCTG

171115	3311	CCTGTCTCCTGTAGGATGGG	215702	47898	ACACGTGGTGCCCCTTGGCC	260289	92485	TTTTACTGACCATGCGAGCT
171116	3312	CCCTGTCTCCTGTAGGATGG	215703	47899	GACACGTGGTGCCCCTTGGC	260290	92486	CTTTTACTGACCATGCGAGC
171117	3313	TCCCTGTCTCCTGTAGGATG	215704	47900	CGACACGTGGTGCCCCTTGG	260291	92487	GCTTTTACTGACCATGCGAG
171118	3314	TTCCCTGTCTCCTGTAGGAT	215705	47901	ACGACACGTGGTGCCCCTTG	260292	92488	TGCTTTTACTGACCATGCGA
171119	3315	TTTCCCTGTCTCCTGTAGGA	215706	47902	CACGACACGTGGTGCCCCTT	260293	92489	TTGCTTTTACTGACCATGCG
171120	3316	ATTTCCCTGTCTCCTGTAGG	215707	47903	CCACGACACGTGGTGCCCCT	260294	92490	TTTGCTTTTACTGACCATGC
171121	3317	CATTTCCCTGTCTCCTGTAG	215708	47904	CCCACGACACGTGGTGCCCC	260295	92491	CTTTGCTTTTACTGACCATG
171122	3318	ACATTTCCCTGTCTCCTGTA	215709	47905	ACCCACGACACGTGGTGCCC	260296	92492	TCTTTGCTTTTACTGACCAT
171123	3319	GACATTTCCCTGTCTCCTGT	215710	47906	TACCCACGACACGTGGTGCC	260297	92493	GTCTTTGCTTTTACTGACCA
171124	3320	AGACATTTCCCTGTCTCCTG	215711	47907	GTACCCACGACACGTGGTGC	260298	92494	CGTCTTTGCTTTTACTGACC
171125	3321	AAGACATTTCCCTGTCTCCT	215712	47908	AGTACCCACGACACGTGGTG	260299	92495	CCGTCTTTGCTTTTACTGAC
171126	3322	AAAGACATTTCCCTGTCTCC	215713	47909	CAGTACCCACGACACGTGGT	260300	92496	CCCGTCTTTGCTTTTACTGA
171127	3323	GAAAGACATTTCCCTGTCTC	215714	47910	ACAGTACCCACGACACGTGG	260301	92497	TCCCGTCTTTGCTTTTACTG
171128	3324	GGAAAGACATTTCCCTGTCT	215715	47911	GACAGTACCCACGACACGTG	260302	92498	GTCCCGTCTTTGCTTTTACT
171129	3325	AGGAAAGACATTTCCCTGTC	215716	47912	TGACAGTACCCACGACACGT	260303	92499	AGTCCCGTCTTTGCTTTTAC
171130	3326	TAGGAAAGACATTTCCCTGT	215717	47913	TTGACAGTACCCACGACACG	260304	92500	CAGTCCCGTCTTTGCTTTTA
171131	3327	GTAGGAAAGACATTTCCCTG	215718	47914	TTTGACAGTACCCACGACAC	260305	92501	CCAGTCCCGTCTTTGCTTTT
171132	3328	GGTAGGAAAGACATTTCCCT	215719	47915	GTTTGACAGTACCCACGACA	260306	92502	TCCAGTCCCGTCTTTGCTTT
171133	3329	CGGTAGGAAAGACATTTCCC	215720	47916	TGTTTGACAGTACCCACGAC	260307	92503	TTCCAGTCCCGTCTTTGCTT
171134	3330	GCGGTAGGAAAGACATTTCC	215721	47917	TTGTTTGACAGTACCCACGA	260308	92504	CTTCCAGTCCCGTCTTTGCT
171135	3331	CGCGGTAGGAAAGACATTTC	215722	47918	CTTGTTTGACAGTACCCACG	260309	92505	GCTTCCAGTCCCGTCTTTGC
171136	3332	CCGCGGTAGGAAAGACATTT	215723	47919	TCTTGTTTGACAGTACCCAC	260310	92506	CGCTTCCAGTCCCGTCTTTG
171137	3333	ACCGCGGTAGGAAAGACATT	215724	47920	CTCTTGTTTGACAGTACCCA	260311	92507	TCGCTTCCAGTCCCGTCTTT
171138	3334	AACCGCGGTAGGAAAGACAT	215725	47921	GCTCTTGTTTGACAGTACCC	260312	92508	ATCGCTTCCAGTCCCGTCTT
171139	3335	CAACCGCGGTAGGAAAGACA	215726	47922	GGCTCTTGTTTGACAGTACC	260313	92509	CATCGCTTCCAGTCCCGTCT
171140	3336	TCAACCGCGGTAGGAAAGAC	215727	47923	AGGCTCTTGTTTGACAGTAC	260314	92510	TCATCGCTTCCAGTCCCGTC
171141	3337	ATCAACCGCGGTAGGAAAGA	215728	47924	AAGGCTCTTGTTTGACAGTA	260315	92511	GTCATCGCTTCCAGTCCCGT
171142	3338	AATCAACCGCGGTAGGAAAG	215729	47925	GAAGGCTCTTGTTTGACAGT	260316	92512	TGTCATCGCTTCCAGTCCCG
171143	3339	GAATCAACCGCGGTAGGAAA	215730	47926	TGAAGGCTCTTGTTTGACAG	260317	92513	TTGTCATCGCTTCCAGTCCC
171144	3340	AGAATCAACCGCGGTAGGAA	215731	47927	CTGAAGGCTCTTGTTTGACA	260318	92514	TTTGTCATCGCTTCCAGTCC
171145	3341	CAGAATCAACCGCGGTAGGA	215732	47928	TCTGAAGGCTCTTGTTTGAC	260319	92515	TTTTGTCATCGCTTCCAGTC
171146	3342	CCAGAATCAACCGCGGTAGG	215733	47929	CTCTGAAGGCTCTTGTTTGA	260320	92516	TTTTTGTCATCGCTTCCAGT
171147	3343	CCCAGAATCAACCGCGGTAG	215734	47930	GCTCTGAAGGCTCTTGTTTG	260321	92517	TTTTTTGTCATCGCTTCCAG
171148	3344	CCCCAGAATCAACCGCGGTA	215735	47931	GGCTCTGAAGGCTCTTGTTT	260322	92518	CTTTTTTGTCATCGCTTCCA
171149	3345	ACCCCAGAATCAACCGCGGT	215736	47932	AGGCTCTGAAGGCTCTTGTT	260323	92519	GCTTTTTTGTCATCGCTTCC
171150	3346	CACCCCAGAATCAACCGCGG	215737	47933	AAGGCTCTGAAGGCTCTTGT	260324	92520	GGCTTTTTTGTCATCGCTTC
171151	3347	ACACCCCAGAATCAACCGCG	215738	47934	GAAGGCTCTGAAGGCTCTTG	260325	92521	TGGCTTTTTTGTCATCGCTT
171152	3348	GACACCCCAGAATCAACCGC	215739	47935	GGAAGGCTCTGAAGGCTCTT	260326	92522	TTGGCTTTTTTGTCATCGCT
171153	3349	TGACACCCCAGAATCAACCG	215740	47936	TGGAAGGCTCTGAAGGCTCT	260327	92523	CTTGGCTTTTTTGTCATCGC
171154	3350	ATGACACCCCAGAATCAACC	215741	47937	GTGGAAGGCTCTGAAGGCTC	260328	92524	CCTTGGCTTTTTTGTCATCG
171155	3351	AATGACACCCCAGAATCAAC	215742	47938	TGTGGAAGGCTCTGAAGGCT	260329	92525	ACCTTGGCTTTTTTGTCATC
171156	3352	AAATGACACCCCAGAATCAA	215743	47939	CTGTGGAAGGCTCTGAAGGC	260330	92526	TACCTTGGCTTTTTTGTCAT
171157	3353	AAAATGACACCCCAGAATCA	215744	47940	ACTGTGGAAGGCTCTGAAGG	260331	92527	TTACCTTGGCTTTTTTGTCA
171158	3354	CAAAATGACACCCCAGAATC	215745	47941	GACTGTGGAAGGCTCTGAAG	260332	92528	CTTACCTTGGCTTTTTTGTC
171159	3355	ACAAAATGACACCCCAGAAT	215746	47942	AGACTGTGGAAGGCTCTGAA	260333	92529	GCTTACCTTGGCTTTTTTGT
171160	3356	CACAAAATGACACCCCAGAA	215747	47943	AAGACTGTGGAAGGCTCTGA	260334	92530	AGCTTACCTTGGCTTTTTTG
171161	3357	ACACAAAATGACACCCCAGA	215748	47944	AAAGACTGTGGAAGGCTCTG	260335	92531	CAGCTTACCTTGGCTTTTTT
171162	3358	AACACAAAATGACACCCCAG	215749	47945	GAAAGACTGTGGAAGGCTCT	260336	92532	TCAGCTTACCTTGGCTTTTT
171163	3359	AAACACAAAATGACACCCCA	215750	47946	AGAAAGACTGTGGAAGGCTC	260337	92533	GTCAGCTTACCTTGGCTTTT
171164	3360	AAAACACAAAATGACACCCC	215751	47947	AAGAAAGACTGTGGAAGGCT	260338	92534	CGTCAGCTTACCTTGGCTTT
171165	3361	CAAAACACAAAATGACACCC	215752	47948	AAAGAAAGACTGTGGAAGGC	260339	92535	TCGTCAGCTTACCTTGGCTT
171166	3362	ACAAAACACAAAATGACACC	215753	47949	AAAAGAAAGACTGTGGAAGG	260340	92536	ATCGTCAGCTTACCTTGGCT
171167	3363	CACAAAACACAAAATGACAC	215754	47950	CAAAAGAAAGACTGTGGAAG	260341	92537	CATCGTCAGCTTACCTTGGC
171168	3364	TCACAAAACACAAAATGACA	215755	47951	GCAAAAGAAAGACTGTGGAA	260342	92538	GCATCGTCAGCTTACCTTGG
171169	3365	ATCACAAAACACAAAATGAC	215756	47952	AGCAAAAGAAAGACTGTGGA	260343	92539	GGCATCGTCAGCTTACCTTG
171170	3366	CATCACAAAACACAAAATGA	215757	47953	AAGCAAAAGAAAGACTGTGG	260344	92540	TGGCATCGTCAGCTTACCTT
171171	3367	CCATCACAAAACACAAAATG	215758	47954	GAAGCAAAAGAAAGACTGTG	260345	92541	GTGGCATCGTCAGCTTACCT
171172	3368	GCCATCACAAAACACAAAAT	215759	47955	GGAAGCAAAAGAAAGACTGT	260346	92542	CGTGGCATCGTCAGCTTACC
171173	3369	AGCCATCACAAAACACAAAA	215760	47956	GGGAAGCAAAAGAAAGACTG	260347	92543	CCGTGGCATCGTCAGCTTAC
171174	3370	CAGCCATCACAAAACACAAA	215761	47957	TGGGAAGCAAAAGAAAGACT	260348	92544	TCCGTGGCATCGTCAGCTTA
171175	3371	GCAGCCATCACAAAACACAA	215762	47958	CTGGGAAGCAAAAGAAAGAC	260349	92545	CTCCGTGGCATCGTCAGCTT
171176	3372	AGCAGCCATCACAAAACACA	215763	47959	GCTGGGAAGCAAAAGAAAGA	260350	92546	GCTCCGTGGCATCGTCAGCT
171177	3373	AAGCAGCCATCACAAAACAC	215764	47960	TGCTGGGAAGCAAAAGAAAG	260351	92547	AGCTCCGTGGCATCGTCAGC
171178	3374	TAAGCAGCCATCACAAAACA	215765	47961	ATGCTGGGAAGCAAAAGAAA	260352	92548	GAGCTCCGTGGCATCGTCAG
171179	3375	ATAAGCAGCCATCACAAAAC	215766	47962	AATGCTGGGAAGCAAAAGAA	260353	92549	AGAGCTCCGTGGCATCGTCA
171180	3376	TATAAGCAGCCATCACAAAA	215767	47963	CAATGCTGGGAAGCAAAAGA	260354	92550	CAGAGCTCCGTGGCATCGTC
171181	3377	ATATAAGCAGCCATCACAAA	215768	47964	GCAATGCTGGGAAGCAAAAG	260355	92551	GCAGAGCTCCGTGGCATCGT
171182	3378	AATATAAGCAGCCATCACAA	215769	47965	AGCAATGCTGGGAAGCAAAA	260356	92552	TGCAGAGCTCCGTGGCATCG
171183	3379	AAATATAAGCAGCCATCACA	215770	47966	AAGCAATGCTGGGAAGCAAA	260357	92553	CTGCAGAGCTCCGTGGCATC
171184	3380	TAAATATAAGCAGCCATCAC	215771	47967	GAAGCAATGCTGGGAAGCAA	260358	92554	GCTGCAGAGCTCCGTGGCAT
171185	3381	GTAAATATAAGCAGCCATCA	215772	47968	GGAAGCAATGCTGGGAAGCA	260359	92555	AGCTGCAGAGCTCCGTGGCA
171186	3382	AGTAAATATAAGCAGCCATC	215773	47969	GGGAAGCAATGCTGGGAAGC	260360	92556	CAGCTGCAGAGCTCCGTGGC

171187	3383	CAGTAAATATAAGCAGCCAT	215774	47970	GGGGAAGCAATGCTGGGAAG	260361	92557	CCAGCTGCAGAGCTCCGTGG
171188	3384	ACAGTAAATATAAGCAGCCA	215775	47971	CGGGGAAGCAATGCTGGGAA	260362	92558	ACCAGCTGCAGAGCTCCGTG
171189	3385	TACAGTAAATATAAGCAGCC	215776	47972	GCGGGGAAGCAATGCTGGGA	260363	92559	GACCAGCTGCAGAGCTCCGT
171190	3386	ATACAGTAAATATAAGCAGC	215777	47973	AGCGGGGAAGCAATGCTGGG	260364	92560	TGACCAGCTGCAGAGCTCCG
171191	3387	TATACAGTAAATATAAGCAG	215778	47974	CAGCGGGGAAGCAATGCTGG	260365	92561	TTGACCAGCTGCAGAGCTCC
171192	3388	TTATACAGTAAATATAAGCA	215779	47975	CCAGCGGGGAAGCAATGCTG	260366	92562	CTTGACCAGCTGCAGAGCTC
171193	3389	CTTATACAGTAAATATAAGC	215780	47976	ACCAGCGGGGAAGCAATGCT	260367	92563	ACTTGACCAGCTGCAGAGCT
171194	3390	GCTTATACAGTAAATATAAG	215781	47977	CACCAGCGGGGAAGCAATGC	260368	92564	AACTTGACCAGCTGCAGAGC
171195	3391	TGCTTATACAGTAAATATAA	215782	47978	CCACCAGCGGGGAAGCAATG	260369	92565	AAACTTGACCAGCTGCAGAG
171196	3392	ATGCTTATACAGTAAATATA	215783	47979	TCCACCAGCGGGGAAGCAAT	260370	92566	TAAACTTGACCAGCTGCAGA
171197	3393	AATGCTTATACAGTAAATAT	215784	47980	GTCCACCAGCGGGGAAGCAA	260371	92567	GTAAACTTGACCAGCTGCAG
171198	3394	CAATGCTTATACAGTAAATA	215785	47981	AGTCCACCAGCGGGGAAGCA	260372	92568	TGTAAACTTGACCAGCTGCA
171199	3395	ACAATGCTTATACAGTAAAT	215786	47982	GAGTCCACCAGCGGGGAAGC	260373	92569	CTGTAAACTTGACCAGCTGC
171200	3396	TACAATGCTTATACAGTAAA	215787	47983	AGAGTCCACCAGCGGGGAAG	260374	92570	TCTGTAAACTTGACCAGCTG
171201	3397	ATACAATGCTTATACAGTAA	215788	47984	CAGAGTCCACCAGCGGGGAA	260375	92571	CTCTGTAAACTTGACCAGCT
171202	3398	AATACAATGCTTATACAGTA	215789	47985	TCAGAGTCCACCAGCGGGGA	260376	92572	TCTCTGTAAACTTGACCAGC
171203	3399	AAATACAATGCTTATACAGT	215790	47986	TTCAGAGTCCACCAGCGGGG	260377	92573	TTCTCTGTAAACTTGACCAG
171204	3400	TAAATACAATGCTTATACAG	215791	47987	ATTCAGAGTCCACCAGCGGG	260378	92574	CTTCTCTGTAAACTTGACCA
171205	3401	GTAAATACAATGCTTATACA	215792	47988	GATTCAGAGTCCACCAGCGG	260379	92575	GCTTCTCTGTAAACTTGACC
171206	3402	AGTAAATACAATGCTTATAC	215793	47989	AGATTCAGAGTCCACCAGCG	260380	92576	AGCTTCTCTGTAAACTTGAC
171207	3403	CAGTAAATACAATGCTTATA	215794	47990	TAGATTCAGAGTCCACCAGC	260381	92577	CAGCTTCTCTGTAAACTTGA
171208	3404	ACAGTAAATACAATGCTTAT	215795	47991	CTAGATTCAGAGTCCACCAG	260382	92578	ACAGCTTCTCTGTAAACTTG
171209	3405	TACAGTAAATACAATGCTTA	215796	47992	TCTAGATTCAGAGTCCACCA	260383	92579	CACAGCTTCTCTGTAAACTT
171210	3406	ATACAGTAAATACAATGCTT	215797	47993	TTCTAGATTCAGAGTCCACC	260384	92580	GCACAGCTTCTCTGTAAACT
171211	3407	TATACAGTAAATACAATGCT	215798	47994	GTTCTAGATTCAGAGTCCAC	260385	92581	AGCACAGCTTCTCTGTAAAC
171212	3408	TTATACAGTAAATACAATGC	215799	47995	AGTTCTAGATTCAGAGTCCA	260386	92582	AAGCACAGCTTCTCTGTAAA
171213	3409	CTTATACAGTAAATACAATG	215800	47996	TAGTTCTAGATTCAGAGTCC	260387	92583	AAAGCACAGCTTCTCTGTAA
171214	3410	GCTTATACAGTAAATACAAT	215801	47997	CTAGTTCTAGATTCAGAGTC	260388	92584	TAAAGCACAGCTTCTCTGTA
171215	3411	TGCTTATACAGTAAATACAA	215802	47998	GCTAGTTCTAGATTCAGAGT	260389	92585	ATAAAGCACAGCTTCTCTGT
171216	3412	ATGCTTATACAGTAAATACA	215803	47999	AGCTAGTTCTAGATTCAGAG	260390	92586	CATAAAGCACAGCTTCTCTG
171217	3413	AATGCTTATACAGTAAATAC	215804	48000	GAGCTAGTTCTAGATTCAGA	260391	92587	ACATAAAGCACAGCTTCTCT
171218	3414	CAATGCTTATACAGTAAATA	215805	48001	GGAGCTAGTTCTAGATTCAG	260392	92588	GACATAAAGCACAGCTTCTC
171219	3415	ACAATGCTTATACAGTAAAT	215806	48002	TGGAGCTAGTTCTAGATTCA	260393	92589	AGACATAAAGCACAGCTTCT
171220	3416	TACAATGCTTATACAGTAAA	215807	48003	CTGGAGCTAGTTCTAGATTC	260394	92590	CAGACATAAAGCACAGCTTC
171221	3417	ATACAATGCTTATACAGTAA	215808	48004	CCTGGAGCTAGTTCTAGATT	260395	92591	TCAGACATAAAGCACAGCTT
171222	3418	AATACAATGCTTATACAGTA	215809	48005	GCCTGGAGCTAGTTCTAGAT	260396	92592	ATCAGACATAAAGCACAGCT
171223	3419	TAATACAATGCTTATACAGT	215810	48006	CGCCTGGAGCTAGTTCTAGA	260397	92593	AATCAGACATAAAGCACAGC
171224	3420	ATAATACAATGCTTATACAG	215811	48007	GCGCCTGGAGCTAGTTCTAG	260398	92594	GAATCAGACATAAAGCACAG
171225	3421	TATAATACAATGCTTATACA	215812	48008	GGCGCCTGGAGCTAGTTCTA	260399	92595	TGAATCAGACATAAAGCACA
171226	3422	TTATAATACAATGCTTATAC	215813	48009	AGGCGCCTGGAGCTAGTTCT	260400	92596	ATGAATCAGACATAAAGCAC
171227	3423	ATTATAATACAATGCTTATA	215814	48010	GAGGCGCCTGGAGCTAGTTC	260401	92597	AATGAATCAGACATAAAGCA
171228	3424	AATTATAATACAATGCTTAT	215815	48011	AGAGGCGCCTGGAGCTAGTT	260402	92598	GAATGAATCAGACATAAAGC
171229	3425	TAATTATAATACAATGCTTA	215816	48012	GAGAGGCGCCTGGAGCTAGT	260403	92599	AGAATGAATCAGACATAAAG
171230	3426	GTAATTATAATACAATGCTT	215817	48013	GGAGAGGCGCCTGGAGCTAG	260404	92600	GAGAATGAATCAGACATAAA
171231	3427	AGTAATTATAATACAATGCT	215818	48014	TGGAGAGGCGCCTGGAGCTA	260405	92601	TGAGAATGAATCAGACATAA
171232	3428	CAGTAATTATAATACAATGC	215819	48015	TTGGAGAGGCGCCTGGAGCT	260406	92602	ATGAGAATGAATCAGACATA
171233	3429	ACAGTAATTATAATACAATG	215820	48016	TTTGGAGAGGCGCCTGGAGC	260407	92603	TATGAGAATGAATCAGACAT
171234	3430	TACAGTAATTATAATACAAT	215821	48017	ATTTGGAGAGGCGCCTGGAG	260408	92604	ATATGAGAATGAATCAGACA
171235	3431	ATACAGTAATTATAATACAA	215822	48018	AATTTGGAGAGGCGCCTGGA	260409	92605	TATATGAGAATGAATCAGAC
171236	3432	TATACAGTAATTATAATACA	215823	48019	GAATTTGGAGAGGCGCCTGG	260410	92606	ATATATGAGAATGAATCAGA
171237	3433	TTATACAGTAATTATAATAC	215824	48020	TGAATTTGGAGAGGCGCCTG	260411	92607	TATATATGAGAATGAATCAG
171238	3434	CTTATACAGTAATTATAATA	215825	48021	CTGAATTTGGAGAGGCGCCT	260412	92608	TTATATATGAGAATGAATCA
171239	3435	GCTTATACAGTAATTATAAT	215826	48022	TCTGAATTTGGAGAGGCGCC	260413	92609	ATTATATATGAGAATGAATC
171240	3436	AGCTTATACAGTAATTATAA	215827	48023	GTCTGAATTTGGAGAGGCGC	260414	92610	CATTATATATGAGAATGAAT
171241	3437	CAGCTTATACAGTAATTATA	215828	48024	CGTCTGAATTTGGAGAGGCG	260415	92611	ACATTATATATGAGAATGAA
171242	3438	GCAGCTTATACAGTAATTAT	215829	48025	CCGTCTGAATTTGGAGAGGC	260416	92612	CACATTATATATGAGAATGA
171243	3439	AGCAGCTTATACAGTAATTA	215830	48026	CCCGTCTGAATTTGGAGAGG	260417	92613	CCACATTATATATGAGAATG
171244	3440	AAGCAGCTTATACAGTAATT	215831	48027	TCCCGTCTGAATTTGGAGAG	260418	92614	CCCACATTATATATGAGAAT
171245	3441	TAAGCAGCTTATACAGTAAT	215832	48028	CTCCCGTCTGAATTTGGAGA	260419	92615	CCCCACATTATATATGAGAA
171246	3442	ATAAGCAGCTTATACAGTAA	215833	48029	GCTCCCGTCTGAATTTGGAG	260420	92616	TCCCCACATTATATATGAGA
171247	3443	TATAAGCAGCTTATACAGTA	215834	48030	AGCTCCCGTCTGAATTTGGA	260421	92617	CTCCCCACATTATATATGAG
171248	3444	ATATAAGCAGCTTATACAGT	215835	48031	CAGCTCCCGTCTGAATTTGG	260422	92618	ACTCCCCACATTATATATGA
171249	3445	AATATAAGCAGCTTATACAG	215836	48032	CCAGCTCCCGTCTGAATTTG	260423	92619	TACTCCCCACATTATATATG
171250	3446	AAATATAAGCAGCTTATACA	215837	48033	CCCAGCTCCCGTCTGAATTT	260424	92620	ATACTCCCCACATTATATAT
171251	3447	TAAATATAAGCAGCTTATAC	215838	48034	CCCCAGCTCCCGTCTGAATT	260425	92621	AATACTCCCCACATTATATA
171252	3448	GTAAATATAAGCAGCTTATA	215839	48035	GCCCCAGCTCCCGTCTGAAT	260426	92622	AAATACTCCCCACATTATAT
171253	3449	AGTAAATATAAGCAGCTTAT	215840	48036	TGCCCCAGCTCCCGTCTGAA	260427	92623	CAAATACTCCCCACATTATA
171254	3450	CAGTAAATATAAGCAGCTTA	215841	48037	GTGCCCCAGCTCCCGTCTGA	260428	92624	ACAAATACTCCCCACATTAT
171255	3451	ACAGTAAATATAAGCAGCTT	215842	48038	AGTGCCCCAGCTCCCGTCTG	260429	92625	GACAAATACTCCCCACATTA
171256	3452	TACAGTAAATATAAGCAGCT	215843	48039	TAGTGCCCCAGCTCCCGTCT	260430	92626	TGACAAATACTCCCCACATT
171257	3453	ATACAGTAAATATAAGCAGC	215844	48040	ATAGTGCCCCAGCTCCCGTC	260431	92627	GTGACAAATACTCCCCACAT
171258	3454	TATACAGTAAATATAAGCAG	215845	48041	AATAGTGCCCCAGCTCCCGT	260432	92628	AGTGACAAATACTCCCCACA

171259	3455	TTATACAGTAAATATAAGCA	215846	48042	TAATAGTGCCCCAGCTCCCG	260433	92629	TAGTGACAAATACTCCCCAC
171260	3456	CTTATACAGTAAATATAAGC	215847	48043	ATAATAGTGCCCCAGCTCCC	260434	92630	TTAGTGACAAATACTCCCCA
171261	3457	GCTTATACAGTAAATATAAG	215848	48044	TATAATAGTGCCCCAGCTCC	260435	92631	TTTAGTGACAAATACTCCCC
171262	3458	TGCTTATACAGTAAATATAA	215849	48045	TTATAATAGTGCCCCAGCTC	260436	92632	CTTTAGTGACAAATACTCCC
171263	3459	ATGCTTATACAGTAAATATA	215850	48046	ATTATAATAGTGCCCCAGCT	260437	92633	ACTTTAGTGACAAATACTCC
171264	3460	GATGCTTATACAGTAAATAT	215851	48047	CATTATAATAGTGCCCCAGC	260438	92634	TACTTTAGTGACAAATACTC
171265	3461	AGATGCTTATACAGTAAATA	215852	48048	GCATTATAATAGTGCCCCAG	260439	92635	GTACTTTAGTGACAAATACT
171266	3462	GAGATGCTTATACAGTAAAT	215853	48049	TGCATTATAATAGTGCCCCA	260440	92636	TGTACTTTAGTGACAAATAC
171267	3463	GGAGATGCTTATACAGTAAA	215854	48050	TTGCATTATAATAGTGCCCC	260441	92637	CTGTACTTTAGTGACAAATA
171268	3464	TGGAGATGCTTATACAGTAA	215855	48051	TTTGCATTATAATAGTGCCC	260442	92638	GCTGTACTTTAGTGACAAAT
171269	3465	TTGGAGATGCTTATACAGTA	215856	48052	ATTTGCATTATAATAGTGCC	260443	92639	AGCTGTACTTTAGTGACAAA
171270	3466	TTTGGAGATGCTTATACAGT	215857	48053	GATTTGCATTATAATAGTGC	260444	92640	CAGCTGTACTTTAGTGACAA
171271	3467	ATTTGGAGATGCTTATACAG	215858	48054	AGATTTGCATTATAATAGTG	260445	92641	ACAGCTGTACTTTAGTGACA
171272	3468	GATTTGGAGATGCTTATACA	215859	48055	TAGATTTGCATTATAATAGT	260446	92642	GACAGCTGTACTTTAGTGAC
171273	3469	GGATTTGGAGATGCTTATAC	215860	48056	CTAGATTTGCATTATAATAG	260447	92643	TGACAGCTGTACTTTAGTGA
171274	3470	AGGATTTGGAGATGCTTATA	215861	48057	CCTAGATTTGCATTATAATA	260448	92644	ATGACAGCTGTACTTTAGTG
171275	3471	GAGGATTTGGAGATGCTTAT	215862	48058	GCCTAGATTTGCATTATAAT	260449	92645	AATGACAGCTGTACTTTAGT
171276	3472	GGAGGATTTGGAGATGCTTA	215863	48059	TGCCTAGATTTGCATTATAA	260450	92646	AAATGACAGCTGTACTTTAG
171277	3473	GGGAGGATTTGGAGATGCTT	215864	48060	TTGCCTAGATTTGCATTATA	260451	92647	TAAATGACAGCTGTACTTTA
171278	3474	AGGGAGGATTTGGAGATGCT	215865	48061	TTTGCCTAGATTTGCATTAT	260452	92648	TTAAATGACAGCTGTACTTT
171279	3475	GAGGGAGGATTTGGAGATGC	215866	48062	CTTTGCCTAGATTTGCATTA	260453	92649	TTTAAATGACAGCTGTACTT
171280	3476	AGAGGGAGGATTTGGAGATG	215867	48063	GCTTTGCCTAGATTTGCATT	260454	92650	CTTTAAATGACAGCTGTACT
171281	3477	TAGAGGGAGGATTTGGAGAT	215868	48064	GGCTTTGCCTAGATTTGCAT	260455	92651	ACTTTAAATGACAGCTGTAC
171282	3478	GTAGAGGGAGGATTTGGAGA	215869	48065	GGGCTTTGCCTAGATTTGCA	260456	92652	CACTTTAAATGACAGCTGTA
171283	3479	CGTAGAGGGAGGATTTGGAG	215870	48066	AGGGCTTTGCCTAGATTTGC	260457	92653	GCACTTTAAATGACAGCTGT
171284	3480	ACGTAGAGGGAGGATTTGGA	215871	48067	GAGGGCTTTGCCTAGATTTG	260458	92654	AGCACTTTAAATGACAGCTG
171285	3481	TACGTAGAGGGAGGATTTGG	215872	48068	GGAGGGCTTTGCCTAGATTT	260459	92655	AAGCACTTTAAATGACAGCT
171286	3482	TTACGTAGAGGGAGGATTTG	215873	48069	GGGAGGGCTTTGCCTAGATT	260460	92656	AAAGCACTTTAAATGACAGC
171287	3483	TTTACGTAGAGGGAGGATTT	215874	48070	TGGGAGGGCTTTGCCTAGAT	260461	92657	CAAAGCACTTTAAATGACAG
171288	3484	GTTTACGTAGAGGGAGGATT	215875	48071	TTGGGAGGGCTTTGCCTAGA	260462	92658	ACAAAGCACTTTAAATGACA
171289	3485	TGTTTACGTAGAGGGAGGAT	215876	48072	ATTGGGAGGGCTTTGCCTAG	260463	92659	TACAAAGCACTTTAAATGAC
171290	3486	TTGTTTACGTAGAGGGAGGA	215877	48073	TATTGGGAGGGCTTTGCCTA	260464	92660	ATACAAAGCACTTTAAATGA
171291	3487	TTTGTTTACGTAGAGGGAGG	215878	48074	GTATTGGGAGGGCTTTGCCT	260465	92661	AATACAAAGCACTTTAAATG
171292	3488	ATTTGTTTACGTAGAGGGAG	215879	48075	GGTATTGGGAGGGCTTTGCC	260466	92662	AAATACAAAGCACTTTAAAT
171293	3489	AATTTGTTTACGTAGAGGGA	215880	48076	TGGTATTGGGAGGGCTTTGC	260467	92663	AAAATACAAAGCACTTTAAA
171294	3490	TAATTTGTTTACGTAGAGGG	215881	48077	CTGGTATTGGGAGGGCTTTG	260468	92664	CAAAATACAAAGCACTTTAA
171295	3491	TTAATTTGTTTACGTAGAGG	215882	48078	CCTGGTATTGGGAGGGCTTT	260469	92665	CCAAAATACAAAGCACTTTA
171296	3492	ATTAATTTGTTTACGTAGAG	215883	48079	TCCTGGTATTGGGAGGGCTT	260470	92666	CCCAAAATACAAAGCACTTT
171297	3493	CATTAATTTGTTTACGTAGA	215884	48080	ATCCTGGTATTGGGAGGGCT	260471	92667	CCCCAAAATACAAAGCACTT
171298	3494	CCATTAATTTGTTTACGTAG	215885	48081	GATCCTGGTATTGGGAGGGC	260472	92668	GCCCCAAAATACAAAGCACT
171299	3495	TCCATTAATTTGTTTACGTA	215886	48082	GGATCCTGGTATTGGGAGGG	260473	92669	TGCCCCAAAATACAAAGCAC
171300	3496	ATCCATTAATTTGTTTACGT	215887	48083	TGGATCCTGGTATTGGGAGG	260474	92670	CTGCCCCAAAATACAAAGCA
171301	3497	TATCCATTAATTTGTTTACG	215888	48084	CTGGATCCTGGTATTGGGAG	260475	92671	CCTGCCCCAAAATACAAAGC
171302	3498	TTATCCATTAATTTGTTTAC	215889	48085	TCTGGATCCTGGTATTGGGA	260476	92672	GCCTGCCCCAAAATACAAAG
171303	3499	TTTATCCATTAATTTGTTTA	215890	48086	TTCTGGATCCTGGTATTGGG	260477	92673	AGCCTGCCCCAAAATACAAA
171304	3500	GTTTATCCATTAATTTGTTT	215891	48087	ATTCTGGATCCTGGTATTGG	260478	92674	AAGCCTGCCCCAAAATACAA
171305	3501	TGTTTATCCATTAATTTGTT	215892	48088	CATTCTGGATCCTGGTATTG	260479	92675	AAAGCCTGCCCCAAAATACA
171306	3502	CTGTTTATCCATTAATTTGT	215893	48089	CCATTCTGGATCCTGGTATT	260480	92676	AAAAGCCTGCCCCAAAATAC
171307	3503	TCTGTTTATCCATTAATTTG	215894	48090	CCCATTCTGGATCCTGGTAT	260481	92677	TAAAAGCCTGCCCCAAAATA
171308	3504	ATCTGTTTATCCATTAATTT	215895	48091	CCCCATTCTGGATCCTGGTA	260482	92678	TTAAAAGCCTGCCCCAAAAT
171309	3505	TATCTGTTTATCCATTAATT	215896	48092	ACCCCATTCTGGATCCTGGT	260483	92679	TTTAAAAGCCTGCCCCAAAA
171310	3506	TTATCTGTTTATCCATTAAT	215897	48093	CACCCCATTCTGGATCCTGG	260484	92680	TTTTAAAAGCCTGCCCCAAA
171311	3507	CTTATCTGTTTATCCATTAA	215898	48094	CCACCCCATTCTGGATCCTG	260485	92681	TTTTTAAAAGCCTGCCCCAA
171312	3508	ACTTATCTGTTTATCCATTA	215899	48095	CCCACCCCATTCTGGATCCT	260486	92682	CTTTTTAAAAGCCTGCCCCA
171313	3509	CACTTATCTGTTTATCCATT	215900	48096	CCCCACCCCATTCTGGATCC	260487	92683	ACTTTTTAAAAGCCTGCCCC
171314	3510	ACACTTATCTGTTTATCCAT	215901	48097	GCCCCACCCCATTCTGGATC	260488	92684	GACTTTTTAAAAGCCTGCCC
171315	3511	TACACTTATCTGTTTATCCA	215902	48098	GGCCCCACCCCATTCTGGAT	260489	92685	GGACTTTTTAAAAGCCTGCC
171316	3512	ATACACTTATCTGTTTATCC	215903	48099	GGGCCCCACCCCATTCTGGA	260490	92686	TGGACTTTTTAAAAGCCTGC
171317	3513	GATACACTTATCTGTTTATC	215904	48100	AGGGCCCCACCCCATTCTGG	260491	92687	CTGGACTTTTTAAAAGCCTG
171318	3514	GGATACACTTATCTGTTTAT	215905	48101	AAGGGCCCCACCCCATTCTG	260492	92688	GCTGGACTTTTTAAAAGCCT
171319	3515	GGGATACACTTATCTGTTTA	215906	48102	AAAGGGCCCCACCCCATTCT	260493	92689	TGCTGGACTTTTTAAAAGCC
171320	3516	GGGGATACACTTATCTGTTT	215907	48103	CAAAGGGCCCCACCCCATTC	260494	92690	ATGCTGGACTTTTTAAAAGC
171321	3517	AGGGGATACACTTATCTGTT	215908	48104	GCAAAGGGCCCCACCCCATT	260495	92691	AATGCTGGACTTTTTAAAAG
171322	3518	CAGGGGATACACTTATCTGT	215909	48105	GGCAAAGGGCCCCACCCCAT	260496	92692	AAATGCTGGACTTTTTAAAA
171323	3519	GCAGGGGATACACTTATCTG	215910	48106	GGGCAAAGGGCCCCACCCCA	260497	92693	TAAATGCTGGACTTTTTAAA
171324	3520	GGCAGGGGATACACTTATCT	215911	48107	AGGGCAAAGGGCCCCACCCC	260498	92694	ATAAATGCTGGACTTTTTAA
171325	3521	GGGCAGGGGATACACTTATC	215912	48108	CAGGGCAAAGGGCCCCACCC	260499	92695	AATAAATGCTGGACTTTTTA
171326	3522	GGGGCAGGGGATACACTTAT	215913	48109	TCAGGGCAAAGGGCCCCACC	260500	92696	TAATAAATGCTGGACTTTTT
171327	3523	GGGGGCAGGGGATACACTTA	215914	48110	TTCAGGGCAAAGGGCCCCAC	260501	92697	CTAATAAATGCTGGACTTTT
171328	3524	TGGGGGCAGGGGATACACTT	215915	48111	TTTCAGGGCAAAGGGCCCCA	260502	92698	ACTAATAAATGCTGGACTTT
171329	3525	GTGGGGGCAGGGGATACACT	215916	48112	TTTTCAGGGCAAAGGGCCCC	260503	92699	AACTAATAAATGCTGGACTT
171330	3526	GGTGGGGGCAGGGGATACAC	215917	48113	CTTTTCAGGGCAAAGGGCCC	260504	92700	AAACTAATAAATGCTGGACT

171331	3527	GGGTGGGGGCAGGGGATACA	215918	48114	GCTTTTCAGGGCAAAGGGCC	260505	92701	AAAACTAATAAATGCTGGAC
171332	3528	GGGGTGGGGGCAGGGGATAC	215919	48115	AGCTTTTCAGGGCAAAGGGC	260506	92702	CAAAACTAATAAATGCTGGA
171333	3529	AGGGGTGGGGGCAGGGGATA	215920	48116	CAGCTTTTCAGGGCAAAGGG	260507	92703	TCAAAACTAATAAATGCTGG
171334	3530	CAGGGGTGGGGGCAGGGGAT	215921	48117	ACAGCTTTTCAGGGCAAAGG	260508	92704	ATCAAAACTAATAAATGCTG
171335	3531	GCAGGGGTGGGGGCAGGGGA	215922	48118	AACAGCTTTTCAGGGCAAAG	260509	92705	TATCAAAACTAATAAATGCT
171336	3532	AGCAGGGGTGGGGGCAGGGG	215923	48119	AAACAGCTTTTCAGGGCAAA	260510	92706	GTATCAAAACTAATAAATGC
171337	3533	TAGCAGGGGTGGGGGCAGGG	215924	48120	TAAACAGCTTTTCAGGGCAA	260511	92707	AGTATCAAAACTAATAAATG
171338	3534	GTAGCAGGGGTGGGGGCAGG	215925	48121	CTAAACAGCTTTTCAGGGCA	260512	92708	AAGTATCAAAACTAATAAAT
171339	3535	CGTAGCAGGGGTGGGGGCAG	215926	48122	ACTAAACAGCTTTTCAGGGC	260513	92709	TAAGTATCAAAACTAATAAA
171340	3536	GCGTAGCAGGGGTGGGGGCA	215927	48123	AACTAAACAGCTTTTCAGGG	260514	92710	GTAAGTATCAAAACTAATAA
171341	3537	TGCGTAGCAGGGGTGGGGGC	215928	48124	AAACTAAACAGCTTTTCAGG	260515	92711	GGTAAGTATCAAAACTAATA
171342	3538	CTGCGTAGCAGGGGTGGGGG	215929	48125	CAAACTAAACAGCTTTTCAG	260516	92712	GGGTAAGTATCAAAACTAAT
171343	3539	CCTGCGTAGCAGGGGTGGGG	215930	48126	TCAAACTAAACAGCTTTTCA	260517	92713	GGGGTAAGTATCAAAACTAA
171344	3540	ACCTGCGTAGCAGGGGTGGG	215931	48127	TTCAAACTAAACAGCTTTTC	260518	92714	TGGGGTAAGTATCAAAACTA
171345	3541	GACCTGCGTAGCAGGGGTGG	215932	48128	TTTCAAACTAAACAGCTTTT	260519	92715	CTGGGGTAAGTATCAAAACT
171346	3542	GGACCTGCGTAGCAGGGGTG	215933	48129	TTTTCAAACTAAACAGCTTT	260520	92716	CCTGGGGTAAGTATCAAAAC
171347	3543	CGGACCTGCGTAGCAGGGGT	215934	48130	ATTTTCAAACTAAACAGCTT	260521	92717	CCCTGGGGTAAGTATCAAAA
171348	3544	CCGGACCTGCGTAGCAGGGG	215935	48131	TATTTTCAAACTAAACAGCT	260522	92718	TCCCTGGGGTAAGTATCAAA
171349	3545	TCCGGACCTGCGTAGCAGGG	215936	48132	GTATTTTCAAACTAAACAGC	260523	92719	TTCCCTGGGGTAAGTATCAA
171350	3546	CTCCGGACCTGCGTAGCAGG	215937	48133	TGTATTTTCAAACTAAACAG	260524	92720	CTTCCCTGGGGTAAGTATCA
171351	3547	ACTCCGGACCTGCGTAGCAG	215938	48134	TTGTATTTTCAAACTAAACA	260525	92721	TCTTCCCTGGGGTAAGTATC
171352	3548	CACTCCGGACCTGCGTAGCA	215939	48135	TTTGTATTTTCAAACTAAAC	260526	92722	CTCTTCCCTGGGGTAAGTAT
171353	3549	TCACTCCGGACCTGCGTAGC	215940	48136	GTTTGTATTTTCAAACTAAA	260527	92723	GCTCTTCCCTGGGGTAAGTA
171354	3550	GTCACTCCGGACCTGCGTAG	215941	48137	TGTTTGTATTTTCAAACTAA	260528	92724	TGCTCTTCCCTGGGGTAAGT
171355	3551	AGTCACTCCGGACCTGCGTA	215942	48138	CTGTTTGTATTTTCAAACTA	260529	92725	CTGCTCTTCCCTGGGGTAAG
171356	3552	GAGTCACTCCGGACCTGCGT	215943	48139	CCTGTTTGTATTTTCAAACT	260530	92726	ACTGCTCTTCCCTGGGGTAA
171357	3553	AGAGTCACTCCGGACCTGCG	215944	48140	TCCTGTTTGTATTTTCAAAC	260531	92727	AACTGCTCTTCCCTGGGGTA
171358	3554	AAGAGTCACTCCGGACCTGC	215945	48141	CTCCTGTTTGTATTTTCAAA	260532	92728	CAACTGCTCTTCCCTGGGGT
171359	3555	CAAGAGTCACTCCGGACCTG	215946	48142	TCTCCTGTTTGTATTTTCAA	260533	92729	CCAACTGCTCTTCCCTGGGG
171360	3556	TCAAGAGTCACTCCGGACCT	215947	48143	GTCTCCTGTTTGTATTTTCA	260534	92730	GCCAACTGCTCTTCCCTGGG
171361	3557	TTCAAGAGTCACTCCGGACC	215948	48144	TGTCTCCTGTTTGTATTTTC	260535	92731	TGCCAACTGCTCTTCCCTGG
171362	3558	CTTCAAGAGTCACTCCGGAC	215949	48145	CTGTCTCCTGTTTGTATTTT	260536	92732	CTGCCAACTGCTCTTCCCTG
171363	3559	GCTTCAAGAGTCACTCCGGA	215950	48146	TCTGTCTCCTGTTTGTATTT	260537	92733	CCTGCCAACTGCTCTTCCCT
171364	3560	AGCTTCAAGAGTCACTCCGG	215951	48147	TTCTGTCTCCTGTTTGTATT	260538	92734	ACCTGCCAACTGCTCTTCCC
171365	3561	GAGCTTCAAGAGTCACTCCG	215952	48148	TTTCTGTCTCCTGTTTGTAT	260539	92735	AACCTGCCAACTGCTCTTCC
171366	3562	TGAGCTTCAAGAGTCACTCC	215953	48149	TTTTCTGTCTCCTGTTTGTA	260540	92736	GAACCTGCCAACTGCTCTTC
171367	3563	ATGAGCTTCAAGAGTCACTC	215954	48150	CTTTTCTGTCTCCTGTTTGT	260541	92737	TGAACCTGCCAACTGCTCTT
171368	3564	TATGAGCTTCAAGAGTCACT	215955	48151	ACTTTTCTGTCTCCTGTTTG	260542	92738	ATGAACCTGCCAACTGCTCT
171369	3565	GTATGAGCTTCAAGAGTCAC	215956	48152	AACTTTTCTGTCTCCTGTTT	260543	92739	CATGAACCTGCCAACTGCTC
171370	3566	TGTATGAGCTTCAAGAGTCA	215957	48153	AAACTTTTCTGTCTCCTGTT	260544	92740	TCATGAACCTGCCAACTGCT
171371	3567	ATGTATGAGCTTCAAGAGTC	215958	48154	CAAACTTTTCTGTCTCCTGT	260545	92741	TTCATGAACCTGCCAACTGC
171372	3568	AATGTATGAGCTTCAAGAGT	215959	48155	CCAAACTTTTCTGTCTCCTG	260546	92742	CTTCATGAACCTGCCAACTG
171373	3569	GAATGTATGAGCTTCAAGAG	215960	48156	GCCAAACTTTTCTGTCTCCT	260547	92743	ACTTCATGAACCTGCCAACT
171374	3570	GGAATGTATGAGCTTCAAGA	215961	48157	AGCCAAACTTTTCTGTCTCC	260548	92744	GACTTCATGAACCTGCCAAC
171375	3571	AGGAATGTATGAGCTTCAAG	215962	48158	TAGCCAAACTTTTCTGTCTC	260549	92745	TGACTTCATGAACCTGCCAA
171376	3572	AAGGAATGTATGAGCTTCAA	215963	48159	TTAGCCAAACTTTTCTGTCT	260550	92746	ATGACTTCATGAACCTGCCA
171377	3573	CAAGGAATGTATGAGCTTCA	215964	48160	TTTAGCCAAACTTTTCTGTC	260551	92747	CATGACTTCATGAACCTGCC
171378	3574	CCAAGGAATGTATGAGCTTC	215965	48161	ATTTAGCCAAACTTTTCTGT	260552	92748	GCATGACTTCATGAACCTGC
171379	3575	GCCAAGGAATGTATGAGCTT	215966	48162	AATTTAGCCAAACTTTTCTG	260553	92749	AGCATGACTTCATGAACCTG
171380	3576	GGCCAAGGAATGTATGAGCT	215967	48163	TAATTTAGCCAAACTTTTCT	260554	92750	GAGCATGACTTCATGAACCT
171381	3577	TGGCCAAGGAATGTATGAGC	215968	48164	TTAATTTAGCCAAACTTTTC	260555	92751	GGAGCATGACTTCATGAACC
171382	3578	TTGGCCAAGGAATGTATGAG	215969	48165	ATTAATTTAGCCAAACTTTT	260556	92752	AGGAGCATGACTTCATGAAC
171383	3579	CTTGGCCAAGGAATGTATGA	215970	48166	CATTAATTTAGCCAAACTTT	260557	92753	TAGGAGCATGACTTCATGAA
171384	3580	ACTTGGCCAAGGAATGTATG	215971	48167	CCATTAATTTAGCCAAACTT	260558	92754	TTAGGAGCATGACTTCATGA
171385	3581	AACTTGGCCAAGGAATGTAT	215972	48168	TCCATTAATTTAGCCAAACT	260559	92755	ATTAGGAGCATGACTTCATG
171386	3582	AAACTTGGCCAAGGAATGTA	215973	48169	ATCCATTAATTTAGCCAAAC	260560	92756	AATTAGGAGCATGACTTCAT
171387	3583	CAAACTTGGCCAAGGAATGT	215974	48170	TATCCATTAATTTAGCCAAA	260561	92757	GAATTAGGAGCATGACTTCA
171388	3584	GCAAACTTGGCCAAGGAATG	215975	48171	TTATCCATTAATTTAGCCAA	260562	92758	GGAATTAGGAGCATGACTTC
171389	3585	AGCAAACTTGGCCAAGGAAT	215976	48172	TTTATCCATTAATTTAGCCA	260563	92759	TGGAATTAGGAGCATGACTT
171390	3586	AAGCAAACTTGGCCAAGGAA	215977	48173	CTTTATCCATTAATTTAGCC	260564	92760	CTGGAATTAGGAGCATGACT
171391	3587	GAAGCAAACTTGGCCAAGGA	215978	48174	ACTTTATCCATTAATTTAGC	260565	92761	GCTGGAATTAGGAGCATGAC
171392	3588	AGAAGCAAACTTGGCCAAGG	215979	48175	AACTTTATCCATTAATTTAG	260566	92762	AGCTGGAATTAGGAGCATGA
171393	3589	GAGAAGCAAACTTGGCCAAG	215980	48176	AAACTTTATCCATTAATTTA	260567	92763	AAGCTGGAATTAGGAGCATG
171394	3590	AGAGAAGCAAACTTGGCCAA	215981	48177	AAAACTTTATCCATTAATTT	260568	92764	AAAGCTGGAATTAGGAGCAT
171395	3591	TAGAGAAGCAAACTTGGCCA	215982	48178	TAAAACTTTATCCATTAATT	260569	92765	GAAAGCTGGAATTAGGAGCA
171396	3592	TTAGAGAAGCAAACTTGGCC	215983	48179	TTAAAACTTTATCCATTAAT	260570	92766	AGAAAGCTGGAATTAGGAGC
171397	3593	GTTAGAGAAGCAAACTTGGC	215984	48180	GTTAAAACTTTATCCATTAA	260571	92767	AAGAAAGCTGGAATTAGGAG
171398	3594	TGTTAGAGAAGCAAACTTGG	215985	48181	CGTTAAAACTTTATCCATTA	260572	92768	TAAGAAAGCTGGAATTAGGA
171399	3595	CTGTTAGAGAAGCAAACTTG	215986	48182	TCGTTAAAACTTTATCCATT	260573	92769	CTAAGAAAGCTGGAATTAGG
171400	3596	TCTGTTAGAGAAGCAAACTT	215987	48183	ATCGTTAAAACTTTATCCAT	260574	92770	ACTAAGAAAGCTGGAATTAG
171401	3597	ATCTGTTAGAGAAGCAAACT	215988	48184	CATCGTTAAAACTTTATCCA	260575	92771	CACTAAGAAAGCTGGAATTA
171402	3598	CATCTGTTAGAGAAGCAAAC	215989	48185	CCATCGTTAAAACTTTATCC	260576	92772	ACACTAAGAAAGCTGGAATT

171403	3599	ACATCTGTTAGAGAAGCAAA	215990	48186	ACCATCGTTAAAACTTTATC	260577	92773	TACACTAAGAAAGCTGGAAT
171404	3600	AACATCTGTTAGAGAAGCAA	215991	48187	TACCATCGTTAAAACTTTAT	260578	92774	GTACACTAAGAAAGCTGGAA
171405	3601	AAACATCTGTTAGAGAAGCA	215992	48188	TTACCATCGTTAAAACTTTA	260579	92775	AGTACACTAAGAAAGCTGGA
171406	3602	TAAACATCTGTTAGAGAAGC	215993	48189	GTTACCATCGTTAAAACTTT	260580	92776	AAGTACACTAAGAAAGCTGG
171407	3603	ATAAACATCTGTTAGAGAAG	215994	48190	GGTTACCATCGTTAAAACTT	260581	92777	AAAGTACACTAAGAAAGCTG
171408	3604	TATAAACATCTGTTAGAGAA	215995	48191	TGGTTACCATCGTTAAAACT	260582	92778	GAAAGTACACTAAGAAAGCT
171409	3605	ATATAAACATCTGTTAGAGA	215996	48192	ATGGTTACCATCGTTAAAAC	260583	92779	TGAAAGTACACTAAGAAAGC
171410	3606	TATATAAACATCTGTTAGAG	215997	48193	TATGGTTACCATCGTTAAAA	260584	92780	CTGAAAGTACACTAAGAAAG
171411	3607	CTATATAAACATCTGTTAGA	215998	48194	CTATGGTTACCATCGTTAAA	260585	92781	ACTGAAAGTACACTAAGAAA
171412	3608	GCTATATAAACATCTGTTAG	215999	48195	ACTATGGTTACCATCGTTAA	260586	92782	CACTGAAAGTACACTAAGAA
171413	3609	TGCTATATAAACATCTGTTA	216000	48196	TACTATGGTTACCATCGTTA	260587	92783	TCACTGAAAGTACACTAAGA
171414	3610	TTGCTATATAAACATCTGTT	216001	48197	CTACTATGGTTACCATCGTT	260588	92784	CTCACTGAAAGTACACTAAG
171415	3611	ATTGCTATATAAACATCTGT	216002	48198	CCTACTATGGTTACCATCGT	260589	92785	TCTCACTGAAAGTACACTAA
171416	3612	TATTGCTATATAAACATCTG	216003	48199	CCCTACTATGGTTACCATCG	260590	92786	GTCTCACTGAAAGTACACTA
171417	3613	TTATTGCTATATAAACATCT	216004	48200	ACCCTACTATGGTTACCATC	260591	92787	GGTCTCACTGAAAGTACACT
171418	3614	GTTATTGCTATATAAACATC	216005	48201	AACCCTACTATGGTTACCAT	260592	92788	GGGTCTCACTGAAAGTACAC
171419	3615	GGTTATTGCTATATAAACAT	216006	48202	GAACCCTACTATGGTTACCA	260593	92789	AGGGTCTCACTGAAAGTACA
171420	3616	AGGTTATTGCTATATAAACA	216007	48203	TGAACCCTACTATGGTTACC	260594	92790	CAGGGTCTCACTGAAAGTAC
171421	3617	CAGGTTATTGCTATATAAAC	216008	48204	ATGAACCCTACTATGGTTAC	260595	92791	TCAGGGTCTCACTGAAAGTA
171422	3618	CCAGGTTATTGCTATATAAA	216009	48205	GATGAACCCTACTATGGTTA	260596	92792	GTCAGGGTCTCACTGAAAGT
171423	3619	GCCAGGTTATTGCTATATAA	216010	48206	CGATGAACCCTACTATGGTT	260597	92793	TGTCAGGGTCTCACTGAAAG
171424	3620	AGCCAGGTTATTGCTATATA	216011	48207	TCGATGAACCCTACTATGGT	260598	92794	CTGTCAGGGTCTCACTGAAA
171425	3621	AAGCCAGGTTATTGCTATAT	216012	48208	GTCGATGAACCCTACTATGG	260599	92795	ACTGTCAGGGTCTCACTGAA
171426	3622	CAAGCCAGGTTATTGCTATA	216013	48209	TGTCGATGAACCCTACTATG	260600	92796	TACTGTCAGGGTCTCACTGA
171427	3623	CCAAGCCAGGTTATTGCTAT	216014	48210	CTGTCGATGAACCCTACTAT	260601	92797	TTACTGTCAGGGTCTCACTG
171428	3624	GCCAAGCCAGGTTATTGCTA	216015	48211	GCTGTCGATGAACCCTACTA	260602	92798	TTTACTGTCAGGGTCTCACT
171429	3625	AGCCAAGCCAGGTTATTGCT	216016	48212	GGCTGTCGATGAACCCTACT	260603	92799	ATTTACTGTCAGGGTCTCAC
171430	3626	GAGCCAAGCCAGGTTATTGC	216017	48213	TGGCTGTCGATGAACCCTAC	260604	92800	CATTTACTGTCAGGGTCTCA
171431	3627	AGAGCCAAGCCAGGTTATTG	216018	48214	CTGGCTGTCGATGAACCCTA	260605	92801	TCATTTACTGTCAGGGTCTC
171432	3628	AAGAGCCAAGCCAGGTTATT	216019	48215	GCTGGCTGTCGATGAACCCT	260606	92802	TTCATTTACTGTCAGGGTCT
171433	3629	CAAGAGCCAAGCCAGGTTAT	216020	48216	CGCTGGCTGTCGATGAACCC	260607	92803	CTTCATTTACTGTCAGGGTC
171434	3630	CCAAGAGCCAAGCCAGGTTA	216021	48217	TCGCTGGCTGTCGATGAACC	260608	92804	CCTTCATTTACTGTCAGGGT
171435	3631	CCCAAGAGCCAAGCCAGGTT	216022	48218	ATCGCTGGCTGTCGATGAAC	260609	92805	ACCTTCATTTACTGTCAGGG
171436	3632	ACCCAAGAGCCAAGCCAGGT	216023	48219	CATCGCTGGCTGTCGATGAA	260610	92806	CACCTTCATTTACTGTCAGG
171437	3633	AACCCAAGAGCCAAGCCAGG	216024	48220	CCATCGCTGGCTGTCGATGA	260611	92807	ACACCTTCATTTACTGTCAG
171438	3634	GAACCCAAGAGCCAAGCCAG	216025	48221	ACCATCGCTGGCTGTCGATG	260612	92808	CACACCTTCATTTACTGTCA
171439	3635	TGAACCCAAGAGCCAAGCCA	216026	48222	AACCATCGCTGGCTGTCGAT	260613	92809	ACACACCTTCATTTACTGTC
171440	3636	GTGAACCCAAGAGCCAAGCC	216027	48223	GAACCATCGCTGGCTGTCGA	260614	92810	AACACACCTTCATTTACTGT
171441	3637	GGTGAACCCAAGAGCCAAGC	216028	48224	AGAACCATCGCTGGCTGTCG	260615	92811	AAACACACCTTCATTTACTG
171442	3638	AGGTGAACCCAAGAGCCAAG	216029	48225	CAGAACCATCGCTGGCTGTC	260616	92812	CAAACACACCTTCATTTACT
171443	3639	AAGGTGAACCCAAGAGCCAA	216030	48226	TCAGAACCATCGCTGGCTGT	260617	92813	TCAAACACACCTTCATTTAC
171444	3640	AAAGGTGAACCCAAGAGCCA	216031	48227	TTCAGAACCATCGCTGGCTG	260618	92814	TTCAAACACACCTTCATTTA
171445	3641	CAAAGGTGAACCCAAGAGCC	216032	48228	GTTCAGAACCATCGCTGGCT	260619	92815	TTTCAAACACACCTTCATTT
171446	3642	CCAAAGGTGAACCCAAGAGC	216033	48229	TGTTCAGAACCATCGCTGGC	260620	92816	TTTTCAAACACACCTTCATT
171447	3643	TCCAAAGGTGAACCCAAGAG	216034	48230	GTGTTCAGAACCATCGCTGG	260621	92817	GTTTTCAAACACACCTTCAT
171448	3644	GTCCAAAGGTGAACCCAAGA	216035	48231	AGTGTTCAGAACCATCGCTG	260622	92818	GGTTTTCAAACACACCTTCA
171449	3645	CGTCCAAAGGTGAACCCAAG	216036	48232	AAGTGTTCAGAACCATCGCT	260623	92819	TGGTTTTCAAACACACCTTC
171450	3646	TCGTCCAAAGGTGAACCCAA	216037	48233	CAAGTGTTCAGAACCATCGC	260624	92820	TTGGTTTTCAAACACACCTT
171451	3647	ATCGTCCAAAGGTGAACCCA	216038	48234	TCAAGTGTTCAGAACCATCG	260625	92821	TTTGGTTTTCAAACACACCT
171452	3648	AATCGTCCAAAGGTGAACCC	216039	48235	GTCAAGTGTTCAGAACCATC	260626	92822	GTTTGGTTTTCAAACACACC
171453	3649	AAATCGTCCAAAGGTGAACC	216040	48236	TGTCAAGTGTTCAGAACCAT	260627	92823	GGTTTGGTTTTCAAACACAC
171454	3650	CAAATCGTCCAAAGGTGAAC	216041	48237	ATGTCAAGTGTTCAGAACCA	260628	92824	GGGTTTGGTTTTCAAACACA
171455	3651	CCAAATCGTCCAAAGGTGAA	216042	48238	CATGTCAAGTGTTCAGAACC	260629	92825	TGGGTTTGGTTTTCAAACAC
171456	3652	CCCAAATCGTCCAAAGGTGA	216043	48239	ACATGTCAAGTGTTCAGAAC	260630	92826	CTGGGTTTGGTTTTCAAACA
171457	3653	CCCCAAATCGTCCAAAGGTG	216044	48240	TACATGTCAAGTGTTCAGAA	260631	92827	CCTGGGTTTGGTTTTCAAAC
171458	3654	TCCCCAAATCGTCCAAAGGT	216045	48241	ATACATGTCAAGTGTTCAGA	260632	92828	TCCTGGGTTTGGTTTTCAAA
171459	3655	TTCCCCAAATCGTCCAAAGG	216046	48242	AATACATGTCAAGTGTTCAG	260633	92829	GTCCTGGGTTTGGTTTTCAA
171460	3656	CTTCCCCAAATCGTCCAAAG	216047	48243	TAATACATGTCAAGTGTTCA	260634	92830	TGTCCTGGGTTTGGTTTTCA
171461	3657	CCTTCCCCAAATCGTCCAAA	216048	48244	TTAATACATGTCAAGTGTTC	260635	92831	CTGTCCTGGGTTTGGTTTTC
171462	3658	CCCTTCCCCAAATCGTCCAA	216049	48245	GTTAATACATGTCAAGTGTT	260636	92832	ACTGTCCTGGGTTTGGTTTT
171463	3659	CCCCTTCCCCAAATCGTCCA	216050	48246	AGTTAATACATGTCAAGTGT	260637	92833	TACTGTCCTGGGTTTGGTTT
171464	3660	GCCCCTTCCCCAAATCGTCC	216051	48247	GAGTTAATACATGTCAAGTG	260638	92834	TTACTGTCCTGGGTTTGGTT
171465	3661	AGCCCCTTCCCCAAATCGTC	216052	48248	TGAGTTAATACATGTCAAGT	260639	92835	TTTACTGTCCTGGGTTTGGT
171466	3662	AAGCCCCTTCCCCAAATCGT	216053	48249	GTGAGTTAATACATGTCAAG	260640	92836	ATTTACTGTCCTGGGTTTGG
171467	3663	CAAGCCCCTTCCCCAAATCG	216054	48250	GGTGAGTTAATACATGTCAA	260641	92837	CATTTACTGTCCTGGGTTTG
171468	3664	ACAAGCCCCTTCCCCAAATC	216055	48251	AGGTGAGTTAATACATGTCA	260642	92838	TCATTTACTGTCCTGGGTTT
171469	3665	AACAAGCCCCTTCCCCAAAT	216056	48252	TAGGTGAGTTAATACATGTC	260643	92839	TTCATTTACTGTCCTGGGTT
171470	3666	CAACAAGCCCCTTCCCCAAA	216057	48253	TTAGGTGAGTTAATACATGT	260644	92840	CTTCATTTACTGTCCTGGGT
171471	3667	CCAACAAGCCCCTTCCCCAA	216058	48254	ATTAGGTGAGTTAATACATG	260645	92841	CCTTCATTTACTGTCCTGGG
171472	3668	GCCAACAAGCCCCTTCCCCA	216059	48255	GATTAGGTGAGTTAATACAT	260646	92842	ACCTTCATTTACTGTCCTGG
171473	3669	AGCCAACAAGCCCCTTCCCC	216060	48256	GGATTAGGTGAGTTAATACA	260647	92843	CACCTTCATTTACTGTCCTG
171474	3670	AAGCCAACAAGCCCCTTCCC	216061	48257	GGGATTAGGTGAGTTAATAC	260648	92844	ACACCTTCATTTACTGTCCT

171475	3671	AAAGCCAACAAGCCCCTTCC	216062	48258	GGGGATTAGGTGAGTTAATA	260649	92845	CACACCTTCATTTACTGTCC
171476	3672	CAAAGCCAACAAGCCCCTTC	216063	48259	TGGGGATTAGGTGAGTTAAT	260650	92846	ACACACCTTCATTTACTGTC
171477	3673	GCAAAGCCAACAAGCCCCTT	216064	48260	GTGGGGATTAGGTGAGTTAA	260651	92847	AACACACCTTCATTTACTGT
171478	3674	AGCAAAGCCAACAAGCCCCT	216065	48261	TGTGGGGATTAGGTGAGTTA	260652	92848	AAACACACCTTCATTTACTG
171479	3675	CAGCAAAGCCAACAAGCCCC	216066	48262	ATGTGGGGATTAGGTGAGTT	260653	92849	CAAACACACCTTCATTTACT
171480	3676	CCAGCAAAGCCAACAAGCCC	216067	48263	AATGTGGGGATTAGGTGAGT	260654	92850	TCAAACACACCTTCATTTAC
171481	3677	CCCAGCAAAGCCAACAAGCC	216068	48264	AAATGTGGGGATTAGGTGAG	260655	92851	TTCAAACACACCTTCATTTA
171482	3678	ACCCAGCAAAGCCAACAAGC	216069	48265	AAAATGTGGGGATTAGGTGA	260656	92852	TTTCAAACACACCTTCATTT
171483	3679	AACCCAGCAAAGCCAACAAG	216070	48266	TAAAATGTGGGGATTAGGTG	260657	92853	TTTTCAAACACACCTTCATT
171484	3680	AAACCCAGCAAAGCCAACAA	216071	48267	GTAAAATGTGGGGATTAGGT	260658	92854	GTTTTCAAACACACCTTCAT
171485	3681	AAAACCCAGCAAAGCCAACA	216072	48268	TGTAAAATGTGGGGATTAGG	260659	92855	GGTTTTCAAACACACCTTCA
171486	3682	CAAAACCCAGCAAAGCCAAC	216073	48269	CTGTAAAATGTGGGGATTAG	260660	92856	TGGTTTTCAAACACACCTTC
171487	3683	CCAAAACCCAGCAAAGCCAA	216074	48270	TCTGTAAAATGTGGGGATTA	260661	92857	CTGGTTTTCAAACACACCTT
171488	3684	TCCAAAACCCAGCAAAGCCA	216075	48271	GTCTGTAAAATGTGGGGATT	260662	92858	GCTGGTTTTCAAACACACCT
171489	3685	ATCCAAAACCCAGCAAAGCC	216076	48272	TGTCTGTAAAATGTGGGGAT	260663	92859	GGCTGGTTTTCAAACACACC
171490	3686	CATCCAAAACCCAGCAAAGC	216077	48273	TTGTCTGTAAAATGTGGGGA	260664	92860	GGGCTGGTTTTCAAACACAC
171491	3687	TCATCCAAAACCCAGCAAAG	216078	48274	ATTGTCTGTAAAATGTGGGG	260665	92861	AGGGCTGGTTTTCAAACACA
171492	3688	CTCATCCAAAACCCAGCAAA	216079	48275	CATTGTCTGTAAAATGTGGG	260666	92862	TAGGGCTGGTTTTCAAACAC
171493	3689	ACTCATCCAAAACCCAGCAA	216080	48276	GCATTGTCTGTAAAATGTGG	260667	92863	CTAGGGCTGGTTTTCAAACA
171494	3690	CACTCATCCAAAACCCAGCA	216081	48277	TGCATTGTCTGTAAAATGTG	260668	92864	CCTAGGGCTGGTTTTCAAAC
171495	3691	TCACTCATCCAAAACCCAGC	216082	48278	TTGCATTGTCTGTAAAATGT	260669	92865	TCCTAGGGCTGGTTTTCAAA
171496	3692	GTCACTCATCCAAAACCCAG	216083	48279	TTTGCATTGTCTGTAAAATG	260670	92866	GTCCTAGGGCTGGTTTTCAA
171497	3693	TGTCACTCATCCAAAACCCA	216084	48280	CTTTGCATTGTCTGTAAAAT	260671	92867	TGTCCTAGGGCTGGTTTTCA
171498	3694	CTGTCACTCATCCAAAACCC	216085	48281	CCTTTGCATTGTCTGTAAAA	260672	92868	CTGTCCTAGGGCTGGTTTTC
171499	3695	ACTGTCACTCATCCAAAACC	216086	48282	TCCTTTGCATTGTCTGTAAA	260673	92869	ACTGTCCTAGGGCTGGTTTT
171500	3696	GACTGTCACTCATCCAAAAC	216087	48283	CTCCTTTGCATTGTCTGTAA	260674	92870	TACTGTCCTAGGGCTGGTTT
171501	3697	GGACTGTCACTCATCCAAAA	216088	48284	CCTCCTTTGCATTGTCTGTA	260675	92871	TTACTGTCCTAGGGCTGGTT
171502	3698	TGGACTGTCACTCATCCAAA	216089	48285	GCCTCCTTTGCATTGTCTGT	260676	92872	TTTACTGTCCTAGGGCTGGT
171503	3699	ATGGACTGTCACTCATCCAA	216090	48286	AGCCTCCTTTGCATTGTCTG	260677	92873	ATTTACTGTCCTAGGGCTGG
171504	3700	CATGGACTGTCACTCATCCA	216091	48287	GAGCCTCCTTTGCATTGTCT	260678	92874	CATTTACTGTCCTAGGGCTG
171505	3701	TCATGGACTGTCACTCATCC	216092	48288	AGAGCCTCCTTTGCATTGTC	260679	92875	TCATTTACTGTCCTAGGGCT
171506	3702	GTCATGGACTGTCACTCATC	216093	48289	CAGAGCCTCCTTTGCATTGT	260680	92876	TTCATTTACTGTCCTAGGGC
171507	3703	AGTCATGGACTGTCACTCAT	216094	48290	CCAGAGCCTCCTTTGCATTG	260681	92877	CTTCATTTACTGTCCTAGGG
171508	3704	CAGTCATGGACTGTCACTCA	216095	48291	CCCAGAGCCTCCTTTGCATT	260682	92878	GCTTCATTTACTGTCCTAGG
171509	3705	ACAGTCATGGACTGTCACTC	216096	48292	TCCCAGAGCCTCCTTTGCAT	260683	92879	GGCTTCATTTACTGTCCTAG
171510	3706	AACAGTCATGGACTGTCACT	216097	48293	CTCCCAGAGCCTCCTTTGCA	260684	92880	TGGCTTCATTTACTGTCCTA
171511	3707	GAACAGTCATGGACTGTCAC	216098	48294	CCTCCCAGAGCCTCCTTTGC	260685	92881	ATGGCTTCATTTACTGTCCT
171512	3708	GGAACAGTCATGGACTGTCA	216099	48295	ACCTCCCAGAGCCTCCTTTG	260686	92882	GATGGCTTCATTTACTGTCC
171513	3709	AGGAACAGTCATGGACTGTC	216100	48296	AACCTCCCAGAGCCTCCTTT	260687	92883	AGATGGCTTCATTTACTGTC
171514	3710	CAGGAACAGTCATGGACTGT	216101	48297	CAACCTCCCAGAGCCTCCTT	260688	92884	AAGATGGCTTCATTTACTGT
171515	3711	GCAGGAACAGTCATGGACTG	216102	48298	TCAACCTCCCAGAGCCTCCT	260689	92885	GAAGATGGCTTCATTTACTG
171516	3712	AGCAGGAACAGTCATGGACT	216103	48299	CTCAACCTCCCAGAGCCTCC	260690	92886	AGAAGATGGCTTCATTTACT
171517	3713	CAGCAGGAACAGTCATGGAC	216104	48300	ACTCAACCTCCCAGAGCCTC	260691	92887	GAGAAGATGGCTTCATTTAC
171518	3714	CCAGCAGGAACAGTCATGGA	216105	48301	CACTCAACCTCCCAGAGCCT	260692	92888	TGAGAAGATGGCTTCATTTA
171519	3715	TCCAGCAGGAACAGTCATGG	216106	48302	TCACTCAACCTCCCAGAGCC	260693	92889	GTGAGAAGATGGCTTCATTT
171520	3716	TTCCAGCAGGAACAGTCATG	216107	48303	GTCACTCAACCTCCCAGAGC	260694	92890	AGTGAGAAGATGGCTTCATT
171521	3717	CTTCCAGCAGGAACAGTCAT	216108	48304	AGTCACTCAACCTCCCAGAG	260695	92891	CAGTGAGAAGATGGCTTCAT
171522	3718	CCTTCCAGCAGGAACAGTCA	216109	48305	AAGTCACTCAACCTCCCAGA	260696	92892	GCAGTGAGAAGATGGCTTCA
171523	3719	CCCTTCCAGCAGGAACAGTC	216110	48306	CAAGTCACTCAACCTCCCAG	260697	92893	TGCAGTGAGAAGATGGCTTC
171524	3720	GCCCTTCCAGCAGGAACAGT	216111	48307	GCAAGTCACTCAACCTCCCA	260698	92894	ATGCAGTGAGAAGATGGCTT
171525	3721	CGCCCTTCCAGCAGGAACAG	216112	48308	GGCAAGTCACTCAACCTCCC	260699	92895	TATGCAGTGAGAAGATGGCT
171526	3722	ACGCCCTTCCAGCAGGAACA	216113	48309	GGGCAAGTCACTCAACCTCC	260700	92896	TTATGCAGTGAGAAGATGGC
171527	3723	CACGCCCTTCCAGCAGGAAC	216114	48310	GGGGCAAGTCACTCAACCTC	260701	92897	TTTATGCAGTGAGAAGATGG
171528	3724	TCACGCCCTTCCAGCAGGAA	216115	48311	TGGGGCAAGTCACTCAACCT	260702	92898	GTTTATGCAGTGAGAAGATG
171529	3725	GTCACGCCCTTCCAGCAGGA	216116	48312	TTGGGGCAAGTCACTCAACC	260703	92899	AGTTTATGCAGTGAGAAGAT
171530	3726	AGTCACGCCCTTCCAGCAGG	216117	48313	TTTGGGGCAAGTCACTCAAC	260704	92900	CAGTTTATGCAGTGAGAAGA
171531	3727	AAGTCACGCCCTTCCAGCAG	216118	48314	CTTTGGGGCAAGTCACTCAA	260705	92901	GCAGTTTATGCAGTGAGAAG
171532	3728	AAAGTCACGCCCTTCCAGCA	216119	48315	ACTTTGGGGCAAGTCACTCA	260706	92902	TGCAGTTTATGCAGTGAGAA
171533	3729	AAAAGTCACGCCCTTCCAGC	216120	48316	GACTTTGGGGCAAGTCACTC	260707	92903	GTGCAGTTTATGCAGTGAGA
171534	3730	TAAAAGTCACGCCCTTCCAG	216121	48317	CGACTTTGGGGCAAGTCACT	260708	92904	GGTGCAGTTTATGCAGTGAG
171535	3731	TTAAAAGTCACGCCCTTCCA	216122	48318	GCGACTTTGGGGCAAGTCAC	260709	92905	GGGTGCAGTTTATGCAGTGA
171536	3732	CTTAAAAGTCACGCCCTTCC	216123	48319	TGCGACTTTGGGGCAAGTCA	260710	92906	TGGGTGCAGTTTATGCAGTG
171537	3733	ACTTAAAAGTCACGCCCTTC	216124	48320	GTGCGACTTTGGGGCAAGTC	260711	92907	CTGGGTGCAGTTTATGCAGT
171538	3734	CACTTAAAAGTCACGCCCTT	216125	48321	TGTGCGACTTTGGGGCAAGT	260712	92908	TCTGGGTGCAGTTTATGCAG
171539	3735	CCACTTAAAAGTCACGCCCT	216126	48322	CTGTGCGACTTTGGGGCAAG	260713	92909	ATCTGGGTGCAGTTTATGCA
171540	3736	ACCACTTAAAAGTCACGCCC	216127	48323	GCTGTGCGACTTTGGGGCAA	260714	92910	GATCTGGGTGCAGTTTATGC
171541	3737	AACCACTTAAAAGTCACGCC	216128	48324	AGCTGTGCGACTTTGGGGCA	260715	92911	AGATCTGGGTGCAGTTTATG
171542	3738	AAACCACTTAAAAGTCACGC	216129	48325	GAGCTGTGCGACTTTGGGGC	260716	92912	AAGATCTGGGTGCAGTTTAT
171543	3739	GAAACCACTTAAAAGTCACG	216130	48326	GGAGCTGTGCGACTTTGGGG	260717	92913	GAAGATCTGGGTGCAGTTTA
171544	3740	AGAAACCACTTAAAAGTCAC	216131	48327	AGGAGCTGTGCGACTTTGGG	260718	92914	CGAAGATCTGGGTGCAGTTT
171545	3741	TAGAAACCACTTAAAAGTCA	216132	48328	TAGGAGCTGTGCGACTTTGG	260719	92915	GCGAAGATCTGGGTGCAGTT
171546	3742	TTAGAAACCACTTAAAAGTC	216133	48329	TTAGGAGCTGTGCGACTTTG	260720	92916	GGCGAAGATCTGGGTGCAGT

171547	3743	ATTAGAAACCACTTAAAAGT	216134	48330	CTTAGGAGCTGTGCGACTTT	260721	92917	GGGCGAAGATCTGGGTGCAG
171548	3744	TATTAGAAACCACTTAAAAG	216135	48331	ACTTAGGAGCTGTGCGACTT	260722	92918	TGGGCGAAGATCTGGGTGCA
171549	3745	ATATTAGAAACCACTTAAAA	216136	48332	CACTTAGGAGCTGTGCGACT	260723	92919	ATGGGCGAAGATCTGGGTGC
171550	3746	GATATTAGAAACCACTTAAA	216137	48333	TCACTTAGGAGCTGTGCGAC	260724	92920	GATGGGCGAAGATCTGGGTG
171551	3747	TGATATTAGAAACCACTTAA	216138	48334	TTCACTTAGGAGCTGTGCGA	260725	92921	GGATGGGCGAAGATCTGGGT
171552	3748	CTGATATTAGAAACCACTTA	216139	48335	CTTCACTTAGGAGCTGTGCG	260726	92922	AGGATGGGCGAAGATCTGGG
171553	3749	CCTGATATTAGAAACCACTT	216140	48336	CCTTCACTTAGGAGCTGTGC	260727	92923	AAGGATGGGCGAAGATCTGG
171554	3750	GCCTGATATTAGAAACCACT	216141	48337	TCCTTCACTTAGGAGCTGTG	260728	92924	GAAGGATGGGCGAAGATCTG
171555	3751	TGCCTGATATTAGAAACCAC	216142	48338	ATCCTTCACTTAGGAGCTGT	260729	92925	AGAAGGATGGGCGAAGATCT
171556	3752	ATGCCTGATATTAGAAACCA	216143	48339	AATCCTTCACTTAGGAGCTG	260730	92926	GAGAAGGATGGGCGAAGATC
171557	3753	AATGCCTGATATTAGAAACC	216144	48340	GAATCCTTCACTTAGGAGCT	260731	92927	TGAGAAGGATGGGCGAAGAT
171558	3754	CAATGCCTGATATTAGAAAC	216145	48341	CGAATCCTTCACTTAGGAGC	260732	92928	CTGAGAAGGATGGGCGAAGA
171559	3755	GCAATGCCTGATATTAGAAA	216146	48342	CCGAATCCTTCACTTAGGAG	260733	92929	ACTGAGAAGGATGGGCGAAG
171560	3756	AGCAATGCCTGATATTAGAA	216147	48343	TCCGAATCCTTCACTTAGGA	260734	92930	TACTGAGAAGGATGGGCGAA
171561	3757	GAGCAATGCCTGATATTAGA	216148	48344	CTCCGAATCCTTCACTTAGG	260735	92931	ATACTGAGAAGGATGGGCGA
171562	3758	GGAGCAATGCCTGATATTAG	216149	48345	ACTCCGAATCCTTCACTTAG	260736	92932	AATACTGAGAAGGATGGGCG
171563	3759	AGGAGCAATGCCTGATATTA	216150	48346	CACTCCGAATCCTTCACTTA	260737	92933	AAATACTGAGAAGGATGGGC
171564	3760	GAGGAGCAATGCCTGATATT	216151	48347	CCACTCCGAATCCTTCACTT	260738	92934	GAAATACTGAGAAGGATGGG
171565	3761	GGAGGAGCAATGCCTGATAT	216152	48348	TCCACTCCGAATCCTTCACT	260739	92935	TGAAATACTGAGAAGGATGG
171566	3762	CGGAGGAGCAATGCCTGATA	216153	48349	GTCCACTCCGAATCCTTCAC	260740	92936	GTGAAATACTGAGAAGGATG
171567	3763	TCGGAGGAGCAATGCCTGAT	216154	48350	AGTCCACTCCGAATCCTTCA	260741	92937	AGTGAAATACTGAGAAGGAT
171568	3764	GTCGGAGGAGCAATGCCTGA	216155	48351	GAGTCCACTCCGAATCCTTC	260742	92938	AAGTGAAATACTGAGAAGGA
171569	3765	TGTCGGAGGAGCAATGCCTG	216156	48352	GGAGTCCACTCCGAATCCTT	260743	92939	GAAGTGAAATACTGAGAAGG
171570	3766	CTGTCGGAGGAGCAATGCCT	216157	48353	TGGAGTCCACTCCGAATCCT	260744	92940	TGAAGTGAAATACTGAGAAG
171571	3767	CCTGTCGGAGGAGCAATGCC	216158	48354	CTGGAGTCCACTCCGAATCC	260745	92941	GTGAAGTGAAATACTGAGAA
171572	3768	TCCTGTCGGAGGAGCAATGC	216159	48355	CCTGGAGTCCACTCCGAATC	260746	92942	GGTGAAGTGAAATACTGAGA
171573	3769	TTCCTGTCGGAGGAGCAATG	216160	48356	GCCTGGAGTCCACTCCGAAT	260747	92943	GGGTGAAGTGAAATACTGAG
171574	3770	GTTCCTGTCGGAGGAGCAAT	216161	48357	TGCCTGGAGTCCACTCCGAA	260748	92944	TGGGTGAAGTGAAATACTGA
171575	3771	TGTTCCTGTCGGAGGAGCAA	216162	48358	CTGCCTGGAGTCCACTCCGA	260749	92945	ATGGGTGAAGTGAAATACTG
171576	3772	TTGTTCCTGTCGGAGGAGCA	216163	48359	GCTGCCTGGAGTCCACTCCG	260750	92946	AATGGGTGAAGTGAAATACT
171577	3773	TTTGTTCCTGTCGGAGGAGC	216164	48360	GGCTGCCTGGAGTCCACTCC	260751	92947	CAATGGGTGAAGTGAAATAC
171578	3774	TTTTGTTCCTGTCGGAGGAG	216165	48361	AGGCTGCCTGGAGTCCACTC	260752	92948	ACAATGGGTGAAGTGAAATA
171579	3775	CTTTTGTTCCTGTCGGAGGA	216166	48362	CAGGCTGCCTGGAGTCCACT	260753	92949	AACAATGGGTGAAGTGAAAT
171580	3776	TCTTTTGTTCCTGTCGGAGG	216167	48363	CCAGGCTGCCTGGAGTCCAC	260754	92950	AAACAATGGGTGAAGTGAAA
171581	3777	TTCTTTTGTTCCTGTCGGAG	216168	48364	ACCAGGCTGCCTGGAGTCCA	260755	92951	TAAACAATGGGTGAAGTGAA
171582	3778	TTTCTTTTGTTCCTGTCGGA	216169	48365	GACCAGGCTGCCTGGAGTCC	260756	92952	GTAAACAATGGGTGAAGTGA
171583	3779	ATTTCTTTTGTTCCTGTCGG	216170	48366	AGACCAGGCTGCCTGGAGTC	260757	92953	AGTAAACAATGGGTGAAGTG
171584	3780	CATTTCTTTTGTTCCTGTCG	216171	48367	CAGACCAGGCTGCCTGGAGT	260758	92954	CAGTAAACAATGGGTGAAGT
171585	3781	CCATTTCTTTTGTTCCTGTC	216172	48368	TCAGACCAGGCTGCCTGGAG	260759	92955	ACAGTAAACAATGGGTGAAG
171586	3782	TCCATTTCTTTTGTTCCTGT	216173	48369	GTCAGACCAGGCTGCCTGGA	260760	92956	GACAGTAAACAATGGGTGAA
171587	3783	ATCCATTTCTTTTGTTCCTG	216174	48370	AGTCAGACCAGGCTGCCTGG	260761	92957	AGACAGTAAACAATGGGTGA
171588	3784	TATCCATTTCTTTTGTTCCT	216175	48371	GAGTCAGACCAGGCTGCCTG	260762	92958	GAGACAGTAAACAATGGGTG
171589	3785	GTATCCATTTCTTTTGTTCC	216176	48372	GGAGTCAGACCAGGCTGCCT	260763	92959	TGAGACAGTAAACAATGGGT
171590	3786	AGTATCCATTTCTTTTGTTC	216177	48373	GGGAGTCAGACCAGGCTGCC	260764	92960	TTGAGACAGTAAACAATGGG
171591	3787	CAGTATCCATTTCTTTTGTT	216178	48374	AGGGAGTCAGACCAGGCTGC	260765	92961	ATTGAGACAGTAAACAATGG
171592	3788	GCAGTATCCATTTCTTTTGT	216179	48375	CAGGGAGTCAGACCAGGCTG	260766	92962	CATTGAGACAGTAAACAATG
171593	3789	GGCAGTATCCATTTCTTTTG	216180	48376	GCAGGGAGTCAGACCAGGCT	260767	92963	TCATTGAGACAGTAAACAAT
171594	3790	GGGCAGTATCCATTTCTTTT	216181	48377	TGCAGGGAGTCAGACCAGGC	260768	92964	GTCATTGAGACAGTAAACAA
171595	3791	TGGGCAGTATCCATTTCTTT	216182	48378	GTGCAGGGAGTCAGACCAGG	260769	92965	AGTCATTGAGACAGTAAACA
171596	3792	ATGGGCAGTATCCATTTCTT	216183	48379	AGTGCAGGGAGTCAGACCAG	260770	92966	CAGTCATTGAGACAGTAAAC
171597	3793	TATGGGCAGTATCCATTTCT	216184	48380	CAGTGCAGGGAGTCAGACCA	260771	92967	CCAGTCATTGAGACAGTAAA
171598	3794	TTATGGGCAGTATCCATTTC	216185	48381	GCAGTGCAGGGAGTCAGACC	260772	92968	CCCAGTCATTGAGACAGTAA
171599	3795	TTTATGGGCAGTATCCATTT	216186	48382	CGCAGTGCAGGGAGTCAGAC	260773	92969	CCCCAGTCATTGAGACAGTA
171600	3796	ATTTATGGGCAGTATCCATT	216187	48383	GCGCAGTGCAGGGAGTCAGA	260774	92970	TCCCCAGTCATTGAGACAGT
171601	3797	AATTTATGGGCAGTATCCAT	216188	48384	AGCGCAGTGCAGGGAGTCAG	260775	92971	TTCCCCAGTCATTGAGACAG
171602	3798	CAATTTATGGGCAGTATCCA	216189	48385	CAGCGCAGTGCAGGGAGTCA	260776	92972	TTTCCCCAGTCATTGAGACA
171603	3799	ACAATTTATGGGCAGTATCC	216190	48386	ACAGCGCAGTGCAGGGAGTC	260777	92973	ATTTCCCCAGTCATTGAGAC
171604	3800	AACAATTTATGGGCAGTATC	216191	48387	CACAGCGCAGTGCAGGGAGT	260778	92974	CATTTCCCCAGTCATTGAGA
171605	3801	TAACAATTTATGGGCAGTAT	216192	48388	GCACAGCGCAGTGCAGGGAG	260779	92975	ACATTTCCCCAGTCATTGAG
171606	3802	CTAACAATTTATGGGCAGTA	216193	48389	AGCACAGCGCAGTGCAGGGA	260780	92976	GACATTTCCCCAGTCATTGA
171607	3803	TCTAACAATTTATGGGCAGT	216194	48390	AAGCACAGCGCAGTGCAGGG	260781	92977	AGACATTTCCCCAGTCATTG
171608	3804	TTCTAACAATTTATGGGCAG	216195	48391	TAAGCACAGCGCAGTGCAGG	260782	92978	CAGACATTTCCCCAGTCATT
171609	3805	TTTCTAACAATTTATGGGCA	216196	48392	ATAAGCACAGCGCAGTGCAG	260783	92979	CCAGACATTTCCCCAGTCAT
171610	3806	TTTTCTAACAATTTATGGGC	216197	48393	GATAAGCACAGCGCAGTGCA	260784	92980	CCCAGACATTTCCCCAGTCA
171611	3807	GTTTTCTAACAATTTATGGG	216198	48394	AGATAAGCACAGCGCAGTGC	260785	92981	CCCCAGACATTTCCCCAGTC
171612	3808	AGTTTTCTAACAATTTATGG	216199	48395	GAGATAAGCACAGCGCAGTG	260786	92982	TCCCCAGACATTTCCCCAGT
171613	3809	AAGTTTTCTAACAATTTATG	216200	48396	AGAGATAAGCACAGCGCAGT	260787	92983	TTCCCCAGACATTTCCCCAG
171614	3810	TAAGTTTTCTAACAATTTAT	216201	48397	CAGAGATAAGCACAGCGCAG	260788	92984	TTTCCCCAGACATTTCCCCA
171615	3811	CTAAGTTTTCTAACAATTTA	216202	48398	CCAGAGATAAGCACAGCGCA	260789	92985	ATTTCCCCAGACATTTCCCC
171616	3812	TCTAAGTTTTCTAACAATTT	216203	48399	GCCAGAGATAAGCACAGCGC	260790	92986	CATTTCCCCAGACATTTCCC
171617	3813	TTCTAAGTTTTCTAACAATT	216204	48400	GGCCAGAGATAAGCACAGCG	260791	92987	GCATTTCCCCAGACATTTCC
171618	3814	ATTCTAAGTTTTCTAACAAT	216205	48401	GGGCCAGAGATAAGCACAGC	260792	92988	AGCATTTCCCCAGACATTTC

171619	3815	GATTCTAAGTTTTCTAACAA	216206	48402	GGGGCCAGAGATAAGCACAG	260793	92989	GAGCATTTCCCCAGACATTT
171620	3816	CGATTCTAAGTTTTCTAACA	216207	48403	TGGGGCCAGAGATAAGCACA	260794	92990	GGAGCATTTCCCCAGACATT
171621	3817	GCGATTCTAAGTTTTCTAAC	216208	48404	TTGGGGCCAGAGATAAGCAC	260795	92991	GGGAGCATTTCCCCAGACAT
171622	3818	AGCGATTCTAAGTTTTCTAA	216209	48405	ATTGGGGCCAGAGATAAGCA	260796	92992	CGGGAGCATTTCCCCAGACA
171623	3819	AAGCGATTCTAAGTTTTCTA	216210	48406	CATTGGGGCCAGAGATAAGC	260797	92993	ACGGGAGCATTTCCCCAGAC
171624	3820	AAAGCGATTCTAAGTTTTCT	216211	48407	GCATTGGGGCCAGAGATAAG	260798	92994	TACGGGAGCATTTCCCCAGA
171625	3821	CAAAGCGATTCTAAGTTTTC	216212	48408	GGCATTGGGGCCAGAGATAA	260799	92995	TTACGGGAGCATTTCCCCAG
171626	3822	TCAAAGCGATTCTAAGTTTT	216213	48409	CGGCATTGGGGCCAGAGATA	260800	92996	ATTACGGGAGCATTTCCCCA
171627	3823	ATCAAAGCGATTCTAAGTTT	216214	48410	GCGGCATTGGGGCCAGAGAT	260801	92997	AATTACGGGAGCATTTCCCC
171628	3824	AATCAAAGCGATTCTAAGTT	216215	48411	GGCGGCATTGGGGCCAGAGA	260802	92998	CAATTACGGGAGCATTTCCC
171629	3825	CAATCAAAGCGATTCTAAGT	216216	48412	TGGCGGCATTGGGGCCAGAG	260803	92999	GCAATTACGGGAGCATTTCC
171630	3826	TCAATCAAAGCGATTCTAAG	216217	48413	ATGGCGGCATTGGGGCCAGA	260804	93000	TGCAATTACGGGAGCATTTC
171631	3827	CTCAATCAAAGCGATTCTAA	216218	48414	CATGGCGGCATTGGGGCCAG	260805	93001	GTGCAATTACGGGAGCATTT
171632	3828	CCTCAATCAAAGCGATTCTA	216219	48415	GCATGGCGGCATTGGGGCCA	260806	93002	TGTGCAATTACGGGAGCATT
171633	3829	TCCTCAATCAAAGCGATTCT	216220	48416	TGCATGGCGGCATTGGGGCC	260807	93003	CTGTGCAATTACGGGAGCAT
171634	3830	TTCCTCAATCAAAGCGATTC	216221	48417	CTGCATGGCGGCATTGGGGC	260808	93004	ACTGTGCAATTACGGGAGCA
171635	3831	TTTCCTCAATCAAAGCGATT	216222	48418	TCTGCATGGCGGCATTGGGG	260809	93005	CACTGTGCAATTACGGGAGC
171636	3832	CTTTCCTCAATCAAAGCGAT	216223	48419	TTCTGCATGGCGGCATTGGG	260810	93006	CCACTGTGCAATTACGGGAG
171637	3833	CCTTTCCTCAATCAAAGCGA	216224	48420	CTTCTGCATGGCGGCATTGG	260811	93007	GCCACTGTGCAATTACGGGA
171638	3834	ACCTTTCCTCAATCAAAGCG	216225	48421	ACTTCTGCATGGCGGCATTG	260812	93008	CGCCACTGTGCAATTACGGG
171639	3835	AACCTTTCCTCAATCAAAGC	216226	48422	CACTTCTGCATGGCGGCATT	260813	93009	ACGCCACTGTGCAATTACGG
171640	3836	TAACCTTTCCTCAATCAAAG	216227	48423	ACACTTCTGCATGGCGGCAT	260814	93010	AACGCCACTGTGCAATTACG
171641	3837	CTAACCTTTCCTCAATCAAA	216228	48424	GACACTTCTGCATGGCGGCA	260815	93011	AAACGCCACTGTGCAATTAC
171642	3838	TCTAACCTTTCCTCAATCAA	216229	48425	AGACACTTCTGCATGGCGGC	260816	93012	AAAACGCCACTGTGCAATTA
171643	3839	ATCTAACCTTTCCTCAATCA	216230	48426	CAGACACTTCTGCATGGCGG	260817	93013	AAAAACGCCACTGTGCAATT
171644	3840	AATCTAACCTTTCCTCAATC	216231	48427	CCAGACACTTCTGCATGGCG	260818	93014	GAAAAACGCCACTGTGCAAT
171645	3841	AAATCTAACCTTTCCTCAAT	216232	48428	CCCAGACACTTCTGCATGGC	260819	93015	GGAAAAACGCCACTGTGCAA
171646	3842	TAAATCTAACCTTTCCTCAA	216233	48429	CCCCAGACACTTCTGCATGG	260820	93016	AGGAAAAACGCCACTGTGCA
171647	3843	ATAAATCTAACCTTTCCTCA	216234	48430	CCCCCAGACACTTCTGCATG	260821	93017	CAGGAAAAACGCCACTGTGC
171648	3844	AATAAATCTAACCTTTCCTC	216235	48431	GCCCCCAGACACTTCTGCAT	260822	93018	CCAGGAAAAACGCCACTGTG
171649	3845	GAATAAATCTAACCTTTCCT	216236	48432	TGCCCCCAGACACTTCTGCA	260823	93019	TCCAGGAAAAACGCCACTGT
171650	3846	GGAATAAATCTAACCTTTCC	216237	48433	GTGCCCCCAGACACTTCTGC	260824	93020	TTCCAGGAAAAACGCCACTG
171651	3847	CGGAATAAATCTAACCTTTC	216238	48434	AGTGCCCCCAGACACTTCTG	260825	93021	TTTCCAGGAAAAACGCCACT
171652	3848	CCGGAATAAATCTAACCTTT	216239	48435	AAGTGCCCCCAGACACTTCT	260826	93022	TTTTCCAGGAAAAACGCCAC
171653	3849	ACCGGAATAAATCTAACCTT	216240	48436	AAAGTGCCCCCAGACACTTC	260827	93023	ATTTTCCAGGAAAAACGCCA
171654	3850	AACCGGAATAAATCTAACCT	216241	48437	CAAAGTGCCCCCAGACACTT	260828	93024	GATTTTCCAGGAAAAACGCC
171655	3851	CAACCGGAATAAATCTAACC	216242	48438	ACAAAGTGCCCCCAGACACT	260829	93025	GGATTTTCCAGGAAAAACGC
171656	3852	CCAACCGGAATAAATCTAAC	216243	48439	GACAAAGTGCCCCCAGACAC	260830	93026	GGGATTTTCCAGGAAAAACG
171657	3853	TCCAACCGGAATAAATCTAA	216244	48440	AGACAAAGTGCCCCCAGACA	260831	93027	TGGGATTTTCCAGGAAAAAC
171658	3854	TTCCAACCGGAATAAATCTA	216245	48441	GAGACAAAGTGCCCCCAGAC	260832	93028	GTGGGATTTTCCAGGAAAAA
171659	3855	TTTCCAACCGGAATAAATCT	216246	48442	AGAGACAAAGTGCCCCCAGA	260833	93029	GGTGGGATTTTCCAGGAAAA
171660	3856	TTTTCCAACCGGAATAAATC	216247	48443	CAGAGACAAAGTGCCCCCAG	260834	93030	TGGTGGGATTTTCCAGGAAA
171661	3857	TTTTTCCAACCGGAATAAAT	216248	48444	ACAGAGACAAAGTGCCCCCA	260835	93031	ATGGTGGGATTTTCCAGGAA
171662	3858	CTTTTTCCAACCGGAATAAA	216249	48445	GACAGAGACAAAGTGCCCCC	260836	93032	CATGGTGGGATTTTCCAGGA
171663	3859	ACTTTTTCCAACCGGAATAA	216250	48446	TGACAGAGACAAAGTGCCCC	260837	93033	CCATGGTGGGATTTTCCAGG
171664	3860	CACTTTTTCCAACCGGAATA	216251	48447	CTGACAGAGACAAAGTGCCC	260838	93034	GCCATGGTGGGATTTTCCAG
171665	3861	CCACTTTTTCCAACCGGAAT	216252	48448	TCTGACAGAGACAAAGTGCC	260839	93035	AGCCATGGTGGGATTTTCCA
171666	3862	GCCACTTTTTCCAACCGGAA	216253	48449	GTCTGACAGAGACAAAGTGC	260840	93036	GAGCCATGGTGGGATTTTCC
171667	3863	GGCCACTTTTTCCAACCGGA	216254	48450	TGTCTGACAGAGACAAAGTG	260841	93037	AGAGCCATGGTGGGATTTTC
171668	3864	AGGCCACTTTTTCCAACCGG	216255	48451	CTGTCTGACAGAGACAAAGT	260842	93038	TAGAGCCATGGTGGGATTTT
171669	3865	AAGGCCACTTTTTCCAACCG	216256	48452	TCTGTCTGACAGAGACAAAG	260843	93039	CTAGAGCCATGGTGGGATTT
171670	3866	AAAGGCCACTTTTTCCAACC	216257	48453	TTCTGTCTGACAGAGACAAA	260844	93040	TCTAGAGCCATGGTGGGATT
171671	3867	GAAAGGCCACTTTTTCCAAC	216258	48454	ATTCTGTCTGACAGAGACAA	260845	93041	ATCTAGAGCCATGGTGGGAT
171672	3868	AGAAAGGCCACTTTTTCCAA	216259	48455	AATTCTGTCTGACAGAGACA	260846	93042	TATCTAGAGCCATGGTGGGA
171673	3869	TAGAAAGGCCACTTTTTCCA	216260	48456	GAATTCTGTCTGACAGAGAC	260847	93043	TTATCTAGAGCCATGGTGGG
171674	3870	ATAGAAAGGCCACTTTTTCC	216261	48457	CGAATTCTGTCTGACAGAGA	260848	93044	CTTATCTAGAGCCATGGTGG
171675	3871	AATAGAAAGGCCACTTTTTC	216262	48458	CCGAATTCTGTCTGACAGAG	260849	93045	TCTTATCTAGAGCCATGGTG
171676	3872	TAATAGAAAGGCCACTTTTT	216263	48459	TCCGAATTCTGTCTGACAGA	260850	93046	GTCTTATCTAGAGCCATGGT
171677	3873	TTAATAGAAAGGCCACTTTT	216264	48460	CTCCGAATTCTGTCTGACAG	260851	93047	GGTCTTATCTAGAGCCATGG
171678	3874	TTTAATAGAAAGGCCACTTT	216265	48461	TCTCCGAATTCTGTCTGACA	260852	93048	AGGTCTTATCTAGAGCCATG
171679	3875	GTTTAATAGAAAGGCCACTT	216266	48462	ATCTCCGAATTCTGTCTGAC	260853	93049	TAGGTCTTATCTAGAGCCAT
171680	3876	CGTTTAATAGAAAGGCCACT	216267	48463	CATCTCCGAATTCTGTCTGA	260854	93050	ATAGGTCTTATCTAGAGCCA
171681	3877	ACGTTTAATAGAAAGGCCAC	216268	48464	ACATCTCCGAATTCTGTCTG	260855	93051	AATAGGTCTTATCTAGAGCC
171682	3878	CACGTTTAATAGAAAGGCCA	216269	48465	CACATCTCCGAATTCTGTCT	260856	93052	AAATAGGTCTTATCTAGAGC
171683	3879	GCACGTTTAATAGAAAGGCC	216270	48466	ACACATCTCCGAATTCTGTC	260857	93053	AAAATAGGTCTTATCTAGAG
171684	3880	GGCACGTTTAATAGAAAGGC	216271	48467	TACACATCTCCGAATTCTGT	260858	93054	AAAAATAGGTCTTATCTAGA
171685	3881	GGGCACGTTTAATAGAAAGG	216272	48468	ATACACATCTCCGAATTCTG	260859	93055	GAAAAATAGGTCTTATCTAG
171686	3882	AGGGCACGTTTAATAGAAAG	216273	48469	CATACACATCTCCGAATTCT	260860	93056	AGAAAAATAGGTCTTATCTA
171687	3883	AAGGGCACGTTTAATAGAAA	216274	48470	GCATACACATCTCCGAATTC	260861	93057	AAGAAAAATAGGTCTTATCT
171688	3884	AAAGGGCACGTTTAATAGAA	216275	48471	AGCATACACATCTCCGAATT	260862	93058	TAAGAAAAATAGGTCTTATC
171689	3885	CAAAGGGCACGTTTAATAGA	216276	48472	AAGCATACACATCTCCGAAT	260863	93059	TTAAGAAAAATAGGTCTTAT
171690	3886	TCAAAGGGCACGTTTAATAG	216277	48473	CAAGCATACACATCTCCGAA	260864	93060	TTTAAGAAAAATAGGTCTTA

171691	3887	GTCAAAGGGCACGTTTAATA	216278	48474	GCAAGCATACACATCTCCGA	260865	93061	CTTTAAGAAAAATAGGTCTT
171692	3888	GGTCAAAGGGCACGTTTAAT	216279	48475	GGCAAGCATACACATCTCCG	260866	93062	CCTTTAAGAAAAATAGGTCT
171693	3889	GGGTCAAAGGGCACGTTTAA	216280	48476	GGGCAAGCATACACATCTCC	260867	93063	ACCTTTAAGAAAAATAGGTC
171694	3890	AGGGTCAAAGGGCACGTTTA	216281	48477	AGGGCAAGCATACACATCTC	260868	93064	TACCTTTAAGAAAAATAGGT
171695	3891	GAGGGTCAAAGGGCACGTTT	216282	48478	CAGGGCAAGCATACACATCT	260869	93065	ATACCTTTAAGAAAAATAGG
171696	3892	TGAGGGTCAAAGGGCACGTT	216283	48479	CCAGGGCAAGCATACACATC	260870	93066	GATACCTTTAAGAAAAATAG
171697	3893	ATGAGGGTCAAAGGGCACGT	216284	48480	ACCAGGGCAAGCATACACAT	260871	93067	AGATACCTTTAAGAAAAATA
171698	3894	CATGAGGGTCAAAGGGCACG	216285	48481	TACCAGGGCAAGCATACACA	260872	93068	TAGATACCTTTAAGAAAAAT
171699	3895	GCATGAGGGTCAAAGGGCAC	216286	48482	ATACCAGGGCAAGCATACAC	260873	93069	TTAGATACCTTTAAGAAAAA
171700	3896	GGCATGAGGGTCAAAGGGCA	216287	48483	CATACCAGGGCAAGCATACA	260874	93070	TTTAGATACCTTTAAGAAAA
171701	3897	GGGCATGAGGGTCAAAGGGC	216288	48484	CCATACCAGGGCAAGCATAC	260875	93071	TTTTAGATACCTTTAAGAAA
171702	3898	AGGGCATGAGGGTCAAAGGG	216289	48485	GCCATACCAGGGCAAGCATA	260876	93072	ATTTTAGATACCTTTAAGAA
171703	3899	AAGGGCATGAGGGTCAAAGG	216290	48486	TGCCATACCAGGGCAAGCAT	260877	93073	AATTTTAGATACCTTTAAGA
171704	3900	CAAGGGCATGAGGGTCAAAG	216291	48487	GTGCCATACCAGGGCAAGCA	260878	93074	AAATTTTAGATACCTTTAAG
171705	3901	CCAAGGGCATGAGGGTCAAA	216292	48488	AGTGCCATACCAGGGCAAGC	260879	93075	GAAATTTTAGATACCTTTAA
171706	3902	TCCAAGGGCATGAGGGTCAA	216293	48489	AAGTGCCATACCAGGGCAAG	260880	93076	GGAAATTTTAGATACCTTTA
171707	3903	CTCCAAGGGCATGAGGGTCA	216294	48490	GAAGTGCCATACCAGGGCAA	260881	93077	TGGAAATTTTAGATACCTTT
171708	3904	CCTCCAAGGGCATGAGGGTC	216295	48491	AGAAGTGCCATACCAGGGCA	260882	93078	CTGGAAATTTTAGATACCTT
171709	3905	ACCTCCAAGGGCATGAGGGT	216296	48492	GAGAAGTGCCATACCAGGGC	260883	93079	GCTGGAAATTTTAGATACCT
171710	3906	GACCTCCAAGGGCATGAGGG	216297	48493	AGAGAAGTGCCATACCAGGG	260884	93080	TGCTGGAAATTTTAGATACC
171711	3907	CGACCTCCAAGGGCATGAGG	216298	48494	AAGAGAAGTGCCATACCAGG	260885	93081	ATGCTGGAAATTTTAGATAC
171712	3908	CCGACCTCCAAGGGCATGAG	216299	48495	AAAGAGAAGTGCCATACCAG	260886	93082	TATGCTGGAAATTTTAGATA
171713	3909	ACCGACCTCCAAGGGCATGA	216300	48496	AAAAGAGAAGTGCCATACCA	260887	93083	TTATGCTGGAAATTTTAGAT
171714	3910	CACCGACCTCCAAGGGCATG	216301	48497	AAAAAGAGAAGTGCCATACC	260888	93084	TTTATGCTGGAAATTTTAGA
171715	3911	GCACCGACCTCCAAGGGCAT	216302	48498	AAAAAAGAGAAGTGCCATAC	260889	93085	ATTTATGCTGGAAATTTTAG
171716	3912	GGCACCGACCTCCAAGGGCA	216303	48499	AAAAAAAGAGAAGTGCCATA	260890	93086	AATTTATGCTGGAAATTTTA
171717	3913	TGGCACCGACCTCCAAGGGC	216304	48500	CAAAAAAAGAGAAGTGCCAT	260891	93087	GAATTTATGCTGGAAATTTT
171718	3914	CTGGCACCGACCTCCAAGGG	216305	48501	TCAAAAAAAGAGAAGTGCCA	260892	93088	AGAATTTATGCTGGAAATTT
171719	3915	GCTGGCACCGACCTCCAAGG	216306	48502	CTCAAAAAAAGAGAAGTGCC	260893	93089	CAGAATTTATGCTGGAAATT
171720	3916	GGCTGGCACCGACCTCCAAG	216307	48503	TCTCAAAAAAAGAGAAGTGC	260894	93090	ACAGAATTTATGCTGGAAAT
171721	3917	AGGCTGGCACCGACCTCCAA	216308	48504	GTCTCAAAAAAAGAGAAGTG	260895	93091	GACAGAATTTATGCTGGAAA
171722	3918	CAGGCTGGCACCGACCTCCA	216309	48505	TGTCTCAAAAAAAGAGAAGT	260896	93092	AGACAGAATTTATGCTGGAA
171723	3919	CCAGGCTGGCACCGACCTCC	216310	48506	CTGTCTCAAAAAAAGAGAAG	260897	93093	CAGACAGAATTTATGCTGGA
171724	3920	TCCAGGCTGGCACCGACCTC	216311	48507	TCTGTCTCAAAAAAAGAGAA	260898	93094	TCAGACAGAATTTATGCTGG
171725	3921	CTCCAGGCTGGCACCGACCT	216312	48508	TTCTGTCTCAAAAAAAGAGA	260899	93095	TTCAGACAGAATTTATGCTG
171726	3922	TCTCCAGGCTGGCACCGACC	216313	48509	ATTCTGTCTCAAAAAAAGAG	260900	93096	TTTCAGACAGAATTTATGCT
171727	3923	ATCTCCAGGCTGGCACCGAC	216314	48510	GATTCTGTCTCAAAAAAAGA	260901	93097	GTTTCAGACAGAATTTATGC
171728	3924	CATCTCCAGGCTGGCACCGA	216315	48511	AGATTCTGTCTCAAAAAAAG	260902	93098	TGTTTCAGACAGAATTTATG
171729	3925	CCATCTCCAGGCTGGCACCG	216316	48512	GAGATTCTGTCTCAAAAAAA	260903	93099	GTGTTTCAGACAGAATTTAT
171730	3926	CCCATCTCCAGGCTGGCACC	216317	48513	TGAGATTCTGTCTCAAAAAA	260904	93100	GGTGTTTCAGACAGAATTTA
171731	3927	TCCCATCTCCAGGCTGGCAC	216318	48514	GTGAGATTCTGTCTCAAAAA	260905	93101	AGGTGTTTCAGACAGAATTT
171732	3928	ATCCCATCTCCAGGCTGGCA	216319	48515	AGTGAGATTCTGTCTCAAAA	260906	93102	CAGGTGTTTCAGACAGAATT
171733	3929	TATCCCATCTCCAGGCTGGC	216320	48516	GAGTGAGATTCTGTCTCAAA	260907	93103	TCAGGTGTTTCAGACAGAAT
171734	3930	TTATCCCATCTCCAGGCTGG	216321	48517	AGAGTGAGATTCTGTCTCAA	260908	93104	TTCAGGTGTTTCAGACAGAA
171735	3931	CTTATCCCATCTCCAGGCTG	216322	48518	CAGAGTGAGATTCTGTCTCA	260909	93105	ATTCAGGTGTTTCAGACAGA
171736	3932	TCTTATCCCATCTCCAGGCT	216323	48519	ACAGAGTGAGATTCTGTCTC	260910	93106	AATTCAGGTGTTTCAGACAG
171737	3933	ATCTTATCCCATCTCCAGGC	216324	48520	GACAGAGTGAGATTCTGTCT	260911	93107	AAATTCAGGTGTTTCAGACA
171738	3934	AATCTTATCCCATCTCCAGG	216325	48521	TGACAGAGTGAGATTCTGTC	260912	93108	AAAATTCAGGTGTTTCAGAC
171739	3935	CAATCTTATCCCATCTCCAG	216326	48522	GTGACAGAGTGAGATTCTGT	260913	93109	TAAAATTCAGGTGTTTCAGA
171740	3936	ACAATCTTATCCCATCTCCA	216327	48523	GGTGACAGAGTGAGATTCTG	260914	93110	TTAAAATTCAGGTGTTTCAG
171741	3937	CACAATCTTATCCCATCTCC	216328	48524	GGGTGACAGAGTGAGATTCT	260915	93111	ATTAAAATTCAGGTGTTTCA
171742	3938	CCACAATCTTATCCCATCTC	216329	48525	AGGGTGACAGAGTGAGATTC	260916	93112	GATTAAAATTCAGGTGTTTC
171743	3939	ACCACAATCTTATCCCATCT	216330	48526	CAGGGTGACAGAGTGAGATT	260917	93113	TGATTAAAATTCAGGTGTTT
171744	3940	AACCACAATCTTATCCCATC	216331	48527	CCAGGGTGACAGAGTGAGAT	260918	93114	CTGATTAAAATTCAGGTGTT
171745	3941	AAACCACAATCTTATCCCAT	216332	48528	GCCAGGGTGACAGAGTGAGA	260919	93115	ACTGATTAAAATTCAGGTGT
171746	3942	AAAACCACAATCTTATCCCA	216333	48529	AGCCAGGGTGACAGAGTGAG	260920	93116	TACTGATTAAAATTCAGGTG
171747	3943	GAAAACCACAATCTTATCCC	216334	48530	CAGCCAGGGTGACAGAGTGA	260921	93117	GTACTGATTAAAATTCAGGT
171748	3944	GGAAAACCACAATCTTATCC	216335	48531	CCAGCCAGGGTGACAGAGTG	260922	93118	AGTACTGATTAAAATTCAGG
171749	3945	AGGAAAACCACAATCTTATC	216336	48532	TCCAGCCAGGGTGACAGAGT	260923	93119	CAGTACTGATTAAAATTCAG
171750	3946	AAGGAAAACCACAATCTTAT	216337	48533	CTCCAGCCAGGGTGACAGAG	260924	93120	CCAGTACTGATTAAAATTCA
171751	3947	GAAGGAAAACCACAATCTTA	216338	48534	ACTCCAGCCAGGGTGACAGA	260925	93121	TCCAGTACTGATTAAAATTC
171752	3948	AGAAGGAAAACCACAATCTT	216339	48535	CACTCCAGCCAGGGTGACAG	260926	93122	CTCCAGTACTGATTAAAATT
171753	3949	CAGAAGGAAAACCACAATCT	216340	48536	GCACTCCAGCCAGGGTGACA	260927	93123	GCTCCAGTACTGATTAAAAT
171754	3950	GCAGAAGGAAAACCACAATC	216341	48537	TGCACTCCAGCCAGGGTGAC	260928	93124	GGCTCCAGTACTGATTAAAA
171755	3951	GGCAGAAGGAAAACCACAAT	216342	48538	CTGCACTCCAGCCAGGGTGA	260929	93125	GGGCTCCAGTACTGATTAAA
171756	3952	AGGCAGAAGGAAAACCACAA	216343	48539	ACTGCACTCCAGCCAGGGTG	260930	93126	CGGGCTCCAGTACTGATTAA
171757	3953	AAGGCAGAAGGAAAACCACA	216344	48540	CACTGCACTCCAGCCAGGGT	260931	93127	CCGGGCTCCAGTACTGATTA
171758	3954	AAAGGCAGAAGGAAAACCAC	216345	48541	CCACTGCACTCCAGCCAGGG	260932	93128	TCCGGGCTCCAGTACTGATT
171759	3955	AAAAGGCAGAAGGAAAACCA	216346	48542	GCCACTGCACTCCAGCCAGG	260933	93129	CTCCGGGCTCCAGTACTGAT
171760	3956	AAAAAGGCAGAAGGAAAACC	216347	48543	TGCCACTGCACTCCAGCCAG	260934	93130	CCTCCGGGCTCCAGTACTGA
171761	3957	TAAAAAGGCAGAAGGAAAAC	216348	48544	ATGCCACTGCACTCCAGCCA	260935	93131	CCCTCCGGGCTCCAGTACTG
171762	3958	TTAAAAAGGCAGAAGGAAAA	216349	48545	CATGCCACTGCACTCCAGCC	260936	93132	GCCCTCCGGGCTCCAGTACT

171763	3959	GTTAAAAAGGCAGAAGGAAA	216350	48546	TCATGCCACTGCACTCCAGC	260937	93133	TGCCCTCCGGGCTCCAGTAC
171764	3960	TGTTAAAAAGGCAGAAGGAA	216351	48547	ATCATGCCACTGCACTCCAG	260938	93134	ATGCCCTCCGGGCTCCAGTA
171765	3961	ATGTTAAAAAGGCAGAAGGA	216352	48548	GATCATGCCACTGCACTCCA	260939	93135	GATGCCCTCCGGGCTCCAGT
171766	3962	GATGTTAAAAAGGCAGAAGG	216353	48549	AGATCATGCCACTGCACTCC	260940	93136	AGATGCCCTCCGGGCTCCAG
171767	3963	AGATGTTAAAAAGGCAGAAG	216354	48550	GAGATCATGCCACTGCACTC	260941	93137	GAGATGCCCTCCGGGCTCCA
171768	3964	CAGATGTTAAAAAGGCAGAA	216355	48551	TGAGATCATGCCACTGCACT	260942	93138	GGAGATGCCCTCCGGGCTCC
171769	3965	ACAGATGTTAAAAAGGCAGA	216356	48552	CTGAGATCATGCCACTGCAC	260943	93139	TGGAGATGCCCTCCGGGCTC
171770	3966	AACAGATGTTAAAAAGGCAG	216357	48553	GCTGAGATCATGCCACTGCA	260944	93140	CTGGAGATGCCCTCCGGGCT
171771	3967	CAACAGATGTTAAAAAGGCA	216358	48554	AGCTGAGATCATGCCACTGC	260945	93141	ACTGGAGATGCCCTCCGGGC
171772	3968	ACAACAGATGTTAAAAAGGC	216359	48555	GAGCTGAGATCATGCCACTG	260946	93142	AACTGGAGATGCCCTCCGGG
171773	3969	AACAACAGATGTTAAAAAGG	216360	48556	TGAGCTGAGATCATGCCACT	260947	93143	CAACTGGAGATGCCCTCCGG
171774	3970	TAACAACAGATGTTAAAAAG	216361	48557	GTGAGCTGAGATCATGCCAC	260948	93144	GCAACTGGAGATGCCCTCCG
171775	3971	GTAACAACAGATGTTAAAAA	216362	48558	AGTGAGCTGAGATCATGCCA	260949	93145	GGCAACTGGAGATGCCCTCC
171776	3972	TGTAACAACAGATGTTAAAA	216363	48559	CAGTGAGCTGAGATCATGCC	260950	93146	TGGCAACTGGAGATGCCCTC
171777	3973	CTGTAACAACAGATGTTAAA	216364	48560	GCAGTGAGCTGAGATCATGC	260951	93147	GTGGCAACTGGAGATGCCCT
171778	3974	ACTGTAACAACAGATGTTAA	216365	48561	TGCAGTGAGCTGAGATCATG	260952	93148	TGTGGCAACTGGAGATGCCC
171779	3975	GACTGTAACAACAGATGTTA	216366	48562	TTGCAGTGAGCTGAGATCAT	260953	93149	ATGTGGCAACTGGAGATGCC
171780	3976	GGACTGTAACAACAGATGTT	216367	48563	GTTGCAGTGAGCTGAGATCA	260954	93150	TATGTGGCAACTGGAGATGC
171781	3977	TGGACTGTAACAACAGATGT	216368	48564	GGTTGCAGTGAGCTGAGATC	260955	93151	CTATGTGGCAACTGGAGATG
171782	3978	ATGGACTGTAACAACAGATG	216369	48565	AGGTTGCAGTGAGCTGAGAT	260956	93152	GCTATGTGGCAACTGGAGAT
171783	3979	AATGGACTGTAACAACAGAT	216370	48566	GAGGTTGCAGTGAGCTGAGA	260957	93153	AGCTATGTGGCAACTGGAGA
171784	3980	AAATGGACTGTAACAACAGA	216371	48567	GGAGGTTGCAGTGAGCTGAG	260958	93154	GAGCTATGTGGCAACTGGAG
171785	3981	CAAATGGACTGTAACAACAG	216372	48568	CGGAGGTTGCAGTGAGCTGA	260959	93155	AGAGCTATGTGGCAACTGGA
171786	3982	ACAAATGGACTGTAACAACA	216373	48569	GCGGAGGTTGCAGTGAGCTG	260960	93156	CAGAGCTATGTGGCAACTGG
171787	3983	AACAAATGGACTGTAACAAC	216374	48570	GGCGGAGGTTGCAGTGAGCT	260961	93157	TCAGAGCTATGTGGCAACTG
171788	3984	CAACAAATGGACTGTAACAA	216375	48571	AGGCGGAGGTTGCAGTGAGC	260962	93158	CTCAGAGCTATGTGGCAACT
171789	3985	TCAACAAATGGACTGTAACA	216376	48572	GAGGCGGAGGTTGCAGTGAG	260963	93159	GCTCAGAGCTATGTGGCAAC
171790	3986	TTCAACAAATGGACTGTAAC	216377	48573	GGAGGCGGAGGTTGCAGTGA	260964	93160	TGCTCAGAGCTATGTGGCAA
171791	3987	TTTCAACAAATGGACTGTAA	216378	48574	GGGAGGCGGAGGTTGCAGTG	260965	93161	ATGCTCAGAGCTATGTGGCA
171792	3988	TTTTCAACAAATGGACTGTA	216379	48575	TGGGAGGCGGAGGTTGCAGT	260966	93162	AATGCTCAGAGCTATGTGGC
171793	3989	ATTTTCAACAAATGGACTGT	216380	48576	CTGGGAGGCGGAGGTTGCAG	260967	93163	GAATGCTCAGAGCTATGTGG
171794	3990	AATTTTCAACAAATGGACTG	216381	48577	CCTGGGAGGCGGAGGTTGCA	260968	93164	TGAATGCTCAGAGCTATGTG
171795	3991	AAATTTTCAACAAATGGACT	216382	48578	ACCTGGGAGGCGGAGGTTGC	260969	93165	CTGAATGCTCAGAGCTATGT
171796	3992	TAAATTTTCAACAAATGGAC	216383	48579	AACCTGGGAGGCGGAGGTTG	260970	93166	ACTGAATGCTCAGAGCTATG
171797	3993	TTAAATTTTCAACAAATGGA	216384	48580	GAACCTGGGAGGCGGAGGTT	260971	93167	CACTGAATGCTCAGAGCTAT
171798	3994	TTTAAATTTTCAACAAATGG	216385	48581	TGAACCTGGGAGGCGGAGGT	260972	93168	CCACTGAATGCTCAGAGCTA
171799	3995	CTTTAAATTTTCAACAAATG	216386	48582	TTGAACCTGGGAGGCGGAGG	260973	93169	ACCACTGAATGCTCAGAGCT
171800	3996	TCTTTAAATTTTCAACAAAT	216387	48583	CTTGAACCTGGGAGGCGGAG	260974	93170	CACCACTGAATGCTCAGAGC
171801	3997	TTCTTTAAATTTTCAACAAA	216388	48584	GCTTGAACCTGGGAGGCGGA	260975	93171	ACACCACTGAATGCTCAGAG
171802	3998	TTTCTTTAAATTTTCAACAA	216389	48585	TGCTTGAACCTGGGAGGCGG	260976	93172	CACACCACTGAATGCTCAGA
171803	3999	GTTTCTTTAAATTTTCAACA	216390	48586	TTGCTTGAACCTGGGAGGCG	260977	93173	ACACACCACTGAATGCTCAG
171804	4000	AGTTTCTTTAAATTTTCAAC	216391	48587	ATTGCTTGAACCTGGGAGGC	260978	93174	AACACACCACTGAATGCTCA
171805	4001	CAGTTTCTTTAAATTTTCAA	216392	48588	AATTGCTTGAACCTGGGAGG	260979	93175	CAACACACCACTGAATGCTC
171806	4002	ACAGTTTCTTTAAATTTTCA	216393	48589	GAATTGCTTGAACCTGGGAG	260980	93176	TCAACACACCACTGAATGCT
171807	4003	AACAGTTTCTTTAAATTTTC	216394	48590	AGAATTGCTTGAACCTGGGA	260981	93177	CTCAACACACCACTGAATGC
171808	4004	AAACAGTTTCTTTAAATTTT	216395	48591	AAGAATTGCTTGAACCTGGG	260982	93178	CCTCAACACACCACTGAATG
171809	4005	AAAACAGTTTCTTTAAATTT	216396	48592	CAAGAATTGCTTGAACCTGG	260983	93179	CCCTCAACACACCACTGAAT
171810	4006	TAAAACAGTTTCTTTAAATT	216397	48593	ACAAGAATTGCTTGAACCTG	260984	93180	GCCCTCAACACACCACTGAA
171811	4007	ATAAAACAGTTTCTTTAAAT	216398	48594	CACAAGAATTGCTTGAACCT	260985	93181	AGCCCTCAACACACCACTGA
171812	4008	AATAAAACAGTTTCTTTAAA	216399	48595	GCACAAGAATTGCTTGAACC	260986	93182	CAGCCCTCAACACACCACTG
171813	4009	GAATAAAACAGTTTCTTTAA	216400	48596	GGCACAAGAATTGCTTGAAC	260987	93183	GCAGCCCTCAACACACCACT
171814	4010	GGAATAAAACAGTTTCTTTA	216401	48597	AGGCACAAGAATTGCTTGAA	260988	93184	AGCAGCCCTCAACACACCAC
171815	4011	TGGAATAAAACAGTTTCTTT	216402	48598	GAGGCACAAGAATTGCTTGA	260989	93185	GAGCAGCCCTCAACACACCA
171816	4012	GTGGAATAAAACAGTTTCTT	216403	48599	TGAGGCACAAGAATTGCTTG	260990	93186	GGAGCAGCCCTCAACACACC
171817	4013	AGTGGAATAAAACAGTTTCT	216404	48600	CTGAGGCACAAGAATTGCTT	260991	93187	GGGAGCAGCCCTCAACACAC
171818	4014	AAGTGGAATAAAACAGTTTC	216405	48601	GCTGAGGCACAAGAATTGCT	260992	93188	CGGGAGCAGCCCTCAACACA
171819	4015	AAAGTGGAATAAAACAGTTT	216406	48602	GGCTGAGGCACAAGAATTGC	260993	93189	CCGGGAGCAGCCCTCAACAC
171820	4016	GAAAGTGGAATAAAACAGTT	216407	48603	AGGCTGAGGCACAAGAATTG	260994	93190	TCCGGGAGCAGCCCTCAACA
171821	4017	GGAAAGTGGAATAAAACAGT	216408	48604	GAGGCTGAGGCACAAGAATT	260995	93191	TTCCGGGAGCAGCCCTCAAC
171822	4018	GGGAAAGTGGAATAAAACAG	216409	48605	GGAGGCTGAGGCACAAGAAT	260996	93192	CTTCCGGGAGCAGCCCTCAA
171823	4019	AGGGAAAGTGGAATAAAACA	216410	48606	GGGAGGCTGAGGCACAAGAA	260997	93193	ACTTCCGGGAGCAGCCCTCA
171824	4020	GAGGGAAAGTGGAATAAAAC	216411	48607	TGGGAGGCTGAGGCACAAGA	260998	93194	CACTTCCGGGAGCAGCCCTC
171825	4021	TGAGGGAAAGTGGAATAAAA	216412	48608	TTGGGAGGCTGAGGCACAAG	260999	93195	GCACTTCCGGGAGCAGCCCT
171826	4022	CTGAGGGAAAGTGGAATAAA	216413	48609	CTTGGGAGGCTGAGGCACAA	261000	93196	GGCACTTCCGGGAGCAGCCC
171827	4023	GCTGAGGGAAAGTGGAATAA	216414	48610	ACTTGGGAGGCTGAGGCACA	261001	93197	AGGCACTTCCGGGAGCAGCC
171828	4024	TGCTGAGGGAAAGTGGAATA	216415	48611	TACTTGGGAGGCTGAGGCAC	261002	93198	CAGGCACTTCCGGGAGCAGC
171829	4025	ATGCTGAGGGAAAGTGGAAT	216416	48612	CTACTTGGGAGGCTGAGGCA	261003	93199	GCAGGCACTTCCGGGAGCAG
171830	4026	AATGCTGAGGGAAAGTGGAA	216417	48613	GCTACTTGGGAGGCTGAGGC	261004	93200	TGCAGGCACTTCCGGGAGCA
171831	4027	AAATGCTGAGGGAAAGTGGA	216418	48614	AGCTACTTGGGAGGCTGAGG	261005	93201	CTGCAGGCACTTCCGGGAGC
171832	4028	TAAATGCTGAGGGAAAGTGG	216419	48615	CAGCTACTTGGGAGGCTGAG	261006	93202	TCTGCAGGCACTTCCGGGAG
171833	4029	ATAAATGCTGAGGGAAAGTG	216420	48616	CCAGCTACTTGGGAGGCTGA	261007	93203	CTCTGCAGGCACTTCCGGGA
171834	4030	CATAAATGCTGAGGGAAAGT	216421	48617	CCCAGCTACTTGGGAGGCTG	261008	93204	ACTCTGCAGGCACTTCCGGG

171835	4031	ACATAAATGCTGAGGGAAAG	216422	48618	TCCCAGCTACTTGGGAGGCT	261009	93205	GACTCTGCAGGCACTTCCGG
171836	4032	CACATAAATGCTGAGGGAAA	216423	48619	ATCCCAGCTACTTGGGAGGC	261010	93206	TGACTCTGCAGGCACTTCCG
171837	4033	ACACATAAATGCTGAGGGAA	216424	48620	AATCCCAGCTACTTGGGAGG	261011	93207	CTGACTCTGCAGGCACTTCC
171838	4034	CACACATAAATGCTGAGGGA	216425	48621	TAATCCCAGCTACTTGGGAG	261012	93208	CCTGACTCTGCAGGCACTTC
171839	4035	ACACACATAAATGCTGAGGG	216426	48622	ATAATCCCAGCTACTTGGGA	261013	93209	CCCTGACTCTGCAGGCACTT
171840	4036	CACACACATAAATGCTGAGG	216427	48623	TATAATCCCAGCTACTTGGG	261014	93210	GCCCTGACTCTGCAGGCACT
171841	4037	CCACACACATAAATGCTGAG	216428	48624	CTATAATCCCAGCTACTTGG	261015	93211	AGCCCTGACTCTGCAGGCAC
171842	4038	ACCACACACATAAATGCTGA	216429	48625	TCTATAATCCCAGCTACTTG	261016	93212	GAGCCCTGACTCTGCAGGCA
171843	4039	AACCACACACATAAATGCTG	216430	48626	ATCTATAATCCCAGCTACTT	261017	93213	GGAGCCCTGACTCTGCAGGC
171844	4040	AAACCACACACATAAATGCT	216431	48627	CATCTATAATCCCAGCTACT	261018	93214	GGGAGCCCTGACTCTGCAGG
171845	4041	GAAACCACACACATAAATGC	216432	48628	ACATCTATAATCCCAGCTAC	261019	93215	GGGGAGCCCTGACTCTGCAG
171846	4042	TGAAACCACACACATAAATG	216433	48629	CACATCTATAATCCCAGCTA	261020	93216	TGGGGAGCCCTGACTCTGCA
171847	4043	CTGAAACCACACACATAAAT	216434	48630	GCACATCTATAATCCCAGCT	261021	93217	CTGGGGAGCCCTGACTCTGC
171848	4044	ACTGAAACCACACACATAAA	216435	48631	TGCACATCTATAATCCCAGC	261022	93218	GCTGGGGAGCCCTGACTCTG
171849	4045	TACTGAAACCACACACATAA	216436	48632	GTGCACATCTATAATCCCAG	261023	93219	GGCTGGGGAGCCCTGACTCT
171850	4046	CTACTGAAACCACACACATA	216437	48633	GGTGCACATCTATAATCCCA	261024	93220	AGGCTGGGGAGCCCTGACTC
171851	4047	GCTACTGAAACCACACACAT	216438	48634	TGGTGCACATCTATAATCCC	261025	93221	GAGGCTGGGGAGCCCTGACT
171852	4048	AGCTACTGAAACCACACACA	216439	48635	ATGGTGCACATCTATAATCC	261026	93222	TGAGGCTGGGGAGCCCTGAC
171853	4049	GAGCTACTGAAACCACACAC	216440	48636	GATGGTGCACATCTATAATC	261027	93223	ATGAGGCTGGGGAGCCCTGA
171854	4050	AGAGCTACTGAAACCACACA	216441	48637	CGATGGTGCACATCTATAAT	261028	93224	GATGAGGCTGGGGAGCCCTG
171855	4051	CAGAGCTACTGAAACCACAC	216442	48638	ACGATGGTGCACATCTATAA	261029	93225	AGATGAGGCTGGGGAGCCCT
171856	4052	ACAGAGCTACTGAAACCACA	216443	48639	CACGATGGTGCACATCTATA	261030	93226	TAGATGAGGCTGGGGAGCCC
171857	4053	CACAGAGCTACTGAAACCAC	216444	48640	GCACGATGGTGCACATCTAT	261031	93227	CTAGATGAGGCTGGGGAGCC
171858	4054	CCACAGAGCTACTGAAACCA	216445	48641	GGCACGATGGTGCACATCTA	261032	93228	ACTAGATGAGGCTGGGGAGC
171859	4055	GCCACAGAGCTACTGAAACC	216446	48642	AGGCACGATGGTGCACATCT	261033	93229	CACTAGATGAGGCTGGGGAG
171860	4056	AGCCACAGAGCTACTGAAAC	216447	48643	TAGGCACGATGGTGCACATC	261034	93230	TCACTAGATGAGGCTGGGGA
171861	4057	TAGCCACAGAGCTACTGAAA	216448	48644	CTAGGCACGATGGTGCACAT	261035	93231	CTCACTAGATGAGGCTGGGG
171862	4058	ATAGCCACAGAGCTACTGAA	216449	48645	GCTAGGCACGATGGTGCACA	261036	93232	CCTCACTAGATGAGGCTGGG
171863	4059	TATAGCCACAGAGCTACTGA	216450	48646	AGCTAGGCACGATGGTGCAC	261037	93233	GCCTCACTAGATGAGGCTGG
171864	4060	ATATAGCCACAGAGCTACTG	216451	48647	TAGCTAGGCACGATGGTGCA	261038	93234	TGCCTCACTAGATGAGGCTG
171865	4061	CATATAGCCACAGAGCTACT	216452	48648	TTAGCTAGGCACGATGGTGC	261039	93235	CTGCCTCACTAGATGAGGCT
171866	4062	ACATATAGCCACAGAGCTAC	216453	48649	TTTAGCTAGGCACGATGGTG	261040	93236	ACTGCCTCACTAGATGAGGC
171867	4063	TACATATAGCCACAGAGCTA	216454	48650	ATTTAGCTAGGCACGATGGT	261041	93237	CACTGCCTCACTAGATGAGG
171868	4064	GTACATATAGCCACAGAGCT	216455	48651	AATTTAGCTAGGCACGATGG	261042	93238	CCACTGCCTCACTAGATGAG
171869	4065	CGTACATATAGCCACAGAGC	216456	48652	AAATTTAGCTAGGCACGATG	261043	93239	TCCACTGCCTCACTAGATGA
171870	4066	TCGTACATATAGCCACAGAG	216457	48653	AAAATTTAGCTAGGCACGAT	261044	93240	TTCCACTGCCTCACTAGATG
171871	4067	TTCGTACATATAGCCACAGA	216458	48654	AAAAATTTAGCTAGGCACGA	261045	93241	CTTCCACTGCCTCACTAGAT
171872	4068	GTTCGTACATATAGCCACAG	216459	48655	CAAAAATTTAGCTAGGCACG	261046	93242	CCTTCCACTGCCTCACTAGA
171873	4069	TGTTCGTACATATAGCCACA	216460	48656	ACAAAAATTTAGCTAGGCAC	261047	93243	CCCTTCCACTGCCTCACTAG
171874	4070	GTGTTCGTACATATAGCCAC	216461	48657	TACAAAAATTTAGCTAGGCA	261048	93244	GCCCTTCCACTGCCTCACTA
171875	4071	CGTGTTCGTACATATAGCCA	216462	48658	GTACAAAAATTTAGCTAGGC	261049	93245	GGCCCTTCCACTGCCTCACT
171876	4072	ACGTGTTCGTACATATAGCC	216463	48659	AGTACAAAAATTTAGCTAGG	261050	93246	AGGCCCTTCCACTGCCTCAC
171877	4073	CACGTGTTCGTACATATAGC	216464	48660	AAGTACAAAAATTTAGCTAG	261051	93247	CAGGCCCTTCCACTGCCTCA
171878	4074	ACACGTGTTCGTACATATAG	216465	48661	AAAGTACAAAAATTTAGCTA	261052	93248	ACAGGCCCTTCCACTGCCTC
171879	4075	AACACGTGTTCGTACATATA	216466	48662	AAAAGTACAAAAATTTAGCT	261053	93249	CACAGGCCCTTCCACTGCCT
171880	4076	TAACACGTGTTCGTACATAT	216467	48663	TAAAAGTACAAAAATTTAGC	261054	93250	CCACAGGCCCTTCCACTGCC
171881	4077	ATAACACGTGTTCGTACATA	216468	48664	CTAAAAGTACAAAAATTTAG	261055	93251	CCCACAGGCCCTTCCACTGC
171882	4078	AATAACACGTGTTCGTACAT	216469	48665	ACTAAAAGTACAAAAATTTA	261056	93252	CCCCACAGGCCCTTCCACTG
171883	4079	AAATAACACGTGTTCGTACA	216470	48666	TACTAAAAGTACAAAAATTT	261057	93253	TCCCCACAGGCCCTTCCACT
171884	4080	AAAATAACACGTGTTCGTAC	216471	48667	TTACTAAAAGTACAAAAATT	261058	93254	ATCCCCACAGGCCCTTCCAC
171885	4081	AAAAATAACACGTGTTCGTA	216472	48668	TTTACTAAAAGTACAAAAAT	261059	93255	AATCCCCACAGGCCCTTCCA
171886	4082	GAAAAATAACACGTGTTCGT	216473	48669	CTTTACTAAAAGTACAAAAA	261060	93256	AAATCCCCACAGGCCCTTCC
171887	4083	GGAAAAATAACACGTGTTCG	216474	48670	TCTTTACTAAAAGTACAAAA	261061	93257	CAAATCCCCACAGGCCCTTC
171888	4084	TGGAAAAATAACACGTGTTC	216475	48671	ATCTTTACTAAAAGTACAAA	261062	93258	CCAAATCCCCACAGGCCCTT
171889	4085	TTGGAAAAATAACACGTGTT	216476	48672	CATCTTTACTAAAAGTACAA	261063	93259	TCCAAATCCCCACAGGCCCT
171890	4086	ATTGGAAAAATAACACGTGT	216477	48673	ACATCTTTACTAAAAGTACA	261064	93260	CTCCAAATCCCCACAGGCCC
171891	4087	AATTGGAAAAATAACACGTG	216478	48674	AACATCTTTACTAAAAGTAC	261065	93261	TCTCCAAATCCCCACAGGCC
171892	4088	CAATTGGAAAAATAACACGT	216479	48675	CAACATCTTTACTAAAAGTA	261066	93262	CTCTCCAAATCCCCACAGGC
171893	4089	CCAATTGGAAAAATAACACG	216480	48676	ACAACATCTTTACTAAAAGT	261067	93263	GCTCTCCAAATCCCCACAGG
171894	4090	TCCAATTGGAAAAATAACAC	216481	48677	AACAACATCTTTACTAAAAG	261068	93264	AGCTCTCCAAATCCCCACAG
171895	4091	GTCCAATTGGAAAAATAACA	216482	48678	AAACAACATCTTTACTAAAA	261069	93265	CAGCTCTCCAAATCCCCACA
171896	4092	TGTCCAATTGGAAAAATAAC	216483	48679	AAAACAACATCTTTACTAAA	261070	93266	CCAGCTCTCCAAATCCCCAC
171897	4093	ATGTCCAATTGGAAAAATAA	216484	48680	CAAAACAACATCTTTACTAA	261071	93267	GCCAGCTCTCCAAATCCCCA
171898	4094	CATGTCCAATTGGAAAAATA	216485	48681	GCAAAACAACATCTTTACTA	261072	93268	GGCCAGCTCTCCAAATCCCC
171899	4095	ACATGTCCAATTGGAAAAAT	216486	48682	AGCAAAACAACATCTTTACT	261073	93269	AGGCCAGCTCTCCAAATCCC
171900	4096	CACATGTCCAATTGGAAAAA	216487	48683	CAGCAAAACAACATCTTTAC	261074	93270	CAGGCCAGCTCTCCAAATCC
171901	4097	TCACATGTCCAATTGGAAAA	216488	48684	ACAGCAAAACAACATCTTTA	261075	93271	CCAGGCCAGCTCTCCAAATC
171902	4098	ATCACATGTCCAATTGGAAA	216489	48685	CACAGCAAAACAACATCTTT	261076	93272	CCCAGGCCAGCTCTCCAAAT
171903	4099	TATCACATGTCCAATTGGAA	216490	48686	ACACAGCAAAACAACATCTT	261077	93273	ACCCAGGCCAGCTCTCCAAA
171904	4100	TTATCACATGTCCAATTGGA	216491	48687	AACACAGCAAAACAACATCT	261078	93274	GACCCAGGCCAGCTCTCCAA
171905	4101	ATTATCACATGTCCAATTGG	216492	48688	CAACACAGCAAAACAACATC	261079	93275	AGACCCAGGCCAGCTCTCCA
171906	4102	AATTATCACATGTCCAATTG	216493	48689	CCAACACAGCAAAACAACAT	261080	93276	GAGACCCAGGCCAGCTCTCC

171907	4103	AAATTATCACATGTCCAATT	216494	48690	GCCAACACAGCAAAACAACA	261081	93277	AGAGACCCAGGCCAGCTCTC
171908	4104	AAAATTATCACATGTCCAAT	216495	48691	GGCCAACACAGCAAAACAAC	261082	93278	CAGAGACCCAGGCCAGCTCT
171909	4105	GAAAATTATCACATGTCCAA	216496	48692	TGGCCAACACAGCAAAACAA	261083	93279	TCAGAGACCCAGGCCAGCTC
171910	4106	GGAAAATTATCACATGTCCA	216497	48693	TTGGCCAACACAGCAAAACA	261084	93280	TTCAGAGACCCAGGCCAGCT
171911	4107	TGGAAAATTATCACATGTCC	216498	48694	CTTGGCCAACACAGCAAAAC	261085	93281	CTTCAGAGACCCAGGCCAGC
171912	4108	TTGGAAAATTATCACATGTC	216499	48695	GCTTGGCCAACACAGCAAAA	261086	93282	ACTTCAGAGACCCAGGCCAG
171913	4109	GTTGGAAAATTATCACATGT	216500	48696	AGCTTGGCCAACACAGCAAA	261087	93283	CACTTCAGAGACCCAGGCCA
171914	4110	AGTTGGAAAATTATCACATG	216501	48697	CAGCTTGGCCAACACAGCAA	261088	93284	TCACTTCAGAGACCCAGGCC
171915	4111	CAGTTGGAAAATTATCACAT	216502	48698	TCAGCTTGGCCAACACAGCA	261089	93285	ATCACTTCAGAGACCCAGGC
171916	4112	CCAGTTGGAAAATTATCACA	216503	48699	ATCAGCTTGGCCAACACAGC	261090	93286	TATCACTTCAGAGACCCAGG
171917	4113	TCCAGTTGGAAAATTATCAC	216504	48700	GATCAGCTTGGCCAACACAG	261091	93287	CTATCACTTCAGAGACCCAG
171918	4114	GTCCAGTTGGAAAATTATCA	216505	48701	AGATCAGCTTGGCCAACACA	261092	93288	ACTATCACTTCAGAGACCCA
171919	4115	GGTCCAGTTGGAAAATTATC	216506	48702	GAGATCAGCTTGGCCAACAC	261093	93289	CACTATCACTTCAGAGACCC
171920	4116	AGGTCCAGTTGGAAAATTAT	216507	48703	CGAGATCAGCTTGGCCAACA	261094	93290	TCACTATCACTTCAGAGACC
171921	4117	AAGGTCCAGTTGGAAAATTA	216508	48704	TCGAGATCAGCTTGGCCAAC	261095	93291	GTCACTATCACTTCAGAGAC
171922	4118	CAAGGTCCAGTTGGAAAATT	216509	48705	TTCGAGATCAGCTTGGCCAA	261096	93292	TGTCACTATCACTTCAGAGA
171923	4119	GCAAGGTCCAGTTGGAAAAT	216510	48706	GTTCGAGATCAGCTTGGCCA	261097	93293	CTGTCACTATCACTTCAGAG
171924	4120	GGCAAGGTCCAGTTGGAAAA	216511	48707	AGTTCGAGATCAGCTTGGCC	261098	93294	GCTGTCACTATCACTTCAGA
171925	4121	AGGCAAGGTCCAGTTGGAAA	216512	48708	AAGTTCGAGATCAGCTTGGC	261099	93295	AGCTGTCACTATCACTTCAG
171926	4122	AAGGCAAGGTCCAGTTGGAA	216513	48709	AAAGTTCGAGATCAGCTTGG	261100	93296	CAGCTGTCACTATCACTTCA
171927	4123	GAAGGCAAGGTCCAGTTGGA	216514	48710	AAAAGTTCGAGATCAGCTTG	261101	93297	GCAGCTGTCACTATCACTTC
171928	4124	AGAAGGCAAGGTCCAGTTGG	216515	48711	CAAAAGTTCGAGATCAGCTT	261102	93298	AGCAGCTGTCACTATCACTT
171929	4125	TAGAAGGCAAGGTCCAGTTG	216516	48712	CCAAAAGTTCGAGATCAGCT	261103	93299	AAGCAGCTGTCACTATCACT
171930	4126	ATAGAAGGCAAGGTCCAGTT	216517	48713	GCCAAAAGTTCGAGATCAGC	261104	93300	CAAGCAGCTGTCACTATCAC
171931	4127	AATAGAAGGCAAGGTCCAGT	216518	48714	GGCCAAAAGTTCGAGATCAG	261105	93301	ACAAGCAGCTGTCACTATCA
171932	4128	CAATAGAAGGCAAGGTCCAG	216519	48715	AGGCCAAAAGTTCGAGATCA	261106	93302	GACAAGCAGCTGTCACTATC
171933	4129	TCAATAGAAGGCAAGGTCCA	216520	48716	GAGGCCAAAAGTTCGAGATC	261107	93303	TGACAAGCAGCTGTCACTAT
171934	4130	ATCAATAGAAGGCAAGGTCC	216521	48717	TGAGGCCAAAAGTTCGAGAT	261108	93304	TTGACAAGCAGCTGTCACTA
171935	4131	CATCAATAGAAGGCAAGGTC	216522	48718	TTGAGGCCAAAAGTTCGAGA	261109	93305	ATTGACAAGCAGCTGTCACT
171936	4132	ACATCAATAGAAGGCAAGGT	216523	48719	CTTGAGGCCAAAAGTTCGAG	261110	93306	GATTGACAAGCAGCTGTCAC
171937	4133	TACATCAATAGAAGGCAAGG	216524	48720	ACTTGAGGCCAAAAGTTCGA	261111	93307	TGATTGACAAGCAGCTGTCA
171938	4134	ATACATCAATAGAAGGCAAG	216525	48721	CACTTGAGGCCAAAAGTTCG	261112	93308	GTGATTGACAAGCAGCTGTC
171939	4135	AATACATCAATAGAAGGCAA	216526	48722	TCACTTGAGGCCAAAAGTTC	261113	93309	CGTGATTGACAAGCAGCTGT
171940	4136	AAATACATCAATAGAAGGCA	216527	48723	ATCACTTGAGGCCAAAAGTT	261114	93310	CCGTGATTGACAAGCAGCTG
171941	4137	TAAATACATCAATAGAAGGC	216528	48724	GATCACTTGAGGCCAAAAGT	261115	93311	ACCGTGATTGACAAGCAGCT
171942	4138	ATAAATACATCAATAGAAGG	216529	48725	AGATCACTTGAGGCCAAAAG	261116	93312	CACCGTGATTGACAAGCAGC
171943	4139	AATAAATACATCAATAGAAG	216530	48726	CAGATCACTTGAGGCCAAAA	261117	93313	GCACCGTGATTGACAAGCAG
171944	4140	AAATAAATACATCAATAGAA	216531	48727	GCAGATCACTTGAGGCCAAA	261118	93314	TGCACCGTGATTGACAAGCA
171945	4141	TAAATAAATACATCAATAGA	216532	48728	GGCAGATCACTTGAGGCCAA	261119	93315	GTGCACCGTGATTGACAAGC
171946	4142	CTAAATAAATACATCAATAG	216533	48729	AGGCAGATCACTTGAGGCCA	261120	93316	TGTGCACCGTGATTGACAAG
171947	4143	GCTAAATAAATACATCAATA	216534	48730	TAGGCAGATCACTTGAGGCC	261121	93317	ATGTGCACCGTGATTGACAA
171948	4144	TGCTAAATAAATACATCAAT	216535	48731	GTAGGCAGATCACTTGAGGC	261122	93318	AATGTGCACCGTGATTGACA
171949	4145	ATGCTAAATAAATACATCAA	216536	48732	GGTAGGCAGATCACTTGAGG	261123	93319	AAATGTGCACCGTGATTGAC
171950	4146	GATGCTAAATAAATACATCA	216537	48733	AGGTAGGCAGATCACTTGAG	261124	93320	TAAATGTGCACCGTGATTGA
171951	4147	AGATGCTAAATAAATACATC	216538	48734	GAGGTAGGCAGATCACTTGA	261125	93321	CTAAATGTGCACCGTGATTG
171952	4148	AAGATGCTAAATAAATACAT	216539	48735	TGAGGTAGGCAGATCACTTG	261126	93322	ACTAAATGTGCACCGTGATT
171953	4149	GAAGATGCTAAATAAATACA	216540	48736	CTGAGGTAGGCAGATCACTT	261127	93323	CACTAAATGTGCACCGTGAT
171954	4150	GGAAGATGCTAAATAAATAC	216541	48737	GCTGAGGTAGGCAGATCACT	261128	93324	GCACTAAATGTGCACCGTGA
171955	4151	AGGAAGATGCTAAATAAATA	216542	48738	GGCTGAGGTAGGCAGATCAC	261129	93325	AGCACTAAATGTGCACCGTG
171956	4152	AAGGAAGATGCTAAATAAAT	216543	48739	AGGCTGAGGTAGGCAGATCA	261130	93326	CAGCACTAAATGTGCACCGT
171957	4153	TAAGGAAGATGCTAAATAAA	216544	48740	GAGGCTGAGGTAGGCAGATC	261131	93327	CCAGCACTAAATGTGCACCG
171958	4154	GTAAGGAAGATGCTAAATAA	216545	48741	GGAGGCTGAGGTAGGCAGAT	261132	93328	CCCAGCACTAAATGTGCACC
171959	4155	AGTAAGGAAGATGCTAAATA	216546	48742	GGGAGGCTGAGGTAGGCAGA	261133	93329	CCCCAGCACTAAATGTGCAC
171960	4156	GAGTAAGGAAGATGCTAAAT	216547	48743	TGGGAGGCTGAGGTAGGCAG	261134	93330	CCCCCAGCACTAAATGTGCA
171961	4157	GGAGTAAGGAAGATGCTAAA	216548	48744	TTGGGAGGCTGAGGTAGGCA	261135	93331	GCCCCCAGCACTAAATGTGC
171962	4158	GGGAGTAAGGAAGATGCTAA	216549	48745	TTTGGGAGGCTGAGGTAGGC	261136	93332	TGCCCCCAGCACTAAATGTG
171963	4159	AGGGAGTAAGGAAGATGCTA	216550	48746	CTTTGGGAGGCTGAGGTAGG	261137	93333	CTGCCCCCAGCACTAAATGT
171964	4160	GAGGGAGTAAGGAAGATGCT	216551	48747	ACTTTGGGAGGCTGAGGTAG	261138	93334	CCTGCCCCCAGCACTAAATG
171965	4161	GGAGGGAGTAAGGAAGATGC	216552	48748	CACTTTGGGAGGCTGAGGTA	261139	93335	CCCTGCCCCCAGCACTAAAT
171966	4162	AGGAGGGAGTAAGGAAGATG	216553	48749	GCACTTTGGGAGGCTGAGGT	261140	93336	CCCCTGCCCCCAGCACTAAA
171967	4163	AAGGAGGGAGTAAGGAAGAT	216554	48750	AGCACTTTGGGAGGCTGAGG	261141	93337	CCCCCTGCCCCCAGCACTAA
171968	4164	CAAGGAGGGAGTAAGGAAGA	216555	48751	CAGCACTTTGGGAGGCTGAG	261142	93338	GCCCCCTGCCCCCAGCACTA
171969	4165	TCAAGGAGGGAGTAAGGAAG	216556	48752	CCAGCACTTTGGGAGGCTGA	261143	93339	TGCCCCCTGCCCCCAGCACT
171970	4166	TTCAAGGAGGGAGTAAGGAA	216557	48753	CCCAGCACTTTGGGAGGCTG	261144	93340	CTGCCCCCTGCCCCCAGCAC
171971	4167	TTTCAAGGAGGGAGTAAGGA	216558	48754	TCCCAGCACTTTGGGAGGCT	261145	93341	CCTGCCCCCTGCCCCCAGCA
171972	4168	TTTTCAAGGAGGGAGTAAGG	216559	48755	ATCCCAGCACTTTGGGAGGC	261146	93342	CCCTGCCCCCTGCCCCCAGC
171973	4169	TTTTTCAAGGAGGGAGTAAG	216560	48756	AATCCCAGCACTTTGGGAGG	261147	93343	TCCCTGCCCCCTGCCCCCAG
171974	4170	CTTTTTCAAGGAGGGAGTAA	216561	48757	TAATCCCAGCACTTTGGGAG	261148	93344	TTCCCTGCCCCCTGCCCCCA
171975	4171	TCTTTTTCAAGGAGGGAGTA	216562	48758	GTAATCCCAGCACTTTGGGA	261149	93345	ATTCCCTGCCCCCTGCCCCC
171976	4172	TTCTTTTTCAAGGAGGGAGT	216563	48759	TGTAATCCCAGCACTTTGGG	261150	93346	TATTCCCTGCCCCCTGCCCC
171977	4173	ATTCTTTTTCAAGGAGGGAG	216564	48760	CTGTAATCCCAGCACTTTGG	261151	93347	GTATTCCCTGCCCCCTGCCC
171978	4174	GATTCTTTTTCAAGGAGGGA	216565	48761	CCTGTAATCCCAGCACTTTG	261152	93348	GGTATTCCCTGCCCCCTGCC

171979	4175	TGATTCTTTTTCAAGGAGGG	216566	48762	GCCTGTAATCCCAGCACTTT	261153	93349	TGGTATTCCCTGCCCCCTGC
171980	4176	GTGATTCTTTTTCAAGGAGG	216567	48763	TGCCTGTAATCCCAGCACTT	261154	93350	CTGGTATTCCCTGCCCCCTG
171981	4177	AGTGATTCTTTTTCAAGGAG	216568	48764	ATGCCTGTAATCCCAGCACT	261155	93351	GCTGGTATTCCCTGCCCCCT
171982	4178	GAGTGATTCTTTTTCAAGGA	216569	48765	CATGCCTGTAATCCCAGCAC	261156	93352	GGCTGGTATTCCCTGCCCCC
171983	4179	TGAGTGATTCTTTTTCAAGG	216570	48766	TCATGCCTGTAATCCCAGCA	261157	93353	AGGCTGGTATTCCCTGCCCC
171984	4180	TTGAGTGATTCTTTTTCAAG	216571	48767	CTCATGCCTGTAATCCCAGC	261158	93354	GAGGCTGGTATTCCCTGCCC
171985	4181	TTTGAGTGATTCTTTTTCAA	216572	48768	GCTCATGCCTGTAATCCCAG	261159	93355	TGAGGCTGGTATTCCCTGCC
171986	4182	TTTTGAGTGATTCTTTTTCA	216573	48769	GGCTCATGCCTGTAATCCCA	261160	93356	ATGAGGCTGGTATTCCCTGC
171987	4183	TTTTTGAGTGATTCTTTTTC	216574	48770	TGGCTCATGCCTGTAATCCC	261161	93357	CATGAGGCTGGTATTCCCTG
171988	4184	GTTTTTGAGTGATTCTTTTT	216575	48771	GTGGCTCATGCCTGTAATCC	261162	93358	GCATGAGGCTGGTATTCCCT
171989	4185	TGTTTTTGAGTGATTCTTTT	216576	48772	GGTGGCTCATGCCTGTAATC	261163	93359	TGCATGAGGCTGGTATTCCC
171990	4186	TTGTTTTTGAGTGATTCTTT	216577	48773	TGGTGGCTCATGCCTGTAAT	261164	93360	ATGCATGAGGCTGGTATTCC
171991	4187	TTTGTTTTTGAGTGATTCTT	216578	48774	ATGGTGGCTCATGCCTGTAA	261165	93361	CATGCATGAGGCTGGTATTC
171992	4188	ATTTGTTTTTGAGTGATTCT	216579	48775	CATGGTGGCTCATGCCTGTA	261166	93362	GCATGCATGAGGCTGGTATT
171993	4189	TATTTGTTTTTGAGTGATTC	216580	48776	GCATGGTGGCTCATGCCTGT	261167	93363	TGCATGCATGAGGCTGGTAT
171994	4190	TTATTTGTTTTTGAGTGATT	216581	48777	GGCATGGTGGCTCATGCCTG	261168	93364	ATGCATGCATGAGGCTGGTA
171995	4191	TTTATTTGTTTTTGAGTGAT	216582	48778	AGGCATGGTGGCTCATGCCT	261169	93365	CATGCATGCATGAGGCTGGT
171996	4192	TTTTATTTGTTTTTGAGTGA	216583	48779	CAGGCATGGTGGCTCATGCC	261170	93366	GCATGCATGCATGAGGCTGG
171997	4193	TTTTTATTTGTTTTTGAGTG	216584	48780	CCAGGCATGGTGGCTCATGC	261171	93367	TGCATGCATGCATGAGGCTG
171998	4194	GTTTTTATTTGTTTTTGAGT	216585	48781	GCCAGGCATGGTGGCTCATG	261172	93368	ATGCATGCATGCATGAGGCT
171999	4195	TGTTTTTATTTGTTTTTGAG	216586	48782	TGCCAGGCATGGTGGCTCAT	261173	93369	AATGCATGCATGCATGAGGC
172000	4196	CTGTTTTTATTTGTTTTTGA	216587	48783	CTGCCAGGCATGGTGGCTCA	261174	93370	GAATGCATGCATGCATGAGG
172001	4197	GCTGTTTTTATTTGTTTTTG	216588	48784	ACTGCCAGGCATGGTGGCTC	261175	93371	TGAATGCATGCATGCATGAG
172002	4198	GGCTGTTTTTATTTGTTTTT	216589	48785	CACTGCCAGGCATGGTGGCT	261176	93372	ATGAATGCATGCATGCATGA
172003	4199	CGGCTGTTTTTATTTGTTTT	216590	48786	ACACTGCCAGGCATGGTGGC	261177	93373	AATGAATGCATGCATGCATG
172004	4200	ACGGCTGTTTTTATTTGTTT	216591	48787	CACACTGCCAGGCATGGTGG	261178	93374	AAATGAATGCATGCATGCAT
172005	4201	TACGGCTGTTTTTATTTGTT	216592	48788	CCACACTGCCAGGCATGGTG	261179	93375	CAAATGAATGCATGCATGCA
172006	4202	CTACGGCTGTTTTTATTTGT	216593	48789	GCCACACTGCCAGGCATGGT	261180	93376	ACAAATGAATGCATGCATGC
172007	4203	CCTACGGCTGTTTTTATTTG	216594	48790	TGCCACACTGCCAGGCATGG	261181	93377	AACAAATGAATGCATGCATG
172008	4204	CCCTACGGCTGTTTTTATTT	216595	48791	GTGCCACACTGCCAGGCATG	261182	93378	GAACAAATGAATGCATGCAT
172009	4205	CCCCTACGGCTGTTTTTATT	216596	48792	AGTGCCACACTGCCAGGCAT	261183	93379	GGAACAAATGAATGCATGCA
172010	4206	GCCCCTACGGCTGTTTTTAT	216597	48793	AAGTGCCACACTGCCAGGCA	261184	93380	AGGAACAAATGAATGCATGC
172011	4207	GGCCCCTACGGCTGTTTTTA	216598	48794	GAAGTGCCACACTGCCAGGC	261185	93381	AAGGAACAAATGAATGCATG
172012	4208	AGGCCCCTACGGCTGTTTTT	216599	48795	AGAAGTGCCACACTGCCAGG	261186	93382	GAAGGAACAAATGAATGCAT
172013	4209	TAGGCCCCTACGGCTGTTTT	216600	48796	AAGAAGTGCCACACTGCCAG	261187	93383	GGAAGGAACAAATGAATGCA
172014	4210	TTAGGCCCCTACGGCTGTTT	216601	48797	TAAGAAGTGCCACACTGCCA	261188	93384	AGGAAGGAACAAATGAATGC
172015	4211	ATTAGGCCCCTACGGCTGTT	216602	48798	GTAAGAAGTGCCACACTGCC	261189	93385	AAGGAAGGAACAAATGAATG
172016	4212	TATTAGGCCCCTACGGCTGT	216603	48799	CGTAAGAAGTGCCACACTGC	261190	93386	GAAGGAAGGAACAAATGAAT
172017	4213	GTATTAGGCCCCTACGGCTG	216604	48800	ACGTAAGAAGTGCCACACTG	261191	93387	TGAAGGAAGGAACAAATGAA
172018	4214	TGTATTAGGCCCCTACGGCT	216605	48801	CACGTAAGAAGTGCCACACT	261192	93388	ATGAAGGAAGGAACAAATGA
172019	4215	CTGTATTAGGCCCCTACGGC	216606	48802	ACACGTAAGAAGTGCCACAC	261193	93389	AATGAAGGAAGGAACAAATG
172020	4216	ACTGTATTAGGCCCCTACGG	216607	48803	CACACGTAAGAAGTGCCACA	261194	93390	GAATGAAGGAAGGAACAAAT
172021	4217	CACTGTATTAGGCCCCTACG	216608	48804	ACACACGTAAGAAGTGCCAC	261195	93391	TGAATGAAGGAAGGAACAAA
172022	4218	GCACTGTATTAGGCCCCTAC	216609	48805	AACACACGTAAGAAGTGCCA	261196	93392	ATGAATGAAGGAAGGAACAA
172023	4219	AGCACTGTATTAGGCCCCTA	216610	48806	GAACACACGTAAGAAGTGCC	261197	93393	AATGAATGAAGGAAGGAACA
172024	4220	TAGCACTGTATTAGGCCCCT	216611	48807	TGAACACACGTAAGAAGTGC	261198	93394	GAATGAATGAAGGAAGGAAC
172025	4221	CTAGCACTGTATTAGGCCCC	216612	48808	CTGAACACACGTAAGAAGTG	261199	93395	TGAATGAATGAAGGAAGGAA
172026	4222	TCTAGCACTGTATTAGGCCC	216613	48809	GCTGAACACACGTAAGAAGT	261200	93396	ATGAATGAATGAAGGAAGGA
172027	4223	GTCTAGCACTGTATTAGGCC	216614	48810	CGCTGAACACACGTAAGAAG	261201	93397	AATGAATGAATGAAGGAAGG
172028	4224	TGTCTAGCACTGTATTAGGC	216615	48811	CCGCTGAACACACGTAAGAA	261202	93398	GAATGAATGAATGAAGGAAG
172029	4225	ATGTCTAGCACTGTATTAGG	216616	48812	TCCGCTGAACACACGTAAGA	261203	93399	TGAATGAATGAATGAAGGAA
172030	4226	TATGTCTAGCACTGTATTAG	216617	48813	GTCCGCTGAACACACGTAAG	261204	93400	CTGAATGAATGAATGAAGGA
172031	4227	GTATGTCTAGCACTGTATTA	216618	48814	TGTCCGCTGAACACACGTAA	261205	93401	ACTGAATGAATGAATGAAGG
172032	4228	TGTATGTCTAGCACTGTATT	216619	48815	GTGTCCGCTGAACACACGTA	261206	93402	TACTGAATGAATGAATGAAG
172033	4229	TTGTATGTCTAGCACTGTAT	216620	48816	AGTGTCCGCTGAACACACGT	261207	93403	GTACTGAATGAATGAATGAA
172034	4230	CTTGTATGTCTAGCACTGTA	216621	48817	CAGTGTCCGCTGAACACACG	261208	93404	TGTACTGAATGAATGAATGA
172035	4231	TCTTGTATGTCTAGCACTGT	216622	48818	ACAGTGTCCGCTGAACACAC	261209	93405	GTGTACTGAATGAATGAATG
172036	4232	CTCTTGTATGTCTAGCACTG	216623	48819	AACAGTGTCCGCTGAACACA	261210	93406	TGTGTACTGAATGAATGAAT
172037	4233	CCTCTTGTATGTCTAGCACT	216624	48820	AAACAGTGTCCGCTGAACAC	261211	93407	ATGTGTACTGAATGAATGAA
172038	4234	ACCTCTTGTATGTCTAGCAC	216625	48821	TAAACAGTGTCCGCTGAACA	261212	93408	CATGTGTACTGAATGAATGA
172039	4235	TACCTCTTGTATGTCTAGCA	216626	48822	ATAAACAGTGTCCGCTGAAC	261213	93409	CCATGTGTACTGAATGAATG
172040	4236	ATACCTCTTGTATGTCTAGC	216627	48823	GATAAACAGTGTCCGCTGAA	261214	93410	CCCATGTGTACTGAATGAAT
172041	4237	AATACCTCTTGTATGTCTAG	216628	48824	AGATAAACAGTGTCCGCTGA	261215	93411	ACCCATGTGTACTGAATGAA
172042	4238	GAATACCTCTTGTATGTCTA	216629	48825	AAGATAAACAGTGTCCGCTG	261216	93412	TACCCATGTGTACTGAATGA
172043	4239	CGAATACCTCTTGTATGTCT	216630	48826	GAAGATAAACAGTGTCCGCT	261217	93413	GTACCCATGTGTACTGAATG
172044	4240	CCGAATACCTCTTGTATGTC	216631	48827	AGAAGATAAACAGTGTCCGC	261218	93414	TGTACCCATGTGTACTGAAT
172045	4241	ACCGAATACCTCTTGTATGT	216632	48828	CAGAAGATAAACAGTGTCCG	261219	93415	TTGTACCCATGTGTACTGAA
172046	4242	GACCGAATACCTCTTGTATG	216633	48829	ACAGAAGATAAACAGTGTCC	261220	93416	GTTGTACCCATGTGTACTGA
172047	4243	GGACCGAATACCTCTTGTAT	216634	48830	GACAGAAGATAAACAGTGTC	261221	93417	TGTTGTACCCATGTGTACTG
172048	4244	TGGACCGAATACCTCTTGTA	216635	48831	GGACAGAAGATAAACAGTGT	261222	93418	ATGTTGTACCCATGTGTACT
172049	4245	ATGGACCGAATACCTCTTGT	216636	48832	GGGACAGAAGATAAACAGTG	261223	93419	GATGTTGTACCCATGTGTAC
172050	4246	TATGGACCGAATACCTCTTG	216637	48833	AGGGACAGAAGATAAACAGT	261224	93420	GGATGTTGTACCCATGTGTA

172051	4247	GTATGGACCGAATACCTCTT	216638	48834	GAGGGACAGAAGATAAACAG	261225	93421	GGGATGTTGTACCCATGTGT
172052	4248	GGTATGGACCGAATACCTCT	216639	48835	GGAGGGACAGAAGATAAACA	261226	93422	AGGGATGTTGTACCCATGTG
172053	4249	TGGTATGGACCGAATACCTC	216640	48836	TGGAGGGACAGAAGATAAAC	261227	93423	CAGGGATGTTGTACCCATGT
172054	4250	TTGGTATGGACCGAATACCT	216641	48837	TTGGAGGGACAGAAGATAAA	261228	93424	GCAGGGATGTTGTACCCATG
172055	4251	TTTGGTATGGACCGAATACC	216642	48838	CTTGGAGGGACAGAAGATAA	261229	93425	GGCAGGGATGTTGTACCCAT
172056	4252	ATTTGGTATGGACCGAATAC	216643	48839	TCTTGGAGGGACAGAAGATA	261230	93426	GGGCAGGGATGTTGTACCCA
172057	4253	CATTTGGTATGGACCGAATA	216644	48840	GTCTTGGAGGGACAGAAGAT	261231	93427	AGGGCAGGGATGTTGTACCC
172058	4254	CCATTTGGTATGGACCGAAT	216645	48841	CGTCTTGGAGGGACAGAAGA	261232	93428	CAGGGCAGGGATGTTGTACC
172059	4255	TCCATTTGGTATGGACCGAA	216646	48842	CCGTCTTGGAGGGACAGAAG	261233	93429	CCAGGGCAGGGATGTTGTAC
172060	4256	ATCCATTTGGTATGGACCGA	216647	48843	ACCGTCTTGGAGGGACAGAA	261234	93430	TCCAGGGCAGGGATGTTGTA
172061	4257	AATCCATTTGGTATGGACCG	216648	48844	CACCGTCTTGGAGGGACAGA	261235	93431	CTCCAGGGCAGGGATGTTGT
172062	4258	AAATCCATTTGGTATGGACC	216649	48845	GCACCGTCTTGGAGGGACAG	261236	93432	ACTCCAGGGCAGGGATGTTG
172063	4259	AAAATCCATTTGGTATGGAC	216650	48846	AGCACCGTCTTGGAGGGACA	261237	93433	AACTCCAGGGCAGGGATGTT
172064	4260	TAAAATCCATTTGGTATGGA	216651	48847	CAGCACCGTCTTGGAGGGAC	261238	93434	CAACTCCAGGGCAGGGATGT
172065	4261	ATAAAATCCATTTGGTATGG	216652	48848	TCAGCACCGTCTTGGAGGGA	261239	93435	GCAACTCCAGGGCAGGGATG
172066	4262	GATAAAATCCATTTGGTATG	216653	48849	CTCAGCACCGTCTTGGAGGG	261240	93436	GGCAACTCCAGGGCAGGGAT
172067	4263	GGATAAAATCCATTTGGTAT	216654	48850	GCTCAGCACCGTCTTGGAGG	261241	93437	GGGCAACTCCAGGGCAGGGA
172068	4264	TGGATAAAATCCATTTGGTA	216655	48851	AGCTCAGCACCGTCTTGGAG	261242	93438	TGGGCAACTCCAGGGCAGGG
172069	4265	ATGGATAAAATCCATTTGGT	216656	48852	GAGCTCAGCACCGTCTTGGA	261243	93439	CTGGGCAACTCCAGGGCAGG
172070	4266	CATGGATAAAATCCATTTGG	216657	48853	TGAGCTCAGCACCGTCTTGG	261244	93440	TCTGGGCAACTCCAGGGCAG
172071	4267	TCATGGATAAAATCCATTTG	216658	48854	CTGAGCTCAGCACCGTCTTG	261245	93441	CTCTGGGCAACTCCAGGGCA
172072	4268	TTCATGGATAAAATCCATTT	216659	48855	CCTGAGCTCAGCACCGTCTT	261246	93442	ACTCTGGGCAACTCCAGGGC
172073	4269	CTTCATGGATAAAATCCATT	216660	48856	ACCTGAGCTCAGCACCGTCT	261247	93443	GACTCTGGGCAACTCCAGGG
172074	4270	CCTTCATGGATAAAATCCAT	216661	48857	GACCTGAGCTCAGCACCGTC	261248	93444	AGACTCTGGGCAACTCCAGG
172075	4271	TCCTTCATGGATAAAATCCA	216662	48858	CGACCTGAGCTCAGCACCGT	261249	93445	TAGACTCTGGGCAACTCCAG
172076	4272	ATCCTTCATGGATAAAATCC	216663	48859	ACGACCTGAGCTCAGCACCG	261250	93446	CTAGACTCTGGGCAACTCCA
172077	4273	TATCCTTCATGGATAAAATC	216664	48860	AACGACCTGAGCTCAGCACC	261251	93447	CCTAGACTCTGGGCAACTCC
172078	4274	TTATCCTTCATGGATAAAAT	216665	48861	GAACGACCTGAGCTCAGCAC	261252	93448	CCCTAGACTCTGGGCAACTC
172079	4275	TTTATCCTTCATGGATAAAA	216666	48862	TGAACGACCTGAGCTCAGCA	261253	93449	TCCCTAGACTCTGGGCAACT
172080	4276	ATTTATCCTTCATGGATAAA	216667	48863	ATGAACGACCTGAGCTCAGC	261254	93450	CTCCCTAGACTCTGGGCAAC
172081	4277	CATTTATCCTTCATGGATAA	216668	48864	AATGAACGACCTGAGCTCAG	261255	93451	CCTCCCTAGACTCTGGGCAA
172082	4278	CCATTTATCCTTCATGGATA	216669	48865	TAATGAACGACCTGAGCTCA	261256	93452	CCCTCCCTAGACTCTGGGCA
172083	4279	CCCATTTATCCTTCATGGAT	216670	48866	GTAATGAACGACCTGAGCTC	261257	93453	CCCCTCCCTAGACTCTGGGC
172084	4280	CCCCATTTATCCTTCATGGA	216671	48867	AGTAATGAACGACCTGAGCT	261258	93454	TCCCCTCCCTAGACTCTGGG
172085	4281	TCCCCATTTATCCTTCATGG	216672	48868	CAGTAATGAACGACCTGAGC	261259	93455	TTCCCCTCCCTAGACTCTGG
172086	4282	TTCCCCATTTATCCTTCATG	216673	48869	CCAGTAATGAACGACCTGAG	261260	93456	TTTCCCCTCCCTAGACTCTG
172087	4283	TTTCCCCATTTATCCTTCAT	216674	48870	GCCAGTAATGAACGACCTGA	261261	93457	CTTTCCCCTCCCTAGACTCT
172088	4284	ATTTCCCCATTTATCCTTCA	216675	48871	TGCCAGTAATGAACGACCTG	261262	93458	TCTTTCCCCTCCCTAGACTC
172089	4285	TATTTCCCCATTTATCCTTC	216676	48872	CTGCCAGTAATGAACGACCT	261263	93459	ATCTTTCCCCTCCCTAGACT
172090	4286	GTATTTCCCCATTTATCCTT	216677	48873	TCTGCCAGTAATGAACGACC	261264	93460	GATCTTTCCCCTCCCTAGAC
172091	4287	TGTATTTCCCCATTTATCCT	216678	48874	GTCTGCCAGTAATGAACGAC	261265	93461	AGATCTTTCCCCTCCCTAGA
172092	4288	CTGTATTTCCCCATTTATCC	216679	48875	TGTCTGCCAGTAATGAACGA	261266	93462	TAGATCTTTCCCCTCCCTAG
172093	4289	ACTGTATTTCCCCATTTATC	216680	48876	TTGTCTGCCAGTAATGAACG	261267	93463	ATAGATCTTTCCCCTCCCTA
172094	4290	CACTGTATTTCCCCATTTAT	216681	48877	GTTGTCTGCCAGTAATGAAC	261268	93464	AATAGATCTTTCCCCTCCCT
172095	4291	CCACTGTATTTCCCCATTTA	216682	48878	AGTTGTCTGCCAGTAATGAA	261269	93465	TAATAGATCTTTCCCCTCCC
172096	4292	CCCACTGTATTTCCCCATTT	216683	48879	CAGTTGTCTGCCAGTAATGA	261270	93466	GTAATAGATCTTTCCCCTCC
172097	4293	TCCCACTGTATTTCCCCATT	216684	48880	GCAGTTGTCTGCCAGTAATG	261271	93467	GGTAATAGATCTTTCCCCTC
172098	4294	TTCCCACTGTATTTCCCCAT	216685	48881	AGCAGTTGTCTGCCAGTAAT	261272	93468	GGGTAATAGATCTTTCCCCT
172099	4295	CTTCCCACTGTATTTCCCCA	216686	48882	CAGCAGTTGTCTGCCAGTAA	261273	93469	AGGGTAATAGATCTTTCCCC
172100	4296	GCTTCCCACTGTATTTCCCC	216687	48883	TCAGCAGTTGTCTGCCAGTA	261274	93470	CAGGGTAATAGATCTTTCCC
172101	4297	TGCTTCCCACTGTATTTCCC	216688	48884	ATCAGCAGTTGTCTGCCAGT	261275	93471	CCAGGGTAATAGATCTTTCC
172102	4298	CTGCTTCCCACTGTATTTCC	216689	48885	AATCAGCAGTTGTCTGCCAG	261276	93472	CCCAGGGTAATAGATCTTTC
172103	4299	CCTGCTTCCCACTGTATTTC	216690	48886	AAATCAGCAGTTGTCTGCCA	261277	93473	GCCCAGGGTAATAGATCTTT
172104	4300	ACCTGCTTCCCACTGTATTT	216691	48887	GAAATCAGCAGTTGTCTGCC	261278	93474	GGCCCAGGGTAATAGATCTT
172105	4301	CACCTGCTTCCCACTGTATT	216692	48888	GGAAATCAGCAGTTGTCTGC	261279	93475	AGGCCCAGGGTAATAGATCT
172106	4302	CCACCTGCTTCCCACTGTAT	216693	48889	TGGAAATCAGCAGTTGTCTG	261280	93476	GAGGCCCAGGGTAATAGATC
172107	4303	CCCACCTGCTTCCCACTGTA	216694	48890	TTGGAAATCAGCAGTTGTCT	261281	93477	CGAGGCCCAGGGTAATAGAT
172108	4304	TCCCACCTGCTTCCCACTGT	216695	48891	GTTGGAAATCAGCAGTTGTC	261282	93478	CCGAGGCCCAGGGTAATAGA
172109	4305	TTCCCACCTGCTTCCCACTG	216696	48892	TGTTGGAAATCAGCAGTTGT	261283	93479	GCCGAGGCCCAGGGTAATAG
172110	4306	TTTCCCACCTGCTTCCCACT	216697	48893	CTGTTGGAAATCAGCAGTTG	261284	93480	GGCCGAGGCCCAGGGTAATA
172111	4307	GTTTCCCACCTGCTTCCCAC	216698	48894	TCTGTTGGAAATCAGCAGTT	261285	93481	TGGCCGAGGCCCAGGGTAAT
172112	4308	AGTTTCCCACCTGCTTCCCA	216699	48895	TTCTGTTGGAAATCAGCAGT	261286	93482	CTGGCCGAGGCCCAGGGTAA
172113	4309	CAGTTTCCCACCTGCTTCCC	216700	48896	ATTCTGTTGGAAATCAGCAG	261287	93483	GCTGGCCGAGGCCCAGGGTA
172114	4310	GCAGTTTCCCACCTGCTTCC	216701	48897	AATTCTGTTGGAAATCAGCA	261288	93484	AGCTGGCCGAGGCCCAGGGT
172115	4311	CGCAGTTTCCCACCTGCTTC	216702	48898	CAATTCTGTTGGAAATCAGC	261289	93485	CAGCTGGCCGAGGCCCAGGG
172116	4312	ACGCAGTTTCCCACCTGCTT	216703	48899	GCAATTCTGTTGGAAATCAG	261290	93486	CCAGCTGGCCGAGGCCCAGG
172117	4313	AACGCAGTTTCCCACCTGCT	216704	48900	GGCAATTCTGTTGGAAATCA	261291	93487	CCCAGCTGGCCGAGGCCCAG
172118	4314	AAACGCAGTTTCCCACCTGC	216705	48901	TGGCAATTCTGTTGGAAATC	261292	93488	CCCCAGCTGGCCGAGGCCCA
172119	4315	CAAACGCAGTTTCCCACCTG	216706	48902	ATGGCAATTCTGTTGGAAAT	261293	93489	TCCCCAGCTGGCCGAGGCCC
172120	4316	TCAAACGCAGTTTCCCACCT	216707	48903	GATGGCAATTCTGTTGGAAA	261294	93490	CTCCCCAGCTGGCCGAGGCC
172121	4317	GTCAAACGCAGTTTCCCACC	216708	48904	GGATGGCAATTCTGTTGGAA	261295	93491	ACTCCCCAGCTGGCCGAGGC
172122	4318	AGTCAAACGCAGTTTCCCAC	216709	48905	AGGATGGCAATTCTGTTGGA	261296	93492	CACTCCCCAGCTGGCCGAGG

172123	4319	GAGTCAAACGCAGTTTCCCA	216710	48906	GAGGATGGCAATTCTGTTGG	261297	93493	GCACTCCCCAGCTGGCCGAG
172124	4320	AGAGTCAAACGCAGTTTCCC	216711	48907	AGAGGATGGCAATTCTGTTG	261298	93494	AGCACTCCCCAGCTGGCCGA
172125	4321	CAGAGTCAAACGCAGTTTCC	216712	48908	AAGAGGATGGCAATTCTGTT	261299	93495	CAGCACTCCCCAGCTGGCCG
172126	4322	GCAGAGTCAAACGCAGTTTC	216713	48909	GAAGAGGATGGCAATTCTGT	261300	93496	GCAGCACTCCCCAGCTGGCC
172127	4323	AGCAGAGTCAAACGCAGTTT	216714	48910	AGAAGAGGATGGCAATTCTG	261301	93497	AGCAGCACTCCCCAGCTGGC
172128	4324	GAGCAGAGTCAAACGCAGTT	216715	48911	GAGAAGAGGATGGCAATTCT	261302	93498	CAGCAGCACTCCCCAGCTGG
172129	4325	AGAGCAGAGTCAAACGCAGT	216716	48912	GGAGAAGAGGATGGCAATTC	261303	93499	CCAGCAGCACTCCCCAGCTG
172130	4326	AAGAGCAGAGTCAAACGCAG	216717	48913	GGGAGAAGAGGATGGCAATT	261304	93500	ACCAGCAGCACTCCCCAGCT
172131	4327	AAAGAGCAGAGTCAAACGCA	216718	48914	GGGGAGAAGAGGATGGCAAT	261305	93501	CACCAGCAGCACTCCCCAGC
172132	4328	GAAAGAGCAGAGTCAAACGC	216719	48915	AGGGGAGAAGAGGATGGCAA	261306	93502	CCACCAGCAGCACTCCCCAG
172133	4329	GGAAAGAGCAGAGTCAAACG	216720	48916	CAGGGGAGAAGAGGATGGCA	261307	93503	TCCACCAGCAGCACTCCCCA
172134	4330	AGGAAAGAGCAGAGTCAAAC	216721	48917	GCAGGGGAGAAGAGGATGGC	261308	93504	CTCCACCAGCAGCACTCCCC
172135	4331	GAGGAAAGAGCAGAGTCAAA	216722	48918	CGCAGGGGAGAAGAGGATGG	261309	93505	TCTCCACCAGCAGCACTCCC
172136	4332	GGAGGAAAGAGCAGAGTCAA	216723	48919	TCGCAGGGGAGAAGAGGATG	261310	93506	CTCTCCACCAGCAGCACTCC
172137	4333	TGGAGGAAAGAGCAGAGTCA	216724	48920	GTCGCAGGGGAGAAGAGGAT	261311	93507	CCTCTCCACCAGCAGCACTC
172138	4334	GTGGAGGAAAGAGCAGAGTC	216725	48921	AGTCGCAGGGGAGAAGAGGA	261312	93508	CCCTCTCCACCAGCAGCACT
172139	4335	GGTGGAGGAAAGAGCAGAGT	216726	48922	AAGTCGCAGGGGAGAAGAGG	261313	93509	CCCCTCTCCACCAGCAGCAC
172140	4336	TGGTGGAGGAAAGAGCAGAG	216727	48923	AAAGTCGCAGGGGAGAAGAG	261314	93510	GCCCCTCTCCACCAGCAGCA
172141	4337	GTGGTGGAGGAAAGAGCAGA	216728	48924	GAAAGTCGCAGGGGAGAAGA	261315	93511	GGCCCCTCTCCACCAGCAGC
172142	4338	GGTGGTGGAGGAAAGAGCAG	216729	48925	TGAAAGTCGCAGGGGAGAAG	261316	93512	CGGCCCCTCTCCACCAGCAG
172143	4339	TGGTGGTGGAGGAAAGAGCA	216730	48926	CTGAAAGTCGCAGGGGAGAA	261317	93513	ACGGCCCCTCTCCACCAGCA
172144	4340	GTGGTGGTGGAGGAAAGAGC	216731	48927	TCTGAAAGTCGCAGGGGAGA	261318	93514	CACGGCCCCTCTCCACCAGC
172145	4341	AGTGGTGGTGGAGGAAAGAG	216732	48928	CTCTGAAAGTCGCAGGGGAG	261319	93515	ACACGGCCCCTCTCCACCAG
172146	4342	AAGTGGTGGTGGAGGAAAGA	216733	48929	ACTCTGAAAGTCGCAGGGGA	261320	93516	CACACGGCCCCTCTCCACCA
172147	4343	AAAGTGGTGGTGGAGGAAAG	216734	48930	CACTCTGAAAGTCGCAGGGG	261321	93517	GCACACGGCCCCTCTCCACC
172148	4344	GAAAGTGGTGGTGGAGGAAA	216735	48931	ACACTCTGAAAGTCGCAGGG	261322	93518	TGCACACGGCCCCTCTCCAC
172149	4345	GGAAAGTGGTGGTGGAGGAA	216736	48932	CACACTCTGAAAGTCGCAGG	261323	93519	CTGCACACGGCCCCTCTCCA
172150	4346	AGGAAAGTGGTGGTGGAGGA	216737	48933	TCACACTCTGAAAGTCGCAG	261324	93520	GCTGCACACGGCCCCTCTCC
172151	4347	GAGGAAAGTGGTGGTGGAGG	216738	48934	GTCACACTCTGAAAGTCGCA	261325	93521	CGCTGCACACGGCCCCTCTC
172152	4348	TGAGGAAAGTGGTGGTGGAG	216739	48935	GGTCACACTCTGAAAGTCGC	261326	93522	TCGCTGCACACGGCCCCTCT
172153	4349	ATGAGGAAAGTGGTGGTGGA	216740	48936	AGGTCACACTCTGAAAGTCG	261327	93523	CTCGCTGCACACGGCCCCTC
172154	4350	GATGAGGAAAGTGGTGGTGG	216741	48937	GAGGTCACACTCTGAAAGTC	261328	93524	CCTCGCTGCACACGGCCCCT
172155	4351	TGATGAGGAAAGTGGTGGTG	216742	48938	TGAGGTCACACTCTGAAAGT	261329	93525	CCCTCGCTGCACACGGCCCC
172156	4352	GTGATGAGGAAAGTGGTGGT	216743	48939	CTGAGGTCACACTCTGAAAG	261330	93526	TCCCTCGCTGCACACGGCCC
172157	4353	GGTGATGAGGAAAGTGGTGG	216744	48940	TCTGAGGTCACACTCTGAAA	261331	93527	TTCCCTCGCTGCACACGGCC
172158	4354	CGGTGATGAGGAAAGTGGTG	216745	48941	GTCTGAGGTCACACTCTGAA	261332	93528	CTTCCCTCGCTGCACACGGC
172159	4355	ACGGTGATGAGGAAAGTGGT	216746	48942	AGTCTGAGGTCACACTCTGA	261333	93529	CCTTCCCTCGCTGCACACGG
172160	4356	CACGGTGATGAGGAAAGTGG	216747	48943	GAGTCTGAGGTCACACTCTG	261334	93530	TCCTTCCCTCGCTGCACACG
172161	4357	ACACGGTGATGAGGAAAGTG	216748	48944	TGAGTCTGAGGTCACACTCT	261335	93531	CTCCTTCCCTCGCTGCACAC
172162	4358	AACACGGTGATGAGGAAAGT	216749	48945	TTGAGTCTGAGGTCACACTC	261336	93532	CCTCCTTCCCTCGCTGCACA
172163	4359	GAACACGGTGATGAGGAAAG	216750	48946	TTTGAGTCTGAGGTCACACT	261337	93533	TCCTCCTTCCCTCGCTGCAC
172164	4360	TGAACACGGTGATGAGGAAA	216751	48947	TTTTGAGTCTGAGGTCACAC	261338	93534	CTCCTCCTTCCCTCGCTGCA
172165	4361	CTGAACACGGTGATGAGGAA	216752	48948	TTTTTGAGTCTGAGGTCACA	261339	93535	ACTCCTCCTTCCCTCGCTGC
172166	4362	TCTGAACACGGTGATGAGGA	216753	48949	ATTTTTGAGTCTGAGGTCAC	261340	93536	GACTCCTCCTTCCCTCGCTG
172167	4363	CTCTGAACACGGTGATGAGG	216754	48950	AATTTTTGAGTCTGAGGTCA	261341	93537	CGACTCCTCCTTCCCTCGCT
172168	4364	TCTCTGAACACGGTGATGAG	216755	48951	TAATTTTTGAGTCTGAGGTC	261342	93538	ACGACTCCTCCTTCCCTCGC
172169	4365	GTCTCTGAACACGGTGATGA	216756	48952	CTAATTTTTGAGTCTGAGGT	261343	93539	GACGACTCCTCCTTCCCTCG
172170	4366	GGTCTCTGAACACGGTGATG	216757	48953	TCTAATTTTTGAGTCTGAGG	261344	93540	TGACGACTCCTCCTTCCCTC
172171	4367	GGGTCTCTGAACACGGTGAT	216758	48954	TTCTAATTTTTGAGTCTGAG	261345	93541	TTGACGACTCCTCCTTCCCT
172172	4368	GGGGTCTCTGAACACGGTGA	216759	48955	CTTCTAATTTTTGAGTCTGA	261346	93542	ATTGACGACTCCTCCTTCCC
172173	4369	GGGGGTCTCTGAACACGGTG	216760	48956	ACTTCTAATTTTTGAGTCTG	261347	93543	TATTGACGACTCCTCCTTCC
172174	4370	TGGGGGTCTCTGAACACGGT	216761	48957	CACTTCTAATTTTTGAGTCT	261348	93544	GTATTGACGACTCCTCCTTC
172175	4371	TTGGGGGTCTCTGAACACGG	216762	48958	TCACTTCTAATTTTTGAGTC	261349	93545	GGTATTGACGACTCCTCCTT
172176	4372	TTTGGGGGTCTCTGAACACG	216763	48959	TTCACTTCTAATTTTTGAGT	261350	93546	GGGTATTGACGACTCCTCCT
172177	4373	CTTTGGGGGTCTCTGAACAC	216764	48960	TTTCACTTCTAATTTTTGAG	261351	93547	GGGGTATTGACGACTCCTCC
172178	4374	GCTTTGGGGGTCTCTGAACA	216765	48961	TTTTCACTTCTAATTTTTGA	261352	93548	GGGGGTATTGACGACTCCTC
172179	4375	GGCTTTGGGGGTCTCTGAAC	216766	48962	GTTTTCACTTCTAATTTTTG	261353	93549	TGGGGGTATTGACGACTCCT
172180	4376	GGGCTTTGGGGGTCTCTGAA	216767	48963	TGTTTTCACTTCTAATTTTT	261354	93550	GTGGGGGTATTGACGACTCC
172181	4377	GGGGCTTTGGGGGTCTCTGA	216768	48964	ATGTTTTCACTTCTAATTTT	261355	93551	GGTGGGGGTATTGACGACTC
172182	4378	GGGGGCTTTGGGGGTCTCTG	216769	48965	GATGTTTTCACTTCTAATTT	261356	93552	GGGTGGGGGTATTGACGACT
172183	4379	AGGGGGCTTTGGGGGTCTCT	216770	48966	AGATGTTTTCACTTCTAATT	261357	93553	GGGGTGGGGGTATTGACGAC
172184	4380	GAGGGGGCTTTGGGGGTCTC	216771	48967	AAGATGTTTTCACTTCTAAT	261358	93554	TGGGGTGGGGGTATTGACGA
172185	4381	TGAGGGGGCTTTGGGGGTCT	216772	48968	TAAGATGTTTTCACTTCTAA	261359	93555	CTGGGGTGGGGGTATTGACG
172186	4382	GTGAGGGGGCTTTGGGGGTC	216773	48969	TTAAGATGTTTTCACTTCTA	261360	93556	GCTGGGGTGGGGGTATTGAC
172187	4383	TGTGAGGGGGCTTTGGGGGT	216774	48970	TTTAAGATGTTTTCACTTCT	261361	93557	AGCTGGGGTGGGGGTATTGA
172188	4384	GTGTGAGGGGGCTTTGGGGG	216775	48971	TTTTAAGATGTTTTCACTTC	261362	93558	AAGCTGGGGTGGGGGTATTG
172189	4385	AGTGTGAGGGGGCTTTGGGG	216776	48972	TTTTTAAGATGTTTTCACTT	261363	93559	AAAGCTGGGGTGGGGGTATT
172190	4386	GAGTGTGAGGGGGCTTTGGG	216777	48973	GTTTTTAAGATGTTTTCACT	261364	93560	CAAAGCTGGGGTGGGGGTAT
172191	4387	GGAGTGTGAGGGGGCTTTGG	216778	48974	AGTTTTTAAGATGTTTTCAC	261365	93561	GCAAAGCTGGGGTGGGGGTA
172192	4388	GGGAGTGTGAGGGGGCTTTG	216779	48975	TAGTTTTTAAGATGTTTTCA	261366	93562	AGCAAAGCTGGGGTGGGGGT
172193	4389	TGGGAGTGTGAGGGGGCTTT	216780	48976	ATAGTTTTTAAGATGTTTTC	261367	93563	AAGCAAAGCTGGGGTGGGGG
172194	4390	CTGGGAGTGTGAGGGGGCTT	216781	48977	GATAGTTTTTAAGATGTTTT	261368	93564	AAAGCAAAGCTGGGGTGGGG

172195	4391	TCTGGGAGTGTGAGGGGGCT	216782	48978	TGATAGTTTTTAAGATGTTT	261369	93565	GAAAGCAAAGCTGGGGTGGG
172196	4392	TTCTGGGAGTGTGAGGGGGC	216783	48979	GTGATAGTTTTTAAGATGTT	261370	93566	AGAAAGCAAAGCTGGGGTGG
172197	4393	TTTCTGGGAGTGTGAGGGGG	216784	48980	GGTGATAGTTTTTAAGATGT	261371	93567	AAGAAAGCAAAGCTGGGGTG
172198	4394	GTTTCTGGGAGTGTGAGGGG	216785	48981	AGGTGATAGTTTTTAAGATG	261372	93568	CAAGAAAGCAAAGCTGGGGT
172199	4395	TGTTTCTGGGAGTGTGAGGG	216786	48982	AAGGTGATAGTTTTTAAGAT	261373	93569	ACAAGAAAGCAAAGCTGGGG
172200	4396	GTGTTTCTGGGAGTGTGAGG	216787	48983	AAAGGTGATAGTTTTTAAGA	261374	93570	GACAAGAAAGCAAAGCTGGG
172201	4397	GGTGTTTCTGGGAGTGTGAG	216788	48984	AAAAGGTGATAGTTTTTAAG	261375	93571	TGACAAGAAAGCAAAGCTGG
172202	4398	GGGTGTTTCTGGGAGTGTGA	216789	48985	GAAAAGGTGATAGTTTTTAA	261376	93572	ATGACAAGAAAGCAAAGCTG
172203	4399	GGGGTGTTTCTGGGAGTGTG	216790	48986	AGAAAAGGTGATAGTTTTTA	261377	93573	GATGACAAGAAAGCAAAGCT
172204	4400	GGGGGTGTTTCTGGGAGTGT	216791	48987	AAGAAAAGGTGATAGTTTTT	261378	93574	TGATGACAAGAAAGCAAAGC
172205	4401	GGGGGGTGTTTCTGGGAGTG	216792	48988	GAAGAAAAGGTGATAGTTTT	261379	93575	CTGATGACAAGAAAGCAAAG
172206	4402	AGGGGGGTGTTTCTGGGAGT	216793	48989	GGAAGAAAAGGTGATAGTTT	261380	93576	GCTGATGACAAGAAAGCAAA
172207	4403	CAGGGGGGTGTTTCTGGGAG	216794	48990	AGGAAGAAAAGGTGATAGTT	261381	93577	GGCTGATGACAAGAAAGCAA
172208	4404	CCAGGGGGGTGTTTCTGGGA	216795	48991	TAGGAAGAAAAGGTGATAGT	261382	93578	GGGCTGATGACAAGAAAGCA
172209	4405	GCCAGGGGGGTGTTTCTGGG	216796	48992	TTAGGAAGAAAAGGTGATAG	261383	93579	GGGGCTGATGACAAGAAAGC
172210	4406	GGCCAGGGGGGTGTTTCTGG	216797	48993	ATTAGGAAGAAAAGGTGATA	261384	93580	TGGGGCTGATGACAAGAAAG
172211	4407	TGGCCAGGGGGGTGTTTCTG	216798	48994	GATTAGGAAGAAAAGGTGAT	261385	93581	CTGGGGCTGATGACAAGAAA
172212	4408	GTGGCCAGGGGGGTGTTTCT	216799	48995	GGATTAGGAAGAAAAGGTGA	261386	93582	CCTGGGGCTGATGACAAGAA
172213	4409	AGTGGCCAGGGGGGTGTTTC	216800	48996	AGGATTAGGAAGAAAAGGTG	261387	93583	CCCTGGGGCTGATGACAAGA
172214	4410	GAGTGGCCAGGGGGGTGTTT	216801	48997	GAGGATTAGGAAGAAAAGGT	261388	93584	GCCCTGGGGCTGATGACAAG
172215	4411	GGAGTGGCCAGGGGGGTGTT	216802	48998	GGAGGATTAGGAAGAAAAGG	261389	93585	GGCCCTGGGGCTGATGACAA
172216	4412	AGGAGTGGCCAGGGGGGTGT	216803	48999	AGGAGGATTAGGAAGAAAAG	261390	93586	GGGCCCTGGGGCTGATGACA
172217	4413	TAGGAGTGGCCAGGGGGGTG	216804	49000	GAGGAGGATTAGGAAGAAAA	261391	93587	GGGGCCCTGGGGCTGATGAC
172218	4414	TTAGGAGTGGCCAGGGGGGT	216805	49001	AGAGGAGGATTAGGAAGAAA	261392	93588	TGGGGCCCTGGGGCTGATGA
172219	4415	GTTAGGAGTGGCCAGGGGGG	216806	49002	GAGAGGAGGATTAGGAAGAA	261393	93589	CTGGGGCCCTGGGGCTGATG
172220	4416	AGTTAGGAGTGGCCAGGGGG	216807	49003	GGAGAGGAGGATTAGGAAGA	261394	93590	GCTGGGGCCCTGGGGCTGAT
172221	4417	AAGTTAGGAGTGGCCAGGGG	216808	49004	GGGAGAGGAGGATTAGGAAG	261395	93591	GGCTGGGGCCCTGGGGCTGA
172222	4418	CAAGTTAGGAGTGGCCAGGG	216809	49005	GGGGAGAGGAGGATTAGGAA	261396	93592	AGGCTGGGGCCCTGGGGCTG
172223	4419	GCAAGTTAGGAGTGGCCAGG	216810	49006	AGGGGAGAGGAGGATTAGGA	261397	93593	CAGGCTGGGGCCCTGGGGCT
172224	4420	GGCAAGTTAGGAGTGGCCAG	216811	49007	GAGGGGAGAGGAGGATTAGG	261398	93594	ACAGGCTGGGGCCCTGGGGC
172225	4421	TGGCAAGTTAGGAGTGGCCA	216812	49008	GGAGGGGAGAGGAGGATTAG	261399	93595	CACAGGCTGGGGCCCTGGGG
172226	4422	ATGGCAAGTTAGGAGTGGCC	216813	49009	GGGAGGGGAGAGGAGGATTA	261400	93596	ACACAGGCTGGGGCCCTGGG
172227	4423	CATGGCAAGTTAGGAGTGGC	216814	49010	AGGGAGGGGAGAGGAGGATT	261401	93597	GACACAGGCTGGGGCCCTGG
172228	4424	GCATGGCAAGTTAGGAGTGG	216815	49011	CAGGGAGGGGAGAGGAGGAT	261402	93598	GGACACAGGCTGGGGCCCTG
172229	4425	GGCATGGCAAGTTAGGAGTG	216816	49012	ACAGGGAGGGGAGAGGAGGA	261403	93599	GGGACACAGGCTGGGGCCCT
172230	4426	GGGCATGGCAAGTTAGGAGT	216817	49013	GACAGGGAGGGGAGAGGAGG	261404	93600	AGGGACACAGGCTGGGGCCC
172231	4427	TGGGCATGGCAAGTTAGGAG	216818	49014	AGACAGGGAGGGGAGAGGAG	261405	93601	GAGGGACACAGGCTGGGGCC
172232	4428	CTGGGCATGGCAAGTTAGGA	216819	49015	AAGACAGGGAGGGGAGAGGA	261406	93602	GGAGGGACACAGGCTGGGGC
172233	4429	CCTGGGCATGGCAAGTTAGG	216820	49016	GAAGACAGGGAGGGGAGAGG	261407	93603	AGGAGGGACACAGGCTGGGG
172234	4430	TCCTGGGCATGGCAAGTTAG	216821	49017	GGAAGACAGGGAGGGGAGAG	261408	93604	GAGGAGGGACACAGGCTGGG
172235	4431	CTCCTGGGCATGGCAAGTTA	216822	49018	AGGAAGACAGGGAGGGGAGA	261409	93605	AGAGGAGGGACACAGGCTGG
172236	4432	ACTCCTGGGCATGGCAAGTT	216823	49019	AAGGAAGACAGGGAGGGGAG	261410	93606	GAGAGGAGGGACACAGGCTG
172237	4433	AACTCCTGGGCATGGCAAGT	216824	49020	CAAGGAAGACAGGGAGGGGA	261411	93607	GGAGAGGAGGGACACAGGCT
172238	4434	TAACTCCTGGGCATGGCAAG	216825	49021	ACAAGGAAGACAGGGAGGGG	261412	93608	GGGAGAGGAGGGACACAGGC
172239	4435	CTAACTCCTGGGCATGGCAA	216826	49022	AACAAGGAAGACAGGGAGGG	261413	93609	TGGGAGAGGAGGGACACAGG
172240	4436	CCTAACTCCTGGGCATGGCA	216827	49023	CAACAAGGAAGACAGGGAGG	261414	93610	ATGGGAGAGGAGGGACACAG
172241	4437	ACCTAACTCCTGGGCATGGC	216828	49024	ACAACAAGGAAGACAGGGAG	261415	93611	AATGGGAGAGGAGGGACACA
172242	4438	CACCTAACTCCTGGGCATGG	216829	49025	GACAACAAGGAAGACAGGGA	261416	93612	CAATGGGAGAGGAGGGACAC
172243	4439	GCACCTAACTCCTGGGCATG	216830	49026	GGACAACAAGGAAGACAGGG	261417	93613	GCAATGGGAGAGGAGGGACA
172244	4440	AGCACCTAACTCCTGGGCAT	216831	49027	GGGACAACAAGGAAGACAGG	261418	93614	AGCAATGGGAGAGGAGGGAC
172245	4441	AAGCACCTAACTCCTGGGCA	216832	49028	GGGGACAACAAGGAAGACAG	261419	93615	TAGCAATGGGAGAGGAGGGA
172246	4442	GAAGCACCTAACTCCTGGGC	216833	49029	TGGGGACAACAAGGAAGACA	261420	93616	GTAGCAATGGGAGAGGAGGG
172247	4443	GGAAGCACCTAACTCCTGGG	216834	49030	ATGGGGACAACAAGGAAGAC	261421	93617	AGTAGCAATGGGAGAGGAGG
172248	4444	TGGAAGCACCTAACTCCTGG	216835	49031	GATGGGGACAACAAGGAAGA	261422	93618	AAGTAGCAATGGGAGAGGAG
172249	4445	GTGGAAGCACCTAACTCCTG	216836	49032	AGATGGGGACAACAAGGAAG	261423	93619	GAAGTAGCAATGGGAGAGGA
172250	4446	AGTGGAAGCACCTAACTCCT	216837	49033	TAGATGGGGACAACAAGGAA	261424	93620	TGAAGTAGCAATGGGAGAGG
172251	4447	TAGTGGAAGCACCTAACTCC	216838	49034	TTAGATGGGGACAACAAGGA	261425	93621	ATGAAGTAGCAATGGGAGAG
172252	4448	CTAGTGGAAGCACCTAACTC	216839	49035	ATTAGATGGGGACAACAAGG	261426	93622	GATGAAGTAGCAATGGGAGA
172253	4449	ACTAGTGGAAGCACCTAACT	216840	49036	CATTAGATGGGGACAACAAG	261427	93623	AGATGAAGTAGCAATGGGAG
172254	4450	CACTAGTGGAAGCACCTAAC	216841	49037	TCATTAGATGGGGACAACAA	261428	93624	GAGATGAAGTAGCAATGGGA
172255	4451	TCACTAGTGGAAGCACCTAA	216842	49038	TTCATTAGATGGGGACAACA	261429	93625	GGAGATGAAGTAGCAATGGG
172256	4452	GTCACTAGTGGAAGCACCTA	216843	49039	GTTCATTAGATGGGGACAAC	261430	93626	AGGAGATGAAGTAGCAATGG
172257	4453	TGTCACTAGTGGAAGCACCT	216844	49040	AGTTCATTAGATGGGGACAA	261431	93627	CAGGAGATGAAGTAGCAATG
172258	4454	ATGTCACTAGTGGAAGCACC	216845	49041	TAGTTCATTAGATGGGGACA	261432	93628	CCAGGAGATGAAGTAGCAAT
172259	4455	CATGTCACTAGTGGAAGCAC	216846	49042	ATAGTTCATTAGATGGGGAC	261433	93629	CCCAGGAGATGAAGTAGCAA
172260	4456	CCATGTCACTAGTGGAAGCA	216847	49043	GATAGTTCATTAGATGGGGA	261434	93630	ACCCAGGAGATGAAGTAGCA
172261	4457	TCCATGTCACTAGTGGAAGC	216848	49044	TGATAGTTCATTAGATGGGG	261435	93631	GACCCAGGAGATGAAGTAGC
172262	4458	CTCCATGTCACTAGTGGAAG	216849	49045	ATGATAGTTCATTAGATGGG	261436	93632	GGACCCAGGAGATGAAGTAG
172263	4459	GCTCCATGTCACTAGTGGAA	216850	49046	CATGATAGTTCATTAGATGG	261437	93633	AGGACCCAGGAGATGAAGTA
172264	4460	AGCTCCATGTCACTAGTGGA	216851	49047	CCATGATAGTTCATTAGATG	261438	93634	GAGGACCCAGGAGATGAAGT
172265	4461	CAGCTCCATGTCACTAGTGG	216852	49048	GCCATGATAGTTCATTAGAT	261439	93635	GGAGGACCCAGGAGATGAAG
172266	4462	CCAGCTCCATGTCACTAGTG	216853	49049	TGCCATGATAGTTCATTAGA	261440	93636	AGGAGGACCCAGGAGATGAA

172267	4463	GCCAGCTCCATGTCACTAGT	216854	49050	TTGCCATGATAGTTCATTAG	261441	93637	AAGGAGGACCCAGGAGATGA
172268	4464	CGCCAGCTCCATGTCACTAG	216855	49051	TTTGCCATGATAGTTCATTA	261442	93638	TAAGGAGGACCCAGGAGATG
172269	4465	ACGCCAGCTCCATGTCACTA	216856	49052	TTTTGCCATGATAGTTCATT	261443	93639	GTAAGGAGGACCCAGGAGAT
172270	4466	AACGCCAGCTCCATGTCACT	216857	49053	TTTTTGCCATGATAGTTCAT	261444	93640	GGTAAGGAGGACCCAGGAGA
172271	4467	AAACGCCAGCTCCATGTCAC	216858	49054	CTTTTTGCCATGATAGTTCA	261445	93641	TGGTAAGGAGGACCCAGGAG
172272	4468	CAAACGCCAGCTCCATGTCA	216859	49055	TCTTTTTGCCATGATAGTTC	261446	93642	TTGGTAAGGAGGACCCAGGA
172273	4469	CCAAACGCCAGCTCCATGTC	216860	49056	CTCTTTTTGCCATGATAGTT	261447	93643	CTTGGTAAGGAGGACCCAGG
172274	4470	CCCAAACGCCAGCTCCATGT	216861	49057	GCTCTTTTTGCCATGATAGT	261448	93644	GCTTGGTAAGGAGGACCCAG
172275	4471	CCCCAAACGCCAGCTCCATG	216862	49058	GGCTCTTTTTGCCATGATAG	261449	93645	GGCTTGGTAAGGAGGACCCA
172276	4472	CCCCCAAACGCCAGCTCCAT	216863	49059	GGGCTCTTTTTGCCATGATA	261450	93646	AGGCTTGGTAAGGAGGACCC
172277	4473	CCCCCCAAACGCCAGCTCCA	216864	49060	TGGGCTCTTTTTGCCATGAT	261451	93647	CAGGCTTGGTAAGGAGGACC
172278	4474	GCCCCCCAAACGCCAGCTCC	216865	49061	ATGGGCTCTTTTTGCCATGA	261452	93648	TCAGGCTTGGTAAGGAGGAC
172279	4475	TGCCCCCCAAACGCCAGCTC	216866	49062	AATGGGCTCTTTTTGCCATG	261453	93649	GTCAGGCTTGGTAAGGAGGA
172280	4476	GTGCCCCCCAAACGCCAGCT	216867	49063	AAATGGGCTCTTTTTGCCAT	261454	93650	GGTCAGGCTTGGTAAGGAGG
172281	4477	GGTGCCCCCCAAACGCCAGC	216868	49064	GAAATGGGCTCTTTTTGCCA	261455	93651	TGGTCAGGCTTGGTAAGGAG
172282	4478	AGGTGCCCCCCAAACGCCAG	216869	49065	AGAAATGGGCTCTTTTTGCC	261456	93652	GTGGTCAGGCTTGGTAAGGA
172283	4479	GAGGTGCCCCCCAAACGCCA	216870	49066	CAGAAATGGGCTCTTTTTGC	261457	93653	TGTGGTCAGGCTTGGTAAGG
172284	4480	TGAGGTGCCCCCCAAACGCC	216871	49067	CCAGAAATGGGCTCTTTTTG	261458	93654	GTGTGGTCAGGCTTGGTAAG
172285	4481	CTGAGGTGCCCCCCAAACGC	216872	49068	ACCAGAAATGGGCTCTTTTT	261459	93655	TGTGTGGTCAGGCTTGGTAA
172286	4482	GCTGAGGTGCCCCCCAAACG	216873	49069	GACCAGAAATGGGCTCTTTT	261460	93656	CTGTGTGGTCAGGCTTGGTA
172287	4483	TGCTGAGGTGCCCCCCAAAC	216874	49070	TGACCAGAAATGGGCTCTTT	261461	93657	TCTGTGTGGTCAGGCTTGGT
172288	4484	CTGCTGAGGTGCCCCCCAAA	216875	49071	ATGACCAGAAATGGGCTCTT	261462	93658	CTCTGTGTGGTCAGGCTTGG
172289	4485	CCTGCTGAGGTGCCCCCCAA	216876	49072	AATGACCAGAAATGGGCTCT	261463	93659	CCTCTGTGTGGTCAGGCTTG
172290	4486	ACCTGCTGAGGTGCCCCCCA	216877	49073	AAATGACCAGAAATGGGCTC	261464	93660	CCCTCTGTGTGGTCAGGCTT
172291	4487	CACCTGCTGAGGTGCCCCCC	216878	49074	AAAATGACCAGAAATGGGCT	261465	93661	GCCCTCTGTGTGGTCAGGCT
172292	4488	TCACCTGCTGAGGTGCCCCC	216879	49075	GAAAATGACCAGAAATGGGC	261466	93662	GGCCCTCTGTGTGGTCAGGC
172293	4489	GTCACCTGCTGAGGTGCCCC	216880	49076	AGAAAATGACCAGAAATGGG	261467	93663	AGGCCCTCTGTGTGGTCAGG
172294	4490	CGTCACCTGCTGAGGTGCCC	216881	49077	CAGAAAATGACCAGAAATGG	261468	93664	AAGGCCCTCTGTGTGGTCAG
172295	4491	CCGTCACCTGCTGAGGTGCC	216882	49078	ACAGAAAATGACCAGAAATG	261469	93665	CAAGGCCCTCTGTGTGGTCA
172296	4492	CCCGTCACCTGCTGAGGTGC	216883	49079	CACAGAAAATGACCAGAAAT	261470	93666	CCAAGGCCCTCTGTGTGGTC
172297	4493	TCCCGTCACCTGCTGAGGTG	216884	49080	CCACAGAAAATGACCAGAAA	261471	93667	GCCAAGGCCCTCTGTGTGGT
172298	4494	TTCCCGTCACCTGCTGAGGT	216885	49081	GCCACAGAAAATGACCAGAA	261472	93668	GGCCAAGGCCCTCTGTGTGG
172299	4495	CTTCCCGTCACCTGCTGAGG	216886	49082	GGCCACAGAAAATGACCAGA	261473	93669	CGGCCAAGGCCCTCTGTGTG
172300	4496	TCTTCCCGTCACCTGCTGAG	216887	49083	AGGCCACAGAAAATGACCAG	261474	93670	GCGGCCAAGGCCCTCTGTGT
172301	4497	CTCTTCCCGTCACCTGCTGA	216888	49084	AAGGCCACAGAAAATGACCA	261475	93671	AGCGGCCAAGGCCCTCTGTG
172302	4498	TCTCTTCCCGTCACCTGCTG	216889	49085	AAAGGCCACAGAAAATGACC	261476	93672	AAGCGGCCAAGGCCCTCTGT
172303	4499	TTCTCTTCCCGTCACCTGCT	216890	49086	GAAAGGCCACAGAAAATGAC	261477	93673	GAAGCGGCCAAGGCCCTCTG
172304	4500	CTTCTCTTCCCGTCACCTGC	216891	49087	TGAAAGGCCACAGAAAATGA	261478	93674	GGAAGCGGCCAAGGCCCTCT
172305	4501	TCTTCTCTTCCCGTCACCTG	216892	49088	TTGAAAGGCCACAGAAAATG	261479	93675	TGGAAGCGGCCAAGGCCCTC
172306	4502	GTCTTCTCTTCCCGTCACCT	216893	49089	TTTGAAAGGCCACAGAAAAT	261480	93676	ATGGAAGCGGCCAAGGCCCT
172307	4503	GGTCTTCTCTTCCCGTCACC	216894	49090	GTTTGAAAGGCCACAGAAAA	261481	93677	CATGGAAGCGGCCAAGGCCC
172308	4504	GGGTCTTCTCTTCCCGTCAC	216895	49091	AGTTTGAAAGGCCACAGAAA	261482	93678	CCATGGAAGCGGCCAAGGCC
172309	4505	GGGGTCTTCTCTTCCCGTCA	216896	49092	GAGTTTGAAAGGCCACAGAA	261483	93679	CCCATGGAAGCGGCCAAGGC
172310	4506	TGGGGTCTTCTCTTCCCGTC	216897	49093	GGAGTTTGAAAGGCCACAGA	261484	93680	CCCCATGGAAGCGGCCAAGG
172311	4507	CTGGGGTCTTCTCTTCCCGT	216898	49094	GGGAGTTTGAAAGGCCACAG	261485	93681	TCCCCATGGAAGCGGCCAAG
172312	4508	GCTGGGGTCTTCTCTTCCCG	216899	49095	TGGGAGTTTGAAAGGCCACA	261486	93682	TTCCCCATGGAAGCGGCCAA
172313	4509	GGCTGGGGTCTTCTCTTCCC	216900	49096	GTGGGAGTTTGAAAGGCCAC	261487	93683	ATTCCCCATGGAAGCGGCCA
172314	4510	AGGCTGGGGTCTTCTCTTCC	216901	49097	GGTGGGAGTTTGAAAGGCCA	261488	93684	AATTCCCCATGGAAGCGGCC
172315	4511	GAGGCTGGGGTCTTCTCTTC	216902	49098	AGGTGGGAGTTTGAAAGGCC	261489	93685	CAATTCCCCATGGAAGCGGC
172316	4512	TGAGGCTGGGGTCTTCTCTT	216903	49099	TAGGTGGGAGTTTGAAAGGC	261490	93686	CCAATTCCCCATGGAAGCGG
172317	4513	GTGAGGCTGGGGTCTTCTCT	216904	49100	GTAGGTGGGAGTTTGAAAGG	261491	93687	TCCAATTCCCCATGGAAGCG
172318	4514	GGTGAGGCTGGGGTCTTCTC	216905	49101	GGTAGGTGGGAGTTTGAAAG	261492	93688	TTCCAATTCCCCATGGAAGC
172319	4515	TGGTGAGGCTGGGGTCTTCT	216906	49102	GGGTAGGTGGGAGTTTGAAA	261493	93689	TTTCCAATTCCCCATGGAAG
172320	4516	CTGGTGAGGCTGGGGTCTTC	216907	49103	GGGGTAGGTGGGAGTTTGAA	261494	93690	CTTTCCAATTCCCCATGGAA
172321	4517	GCTGGTGAGGCTGGGGTCTT	216908	49104	TGGGGTAGGTGGGAGTTTGA	261495	93691	GCTTTCCAATTCCCCATGGA
172322	4518	AGCTGGTGAGGCTGGGGTCT	216909	49105	GTGGGGTAGGTGGGAGTTTG	261496	93692	TGCTTTCCAATTCCCCATGG
172323	4519	CAGCTGGTGAGGCTGGGGTC	216910	49106	AGTGGGGTAGGTGGGAGTTT	261497	93693	TTGCTTTCCAATTCCCCATG
172324	4520	CCAGCTGGTGAGGCTGGGGT	216911	49107	CAGTGGGGTAGGTGGGAGTT	261498	93694	ATTGCTTTCCAATTCCCCAT
172325	4521	CCCAGCTGGTGAGGCTGGGG	216912	49108	GCAGTGGGGTAGGTGGGAGT	261499	93695	TATTGCTTTCCAATTCCCCA
172326	4522	GCCCAGCTGGTGAGGCTGGG	216913	49109	AGCAGTGGGGTAGGTGGGAG	261500	93696	TTATTGCTTTCCAATTCCCC
172327	4523	AGCCCAGCTGGTGAGGCTGG	216914	49110	GAGCAGTGGGGTAGGTGGGA	261501	93697	CTTATTGCTTTCCAATTCCC
172328	4524	CAGCCCAGCTGGTGAGGCTG	216915	49111	GGAGCAGTGGGGTAGGTGGG	261502	93698	TCTTATTGCTTTCCAATTCC
172329	4525	GCAGCCCAGCTGGTGAGGCT	216916	49112	AGGAGCAGTGGGGTAGGTGG	261503	93699	ATCTTATTGCTTTCCAATTC
172330	4526	TGCAGCCCAGCTGGTGAGGC	216917	49113	CAGGAGCAGTGGGGTAGGTG	261504	93700	TATCTTATTGCTTTCCAATT
172331	4527	CTGCAGCCCAGCTGGTGAGG	216918	49114	CCAGGAGCAGTGGGGTAGGT	261505	93701	CTATCTTATTGCTTTCCAAT
172332	4528	GCTGCAGCCCAGCTGGTGAG	216919	49115	CCCAGGAGCAGTGGGGTAGG	261506	93702	GCTATCTTATTGCTTTCCAA
172333	4529	TGCTGCAGCCCAGCTGGTGA	216920	49116	ACCCAGGAGCAGTGGGGTAG	261507	93703	TGCTATCTTATTGCTTTCCA
172334	4530	CTGCTGCAGCCCAGCTGGTG	216921	49117	CACCCAGGAGCAGTGGGGTA	261508	93704	ATGCTATCTTATTGCTTTCC
172335	4531	CCTGCTGCAGCCCAGCTGGT	216922	49118	GCACCCAGGAGCAGTGGGGT	261509	93705	GATGCTATCTTATTGCTTTC
172336	4532	CCCTGCTGCAGCCCAGCTGG	216923	49119	TGCACCCAGGAGCAGTGGGG	261510	93706	GGATGCTATCTTATTGCTTT
172337	4533	TCCCTGCTGCAGCCCAGCTG	216924	49120	ATGCACCCAGGAGCAGTGGG	261511	93707	GGGATGCTATCTTATTGCTT
172338	4534	CTCCCTGCTGCAGCCCAGCT	216925	49121	AATGCACCCAGGAGCAGTGG	261512	93708	GGGGATGCTATCTTATTGCT

172339	4535	TCTCCCTGCTGCAGCCCAGC	216926	49122	TAATGCACCCAGGAGCAGTG	261513	93709	AGGGGATGCTATCTTATTGC
172340	4536	CTCTCCCTGCTGCAGCCCAG	216927	49123	GTAATGCACCCAGGAGCAGT	261514	93710	TAGGGGATGCTATCTTATTG
172341	4537	CCTCTCCCTGCTGCAGCCCA	216928	49124	GGTAATGCACCCAGGAGCAG	261515	93711	CTAGGGGATGCTATCTTATT
172342	4538	TCCTCTCCCTGCTGCAGCCC	216929	49125	GGGTAATGCACCCAGGAGCA	261516	93712	TCTAGGGGATGCTATCTTAT
172343	4539	CTCCTCTCCCTGCTGCAGCC	216930	49126	CGGGTAATGCACCCAGGAGC	261517	93713	TTCTAGGGGATGCTATCTTA
172344	4540	ACTCCTCTCCCTGCTGCAGC	216931	49127	TCGGGTAATGCACCCAGGAG	261518	93714	CTTCTAGGGGATGCTATCTT
172345	4541	GACTCCTCTCCCTGCTGCAG	216932	49128	TTCGGGTAATGCACCCAGGA	261519	93715	GCTTCTAGGGGATGCTATCT
172346	4542	GGACTCCTCTCCCTGCTGCA	216933	49129	TTTCGGGTAATGCACCCAGG	261520	93716	GGCTTCTAGGGGATGCTATC
172347	4543	AGGACTCCTCTCCCTGCTGC	216934	49130	CTTTCGGGTAATGCACCCAG	261521	93717	GGGCTTCTAGGGGATGCTAT
172348	4544	GAGGACTCCTCTCCCTGCTG	216935	49131	GCTTTCGGGTAATGCACCCA	261522	93718	TGGGCTTCTAGGGGATGCTA
172349	4545	TGAGGACTCCTCTCCCTGCT	216936	49132	AGCTTTCGGGTAATGCACCC	261523	93719	CTGGGCTTCTAGGGGATGCT
172350	4546	ATGAGGACTCCTCTCCCTGC	216937	49133	CAGCTTTCGGGTAATGCACC	261524	93720	ACTGGGCTTCTAGGGGATGC
172351	4547	CATGAGGACTCCTCTCCCTG	216938	49134	TCAGCTTTCGGGTAATGCAC	261525	93721	CACTGGGCTTCTAGGGGATG
172352	4548	ACATGAGGACTCCTCTCCCT	216939	49135	CTCAGCTTTCGGGTAATGCA	261526	93722	TCACTGGGCTTCTAGGGGAT
172353	4549	AACATGAGGACTCCTCTCCC	216940	49136	TCTCAGCTTTCGGGTAATGC	261527	93723	TTCACTGGGCTTCTAGGGGA
172354	4550	GAACATGAGGACTCCTCTCC	216941	49137	GTCTCAGCTTTCGGGTAATG	261528	93724	CTTCACTGGGCTTCTAGGGG
172355	4551	GGAACATGAGGACTCCTCTC	216942	49138	AGTCTCAGCTTTCGGGTAAT	261529	93725	ACTTCACTGGGCTTCTAGGG
172356	4552	TGGAACATGAGGACTCCTCT	216943	49139	AAGTCTCAGCTTTCGGGTAA	261530	93726	GACTTCACTGGGCTTCTAGG
172357	4553	CTGGAACATGAGGACTCCTC	216944	49140	GAAGTCTCAGCTTTCGGGTA	261531	93727	AGACTTCACTGGGCTTCTAG
172358	4554	GCTGGAACATGAGGACTCCT	216945	49141	TGAAGTCTCAGCTTTCGGGT	261532	93728	CAGACTTCACTGGGCTTCTA
172359	4555	TGCTGGAACATGAGGACTCC	216946	49142	CTGAAGTCTCAGCTTTCGGG	261533	93729	CCAGACTTCACTGGGCTTCT
172360	4556	CTGCTGGAACATGAGGACTC	216947	49143	ACTGAAGTCTCAGCTTTCGG	261534	93730	CCCAGACTTCACTGGGCTTC
172361	4557	CCTGCTGGAACATGAGGACT	216948	49144	CACTGAAGTCTCAGCTTTCG	261535	93731	TCCCAGACTTCACTGGGCTT
172362	4558	CCCTGCTGGAACATGAGGAC	216949	49145	GCACTGAAGTCTCAGCTTTC	261536	93732	GTCCCAGACTTCACTGGGCT
172363	4559	TCCCTGCTGGAACATGAGGA	216950	49146	TGCACTGAAGTCTCAGCTTT	261537	93733	TGTCCCAGACTTCACTGGGC
172364	4560	GTCCCTGCTGGAACATGAGG	216951	49147	CTGCACTGAAGTCTCAGCTT	261538	93734	CTGTCCCAGACTTCACTGGG
172365	4561	AGTCCCTGCTGGAACATGAG	216952	49148	TCTGCACTGAAGTCTCAGCT	261539	93735	CCTGTCCCAGACTTCACTGG
172366	4562	GAGTCCCTGCTGGAACATGA	216953	49149	TTCTGCACTGAAGTCTCAGC	261540	93736	TCCTGTCCCAGACTTCACTG
172367	4563	AGAGTCCCTGCTGGAACATG	216954	49150	TTTCTGCACTGAAGTCTCAG	261541	93737	GTCCTGTCCCAGACTTCACT
172368	4564	GAGAGTCCCTGCTGGAACAT	216955	49151	CTTTCTGCACTGAAGTCTCA	261542	93738	GGTCCTGTCCCAGACTTCAC
172369	4565	TGAGAGTCCCTGCTGGAACA	216956	49152	ACTTTCTGCACTGAAGTCTC	261543	93739	GGGTCCTGTCCCAGACTTCA
172370	4566	CTGAGAGTCCCTGCTGGAAC	216957	49153	CACTTTCTGCACTGAAGTCT	261544	93740	AGGGTCCTGTCCCAGACTTC
172371	4567	GCTGAGAGTCCCTGCTGGAA	216958	49154	GCACTTTCTGCACTGAAGTC	261545	93741	AAGGGTCCTGTCCCAGACTT
172372	4568	AGCTGAGAGTCCCTGCTGGA	216959	49155	GGCACTTTCTGCACTGAAGT	261546	93742	GAAGGGTCCTGTCCCAGACT
172373	4569	CAGCTGAGAGTCCCTGCTGG	216960	49156	TGGCACTTTCTGCACTGAAG	261547	93743	AGAAGGGTCCTGTCCCAGAC
172374	4570	ACAGCTGAGAGTCCCTGCTG	216961	49157	CTGGCACTTTCTGCACTGAA	261548	93744	GAGAAGGGTCCTGTCCCAGA
172375	4571	AACAGCTGAGAGTCCCTGCT	216962	49158	CCTGGCACTTTCTGCACTGA	261549	93745	AGAGAAGGGTCCTGTCCCAG
172376	4572	AAACAGCTGAGAGTCCCTGC	216963	49159	GCCTGGCACTTTCTGCACTG	261550	93746	CAGAGAAGGGTCCTGTCCCA
172377	4573	AAAACAGCTGAGAGTCCCTG	216964	49160	GGCCTGGCACTTTCTGCACT	261551	93747	TCAGAGAAGGGTCCTGTCCC
172378	4574	GAAAACAGCTGAGAGTCCCT	216965	49161	GGGCCTGGCACTTTCTGCAC	261552	93748	CTCAGAGAAGGGTCCTGTCC
172379	4575	GGAAAACAGCTGAGAGTCCC	216966	49162	AGGGCCTGGCACTTTCTGCA	261553	93749	GCTCAGAGAAGGGTCCTGTC
172380	4576	AGGAAAACAGCTGAGAGTCC	216967	49163	GAGGGCCTGGCACTTTCTGC	261554	93750	AGCTCAGAGAAGGGTCCTGT
172381	4577	CAGGAAAACAGCTGAGAGTC	216968	49164	AGAGGGCCTGGCACTTTCTG	261555	93751	GAGCTCAGAGAAGGGTCCTG
172382	4578	ACAGGAAAACAGCTGAGAGT	216969	49165	CAGAGGGCCTGGCACTTTCT	261556	93752	AGAGCTCAGAGAAGGGTCCT
172383	4579	TACAGGAAAACAGCTGAGAG	216970	49166	ACAGAGGGCCTGGCACTTTC	261557	93753	CAGAGCTCAGAGAAGGGTCC
172384	4580	TTACAGGAAAACAGCTGAGA	216971	49167	GACAGAGGGCCTGGCACTTT	261558	93754	TCAGAGCTCAGAGAAGGGTC
172385	4581	TTTACAGGAAAACAGCTGAG	216972	49168	GGACAGAGGGCCTGGCACTT	261559	93755	GTCAGAGCTCAGAGAAGGGT
172386	4582	TTTTACAGGAAAACAGCTGA	216973	49169	GGGACAGAGGGCCTGGCACT	261560	93756	AGTCAGAGCTCAGAGAAGGG
172387	4583	GTTTTACAGGAAAACAGCTG	216974	49170	GGGGACAGAGGGCCTGGCAC	261561	93757	AAGTCAGAGCTCAGAGAAGG
172388	4584	GGTTTTACAGGAAAACAGCT	216975	49171	GGGGGACAGAGGGCCTGGCA	261562	93758	CAAGTCAGAGCTCAGAGAAG
172389	4585	TGGTTTTACAGGAAAACAGC	216976	49172	GGGGGGACAGAGGGCCTGGC	261563	93759	GCAAGTCAGAGCTCAGAGAA
172390	4586	ATGGTTTTACAGGAAAACAG	216977	49173	TGGGGGGACAGAGGGCCTGG	261564	93760	AGCAAGTCAGAGCTCAGAGA
172391	4587	CATGGTTTTACAGGAAAACA	216978	49174	CTGGGGGGACAGAGGGCCTG	261565	93761	GAGCAAGTCAGAGCTCAGAG
172392	4588	CCATGGTTTTACAGGAAAAC	216979	49175	TCTGGGGGGACAGAGGGCCT	261566	93762	AGAGCAAGTCAGAGCTCAGA
172393	4589	ACCATGGTTTTACAGGAAAA	216980	49176	ATCTGGGGGGACAGAGGGCC	261567	93763	AAGAGCAAGTCAGAGCTCAG
172394	4590	AACCATGGTTTTACAGGAAA	216981	49177	GATCTGGGGGGACAGAGGGC	261568	93764	CAAGAGCAAGTCAGAGCTCA
172395	4591	GAACCATGGTTTTACAGGAA	216982	49178	CGATCTGGGGGGACAGAGGG	261569	93765	CCAAGAGCAAGTCAGAGCTC
172396	4592	AGAACCATGGTTTTACAGGA	216983	49179	GCGATCTGGGGGGACAGAGG	261570	93766	TCCAAGAGCAAGTCAGAGCT
172397	4593	GAGAACCATGGTTTTACAGG	216984	49180	GGCGATCTGGGGGGACAGAG	261571	93767	TTCCAAGAGCAAGTCAGAGC
172398	4594	TGAGAACCATGGTTTTACAG	216985	49181	AGGCGATCTGGGGGGACAGA	261572	93768	TTTCCAAGAGCAAGTCAGAG
172399	4595	TTGAGAACCATGGTTTTACA	216986	49182	AAGGCGATCTGGGGGGACAG	261573	93769	GTTTCCAAGAGCAAGTCAGA
172400	4596	GTTGAGAACCATGGTTTTAC	216987	49183	GAAGGCGATCTGGGGGGACA	261574	93770	TGTTTCCAAGAGCAAGTCAG
172401	4597	AGTTGAGAACCATGGTTTTA	216988	49184	GGAAGGCGATCTGGGGGGAC	261575	93771	GTGTTTCCAAGAGCAAGTCA
172402	4598	CAGTTGAGAACCATGGTTTT	216989	49185	AGGAAGGCGATCTGGGGGGA	261576	93772	AGTGTTTCCAAGAGCAAGTC
172403	4599	CCAGTTGAGAACCATGGTTT	216990	49186	AAGGAAGGCGATCTGGGGGG	261577	93773	AAGTGTTTCCAAGAGCAAGT
172404	4600	CCCAGTTGAGAACCATGGTT	216991	49187	CAAGGAAGGCGATCTGGGGG	261578	93774	GAAGTGTTTCCAAGAGCAAG
172405	4601	CCCCAGTTGAGAACCATGGT	216992	49188	ACAAGGAAGGCGATCTGGGG	261579	93775	CGAAGTGTTTCCAAGAGCAA
172406	4602	CCCCCAGTTGAGAACCATGG	216993	49189	GACAAGGAAGGCGATCTGGG	261580	93776	TCGAAGTGTTTCCAAGAGCA
172407	4603	GCCCCCAGTTGAGAACCATG	216994	49190	AGACAAGGAAGGCGATCTGG	261581	93777	CTCGAAGTGTTTCCAAGAGC
172408	4604	GGCCCCCAGTTGAGAACCAT	216995	49191	AAGACAAGGAAGGCGATCTG	261582	93778	CCTCGAAGTGTTTCCAAGAG
172409	4605	TGGCCCCCAGTTGAGAACCA	216996	49192	GAAGACAAGGAAGGCGATCT	261583	93779	GCCTCGAAGTGTTTCCAAGA
172410	4606	GTGGCCCCCAGTTGAGAACC	216997	49193	GGAAGACAAGGAAGGCGATC	261584	93780	AGCCTCGAAGTGTTTCCAAG

172411	4607	AGTGGCCCCCAGTTGAGAAC	216998	49194	GGGAAGACAAGGAAGGCGAT	261585	93781	AAGCCTCGAAGTGTTTCCAA
172412	4608	CAGTGGCCCCCAGTTGAGAA	216999	49195	AGGGAAGACAAGGAAGGCGA	261586	93782	TAAGCCTCGAAGTGTTTCCA
172413	4609	TCAGTGGCCCCCAGTTGAGA	217000	49196	CAGGGAAGACAAGGAAGGCG	261587	93783	CTAAGCCTCGAAGTGTTTCC
172414	4610	CTCAGTGGCCCCCAGTTGAG	217001	49197	ACAGGGAAGACAAGGAAGGC	261588	93784	GCTAAGCCTCGAAGTGTTTC
172415	4611	TCTCAGTGGCCCCCAGTTGA	217002	49198	CACAGGGAAGACAAGGAAGG	261589	93785	GGCTAAGCCTCGAAGTGTTT
172416	4612	ATCTCAGTGGCCCCCAGTTG	217003	49199	GCACAGGGAAGACAAGGAAG	261590	93786	AGGCTAAGCCTCGAAGTGTT
172417	4613	CATCTCAGTGGCCCCCAGTT	217004	49200	AGCACAGGGAAGACAAGGAA	261591	93787	GAGGCTAAGCCTCGAAGTGT
172418	4614	ACATCTCAGTGGCCCCCAGT	217005	49201	AAGCACAGGGAAGACAAGGA	261592	93788	GGAGGCTAAGCCTCGAAGTG
172419	4615	GACATCTCAGTGGCCCCCAG	217006	49202	CAAGCACAGGGAAGACAAGG	261593	93789	GGGAGGCTAAGCCTCGAAGT
172420	4616	AGACATCTCAGTGGCCCCCA	217007	49203	GCAAGCACAGGGAAGACAAG	261594	93790	GGGGAGGCTAAGCCTCGAAG
172421	4617	TAGACATCTCAGTGGCCCCC	217008	49204	GGCAAGCACAGGGAAGACAA	261595	93791	TGGGGAGGCTAAGCCTCGAA
172422	4618	CTAGACATCTCAGTGGCCCC	217009	49205	AGGCAAGCACAGGGAAGACA	261596	93792	GTGGGGAGGCTAAGCCTCGA
172423	4619	TCTAGACATCTCAGTGGCCC	217010	49206	CAGGCAAGCACAGGGAAGAC	261597	93793	AGTGGGGAGGCTAAGCCTCG
172424	4620	CTCTAGACATCTCAGTGGCC	217011	49207	ACAGGCAAGCACAGGGAAGA	261598	93794	AAGTGGGGAGGCTAAGCCTC
172425	4621	TCTCTAGACATCTCAGTGGC	217012	49208	GACAGGCAAGCACAGGGAAG	261599	93795	AAAGTGGGGAGGCTAAGCCT
172426	4622	CTCTCTAGACATCTCAGTGG	217013	49209	TGACAGGCAAGCACAGGGAA	261600	93796	CAAAGTGGGGAGGCTAAGCC
172427	4623	TCTCTCTAGACATCTCAGTG	217014	49210	GTGACAGGCAAGCACAGGGA	261601	93797	ACAAAGTGGGGAGGCTAAGC
172428	4624	ATCTCTCTAGACATCTCAGT	217015	49211	TGTGACAGGCAAGCACAGGG	261602	93798	AACAAAGTGGGGAGGCTAAG
172429	4625	CATCTCTCTAGACATCTCAG	217016	49212	ATGTGACAGGCAAGCACAGG	261603	93799	AAACAAAGTGGGGAGGCTAA
172430	4626	ACATCTCTCTAGACATCTCA	217017	49213	AATGTGACAGGCAAGCACAG	261604	93800	GAAACAAAGTGGGGAGGCTA
172431	4627	AACATCTCTCTAGACATCTC	217018	49214	CAATGTGACAGGCAAGCACA	261605	93801	GGAAACAAAGTGGGGAGGCT
172432	4628	AAACATCTCTCTAGACATCT	217019	49215	ACAATGTGACAGGCAAGCAC	261606	93802	GGGAAACAAAGTGGGGAGGC
172433	4629	AAAACATCTCTCTAGACATC	217020	49216	CACAATGTGACAGGCAAGCA	261607	93803	CGGGAAACAAAGTGGGGAGG
172434	4630	AAAAACATCTCTCTAGACAT	217021	49217	ACACAATGTGACAGGCAAGC	261608	93804	TCGGGAAACAAAGTGGGGAG
172435	4631	CAAAAACATCTCTCTAGACA	217022	49218	CACACAATGTGACAGGCAAG	261609	93805	CTCGGGAAACAAAGTGGGGA
172436	4632	ACAAAAACATCTCTCTAGAC	217023	49219	CCACACAATGTGACAGGCAA	261610	93806	TCTCGGGAAACAAAGTGGGG
172437	4633	AACAAAAACATCTCTCTAGA	217024	49220	CCCACACAATGTGACAGGCA	261611	93807	CTCTCGGGAAACAAAGTGGG
172438	4634	AAACAAAAACATCTCTCTAG	217025	49221	ACCCACACAATGTGACAGGC	261612	93808	ACTCTCGGGAAACAAAGTGG
172439	4635	AAAACAAAAACATCTCTCTA	217026	49222	AACCCACACAATGTGACAGG	261613	93809	CACTCTCGGGAAACAAAGTG
172440	4636	GAAAACAAAAACATCTCTCT	217027	49223	GAACCCACACAATGTGACAG	261614	93810	ACACTCTCGGGAAACAAAGT
172441	4637	TGAAAACAAAAACATCTCTC	217028	49224	GGAACCCACACAATGTGACA	261615	93811	CACACTCTCGGGAAACAAAG
172442	4638	GTGAAAACAAAAACATCTCT	217029	49225	TGGAACCCACACAATGTGAC	261616	93812	TCACACTCTCGGGAAACAAA
172443	4639	TGTGAAAACAAAAACATCTC	217030	49226	CTGGAACCCACACAATGTGA	261617	93813	GTCACACTCTCGGGAAACAA
172444	4640	TTGTGAAAACAAAAACATCT	217031	49227	GCTGGAACCCACACAATGTG	261618	93814	GGTCACACTCTCGGGAAACA
172445	4641	GTTGTGAAAACAAAAACATC	217032	49228	CGCTGGAACCCACACAATGT	261619	93815	AGGTCACACTCTCGGGAAAC
172446	4642	AGTTGTGAAAACAAAAACAT	217033	49229	GCGCTGGAACCCACACAATG	261620	93816	CAGGTCACACTCTCGGGAAA
172447	4643	GAGTTGTGAAAACAAAAACA	217034	49230	AGCGCTGGAACCCACACAAT	261621	93817	ACAGGTCACACTCTCGGGAA
172448	4644	CGAGTTGTGAAAACAAAAAC	217035	49231	CAGCGCTGGAACCCACACAA	261622	93818	AACAGGTCACACTCTCGGGA
172449	4645	CCGAGTTGTGAAAACAAAAA	217036	49232	CCAGCGCTGGAACCCACACA	261623	93819	GAACAGGTCACACTCTCGGG
172450	4646	CCCGAGTTGTGAAAACAAAA	217037	49233	TCCAGCGCTGGAACCCACAC	261624	93820	GGAACAGGTCACACTCTCGG
172451	4647	CCCCGAGTTGTGAAAACAAA	217038	49234	TTCCAGCGCTGGAACCCACA	261625	93821	GGGAACAGGTCACACTCTCG
172452	4648	TCCCCGAGTTGTGAAAACAA	217039	49235	CTTCCAGCGCTGGAACCCAC	261626	93822	GGGGAACAGGTCACACTCTC
172453	4649	CTCCCCGAGTTGTGAAAACA	217040	49236	CCTTCCAGCGCTGGAACCCA	261627	93823	AGGGGAACAGGTCACACTCT
172454	4650	CCTCCCCGAGTTGTGAAAAC	217041	49237	TCCTTCCAGCGCTGGAACCC	261628	93824	GAGGGGAACAGGTCACACTC
172455	4651	CCCTCCCCGAGTTGTGAAAA	217042	49238	TTCCTTCCAGCGCTGGAACC	261629	93825	GGAGGGGAACAGGTCACACT
172456	4652	ACCCTCCCCGAGTTGTGAAA	217043	49239	ATTCCTTCCAGCGCTGGAAC	261630	93826	TGGAGGGGAACAGGTCACAC
172457	4653	CACCCTCCCCGAGTTGTGAA	217044	49240	CATTCCTTCCAGCGCTGGAA	261631	93827	TTGGAGGGGAACAGGTCACA
172458	4654	GCACCCTCCCCGAGTTGTGA	217045	49241	TCATTCCTTCCAGCGCTGGA	261632	93828	TTTGGAGGGGAACAGGTCAC
172459	4655	AGCACCCTCCCCGAGTTGTG	217046	49242	CTCATTCCTTCCAGCGCTGG	261633	93829	GTTTGGAGGGGAACAGGTCA
172460	4656	TAGCACCCTCCCCGAGTTGT	217047	49243	CCTCATTCCTTCCAGCGCTG	261634	93830	TGTTTGGAGGGGAACAGGTC
172461	4657	GTAGCACCCTCCCCGAGTTG	217048	49244	TCCTCATTCCTTCCAGCGCT	261635	93831	GTGTTTGGAGGGGAACAGGT
172462	4658	AGTAGCACCCTCCCCGAGTT	217049	49245	TTCCTCATTCCTTCCAGCGC	261636	93832	GGTGTTTGGAGGGGAACAGG
172463	4659	CAGTAGCACCCTCCCCGAGT	217050	49246	GTTCCTCATTCCTTCCAGCG	261637	93833	GGGTGTTTGGAGGGGAACAG
172464	4660	TCAGTAGCACCCTCCCCGAG	217051	49247	TGTTCCTCATTCCTTCCAGC	261638	93834	GGGGTGTTTGGAGGGGAACA
172465	4661	GTCAGTAGCACCCTCCCCGA	217052	49248	CTGTTCCTCATTCCTTCCAG	261639	93835	GGGGGTGTTTGGAGGGGAAC
172466	4662	TGTCAGTAGCACCCTCCCCG	217053	49249	TCTGTTCCTCATTCCTTCCA	261640	93836	AGGGGGTGTTTGGAGGGGAA
172467	4663	ATGTCAGTAGCACCCTCCCC	217054	49250	ATCTGTTCCTCATTCCTTCC	261641	93837	AAGGGGGTGTTTGGAGGGGA
172468	4664	GATGTCAGTAGCACCCTCCC	217055	49251	AATCTGTTCCTCATTCCTTC	261642	93838	GAAGGGGGTGTTTGGAGGGG
172469	4665	AGATGTCAGTAGCACCCTCC	217056	49252	GAATCTGTTCCTCATTCCTT	261643	93839	AGAAGGGGGTGTTTGGAGGG
172470	4666	AAGATGTCAGTAGCACCCTC	217057	49253	AGAATCTGTTCCTCATTCCT	261644	93840	GAGAAGGGGGTGTTTGGAGG
172471	4667	CAAGATGTCAGTAGCACCCT	217058	49254	GAGAATCTGTTCCTCATTCC	261645	93841	GGAGAAGGGGGTGTTTGGAG
172472	4668	ACAAGATGTCAGTAGCACCC	217059	49255	AGAGAATCTGTTCCTCATTC	261646	93842	AGGAGAAGGGGGTGTTTGGA
172473	4669	CACAAGATGTCAGTAGCACC	217060	49256	CAGAGAATCTGTTCCTCATT	261647	93843	GAGGAGAAGGGGGTGTTTGG
172474	4670	CCACAAGATGTCAGTAGCAC	217061	49257	CCAGAGAATCTGTTCCTCAT	261648	93844	GGAGGAGAAGGGGGTGTTTG
172475	4671	CCCACAAGATGTCAGTAGCA	217062	49258	ACCAGAGAATCTGTTCCTCA	261649	93845	TGGAGGAGAAGGGGGTGTTT
172476	4672	ACCCACAAGATGTCAGTAGC	217063	49259	AACCAGAGAATCTGTTCCTC	261650	93846	CTGGAGGAGAAGGGGGTGTT
172477	4673	TACCCACAAGATGTCAGTAG	217064	49260	GAACCAGAGAATCTGTTCCT	261651	93847	CCTGGAGGAGAAGGGGGTGT
172478	4674	CTACCCACAAGATGTCAGTA	217065	49261	AGAACCAGAGAATCTGTTCC	261652	93848	CCCTGGAGGAGAAGGGGGTG
172479	4675	TCTACCCACAAGATGTCAGT	217066	49262	GAGAACCAGAGAATCTGTTC	261653	93849	GCCCTGGAGGAGAAGGGGGT
172480	4676	CTCTACCCACAAGATGTCAG	217067	49263	GGAGAACCAGAGAATCTGTT	261654	93850	GGCCCTGGAGGAGAAGGGGG
172481	4677	CCTCTACCCACAAGATGTCA	217068	49264	AGGAGAACCAGAGAATCTGT	261655	93851	TGGCCCTGGAGGAGAAGGGG
172482	4678	GCCTCTACCCACAAGATGTC	217069	49265	AAGGAGAACCAGAGAATCTG	261656	93852	ATGGCCCTGGAGGAGAAGGG

172483	4679	GGCCTCTACCCACAAGATGT	217070	49266	AAAGGAGAACCAGAGAATCT	261657	93853	CATGGCCCTGGAGGAGAAGG
172484	4680	TGGCCTCTACCCACAAGATG	217071	49267	AAAAGGAGAACCAGAGAATC	261658	93854	GCATGGCCCTGGAGGAGAAG
172485	4681	CTGGCCTCTACCCACAAGAT	217072	49268	CAAAAGGAGAACCAGAGAAT	261659	93855	GGCATGGCCCTGGAGGAGAA
172486	4682	CCTGGCCTCTACCCACAAGA	217073	49269	TCAAAAGGAGAACCAGAGAA	261660	93856	GGGCATGGCCCTGGAGGAGA
172487	4683	TCCTGGCCTCTACCCACAAG	217074	49270	TTCAAAAGGAGAACCAGAGA	261661	93857	TGGGCATGGCCCTGGAGGAG
172488	4684	TTCCTGGCCTCTACCCACAA	217075	49271	CTTCAAAAGGAGAACCAGAG	261662	93858	GTGGGCATGGCCCTGGAGGA
172489	4685	ATTCCTGGCCTCTACCCACA	217076	49272	ACTTCAAAAGGAGAACCAGA	261663	93859	GGTGGGCATGGCCCTGGAGG
172490	4686	CATTCCTGGCCTCTACCCAC	217077	49273	AACTTCAAAAGGAGAACCAG	261664	93860	GGGTGGGCATGGCCCTGGAG
172491	4687	GCATTCCTGGCCTCTACCCA	217078	49274	AAACTTCAAAAGGAGAACCA	261665	93861	CGGGTGGGCATGGCCCTGGA
172492	4688	AGCATTCCTGGCCTCTACCC	217079	49275	TAAACTTCAAAAGGAGAACC	261666	93862	ACGGGTGGGCATGGCCCTGG
172493	4689	CAGCATTCCTGGCCTCTACC	217080	49276	GTAAACTTCAAAAGGAGAAC	261667	93863	GACGGGTGGGCATGGCCCTG
172494	4690	ACAGCATTCCTGGCCTCTAC	217081	49277	GGTAAACTTCAAAAGGAGAA	261668	93864	TGACGGGTGGGCATGGCCCT
172495	4691	AACAGCATTCCTGGCCTCTA	217082	49278	AGGTAAACTTCAAAAGGAGA	261669	93865	TTGACGGGTGGGCATGGCCC
172496	4692	TAACAGCATTCCTGGCCTCT	217083	49279	AAGGTAAACTTCAAAAGGAG	261670	93866	TTTGACGGGTGGGCATGGCC
172497	4693	TTAACAGCATTCCTGGCCTC	217084	49280	GAAGGTAAACTTCAAAAGGA	261671	93867	TTTTGACGGGTGGGCATGGC
172498	4694	TTTAACAGCATTCCTGGCCT	217085	49281	CGAAGGTAAACTTCAAAAGG	261672	93868	ATTTTGACGGGTGGGCATGG
172499	4695	GTTTAACAGCATTCCTGGCC	217086	49282	GCGAAGGTAAACTTCAAAAG	261673	93869	GATTTTGACGGGTGGGCATG
172500	4696	TGTTTAACAGCATTCCTGGC	217087	49283	AGCGAAGGTAAACTTCAAAA	261674	93870	GGATTTTGACGGGTGGGCAT
172501	4697	ATGTTTAACAGCATTCCTGG	217088	49284	GAGCGAAGGTAAACTTCAAA	261675	93871	GGGATTTTGACGGGTGGGCA
172502	4698	GATGTTTAACAGCATTCCTG	217089	49285	GGAGCGAAGGTAAACTTCAA	261676	93872	GGGGATTTTGACGGGTGGGC
172503	4699	GGATGTTTAACAGCATTCCT	217090	49286	TGGAGCGAAGGTAAACTTCA	261677	93873	GGGGGATTTTGACGGGTGGG
172504	4700	AGGATGTTTAACAGCATTCC	217091	49287	GTGGAGCGAAGGTAAACTTC	261678	93874	TGGGGGATTTTGACGGGTGG
172505	4701	TAGGATGTTTAACAGCATTC	217092	49288	GGTGGAGCGAAGGTAAACTT	261679	93875	GTGGGGGATTTTGACGGGTG
172506	4702	GTAGGATGTTTAACAGCATT	217093	49289	TGGTGGAGCGAAGGTAAACT	261680	93876	CGTGGGGGATTTTGACGGGT
172507	4703	TGTAGGATGTTTAACAGCAT	217094	49290	GTGGTGGAGCGAAGGTAAAC	261681	93877	CCGTGGGGGATTTTGACGGG
172508	4704	TTGTAGGATGTTTAACAGCA	217095	49291	AGTGGTGGAGCGAAGGTAAA	261682	93878	CCCGTGGGGGATTTTGACGG
172509	4705	CTTGTAGGATGTTTAACAGC	217096	49292	AAGTGGTGGAGCGAAGGTAA	261683	93879	GCCCGTGGGGGATTTTGACG
172510	4706	CCTTGTAGGATGTTTAACAG	217097	49293	GAAGTGGTGGAGCGAAGGTA	261684	93880	TGCCCGTGGGGGATTTTGAC
172511	4707	TCCTTGTAGGATGTTTAACA	217098	49294	AGAAGTGGTGGAGCGAAGGT	261685	93881	CTGCCCGTGGGGGATTTTGA
172512	4708	TTCCTTGTAGGATGTTTAAC	217099	49295	CAGAAGTGGTGGAGCGAAGG	261686	93882	CCTGCCCGTGGGGGATTTTG
172513	4709	CTTCCTTGTAGGATGTTTAA	217100	49296	TCAGAAGTGGTGGAGCGAAG	261687	93883	TCCTGCCCGTGGGGGATTTT
172514	4710	CCTTCCTTGTAGGATGTTTA	217101	49297	CTCAGAAGTGGTGGAGCGAA	261688	93884	GTCCTGCCCGTGGGGGATTT
172515	4711	GCCTTCCTTGTAGGATGTTT	217102	49298	TCTCAGAAGTGGTGGAGCGA	261689	93885	CGTCCTGCCCGTGGGGGATT
172516	4712	TGCCTTCCTTGTAGGATGTT	217103	49299	GTCTCAGAAGTGGTGGAGCG	261690	93886	TCGTCCTGCCCGTGGGGGAT
172517	4713	GTGCCTTCCTTGTAGGATGT	217104	49300	GGTCTCAGAAGTGGTGGAGC	261691	93887	TTCGTCCTGCCCGTGGGGGA
172518	4714	TGTGCCTTCCTTGTAGGATG	217105	49301	AGGTCTCAGAAGTGGTGGAG	261692	93888	GTTCGTCCTGCCCGTGGGGG
172519	4715	CTGTGCCTTCCTTGTAGGAT	217106	49302	AAGGTCTCAGAAGTGGTGGA	261693	93889	AGTTCGTCCTGCCCGTGGGG
172520	4716	CCTGTGCCTTCCTTGTAGGA	217107	49303	GAAGGTCTCAGAAGTGGTGG	261694	93890	CAGTTCGTCCTGCCCGTGGG
172521	4717	TCCTGTGCCTTCCTTGTAGG	217108	49304	GGAAGGTCTCAGAAGTGGTG	261695	93891	ACAGTTCGTCCTGCCCGTGG
172522	4718	GTCCTGTGCCTTCCTTGTAG	217109	49305	GGGAAGGTCTCAGAAGTGGT	261696	93892	CACAGTTCGTCCTGCCCGTG
172523	4719	TGTCCTGTGCCTTCCTTGTA	217110	49306	CGGGAAGGTCTCAGAAGTGG	261697	93893	CCACAGTTCGTCCTGCCCGT
172524	4720	CTGTCCTGTGCCTTCCTTGT	217111	49307	CCGGGAAGGTCTCAGAAGTG	261698	93894	CCCACAGTTCGTCCTGCCCG
172525	4721	ACTGTCCTGTGCCTTCCTTG	217112	49308	TCCGGGAAGGTCTCAGAAGT	261699	93895	ACCCACAGTTCGTCCTGCCC
172526	4722	GACTGTCCTGTGCCTTCCTT	217113	49309	TTCCGGGAAGGTCTCAGAAG	261700	93896	CACCCACAGTTCGTCCTGCC
172527	4723	AGACTGTCCTGTGCCTTCCT	217114	49310	CTTCCGGGAAGGTCTCAGAA	261701	93897	ACACCCACAGTTCGTCCTGC
172528	4724	GAGACTGTCCTGTGCCTTCC	217115	49311	ACTTCCGGGAAGGTCTCAGA	261702	93898	GACACCCACAGTTCGTCCTG
172529	4725	GGAGACTGTCCTGTGCCTTC	217116	49312	AACTTCCGGGAAGGTCTCAG	261703	93899	TGACACCCACAGTTCGTCCT
172530	4726	AGGAGACTGTCCTGTGCCTT	217117	49313	CAACTTCCGGGAAGGTCTCA	261704	93900	CTGACACCCACAGTTCGTCC
172531	4727	TAGGAGACTGTCCTGTGCCT	217118	49314	GCAACTTCCGGGAAGGTCTC	261705	93901	ACTGACACCCACAGTTCGTC
172532	4728	GTAGGAGACTGTCCTGTGCC	217119	49315	GGCAACTTCCGGGAAGGTCT	261706	93902	GACTGACACCCACAGTTCGT
172533	4729	TGTAGGAGACTGTCCTGTGC	217120	49316	GGGCAACTTCCGGGAAGGTC	261707	93903	TGACTGACACCCACAGTTCG
172534	4730	ATGTAGGAGACTGTCCTGTG	217121	49317	GGGGCAACTTCCGGGAAGGT	261708	93904	GTGACTGACACCCACAGTTC
172535	4731	GATGTAGGAGACTGTCCTGT	217122	49318	AGGGGCAACTTCCGGGAAGG	261709	93905	GGTGACTGACACCCACAGTT
172536	4732	TGATGTAGGAGACTGTCCTG	217123	49319	AAGGGGCAACTTCCGGGAAG	261710	93906	TGGTGACTGACACCCACAGT
172537	4733	TTGATGTAGGAGACTGTCCT	217124	49320	CAAGGGGCAACTTCCGGGAA	261711	93907	ATGGTGACTGACACCCACAG
172538	4734	TTTGATGTAGGAGACTGTCC	217125	49321	ACAAGGGGCAACTTCCGGGA	261712	93908	GATGGTGACTGACACCCACA
172539	4735	TTTTGATGTAGGAGACTGTC	217126	49322	AACAAGGGGCAACTTCCGGG	261713	93909	AGATGGTGACTGACACCCAC
172540	4736	ATTTTGATGTAGGAGACTGT	217127	49323	AAACAAGGGGCAACTTCCGG	261714	93910	TAGATGGTGACTGACACCCA
172541	4737	TATTTTGATGTAGGAGACTG	217128	49324	GAAACAAGGGGCAACTTCCG	261715	93911	ATAGATGGTGACTGACACCC
172542	4738	ATATTTTGATGTAGGAGACT	217129	49325	AGAAACAAGGGGCAACTTCC	261716	93912	GATAGATGGTGACTGACACC
172543	4739	CATATTTTGATGTAGGAGAC	217130	49326	GAGAAACAAGGGGCAACTTC	261717	93913	GGATAGATGGTGACTGACAC
172544	4740	TCATATTTTGATGTAGGAGA	217131	49327	AGAGAAACAAGGGGCAACTT	261718	93914	AGGATAGATGGTGACTGACA
172545	4741	GTCATATTTTGATGTAGGAG	217132	49328	GAGAGAAACAAGGGGCAACT	261719	93915	CAGGATAGATGGTGACTGAC
172546	4742	GGTCATATTTTGATGTAGGA	217133	49329	GGAGAGAAACAAGGGGCAAC	261720	93916	GCAGGATAGATGGTGACTGA
172547	4743	GGGTCATATTTTGATGTAGG	217134	49330	AGGAGAGAAACAAGGGGCAA	261721	93917	TGCAGGATAGATGGTGACTG
172548	4744	TGGGTCATATTTTGATGTAG	217135	49331	GAGGAGAGAAACAAGGGGCA	261722	93918	ATGCAGGATAGATGGTGACT
172549	4745	CTGGGTCATATTTTGATGTA	217136	49332	AGAGGAGAGAAACAAGGGGC	261723	93919	GATGCAGGATAGATGGTGAC
172550	4746	ACTGGGTCATATTTTGATGT	217137	49333	GAGAGGAGAGAAACAAGGGG	261724	93920	GGATGCAGGATAGATGGTGA
172551	4747	GACTGGGTCATATTTTGATG	217138	49334	GGAGAGGAGAGAAACAAGGG	261725	93921	AGGATGCAGGATAGATGGTG
172552	4748	GGACTGGGTCATATTTTGAT	217139	49335	TGGAGAGGAGAGAAACAAGG	261726	93922	CAGGATGCAGGATAGATGGT
172553	4749	GGGACTGGGTCATATTTTGA	217140	49336	CTGGAGAGGAGAGAAACAAG	261727	93923	CCAGGATGCAGGATAGATGG
172554	4750	TGGGACTGGGTCATATTTTG	217141	49337	CCTGGAGAGGAGAGAAACAA	261728	93924	ACCAGGATGCAGGATAGATG

172555	4751	TTGGGACTGGGTCATATTTT	217142	49338	CCCTGGAGAGGAGAGAAACA	261729	93925	AACCAGGATGCAGGATAGAT
172556	4752	ATTGGGACTGGGTCATATTT	217143	49339	GCCCTGGAGAGGAGAGAAAC	261730	93926	GAACCAGGATGCAGGATAGA
172557	4753	CATTGGGACTGGGTCATATT	217144	49340	AGCCCTGGAGAGGAGAGAAA	261731	93927	GGAACCAGGATGCAGGATAG
172558	4754	ACATTGGGACTGGGTCATAT	217145	49341	CAGCCCTGGAGAGGAGAGAA	261732	93928	TGGAACCAGGATGCAGGATA
172559	4755	GACATTGGGACTGGGTCATA	217146	49342	GCAGCCCTGGAGAGGAGAGA	261733	93929	CTGGAACCAGGATGCAGGAT
172560	4756	TGACATTGGGACTGGGTCAT	217147	49343	GGCAGCCCTGGAGAGGAGAG	261734	93930	CCTGGAACCAGGATGCAGGA
172561	4757	GTGACATTGGGACTGGGTCA	217148	49344	GGGCAGCCCTGGAGAGGAGA	261735	93931	CCCTGGAACCAGGATGCAGG
172562	4758	GGTGACATTGGGACTGGGTC	217149	49345	GGGGCAGCCCTGGAGAGGAG	261736	93932	GCCCTGGAACCAGGATGCAG
172563	4759	TGGTGACATTGGGACTGGGT	217150	49346	TGGGGCAGCCCTGGAGAGGA	261737	93933	GGCCCTGGAACCAGGATGCA
172564	4760	GTGGTGACATTGGGACTGGG	217151	49347	CTGGGGCAGCCCTGGAGAGG	261738	93934	GGGCCCTGGAACCAGGATGC
172565	4761	AGTGGTGACATTGGGACTGG	217152	49348	TCTGGGGCAGCCCTGGAGAG	261739	93935	GGGGCCCTGGAACCAGGATG
172566	4762	CAGTGGTGACATTGGGACTG	217153	49349	CTCTGGGGCAGCCCTGGAGA	261740	93936	GGGGGCCCTGGAACCAGGAT
172567	4763	GCAGTGGTGACATTGGGACT	217154	49350	GCTCTGGGGCAGCCCTGGAG	261741	93937	GGGGGGCCCTGGAACCAGGA
172568	4764	AGCAGTGGTGACATTGGGAC	217155	49351	AGCTCTGGGGCAGCCCTGGA	261742	93938	GGGGGGGCCCTGGAACCAGG
172569	4765	CAGCAGTGGTGACATTGGGA	217156	49352	CAGCTCTGGGGCAGCCCTGG	261743	93939	GGGGGGGGCCCTGGAACCAG
172570	4766	CCAGCAGTGGTGACATTGGG	217157	49353	GCAGCTCTGGGGCAGCCCTG	261744	93940	TGGGGGGGGCCCTGGAACCA
172571	4767	CCCAGCAGTGGTGACATTGG	217158	49354	GGCAGCTCTGGGGCAGCCCT	261745	93941	CTGGGGGGGGCCCTGGAACC
172572	4768	CCCCAGCAGTGGTGACATTG	217159	49355	AGGCAGCTCTGGGGCAGCCC	261746	93942	GCTGGGGGGGGCCCTGGAAC
172573	4769	ACCCCAGCAGTGGTGACATT	217160	49356	GAGGCAGCTCTGGGGCAGCC	261747	93943	GGCTGGGGGGGGCCCTGGAA
172574	4770	AACCCCAGCAGTGGTGACAT	217161	49357	AGAGGCAGCTCTGGGGCAGC	261748	93944	GGGCTGGGGGGGGCCCTGGA
172575	4771	CAACCCCAGCAGTGGTGACA	217162	49358	GAGAGGCAGCTCTGGGGCAG	261749	93945	GGGGCTGGGGGGGGCCCTGG
172576	4772	TCAACCCCAGCAGTGGTGAC	217163	49359	TGAGAGGCAGCTCTGGGGCA	261750	93946	CGGGGCTGGGGGGGGCCCTG
172577	4773	GTCAACCCCAGCAGTGGTGA	217164	49360	GTGAGAGGCAGCTCTGGGGC	261751	93947	GCGGGGCTGGGGGGGGCCCT
172578	4774	TGTCAACCCCAGCAGTGGTG	217165	49361	GGTGAGAGGCAGCTCTGGGG	261752	93948	GGCGGGGCTGGGGGGGGCCC
172579	4775	GTGTCAACCCCAGCAGTGGT	217166	49362	AGGTGAGAGGCAGCTCTGGG	261753	93949	AGGCGGGGCTGGGGGGGGCC
172580	4776	AGTGTCAACCCCAGCAGTGG	217167	49363	GAGGTGAGAGGCAGCTCTGG	261754	93950	GAGGCGGGGCTGGGGGGGGC
172581	4777	CAGTGTCAACCCCAGCAGTG	217168	49364	AGAGGTGAGAGGCAGCTCTG	261755	93951	GGAGGCGGGGCTGGGGGGGG
172582	4778	CCAGTGTCAACCCCAGCAGT	217169	49365	AAGAGGTGAGAGGCAGCTCT	261756	93952	TGGAGGCGGGGCTGGGGGGG
172583	4779	GCCAGTGTCAACCCCAGCAG	217170	49366	GAAGAGGTGAGAGGCAGCTC	261757	93953	ATGGAGGCGGGGCTGGGGGG
172584	4780	TGCCAGTGTCAACCCCAGCA	217171	49367	GGAAGAGGTGAGAGGCAGCT	261758	93954	TATGGAGGCGGGGCTGGGGG
172585	4781	GTGCCAGTGTCAACCCCAGC	217172	49368	AGGAAGAGGTGAGAGGCAGC	261759	93955	CTATGGAGGCGGGGCTGGGG
172586	4782	AGTGCCAGTGTCAACCCCAG	217173	49369	CAGGAAGAGGTGAGAGGCAG	261760	93956	CCTATGGAGGCGGGGCTGGG
172587	4783	CAGTGCCAGTGTCAACCCCA	217174	49370	GCAGGAAGAGGTGAGAGGCA	261761	93957	CCCTATGGAGGCGGGGCTGG
172588	4784	GCAGTGCCAGTGTCAACCCC	217175	49371	AGCAGGAAGAGGTGAGAGGC	261762	93958	TCCCTATGGAGGCGGGGCTG
172589	4785	AGCAGTGCCAGTGTCAACCC	217176	49372	CAGCAGGAAGAGGTGAGAGG	261763	93959	GTCCCTATGGAGGCGGGGCT
172590	4786	TAGCAGTGCCAGTGTCAACC	217177	49373	ACAGCAGGAAGAGGTGAGAG	261764	93960	TGTCCCTATGGAGGCGGGGC
172591	4787	ATAGCAGTGCCAGTGTCAAC	217178	49374	GACAGCAGGAAGAGGTGAGA	261765	93961	CTGTCCCTATGGAGGCGGGG
172592	4788	GATAGCAGTGCCAGTGTCAA	217179	49375	TGACAGCAGGAAGAGGTGAG	261766	93962	CCTGTCCCTATGGAGGCGGG
172593	4789	AGATAGCAGTGCCAGTGTCA	217180	49376	GTGACAGCAGGAAGAGGTGA	261767	93963	GCCTGTCCCTATGGAGGCGG
172594	4790	AAGATAGCAGTGCCAGTGTC	217181	49377	GGTGACAGCAGGAAGAGGTG	261768	93964	CGCCTGTCCCTATGGAGGCG
172595	4791	TAAGATAGCAGTGCCAGTGT	217182	49378	GGGTGACAGCAGGAAGAGGT	261769	93965	ACGCCTGTCCCTATGGAGGC
172596	4792	TTAAGATAGCAGTGCCAGTG	217183	49379	GGGGTGACAGCAGGAAGAGG	261770	93966	CACGCCTGTCCCTATGGAGG
172597	4793	ATTAAGATAGCAGTGCCAGT	217184	49380	TGGGGTGACAGCAGGAAGAG	261771	93967	GCACGCCTGTCCCTATGGAG
172598	4794	AATTAAGATAGCAGTGCCAG	217185	49381	GTGGGGTGACAGCAGGAAGA	261772	93968	TGCACGCCTGTCCCTATGGA
172599	4795	TAATTAAGATAGCAGTGCCA	217186	49382	GGTGGGGTGACAGCAGGAAG	261773	93969	CTGCACGCCTGTCCCTATGG
172600	4796	GTAATTAAGATAGCAGTGCC	217187	49383	TGGTGGGGTGACAGCAGGAA	261774	93970	TCTGCACGCCTGTCCCTATG
172601	4797	TGTAATTAAGATAGCAGTGC	217188	49384	GTGGTGGGGTGACAGCAGGA	261775	93971	GTCTGCACGCCTGTCCCTAT
172602	4798	ATGTAATTAAGATAGCAGTG	217189	49385	GGTGGTGGGGTGACAGCAGG	261776	93972	TGTCTGCACGCCTGTCCCTA
172603	4799	AATGTAATTAAGATAGCAGT	217190	49386	TGGTGGTGGGGTGACAGCAG	261777	93973	GTGTCTGCACGCCTGTCCCT
172604	4800	GAATGTAATTAAGATAGCAG	217191	49387	ATGGTGGTGGGGTGACAGCA	261778	93974	GGTGTCTGCACGCCTGTCCC
172605	4801	TGAATGTAATTAAGATAGCA	217192	49388	GATGGTGGTGGGGTGACAGC	261779	93975	GGGTGTCTGCACGCCTGTCC
172606	4802	ATGAATGTAATTAAGATAGC	217193	49389	TGATGGTGGTGGGGTGACAG	261780	93976	CGGGTGTCTGCACGCCTGTC
172607	4803	AATGAATGTAATTAAGATAG	217194	49390	CTGATGGTGGTGGGGTGACA	261781	93977	ACGGGTGTCTGCACGCCTGT
172608	4804	CAATGAATGTAATTAAGATA	217195	49391	CCTGATGGTGGTGGGGTGAC	261782	93978	GACGGGTGTCTGCACGCCTG
172609	4805	TCAATGAATGTAATTAAGAT	217196	49392	CCCTGATGGTGGTGGGGTGA	261783	93979	GGACGGGTGTCTGCACGCCT
172610	4806	CTCAATGAATGTAATTAAGA	217197	49393	GCCCTGATGGTGGTGGGGTG	261784	93980	GGGACGGGTGTCTGCACGCC
172611	4807	ACTCAATGAATGTAATTAAG	217198	49394	TGCCCTGATGGTGGTGGGGT	261785	93981	AGGGACGGGTGTCTGCACGC
172612	4808	CACTCAATGAATGTAATTAA	217199	49395	CTGCCCTGATGGTGGTGGGG	261786	93982	CAGGGACGGGTGTCTGCACG
172613	4809	ACACTCAATGAATGTAATTA	217200	49396	TCTGCCCTGATGGTGGTGGG	261787	93983	CCAGGGACGGGTGTCTGCAC
172614	4810	GACACTCAATGAATGTAATT	217201	49397	TTCTGCCCTGATGGTGGTGG	261788	93984	GCCAGGGACGGGTGTCTGCA
172615	4811	AGACACTCAATGAATGTAAT	217202	49398	CTTCTGCCCTGATGGTGGTG	261789	93985	AGCCAGGGACGGGTGTCTGC
172616	4812	AAGACACTCAATGAATGTAA	217203	49399	ACTTCTGCCCTGATGGTGGT	261790	93986	CAGCCAGGGACGGGTGTCTG
172617	4813	AAAGACACTCAATGAATGTA	217204	49400	AACTTCTGCCCTGATGGTGG	261791	93987	GCAGCCAGGGACGGGTGTCT
172618	4814	AAAAGACACTCAATGAATGT	217205	49401	CAACTTCTGCCCTGATGGTG	261792	93988	AGCAGCCAGGGACGGGTGTC
172619	4815	TAAAAGACACTCAATGAATG	217206	49402	CCAACTTCTGCCCTGATGGT	261793	93989	AAGCAGCCAGGGACGGGTGT
172620	4816	CTAAAAGACACTCAATGAAT	217207	49403	CCCAACTTCTGCCCTGATGG	261794	93990	GAAGCAGCCAGGGACGGGTG
172621	4817	CCTAAAAGACACTCAATGAA	217208	49404	TCCCAACTTCTGCCCTGATG	261795	93991	GGAAGCAGCCAGGGACGGGT
172622	4818	TCCTAAAAGACACTCAATGA	217209	49405	GTCCCAACTTCTGCCCTGAT	261796	93992	AGGAAGCAGCCAGGGACGGG
172623	4819	CTCCTAAAAGACACTCAATG	217210	49406	TGTCCCAACTTCTGCCCTGA	261797	93993	GAGGAAGCAGCCAGGGACGG
172624	4820	CCTCCTAAAAGACACTCAAT	217211	49407	TTGTCCCAACTTCTGCCCTG	261798	93994	AGAGGAAGCAGCCAGGGACG
172625	4821	GCCTCCTAAAAGACACTCAA	217212	49408	TTTGTCCCAACTTCTGCCCT	261799	93995	AAGAGGAAGCAGCCAGGGAC
172626	4822	GGCCTCCTAAAAGACACTCA	217213	49409	CTTTGTCCCAACTTCTGCCC	261800	93996	CAAGAGGAAGCAGCCAGGGA

172627	4823	GGGCCTCCTAAAAGACACTC	217214	49410	GCTTTGTCCCAACTTCTGCC	261801	93997	ACAAGAGGAAGCAGCCAGGG
172628	4824	AGGGCCTCCTAAAAGACACT	217215	49411	GGCTTTGTCCCAACTTCTGC	261802	93998	CACAAGAGGAAGCAGCCAGG
172629	4825	TAGGGCCTCCTAAAAGACAC	217216	49412	AGGCTTTGTCCCAACTTCTG	261803	93999	CCACAAGAGGAAGCAGCCAG
172630	4826	ATAGGGCCTCCTAAAAGACA	217217	49413	GAGGCTTTGTCCCAACTTCT	261804	94000	TCCACAAGAGGAAGCAGCCA
172631	4827	AATAGGGCCTCCTAAAAGAC	217218	49414	AGAGGCTTTGTCCCAACTTC	261805	94001	TTCCACAAGAGGAAGCAGCC
172632	4828	GAATAGGGCCTCCTAAAAGA	217219	49415	GAGAGGCTTTGTCCCAACTT	261806	94002	ATTCCACAAGAGGAAGCAGC
172633	4829	AGAATAGGGCCTCCTAAAAG	217220	49416	GGAGAGGCTTTGTCCCAACT	261807	94003	CATTCCACAAGAGGAAGCAG
172634	4830	TAGAATAGGGCCTCCTAAAA	217221	49417	AGGAGAGGCTTTGTCCCAAC	261808	94004	CCATTCCACAAGAGGAAGCA
172635	4831	TTAGAATAGGGCCTCCTAAA	217222	49418	TAGGAGAGGCTTTGTCCCAA	261809	94005	CCCATTCCACAAGAGGAAGC
172636	4832	CTTAGAATAGGGCCTCCTAA	217223	49419	GTAGGAGAGGCTTTGTCCCA	261810	94006	ACCCATTCCACAAGAGGAAG
172637	4833	ACTTAGAATAGGGCCTCCTA	217224	49420	AGTAGGAGAGGCTTTGTCCC	261811	94007	AACCCATTCCACAAGAGGAA
172638	4834	CACTTAGAATAGGGCCTCCT	217225	49421	CAGTAGGAGAGGCTTTGTCC	261812	94008	GAACCCATTCCACAAGAGGA
172639	4835	GCACTTAGAATAGGGCCTCC	217226	49422	CCAGTAGGAGAGGCTTTGTC	261813	94009	TGAACCCATTCCACAAGAGG
172640	4836	AGCACTTAGAATAGGGCCTC	217227	49423	GCCAGTAGGAGAGGCTTTGT	261814	94010	TTGAACCCATTCCACAAGAG
172641	4837	AAGCACTTAGAATAGGGCCT	217228	49424	AGCCAGTAGGAGAGGCTTTG	261815	94011	TTTGAACCCATTCCACAAGA
172642	4838	CAAGCACTTAGAATAGGGCC	217229	49425	GAGCCAGTAGGAGAGGCTTT	261816	94012	TTTTGAACCCATTCCACAAG
172643	4839	GCAAGCACTTAGAATAGGGC	217230	49426	GGAGCCAGTAGGAGAGGCTT	261817	94013	CTTTTGAACCCATTCCACAA
172644	4840	AGCAAGCACTTAGAATAGGG	217231	49427	AGGAGCCAGTAGGAGAGGCT	261818	94014	ACTTTTGAACCCATTCCACA
172645	4841	TAGCAAGCACTTAGAATAGG	217232	49428	CAGGAGCCAGTAGGAGAGGC	261819	94015	TACTTTTGAACCCATTCCAC
172646	4842	TTAGCAAGCACTTAGAATAG	217233	49429	GCAGGAGCCAGTAGGAGAGG	261820	94016	TTACTTTTGAACCCATTCCA
172647	4843	CTTAGCAAGCACTTAGAATA	217234	49430	AGCAGGAGCCAGTAGGAGAG	261821	94017	CTTACTTTTGAACCCATTCC
172648	4844	TCTTAGCAAGCACTTAGAAT	217235	49431	AAGCAGGAGCCAGTAGGAGA	261822	94018	GCTTACTTTTGAACCCATTC
172649	4845	ATCTTAGCAAGCACTTAGAA	217236	49432	AAAGCAGGAGCCAGTAGGAG	261823	94019	TGCTTACTTTTGAACCCATT
172650	4846	AATCTTAGCAAGCACTTAGA	217237	49433	AAAAGCAGGAGCCAGTAGGA	261824	94020	CTGCTTACTTTTGAACCCAT
172651	4847	TAATCTTAGCAAGCACTTAG	217238	49434	GAAAAGCAGGAGCCAGTAGG	261825	94021	ACTGCTTACTTTTGAACCCA
172652	4848	ATAATCTTAGCAAGCACTTA	217239	49435	AGAAAAGCAGGAGCCAGTAG	261826	94022	CACTGCTTACTTTTGAACCC
172653	4849	GATAATCTTAGCAAGCACTT	217240	49436	GAGAAAAGCAGGAGCCAGTA	261827	94023	ACACTGCTTACTTTTGAACC
172654	4850	AGATAATCTTAGCAAGCACT	217241	49437	GGAGAAAAGCAGGAGCCAGT	261828	94024	AACACTGCTTACTTTTGAAC
172655	4851	GAGATAATCTTAGCAAGCAC	217242	49438	GGGAGAAAAGCAGGAGCCAG	261829	94025	CAACACTGCTTACTTTTGAA
172656	4852	TGAGATAATCTTAGCAAGCA	217243	49439	AGGGAGAAAAGCAGGAGCCA	261830	94026	ACAACACTGCTTACTTTTGA
172657	4853	ATGAGATAATCTTAGCAAGC	217244	49440	AAGGGAGAAAAGCAGGAGCC	261831	94027	AACAACACTGCTTACTTTTG
172658	4854	AATGAGATAATCTTAGCAAG	217245	49441	TAAGGGAGAAAAGCAGGAGC	261832	94028	AAACAACACTGCTTACTTTT
172659	4855	AAATGAGATAATCTTAGCAA	217246	49442	CTAAGGGAGAAAAGCAGGAG	261833	94029	TAAACAACACTGCTTACTTT
172660	4856	TAAATGAGATAATCTTAGCA	217247	49443	CCTAAGGGAGAAAAGCAGGA	261834	94030	GTAAACAACACTGCTTACTT
172661	4857	TTAAATGAGATAATCTTAGC	217248	49444	ACCTAAGGGAGAAAAGCAGG	261835	94031	TGTAAACAACACTGCTTACT
172662	4858	ATTAAATGAGATAATCTTAG	217249	49445	GACCTAAGGGAGAAAAGCAG	261836	94032	GTGTAAACAACACTGCTTAC
172663	4859	GATTAAATGAGATAATCTTA	217250	49446	GGACCTAAGGGAGAAAAGCA	261837	94033	AGTGTAAACAACACTGCTTA
172664	4860	GGATTAAATGAGATAATCTT	217251	49447	TGGACCTAAGGGAGAAAAGC	261838	94034	CAGTGTAAACAACACTGCTT
172665	4861	AGGATTAAATGAGATAATCT	217252	49448	CTGGACCTAAGGGAGAAAAG	261839	94035	TCAGTGTAAACAACACTGCT
172666	4862	GAGGATTAAATGAGATAATC	217253	49449	GCTGGACCTAAGGGAGAAAA	261840	94036	GTCAGTGTAAACAACACTGC
172667	4863	TGAGGATTAAATGAGATAAT	217254	49450	GGCTGGACCTAAGGGAGAAA	261841	94037	TGTCAGTGTAAACAACACTG
172668	4864	GTGAGGATTAAATGAGATAA	217255	49451	AGGCTGGACCTAAGGGAGAA	261842	94038	TTGTCAGTGTAAACAACACT
172669	4865	TGTGAGGATTAAATGAGATA	217256	49452	GAGGCTGGACCTAAGGGAGA	261843	94039	TTTGTCAGTGTAAACAACAC
172670	4866	TTGTGAGGATTAAATGAGAT	217257	49453	GGAGGCTGGACCTAAGGGAG	261844	94040	GTTTGTCAGTGTAAACAACA
172671	4867	GTTGTGAGGATTAAATGAGA	217258	49454	AGGAGGCTGGACCTAAGGGA	261845	94041	AGTTTGTCAGTGTAAACAAC
172672	4868	TGTTGTGAGGATTAAATGAG	217259	49455	GAGGAGGCTGGACCTAAGGG	261846	94042	CAGTTTGTCAGTGTAAACAA
172673	4869	GTGTTGTGAGGATTAAATGA	217260	49456	AGAGGAGGCTGGACCTAAGG	261847	94043	TCAGTTTGTCAGTGTAAACA
172674	4870	AGTGTTGTGAGGATTAAATG	217261	49457	AAGAGGAGGCTGGACCTAAG	261848	94044	TTCAGTTTGTCAGTGTAAAC
172675	4871	AAGTGTTGTGAGGATTAAAT	217262	49458	GAAGAGGAGGCTGGACCTAA	261849	94045	TTTCAGTTTGTCAGTGTAAA
172676	4872	GAAGTGTTGTGAGGATTAAA	217263	49459	AGAAGAGGAGGCTGGACCTA	261850	94046	TTTTCAGTTTGTCAGTGTAA
172677	4873	GGAAGTGTTGTGAGGATTAA	217264	49460	GAGAAGAGGAGGCTGGACCT	261851	94047	TTTTTCAGTTTGTCAGTGTA
172678	4874	CGGAAGTGTTGTGAGGATTA	217265	49461	GGAGAAGAGGAGGCTGGACC	261852	94048	TTTTTTCAGTTTGTCAGTGT
172679	4875	GCGGAAGTGTTGTGAGGATT	217266	49462	TGGAGAAGAGGAGGCTGGAC	261853	94049	TTTTTTTCAGTTTGTCAGTG
172680	4876	AGCGGAAGTGTTGTGAGGAT	217267	49463	ATGGAGAAGAGGAGGCTGGA	261854	94050	TTTTTTTTCAGTTTGTCAGT
172681	4877	TAGCGGAAGTGTTGTGAGGA	217268	49464	GATGGAGAAGAGGAGGCTGG	261855	94051	TTTTTTTTTCAGTTTGTCAG
172682	4878	ATAGCGGAAGTGTTGTGAGG	217269	49465	AGATGGAGAAGAGGAGGCTG	261856	94052	CTTTTTTTTTCAGTTTGTCA
172683	4879	CATAGCGGAAGTGTTGTGAG	217270	49466	AAGATGGAGAAGAGGAGGCT	261857	94053	TCTTTTTTTTTCAGTTTGTC
172684	4880	ACATAGCGGAAGTGTTGTGA	217271	49467	GAAGATGGAGAAGAGGAGGC	261858	94054	TTCTTTTTTTTTCAGTTTGT
172685	4881	TACATAGCGGAAGTGTTGTG	217272	49468	TGAAGATGGAGAAGAGGAGG	261859	94055	TTTCTTTTTTTTTCAGTTTG
172686	4882	CTACATAGCGGAAGTGTTGT	217273	49469	CTGAAGATGGAGAAGAGGAG	261860	94056	TTTTCTTTTTTTTTCAGTTT
172687	4883	GCTACATAGCGGAAGTGTTG	217274	49470	CCTGAAGATGGAGAAGAGGA	261861	94057	TTTTTCTTTTTTTTTCAGTT
172688	4884	TGCTACATAGCGGAAGTGTT	217275	49471	TCCTGAAGATGGAGAAGAGG	261862	94058	CTTTTTCTTTTTTTTTCAGT
172689	4885	CTGCTACATAGCGGAAGTGT	217276	49472	CTCCTGAAGATGGAGAAGAG	261863	94059	TCTTTTTCTTTTTTTTTCAG
172690	4886	CCTGCTACATAGCGGAAGTG	217277	49473	ACTCCTGAAGATGGAGAAGA	261864	94060	CTCTTTTTCTTTTTTTTTCA
172691	4887	ACCTGCTACATAGCGGAAGT	217278	49474	GACTCCTGAAGATGGAGAAG	261865	94061	TCTCTTTTTCTTTTTTTTTC
172692	4888	CACCTGCTACATAGCGGAAG	217279	49475	AGACTCCTGAAGATGGAGAA	261866	94062	ATCTCTTTTTCTTTTTTTTT
172693	4889	GCACCTGCTACATAGCGGAA	217280	49476	GAGACTCCTGAAGATGGAGA	261867	94063	TATCTCTTTTTCTTTTTTTT
172694	4890	AGCACCTGCTACATAGCGGA	217281	49477	GGAGACTCCTGAAGATGGAG	261868	94064	TTATCTCTTTTTCTTTTTTT
172695	4891	CAGCACCTGCTACATAGCGG	217282	49478	AGGAGACTCCTGAAGATGGA	261869	94065	GTTATCTCTTTTTCTTTTTT
172696	4892	ACAGCACCTGCTACATAGCG	217283	49479	AAGGAGACTCCTGAAGATGG	261870	94066	TGTTATCTCTTTTTCTTTTT
172697	4893	AACAGCACCTGCTACATAGC	217284	49480	GAAGGAGACTCCTGAAGATG	261871	94067	ATGTTATCTCTTTTTCTTTT
172698	4894	TAACAGCACCTGCTACATAG	217285	49481	AGAAGGAGACTCCTGAAGAT	261872	94068	AATGTTATCTCTTTTTCTTT

172699	4895	ATAACAGCACCTGCTACATA	217286	49482	GAGAAGGAGACTCCTGAAGA	261873	94069	CAATGTTATCTCTTTTTCTT
172700	4896	AATAACAGCACCTGCTACAT	217287	49483	GGAGAAGGAGACTCCTGAAG	261874	94070	CCAATGTTATCTCTTTTTCT
172701	4897	TAATAACAGCACCTGCTACA	217288	49484	TGGAGAAGGAGACTCCTGAA	261875	94071	TCCAATGTTATCTCTTTTTC
172702	4898	ATAATAACAGCACCTGCTAC	217289	49485	GTGGAGAAGGAGACTCCTGA	261876	94072	CTCCAATGTTATCTCTTTTT
172703	4899	GATAATAACAGCACCTGCTA	217290	49486	AGTGGAGAAGGAGACTCCTG	261877	94073	CCTCCAATGTTATCTCTTTT
172704	4900	AGATAATAACAGCACCTGCT	217291	49487	GAGTGGAGAAGGAGACTCCT	261878	94074	GCCTCCAATGTTATCTCTTT
172705	4901	GAGATAATAACAGCACCTGC	217292	49488	TGAGTGGAGAAGGAGACTCC	261879	94075	AGCCTCCAATGTTATCTCTT
172706	4902	GGAGATAATAACAGCACCTG	217293	49489	GTGAGTGGAGAAGGAGACTC	261880	94076	AAGCCTCCAATGTTATCTCT
172707	4903	CGGAGATAATAACAGCACCT	217294	49490	TGTGAGTGGAGAAGGAGACT	261881	94077	CAAGCCTCCAATGTTATCTC
172708	4904	ACGGAGATAATAACAGCACC	217295	49491	GTGTGAGTGGAGAAGGAGAC	261882	94078	CCAAGCCTCCAATGTTATCT
172709	4905	CACGGAGATAATAACAGCAC	217296	49492	CGTGTGAGTGGAGAAGGAGA	261883	94079	GCCAAGCCTCCAATGTTATC
172710	4906	TCACGGAGATAATAACAGCA	217297	49493	ACGTGTGAGTGGAGAAGGAG	261884	94080	TGCCAAGCCTCCAATGTTAT
172711	4907	ATCACGGAGATAATAACAGC	217298	49494	GACGTGTGAGTGGAGAAGGA	261885	94081	GTGCCAAGCCTCCAATGTTA
172712	4908	CATCACGGAGATAATAACAG	217299	49495	TGACGTGTGAGTGGAGAAGG	261886	94082	TGTGCCAAGCCTCCAATGTT
172713	4909	CCATCACGGAGATAATAACA	217300	49496	ATGACGTGTGAGTGGAGAAG	261887	94083	CTGTGCCAAGCCTCCAATGT
172714	4910	CCCATCACGGAGATAATAAC	217301	49497	CATGACGTGTGAGTGGAGAA	261888	94084	ACTGTGCCAAGCCTCCAATG
172715	4911	CCCCATCACGGAGATAATAA	217302	49498	TCATGACGTGTGAGTGGAGA	261889	94085	CACTGTGCCAAGCCTCCAAT
172716	4912	TCCCCATCACGGAGATAATA	217303	49499	GTCATGACGTGTGAGTGGAG	261890	94086	CCACTGTGCCAAGCCTCCAA
172717	4913	TTCCCCATCACGGAGATAAT	217304	49500	AGTCATGACGTGTGAGTGGA	261891	94087	GCCACTGTGCCAAGCCTCCA
172718	4914	TTTCCCCATCACGGAGATAA	217305	49501	AAGTCATGACGTGTGAGTGG	261892	94088	AGCCACTGTGCCAAGCCTCC
172719	4915	GTTTCCCCATCACGGAGATA	217306	49502	GAAGTCATGACGTGTGAGTG	261893	94089	GAGCCACTGTGCCAAGCCTC
172720	4916	AGTTTCCCCATCACGGAGAT	217307	49503	TGAAGTCATGACGTGTGAGT	261894	94090	TGAGCCACTGTGCCAAGCCT
172721	4917	CAGTTTCCCCATCACGGAGA	217308	49504	CTGAAGTCATGACGTGTGAG	261895	94091	ATGAGCCACTGTGCCAAGCC
172722	4918	TCAGTTTCCCCATCACGGAG	217309	49505	GCTGAAGTCATGACGTGTGA	261896	94092	CATGAGCCACTGTGCCAAGC
172723	4919	TTCAGTTTCCCCATCACGGA	217310	49506	TGCTGAAGTCATGACGTGTG	261897	94093	GCATGAGCCACTGTGCCAAG
172724	4920	CTTCAGTTTCCCCATCACGG	217311	49507	GTGCTGAAGTCATGACGTGT	261898	94094	GGCATGAGCCACTGTGCCAA
172725	4921	GCTTCAGTTTCCCCATCACG	217312	49508	GGTGCTGAAGTCATGACGTG	261899	94095	AGGCATGAGCCACTGTGCCA
172726	4922	TGCTTCAGTTTCCCCATCAC	217313	49509	AGGTGCTGAAGTCATGACGT	261900	94096	CAGGCATGAGCCACTGTGCC
172727	4923	GTGCTTCAGTTTCCCCATCA	217314	49510	GAGGTGCTGAAGTCATGACG	261901	94097	ACAGGCATGAGCCACTGTGC
172728	4924	TGTGCTTCAGTTTCCCCATC	217315	49511	CGAGGTGCTGAAGTCATGAC	261902	94098	TACAGGCATGAGCCACTGTG
172729	4925	CTGTGCTTCAGTTTCCCCAT	217316	49512	GCGAGGTGCTGAAGTCATGA	261903	94099	TTACAGGCATGAGCCACTGT
172730	4926	TCTGTGCTTCAGTTTCCCCA	217317	49513	TGCGAGGTGCTGAAGTCATG	261904	94100	ATTACAGGCATGAGCCACTG
172731	4927	CTCTGTGCTTCAGTTTCCCC	217318	49514	ATGCGAGGTGCTGAAGTCAT	261905	94101	GATTACAGGCATGAGCCACT
172732	4928	TCTCTGTGCTTCAGTTTCCC	217319	49515	GATGCGAGGTGCTGAAGTCA	261906	94102	GGATTACAGGCATGAGCCAC
172733	4929	CTCTCTGTGCTTCAGTTTCC	217320	49516	TGATGCGAGGTGCTGAAGTC	261907	94103	GGGATTACAGGCATGAGCCA
172734	4930	CCTCTCTGTGCTTCAGTTTC	217321	49517	CTGATGCGAGGTGCTGAAGT	261908	94104	TGGGATTACAGGCATGAGCC
172735	4931	CCCTCTCTGTGCTTCAGTTT	217322	49518	ACTGATGCGAGGTGCTGAAG	261909	94105	CTGGGATTACAGGCATGAGC
172736	4932	ACCCTCTCTGTGCTTCAGTT	217323	49519	GACTGATGCGAGGTGCTGAA	261910	94106	GCTGGGATTACAGGCATGAG
172737	4933	AACCCTCTCTGTGCTTCAGT	217324	49520	GGACTGATGCGAGGTGCTGA	261911	94107	TGCTGGGATTACAGGCATGA
172738	4934	TAACCCTCTCTGTGCTTCAG	217325	49521	TGGACTGATGCGAGGTGCTG	261912	94108	GTGCTGGGATTACAGGCATG
172739	4935	CTAACCCTCTCTGTGCTTCA	217326	49522	CTGGACTGATGCGAGGTGCT	261913	94109	AGTGCTGGGATTACAGGCAT
172740	4936	ACTAACCCTCTCTGTGCTTC	217327	49523	TCTGGACTGATGCGAGGTGC	261914	94110	AAGTGCTGGGATTACAGGCA
172741	4937	TACTAACCCTCTCTGTGCTT	217328	49524	TTCTGGACTGATGCGAGGTG	261915	94111	AAAGTGCTGGGATTACAGGC
172742	4938	TTACTAACCCTCTCTGTGCT	217329	49525	ATTCTGGACTGATGCGAGGT	261916	94112	CAAAGTGCTGGGATTACAGG
172743	4939	GTTACTAACCCTCTCTGTGC	217330	49526	TATTCTGGACTGATGCGAGG	261917	94113	CCAAAGTGCTGGGATTACAG
172744	4940	AGTTACTAACCCTCTCTGTG	217331	49527	ATATTCTGGACTGATGCGAG	261918	94114	CCCAAAGTGCTGGGATTACA
172745	4941	AAGTTACTAACCCTCTCTGT	217332	49528	CATATTCTGGACTGATGCGA	261919	94115	TCCCAAAGTGCTGGGATTAC
172746	4942	CAAGTTACTAACCCTCTCTG	217333	49529	TCATATTCTGGACTGATGCG	261920	94116	CTCCCAAAGTGCTGGGATTA
172747	4943	GCAAGTTACTAACCCTCTCT	217334	49530	GTCATATTCTGGACTGATGC	261921	94117	CCTCCCAAAGTGCTGGGATT
172748	4944	AGCAAGTTACTAACCCTCTC	217335	49531	AGTCATATTCTGGACTGATG	261922	94118	GCCTCCCAAAGTGCTGGGAT
172749	4945	TAGCAAGTTACTAACCCTCT	217336	49532	CAGTCATATTCTGGACTGAT	261923	94119	AGCCTCCCAAAGTGCTGGGA
172750	4946	TTAGCAAGTTACTAACCCTC	217337	49533	GCAGTCATATTCTGGACTGA	261924	94120	TAGCCTCCCAAAGTGCTGGG
172751	4947	TTTAGCAAGTTACTAACCCT	217338	49534	AGCAGTCATATTCTGGACTG	261925	94121	TTAGCCTCCCAAAGTGCTGG
172752	4948	CTTTAGCAAGTTACTAACCC	217339	49535	AAGCAGTCATATTCTGGACT	261926	94122	CTTAGCCTCCCAAAGTGCTG
172753	4949	CCTTTAGCAAGTTACTAACC	217340	49536	CAAGCAGTCATATTCTGGAC	261927	94123	CCTTAGCCTCCCAAAGTGCT
172754	4950	ACCTTTAGCAAGTTACTAAC	217341	49537	ACAAGCAGTCATATTCTGGA	261928	94124	ACCTTAGCCTCCCAAAGTGC
172755	4951	GACCTTTAGCAAGTTACTAA	217342	49538	AACAAGCAGTCATATTCTGG	261929	94125	CACCTTAGCCTCCCAAAGTG
172756	4952	TGACCTTTAGCAAGTTACTA	217343	49539	GAACAAGCAGTCATATTCTG	261930	94126	CCACCTTAGCCTCCCAAAGT
172757	4953	GTGACCTTTAGCAAGTTACT	217344	49540	TGAACAAGCAGTCATATTCT	261931	94127	CCCACCTTAGCCTCCCAAAG
172758	4954	TGTGACCTTTAGCAAGTTAC	217345	49541	TTGAACAAGCAGTCATATTC	261932	94128	TCCCACCTTAGCCTCCCAAA
172759	4955	CTGTGACCTTTAGCAAGTTA	217346	49542	CTTGAACAAGCAGTCATATT	261933	94129	CTCCCACCTTAGCCTCCCAA
172760	4956	TCTGTGACCTTTAGCAAGTT	217347	49543	ACTTGAACAAGCAGTCATAT	261934	94130	CCTCCCACCTTAGCCTCCCA
172761	4957	CTCTGTGACCTTTAGCAAGT	217348	49544	CACTTGAACAAGCAGTCATA	261935	94131	TCCTCCCACCTTAGCCTCCC
172762	4958	GCTCTGTGACCTTTAGCAAG	217349	49545	GCACTTGAACAAGCAGTCAT	261936	94132	ATCCTCCCACCTTAGCCTCC
172763	4959	GGCTCTGTGACCTTTAGCAA	217350	49546	GGCACTTGAACAAGCAGTCA	261937	94133	CATCCTCCCACCTTAGCCTC
172764	4960	TGGCTCTGTGACCTTTAGCA	217351	49547	TGGCACTTGAACAAGCAGTC	261938	94134	ACATCCTCCCACCTTAGCCT
172765	4961	CTGGCTCTGTGACCTTTAGC	217352	49548	GTGGCACTTGAACAAGCAGT	261939	94135	GACATCCTCCCACCTTAGCC
172766	4962	ACTGGCTCTGTGACCTTTAG	217353	49549	GGTGGCACTTGAACAAGCAG	261940	94136	GGACATCCTCCCACCTTAGC
172767	4963	CACTGGCTCTGTGACCTTTA	217354	49550	AGGTGGCACTTGAACAAGCA	261941	94137	GGGACATCCTCCCACCTTAG
172768	4964	CCACTGGCTCTGTGACCTTT	217355	49551	AAGGTGGCACTTGAACAAGC	261942	94138	GGGGACATCCTCCCACCTTA
172769	4965	CCCACTGGCTCTGTGACCTT	217356	49552	AAAGGTGGCACTTGAACAAG	261943	94139	TGGGGACATCCTCCCACCTT
172770	4966	ACCCACTGGCTCTGTGACCT	217357	49553	GAAAGGTGGCACTTGAACAA	261944	94140	CTGGGGACATCCTCCCACCT

172771	4967	CACCCACTGGCTCTGTGACC	217358	49554	AGAAAGGTGGCACTTGAACA	261945	94141	GCTGGGGACATCCTCCCACC
172772	4968	CCACCCACTGGCTCTGTGAC	217359	49555	GAGAAAGGTGGCACTTGAAC	261946	94142	GGCTGGGGACATCCTCCCAC
172773	4969	ACCACCCACTGGCTCTGTGA	217360	49556	TGAGAAAGGTGGCACTTGAA	261947	94143	GGGCTGGGGACATCCTCCCA
172774	4970	CACCACCCACTGGCTCTGTG	217361	49557	ATGAGAAAGGTGGCACTTGA	261948	94144	TGGGCTGGGGACATCCTCCC
172775	4971	CCACCACCCACTGGCTCTGT	217362	49558	CATGAGAAAGGTGGCACTTG	261949	94145	TTGGGCTGGGGACATCCTCC
172776	4972	TCCACCACCCACTGGCTCTG	217363	49559	GCATGAGAAAGGTGGCACTT	261950	94146	CTTGGGCTGGGGACATCCTC
172777	4973	CTCCACCACCCACTGGCTCT	217364	49560	TGCATGAGAAAGGTGGCACT	261951	94147	TCTTGGGCTGGGGACATCCT
172778	4974	GCTCCACCACCCACTGGCTC	217365	49561	ATGCATGAGAAAGGTGGCAC	261952	94148	CTCTTGGGCTGGGGACATCC
172779	4975	AGCTCCACCACCCACTGGCT	217366	49562	AATGCATGAGAAAGGTGGCA	261953	94149	ACTCTTGGGCTGGGGACATC
172780	4976	CAGCTCCACCACCCACTGGC	217367	49563	AAATGCATGAGAAAGGTGGC	261954	94150	AACTCTTGGGCTGGGGACAT
172781	4977	CCAGCTCCACCACCCACTGG	217368	49564	AAAATGCATGAGAAAGGTGG	261955	94151	GAACTCTTGGGCTGGGGACA
172782	4978	ACCAGCTCCACCACCCACTG	217369	49565	AAAAATGCATGAGAAAGGTG	261956	94152	AGAACTCTTGGGCTGGGGAC
172783	4979	AACCAGCTCCACCACCCACT	217370	49566	AAAAAATGCATGAGAAAGGT	261957	94153	TAGAACTCTTGGGCTGGGGA
172784	4980	CAACCAGCTCCACCACCCAC	217371	49567	AAAAAAATGCATGAGAAAGG	261958	94154	CTAGAACTCTTGGGCTGGGG
172785	4981	GCAACCAGCTCCACCACCCA	217372	49568	GAAAAAAATGCATGAGAAAG	261959	94155	TCTAGAACTCTTGGGCTGGG
172786	4982	GGCAACCAGCTCCACCACCC	217373	49569	AGAAAAAAATGCATGAGAAA	261960	94156	GTCTAGAACTCTTGGGCTGG
172787	4983	AGGCAACCAGCTCCACCACC	217374	49570	TAGAAAAAAATGCATGAGAA	261961	94157	GGTCTAGAACTCTTGGGCTG
172788	4984	CAGGCAACCAGCTCCACCAC	217375	49571	CTAGAAAAAAATGCATGAGA	261962	94158	TGGTCTAGAACTCTTGGGCT
172789	4985	TCAGGCAACCAGCTCCACCA	217376	49572	ACTAGAAAAAAATGCATGAG	261963	94159	CTGGTCTAGAACTCTTGGGC
172790	4986	GTCAGGCAACCAGCTCCACC	217377	49573	CACTAGAAAAAAATGCATGA	261964	94160	GCTGGTCTAGAACTCTTGGG
172791	4987	TGTCAGGCAACCAGCTCCAC	217378	49574	TCACTAGAAAAAAATGCATG	261965	94161	GGCTGGTCTAGAACTCTTGG
172792	4988	GTGTCAGGCAACCAGCTCCA	217379	49575	GTCACTAGAAAAAAATGCAT	261966	94162	AGGCTGGTCTAGAACTCTTG
172793	4989	AGTGTCAGGCAACCAGCTCC	217380	49576	TGTCACTAGAAAAAAATGCA	261967	94163	CAGGCTGGTCTAGAACTCTT
172794	4990	TAGTGTCAGGCAACCAGCTC	217381	49577	TTGTCACTAGAAAAAAATGC	261968	94164	CCAGGCTGGTCTAGAACTCT
172795	4991	CTAGTGTCAGGCAACCAGCT	217382	49578	ATTGTCACTAGAAAAAAATG	261969	94165	CCCAGGCTGGTCTAGAACTC
172796	4992	ACTAGTGTCAGGCAACCAGC	217383	49579	GATTGTCACTAGAAAAAAAT	261970	94166	GCCCAGGCTGGTCTAGAACT
172797	4993	AACTAGTGTCAGGCAACCAG	217384	49580	TGATTGTCACTAGAAAAAAA	261971	94167	TGCCCAGGCTGGTCTAGAAC
172798	4994	GAACTAGTGTCAGGCAACCA	217385	49581	GTGATTGTCACTAGAAAAAA	261972	94168	TTGCCCAGGCTGGTCTAGAA
172799	4995	GGAACTAGTGTCAGGCAACC	217386	49582	TGTGATTGTCACTAGAAAAA	261973	94169	GTTGCCCAGGCTGGTCTAGA
172800	4996	GGGAACTAGTGTCAGGCAAC	217387	49583	CTGTGATTGTCACTAGAAAA	261974	94170	TGTTGCCCAGGCTGGTCTAG
172801	4997	AGGGAACTAGTGTCAGGCAA	217388	49584	GCTGTGATTGTCACTAGAAA	261975	94171	ATGTTGCCCAGGCTGGTCTA
172802	4998	GAGGGAACTAGTGTCAGGCA	217389	49585	GGCTGTGATTGTCACTAGAA	261976	94172	TATGTTGCCCAGGCTGGTCT
172803	4999	GGAGGGAACTAGTGTCAGGC	217390	49586	TGGCTGTGATTGTCACTAGA	261977	94173	CTATGTTGCCCAGGCTGGTC
172804	5000	GGGAGGGAACTAGTGTCAGG	217391	49587	GTGGCTGTGATTGTCACTAG	261978	94174	GCTATGTTGCCCAGGCTGGT
172805	5001	GGGGAGGGAACTAGTGTCAG	217392	49588	GGTGGCTGTGATTGTCACTA	261979	94175	TGCTATGTTGCCCAGGCTGG
172806	5002	AGGGGAGGGAACTAGTGTCA	217393	49589	GGGTGGCTGTGATTGTCACT	261980	94176	TTGCTATGTTGCCCAGGCTG
172807	5003	GAGGGGAGGGAACTAGTGTC	217394	49590	AGGGTGGCTGTGATTGTCAC	261981	94177	CTTGCTATGTTGCCCAGGCT
172808	5004	AGAGGGGAGGGAACTAGTGT	217395	49591	CAGGGTGGCTGTGATTGTCA	261982	94178	TCTTGCTATGTTGCCCAGGC
172809	5005	GAGAGGGGAGGGAACTAGTG	217396	49592	ACAGGGTGGCTGTGATTGTC	261983	94179	GTCTTGCTATGTTGCCCAGG
172810	5006	TGAGAGGGGAGGGAACTAGT	217397	49593	CACAGGGTGGCTGTGATTGT	261984	94180	GGTCTTGCTATGTTGCCCAG
172811	5007	CTGAGAGGGGAGGGAACTAG	217398	49594	CCACAGGGTGGCTGTGATTG	261985	94181	GGGTCTTGCTATGTTGCCCA
172812	5008	GCTGAGAGGGGAGGGAACTA	217399	49595	CCCACAGGGTGGCTGTGATT	261986	94182	GGGGTCTTGCTATGTTGCCC
172813	5009	GGCTGAGAGGGGAGGGAACT	217400	49596	CCCCACAGGGTGGCTGTGAT	261987	94183	TGGGGTCTTGCTATGTTGCC
172814	5010	TGGCTGAGAGGGGAGGGAAC	217401	49597	GCCCCACAGGGTGGCTGTGA	261988	94184	ATGGGGTCTTGCTATGTTGC
172815	5011	GTGGCTGAGAGGGGAGGGAA	217402	49598	TGCCCCACAGGGTGGCTGTG	261989	94185	GATGGGGTCTTGCTATGTTG
172816	5012	TGTGGCTGAGAGGGGAGGGA	217403	49599	CTGCCCCACAGGGTGGCTGT	261990	94186	AGATGGGGTCTTGCTATGTT
172817	5013	ATGTGGCTGAGAGGGGAGGG	217404	49600	CCTGCCCCACAGGGTGGCTG	261991	94187	GAGATGGGGTCTTGCTATGT
172818	5014	CATGTGGCTGAGAGGGGAGG	217405	49601	TCCTGCCCCACAGGGTGGCT	261992	94188	TGAGATGGGGTCTTGCTATG
172819	5015	ACATGTGGCTGAGAGGGGAG	217406	49602	CTCCTGCCCCACAGGGTGGC	261993	94189	TTGAGATGGGGTCTTGCTAT
172820	5016	CACATGTGGCTGAGAGGGGA	217407	49603	ACTCCTGCCCCACAGGGTGG	261994	94190	TTTGAGATGGGGTCTTGCTA
172821	5017	CCACATGTGGCTGAGAGGGG	217408	49604	CACTCCTGCCCCACAGGGTG	261995	94191	TTTTGAGATGGGGTCTTGCT
172822	5018	CCCACATGTGGCTGAGAGGG	217409	49605	ACACTCCTGCCCCACAGGGT	261996	94192	TTTTTGAGATGGGGTCTTGC
172823	5019	ACCCACATGTGGCTGAGAGG	217410	49606	GACACTCCTGCCCCACAGGG	261997	94193	TTTTTTGAGATGGGGTCTTG
172824	5020	AACCCACATGTGGCTGAGAG	217411	49607	TGACACTCCTGCCCCACAGG	261998	94194	TTTTTTTGAGATGGGGTCTT
172825	5021	AAACCCACATGTGGCTGAGA	217412	49608	ATGACACTCCTGCCCCACAG	261999	94195	TTTTTTTTGAGATGGGGTCT
172826	5022	TAAACCCACATGTGGCTGAG	217413	49609	GATGACACTCCTGCCCCACA	262000	94196	TTTTTTTTTGAGATGGGGTC
172827	5023	GTAAACCCACATGTGGCTGA	217414	49610	TGATGACACTCCTGCCCCAC	262001	94197	TTTTTTTTTTGAGATGGGGT
172828	5024	AGTAAACCCACATGTGGCTG	217415	49611	ATGATGACACTCCTGCCCCA	262002	94198	ATTTTTTTTTTGAGATGGGG
172829	5025	AAGTAAACCCACATGTGGCT	217416	49612	GATGATGACACTCCTGCCCC	262003	94199	AATTTTTTTTTTGAGATGGG
172830	5026	CAAGTAAACCCACATGTGGC	217417	49613	GGATGATGACACTCCTGCCC	262004	94200	AAATTTTTTTTTTGAGATGG
172831	5027	CCAAGTAAACCCACATGTGG	217418	49614	GGGATGATGACACTCCTGCC	262005	94201	TAAATTTTTTTTTTGAGATG
172832	5028	GCCAAGTAAACCCACATGTG	217419	49615	GGGGATGATGACACTCCTGC	262006	94202	TTAAATTTTTTTTTTGAGAT
172833	5029	GGCCAAGTAAACCCACATGT	217420	49616	TGGGGATGATGACACTCCTG	262007	94203	ATTAAATTTTTTTTTTGAGA
172834	5030	TGGCCAAGTAAACCCACATG	217421	49617	ATGGGGATGATGACACTCCT	262008	94204	AATTAAATTTTTTTTTTGAG
172835	5031	ATGGCCAAGTAAACCCACAT	217422	49618	CATGGGGATGATGACACTCC	262009	94205	CAATTAAATTTTTTTTTTGA
172836	5032	AATGGCCAAGTAAACCCACA	217423	49619	ACATGGGGATGATGACACTC	262010	94206	CCAATTAAATTTTTTTTTTG
172837	5033	CAATGGCCAAGTAAACCCAC	217424	49620	AACATGGGGATGATGACACT	262011	94207	GCCAATTAAATTTTTTTTTT
172838	5034	ACAATGGCCAAGTAAACCCA	217425	49621	AAACATGGGGATGATGACAC	262012	94208	GGCCAATTAAATTTTTTTTT
172839	5035	CACAATGGCCAAGTAAACCC	217426	49622	GAAACATGGGGATGATGACA	262013	94209	TGGCCAATTAAATTTTTTTT
172840	5036	CCACAATGGCCAAGTAAACC	217427	49623	TGAAACATGGGGATGATGAC	262014	94210	CTGGCCAATTAAATTTTTTT
172841	5037	TCCACAATGGCCAAGTAAAC	217428	49624	TTGAAACATGGGGATGATGA	262015	94211	CCTGGCCAATTAAATTTTTT
172842	5038	GTCCACAATGGCCAAGTAAA	217429	49625	TTTGAAACATGGGGATGATG	262016	94212	GCCTGGCCAATTAAATTTTT

172843	5039	AGTCCACAATGGCCAAGTAA	217430	49626	ATTTGAAACATGGGGATGAT	262017	94213	TGCCTGGCCAATTAAATTTT
172844	5040	TAGTCCACAATGGCCAAGTA	217431	49627	CATTTGAAACATGGGGATGA	262018	94214	CTGCCTGGCCAATTAAATTT
172845	5041	CTAGTCCACAATGGCCAAGT	217432	49628	TCATTTGAAACATGGGGATG	262019	94215	TCTGCCTGGCCAATTAAATT
172846	5042	ACTAGTCCACAATGGCCAAG	217433	49629	TTCATTTGAAACATGGGGAT	262020	94216	CTCTGCCTGGCCAATTAAAT
172847	5043	GACTAGTCCACAATGGCCAA	217434	49630	CTTCATTTGAAACATGGGGA	262021	94217	CCTCTGCCTGGCCAATTAAA
172848	5044	AGACTAGTCCACAATGGCCA	217435	49631	TCTTCATTTGAAACATGGGG	262022	94218	ACCTCTGCCTGGCCAATTAA
172849	5045	CAGACTAGTCCACAATGGCC	217436	49632	TTCTTCATTTGAAACATGGG	262023	94219	CACCTCTGCCTGGCCAATTA
172850	5046	CCAGACTAGTCCACAATGGC	217437	49633	ATTCTTCATTTGAAACATGG	262024	94220	CCACCTCTGCCTGGCCAATT
172851	5047	CCCAGACTAGTCCACAATGG	217438	49634	AATTCTTCATTTGAAACATG	262025	94221	CCCACCTCTGCCTGGCCAAT
172852	5048	TCCCAGACTAGTCCACAATG	217439	49635	CAATTCTTCATTTGAAACAT	262026	94222	TCCCACCTCTGCCTGGCCAA
172853	5049	TTCCCAGACTAGTCCACAAT	217440	49636	GCAATTCTTCATTTGAAACA	262027	94223	CTCCCACCTCTGCCTGGCCA
172854	5050	GTTCCCAGACTAGTCCACAA	217441	49637	TGCAATTCTTCATTTGAAAC	262028	94224	CCTCCCACCTCTGCCTGGCC
172855	5051	GGTTCCCAGACTAGTCCACA	217442	49638	CTGCAATTCTTCATTTGAAA	262029	94225	TCCTCCCACCTCTGCCTGGC
172856	5052	GGGTTCCCAGACTAGTCCAC	217443	49639	ACTGCAATTCTTCATTTGAA	262030	94226	ATCCTCCCACCTCTGCCTGG
172857	5053	TGGGTTCCCAGACTAGTCCA	217444	49640	AACTGCAATTCTTCATTTGA	262031	94227	GATCCTCCCACCTCTGCCTG
172858	5054	CTGGGTTCCCAGACTAGTCC	217445	49641	GAACTGCAATTCTTCATTTG	262032	94228	TGATCCTCCCACCTCTGCCT
172859	5055	TCTGGGTTCCCAGACTAGTC	217446	49642	TGAACTGCAATTCTTCATTT	262033	94229	GTGATCCTCCCACCTCTGCC
172860	5056	ATCTGGGTTCCCAGACTAGT	217447	49643	CTGAACTGCAATTCTTCATT	262034	94230	AGTGATCCTCCCACCTCTGC
172861	5057	TATCTGGGTTCCCAGACTAG	217448	49644	TCTGAACTGCAATTCTTCAT	262035	94231	AAGTGATCCTCCCACCTCTG
172862	5058	ATATCTGGGTTCCCAGACTA	217449	49645	CTCTGAACTGCAATTCTTCA	262036	94232	CAAGTGATCCTCCCACCTCT
172863	5059	CATATCTGGGTTCCCAGACT	217450	49646	TCTCTGAACTGCAATTCTTC	262037	94233	TCAAGTGATCCTCCCACCTC
172864	5060	TCATATCTGGGTTCCCAGAC	217451	49647	CTCTCTGAACTGCAATTCTT	262038	94234	TTCAAGTGATCCTCCCACCT
172865	5061	ATCATATCTGGGTTCCCAGA	217452	49648	CCTCTCTGAACTGCAATTCT	262039	94235	GTTCAAGTGATCCTCCCACC
172866	5062	GATCATATCTGGGTTCCCAG	217453	49649	CCCTCTCTGAACTGCAATTC	262040	94236	GGTTCAAGTGATCCTCCCAC
172867	5063	AGATCATATCTGGGTTCCCA	217454	49650	GCCCTCTCTGAACTGCAATT	262041	94237	GGGTTCAAGTGATCCTCCCA
172868	5064	TAGATCATATCTGGGTTCCC	217455	49651	TGCCCTCTCTGAACTGCAAT	262042	94238	TGGGTTCAAGTGATCCTCCC
172869	5065	ATAGATCATATCTGGGTTCC	217456	49652	TTGCCCTCTCTGAACTGCAA	262043	94239	TTGGGTTCAAGTGATCCTCC
172870	5066	TATAGATCATATCTGGGTTC	217457	49653	CTTGCCCTCTCTGAACTGCA	262044	94240	TTTGGGTTCAAGTGATCCTC
172871	5067	TTATAGATCATATCTGGGTT	217458	49654	ACTTGCCCTCTCTGAACTGC	262045	94241	CTTTGGGTTCAAGTGATCCT
172872	5068	GTTATAGATCATATCTGGGT	217459	49655	CACTTGCCCTCTCTGAACTG	262046	94242	CCTTTGGGTTCAAGTGATCC
172873	5069	TGTTATAGATCATATCTGGG	217460	49656	TCACTTGCCCTCTCTGAACT	262047	94243	CCCTTTGGGTTCAAGTGATC
172874	5070	ATGTTATAGATCATATCTGG	217461	49657	GTCACTTGCCCTCTCTGAAC	262048	94244	ACCCTTTGGGTTCAAGTGAT
172875	5071	AATGTTATAGATCATATCTG	217462	49658	AGTCACTTGCCCTCTCTGAA	262049	94245	CACCCTTTGGGTTCAAGTGA
172876	5072	CAATGTTATAGATCATATCT	217463	49659	CAGTCACTTGCCCTCTCTGA	262050	94246	CCACCCTTTGGGTTCAAGTG
172877	5073	TCAATGTTATAGATCATATC	217464	49660	CCAGTCACTTGCCCTCTCTG	262051	94247	TCCACCCTTTGGGTTCAAGT
172878	5074	GTCAATGTTATAGATCATAT	217465	49661	GCCAGTCACTTGCCCTCTCT	262052	94248	CTCCACCCTTTGGGTTCAAG
172879	5075	GGTCAATGTTATAGATCATA	217466	49662	GGCCAGTCACTTGCCCTCTC	262053	94249	CCTCCACCCTTTGGGTTCAA
172880	5076	GGGTCAATGTTATAGATCAT	217467	49663	GGGCCAGTCACTTGCCCTCT	262054	94250	GCCTCCACCCTTTGGGTTCA
172881	5077	TGGGTCAATGTTATAGATCA	217468	49664	TGGGCCAGTCACTTGCCCTC	262055	94251	AGCCTCCACCCTTTGGGTTC
172882	5078	CTGGGTCAATGTTATAGATC	217469	49665	CTGGGCCAGTCACTTGCCCT	262056	94252	CAGCCTCCACCCTTTGGGTT
172883	5079	ACTGGGTCAATGTTATAGAT	217470	49666	GCTGGGCCAGTCACTTGCCC	262057	94253	GCAGCCTCCACCCTTTGGGT
172884	5080	TACTGGGTCAATGTTATAGA	217471	49667	GGCTGGGCCAGTCACTTGCC	262058	94254	TGCAGCCTCCACCCTTTGGG
172885	5081	CTACTGGGTCAATGTTATAG	217472	49668	AGGCTGGGCCAGTCACTTGC	262059	94255	CTGCAGCCTCCACCCTTTGG
172886	5082	TCTACTGGGTCAATGTTATA	217473	49669	GAGGCTGGGCCAGTCACTTG	262060	94256	ACTGCAGCCTCCACCCTTTG
172887	5083	TTCTACTGGGTCAATGTTAT	217474	49670	TGAGGCTGGGCCAGTCACTT	262061	94257	CACTGCAGCCTCCACCCTTT
172888	5084	ATTCTACTGGGTCAATGTTA	217475	49671	TTGAGGCTGGGCCAGTCACT	262062	94258	TCACTGCAGCCTCCACCCTT
172889	5085	TATTCTACTGGGTCAATGTT	217476	49672	GTTGAGGCTGGGCCAGTCAC	262063	94259	CTCACTGCAGCCTCCACCCT
172890	5086	ATATTCTACTGGGTCAATGT	217477	49673	TGTTGAGGCTGGGCCAGTCA	262064	94260	GCTCACTGCAGCCTCCACCC
172891	5087	AATATTCTACTGGGTCAATG	217478	49674	CTGTTGAGGCTGGGCCAGTC	262065	94261	GGCTCACTGCAGCCTCCACC
172892	5088	CAATATTCTACTGGGTCAAT	217479	49675	GCTGTTGAGGCTGGGCCAGT	262066	94262	CGGCTCACTGCAGCCTCCAC
172893	5089	TCAATATTCTACTGGGTCAA	217480	49676	AGCTGTTGAGGCTGGGCCAG	262067	94263	ACGGCTCACTGCAGCCTCCA
172894	5090	ATCAATATTCTACTGGGTCA	217481	49677	TAGCTGTTGAGGCTGGGCCA	262068	94264	CACGGCTCACTGCAGCCTCC
172895	5091	AATCAATATTCTACTGGGTC	217482	49678	CTAGCTGTTGAGGCTGGGCC	262069	94265	TCACGGCTCACTGCAGCCTC
172896	5092	GAATCAATATTCTACTGGGT	217483	49679	GCTAGCTGTTGAGGCTGGGC	262070	94266	ATCACGGCTCACTGCAGCCT
172897	5093	GGAATCAATATTCTACTGGG	217484	49680	GGCTAGCTGTTGAGGCTGGG	262071	94267	CATCACGGCTCACTGCAGCC
172898	5094	TGGAATCAATATTCTACTGG	217485	49681	TGGCTAGCTGTTGAGGCTGG	262072	94268	CCATCACGGCTCACTGCAGC
172899	5095	TTGGAATCAATATTCTACTG	217486	49682	CTGGCTAGCTGTTGAGGCTG	262073	94269	GCCATCACGGCTCACTGCAG
172900	5096	TTTGGAATCAATATTCTACT	217487	49683	ACTGGCTAGCTGTTGAGGCT	262074	94270	TGCCATCACGGCTCACTGCA
172901	5097	TTTTGGAATCAATATTCTAC	217488	49684	CACTGGCTAGCTGTTGAGGC	262075	94271	GTGCCATCACGGCTCACTGC
172902	5098	GTTTTGGAATCAATATTCTA	217489	49685	CCACTGGCTAGCTGTTGAGG	262076	94272	GGTGCCATCACGGCTCACTG
172903	5099	GGTTTTGGAATCAATATTCT	217490	49686	TCCACTGGCTAGCTGTTGAG	262077	94273	TGGTGCCATCACGGCTCACT
172904	5100	TGGTTTTGGAATCAATATTC	217491	49687	GTCCACTGGCTAGCTGTTGA	262078	94274	GTGGTGCCATCACGGCTCAC
172905	5101	GTGGTTTTGGAATCAATATT	217492	49688	GGTCCACTGGCTAGCTGTTG	262079	94275	AGTGGTGCCATCACGGCTCA
172906	5102	AGTGGTTTTGGAATCAATAT	217493	49689	GGGTCCACTGGCTAGCTGTT	262080	94276	CAGTGGTGCCATCACGGCTC
172907	5103	CAGTGGTTTTGGAATCAATA	217494	49690	GGGGTCCACTGGCTAGCTGT	262081	94277	GCAGTGGTGCCATCACGGCT
172908	5104	ACAGTGGTTTTGGAATCAAT	217495	49691	TGGGGTCCACTGGCTAGCTG	262082	94278	TGCAGTGGTGCCATCACGGC
172909	5105	GACAGTGGTTTTGGAATCAA	217496	49692	GTGGGGTCCACTGGCTAGCT	262083	94279	GTGCAGTGGTGCCATCACGG
172910	5106	AGACAGTGGTTTTGGAATCA	217497	49693	GGTGGGGTCCACTGGCTAGC	262084	94280	AGTGCAGTGGTGCCATCACG
172911	5107	GAGACAGTGGTTTTGGAATC	217498	49694	TGGTGGGGTCCACTGGCTAG	262085	94281	GAGTGCAGTGGTGCCATCAC
172912	5108	TGAGACAGTGGTTTTGGAAT	217499	49695	CTGGTGGGGTCCACTGGCTA	262086	94282	GGAGTGCAGTGGTGCCATCA
172913	5109	GTGAGACAGTGGTTTTGGAA	217500	49696	CCTGGTGGGGTCCACTGGCT	262087	94283	TGGAGTGCAGTGGTGCCATC
172914	5110	TGTGAGACAGTGGTTTTGGA	217501	49697	CCCTGGTGGGGTCCACTGGC	262088	94284	CTGGAGTGCAGTGGTGCCAT

172915	5111	TTGTGAGACAGTGGTTTTGG	217502	49698	GCCCTGGTGGGGTCCACTGG	262089	94285	GCTGGAGTGCAGTGGTGCCA
172916	5112	TTTGTGAGACAGTGGTTTTG	217503	49699	AGCCCTGGTGGGGTCCACTG	262090	94286	GGCTGGAGTGCAGTGGTGCC
172917	5113	ATTTGTGAGACAGTGGTTTT	217504	49700	AAGCCCTGGTGGGGTCCACT	262091	94287	TGGCTGGAGTGCAGTGGTGC
172918	5114	CATTTGTGAGACAGTGGTTT	217505	49701	GAAGCCCTGGTGGGGTCCAC	262092	94288	CTGGCTGGAGTGCAGTGGTG
172919	5115	TCATTTGTGAGACAGTGGTT	217506	49702	AGAAGCCCTGGTGGGGTCCA	262093	94289	CCTGGCTGGAGTGCAGTGGT
172920	5116	TTCATTTGTGAGACAGTGGT	217507	49703	CAGAAGCCCTGGTGGGGTCC	262094	94290	CCCTGGCTGGAGTGCAGTGG
172921	5117	ATTCATTTGTGAGACAGTGG	217508	49704	TCAGAAGCCCTGGTGGGGTC	262095	94291	GCCCTGGCTGGAGTGCAGTG
172922	5118	AATTCATTTGTGAGACAGTG	217509	49705	GTCAGAAGCCCTGGTGGGGT	262096	94292	TGCCCTGGCTGGAGTGCAGT
172923	5119	AAATTCATTTGTGAGACAGT	217510	49706	AGTCAGAAGCCCTGGTGGGG	262097	94293	TTGCCCTGGCTGGAGTGCAG
172924	5120	AAAATTCATTTGTGAGACAG	217511	49707	GAGTCAGAAGCCCTGGTGGG	262098	94294	GTTGCCCTGGCTGGAGTGCA
172925	5121	AAAAATTCATTTGTGAGACA	217512	49708	GGAGTCAGAAGCCCTGGTGG	262099	94295	TGTTGCCCTGGCTGGAGTGC
172926	5122	TAAAAATTCATTTGTGAGAC	217513	49709	TGGAGTCAGAAGCCCTGGTG	262100	94296	CTGTTGCCCTGGCTGGAGTG
172927	5123	GTAAAAATTCATTTGTGAGA	217514	49710	CTGGAGTCAGAAGCCCTGGT	262101	94297	TCTGTTGCCCTGGCTGGAGT
172928	5124	TGTAAAAATTCATTTGTGAG	217515	49711	ACTGGAGTCAGAAGCCCTGG	262102	94298	CTCTGTTGCCCTGGCTGGAG
172929	5125	TTGTAAAAATTCATTTGTGA	217516	49712	GACTGGAGTCAGAAGCCCTG	262103	94299	CCTCTGTTGCCCTGGCTGGA
172930	5126	CTTGTAAAAATTCATTTGTG	217517	49713	GGACTGGAGTCAGAAGCCCT	262104	94300	CCCTCTGTTGCCCTGGCTGG
172931	5127	TCTTGTAAAAATTCATTTGT	217518	49714	CGGACTGGAGTCAGAAGCCC	262105	94301	TCCCTCTGTTGCCCTGGCTG
172932	5128	CTCTTGTAAAAATTCATTTG	217519	49715	CCGGACTGGAGTCAGAAGCC	262106	94302	CTCCCTCTGTTGCCCTGGCT
172933	5129	ACTCTTGTAAAAATTCATTT	217520	49716	CCCGGACTGGAGTCAGAAGC	262107	94303	TCTCCCTCTGTTGCCCTGGC
172934	5130	GACTCTTGTAAAAATTCATT	217521	49717	ACCCGGACTGGAGTCAGAAG	262108	94304	GTCTCCCTCTGTTGCCCTGG
172935	5131	AGACTCTTGTAAAAATTCAT	217522	49718	AACCCGGACTGGAGTCAGAA	262109	94305	GGTCTCCCTCTGTTGCCCTG
172936	5132	CAGACTCTTGTAAAAATTCA	217523	49719	GAACCCGGACTGGAGTCAGA	262110	94306	GGGTCTCCCTCTGTTGCCCT
172937	5133	ACAGACTCTTGTAAAAATTC	217524	49720	GGAACCCGGACTGGAGTCAG	262111	94307	AGGGTCTCCCTCTGTTGCCC
172938	5134	TACAGACTCTTGTAAAAATT	217525	49721	GGGAACCCGGACTGGAGTCA	262112	94308	CAGGGTCTCCCTCTGTTGCC
172939	5135	TTACAGACTCTTGTAAAAAT	217526	49722	AGGGAACCCGGACTGGAGTC	262113	94309	ACAGGGTCTCCCTCTGTTGC
172940	5136	ATTACAGACTCTTGTAAAAA	217527	49723	AAGGGAACCCGGACTGGAGT	262114	94310	GACAGGGTCTCCCTCTGTTG
172941	5137	GATTACAGACTCTTGTAAAA	217528	49724	AAAGGGAACCCGGACTGGAG	262115	94311	AGACAGGGTCTCCCTCTGTT
172942	5138	CGATTACAGACTCTTGTAAA	217529	49725	GAAAGGGAACCCGGACTGGA	262116	94312	GAGACAGGGTCTCCCTCTGT
172943	5139	CCGATTACAGACTCTTGTAA	217530	49726	GGAAAGGGAACCCGGACTGG	262117	94313	AGAGACAGGGTCTCCCTCTG
172944	5140	TCCGATTACAGACTCTTGTA	217531	49727	TGGAAAGGGAACCCGGACTG	262118	94314	TAGAGACAGGGTCTCCCTCT
172945	5141	CTCCGATTACAGACTCTTGT	217532	49728	GTGGAAAGGGAACCCGGACT	262119	94315	TTAGAGACAGGGTCTCCCTC
172946	5142	GCTCCGATTACAGACTCTTG	217533	49729	GGTGGAAAGGGAACCCGGAC	262120	94316	TTTAGAGACAGGGTCTCCCT
172947	5143	TGCTCCGATTACAGACTCTT	217534	49730	GGGTGGAAAGGGAACCCGGA	262121	94317	TTTTAGAGACAGGGTCTCCC
172948	5144	ATGCTCCGATTACAGACTCT	217535	49731	TGGGTGGAAAGGGAACCCGG	262122	94318	GTTTTAGAGACAGGGTCTCC
172949	5145	CATGCTCCGATTACAGACTC	217536	49732	TTGGGTGGAAAGGGAACCCG	262123	94319	TGTTTTAGAGACAGGGTCTC
172950	5146	TCATGCTCCGATTACAGACT	217537	49733	TTTGGGTGGAAAGGGAACCC	262124	94320	TTGTTTTAGAGACAGGGTCT
172951	5147	GTCATGCTCCGATTACAGAC	217538	49734	ATTTGGGTGGAAAGGGAACC	262125	94321	TTTGTTTTAGAGACAGGGTC
172952	5148	GGTCATGCTCCGATTACAGA	217539	49735	GATTTGGGTGGAAAGGGAAC	262126	94322	GTTTGTTTTAGAGACAGGGT
172953	5149	GGGTCATGCTCCGATTACAG	217540	49736	GGATTTGGGTGGAAAGGGAA	262127	94323	TGTTTGTTTTAGAGACAGGG
172954	5150	TGGGTCATGCTCCGATTACA	217541	49737	TGGATTTGGGTGGAAAGGGA	262128	94324	TTGTTTGTTTTAGAGACAGG
172955	5151	CTGGGTCATGCTCCGATTAC	217542	49738	ATGGATTTGGGTGGAAAGGG	262129	94325	TTTGTTTGTTTTAGAGACAG
172956	5152	TCTGGGTCATGCTCCGATTA	217543	49739	CATGGATTTGGGTGGAAAGG	262130	94326	GTTTGTTTGTTTTAGAGACA
172957	5153	TTCTGGGTCATGCTCCGATT	217544	49740	CCATGGATTTGGGTGGAAAG	262131	94327	TGTTTGTTTGTTTTAGAGAC
172958	5154	ATTCTGGGTCATGCTCCGAT	217545	49741	TCCATGGATTTGGGTGGAAA	262132	94328	TTGTTTGTTTGTTTTAGAGA
172959	5155	TATTCTGGGTCATGCTCCGA	217546	49742	CTCCATGGATTTGGGTGGAA	262133	94329	TTTGTTTGTTTGTTTTAGAG
172960	5156	TTATTCTGGGTCATGCTCCG	217547	49743	CCTCCATGGATTTGGGTGGA	262134	94330	GTTTGTTTGTTTGTTTTAGA
172961	5157	CTTATTCTGGGTCATGCTCC	217548	49744	CCCTCCATGGATTTGGGTGG	262135	94331	TGTTTGTTTGTTTGTTTTAG
172962	5158	CCTTATTCTGGGTCATGCTC	217549	49745	TCCCTCCATGGATTTGGGTG	262136	94332	TTGTTTGTTTGTTTGTTTTA
172963	5159	ACCTTATTCTGGGTCATGCT	217550	49746	CTCCCTCCATGGATTTGGGT	262137	94333	TTTGTTTGTTTGTTTGTTTT
172964	5160	AACCTTATTCTGGGTCATGC	217551	49747	GCTCCCTCCATGGATTTGGG	262138	94334	GTTTGTTTGTTTGTTTGTTT
172965	5161	TAACCTTATTCTGGGTCATG	217552	49748	AGCTCCCTCCATGGATTTGG	262139	94335	TGTTTGTTTGTTTGTTTGTT
172966	5162	CTAACCTTATTCTGGGTCAT	217553	49749	CAGCTCCCTCCATGGATTTG	262140	94336	TTGTTTGTTTGTTTGTTTGT
172967	5163	CCTAACCTTATTCTGGGTCA	217554	49750	TCAGCTCCCTCCATGGATTT	262141	94337	TTTGTTTGTTTGTTTGTTTG
172968	5164	CCCTAACCTTATTCTGGGTC	217555	49751	CTCAGCTCCCTCCATGGATT	262142	94338	GTTTGTTTGTTTGTTTGTTT
172969	5165	TCCCTAACCTTATTCTGGGT	217556	49752	GCTCAGCTCCCTCCATGGAT	262143	94339	TGTTTGTTTGTTTGTTTGTT
172970	5166	CTCCCTAACCTTATTCTGGG	217557	49753	GGCTCAGCTCCCTCCATGGA	262144	94340	TTGTTTGTTTGTTTGTTTGT
172971	5167	TCTCCCTAACCTTATTCTGG	217558	49754	CGGCTCAGCTCCCTCCATGG	262145	94341	TTTGTTTGTTTGTTTGTTTG
172972	5168	ATCTCCCTAACCTTATTCTG	217559	49755	TCGGCTCAGCTCCCTCCATG	262146	94342	TTTTGTTTGTTTGTTTGTTT
172973	5169	CATCTCCCTAACCTTATTCT	217560	49756	CTCGGCTCAGCTCCCTCCAT	262147	94343	CTTTTGTTTGTTTGTTTGTT
172974	5170	ACATCTCCCTAACCTTATTC	217561	49757	TCTCGGCTCAGCTCCCTCCA	262148	94344	TCTTTTGTTTGTTTGTTTGT
172975	5171	CACATCTCCCTAACCTTATT	217562	49758	TTCTCGGCTCAGCTCCCTCC	262149	94345	CTCTTTTGTTTGTTTGTTTG
172976	5172	CCACATCTCCCTAACCTTAT	217563	49759	GTTCTCGGCTCAGCTCCCTC	262150	94346	ACTCTTTTGTTTGTTTGTTT
172977	5173	TCCACATCTCCCTAACCTTA	217564	49760	TGTTCTCGGCTCAGCTCCCT	262151	94347	AACTCTTTTGTTTGTTTGTT
172978	5174	CTCCACATCTCCCTAACCTT	217565	49761	CTGTTCTCGGCTCAGCTCCC	262152	94348	TAACTCTTTTGTTTGTTTGT
172979	5175	ACTCCACATCTCCCTAACCT	217566	49762	CCTGTTCTCGGCTCAGCTCC	262153	94349	TTAACTCTTTTGTTTGTTTG
172980	5176	AACTCCACATCTCCCTAACC	217567	49763	ACCTGTTCTCGGCTCAGCTC	262154	94350	GTTAACTCTTTTGTTTGTTT
172981	5177	TAACTCCACATCTCCCTAAC	217568	49764	CACCTGTTCTCGGCTCAGCT	262155	94351	TGTTAACTCTTTTGTTTGTT
172982	5178	TTAACTCCACATCTCCCTAA	217569	49765	ACACCTGTTCTCGGCTCAGC	262156	94352	ATGTTAACTCTTTTGTTTGT
172983	5179	TTTAACTCCACATCTCCCTA	217570	49766	GACACCTGTTCTCGGCTCAG	262157	94353	AATGTTAACTCTTTTGTTTG
172984	5180	CTTTAACTCCACATCTCCCT	217571	49767	GGACACCTGTTCTCGGCTCA	262158	94354	CAATGTTAACTCTTTTGTTT
172985	5181	GCTTTAACTCCACATCTCCC	217572	49768	AGGACACCTGTTCTCGGCTC	262159	94355	CCAATGTTAACTCTTTTGTT
172986	5182	AGCTTTAACTCCACATCTCC	217573	49769	AAGGACACCTGTTCTCGGCT	262160	94356	GCCAATGTTAACTCTTTTGT

172987	5183	GAGCTTTAACTCCACATCTC	217574	49770	GAAGGACACCTGTTCTCGGC	262161	94357	GGCCAATGTTAACTCTTTTG
172988	5184	AGAGCTTTAACTCCACATCT	217575	49771	TGAAGGACACCTGTTCTCGG	262162	94358	TGGCCAATGTTAACTCTTTT
172989	5185	GAGAGCTTTAACTCCACATC	217576	49772	CTGAAGGACACCTGTTCTCG	262163	94359	CTGGCCAATGTTAACTCTTT
172990	5186	TGAGAGCTTTAACTCCACAT	217577	49773	CCTGAAGGACACCTGTTCTC	262164	94360	TCTGGCCAATGTTAACTCTT
172991	5187	TTGAGAGCTTTAACTCCACA	217578	49774	TCCTGAAGGACACCTGTTCT	262165	94361	ATCTGGCCAATGTTAACTCT
172992	5188	ATTGAGAGCTTTAACTCCAC	217579	49775	TTCCTGAAGGACACCTGTTC	262166	94362	AATCTGGCCAATGTTAACTC
172993	5189	AATTGAGAGCTTTAACTCCA	217580	49776	CTTCCTGAAGGACACCTGTT	262167	94363	TAATCTGGCCAATGTTAACT
172994	5190	AAATTGAGAGCTTTAACTCC	217581	49777	TCTTCCTGAAGGACACCTGT	262168	94364	CTAATCTGGCCAATGTTAAC
172995	5191	GAAATTGAGAGCTTTAACTC	217582	49778	GTCTTCCTGAAGGACACCTG	262169	94365	CCTAATCTGGCCAATGTTAA
172996	5192	AGAAATTGAGAGCTTTAACT	217583	49779	CGTCTTCCTGAAGGACACCT	262170	94366	TCCTAATCTGGCCAATGTTA
172997	5193	AAGAAATTGAGAGCTTTAAC	217584	49780	ACGTCTTCCTGAAGGACACC	262171	94367	ATCCTAATCTGGCCAATGTT
172998	5194	TAAGAAATTGAGAGCTTTAA	217585	49781	CACGTCTTCCTGAAGGACAC	262172	94368	AATCCTAATCTGGCCAATGT
172999	5195	ATAAGAAATTGAGAGCTTTA	217586	49782	TCACGTCTTCCTGAAGGACA	262173	94369	GAATCCTAATCTGGCCAATG
173000	5196	GATAAGAAATTGAGAGCTTT	217587	49783	TTCACGTCTTCCTGAAGGAC	262174	94370	TGAATCCTAATCTGGCCAAT
173001	5197	AGATAAGAAATTGAGAGCTT	217588	49784	CTTCACGTCTTCCTGAAGGA	262175	94371	GTGAATCCTAATCTGGCCAA
173002	5198	CAGATAAGAAATTGAGAGCT	217589	49785	GCTTCACGTCTTCCTGAAGG	262176	94372	GGTGAATCCTAATCTGGCCA
173003	5199	CCAGATAAGAAATTGAGAGC	217590	49786	GGCTTCACGTCTTCCTGAAG	262177	94373	TGGTGAATCCTAATCTGGCC
173004	5200	GCCAGATAAGAAATTGAGAG	217591	49787	TGGCTTCACGTCTTCCTGAA	262178	94374	CTGGTGAATCCTAATCTGGC
173005	5201	GGCCAGATAAGAAATTGAGA	217592	49788	TTGGCTTCACGTCTTCCTGA	262179	94375	TCTGGTGAATCCTAATCTGG
173006	5202	GGGCCAGATAAGAAATTGAG	217593	49789	TTTGGCTTCACGTCTTCCTG	262180	94376	ATCTGGTGAATCCTAATCTG
173007	5203	GGGGCCAGATAAGAAATTGA	217594	49790	CTTTGGCTTCACGTCTTCCT	262181	94377	TATCTGGTGAATCCTAATCT
173008	5204	CGGGGCCAGATAAGAAATTG	217595	49791	GCTTTGGCTTCACGTCTTCC	262182	94378	CTATCTGGTGAATCCTAATC
173009	5205	TCGGGGCCAGATAAGAAATT	217596	49792	GGCTTTGGCTTCACGTCTTC	262183	94379	ACTATCTGGTGAATCCTAAT
173010	5206	GTCGGGGCCAGATAAGAAAT	217597	49793	AGGCTTTGGCTTCACGTCTT	262184	94380	CACTATCTGGTGAATCCTAA
173011	5207	TGTCGGGGCCAGATAAGAAA	217598	49794	GAGGCTTTGGCTTCACGTCT	262185	94381	ACACTATCTGGTGAATCCTA
173012	5208	GTGTCGGGGCCAGATAAGAA	217599	49795	GGAGGCTTTGGCTTCACGTC	262186	94382	AACACTATCTGGTGAATCCT
173013	5209	TGTGTCGGGGCCAGATAAGA	217600	49796	TGGAGGCTTTGGCTTCACGT	262187	94383	TAACACTATCTGGTGAATCC
173014	5210	CTGTGTCGGGGCCAGATAAG	217601	49797	GTGGAGGCTTTGGCTTCACG	262188	94384	TTAACACTATCTGGTGAATC
173015	5211	TCTGTGTCGGGGCCAGATAA	217602	49798	GGTGGAGGCTTTGGCTTCAC	262189	94385	ATTAACACTATCTGGTGAAT
173016	5212	CTCTGTGTCGGGGCCAGATA	217603	49799	AGGTGGAGGCTTTGGCTTCA	262190	94386	TATTAACACTATCTGGTGAA
173017	5213	TCTCTGTGTCGGGGCCAGAT	217604	49800	GAGGTGGAGGCTTTGGCTTC	262191	94387	ATATTAACACTATCTGGTGA
173018	5214	CTCTCTGTGTCGGGGCCAGA	217605	49801	GGAGGTGGAGGCTTTGGCTT	262192	94388	AATATTAACACTATCTGGTG
173019	5215	GCTCTCTGTGTCGGGGCCAG	217606	49802	TGGAGGTGGAGGCTTTGGCT	262193	94389	TAATATTAACACTATCTGGT
173020	5216	TGCTCTCTGTGTCGGGGCCA	217607	49803	TTGGAGGTGGAGGCTTTGGC	262194	94390	CTAATATTAACACTATCTGG
173021	5217	TTGCTCTCTGTGTCGGGGCC	217608	49804	TTTGGAGGTGGAGGCTTTGG	262195	94391	ACTAATATTAACACTATCTG
173022	5218	CTTGCTCTCTGTGTCGGGGC	217609	49805	GTTTGGAGGTGGAGGCTTTG	262196	94392	AACTAATATTAACACTATCT
173023	5219	CCTTGCTCTCTGTGTCGGGG	217610	49806	AGTTTGGAGGTGGAGGCTTT	262197	94393	AAACTAATATTAACACTATC
173024	5220	GCCTTGCTCTCTGTGTCGGG	217611	49807	GAGTTTGGAGGTGGAGGCTT	262198	94394	CAAACTAATATTAACACTAT
173025	5221	TGCCTTGCTCTCTGTGTCGG	217612	49808	TGAGTTTGGAGGTGGAGGCT	262199	94395	TCAAACTAATATTAACACTA
173026	5222	ATGCCTTGCTCTCTGTGTCG	217613	49809	CTGAGTTTGGAGGTGGAGGC	262200	94396	ATCAAACTAATATTAACACT
173027	5223	AATGCCTTGCTCTCTGTGTC	217614	49810	CCTGAGTTTGGAGGTGGAGG	262201	94397	AATCAAACTAATATTAACAC
173028	5224	AAATGCCTTGCTCTCTGTGT	217615	49811	CCCTGAGTTTGGAGGTGGAG	262202	94398	AAATCAAACTAATATTAACA
173029	5225	GAAATGCCTTGCTCTCTGTG	217616	49812	CCCCTGAGTTTGGAGGTGGA	262203	94399	CAAATCAAACTAATATTAAC
173030	5226	TGAAATGCCTTGCTCTCTGT	217617	49813	GCCCCTGAGTTTGGAGGTGG	262204	94400	TCAAATCAAACTAATATTAA
173031	5227	GTGAAATGCCTTGCTCTCTG	217618	49814	GGCCCCTGAGTTTGGAGGTG	262205	94401	CTCAAATCAAACTAATATTA
173032	5228	AGTGAAATGCCTTGCTCTCT	217619	49815	GGGCCCCTGAGTTTGGAGGT	262206	94402	TCTCAAATCAAACTAATATT
173033	5229	GAGTGAAATGCCTTGCTCTC	217620	49816	TGGGCCCCTGAGTTTGGAGG	262207	94403	GTCTCAAATCAAACTAATAT
173034	5230	AGAGTGAAATGCCTTGCTCT	217621	49817	CTGGGCCCCTGAGTTTGGAG	262208	94404	AGTCTCAAATCAAACTAATA
173035	5231	TAGAGTGAAATGCCTTGCTC	217622	49818	CCTGGGCCCCTGAGTTTGGA	262209	94405	AAGTCTCAAATCAAACTAAT
173036	5232	GTAGAGTGAAATGCCTTGCT	217623	49819	CCCTGGGCCCCTGAGTTTGG	262210	94406	AAAGTCTCAAATCAAACTAA
173037	5233	TGTAGAGTGAAATGCCTTGC	217624	49820	TCCCTGGGCCCCTGAGTTTG	262211	94407	TAAAGTCTCAAATCAAACTA
173038	5234	ATGTAGAGTGAAATGCCTTG	217625	49821	CTCCCTGGGCCCCTGAGTTT	262212	94408	TTAAAGTCTCAAATCAAACT
173039	5235	AATGTAGAGTGAAATGCCTT	217626	49822	ACTCCCTGGGCCCCTGAGTT	262213	94409	ATTAAAGTCTCAAATCAAAC
173040	5236	CAATGTAGAGTGAAATGCCT	217627	49823	GACTCCCTGGGCCCCTGAGT	262214	94410	GATTAAAGTCTCAAATCAAA
173041	5237	CCAATGTAGAGTGAAATGCC	217628	49824	GGACTCCCTGGGCCCCTGAG	262215	94411	TGATTAAAGTCTCAAATCAA
173042	5238	ACCAATGTAGAGTGAAATGC	217629	49825	TGGACTCCCTGGGCCCCTGA	262216	94412	CTGATTAAAGTCTCAAATCA
173043	5239	CACCAATGTAGAGTGAAATG	217630	49826	CTGGACTCCCTGGGCCCCTG	262217	94413	TCTGATTAAAGTCTCAAATC
173044	5240	GCACCAATGTAGAGTGAAAT	217631	49827	CCTGGACTCCCTGGGCCCCT	262218	94414	TTCTGATTAAAGTCTCAAAT
173045	5241	AGCACCAATGTAGAGTGAAA	217632	49828	GCCTGGACTCCCTGGGCCCC	262219	94415	TTTCTGATTAAAGTCTCAAA
173046	5242	GAGCACCAATGTAGAGTGAA	217633	49829	TGCCTGGACTCCCTGGGCCC	262220	94416	CTTTCTGATTAAAGTCTCAA
173047	5243	AGAGCACCAATGTAGAGTGA	217634	49830	GTGCCTGGACTCCCTGGGCC	262221	94417	GCTTTCTGATTAAAGTCTCA
173048	5244	CAGAGCACCAATGTAGAGTG	217635	49831	GGTGCCTGGACTCCCTGGGC	262222	94418	TGCTTTCTGATTAAAGTCTC
173049	5245	ACAGAGCACCAATGTAGAGT	217636	49832	GGGTGCCTGGACTCCCTGGG	262223	94419	GTGCTTTCTGATTAAAGTCT
173050	5246	AACAGAGCACCAATGTAGAG	217637	49833	TGGGTGCCTGGACTCCCTGG	262224	94420	TGTGCTTTCTGATTAAAGTC
173051	5247	AAACAGAGCACCAATGTAGA	217638	49834	ATGGGTGCCTGGACTCCCTG	262225	94421	ATGTGCTTTCTGATTAAAGT
173052	5248	TAAACAGAGCACCAATGTAG	217639	49835	GATGGGTGCCTGGACTCCCT	262226	94422	CATGTGCTTTCTGATTAAAG
173053	5249	ATAAACAGAGCACCAATGTA	217640	49836	GGATGGGTGCCTGGACTCCC	262227	94423	ACATGTGCTTTCTGATTAAA
173054	5250	TATAAACAGAGCACCAATGT	217641	49837	TGGATGGGTGCCTGGACTCC	262228	94424	CACATGTGCTTTCTGATTAA
173055	5251	TTATAAACAGAGCACCAATG	217642	49838	GTGGATGGGTGCCTGGACTC	262229	94425	ACACATGTGCTTTCTGATTA
173056	5252	TTTATAAACAGAGCACCAAT	217643	49839	AGTGGATGGGTGCCTGGACT	262230	94426	CACACATGTGCTTTCTGATT
173057	5253	TTTTATAAACAGAGCACCAA	217644	49840	GAGTGGATGGGTGCCTGGAC	262231	94427	CCACACATGTGCTTTCTGAT
173058	5254	GTTTTATAAACAGAGCACCA	217645	49841	TGAGTGGATGGGTGCCTGGA	262232	94428	ACCACACATGTGCTTTCTGA

173059	5255	TGTTTTATAAACAGAGCACC	217646	49842	GTGAGTGGATGGGTGCCTGG	262233	94429	CACCACACATGTGCTTTCTG
173060	5256	TTGTTTTATAAACAGAGCAC	217647	49843	TGTGAGTGGATGGGTGCCTG	262234	94430	CCACCACACATGTGCTTTCT
173061	5257	TTTGTTTTATAAACAGAGCA	217648	49844	TTGTGAGTGGATGGGTGCCT	262235	94431	CCCACCACACATGTGCTTTC
173062	5258	CTTTGTTTTATAAACAGAGC	217649	49845	CTTGTGAGTGGATGGGTGCC	262236	94432	CCCCACCACACATGTGCTTT
173063	5259	TCTTTGTTTTATAAACAGAG	217650	49846	CCTTGTGAGTGGATGGGTGC	262237	94433	CCCCCACCACACATGTGCTT
173064	5260	CTCTTTGTTTTATAAACAGA	217651	49847	GCCTTGTGAGTGGATGGGTG	262238	94434	ACCCCCACCACACATGTGCT
173065	5261	GCTCTTTGTTTTATAAACAG	217652	49848	AGCCTTGTGAGTGGATGGGT	262239	94435	CACCCCCACCACACATGTGC
173066	5262	TGCTCTTTGTTTTATAAACA	217653	49849	CAGCCTTGTGAGTGGATGGG	262240	94436	CCACCCCCACCACACATGTG
173067	5263	TTGCTCTTTGTTTTATAAAC	217654	49850	CCAGCCTTGTGAGTGGATGG	262241	94437	CCCACCCCCACCACACATGT
173068	5264	TTTGCTCTTTGTTTTATAAA	217655	49851	TCCAGCCTTGTGAGTGGATG	262242	94438	ACCCACCCCCACCACACATG
173069	5265	ATTTGCTCTTTGTTTTATAA	217656	49852	ATCCAGCCTTGTGAGTGGAT	262243	94439	CACCCACCCCCACCACACAT
173070	5266	TATTTGCTCTTTGTTTTATA	217657	49853	TATCCAGCCTTGTGAGTGGA	262244	94440	ACACCCACCCCCACCACACA
173071	5267	ATATTTGCTCTTTGTTTTAT	217658	49854	ATATCCAGCCTTGTGAGTGG	262245	94441	TACACCCACCCCCACCACAC
173072	5268	GATATTTGCTCTTTGTTTTA	217659	49855	CATATCCAGCCTTGTGAGTG	262246	94442	TTACACCCACCCCCACCACA
173073	5269	AGATATTTGCTCTTTGTTTT	217660	49856	CCATATCCAGCCTTGTGAGT	262247	94443	GTTACACCCACCCCCACCAC
173074	5270	GAGATATTTGCTCTTTGTTT	217661	49857	ACCATATCCAGCCTTGTGAG	262248	94444	GGTTACACCCACCCCCACCA
173075	5271	AGAGATATTTGCTCTTTGTT	217662	49858	CACCATATCCAGCCTTGTGA	262249	94445	AGGTTACACCCACCCCCACC
173076	5272	AAGAGATATTTGCTCTTTGT	217663	49859	GCACCATATCCAGCCTTGTG	262250	94446	TAGGTTACACCCACCCCCAC
173077	5273	GAAGAGATATTTGCTCTTTG	217664	49860	TGCACCATATCCAGCCTTGT	262251	94447	TTAGGTTACACCCACCCCCA
173078	5274	GGAAGAGATATTTGCTCTTT	217665	49861	ATGCACCATATCCAGCCTTG	262252	94448	CTTAGGTTACACCCACCCCC
173079	5275	AGGAAGAGATATTTGCTCTT	217666	49862	AATGCACCATATCCAGCCTT	262253	94449	ACTTAGGTTACACCCACCCC
173080	5276	TAGGAAGAGATATTTGCTCT	217667	49863	GAATGCACCATATCCAGCCT	262254	94450	GACTTAGGTTACACCCACCC
173081	5277	TTAGGAAGAGATATTTGCTC	217668	49864	GGAATGCACCATATCCAGCC	262255	94451	TGACTTAGGTTACACCCACC
173082	5278	CTTAGGAAGAGATATTTGCT	217669	49865	TGGAATGCACCATATCCAGC	262256	94452	CTGACTTAGGTTACACCCAC
173083	5279	CCTTAGGAAGAGATATTTGC	217670	49866	CTGGAATGCACCATATCCAG	262257	94453	CCTGACTTAGGTTACACCCA
173084	5280	ACCTTAGGAAGAGATATTTG	217671	49867	CCTGGAATGCACCATATCCA	262258	94454	ACCTGACTTAGGTTACACCC
173085	5281	GACCTTAGGAAGAGATATTT	217672	49868	TCCTGGAATGCACCATATCC	262259	94455	TACCTGACTTAGGTTACACC
173086	5282	GGACCTTAGGAAGAGATATT	217673	49869	CTCCTGGAATGCACCATATC	262260	94456	CTACCTGACTTAGGTTACAC
173087	5283	AGGACCTTAGGAAGAGATAT	217674	49870	TCTCCTGGAATGCACCATAT	262261	94457	TCTACCTGACTTAGGTTACA
173088	5284	AAGGACCTTAGGAAGAGATA	217675	49871	CTCTCCTGGAATGCACCATA	262262	94458	TTCTACCTGACTTAGGTTAC
173089	5285	TAAGGACCTTAGGAAGAGAT	217676	49872	CCTCTCCTGGAATGCACCAT	262263	94459	ATTCTACCTGACTTAGGTTA
173090	5286	TTAAGGACCTTAGGAAGAGA	217677	49873	CCCTCTCCTGGAATGCACCA	262264	94460	GATTCTACCTGACTTAGGTT
173091	5287	TTTAAGGACCTTAGGAAGAG	217678	49874	CCCCTCTCCTGGAATGCACC	262265	94461	AGATTCTACCTGACTTAGGT
173092	5288	GTTTAAGGACCTTAGGAAGA	217679	49875	ACCCCTCTCCTGGAATGCAC	262266	94462	AAGATTCTACCTGACTTAGG
173093	5289	GGTTTAAGGACCTTAGGAAG	217680	49876	AACCCCTCTCCTGGAATGCA	262267	94463	AAAGATTCTACCTGACTTAG
173094	5290	AGGTTTAAGGACCTTAGGAA	217681	49877	CAACCCCTCTCCTGGAATGC	262268	94464	GAAAGATTCTACCTGACTTA
173095	5291	GAGGTTTAAGGACCTTAGGA	217682	49878	CCAACCCCTCTCCTGGAATG	262269	94465	GGAAAGATTCTACCTGACTT
173096	5292	AGAGGTTTAAGGACCTTAGG	217683	49879	CCCAACCCCTCTCCTGGAAT	262270	94466	TGGAAAGATTCTACCTGACT
173097	5293	AAGAGGTTTAAGGACCTTAG	217684	49880	CCCCAACCCCTCTCCTGGAA	262271	94467	TTGGAAAGATTCTACCTGAC
173098	5294	GAAGAGGTTTAAGGACCTTA	217685	49881	CCCCCAACCCCTCTCCTGGA	262272	94468	GTTGGAAAGATTCTACCTGA
173099	5295	GGAAGAGGTTTAAGGACCTT	217686	49882	GCCCCCAACCCCTCTCCTGG	262273	94469	AGTTGGAAAGATTCTACCTG
173100	5296	GGGAAGAGGTTTAAGGACCT	217687	49883	CGCCCCCAACCCCTCTCCTG	262274	94470	AAGTTGGAAAGATTCTACCT
173101	5297	GGGGAAGAGGTTTAAGGACC	217688	49884	TCGCCCCCAACCCCTCTCCT	262275	94471	CAAGTTGGAAAGATTCTACC
173102	5298	GGGGGAAGAGGTTTAAGGAC	217689	49885	CTCGCCCCCAACCCCTCTCC	262276	94472	CCAAGTTGGAAAGATTCTAC
173103	5299	TGGGGGAAGAGGTTTAAGGA	217690	49886	ACTCGCCCCCAACCCCTCTC	262277	94473	CCCAAGTTGGAAAGATTCTA
173104	5300	TTGGGGGAAGAGGTTTAAGG	217691	49887	CACTCGCCCCCAACCCCTCT	262278	94474	CCCCAAGTTGGAAAGATTCT
173105	5301	ATTGGGGGAAGAGGTTTAAG	217692	49888	CCACTCGCCCCCAACCCCTC	262279	94475	CCCCCAAGTTGGAAAGATTC
173106	5302	GATTGGGGGAAGAGGTTTAA	217693	49889	GCCACTCGCCCCCAACCCCT	262280	94476	CCCCCCAAGTTGGAAAGATT
173107	5303	GGATTGGGGGAAGAGGTTTA	217694	49890	GGCCACTCGCCCCCAACCCC	262281	94477	CCCCCCCAAGTTGGAAAGAT
173108	5304	TGGATTGGGGGAAGAGGTTT	217695	49891	AGGCCACTCGCCCCCAACCC	262282	94478	CCCCCCCCAAGTTGGAAAGA
173109	5305	CTGGATTGGGGGAAGAGGTT	217696	49892	GAGGCCACTCGCCCCCAACC	262283	94479	GCCCCCCCCAAGTTGGAAAG
173110	5306	CCTGGATTGGGGGAAGAGGT	217697	49893	AGAGGCCACTCGCCCCCAAC	262284	94480	TGCCCCCCCCAAGTTGGAAA
173111	5307	CCCTGGATTGGGGGAAGAGG	217698	49894	GAGAGGCCACTCGCCCCCAA	262285	94481	GTGCCCCCCCCAAGTTGGAA
173112	5308	ACCCTGGATTGGGGGAAGAG	217699	49895	AGAGAGGCCACTCGCCCCCA	262286	94482	TGTGCCCCCCCCAAGTTGGA
173113	5309	AACCCTGGATTGGGGGAAGA	217700	49896	CAGAGAGGCCACTCGCCCCC	262287	94483	GTGTGCCCCCCCCAAGTTGG
173114	5310	AAACCCTGGATTGGGGGAAG	217701	49897	ACAGAGAGGCCACTCGCCCC	262288	94484	AGTGTGCCCCCCCCAAGTTG
173115	5311	GAAACCCTGGATTGGGGGAA	217702	49898	CACAGAGAGGCCACTCGCCC	262289	94485	GAGTGTGCCCCCCCCAAGTT
173116	5312	AGAAACCCTGGATTGGGGGA	217703	49899	ACACAGAGAGGCCACTCGCC	262290	94486	GGAGTGTGCCCCCCCCAAGT
173117	5313	CAGAAACCCTGGATTGGGGG	217704	49900	TACACAGAGAGGCCACTCGC	262291	94487	AGGAGTGTGCCCCCCCCAAG
173118	5314	CCAGAAACCCTGGATTGGGG	217705	49901	GTACACAGAGAGGCCACTCG	262292	94488	CAGGAGTGTGCCCCCCCCAA
173119	5315	TCCAGAAACCCTGGATTGGG	217706	49902	GGTACACAGAGAGGCCACTC	262293	94489	TCAGGAGTGTGCCCCCCCCA
173120	5316	GTCCAGAAACCCTGGATTGG	217707	49903	GGGTACACAGAGAGGCCACT	262294	94490	ATCAGGAGTGTGCCCCCCCC
173121	5317	AGTCCAGAAACCCTGGATTG	217708	49904	CGGGTACACAGAGAGGCCAC	262295	94491	AATCAGGAGTGTGCCCCCCC
173122	5318	CAGTCCAGAAACCCTGGATT	217709	49905	ACGGGTACACAGAGAGGCCA	262296	94492	CAATCAGGAGTGTGCCCCCC
173123	5319	GCAGTCCAGAAACCCTGGAT	217710	49906	CACGGGTACACAGAGAGGCC	262297	94493	ACAATCAGGAGTGTGCCCCC
173124	5320	AGCAGTCCAGAAACCCTGGA	217711	49907	CCACGGGTACACAGAGAGGC	262298	94494	TACAATCAGGAGTGTGCCCC
173125	5321	GAGCAGTCCAGAAACCCTGG	217712	49908	CCCACGGGTACACAGAGAGG	262299	94495	CTACAATCAGGAGTGTGCCC
173126	5322	AGAGCAGTCCAGAAACCCTG	217713	49909	CCCCACGGGTACACAGAGAG	262300	94496	GCTACAATCAGGAGTGTGCC
173127	5323	CAGAGCAGTCCAGAAACCCT	217714	49910	TCCCCACGGGTACACAGAGA	262301	94497	GGCTACAATCAGGAGTGTGC
173128	5324	GCAGAGCAGTCCAGAAACCC	217715	49911	ATCCCCACGGGTACACAGAG	262302	94498	TGGCTACAATCAGGAGTGTG
173129	5325	GGCAGAGCAGTCCAGAAACC	217716	49912	TATCCCCACGGGTACACAGA	262303	94499	ATGGCTACAATCAGGAGTGT
173130	5326	TGGCAGAGCAGTCCAGAAAC	217717	49913	CTATCCCCACGGGTACACAG	262304	94500	TATGGCTACAATCAGGAGTG

173131	5327	ATGGCAGAGCAGTCCAGAAA	217718	49914	TCTATCCCCACGGGTACACA	262305	94501	ATATGGCTACAATCAGGAGT
173132	5328	TATGGCAGAGCAGTCCAGAA	217719	49915	ATCTATCCCCACGGGTACAC	262306	94502	CATATGGCTACAATCAGGAG
173133	5329	ATATGGCAGAGCAGTCCAGA	217720	49916	CATCTATCCCCACGGGTACA	262307	94503	TCATATGGCTACAATCAGGA
173134	5330	CATATGGCAGAGCAGTCCAG	217721	49917	GCATCTATCCCCACGGGTAC	262308	94504	CTCATATGGCTACAATCAGG
173135	5331	TCATATGGCAGAGCAGTCCA	217722	49918	CGCATCTATCCCCACGGGTA	262309	94505	ACTCATATGGCTACAATCAG
173136	5332	GTCATATGGCAGAGCAGTCC	217723	49919	GCGCATCTATCCCCACGGGT	262310	94506	GACTCATATGGCTACAATCA
173137	5333	CGTCATATGGCAGAGCAGTC	217724	49920	TGCGCATCTATCCCCACGGG	262311	94507	AGACTCATATGGCTACAATC
173138	5334	CCGTCATATGGCAGAGCAGT	217725	49921	TTGCGCATCTATCCCCACGG	262312	94508	CAGACTCATATGGCTACAAT
173139	5335	CCCGTCATATGGCAGAGCAG	217726	49922	CTTGCGCATCTATCCCCACG	262313	94509	ACAGACTCATATGGCTACAA
173140	5336	CCCCGTCATATGGCAGAGCA	217727	49923	ACTTGCGCATCTATCCCCAC	262314	94510	GACAGACTCATATGGCTACA
173141	5337	GCCCCGTCATATGGCAGAGC	217728	49924	CACTTGCGCATCTATCCCCA	262315	94511	TGACAGACTCATATGGCTAC
173142	5338	TGCCCCGTCATATGGCAGAG	217729	49925	CCACTTGCGCATCTATCCCC	262316	94512	CTGACAGACTCATATGGCTA
173143	5339	CTGCCCCGTCATATGGCAGA	217730	49926	GCCACTTGCGCATCTATCCC	262317	94513	ACTGACAGACTCATATGGCT
173144	5340	GCTGCCCCGTCATATGGCAG	217731	49927	TGCCACTTGCGCATCTATCC	262318	94514	CACTGACAGACTCATATGGC
173145	5341	AGCTGCCCCGTCATATGGCA	217732	49928	ATGCCACTTGCGCATCTATC	262319	94515	ACACTGACAGACTCATATGG
173146	5342	CAGCTGCCCCGTCATATGGC	217733	49929	GATGCCACTTGCGCATCTAT	262320	94516	CACACTGACAGACTCATATG
173147	5343	CCAGCTGCCCCGTCATATGG	217734	49930	CGATGCCACTTGCGCATCTA	262321	94517	CCACACTGACAGACTCATAT
173148	5344	ACCAGCTGCCCCGTCATATG	217735	49931	GCGATGCCACTTGCGCATCT	262322	94518	ACCACACTGACAGACTCATA
173149	5345	AACCAGCTGCCCCGTCATAT	217736	49932	GGCGATGCCACTTGCGCATC	262323	94519	CACCACACTGACAGACTCAT
173150	5346	AAACCAGCTGCCCCGTCATA	217737	49933	TGGCGATGCCACTTGCGCAT	262324	94520	CCACCACACTGACAGACTCA
173151	5347	CAAACCAGCTGCCCCGTCAT	217738	49934	GTGGCGATGCCACTTGCGCA	262325	94521	TCCACCACACTGACAGACTC
173152	5348	TCAAACCAGCTGCCCCGTCA	217739	49935	TGTGGCGATGCCACTTGCGC	262326	94522	TTCCACCACACTGACAGACT
173153	5349	ATCAAACCAGCTGCCCCGTC	217740	49936	ATGTGGCGATGCCACTTGCG	262327	94523	CTTCCACCACACTGACAGAC
173154	5350	AATCAAACCAGCTGCCCCGT	217741	49937	GATGTGGCGATGCCACTTGC	262328	94524	TCTTCCACCACACTGACAGA
173155	5351	CAATCAAACCAGCTGCCCCG	217742	49938	CGATGTGGCGATGCCACTTG	262329	94525	CTCTTCCACCACACTGACAG
173156	5352	TCAATCAAACCAGCTGCCCC	217743	49939	ACGATGTGGCGATGCCACTT	262330	94526	CCTCTTCCACCACACTGACA
173157	5353	GTCAATCAAACCAGCTGCCC	217744	49940	CACGATGTGGCGATGCCACT	262331	94527	GCCTCTTCCACCACACTGAC
173158	5354	GGTCAATCAAACCAGCTGCC	217745	49941	TCACGATGTGGCGATGCCAC	262332	94528	GGCCTCTTCCACCACACTGA
173159	5355	GGGTCAATCAAACCAGCTGC	217746	49942	CTCACGATGTGGCGATGCCA	262333	94529	TGGCCTCTTCCACCACACTG
173160	5356	TGGGTCAATCAAACCAGCTG	217747	49943	ACTCACGATGTGGCGATGCC	262334	94530	ATGGCCTCTTCCACCACACT
173161	5357	CTGGGTCAATCAAACCAGCT	217748	49944	GACTCACGATGTGGCGATGC	262335	94531	CATGGCCTCTTCCACCACAC
173162	5358	CCTGGGTCAATCAAACCAGC	217749	49945	GGACTCACGATGTGGCGATG	262336	94532	CCATGGCCTCTTCCACCACA
173163	5359	CCCTGGGTCAATCAAACCAG	217750	49946	AGGACTCACGATGTGGCGAT	262337	94533	CCCATGGCCTCTTCCACCAC
173164	5360	TCCCTGGGTCAATCAAACCA	217751	49947	CAGGACTCACGATGTGGCGA	262338	94534	ACCCATGGCCTCTTCCACCA
173165	5361	TTCCCTGGGTCAATCAAACC	217752	49948	CCAGGACTCACGATGTGGCG	262339	94535	AACCCATGGCCTCTTCCACC
173166	5362	CTTCCCTGGGTCAATCAAAC	217753	49949	GCCAGGACTCACGATGTGGC	262340	94536	TAACCCATGGCCTCTTCCAC
173167	5363	CCTTCCCTGGGTCAATCAAA	217754	49950	AGCCAGGACTCACGATGTGG	262341	94537	TTAACCCATGGCCTCTTCCA
173168	5364	GCCTTCCCTGGGTCAATCAA	217755	49951	AAGCCAGGACTCACGATGTG	262342	94538	ATTAACCCATGGCCTCTTCC
173169	5365	AGCCTTCCCTGGGTCAATCA	217756	49952	GAAGCCAGGACTCACGATGT	262343	94539	CATTAACCCATGGCCTCTTC
173170	5366	CAGCCTTCCCTGGGTCAATC	217757	49953	TGAAGCCAGGACTCACGATG	262344	94540	CCATTAACCCATGGCCTCTT
173171	5367	CCAGCCTTCCCTGGGTCAAT	217758	49954	ATGAAGCCAGGACTCACGAT	262345	94541	CCCATTAACCCATGGCCTCT
173172	5368	TCCAGCCTTCCCTGGGTCAA	217759	49955	CATGAAGCCAGGACTCACGA	262346	94542	GCCCATTAACCCATGGCCTC
173173	5369	TTCCAGCCTTCCCTGGGTCA	217760	49956	CCATGAAGCCAGGACTCACG	262347	94543	TGCCCATTAACCCATGGCCT
173174	5370	TTTCCAGCCTTCCCTGGGTC	217761	49957	CCCATGAAGCCAGGACTCAC	262348	94544	CTGCCCATTAACCCATGGCC
173175	5371	ATTTCCAGCCTTCCCTGGGT	217762	49958	ACCCATGAAGCCAGGACTCA	262349	94545	CCTGCCCATTAACCCATGGC
173176	5372	GATTTCCAGCCTTCCCTGGG	217763	49959	CACCCATGAAGCCAGGACTC	262350	94546	ACCTGCCCATTAACCCATGG
173177	5373	TGATTTCCAGCCTTCCCTGG	217764	49960	TCACCCATGAAGCCAGGACT	262351	94547	TACCTGCCCATTAACCCATG
173178	5374	TTGATTTCCAGCCTTCCCTG	217765	49961	CTCACCCATGAAGCCAGGAC	262352	94548	TTACCTGCCCATTAACCCAT
173179	5375	CTTGATTTCCAGCCTTCCCT	217766	49962	GCTCACCCATGAAGCCAGGA	262353	94549	TTTACCTGCCCATTAACCCA
173180	5376	TCTTGATTTCCAGCCTTCCC	217767	49963	AGCTCACCCATGAAGCCAGG	262354	94550	TTTTACCTGCCCATTAACCC
173181	5377	GTCTTGATTTCCAGCCTTCC	217768	49964	GAGCTCACCCATGAAGCCAG	262355	94551	TTTTTACCTGCCCATTAACC
173182	5378	AGTCTTGATTTCCAGCCTTC	217769	49965	GGAGCTCACCCATGAAGCCA	262356	94552	TTTTTTACCTGCCCATTAAC
173183	5379	CAGTCTTGATTTCCAGCCTT	217770	49966	TGGAGCTCACCCATGAAGCC	262357	94553	CTTTTTTACCTGCCCATTAA
173184	5380	CCAGTCTTGATTTCCAGCCT	217771	49967	CTGGAGCTCACCCATGAAGC	262358	94554	GCTTTTTTACCTGCCCATTA
173185	5381	CCCAGTCTTGATTTCCAGCC	217772	49968	CCTGGAGCTCACCCATGAAG	262359	94555	TGCTTTTTTACCTGCCCATT
173186	5382	CCCCAGTCTTGATTTCCAGC	217773	49969	ACCTGGAGCTCACCCATGAA	262360	94556	GTGCTTTTTTACCTGCCCAT
173187	5383	CCCCCAGTCTTGATTTCCAG	217774	49970	GACCTGGAGCTCACCCATGA	262361	94557	GGTGCTTTTTTACCTGCCCA
173188	5384	TCCCCCAGTCTTGATTTCCA	217775	49971	GGACCTGGAGCTCACCCATG	262362	94558	AGGTGCTTTTTTACCTGCCC
173189	5385	ATCCCCCAGTCTTGATTTCC	217776	49972	TGGACCTGGAGCTCACCCAT	262363	94559	AAGGTGCTTTTTTACCTGCC
173190	5386	GATCCCCCAGTCTTGATTTC	217777	49973	TTGGACCTGGAGCTCACCCA	262364	94560	CAAGGTGCTTTTTTACCTGC
173191	5387	TGATCCCCCAGTCTTGATTT	217778	49974	GTTGGACCTGGAGCTCACCC	262365	94561	GCAAGGTGCTTTTTTACCTG
173192	5388	TTGATCCCCCAGTCTTGATT	217779	49975	CGTTGGACCTGGAGCTCACC	262366	94562	GGCAAGGTGCTTTTTTACCT
173193	5389	CTTGATCCCCCAGTCTTGAT	217780	49976	TCGTTGGACCTGGAGCTCAC	262367	94563	AGGCAAGGTGCTTTTTTACC
173194	5390	TCTTGATCCCCCAGTCTTGA	217781	49977	CTCGTTGGACCTGGAGCTCA	262368	94564	CAGGCAAGGTGCTTTTTTAC
173195	5391	GTCTTGATCCCCCAGTCTTG	217782	49978	TCTCGTTGGACCTGGAGCTC	262369	94565	CCAGGCAAGGTGCTTTTTTA
173196	5392	CGTCTTGATCCCCCAGTCTT	217783	49979	TTCTCGTTGGACCTGGAGCT	262370	94566	TCCAGGCAAGGTGCTTTTTT
173197	5393	ACGTCTTGATCCCCCAGTCT	217784	49980	CTTCTCGTTGGACCTGGAGC	262371	94567	TTCCAGGCAAGGTGCTTTTT
173198	5394	TACGTCTTGATCCCCCAGTC	217785	49981	GCTTCTCGTTGGACCTGGAG	262372	94568	ATTCCAGGCAAGGTGCTTTT
173199	5395	CTACGTCTTGATCCCCCAGT	217786	49982	GGCTTCTCGTTGGACCTGGA	262373	94569	AATTCCAGGCAAGGTGCTTT
173200	5396	TCTACGTCTTGATCCCCCAG	217787	49983	TGGCTTCTCGTTGGACCTGG	262374	94570	CAATTCCAGGCAAGGTGCTT
173201	5397	ATCTACGTCTTGATCCCCCA	217788	49984	TTGGCTTCTCGTTGGACCTG	262375	94571	TCAATTCCAGGCAAGGTGCT
173202	5398	AATCTACGTCTTGATCCCCC	217789	49985	CTTGGCTTCTCGTTGGACCT	262376	94572	CTCAATTCCAGGCAAGGTGC

173203	5399	GAATCTACGTCTTGATCCCC	217790	49986	GCTTGGCTTCTCGTTGGACC	262377	94573	ACTCAATTCCAGGCAAGGTG
173204	5400	TGAATCTACGTCTTGATCCC	217791	49987	TGCTTGGCTTCTCGTTGGAC	262378	94574	TACTCAATTCCAGGCAAGGT
173205	5401	CTGAATCTACGTCTTGATCC	217792	49988	CTGCTTGGCTTCTCGTTGGA	262379	94575	CTACTCAATTCCAGGCAAGG
173206	5402	ACTGAATCTACGTCTTGATC	217793	49989	CCTGCTTGGCTTCTCGTTGG	262380	94576	TCTACTCAATTCCAGGCAAG
173207	5403	CACTGAATCTACGTCTTGAT	217794	49990	CCCTGCTTGGCTTCTCGTTG	262381	94577	TTCTACTCAATTCCAGGCAA
173208	5404	ACACTGAATCTACGTCTTGA	217795	49991	CCCCTGCTTGGCTTCTCGTT	262382	94578	TTTCTACTCAATTCCAGGCA
173209	5405	CACACTGAATCTACGTCTTG	217796	49992	CCCCCTGCTTGGCTTCTCGT	262383	94579	CTTTCTACTCAATTCCAGGC
173210	5406	CCACACTGAATCTACGTCTT	217797	49993	GCCCCCTGCTTGGCTTCTCG	262384	94580	ACTTTCTACTCAATTCCAGG
173211	5407	GCCACACTGAATCTACGTCT	217798	49994	GGCCCCCTGCTTGGCTTCTC	262385	94581	TACTTTCTACTCAATTCCAG
173212	5408	GGCCACACTGAATCTACGTC	217799	49995	GGGCCCCCTGCTTGGCTTCT	262386	94582	TTACTTTCTACTCAATTCCA
173213	5409	TGGCCACACTGAATCTACGT	217800	49996	AGGGCCCCCTGCTTGGCTTC	262387	94583	CTTACTTTCTACTCAATTCC
173214	5410	TTGGCCACACTGAATCTACG	217801	49997	AAGGGCCCCCTGCTTGGCTT	262388	94584	CCTTACTTTCTACTCAATTC
173215	5411	CTTGGCCACACTGAATCTAC	217802	49998	GAAGGGCCCCCTGCTTGGCT	262389	94585	GCCTTACTTTCTACTCAATT
173216	5412	CCTTGGCCACACTGAATCTA	217803	49999	TGAAGGGCCCCCTGCTTGGC	262390	94586	GGCCTTACTTTCTACTCAAT
173217	5413	ACCTTGGCCACACTGAATCT	217804	50000	TTGAAGGGCCCCCTGCTTGG	262391	94587	GGGCCTTACTTTCTACTCAA
173218	5414	GACCTTGGCCACACTGAATC	217805	50001	CTTGAAGGGCCCCCTGCTTG	262392	94588	AGGGCCTTACTTTCTACTCA
173219	5415	TGACCTTGGCCACACTGAAT	217806	50002	GCTTGAAGGGCCCCCTGCTT	262393	94589	AAGGGCCTTACTTTCTACTC
173220	5416	TTGACCTTGGCCACACTGAA	217807	50003	AGCTTGAAGGGCCCCCTGCT	262394	94590	GAAGGGCCTTACTTTCTACT
173221	5417	CTTGACCTTGGCCACACTGA	217808	50004	GAGCTTGAAGGGCCCCCTGC	262395	94591	TGAAGGGCCTTACTTTCTAC
173222	5418	ACTTGACCTTGGCCACACTG	217809	50005	TGAGCTTGAAGGGCCCCCTG	262396	94592	CTGAAGGGCCTTACTTTCTA
173223	5419	GACTTGACCTTGGCCACACT	217810	50006	CTGAGCTTGAAGGGCCCCCT	262397	94593	TCTGAAGGGCCTTACTTTCT
173224	5420	AGACTTGACCTTGGCCACAC	217811	50007	GCTGAGCTTGAAGGGCCCCC	262398	94594	GTCTGAAGGGCCTTACTTTC
173225	5421	GAGACTTGACCTTGGCCACA	217812	50008	AGCTGAGCTTGAAGGGCCCC	262399	94595	GGTCTGAAGGGCCTTACTTT
173226	5422	AGAGACTTGACCTTGGCCAC	217813	50009	AAGCTGAGCTTGAAGGGCCC	262400	94596	GGGTCTGAAGGGCCTTACTT
173227	5423	CAGAGACTTGACCTTGGCCA	217814	50010	AAAGCTGAGCTTGAAGGGCC	262401	94597	GGGGTCTGAAGGGCCTTACT
173228	5424	TCAGAGACTTGACCTTGGCC	217815	50011	CAAAGCTGAGCTTGAAGGGC	262402	94598	CGGGGTCTGAAGGGCCTTAC
173229	5425	CTCAGAGACTTGACCTTGGC	217816	50012	CCAAAGCTGAGCTTGAAGGG	262403	94599	ACGGGGTCTGAAGGGCCTTA
173230	5426	CCTCAGAGACTTGACCTTGG	217817	50013	CCCAAAGCTGAGCTTGAAGG	262404	94600	CACGGGGTCTGAAGGGCCTT
173231	5427	ACCTCAGAGACTTGACCTTG	217818	50014	GCCCAAAGCTGAGCTTGAAG	262405	94601	TCACGGGGTCTGAAGGGCCT
173232	5428	AACCTCAGAGACTTGACCTT	217819	50015	GGCCCAAAGCTGAGCTTGAA	262406	94602	GTCACGGGGTCTGAAGGGCC
173233	5429	AAACCTCAGAGACTTGACCT	217820	50016	GGGCCCAAAGCTGAGCTTGA	262407	94603	TGTCACGGGGTCTGAAGGGC
173234	5430	TAAACCTCAGAGACTTGACC	217821	50017	CGGGCCCAAAGCTGAGCTTG	262408	94604	GTGTCACGGGGTCTGAAGGG
173235	5431	CTAAACCTCAGAGACTTGAC	217822	50018	CCGGGCCCAAAGCTGAGCTT	262409	94605	TGTGTCACGGGGTCTGAAGG
173236	5432	CCTAAACCTCAGAGACTTGA	217823	50019	CCCGGGCCCAAAGCTGAGCT	262410	94606	GTGTGTCACGGGGTCTGAAG
173237	5433	CCCTAAACCTCAGAGACTTG	217824	50020	ACCCGGGCCCAAAGCTGAGC	262411	94607	AGTGTGTCACGGGGTCTGAA
173238	5434	TCCCTAAACCTCAGAGACTT	217825	50021	GACCCGGGCCCAAAGCTGAG	262412	94608	AAGTGTGTCACGGGGTCTGA
173239	5435	GTCCCTAAACCTCAGAGACT	217826	50022	CGACCCGGGCCCAAAGCTGA	262413	94609	CAAGTGTGTCACGGGGTCTG
173240	5436	TGTCCCTAAACCTCAGAGAC	217827	50023	CCGACCCGGGCCCAAAGCTG	262414	94610	CCAAGTGTGTCACGGGGTCT
173241	5437	ATGTCCCTAAACCTCAGAGA	217828	50024	CCCGACCCGGGCCCAAAGCT	262415	94611	CCCAAGTGTGTCACGGGGTC
173242	5438	GATGTCCCTAAACCTCAGAG	217829	50025	CCCCGACCCGGGCCCAAAGC	262416	94612	CCCCAAGTGTGTCACGGGGT
173243	5439	TGATGTCCCTAAACCTCAGA	217830	50026	ACCCCGACCCGGGCCCAAAG	262417	94613	TCCCCAAGTGTGTCACGGGG
173244	5440	CTGATGTCCCTAAACCTCAG	217831	50027	TACCCCGACCCGGGCCCAAA	262418	94614	GTCCCCAAGTGTGTCACGGG
173245	5441	TCTGATGTCCCTAAACCTCA	217832	50028	GTACCCCGACCCGGGCCCAA	262419	94615	TGTCCCCAAGTGTGTCACGG
173246	5442	ATCTGATGTCCCTAAACCTC	217833	50029	TGTACCCCGACCCGGGCCCA	262420	94616	ATGTCCCCAAGTGTGTCACG
173247	5443	GATCTGATGTCCCTAAACCT	217834	50030	CTGTACCCCGACCCGGGCCC	262421	94617	AATGTCCCCAAGTGTGTCAC
173248	5444	GGATCTGATGTCCCTAAACC	217835	50031	CCTGTACCCCGACCCGGGCC	262422	94618	AAATGTCCCCAAGTGTGTCA
173249	5445	GGGATCTGATGTCCCTAAAC	217836	50032	CCCTGTACCCCGACCCGGGC	262423	94619	AAAATGTCCCCAAGTGTGTC
173250	5446	GGGGATCTGATGTCCCTAAA	217837	50033	ACCCTGTACCCCGACCCGGG	262424	94620	GAAAATGTCCCCAAGTGTGT
173251	5447	TGGGGATCTGATGTCCCTAA	217838	50034	TACCCTGTACCCCGACCCGG	262425	94621	AGAAAATGTCCCCAAGTGTG
173252	5448	CTGGGGATCTGATGTCCCTA	217839	50035	CTACCCTGTACCCCGACCCG	262426	94622	AAGAAAATGTCCCCAAGTGT
173253	5449	GCTGGGGATCTGATGTCCCT	217840	50036	TCTACCCTGTACCCCGACCC	262427	94623	CAAGAAAATGTCCCCAAGTG
173254	5450	AGCTGGGGATCTGATGTCCC	217841	50037	CTCTACCCTGTACCCCGACC	262428	94624	TCAAGAAAATGTCCCCAAGT
173255	5451	AAGCTGGGGATCTGATGTCC	217842	50038	GCTCTACCCTGTACCCCGAC	262429	94625	CTCAAGAAAATGTCCCCAAG
173256	5452	TAAGCTGGGGATCTGATGTC	217843	50039	CGCTCTACCCTGTACCCCGA	262430	94626	ACTCAAGAAAATGTCCCCAA
173257	5453	CTAAGCTGGGGATCTGATGT	217844	50040	CCGCTCTACCCTGTACCCCG	262431	94627	TACTCAAGAAAATGTCCCCA
173258	5454	CCTAAGCTGGGGATCTGATG	217845	50041	CCCGCTCTACCCTGTACCCC	262432	94628	TTACTCAAGAAAATGTCCCC
173259	5455	ACCTAAGCTGGGGATCTGAT	217846	50042	GCCCGCTCTACCCTGTACCC	262433	94629	GTTACTCAAGAAAATGTCCC
173260	5456	AACCTAAGCTGGGGATCTGA	217847	50043	GGCCCGCTCTACCCTGTACC	262434	94630	TGTTACTCAAGAAAATGTCC
173261	5457	GAACCTAAGCTGGGGATCTG	217848	50044	AGGCCCGCTCTACCCTGTAC	262435	94631	ATGTTACTCAAGAAAATGTC
173262	5458	AGAACCTAAGCTGGGGATCT	217849	50045	GAGGCCCGCTCTACCCTGTA	262436	94632	GATGTTACTCAAGAAAATGT
173263	5459	CAGAACCTAAGCTGGGGATC	217850	50046	GGAGGCCCGCTCTACCCTGT	262437	94633	GGATGTTACTCAAGAAAATG
173264	5460	ACAGAACCTAAGCTGGGGAT	217851	50047	GGGAGGCCCGCTCTACCCTG	262438	94634	AGGATGTTACTCAAGAAAAT
173265	5461	TACAGAACCTAAGCTGGGGA	217852	50048	GGGGAGGCCCGCTCTACCCT	262439	94635	TAGGATGTTACTCAAGAAAA
173266	5462	GTACAGAACCTAAGCTGGGG	217853	50049	TGGGGAGGCCCGCTCTACCC	262440	94636	TTAGGATGTTACTCAAGAAA
173267	5463	GGTACAGAACCTAAGCTGGG	217854	50050	CTGGGGAGGCCCGCTCTACC	262441	94637	CTTAGGATGTTACTCAAGAA
173268	5464	AGGTACAGAACCTAAGCTGG	217855	50051	GCTGGGGAGGCCCGCTCTAC	262442	94638	TCTTAGGATGTTACTCAAGA
173269	5465	GAGGTACAGAACCTAAGCTG	217856	50052	GGCTGGGGAGGCCCGCTCTA	262443	94639	ATCTTAGGATGTTACTCAAG
173270	5466	CGAGGTACAGAACCTAAGCT	217857	50053	GGGCTGGGGAGGCCCGCTCT	262444	94640	AATCTTAGGATGTTACTCAA
173271	5467	CCGAGGTACAGAACCTAAGC	217858	50054	GGGGCTGGGGAGGCCCGCTC	262445	94641	GAATCTTAGGATGTTACTCA
173272	5468	GCCGAGGTACAGAACCTAAG	217859	50055	AGGGGCTGGGGAGGCCCGCT	262446	94642	TGAATCTTAGGATGTTACTC
173273	5469	TGCCGAGGTACAGAACCTAA	217860	50056	CAGGGGCTGGGGAGGCCCGC	262447	94643	ATGAATCTTAGGATGTTACT
173274	5470	TTGCCGAGGTACAGAACCTA	217861	50057	GCAGGGGCTGGGGAGGCCCG	262448	94644	CATGAATCTTAGGATGTTAC

173275	5471	CTTGCCGAGGTACAGAACCT	217862	50058	GGCAGGGGCTGGGGAGGCCC	262449	94645	ACATGAATCTTAGGATGTTA
173276	5472	CCTTGCCGAGGTACAGAACC	217863	50059	TGGCAGGGGCTGGGGAGGCC	262450	94646	TACATGAATCTTAGGATGTT
173277	5473	ACCTTGCCGAGGTACAGAAC	217864	50060	ATGGCAGGGGCTGGGGAGGC	262451	94647	GTACATGAATCTTAGGATGT
173278	5474	CACCTTGCCGAGGTACAGAA	217865	50061	CATGGCAGGGGCTGGGGAGG	262452	94648	GGTACATGAATCTTAGGATG
173279	5475	TCACCTTGCCGAGGTACAGA	217866	50062	TCATGGCAGGGGCTGGGGAG	262453	94649	AGGTACATGAATCTTAGGAT
173280	5476	TTCACCTTGCCGAGGTACAG	217867	50063	CTCATGGCAGGGGCTGGGGA	262454	94650	AAGGTACATGAATCTTAGGA
173281	5477	TTTCACCTTGCCGAGGTACA	217868	50064	CCTCATGGCAGGGGCTGGGG	262455	94651	CAAGGTACATGAATCTTAGG
173282	5478	CTTTCACCTTGCCGAGGTAC	217869	50065	GCCTCATGGCAGGGGCTGGG	262456	94652	TCAAGGTACATGAATCTTAG
173283	5479	GCTTTCACCTTGCCGAGGTA	217870	50066	GGCCTCATGGCAGGGGCTGG	262457	94653	ATCAAGGTACATGAATCTTA
173284	5480	CGCTTTCACCTTGCCGAGGT	217871	50067	TGGCCTCATGGCAGGGGCTG	262458	94654	CATCAAGGTACATGAATCTT
173285	5481	ACGCTTTCACCTTGCCGAGG	217872	50068	TTGGCCTCATGGCAGGGGCT	262459	94655	TCATCAAGGTACATGAATCT
173286	5482	AACGCTTTCACCTTGCCGAG	217873	50069	CTTGGCCTCATGGCAGGGGC	262460	94656	ATCATCAAGGTACATGAATC
173287	5483	CAACGCTTTCACCTTGCCGA	217874	50070	CCTTGGCCTCATGGCAGGGG	262461	94657	GATCATCAAGGTACATGAAT
173288	5484	CCAACGCTTTCACCTTGCCG	217875	50071	GCCTTGGCCTCATGGCAGGG	262462	94658	AGATCATCAAGGTACATGAA
173289	5485	GCCAACGCTTTCACCTTGCC	217876	50072	TGCCTTGGCCTCATGGCAGG	262463	94659	GAGATCATCAAGGTACATGA
173290	5486	CGCCAACGCTTTCACCTTGC	217877	50073	CTGCCTTGGCCTCATGGCAG	262464	94660	GGAGATCATCAAGGTACATG
173291	5487	GCGCCAACGCTTTCACCTTG	217878	50074	ACTGCCTTGGCCTCATGGCA	262465	94661	TGGAGATCATCAAGGTACAT
173292	5488	GGCGCCAACGCTTTCACCTT	217879	50075	CACTGCCTTGGCCTCATGGC	262466	94662	ATGGAGATCATCAAGGTACA
173293	5489	GGGCGCCAACGCTTTCACCT	217880	50076	GCACTGCCTTGGCCTCATGG	262467	94663	GATGGAGATCATCAAGGTAC
173294	5490	TGGGCGCCAACGCTTTCACC	217881	50077	TGCACTGCCTTGGCCTCATG	262468	94664	TGATGGAGATCATCAAGGTA
173295	5491	GTGGGCGCCAACGCTTTCAC	217882	50078	ATGCACTGCCTTGGCCTCAT	262469	94665	TTGATGGAGATCATCAAGGT
173296	5492	AGTGGGCGCCAACGCTTTCA	217883	50079	GATGCACTGCCTTGGCCTCA	262470	94666	GTTGATGGAGATCATCAAGG
173297	5493	CAGTGGGCGCCAACGCTTTC	217884	50080	CGATGCACTGCCTTGGCCTC	262471	94667	AGTTGATGGAGATCATCAAG
173298	5494	TCAGTGGGCGCCAACGCTTT	217885	50081	ACGATGCACTGCCTTGGCCT	262472	94668	AAGTTGATGGAGATCATCAA
173299	5495	ATCAGTGGGCGCCAACGCTT	217886	50082	AACGATGCACTGCCTTGGCC	262473	94669	TAAGTTGATGGAGATCATCA
173300	5496	CATCAGTGGGCGCCAACGCT	217887	50083	GAACGATGCACTGCCTTGGC	262474	94670	GTAAGTTGATGGAGATCATC
173301	5497	TCATCAGTGGGCGCCAACGC	217888	50084	CGAACGATGCACTGCCTTGG	262475	94671	AGTAAGTTGATGGAGATCAT
173302	5498	CTCATCAGTGGGCGCCAACG	217889	50085	GCGAACGATGCACTGCCTTG	262476	94672	GAGTAAGTTGATGGAGATCA
173303	5499	CCTCATCAGTGGGCGCCAAC	217890	50086	TGCGAACGATGCACTGCCTT	262477	94673	TGAGTAAGTTGATGGAGATC
173304	5500	GCCTCATCAGTGGGCGCCAA	217891	50087	CTGCGAACGATGCACTGCCT	262478	94674	ATGAGTAAGTTGATGGAGAT
173305	5501	GGCCTCATCAGTGGGCGCCA	217892	50088	GCTGCGAACGATGCACTGCC	262479	94675	CATGAGTAAGTTGATGGAGA
173306	5502	AGGCCTCATCAGTGGGCGCC	217893	50089	CGCTGCGAACGATGCACTGC	262480	94676	ACATGAGTAAGTTGATGGAG
173307	5503	CAGGCCTCATCAGTGGGCGC	217894	50090	ACGCTGCGAACGATGCACTG	262481	94677	CACATGAGTAAGTTGATGGA
173308	5504	GCAGGCCTCATCAGTGGGCG	217895	50091	TACGCTGCGAACGATGCACT	262482	94678	TCACATGAGTAAGTTGATGG
173309	5505	AGCAGGCCTCATCAGTGGGC	217896	50092	GTACGCTGCGAACGATGCAC	262483	94679	TTCACATGAGTAAGTTGATG
173310	5506	GAGCAGGCCTCATCAGTGGG	217897	50093	TGTACGCTGCGAACGATGCA	262484	94680	CTTCACATGAGTAAGTTGAT
173311	5507	AGAGCAGGCCTCATCAGTGG	217898	50094	ATGTACGCTGCGAACGATGC	262485	94681	GCTTCACATGAGTAAGTTGA
173312	5508	CAGAGCAGGCCTCATCAGTG	217899	50095	AATGTACGCTGCGAACGATG	262486	94682	TGCTTCACATGAGTAAGTTG
173313	5509	TCAGAGCAGGCCTCATCAGT	217900	50096	GAATGTACGCTGCGAACGAT	262487	94683	GTGCTTCACATGAGTAAGTT
173314	5510	CTCAGAGCAGGCCTCATCAG	217901	50097	TGAATGTACGCTGCGAACGA	262488	94684	GGTGCTTCACATGAGTAAGT
173315	5511	TCTCAGAGCAGGCCTCATCA	217902	50098	CTGAATGTACGCTGCGAACG	262489	94685	AGGTGCTTCACATGAGTAAG
173316	5512	ATCTCAGAGCAGGCCTCATC	217903	50099	TCTGAATGTACGCTGCGAAC	262490	94686	AAGGTGCTTCACATGAGTAA
173317	5513	AATCTCAGAGCAGGCCTCAT	217904	50100	TTCTGAATGTACGCTGCGAA	262491	94687	AAAGGTGCTTCACATGAGTA
173318	5514	CAATCTCAGAGCAGGCCTCA	217905	50101	TTTCTGAATGTACGCTGCGA	262492	94688	TAAAGGTGCTTCACATGAGT
173319	5515	ACAATCTCAGAGCAGGCCTC	217906	50102	GTTTCTGAATGTACGCTGCG	262493	94689	TTAAAGGTGCTTCACATGAG
173320	5516	CACAATCTCAGAGCAGGCCT	217907	50103	GGTTTCTGAATGTACGCTGC	262494	94690	TTTAAAGGTGCTTCACATGA
173321	5517	CCACAATCTCAGAGCAGGCC	217908	50104	TGGTTTCTGAATGTACGCTG	262495	94691	GTTTAAAGGTGCTTCACATG
173322	5518	CCCACAATCTCAGAGCAGGC	217909	50105	TTGGTTTCTGAATGTACGCT	262496	94692	GGTTTAAAGGTGCTTCACAT
173323	5519	ACCCACAATCTCAGAGCAGG	217910	50106	TTTGGTTTCTGAATGTACGC	262497	94693	TGGTTTAAAGGTGCTTCACA
173324	5520	CACCCACAATCTCAGAGCAG	217911	50107	CTTTGGTTTCTGAATGTACG	262498	94694	CTGGTTTAAAGGTGCTTCAC
173325	5521	ACACCCACAATCTCAGAGCA	217912	50108	GCTTTGGTTTCTGAATGTAC	262499	94695	ACTGGTTTAAAGGTGCTTCA
173326	5522	CACACCCACAATCTCAGAGC	217913	50109	GGCTTTGGTTTCTGAATGTA	262500	94696	GACTGGTTTAAAGGTGCTTC
173327	5523	CCACACCCACAATCTCAGAG	217914	50110	AGGCTTTGGTTTCTGAATGT	262501	94697	CGACTGGTTTAAAGGTGCTT
173328	5524	CCCACACCCACAATCTCAGA	217915	50111	TAGGCTTTGGTTTCTGAATG	262502	94698	ACGACTGGTTTAAAGGTGCT
173329	5525	ACCCACACCCACAATCTCAG	217916	50112	CTAGGCTTTGGTTTCTGAAT	262503	94699	GACGACTGGTTTAAAGGTGC
173330	5526	AACCCACACCCACAATCTCA	217917	50113	CCTAGGCTTTGGTTTCTGAA	262504	94700	AGACGACTGGTTTAAAGGTG
173331	5527	CAACCCACACCCACAATCTC	217918	50114	TCCTAGGCTTTGGTTTCTGA	262505	94701	GAGACGACTGGTTTAAAGGT
173332	5528	TCAACCCACACCCACAATCT	217919	50115	CTCCTAGGCTTTGGTTTCTG	262506	94702	GGAGACGACTGGTTTAAAGG
173333	5529	CTCAACCCACACCCACAATC	217920	50116	GCTCCTAGGCTTTGGTTTCT	262507	94703	TGGAGACGACTGGTTTAAAG
173334	5530	ACTCAACCCACACCCACAAT	217921	50117	AGCTCCTAGGCTTTGGTTTC	262508	94704	TTGGAGACGACTGGTTTAAA
173335	5531	AACTCAACCCACACCCACAA	217922	50118	CAGCTCCTAGGCTTTGGTTT	262509	94705	TTTGGAGACGACTGGTTTAA
173336	5532	CAACTCAACCCACACCCACA	217923	50119	CCAGCTCCTAGGCTTTGGTT	262510	94706	ATTTGGAGACGACTGGTTTA
173337	5533	CCAACTCAACCCACACCCAC	217924	50120	ACCAGCTCCTAGGCTTTGGT	262511	94707	AATTTGGAGACGACTGGTTT
173338	5534	CCCAACTCAACCCACACCCA	217925	50121	AACCAGCTCCTAGGCTTTGG	262512	94708	GAATTTGGAGACGACTGGTT
173339	5535	ACCCAACTCAACCCACACCC	217926	50122	TAACCAGCTCCTAGGCTTTG	262513	94709	TGAATTTGGAGACGACTGGT
173340	5536	CACCCAACTCAACCCACACC	217927	50123	ATAACCAGCTCCTAGGCTTT	262514	94710	CTGAATTTGGAGACGACTGG
173341	5537	CCACCCAACTCAACCCACAC	217928	50124	GATAACCAGCTCCTAGGCTT	262515	94711	CCTGAATTTGGAGACGACTG
173342	5538	CCCACCCAACTCAACCCACA	217929	50125	TGATAACCAGCTCCTAGGCT	262516	94712	CCCTGAATTTGGAGACGACT
173343	5539	GCCCACCCAACTCAACCCAC	217930	50126	ATGATAACCAGCTCCTAGGC	262517	94713	CCCCTGAATTTGGAGACGAC
173344	5540	TGCCCACCCAACTCAACCCA	217931	50127	AATGATAACCAGCTCCTAGG	262518	94714	GCCCCTGAATTTGGAGACGA
173345	5541	ATGCCCACCCAACTCAACCC	217932	50128	GAATGATAACCAGCTCCTAG	262519	94715	TGCCCCTGAATTTGGAGACG
173346	5542	TATGCCCACCCAACTCAACC	217933	50129	GGAATGATAACCAGCTCCTA	262520	94716	GTGCCCCTGAATTTGGAGAC

173347	5543	CTATGCCCACCCAACTCAAC	217934	50130	CGGAATGATAACCAGCTCCT	262521	94717	TGTGCCCCTGAATTTGGAGA
173348	5544	CCTATGCCCACCCAACTCAA	217935	50131	CCGGAATGATAACCAGCTCC	262522	94718	CTGTGCCCCTGAATTTGGAG
173349	5545	GCCTATGCCCACCCAACTCA	217936	50132	ACCGGAATGATAACCAGCTC	262523	94719	ACTGTGCCCCTGAATTTGGA
173350	5546	TGCCTATGCCCACCCAACTC	217937	50133	AACCGGAATGATAACCAGCT	262524	94720	TACTGTGCCCCTGAATTTGG
173351	5547	TTGCCTATGCCCACCCAACT	217938	50134	AAACCGGAATGATAACCAGC	262525	94721	TTACTGTGCCCCTGAATTTG
173352	5548	CTTGCCTATGCCCACCCAAC	217939	50135	TAAACCGGAATGATAACCAG	262526	94722	GTTACTGTGCCCCTGAATTT
173353	5549	ACTTGCCTATGCCCACCCAA	217940	50136	GTAAACCGGAATGATAACCA	262527	94723	TGTTACTGTGCCCCTGAATT
173354	5550	GACTTGCCTATGCCCACCCA	217941	50137	TGTAAACCGGAATGATAACC	262528	94724	ATGTTACTGTGCCCCTGAAT
173355	5551	GGACTTGCCTATGCCCACCC	217942	50138	CTGTAAACCGGAATGATAAC	262529	94725	GATGTTACTGTGCCCCTGAA
173356	5552	AGGACTTGCCTATGCCCACC	217943	50139	GCTGTAAACCGGAATGATAA	262530	94726	GGATGTTACTGTGCCCCTGA
173357	5553	GAGGACTTGCCTATGCCCAC	217944	50140	AGCTGTAAACCGGAATGATA	262531	94727	TGGATGTTACTGTGCCCCTG
173358	5554	AGAGGACTTGCCTATGCCCA	217945	50141	CAGCTGTAAACCGGAATGAT	262532	94728	TTGGATGTTACTGTGCCCCT
173359	5555	AAGAGGACTTGCCTATGCCC	217946	50142	TCAGCTGTAAACCGGAATGA	262533	94729	GTTGGATGTTACTGTGCCCC
173360	5556	CAAGAGGACTTGCCTATGCC	217947	50143	ATCAGCTGTAAACCGGAATG	262534	94730	TGTTGGATGTTACTGTGCCC
173361	5557	ACAAGAGGACTTGCCTATGC	217948	50144	CATCAGCTGTAAACCGGAAT	262535	94731	CTGTTGGATGTTACTGTGCC
173362	5558	TACAAGAGGACTTGCCTATG	217949	50145	CCATCAGCTGTAAACCGGAA	262536	94732	CCTGTTGGATGTTACTGTGC
173363	5559	TTACAAGAGGACTTGCCTAT	217950	50146	TCCATCAGCTGTAAACCGGA	262537	94733	GCCTGTTGGATGTTACTGTG
173364	5560	CTTACAAGAGGACTTGCCTA	217951	50147	TTCCATCAGCTGTAAACCGG	262538	94734	AGCCTGTTGGATGTTACTGT
173365	5561	TCTTACAAGAGGACTTGCCT	217952	50148	CTTCCATCAGCTGTAAACCG	262539	94735	CAGCCTGTTGGATGTTACTG
173366	5562	TTCTTACAAGAGGACTTGCC	217953	50149	TCTTCCATCAGCTGTAAACC	262540	94736	CCAGCCTGTTGGATGTTACT
173367	5563	ATTCTTACAAGAGGACTTGC	217954	50150	CTCTTCCATCAGCTGTAAAC	262541	94737	TCCAGCCTGTTGGATGTTAC
173368	5564	GATTCTTACAAGAGGACTTG	217955	50151	GCTCTTCCATCAGCTGTAAA	262542	94738	CTCCAGCCTGTTGGATGTTA
173369	5565	AGATTCTTACAAGAGGACTT	217956	50152	TGCTCTTCCATCAGCTGTAA	262543	94739	TCTCCAGCCTGTTGGATGTT
173370	5566	AAGATTCTTACAAGAGGACT	217957	50153	CTGCTCTTCCATCAGCTGTA	262544	94740	TTCTCCAGCCTGTTGGATGT
173371	5567	AAAGATTCTTACAAGAGGAC	217958	50154	CCTGCTCTTCCATCAGCTGT	262545	94741	TTTCTCCAGCCTGTTGGATG
173372	5568	AAAAGATTCTTACAAGAGGA	217959	50155	ACCTGCTCTTCCATCAGCTG	262546	94742	CTTTCTCCAGCCTGTTGGAT
173373	5569	CAAAAGATTCTTACAAGAGG	217960	50156	CACCTGCTCTTCCATCAGCT	262547	94743	TCTTTCTCCAGCCTGTTGGA
173374	5570	CCAAAAGATTCTTACAAGAG	217961	50157	GCACCTGCTCTTCCATCAGC	262548	94744	TTCTTTCTCCAGCCTGTTGG
173375	5571	GCCAAAAGATTCTTACAAGA	217962	50158	AGCACCTGCTCTTCCATCAG	262549	94745	GTTCTTTCTCCAGCCTGTTG
173376	5572	TGCCAAAAGATTCTTACAAG	217963	50159	AAGCACCTGCTCTTCCATCA	262550	94746	CGTTCTTTCTCCAGCCTGTT
173377	5573	TTGCCAAAAGATTCTTACAA	217964	50160	GAAGCACCTGCTCTTCCATC	262551	94747	ACGTTCTTTCTCCAGCCTGT
173378	5574	TTTGCCAAAAGATTCTTACA	217965	50161	GGAAGCACCTGCTCTTCCAT	262552	94748	TACGTTCTTTCTCCAGCCTG
173379	5575	CTTTGCCAAAAGATTCTTAC	217966	50162	CGGAAGCACCTGCTCTTCCA	262553	94749	GTACGTTCTTTCTCCAGCCT
173380	5576	TCTTTGCCAAAAGATTCTTA	217967	50163	TCGGAAGCACCTGCTCTTCC	262554	94750	AGTACGTTCTTTCTCCAGCC
173381	5577	ATCTTTGCCAAAAGATTCTT	217968	50164	CTCGGAAGCACCTGCTCTTC	262555	94751	TAGTACGTTCTTTCTCCAGC
173382	5578	CATCTTTGCCAAAAGATTCT	217969	50165	TCTCGGAAGCACCTGCTCTT	262556	94752	CTAGTACGTTCTTTCTCCAG
173383	5579	CCATCTTTGCCAAAAGATTC	217970	50166	TTCTCGGAAGCACCTGCTCT	262557	94753	TCTAGTACGTTCTTTCTCCA
173384	5580	CCCATCTTTGCCAAAAGATT	217971	50167	GTTCTCGGAAGCACCTGCTC	262558	94754	TTCTAGTACGTTCTTTCTCC
173385	5581	GCCCATCTTTGCCAAAAGAT	217972	50168	GGTTCTCGGAAGCACCTGCT	262559	94755	GTTCTAGTACGTTCTTTCTC
173386	5582	GGCCCATCTTTGCCAAAAGA	217973	50169	GGGTTCTCGGAAGCACCTGC	262560	94756	AGTTCTAGTACGTTCTTTCT
173387	5583	AGGCCCATCTTTGCCAAAAG	217974	50170	TGGGTTCTCGGAAGCACCTG	262561	94757	AAGTTCTAGTACGTTCTTTC
173388	5584	CAGGCCCATCTTTGCCAAAA	217975	50171	GTGGGTTCTCGGAAGCACCT	262562	94758	GAAGTTCTAGTACGTTCTTT
173389	5585	CCAGGCCCATCTTTGCCAAA	217976	50172	TGTGGGTTCTCGGAAGCACC	262563	94759	GGAAGTTCTAGTACGTTCTT
173390	5586	CCCAGGCCCATCTTTGCCAA	217977	50173	CTGTGGGTTCTCGGAAGCAC	262564	94760	TGGAAGTTCTAGTACGTTCT
173391	5587	TCCCAGGCCCATCTTTGCCA	217978	50174	ACTGTGGGTTCTCGGAAGCA	262565	94761	ATGGAAGTTCTAGTACGTTC
173392	5588	CTCCCAGGCCCATCTTTGCC	217979	50175	CACTGTGGGTTCTCGGAAGC	262566	94762	AATGGAAGTTCTAGTACGTT
173393	5589	CCTCCCAGGCCCATCTTTGC	217980	50176	GCACTGTGGGTTCTCGGAAG	262567	94763	GAATGGAAGTTCTAGTACGT
173394	5590	GCCTCCCAGGCCCATCTTTG	217981	50177	AGCACTGTGGGTTCTCGGAA	262568	94764	GGAATGGAAGTTCTAGTACG
173395	5591	AGCCTCCCAGGCCCATCTTT	217982	50178	GAGCACTGTGGGTTCTCGGA	262569	94765	AGGAATGGAAGTTCTAGTAC
173396	5592	AAGCCTCCCAGGCCCATCTT	217983	50179	AGAGCACTGTGGGTTCTCGG	262570	94766	AAGGAATGGAAGTTCTAGTA
173397	5593	AAAGCCTCCCAGGCCCATCT	217984	50180	AAGAGCACTGTGGGTTCTCG	262571	94767	AAAGGAATGGAAGTTCTAGT
173398	5594	AAAAGCCTCCCAGGCCCATC	217985	50181	AAAGAGCACTGTGGGTTCTC	262572	94768	AAAAGGAATGGAAGTTCTAG
173399	5595	GAAAAGCCTCCCAGGCCCAT	217986	50182	CAAAGAGCACTGTGGGTTCT	262573	94769	AAAAAGGAATGGAAGTTCTA
173400	5596	AGAAAAGCCTCCCAGGCCCA	217987	50183	CCAAAGAGCACTGTGGGTTC	262574	94770	GAAAAAGGAATGGAAGTTCT
173401	5597	GAGAAAAGCCTCCCAGGCCC	217988	50184	GCCAAAGAGCACTGTGGGTT	262575	94771	TGAAAAAGGAATGGAAGTTC
173402	5598	TGAGAAAAGCCTCCCAGGCC	217989	50185	GGCCAAAGAGCACTGTGGGT	262576	94772	ATGAAAAAGGAATGGAAGTT
173403	5599	GTGAGAAAAGCCTCCCAGGC	217990	50186	TGGCCAAAGAGCACTGTGGG	262577	94773	CATGAAAAAGGAATGGAAGT
173404	5600	AGTGAGAAAAGCCTCCCAGG	217991	50187	CTGGCCAAAGAGCACTGTGG	262578	94774	ACATGAAAAAGGAATGGAAG
173405	5601	AAGTGAGAAAAGCCTCCCAG	217992	50188	ACTGGCCAAAGAGCACTGTG	262579	94775	GACATGAAAAAGGAATGGAA
173406	5602	GAAGTGAGAAAAGCCTCCCA	217993	50189	CACTGGCCAAAGAGCACTGT	262580	94776	GGACATGAAAAAGGAATGGA
173407	5603	GGAAGTGAGAAAAGCCTCCC	217994	50190	TCACTGGCCAAAGAGCACTG	262581	94777	AGGACATGAAAAAGGAATGG
173408	5604	AGGAAGTGAGAAAAGCCTCC	217995	50191	GTCACTGGCCAAAGAGCACT	262582	94778	GAGGACATGAAAAAGGAATG
173409	5605	CAGGAAGTGAGAAAAGCCTC	217996	50192	GGTCACTGGCCAAAGAGCAC	262583	94779	AGAGGACATGAAAAAGGAAT
173410	5606	CCAGGAAGTGAGAAAAGCCT	217997	50193	GGGTCACTGGCCAAAGAGCA	262584	94780	AAGAGGACATGAAAAAGGAA
173411	5607	CCCAGGAAGTGAGAAAAGCC	217998	50194	TGGGTCACTGGCCAAAGAGC	262585	94781	GAAGAGGACATGAAAAAGGA
173412	5608	CCCCAGGAAGTGAGAAAAGC	217999	50195	TTGGGTCACTGGCCAAAGAG	262586	94782	AGAAGAGGACATGAAAAAGG
173413	5609	GCCCCAGGAAGTGAGAAAAG	218000	50196	CTTGGGTCACTGGCCAAAGA	262587	94783	TAGAAGAGGACATGAAAAAG
173414	5610	GGCCCCAGGAAGTGAGAAAA	218001	50197	CCTTGGGTCACTGGCCAAAG	262588	94784	TTAGAAGAGGACATGAAAAA
173415	5611	GGGCCCCAGGAAGTGAGAAA	218002	50198	CCCTTGGGTCACTGGCCAAA	262589	94785	TTTAGAAGAGGACATGAAAA
173416	5612	TGGGCCCCAGGAAGTGAGAA	218003	50199	ACCCTTGGGTCACTGGCCAA	262590	94786	TTTTAGAAGAGGACATGAAA
173417	5613	CTGGGCCCCAGGAAGTGAGA	218004	50200	CACCCTTGGGTCACTGGCCA	262591	94787	CTTTTAGAAGAGGACATGAA
173418	5614	CCTGGGCCCCAGGAAGTGAG	218005	50201	GCACCCTTGGGTCACTGGCC	262592	94788	GCTTTTAGAAGAGGACATGA

173419	5615	GCCTGGGCCCCAGGAAGTGA	218006	50202	GGCACCCTTGGGTCACTGGC	262593	94789	AGCTTTTAGAAGAGGACATG
173420	5616	AGCCTGGGCCCCAGGAAGTG	218007	50203	AGGCACCCTTGGGTCACTGG	262594	94790	AAGCTTTTAGAAGAGGACAT
173421	5617	AAGCCTGGGCCCCAGGAAGT	218008	50204	GAGGCACCCTTGGGTCACTG	262595	94791	AAAGCTTTTAGAAGAGGACA
173422	5618	AAAGCCTGGGCCCCAGGAAG	218009	50205	AGAGGCACCCTTGGGTCACT	262596	94792	CAAAGCTTTTAGAAGAGGAC
173423	5619	CAAAGCCTGGGCCCCAGGAA	218010	50206	CAGAGGCACCCTTGGGTCAC	262597	94793	ACAAAGCTTTTAGAAGAGGA
173424	5620	GCAAAGCCTGGGCCCCAGGA	218011	50207	TCAGAGGCACCCTTGGGTCA	262598	94794	GACAAAGCTTTTAGAAGAGG
173425	5621	TGCAAAGCCTGGGCCCCAGG	218012	50208	CTCAGAGGCACCCTTGGGTC	262599	94795	TGACAAAGCTTTTAGAAGAG
173426	5622	TTGCAAAGCCTGGGCCCCAG	218013	50209	TCTCAGAGGCACCCTTGGGT	262600	94796	CTGACAAAGCTTTTAGAAGA
173427	5623	ATTGCAAAGCCTGGGCCCCA	218014	50210	CTCTCAGAGGCACCCTTGGG	262601	94797	CCTGACAAAGCTTTTAGAAG
173428	5624	TATTGCAAAGCCTGGGCCCC	218015	50211	CCTCTCAGAGGCACCCTTGG	262602	94798	CCCTGACAAAGCTTTTAGAA
173429	5625	TTATTGCAAAGCCTGGGCCC	218016	50212	GCCTCTCAGAGGCACCCTTG	262603	94799	GCCCTGACAAAGCTTTTAGA
173430	5626	CTTATTGCAAAGCCTGGGCC	218017	50213	GGCCTCTCAGAGGCACCCTT	262604	94800	GGCCCTGACAAAGCTTTTAG
173431	5627	ACTTATTGCAAAGCCTGGGC	218018	50214	AGGCCTCTCAGAGGCACCCT	262605	94801	TGGCCCTGACAAAGCTTTTA
173432	5628	TACTTATTGCAAAGCCTGGG	218019	50215	GAGGCCTCTCAGAGGCACCC	262606	94802	CTGGCCCTGACAAAGCTTTT
173433	5629	ATACTTATTGCAAAGCCTGG	218020	50216	CGAGGCCTCTCAGAGGCACC	262607	94803	CCTGGCCCTGACAAAGCTTT
173434	5630	AATACTTATTGCAAAGCCTG	218021	50217	GCGAGGCCTCTCAGAGGCAC	262608	94804	GCCTGGCCCTGACAAAGCTT
173435	5631	GAATACTTATTGCAAAGCCT	218022	50218	TGCGAGGCCTCTCAGAGGCA	262609	94805	CGCCTGGCCCTGACAAAGCT
173436	5632	GGAATACTTATTGCAAAGCC	218023	50219	CTGCGAGGCCTCTCAGAGGC	262610	94806	GCGCCTGGCCCTGACAAAGC
173437	5633	TGGAATACTTATTGCAAAGC	218024	50220	GCTGCGAGGCCTCTCAGAGG	262611	94807	CGCGCCTGGCCCTGACAAAG
173438	5634	ATGGAATACTTATTGCAAAG	218025	50221	TGCTGCGAGGCCTCTCAGAG	262612	94808	CCGCGCCTGGCCCTGACAAA
173439	5635	AATGGAATACTTATTGCAAA	218026	50222	GTGCTGCGAGGCCTCTCAGA	262613	94809	ACCGCGCCTGGCCCTGACAA
173440	5636	TAATGGAATACTTATTGCAA	218027	50223	GGTGCTGCGAGGCCTCTCAG	262614	94810	CACCGCGCCTGGCCCTGACA
173441	5637	ATAATGGAATACTTATTGCA	218028	50224	GGGTGCTGCGAGGCCTCTCA	262615	94811	CCACCGCGCCTGGCCCTGAC
173442	5638	TATAATGGAATACTTATTGC	218029	50225	CGGGTGCTGCGAGGCCTCTC	262616	94812	GCCACCGCGCCTGGCCCTGA
173443	5639	GTATAATGGAATACTTATTG	218030	50226	CCGGGTGCTGCGAGGCCTCT	262617	94813	AGCCACCGCGCCTGGCCCTG
173444	5640	AGTATAATGGAATACTTATT	218031	50227	TCCGGGTGCTGCGAGGCCTC	262618	94814	GAGCCACCGCGCCTGGCCCT
173445	5641	CAGTATAATGGAATACTTAT	218032	50228	CTCCGGGTGCTGCGAGGCCT	262619	94815	TGAGCCACCGCGCCTGGCCC
173446	5642	ACAGTATAATGGAATACTTA	218033	50229	CCTCCGGGTGCTGCGAGGCC	262620	94816	GTGAGCCACCGCGCCTGGCC
173447	5643	CACAGTATAATGGAATACTT	218034	50230	ACCTCCGGGTGCTGCGAGGC	262621	94817	CGTGAGCCACCGCGCCTGGC
173448	5644	CCACAGTATAATGGAATACT	218035	50231	CACCTCCGGGTGCTGCGAGG	262622	94818	GCGTGAGCCACCGCGCCTGG
173449	5645	ACCACAGTATAATGGAATAC	218036	50232	GCACCTCCGGGTGCTGCGAG	262623	94819	GGCGTGAGCCACCGCGCCTG
173450	5646	TACCACAGTATAATGGAATA	218037	50233	AGCACCTCCGGGTGCTGCGA	262624	94820	AGGCGTGAGCCACCGCGCCT
173451	5647	GTACCACAGTATAATGGAAT	218038	50234	CAGCACCTCCGGGTGCTGCG	262625	94821	CAGGCGTGAGCCACCGCGCC
173452	5648	GGTACCACAGTATAATGGAA	218039	50235	GCAGCACCTCCGGGTGCTGC	262626	94822	ACAGGCGTGAGCCACCGCGC
173453	5649	AGGTACCACAGTATAATGGA	218040	50236	AGCAGCACCTCCGGGTGCTG	262627	94823	TACAGGCGTGAGCCACCGCG
173454	5650	AAGGTACCACAGTATAATGG	218041	50237	CAGCAGCACCTCCGGGTGCT	262628	94824	TTACAGGCGTGAGCCACCGC
173455	5651	CAAGGTACCACAGTATAATG	218042	50238	TCAGCAGCACCTCCGGGTGC	262629	94825	ATTACAGGCGTGAGCCACCG
173456	5652	CCAAGGTACCACAGTATAAT	218043	50239	CTCAGCAGCACCTCCGGGTG	262630	94826	GATTACAGGCGTGAGCCACC
173457	5653	CCCAAGGTACCACAGTATAA	218044	50240	CCTCAGCAGCACCTCCGGGT	262631	94827	GGATTACAGGCGTGAGCCAC
173458	5654	CCCCAAGGTACCACAGTATA	218045	50241	GCCTCAGCAGCACCTCCGGG	262632	94828	GGGATTACAGGCGTGAGCCA
173459	5655	GCCCCAAGGTACCACAGTAT	218046	50242	TGCCTCAGCAGCACCTCCGG	262633	94829	TGGGATTACAGGCGTGAGCC
173460	5656	AGCCCCAAGGTACCACAGTA	218047	50243	TTGCCTCAGCAGCACCTCCG	262634	94830	CTGGGATTACAGGCGTGAGC
173461	5657	TAGCCCCAAGGTACCACAGT	218048	50244	GTTGCCTCAGCAGCACCTCC	262635	94831	GCTGGGATTACAGGCGTGAG
173462	5658	GTAGCCCCAAGGTACCACAG	218049	50245	CGTTGCCTCAGCAGCACCTC	262636	94832	TGCTGGGATTACAGGCGTGA
173463	5659	GGTAGCCCCAAGGTACCACA	218050	50246	GCGTTGCCTCAGCAGCACCT	262637	94833	GTGCTGGGATTACAGGCGTG
173464	5660	AGGTAGCCCCAAGGTACCAC	218051	50247	GGCGTTGCCTCAGCAGCACC	262638	94834	AGTGCTGGGATTACAGGCGT
173465	5661	CAGGTAGCCCCAAGGTACCA	218052	50248	GGGCGTTGCCTCAGCAGCAC	262639	94835	AAGTGCTGGGATTACAGGCG
173466	5662	TCAGGTAGCCCCAAGGTACC	218053	50249	AGGGCGTTGCCTCAGCAGCA	262640	94836	AAAGTGCTGGGATTACAGGC
173467	5663	CTCAGGTAGCCCCAAGGTAC	218054	50250	CAGGGCGTTGCCTCAGCAGC	262641	94837	CAAAGTGCTGGGATTACAGG
173468	5664	TCTCAGGTAGCCCCAAGGTA	218055	50251	TCAGGGCGTTGCCTCAGCAG	262642	94838	CCAAAGTGCTGGGATTACAG
173469	5665	TTCTCAGGTAGCCCCAAGGT	218056	50252	GTCAGGGCGTTGCCTCAGCA	262643	94839	CCCAAAGTGCTGGGATTACA
173470	5666	ATTCTCAGGTAGCCCCAAGG	218057	50253	AGTCAGGGCGTTGCCTCAGC	262644	94840	TCCCAAAGTGCTGGGATTAC
173471	5667	GATTCTCAGGTAGCCCCAAG	218058	50254	CAGTCAGGGCGTTGCCTCAG	262645	94841	CTCCCAAAGTGCTGGGATTA
173472	5668	GGATTCTCAGGTAGCCCCAA	218059	50255	ACAGTCAGGGCGTTGCCTCA	262646	94842	CCTCCCAAAGTGCTGGGATT
173473	5669	AGGATTCTCAGGTAGCCCCA	218060	50256	TACAGTCAGGGCGTTGCCTC	262647	94843	GCCTCCCAAAGTGCTGGGAT
173474	5670	GAGGATTCTCAGGTAGCCCC	218061	50257	TTACAGTCAGGGCGTTGCCT	262648	94844	GGCCTCCCAAAGTGCTGGGA
173475	5671	AGAGGATTCTCAGGTAGCCC	218062	50258	CTTACAGTCAGGGCGTTGCC	262649	94845	CGGCCTCCCAAAGTGCTGGG
173476	5672	CAGAGGATTCTCAGGTAGCC	218063	50259	TCTTACAGTCAGGGCGTTGC	262650	94846	TCGGCCTCCCAAAGTGCTGG
173477	5673	ACAGAGGATTCTCAGGTAGC	218064	50260	TTCTTACAGTCAGGGCGTTG	262651	94847	CTCGGCCTCCCAAAGTGCTG
173478	5674	GACAGAGGATTCTCAGGTAG	218065	50261	CTTCTTACAGTCAGGGCGTT	262652	94848	TCTCGGCCTCCCAAAGTGCT
173479	5675	AGACAGAGGATTCTCAGGTA	218066	50262	CCTTCTTACAGTCAGGGCGT	262653	94849	GTCTCGGCCTCCCAAAGTGC
173480	5676	GAGACAGAGGATTCTCAGGT	218067	50263	TCCTTCTTACAGTCAGGGCG	262654	94850	CGTCTCGGCCTCCCAAAGTG
173481	5677	CGAGACAGAGGATTCTCAGG	218068	50264	GTCCTTCTTACAGTCAGGGC	262655	94851	CCGTCTCGGCCTCCCAAAGT
173482	5678	GCGAGACAGAGGATTCTCAG	218069	50265	GGTCCTTCTTACAGTCAGGG	262656	94852	CCCGTCTCGGCCTCCCAAAG
173483	5679	GGCGAGACAGAGGATTCTCA	218070	50266	TGGTCCTTCTTACAGTCAGG	262657	94853	ACCCGTCTCGGCCTCCCAAA
173484	5680	GGGCGAGACAGAGGATTCTC	218071	50267	ATGGTCCTTCTTACAGTCAG	262658	94854	CACCCGTCTCGGCCTCCCAA
173485	5681	GGGGCGAGACAGAGGATTCT	218072	50268	AATGGTCCTTCTTACAGTCA	262659	94855	CCACCCGTCTCGGCCTCCCA
173486	5682	AGGGGCGAGACAGAGGATTC	218073	50269	GAATGGTCCTTCTTACAGTC	262660	94856	TCCACCCGTCTCGGCCTCCC
173487	5683	CAGGGGCGAGACAGAGGATT	218074	50270	TGAATGGTCCTTCTTACAGT	262661	94857	ATCCACCCGTCTCGGCCTCC
173488	5684	ACAGGGGCGAGACAGAGGAT	218075	50271	ATGAATGGTCCTTCTTACAG	262662	94858	GATCCACCCGTCTCGGCCTC
173489	5685	AACAGGGGCGAGACAGAGGA	218076	50272	GATGAATGGTCCTTCTTACA	262663	94859	TGATCCACCCGTCTCGGCCT
173490	5686	CAACAGGGGCGAGACAGAGG	218077	50273	GGATGAATGGTCCTTCTTAC	262664	94860	GTGATCCACCCGTCTCGGCC

173491	5687	GCAACAGGGGCGAGACAGAG	218078	50274	AGGATGAATGGTCCTTCTTA	262665	94861	CGTGATCCACCCGTCTCGGC
173492	5688	GGCAACAGGGGCGAGACAGA	218079	50275	GAGGATGAATGGTCCTTCTT	262666	94862	TCGTGATCCACCCGTCTCGG
173493	5689	AGGCAACAGGGGCGAGACAG	218080	50276	TGAGGATGAATGGTCCTTCT	262667	94863	CTCGTGATCCACCCGTCTCG
173494	5690	AAGGCAACAGGGGCGAGACA	218081	50277	CTGAGGATGAATGGTCCTTC	262668	94864	CCTCGTGATCCACCCGTCTC
173495	5691	CAAGGCAACAGGGGCGAGAC	218082	50278	TCTGAGGATGAATGGTCCTT	262669	94865	ACCTCGTGATCCACCCGTCT
173496	5692	GCAAGGCAACAGGGGCGAGA	218083	50279	CTCTGAGGATGAATGGTCCT	262670	94866	GACCTCGTGATCCACCCGTC
173497	5693	GGCAAGGCAACAGGGGCGAG	218084	50280	TCTCTGAGGATGAATGGTCC	262671	94867	TGACCTCGTGATCCACCCGT
173498	5694	TGGCAAGGCAACAGGGGCGA	218085	50281	CTCTCTGAGGATGAATGGTC	262672	94868	CTGACCTCGTGATCCACCCG
173499	5695	TTGGCAAGGCAACAGGGGCG	218086	50282	ACTCTCTGAGGATGAATGGT	262673	94869	CCTGACCTCGTGATCCACCC
173500	5696	TTTGGCAAGGCAACAGGGGC	218087	50283	CACTCTCTGAGGATGAATGG	262674	94870	TCCTGACCTCGTGATCCACC
173501	5697	CTTTGGCAAGGCAACAGGGG	218088	50284	CCACTCTCTGAGGATGAATG	262675	94871	CTCCTGACCTCGTGATCCAC
173502	5698	TCTTTGGCAAGGCAACAGGG	218089	50285	GCCACTCTCTGAGGATGAAT	262676	94872	TCTCCTGACCTCGTGATCCA
173503	5699	CTCTTTGGCAAGGCAACAGG	218090	50286	GGCCACTCTCTGAGGATGAA	262677	94873	ATCTCCTGACCTCGTGATCC
173504	5700	ACTCTTTGGCAAGGCAACAG	218091	50287	CGGCCACTCTCTGAGGATGA	262678	94874	GATCTCCTGACCTCGTGATC
173505	5701	AACTCTTTGGCAAGGCAACA	218092	50288	ACGGCCACTCTCTGAGGATG	262679	94875	CGATCTCCTGACCTCGTGAT
173506	5702	AAACTCTTTGGCAAGGCAAC	218093	50289	CACGGCCACTCTCTGAGGAT	262680	94876	TCGATCTCCTGACCTCGTGA
173507	5703	CAAACTCTTTGGCAAGGCAA	218094	50290	TCACGGCCACTCTCTGAGGA	262681	94877	CTCGATCTCCTGACCTCGTG
173508	5704	GCAAACTCTTTGGCAAGGCA	218095	50291	ATCACGGCCACTCTCTGAGG	262682	94878	TCTCGATCTCCTGACCTCGT
173509	5705	AGCAAACTCTTTGGCAAGGC	218096	50292	CATCACGGCCACTCTCTGAG	262683	94879	GTCTCGATCTCCTGACCTCG
173510	5706	CAGCAAACTCTTTGGCAAGG	218097	50293	GCATCACGGCCACTCTCTGA	262684	94880	GGTCTCGATCTCCTGACCTC
173511	5707	ACAGCAAACTCTTTGGCAAG	218098	50294	AGCATCACGGCCACTCTCTG	262685	94881	TGGTCTCGATCTCCTGACCT
173512	5708	GACAGCAAACTCTTTGGCAA	218099	50295	CAGCATCACGGCCACTCTCT	262686	94882	ATGGTCTCGATCTCCTGACC
173513	5709	GGACAGCAAACTCTTTGGCA	218100	50296	GCAGCATCACGGCCACTCTC	262687	94883	GATGGTCTCGATCTCCTGAC
173514	5710	TGGACAGCAAACTCTTTGGC	218101	50297	AGCAGCATCACGGCCACTCT	262688	94884	GGATGGTCTCGATCTCCTGA
173515	5711	TTGGACAGCAAACTCTTTGG	218102	50298	CAGCAGCATCACGGCCACTC	262689	94885	AGGATGGTCTCGATCTCCTG
173516	5712	CTTGGACAGCAAACTCTTTG	218103	50299	GCAGCAGCATCACGGCCACT	262690	94886	CAGGATGGTCTCGATCTCCT
173517	5713	TCTTGGACAGCAAACTCTTT	218104	50300	CGCAGCAGCATCACGGCCAC	262691	94887	CCAGGATGGTCTCGATCTCC
173518	5714	TTCTTGGACAGCAAACTCTT	218105	50301	TCGCAGCAGCATCACGGCCA	262692	94888	GCCAGGATGGTCTCGATCTC
173519	5715	ATTCTTGGACAGCAAACTCT	218106	50302	GTCGCAGCAGCATCACGGCC	262693	94889	AGCCAGGATGGTCTCGATCT
173520	5716	AATTCTTGGACAGCAAACTC	218107	50303	TGTCGCAGCAGCATCACGGC	262694	94890	TAGCCAGGATGGTCTCGATC
173521	5717	GAATTCTTGGACAGCAAACT	218108	50304	CTGTCGCAGCAGCATCACGG	262695	94891	TTAGCCAGGATGGTCTCGAT
173522	5718	GGAATTCTTGGACAGCAAAC	218109	50305	ACTGTCGCAGCAGCATCACG	262696	94892	GTTAGCCAGGATGGTCTCGA
173523	5719	AGGAATTCTTGGACAGCAAA	218110	50306	GACTGTCGCAGCAGCATCAC	262697	94893	TGTTAGCCAGGATGGTCTCG
173524	5720	AAGGAATTCTTGGACAGCAA	218111	50307	GGACTGTCGCAGCAGCATCA	262698	94894	GTGTTAGCCAGGATGGTCTC
173525	5721	AAAGGAATTCTTGGACAGCA	218112	50308	GGGACTGTCGCAGCAGCATC	262699	94895	TGTGTTAGCCAGGATGGTCT
173526	5722	GAAAGGAATTCTTGGACAGC	218113	50309	TGGGACTGTCGCAGCAGCAT	262700	94896	CTGTGTTAGCCAGGATGGTC
173527	5723	GGAAAGGAATTCTTGGACAG	218114	50310	GTGGGACTGTCGCAGCAGCA	262701	94897	ACTGTGTTAGCCAGGATGGT
173528	5724	AGGAAAGGAATTCTTGGACA	218115	50311	GGTGGGACTGTCGCAGCAGC	262702	94898	CACTGTGTTAGCCAGGATGG
173529	5725	CAGGAAAGGAATTCTTGGAC	218116	50312	TGGTGGGACTGTCGCAGCAG	262703	94899	TCACTGTGTTAGCCAGGATG
173530	5726	ACAGGAAAGGAATTCTTGGA	218117	50313	ATGGTGGGACTGTCGCAGCA	262704	94900	TTCACTGTGTTAGCCAGGAT
173531	5727	GACAGGAAAGGAATTCTTGG	218118	50314	GATGGTGGGACTGTCGCAGC	262705	94901	TTTCACTGTGTTAGCCAGGA
173532	5728	AGACAGGAAAGGAATTCTTG	218119	50315	GGATGGTGGGACTGTCGCAG	262706	94902	GTTTCACTGTGTTAGCCAGG
173533	5729	GAGACAGGAAAGGAATTCTT	218120	50316	GGGATGGTGGGACTGTCGCA	262707	94903	GGTTTCACTGTGTTAGCCAG
173534	5730	GGAGACAGGAAAGGAATTCT	218121	50317	AGGGATGGTGGGACTGTCGC	262708	94904	GGGTTTCACTGTGTTAGCCA
173535	5731	TGGAGACAGGAAAGGAATTC	218122	50318	GAGGGATGGTGGGACTGTCG	262709	94905	GGGGTTTCACTGTGTTAGCC
173536	5732	CTGGAGACAGGAAAGGAATT	218123	50319	GGAGGGATGGTGGGACTGTC	262710	94906	TGGGGTTTCACTGTGTTAGC
173537	5733	CCTGGAGACAGGAAAGGAAT	218124	50320	GGGAGGGATGGTGGGACTGT	262711	94907	ATGGGGTTTCACTGTGTTAG
173538	5734	ACCTGGAGACAGGAAAGGAA	218125	50321	CGGGAGGGATGGTGGGACTG	262712	94908	GATGGGGTTTCACTGTGTTA
173539	5735	CACCTGGAGACAGGAAAGGA	218126	50322	TCGGGAGGGATGGTGGGACT	262713	94909	AGATGGGGTTTCACTGTGTT
173540	5736	GCACCTGGAGACAGGAAAGG	218127	50323	GTCGGGAGGGATGGTGGGAC	262714	94910	GAGATGGGGTTTCACTGTGT
173541	5737	GGCACCTGGAGACAGGAAAG	218128	50324	AGTCGGGAGGGATGGTGGGA	262715	94911	AGAGATGGGGTTTCACTGTG
173542	5738	TGGCACCTGGAGACAGGAAA	218129	50325	GAGTCGGGAGGGATGGTGGG	262716	94912	TAGAGATGGGGTTTCACTGT
173543	5739	ATGGCACCTGGAGACAGGAA	218130	50326	AGAGTCGGGAGGGATGGTGG	262717	94913	GTAGAGATGGGGTTTCACTG
173544	5740	CATGGCACCTGGAGACAGGA	218131	50327	GAGAGTCGGGAGGGATGGTG	262718	94914	AGTAGAGATGGGGTTTCACT
173545	5741	GCATGGCACCTGGAGACAGG	218132	50328	TGAGAGTCGGGAGGGATGGT	262719	94915	TAGTAGAGATGGGGTTTCAC
173546	5742	AGCATGGCACCTGGAGACAG	218133	50329	GTGAGAGTCGGGAGGGATGG	262720	94916	TTAGTAGAGATGGGGTTTCA
173547	5743	GAGCATGGCACCTGGAGACA	218134	50330	AGTGAGAGTCGGGAGGGATG	262721	94917	TTTAGTAGAGATGGGGTTTC
173548	5744	GGAGCATGGCACCTGGAGAC	218135	50331	GAGTGAGAGTCGGGAGGGAT	262722	94918	TTTTAGTAGAGATGGGGTTT
173549	5745	AGGAGCATGGCACCTGGAGA	218136	50332	GGAGTGAGAGTCGGGAGGGA	262723	94919	TTTTTAGTAGAGATGGGGTT
173550	5746	CAGGAGCATGGCACCTGGAG	218137	50333	GGGAGTGAGAGTCGGGAGGG	262724	94920	ATTTTTAGTAGAGATGGGGT
173551	5747	GCAGGAGCATGGCACCTGGA	218138	50334	TGGGAGTGAGAGTCGGGAGG	262725	94921	TATTTTTAGTAGAGATGGGG
173552	5748	GGCAGGAGCATGGCACCTGG	218139	50335	TTGGGAGTGAGAGTCGGGAG	262726	94922	GTATTTTTAGTAGAGATGGG
173553	5749	TGGCAGGAGCATGGCACCTG	218140	50336	GTTGGGAGTGAGAGTCGGGA	262727	94923	TGTATTTTTAGTAGAGATGG
173554	5750	GTGGCAGGAGCATGGCACCT	218141	50337	TGTTGGGAGTGAGAGTCGGG	262728	94924	TTGTATTTTTAGTAGAGATG
173555	5751	GGTGGCAGGAGCATGGCACC	218142	50338	CTGTTGGGAGTGAGAGTCGG	262729	94925	TTTGTATTTTTAGTAGAGAT
173556	5752	AGGTGGCAGGAGCATGGCAC	218143	50339	TCTGTTGGGAGTGAGAGTCG	262730	94926	TTTTGTATTTTTAGTAGAGA
173557	5753	GAGGTGGCAGGAGCATGGCA	218144	50340	GTCTGTTGGGAGTGAGAGTC	262731	94927	TTTTTGTATTTTTAGTAGAG
173558	5754	AGAGGTGGCAGGAGCATGGC	218145	50341	AGTCTGTTGGGAGTGAGAGT	262732	94928	TTTTTTGTATTTTTAGTAGA
173559	5755	CAGAGGTGGCAGGAGCATGG	218146	50342	AAGTCTGTTGGGAGTGAGAG	262733	94929	TTTTTTTGTATTTTTAGTAG
173560	5756	GCAGAGGTGGCAGGAGCATG	218147	50343	GAAGTCTGTTGGGAGTGAGA	262734	94930	GTTTTTTTGTATTTTTAGTA
173561	5757	GGCAGAGGTGGCAGGAGCAT	218148	50344	GGAAGTCTGTTGGGAGTGAG	262735	94931	CGTTTTTTTGTATTTTTAGT
173562	5758	TGGCAGAGGTGGCAGGAGCA	218149	50345	GGGAAGTCTGTTGGGAGTGA	262736	94932	TCGTTTTTTTGTATTTTTAG

173563	5759	CTGGCAGAGGTGGCAGGAGC	218150	50346	TGGGAAGTCTGTTGGGAGTG	262737	94933	CTCGTTTTTTTGTATTTTTA
173564	5760	CCTGGCAGAGGTGGCAGGAG	218151	50347	GTGGGAAGTCTGTTGGGAGT	262738	94934	GCTCGTTTTTTTGTATTTTT
173565	5761	ACCTGGCAGAGGTGGCAGGA	218152	50348	AGTGGGAAGTCTGTTGGGAG	262739	94935	GGCTCGTTTTTTTGTATTTT
173566	5762	AACCTGGCAGAGGTGGCAGG	218153	50349	CAGTGGGAAGTCTGTTGGGA	262740	94936	CGGCTCGTTTTTTTGTATTT
173567	5763	GAACCTGGCAGAGGTGGCAG	218154	50350	ACAGTGGGAAGTCTGTTGGG	262741	94937	CCGGCTCGTTTTTTTGTATT
173568	5764	GGAACCTGGCAGAGGTGGCA	218155	50351	TACAGTGGGAAGTCTGTTGG	262742	94938	CCCGGCTCGTTTTTTTGTAT
173569	5765	GGGAACCTGGCAGAGGTGGC	218156	50352	TTACAGTGGGAAGTCTGTTG	262743	94939	GCCCGGCTCGTTTTTTTGTA
173570	5766	AGGGAACCTGGCAGAGGTGG	218157	50353	TTTACAGTGGGAAGTCTGTT	262744	94940	CGCCCGGCTCGTTTTTTTGT
173571	5767	CAGGGAACCTGGCAGAGGTG	218158	50354	CTTTACAGTGGGAAGTCTGT	262745	94941	ACGCCCGGCTCGTTTTTTTG
173572	5768	GCAGGGAACCTGGCAGAGGT	218159	50355	GCTTTACAGTGGGAAGTCTG	262746	94942	CACGCCCGGCTCGTTTTTTT
173573	5769	GGCAGGGAACCTGGCAGAGG	218160	50356	AGCTTTACAGTGGGAAGTCT	262747	94943	CCACGCCCGGCTCGTTTTTT
173574	5770	AGGCAGGGAACCTGGCAGAG	218161	50357	CAGCTTTACAGTGGGAAGTC	262748	94944	ACCACGCCCGGCTCGTTTTT
173575	5771	CAGGCAGGGAACCTGGCAGA	218162	50358	TCAGCTTTACAGTGGGAAGT	262749	94945	CACCACGCCCGGCTCGTTTT
173576	5772	GCAGGCAGGGAACCTGGCAG	218163	50359	TTCAGCTTTACAGTGGGAAG	262750	94946	CCACCACGCCCGGCTCGTTT
173577	5773	GGCAGGCAGGGAACCTGGCA	218164	50360	GTTCAGCTTTACAGTGGGAA	262751	94947	ACCACCACGCCCGGCTCGTT
173578	5774	GGGCAGGCAGGGAACCTGGC	218165	50361	AGTTCAGCTTTACAGTGGGA	262752	94948	CACCACCACGCCCGGCTCGT
173579	5775	TGGGCAGGCAGGGAACCTGG	218166	50362	GAGTTCAGCTTTACAGTGGG	262753	94949	CCACCACCACGCCCGGCTCG
173580	5776	CTGGGCAGGCAGGGAACCTG	218167	50363	AGAGTTCAGCTTTACAGTGG	262754	94950	CCCACCACCACGCCCGGCTC
173581	5777	TCTGGGCAGGCAGGGAACCT	218168	50364	GAGAGTTCAGCTTTACAGTG	262755	94951	GCCCACCACCACGCCCGGCT
173582	5778	ATCTGGGCAGGCAGGGAACC	218169	50365	GGAGAGTTCAGCTTTACAGT	262756	94952	CGCCCACCACCACGCCCGGC
173583	5779	CATCTGGGCAGGCAGGGAAC	218170	50366	TGGAGAGTTCAGCTTTACAG	262757	94953	GCGCCCACCACCACGCCCGG
173584	5780	CCATCTGGGCAGGCAGGGAA	218171	50367	CTGGAGAGTTCAGCTTTACA	262758	94954	GGCGCCCACCACCACGCCCG
173585	5781	GCCATCTGGGCAGGCAGGGA	218172	50368	GCTGGAGAGTTCAGCTTTAC	262759	94955	AGGCGCCCACCACCACGCCC
173586	5782	AGCCATCTGGGCAGGCAGGG	218173	50369	TGCTGGAGAGTTCAGCTTTA	262760	94956	CAGGCGCCCACCACCACGCC
173587	5783	GAGCCATCTGGGCAGGCAGG	218174	50370	TTGCTGGAGAGTTCAGCTTT	262761	94957	ACAGGCGCCCACCACCACGC
173588	5784	GGAGCCATCTGGGCAGGCAG	218175	50371	TTTGCTGGAGAGTTCAGCTT	262762	94958	TACAGGCGCCCACCACCACG
173589	5785	GGGAGCCATCTGGGCAGGCA	218176	50372	ATTTGCTGGAGAGTTCAGCT	262763	94959	CTACAGGCGCCCACCACCAC
173590	5786	TGGGAGCCATCTGGGCAGGC	218177	50373	GATTTGCTGGAGAGTTCAGC	262764	94960	ACTACAGGCGCCCACCACCA
173591	5787	TTGGGAGCCATCTGGGCAGG	218178	50374	TGATTTGCTGGAGAGTTCAG	262765	94961	GACTACAGGCGCCCACCACC
173592	5788	GTTGGGAGCCATCTGGGCAG	218179	50375	GTGATTTGCTGGAGAGTTCA	262766	94962	GGACTACAGGCGCCCACCAC
173593	5789	AGTTGGGAGCCATCTGGGCA	218180	50376	GGTGATTTGCTGGAGAGTTC	262767	94963	GGGACTACAGGCGCCCACCA
173594	5790	CAGTTGGGAGCCATCTGGGC	218181	50377	AGGTGATTTGCTGGAGAGTT	262768	94964	TGGGACTACAGGCGCCCACC
173595	5791	TCAGTTGGGAGCCATCTGGG	218182	50378	GAGGTGATTTGCTGGAGAGT	262769	94965	CTGGGACTACAGGCGCCCAC
173596	5792	CTCAGTTGGGAGCCATCTGG	218183	50379	AGAGGTGATTTGCTGGAGAG	262770	94966	GCTGGGACTACAGGCGCCCA
173597	5793	ACTCAGTTGGGAGCCATCTG	218184	50380	GAGAGGTGATTTGCTGGAGA	262771	94967	AGCTGGGACTACAGGCGCCC
173598	5794	CACTCAGTTGGGAGCCATCT	218185	50381	CGAGAGGTGATTTGCTGGAG	262772	94968	TAGCTGGGACTACAGGCGCC
173599	5795	ACACTCAGTTGGGAGCCATC	218186	50382	GCGAGAGGTGATTTGCTGGA	262773	94969	GTAGCTGGGACTACAGGCGC
173600	5796	CACACTCAGTTGGGAGCCAT	218187	50383	GGCGAGAGGTGATTTGCTGG	262774	94970	AGTAGCTGGGACTACAGGCG
173601	5797	TCACACTCAGTTGGGAGCCA	218188	50384	TGGCGAGAGGTGATTTGCTG	262775	94971	GAGTAGCTGGGACTACAGGC
173602	5798	CTCACACTCAGTTGGGAGCC	218189	50385	CTGGCGAGAGGTGATTTGCT	262776	94972	CGAGTAGCTGGGACTACAGG
173603	5799	CCTCACACTCAGTTGGGAGC	218190	50386	TCTGGCGAGAGGTGATTTGC	262777	94973	CCGAGTAGCTGGGACTACAG
173604	5800	TCCTCACACTCAGTTGGGAG	218191	50387	GTCTGGCGAGAGGTGATTTG	262778	94974	CCCGAGTAGCTGGGACTACA
173605	5801	CTCCTCACACTCAGTTGGGA	218192	50388	AGTCTGGCGAGAGGTGATTT	262779	94975	TCCCGAGTAGCTGGGACTAC
173606	5802	CCTCCTCACACTCAGTTGGG	218193	50389	GAGTCTGGCGAGAGGTGATT	262780	94976	CTCCCGAGTAGCTGGGACTA
173607	5803	TCCTCCTCACACTCAGTTGG	218194	50390	AGAGTCTGGCGAGAGGTGAT	262781	94977	CCTCCCGAGTAGCTGGGACT
173608	5804	TTCCTCCTCACACTCAGTTG	218195	50391	GAGAGTCTGGCGAGAGGTGA	262782	94978	GCCTCCCGAGTAGCTGGGAC
173609	5805	ATTCCTCCTCACACTCAGTT	218196	50392	AGAGAGTCTGGCGAGAGGTG	262783	94979	AGCCTCCCGAGTAGCTGGGA
173610	5806	AATTCCTCCTCACACTCAGT	218197	50393	GAGAGAGTCTGGCGAGAGGT	262784	94980	CAGCCTCCCGAGTAGCTGGG
173611	5807	AAATTCCTCCTCACACTCAG	218198	50394	GGAGAGAGTCTGGCGAGAGG	262785	94981	TCAGCCTCCCGAGTAGCTGG
173612	5808	CAAATTCCTCCTCACACTCA	218199	50395	AGGAGAGAGTCTGGCGAGAG	262786	94982	CTCAGCCTCCCGAGTAGCTG
173613	5809	TCAAATTCCTCCTCACACTC	218200	50396	GAGGAGAGAGTCTGGCGAGA	262787	94983	CCTCAGCCTCCCGAGTAGCT
173614	5810	CTCAAATTCCTCCTCACACT	218201	50397	TGAGGAGAGAGTCTGGCGAG	262788	94984	GCCTCAGCCTCCCGAGTAGC
173615	5811	TCTCAAATTCCTCCTCACAC	218202	50398	GTGAGGAGAGAGTCTGGCGA	262789	94985	TGCCTCAGCCTCCCGAGTAG
173616	5812	GTCTCAAATTCCTCCTCACA	218203	50399	AGTGAGGAGAGAGTCTGGCG	262790	94986	CTGCCTCAGCCTCCCGAGTA
173617	5813	TGTCTCAAATTCCTCCTCAC	218204	50400	GAGTGAGGAGAGAGTCTGGC	262791	94987	CCTGCCTCAGCCTCCCGAGT
173618	5814	CTGTCTCAAATTCCTCCTCA	218205	50401	AGAGTGAGGAGAGAGTCTGG	262792	94988	TCCTGCCTCAGCCTCCCGAG
173619	5815	CCTGTCTCAAATTCCTCCTC	218206	50402	GAGAGTGAGGAGAGAGTCTG	262793	94989	CTCCTGCCTCAGCCTCCCGA
173620	5816	ACCTGTCTCAAATTCCTCCT	218207	50403	AGAGAGTGAGGAGAGAGTCT	262794	94990	TCTCCTGCCTCAGCCTCCCG
173621	5817	AACCTGTCTCAAATTCCTCC	218208	50404	GAGAGAGTGAGGAGAGAGTC	262795	94991	TTCTCCTGCCTCAGCCTCCC
173622	5818	AAACCTGTCTCAAATTCCTC	218209	50405	AGAGAGAGTGAGGAGAGAGT	262796	94992	ATTCTCCTGCCTCAGCCTCC
173623	5819	AAAACCTGTCTCAAATTCCT	218210	50406	CAGAGAGAGTGAGGAGAGAG	262797	94993	CATTCTCCTGCCTCAGCCTC
173624	5820	CAAAACCTGTCTCAAATTCC	218211	50407	CCAGAGAGAGTGAGGAGAGA	262798	94994	CCATTCTCCTGCCTCAGCCT
173625	5821	TCAAAACCTGTCTCAAATTC	218212	50408	CCCAGAGAGAGTGAGGAGAG	262799	94995	GCCATTCTCCTGCCTCAGCC
173626	5822	CTCAAAACCTGTCTCAAATT	218213	50409	ACCCAGAGAGAGTGAGGAGA	262800	94996	CGCCATTCTCCTGCCTCAGC
173627	5823	GCTCAAAACCTGTCTCAAAT	218214	50410	GACCCAGAGAGAGTGAGGAG	262801	94997	ACGCCATTCTCCTGCCTCAG
173628	5824	AGCTCAAAACCTGTCTCAAA	218215	50411	GGACCCAGAGAGAGTGAGGA	262802	94998	CACGCCATTCTCCTGCCTCA
173629	5825	AAGCTCAAAACCTGTCTCAA	218216	50412	TGGACCCAGAGAGAGTGAGG	262803	94999	TCACGCCATTCTCCTGCCTC
173630	5826	AAAGCTCAAAACCTGTCTCA	218217	50413	GTGGACCCAGAGAGAGTGAG	262804	95000	TTCACGCCATTCTCCTGCCT
173631	5827	GAAAGCTCAAAACCTGTCTC	218218	50414	AGTGGACCCAGAGAGAGTGA	262805	95001	GTTCACGCCATTCTCCTGCC
173632	5828	AGAAAGCTCAAAACCTGTCT	218219	50415	TAGTGGACCCAGAGAGAGTG	262806	95002	GGTTCACGCCATTCTCCTGC
173633	5829	CAGAAAGCTCAAAACCTGTC	218220	50416	CTAGTGGACCCAGAGAGAGT	262807	95003	GGGTTCACGCCATTCTCCTG
173634	5830	CCAGAAAGCTCAAAACCTGT	218221	50417	TCTAGTGGACCCAGAGAGAG	262808	95004	TGGGTTCACGCCATTCTCCT

173635	5831	CCCAGAAAGCTCAAAACCTG	218222	50418	CTCTAGTGGACCCAGAGAGA	262809	95005	CTGGGTTCACGCCATTCTCC
173636	5832	ACCCAGAAAGCTCAAAACCT	218223	50419	CCTCTAGTGGACCCAGAGAG	262810	95006	CCTGGGTTCACGCCATTCTC
173637	5833	AACCCAGAAAGCTCAAAACC	218224	50420	ACCTCTAGTGGACCCAGAGA	262811	95007	TCCTGGGTTCACGCCATTCT
173638	5834	GAACCCAGAAAGCTCAAAAC	218225	50421	AACCTCTAGTGGACCCAGAG	262812	95008	CTCCTGGGTTCACGCCATTC
173639	5835	AGAACCCAGAAAGCTCAAAA	218226	50422	GAACCTCTAGTGGACCCAGA	262813	95009	CCTCCTGGGTTCACGCCATT
173640	5836	GAGAACCCAGAAAGCTCAAA	218227	50423	GGAACCTCTAGTGGACCCAG	262814	95010	GCCTCCTGGGTTCACGCCAT
173641	5837	GGAGAACCCAGAAAGCTCAA	218228	50424	AGGAACCTCTAGTGGACCCA	262815	95011	TGCCTCCTGGGTTCACGCCA
173642	5838	TGGAGAACCCAGAAAGCTCA	218229	50425	GAGGAACCTCTAGTGGACCC	262816	95012	CTGCCTCCTGGGTTCACGCC
173643	5839	CTGGAGAACCCAGAAAGCTC	218230	50426	TGAGGAACCTCTAGTGGACC	262817	95013	TCTGCCTCCTGGGTTCACGC
173644	5840	ACTGGAGAACCCAGAAAGCT	218231	50427	CTGAGGAACCTCTAGTGGAC	262818	95014	CTCTGCCTCCTGGGTTCACG
173645	5841	AACTGGAGAACCCAGAAAGC	218232	50428	GCTGAGGAACCTCTAGTGGA	262819	95015	GCTCTGCCTCCTGGGTTCAC
173646	5842	TAACTGGAGAACCCAGAAAG	218233	50429	GGCTGAGGAACCTCTAGTGG	262820	95016	AGCTCTGCCTCCTGGGTTCA
173647	5843	CTAACTGGAGAACCCAGAAA	218234	50430	AGGCTGAGGAACCTCTAGTG	262821	95017	AAGCTCTGCCTCCTGGGTTC
173648	5844	CCTAACTGGAGAACCCAGAA	218235	50431	GAGGCTGAGGAACCTCTAGT	262822	95018	CAAGCTCTGCCTCCTGGGTT
173649	5845	TCCTAACTGGAGAACCCAGA	218236	50432	AGAGGCTGAGGAACCTCTAG	262823	95019	GCAAGCTCTGCCTCCTGGGT
173650	5846	TTCCTAACTGGAGAACCCAG	218237	50433	GAGAGGCTGAGGAACCTCTA	262824	95020	TGCAAGCTCTGCCTCCTGGG
173651	5847	TTTCCTAACTGGAGAACCCA	218238	50434	AGAGAGGCTGAGGAACCTCT	262825	95021	CTGCAAGCTCTGCCTCCTGG
173652	5848	GTTTCCTAACTGGAGAACCC	218239	50435	AAGAGAGGCTGAGGAACCTC	262826	95022	ACTGCAAGCTCTGCCTCCTG
173653	5849	AGTTTCCTAACTGGAGAACC	218240	50436	AAAGAGAGGCTGAGGAACCT	262827	95023	CACTGCAAGCTCTGCCTCCT
173654	5850	AAGTTTCCTAACTGGAGAAC	218241	50437	CAAAGAGAGGCTGAGGAACC	262828	95024	TCACTGCAAGCTCTGCCTCC
173655	5851	AAAGTTTCCTAACTGGAGAA	218242	50438	GCAAAGAGAGGCTGAGGAAC	262829	95025	CTCACTGCAAGCTCTGCCTC
173656	5852	GAAAGTTTCCTAACTGGAGA	218243	50439	GGCAAAGAGAGGCTGAGGAA	262830	95026	GCTCACTGCAAGCTCTGCCT
173657	5853	AGAAAGTTTCCTAACTGGAG	218244	50440	AGGCAAAGAGAGGCTGAGGA	262831	95027	GGCTCACTGCAAGCTCTGCC
173658	5854	CAGAAAGTTTCCTAACTGGA	218245	50441	AAGGCAAAGAGAGGCTGAGG	262832	95028	CGGCTCACTGCAAGCTCTGC
173659	5855	ACAGAAAGTTTCCTAACTGG	218246	50442	CAAGGCAAAGAGAGGCTGAG	262833	95029	TCGGCTCACTGCAAGCTCTG
173660	5856	TACAGAAAGTTTCCTAACTG	218247	50443	CCAAGGCAAAGAGAGGCTGA	262834	95030	CTCGGCTCACTGCAAGCTCT
173661	5857	TTACAGAAAGTTTCCTAACT	218248	50444	ACCAAGGCAAAGAGAGGCTG	262835	95031	TCTCGGCTCACTGCAAGCTC
173662	5858	CTTACAGAAAGTTTCCTAAC	218249	50445	AACCAAGGCAAAGAGAGGCT	262836	95032	ATCTCGGCTCACTGCAAGCT
173663	5859	GCTTACAGAAAGTTTCCTAA	218250	50446	AAACCAAGGCAAAGAGAGGC	262837	95033	AATCTCGGCTCACTGCAAGC
173664	5860	TGCTTACAGAAAGTTTCCTA	218251	50447	AAAACCAAGGCAAAGAGAGG	262838	95034	CAATCTCGGCTCACTGCAAG
173665	5861	ATGCTTACAGAAAGTTTCCT	218252	50448	GAAAACCAAGGCAAAGAGAG	262839	95035	GCAATCTCGGCTCACTGCAA
173666	5862	CATGCTTACAGAAAGTTTCC	218253	50449	GGAAAACCAAGGCAAAGAGA	262840	95036	TGCAATCTCGGCTCACTGCA
173667	5863	GCATGCTTACAGAAAGTTTC	218254	50450	GGGAAAACCAAGGCAAAGAG	262841	95037	GTGCAATCTCGGCTCACTGC
173668	5864	TGCATGCTTACAGAAAGTTT	218255	50451	TGGGAAAACCAAGGCAAAGA	262842	95038	GGTGCAATCTCGGCTCACTG
173669	5865	CTGCATGCTTACAGAAAGTT	218256	50452	CTGGGAAAACCAAGGCAAAG	262843	95039	TGGTGCAATCTCGGCTCACT
173670	5866	TCTGCATGCTTACAGAAAGT	218257	50453	GCTGGGAAAACCAAGGCAAA	262844	95040	GTGGTGCAATCTCGGCTCAC
173671	5867	ATCTGCATGCTTACAGAAAG	218258	50454	AGCTGGGAAAACCAAGGCAA	262845	95041	AGTGGTGCAATCTCGGCTCA
173672	5868	TATCTGCATGCTTACAGAAA	218259	50455	CAGCTGGGAAAACCAAGGCA	262846	95042	CAGTGGTGCAATCTCGGCTC
173673	5869	CTATCTGCATGCTTACAGAA	218260	50456	ACAGCTGGGAAAACCAAGGC	262847	95043	GCAGTGGTGCAATCTCGGCT
173674	5870	TCTATCTGCATGCTTACAGA	218261	50457	TACAGCTGGGAAAACCAAGG	262848	95044	TGCAGTGGTGCAATCTCGGC
173675	5871	TTCTATCTGCATGCTTACAG	218262	50458	TTACAGCTGGGAAAACCAAG	262849	95045	CTGCAGTGGTGCAATCTCGG
173676	5872	ATTCTATCTGCATGCTTACA	218263	50459	TTTACAGCTGGGAAAACCAA	262850	95046	ACTGCAGTGGTGCAATCTCG
173677	5873	CATTCTATCTGCATGCTTAC	218264	50460	TTTTACAGCTGGGAAAACCA	262851	95047	GACTGCAGTGGTGCAATCTC
173678	5874	CCATTCTATCTGCATGCTTA	218265	50461	ATTTTACAGCTGGGAAAACC	262852	95048	GGACTGCAGTGGTGCAATCT
173679	5875	CCCATTCTATCTGCATGCTT	218266	50462	CATTTTACAGCTGGGAAAAC	262853	95049	TGGACTGCAGTGGTGCAATC
173680	5876	GCCCATTCTATCTGCATGCT	218267	50463	CCATTTTACAGCTGGGAAAA	262854	95050	CTGGACTGCAGTGGTGCAAT
173681	5877	AGCCCATTCTATCTGCATGC	218268	50464	TCCATTTTACAGCTGGGAAA	262855	95051	GCTGGACTGCAGTGGTGCAA
173682	5878	AAGCCCATTCTATCTGCATG	218269	50465	CTCCATTTTACAGCTGGGAA	262856	95052	GGCTGGACTGCAGTGGTGCA
173683	5879	GAAGCCCATTCTATCTGCAT	218270	50466	GCTCCATTTTACAGCTGGGA	262857	95053	AGGCTGGACTGCAGTGGTGC
173684	5880	TGAAGCCCATTCTATCTGCA	218271	50467	TGCTCCATTTTACAGCTGGG	262858	95054	CAGGCTGGACTGCAGTGGTG
173685	5881	CTGAAGCCCATTCTATCTGC	218272	50468	TTGCTCCATTTTACAGCTGG	262859	95055	CCAGGCTGGACTGCAGTGGT
173686	5882	GCTGAAGCCCATTCTATCTG	218273	50469	TTTGCTCCATTTTACAGCTG	262860	95056	CCCAGGCTGGACTGCAGTGG
173687	5883	TGCTGAAGCCCATTCTATCT	218274	50470	CTTTGCTCCATTTTACAGCT	262861	95057	GCCCAGGCTGGACTGCAGTG
173688	5884	TTGCTGAAGCCCATTCTATC	218275	50471	TCTTTGCTCCATTTTACAGC	262862	95058	CGCCCAGGCTGGACTGCAGT
173689	5885	TTTGCTGAAGCCCATTCTAT	218276	50472	CTCTTTGCTCCATTTTACAG	262863	95059	TCGCCCAGGCTGGACTGCAG
173690	5886	TTTTGCTGAAGCCCATTCTA	218277	50473	CCTCTTTGCTCCATTTTACA	262864	95060	GTCGCCCAGGCTGGACTGCA
173691	5887	ATTTTGCTGAAGCCCATTCT	218278	50474	CCCTCTTTGCTCCATTTTAC	262865	95061	TGTCGCCCAGGCTGGACTGC
173692	5888	TATTTTGCTGAAGCCCATTC	218279	50475	GCCCTCTTTGCTCCATTTTA	262866	95062	CTGTCGCCCAGGCTGGACTG
173693	5889	GTATTTTGCTGAAGCCCATT	218280	50476	GGCCCTCTTTGCTCCATTTT	262867	95063	TCTGTCGCCCAGGCTGGACT
173694	5890	TGTATTTTGCTGAAGCCCAT	218281	50477	AGGCCCTCTTTGCTCCATTT	262868	95064	CTCTGTCGCCCAGGCTGGAC
173695	5891	TTGTATTTTGCTGAAGCCCA	218282	50478	TAGGCCCTCTTTGCTCCATT	262869	95065	GCTCTGTCGCCCAGGCTGGA
173696	5892	TTTGTATTTTGCTGAAGCCC	218283	50479	ATAGGCCCTCTTTGCTCCAT	262870	95066	CGCTCTGTCGCCCAGGCTGG
173697	5893	GTTTGTATTTTGCTGAAGCC	218284	50480	CATAGGCCCTCTTTGCTCCA	262871	95067	TCGCTCTGTCGCCCAGGCTG
173698	5894	AGTTTGTATTTTGCTGAAGC	218285	50481	ACATAGGCCCTCTTTGCTCC	262872	95068	CTCGCTCTGTCGCCCAGGCT
173699	5895	GAGTTTGTATTTTGCTGAAG	218286	50482	TACATAGGCCCTCTTTGCTC	262873	95069	TCTCGCTCTGTCGCCCAGGC
173700	5896	CGAGTTTGTATTTTGCTGAA	218287	50483	GTACATAGGCCCTCTTTGCT	262874	95070	GTCTCGCTCTGTCGCCCAGG
173701	5897	TCGAGTTTGTATTTTGCTGA	218288	50484	GGTACATAGGCCCTCTTTGC	262875	95071	AGTCTCGCTCTGTCGCCCAG
173702	5898	TTCGAGTTTGTATTTTGCTG	218289	50485	GGGTACATAGGCCCTCTTTG	262876	95072	GAGTCTCGCTCTGTCGCCCA
173703	5899	GTTCGAGTTTGTATTTTGCT	218290	50486	TGGGTACATAGGCCCTCTTT	262877	95073	GGAGTCTCGCTCTGTCGCCC
173704	5900	TGTTCGAGTTTGTATTTTGC	218291	50487	GTGGGTACATAGGCCCTCTT	262878	95074	CGGAGTCTCGCTCTGTCGCC
173705	5901	TTGTTCGAGTTTGTATTTTG	218292	50488	TGTGGGTACATAGGCCCTCT	262879	95075	ACGGAGTCTCGCTCTGTCGC
173706	5902	GTTGTTCGAGTTTGTATTTT	218293	50489	TTGTGGGTACATAGGCCCTC	262880	95076	GACGGAGTCTCGCTCTGTCG

173707	5903	AGTTGTTCGAGTTTGTATTT	218294	50490	TTTGTGGGTACATAGGCCCT	262881	95077	AGACGGAGTCTCGCTCTGTC
173708	5904	AAGTTGTTCGAGTTTGTATT	218295	50491	CTTTGTGGGTACATAGGCCC	262882	95078	GAGACGGAGTCTCGCTCTGT
173709	5905	GAAGTTGTTCGAGTTTGTAT	218296	50492	CCTTTGTGGGTACATAGGCC	262883	95079	TGAGACGGAGTCTCGCTCTG
173710	5906	GGAAGTTGTTCGAGTTTGTA	218297	50493	ACCTTTGTGGGTACATAGGC	262884	95080	TTGAGACGGAGTCTCGCTCT
173711	5907	TGGAAGTTGTTCGAGTTTGT	218298	50494	CACCTTTGTGGGTACATAGG	262885	95081	TTTGAGACGGAGTCTCGCTC
173712	5908	ATGGAAGTTGTTCGAGTTTG	218299	50495	ACACCTTTGTGGGTACATAG	262886	95082	TTTTGAGACGGAGTCTCGCT
173713	5909	CATGGAAGTTGTTCGAGTTT	218300	50496	CACACCTTTGTGGGTACATA	262887	95083	TTTTTGAGACGGAGTCTCGC
173714	5910	ACATGGAAGTTGTTCGAGTT	218301	50497	CCACACCTTTGTGGGTACAT	262888	95084	TTTTTTGAGACGGAGTCTCG
173715	5911	TACATGGAAGTTGTTCGAGT	218302	50498	ACCACACCTTTGTGGGTACA	262889	95085	CTTTTTTGAGACGGAGTCTC
173716	5912	ATACATGGAAGTTGTTCGAG	218303	50499	AACCACACCTTTGTGGGTAC	262890	95086	TCTTTTTTGAGACGGAGTCT
173717	5913	TATACATGGAAGTTGTTCGA	218304	50500	CAACCACACCTTTGTGGGTA	262891	95087	TTCTTTTTTGAGACGGAGTC
173718	5914	CTATACATGGAAGTTGTTCG	218305	50501	CCAACCACACCTTTGTGGGT	262892	95088	TTTCTTTTTTGAGACGGAGT
173719	5915	ACTATACATGGAAGTTGTTC	218306	50502	TCCAACCACACCTTTGTGGG	262893	95089	TTTTCTTTTTTGAGACGGAG
173720	5916	GACTATACATGGAAGTTGTT	218307	50503	CTCCAACCACACCTTTGTGG	262894	95090	TTTTTCTTTTTTGAGACGGA
173721	5917	GGACTATACATGGAAGTTGT	218308	50504	GCTCCAACCACACCTTTGTG	262895	95091	CTTTTTCTTTTTTGAGACGG
173722	5918	GGGACTATACATGGAAGTTG	218309	50505	CGCTCCAACCACACCTTTGT	262896	95092	TCTTTTTCTTTTTTGAGACG
173723	5919	AGGGACTATACATGGAAGTT	218310	50506	TCGCTCCAACCACACCTTTG	262897	95093	TTCTTTTTCTTTTTTGAGAC
173724	5920	AAGGGACTATACATGGAAGT	218311	50507	GTCGCTCCAACCACACCTTT	262898	95094	TTTCTTTTTCTTTTTTGAGA
173725	5921	TAAGGGACTATACATGGAAG	218312	50508	AGTCGCTCCAACCACACCTT	262899	95095	TTTTCTTTTTCTTTTTTGAG
173726	5922	TTAAGGGACTATACATGGAA	218313	50509	GAGTCGCTCCAACCACACCT	262900	95096	TTTTTCTTTTTCTTTTTTGA
173727	5923	ATTAAGGGACTATACATGGA	218314	50510	GGAGTCGCTCCAACCACACC	262901	95097	CTTTTTCTTTTTCTTTTTTG
173728	5924	AATTAAGGGACTATACATGG	218315	50511	AGGAGTCGCTCCAACCACAC	262902	95098	TCTTTTTCTTTTTCTTTTTT
173729	5925	AAATTAAGGGACTATACATG	218316	50512	GAGGAGTCGCTCCAACCACA	262903	95099	TTCTTTTTCTTTTTCTTTTT
173730	5926	AAAATTAAGGGACTATACAT	218317	50513	GGAGGAGTCGCTCCAACCAC	262904	95100	TTTCTTTTTCTTTTTCTTTT
173731	5927	GAAAATTAAGGGACTATACA	218318	50514	AGGAGGAGTCGCTCCAACCA	262905	95101	TTTTCTTTTTCTTTTTCTTT
173732	5928	AGAAAATTAAGGGACTATAC	218319	50515	TAGGAGGAGTCGCTCCAACC	262906	95102	TTTTTCTTTTTCTTTTTCTT
173733	5929	AAGAAAATTAAGGGACTATA	218320	50516	GTAGGAGGAGTCGCTCCAAC	262907	95103	CTTTTTCTTTTTCTTTTTCT
173734	5930	AAAGAAAATTAAGGGACTAT	218321	50517	TGTAGGAGGAGTCGCTCCAA	262908	95104	TCTTTTTCTTTTTCTTTTTC
173735	5931	CAAAGAAAATTAAGGGACTA	218322	50518	ATGTAGGAGGAGTCGCTCCA	262909	95105	TTCTTTTTCTTTTTCTTTTT
173736	5932	GCAAAGAAAATTAAGGGACT	218323	50519	AATGTAGGAGGAGTCGCTCC	262910	95106	GTTCTTTTTCTTTTTCTTTT
173737	5933	AGCAAAGAAAATTAAGGGAC	218324	50520	TAATGTAGGAGGAGTCGCTC	262911	95107	AGTTCTTTTTCTTTTTCTTT
173738	5934	AAGCAAAGAAAATTAAGGGA	218325	50521	CTAATGTAGGAGGAGTCGCT	262912	95108	CAGTTCTTTTTCTTTTTCTT
173739	5935	AAAGCAAAGAAAATTAAGGG	218326	50522	CCTAATGTAGGAGGAGTCGC	262913	95109	ACAGTTCTTTTTCTTTTTCT
173740	5936	AAAAGCAAAGAAAATTAAGG	218327	50523	CCCTAATGTAGGAGGAGTCG	262914	95110	CACAGTTCTTTTTCTTTTTC
173741	5937	AAAAAGCAAAGAAAATTAAG	218328	50524	GCCCTAATGTAGGAGGAGTC	262915	95111	TCACAGTTCTTTTTCTTTTT
173742	5938	AAAAAAGCAAAGAAAATTAA	218329	50525	GGCCCTAATGTAGGAGGAGT	262916	95112	ATCACAGTTCTTTTTCTTTT
173743	5939	GAAAAAAGCAAAGAAAATTA	218330	50526	AGGCCCTAATGTAGGAGGAG	262917	95113	AATCACAGTTCTTTTTCTTT
173744	5940	TGAAAAAAGCAAAGAAAATT	218331	50527	GAGGCCCTAATGTAGGAGGA	262918	95114	CAATCACAGTTCTTTTTCTT
173745	5941	ATGAAAAAAGCAAAGAAAAT	218332	50528	CGAGGCCCTAATGTAGGAGG	262919	95115	CCAATCACAGTTCTTTTTCT
173746	5942	TATGAAAAAAGCAAAGAAAA	218333	50529	TCGAGGCCCTAATGTAGGAG	262920	95116	CCCAATCACAGTTCTTTTTC
173747	5943	ATATGAAAAAAGCAAAGAAA	218334	50530	CTCGAGGCCCTAATGTAGGA	262921	95117	CCCCAATCACAGTTCTTTTT
173748	5944	AATATGAAAAAAGCAAAGAA	218335	50531	ACTCGAGGCCCTAATGTAGG	262922	95118	TCCCCAATCACAGTTCTTTT
173749	5945	AAATATGAAAAAAGCAAAGA	218336	50532	CACTCGAGGCCCTAATGTAG	262923	95119	CTCCCCAATCACAGTTCTTT
173750	5946	GAAATATGAAAAAAGCAAAG	218337	50533	CCACTCGAGGCCCTAATGTA	262924	95120	CCTCCCCAATCACAGTTCTT
173751	5947	TGAAATATGAAAAAAGCAAA	218338	50534	CCCACTCGAGGCCCTAATGT	262925	95121	TCCTCCCCAATCACAGTTCT
173752	5948	ATGAAATATGAAAAAAGCAA	218339	50535	CCCCACTCGAGGCCCTAATG	262926	95122	GTCCTCCCCAATCACAGTTC
173753	5949	GATGAAATATGAAAAAAGCA	218340	50536	GCCCCACTCGAGGCCCTAAT	262927	95123	CGTCCTCCCCAATCACAGTT
173754	5950	TGATGAAATATGAAAAAAGC	218341	50537	AGCCCCACTCGAGGCCCTAA	262928	95124	CCGTCCTCCCCAATCACAGT
173755	5951	CTGATGAAATATGAAAAAAG	218342	50538	AAGCCCCACTCGAGGCCCTA	262929	95125	ACCGTCCTCCCCAATCACAG
173756	5952	CCTGATGAAATATGAAAAAA	218343	50539	GAAGCCCCACTCGAGGCCCT	262930	95126	GACCGTCCTCCCCAATCACA
173757	5953	GCCTGATGAAATATGAAAAA	218344	50540	TGAAGCCCCACTCGAGGCCC	262931	95127	TGACCGTCCTCCCCAATCAC
173758	5954	AGCCTGATGAAATATGAAAA	218345	50541	ATGAAGCCCCACTCGAGGCC	262932	95128	GTGACCGTCCTCCCCAATCA
173759	5955	GAGCCTGATGAAATATGAAA	218346	50542	CATGAAGCCCCACTCGAGGC	262933	95129	AGTGACCGTCCTCCCCAATC
173760	5956	GGAGCCTGATGAAATATGAA	218347	50543	TCATGAAGCCCCACTCGAGG	262934	95130	AAGTGACCGTCCTCCCCAAT
173761	5957	TGGAGCCTGATGAAATATGA	218348	50544	ATCATGAAGCCCCACTCGAG	262935	95131	AAAGTGACCGTCCTCCCCAA
173762	5958	ATGGAGCCTGATGAAATATG	218349	50545	AATCATGAAGCCCCACTCGA	262936	95132	GAAAGTGACCGTCCTCCCCA
173763	5959	CATGGAGCCTGATGAAATAT	218350	50546	CAATCATGAAGCCCCACTCG	262937	95133	GGAAAGTGACCGTCCTCCCC
173764	5960	GCATGGAGCCTGATGAAATA	218351	50547	CCAATCATGAAGCCCCACTC	262938	95134	AGGAAAGTGACCGTCCTCCC
173765	5961	AGCATGGAGCCTGATGAAAT	218352	50548	ACCAATCATGAAGCCCCACT	262939	95135	CAGGAAAGTGACCGTCCTCC
173766	5962	CAGCATGGAGCCTGATGAAA	218353	50549	AACCAATCATGAAGCCCCAC	262940	95136	ACAGGAAAGTGACCGTCCTC
173767	5963	TCAGCATGGAGCCTGATGAA	218354	50550	CAACCAATCATGAAGCCCCA	262941	95137	AACAGGAAAGTGACCGTCCT
173768	5964	CTCAGCATGGAGCCTGATGA	218355	50551	CCAACCAATCATGAAGCCCC	262942	95138	GAACAGGAAAGTGACCGTCC
173769	5965	GCTCAGCATGGAGCCTGATG	218356	50552	ACCAACCAATCATGAAGCCC	262943	95139	AGAACAGGAAAGTGACCGTC
173770	5966	GGCTCAGCATGGAGCCTGAT	218357	50553	CACCAACCAATCATGAAGCC	262944	95140	AAGAACAGGAAAGTGACCGT
173771	5967	GGGCTCAGCATGGAGCCTGA	218358	50554	CCACCAACCAATCATGAAGC	262945	95141	TAAGAACAGGAAAGTGACCG
173772	5968	TGGGCTCAGCATGGAGCCTG	218359	50555	TCCACCAACCAATCATGAAG	262946	95142	GTAAGAACAGGAAAGTGACC
173773	5969	TTGGGCTCAGCATGGAGCCT	218360	50556	CTCCACCAACCAATCATGAA	262947	95143	AGTAAGAACAGGAAAGTGAC
173774	5970	ATTGGGCTCAGCATGGAGCC	218361	50557	CCTCCACCAACCAATCATGA	262948	95144	CAGTAAGAACAGGAAAGTGA
173775	5971	GATTGGGCTCAGCATGGAGC	218362	50558	ACCTCCACCAACCAATCATG	262949	95145	TCAGTAAGAACAGGAAAGTG
173776	5972	TGATTGGGCTCAGCATGGAG	218363	50559	GACCTCCACCAACCAATCAT	262950	95146	ATCAGTAAGAACAGGAAAGT
173777	5973	CTGATTGGGCTCAGCATGGA	218364	50560	AGACCTCCACCAACCAATCA	262951	95147	GATCAGTAAGAACAGGAAAG
173778	5974	CCTGATTGGGCTCAGCATGG	218365	50561	GAGACCTCCACCAACCAATC	262952	95148	TGATCAGTAAGAACAGGAAA

173779	5975	CCCTGATTGGGCTCAGCATG	218366	50562	GGAGACCTCCACCAACCAAT	262953	95149	CTGATCAGTAAGAACAGGAA
173780	5976	TCCCTGATTGGGCTCAGCAT	218367	50563	TGGAGACCTCCACCAACCAA	262954	95150	TCTGATCAGTAAGAACAGGA
173781	5977	GTCCCTGATTGGGCTCAGCA	218368	50564	TTGGAGACCTCCACCAACCA	262955	95151	TTCTGATCAGTAAGAACAGG
173782	5978	GGTCCCTGATTGGGCTCAGC	218369	50565	TTTGGAGACCTCCACCAACC	262956	95152	CTTCTGATCAGTAAGAACAG
173783	5979	GGGTCCCTGATTGGGCTCAG	218370	50566	GTTTGGAGACCTCCACCAAC	262957	95153	CCTTCTGATCAGTAAGAACA
173784	5980	CGGGTCCCTGATTGGGCTCA	218371	50567	GGTTTGGAGACCTCCACCAA	262958	95154	CCCTTCTGATCAGTAAGAAC
173785	5981	TCGGGTCCCTGATTGGGCTC	218372	50568	GGGTTTGGAGACCTCCACCA	262959	95155	TCCCTTCTGATCAGTAAGAA
173786	5982	ATCGGGTCCCTGATTGGGCT	218373	50569	TGGGTTTGGAGACCTCCACC	262960	95156	ATCCCTTCTGATCAGTAAGA
173787	5983	TATCGGGTCCCTGATTGGGC	218374	50570	GTGGGTTTGGAGACCTCCAC	262961	95157	TATCCCTTCTGATCAGTAAG
173788	5984	CTATCGGGTCCCTGATTGGG	218375	50571	GGTGGGTTTGGAGACCTCCA	262962	95158	ATATCCCTTCTGATCAGTAA
173789	5985	TCTATCGGGTCCCTGATTGG	218376	50572	GGGTGGGTTTGGAGACCTCC	262963	95159	AATATCCCTTCTGATCAGTA
173790	5986	TTCTATCGGGTCCCTGATTG	218377	50573	TGGGTGGGTTTGGAGACCTC	262964	95160	TAATATCCCTTCTGATCAGT
173791	5987	TTTCTATCGGGTCCCTGATT	218378	50574	CTGGGTGGGTTTGGAGACCT	262965	95161	TTAATATCCCTTCTGATCAG
173792	5988	ATTTCTATCGGGTCCCTGAT	218379	50575	ACTGGGTGGGTTTGGAGACC	262966	95162	CTTAATATCCCTTCTGATCA
173793	5989	GATTTCTATCGGGTCCCTGA	218380	50576	CACTGGGTGGGTTTGGAGAC	262967	95163	CCTTAATATCCCTTCTGATC
173794	5990	GGATTTCTATCGGGTCCCTG	218381	50577	GCACTGGGTGGGTTTGGAGA	262968	95164	CCCTTAATATCCCTTCTGAT
173795	5991	TGGATTTCTATCGGGTCCCT	218382	50578	GGCACTGGGTGGGTTTGGAG	262969	95165	ACCCTTAATATCCCTTCTGA
173796	5992	TTGGATTTCTATCGGGTCCC	218383	50579	TGGCACTGGGTGGGTTTGGA	262970	95166	TACCCTTAATATCCCTTCTG
173797	5993	TTTGGATTTCTATCGGGTCC	218384	50580	GTGGCACTGGGTGGGTTTGG	262971	95167	GTACCCTTAATATCCCTTCT
173798	5994	GTTTGGATTTCTATCGGGTC	218385	50581	GGTGGCACTGGGTGGGTTTG	262972	95168	GGTACCCTTAATATCCCTTC
173799	5995	TGTTTGGATTTCTATCGGGT	218386	50582	CGGTGGCACTGGGTGGGTTT	262973	95169	AGGTACCCTTAATATCCCTT
173800	5996	GTGTTTGGATTTCTATCGGG	218387	50583	TCGGTGGCACTGGGTGGGTT	262974	95170	CAGGTACCCTTAATATCCCT
173801	5997	GGTGTTTGGATTTCTATCGG	218388	50584	TTCGGTGGCACTGGGTGGGT	262975	95171	TCAGGTACCCTTAATATCCC
173802	5998	TGGTGTTTGGATTTCTATCG	218389	50585	CTTCGGTGGCACTGGGTGGG	262976	95172	ATCAGGTACCCTTAATATCC
173803	5999	ATGGTGTTTGGATTTCTATC	218390	50586	CCTTCGGTGGCACTGGGTGG	262977	95173	AATCAGGTACCCTTAATATC
173804	6000	CATGGTGTTTGGATTTCTAT	218391	50587	GCCTTCGGTGGCACTGGGTG	262978	95174	GAATCAGGTACCCTTAATAT
173805	6001	ACATGGTGTTTGGATTTCTA	218392	50588	AGCCTTCGGTGGCACTGGGT	262979	95175	TGAATCAGGTACCCTTAATA
173806	6002	GACATGGTGTTTGGATTTCT	218393	50589	CAGCCTTCGGTGGCACTGGG	262980	95176	TTGAATCAGGTACCCTTAAT
173807	6003	TGACATGGTGTTTGGATTTC	218394	50590	TCAGCCTTCGGTGGCACTGG	262981	95177	TTTGAATCAGGTACCCTTAA
173808	6004	CTGACATGGTGTTTGGATTT	218395	50591	CTCAGCCTTCGGTGGCACTG	262982	95178	GTTTGAATCAGGTACCCTTA
173809	6005	GCTGACATGGTGTTTGGATT	218396	50592	TCTCAGCCTTCGGTGGCACT	262983	95179	TGTTTGAATCAGGTACCCTT
173810	6006	CGCTGACATGGTGTTTGGAT	218397	50593	GTCTCAGCCTTCGGTGGCAC	262984	95180	CTGTTTGAATCAGGTACCCT
173811	6007	TCGCTGACATGGTGTTTGGA	218398	50594	AGTCTCAGCCTTCGGTGGCA	262985	95181	GCTGTTTGAATCAGGTACCC
173812	6008	CTCGCTGACATGGTGTTTGG	218399	50595	CAGTCTCAGCCTTCGGTGGC	262986	95182	GGCTGTTTGAATCAGGTACC
173813	6009	ACTCGCTGACATGGTGTTTG	218400	50596	GCAGTCTCAGCCTTCGGTGG	262987	95183	AGGCTGTTTGAATCAGGTAC
173814	6010	GACTCGCTGACATGGTGTTT	218401	50597	TGCAGTCTCAGCCTTCGGTG	262988	95184	CAGGCTGTTTGAATCAGGTA
173815	6011	GGACTCGCTGACATGGTGTT	218402	50598	CTGCAGTCTCAGCCTTCGGT	262989	95185	CCAGGCTGTTTGAATCAGGT
173816	6012	GGGACTCGCTGACATGGTGT	218403	50599	TCTGCAGTCTCAGCCTTCGG	262990	95186	TCCAGGCTGTTTGAATCAGG
173817	6013	GGGGACTCGCTGACATGGTG	218404	50600	ATCTGCAGTCTCAGCCTTCG	262991	95187	CTCCAGGCTGTTTGAATCAG
173818	6014	TGGGGACTCGCTGACATGGT	218405	50601	CATCTGCAGTCTCAGCCTTC	262992	95188	TCTCCAGGCTGTTTGAATCA
173819	6015	TTGGGGACTCGCTGACATGG	218406	50602	GCATCTGCAGTCTCAGCCTT	262993	95189	ATCTCCAGGCTGTTTGAATC
173820	6016	CTTGGGGACTCGCTGACATG	218407	50603	TGCATCTGCAGTCTCAGCCT	262994	95190	GATCTCCAGGCTGTTTGAAT
173821	6017	TCTTGGGGACTCGCTGACAT	218408	50604	TTGCATCTGCAGTCTCAGCC	262995	95191	TGATCTCCAGGCTGTTTGAA
173822	6018	TTCTTGGGGACTCGCTGACA	218409	50605	ATTGCATCTGCAGTCTCAGC	262996	95192	GTGATCTCCAGGCTGTTTGA
173823	6019	TTTCTTGGGGACTCGCTGAC	218410	50606	CATTGCATCTGCAGTCTCAG	262997	95193	AGTGATCTCCAGGCTGTTTG
173824	6020	ATTTCTTGGGGACTCGCTGA	218411	50607	GCATTGCATCTGCAGTCTCA	262998	95194	CAGTGATCTCCAGGCTGTTT
173825	6021	CATTTCTTGGGGACTCGCTG	218412	50608	GGCATTGCATCTGCAGTCTC	262999	95195	GCAGTGATCTCCAGGCTGTT
173826	6022	GCATTTCTTGGGGACTCGCT	218413	50609	TGGCATTGCATCTGCAGTCT	263000	95196	AGCAGTGATCTCCAGGCTGT
173827	6023	TGCATTTCTTGGGGACTCGC	218414	50610	GTGGCATTGCATCTGCAGTC	263001	95197	AAGCAGTGATCTCCAGGCTG
173828	6024	ATGCATTTCTTGGGGACTCG	218415	50611	TGTGGCATTGCATCTGCAGT	263002	95198	AAAGCAGTGATCTCCAGGCT
173829	6025	AATGCATTTCTTGGGGACTC	218416	50612	CTGTGGCATTGCATCTGCAG	263003	95199	GAAAGCAGTGATCTCCAGGC
173830	6026	AAATGCATTTCTTGGGGACT	218417	50613	CCTGTGGCATTGCATCTGCA	263004	95200	TGAAAGCAGTGATCTCCAGG
173831	6027	AAAATGCATTTCTTGGGGAC	218418	50614	ACCTGTGGCATTGCATCTGC	263005	95201	TTGAAAGCAGTGATCTCCAG
173832	6028	CAAAATGCATTTCTTGGGGA	218419	50615	CACCTGTGGCATTGCATCTG	263006	95202	GTTGAAAGCAGTGATCTCCA
173833	6029	ACAAAATGCATTTCTTGGGG	218420	50616	ACACCTGTGGCATTGCATCT	263007	95203	GGTTGAAAGCAGTGATCTCC
173834	6030	CACAAAATGCATTTCTTGGG	218421	50617	GACACCTGTGGCATTGCATC	263008	95204	TGGTTGAAAGCAGTGATCTC
173835	6031	GCACAAAATGCATTTCTTGG	218422	50618	GGACACCTGTGGCATTGCAT	263009	95205	ATGGTTGAAAGCAGTGATCT
173836	6032	GGCACAAAATGCATTTCTTG	218423	50619	AGGACACCTGTGGCATTGCA	263010	95206	AATGGTTGAAAGCAGTGATC
173837	6033	TGGCACAAAATGCATTTCTT	218424	50620	AAGGACACCTGTGGCATTGC	263011	95207	TAATGGTTGAAAGCAGTGAT
173838	6034	TTGGCACAAAATGCATTTCT	218425	50621	GAAGGACACCTGTGGCATTG	263012	95208	GTAATGGTTGAAAGCAGTGA
173839	6035	CTTGGCACAAAATGCATTTC	218426	50622	GGAAGGACACCTGTGGCATT	263013	95209	GGTAATGGTTGAAAGCAGTG
173840	6036	CCTTGGCACAAAATGCATTT	218427	50623	AGGAAGGACACCTGTGGCAT	263014	95210	AGGTAATGGTTGAAAGCAGT
173841	6037	GCCTTGGCACAAAATGCATT	218428	50624	GAGGAAGGACACCTGTGGCA	263015	95211	CAGGTAATGGTTGAAAGCAG
173842	6038	AGCCTTGGCACAAAATGCAT	218429	50625	TGAGGAAGGACACCTGTGGC	263016	95212	GCAGGTAATGGTTGAAAGCA
173843	6039	TAGCCTTGGCACAAAATGCA	218430	50626	CTGAGGAAGGACACCTGTGG	263017	95213	GGCAGGTAATGGTTGAAAGC
173844	6040	ATAGCCTTGGCACAAAATGC	218431	50627	GCTGAGGAAGGACACCTGTG	263018	95214	AGGCAGGTAATGGTTGAAAG
173845	6041	AATAGCCTTGGCACAAAATG	218432	50628	GGCTGAGGAAGGACACCTGT	263019	95215	AAGGCAGGTAATGGTTGAAA
173846	6042	GAATAGCCTTGGCACAAAAT	218433	50629	AGGCTGAGGAAGGACACCTG	263020	95216	TAAGGCAGGTAATGGTTGAA
173847	6043	TGAATAGCCTTGGCACAAAA	218434	50630	CAGGCTGAGGAAGGACACCT	263021	95217	ATAAGGCAGGTAATGGTTGA
173848	6044	TTGAATAGCCTTGGCACAAA	218435	50631	CCAGGCTGAGGAAGGACACC	263022	95218	AATAAGGCAGGTAATGGTTG
173849	6045	CTTGAATAGCCTTGGCACAA	218436	50632	CCCAGGCTGAGGAAGGACAC	263023	95219	AAATAAGGCAGGTAATGGTT
173850	6046	CCTTGAATAGCCTTGGCACA	218437	50633	GCCCAGGCTGAGGAAGGACA	263024	95220	TAAATAAGGCAGGTAATGGT

173851	6047	TCCTTGAATAGCCTTGGCAC	218438	50634	TGCCCAGGCTGAGGAAGGAC	263025	95221	ATAAATAAGGCAGGTAATGG
173852	6048	TTCCTTGAATAGCCTTGGCA	218439	50635	CTGCCCAGGCTGAGGAAGGA	263026	95222	AATAAATAAGGCAGGTAATG
173853	6049	CTTCCTTGAATAGCCTTGGC	218440	50636	GCTGCCCAGGCTGAGGAAGG	263027	95223	AAATAAATAAGGCAGGTAAT
173854	6050	CCTTCCTTGAATAGCCTTGG	218441	50637	AGCTGCCCAGGCTGAGGAAG	263028	95224	AAAATAAATAAGGCAGGTAA
173855	6051	ACCTTCCTTGAATAGCCTTG	218442	50638	CAGCTGCCCAGGCTGAGGAA	263029	95225	AAAAATAAATAAGGCAGGTA
173856	6052	AACCTTCCTTGAATAGCCTT	218443	50639	TCAGCTGCCCAGGCTGAGGA	263030	95226	TAAAAATAAATAAGGCAGGT
173857	6053	AAACCTTCCTTGAATAGCCT	218444	50640	TTCAGCTGCCCAGGCTGAGG	263031	95227	CTAAAAATAAATAAGGCAGG
173858	6054	CAAACCTTCCTTGAATAGCC	218445	50641	GTTCAGCTGCCCAGGCTGAG	263032	95228	ACTAAAAATAAATAAGGCAG
173859	6055	CCAAACCTTCCTTGAATAGC	218446	50642	TGTTCAGCTGCCCAGGCTGA	263033	95229	AACTAAAAATAAATAAGGCA
173860	6056	CCCAAACCTTCCTTGAATAG	218447	50643	ATGTTCAGCTGCCCAGGCTG	263034	95230	TAACTAAAAATAAATAAGGC
173861	6057	TCCCAAACCTTCCTTGAATA	218448	50644	GATGTTCAGCTGCCCAGGCT	263035	95231	GTAACTAAAAATAAATAAGG
173862	6058	CTCCCAAACCTTCCTTGAAT	218449	50645	TGATGTTCAGCTGCCCAGGC	263036	95232	AGTAACTAAAAATAAATAAG
173863	6059	GCTCCCAAACCTTCCTTGAA	218450	50646	ATGATGTTCAGCTGCCCAGG	263037	95233	CAGTAACTAAAAATAAATAA
173864	6060	TGCTCCCAAACCTTCCTTGA	218451	50647	CATGATGTTCAGCTGCCCAG	263038	95234	ACAGTAACTAAAAATAAATA
173865	6061	CTGCTCCCAAACCTTCCTTG	218452	50648	ACATGATGTTCAGCTGCCCA	263039	95235	GACAGTAACTAAAAATAAAT
173866	6062	GCTGCTCCCAAACCTTCCTT	218453	50649	CACATGATGTTCAGCTGCCC	263040	95236	GGACAGTAACTAAAAATAAA
173867	6063	AGCTGCTCCCAAACCTTCCT	218454	50650	ACACATGATGTTCAGCTGCC	263041	95237	AGGACAGTAACTAAAAATAA
173868	6064	GAGCTGCTCCCAAACCTTCC	218455	50651	TACACATGATGTTCAGCTGC	263042	95238	AAGGACAGTAACTAAAAATA
173869	6065	TGAGCTGCTCCCAAACCTTC	218456	50652	TTACACATGATGTTCAGCTG	263043	95239	AAAGGACAGTAACTAAAAAT
173870	6066	TTGAGCTGCTCCCAAACCTT	218457	50653	TTTACACATGATGTTCAGCT	263044	95240	AAAAGGACAGTAACTAAAAA
173871	6067	CTTGAGCTGCTCCCAAACCT	218458	50654	TTTTACACATGATGTTCAGC	263045	95241	AAAAAGGACAGTAACTAAAA
173872	6068	CCTTGAGCTGCTCCCAAACC	218459	50655	GTTTTACACATGATGTTCAG	263046	95242	AAAAAAGGACAGTAACTAAA
173873	6069	CCCTTGAGCTGCTCCCAAAC	218460	50656	CGTTTTACACATGATGTTCA	263047	95243	GAAAAAAGGACAGTAACTAA
173874	6070	GCCCTTGAGCTGCTCCCAAA	218461	50657	CCGTTTTACACATGATGTTC	263048	95244	TGAAAAAAGGACAGTAACTA
173875	6071	TGCCCTTGAGCTGCTCCCAA	218462	50658	CCCGTTTTACACATGATGTT	263049	95245	CTGAAAAAAGGACAGTAACT
173876	6072	CTGCCCTTGAGCTGCTCCCA	218463	50659	CCCCGTTTTACACATGATGT	263050	95246	ACTGAAAAAAGGACAGTAAC
173877	6073	TCTGCCCTTGAGCTGCTCCC	218464	50660	TCCCCGTTTTACACATGATG	263051	95247	AACTGAAAAAAGGACAGTAA
173878	6074	GTCTGCCCTTGAGCTGCTCC	218465	50661	ATCCCCGTTTTACACATGAT	263052	95248	AAACTGAAAAAAGGACAGTA
173879	6075	TGTCTGCCCTTGAGCTGCTC	218466	50662	TATCCCCGTTTTACACATGA	263053	95249	CAAACTGAAAAAAGGACAGT
173880	6076	GTGTCTGCCCTTGAGCTGCT	218467	50663	TTATCCCCGTTTTACACATG	263054	95250	ACAAACTGAAAAAAGGACAG
173881	6077	AGTGTCTGCCCTTGAGCTGC	218468	50664	ATTATCCCCGTTTTACACAT	263055	95251	AACAAACTGAAAAAAGGACA
173882	6078	CAGTGTCTGCCCTTGAGCTG	218469	50665	TATTATCCCCGTTTTACACA	263056	95252	AAACAAACTGAAAAAAGGAC
173883	6079	ACAGTGTCTGCCCTTGAGCT	218470	50666	TTATTATCCCCGTTTTACAC	263057	95253	GAAACAAACTGAAAAAAGGA
173884	6080	AACAGTGTCTGCCCTTGAGC	218471	50667	CTTATTATCCCCGTTTTACA	263058	95254	GGAAACAAACTGAAAAAAGG
173885	6081	TAACAGTGTCTGCCCTTGAG	218472	50668	TCTTATTATCCCCGTTTTAC	263059	95255	GGGAAACAAACTGAAAAAAG
173886	6082	GTAACAGTGTCTGCCCTTGA	218473	50669	ATCTTATTATCCCCGTTTTA	263060	95256	AGGGAAACAAACTGAAAAAA
173887	6083	GGTAACAGTGTCTGCCCTTG	218474	50670	TATCTTATTATCCCCGTTTT	263061	95257	GAGGGAAACAAACTGAAAAA
173888	6084	GGGTAACAGTGTCTGCCCTT	218475	50671	TTATCTTATTATCCCCGTTT	263062	95258	GGAGGGAAACAAACTGAAAA
173889	6085	AGGGTAACAGTGTCTGCCCT	218476	50672	ATTATCTTATTATCCCCGTT	263063	95259	AGGAGGGAAACAAACTGAAA
173890	6086	GAGGGTAACAGTGTCTGCCC	218477	50673	TATTATCTTATTATCCCCGT	263064	95260	GAGGAGGGAAACAAACTGAA
173891	6087	GGAGGGTAACAGTGTCTGCC	218478	50674	TTATTATCTTATTATCCCCG	263065	95261	GGAGGAGGGAAACAAACTGA
173892	6088	GGGAGGGTAACAGTGTCTGC	218479	50675	GTTATTATCTTATTATCCCC	263066	95262	TGGAGGAGGGAAACAAACTG
173893	6089	GGGGAGGGTAACAGTGTCTG	218480	50676	TGTTATTATCTTATTATCCC	263067	95263	ATGGAGGAGGGAAACAAACT
173894	6090	GGGGGAGGGTAACAGTGTCT	218481	50677	CTGTTATTATCTTATTATCC	263068	95264	CATGGAGGAGGGAAACAAAC
173895	6091	TGGGGGAGGGTAACAGTGTC	218482	50678	GCTGTTATTATCTTATTATC	263069	95265	ACATGGAGGAGGGAAACAAA
173896	6092	CTGGGGGAGGGTAACAGTGT	218483	50679	GGCTGTTATTATCTTATTAT	263070	95266	CACATGGAGGAGGGAAACAA
173897	6093	CCTGGGGGAGGGTAACAGTG	218484	50680	GGGCTGTTATTATCTTATTA	263071	95267	GCACATGGAGGAGGGAAACA
173898	6094	ACCTGGGGGAGGGTAACAGT	218485	50681	GGGGCTGTTATTATCTTATT	263072	95268	AGCACATGGAGGAGGGAAAC
173899	6095	GACCTGGGGGAGGGTAACAG	218486	50682	AGGGGCTGTTATTATCTTAT	263073	95269	CAGCACATGGAGGAGGGAAA
173900	6096	GGACCTGGGGGAGGGTAACA	218487	50683	AAGGGGCTGTTATTATCTTA	263074	95270	TCAGCACATGGAGGAGGGAA
173901	6097	GGGACCTGGGGGAGGGTAAC	218488	50684	CAAGGGGCTGTTATTATCTT	263075	95271	GTCAGCACATGGAGGAGGGA
173902	6098	GGGGACCTGGGGGAGGGTAA	218489	50685	GCAAGGGGCTGTTATTATCT	263076	95272	AGTCAGCACATGGAGGAGGG
173903	6099	TGGGGACCTGGGGGAGGGTA	218490	50686	TGCAAGGGGCTGTTATTATC	263077	95273	AAGTCAGCACATGGAGGAGG
173904	6100	CTGGGGACCTGGGGGAGGGT	218491	50687	GTGCAAGGGGCTGTTATTAT	263078	95274	AAAGTCAGCACATGGAGGAG
173905	6101	ACTGGGGACCTGGGGGAGGG	218492	50688	GGTGCAAGGGGCTGTTATTA	263079	95275	AAAAGTCAGCACATGGAGGA
173906	6102	CACTGGGGACCTGGGGGAGG	218493	50689	AGGTGCAAGGGGCTGTTATT	263080	95276	TAAAAGTCAGCACATGGAGG
173907	6103	GCACTGGGGACCTGGGGGAG	218494	50690	TAGGTGCAAGGGGCTGTTAT	263081	95277	ATAAAAGTCAGCACATGGAG
173908	6104	TGCACTGGGGACCTGGGGGA	218495	50691	ATAGGTGCAAGGGGCTGTTA	263082	95278	AATAAAAGTCAGCACATGGA
173909	6105	CTGCACTGGGGACCTGGGGG	218496	50692	CATAGGTGCAAGGGGCTGTT	263083	95279	AAATAAAAGTCAGCACATGG
173910	6106	CCTGCACTGGGGACCTGGGG	218497	50693	ACATAGGTGCAAGGGGCTGT	263084	95280	AAAATAAAAGTCAGCACATG
173911	6107	CCCTGCACTGGGGACCTGGG	218498	50694	CACATAGGTGCAAGGGGCTG	263085	95281	CAAAATAAAAGTCAGCACAT
173912	6108	GCCCTGCACTGGGGACCTGG	218499	50695	CCACATAGGTGCAAGGGGCT	263086	95282	TCAAAATAAAAGTCAGCACA
173913	6109	TGCCCTGCACTGGGGACCTG	218500	50696	GCCACATAGGTGCAAGGGGC	263087	95283	ATCAAAATAAAAGTCAGCAC
173914	6110	CTGCCCTGCACTGGGGACCT	218501	50697	AGCCACATAGGTGCAAGGGG	263088	95284	AATCAAAATAAAAGTCAGCA
173915	6111	ACTGCCCTGCACTGGGGACC	218502	50698	CAGCCACATAGGTGCAAGGG	263089	95285	AAATCAAAATAAAAGTCAGC
173916	6112	CACTGCCCTGCACTGGGGAC	218503	50699	ACAGCCACATAGGTGCAAGG	263090	95286	AAAATCAAAATAAAAGTCAG
173917	6113	ACACTGCCCTGCACTGGGGA	218504	50700	CACAGCCACATAGGTGCAAG	263091	95287	TAAAATCAAAATAAAAGTCA
173918	6114	AACACTGCCCTGCACTGGGG	218505	50701	TCACAGCCACATAGGTGCAA	263092	95288	ATAAAATCAAAATAAAAGTC
173919	6115	GAACACTGCCCTGCACTGGG	218506	50702	CTCACAGCCACATAGGTGCA	263093	95289	AATAAAATCAAAATAAAAGT
173920	6116	AGAACACTGCCCTGCACTGG	218507	50703	CCTCACAGCCACATAGGTGC	263094	95290	AAATAAAATCAAAATAAAAG
173921	6117	CAGAACACTGCCCTGCACTG	218508	50704	TCCTCACAGCCACATAGGTG	263095	95291	TAAATAAAATCAAAATAAAA
173922	6118	GCAGAACACTGCCCTGCACT	218509	50705	ATCCTCACAGCCACATAGGT	263096	95292	ATAAATAAAATCAAAATAAA

173923	6119	TGCAGAACACTGCCCTGCAC	218510	50706	AATCCTCACAGCCACATAGG	263097	95293	CATAAATAAAATCAAAATAA
173924	6120	ATGCAGAACACTGCCCTGCA	218511	50707	TAATCCTCACAGCCACATAG	263098	95294	ACATAAATAAAATCAAAATA
173925	6121	CATGCAGAACACTGCCCTGC	218512	50708	TTAATCCTCACAGCCACATA	263099	95295	AACATAAATAAAATCAAAAT
173926	6122	ACATGCAGAACACTGCCCTG	218513	50709	TTTAATCCTCACAGCCACAT	263100	95296	AAACATAAATAAAATCAAAA
173927	6123	CACATGCAGAACACTGCCCT	218514	50710	GTTTAATCCTCACAGCCACA	263101	95297	TAAACATAAATAAAATCAAA
173928	6124	CCACATGCAGAACACTGCCC	218515	50711	TGTTTAATCCTCACAGCCAC	263102	95298	ATAAACATAAATAAAATCAA
173929	6125	TCCACATGCAGAACACTGCC	218516	50712	TTGTTTAATCCTCACAGCCA	263103	95299	CATAAACATAAATAAAATCA
173930	6126	CTCCACATGCAGAACACTGC	218517	50713	CTTGTTTAATCCTCACAGCC	263104	95300	ACATAAACATAAATAAAATC
173931	6127	CCTCCACATGCAGAACACTG	218518	50714	TCTTGTTTAATCCTCACAGC	263105	95301	AACATAAACATAAATAAAAT
173932	6128	GCCTCCACATGCAGAACACT	218519	50715	ATCTTGTTTAATCCTCACAG	263106	95302	AAACATAAACATAAATAAAA
173933	6129	TGCCTCCACATGCAGAACAC	218520	50716	TATCTTGTTTAATCCTCACA	263107	95303	TAAACATAAACATAAATAAA
173934	6130	CTGCCTCCACATGCAGAACA	218521	50717	TTATCTTGTTTAATCCTCAC	263108	95304	TTAAACATAAACATAAATAA
173935	6131	ACTGCCTCCACATGCAGAAC	218522	50718	TTTATCTTGTTTAATCCTCA	263109	95305	CTTAAACATAAACATAAATA
173936	6132	AACTGCCTCCACATGCAGAA	218523	50719	ATTTATCTTGTTTAATCCTC	263110	95306	TCTTAAACATAAACATAAAT
173937	6133	AAACTGCCTCCACATGCAGA	218524	50720	CATTTATCTTGTTTAATCCT	263111	95307	GTCTTAAACATAAACATAAA
173938	6134	CAAACTGCCTCCACATGCAG	218525	50721	ACATTTATCTTGTTTAATCC	263112	95308	TGTCTTAAACATAAACATAA
173939	6135	CCAAACTGCCTCCACATGCA	218526	50722	CACATTTATCTTGTTTAATC	263113	95309	ATGTCTTAAACATAAACATA
173940	6136	GCCAAACTGCCTCCACATGC	218527	50723	ACACATTTATCTTGTTTAAT	263114	95310	GATGTCTTAAACATAAACAT
173941	6137	GGCCAAACTGCCTCCACATG	218528	50724	TACACATTTATCTTGTTTAA	263115	95311	GGATGTCTTAAACATAAACA
173942	6138	AGGCCAAACTGCCTCCACAT	218529	50725	TTACACATTTATCTTGTTTA	263116	95312	TGGATGTCTTAAACATAAAC
173943	6139	TAGGCCAAACTGCCTCCACA	218530	50726	GTTACACATTTATCTTGTTT	263117	95313	GTGGATGTCTTAAACATAAA
173944	6140	TTAGGCCAAACTGCCTCCAC	218531	50727	TGTTACACATTTATCTTGTT	263118	95314	TGTGGATGTCTTAAACATAA
173945	6141	ATTAGGCCAAACTGCCTCCA	218532	50728	CTGTTACACATTTATCTTGT	263119	95315	GTGTGGATGTCTTAAACATA
173946	6142	CATTAGGCCAAACTGCCTCC	218533	50729	ACTGTTACACATTTATCTTG	263120	95316	CGTGTGGATGTCTTAAACAT
173947	6143	CCATTAGGCCAAACTGCCTC	218534	50730	CACTGTTACACATTTATCTT	263121	95317	ACGTGTGGATGTCTTAAACA
173948	6144	ACCATTAGGCCAAACTGCCT	218535	50731	GCACTGTTACACATTTATCT	263122	95318	AACGTGTGGATGTCTTAAAC
173949	6145	AACCATTAGGCCAAACTGCC	218536	50732	GGCACTGTTACACATTTATC	263123	95319	GAACGTGTGGATGTCTTAAA
173950	6146	TAACCATTAGGCCAAACTGC	218537	50733	AGGCACTGTTACACATTTAT	263124	95320	GGAACGTGTGGATGTCTTAA
173951	6147	TTAACCATTAGGCCAAACTG	218538	50734	CAGGCACTGTTACACATTTA	263125	95321	AGGAACGTGTGGATGTCTTA
173952	6148	CTTAACCATTAGGCCAAACT	218539	50735	CCAGGCACTGTTACACATTT	263126	95322	GAGGAACGTGTGGATGTCTT
173953	6149	CCTTAACCATTAGGCCAAAC	218540	50736	GCCAGGCACTGTTACACATT	263127	95323	AGAGGAACGTGTGGATGTCT
173954	6150	TCCTTAACCATTAGGCCAAA	218541	50737	AGCCAGGCACTGTTACACAT	263128	95324	CAGAGGAACGTGTGGATGTC
173955	6151	CTCCTTAACCATTAGGCCAA	218542	50738	TAGCCAGGCACTGTTACACA	263129	95325	GCAGAGGAACGTGTGGATGT
173956	6152	CCTCCTTAACCATTAGGCCA	218543	50739	ATAGCCAGGCACTGTTACAC	263130	95326	AGCAGAGGAACGTGTGGATG
173957	6153	ACCTCCTTAACCATTAGGCC	218544	50740	TATAGCCAGGCACTGTTACA	263131	95327	TAGCAGAGGAACGTGTGGAT
173958	6154	TACCTCCTTAACCATTAGGC	218545	50741	CTATAGCCAGGCACTGTTAC	263132	95328	TTAGCAGAGGAACGTGTGGA
173959	6155	CTACCTCCTTAACCATTAGG	218546	50742	TCTATAGCCAGGCACTGTTA	263133	95329	TTTAGCAGAGGAACGTGTGG
173960	6156	CCTACCTCCTTAACCATTAG	218547	50743	TTCTATAGCCAGGCACTGTT	263134	95330	TTTTAGCAGAGGAACGTGTG
173961	6157	GCCTACCTCCTTAACCATTA	218548	50744	TTTCTATAGCCAGGCACTGT	263135	95331	GTTTTAGCAGAGGAACGTGT
173962	6158	AGCCTACCTCCTTAACCATT	218549	50745	ATTTCTATAGCCAGGCACTG	263136	95332	GGTTTTAGCAGAGGAACGTG
173963	6159	GAGCCTACCTCCTTAACCAT	218550	50746	TATTTCTATAGCCAGGCACT	263137	95333	AGGTTTTAGCAGAGGAACGT
173964	6160	AGAGCCTACCTCCTTAACCA	218551	50747	ATATTTCTATAGCCAGGCAC	263138	95334	AAGGTTTTAGCAGAGGAACG
173965	6161	CAGAGCCTACCTCCTTAACC	218552	50748	AATATTTCTATAGCCAGGCA	263139	95335	CAAGGTTTTAGCAGAGGAAC
173966	6162	TCAGAGCCTACCTCCTTAAC	218553	50749	AAATATTTCTATAGCCAGGC	263140	95336	TCAAGGTTTTAGCAGAGGAA
173967	6163	ATCAGAGCCTACCTCCTTAA	218554	50750	TAAATATTTCTATAGCCAGG	263141	95337	TTCAAGGTTTTAGCAGAGGA
173968	6164	GATCAGAGCCTACCTCCTTA	218555	50751	GTAAATATTTCTATAGCCAG	263142	95338	TTTCAAGGTTTTAGCAGAGG
173969	6165	CGATCAGAGCCTACCTCCTT	218556	50752	AGTAAATATTTCTATAGCCA	263143	95339	TTTTCAAGGTTTTAGCAGAG
173970	6166	CCGATCAGAGCCTACCTCCT	218557	50753	GAGTAAATATTTCTATAGCC	263144	95340	TTTTTCAAGGTTTTAGCAGA
173971	6167	CCCGATCAGAGCCTACCTCC	218558	50754	AGAGTAAATATTTCTATAGC	263145	95341	ATTTTTCAAGGTTTTAGCAG
173972	6168	GCCCGATCAGAGCCTACCTC	218559	50755	AAGAGTAAATATTTCTATAG	263146	95342	TATTTTTCAAGGTTTTAGCA
173973	6169	GGCCCGATCAGAGCCTACCT	218560	50756	CAAGAGTAAATATTTCTATA	263147	95343	CTATTTTTCAAGGTTTTAGC
173974	6170	AGGCCCGATCAGAGCCTACC	218561	50757	ACAAGAGTAAATATTTCTAT	263148	95344	CCTATTTTTCAAGGTTTTAG
173975	6171	GAGGCCCGATCAGAGCCTAC	218562	50758	AACAAGAGTAAATATTTCTA	263149	95345	GCCTATTTTTCAAGGTTTTA
173976	6172	GGAGGCCCGATCAGAGCCTA	218563	50759	TAACAAGAGTAAATATTTCT	263150	95346	GGCCTATTTTTCAAGGTTTT
173977	6173	AGGAGGCCCGATCAGAGCCT	218564	50760	ATAACAAGAGTAAATATTTC	263151	95347	AGGCCTATTTTTCAAGGTTT
173978	6174	CAGGAGGCCCGATCAGAGCC	218565	50761	AATAACAAGAGTAAATATTT	263152	95348	AAGGCCTATTTTTCAAGGTT
173979	6175	CCAGGAGGCCCGATCAGAGC	218566	50762	TAATAACAAGAGTAAATATT	263153	95349	CAAGGCCTATTTTTCAAGGT
173980	6176	CCCAGGAGGCCCGATCAGAG	218567	50763	TTAATAACAAGAGTAAATAT	263154	95350	GCAAGGCCTATTTTTCAAGG
173981	6177	GCCCAGGAGGCCCGATCAGA	218568	50764	CTTAATAACAAGAGTAAATA	263155	95351	GGCAAGGCCTATTTTTCAAG
173982	6178	TGCCCAGGAGGCCCGATCAG	218569	50765	CCTTAATAACAAGAGTAAAT	263156	95352	AGGCAAGGCCTATTTTTCAA
173983	6179	GTGCCCAGGAGGCCCGATCA	218570	50766	CCCTTAATAACAAGAGTAAA	263157	95353	AAGGCAAGGCCTATTTTTCA
173984	6180	TGTGCCCAGGAGGCCCGATC	218571	50767	TCCCTTAATAACAAGAGTAA	263158	95354	TAAGGCAAGGCCTATTTTTC
173985	6181	TTGTGCCCAGGAGGCCCGAT	218572	50768	TTCCCTTAATAACAAGAGTA	263159	95355	CTAAGGCAAGGCCTATTTTT
173986	6182	TTTGTGCCCAGGAGGCCCGA	218573	50769	CTTCCCTTAATAACAAGAGT	263160	95356	GCTAAGGCAAGGCCTATTTT
173987	6183	ATTTGTGCCCAGGAGGCCCG	218574	50770	TCTTCCCTTAATAACAAGAG	263161	95357	GGCTAAGGCAAGGCCTATTT
173988	6184	GATTTGTGCCCAGGAGGCCC	218575	50771	TTCTTCCCTTAATAACAAGA	263162	95358	GGGCTAAGGCAAGGCCTATT
173989	6185	GGATTTGTGCCCAGGAGGCC	218576	50772	ATTCTTCCCTTAATAACAAG	263163	95359	GGGGCTAAGGCAAGGCCTAT
173990	6186	GGGATTTGTGCCCAGGAGGC	218577	50773	TATTCTTCCCTTAATAACAA	263164	95360	TGGGGCTAAGGCAAGGCCTA
173991	6187	TGGGATTTGTGCCCAGGAGG	218578	50774	ATATTCTTCCCTTAATAACA	263165	95361	TTGGGGCTAAGGCAAGGCCT
173992	6188	CTGGGATTTGTGCCCAGGAG	218579	50775	CATATTCTTCCCTTAATAAC	263166	95362	TTTGGGGCTAAGGCAAGGCC
173993	6189	GCTGGGATTTGTGCCCAGGA	218580	50776	ACATATTCTTCCCTTAATAA	263167	95363	GTTTGGGGCTAAGGCAAGGC
173994	6190	AGCTGGGATTTGTGCCCAGG	218581	50777	CACATATTCTTCCCTTAATA	263168	95364	TGTTTGGGGCTAAGGCAAGG

173995	6191	GAGCTGGGATTTGTGCCCAG	218582	50778	ACACATATTCTTCCCTTAAT	263169	95365	GTGTTTGGGGCTAAGGCAAG
173996	6192	GGAGCTGGGATTTGTGCCCA	218583	50779	CACACATATTCTTCCCTTAA	263170	95366	GGTGTTTGGGGCTAAGGCAA
173997	6193	GGGAGCTGGGATTTGTGCCC	218584	50780	CCACACATATTCTTCCCTTA	263171	95367	GGGTGTTTGGGGCTAAGGCA
173998	6194	AGGGAGCTGGGATTTGTGCC	218585	50781	GCCACACATATTCTTCCCTT	263172	95368	GGGGTGTTTGGGGCTAAGGC
173999	6195	CAGGGAGCTGGGATTTGTGC	218586	50782	AGCCACACATATTCTTCCCT	263173	95369	TGGGGTGTTTGGGGCTAAGG
174000	6196	GCAGGGAGCTGGGATTTGTG	218587	50783	TAGCCACACATATTCTTCCC	263174	95370	GTGGGGTGTTTGGGGCTAAG
174001	6197	AGCAGGGAGCTGGGATTTGT	218588	50784	TTAGCCACACATATTCTTCC	263175	95371	AGTGGGGTGTTTGGGGCTAA
174002	6198	GAGCAGGGAGCTGGGATTTG	218589	50785	TTTAGCCACACATATTCTTC	263176	95372	GAGTGGGGTGTTTGGGGCTA
174003	6199	TGAGCAGGGAGCTGGGATTT	218590	50786	TTTTAGCCACACATATTCTT	263177	95373	GGAGTGGGGTGTTTGGGGCT
174004	6200	GTGAGCAGGGAGCTGGGATT	218591	50787	TTTTTAGCCACACATATTCT	263178	95374	AGGAGTGGGGTGTTTGGGGC
174005	6201	AGTGAGCAGGGAGCTGGGAT	218592	50788	CTTTTTAGCCACACATATTC	263179	95375	CAGGAGTGGGGTGTTTGGGG
174006	6202	CAGTGAGCAGGGAGCTGGGA	218593	50789	CCTTTTTAGCCACACATATT	263180	95376	CCAGGAGTGGGGTGTTTGGG
174007	6203	ACAGTGAGCAGGGAGCTGGG	218594	50790	CCCTTTTTAGCCACACATAT	263181	95377	ACCAGGAGTGGGGTGTTTGG
174008	6204	CACAGTGAGCAGGGAGCTGG	218595	50791	TCCCTTTTTAGCCACACATA	263182	95378	TACCAGGAGTGGGGTGTTTG
174009	6205	TCACAGTGAGCAGGGAGCTG	218596	50792	ATCCCTTTTTAGCCACACAT	263183	95379	CTACCAGGAGTGGGGTGTTT
174010	6206	CTCACAGTGAGCAGGGAGCT	218597	50793	GATCCCTTTTTAGCCACACA	263184	95380	GCTACCAGGAGTGGGGTGTT
174011	6207	TCTCACAGTGAGCAGGGAGC	218598	50794	CGATCCCTTTTTAGCCACAC	263185	95381	AGCTACCAGGAGTGGGGTGT
174012	6208	GTCTCACAGTGAGCAGGGAG	218599	50795	TCGATCCCTTTTTAGCCACA	263186	95382	GAGCTACCAGGAGTGGGGTG
174013	6209	GGTCTCACAGTGAGCAGGGA	218600	50796	TTCGATCCCTTTTTAGCCAC	263187	95383	TGAGCTACCAGGAGTGGGGT
174014	6210	AGGTCTCACAGTGAGCAGGG	218601	50797	CTTCGATCCCTTTTTAGCCA	263188	95384	CTGAGCTACCAGGAGTGGGG
174015	6211	TAGGTCTCACAGTGAGCAGG	218602	50798	TCTTCGATCCCTTTTTAGCC	263189	95385	TCTGAGCTACCAGGAGTGGG
174016	6212	TTAGGTCTCACAGTGAGCAG	218603	50799	ATCTTCGATCCCTTTTTAGC	263190	95386	GTCTGAGCTACCAGGAGTGG
174017	6213	CTTAGGTCTCACAGTGAGCA	218604	50800	CATCTTCGATCCCTTTTTAG	263191	95387	GGTCTGAGCTACCAGGAGTG
174018	6214	GCTTAGGTCTCACAGTGAGC	218605	50801	ACATCTTCGATCCCTTTTTA	263192	95388	GGGTCTGAGCTACCAGGAGT
174019	6215	GGCTTAGGTCTCACAGTGAG	218606	50802	TACATCTTCGATCCCTTTTT	263193	95389	AGGGTCTGAGCTACCAGGAG
174020	6216	TGGCTTAGGTCTCACAGTGA	218607	50803	TTACATCTTCGATCCCTTTT	263194	95390	GAGGGTCTGAGCTACCAGGA
174021	6217	ATGGCTTAGGTCTCACAGTG	218608	50804	TTTACATCTTCGATCCCTTT	263195	95391	AGAGGGTCTGAGCTACCAGG
174022	6218	TATGGCTTAGGTCTCACAGT	218609	50805	TTTTACATCTTCGATCCCTT	263196	95392	CAGAGGGTCTGAGCTACCAG
174023	6219	ATATGGCTTAGGTCTCACAG	218610	50806	CTTTTACATCTTCGATCCCT	263197	95393	TCAGAGGGTCTGAGCTACCA
174024	6220	AATATGGCTTAGGTCTCACA	218611	50807	GCTTTTACATCTTCGATCCC	263198	95394	ATCAGAGGGTCTGAGCTACC
174025	6221	CAATATGGCTTAGGTCTCAC	218612	50808	GGCTTTTACATCTTCGATCC	263199	95395	GATCAGAGGGTCTGAGCTAC
174026	6222	ACAATATGGCTTAGGTCTCA	218613	50809	TGGCTTTTACATCTTCGATC	263200	95396	GGATCAGAGGGTCTGAGCTA
174027	6223	AACAATATGGCTTAGGTCTC	218614	50810	TTGGCTTTTACATCTTCGAT	263201	95397	TGGATCAGAGGGTCTGAGCT
174028	6224	AAACAATATGGCTTAGGTCT	218615	50811	ATTGGCTTTTACATCTTCGA	263202	95398	TTGGATCAGAGGGTCTGAGC
174029	6225	TAAACAATATGGCTTAGGTC	218616	50812	GATTGGCTTTTACATCTTCG	263203	95399	GTTGGATCAGAGGGTCTGAG
174030	6226	CTAAACAATATGGCTTAGGT	218617	50813	GGATTGGCTTTTACATCTTC	263204	95400	GGTTGGATCAGAGGGTCTGA
174031	6227	GCTAAACAATATGGCTTAGG	218618	50814	GGGATTGGCTTTTACATCTT	263205	95401	GGGTTGGATCAGAGGGTCTG
174032	6228	AGCTAAACAATATGGCTTAG	218619	50815	AGGGATTGGCTTTTACATCT	263206	95402	AGGGTTGGATCAGAGGGTCT
174033	6229	CAGCTAAACAATATGGCTTA	218620	50816	GAGGGATTGGCTTTTACATC	263207	95403	GAGGGTTGGATCAGAGGGTC
174034	6230	GCAGCTAAACAATATGGCTT	218621	50817	GGAGGGATTGGCTTTTACAT	263208	95404	GGAGGGTTGGATCAGAGGGT
174035	6231	AGCAGCTAAACAATATGGCT	218622	50818	GGGAGGGATTGGCTTTTACA	263209	95405	TGGAGGGTTGGATCAGAGGG
174036	6232	AAGCAGCTAAACAATATGGC	218623	50819	GGGGAGGGATTGGCTTTTAC	263210	95406	CTGGAGGGTTGGATCAGAGG
174037	6233	CAAGCAGCTAAACAATATGG	218624	50820	GGGGGAGGGATTGGCTTTTA	263211	95407	GCTGGAGGGTTGGATCAGAG
174038	6234	CCAAGCAGCTAAACAATATG	218625	50821	AGGGGGAGGGATTGGCTTTT	263212	95408	GGCTGGAGGGTTGGATCAGA
174039	6235	TCCAAGCAGCTAAACAATAT	218626	50822	GAGGGGGAGGGATTGGCTTT	263213	95409	GGGCTGGAGGGTTGGATCAG
174040	6236	CTCCAAGCAGCTAAACAATA	218627	50823	AGAGGGGGAGGGATTGGCTT	263214	95410	AGGGCTGGAGGGTTGGATCA
174041	6237	TCTCCAAGCAGCTAAACAAT	218628	50824	TAGAGGGGGAGGGATTGGCT	263215	95411	CAGGGCTGGAGGGTTGGATC
174042	6238	CTCTCCAAGCAGCTAAACAA	218629	50825	CTAGAGGGGGAGGGATTGGC	263216	95412	GCAGGGCTGGAGGGTTGGAT
174043	6239	ACTCTCCAAGCAGCTAAACA	218630	50826	GCTAGAGGGGGAGGGATTGG	263217	95413	AGCAGGGCTGGAGGGTTGGA
174044	6240	AACTCTCCAAGCAGCTAAAC	218631	50827	TGCTAGAGGGGGAGGGATTG	263218	95414	CAGCAGGGCTGGAGGGTTGG
174045	6241	AAACTCTCCAAGCAGCTAAA	218632	50828	ATGCTAGAGGGGGAGGGATT	263219	95415	ACAGCAGGGCTGGAGGGTTG
174046	6242	AAAACTCTCCAAGCAGCTAA	218633	50829	TATGCTAGAGGGGGAGGGAT	263220	95416	CACAGCAGGGCTGGAGGGTT
174047	6243	AAAAACTCTCCAAGCAGCTA	218634	50830	ATATGCTAGAGGGGGAGGGA	263221	95417	ACACAGCAGGGCTGGAGGGT
174048	6244	AAAAAACTCTCCAAGCAGCT	218635	50831	AATATGCTAGAGGGGGAGGG	263222	95418	CACACAGCAGGGCTGGAGGG
174049	6245	CAAAAAACTCTCCAAGCAGC	218636	50832	AAATATGCTAGAGGGGGAGG	263223	95419	GCACACAGCAGGGCTGGAGG
174050	6246	ACAAAAAACTCTCCAAGCAG	218637	50833	TAAATATGCTAGAGGGGGAG	263224	95420	GGCACACAGCAGGGCTGGAG
174051	6247	GACAAAAAACTCTCCAAGCA	218638	50834	TTAAATATGCTAGAGGGGGA	263225	95421	GGGCACACAGCAGGGCTGGA
174052	6248	TGACAAAAAACTCTCCAAGC	218639	50835	CTTAAATATGCTAGAGGGGG	263226	95422	TGGGCACACAGCAGGGCTGG
174053	6249	ATGACAAAAAACTCTCCAAG	218640	50836	CCTTAAATATGCTAGAGGGG	263227	95423	CTGGGCACACAGCAGGGCTG
174054	6250	GATGACAAAAAACTCTCCAA	218641	50837	CCCTTAAATATGCTAGAGGG	263228	95424	TCTGGGCACACAGCAGGGCT
174055	6251	GGATGACAAAAAACTCTCCA	218642	50838	ACCCTTAAATATGCTAGAGG	263229	95425	CTCTGGGCACACAGCAGGGC
174056	6252	TGGATGACAAAAAACTCTCC	218643	50839	TACCCTTAAATATGCTAGAG	263230	95426	GCTCTGGGCACACAGCAGGG
174057	6253	GTGGATGACAAAAAACTCTC	218644	50840	TTACCCTTAAATATGCTAGA	263231	95427	GGCTCTGGGCACACAGCAGG
174058	6254	TGTGGATGACAAAAAACTCT	218645	50841	ATTACCCTTAAATATGCTAG	263232	95428	TGGCTCTGGGCACACAGCAG
174059	6255	TTGTGGATGACAAAAAACTC	218646	50842	CATTACCCTTAAATATGCTA	263233	95429	GTGGCTCTGGGCACACAGCA
174060	6256	GTTGTGGATGACAAAAAACT	218647	50843	ACATTACCCTTAAATATGCT	263234	95430	GGTGGCTCTGGGCACACAGC
174061	6257	AGTTGTGGATGACAAAAAAC	218648	50844	AACATTACCCTTAAATATGC	263235	95431	AGGTGGCTCTGGGCACACAG
174062	6258	AAGTTGTGGATGACAAAAAA	218649	50845	CAACATTACCCTTAAATATG	263236	95432	AAGGTGGCTCTGGGCACACA
174063	6259	CAAGTTGTGGATGACAAAAA	218650	50846	TCAACATTACCCTTAAATAT	263237	95433	GAAGGTGGCTCTGGGCACAC
174064	6260	CCAAGTTGTGGATGACAAAA	218651	50847	CTCAACATTACCCTTAAATA	263238	95434	GGAAGGTGGCTCTGGGCACA
174065	6261	TCCAAGTTGTGGATGACAAA	218652	50848	ACTCAACATTACCCTTAAAT	263239	95435	AGGAAGGTGGCTCTGGGCAC
174066	6262	CTCCAAGTTGTGGATGACAA	218653	50849	AACTCAACATTACCCTTAAA	263240	95436	GAGGAAGGTGGCTCTGGGCA

174067	6263	ACTCCAAGTTGTGGATGACA	218654	50850	CAACTCAACATTACCCTTAA	263241	95437	AGAGGAAGGTGGCTCTGGGC
174068	6264	TACTCCAAGTTGTGGATGAC	218655	50851	CCAACTCAACATTACCCTTA	263242	95438	GAGAGGAAGGTGGCTCTGGG
174069	6265	ATACTCCAAGTTGTGGATGA	218656	50852	ACCAACTCAACATTACCCTT	263243	95439	GGAGAGGAAGGTGGCTCTGG
174070	6266	CATACTCCAAGTTGTGGATG	218657	50853	AACCAACTCAACATTACCCT	263244	95440	AGGAGAGGAAGGTGGCTCTG
174071	6267	TCATACTCCAAGTTGTGGAT	218658	50854	AAACCAACTCAACATTACCC	263245	95441	TAGGAGAGGAAGGTGGCTCT
174072	6268	ATCATACTCCAAGTTGTGGA	218659	50855	CAAACCAACTCAACATTACC	263246	95442	TTAGGAGAGGAAGGTGGCTC
174073	6269	CATCATACTCCAAGTTGTGG	218660	50856	ACAAACCAACTCAACATTAC	263247	95443	TTTAGGAGAGGAAGGTGGCT
174074	6270	CCATCATACTCCAAGTTGTG	218661	50857	CACAAACCAACTCAACATTA	263248	95444	ATTTAGGAGAGGAAGGTGGC
174075	6271	ACCATCATACTCCAAGTTGT	218662	50858	CCACAAACCAACTCAACATT	263249	95445	TATTTAGGAGAGGAAGGTGG
174076	6272	TACCATCATACTCCAAGTTG	218663	50859	TCCACAAACCAACTCAACAT	263250	95446	GTATTTAGGAGAGGAAGGTG
174077	6273	GTACCATCATACTCCAAGTT	218664	50860	GTCCACAAACCAACTCAACA	263251	95447	CGTATTTAGGAGAGGAAGGT
174078	6274	GGTACCATCATACTCCAAGT	218665	50861	GGTCCACAAACCAACTCAAC	263252	95448	ACGTATTTAGGAGAGGAAGG
174079	6275	AGGTACCATCATACTCCAAG	218666	50862	TGGTCCACAAACCAACTCAA	263253	95449	GACGTATTTAGGAGAGGAAG
174080	6276	CAGGTACCATCATACTCCAA	218667	50863	ATGGTCCACAAACCAACTCA	263254	95450	AGACGTATTTAGGAGAGGAA
174081	6277	ACAGGTACCATCATACTCCA	218668	50864	AATGGTCCACAAACCAACTC	263255	95451	GAGACGTATTTAGGAGAGGA
174082	6278	GACAGGTACCATCATACTCC	218669	50865	AAATGGTCCACAAACCAACT	263256	95452	AGAGACGTATTTAGGAGAGG
174083	6279	AGACAGGTACCATCATACTC	218670	50866	CAAATGGTCCACAAACCAAC	263257	95453	AAGAGACGTATTTAGGAGAG
174084	6280	GAGACAGGTACCATCATACT	218671	50867	GCAAATGGTCCACAAACCAA	263258	95454	GAAGAGACGTATTTAGGAGA
174085	6281	TGAGACAGGTACCATCATAC	218672	50868	AGCAAATGGTCCACAAACCA	263259	95455	AGAAGAGACGTATTTAGGAG
174086	6282	GTGAGACAGGTACCATCATA	218673	50869	CAGCAAATGGTCCACAAACC	263260	95456	CAGAAGAGACGTATTTAGGA
174087	6283	CGTGAGACAGGTACCATCAT	218674	50870	GCAGCAAATGGTCCACAAAC	263261	95457	ACAGAAGAGACGTATTTAGG
174088	6284	CCGTGAGACAGGTACCATCA	218675	50871	GGCAGCAAATGGTCCACAAA	263262	95458	GACAGAAGAGACGTATTTAG
174089	6285	CCCGTGAGACAGGTACCATC	218676	50872	AGGCAGCAAATGGTCCACAA	263263	95459	TGACAGAAGAGACGTATTTA
174090	6286	ACCCGTGAGACAGGTACCAT	218677	50873	CAGGCAGCAAATGGTCCACA	263264	95460	GTGACAGAAGAGACGTATTT
174091	6287	AACCCGTGAGACAGGTACCA	218678	50874	ACAGGCAGCAAATGGTCCAC	263265	95461	AGTGACAGAAGAGACGTATT
174092	6288	CAACCCGTGAGACAGGTACC	218679	50875	AACAGGCAGCAAATGGTCCA	263266	95462	AAGTGACAGAAGAGACGTAT
174093	6289	GCAACCCGTGAGACAGGTAC	218680	50876	TAACAGGCAGCAAATGGTCC	263267	95463	GAAGTGACAGAAGAGACGTA
174094	6290	GGCAACCCGTGAGACAGGTA	218681	50877	CTAACAGGCAGCAAATGGTC	263268	95464	GGAAGTGACAGAAGAGACGT
174095	6291	TGGCAACCCGTGAGACAGGT	218682	50878	TCTAACAGGCAGCAAATGGT	263269	95465	GGGAAGTGACAGAAGAGACG
174096	6292	ATGGCAACCCGTGAGACAGG	218683	50879	CTCTAACAGGCAGCAAATGG	263270	95466	CGGGAAGTGACAGAAGAGAC
174097	6293	CATGGCAACCCGTGAGACAG	218684	50880	GCTCTAACAGGCAGCAAATG	263271	95467	TCGGGAAGTGACAGAAGAGA
174098	6294	CCATGGCAACCCGTGAGACA	218685	50881	AGCTCTAACAGGCAGCAAAT	263272	95468	TTCGGGAAGTGACAGAAGAG
174099	6295	CCCATGGCAACCCGTGAGAC	218686	50882	CAGCTCTAACAGGCAGCAAA	263273	95469	GTTCGGGAAGTGACAGAAGA
174100	6296	CCCCATGGCAACCCGTGAGA	218687	50883	CCAGCTCTAACAGGCAGCAA	263274	95470	AGTTCGGGAAGTGACAGAAG
174101	6297	ACCCCATGGCAACCCGTGAG	218688	50884	TCCAGCTCTAACAGGCAGCA	263275	95471	CAGTTCGGGAAGTGACAGAA
174102	6298	AACCCCATGGCAACCCGTGA	218689	50885	TTCCAGCTCTAACAGGCAGC	263276	95472	CCAGTTCGGGAAGTGACAGA
174103	6299	GAACCCCATGGCAACCCGTG	218690	50886	CTTCCAGCTCTAACAGGCAG	263277	95473	GCCAGTTCGGGAAGTGACAG
174104	6300	TGAACCCCATGGCAACCCGT	218691	50887	CCTTCCAGCTCTAACAGGCA	263278	95474	TGCCAGTTCGGGAAGTGACA
174105	6301	GTGAACCCCATGGCAACCCG	218692	50888	ACCTTCCAGCTCTAACAGGC	263279	95475	CTGCCAGTTCGGGAAGTGAC
174106	6302	TGTGAACCCCATGGCAACCC	218693	50889	TACCTTCCAGCTCTAACAGG	263280	95476	ACTGCCAGTTCGGGAAGTGA
174107	6303	GTGTGAACCCCATGGCAACC	218694	50890	CTACCTTCCAGCTCTAACAG	263281	95477	AACTGCCAGTTCGGGAAGTG
174108	6304	TGTGTGAACCCCATGGCAAC	218695	50891	CCTACCTTCCAGCTCTAACA	263282	95478	GAACTGCCAGTTCGGGAAGT
174109	6305	TTGTGTGAACCCCATGGCAA	218696	50892	CCCTACCTTCCAGCTCTAAC	263283	95479	AGAACTGCCAGTTCGGGAAG
174110	6306	CTTGTGTGAACCCCATGGCA	218697	50893	TCCCTACCTTCCAGCTCTAA	263284	95480	CAGAACTGCCAGTTCGGGAA
174111	6307	GCTTGTGTGAACCCCATGGC	218698	50894	GTCCCTACCTTCCAGCTCTA	263285	95481	CCAGAACTGCCAGTTCGGGA
174112	6308	AGCTTGTGTGAACCCCATGG	218699	50895	GGTCCCTACCTTCCAGCTCT	263286	95482	TCCAGAACTGCCAGTTCGGG
174113	6309	TAGCTTGTGTGAACCCCATG	218700	50896	GGGTCCCTACCTTCCAGCTC	263287	95483	CTCCAGAACTGCCAGTTCGG
174114	6310	TTAGCTTGTGTGAACCCCAT	218701	50897	GGGGTCCCTACCTTCCAGCT	263288	95484	GCTCCAGAACTGCCAGTTCG
174115	6311	GTTAGCTTGTGTGAACCCCA	218702	50898	GGGGGTCCCTACCTTCCAGC	263289	95485	TGCTCCAGAACTGCCAGTTC
174116	6312	GGTTAGCTTGTGTGAACCCC	218703	50899	AGGGGGTCCCTACCTTCCAG	263290	95486	TTGCTCCAGAACTGCCAGTT
174117	6313	GGGTTAGCTTGTGTGAACCC	218704	50900	GAGGGGGTCCCTACCTTCCA	263291	95487	TTTGCTCCAGAACTGCCAGT
174118	6314	CGGGTTAGCTTGTGTGAACC	218705	50901	AGAGGGGGTCCCTACCTTCC	263292	95488	CTTTGCTCCAGAACTGCCAG
174119	6315	CCGGGTTAGCTTGTGTGAAC	218706	50902	GAGAGGGGGTCCCTACCTTC	263293	95489	CCTTTGCTCCAGAACTGCCA
174120	6316	ACCGGGTTAGCTTGTGTGAA	218707	50903	TGAGAGGGGGTCCCTACCTT	263294	95490	TCCTTTGCTCCAGAACTGCC
174121	6317	TACCGGGTTAGCTTGTGTGA	218708	50904	TTGAGAGGGGGTCCCTACCT	263295	95491	CTCCTTTGCTCCAGAACTGC
174122	6318	GTACCGGGTTAGCTTGTGTG	218709	50905	GTTGAGAGGGGGTCCCTACC	263296	95492	TCTCCTTTGCTCCAGAACTG
174123	6319	AGTACCGGGTTAGCTTGTGT	218710	50906	TGTTGAGAGGGGGTCCCTAC	263297	95493	ATCTCCTTTGCTCCAGAACT
174124	6320	GAGTACCGGGTTAGCTTGTG	218711	50907	CTGTTGAGAGGGGGTCCCTA	263298	95494	CATCTCCTTTGCTCCAGAAC
174125	6321	TGAGTACCGGGTTAGCTTGT	218712	50908	GCTGTTGAGAGGGGGTCCCT	263299	95495	TCATCTCCTTTGCTCCAGAA
174126	6322	GTGAGTACCGGGTTAGCTTG	218713	50909	CGCTGTTGAGAGGGGGTCCC	263300	95496	TTCATCTCCTTTGCTCCAGA
174127	6323	AGTGAGTACCGGGTTAGCTT	218714	50910	TCGCTGTTGAGAGGGGGTCC	263301	95497	TTTCATCTCCTTTGCTCCAG
174128	6324	TAGTGAGTACCGGGTTAGCT	218715	50911	ATCGCTGTTGAGAGGGGGTC	263302	95498	GTTTCATCTCCTTTGCTCCA
174129	6325	CTAGTGAGTACCGGGTTAGC	218716	50912	CATCGCTGTTGAGAGGGGGT	263303	95499	AGTTTCATCTCCTTTGCTCC
174130	6326	CCTAGTGAGTACCGGGTTAG	218717	50913	GCATCGCTGTTGAGAGGGGG	263304	95500	GAGTTTCATCTCCTTTGCTC
174131	6327	CCCTAGTGAGTACCGGGTTA	218718	50914	AGCATCGCTGTTGAGAGGGG	263305	95501	TGAGTTTCATCTCCTTTGCT
174132	6328	GCCCTAGTGAGTACCGGGTT	218719	50915	TAGCATCGCTGTTGAGAGGG	263306	95502	TTGAGTTTCATCTCCTTTGC
174133	6329	GGCCCTAGTGAGTACCGGGT	218720	50916	GTAGCATCGCTGTTGAGAGG	263307	95503	CTTGAGTTTCATCTCCTTTG
174134	6330	TGGCCCTAGTGAGTACCGGG	218721	50917	TGTAGCATCGCTGTTGAGAG	263308	95504	CCTTGAGTTTCATCTCCTTT
174135	6331	TTGGCCCTAGTGAGTACCGG	218722	50918	TTGTAGCATCGCTGTTGAGA	263309	95505	ACCTTGAGTTTCATCTCCTT
174136	6332	CTTGGCCCTAGTGAGTACCG	218723	50919	TTTGTAGCATCGCTGTTGAG	263310	95506	TACCTTGAGTTTCATCTCCT
174137	6333	GCTTGGCCCTAGTGAGTACC	218724	50920	ATTTGTAGCATCGCTGTTGA	263311	95507	TTACCTTGAGTTTCATCTCC
174138	6334	TGCTTGGCCCTAGTGAGTAC	218725	50921	AATTTGTAGCATCGCTGTTG	263312	95508	CTTACCTTGAGTTTCATCTC

174139	6335	GTGCTTGGCCCTAGTGAGTA	218726	50922	TAATTTGTAGCATCGCTGTT	263313	95509	CCTTACCTTGAGTTTCATCT
174140	6336	TGTGCTTGGCCCTAGTGAGT	218727	50923	ATAATTTGTAGCATCGCTGT	263314	95510	TCCTTACCTTGAGTTTCATC
174141	6337	ATGTGCTTGGCCCTAGTGAG	218728	50924	TATAATTTGTAGCATCGCTG	263315	95511	TTCCTTACCTTGAGTTTCAT
174142	6338	TATGTGCTTGGCCCTAGTGA	218729	50925	GTATAATTTGTAGCATCGCT	263316	95512	TTTCCTTACCTTGAGTTTCA
174143	6339	CTATGTGCTTGGCCCTAGTG	218730	50926	GGTATAATTTGTAGCATCGC	263317	95513	GTTTCCTTACCTTGAGTTTC
174144	6340	ACTATGTGCTTGGCCCTAGT	218731	50927	GGGTATAATTTGTAGCATCG	263318	95514	GGTTTCCTTACCTTGAGTTT
174145	6341	TACTATGTGCTTGGCCCTAG	218732	50928	TGGGTATAATTTGTAGCATC	263319	95515	TGGTTTCCTTACCTTGAGTT
174146	6342	TTACTATGTGCTTGGCCCTA	218733	50929	ATGGGTATAATTTGTAGCAT	263320	95516	GTGGTTTCCTTACCTTGAGT
174147	6343	GTTACTATGTGCTTGGCCCT	218734	50930	AATGGGTATAATTTGTAGCA	263321	95517	GGTGGTTTCCTTACCTTGAG
174148	6344	AGTTACTATGTGCTTGGCCC	218735	50931	CAATGGGTATAATTTGTAGC	263322	95518	AGGTGGTTTCCTTACCTTGA
174149	6345	CAGTTACTATGTGCTTGGCC	218736	50932	CCAATGGGTATAATTTGTAG	263323	95519	AAGGTGGTTTCCTTACCTTG
174150	6346	GCAGTTACTATGTGCTTGGC	218737	50933	TCCAATGGGTATAATTTGTA	263324	95520	AAAGGTGGTTTCCTTACCTT
174151	6347	AGCAGTTACTATGTGCTTGG	218738	50934	CTCCAATGGGTATAATTTGT	263325	95521	CAAAGGTGGTTTCCTTACCT
174152	6348	GAGCAGTTACTATGTGCTTG	218739	50935	CCTCCAATGGGTATAATTTG	263326	95522	TCAAAGGTGGTTTCCTTACC
174153	6349	TGAGCAGTTACTATGTGCTT	218740	50936	ACCTCCAATGGGTATAATTT	263327	95523	TTCAAAGGTGGTTTCCTTAC
174154	6350	CTGAGCAGTTACTATGTGCT	218741	50937	GACCTCCAATGGGTATAATT	263328	95524	TTTCAAAGGTGGTTTCCTTA
174155	6351	ACTGAGCAGTTACTATGTGC	218742	50938	TGACCTCCAATGGGTATAAT	263329	95525	TTTTCAAAGGTGGTTTCCTT
174156	6352	TACTGAGCAGTTACTATGTG	218743	50939	TTGACCTCCAATGGGTATAA	263330	95526	CTTTTCAAAGGTGGTTTCCT
174157	6353	TTACTGAGCAGTTACTATGT	218744	50940	GTTGACCTCCAATGGGTATA	263331	95527	TCTTTTCAAAGGTGGTTTCC
174158	6354	TTTACTGAGCAGTTACTATG	218745	50941	GGTTGACCTCCAATGGGTAT	263332	95528	TTCTTTTCAAAGGTGGTTTC
174159	6355	ATTTACTGAGCAGTTACTAT	218746	50942	TGGTTGACCTCCAATGGGTA	263333	95529	GTTCTTTTCAAAGGTGGTTT
174160	6356	CATTTACTGAGCAGTTACTA	218747	50943	TTGGTTGACCTCCAATGGGT	263334	95530	GGTTCTTTTCAAAGGTGGTT
174161	6357	CCATTTACTGAGCAGTTACT	218748	50944	TTTGGTTGACCTCCAATGGG	263335	95531	TGGTTCTTTTCAAAGGTGGT
174162	6358	GCCATTTACTGAGCAGTTAC	218749	50945	TTTTGGTTGACCTCCAATGG	263336	95532	CTGGTTCTTTTCAAAGGTGG
174163	6359	TGCCATTTACTGAGCAGTTA	218750	50946	CTTTTGGTTGACCTCCAATG	263337	95533	CCTGGTTCTTTTCAAAGGTG
174164	6360	ATGCCATTTACTGAGCAGTT	218751	50947	TCTTTTGGTTGACCTCCAAT	263338	95534	GCCTGGTTCTTTTCAAAGGT
174165	6361	GATGCCATTTACTGAGCAGT	218752	50948	GTCTTTTGGTTGACCTCCAA	263339	95535	AGCCTGGTTCTTTTCAAAGG
174166	6362	TGATGCCATTTACTGAGCAG	218753	50949	TGTCTTTTGGTTGACCTCCA	263340	95536	CAGCCTGGTTCTTTTCAAAG
174167	6363	ATGATGCCATTTACTGAGCA	218754	50950	TTGTCTTTTGGTTGACCTCC	263341	95537	GCAGCCTGGTTCTTTTCAAA
174168	6364	GATGATGCCATTTACTGAGC	218755	50951	TTTGTCTTTTGGTTGACCTC	263342	95538	AGCAGCCTGGTTCTTTTCAA
174169	6365	CGATGATGCCATTTACTGAG	218756	50952	CTTTGTCTTTTGGTTGACCT	263343	95539	GAGCAGCCTGGTTCTTTTCA
174170	6366	CCGATGATGCCATTTACTGA	218757	50953	GCTTTGTCTTTTGGTTGACC	263344	95540	AGAGCAGCCTGGTTCTTTTC
174171	6367	GCCGATGATGCCATTTACTG	218758	50954	AGCTTTGTCTTTTGGTTGAC	263345	95541	CAGAGCAGCCTGGTTCTTTT
174172	6368	CGCCGATGATGCCATTTACT	218759	50955	AAGCTTTGTCTTTTGGTTGA	263346	95542	GCAGAGCAGCCTGGTTCTTT
174173	6369	CCGCCGATGATGCCATTTAC	218760	50956	TAAGCTTTGTCTTTTGGTTG	263347	95543	AGCAGAGCAGCCTGGTTCTT
174174	6370	ACCGCCGATGATGCCATTTA	218761	50957	ATAAGCTTTGTCTTTTGGTT	263348	95544	CAGCAGAGCAGCCTGGTTCT
174175	6371	CACCGCCGATGATGCCATTT	218762	50958	AATAAGCTTTGTCTTTTGGT	263349	95545	ACAGCAGAGCAGCCTGGTTC
174176	6372	ACACCGCCGATGATGCCATT	218763	50959	CAATAAGCTTTGTCTTTTGG	263350	95546	CACAGCAGAGCAGCCTGGTT
174177	6373	GACACCGCCGATGATGCCAT	218764	50960	CCAATAAGCTTTGTCTTTTG	263351	95547	CCACAGCAGAGCAGCCTGGT
174178	6374	GGACACCGCCGATGATGCCA	218765	50961	GCCAATAAGCTTTGTCTTTT	263352	95548	ACCACAGCAGAGCAGCCTGG
174179	6375	AGGACACCGCCGATGATGCC	218766	50962	AGCCAATAAGCTTTGTCTTT	263353	95549	AACCACAGCAGAGCAGCCTG
174180	6376	CAGGACACCGCCGATGATGC	218767	50963	CAGCCAATAAGCTTTGTCTT	263354	95550	AAACCACAGCAGAGCAGCCT
174181	6377	ACAGGACACCGCCGATGATG	218768	50964	CCAGCCAATAAGCTTTGTCT	263355	95551	CAAACCACAGCAGAGCAGCC
174182	6378	CACAGGACACCGCCGATGAT	218769	50965	TCCAGCCAATAAGCTTTGTC	263356	95552	GCAAACCACAGCAGAGCAGC
174183	6379	CCACAGGACACCGCCGATGA	218770	50966	GTCCAGCCAATAAGCTTTGT	263357	95553	TGCAAACCACAGCAGAGCAG
174184	6380	TCCACAGGACACCGCCGATG	218771	50967	TGTCCAGCCAATAAGCTTTG	263358	95554	TTGCAAACCACAGCAGAGCA
174185	6381	ATCCACAGGACACCGCCGAT	218772	50968	ATGTCCAGCCAATAAGCTTT	263359	95555	TTTGCAAACCACAGCAGAGC
174186	6382	CATCCACAGGACACCGCCGA	218773	50969	CATGTCCAGCCAATAAGCTT	263360	95556	ATTTGCAAACCACAGCAGAG
174187	6383	TCATCCACAGGACACCGCCG	218774	50970	CCATGTCCAGCCAATAAGCT	263361	95557	CATTTGCAAACCACAGCAGA
174188	6384	CTCATCCACAGGACACCGCC	218775	50971	ACCATGTCCAGCCAATAAGC	263362	95558	ACATTTGCAAACCACAGCAG
174189	6385	ACTCATCCACAGGACACCGC	218776	50972	CACCATGTCCAGCCAATAAG	263363	95559	CACATTTGCAAACCACAGCA
174190	6386	CACTCATCCACAGGACACCG	218777	50973	CCACCATGTCCAGCCAATAA	263364	95560	CCACATTTGCAAACCACAGC
174191	6387	GCACTCATCCACAGGACACC	218778	50974	GCCACCATGTCCAGCCAATA	263365	95561	CCCACATTTGCAAACCACAG
174192	6388	AGCACTCATCCACAGGACAC	218779	50975	AGCCACCATGTCCAGCCAAT	263366	95562	CCCCACATTTGCAAACCACA
174193	6389	AAGCACTCATCCACAGGACA	218780	50976	GAGCCACCATGTCCAGCCAA	263367	95563	ACCCCACATTTGCAAACCAC
174194	6390	CAAGCACTCATCCACAGGAC	218781	50977	TGAGCCACCATGTCCAGCCA	263368	95564	AACCCCACATTTGCAAACCA
174195	6391	ACAAGCACTCATCCACAGGA	218782	50978	GTGAGCCACCATGTCCAGCC	263369	95565	AAACCCCACATTTGCAAACC
174196	6392	CACAAGCACTCATCCACAGG	218783	50979	TGTGAGCCACCATGTCCAGC	263370	95566	CAAACCCCACATTTGCAAAC
174197	6393	TCACAAGCACTCATCCACAG	218784	50980	GTGTGAGCCACCATGTCCAG	263371	95567	ACAAACCCCACATTTGCAAA
174198	6394	ATCACAAGCACTCATCCACA	218785	50981	GGTGTGAGCCACCATGTCCA	263372	95568	AACAAACCCCACATTTGCAA
174199	6395	AATCACAAGCACTCATCCAC	218786	50982	AGGTGTGAGCCACCATGTCC	263373	95569	AAACAAACCCCACATTTGCA
174200	6396	CAATCACAAGCACTCATCCA	218787	50983	CAGGTGTGAGCCACCATGTC	263374	95570	TAAACAAACCCCACATTTGC
174201	6397	CCAATCACAAGCACTCATCC	218788	50984	ACAGGTGTGAGCCACCATGT	263375	95571	ATAAACAAACCCCACATTTG
174202	6398	GCCAATCACAAGCACTCATC	218789	50985	TACAGGTGTGAGCCACCATG	263376	95572	AATAAACAAACCCCACATTT
174203	6399	AGCCAATCACAAGCACTCAT	218790	50986	TTACAGGTGTGAGCCACCAT	263377	95573	AAATAAACAAACCCCACATT
174204	6400	CAGCCAATCACAAGCACTCA	218791	50987	ATTACAGGTGTGAGCCACCA	263378	95574	CAAATAAACAAACCCCACAT
174205	6401	TCAGCCAATCACAAGCACTC	218792	50988	GATTACAGGTGTGAGCCACC	263379	95575	ACAAATAAACAAACCCCACA
174206	6402	TTCAGCCAATCACAAGCACT	218793	50989	GGATTACAGGTGTGAGCCAC	263380	95576	AACAAATAAACAAACCCCAC
174207	6403	ATTCAGCCAATCACAAGCAC	218794	50990	AGGATTACAGGTGTGAGCCA	263381	95577	AAACAAATAAACAAACCCCA
174208	6404	CATTCAGCCAATCACAAGCA	218795	50991	TAGGATTACAGGTGTGAGCC	263382	95578	AAAACAAATAAACAAACCCC
174209	6405	TCATTCAGCCAATCACAAGC	218796	50992	CTAGGATTACAGGTGTGAGC	263383	95579	AAAAACAAATAAACAAACCC
174210	6406	GTCATTCAGCCAATCACAAG	218797	50993	GCTAGGATTACAGGTGTGAG	263384	95580	AAAAAACAAATAAACAAACC

174211	6407	GGTCATTCAGCCAATCACAA	218798	50994	TGCTAGGATTACAGGTGTGA	263385	95581	TAAAAAACAAATAAACAAAC
174212	6408	TGGTCATTCAGCCAATCACA	218799	50995	GTGCTAGGATTACAGGTGTG	263386	95582	CTAAAAAACAAATAAACAAA
174213	6409	CTGGTCATTCAGCCAATCAC	218800	50996	AGTGCTAGGATTACAGGTGT	263387	95583	GCTAAAAAACAAATAAACAA
174214	6410	TCTGGTCATTCAGCCAATCA	218801	50997	AAGTGCTAGGATTACAGGTG	263388	95584	GGCTAAAAAACAAATAAACA
174215	6411	CTCTGGTCATTCAGCCAATC	218802	50998	AAAGTGCTAGGATTACAGGT	263389	95585	AGGCTAAAAAACAAATAAAC
174216	6412	CCTCTGGTCATTCAGCCAAT	218803	50999	CAAAGTGCTAGGATTACAGG	263390	95586	GAGGCTAAAAAACAAATAAA
174217	6413	CCCTCTGGTCATTCAGCCAA	218804	51000	CCAAAGTGCTAGGATTACAG	263391	95587	TGAGGCTAAAAAACAAATAA
174218	6414	CCCCTCTGGTCATTCAGCCA	218805	51001	CCCAAAGTGCTAGGATTACA	263392	95588	TTGAGGCTAAAAAACAAATA
174219	6415	ACCCCTCTGGTCATTCAGCC	218806	51002	TCCCAAAGTGCTAGGATTAC	263393	95589	TTTGAGGCTAAAAAACAAAT
174220	6416	GACCCCTCTGGTCATTCAGC	218807	51003	CTCCCAAAGTGCTAGGATTA	263394	95590	CTTTGAGGCTAAAAAACAAA
174221	6417	AGACCCCTCTGGTCATTCAG	218808	51004	CCTCCCAAAGTGCTAGGATT	263395	95591	TCTTTGAGGCTAAAAAACAA
174222	6418	TAGACCCCTCTGGTCATTCA	218809	51005	GCCTCCCAAAGTGCTAGGAT	263396	95592	GTCTTTGAGGCTAAAAAACA
174223	6419	TTAGACCCCTCTGGTCATTC	218810	51006	GGCCTCCCAAAGTGCTAGGA	263397	95593	GGTCTTTGAGGCTAAAAAAC
174224	6420	TTTAGACCCCTCTGGTCATT	218811	51007	TGGCCTCCCAAAGTGCTAGG	263398	95594	AGGTCTTTGAGGCTAAAAAA
174225	6421	CTTTAGACCCCTCTGGTCAT	218812	51008	TTGGCCTCCCAAAGTGCTAG	263399	95595	AAGGTCTTTGAGGCTAAAAA
174226	6422	TCTTTAGACCCCTCTGGTCA	218813	51009	CTTGGCCTCCCAAAGTGCTA	263400	95596	AAAGGTCTTTGAGGCTAAAA
174227	6423	ATCTTTAGACCCCTCTGGTC	218814	51010	CCTTGGCCTCCCAAAGTGCT	263401	95597	GAAAGGTCTTTGAGGCTAAA
174228	6424	GATCTTTAGACCCCTCTGGT	218815	51011	GCCTTGGCCTCCCAAAGTGC	263402	95598	AGAAAGGTCTTTGAGGCTAA
174229	6425	GGATCTTTAGACCCCTCTGG	218816	51012	TGCCTTGGCCTCCCAAAGTG	263403	95599	AAGAAAGGTCTTTGAGGCTA
174230	6426	AGGATCTTTAGACCCCTCTG	218817	51013	CTGCCTTGGCCTCCCAAAGT	263404	95600	GAAGAAAGGTCTTTGAGGCT
174231	6427	CAGGATCTTTAGACCCCTCT	218818	51014	CCTGCCTTGGCCTCCCAAAG	263405	95601	TGAAGAAAGGTCTTTGAGGC
174232	6428	CCAGGATCTTTAGACCCCTC	218819	51015	GCCTGCCTTGGCCTCCCAAA	263406	95602	TTGAAGAAAGGTCTTTGAGG
174233	6429	ACCAGGATCTTTAGACCCCT	218820	51016	CGCCTGCCTTGGCCTCCCAA	263407	95603	TTTGAAGAAAGGTCTTTGAG
174234	6430	CACCAGGATCTTTAGACCCC	218821	51017	CCGCCTGCCTTGGCCTCCCA	263408	95604	ATTTGAAGAAAGGTCTTTGA
174235	6431	TCACCAGGATCTTTAGACCC	218822	51018	TCCGCCTGCCTTGGCCTCCC	263409	95605	CATTTGAAGAAAGGTCTTTG
174236	6432	ATCACCAGGATCTTTAGACC	218823	51019	ATCCGCCTGCCTTGGCCTCC	263410	95606	TCATTTGAAGAAAGGTCTTT
174237	6433	CATCACCAGGATCTTTAGAC	218824	51020	GATCCGCCTGCCTTGGCCTC	263411	95607	CTCATTTGAAGAAAGGTCTT
174238	6434	CCATCACCAGGATCTTTAGA	218825	51021	TGATCCGCCTGCCTTGGCCT	263412	95608	ACTCATTTGAAGAAAGGTCT
174239	6435	TCCATCACCAGGATCTTTAG	218826	51022	GTGATCCGCCTGCCTTGGCC	263413	95609	AACTCATTTGAAGAAAGGTC
174240	6436	TTCCATCACCAGGATCTTTA	218827	51023	AGTGATCCGCCTGCCTTGGC	263414	95610	GAACTCATTTGAAGAAAGGT
174241	6437	ATTCCATCACCAGGATCTTT	218828	51024	AAGTGATCCGCCTGCCTTGG	263415	95611	AGAACTCATTTGAAGAAAGG
174242	6438	GATTCCATCACCAGGATCTT	218829	51025	CAAGTGATCCGCCTGCCTTG	263416	95612	CAGAACTCATTTGAAGAAAG
174243	6439	TGATTCCATCACCAGGATCT	218830	51026	TCAAGTGATCCGCCTGCCTT	263417	95613	CCAGAACTCATTTGAAGAAA
174244	6440	CTGATTCCATCACCAGGATC	218831	51027	CTCAAGTGATCCGCCTGCCT	263418	95614	GCCAGAACTCATTTGAAGAA
174245	6441	ACTGATTCCATCACCAGGAT	218832	51028	TCTCAAGTGATCCGCCTGCC	263419	95615	TGCCAGAACTCATTTGAAGA
174246	6442	AACTGATTCCATCACCAGGA	218833	51029	ATCTCAAGTGATCCGCCTGC	263420	95616	ATGCCAGAACTCATTTGAAG
174247	6443	CAACTGATTCCATCACCAGG	218834	51030	GATCTCAAGTGATCCGCCTG	263421	95617	TATGCCAGAACTCATTTGAA
174248	6444	ACAACTGATTCCATCACCAG	218835	51031	TGATCTCAAGTGATCCGCCT	263422	95618	CTATGCCAGAACTCATTTGA
174249	6445	TACAACTGATTCCATCACCA	218836	51032	CTGATCTCAAGTGATCCGCC	263423	95619	TCTATGCCAGAACTCATTTG
174250	6446	GTACAACTGATTCCATCACC	218837	51033	CCTGATCTCAAGTGATCCGC	263424	95620	TTCTATGCCAGAACTCATTT
174251	6447	TGTACAACTGATTCCATCAC	218838	51034	TCCTGATCTCAAGTGATCCG	263425	95621	CTTCTATGCCAGAACTCATT
174252	6448	CTGTACAACTGATTCCATCA	218839	51035	CTCCTGATCTCAAGTGATCC	263426	95622	GCTTCTATGCCAGAACTCAT
174253	6449	TCTGTACAACTGATTCCATC	218840	51036	ACTCCTGATCTCAAGTGATC	263427	95623	TGCTTCTATGCCAGAACTCA
174254	6450	ATCTGTACAACTGATTCCAT	218841	51037	AACTCCTGATCTCAAGTGAT	263428	95624	GTGCTTCTATGCCAGAACTC
174255	6451	TATCTGTACAACTGATTCCA	218842	51038	GAACTCCTGATCTCAAGTGA	263429	95625	GGTGCTTCTATGCCAGAACT
174256	6452	TTATCTGTACAACTGATTCC	218843	51039	CGAACTCCTGATCTCAAGTG	263430	95626	CGGTGCTTCTATGCCAGAAC
174257	6453	TTTATCTGTACAACTGATTC	218844	51040	TCGAACTCCTGATCTCAAGT	263431	95627	ACGGTGCTTCTATGCCAGAA
174258	6454	ATTTATCTGTACAACTGATT	218845	51041	CTCGAACTCCTGATCTCAAG	263432	95628	CACGGTGCTTCTATGCCAGA
174259	6455	AATTTATCTGTACAACTGAT	218846	51042	TCTCGAACTCCTGATCTCAA	263433	95629	ACACGGTGCTTCTATGCCAG
174260	6456	CAATTTATCTGTACAACTGA	218847	51043	GTCTCGAACTCCTGATCTCA	263434	95630	TACACGGTGCTTCTATGCCA
174261	6457	ACAATTTATCTGTACAACTG	218848	51044	GGTCTCGAACTCCTGATCTC	263435	95631	TTACACGGTGCTTCTATGCC
174262	6458	AACAATTTATCTGTACAACT	218849	51045	TGGTCTCGAACTCCTGATCT	263436	95632	TTTACACGGTGCTTCTATGC
174263	6459	TAACAATTTATCTGTACAAC	218850	51046	CTGGTCTCGAACTCCTGATC	263437	95633	TTTTACACGGTGCTTCTATG
174264	6460	GTAACAATTTATCTGTACAA	218851	51047	GCTGGTCTCGAACTCCTGAT	263438	95634	ATTTTACACGGTGCTTCTAT
174265	6461	TGTAACAATTTATCTGTACA	218852	51048	GGCTGGTCTCGAACTCCTGA	263439	95635	TATTTTACACGGTGCTTCTA
174266	6462	GTGTAACAATTTATCTGTAC	218853	51049	AGGCTGGTCTCGAACTCCTG	263440	95636	CTATTTTACACGGTGCTTCT
174267	6463	AGTGTAACAATTTATCTGTA	218854	51050	CAGGCTGGTCTCGAACTCCT	263441	95637	ACTATTTTACACGGTGCTTC
174268	6464	CAGTGTAACAATTTATCTGT	218855	51051	CCAGGCTGGTCTCGAACTCC	263442	95638	AACTATTTTACACGGTGCTT
174269	6465	TCAGTGTAACAATTTATCTG	218856	51052	GCCAGGCTGGTCTCGAACTC	263443	95639	TAACTATTTTACACGGTGCT
174270	6466	CTCAGTGTAACAATTTATCT	218857	51053	GGCCAGGCTGGTCTCGAACT	263444	95640	CTAACTATTTTACACGGTGC
174271	6467	ACTCAGTGTAACAATTTATC	218858	51054	TGGCCAGGCTGGTCTCGAAC	263445	95641	TCTAACTATTTTACACGGTG
174272	6468	TACTCAGTGTAACAATTTAT	218859	51055	TTGGCCAGGCTGGTCTCGAA	263446	95642	TTCTAACTATTTTACACGGT
174273	6469	CTACTCAGTGTAACAATTTA	218860	51056	GTTGGCCAGGCTGGTCTCGA	263447	95643	ATTCTAACTATTTTACACGG
174274	6470	CCTACTCAGTGTAACAATTT	218861	51057	TGTTGGCCAGGCTGGTCTCG	263448	95644	AATTCTAACTATTTTACACG
174275	6471	CCCTACTCAGTGTAACAATT	218862	51058	ATGTTGGCCAGGCTGGTCTC	263449	95645	GAATTCTAACTATTTTACAC
174276	6472	TCCCTACTCAGTGTAACAAT	218863	51059	CATGTTGGCCAGGCTGGTCT	263450	95646	AGAATTCTAACTATTTTACA
174277	6473	ATCCCTACTCAGTGTAACAA	218864	51060	CCATGTTGGCCAGGCTGGTC	263451	95647	CAGAATTCTAACTATTTTAC
174278	6474	GATCCCTACTCAGTGTAACA	218865	51061	ACCATGTTGGCCAGGCTGGT	263452	95648	CCAGAATTCTAACTATTTTA
174279	6475	TGATCCCTACTCAGTGTAAC	218866	51062	CACCATGTTGGCCAGGCTGG	263453	95649	CCCAGAATTCTAACTATTTT
174280	6476	TTGATCCCTACTCAGTGTAA	218867	51063	TCACCATGTTGGCCAGGCTG	263454	95650	GCCCAGAATTCTAACTATTT
174281	6477	CTTGATCCCTACTCAGTGTA	218868	51064	TTCACCATGTTGGCCAGGCT	263455	95651	TGCCCAGAATTCTAACTATT
174282	6478	TCTTGATCCCTACTCAGTGT	218869	51065	TTTCACCATGTTGGCCAGGC	263456	95652	TTGCCCAGAATTCTAACTAT

174283	6479	ATCTTGATCCCTACTCAGTG	218870	51066	GTTTCACCATGTTGGCCAGG	263457	95653	TTTGCCCAGAATTCTAACTA
174284	6480	TATCTTGATCCCTACTCAGT	218871	51067	GGTTTCACCATGTTGGCCAG	263458	95654	CTTTGCCCAGAATTCTAACT
174285	6481	CTATCTTGATCCCTACTCAG	218872	51068	GGGTTTCACCATGTTGGCCA	263459	95655	CCTTTGCCCAGAATTCTAAC
174286	6482	CCTATCTTGATCCCTACTCA	218873	51069	GGGGTTTCACCATGTTGGCC	263460	95656	CCCTTTGCCCAGAATTCTAA
174287	6483	TCCTATCTTGATCCCTACTC	218874	51070	TGGGGTTTCACCATGTTGGC	263461	95657	CCCCTTTGCCCAGAATTCTA
174288	6484	TTCCTATCTTGATCCCTACT	218875	51071	ATGGGGTTTCACCATGTTGG	263462	95658	TCCCCTTTGCCCAGAATTCT
174289	6485	TTTCCTATCTTGATCCCTAC	218876	51072	GATGGGGTTTCACCATGTTG	263463	95659	TTCCCCTTTGCCCAGAATTC
174290	6486	TTTTCCTATCTTGATCCCTA	218877	51073	GGATGGGGTTTCACCATGTT	263464	95660	TTTCCCCTTTGCCCAGAATT
174291	6487	CTTTTCCTATCTTGATCCCT	218878	51074	GGGATGGGGTTTCACCATGT	263465	95661	TTTTCCCCTTTGCCCAGAAT
174292	6488	ACTTTTCCTATCTTGATCCC	218879	51075	AGGGATGGGGTTTCACCATG	263466	95662	CTTTTCCCCTTTGCCCAGAA
174293	6489	GACTTTTCCTATCTTGATCC	218880	51076	TAGGGATGGGGTTTCACCAT	263467	95663	TCTTTTCCCCTTTGCCCAGA
174294	6490	CGACTTTTCCTATCTTGATC	218881	51077	GTAGGGATGGGGTTTCACCA	263468	95664	CTCTTTTCCCCTTTGCCCAG
174295	6491	CCGACTTTTCCTATCTTGAT	218882	51078	AGTAGGGATGGGGTTTCACC	263469	95665	TCTCTTTTCCCCTTTGCCCA
174296	6492	GCCGACTTTTCCTATCTTGA	218883	51079	TAGTAGGGATGGGGTTTCAC	263470	95666	CTCTCTTTTCCCCTTTGCCC
174297	6493	TGCCGACTTTTCCTATCTTG	218884	51080	TTAGTAGGGATGGGGTTTCA	263471	95667	GCTCTCTTTTCCCCTTTGCC
174298	6494	TTGCCGACTTTTCCTATCTT	218885	51081	TTTAGTAGGGATGGGGTTTC	263472	95668	AGCTCTCTTTTCCCCTTTGC
174299	6495	GTTGCCGACTTTTCCTATCT	218886	51082	TTTTAGTAGGGATGGGGTTT	263473	95669	CAGCTCTCTTTTCCCCTTTG
174300	6496	AGTTGCCGACTTTTCCTATC	218887	51083	TTTTTAGTAGGGATGGGGTT	263474	95670	CCAGCTCTCTTTTCCCCTTT
174301	6497	TAGTTGCCGACTTTTCCTAT	218888	51084	ATTTTTAGTAGGGATGGGGT	263475	95671	CCCAGCTCTCTTTTCCCCTT
174302	6498	GTAGTTGCCGACTTTTCCTA	218889	51085	TATTTTTAGTAGGGATGGGG	263476	95672	CCCCAGCTCTCTTTTCCCCT
174303	6499	GGTAGTTGCCGACTTTTCCT	218890	51086	GTATTTTTAGTAGGGATGGG	263477	95673	CCCCCAGCTCTCTTTTCCCC
174304	6500	GGGTAGTTGCCGACTTTTCC	218891	51087	TGTATTTTTAGTAGGGATGG	263478	95674	GCCCCCAGCTCTCTTTTCCC
174305	6501	TGGGTAGTTGCCGACTTTTC	218892	51088	TTGTATTTTTAGTAGGGATG	263479	95675	GGCCCCCAGCTCTCTTTTCC
174306	6502	CTGGGTAGTTGCCGACTTTT	218893	51089	TTTGTATTTTTAGTAGGGAT	263480	95676	TGGCCCCCAGCTCTCTTTTC
174307	6503	GCTGGGTAGTTGCCGACTTT	218894	51090	TTTTGTATTTTTAGTAGGGA	263481	95677	ATGGCCCCCAGCTCTCTTTT
174308	6504	AGCTGGGTAGTTGCCGACTT	218895	51091	TTTTTGTATTTTTAGTAGGG	263482	95678	GATGGCCCCCAGCTCTCTTT
174309	6505	GAGCTGGGTAGTTGCCGACT	218896	51092	ATTTTTGTATTTTTAGTAGG	263483	95679	GGATGGCCCCCAGCTCTCTT
174310	6506	GGAGCTGGGTAGTTGCCGAC	218897	51093	AATTTTTGTATTTTTAGTAG	263484	95680	GGGATGGCCCCCAGCTCTCT
174311	6507	GGGAGCTGGGTAGTTGCCGA	218898	51094	TAATTTTTGTATTTTTAGTA	263485	95681	AGGGATGGCCCCCAGCTCTC
174312	6508	GGGGAGCTGGGTAGTTGCCG	218899	51095	CTAATTTTTGTATTTTTAGT	263486	95682	GAGGGATGGCCCCCAGCTCT
174313	6509	AGGGGAGCTGGGTAGTTGCC	218900	51096	GCTAATTTTTGTATTTTTAG	263487	95683	AGAGGGATGGCCCCCAGCTC
174314	6510	CAGGGGAGCTGGGTAGTTGC	218901	51097	AGCTAATTTTTGTATTTTTA	263488	95684	GAGAGGGATGGCCCCCAGCT
174315	6511	GCAGGGGAGCTGGGTAGTTG	218902	51098	CAGCTAATTTTTGTATTTTT	263489	95685	TGAGAGGGATGGCCCCCAGC
174316	6512	TGCAGGGGAGCTGGGTAGTT	218903	51099	CCAGCTAATTTTTGTATTTT	263490	95686	CTGAGAGGGATGGCCCCCAG
174317	6513	GTGCAGGGGAGCTGGGTAGT	218904	51100	CCCAGCTAATTTTTGTATTT	263491	95687	GCTGAGAGGGATGGCCCCCA
174318	6514	GGTGCAGGGGAGCTGGGTAG	218905	51101	GCCCAGCTAATTTTTGTATT	263492	95688	TGCTGAGAGGGATGGCCCCC
174319	6515	TGGTGCAGGGGAGCTGGGTA	218906	51102	CGCCCAGCTAATTTTTGTAT	263493	95689	GTGCTGAGAGGGATGGCCCC
174320	6516	TTGGTGCAGGGGAGCTGGGT	218907	51103	ACGCCCAGCTAATTTTTGTA	263494	95690	GGTGCTGAGAGGGATGGCCC
174321	6517	TTTGGTGCAGGGGAGCTGGG	218908	51104	CACGCCCAGCTAATTTTTGT	263495	95691	GGGTGCTGAGAGGGATGGCC
174322	6518	GTTTGGTGCAGGGGAGCTGG	218909	51105	CCACGCCCAGCTAATTTTTG	263496	95692	GGGGTGCTGAGAGGGATGGC
174323	6519	AGTTTGGTGCAGGGGAGCTG	218910	51106	ACCACGCCCAGCTAATTTTT	263497	95693	TGGGGTGCTGAGAGGGATGG
174324	6520	CAGTTTGGTGCAGGGGAGCT	218911	51107	CACCACGCCCAGCTAATTTT	263498	95694	GTGGGGTGCTGAGAGGGATG
174325	6521	CCAGTTTGGTGCAGGGGAGC	218912	51108	CCACCACGCCCAGCTAATTT	263499	95695	TGTGGGGTGCTGAGAGGGAT
174326	6522	CCCAGTTTGGTGCAGGGGAG	218913	51109	ACCACCACGCCCAGCTAATT	263500	95696	CTGTGGGGTGCTGAGAGGGA
174327	6523	GCCCAGTTTGGTGCAGGGGA	218914	51110	CACCACCACGCCCAGCTAAT	263501	95697	CCTGTGGGGTGCTGAGAGGG
174328	6524	TGCCCAGTTTGGTGCAGGGG	218915	51111	GCACCACCACGCCCAGCTAA	263502	95698	GCCTGTGGGGTGCTGAGAGG
174329	6525	CTGCCCAGTTTGGTGCAGGG	218916	51112	TGCACCACCACGCCCAGCTA	263503	95699	AGCCTGTGGGGTGCTGAGAG
174330	6526	TCTGCCCAGTTTGGTGCAGG	218917	51113	GTGCACCACCACGCCCAGCT	263504	95700	GAGCCTGTGGGGTGCTGAGA
174331	6527	TTCTGCCCAGTTTGGTGCAG	218918	51114	TGTGCACCACCACGCCCAGC	263505	95701	AGAGCCTGTGGGGTGCTGAG
174332	6528	CTTCTGCCCAGTTTGGTGCA	218919	51115	GTGTGCACCACCACGCCCAG	263506	95702	GAGAGCCTGTGGGGTGCTGA
174333	6529	ACTTCTGCCCAGTTTGGTGC	218920	51116	GGTGTGCACCACCACGCCCA	263507	95703	TGAGAGCCTGTGGGGTGCTG
174334	6530	CACTTCTGCCCAGTTTGGTG	218921	51117	AGGTGTGCACCACCACGCCC	263508	95704	ATGAGAGCCTGTGGGGTGCT
174335	6531	CCACTTCTGCCCAGTTTGGT	218922	51118	CAGGTGTGCACCACCACGCC	263509	95705	TATGAGAGCCTGTGGGGTGC
174336	6532	TCCACTTCTGCCCAGTTTGG	218923	51119	ACAGGTGTGCACCACCACGC	263510	95706	CTATGAGAGCCTGTGGGGTG
174337	6533	ATCCACTTCTGCCCAGTTTG	218924	51120	TACAGGTGTGCACCACCACG	263511	95707	GCTATGAGAGCCTGTGGGGT
174338	6534	GATCCACTTCTGCCCAGTTT	218925	51121	TTACAGGTGTGCACCACCAC	263512	95708	TGCTATGAGAGCCTGTGGGG
174339	6535	GGATCCACTTCTGCCCAGTT	218926	51122	ATTACAGGTGTGCACCACCA	263513	95709	CTGCTATGAGAGCCTGTGGG
174340	6536	AGGATCCACTTCTGCCCAGT	218927	51123	GATTACAGGTGTGCACCACC	263514	95710	GCTGCTATGAGAGCCTGTGG
174341	6537	GAGGATCCACTTCTGCCCAG	218928	51124	GGATTACAGGTGTGCACCAC	263515	95711	TGCTGCTATGAGAGCCTGTG
174342	6538	AGAGGATCCACTTCTGCCCA	218929	51125	GGGATTACAGGTGTGCACCA	263516	95712	CTGCTGCTATGAGAGCCTGT
174343	6539	CAGAGGATCCACTTCTGCCC	218930	51126	TGGGATTACAGGTGTGCACC	263517	95713	GCTGCTGCTATGAGAGCCTG
174344	6540	TCAGAGGATCCACTTCTGCC	218931	51127	CTGGGATTACAGGTGTGCAC	263518	95714	AGCTGCTGCTATGAGAGCCT
174345	6541	TTCAGAGGATCCACTTCTGC	218932	51128	GCTGGGATTACAGGTGTGCA	263519	95715	GAGCTGCTGCTATGAGAGCC
174346	6542	TTTCAGAGGATCCACTTCTG	218933	51129	AGCTGGGATTACAGGTGTGC	263520	95716	GGAGCTGCTGCTATGAGAGC
174347	6543	TTTTCAGAGGATCCACTTCT	218934	51130	TAGCTGGGATTACAGGTGTG	263521	95717	AGGAGCTGCTGCTATGAGAG
174348	6544	ATTTTCAGAGGATCCACTTC	218935	51131	GTAGCTGGGATTACAGGTGT	263522	95718	TAGGAGCTGCTGCTATGAGA
174349	6545	AATTTTCAGAGGATCCACTT	218936	51132	AGTAGCTGGGATTACAGGTG	263523	95719	TTAGGAGCTGCTGCTATGAG
174350	6546	CAATTTTCAGAGGATCCACT	218937	51133	GAGTAGCTGGGATTACAGGT	263524	95720	CTTAGGAGCTGCTGCTATGA
174351	6547	GCAATTTTCAGAGGATCCAC	218938	51134	TGAGTAGCTGGGATTACAGG	263525	95721	TCTTAGGAGCTGCTGCTATG
174352	6548	TGCAATTTTCAGAGGATCCA	218939	51135	CTGAGTAGCTGGGATTACAG	263526	95722	GTCTTAGGAGCTGCTGCTAT
174353	6549	GTGCAATTTTCAGAGGATCC	218940	51136	CCTGAGTAGCTGGGATTACA	263527	95723	TGTCTTAGGAGCTGCTGCTA
174354	6550	TGTGCAATTTTCAGAGGATC	218941	51137	TCCTGAGTAGCTGGGATTAC	263528	95724	GTGTCTTAGGAGCTGCTGCT

174355	6551	GTGTGCAATTTTCAGAGGAT	218942	51138	CTCCTGAGTAGCTGGGATTA	263529	95725	GGTGTCTTAGGAGCTGCTGC
174356	6552	TGTGTGCAATTTTCAGAGGA	218943	51139	CCTCCTGAGTAGCTGGGATT	263530	95726	AGGTGTCTTAGGAGCTGCTG
174357	6553	GTGTGTGCAATTTTCAGAGG	218944	51140	GCCTCCTGAGTAGCTGGGAT	263531	95727	CAGGTGTCTTAGGAGCTGCT
174358	6554	GGTGTGTGCAATTTTCAGAG	218945	51141	AGCCTCCTGAGTAGCTGGGA	263532	95728	CCAGGTGTCTTAGGAGCTGC
174359	6555	GGGTGTGTGCAATTTTCAGA	218946	51142	CAGCCTCCTGAGTAGCTGGG	263533	95729	ACCAGGTGTCTTAGGAGCTG
174360	6556	TGGGTGTGTGCAATTTTCAG	218947	51143	TCAGCCTCCTGAGTAGCTGG	263534	95730	CACCAGGTGTCTTAGGAGCT
174361	6557	ATGGGTGTGTGCAATTTTCA	218948	51144	CTCAGCCTCCTGAGTAGCTG	263535	95731	CCACCAGGTGTCTTAGGAGC
174362	6558	CATGGGTGTGTGCAATTTTC	218949	51145	CCTCAGCCTCCTGAGTAGCT	263536	95732	CCCACCAGGTGTCTTAGGAG
174363	6559	ACATGGGTGTGTGCAATTTT	218950	51146	GCCTCAGCCTCCTGAGTAGC	263537	95733	TCCCACCAGGTGTCTTAGGA
174364	6560	AACATGGGTGTGTGCAATTT	218951	51147	TGCCTCAGCCTCCTGAGTAG	263538	95734	GTCCCACCAGGTGTCTTAGG
174365	6561	AAACATGGGTGTGTGCAATT	218952	51148	CTGCCTCAGCCTCCTGAGTA	263539	95735	GGTCCCACCAGGTGTCTTAG
174366	6562	TAAACATGGGTGTGTGCAAT	218953	51149	CCTGCCTCAGCCTCCTGAGT	263540	95736	AGGTCCCACCAGGTGTCTTA
174367	6563	TTAAACATGGGTGTGTGCAA	218954	51150	TCCTGCCTCAGCCTCCTGAG	263541	95737	AAGGTCCCACCAGGTGTCTT
174368	6564	TTTAAACATGGGTGTGTGCA	218955	51151	CTCCTGCCTCAGCCTCCTGA	263542	95738	CAAGGTCCCACCAGGTGTCT
174369	6565	ATTTAAACATGGGTGTGTGC	218956	51152	TCTCCTGCCTCAGCCTCCTG	263543	95739	CCAAGGTCCCACCAGGTGTC
174370	6566	CATTTAAACATGGGTGTGTG	218957	51153	TTCTCCTGCCTCAGCCTCCT	263544	95740	ACCAAGGTCCCACCAGGTGT
174371	6567	ACATTTAAACATGGGTGTGT	218958	51154	ATTCTCCTGCCTCAGCCTCC	263545	95741	AACCAAGGTCCCACCAGGTG
174372	6568	TACATTTAAACATGGGTGTG	218959	51155	GATTCTCCTGCCTCAGCCTC	263546	95742	AAACCAAGGTCCCACCAGGT
174373	6569	GTACATTTAAACATGGGTGT	218960	51156	TGATTCTCCTGCCTCAGCCT	263547	95743	GAAACCAAGGTCCCACCAGG
174374	6570	TGTACATTTAAACATGGGTG	218961	51157	GTGATTCTCCTGCCTCAGCC	263548	95744	CGAAACCAAGGTCCCACCAG
174375	6571	GTGTACATTTAAACATGGGT	218962	51158	AGTGATTCTCCTGCCTCAGC	263549	95745	TCGAAACCAAGGTCCCACCA
174376	6572	TGTGTACATTTAAACATGGG	218963	51159	TAGTGATTCTCCTGCCTCAG	263550	95746	TTCGAAACCAAGGTCCCACC
174377	6573	GTGTGTACATTTAAACATGG	218964	51160	CTAGTGATTCTCCTGCCTCA	263551	95747	TTTCGAAACCAAGGTCCCAC
174378	6574	TGTGTGTACATTTAAACATG	218965	51161	TCTAGTGATTCTCCTGCCTC	263552	95748	ATTTCGAAACCAAGGTCCCA
174379	6575	CTGTGTGTACATTTAAACAT	218966	51162	TTCTAGTGATTCTCCTGCCT	263553	95749	GATTTCGAAACCAAGGTCCC
174380	6576	TCTGTGTGTACATTTAAACA	218967	51163	GTTCTAGTGATTCTCCTGCC	263554	95750	CGATTTCGAAACCAAGGTCC
174381	6577	TTCTGTGTGTACATTTAAAC	218968	51164	GGTTCTAGTGATTCTCCTGC	263555	95751	GCGATTTCGAAACCAAGGTC
174382	6578	GTTCTGTGTGTACATTTAAA	218969	51165	GGGTTCTAGTGATTCTCCTG	263556	95752	AGCGATTTCGAAACCAAGGT
174383	6579	AGTTCTGTGTGTACATTTAA	218970	51166	TGGGTTCTAGTGATTCTCCT	263557	95753	TAGCGATTTCGAAACCAAGG
174384	6580	GAGTTCTGTGTGTACATTTA	218971	51167	CTGGGTTCTAGTGATTCTCC	263558	95754	GTAGCGATTTCGAAACCAAG
174385	6581	AGAGTTCTGTGTGTACATTT	218972	51168	CCTGGGTTCTAGTGATTCTC	263559	95755	AGTAGCGATTTCGAAACCAA
174386	6582	AAGAGTTCTGTGTGTACATT	218973	51169	TCCTGGGTTCTAGTGATTCT	263560	95756	GAGTAGCGATTTCGAAACCA
174387	6583	CAAGAGTTCTGTGTGTACAT	218974	51170	CTCCTGGGTTCTAGTGATTC	263561	95757	AGAGTAGCGATTTCGAAACC
174388	6584	GCAAGAGTTCTGTGTGTACA	218975	51171	CCTCCTGGGTTCTAGTGATT	263562	95758	TAGAGTAGCGATTTCGAAAC
174389	6585	GGCAAGAGTTCTGTGTGTAC	218976	51172	ACCTCCTGGGTTCTAGTGAT	263563	95759	TTAGAGTAGCGATTTCGAAA
174390	6586	TGGCAAGAGTTCTGTGTGTA	218977	51173	CACCTCCTGGGTTCTAGTGA	263564	95760	CTTAGAGTAGCGATTTCGAA
174391	6587	GTGGCAAGAGTTCTGTGTGT	218978	51174	TCACCTCCTGGGTTCTAGTG	263565	95761	CCTTAGAGTAGCGATTTCGA
174392	6588	TGTGGCAAGAGTTCTGTGTG	218979	51175	TTCACCTCCTGGGTTCTAGT	263566	95762	GCCTTAGAGTAGCGATTTCG
174393	6589	CTGTGGCAAGAGTTCTGTGT	218980	51176	CTTCACCTCCTGGGTTCTAG	263567	95763	AGCCTTAGAGTAGCGATTTC
174394	6590	CCTGTGGCAAGAGTTCTGTG	218981	51177	CCTTCACCTCCTGGGTTCTA	263568	95764	CAGCCTTAGAGTAGCGATTT
174395	6591	GCCTGTGGCAAGAGTTCTGT	218982	51178	ACCTTCACCTCCTGGGTTCT	263569	95765	CCAGCCTTAGAGTAGCGATT
174396	6592	TGCCTGTGGCAAGAGTTCTG	218983	51179	AACCTTCACCTCCTGGGTTC	263570	95766	CCCAGCCTTAGAGTAGCGAT
174397	6593	TTGCCTGTGGCAAGAGTTCT	218984	51180	CAACCTTCACCTCCTGGGTT	263571	95767	GCCCAGCCTTAGAGTAGCGA
174398	6594	CTTGCCTGTGGCAAGAGTTC	218985	51181	GCAACCTTCACCTCCTGGGT	263572	95768	TGCCCAGCCTTAGAGTAGCG
174399	6595	GCTTGCCTGTGGCAAGAGTT	218986	51182	TGCAACCTTCACCTCCTGGG	263573	95769	GTGCCCAGCCTTAGAGTAGC
174400	6596	CGCTTGCCTGTGGCAAGAGT	218987	51183	CTGCAACCTTCACCTCCTGG	263574	95770	CGTGCCCAGCCTTAGAGTAG
174401	6597	CCGCTTGCCTGTGGCAAGAG	218988	51184	ACTGCAACCTTCACCTCCTG	263575	95771	CCGTGCCCAGCCTTAGAGTA
174402	6598	TCCGCTTGCCTGTGGCAAGA	218989	51185	CACTGCAACCTTCACCTCCT	263576	95772	ACCGTGCCCAGCCTTAGAGT
174403	6599	CTCCGCTTGCCTGTGGCAAG	218990	51186	TCACTGCAACCTTCACCTCC	263577	95773	CACCGTGCCCAGCCTTAGAG
174404	6600	TCTCCGCTTGCCTGTGGCAA	218991	51187	CTCACTGCAACCTTCACCTC	263578	95774	CCACCGTGCCCAGCCTTAGA
174405	6601	ATCTCCGCTTGCCTGTGGCA	218992	51188	GCTCACTGCAACCTTCACCT	263579	95775	GCCACCGTGCCCAGCCTTAG
174406	6602	AATCTCCGCTTGCCTGTGGC	218993	51189	GGCTCACTGCAACCTTCACC	263580	95776	AGCCACCGTGCCCAGCCTTA
174407	6603	AAATCTCCGCTTGCCTGTGG	218994	51190	CGGCTCACTGCAACCTTCAC	263581	95777	GAGCCACCGTGCCCAGCCTT
174408	6604	CAAATCTCCGCTTGCCTGTG	218995	51191	TCGGCTCACTGCAACCTTCA	263582	95778	TGAGCCACCGTGCCCAGCCT
174409	6605	ACAAATCTCCGCTTGCCTGT	218996	51192	CTCGGCTCACTGCAACCTTC	263583	95779	GTGAGCCACCGTGCCCAGCC
174410	6606	GACAAATCTCCGCTTGCCTG	218997	51193	TCTCGGCTCACTGCAACCTT	263584	95780	TGTGAGCCACCGTGCCCAGC
174411	6607	TGACAAATCTCCGCTTGCCT	218998	51194	ATCTCGGCTCACTGCAACCT	263585	95781	GTGTGAGCCACCGTGCCCAG
174412	6608	ATGACAAATCTCCGCTTGCC	218999	51195	GATCTCGGCTCACTGCAACC	263586	95782	GGTGTGAGCCACCGTGCCCA
174413	6609	GATGACAAATCTCCGCTTGC	219000	51196	CGATCTCGGCTCACTGCAAC	263587	95783	AGGTGTGAGCCACCGTGCCC
174414	6610	AGATGACAAATCTCCGCTTG	219001	51197	GCGATCTCGGCTCACTGCAA	263588	95784	CAGGTGTGAGCCACCGTGCC
174415	6611	CAGATGACAAATCTCCGCTT	219002	51198	TGCGATCTCGGCTCACTGCA	263589	95785	ACAGGTGTGAGCCACCGTGC
174416	6612	GCAGATGACAAATCTCCGCT	219003	51199	GTGCGATCTCGGCTCACTGC	263590	95786	TACAGGTGTGAGCCACCGTG
174417	6613	AGCAGATGACAAATCTCCGC	219004	51200	GGTGCGATCTCGGCTCACTG	263591	95787	TTACAGGTGTGAGCCACCGT
174418	6614	CAGCAGATGACAAATCTCCG	219005	51201	TGGTGCGATCTCGGCTCACT	263592	95788	ATTACAGGTGTGAGCCACCG
174419	6615	ACAGCAGATGACAAATCTCC	219006	51202	GTGGTGCGATCTCGGCTCAC	263593	95789	GATTACAGGTGTGAGCCACC
174420	6616	GACAGCAGATGACAAATCTC	219007	51203	AGTGGTGCGATCTCGGCTCA	263594	95790	GGATTACAGGTGTGAGCCAC
174421	6617	GGACAGCAGATGACAAATCT	219008	51204	CAGTGGTGCGATCTCGGCTC	263595	95791	GGGATTACAGGTGTGAGCCA
174422	6618	GGGACAGCAGATGACAAATC	219009	51205	ACAGTGGTGCGATCTCGGCT	263596	95792	TGGGATTACAGGTGTGAGCC
174423	6619	AGGGACAGCAGATGACAAAT	219010	51206	TACAGTGGTGCGATCTCGGC	263597	95793	CTGGGATTACAGGTGTGAGC
174424	6620	CAGGGACAGCAGATGACAAA	219011	51207	GTACAGTGGTGCGATCTCGG	263598	95794	GCTGGGATTACAGGTGTGAG
174425	6621	GCAGGGACAGCAGATGACAA	219012	51208	AGTACAGTGGTGCGATCTCG	263599	95795	AGCTGGGATTACAGGTGTGA
174426	6622	GGCAGGGACAGCAGATGACA	219013	51209	GAGTACAGTGGTGCGATCTC	263600	95796	GAGCTGGGATTACAGGTGTG

174427	6623	AGGCAGGGACAGCAGATGAC	219014	51210	TGAGTACAGTGGTGCGATCT	263601	95797	AGAGCTGGGATTACAGGTGT
174428	6624	GAGGCAGGGACAGCAGATGA	219015	51211	TTGAGTACAGTGGTGCGATC	263602	95798	AAGAGCTGGGATTACAGGTG
174429	6625	TGAGGCAGGGACAGCAGATG	219016	51212	TTTGAGTACAGTGGTGCGAT	263603	95799	AAAGAGCTGGGATTACAGGT
174430	6626	ATGAGGCAGGGACAGCAGAT	219017	51213	GTTTGAGTACAGTGGTGCGA	263604	95800	TAAAGAGCTGGGATTACAGG
174431	6627	GATGAGGCAGGGACAGCAGA	219018	51214	GGTTTGAGTACAGTGGTGCG	263605	95801	CTAAAGAGCTGGGATTACAG
174432	6628	AGATGAGGCAGGGACAGCAG	219019	51215	CGGTTTGAGTACAGTGGTGC	263606	95802	CCTAAAGAGCTGGGATTACA
174433	6629	AAGATGAGGCAGGGACAGCA	219020	51216	TCGGTTTGAGTACAGTGGTG	263607	95803	TCCTAAAGAGCTGGGATTAC
174434	6630	GAAGATGAGGCAGGGACAGC	219021	51217	CTCGGTTTGAGTACAGTGGT	263608	95804	CTCCTAAAGAGCTGGGATTA
174435	6631	AGAAGATGAGGCAGGGACAG	219022	51218	CCTCGGTTTGAGTACAGTGG	263609	95805	CCTCCTAAAGAGCTGGGATT
174436	6632	AAGAAGATGAGGCAGGGACA	219023	51219	GCCTCGGTTTGAGTACAGTG	263610	95806	GCCTCCTAAAGAGCTGGGAT
174437	6633	GAAGAAGATGAGGCAGGGAC	219024	51220	TGCCTCGGTTTGAGTACAGT	263611	95807	GGCCTCCTAAAGAGCTGGGA
174438	6634	GGAAGAAGATGAGGCAGGGA	219025	51221	TTGCCTCGGTTTGAGTACAG	263612	95808	CGGCCTCCTAAAGAGCTGGG
174439	6635	AGGAAGAAGATGAGGCAGGG	219026	51222	GTTGCCTCGGTTTGAGTACA	263613	95809	TCGGCCTCCTAAAGAGCTGG
174440	6636	CAGGAAGAAGATGAGGCAGG	219027	51223	TGTTGCCTCGGTTTGAGTAC	263614	95810	CTCGGCCTCCTAAAGAGCTG
174441	6637	TCAGGAAGAAGATGAGGCAG	219028	51224	CTGTTGCCTCGGTTTGAGTA	263615	95811	CCTCGGCCTCCTAAAGAGCT
174442	6638	TTCAGGAAGAAGATGAGGCA	219029	51225	TCTGTTGCCTCGGTTTGAGT	263616	95812	TCCTCGGCCTCCTAAAGAGC
174443	6639	TTTCAGGAAGAAGATGAGGC	219030	51226	CTCTGTTGCCTCGGTTTGAG	263617	95813	CTCCTCGGCCTCCTAAAGAG
174444	6640	ATTTCAGGAAGAAGATGAGG	219031	51227	CCTCTGTTGCCTCGGTTTGA	263618	95814	CCTCCTCGGCCTCCTAAAGA
174445	6641	GATTTCAGGAAGAAGATGAG	219032	51228	CCCTCTGTTGCCTCGGTTTG	263619	95815	CCCTCCTCGGCCTCCTAAAG
174446	6642	GGATTTCAGGAAGAAGATGA	219033	51229	TCCCTCTGTTGCCTCGGTTT	263620	95816	ACCCTCCTCGGCCTCCTAAA
174447	6643	TGGATTTCAGGAAGAAGATG	219034	51230	CTCCCTCTGTTGCCTCGGTT	263621	95817	CACCCTCCTCGGCCTCCTAA
174448	6644	GTGGATTTCAGGAAGAAGAT	219035	51231	TCTCCCTCTGTTGCCTCGGT	263622	95818	CCACCCTCCTCGGCCTCCTA
174449	6645	AGTGGATTTCAGGAAGAAGA	219036	51232	GTCTCCCTCTGTTGCCTCGG	263623	95819	TCCACCCTCCTCGGCCTCCT
174450	6646	GAGTGGATTTCAGGAAGAAG	219037	51233	CGTCTCCCTCTGTTGCCTCG	263624	95820	ATCCACCCTCCTCGGCCTCC
174451	6647	GGAGTGGATTTCAGGAAGAA	219038	51234	GCGTCTCCCTCTGTTGCCTC	263625	95821	GATCCACCCTCCTCGGCCTC
174452	6648	TGGAGTGGATTTCAGGAAGA	219039	51235	TGCGTCTCCCTCTGTTGCCT	263626	95822	TGATCCACCCTCCTCGGCCT
174453	6649	ATGGAGTGGATTTCAGGAAG	219040	51236	TTGCGTCTCCCTCTGTTGCC	263627	95823	GTGATCCACCCTCCTCGGCC
174454	6650	CATGGAGTGGATTTCAGGAA	219041	51237	ATTGCGTCTCCCTCTGTTGC	263628	95824	GGTGATCCACCCTCCTCGGC
174455	6651	GCATGGAGTGGATTTCAGGA	219042	51238	GATTGCGTCTCCCTCTGTTG	263629	95825	AGGTGATCCACCCTCCTCGG
174456	6652	GGCATGGAGTGGATTTCAGG	219043	51239	AGATTGCGTCTCCCTCTGTT	263630	95826	CAGGTGATCCACCCTCCTCG
174457	6653	TGGCATGGAGTGGATTTCAG	219044	51240	GAGATTGCGTCTCCCTCTGT	263631	95827	TCAGGTGATCCACCCTCCTC
174458	6654	CTGGCATGGAGTGGATTTCA	219045	51241	TGAGATTGCGTCTCCCTCTG	263632	95828	CTCAGGTGATCCACCCTCCT
174459	6655	CCTGGCATGGAGTGGATTTC	219046	51242	TTGAGATTGCGTCTCCCTCT	263633	95829	TCTCAGGTGATCCACCCTCC
174460	6656	TCCTGGCATGGAGTGGATTT	219047	51243	TTTGAGATTGCGTCTCCCTC	263634	95830	ATCTCAGGTGATCCACCCTC
174461	6657	TTCCTGGCATGGAGTGGATT	219048	51244	TTTTGAGATTGCGTCTCCCT	263635	95831	GATCTCAGGTGATCCACCCT
174462	6658	ATTCCTGGCATGGAGTGGAT	219049	51245	TTTTTGAGATTGCGTCTCCC	263636	95832	TGATCTCAGGTGATCCACCC
174463	6659	TATTCCTGGCATGGAGTGGA	219050	51246	TTTTTTGAGATTGCGTCTCC	263637	95833	CTGATCTCAGGTGATCCACC
174464	6660	TTATTCCTGGCATGGAGTGG	219051	51247	TTTTTTTGAGATTGCGTCTC	263638	95834	CCTGATCTCAGGTGATCCAC
174465	6661	TTTATTCCTGGCATGGAGTG	219052	51248	TTTTTTTTGAGATTGCGTCT	263639	95835	TCCTGATCTCAGGTGATCCA
174466	6662	GTTTATTCCTGGCATGGAGT	219053	51249	TTTTTTTTTGAGATTGCGTC	263640	95836	CTCCTGATCTCAGGTGATCC
174467	6663	AGTTTATTCCTGGCATGGAG	219054	51250	CTTTTTTTTTGAGATTGCGT	263641	95837	ACTCCTGATCTCAGGTGATC
174468	6664	CAGTTTATTCCTGGCATGGA	219055	51251	TCTTTTTTTTTGAGATTGCG	263642	95838	AACTCCTGATCTCAGGTGAT
174469	6665	GCAGTTTATTCCTGGCATGG	219056	51252	TTCTTTTTTTTTGAGATTGC	263643	95839	GAACTCCTGATCTCAGGTGA
174470	6666	TGCAGTTTATTCCTGGCATG	219057	51253	TTTCTTTTTTTTTGAGATTG	263644	95840	CGAACTCCTGATCTCAGGTG
174471	6667	ATGCAGTTTATTCCTGGCAT	219058	51254	TTTTCTTTTTTTTTGAGATT	263645	95841	TCGAACTCCTGATCTCAGGT
174472	6668	CATGCAGTTTATTCCTGGCA	219059	51255	TTTTTCTTTTTTTTTGAGAT	263646	95842	CTCGAACTCCTGATCTCAGG
174473	6669	GCATGCAGTTTATTCCTGGC	219060	51256	TTTTTTCTTTTTTTTTGAGA	263647	95843	TCTCGAACTCCTGATCTCAG
174474	6670	AGCATGCAGTTTATTCCTGG	219061	51257	TTTTTTTCTTTTTTTTTGAG	263648	95844	GTCTCGAACTCCTGATCTCA
174475	6671	GAGCATGCAGTTTATTCCTG	219062	51258	CTTTTTTTCTTTTTTTTTGA	263649	95845	GGTCTCGAACTCCTGATCTC
174476	6672	AGAGCATGCAGTTTATTCCT	219063	51259	TCTTTTTTTCTTTTTTTTTG	263650	95846	TGGTCTCGAACTCCTGATCT
174477	6673	GAGAGCATGCAGTTTATTCC	219064	51260	GTCTTTTTTTCTTTTTTTTT	263651	95847	CTGGTCTCGAACTCCTGATC
174478	6674	GGAGAGCATGCAGTTTATTC	219065	51261	TGTCTTTTTTTCTTTTTTTT	263652	95848	GCTGGTCTCGAACTCCTGAT
174479	6675	TGGAGAGCATGCAGTTTATT	219066	51262	TTGTCTTTTTTTCTTTTTTT	263653	95849	GGCTGGTCTCGAACTCCTGA
174480	6676	GTGGAGAGCATGCAGTTTAT	219067	51263	TTTGTCTTTTTTTCTTTTTT	263654	95850	AGGCTGGTCTCGAACTCCTG
174481	6677	GGTGGAGAGCATGCAGTTTA	219068	51264	CTTTGTCTTTTTTTCTTTTT	263655	95851	CAGGCTGGTCTCGAACTCCT
174482	6678	TGGTGGAGAGCATGCAGTTT	219069	51265	GCTTTGTCTTTTTTTCTTTT	263656	95852	CCAGGCTGGTCTCGAACTCC
174483	6679	CTGGTGGAGAGCATGCAGTT	219070	51266	AGCTTTGTCTTTTTTTCTTT	263657	95853	GCCAGGCTGGTCTCGAACTC
174484	6680	GCTGGTGGAGAGCATGCAGT	219071	51267	AAGCTTTGTCTTTTTTTCTT	263658	95854	AGCCAGGCTGGTCTCGAACT
174485	6681	GGCTGGTGGAGAGCATGCAG	219072	51268	CAAGCTTTGTCTTTTTTTCT	263659	95855	TAGCCAGGCTGGTCTCGAAC
174486	6682	GGGCTGGTGGAGAGCATGCA	219073	51269	ACAAGCTTTGTCTTTTTTTC	263660	95856	TTAGCCAGGCTGGTCTCGAA
174487	6683	TGGGCTGGTGGAGAGCATGC	219074	51270	AACAAGCTTTGTCTTTTTTT	263661	95857	GTTAGCCAGGCTGGTCTCGA
174488	6684	TTGGGCTGGTGGAGAGCATG	219075	51271	TAACAAGCTTTGTCTTTTTT	263662	95858	TGTTAGCCAGGCTGGTCTCG
174489	6685	TTTGGGCTGGTGGAGAGCAT	219076	51272	TTAACAAGCTTTGTCTTTTT	263663	95859	ATGTTAGCCAGGCTGGTCTC
174490	6686	GTTTGGGCTGGTGGAGAGCA	219077	51273	ATTAACAAGCTTTGTCTTTT	263664	95860	CATGTTAGCCAGGCTGGTCT
174491	6687	AGTTTGGGCTGGTGGAGAGC	219078	51274	TATTAACAAGCTTTGTCTTT	263665	95861	CCATGTTAGCCAGGCTGGTC
174492	6688	CAGTTTGGGCTGGTGGAGAG	219079	51275	GTATTAACAAGCTTTGTCTT	263666	95862	GCCATGTTAGCCAGGCTGGT
174493	6689	TCAGTTTGGGCTGGTGGAGA	219080	51276	GGTATTAACAAGCTTTGTCT	263667	95863	TGCCATGTTAGCCAGGCTGG
174494	6690	GTCAGTTTGGGCTGGTGGAG	219081	51277	TGGTATTAACAAGCTTTGTC	263668	95864	TTGCCATGTTAGCCAGGCTG
174495	6691	GGTCAGTTTGGGCTGGTGGA	219082	51278	CTGGTATTAACAAGCTTTGT	263669	95865	TTTGCCATGTTAGCCAGGCT
174496	6692	AGGTCAGTTTGGGCTGGTGG	219083	51279	GCTGGTATTAACAAGCTTTG	263670	95866	TTTTGCCATGTTAGCCAGGC
174497	6693	CAGGTCAGTTTGGGCTGGTG	219084	51280	TGCTGGTATTAACAAGCTTT	263671	95867	GTTTTGCCATGTTAGCCAGG
174498	6694	GCAGGTCAGTTTGGGCTGGT	219085	51281	ATGCTGGTATTAACAAGCTT	263672	95868	GGTTTTGCCATGTTAGCCAG

174499	6695	GGCAGGTCAGTTTGGGCTGG	219086	51282	TATGCTGGTATTAACAAGCT	263673	95869	GGGTTTTGCCATGTTAGCCA
174500	6696	AGGCAGGTCAGTTTGGGCTG	219087	51283	ATATGCTGGTATTAACAAGC	263674	95870	AGGGTTTTGCCATGTTAGCC
174501	6697	AAGGCAGGTCAGTTTGGGCT	219088	51284	AATATGCTGGTATTAACAAG	263675	95871	CAGGGTTTTGCCATGTTAGC
174502	6698	GAAGGCAGGTCAGTTTGGGC	219089	51285	CAATATGCTGGTATTAACAA	263676	95872	ACAGGGTTTTGCCATGTTAG
174503	6699	GGAAGGCAGGTCAGTTTGGG	219090	51286	ACAATATGCTGGTATTAACA	263677	95873	GACAGGGTTTTGCCATGTTA
174504	6700	GGGAAGGCAGGTCAGTTTGG	219091	51287	AACAATATGCTGGTATTAAC	263678	95874	AGACAGGGTTTTGCCATGTT
174505	6701	CGGGAAGGCAGGTCAGTTTG	219092	51288	TAACAATATGCTGGTATTAA	263679	95875	GAGACAGGGTTTTGCCATGT
174506	6702	GCGGGAAGGCAGGTCAGTTT	219093	51289	TTAACAATATGCTGGTATTA	263680	95876	AGAGACAGGGTTTTGCCATG
174507	6703	GGCGGGAAGGCAGGTCAGTT	219094	51290	CTTAACAATATGCTGGTATT	263681	95877	TAGAGACAGGGTTTTGCCAT
174508	6704	TGGCGGGAAGGCAGGTCAGT	219095	51291	CCTTAACAATATGCTGGTAT	263682	95878	GTAGAGACAGGGTTTTGCCA
174509	6705	CTGGCGGGAAGGCAGGTCAG	219096	51292	CCCTTAACAATATGCTGGTA	263683	95879	AGTAGAGACAGGGTTTTGCC
174510	6706	GCTGGCGGGAAGGCAGGTCA	219097	51293	TCCCTTAACAATATGCTGGT	263684	95880	TAGTAGAGACAGGGTTTTGC
174511	6707	GGCTGGCGGGAAGGCAGGTC	219098	51294	TTCCCTTAACAATATGCTGG	263685	95881	TTAGTAGAGACAGGGTTTTG
174512	6708	TGGCTGGCGGGAAGGCAGGT	219099	51295	ATTCCCTTAACAATATGCTG	263686	95882	TTTAGTAGAGACAGGGTTTT
174513	6709	ATGGCTGGCGGGAAGGCAGG	219100	51296	TATTCCCTTAACAATATGCT	263687	95883	TTTTAGTAGAGACAGGGTTT
174514	6710	GATGGCTGGCGGGAAGGCAG	219101	51297	TTATTCCCTTAACAATATGC	263688	95884	TTTTTAGTAGAGACAGGGTT
174515	6711	GGATGGCTGGCGGGAAGGCA	219102	51298	TTTATTCCCTTAACAATATG	263689	95885	ATTTTTAGTAGAGACAGGGT
174516	6712	GGGATGGCTGGCGGGAAGGC	219103	51299	CTTTATTCCCTTAACAATAT	263690	95886	TATTTTTAGTAGAGACAGGG
174517	6713	CGGGATGGCTGGCGGGAAGG	219104	51300	ACTTTATTCCCTTAACAATA	263691	95887	GTATTTTTAGTAGAGACAGG
174518	6714	CCGGGATGGCTGGCGGGAAG	219105	51301	TACTTTATTCCCTTAACAAT	263692	95888	TGTATTTTTAGTAGAGACAG
174519	6715	CCCGGGATGGCTGGCGGGAA	219106	51302	CTACTTTATTCCCTTAACAA	263693	95889	TTGTATTTTTAGTAGAGACA
174520	6716	GCCCGGGATGGCTGGCGGGA	219107	51303	CCTACTTTATTCCCTTAACA	263694	95890	TTTGTATTTTTAGTAGAGAC
174521	6717	TGCCCGGGATGGCTGGCGGG	219108	51304	GCCTACTTTATTCCCTTAAC	263695	95891	TTTTGTATTTTTAGTAGAGA
174522	6718	CTGCCCGGGATGGCTGGCGG	219109	51305	AGCCTACTTTATTCCCTTAA	263696	95892	TTTTTGTATTTTTAGTAGAG
174523	6719	CCTGCCCGGGATGGCTGGCG	219110	51306	CAGCCTACTTTATTCCCTTA	263697	95893	ATTTTTGTATTTTTAGTAGA
174524	6720	CCCTGCCCGGGATGGCTGGC	219111	51307	GCAGCCTACTTTATTCCCTT	263698	95894	AATTTTTGTATTTTTAGTAG
174525	6721	ACCCTGCCCGGGATGGCTGG	219112	51308	TGCAGCCTACTTTATTCCCT	263699	95895	TAATTTTTGTATTTTTAGTA
174526	6722	CACCCTGCCCGGGATGGCTG	219113	51309	CTGCAGCCTACTTTATTCCC	263700	95896	CTAATTTTTGTATTTTTAGT
174527	6723	TCACCCTGCCCGGGATGGCT	219114	51310	TCTGCAGCCTACTTTATTCC	263701	95897	GCTAATTTTTGTATTTTTAG
174528	6724	GTCACCCTGCCCGGGATGGC	219115	51311	TTCTGCAGCCTACTTTATTC	263702	95898	GGCTAATTTTTGTATTTTTA
174529	6725	GGTCACCCTGCCCGGGATGG	219116	51312	GTTCTGCAGCCTACTTTATT	263703	95899	CGGCTAATTTTTGTATTTTT
174530	6726	AGGTCACCCTGCCCGGGATG	219117	51313	TGTTCTGCAGCCTACTTTAT	263704	95900	CCGGCTAATTTTTGTATTTT
174531	6727	CAGGTCACCCTGCCCGGGAT	219118	51314	TTGTTCTGCAGCCTACTTTA	263705	95901	CCCGGCTAATTTTTGTATTT
174532	6728	CCAGGTCACCCTGCCCGGGA	219119	51315	GTTGTTCTGCAGCCTACTTT	263706	95902	GCCCGGCTAATTTTTGTATT
174533	6729	GCCAGGTCACCCTGCCCGGG	219120	51316	AGTTGTTCTGCAGCCTACTT	263707	95903	CGCCCGGCTAATTTTTGTAT
174534	6730	AGCCAGGTCACCCTGCCCGG	219121	51317	CAGTTGTTCTGCAGCCTACT	263708	95904	ACGCCCGGCTAATTTTTGTA
174535	6731	AAGCCAGGTCACCCTGCCCG	219122	51318	CCAGTTGTTCTGCAGCCTAC	263709	95905	CACGCCCGGCTAATTTTTGT
174536	6732	TAAGCCAGGTCACCCTGCCC	219123	51319	ACCAGTTGTTCTGCAGCCTA	263710	95906	CCACGCCCGGCTAATTTTTG
174537	6733	CTAAGCCAGGTCACCCTGCC	219124	51320	CACCAGTTGTTCTGCAGCCT	263711	95907	ACCACGCCCGGCTAATTTTT
174538	6734	ACTAAGCCAGGTCACCCTGC	219125	51321	ACACCAGTTGTTCTGCAGCC	263712	95908	CACCACGCCCGGCTAATTTT
174539	6735	TACTAAGCCAGGTCACCCTG	219126	51322	TACACCAGTTGTTCTGCAGC	263713	95909	CCACCACGCCCGGCTAATTT
174540	6736	GTACTAAGCCAGGTCACCCT	219127	51323	TTACACCAGTTGTTCTGCAG	263714	95910	ACCACCACGCCCGGCTAATT
174541	6737	TGTACTAAGCCAGGTCACCC	219128	51324	ATTACACCAGTTGTTCTGCA	263715	95911	TACCACCACGCCCGGCTAAT
174542	6738	ATGTACTAAGCCAGGTCACC	219129	51325	TATTACACCAGTTGTTCTGC	263716	95912	ATACCACCACGCCCGGCTAA
174543	6739	GATGTACTAAGCCAGGTCAC	219130	51326	ATATTACACCAGTTGTTCTG	263717	95913	CATACCACCACGCCCGGCTA
174544	6740	CGATGTACTAAGCCAGGTCA	219131	51327	CATATTACACCAGTTGTTCT	263718	95914	GCATACCACCACGCCCGGCT
174545	6741	CCGATGTACTAAGCCAGGTC	219132	51328	CCATATTACACCAGTTGTTC	263719	95915	CGCATACCACCACGCCCGGC
174546	6742	CCCGATGTACTAAGCCAGGT	219133	51329	ACCATATTACACCAGTTGTT	263720	95916	ACGCATACCACCACGCCCGG
174547	6743	ACCCGATGTACTAAGCCAGG	219134	51330	CACCATATTACACCAGTTGT	263721	95917	CACGCATACCACCACGCCCG
174548	6744	AACCCGATGTACTAAGCCAG	219135	51331	GCACCATATTACACCAGTTG	263722	95918	CCACGCATACCACCACGCCC
174549	6745	GAACCCGATGTACTAAGCCA	219136	51332	GGCACCATATTACACCAGTT	263723	95919	ACCACGCATACCACCACGCC
174550	6746	TGAACCCGATGTACTAAGCC	219137	51333	TGGCACCATATTACACCAGT	263724	95920	CACCACGCATACCACCACGC
174551	6747	CTGAACCCGATGTACTAAGC	219138	51334	ATGGCACCATATTACACCAG	263725	95921	CCACCACGCATACCACCACG
174552	6748	TCTGAACCCGATGTACTAAG	219139	51335	CATGGCACCATATTACACCA	263726	95922	ACCACCACGCATACCACCAC
174553	6749	CTCTGAACCCGATGTACTAA	219140	51336	ACATGGCACCATATTACACC	263727	95923	TACCACCACGCATACCACCA
174554	6750	TCTCTGAACCCGATGTACTA	219141	51337	TACATGGCACCATATTACAC	263728	95924	TTACCACCACGCATACCACC
174555	6751	ATCTCTGAACCCGATGTACT	219142	51338	CTACATGGCACCATATTACA	263729	95925	ATTACCACCACGCATACCAC
174556	6752	GATCTCTGAACCCGATGTAC	219143	51339	CCTACATGGCACCATATTAC	263730	95926	GATTACCACCACGCATACCA
174557	6753	AGATCTCTGAACCCGATGTA	219144	51340	CCCTACATGGCACCATATTA	263731	95927	CGATTACCACCACGCATACC
174558	6754	AAGATCTCTGAACCCGATGT	219145	51341	TCCCTACATGGCACCATATT	263732	95928	GCGATTACCACCACGCATAC
174559	6755	AAAGATCTCTGAACCCGATG	219146	51342	TTCCCTACATGGCACCATAT	263733	95929	TGCGATTACCACCACGCATA
174560	6756	GAAAGATCTCTGAACCCGAT	219147	51343	TTTCCCTACATGGCACCATA	263734	95930	CTGCGATTACCACCACGCAT
174561	6757	GGAAAGATCTCTGAACCCGA	219148	51344	TTTTCCCTACATGGCACCAT	263735	95931	GCTGCGATTACCACCACGCA
174562	6758	TGGAAAGATCTCTGAACCCG	219149	51345	ATTTTCCCTACATGGCACCA	263736	95932	AGCTGCGATTACCACCACGC
174563	6759	CTGGAAAGATCTCTGAACCC	219150	51346	AATTTTCCCTACATGGCACC	263737	95933	TAGCTGCGATTACCACCACG
174564	6760	ACTGGAAAGATCTCTGAACC	219151	51347	TAATTTTCCCTACATGGCAC	263738	95934	GTAGCTGCGATTACCACCAC
174565	6761	AACTGGAAAGATCTCTGAAC	219152	51348	GTAATTTTCCCTACATGGCA	263739	95935	AGTAGCTGCGATTACCACCA
174566	6762	AAACTGGAAAGATCTCTGAA	219153	51349	TGTAATTTTCCCTACATGGC	263740	95936	GAGTAGCTGCGATTACCACC
174567	6763	TAAACTGGAAAGATCTCTGA	219154	51350	ATGTAATTTTCCCTACATGG	263741	95937	CGAGTAGCTGCGATTACCAC
174568	6764	GTAAACTGGAAAGATCTCTG	219155	51351	CATGTAATTTTCCCTACATG	263742	95938	CCGAGTAGCTGCGATTACCA
174569	6765	AGTAAACTGGAAAGATCTCT	219156	51352	ACATGTAATTTTCCCTACAT	263743	95939	CCCGAGTAGCTGCGATTACC
174570	6766	GAGTAAACTGGAAAGATCTC	219157	51353	CACATGTAATTTTCCCTACA	263744	95940	TCCCGAGTAGCTGCGATTAC

174571	6767	CGAGTAAACTGGAAAGATCT	219158	51354	ACACATGTAATTTTCCCTAC	263745	95941	CTCCCGAGTAGCTGCGATTA
174572	6768	ACGAGTAAACTGGAAAGATC	219159	51355	CACACATGTAATTTTCCCTA	263746	95942	CCTCCCGAGTAGCTGCGATT
174573	6769	AACGAGTAAACTGGAAAGAT	219160	51356	GCACACATGTAATTTTCCCT	263747	95943	GCCTCCCGAGTAGCTGCGAT
174574	6770	CAACGAGTAAACTGGAAAGA	219161	51357	TGCACACATGTAATTTTCCC	263748	95944	AGCCTCCCGAGTAGCTGCGA
174575	6771	TCAACGAGTAAACTGGAAAG	219162	51358	ATGCACACATGTAATTTTCC	263749	95945	CAGCCTCCCGAGTAGCTGCG
174576	6772	TTCAACGAGTAAACTGGAAA	219163	51359	TATGCACACATGTAATTTTC	263750	95946	TCAGCCTCCCGAGTAGCTGC
174577	6773	ATTCAACGAGTAAACTGGAA	219164	51360	CTATGCACACATGTAATTTT	263751	95947	CTCAGCCTCCCGAGTAGCTG
174578	6774	TATTCAACGAGTAAACTGGA	219165	51361	CCTATGCACACATGTAATTT	263752	95948	CCTCAGCCTCCCGAGTAGCT
174579	6775	TTATTCAACGAGTAAACTGG	219166	51362	TCCTATGCACACATGTAATT	263753	95949	GCCTCAGCCTCCCGAGTAGC
174580	6776	TTTATTCAACGAGTAAACTG	219167	51363	CTCCTATGCACACATGTAAT	263754	95950	TGCCTCAGCCTCCCGAGTAG
174581	6777	TTTTATTCAACGAGTAAACT	219168	51364	TCTCCTATGCACACATGTAA	263755	95951	GTGCCTCAGCCTCCCGAGTA
174582	6778	TTTTTATTCAACGAGTAAAC	219169	51365	CTCTCCTATGCACACATGTA	263756	95952	TGTGCCTCAGCCTCCCGAGT
174583	6779	CTTTTTATTCAACGAGTAAA	219170	51366	CCTCTCCTATGCACACATGT	263757	95953	TTGTGCCTCAGCCTCCCGAG
174584	6780	ACTTTTTATTCAACGAGTAA	219171	51367	CCCTCTCCTATGCACACATG	263758	95954	CTTGTGCCTCAGCCTCCCGA
174585	6781	CACTTTTTATTCAACGAGTA	219172	51368	CCCCTCTCCTATGCACACAT	263759	95955	CCTTGTGCCTCAGCCTCCCG
174586	6782	TCACTTTTTATTCAACGAGT	219173	51369	ACCCCTCTCCTATGCACACA	263760	95956	TCCTTGTGCCTCAGCCTCCC
174587	6783	CTCACTTTTTATTCAACGAG	219174	51370	GACCCCTCTCCTATGCACAC	263761	95957	ATCCTTGTGCCTCAGCCTCC
174588	6784	CCTCACTTTTTATTCAACGA	219175	51371	AGACCCCTCTCCTATGCACA	263762	95958	AATCCTTGTGCCTCAGCCTC
174589	6785	CCCTCACTTTTTATTCAACG	219176	51372	CAGACCCCTCTCCTATGCAC	263763	95959	CAATCCTTGTGCCTCAGCCT
174590	6786	GCCCTCACTTTTTATTCAAC	219177	51373	GCAGACCCCTCTCCTATGCA	263764	95960	GCAATCCTTGTGCCTCAGCC
174591	6787	AGCCCTCACTTTTTATTCAA	219178	51374	TGCAGACCCCTCTCCTATGC	263765	95961	AGCAATCCTTGTGCCTCAGC
174592	6788	CAGCCCTCACTTTTTATTCA	219179	51375	TTGCAGACCCCTCTCCTATG	263766	95962	AAGCAATCCTTGTGCCTCAG
174593	6789	TCAGCCCTCACTTTTTATTC	219180	51376	CTTGCAGACCCCTCTCCTAT	263767	95963	CAAGCAATCCTTGTGCCTCA
174594	6790	ATCAGCCCTCACTTTTTATT	219181	51377	CCTTGCAGACCCCTCTCCTA	263768	95964	TCAAGCAATCCTTGTGCCTC
174595	6791	GATCAGCCCTCACTTTTTAT	219182	51378	ACCTTGCAGACCCCTCTCCT	263769	95965	TTCAAGCAATCCTTGTGCCT
174596	6792	CGATCAGCCCTCACTTTTTA	219183	51379	AACCTTGCAGACCCCTCTCC	263770	95966	GTTCAAGCAATCCTTGTGCC
174597	6793	TCGATCAGCCCTCACTTTTT	219184	51380	CAACCTTGCAGACCCCTCTC	263771	95967	GGTTCAAGCAATCCTTGTGC
174598	6794	CTCGATCAGCCCTCACTTTT	219185	51381	ACAACCTTGCAGACCCCTCT	263772	95968	GGGTTCAAGCAATCCTTGTG
174599	6795	TCTCGATCAGCCCTCACTTT	219186	51382	CACAACCTTGCAGACCCCTC	263773	95969	GGGGTTCAAGCAATCCTTGT
174600	6796	TTCTCGATCAGCCCTCACTT	219187	51383	GCACAACCTTGCAGACCCCT	263774	95970	TGGGGTTCAAGCAATCCTTG
174601	6797	TTTCTCGATCAGCCCTCACT	219188	51384	GGCACAACCTTGCAGACCCC	263775	95971	CTGGGGTTCAAGCAATCCTT
174602	6798	CTTTCTCGATCAGCCCTCAC	219189	51385	GGGCACAACCTTGCAGACCC	263776	95972	TCTGGGGTTCAAGCAATCCT
174603	6799	ACTTTCTCGATCAGCCCTCA	219190	51386	AGGGCACAACCTTGCAGACC	263777	95973	CTCTGGGGTTCAAGCAATCC
174604	6800	TACTTTCTCGATCAGCCCTC	219191	51387	TAGGGCACAACCTTGCAGAC	263778	95974	CCTCTGGGGTTCAAGCAATC
174605	6801	TTACTTTCTCGATCAGCCCT	219192	51388	TTAGGGCACAACCTTGCAGA	263779	95975	GCCTCTGGGGTTCAAGCAAT
174606	6802	ATTACTTTCTCGATCAGCCC	219193	51389	CTTAGGGCACAACCTTGCAG	263780	95976	TGCCTCTGGGGTTCAAGCAA
174607	6803	CATTACTTTCTCGATCAGCC	219194	51390	TCTTAGGGCACAACCTTGCA	263781	95977	CTGCCTCTGGGGTTCAAGCA
174608	6804	CCATTACTTTCTCGATCAGC	219195	51391	ATCTTAGGGCACAACCTTGC	263782	95978	TCTGCCTCTGGGGTTCAAGC
174609	6805	GCCATTACTTTCTCGATCAG	219196	51392	CATCTTAGGGCACAACCTTG	263783	95979	CTCTGCCTCTGGGGTTCAAG
174610	6806	TGCCATTACTTTCTCGATCA	219197	51393	ACATCTTAGGGCACAACCTT	263784	95980	CCTCTGCCTCTGGGGTTCAA
174611	6807	CTGCCATTACTTTCTCGATC	219198	51394	AACATCTTAGGGCACAACCT	263785	95981	ACCTCTGCCTCTGGGGTTCA
174612	6808	ACTGCCATTACTTTCTCGAT	219199	51395	TAACATCTTAGGGCACAACC	263786	95982	AACCTCTGCCTCTGGGGTTC
174613	6809	GACTGCCATTACTTTCTCGA	219200	51396	CTAACATCTTAGGGCACAAC	263787	95983	CAACCTCTGCCTCTGGGGTT
174614	6810	TGACTGCCATTACTTTCTCG	219201	51397	TCTAACATCTTAGGGCACAA	263788	95984	ACAACCTCTGCCTCTGGGGT
174615	6811	CTGACTGCCATTACTTTCTC	219202	51398	CTCTAACATCTTAGGGCACA	263789	95985	TACAACCTCTGCCTCTGGGG
174616	6812	CCTGACTGCCATTACTTTCT	219203	51399	ACTCTAACATCTTAGGGCAC	263790	95986	CTACAACCTCTGCCTCTGGG
174617	6813	CCCTGACTGCCATTACTTTC	219204	51400	CACTCTAACATCTTAGGGCA	263791	95987	ACTACAACCTCTGCCTCTGG
174618	6814	TCCCTGACTGCCATTACTTT	219205	51401	CCACTCTAACATCTTAGGGC	263792	95988	AACTACAACCTCTGCCTCTG
174619	6815	TTCCCTGACTGCCATTACTT	219206	51402	ACCACTCTAACATCTTAGGG	263793	95989	TAACTACAACCTCTGCCTCT
174620	6816	CTTCCCTGACTGCCATTACT	219207	51403	AACCACTCTAACATCTTAGG	263794	95990	CTAACTACAACCTCTGCCTC
174621	6817	CCTTCCCTGACTGCCATTAC	219208	51404	GAACCACTCTAACATCTTAG	263795	95991	GCTAACTACAACCTCTGCCT
174622	6818	GCCTTCCCTGACTGCCATTA	219209	51405	GGAACCACTCTAACATCTTA	263796	95992	AGCTAACTACAACCTCTGCC
174623	6819	CGCCTTCCCTGACTGCCATT	219210	51406	AGGAACCACTCTAACATCTT	263797	95993	GAGCTAACTACAACCTCTGC
174624	6820	TCGCCTTCCCTGACTGCCAT	219211	51407	AAGGAACCACTCTAACATCT	263798	95994	GGAGCTAACTACAACCTCTG
174625	6821	TTCGCCTTCCCTGACTGCCA	219212	51408	AAAGGAACCACTCTAACATC	263799	95995	TGGAGCTAACTACAACCTCT
174626	6822	CTTCGCCTTCCCTGACTGCC	219213	51409	CAAAGGAACCACTCTAACAT	263800	95996	CTGGAGCTAACTACAACCTC
174627	6823	CCTTCGCCTTCCCTGACTGC	219214	51410	GCAAAGGAACCACTCTAACA	263801	95997	GCTGGAGCTAACTACAACCT
174628	6824	TCCTTCGCCTTCCCTGACTG	219215	51411	AGCAAAGGAACCACTCTAAC	263802	95998	AGCTGGAGCTAACTACAACC
174629	6825	CTCCTTCGCCTTCCCTGACT	219216	51412	AAGCAAAGGAACCACTCTAA	263803	95999	AAGCTGGAGCTAACTACAAC
174630	6826	CCTCCTTCGCCTTCCCTGAC	219217	51413	AAAGCAAAGGAACCACTCTA	263804	96000	CAAGCTGGAGCTAACTACAA
174631	6827	ACCTCCTTCGCCTTCCCTGA	219218	51414	AAAAGCAAAGGAACCACTCT	263805	96001	CCAAGCTGGAGCTAACTACA
174632	6828	TACCTCCTTCGCCTTCCCTG	219219	51415	GAAAAGCAAAGGAACCACTC	263806	96002	CCCAAGCTGGAGCTAACTAC
174633	6829	TTACCTCCTTCGCCTTCCCT	219220	51416	AGAAAAGCAAAGGAACCACT	263807	96003	GCCCAAGCTGGAGCTAACTA
174634	6830	TTTACCTCCTTCGCCTTCCC	219221	51417	GAGAAAAGCAAAGGAACCAC	263808	96004	CGCCCAAGCTGGAGCTAACT
174635	6831	CTTTACCTCCTTCGCCTTCC	219222	51418	AGAGAAAAGCAAAGGAACCA	263809	96005	TCGCCCAAGCTGGAGCTAAC
174636	6832	TCTTTACCTCCTTCGCCTTC	219223	51419	AAGAGAAAAGCAAAGGAACC	263810	96006	GTCGCCCAAGCTGGAGCTAA
174637	6833	TTCTTTACCTCCTTCGCCTT	219224	51420	AAAGAGAAAAGCAAAGGAAC	263811	96007	TGTCGCCCAAGCTGGAGCTA
174638	6834	CTTCTTTACCTCCTTCGCCT	219225	51421	AAAAGAGAAAAGCAAAGGAA	263812	96008	CTGTCGCCCAAGCTGGAGCT
174639	6835	TCTTCTTTACCTCCTTCGCC	219226	51422	TAAAAGAGAAAAGCAAAGGA	263813	96009	TCTGTCGCCCAAGCTGGAGC
174640	6836	CTCTTCTTTACCTCCTTCGC	219227	51423	ATAAAAGAGAAAAGCAAAGG	263814	96010	CTCTGTCGCCCAAGCTGGAG
174641	6837	TCTCTTCTTTACCTCCTTCG	219228	51424	TATAAAAGAGAAAAGCAAAG	263815	96011	GCTCTGTCGCCCAAGCTGGA
174642	6838	ATCTCTTCTTTACCTCCTTC	219229	51425	TTATAAAAGAGAAAAGCAAA	263816	96012	TGCTCTGTCGCCCAAGCTGG

174643	6839	AATCTCTTCTTTACCTCCTT	219230	51426	ATTATAAAAGAGAAAAGCAA	263817	96013	TTGCTCTGTCGCCCAAGCTG
174644	6840	AAATCTCTTCTTTACCTCCT	219231	51427	AATTATAAAAGAGAAAAGCA	263818	96014	CTTGCTCTGTCGCCCAAGCT
174645	6841	AAAATCTCTTCTTTACCTCC	219232	51428	AAATTATAAAAGAGAAAAGC	263819	96015	TCTTGCTCTGTCGCCCAAGC
174646	6842	TAAAATCTCTTCTTTACCTC	219233	51429	AAAATTATAAAAGAGAAAAG	263820	96016	GTCTTGCTCTGTCGCCCAAG
174647	6843	GTAAAATCTCTTCTTTACCT	219234	51430	CAAAATTATAAAAGAGAAAA	263821	96017	GGTCTTGCTCTGTCGCCCAA
174648	6844	TGTAAAATCTCTTCTTTACC	219235	51431	ACAAAATTATAAAAGAGAAA	263822	96018	GGGTCTTGCTCTGTCGCCCA
174649	6845	TTGTAAAATCTCTTCTTTAC	219236	51432	TACAAAATTATAAAAGAGAA	263823	96019	AGGGTCTTGCTCTGTCGCCC
174650	6846	TTTGTAAAATCTCTTCTTTA	219237	51433	ATACAAAATTATAAAAGAGA	263824	96020	CAGGGTCTTGCTCTGTCGCC
174651	6847	ATTTGTAAAATCTCTTCTTT	219238	51434	AATACAAAATTATAAAAGAG	263825	96021	ACAGGGTCTTGCTCTGTCGC
174652	6848	CATTTGTAAAATCTCTTCTT	219239	51435	AAATACAAAATTATAAAAGA	263826	96022	GACAGGGTCTTGCTCTGTCG
174653	6849	TCATTTGTAAAATCTCTTCT	219240	51436	CAAATACAAAATTATAAAAG	263827	96023	CGACAGGGTCTTGCTCTGTC
174654	6850	TTCATTTGTAAAATCTCTTC	219241	51437	TCAAATACAAAATTATAAAA	263828	96024	GCGACAGGGTCTTGCTCTGT
174655	6851	CTTCATTTGTAAAATCTCTT	219242	51438	GTCAAATACAAAATTATAAA	263829	96025	TGCGACAGGGTCTTGCTCTG
174656	6852	ACTTCATTTGTAAAATCTCT	219243	51439	AGTCAAATACAAAATTATAA	263830	96026	TTGCGACAGGGTCTTGCTCT
174657	6853	TACTTCATTTGTAAAATCTC	219244	51440	AAGTCAAATACAAAATTATA	263831	96027	TTTGCGACAGGGTCTTGCTC
174658	6854	TTACTTCATTTGTAAAATCT	219245	51441	AAAGTCAAATACAAAATTAT	263832	96028	TTTTGCGACAGGGTCTTGCT
174659	6855	ATTACTTCATTTGTAAAATC	219246	51442	AAAAGTCAAATACAAAATTA	263833	96029	TTTTTGCGACAGGGTCTTGC
174660	6856	AATTACTTCATTTGTAAAAT	219247	51443	TAAAAGTCAAATACAAAATT	263834	96030	ATTTTTGCGACAGGGTCTTG
174661	6857	GAATTACTTCATTTGTAAAA	219248	51444	TTAAAAGTCAAATACAAAAT	263835	96031	AATTTTTGCGACAGGGTCTT
174662	6858	TGAATTACTTCATTTGTAAA	219249	51445	TTTAAAAGTCAAATACAAAA	263836	96032	CAATTTTTGCGACAGGGTCT
174663	6859	TTGAATTACTTCATTTGTAA	219250	51446	ATTTAAAAGTCAAATACAAA	263837	96033	ACAATTTTTGCGACAGGGTC
174664	6860	GTTGAATTACTTCATTTGTA	219251	51447	TATTTAAAAGTCAAATACAA	263838	96034	AACAATTTTTGCGACAGGGT
174665	6861	TGTTGAATTACTTCATTTGT	219252	51448	TTATTTAAAAGTCAAATACA	263839	96035	AAACAATTTTTGCGACAGGG
174666	6862	CTGTTGAATTACTTCATTTG	219253	51449	CTTATTTAAAAGTCAAATAC	263840	96036	TAAACAATTTTTGCGACAGG
174667	6863	TCTGTTGAATTACTTCATTT	219254	51450	CCTTATTTAAAAGTCAAATA	263841	96037	TTAAACAATTTTTGCGACAG
174668	6864	CTCTGTTGAATTACTTCATT	219255	51451	TCCTTATTTAAAAGTCAAAT	263842	96038	TTTAAACAATTTTTGCGACA
174669	6865	ACTCTGTTGAATTACTTCAT	219256	51452	GTCCTTATTTAAAAGTCAAA	263843	96039	TTTTAAACAATTTTTGCGAC
174670	6866	CACTCTGTTGAATTACTTCA	219257	51453	GGTCCTTATTTAAAAGTCAA	263844	96040	TTTTTAAACAATTTTTGCGA
174671	6867	GCACTCTGTTGAATTACTTC	219258	51454	TGGTCCTTATTTAAAAGTCA	263845	96041	TTTTTTAAACAATTTTTGCG
174672	6868	AGCACTCTGTTGAATTACTT	219259	51455	ATGGTCCTTATTTAAAAGTC	263846	96042	GTTTTTTAAACAATTTTTGC
174673	6869	CAGCACTCTGTTGAATTACT	219260	51456	TATGGTCCTTATTTAAAAGT	263847	96043	TGTTTTTTAAACAATTTTTG
174674	6870	TCAGCACTCTGTTGAATTAC	219261	51457	TTATGGTCCTTATTTAAAAG	263848	96044	TTGTTTTTTAAACAATTTTT
174675	6871	GTCAGCACTCTGTTGAATTA	219262	51458	TTTATGGTCCTTATTTAAAA	263849	96045	TTTGTTTTTTAAACAATTTT
174676	6872	TGTCAGCACTCTGTTGAATT	219263	51459	ATTTATGGTCCTTATTTAAA	263850	96046	GTTTGTTTTTTAAACAATTT
174677	6873	ATGTCAGCACTCTGTTGAAT	219264	51460	GATTTATGGTCCTTATTTAA	263851	96047	GGTTTGTTTTTTAAACAATT
174678	6874	AATGTCAGCACTCTGTTGAA	219265	51461	TGATTTATGGTCCTTATTTA	263852	96048	GGGTTTGTTTTTTAAACAAT
174679	6875	CAATGTCAGCACTCTGTTGA	219266	51462	GTGATTTATGGTCCTTATTT	263853	96049	TGGGTTTGTTTTTTAAACAA
174680	6876	CCAATGTCAGCACTCTGTTG	219267	51463	AGTGATTTATGGTCCTTATT	263854	96050	TTGGGTTTGTTTTTTAAACA
174681	6877	ACCAATGTCAGCACTCTGTT	219268	51464	AAGTGATTTATGGTCCTTAT	263855	96051	TTTGGGTTTGTTTTTTAAAC
174682	6878	TACCAATGTCAGCACTCTGT	219269	51465	AAAGTGATTTATGGTCCTTA	263856	96052	TTTTGGGTTTGTTTTTTAAA
174683	6879	TTACCAATGTCAGCACTCTG	219270	51466	AAAAGTGATTTATGGTCCTT	263857	96053	ATTTTGGGTTTGTTTTTTAA
174684	6880	TTTACCAATGTCAGCACTCT	219271	51467	TAAAAGTGATTTATGGTCCT	263858	96054	AATTTTGGGTTTGTTTTTTA
174685	6881	GTTTACCAATGTCAGCACTC	219272	51468	ATAAAAGTGATTTATGGTCC	263859	96055	CAATTTTGGGTTTGTTTTTT
174686	6882	AGTTTACCAATGTCAGCACT	219273	51469	TATAAAAGTGATTTATGGTC	263860	96056	GCAATTTTGGGTTTGTTTTT
174687	6883	CAGTTTACCAATGTCAGCAC	219274	51470	TTATAAAAGTGATTTATGGT	263861	96057	AGCAATTTTGGGTTTGTTTT
174688	6884	CCAGTTTACCAATGTCAGCA	219275	51471	TTTATAAAAGTGATTTATGG	263862	96058	TAGCAATTTTGGGTTTGTTT
174689	6885	GCCAGTTTACCAATGTCAGC	219276	51472	TTTTATAAAAGTGATTTATG	263863	96059	GTAGCAATTTTGGGTTTGTT
174690	6886	TGCCAGTTTACCAATGTCAG	219277	51473	ATTTTATAAAAGTGATTTAT	263864	96060	AGTAGCAATTTTGGGTTTGT
174691	6887	TTGCCAGTTTACCAATGTCA	219278	51474	TATTTTATAAAAGTGATTTA	263865	96061	GAGTAGCAATTTTGGGTTTG
174692	6888	TTTGCCAGTTTACCAATGTC	219279	51475	GTATTTTATAAAAGTGATTT	263866	96062	AGAGTAGCAATTTTGGGTTT
174693	6889	GTTTGCCAGTTTACCAATGT	219280	51476	TGTATTTTATAAAAGTGATT	263867	96063	GAGAGTAGCAATTTTGGGTT
174694	6890	TGTTTGCCAGTTTACCAATG	219281	51477	ATGTATTTTATAAAAGTGAT	263868	96064	TGAGAGTAGCAATTTTGGGT
174695	6891	CTGTTTGCCAGTTTACCAAT	219282	51478	AATGTATTTTATAAAAGTGA	263869	96065	ATGAGAGTAGCAATTTTGGG
174696	6892	TCTGTTTGCCAGTTTACCAA	219283	51479	GAATGTATTTTATAAAAGTG	263870	96066	AATGAGAGTAGCAATTTTGG
174697	6893	ATCTGTTTGCCAGTTTACCA	219284	51480	AGAATGTATTTTATAAAAGT	263871	96067	CAATGAGAGTAGCAATTTTG
174698	6894	AATCTGTTTGCCAGTTTACC	219285	51481	GAGAATGTATTTTATAAAAG	263872	96068	CCAATGAGAGTAGCAATTTT
174699	6895	AAATCTGTTTGCCAGTTTAC	219286	51482	AGAGAATGTATTTTATAAAA	263873	96069	CCCAATGAGAGTAGCAATTT
174700	6896	GAAATCTGTTTGCCAGTTTA	219287	51483	GAGAGAATGTATTTTATAAA	263874	96070	ACCCAATGAGAGTAGCAATT
174701	6897	TGAAATCTGTTTGCCAGTTT	219288	51484	GGAGAGAATGTATTTTATAA	263875	96071	AACCCAATGAGAGTAGCAAT
174702	6898	CTGAAATCTGTTTGCCAGTT	219289	51485	TGGAGAGAATGTATTTTATA	263876	96072	GAACCCAATGAGAGTAGCAA
174703	6899	CCTGAAATCTGTTTGCCAGT	219290	51486	CTGGAGAGAATGTATTTTAT	263877	96073	GGAACCCAATGAGAGTAGCA
174704	6900	CCCTGAAATCTGTTTGCCAG	219291	51487	GCTGGAGAGAATGTATTTTA	263878	96074	AGGAACCCAATGAGAGTAGC
174705	6901	ACCCTGAAATCTGTTTGCCA	219292	51488	GGCTGGAGAGAATGTATTTT	263879	96075	AAGGAACCCAATGAGAGTAG
174706	6902	CACCCTGAAATCTGTTTGCC	219293	51489	GGGCTGGAGAGAATGTATTT	263880	96076	AAAGGAACCCAATGAGAGTA
174707	6903	CCACCCTGAAATCTGTTTGC	219294	51490	GGGGCTGGAGAGAATGTATT	263881	96077	CAAAGGAACCCAATGAGAGT
174708	6904	ACCACCCTGAAATCTGTTTG	219295	51491	AGGGGCTGGAGAGAATGTAT	263882	96078	GCAAAGGAACCCAATGAGAG
174709	6905	AACCACCCTGAAATCTGTTT	219296	51492	TAGGGGCTGGAGAGAATGTA	263883	96079	GGCAAAGGAACCCAATGAGA
174710	6906	CAACCACCCTGAAATCTGTT	219297	51493	GTAGGGGCTGGAGAGAATGT	263884	96080	GGGCAAAGGAACCCAATGAG
174711	6907	CCAACCACCCTGAAATCTGT	219298	51494	AGTAGGGGCTGGAGAGAATG	263885	96081	TGGGCAAAGGAACCCAATGA
174712	6908	ACCAACCACCCTGAAATCTG	219299	51495	TAGTAGGGGCTGGAGAGAAT	263886	96082	ATGGGCAAAGGAACCCAATG
174713	6909	AACCAACCACCCTGAAATCT	219300	51496	GTAGTAGGGGCTGGAGAGAA	263887	96083	AATGGGCAAAGGAACCCAAT
174714	6910	CAACCAACCACCCTGAAATC	219301	51497	AGTAGTAGGGGCTGGAGAGA	263888	96084	GAATGGGCAAAGGAACCCAA

174715	6911	TCAACCAACCACCCTGAAAT	219302	51498	GAGTAGTAGGGGCTGGAGAG	263889	96085	GGAATGGGCAAAGGAACCCA
174716	6912	CTCAACCAACCACCCTGAAA	219303	51499	GGAGTAGTAGGGGCTGGAGA	263890	96086	AGGAATGGGCAAAGGAACCC
174717	6913	TCTCAACCAACCACCCTGAA	219304	51500	AGGAGTAGTAGGGGCTGGAG	263891	96087	CAGGAATGGGCAAAGGAACC
174718	6914	CTCTCAACCAACCACCCTGA	219305	51501	AAGGAGTAGTAGGGGCTGGA	263892	96088	TCAGGAATGGGCAAAGGAAC
174719	6915	ACTCTCAACCAACCACCCTG	219306	51502	AAAGGAGTAGTAGGGGCTGG	263893	96089	ATCAGGAATGGGCAAAGGAA
174720	6916	TACTCTCAACCAACCACCCT	219307	51503	TAAAGGAGTAGTAGGGGCTG	263894	96090	AATCAGGAATGGGCAAAGGA
174721	6917	CTACTCTCAACCAACCACCC	219308	51504	TTAAAGGAGTAGTAGGGGCT	263895	96091	AAATCAGGAATGGGCAAAGG
174722	6918	TCTACTCTCAACCAACCACC	219309	51505	TTTAAAGGAGTAGTAGGGGC	263896	96092	AAAATCAGGAATGGGCAAAG
174723	6919	CTCTACTCTCAACCAACCAC	219310	51506	CTTTAAAGGAGTAGTAGGGG	263897	96093	CAAAATCAGGAATGGGCAAA
174724	6920	ACTCTACTCTCAACCAACCA	219311	51507	TCTTTAAAGGAGTAGTAGGG	263898	96094	CCAAAATCAGGAATGGGCAA
174725	6921	TACTCTACTCTCAACCAACC	219312	51508	TTCTTTAAAGGAGTAGTAGG	263899	96095	GCCAAAATCAGGAATGGGCA
174726	6922	CTACTCTACTCTCAACCAAC	219313	51509	ATTCTTTAAAGGAGTAGTAG	263900	96096	TGCCAAAATCAGGAATGGGC
174727	6923	TCTACTCTACTCTCAACCAA	219314	51510	TATTCTTTAAAGGAGTAGTA	263901	96097	TTGCCAAAATCAGGAATGGG
174728	6924	TTCTACTCTACTCTCAACCA	219315	51511	TTATTCTTTAAAGGAGTAGT	263902	96098	CTTGCCAAAATCAGGAATGG
174729	6925	TTTCTACTCTACTCTCAACC	219316	51512	CTTATTCTTTAAAGGAGTAG	263903	96099	TCTTGCCAAAATCAGGAATG
174730	6926	TTTTCTACTCTACTCTCAAC	219317	51513	TCTTATTCTTTAAAGGAGTA	263904	96100	CTCTTGCCAAAATCAGGAAT
174731	6927	CTTTTCTACTCTACTCTCAA	219318	51514	CTCTTATTCTTTAAAGGAGT	263905	96101	TCTCTTGCCAAAATCAGGAA
174732	6928	CCTTTTCTACTCTACTCTCA	219319	51515	ACTCTTATTCTTTAAAGGAG	263906	96102	TTCTCTTGCCAAAATCAGGA
174733	6929	TCCTTTTCTACTCTACTCTC	219320	51516	CACTCTTATTCTTTAAAGGA	263907	96103	TTTCTCTTGCCAAAATCAGG
174734	6930	ATCCTTTTCTACTCTACTCT	219321	51517	CCACTCTTATTCTTTAAAGG	263908	96104	ATTTCTCTTGCCAAAATCAG
174735	6931	AATCCTTTTCTACTCTACTC	219322	51518	ACCACTCTTATTCTTTAAAG	263909	96105	CATTTCTCTTGCCAAAATCA
174736	6932	TAATCCTTTTCTACTCTACT	219323	51519	AACCACTCTTATTCTTTAAA	263910	96106	GCATTTCTCTTGCCAAAATC
174737	6933	TTAATCCTTTTCTACTCTAC	219324	51520	AAACCACTCTTATTCTTTAA	263911	96107	AGCATTTCTCTTGCCAAAAT
174738	6934	TTTAATCCTTTTCTACTCTA	219325	51521	CAAACCACTCTTATTCTTTA	263912	96108	AAGCATTTCTCTTGCCAAAA
174739	6935	ATTTAATCCTTTTCTACTCT	219326	51522	GCAAACCACTCTTATTCTTT	263913	96109	GAAGCATTTCTCTTGCCAAA
174740	6936	TATTTAATCCTTTTCTACTC	219327	51523	GGCAAACCACTCTTATTCTT	263914	96110	GGAAGCATTTCTCTTGCCAA
174741	6937	TTATTTAATCCTTTTCTACT	219328	51524	GGGCAAACCACTCTTATTCT	263915	96111	TGGAAGCATTTCTCTTGCCA
174742	6938	TTTATTTAATCCTTTTCTAC	219329	51525	TGGGCAAACCACTCTTATTC	263916	96112	CTGGAAGCATTTCTCTTGCC
174743	6939	CTTTATTTAATCCTTTTCTA	219330	51526	TTGGGCAAACCACTCTTATT	263917	96113	TCTGGAAGCATTTCTCTTGC
174744	6940	GCTTTATTTAATCCTTTTCT	219331	51527	CTTGGGCAAACCACTCTTAT	263918	96114	ATCTGGAAGCATTTCTCTTG
174745	6941	TGCTTTATTTAATCCTTTTC	219332	51528	TCTTGGGCAAACCACTCTTA	263919	96115	AATCTGGAAGCATTTCTCTT
174746	6942	TTGCTTTATTTAATCCTTTT	219333	51529	TTCTTGGGCAAACCACTCTT	263920	96116	CAATCTGGAAGCATTTCTCT
174747	6943	TTTGCTTTATTTAATCCTTT	219334	51530	TTTCTTGGGCAAACCACTCT	263921	96117	GCAATCTGGAAGCATTTCTC
174748	6944	GTTTGCTTTATTTAATCCTT	219335	51531	CTTTCTTGGGCAAACCACTC	263922	96118	GGCAATCTGGAAGCATTTCT
174749	6945	AGTTTGCTTTATTTAATCCT	219336	51532	TCTTTCTTGGGCAAACCACT	263923	96119	GGGCAATCTGGAAGCATTTC
174750	6946	AAGTTTGCTTTATTTAATCC	219337	51533	GTCTTTCTTGGGCAAACCAC	263924	96120	AGGGCAATCTGGAAGCATTT
174751	6947	CAAGTTTGCTTTATTTAATC	219338	51534	TGTCTTTCTTGGGCAAACCA	263925	96121	CAGGGCAATCTGGAAGCATT
174752	6948	ACAAGTTTGCTTTATTTAAT	219339	51535	CTGTCTTTCTTGGGCAAACC	263926	96122	TCAGGGCAATCTGGAAGCAT
174753	6949	CACAAGTTTGCTTTATTTAA	219340	51536	ACTGTCTTTCTTGGGCAAAC	263927	96123	ATCAGGGCAATCTGGAAGCA
174754	6950	CCACAAGTTTGCTTTATTTA	219341	51537	AACTGTCTTTCTTGGGCAAA	263928	96124	GATCAGGGCAATCTGGAAGC
174755	6951	ACCACAAGTTTGCTTTATTT	219342	51538	AAACTGTCTTTCTTGGGCAA	263929	96125	AGATCAGGGCAATCTGGAAG
174756	6952	CACCACAAGTTTGCTTTATT	219343	51539	AAAACTGTCTTTCTTGGGCA	263930	96126	CAGATCAGGGCAATCTGGAA
174757	6953	ACACCACAAGTTTGCTTTAT	219344	51540	AAAAACTGTCTTTCTTGGGC	263931	96127	CCAGATCAGGGCAATCTGGA
174758	6954	TACACCACAAGTTTGCTTTA	219345	51541	AAAAAACTGTCTTTCTTGGG	263932	96128	CCCAGATCAGGGCAATCTGG
174759	6955	GTACACCACAAGTTTGCTTT	219346	51542	AAAAAAACTGTCTTTCTTGG	263933	96129	ACCCAGATCAGGGCAATCTG
174760	6956	AGTACACCACAAGTTTGCTT	219347	51543	AAAAAAAACTGTCTTTCTTG	263934	96130	TACCCAGATCAGGGCAATCT
174761	6957	CAGTACACCACAAGTTTGCT	219348	51544	CAAAAAAAACTGTCTTTCTT	263935	96131	CTACCCAGATCAGGGCAATC
174762	6958	TCAGTACACCACAAGTTTGC	219349	51545	GCAAAAAAAACTGTCTTTCT	263936	96132	CCTACCCAGATCAGGGCAAT
174763	6959	TTCAGTACACCACAAGTTTG	219350	51546	AGCAAAAAAAACTGTCTTTC	263937	96133	TCCTACCCAGATCAGGGCAA
174764	6960	ATTCAGTACACCACAAGTTT	219351	51547	GAGCAAAAAAAACTGTCTTT	263938	96134	GTCCTACCCAGATCAGGGCA
174765	6961	GATTCAGTACACCACAAGTT	219352	51548	AGAGCAAAAAAAACTGTCTT	263939	96135	TGTCCTACCCAGATCAGGGC
174766	6962	AGATTCAGTACACCACAAGT	219353	51549	CAGAGCAAAAAAAACTGTCT	263940	96136	CTGTCCTACCCAGATCAGGG
174767	6963	AAGATTCAGTACACCACAAG	219354	51550	CCAGAGCAAAAAAAACTGTC	263941	96137	GCTGTCCTACCCAGATCAGG
174768	6964	TAAGATTCAGTACACCACAA	219355	51551	ACCAGAGCAAAAAAAACTGT	263942	96138	TGCTGTCCTACCCAGATCAG
174769	6965	CTAAGATTCAGTACACCACA	219356	51552	AACCAGAGCAAAAAAAACTG	263943	96139	ATGCTGTCCTACCCAGATCA
174770	6966	CCTAAGATTCAGTACACCAC	219357	51553	AAACCAGAGCAAAAAAAACT	263944	96140	GATGCTGTCCTACCCAGATC
174771	6967	TCCTAAGATTCAGTACACCA	219358	51554	AAAACCAGAGCAAAAAAAAC	263945	96141	TGATGCTGTCCTACCCAGAT
174772	6968	TTCCTAAGATTCAGTACACC	219359	51555	GAAAACCAGAGCAAAAAAAA	263946	96142	GTGATGCTGTCCTACCCAGA
174773	6969	ATTCCTAAGATTCAGTACAC	219360	51556	AGAAAACCAGAGCAAAAAAA	263947	96143	CGTGATGCTGTCCTACCCAG
174774	6970	AATTCCTAAGATTCAGTACA	219361	51557	AAGAAAACCAGAGCAAAAAA	263948	96144	GCGTGATGCTGTCCTACCCA
174775	6971	GAATTCCTAAGATTCAGTAC	219362	51558	CAAGAAAACCAGAGCAAAAA	263949	96145	GGCGTGATGCTGTCCTACCC
174776	6972	GGAATTCCTAAGATTCAGTA	219363	51559	TCAAGAAAACCAGAGCAAAA	263950	96146	TGGCGTGATGCTGTCCTACC
174777	6973	TGGAATTCCTAAGATTCAGT	219364	51560	ATCAAGAAAACCAGAGCAAA	263951	96147	ATGGCGTGATGCTGTCCTAC
174778	6974	ATGGAATTCCTAAGATTCAG	219365	51561	AATCAAGAAAACCAGAGCAA	263952	96148	TATGGCGTGATGCTGTCCTA
174779	6975	CATGGAATTCCTAAGATTCA	219366	51562	GAATCAAGAAAACCAGAGCA	263953	96149	CTATGGCGTGATGCTGTCCT
174780	6976	ACATGGAATTCCTAAGATTC	219367	51563	AGAATCAAGAAAACCAGAGC	263954	96150	GCTATGGCGTGATGCTGTCC
174781	6977	TACATGGAATTCCTAAGATT	219368	51564	CAGAATCAAGAAAACCAGAG	263955	96151	TGCTATGGCGTGATGCTGTC
174782	6978	ATACATGGAATTCCTAAGAT	219369	51565	TCAGAATCAAGAAAACCAGA	263956	96152	TTGCTATGGCGTGATGCTGT
174783	6979	GATACATGGAATTCCTAAGA	219370	51566	GTCAGAATCAAGAAAACCAG	263957	96153	GTTGCTATGGCGTGATGCTG
174784	6980	GGATACATGGAATTCCTAAG	219371	51567	TGTCAGAATCAAGAAAACCA	263958	96154	TGTTGCTATGGCGTGATGCT
174785	6981	TGGATACATGGAATTCCTAA	219372	51568	ATGTCAGAATCAAGAAAACC	263959	96155	GTGTTGCTATGGCGTGATGC
174786	6982	TTGGATACATGGAATTCCTA	219373	51569	GATGTCAGAATCAAGAAAAC	263960	96156	AGTGTTGCTATGGCGTGATG

174787	6983	ATTGGATACATGGAATTCCT	219374	51570	TGATGTCAGAATCAAGAAAA	263961	96157	CAGTGTTGCTATGGCGTGAT
174788	6984	TATTGGATACATGGAATTCC	219375	51571	CTGATGTCAGAATCAAGAAA	263962	96158	GCAGTGTTGCTATGGCGTGA
174789	6985	TTATTGGATACATGGAATTC	219376	51572	TCTGATGTCAGAATCAAGAA	263963	96159	GGCAGTGTTGCTATGGCGTG
174790	6986	CTTATTGGATACATGGAATT	219377	51573	CTCTGATGTCAGAATCAAGA	263964	96160	GGGCAGTGTTGCTATGGCGT
174791	6987	ACTTATTGGATACATGGAAT	219378	51574	CCTCTGATGTCAGAATCAAG	263965	96161	GGGGCAGTGTTGCTATGGCG
174792	6988	TACTTATTGGATACATGGAA	219379	51575	TCCTCTGATGTCAGAATCAA	263966	96162	CGGGGCAGTGTTGCTATGGC
174793	6989	ATACTTATTGGATACATGGA	219380	51576	TTCCTCTGATGTCAGAATCA	263967	96163	ACGGGGCAGTGTTGCTATGG
174794	6990	TATACTTATTGGATACATGG	219381	51577	TTTCCTCTGATGTCAGAATC	263968	96164	CACGGGGCAGTGTTGCTATG
174795	6991	CTATACTTATTGGATACATG	219382	51578	GTTTCCTCTGATGTCAGAAT	263969	96165	TCACGGGGCAGTGTTGCTAT
174796	6992	ACTATACTTATTGGATACAT	219383	51579	AGTTTCCTCTGATGTCAGAA	263970	96166	CTCACGGGGCAGTGTTGCTA
174797	6993	GACTATACTTATTGGATACA	219384	51580	CAGTTTCCTCTGATGTCAGA	263971	96167	GCTCACGGGGCAGTGTTGCT
174798	6994	TGACTATACTTATTGGATAC	219385	51581	GCAGTTTCCTCTGATGTCAG	263972	96168	AGCTCACGGGGCAGTGTTGC
174799	6995	ATGACTATACTTATTGGATA	219386	51582	AGCAGTTTCCTCTGATGTCA	263973	96169	GAGCTCACGGGGCAGTGTTG
174800	6996	AATGACTATACTTATTGGAT	219387	51583	AAGCAGTTTCCTCTGATGTC	263974	96170	TGAGCTCACGGGGCAGTGTT
174801	6997	AAATGACTATACTTATTGGA	219388	51584	GAAGCAGTTTCCTCTGATGT	263975	96171	GTGAGCTCACGGGGCAGTGT
174802	6998	TAAATGACTATACTTATTGG	219389	51585	AGAAGCAGTTTCCTCTGATG	263976	96172	AGTGAGCTCACGGGGCAGTG
174803	6999	ATAAATGACTATACTTATTG	219390	51586	GAGAAGCAGTTTCCTCTGAT	263977	96173	CAGTGAGCTCACGGGGCAGT
174804	7000	CATAAATGACTATACTTATT	219391	51587	TGAGAAGCAGTTTCCTCTGA	263978	96174	GCAGTGAGCTCACGGGGCAG
174805	7001	TCATAAATGACTATACTTAT	219392	51588	ATGAGAAGCAGTTTCCTCTG	263979	96175	GGCAGTGAGCTCACGGGGCA
174806	7002	TTCATAAATGACTATACTTA	219393	51589	GATGAGAAGCAGTTTCCTCT	263980	96176	GGGCAGTGAGCTCACGGGGC
174807	7003	ATTCATAAATGACTATACTT	219394	51590	GGATGAGAAGCAGTTTCCTC	263981	96177	GGGGCAGTGAGCTCACGGGG
174808	7004	AATTCATAAATGACTATACT	219395	51591	TGGATGAGAAGCAGTTTCCT	263982	96178	GGGGGCAGTGAGCTCACGGG
174809	7005	TAATTCATAAATGACTATAC	219396	51592	GTGGATGAGAAGCAGTTTCC	263983	96179	AGGGGGCAGTGAGCTCACGG
174810	7006	TTAATTCATAAATGACTATA	219397	51593	AGTGGATGAGAAGCAGTTTC	263984	96180	GAGGGGGCAGTGAGCTCACG
174811	7007	ATTAATTCATAAATGACTAT	219398	51594	AAGTGGATGAGAAGCAGTTT	263985	96181	TGAGGGGGCAGTGAGCTCAC
174812	7008	TATTAATTCATAAATGACTA	219399	51595	CAAGTGGATGAGAAGCAGTT	263986	96182	TTGAGGGGGCAGTGAGCTCA
174813	7009	TTATTAATTCATAAATGACT	219400	51596	CCAAGTGGATGAGAAGCAGT	263987	96183	GTTGAGGGGGCAGTGAGCTC
174814	7010	TTTATTAATTCATAAATGAC	219401	51597	CCCAAGTGGATGAGAAGCAG	263988	96184	AGTTGAGGGGGCAGTGAGCT
174815	7011	ATTTATTAATTCATAAATGA	219402	51598	CCCCAAGTGGATGAGAAGCA	263989	96185	TAGTTGAGGGGGCAGTGAGC
174816	7012	AATTTATTAATTCATAAATG	219403	51599	GCCCCAAGTGGATGAGAAGC	263990	96186	CTAGTTGAGGGGGCAGTGAG
174817	7013	GAATTTATTAATTCATAAAT	219404	51600	AGCCCCAAGTGGATGAGAAG	263991	96187	GCTAGTTGAGGGGGCAGTGA
174818	7014	CGAATTTATTAATTCATAAA	219405	51601	GAGCCCCAAGTGGATGAGAA	263992	96188	AGCTAGTTGAGGGGGCAGTG
174819	7015	CCGAATTTATTAATTCATAA	219406	51602	AGAGCCCCAAGTGGATGAGA	263993	96189	AAGCTAGTTGAGGGGGCAGT
174820	7016	GCCGAATTTATTAATTCATA	219407	51603	CAGAGCCCCAAGTGGATGAG	263994	96190	CAAGCTAGTTGAGGGGGCAG
174821	7017	GGCCGAATTTATTAATTCAT	219408	51604	CCAGAGCCCCAAGTGGATGA	263995	96191	ACAAGCTAGTTGAGGGGGCA
174822	7018	AGGCCGAATTTATTAATTCA	219409	51605	CCCAGAGCCCCAAGTGGATG	263996	96192	CACAAGCTAGTTGAGGGGGC
174823	7019	TAGGCCGAATTTATTAATTC	219410	51606	ACCCAGAGCCCCAAGTGGAT	263997	96193	CCACAAGCTAGTTGAGGGGG
174824	7020	TTAGGCCGAATTTATTAATT	219411	51607	AACCCAGAGCCCCAAGTGGA	263998	96194	ACCACAAGCTAGTTGAGGGG
174825	7021	CTTAGGCCGAATTTATTAAT	219412	51608	GAACCCAGAGCCCCAAGTGG	263999	96195	GACCACAAGCTAGTTGAGGG
174826	7022	TCTTAGGCCGAATTTATTAA	219413	51609	TGAACCCAGAGCCCCAAGTG	264000	96196	GGACCACAAGCTAGTTGAGG
174827	7023	TTCTTAGGCCGAATTTATTA	219414	51610	CTGAACCCAGAGCCCCAAGT	264001	96197	AGGACCACAAGCTAGTTGAG
174828	7024	CTTCTTAGGCCGAATTTATT	219415	51611	CCTGAACCCAGAGCCCCAAG	264002	96198	AAGGACCACAAGCTAGTTGA
174829	7025	GCTTCTTAGGCCGAATTTAT	219416	51612	CCCTGAACCCAGAGCCCCAA	264003	96199	CAAGGACCACAAGCTAGTTG
174830	7026	GGCTTCTTAGGCCGAATTTA	219417	51613	CCCCTGAACCCAGAGCCCCA	264004	96200	CCAAGGACCACAAGCTAGTT
174831	7027	AGGCTTCTTAGGCCGAATTT	219418	51614	TCCCCTGAACCCAGAGCCCC	264005	96201	ACCAAGGACCACAAGCTAGT
174832	7028	AAGGCTTCTTAGGCCGAATT	219419	51615	ATCCCCTGAACCCAGAGCCC	264006	96202	AACCAAGGACCACAAGCTAG
174833	7029	GAAGGCTTCTTAGGCCGAAT	219420	51616	AATCCCCTGAACCCAGAGCC	264007	96203	TAACCAAGGACCACAAGCTA
174834	7030	AGAAGGCTTCTTAGGCCGAA	219421	51617	GAATCCCCTGAACCCAGAGC	264008	96204	TTAACCAAGGACCACAAGCT
174835	7031	AAGAAGGCTTCTTAGGCCGA	219422	51618	TGAATCCCCTGAACCCAGAG	264009	96205	ATTAACCAAGGACCACAAGC
174836	7032	TAAGAAGGCTTCTTAGGCCG	219423	51619	ATGAATCCCCTGAACCCAGA	264010	96206	CATTAACCAAGGACCACAAG
174837	7033	ATAAGAAGGCTTCTTAGGCC	219424	51620	AATGAATCCCCTGAACCCAG	264011	96207	ACATTAACCAAGGACCACAA
174838	7034	GATAAGAAGGCTTCTTAGGC	219425	51621	AAATGAATCCCCTGAACCCA	264012	96208	GACATTAACCAAGGACCACA
174839	7035	CGATAAGAAGGCTTCTTAGG	219426	51622	GAAATGAATCCCCTGAACCC	264013	96209	TGACATTAACCAAGGACCAC
174840	7036	GCGATAAGAAGGCTTCTTAG	219427	51623	TGAAATGAATCCCCTGAACC	264014	96210	CTGACATTAACCAAGGACCA
174841	7037	AGCGATAAGAAGGCTTCTTA	219428	51624	CTGAAATGAATCCCCTGAAC	264015	96211	ACTGACATTAACCAAGGACC
174842	7038	AAGCGATAAGAAGGCTTCTT	219429	51625	CCTGAAATGAATCCCCTGAA	264016	96212	AACTGACATTAACCAAGGAC
174843	7039	TAAGCGATAAGAAGGCTTCT	219430	51626	GCCTGAAATGAATCCCCTGA	264017	96213	AAACTGACATTAACCAAGGA
174844	7040	TTAAGCGATAAGAAGGCTTC	219431	51627	TGCCTGAAATGAATCCCCTG	264018	96214	GAAACTGACATTAACCAAGG
174845	7041	TTTAAGCGATAAGAAGGCTT	219432	51628	CTGCCTGAAATGAATCCCCT	264019	96215	AGAAACTGACATTAACCAAG
174846	7042	ATTTAAGCGATAAGAAGGCT	219433	51629	TCTGCCTGAAATGAATCCCC	264020	96216	AAGAAACTGACATTAACCAA
174847	7043	GATTTAAGCGATAAGAAGGC	219434	51630	ATCTGCCTGAAATGAATCCC	264021	96217	AAAGAAACTGACATTAACCA
174848	7044	TGATTTAAGCGATAAGAAGG	219435	51631	AATCTGCCTGAAATGAATCC	264022	96218	AAAAGAAACTGACATTAACC
174849	7045	TTGATTTAAGCGATAAGAAG	219436	51632	TAATCTGCCTGAAATGAATC	264023	96219	AAAAAGAAACTGACATTAAC
174850	7046	CTTGATTTAAGCGATAAGAA	219437	51633	TTAATCTGCCTGAAATGAAT	264024	96220	AAAAAAGAAACTGACATTAA
174851	7047	TCTTGATTTAAGCGATAAGA	219438	51634	TTTAATCTGCCTGAAATGAA	264025	96221	CAAAAAAGAAACTGACATTA
174852	7048	GTCTTGATTTAAGCGATAAG	219439	51635	CTTTAATCTGCCTGAAATGA	264026	96222	TCAAAAAAGAAACTGACATT
174853	7049	AGTCTTGATTTAAGCGATAA	219440	51636	ACTTTAATCTGCCTGAAATG	264027	96223	CTCAAAAAAGAAACTGACAT
174854	7050	TAGTCTTGATTTAAGCGATA	219441	51637	CACTTTAATCTGCCTGAAAT	264028	96224	ACTCAAAAAAGAAACTGACA
174855	7051	TTAGTCTTGATTTAAGCGAT	219442	51638	CCACTTTAATCTGCCTGAAA	264029	96225	AACTCAAAAAAGAAACTGAC
174856	7052	CTTAGTCTTGATTTAAGCGA	219443	51639	ACCACTTTAATCTGCCTGAA	264030	96226	AAACTCAAAAAAGAAACTGA
174857	7053	ACTTAGTCTTGATTTAAGCG	219444	51640	CACCACTTTAATCTGCCTGA	264031	96227	CAAACTCAAAAAAGAAACTG
174858	7054	TACTTAGTCTTGATTTAAGC	219445	51641	TCACCACTTTAATCTGCCTG	264032	96228	ACAAACTCAAAAAAGAAACT

174859	7055	TTACTTAGTCTTGATTTAAG	219446	51642	GTCACCACTTTAATCTGCCT	264033	96229	CACAAACTCAAAAAAGAAAC
174860	7056	GTTACTTAGTCTTGATTTAA	219447	51643	GGTCACCACTTTAATCTGCC	264034	96230	ACACAAACTCAAAAAAGAAA
174861	7057	TGTTACTTAGTCTTGATTTA	219448	51644	TGGTCACCACTTTAATCTGC	264035	96231	AACACAAACTCAAAAAAGAA
174862	7058	TTGTTACTTAGTCTTGATTT	219449	51645	CTGGTCACCACTTTAATCTG	264036	96232	TAACACAAACTCAAAAAAGA
174863	7059	ATTGTTACTTAGTCTTGATT	219450	51646	CCTGGTCACCACTTTAATCT	264037	96233	ATAACACAAACTCAAAAAAG
174864	7060	TATTGTTACTTAGTCTTGAT	219451	51647	CCCTGGTCACCACTTTAATC	264038	96234	CATAACACAAACTCAAAAAA
174865	7061	ATATTGTTACTTAGTCTTGA	219452	51648	CCCCTGGTCACCACTTTAAT	264039	96235	ACATAACACAAACTCAAAAA
174866	7062	TATATTGTTACTTAGTCTTG	219453	51649	GCCCCTGGTCACCACTTTAA	264040	96236	GACATAACACAAACTCAAAA
174867	7063	ATATATTGTTACTTAGTCTT	219454	51650	TGCCCCTGGTCACCACTTTA	264041	96237	AGACATAACACAAACTCAAA
174868	7064	GATATATTGTTACTTAGTCT	219455	51651	ATGCCCCTGGTCACCACTTT	264042	96238	TAGACATAACACAAACTCAA
174869	7065	TGATATATTGTTACTTAGTC	219456	51652	AATGCCCCTGGTCACCACTT	264043	96239	TTAGACATAACACAAACTCA
174870	7066	CTGATATATTGTTACTTAGT	219457	51653	GAATGCCCCTGGTCACCACT	264044	96240	CTTAGACATAACACAAACTC
174871	7067	ACTGATATATTGTTACTTAG	219458	51654	CGAATGCCCCTGGTCACCAC	264045	96241	CCTTAGACATAACACAAACT
174872	7068	AACTGATATATTGTTACTTA	219459	51655	ACGAATGCCCCTGGTCACCA	264046	96242	CCCTTAGACATAACACAAAC
174873	7069	AAACTGATATATTGTTACTT	219460	51656	CACGAATGCCCCTGGTCACC	264047	96243	ACCCTTAGACATAACACAAA
174874	7070	AAAACTGATATATTGTTACT	219461	51657	CCACGAATGCCCCTGGTCAC	264048	96244	GACCCTTAGACATAACACAA
174875	7071	TAAAACTGATATATTGTTAC	219462	51658	TCCACGAATGCCCCTGGTCA	264049	96245	TGACCCTTAGACATAACACA
174876	7072	TTAAAACTGATATATTGTTA	219463	51659	GTCCACGAATGCCCCTGGTC	264050	96246	ATGACCCTTAGACATAACAC
174877	7073	TTTAAAACTGATATATTGTT	219464	51660	TGTCCACGAATGCCCCTGGT	264051	96247	GATGACCCTTAGACATAACA
174878	7074	TTTTAAAACTGATATATTGT	219465	51661	GTGTCCACGAATGCCCCTGG	264052	96248	AGATGACCCTTAGACATAAC
174879	7075	TTTTTAAAACTGATATATTG	219466	51662	TGTGTCCACGAATGCCCCTG	264053	96249	CAGATGACCCTTAGACATAA
174880	7076	CTTTTTAAAACTGATATATT	219467	51663	CTGTGTCCACGAATGCCCCT	264054	96250	GCAGATGACCCTTAGACATA
174881	7077	ACTTTTTAAAACTGATATAT	219468	51664	CCTGTGTCCACGAATGCCCC	264055	96251	AGCAGATGACCCTTAGACAT
174882	7078	GACTTTTTAAAACTGATATA	219469	51665	CCCTGTGTCCACGAATGCCC	264056	96252	CAGCAGATGACCCTTAGACA
174883	7079	TGACTTTTTAAAACTGATAT	219470	51666	TCCCTGTGTCCACGAATGCC	264057	96253	CCAGCAGATGACCCTTAGAC
174884	7080	ATGACTTTTTAAAACTGATA	219471	51667	CTCCCTGTGTCCACGAATGC	264058	96254	CCCAGCAGATGACCCTTAGA
174885	7081	AATGACTTTTTAAAACTGAT	219472	51668	CCTCCCTGTGTCCACGAATG	264059	96255	ACCCAGCAGATGACCCTTAG
174886	7082	TAATGACTTTTTAAAACTGA	219473	51669	CCCTCCCTGTGTCCACGAAT	264060	96256	TACCCAGCAGATGACCCTTA
174887	7083	ATAATGACTTTTTAAAACTG	219474	51670	TCCCTCCCTGTGTCCACGAA	264061	96257	TTACCCAGCAGATGACCCTT
174888	7084	TATAATGACTTTTTAAAACT	219475	51671	GTCCCTCCCTGTGTCCACGA	264062	96258	GTTACCCAGCAGATGACCCT
174889	7085	ATATAATGACTTTTTAAAAC	219476	51672	TGTCCCTCCCTGTGTCCACG	264063	96259	CGTTACCCAGCAGATGACCC
174890	7086	GATATAATGACTTTTTAAAA	219477	51673	CTGTCCCTCCCTGTGTCCAC	264064	96260	CCGTTACCCAGCAGATGACC
174891	7087	TGATATAATGACTTTTTAAA	219478	51674	CCTGTCCCTCCCTGTGTCCA	264065	96261	TCCGTTACCCAGCAGATGAC
174892	7088	CTGATATAATGACTTTTTAA	219479	51675	TCCTGTCCCTCCCTGTGTCC	264066	96262	TTCCGTTACCCAGCAGATGA
174893	7089	TCTGATATAATGACTTTTTA	219480	51676	CTCCTGTCCCTCCCTGTGTC	264067	96263	GTTCCGTTACCCAGCAGATG
174894	7090	TTCTGATATAATGACTTTTT	219481	51677	GCTCCTGTCCCTCCCTGTGT	264068	96264	GGTTCCGTTACCCAGCAGAT
174895	7091	TTTCTGATATAATGACTTTT	219482	51678	TGCTCCTGTCCCTCCCTGTG	264069	96265	GGGTTCCGTTACCCAGCAGA
174896	7092	TTTTCTGATATAATGACTTT	219483	51679	GTGCTCCTGTCCCTCCCTGT	264070	96266	TGGGTTCCGTTACCCAGCAG
174897	7093	ATTTTCTGATATAATGACTT	219484	51680	GGTGCTCCTGTCCCTCCCTG	264071	96267	CTGGGTTCCGTTACCCAGCA
174898	7094	GATTTTCTGATATAATGACT	219485	51681	TGGTGCTCCTGTCCCTCCCT	264072	96268	CCTGGGTTCCGTTACCCAGC
174899	7095	TGATTTTCTGATATAATGAC	219486	51682	ATGGTGCTCCTGTCCCTCCC	264073	96269	CCCTGGGTTCCGTTACCCAG
174900	7096	ATGATTTTCTGATATAATGA	219487	51683	GATGGTGCTCCTGTCCCTCC	264074	96270	TCCCTGGGTTCCGTTACCCA
174901	7097	AATGATTTTCTGATATAATG	219488	51684	TGATGGTGCTCCTGTCCCTC	264075	96271	GTCCCTGGGTTCCGTTACCC
174902	7098	AAATGATTTTCTGATATAAT	219489	51685	CTGATGGTGCTCCTGTCCCT	264076	96272	AGTCCCTGGGTTCCGTTACC
174903	7099	TAAATGATTTTCTGATATAA	219490	51686	ACTGATGGTGCTCCTGTCCC	264077	96273	CAGTCCCTGGGTTCCGTTAC
174904	7100	TTAAATGATTTTCTGATATA	219491	51687	AACTGATGGTGCTCCTGTCC	264078	96274	GCAGTCCCTGGGTTCCGTTA
174905	7101	TTTAAATGATTTTCTGATAT	219492	51688	AAACTGATGGTGCTCCTGTC	264079	96275	GGCAGTCCCTGGGTTCCGTT
174906	7102	ATTTAAATGATTTTCTGATA	219493	51689	CAAACTGATGGTGCTCCTGT	264080	96276	GGGCAGTCCCTGGGTTCCGT
174907	7103	CATTTAAATGATTTTCTGAT	219494	51690	ACAAACTGATGGTGCTCCTG	264081	96277	AGGGCAGTCCCTGGGTTCCG
174908	7104	TCATTTAAATGATTTTCTGA	219495	51691	GACAAACTGATGGTGCTCCT	264082	96278	TAGGGCAGTCCCTGGGTTCC
174909	7105	ATCATTTAAATGATTTTCTG	219496	51692	AGACAAACTGATGGTGCTCC	264083	96279	CTAGGGCAGTCCCTGGGTTC
174910	7106	TATCATTTAAATGATTTTCT	219497	51693	GAGACAAACTGATGGTGCTC	264084	96280	ACTAGGGCAGTCCCTGGGTT
174911	7107	GTATCATTTAAATGATTTTC	219498	51694	TGAGACAAACTGATGGTGCT	264085	96281	GACTAGGGCAGTCCCTGGGT
174912	7108	TGTATCATTTAAATGATTTT	219499	51695	GTGAGACAAACTGATGGTGC	264086	96282	GGACTAGGGCAGTCCCTGGG
174913	7109	GTGTATCATTTAAATGATTT	219500	51696	TGTGAGACAAACTGATGGTG	264087	96283	GGGACTAGGGCAGTCCCTGG
174914	7110	TGTGTATCATTTAAATGATT	219501	51697	GTGTGAGACAAACTGATGGT	264088	96284	AGGGACTAGGGCAGTCCCTG
174915	7111	ATGTGTATCATTTAAATGAT	219502	51698	TGTGTGAGACAAACTGATGG	264089	96285	TAGGGACTAGGGCAGTCCCT
174916	7112	TATGTGTATCATTTAAATGA	219503	51699	TTGTGTGAGACAAACTGATG	264090	96286	CTAGGGACTAGGGCAGTCCC
174917	7113	CTATGTGTATCATTTAAATG	219504	51700	GTTGTGTGAGACAAACTGAT	264091	96287	TCTAGGGACTAGGGCAGTCC
174918	7114	TCTATGTGTATCATTTAAAT	219505	51701	GGTTGTGTGAGACAAACTGA	264092	96288	GTCTAGGGACTAGGGCAGTC
174919	7115	ATCTATGTGTATCATTTAAA	219506	51702	TGGTTGTGTGAGACAAACTG	264093	96289	AGTCTAGGGACTAGGGCAGT
174920	7116	AATCTATGTGTATCATTTAA	219507	51703	GTGGTTGTGTGAGACAAACT	264094	96290	CAGTCTAGGGACTAGGGCAG
174921	7117	AAATCTATGTGTATCATTTA	219508	51704	AGTGGTTGTGTGAGACAAAC	264095	96291	ACAGTCTAGGGACTAGGGCA
174922	7118	GAAATCTATGTGTATCATTT	219509	51705	CAGTGGTTGTGTGAGACAAA	264096	96292	CACAGTCTAGGGACTAGGGC
174923	7119	GGAAATCTATGTGTATCATT	219510	51706	ACAGTGGTTGTGTGAGACAA	264097	96293	GCACAGTCTAGGGACTAGGG
174924	7120	TGGAAATCTATGTGTATCAT	219511	51707	GACAGTGGTTGTGTGAGACA	264098	96294	GGCACAGTCTAGGGACTAGG
174925	7121	TTGGAAATCTATGTGTATCA	219512	51708	TGACAGTGGTTGTGTGAGAC	264099	96295	TGGCACAGTCTAGGGACTAG
174926	7122	CTTGGAAATCTATGTGTATC	219513	51709	ATGACAGTGGTTGTGTGAGA	264100	96296	ATGGCACAGTCTAGGGACTA
174927	7123	TCTTGGAAATCTATGTGTAT	219514	51710	GATGACAGTGGTTGTGTGAG	264101	96297	CATGGCACAGTCTAGGGACT
174928	7124	ATCTTGGAAATCTATGTGTA	219515	51711	GGATGACAGTGGTTGTGTGA	264102	96298	GCATGGCACAGTCTAGGGAC
174929	7125	AATCTTGGAAATCTATGTGT	219516	51712	AGGATGACAGTGGTTGTGTG	264103	96299	GGCATGGCACAGTCTAGGGA
174930	7126	AAATCTTGGAAATCTATGTG	219517	51713	GAGGATGACAGTGGTTGTGT	264104	96300	GGGCATGGCACAGTCTAGGG

174931	7127	AAAATCTTGGAAATCTATGT	219518	51714	TGAGGATGACAGTGGTTGTG	264105	96301	CGGGCATGGCACAGTCTAGG
174932	7128	TAAAATCTTGGAAATCTATG	219519	51715	GTGAGGATGACAGTGGTTGT	264106	96302	TCGGGCATGGCACAGTCTAG
174933	7129	GTAAAATCTTGGAAATCTAT	219520	51716	AGTGAGGATGACAGTGGTTG	264107	96303	GTCGGGCATGGCACAGTCTA
174934	7130	AGTAAAATCTTGGAAATCTA	219521	51717	CAGTGAGGATGACAGTGGTT	264108	96304	AGTCGGGCATGGCACAGTCT
174935	7131	AAGTAAAATCTTGGAAATCT	219522	51718	TCAGTGAGGATGACAGTGGT	264109	96305	GAGTCGGGCATGGCACAGTC
174936	7132	AAAGTAAAATCTTGGAAATC	219523	51719	TTCAGTGAGGATGACAGTGG	264110	96306	AGAGTCGGGCATGGCACAGT
174937	7133	TAAAGTAAAATCTTGGAAAT	219524	51720	CTTCAGTGAGGATGACAGTG	264111	96307	CAGAGTCGGGCATGGCACAG
174938	7134	TTAAAGTAAAATCTTGGAAA	219525	51721	CCTTCAGTGAGGATGACAGT	264112	96308	GCAGAGTCGGGCATGGCACA
174939	7135	GTTAAAGTAAAATCTTGGAA	219526	51722	GCCTTCAGTGAGGATGACAG	264113	96309	GGCAGAGTCGGGCATGGCAC
174940	7136	GGTTAAAGTAAAATCTTGGA	219527	51723	AGCCTTCAGTGAGGATGACA	264114	96310	TGGCAGAGTCGGGCATGGCA
174941	7137	CGGTTAAAGTAAAATCTTGG	219528	51724	CAGCCTTCAGTGAGGATGAC	264115	96311	CTGGCAGAGTCGGGCATGGC
174942	7138	TCGGTTAAAGTAAAATCTTG	219529	51725	ACAGCCTTCAGTGAGGATGA	264116	96312	GCTGGCAGAGTCGGGCATGG
174943	7139	TTCGGTTAAAGTAAAATCTT	219530	51726	AACAGCCTTCAGTGAGGATG	264117	96313	AGCTGGCAGAGTCGGGCATG
174944	7140	TTTCGGTTAAAGTAAAATCT	219531	51727	CAACAGCCTTCAGTGAGGAT	264118	96314	AAGCTGGCAGAGTCGGGCAT
174945	7141	GTTTCGGTTAAAGTAAAATC	219532	51728	GCAACAGCCTTCAGTGAGGA	264119	96315	AAAGCTGGCAGAGTCGGGCA
174946	7142	AGTTTCGGTTAAAGTAAAAT	219533	51729	GGCAACAGCCTTCAGTGAGG	264120	96316	CAAAGCTGGCAGAGTCGGGC
174947	7143	TAGTTTCGGTTAAAGTAAAA	219534	51730	AGGCAACAGCCTTCAGTGAG	264121	96317	ACAAAGCTGGCAGAGTCGGG
174948	7144	ATAGTTTCGGTTAAAGTAAA	219535	51731	CAGGCAACAGCCTTCAGTGA	264122	96318	GACAAAGCTGGCAGAGTCGG
174949	7145	TATAGTTTCGGTTAAAGTAA	219536	51732	TCAGGCAACAGCCTTCAGTG	264123	96319	TGACAAAGCTGGCAGAGTCG
174950	7146	ATATAGTTTCGGTTAAAGTA	219537	51733	ATCAGGCAACAGCCTTCAGT	264124	96320	CTGACAAAGCTGGCAGAGTC
174951	7147	TATATAGTTTCGGTTAAAGT	219538	51734	GATCAGGCAACAGCCTTCAG	264125	96321	ACTGACAAAGCTGGCAGAGT
174952	7148	TTATATAGTTTCGGTTAAAG	219539	51735	TGATCAGGCAACAGCCTTCA	264126	96322	CACTGACAAAGCTGGCAGAG
174953	7149	TTTATATAGTTTCGGTTAAA	219540	51736	TTGATCAGGCAACAGCCTTC	264127	96323	TCACTGACAAAGCTGGCAGA
174954	7150	ATTTATATAGTTTCGGTTAA	219541	51737	TTTGATCAGGCAACAGCCTT	264128	96324	ATCACTGACAAAGCTGGCAG
174955	7151	CATTTATATAGTTTCGGTTA	219542	51738	TTTTGATCAGGCAACAGCCT	264129	96325	CATCACTGACAAAGCTGGCA
174956	7152	ACATTTATATAGTTTCGGTT	219543	51739	TTTTTGATCAGGCAACAGCC	264130	96326	GCATCACTGACAAAGCTGGC
174957	7153	CACATTTATATAGTTTCGGT	219544	51740	GTTTTTGATCAGGCAACAGC	264131	96327	AGCATCACTGACAAAGCTGG
174958	7154	TCACATTTATATAGTTTCGG	219545	51741	TGTTTTTGATCAGGCAACAG	264132	96328	CAGCATCACTGACAAAGCTG
174959	7155	TTCACATTTATATAGTTTCG	219546	51742	CTGTTTTTGATCAGGCAACA	264133	96329	CCAGCATCACTGACAAAGCT
174960	7156	ATTCACATTTATATAGTTTC	219547	51743	ACTGTTTTTGATCAGGCAAC	264134	96330	ACCAGCATCACTGACAAAGC
174961	7157	AATTCACATTTATATAGTTT	219548	51744	TACTGTTTTTGATCAGGCAA	264135	96331	CACCAGCATCACTGACAAAG
174962	7158	AAATTCACATTTATATAGTT	219549	51745	ATACTGTTTTTGATCAGGCA	264136	96332	GCACCAGCATCACTGACAAA
174963	7159	CAAATTCACATTTATATAGT	219550	51746	AATACTGTTTTTGATCAGGC	264137	96333	AGCACCAGCATCACTGACAA
174964	7160	ACAAATTCACATTTATATAG	219551	51747	CAATACTGTTTTTGATCAGG	264138	96334	GAGCACCAGCATCACTGACA
174965	7161	AACAAATTCACATTTATATA	219552	51748	CCAATACTGTTTTTGATCAG	264139	96335	CGAGCACCAGCATCACTGAC
174966	7162	GAACAAATTCACATTTATAT	219553	51749	CCCAATACTGTTTTTGATCA	264140	96336	GCGAGCACCAGCATCACTGA
174967	7163	TGAACAAATTCACATTTATA	219554	51750	GCCCAATACTGTTTTTGATC	264141	96337	GGCGAGCACCAGCATCACTG
174968	7164	GTGAACAAATTCACATTTAT	219555	51751	GGCCCAATACTGTTTTTGAT	264142	96338	AGGCGAGCACCAGCATCACT
174969	7165	GGTGAACAAATTCACATTTA	219556	51752	TGGCCCAATACTGTTTTTGA	264143	96339	GAGGCGAGCACCAGCATCAC
174970	7166	GGGTGAACAAATTCACATTT	219557	51753	CTGGCCCAATACTGTTTTTG	264144	96340	GGAGGCGAGCACCAGCATCA
174971	7167	TGGGTGAACAAATTCACATT	219558	51754	CCTGGCCCAATACTGTTTTT	264145	96341	AGGAGGCGAGCACCAGCATC
174972	7168	ATGGGTGAACAAATTCACAT	219559	51755	GCCTGGCCCAATACTGTTTT	264146	96342	GAGGAGGCGAGCACCAGCAT
174973	7169	GATGGGTGAACAAATTCACA	219560	51756	TGCCTGGCCCAATACTGTTT	264147	96343	CGAGGAGGCGAGCACCAGCA
174974	7170	AGATGGGTGAACAAATTCAC	219561	51757	GTGCCTGGCCCAATACTGTT	264148	96344	CCGAGGAGGCGAGCACCAGC
174975	7171	AAGATGGGTGAACAAATTCA	219562	51758	CGTGCCTGGCCCAATACTGT	264149	96345	CCCGAGGAGGCGAGCACCAG
174976	7172	AAAGATGGGTGAACAAATTC	219563	51759	CCGTGCCTGGCCCAATACTG	264150	96346	ACCCGAGGAGGCGAGCACCA
174977	7173	AAAAGATGGGTGAACAAATT	219564	51760	ACCGTGCCTGGCCCAATACT	264151	96347	CACCCGAGGAGGCGAGCACC
174978	7174	CAAAAGATGGGTGAACAAAT	219565	51761	CACCGTGCCTGGCCCAATAC	264152	96348	GCACCCGAGGAGGCGAGCAC
174979	7175	TCAAAAGATGGGTGAACAAA	219566	51762	CCACCGTGCCTGGCCCAATA	264153	96349	AGCACCCGAGGAGGCGAGCA
174980	7176	GTCAAAAGATGGGTGAACAA	219567	51763	GCCACCGTGCCTGGCCCAAT	264154	96350	GAGCACCCGAGGAGGCGAGC
174981	7177	TGTCAAAAGATGGGTGAACA	219568	51764	AGCCACCGTGCCTGGCCCAA	264155	96351	CGAGCACCCGAGGAGGCGAG
174982	7178	GTGTCAAAAGATGGGTGAAC	219569	51765	GAGCCACCGTGCCTGGCCCA	264156	96352	GCGAGCACCCGAGGAGGCGA
174983	7179	TGTGTCAAAAGATGGGTGAA	219570	51766	TGAGCCACCGTGCCTGGCCC	264157	96353	GGCGAGCACCCGAGGAGGCG
174984	7180	CTGTGTCAAAAGATGGGTGA	219571	51767	GTGAGCCACCGTGCCTGGCC	264158	96354	AGGCGAGCACCCGAGGAGGC
174985	7181	CCTGTGTCAAAAGATGGGTG	219572	51768	TGTGAGCCACCGTGCCTGGC	264159	96355	CAGGCGAGCACCCGAGGAGG
174986	7182	CCCTGTGTCAAAAGATGGGT	219573	51769	GTGTGAGCCACCGTGCCTGG	264160	96356	CCAGGCGAGCACCCGAGGAG
174987	7183	GCCCTGTGTCAAAAGATGGG	219574	51770	GGTGTGAGCCACCGTGCCTG	264161	96357	ACCAGGCGAGCACCCGAGGA
174988	7184	AGCCCTGTGTCAAAAGATGG	219575	51771	AGGTGTGAGCCACCGTGCCT	264162	96358	GACCAGGCGAGCACCCGAGG
174989	7185	GAGCCCTGTGTCAAAAGATG	219576	51772	CAGGTGTGAGCCACCGTGCC	264163	96359	AGACCAGGCGAGCACCCGAG
174990	7186	TGAGCCCTGTGTCAAAAGAT	219577	51773	ACAGGTGTGAGCCACCGTGC	264164	96360	CAGACCAGGCGAGCACCCGA
174991	7187	CTGAGCCCTGTGTCAAAAGA	219578	51774	TACAGGTGTGAGCCACCGTG	264165	96361	TCAGACCAGGCGAGCACCCG
174992	7188	CCTGAGCCCTGTGTCAAAAG	219579	51775	TTACAGGTGTGAGCCACCGT	264166	96362	CTCAGACCAGGCGAGCACCC
174993	7189	ACCTGAGCCCTGTGTCAAAA	219580	51776	ATTACAGGTGTGAGCCACCG	264167	96363	GCTCAGACCAGGCGAGCACC
174994	7190	GACCTGAGCCCTGTGTCAAA	219581	51777	TATTACAGGTGTGAGCCACC	264168	96364	TGCTCAGACCAGGCGAGCAC
174995	7191	AGACCTGAGCCCTGTGTCAA	219582	51778	GTATTACAGGTGTGAGCCAC	264169	96365	GTGCTCAGACCAGGCGAGCA
174996	7192	AAGACCTGAGCCCTGTGTCA	219583	51779	GGTATTACAGGTGTGAGCCA	264170	96366	TGTGCTCAGACCAGGCGAGC
174997	7193	GAAGACCTGAGCCCTGTGTC	219584	51780	TGGTATTACAGGTGTGAGCC	264171	96367	GTGTGCTCAGACCAGGCGAG
174998	7194	AGAAGACCTGAGCCCTGTGT	219585	51781	GTGGTATTACAGGTGTGAGC	264172	96368	GGTGTGCTCAGACCAGGCGA
174999	7195	GAGAAGACCTGAGCCCTGTG	219586	51782	GGTGGTATTACAGGTGTGAG	264173	96369	GGGTGTGCTCAGACCAGGCG
175000	7196	AGAGAAGACCTGAGCCCTGT	219587	51783	TGGTGGTATTACAGGTGTGA	264174	96370	TGGGTGTGCTCAGACCAGGC
175001	7197	AAGAGAAGACCTGAGCCCTG	219588	51784	GTGGTGGTATTACAGGTGTG	264175	96371	TTGGGTGTGCTCAGACCAGG
175002	7198	CAAGAGAAGACCTGAGCCCT	219589	51785	AGTGGTGGTATTACAGGTGT	264176	96372	CTTGGGTGTGCTCAGACCAG

175003	7199	CCAAGAGAAGACCTGAGCCC	219590	51786	AAGTGGTGGTATTACAGGTG	264177	96373	CCTTGGGTGTGCTCAGACCA
175004	7200	ACCAAGAGAAGACCTGAGCC	219591	51787	AAAGTGGTGGTATTACAGGT	264178	96374	TCCTTGGGTGTGCTCAGACC
175005	7201	CACCAAGAGAAGACCTGAGC	219592	51788	CAAAGTGGTGGTATTACAGG	264179	96375	CTCCTTGGGTGTGCTCAGAC
175006	7202	ACACCAAGAGAAGACCTGAG	219593	51789	CCAAAGTGGTGGTATTACAG	264180	96376	ACTCCTTGGGTGTGCTCAGA
175007	7203	GACACCAAGAGAAGACCTGA	219594	51790	CCCAAAGTGGTGGTATTACA	264181	96377	AACTCCTTGGGTGTGCTCAG
175008	7204	AGACACCAAGAGAAGACCTG	219595	51791	TCCCAAAGTGGTGGTATTAC	264182	96378	GAACTCCTTGGGTGTGCTCA
175009	7205	CAGACACCAAGAGAAGACCT	219596	51792	CTCCCAAAGTGGTGGTATTA	264183	96379	AGAACTCCTTGGGTGTGCTC
175010	7206	CCAGACACCAAGAGAAGACC	219597	51793	CCTCCCAAAGTGGTGGTATT	264184	96380	AAGAACTCCTTGGGTGTGCT
175011	7207	TCCAGACACCAAGAGAAGAC	219598	51794	GCCTCCCAAAGTGGTGGTAT	264185	96381	CAAGAACTCCTTGGGTGTGC
175012	7208	ATCCAGACACCAAGAGAAGA	219599	51795	AGCCTCCCAAAGTGGTGGTA	264186	96382	TCAAGAACTCCTTGGGTGTG
175013	7209	GATCCAGACACCAAGAGAAG	219600	51796	CAGCCTCCCAAAGTGGTGGT	264187	96383	CTCAAGAACTCCTTGGGTGT
175014	7210	TGATCCAGACACCAAGAGAA	219601	51797	TCAGCCTCCCAAAGTGGTGG	264188	96384	CCTCAAGAACTCCTTGGGTG
175015	7211	CTGATCCAGACACCAAGAGA	219602	51798	CTCAGCCTCCCAAAGTGGTG	264189	96385	GCCTCAAGAACTCCTTGGGT
175016	7212	GCTGATCCAGACACCAAGAG	219603	51799	CCTCAGCCTCCCAAAGTGGT	264190	96386	GGCCTCAAGAACTCCTTGGG
175017	7213	GGCTGATCCAGACACCAAGA	219604	51800	ACCTCAGCCTCCCAAAGTGG	264191	96387	AGGCCTCAAGAACTCCTTGG
175018	7214	TGGCTGATCCAGACACCAAG	219605	51801	CACCTCAGCCTCCCAAAGTG	264192	96388	AAGGCCTCAAGAACTCCTTG
175019	7215	CTGGCTGATCCAGACACCAA	219606	51802	TCACCTCAGCCTCCCAAAGT	264193	96389	TAAGGCCTCAAGAACTCCTT
175020	7216	ACTGGCTGATCCAGACACCA	219607	51803	CTCACCTCAGCCTCCCAAAG	264194	96390	CTAAGGCCTCAAGAACTCCT
175021	7217	AACTGGCTGATCCAGACACC	219608	51804	ACTCACCTCAGCCTCCCAAA	264195	96391	CCTAAGGCCTCAAGAACTCC
175022	7218	CAACTGGCTGATCCAGACAC	219609	51805	CACTCACCTCAGCCTCCCAA	264196	96392	CCCTAAGGCCTCAAGAACTC
175023	7219	TCAACTGGCTGATCCAGACA	219610	51806	CCACTCACCTCAGCCTCCCA	264197	96393	ACCCTAAGGCCTCAAGAACT
175024	7220	TTCAACTGGCTGATCCAGAC	219611	51807	TCCACTCACCTCAGCCTCCC	264198	96394	AACCCTAAGGCCTCAAGAAC
175025	7221	TTTCAACTGGCTGATCCAGA	219612	51808	ATCCACTCACCTCAGCCTCC	264199	96395	CAACCCTAAGGCCTCAAGAA
175026	7222	ATTTCAACTGGCTGATCCAG	219613	51809	GATCCACTCACCTCAGCCTC	264200	96396	ACAACCCTAAGGCCTCAAGA
175027	7223	AATTTCAACTGGCTGATCCA	219614	51810	TGATCCACTCACCTCAGCCT	264201	96397	AACAACCCTAAGGCCTCAAG
175028	7224	AAATTTCAACTGGCTGATCC	219615	51811	GTGATCCACTCACCTCAGCC	264202	96398	AAACAACCCTAAGGCCTCAA
175029	7225	GAAATTTCAACTGGCTGATC	219616	51812	AGTGATCCACTCACCTCAGC	264203	96399	CAAACAACCCTAAGGCCTCA
175030	7226	AGAAATTTCAACTGGCTGAT	219617	51813	AAGTGATCCACTCACCTCAG	264204	96400	GCAAACAACCCTAAGGCCTC
175031	7227	AAGAAATTTCAACTGGCTGA	219618	51814	CAAGTGATCCACTCACCTCA	264205	96401	CGCAAACAACCCTAAGGCCT
175032	7228	CAAGAAATTTCAACTGGCTG	219619	51815	TCAAGTGATCCACTCACCTC	264206	96402	TCGCAAACAACCCTAAGGCC
175033	7229	ACAAGAAATTTCAACTGGCT	219620	51816	CTCAAGTGATCCACTCACCT	264207	96403	CTCGCAAACAACCCTAAGGC
175034	7230	GACAAGAAATTTCAACTGGC	219621	51817	CCTCAAGTGATCCACTCACC	264208	96404	TCTCGCAAACAACCCTAAGG
175035	7231	AGACAAGAAATTTCAACTGG	219622	51818	ACCTCAAGTGATCCACTCAC	264209	96405	CTCTCGCAAACAACCCTAAG
175036	7232	CAGACAAGAAATTTCAACTG	219623	51819	GACCTCAAGTGATCCACTCA	264210	96406	TCTCTCGCAAACAACCCTAA
175037	7233	ACAGACAAGAAATTTCAACT	219624	51820	TGACCTCAAGTGATCCACTC	264211	96407	TTCTCTCGCAAACAACCCTA
175038	7234	AACAGACAAGAAATTTCAAC	219625	51821	CTGACCTCAAGTGATCCACT	264212	96408	ATTCTCTCGCAAACAACCCT
175039	7235	AAACAGACAAGAAATTTCAA	219626	51822	CCTGACCTCAAGTGATCCAC	264213	96409	CATTCTCTCGCAAACAACCC
175040	7236	AAAACAGACAAGAAATTTCA	219627	51823	TCCTGACCTCAAGTGATCCA	264214	96410	TCATTCTCTCGCAAACAACC
175041	7237	CAAAACAGACAAGAAATTTC	219628	51824	CTCCTGACCTCAAGTGATCC	264215	96411	TTCATTCTCTCGCAAACAAC
175042	7238	GCAAAACAGACAAGAAATTT	219629	51825	ACTCCTGACCTCAAGTGATC	264216	96412	TTTCATTCTCTCGCAAACAA
175043	7239	GGCAAAACAGACAAGAAATT	219630	51826	AACTCCTGACCTCAAGTGAT	264217	96413	CTTTCATTCTCTCGCAAACA
175044	7240	AGGCAAAACAGACAAGAAAT	219631	51827	GAACTCCTGACCTCAAGTGA	264218	96414	TCTTTCATTCTCTCGCAAAC
175045	7241	TAGGCAAAACAGACAAGAAA	219632	51828	CGAACTCCTGACCTCAAGTG	264219	96415	TTCTTTCATTCTCTCGCAAA
175046	7242	ATAGGCAAAACAGACAAGAA	219633	51829	TCGAACTCCTGACCTCAAGT	264220	96416	GTTCTTTCATTCTCTCGCAA
175047	7243	CATAGGCAAAACAGACAAGA	219634	51830	CTCGAACTCCTGACCTCAAG	264221	96417	TGTTCTTTCATTCTCTCGCA
175048	7244	GCATAGGCAAAACAGACAAG	219635	51831	TCTCGAACTCCTGACCTCAA	264222	96418	GTGTTCTTTCATTCTCTCGC
175049	7245	GGCATAGGCAAAACAGACAA	219636	51832	ATCTCGAACTCCTGACCTCA	264223	96419	CGTGTTCTTTCATTCTCTCG
175050	7246	TGGCATAGGCAAAACAGACA	219637	51833	GATCTCGAACTCCTGACCTC	264224	96420	TCGTGTTCTTTCATTCTCTC
175051	7247	GTGGCATAGGCAAAACAGAC	219638	51834	TGATCTCGAACTCCTGACCT	264225	96421	GTCGTGTTCTTTCATTCTCT
175052	7248	TGTGGCATAGGCAAAACAGA	219639	51835	TTGATCTCGAACTCCTGACC	264226	96422	GGTCGTGTTCTTTCATTCTC
175053	7249	ATGTGGCATAGGCAAAACAG	219640	51836	GTTGATCTCGAACTCCTGAC	264227	96423	AGGTCGTGTTCTTTCATTCT
175054	7250	AATGTGGCATAGGCAAAACA	219641	51837	GGTTGATCTCGAACTCCTGA	264228	96424	TAGGTCGTGTTCTTTCATTC
175055	7251	TAATGTGGCATAGGCAAAAC	219642	51838	AGGTTGATCTCGAACTCCTG	264229	96425	CTAGGTCGTGTTCTTTCATT
175056	7252	TTAATGTGGCATAGGCAAAA	219643	51839	CAGGTTGATCTCGAACTCCT	264230	96426	GCTAGGTCGTGTTCTTTCAT
175057	7253	ATTAATGTGGCATAGGCAAA	219644	51840	CCAGGTTGATCTCGAACTCC	264231	96427	AGCTAGGTCGTGTTCTTTCA
175058	7254	TATTAATGTGGCATAGGCAA	219645	51841	GCCAGGTTGATCTCGAACTC	264232	96428	GAGCTAGGTCGTGTTCTTTC
175059	7255	TTATTAATGTGGCATAGGCA	219646	51842	GGCCAGGTTGATCTCGAACT	264233	96429	AGAGCTAGGTCGTGTTCTTT
175060	7256	ATTATTAATGTGGCATAGGC	219647	51843	TGGCCAGGTTGATCTCGAAC	264234	96430	GAGAGCTAGGTCGTGTTCTT
175061	7257	CATTATTAATGTGGCATAGG	219648	51844	TTGGCCAGGTTGATCTCGAA	264235	96431	AGAGAGCTAGGTCGTGTTCT
175062	7258	GCATTATTAATGTGGCATAG	219649	51845	GTTGGCCAGGTTGATCTCGA	264236	96432	AAGAGAGCTAGGTCGTGTTC
175063	7259	TGCATTATTAATGTGGCATA	219650	51846	TGTTGGCCAGGTTGATCTCG	264237	96433	AAAGAGAGCTAGGTCGTGTT
175064	7260	GTGCATTATTAATGTGGCAT	219651	51847	ATGTTGGCCAGGTTGATCTC	264238	96434	TAAAGAGAGCTAGGTCGTGT
175065	7261	AGTGCATTATTAATGTGGCA	219652	51848	CATGTTGGCCAGGTTGATCT	264239	96435	CTAAAGAGAGCTAGGTCGTG
175066	7262	CAGTGCATTATTAATGTGGC	219653	51849	CCATGTTGGCCAGGTTGATC	264240	96436	GCTAAAGAGAGCTAGGTCGT
175067	7263	ACAGTGCATTATTAATGTGG	219654	51850	ACCATGTTGGCCAGGTTGAT	264241	96437	TGCTAAAGAGAGCTAGGTCG
175068	7264	GACAGTGCATTATTAATGTG	219655	51851	CACCATGTTGGCCAGGTTGA	264242	96438	ATGCTAAAGAGAGCTAGGTC
175069	7265	AGACAGTGCATTATTAATGT	219656	51852	TCACCATGTTGGCCAGGTTG	264243	96439	GATGCTAAAGAGAGCTAGGT
175070	7266	CAGACAGTGCATTATTAATG	219657	51853	TTCACCATGTTGGCCAGGTT	264244	96440	GGATGCTAAAGAGAGCTAGG
175071	7267	CCAGACAGTGCATTATTAAT	219658	51854	TTTCACCATGTTGGCCAGGT	264245	96441	AGGATGCTAAAGAGAGCTAG
175072	7268	CCCAGACAGTGCATTATTAA	219659	51855	GTTTCACCATGTTGGCCAGG	264246	96442	AAGGATGCTAAAGAGAGCTA
175073	7269	ACCCAGACAGTGCATTATTA	219660	51856	GGTTTCACCATGTTGGCCAG	264247	96443	CAAGGATGCTAAAGAGAGCT
175074	7270	GACCCAGACAGTGCATTATT	219661	51857	AGGTTTCACCATGTTGGCCA	264248	96444	CCAAGGATGCTAAAGAGAGC

175075	7271	GGACCCAGACAGTGCATTAT	219662	51858	AAGGTTTCACCATGTTGGCC	264249	96445	ACCAAGGATGCTAAAGAGAG
175076	7272	AGGACCCAGACAGTGCATTA	219663	51859	CAAGGTTTCACCATGTTGGC	264250	96446	GACCAAGGATGCTAAAGAGA
175077	7273	GAGGACCCAGACAGTGCATT	219664	51860	ACAAGGTTTCACCATGTTGG	264251	96447	TGACCAAGGATGCTAAAGAG
175078	7274	GGAGGACCCAGACAGTGCAT	219665	51861	GACAAGGTTTCACCATGTTG	264252	96448	CTGACCAAGGATGCTAAAGA
175079	7275	CGGAGGACCCAGACAGTGCA	219666	51862	AGACAAGGTTTCACCATGTT	264253	96449	CCTGACCAAGGATGCTAAAG
175080	7276	TCGGAGGACCCAGACAGTGC	219667	51863	GAGACAAGGTTTCACCATGT	264254	96450	ACCTGACCAAGGATGCTAAA
175081	7277	ATCGGAGGACCCAGACAGTG	219668	51864	AGAGACAAGGTTTCACCATG	264255	96451	AACCTGACCAAGGATGCTAA
175082	7278	AATCGGAGGACCCAGACAGT	219669	51865	TAGAGACAAGGTTTCACCAT	264256	96452	GAACCTGACCAAGGATGCTA
175083	7279	AAATCGGAGGACCCAGACAG	219670	51866	GTAGAGACAAGGTTTCACCA	264257	96453	TGAACCTGACCAAGGATGCT
175084	7280	GAAATCGGAGGACCCAGACA	219671	51867	AGTAGAGACAAGGTTTCACC	264258	96454	TTGAACCTGACCAAGGATGC
175085	7281	TGAAATCGGAGGACCCAGAC	219672	51868	TAGTAGAGACAAGGTTTCAC	264259	96455	GTTGAACCTGACCAAGGATG
175086	7282	CTGAAATCGGAGGACCCAGA	219673	51869	TTAGTAGAGACAAGGTTTCA	264260	96456	TGTTGAACCTGACCAAGGAT
175087	7283	ACTGAAATCGGAGGACCCAG	219674	51870	TTTAGTAGAGACAAGGTTTC	264261	96457	GTGTTGAACCTGACCAAGGA
175088	7284	AACTGAAATCGGAGGACCCA	219675	51871	TTTTAGTAGAGACAAGGTTT	264262	96458	AGTGTTGAACCTGACCAAGG
175089	7285	AAACTGAAATCGGAGGACCC	219676	51872	CTTTTAGTAGAGACAAGGTT	264263	96459	CAGTGTTGAACCTGACCAAG
175090	7286	CAAACTGAAATCGGAGGACC	219677	51873	ACTTTTAGTAGAGACAAGGT	264264	96460	GCAGTGTTGAACCTGACCAA
175091	7287	CCAAACTGAAATCGGAGGAC	219678	51874	AACTTTTAGTAGAGACAAGG	264265	96461	GGCAGTGTTGAACCTGACCA
175092	7288	TCCAAACTGAAATCGGAGGA	219679	51875	GAACTTTTAGTAGAGACAAG	264266	96462	GGGCAGTGTTGAACCTGACC
175093	7289	ATCCAAACTGAAATCGGAGG	219680	51876	TGAACTTTTAGTAGAGACAA	264267	96463	GGGGCAGTGTTGAACCTGAC
175094	7290	AATCCAAACTGAAATCGGAG	219681	51877	TTGAACTTTTAGTAGAGACA	264268	96464	GGGGGCAGTGTTGAACCTGA
175095	7291	AAATCCAAACTGAAATCGGA	219682	51878	TTTGAACTTTTAGTAGAGAC	264269	96465	TGGGGGCAGTGTTGAACCTG
175096	7292	AAAATCCAAACTGAAATCGG	219683	51879	TTTTGAACTTTTAGTAGAGA	264270	96466	CTGGGGGCAGTGTTGAACCT
175097	7293	CAAAATCCAAACTGAAATCG	219684	51880	TTTTTGAACTTTTAGTAGAG	264271	96467	CCTGGGGGCAGTGTTGAACC
175098	7294	CCAAAATCCAAACTGAAATC	219685	51881	ATTTTTGAACTTTTAGTAGA	264272	96468	CCCTGGGGGCAGTGTTGAAC
175099	7295	CCCAAAATCCAAACTGAAAT	219686	51882	AATTTTTGAACTTTTAGTAG	264273	96469	CCCCTGGGGGCAGTGTTGAA
175100	7296	ACCCAAAATCCAAACTGAAA	219687	51883	TAATTTTTGAACTTTTAGTA	264274	96470	GCCCCTGGGGGCAGTGTTGA
175101	7297	AACCCAAAATCCAAACTGAA	219688	51884	CTAATTTTTGAACTTTTAGT	264275	96471	GGCCCCTGGGGGCAGTGTTG
175102	7298	AAACCCAAAATCCAAACTGA	219689	51885	GCTAATTTTTGAACTTTTAG	264276	96472	AGGCCCCTGGGGGCAGTGTT
175103	7299	TAAACCCAAAATCCAAACTG	219690	51886	GGCTAATTTTTGAACTTTTA	264277	96473	GAGGCCCCTGGGGGCAGTGT
175104	7300	GTAAACCCAAAATCCAAACT	219691	51887	TGGCTAATTTTTGAACTTTT	264278	96474	AGAGGCCCCTGGGGGCAGTG
175105	7301	TGTAAACCCAAAATCCAAAC	219692	51888	CTGGCTAATTTTTGAACTTT	264279	96475	CAGAGGCCCCTGGGGGCAGT
175106	7302	ATGTAAACCCAAAATCCAAA	219693	51889	CCTGGCTAATTTTTGAACTT	264280	96476	CCAGAGGCCCCTGGGGGCAG
175107	7303	AATGTAAACCCAAAATCCAA	219694	51890	GCCTGGCTAATTTTTGAACT	264281	96477	ACCAGAGGCCCCTGGGGGCA
175108	7304	CAATGTAAACCCAAAATCCA	219695	51891	CGCCTGGCTAATTTTTGAAC	264282	96478	CACCAGAGGCCCCTGGGGGC
175109	7305	ACAATGTAAACCCAAAATCC	219696	51892	ACGCCTGGCTAATTTTTGAA	264283	96479	CCACCAGAGGCCCCTGGGGG
175110	7306	CACAATGTAAACCCAAAATC	219697	51893	CACGCCTGGCTAATTTTTGA	264284	96480	TCCACCAGAGGCCCCTGGGG
175111	7307	CCACAATGTAAACCCAAAAT	219698	51894	CCACGCCTGGCTAATTTTTG	264285	96481	CTCCACCAGAGGCCCCTGGG
175112	7308	TCCACAATGTAAACCCAAAA	219699	51895	ACCACGCCTGGCTAATTTTT	264286	96482	GCTCCACCAGAGGCCCCTGG
175113	7309	CTCCACAATGTAAACCCAAA	219700	51896	CACCACGCCTGGCTAATTTT	264287	96483	GGCTCCACCAGAGGCCCCTG
175114	7310	ACTCCACAATGTAAACCCAA	219701	51897	CCACCACGCCTGGCTAATTT	264288	96484	TGGCTCCACCAGAGGCCCCT
175115	7311	GACTCCACAATGTAAACCCA	219702	51898	CCCACCACGCCTGGCTAATT	264289	96485	TTGGCTCCACCAGAGGCCCC
175116	7312	TGACTCCACAATGTAAACCC	219703	51899	ACCCACCACGCCTGGCTAAT	264290	96486	GTTGGCTCCACCAGAGGCCC
175117	7313	ATGACTCCACAATGTAAACC	219704	51900	CACCCACCACGCCTGGCTAA	264291	96487	GGTTGGCTCCACCAGAGGCC
175118	7314	GATGACTCCACAATGTAAAC	219705	51901	GCACCCACCACGCCTGGCTA	264292	96488	TGGTTGGCTCCACCAGAGGC
175119	7315	AGATGACTCCACAATGTAAA	219706	51902	GGCACCCACCACGCCTGGCT	264293	96489	GTGGTTGGCTCCACCAGAGG
175120	7316	CAGATGACTCCACAATGTAA	219707	51903	AGGCACCCACCACGCCTGGC	264294	96490	GGTGGTTGGCTCCACCAGAG
175121	7317	TCAGATGACTCCACAATGTA	219708	51904	CAGGCACCCACCACGCCTGG	264295	96491	TGGTGGTTGGCTCCACCAGA
175122	7318	TTCAGATGACTCCACAATGT	219709	51905	ACAGGCACCCACCACGCCTG	264296	96492	ATGGTGGTTGGCTCCACCAG
175123	7319	ATTCAGATGACTCCACAATG	219710	51906	TACAGGCACCCACCACGCCT	264297	96493	GATGGTGGTTGGCTCCACCA
175124	7320	CATTCAGATGACTCCACAAT	219711	51907	CTACAGGCACCCACCACGCC	264298	96494	TGATGGTGGTTGGCTCCACC
175125	7321	GCATTCAGATGACTCCACAA	219712	51908	ACTACAGGCACCCACCACGC	264299	96495	CTGATGGTGGTTGGCTCCAC
175126	7322	TGCATTCAGATGACTCCACA	219713	51909	GACTACAGGCACCCACCACG	264300	96496	GCTGATGGTGGTTGGCTCCA
175127	7323	CTGCATTCAGATGACTCCAC	219714	51910	GGACTACAGGCACCCACCAC	264301	96497	GGCTGATGGTGGTTGGCTCC
175128	7324	TCTGCATTCAGATGACTCCA	219715	51911	GGGACTACAGGCACCCACCA	264302	96498	TGGCTGATGGTGGTTGGCTC
175129	7325	TTCTGCATTCAGATGACTCC	219716	51912	TGGGACTACAGGCACCCACC	264303	96499	TTGGCTGATGGTGGTTGGCT
175130	7326	ATTCTGCATTCAGATGACTC	219717	51913	CTGGGACTACAGGCACCCAC	264304	96500	TTTGGCTGATGGTGGTTGGC
175131	7327	GATTCTGCATTCAGATGACT	219718	51914	GCTGGGACTACAGGCACCCA	264305	96501	ATTTGGCTGATGGTGGTTGG
175132	7328	GGATTCTGCATTCAGATGAC	219719	51915	AGCTGGGACTACAGGCACCC	264306	96502	TATTTGGCTGATGGTGGTTG
175133	7329	AGGATTCTGCATTCAGATGA	219720	51916	TAGCTGGGACTACAGGCACC	264307	96503	TTATTTGGCTGATGGTGGTT
175134	7330	AAGGATTCTGCATTCAGATG	219721	51917	GTAGCTGGGACTACAGGCAC	264308	96504	TTTATTTGGCTGATGGTGGT
175135	7331	GAAGGATTCTGCATTCAGAT	219722	51918	AGTAGCTGGGACTACAGGCA	264309	96505	ATTTATTTGGCTGATGGTGG
175136	7332	TGAAGGATTCTGCATTCAGA	219723	51919	AAGTAGCTGGGACTACAGGC	264310	96506	GATTTATTTGGCTGATGGTG
175137	7333	CTGAAGGATTCTGCATTCAG	219724	51920	CAAGTAGCTGGGACTACAGG	264311	96507	GGATTTATTTGGCTGATGGT
175138	7334	CCTGAAGGATTCTGCATTCA	219725	51921	CCAAGTAGCTGGGACTACAG	264312	96508	TGGATTTATTTGGCTGATGG
175139	7335	CCCTGAAGGATTCTGCATTC	219726	51922	CCCAAGTAGCTGGGACTACA	264313	96509	ATGGATTTATTTGGCTGATG
175140	7336	TCCCTGAAGGATTCTGCATT	219727	51923	TCCCAAGTAGCTGGGACTAC	264314	96510	TATGGATTTATTTGGCTGAT
175141	7337	ATCCCTGAAGGATTCTGCAT	219728	51924	CTCCCAAGTAGCTGGGACTA	264315	96511	TTATGGATTTATTTGGCTGA
175142	7338	AATCCCTGAAGGATTCTGCA	219729	51925	CCTCCCAAGTAGCTGGGACT	264316	96512	ATTATGGATTTATTTGGCTG
175143	7339	AAATCCCTGAAGGATTCTGC	219730	51926	GCCTCCCAAGTAGCTGGGAC	264317	96513	AATTATGGATTTATTTGGCT
175144	7340	AAAATCCCTGAAGGATTCTG	219731	51927	AGCCTCCCAAGTAGCTGGGA	264318	96514	TAATTATGGATTTATTTGGC
175145	7341	TAAAATCCCTGAAGGATTCT	219732	51928	CAGCCTCCCAAGTAGCTGGG	264319	96515	CTAATTATGGATTTATTTGG
175146	7342	GTAAAATCCCTGAAGGATTC	219733	51929	TCAGCCTCCCAAGTAGCTGG	264320	96516	TCTAATTATGGATTTATTTG

175147	7343	AGTAAAATCCCTGAAGGATT	219734	51930	CTCAGCCTCCCAAGTAGCTG	264321	96517	CTCTAATTATGGATTTATTT
175148	7344	AAGTAAAATCCCTGAAGGAT	219735	51931	CCTCAGCCTCCCAAGTAGCT	264322	96518	ACTCTAATTATGGATTTATT
175149	7345	AAAGTAAAATCCCTGAAGGA	219736	51932	GCCTCAGCCTCCCAAGTAGC	264323	96519	GACTCTAATTATGGATTTAT
175150	7346	AAAAGTAAAATCCCTGAAGG	219737	51933	TGCCTCAGCCTCCCAAGTAG	264324	96520	TGACTCTAATTATGGATTTA
175151	7347	AAAAAGTAAAATCCCTGAAG	219738	51934	CTGCCTCAGCCTCCCAAGTA	264325	96521	CTGACTCTAATTATGGATTT
175152	7348	AAAAAAGTAAAATCCCTGAA	219739	51935	CCTGCCTCAGCCTCCCAAGT	264326	96522	TCTGACTCTAATTATGGATT
175153	7349	AAAAAAAGTAAAATCCCTGA	219740	51936	TCCTGCCTCAGCCTCCCAAG	264327	96523	TTCTGACTCTAATTATGGAT
175154	7350	AAAAAAAAGTAAAATCCCTG	219741	51937	CTCCTGCCTCAGCCTCCCAA	264328	96524	TTTCTGACTCTAATTATGGA
175155	7351	AAAAAAAAAGTAAAATCCCT	219742	51938	TCTCCTGCCTCAGCCTCCCA	264329	96525	TTTTCTGACTCTAATTATGG
175156	7352	AAAAAAAAAAGTAAAATCCC	219743	51939	TTCTCCTGCCTCAGCCTCCC	264330	96526	ATTTTCTGACTCTAATTATG
175157	7353	AAAAAAAAAAAGTAAAATCC	219744	51940	ATTCTCCTGCCTCAGCCTCC	264331	96527	CATTTTCTGACTCTAATTAT
175158	7354	AAAAAAAAAAAAGTAAAATC	219745	51941	AATTCTCCTGCCTCAGCCTC	264332	96528	CCATTTTCTGACTCTAATTA
175159	7355	AAAAAAAAAAAAAGTAAAAT	219746	51942	CAATTCTCCTGCCTCAGCCT	264333	96529	TCCATTTTCTGACTCTAATT
175160	7356	AAAAAAAAAAAAAAGTAAAA	219747	51943	GCAATTCTCCTGCCTCAGCC	264334	96530	ATCCATTTTCTGACTCTAAT
175161	7357	AAAAAAAAAAAAAAAGTAAA	219748	51944	AGCAATTCTCCTGCCTCAGC	264335	96531	CATCCATTTTCTGACTCTAA
175162	7358	AAAAAAAAAAAAAAAAGTAA	219749	51945	AAGCAATTCTCCTGCCTCAG	264336	96532	ACATCCATTTTCTGACTCTA
175163	7359	GAAAAAAAAAAAAAAAAGTA	219750	51946	CAAGCAATTCTCCTGCCTCA	264337	96533	GACATCCATTTTCTGACTCT
175164	7360	TGAAAAAAAAAAAAAAAAGT	219751	51947	TCAAGCAATTCTCCTGCCTC	264338	96534	AGACATCCATTTTCTGACTC
175165	7361	ATGAAAAAAAAAAAAAAAAG	219752	51948	TTCAAGCAATTCTCCTGCCT	264339	96535	CAGACATCCATTTTCTGACT
175166	7362	CATGAAAAAAAAAAAAAAAA	219753	51949	GTTCAAGCAATTCTCCTGCC	264340	96536	GCAGACATCCATTTTCTGAC
175167	7363	CCATGAAAAAAAAAAAAAAA	219754	51950	GGTTCAAGCAATTCTCCTGC	264341	96537	TGCAGACATCCATTTTCTGA
175168	7364	ACCATGAAAAAAAAAAAAAA	219755	51951	GGGTTCAAGCAATTCTCCTG	264342	96538	ATGCAGACATCCATTTTCTG
175169	7365	GACCATGAAAAAAAAAAAAA	219756	51952	CGGGTTCAAGCAATTCTCCT	264343	96539	TATGCAGACATCCATTTTCT
175170	7366	AGACCATGAAAAAAAAAAAA	219757	51953	TCGGGTTCAAGCAATTCTCC	264344	96540	ATATGCAGACATCCATTTTC
175171	7367	AAGACCATGAAAAAAAAAAA	219758	51954	CTCGGGTTCAAGCAATTCTC	264345	96541	CATATGCAGACATCCATTTT
175172	7368	AAAGACCATGAAAAAAAAAA	219759	51955	TCTCGGGTTCAAGCAATTCT	264346	96542	ACATATGCAGACATCCATTT
175173	7369	TAAAGACCATGAAAAAAAAA	219760	51956	CTCTCGGGTTCAAGCAATTC	264347	96543	CACATATGCAGACATCCATT
175174	7370	GTAAAGACCATGAAAAAAAA	219761	51957	CCTCTCGGGTTCAAGCAATT	264348	96544	ACACATATGCAGACATCCAT
175175	7371	GGTAAAGACCATGAAAAAAA	219762	51958	ACCTCTCGGGTTCAAGCAAT	264349	96545	TACACATATGCAGACATCCA
175176	7372	TGGTAAAGACCATGAAAAAA	219763	51959	TACCTCTCGGGTTCAAGCAA	264350	96546	CTACACATATGCAGACATCC
175177	7373	ATGGTAAAGACCATGAAAAA	219764	51960	CTACCTCTCGGGTTCAAGCA	264351	96547	ACTACACATATGCAGACATC
175178	7374	GATGGTAAAGACCATGAAAA	219765	51961	TCTACCTCTCGGGTTCAAGC	264352	96548	CACTACACATATGCAGACAT
175179	7375	GGATGGTAAAGACCATGAAA	219766	51962	CTCTACCTCTCGGGTTCAAG	264353	96549	GCACTACACATATGCAGACA
175180	7376	GGGATGGTAAAGACCATGAA	219767	51963	CCTCTACCTCTCGGGTTCAA	264354	96550	TGCACTACACATATGCAGAC
175181	7377	TGGGATGGTAAAGACCATGA	219768	51964	ACCTCTACCTCTCGGGTTCA	264355	96551	GTGCACTACACATATGCAGA
175182	7378	ATGGGATGGTAAAGACCATG	219769	51965	AACCTCTACCTCTCGGGTTC	264356	96552	AGTGCACTACACATATGCAG
175183	7379	AATGGGATGGTAAAGACCAT	219770	51966	CAACCTCTACCTCTCGGGTT	264357	96553	TAGTGCACTACACATATGCA
175184	7380	AAATGGGATGGTAAAGACCA	219771	51967	GCAACCTCTACCTCTCGGGT	264358	96554	TTAGTGCACTACACATATGC
175185	7381	CAAATGGGATGGTAAAGACC	219772	51968	TGCAACCTCTACCTCTCGGG	264359	96555	ATTAGTGCACTACACATATG
175186	7382	TCAAATGGGATGGTAAAGAC	219773	51969	CTGCAACCTCTACCTCTCGG	264360	96556	CATTAGTGCACTACACATAT
175187	7383	ATCAAATGGGATGGTAAAGA	219774	51970	ACTGCAACCTCTACCTCTCG	264361	96557	ACATTAGTGCACTACACATA
175188	7384	TATCAAATGGGATGGTAAAG	219775	51971	CACTGCAACCTCTACCTCTC	264362	96558	GACATTAGTGCACTACACAT
175189	7385	CTATCAAATGGGATGGTAAA	219776	51972	TCACTGCAACCTCTACCTCT	264363	96559	GGACATTAGTGCACTACACA
175190	7386	ACTATCAAATGGGATGGTAA	219777	51973	CTCACTGCAACCTCTACCTC	264364	96560	AGGACATTAGTGCACTACAC
175191	7387	TACTATCAAATGGGATGGTA	219778	51974	GCTCACTGCAACCTCTACCT	264365	96561	CAGGACATTAGTGCACTACA
175192	7388	TTACTATCAAATGGGATGGT	219779	51975	GGCTCACTGCAACCTCTACC	264366	96562	GCAGGACATTAGTGCACTAC
175193	7389	TTTACTATCAAATGGGATGG	219780	51976	CGGCTCACTGCAACCTCTAC	264367	96563	GGCAGGACATTAGTGCACTA
175194	7390	ATTTACTATCAAATGGGATG	219781	51977	TCGGCTCACTGCAACCTCTA	264368	96564	CGGCAGGACATTAGTGCACT
175195	7391	TATTTACTATCAAATGGGAT	219782	51978	CTCGGCTCACTGCAACCTCT	264369	96565	TCGGCAGGACATTAGTGCAC
175196	7392	ATATTTACTATCAAATGGGA	219783	51979	TCTCGGCTCACTGCAACCTC	264370	96566	ATCGGCAGGACATTAGTGCA
175197	7393	AATATTTACTATCAAATGGG	219784	51980	ATCTCGGCTCACTGCAACCT	264371	96567	CATCGGCAGGACATTAGTGC
175198	7394	TAATATTTACTATCAAATGG	219785	51981	CATCTCGGCTCACTGCAACC	264372	96568	TCATCGGCAGGACATTAGTG
175199	7395	GTAATATTTACTATCAAATG	219786	51982	CCATCTCGGCTCACTGCAAC	264373	96569	ATCATCGGCAGGACATTAGT
175200	7396	AGTAATATTTACTATCAAAT	219787	51983	GCCATCTCGGCTCACTGCAA	264374	96570	AATCATCGGCAGGACATTAG
175201	7397	GAGTAATATTTACTATCAAA	219788	51984	TGCCATCTCGGCTCACTGCA	264375	96571	CAATCATCGGCAGGACATTA
175202	7398	TGAGTAATATTTACTATCAA	219789	51985	GTGCCATCTCGGCTCACTGC	264376	96572	TCAATCATCGGCAGGACATT
175203	7399	GTGAGTAATATTTACTATCA	219790	51986	GGTGCCATCTCGGCTCACTG	264377	96573	GTCAATCATCGGCAGGACAT
175204	7400	GGTGAGTAATATTTACTATC	219791	51987	TGGTGCCATCTCGGCTCACT	264378	96574	TGTCAATCATCGGCAGGACA
175205	7401	AGGTGAGTAATATTTACTAT	219792	51988	GTGGTGCCATCTCGGCTCAC	264379	96575	ATGTCAATCATCGGCAGGAC
175206	7402	AAGGTGAGTAATATTTACTA	219793	51989	GGTGGTGCCATCTCGGCTCA	264380	96576	CATGTCAATCATCGGCAGGA
175207	7403	AAAGGTGAGTAATATTTACT	219794	51990	TGGTGGTGCCATCTCGGCTC	264381	96577	CCATGTCAATCATCGGCAGG
175208	7404	TAAAGGTGAGTAATATTTAC	219795	51991	GTGGTGGTGCCATCTCGGCT	264382	96578	TCCATGTCAATCATCGGCAG
175209	7405	ATAAAGGTGAGTAATATTTA	219796	51992	TGTGGTGGTGCCATCTCGGC	264383	96579	CTCCATGTCAATCATCGGCA
175210	7406	CATAAAGGTGAGTAATATTT	219797	51993	GTGTGGTGGTGCCATCTCGG	264384	96580	ACTCCATGTCAATCATCGGC
175211	7407	TCATAAAGGTGAGTAATATT	219798	51994	AGTGTGGTGGTGCCATCTCG	264385	96581	CACTCCATGTCAATCATCGG
175212	7408	TTCATAAAGGTGAGTAATAT	219799	51995	GAGTGTGGTGGTGCCATCTC	264386	96582	CCACTCCATGTCAATCATCG
175213	7409	CTTCATAAAGGTGAGTAATA	219800	51996	GGAGTGTGGTGGTGCCATCT	264387	96583	TCCACTCCATGTCAATCATC
175214	7410	ACTTCATAAAGGTGAGTAAT	219801	51997	TGGAGTGTGGTGGTGCCATC	264388	96584	CTCCACTCCATGTCAATCAT
175215	7411	GACTTCATAAAGGTGAGTAA	219802	51998	CTGGAGTGTGGTGGTGCCAT	264389	96585	TCTCCACTCCATGTCAATCA
175216	7412	AGACTTCATAAAGGTGAGTA	219803	51999	GCTGGAGTGTGGTGGTGCCA	264390	96586	CTCTCCACTCCATGTCAATC
175217	7413	AAGACTTCATAAAGGTGAGT	219804	52000	GGCTGGAGTGTGGTGGTGCC	264391	96587	ACTCTCCACTCCATGTCAAT
175218	7414	AAAGACTTCATAAAGGTGAG	219805	52001	AGGCTGGAGTGTGGTGGTGC	264392	96588	CACTCTCCACTCCATGTCAA

175219	7415	GAAAGACTTCATAAAGGTGA	219806	52002	CAGGCTGGAGTGTGGTGGTG	264393	96589	TCACTCTCCACTCCATGTCA
175220	7416	GGAAAGACTTCATAAAGGTG	219807	52003	CCAGGCTGGAGTGTGGTGGT	264394	96590	GTCACTCTCCACTCCATGTC
175221	7417	TGGAAAGACTTCATAAAGGT	219808	52004	CCCAGGCTGGAGTGTGGTGG	264395	96591	GGTCACTCTCCACTCCATGT
175222	7418	TTGGAAAGACTTCATAAAGG	219809	52005	GCCCAGGCTGGAGTGTGGTG	264396	96592	AGGTCACTCTCCACTCCATG
175223	7419	TTTGGAAAGACTTCATAAAG	219810	52006	CGCCCAGGCTGGAGTGTGGT	264397	96593	CAGGTCACTCTCCACTCCAT
175224	7420	TTTTGGAAAGACTTCATAAA	219811	52007	TCGCCCAGGCTGGAGTGTGG	264398	96594	TCAGGTCACTCTCCACTCCA
175225	7421	GTTTTGGAAAGACTTCATAA	219812	52008	GTCGCCCAGGCTGGAGTGTG	264399	96595	ATCAGGTCACTCTCCACTCC
175226	7422	TGTTTTGGAAAGACTTCATA	219813	52009	GGTCGCCCAGGCTGGAGTGT	264400	96596	GATCAGGTCACTCTCCACTC
175227	7423	ATGTTTTGGAAAGACTTCAT	219814	52010	CGGTCGCCCAGGCTGGAGTG	264401	96597	TGATCAGGTCACTCTCCACT
175228	7424	AATGTTTTGGAAAGACTTCA	219815	52011	TCGGTCGCCCAGGCTGGAGT	264402	96598	ATGATCAGGTCACTCTCCAC
175229	7425	GAATGTTTTGGAAAGACTTC	219816	52012	CTCGGTCGCCCAGGCTGGAG	264403	96599	AATGATCAGGTCACTCTCCA
175230	7426	TGAATGTTTTGGAAAGACTT	219817	52013	CCTCGGTCGCCCAGGCTGGA	264404	96600	CAATGATCAGGTCACTCTCC
175231	7427	TTGAATGTTTTGGAAAGACT	219818	52014	CCCTCGGTCGCCCAGGCTGG	264405	96601	GCAATGATCAGGTCACTCTC
175232	7428	GTTGAATGTTTTGGAAAGAC	219819	52015	CCCCTCGGTCGCCCAGGCTG	264406	96602	AGCAATGATCAGGTCACTCT
175233	7429	AGTTGAATGTTTTGGAAAGA	219820	52016	CCCCCTCGGTCGCCCAGGCT	264407	96603	CAGCAATGATCAGGTCACTC
175234	7430	TAGTTGAATGTTTTGGAAAG	219821	52017	TCCCCCTCGGTCGCCCAGGC	264408	96604	ACAGCAATGATCAGGTCACT
175235	7431	TTAGTTGAATGTTTTGGAAA	219822	52018	GTCCCCCTCGGTCGCCCAGG	264409	96605	CACAGCAATGATCAGGTCAC
175236	7432	TTTAGTTGAATGTTTTGGAA	219823	52019	AGTCCCCCTCGGTCGCCCAG	264410	96606	TCACAGCAATGATCAGGTCA
175237	7433	ATTTAGTTGAATGTTTTGGA	219824	52020	GAGTCCCCCTCGGTCGCCCA	264411	96607	CTCACAGCAATGATCAGGTC
175238	7434	AATTTAGTTGAATGTTTTGG	219825	52021	AGAGTCCCCCTCGGTCGCCC	264412	96608	GCTCACAGCAATGATCAGGT
175239	7435	AAATTTAGTTGAATGTTTTG	219826	52022	CAGAGTCCCCCTCGGTCGCC	264413	96609	AGCTCACAGCAATGATCAGG
175240	7436	AAAATTTAGTTGAATGTTTT	219827	52023	ACAGAGTCCCCCTCGGTCGC	264414	96610	GAGCTCACAGCAATGATCAG
175241	7437	GAAAATTTAGTTGAATGTTT	219828	52024	GACAGAGTCCCCCTCGGTCG	264415	96611	AGAGCTCACAGCAATGATCA
175242	7438	AGAAAATTTAGTTGAATGTT	219829	52025	AGACAGAGTCCCCCTCGGTC	264416	96612	CAGAGCTCACAGCAATGATC
175243	7439	AAGAAAATTTAGTTGAATGT	219830	52026	AAGACAGAGTCCCCCTCGGT	264417	96613	GCAGAGCTCACAGCAATGAT
175244	7440	TAAGAAAATTTAGTTGAATG	219831	52027	TAAGACAGAGTCCCCCTCGG	264418	96614	AGCAGAGCTCACAGCAATGA
175245	7441	TTAAGAAAATTTAGTTGAAT	219832	52028	TTAAGACAGAGTCCCCCTCG	264419	96615	CAGCAGAGCTCACAGCAATG
175246	7442	TTTAAGAAAATTTAGTTGAA	219833	52029	TTTAAGACAGAGTCCCCCTC	264420	96616	CCAGCAGAGCTCACAGCAAT
175247	7443	TTTTAAGAAAATTTAGTTGA	219834	52030	TTTTAAGACAGAGTCCCCCT	264421	96617	GCCAGCAGAGCTCACAGCAA
175248	7444	ATTTTAAGAAAATTTAGTTG	219835	52031	TTTTTAAGACAGAGTCCCCC	264422	96618	GGCCAGCAGAGCTCACAGCA
175249	7445	GATTTTAAGAAAATTTAGTT	219836	52032	TTTTTTAAGACAGAGTCCCC	264423	96619	AGGCCAGCAGAGCTCACAGC
175250	7446	TGATTTTAAGAAAATTTAGT	219837	52033	TTTTTTTAAGACAGAGTCCC	264424	96620	AAGGCCAGCAGAGCTCACAG
175251	7447	ATGATTTTAAGAAAATTTAG	219838	52034	TTTTTTTTAAGACAGAGTCC	264425	96621	CAAGGCCAGCAGAGCTCACA
175252	7448	AATGATTTTAAGAAAATTTA	219839	52035	TTTTTTTTTAAGACAGAGTC	264426	96622	CCAAGGCCAGCAGAGCTCAC
175253	7449	CAATGATTTTAAGAAAATTT	219840	52036	TTTTTTTTTTAAGACAGAGT	264427	96623	GCCAAGGCCAGCAGAGCTCA
175254	7450	TCAATGATTTTAAGAAAATT	219841	52037	TTTTTTTTTTTAAGACAGAG	264428	96624	TGCCAAGGCCAGCAGAGCTC
175255	7451	TTCAATGATTTTAAGAAAAT	219842	52038	TTTTTTTTTTTTAAGACAGA	264429	96625	GTGCCAAGGCCAGCAGAGCT
175256	7452	ATTCAATGATTTTAAGAAAA	219843	52039	TTTTTTTTTTTTTAAGACAG	264430	96626	TGTGCCAAGGCCAGCAGAGC
175257	7453	CATTCAATGATTTTAAGAAA	219844	52040	TTTTTTTTTTTTTTAAGACA	264431	96627	TTGTGCCAAGGCCAGCAGAG
175258	7454	TCATTCAATGATTTTAAGAA	219845	52041	TTTTTTTTTTTTTTTAAGAC	264432	96628	GTTGTGCCAAGGCCAGCAGA
175259	7455	ATCATTCAATGATTTTAAGA	219846	52042	TTTTTTTTTTTTTTTTAAGA	264433	96629	AGTTGTGCCAAGGCCAGCAG
175260	7456	AATCATTCAATGATTTTAAG	219847	52043	TTTTTTTTTTTTTTTTTAAG	264434	96630	GAGTTGTGCCAAGGCCAGCA
175261	7457	AAATCATTCAATGATTTTAA	219848	52044	TTTTTTTTTTTTTTTTTAA	264435	96631	TGAGTTGTGCCAAGGCCAGC
175262	7458	CAAATCATTCAATGATTTTA	219849	52045	ATTTTTTTTTTTTTTTTTA	264436	96632	ATGAGTTGTGCCAAGGCCAG
175263	7459	TCAAATCATTCAATGATTTT	219850	52046	TATTTTTTTTTTTTTTTTT	264437	96633	CATGAGTTGTGCCAAGGCCA
175264	7460	TTCAAATCATTCAATGATTT	219851	52047	ATATTTTTTTTTTTTTTTT	264438	96634	GCATGAGTTGTGCCAAGGCC
175265	7461	CTTCAAATCATTCAATGATT	219852	52048	TATATTTTTTTTTTTTTTT	264439	96635	AGCATGAGTTGTGCCAAGGC
175266	7462	TCTTCAAATCATTCAATGAT	219853	52049	ATATATTTTTTTTTTTTTT	264440	96636	CAGCATGAGTTGTGCCAAGG
175267	7463	CTCTTCAAATCATTCAATGA	219854	52050	TATATATTTTTTTTTTTTT	264441	96637	TCAGCATGAGTTGTGCCAAG
175268	7464	GCTCTTCAAATCATTCAATG	219855	52051	ATATATATTTTTTTTTTTT	264442	96638	ATCAGCATGAGTTGTGCCAA
175269	7465	AGCTCTTCAAATCATTCAAT	219856	52052	TATATATATTTTTTTTTTT	264443	96639	TATCAGCATGAGTTGTGCCA
175270	7466	AAGCTCTTCAAATCATTCAA	219857	52053	ATATATATATTTTTTTTTT	264444	96640	TTATCAGCATGAGTTGTGCC
175271	7467	TAAGCTCTTCAAATCATTCA	219858	52054	TATATATATATTTTTTTTT	264445	96641	GTTATCAGCATGAGTTGTGC
175272	7468	ATAAGCTCTTCAAATCATTC	219859	52055	ATATATATATATTTTTTTT	264446	96642	AGTTATCAGCATGAGTTGTG
175273	7469	AATAAGCTCTTCAAATCATT	219860	52056	TATATATATATATTTTTTT	264447	96643	TAGTTATCAGCATGAGTTGT
175274	7470	GAATAAGCTCTTCAAATCAT	219861	52057	ATATATATATATATTTTTT	264448	96644	TTAGTTATCAGCATGAGTTG
175275	7471	GGAATAAGCTCTTCAAATCA	219862	52058	TATATATATATATATTTTT	264449	96645	ATTAGTTATCAGCATGAGTT
175276	7472	AGGAATAAGCTCTTCAAATC	219863	52059	ATATATATATATATATTTT	264450	96646	CATTAGTTATCAGCATGAGT
175277	7473	GAGGAATAAGCTCTTCAAAT	219864	52060	TATATATATATATATATTT	264451	96647	GCATTAGTTATCAGCATGAG
175278	7474	TGAGGAATAAGCTCTTCAAA	219865	52061	ATATATATATATATATATT	264452	96648	TGCATTAGTTATCAGCATGA
175279	7475	CTGAGGAATAAGCTCTTCAA	219866	52062	TATATATATATATATATAT	264453	96649	GTGCATTAGTTATCAGCATG
175280	7476	GCTGAGGAATAAGCTCTTCA	219867	52063	ATATATATATATATATATA	264454	96650	TGTGCATTAGTTATCAGCAT
175281	7477	TGCTGAGGAATAAGCTCTTC	219868	52064	TATATATATATATATATATA	264455	96651	GTGTGCATTAGTTATCAGCA
175282	7478	GTGCTGAGGAATAAGCTCTT	219869	52065	ATATATATATATATATATAT	264456	96652	TGTGTGCATTAGTTATCAGC
175283	7479	AGTGCTGAGGAATAAGCTCT	219870	52066	TATATATATATATATATATA	264457	96653	CTGTGTGCATTAGTTATCAG
175284	7480	AAGTGCTGAGGAATAAGCTC	219871	52067	ATATATATATATATATATAT	264458	96654	ACTGTGTGCATTAGTTATCA
175285	7481	AAAGTGCTGAGGAATAAGCT	219872	52068	CATATATATATATATATATA	264459	96655	AACTGTGTGCATTAGTTATC
175286	7482	AAAAGTGCTGAGGAATAAGC	219873	52069	ACATATATATATATATATAT	264460	96656	GAACTGTGTGCATTAGTTAT
175287	7483	TAAAAGTGCTGAGGAATAAG	219874	52070	GACATATATATATATATATA	264461	96657	GGAACTGTGTGCATTAGTTA
175288	7484	GTAAAAGTGCTGAGGAATAA	219875	52071	TGACATATATATATATATAT	264462	96658	AGGAACTGTGTGCATTAGTT
175289	7485	AGTAAAAGTGCTGAGGAATA	219876	52072	TTGACATATATATATATATA	264463	96659	GAGGAACTGTGTGCATTAGT
175290	7486	GAGTAAAAGTGCTGAGGAAT	219877	52073	TTTGACATATATATATATAT	264464	96660	AGAGGAACTGTGTGCATTAG

175291	7487	GGAGTAAAAGTGCTGAGGAA	219878	52074	TTTTGACATATATATATATA	264465	96661	CAGAGGAACTGTGTGCATTA
175292	7488	TGGAGTAAAAGTGCTGAGGA	219879	52075	TTTTTGACATATATATATAT	264466	96662	CCAGAGGAACTGTGTGCATT
175293	7489	ATGGAGTAAAAGTGCTGAGG	219880	52076	ATTTTTGACATATATATATA	264467	96663	CCCAGAGGAACTGTGTGCAT
175294	7490	GATGGAGTAAAAGTGCTGAG	219881	52077	CATTTTTGACATATATATAT	264468	96664	TCCCAGAGGAACTGTGTGCA
175295	7491	TGATGGAGTAAAAGTGCTGA	219882	52078	CCATTTTTGACATATATATA	264469	96665	CTCCCAGAGGAACTGTGTGC
175296	7492	CTGATGGAGTAAAAGTGCTG	219883	52079	CCCATTTTTGACATATATAT	264470	96666	CCTCCCAGAGGAACTGTGTG
175297	7493	GCTGATGGAGTAAAAGTGCT	219884	52080	CCCCATTTTTGACATATATA	264471	96667	TCCTCCCAGAGGAACTGTGT
175298	7494	AGCTGATGGAGTAAAAGTGC	219885	52081	ACCCCATTTTTGACATATAT	264472	96668	TTCCTCCCAGAGGAACTGTG
175299	7495	AAGCTGATGGAGTAAAAGTG	219886	52082	TACCCCATTTTTGACATATA	264473	96669	TTTCCTCCCAGAGGAACTGT
175300	7496	CAAGCTGATGGAGTAAAAGT	219887	52083	CTACCCCATTTTTGACATAT	264474	96670	ATTTCCTCCCAGAGGAACTG
175301	7497	GCAAGCTGATGGAGTAAAAG	219888	52084	ACTACCCCATTTTTGACATA	264475	96671	CATTTCCTCCCAGAGGAACT
175302	7498	TGCAAGCTGATGGAGTAAAA	219889	52085	AACTACCCCATTTTTGACAT	264476	96672	ACATTTCCTCCCAGAGGAAC
175303	7499	GTGCAAGCTGATGGAGTAAA	219890	52086	AAACTACCCCATTTTTGACA	264477	96673	GACATTTCCTCCCAGAGGAA
175304	7500	GGTGCAAGCTGATGGAGTAA	219891	52087	AAAACTACCCCATTTTTGAC	264478	96674	GGACATTTCCTCCCAGAGGA
175305	7501	AGGTGCAAGCTGATGGAGTA	219892	52088	AAAAACTACCCCATTTTTGA	264479	96675	AGGACATTTCCTCCCAGAGG
175306	7502	AAGGTGCAAGCTGATGGAGT	219893	52089	TAAAAACTACCCCATTTTTG	264480	96676	GAGGACATTTCCTCCCAGAG
175307	7503	TAAGGTGCAAGCTGATGGAG	219894	52090	CTAAAAACTACCCCATTTTT	264481	96677	TGAGGACATTTCCTCCCAGA
175308	7504	ATAAGGTGCAAGCTGATGGA	219895	52091	TCTAAAAACTACCCCATTTT	264482	96678	CTGAGGACATTTCCTCCCAG
175309	7505	AATAAGGTGCAAGCTGATGG	219896	52092	ATCTAAAAACTACCCCATTT	264483	96679	CCTGAGGACATTTCCTCCCA
175310	7506	AAATAAGGTGCAAGCTGATG	219897	52093	GATCTAAAAACTACCCCATT	264484	96680	CCCTGAGGACATTTCCTCCC
175311	7507	AAAATAAGGTGCAAGCTGAT	219898	52094	AGATCTAAAAACTACCCCAT	264485	96681	TCCCTGAGGACATTTCCTCC
175312	7508	AAAAATAAGGTGCAAGCTGA	219899	52095	TAGATCTAAAAACTACCCCA	264486	96682	TTCCCTGAGGACATTTCCTC
175313	7509	AAAAAATAAGGTGCAAGCTG	219900	52096	ATAGATCTAAAAACTACCCC	264487	96683	GTTCCCTGAGGACATTTCCT
175314	7510	TAAAAAATAAGGTGCAAGCT	219901	52097	TATAGATCTAAAAACTACCC	264488	96684	AGTTCCCTGAGGACATTTCC
175315	7511	TTAAAAAATAAGGTGCAAGC	219902	52098	CTATAGATCTAAAAACTACC	264489	96685	AAGTTCCCTGAGGACATTTC
175316	7512	ATTAAAAAATAAGGTGCAAG	219903	52099	ACTATAGATCTAAAAACTAC	264490	96686	CAAGTTCCCTGAGGACATTT
175317	7513	GATTAAAAAATAAGGTGCAA	219904	52100	TACTATAGATCTAAAAACTA	264491	96687	CCAAGTTCCCTGAGGACATT
175318	7514	AGATTAAAAAATAAGGTGCA	219905	52101	CTACTATAGATCTAAAAACT	264492	96688	TCCAAGTTCCCTGAGGACAT
175319	7515	AAGATTAAAAAATAAGGTGC	219906	52102	ACTACTATAGATCTAAAAAC	264493	96689	CTCCAAGTTCCCTGAGGACA
175320	7516	AAAGATTAAAAAATAAGGTG	219907	52103	AACTACTATAGATCTAAAAA	264494	96690	ACTCCAAGTTCCCTGAGGAC
175321	7517	AAAAGATTAAAAAATAAGGT	219908	52104	GAACTACTATAGATCTAAAA	264495	96691	AACTCCAAGTTCCCTGAGGA
175322	7518	AAAAAGATTAAAAAATAAGG	219909	52105	AGAACTACTATAGATCTAAA	264496	96692	AAACTCCAAGTTCCCTGAGG
175323	7519	AAAAAAGATTAAAAAATAAG	219910	52106	TAGAACTACTATAGATCTAA	264497	96693	CAAACTCCAAGTTCCCTGAG
175324	7520	AAAAAAAGATTAAAAAATAA	219911	52107	TTAGAACTACTATAGATCTA	264498	96694	CCAAACTCCAAGTTCCCTGA
175325	7521	CAAAAAAAGATTAAAAAATA	219912	52108	TTTAGAACTACTATAGATCT	264499	96695	CCCAAACTCCAAGTTCCCTG
175326	7522	TCAAAAAAAGATTAAAAAAT	219913	52109	TTTTAGAACTACTATAGATC	264500	96696	ACCCAAACTCCAAGTTCCCT
175327	7523	CTCAAAAAAAGATTAAAAAA	219914	52110	TTTTTAGAACTACTATAGAT	264501	96697	CACCCAAACTCCAAGTTCCC
175328	7524	TCTCAAAAAAAGATTAAAAA	219915	52111	GTTTTTAGAACTACTATAGA	264502	96698	CCACCCAAACTCCAAGTTCC
175329	7525	GTCTCAAAAAAAGATTAAAA	219916	52112	TGTTTTTAGAACTACTATAG	264503	96699	CCCACCCAAACTCCAAGTTC
175330	7526	CGTCTCAAAAAAAGATTAAA	219917	52113	TTGTTTTTAGAACTACTATA	264504	96700	CCCCACCCAAACTCCAAGTT
175331	7527	CCGTCTCAAAAAAAGATTAA	219918	52114	TTTGTTTTTAGAACTACTAT	264505	96701	TCCCCACCCAAACTCCAAGT
175332	7528	TCCGTCTCAAAAAAAGATTA	219919	52115	CTTTGTTTTTAGAACTACTA	264506	96702	ATCCCCACCCAAACTCCAAG
175333	7529	CTCCGTCTCAAAAAAAGATT	219920	52116	CCTTTGTTTTTAGAACTACT	264507	96703	CATCCCCACCCAAACTCCAA
175334	7530	ACTCCGTCTCAAAAAAAGAT	219921	52117	GCCTTTGTTTTTAGAACTAC	264508	96704	ACATCCCCACCCAAACTCCA
175335	7531	GACTCCGTCTCAAAAAAAGA	219922	52118	GGCCTTTGTTTTTAGAACTA	264509	96705	CACATCCCCACCCAAACTCC
175336	7532	AGACTCCGTCTCAAAAAAAG	219923	52119	TGGCCTTTGTTTTTAGAACT	264510	96706	CCACATCCCCACCCAAACTC
175337	7533	GAGACTCCGTCTCAAAAAAA	219924	52120	ATGGCCTTTGTTTTTAGAAC	264511	96707	CCCACATCCCCACCCAAACT
175338	7534	CGAGACTCCGTCTCAAAAAA	219925	52121	GATGGCCTTTGTTTTTAGAA	264512	96708	ACCCACATCCCCACCCAAAC
175339	7535	GCGAGACTCCGTCTCAAAAA	219926	52122	GGATGGCCTTTGTTTTTAGA	264513	96709	AACCCACATCCCCACCCAAA
175340	7536	AGCGAGACTCCGTCTCAAAA	219927	52123	TGGATGGCCTTTGTTTTTAG	264514	96710	AAACCCACATCCCCACCCAA
175341	7537	GAGCGAGACTCCGTCTCAAA	219928	52124	TTGGATGGCCTTTGTTTTTA	264515	96711	CAAACCCACATCCCCACCCA
175342	7538	AGAGCGAGACTCCGTCTCAA	219929	52125	CTTGGATGGCCTTTGTTTTT	264516	96712	ACAAACCCACATCCCCACCC
175343	7539	TAGAGCGAGACTCCGTCTCA	219930	52126	GCTTGGATGGCCTTTGTTTT	264517	96713	CACAAACCCACATCCCCACC
175344	7540	ATAGAGCGAGACTCCGTCTC	219931	52127	TGCTTGGATGGCCTTTGTTT	264518	96714	ACACAAACCCACATCCCCAC
175345	7541	GATAGAGCGAGACTCCGTCT	219932	52128	ATGCTTGGATGGCCTTTGTT	264519	96715	CACACAAACCCACATCCCCA
175346	7542	CGATAGAGCGAGACTCCGTC	219933	52129	CATGCTTGGATGGCCTTTGT	264520	96716	GCACACAAACCCACATCCCC
175347	7543	GCGATAGAGCGAGACTCCGT	219934	52130	TCATGCTTGGATGGCCTTTG	264521	96717	GGCACACAAACCCACATCCC
175348	7544	GGCGATAGAGCGAGACTCCG	219935	52131	GTCATGCTTGGATGGCCTTT	264522	96718	GGGCACACAAACCCACATCC
175349	7545	GGGCGATAGAGCGAGACTCC	219936	52132	TGTCATGCTTGGATGGCCTT	264523	96719	TGGGCACACAAACCCACATC
175350	7546	TGGGCGATAGAGCGAGACTC	219937	52133	CTGTCATGCTTGGATGGCCT	264524	96720	CTGGGCACACAAACCCACAT
175351	7547	CTGGGCGATAGAGCGAGACT	219938	52134	TCTGTCATGCTTGGATGGCC	264525	96721	GCTGGGCACACAAACCCACA
175352	7548	CCTGGGCGATAGAGCGAGAC	219939	52135	ATCTGTCATGCTTGGATGGC	264526	96722	TGCTGGGCACACAAACCCAC
175353	7549	GCCTGGGCGATAGAGCGAGA	219940	52136	AATCTGTCATGCTTGGATGG	264527	96723	TTGCTGGGCACACAAACCCA
175354	7550	AGCCTGGGCGATAGAGCGAG	219941	52137	AAATCTGTCATGCTTGGATG	264528	96724	CTTGCTGGGCACACAAACCC
175355	7551	AAGCCTGGGCGATAGAGCGA	219942	52138	TAAATCTGTCATGCTTGGAT	264529	96725	GCTTGCTGGGCACACAAACC
175356	7552	TAAGCCTGGGCGATAGAGCG	219943	52139	GTAAATCTGTCATGCTTGGA	264530	96726	GGCTTGCTGGGCACACAAAC
175357	7553	TTAAGCCTGGGCGATAGAGC	219944	52140	TGTAAATCTGTCATGCTTGG	264531	96727	GGGCTTGCTGGGCACACAAA
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175359	7555	ACTTAAGCCTGGGCGATAGA	219946	52142	CTTGTAAATCTGTCATGCTT	264533	96729	AAGGGCTTGCTGGGCACACA
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175361	7557	GCACTTAAGCCTGGGCGATA	219948	52144	TGCTTGTAAATCTGTCATGC	264535	96731	ACAAGGGCTTGCTGGGCACA
175362	7558	TGCACTTAAGCCTGGGCGAT	219949	52145	GTGCTTGTAAATCTGTCATG	264536	96732	CACAAGGGCTTGCTGGGCAC

175363	7559	TTGCACTTAAGCCTGGGCGA	219950	52146	AGTGCTTGTAAATCTGTCAT	264537	96733	CCACAAGGGCTTGCTGGGCA
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175365	7561	CATTGCACTTAAGCCTGGGC	219952	52148	ATAGTGCTTGTAAATCTGTC	264539	96735	AACCACAAGGGCTTGCTGGG
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175379	7575	AGCCAAGATCGCGCCATTGC	219966	52162	TACTGGAATAGCCAATAGTG	264553	96749	CTAGTGTCTGCTACAACCAC
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175384	7580	CAGTGAGCCAAGATCGCGCC	219971	52167	GTAACTACTGGAATAGCCAA	264558	96754	TGCCACTAGTGTCTGCTACA
175385	7581	GCAGTGAGCCAAGATCGCGC	219972	52168	TGTAACTACTGGAATAGCCA	264559	96755	ATGCCACTAGTGTCTGCTAC
175386	7582	CGCAGTGAGCCAAGATCGCG	219973	52169	TTGTAACTACTGGAATAGCC	264560	96756	GATGCCACTAGTGTCTGCTA
175387	7583	TCGCAGTGAGCCAAGATCGC	219974	52170	ATTGTAACTACTGGAATAGC	264561	96757	AGATGCCACTAGTGTCTGCT
175388	7584	GTCGCAGTGAGCCAAGATCG	219975	52171	CATTGTAACTACTGGAATAG	264562	96758	TAGATGCCACTAGTGTCTGC
175389	7585	GGTCGCAGTGAGCCAAGATC	219976	52172	CCATTGTAACTACTGGAATA	264563	96759	CTAGATGCCACTAGTGTCTG
175390	7586	AGGTCGCAGTGAGCCAAGAT	219977	52173	TCCATTGTAACTACTGGAAT	264564	96760	CCTAGATGCCACTAGTGTCT
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175392	7588	GGAGGTCGCAGTGAGCCAAG	219979	52175	CCTCCATTGTAACTACTGGA	264566	96762	CTCCTAGATGCCACTAGTGT
175393	7589	TGGAGGTCGCAGTGAGCCAA	219980	52176	TCCTCCATTGTAACTACTGG	264567	96763	CCTCCTAGATGCCACTAGTG
175394	7590	GTGGAGGTCGCAGTGAGCCA	219981	52177	CTCCTCCATTGTAACTACTG	264568	96764	GCCTCCTAGATGCCACTAGT
175395	7591	GGTGGAGGTCGCAGTGAGCC	219982	52178	TCTCCTCCATTGTAACTACT	264569	96765	TGCCTCCTAGATGCCACTAG
175396	7592	AGGTGGAGGTCGCAGTGAGC	219983	52179	CTCTCCTCCATTGTAACTAC	264570	96766	TTGCCTCCTAGATGCCACTA
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175398	7594	GGAGGTGGAGGTCGCAGTGA	219985	52181	TTCTCTCCTCCATTGTAACT	264572	96768	CTTTGCCTCCTAGATGCCAC
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175402	7598	CCCAGGAGGTGGAGGTCGCA	219989	52185	AAGCTTCTCTCCTCCATTGT	264576	96772	GACCCTTTGCCTCCTAGATG
175403	7599	ACCCAGGAGGTGGAGGTCGC	219990	52186	AAAGCTTCTCTCCTCCATTG	264577	96773	TGACCCTTTGCCTCCTAGAT
175404	7600	AACCCAGGAGGTGGAGGTCG	219991	52187	AAAAGCTTCTCTCCTCCATT	264578	96774	GTGACCCTTTGCCTCCTAGA
175405	7601	GAACCCAGGAGGTGGAGGTC	219992	52188	TAAAAGCTTCTCTCCTCCAT	264579	96775	GGTGACCCTTTGCCTCCTAG
175406	7602	TGAACCCAGGAGGTGGAGGT	219993	52189	CTAAAAGCTTCTCTCCTCCA	264580	96776	GGGTGACCCTTTGCCTCCTA
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175408	7604	CTTGAACCCAGGAGGTGGAG	219995	52191	AACTAAAAGCTTCTCTCCTC	264582	96778	TGGGGTGACCCTTTGCCTCC
175409	7605	GCTTGAACCCAGGAGGTGGA	219996	52192	TAACTAAAAGCTTCTCTCCT	264583	96779	CTGGGGTGACCCTTTGCCTC
175410	7606	TGCTTGAACCCAGGAGGTGG	219997	52193	TTAACTAAAAGCTTCTCTCC	264584	96780	ACTGGGGTGACCCTTTGCCT
175411	7607	TTGCTTGAACCCAGGAGGTG	219998	52194	TTTAACTAAAAGCTTCTCTC	264585	96781	GACTGGGGTGACCCTTTGCC
175412	7608	ATTGCTTGAACCCAGGAGGT	219999	52195	TTTTAACTAAAAGCTTCTCT	264586	96782	AGACTGGGGTGACCCTTTGC
175413	7609	AATTGCTTGAACCCAGGAGG	220000	52196	GTTTTAACTAAAAGCTTCTC	264587	96783	AAGACTGGGGTGACCCTTTG
175414	7610	GAATTGCTTGAACCCAGGAG	220001	52197	TGTTTTAACTAAAAGCTTCT	264588	96784	TAAGACTGGGGTGACCCTTT
175415	7611	GGAATTGCTTGAACCCAGGA	220002	52198	TTGTTTTAACTAAAAGCTTC	264589	96785	CTAAGACTGGGGTGACCCTT
175416	7612	CGGAATTGCTTGAACCCAGG	220003	52199	TTTGTTTTAACTAAAAGCTT	264590	96786	GCTAAGACTGGGGTGACCCT
175417	7613	GCGGAATTGCTTGAACCCAG	220004	52200	GTTTGTTTTAACTAAAAGCT	264591	96787	GGCTAAGACTGGGGTGACCC
175418	7614	GGCGGAATTGCTTGAACCCA	220005	52201	TGTTTGTTTTAACTAAAAGC	264592	96788	TGGCTAAGACTGGGGTGACC
175419	7615	AGGCGGAATTGCTTGAACCC	220006	52202	TTGTTTGTTTTAACTAAAAG	264593	96789	GTGGCTAAGACTGGGGTGAC
175420	7616	GAGGCGGAATTGCTTGAACC	220007	52203	TTTGTTTGTTTTAACTAAAA	264594	96790	CGTGGCTAAGACTGGGGTGA
175421	7617	TGAGGCGGAATTGCTTGAAC	220008	52204	GTTTGTTTGTTTTAACTAAA	264595	96791	ACGTGGCTAAGACTGGGGTG
175422	7618	CTGAGGCGGAATTGCTTGAA	220009	52205	TGTTTGTTTGTTTTAACTAA	264596	96792	AACGTGGCTAAGACTGGGGT
175423	7619	GCTGAGGCGGAATTGCTTGA	220010	52206	TTGTTTGTTTGTTTTAACTA	264597	96793	AAACGTGGCTAAGACTGGGG
175424	7620	GGCTGAGGCGGAATTGCTTG	220011	52207	GTTGTTTGTTTGTTTTAACT	264598	96794	AAAACGTGGCTAAGACTGGG
175425	7621	AGGCTGAGGCGGAATTGCTT	220012	52208	TGTTGTTTGTTTGTTTTAAC	264599	96795	CAAAACGTGGCTAAGACTGG
175426	7622	GAGGCTGAGGCGGAATTGCT	220013	52209	GTGTTGTTTGTTTGTTTTAA	264600	96796	TCAAAACGTGGCTAAGACTG
175427	7623	GGAGGCTGAGGCGGAATTGC	220014	52210	TGTGTTGTTTGTTTGTTTTA	264601	96797	CTCAAAACGTGGCTAAGACT
175428	7624	CGGAGGCTGAGGCGGAATTG	220015	52211	TTGTGTTGTTTGTTTGTTTT	264602	96798	ACTCAAAACGTGGCTAAGAC
175429	7625	GCGGAGGCTGAGGCGGAATT	220016	52212	GTTGTGTTGTTTGTTTGTTT	264603	96799	GACTCAAAACGTGGCTAAGA
175430	7626	GGCGGAGGCTGAGGCGGAAT	220017	52213	TGTTGTGTTGTTTGTTTGTT	264604	96800	TGACTCAAAACGTGGCTAAG
175431	7627	CGGCGGAGGCTGAGGCGGAA	220018	52214	TTGTTGTGTTGTTTGTTTGT	264605	96801	TTGACTCAAAACGTGGCTAA
175432	7628	ACGGCGGAGGCTGAGGCGGA	220019	52215	TTTGTTGTGTTGTTTGTTTG	264606	96802	CTTGACTCAAAACGTGGCTA
175433	7629	TACGGCGGAGGCTGAGGCGG	220020	52216	GTTTGTTGTGTTGTTTGTTT	264607	96803	CCTTGACTCAAAACGTGGCT
175434	7630	CTACGGCGGAGGCTGAGGCG	220021	52217	GGTTTGTTGTGTTGTTTGTT	264608	96804	ACCTTGACTCAAAACGTGGC

175435	7631	GCTACGGCGGAGGCTGAGGC	220022	52218	GGGTTTGTTGTGTTGTTTGT	264609	96805	CACCTTGACTCAAAACGTGG
175436	7632	GGCTACGGCGGAGGCTGAGG	220023	52219	TGGGTTTGTTGTGTTGTTTG	264610	96806	CCACCTTGACTCAAAACGTG
175437	7633	CGGCTACGGCGGAGGCTGAG	220024	52220	CTGGGTTTGTTGTGTTGTTT	264611	96807	GCCACCTTGACTCAAAACGT
175438	7634	CCGGCTACGGCGGAGGCTGA	220025	52221	TCTGGGTTTGTTGTGTTGTT	264612	96808	CGCCACCTTGACTCAAAACG
175439	7635	CCCGGCTACGGCGGAGGCTG	220026	52222	TTCTGGGTTTGTTGTGTTGT	264613	96809	CCGCCACCTTGACTCAAAAC
175440	7636	TCCCGGCTACGGCGGAGGCT	220027	52223	TTTCTGGGTTTGTTGTGTTG	264614	96810	TCCGCCACCTTGACTCAAAA
175441	7637	GTCCCGGCTACGGCGGAGGC	220028	52224	GTTTCTGGGTTTGTTGTGTT	264615	96811	CTCCGCCACCTTGACTCAAA
175442	7638	AGTCCCGGCTACGGCGGAGG	220029	52225	GGTTTCTGGGTTTGTTGTGT	264616	96812	ACTCCGCCACCTTGACTCAA
175443	7639	TAGTCCCGGCTACGGCGGAG	220030	52226	AGGTTTCTGGGTTTGTTGTG	264617	96813	CACTCCGCCACCTTGACTCA
175444	7640	GTAGTCCCGGCTACGGCGGA	220031	52227	AAGGTTTCTGGGTTTGTTGT	264618	96814	CCACTCCGCCACCTTGACTC
175445	7641	TGTAGTCCCGGCTACGGCGG	220032	52228	TAAGGTTTCTGGGTTTGTTG	264619	96815	CCCACTCCGCCACCTTGACT
175446	7642	CTGTAGTCCCGGCTACGGCG	220033	52229	CTAAGGTTTCTGGGTTTGTT	264620	96816	CCCCACTCCGCCACCTTGAC
175447	7643	CCTGTAGTCCCGGCTACGGC	220034	52230	CCTAAGGTTTCTGGGTTTGT	264621	96817	GCCCCACTCCGCCACCTTGA
175448	7644	ACCTGTAGTCCCGGCTACGG	220035	52231	ACCTAAGGTTTCTGGGTTTG	264622	96818	AGCCCCACTCCGCCACCTTG
175449	7645	TACCTGTAGTCCCGGCTACG	220036	52232	GACCTAAGGTTTCTGGGTTT	264623	96819	CAGCCCCACTCCGCCACCTT
175450	7646	GTACCTGTAGTCCCGGCTAC	220037	52233	TGACCTAAGGTTTCTGGGTT	264624	96820	CCAGCCCCACTCCGCCACCT
175451	7647	TGTACCTGTAGTCCCGGCTA	220038	52234	TTGACCTAAGGTTTCTGGGT	264625	96821	ACCAGCCCCACTCCGCCACC
175452	7648	GTGTACCTGTAGTCCCGGCT	220039	52235	TTTGACCTAAGGTTTCTGGG	264626	96822	CACCAGCCCCACTCCGCCAC
175453	7649	TGTGTACCTGTAGTCCCGGC	220040	52236	TTTTGACCTAAGGTTTCTGG	264627	96823	ACACCAGCCCCACTCCGCCA
175454	7650	GTGTGTACCTGTAGTCCCGG	220041	52237	GTTTTGACCTAAGGTTTCTG	264628	96824	AACACCAGCCCCACTCCGCC
175455	7651	GGTGTGTACCTGTAGTCCCG	220042	52238	GGTTTTGACCTAAGGTTTCT	264629	96825	CAACACCAGCCCCACTCCGC
175456	7652	TGGTGTGTACCTGTAGTCCC	220043	52239	TGGTTTTGACCTAAGGTTTC	264630	96826	TCAACACCAGCCCCACTCCG
175457	7653	ATGGTGTGTACCTGTAGTCC	220044	52240	TTGGTTTTGACCTAAGGTTT	264631	96827	GTCAACACCAGCCCCACTCC
175458	7654	TATGGTGTGTACCTGTAGTC	220045	52241	TTTGGTTTTGACCTAAGGTT	264632	96828	AGTCAACACCAGCCCCACTC
175459	7655	TTATGGTGTGTACCTGTAGT	220046	52242	TTTTGGTTTTGACCTAAGGT	264633	96829	GAGTCAACACCAGCCCCACT
175460	7656	ATTATGGTGTGTACCTGTAG	220047	52243	ATTTTGGTTTTGACCTAAGG	264634	96830	AGAGTCAACACCAGCCCCAC
175461	7657	CATTATGGTGTGTACCTGTA	220048	52244	AATTTTGGTTTTGACCTAAG	264635	96831	AAGAGTCAACACCAGCCCCA
175462	7658	GCATTATGGTGTGTACCTGT	220049	52245	CAATTTTGGTTTTGACCTAA	264636	96832	CAAGAGTCAACACCAGCCCC
175463	7659	AGCATTATGGTGTGTACCTG	220050	52246	ACAATTTTGGTTTTGACCTA	264637	96833	CCAAGAGTCAACACCAGCCC
175464	7660	GAGCATTATGGTGTGTACCT	220051	52247	GACAATTTTGGTTTTGACCT	264638	96834	ACCAAGAGTCAACACCAGCC
175465	7661	CGAGCATTATGGTGTGTACC	220052	52248	GGACAATTTTGGTTTTGACC	264639	96835	CACCAAGAGTCAACACCAGC
175466	7662	CCGAGCATTATGGTGTGTAC	220053	52249	AGGACAATTTTGGTTTTGAC	264640	96836	CCACCAAGAGTCAACACCAG
175467	7663	GCCGAGCATTATGGTGTGTA	220054	52250	GAGGACAATTTTGGTTTTGA	264641	96837	GCCACCAAGAGTCAACACCA
175468	7664	AGCCGAGCATTATGGTGTGT	220055	52251	AGAGGACAATTTTGGTTTTG	264642	96838	TGCCACCAAGAGTCAACACC
175469	7665	CAGCCGAGCATTATGGTGTG	220056	52252	GAGAGGACAATTTTGGTTTT	264643	96839	CTGCCACCAAGAGTCAACAC
175470	7666	TCAGCCGAGCATTATGGTGT	220057	52253	TGAGAGGACAATTTTGGTTT	264644	96840	ACTGCCACCAAGAGTCAACA
175471	7667	ATCAGCCGAGCATTATGGTG	220058	52254	CTGAGAGGACAATTTTGGTT	264645	96841	TACTGCCACCAAGAGTCAAC
175472	7668	AATCAGCCGAGCATTATGGT	220059	52255	TCTGAGAGGACAATTTTGGT	264646	96842	TTACTGCCACCAAGAGTCAA
175473	7669	AAATCAGCCGAGCATTATGG	220060	52256	GTCTGAGAGGACAATTTTGG	264647	96843	GTTACTGCCACCAAGAGTCA
175474	7670	AAAATCAGCCGAGCATTATG	220061	52257	TGTCTGAGAGGACAATTTTG	264648	96844	AGTTACTGCCACCAAGAGTC
175475	7671	AAAAATCAGCCGAGCATTAT	220062	52258	GTGTCTGAGAGGACAATTTT	264649	96845	AAGTTACTGCCACCAAGAGT
175476	7672	CAAAAATCAGCCGAGCATTA	220063	52259	TGTGTCTGAGAGGACAATTT	264650	96846	AAAGTTACTGCCACCAAGAG
175477	7673	ACAAAAATCAGCCGAGCATT	220064	52260	TTGTGTCTGAGAGGACAATT	264651	96847	AAAAGTTACTGCCACCAAGA
175478	7674	TACAAAAATCAGCCGAGCAT	220065	52261	ATTGTGTCTGAGAGGACAAT	264652	96848	GAAAAGTTACTGCCACCAAG
175479	7675	ATACAAAAATCAGCCGAGCA	220066	52262	GATTGTGTCTGAGAGGACAA	264653	96849	GGAAAAGTTACTGCCACCAA
175480	7676	AATACAAAAATCAGCCGAGC	220067	52263	AGATTGTGTCTGAGAGGACA	264654	96850	GGGAAAAGTTACTGCCACCA
175481	7677	AAATACAAAAATCAGCCGAG	220068	52264	CAGATTGTGTCTGAGAGGAC	264655	96851	TGGGAAAAGTTACTGCCACC
175482	7678	AAAATACAAAAATCAGCCGA	220069	52265	CCAGATTGTGTCTGAGAGGA	264656	96852	TTGGGAAAAGTTACTGCCAC
175483	7679	AAAAATACAAAAATCAGCCG	220070	52266	CCCAGATTGTGTCTGAGAGG	264657	96853	ATTGGGAAAAGTTACTGCCA
175484	7680	CAAAAATACAAAAATCAGCC	220071	52267	TCCCAGATTGTGTCTGAGAG	264658	96854	CATTGGGAAAAGTTACTGCC
175485	7681	ACAAAAATACAAAAATCAGC	220072	52268	TTCCCAGATTGTGTCTGAGA	264659	96855	CCATTGGGAAAAGTTACTGC
175486	7682	TACAAAAATACAAAAATCAG	220073	52269	ATTCCCAGATTGTGTCTGAG	264660	96856	ACCATTGGGAAAAGTTACTG
175487	7683	CTACAAAAATACAAAAATCA	220074	52270	AATTCCCAGATTGTGTCTGA	264661	96857	CACCATTGGGAAAAGTTACT
175488	7684	CCTACAAAAATACAAAAATC	220075	52271	AAATTCCCAGATTGTGTCTG	264662	96858	TCACCATTGGGAAAAGTTAC
175489	7685	CCCTACAAAAATACAAAAAT	220076	52272	AAAATTCCCAGATTGTGTCT	264663	96859	TTCACCATTGGGAAAAGTTA
175490	7686	TCCCTACAAAAATACAAAAA	220077	52273	GAAAATTCCCAGATTGTGTC	264664	96860	TTTCACCATTGGGAAAAGTT
175491	7687	ATCCCTACAAAAATACAAAA	220078	52274	AGAAAATTCCCAGATTGTGT	264665	96861	TTTTCACCATTGGGAAAAGT
175492	7688	CATCCCTACAAAAATACAAA	220079	52275	GAGAAAATTCCCAGATTGTG	264666	96862	TTTTTCACCATTGGGAAAAG
175493	7689	CCATCCCTACAAAAATACAA	220080	52276	TGAGAAAATTCCCAGATTGT	264667	96863	GTTTTTCACCATTGGGAAAA
175494	7690	CCCATCCCTACAAAAATACA	220081	52277	ATGAGAAAATTCCCAGATTG	264668	96864	GGTTTTTCACCATTGGGAAA
175495	7691	CCCCATCCCTACAAAAATAC	220082	52278	CATGAGAAAATTCCCAGATT	264669	96865	GGGTTTTTCACCATTGGGAA
175496	7692	ACCCCATCCCTACAAAAATA	220083	52279	TCATGAGAAAATTCCCAGAT	264670	96866	GGGGTTTTTCACCATTGGGA
175497	7693	TACCCCATCCCTACAAAAAT	220084	52280	GTCATGAGAAAATTCCCAGA	264671	96867	AGGGGTTTTTCACCATTGGG
175498	7694	ATACCCCATCCCTACAAAAA	220085	52281	TGTCATGAGAAAATTCCCAG	264672	96868	GAGGGGTTTTTCACCATTGG
175499	7695	GATACCCCATCCCTACAAAA	220086	52282	CTGTCATGAGAAAATTCCCA	264673	96869	AGAGGGGTTTTTCACCATTG
175500	7696	CGATACCCCATCCCTACAAA	220087	52283	ACTGTCATGAGAAAATTCCC	264674	96870	TAGAGGGGTTTTTCACCATT
175501	7697	GCGATACCCCATCCCTACAA	220088	52284	CACTGTCATGAGAAAATTCC	264675	96871	ATAGAGGGGTTTTTCACCAT
175502	7698	GGCGATACCCCATCCCTACA	220089	52285	CCACTGTCATGAGAAAATTC	264676	96872	GATAGAGGGGTTTTTCACCA
175503	7699	TGGCGATACCCCATCCCTAC	220090	52286	CCCACTGTCATGAGAAAATT	264677	96873	TGATAGAGGGGTTTTTCACC
175504	7700	ATGGCGATACCCCATCCCTA	220091	52287	GCCCACTGTCATGAGAAAAT	264678	96874	ATGATAGAGGGGTTTTTCAC
175505	7701	CATGGCGATACCCCATCCCT	220092	52288	TGCCCACTGTCATGAGAAAA	264679	96875	CATGATAGAGGGGTTTTTCA
175506	7702	ACATGGCGATACCCCATCCC	220093	52289	ATGCCCACTGTCATGAGAAA	264680	96876	ACATGATAGAGGGGTTTTTC

175507	7703	AACATGGCGATACCCCATCC	220094	52290	AATGCCCACTGTCATGAGAA	264681	96877	AACATGATAGAGGGGTTTTT
175508	7704	CAACATGGCGATACCCCATC	220095	52291	TAATGCCCACTGTCATGAGA	264682	96878	AAACATGATAGAGGGGTTTT
175509	7705	CCAACATGGCGATACCCCAT	220096	52292	CTAATGCCCACTGTCATGAG	264683	96879	GAAACATGATAGAGGGGTTT
175510	7706	GCCAACATGGCGATACCCCA	220097	52293	GCTAATGCCCACTGTCATGA	264684	96880	TGAAACATGATAGAGGGGTT
175511	7707	GGCCAACATGGCGATACCCC	220098	52294	GGCTAATGCCCACTGTCATG	264685	96881	ATGAAACATGATAGAGGGGT
175512	7708	TGGCCAACATGGCGATACCC	220099	52295	TGGCTAATGCCCACTGTCAT	264686	96882	AATGAAACATGATAGAGGGG
175513	7709	CTGGCCAACATGGCGATACC	220100	52296	TTGGCTAATGCCCACTGTCA	264687	96883	AAATGAAACATGATAGAGGG
175514	7710	CCTGGCCAACATGGCGATAC	220101	52297	GTTGGCTAATGCCCACTGTC	264688	96884	TAAATGAAACATGATAGAGG
175515	7711	GCCTGGCCAACATGGCGATA	220102	52298	AGTTGGCTAATGCCCACTGT	264689	96885	GTAAATGAAACATGATAGAG
175516	7712	AGCCTGGCCAACATGGCGAT	220103	52299	CAGTTGGCTAATGCCCACTG	264690	96886	TGTAAATGAAACATGATAGA
175517	7713	CAGCCTGGCCAACATGGCGA	220104	52300	TCAGTTGGCTAATGCCCACT	264691	96887	CTGTAAATGAAACATGATAG
175518	7714	CCAGCCTGGCCAACATGGCG	220105	52301	GTCAGTTGGCTAATGCCCAC	264692	96888	CCTGTAAATGAAACATGATA
175519	7715	ACCAGCCTGGCCAACATGGC	220106	52302	TGTCAGTTGGCTAATGCCCA	264693	96889	CCCTGTAAATGAAACATGAT
175520	7716	GACCAGCCTGGCCAACATGG	220107	52303	ATGTCAGTTGGCTAATGCCC	264694	96890	CCCCTGTAAATGAAACATGA
175521	7717	GGACCAGCCTGGCCAACATG	220108	52304	GATGTCAGTTGGCTAATGCC	264695	96891	CCCCCTGTAAATGAAACATG
175522	7718	GGGACCAGCCTGGCCAACAT	220109	52305	TGATGTCAGTTGGCTAATGC	264696	96892	GCCCCCTGTAAATGAAACAT
175523	7719	CGGGACCAGCCTGGCCAACA	220110	52306	CTGATGTCAGTTGGCTAATG	264697	96893	AGCCCCCTGTAAATGAAACA
175524	7720	TCGGGACCAGCCTGGCCAAC	220111	52307	GCTGATGTCAGTTGGCTAAT	264698	96894	CAGCCCCCTGTAAATGAAAC
175525	7721	TTCGGGACCAGCCTGGCCAA	220112	52308	TGCTGATGTCAGTTGGCTAA	264699	96895	TCAGCCCCCTGTAAATGAAA
175526	7722	GTTCGGGACCAGCCTGGCCA	220113	52309	CTGCTGATGTCAGTTGGCTA	264700	96896	ATCAGCCCCCTGTAAATGAA
175527	7723	AGTTCGGGACCAGCCTGGCC	220114	52310	GCTGCTGATGTCAGTTGGCT	264701	96897	CATCAGCCCCCTGTAAATGA
175528	7724	AAGTTCGGGACCAGCCTGGC	220115	52311	TGCTGCTGATGTCAGTTGGC	264702	96898	CCATCAGCCCCCTGTAAATG
175529	7725	GAAGTTCGGGACCAGCCTGG	220116	52312	TTGCTGCTGATGTCAGTTGG	264703	96899	ACCATCAGCCCCCTGTAAAT
175530	7726	AGAAGTTCGGGACCAGCCTG	220117	52313	GTTGCTGCTGATGTCAGTTG	264704	96900	TACCATCAGCCCCCTGTAAA
175531	7727	CAGAAGTTCGGGACCAGCCT	220118	52314	GGTTGCTGCTGATGTCAGTT	264705	96901	TTACCATCAGCCCCCTGTAA
175532	7728	TCAGAAGTTCGGGACCAGCC	220119	52315	TGGTTGCTGCTGATGTCAGT	264706	96902	TTTACCATCAGCCCCCTGTA
175533	7729	GTCAGAAGTTCGGGACCAGC	220120	52316	ATGGTTGCTGCTGATGTCAG	264707	96903	TTTTACCATCAGCCCCCTGT
175534	7730	GGTCAGAAGTTCGGGACCAG	220121	52317	GATGGTTGCTGCTGATGTCA	264708	96904	GTTTTACCATCAGCCCCCTG
175535	7731	GGGTCAGAAGTTCGGGACCA	220122	52318	GGATGGTTGCTGCTGATGTC	264709	96905	CGTTTTACCATCAGCCCCCT
175536	7732	TGGGTCAGAAGTTCGGGACC	220123	52319	CGGATGGTTGCTGCTGATGT	264710	96906	TCGTTTTACCATCAGCCCCC
175537	7733	TTGGGTCAGAAGTTCGGGAC	220124	52320	ACGGATGGTTGCTGCTGATG	264711	96907	TTCGTTTTACCATCAGCCCC
175538	7734	CTTGGGTCAGAAGTTCGGGA	220125	52321	CACGGATGGTTGCTGCTGAT	264712	96908	CTTCGTTTTACCATCAGCCC
175539	7735	ACTTGGGTCAGAAGTTCGGG	220126	52322	ACACGGATGGTTGCTGCTGA	264713	96909	TCTTCGTTTTACCATCAGCC
175540	7736	CACTTGGGTCAGAAGTTCGG	220127	52323	CACACGGATGGTTGCTGCTG	264714	96910	ATCTTCGTTTTACCATCAGC
175541	7737	TCACTTGGGTCAGAAGTTCG	220128	52324	GCACACGGATGGTTGCTGCT	264715	96911	GATCTTCGTTTTACCATCAG
175542	7738	ATCACTTGGGTCAGAAGTTC	220129	52325	TGCACACGGATGGTTGCTGC	264716	96912	CGATCTTCGTTTTACCATCA
175543	7739	GATCACTTGGGTCAGAAGTT	220130	52326	GTGCACACGGATGGTTGCTG	264717	96913	GCGATCTTCGTTTTACCATC
175544	7740	GGATCACTTGGGTCAGAAGT	220131	52327	TGTGCACACGGATGGTTGCT	264718	96914	GGCGATCTTCGTTTTACCAT
175545	7741	TGGATCACTTGGGTCAGAAG	220132	52328	GTGTGCACACGGATGGTTGC	264719	96915	TGGCGATCTTCGTTTTACCA
175546	7742	GTGGATCACTTGGGTCAGAA	220133	52329	TGTGTGCACACGGATGGTTG	264720	96916	GTGGCGATCTTCGTTTTACC
175547	7743	GGTGGATCACTTGGGTCAGA	220134	52330	CTGTGTGCACACGGATGGTT	264721	96917	TGTGGCGATCTTCGTTTTAC
175548	7744	GGGTGGATCACTTGGGTCAG	220135	52331	ACTGTGTGCACACGGATGGT	264722	96918	GTGTGGCGATCTTCGTTTTA
175549	7745	TGGGTGGATCACTTGGGTCA	220136	52332	CACTGTGTGCACACGGATGG	264723	96919	GGTGTGGCGATCTTCGTTTT
175550	7746	GTGGGTGGATCACTTGGGTC	220137	52333	CCACTGTGTGCACACGGATG	264724	96920	CGGTGTGGCGATCTTCGTTT
175551	7747	GGTGGGTGGATCACTTGGGT	220138	52334	GCCACTGTGTGCACACGGAT	264725	96921	GCGGTGTGGCGATCTTCGTT
175552	7748	AGGTGGGTGGATCACTTGGG	220139	52335	TGCCACTGTGTGCACACGGA	264726	96922	CGCGGTGTGGCGATCTTCGT
175553	7749	GAGGTGGGTGGATCACTTGG	220140	52336	GTGCCACTGTGTGCACACGG	264727	96923	CCGCGGTGTGGCGATCTTCG
175554	7750	CGAGGTGGGTGGATCACTTG	220141	52337	GGTGCCACTGTGTGCACACG	264728	96924	CCCGCGGTGTGGCGATCTTC
175555	7751	CCGAGGTGGGTGGATCACTT	220142	52338	TGGTGCCACTGTGTGCACAC	264729	96925	CCCCGCGGTGTGGCGATCTT
175556	7752	GCCGAGGTGGGTGGATCACT	220143	52339	GTGGTGCCACTGTGTGCACA	264730	96926	TCCCCGCGGTGTGGCGATCT
175557	7753	GGCCGAGGTGGGTGGATCAC	220144	52340	GGTGGTGCCACTGTGTGCAC	264731	96927	CTCCCCGCGGTGTGGCGATC
175558	7754	AGGCCGAGGTGGGTGGATCA	220145	52341	AGGTGGTGCCACTGTGTGCA	264732	96928	GCTCCCCGCGGTGTGGCGAT
175559	7755	GAGGCCGAGGTGGGTGGATC	220146	52342	GAGGTGGTGCCACTGTGTGC	264733	96929	TGCTCCCCGCGGTGTGGCGA
175560	7756	GGAGGCCGAGGTGGGTGGAT	220147	52343	GGAGGTGGTGCCACTGTGTG	264734	96930	CTGCTCCCCGCGGTGTGGCG
175561	7757	GGGAGGCCGAGGTGGGTGGA	220148	52344	AGGAGGTGGTGCCACTGTGT	264735	96931	GCTGCTCCCCGCGGTGTGGC
175562	7758	TGGGAGGCCGAGGTGGGTGG	220149	52345	GAGGAGGTGGTGCCACTGTG	264736	96932	GGCTGCTCCCCGCGGTGTGG
175563	7759	TTGGGAGGCCGAGGTGGGTG	220150	52346	GGAGGAGGTGGTGCCACTGT	264737	96933	GGGCTGCTCCCCGCGGTGTG
175564	7760	TTTGGGAGGCCGAGGTGGGT	220151	52347	GGGAGGAGGTGGTGCCACTG	264738	96934	GGGGCTGCTCCCCGCGGTGT
175565	7761	CTTTGGGAGGCCGAGGTGGG	220152	52348	TGGGAGGAGGTGGTGCCACT	264739	96935	AGGGGCTGCTCCCCGCGGTG
175566	7762	ACTTTGGGAGGCCGAGGTGG	220153	52349	TTGGGAGGAGGTGGTGCCAC	264740	96936	GAGGGGCTGCTCCCCGCGGT
175567	7763	CACTTTGGGAGGCCGAGGTG	220154	52350	TTTGGGAGGAGGTGGTGCCA	264741	96937	GGAGGGGCTGCTCCCCGCGG
175568	7764	GCACTTTGGGAGGCCGAGGT	220155	52351	TTTTGGGAGGAGGTGGTGCC	264742	96938	TGGAGGGGCTGCTCCCCGCG
175569	7765	AGCACTTTGGGAGGCCGAGG	220156	52352	TTTTTGGGAGGAGGTGGTGC	264743	96939	CTGGAGGGGCTGCTCCCCGC
175570	7766	CAGCACTTTGGGAGGCCGAG	220157	52353	CTTTTTGGGAGGAGGTGGTG	264744	96940	CCTGGAGGGGCTGCTCCCCG
175571	7767	CCAGCACTTTGGGAGGCCGA	220158	52354	GCTTTTTGGGAGGAGGTGGT	264745	96941	GCCTGGAGGGGCTGCTCCCC
175572	7768	CCCAGCACTTTGGGAGGCCG	220159	52355	TGCTTTTTGGGAGGAGGTGG	264746	96942	GGCCTGGAGGGGCTGCTCCC
175573	7769	TCCCAGCACTTTGGGAGGCC	220160	52356	CTGCTTTTTGGGAGGAGGTG	264747	96943	TGGCCTGGAGGGGCTGCTCC
175574	7770	ATCCCAGCACTTTGGGAGGC	220161	52357	GCTGCTTTTTGGGAGGAGGT	264748	96944	CTGGCCTGGAGGGGCTGCTC
175575	7771	AATCCCAGCACTTTGGGAGG	220162	52358	GGCTGCTTTTTGGGAGGAGG	264749	96945	TCTGGCCTGGAGGGGCTGCT
175576	7772	TAATCCCAGCACTTTGGGAG	220163	52359	AGGCTGCTTTTTGGGAGGAG	264750	96946	TTCTGGCCTGGAGGGGCTGC
175577	7773	GTAATCCCAGCACTTTGGGA	220164	52360	AAGGCTGCTTTTTGGGAGGA	264751	96947	CTTCTGGCCTGGAGGGGCTG
175578	7774	TGTAATCCCAGCACTTTGGG	220165	52361	GAAGGCTGCTTTTTGGGAGG	264752	96948	CCTTCTGGCCTGGAGGGGCT

175579	7775	CTGTAATCCCAGCACTTTGG	220166	52362	TGAAGGCTGCTTTTTGGGAG	264753	96949	CCCTTCTGGCCTGGAGGGGC
175580	7776	CCTGTAATCCCAGCACTTTG	220167	52363	ATGAAGGCTGCTTTTTGGGA	264754	96950	GCCCTTCTGGCCTGGAGGGG
175581	7777	ACCTGTAATCCCAGCACTTT	220168	52364	GATGAAGGCTGCTTTTTGGG	264755	96951	GGCCCTTCTGGCCTGGAGGG
175582	7778	CACCTGTAATCCCAGCACTT	220169	52365	AGATGAAGGCTGCTTTTTGG	264756	96952	TGGCCCTTCTGGCCTGGAGG
175583	7779	ACACCTGTAATCCCAGCACT	220170	52366	TAGATGAAGGCTGCTTTTTG	264757	96953	CTGGCCCTTCTGGCCTGGAG
175584	7780	CACACCTGTAATCCCAGCAC	220171	52367	ATAGATGAAGGCTGCTTTTT	264758	96954	CCTGGCCCTTCTGGCCTGGA
175585	7781	TCACACCTGTAATCCCAGCA	220172	52368	CATAGATGAAGGCTGCTTTT	264759	96955	GCCTGGCCCTTCTGGCCTGG
175586	7782	CTCACACCTGTAATCCCAGC	220173	52369	GCATAGATGAAGGCTGCTTT	264760	96956	GGCCTGGCCCTTCTGGCCTG
175587	7783	GCTCACACCTGTAATCCCAG	220174	52370	GGCATAGATGAAGGCTGCTT	264761	96957	TGGCCTGGCCCTTCTGGCCT
175588	7784	GGCTCACACCTGTAATCCCA	220175	52371	GGGCATAGATGAAGGCTGCT	264762	96958	TTGGCCTGGCCCTTCTGGCC
175589	7785	TGGCTCACACCTGTAATCCC	220176	52372	AGGGCATAGATGAAGGCTGC	264763	96959	GTTGGCCTGGCCCTTCTGGC
175590	7786	GTGGCTCACACCTGTAATCC	220177	52373	GAGGGCATAGATGAAGGCTG	264764	96960	CGTTGGCCTGGCCCTTCTGG
175591	7787	GGTGGCTCACACCTGTAATC	220178	52374	TGAGGGCATAGATGAAGGCT	264765	96961	GCGTTGGCCTGGCCCTTCTG
175592	7788	CGGTGGCTCACACCTGTAAT	220179	52375	ATGAGGGCATAGATGAAGGC	264766	96962	GGCGTTGGCCTGGCCCTTCT
175593	7789	GCGGTGGCTCACACCTGTAA	220180	52376	TATGAGGGCATAGATGAAGG	264767	96963	TGGCGTTGGCCTGGCCCTTC
175594	7790	CGCGGTGGCTCACACCTGTA	220181	52377	GTATGAGGGCATAGATGAAG	264768	96964	GTGGCGTTGGCCTGGCCCTT
175595	7791	GCGCGGTGGCTCACACCTGT	220182	52378	TGTATGAGGGCATAGATGAA	264769	96965	GGTGGCGTTGGCCTGGCCCT
175596	7792	GGCGCGGTGGCTCACACCTG	220183	52379	TTGTATGAGGGCATAGATGA	264770	96966	TGGTGGCGTTGGCCTGGCCC
175597	7793	GGGCGCGGTGGCTCACACCT	220184	52380	ATTGTATGAGGGCATAGATG	264771	96967	CTGGTGGCGTTGGCCTGGCC
175598	7794	CGGGCGCGGTGGCTCACACC	220185	52381	GATTGTATGAGGGCATAGAT	264772	96968	CCTGGTGGCGTTGGCCTGGC
175599	7795	CCGGGCGCGGTGGCTCACAC	220186	52382	CGATTGTATGAGGGCATAGA	264773	96969	TCCTGGTGGCGTTGGCCTGG
175600	7796	GCCGGGCGCGGTGGCTCACA	220187	52383	ACGATTGTATGAGGGCATAG	264774	96970	ATCCTGGTGGCGTTGGCCTG
175601	7797	GGCCGGGCGCGGTGGCTCAC	220188	52384	AACGATTGTATGAGGGCATA	264775	96971	AATCCTGGTGGCGTTGGCCT
175602	7798	TGGCCGGGCGCGGTGGCTCA	220189	52385	CAACGATTGTATGAGGGCAT	264776	96972	GAATCCTGGTGGCGTTGGCC
175603	7799	CTGGCCGGGCGCGGTGGCTC	220190	52386	TCAACGATTGTATGAGGGCA	264777	96973	GGAATCCTGGTGGCGTTGGC
175604	7800	GCTGGCCGGGCGCGGTGGCT	220191	52387	ATCAACGATTGTATGAGGGC	264778	96974	TGGAATCCTGGTGGCGTTGG
175605	7801	AGCTGGCCGGGCGCGGTGGC	220192	52388	AATCAACGATTGTATGAGGG	264779	96975	CTGGAATCCTGGTGGCGTTG
175606	7802	AAGCTGGCCGGGCGCGGTGG	220193	52389	TAATCAACGATTGTATGAGG	264780	96976	GCTGGAATCCTGGTGGCGTT
175607	7803	CAAGCTGGCCGGGCGCGGTG	220194	52390	ATAATCAACGATTGTATGAG	264781	96977	TGCTGGAATCCTGGTGGCGT
175608	7804	GCAAGCTGGCCGGGCGCGGT	220195	52391	AATAATCAACGATTGTATGA	264782	96978	TTGCTGGAATCCTGGTGGCG
175609	7805	TGCAAGCTGGCCGGGCGCGG	220196	52392	GAATAATCAACGATTGTATG	264783	96979	TTTGCTGGAATCCTGGTGGC
175610	7806	GTGCAAGCTGGCCGGGCGCG	220197	52393	AGAATAATCAACGATTGTAT	264784	96980	TTTTGCTGGAATCCTGGTGG
175611	7807	GGTGCAAGCTGGCCGGGCGC	220198	52394	GAGAATAATCAACGATTGTA	264785	96981	TTTTTGCTGGAATCCTGGTG
175612	7808	AGGTGCAAGCTGGCCGGGCG	220199	52395	AGAGAATAATCAACGATTGT	264786	96982	GTTTTTGCTGGAATCCTGGT
175613	7809	AAGGTGCAAGCTGGCCGGGC	220200	52396	AAGAGAATAATCAACGATTG	264787	96983	GGTTTTTGCTGGAATCCTGG
175614	7810	TAAGGTGCAAGCTGGCCGGG	220201	52397	AAAGAGAATAATCAACGATT	264788	96984	GGGTTTTTGCTGGAATCCTG
175615	7811	ATAAGGTGCAAGCTGGCCGG	220202	52398	CAAAGAGAATAATCAACGAT	264789	96985	GGGGTTTTTGCTGGAATCCT
175616	7812	AATAAGGTGCAAGCTGGCCG	220203	52399	CCAAAGAGAATAATCAACGA	264790	96986	CGGGGTTTTTGCTGGAATCC
175617	7813	AAATAAGGTGCAAGCTGGCC	220204	52400	TCCAAAGAGAATAATCAACG	264791	96987	GCGGGGTTTTTGCTGGAATC
175618	7814	TAAATAAGGTGCAAGCTGGC	220205	52401	ATCCAAAGAGAATAATCAAC	264792	96988	GGCGGGGTTTTTGCTGGAAT
175619	7815	CTAAATAAGGTGCAAGCTGG	220206	52402	AATCCAAAGAGAATAATCAA	264793	96989	GGGCGGGGTTTTTGCTGGAA
175620	7816	CCTAAATAAGGTGCAAGCTG	220207	52403	CAATCCAAAGAGAATAATCA	264794	96990	CGGGCGGGGTTTTTGCTGGA
175621	7817	TCCTAAATAAGGTGCAAGCT	220208	52404	TCAATCCAAAGAGAATAATC	264795	96991	GCGGGCGGGGTTTTTGCTGG
175622	7818	ATCCTAAATAAGGTGCAAGC	220209	52405	CTCAATCCAAAGAGAATAAT	264796	96992	AGCGGGCGGGGTTTTTGCTG
175623	7819	TATCCTAAATAAGGTGCAAG	220210	52406	CCTCAATCCAAAGAGAATAA	264797	96993	GAGCGGGCGGGGTTTTTGCT
175624	7820	ATATCCTAAATAAGGTGCAA	220211	52407	GCCTCAATCCAAAGAGAATA	264798	96994	GGAGCGGGCGGGGTTTTTGC
175625	7821	CATATCCTAAATAAGGTGCA	220212	52408	GGCCTCAATCCAAAGAGAAT	264799	96995	TGGAGCGGGCGGGGTTTTTG
175626	7822	ACATATCCTAAATAAGGTGC	220213	52409	GGGCCTCAATCCAAAGAGAA	264800	96996	TTGGAGCGGGCGGGGTTTTT
175627	7823	CACATATCCTAAATAAGGTG	220214	52410	CGGGCCTCAATCCAAAGAGA	264801	96997	TTTGGAGCGGGCGGGGTTTT
175628	7824	TCACATATCCTAAATAAGGT	220215	52411	CCGGGCCTCAATCCAAAGAG	264802	96998	CTTTGGAGCGGGCGGGGTTT
175629	7825	ATCACATATCCTAAATAAGG	220216	52412	TCCGGGCCTCAATCCAAAGA	264803	96999	TCTTTGGAGCGGGCGGGGTT
175630	7826	AATCACATATCCTAAATAAG	220217	52413	TTCCGGGCCTCAATCCAAAG	264804	97000	GTCTTTGGAGCGGGCGGGGT
175631	7827	TAATCACATATCCTAAATAA	220218	52414	ATTCCGGGCCTCAATCCAAA	264805	97001	TGTCTTTGGAGCGGGCGGGG
175632	7828	ATAATCACATATCCTAAATA	220219	52415	AATTCCGGGCCTCAATCCAA	264806	97002	GTGTCTTTGGAGCGGGCGGG
175633	7829	AATAATCACATATCCTAAAT	220220	52416	TAATTCCGGGCCTCAATCCA	264807	97003	GGTGTCTTTGGAGCGGGCGG
175634	7830	TAATAATCACATATCCTAAA	220221	52417	ATAATTCCGGGCCTCAATCC	264808	97004	TGGTGTCTTTGGAGCGGGCG
175635	7831	ATAATAATCACATATCCTAA	220222	52418	AATAATTCCGGGCCTCAATC	264809	97005	GTGGTGTCTTTGGAGCGGGC
175636	7832	TATAATAATCACATATCCTA	220223	52419	AAATAATTCCGGGCCTCAAT	264810	97006	GGTGGTGTCTTTGGAGCGGG
175637	7833	CTATAATAATCACATATCCT	220224	52420	TAAATAATTCCGGGCCTCAA	264811	97007	GGGTGGTGTCTTTGGAGCGG
175638	7834	GCTATAATAATCACATATCC	220225	52421	TTAAATAATTCCGGGCCTCA	264812	97008	TGGGTGGTGTCTTTGGAGCG
175639	7835	TGCTATAATAATCACATATC	220226	52422	CTTAAATAATTCCGGGCCTC	264813	97009	CTGGGTGGTGTCTTTGGAGC
175640	7836	TTGCTATAATAATCACATAT	220227	52423	ACTTAAATAATTCCGGGCCT	264814	97010	GCTGGGTGGTGTCTTTGGAG
175641	7837	CTTGCTATAATAATCACATA	220228	52424	AACTTAAATAATTCCGGGCC	264815	97011	AGCTGGGTGGTGTCTTTGGA
175642	7838	ACTTGCTATAATAATCACAT	220229	52425	AAACTTAAATAATTCCGGGC	264816	97012	GAGCTGGGTGGTGTCTTTGG
175643	7839	GACTTGCTATAATAATCACA	220230	52426	GAAACTTAAATAATTCCGGG	264817	97013	AGAGCTGGGTGGTGTCTTTG
175644	7840	AGACTTGCTATAATAATCAC	220231	52427	AGAAACTTAAATAATTCCGG	264818	97014	CAGAGCTGGGTGGTGTCTTT
175645	7841	CAGACTTGCTATAATAATCA	220232	52428	AAGAAACTTAAATAATTCCG	264819	97015	CCAGAGCTGGGTGGTGTCTT
175646	7842	CCAGACTTGCTATAATAATC	220233	52429	GAAGAAACTTAAATAATTCC	264820	97016	ACCAGAGCTGGGTGGTGTCT
175647	7843	ACCAGACTTGCTATAATAAT	220234	52430	AGAAGAAACTTAAATAATTC	264821	97017	TACCAGAGCTGGGTGGTGTC
175648	7844	CACCAGACTTGCTATAATAA	220235	52431	AAGAAGAAACTTAAATAATT	264822	97018	TTACCAGAGCTGGGTGGTGT
175649	7845	ACACCAGACTTGCTATAATA	220236	52432	CAAGAAGAAACTTAAATAAT	264823	97019	CTTACCAGAGCTGGGTGGTG
175650	7846	TACACCAGACTTGCTATAAT	220237	52433	GCAAGAAGAAACTTAAATAA	264824	97020	TCTTACCAGAGCTGGGTGGT

175651	7847	GTACACCAGACTTGCTATAA	220238	52434	GGCAAGAAGAAACTTAAATA	264825	97021	TTCTTACCAGAGCTGGGTGG
175652	7848	TGTACACCAGACTTGCTATA	220239	52435	TGGCAAGAAGAAACTTAAAT	264826	97022	CTTCTTACCAGAGCTGGGTG
175653	7849	ATGTACACCAGACTTGCTAT	220240	52436	CTGGCAAGAAGAAACTTAAA	264827	97023	TCTTCTTACCAGAGCTGGGT
175654	7850	TATGTACACCAGACTTGCTA	220241	52437	GCTGGCAAGAAGAAACTTAA	264828	97024	TTCTTCTTACCAGAGCTGGG
175655	7851	GTATGTACACCAGACTTGCT	220242	52438	TGCTGGCAAGAAGAAACTTA	264829	97025	GTTCTTCTTACCAGAGCTGG
175656	7852	TGTATGTACACCAGACTTGC	220243	52439	ATGCTGGCAAGAAGAAACTT	264830	97026	CGTTCTTCTTACCAGAGCTG
175657	7853	TTGTATGTACACCAGACTTG	220244	52440	CATGCTGGCAAGAAGAAACT	264831	97027	ACGTTCTTCTTACCAGAGCT
175658	7854	CTTGTATGTACACCAGACTT	220245	52441	TCATGCTGGCAAGAAGAAAC	264832	97028	AACGTTCTTCTTACCAGAGC
175659	7855	TCTTGTATGTACACCAGACT	220246	52442	CTCATGCTGGCAAGAAGAAA	264833	97029	GAACGTTCTTCTTACCAGAG
175660	7856	ATCTTGTATGTACACCAGAC	220247	52443	ACTCATGCTGGCAAGAAGAA	264834	97030	AGAACGTTCTTCTTACCAGA
175661	7857	AATCTTGTATGTACACCAGA	220248	52444	GACTCATGCTGGCAAGAAGA	264835	97031	GAGAACGTTCTTCTTACCAG
175662	7858	AAATCTTGTATGTACACCAG	220249	52445	AGACTCATGCTGGCAAGAAG	264836	97032	AGAGAACGTTCTTCTTACCA
175663	7859	AAAATCTTGTATGTACACCA	220250	52446	AAGACTCATGCTGGCAAGAA	264837	97033	AAGAGAACGTTCTTCTTACC
175664	7860	CAAAATCTTGTATGTACACC	220251	52447	AAAGACTCATGCTGGCAAGA	264838	97034	CAAGAGAACGTTCTTCTTAC
175665	7861	TCAAAATCTTGTATGTACAC	220252	52448	GAAAGACTCATGCTGGCAAG	264839	97035	TCAAGAGAACGTTCTTCTTA
175666	7862	TTCAAAATCTTGTATGTACA	220253	52449	GGAAAGACTCATGCTGGCAA	264840	97036	TTCAAGAGAACGTTCTTCTT
175667	7863	ATTCAAAATCTTGTATGTAC	220254	52450	AGGAAAGACTCATGCTGGCA	264841	97037	ATTCAAGAGAACGTTCTTCT
175668	7864	CATTCAAAATCTTGTATGTA	220255	52451	AAGGAAAGACTCATGCTGGC	264842	97038	GATTCAAGAGAACGTTCTTC
175669	7865	CCATTCAAAATCTTGTATGT	220256	52452	AAAGGAAAGACTCATGCTGG	264843	97039	AGATTCAAGAGAACGTTCTT
175670	7866	CCCATTCAAAATCTTGTATG	220257	52453	GAAAGGAAAGACTCATGCTG	264844	97040	AAGATTCAAGAGAACGTTCT
175671	7867	GCCCATTCAAAATCTTGTAT	220258	52454	AGAAAGGAAAGACTCATGCT	264845	97041	TAAGATTCAAGAGAACGTTC
175672	7868	TGCCCATTCAAAATCTTGTA	220259	52455	CAGAAAGGAAAGACTCATGC	264846	97042	CTAAGATTCAAGAGAACGTT
175673	7869	GTGCCCATTCAAAATCTTGT	220260	52456	ACAGAAAGGAAAGACTCATG	264847	97043	TCTAAGATTCAAGAGAACGT
175674	7870	TGTGCCCATTCAAAATCTTG	220261	52457	TACAGAAAGGAAAGACTCAT	264848	97044	CTCTAAGATTCAAGAGAACG
175675	7871	CTGTGCCCATTCAAAATCTT	220262	52458	ATACAGAAAGGAAAGACTCA	264849	97045	CCTCTAAGATTCAAGAGAAC
175676	7872	TCTGTGCCCATTCAAAATCT	220263	52459	CATACAGAAAGGAAAGACTC	264850	97046	TCCTCTAAGATTCAAGAGAA
175677	7873	ATCTGTGCCCATTCAAAATC	220264	52460	GCATACAGAAAGGAAAGACT	264851	97047	TTCCTCTAAGATTCAAGAGA
175678	7874	CATCTGTGCCCATTCAAAAT	220265	52461	AGCATACAGAAAGGAAAGAC	264852	97048	CTTCCTCTAAGATTCAAGAG
175679	7875	TCATCTGTGCCCATTCAAAA	220266	52462	GAGCATACAGAAAGGAAAGA	264853	97049	GCTTCCTCTAAGATTCAAGA
175680	7876	GTCATCTGTGCCCATTCAAA	220267	52463	GGAGCATACAGAAAGGAAAG	264854	97050	AGCTTCCTCTAAGATTCAAG
175681	7877	GGTCATCTGTGCCCATTCAA	220268	52464	AGGAGCATACAGAAAGGAAA	264855	97051	CAGCTTCCTCTAAGATTCAA
175682	7878	AGGTCATCTGTGCCCATTCA	220269	52465	AAGGAGCATACAGAAAGGAA	264856	97052	TCAGCTTCCTCTAAGATTCA
175683	7879	AAGGTCATCTGTGCCCATTC	220270	52466	TAAGGAGCATACAGAAAGGA	264857	97053	TTCAGCTTCCTCTAAGATTC
175684	7880	AAAGGTCATCTGTGCCCATT	220271	52467	ATAAGGAGCATACAGAAAGG	264858	97054	CTTCAGCTTCCTCTAAGATT
175685	7881	TAAAGGTCATCTGTGCCCAT	220272	52468	GATAAGGAGCATACAGAAAG	264859	97055	GCTTCAGCTTCCTCTAAGAT
175686	7882	CTAAAGGTCATCTGTGCCCA	220273	52469	AGATAAGGAGCATACAGAAA	264860	97056	AGCTTCAGCTTCCTCTAAGA
175687	7883	ACTAAAGGTCATCTGTGCCC	220274	52470	AAGATAAGGAGCATACAGAA	264861	97057	GAGCTTCAGCTTCCTCTAAG
175688	7884	TACTAAAGGTCATCTGTGCC	220275	52471	GAAGATAAGGAGCATACAGA	264862	97058	AGAGCTTCAGCTTCCTCTAA
175689	7885	TTACTAAAGGTCATCTGTGC	220276	52472	AGAAGATAAGGAGCATACAG	264863	97059	GAGAGCTTCAGCTTCCTCTA
175690	7886	CTTACTAAAGGTCATCTGTG	220277	52473	GAGAAGATAAGGAGCATACA	264864	97060	TGAGAGCTTCAGCTTCCTCT
175691	7887	ACTTACTAAAGGTCATCTGT	220278	52474	AGAGAAGATAAGGAGCATAC	264865	97061	CTGAGAGCTTCAGCTTCCTC
175692	7888	CACTTACTAAAGGTCATCTG	220279	52475	GAGAGAAGATAAGGAGCATA	264866	97062	TCTGAGAGCTTCAGCTTCCT
175693	7889	GCACTTACTAAAGGTCATCT	220280	52476	AGAGAGAAGATAAGGAGCAT	264867	97063	CTCTGAGAGCTTCAGCTTCC
175694	7890	AGCACTTACTAAAGGTCATC	220281	52477	AAGAGAGAAGATAAGGAGCA	264868	97064	CCTCTGAGAGCTTCAGCTTC
175695	7891	AAGCACTTACTAAAGGTCAT	220282	52478	AAAGAGAGAAGATAAGGAGC	264869	97065	ACCTCTGAGAGCTTCAGCTT
175696	7892	CAAGCACTTACTAAAGGTCA	220283	52479	TAAAGAGAGAAGATAAGGAG	264870	97066	TACCTCTGAGAGCTTCAGCT
175697	7893	CCAAGCACTTACTAAAGGTC	220284	52480	TTAAAGAGAGAAGATAAGGA	264871	97067	GTACCTCTGAGAGCTTCAGC
175698	7894	GCCAAGCACTTACTAAAGGT	220285	52481	ATTAAAGAGAGAAGATAAGG	264872	97068	TGTACCTCTGAGAGCTTCAG
175699	7895	AGCCAAGCACTTACTAAAGG	220286	52482	AATTAAAGAGAGAAGATAAG	264873	97069	CTGTACCTCTGAGAGCTTCA
175700	7896	CAGCCAAGCACTTACTAAAG	220287	52483	AAATTAAAGAGAGAAGATAA	264874	97070	GCTGTACCTCTGAGAGCTTC
175701	7897	ACAGCCAAGCACTTACTAAA	220288	52484	CAAATTAAAGAGAGAAGATA	264875	97071	GGCTGTACCTCTGAGAGCTT
175702	7898	CACAGCCAAGCACTTACTAA	220289	52485	CCAAATTAAAGAGAGAAGAT	264876	97072	AGGCTGTACCTCTGAGAGCT
175703	7899	TCACAGCCAAGCACTTACTA	220290	52486	GCCAAATTAAAGAGAGAAGA	264877	97073	AAGGCTGTACCTCTGAGAGC
175704	7900	ATCACAGCCAAGCACTTACT	220291	52487	TGCCAAATTAAAGAGAGAAG	264878	97074	GAAGGCTGTACCTCTGAGAG
175705	7901	TATCACAGCCAAGCACTTAC	220292	52488	CTGCCAAATTAAAGAGAGAA	264879	97075	TGAAGGCTGTACCTCTGAGA
175706	7902	TTATCACAGCCAAGCACTTA	220293	52489	ACTGCCAAATTAAAGAGAGA	264880	97076	ATGAAGGCTGTACCTCTGAG
175707	7903	CTTATCACAGCCAAGCACTT	220294	52490	AACTGCCAAATTAAAGAGAG	264881	97077	AATGAAGGCTGTACCTCTGA
175708	7904	TCTTATCACAGCCAAGCACT	220295	52491	GAACTGCCAAATTAAAGAGA	264882	97078	AAATGAAGGCTGTACCTCTG
175709	7905	CTCTTATCACAGCCAAGCAC	220296	52492	AGAACTGCCAAATTAAAGAG	264883	97079	AAAATGAAGGCTGTACCTCT
175710	7906	CCTCTTATCACAGCCAAGCA	220297	52493	CAGAACTGCCAAATTAAAGA	264884	97080	TAAAATGAAGGCTGTACCTC
175711	7907	GCCTCTTATCACAGCCAAGC	220298	52494	GCAGAACTGCCAAATTAAAG	264885	97081	CTAAAATGAAGGCTGTACCT
175712	7908	TGCCTCTTATCACAGCCAAG	220299	52495	AGCAGAACTGCCAAATTAAA	264886	97082	CCTAAAATGAAGGCTGTACC
175713	7909	CTGCCTCTTATCACAGCCAA	220300	52496	AAGCAGAACTGCCAAATTAA	264887	97083	TCCTAAAATGAAGGCTGTAC
175714	7910	ACTGCCTCTTATCACAGCCA	220301	52497	CAAGCAGAACTGCCAAATTA	264888	97084	CTCCTAAAATGAAGGCTGTA
175715	7911	GACTGCCTCTTATCACAGCC	220302	52498	TCAAGCAGAACTGCCAAATT	264889	97085	CCTCCTAAAATGAAGGCTGT
175716	7912	GGACTGCCTCTTATCACAGC	220303	52499	TTCAAGCAGAACTGCCAAAT	264890	97086	GCCTCCTAAAATGAAGGCTG
175717	7913	AGGACTGCCTCTTATCACAG	220304	52500	TTTCAAGCAGAACTGCCAAA	264891	97087	GGCCTCCTAAAATGAAGGCT
175718	7914	CAGGACTGCCTCTTATCACA	220305	52501	ATTTCAAGCAGAACTGCCAA	264892	97088	AGGCCTCCTAAAATGAAGGC
175719	7915	TCAGGACTGCCTCTTATCAC	220306	52502	GATTTCAAGCAGAACTGCCA	264893	97089	AAGGCCTCCTAAAATGAAGG
175720	7916	GTCAGGACTGCCTCTTATCA	220307	52503	AGATTTCAAGCAGAACTGCC	264894	97090	TAAGGCCTCCTAAAATGAAG
175721	7917	AGTCAGGACTGCCTCTTATC	220308	52504	CAGATTTCAAGCAGAACTGC	264895	97091	CTAAGGCCTCCTAAAATGAA
175722	7918	CAGTCAGGACTGCCTCTTAT	220309	52505	CCAGATTTCAAGCAGAACTG	264896	97092	CCTAAGGCCTCCTAAAATGA

175723	7919	GCAGTCAGGACTGCCTCTTA	220310	52506	CCCAGATTTCAAGCAGAACT	264897	97093	GCCTAAGGCCTCCTAAAATG
175724	7920	TGCAGTCAGGACTGCCTCTT	220311	52507	ACCCAGATTTCAAGCAGAAC	264898	97094	GGCCTAAGGCCTCCTAAAAT
175725	7921	CTGCAGTCAGGACTGCCTCT	220312	52508	GACCCAGATTTCAAGCAGAA	264899	97095	TGGCCTAAGGCCTCCTAAAA
175726	7922	TCTGCAGTCAGGACTGCCTC	220313	52509	AGACCCAGATTTCAAGCAGA	264900	97096	GTGGCCTAAGGCCTCCTAAA
175727	7923	ATCTGCAGTCAGGACTGCCT	220314	52510	AAGACCCAGATTTCAAGCAG	264901	97097	AGTGGCCTAAGGCCTCCTAA
175728	7924	GATCTGCAGTCAGGACTGCC	220315	52511	AAAGACCCAGATTTCAAGCA	264902	97098	CAGTGGCCTAAGGCCTCCTA
175729	7925	TGATCTGCAGTCAGGACTGC	220316	52512	GAAAGACCCAGATTTCAAGC	264903	97099	TCAGTGGCCTAAGGCCTCCT
175730	7926	CTGATCTGCAGTCAGGACTG	220317	52513	TGAAAGACCCAGATTTCAAG	264904	97100	CTCAGTGGCCTAAGGCCTCC
175731	7927	CCTGATCTGCAGTCAGGACT	220318	52514	ATGAAAGACCCAGATTTCAA	264905	97101	TCTCAGTGGCCTAAGGCCTC
175732	7928	GCCTGATCTGCAGTCAGGAC	220319	52515	AATGAAAGACCCAGATTTCA	264906	97102	TTCTCAGTGGCCTAAGGCCT
175733	7929	AGCCTGATCTGCAGTCAGGA	220320	52516	TAATGAAAGACCCAGATTTC	264907	97103	ATTCTCAGTGGCCTAAGGCC
175734	7930	CAGCCTGATCTGCAGTCAGG	220321	52517	CTAATGAAAGACCCAGATTT	264908	97104	CATTCTCAGTGGCCTAAGGC
175735	7931	ACAGCCTGATCTGCAGTCAG	220322	52518	ACTAATGAAAGACCCAGATT	264909	97105	TCATTCTCAGTGGCCTAAGG
175736	7932	CACAGCCTGATCTGCAGTCA	220323	52519	TACTAATGAAAGACCCAGAT	264910	97106	TTCATTCTCAGTGGCCTAAG
175737	7933	ACACAGCCTGATCTGCAGTC	220324	52520	CTACTAATGAAAGACCCAGA	264911	97107	ATTCATTCTCAGTGGCCTAA
175738	7934	CACACAGCCTGATCTGCAGT	220325	52521	ACTACTAATGAAAGACCCAG	264912	97108	TATTCATTCTCAGTGGCCTA
175739	7935	CCACACAGCCTGATCTGCAG	220326	52522	TACTACTAATGAAAGACCCA	264913	97109	TTATTCATTCTCAGTGGCCT
175740	7936	TCCACACAGCCTGATCTGCA	220327	52523	CTACTACTAATGAAAGACCC	264914	97110	GTTATTCATTCTCAGTGGCC
175741	7937	GTCCACACAGCCTGATCTGC	220328	52524	ACTACTACTAATGAAAGACC	264915	97111	GGTTATTCATTCTCAGTGGC
175742	7938	GGTCCACACAGCCTGATCTG	220329	52525	AACTACTACTAATGAAAGAC	264916	97112	GGGTTATTCATTCTCAGTGG
175743	7939	GGGTCCACACAGCCTGATCT	220330	52526	GAACTACTACTAATGAAAGA	264917	97113	GGGGTTATTCATTCTCAGTG
175744	7940	GGGGTCCACACAGCCTGATC	220331	52527	TGAACTACTACTAATGAAAG	264918	97114	AGGGGTTATTCATTCTCAGT
175745	7941	TGGGGTCCACACAGCCTGAT	220332	52528	TTGAACTACTACTAATGAAA	264919	97115	CAGGGGTTATTCATTCTCAG
175746	7942	CTGGGGTCCACACAGCCTGA	220333	52529	ATTGAACTACTACTAATGAA	264920	97116	CCAGGGGTTATTCATTCTCA
175747	7943	GCTGGGGTCCACACAGCCTG	220334	52530	AATTGAACTACTACTAATGA	264921	97117	GCCAGGGGTTATTCATTCTC
175748	7944	GGCTGGGGTCCACACAGCCT	220335	52531	AAATTGAACTACTACTAATG	264922	97118	TGCCAGGGGTTATTCATTCT
175749	7945	AGGCTGGGGTCCACACAGCC	220336	52532	CAAATTGAACTACTACTAAT	264923	97119	CTGCCAGGGGTTATTCATTC
175750	7946	AAGGCTGGGGTCCACACAGC	220337	52533	CCAAATTGAACTACTACTAA	264924	97120	GCTGCCAGGGGTTATTCATT
175751	7947	CAAGGCTGGGGTCCACACAG	220338	52534	ACCAAATTGAACTACTACTA	264925	97121	AGCTGCCAGGGGTTATTCAT
175752	7948	GCAAGGCTGGGGTCCACACA	220339	52535	AACCAAATTGAACTACTACT	264926	97122	CAGCTGCCAGGGGTTATTCA
175753	7949	TGCAAGGCTGGGGTCCACAC	220340	52536	GAACCAAATTGAACTACTAC	264927	97123	CCAGCTGCCAGGGGTTATTC
175754	7950	ATGCAAGGCTGGGGTCCACA	220341	52537	GGAACCAAATTGAACTACTA	264928	97124	ACCAGCTGCCAGGGGTTATT
175755	7951	CATGCAAGGCTGGGGTCCAC	220342	52538	TGGAACCAAATTGAACTACT	264929	97125	GACCAGCTGCCAGGGGTTAT
175756	7952	ACATGCAAGGCTGGGGTCCA	220343	52539	CTGGAACCAAATTGAACTAC	264930	97126	TGACCAGCTGCCAGGGGTTA
175757	7953	AACATGCAAGGCTGGGGTCC	220344	52540	TCTGGAACCAAATTGAACTA	264931	97127	CTGACCAGCTGCCAGGGGTT
175758	7954	AAACATGCAAGGCTGGGGTC	220345	52541	TTCTGGAACCAAATTGAACT	264932	97128	GCTGACCAGCTGCCAGGGGT
175759	7955	TAAACATGCAAGGCTGGGGT	220346	52542	GTTCTGGAACCAAATTGAAC	264933	97129	TGCTGACCAGCTGCCAGGGG
175760	7956	GTAAACATGCAAGGCTGGGG	220347	52543	TGTTCTGGAACCAAATTGAA	264934	97130	CTGCTGACCAGCTGCCAGGG
175761	7957	TGTAAACATGCAAGGCTGGG	220348	52544	ATGTTCTGGAACCAAATTGA	264935	97131	GCTGCTGACCAGCTGCCAGG
175762	7958	CTGTAAACATGCAAGGCTGG	220349	52545	AATGTTCTGGAACCAAATTG	264936	97132	AGCTGCTGACCAGCTGCCAG
175763	7959	TCTGTAAACATGCAAGGCTG	220350	52546	GAATGTTCTGGAACCAAATT	264937	97133	AAGCTGCTGACCAGCTGCCA
175764	7960	GTCTGTAAACATGCAAGGCT	220351	52547	AGAATGTTCTGGAACCAAAT	264938	97134	CAAGCTGCTGACCAGCTGCC
175765	7961	GGTCTGTAAACATGCAAGGC	220352	52548	CAGAATGTTCTGGAACCAAA	264939	97135	GCAAGCTGCTGACCAGCTGC
175766	7962	AGGTCTGTAAACATGCAAGG	220353	52549	ACAGAATGTTCTGGAACCAA	264940	97136	TGCAAGCTGCTGACCAGCTG
175767	7963	AAGGTCTGTAAACATGCAAG	220354	52550	CACAGAATGTTCTGGAACCA	264941	97137	CTGCAAGCTGCTGACCAGCT
175768	7964	GAAGGTCTGTAAACATGCAA	220355	52551	CCACAGAATGTTCTGGAACC	264942	97138	ACTGCAAGCTGCTGACCAGC
175769	7965	TGAAGGTCTGTAAACATGCA	220356	52552	ACCACAGAATGTTCTGGAAC	264943	97139	AACTGCAAGCTGCTGACCAG
175770	7966	ATGAAGGTCTGTAAACATGC	220357	52553	CACCACAGAATGTTCTGGAA	264944	97140	AAACTGCAAGCTGCTGACCA
175771	7967	CATGAAGGTCTGTAAACATG	220358	52554	ACACCACAGAATGTTCTGGA	264945	97141	TAAACTGCAAGCTGCTGACC
175772	7968	ACATGAAGGTCTGTAAACAT	220359	52555	CACACCACAGAATGTTCTGG	264946	97142	GTAAACTGCAAGCTGCTGAC
175773	7969	GACATGAAGGTCTGTAAACA	220360	52556	TCACACCACAGAATGTTCTG	264947	97143	AGTAAACTGCAAGCTGCTGA
175774	7970	AGACATGAAGGTCTGTAAAC	220361	52557	ATCACACCACAGAATGTTCT	264948	97144	TAGTAAACTGCAAGCTGCTG
175775	7971	AAGACATGAAGGTCTGTAAA	220362	52558	CATCACACCACAGAATGTTC	264949	97145	TTAGTAAACTGCAAGCTGCT
175776	7972	TAAGACATGAAGGTCTGTAA	220363	52559	GCATCACACCACAGAATGTT	264950	97146	CTTAGTAAACTGCAAGCTGC
175777	7973	ATAAGACATGAAGGTCTGTA	220364	52560	TGCATCACACCACAGAATGT	264951	97147	GCTTAGTAAACTGCAAGCTG
175778	7974	AATAAGACATGAAGGTCTGT	220365	52561	TTGCATCACACCACAGAATG	264952	97148	TGCTTAGTAAACTGCAAGCT
175779	7975	GAATAAGACATGAAGGTCTG	220366	52562	ATTGCATCACACCACAGAAT	264953	97149	GTGCTTAGTAAACTGCAAGC
175780	7976	AGAATAAGACATGAAGGTCT	220367	52563	CATTGCATCACACCACAGAA	264954	97150	AGTGCTTAGTAAACTGCAAG
175781	7977	AAGAATAAGACATGAAGGTC	220368	52564	ACATTGCATCACACCACAGA	264955	97151	CAGTGCTTAGTAAACTGCAA
175782	7978	TAAGAATAAGACATGAAGGT	220369	52565	CACATTGCATCACACCACAG	264956	97152	CCAGTGCTTAGTAAACTGCA
175783	7979	GTAAGAATAAGACATGAAGG	220370	52566	TCACATTGCATCACACCACA	264957	97153	TCCAGTGCTTAGTAAACTGC
175784	7980	TGTAAGAATAAGACATGAAG	220371	52567	GTCACATTGCATCACACCAC	264958	97154	CTCCAGTGCTTAGTAAACTG
175785	7981	CTGTAAGAATAAGACATGAA	220372	52568	GGTCACATTGCATCACACCA	264959	97155	ACTCCAGTGCTTAGTAAACT
175786	7982	CCTGTAAGAATAAGACATGA	220373	52569	TGGTCACATTGCATCACACC	264960	97156	GACTCCAGTGCTTAGTAAAC
175787	7983	CCCTGTAAGAATAAGACATG	220374	52570	CTGGTCACATTGCATCACAC	264961	97157	AGACTCCAGTGCTTAGTAAA
175788	7984	ACCCTGTAAGAATAAGACAT	220375	52571	TCTGGTCACATTGCATCACA	264962	97158	AAGACTCCAGTGCTTAGTAA
175789	7985	TACCCTGTAAGAATAAGACA	220376	52572	CTCTGGTCACATTGCATCAC	264963	97159	GAAGACTCCAGTGCTTAGTA
175790	7986	ATACCCTGTAAGAATAAGAC	220377	52573	GCTCTGGTCACATTGCATCA	264964	97160	TGAAGACTCCAGTGCTTAGT
175791	7987	GATACCCTGTAAGAATAAGA	220378	52574	AGCTCTGGTCACATTGCATC	264965	97161	ATGAAGACTCCAGTGCTTAG
175792	7988	TGATACCCTGTAAGAATAAG	220379	52575	GAGCTCTGGTCACATTGCAT	264966	97162	AATGAAGACTCCAGTGCTTA
175793	7989	CTGATACCCTGTAAGAATAA	220380	52576	TGAGCTCTGGTCACATTGCA	264967	97163	CAATGAAGACTCCAGTGCTT
175794	7990	TCTGATACCCTGTAAGAATA	220381	52577	GTGAGCTCTGGTCACATTGC	264968	97164	GCAATGAAGACTCCAGTGCT

175795	7991	TTCTGATACCCTGTAAGAAT	220382	52578	TGTGAGCTCTGGTCACATTG	264969	97165	GGCAATGAAGACTCCAGTGC
175796	7992	CTTCTGATACCCTGTAAGAA	220383	52579	GTGTGAGCTCTGGTCACATT	264970	97166	AGGCAATGAAGACTCCAGTG
175797	7993	TCTTCTGATACCCTGTAAGA	220384	52580	AGTGTGAGCTCTGGTCACAT	264971	97167	AAGGCAATGAAGACTCCAGT
175798	7994	TTCTTCTGATACCCTGTAAG	220385	52581	AAGTGTGAGCTCTGGTCACA	264972	97168	GAAGGCAATGAAGACTCCAG
175799	7995	GTTCTTCTGATACCCTGTAA	220386	52582	GAAGTGTGAGCTCTGGTCAC	264973	97169	AGAAGGCAATGAAGACTCCA
175800	7996	TGTTCTTCTGATACCCTGTA	220387	52583	TGAAGTGTGAGCTCTGGTCA	264974	97170	GAGAAGGCAATGAAGACTCC
175801	7997	GTGTTCTTCTGATACCCTGT	220388	52584	CTGAAGTGTGAGCTCTGGTC	264975	97171	TGAGAAGGCAATGAAGACTC
175802	7998	GGTGTTCTTCTGATACCCTG	220389	52585	TCTGAAGTGTGAGCTCTGGT	264976	97172	CTGAGAAGGCAATGAAGACT
175803	7999	AGGTGTTCTTCTGATACCCT	220390	52586	CTCTGAAGTGTGAGCTCTGG	264977	97173	ACTGAGAAGGCAATGAAGAC
175804	8000	TAGGTGTTCTTCTGATACCC	220391	52587	GCTCTGAAGTGTGAGCTCTG	264978	97174	GACTGAGAAGGCAATGAAGA
175805	8001	GTAGGTGTTCTTCTGATACC	220392	52588	AGCTCTGAAGTGTGAGCTCT	264979	97175	GGACTGAGAAGGCAATGAAG
175806	8002	AGTAGGTGTTCTTCTGATAC	220393	52589	GAGCTCTGAAGTGTGAGCTC	264980	97176	AGGACTGAGAAGGCAATGAA
175807	8003	CAGTAGGTGTTCTTCTGATA	220394	52590	AGAGCTCTGAAGTGTGAGCT	264981	97177	AAGGACTGAGAAGGCAATGA
175808	8004	CCAGTAGGTGTTCTTCTGAT	220395	52591	AAGAGCTCTGAAGTGTGAGC	264982	97178	AAAGGACTGAGAAGGCAATG
175809	8005	CCCAGTAGGTGTTCTTCTGA	220396	52592	GAAGAGCTCTGAAGTGTGAG	264983	97179	AAAAGGACTGAGAAGGCAAT
175810	8006	CCCCAGTAGGTGTTCTTCTG	220397	52593	TGAAGAGCTCTGAAGTGTGA	264984	97180	CAAAAGGACTGAGAAGGCAA
175811	8007	TCCCCAGTAGGTGTTCTTCT	220398	52594	TTGAAGAGCTCTGAAGTGTG	264985	97181	TCAAAAGGACTGAGAAGGCA
175812	8008	TTCCCCAGTAGGTGTTCTTC	220399	52595	CTTGAAGAGCTCTGAAGTGT	264986	97182	ATCAAAAGGACTGAGAAGGC
175813	8009	TTTCCCCAGTAGGTGTTCTT	220400	52596	CCTTGAAGAGCTCTGAAGTG	264987	97183	AATCAAAAGGACTGAGAAGG
175814	8010	GTTTCCCCAGTAGGTGTTCT	220401	52597	CCCTTGAAGAGCTCTGAAGT	264988	97184	AAATCAAAAGGACTGAGAAG
175815	8011	AGTTTCCCCAGTAGGTGTTC	220402	52598	GCCCTTGAAGAGCTCTGAAG	264989	97185	GAAATCAAAAGGACTGAGAA
175816	8012	AAGTTTCCCCAGTAGGTGTT	220403	52599	GGCCCTTGAAGAGCTCTGAA	264990	97186	AGAAATCAAAAGGACTGAGA
175817	8013	TAAGTTTCCCCAGTAGGTGT	220404	52600	TGGCCCTTGAAGAGCTCTGA	264991	97187	CAGAAATCAAAAGGACTGAG
175818	8014	ATAAGTTTCCCCAGTAGGTG	220405	52601	CTGGCCCTTGAAGAGCTCTG	264992	97188	TCAGAAATCAAAAGGACTGA
175819	8015	TATAAGTTTCCCCAGTAGGT	220406	52602	ACTGGCCCTTGAAGAGCTCT	264993	97189	CTCAGAAATCAAAAGGACTG
175820	8016	TTATAAGTTTCCCCAGTAGG	220407	52603	GACTGGCCCTTGAAGAGCTC	264994	97190	CCTCAGAAATCAAAAGGACT
175821	8017	TTTATAAGTTTCCCCAGTAG	220408	52604	AGACTGGCCCTTGAAGAGCT	264995	97191	GCCTCAGAAATCAAAAGGAC
175822	8018	ATTTATAAGTTTCCCCAGTA	220409	52605	AAGACTGGCCCTTGAAGAGC	264996	97192	TGCCTCAGAAATCAAAAGGA
175823	8019	AATTTATAAGTTTCCCCAGT	220410	52606	TAAGACTGGCCCTTGAAGAG	264997	97193	TTGCCTCAGAAATCAAAAGG
175824	8020	TAATTTATAAGTTTCCCCAG	220411	52607	GTAAGACTGGCCCTTGAAGA	264998	97194	TTTGCCTCAGAAATCAAAAG
175825	8021	CTAATTTATAAGTTTCCCCA	220412	52608	AGTAAGACTGGCCCTTGAAG	264999	97195	ATTTGCCTCAGAAATCAAAA
175826	8022	ACTAATTTATAAGTTTCCCC	220413	52609	CAGTAAGACTGGCCCTTGAA	265000	97196	CATTTGCCTCAGAAATCAAA
175827	8023	TACTAATTTATAAGTTTCCC	220414	52610	TCAGTAAGACTGGCCCTTGA	265001	97197	ACATTTGCCTCAGAAATCAA
175828	8024	TTACTAATTTATAAGTTTCC	220415	52611	CTCAGTAAGACTGGCCCTTG	265002	97198	AACATTTGCCTCAGAAATCA
175829	8025	TTTACTAATTTATAAGTTTC	220416	52612	GCTCAGTAAGACTGGCCCTT	265003	97199	CAACATTTGCCTCAGAAATC
175830	8026	TTTTACTAATTTATAAGTTT	220417	52613	TGCTCAGTAAGACTGGCCCT	265004	97200	TCAACATTTGCCTCAGAAAT
175831	8027	CTTTTACTAATTTATAAGTT	220418	52614	GTGCTCAGTAAGACTGGCCC	265005	97201	TTCAACATTTGCCTCAGAAA
175832	8028	CCTTTTACTAATTTATAAGT	220419	52615	GGTGCTCAGTAAGACTGGCC	265006	97202	ATTCAACATTTGCCTCAGAA
175833	8029	ACCTTTTACTAATTTATAAG	220420	52616	AGGTGCTCAGTAAGACTGGC	265007	97203	GATTCAACATTTGCCTCAGA
175834	8030	CACCTTTTACTAATTTATAA	220421	52617	GAGGTGCTCAGTAAGACTGG	265008	97204	GGATTCAACATTTGCCTCAG
175835	8031	CCACCTTTTACTAATTTATA	220422	52618	GGAGGTGCTCAGTAAGACTG	265009	97205	GGGATTCAACATTTGCCTCA
175836	8032	CCCACCTTTTACTAATTTAT	220423	52619	GGGAGGTGCTCAGTAAGACT	265010	97206	AGGGATTCAACATTTGCCTC
175837	8033	GCCCACCTTTTACTAATTTA	220424	52620	TGGGAGGTGCTCAGTAAGAC	265011	97207	TAGGGATTCAACATTTGCCT
175838	8034	TGCCCACCTTTTACTAATTT	220425	52621	CTGGGAGGTGCTCAGTAAGA	265012	97208	GTAGGGATTCAACATTTGCC
175839	8035	ATGCCCACCTTTTACTAATT	220426	52622	ACTGGGAGGTGCTCAGTAAG	265013	97209	GGTAGGGATTCAACATTTGC
175840	8036	AATGCCCACCTTTTACTAAT	220427	52623	CACTGGGAGGTGCTCAGTAA	265014	97210	AGGTAGGGATTCAACATTTG
175841	8037	GAATGCCCACCTTTTACTAA	220428	52624	CCACTGGGAGGTGCTCAGTA	265015	97211	AAGGTAGGGATTCAACATTT
175842	8038	AGAATGCCCACCTTTTACTA	220429	52625	GCCACTGGGAGGTGCTCAGT	265016	97212	AAAGGTAGGGATTCAACATT
175843	8039	GAGAATGCCCACCTTTTACT	220430	52626	AGCCACTGGGAGGTGCTCAG	265017	97213	AAAAGGTAGGGATTCAACAT
175844	8040	GGAGAATGCCCACCTTTTAC	220431	52627	CAGCCACTGGGAGGTGCTCA	265018	97214	AAAAAGGTAGGGATTCAACA
175845	8041	GGGAGAATGCCCACCTTTTA	220432	52628	GCAGCCACTGGGAGGTGCTC	265019	97215	AAAAAAGGTAGGGATTCAAC
175846	8042	GGGGAGAATGCCCACCTTTT	220433	52629	GGCAGCCACTGGGAGGTGCT	265020	97216	AAAAAAAGGTAGGGATTCAA
175847	8043	CGGGGAGAATGCCCACCTTT	220434	52630	AGGCAGCCACTGGGAGGTGC	265021	97217	AAAAAAAAGGTAGGGATTCA
175848	8044	GCGGGGAGAATGCCCACCTT	220435	52631	CAGGCAGCCACTGGGAGGTG	265022	97218	AAAAAAAAAGGTAGGGATTC
175849	8045	GGCGGGGAGAATGCCCACCT	220436	52632	ACAGGCAGCCACTGGGAGGT	265023	97219	AAAAAAAAAAGGTAGGGATT
175850	8046	GGGCGGGGAGAATGCCCACC	220437	52633	CACAGGCAGCCACTGGGAGG	265024	97220	AAAAAAAAAAAGGTAGGGAT
175851	8047	TGGGCGGGGAGAATGCCCAC	220438	52634	ACACAGGCAGCCACTGGGAG	265025	97221	AAAAAAAAAAAAGGTAGGGA
175852	8048	ATGGGCGGGGAGAATGCCCA	220439	52635	CACACAGGCAGCCACTGGGA	265026	97222	AAAAAAAAAAAAAGGTAGGG
175853	8049	GATGGGCGGGGAGAATGCCC	220440	52636	GCACACAGGCAGCCACTGGG	265027	97223	AAAAAAAAAAAAAAGGTAGG
175854	8050	AGATGGGCGGGGAGAATGCC	220441	52637	AGCACACAGGCAGCCACTGG	265028	97224	AAAAAAAAAAAAAAAGGTAG
175855	8051	AAGATGGGCGGGGAGAATGC	220442	52638	CAGCACACAGGCAGCCACTG	265029	97225	GAAAAAAAAAAAAAAAGGTA
175856	8052	GAAGATGGGCGGGGAGAATG	220443	52639	CCAGCACACAGGCAGCCACT	265030	97226	AGAAAAAAAAAAAAAAAGGT
175857	8053	AGAAGATGGGCGGGGAGAAT	220444	52640	CCCAGCACACAGGCAGCCAC	265031	97227	AAGAAAAAAAAAAAAAAAGG
175858	8054	CAGAAGATGGGCGGGGAGAA	220445	52641	GCCCAGCACACAGGCAGCCA	265032	97228	AAAGAAAAAAAAAAAAAAAG
175859	8055	ACAGAAGATGGGCGGGGAGA	220446	52642	CGCCCAGCACACAGGCAGCC	265033	97229	AAAAGAAAAAAAAAAAAAAA
175860	8056	GACAGAAGATGGGCGGGGAG	220447	52643	GCGCCCAGCACACAGGCAGC	265034	97230	CAAAAGAAAAAAAAAAAAAA
175861	8057	AGACAGAAGATGGGCGGGGA	220448	52644	GGCGCCCAGCACACAGGCAG	265035	97231	TCAAAAGAAAAAAAAAAAAA
175862	8058	CAGACAGAAGATGGGCGGGG	220449	52645	TGGCGCCCAGCACACAGGCA	265036	97232	CTCAAAAGAAAAAAAAAAAA
175863	8059	ACAGACAGAAGATGGGCGGG	220450	52646	GTGGCGCCCAGCACACAGGC	265037	97233	TCTCAAAAGAAAAAAAAAAA
175864	8060	GACAGACAGAAGATGGGCGG	220451	52647	AGTGGCGCCCAGCACACAGG	265038	97234	GTCTCAAAAGAAAAAAAAAA
175865	8061	AGACAGACAGAAGATGGGCG	220452	52648	AAGTGGCGCCCAGCACACAG	265039	97235	TGTCTCAAAAGAAAAAAAAA
175866	8062	CAGACAGACAGAAGATGGGC	220453	52649	CAAGTGGCGCCCAGCACACA	265040	97236	CTGTCTCAAAAGAAAAAAAA

175867	8063	GCAGACAGACAGAAGATGGG	220454	52650	ACAAGTGGCGCCCAGCACAC	265041	97237	TCTGTCTCAAAAGAAAAAAA
175868	8064	GGCAGACAGACAGAAGATGG	220455	52651	CACAAGTGGCGCCCAGCACA	265042	97238	CTCTGTCTCAAAAGAAAAAA
175869	8065	TGGCAGACAGACAGAAGATG	220456	52652	CCACAAGTGGCGCCCAGCAC	265043	97239	ACTCTGTCTCAAAAGAAAAA
175870	8066	CTGGCAGACAGACAGAAGAT	220457	52653	ACCACAAGTGGCGCCCAGCA	265044	97240	AACTCTGTCTCAAAAGAAAA
175871	8067	CCTGGCAGACAGACAGAAGA	220458	52654	CACCACAAGTGGCGCCCAGC	265045	97241	AAACTCTGTCTCAAAAGAAA
175872	8068	TCCTGGCAGACAGACAGAAG	220459	52655	CCACCACAAGTGGCGCCCAG	265046	97242	GAAACTCTGTCTCAAAAGAA
175873	8069	GTCCTGGCAGACAGACAGAA	220460	52656	CCCACCACAAGTGGCGCCCA	265047	97243	CGAAACTCTGTCTCAAAAGA
175874	8070	AGTCCTGGCAGACAGACAGA	220461	52657	GCCCACCACAAGTGGCGCCC	265048	97244	GCGAAACTCTGTCTCAAAAG
175875	8071	TAGTCCTGGCAGACAGACAG	220462	52658	TGCCCACCACAAGTGGCGCC	265049	97245	AGCGAAACTCTGTCTCAAAA
175876	8072	CTAGTCCTGGCAGACAGACA	220463	52659	CTGCCCACCACAAGTGGCGC	265050	97246	AAGCGAAACTCTGTCTCAAA
175877	8073	GCTAGTCCTGGCAGACAGAC	220464	52660	CCTGCCCACCACAAGTGGCG	265051	97247	AAAGCGAAACTCTGTCTCAA
175878	8074	TGCTAGTCCTGGCAGACAGA	220465	52661	TCCTGCCCACCACAAGTGGC	265052	97248	AAAAGCGAAACTCTGTCTCA
175879	8075	GTGCTAGTCCTGGCAGACAG	220466	52662	CTCCTGCCCACCACAAGTGG	265053	97249	CAAAAGCGAAACTCTGTCTC
175880	8076	TGTGCTAGTCCTGGCAGACA	220467	52663	TCTCCTGCCCACCACAAGTG	265054	97250	ACAAAAGCGAAACTCTGTCT
175881	8077	CTGTGCTAGTCCTGGCAGAC	220468	52664	CTCTCCTGCCCACCACAAGT	265055	97251	AACAAAAGCGAAACTCTGTC
175882	8078	GCTGTGCTAGTCCTGGCAGA	220469	52665	TCTCTCCTGCCCACCACAAG	265056	97252	TAACAAAAGCGAAACTCTGT
175883	8079	TGCTGTGCTAGTCCTGGCAG	220470	52666	CTCTCTCCTGCCCACCACAA	265057	97253	ATAACAAAAGCGAAACTCTG
175884	8080	GTGCTGTGCTAGTCCTGGCA	220471	52667	CCTCTCTCCTGCCCACCACA	265058	97254	GATAACAAAAGCGAAACTCT
175885	8081	AGTGCTGTGCTAGTCCTGGC	220472	52668	TCCTCTCTCCTGCCCACCAC	265059	97255	GGATAACAAAAGCGAAACTC
175886	8082	AAGTGCTGTGCTAGTCCTGG	220473	52669	CTCCTCTCTCCTGCCCACCA	265060	97256	TGGATAACAAAAGCGAAACT
175887	8083	AAAGTGCTGTGCTAGTCCTG	220474	52670	CCTCCTCTCTCCTGCCCACC	265061	97257	CTGGATAACAAAAGCGAAAC
175888	8084	CAAAGTGCTGTGCTAGTCCT	220475	52671	CCCTCCTCTCTCCTGCCCAC	265062	97258	CCTGGATAACAAAAGCGAAA
175889	8085	TCAAAGTGCTGTGCTAGTCC	220476	52672	CCCCTCCTCTCTCCTGCCCA	265063	97259	GCCTGGATAACAAAAGCGAA
175890	8086	TTCAAAGTGCTGTGCTAGTC	220477	52673	TCCCCTCCTCTCTCCTGCCC	265064	97260	GGCCTGGATAACAAAAGCGA
175891	8087	CTTCAAAGTGCTGTGCTAGT	220478	52674	GTCCCCTCCTCTCTCCTGCC	265065	97261	CGGCCTGGATAACAAAAGCG
175892	8088	ACTTCAAAGTGCTGTGCTAG	220479	52675	TGTCCCCTCCTCTCTCCTGC	265066	97262	CCGGCCTGGATAACAAAAGC
175893	8089	GACTTCAAAGTGCTGTGCTA	220480	52676	GTGTCCCCTCCTCTCTCCTG	265067	97263	TCCGGCCTGGATAACAAAAG
175894	8090	TGACTTCAAAGTGCTGTGCT	220481	52677	TGTGTCCCCTCCTCTCTCCT	265068	97264	CTCCGGCCTGGATAACAAAA
175895	8091	ATGACTTCAAAGTGCTGTGC	220482	52678	TTGTGTCCCCTCCTCTCTCC	265069	97265	ACTCCGGCCTGGATAACAAA
175896	8092	AATGACTTCAAAGTGCTGTG	220483	52679	TTTGTGTCCCCTCCTCTCTC	265070	97266	CACTCCGGCCTGGATAACAA
175897	8093	GAATGACTTCAAAGTGCTGT	220484	52680	TTTTGTGTCCCCTCCTCTCT	265071	97267	GCACTCCGGCCTGGATAACA
175898	8094	TGAATGACTTCAAAGTGCTG	220485	52681	CTTTTGTGTCCCCTCCTCTC	265072	97268	TGCACTCCGGCCTGGATAAC
175899	8095	GTGAATGACTTCAAAGTGCT	220486	52682	CCTTTTGTGTCCCCTCCTCT	265073	97269	CTGCACTCCGGCCTGGATAA
175900	8096	TGTGAATGACTTCAAAGTGC	220487	52683	TCCTTTTGTGTCCCCTCCTC	265074	97270	ACTGCACTCCGGCCTGGATA
175901	8097	ATGTGAATGACTTCAAAGTG	220488	52684	CTCCTTTTGTGTCCCCTCCT	265075	97271	CACTGCACTCCGGCCTGGAT
175902	8098	TATGTGAATGACTTCAAAGT	220489	52685	TCTCCTTTTGTGTCCCCTCC	265076	97272	CCACTGCACTCCGGCCTGGA
175903	8099	CTATGTGAATGACTTCAAAG	220490	52686	GTCTCCTTTTGTGTCCCCTC	265077	97273	ACCACTGCACTCCGGCCTGG
175904	8100	TCTATGTGAATGACTTCAAA	220491	52687	TGTCTCCTTTTGTGTCCCCT	265078	97274	CACCACTGCACTCCGGCCTG
175905	8101	TTCTATGTGAATGACTTCAA	220492	52688	GTGTCTCCTTTTGTGTCCCC	265079	97275	ACACCACTGCACTCCGGCCT
175906	8102	ATTCTATGTGAATGACTTCA	220493	52689	TGTGTCTCCTTTTGTGTCCC	265080	97276	CACACCACTGCACTCCGGCC
175907	8103	GATTCTATGTGAATGACTTC	220494	52690	CTGTGTCTCCTTTTGTGTCC	265081	97277	TCACACCACTGCACTCCGGC
175908	8104	GGATTCTATGTGAATGACTT	220495	52691	GCTGTGTCTCCTTTTGTGTC	265082	97278	ATCACACCACTGCACTCCGG
175909	8105	GGGATTCTATGTGAATGACT	220496	52692	AGCTGTGTCTCCTTTTGTGT	265083	97279	GATCACACCACTGCACTCCG
175910	8106	TGGGATTCTATGTGAATGAC	220497	52693	GAGCTGTGTCTCCTTTTGTG	265084	97280	AGATCACACCACTGCACTCC
175911	8107	TTGGGATTCTATGTGAATGA	220498	52694	GGAGCTGTGTCTCCTTTTGT	265085	97281	GAGATCACACCACTGCACTC
175912	8108	GTTGGGATTCTATGTGAATG	220499	52695	AGGAGCTGTGTCTCCTTTTG	265086	97282	TGAGATCACACCACTGCACT
175913	8109	AGTTGGGATTCTATGTGAAT	220500	52696	AAGGAGCTGTGTCTCCTTTT	265087	97283	CTGAGATCACACCACTGCAC
175914	8110	AAGTTGGGATTCTATGTGAA	220501	52697	GAAGGAGCTGTGTCTCCTTT	265088	97284	GCTGAGATCACACCACTGCA
175915	8111	TAAGTTGGGATTCTATGTGA	220502	52698	AGAAGGAGCTGTGTCTCCTT	265089	97285	AGCTGAGATCACACCACTGC
175916	8112	TTAAGTTGGGATTCTATGTG	220503	52699	AAGAAGGAGCTGTGTCTCCT	265090	97286	GAGCTGAGATCACACCACTG
175917	8113	CTTAAGTTGGGATTCTATGT	220504	52700	TAAGAAGGAGCTGTGTCTCC	265091	97287	TGAGCTGAGATCACACCACT
175918	8114	TCTTAAGTTGGGATTCTATG	220505	52701	CTAAGAAGGAGCTGTGTCTC	265092	97288	GTGAGCTGAGATCACACCAC
175919	8115	CTCTTAAGTTGGGATTCTAT	220506	52702	TCTAAGAAGGAGCTGTGTCT	265093	97289	AGTGAGCTGAGATCACACCA
175920	8116	CCTCTTAAGTTGGGATTCTA	220507	52703	TTCTAAGAAGGAGCTGTGTC	265094	97290	CAGTGAGCTGAGATCACACC
175921	8117	CCCTCTTAAGTTGGGATTCT	220508	52704	CTTCTAAGAAGGAGCTGTGT	265095	97291	GCAGTGAGCTGAGATCACAC
175922	8118	ACCCTCTTAAGTTGGGATTC	220509	52705	GCTTCTAAGAAGGAGCTGTG	265096	97292	TGCAGTGAGCTGAGATCACA
175923	8119	TACCCTCTTAAGTTGGGATT	220510	52706	AGCTTCTAAGAAGGAGCTGT	265097	97293	ATGCAGTGAGCTGAGATCAC
175924	8120	TTACCCTCTTAAGTTGGGAT	220511	52707	GAGCTTCTAAGAAGGAGCTG	265098	97294	GATGCAGTGAGCTGAGATCA
175925	8121	TTTACCCTCTTAAGTTGGGA	220512	52708	TGAGCTTCTAAGAAGGAGCT	265099	97295	GGATGCAGTGAGCTGAGATC
175926	8122	TTTTACCCTCTTAAGTTGGG	220513	52709	TTGAGCTTCTAAGAAGGAGC	265100	97296	AGGATGCAGTGAGCTGAGAT
175927	8123	ATTTTACCCTCTTAAGTTGG	220514	52710	TTTGAGCTTCTAAGAAGGAG	265101	97297	GAGGATGCAGTGAGCTGAGA
175928	8124	GATTTTACCCTCTTAAGTTG	220515	52711	CTTTGAGCTTCTAAGAAGGA	265102	97298	GGAGGATGCAGTGAGCTGAG
175929	8125	GGATTTTACCCTCTTAAGTT	220516	52712	ACTTTGAGCTTCTAAGAAGG	265103	97299	TGGAGGATGCAGTGAGCTGA
175930	8126	AGGATTTTACCCTCTTAAGT	220517	52713	AACTTTGAGCTTCTAAGAAG	265104	97300	GTGGAGGATGCAGTGAGCTG
175931	8127	GAGGATTTTACCCTCTTAAG	220518	52714	CAACTTTGAGCTTCTAAGAA	265105	97301	GGTGGAGGATGCAGTGAGCT
175932	8128	GGAGGATTTTACCCTCTTAA	220519	52715	CCAACTTTGAGCTTCTAAGA	265106	97302	AGGTGGAGGATGCAGTGAGC
175933	8129	AGGAGGATTTTACCCTCTTA	220520	52716	CCCAACTTTGAGCTTCTAAG	265107	97303	GAGGTGGAGGATGCAGTGAG
175934	8130	GAGGAGGATTTTACCCTCTT	220521	52717	CCCCAACTTTGAGCTTCTAA	265108	97304	GGAGGTGGAGGATGCAGTGA
175935	8131	TGAGGAGGATTTTACCCTCT	220522	52718	TCCCCAACTTTGAGCTTCTA	265109	97305	GGGAGGTGGAGGATGCAGTG
175936	8132	TTGAGGAGGATTTTACCCTC	220523	52719	GTCCCCAACTTTGAGCTTCT	265110	97306	TGGGAGGTGGAGGATGCAGT
175937	8133	GTTGAGGAGGATTTTACCCT	220524	52720	GGTCCCCAACTTTGAGCTTC	265111	97307	CTGGGAGGTGGAGGATGCAG
175938	8134	TGTTGAGGAGGATTTTACCC	220525	52721	TGGTCCCCAACTTTGAGCTT	265112	97308	CCTGGGAGGTGGAGGATGCA

175939	8135	CTGTTGAGGAGGATTTTACC	220526	52722	CTGGTCCCCAACTTTGAGCT	265113	97309	ACCTGGGAGGTGGAGGATGC
175940	8136	TCTGTTGAGGAGGATTTTAC	220527	52723	GCTGGTCCCCAACTTTGAGC	265114	97310	AACCTGGGAGGTGGAGGATG
175941	8137	GTCTGTTGAGGAGGATTTTA	220528	52724	AGCTGGTCCCCAACTTTGAG	265115	97311	GAACCTGGGAGGTGGAGGAT
175942	8138	AGTCTGTTGAGGAGGATTTT	220529	52725	CAGCTGGTCCCCAACTTTGA	265116	97312	TGAACCTGGGAGGTGGAGGA
175943	8139	CAGTCTGTTGAGGAGGATTT	220530	52726	GCAGCTGGTCCCCAACTTTG	265117	97313	TTGAACCTGGGAGGTGGAGG
175944	8140	TCAGTCTGTTGAGGAGGATT	220531	52727	GGCAGCTGGTCCCCAACTTT	265118	97314	CTTGAACCTGGGAGGTGGAG
175945	8141	TTCAGTCTGTTGAGGAGGAT	220532	52728	TGGCAGCTGGTCCCCAACTT	265119	97315	GCTTGAACCTGGGAGGTGGA
175946	8142	TTTCAGTCTGTTGAGGAGGA	220533	52729	GTGGCAGCTGGTCCCCAACT	265120	97316	CGCTTGAACCTGGGAGGTGG
175947	8143	TTTTCAGTCTGTTGAGGAGG	220534	52730	TGTGGCAGCTGGTCCCCAAC	265121	97317	TCGCTTGAACCTGGGAGGTG
175948	8144	ATTTTCAGTCTGTTGAGGAG	220535	52731	CTGTGGCAGCTGGTCCCCAA	265122	97318	ATCGCTTGAACCTGGGAGGT
175949	8145	TATTTTCAGTCTGTTGAGGA	220536	52732	TCTGTGGCAGCTGGTCCCCA	265123	97319	AATCGCTTGAACCTGGGAGG
175950	8146	TTATTTTCAGTCTGTTGAGG	220537	52733	TTCTGTGGCAGCTGGTCCCC	265124	97320	GAATCGCTTGAACCTGGGAG
175951	8147	CTTATTTTCAGTCTGTTGAG	220538	52734	CTTCTGTGGCAGCTGGTCCC	265125	97321	AGAATCGCTTGAACCTGGGA
175952	8148	ACTTATTTTCAGTCTGTTGA	220539	52735	TCTTCTGTGGCAGCTGGTCC	265126	97322	GAGAATCGCTTGAACCTGGG
175953	8149	AACTTATTTTCAGTCTGTTG	220540	52736	CTCTTCTGTGGCAGCTGGTC	265127	97323	GGAGAATCGCTTGAACCTGG
175954	8150	AAACTTATTTTCAGTCTGTT	220541	52737	ACTCTTCTGTGGCAGCTGGT	265128	97324	AGGAGAATCGCTTGAACCTG
175955	8151	TAAACTTATTTTCAGTCTGT	220542	52738	TACTCTTCTGTGGCAGCTGG	265129	97325	TAGGAGAATCGCTTGAACCT
175956	8152	TTAAACTTATTTTCAGTCTG	220543	52739	ATACTCTTCTGTGGCAGCTG	265130	97326	GTAGGAGAATCGCTTGAACC
175957	8153	TTTAAACTTATTTTCAGTCT	220544	52740	CATACTCTTCTGTGGCAGCT	265131	97327	GGTAGGAGAATCGCTTGAAC
175958	8154	ATTTAAACTTATTTTCAGTC	220545	52741	ACATACTCTTCTGTGGCAGC	265132	97328	AGGTAGGAGAATCGCTTGAA
175959	8155	AATTTAAACTTATTTTCAGT	220546	52742	AACATACTCTTCTGTGGCAG	265133	97329	GAGGTAGGAGAATCGCTTGA
175960	8156	GAATTTAAACTTATTTTCAG	220547	52743	AAACATACTCTTCTGTGGCA	265134	97330	TGAGGTAGGAGAATCGCTTG
175961	8157	GGAATTTAAACTTATTTTCA	220548	52744	TAAACATACTCTTCTGTGGC	265135	97331	CTGAGGTAGGAGAATCGCTT
175962	8158	GGGAATTTAAACTTATTTTC	220549	52745	CTAAACATACTCTTCTGTGG	265136	97332	GCTGAGGTAGGAGAATCGCT
175963	8159	AGGGAATTTAAACTTATTTT	220550	52746	GCTAAACATACTCTTCTGTG	265137	97333	GGCTGAGGTAGGAGAATCGC
175964	8160	AAGGGAATTTAAACTTATTT	220551	52747	TGCTAAACATACTCTTCTGT	265138	97334	AGGCTGAGGTAGGAGAATCG
175965	8161	AAAGGGAATTTAAACTTATT	220552	52748	ATGCTAAACATACTCTTCTG	265139	97335	GAGGCTGAGGTAGGAGAATC
175966	8162	CAAAGGGAATTTAAACTTAT	220553	52749	GATGCTAAACATACTCTTCT	265140	97336	GGAGGCTGAGGTAGGAGAAT
175967	8163	GCAAAGGGAATTTAAACTTA	220554	52750	AGATGCTAAACATACTCTTC	265141	97337	GGGAGGCTGAGGTAGGAGAA
175968	8164	AGCAAAGGGAATTTAAACTT	220555	52751	CAGATGCTAAACATACTCTT	265142	97338	AGGGAGGCTGAGGTAGGAGA
175969	8165	TAGCAAAGGGAATTTAAACT	220556	52752	TCAGATGCTAAACATACTCT	265143	97339	TAGGGAGGCTGAGGTAGGAG
175970	8166	ATAGCAAAGGGAATTTAAAC	220557	52753	CTCAGATGCTAAACATACTC	265144	97340	CTAGGGAGGCTGAGGTAGGA
175971	8167	TATAGCAAAGGGAATTTAAA	220558	52754	TCTCAGATGCTAAACATACT	265145	97341	ACTAGGGAGGCTGAGGTAGG
175972	8168	ATATAGCAAAGGGAATTTAA	220559	52755	GTCTCAGATGCTAAACATAC	265146	97342	TACTAGGGAGGCTGAGGTAG
175973	8169	AATATAGCAAAGGGAATTTA	220560	52756	TGTCTCAGATGCTAAACATA	265147	97343	CTACTAGGGAGGCTGAGGTA
175974	8170	TAATATAGCAAAGGGAATTT	220561	52757	GTGTCTCAGATGCTAAACAT	265148	97344	GCTACTAGGGAGGCTGAGGT
175975	8171	TTAATATAGCAAAGGGAATT	220562	52758	GGTGTCTCAGATGCTAAACA	265149	97345	AGCTACTAGGGAGGCTGAGG
175976	8172	GTTAATATAGCAAAGGGAAT	220563	52759	TGGTGTCTCAGATGCTAAAC	265150	97346	CAGCTACTAGGGAGGCTGAG
175977	8173	AGTTAATATAGCAAAGGGAA	220564	52760	TTGGTGTCTCAGATGCTAAA	265151	97347	CCAGCTACTAGGGAGGCTGA
175978	8174	GAGTTAATATAGCAAAGGGA	220565	52761	CTTGGTGTCTCAGATGCTAA	265152	97348	CCCAGCTACTAGGGAGGCTG
175979	8175	GGAGTTAATATAGCAAAGGG	220566	52762	TCTTGGTGTCTCAGATGCTA	265153	97349	TCCCAGCTACTAGGGAGGCT
175980	8176	GGGAGTTAATATAGCAAAGG	220567	52763	ATCTTGGTGTCTCAGATGCT	265154	97350	ATCCCAGCTACTAGGGAGGC
175981	8177	GGGGAGTTAATATAGCAAAG	220568	52764	GATCTTGGTGTCTCAGATGC	265155	97351	AATCCCAGCTACTAGGGAGG
175982	8178	AGGGGAGTTAATATAGCAAA	220569	52765	GGATCTTGGTGTCTCAGATG	265156	97352	TAATCCCAGCTACTAGGGAG
175983	8179	CAGGGGAGTTAATATAGCAA	220570	52766	TGGATCTTGGTGTCTCAGAT	265157	97353	GTAATCCCAGCTACTAGGGA
175984	8180	TCAGGGGAGTTAATATAGCA	220571	52767	CTGGATCTTGGTGTCTCAGA	265158	97354	TGTAATCCCAGCTACTAGGG
175985	8181	CTCAGGGGAGTTAATATAGC	220572	52768	GCTGGATCTTGGTGTCTCAG	265159	97355	CTGTAATCCCAGCTACTAGG
175986	8182	CCTCAGGGGAGTTAATATAG	220573	52769	CGCTGGATCTTGGTGTCTCA	265160	97356	CCTGTAATCCCAGCTACTAG
175987	8183	TCCTCAGGGGAGTTAATATA	220574	52770	ACGCTGGATCTTGGTGTCTC	265161	97357	GCCTGTAATCCCAGCTACTA
175988	8184	TTCCTCAGGGGAGTTAATAT	220575	52771	GACGCTGGATCTTGGTGTCT	265162	97358	TGCCTGTAATCCCAGCTACT
175989	8185	TTTCCTCAGGGGAGTTAATA	220576	52772	TGACGCTGGATCTTGGTGTC	265163	97359	GTGCCTGTAATCCCAGCTAC
175990	8186	CTTTCCTCAGGGGAGTTAAT	220577	52773	GTGACGCTGGATCTTGGTGT	265164	97360	GGTGCCTGTAATCCCAGCTA
175991	8187	TCTTTCCTCAGGGGAGTTAA	220578	52774	TGTGACGCTGGATCTTGGTG	265165	97361	AGGTGCCTGTAATCCCAGCT
175992	8188	CTCTTTCCTCAGGGGAGTTA	220579	52775	TTGTGACGCTGGATCTTGGT	265166	97362	CAGGTGCCTGTAATCCCAGC
175993	8189	ACTCTTTCCTCAGGGGAGTT	220580	52776	CTTGTGACGCTGGATCTTGG	265167	97363	GCAGGTGCCTGTAATCCCAG
175994	8190	GACTCTTTCCTCAGGGGAGT	220581	52777	CCTTGTGACGCTGGATCTTG	265168	97364	GGCAGGTGCCTGTAATCCCA
175995	8191	AGACTCTTTCCTCAGGGGAG	220582	52778	CCCTTGTGACGCTGGATCTT	265169	97365	TGGCAGGTGCCTGTAATCCC
175996	8192	AAGACTCTTTCCTCAGGGGA	220583	52779	ACCCTTGTGACGCTGGATCT	265170	97366	GTGGCAGGTGCCTGTAATCC
175997	8193	TAAGACTCTTTCCTCAGGGG	220584	52780	CACCCTTGTGACGCTGGATC	265171	97367	AGTGGCAGGTGCCTGTAATC
175998	8194	CTAAGACTCTTTCCTCAGGG	220585	52781	ACACCCTTGTGACGCTGGAT	265172	97368	TAGTGGCAGGTGCCTGTAAT
175999	8195	TCTAAGACTCTTTCCTCAGG	220586	52782	AACACCCTTGTGACGCTGGA	265173	97369	ATAGTGGCAGGTGCCTGTAA
176000	8196	ATCTAAGACTCTTTCCTCAG	220587	52783	AAACACCCTTGTGACGCTGG	265174	97370	CATAGTGGCAGGTGCCTGTA
176001	8197	GATCTAAGACTCTTTCCTCA	220588	52784	TAAACACCCTTGTGACGCTG	265175	97371	GCATAGTGGCAGGTGCCTGT
176002	8198	TGATCTAAGACTCTTTCCTC	220589	52785	ATAAACACCCTTGTGACGCT	265176	97372	GGCATAGTGGCAGGTGCCTG
176003	8199	TTGATCTAAGACTCTTTCCT	220590	52786	AATAAACACCCTTGTGACGC	265177	97373	GGGCATAGTGGCAGGTGCCT
176004	8200	ATTGATCTAAGACTCTTTCC	220591	52787	TAATAAACACCCTTGTGACG	265178	97374	CGGGCATAGTGGCAGGTGCC
176005	8201	CATTGATCTAAGACTCTTTC	220592	52788	TTAATAAACACCCTTGTGAC	265179	97375	CCGGGCATAGTGGCAGGTGC
176006	8202	ACATTGATCTAAGACTCTTT	220593	52789	CTTAATAAACACCCTTGTGA	265180	97376	GCCGGGCATAGTGGCAGGTG
176007	8203	GACATTGATCTAAGACTCTT	220594	52790	GCTTAATAAACACCCTTGTG	265181	97377	AGCCGGGCATAGTGGCAGGT
176008	8204	GGACATTGATCTAAGACTCT	220595	52791	GGCTTAATAAACACCCTTGT	265182	97378	TAGCCGGGCATAGTGGCAGG
176009	8205	TGGACATTGATCTAAGACTC	220596	52792	AGGCTTAATAAACACCCTTG	265183	97379	TTAGCCGGGCATAGTGGCAG
176010	8206	TTGGACATTGATCTAAGACT	220597	52793	GAGGCTTAATAAACACCCTT	265184	97380	ATTAGCCGGGCATAGTGGCA

176011	8207	GTTGGACATTGATCTAAGAC	220598	52794	GGAGGCTTAATAAACACCCT	265185	97381	AATTAGCCGGGCATAGTGGC
176012	8208	TGTTGGACATTGATCTAAGA	220599	52795	AGGAGGCTTAATAAACACCC	265186	97382	AAATTAGCCGGGCATAGTGG
176013	8209	GTGTTGGACATTGATCTAAG	220600	52796	GAGGAGGCTTAATAAACACC	265187	97383	AAAATTAGCCGGGCATAGTG
176014	8210	AGTGTTGGACATTGATCTAA	220601	52797	TGAGGAGGCTTAATAAACAC	265188	97384	AAAAATTAGCCGGGCATAGT
176015	8211	TAGTGTTGGACATTGATCTA	220602	52798	ATGAGGAGGCTTAATAAACA	265189	97385	AAAAAATTAGCCGGGCATAG
176016	8212	TTAGTGTTGGACATTGATCT	220603	52799	GATGAGGAGGCTTAATAAAC	265190	97386	CAAAAAATTAGCCGGGCATA
176017	8213	TTTAGTGTTGGACATTGATC	220604	52800	AGATGAGGAGGCTTAATAAA	265191	97387	ACAAAAAATTAGCCGGGCAT
176018	8214	TTTTAGTGTTGGACATTGAT	220605	52801	GAGATGAGGAGGCTTAATAA	265192	97388	TACAAAAAATTAGCCGGGCA
176019	8215	TTTTTAGTGTTGGACATTGA	220606	52802	AGAGATGAGGAGGCTTAATA	265193	97389	ATACAAAAAATTAGCCGGGC
176020	8216	GTTTTTAGTGTTGGACATTG	220607	52803	AAGAGATGAGGAGGCTTAAT	265194	97390	AATACAAAAAATTAGCCGGG
176021	8217	TGTTTTTAGTGTTGGACATT	220608	52804	AAAGAGATGAGGAGGCTTAA	265195	97391	AAATACAAAAAATTAGCCGG
176022	8218	CTGTTTTTAGTGTTGGACAT	220609	52805	GAAAGAGATGAGGAGGCTTA	265196	97392	AAAATACAAAAAATTAGCCG
176023	8219	ACTGTTTTTAGTGTTGGACA	220610	52806	AGAAAGAGATGAGGAGGCTT	265197	97393	AAAAATACAAAAAATTAGCC
176024	8220	AACTGTTTTTAGTGTTGGAC	220611	52807	AAGAAAGAGATGAGGAGGCT	265198	97394	TAAAAATACAAAAAATTAGC
176025	8221	AAACTGTTTTTAGTGTTGGA	220612	52808	AAAGAAAGAGATGAGGAGGC	265199	97395	CTAAAAATACAAAAAATTAG
176026	8222	AAAACTGTTTTTAGTGTTGG	220613	52809	AAAAGAAAGAGATGAGGAGG	265200	97396	ACTAAAAATACAAAAAATTA
176027	8223	TAAAACTGTTTTTAGTGTTG	220614	52810	AAAAAGAAAGAGATGAGGAG	265201	97397	TACTAAAAATACAAAAAATT
176028	8224	TTAAAACTGTTTTTAGTGTT	220615	52811	GAAAAAGAAAGAGATGAGGA	265202	97398	CTACTAAAAATACAAAAAAT
176029	8225	TTTAAAACTGTTTTTAGTGT	220616	52812	AGAAAAAGAAAGAGATGAGG	265203	97399	TCTACTAAAAATACAAAAAA
176030	8226	ATTTAAAACTGTTTTTAGTG	220617	52813	AAGAAAAAGAAAGAGATGAG	265204	97400	CTCTACTAAAAATACAAAAA
176031	8227	GATTTAAAACTGTTTTTAGT	220618	52814	AAAGAAAAAGAAAGAGATGA	265205	97401	TCTCTACTAAAAATACAAAA
176032	8228	TGATTTAAAACTGTTTTTAG	220619	52815	AAAAGAAAAAGAAAGAGATG	265206	97402	GTCTCTACTAAAAATACAAA
176033	8229	CTGATTTAAAACTGTTTTTA	220620	52816	AAAAAGAAAAAGAAAGAGAT	265207	97403	TGTCTCTACTAAAAATACAA
176034	8230	GCTGATTTAAAACTGTTTTT	220621	52817	AAAAAAGAAAAAGAAAGAGA	265208	97404	CTGTCTCTACTAAAAATACA
176035	8231	TGCTGATTTAAAACTGTTTT	220622	52818	AAAAAAAGAAAAAGAAAGAG	265209	97405	CCTGTCTCTACTAAAAATAC
176036	8232	TTGCTGATTTAAAACTGTTT	220623	52819	AAAAAAAAGAAAAAGAAAGA	265210	97406	CCCTGTCTCTACTAAAAATA
176037	8233	CTTGCTGATTTAAAACTGTT	220624	52820	AAAAAAAAAGAAAAAGAAAG	265211	97407	ACCCTGTCTCTACTAAAAAT
176038	8234	ACTTGCTGATTTAAAACTGT	220625	52821	AAAAAAAAAAGAAAAAGAAA	265212	97408	AACCCTGTCTCTACTAAAAA
176039	8235	CACTTGCTGATTTAAAACTG	220626	52822	AAAAAAAAAAAGAAAAAGAA	265213	97409	AAACCCTGTCTCTACTAAAA
176040	8236	TCACTTGCTGATTTAAAACT	220627	52823	AAAAAAAAAAAAGAAAAAGA	265214	97410	GAAACCCTGTCTCTACTAAA
176041	8237	CTCACTTGCTGATTTAAAAC	220628	52824	AAAAAAAAAAAAAGAAAAAG	265215	97411	TGAAACCCTGTCTCTACTAA
176042	8238	TCTCACTTGCTGATTTAAAA	220629	52825	AAAAAAAAAAAAAAGAAAAA	265216	97412	GTGAAACCCTGTCTCTACTA
176043	8239	TTCTCACTTGCTGATTTAAA	220630	52826	AAAAAAAAAAAAAAAGAAAA	265217	97413	GGTGAAACCCTGTCTCTACT
176044	8240	ATTCTCACTTGCTGATTTAA	220631	52827	AAAAAAAAAAAAAAAAGAAA	265218	97414	TGGTGAAACCCTGTCTCTAC
176045	8241	AATTCTCACTTGCTGATTTA	220632	52828	AAAAAAAAAAAAAAAAAGAA	265219	97415	ATGGTGAAACCCTGTCTCTA
176046	8242	TAATTCTCACTTGCTGATTT	220633	52829	GAAAAAAAAAAAAAAAAAGA	265220	97416	CATGGTGAAACCCTGTCTCT
176047	8243	TTAATTCTCACTTGCTGATT	220634	52830	GGAAAAAAAAAAAAAAAAAG	265221	97417	ACATGGTGAAACCCTGTCTC
176048	8244	TTTAATTCTCACTTGCTGAT	220635	52831	AGGAAAAAAAAAAAAAAAAA	265222	97418	AACATGGTGAAACCCTGTCT
176049	8245	ATTTAATTCTCACTTGCTGA	220636	52832	GAGGAAAAAAAAAAAAAAAA	265223	97419	CAACATGGTGAAACCCTGTC
176050	8246	GATTTAATTCTCACTTGCTG	220637	52833	TGAGGAAAAAAAAAAAAAAA	265224	97420	CCAACATGGTGAAACCCTGT
176051	8247	AGATTTAATTCTCACTTGCT	220638	52834	CTGAGGAAAAAAAAAAAAAA	265225	97421	GCCAACATGGTGAAACCCTG
176052	8248	CAGATTTAATTCTCACTTGC	220639	52835	CCTGAGGAAAAAAAAAAAAA	265226	97422	GGCCAACATGGTGAAACCCT
176053	8249	TCAGATTTAATTCTCACTTG	220640	52836	GCCTGAGGAAAAAAAAAAAA	265227	97423	TGGCCAACATGGTGAAACCC
176054	8250	TTCAGATTTAATTCTCACTT	220641	52837	TGCCTGAGGAAAAAAAAAAA	265228	97424	CTGGCCAACATGGTGAAACC
176055	8251	CTTCAGATTTAATTCTCACT	220642	52838	CTGCCTGAGGAAAAAAAAAA	265229	97425	CCTGGCCAACATGGTGAAAC
176056	8252	GCTTCAGATTTAATTCTCAC	220643	52839	ACTGCCTGAGGAAAAAAAAA	265230	97426	GCCTGGCCAACATGGTGAAA
176057	8253	TGCTTCAGATTTAATTCTCA	220644	52840	GACTGCCTGAGGAAAAAAAA	265231	97427	AGCCTGGCCAACATGGTGAA
176058	8254	TTGCTTCAGATTTAATTCTC	220645	52841	AGACTGCCTGAGGAAAAAAA	265232	97428	CAGCCTGGCCAACATGGTGA
176059	8255	ATTGCTTCAGATTTAATTCT	220646	52842	AAGACTGCCTGAGGAAAAAA	265233	97429	CCAGCCTGGCCAACATGGTG
176060	8256	AATTGCTTCAGATTTAATTC	220647	52843	TAAGACTGCCTGAGGAAAAA	265234	97430	ACCAGCCTGGCCAACATGGT
176061	8257	CAATTGCTTCAGATTTAATT	220648	52844	GTAAGACTGCCTGAGGAAAA	265235	97431	GACCAGCCTGGCCAACATGG
176062	8258	TCAATTGCTTCAGATTTAAT	220649	52845	AGTAAGACTGCCTGAGGAAA	265236	97432	AGACCAGCCTGGCCAACATG
176063	8259	ATCAATTGCTTCAGATTTAA	220650	52846	GAGTAAGACTGCCTGAGGAA	265237	97433	GAGACCAGCCTGGCCAACAT
176064	8260	TATCAATTGCTTCAGATTTA	220651	52847	AGAGTAAGACTGCCTGAGGA	265238	97434	CGAGACCAGCCTGGCCAACA
176065	8261	TTATCAATTGCTTCAGATTT	220652	52848	CAGAGTAAGACTGCCTGAGG	265239	97435	TCGAGACCAGCCTGGCCAAC
176066	8262	ATTATCAATTGCTTCAGATT	220653	52849	ACAGAGTAAGACTGCCTGAG	265240	97436	TTCGAGACCAGCCTGGCCAA
176067	8263	TATTATCAATTGCTTCAGAT	220654	52850	GACAGAGTAAGACTGCCTGA	265241	97437	GTTCGAGACCAGCCTGGCCA
176068	8264	TTATTATCAATTGCTTCAGA	220655	52851	TGACAGAGTAAGACTGCCTG	265242	97438	CGTTCGAGACCAGCCTGGCC
176069	8265	ATTATTATCAATTGCTTCAG	220656	52852	GTGACAGAGTAAGACTGCCT	265243	97439	GCGTTCGAGACCAGCCTGGC
176070	8266	CATTATTATCAATTGCTTCA	220657	52853	GGTGACAGAGTAAGACTGCC	265244	97440	GGCGTTCGAGACCAGCCTGG
176071	8267	ACATTATTATCAATTGCTTC	220658	52854	GGGTGACAGAGTAAGACTGC	265245	97441	AGGCGTTCGAGACCAGCCTG
176072	8268	AACATTATTATCAATTGCTT	220659	52855	TGGGTGACAGAGTAAGACTG	265246	97442	CAGGCGTTCGAGACCAGCCT
176073	8269	AAACATTATTATCAATTGCT	220660	52856	CTGGGTGACAGAGTAAGACT	265247	97443	TCAGGCGTTCGAGACCAGCC
176074	8270	GAAACATTATTATCAATTGC	220661	52857	CCTGGGTGACAGAGTAAGAC	265248	97444	GTCAGGCGTTCGAGACCAGC
176075	8271	TGAAACATTATTATCAATTG	220662	52858	GCCTGGGTGACAGAGTAAGA	265249	97445	GGTCAGGCGTTCGAGACCAG
176076	8272	ATGAAACATTATTATCAATT	220663	52859	AGCCTGGGTGACAGAGTAAG	265250	97446	AGGTCAGGCGTTCGAGACCA
176077	8273	AATGAAACATTATTATCAAT	220664	52860	CAGCCTGGGTGACAGAGTAA	265251	97447	GAGGTCAGGCGTTCGAGACC
176078	8274	GAATGAAACATTATTATCAA	220665	52861	CCAGCCTGGGTGACAGAGTA	265252	97448	TGAGGTCAGGCGTTCGAGAC
176079	8275	TGAATGAAACATTATTATCA	220666	52862	TCCAGCCTGGGTGACAGAGT	265253	97449	CTGAGGTCAGGCGTTCGAGA
176080	8276	ATGAATGAAACATTATTATC	220667	52863	CTCCAGCCTGGGTGACAGAG	265254	97450	CCTGAGGTCAGGCGTTCGAG
176081	8277	AATGAATGAAACATTATTAT	220668	52864	ACTCCAGCCTGGGTGACAGA	265255	97451	ACCTGAGGTCAGGCGTTCGA
176082	8278	GAATGAATGAAACATTATTA	220669	52865	CACTCCAGCCTGGGTGACAG	265256	97452	CACCTGAGGTCAGGCGTTCG

176083	8279	GGAATGAATGAAACATTATT	220670	52866	GCACTCCAGCCTGGGTGACA	265257	97453	TCACCTGAGGTCAGGCGTTC
176084	8280	AGGAATGAATGAAACATTAT	220671	52867	TGCACTCCAGCCTGGGTGAC	265258	97454	ATCACCTGAGGTCAGGCGTT
176085	8281	GAGGAATGAATGAAACATTA	220672	52868	CTGCACTCCAGCCTGGGTGA	265259	97455	GATCACCTGAGGTCAGGCGT
176086	8282	AGAGGAATGAATGAAACATT	220673	52869	ACTGCACTCCAGCCTGGGTG	265260	97456	GGATCACCTGAGGTCAGGCG
176087	8283	GAGAGGAATGAATGAAACAT	220674	52870	CACTGCACTCCAGCCTGGGT	265261	97457	TGGATCACCTGAGGTCAGGC
176088	8284	GGAGAGGAATGAATGAAACA	220675	52871	CCACTGCACTCCAGCCTGGG	265262	97458	GTGGATCACCTGAGGTCAGG
176089	8285	AGGAGAGGAATGAATGAAAC	220676	52872	GCCACTGCACTCCAGCCTGG	265263	97459	GGTGGATCACCTGAGGTCAG
176090	8286	AAGGAGAGGAATGAATGAAA	220677	52873	TGCCACTGCACTCCAGCCTG	265264	97460	AGGTGGATCACCTGAGGTCA
176091	8287	AAAGGAGAGGAATGAATGAA	220678	52874	ATGCCACTGCACTCCAGCCT	265265	97461	CAGGTGGATCACCTGAGGTC
176092	8288	CAAAGGAGAGGAATGAATGA	220679	52875	CATGCCACTGCACTCCAGCC	265266	97462	GCAGGTGGATCACCTGAGGT
176093	8289	CCAAAGGAGAGGAATGAATG	220680	52876	TCATGCCACTGCACTCCAGC	265267	97463	GGCAGGTGGATCACCTGAGG
176094	8290	GCCAAAGGAGAGGAATGAAT	220681	52877	ATCATGCCACTGCACTCCAG	265268	97464	AGGCAGGTGGATCACCTGAG
176095	8291	GGCCAAAGGAGAGGAATGAA	220682	52878	GATCATGCCACTGCACTCCA	265269	97465	GAGGCAGGTGGATCACCTGA
176096	8292	GGGCCAAAGGAGAGGAATGA	220683	52879	AGATCATGCCACTGCACTCC	265270	97466	CGAGGCAGGTGGATCACCTG
176097	8293	GGGGCCAAAGGAGAGGAATG	220684	52880	GAGATCATGCCACTGCACTC	265271	97467	CCGAGGCAGGTGGATCACCT
176098	8294	CGGGGCCAAAGGAGAGGAAT	220685	52881	CGAGATCATGCCACTGCACT	265272	97468	GCCGAGGCAGGTGGATCACC
176099	8295	ACGGGGCCAAAGGAGAGGAA	220686	52882	CCGAGATCATGCCACTGCAC	265273	97469	GGCCGAGGCAGGTGGATCAC
176100	8296	GACGGGGCCAAAGGAGAGGA	220687	52883	GCCGAGATCATGCCACTGCA	265274	97470	AGGCCGAGGCAGGTGGATCA
176101	8297	GGACGGGGCCAAAGGAGAGG	220688	52884	AGCCGAGATCATGCCACTGC	265275	97471	GAGGCCGAGGCAGGTGGATC
176102	8298	TGGACGGGGCCAAAGGAGAG	220689	52885	GAGCCGAGATCATGCCACTG	265276	97472	GGAGGCCGAGGCAGGTGGAT
176103	8299	GTGGACGGGGCCAAAGGAGA	220690	52886	TGAGCCGAGATCATGCCACT	265277	97473	GGGAGGCCGAGGCAGGTGGA
176104	8300	GGTGGACGGGGCCAAAGGAG	220691	52887	GTGAGCCGAGATCATGCCAC	265278	97474	TGGGAGGCCGAGGCAGGTGG
176105	8301	GGGTGGACGGGGCCAAAGGA	220692	52888	AGTGAGCCGAGATCATGCCA	265279	97475	TTGGGAGGCCGAGGCAGGTG
176106	8302	AGGGTGGACGGGGCCAAAGG	220693	52889	CAGTGAGCCGAGATCATGCC	265280	97476	TTTGGGAGGCCGAGGCAGGT
176107	8303	TAGGGTGGACGGGGCCAAAG	220694	52890	GCAGTGAGCCGAGATCATGC	265281	97477	CTTTGGGAGGCCGAGGCAGG
176108	8304	GTAGGGTGGACGGGGCCAAA	220695	52891	TGCAGTGAGCCGAGATCATG	265282	97478	ACTTTGGGAGGCCGAGGCAG
176109	8305	AGTAGGGTGGACGGGGCCAA	220696	52892	ATGCAGTGAGCCGAGATCAT	265283	97479	CACTTTGGGAGGCCGAGGCA
176110	8306	CAGTAGGGTGGACGGGGCCA	220697	52893	CATGCAGTGAGCCGAGATCA	265284	97480	GCACTTTGGGAGGCCGAGGC
176111	8307	GCAGTAGGGTGGACGGGGCC	220698	52894	GCATGCAGTGAGCCGAGATC	265285	97481	AGCACTTTGGGAGGCCGAGG
176112	8308	AGCAGTAGGGTGGACGGGGC	220699	52895	TGCATGCAGTGAGCCGAGAT	265286	97482	CAGCACTTTGGGAGGCCGAG
176113	8309	TAGCAGTAGGGTGGACGGGG	220700	52896	TTGCATGCAGTGAGCCGAGA	265287	97483	CCAGCACTTTGGGAGGCCGA
176114	8310	TTAGCAGTAGGGTGGACGGG	220701	52897	GTTGCATGCAGTGAGCCGAG	265288	97484	CCCAGCACTTTGGGAGGCCG
176115	8311	TTTAGCAGTAGGGTGGACGG	220702	52898	GGTTGCATGCAGTGAGCCGA	265289	97485	TCCCAGCACTTTGGGAGGCC
176116	8312	ATTTAGCAGTAGGGTGGACG	220703	52899	TGGTTGCATGCAGTGAGCCG	265290	97486	ATCCCAGCACTTTGGGAGGC
176117	8313	GATTTAGCAGTAGGGTGGAC	220704	52900	GTGGTTGCATGCAGTGAGCC	265291	97487	AATCCCAGCACTTTGGGAGG
176118	8314	GGATTTAGCAGTAGGGTGGA	220705	52901	GGTGGTTGCATGCAGTGAGC	265292	97488	TAATCCCAGCACTTTGGGAG
176119	8315	TGGATTTAGCAGTAGGGTGG	220706	52902	TGGTGGTTGCATGCAGTGAG	265293	97489	GTAATCCCAGCACTTTGGGA
176120	8316	CTGGATTTAGCAGTAGGGTG	220707	52903	GTGGTGGTTGCATGCAGTGA	265294	97490	TGTAATCCCAGCACTTTGGG
176121	8317	CCTGGATTTAGCAGTAGGGT	220708	52904	GGTGGTGGTTGCATGCAGTG	265295	97491	CTGTAATCCCAGCACTTTGG
176122	8318	GCCTGGATTTAGCAGTAGGG	220709	52905	AGGTGGTGGTTGCATGCAGT	265296	97492	CCTGTAATCCCAGCACTTTG
176123	8319	TGCCTGGATTTAGCAGTAGG	220710	52906	GAGGTGGTGGTTGCATGCAG	265297	97493	GCCTGTAATCCCAGCACTTT
176124	8320	ATGCCTGGATTTAGCAGTAG	220711	52907	GGAGGTGGTGGTTGCATGCA	265298	97494	TGCCTGTAATCCCAGCACTT
176125	8321	GATGCCTGGATTTAGCAGTA	220712	52908	GGGAGGTGGTGGTTGCATGC	265299	97495	ATGCCTGTAATCCCAGCACT
176126	8322	TGATGCCTGGATTTAGCAGT	220713	52909	CGGGAGGTGGTGGTTGCATG	265300	97496	CATGCCTGTAATCCCAGCAC
176127	8323	TTGATGCCTGGATTTAGCAG	220714	52910	CCGGGAGGTGGTGGTTGCAT	265301	97497	TCATGCCTGTAATCCCAGCA
176128	8324	TTTGATGCCTGGATTTAGCA	220715	52911	CCCGGGAGGTGGTGGTTGCA	265302	97498	CTCATGCCTGTAATCCCAGC
176129	8325	CTTTGATGCCTGGATTTAGC	220716	52912	ACCCGGGAGGTGGTGGTTGC	265303	97499	GCTCATGCCTGTAATCCCAG
176130	8326	TCTTTGATGCCTGGATTTAG	220717	52913	AACCCGGGAGGTGGTGGTTG	265304	97500	GGCTCATGCCTGTAATCCCA
176131	8327	CTCTTTGATGCCTGGATTTA	220718	52914	AAACCCGGGAGGTGGTGGTT	265305	97501	TGGCTCATGCCTGTAATCCC
176132	8328	TCTCTTTGATGCCTGGATTT	220719	52915	TAAACCCGGGAGGTGGTGGT	265306	97502	GTGGCTCATGCCTGTAATCC
176133	8329	TTCTCTTTGATGCCTGGATT	220720	52916	TTAAACCCGGGAGGTGGTGG	265307	97503	GGTGGCTCATGCCTGTAATC
176134	8330	CTTCTCTTTGATGCCTGGAT	220721	52917	CTTAAACCCGGGAGGTGGTG	265308	97504	TGGTGGCTCATGCCTGTAAT
176135	8331	TCTTCTCTTTGATGCCTGGA	220722	52918	GCTTAAACCCGGGAGGTGGT	265309	97505	GTGGTGGCTCATGCCTGTAA
176136	8332	CTCTTCTCTTTGATGCCTGG	220723	52919	TGCTTAAACCCGGGAGGTGG	265310	97506	AGTGGTGGCTCATGCCTGTA
176137	8333	CCTCTTCTCTTTGATGCCTG	220724	52920	TTGCTTAAACCCGGGAGGTG	265311	97507	GAGTGGTGGCTCATGCCTGT
176138	8334	CCCTCTTCTCTTTGATGCCT	220725	52921	ATTGCTTAAACCCGGGAGGT	265312	97508	GGAGTGGTGGCTCATGCCTG
176139	8335	TCCCTCTTCTCTTTGATGCC	220726	52922	AATTGCTTAAACCCGGGAGG	265313	97509	GGGAGTGGTGGCTCATGCCT
176140	8336	GTCCCTCTTCTCTTTGATGC	220727	52923	GAATTGCTTAAACCCGGGAG	265314	97510	TGGGAGTGGTGGCTCATGCC
176141	8337	TGTCCCTCTTCTCTTTGATG	220728	52924	AGAATTGCTTAAACCCGGGA	265315	97511	CTGGGAGTGGTGGCTCATGC
176142	8338	ATGTCCCTCTTCTCTTTGAT	220729	52925	GAGAATTGCTTAAACCCGGG	265316	97512	GCTGGGAGTGGTGGCTCATG
176143	8339	TATGTCCCTCTTCTCTTTGA	220730	52926	GGAGAATTGCTTAAACCCGG	265317	97513	GGCTGGGAGTGGTGGCTCAT
176144	8340	TTATGTCCCTCTTCTCTTTG	220731	52927	AGGAGAATTGCTTAAACCCG	265318	97514	AGGCTGGGAGTGGTGGCTCA
176145	8341	ATTATGTCCCTCTTCTCTTT	220732	52928	CAGGAGAATTGCTTAAACCC	265319	97515	CAGGCTGGGAGTGGTGGCTC
176146	8342	AATTATGTCCCTCTTCTCTT	220733	52929	GCAGGAGAATTGCTTAAACC	265320	97516	TCAGGCTGGGAGTGGTGGCT
176147	8343	TAATTATGTCCCTCTTCTCT	220734	52930	GGCAGGAGAATTGCTTAAAC	265321	97517	TTCAGGCTGGGAGTGGTGGC
176148	8344	ATAATTATGTCCCTCTTCTC	220735	52931	AGGCAGGAGAATTGCTTAAA	265322	97518	ATTCAGGCTGGGAGTGGTGG
176149	8345	GATAATTATGTCCCTCTTCT	220736	52932	GAGGCAGGAGAATTGCTTAA	265323	97519	GATTCAGGCTGGGAGTGGTG
176150	8346	AGATAATTATGTCCCTCTTC	220737	52933	TGAGGCAGGAGAATTGCTTA	265324	97520	GGATTCAGGCTGGGAGTGGT
176151	8347	GAGATAATTATGTCCCTCTT	220738	52934	CTGAGGCAGGAGAATTGCTT	265325	97521	AGGATTCAGGCTGGGAGTGG
176152	8348	AGAGATAATTATGTCCCTCT	220739	52935	GCTGAGGCAGGAGAATTGCT	265326	97522	GAGGATTCAGGCTGGGAGTG
176153	8349	TAGAGATAATTATGTCCCTC	220740	52936	GGCTGAGGCAGGAGAATTGC	265327	97523	TGAGGATTCAGGCTGGGAGT
176154	8350	CTAGAGATAATTATGTCCCT	220741	52937	AGGCTGAGGCAGGAGAATTG	265328	97524	GTGAGGATTCAGGCTGGGAG

176155	8351	ACTAGAGATAATTATGTCCC	220742	52938	GAGGCTGAGGCAGGAGAATT	265329	97525	AGTGAGGATTCAGGCTGGGA
176156	8352	GACTAGAGATAATTATGTCC	220743	52939	GGAGGCTGAGGCAGGAGAAT	265330	97526	AAGTGAGGATTCAGGCTGGG
176157	8353	GGACTAGAGATAATTATGTC	220744	52940	GGGAGGCTGAGGCAGGAGAA	265331	97527	AAAGTGAGGATTCAGGCTGG
176158	8354	GGGACTAGAGATAATTATGT	220745	52941	GGGGAGGCTGAGGCAGGAGA	265332	97528	AAAAGTGAGGATTCAGGCTG
176159	8355	TGGGACTAGAGATAATTATG	220746	52942	TGGGGAGGCTGAGGCAGGAG	265333	97529	AAAAAGTGAGGATTCAGGCT
176160	8356	CTGGGACTAGAGATAATTAT	220747	52943	CTGGGGAGGCTGAGGCAGGA	265334	97530	TAAAAAGTGAGGATTCAGGC
176161	8357	GCTGGGACTAGAGATAATTA	220748	52944	ACTGGGGAGGCTGAGGCAGG	265335	97531	ATAAAAAGTGAGGATTCAGG
176162	8358	AGCTGGGACTAGAGATAATT	220749	52945	TACTGGGGAGGCTGAGGCAG	265336	97532	GATAAAAAGTGAGGATTCAG
176163	8359	CAGCTGGGACTAGAGATAAT	220750	52946	CTACTGGGGAGGCTGAGGCA	265337	97533	TGATAAAAAGTGAGGATTCA
176164	8360	GCAGCTGGGACTAGAGATAA	220751	52947	GCTACTGGGGAGGCTGAGGC	265338	97534	TTGATAAAAAGTGAGGATTC
176165	8361	AGCAGCTGGGACTAGAGATA	220752	52948	AGCTACTGGGGAGGCTGAGG	265339	97535	ATTGATAAAAAGTGAGGATT
176166	8362	CAGCAGCTGGGACTAGAGAT	220753	52949	CAGCTACTGGGGAGGCTGAG	265340	97536	CATTGATAAAAAGTGAGGAT
176167	8363	CCAGCAGCTGGGACTAGAGA	220754	52950	CCAGCTACTGGGGAGGCTGA	265341	97537	TCATTGATAAAAAGTGAGGA
176168	8364	ACCAGCAGCTGGGACTAGAG	220755	52951	CCCAGCTACTGGGGAGGCTG	265342	97538	TTCATTGATAAAAAGTGAGG
176169	8365	AACCAGCAGCTGGGACTAGA	220756	52952	TCCCAGCTACTGGGGAGGCT	265343	97539	CTTCATTGATAAAAAGTGAG
176170	8366	AAACCAGCAGCTGGGACTAG	220757	52953	ATCCCAGCTACTGGGGAGGC	265344	97540	TCTTCATTGATAAAAAGTGA
176171	8367	AAAACCAGCAGCTGGGACTA	220758	52954	AATCCCAGCTACTGGGGAGG	265345	97541	TTCTTCATTGATAAAAAGTG
176172	8368	GAAAACCAGCAGCTGGGACT	220759	52955	TAATCCCAGCTACTGGGGAG	265346	97542	TTTCTTCATTGATAAAAAGT
176173	8369	GGAAAACCAGCAGCTGGGAC	220760	52956	GTAATCCCAGCTACTGGGGA	265347	97543	ATTTCTTCATTGATAAAAAG
176174	8370	AGGAAAACCAGCAGCTGGGA	220761	52957	TGTAATCCCAGCTACTGGGG	265348	97544	AATTTCTTCATTGATAAAAA
176175	8371	AAGGAAAACCAGCAGCTGGG	220762	52958	CTGTAATCCCAGCTACTGGG	265349	97545	CAATTTCTTCATTGATAAAA
176176	8372	GAAGGAAAACCAGCAGCTGG	220763	52959	CCTGTAATCCCAGCTACTGG	265350	97546	TCAATTTCTTCATTGATAAA
176177	8373	GGAAGGAAAACCAGCAGCTG	220764	52960	ACCTGTAATCCCAGCTACTG	265351	97547	CTCAATTTCTTCATTGATAA
176178	8374	TGGAAGGAAAACCAGCAGCT	220765	52961	CACCTGTAATCCCAGCTACT	265352	97548	CCTCAATTTCTTCATTGATA
176179	8375	CTGGAAGGAAAACCAGCAGC	220766	52962	GCACCTGTAATCCCAGCTAC	265353	97549	GCCTCAATTTCTTCATTGAT
176180	8376	GCTGGAAGGAAAACCAGCAG	220767	52963	GGCACCTGTAATCCCAGCTA	265354	97550	AGCCTCAATTTCTTCATTGA
176181	8377	GGCTGGAAGGAAAACCAGCA	220768	52964	GGGCACCTGTAATCCCAGCT	265355	97551	CAGCCTCAATTTCTTCATTG
176182	8378	AGGCTGGAAGGAAAACCAGC	220769	52965	TGGGCACCTGTAATCCCAGC	265356	97552	TCAGCCTCAATTTCTTCATT
176183	8379	TAGGCTGGAAGGAAAACCAG	220770	52966	GTGGGCACCTGTAATCCCAG	265357	97553	ATCAGCCTCAATTTCTTCAT
176184	8380	ATAGGCTGGAAGGAAAACCA	220771	52967	GGTGGGCACCTGTAATCCCA	265358	97554	AATCAGCCTCAATTTCTTCA
176185	8381	CATAGGCTGGAAGGAAAACC	220772	52968	TGGTGGGCACCTGTAATCCC	265359	97555	GAATCAGCCTCAATTTCTTC
176186	8382	CCATAGGCTGGAAGGAAAAC	220773	52969	GTGGTGGGCACCTGTAATCC	265360	97556	AGAATCAGCCTCAATTTCTT
176187	8383	GCCATAGGCTGGAAGGAAAA	220774	52970	GGTGGTGGGCACCTGTAATC	265361	97557	CAGAATCAGCCTCAATTTCT
176188	8384	GGCCATAGGCTGGAAGGAAA	220775	52971	TGGTGGTGGGCACCTGTAAT	265362	97558	GCAGAATCAGCCTCAATTTC
176189	8385	GGGCCATAGGCTGGAAGGAA	220776	52972	GTGGTGGTGGGCACCTGTAA	265363	97559	TGCAGAATCAGCCTCAATTT
176190	8386	TGGGCCATAGGCTGGAAGGA	220777	52973	TGTGGTGGTGGGCACCTGTA	265364	97560	CTGCAGAATCAGCCTCAATT
176191	8387	CTGGGCCATAGGCTGGAAGG	220778	52974	GTGTGGTGGTGGGCACCTGT	265365	97561	GCTGCAGAATCAGCCTCAAT
176192	8388	ACTGGGCCATAGGCTGGAAG	220779	52975	GGTGTGGTGGTGGGCACCTG	265366	97562	TGCTGCAGAATCAGCCTCAA
176193	8389	AACTGGGCCATAGGCTGGAA	220780	52976	GGGTGTGGTGGTGGGCACCT	265367	97563	ATGCTGCAGAATCAGCCTCA
176194	8390	AAACTGGGCCATAGGCTGGA	220781	52977	TGGGTGTGGTGGTGGGCACC	265368	97564	CATGCTGCAGAATCAGCCTC
176195	8391	AAAACTGGGCCATAGGCTGG	220782	52978	CTGGGTGTGGTGGTGGGCAC	265369	97565	TCATGCTGCAGAATCAGCCT
176196	8392	GAAAACTGGGCCATAGGCTG	220783	52979	GCTGGGTGTGGTGGTGGGCA	265370	97566	ATCATGCTGCAGAATCAGCC
176197	8393	AGAAAACTGGGCCATAGGCT	220784	52980	AGCTGGGTGTGGTGGTGGGC	265371	97567	TATCATGCTGCAGAATCAGC
176198	8394	CAGAAAACTGGGCCATAGGC	220785	52981	TAGCTGGGTGTGGTGGTGGG	265372	97568	TTATCATGCTGCAGAATCAG
176199	8395	ACAGAAAACTGGGCCATAGG	220786	52982	TTAGCTGGGTGTGGTGGTGG	265373	97569	TTTATCATGCTGCAGAATCA
176200	8396	AACAGAAAACTGGGCCATAG	220787	52983	ATTAGCTGGGTGTGGTGGTG	265374	97570	TTTTATCATGCTGCAGAATC
176201	8397	AAACAGAAAACTGGGCCATA	220788	52984	AATTAGCTGGGTGTGGTGGT	265375	97571	TTTTTATCATGCTGCAGAAT
176202	8398	AAAACAGAAAACTGGGCCAT	220789	52985	AAATTAGCTGGGTGTGGTGG	265376	97572	TTTTTTATCATGCTGCAGAA
176203	8399	TAAAACAGAAAACTGGGCCA	220790	52986	AAAATTAGCTGGGTGTGGTG	265377	97573	TTTTTTTATCATGCTGCAGA
176204	8400	GTAAAACAGAAAACTGGGCC	220791	52987	AAAAATTAGCTGGGTGTGGT	265378	97574	TTTTTTTTATCATGCTGCAG
176205	8401	AGTAAAACAGAAAACTGGGC	220792	52988	CAAAAATTAGCTGGGTGTGG	265379	97575	TTTTTTTTTATCATGCTGCA
176206	8402	CAGTAAAACAGAAAACTGGG	220793	52989	ACAAAAATTAGCTGGGTGTG	265380	97576	ATTTTTTTTTATCATGCTGC
176207	8403	TCAGTAAAACAGAAAACTGG	220794	52990	CACAAAAATTAGCTGGGTGT	265381	97577	TATTTTTTTTTATCATGCTG
176208	8404	CTCAGTAAAACAGAAAACTG	220795	52991	ACACAAAAATTAGCTGGGTG	265382	97578	GTATTTTTTTTTATCATGCT
176209	8405	TCTCAGTAAAACAGAAAACT	220796	52992	AACACAAAAATTAGCTGGGT	265383	97579	TGTATTTTTTTTTATCATGC
176210	8406	TTCTCAGTAAAACAGAAAAC	220797	52993	AAACACAAAAATTAGCTGGG	265384	97580	CTGTATTTTTTTTTATCATG
176211	8407	CTTCTCAGTAAAACAGAAAA	220798	52994	AAAACACAAAAATTAGCTGG	265385	97581	TCTGTATTTTTTTTTATCAT
176212	8408	CCTTCTCAGTAAAACAGAAA	220799	52995	AAAAACACAAAAATTAGCTG	265386	97582	TTCTGTATTTTTTTTTATCA
176213	8409	GCCTTCTCAGTAAAACAGAA	220800	52996	TAAAAACACAAAAATTAGCT	265387	97583	TTTCTGTATTTTTTTTTATC
176214	8410	AGCCTTCTCAGTAAAACAGA	220801	52997	CTAAAAACACAAAAATTAGC	265388	97584	TTTTCTGTATTTTTTTTTAT
176215	8411	CAGCCTTCTCAGTAAAACAG	220802	52998	ACTAAAAACACAAAAATTAG	265389	97585	TTTTTCTGTATTTTTTTTTA
176216	8412	CCAGCCTTCTCAGTAAAACA	220803	52999	TACTAAAAACACAAAAATTA	265390	97586	CTTTTTCTGTATTTTTTTTT
176217	8413	ACCAGCCTTCTCAGTAAAAC	220804	53000	CTACTAAAAACACAAAAATT	265391	97587	CCTTTTTCTGTATTTTTTTT
176218	8414	CACCAGCCTTCTCAGTAAAA	220805	53001	CTACTAAAAACACAAAAAT	265392	97588	TCCTTTTTCTGTATTTTTTT
176219	8415	TCACCAGCCTTCTCAGTAAA	220806	53002	CTCTACTAAAAACACAAAAA	265393	97589	TTCCTTTTTCTGTATTTTTT
176220	8416	ATCACCAGCCTTCTCAGTAA	220807	53003	TCTCTACTAAAAACACAAAA	265394	97590	TTTCCTTTTTCTGTATTTTT
176221	8417	CATCACCAGCCTTCTCAGTA	220808	53004	GTCTCTACTAAAAACACAAA	265395	97591	TTTTCCTTTTTCTGTATTTT
176222	8418	ACATCACCAGCCTTCTCAGT	220809	53005	TGTCTCTACTAAAAACACAA	265396	97592	TTTTTCCTTTTTCTGTATTT
176223	8419	AACATCACCAGCCTTCTCAG	220810	53006	CTGTCTCTACTAAAAACACA	265397	97593	TTTTTTCCTTTTTCTGTATT
176224	8420	TAACATCACCAGCCTTCTCA	220811	53007	CCTGTCTCTACTAAAAACAC	265398	97594	TTTTTTTCCTTTTTCTGTAT
176225	8421	ATAACATCACCAGCCTTCTC	220812	53008	CCCTGTCTCTACTAAAAACA	265399	97595	TTTTTTTTCCTTTTTCTGTA
176226	8422	GATAACATCACCAGCCTTCT	220813	53009	ACCCTGTCTCTACTAAAAAC	265400	97596	CTTTTTTTTCCTTTTTCTGT

176227	8423	AGATAACATCACCAGCCTTC	220814	53010	AACCCTGTCTCTACTAAAAA	265401	97597	TCTTTTTTTTCCTTTTTCTG
176228	8424	AAGATAACATCACCAGCCTT	220815	53011	AAACCCTGTCTCTACTAAAA	265402	97598	TTCTTTTTTTTCCTTTTTCT
176229	8425	CAAGATAACATCACCAGCCT	220816	53012	GAAACCCTGTCTCTACTAAA	265403	97599	TTTCTTTTTTTTCCTTTTTC
176230	8426	CCAAGATAACATCACCAGCC	220817	53013	TGAAACCCTGTCTCTACTAA	265404	97600	CTTTCTTTTTTTTCCTTTTT
176231	8427	CCCAAGATAACATCACCAGC	220818	53014	GTGAAACCCTGTCTCTACTA	265405	97601	TCTTTCTTTTTTTTCCTTTT
176232	8428	TCCCAAGATAACATCACCAG	220819	53015	GGTGAAACCCTGTCTCTACT	265406	97602	TTCTTTCTTTTTTTTCCTTT
176233	8429	ATCCCAAGATAACATCACCA	220820	53016	TGGTGAAACCCTGTCTCTAC	265407	97603	TTTCTTTCTTTTTTTTCCTT
176234	8430	GATCCCAAGATAACATCACC	220821	53017	ATGGTGAAACCCTGTCTCTA	265408	97604	ATTTCTTTCTTTTTTTTCCT
176235	8431	AGATCCCAAGATAACATCAC	220822	53018	CATGGTGAAACCCTGTCTCT	265409	97605	GATTTCTTTCTTTTTTTTCC
176236	8432	TAGATCCCAAGATAACATCA	220823	53019	ACATGGTGAAACCCTGTCTC	265410	97606	CGATTTCTTTCTTTTTTTTC
176237	8433	TTAGATCCCAAGATAACATC	220824	53020	AACATGGTGAAACCCTGTCT	265411	97607	TCGATTTCTTTCTTTTTTTT
176238	8434	CTTAGATCCCAAGATAACAT	220825	53021	CAACATGGTGAAACCCTGTC	265412	97608	CTCGATTTCTTTCTTTTTTT
176239	8435	ACTTAGATCCCAAGATAACA	220826	53022	CCAACATGGTGAAACCCTGT	265413	97609	GCTCGATTTCTTTCTTTTTT
176240	8436	GACTTAGATCCCAAGATAAC	220827	53023	ACCAACATGGTGAAACCCTG	265414	97610	GGCTCGATTTCTTTCTTTTT
176241	8437	AGACTTAGATCCCAAGATAA	220828	53024	GACCAACATGGTGAAACCCT	265415	97611	AGGCTCGATTTCTTTCTTTT
176242	8438	CAGACTTAGATCCCAAGATA	220829	53025	TGACCAACATGGTGAAACCC	265416	97612	GAGGCTCGATTTCTTTCTTT
176243	8439	GCAGACTTAGATCCCAAGAT	220830	53026	CTGACCAACATGGTGAAACC	265417	97613	AGAGGCTCGATTTCTTTCTT
176244	8440	TGCAGACTTAGATCCCAAGA	220831	53027	CCTGACCAACATGGTGAAAC	265418	97614	CAGAGGCTCGATTTCTTTCT
176245	8441	CTGCAGACTTAGATCCCAAG	220832	53028	GCCTGACCAACATGGTGAAA	265419	97615	TCAGAGGCTCGATTTCTTTC
176246	8442	ACTGCAGACTTAGATCCCAA	220833	53029	AGCCTGACCAACATGGTGAA	265420	97616	CTCAGAGGCTCGATTTCTTT
176247	8443	AACTGCAGACTTAGATCCCA	220834	53030	CAGCCTGACCAACATGGTGA	265421	97617	TCTCAGAGGCTCGATTTCTT
176248	8444	AAACTGCAGACTTAGATCCC	220835	53031	CCAGCCTGACCAACATGGTG	265422	97618	CTCTCAGAGGCTCGATTTCT
176249	8445	GAAACTGCAGACTTAGATCC	220836	53032	ACCAGCCTGACCAACATGGT	265423	97619	ACTCTCAGAGGCTCGATTTC
176250	8446	TGAAACTGCAGACTTAGATC	220837	53033	GACCAGCCTGACCAACATGG	265424	97620	AACTCTCAGAGGCTCGATTT
176251	8447	GTGAAACTGCAGACTTAGAT	220838	53034	AGACCAGCCTGACCAACATG	265425	97621	AAACTCTCAGAGGCTCGATT
176252	8448	GGTGAAACTGCAGACTTAGA	220839	53035	GAGACCAGCCTGACCAACAT	265426	97622	CAAACTCTCAGAGGCTCGAT
176253	8449	TGGTGAAACTGCAGACTTAG	220840	53036	CGAGACCAGCCTGACCAACA	265427	97623	GCAAACTCTCAGAGGCTCGA
176254	8450	GTGGTGAAACTGCAGACTTA	220841	53037	TCGAGACCAGCCTGACCAAC	265428	97624	AGCAAACTCTCAGAGGCTCG
176255	8451	TGTGGTGAAACTGCAGACTT	220842	53038	TTCGAGACCAGCCTGACCAA	265429	97625	AAGCAAACTCTCAGAGGCTC
176256	8452	TTGTGGTGAAACTGCAGACT	220843	53039	GTTCGAGACCAGCCTGACCA	265430	97626	CAAGCAAACTCTCAGAGGCT
176257	8453	TTTGTGGTGAAACTGCAGAC	220844	53040	AGTTCGAGACCAGCCTGACC	265431	97627	TCAAGCAAACTCTCAGAGGC
176258	8454	TTTTGTGGTGAAACTGCAGA	220845	53041	GAGTTCGAGACCAGCCTGAC	265432	97628	GTCAAGCAAACTCTCAGAGG
176259	8455	TTTTTGTGGTGAAACTGCAG	220846	53042	GGAGTTCGAGACCAGCCTGA	265433	97629	AGTCAAGCAAACTCTCAGAG
176260	8456	CTTTTTGTGGTGAAACTGCA	220847	53043	AGGAGTTCGAGACCAGCCTG	265434	97630	CAGTCAAGCAAACTCTCAGA
176261	8457	ACTTTTTGTGGTGAAACTGC	220848	53044	CAGGAGTTCGAGACCAGCCT	265435	97631	TCAGTCAAGCAAACTCTCAG
176262	8458	GACTTTTTGTGGTGAAACTG	220849	53045	TCAGGAGTTCGAGACCAGCC	265436	97632	CTCAGTCAAGCAAACTCTCA
176263	8459	GGACTTTTTGTGGTGAAACT	220850	53046	GTCAGGAGTTCGAGACCAGC	265437	97633	ACTCAGTCAAGCAAACTCTC
176264	8460	TGGACTTTTTGTGGTGAAAC	220851	53047	GGTCAGGAGTTCGAGACCAG	265438	97634	GACTCAGTCAAGCAAACTCT
176265	8461	CTGGACTTTTTGTGGTGAAA	220852	53048	AGGTCAGGAGTTCGAGACCA	265439	97635	AGACTCAGTCAAGCAAACTC
176266	8462	CCTGGACTTTTTGTGGTGAA	220853	53049	GAGGTCAGGAGTTCGAGACC	265440	97636	TAGACTCAGTCAAGCAAACT
176267	8463	CCCTGGACTTTTTGTGGTGA	220854	53050	TGAGGTCAGGAGTTCGAGAC	265441	97637	TTAGACTCAGTCAAGCAAAC
176268	8464	TCCCTGGACTTTTTGTGGTG	220855	53051	CTGAGGTCAGGAGTTCGAGA	265442	97638	GTTAGACTCAGTCAAGCAAA
176269	8465	ATCCCTGGACTTTTTGTGGT	220856	53052	TCTGAGGTCAGGAGTTCGAG	265443	97639	GGTTAGACTCAGTCAAGCAA
176270	8466	CATCCCTGGACTTTTTGTGG	220857	53053	ATCTGAGGTCAGGAGTTCGA	265444	97640	TGGTTAGACTCAGTCAAGCA
176271	8467	GCATCCCTGGACTTTTTGTG	220858	53054	CATCTGAGGTCAGGAGTTCG	265445	97641	CTGGTTAGACTCAGTCAAGC
176272	8468	TGCATCCCTGGACTTTTTGT	220859	53055	TCATCTGAGGTCAGGAGTTC	265446	97642	GCTGGTTAGACTCAGTCAAG
176273	8469	GTGCATCCCTGGACTTTTTG	220860	53056	ATCATCTGAGGTCAGGAGTT	265447	97643	AGCTGGTTAGACTCAGTCAA
176274	8470	AGTGCATCCCTGGACTTTTT	220861	53057	AATCATCTGAGGTCAGGAGT	265448	97644	GAGCTGGTTAGACTCAGTCA
176275	8471	AAGTGCATCCCTGGACTTTT	220862	53058	GAATCATCTGAGGTCAGGAG	265449	97645	TGAGCTGGTTAGACTCAGTC
176276	8472	AAAGTGCATCCCTGGACTTT	220863	53059	TGAATCATCTGAGGTCAGGA	265450	97646	ATGAGCTGGTTAGACTCAGT
176277	8473	GAAAGTGCATCCCTGGACTT	220864	53060	GTGAATCATCTGAGGTCAGG	265451	97647	AATGAGCTGGTTAGACTCAG
176278	8474	TGAAAGTGCATCCCTGGACT	220865	53061	GGTGAATCATCTGAGGTCAG	265452	97648	AAATGAGCTGGTTAGACTCA
176279	8475	ATGAAAGTGCATCCCTGGAC	220866	53062	GGGTGAATCATCTGAGGTCA	265453	97649	AAAATGAGCTGGTTAGACTC
176280	8476	CATGAAAGTGCATCCCTGGA	220867	53063	TGGGTGAATCATCTGAGGTC	265454	97650	TAAAATGAGCTGGTTAGACT
176281	8477	GCATGAAAGTGCATCCCTGG	220868	53064	GTGGGTGAATCATCTGAGGT	265455	97651	TTAAAATGAGCTGGTTAGAC
176282	8478	AGCATGAAAGTGCATCCCTG	220869	53065	GGTGGGTGAATCATCTGAGG	265456	97652	TTTAAAATGAGCTGGTTAGA
176283	8479	AAGCATGAAAGTGCATCCCT	220870	53066	AGGTGGGTGAATCATCTGAG	265457	97653	GTTTAAAATGAGCTGGTTAG
176284	8480	CAAGCATGAAAGTGCATCCC	220871	53067	GAGGTGGGTGAATCATCTGA	265458	97654	GGTTTAAAATGAGCTGGTTA
176285	8481	ACAAGCATGAAAGTGCATCC	220872	53068	CGAGGTGGGTGAATCATCTG	265459	97655	GGGTTTAAAATGAGCTGGTT
176286	8482	CACAAGCATGAAAGTGCATC	220873	53069	CCGAGGTGGGTGAATCATCT	265460	97656	CGGGTTTAAAATGAGCTGGT
176287	8483	ACACAAGCATGAAAGTGCAT	220874	53070	GCCGAGGTGGGTGAATCATC	265461	97657	TCGGGTTTAAAATGAGCTGG
176288	8484	GACACAAGCATGAAAGTGCA	220875	53071	GGCCGAGGTGGGTGAATCAT	265462	97658	CTCGGGTTTAAAATGAGCTG
176289	8485	GGACACAAGCATGAAAGTGC	220876	53072	AGGCCGAGGTGGGTGAATCA	265463	97659	CCTCGGGTTTAAAATGAGCT
176290	8486	AGGACACAAGCATGAAAGTG	220877	53073	GAGGCCGAGGTGGGTGAATC	265464	97660	TCCTCGGGTTTAAAATGAGC
176291	8487	GAGGACACAAGCATGAAAGT	220878	53074	GGAGGCCGAGGTGGGTGAAT	265465	97661	TTCCTCGGGTTTAAAATGAG
176292	8488	GGAGGACACAAGCATGAAAG	220879	53075	GGGAGGCCGAGGTGGGTGAA	265466	97662	TTTCCTCGGGTTTAAAATGA
176293	8489	AGGAGGACACAAGCATGAAA	220880	53076	TGGGAGGCCGAGGTGGGTGA	265467	97663	TTTTCCTCGGGTTTAAAATG
176294	8490	GAGGAGGACACAAGCATGAA	220881	53077	CTGGGAGGCCGAGGTGGGTG	265468	97664	ATTTTCCTCGGGTTTAAAAT
176295	8491	GGAGGAGGACACAAGCATGA	220882	53078	ACTGGGAGGCCGAGGTGGGT	265469	97665	CATTTTCCTCGGGTTTAAAA
176296	8492	GGGAGGAGGACACAAGCATG	220883	53079	CACTGGGAGGCCGAGGTGGG	265470	97666	GCATTTTCCTCGGGTTTAAA
176297	8493	AGGGAGGAGGACACAAGCAT	220884	53080	ACACTGGGAGGCCGAGGTGG	265471	97667	TGCATTTTCCTCGGGTTTAA
176298	8494	CAGGGAGGAGGACACAAGCA	220885	53081	CACACTGGGAGGCCGAGGTG	265472	97668	CTGCATTTTCCTCGGGTTTA

176299	8495	CCAGGGAGGAGGACACAAGC	220886	53082	GCACACTGGGAGGCCGAGGT	265473	97669	ACTGCATTTTCCTCGGGTTT
176300	8496	CCCAGGGAGGAGGACACAAG	220887	53083	AGCACACTGGGAGGCCGAGG	265474	97670	GACTGCATTTTCCTCGGGTT
176301	8497	TCCCAGGGAGGAGGACACAA	220888	53084	CAGCACACTGGGAGGCCGAG	265475	97671	TGACTGCATTTTCCTCGGGT
176302	8498	ATCCCAGGGAGGAGGACACA	220889	53085	CCAGCACACTGGGAGGCCGA	265476	97672	GTGACTGCATTTTCCTCGGG
176303	8499	TATCCCAGGGAGGAGGACAC	220890	53086	CCCAGCACACTGGGAGGCCG	265477	97673	TGTGACTGCATTTTCCTCGG
176304	8500	CTATCCCAGGGAGGAGGACA	220891	53087	TCCCAGCACACTGGGAGGCC	265478	97674	ATGTGACTGCATTTTCCTCG
176305	8501	GCTATCCCAGGGAGGAGGAC	220892	53088	ATCCCAGCACACTGGGAGGC	265479	97675	CATGTGACTGCATTTTCCTC
176306	8502	TGCTATCCCAGGGAGGAGGA	220893	53089	AATCCCAGCACACTGGGAGG	265480	97676	TCATGTGACTGCATTTTCCT
176307	8503	TTGCTATCCCAGGGAGGAGG	220894	53090	TAATCCCAGCACACTGGGAG	265481	97677	GTCATGTGACTGCATTTTCC
176308	8504	CTTGCTATCCCAGGGAGGAG	220895	53091	GTAATCCCAGCACACTGGGA	265482	97678	AGTCATGTGACTGCATTTTC
176309	8505	CCTTGCTATCCCAGGGAGGA	220896	53092	TGTAATCCCAGCACACTGGG	265483	97679	TAGTCATGTGACTGCATTTT
176310	8506	TCCTTGCTATCCCAGGGAGG	220897	53093	CTGTAATCCCAGCACACTGG	265484	97680	GTAGTCATGTGACTGCATTT
176311	8507	ATCCTTGCTATCCCAGGGAG	220898	53094	CCTGTAATCCCAGCACACTG	265485	97681	AGTAGTCATGTGACTGCATT
176312	8508	TATCCTTGCTATCCCAGGGA	220899	53095	ACCTGTAATCCCAGCACACT	265486	97682	TAGTAGTCATGTGACTGCAT
176313	8509	ATATCCTTGCTATCCCAGGG	220900	53096	CACCTGTAATCCCAGCACAC	265487	97683	TTAGTAGTCATGTGACTGCA
176314	8510	AATATCCTTGCTATCCCAGG	220901	53097	ACACCTGTAATCCCAGCACA	265488	97684	CTTAGTAGTCATGTGACTGC
176315	8511	TAATATCCTTGCTATCCCAG	220902	53098	CACACCTGTAATCCCAGCAC	265489	97685	ACTTAGTAGTCATGTGACTG
176316	8512	CTAATATCCTTGCTATCCCA	220903	53099	TCACACCTGTAATCCCAGCA	265490	97686	CACTTAGTAGTCATGTGACT
176317	8513	TCTAATATCCTTGCTATCCC	220904	53100	CTCACACCTGTAATCCCAGC	265491	97687	CCACTTAGTAGTCATGTGAC
176318	8514	TTCTAATATCCTTGCTATCC	220905	53101	GCTCACACCTGTAATCCCAG	265492	97688	GCCACTTAGTAGTCATGTGA
176319	8515	CTTCTAATATCCTTGCTATC	220906	53102	GGCTCACACCTGTAATCCCA	265493	97689	TGCCACTTAGTAGTCATGTG
176320	8516	TCTTCTAATATCCTTGCTAT	220907	53103	TGGCTCACACCTGTAATCCC	265494	97690	CTGCCACTTAGTAGTCATGT
176321	8517	GTCTTCTAATATCCTTGCTA	220908	53104	GTGGCTCACACCTGTAATCC	265495	97691	GCTGCCACTTAGTAGTCATG
176322	8518	GGTCTTCTAATATCCTTGCT	220909	53105	GGTGGCTCACACCTGTAATC	265496	97692	AGCTGCCACTTAGTAGTCAT
176323	8519	GGGTCTTCTAATATCCTTGC	220910	53106	CGGTGGCTCACACCTGTAAT	265497	97693	GAGCTGCCACTTAGTAGTCA
176324	8520	GGGGTCTTCTAATATCCTTG	220911	53107	GCGGTGGCTCACACCTGTAA	265498	97694	AGAGCTGCCACTTAGTAGTC
176325	8521	AGGGGTCTTCTAATATCCTT	220912	53108	CGCGGTGGCTCACACCTGTA	265499	97695	GAGAGCTGCCACTTAGTAGT
176326	8522	CAGGGGTCTTCTAATATCCT	220913	53109	GCGCGGTGGCTCACACCTGT	265500	97696	CGAGAGCTGCCACTTAGTAG
176327	8523	CCAGGGGTCTTCTAATATCC	220914	53110	GGCGCGGTGGCTCACACCTG	265501	97697	CCGAGAGCTGCCACTTAGTA
176328	8524	GCCAGGGGTCTTCTAATATC	220915	53111	AGGCGCGGTGGCTCACACCT	265502	97698	TCCGAGAGCTGCCACTTAGT
176329	8525	AGCCAGGGGTCTTCTAATAT	220916	53112	CAGGCGCGGTGGCTCACACC	265503	97699	CTCCGAGAGCTGCCACTTAG
176330	8526	GAGCCAGGGGTCTTCTAATA	220917	53113	CCAGGCGCGGTGGCTCACAC	265504	97700	GCTCCGAGAGCTGCCACTTA
176331	8527	AGAGCCAGGGGTCTTCTAAT	220918	53114	GCCAGGCGCGGTGGCTCACA	265505	97701	GGCTCCGAGAGCTGCCACTT
176332	8528	CAGAGCCAGGGGTCTTCTAA	220919	53115	GGCCAGGCGCGGTGGCTCAC	265506	97702	AGGCTCCGAGAGCTGCCACT
176333	8529	ACAGAGCCAGGGGTCTTCTA	220920	53116	AGGCCAGGCGCGGTGGCTCA	265507	97703	GAGGCTCCGAGAGCTGCCAC
176334	8530	TACAGAGCCAGGGGTCTTCT	220921	53117	AAGGCCAGGCGCGGTGGCTC	265508	97704	AGAGGCTCCGAGAGCTGCCA
176335	8531	TTACAGAGCCAGGGGTCTTC	220922	53118	CAAGGCCAGGCGCGGTGGCT	265509	97705	GAGAGGCTCCGAGAGCTGCC
176336	8532	ATTACAGAGCCAGGGGTCTT	220923	53119	GCAAGGCCAGGCGCGGTGGC	265510	97706	AGAGAGGCTCCGAGAGCTGC
176337	8533	AATTACAGAGCCAGGGGTCT	220924	53120	AGCAAGGCCAGGCGCGGTGG	265511	97707	CAGAGAGGCTCCGAGAGCTG
176338	8534	CAATTACAGAGCCAGGGGTC	220925	53121	CAGCAAGGCCAGGCGCGGTG	265512	97708	CCAGAGAGGCTCCGAGAGCT
176339	8535	GCAATTACAGAGCCAGGGGT	220926	53122	ACAGCAAGGCCAGGCGCGGT	265513	97709	GCCAGAGAGGCTCCGAGAGC
176340	8536	AGCAATTACAGAGCCAGGGG	220927	53123	AACAGCAAGGCCAGGCGCGG	265514	97710	GGCCAGAGAGGCTCCGAGAG
176341	8537	AAGCAATTACAGAGCCAGGG	220928	53124	CAACAGCAAGGCCAGGCGCG	265515	97711	GGGCCAGAGAGGCTCCGAGA
176342	8538	CAAGCAATTACAGAGCCAGG	220929	53125	TCAACAGCAAGGCCAGGCGC	265516	97712	GGGGCCAGAGAGGCTCCGAG
176343	8539	ACAAGCAATTACAGAGCCAG	220930	53126	ATCAACAGCAAGGCCAGGCG	265517	97713	TGGGGCCAGAGAGGCTCCGA
176344	8540	GACAAGCAATTACAGAGCCA	220931	53127	AATCAACAGCAAGGCCAGGC	265518	97714	TTGGGGCCAGAGAGGCTCCG
176345	8541	TGACAAGCAATTACAGAGCC	220932	53128	GAATCAACAGCAAGGCCAGG	265519	97715	CTTGGGGCCAGAGAGGCTCC
176346	8542	ATGACAAGCAATTACAGAGC	220933	53129	TGAATCAACAGCAAGGCCAG	265520	97716	ACTTGGGGCCAGAGAGGCTC
176347	8543	CATGACAAGCAATTACAGAG	220934	53130	ATGAATCAACAGCAAGGCCA	265521	97717	GACTTGGGGCCAGAGAGGCT
176348	8544	ACATGACAAGCAATTACAGA	220935	53131	GATGAATCAACAGCAAGGCC	265522	97718	GGACTTGGGGCCAGAGAGGC
176349	8545	CACATGACAAGCAATTACAG	220936	53132	AGATGAATCAACAGCAAGGC	265523	97719	TGGACTTGGGGCCAGAGAGG
176350	8546	GCACATGACAAGCAATTACA	220937	53133	TAGATGAATCAACAGCAAGG	265524	97720	CTGGACTTGGGGCCAGAGAG
176351	8547	AGCACATGACAAGCAATTAC	220938	53134	ATAGATGAATCAACAGCAAG	265525	97721	CCTGGACTTGGGGCCAGAGA
176352	8548	GAGCACATGACAAGCAATTA	220939	53135	TATAGATGAATCAACAGCAA	265526	97722	CCCTGGACTTGGGGCCAGAG
176353	8549	AGAGCACATGACAAGCAATT	220940	53136	CTATAGATGAATCAACAGCA	265527	97723	ACCCTGGACTTGGGGCCAGA
176354	8550	TAGAGCACATGACAAGCAAT	220941	53137	ACTATAGATGAATCAACAGC	265528	97724	AACCCTGGACTTGGGGCCAG
176355	8551	GTAGAGCACATGACAAGCAA	220942	53138	TACTATAGATGAATCAACAG	265529	97725	GAACCCTGGACTTGGGGCCA
176356	8552	TGTAGAGCACATGACAAGCA	220943	53139	ATACTATAGATGAATCAACA	265530	97726	GGAACCCTGGACTTGGGGCC
176357	8553	CTGTAGAGCACATGACAAGC	220944	53140	CATACTATAGATGAATCAAC	265531	97727	TGGAACCCTGGACTTGGGGC
176358	8554	TCTGTAGAGCACATGACAAG	220945	53141	ACATACTATAGATGAATCAA	265532	97728	ATGGAACCCTGGACTTGGGG
176359	8555	GTCTGTAGAGCACATGACAA	220946	53142	AACATACTATAGATGAATCA	265533	97729	TATGGAACCCTGGACTTGGG
176360	8556	CGTCTGTAGAGCACATGACA	220947	53143	AAACATACTATAGATGAATC	265534	97730	CTATGGAACCCTGGACTTGG
176361	8557	GCGTCTGTAGAGCACATGAC	220948	53144	CAAACATACTATAGATGAAT	265535	97731	TCTATGGAACCCTGGACTTG
176362	8558	GGCGTCTGTAGAGCACATGA	220949	53145	TCAAACATACTATAGATGAA	265536	97732	CTCTATGGAACCCTGGACTT
176363	8559	TGGCGTCTGTAGAGCACATG	220950	53146	GTCAAACATACTATAGATGA	265537	97733	CCTCTATGGAACCCTGGACT
176364	8560	GTGGCGTCTGTAGAGCACAT	220951	53147	AGTCAAACATACTATAGATG	265538	97734	GCCTCTATGGAACCCTGGAC
176365	8561	TGTGGCGTCTGTAGAGCACA	220952	53148	AAGTCAAACATACTATAGAT	265539	97735	TGCCTCTATGGAACCCTGGA
176366	8562	CTGTGGCGTCTGTAGAGCAC	220953	53149	CAAGTCAAACATACTATAGA	265540	97736	CTGCCTCTATGGAACCCTGG
176367	8563	TCTGTGGCGTCTGTAGAGCA	220954	53150	TCAAGTCAAACATACTATAG	265541	97737	GCTGCCTCTATGGAACCCTG
176368	8564	TTCTGTGGCGTCTGTAGAGC	220955	53151	ATCAAGTCAAACATACTATA	265542	97738	GGCTGCCTCTATGGAACCCT
176369	8565	ATTCTGTGGCGTCTGTAGAG	220956	53152	CATCAAGTCAAACATACTAT	265543	97739	GGGCTGCCTCTATGGAACCC
176370	8566	CATTCTGTGGCGTCTGTAGA	220957	53153	TCATCAAGTCAAACATACTA	265544	97740	GGGGCTGCCTCTATGGAACC

176371	8567	GCATTCTGTGGCGTCTGTAG	220958	53154	GTCATCAAGTCAAACATACT	265545	97741	TGGGGCTGCCTCTATGGAAC
176372	8568	GGCATTCTGTGGCGTCTGTA	220959	53155	GGTCATCAAGTCAAACATAC	265546	97742	CTGGGGCTGCCTCTATGGAA
176373	8569	TGGCATTCTGTGGCGTCTGT	220960	53156	AGGTCATCAAGTCAAACATA	265547	97743	GCTGGGGCTGCCTCTATGGA
176374	8570	TTGGCATTCTGTGGCGTCTG	220961	53157	GAGGTCATCAAGTCAAACAT	265548	97744	TGCTGGGGCTGCCTCTATGG
176375	8571	CTTGGCATTCTGTGGCGTCT	220962	53158	GGAGGTCATCAAGTCAAACA	265549	97745	ATGCTGGGGCTGCCTCTATG
176376	8572	TCTTGGCATTCTGTGGCGTC	220963	53159	TGGAGGTCATCAAGTCAAAC	265550	97746	CATGCTGGGGCTGCCTCTAT
176377	8573	TTCTTGGCATTCTGTGGCGT	220964	53160	CTGGAGGTCATCAAGTCAAA	265551	97747	CCATGCTGGGGCTGCCTCTA
176378	8574	GTTCTTGGCATTCTGTGGCG	220965	53161	ACTGGAGGTCATCAAGTCAA	265552	97748	GCCATGCTGGGGCTGCCTCT
176379	8575	CGTTCTTGGCATTCTGTGGC	220966	53162	AACTGGAGGTCATCAAGTCA	265553	97749	TGCCATGCTGGGGCTGCCTC
176380	8576	TCGTTCTTGGCATTCTGTGG	220967	53163	TAACTGGAGGTCATCAAGTC	265554	97750	ATGCCATGCTGGGGCTGCCT
176381	8577	TTCGTTCTTGGCATTCTGTG	220968	53164	GTAACTGGAGGTCATCAAGT	265555	97751	CATGCCATGCTGGGGCTGCC
176382	8578	CTTCGTTCTTGGCATTCTGT	220969	53165	GGTAACTGGAGGTCATCAAG	265556	97752	ACATGCCATGCTGGGGCTGC
176383	8579	ACTTCGTTCTTGGCATTCTG	220970	53166	AGGTAACTGGAGGTCATCAA	265557	97753	AACATGCCATGCTGGGGCTG
176384	8580	CACTTCGTTCTTGGCATTCT	220971	53167	AAGGTAACTGGAGGTCATCA	265558	97754	AAACATGCCATGCTGGGGCT
176385	8581	GCACTTCGTTCTTGGCATTC	220972	53168	TAAGGTAACTGGAGGTCATC	265559	97755	AAAACATGCCATGCTGGGGC
176386	8582	AGCACTTCGTTCTTGGCATT	220973	53169	CTAAGGTAACTGGAGGTCAT	265560	97756	GAAAACATGCCATGCTGGGG
176387	8583	CAGCACTTCGTTCTTGGCAT	220974	53170	TCTAAGGTAACTGGAGGTCA	265561	97757	TGAAAACATGCCATGCTGGG
176388	8584	CCAGCACTTCGTTCTTGGCA	220975	53171	GTCTAAGGTAACTGGAGGTC	265562	97758	CTGAAAACATGCCATGCTGG
176389	8585	CCCAGCACTTCGTTCTTGGC	220976	53172	TGTCTAAGGTAACTGGAGGT	265563	97759	ACTGAAAACATGCCATGCTG
176390	8586	TCCCAGCACTTCGTTCTTGG	220977	53173	CTGTCTAAGGTAACTGGAGG	265564	97760	GACTGAAAACATGCCATGCT
176391	8587	TTCCCAGCACTTCGTTCTTG	220978	53174	TCTGTCTAAGGTAACTGGAG	265565	97761	GGACTGAAAACATGCCATGC
176392	8588	CTTCCCAGCACTTCGTTCTT	220979	53175	CTCTGTCTAAGGTAACTGGA	265566	97762	GGGACTGAAAACATGCCATG
176393	8589	CCTTCCCAGCACTTCGTTCT	220980	53176	CCTCTGTCTAAGGTAACTGG	265567	97763	GGGGACTGAAAACATGCCAT
176394	8590	TCCTTCCCAGCACTTCGTTC	220981	53177	ACCTCTGTCTAAGGTAACTG	265568	97764	TGGGGACTGAAAACATGCCA
176395	8591	GTCCTTCCCAGCACTTCGTT	220982	53178	AACCTCTGTCTAAGGTAACT	265569	97765	TTGGGGACTGAAAACATGCC
176396	8592	TGTCCTTCCCAGCACTTCGT	220983	53179	GAACCTCTGTCTAAGGTAAC	265570	97766	TTTGGGGACTGAAAACATGC
176397	8593	TTGTCCTTCCCAGCACTTCG	220984	53180	AGAACCTCTGTCTAAGGTAA	265571	97767	ATTTGGGGACTGAAAACATG
176398	8594	TTTGTCCTTCCCAGCACTTC	220985	53181	GAGAACCTCTGTCTAAGGTA	265572	97768	CATTTGGGGACTGAAAACAT
176399	8595	ATTTGTCCTTCCCAGCACTT	220986	53182	TGAGAACCTCTGTCTAAGGT	265573	97769	TCATTTGGGGACTGAAAACA
176400	8596	AATTTGTCCTTCCCAGCACT	220987	53183	ATGAGAACCTCTGTCTAAGG	265574	97770	CTCATTTGGGGACTGAAAAC
176401	8597	GAATTTGTCCTTCCCAGCAC	220988	53184	GATGAGAACCTCTGTCTAAG	265575	97771	TCTCATTTGGGGACTGAAAA
176402	8598	TGAATTTGTCCTTCCCAGCA	220989	53185	AGATGAGAACCTCTGTCTAA	265576	97772	GTCTCATTTGGGGACTGAAA
176403	8599	ATGAATTTGTCCTTCCCAGC	220990	53186	TAGATGAGAACCTCTGTCTA	265577	97773	AGTCTCATTTGGGGACTGAA
176404	8600	CATGAATTTGTCCTTCCCAG	220991	53187	TTAGATGAGAACCTCTGTCT	265578	97774	GAGTCTCATTTGGGGACTGA
176405	8601	CCATGAATTTGTCCTTCCCA	220992	53188	CTTAGATGAGAACCTCTGTC	265579	97775	AGAGTCTCATTTGGGGACTG
176406	8602	TCCATGAATTTGTCCTTCCC	220993	53189	GCTTAGATGAGAACCTCTGT	265580	97776	CAGAGTCTCATTTGGGGACT
176407	8603	TTCCATGAATTTGTCCTTCC	220994	53190	AGCTTAGATGAGAACCTCTG	265581	97777	CCAGAGTCTCATTTGGGGAC
176408	8604	GTTCCATGAATTTGTCCTTC	220995	53191	GAGCTTAGATGAGAACCTCT	265582	97778	TCCAGAGTCTCATTTGGGGA
176409	8605	GGTTCCATGAATTTGTCCTT	220996	53192	GGAGCTTAGATGAGAACCTC	265583	97779	CTCCAGAGTCTCATTTGGGG
176410	8606	CGGTTCCATGAATTTGTCCT	220997	53193	TGGAGCTTAGATGAGAACCT	265584	97780	TCTCCAGAGTCTCATTTGGG
176411	8607	ACGGTTCCATGAATTTGTCC	220998	53194	TTGGAGCTTAGATGAGAACC	265585	97781	GTCTCCAGAGTCTCATTTGG
176412	8608	CACGGTTCCATGAATTTGTC	220999	53195	GTTGGAGCTTAGATGAGAAC	265586	97782	TGTCTCCAGAGTCTCATTTG
176413	8609	CCACGGTTCCATGAATTTGT	221000	53196	AGTTGGAGCTTAGATGAGAA	265587	97783	TTGTCTCCAGAGTCTCATTT
176414	8610	CCCACGGTTCCATGAATTTG	221001	53197	AAGTTGGAGCTTAGATGAGA	265588	97784	TTTGTCTCCAGAGTCTCATT
176415	8611	TCCCACGGTTCCATGAATTT	221002	53198	AAAGTTGGAGCTTAGATGAG	265589	97785	ATTTGTCTCCAGAGTCTCAT
176416	8612	GTCCCACGGTTCCATGAATT	221003	53199	GAAAGTTGGAGCTTAGATGA	265590	97786	CATTTGTCTCCAGAGTCTCA
176417	8613	CGTCCCACGGTTCCATGAAT	221004	53200	GGAAAGTTGGAGCTTAGATG	265591	97787	ACATTTGTCTCCAGAGTCTC
176418	8614	CCGTCCCACGGTTCCATGAA	221005	53201	TGGAAAGTTGGAGCTTAGAT	265592	97788	GACATTTGTCTCCAGAGTCT
176419	8615	ACCGTCCCACGGTTCCATGA	221006	53202	ATGGAAAGTTGGAGCTTAGA	265593	97789	AGACATTTGTCTCCAGAGTC
176420	8616	CACCGTCCCACGGTTCCATG	221007	53203	AATGGAAAGTTGGAGCTTAG	265594	97790	GAGACATTTGTCTCCAGAGT
176421	8617	GCACCGTCCCACGGTTCCAT	221008	53204	AAATGGAAAGTTGGAGCTTA	265595	97791	AGAGACATTTGTCTCCAGAG
176422	8618	AGCACCGTCCCACGGTTCCA	221009	53205	GAAATGGAAAGTTGGAGCTT	265596	97792	CAGAGACATTTGTCTCCAGA
176423	8619	GAGCACCGTCCCACGGTTCC	221010	53206	GGAAATGGAAAGTTGGAGCT	265597	97793	CCAGAGACATTTGTCTCCAG
176424	8620	GGAGCACCGTCCCACGGTTC	221011	53207	AGGAAATGGAAAGTTGGAGC	265598	97794	TCCAGAGACATTTGTCTCCA
176425	8621	AGGAGCACCGTCCCACGGTT	221012	53208	AAGGAAATGGAAAGTTGGAG	265599	97795	CTCCAGAGACATTTGTCTCC
176426	8622	GAGGAGCACCGTCCCACGGT	221013	53209	AAAGGAAATGGAAAGTTGGA	265600	97796	TCTCCAGAGACATTTGTCTC
176427	8623	GGAGGAGCACCGTCCCACGG	221014	53210	CAAAGGAAATGGAAAGTTGG	265601	97797	GTCTCCAGAGACATTTGTCT
176428	8624	GGGAGGAGCACCGTCCCACG	221015	53211	ACAAAGGAAATGGAAAGTTG	265602	97798	TGTCTCCAGAGACATTTGTC
176429	8625	GGGGAGGAGCACCGTCCCAC	221016	53212	GACAAAGGAAATGGAAAGTT	265603	97799	CTGTCTCCAGAGACATTTGT
176430	8626	GGGGGAGGAGCACCGTCCCA	221017	53213	GGACAAAGGAAATGGAAAGT	265604	97800	TCTGTCTCCAGAGACATTTG
176431	8627	TGGGGGAGGAGCACCGTCCC	221018	53214	AGGACAAAGGAAATGGAAAG	265605	97801	CTCTGTCTCCAGAGACATTT
176432	8628	CTGGGGGAGGAGCACCGTCC	221019	53215	GAGGACAAAGGAAATGGAAA	265606	97802	GCTCTGTCTCCAGAGACATT
176433	8629	GCTGGGGGAGGAGCACCGTC	221020	53216	CGAGGACAAAGGAAATGGAA	265607	97803	TGCTCTGTCTCCAGAGACAT
176434	8630	CGCTGGGGGAGGAGCACCGT	221021	53217	ACGAGGACAAAGGAAATGGA	265608	97804	CTGCTCTGTCTCCAGAGACA
176435	8631	ACGCTGGGGGAGGAGCACCG	221022	53218	GACGAGGACAAAGGAAATGG	265609	97805	GCTGCTCTGTCTCCAGAGAC
176436	8632	TACGCTGGGGGAGGAGCACC	221023	53219	AGACGAGGACAAAGGAAATG	265610	97806	TGCTGCTCTGTCTCCAGAGA
176437	8633	TTACGCTGGGGGAGGAGCAC	221024	53220	AAGACGAGGACAAAGGAAAT	265611	97807	CTGCTGCTCTGTCTCCAGAG
176438	8634	TTTACGCTGGGGGAGGAGCA	221025	53221	AAAGACGAGGACAAAGGAAA	265612	97808	GCTGCTGCTCTGTCTCCAGA
176439	8635	CTTTACGCTGGGGGAGGAGC	221026	53222	GAAAGACGAGGACAAAGGAA	265613	97809	GGCTGCTGCTCTGTCTCCAG
176440	8636	CCTTTACGCTGGGGGAGGAG	221027	53223	GGAAAGACGAGGACAAAGGA	265614	97810	AGGCTGCTGCTCTGTCTCCA
176441	8637	TCCTTTACGCTGGGGGAGGA	221028	53224	GGGAAAGACGAGGACAAAGG	265615	97811	CAGGCTGCTGCTCTGTCTCC
176442	8638	GTCCTTTACGCTGGGGGAGG	221029	53225	GGGGAAAGACGAGGACAAAG	265616	97812	CCAGGCTGCTGCTCTGTCTC

176443	8639	TGTCCTTTACGCTGGGGGAG	221030	53226	AGGGGAAAGACGAGGACAAA	265617	97813	TCCAGGCTGCTGCTCTGTCT
176444	8640	CTGTCCTTTACGCTGGGGGA	221031	53227	AAGGGGAAAGACGAGGACAA	265618	97814	ATCCAGGCTGCTGCTCTGTC
176445	8641	GCTGTCCTTTACGCTGGGGG	221032	53228	TAAGGGGAAAGACGAGGACA	265619	97815	TATCCAGGCTGCTGCTCTGT
176446	8642	AGCTGTCCTTTACGCTGGGG	221033	53229	TTAAGGGGAAAGACGAGGAC	265620	97816	TTATCCAGGCTGCTGCTCTG
176447	8643	GAGCTGTCCTTTACGCTGGG	221034	53230	GTTAAGGGGAAAGACGAGGA	265621	97817	CTTATCCAGGCTGCTGCTCT
176448	8644	GGAGCTGTCCTTTACGCTGG	221035	53231	GGTTAAGGGGAAAGACGAGG	265622	97818	ACTTATCCAGGCTGCTGCTC
176449	8645	AGGAGCTGTCCTTTACGCTG	221036	53232	GGGTTAAGGGGAAAGACGAG	265623	97819	GACTTATCCAGGCTGCTGCT
176450	8646	GAGGAGCTGTCCTTTACGCT	221037	53233	GGGGTTAAGGGGAAAGACGA	265624	97820	TGACTTATCCAGGCTGCTGC
176451	8647	GGAGGAGCTGTCCTTTACGC	221038	53234	AGGGGTTAAGGGGAAAGACG	265625	97821	GTGACTTATCCAGGCTGCTG
176452	8648	AGGAGGAGCTGTCCTTTACG	221039	53235	GAGGGGTTAAGGGGAAAGAC	265626	97822	TGTGACTTATCCAGGCTGCT
176453	8649	GAGGAGGAGCTGTCCTTTAC	221040	53236	GGAGGGGTTAAGGGGAAAGA	265627	97823	TTGTGACTTATCCAGGCTGC
176454	8650	GGAGGAGGAGCTGTCCTTTA	221041	53237	TGGAGGGGTTAAGGGGAAAG	265628	97824	ATTGTGACTTATCCAGGCTG
176455	8651	AGGAGGAGGAGCTGTCCTTT	221042	53238	GTGGAGGGGTTAAGGGGAAA	265629	97825	CATTGTGACTTATCCAGGCT
176456	8652	CAGGAGGAGGAGCTGTCCTT	221043	53239	TGTGGAGGGGTTAAGGGGAA	265630	97826	CCATTGTGACTTATCCAGGC
176457	8653	TCAGGAGGAGGAGCTGTCCT	221044	53240	ATGTGGAGGGGTTAAGGGGA	265631	97827	CCCATTGTGACTTATCCAGG
176458	8654	TTCAGGAGGAGGAGCTGTCC	221045	53241	AATGTGGAGGGGTTAAGGGG	265632	97828	ACCCATTGTGACTTATCCAG
176459	8655	ATTCAGGAGGAGGAGCTGTC	221046	53242	AAATGTGGAGGGGTTAAGGG	265633	97829	CACCCATTGTGACTTATCCA
176460	8656	AATTCAGGAGGAGGAGCTGT	221047	53243	GAAATGTGGAGGGGTTAAGG	265634	97830	TCACCCATTGTGACTTATCC
176461	8657	CAATTCAGGAGGAGGAGCTG	221048	53244	AGAAATGTGGAGGGGTTAAG	265635	97831	GTCACCCATTGTGACTTATC
176462	8658	CCAATTCAGGAGGAGGAGCT	221049	53245	GAGAAATGTGGAGGGGTTAA	265636	97832	CGTCACCCATTGTGACTTAT
176463	8659	TCCAATTCAGGAGGAGGAGC	221050	53246	AGAGAAATGTGGAGGGGTTA	265637	97833	ACGTCACCCATTGTGACTTA
176464	8660	CTCCAATTCAGGAGGAGGAG	221051	53247	GAGAGAAATGTGGAGGGGTT	265638	97834	GACGTCACCCATTGTGACTT
176465	8661	GCTCCAATTCAGGAGGAGGA	221052	53248	TGAGAGAAATGTGGAGGGGT	265639	97835	TGACGTCACCCATTGTGACT
176466	8662	GGCTCCAATTCAGGAGGAGG	221053	53249	TTGAGAGAAATGTGGAGGGG	265640	97836	GTGACGTCACCCATTGTGAC
176467	8663	TGGCTCCAATTCAGGAGGAG	221054	53250	TTTGAGAGAAATGTGGAGGG	265641	97837	AGTGACGTCACCCATTGTGA
176468	8664	CTGGCTCCAATTCAGGAGGA	221055	53251	TTTTGAGAGAAATGTGGAGG	265642	97838	GAGTGACGTCACCCATTGTG
176469	8665	GCTGGCTCCAATTCAGGAGG	221056	53252	ATTTTGAGAGAAATGTGGAG	265643	97839	TGAGTGACGTCACCCATTGT
176470	8666	CGCTGGCTCCAATTCAGGAG	221057	53253	GATTTTGAGAGAAATGTGGA	265644	97840	CTGAGTGACGTCACCCATTG
176471	8667	ACGCTGGCTCCAATTCAGGA	221058	53254	TGATTTTGAGAGAAATGTGG	265645	97841	CCTGAGTGACGTCACCCATT
176472	8668	AACGCTGGCTCCAATTCAGG	221059	53255	GTGATTTTGAGAGAAATGTG	265646	97842	CCCTGAGTGACGTCACCCAT
176473	8669	GAACGCTGGCTCCAATTCAG	221060	53256	GGTGATTTTGAGAGAAATGT	265647	97843	GCCCTGAGTGACGTCACCCA
176474	8670	AGAACGCTGGCTCCAATTCA	221061	53257	GGGTGATTTTGAGAGAAATG	265648	97844	AGCCCTGAGTGACGTCACCC
176475	8671	TAGAACGCTGGCTCCAATTC	221062	53258	GGGGTGATTTTGAGAGAAAT	265649	97845	GAGCCCTGAGTGACGTCACC
176476	8672	TTAGAACGCTGGCTCCAATT	221063	53259	TGGGGTGATTTTGAGAGAAA	265650	97846	TGAGCCCTGAGTGACGTCAC
176477	8673	TTTAGAACGCTGGCTCCAAT	221064	53260	GTGGGGTGATTTTGAGAGAA	265651	97847	TTGAGCCCTGAGTGACGTCA
176478	8674	ATTTAGAACGCTGGCTCCAA	221065	53261	AGTGGGGTGATTTTGAGAGA	265652	97848	GTTGAGCCCTGAGTGACGTC
176479	8675	GATTTAGAACGCTGGCTCCA	221066	53262	AAGTGGGGTGATTTTGAGAG	265653	97849	GGTTGAGCCCTGAGTGACGT
176480	8676	TGATTTAGAACGCTGGCTCC	221067	53263	GAAGTGGGGTGATTTTGAGA	265654	97850	GGGTTGAGCCCTGAGTGACG
176481	8677	ATGATTTAGAACGCTGGCTC	221068	53264	AGAAGTGGGGTGATTTTGAG	265655	97851	GGGGTTGAGCCCTGAGTGAC
176482	8678	CATGATTTAGAACGCTGGCT	221069	53265	TAGAAGTGGGGTGATTTTGA	265656	97852	AGGGGTTGAGCCCTGAGTGA
176483	8679	ACATGATTTAGAACGCTGGC	221070	53266	TTAGAAGTGGGGTGATTTTG	265657	97853	CAGGGGTTGAGCCCTGAGTG
176484	8680	CACATGATTTAGAACGCTGG	221071	53267	TTTAGAAGTGGGGTGATTTT	265658	97854	CCAGGGGTTGAGCCCTGAGT
176485	8681	ACACATGATTTAGAACGCTG	221072	53268	TTTTAGAAGTGGGGTGATTT	265659	97855	CCCAGGGGTTGAGCCCTGAG
176486	8682	GACACATGATTTAGAACGCT	221073	53269	TTTTTAGAAGTGGGGTGATT	265660	97856	GCCCAGGGGTTGAGCCCTGA
176487	8683	TGACACATGATTTAGAACGC	221074	53270	TTTTTTAGAAGTGGGGTGAT	265661	97857	TGCCCAGGGGTTGAGCCCTG
176488	8684	TTGACACATGATTTAGAACG	221075	53271	ATTTTTTAGAAGTGGGGTGA	265662	97858	CTGCCCAGGGGTTGAGCCCT
176489	8685	GTTGACACATGATTTAGAAC	221076	53272	TATTTTTTAGAAGTGGGGTG	265663	97859	GCTGCCCAGGGGTTGAGCCC
176490	8686	TGTTGACACATGATTTAGAA	221077	53273	GTATTTTTTAGAAGTGGGGT	265664	97860	AGCTGCCCAGGGGTTGAGCC
176491	8687	CTGTTGACACATGATTTAGA	221078	53274	AGTATTTTTTAGAAGTGGGG	265665	97861	AAGCTGCCCAGGGGTTGAGC
176492	8688	TCTGTTGACACATGATTTAG	221079	53275	CAGTATTTTTTAGAAGTGGG	265666	97862	TAAGCTGCCCAGGGGTTGAG
176493	8689	CTCTGTTGACACATGATTTA	221080	53276	ACAGTATTTTTTAGAAGTGG	265667	97863	TTAAGCTGCCCAGGGGTTGA
176494	8690	ACTCTGTTGACACATGATTT	221081	53277	AACAGTATTTTTTAGAAGTG	265668	97864	GTTAAGCTGCCCAGGGGTTG
176495	8691	AACTCTGTTGACACATGATT	221082	53278	AAACAGTATTTTTTAGAAGT	265669	97865	AGTTAAGCTGCCCAGGGGTT
176496	8692	CAACTCTGTTGACACATGAT	221083	53279	TAAACAGTATTTTTTAGAAG	265670	97866	AAGTTAAGCTGCCCAGGGGT
176497	8693	ACAACTCTGTTGACACATGA	221084	53280	ATAAACAGTATTTTTTAGAA	265671	97867	CAAGTTAAGCTGCCCAGGGG
176498	8694	GACAACTCTGTTGACACATG	221085	53281	AATAAACAGTATTTTTTAGA	265672	97868	GCAAGTTAAGCTGCCCAGGG
176499	8695	GGACAACTCTGTTGACACAT	221086	53282	AAATAAACAGTATTTTTTAG	265673	97869	AGCAAGTTAAGCTGCCCAGG
176500	8696	AGGACAACTCTGTTGACACA	221087	53283	AAAATAAACAGTATTTTTTA	265674	97870	TAGCAAGTTAAGCTGCCCAG
176501	8697	CAGGACAACTCTGTTGACAC	221088	53284	AAAAATAAACAGTATTTTTT	265675	97871	CTAGCAAGTTAAGCTGCCCA
176502	8698	CCAGGACAACTCTGTTGACA	221089	53285	GAAAAATAAACAGTATTTTT	265676	97872	CCTAGCAAGTTAAGCTGCCC
176503	8699	TCCAGGACAACTCTGTTGAC	221090	53286	AGAAAAATAAACAGTATTTT	265677	97873	CCCTAGCAAGTTAAGCTGCC
176504	8700	ATCCAGGACAACTCTGTTGA	221091	53287	AAGAAAAATAAACAGTATTT	265678	97874	TCCCTAGCAAGTTAAGCTGC
176505	8701	GATCCAGGACAACTCTGTTG	221092	53288	AAAGAAAAATAAACAGTATT	265679	97875	GTCCCTAGCAAGTTAAGCTG
176506	8702	CGATCCAGGACAACTCTGTT	221093	53289	AAAAGAAAAATAAACAGTAT	265680	97876	CGTCCCTAGCAAGTTAAGCT
176507	8703	CCGATCCAGGACAACTCTGT	221094	53290	TAAAAGAAAAATAAACAGTA	265681	97877	ACGTCCCTAGCAAGTTAAGC
176508	8704	TCCGATCCAGGACAACTCTG	221095	53291	TTAAAAGAAAAATAAACAGT	265682	97878	AACGTCCCTAGCAAGTTAAG
176509	8705	ATCCGATCCAGGACAACTCT	221096	53292	TTTAAAAGAAAAATAAACAG	265683	97879	TAACGTCCCTAGCAAGTTAA
176510	8706	GATCCGATCCAGGACAACTC	221097	53293	ATTTAAAAGAAAAATAAACA	265684	97880	CTAACGTCCCTAGCAAGTTA
176511	8707	GGATCCGATCCAGGACAACT	221098	53294	AATTTAAAAGAAAAATAAAC	265685	97881	CCTAACGTCCCTAGCAAGTT
176512	8708	TGGATCCGATCCAGGACAAC	221099	53295	AAATTTAAAAGAAAAATAAA	265686	97882	TCCTAACGTCCCTAGCAAGT
176513	8709	CTGGATCCGATCCAGGACAA	221100	53296	GAAATTTAAAAGAAAAATAA	265687	97883	CTCCTAACGTCCCTAGCAAG
176514	8710	ACTGGATCCGATCCAGGACA	221101	53297	TGAAATTTAAAAGAAAAATA	265688	97884	ACTCCTAACGTCCCTAGCAA

176515	8711	AACTGGATCCGATCCAGGAC	221102	53298	TTGAAATTTAAAAGAAAAAT	265689	97885	GACTCCTAACGTCCCTAGCA
176516	8712	GAACTGGATCCGATCCAGGA	221103	53299	TTTGAAATTTAAAAGAAAAA	265690	97886	AGACTCCTAACGTCCCTAGC
176517	8713	AGAACTGGATCCGATCCAGG	221104	53300	ATTTGAAATTTAAAAGAAAA	265691	97887	CAGACTCCTAACGTCCCTAG
176518	8714	CAGAACTGGATCCGATCCAG	221105	53301	AATTTGAAATTTAAAAGAAA	265692	97888	GCAGACTCCTAACGTCCCTA
176519	8715	GCAGAACTGGATCCGATCCA	221106	53302	TAATTTGAAATTTAAAAGAA	265693	97889	AGCAGACTCCTAACGTCCCT
176520	8716	GGCAGAACTGGATCCGATCC	221107	53303	ATAATTTGAAATTTAAAAGA	265694	97890	CAGCAGACTCCTAACGTCCC
176521	8717	TGGCAGAACTGGATCCGATC	221108	53304	GATAATTTGAAATTTAAAAG	265695	97891	GCAGCAGACTCCTAACGTCC
176522	8718	ATGGCAGAACTGGATCCGAT	221109	53305	AGATAATTTGAAATTTAAAA	265696	97892	TGCAGCAGACTCCTAACGTC
176523	8719	AATGGCAGAACTGGATCCGA	221110	53306	TAGATAATTTGAAATTTAAA	265697	97893	TTGCAGCAGACTCCTAACGT
176524	8720	CAATGGCAGAACTGGATCCG	221111	53307	ATAGATAATTTGAAATTTAA	265698	97894	TTTGCAGCAGACTCCTAACG
176525	8721	TCAATGGCAGAACTGGATCC	221112	53308	TATAGATAATTTGAAATTTA	265699	97895	TTTTGCAGCAGACTCCTAAC
176526	8722	ATCAATGGCAGAACTGGATC	221113	53309	GTATAGATAATTTGAAATTT	265700	97896	GTTTTGCAGCAGACTCCTAA
176527	8723	AATCAATGGCAGAACTGGAT	221114	53310	AGTATAGATAATTTGAAATT	265701	97897	GGTTTTGCAGCAGACTCCTA
176528	8724	AAATCAATGGCAGAACTGGA	221115	53311	GAGTATAGATAATTTGAAAT	265702	97898	AGGTTTTGCAGCAGACTCCT
176529	8725	CAAATCAATGGCAGAACTGG	221116	53312	TGAGTATAGATAATTTGAAA	265703	97899	CAGGTTTTGCAGCAGACTCC
176530	8726	GCAAATCAATGGCAGAACTG	221117	53313	ATGAGTATAGATAATTTGAA	265704	97900	TCAGGTTTTGCAGCAGACTC
176531	8727	TGCAAATCAATGGCAGAACT	221118	53314	AATGAGTATAGATAATTTGA	265705	97901	CTCAGGTTTTGCAGCAGACT
176532	8728	CTGCAAATCAATGGCAGAAC	221119	53315	CAATGAGTATAGATAATTTG	265706	97902	CCTCAGGTTTTGCAGCAGAC
176533	8729	CCTGCAAATCAATGGCAGAA	221120	53316	TCAATGAGTATAGATAATTT	265707	97903	CCCTCAGGTTTTGCAGCAGA
176534	8730	ACCTGCAAATCAATGGCAGA	221121	53317	TTCAATGAGTATAGATAATT	265708	97904	ACCCTCAGGTTTTGCAGCAG
176535	8731	GACCTGCAAATCAATGGCAG	221122	53318	TTTCAATGAGTATAGATAAT	265709	97905	GACCCTCAGGTTTTGCAGCA
176536	8732	TGACCTGCAAATCAATGGCA	221123	53319	ATTTCAATGAGTATAGATAA	265710	97906	AGACCCTCAGGTTTTGCAGC
176537	8733	ATGACCTGCAAATCAATGGC	221124	53320	TATTTCAATGAGTATAGATA	265711	97907	AAGACCCTCAGGTTTTGCAG
176538	8734	AATGACCTGCAAATCAATGG	221125	53321	TTATTTCAATGAGTATAGAT	265712	97908	TAAGACCCTCAGGTTTTGCA
176539	8735	AAATGACCTGCAAATCAATG	221126	53322	TTTATTTCAATGAGTATAGA	265713	97909	CTAAGACCCTCAGGTTTTGC
176540	8736	GAAATGACCTGCAAATCAAT	221127	53323	ATTTATTTCAATGAGTATAG	265714	97910	GCTAAGACCCTCAGGTTTTG
176541	8737	TGAAATGACCTGCAAATCAA	221128	53324	GATTTATTTCAATGAGTATA	265715	97911	AGCTAAGACCCTCAGGTTTT
176542	8738	CTGAAATGACCTGCAAATCA	221129	53325	TGATTTATTTCAATGAGTAT	265716	97912	CAGCTAAGACCCTCAGGTTT
176543	8739	ACTGAAATGACCTGCAAATC	221130	53326	TTGATTTATTTCAATGAGTA	265717	97913	TCAGCTAAGACCCTCAGGTT
176544	8740	CACTGAAATGACCTGCAAAT	221131	53327	TTTGATTTATTTCAATGAGT	265718	97914	CTCAGCTAAGACCCTCAGGT
176545	8741	CCACTGAAATGACCTGCAAA	221132	53328	TTTTGATTTATTTCAATGAG	265719	97915	GCTCAGCTAAGACCCTCAGG
176546	8742	ACCACTGAAATGACCTGCAA	221133	53329	ATTTTGATTTATTTCAATGA	265720	97916	TGCTCAGCTAAGACCCTCAG
176547	8743	TACCACTGAAATGACCTGCA	221134	53330	TATTTTGATTTATTTCAATG	265721	97917	CTGCTCAGCTAAGACCCTCA
176548	8744	GTACCACTGAAATGACCTGC	221135	53331	CTATTTTGATTTATTTCAAT	265722	97918	ACTGCTCAGCTAAGACCCTC
176549	8745	GGTACCACTGAAATGACCTG	221136	53332	GCTATTTTGATTTATTTCAA	265723	97919	GACTGCTCAGCTAAGACCCT
176550	8746	AGGTACCACTGAAATGACCT	221137	53333	TGCTATTTTGATTTATTTCA	265724	97920	TGACTGCTCAGCTAAGACCC
176551	8747	CAGGTACCACTGAAATGACC	221138	53334	ATGCTATTTTGATTTATTTC	265725	97921	GTGACTGCTCAGCTAAGACC
176552	8748	ACAGGTACCACTGAAATGAC	221139	53335	CATGCTATTTTGATTTATTT	265726	97922	TGTGACTGCTCAGCTAAGAC
176553	8749	AACAGGTACCACTGAAATGA	221140	53336	CCATGCTATTTTGATTTATT	265727	97923	CTGTGACTGCTCAGCTAAGA
176554	8750	AAACAGGTACCACTGAAATG	221141	53337	TCCATGCTATTTTGATTTAT	265728	97924	CCTGTGACTGCTCAGCTAAG
176555	8751	GAAACAGGTACCACTGAAAT	221142	53338	TTCCATGCTATTTTGATTTA	265729	97925	GCCTGTGACTGCTCAGCTAA
176556	8752	GGAAACAGGTACCACTGAAA	221143	53339	ATTCCATGCTATTTTGATTT	265730	97926	AGCCTGTGACTGCTCAGCTA
176557	8753	TGGAAACAGGTACCACTGAA	221144	53340	TATTCCATGCTATTTTGATT	265731	97927	CAGCCTGTGACTGCTCAGCT
176558	8754	CTGGAAACAGGTACCACTGA	221145	53341	TTATTCCATGCTATTTTGAT	265732	97928	CCAGCCTGTGACTGCTCAGC
176559	8755	ACTGGAAACAGGTACCACTG	221146	53342	CTTATTCCATGCTATTTTGA	265733	97929	CCCAGCCTGTGACTGCTCAG
176560	8756	AACTGGAAACAGGTACCACT	221147	53343	GCTTATTCCATGCTATTTTG	265734	97930	GCCCAGCCTGTGACTGCTCA
176561	8757	CAACTGGAAACAGGTACCAC	221148	53344	CGCTTATTCCATGCTATTTT	265735	97931	GGCCCAGCCTGTGACTGCTC
176562	8758	ACAACTGGAAACAGGTACCA	221149	53345	TCGCTTATTCCATGCTATTT	265736	97932	GGGCCCAGCCTGTGACTGCT
176563	8759	AACAACTGGAAACAGGTACC	221150	53346	TTCGCTTATTCCATGCTATT	265737	97933	CGGGCCCAGCCTGTGACTGC
176564	8760	GAACAACTGGAAACAGGTAC	221151	53347	TTTCGCTTATTCCATGCTAT	265738	97934	ACGGGCCCAGCCTGTGACTG
176565	8761	AGAACAACTGGAAACAGGTA	221152	53348	TTTTCGCTTATTCCATGCTA	265739	97935	AACGGGCCCAGCCTGTGACT
176566	8762	AAGAACAACTGGAAACAGGT	221153	53349	TTTTTCGCTTATTCCATGCT	265740	97936	CAACGGGCCCAGCCTGTGAC
176567	8763	TAAGAACAACTGGAAACAGG	221154	53350	TTTTTTCGCTTATTCCATGC	265741	97937	GCAACGGGCCCAGCCTGTGA
176568	8764	TTAAGAACAACTGGAAACAG	221155	53351	TTTTTTTCGCTTATTCCATG	265742	97938	GGCAACGGGCCCAGCCTGTG
176569	8765	ATTAAGAACAACTGGAAACA	221156	53352	ATTTTTTTCGCTTATTCCAT	265743	97939	GGGCAACGGGCCCAGCCTGT
176570	8766	AATTAAGAACAACTGGAAAC	221157	53353	CATTTTTTTCGCTTATTCCA	265744	97940	AGGGCAACGGGCCCAGCCTG
176571	8767	CAATTAAGAACAACTGGAAA	221158	53354	CCATTTTTTTCGCTTATTCC	265745	97941	CAGGGCAACGGGCCCAGCCT
176572	8768	TCAATTAAGAACAACTGGAA	221159	53355	TCCATTTTTTTCGCTTATTC	265746	97942	CCAGGGCAACGGGCCCAGCC
176573	8769	TTCAATTAAGAACAACTGGA	221160	53356	ATCCATTTTTTTCGCTTATT	265747	97943	CCCAGGGCAACGGGCCCAGC
176574	8770	GTTCAATTAAGAACAACTGG	221161	53357	GATCCATTTTTTTCGCTTAT	265748	97944	GCCCAGGGCAACGGGCCCAG
176575	8771	TGTTCAATTAAGAACAACTG	221162	53358	GGATCCATTTTTTTCGCTTA	265749	97945	AGCCCAGGGCAACGGGCCCA
176576	8772	CTGTTCAATTAAGAACAACT	221163	53359	GGGATCCATTTTTTTCGCTT	265750	97946	GAGCCCAGGGCAACGGGCCC
176577	8773	ACTGTTCAATTAAGAACAAC	221164	53360	TGGGATCCATTTTTTTCGCT	265751	97947	GGAGCCCAGGGCAACGGGCC
176578	8774	CACTGTTCAATTAAGAACAA	221165	53361	GTGGGATCCATTTTTTTCGC	265752	97948	AGGAGCCCAGGGCAACGGGC
176579	8775	CCACTGTTCAATTAAGAACA	221166	53362	GGTGGGATCCATTTTTTTCG	265753	97949	CAGGAGCCCAGGGCAACGGG
176580	8776	GCCACTGTTCAATTAAGAAC	221167	53363	GGGTGGGATCCATTTTTTTC	265754	97950	ACAGGAGCCCAGGGCAACGG
176581	8777	TGCCACTGTTCAATTAAGAA	221168	53364	AGGGTGGGATCCATTTTTTT	265755	97951	CACAGGAGCCCAGGGCAACG
176582	8778	GTGCCACTGTTCAATTAAGA	221169	53365	AAGGGTGGGATCCATTTTTT	265756	97952	TCACAGGAGCCCAGGGCAAC
176583	8779	GGTGCCACTGTTCAATTAAG	221170	53366	GAAGGGTGGGATCCATTTTT	265757	97953	CTCACAGGAGCCCAGGGCAA
176584	8780	TGGTGCCACTGTTCAATTAA	221171	53367	GGAAGGGTGGGATCCATTTT	265758	97954	ACTCACAGGAGCCCAGGGCA
176585	8781	TTGGTGCCACTGTTCAATTA	221172	53368	GGGAAGGGTGGGATCCATTT	265759	97955	TACTCACAGGAGCCCAGGGC
176586	8782	TTTGGTGCCACTGTTCAATT	221173	53369	GGGGAAGGGTGGGATCCATT	265760	97956	TTACTCACAGGAGCCCAGGG

176587	8783	GTTTGGTGCCACTGTTCAAT	221174	53370	TGGGGAAGGGTGGGATCCAT	265761	97957	TTTACTCACAGGAGCCCAGG
176588	8784	AGTTTGGTGCCACTGTTCAA	221175	53371	GTGGGGAAGGGTGGGATCCA	265762	97958	TTTTACTCACAGGAGCCCAG
176589	8785	TAGTTTGGTGCCACTGTTCA	221176	53372	AGTGGGGAAGGGTGGGATCC	265763	97959	GTTTTACTCACAGGAGCCCA
176590	8786	ATAGTTTGGTGCCACTGTTC	221177	53373	GAGTGGGGAAGGGTGGGATC	265764	97960	GGTTTTACTCACAGGAGCCC
176591	8787	AATAGTTTGGTGCCACTGTT	221178	53374	GGAGTGGGGAAGGGTGGGAT	265765	97961	GGGTTTTACTCACAGGAGCC
176592	8788	CAATAGTTTGGTGCCACTGT	221179	53375	GGGAGTGGGGAAGGGTGGGA	265766	97962	TGGGTTTTACTCACAGGAGC
176593	8789	ACAATAGTTTGGTGCCACTG	221180	53376	TGGGAGTGGGGAAGGGTGGG	265767	97963	CTGGGTTTTACTCACAGGAG
176594	8790	GACAATAGTTTGGTGCCACT	221181	53377	ATGGGAGTGGGGAAGGGTGG	265768	97964	ACTGGGTTTTACTCACAGGA
176595	8791	AGACAATAGTTTGGTGCCAC	221182	53378	AATGGGAGTGGGGAAGGGTG	265769	97965	GACTGGGTTTTACTCACAGG
176596	8792	AAGACAATAGTTTGGTGCCA	221183	53379	GAATGGGAGTGGGGAAGGGT	265770	97966	TGACTGGGTTTTACTCACAG
176597	8793	CAAGACAATAGTTTGGTGCC	221184	53380	GGAATGGGAGTGGGGAAGGG	265771	97967	TTGACTGGGTTTTACTCACA
176598	8794	GCAAGACAATAGTTTGGTGC	221185	53381	GGGAATGGGAGTGGGGAAGG	265772	97968	ATTGACTGGGTTTTACTCAC
176599	8795	GGCAAGACAATAGTTTGGTG	221186	53382	AGGGAATGGGAGTGGGGAAG	265773	97969	AATTGACTGGGTTTTACTCA
176600	8796	AGGCAAGACAATAGTTTGGT	221187	53383	TAGGGAATGGGAGTGGGGAA	265774	97970	AAATTGACTGGGTTTTACTC
176601	8797	GAGGCAAGACAATAGTTTGG	221188	53384	CTAGGGAATGGGAGTGGGGA	265775	97971	AAAATTGACTGGGTTTTACT
176602	8798	TGAGGCAAGACAATAGTTTG	221189	53385	CCTAGGGAATGGGAGTGGGG	265776	97972	CAAAATTGACTGGGTTTTAC
176603	8799	ATGAGGCAAGACAATAGTTT	221190	53386	CCCTAGGGAATGGGAGTGGG	265777	97973	TCAAAATTGACTGGGTTTTA
176604	8800	GATGAGGCAAGACAATAGTT	221191	53387	GCCCTAGGGAATGGGAGTGG	265778	97974	CTCAAAATTGACTGGGTTTT
176605	8801	GGATGAGGCAAGACAATAGT	221192	53388	AGCCCTAGGGAATGGGAGTG	265779	97975	ACTCAAAATTGACTGGGTTT
176606	8802	GGGATGAGGCAAGACAATAG	221193	53389	TAGCCCTAGGGAATGGGAGT	265780	97976	TACTCAAAATTGACTGGGTT
176607	8803	GGGGATGAGGCAAGACAATA	221194	53390	TTAGCCCTAGGGAATGGGAG	265781	97977	GTACTCAAAATTGACTGGGT
176608	8804	GGGGGATGAGGCAAGACAAT	221195	53391	GTTAGCCCTAGGGAATGGGA	265782	97978	GGTACTCAAAATTGACTGGG
176609	8805	AGGGGGATGAGGCAAGACAA	221196	53392	GGTTAGCCCTAGGGAATGGG	265783	97979	GGGTACTCAAAATTGACTGG
176610	8806	GAGGGGGATGAGGCAAGACA	221197	53393	TGGTTAGCCCTAGGGAATGG	265784	97980	TGGGTACTCAAAATTGACTG
176611	8807	GGAGGGGGATGAGGCAAGAC	221198	53394	ATGGTTAGCCCTAGGGAATG	265785	97981	CTGGGTACTCAAAATTGACT
176612	8808	GGGAGGGGGATGAGGCAAGA	221199	53395	TATGGTTAGCCCTAGGGAAT	265786	97982	ACTGGGTACTCAAAATTGAC
176613	8809	TGGGAGGGGGATGAGGCAAG	221200	53396	CTATGGTTAGCCCTAGGGAA	265787	97983	TACTGGGTACTCAAAATTGA
176614	8810	ATGGGAGGGGGATGAGGCAA	221201	53397	ACTATGGTTAGCCCTAGGGA	265788	97984	TTACTGGGTACTCAAAATTG
176615	8811	CATGGGAGGGGGATGAGGCA	221202	53398	AACTATGGTTAGCCCTAGGG	265789	97985	CTTACTGGGTACTCAAAATT
176616	8812	CCATGGGAGGGGGATGAGGC	221203	53399	TAACTATGGTTAGCCCTAGG	265790	97986	CCTTACTGGGTACTCAAAAT
176617	8813	GCCATGGGAGGGGGATGAGG	221204	53400	TTAACTATGGTTAGCCCTAG	265791	97987	GCCTTACTGGGTACTCAAAA
176618	8814	GGCCATGGGAGGGGGATGAG	221205	53401	GTTAACTATGGTTAGCCCTA	265792	97988	TGCCTTACTGGGTACTCAAA
176619	8815	AGGCCATGGGAGGGGGATGA	221206	53402	GGTTAACTATGGTTAGCCCT	265793	97989	ATGCCTTACTGGGTACTCAA
176620	8816	CAGGCCATGGGAGGGGGATG	221207	53403	TGGTTAACTATGGTTAGCCC	265794	97990	GATGCCTTACTGGGTACTCA
176621	8817	ACAGGCCATGGGAGGGGGAT	221208	53404	ATGGTTAACTATGGTTAGCC	265795	97991	GGATGCCTTACTGGGTACTC
176622	8818	GACAGGCCATGGGAGGGGGA	221209	53405	AATGGTTAACTATGGTTAGC	265796	97992	TGGATGCCTTACTGGGTACT
176623	8819	GGACAGGCCATGGGAGGGGG	221210	53406	AAATGGTTAACTATGGTTAG	265797	97993	ATGGATGCCTTACTGGGTAC
176624	8820	GGGACAGGCCATGGGAGGGG	221211	53407	TAAATGGTTAACTATGGTTA	265798	97994	AATGGATGCCTTACTGGGTA
176625	8821	GGGGACAGGCCATGGGAGGG	221212	53408	TTAAATGGTTAACTATGGTT	265799	97995	CAATGGATGCCTTACTGGGT
176626	8822	GGGGGACAGGCCATGGGAGG	221213	53409	ATTAAATGGTTAACTATGGT	265800	97996	TCAATGGATGCCTTACTGGG
176627	8823	TGGGGGACAGGCCATGGGAG	221214	53410	CATTAAATGGTTAACTATGG	265801	97997	CTCAATGGATGCCTTACTGG
176628	8824	TTGGGGGACAGGCCATGGGA	221215	53411	TCATTAAATGGTTAACTATG	265802	97998	ACTCAATGGATGCCTTACTG
176629	8825	TTTGGGGGACAGGCCATGGG	221216	53412	GTCATTAAATGGTTAACTAT	265803	97999	AACTCAATGGATGCCTTACT
176630	8826	TTTTGGGGGACAGGCCATGG	221217	53413	AGTCATTAAATGGTTAACTA	265804	98000	TAACTCAATGGATGCCTTAC
176631	8827	TTTTTGGGGGACAGGCCATG	221218	53414	TAGTCATTAAATGGTTAACT	265805	98001	ATAACTCAATGGATGCCTTA
176632	8828	CTTTTTGGGGGACAGGCCAT	221219	53415	CTAGTCATTAAATGGTTAAC	265806	98002	AATAACTCAATGGATGCCTT
176633	8829	TCTTTTTGGGGGACAGGCCA	221220	53416	CCTAGTCATTAAATGGTTAA	265807	98003	AAATAACTCAATGGATGCCT
176634	8830	CTCTTTTTGGGGGACAGGCC	221221	53417	ACCTAGTCATTAAATGGTTA	265808	98004	AAAATAACTCAATGGATGCC
176635	8831	TCTCTTTTTGGGGGACAGGC	221222	53418	AACCTAGTCATTAAATGGTT	265809	98005	CAAAATAACTCAATGGATGC
176636	8832	GTCTCTTTTTGGGGGACAGG	221223	53419	AAACCTAGTCATTAAATGGT	265810	98006	GCAAAATAACTCAATGGATG
176637	8833	AGTCTCTTTTTGGGGGACAG	221224	53420	AAAACCTAGTCATTAAATGG	265811	98007	TGCAAAATAACTCAATGGAT
176638	8834	AAGTCTCTTTTTGGGGGACA	221225	53421	AAAAACCTAGTCATTAAATG	265812	98008	CTGCAAAATAACTCAATGGA
176639	8835	GAAGTCTCTTTTTGGGGGAC	221226	53422	AAAAAACCTAGTCATTAAAT	265813	98009	GCTGCAAAATAACTCAATGG
176640	8836	AGAAGTCTCTTTTTGGGGGA	221227	53423	AAAAAAACCTAGTCATTAAA	265814	98010	GGCTGCAAAATAACTCAATG
176641	8837	AAGAAGTCTCTTTTTGGGGG	221228	53424	CAAAAAAACCTAGTCATTAA	265815	98011	TGGCTGCAAAATAACTCAAT
176642	8838	CAAGAAGTCTCTTTTTGGGG	221229	53425	ACAAAAAAACCTAGTCATTA	265816	98012	CTGGCTGCAAAATAACTCAA
176643	8839	CCAAGAAGTCTCTTTTTGGG	221230	53426	AACAAAAAAACCTAGTCATT	265817	98013	CCTGGCTGCAAAATAACTCA
176644	8840	CCCAAGAAGTCTCTTTTTGG	221231	53427	CAACAAAAAAACCTAGTCAT	265818	98014	TCCTGGCTGCAAAATAACTC
176645	8841	ACCCAAGAAGTCTCTTTTTG	221232	53428	ACAACAAAAAAACCTAGTCA	265819	98015	CTCCTGGCTGCAAAATAACT
176646	8842	TACCCAAGAAGTCTCTTTTT	221233	53429	AACAACAAAAAAACCTAGTC	265820	98016	ACTCCTGGCTGCAAAATAAC
176647	8843	TTACCCAAGAAGTCTCTTTT	221234	53430	CAACAACAAAAAAACCTAGT	265821	98017	CACTCCTGGCTGCAAAATAA
176648	8844	ATTACCCAAGAAGTCTCTTT	221235	53431	ACAACAACAAAAAAACCTAG	265822	98018	GCACTCCTGGCTGCAAAATA
176649	8845	AATTACCCAAGAAGTCTCTT	221236	53432	AACAACAACAAAAAAACCTA	265823	98019	AGCACTCCTGGCTGCAAAAT
176650	8846	TAATTACCCAAGAAGTCTCT	221237	53433	TAACAACAACAAAAAAACCT	265824	98020	TAGCACTCCTGGCTGCAAAA
176651	8847	TTAATTACCCAAGAAGTCTC	221238	53434	ATAACAACAACAAAAAAACC	265825	98021	ATAGCACTCCTGGCTGCAAA
176652	8848	ATTAATTACCCAAGAAGTCT	221239	53435	AATAACAACAACAAAAAAAC	265826	98022	AATAGCACTCCTGGCTGCAA
176653	8849	GATTAATTACCCAAGAAGTC	221240	53436	AAATAACAACAACAAAAAAA	265827	98023	TAATAGCACTCCTGGCTGCA
176654	8850	TGATTAATTACCCAAGAAGT	221241	53437	AAAATAACAACAACAAAAAA	265828	98024	TTAATAGCACTCCTGGCTGC
176655	8851	CTGATTAATTACCCAAGAAG	221242	53438	AAAAATAACAACAACAAAAA	265829	98025	CTTAATAGCACTCCTGGCTG
176656	8852	CCTGATTAATTACCCAAGAA	221243	53439	AAAAAATAACAACAACAAAA	265830	98026	TCTTAATAGCACTCCTGGCT
176657	8853	CCCTGATTAATTACCCAAGA	221244	53440	TAAAAAATAACAACAACAAA	265831	98027	TTCTTAATAGCACTCCTGGC
176658	8854	GCCCTGATTAATTACCCAAG	221245	53441	ATAAAAAATAACAACAACAA	265832	98028	GTTCTTAATAGCACTCCTGG

176659	8855	TGCCCTGATTAATTACCCAA	221246	53442	AATAAAAAATAACAACAACA	265833	98029	TGTTCTTAATAGCACTCCTG
176660	8856	TTGCCCTGATTAATTACCCA	221247	53443	AAATAAAAAATAACAACAAC	265834	98030	CTGTTCTTAATAGCACTCCT
176661	8857	GTTGCCCTGATTAATTACCC	221248	53444	TAAATAAAAAATAACAACAA	265835	98031	ACTGTTCTTAATAGCACTCC
176662	8858	TGTTGCCCTGATTAATTACC	221249	53445	ATAAATAAAAAATAACAACA	265836	98032	GACTGTTCTTAATAGCACTC
176663	8859	ATGTTGCCCTGATTAATTAC	221250	53446	AATAAATAAAAAATAACAAC	265837	98033	CGACTGTTCTTAATAGCACT
176664	8860	GATGTTGCCCTGATTAATTA	221251	53447	AAATAAATAAAAAATAACAA	265838	98034	GCGACTGTTCTTAATAGCAC
176665	8861	TGATGTTGCCCTGATTAATT	221252	53448	TAAATAAATAAAAAATAACA	265839	98035	CGCGACTGTTCTTAATAGCA
176666	8862	CTGATGTTGCCCTGATTAAT	221253	53449	ATAAATAAATAAAAAATAAC	265840	98036	CCGCGACTGTTCTTAATAGC
176667	8863	CCTGATGTTGCCCTGATTAA	221254	53450	AATAAATAAATAAAAAATAA	265841	98037	GCCGCGACTGTTCTTAATAG
176668	8864	GCCTGATGTTGCCCTGATTA	221255	53451	AAATAAATAAATAAAAAATA	265842	98038	AGCCGCGACTGTTCTTAATA
176669	8865	TGCCTGATGTTGCCCTGATT	221256	53452	AAAATAAATAAATAAAAAAT	265843	98039	CAGCCGCGACTGTTCTTAAT
176670	8866	CTGCCTGATGTTGCCCTGAT	221257	53453	CAAAATAAATAAATAAAAAA	265844	98040	CCAGCCGCGACTGTTCTTAA
176671	8867	ACTGCCTGATGTTGCCCTGA	221258	53454	TCAAAATAAATAAATAAAAA	265845	98041	CCCAGCCGCGACTGTTCTTA
176672	8868	GACTGCCTGATGTTGCCCTG	221259	53455	CTCAAAATAAATAAATAAAA	265846	98042	GCCCAGCCGCGACTGTTCTT
176673	8869	AGACTGCCTGATGTTGCCCT	221260	53456	TCTCAAAATAAATAAATAAA	265847	98043	CGCCCAGCCGCGACTGTTCT
176674	8870	CAGACTGCCTGATGTTGCCC	221261	53457	GTCTCAAAATAAATAAATAA	265848	98044	ACGCCCAGCCGCGACTGTTC
176675	8871	CCAGACTGCCTGATGTTGCC	221262	53458	TGTCTCAAAATAAATAAATA	265849	98045	CACGCCCAGCCGCGACTGTT
176676	8872	CCCAGACTGCCTGATGTTGC	221263	53459	CTGTCTCAAAATAAATAAAT	265850	98046	CCACGCCCAGCCGCGACTGT
176677	8873	GCCCAGACTGCCTGATGTTG	221264	53460	TCTGTCTCAAAATAAATAAA	265851	98047	ACCACGCCCAGCCGCGACTG
176678	8874	CGCCCAGACTGCCTGATGTT	221265	53461	CTCTGTCTCAAAATAAATAA	265852	98048	CACCACGCCCAGCCGCGACT
176679	8875	GCGCCCAGACTGCCTGATGT	221266	53462	ACTCTGTCTCAAAATAAATA	265853	98049	CCACCACGCCCAGCCGCGAC
176680	8876	CGCGCCCAGACTGCCTGATG	221267	53463	GACTCTGTCTCAAAATAAAT	265854	98050	GCCACCACGCCCAGCCGCGA
176681	8877	CCGCGCCCAGACTGCCTGAT	221268	53464	AGACTCTGTCTCAAAATAAA	265855	98051	AGCCACCACGCCCAGCCGCG
176682	8878	ACCGCGCCCAGACTGCCTGA	221269	53465	AAGACTCTGTCTCAAAATAA	265856	98052	GAGCCACCACGCCCAGCCGC
176683	8879	CACCGCGCCCAGACTGCCTG	221270	53466	TAAGACTCTGTCTCAAAATA	265857	98053	TGAGCCACCACGCCCAGCCG
176684	8880	CCACCGCGCCCAGACTGCCT	221271	53467	GTAAGACTCTGTCTCAAAAT	265858	98054	ATGAGCCACCACGCCCAGCC
176685	8881	GCCACCGCGCCCAGACTGCC	221272	53468	AGTAAGACTCTGTCTCAAAA	265859	98055	CATGAGCCACCACGCCCAGC
176686	8882	AGCCACCGCGCCCAGACTGC	221273	53469	GAGTAAGACTCTGTCTCAAA	265860	98056	GCATGAGCCACCACGCCCAG
176687	8883	GAGCCACCGCGCCCAGACTG	221274	53470	AGAGTAAGACTCTGTCTCAA	265861	98057	GGCATGAGCCACCACGCCCA
176688	8884	TGAGCCACCGCGCCCAGACT	221275	53471	CAGAGTAAGACTCTGTCTCA	265862	98058	AGGCATGAGCCACCACGCCC
176689	8885	GTGAGCCACCGCGCCCAGAC	221276	53472	ACAGAGTAAGACTCTGTCTC	265863	98059	CAGGCATGAGCCACCACGCC
176690	8886	CGTGAGCCACCGCGCCCAGA	221277	53473	GACAGAGTAAGACTCTGTCT	265864	98060	ACAGGCATGAGCCACCACGC
176691	8887	GCGTGAGCCACCGCGCCCAG	221278	53474	TGACAGAGTAAGACTCTGTC	265865	98061	TACAGGCATGAGCCACCACG
176692	8888	GGCGTGAGCCACCGCGCCCA	221279	53475	GTGACAGAGTAAGACTCTGT	265866	98062	TTACAGGCATGAGCCACCAC
176693	8889	AGGCGTGAGCCACCGCGCCC	221280	53476	GGTGACAGAGTAAGACTCTG	265867	98063	ATTACAGGCATGAGCCACCA
176694	8890	CAGGCGTGAGCCACCGCGCC	221281	53477	GGGTGACAGAGTAAGACTCT	265868	98064	GATTACAGGCATGAGCCACC
176695	8891	ACAGGCGTGAGCCACCGCGC	221282	53478	TGGGTGACAGAGTAAGACTC	265869	98065	GGATTACAGGCATGAGCCAC
176696	8892	TACAGGCGTGAGCCACCGCG	221283	53479	CTGGGTGACAGAGTAAGACT	265870	98066	GGGATTACAGGCATGAGCCA
176697	8893	TTACAGGCGTGAGCCACCGC	221284	53480	CCTGGGTGACAGAGTAAGAC	265871	98067	TGGGATTACAGGCATGAGCC
176698	8894	ATTACAGGCGTGAGCCACCG	221285	53481	GCCTGGGTGACAGAGTAAGA	265872	98068	CTGGGATTACAGGCATGAGC
176699	8895	GATTACAGGCGTGAGCCACC	221286	53482	AGCCTGGGTGACAGAGTAAG	265873	98069	GCTGGGATTACAGGCATGAG
176700	8896	GGATTACAGGCGTGAGCCAC	221287	53483	CAGCCTGGGTGACAGAGTAA	265874	98070	TGCTGGGATTACAGGCATGA
176701	8897	GGGATTACAGGCGTGAGCCA	221288	53484	CCAGCCTGGGTGACAGAGTA	265875	98071	GTGCTGGGATTACAGGCATG
176702	8898	TGGGATTACAGGCGTGAGCC	221289	53485	TCCAGCCTGGGTGACAGAGT	265876	98072	AGTGCTGGGATTACAGGCAT
176703	8899	CTGGGATTACAGGCGTGAGC	221290	53486	CTCCAGCCTGGGTGACAGAG	265877	98073	AAGTGCTGGGATTACAGGCA
176704	8900	GCTGGGATTACAGGCGTGAG	221291	53487	ACTCCAGCCTGGGTGACAGA	265878	98074	AAAGTGCTGGGATTACAGGC
176705	8901	TGCTGGGATTACAGGCGTGA	221292	53488	CACTCCAGCCTGGGTGACAG	265879	98075	CAAAGTGCTGGGATTACAGG
176706	8902	GTGCTGGGATTACAGGCGTG	221293	53489	GCACTCCAGCCTGGGTGACA	265880	98076	CCAAAGTGCTGGGATTACAG
176707	8903	AGTGCTGGGATTACAGGCGT	221294	53490	TGCACTCCAGCCTGGGTGAC	265881	98077	CCCAAAGTGCTGGGATTACA
176708	8904	AAGTGCTGGGATTACAGGCG	221295	53491	CTGCACTCCAGCCTGGGTGA	265882	98078	TCCCAAAGTGCTGGGATTAC
176709	8905	AAAGTGCTGGGATTACAGGC	221296	53492	ACTGCACTCCAGCCTGGGTG	265883	98079	CTCCCAAAGTGCTGGGATTA
176710	8906	CAAAGTGCTGGGATTACAGG	221297	53493	CACTGCACTCCAGCCTGGGT	265884	98080	CCTCCCAAAGTGCTGGGATT
176711	8907	CCAAAGTGCTGGGATTACAG	221298	53494	CCACTGCACTCCAGCCTGGG	265885	98081	GCCTCCCAAAGTGCTGGGAT
176712	8908	CCCAAAGTGCTGGGATTACA	221299	53495	ACCACTGCACTCCAGCCTGG	265886	98082	GGCCTCCCAAAGTGCTGGGA
176713	8909	TCCCAAAGTGCTGGGATTAC	221300	53496	CACCACTGCACTCCAGCCTG	265887	98083	TGGCCTCCCAAAGTGCTGGG
176714	8910	CTCCCAAAGTGCTGGGATTA	221301	53497	ACACCACTGCACTCCAGCCT	265888	98084	TTGGCCTCCCAAAGTGCTGG
176715	8911	CCTCCCAAAGTGCTGGGATT	221302	53498	CACACCACTGCACTCCAGCC	265889	98085	CTTGGCCTCCCAAAGTGCTG
176716	8912	GCCTCCCAAAGTGCTGGGAT	221303	53499	TCACACCACTGCACTCCAGC	265890	98086	CCTTGGCCTCCCAAAGTGCT
176717	8913	GGCCTCCCAAAGTGCTGGGA	221304	53500	ATCACACCACTGCACTCCAG	265891	98087	ACCTTGGCCTCCCAAAGTGC
176718	8914	CGGCCTCCCAAAGTGCTGGG	221305	53501	GATCACACCACTGCACTCCA	265892	98088	CACCTTGGCCTCCCAAAGTG
176719	8915	TCGGCCTCCCAAAGTGCTGG	221306	53502	AGATCACACCACTGCACTCC	265893	98089	CCACCTTGGCCTCCCAAAGT
176720	8916	CTCGGCCTCCCAAAGTGCTG	221307	53503	GAGATCACACCACTGCACTC	265894	98090	CCCACCTTGGCCTCCCAAAG
176721	8917	CCTCGGCCTCCCAAAGTGCT	221308	53504	CGAGATCACACCACTGCACT	265895	98091	GCCCACCTTGGCCTCCCAAA
176722	8918	GCCTCGGCCTCCCAAAGTGC	221309	53505	CCGAGATCACACCACTGCAC	265896	98092	CGCCCACCTTGGCCTCCCAA
176723	8919	CGCCTCGGCCTCCCAAAGTG	221310	53506	GCCGAGATCACACCACTGCA	265897	98093	CCGCCCACCTTGGCCTCCCA
176724	8920	CCGCCTCGGCCTCCCAAAGT	221311	53507	AGCCGAGATCACACCACTGC	265898	98094	TCCGCCCACCTTGGCCTCCC
176725	8921	CCCGCCTCGGCCTCCCAAAG	221312	53508	GAGCCGAGATCACACCACTG	265899	98095	ATCCGCCCACCTTGGCCTCC
176726	8922	GCCCGCCTCGGCCTCCCAAA	221313	53509	TGAGCCGAGATCACACCACT	265900	98096	GATCCGCCCACCTTGGCCTC
176727	8923	TGCCCGCCTCGGCCTCCCAA	221314	53510	GTGAGCCGAGATCACACCAC	265901	98097	TGATCCGCCCACCTTGGCCT
176728	8924	CTGCCCGCCTCGGCCTCCCA	221315	53511	AGTGAGCCGAGATCACACCA	265902	98098	GTGATCCGCCCACCTTGGCC
176729	8925	TCTGCCCGCCTCGGCCTCCC	221316	53512	CAGTGAGCCGAGATCACACC	265903	98099	GGTGATCCGCCCACCTTGGC
176730	8926	ATCTGCCCGCCTCGGCCTCC	221317	53513	GCAGTGAGCCGAGATCACAC	265904	98100	AGGTGATCCGCCCACCTTGG

176731	8927	GATCTGCCCGCCTCGGCCTC	221318	53514	TGCAGTGAGCCGAGATCACA	265905	98101	CAGGTGATCCGCCCACCTTG
176732	8928	TGATCTGCCCGCCTCGGCCT	221319	53515	TTGCAGTGAGCCGAGATCAC	265906	98102	TCAGGTGATCCGCCCACCTT
176733	8929	ATGATCTGCCCGCCTCGGCC	221320	53516	GTTGCAGTGAGCCGAGATCA	265907	98103	CTCAGGTGATCCGCCCACCT
176734	8930	CATGATCTGCCCGCCTCGGC	221321	53517	GGTTGCAGTGAGCCGAGATC	265908	98104	CCTCAGGTGATCCGCCCACC
176735	8931	TCATGATCTGCCCGCCTCGG	221322	53518	AGGTTGCAGTGAGCCGAGAT	265909	98105	ACCTCAGGTGATCCGCCCAC
176736	8932	CTCATGATCTGCCCGCCTCG	221323	53519	GAGGTTGCAGTGAGCCGAGA	265910	98106	GACCTCAGGTGATCCGCCCA
176737	8933	CCTCATGATCTGCCCGCCTC	221324	53520	AGAGGTTGCAGTGAGCCGAG	265911	98107	TGACCTCAGGTGATCCGCCC
176738	8934	ACCTCATGATCTGCCCGCCT	221325	53521	CAGAGGTTGCAGTGAGCCGA	265912	98108	CTGACCTCAGGTGATCCGCC
176739	8935	AACCTCATGATCTGCCCGCC	221326	53522	GCAGAGGTTGCAGTGAGCCG	265913	98109	CCTGACCTCAGGTGATCCGC
176740	8936	TAACCTCATGATCTGCCCGC	221327	53523	GGCAGAGGTTGCAGTGAGCC	265914	98110	TCCTGACCTCAGGTGATCCG
176741	8937	CTAACCTCATGATCTGCCCG	221328	53524	AGGCAGAGGTTGCAGTGAGC	265915	98111	CTCCTGACCTCAGGTGATCC
176742	8938	CCTAACCTCATGATCTGCCC	221329	53525	GAGGCAGAGGTTGCAGTGAG	265916	98112	ACTCCTGACCTCAGGTGATC
176743	8939	TCCTAACCTCATGATCTGCC	221330	53526	GGAGGCAGAGGTTGCAGTGA	265917	98113	AACTCCTGACCTCAGGTGAT
176744	8940	CTCCTAACCTCATGATCTGC	221331	53527	GGGAGGCAGAGGTTGCAGTG	265918	98114	GAACTCCTGACCTCAGGTGA
176745	8941	TCTCCTAACCTCATGATCTG	221332	53528	TGGGAGGCAGAGGTTGCAGT	265919	98115	CGAACTCCTGACCTCAGGTG
176746	8942	ATCTCCTAACCTCATGATCT	221333	53529	CTGGGAGGCAGAGGTTGCAG	265920	98116	TCGAACTCCTGACCTCAGGT
176747	8943	AATCTCCTAACCTCATGATC	221334	53530	CCTGGGAGGCAGAGGTTGCA	265921	98117	CTCGAACTCCTGACCTCAGG
176748	8944	CAATCTCCTAACCTCATGAT	221335	53531	ACCTGGGAGGCAGAGGTTGC	265922	98118	TCTCGAACTCCTGACCTCAG
176749	8945	TCAATCTCCTAACCTCATGA	221336	53532	AACCTGGGAGGCAGAGGTTG	265923	98119	GTCTCGAACTCCTGACCTCA
176750	8946	CTCAATCTCCTAACCTCATG	221337	53533	GAACCTGGGAGGCAGAGGTT	265924	98120	GGTCTCGAACTCCTGACCTC
176751	8947	TCTCAATCTCCTAACCTCAT	221338	53534	TGAACCTGGGAGGCAGAGGT	265925	98121	TGGTCTCGAACTCCTGACCT
176752	8948	GTCTCAATCTCCTAACCTCA	221339	53535	TTGAACCTGGGAGGCAGAGG	265926	98122	CTGGTCTCGAACTCCTGACC
176753	8949	GGTCTCAATCTCCTAACCTC	221340	53536	CTTGAACCTGGGAGGCAGAG	265927	98123	GCTGGTCTCGAACTCCTGAC
176754	8950	TGGTCTCAATCTCCTAACCT	221341	53537	GCTTGAACCTGGGAGGCAGA	265928	98124	AGCTGGTCTCGAACTCCTGA
176755	8951	ATGGTCTCAATCTCCTAACC	221342	53538	TGCTTGAACCTGGGAGGCAG	265929	98125	AAGCTGGTCTCGAACTCCTG
176756	8952	GATGGTCTCAATCTCCTAAC	221343	53539	ATGCTTGAACCTGGGAGGCA	265930	98126	CAAGCTGGTCTCGAACTCCT
176757	8953	GGATGGTCTCAATCTCCTAA	221344	53540	AATGCTTGAACCTGGGAGGC	265931	98127	CCAAGCTGGTCTCGAACTCC
176758	8954	AGGATGGTCTCAATCTCCTA	221345	53541	GAATGCTTGAACCTGGGAGG	265932	98128	GCCAAGCTGGTCTCGAACTC
176759	8955	CAGGATGGTCTCAATCTCCT	221346	53542	AGAATGCTTGAACCTGGGAG	265933	98129	GGCCAAGCTGGTCTCGAACT
176760	8956	CCAGGATGGTCTCAATCTCC	221347	53543	GAGAATGCTTGAACCTGGGA	265934	98130	TGGCCAAGCTGGTCTCGAAC
176761	8957	GCCAGGATGGTCTCAATCTC	221348	53544	GGAGAATGCTTGAACCTGGG	265935	98131	TTGGCCAAGCTGGTCTCGAA
176762	8958	AGCCAGGATGGTCTCAATCT	221349	53545	AGGAGAATGCTTGAACCTGG	265936	98132	GTTGGCCAAGCTGGTCTCGA
176763	8959	AAGCCAGGATGGTCTCAATC	221350	53546	CAGGAGAATGCTTGAACCTG	265937	98133	TGTTGGCCAAGCTGGTCTCG
176764	8960	AAAGCCAGGATGGTCTCAAT	221351	53547	GCAGGAGAATGCTTGAACCT	265938	98134	ATGTTGGCCAAGCTGGTCTC
176765	8961	CAAAGCCAGGATGGTCTCAA	221352	53548	GGCAGGAGAATGCTTGAACC	265939	98135	CATGTTGGCCAAGCTGGTCT
176766	8962	ACAAAGCCAGGATGGTCTCA	221353	53549	AGGCAGGAGAATGCTTGAAC	265940	98136	CCATGTTGGCCAAGCTGGTC
176767	8963	CACAAAGCCAGGATGGTCTC	221354	53550	GAGGCAGGAGAATGCTTGAA	265941	98137	GCCATGTTGGCCAAGCTGGT
176768	8964	TCACAAAGCCAGGATGGTCT	221355	53551	AGAGGCAGGAGAATGCTTGA	265942	98138	TGCCATGTTGGCCAAGCTGG
176769	8965	TTCACAAAGCCAGGATGGTC	221356	53552	CAGAGGCAGGAGAATGCTTG	265943	98139	TTGCCATGTTGGCCAAGCTG
176770	8966	TTTCACAAAGCCAGGATGGT	221357	53553	GCAGAGGCAGGAGAATGCTT	265944	98140	TTTGCCATGTTGGCCAAGCT
176771	8967	GTTTCACAAAGCCAGGATGG	221358	53554	GGCAGAGGCAGGAGAATGCT	265945	98141	TTTTGCCATGTTGGCCAAGC
176772	8968	GGTTTCACAAAGCCAGGATG	221359	53555	AGGCAGAGGCAGGAGAATGC	265946	98142	GTTTTGCCATGTTGGCCAAG
176773	8969	GGGTTTCACAAAGCCAGGAT	221360	53556	GAGGCAGAGGCAGGAGAATG	265947	98143	GGTTTTGCCATGTTGGCCAA
176774	8970	GGGGTTTCACAAAGCCAGGA	221361	53557	GGAGGCAGAGGCAGGAGAAT	265948	98144	GGGTTTTGCCATGTTGGCCA
176775	8971	CGGGGTTTCACAAAGCCAGG	221362	53558	AGGAGGCAGAGGCAGGAGAA	265949	98145	GGGGTTTTGCCATGTTGGCC
176776	8972	ACGGGGTTTCACAAAGCCAG	221363	53559	CAGGAGGCAGAGGCAGGAGA	265950	98146	CGGGGTTTTGCCATGTTGGC
176777	8973	GACGGGGTTTCACAAAGCCA	221364	53560	TCAGGAGGCAGAGGCAGGAG	265951	98147	ACGGGGTTTTGCCATGTTGG
176778	8974	AGACGGGGTTTCACAAAGCC	221365	53561	CTCAGGAGGCAGAGGCAGGA	265952	98148	GACGGGGTTTTGCCATGTTG
176779	8975	GAGACGGGGTTTCACAAAGC	221366	53562	ACTCAGGAGGCAGAGGCAGG	265953	98149	AGACGGGGTTTTGCCATGTT
176780	8976	AGAGACGGGGTTTCACAAAG	221367	53563	TACTCAGGAGGCAGAGGCAG	265954	98150	GAGACGGGGTTTTGCCATGT
176781	8977	TAGAGACGGGGTTTCACAAA	221368	53564	CTACTCAGGAGGCAGAGGCA	265955	98151	AGAGACGGGGTTTTGCCATG
176782	8978	GTAGAGACGGGGTTTCACAA	221369	53565	GCTACTCAGGAGGCAGAGGC	265956	98152	TAGAGACGGGGTTTTGCCAT
176783	8979	AGTAGAGACGGGGTTTCACA	221370	53566	AGCTACTCAGGAGGCAGAGG	265957	98153	TTAGAGACGGGGTTTTGCCA
176784	8980	TAGTAGAGACGGGGTTTCAC	221371	53567	CAGCTACTCAGGAGGCAGAG	265958	98154	ATTAGAGACGGGGTTTTGCC
176785	8981	TTAGTAGAGACGGGGTTTCA	221372	53568	CCAGCTACTCAGGAGGCAGA	265959	98155	TATTAGAGACGGGGTTTTGC
176786	8982	TTTAGTAGAGACGGGGTTTC	221373	53569	CCCAGCTACTCAGGAGGCAG	265960	98156	TTATTAGAGACGGGGTTTTG
176787	8983	TTTTAGTAGAGACGGGGTTT	221374	53570	TCCCAGCTACTCAGGAGGCA	265961	98157	TTTATTAGAGACGGGGTTTT
176788	8984	TTTTTAGTAGAGACGGGGTT	221375	53571	ATCCCAGCTACTCAGGAGGC	265962	98158	TTTTATTAGAGACGGGGTTT
176789	8985	ATTTTTAGTAGAGACGGGGT	221376	53572	AATCCCAGCTACTCAGGAGG	265963	98159	TTTTTATTAGAGACGGGGTT
176790	8986	TATTTTTAGTAGAGACGGGG	221377	53573	TAATCCCAGCTACTCAGGAG	265964	98160	ATTTTTATTAGAGACGGGGT
176791	8987	GTATTTTTAGTAGAGACGGG	221378	53574	GTAATCCCAGCTACTCAGGA	265965	98161	TATTTTTATTAGAGACGGGG
176792	8988	TGTATTTTTAGTAGAGACGG	221379	53575	TGTAATCCCAGCTACTCAGG	265966	98162	GTATTTTTATTAGAGACGGG
176793	8989	TTGTATTTTTAGTAGAGACG	221380	53576	CTGTAATCCCAGCTACTCAG	265967	98163	TGTATTTTTATTAGAGACGG
176794	8990	TTTGTATTTTTAGTAGAGAC	221381	53577	CCTGTAATCCCAGCTACTCA	265968	98164	TTGTATTTTTATTAGAGACG
176795	8991	TTTTGTATTTTTAGTAGAGA	221382	53578	ACCTGTAATCCCAGCTACTC	265969	98165	TTTGTATTTTTATTAGAGAC
176796	8992	TTTTTGTATTTTTAGTAGAG	221383	53579	CACCTGTAATCCCAGCTACT	265970	98166	TTTTGTATTTTTATTAGAGA
176797	8993	TTTTTTGTATTTTTAGTAGA	221384	53580	GCACCTGTAATCCCAGCTAC	265971	98167	ATTTTGTATTTTTATTAGAG
176798	8994	ATTTTTTGTATTTTTAGTAG	221385	53581	GGCACCTGTAATCCCAGCTA	265972	98168	TATTTTGTATTTTTATTAGA
176799	8995	AATTTTTTGTATTTTTAGTA	221386	53582	AGGCACCTGTAATCCCAGCT	265973	98169	TTATTTTGTATTTTTATTAG
176800	8996	TAATTTTTTGTATTTTTAGT	221387	53583	CAGGCACCTGTAATCCCAGC	265974	98170	ATTATTTTGTATTTTTATTA
176801	8997	CTAATTTTTTGTATTTTTAG	221388	53584	GCAGGCACCTGTAATCCCAG	265975	98171	AATTATTTTGTATTTTTATT
176802	8998	GCTAATTTTTTGTATTTTTA	221389	53585	GGCAGGCACCTGTAATCCCA	265976	98172	TAATTATTTTGTATTTTTAT

176803	8999	GGCTAATTTTTTGTATTTTT	221390	53586	TGGCAGGCACCTGTAATCCC	265977	98173	CTAATTATTTTGTATTTTTA
176804	9000	CGGCTAATTTTTTGTATTTT	221391	53587	GTGGCAGGCACCTGTAATCC	265978	98174	GCTAATTATTTTGTATTTTT
176805	9001	CCGGCTAATTTTTTGTATTT	221392	53588	GGTGGCAGGCACCTGTAATC	265979	98175	AGCTAATTATTTTGTATTTT
176806	9002	CCCGGCTAATTTTTTGTATT	221393	53589	TGGTGGCAGGCACCTGTAAT	265980	98176	CAGCTAATTATTTTGTATTT
176807	9003	GCCCGGCTAATTTTTTGTAT	221394	53590	GTGGTGGCAGGCACCTGTAA	265981	98177	CCAGCTAATTATTTTGTATT
176808	9004	CGCCCGGCTAATTTTTTGTA	221395	53591	TGTGGTGGCAGGCACCTGTA	265982	98178	CCCAGCTAATTATTTTGTAT
176809	9005	ACGCCCGGCTAATTTTTTGT	221396	53592	GTGTGGTGGCAGGCACCTGT	265983	98179	GCCCAGCTAATTATTTTGTA
176810	9006	CACGCCCGGCTAATTTTTTG	221397	53593	GGTGTGGTGGCAGGCACCTG	265984	98180	CGCCCAGCTAATTATTTTGT
176811	9007	CCACGCCCGGCTAATTTTTT	221398	53594	AGGTGTGGTGGCAGGCACCT	265985	98181	ACGCCCAGCTAATTATTTTG
176812	9008	ACCACGCCCGGCTAATTTTT	221399	53595	CAGGTGTGGTGGCAGGCACC	265986	98182	CACGCCCAGCTAATTATTTT
176813	9009	CACCACGCCCGGCTAATTTT	221400	53596	CCAGGTGTGGTGGCAGGCAC	265987	98183	CCACGCCCAGCTAATTATTT
176814	9010	CCACCACGCCCGGCTAATTT	221401	53597	GCCAGGTGTGGTGGCAGGCA	265988	98184	ACCACGCCCAGCTAATTATT
176815	9011	GCCACCACGCCCGGCTAATT	221402	53598	AGCCAGGTGTGGTGGCAGGC	265989	98185	CACCACGCCCAGCTAATTAT
176816	9012	CGCCACCACGCCCGGCTAAT	221403	53599	TAGCCAGGTGTGGTGGCAGG	265990	98186	CCACCACGCCCAGCTAATTA
176817	9013	CCGCCACCACGCCCGGCTAA	221404	53600	TTAGCCAGGTGTGGTGGCAG	265991	98187	GCCACCACGCCCAGCTAATT
176818	9014	CCCGCCACCACGCCCGGCTA	221405	53601	ATTAGCCAGGTGTGGTGGCA	265992	98188	CGCCACCACGCCCAGCTAAT
176819	9015	GCCCGCCACCACGCCCGGCT	221406	53602	AATTAGCCAGGTGTGGTGGC	265993	98189	CCGCCACCACGCCCAGCTAA
176820	9016	CGCCCGCCACCACGCCCGGC	221407	53603	AAATTAGCCAGGTGTGGTGG	265994	98190	CCCGCCACCACGCCCAGCTA
176821	9017	GCGCCCGCCACCACGCCCGG	221408	53604	AAAATTAGCCAGGTGTGGTG	265995	98191	GCCCGCCACCACGCCCAGCT
176822	9018	GGCGCCCGCCACCACGCCCG	221409	53605	AAAAATTAGCCAGGTGTGGT	265996	98192	CGCCCGCCACCACGCCCAGC
176823	9019	AGGCGCCCGCCACCACGCCC	221410	53606	CAAAAATTAGCCAGGTGTGG	265997	98193	GCGCCCGCCACCACGCCCAG
176824	9020	CAGGCGCCCGCCACCACGCC	221411	53607	ACAAAAATTAGCCAGGTGTG	265998	98194	GGCGCCCGCCACCACGCCCA
176825	9021	ACAGGCGCCCGCCACCACGC	221412	53608	TACAAAAATTAGCCAGGTGT	265999	98195	AGGCGCCCGCCACCACGCCC
176826	9022	TACAGGCGCCCGCCACCACG	221413	53609	GTACAAAAATTAGCCAGGTG	266000	98196	CAGGCGCCCGCCACCACGCC
176827	9023	CTACAGGCGCCCGCCACCAC	221414	53610	AGTACAAAAATTAGCCAGGT	266001	98197	ACAGGCGCCCGCCACCACGC
176828	9024	ACTACAGGCGCCCGCCACCA	221415	53611	AAGTACAAAAATTAGCCAGG	266002	98198	TACAGGCGCCCGCCACCACG
176829	9025	GACTACAGGCGCCCGCCACC	221416	53612	AAAGTACAAAAATTAGCCAG	266003	98199	TTACAGGCGCCCGCCACCAC
176830	9026	GGACTACAGGCGCCCGCCAC	221417	53613	AAAAGTACAAAAATTAGCCA	266004	98200	ATTACAGGCGCCCGCCACCA
176831	9027	GGGACTACAGGCGCCCGCCA	221418	53614	CAAAAGTACAAAAATTAGCC	266005	98201	GATTACAGGCGCCCGCCACC
176832	9028	TGGGACTACAGGCGCCCGCC	221419	53615	CCAAAAGTACAAAAATTAGC	266006	98202	GGATTACAGGCGCCCGCCAC
176833	9029	CTGGGACTACAGGCGCCCGC	221420	53616	ACCAAAAGTACAAAAATTAG	266007	98203	GGGATTACAGGCGCCCGCCA
176834	9030	GCTGGGACTACAGGCGCCCG	221421	53617	TACCAAAAGTACAAAAATTA	266008	98204	TGGGATTACAGGCGCCCGCC
176835	9031	AGCTGGGACTACAGGCGCCC	221422	53618	CTACCAAAAGTACAAAAATT	266009	98205	CTGGGATTACAGGCGCCCGC
176836	9032	TAGCTGGGACTACAGGCGCC	221423	53619	TCTACCAAAAGTACAAAAAT	266010	98206	GCTGGGATTACAGGCGCCCG
176837	9033	GTAGCTGGGACTACAGGCGC	221424	53620	CTCTACCAAAAGTACAAAAA	266011	98207	AGCTGGGATTACAGGCGCCC
176838	9034	AGTAGCTGGGACTACAGGCG	221425	53621	TCTCTACCAAAAGTACAAAA	266012	98208	AAGCTGGGATTACAGGCGCC
176839	9035	GAGTAGCTGGGACTACAGGC	221426	53622	GTCTCTACCAAAAGTACAAA	266013	98209	GAAGCTGGGATTACAGGCGC
176840	9036	CGAGTAGCTGGGACTACAGG	221427	53623	TGTCTCTACCAAAAGTACAA	266014	98210	AGAAGCTGGGATTACAGGCG
176841	9037	TCGAGTAGCTGGGACTACAG	221428	53624	CTGTCTCTACCAAAAGTACA	266015	98211	GAGAAGCTGGGATTACAGGC
176842	9038	CTCGAGTAGCTGGGACTACA	221429	53625	CCTGTCTCTACCAAAAGTAC	266016	98212	TGAGAAGCTGGGATTACAGG
176843	9039	TCTCGAGTAGCTGGGACTAC	221430	53626	CCCTGTCTCTACCAAAAGTA	266017	98213	CTGAGAAGCTGGGATTACAG
176844	9040	CTCTCGAGTAGCTGGGACTA	221431	53627	ACCCTGTCTCTACCAAAAGT	266018	98214	CCTGAGAAGCTGGGATTACA
176845	9041	CCTCTCGAGTAGCTGGGACT	221432	53628	AACCCTGTCTCTACCAAAAG	266019	98215	TCCTGAGAAGCTGGGATTAC
176846	9042	GCCTCTCGAGTAGCTGGGAC	221433	53629	AAACCCTGTCTCTACCAAAA	266020	98216	CTCCTGAGAAGCTGGGATTA
176847	9043	AGCCTCTCGAGTAGCTGGGA	221434	53630	GAAACCCTGTCTCTACCAAA	266021	98217	CCTCCTGAGAAGCTGGGATT
176848	9044	CAGCCTCTCGAGTAGCTGGG	221435	53631	AGAAACCCTGTCTCTACCAA	266022	98218	CCCTCCTGAGAAGCTGGGAT
176849	9045	TCAGCCTCTCGAGTAGCTGG	221436	53632	GAGAAACCCTGTCTCTACCA	266023	98219	ACCCTCCTGAGAAGCTGGGA
176850	9046	CTCAGCCTCTCGAGTAGCTG	221437	53633	TGAGAAACCCTGTCTCTACC	266024	98220	CACCCTCCTGAGAAGCTGGG
176851	9047	CCTCAGCCTCTCGAGTAGCT	221438	53634	TTGAGAAACCCTGTCTCTAC	266025	98221	TCACCCTCCTGAGAAGCTGG
176852	9048	GCCTCAGCCTCTCGAGTAGC	221439	53635	ATTGAGAAACCCTGTCTCTA	266026	98222	CTCACCCTCCTGAGAAGCTG
176853	9049	TGCCTCAGCCTCTCGAGTAG	221440	53636	CATTGAGAAACCCTGTCTCT	266027	98223	CCTCACCCTCCTGAGAAGCT
176854	9050	CTGCCTCAGCCTCTCGAGTA	221441	53637	ACATTGAGAAACCCTGTCTC	266028	98224	TCCTCACCCTCCTGAGAAGC
176855	9051	CCTGCCTCAGCCTCTCGAGT	221442	53638	AACATTGAGAAACCCTGTCT	266029	98225	TTCCTCACCCTCCTGAGAAG
176856	9052	CCCTGCCTCAGCCTCTCGAG	221443	53639	TAACATTGAGAAACCCTGTC	266030	98226	CTTCCTCACCCTCCTGAGAA
176857	9053	CCCCTGCCTCAGCCTCTCGA	221444	53640	CTAACATTGAGAAACCCTGT	266031	98227	CCTTCCTCACCCTCCTGAGA
176858	9054	TCCCCTGCCTCAGCCTCTCG	221445	53641	GCTAACATTGAGAAACCCTG	266032	98228	TCCTTCCTCACCCTCCTGAG
176859	9055	TTCCCCTGCCTCAGCCTCTC	221446	53642	GGCTAACATTGAGAAACCCT	266033	98229	CTCCTTCCTCACCCTCCTGA
176860	9056	ATTCCCCTGCCTCAGCCTCT	221447	53643	TGGCTAACATTGAGAAACCC	266034	98230	TCTCCTTCCTCACCCTCCTG
176861	9057	CATTCCCCTGCCTCAGCCTC	221448	53644	CTGGCTAACATTGAGAAACC	266035	98231	TTCTCCTTCCTCACCCTCCT
176862	9058	CCATTCCCCTGCCTCAGCCT	221449	53645	CCTGGCTAACATTGAGAAAC	266036	98232	ATTCTCCTTCCTCACCCTCC
176863	9059	GCCATTCCCCTGCCTCAGCC	221450	53646	GCCTGGCTAACATTGAGAAA	266037	98233	GATTCTCCTTCCTCACCCTC
176864	9060	CGCCATTCCCCTGCCTCAGC	221451	53647	AGCCTGGCTAACATTGAGAA	266038	98234	TGATTCTCCTTCCTCACCCT
176865	9061	ACGCCATTCCCCTGCCTCAG	221452	53648	CAGCCTGGCTAACATTGAGA	266039	98235	GTGATTCTCCTTCCTCACCC
176866	9062	CACGCCATTCCCCTGCCTCA	221453	53649	CCAGCCTGGCTAACATTGAG	266040	98236	AGTGATTCTCCTTCCTCACC
176867	9063	TCACGCCATTCCCCTGCCTC	221454	53650	ACCAGCCTGGCTAACATTGA	266041	98237	AAGTGATTCTCCTTCCTCAC
176868	9064	TTCACGCCATTCCCCTGCCT	221455	53651	GACCAGCCTGGCTAACATTG	266042	98238	CAAGTGATTCTCCTTCCTCA
176869	9065	GTTCACGCCATTCCCCTGCC	221456	53652	AGACCAGCCTGGCTAACATT	266043	98239	TCAAGTGATTCTCCTTCCTC
176870	9066	GGTTCACGCCATTCCCCTGC	221457	53653	GAGACCAGCCTGGCTAACAT	266044	98240	TTCAAGTGATTCTCCTTCCT
176871	9067	GGGTTCACGCCATTCCCCTG	221458	53654	CGAGACCAGCCTGGCTAACA	266045	98241	GTTCAAGTGATTCTCCTTCC
176872	9068	CGGGTTCACGCCATTCCCCT	221459	53655	TCGAGACCAGCCTGGCTAAC	266046	98242	GGTTCAAGTGATTCTCCTTC
176873	9069	CCGGGTTCACGCCATTCCCC	221460	53656	TTCGAGACCAGCCTGGCTAA	266047	98243	GGGTTCAAGTGATTCTCCTT
176874	9070	CCCGGGTTCACGCCATTCCC	221461	53657	GTTCGAGACCAGCCTGGCTA	266048	98244	TGGGTTCAAGTGATTCTCCT

176875	9071	TCCCGGGTTCACGCCATTCC	221462	53658	AGTTCGAGACCAGCCTGGCT	266049	98245	CTGGGTTCAAGTGATTCTCC
176876	9072	CTCCCGGGTTCACGCCATTC	221463	53659	GAGTTCGAGACCAGCCTGGC	266050	98246	CCTGGGTTCAAGTGATTCTC
176877	9073	CCTCCCGGGTTCACGCCATT	221464	53660	GGAGTTCGAGACCAGCCTGG	266051	98247	TCCTGGGTTCAAGTGATTCT
176878	9074	ACCTCCCGGGTTCACGCCAT	221465	53661	AGGAGTTCGAGACCAGCCTG	266052	98248	CTCCTGGGTTCAAGTGATTC
176879	9075	CACCTCCCGGGTTCACGCCA	221466	53662	CAGGAGTTCGAGACCAGCCT	266053	98249	CCTCCTGGGTTCAAGTGATT
176880	9076	CCACCTCCCGGGTTCACGCC	221467	53663	CCAGGAGTTCGAGACCAGCC	266054	98250	GCCTCCTGGGTTCAAGTGAT
176881	9077	TCCACCTCCCGGGTTCACGC	221468	53664	GCCAGGAGTTCGAGACCAGC	266055	98251	TGCCTCCTGGGTTCAAGTGA
176882	9078	CTCCACCTCCCGGGTTCACG	221469	53665	GGCCAGGAGTTCGAGACCAG	266056	98252	CTGCCTCCTGGGTTCAAGTG
176883	9079	CCTCCACCTCCCGGGTTCAC	221470	53666	AGGCCAGGAGTTCGAGACCA	266057	98253	TCTGCCTCCTGGGTTCAAGT
176884	9080	ACCTCCACCTCCCGGGTTCA	221471	53667	GAGGCCAGGAGTTCGAGACC	266058	98254	CTCTGCCTCCTGGGTTCAAG
176885	9081	AACCTCCACCTCCCGGGTTC	221472	53668	TGAGGCCAGGAGTTCGAGAC	266059	98255	CCTCTGCCTCCTGGGTTCAA
176886	9082	CAACCTCCACCTCCCGGGTT	221473	53669	TTGAGGCCAGGAGTTCGAGA	266060	98256	ACCTCTGCCTCCTGGGTTCA
176887	9083	GCAACCTCCACCTCCCGGGT	221474	53670	CTTGAGGCCAGGAGTTCGAG	266061	98257	AACCTCTGCCTCCTGGGTTC
176888	9084	TGCAACCTCCACCTCCCGGG	221475	53671	ACTTGAGGCCAGGAGTTCGA	266062	98258	CAACCTCTGCCTCCTGGGTT
176889	9085	CTGCAACCTCCACCTCCCGG	221476	53672	CACTTGAGGCCAGGAGTTCG	266063	98259	GCAACCTCTGCCTCCTGGGT
176890	9086	ACTGCAACCTCCACCTCCCG	221477	53673	TCACTTGAGGCCAGGAGTTC	266064	98260	TGCAACCTCTGCCTCCTGGG
176891	9087	CACTGCAACCTCCACCTCCC	221478	53674	ATCACTTGAGGCCAGGAGTT	266065	98261	CTGCAACCTCTGCCTCCTGG
176892	9088	TCACTGCAACCTCCACCTCC	221479	53675	GATCACTTGAGGCCAGGAGT	266066	98262	ACTGCAACCTCTGCCTCCTG
176893	9089	CTCACTGCAACCTCCACCTC	221480	53676	AGATCACTTGAGGCCAGGAG	266067	98263	CACTGCAACCTCTGCCTCCT
176894	9090	GCTCACTGCAACCTCCACCT	221481	53677	CAGATCACTTGAGGCCAGGA	266068	98264	TCACTGCAACCTCTGCCTCC
176895	9091	GGCTCACTGCAACCTCCACC	221482	53678	GCAGATCACTTGAGGCCAGG	266069	98265	CTCACTGCAACCTCTGCCTC
176896	9092	CGGCTCACTGCAACCTCCAC	221483	53679	GGCAGATCACTTGAGGCCAG	266070	98266	GCTCACTGCAACCTCTGCCT
176897	9093	TCGGCTCACTGCAACCTCCA	221484	53680	GGGCAGATCACTTGAGGCCA	266071	98267	AGCTCACTGCAACCTCTGCC
176898	9094	CTCGGCTCACTGCAACCTCC	221485	53681	TGGGCAGATCACTTGAGGCC	266072	98268	CAGCTCACTGCAACCTCTGC
176899	9095	TCTCGGCTCACTGCAACCTC	221486	53682	GTGGGCAGATCACTTGAGGC	266073	98269	TCAGCTCACTGCAACCTCTG
176900	9096	ATCTCGGCTCACTGCAACCT	221487	53683	GGTGGGCAGATCACTTGAGG	266074	98270	CTCAGCTCACTGCAACCTCT
176901	9097	GATCTCGGCTCACTGCAACC	221488	53684	AGGTGGGCAGATCACTTGAG	266075	98271	TCTCAGCTCACTGCAACCTC
176902	9098	CGATCTCGGCTCACTGCAAC	221489	53685	AAGGTGGGCAGATCACTTGA	266076	98272	ATCTCAGCTCACTGCAACCT
176903	9099	GCGATCTCGGCTCACTGCAA	221490	53686	CAAGGTGGGCAGATCACTTG	266077	98273	GATCTCAGCTCACTGCAACC
176904	9100	TGCGATCTCGGCTCACTGCA	221491	53687	CCAAGGTGGGCAGATCACTT	266078	98274	CGATCTCAGCTCACTGCAAC
176905	9101	GTGCGATCTCGGCTCACTGC	221492	53688	GCCAAGGTGGGCAGATCACT	266079	98275	GCGATCTCAGCTCACTGCAA
176906	9102	GGTGCGATCTCGGCTCACTG	221493	53689	GGCCAAGGTGGGCAGATCAC	266080	98276	TGCGATCTCAGCTCACTGCA
176907	9103	TGGTGCGATCTCGGCTCACT	221494	53690	AGGCCAAGGTGGGCAGATCA	266081	98277	GTGCGATCTCAGCTCACTGC
176908	9104	GTGGTGCGATCTCGGCTCAC	221495	53691	AAGGCCAAGGTGGGCAGATC	266082	98278	GGTGCGATCTCAGCTCACTG
176909	9105	AGTGGTGCGATCTCGGCTCA	221496	53692	GAAGGCCAAGGTGGGCAGAT	266083	98279	TGGTGCGATCTCAGCTCACT
176910	9106	CAGTGGTGCGATCTCGGCTC	221497	53693	GGAAGGCCAAGGTGGGCAGA	266084	98280	ATGGTGCGATCTCAGCTCAC
176911	9107	GCAGTGGTGCGATCTCGGCT	221498	53694	TGGAAGGCCAAGGTGGGCAG	266085	98281	AATGGTGCGATCTCAGCTCA
176912	9108	TGCAGTGGTGCGATCTCGGC	221499	53695	TTGGAAGGCCAAGGTGGGCA	266086	98282	CAATGGTGCGATCTCAGCTC
176913	9109	GTGCAGTGGTGCGATCTCGG	221500	53696	TTTGGAAGGCCAAGGTGGGC	266087	98283	GCAATGGTGCGATCTCAGCT
176914	9110	AGTGCAGTGGTGCGATCTCG	221501	53697	TTTTGGAAGGCCAAGGTGGG	266088	98284	TGCAATGGTGCGATCTCAGC
176915	9111	GAGTGCAGTGGTGCGATCTC	221502	53698	ATTTTGGAAGGCCAAGGTGG	266089	98285	GTGCAATGGTGCGATCTCAG
176916	9112	AGAGTGCAGTGGTGCGATCT	221503	53699	TATTTTGGAAGGCCAAGGTG	266090	98286	AGTGCAATGGTGCGATCTCA
176917	9113	TAGAGTGCAGTGGTGCGATC	221504	53700	GTATTTTGGAAGGCCAAGGT	266091	98287	GAGTGCAATGGTGCGATCTC
176918	9114	CTAGAGTGCAGTGGTGCGAT	221505	53701	AGTATTTTGGAAGGCCAAGG	266092	98288	GGAGTGCAATGGTGCGATCT
176919	9115	GCTAGAGTGCAGTGGTGCGA	221506	53702	CAGTATTTTGGAAGGCCAAG	266093	98289	TGGAGTGCAATGGTGCGATC
176920	9116	GGCTAGAGTGCAGTGGTGCG	221507	53703	CCAGTATTTTGGAAGGCCAA	266094	98290	CTGGAGTGCAATGGTGCGAT
176921	9117	AGGCTAGAGTGCAGTGGTGC	221508	53704	CCCAGTATTTTGGAAGGCCA	266095	98291	GCTGGAGTGCAATGGTGCGA
176922	9118	CAGGCTAGAGTGCAGTGGTG	221509	53705	TCCCAGTATTTTGGAAGGCC	266096	98292	GGCTGGAGTGCAATGGTGCG
176923	9119	CCAGGCTAGAGTGCAGTGGT	221510	53706	ATCCCAGTATTTTGGAAGGC	266097	98293	AGGCTGGAGTGCAATGGTGC
176924	9120	CCCAGGCTAGAGTGCAGTGG	221511	53707	AATCCCAGTATTTTGGAAGG	266098	98294	CAGGCTGGAGTGCAATGGTG
176925	9121	GCCCAGGCTAGAGTGCAGTG	221512	53708	TAATCCCAGTATTTTGGAAG	266099	98295	CCAGGCTGGAGTGCAATGGT
176926	9122	CGCCCAGGCTAGAGTGCAGT	221513	53709	TTAATCCCAGTATTTTGGAA	266100	98296	TCCAGGCTGGAGTGCAATGG
176927	9123	TCGCCCAGGCTAGAGTGCAG	221514	53710	CTTAATCCCAGTATTTTGGA	266101	98297	ATCCAGGCTGGAGTGCAATG
176928	9124	GTCGCCCAGGCTAGAGTGCA	221515	53711	CCTTAATCCCAGTATTTTGG	266102	98298	CATCCAGGCTGGAGTGCAAT
176929	9125	TGTCGCCCAGGCTAGAGTGC	221516	53712	ACCTTAATCCCAGTATTTTG	266103	98299	TCATCCAGGCTGGAGTGCAA
176930	9126	CTGTCGCCCAGGCTAGAGTG	221517	53713	TACCTTAATCCCAGTATTTT	266104	98300	GTCATCCAGGCTGGAGTGCA
176931	9127	TCTGTCGCCCAGGCTAGAGT	221518	53714	ATACCTTAATCCCAGTATTT	266105	98301	TGTCATCCAGGCTGGAGTGC
176932	9128	CTCTGTCGCCCAGGCTAGAG	221519	53715	CATACCTTAATCCCAGTATT	266106	98302	TTGTCATCCAGGCTGGAGTG
176933	9129	GCTCTGTCGCCCAGGCTAGA	221520	53716	TCATACCTTAATCCCAGTAT	266107	98303	TTTGTCATCCAGGCTGGAGT
176934	9130	AGCTCTGTCGCCCAGGCTAG	221521	53717	CTCATACCTTAATCCCAGTA	266108	98304	TTTTGTCATCCAGGCTGGAG
176935	9131	TAGCTCTGTCGCCCAGGCTA	221522	53718	GCTCATACCTTAATCCCAGT	266109	98305	CTTTTGTCATCCAGGCTGGA
176936	9132	CTAGCTCTGTCGCCCAGGCT	221523	53719	GGCTCATACCTTAATCCCAG	266110	98306	ACTTTTGTCATCCAGGCTGG
176937	9133	TCTAGCTCTGTCGCCCAGGC	221524	53720	TGGCTCATACCTTAATCCCA	266111	98307	CACTTTTGTCATCCAGGCTG
176938	9134	GTCTAGCTCTGTCGCCCAGG	221525	53721	GTGGCTCATACCTTAATCCC	266112	98308	TCACTTTTGTCATCCAGGCT
176939	9135	AGTCTAGCTCTGTCGCCCAG	221526	53722	GGTGGCTCATACCTTAATCC	266113	98309	CTCACTTTTGTCATCCAGGC
176940	9136	AAGTCTAGCTCTGTCGCCCA	221527	53723	CGGTGGCTCATACCTTAATC	266114	98310	TCTCACTTTTGTCATCCAGG
176941	9137	GAAGTCTAGCTCTGTCGCCC	221528	53724	GCGGTGGCTCATACCTTAAT	266115	98311	ATCTCACTTTTGTCATCCAG
176942	9138	AGAAGTCTAGCTCTGTCGCC	221529	53725	TGCGGTGGCTCATACCTTAA	266116	98312	AATCTCACTTTTGTCATCCA
176943	9139	AAGAAGTCTAGCTCTGTCGC	221530	53726	GTGCGGTGGCTCATACCTTA	266117	98313	GAATCTCACTTTTGTCATCC
176944	9140	GAAGAAGTCTAGCTCTGTCG	221531	53727	GGTGCGGTGGCTCATACCTT	266118	98314	GGAATCTCACTTTTGTCATC
176945	9141	AGAAGAAGTCTAGCTCTGTC	221532	53728	GGGTGCGGTGGCTCATACCT	266119	98315	AGGAATCTCACTTTTGTCAT
176946	9142	GAGAAGAAGTCTAGCTCTGT	221533	53729	TGGGTGCGGTGGCTCATACC	266120	98316	AAGGAATCTCACTTTTGTCA

176947	9143	TGAGAAGAAGTCTAGCTCTG	221534	53730	CTGGGTGCGGTGGCTCATAC	266121	98317	GAAGGAATCTCACTTTTGTC
176948	9144	TTGAGAAGAAGTCTAGCTCT	221535	53731	GCTGGGTGCGGTGGCTCATA	266122	98318	AGAAGGAATCTCACTTTTGT
176949	9145	TTTGAGAAGAAGTCTAGCTC	221536	53732	GGCTGGGTGCGGTGGCTCAT	266123	98319	GAGAAGGAATCTCACTTTTG
176950	9146	TTTTGAGAAGAAGTCTAGCT	221537	53733	GGGCTGGGTGCGGTGGCTCA	266124	98320	TGAGAAGGAATCTCACTTTT
176951	9147	TTTTTGAGAAGAAGTCTAGC	221538	53734	AGGGCTGGGTGCGGTGGCTC	266125	98321	TTGAGAAGGAATCTCACTTT
176952	9148	TTTTTTGAGAAGAAGTCTAG	221539	53735	GAGGGCTGGGTGCGGTGGCT	266126	98322	TTTGAGAAGGAATCTCACTT
176953	9149	TTTTTTTGAGAAGAAGTCTA	221540	53736	GGAGGGCTGGGTGCGGTGGC	266127	98323	TTTTGAGAAGGAATCTCACT
176954	9150	TTTTTTTTGAGAAGAAGTCT	221541	53737	AGGAGGGCTGGGTGCGGTGG	266128	98324	TTTTTGAGAAGGAATCTCAC
176955	9151	TTTTTTTTTGAGAAGAAGTC	221542	53738	CAGGAGGGCTGGGTGCGGTG	266129	98325	TTTTTTGAGAAGGAATCTCA
176956	9152	TTTTTTTTTTGAGAAGAAGT	221543	53739	CCAGGAGGGCTGGGTGCGGT	266130	98326	TTTTTTTGAGAAGGAATCTC
176957	9153	TTTTTTTTTTTGAGAAGAAG	221544	53740	CCCAGGAGGGCTGGGTGCGG	266131	98327	TTTTTTTTGAGAAGGAATCT
176958	9154	TTTTTTTTTTTTGAGAAGAA	221545	53741	GCCCAGGAGGGCTGGGTGCG	266132	98328	TTTTTTTTTGAGAAGGAATC
176959	9155	TTTTTTTTTTTTTGAGAAGA	221546	53742	AGCCCAGGAGGGCTGGGTGC	266133	98329	TTTTTTTTTTGAGAAGGAAT
176960	9156	TTTTTTTTTTTTTTGAGAAG	221547	53743	GAGCCCAGGAGGGCTGGGTG	266134	98330	TTTTTTTTTTTGAGAAGGAA
176961	9157	TTTTTTTTTTTTTTTGAGAA	221548	53744	AGAGCCCAGGAGGGCTGGGT	266135	98331	TTTTTTTTTTTTGAGAAGGA
176962	9158	TTTTTTTTTTTTTTTTGAGA	221549	53745	AAGAGCCCAGGAGGGCTGGG	266136	98332	TTTTTTTTTTTTTGAGAAGG
176963	9159	TTTTTTTTTTTTTTTTTGAG	221550	53746	AAAGAGCCCAGGAGGGCTGG	266137	98333	TTTTTTTTTTTTTTGAGAAG
176964	9160	CTTTTTTTTTTTTTTTTGA	221551	53747	AAAAGAGCCCAGGAGGGCTG	266138	98334	TTTTTTTTTTTTTTGAGAA
176965	9161	CCTTTTTTTTTTTTTTTTG	221552	53748	GAAAAGAGCCCAGGAGGGCT	266139	98335	TTTTTTTTTTTTTTTGAGA
176966	9162	TCCTTTTTTTTTTTTTTTT	221553	53749	GGAAAAGAGCCCAGGAGGGC	266140	98336	TTTTTTTTTTTTTTTTGAG
176967	9163	TTCCTTTTTTTTTTTTTTT	221554	53750	AGGAAAAGAGCCCAGGAGGG	266141	98337	TTTTTTTTTTTTTTTTTGA
176968	9164	ATTCCTTTTTTTTTTTTTT	221555	53751	AAGGAAAAGAGCCCAGGAGG	266142	98338	TTTTTTTTTTTTTTTTTTG
176969	9165	GATTCCTTTTTTTTTTTTT	221556	53752	AAAGGAAAAGAGCCCAGGAG	266143	98339	GTTTTTTTTTTTTTTTTTT
176970	9166	AGATTCCTTTTTTTTTTTT	221557	53753	TAAAGGAAAAGAGCCCAGGA	266144	98340	TGTTTTTTTTTTTTTTTTT
176971	9167	GAGATTCCTTTTTTTTTTT	221558	53754	CTAAAGGAAAAGAGCCCAGG	266145	98341	CTGTTTTTTTTTTTTTTTT
176972	9168	AGAGATTCCTTTTTTTTTT	221559	53755	ACTAAAGGAAAAGAGCCCAG	266146	98342	ACTGTTTTTTTTTTTTTTT
176973	9169	AAGAGATTCCTTTTTTTTT	221560	53756	AACTAAAGGAAAAGAGCCCA	266147	98343	GACTGTTTTTTTTTTTTTT
176974	9170	AAAGAGATTCCTTTTTTTT	221561	53757	CAACTAAAGGAAAAGAGCCC	266148	98344	CGACTGTTTTTTTTTTTTT
176975	9171	CAAAGAGATTCCTTTTTTT	221562	53758	GCAACTAAAGGAAAAGAGCC	266149	98345	ACGACTGTTTTTTTTTTTT
176976	9172	CCAAAGAGATTCCTTTTTT	221563	53759	TGCAACTAAAGGAAAAGAGC	266150	98346	GACGACTGTTTTTTTTTTT
176977	9173	ACCAAAGAGATTCCTTTTT	221564	53760	GTGCAACTAAAGGAAAAGAG	266151	98347	GGACGACTGTTTTTTTTTT
176978	9174	AACCAAAGAGATTCCTTTT	221565	53761	AGTGCAACTAAAGGAAAAGA	266152	98348	AGGACGACTGTTTTTTTTT
176979	9175	AAACCAAAGAGATTCCTTT	221566	53762	GAGTGCAACTAAAGGAAAAG	266153	98349	GAGGACGACTGTTTTTTTT
176980	9176	AAAACCAAAGAGATTCCTT	221567	53763	CGAGTGCAACTAAAGGAAAA	266154	98350	AGAGGACGACTGTTTTTTT
176981	9177	TAAAACCAAAGAGATTCCTT	221568	53764	GCGAGTGCAACTAAAGGAAA	266155	98351	AAGAGGACGACTGTTTTTT
176982	9178	ATAAAACCAAAGAGATTCCT	221569	53765	AGCGAGTGCAACTAAAGGAA	266156	98352	AAAGAGGACGACTGTTTTT
176983	9179	TATAAAACCAAAGAGATTCC	221570	53766	GAGCGAGTGCAACTAAAGGA	266157	98353	CAAAGAGGACGACTGTTTT
176984	9180	ATATAAAACCAAAGAGATTC	221571	53767	GGAGCGAGTGCAACTAAAGG	266158	98354	CCAAAGAGGACGACTGTTT
176985	9181	TATATAAAACCAAAGAGATT	221572	53768	GGGAGCGAGTGCAACTAAAG	266159	98355	CCCAAAGAGGACGACTGTT
176986	9182	ATATATAAAACCAAAGAGAT	221573	53769	GGGGAGCGAGTGCAACTAAA	266160	98356	CCCCAAAGAGGACGACTGT
176987	9183	TATATATAAAACCAAAGAGA	221574	53770	CGGGGAGCGAGTGCAACTAA	266161	98357	TCCCCAAAGAGGACGACTGT
176988	9184	ATATATATAAAACCAAAGAG	221575	53771	GCGGGGAGCGAGTGCAACTA	266162	98358	ATCCCCAAAGAGGACGACTG
176989	9185	AATATATATAAAACCAAAGA	221576	53772	AGCGGGGAGCGAGTGCAACT	266163	98359	AATCCCCAAAGAGGACGACT
176990	9186	AAATATATATAAAACCAAAG	221577	53773	GAGCGGGGAGCGAGTGCAAC	266164	98360	TAATCCCCAAAGAGGACGAC
176991	9187	AAAATATATATAAAACCAAA	221578	53774	GGAGCGGGGAGCGAGTGCAA	266165	98361	CTAATCCCCAAAGAGGACGA
176992	9188	AAAAATATATATAAAACCAA	221579	53775	AGGAGCGGGGAGCGAGTGCA	266166	98362	CCTAATCCCCAAAGAGGACG
176993	9189	AAAAAATATATATAAAACCA	221580	53776	CAGGAGCGGGGAGCGAGTGC	266167	98363	CCCTAATCCCCAAAGAGGAC
176994	9190	AAAAAAATATATATAAAACC	221581	53777	CCAGGAGCGGGGAGCGAGTG	266168	98364	TCCCTAATCCCCAAAGAGGA
176995	9191	AAAAAAAATATATATAAAAC	221582	53778	TCCAGGAGCGGGGAGCGAGT	266169	98365	GTCCCTAATCCCCAAAGAGG
176996	9192	TAAAAAAAATATATATAAAA	221583	53779	CTCCAGGAGCGGGGAGCGAG	266170	98366	TGTCCCTAATCCCCAAAGAG
176997	9193	ATAAAAAAAATATATATAAA	221584	53780	ACTCCAGGAGCGGGGAGCGA	266171	98367	CTGTCCCTAATCCCCAAAGA
176998	9194	TATAAAAAAAATATATATAA	221585	53781	TACTCCAGGAGCGGGGAGCG	266172	98368	GCTGTCCCTAATCCCCAAAG
176999	9195	ATATAAAAAAAATATATATA	221586	53782	CTACTCCAGGAGCGGGGAGC	266173	98369	GGCTGTCCCTAATCCCCAAA
177000	9196	TATATAAAAAAAATATATAT	221587	53783	TCTACTCCAGGAGCGGGGAG	266174	98370	AGGCTGTCCCTAATCCCCAA
177001	9197	ATATATAAAAAAAATATATA	221588	53784	CTCTACTCCAGGAGCGGGGA	266175	98371	CAGGCTGTCCCTAATCCCCA
177002	9198	TATATATAAAAAAAATATAT	221589	53785	CCTCTACTCCAGGAGCGGGG	266176	98372	GCAGGCTGTCCCTAATCCCC
177003	9199	ATATATATAAAAAAAATATA	221590	53786	CCCTCTACTCCAGGAGCGGG	266177	98373	GGCAGGCTGTCCCTAATCCC
177004	9200	TATATATATAAAAAAAATAT	221591	53787	TCCCTCTACTCCAGGAGCGG	266178	98374	AGGCAGGCTGTCCCTAATCC
177005	9201	TTATATATATAAAAAAAATA	221592	53788	ATCCCTCTACTCCAGGAGCG	266179	98375	CAGGCAGGCTGTCCCTAATC
177006	9202	ATTATATATATAAAAAAAAT	221593	53789	AATCCCTCTACTCCAGGAGC	266180	98376	GCAGGCAGGCTGTCCCTAAT
177007	9203	TATTATATATATAAAAAAAA	221594	53790	AAATCCCTCTACTCCAGGAG	266181	98377	GGCAGGCAGGCTGTCCCTAA
177008	9204	ATATTATATATATAAAAAAA	221595	53791	GAAATCCCTCTACTCCAGGA	266182	98378	AGGCAGGCAGGCTGTCCCTA
177009	9205	TATATTATATATATAAAAAA	221596	53792	GGAAATCCCTCTACTCCAGG	266183	98379	CAGGCAGGCAGGCTGTCCCT
177010	9206	ATATATTATATATATAAAAA	221597	53793	CGGAAATCCCTCTACTCCAG	266184	98380	GCAGGCAGGCAGGCTGTCCC
177011	9207	TATATATTATATATATAAAA	221598	53794	TCGGAAATCCCTCTACTCCA	266185	98381	GGCAGGCAGGCAGGCTGTCC
177012	9208	ATATATATTATATATATAAA	221599	53795	CTCGGAAATCCCTCTACTCC	266186	98382	GGGCAGGCAGGCAGGCTGTC
177013	9209	AATATATATTATATATATAA	221600	53796	TCTCGGAAATCCCTCTACTC	266187	98383	CGGGCAGGCAGGCAGGCTGT
177014	9210	TAATATATATTATATATATA	221601	53797	CTCTCGGAAATCCCTCTACT	266188	98384	TCGGGCAGGCAGGCAGGCTG
177015	9211	TTAATATATATTATATATAT	221602	53798	TCTCTCGGAAATCCCTCTAC	266189	98385	CTCGGGCAGGCAGGCAGGCT
177016	9212	TTTAATATATATTATATATA	221603	53799	GTCTCTCGGAAATCCCTCTA	266190	98386	GCTCGGGCAGGCAGGCAGGC
177017	9213	TTTTAATATATATTATATAT	221604	53800	AGTCTCTCGGAAATCCCTCT	266191	98387	TGCTCGGGCAGGCAGGCAGG
177018	9214	ATTTTAATATATATTATATA	221605	53801	CAGTCTCTCGGAAATCCCTC	266192	98388	GTGCTCGGGCAGGCAGGCAG

177019	9215	TATTTTAATATATATTATAT	221606	53802	ACAGTCTCTCGGAAATCCCT	266193	98389	AGTGCTCGGGCAGGCAGGCA
177020	9216	ATATTTTAATATATATTATA	221607	53803	CACAGTCTCTCGGAAATCCC	266194	98390	AAGTGCTCGGGCAGGCAGGC
177021	9217	TATATTTTAATATATATTAT	221608	53804	CCACAGTCTCTCGGAAATCC	266195	98391	GAAGTGCTCGGGCAGGCAGG
177022	9218	TTATATTTTAATATATATTA	221609	53805	CCCACAGTCTCTCGGAAATC	266196	98392	AGAAGTGCTCGGGCAGGCAG
177023	9219	ATTATATTTTAATATATATT	221610	53806	GCCCACAGTCTCTCGGAAAT	266197	98393	GAGAAGTGCTCGGGCAGGCA
177024	9220	TATTATATTTTAATATATAT	221611	53807	AGCCCACAGTCTCTCGGAAA	266198	98394	AGAGAAGTGCTCGGGCAGGC
177025	9221	ATATTATATTTTAATATATA	221612	53808	GAGCCCACAGTCTCTCGGAA	266199	98395	GAGAGAAGTGCTCGGGCAGG
177026	9222	TATATTATATTTTAATATAT	221613	53809	GGAGCCCACAGTCTCTCGGA	266200	98396	AGAGAGAAGTGCTCGGGCAG
177027	9223	ATATATTATATTTTAATATA	221614	53810	TGGAGCCCACAGTCTCTCGG	266201	98397	AAGAGAGAAGTGCTCGGGCA
177028	9224	TATATATTATATTTTAATAT	221615	53811	CTGGAGCCCACAGTCTCTCG	266202	98398	GAAGAGAGAAGTGCTCGGGC
177029	9225	ATATATATTATATTTTAATA	221616	53812	GCTGGAGCCCACAGTCTCTC	266203	98399	GGAAGAGAGAAGTGCTCGGG
177030	9226	TATATATATTATATTTTAAT	221617	53813	GGCTGGAGCCCACAGTCTCT	266204	98400	TGGAAGAGAGAAGTGCTCGG
177031	9227	ATATATATATTATATTTTAA	221618	53814	AGGCTGGAGCCCACAGTCTC	266205	98401	ATGGAAGAGAGAAGTGCTCG
177032	9228	AATATATATATTATATTTTA	221619	53815	AAGGCTGGAGCCCACAGTCT	266206	98402	AATGGAAGAGAGAAGTGCTC
177033	9229	AAATATATATATTATATTTT	221620	53816	GAAGGCTGGAGCCCACAGTC	266207	98403	CAATGGAAGAGAGAAGTGCT
177034	9230	TAAATATATATATTATATTT	221621	53817	TGAAGGCTGGAGCCCACAGT	266208	98404	GCAATGGAAGAGAGAAGTGC
177035	9231	ATAAATATATATATTATATT	221622	53818	GTGAAGGCTGGAGCCCACAG	266209	98405	GGCAATGGAAGAGAGAAGTG
177036	9232	TATAAATATATATATTATAT	221623	53819	GGTGAAGGCTGGAGCCCACA	266210	98406	GGGCAATGGAAGAGAGAAGT
177037	9233	ATATAAATATATATATTATA	221624	53820	AGGTGAAGGCTGGAGCCCAC	266211	98407	GGGGCAATGGAAGAGAGAAG
177038	9234	TATATAAATATATATATTAT	221625	53821	TAGGTGAAGGCTGGAGCCCA	266212	98408	TGGGGCAATGGAAGAGAGAA
177039	9235	TTATATAAATATATATATTA	221626	53822	CTAGGTGAAGGCTGGAGCCC	266213	98409	CTGGGGCAATGGAAGAGAGA
177040	9236	ATTATATAAATATATATATT	221627	53823	CCTAGGTGAAGGCTGGAGCC	266214	98410	ACTGGGGCAATGGAAGAGAG
177041	9237	TATTATATAAATATATATAT	221628	53824	GCCTAGGTGAAGGCTGGAGC	266215	98411	CACTGGGGCAATGGAAGAGA
177042	9238	ATATTATATAAATATATATA	221629	53825	GGCCTAGGTGAAGGCTGGAG	266216	98412	TCACTGGGGCAATGGAAGAG
177043	9239	TATATTATATAAATATATAT	221630	53826	GGGCCTAGGTGAAGGCTGGA	266217	98413	TTCACTGGGGCAATGGAAGA
177044	9240	TTATATTATATAAATATATA	221631	53827	TGGGCCTAGGTGAAGGCTGG	266218	98414	CTTCACTGGGGCAATGGAAG
177045	9241	ATTATATTATATAAATATAT	221632	53828	CTGGGCCTAGGTGAAGGCTG	266219	98415	ACTTCACTGGGGCAATGGAA
177046	9242	TATTATATTATATAAATATA	221633	53829	CCTGGGCCTAGGTGAAGGCT	266220	98416	TACTTCACTGGGGCAATGGA
177047	9243	ATATTATATTATATAAATAT	221634	53830	TCCTGGGCCTAGGTGAAGGC	266221	98417	ATACTTCACTGGGGCAATGG
177048	9244	TATATTATATTATATAAATA	221635	53831	GTCCTGGGCCTAGGTGAAGG	266222	98418	AATACTTCACTGGGGCAATG
177049	9245	ATATATTATATTATATAAAT	221636	53832	AGTCCTGGGCCTAGGTGAAG	266223	98419	GAATACTTCACTGGGGCAAT
177050	9246	TATATATTATATTATATAAA	221637	53833	TAGTCCTGGGCCTAGGTGAA	266224	98420	GGAATACTTCACTGGGGCAA
177051	9247	TTATATATTATATTATATAA	221638	53834	CTAGTCCTGGGCCTAGGTGA	266225	98421	TGGAATACTTCACTGGGGCA
177052	9248	TTTATATATTATATTATATA	221639	53835	CCTAGTCCTGGGCCTAGGTG	266226	98422	CTGGAATACTTCACTGGGGC
177053	9249	ATTTATATATTATATTATAT	221640	53836	TCCTAGTCCTGGGCCTAGGT	266227	98423	CCTGGAATACTTCACTGGGG
177054	9250	TATTTATATATTATATTATA	221641	53837	ATCCTAGTCCTGGGCCTAGG	266228	98424	GCCTGGAATACTTCACTGGG
177055	9251	ATATTTATATATTATATTAT	221642	53838	CATCCTAGTCCTGGGCCTAG	266229	98425	GGCCTGGAATACTTCACTGG
177056	9252	TATATTTATATATTATATTA	221643	53839	GCATCCTAGTCCTGGGCCTA	266230	98426	GGGCCTGGAATACTTCACTG
177057	9253	ATATATTTATATATTATATT	221644	53840	GGCATCCTAGTCCTGGGCCT	266231	98427	GGGGCCTGGAATACTTCACT
177058	9254	AATATATTTATATATTATAT	221645	53841	AGGCATCCTAGTCCTGGGCC	266232	98428	AGGGGCCTGGAATACTTCAC
177059	9255	TAATATATTTATATATTATA	221646	53842	CAGGCATCCTAGTCCTGGGC	266233	98429	CAGGGGCCTGGAATACTTCA
177060	9256	ATAATATATTTATATATTAT	221647	53843	GCAGGCATCCTAGTCCTGGG	266234	98430	CCAGGGGCCTGGAATACTTC
177061	9257	TATAATATATTTATATATTA	221648	53844	GGCAGGCATCCTAGTCCTGG	266235	98431	CCCAGGGGCCTGGAATACTT
177062	9258	ATATAATATATTTATATATT	221649	53845	GGGCAGGCATCCTAGTCCTG	266236	98432	ACCCAGGGGCCTGGAATACT
177063	9259	TATATAATATATTTATATAT	221650	53846	AGGGCAGGCATCCTAGTCCT	266237	98433	AACCCAGGGGCCTGGAATAC
177064	9260	ATATATAATATATTTATATA	221651	53847	TAGGGCAGGCATCCTAGTCC	266238	98434	AAACCCAGGGGCCTGGAATA
177065	9261	AATATATAATATATTTATAT	221652	53848	TTAGGGCAGGCATCCTAGTC	266239	98435	TAAACCCAGGGGCCTGGAAT
177066	9262	TAATATATAATATATTTATA	221653	53849	GTTAGGGCAGGCATCCTAGT	266240	98436	CTAAACCCAGGGGCCTGGAA
177067	9263	ATAATATATAATATATTTAT	221654	53850	TGTTAGGGCAGGCATCCTAG	266241	98437	TCTAAACCCAGGGGCCTGGA
177068	9264	TATAATATATAATATATTTA	221655	53851	ATGTTAGGGCAGGCATCCTA	266242	98438	GTCTAAACCCAGGGGCCTGG
177069	9265	ATATAATATATAATATATTT	221656	53852	AATGTTAGGGCAGGCATCCT	266243	98439	AGTCTAAACCCAGGGGCCTG
177070	9266	TATATAATATATAATATATT	221657	53853	AAATGTTAGGGCAGGCATCC	266244	98440	GAGTCTAAACCCAGGGGCCT
177071	9267	ATATATAATATATAATATAT	221658	53854	TAAATGTTAGGGCAGGCATC	266245	98441	AGAGTCTAAACCCAGGGGCC
177072	9268	AATATATAATATATAATATA	221659	53855	ATAAATGTTAGGGCAGGCAT	266246	98442	CAGAGTCTAAACCCAGGGGC
177073	9269	AAATATATAATATATAATAT	221660	53856	GATAAATGTTAGGGCAGGCA	266247	98443	GCAGAGTCTAAACCCAGGGG
177074	9270	AAAATATATAATATATAATA	221661	53857	AGATAAATGTTAGGGCAGGC	266248	98444	TGCAGAGTCTAAACCCAGGG
177075	9271	TAAAATATATAATATATAAT	221662	53858	AAGATAAATGTTAGGGCAGG	266249	98445	GTGCAGAGTCTAAACCCAGG
177076	9272	ATAAAATATATAATATATAA	221663	53859	AAAGATAAATGTTAGGGCAG	266250	98446	GGTGCAGAGTCTAAACCCAG
177077	9273	TATAAAATATATAATATATA	221664	53860	TAAAGATAAATGTTAGGGCA	266251	98447	TGGTGCAGAGTCTAAACCCA
177078	9274	ATATAAAATATATAATATAT	221665	53861	ATAAAGATAAATGTTAGGGC	266252	98448	ATGGTGCAGAGTCTAAACCC
177079	9275	TATATAAAATATATAATATA	221666	53862	TATAAAGATAAATGTTAGGG	266253	98449	CATGGTGCAGAGTCTAAACC
177080	9276	ATATATAAAATATATAATAT	221667	53863	GTATAAAGATAAATGTTAGG	266254	98450	ACATGGTGCAGAGTCTAAAC
177081	9277	AATATATAAAATATATAATA	221668	53864	GGTATAAAGATAAATGTTAG	266255	98451	TACATGGTGCAGAGTCTAAA
177082	9278	TAATATATAAAATATATAAT	221669	53865	AGGTATAAAGATAAATGTTA	266256	98452	CTACATGGTGCAGAGTCTAA
177083	9279	ATAATATATAAAATATATAA	221670	53866	AAGGTATAAAGATAAATGTT	266257	98453	CCTACATGGTGCAGAGTCTA
177084	9280	TATAATATATAAAATATATA	221671	53867	TAAGGTATAAAGATAAATGT	266258	98454	CCCTACATGGTGCAGAGTCT
177085	9281	ATATAATATATAAAATATAT	221672	53868	TTAAGGTATAAAGATAAATG	266259	98455	CCCCTACATGGTGCAGAGTC
177086	9282	TATATAATATATAAAATATA	221673	53869	TTTAAGGTATAAAGATAAAT	266260	98456	ACCCCTACATGGTGCAGAGT
177087	9283	ATATATAATATATAAAATAT	221674	53870	CTTTAAGGTATAAAGATAAA	266261	98457	CACCCCTACATGGTGCAGAG
177088	9284	AATATATAATATATAAAATA	221675	53871	GCTTTAAGGTATAAAGATAA	266262	98458	ACACCCCTACATGGTGCAGA
177089	9285	TAATATATAATATATAAAAT	221676	53872	TGCTTTAAGGTATAAAGATA	266263	98459	GACACCCCTACATGGTGCAG
177090	9286	ATAATATATAATATATAAAA	221677	53873	TTGCTTTAAGGTATAAAGAT	266264	98460	AGACACCCCTACATGGTGCA

177091	9287	TATAATATATAATATATAAA	221678	53874	TTTGCTTTAAGGTATAAAGA	266265	98461	CAGACACCCCTACATGGTGC
177092	9288	ATATAATATATAATATATAA	221679	53875	TTTTGCTTTAAGGTATAAAG	266266	98462	TCAGACACCCCTACATGGTG
177093	9289	TATATAATATATAATATATA	221680	53876	GTTTTGCTTTAAGGTATAAA	266267	98463	GTCAGACACCCCTACATGGT
177094	9290	ATATATAATATATAATATAT	221681	53877	TGTTTTGCTTTAAGGTATAA	266268	98464	GGTCAGACACCCCTACATGG
177095	9291	TATATATAATATATAATATA	221682	53878	CTGTTTTGCTTTAAGGTATA	266269	98465	AGGTCAGACACCCCTACATG
177096	9292	ATATATATAATATATAATAT	221683	53879	GCTGTTTTGCTTTAAGGTAT	266270	98466	CAGGTCAGACACCCCTACAT
177097	9293	AATATATATAATATATAATA	221684	53880	AGCTGTTTTGCTTTAAGGTA	266271	98467	GCAGGTCAGACACCCCTACA
177098	9294	TAATATATATAATATATAAT	221685	53881	CAGCTGTTTTGCTTTAAGGT	266272	98468	TGCAGGTCAGACACCCCTAC
177099	9295	ATAATATATATAATATATAA	221686	53882	CCAGCTGTTTTGCTTTAAGG	266273	98469	GTGCAGGTCAGACACCCCTA
177100	9296	TATAATATATATAATATATA	221687	53883	TCCAGCTGTTTTGCTTTAAG	266274	98470	AGTGCAGGTCAGACACCCCT
177101	9297	ATATAATATATATAATATAT	221688	53884	GTCCAGCTGTTTTGCTTTAA	266275	98471	AAGTGCAGGTCAGACACCCC
177102	9298	TATATAATATATATAATATA	221689	53885	GGTCCAGCTGTTTTGCTTTA	266276	98472	CAAGTGCAGGTCAGACACCC
177103	9299	ATATATAATATATATAATAT	221690	53886	TGGTCCAGCTGTTTTGCTTT	266277	98473	GCAAGTGCAGGTCAGACACC
177104	9300	AATATATAATATATATAATA	221691	53887	ATGGTCCAGCTGTTTTGCTT	266278	98474	AGCAAGTGCAGGTCAGACAC
177105	9301	TAATATATAATATATATAAT	221692	53888	TATGGTCCAGCTGTTTTGCT	266279	98475	GAGCAAGTGCAGGTCAGACA
177106	9302	ATAATATATAATATATATAA	221693	53889	TTATGGTCCAGCTGTTTTGC	266280	98476	GGAGCAAGTGCAGGTCAGAC
177107	9303	TATAATATATAATATATATA	221694	53890	CTTATGGTCCAGCTGTTTTG	266281	98477	AGGAGCAAGTGCAGGTCAGA
177108	9304	ATATAATATATAATATATAT	221695	53891	GCTTATGGTCCAGCTGTTTT	266282	98478	AAGGAGCAAGTGCAGGTCAG
177109	9305	TATATAATATATAATATATA	221696	53892	TGCTTATGGTCCAGCTGTTT	266283	98479	CAAGGAGCAAGTGCAGGTCA
177110	9306	ATATATAATATATAATATAT	221697	53893	ATGCTTATGGTCCAGCTGTT	266284	98480	CCAAGGAGCAAGTGCAGGTC
177111	9307	AATATATAATATATAATATA	221698	53894	AATGCTTATGGTCCAGCTGT	266285	98481	ACCAAGGAGCAAGTGCAGGT
177112	9308	AAATATATAATATATAATAT	221699	53895	GAATGCTTATGGTCCAGCTG	266286	98482	CACCAAGGAGCAAGTGCAGG
177113	9309	TAAATATATAATATATAATA	221700	53896	TGAATGCTTATGGTCCAGCT	266287	98483	CCACCAAGGAGCAAGTGCAG
177114	9310	ATAAATATATAATATATAAT	221701	53897	TTGAATGCTTATGGTCCAGC	266288	98484	GCCACCAAGGAGCAAGTGCA
177115	9311	TATAAATATATAATATATAA	221702	53898	CTTGAATGCTTATGGTCCAG	266289	98485	TGCCACCAAGGAGCAAGTGC
177116	9312	ATATAAATATATAATATATA	221703	53899	TCTTGAATGCTTATGGTCCA	266290	98486	GTGCCACCAAGGAGCAAGTG
177117	9313	TATATAAATATATAATATAT	221704	53900	TTCTTGAATGCTTATGGTCC	266291	98487	CGTGCCACCAAGGAGCAAGT
177118	9314	ATATATAAATATATAATATA	221705	53901	GTTCTTGAATGCTTATGGTC	266292	98488	CCGTGCCACCAAGGAGCAAG
177119	9315	AATATATAAATATATAATAT	221706	53902	TGTTCTTGAATGCTTATGGT	266293	98489	CCCGTGCCACCAAGGAGCAA
177120	9316	AAATATATAAATATATAATA	221707	53903	TTGTTCTTGAATGCTTATGG	266294	98490	GCCCGTGCCACCAAGGAGCA
177121	9317	TAAATATATAAATATATAAT	221708	53904	TTTGTTCTTGAATGCTTATG	266295	98491	TGCCCGTGCCACCAAGGAGC
177122	9318	ATAAATATATAAATATATAA	221709	53905	GTTTGTTCTTGAATGCTTAT	266296	98492	CTGCCCGTGCCACCAAGGAG
177123	9319	TATAAATATATAAATATATA	221710	53906	AGTTTGTTCTTGAATGCTTA	266297	98493	GCTGCCCGTGCCACCAAGGA
177124	9320	ATATAAATATATAAATATAT	221711	53907	CAGTTTGTTCTTGAATGCTT	266298	98494	GGCTGCCCGTGCCACCAAGG
177125	9321	TATATAAATATATAAATATA	221712	53908	ACAGTTTGTTCTTGAATGCT	266299	98495	AGGCTGCCCGTGCCACCAAG
177126	9322	ATATATAAATATATAAATAT	221713	53909	CACAGTTTGTTCTTGAATGC	266300	98496	TAGGCTGCCCGTGCCACCAA
177127	9323	AATATATAAATATATAAATA	221714	53910	TCACAGTTTGTTCTTGAATG	266301	98497	ATAGGCTGCCCGTGCCACCA
177128	9324	TAATATATAAATATATAAAT	221715	53911	TTCACAGTTTGTTCTTGAAT	266302	98498	CATAGGCTGCCCGTGCCACC
177129	9325	ATAATATATAAATATATAAA	221716	53912	ATTCACAGTTTGTTCTTGAA	266303	98499	CCATAGGCTGCCCGTGCCAC
177130	9326	TATAATATATAAATATATAA	221717	53913	TATTCACAGTTTGTTCTTGA	266304	98500	GCCATAGGCTGCCCGTGCCA
177131	9327	ATATAATATATAAATATATA	221718	53914	TTATTCACAGTTTGTTCTTG	266305	98501	TGCCATAGGCTGCCCGTGCC
177132	9328	TATATAATATATAAATATAT	221719	53915	CTTATTCACAGTTTGTTCTT	266306	98502	GTGCCATAGGCTGCCCGTGC
177133	9329	ATATATAATATATAAATATA	221720	53916	CCTTATTCACAGTTTGTTCT	266307	98503	AGTGCCATAGGCTGCCCGTG
177134	9330	TATATATAATATATAAATAT	221721	53917	TCCTTATTCACAGTTTGTTC	266308	98504	AAGTGCCATAGGCTGCCCGT
177135	9331	ATATATATAATATATAAATA	221722	53918	CTCCTTATTCACAGTTTGTT	266309	98505	CAAGTGCCATAGGCTGCCCG
177136	9332	AATATATATAATATATAAAT	221723	53919	TCTCCTTATTCACAGTTTGT	266310	98506	GCAAGTGCCATAGGCTGCCC
177137	9333	AAATATATATAATATATAAA	221724	53920	TTCTCCTTATTCACAGTTTG	266311	98507	AGCAAGTGCCATAGGCTGCC
177138	9334	TAAATATATATAATATATAA	221725	53921	TTTCTCCTTATTCACAGTTT	266312	98508	CAGCAAGTGCCATAGGCTGC
177139	9335	ATAAATATATATAATATATA	221726	53922	CTTTCTCCTTATTCACAGTT	266313	98509	GCAGCAAGTGCCATAGGCTG
177140	9336	TATAAATATATATAATATAT	221727	53923	ACTTTCTCCTTATTCACAGT	266314	98510	CGCAGCAAGTGCCATAGGCT
177141	9337	ATATAAATATATATAATATA	221728	53924	AACTTTCTCCTTATTCACAG	266315	98511	CCGCAGCAAGTGCCATAGGC
177142	9338	TATATAAATATATATAATAT	221729	53925	GAACTTTCTCCTTATTCACA	266316	98512	CCCGCAGCAAGTGCCATAGG
177143	9339	ATATATAAATATATATAATA	221730	53926	AGAACTTTCTCCTTATTCAC	266317	98513	GCCCGCAGCAAGTGCCATAG
177144	9340	AATATATAAATATATATAAT	221731	53927	GAGAACTTTCTCCTTATTCA	266318	98514	AGCCCGCAGCAAGTGCCATA
177145	9341	TAATATATAAATATATATAA	221732	53928	GGAGAACTTTCTCCTTATTC	266319	98515	CAGCCCGCAGCAAGTGCCAT
177146	9342	ATAATATATAAATATATATA	221733	53929	GGGAGAACTTTCTCCTTATT	266320	98516	ACAGCCCGCAGCAAGTGCCA
177147	9343	TATAATATATAAATATATAT	221734	53930	TGGGAGAACTTTCTCCTTAT	266321	98517	CACAGCCCGCAGCAAGTGCC
177148	9344	ATATAATATATAAATATATA	221735	53931	CTGGGAGAACTTTCTCCTTA	266322	98518	TCACAGCCCGCAGCAAGTGC
177149	9345	TATATAATATATAAATATAT	221736	53932	CCTGGGAGAACTTTCTCCTT	266323	98519	GTCACAGCCCGCAGCAAGTG
177150	9346	ATATATAATATATAAATATA	221737	53933	TCCTGGGAGAACTTTCTCCT	266324	98520	GGTCACAGCCCGCAGCAAGT
177151	9347	AATATATAATATATAAATAT	221738	53934	TTCCTGGGAGAACTTTCTCC	266325	98521	TGGTCACAGCCCGCAGCAAG
177152	9348	AAATATATAATATATAAATA	221739	53935	TTTCCTGGGAGAACTTTCTC	266326	98522	TTGGTCACAGCCCGCAGCAA
177153	9349	TAAATATATAATATATAAAT	221740	53936	GTTTCCTGGGAGAACTTTCT	266327	98523	TTTGGTCACAGCCCGCAGCA
177154	9350	ATAAATATATAATATATAAA	221741	53937	TGTTTCCTGGGAGAACTTTC	266328	98524	CTTTGGTCACAGCCCGCAGC
177155	9351	TATAAATATATAATATATAA	221742	53938	TTGTTTCCTGGGAGAACTTT	266329	98525	GCTTTGGTCACAGCCCGCAG
177156	9352	ATATAAATATATAATATATA	221743	53939	CTTGTTTCCTGGGAGAACTT	266330	98526	GGCTTTGGTCACAGCCCGCA
177157	9353	TATATAAATATATAATATAT	221744	53940	TCTTGTTTCCTGGGAGAACT	266331	98527	AGGCTTTGGTCACAGCCCGC
177158	9354	ATATATAAATATATAATATA	221745	53941	CTCTTGTTTCCTGGGAGAAC	266332	98528	CAGGCTTTGGTCACAGCCCG
177159	9355	TATATATAAATATATAATAT	221746	53942	GCTCTTGTTTCCTGGGAGAA	266333	98529	CCAGGCTTTGGTCACAGCCC
177160	9356	ATATATATAAATATATAATA	221747	53943	AGCTCTTGTTTCCTGGGAGA	266334	98530	GCCAGGCTTTGGTCACAGCC
177161	9357	AATATATATAAATATATAAT	221748	53944	AAGCTCTTGTTTCCTGGGAG	266335	98531	GGCCAGGCTTTGGTCACAGC
177162	9358	TAATATATATAAATATATAA	221749	53945	AAAGCTCTTGTTTCCTGGGA	266336	98532	AGGCCAGGCTTTGGTCACAG

177163	9359	ATAATATATATAAATATATA	221750	53946	TAAAGCTCTTGTTTCCTGGG	266337	98533	CAGGCCAGGCTTTGGTCACA
177164	9360	TATAATATATATAAATATAT	221751	53947	CTAAAGCTCTTGTTTCCTGG	266338	98534	CCAGGCCAGGCTTTGGTCAC
177165	9361	ATATAATATATATAAATATA	221752	53948	ACTAAAGCTCTTGTTTCCTG	266339	98535	TCCAGGCCAGGCTTTGGTCA
177166	9362	TATATAATATATATAAATAT	221753	53949	AACTAAAGCTCTTGTTTCCT	266340	98536	ATCCAGGCCAGGCTTTGGTC
177167	9363	ATATATAATATATATAAATA	221754	53950	GAACTAAAGCTCTTGTTTCC	266341	98537	GATCCAGGCCAGGCTTTGGT
177168	9364	AATATATAATATATATAAAT	221755	53951	AGAACTAAAGCTCTTGTTTC	266342	98538	AGATCCAGGCCAGGCTTTGG
177169	9365	AAATATATAATATATATAAA	221756	53952	CAGAACTAAAGCTCTTGTTT	266343	98539	AAGATCCAGGCCAGGCTTTG
177170	9366	TAAATATATAATATATATAA	221757	53953	ACAGAACTAAAGCTCTTGTT	266344	98540	CAAGATCCAGGCCAGGCTTT
177171	9367	ATAAATATATAATATATATA	221758	53954	AACAGAACTAAAGCTCTTGT	266345	98541	CCAAGATCCAGGCCAGGCTT
177172	9368	TATAAATATATAATATATAT	221759	53955	CAACAGAACTAAAGCTCTTG	266346	98542	TCCAAGATCCAGGCCAGGCT
177173	9369	ATATAAATATATAATATATA	221760	53956	CCAACAGAACTAAAGCTCTT	266347	98543	ATCCAAGATCCAGGCCAGGC
177174	9370	TATATAAATATATAATATAT	221761	53957	CCCAACAGAACTAAAGCTCT	266348	98544	GATCCAAGATCCAGGCCAGG
177175	9371	ATATATAAATATATAATATA	221762	53958	GCCCAACAGAACTAAAGCTC	266349	98545	AGATCCAAGATCCAGGCCAG
177176	9372	TATATATAAATATATAATAT	221763	53959	GGCCCAACAGAACTAAAGCT	266350	98546	AAGATCCAAGATCCAGGCCA
177177	9373	TTATATATAAATATATAATA	221764	53960	TGGCCCAACAGAACTAAAGC	266351	98547	CAAGATCCAAGATCCAGGCC
177178	9374	ATTATATATAAATATATAAT	221765	53961	CTGGCCCAACAGAACTAAAG	266352	98548	CCAAGATCCAAGATCCAGGC
177179	9375	TATTATATATAAATATATAA	221766	53962	GCTGGCCCAACAGAACTAAA	266353	98549	ACCAAGATCCAAGATCCAGG
177180	9376	ATATTATATATAAATATATA	221767	53963	GGCTGGCCCAACAGAACTAA	266354	98550	CACCAAGATCCAAGATCCAG
177181	9377	TATATTATATATAAATATAT	221768	53964	GGGCTGGCCCAACAGAACTA	266355	98551	TCACCAAGATCCAAGATCCA
177182	9378	ATATATTATATATAAATATA	221769	53965	AGGGCTGGCCCAACAGAACT	266356	98552	GTCACCAAGATCCAAGATCC
177183	9379	TATATATTATATATAAATAT	221770	53966	AAGGGCTGGCCCAACAGAAC	266357	98553	AGTCACCAAGATCCAAGATC
177184	9380	ATATATATTATATATAAATA	221771	53967	TAAGGGCTGGCCCAACAGAA	266358	98554	GAGTCACCAAGATCCAAGAT
177185	9381	AATATATATTATATATAAAT	221772	53968	ATAAGGGCTGGCCCAACAGA	266359	98555	AGAGTCACCAAGATCCAAGA
177186	9382	TAATATATATTATATATAAA	221773	53969	TATAAGGGCTGGCCCAACAG	266360	98556	CAGAGTCACCAAGATCCAAG
177187	9383	ATAATATATATTATATATAA	221774	53970	ATATAAGGGCTGGCCCAACA	266361	98557	GCAGAGTCACCAAGATCCAA
177188	9384	TATAATATATATTATATATA	221775	53971	AATATAAGGGCTGGCCCAAC	266362	98558	AGCAGAGTCACCAAGATCCA
177189	9385	ATATAATATATATTATATAT	221776	53972	GAATATAAGGGCTGGCCCAA	266363	98559	AAGCAGAGTCACCAAGATCC
177190	9386	TATATAATATATATTATATA	221777	53973	GGAATATAAGGGCTGGCCCA	266364	98560	GAAGCAGAGTCACCAAGATC
177191	9387	ATATATAATATATATTATAT	221778	53974	AGGAATATAAGGGCTGGCCC	266365	98561	AGAAGCAGAGTCACCAAGAT
177192	9388	AATATATAATATATATTATA	221779	53975	AAGGAATATAAGGGCTGGCC	266366	98562	GAGAAGCAGAGTCACCAAGA
177193	9389	TAATATATAATATATATTAT	221780	53976	TAAGGAATATAAGGGCTGGC	266367	98563	GGAGAAGCAGAGTCACCAAG
177194	9390	ATAATATATAATATATATTA	221781	53977	CTAAGGAATATAAGGGCTGG	266368	98564	GGGAGAAGCAGAGTCACCAA
177195	9391	TATAATATATAATATATATT	221782	53978	GCTAAGGAATATAAGGGCTG	266369	98565	AGGGAGAAGCAGAGTCACCA
177196	9392	ATATAATATATAATATATAT	221783	53979	AGCTAAGGAATATAAGGGCT	266370	98566	CAGGGAGAAGCAGAGTCACC
177197	9393	TATATAATATATAATATATA	221784	53980	CAGCTAAGGAATATAAGGGC	266371	98567	CCAGGGAGAAGCAGAGTCAC
177198	9394	ATATATAATATATAATATAT	221785	53981	ACAGCTAAGGAATATAAGGG	266372	98568	GCCAGGGAGAAGCAGAGTCA
177199	9395	AATATATAATATATAATATA	221786	53982	AACAGCTAAGGAATATAAGG	266373	98569	GGCCAGGGAGAAGCAGAGTC
177200	9396	TAATATATAATATATAATAT	221787	53983	TAACAGCTAAGGAATATAAG	266374	98570	AGGCCAGGGAGAAGCAGAGT
177201	9397	ATAATATATAATATATAATA	221788	53984	GTAACAGCTAAGGAATATAA	266375	98571	CAGGCCAGGGAGAAGCAGAG
177202	9398	TATAATATATAATATATAAT	221789	53985	GGTAACAGCTAAGGAATATA	266376	98572	TCAGGCCAGGGAGAAGCAGA
177203	9399	ATATAATATATAATATATAA	221790	53986	TGGTAACAGCTAAGGAATAT	266377	98573	CTCAGGCCAGGGAGAAGCAG
177204	9400	TATATAATATATAATATATA	221791	53987	CTGGTAACAGCTAAGGAATA	266378	98574	CCTCAGGCCAGGGAGAAGCA
177205	9401	ATATATAATATATAATATAT	221792	53988	ACTGGTAACAGCTAAGGAAT	266379	98575	CCCTCAGGCCAGGGAGAAGC
177206	9402	AATATATAATATATAATATA	221793	53989	GACTGGTAACAGCTAAGGAA	266380	98576	TCCCTCAGGCCAGGGAGAAG
177207	9403	TAATATATAATATATAATAT	221794	53990	TGACTGGTAACAGCTAAGGA	266381	98577	CTCCCTCAGGCCAGGGAGAA
177208	9404	ATAATATATAATATATAATA	221795	53991	GTGACTGGTAACAGCTAAGG	266382	98578	GCTCCCTCAGGCCAGGGAGA
177209	9405	TATAATATATAATATATAAT	221796	53992	AGTGACTGGTAACAGCTAAG	266383	98579	AGCTCCCTCAGGCCAGGGAG
177210	9406	ATATAATATATAATATATAA	221797	53993	CAGTGACTGGTAACAGCTAA	266384	98580	CAGCTCCCTCAGGCCAGGGA
177211	9407	TATATAATATATAATATATA	221798	53994	GCAGTGACTGGTAACAGCTA	266385	98581	GCAGCTCCCTCAGGCCAGGG
177212	9408	ATATATAATATATAATATAT	221799	53995	AGCAGTGACTGGTAACAGCT	266386	98582	GGCAGCTCCCTCAGGCCAGG
177213	9409	AATATATAATATATAATATA	221800	53996	AAGCAGTGACTGGTAACAGC	266387	98583	GGGCAGCTCCCTCAGGCCAG
177214	9410	TAATATATAATATATAATAT	221801	53997	CAAGCAGTGACTGGTAACAG	266388	98584	TGGGCAGCTCCCTCAGGCCA
177215	9411	ATAATATATAATATATAATA	221802	53998	TCAAGCAGTGACTGGTAACA	266389	98585	CTGGGCAGCTCCCTCAGGCC
177216	9412	TATAATATATAATATATAAT	221803	53999	ATCAAGCAGTGACTGGTAAC	266390	98586	TCTGGGCAGCTCCCTCAGGC
177217	9413	ATATAATATATAATATATAA	221804	54000	AATCAAGCAGTGACTGGTAA	266391	98587	CTCTGGGCAGCTCCCTCAGG
177218	9414	TATATAATATATAATATATA	221805	54001	AAATCAAGCAGTGACTGGTA	266392	98588	GCTCTGGGCAGCTCCCTCAG
177219	9415	ATATATAATATATAATATAT	221806	54002	TAAATCAAGCAGTGACTGGT	266393	98589	GGCTCTGGGCAGCTCCCTCA
177220	9416	AATATATAATATATAATATA	221807	54003	TTAAATCAAGCAGTGACTGG	266394	98590	AGGCTCTGGGCAGCTCCCTC
177221	9417	AAATATATAATATATAATAT	221808	54004	ATTAAATCAAGCAGTGACTG	266395	98591	CAGGCTCTGGGCAGCTCCCT
177222	9418	TAAATATATAATATATAATA	221809	54005	GATTAAATCAAGCAGTGACT	266396	98592	GCAGGCTCTGGGCAGCTCCC
177223	9419	ATAAATATATAATATATAAT	221810	54006	AGATTAAATCAAGCAGTGAC	266397	98593	GGCAGGCTCTGGGCAGCTCC
177224	9420	TATAAATATATAATATATAA	221811	54007	GAGATTAAATCAAGCAGTGA	266398	98594	GGGCAGGCTCTGGGCAGCTC
177225	9421	ATATAAATATATAATATATA	221812	54008	CGAGATTAAATCAAGCAGTG	266399	98595	TGGGCAGGCTCTGGGCAGCT
177226	9422	TATATAAATATATAATATAT	221813	54009	CCGAGATTAAATCAAGCAGT	266400	98596	GTGGGCAGGCTCTGGGCAGC
177227	9423	ATATATAAATATATAATATA	221814	54010	GCCGAGATTAAATCAAGCAG	266401	98597	GGTGGGCAGGCTCTGGGCAG
177228	9424	TATATATAAATATATAATAT	221815	54011	AGCCGAGATTAAATCAAGCA	266402	98598	TGGTGGGCAGGCTCTGGGCA
177229	9425	ATATATATAAATATATAATA	221816	54012	TAGCCGAGATTAAATCAAGC	266403	98599	GTGGTGGGCAGGCTCTGGGC
177230	9426	AATATATATAAATATATAAT	221817	54013	ATAGCCGAGATTAAATCAAG	266404	98600	GGTGGTGGGCAGGCTCTGGG
177231	9427	TAATATATATAAATATATAA	221818	54014	GATAGCCGAGATTAAATCAA	266405	98601	AGGTGGTGGGCAGGCTCTGG
177232	9428	ATAATATATATAAATATATA	221819	54015	TGATAGCCGAGATTAAATCA	266406	98602	CAGGTGGTGGGCAGGCTCTG
177233	9429	TATAATATATATAAATATAT	221820	54016	GTGATAGCCGAGATTAAATC	266407	98603	GCAGGTGGTGGGCAGGCTCT
177234	9430	ATATAATATATATAAATATA	221821	54017	AGTGATAGCCGAGATTAAAT	266408	98604	AGCAGGTGGTGGGCAGGCTC

177235	9431	TATATAATATATATAAATAT	221822	54018	AAGTGATAGCCGAGATTAAA	266409	98605	CAGCAGGTGGTGGGCAGGCT
177236	9432	ATATATAATATATATAAATA	221823	54019	CAAGTGATAGCCGAGATTAA	266410	98606	GCAGCAGGTGGTGGGCAGGC
177237	9433	AATATATAATATATATAAAT	221824	54020	CCAAGTGATAGCCGAGATTA	266411	98607	CGCAGCAGGTGGTGGGCAGG
177238	9434	TAATATATAATATATATAAA	221825	54021	GCCAAGTGATAGCCGAGATT	266412	98608	ACGCAGCAGGTGGTGGGCAG
177239	9435	ATAATATATAATATATATAA	221826	54022	GGCCAAGTGATAGCCGAGAT	266413	98609	CACGCAGCAGGTGGTGGGCA
177240	9436	TATAATATATAATATATATA	221827	54023	AGGCCAAGTGATAGCCGAGA	266414	98610	ACACGCAGCAGGTGGTGGGC
177241	9437	ATATAATATATAATATATAT	221828	54024	CAGGCCAAGTGATAGCCGAG	266415	98611	GACACGCAGCAGGTGGTGGG
177242	9438	TATATAATATATAATATATA	221829	54025	TCAGGCCAAGTGATAGCCGA	266416	98612	AGACACGCAGCAGGTGGTGG
177243	9439	ATATATAATATATAATATAT	221830	54026	GTCAGGCCAAGTGATAGCCG	266417	98613	AAGACACGCAGCAGGTGGTG
177244	9440	TATATATAATATATAATATA	221831	54027	TGTCAGGCCAAGTGATAGCC	266418	98614	AAAGACACGCAGCAGGTGGT
177245	9441	ATATATATAATATATAATAT	221832	54028	CTGTCAGGCCAAGTGATAGC	266419	98615	CAAAGACACGCAGCAGGTGG
177246	9442	AATATATATAATATATAATA	221833	54029	CCTGTCAGGCCAAGTGATAG	266420	98616	GCAAAGACACGCAGCAGGTG
177247	9443	TAATATATATAATATATAAT	221834	54030	ACCTGTCAGGCCAAGTGATA	266421	98617	CGCAAAGACACGCAGCAGGT
177248	9444	ATAATATATATAATATATAA	221835	54031	GACCTGTCAGGCCAAGTGAT	266422	98618	CCGCAAAGACACGCAGCAGG
177249	9445	TATAATATATATAATATATA	221836	54032	AGACCTGTCAGGCCAAGTGA	266423	98619	ACCGCAAAGACACGCAGCAG
177250	9446	ATATAATATATATAATATAT	221837	54033	CAGACCTGTCAGGCCAAGTG	266424	98620	CACCGCAAAGACACGCAGCA
177251	9447	TATATAATATATATAATATA	221838	54034	GCAGACCTGTCAGGCCAAGT	266425	98621	CCACCGCAAAGACACGCAGC
177252	9448	ATATATAATATATATAATAT	221839	54035	AGCAGACCTGTCAGGCCAAG	266426	98622	GCCACCGCAAAGACACGCAG
177253	9449	AATATATAATATATATAATA	221840	54036	CAGCAGACCTGTCAGGCCAA	266427	98623	TGCCACCGCAAAGACACGCA
177254	9450	TAATATATAATATATATAAT	221841	54037	GCAGCAGACCTGTCAGGCCA	266428	98624	ATGCCACCGCAAAGACACGC
177255	9451	ATAATATATAATATATATAA	221842	54038	AGCAGCAGACCTGTCAGGCC	266429	98625	AATGCCACCGCAAAGACACG
177256	9452	TATAATATATAATATATATA	221843	54039	CAGCAGCAGACCTGTCAGGC	266430	98626	AAATGCCACCGCAAAGACAC
177257	9453	ATATAATATATAATATATAT	221844	54040	CCAGCAGCAGACCTGTCAGG	266431	98627	GAAATGCCACCGCAAAGACA
177258	9454	TATATAATATATAATATATA	221845	54041	ACCAGCAGCAGACCTGTCAG	266432	98628	AGAAATGCCACCGCAAAGAC
177259	9455	ATATATAATATATAATATAT	221846	54042	CACCAGCAGCAGACCTGTCA	266433	98629	GAGAAATGCCACCGCAAAGA
177260	9456	AATATATAATATATAATATA	221847	54043	GCACCAGCAGCAGACCTGTC	266434	98630	CGAGAAATGCCACCGCAAAG
177261	9457	AAATATATAATATATAATAT	221848	54044	GGCACCAGCAGCAGACCTGT	266435	98631	GCGAGAAATGCCACCGCAAA
177262	9458	TAAATATATAATATATAATA	221849	54045	TGGCACCAGCAGCAGACCTG	266436	98632	TGCGAGAAATGCCACCGCAA
177263	9459	ATAAATATATAATATATAAT	221850	54046	CTGGCACCAGCAGCAGACCT	266437	98633	GTGCGAGAAATGCCACCGCA
177264	9460	TATAAATATATAATATATAA	221851	54047	CCTGGCACCAGCAGCAGACC	266438	98634	TGTGCGAGAAATGCCACCGC
177265	9461	ATATAAATATATAATATATA	221852	54048	TCCTGGCACCAGCAGCAGAC	266439	98635	GTGTGCGAGAAATGCCACCG
177266	9462	TATATAAATATATAATATAT	221853	54049	ATCCTGGCACCAGCAGCAGA	266440	98636	TGTGTGCGAGAAATGCCACC
177267	9463	ATATATAAATATATAATATA	221854	54050	CATCCTGGCACCAGCAGCAG	266441	98637	ATGTGTGCGAGAAATGCCAC
177268	9464	AATATATAAATATATAATAT	221855	54051	ACATCCTGGCACCAGCAGCA	266442	98638	CATGTGTGCGAGAAATGCCA
177269	9465	TAATATATAAATATATAATA	221856	54052	GACATCCTGGCACCAGCAGC	266443	98639	GCATGTGTGCGAGAAATGCC
177270	9466	ATAATATATAAATATATAAT	221857	54053	AGACATCCTGGCACCAGCAG	266444	98640	GGCATGTGTGCGAGAAATGC
177271	9467	TATAATATATAAATATATAA	221858	54054	CAGACATCCTGGCACCAGCA	266445	98641	CGGCATGTGTGCGAGAAATG
177272	9468	ATATAATATATAAATATATA	221859	54055	CCAGACATCCTGGCACCAGC	266446	98642	ACGGCATGTGTGCGAGAAAT
177273	9469	TATATAATATATAAATATAT	221860	54056	CCCAGACATCCTGGCACCAG	266447	98643	CACGGCATGTGTGCGAGAAA
177274	9470	ATATATAATATATAAATATA	221861	54057	ACCCAGACATCCTGGCACCA	266448	98644	GCACGGCATGTGTGCGAGAA
177275	9471	AATATATAATATATAAATAT	221862	54058	AACCCAGACATCCTGGCACC	266449	98645	TGCACGGCATGTGTGCGAGA
177276	9472	AAATATATAATATATAAATA	221863	54059	AAACCCAGACATCCTGGCAC	266450	98646	CTGCACGGCATGTGTGCGAG
177277	9473	TAAATATATAATATATAAAT	221864	54060	AAAACCCAGACATCCTGGCA	266451	98647	ACTGCACGGCATGTGTGCGA
177278	9474	ATAAATATATAATATATAAA	221865	54061	CAAAACCCAGACATCCTGGC	266452	98648	CACTGCACGGCATGTGTGCG
177279	9475	TATAAATATATAATATATAA	221866	54062	TCAAAACCCAGACATCCTGG	266453	98649	CCACTGCACGGCATGTGTGC
177280	9476	ATATAAATATATAATATATA	221867	54063	TTCAAAACCCAGACATCCTG	266454	98650	GCCACTGCACGGCATGTGTG
177281	9477	TATATAAATATATAATATAT	221868	54064	CTTCAAAACCCAGACATCCT	266455	98651	TGCCACTGCACGGCATGTGT
177282	9478	ATATATAAATATATAATATA	221869	54065	GCTTCAAAACCCAGACATCC	266456	98652	GTGCCACTGCACGGCATGTG
177283	9479	TATATATAAATATATAATAT	221870	54066	GGCTTCAAAACCCAGACATC	266457	98653	GGTGCCACTGCACGGCATGT
177284	9480	ATATATATAAATATATAATA	221871	54067	AGGCTTCAAAACCCAGACAT	266458	98654	GGGTGCCACTGCACGGCATG
177285	9481	AATATATATAAATATATAAT	221872	54068	CAGGCTTCAAAACCCAGACA	266459	98655	GGGGTGCCACTGCACGGCAT
177286	9482	TAATATATATAAATATATAA	221873	54069	CCAGGCTTCAAAACCCAGAC	266460	98656	GGGGGTGCCACTGCACGGCA
177287	9483	ATAATATATATAAATATATA	221874	54070	GCCAGGCTTCAAAACCCAGA	266461	98657	TGGGGGTGCCACTGCACGGC
177288	9484	TATAATATATATAAATATAT	221875	54071	AGCCAGGCTTCAAAACCCAG	266462	98658	TTGGGGGTGCCACTGCACGG
177289	9485	ATATAATATATATAAATATA	221876	54072	GAGCCAGGCTTCAAAACCCA	266463	98659	CTTGGGGGTGCCACTGCACG
177290	9486	TATATAATATATATAAATAT	221877	54073	GGAGCCAGGCTTCAAAACCC	266464	98660	CCTTGGGGGTGCCACTGCAC
177291	9487	ATATATAATATATATAAATA	221878	54074	TGGAGCCAGGCTTCAAAACC	266465	98661	TCCTTGGGGGTGCCACTGCA
177292	9488	AATATATAATATATATAAAT	221879	54075	ATGGAGCCAGGCTTCAAAAC	266466	98662	ATCCTTGGGGGTGCCACTGC
177293	9489	TAATATATAATATATATAAA	221880	54076	AATGGAGCCAGGCTTCAAAA	266467	98663	CATCCTTGGGGGTGCCACTG
177294	9490	ATAATATATAATATATATAA	221881	54077	TAATGGAGCCAGGCTTCAAA	266468	98664	CCATCCTTGGGGGTGCCACT
177295	9491	TATAATATATAATATATATA	221882	54078	GTAATGGAGCCAGGCTTCAA	266469	98665	GCCATCCTTGGGGGTGCCAC
177296	9492	ATATAATATATAATATATAT	221883	54079	TGTAATGGAGCCAGGCTTCA	266470	98666	GGCCATCCTTGGGGGTGCCA
177297	9493	TATATAATATATAATATATA	221884	54080	ATGTAATGGAGCCAGGCTTC	266471	98667	TGGCCATCCTTGGGGGTGCC
177298	9494	ATATATAATATATAATATAT	221885	54081	TATGTAATGGAGCCAGGCTT	266472	98668	ATGGCCATCCTTGGGGGTGC
177299	9495	AATATATAATATATAATATA	221886	54082	GTATGTAATGGAGCCAGGCT	266473	98669	AATGGCCATCCTTGGGGGTG
177300	9496	TAATATATAATATATAATAT	221887	54083	AGTATGTAATGGAGCCAGGC	266474	98670	GAATGGCCATCCTTGGGGGT
177301	9497	ATAATATATAATATATAATA	221888	54084	AAGTATGTAATGGAGCCAGG	266475	98671	TGAATGGCCATCCTTGGGGG
177302	9498	TATAATATATAATATATAAT	221889	54085	GAAGTATGTAATGGAGCCAG	266476	98672	GTGAATGGCCATCCTTGGGG
177303	9499	ATATAATATATAATATATAA	221890	54086	GGAAGTATGTAATGGAGCCA	266477	98673	AGTGAATGGCCATCCTTGGG
177304	9500	TATATAATATATAATATATA	221891	54087	AGGAAGTATGTAATGGAGCC	266478	98674	TAGTGAATGGCCATCCTTGG
177305	9501	ATATATAATATATAATATAT	221892	54088	CAGGAAGTATGTAATGGAGC	266479	98675	TTAGTGAATGGCCATCCTTG
177306	9502	AATATATAATATATAATATA	221893	54089	ACAGGAAGTATGTAATGGAG	266480	98676	CTTAGTGAATGGCCATCCTT

177307	9503	AAATATATAATATATAATAT	221894	54090	CACAGGAAGTATGTAATGGA	266481	98677	CCTTAGTGAATGGCCATCCT
177308	9504	TAAATATATAATATATAATA	221895	54091	ACACAGGAAGTATGTAATGG	266482	98678	GCCTTAGTGAATGGCCATCC
177309	9505	ATAAATATATAATATATAAT	221896	54092	CACACAGGAAGTATGTAATG	266483	98679	GGCCTTAGTGAATGGCCATC
177310	9506	TATAAATATATAATATATAA	221897	54093	TCACACAGGAAGTATGTAAT	266484	98680	GGGCCTTAGTGAATGGCCAT
177311	9507	ATATAAATATATAATATATA	221898	54094	GTCACACAGGAAGTATGTAA	266485	98681	TGGGCCTTAGTGAATGGCCA
177312	9508	TATATAAATATATAATATAT	221899	54095	GGTCACACAGGAAGTATGTA	266486	98682	ATGGGCCTTAGTGAATGGCC
177313	9509	ATATATAAATATATAATATA	221900	54096	AGGTCACACAGGAAGTATGT	266487	98683	AATGGGCCTTAGTGAATGGC
177314	9510	AATATATAAATATATAATAT	221901	54097	AAGGTCACACAGGAAGTATG	266488	98684	CAATGGGCCTTAGTGAATGG
177315	9511	TAATATATAAATATATAATA	221902	54098	CAAGGTCACACAGGAAGTAT	266489	98685	ACAATGGGCCTTAGTGAATG
177316	9512	ATAATATATAAATATATAAT	221903	54099	CCAAGGTCACACAGGAAGTA	266490	98686	AACAATGGGCCTTAGTGAAT
177317	9513	TATAATATATAAATATATAA	221904	54100	CCCAAGGTCACACAGGAAGT	266491	98687	AAACAATGGGCCTTAGTGAA
177318	9514	ATATAATATATAAATATATA	221905	54101	GCCCAAGGTCACACAGGAAG	266492	98688	AAAACAATGGGCCTTAGTGA
177319	9515	TATATAATATATAAATATAT	221906	54102	TGCCCAAGGTCACACAGGAA	266493	98689	AAAAACAATGGGCCTTAGTG
177320	9516	ATATATAATATATAAATATA	221907	54103	TTGCCCAAGGTCACACAGGA	266494	98690	CAAAAACAATGGGCCTTAGT
177321	9517	AATATATAATATATAAATAT	221908	54104	GTTGCCCAAGGTCACACAGG	266495	98691	ACAAAAACAATGGGCCTTAG
177322	9518	AAATATATAATATATAAATA	221909	54105	AGTTGCCCAAGGTCACACAG	266496	98692	GACAAAAACAATGGGCCTTA
177323	9519	TAAATATATAATATATAAAT	221910	54106	AAGTTGCCCAAGGTCACACA	266497	98693	AGACAAAAACAATGGGCCTT
177324	9520	ATAAATATATAATATATAAA	221911	54107	TAAGTTGCCCAAGGTCACAC	266498	98694	AAGACAAAAACAATGGGCCT
177325	9521	TATAAATATATAATATATAA	221912	54108	GTAAGTTGCCCAAGGTCACA	266499	98695	AAAGACAAAAACAATGGGCC
177326	9522	ATATAAATATATAATATATA	221913	54109	AGTAAGTTGCCCAAGGTCAC	266500	98696	AAAAGACAAAAACAATGGGC
177327	9523	TATATAAATATATAATATAT	221914	54110	GAGTAAGTTGCCCAAGGTCA	266501	98697	GAAAAGACAAAAACAATGGG
177328	9524	ATATATAAATATATAATATA	221915	54111	TGAGTAAGTTGCCCAAGGTC	266502	98698	CGAAAAGACAAAAACAATGG
177329	9525	AATATATAAATATATAATAT	221916	54112	TTGAGTAAGTTGCCCAAGGT	266503	98699	GCGAAAAGACAAAAACAATG
177330	9526	TAATATATAAATATATAATA	221917	54113	GTTGAGTAAGTTGCCCAAGG	266504	98700	AGCGAAAAGACAAAAACAAT
177331	9527	ATAATATATAAATATATAAT	221918	54114	GGTTGAGTAAGTTGCCCAAG	266505	98701	AAGCGAAAAGACAAAAACAA
177332	9528	TATAATATATAAATATATAA	221919	54115	AGGTTGAGTAAGTTGCCCAA	266506	98702	GAAGCGAAAAGACAAAAACA
177333	9529	ATATAATATATAAATATATA	221920	54116	CAGGTTGAGTAAGTTGCCCA	266507	98703	CGAAGCGAAAAGACAAAAAC
177334	9530	TATATAATATATAAATATAT	221921	54117	ACAGGTTGAGTAAGTTGCCC	266508	98704	ACGAAGCGAAAAGACAAAAA
177335	9531	ATATATAATATATAAATATA	221922	54118	GACAGGTTGAGTAAGTTGCC	266509	98705	CACGAAGCGAAAAGACAAAA
177336	9532	TATATATAATATATAAATAT	221923	54119	AGACAGGTTGAGTAAGTTGC	266510	98706	ACACGAAGCGAAAAGACAAA
177337	9533	ATATATATAATATATAAATA	221924	54120	CAGACAGGTTGAGTAAGTTG	266511	98707	AACACGAAGCGAAAAGACAA
177338	9534	AATATATATAATATATAAAT	221925	54121	ACAGACAGGTTGAGTAAGTT	266512	98708	AAACACGAAGCGAAAAGACA
177339	9535	AAATATATATAATATATAAA	221926	54122	AACAGACAGGTTGAGTAAGT	266513	98709	AAAACACGAAGCGAAAAGAC
177340	9536	TAAATATATATAATATATAA	221927	54123	GAACAGACAGGTTGAGTAAG	266514	98710	GAAAACACGAAGCGAAAAGA
177341	9537	ATAAATATATATAATATATA	221928	54124	GGAACAGACAGGTTGAGTAA	266515	98711	AGAAAACACGAAGCGAAAAG
177342	9538	TATAAATATATATAATATAT	221929	54125	AGGAACAGACAGGTTGAGTA	266516	98712	CAGAAAACACGAAGCGAAAA
177343	9539	ATATAAATATATATAATATA	221930	54126	GAGGAACAGACAGGTTGAGT	266517	98713	CCAGAAAACACGAAGCGAAA
177344	9540	TATATAAATATATATAATAT	221931	54127	TGAGGAACAGACAGGTTGAG	266518	98714	GCCAGAAAACACGAAGCGAA
177345	9541	ATATATAAATATATATAATA	221932	54128	CTGAGGAACAGACAGGTTGA	266519	98715	GGCCAGAAAACACGAAGCGA
177346	9542	TATATATAAATATATATAAT	221933	54129	ACTGAGGAACAGACAGGTTG	266520	98716	AGGCCAGAAAACACGAAGCG
177347	9543	ATATATATAAATATATATAA	221934	54130	AACTGAGGAACAGACAGGTT	266521	98717	CAGGCCAGAAAACACGAAGC
177348	9544	AATATATATAAATATATATA	221935	54131	AAACTGAGGAACAGACAGGT	266522	98718	CCAGGCCAGAAAACACGAAG
177349	9545	TAATATATATAAATATATAT	221936	54132	GAAACTGAGGAACAGACAGG	266523	98719	ACCAGGCCAGAAAACACGAA
177350	9546	ATAATATATATAAATATATA	221937	54133	GGAAACTGAGGAACAGACAG	266524	98720	CACCAGGCCAGAAAACACGA
177351	9547	TATAATATATATAAATATAT	221938	54134	GGGAAACTGAGGAACAGACA	266525	98721	ACACCAGGCCAGAAAACACG
177352	9548	ATATAATATATATAAATATA	221939	54135	GGGGAAACTGAGGAACAGAC	266526	98722	AACACCAGGCCAGAAAACAC
177353	9549	TATATAATATATATAAATAT	221940	54136	TGGGGAAACTGAGGAACAGA	266527	98723	AAACACCAGGCCAGAAAACA
177354	9550	ATATATAATATATATAAATA	221941	54137	CTGGGGAAACTGAGGAACAG	266528	98724	AAAACACCAGGCCAGAAAAC
177355	9551	AATATATAATATATATAAAT	221942	54138	GCTGGGGAAACTGAGGAACA	266529	98725	AAAAACACCAGGCCAGAAAA
177356	9552	TAATATATAATATATATAAA	221943	54139	AGCTGGGGAAACTGAGGAAC	266530	98726	GAAAAACACCAGGCCAGAAA
177357	9553	ATAATATATAATATATATAA	221944	54140	CAGCTGGGGAAACTGAGGAA	266531	98727	AGAAAAACACCAGGCCAGAA
177358	9554	TATAATATATAATATATATA	221945	54141	ACAGCTGGGGAAACTGAGGA	266532	98728	GAGAAAAACACCAGGCCAGA
177359	9555	ATATAATATATAATATATAT	221946	54142	TACAGCTGGGGAAACTGAGG	266533	98729	TGAGAAAAACACCAGGCCAG
177360	9556	TATATAATATATAATATATA	221947	54143	ATACAGCTGGGGAAACTGAG	266534	98730	ATGAGAAAAACACCAGGCCA
177361	9557	ATATATAATATATAATATAT	221948	54144	AATACAGCTGGGGAAACTGA	266535	98731	TATGAGAAAAACACCAGGCC
177362	9558	AATATATAATATATAATATA	221949	54145	TAATACAGCTGGGGAAACTG	266536	98732	ATATGAGAAAAACACCAGGC
177363	9559	TAATATATAATATATAATAT	221950	54146	ATAATACAGCTGGGGAAACT	266537	98733	TATATGAGAAAAACACCAGG
177364	9560	ATAATATATAATATATAATA	221951	54147	CATAATACAGCTGGGGAAAC	266538	98734	GTATATGAGAAAAACACCAG
177365	9561	TATAATATATAATATATAAT	221952	54148	ACATAATACAGCTGGGGAAA	266539	98735	TGTATATGAGAAAAACACCA
177366	9562	ATATAATATATAATATATAA	221953	54149	GACATAATACAGCTGGGGAA	266540	98736	ATGTATATGAGAAAAACACC
177367	9563	TATATAATATATAATATATA	221954	54150	TGACATAATACAGCTGGGGA	266541	98737	CATGTATATGAGAAAAACAC
177368	9564	ATATATAATATATAATATAT	221955	54151	CTGACATAATACAGCTGGGG	266542	98738	ACATGTATATGAGAAAAACA
177369	9565	CATATATAATATATAATATA	221956	54152	GCTGACATAATACAGCTGGG	266543	98739	CACATGTATATGAGAAAAAC
177370	9566	ACATATATAATATATAATAT	221957	54153	TGCTGACATAATACAGCTGG	266544	98740	TCACATGTATATGAGAAAAA
177371	9567	TACATATATAATATATAATA	221958	54154	ATGCTGACATAATACAGCTG	266545	98741	ATCACATGTATATGAGAAAA
177372	9568	ATACATATATAATATATAAT	221959	54155	TATGCTGACATAATACAGCT	266546	98742	GATCACATGTATATGAGAAA
177373	9569	TATACATATATAATATATAA	221960	54156	TTATGCTGACATAATACAGC	266547	98743	GGATCACATGTATATGAGAA
177374	9570	ATATACATATATAATATATA	221961	54157	ATTATGCTGACATAATACAG	266548	98744	TGGATCACATGTATATGAGA
177375	9571	TATATACATATATAATATAT	221962	54158	TATTATGCTGACATAATACA	266549	98745	CTGGATCACATGTATATGAG
177376	9572	ATATATACATATATAATATA	221963	54159	CTATTATGCTGACATAATAC	266550	98746	CCTGGATCACATGTATATGA
177377	9573	AATATATACATATATAATAT	221964	54160	ACTATTATGCTGACATAATA	266551	98747	CCCTGGATCACATGTATATG
177378	9574	TAATATATACATATATAATA	221965	54161	AACTATTATGCTGACATAAT	266552	98748	TCCCTGGATCACATGTATAT

177379	9575	ATAATATATACATATATAAT	221966	54162	AAACTATTATGCTGACATAA	266553	98749	ATCCCTGGATCACATGTATA
177380	9576	TATAATATATACATATATAA	221967	54163	CAAACTATTATGCTGACATA	266554	98750	TATCCCTGGATCACATGTAT
177381	9577	ATATAATATATACATATATA	221968	54164	ACAAACTATTATGCTGACAT	266555	98751	TTATCCCTGGATCACATGTA
177382	9578	TATATAATATATACATATAT	221969	54165	AACAAACTATTATGCTGACA	266556	98752	ATTATCCCTGGATCACATGT
177383	9579	ATATATAATATATACATATA	221970	54166	CAACAAACTATTATGCTGAC	266557	98753	AATTATCCCTGGATCACATG
177384	9580	CATATATAATATATACATAT	221971	54167	ACAACAAACTATTATGCTGA	266558	98754	GAATTATCCCTGGATCACAT
177385	9581	ACATATATAATATATACATA	221972	54168	CACAACAAACTATTATGCTG	266559	98755	GGAATTATCCCTGGATCACA
177386	9582	AACATATATAATATATACAT	221973	54169	ACACAACAAACTATTATGCT	266560	98756	GGGAATTATCCCTGGATCAC
177387	9583	TAACATATATAATATATACA	221974	54170	CACACAACAAACTATTATGC	266561	98757	TGGGAATTATCCCTGGATCA
177388	9584	ATAACATATATAATATATAC	221975	54171	TCACACAACAAACTATTATG	266562	98758	CTGGGAATTATCCCTGGATC
177389	9585	TATAACATATATAATATATA	221976	54172	TTCACACAACAAACTATTAT	266563	98759	TCTGGGAATTATCCCTGGAT
177390	9586	ATATAACATATATAATATAT	221977	54173	ATTCACACAACAAACTATTA	266564	98760	TTCTGGGAATTATCCCTGGA
177391	9587	TATATAACATATATAATATA	221978	54174	AATTCACACAACAAACTATT	266565	98761	ATTCTGGGAATTATCCCTGG
177392	9588	ATATATAACATATATAATAT	221979	54175	TAATTCACACAACAAACTAT	266566	98762	AATTCTGGGAATTATCCCTG
177393	9589	AATATATAACATATATAATA	221980	54176	TTAATTCACACAACAAACTA	266567	98763	AAATTCTGGGAATTATCCCT
177394	9590	TAATATATAACATATATAAT	221981	54177	TTTAATTCACACAACAAACT	266568	98764	AAAATTCTGGGAATTATCCC
177395	9591	ATAATATATAACATATATAA	221982	54178	ATTTAATTCACACAACAAAC	266569	98765	CAAAATTCTGGGAATTATCC
177396	9592	TATAATATATAACATATATA	221983	54179	CATTTAATTCACACAACAAA	266570	98766	TCAAAATTCTGGGAATTATC
177397	9593	ATATAATATATAACATATAT	221984	54180	TCATTTAATTCACACAACAA	266571	98767	GTCAAAATTCTGGGAATTAT
177398	9594	TATATAATATATAACATATA	221985	54181	CTCATTTAATTCACACAACA	266572	98768	TGTCAAAATTCTGGGAATTA
177399	9595	ATATATAATATATAACATAT	221986	54182	CCTCATTTAATTCACACAAC	266573	98769	CTGTCAAAATTCTGGGAATT
177400	9596	TATATATAATATATAACATA	221987	54183	ACCTCATTTAATTCACACAA	266574	98770	CCTGTCAAAATTCTGGGAAT
177401	9597	ATATATATAATATATAACAT	221988	54184	TACCTCATTTAATTCACACA	266575	98771	TCCTGTCAAAATTCTGGGAA
177402	9598	AATATATATAATATATAACA	221989	54185	TTACCTCATTTAATTCACAC	266576	98772	ATCCTGTCAAAATTCTGGGA
177403	9599	AAATATATATAATATATAAC	221990	54186	ATTACCTCATTTAATTCACA	266577	98773	AATCCTGTCAAAATTCTGGG
177404	9600	TAAATATATATAATATATAA	221991	54187	TATTACCTCATTTAATTCAC	266578	98774	AAATCCTGTCAAAATTCTGG
177405	9601	ATAAATATATATAATATATA	221992	54188	TTATTACCTCATTTAATTCA	266579	98775	AAAATCCTGTCAAAATTCTG
177406	9602	TATAAATATATATAATATAT	221993	54189	GTTATTACCTCATTTAATTC	266580	98776	TAAAATCCTGTCAAAATTCT
177407	9603	ATATAAATATATATAATATA	221994	54190	AGTTATTACCTCATTTAATT	266581	98777	TTAAAATCCTGTCAAAATTC
177408	9604	TATATAAATATATATAATAT	221995	54191	CAGTTATTACCTCATTTAAT	266582	98778	CTTAAAATCCTGTCAAAATT
177409	9605	ATATATAAATATATATAATA	221996	54192	CCAGTTATTACCTCATTTAA	266583	98779	ACTTAAAATCCTGTCAAAAT
177410	9606	TATATATAAATATATATAAT	221997	54193	TCCAGTTATTACCTCATTTA	266584	98780	TACTTAAAATCCTGTCAAAA
177411	9607	ATATATATAAATATATATAA	221998	54194	TTCCAGTTATTACCTCATTT	266585	98781	CTACTTAAAATCCTGTCAAA
177412	9608	TATATATATAAATATATATA	221999	54195	TTTCCAGTTATTACCTCATT	266586	98782	GCTACTTAAAATCCTGTCAA
177413	9609	TTATATATATAAATATATAT	222000	54196	ATTTCCAGTTATTACCTCAT	266587	98783	CGCTACTTAAAATCCTGTCA
177414	9610	ATTATATATATAAATATATA	222001	54197	CATTTCCAGTTATTACCTCA	266588	98784	ACGCTACTTAAAATCCTGTC
177415	9611	TATTATATATATAAATATAT	222002	54198	GCATTTCCAGTTATTACCTC	266589	98785	AACGCTACTTAAAATCCTGT
177416	9612	ATATTATATATATAAATATA	222003	54199	AGCATTTCCAGTTATTACCT	266590	98786	AAACGCTACTTAAAATCCTG
177417	9613	TATATTATATATATAAATAT	222004	54200	AAGCATTTCCAGTTATTACC	266591	98787	CAAACGCTACTTAAAATCCT
177418	9614	ATATATTATATATATAAATA	222005	54201	GAAGCATTTCCAGTTATTAC	266592	98788	CCAAACGCTACTTAAAATCC
177419	9615	AATATATTATATATATAAAT	222006	54202	TGAAGCATTTCCAGTTATTA	266593	98789	TCCAAACGCTACTTAAAATC
177420	9616	CAATATATTATATATATAAA	222007	54203	TTGAAGCATTTCCAGTTATT	266594	98790	ATCCAAACGCTACTTAAAAT
177421	9617	ACAATATATTATATATATAA	222008	54204	TTTGAAGCATTTCCAGTTAT	266595	98791	GATCCAAACGCTACTTAAAA
177422	9618	TACAATATATTATATATATA	222009	54205	GTTTGAAGCATTTCCAGTTA	266596	98792	GGATCCAAACGCTACTTAAA
177423	9619	ATACAATATATTATATATAT	222010	54206	TGTTTGAAGCATTTCCAGTT	266597	98793	AGGATCCAAACGCTACTTAA
177424	9620	TATACAATATATTATATATA	222011	54207	ATGTTTGAAGCATTTCCAGT	266598	98794	CAGGATCCAAACGCTACTTA
177425	9621	ATATACAATATATTATATAT	222012	54208	CATGTTTGAAGCATTTCCAG	266599	98795	GCAGGATCCAAACGCTACTT
177426	9622	TATATACAATATATTATATA	222013	54209	CCATGTTTGAAGCATTTCCA	266600	98796	AGCAGGATCCAAACGCTACT
177427	9623	ATATATACAATATATTATAT	222014	54210	ACCATGTTTGAAGCATTTCC	266601	98797	CAGCAGGATCCAAACGCTAC
177428	9624	AATATATACAATATATTATA	222015	54211	AACCATGTTTGAAGCATTTC	266602	98798	ACAGCAGGATCCAAACGCTA
177429	9625	TAATATATACAATATATTAT	222016	54212	GAACCATGTTTGAAGCATTT	266603	98799	AACAGCAGGATCCAAACGCT
177430	9626	ATAATATATACAATATATTA	222017	54213	GGAACCATGTTTGAAGCATT	266604	98800	AAACAGCAGGATCCAAACGC
177431	9627	TATAATATATACAATATATT	222018	54214	AGGAACCATGTTTGAAGCAT	266605	98801	AAAACAGCAGGATCCAAACG
177432	9628	ATATAATATATACAATATAT	222019	54215	TAGGAACCATGTTTGAAGCA	266606	98802	AAAAACAGCAGGATCCAAAC
177433	9629	TATATAATATATACAATATA	222020	54216	ATAGGAACCATGTTTGAAGC	266607	98803	AAAAAACAGCAGGATCCAAA
177434	9630	ATATATAATATATACAATAT	222021	54217	GATAGGAACCATGTTTGAAG	266608	98804	AAAAAAACAGCAGGATCCAA
177435	9631	GATATATAATATATACAATA	222022	54218	TGATAGGAACCATGTTTGAA	266609	98805	AAAAAAAACAGCAGGATCCA
177436	9632	AGATATATAATATATACAAT	222023	54219	ATGATAGGAACCATGTTTGA	266610	98806	AAAAAAAAACAGCAGGATCC
177437	9633	TAGATATATAATATATACAA	222024	54220	CATGATAGGAACCATGTTTG	266611	98807	GAAAAAAAAACAGCAGGATC
177438	9634	TTAGATATATAATATATACA	222025	54221	TCATGATAGGAACCATGTTT	266612	98808	TGAAAAAAAAACAGCAGGAT
177439	9635	ATTAGATATATAATATATAC	222026	54222	CTCATGATAGGAACCATGTT	266613	98809	GTGAAAAAAAAACAGCAGGA
177440	9636	TATTAGATATATAATATATA	222027	54223	TCTCATGATAGGAACCATGT	266614	98810	AGTGAAAAAAAAACAGCAGG
177441	9637	ATATTAGATATATAATATAT	222028	54224	TTCTCATGATAGGAACCATG	266615	98811	AAGTGAAAAAAAAACAGCAG
177442	9638	TATATTAGATATATAATATA	222029	54225	TTTCTCATGATAGGAACCAT	266616	98812	TAAGTGAAAAAAAAACAGCA
177443	9639	ATATATTAGATATATAATAT	222030	54226	ATTTCTCATGATAGGAACCA	266617	98813	TTAAGTGAAAAAAAAACAGC
177444	9640	AATATATTAGATATATAATA	222031	54227	GATTTCTCATGATAGGAACC	266618	98814	GTTAAGTGAAAAAAAAACAG
177445	9641	TAATATATTAGATATATAAT	222032	54228	GGATTTCTCATGATAGGAAC	266619	98815	TGTTAAGTGAAAAAAAAACA
177446	9642	ATAATATATTAGATATATAA	222033	54229	AGGATTTCTCATGATAGGAA	266620	98816	ATGTTAAGTGAAAAAAAAAC
177447	9643	TATAATATATTAGATATATA	222034	54230	CAGGATTTCTCATGATAGGA	266621	98817	GATGTTAAGTGAAAAAAAAA
177448	9644	ATATAATATATTAGATATAT	222035	54231	GCAGGATTTCTCATGATAGG	266622	98818	CGATGTTAAGTGAAAAAAAA
177449	9645	TATATAATATATTAGATATA	222036	54232	AGCAGGATTTCTCATGATAG	266623	98819	CCGATGTTAAGTGAAAAAAA
177450	9646	ATATATAATATATTAGATAT	222037	54233	AAGCAGGATTTCTCATGATA	266624	98820	CCCGATGTTAAGTGAAAAAA

177451	9647	TATATATAATATATTAGATA	222038	54234	AAAGCAGGATTTCTCATGAT	266625	98821	GCCCGATGTTAAGTGAAAAA
177452	9648	ATATATATAATATATTAGAT	222039	54235	GAAAGCAGGATTTCTCATGA	266626	98822	GGCCCGATGTTAAGTGAAAA
177453	9649	AATATATATAATATATTAGA	222040	54236	GGAAAGCAGGATTTCTCATG	266627	98823	TGGCCCGATGTTAAGTGAAA
177454	9650	TAATATATATAATATATTAG	222041	54237	CGGAAAGCAGGATTTCTCAT	266628	98824	CTGGCCCGATGTTAAGTGAA
177455	9651	ATAATATATATAATATATTA	222042	54238	GCGGAAAGCAGGATTTCTCA	266629	98825	ACTGGCCCGATGTTAAGTGA
177456	9652	TATAATATATATAATATATT	222043	54239	GGCGGAAAGCAGGATTTCTC	266630	98826	AACTGGCCCGATGTTAAGTG
177457	9653	ATATAATATATATAATATAT	222044	54240	AGGCGGAAAGCAGGATTTCT	266631	98827	CAACTGGCCCGATGTTAAGT
177458	9654	TATATAATATATATAATATA	222045	54241	TAGGCGGAAAGCAGGATTTC	266632	98828	TCAACTGGCCCGATGTTAAG
177459	9655	ATATATAATATATATAATAT	222046	54242	TTAGGCGGAAAGCAGGATTT	266633	98829	GTCAACTGGCCCGATGTTAA
177460	9656	TATATATAATATATATAATA	222047	54243	TTTAGGCGGAAAGCAGGATT	266634	98830	AGTCAACTGGCCCGATGTTA
177461	9657	ATATATATAATATATATAAT	222048	54244	ATTTAGGCGGAAAGCAGGAT	266635	98831	GAGTCAACTGGCCCGATGTT
177462	9658	AATATATATAATATATATAA	222049	54245	CATTTAGGCGGAAAGCAGGA	266636	98832	TGAGTCAACTGGCCCGATGT
177463	9659	TAATATATATAATATATATA	222050	54246	ACATTTAGGCGGAAAGCAGG	266637	98833	GTGAGTCAACTGGCCCGATG
177464	9660	ATAATATATATAATATATAT	222051	54247	CACATTTAGGCGGAAAGCAG	266638	98834	TGTGAGTCAACTGGCCCGAT
177465	9661	TATAATATATATAATATATA	222052	54248	GCACATTTAGGCGGAAAGCA	266639	98835	GTGTGAGTCAACTGGCCCGA
177466	9662	ATATAATATATATAATATAT	222053	54249	AGCACATTTAGGCGGAAAGC	266640	98836	AGTGTGAGTCAACTGGCCCG
177467	9663	TATATAATATATATAATATA	222054	54250	CAGCACATTTAGGCGGAAAG	266641	98837	GAGTGTGAGTCAACTGGCCC
177468	9664	ATATATAATATATATAATAT	222055	54251	CCAGCACATTTAGGCGGAAA	266642	98838	AGAGTGTGAGTCAACTGGCC
177469	9665	AATATATAATATATATAATA	222056	54252	TCCAGCACATTTAGGCGGAA	266643	98839	CAGAGTGTGAGTCAACTGGC
177470	9666	TAATATATAATATATATAAT	222057	54253	TTCCAGCACATTTAGGCGGA	266644	98840	ACAGAGTGTGAGTCAACTGG
177471	9667	ATAATATATAATATATATAA	222058	54254	TTTCCAGCACATTTAGGCGG	266645	98841	AACAGAGTGTGAGTCAACTG
177472	9668	TATAATATATAATATATATA	222059	54255	TTTTCCAGCACATTTAGGCG	266646	98842	AAACAGAGTGTGAGTCAACT
177473	9669	TTATAATATATAATATATAT	222060	54256	ATTTTCCAGCACATTTAGGC	266647	98843	AAAACAGAGTGTGAGTCAAC
177474	9670	ATTATAATATATAATATATA	222061	54257	AATTTTCCAGCACATTTAGG	266648	98844	AAAAACAGAGTGTGAGTCAA
177475	9671	TATTATAATATATAATATAT	222062	54258	GAATTTTCCAGCACATTTAG	266649	98845	AAAAAACAGAGTGTGAGTCA
177476	9672	ATATTATAATATATAATATA	222063	54259	GGAATTTTCCAGCACATTTA	266650	98846	CAAAAAACAGAGTGTGAGTC
177477	9673	TATATTATAATATATAATAT	222064	54260	AGGAATTTTCCAGCACATTT	266651	98847	ACAAAAAACAGAGTGTGAGT
177478	9674	ATATATTATAATATATAATA	222065	54261	CAGGAATTTTCCAGCACATT	266652	98848	AACAAAAAACAGAGTGTGAG
177479	9675	TATATATTATAATATATAAT	222066	54262	CCAGGAATTTTCCAGCACAT	266653	98849	CAACAAAAAACAGAGTGTGA
177480	9676	ATATATATTATAATATATAA	222067	54263	ACCAGGAATTTTCCAGCACA	266654	98850	ACAACAAAAAACAGAGTGTG
177481	9677	AATATATATTATAATATATA	222068	54264	CACCAGGAATTTTCCAGCAC	266655	98851	AACAACAAAAAACAGAGTGT
177482	9678	TAATATATATTATAATATAT	222069	54265	CCACCAGGAATTTTCCAGCA	266656	98852	CAACAACAAAAAACAGAGTG
177483	9679	ATAATATATATTATAATATA	222070	54266	ACCACCAGGAATTTTCCAGC	266657	98853	ACAACAACAAAAAACAGAGT
177484	9680	TATAATATATATTATAATAT	222071	54267	CACCACCAGGAATTTTCCAG	266658	98854	AACAACAACAAAAAACAGAG
177485	9681	ATATAATATATATTATAATA	222072	54268	GCACCACCAGGAATTTTCCA	266659	98855	AAACAACAACAAAAAACAGA
177486	9682	TATATAATATATATTATAAT	222073	54269	TGCACCACCAGGAATTTTCC	266660	98856	AAAACAACAACAAAAAACAG
177487	9683	ATATATAATATATATTATAA	222074	54270	CTGCACCACCAGGAATTTTC	266661	98857	AAAAACAACAACAAAAAACA
177488	9684	AATATATAATATATATTATA	222075	54271	TCTGCACCACCAGGAATTTT	266662	98858	AAAAAACAACAACAAAAAAC
177489	9685	TAATATATAATATATATTAT	222076	54272	TTCTGCACCACCAGGAATTT	266663	98859	AAAAAAACAACAACAAAAAA
177490	9686	ATAATATATAATATATATTA	222077	54273	GTTCTGCACCACCAGGAATT	266664	98860	CAAAAAAACAACAACAAAAA
177491	9687	TATAATATATAATATATATT	222078	54274	TGTTCTGCACCACCAGGAAT	266665	98861	TCAAAAAAACAACAACAAAA
177492	9688	ATATAATATATAATATATAT	222079	54275	CTGTTCTGCACCACCAGGAA	266666	98862	CTCAAAAAAACAACAACAAA
177493	9689	TATATAATATATAATATATA	222080	54276	CCTGTTCTGCACCACCAGGA	266667	98863	TCTCAAAAAAACAACAACAA
177494	9690	ATATATAATATATAATATAT	222081	54277	TCCTGTTCTGCACCACCAGG	266668	98864	GTCTCAAAAAAACAACAACA
177495	9691	AATATATAATATATAATATA	222082	54278	CTCCTGTTCTGCACCACCAG	266669	98865	CGTCTCAAAAAAACAACAAC
177496	9692	TAATATATAATATATAATAT	222083	54279	TCTCCTGTTCTGCACCACCA	266670	98866	CCGTCTCAAAAAAACAACAA
177497	9693	ATAATATATAATATATAATA	222084	54280	GTCTCCTGTTCTGCACCACC	266671	98867	TCCGTCTCAAAAAAACAACA
177498	9694	TATAATATATAATATATAAT	222085	54281	GGTCTCCTGTTCTGCACCAC	266672	98868	CTCCGTCTCAAAAAAACAAC
177499	9695	ATATAATATATAATATATAA	222086	54282	TGGTCTCCTGTTCTGCACCA	266673	98869	ACTCCGTCTCAAAAAAACAA
177500	9696	TATATAATATATAATATATA	222087	54283	CTGGTCTCCTGTTCTGCACC	266674	98870	GACTCCGTCTCAAAAAAACA
177501	9697	ATATATAATATATAATATAT	222088	54284	TCTGGTCTCCTGTTCTGCAC	266675	98871	AGACTCCGTCTCAAAAAAAC
177502	9698	TATATATAATATATAATATA	222089	54285	CTCTGGTCTCCTGTTCTGCA	266676	98872	GAGACTCCGTCTCAAAAAAA
177503	9699	ATATATATAATATATAATAT	222090	54286	GCTCTGGTCTCCTGTTCTGC	266677	98873	TGAGACTCCGTCTCAAAAAA
177504	9700	AATATATATAATATATAATA	222091	54287	TGCTCTGGTCTCCTGTTCTG	266678	98874	GTGAGACTCCGTCTCAAAAA
177505	9701	AAATATATATAATATATAAT	222092	54288	TTGCTCTGGTCTCCTGTTCT	266679	98875	AGTGAGACTCCGTCTCAAAA
177506	9702	AAAATATATATAATATATAA	222093	54289	TTTGCTCTGGTCTCCTGTTC	266680	98876	CAGTGAGACTCCGTCTCAAA
177507	9703	AAAAATATATATAATATATA	222094	54290	CTTTGCTCTGGTCTCCTGTT	266681	98877	ACAGTGAGACTCCGTCTCAA
177508	9704	TAAAAATATATATAATATAT	222095	54291	CCTTTGCTCTGGTCTCCTGT	266682	98878	CACAGTGAGACTCCGTCTCA
177509	9705	ATAAAAATATATATAATATA	222096	54292	TCCTTTGCTCTGGTCTCCTG	266683	98879	ACACAGTGAGACTCCGTCTC
177510	9706	TATAAAAATATATATAATAT	222097	54293	TTCCTTTGCTCTGGTCTCCT	266684	98880	GACACAGTGAGACTCCGTCT
177511	9707	ATATAAAAATATATATAATA	222098	54294	TTTCCTTTGCTCTGGTCTCC	266685	98881	TGACACAGTGAGACTCCGTC
177512	9708	TATATAAAAATATATATAAT	222099	54295	CTTTCCTTTGCTCTGGTCTC	266686	98882	GTGACACAGTGAGACTCCGT
177513	9709	ATATATAAAAATATATATAA	222100	54296	TCTTTCCTTTGCTCTGGTCT	266687	98883	GGTGACACAGTGAGACTCCG
177514	9710	TATATATAAAAATATATATA	222101	54297	GTCTTTCCTTTGCTCTGGTC	266688	98884	GGGTGACACAGTGAGACTCC
177515	9711	ATATATATAAAAATATATAT	222102	54298	TGTCTTTCCTTTGCTCTGGT	266689	98885	TGGGTGACACAGTGAGACTC
177516	9712	TATATATATAAAAATATATA	222103	54299	CTGTCTTTCCTTTGCTCTGG	266690	98886	CTGGGTGACACAGTGAGACT
177517	9713	TTATATATATAAAAATATAT	222104	54300	CCTGTCTTTCCTTTGCTCTG	266691	98887	CCTGGGTGACACAGTGAGAC
177518	9714	ATTATATATATAAAAATATA	222105	54301	CCCTGTCTTTCCTTTGCTCT	266692	98888	GCCTGGGTGACACAGTGAGA
177519	9715	TATTATATATATAAAAATAT	222106	54302	ACCCTGTCTTTCCTTTGCTC	266693	98889	AGCCTGGGTGACACAGTGAG
177520	9716	ATATTATATATATAAAAATA	222107	54303	CACCCTGTCTTTCCTTTGCT	266694	98890	CAGCCTGGGTGACACAGTGA
177521	9717	CATATTATATATATAAAAAT	222108	54304	GCACCCTGTCTTTCCTTTGC	266695	98891	TCAGCCTGGGTGACACAGTG
177522	9718	ACATATTATATATATAAAAA	222109	54305	TGCACCCTGTCTTTCCTTTG	266696	98892	TTCAGCCTGGGTGACACAGT

177523	9719	TACATATTATATATATAAAA	222110	54306	CTGCACCCTGTCTTTCCTTT	266697	98893	CTTCAGCCTGGGTGACACAG
177524	9720	ATACATATTATATATATAAA	222111	54307	TCTGCACCCTGTCTTTCCTT	266698	98894	ACTTCAGCCTGGGTGACACA
177525	9721	TATACATATTATATATATAA	222112	54308	TTCTGCACCCTGTCTTTCCT	266699	98895	CACTTCAGCCTGGGTGACAC
177526	9722	TTATACATATTATATATATA	222113	54309	CTTCTGCACCCTGTCTTTCC	266700	98896	GCACTTCAGCCTGGGTGACA
177527	9723	ATTATACATATTATATATAT	222114	54310	GCTTCTGCACCCTGTCTTTC	266701	98897	TGCACTTCAGCCTGGGTGAC
177528	9724	TATTATACATATTATATATA	222115	54311	GGCTTCTGCACCCTGTCTTT	266702	98898	CTGCACTTCAGCCTGGGTGA
177529	9725	ATATTATACATATTATATAT	222116	54312	TGGCTTCTGCACCCTGTCTT	266703	98899	ACTGCACTTCAGCCTGGGTG
177530	9726	TATATTATACATATTATATA	222117	54313	TTGGCTTCTGCACCCTGTCT	266704	98900	CACTGCACTTCAGCCTGGGT
177531	9727	ATATATTATACATATTATAT	222118	54314	TTTGGCTTCTGCACCCTGTC	266705	98901	CCACTGCACTTCAGCCTGGG
177532	9728	TATATATTATACATATTATA	222119	54315	TTTTGGCTTCTGCACCCTGT	266706	98902	GCCACTGCACTTCAGCCTGG
177533	9729	TTATATATTATACATATTAT	222120	54316	TTTTTGGCTTCTGCACCCTG	266707	98903	TGCCACTGCACTTCAGCCTG
177534	9730	ATTATATATTATACATATTA	222121	54317	ATTTTTGGCTTCTGCACCCT	266708	98904	GTGCCACTGCACTTCAGCCT
177535	9731	TATTATATATTATACATATT	222122	54318	AATTTTTGGCTTCTGCACCC	266709	98905	TGTGCCACTGCACTTCAGCC
177536	9732	ATATTATATATTATACATAT	222123	54319	TAATTTTTGGCTTCTGCACC	266710	98906	TTGTGCCACTGCACTTCAGC
177537	9733	TATATTATATATTATACATA	222124	54320	GTAATTTTTGGCTTCTGCAC	266711	98907	ATTGTGCCACTGCACTTCAG
177538	9734	ATATATTATATATTATACAT	222125	54321	GGTAATTTTTGGCTTCTGCA	266712	98908	GATTGTGCCACTGCACTTCA
177539	9735	TATATATTATATATTATACA	222126	54322	AGGTAATTTTTGGCTTCTGC	266713	98909	AGATTGTGCCACTGCACTTC
177540	9736	ATATATATTATATATTATAC	222127	54323	AAGGTAATTTTTGGCTTCTG	266714	98910	AAGATTGTGCCACTGCACTT
177541	9737	TATATATATTATATATTATA	222128	54324	CAAGGTAATTTTTGGCTTCT	266715	98911	CAAGATTGTGCCACTGCACT
177542	9738	TTATATATATTATATATTAT	222129	54325	CCAAGGTAATTTTTGGCTTC	266716	98912	CCAAGATTGTGCCACTGCAC
177543	9739	TTTATATATATTATATATTA	222130	54326	TCCAAGGTAATTTTTGGCTT	266717	98913	GCCAAGATTGTGCCACTGCA
177544	9740	TTTTATATATATTATATATT	222131	54327	CTCCAAGGTAATTTTTGGCT	266718	98914	TGCCAAGATTGTGCCACTGC
177545	9741	TTTTTATATATATTATATAT	222132	54328	TCTCCAAGGTAATTTTTGGC	266719	98915	ATGCCAAGATTGTGCCACTG
177546	9742	GTTTTTATATATATTATATA	222133	54329	TTCTCCAAGGTAATTTTTGG	266720	98916	TATGCCAAGATTGTGCCACT
177547	9743	TGTTTTTATATATATTATAT	222134	54330	GTTCTCCAAGGTAATTTTTG	266721	98917	GTATGCCAAGATTGTGCCAC
177548	9744	ATGTTTTTATATATATTATA	222135	54331	TGTTCTCCAAGGTAATTTTT	266722	98918	AGTATGCCAAGATTGTGCCA
177549	9745	TATGTTTTTATATATATTAT	222136	54332	TTGTTCTCCAAGGTAATTTT	266723	98919	CAGTATGCCAAGATTGTGCC
177550	9746	ATATGTTTTTATATATATTA	222137	54333	TTTGTTCTCCAAGGTAATTT	266724	98920	GCAGTATGCCAAGATTGTGC
177551	9747	TATATGTTTTTATATATATT	222138	54334	CTTTGTTCTCCAAGGTAATT	266725	98921	TGCAGTATGCCAAGATTGTG
177552	9748	ATATATGTTTTTATATATAT	222139	54335	GCTTTGTTCTCCAAGGTAAT	266726	98922	TTGCAGTATGCCAAGATTGT
177553	9749	TATATATGTTTTTATATATA	222140	54336	CGCTTTGTTCTCCAAGGTAA	266727	98923	GTTGCAGTATGCCAAGATTG
177554	9750	TTATATATGTTTTTATATAT	222141	54337	GCGCTTTGTTCTCCAAGGTA	266728	98924	GGTTGCAGTATGCCAAGATT
177555	9751	ATTATATATGTTTTTATATA	222142	54338	TGCGCTTTGTTCTCCAAGGT	266729	98925	AGGTTGCAGTATGCCAAGAT
177556	9752	TATTATATATGTTTTTATAT	222143	54339	ATGCGCTTTGTTCTCCAAGG	266730	98926	GAGGTTGCAGTATGCCAAGA
177557	9753	ATATTATATATGTTTTTATA	222144	54340	CATGCGCTTTGTTCTCCAAG	266731	98927	AGAGGTTGCAGTATGCCAAG
177558	9754	TATATTATATATGTTTTTAT	222145	54341	ACATGCGCTTTGTTCTCCAA	266732	98928	CAGAGGTTGCAGTATGCCAA
177559	9755	ATATATTATATATGTTTTTA	222146	54342	AACATGCGCTTTGTTCTCCA	266733	98929	GCAGAGGTTGCAGTATGCCA
177560	9756	TATATATTATATATGTTTTT	222147	54343	TAACATGCGCTTTGTTCTCC	266734	98930	AGCAGAGGTTGCAGTATGCC
177561	9757	ATATATATTATATATGTTTT	222148	54344	TTAACATGCGCTTTGTTCTC	266735	98931	AAGCAGAGGTTGCAGTATGC
177562	9758	AATATATATTATATATGTTT	222149	54345	CTTAACATGCGCTTTGTTCT	266736	98932	GAAGCAGAGGTTGCAGTATG
177563	9759	TAATATATATTATATATGTT	222150	54346	CCTTAACATGCGCTTTGTTC	266737	98933	GGAAGCAGAGGTTGCAGTAT
177564	9760	ATAATATATATTATATATGT	222151	54347	ACCTTAACATGCGCTTTGTT	266738	98934	GGGAAGCAGAGGTTGCAGTA
177565	9761	TATAATATATATTATATATG	222152	54348	AACCTTAACATGCGCTTTGT	266739	98935	TGGGAAGCAGAGGTTGCAGT
177566	9762	ATATAATATATATTATATAT	222153	54349	TAACCTTAACATGCGCTTTG	266740	98936	TTGGGAAGCAGAGGTTGCAG
177567	9763	TATATAATATATATTATATA	222154	54350	ATAACCTTAACATGCGCTTT	266741	98937	TTTGGGAAGCAGAGGTTGCA
177568	9764	ATATATAATATATATTATAT	222155	54351	AATAACCTTAACATGCGCTT	266742	98938	ATTTGGGAAGCAGAGGTTGC
177569	9765	AATATATAATATATATTATA	222156	54352	AAATAACCTTAACATGCGCT	266743	98939	AATTTGGGAAGCAGAGGTTG
177570	9766	TAATATATAATATATATTAT	222157	54353	AAAATAACCTTAACATGCGC	266744	98940	GAATTTGGGAAGCAGAGGTT
177571	9767	ATAATATATAATATATATTA	222158	54354	AAAAATAACCTTAACATGCG	266745	98941	TGAATTTGGGAAGCAGAGGT
177572	9768	TATAATATATAATATATATT	222159	54355	CAAAAATAACCTTAACATGC	266746	98942	TTGAATTTGGGAAGCAGAGG
177573	9769	ATATAATATATAATATATAT	222160	54356	CCAAAAATAACCTTAACATG	266747	98943	CTTGAATTTGGGAAGCAGAG
177574	9770	TATATAATATATAATATATA	222161	54357	TCCAAAAATAACCTTAACAT	266748	98944	GCTTGAATTTGGGAAGCAGA
177575	9771	ATATATAATATATAATATAT	222162	54358	ATCCAAAAATAACCTTAACA	266749	98945	TGCTTGAATTTGGGAAGCAG
177576	9772	TATATATAATATATAATATA	222163	54359	AATCCAAAAATAACCTTAAC	266750	98946	CTGCTTGAATTTGGGAAGCA
177577	9773	ATATATATAATATATAATAT	222164	54360	GAATCCAAAAATAACCTTAA	266751	98947	ACTGCTTGAATTTGGGAAGC
177578	9774	TATATATATAATATATAATA	222165	54361	AGAATCCAAAAATAACCTTA	266752	98948	AACTGCTTGAATTTGGGAAG
177579	9775	ATATATATATAATATATAAT	222166	54362	TAGAATCCAAAAATAACCTT	266753	98949	AAACTGCTTGAATTTGGGAA
177580	9776	AATATATATATAATATATAA	222167	54363	CTAGAATCCAAAAATAACCT	266754	98950	AAAACTGCTTGAATTTGGGA
177581	9777	TAATATATATATAATATATA	222168	54364	CCTAGAATCCAAAAATAACC	266755	98951	GAAAACTGCTTGAATTTGGG
177582	9778	ATAATATATATATAATATAT	222169	54365	ACCTAGAATCCAAAAATAAC	266756	98952	GGAAAACTGCTTGAATTTGG
177583	9779	TATAATATATATATAATATA	222170	54366	AACCTAGAATCCAAAAATAA	266757	98953	AGGAAAACTGCTTGAATTTG
177584	9780	ATATAATATATATATAATAT	222171	54367	AAACCTAGAATCCAAAAATA	266758	98954	CAGGAAAACTGCTTGAATTT
177585	9781	TATATAATATATATATAATA	222172	54368	TAAACCTAGAATCCAAAAAT	266759	98955	GCAGGAAAACTGCTTGAATT
177586	9782	ATATATAATATATATATAAT	222173	54369	ATAAACCTAGAATCCAAAAA	266760	98956	GGCAGGAAAACTGCTTGAAT
177587	9783	TATATATAATATATATATAA	222174	54370	GATAAACCTAGAATCCAAAA	266761	98957	AGGCAGGAAAACTGCTTGAA
177588	9784	ATATATATAATATATATATA	222175	54371	AGATAAACCTAGAATCCAAA	266762	98958	GAGGCAGGAAAACTGCTTGA
177589	9785	AATATATATAATATATATAT	222176	54372	GAGATAAACCTAGAATCCAA	266763	98959	TGAGGCAGGAAAACTGCTTG
177590	9786	TAATATATATAATATATATA	222177	54373	AGAGATAAACCTAGAATCCA	266764	98960	CTGAGGCAGGAAAACTGCTT
177591	9787	ATAATATATATAATATATAT	222178	54374	CAGAGATAAACCTAGAATCC	266765	98961	GCTGAGGCAGGAAAACTGCT
177592	9788	TATAATATATATAATATATA	222179	54375	GCAGAGATAAACCTAGAATC	266766	98962	GGCTGAGGCAGGAAAACTGC
177593	9789	ATATAATATATATAATATAT	222180	54376	AGCAGAGATAAACCTAGAAT	266767	98963	AGGCTGAGGCAGGAAAACTG
177594	9790	TATATAATATATATAATATA	222181	54377	AAGCAGAGATAAACCTAGAA	266768	98964	GAGGCTGAGGCAGGAAAACT

177595	9791	ATATATAATATATATAATAT	222182	54378	CAAGCAGAGATAAACCTAGA	266769	98965	GGAGGCTGAGGCAGGAAAAC
177596	9792	TATATATAATATATATAATA	222183	54379	CCAAGCAGAGATAAACCTAG	266770	98966	AGGAGGCTGAGGCAGGAAAA
177597	9793	ATATATATAATATATATAAT	222184	54380	ACCAAGCAGAGATAAACCTA	266771	98967	CAGGAGGCTGAGGCAGGAAA
177598	9794	AATATATATAATATATATAA	222185	54381	GACCAAGCAGAGATAAACCT	266772	98968	TCAGGAGGCTGAGGCAGGAA
177599	9795	TAATATATATAATATATATA	222186	54382	AGACCAAGCAGAGATAAACC	266773	98969	CTCAGGAGGCTGAGGCAGGA
177600	9796	TTAATATATATAATATATAT	222187	54383	AAGACCAAGCAGAGATAAAC	266774	98970	ACTCAGGAGGCTGAGGCAGG
177601	9797	TTTAATATATATAATATATA	222188	54384	GAAGACCAAGCAGAGATAAA	266775	98971	TACTCAGGAGGCTGAGGCAG
177602	9798	ATTTAATATATATAATATAT	222189	54385	TGAAGACCAAGCAGAGATAA	266776	98972	CTACTCAGGAGGCTGAGGCA
177603	9799	TATTTAATATATATAATATA	222190	54386	CTGAAGACCAAGCAGAGATA	266777	98973	GCTACTCAGGAGGCTGAGGC
177604	9800	ATATTTAATATATATAATAT	222191	54387	ACTGAAGACCAAGCAGAGAT	266778	98974	AGCTACTCAGGAGGCTGAGG
177605	9801	TATATTTAATATATATAATA	222192	54388	AACTGAAGACCAAGCAGAGA	266779	98975	CAGCTACTCAGGAGGCTGAG
177606	9802	ATATATTTAATATATATAAT	222193	54389	TAACTGAAGACCAAGCAGAG	266780	98976	CCAGCTACTCAGGAGGCTGA
177607	9803	AATATATTTAATATATATAA	222194	54390	GTAACTGAAGACCAAGCAGA	266781	98977	CCCAGCTACTCAGGAGGCTG
177608	9804	AAATATATTTAATATATATA	222195	54391	GGTAACTGAAGACCAAGCAG	266782	98978	TCCCAGCTACTCAGGAGGCT
177609	9805	AAAATATATTTAATATATAT	222196	54392	AGGTAACTGAAGACCAAGCA	266783	98979	GTCCCAGCTACTCAGGAGGC
177610	9806	TAAAATATATTTAATATATA	222197	54393	CAGGTAACTGAAGACCAAGC	266784	98980	AGTCCCAGCTACTCAGGAGG
177611	9807	ATAAAATATATTTAATATAT	222198	54394	GCAGGTAACTGAAGACCAAG	266785	98981	TAGTCCCAGCTACTCAGGAG
177612	9808	TATAAAATATATTTAATATA	222199	54395	TGCAGGTAACTGAAGACCAA	266786	98982	GTAGTCCCAGCTACTCAGGA
177613	9809	ATATAAAATATATTTAATAT	222200	54396	TTGCAGGTAACTGAAGACCA	266787	98983	TGTAGTCCCAGCTACTCAGG
177614	9810	TATATAAAATATATTTAATA	222201	54397	CTTGCAGGTAACTGAAGACC	266788	98984	CTGTAGTCCCAGCTACTCAG
177615	9811	ATATATAAAATATATTTAAT	222202	54398	TCTTGCAGGTAACTGAAGAC	266789	98985	CCTGTAGTCCCAGCTACTCA
177616	9812	TATATATAAAATATATTTAA	222203	54399	CTCTTGCAGGTAACTGAAGA	266790	98986	GCCTGTAGTCCCAGCTACTC
177617	9813	ATATATATAAAATATATTTA	222204	54400	TCTCTTGCAGGTAACTGAAG	266791	98987	TGCCTGTAGTCCCAGCTACT
177618	9814	AATATATATAAAATATATTT	222205	54401	ATCTCTTGCAGGTAACTGAA	266792	98988	GTGCCTGTAGTCCCAGCTAC
177619	9815	TAATATATATAAAATATATT	222206	54402	GATCTCTTGCAGGTAACTGA	266793	98989	TGTGCCTGTAGTCCCAGCTA
177620	9816	ATAATATATATAAAATATAT	222207	54403	GGATCTCTTGCAGGTAACTG	266794	98990	CTGTGCCTGTAGTCCCAGCT
177621	9817	TATAATATATATAAAATATA	222208	54404	TGGATCTCTTGCAGGTAACT	266795	98991	CCTGTGCCTGTAGTCCCAGC
177622	9818	ATATAATATATATAAAATAT	222209	54405	ATGGATCTCTTGCAGGTAAC	266796	98992	GCCTGTGCCTGTAGTCCCAG
177623	9819	TATATAATATATATAAAATA	222210	54406	AATGGATCTCTTGCAGGTAA	266797	98993	GGCCTGTGCCTGTAGTCCCA
177624	9820	ATATATAATATATATAAAAT	222211	54407	AAATGGATCTCTTGCAGGTA	266798	98994	TGGCCTGTGCCTGTAGTCCC
177625	9821	TATATATAATATATATAAAA	222212	54408	TAAATGGATCTCTTGCAGGT	266799	98995	GTGGCCTGTGCCTGTAGTCC
177626	9822	ATATATATAATATATATAAA	222213	54409	CTAAATGGATCTCTTGCAGG	266800	98996	GGTGGCCTGTGCCTGTAGTC
177627	9823	TATATATATAATATATATAA	222214	54410	CCTAAATGGATCTCTTGCAG	266801	98997	TGGTGGCCTGTGCCTGTAGT
177628	9824	ATATATATATAATATATATA	222215	54411	CCCTAAATGGATCTCTTGCA	266802	98998	GTGGTGGCCTGTGCCTGTAG
177629	9825	TATATATATATAATATATAT	222216	54412	CCCCTAAATGGATCTCTTGC	266803	98999	CGTGGTGGCCTGTGCCTGTA
177630	9826	GTATATATATATAATATATA	222217	54413	TCCCCTAAATGGATCTCTTG	266804	99000	GCGTGGTGGCCTGTGCCTGT
177631	9827	TGTATATATATATAATATAT	222218	54414	ATCCCCTAAATGGATCTCTT	266805	99001	GGCGTGGTGGCCTGTGCCTG
177632	9828	GTGTATATATATATAATATA	222219	54415	AATCCCCTAAATGGATCTCT	266806	99002	GGGCGTGGTGGCCTGTGCCT
177633	9829	TGTGTATATATATATAATAT	222220	54416	AAATCCCCTAAATGGATCTC	266807	99003	AGGGCGTGGTGGCCTGTGCC
177634	9830	ATGTGTATATATATATAATA	222221	54417	AAAATCCCCTAAATGGATCT	266808	99004	CAGGGCGTGGTGGCCTGTGC
177635	9831	TATGTGTATATATATATAAT	222222	54418	AAAAATCCCCTAAATGGATC	266809	99005	GCAGGGCGTGGTGGCCTGTG
177636	9832	ATATGTGTATATATATATAA	222223	54419	CAAAAATCCCCTAAATGGAT	266810	99006	AGCAGGGCGTGGTGGCCTGT
177637	9833	TATATGTGTATATATATATA	222224	54420	ACAAAAATCCCCTAAATGGA	266811	99007	TAGCAGGGCGTGGTGGCCTG
177638	9834	ATATATGTGTATATATATAT	222225	54421	AACAAAAATCCCCTAAATGG	266812	99008	TTAGCAGGGCGTGGTGGCCT
177639	9835	TATATATGTGTATATATATA	222226	54422	AAACAAAAATCCCCTAAATG	266813	99009	ATTAGCAGGGCGTGGTGGCC
177640	9836	ATATATATGTGTATATATAT	222227	54423	CAAACAAAAATCCCCTAAAT	266814	99010	AATTAGCAGGGCGTGGTGGC
177641	9837	TATATATATGTGTATATATA	222228	54424	ACAAACAAAAATCCCCTAAA	266815	99011	AAATTAGCAGGGCGTGGTGG
177642	9838	ATATATATATGTGTATATAT	222229	54425	AACAAACAAAAATCCCCTAA	266816	99012	AAAATTAGCAGGGCGTGGTG
177643	9839	TATATATATATGTGTATATA	222230	54426	AAACAAACAAAAATCCCCTA	266817	99013	AAAAATTAGCAGGGCGTGGT
177644	9840	ATATATATATATGTGTATAT	222231	54427	AAAACAAACAAAAATCCCCT	266818	99014	CAAAAATTAGCAGGGCGTGG
177645	9841	TATATATATATATGTGTATA	222232	54428	AAAAACAAACAAAAATCCCC	266819	99015	ACAAAAATTAGCAGGGCGTG
177646	9842	TTATATATATATATGTGTAT	222233	54429	TAAAAACAAACAAAAATCCC	266820	99016	TACAAAAATTAGCAGGGCGT
177647	9843	TTTATATATATATATGTGTA	222234	54430	TTAAAAACAAACAAAAATCC	266821	99017	ATACAAAAATTAGCAGGGCG
177648	9844	ATTTATATATATATATGTGT	222235	54431	GTTAAAAACAAACAAAAATC	266822	99018	AATACAAAAATTAGCAGGGC
177649	9845	CATTTATATATATATATGTG	222236	54432	CGTTAAAAACAAACAAAAAT	266823	99019	AAATACAAAAATTAGCAGGG
177650	9846	TCATTTATATATATATATGT	222237	54433	TCGTTAAAAACAAACAAAAA	266824	99020	AAAATACAAAAATTAGCAGG
177651	9847	CTCATTTATATATATATATG	222238	54434	ATCGTTAAAAACAAACAAAA	266825	99021	AAAAATACAAAAATTAGCAG
177652	9848	CCTCATTTATATATATATAT	222239	54435	TATCGTTAAAAACAAACAAA	266826	99022	TAAAAATACAAAAATTAGCA
177653	9849	GCCTCATTTATATATATATA	222240	54436	CTATCGTTAAAAACAAACAA	266827	99023	CTAAAAATACAAAAATTAGC
177654	9850	GGCCTCATTTATATATATAT	222241	54437	GCTATCGTTAAAAACAAACA	266828	99024	ACTAAAAATACAAAAATTAG
177655	9851	TGGCCTCATTTATATATATA	222242	54438	AGCTATCGTTAAAAACAAAC	266829	99025	TACTAAAAATACAAAAATTA
177656	9852	CTGGCCTCATTTATATATAT	222243	54439	AAGCTATCGTTAAAAACAAA	266830	99026	TTACTAAAAATACAAAAATT
177657	9853	CCTGGCCTCATTTATATATA	222244	54440	AAAGCTATCGTTAAAAACAA	266831	99027	TTTACTAAAAATACAAAAAT
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177659	9855	AGCCTGGCCTCATTTATATA	222246	54442	ATAAAGCTATCGTTAAAAAC	266833	99029	TCTTTACTAAAAATACAAAA
177660	9856	GAGCCTGGCCTCATTTATAT	222247	54443	AATAAAGCTATCGTTAAAAA	266834	99030	GTCTTTACTAAAAATACAAA
177661	9857	CGAGCCTGGCCTCATTTATA	222248	54444	CAATAAAGCTATCGTTAAAA	266835	99031	TGTCTTTACTAAAAATACAA
177662	9858	CCGAGCCTGGCCTCATTTAT	222249	54445	TCAATAAAGCTATCGTTAAA	266836	99032	CTGTCTTTACTAAAAATACA
177663	9859	ACCGAGCCTGGCCTCATTTA	222250	54446	CTCAATAAAGCTATCGTTAA	266837	99033	CCTGTCTTTACTAAAAATAC
177664	9860	CACCGAGCCTGGCCTCATTT	222251	54447	TCTCAATAAAGCTATCGTTA	266838	99034	CCCTGTCTTTACTAAAAATA
177665	9861	CCACCGAGCCTGGCCTCATT	222252	54448	ATCTCAATAAAGCTATCGTT	266839	99035	ACCCTGTCTTTACTAAAAAT
177666	9862	GCCACCGAGCCTGGCCTCAT	222253	54449	TATCTCAATAAAGCTATCGT	266840	99036	AACCCTGTCTTTACTAAAAA

177667	9863	AGCCACCGAGCCTGGCCTCA	222254	54450	ATATCTCAATAAAGCTATCG	266841	99037	AAACCCTGTCTTTACTAAAA
177668	9864	GAGCCACCGAGCCTGGCCTC	222255	54451	TATATCTCAATAAAGCTATC	266842	99038	GAAACCCTGTCTTTACTAAA
177669	9865	TGAGCCACCGAGCCTGGCCT	222256	54452	TTATATCTCAATAAAGCTAT	266843	99039	TGAAACCCTGTCTTTACTAA
177670	9866	GTGAGCCACCGAGCCTGGCC	222257	54453	ATTATATCTCAATAAAGCTA	266844	99040	GTGAAACCCTGTCTTTACTA
177671	9867	TGTGAGCCACCGAGCCTGGC	222258	54454	AATTATATCTCAATAAAGCT	266845	99041	GGTGAAACCCTGTCTTTACT
177672	9868	GTGTGAGCCACCGAGCCTGG	222259	54455	GAATTATATCTCAATAAAGC	266846	99042	TGGTGAAACCCTGTCTTTAC
177673	9869	AGTGTGAGCCACCGAGCCTG	222260	54456	TGAATTATATCTCAATAAAG	266847	99043	ATGGTGAAACCCTGTCTTTA
177674	9870	AAGTGTGAGCCACCGAGCCT	222261	54457	ATGAATTATATCTCAATAAA	266848	99044	AATGGTGAAACCCTGTCTTT
177675	9871	CAAGTGTGAGCCACCGAGCC	222262	54458	TATGAATTATATCTCAATAA	266849	99045	AAATGGTGAAACCCTGTCTT
177676	9872	ACAAGTGTGAGCCACCGAGC	222263	54459	ATATGAATTATATCTCAATA	266850	99046	AAAATGGTGAAACCCTGTCT
177677	9873	TACAAGTGTGAGCCACCGAG	222264	54460	CATATGAATTATATCTCAAT	266851	99047	CAAAATGGTGAAACCCTGTC
177678	9874	TTACAAGTGTGAGCCACCGA	222265	54461	GCATATGAATTATATCTCAA	266852	99048	CCAAAATGGTGAAACCCTGT
177679	9875	ATTACAAGTGTGAGCCACCG	222266	54462	GGCATATGAATTATATCTCA	266853	99049	GCCAAAATGGTGAAACCCTG
177680	9876	GATTACAAGTGTGAGCCACC	222267	54463	TGGCATATGAATTATATCTC	266854	99050	GGCCAAAATGGTGAAACCCT
177681	9877	GGATTACAAGTGTGAGCCAC	222268	54464	ATGGCATATGAATTATATCT	266855	99051	TGGCCAAAATGGTGAAACCC
177682	9878	GGGATTACAAGTGTGAGCCA	222269	54465	TATGGCATATGAATTATATC	266856	99052	CTGGCCAAAATGGTGAAACC
177683	9879	TGGGATTACAAGTGTGAGCC	222270	54466	TTATGGCATATGAATTATAT	266857	99053	GCTGGCCAAAATGGTGAAAC
177684	9880	CTGGGATTACAAGTGTGAGC	222271	54467	TTTATGGCATATGAATTATA	266858	99054	GGCTGGCCAAAATGGTGAAA
177685	9881	GCTGGGATTACAAGTGTGAG	222272	54468	TTTTATGGCATATGAATTAT	266859	99055	AGGCTGGCCAAAATGGTGAA
177686	9882	TGCTGGGATTACAAGTGTGA	222273	54469	CTTTTATGGCATATGAATTA	266860	99056	TAGGCTGGCCAAAATGGTGA
177687	9883	GTGCTGGGATTACAAGTGTG	222274	54470	ACTTTTATGGCATATGAATT	266861	99057	CTAGGCTGGCCAAAATGGTG
177688	9884	AGTGCTGGGATTACAAGTGT	222275	54471	GACTTTTATGGCATATGAAT	266862	99058	ACTAGGCTGGCCAAAATGGT
177689	9885	CAGTGCTGGGATTACAAGTG	222276	54472	TGACTTTTATGGCATATGAA	266863	99059	GACTAGGCTGGCCAAAATGG
177690	9886	ACAGTGCTGGGATTACAAGT	222277	54473	GTGACTTTTATGGCATATGA	266864	99060	AGACTAGGCTGGCCAAAATG
177691	9887	CACAGTGCTGGGATTACAAG	222278	54474	AGTGACTTTTATGGCATATG	266865	99061	GAGACTAGGCTGGCCAAAAT
177692	9888	CCACAGTGCTGGGATTACAA	222279	54475	GAGTGACTTTTATGGCATAT	266866	99062	CGAGACTAGGCTGGCCAAAA
177693	9889	CCCACAGTGCTGGGATTACA	222280	54476	AGAGTGACTTTTATGGCATA	266867	99063	TCGAGACTAGGCTGGCCAAA
177694	9890	TCCCACAGTGCTGGGATTAC	222281	54477	AAGAGTGACTTTTATGGCAT	266868	99064	TTCGAGACTAGGCTGGCCAA
177695	9891	CTCCCACAGTGCTGGGATTA	222282	54478	AAAGAGTGACTTTTATGGCA	266869	99065	GTTCGAGACTAGGCTGGCCA
177696	9892	CCTCCCACAGTGCTGGGATT	222283	54479	AAAAGAGTGACTTTTATGGC	266870	99066	AGTTCGAGACTAGGCTGGCC
177697	9893	TCCTCCCACAGTGCTGGGAT	222284	54480	TAAAAGAGTGACTTTTATGG	266871	99067	GAGTTCGAGACTAGGCTGGC
177698	9894	ATCCTCCCACAGTGCTGGGA	222285	54481	TTAAAAGAGTGACTTTTATG	266872	99068	GGAGTTCGAGACTAGGCTGG
177699	9895	GATCCTCCCACAGTGCTGGG	222286	54482	TTTAAAAGAGTGACTTTTAT	266873	99069	AGGAGTTCGAGACTAGGCTG
177700	9896	TGATCCTCCCACAGTGCTGG	222287	54483	TTTTAAAAGAGTGACTTTTA	266874	99070	CAGGAGTTCGAGACTAGGCT
177701	9897	GTGATCCTCCCACAGTGCTG	222288	54484	ATTTTAAAAGAGTGACTTTT	266875	99071	TCAGGAGTTCGAGACTAGGC
177702	9898	AGTGATCCTCCCACAGTGCT	222289	54485	CATTTTAAAAGAGTGACTTT	266876	99072	GTCAGGAGTTCGAGACTAGG
177703	9899	AAGTGATCCTCCCACAGTGC	222290	54486	ACATTTTAAAAGAGTGACTT	266877	99073	GGTCAGGAGTTCGAGACTAG
177704	9900	CAAGTGATCCTCCCACAGTG	222291	54487	AACATTTTAAAAGAGTGACT	266878	99074	AGGTCAGGAGTTCGAGACTA
177705	9901	TCAAGTGATCCTCCCACAGT	222292	54488	AAACATTTTAAAAGAGTGAC	266879	99075	GAGGTCAGGAGTTCGAGACT
177706	9902	TTCAAGTGATCCTCCCACAG	222293	54489	GAAACATTTTAAAAGAGTGA	266880	99076	TGAGGTCAGGAGTTCGAGAC
177707	9903	CTTCAAGTGATCCTCCCACA	222294	54490	GGAAACATTTTAAAAGAGTG	266881	99077	TTGAGGTCAGGAGTTCGAGA
177708	9904	GCTTCAAGTGATCCTCCCAC	222295	54491	CGGAAACATTTTAAAAGAGT	266882	99078	CTTGAGGTCAGGAGTTCGAG
177709	9905	GGCTTCAAGTGATCCTCCCA	222296	54492	CCGGAAACATTTTAAAAGAG	266883	99079	ACTTGAGGTCAGGAGTTCGA
177710	9906	TGGCTTCAAGTGATCCTCCC	222297	54493	ACCGGAAACATTTTAAAAGA	266884	99080	CACTTGAGGTCAGGAGTTCG
177711	9907	CTGGCTTCAAGTGATCCTCC	222298	54494	TACCGGAAACATTTTAAAAG	266885	99081	TCACTTGAGGTCAGGAGTTC
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177713	9909	TCCTGGCTTCAAGTGATCCT	222300	54496	TATACCGGAAACATTTTAAA	266887	99083	GATCACTTGAGGTCAGGAGT
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177715	9911	ACTCCTGGCTTCAAGTGATC	222302	54498	AATATACCGGAAACATTTTA	266889	99085	CGGATCACTTGAGGTCAGGA
177716	9912	GACTCCTGGCTTCAAGTGAT	222303	54499	GAATATACCGGAAACATTTT	266890	99086	GCGGATCACTTGAGGTCAGG
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177723	9919	AGTCTCAGACTCCTGGCTTC	222310	54506	GCCTTGTGAATATACCGGAA	266897	99093	GAGGTGGGCGGATCACTTGA
177724	9920	TAGTCTCAGACTCCTGGCTT	222311	54507	AGCCTTGTGAATATACCGGA	266898	99094	CGAGGTGGGCGGATCACTTG
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177726	9922	GCTAGTCTCAGACTCCTGGC	222313	54509	ACAGCCTTGTGAATATACCG	266900	99096	GCCGAGGTGGGCGGATCACT
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177734	9930	TTGCCCAGGCTAGTCTCAGA	222321	54517	AAGGCTGCACAGCCTTGTGA	266908	99104	TTTGGGAGGCCGAGGTGGGC
177735	9931	GTTGCCCAGGCTAGTCTCAG	222322	54518	GAAGGCTGCACAGCCTTGTG	266909	99105	CTTTGGGAGGCCGAGGTGGG
177736	9932	TGTTGCCCAGGCTAGTCTCA	222323	54519	GGAAGGCTGCACAGCCTTGT	266910	99106	ACTTTGGGAGGCCGAGGTGG
177737	9933	TTGTTGCCCAGGCTAGTCTC	222324	54520	GGGAAGGCTGCACAGCCTTG	266911	99107	CACTTTGGGAGGCCGAGGTG
177738	9934	TTTGTTGCCCAGGCTAGTCT	222325	54521	AGGGAAGGCTGCACAGCCTT	266912	99108	GCACTTTGGGAGGCCGAGGT

177739	9935	TTTTGTTGCCCAGGCTAGTC	222326	54522	CAGGGAAGGCTGCACAGCCT	266913	99109	AGCACTTTGGGAGGCCGAGG
177740	9936	GTTTTGTTGCCCAGGCTAGT	222327	54523	ACAGGGAAGGCTGCACAGCC	266914	99110	CAGCACTTTGGGAGGCCGAG
177741	9937	TGTTTTGTTGCCCAGGCTAG	222328	54524	GACAGGGAAGGCTGCACAGC	266915	99111	CCAGCACTTTGGGAGGCCGA
177742	9938	TTGTTTTGTTGCCCAGGCTA	222329	54525	GGACAGGGAAGGCTGCACAG	266916	99112	CCCAGCACTTTGGGAGGCCG
177743	9939	CTTGTTTTGTTGCCCAGGCT	222330	54526	AGGACAGGGAAGGCTGCACA	266917	99113	TCCCAGCACTTTGGGAGGCC
177744	9940	TCTTGTTTTGTTGCCCAGGC	222331	54527	AAGGACAGGGAAGGCTGCAC	266918	99114	ATCCCAGCACTTTGGGAGGC
177745	9941	ATCTTGTTTTGTTGCCCAGG	222332	54528	CAAGGACAGGGAAGGCTGCA	266919	99115	AATCCCAGCACTTTGGGAGG
177746	9942	GATCTTGTTTTGTTGCCCAG	222333	54529	TCAAGGACAGGGAAGGCTGC	266920	99116	TAATCCCAGCACTTTGGGAG
177747	9943	GGATCTTGTTTTGTTGCCCA	222334	54530	ATCAAGGACAGGGAAGGCTG	266921	99117	GTAATCCCAGCACTTTGGGA
177748	9944	AGGATCTTGTTTTGTTGCCC	222335	54531	AATCAAGGACAGGGAAGGCT	266922	99118	TGTAATCCCAGCACTTTGGG
177749	9945	CAGGATCTTGTTTTGTTGCC	222336	54532	GAATCAAGGACAGGGAAGGC	266923	99119	CTGTAATCCCAGCACTTTGG
177750	9946	ACAGGATCTTGTTTTGTTGC	222337	54533	GGAATCAAGGACAGGGAAGG	266924	99120	CCTGTAATCCCAGCACTTTG
177751	9947	GACAGGATCTTGTTTTGTTG	222338	54534	TGGAATCAAGGACAGGGAAG	266925	99121	CCCTGTAATCCCAGCACTTT
177752	9948	AGACAGGATCTTGTTTTGTT	222339	54535	CTGGAATCAAGGACAGGGAA	266926	99122	CCCCTGTAATCCCAGCACTT
177753	9949	GAGACAGGATCTTGTTTTGT	222340	54536	ACTGGAATCAAGGACAGGGA	266927	99123	TCCCCTGTAATCCCAGCACT
177754	9950	AGAGACAGGATCTTGTTTTG	222341	54537	GACTGGAATCAAGGACAGGG	266928	99124	GTCCCCTGTAATCCCAGCAC
177755	9951	TAGAGACAGGATCTTGTTTT	222342	54538	AGACTGGAATCAAGGACAGG	266929	99125	AGTCCCCTGTAATCCCAGCA
177756	9952	GTAGAGACAGGATCTTGTTT	222343	54539	CAGACTGGAATCAAGGACAG	266930	99126	GAGTCCCCTGTAATCCCAGC
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177758	9954	TTGTAGAGACAGGATCTTGT	222345	54541	CTCAGACTGGAATCAAGGAC	266932	99128	GTGAGTCCCCTGTAATCCCA
177759	9955	TTTGTAGAGACAGGATCTTG	222346	54542	ACTCAGACTGGAATCAAGGA	266933	99129	TGTGAGTCCCCTGTAATCCC
177760	9956	TTTTGTAGAGACAGGATCTT	222347	54543	AACTCAGACTGGAATCAAGG	266934	99130	GTGTGAGTCCCCTGTAATCC
177761	9957	CTTTTGTAGAGACAGGATCT	222348	54544	AAACTCAGACTGGAATCAAG	266935	99131	AGTGTGAGTCCCCTGTAATC
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177763	9959	TCCTTTTGTAGAGACAGGAT	222350	54546	AAAAACTCAGACTGGAATCA	266937	99133	AAAGTGTGAGTCCCCTGTAA
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177772	9968	TTTACAGTTTCCTTTTGTAG	222359	54555	CCTTCAGTTAAAAACTCAGA	266946	99142	GGTTGTTACAAAGTGTGAGT
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177775	9971	ATTTTTACAGTTTCCTTTTG	222362	54558	ATCCCTTCAGTTAAAAACTC	266949	99145	TCAGGTTGTTACAAAGTGTG
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177780	9976	AGCTAATTTTTACAGTTTCC	222367	54563	TCCTTATCCCTTCAGTTAAA	266954	99150	TTGTTTCAGGTTGTTACAAA
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177782	9978	CCAGCTAATTTTTACAGTTT	222369	54565	CCTCCTTATCCCTTCAGTTA	266956	99152	CGTTGTTTCAGGTTGTTACA
177783	9979	CCCAGCTAATTTTTACAGTT	222370	54566	TCCTCCTTATCCCTTCAGTT	266957	99153	ACGTTGTTTCAGGTTGTTAC
177784	9980	GCCCAGCTAATTTTTACAGT	222371	54567	GTCCTCCTTATCCCTTCAGT	266958	99154	CACGTTGTTTCAGGTTGTTA
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177786	9982	ATGCCCAGCTAATTTTTACA	222373	54569	TGGTCCTCCTTATCCCTTCA	266960	99156	ATCACGTTGTTTCAGGTTGT
177787	9983	CATGCCCAGCTAATTTTTAC	222374	54570	GTGGTCCTCCTTATCCCTTC	266961	99157	CATCACGTTGTTTCAGGTTG
177788	9984	TCATGCCCAGCTAATTTTTA	222375	54571	CGTGGTCCTCCTTATCCCTT	266962	99158	GCATCACGTTGTTTCAGGTT
177789	9985	ATCATGCCCAGCTAATTTTT	222376	54572	GCGTGGTCCTCCTTATCCCT	266963	99159	TGCATCACGTTGTTTCAGGT
177790	9986	CATCATGCCCAGCTAATTTT	222377	54573	AGCGTGGTCCTCCTTATCCC	266964	99160	ATGCATCACGTTGTTTCAGG
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177792	9988	GCCATCATGCCCAGCTAATT	222379	54575	AAAGCGTGGTCCTCCTTATC	266966	99162	AAATGCATCACGTTGTTTCA
177793	9989	TGCCATCATGCCCAGCTAAT	222380	54576	GAAAGCGTGGTCCTCCTTAT	266967	99163	GAAATGCATCACGTTGTTTC
177794	9990	ATGCCATCATGCCCAGCTAA	222381	54577	GGAAAGCGTGGTCCTCCTTA	266968	99164	GGAAATGCATCACGTTGTTT
177795	9991	CATGCCATCATGCCCAGCTA	222382	54578	GGGAAAGCGTGGTCCTCCTT	266969	99165	GGGAAATGCATCACGTTGTT
177796	9992	ACATGCCATCATGCCCAGCT	222383	54579	GGGGAAAGCGTGGTCCTCCT	266970	99166	AGGGAAATGCATCACGTTGT
177797	9993	CACATGCCATCATGCCCAGC	222384	54580	TGGGGAAAGCGTGGTCCTCC	266971	99167	AAGGGAAATGCATCACGTTG
177798	9994	ACACATGCCATCATGCCCAG	222385	54581	CTGGGGAAAGCGTGGTCCTC	266972	99168	AAAGGGAAATGCATCACGTT
177799	9995	GACACATGCCATCATGCCCA	222386	54582	TCTGGGGAAAGCGTGGTCCT	266973	99169	CAAAGGGAAATGCATCACGT
177800	9996	AGACACATGCCATCATGCCC	222387	54583	GTCTGGGGAAAGCGTGGTCC	266974	99170	CCAAAGGGAAATGCATCACG
177801	9997	CAGACACATGCCATCATGCC	222388	54584	GGTCTGGGGAAAGCGTGGTC	266975	99171	CCCAAAGGGAAATGCATCAC
177802	9998	ACAGACACATGCCATCATGC	222389	54585	TGGTCTGGGGAAAGCGTGGT	266976	99172	ACCCAAAGGGAAATGCATCA
177803	9999	TACAGACACATGCCATCATG	222390	54586	CTGGTCTGGGGAAAGCGTGG	266977	99173	GACCCAAAGGGAAATGCATC
177804	10000	CTACAGACACATGCCATCAT	222391	54587	TCTGGTCTGGGGAAAGCGTG	266978	99174	AGACCCAAAGGGAAATGCAT
177805	10001	GCTACAGACACATGCCATCA	222392	54588	TTCTGGTCTGGGGAAAGCGT	266979	99175	AAGACCCAAAGGGAAATGCA
177806	10002	GGCTACAGACACATGCCATC	222393	54589	GTTCTGGTCTGGGGAAAGCG	266980	99176	TAAGACCCAAAGGGAAATGC
177807	10003	GGGCTACAGACACATGCCAT	222394	54590	GGTTCTGGTCTGGGGAAAGC	266981	99177	GTAAGACCCAAAGGGAAATG
177808	10004	AGGGCTACAGACACATGCCA	222395	54591	CGGTTCTGGTCTGGGGAAAG	266982	99178	GGTAAGACCCAAAGGGAAAT
177809	10005	TAGGGCTACAGACACATGCC	222396	54592	GCGGTTCTGGTCTGGGGAAA	266983	99179	AGGTAAGACCCAAAGGGAAA
177810	10006	CTAGGGCTACAGACACATGC	222397	54593	CGCGGTTCTGGTCTGGGGAA	266984	99180	CAGGTAAGACCCAAAGGGAA

177811	10007	GCTAGGGCTACAGACACATG	222398	54594	CCGCGGTTCTGGTCTGGGGA	266985	99181	GCAGGTAAGACCCAAAGGGA
177812	10008	AGCTAGGGCTACAGACACAT	222399	54595	CCCGCGGTTCTGGTCTGGGG	266986	99182	AGCAGGTAAGACCCAAAGGG
177813	10009	TAGCTAGGGCTACAGACACA	222400	54596	GCCCGCGGTTCTGGTCTGGG	266987	99183	GAGCAGGTAAGACCCAAAGG
177814	10010	GTAGCTAGGGCTACAGACAC	222401	54597	GGCCCGCGGTTCTGGTCTGG	266988	99184	AGAGCAGGTAAGACCCAAAG
177815	10011	AGTAGCTAGGGCTACAGACA	222402	54598	TGGCCCGCGGTTCTGGTCTG	266989	99185	AAGAGCAGGTAAGACCCAAA
177816	10012	AAGTAGCTAGGGCTACAGAC	222403	54599	CTGGCCCGCGGTTCTGGTCT	266990	99186	GAAGAGCAGGTAAGACCCAA
177817	10013	CAAGTAGCTAGGGCTACAGA	222404	54600	CCTGGCCCGCGGTTCTGGTC	266991	99187	CGAAGAGCAGGTAAGACCCA
177818	10014	CCAAGTAGCTAGGGCTACAG	222405	54601	CCCTGGCCCGCGGTTCTGGT	266992	99188	CCGAAGAGCAGGTAAGACCC
177819	10015	CCCAAGTAGCTAGGGCTACA	222406	54602	CCCCTGGCCCGCGGTTCTGG	266993	99189	ACCGAAGAGCAGGTAAGACC
177820	10016	TCCCAAGTAGCTAGGGCTAC	222407	54603	CCCCCTGGCCCGCGGTTCTG	266994	99190	CACCGAAGAGCAGGTAAGAC
177821	10017	CTCCCAAGTAGCTAGGGCTA	222408	54604	GCCCCCTGGCCCGCGGTTCT	266995	99191	CCACCGAAGAGCAGGTAAGA
177822	10018	CCTCCCAAGTAGCTAGGGCT	222409	54605	CGCCCCCTGGCCCGCGGTTC	266996	99192	GCCACCGAAGAGCAGGTAAG
177823	10019	GCCTCCCAAGTAGCTAGGGC	222410	54606	TCGCCCCCTGGCCCGCGGTT	266997	99193	AGCCACCGAAGAGCAGGTAA
177824	10020	GGCCTCCCAAGTAGCTAGGG	222411	54607	ATCGCCCCCTGGCCCGCGGT	266998	99194	CAGCCACCGAAGAGCAGGTA
177825	10021	CGGCCTCCCAAGTAGCTAGG	222412	54608	AATCGCCCCCTGGCCCGCGG	266999	99195	GCAGCCACCGAAGAGCAGGT
177826	10022	TCGGCCTCCCAAGTAGCTAG	222413	54609	GAATCGCCCCCTGGCCCGCG	267000	99196	GGCAGCCACCGAAGAGCAGG
177827	10023	TTCGGCCTCCCAAGTAGCTA	222414	54610	AGAATCGCCCCCTGGCCCGC	267001	99197	AGGCAGCCACCGAAGAGCAG
177828	10024	CTTCGGCCTCCCAAGTAGCT	222415	54611	CAGAATCGCCCCCTGGCCCG	267002	99198	CAGGCAGCCACCGAAGAGCA
177829	10025	GCTTCGGCCTCCCAAGTAGC	222416	54612	GCAGAATCGCCCCCTGGCCC	267003	99199	GCAGGCAGCCACCGAAGAGC
177830	10026	TGCTTCGGCCTCCCAAGTAG	222417	54613	AGCAGAATCGCCCCCTGGCC	267004	99200	TGCAGGCAGCCACCGAAGAG
177831	10027	CTGCTTCGGCCTCCCAAGTA	222418	54614	CAGCAGAATCGCCCCCTGGC	267005	99201	CTGCAGGCAGCCACCGAAGA
177832	10028	CCTGCTTCGGCCTCCCAAGT	222419	54615	TCAGCAGAATCGCCCCCTGG	267006	99202	CCTGCAGGCAGCCACCGAAG
177833	10029	TCCTGCTTCGGCCTCCCAAG	222420	54616	CTCAGCAGAATCGCCCCCTG	267007	99203	ACCTGCAGGCAGCCACCGAA
177834	10030	CTCCTGCTTCGGCCTCCCAA	222421	54617	ACTCAGCAGAATCGCCCCCT	267008	99204	CACCTGCAGGCAGCCACCGA
177835	10031	CCTCCTGCTTCGGCCTCCCA	222422	54618	GACTCAGCAGAATCGCCCCC	267009	99205	CCACCTGCAGGCAGCCACCG
177836	10032	TCCTCCTGCTTCGGCCTCCC	222423	54619	TGACTCAGCAGAATCGCCCC	267010	99206	TCCACCTGCAGGCAGCCACC
177837	10033	ATCCTCCTGCTTCGGCCTCC	222424	54620	GTGACTCAGCAGAATCGCCC	267011	99207	CTCCACCTGCAGGCAGCCAC
177838	10034	GATCCTCCTGCTTCGGCCTC	222425	54621	GGTGACTCAGCAGAATCGCC	267012	99208	TCTCCACCTGCAGGCAGCCA
177839	10035	CGATCCTCCTGCTTCGGCCT	222426	54622	CGGTGACTCAGCAGAATCGC	267013	99209	CTCTCCACCTGCAGGCAGCC
177840	10036	GCGATCCTCCTGCTTCGGCC	222427	54623	GCGGTGACTCAGCAGAATCG	267014	99210	TCTCTCCACCTGCAGGCAGC
177841	10037	AGCGATCCTCCTGCTTCGGC	222428	54624	CGCGGTGACTCAGCAGAATC	267015	99211	GTCTCTCCACCTGCAGGCAG
177842	10038	AAGCGATCCTCCTGCTTCGG	222429	54625	CCGCGGTGACTCAGCAGAAT	267016	99212	GGTCTCTCCACCTGCAGGCA
177843	10039	CAAGCGATCCTCCTGCTTCG	222430	54626	CCCGCGGTGACTCAGCAGAA	267017	99213	GGGTCTCTCCACCTGCAGGC
177844	10040	TCAAGCGATCCTCCTGCTTC	222431	54627	GCCCGCGGTGACTCAGCAGA	267018	99214	AGGGTCTCTCCACCTGCAGG
177845	10041	CTCAAGCGATCCTCCTGCTT	222432	54628	CGCCCGCGGTGACTCAGCAG	267019	99215	GAGGGTCTCTCCACCTGCAG
177846	10042	GCTCAAGCGATCCTCCTGCT	222433	54629	GCGCCCGCGGTGACTCAGCA	267020	99216	GGAGGGTCTCTCCACCTGCA
177847	10043	GGCTCAAGCGATCCTCCTGC	222434	54630	GGCGCCCGCGGTGACTCAGC	267021	99217	GGGAGGGTCTCTCCACCTGC
177848	10044	GGGCTCAAGCGATCCTCCTG	222435	54631	AGGCGCCCGCGGTGACTCAG	267022	99218	GGGGAGGGTCTCTCCACCTG
177849	10045	TGGGCTCAAGCGATCCTCCT	222436	54632	CAGGCGCCCGCGGTGACTCA	267023	99219	GGGGGAGGGTCTCTCCACCT
177850	10046	CTGGGCTCAAGCGATCCTCC	222437	54633	CCAGGCGCCCGCGGTGACTC	267024	99220	AGGGGGAGGGTCTCTCCACC
177851	10047	CCTGGGCTCAAGCGATCCTC	222438	54634	ACCAGGCGCCCGCGGTGACT	267025	99221	AAGGGGGAGGGTCTCTCCAC
177852	10048	TCCTGGGCTCAAGCGATCCT	222439	54635	CACCAGGCGCCCGCGGTGAC	267026	99222	CAAGGGGGAGGGTCTCTCCA
177853	10049	CTCCTGGGCTCAAGCGATCC	222440	54636	GCACCAGGCGCCCGCGGTGA	267027	99223	CCAAGGGGGAGGGTCTCTCC
177854	10050	ACTCCTGGGCTCAAGCGATC	222441	54637	CGCACCAGGCGCCCGCGGTG	267028	99224	CCCAAGGGGGAGGGTCTCTC
177855	10051	AACTCCTGGGCTCAAGCGAT	222442	54638	GCGCACCAGGCGCCCGCGGT	267029	99225	GCCCAAGGGGGAGGGTCTCT
177856	10052	GAACTCCTGGGCTCAAGCGA	222443	54639	CGCGCACCAGGCGCCCGCGG	267030	99226	GGCCCAAGGGGGAGGGTCTC
177857	10053	TGAACTCCTGGGCTCAAGCG	222444	54640	CCGCGCACCAGGCGCCCGCG	267031	99227	GGGCCCAAGGGGGAGGGTCT
177858	10054	TTGAACTCCTGGGCTCAAGC	222445	54641	GCCGCGCACCAGGCGCCCGC	267032	99228	GGGGCCCAAGGGGGAGGGTC
177859	10055	CTTGAACTCCTGGGCTCAAG	222446	54642	CGCCGCGCACCAGGCGCCCG	267033	99229	AGGGGCCCAAGGGGGAGGGT
177860	10056	CCTTGAACTCCTGGGCTCAA	222447	54643	CCGCCGCGCACCAGGCGCCC	267034	99230	GAGGGGCCCAAGGGGGAGGG
177861	10057	GCCTTGAACTCCTGGGCTCA	222448	54644	GCCGCCGCGCACCAGGCGCC	267035	99231	CGAGGGGCCCAAGGGGGAGG
177862	10058	AGCCTTGAACTCCTGGGCTC	222449	54645	CGCCGCCGCGCACCAGGCGC	267036	99232	TCGAGGGGCCCAAGGGGGAG
177863	10059	TAGCCTTGAACTCCTGGGCT	222450	54646	CCGCCGCCGCGCACCAGGCG	267037	99233	GTCGAGGGGCCCAAGGGGGA
177864	10060	GTAGCCTTGAACTCCTGGGC	222451	54647	TCCGCCGCCGCGCACCAGGC	267038	99234	GGTCGAGGGGCCCAAGGGGG
177865	10061	TGTAGCCTTGAACTCCTGGG	222452	54648	CTCCGCCGCCGCGCACCAGG	267039	99235	AGGTCGAGGGGCCCAAGGGG
177866	10062	CTGTAGCCTTGAACTCCTGG	222453	54649	GCTCCGCCGCCGCGCACCAG	267040	99236	AAGGTCGAGGGGCCCAAGGG
177867	10063	ACTGTAGCCTTGAACTCCTG	222454	54650	GGCTCCGCCGCCGCGCACCA	267041	99237	CAAGGTCGAGGGGCCCAAGG
177868	10064	CACTGTAGCCTTGAACTCCT	222455	54651	GGGCTCCGCCGCCGCGCACC	267042	99238	ACAAGGTCGAGGGGCCCAAG
177869	10065	TCACTGTAGCCTTGAACTCC	222456	54652	CGGGCTCCGCCGCCGCGCAC	267043	99239	AACAAGGTCGAGGGGCCCAA
177870	10066	CTCACTGTAGCCTTGAACTC	222457	54653	CCGGGCTCCGCCGCCGCGCA	267044	99240	AAACAAGGTCGAGGGGCCCA
177871	10067	GCTCACTGTAGCCTTGAACT	222458	54654	CCCGGGCTCCGCCGCCGCGC	267045	99241	GAAACAAGGTCGAGGGGCCC
177872	10068	AGCTCACTGTAGCCTTGAAC	222459	54655	TCCCGGGCTCCGCCGCCGCG	267046	99242	TGAAACAAGGTCGAGGGGCC
177873	10069	TAGCTCACTGTAGCCTTGAA	222460	54656	GTCCCGGGCTCCGCCGCCGC	267047	99243	CTGAAACAAGGTCGAGGGGC
177874	10070	ATAGCTCACTGTAGCCTTGA	222461	54657	GGTCCCGGGCTCCGCCGCCG	267048	99244	TCTGAAACAAGGTCGAGGGG
177875	10071	CATAGCTCACTGTAGCCTTG	222462	54658	AGGTCCCGGGCTCCGCCGCC	267049	99245	TTCTGAAACAAGGTCGAGGG
177876	10072	TCATAGCTCACTGTAGCCTT	222463	54659	AAGGTCCCGGGCTCCGCCGC	267050	99246	ATTCTGAAACAAGGTCGAGG
177877	10073	ATCATAGCTCACTGTAGCCT	222464	54660	GAAGGTCCCGGGCTCCGCCG	267051	99247	CATTCTGAAACAAGGTCGAG
177878	10074	AATCATAGCTCACTGTAGCC	222465	54661	GGAAGGTCCCGGGCTCCGCC	267052	99248	CCATTCTGAAACAAGGTCGA
177879	10075	CAATCATAGCTCACTGTAGC	222466	54662	AGGAAGGTCCCGGGCTCCGC	267053	99249	CCCATTCTGAAACAAGGTCG
177880	10076	ACAATCATAGCTCACTGTAG	222467	54663	AAGGAAGGTCCCGGGCTCCG	267054	99250	CCCCATTCTGAAACAAGGTC
177881	10077	GACAATCATAGCTCACTGTA	222468	54664	CAAGGAAGGTCCCGGGCTCC	267055	99251	GCCCCATTCTGAAACAAGGT
177882	10078	GGACAATCATAGCTCACTGT	222469	54665	CCAAGGAAGGTCCCGGGCTC	267056	99252	GGCCCCATTCTGAAACAAGG

177883	10079	GGGACAATCATAGCTCACTG	222470	54666	GCCAAGGAAGGTCCCGGGCT	267057	99253	GGGCCCCATTCTGAAACAAG
177884	10080	TGGGACAATCATAGCTCACT	222471	54667	AGCCAAGGAAGGTCCCGGGC	267058	99254	GGGGCCCCATTCTGAAACAA
177885	10081	ATGGGACAATCATAGCTCAC	222472	54668	CAGCCAAGGAAGGTCCCGGG	267059	99255	AGGGGCCCCATTCTGAAACA
177886	10082	TATGGGACAATCATAGCTCA	222473	54669	GCAGCCAAGGAAGGTCCCGG	267060	99256	CAGGGGCCCCATTCTGAAAC
177887	10083	CTATGGGACAATCATAGCTC	222474	54670	GGCAGCCAAGGAAGGTCCCG	267061	99257	GCAGGGGCCCCATTCTGAAA
177888	10084	GCTATGGGACAATCATAGCT	222475	54671	GGGCAGCCAAGGAAGGTCCC	267062	99258	AGCAGGGGCCCCATTCTGAA
177889	10085	TGCTATGGGACAATCATAGC	222476	54672	GGGGCAGCCAAGGAAGGTCC	267063	99259	CAGCAGGGGCCCCATTCTGA
177890	10086	GTGCTATGGGACAATCATAG	222477	54673	GGGGGCAGCCAAGGAAGGTC	267064	99260	CCAGCAGGGGCCCCATTCTG
177891	10087	AGTGCTATGGGACAATCATA	222478	54674	AGGGGGCAGCCAAGGAAGGT	267065	99261	CCCAGCAGGGGCCCCATTCT
177892	10088	GAGTGCTATGGGACAATCAT	222479	54675	TAGGGGGCAGCCAAGGAAGG	267066	99262	GCCCAGCAGGGGCCCCATTC
177893	10089	GGAGTGCTATGGGACAATCA	222480	54676	CTAGGGGGCAGCCAAGGAAG	267067	99263	GGCCCAGCAGGGGCCCCATT
177894	10090	TGGAGTGCTATGGGACAATC	222481	54677	GCTAGGGGGCAGCCAAGGAA	267068	99264	TGGCCCAGCAGGGGCCCCAT
177895	10091	CTGGAGTGCTATGGGACAAT	222482	54678	CGCTAGGGGGCAGCCAAGGA	267069	99265	CTGGCCCAGCAGGGGCCCCA
177896	10092	GCTGGAGTGCTATGGGACAA	222483	54679	TCGCTAGGGGGCAGCCAAGG	267070	99266	GCTGGCCCAGCAGGGGCCCC
177897	10093	GGCTGGAGTGCTATGGGACA	222484	54680	CTCGCTAGGGGGCAGCCAAG	267071	99267	AGCTGGCCCAGCAGGGGCCC
177898	10094	AGGCTGGAGTGCTATGGGAC	222485	54681	CCTCGCTAGGGGGCAGCCAA	267072	99268	CAGCTGGCCCAGCAGGGGCC
177899	10095	CAGGCTGGAGTGCTATGGGA	222486	54682	CCCTCGCTAGGGGGCAGCCA	267073	99269	ACAGCTGGCCCAGCAGGGGC
177900	10096	CCAGGCTGGAGTGCTATGGG	222487	54683	GCCCTCGCTAGGGGGCAGCC	267074	99270	CACAGCTGGCCCAGCAGGGG
177901	10097	CCCAGGCTGGAGTGCTATGG	222488	54684	GGCCCTCGCTAGGGGGCAGC	267075	99271	CCACAGCTGGCCCAGCAGGG
177902	10098	ACCCAGGCTGGAGTGCTATG	222489	54685	CGGCCCTCGCTAGGGGGCAG	267076	99272	CCCACAGCTGGCCCAGCAGG
177903	10099	TACCCAGGCTGGAGTGCTAT	222490	54686	GCGGCCCTCGCTAGGGGGCA	267077	99273	ACCCACAGCTGGCCCAGCAG
177904	10100	TTACCCAGGCTGGAGTGCTA	222491	54687	TGCGGCCCTCGCTAGGGGGC	267078	99274	CACCCACAGCTGGCCCAGCA
177905	10101	GTTACCCAGGCTGGAGTGCT	222492	54688	CTGCGGCCCTCGCTAGGGGG	267079	99275	GCACCCACAGCTGGCCCAGC
177906	10102	TGTTACCCAGGCTGGAGTGC	222493	54689	GCTGCGGCCCTCGCTAGGGG	267080	99276	GGCACCCACAGCTGGCCCAG
177907	10103	GTGTTACCCAGGCTGGAGTG	222494	54690	CGCTGCGGCCCTCGCTAGGG	267081	99277	AGGCACCCACAGCTGGCCCA
177908	10104	TGTGTTACCCAGGCTGGAGT	222495	54691	GCGCTGCGGCCCTCGCTAGG	267082	99278	CAGGCACCCACAGCTGGCCC
177909	10105	CTGTGTTACCCAGGCTGGAG	222496	54692	TGCGCTGCGGCCCTCGCTAG	267083	99279	GCAGGCACCCACAGCTGGCC
177910	10106	GCTGTGTTACCCAGGCTGGA	222497	54693	CTGCGCTGCGGCCCTCGCTA	267084	99280	GGCAGGCACCCACAGCTGGC
177911	10107	TGCTGTGTTACCCAGGCTGG	222498	54694	GCTGCGCTGCGGCCCTCGCT	267085	99281	TGGCAGGCACCCACAGCTGG
177912	10108	TTGCTGTGTTACCCAGGCTG	222499	54695	GGCTGCGCTGCGGCCCTCGC	267086	99282	GTGGCAGGCACCCACAGCTG
177913	10109	CTTGCTGTGTTACCCAGGCT	222500	54696	AGGCTGCGCTGCGGCCCTCG	267087	99283	CGTGGCAGGCACCCACAGCT
177914	10110	CCTTGCTGTGTTACCCAGGC	222501	54697	CAGGCTGCGCTGCGGCCCTC	267088	99284	ACGTGGCAGGCACCCACAGC
177915	10111	GCCTTGCTGTGTTACCCAGG	222502	54698	TCAGGCTGCGCTGCGGCCCT	267089	99285	CACGTGGCAGGCACCCACAG
177916	10112	GGCCTTGCTGTGTTACCCAG	222503	54699	CTCAGGCTGCGCTGCGGCCC	267090	99286	TCACGTGGCAGGCACCCACA
177917	10113	GGGCCTTGCTGTGTTACCCA	222504	54700	TCTCAGGCTGCGCTGCGGCC	267091	99287	TTCACGTGGCAGGCACCCAC
177918	10114	AGGGCCTTGCTGTGTTACCC	222505	54701	GTCTCAGGCTGCGCTGCGGC	267092	99288	CTTCACGTGGCAGGCACCCA
177919	10115	CAGGGCCTTGCTGTGTTACC	222506	54702	TGTCTCAGGCTGCGCTGCGG	267093	99289	CCTTCACGTGGCAGGCACCC
177920	10116	ACAGGGCCTTGCTGTGTTAC	222507	54703	GTGTCTCAGGCTGCGCTGCG	267094	99290	TCCTTCACGTGGCAGGCACC
177921	10117	GACAGGGCCTTGCTGTGTTA	222508	54704	GGTGTCTCAGGCTGCGCTGC	267095	99291	GTCCTTCACGTGGCAGGCAC
177922	10118	AGACAGGGCCTTGCTGTGTT	222509	54705	GGGTGTCTCAGGCTGCGCTG	267096	99292	AGTCCTTCACGTGGCAGGCA
177923	10119	GAGACAGGGCCTTGCTGTGT	222510	54706	CGGGTGTCTCAGGCTGCGCT	267097	99293	GAGTCCTTCACGTGGCAGGC
177924	10120	AGAGACAGGGCCTTGCTGTG	222511	54707	GCGGGTGTCTCAGGCTGCGC	267098	99294	TGAGTCCTTCACGTGGCAGG
177925	10121	TAGAGACAGGGCCTTGCTGT	222512	54708	GGCGGGTGTCTCAGGCTGCG	267099	99295	ATGAGTCCTTCACGTGGCAG
177926	10122	TTAGAGACAGGGCCTTGCTG	222513	54709	CGGCGGGTGTCTCAGGCTGC	267100	99296	AATGAGTCCTTCACGTGGCA
177927	10123	TTTAGAGACAGGGCCTTGCT	222514	54710	CCGGCGGGTGTCTCAGGCTG	267101	99297	TAATGAGTCCTTCACGTGGC
177928	10124	GTTTAGAGACAGGGCCTTGC	222515	54711	CCCGGCGGGTGTCTCAGGCT	267102	99298	TTAATGAGTCCTTCACGTGG
177929	10125	AGTTTAGAGACAGGGCCTTG	222516	54712	CCCCGGCGGGTGTCTCAGGC	267103	99299	CTTAATGAGTCCTTCACGTG
177930	10126	AAGTTTAGAGACAGGGCCTT	222517	54713	GCCCCGGCGGGTGTCTCAGG	267104	99300	CCTTAATGAGTCCTTCACGT
177931	10127	AAAGTTTAGAGACAGGGCCT	222518	54714	GGCCCCGGCGGGTGTCTCAG	267105	99301	GCCTTAATGAGTCCTTCACG
177932	10128	AAAAGTTTAGAGACAGGGCC	222519	54715	CGGCCCCGGCGGGTGTCTCA	267106	99302	GGCCTTAATGAGTCCTTCAC
177933	10129	AAAAAGTTTAGAGACAGGGC	222520	54716	GCGGCCCCGGCGGGTGTCTC	267107	99303	GGGCCTTAATGAGTCCTTCA
177934	10130	AAAAAAGTTTAGAGACAGGG	222521	54717	AGCGGCCCCGGCGGGTGTCT	267108	99304	AGGGCCTTAATGAGTCCTTC
177935	10131	AAAAAAAGTTTAGAGACAGG	222522	54718	GAGCGGCCCCGGCGGGTGTC	267109	99305	CAGGGCCTTAATGAGTCCTT
177936	10132	AAAAAAAAGTTTAGAGACAG	222523	54719	GGAGCGGCCCCGGCGGGTGT	267110	99306	ACAGGGCCTTAATGAGTCCT
177937	10133	AAAAAAAAAGTTTAGAGACA	222524	54720	TGGAGCGGCCCCGGCGGGTG	267111	99307	AACAGGGCCTTAATGAGTCC
177938	10134	AAAAAAAAAAGTTTAGAGAC	222525	54721	GTGGAGCGGCCCCGGCGGGT	267112	99308	AAACAGGGCCTTAATGAGTC
177939	10135	AAAAAAAAAAAGTTTAGAGA	222526	54722	CGTGGAGCGGCCCCGGCGGG	267113	99309	TAAACAGGGCCTTAATGAGT
177940	10136	TAAAAAAAAAAAGTTTAGAG	222527	54723	CCGTGGAGCGGCCCCGGCGG	267114	99310	TTAAACAGGGCCTTAATGAG
177941	10137	TTAAAAAAAAAAAGTTTAGA	222528	54724	GCCGTGGAGCGGCCCCGGCG	267115	99311	CTTAAACAGGGCCTTAATGA
177942	10138	ATTAAAAAAAAAAAGTTTAG	222529	54725	GGCCGTGGAGCGGCCCCGGC	267116	99312	GCTTAAACAGGGCCTTAATG
177943	10139	AATTAAAAAAAAAAAGTTTA	222530	54726	CGGCCGTGGAGCGGCCCCGG	267117	99313	GGCTTAAACAGGGCCTTAAT
177944	10140	GAATTAAAAAAAAAAAGTTT	222531	54727	ACGGCCGTGGAGCGGCCCCG	267118	99314	AGGCTTAAACAGGGCCTTAA
177945	10141	AGAATTAAAAAAAAAAAGTT	222532	54728	GACGGCCGTGGAGCGGCCCC	267119	99315	CAGGCTTAAACAGGGCCTTA
177946	10142	TAGAATTAAAAAAAAAAAGT	222533	54729	CGACGGCCGTGGAGCGGCCC	267120	99316	TCAGGCTTAAACAGGGCCTT
177947	10143	ATAGAATTAAAAAAAAAAAG	222534	54730	CCGACGGCCGTGGAGCGGCC	267121	99317	ATCAGGCTTAAACAGGGCCT
177948	10144	AATAGAATTAAAAAAAAAAA	222535	54731	TCCGACGGCCGTGGAGCGGC	267122	99318	CATCAGGCTTAAACAGGGCC
177949	10145	AAATAGAATTAAAAAAAAAA	222536	54732	ATCCGACGGCCGTGGAGCGG	267123	99319	TCATCAGGCTTAAACAGGGC
177950	10146	TAAATAGAATTAAAAAAAAA	222537	54733	AATCCGACGGCCGTGGAGCG	267124	99320	ATCATCAGGCTTAAACAGGG
177951	10147	ATAAATAGAATTAAAAAAAA	222538	54734	AAATCCGACGGCCGTGGAGC	267125	99321	TATCATCAGGCTTAAACAGG
177952	10148	TATAAATAGAATTAAAAAAA	222539	54735	TAAATCCGACGGCCGTGGAG	267126	99322	TTATCATCAGGCTTAAACAG
177953	10149	ATATAAATAGAATTAAAAAA	222540	54736	CTAAATCCGACGGCCGTGGA	267127	99323	ATTATCATCAGGCTTAAACA
177954	10150	AATATAAATAGAATTAAAAA	222541	54737	TCTAAATCCGACGGCCGTGG	267128	99324	TATTATCATCAGGCTTAAAC

177955	10151	AAATATAAATAGAATTAAAA	222542	54738	GTCTAAATCCGACGGCCGTG	267129	99325	TTATTATCATCAGGCTTAAA
177956	10152	TAAATATAAATAGAATTAAA	222543	54739	AGTCTAAATCCGACGGCCGT	267130	99326	CTTATTATCATCAGGCTTAA
177957	10153	GTAAATATAAATAGAATTAA	222544	54740	CAGTCTAAATCCGACGGCCG	267131	99327	CCTTATTATCATCAGGCTTA
177958	10154	TGTAAATATAAATAGAATTA	222545	54741	CCAGTCTAAATCCGACGGCC	267132	99328	GCCTTATTATCATCAGGCTT
177959	10155	ATGTAAATATAAATAGAATT	222546	54742	TCCAGTCTAAATCCGACGGC	267133	99329	AGCCTTATTATCATCAGGCT
177960	10156	CATGTAAATATAAATAGAAT	222547	54743	TTCCAGTCTAAATCCGACGG	267134	99330	AAGCCTTATTATCATCAGGC
177961	10157	ACATGTAAATATAAATAGAA	222548	54744	CTTCCAGTCTAAATCCGACG	267135	99331	AAAGCCTTATTATCATCAGG
177962	10158	TACATGTAAATATAAATAGA	222549	54745	GCTTCCAGTCTAAATCCGAC	267136	99332	GAAAGCCTTATTATCATCAG
177963	10159	ATACATGTAAATATAAATAG	222550	54746	AGCTTCCAGTCTAAATCCGA	267137	99333	CGAAAGCCTTATTATCATCA
177964	10160	AATACATGTAAATATAAATA	222551	54747	GAGCTTCCAGTCTAAATCCG	267138	99334	ACGAAAGCCTTATTATCATC
177965	10161	AAATACATGTAAATATAAAT	222552	54748	CGAGCTTCCAGTCTAAATCC	267139	99335	CACGAAAGCCTTATTATCAT
177966	10162	TAAATACATGTAAATATAAA	222553	54749	CCGAGCTTCCAGTCTAAATC	267140	99336	CCACGAAAGCCTTATTATCA
177967	10163	TTAAATACATGTAAATATAA	222554	54750	ACCGAGCTTCCAGTCTAAAT	267141	99337	TCCACGAAAGCCTTATTATC
177968	10164	TTTAAATACATGTAAATATA	222555	54751	GACCGAGCTTCCAGTCTAAA	267142	99338	ATCCACGAAAGCCTTATTAT
177969	10165	ATTTAAATACATGTAAATAT	222556	54752	GGACCGAGCTTCCAGTCTAA	267143	99339	AATCCACGAAAGCCTTATTA
177970	10166	CATTTAAATACATGTAAATA	222557	54753	TGGACCGAGCTTCCAGTCTA	267144	99340	AAATCCACGAAAGCCTTATT
177971	10167	ACATTTAAATACATGTAAAT	222558	54754	CTGGACCGAGCTTCCAGTCT	267145	99341	AAAATCCACGAAAGCCTTAT
177972	10168	CACATTTAAATACATGTAAA	222559	54755	CCTGGACCGAGCTTCCAGTC	267146	99342	AAAAATCCACGAAAGCCTTA
177973	10169	TCACATTTAAATACATGTAA	222560	54756	ACCTGGACCGAGCTTCCAGT	267147	99343	GAAAAATCCACGAAAGCCTT
177974	10170	TTCACATTTAAATACATGTA	222561	54757	GACCTGGACCGAGCTTCCAG	267148	99344	AGAAAAATCCACGAAAGCCT
177975	10171	ATTCACATTTAAATACATGT	222562	54758	GGACCTGGACCGAGCTTCCA	267149	99345	GAGAAAAATCCACGAAAGCC
177976	10172	TATTCACATTTAAATACATG	222563	54759	GGGACCTGGACCGAGCTTCC	267150	99346	AGAGAAAAATCCACGAAAGC
177977	10173	ATATTCACATTTAAATACAT	222564	54760	GGGGACCTGGACCGAGCTTC	267151	99347	AAGAGAAAAATCCACGAAAG
177978	10174	AATATTCACATTTAAATACA	222565	54761	TGGGGACCTGGACCGAGCTT	267152	99348	AAAGAGAAAAATCCACGAAA
177979	10175	GAATATTCACATTTAAATAC	222566	54762	CTGGGGACCTGGACCGAGCT	267153	99349	TAAAGAGAAAAATCCACGAA
177980	10176	TGAATATTCACATTTAAATA	222567	54763	GCTGGGGACCTGGACCGAGC	267154	99350	TTAAAGAGAAAAATCCACGA
177981	10177	GTGAATATTCACATTTAAAT	222568	54764	AGCTGGGGACCTGGACCGAG	267155	99351	CTTAAAGAGAAAAATCCACG
177982	10178	AGTGAATATTCACATTTAAA	222569	54765	AAGCTGGGGACCTGGACCGA	267156	99352	GCTTAAAGAGAAAAATCCAC
177983	10179	TAGTGAATATTCACATTTAA	222570	54766	CAAGCTGGGGACCTGGACCG	267157	99353	CGCTTAAAGAGAAAAATCCA
177984	10180	GTAGTGAATATTCACATTTA	222571	54767	TCAAGCTGGGGACCTGGACC	267158	99354	TCGCTTAAAGAGAAAAATCC
177985	10181	GGTAGTGAATATTCACATTT	222572	54768	ATCAAGCTGGGGACCTGGAC	267159	99355	GTCGCTTAAAGAGAAAAATC
177986	10182	AGGTAGTGAATATTCACATT	222573	54769	CATCAAGCTGGGGACCTGGA	267160	99356	AGTCGCTTAAAGAGAAAAAT
177987	10183	TAGGTAGTGAATATTCACAT	222574	54770	GCATCAAGCTGGGGACCTGG	267161	99357	TAGTCGCTTAAAGAGAAAAA
177988	10184	ATAGGTAGTGAATATTCACA	222575	54771	CGCATCAAGCTGGGGACCTG	267162	99358	TTAGTCGCTTAAAGAGAAAA
177989	10185	AATAGGTAGTGAATATTCAC	222576	54772	GCGCATCAAGCTGGGGACCT	267163	99359	CTTAGTCGCTTAAAGAGAAA
177990	10186	AAATAGGTAGTGAATATTCA	222577	54773	GGCGCATCAAGCTGGGGACC	267164	99360	GCTTAGTCGCTTAAAGAGAA
177991	10187	CAAATAGGTAGTGAATATTC	222578	54774	GGGCGCATCAAGCTGGGGAC	267165	99361	TGCTTAGTCGCTTAAAGAGA
177992	10188	ACAAATAGGTAGTGAATATT	222579	54775	CGGGCGCATCAAGCTGGGGA	267166	99362	TTGCTTAGTCGCTTAAAGAG
177993	10189	AACAAATAGGTAGTGAATAT	222580	54776	GCGGGCGCATCAAGCTGGGG	267167	99363	CTTGCTTAGTCGCTTAAAGA
177994	10190	CAACAAATAGGTAGTGAATA	222581	54777	CGCGGGCGCATCAAGCTGGG	267168	99364	ACTTGCTTAGTCGCTTAAAG
177995	10191	GCAACAAATAGGTAGTGAAT	222582	54778	CCGCGGGCGCATCAAGCTGG	267169	99365	GACTTGCTTAGTCGCTTAAA
177996	10192	TGCAACAAATAGGTAGTGAA	222583	54779	ACCGCGGGCGCATCAAGCTG	267170	99366	GGACTTGCTTAGTCGCTTAA
177997	10193	ATGCAACAAATAGGTAGTGA	222584	54780	CACCGCGGGCGCATCAAGCT	267171	99367	TGGACTTGCTTAGTCGCTTA
177998	10194	CATGCAACAAATAGGTAGTG	222585	54781	ACACCGCGGGCGCATCAAGC	267172	99368	CTGGACTTGCTTAGTCGCTT
177999	10195	GCATGCAACAAATAGGTAGT	222586	54782	TACACCGCGGGCGCATCAAG	267173	99369	TCTGGACTTGCTTAGTCGCT
178000	10196	GGCATGCAACAAATAGGTAG	222587	54783	CTACACCGCGGGCGCATCAA	267174	99370	CTCTGGACTTGCTTAGTCGC
178001	10197	AGGCATGCAACAAATAGGTA	222588	54784	CCTACACCGCGGGCGCATCA	267175	99371	TCTCTGGACTTGCTTAGTCG
178002	10198	CAGGCATGCAACAAATAGGT	222589	54785	TCCTACACCGCGGGCGCATC	267176	99372	TTCTCTGGACTTGCTTAGTC
178003	10199	GCAGGCATGCAACAAATAGG	222590	54786	CTCCTACACCGCGGGCGCAT	267177	99373	CTTCTCTGGACTTGCTTAGT
178004	10200	TGCAGGCATGCAACAAATAG	222591	54787	TCTCCTACACCGCGGGCGCA	267178	99374	TCTTCTCTGGACTTGCTTAG
178005	10201	ATGCAGGCATGCAACAAATA	222592	54788	GTCTCCTACACCGCGGGCGC	267179	99375	GTCTTCTCTGGACTTGCTTA
178006	10202	AATGCAGGCATGCAACAAAT	222593	54789	GGTCTCCTACACCGCGGGCG	267180	99376	GGTCTTCTCTGGACTTGCTT
178007	10203	AAATGCAGGCATGCAACAAA	222594	54790	TGGTCTCCTACACCGCGGGC	267181	99377	TGGTCTTCTCTGGACTTGCT
178008	10204	AAAATGCAGGCATGCAACAA	222595	54791	CTGGTCTCCTACACCGCGGG	267182	99378	GTGGTCTTCTCTGGACTTGC
178009	10205	AAAAATGCAGGCATGCAACA	222596	54792	GCTGGTCTCCTACACCGCGG	267183	99379	GGTGGTCTTCTCTGGACTTG
178010	10206	AAAAAATGCAGGCATGCAAC	222597	54793	GGCTGGTCTCCTACACCGCG	267184	99380	GGGTGGTCTTCTCTGGACTT
178011	10207	TAAAAAATGCAGGCATGCAA	222598	54794	GGGCTGGTCTCCTACACCGC	267185	99381	GGGGTGGTCTTCTCTGGACT
178012	10208	ATAAAAAATGCAGGCATGCA	222599	54795	CGGGCTGGTCTCCTACACCG	267186	99382	GGGGGTGGTCTTCTCTGGAC
178013	10209	TATAAAAAATGCAGGCATGC	222600	54796	TCGGGCTGGTCTCCTACACC	267187	99383	AGGGGGTGGTCTTCTCTGGA
178014	10210	GTATAAAAAATGCAGGCATG	222601	54797	GTCGGGCTGGTCTCCTACAC	267188	99384	CAGGGGGTGGTCTTCTCTGG
178015	10211	AGTATAAAAAATGCAGGCAT	222602	54798	AGTCGGGCTGGTCTCCTACA	267189	99385	GCAGGGGGTGGTCTTCTCTG
178016	10212	CAGTATAAAAAATGCAGGCA	222603	54799	GAGTCGGGCTGGTCTCCTAC	267190	99386	TGCAGGGGGTGGTCTTCTCT
178017	10213	CCAGTATAAAAAATGCAGGC	222604	54800	CGAGTCGGGCTGGTCTCCTA	267191	99387	CTGCAGGGGGTGGTCTTCTC
178018	10214	CCCAGTATAAAAAATGCAGG	222605	54801	CCGAGTCGGGCTGGTCTCCT	267192	99388	CCTGCAGGGGGTGGTCTTCT
178019	10215	GCCCAGTATAAAAAATGCAG	222606	54802	CCCGAGTCGGGCTGGTCTCC	267193	99389	CCCTGCAGGGGGTGGTCTTC
178020	10216	AGCCCAGTATAAAAAATGCA	222607	54803	GCCCGAGTCGGGCTGGTCTC	267194	99390	GCCCTGCAGGGGGTGGTCTT
178021	10217	AAGCCCAGTATAAAAAATGC	222608	54804	AGCCCGAGTCGGGCTGGTCT	267195	99391	GGCCCTGCAGGGGGTGGTCT
178022	10218	CAAGCCCAGTATAAAAAATG	222609	54805	AAGCCCGAGTCGGGCTGGTC	267196	99392	GGGCCCTGCAGGGGGTGGTC
178023	10219	GCAAGCCCAGTATAAAAAAT	222610	54806	GAAGCCCGAGTCGGGCTGGT	267197	99393	TGGGCCCTGCAGGGGGTGGT
178024	10220	GGCAAGCCCAGTATAAAAAA	222611	54807	GGAAGCCCGAGTCGGGCTGG	267198	99394	CTGGGCCCTGCAGGGGGTGG
178025	10221	TGGCAAGCCCAGTATAAAAA	222612	54808	GGGAAGCCCGAGTCGGGCTG	267199	99395	TCTGGGCCCTGCAGGGGGTG
178026	10222	TTGGCAAGCCCAGTATAAAA	222613	54809	GGGGAAGCCCGAGTCGGGCT	267200	99396	ATCTGGGCCCTGCAGGGGGT

178027	10223	TTTGGCAAGCCCAGTATAAA	222614	54810	AGGGGAAGCCCGAGTCGGGC	267201	99397	GATCTGGGCCCTGCAGGGGG
178028	10224	TTTTGGCAAGCCCAGTATAA	222615	54811	CAGGGGAAGCCCGAGTCGGG	267202	99398	AGATCTGGGCCCTGCAGGGG
178029	10225	TTTTTGGCAAGCCCAGTATA	222616	54812	TCAGGGGAAGCCCGAGTCGG	267203	99399	CAGATCTGGGCCCTGCAGGG
178030	10226	GTTTTTGGCAAGCCCAGTAT	222617	54813	CTCAGGGGAAGCCCGAGTCG	267204	99400	TCAGATCTGGGCCCTGCAGG
178031	10227	GGTTTTTGGCAAGCCCAGTA	222618	54814	GCTCAGGGGAAGCCCGAGTC	267205	99401	CTCAGATCTGGGCCCTGCAG
178032	10228	GGGTTTTTGGCAAGCCCAGT	222619	54815	GGCTCAGGGGAAGCCCGAGT	267206	99402	TCTCAGATCTGGGCCCTGCA
178033	10229	CGGGTTTTTGGCAAGCCCAG	222620	54816	GGGCTCAGGGGAAGCCCGAG	267207	99403	CTCTCAGATCTGGGCCCTGC
178034	10230	TCGGGTTTTTGGCAAGCCCA	222621	54817	GGGGCTCAGGGGAAGCCCGA	267208	99404	TCTCTCAGATCTGGGCCCTG
178035	10231	TTCGGGTTTTTGGCAAGCCC	222622	54818	AGGGGCTCAGGGGAAGCCCG	267209	99405	CTCTCTCAGATCTGGGCCCT
178036	10232	GTTCGGGTTTTTGGCAAGCC	222623	54819	CAGGGGCTCAGGGGAAGCCC	267210	99406	CCTCTCTCAGATCTGGGCCC
178037	10233	TGTTCGGGTTTTTGGCAAGC	222624	54820	CCAGGGGCTCAGGGGAAGCC	267211	99407	ACCTCTCTCAGATCTGGGCC
178038	10234	CTGTTCGGGTTTTTGGCAAG	222625	54821	TCCAGGGGCTCAGGGGAAGC	267212	99408	TACCTCTCTCAGATCTGGGC
178039	10235	GCTGTTCGGGTTTTTGGCAA	222626	54822	GTCCAGGGGCTCAGGGGAAG	267213	99409	GTACCTCTCTCAGATCTGGG
178040	10236	AGCTGTTCGGGTTTTTGGCA	222627	54823	AGTCCAGGGGCTCAGGGGAA	267214	99410	AGTACCTCTCTCAGATCTGG
178041	10237	AAGCTGTTCGGGTTTTTGGC	222628	54824	GAGTCCAGGGGCTCAGGGGA	267215	99411	GAGTACCTCTCTCAGATCTG
178042	10238	AAAGCTGTTCGGGTTTTTGG	222629	54825	AGAGTCCAGGGGCTCAGGGG	267216	99412	CGAGTACCTCTCTCAGATCT
178043	10239	GAAAGCTGTTCGGGTTTTTG	222630	54826	AAGAGTCCAGGGGCTCAGGG	267217	99413	CCGAGTACCTCTCTCAGATC
178044	10240	AGAAAGCTGTTCGGGTTTTT	222631	54827	CAAGAGTCCAGGGGCTCAGG	267218	99414	CCCGAGTACCTCTCTCAGAT
178045	10241	TAGAAAGCTGTTCGGGTTTT	222632	54828	TCAAGAGTCCAGGGGCTCAG	267219	99415	TCCCGAGTACCTCTCTCAGA
178046	10242	GTAGAAAGCTGTTCGGGTTT	222633	54829	GTCAAGAGTCCAGGGGCTCA	267220	99416	CTCCCGAGTACCTCTCTCAG
178047	10243	AGTAGAAAGCTGTTCGGGTT	222634	54830	AGTCAAGAGTCCAGGGGCTC	267221	99417	GCTCCCGAGTACCTCTCTCA
178048	10244	AAGTAGAAAGCTGTTCGGGT	222635	54831	GAGTCAAGAGTCCAGGGGCT	267222	99418	GGCTCCCGAGTACCTCTCTC
178049	10245	AAAGTAGAAAGCTGTTCGGG	222636	54832	GGAGTCAAGAGTCCAGGGGC	267223	99419	AGGCTCCCGAGTACCTCTCT
178050	10246	CAAAGTAGAAAGCTGTTCGG	222637	54833	TGGAGTCAAGAGTCCAGGGG	267224	99420	TAGGCTCCCGAGTACCTCTC
178051	10247	TCAAAGTAGAAAGCTGTTCG	222638	54834	CTGGAGTCAAGAGTCCAGGG	267225	99421	GTAGGCTCCCGAGTACCTCT
178052	10248	GTCAAAGTAGAAAGCTGTTC	222639	54835	GCTGGAGTCAAGAGTCCAGG	267226	99422	AGTAGGCTCCCGAGTACCTC
178053	10249	TGTCAAAGTAGAAAGCTGTT	222640	54836	TGCTGGAGTCAAGAGTCCAG	267227	99423	AAGTAGGCTCCCGAGTACCT
178054	10250	TTGTCAAAGTAGAAAGCTGT	222641	54837	CTGCTGGAGTCAAGAGTCCA	267228	99424	GAAGTAGGCTCCCGAGTACC
178055	10251	ATTGTCAAAGTAGAAAGCTG	222642	54838	CCTGCTGGAGTCAAGAGTCC	267229	99425	CGAAGTAGGCTCCCGAGTAC
178056	10252	CATTGTCAAAGTAGAAAGCT	222643	54839	CCCTGCTGGAGTCAAGAGTC	267230	99426	GCGAAGTAGGCTCCCGAGTA
178057	10253	ACATTGTCAAAGTAGAAAGC	222644	54840	GCCCTGCTGGAGTCAAGAGT	267231	99427	AGCGAAGTAGGCTCCCGAGT
178058	10254	TACATTGTCAAAGTAGAAAG	222645	54841	GGCCCTGCTGGAGTCAAGAG	267232	99428	CAGCGAAGTAGGCTCCCGAG
178059	10255	ATACATTGTCAAAGTAGAAA	222646	54842	AGGCCCTGCTGGAGTCAAGA	267233	99429	CCAGCGAAGTAGGCTCCCGA
178060	10256	GATACATTGTCAAAGTAGAA	222647	54843	CAGGCCCTGCTGGAGTCAAG	267234	99430	CCCAGCGAAGTAGGCTCCCG
178061	10257	TGATACATTGTCAAAGTAGA	222648	54844	CCAGGCCCTGCTGGAGTCAA	267235	99431	TCCCAGCGAAGTAGGCTCCC
178062	10258	CTGATACATTGTCAAAGTAG	222649	54845	CCCAGGCCCTGCTGGAGTCA	267236	99432	CTCCCAGCGAAGTAGGCTCC
178063	10259	TCTGATACATTGTCAAAGTA	222650	54846	ACCCAGGCCCTGCTGGAGTC	267237	99433	GCTCCCAGCGAAGTAGGCTC
178064	10260	TTCTGATACATTGTCAAAGT	222651	54847	TACCCAGGCCCTGCTGGAGT	267238	99434	TGCTCCCAGCGAAGTAGGCT
178065	10261	ATTCTGATACATTGTCAAAG	222652	54848	TTACCCAGGCCCTGCTGGAG	267239	99435	CTGCTCCCAGCGAAGTAGGC
178066	10262	AATTCTGATACATTGTCAAA	222653	54849	ATTACCCAGGCCCTGCTGGA	267240	99436	GCTGCTCCCAGCGAAGTAGG
178067	10263	AAATTCTGATACATTGTCAA	222654	54850	CATTACCCAGGCCCTGCTGG	267241	99437	GGCTGCTCCCAGCGAAGTAG
178068	10264	TAAATTCTGATACATTGTCA	222655	54851	TCATTACCCAGGCCCTGCTG	267242	99438	AGGCTGCTCCCAGCGAAGTA
178069	10265	TTAAATTCTGATACATTGTC	222656	54852	TTCATTACCCAGGCCCTGCT	267243	99439	GAGGCTGCTCCCAGCGAAGT
178070	10266	TTTAAATTCTGATACATTGT	222657	54853	GTTCATTACCCAGGCCCTGC	267244	99440	GGAGGCTGCTCCCAGCGAAG
178071	10267	ATTTAAATTCTGATACATTG	222658	54854	CGTTCATTACCCAGGCCCTG	267245	99441	GGGAGGCTGCTCCCAGCGAA
178072	10268	GATTTAAATTCTGATACATT	222659	54855	ACGTTCATTACCCAGGCCCT	267246	99442	AGGGAGGCTGCTCCCAGCGA
178073	10269	TGATTTAAATTCTGATACAT	222660	54856	GACGTTCATTACCCAGGCCC	267247	99443	AAGGGAGGCTGCTCCCAGCG
178074	10270	CTGATTTAAATTCTGATACA	222661	54857	TGACGTTCATTACCCAGGCC	267248	99444	AAAGGGAGGCTGCTCCCAGC
178075	10271	GCTGATTTAAATTCTGATAC	222662	54858	CTGACGTTCATTACCCAGGC	267249	99445	CAAAGGGAGGCTGCTCCCAG
178076	10272	TGCTGATTTAAATTCTGATA	222663	54859	GCTGACGTTCATTACCCAGG	267250	99446	GCAAAGGGAGGCTGCTCCCA
178077	10273	TTGCTGATTTAAATTCTGAT	222664	54860	AGCTGACGTTCATTACCCAG	267251	99447	CGCAAAGGGAGGCTGCTCCC
178078	10274	ATTGCTGATTTAAATTCTGA	222665	54861	GAGCTGACGTTCATTACCCA	267252	99448	ACGCAAAGGGAGGCTGCTCC
178079	10275	TATTGCTGATTTAAATTCTG	222666	54862	GGAGCTGACGTTCATTACCC	267253	99449	CACGCAAAGGGAGGCTGCTC
178080	10276	ATATTGCTGATTTAAATTCT	222667	54863	GGGAGCTGACGTTCATTACC	267254	99450	ACACGCAAAGGGAGGCTGCT
178081	10277	CATATTGCTGATTTAAATTC	222668	54864	GGGGAGCTGACGTTCATTAC	267255	99451	CACACGCAAAGGGAGGCTGC
178082	10278	ACATATTGCTGATTTAAATT	222669	54865	AGGGGAGCTGACGTTCATTA	267256	99452	ACACACGCAAAGGGAGGCTG
178083	10279	AACATATTGCTGATTTAAAT	222670	54866	AAGGGGAGCTGACGTTCATT	267257	99453	CACACACGCAAAGGGAGGCT
178084	10280	TAACATATTGCTGATTTAAA	222671	54867	AAAGGGGAGCTGACGTTCAT	267258	99454	CCACACACGCAAAGGGAGGC
178085	10281	TTAACATATTGCTGATTTAA	222672	54868	GAAAGGGGAGCTGACGTTCA	267259	99455	GCCACACACGCAAAGGGAGG
178086	10282	ATTAACATATTGCTGATTTA	222673	54869	GGAAAGGGGAGCTGACGTTC	267260	99456	GGCCACACACGCAAAGGGAG
178087	10283	TATTAACATATTGCTGATTT	222674	54870	GGGAAAGGGGAGCTGACGTT	267261	99457	TGGCCACACACGCAAAGGGA
178088	10284	TTATTAACATATTGCTGATT	222675	54871	TGGGAAAGGGGAGCTGACGT	267262	99458	ATGGCCACACACGCAAAGGG
178089	10285	CTTATTAACATATTGCTGAT	222676	54872	TTGGGAAAGGGGAGCTGACG	267263	99459	AATGGCCACACACGCAAAGG
178090	10286	GCTTATTAACATATTGCTGA	222677	54873	TTTGGGAAAGGGGAGCTGAC	267264	99460	GAATGGCCACACACGCAAAG
178091	10287	GGCTTATTAACATATTGCTG	222678	54874	CTTTGGGAAAGGGGAGCTGA	267265	99461	TGAATGGCCACACACGCAAA
178092	10288	TGGCTTATTAACATATTGCT	222679	54875	CCTTTGGGAAAGGGGAGCTG	267266	99462	GTGAATGGCCACACACGCAA
178093	10289	TTGGCTTATTAACATATTGC	222680	54876	CCCTTTGGGAAAGGGGAGCT	267267	99463	AGTGAATGGCCACACACGCA
178094	10290	CTTGGCTTATTAACATATTG	222681	54877	CCCCTTTGGGAAAGGGGAGC	267268	99464	CAGTGAATGGCCACACACGC
178095	10291	GCTTGGCTTATTAACATATT	222682	54878	ACCCCTTTGGGAAAGGGGAG	267269	99465	CCAGTGAATGGCCACACACG
178096	10292	TGCTTGGCTTATTAACATAT	222683	54879	AACCCCTTTGGGAAAGGGGA	267270	99466	GCCAGTGAATGGCCACACAC
178097	10293	TTGCTTGGCTTATTAACATA	222684	54880	CAACCCCTTTGGGAAAGGGG	267271	99467	AGCCAGTGAATGGCCACACA
178098	10294	TTTGCTTGGCTTATTAACAT	222685	54881	GCAACCCCTTTGGGAAAGGG	267272	99468	AAGCCAGTGAATGGCCACAC

178099	10295	CTTTGCTTGGCTTATTAACA	222686	54882	AGCAACCCCTTTGGGAAAGG	267273	99469	CAAGCCAGTGAATGGCCACA
178100	10296	CCTTTGCTTGGCTTATTAAC	222687	54883	GAGCAACCCCTTTGGGAAAG	267274	99470	ACAAGCCAGTGAATGGCCAC
178101	10297	ACCTTTGCTTGGCTTATTAA	222688	54884	AGAGCAACCCCTTTGGGAAA	267275	99471	CACAAGCCAGTGAATGGCCA
178102	10298	AACCTTTGCTTGGCTTATTA	222689	54885	CAGAGCAACCCCTTTGGGAA	267276	99472	ACACAAGCCAGTGAATGGCC
178103	10299	TAACCTTTGCTTGGCTTATT	222690	54886	ACAGAGCAACCCCTTTGGGA	267277	99473	AACACAAGCCAGTGAATGGC
178104	10300	ATAACCTTTGCTTGGCTTAT	222691	54887	AACAGAGCAACCCCTTTGGG	267278	99474	AAACACAAGCCAGTGAATGG
178105	10301	TATAACCTTTGCTTGGCTTA	222692	54888	CAACAGAGCAACCCCTTTGG	267279	99475	GAAACACAAGCCAGTGAATG
178106	10302	ATATAACCTTTGCTTGGCTT	222693	54889	CCAACAGAGCAACCCCTTTG	267280	99476	AGAAACACAAGCCAGTGAAT
178107	10303	TATATAACCTTTGCTTGGCT	222694	54890	CCCAACAGAGCAACCCCTTT	267281	99477	TAGAAACACAAGCCAGTGAA
178108	10304	ATATATAACCTTTGCTTGGC	222695	54891	TCCCAACAGAGCAACCCCTT	267282	99478	CTAGAAACACAAGCCAGTGA
178109	10305	CATATATAACCTTTGCTTGG	222696	54892	TTCCCAACAGAGCAACCCCT	267283	99479	TCTAGAAACACAAGCCAGTG
178110	10306	GCATATATAACCTTTGCTTG	222697	54893	CTTCCCAACAGAGCAACCCC	267284	99480	CTCTAGAAACACAAGCCAGT
178111	10307	TGCATATATAACCTTTGCTT	222698	54894	CCTTCCCAACAGAGCAACCC	267285	99481	GCTCTAGAAACACAAGCCAG
178112	10308	TTGCATATATAACCTTTGCT	222699	54895	GCCTTCCCAACAGAGCAACC	267286	99482	GGCTCTAGAAACACAAGCCA
178113	10309	TTTGCATATATAACCTTTGC	222700	54896	TGCCTTCCCAACAGAGCAAC	267287	99483	CGGCTCTAGAAACACAAGCC
178114	10310	ATTTGCATATATAACCTTTG	222701	54897	GTGCCTTCCCAACAGAGCAA	267288	99484	CCGGCTCTAGAAACACAAGC
178115	10311	TATTTGCATATATAACCTTT	222702	54898	GGTGCCTTCCCAACAGAGCA	267289	99485	CCCGGCTCTAGAAACACAAG
178116	10312	TTATTTGCATATATAACCTT	222703	54899	GGGTGCCTTCCCAACAGAGC	267290	99486	TCCCGGCTCTAGAAACACAA
178117	10313	TTTATTTGCATATATAACCT	222704	54900	CGGGTGCCTTCCCAACAGAG	267291	99487	CTCCCGGCTCTAGAAACACA
178118	10314	TTTTATTTGCATATATAACC	222705	54901	ACGGGTGCCTTCCCAACAGA	267292	99488	CCTCCCGGCTCTAGAAACAC
178119	10315	GTTTTATTTGCATATATAAC	222706	54902	AACGGGTGCCTTCCCAACAG	267293	99489	TCCTCCCGGCTCTAGAAACA
178120	10316	AGTTTTATTTGCATATATAA	222707	54903	AAACGGGTGCCTTCCCAACA	267294	99490	GTCCTCCCGGCTCTAGAAAC
178121	10317	CAGTTTTATTTGCATATATA	222708	54904	CAAACGGGTGCCTTCCCAAC	267295	99491	GGTCCTCCCGGCTCTAGAAA
178122	10318	ACAGTTTTATTTGCATATAT	222709	54905	TCAAACGGGTGCCTTCCCAA	267296	99492	GGGTCCTCCCGGCTCTAGAA
178123	10319	AACAGTTTTATTTGCATATA	222710	54906	ATCAAACGGGTGCCTTCCCA	267297	99493	AGGGTCCTCCCGGCTCTAGA
178124	10320	CAACAGTTTTATTTGCATAT	222711	54907	TATCAAACGGGTGCCTTCCC	267298	99494	AAGGGTCCTCCCGGCTCTAG
178125	10321	ACAACAGTTTTATTTGCATA	222712	54908	GTATCAAACGGGTGCCTTCC	267299	99495	AAAGGGTCCTCCCGGCTCTA
178126	10322	GACAACAGTTTTATTTGCAT	222713	54909	TGTATCAAACGGGTGCCTTC	267300	99496	AAAAGGGTCCTCCCGGCTCT
178127	10323	AGACAACAGTTTTATTTGCA	222714	54910	CTGTATCAAACGGGTGCCTT	267301	99497	GAAAAGGGTCCTCCCGGCTC
178128	10324	TAGACAACAGTTTTATTTGC	222715	54911	ACTGTATCAAACGGGTGCCT	267302	99498	AGAAAAGGGTCCTCCCGGCT
178129	10325	ATAGACAACAGTTTTATTTG	222716	54912	TACTGTATCAAACGGGTGCC	267303	99499	CAGAAAAGGGTCCTCCCGGC
178130	10326	TATAGACAACAGTTTTATTT	222717	54913	CTACTGTATCAAACGGGTGC	267304	99500	GCAGAAAAGGGTCCTCCCGG
178131	10327	TTATAGACAACAGTTTTATT	222718	54914	GCTACTGTATCAAACGGGTG	267305	99501	TGCAGAAAAGGGTCCTCCCG
178132	10328	GTTATAGACAACAGTTTTAT	222719	54915	TGCTACTGTATCAAACGGGT	267306	99502	TTGCAGAAAAGGGTCCTCCC
178133	10329	GGTTATAGACAACAGTTTTA	222720	54916	ATGCTACTGTATCAAACGGG	267307	99503	ATTGCAGAAAAGGGTCCTCC
178134	10330	AGGTTATAGACAACAGTTTT	222721	54917	TATGCTACTGTATCAAACGG	267308	99504	CATTGCAGAAAAGGGTCCTC
178135	10331	GAGGTTATAGACAACAGTTT	222722	54918	CTATGCTACTGTATCAAACG	267309	99505	GCATTGCAGAAAAGGGTCCT
178136	10332	GGAGGTTATAGACAACAGTT	222723	54919	TCTATGCTACTGTATCAAAC	267310	99506	TGCATTGCAGAAAAGGGTCC
178137	10333	AGGAGGTTATAGACAACAGT	222724	54920	CTCTATGCTACTGTATCAAA	267311	99507	CTGCATTGCAGAAAAGGGTC
178138	10334	CAGGAGGTTATAGACAACAG	222725	54921	TCTCTATGCTACTGTATCAA	267312	99508	CCTGCATTGCAGAAAAGGGT
178139	10335	ACAGGAGGTTATAGACAACA	222726	54922	ATCTCTATGCTACTGTATCA	267313	99509	CCCTGCATTGCAGAAAAGGG
178140	10336	AACAGGAGGTTATAGACAAC	222727	54923	CATCTCTATGCTACTGTATC	267314	99510	ACCCTGCATTGCAGAAAAGG
178141	10337	TAACAGGAGGTTATAGACAA	222728	54924	CCATCTCTATGCTACTGTAT	267315	99511	AACCCTGCATTGCAGAAAAG
178142	10338	GTAACAGGAGGTTATAGACA	222729	54925	CCCATCTCTATGCTACTGTA	267316	99512	GAACCCTGCATTGCAGAAAA
178143	10339	TGTAACAGGAGGTTATAGAC	222730	54926	ACCCATCTCTATGCTACTGT	267317	99513	TGAACCCTGCATTGCAGAAA
178144	10340	GTGTAACAGGAGGTTATAGA	222731	54927	AACCCATCTCTATGCTACTG	267318	99514	GTGAACCCTGCATTGCAGAA
178145	10341	AGTGTAACAGGAGGTTATAG	222732	54928	AAACCCATCTCTATGCTACT	267319	99515	TGTGAACCCTGCATTGCAGA
178146	10342	CAGTGTAACAGGAGGTTATA	222733	54929	AAAACCCATCTCTATGCTAC	267320	99516	GTGTGAACCCTGCATTGCAG
178147	10343	CCAGTGTAACAGGAGGTTAT	222734	54930	TAAAACCCATCTCTATGCTA	267321	99517	TGTGTGAACCCTGCATTGCA
178148	10344	CCCAGTGTAACAGGAGGTTA	222735	54931	CTAAAACCCATCTCTATGCT	267322	99518	CTGTGTGAACCCTGCATTGC
178149	10345	CCCCAGTGTAACAGGAGGTT	222736	54932	GCTAAAACCCATCTCTATGC	267323	99519	CCTGTGTGAACCCTGCATTG
178150	10346	GCCCCAGTGTAACAGGAGGT	222737	54933	TGCTAAAACCCATCTCTATG	267324	99520	CCCTGTGTGAACCCTGCATT
178151	10347	TGCCCCAGTGTAACAGGAGG	222738	54934	ATGCTAAAACCCATCTCTAT	267325	99521	ACCCTGTGTGAACCCTGCAT
178152	10348	GTGCCCCAGTGTAACAGGAG	222739	54935	GATGCTAAAACCCATCTCTA	267326	99522	AACCCTGTGTGAACCCTGCA
178153	10349	TGTGCCCCAGTGTAACAGGA	222740	54936	TGATGCTAAAACCCATCTCT	267327	99523	GAACCCTGTGTGAACCCTGC
178154	10350	CTGTGCCCCAGTGTAACAGG	222741	54937	TTGATGCTAAAACCCATCTC	267328	99524	CGAACCCTGTGTGAACCCTG
178155	10351	GCTGTGCCCCAGTGTAACAG	222742	54938	TTTGATGCTAAAACCCATCT	267329	99525	GCGAACCCTGTGTGAACCCT
178156	10352	TGCTGTGCCCCAGTGTAACA	222743	54939	TTTTGATGCTAAAACCCATC	267330	99526	TGCGAACCCTGTGTGAACCC
178157	10353	TTGCTGTGCCCCAGTGTAAC	222744	54940	ATTTTGATGCTAAAACCCAT	267331	99527	CTGCGAACCCTGTGTGAACC
178158	10354	TTTGCTGTGCCCCAGTGTAA	222745	54941	TATTTTGATGCTAAAACCCA	267332	99528	GCTGCGAACCCTGTGTGAAC
178159	10355	TTTTGCTGTGCCCCAGTGTA	222746	54942	ATATTTTGATGCTAAAACCC	267333	99529	GGCTGCGAACCCTGTGTGAA
178160	10356	CTTTTGCTGTGCCCCAGTGT	222747	54943	GATATTTTGATGCTAAAACC	267334	99530	AGGCTGCGAACCCTGTGTGA
178161	10357	ACTTTTGCTGTGCCCCAGTG	222748	54944	TGATATTTTGATGCTAAAAC	267335	99531	CAGGCTGCGAACCCTGTGTG
178162	10358	GACTTTTGCTGTGCCCCAGT	222749	54945	CTGATATTTTGATGCTAAAA	267336	99532	TCAGGCTGCGAACCCTGTGT
178163	10359	TGACTTTTGCTGTGCCCCAG	222750	54946	TCTGATATTTTGATGCTAAA	267337	99533	TTCAGGCTGCGAACCCTGTG
178164	10360	ATGACTTTTGCTGTGCCCCA	222751	54947	TTCTGATATTTTGATGCTAA	267338	99534	CTTCAGGCTGCGAACCCTGT
178165	10361	CATGACTTTTGCTGTGCCCC	222752	54948	ATTCTGATATTTTGATGCTA	267339	99535	TCTTCAGGCTGCGAACCCTG
178166	10362	CCATGACTTTTGCTGTGCCC	222753	54949	AATTCTGATATTTTGATGCT	267340	99536	ATCTTCAGGCTGCGAACCCT
178167	10363	ACCATGACTTTTGCTGTGCC	222754	54950	GAATTCTGATATTTTGATGC	267341	99537	CATCTTCAGGCTGCGAACCC
178168	10364	CACCATGACTTTTGCTGTGC	222755	54951	TGAATTCTGATATTTTGATG	267342	99538	CCATCTTCAGGCTGCGAACC
178169	10365	ACACCATGACTTTTGCTGTG	222756	54952	TTGAATTCTGATATTTTGAT	267343	99539	TCCATCTTCAGGCTGCGAAC
178170	10366	TACACCATGACTTTTGCTGT	222757	54953	CTTGAATTCTGATATTTTGA	267344	99540	CTCCATCTTCAGGCTGCGAA

178171	10367	CTACACCATGACTTTTGCTG	222758	54954	GCTTGAATTCTGATATTTTG	267345	99541	GCTCCATCTTCAGGCTGCGA
178172	10368	ACTACACCATGACTTTTGCT	222759	54955	GGCTTGAATTCTGATATTTT	267346	99542	TGCTCCATCTTCAGGCTGCG
178173	10369	GACTACACCATGACTTTTGC	222760	54956	AGGCTTGAATTCTGATATTT	267347	99543	CTGCTCCATCTTCAGGCTGC
178174	10370	CGACTACACCATGACTTTTG	222761	54957	AAGGCTTGAATTCTGATATT	267348	99544	ACTGCTCCATCTTCAGGCTG
178175	10371	GCGACTACACCATGACTTTT	222762	54958	CAAGGCTTGAATTCTGATAT	267349	99545	GACTGCTCCATCTTCAGGCT
178176	10372	TGCGACTACACCATGACTTT	222763	54959	GCAAGGCTTGAATTCTGATA	267350	99546	GGACTGCTCCATCTTCAGGC
178177	10373	ATGCGACTACACCATGACTT	222764	54960	AGCAAGGCTTGAATTCTGAT	267351	99547	CGGACTGCTCCATCTTCAGG
178178	10374	CATGCGACTACACCATGACT	222765	54961	GAGCAAGGCTTGAATTCTGA	267352	99548	TCGGACTGCTCCATCTTCAG
178179	10375	ACATGCGACTACACCATGAC	222766	54962	AGAGCAAGGCTTGAATTCTG	267353	99549	TTCGGACTGCTCCATCTTCA
178180	10376	CACATGCGACTACACCATGA	222767	54963	GAGAGCAAGGCTTGAATTCT	267354	99550	ATTCGGACTGCTCCATCTTC
178181	10377	TCACATGCGACTACACCATG	222768	54964	AGAGAGCAAGGCTTGAATTC	267355	99551	AATTCGGACTGCTCCATCTT
178182	10378	TTCACATGCGACTACACCAT	222769	54965	CAGAGAGCAAGGCTTGAATT	267356	99552	GAATTCGGACTGCTCCATCT
178183	10379	GTTCACATGCGACTACACCA	222770	54966	GCAGAGAGCAAGGCTTGAAT	267357	99553	AGAATTCGGACTGCTCCATC
178184	10380	GGTTCACATGCGACTACACC	222771	54967	AGCAGAGAGCAAGGCTTGAA	267358	99554	GAGAATTCGGACTGCTCCAT
178185	10381	AGGTTCACATGCGACTACAC	222772	54968	AAGCAGAGAGCAAGGCTTGA	267359	99555	AGAGAATTCGGACTGCTCCA
178186	10382	CAGGTTCACATGCGACTACA	222773	54969	TAAGCAGAGAGCAAGGCTTG	267360	99556	AAGAGAATTCGGACTGCTCC
178187	10383	ACAGGTTCACATGCGACTAC	222774	54970	GTAAGCAGAGAGCAAGGCTT	267361	99557	GAAGAGAATTCGGACTGCTC
178188	10384	GACAGGTTCACATGCGACTA	222775	54971	AGTAAGCAGAGAGCAAGGCT	267362	99558	GGAAGAGAATTCGGACTGCT
178189	10385	GGACAGGTTCACATGCGACT	222776	54972	TAGTAAGCAGAGAGCAAGGC	267363	99559	GGGAAGAGAATTCGGACTGC
178190	10386	GGGACAGGTTCACATGCGAC	222777	54973	CTAGTAAGCAGAGAGCAAGG	267364	99560	AGGGAAGAGAATTCGGACTG
178191	10387	AGGGACAGGTTCACATGCGA	222778	54974	GCTAGTAAGCAGAGAGCAAG	267365	99561	CAGGGAAGAGAATTCGGACT
178192	10388	AAGGGACAGGTTCACATGCG	222779	54975	AGCTAGTAAGCAGAGAGCAA	267366	99562	ACAGGGAAGAGAATTCGGAC
178193	10389	AAAGGGACAGGTTCACATGC	222780	54976	CAGCTAGTAAGCAGAGAGCA	267367	99563	CACAGGGAAGAGAATTCGGA
178194	10390	GAAAGGGACAGGTTCACATG	222781	54977	ACAGCTAGTAAGCAGAGAGC	267368	99564	GCACAGGGAAGAGAATTCGG
178195	10391	TGAAAGGGACAGGTTCACAT	222782	54978	CACAGCTAGTAAGCAGAGAG	267369	99565	TGCACAGGGAAGAGAATTCG
178196	10392	ATGAAAGGGACAGGTTCACA	222783	54979	ACACAGCTAGTAAGCAGAGA	267370	99566	CTGCACAGGGAAGAGAATTC
178197	10393	TATGAAAGGGACAGGTTCAC	222784	54980	CACACAGCTAGTAAGCAGAG	267371	99567	ACTGCACAGGGAAGAGAATT
178198	10394	CTATGAAAGGGACAGGTTCA	222785	54981	TCACACAGCTAGTAAGCAGA	267372	99568	AACTGCACAGGGAAGAGAAT
178199	10395	GCTATGAAAGGGACAGGTTC	222786	54982	GTCACACAGCTAGTAAGCAG	267373	99569	AAACTGCACAGGGAAGAGAA
178200	10396	AGCTATGAAAGGGACAGGTT	222787	54983	GGTCACACAGCTAGTAAGCA	267374	99570	CAAACTGCACAGGGAAGAGA
178201	10397	CAGCTATGAAAGGGACAGGT	222788	54984	GGGTCACACAGCTAGTAAGC	267375	99571	GCAAACTGCACAGGGAAGAG
178202	10398	GCAGCTATGAAAGGGACAGG	222789	54985	AGGGTCACACAGCTAGTAAG	267376	99572	CGCAAACTGCACAGGGAAGA
178203	10399	AGCAGCTATGAAAGGGACAG	222790	54986	TAGGGTCACACAGCTAGTAA	267377	99573	GCGCAAACTGCACAGGGAAG
178204	10400	GAGCAGCTATGAAAGGGACA	222791	54987	TTAGGGTCACACAGCTAGTA	267378	99574	TGCGCAAACTGCACAGGGAA
178205	10401	TGAGCAGCTATGAAAGGGAC	222792	54988	TTTAGGGTCACACAGCTAGT	267379	99575	CTGCGCAAACTGCACAGGGA
178206	10402	ATGAGCAGCTATGAAAGGGA	222793	54989	TTTTAGGGTCACACAGCTAG	267380	99576	GCTGCGCAAACTGCACAGGG
178207	10403	AATGAGCAGCTATGAAAGGG	222794	54990	TTTTTAGGGTCACACAGCTA	267381	99577	AGCTGCGCAAACTGCACAGG
178208	10404	CAATGAGCAGCTATGAAAGG	222795	54991	CTTTTTAGGGTCACACAGCT	267382	99578	CAGCTGCGCAAACTGCACAG
178209	10405	GCAATGAGCAGCTATGAAAG	222796	54992	CCTTTTTAGGGTCACACAGC	267383	99579	ACAGCTGCGCAAACTGCACA
178210	10406	GGCAATGAGCAGCTATGAAA	222797	54993	ACCTTTTTAGGGTCACACAG	267384	99580	CACAGCTGCGCAAACTGCAC
178211	10407	TGGCAATGAGCAGCTATGAA	222798	54994	AACCTTTTTAGGGTCACACA	267385	99581	ACACAGCTGCGCAAACTGCA
178212	10408	CTGGCAATGAGCAGCTATGA	222799	54995	AAACCTTTTTAGGGTCACAC	267386	99582	AACACAGCTGCGCAAACTGC
178213	10409	CCTGGCAATGAGCAGCTATG	222800	54996	GAAACCTTTTTAGGGTCACA	267387	99583	AAACACAGCTGCGCAAACTG
178214	10410	TCCTGGCAATGAGCAGCTAT	222801	54997	AGAAACCTTTTTAGGGTCAC	267388	99584	CAAACACAGCTGCGCAAACT
178215	10411	TTCCTGGCAATGAGCAGCTA	222802	54998	CAGAAACCTTTTTAGGGTCA	267389	99585	ACAAACACAGCTGCGCAAAC
178216	10412	TTTCCTGGCAATGAGCAGCT	222803	54999	TCAGAAACCTTTTTAGGGTC	267390	99586	GACAAACACAGCTGCGCAAA
178217	10413	GTTTCCTGGCAATGAGCAGC	222804	55000	TTCAGAAACCTTTTTAGGGT	267391	99587	AGACAAACACAGCTGCGCAA
178218	10414	TGTTTCCTGGCAATGAGCAG	222805	55001	GTTCAGAAACCTTTTTAGGG	267392	99588	CAGACAAACACAGCTGCGCA
178219	10415	ATGTTTCCTGGCAATGAGCA	222806	55002	CGTTCAGAAACCTTTTTAGG	267393	99589	TCAGACAAACACAGCTGCGC
178220	10416	GATGTTTCCTGGCAATGAGC	222807	55003	ACGTTCAGAAACCTTTTTAG	267394	99590	ATCAGACAAACACAGCTGCG
178221	10417	TGATGTTTCCTGGCAATGAG	222808	55004	GACGTTCAGAAACCTTTTTA	267395	99591	CATCAGACAAACACAGCTGC
178222	10418	CTGATGTTTCCTGGCAATGA	222809	55005	AGACGTTCAGAAACCTTTTT	267396	99592	CCATCAGACAAACACAGCTG
178223	10419	CCTGATGTTTCCTGGCAATG	222810	55006	GAGACGTTCAGAAACCTTTT	267397	99593	CCCATCAGACAAACACAGCT
178224	10420	TCCTGATGTTTCCTGGCAAT	222811	55007	AGAGACGTTCAGAAACCTTT	267398	99594	GCCCATCAGACAAACACAGC
178225	10421	TTCCTGATGTTTCCTGGCAA	222812	55008	CAGAGACGTTCAGAAACCTT	267399	99595	AGCCCATCAGACAAACACAG
178226	10422	ATTCCTGATGTTTCCTGGCA	222813	55009	TCAGAGACGTTCAGAAACCT	267400	99596	AAGCCCATCAGACAAACACA
178227	10423	TATTCCTGATGTTTCCTGGC	222814	55010	CTCAGAGACGTTCAGAAACC	267401	99597	AAAGCCCATCAGACAAACAC
178228	10424	CTATTCCTGATGTTTCCTGG	222815	55011	GCTCAGAGACGTTCAGAAAC	267402	99598	GAAAGCCCATCAGACAAACA
178229	10425	GCTATTCCTGATGTTTCCTG	222816	55012	AGCTCAGAGACGTTCAGAAA	267403	99599	AGAAAGCCCATCAGACAAAC
178230	10426	GGCTATTCCTGATGTTTCCT	222817	55013	AAGCTCAGAGACGTTCAGAA	267404	99600	TAGAAAGCCCATCAGACAAA
178231	10427	TGGCTATTCCTGATGTTTCC	222818	55014	GAAGCTCAGAGACGTTCAGA	267405	99601	TTAGAAAGCCCATCAGACAA
178232	10428	ATGGCTATTCCTGATGTTTC	222819	55015	TGAAGCTCAGAGACGTTCAG	267406	99602	ATTAGAAAGCCCATCAGACA
178233	10429	AATGGCTATTCCTGATGTTT	222820	55016	CTGAAGCTCAGAGACGTTCA	267407	99603	GATTAGAAAGCCCATCAGAC
178234	10430	AAATGGCTATTCCTGATGTT	222821	55017	ACTGAAGCTCAGAGACGTTC	267408	99604	GGATTAGAAAGCCCATCAGA
178235	10431	CAAATGGCTATTCCTGATGT	222822	55018	AACTGAAGCTCAGAGACGTT	267409	99605	AGGATTAGAAAGCCCATCAG
178236	10432	CCAAATGGCTATTCCTGATG	222823	55019	AAACTGAAGCTCAGAGACGT	267410	99606	CAGGATTAGAAAGCCCATCA
178237	10433	TCCAAATGGCTATTCCTGAT	222824	55020	GAAACTGAAGCTCAGAGACG	267411	99607	ACAGGATTAGAAAGCCCATC
178238	10434	TTCCAAATGGCTATTCCTGA	222825	55021	GGAAACTGAAGCTCAGAGAC	267412	99608	CACAGGATTAGAAAGCCCAT
178239	10435	CTTCCAAATGGCTATTCCTG	222826	55022	AGGAAACTGAAGCTCAGAGA	267413	99609	ACACAGGATTAGAAAGCCCA
178240	10436	TCTTCCAAATGGCTATTCCT	222827	55023	GAGGAAACTGAAGCTCAGAG	267414	99610	CACACAGGATTAGAAAGCCC
178241	10437	CTCTTCCAAATGGCTATTCC	222828	55024	TGAGGAAACTGAAGCTCAGA	267415	99611	GCACACAGGATTAGAAAGCC
178242	10438	ACTCTTCCAAATGGCTATTC	222829	55025	ATGAGGAAACTGAAGCTCAG	267416	99612	AGCACACAGGATTAGAAAGC

178243	10439	GACTCTTCCAAATGGCTATT	222830	55026	GATGAGGAAACTGAAGCTCA	267417	99613	GAGCACACAGGATTAGAAAG
178244	10440	TGACTCTTCCAAATGGCTAT	222831	55027	TGATGAGGAAACTGAAGCTC	267418	99614	AGAGCACACAGGATTAGAAA
178245	10441	ATGACTCTTCCAAATGGCTA	222832	55028	ATGATGAGGAAACTGAAGCT	267419	99615	GAGAGCACACAGGATTAGAA
178246	10442	GATGACTCTTCCAAATGGCT	222833	55029	AATGATGAGGAAACTGAAGC	267420	99616	GGAGAGCACACAGGATTAGA
178247	10443	TGATGACTCTTCCAAATGGC	222834	55030	GAATGATGAGGAAACTGAAG	267421	99617	AGGAGAGCACACAGGATTAG
178248	10444	CTGATGACTCTTCCAAATGG	222835	55031	GGAATGATGAGGAAACTGAA	267422	99618	AAGGAGAGCACACAGGATTA
178249	10445	GCTGATGACTCTTCCAAATG	222836	55032	AGGAATGATGAGGAAACTGA	267423	99619	CAAGGAGAGCACACAGGATT
178250	10446	GGCTGATGACTCTTCCAAAT	222837	55033	AAGGAATGATGAGGAAACTG	267424	99620	TCAAGGAGAGCACACAGGAT
178251	10447	GGGCTGATGACTCTTCCAAA	222838	55034	GAAGGAATGATGAGGAAACT	267425	99621	GTCAAGGAGAGCACACAGGA
178252	10448	AGGGCTGATGACTCTTCCAA	222839	55035	AGAAGGAATGATGAGGAAAC	267426	99622	AGTCAAGGAGAGCACACAGG
178253	10449	GAGGGCTGATGACTCTTCCA	222840	55036	GAGAAGGAATGATGAGGAAA	267427	99623	AAGTCAAGGAGAGCACACAG
178254	10450	GGAGGGCTGATGACTCTTCC	222841	55037	TGAGAAGGAATGATGAGGAA	267428	99624	GAAGTCAAGGAGAGCACACA
178255	10451	GGGAGGGCTGATGACTCTTC	222842	55038	GTGAGAAGGAATGATGAGGA	267429	99625	TGAAGTCAAGGAGAGCACAC
178256	10452	TGGGAGGGCTGATGACTCTT	222843	55039	CGTGAGAAGGAATGATGAGG	267430	99626	CTGAAGTCAAGGAGAGCACA
178257	10453	GTGGGAGGGCTGATGACTCT	222844	55040	CCGTGAGAAGGAATGATGAG	267431	99627	CCTGAAGTCAAGGAGAGCAC
178258	10454	GGTGGGAGGGCTGATGACTC	222845	55041	CCCGTGAGAAGGAATGATGA	267432	99628	CCCTGAAGTCAAGGAGAGCA
178259	10455	TGGTGGGAGGGCTGATGACT	222846	55042	CCCCGTGAGAAGGAATGATG	267433	99629	TCCCTGAAGTCAAGGAGAGC
178260	10456	ATGGTGGGAGGGCTGATGAC	222847	55043	ACCCCGTGAGAAGGAATGAT	267434	99630	GTCCCTGAAGTCAAGGAGAG
178261	10457	GATGGTGGGAGGGCTGATGA	222848	55044	CACCCCGTGAGAAGGAATGA	267435	99631	TGTCCCTGAAGTCAAGGAGA
178262	10458	GGATGGTGGGAGGGCTGATG	222849	55045	CCACCCCGTGAGAAGGAATG	267436	99632	TTGTCCCTGAAGTCAAGGAG
178263	10459	CGGATGGTGGGAGGGCTGAT	222850	55046	ACCACCCCGTGAGAAGGAAT	267437	99633	ATTGTCCCTGAAGTCAAGGA
178264	10460	ACGGATGGTGGGAGGGCTGA	222851	55047	AACCACCCCGTGAGAAGGAA	267438	99634	CATTGTCCCTGAAGTCAAGG
178265	10461	AACGGATGGTGGGAGGGCTG	222852	55048	CAACCACCCCGTGAGAAGGA	267439	99635	CCATTGTCCCTGAAGTCAAG
178266	10462	AAACGGATGGTGGGAGGGCT	222853	55049	ACAACCACCCCGTGAGAAGG	267440	99636	GCCATTGTCCCTGAAGTCAA
178267	10463	AAAACGGATGGTGGGAGGGC	222854	55050	CACAACCACCCCGTGAGAAG	267441	99637	TGCCATTGTCCCTGAAGTCA
178268	10464	GAAAACGGATGGTGGGAGGG	222855	55051	TCACAACCACCCCGTGAGAA	267442	99638	ATGCCATTGTCCCTGAAGTC
178269	10465	AGAAAACGGATGGTGGGAGG	222856	55052	CTCACAACCACCCCGTGAGA	267443	99639	AATGCCATTGTCCCTGAAGT
178270	10466	CAGAAAACGGATGGTGGGAG	222857	55053	GCTCACAACCACCCCGTGAG	267444	99640	TAATGCCATTGTCCCTGAAG
178271	10467	ACAGAAAACGGATGGTGGGA	222858	55054	TGCTCACAACCACCCCGTGA	267445	99641	GTAATGCCATTGTCCCTGAA
178272	10468	GACAGAAAACGGATGGTGGG	222859	55055	ATGCTCACAACCACCCCGTG	267446	99642	TGTAATGCCATTGTCCCTGA
178273	10469	AGACAGAAAACGGATGGTGG	222860	55056	AATGCTCACAACCACCCCGT	267447	99643	CTGTAATGCCATTGTCCCTG
178274	10470	AAGACAGAAAACGGATGGTG	222861	55057	TAATGCTCACAACCACCCCG	267448	99644	CCTGTAATGCCATTGTCCCT
178275	10471	CAAGACAGAAAACGGATGGT	222862	55058	GTAATGCTCACAACCACCCC	267449	99645	GCCTGTAATGCCATTGTCCC
178276	10472	ACAAGACAGAAAACGGATGG	222863	55059	TGTAATGCTCACAACCACCC	267450	99646	TGCCTGTAATGCCATTGTCC
178277	10473	GACAAGACAGAAAACGGATG	222864	55060	CTGTAATGCTCACAACCACC	267451	99647	ATGCCTGTAATGCCATTGTC
178278	10474	AGACAAGACAGAAAACGGAT	222865	55061	TCTGTAATGCTCACAACCAC	267452	99648	CATGCCTGTAATGCCATTGT
178279	10475	AAGACAAGACAGAAAACGGA	222866	55062	CTCTGTAATGCTCACAACCA	267453	99649	TCATGCCTGTAATGCCATTG
178280	10476	AAAGACAAGACAGAAAACGG	222867	55063	TCTCTGTAATGCTCACAACC	267454	99650	CTCATGCCTGTAATGCCATT
178281	10477	AAAAGACAAGACAGAAAACG	222868	55064	ATCTCTGTAATGCTCACAAC	267455	99651	GCTCATGCCTGTAATGCCAT
178282	10478	GAAAAGACAAGACAGAAAAC	222869	55065	GATCTCTGTAATGCTCACAA	267456	99652	GGCTCATGCCTGTAATGCCA
178283	10479	GGAAAAGACAAGACAGAAAA	222870	55066	GGATCTCTGTAATGCTCACA	267457	99653	TGGCTCATGCCTGTAATGCC
178284	10480	GGGAAAAGACAAGACAGAAA	222871	55067	AGGATCTCTGTAATGCTCAC	267458	99654	GTGGCTCATGCCTGTAATGC
178285	10481	AGGGAAAAGACAAGACAGAA	222872	55068	GAGGATCTCTGTAATGCTCA	267459	99655	GGTGGCTCATGCCTGTAATG
178286	10482	TAGGGAAAAGACAAGACAGA	222873	55069	AGAGGATCTCTGTAATGCTC	267460	99656	TGGTGGCTCATGCCTGTAAT
178287	10483	ATAGGGAAAAGACAAGACAG	222874	55070	GAGAGGATCTCTGTAATGCT	267461	99657	ATGGTGGCTCATGCCTGTAA
178288	10484	CATAGGGAAAAGACAAGACA	222875	55071	AGAGAGGATCTCTGTAATGC	267462	99658	CATGGTGGCTCATGCCTGTA
178289	10485	TCATAGGGAAAAGACAAGAC	222876	55072	CAGAGAGGATCTCTGTAATG	267463	99659	GCATGGTGGCTCATGCCTGT
178290	10486	CTCATAGGGAAAAGACAAGA	222877	55073	ACAGAGAGGATCTCTGTAAT	267464	99660	GGCATGGTGGCTCATGCCTG
178291	10487	GCTCATAGGGAAAAGACAAG	222878	55074	CACAGAGAGGATCTCTGTAA	267465	99661	AGGCATGGTGGCTCATGCCT
178292	10488	TGCTCATAGGGAAAAGACAA	222879	55075	TCACAGAGAGGATCTCTGTA	267466	99662	CAGGCATGGTGGCTCATGCC
178293	10489	CTGCTCATAGGGAAAAGACA	222880	55076	TTCACAGAGAGGATCTCTGT	267467	99663	CCAGGCATGGTGGCTCATGC
178294	10490	CCTGCTCATAGGGAAAAGAC	222881	55077	CTTCACAGAGAGGATCTCTG	267468	99664	GCCAGGCATGGTGGCTCATG
178295	10491	CCCTGCTCATAGGGAAAAGA	222882	55078	GCTTCACAGAGAGGATCTCT	267469	99665	AGCCAGGCATGGTGGCTCAT
178296	10492	CCCCTGCTCATAGGGAAAAG	222883	55079	GGCTTCACAGAGAGGATCTC	267470	99666	CAGCCAGGCATGGTGGCTCA
178297	10493	TCCCCTGCTCATAGGGAAAA	222884	55080	GGGCTTCACAGAGAGGATCT	267471	99667	ACAGCCAGGCATGGTGGCTC
178298	10494	TTCCCCTGCTCATAGGGAAA	222885	55081	GGGGCTTCACAGAGAGGATC	267472	99668	GACAGCCAGGCATGGTGGCT
178299	10495	TTTCCCCTGCTCATAGGGAA	222886	55082	AGGGGCTTCACAGAGAGGAT	267473	99669	AGACAGCCAGGCATGGTGGC
178300	10496	ATTTCCCCTGCTCATAGGGA	222887	55083	CAGGGGCTTCACAGAGAGGA	267474	99670	GAGACAGCCAGGCATGGTGG
178301	10497	AATTTCCCCTGCTCATAGGG	222888	55084	ACAGGGGCTTCACAGAGAGG	267475	99671	GGAGACAGCCAGGCATGGTG
178302	10498	GAATTTCCCCTGCTCATAGG	222889	55085	CACAGGGGCTTCACAGAGAG	267476	99672	GGGAGACAGCCAGGCATGGT
178303	10499	GGAATTTCCCCTGCTCATAG	222890	55086	TCACAGGGGCTTCACAGAGA	267477	99673	AGGGAGACAGCCAGGCATGG
178304	10500	TGGAATTTCCCCTGCTCATA	222891	55087	CTCACAGGGGCTTCACAGAG	267478	99674	TAGGGAGACAGCCAGGCATG
178305	10501	GTGGAATTTCCCCTGCTCAT	222892	55088	ACTCACAGGGGCTTCACAGA	267479	99675	ATAGGGAGACAGCCAGGCAT
178306	10502	CGTGGAATTTCCCCTGCTCA	222893	55089	CACTCACAGGGGCTTCACAG	267480	99676	CATAGGGAGACAGCCAGGCA
178307	10503	GCGTGGAATTTCCCCTGCTC	222894	55090	CCACTCACAGGGGCTTCACA	267481	99677	ACATAGGGAGACAGCCAGGC
178308	10504	AGCGTGGAATTTCCCCTGCT	222895	55091	GCCACTCACAGGGGCTTCAC	267482	99678	AACATAGGGAGACAGCCAGG
178309	10505	CAGCGTGGAATTTCCCCTGC	222896	55092	AGCCACTCACAGGGGCTTCA	267483	99679	AAACATAGGGAGACAGCCAG
178310	10506	CCAGCGTGGAATTTCCCCTG	222897	55093	GAGCCACTCACAGGGGCTTC	267484	99680	GAAACATAGGGAGACAGCCA
178311	10507	GCCAGCGTGGAATTTCCCCT	222898	55094	TGAGCCACTCACAGGGGCTT	267485	99681	TGAAACATAGGGAGACAGCC
178312	10508	GGCCAGCGTGGAATTTCCCC	222899	55095	ATGAGCCACTCACAGGGGCT	267486	99682	CTGAAACATAGGGAGACAGC
178313	10509	GGGCCAGCGTGGAATTTCCC	222900	55096	GATGAGCCACTCACAGGGGC	267487	99683	TCTGAAACATAGGGAGACAG
178314	10510	GGGGCCAGCGTGGAATTTCC	222901	55097	GGATGAGCCACTCACAGGGG	267488	99684	ATCTGAAACATAGGGAGACA

178315	10511	TGGGGCCAGCGTGGAATTTC	222902	55098	AGGATGAGCCACTCACAGGG	267489	99685	CATCTGAAACATAGGGAGAC
178316	10512	TTGGGGCCAGCGTGGAATTT	222903	55099	CAGGATGAGCCACTCACAGG	267490	99686	TCATCTGAAACATAGGGAGA
178317	10513	ATTGGGGCCAGCGTGGAATT	222904	55100	TCAGGATGAGCCACTCACAG	267491	99687	TTCATCTGAAACATAGGGAG
178318	10514	GATTGGGGCCAGCGTGGAAT	222905	55101	CTCAGGATGAGCCACTCACA	267492	99688	CTTCATCTGAAACATAGGGA
178319	10515	GGATTGGGGCCAGCGTGGAA	222906	55102	CCTCAGGATGAGCCACTCAC	267493	99689	TCTTCATCTGAAACATAGGG
178320	10516	GGGATTGGGGCCAGCGTGGA	222907	55103	CCCTCAGGATGAGCCACTCA	267494	99690	GTCTTCATCTGAAACATAGG
178321	10517	GGGGATTGGGGCCAGCGTGG	222908	55104	GCCCTCAGGATGAGCCACTC	267495	99691	TGTCTTCATCTGAAACATAG
178322	10518	TGGGGATTGGGGCCAGCGTG	222909	55105	AGCCCTCAGGATGAGCCACT	267496	99692	ATGTCTTCATCTGAAACATA
178323	10519	CTGGGGATTGGGGCCAGCGT	222910	55106	CAGCCCTCAGGATGAGCCAC	267497	99693	TATGTCTTCATCTGAAACAT
178324	10520	ACTGGGGATTGGGGCCAGCG	222911	55107	TCAGCCCTCAGGATGAGCCA	267498	99694	CTATGTCTTCATCTGAAACA
178325	10521	CACTGGGGATTGGGGCCAGC	222912	55108	TTCAGCCCTCAGGATGAGCC	267499	99695	CCTATGTCTTCATCTGAAAC
178326	10522	GCACTGGGGATTGGGGCCAG	222913	55109	TTTCAGCCCTCAGGATGAGC	267500	99696	GCCTATGTCTTCATCTGAAA
178327	10523	TGCACTGGGGATTGGGGCCA	222914	55110	ATTTCAGCCCTCAGGATGAG	267501	99697	AGCCTATGTCTTCATCTGAA
178328	10524	CTGCACTGGGGATTGGGGCC	222915	55111	TATTTCAGCCCTCAGGATGA	267502	99698	AAGCCTATGTCTTCATCTGA
178329	10525	GCTGCACTGGGGATTGGGGC	222916	55112	TTATTTCAGCCCTCAGGATG	267503	99699	TAAGCCTATGTCTTCATCTG
178330	10526	CGCTGCACTGGGGATTGGGG	222917	55113	TTTATTTCAGCCCTCAGGAT	267504	99700	TTAAGCCTATGTCTTCATCT
178331	10527	CCGCTGCACTGGGGATTGGG	222918	55114	GTTTATTTCAGCCCTCAGGA	267505	99701	CTTAAGCCTATGTCTTCATC
178332	10528	GCCGCTGCACTGGGGATTGG	222919	55115	TGTTTATTTCAGCCCTCAGG	267506	99702	CCTTAAGCCTATGTCTTCAT
178333	10529	AGCCGCTGCACTGGGGATTG	222920	55116	ATGTTTATTTCAGCCCTCAG	267507	99703	TCCTTAAGCCTATGTCTTCA
178334	10530	GAGCCGCTGCACTGGGGATT	222921	55117	CATGTTTATTTCAGCCCTCA	267508	99704	CTCCTTAAGCCTATGTCTTC
178335	10531	TGAGCCGCTGCACTGGGGAT	222922	55118	ACATGTTTATTTCAGCCCTC	267509	99705	CCTCCTTAAGCCTATGTCTT
178336	10532	CTGAGCCGCTGCACTGGGGA	222923	55119	AACATGTTTATTTCAGCCCT	267510	99706	ACCTCCTTAAGCCTATGTCT
178337	10533	GCTGAGCCGCTGCACTGGGG	222924	55120	TAACATGTTTATTTCAGCCC	267511	99707	GACCTCCTTAAGCCTATGTC
178338	10534	GGCTGAGCCGCTGCACTGGG	222925	55121	ATAACATGTTTATTTCAGCC	267512	99708	TGACCTCCTTAAGCCTATGT
178339	10535	AGGCTGAGCCGCTGCACTGG	222926	55122	AATAACATGTTTATTTCAGC	267513	99709	CTGACCTCCTTAAGCCTATG
178340	10536	GAGGCTGAGCCGCTGCACTG	222927	55123	TAATAACATGTTTATTTCAG	267514	99710	CCTGACCTCCTTAAGCCTAT
178341	10537	AGAGGCTGAGCCGCTGCACT	222928	55124	TTAATAACATGTTTATTTCA	267515	99711	ACCTGACCTCCTTAAGCCTA
178342	10538	CAGAGGCTGAGCCGCTGCAC	222929	55125	ATTAATAACATGTTTATTTC	267516	99712	CACCTGACCTCCTTAAGCCT
178343	10539	GCAGAGGCTGAGCCGCTGCA	222930	55126	TATTAATAACATGTTTATTT	267517	99713	TCACCTGACCTCCTTAAGCC
178344	10540	GGCAGAGGCTGAGCCGCTGC	222931	55127	TTATTAATAACATGTTTATT	267518	99714	GTCACCTGACCTCCTTAAGC
178345	10541	AGGCAGAGGCTGAGCCGCTG	222932	55128	ATTATTAATAACATGTTTAT	267519	99715	AGTCACCTGACCTCCTTAAG
178346	10542	GAGGCAGAGGCTGAGCCGCT	222933	55129	GATTATTAATAACATGTTTA	267520	99716	AAGTCACCTGACCTCCTTAA
178347	10543	AGAGGCAGAGGCTGAGCCGC	222934	55130	GGATTATTAATAACATGTTT	267521	99717	CAAGTCACCTGACCTCCTTA
178348	10544	CAGAGGCAGAGGCTGAGCCG	222935	55131	TGGATTATTAATAACATGTT	267522	99718	GCAAGTCACCTGACCTCCTT
178349	10545	GCAGAGGCAGAGGCTGAGCC	222936	55132	TTGGATTATTAATAACATGT	267523	99719	GGCAAGTCACCTGACCTCCT
178350	10546	AGCAGAGGCAGAGGCTGAGC	222937	55133	TTTGGATTATTAATAACATG	267524	99720	GGGCAAGTCACCTGACCTCC
178351	10547	CAGCAGAGGCAGAGGCTGAG	222938	55134	TTTTGGATTATTAATAACAT	267525	99721	TGGGCAAGTCACCTGACCTC
178352	10548	GCAGCAGAGGCAGAGGCTGA	222939	55135	GTTTTGGATTATTAATAACA	267526	99722	GTGGGCAAGTCACCTGACCT
178353	10549	AGCAGCAGAGGCAGAGGCTG	222940	55136	AGTTTTGGATTATTAATAAC	267527	99723	CGTGGGCAAGTCACCTGACC
178354	10550	CAGCAGCAGAGGCAGAGGCT	222941	55137	CAGTTTTGGATTATTAATAA	267528	99724	TCGTGGGCAAGTCACCTGAC
178355	10551	CCAGCAGCAGAGGCAGAGGC	222942	55138	CCAGTTTTGGATTATTAATA	267529	99725	GTCGTGGGCAAGTCACCTGA
178356	10552	ACCAGCAGCAGAGGCAGAGG	222943	55139	GCCAGTTTTGGATTATTAAT	267530	99726	GGTCGTGGGCAAGTCACCTG
178357	10553	GACCAGCAGCAGAGGCAGAG	222944	55140	TGCCAGTTTTGGATTATTAA	267531	99727	TGGTCGTGGGCAAGTCACCT
178358	10554	GGACCAGCAGCAGAGGCAGA	222945	55141	TTGCCAGTTTTGGATTATTA	267532	99728	GTGGTCGTGGGCAAGTCACC
178359	10555	GGGACCAGCAGCAGAGGCAG	222946	55142	CTTGCCAGTTTTGGATTATT	267533	99729	AGTGGTCGTGGGCAAGTCAC
178360	10556	GGGGACCAGCAGCAGAGGCA	222947	55143	CCTTGCCAGTTTTGGATTAT	267534	99730	GAGTGGTCGTGGGCAAGTCA
178361	10557	TGGGGACCAGCAGCAGAGGC	222948	55144	CCCTTGCCAGTTTTGGATTA	267535	99731	AGAGTGGTCGTGGGCAAGTC
178362	10558	ATGGGGACCAGCAGCAGAGG	222949	55145	TCCCTTGCCAGTTTTGGATT	267536	99732	CAGAGTGGTCGTGGGCAAGT
178363	10559	CATGGGGACCAGCAGCAGAG	222950	55146	ATCCCTTGCCAGTTTTGGAT	267537	99733	ACAGAGTGGTCGTGGGCAAG
178364	10560	TCATGGGGACCAGCAGCAGA	222951	55147	CATCCCTTGCCAGTTTTGGA	267538	99734	TACAGAGTGGTCGTGGGCAA
178365	10561	CTCATGGGGACCAGCAGCAG	222952	55148	ACATCCCTTGCCAGTTTTGG	267539	99735	TTACAGAGTGGTCGTGGGCA
178366	10562	CCTCATGGGGACCAGCAGCA	222953	55149	AACATCCCTTGCCAGTTTTG	267540	99736	TTTACAGAGTGGTCGTGGGC
178367	10563	GCCTCATGGGGACCAGCAGC	222954	55150	CAACATCCCTTGCCAGTTTT	267541	99737	ATTTACAGAGTGGTCGTGGG
178368	10564	GGCCTCATGGGGACCAGCAG	222955	55151	TCAACATCCCTTGCCAGTTT	267542	99738	TATTTACAGAGTGGTCGTGG
178369	10565	TGGCCTCATGGGGACCAGCA	222956	55152	GTCAACATCCCTTGCCAGTT	267543	99739	TTATTTACAGAGTGGTCGTG
178370	10566	CTGGCCTCATGGGGACCAGC	222957	55153	AGTCAACATCCCTTGCCAGT	267544	99740	CTTATTTACAGAGTGGTCGT
178371	10567	GCTGGCCTCATGGGGACCAG	222958	55154	CAGTCAACATCCCTTGCCAG	267545	99741	TCTTATTTACAGAGTGGTCG
178372	10568	AGCTGGCCTCATGGGGACCA	222959	55155	CCAGTCAACATCCCTTGCCA	267546	99742	CTCTTATTTACAGAGTGGTC
178373	10569	AAGCTGGCCTCATGGGGACC	222960	55156	ACCAGTCAACATCCCTTGCC	267547	99743	CCTCTTATTTACAGAGTGGT
178374	10570	TAAGCTGGCCTCATGGGGAC	222961	55157	GACCAGTCAACATCCCTTGC	267548	99744	GCCTCTTATTTACAGAGTGG
178375	10571	CTAAGCTGGCCTCATGGGGA	222962	55158	GGACCAGTCAACATCCCTTG	267549	99745	TGCCTCTTATTTACAGAGTG
178376	10572	TCTAAGCTGGCCTCATGGGG	222963	55159	GGGACCAGTCAACATCCCTT	267550	99746	ATGCCTCTTATTTACAGAGT
178377	10573	TTCTAAGCTGGCCTCATGGG	222964	55160	GGGGACCAGTCAACATCCCT	267551	99747	CATGCCTCTTATTTACAGAG
178378	10574	TTTCTAAGCTGGCCTCATGG	222965	55161	GGGGGACCAGTCAACATCCC	267552	99748	TCATGCCTCTTATTTACAGA
178379	10575	GTTTCTAAGCTGGCCTCATG	222966	55162	AGGGGGACCAGTCAACATCC	267553	99749	TTCATGCCTCTTATTTACAG
178380	10576	CGTTTCTAAGCTGGCCTCAT	222967	55163	GAGGGGGACCAGTCAACATC	267554	99750	TTTCATGCCTCTTATTTACA
178381	10577	CCGTTTCTAAGCTGGCCTCA	222968	55164	GGAGGGGGACCAGTCAACAT	267555	99751	TTTTCATGCCTCTTATTTAC
178382	10578	TCCGTTTCTAAGCTGGCCTC	222969	55165	GGGAGGGGGACCAGTCAACA	267556	99752	CTTTTCATGCCTCTTATTTA
178383	10579	CTCCGTTTCTAAGCTGGCCT	222970	55166	AGGGAGGGGGACCAGTCAAC	267557	99753	ACTTTTCATGCCTCTTATTT
178384	10580	CCTCCGTTTCTAAGCTGGCC	222971	55167	AAGGGAGGGGGACCAGTCAA	267558	99754	TACTTTTCATGCCTCTTATT
178385	10581	TCCTCCGTTTCTAAGCTGGC	222972	55168	CAAGGGAGGGGGACCAGTCA	267559	99755	ATACTTTTCATGCCTCTTAT
178386	10582	ATCCTCCGTTTCTAAGCTGG	222973	55169	GCAAGGGAGGGGGACCAGTC	267560	99756	AATACTTTTCATGCCTCTTA

178387	10583	AATCCTCCGTTTCTAAGCTG	222974	55170	GGCAAGGGAGGGGGACCAGT	267561	99757	AAATACTTTTCATGCCTCTT
178388	10584	AAATCCTCCGTTTCTAAGCT	222975	55171	GGGCAAGGGAGGGGGACCAG	267562	99758	CAAATACTTTTCATGCCTCT
178389	10585	AAAATCCTCCGTTTCTAAGC	222976	55172	TGGGCAAGGGAGGGGGACCA	267563	99759	CCAAATACTTTTCATGCCTC
178390	10586	CAAAATCCTCCGTTTCTAAG	222977	55173	TTGGGCAAGGGAGGGGGACC	267564	99760	TCCAAATACTTTTCATGCCT
178391	10587	GCAAAATCCTCCGTTTCTAA	222978	55174	CTTGGGCAAGGGAGGGGGAC	267565	99761	CTCCAAATACTTTTCATGCC
178392	10588	TGCAAAATCCTCCGTTTCTA	222979	55175	CCTTGGGCAAGGGAGGGGGA	267566	99762	GCTCCAAATACTTTTCATGC
178393	10589	CTGCAAAATCCTCCGTTTCT	222980	55176	TCCTTGGGCAAGGGAGGGGG	267567	99763	GGCTCCAAATACTTTTCATG
178394	10590	TCTGCAAAATCCTCCGTTTC	222981	55177	CTCCTTGGGCAAGGGAGGGG	267568	99764	TGGCTCCAAATACTTTTCAT
178395	10591	TTCTGCAAAATCCTCCGTTT	222982	55178	GCTCCTTGGGCAAGGGAGGG	267569	99765	GTGGCTCCAAATACTTTTCA
178396	10592	GTTCTGCAAAATCCTCCGTT	222983	55179	AGCTCCTTGGGCAAGGGAGG	267570	99766	GGTGGCTCCAAATACTTTTC
178397	10593	TGTTCTGCAAAATCCTCCGT	222984	55180	AAGCTCCTTGGGCAAGGGAG	267571	99767	TGGTGGCTCCAAATACTTTT
178398	10594	ATGTTCTGCAAAATCCTCCG	222985	55181	AAAGCTCCTTGGGCAAGGGA	267572	99768	GTGGTGGCTCCAAATACTTT
178399	10595	GATGTTCTGCAAAATCCTCC	222986	55182	GAAAGCTCCTTGGGCAAGGG	267573	99769	GGTGGTGGCTCCAAATACTT
178400	10596	GGATGTTCTGCAAAATCCTC	222987	55183	AGAAAGCTCCTTGGGCAAGG	267574	99770	TGGTGGTGGCTCCAAATACT
178401	10597	GGGATGTTCTGCAAAATCCT	222988	55184	TAGAAAGCTCCTTGGGCAAG	267575	99771	GTGGTGGTGGCTCCAAATAC
178402	10598	AGGGATGTTCTGCAAAATCC	222989	55185	CTAGAAAGCTCCTTGGGCAA	267576	99772	GGTGGTGGTGGCTCCAAATA
178403	10599	TAGGGATGTTCTGCAAAATC	222990	55186	TCTAGAAAGCTCCTTGGGCA	267577	99773	TGGTGGTGGTGGCTCCAAAT
178404	10600	TTAGGGATGTTCTGCAAAAT	222991	55187	TTCTAGAAAGCTCCTTGGGC	267578	99774	TTGGTGGTGGTGGCTCCAAA
178405	10601	TTTAGGGATGTTCTGCAAAA	222992	55188	GTTCTAGAAAGCTCCTTGGG	267579	99775	CTTGGTGGTGGTGGCTCCAA
178406	10602	ATTTAGGGATGTTCTGCAAA	222993	55189	GGTTCTAGAAAGCTCCTTGG	267580	99776	GCTTGGTGGTGGTGGCTCCA
178407	10603	GATTTAGGGATGTTCTGCAA	222994	55190	AGGTTCTAGAAAGCTCCTTG	267581	99777	GGCTTGGTGGTGGTGGCTCC
178408	10604	GGATTTAGGGATGTTCTGCA	222995	55191	CAGGTTCTAGAAAGCTCCTT	267582	99778	GGGCTTGGTGGTGGTGGCTC
178409	10605	CGGATTTAGGGATGTTCTGC	222996	55192	TCAGGTTCTAGAAAGCTCCT	267583	99779	TGGGCTTGGTGGTGGTGGCT
178410	10606	GCGGATTTAGGGATGTTCTG	222997	55193	CTCAGGTTCTAGAAAGCTCC	267584	99780	GTGGGCTTGGTGGTGGTGGC
178411	10607	AGCGGATTTAGGGATGTTCT	222998	55194	ACTCAGGTTCTAGAAAGCTC	267585	99781	AGTGGGCTTGGTGGTGGTGG
178412	10608	AAGCGGATTTAGGGATGTTC	222999	55195	AACTCAGGTTCTAGAAAGCT	267586	99782	CAGTGGGCTTGGTGGTGGTG
178413	10609	CAAGCGGATTTAGGGATGTT	223000	55196	TAACTCAGGTTCTAGAAAGC	267587	99783	CCAGTGGGCTTGGTGGTGGT
178414	10610	TCAAGCGGATTTAGGGATGT	223001	55197	ATAACTCAGGTTCTAGAAAG	267588	99784	ACCAGTGGGCTTGGTGGTGG
178415	10611	TTCAAGCGGATTTAGGGATG	223002	55198	GATAACTCAGGTTCTAGAAA	267589	99785	GACCAGTGGGCTTGGTGGTG
178416	10612	ATTCAAGCGGATTTAGGGAT	223003	55199	TGATAACTCAGGTTCTAGAA	267590	99786	TGACCAGTGGGCTTGGTGGT
178417	10613	TATTCAAGCGGATTTAGGGA	223004	55200	ATGATAACTCAGGTTCTAGA	267591	99787	GTGACCAGTGGGCTTGGTGG
178418	10614	TTATTCAAGCGGATTTAGGG	223005	55201	AATGATAACTCAGGTTCTAG	267592	99788	GGTGACCAGTGGGCTTGGTG
178419	10615	ATTATTCAAGCGGATTTAGG	223006	55202	TAATGATAACTCAGGTTCTA	267593	99789	GGGTGACCAGTGGGCTTGGT
178420	10616	CATTATTCAAGCGGATTTAG	223007	55203	GTAATGATAACTCAGGTTCT	267594	99790	AGGGTGACCAGTGGGCTTGG
178421	10617	TCATTATTCAAGCGGATTTA	223008	55204	GGTAATGATAACTCAGGTTC	267595	99791	CAGGGTGACCAGTGGGCTTG
178422	10618	TTCATTATTCAAGCGGATTT	223009	55205	TGGTAATGATAACTCAGGTT	267596	99792	CCAGGGTGACCAGTGGGCTT
178423	10619	CTTCATTATTCAAGCGGATT	223010	55206	TTGGTAATGATAACTCAGGT	267597	99793	CCCAGGGTGACCAGTGGGCT
178424	10620	ACTTCATTATTCAAGCGGAT	223011	55207	TTTGGTAATGATAACTCAGG	267598	99794	ACCCAGGGTGACCAGTGGGC
178425	10621	CACTTCATTATTCAAGCGGA	223012	55208	GTTTGGTAATGATAACTCAG	267599	99795	GACCCAGGGTGACCAGTGGG
178426	10622	TCACTTCATTATTCAAGCGG	223013	55209	AGTTTGGTAATGATAACTCA	267600	99796	AGACCCAGGGTGACCAGTGG
178427	10623	ATCACTTCATTATTCAAGCG	223014	55210	CAGTTTGGTAATGATAACTC	267601	99797	GAGACCCAGGGTGACCAGTG
178428	10624	GATCACTTCATTATTCAAGC	223015	55211	ACAGTTTGGTAATGATAACT	267602	99798	AGAGACCCAGGGTGACCAGT
178429	10625	TGATCACTTCATTATTCAAG	223016	55212	TACAGTTTGGTAATGATAAC	267603	99799	CAGAGACCCAGGGTGACCAG
178430	10626	ATGATCACTTCATTATTCAA	223017	55213	GTACAGTTTGGTAATGATAA	267604	99800	TCAGAGACCCAGGGTGACCA
178431	10627	AATGATCACTTCATTATTCA	223018	55214	AGTACAGTTTGGTAATGATA	267605	99801	TTCAGAGACCCAGGGTGACC
178432	10628	GAATGATCACTTCATTATTC	223019	55215	CAGTACAGTTTGGTAATGAT	267606	99802	CTTCAGAGACCCAGGGTGAC
178433	10629	TGAATGATCACTTCATTATT	223020	55216	GCAGTACAGTTTGGTAATGA	267607	99803	ACTTCAGAGACCCAGGGTGA
178434	10630	ATGAATGATCACTTCATTAT	223021	55217	GGCAGTACAGTTTGGTAATG	267608	99804	GACTTCAGAGACCCAGGGTG
178435	10631	TATGAATGATCACTTCATTA	223022	55218	AGGCAGTACAGTTTGGTAAT	267609	99805	TGACTTCAGAGACCCAGGGT
178436	10632	TTATGAATGATCACTTCATT	223023	55219	AAGGCAGTACAGTTTGGTAA	267610	99806	CTGACTTCAGAGACCCAGGG
178437	10633	TTTATGAATGATCACTTCAT	223024	55220	CAAGGCAGTACAGTTTGGTA	267611	99807	CCTGACTTCAGAGACCCAGG
178438	10634	GTTTATGAATGATCACTTCA	223025	55221	TCAAGGCAGTACAGTTTGGT	267612	99808	CCCTGACTTCAGAGACCCAG
178439	10635	AGTTTATGAATGATCACTTC	223026	55222	CTCAAGGCAGTACAGTTTGG	267613	99809	TCCCTGACTTCAGAGACCCA
178440	10636	GAGTTTATGAATGATCACTT	223027	55223	ACTCAAGGCAGTACAGTTTG	267614	99810	CTCCCTGACTTCAGAGACCC
178441	10637	TGAGTTTATGAATGATCACT	223028	55224	TACTCAAGGCAGTACAGTTT	267615	99811	CCTCCCTGACTTCAGAGACC
178442	10638	GTGAGTTTATGAATGATCAC	223029	55225	TTACTCAAGGCAGTACAGTT	267616	99812	GCCTCCCTGACTTCAGAGAC
178443	10639	GGTGAGTTTATGAATGATCA	223030	55226	CTTACTCAAGGCAGTACAGT	267617	99813	TGCCTCCCTGACTTCAGAGA
178444	10640	AGGTGAGTTTATGAATGATC	223031	55227	TCTTACTCAAGGCAGTACAG	267618	99814	CTGCCTCCCTGACTTCAGAG
178445	10641	CAGGTGAGTTTATGAATGAT	223032	55228	TTCTTACTCAAGGCAGTACA	267619	99815	CCTGCCTCCCTGACTTCAGA
178446	10642	TCAGGTGAGTTTATGAATGA	223033	55229	TTTCTTACTCAAGGCAGTAC	267620	99816	TCCTGCCTCCCTGACTTCAG
178447	10643	TTCAGGTGAGTTTATGAATG	223034	55230	CTTTCTTACTCAAGGCAGTA	267621	99817	CTCCTGCCTCCCTGACTTCA
178448	10644	GTTCAGGTGAGTTTATGAAT	223035	55231	ACTTTCTTACTCAAGGCAGT	267622	99818	CCTCCTGCCTCCCTGACTTC
178449	10645	GGTTCAGGTGAGTTTATGAA	223036	55232	AACTTTCTTACTCAAGGCAG	267623	99819	TCCTCCTGCCTCCCTGACTT
178450	10646	AGGTTCAGGTGAGTTTATGA	223037	55233	TAACTTTCTTACTCAAGGCA	267624	99820	ATCCTCCTGCCTCCCTGACT
178451	10647	AAGGTTCAGGTGAGTTTATG	223038	55234	CTAACTTTCTTACTCAAGGC	267625	99821	CATCCTCCTGCCTCCCTGAC
178452	10648	TAAGGTTCAGGTGAGTTTAT	223039	55235	TCTAACTTTCTTACTCAAGG	267626	99822	CCATCCTCCTGCCTCCCTGA
178453	10649	ATAAGGTTCAGGTGAGTTTA	223040	55236	TTCTAACTTTCTTACTCAAG	267627	99823	CCCATCCTCCTGCCTCCCTG
178454	10650	AATAAGGTTCAGGTGAGTTT	223041	55237	CTTCTAACTTTCTTACTCAA	267628	99824	TCCCATCCTCCTGCCTCCCT
178455	10651	TAATAAGGTTCAGGTGAGTT	223042	55238	CCTTCTAACTTTCTTACTCA	267629	99825	CTCCCATCCTCCTGCCTCCC
178456	10652	TTAATAAGGTTCAGGTGAGT	223043	55239	TCCTTCTAACTTTCTTACTC	267630	99826	CCTCCCATCCTCCTGCCTCC
178457	10653	TTTAATAAGGTTCAGGTGAG	223044	55240	TTCCTTCTAACTTTCTTACT	267631	99827	ACCTCCCATCCTCCTGCCTC
178458	10654	TTTTAATAAGGTTCAGGTGA	223045	55241	ATTCCTTCTAACTTTCTTAC	267632	99828	GACCTCCCATCCTCCTGCCT

178459	10655	GTTTTAATAAGGTTCAGGTG	223046	55242	CATTCCTTCTAACTTTCTTA	267633	99829	AGACCTCCCATCCTCCTGCC
178460	10656	GGTTTTAATAAGGTTCAGGT	223047	55243	CCATTCCTTCTAACTTTCTT	267634	99830	CAGACCTCCCATCCTCCTGC
178461	10657	AGGTTTTAATAAGGTTCAGG	223048	55244	CCCATTCCTTCTAACTTTCT	267635	99831	TCAGACCTCCCATCCTCCTG
178462	10658	TAGGTTTTAATAAGGTTCAG	223049	55245	TCCCATTCCTTCTAACTTTC	267636	99832	CTCAGACCTCCCATCCTCCT
178463	10659	ATAGGTTTTAATAAGGTTCA	223050	55246	TTCCCATTCCTTCTAACTTT	267637	99833	CCTCAGACCTCCCATCCTCC
178464	10660	AATAGGTTTTAATAAGGTTC	223051	55247	CTTCCCATTCCTTCTAACTT	267638	99834	TCCTCAGACCTCCCATCCTC
178465	10661	AAATAGGTTTTAATAAGGTT	223052	55248	CCTTCCCATTCCTTCTAACT	267639	99835	CTCCTCAGACCTCCCATCCT
178466	10662	TAAATAGGTTTTAATAAGGT	223053	55249	TCCTTCCCATTCCTTCTAAC	267640	99836	CCTCCTCAGACCTCCCATCC
178467	10663	TTAAATAGGTTTTAATAAGG	223054	55250	ATCCTTCCCATTCCTTCTAA	267641	99837	GCCTCCTCAGACCTCCCATC
178468	10664	ATTAAATAGGTTTTAATAAG	223055	55251	CATCCTTCCCATTCCTTCTA	267642	99838	TGCCTCCTCAGACCTCCCAT
178469	10665	TATTAAATAGGTTTTAATAA	223056	55252	CCATCCTTCCCATTCCTTCT	267643	99839	CTGCCTCCTCAGACCTCCCA
178470	10666	ATATTAAATAGGTTTTAATA	223057	55253	ACCATCCTTCCCATTCCTTC	267644	99840	TCTGCCTCCTCAGACCTCCC
178471	10667	AATATTAAATAGGTTTTAAT	223058	55254	CACCATCCTTCCCATTCCTT	267645	99841	CTCTGCCTCCTCAGACCTCC
178472	10668	AAATATTAAATAGGTTTTAA	223059	55255	CCACCATCCTTCCCATTCCT	267646	99842	TCTCTGCCTCCTCAGACCTC
178473	10669	AAAATATTAAATAGGTTTTA	223060	55256	GCCACCATCCTTCCCATTCC	267647	99843	CTCTCTGCCTCCTCAGACCT
178474	10670	AAAAATATTAAATAGGTTTT	223061	55257	TGCCACCATCCTTCCCATTC	267648	99844	CCTCTCTGCCTCCTCAGACC
178475	10671	GAAAAATATTAAATAGGTTT	223062	55258	CTGCCACCATCCTTCCCATT	267649	99845	GCCTCTCTGCCTCCTCAGAC
178476	10672	GGAAAAATATTAAATAGGTT	223063	55259	CCTGCCACCATCCTTCCCAT	267650	99846	AGCCTCTCTGCCTCCTCAGA
178477	10673	AGGAAAAATATTAAATAGGT	223064	55260	ACCTGCCACCATCCTTCCCA	267651	99847	CAGCCTCTCTGCCTCCTCAG
178478	10674	CAGGAAAAATATTAAATAGG	223065	55261	CACCTGCCACCATCCTTCCC	267652	99848	TCAGCCTCTCTGCCTCCTCA
178479	10675	CCAGGAAAAATATTAAATAG	223066	55262	CCACCTGCCACCATCCTTCC	267653	99849	CTCAGCCTCTCTGCCTCCTC
178480	10676	TCCAGGAAAAATATTAAATA	223067	55263	TCCACCTGCCACCATCCTTC	267654	99850	GCTCAGCCTCTCTGCCTCCT
178481	10677	ATCCAGGAAAAATATTAAAT	223068	55264	CTCCACCTGCCACCATCCTT	267655	99851	GGCTCAGCCTCTCTGCCTCC
178482	10678	TATCCAGGAAAAATATTAAA	223069	55265	CCTCCACCTGCCACCATCCT	267656	99852	AGGCTCAGCCTCTCTGCCTC
178483	10679	TTATCCAGGAAAAATATTAA	223070	55266	TCCTCCACCTGCCACCATCC	267657	99853	CAGGCTCAGCCTCTCTGCCT
178484	10680	ATTATCCAGGAAAAATATTA	223071	55267	TTCCTCCACCTGCCACCATC	267658	99854	CCAGGCTCAGCCTCTCTGCC
178485	10681	GATTATCCAGGAAAAATATT	223072	55268	CTTCCTCCACCTGCCACCAT	267659	99855	TCCAGGCTCAGCCTCTCTGC
178486	10682	GGATTATCCAGGAAAAATAT	223073	55269	CCTTCCTCCACCTGCCACCA	267660	99856	CTCCAGGCTCAGCCTCTCTG
178487	10683	AGGATTATCCAGGAAAAATA	223074	55270	GCCTTCCTCCACCTGCCACC	267661	99857	CCTCCAGGCTCAGCCTCTCT
178488	10684	TAGGATTATCCAGGAAAAAT	223075	55271	CGCCTTCCTCCACCTGCCAC	267662	99858	GCCTCCAGGCTCAGCCTCTC
178489	10685	ATAGGATTATCCAGGAAAAA	223076	55272	CCGCCTTCCTCCACCTGCCA	267663	99859	GGCCTCCAGGCTCAGCCTCT
178490	10686	TATAGGATTATCCAGGAAAA	223077	55273	TCCGCCTTCCTCCACCTGCC	267664	99860	GGGCCTCCAGGCTCAGCCTC
178491	10687	CTATAGGATTATCCAGGAAA	223078	55274	ATCCGCCTTCCTCCACCTGC	267665	99861	AGGGCCTCCAGGCTCAGCCT
178492	10688	CCTATAGGATTATCCAGGAA	223079	55275	AATCCGCCTTCCTCCACCTG	267666	99862	CAGGGCCTCCAGGCTCAGCC
178493	10689	CCCTATAGGATTATCCAGGA	223080	55276	CAATCCGCCTTCCTCCACCT	267667	99863	CCAGGGCCTCCAGGCTCAGC
178494	10690	TCCCTATAGGATTATCCAGG	223081	55277	CCAATCCGCCTTCCTCCACC	267668	99864	TCCAGGGCCTCCAGGCTCAG
178495	10691	ATCCCTATAGGATTATCCAG	223082	55278	ACCAATCCGCCTTCCTCCAC	267669	99865	CTCCAGGGCCTCCAGGCTCA
178496	10692	TATCCCTATAGGATTATCCA	223083	55279	GACCAATCCGCCTTCCTCCA	267670	99866	CCTCCAGGGCCTCCAGGCTC
178497	10693	TTATCCCTATAGGATTATCC	223084	55280	TGACCAATCCGCCTTCCTCC	267671	99867	GCCTCCAGGGCCTCCAGGCT
178498	10694	GTTATCCCTATAGGATTATC	223085	55281	ATGACCAATCCGCCTTCCTC	267672	99868	GGCCTCCAGGGCCTCCAGGC
178499	10695	AGTTATCCCTATAGGATTAT	223086	55282	GATGACCAATCCGCCTTCCT	267673	99869	CGGCCTCCAGGGCCTCCAGG
178500	10696	AAGTTATCCCTATAGGATTA	223087	55283	TGATGACCAATCCGCCTTCC	267674	99870	TCGGCCTCCAGGGCCTCCAG
178501	10697	CAAGTTATCCCTATAGGATT	223088	55284	GTGATGACCAATCCGCCTTC	267675	99871	CTCGGCCTCCAGGGCCTCCA
178502	10698	GCAAGTTATCCCTATAGGAT	223089	55285	GGTGATGACCAATCCGCCTT	267676	99872	CCTCGGCCTCCAGGGCCTCC
178503	10699	GGCAAGTTATCCCTATAGGA	223090	55286	AGGTGATGACCAATCCGCCT	267677	99873	GCCTCGGCCTCCAGGGCCTC
178504	10700	AGGCAAGTTATCCCTATAGG	223091	55287	GAGGTGATGACCAATCCGCC	267678	99874	GGCCTCGGCCTCCAGGGCCT
178505	10701	GAGGCAAGTTATCCCTATAG	223092	55288	GGAGGTGATGACCAATCCGC	267679	99875	GGGCCTCGGCCTCCAGGGCC
178506	10702	GGAGGCAAGTTATCCCTATA	223093	55289	AGGAGGTGATGACCAATCCG	267680	99876	GGGGCCTCGGCCTCCAGGGC
178507	10703	AGGAGGCAAGTTATCCCTAT	223094	55290	AAGGAGGTGATGACCAATCC	267681	99877	TGGGGCCTCGGCCTCCAGGG
178508	10704	CAGGAGGCAAGTTATCCCTA	223095	55291	CAAGGAGGTGATGACCAATC	267682	99878	ATGGGGCCTCGGCCTCCAGG
178509	10705	CCAGGAGGCAAGTTATCCCT	223096	55292	GCAAGGAGGTGATGACCAAT	267683	99879	GATGGGGCCTCGGCCTCCAG
178510	10706	CCCAGGAGGCAAGTTATCCC	223097	55293	TGCAAGGAGGTGATGACCAA	267684	99880	AGATGGGGCCTCGGCCTCCA
178511	10707	GCCCAGGAGGCAAGTTATCC	223098	55294	CTGCAAGGAGGTGATGACCA	267685	99881	CAGATGGGGCCTCGGCCTCC
178512	10708	AGCCCAGGAGGCAAGTTATC	223099	55295	GCTGCAAGGAGGTGATGACC	267686	99882	ACAGATGGGGCCTCGGCCTC
178513	10709	AAGCCCAGGAGGCAAGTTAT	223100	55296	TGCTGCAAGGAGGTGATGAC	267687	99883	AACAGATGGGGCCTCGGCCT
178514	10710	GAAGCCCAGGAGGCAAGTTA	223101	55297	TTGCTGCAAGGAGGTGATGA	267688	99884	CAACAGATGGGGCCTCGGCC
178515	10711	AGAAGCCCAGGAGGCAAGTT	223102	55298	CTTGCTGCAAGGAGGTGATG	267689	99885	ACAACAGATGGGGCCTCGGC
178516	10712	GAGAAGCCCAGGAGGCAAGT	223103	55299	TCTTGCTGCAAGGAGGTGAT	267690	99886	AACAACAGATGGGGCCTCGG
178517	10713	AGAGAAGCCCAGGAGGCAAG	223104	55300	TTCTTGCTGCAAGGAGGTGA	267691	99887	AAACAACAGATGGGGCCTCG
178518	10714	GAGAGAAGCCCAGGAGGCAA	223105	55301	TTTCTTGCTGCAAGGAGGTG	267692	99888	GAAACAACAGATGGGGCCTC
178519	10715	GGAGAGAAGCCCAGGAGGCA	223106	55302	GTTTCTTGCTGCAAGGAGGT	267693	99889	GGAAACAACAGATGGGGCCT
178520	10716	TGGAGAGAAGCCCAGGAGGC	223107	55303	TGTTTCTTGCTGCAAGGAGG	267694	99890	AGGAAACAACAGATGGGGCC
178521	10717	GTGGAGAGAAGCCCAGGAGG	223108	55304	CTGTTTCTTGCTGCAAGGAG	267695	99891	AAGGAAACAACAGATGGGGC
178522	10718	GGTGGAGAGAAGCCCAGGAG	223109	55305	GCTGTTTCTTGCTGCAAGGA	267696	99892	TAAGGAAACAACAGATGGGG
178523	10719	CGGTGGAGAGAAGCCCAGGA	223110	55306	GGCTGTTTCTTGCTGCAAGG	267697	99893	ATAAGGAAACAACAGATGGG
178524	10720	CCGGTGGAGAGAAGCCCAGG	223111	55307	GGGCTGTTTCTTGCTGCAAG	267698	99894	CATAAGGAAACAACAGATGG
178525	10721	CCCGGTGGAGAGAAGCCCAG	223112	55308	GGGGCTGTTTCTTGCTGCAA	267699	99895	ACATAAGGAAACAACAGATG
178526	10722	ACCCGGTGGAGAGAAGCCCA	223113	55309	TGGGGCTGTTTCTTGCTGCA	267700	99896	CACATAAGGAAACAACAGAT
178527	10723	AACCCGGTGGAGAGAAGCCC	223114	55310	CTGGGGCTGTTTCTTGCTGC	267701	99897	CCACATAAGGAAACAACAGA
178528	10724	GAACCCGGTGGAGAGAAGCC	223115	55311	TCTGGGGCTGTTTCTTGCTG	267702	99898	TCCACATAAGGAAACAACAG
178529	10725	TGAACCCGGTGGAGAGAAGC	223116	55312	ATCTGGGGCTGTTTCTTGCT	267703	99899	TTCCACATAAGGAAACAACA
178530	10726	CTGAACCCGGTGGAGAGAAG	223117	55313	GATCTGGGGCTGTTTCTTGC	267704	99900	TTTCCACATAAGGAAACAAC

178531	10727	ACTGAACCCGGTGGAGAGAA	223118	55314	CGATCTGGGGCTGTTTCTTG	267705	99901	TTTTCCACATAAGGAAACAA
178532	10728	AACTGAACCCGGTGGAGAGA	223119	55315	ACGATCTGGGGCTGTTTCTT	267706	99902	ATTTTCCACATAAGGAAACA
178533	10729	GAACTGAACCCGGTGGAGAG	223120	55316	CACGATCTGGGGCTGTTTCT	267707	99903	TATTTTCCACATAAGGAAAC
178534	10730	AGAACTGAACCCGGTGGAGA	223121	55317	CCACGATCTGGGGCTGTTTC	267708	99904	TTATTTTCCACATAAGGAAA
178535	10731	AAGAACTGAACCCGGTGGAG	223122	55318	CCCACGATCTGGGGCTGTTT	267709	99905	CTTATTTTCCACATAAGGAA
178536	10732	GAAGAACTGAACCCGGTGGA	223123	55319	TCCCACGATCTGGGGCTGTT	267710	99906	TCTTATTTTCCACATAAGGA
178537	10733	GGAAGAACTGAACCCGGTGG	223124	55320	TTCCCACGATCTGGGGCTGT	267711	99907	CTCTTATTTTCCACATAAGG
178538	10734	AGGAAGAACTGAACCCGGTG	223125	55321	TTTCCCACGATCTGGGGCTG	267712	99908	CCTCTTATTTTCCACATAAG
178539	10735	AAGGAAGAACTGAACCCGGT	223126	55322	GTTTCCCACGATCTGGGGCT	267713	99909	GCCTCTTATTTTCCACATAA
178540	10736	AAAGGAAGAACTGAACCCGG	223127	55323	GGTTTCCCACGATCTGGGGC	267714	99910	AGCCTCTTATTTTCCACATA
178541	10737	TAAAGGAAGAACTGAACCCG	223128	55324	AGGTTTCCCACGATCTGGGG	267715	99911	AAGCCTCTTATTTTCCACAT
178542	10738	CTAAAGGAAGAACTGAACCC	223129	55325	TAGGTTTCCCACGATCTGGG	267716	99912	GAAGCCTCTTATTTTCCACA
178543	10739	ACTAAAGGAAGAACTGAACC	223130	55326	GTAGGTTTCCCACGATCTGG	267717	99913	CGAAGCCTCTTATTTTCCAC
178544	10740	CACTAAAGGAAGAACTGAAC	223131	55327	TGTAGGTTTCCCACGATCTG	267718	99914	ACGAAGCCTCTTATTTTCCA
178545	10741	CCACTAAAGGAAGAACTGAA	223132	55328	CTGTAGGTTTCCCACGATCT	267719	99915	AACGAAGCCTCTTATTTTCC
178546	10742	ACCACTAAAGGAAGAACTGA	223133	55329	TCTGTAGGTTTCCCACGATC	267720	99916	AAACGAAGCCTCTTATTTTC
178547	10743	CACCACTAAAGGAAGAACTG	223134	55330	GTCTGTAGGTTTCCCACGAT	267721	99917	CAAACGAAGCCTCTTATTTT
178548	10744	TCACCACTAAAGGAAGAACT	223135	55331	GGTCTGTAGGTTTCCCACGA	267722	99918	ACAAACGAAGCCTCTTATTT
178549	10745	TTCACCACTAAAGGAAGAAC	223136	55332	AGGTCTGTAGGTTTCCCACG	267723	99919	GACAAACGAAGCCTCTTATT
178550	10746	CTTCACCACTAAAGGAAGAA	223137	55333	CAGGTCTGTAGGTTTCCCAC	267724	99920	GGACAAACGAAGCCTCTTAT
178551	10747	ACTTCACCACTAAAGGAAGA	223138	55334	GCAGGTCTGTAGGTTTCCCA	267725	99921	AGGACAAACGAAGCCTCTTA
178552	10748	AACTTCACCACTAAAGGAAG	223139	55335	AGCAGGTCTGTAGGTTTCCC	267726	99922	TAGGACAAACGAAGCCTCTT
178553	10749	GAACTTCACCACTAAAGGAA	223140	55336	TAGCAGGTCTGTAGGTTTCC	267727	99923	ATAGGACAAACGAAGCCTCT
178554	10750	GGAACTTCACCACTAAAGGA	223141	55337	CTAGCAGGTCTGTAGGTTTC	267728	99924	AATAGGACAAACGAAGCCTC
178555	10751	AGGAACTTCACCACTAAAGG	223142	55338	TCTAGCAGGTCTGTAGGTTT	267729	99925	CAATAGGACAAACGAAGCCT
178556	10752	GAGGAACTTCACCACTAAAG	223143	55339	GTCTAGCAGGTCTGTAGGTT	267730	99926	GCAATAGGACAAACGAAGCC
178557	10753	GGAGGAACTTCACCACTAAA	223144	55340	TGTCTAGCAGGTCTGTAGGT	267731	99927	GGCAATAGGACAAACGAAGC
178558	10754	GGGAGGAACTTCACCACTAA	223145	55341	CTGTCTAGCAGGTCTGTAGG	267732	99928	TGGCAATAGGACAAACGAAG
178559	10755	AGGGAGGAACTTCACCACTA	223146	55342	TCTGTCTAGCAGGTCTGTAG	267733	99929	GTGGCAATAGGACAAACGAA
178560	10756	AAGGGAGGAACTTCACCACT	223147	55343	GTCTGTCTAGCAGGTCTGTA	267734	99930	TGTGGCAATAGGACAAACGA
178561	10757	GAAGGGAGGAACTTCACCAC	223148	55344	AGTCTGTCTAGCAGGTCTGT	267735	99931	CTGTGGCAATAGGACAAACG
178562	10758	AGAAGGGAGGAACTTCACCA	223149	55345	TAGTCTGTCTAGCAGGTCTG	267736	99932	TCTGTGGCAATAGGACAAAC
178563	10759	AAGAAGGGAGGAACTTCACC	223150	55346	CTAGTCTGTCTAGCAGGTCT	267737	99933	CTCTGTGGCAATAGGACAAA
178564	10760	TAAGAAGGGAGGAACTTCAC	223151	55347	CCTAGTCTGTCTAGCAGGTC	267738	99934	GCTCTGTGGCAATAGGACAA
178565	10761	CTAAGAAGGGAGGAACTTCA	223152	55348	TCCTAGTCTGTCTAGCAGGT	267739	99935	CGCTCTGTGGCAATAGGACA
178566	10762	GCTAAGAAGGGAGGAACTTC	223153	55349	CTCCTAGTCTGTCTAGCAGG	267740	99936	ACGCTCTGTGGCAATAGGAC
178567	10763	TGCTAAGAAGGGAGGAACTT	223154	55350	GCTCCTAGTCTGTCTAGCAG	267741	99937	TACGCTCTGTGGCAATAGGA
178568	10764	ATGCTAAGAAGGGAGGAACT	223155	55351	TGCTCCTAGTCTGTCTAGCA	267742	99938	GTACGCTCTGTGGCAATAGG
178569	10765	GATGCTAAGAAGGGAGGAAC	223156	55352	TTGCTCCTAGTCTGTCTAGC	267743	99939	AGTACGCTCTGTGGCAATAG
178570	10766	AGATGCTAAGAAGGGAGGAA	223157	55353	TTTGCTCCTAGTCTGTCTAG	267744	99940	TAGTACGCTCTGTGGCAATA
178571	10767	GAGATGCTAAGAAGGGAGGA	223158	55354	TTTTGCTCCTAGTCTGTCTA	267745	99941	GTAGTACGCTCTGTGGCAAT
178572	10768	TGAGATGCTAAGAAGGGAGG	223159	55355	CTTTTGCTCCTAGTCTGTCT	267746	99942	AGTAGTACGCTCTGTGGCAA
178573	10769	TTGAGATGCTAAGAAGGGAG	223160	55356	GCTTTTGCTCCTAGTCTGTC	267747	99943	AAGTAGTACGCTCTGTGGCA
178574	10770	GTTGAGATGCTAAGAAGGGA	223161	55357	AGCTTTTGCTCCTAGTCTGT	267748	99944	GAAGTAGTACGCTCTGTGGC
178575	10771	AGTTGAGATGCTAAGAAGGG	223162	55358	CAGCTTTTGCTCCTAGTCTG	267749	99945	TGAAGTAGTACGCTCTGTGG
178576	10772	CAGTTGAGATGCTAAGAAGG	223163	55359	CCAGCTTTTGCTCCTAGTCT	267750	99946	CTGAAGTAGTACGCTCTGTG
178577	10773	ACAGTTGAGATGCTAAGAAG	223164	55360	CCCAGCTTTTGCTCCTAGTC	267751	99947	CCTGAAGTAGTACGCTCTGT
178578	10774	CACAGTTGAGATGCTAAGAA	223165	55361	CCCCAGCTTTTGCTCCTAGT	267752	99948	TCCTGAAGTAGTACGCTCTG
178579	10775	GCACAGTTGAGATGCTAAGA	223166	55362	GCCCCAGCTTTTGCTCCTAG	267753	99949	TTCCTGAAGTAGTACGCTCT
178580	10776	GGCACAGTTGAGATGCTAAG	223167	55363	AGCCCCAGCTTTTGCTCCTA	267754	99950	GTTCCTGAAGTAGTACGCTC
178581	10777	AGGCACAGTTGAGATGCTAA	223168	55364	AAGCCCCAGCTTTTGCTCCT	267755	99951	TGTTCCTGAAGTAGTACGCT
178582	10778	CAGGCACAGTTGAGATGCTA	223169	55365	AAAGCCCCAGCTTTTGCTCC	267756	99952	ATGTTCCTGAAGTAGTACGC
178583	10779	TCAGGCACAGTTGAGATGCT	223170	55366	TAAAGCCCCAGCTTTTGCTC	267757	99953	GATGTTCCTGAAGTAGTACG
178584	10780	CTCAGGCACAGTTGAGATGC	223171	55367	TTAAAGCCCCAGCTTTTGCT	267758	99954	GGATGTTCCTGAAGTAGTAC
178585	10781	TCTCAGGCACAGTTGAGATG	223172	55368	CTTAAAGCCCCAGCTTTTGC	267759	99955	TGGATGTTCCTGAAGTAGTA
178586	10782	TTCTCAGGCACAGTTGAGAT	223173	55369	TCTTAAAGCCCCAGCTTTTG	267760	99956	TTGGATGTTCCTGAAGTAGT
178587	10783	TTTCTCAGGCACAGTTGAGA	223174	55370	TTCTTAAAGCCCCAGCTTTT	267761	99957	CTTGGATGTTCCTGAAGTAG
178588	10784	TTTTCTCAGGCACAGTTGAG	223175	55371	ATTCTTAAAGCCCCAGCTTT	267762	99958	TCTTGGATGTTCCTGAAGTA
178589	10785	CTTTTCTCAGGCACAGTTGA	223176	55372	GATTCTTAAAGCCCCAGCTT	267763	99959	GTCTTGGATGTTCCTGAAGT
178590	10786	CCTTTTCTCAGGCACAGTTG	223177	55373	GGATTCTTAAAGCCCCAGCT	267764	99960	TGTCTTGGATGTTCCTGAAG
178591	10787	GCCTTTTCTCAGGCACAGTT	223178	55374	GGGATTCTTAAAGCCCCAGC	267765	99961	ATGTCTTGGATGTTCCTGAA
178592	10788	GGCCTTTTCTCAGGCACAGT	223179	55375	GGGGATTCTTAAAGCCCCAG	267766	99962	CATGTCTTGGATGTTCCTGA
178593	10789	TGGCCTTTTCTCAGGCACAG	223180	55376	TGGGGATTCTTAAAGCCCCA	267767	99963	CCATGTCTTGGATGTTCCTG
178594	10790	CTGGCCTTTTCTCAGGCACA	223181	55377	CTGGGGATTCTTAAAGCCCC	267768	99964	TCCATGTCTTGGATGTTCCT
178595	10791	ACTGGCCTTTTCTCAGGCAC	223182	55378	CCTGGGGATTCTTAAAGCCC	267769	99965	TTCCATGTCTTGGATGTTCC
178596	10792	CACTGGCCTTTTCTCAGGCA	223183	55379	CCCTGGGGATTCTTAAAGCC	267770	99966	TTTCCATGTCTTGGATGTTC
178597	10793	CCACTGGCCTTTTCTCAGGC	223184	55380	TCCCTGGGGATTCTTAAAGC	267771	99967	ATTTCCATGTCTTGGATGTT
178598	10794	GCCACTGGCCTTTTCTCAGG	223185	55381	CTCCCTGGGGATTCTTAAAG	267772	99968	GATTTCCATGTCTTGGATGT
178599	10795	CGCCACTGGCCTTTTCTCAG	223186	55382	CCTCCCTGGGGATTCTTAAA	267773	99969	GGATTTCCATGTCTTGGATG
178600	10796	CCGCCACTGGCCTTTTCTCA	223187	55383	ACCTCCCTGGGGATTCTTAA	267774	99970	CGGATTTCCATGTCTTGGAT
178601	10797	GCCGCCACTGGCCTTTTCTC	223188	55384	AACCTCCCTGGGGATTCTTA	267775	99971	GCGGATTTCCATGTCTTGGA
178602	10798	AGCCGCCACTGGCCTTTTCT	223189	55385	GAACCTCCCTGGGGATTCTT	267776	99972	TGCGGATTTCCATGTCTTGG

178603	10799	CAGCCGCCACTGGCCTTTTC	223190	55386	AGAACCTCCCTGGGGATTCT	267777	99973	CTGCGGATTTCCATGTCTTG
178604	10800	GCAGCCGCCACTGGCCTTTT	223191	55387	GAGAACCTCCCTGGGGATTC	267778	99974	CCTGCGGATTTCCATGTCTT
178605	10801	TGCAGCCGCCACTGGCCTTT	223192	55388	GGAGAACCTCCCTGGGGATT	267779	99975	CCCTGCGGATTTCCATGTCT
178606	10802	GTGCAGCCGCCACTGGCCTT	223193	55389	AGGAGAACCTCCCTGGGGAT	267780	99976	GCCCTGCGGATTTCCATGTC
178607	10803	AGTGCAGCCGCCACTGGCCT	223194	55390	CAGGAGAACCTCCCTGGGGA	267781	99977	TGCCCTGCGGATTTCCATGT
178608	10804	GAGTGCAGCCGCCACTGGCC	223195	55391	TCAGGAGAACCTCCCTGGGG	267782	99978	GTGCCCTGCGGATTTCCATG
178609	10805	AGAGTGCAGCCGCCACTGGC	223196	55392	CTCAGGAGAACCTCCCTGGG	267783	99979	CGTGCCCTGCGGATTTCCAT
178610	10806	CAGAGTGCAGCCGCCACTGG	223197	55393	TCTCAGGAGAACCTCCCTGG	267784	99980	CCGTGCCCTGCGGATTTCCA
178611	10807	ACAGAGTGCAGCCGCCACTG	223198	55394	CTCTCAGGAGAACCTCCCTG	267785	99981	ACCGTGCCCTGCGGATTTCC
178612	10808	AACAGAGTGCAGCCGCCACT	223199	55395	TCTCTCAGGAGAACCTCCCT	267786	99982	CACCGTGCCCTGCGGATTTC
178613	10809	GAACAGAGTGCAGCCGCCAC	223200	55396	CTCTCTCAGGAGAACCTCCC	267787	99983	CCACCGTGCCCTGCGGATTT
178614	10810	GGAACAGAGTGCAGCCGCCA	223201	55397	ACTCTCTCAGGAGAACCTCC	267788	99984	GCCACCGTGCCCTGCGGATT
178615	10811	GGGAACAGAGTGCAGCCGCC	223202	55398	TACTCTCTCAGGAGAACCTC	267789	99985	AGCCACCGTGCCCTGCGGAT
178616	10812	AGGGAACAGAGTGCAGCCGC	223203	55399	CTACTCTCTCAGGAGAACCT	267790	99986	GAGCCACCGTGCCCTGCGGA
178617	10813	CAGGGAACAGAGTGCAGCCG	223204	55400	GCTACTCTCTCAGGAGAACC	267791	99987	TGAGCCACCGTGCCCTGCGG
178618	10814	ACAGGGAACAGAGTGCAGCC	223205	55401	GGCTACTCTCTCAGGAGAAC	267792	99988	GTGAGCCACCGTGCCCTGCG
178619	10815	CACAGGGAACAGAGTGCAGC	223206	55402	TGGCTACTCTCTCAGGAGAA	267793	99989	CGTGAGCCACCGTGCCCTGC
178620	10816	CCACAGGGAACAGAGTGCAG	223207	55403	CTGGCTACTCTCTCAGGAGA	267794	99990	ACGTGAGCCACCGTGCCCTG
178621	10817	TCCACAGGGAACAGAGTGCA	223208	55404	ACTGGCTACTCTCTCAGGAG	267795	99991	GACGTGAGCCACCGTGCCCT
178622	10818	CTCCACAGGGAACAGAGTGC	223209	55405	AACTGGCTACTCTCTCAGGA	267796	99992	AGACGTGAGCCACCGTGCCC
178623	10819	ACTCCACAGGGAACAGAGTG	223210	55406	CAACTGGCTACTCTCTCAGG	267797	99993	TAGACGTGAGCCACCGTGCC
178624	10820	CACTCCACAGGGAACAGAGT	223211	55407	CCAACTGGCTACTCTCTCAG	267798	99994	ATAGACGTGAGCCACCGTGC
178625	10821	ACACTCCACAGGGAACAGAG	223212	55408	TCCAACTGGCTACTCTCTCA	267799	99995	TATAGACGTGAGCCACCGTG
178626	10822	AACACTCCACAGGGAACAGA	223213	55409	ATCCAACTGGCTACTCTCTC	267800	99996	TTATAGACGTGAGCCACCGT
178627	10823	TAACACTCCACAGGGAACAG	223214	55410	AATCCAACTGGCTACTCTCT	267801	99997	ATTATAGACGTGAGCCACCG
178628	10824	TTAACACTCCACAGGGAACA	223215	55411	AAATCCAACTGGCTACTCTC	267802	99998	GATTATAGACGTGAGCCACC
178629	10825	ATTAACACTCCACAGGGAAC	223216	55412	AAAATCCAACTGGCTACTCT	267803	99999	GGATTATAGACGTGAGCCAC
178630	10826	TATTAACACTCCACAGGGAA	223217	55413	CAAAATCCAACTGGCTACTC	267804	100000	GGGATTATAGACGTGAGCCA
178631	10827	TTATTAACACTCCACAGGGA	223218	55414	ACAAAATCCAACTGGCTACT	267805	100001	CGGGATTATAGACGTGAGCC
178632	10828	TTTATTAACACTCCACAGGG	223219	55415	TACAAAATCCAACTGGCTAC	267806	100002	CCGGGATTATAGACGTGAGC
178633	10829	CTTTATTAACACTCCACAGG	223220	55416	TTACAAAATCCAACTGGCTA	267807	100003	GCCGGGATTATAGACGTGAG
178634	10830	TCTTTATTAACACTCCACAG	223221	55417	CTTACAAAATCCAACTGGCT	267808	100004	TGCCGGGATTATAGACGTGA
178635	10831	GTCTTTATTAACACTCCACA	223222	55418	GCTTACAAAATCCAACTGGC	267809	100005	GTGCCGGGATTATAGACGTG
178636	10832	AGTCTTTATTAACACTCCAC	223223	55419	TGCTTACAAAATCCAACTGG	267810	100006	AGTGCCGGGATTATAGACGT
178637	10833	CAGTCTTTATTAACACTCCA	223224	55420	CTGCTTACAAAATCCAACTG	267811	100007	AAGTGCCGGGATTATAGACG
178638	10834	TCAGTCTTTATTAACACTCC	223225	55421	TCTGCTTACAAAATCCAACT	267812	100008	AAAGTGCCGGGATTATAGAC
178639	10835	TTCAGTCTTTATTAACACTC	223226	55422	CTCTGCTTACAAAATCCAAC	267813	100009	CAAAGTGCCGGGATTATAGA
178640	10836	ATTCAGTCTTTATTAACACT	223227	55423	TCTCTGCTTACAAAATCCAA	267814	100010	CCAAAGTGCCGGGATTATAG
178641	10837	TATTCAGTCTTTATTAACAC	223228	55424	ATCTCTGCTTACAAAATCCA	267815	100011	CCCAAAGTGCCGGGATTATA
178642	10838	TTATTCAGTCTTTATTAACA	223229	55425	AATCTCTGCTTACAAAATCC	267816	100012	TCCCAAAGTGCCGGGATTAT
178643	10839	TTTATTCAGTCTTTATTAAC	223230	55426	AAATCTCTGCTTACAAAATC	267817	100013	CTCCCAAAGTGCCGGGATTA
178644	10840	ATTTATTCAGTCTTTATTAA	223231	55427	CAAATCTCTGCTTACAAAAT	267818	100014	CCTCCCAAAGTGCCGGGATT
178645	10841	AATTTATTCAGTCTTTATTA	223232	55428	ACAAATCTCTGCTTACAAAA	267819	100015	ACCTCCCAAAGTGCCGGGAT
178646	10842	CAATTTATTCAGTCTTTATT	223233	55429	AACAAATCTCTGCTTACAAA	267820	100016	AACCTCCCAAAGTGCCGGGA
178647	10843	TCAATTTATTCAGTCTTTAT	223234	55430	AAACAAATCTCTGCTTACAA	267821	100017	CAACCTCCCAAAGTGCCGGG
178648	10844	TTCAATTTATTCAGTCTTTA	223235	55431	CAAACAAATCTCTGCTTACA	267822	100018	TCAACCTCCCAAAGTGCCGG
178649	10845	TTTCAATTTATTCAGTCTTT	223236	55432	CCAAACAAATCTCTGCTTAC	267823	100019	CTCAACCTCCCAAAGTGCCG
178650	10846	ATTTCAATTTATTCAGTCTT	223237	55433	CCCAAACAAATCTCTGCTTA	267824	100020	CCTCAACCTCCCAAAGTGCC
178651	10847	TATTTCAATTTATTCAGTCT	223238	55434	CCCCAAACAAATCTCTGCTT	267825	100021	ACCTCAACCTCCCAAAGTGC
178652	10848	TTATTTCAATTTATTCAGTC	223239	55435	TCCCCAAACAAATCTCTGCT	267826	100022	CACCTCAACCTCCCAAAGTG
178653	10849	TTTATTTCAATTTATTCAGT	223240	55436	CTCCCCAAACAAATCTCTGC	267827	100023	CCACCTCAACCTCCCAAAGT
178654	10850	ATTTATTTCAATTTATTCAG	223241	55437	CCTCCCCAAACAAATCTCTG	267828	100024	CCCACCTCAACCTCCCAAAG
178655	10851	GATTTATTTCAATTTATTCA	223242	55438	TCCTCCCCAAACAAATCTCT	267829	100025	TCCCACCTCAACCTCCCAAA
178656	10852	GGATTTATTTCAATTTATTC	223243	55439	CTCCTCCCCAAACAAATCTC	267830	100026	CTCCCACCTCAACCTCCCAA
178657	10853	GGGATTTATTTCAATTTATT	223244	55440	CCTCCTCCCCAAACAAATCT	267831	100027	TCTCCCACCTCAACCTCCCA
178658	10854	AGGGATTTATTTCAATTTAT	223245	55441	ACCTCCTCCCCAAACAAATC	267832	100028	TTCTCCCACCTCAACCTCCC
178659	10855	AAGGGATTTATTTCAATTTA	223246	55442	CACCTCCTCCCCAAACAAAT	267833	100029	ATTCTCCCACCTCAACCTCC
178660	10856	AAAGGGATTTATTTCAATTT	223247	55443	TCACCTCCTCCCCAAACAAA	267834	100030	GATTCTCCCACCTCAACCTC
178661	10857	GAAAGGGATTTATTTCAATT	223248	55444	GTCACCTCCTCCCCAAACAA	267835	100031	CGATTCTCCCACCTCAACCT
178662	10858	TGAAAGGGATTTATTTCAAT	223249	55445	TGTCACCTCCTCCCCAAACA	267836	100032	GCGATTCTCCCACCTCAACC
178663	10859	TTGAAAGGGATTTATTTCAA	223250	55446	TTGTCACCTCCTCCCCAAAC	267837	100033	AGCGATTCTCCCACCTCAAC
178664	10860	ATTGAAAGGGATTTATTTCA	223251	55447	GTTGTCACCTCCTCCCCAAA	267838	100034	AAGCGATTCTCCCACCTCAA
178665	10861	CATTGAAAGGGATTTATTTC	223252	55448	CGTTGTCACCTCCTCCCCAA	267839	100035	CAAGCGATTCTCCCACCTCA
178666	10862	ACATTGAAAGGGATTTATTT	223253	55449	ACGTTGTCACCTCCTCCCCA	267840	100036	TCAAGCGATTCTCCCACCTC
178667	10863	GACATTGAAAGGGATTTATT	223254	55450	TACGTTGTCACCTCCTCCCC	267841	100037	CTCAAGCGATTCTCCCACCT
178668	10864	TGACATTGAAAGGGATTTAT	223255	55451	CTACGTTGTCACCTCCTCCC	267842	100038	CCTCAAGCGATTCTCCCACC
178669	10865	ATGACATTGAAAGGGATTTA	223256	55452	CCTACGTTGTCACCTCCTCC	267843	100039	GCCTCAAGCGATTCTCCCAC
178670	10866	AATGACATTGAAAGGGATTT	223257	55453	CCCTACGTTGTCACCTCCTC	267844	100040	GGCCTCAAGCGATTCTCCCA
178671	10867	TAATGACATTGAAAGGGATT	223258	55454	TCCCTACGTTGTCACCTCCT	267845	100041	TGGCCTCAAGCGATTCTCCC
178672	10868	TTAATGACATTGAAAGGGAT	223259	55455	CTCCCTACGTTGTCACCTCC	267846	100042	CTGGCCTCAAGCGATTCTCC
178673	10869	CTTAATGACATTGAAAGGGA	223260	55456	GCTCCCTACGTTGTCACCTC	267847	100043	TCTGGCCTCAAGCGATTCTC
178674	10870	ACTTAATGACATTGAAAGGG	223261	55457	TGCTCCCTACGTTGTCACCT	267848	100044	TTCTGGCCTCAAGCGATTCT

178675	10871	CACTTAATGACATTGAAAGG	223262	55458	CTGCTCCCTACGTTGTCACC	267849	100045	CTTCTGGCCTCAAGCGATTC
178676	10872	GCACTTAATGACATTGAAAG	223263	55459	TCTGCTCCCTACGTTGTCAC	267850	100046	ACTTCTGGCCTCAAGCGATT
178677	10873	AGCACTTAATGACATTGAAA	223264	55460	CTCTGCTCCCTACGTTGTCA	267851	100047	AACTTCTGGCCTCAAGCGAT
178678	10874	TAGCACTTAATGACATTGAA	223265	55461	CCTCTGCTCCCTACGTTGTC	267852	100048	GAACTTCTGGCCTCAAGCGA
178679	10875	ATAGCACTTAATGACATTGA	223266	55462	CCCTCTGCTCCCTACGTTGT	267853	100049	TGAACTTCTGGCCTCAAGCG
178680	10876	TATAGCACTTAATGACATTG	223267	55463	CCCCTCTGCTCCCTACGTTG	267854	100050	TTGAACTTCTGGCCTCAAGC
178681	10877	TTATAGCACTTAATGACATT	223268	55464	GCCCCTCTGCTCCCTACGTT	267855	100051	CTTGAACTTCTGGCCTCAAG
178682	10878	TTTATAGCACTTAATGACAT	223269	55465	TGCCCCTCTGCTCCCTACGT	267856	100052	TCTTGAACTTCTGGCCTCAA
178683	10879	ATTTATAGCACTTAATGACA	223270	55466	TTGCCCCTCTGCTCCCTACG	267857	100053	GTCTTGAACTTCTGGCCTCA
178684	10880	TATTTATAGCACTTAATGAC	223271	55467	TTTGCCCCTCTGCTCCCTAC	267858	100054	GGTCTTGAACTTCTGGCCTC
178685	10881	TTATTTATAGCACTTAATGA	223272	55468	CTTTGCCCCTCTGCTCCCTA	267859	100055	TGGTCTTGAACTTCTGGCCT
178686	10882	ATTATTTATAGCACTTAATG	223273	55469	GCTTTGCCCCTCTGCTCCCT	267860	100056	CTGGTCTTGAACTTCTGGCC
178687	10883	GATTATTTATAGCACTTAAT	223274	55470	AGCTTTGCCCCTCTGCTCCC	267861	100057	GCTGGTCTTGAACTTCTGGC
178688	10884	TGATTATTTATAGCACTTAA	223275	55471	CAGCTTTGCCCCTCTGCTCC	267862	100058	GGCTGGTCTTGAACTTCTGG
178689	10885	ATGATTATTTATAGCACTTA	223276	55472	ACAGCTTTGCCCCTCTGCTC	267863	100059	AGGCTGGTCTTGAACTTCTG
178690	10886	CATGATTATTTATAGCACTT	223277	55473	GACAGCTTTGCCCCTCTGCT	267864	100060	CAGGCTGGTCTTGAACTTCT
178691	10887	TCATGATTATTTATAGCACT	223278	55474	CGACAGCTTTGCCCCTCTGC	267865	100061	TCAGGCTGGTCTTGAACTTC
178692	10888	TTCATGATTATTTATAGCAC	223279	55475	CCGACAGCTTTGCCCCTCTG	267866	100062	CTCAGGCTGGTCTTGAACTT
178693	10889	GTTCATGATTATTTATAGCA	223280	55476	CCCGACAGCTTTGCCCCTCT	267867	100063	GCTCAGGCTGGTCTTGAACT
178694	10890	GGTTCATGATTATTTATAGC	223281	55477	TCCCGACAGCTTTGCCCCTC	267868	100064	TGCTCAGGCTGGTCTTGAAC
178695	10891	TGGTTCATGATTATTTATAG	223282	55478	TTCCCGACAGCTTTGCCCCT	267869	100065	TTGCTCAGGCTGGTCTTGAA
178696	10892	TTGGTTCATGATTATTTATA	223283	55479	ATTCCCGACAGCTTTGCCCC	267870	100066	GTTGCTCAGGCTGGTCTTGA
178697	10893	ATTGGTTCATGATTATTTAT	223284	55480	GATTCCCGACAGCTTTGCCC	267871	100067	TGTTGCTCAGGCTGGTCTTG
178698	10894	CATTGGTTCATGATTATTTA	223285	55481	GGATTCCCGACAGCTTTGCC	267872	100068	ATGTTGCTCAGGCTGGTCTT
178699	10895	ACATTGGTTCATGATTATTT	223286	55482	AGGATTCCCGACAGCTTTGC	267873	100069	TATGTTGCTCAGGCTGGTCT
178700	10896	AACATTGGTTCATGATTATT	223287	55483	CAGGATTCCCGACAGCTTTG	267874	100070	CTATGTTGCTCAGGCTGGTC
178701	10897	GAACATTGGTTCATGATTAT	223288	55484	GCAGGATTCCCGACAGCTTT	267875	100071	ACTATGTTGCTCAGGCTGGT
178702	10898	CGAACATTGGTTCATGATTA	223289	55485	GGCAGGATTCCCGACAGCTT	267876	100072	GACTATGTTGCTCAGGCTGG
178703	10899	TCGAACATTGGTTCATGATT	223290	55486	AGGCAGGATTCCCGACAGCT	267877	100073	TGACTATGTTGCTCAGGCTG
178704	10900	ATCGAACATTGGTTCATGAT	223291	55487	AAGGCAGGATTCCCGACAGC	267878	100074	CTGACTATGTTGCTCAGGCT
178705	10901	CATCGAACATTGGTTCATGA	223292	55488	CAAGGCAGGATTCCCGACAG	267879	100075	TCTGACTATGTTGCTCAGGC
178706	10902	CCATCGAACATTGGTTCATG	223293	55489	TCAAGGCAGGATTCCCGACA	267880	100076	GTCTGACTATGTTGCTCAGG
178707	10903	GCCATCGAACATTGGTTCAT	223294	55490	CTCAAGGCAGGATTCCCGAC	267881	100077	GGTCTGACTATGTTGCTCAG
178708	10904	AGCCATCGAACATTGGTTCA	223295	55491	CCTCAAGGCAGGATTCCCGA	267882	100078	GGGTCTGACTATGTTGCTCA
178709	10905	CAGCCATCGAACATTGGTTC	223296	55492	CCCTCAAGGCAGGATTCCCG	267883	100079	GGGGTCTGACTATGTTGCTC
178710	10906	TCAGCCATCGAACATTGGTT	223297	55493	GCCCTCAAGGCAGGATTCCC	267884	100080	CGGGGTCTGACTATGTTGCT
178711	10907	ATCAGCCATCGAACATTGGT	223298	55494	TGCCCTCAAGGCAGGATTCC	267885	100081	ACGGGGTCTGACTATGTTGC
178712	10908	CATCAGCCATCGAACATTGG	223299	55495	CTGCCCTCAAGGCAGGATTC	267886	100082	GACGGGGTCTGACTATGTTG
178713	10909	TCATCAGCCATCGAACATTG	223300	55496	CCTGCCCTCAAGGCAGGATT	267887	100083	AGACGGGGTCTGACTATGTT
178714	10910	CTCATCAGCCATCGAACATT	223301	55497	CCCTGCCCTCAAGGCAGGAT	267888	100084	GAGACGGGGTCTGACTATGT
178715	10911	TCTCATCAGCCATCGAACAT	223302	55498	TCCCTGCCCTCAAGGCAGGA	267889	100085	AGAGACGGGGTCTGACTATG
178716	10912	TTCTCATCAGCCATCGAACA	223303	55499	ATCCCTGCCCTCAAGGCAGG	267890	100086	TAGAGACGGGGTCTGACTAT
178717	10913	TTTCTCATCAGCCATCGAAC	223304	55500	CATCCCTGCCCTCAAGGCAG	267891	100087	ATAGAGACGGGGTCTGACTA
178718	10914	ATTTCTCATCAGCCATCGAA	223305	55501	ACATCCCTGCCCTCAAGGCA	267892	100088	TATAGAGACGGGGTCTGACT
178719	10915	CATTTCTCATCAGCCATCGA	223306	55502	CACATCCCTGCCCTCAAGGC	267893	100089	TTATAGAGACGGGGTCTGAC
178720	10916	GCATTTCTCATCAGCCATCG	223307	55503	ACACATCCCTGCCCTCAAGG	267894	100090	TTTATAGAGACGGGGTCTGA
178721	10917	TGCATTTCTCATCAGCCATC	223308	55504	CACACATCCCTGCCCTCAAG	267895	100091	TTTTATAGAGACGGGGTCTG
178722	10918	TTGCATTTCTCATCAGCCAT	223309	55505	ACACACATCCCTGCCCTCAA	267896	100092	TTTTTATAGAGACGGGGTCT
178723	10919	CTTGCATTTCTCATCAGCCA	223310	55506	AACACACATCCCTGCCCTCA	267897	100093	TTTTTTATAGAGACGGGGTC
178724	10920	TCTTGCATTTCTCATCAGCC	223311	55507	CAACACACATCCCTGCCCTC	267898	100094	GTTTTTTATAGAGACGGGGT
178725	10921	TTCTTGCATTTCTCATCAGC	223312	55508	CCAACACACATCCCTGCCCT	267899	100095	TGTTTTTTATAGAGACGGGG
178726	10922	TTTCTTGCATTTCTCATCAG	223313	55509	CCCAACACACATCCCTGCCC	267900	100096	ATGTTTTTTATAGAGACGGG
178727	10923	TTTTCTTGCATTTCTCATCA	223314	55510	CCCCAACACACATCCCTGCC	267901	100097	AATGTTTTTTATAGAGACGG
178728	10924	TTTTTCTTGCATTTCTCATC	223315	55511	CCCCCAACACACATCCCTGC	267902	100098	TAATGTTTTTTATAGAGACG
178729	10925	TTTTTTCTTGCATTTCTCAT	223316	55512	CCCCCCAACACACATCCCTG	267903	100099	ATAATGTTTTTTATAGAGAC
178730	10926	ATTTTTTCTTGCATTTCTCA	223317	55513	TCCCCCCAACACACATCCCT	267904	100100	AATAATGTTTTTTATAGAGA
178731	10927	AATTTTTTCTTGCATTTCTC	223318	55514	CTCCCCCCAACACACATCCC	267905	100101	AAATAATGTTTTTTATAGAG
178732	10928	AAATTTTTTCTTGCATTTCT	223319	55515	ACTCCCCCCAACACACATCC	267906	100102	AAAATAATGTTTTTTATAGA
178733	10929	AAAATTTTTTCTTGCATTTC	223320	55516	AACTCCCCCCAACACACATC	267907	100103	AAAAATAATGTTTTTTATAG
178734	10930	AAAAATTTTTTCTTGCATTT	223321	55517	CAACTCCCCCCAACACACAT	267908	100104	TAAAAATAATGTTTTTTATA
178735	10931	TAAAAATTTTTTCTTGCATT	223322	55518	CCAACTCCCCCCAACACACA	267909	100105	TTAAAAATAATGTTTTTTAT
178736	10932	TTAAAAATTTTTTCTTGCAT	223323	55519	CCCAACTCCCCCCAACACAC	267910	100106	TTTAAAAATAATGTTTTTTA
178737	10933	ATTAAAAATTTTTTCTTGCA	223324	55520	ACCCAACTCCCCCCAACACA	267911	100107	TTTTAAAAATAATGTTTTTT
178738	10934	GATTAAAAATTTTTTCTTGC	223325	55521	GACCCAACTCCCCCCAACAC	267912	100108	TTTTTAAAAATAATGTTTTT
178739	10935	TGATTAAAAATTTTTTCTTG	223326	55522	TGACCCAACTCCCCCCAACA	267913	100109	TTTTTTAAAAATAATGTTTT
178740	10936	CTGATTAAAAATTTTTTCTT	223327	55523	GTGACCCAACTCCCCCCAAC	267914	100110	CTTTTTTAAAAATAATGTTT
178741	10937	ACTGATTAAAAATTTTTTCT	223328	55524	AGTGACCCAACTCCCCCCAA	267915	100111	TCTTTTTTAAAAATAATGTT
178742	10938	TACTGATTAAAAATTTTTTC	223329	55525	CAGTGACCCAACTCCCCCCA	267916	100112	GTCTTTTTTAAAAATAATGT
178743	10939	CTACTGATTAAAAATTTTTT	223330	55526	CCAGTGACCCAACTCCCCCC	267917	100113	TGTCTTTTTTAAAAATAATG
178744	10940	CCTACTGATTAAAAATTTTT	223331	55527	CCCAGTGACCCAACTCCCCC	267918	100114	ATGTCTTTTTTAAAAATAAT
178745	10941	TCCTACTGATTAAAAATTTT	223332	55528	CCCCAGTGACCCAACTCCCC	267919	100115	CATGTCTTTTTTAAAAATAA
178746	10942	ATCCTACTGATTAAAAATTT	223333	55529	GCCCCAGTGACCCAACTCCC	267920	100116	CCATGTCTTTTTTAAAAATA

178747	10943	AATCCTACTGATTAAAAATT	223334	55530	AGCCCCAGTGACCCAACTCC	267921	100117	TCCATGTCTTTTTTAAAAAT
178748	10944	GAATCCTACTGATTAAAAAT	223335	55531	GAGCCCCAGTGACCCAACTC	267922	100118	TTCCATGTCTTTTTTAAAAA
178749	10945	TGAATCCTACTGATTAAAAA	223336	55532	CGAGCCCCAGTGACCCAACT	267923	100119	CTTCCATGTCTTTTTTAAAA
178750	10946	ATGAATCCTACTGATTAAAA	223337	55533	CCGAGCCCCAGTGACCCAAC	267924	100120	ACTTCCATGTCTTTTTTAAA
178751	10947	TATGAATCCTACTGATTAAA	223338	55534	ACCGAGCCCCAGTGACCCAA	267925	100121	GACTTCCATGTCTTTTTTAA
178752	10948	TTATGAATCCTACTGATTAA	223339	55535	CACCGAGCCCCAGTGACCCA	267926	100122	TGACTTCCATGTCTTTTTTA
178753	10949	CTTATGAATCCTACTGATTA	223340	55536	CCACCGAGCCCCAGTGACCC	267927	100123	TTGACTTCCATGTCTTTTTT
178754	10950	ACTTATGAATCCTACTGATT	223341	55537	GCCACCGAGCCCCAGTGACC	267928	100124	TTTGACTTCCATGTCTTTTT
178755	10951	AACTTATGAATCCTACTGAT	223342	55538	GGCCACCGAGCCCCAGTGAC	267929	100125	ATTTGACTTCCATGTCTTTT
178756	10952	CAACTTATGAATCCTACTGA	223343	55539	AGGCCACCGAGCCCCAGTGA	267930	100126	AATTTGACTTCCATGTCTTT
178757	10953	TCAACTTATGAATCCTACTG	223344	55540	AAGGCCACCGAGCCCCAGTG	267931	100127	GAATTTGACTTCCATGTCTT
178758	10954	GTCAACTTATGAATCCTACT	223345	55541	CAAGGCCACCGAGCCCCAGT	267932	100128	AGAATTTGACTTCCATGTCT
178759	10955	TGTCAACTTATGAATCCTAC	223346	55542	CCAAGGCCACCGAGCCCCAG	267933	100129	TAGAATTTGACTTCCATGTC
178760	10956	TTGTCAACTTATGAATCCTA	223347	55543	CCCAAGGCCACCGAGCCCCA	267934	100130	TTAGAATTTGACTTCCATGT
178761	10957	ATTGTCAACTTATGAATCCT	223348	55544	GCCCAAGGCCACCGAGCCCC	267935	100131	TTTAGAATTTGACTTCCATG
178762	10958	GATTGTCAACTTATGAATCC	223349	55545	TGCCCAAGGCCACCGAGCCC	267936	100132	TTTTAGAATTTGACTTCCAT
178763	10959	AGATTGTCAACTTATGAATC	223350	55546	TTGCCCAAGGCCACCGAGCC	267937	100133	TTTTTAGAATTTGACTTCCA
178764	10960	CAGATTGTCAACTTATGAAT	223351	55547	CTTGCCCAAGGCCACCGAGC	267938	100134	GTTTTTAGAATTTGACTTCC
178765	10961	CCAGATTGTCAACTTATGAA	223352	55548	ACTTGCCCAAGGCCACCGAG	267939	100135	AGTTTTTAGAATTTGACTTC
178766	10962	CCCAGATTGTCAACTTATGA	223353	55549	AACTTGCCCAAGGCCACCGA	267940	100136	CAGTTTTTAGAATTTGACTT
178767	10963	GCCCAGATTGTCAACTTATG	223354	55550	AAACTTGCCCAAGGCCACCG	267941	100137	CCAGTTTTTAGAATTTGACT
178768	10964	GGCCCAGATTGTCAACTTAT	223355	55551	GAAACTTGCCCAAGGCCACC	267942	100138	ACCAGTTTTTAGAATTTGAC
178769	10965	TGGCCCAGATTGTCAACTTA	223356	55552	AGAAACTTGCCCAAGGCCAC	267943	100139	CACCAGTTTTTAGAATTTGA
178770	10966	TTGGCCCAGATTGTCAACTT	223357	55553	TAGAAACTTGCCCAAGGCCA	267944	100140	GCACCAGTTTTTAGAATTTG
178771	10967	CTTGGCCCAGATTGTCAACT	223358	55554	GTAGAAACTTGCCCAAGGCC	267945	100141	AGCACCAGTTTTTAGAATTT
178772	10968	ACTTGGCCCAGATTGTCAAC	223359	55555	GGTAGAAACTTGCCCAAGGC	267946	100142	CAGCACCAGTTTTTAGAATT
178773	10969	AACTTGGCCCAGATTGTCAA	223360	55556	AGGTAGAAACTTGCCCAAGG	267947	100143	CCAGCACCAGTTTTTAGAAT
178774	10970	TAACTTGGCCCAGATTGTCA	223361	55557	GAGGTAGAAACTTGCCCAAG	267948	100144	GCCAGCACCAGTTTTTAGAA
178775	10971	TTAACTTGGCCCAGATTGTC	223362	55558	AGAGGTAGAAACTTGCCCAA	267949	100145	AGCCAGCACCAGTTTTTAGA
178776	10972	TTTAACTTGGCCCAGATTGT	223363	55559	GAGAGGTAGAAACTTGCCCA	267950	100146	CAGCCAGCACCAGTTTTTAG
178777	10973	TTTTAACTTGGCCCAGATTG	223364	55560	TGAGAGGTAGAAACTTGCCC	267951	100147	CCAGCCAGCACCAGTTTTTA
178778	10974	TTTTTAACTTGGCCCAGATT	223365	55561	CTGAGAGGTAGAAACTTGCC	267952	100148	CCCAGCCAGCACCAGTTTTT
178779	10975	TTTTTTAACTTGGCCCAGAT	223366	55562	CCTGAGAGGTAGAAACTTGC	267953	100149	ACCCAGCCAGCACCAGTTTT
178780	10976	TTTTTTTAACTTGGCCCAGA	223367	55563	ACCTGAGAGGTAGAAACTTG	267954	100150	CACCCAGCCAGCACCAGTTT
178781	10977	TTTTTTTTAACTTGGCCCAG	223368	55564	GACCTGAGAGGTAGAAACTT	267955	100151	GCACCCAGCCAGCACCAGTT
178782	10978	ATTTTTTTTAACTTGGCCCA	223369	55565	GGACCTGAGAGGTAGAAACT	267956	100152	CGCACCCAGCCAGCACCAGT
178783	10979	TATTTTTTTTAACTTGGCCC	223370	55566	AGGACCTGAGAGGTAGAAAC	267957	100153	CCGCACCCAGCCAGCACCAG
178784	10980	TTATTTTTTTTAACTTGGCC	223371	55567	AAGGACCTGAGAGGTAGAAA	267958	100154	ACCGCACCCAGCCAGCACCA
178785	10981	TTTATTTTTTTTAACTTGGC	223372	55568	AAAGGACCTGAGAGGTAGAA	267959	100155	CACCGCACCCAGCCAGCACC
178786	10982	TTTTATTTTTTTTAACTTGG	223373	55569	TAAAGGACCTGAGAGGTAGA	267960	100156	CCACCGCACCCAGCCAGCAC
178787	10983	TTTTTATTTTTTTTAACTTG	223374	55570	GTAAAGGACCTGAGAGGTAG	267961	100157	GCCACCGCACCCAGCCAGCA
178788	10984	ATTTTTATTTTTTTTAACTT	223375	55571	GGTAAAGGACCTGAGAGGTA	267962	100158	AGCCACCGCACCCAGCCAGC
178789	10985	TATTTTTATTTTTTTTAACT	223376	55572	GGGTAAAGGACCTGAGAGGT	267963	100159	GAGCCACCGCACCCAGCCAG
178790	10986	TTATTTTTATTTTTTTTAAC	223377	55573	TGGGTAAAGGACCTGAGAGG	267964	100160	TGAGCCACCGCACCCAGCCA
178791	10987	TTTATTTTTATTTTTTTTAA	223378	55574	GTGGGTAAAGGACCTGAGAG	267965	100161	ATGAGCCACCGCACCCAGCC
178792	10988	TTTTATTTTTATTTTTTTTA	223379	55575	GGTGGGTAAAGGACCTGAGA	267966	100162	CATGAGCCACCGCACCCAGC
178793	10989	TTTTTATTTTTATTTTTTTT	223380	55576	AGGTGGGTAAAGGACCTGAG	267967	100163	GCATGAGCCACCGCACCCAG
178794	10990	CTTTTTATTTTTATTTTTTT	223381	55577	TAGGTGGGTAAAGGACCTGA	267968	100164	GGCATGAGCCACCGCACCCA
178795	10991	TCTTTTTATTTTTATTTTTT	223382	55578	CTAGGTGGGTAAAGGACCTG	267969	100165	AGGCATGAGCCACCGCACCC
178796	10992	GTCTTTTTATTTTTATTTTT	223383	55579	CCTAGGTGGGTAAAGGACCT	267970	100166	TAGGCATGAGCCACCGCACC
178797	10993	AGTCTTTTTATTTTTATTTT	223384	55580	CCCTAGGTGGGTAAAGGACC	267971	100167	ATAGGCATGAGCCACCGCAC
178798	10994	AAGTCTTTTTATTTTTATTT	223385	55581	ACCCTAGGTGGGTAAAGGAC	267972	100168	TATAGGCATGAGCCACCGCA
178799	10995	AAAGTCTTTTTATTTTTATT	223386	55582	GACCCTAGGTGGGTAAAGGA	267973	100169	TTATAGGCATGAGCCACCGC
178800	10996	AAAAGTCTTTTTATTTTTAT	223387	55583	CGACCCTAGGTGGGTAAAGG	267974	100170	ATTATAGGCATGAGCCACCG
178801	10997	TAAAAGTCTTTTTATTTTTA	223388	55584	GCGACCCTAGGTGGGTAAAG	267975	100171	GATTATAGGCATGAGCCACC
178802	10998	TTAAAAGTCTTTTTATTTTT	223389	55585	GGCGACCCTAGGTGGGTAAA	267976	100172	GGATTATAGGCATGAGCCAC
178803	10999	TTTAAAAGTCTTTTTATTTT	223390	55586	TGGCGACCCTAGGTGGGTAA	267977	100173	GGGATTATAGGCATGAGCCA
178804	11000	TTTTAAAAGTCTTTTTATTT	223391	55587	ATGGCGACCCTAGGTGGGTA	267978	100174	TGGGATTATAGGCATGAGCC
178805	11001	TTTTTAAAAGTCTTTTTATT	223392	55588	GATGGCGACCCTAGGTGGGT	267979	100175	CTGGGATTATAGGCATGAGC
178806	11002	CTTTTTAAAAGTCTTTTTAT	223393	55589	GGATGGCGACCCTAGGTGGG	267980	100176	GCTGGGATTATAGGCATGAG
178807	11003	TCTTTTTAAAAGTCTTTTTA	223394	55590	AGGATGGCGACCCTAGGTGG	267981	100177	TGCTGGGATTATAGGCATGA
178808	11004	ATCTTTTTAAAAGTCTTTTT	223395	55591	CAGGATGGCGACCCTAGGTG	267982	100178	GTGCTGGGATTATAGGCATG
178809	11005	GATCTTTTTAAAAGTCTTTT	223396	55592	GCAGGATGGCGACCCTAGGT	267983	100179	AGTGCTGGGATTATAGGCAT
178810	11006	AGATCTTTTTAAAAGTCTTT	223397	55593	GGCAGGATGGCGACCCTAGG	267984	100180	AAGTGCTGGGATTATAGGCA
178811	11007	AAGATCTTTTTAAAAGTCTT	223398	55594	GGGCAGGATGGCGACCCTAG	267985	100181	AAAGTGCTGGGATTATAGGC
178812	11008	TAAGATCTTTTTAAAAGTCT	223399	55595	TGGGCAGGATGGCGACCCTA	267986	100182	CAAAGTGCTGGGATTATAGG
178813	11009	ATAAGATCTTTTTAAAAGTC	223400	55596	GTGGGCAGGATGGCGACCCT	267987	100183	CCAAAGTGCTGGGATTATAG
178814	11010	GATAAGATCTTTTTAAAAGT	223401	55597	GGTGGGCAGGATGGCGACCC	267988	100184	CCCAAAGTGCTGGGATTATA
178815	11011	CGATAAGATCTTTTTAAAAG	223402	55598	AGGTGGGCAGGATGGCGACC	267989	100185	TCCCAAAGTGCTGGGATTAT
178816	11012	ACGATAAGATCTTTTTAAAA	223403	55599	GAGGTGGGCAGGATGGCGAC	267990	100186	CTCCCAAAGTGCTGGGATTA
178817	11013	AACGATAAGATCTTTTTAAA	223404	55600	TGAGGTGGGCAGGATGGCGA	267991	100187	CCTCCCAAAGTGCTGGGATT
178818	11014	AAACGATAAGATCTTTTTAA	223405	55601	GTGAGGTGGGCAGGATGGCG	267992	100188	GCCTCCCAAAGTGCTGGGAT

178819	11015	CAAACGATAAGATCTTTTTA	223406	55602	TGTGAGGTGGGCAGGATGGC	267993	100189	GGCCTCCCAAAGTGCTGGGA
178820	11016	ACAAACGATAAGATCTTTTT	223407	55603	CTGTGAGGTGGGCAGGATGG	267994	100190	CGGCCTCCCAAAGTGCTGGG
178821	11017	AACAAACGATAAGATCTTTT	223408	55604	CCTGTGAGGTGGGCAGGATG	267995	100191	TCGGCCTCCCAAAGTGCTGG
178822	11018	TAACAAACGATAAGATCTTT	223409	55605	ACCTGTGAGGTGGGCAGGAT	267996	100192	CTCGGCCTCCCAAAGTGCTG
178823	11019	GTAACAAACGATAAGATCTT	223410	55606	AACCTGTGAGGTGGGCAGGA	267997	100193	CCTCGGCCTCCCAAAGTGCT
178824	11020	GGTAACAAACGATAAGATCT	223411	55607	TAACCTGTGAGGTGGGCAGG	267998	100194	GCCTCGGCCTCCCAAAGTGC
178825	11021	TGGTAACAAACGATAAGATC	223412	55608	GTAACCTGTGAGGTGGGCAG	267999	100195	CGCCTCGGCCTCCCAAAGTG
178826	11022	CTGGTAACAAACGATAAGAT	223413	55609	TGTAACCTGTGAGGTGGGCA	268000	100196	CCGCCTCGGCCTCCCAAAGT
178827	11023	ACTGGTAACAAACGATAAGA	223414	55610	CTGTAACCTGTGAGGTGGGC	268001	100197	CCCGCCTCGGCCTCCCAAAG
178828	11024	TACTGGTAACAAACGATAAG	223415	55611	ACTGTAACCTGTGAGGTGGG	268002	100198	ACCCGCCTCGGCCTCCCAAA
178829	11025	TTACTGGTAACAAACGATAA	223416	55612	CACTGTAACCTGTGAGGTGG	268003	100199	CACCCGCCTCGGCCTCCCAA
178830	11026	CTTACTGGTAACAAACGATA	223417	55613	TCACTGTAACCTGTGAGGTG	268004	100200	CCACCCGCCTCGGCCTCCCA
178831	11027	TCTTACTGGTAACAAACGAT	223418	55614	CTCACTGTAACCTGTGAGGT	268005	100201	TCCACCCGCCTCGGCCTCCC
178832	11028	GTCTTACTGGTAACAAACGA	223419	55615	GCTCACTGTAACCTGTGAGG	268006	100202	ATCCACCCGCCTCGGCCTCC
178833	11029	AGTCTTACTGGTAACAAACG	223420	55616	GGCTCACTGTAACCTGTGAG	268007	100203	GATCCACCCGCCTCGGCCTC
178834	11030	CAGTCTTACTGGTAACAAAC	223421	55617	AGGCTCACTGTAACCTGTGA	268008	100204	TGATCCACCCGCCTCGGCCT
178835	11031	TCAGTCTTACTGGTAACAAA	223422	55618	CAGGCTCACTGTAACCTGTG	268009	100205	GTGATCCACCCGCCTCGGCC
178836	11032	TTCAGTCTTACTGGTAACAA	223423	55619	CCAGGCTCACTGTAACCTGT	268010	100206	GGTGATCCACCCGCCTCGGC
178837	11033	ATTCAGTCTTACTGGTAACA	223424	55620	TCCAGGCTCACTGTAACCTG	268011	100207	AGGTGATCCACCCGCCTCGG
178838	11034	AATTCAGTCTTACTGGTAAC	223425	55621	ATCCAGGCTCACTGTAACCT	268012	100208	CAGGTGATCCACCCGCCTCG
178839	11035	GAATTCAGTCTTACTGGTAA	223426	55622	CATCCAGGCTCACTGTAACC	268013	100209	TCAGGTGATCCACCCGCCTC
178840	11036	GGAATTCAGTCTTACTGGTA	223427	55623	GCATCCAGGCTCACTGTAAC	268014	100210	CTCAGGTGATCCACCCGCCT
178841	11037	TGGAATTCAGTCTTACTGGT	223428	55624	TGCATCCAGGCTCACTGTAA	268015	100211	CCTCAGGTGATCCACCCGCC
178842	11038	CTGGAATTCAGTCTTACTGG	223429	55625	GTGCATCCAGGCTCACTGTA	268016	100212	ACCTCAGGTGATCCACCCGC
178843	11039	TCTGGAATTCAGTCTTACTG	223430	55626	AGTGCATCCAGGCTCACTGT	268017	100213	GACCTCAGGTGATCCACCCG
178844	11040	TTCTGGAATTCAGTCTTACT	223431	55627	CAGTGCATCCAGGCTCACTG	268018	100214	TGACCTCAGGTGATCCACCC
178845	11041	CTTCTGGAATTCAGTCTTAC	223432	55628	ACAGTGCATCCAGGCTCACT	268019	100215	CTGACCTCAGGTGATCCACC
178846	11042	GCTTCTGGAATTCAGTCTTA	223433	55629	GACAGTGCATCCAGGCTCAC	268020	100216	CCTGACCTCAGGTGATCCAC
178847	11043	TGCTTCTGGAATTCAGTCTT	223434	55630	TGACAGTGCATCCAGGCTCA	268021	100217	TCCTGACCTCAGGTGATCCA
178848	11044	TTGCTTCTGGAATTCAGTCT	223435	55631	ATGACAGTGCATCCAGGCTC	268022	100218	CTCCTGACCTCAGGTGATCC
178849	11045	CTTGCTTCTGGAATTCAGTC	223436	55632	CATGACAGTGCATCCAGGCT	268023	100219	ACTCCTGACCTCAGGTGATC
178850	11046	GCTTGCTTCTGGAATTCAGT	223437	55633	CCATGACAGTGCATCCAGGC	268024	100220	AACTCCTGACCTCAGGTGAT
178851	11047	AGCTTGCTTCTGGAATTCAG	223438	55634	CCCATGACAGTGCATCCAGG	268025	100221	GAACTCCTGACCTCAGGTGA
178852	11048	TAGCTTGCTTCTGGAATTCA	223439	55635	GCCCATGACAGTGCATCCAG	268026	100222	TGAACTCCTGACCTCAGGTG
178853	11049	GTAGCTTGCTTCTGGAATTC	223440	55636	TGCCCATGACAGTGCATCCA	268027	100223	TTGAACTCCTGACCTCAGGT
178854	11050	AGTAGCTTGCTTCTGGAATT	223441	55637	CTGCCCATGACAGTGCATCC	268028	100224	CTTGAACTCCTGACCTCAGG
178855	11051	GAGTAGCTTGCTTCTGGAAT	223442	55638	CCTGCCCATGACAGTGCATC	268029	100225	TCTTGAACTCCTGACCTCAG
178856	11052	GGAGTAGCTTGCTTCTGGAA	223443	55639	ACCTGCCCATGACAGTGCAT	268030	100226	GTCTTGAACTCCTGACCTCA
178857	11053	GGGAGTAGCTTGCTTCTGGA	223444	55640	CACCTGCCCATGACAGTGCA	268031	100227	GGTCTTGAACTCCTGACCTC
178858	11054	AGGGAGTAGCTTGCTTCTGG	223445	55641	GCACCTGCCCATGACAGTGC	268032	100228	TGGTCTTGAACTCCTGACCT
178859	11055	GAGGGAGTAGCTTGCTTCTG	223446	55642	GGCACCTGCCCATGACAGTG	268033	100229	CTGGTCTTGAACTCCTGACC
178860	11056	TGAGGGAGTAGCTTGCTTCT	223447	55643	GGGCACCTGCCCATGACAGT	268034	100230	GCTGGTCTTGAACTCCTGAC
178861	11057	ATGAGGGAGTAGCTTGCTTC	223448	55644	TGGGCACCTGCCCATGACAG	268035	100231	GGCTGGTCTTGAACTCCTGA
178862	11058	AATGAGGGAGTAGCTTGCTT	223449	55645	CTGGGCACCTGCCCATGACA	268036	100232	AGGCTGGTCTTGAACTCCTG
178863	11059	AAATGAGGGAGTAGCTTGCT	223450	55646	CCTGGGCACCTGCCCATGAC	268037	100233	CAGGCTGGTCTTGAACTCCT
178864	11060	CAAATGAGGGAGTAGCTTGC	223451	55647	TCCTGGGCACCTGCCCATGA	268038	100234	CCAGGCTGGTCTTGAACTCC
178865	11061	ACAAATGAGGGAGTAGCTTG	223452	55648	TTCCTGGGCACCTGCCCATG	268039	100235	GCCAGGCTGGTCTTGAACTC
178866	11062	CACAAATGAGGGAGTAGCTT	223453	55649	TTTCCTGGGCACCTGCCCAT	268040	100236	GGCCAGGCTGGTCTTGAACT
178867	11063	CCACAAATGAGGGAGTAGCT	223454	55650	TTTTCCTGGGCACCTGCCCA	268041	100237	TGGCCAGGCTGGTCTTGAAC
178868	11064	CCCACAAATGAGGGAGTAGC	223455	55651	ATTTTCCTGGGCACCTGCCC	268042	100238	TTGGCCAGGCTGGTCTTGAA
178869	11065	GCCCACAAATGAGGGAGTAG	223456	55652	CATTTTCCTGGGCACCTGCC	268043	100239	GTTGGCCAGGCTGGTCTTGA
178870	11066	GGCCCACAAATGAGGGAGTA	223457	55653	CCATTTTCCTGGGCACCTGC	268044	100240	TGTTGGCCAGGCTGGTCTTG
178871	11067	GGGCCCACAAATGAGGGAGT	223458	55654	GCCATTTTCCTGGGCACCTG	268045	100241	ATGTTGGCCAGGCTGGTCTT
178872	11068	GGGGCCCACAAATGAGGGAG	223459	55655	TGCCATTTTCCTGGGCACCT	268046	100242	CATGTTGGCCAGGCTGGTCT
178873	11069	AGGGGCCCACAAATGAGGGA	223460	55656	CTGCCATTTTCCTGGGCACC	268047	100243	CCATGTTGGCCAGGCTGGTC
178874	11070	CAGGGGCCCACAAATGAGGG	223461	55657	TCTGCCATTTTCCTGGGCAC	268048	100244	ACCATGTTGGCCAGGCTGGT
178875	11071	ACAGGGGCCCACAAATGAGG	223462	55658	GTCTGCCATTTTCCTGGGCA	268049	100245	TACCATGTTGGCCAGGCTGG
178876	11072	AACAGGGGCCCACAAATGAG	223463	55659	TGTCTGCCATTTTCCTGGGC	268050	100246	TTACCATGTTGGCCAGGCTG
178877	11073	TAACAGGGGCCCACAAATGA	223464	55660	ATGTCTGCCATTTTCCTGGG	268051	100247	TTTACCATGTTGGCCAGGCT
178878	11074	ATAACAGGGGCCCACAAATG	223465	55661	CATGTCTGCCATTTTCCTGG	268052	100248	TTTTACCATGTTGGCCAGGC
178879	11075	GATAACAGGGGCCCACAAAT	223466	55662	ACATGTCTGCCATTTTCCTG	268053	100249	GTTTTACCATGTTGGCCAGG
178880	11076	TGATAACAGGGGCCCACAAA	223467	55663	AACATGTCTGCCATTTTCCT	268054	100250	GGTTTTACCATGTTGGCCAG
178881	11077	GTGATAACAGGGGCCCACAA	223468	55664	GAACATGTCTGCCATTTTCC	268055	100251	AGGTTTTACCATGTTGGCCA
178882	11078	AGTGATAACAGGGGCCCACA	223469	55665	GGAACATGTCTGCCATTTTC	268056	100252	GAGGTTTTACCATGTTGGCC
178883	11079	CAGTGATAACAGGGGCCCAC	223470	55666	TGGAACATGTCTGCCATTTT	268057	100253	AGAGGTTTTACCATGTTGGC
178884	11080	CCAGTGATAACAGGGGCCCA	223471	55667	TTGGAACATGTCTGCCATTT	268058	100254	TAGAGGTTTTACCATGTTGG
178885	11081	GCCAGTGATAACAGGGGCCC	223472	55668	TTTGGAACATGTCTGCCATT	268059	100255	GTAGAGGTTTTACCATGTTG
178886	11082	AGCCAGTGATAACAGGGGCC	223473	55669	GTTTGGAACATGTCTGCCAT	268060	100256	AGTAGAGGTTTTACCATGTT
178887	11083	CAGCCAGTGATAACAGGGGC	223474	55670	TGTTTGGAACATGTCTGCCA	268061	100257	TAGTAGAGGTTTTACCATGT
178888	11084	GCAGCCAGTGATAACAGGGG	223475	55671	CTGTTTGGAACATGTCTGCC	268062	100258	TTAGTAGAGGTTTTACCATG
178889	11085	AGCAGCCAGTGATAACAGGG	223476	55672	GCTGTTTGGAACATGTCTGC	268063	100259	TTTAGTAGAGGTTTTACCAT
178890	11086	AAGCAGCCAGTGATAACAGG	223477	55673	TGCTGTTTGGAACATGTCTG	268064	100260	CTTTAGTAGAGGTTTTACCA

178891	11087	TAAGCAGCCAGTGATAACAG	223478	55674	GTGCTGTTTGGAACATGTCT	268065	100261	TCTTTAGTAGAGGTTTTACC
178892	11088	CTAAGCAGCCAGTGATAACA	223479	55675	CGTGCTGTTTGGAACATGTC	268066	100262	TTCTTTAGTAGAGGTTTTAC
178893	11089	CCTAAGCAGCCAGTGATAAC	223480	55676	GCGTGCTGTTTGGAACATGT	268067	100263	TTTCTTTAGTAGAGGTTTTA
178894	11090	CCCTAAGCAGCCAGTGATAA	223481	55677	TGCGTGCTGTTTGGAACATG	268068	100264	ATTTCTTTAGTAGAGGTTTT
178895	11091	ACCCTAAGCAGCCAGTGATA	223482	55678	CTGCGTGCTGTTTGGAACAT	268069	100265	GATTTCTTTAGTAGAGGTTT
178896	11092	AACCCTAAGCAGCCAGTGAT	223483	55679	GCTGCGTGCTGTTTGGAACA	268070	100266	AGATTTCTTTAGTAGAGGTT
178897	11093	CAACCCTAAGCAGCCAGTGA	223484	55680	TGCTGCGTGCTGTTTGGAAC	268071	100267	AAGATTTCTTTAGTAGAGGT
178898	11094	GCAACCCTAAGCAGCCAGTG	223485	55681	ATGCTGCGTGCTGTTTGGAA	268072	100268	AAAGATTTCTTTAGTAGAGG
178899	11095	GGCAACCCTAAGCAGCCAGT	223486	55682	AATGCTGCGTGCTGTTTGGA	268073	100269	TAAAGATTTCTTTAGTAGAG
178900	11096	TGGCAACCCTAAGCAGCCAG	223487	55683	GAATGCTGCGTGCTGTTTGG	268074	100270	GTAAAGATTTCTTTAGTAGA
178901	11097	TTGGCAACCCTAAGCAGCCA	223488	55684	GGAATGCTGCGTGCTGTTTG	268075	100271	AGTAAAGATTTCTTTAGTAG
178902	11098	CTTGGCAACCCTAAGCAGCC	223489	55685	GGGAATGCTGCGTGCTGTTT	268076	100272	CAGTAAAGATTTCTTTAGTA
178903	11099	GCTTGGCAACCCTAAGCAGC	223490	55686	GGGGAATGCTGCGTGCTGTT	268077	100273	TCAGTAAAGATTTCTTTAGT
178904	11100	GGCTTGGCAACCCTAAGCAG	223491	55687	TGGGGAATGCTGCGTGCTGT	268078	100274	TTCAGTAAAGATTTCTTTAG
178905	11101	GGGCTTGGCAACCCTAAGCA	223492	55688	CTGGGGAATGCTGCGTGCTG	268079	100275	TTTCAGTAAAGATTTCTTTA
178906	11102	AGGGCTTGGCAACCCTAAGC	223493	55689	ACTGGGGAATGCTGCGTGCT	268080	100276	TTTTCAGTAAAGATTTCTTT
178907	11103	CAGGGCTTGGCAACCCTAAG	223494	55690	CACTGGGGAATGCTGCGTGC	268081	100277	ATTTTCAGTAAAGATTTCTT
178908	11104	TCAGGGCTTGGCAACCCTAA	223495	55691	TCACTGGGGAATGCTGCGTG	268082	100278	TATTTTCAGTAAAGATTTCT
178909	11105	TTCAGGGCTTGGCAACCCTA	223496	55692	ATCACTGGGGAATGCTGCGT	268083	100279	GTATTTTCAGTAAAGATTTC
178910	11106	ATTCAGGGCTTGGCAACCCT	223497	55693	CATCACTGGGGAATGCTGCG	268084	100280	TGTATTTTCAGTAAAGATTT
178911	11107	AATTCAGGGCTTGGCAACCC	223498	55694	GCATCACTGGGGAATGCTGC	268085	100281	TTGTATTTTCAGTAAAGATT
178912	11108	GAATTCAGGGCTTGGCAACC	223499	55695	GGCATCACTGGGGAATGCTG	268086	100282	TTTGTATTTTCAGTAAAGAT
178913	11109	TGAATTCAGGGCTTGGCAAC	223500	55696	GGGCATCACTGGGGAATGCT	268087	100283	TTTTGTATTTTCAGTAAAGA
178914	11110	ATGAATTCAGGGCTTGGCAA	223501	55697	TGGGCATCACTGGGGAATGC	268088	100284	TTTTTGTATTTTCAGTAAAG
178915	11111	AATGAATTCAGGGCTTGGCA	223502	55698	CTGGGCATCACTGGGGAATG	268089	100285	ATTTTTGTATTTTCAGTAAA
178916	11112	AAATGAATTCAGGGCTTGGC	223503	55699	CCTGGGCATCACTGGGGAAT	268090	100286	GATTTTTGTATTTTCAGTAA
178917	11113	CAAATGAATTCAGGGCTTGG	223504	55700	CCCTGGGCATCACTGGGGAA	268091	100287	GGATTTTTGTATTTTCAGTA
178918	11114	ACAAATGAATTCAGGGCTTG	223505	55701	ACCCTGGGCATCACTGGGGA	268092	100288	TGGATTTTTGTATTTTCAGT
178919	11115	GACAAATGAATTCAGGGCTT	223506	55702	GACCCTGGGCATCACTGGGG	268093	100289	CTGGATTTTTGTATTTTCAG
178920	11116	TGACAAATGAATTCAGGGCT	223507	55703	TGACCCTGGGCATCACTGGG	268094	100290	ACTGGATTTTTGTATTTTCA
178921	11117	TTGACAAATGAATTCAGGGC	223508	55704	GTGACCCTGGGCATCACTGG	268095	100291	GACTGGATTTTTGTATTTTC
178922	11118	GTTGACAAATGAATTCAGGG	223509	55705	GGTGACCCTGGGCATCACTG	268096	100292	AGACTGGATTTTTGTATTTT
178923	11119	AGTTGACAAATGAATTCAGG	223510	55706	AGGTGACCCTGGGCATCACT	268097	100293	GAGACTGGATTTTTGTATTT
178924	11120	TAGTTGACAAATGAATTCAG	223511	55707	AAGGTGACCCTGGGCATCAC	268098	100294	AGAGACTGGATTTTTGTATT
178925	11121	TTAGTTGACAAATGAATTCA	223512	55708	CAAGGTGACCCTGGGCATCA	268099	100295	TAGAGACTGGATTTTTGTAT
178926	11122	CTTAGTTGACAAATGAATTC	223513	55709	CCAAGGTGACCCTGGGCATC	268100	100296	GTAGAGACTGGATTTTTGTA
178927	11123	TCTTAGTTGACAAATGAATT	223514	55710	TCCAAGGTGACCCTGGGCAT	268101	100297	AGTAGAGACTGGATTTTTGT
178928	11124	CTCTTAGTTGACAAATGAAT	223515	55711	CTCCAAGGTGACCCTGGGCA	268102	100298	TAGTAGAGACTGGATTTTTG
178929	11125	TCTCTTAGTTGACAAATGAA	223516	55712	CCTCCAAGGTGACCCTGGGC	268103	100299	TTAGTAGAGACTGGATTTTT
178930	11126	ATCTCTTAGTTGACAAATGA	223517	55713	ACCTCCAAGGTGACCCTGGG	268104	100300	TTTAGTAGAGACTGGATTTT
178931	11127	AATCTCTTAGTTGACAAATG	223518	55714	CACCTCCAAGGTGACCCTGG	268105	100301	TTTTAGTAGAGACTGGATTT
178932	11128	AAATCTCTTAGTTGACAAAT	223519	55715	CCACCTCCAAGGTGACCCTG	268106	100302	ATTTTAGTAGAGACTGGATT
178933	11129	AAAATCTCTTAGTTGACAAA	223520	55716	CCCACCTCCAAGGTGACCCT	268107	100303	TATTTTAGTAGAGACTGGAT
178934	11130	AAAAATCTCTTAGTTGACAA	223521	55717	GCCCACCTCCAAGGTGACCC	268108	100304	TTATTTTAGTAGAGACTGGA
178935	11131	CAAAAATCTCTTAGTTGACA	223522	55718	CGCCCACCTCCAAGGTGACC	268109	100305	CTTATTTTAGTAGAGACTGG
178936	11132	CCAAAAATCTCTTAGTTGAC	223523	55719	TCGCCCACCTCCAAGGTGAC	268110	100306	ACTTATTTTAGTAGAGACTG
178937	11133	GCCAAAAATCTCTTAGTTGA	223524	55720	CTCGCCCACCTCCAAGGTGA	268111	100307	GACTTATTTTAGTAGAGACT
178938	11134	GGCCAAAAATCTCTTAGTTG	223525	55721	TCTCGCCCACCTCCAAGGTG	268112	100308	AGACTTATTTTAGTAGAGAC
178939	11135	TGGCCAAAAATCTCTTAGTT	223526	55722	ATCTCGCCCACCTCCAAGGT	268113	100309	GAGACTTATTTTAGTAGAGA
178940	11136	TTGGCCAAAAATCTCTTAGT	223527	55723	CATCTCGCCCACCTCCAAGG	268114	100310	AGAGACTTATTTTAGTAGAG
178941	11137	CTTGGCCAAAAATCTCTTAG	223528	55724	GCATCTCGCCCACCTCCAAG	268115	100311	TAGAGACTTATTTTAGTAGA
178942	11138	TCTTGGCCAAAAATCTCTTA	223529	55725	GGCATCTCGCCCACCTCCAA	268116	100312	GTAGAGACTTATTTTAGTAG
178943	11139	ATCTTGGCCAAAAATCTCTT	223530	55726	AGGCATCTCGCCCACCTCCA	268117	100313	AGTAGAGACTTATTTTAGTA
178944	11140	AATCTTGGCCAAAAATCTCT	223531	55727	CAGGCATCTCGCCCACCTCC	268118	100314	TAGTAGAGACTTATTTTAGT
178945	11141	TAATCTTGGCCAAAAATCTC	223532	55728	CCAGGCATCTCGCCCACCTC	268119	100315	TTAGTAGAGACTTATTTTAG
178946	11142	TTAATCTTGGCCAAAAATCT	223533	55729	CCCAGGCATCTCGCCCACCT	268120	100316	TTTAGTAGAGACTTATTTTA
178947	11143	CTTAATCTTGGCCAAAAATC	223534	55730	CCCCAGGCATCTCGCCCACC	268121	100317	TTTTAGTAGAGACTTATTTT
178948	11144	TCTTAATCTTGGCCAAAAAT	223535	55731	ACCCCAGGCATCTCGCCCAC	268122	100318	TTTTTAGTAGAGACTTATTT
178949	11145	ATCTTAATCTTGGCCAAAAA	223536	55732	AACCCCAGGCATCTCGCCCA	268123	100319	ATTTTTAGTAGAGACTTATT
178950	11146	AATCTTAATCTTGGCCAAAA	223537	55733	AAACCCCAGGCATCTCGCCC	268124	100320	TATTTTTAGTAGAGACTTAT
178951	11147	AAATCTTAATCTTGGCCAAA	223538	55734	GAAACCCCAGGCATCTCGCC	268125	100321	GTATTTTTAGTAGAGACTTA
178952	11148	GAAATCTTAATCTTGGCCAA	223539	55735	AGAAACCCCAGGCATCTCGC	268126	100322	TGTATTTTTAGTAGAGACTT
178953	11149	GGAAATCTTAATCTTGGCCA	223540	55736	GAGAAACCCCAGGCATCTCG	268127	100323	TTGTATTTTTAGTAGAGACT
178954	11150	GGGAAATCTTAATCTTGGCC	223541	55737	CGAGAAACCCCAGGCATCTC	268128	100324	TTTGTATTTTTAGTAGAGAC
178955	11151	TGGGAAATCTTAATCTTGGC	223542	55738	ACGAGAAACCCCAGGCATCT	268129	100325	TTTTGTATTTTTAGTAGAGA
178956	11152	ATGGGAAATCTTAATCTTGG	223543	55739	GACGAGAAACCCCAGGCATC	268130	100326	TTTTTGTATTTTTAGTAGAG
178957	11153	CATGGGAAATCTTAATCTTG	223544	55740	GGACGAGAAACCCCAGGCAT	268131	100327	ATTTTTGTATTTTTAGTAGA
178958	11154	GCATGGGAAATCTTAATCTT	223545	55741	TGGACGAGAAACCCCAGGCA	268132	100328	AATTTTTGTATTTTTAGTAG
178959	11155	GGCATGGGAAATCTTAATCT	223546	55742	GTGGACGAGAAACCCCAGGC	268133	100329	TAATTTTTGTATTTTTAGTA
178960	11156	AGGCATGGGAAATCTTAATC	223547	55743	GGTGGACGAGAAACCCCAGG	268134	100330	CTAATTTTTGTATTTTTAGT
178961	11157	GAGGCATGGGAAATCTTAAT	223548	55744	GGGTGGACGAGAAACCCCAG	268135	100331	GCTAATTTTTGTATTTTTAG
178962	11158	GGAGGCATGGGAAATCTTAA	223549	55745	GGGGTGGACGAGAAACCCCA	268136	100332	GGCTAATTTTTGTATTTTTA

178963	11159	TGGAGGCATGGGAAATCTTA	223550	55746	TGGGGTGGACGAGAAACCCC	268137	100333	TGGCTAATTTTTGTATTTTT
178964	11160	ATGGAGGCATGGGAAATCTT	223551	55747	GTGGGGTGGACGAGAAACCC	268138	100334	CTGGCTAATTTTTGTATTTT
178965	11161	TATGGAGGCATGGGAAATCT	223552	55748	TGTGGGGTGGACGAGAAACC	268139	100335	CCTGGCTAATTTTTGTATTT
178966	11162	ATATGGAGGCATGGGAAATC	223553	55749	TTGTGGGGTGGACGAGAAAC	268140	100336	GCCTGGCTAATTTTTGTATT
178967	11163	AATATGGAGGCATGGGAAAT	223554	55750	GTTGTGGGGTGGACGAGAAA	268141	100337	CGCCTGGCTAATTTTTGTAT
178968	11164	AAATATGGAGGCATGGGAAA	223555	55751	TGTTGTGGGGTGGACGAGAA	268142	100338	ACGCCTGGCTAATTTTTGTA
178969	11165	GAAATATGGAGGCATGGGAA	223556	55752	GTGTTGTGGGGTGGACGAGA	268143	100339	CACGCCTGGCTAATTTTTGT
178970	11166	GGAAATATGGAGGCATGGGA	223557	55753	GGTGTTGTGGGGTGGACGAG	268144	100340	CCACGCCTGGCTAATTTTTG
178971	11167	TGGAAATATGGAGGCATGGG	223558	55754	AGGTGTTGTGGGGTGGACGA	268145	100341	ACCACGCCTGGCTAATTTTT
178972	11168	ATGGAAATATGGAGGCATGG	223559	55755	GAGGTGTTGTGGGGTGGACG	268146	100342	CACCACGCCTGGCTAATTTT
178973	11169	GATGGAAATATGGAGGCATG	223560	55756	TGAGGTGTTGTGGGGTGGAC	268147	100343	GCACCACGCCTGGCTAATTT
178974	11170	AGATGGAAATATGGAGGCAT	223561	55757	CTGAGGTGTTGTGGGGTGGA	268148	100344	AGCACCACGCCTGGCTAATT
178975	11171	CAGATGGAAATATGGAGGCA	223562	55758	CCTGAGGTGTTGTGGGGTGG	268149	100345	CAGCACCACGCCTGGCTAAT
178976	11172	TCAGATGGAAATATGGAGGC	223563	55759	CCCTGAGGTGTTGTGGGGTG	268150	100346	GCAGCACCACGCCTGGCTAA
178977	11173	CTCAGATGGAAATATGGAGG	223564	55760	CCCCTGAGGTGTTGTGGGGT	268151	100347	TGCAGCACCACGCCTGGCTA
178978	11174	TCTCAGATGGAAATATGGAG	223565	55761	TCCCCTGAGGTGTTGTGGGG	268152	100348	GTGCAGCACCACGCCTGGCT
178979	11175	TTCTCAGATGGAAATATGGA	223566	55762	GTCCCCTGAGGTGTTGTGGG	268153	100349	TGTGCAGCACCACGCCTGGC
178980	11176	TTTCTCAGATGGAAATATGG	223567	55763	TGTCCCCTGAGGTGTTGTGG	268154	100350	GTGTGCAGCACCACGCCTGG
178981	11177	ATTTCTCAGATGGAAATATG	223568	55764	CTGTCCCCTGAGGTGTTGTG	268155	100351	GGTGTGCAGCACCACGCCTG
178982	11178	CATTTCTCAGATGGAAATAT	223569	55765	GCTGTCCCCTGAGGTGTTGT	268156	100352	AGGTGTGCAGCACCACGCCT
178983	11179	CCATTTCTCAGATGGAAATA	223570	55766	GGCTGTCCCCTGAGGTGTTG	268157	100353	CAGGTGTGCAGCACCACGCC
178984	11180	TCCATTTCTCAGATGGAAAT	223571	55767	TGGCTGTCCCCTGAGGTGTT	268158	100354	ACAGGTGTGCAGCACCACGC
178985	11181	CTCCATTTCTCAGATGGAAA	223572	55768	TTGGCTGTCCCCTGAGGTGT	268159	100355	TACAGGTGTGCAGCACCACG
178986	11182	TCTCCATTTCTCAGATGGAA	223573	55769	TTTGGCTGTCCCCTGAGGTG	268160	100356	TTACAGGTGTGCAGCACCAC
178987	11183	ATCTCCATTTCTCAGATGGA	223574	55770	CTTTGGCTGTCCCCTGAGGT	268161	100357	ATTACAGGTGTGCAGCACCA
178988	11184	AATCTCCATTTCTCAGATGG	223575	55771	GCTTTGGCTGTCCCCTGAGG	268162	100358	TATTACAGGTGTGCAGCACC
178989	11185	TAATCTCCATTTCTCAGATG	223576	55772	AGCTTTGGCTGTCCCCTGAG	268163	100359	ATATTACAGGTGTGCAGCAC
178990	11186	ATAATCTCCATTTCTCAGAT	223577	55773	CAGCTTTGGCTGTCCCCTGA	268164	100360	GATATTACAGGTGTGCAGCA
178991	11187	TATAATCTCCATTTCTCAGA	223578	55774	ACAGCTTTGGCTGTCCCCTG	268165	100361	TGATATTACAGGTGTGCAGC
178992	11188	GTATAATCTCCATTTCTCAG	223579	55775	GACAGCTTTGGCTGTCCCCT	268166	100362	CTGATATTACAGGTGTGCAG
178993	11189	AGTATAATCTCCATTTCTCA	223580	55776	GGACAGCTTTGGCTGTCCCC	268167	100363	GCTGATATTACAGGTGTGCA
178994	11190	CAGTATAATCTCCATTTCTC	223581	55777	GGGACAGCTTTGGCTGTCCC	268168	100364	AGCTGATATTACAGGTGTGC
178995	11191	ACAGTATAATCTCCATTTCT	223582	55778	AGGGACAGCTTTGGCTGTCC	268169	100365	TAGCTGATATTACAGGTGTG
178996	11192	GACAGTATAATCTCCATTTC	223583	55779	AAGGGACAGCTTTGGCTGTC	268170	100366	GTAGCTGATATTACAGGTGT
178997	11193	AGACAGTATAATCTCCATTT	223584	55780	GAAGGGACAGCTTTGGCTGT	268171	100367	AGTAGCTGATATTACAGGTG
178998	11194	AAGACAGTATAATCTCCATT	223585	55781	TGAAGGGACAGCTTTGGCTG	268172	100368	GAGTAGCTGATATTACAGGT
178999	11195	GAAGACAGTATAATCTCCAT	223586	55782	CTGAAGGGACAGCTTTGGCT	268173	100369	CGAGTAGCTGATATTACAGG
179000	11196	GGAAGACAGTATAATCTCCA	223587	55783	CCTGAAGGGACAGCTTTGGC	268174	100370	CCGAGTAGCTGATATTACAG
179001	11197	GGGAAGACAGTATAATCTCC	223588	55784	ACCTGAAGGGACAGCTTTGG	268175	100371	CCCGAGTAGCTGATATTACA
179002	11198	GGGGAAGACAGTATAATCTC	223589	55785	TACCTGAAGGGACAGCTTTG	268176	100372	TCCCGAGTAGCTGATATTAC
179003	11199	GGGGGAAGACAGTATAATCT	223590	55786	TTACCTGAAGGGACAGCTTT	268177	100373	CTCCCGAGTAGCTGATATTA
179004	11200	AGGGGGAAGACAGTATAATC	223591	55787	CTTACCTGAAGGGACAGCTT	268178	100374	CCTCCCGAGTAGCTGATATT
179005	11201	GAGGGGGAAGACAGTATAAT	223592	55788	GCTTACCTGAAGGGACAGCT	268179	100375	GCCTCCCGAGTAGCTGATAT
179006	11202	TGAGGGGGAAGACAGTATAA	223593	55789	AGCTTACCTGAAGGGACAGC	268180	100376	AGCCTCCCGAGTAGCTGATA
179007	11203	CTGAGGGGGAAGACAGTATA	223594	55790	CAGCTTACCTGAAGGGACAG	268181	100377	CAGCCTCCCGAGTAGCTGAT
179008	11204	TCTGAGGGGGAAGACAGTAT	223595	55791	GCAGCTTACCTGAAGGGACA	268182	100378	TCAGCCTCCCGAGTAGCTGA
179009	11205	TTCTGAGGGGGAAGACAGTA	223596	55792	TGCAGCTTACCTGAAGGGAC	268183	100379	CTCAGCCTCCCGAGTAGCTG
179010	11206	ATTCTGAGGGGGAAGACAGT	223597	55793	GTGCAGCTTACCTGAAGGGA	268184	100380	CCTCAGCCTCCCGAGTAGCT
179011	11207	CATTCTGAGGGGGAAGACAG	223598	55794	TGTGCAGCTTACCTGAAGGG	268185	100381	GCCTCAGCCTCCCGAGTAGC
179012	11208	CCATTCTGAGGGGGAAGACA	223599	55795	CTGTGCAGCTTACCTGAAGG	268186	100382	TGCCTCAGCCTCCCGAGTAG
179013	11209	TCCATTCTGAGGGGGAAGAC	223600	55796	TCTGTGCAGCTTACCTGAAG	268187	100383	CTGCCTCAGCCTCCCGAGTA
179014	11210	ATCCATTCTGAGGGGGAAGA	223601	55797	TTCTGTGCAGCTTACCTGAA	268188	100384	CCTGCCTCAGCCTCCCGAGT
179015	11211	CATCCATTCTGAGGGGGAAG	223602	55798	CTTCTGTGCAGCTTACCTGA	268189	100385	TCCTGCCTCAGCCTCCCGAG
179016	11212	TCATCCATTCTGAGGGGGAA	223603	55799	TCTTCTGTGCAGCTTACCTG	268190	100386	CTCCTGCCTCAGCCTCCCGA
179017	11213	ATCATCCATTCTGAGGGGGA	223604	55800	ATCTTCTGTGCAGCTTACCT	268191	100387	TCTCCTGCCTCAGCCTCCCG
179018	11214	TATCATCCATTCTGAGGGGG	223605	55801	CATCTTCTGTGCAGCTTACC	268192	100388	GTCTCCTGCCTCAGCCTCCC
179019	11215	TTATCATCCATTCTGAGGGG	223606	55802	ACATCTTCTGTGCAGCTTAC	268193	100389	AGTCTCCTGCCTCAGCCTCC
179020	11216	ATTATCATCCATTCTGAGGG	223607	55803	CACATCTTCTGTGCAGCTTA	268194	100390	GAGTCTCCTGCCTCAGCCTC
179021	11217	CATTATCATCCATTCTGAGG	223608	55804	TCACATCTTCTGTGCAGCTT	268195	100391	CGAGTCTCCTGCCTCAGCCT
179022	11218	ACATTATCATCCATTCTGAG	223609	55805	TTCACATCTTCTGTGCAGCT	268196	100392	GCGAGTCTCCTGCCTCAGCC
179023	11219	CACATTATCATCCATTCTGA	223610	55806	GTTCACATCTTCTGTGCAGC	268197	100393	AGCGAGTCTCCTGCCTCAGC
179024	11220	CCACATTATCATCCATTCTG	223611	55807	AGTTCACATCTTCTGTGCAG	268198	100394	AAGCGAGTCTCCTGCCTCAG
179025	11221	ACCACATTATCATCCATTCT	223612	55808	GAGTTCACATCTTCTGTGCA	268199	100395	CAAGCGAGTCTCCTGCCTCA
179026	11222	GACCACATTATCATCCATTC	223613	55809	AGAGTTCACATCTTCTGTGC	268200	100396	TCAAGCGAGTCTCCTGCCTC
179027	11223	AGACCACATTATCATCCATT	223614	55810	CAGAGTTCACATCTTCTGTG	268201	100397	ATCAAGCGAGTCTCCTGCCT
179028	11224	GAGACCACATTATCATCCAT	223615	55811	GCAGAGTTCACATCTTCTGT	268202	100398	GATCAAGCGAGTCTCCTGCC
179029	11225	AGAGACCACATTATCATCCA	223616	55812	AGCAGAGTTCACATCTTCTG	268203	100399	GGATCAAGCGAGTCTCCTGC
179030	11226	GAGAGACCACATTATCATCC	223617	55813	CAGCAGAGTTCACATCTTCT	268204	100400	GGGATCAAGCGAGTCTCCTG
179031	11227	AGAGAGACCACATTATCATC	223618	55814	GCAGCAGAGTTCACATCTTC	268205	100401	TGGGATCAAGCGAGTCTCCT
179032	11228	AAGAGAGACCACATTATCAT	223619	55815	TGCAGCAGAGTTCACATCTT	268206	100402	ATGGGATCAAGCGAGTCTCC
179033	11229	GAAGAGAGACCACATTATCA	223620	55816	TTGCAGCAGAGTTCACATCT	268207	100403	CATGGGATCAAGCGAGTCTC
179034	11230	AGAAGAGAGACCACATTATC	223621	55817	TTTGCAGCAGAGTTCACATC	268208	100404	GCATGGGATCAAGCGAGTCT

179035	11231	CAGAAGAGAGACCACATTAT	223622	55818	CTTTGCAGCAGAGTTCACAT	268209	100405	TGCATGGGATCAAGCGAGTC
179036	11232	ACAGAAGAGAGACCACATTA	223623	55819	TCTTTGCAGCAGAGTTCACA	268210	100406	CTGCATGGGATCAAGCGAGT
179037	11233	AACAGAAGAGAGACCACATT	223624	55820	GTCTTTGCAGCAGAGTTCAC	268211	100407	GCTGCATGGGATCAAGCGAG
179038	11234	GAACAGAAGAGAGACCACAT	223625	55821	AGTCTTTGCAGCAGAGTTCA	268212	100408	CGCTGCATGGGATCAAGCGA
179039	11235	CGAACAGAAGAGAGACCACA	223626	55822	GAGTCTTTGCAGCAGAGTTC	268213	100409	CCGCTGCATGGGATCAAGCG
179040	11236	GCGAACAGAAGAGAGACCAC	223627	55823	AGAGTCTTTGCAGCAGAGTT	268214	100410	TCCGCTGCATGGGATCAAGC
179041	11237	TGCGAACAGAAGAGAGACCA	223628	55824	TAGAGTCTTTGCAGCAGAGT	268215	100411	CTCCGCTGCATGGGATCAAG
179042	11238	ATGCGAACAGAAGAGAGACC	223629	55825	ATAGAGTCTTTGCAGCAGAG	268216	100412	CCTCCGCTGCATGGGATCAA
179043	11239	TATGCGAACAGAAGAGAGAC	223630	55826	AATAGAGTCTTTGCAGCAGA	268217	100413	ACCTCCGCTGCATGGGATCA
179044	11240	CTATGCGAACAGAAGAGAGA	223631	55827	GAATAGAGTCTTTGCAGCAG	268218	100414	AACCTCCGCTGCATGGGATC
179045	11241	ACTATGCGAACAGAAGAGAG	223632	55828	AGAATAGAGTCTTTGCAGCA	268219	100415	CAACCTCCGCTGCATGGGAT
179046	11242	GACTATGCGAACAGAAGAGA	223633	55829	AAGAATAGAGTCTTTGCAGC	268220	100416	GCAACCTCCGCTGCATGGGA
179047	11243	TGACTATGCGAACAGAAGAG	223634	55830	AAAGAATAGAGTCTTTGCAG	268221	100417	TGCAACCTCCGCTGCATGGG
179048	11244	ATGACTATGCGAACAGAAGA	223635	55831	CAAAGAATAGAGTCTTTGCA	268222	100418	CTGCAACCTCCGCTGCATGG
179049	11245	TATGACTATGCGAACAGAAG	223636	55832	CCAAAGAATAGAGTCTTTGC	268223	100419	ACTGCAACCTCCGCTGCATG
179050	11246	CTATGACTATGCGAACAGAA	223637	55833	CCCAAAGAATAGAGTCTTTG	268224	100420	CACTGCAACCTCCGCTGCAT
179051	11247	TCTATGACTATGCGAACAGA	223638	55834	TCCCAAAGAATAGAGTCTTT	268225	100421	TCACTGCAACCTCCGCTGCA
179052	11248	TTCTATGACTATGCGAACAG	223639	55835	CTCCCAAAGAATAGAGTCTT	268226	100422	CTCACTGCAACCTCCGCTGC
179053	11249	GTTCTATGACTATGCGAACA	223640	55836	GCTCCCAAAGAATAGAGTCT	268227	100423	GCTCACTGCAACCTCCGCTG
179054	11250	AGTTCTATGACTATGCGAAC	223641	55837	TGCTCCCAAAGAATAGAGTC	268228	100424	GGCTCACTGCAACCTCCGCT
179055	11251	CAGTTCTATGACTATGCGAA	223642	55838	TTGCTCCCAAAGAATAGAGT	268229	100425	CGGCTCACTGCAACCTCCGC
179056	11252	TCAGTTCTATGACTATGCGA	223643	55839	TTTGCTCCCAAAGAATAGAG	268230	100426	TCGGCTCACTGCAACCTCCG
179057	11253	TTCAGTTCTATGACTATGCG	223644	55840	TTTTGCTCCCAAAGAATAGA	268231	100427	CTCGGCTCACTGCAACCTCC
179058	11254	TTTCAGTTCTATGACTATGC	223645	55841	CTTTTGCTCCCAAAGAATAG	268232	100428	TCTCGGCTCACTGCAACCTC
179059	11255	ATTTCAGTTCTATGACTATG	223646	55842	CCTTTTGCTCCCAAAGAATA	268233	100429	ATCTCGGCTCACTGCAACCT
179060	11256	TATTTCAGTTCTATGACTAT	223647	55843	CCCTTTTGCTCCCAAAGAAT	268234	100430	GATCTCGGCTCACTGCAACC
179061	11257	TTATTTCAGTTCTATGACTA	223648	55844	TCCCTTTTGCTCCCAAAGAA	268235	100431	TGATCTCGGCTCACTGCAAC
179062	11258	TTTATTTCAGTTCTATGACT	223649	55845	GTCCCTTTTGCTCCCAAAGA	268236	100432	GTGATCTCGGCTCACTGCAA
179063	11259	TTTTATTTCAGTTCTATGAC	223650	55846	GGTCCCTTTTGCTCCCAAAG	268237	100433	CGTGATCTCGGCTCACTGCA
179064	11260	GTTTTATTTCAGTTCTATGA	223651	55847	GGGTCCCTTTTGCTCCCAAA	268238	100434	GCGTGATCTCGGCTCACTGC
179065	11261	TGTTTTATTTCAGTTCTATG	223652	55848	TGGGTCCCTTTTGCTCCCAA	268239	100435	GGCGTGATCTCGGCTCACTG
179066	11262	TTGTTTTATTTCAGTTCTAT	223653	55849	CTGGGTCCCTTTTGCTCCCA	268240	100436	TGGCGTGATCTCGGCTCACT
179067	11263	GTTGTTTTATTTCAGTTCTA	223654	55850	CCTGGGTCCCTTTTGCTCCC	268241	100437	ATGGCGTGATCTCGGCTCAC
179068	11264	AGTTGTTTTATTTCAGTTCT	223655	55851	CCCTGGGTCCCTTTTGCTCC	268242	100438	AATGGCGTGATCTCGGCTCA
179069	11265	AAGTTGTTTTATTTCAGTTC	223656	55852	ACCCTGGGTCCCTTTTGCTC	268243	100439	CAATGGCGTGATCTCGGCTC
179070	11266	TAAGTTGTTTTATTTCAGTT	223657	55853	GACCCTGGGTCCCTTTTGCT	268244	100440	GCAATGGCGTGATCTCGGCT
179071	11267	TTAAGTTGTTTTATTTCAGT	223658	55854	AGACCCTGGGTCCCTTTTGC	268245	100441	TGCAATGGCGTGATCTCGGC
179072	11268	CTTAAGTTGTTTTATTTCAG	223659	55855	GAGACCCTGGGTCCCTTTTG	268246	100442	GTGCAATGGCGTGATCTCGG
179073	11269	TCTTAAGTTGTTTTATTTCA	223660	55856	TGAGACCCTGGGTCCCTTTT	268247	100443	AGTGCAATGGCGTGATCTCG
179074	11270	CTCTTAAGTTGTTTTATTTC	223661	55857	GTGAGACCCTGGGTCCCTTT	268248	100444	GAGTGCAATGGCGTGATCTC
179075	11271	TCTCTTAAGTTGTTTTATTT	223662	55858	GGTGAGACCCTGGGTCCCTT	268249	100445	GGAGTGCAATGGCGTGATCT
179076	11272	TTCTCTTAAGTTGTTTTATT	223663	55859	AGGTGAGACCCTGGGTCCCT	268250	100446	TGGAGTGCAATGGCGTGATC
179077	11273	ATTCTCTTAAGTTGTTTTAT	223664	55860	CAGGTGAGACCCTGGGTCCC	268251	100447	CTGGAGTGCAATGGCGTGAT
179078	11274	AATTCTCTTAAGTTGTTTTA	223665	55861	GCAGGTGAGACCCTGGGTCC	268252	100448	GCTGGAGTGCAATGGCGTGA
179079	11275	GAATTCTCTTAAGTTGTTTT	223666	55862	TGCAGGTGAGACCCTGGGTC	268253	100449	GGCTGGAGTGCAATGGCGTG
179080	11276	GGAATTCTCTTAAGTTGTTT	223667	55863	GTGCAGGTGAGACCCTGGGT	268254	100450	AGGCTGGAGTGCAATGGCGT
179081	11277	AGGAATTCTCTTAAGTTGTT	223668	55864	TGTGCAGGTGAGACCCTGGG	268255	100451	CAGGCTGGAGTGCAATGGCG
179082	11278	AAGGAATTCTCTTAAGTTGT	223669	55865	ATGTGCAGGTGAGACCCTGG	268256	100452	CCAGGCTGGAGTGCAATGGC
179083	11279	AAAGGAATTCTCTTAAGTTG	223670	55866	GATGTGCAGGTGAGACCCTG	268257	100453	CCCAGGCTGGAGTGCAATGG
179084	11280	CAAAGGAATTCTCTTAAGTT	223671	55867	GGATGTGCAGGTGAGACCCT	268258	100454	GCCCAGGCTGGAGTGCAATG
179085	11281	TCAAAGGAATTCTCTTAAGT	223672	55868	GGGATGTGCAGGTGAGACCC	268259	100455	TGCCCAGGCTGGAGTGCAAT
179086	11282	CTCAAAGGAATTCTCTTAAG	223673	55869	AGGGATGTGCAGGTGAGACC	268260	100456	ATGCCCAGGCTGGAGTGCAA
179087	11283	GCTCAAAGGAATTCTCTTAA	223674	55870	CAGGGATGTGCAGGTGAGAC	268261	100457	GATGCCCAGGCTGGAGTGCA
179088	11284	AGCTCAAAGGAATTCTCTTA	223675	55871	ACAGGGATGTGCAGGTGAGA	268262	100458	TGATGCCCAGGCTGGAGTGC
179089	11285	AAGCTCAAAGGAATTCTCTT	223676	55872	GACAGGGATGTGCAGGTGAG	268263	100459	CTGATGCCCAGGCTGGAGTG
179090	11286	GAAGCTCAAAGGAATTCTCT	223677	55873	GGACAGGGATGTGCAGGTGA	268264	100460	TCTGATGCCCAGGCTGGAGT
179091	11287	AGAAGCTCAAAGGAATTCTC	223678	55874	GGGACAGGGATGTGCAGGTG	268265	100461	TTCTGATGCCCAGGCTGGAG
179092	11288	GAGAAGCTCAAAGGAATTCT	223679	55875	AGGGACAGGGATGTGCAGGT	268266	100462	ATTCTGATGCCCAGGCTGGA
179093	11289	TGAGAAGCTCAAAGGAATTC	223680	55876	CAGGGACAGGGATGTGCAGG	268267	100463	TATTCTGATGCCCAGGCTGG
179094	11290	CTGAGAAGCTCAAAGGAATT	223681	55877	TCAGGGACAGGGATGTGCAG	268268	100464	TTATTCTGATGCCCAGGCTG
179095	11291	TCTGAGAAGCTCAAAGGAAT	223682	55878	CTCAGGGACAGGGATGTGCA	268269	100465	CTTATTCTGATGCCCAGGCT
179096	11292	TTCTGAGAAGCTCAAAGGAA	223683	55879	CCTCAGGGACAGGGATGTGC	268270	100466	TCTTATTCTGATGCCCAGGC
179097	11293	CTTCTGAGAAGCTCAAAGGA	223684	55880	CCCTCAGGGACAGGGATGTG	268271	100467	GTCTTATTCTGATGCCCAGG
179098	11294	ACTTCTGAGAAGCTCAAAGG	223685	55881	GCCCTCAGGGACAGGGATGT	268272	100468	AGTCTTATTCTGATGCCCAG
179099	11295	CACTTCTGAGAAGCTCAAAG	223686	55882	GGCCCTCAGGGACAGGGATG	268273	100469	GAGTCTTATTCTGATGCCCA
179100	11296	GCACTTCTGAGAAGCTCAAA	223687	55883	AGGCCCTCAGGGACAGGGAT	268274	100470	GGAGTCTTATTCTGATGCCC
179101	11297	AGCACTTCTGAGAAGCTCAA	223688	55884	TAGGCCCTCAGGGACAGGGA	268275	100471	CGGAGTCTTATTCTGATGCC
179102	11298	CAGCACTTCTGAGAAGCTCA	223689	55885	CTAGGCCCTCAGGGACAGGG	268276	100472	ACGGAGTCTTATTCTGATGC
179103	11299	GCAGCACTTCTGAGAAGCTC	223690	55886	CCTAGGCCCTCAGGGACAGG	268277	100473	GACGGAGTCTTATTCTGATG
179104	11300	TGCAGCACTTCTGAGAAGCT	223691	55887	CCCTAGGCCCTCAGGGACAG	268278	100474	AGACGGAGTCTTATTCTGAT
179105	11301	CTGCAGCACTTCTGAGAAGC	223692	55888	CCCCTAGGCCCTCAGGGACA	268279	100475	GAGACGGAGTCTTATTCTGA
179106	11302	CCTGCAGCACTTCTGAGAAG	223693	55889	ACCCCTAGGCCCTCAGGGAC	268280	100476	TGAGACGGAGTCTTATTCTG

179107	11303	CCCTGCAGCACTTCTGAGAA	223694	55890	AACCCCTAGGCCCTCAGGGA	268281	100477	TTGAGACGGAGTCTTATTCT
179108	11304	GCCCTGCAGCACTTCTGAGA	223695	55891	GAACCCCTAGGCCCTCAGGG	268282	100478	TTTGAGACGGAGTCTTATTC
179109	11305	AGCCCTGCAGCACTTCTGAG	223696	55892	AGAACCCCTAGGCCCTCAGG	268283	100479	TTTTGAGACGGAGTCTTATT
179110	11306	CAGCCCTGCAGCACTTCTGA	223697	55893	AAGAACCCCTAGGCCCTCAG	268284	100480	TTTTTGAGACGGAGTCTTAT
179111	11307	CCAGCCCTGCAGCACTTCTG	223698	55894	CAAGAACCCCTAGGCCCTCA	268285	100481	TTTTTTGAGACGGAGTCTTA
179112	11308	CCCAGCCCTGCAGCACTTCT	223699	55895	CCAAGAACCCCTAGGCCCTC	268286	100482	TTTTTTTGAGACGGAGTCTT
179113	11309	CCCCAGCCCTGCAGCACTTC	223700	55896	TCCAAGAACCCCTAGGCCCT	268287	100483	TTTTTTTTGAGACGGAGTCT
179114	11310	CCCCCAGCCCTGCAGCACTT	223701	55897	CTCCAAGAACCCCTAGGCCC	268288	100484	TTTTTTTTTGAGACGGAGTC
179115	11311	TCCCCCAGCCCTGCAGCACT	223702	55898	CCTCCAAGAACCCCTAGGCC	268289	100485	TTTTTTTTTTGAGACGGAGT
179116	11312	ATCCCCCAGCCCTGCAGCAC	223703	55899	GCCTCCAAGAACCCCTAGGC	268290	100486	GTTTTTTTTTTGAGACGGAG
179117	11313	CATCCCCCAGCCCTGCAGCA	223704	55900	GGCCTCCAAGAACCCCTAGG	268291	100487	GGTTTTTTTTTTGAGACGGA
179118	11314	GCATCCCCCAGCCCTGCAGC	223705	55901	GGGCCTCCAAGAACCCCTAG	268292	100488	TGGTTTTTTTTTTGAGACGG
179119	11315	GGCATCCCCCAGCCCTGCAG	223706	55902	GGGGCCTCCAAGAACCCCTA	268293	100489	GTGGTTTTTTTTTTGAGACG
179120	11316	AGGCATCCCCCAGCCCTGCA	223707	55903	TGGGGCCTCCAAGAACCCCT	268294	100490	TGTGGTTTTTTTTTTGAGAC
179121	11317	GAGGCATCCCCCAGCCCTGC	223708	55904	CTGGGGCCTCCAAGAACCCC	268295	100491	TTGTGGTTTTTTTTTTGAGA
179122	11318	GGAGGCATCCCCCAGCCCTG	223709	55905	GCTGGGGCCTCCAAGAACCC	268296	100492	TTTGTGGTTTTTTTTTTGAG
179123	11319	GGGAGGCATCCCCCAGCCCT	223710	55906	GGCTGGGGCCTCCAAGAACC	268297	100493	TTTTGTGGTTTTTTTTTTGA
179124	11320	TGGGAGGCATCCCCCAGCCC	223711	55907	AGGCTGGGGCCTCCAAGAAC	268298	100494	TTTTTGTGGTTTTTTTTTTG
179125	11321	CTGGGAGGCATCCCCCAGCC	223712	55908	AAGGCTGGGGCCTCCAAGAA	268299	100495	TTTTTTGTGGTTTTTTTTTT
179126	11322	CCTGGGAGGCATCCCCCAGC	223713	55909	CAAGGCTGGGGCCTCCAAGA	268300	100496	TTTTTTTGTGGTTTTTTTTT
179127	11323	TCCTGGGAGGCATCCCCCAG	223714	55910	CCAAGGCTGGGGCCTCCAAG	268301	100497	GTTTTTTTGTGGTTTTTTTT
179128	11324	CTCCTGGGAGGCATCCCCCA	223715	55911	GCCAAGGCTGGGGCCTCCAA	268302	100498	TGTTTTTTTGTGGTTTTTTT
179129	11325	GCTCCTGGGAGGCATCCCCC	223716	55912	TGCCAAGGCTGGGGCCTCCA	268303	100499	TTGTTTTTTTGTGGTTTTTT
179130	11326	GGCTCCTGGGAGGCATCCCC	223717	55913	TTGCCAAGGCTGGGGCCTCC	268304	100500	TTTGTTTTTTTGTGGTTTTT
179131	11327	CGGCTCCTGGGAGGCATCCC	223718	55914	TTTGCCAAGGCTGGGGCCTC	268305	100501	TTTTGTTTTTTTGTGGTTTT
179132	11328	GCGGCTCCTGGGAGGCATCC	223719	55915	TTTTGCCAAGGCTGGGGCCT	268306	100502	GTTTTGTTTTTTTGTGGTTT
179133	11329	TGCGGCTCCTGGGAGGCATC	223720	55916	ATTTTGCCAAGGCTGGGGCC	268307	100503	TGTTTTGTTTTTTTGTGGTT
179134	11330	CTGCGGCTCCTGGGAGGCAT	223721	55917	CATTTTGCCAAGGCTGGGGC	268308	100504	TTGTTTTGTTTTTTTGTGGT
179135	11331	ACTGCGGCTCCTGGGAGGCA	223722	55918	TCATTTTGCCAAGGCTGGGG	268309	100505	GTTGTTTTGTTTTTTTGTGG
179136	11332	GACTGCGGCTCCTGGGAGGC	223723	55919	CTCATTTTGCCAAGGCTGGG	268310	100506	TGTTGTTTTGTTTTTTTGTG
179137	11333	TGACTGCGGCTCCTGGGAGG	223724	55920	CCTCATTTTGCCAAGGCTGG	268311	100507	TTGTTGTTTTGTTTTTTTGT
179138	11334	CTGACTGCGGCTCCTGGGAG	223725	55921	TCCTCATTTTGCCAAGGCTG	268312	100508	GTTGTTGTTTTGTTTTTTTG
179139	11335	CCTGACTGCGGCTCCTGGGA	223726	55922	TTCCTCATTTTGCCAAGGCT	268313	100509	TGTTGTTGTTTTGTTTTTTT
179140	11336	ACCTGACTGCGGCTCCTGGG	223727	55923	CTTCCTCATTTTGCCAAGGC	268314	100510	TTGTTGTTGTTTTGTTTTTT
179141	11337	CACCTGACTGCGGCTCCTGG	223728	55924	TCTTCCTCATTTTGCCAAGG	268315	100511	TTTGTTGTTGTTTTGTTTTT
179142	11338	GCACCTGACTGCGGCTCCTG	223729	55925	TTCTTCCTCATTTTGCCAAG	268316	100512	TTTTGTTGTTGTTTTGTTTT
179143	11339	AGCACCTGACTGCGGCTCCT	223730	55926	CTTCTTCCTCATTTTGCCAA	268317	100513	CTTTTGTTGTTGTTTTGTTT
179144	11340	CAGCACCTGACTGCGGCTCC	223731	55927	CCTTCTTCCTCATTTTGCCA	268318	100514	TCTTTTGTTGTTGTTTTGTT
179145	11341	TCAGCACCTGACTGCGGCTC	223732	55928	ACCTTCTTCCTCATTTTGCC	268319	100515	TTCTTTTGTTGTTGTTTTGT
179146	11342	ATCAGCACCTGACTGCGGCT	223733	55929	CACCTTCTTCCTCATTTTGC	268320	100516	TTTCTTTTGTTGTTGTTTTG
179147	11343	GATCAGCACCTGACTGCGGC	223734	55930	TCACCTTCTTCCTCATTTTG	268321	100517	TTTTCTTTTGTTGTTGTTTT
179148	11344	AGATCAGCACCTGACTGCGG	223735	55931	TTCACCTTCTTCCTCATTTT	268322	100518	GTTTTCTTTTGTTGTTGTTT
179149	11345	CAGATCAGCACCTGACTGCG	223736	55932	CTTCACCTTCTTCCTCATTT	268323	100519	AGTTTTCTTTTGTTGTTGTT
179150	11346	TCAGATCAGCACCTGACTGC	223737	55933	CCTTCACCTTCTTCCTCATT	268324	100520	TAGTTTTCTTTTGTTGTTGT
179151	11347	TTCAGATCAGCACCTGACTG	223738	55934	ACCTTCACCTTCTTCCTCAT	268325	100521	CTAGTTTTCTTTTGTTGTTG
179152	11348	CTTCAGATCAGCACCTGACT	223739	55935	AACCTTCACCTTCTTCCTCA	268326	100522	ACTAGTTTTCTTTTGTTGTT
179153	11349	ACTTCAGATCAGCACCTGAC	223740	55936	CAACCTTCACCTTCTTCCTC	268327	100523	CACTAGTTTTCTTTTGTTGT
179154	11350	GACTTCAGATCAGCACCTGA	223741	55937	ACAACCTTCACCTTCTTCCT	268328	100524	GCACTAGTTTTCTTTTGTTG
179155	11351	AGACTTCAGATCAGCACCTG	223742	55938	GACAACCTTCACCTTCTTCC	268329	100525	AGCACTAGTTTTCTTTTGTT
179156	11352	AAGACTTCAGATCAGCACCT	223743	55939	AGACAACCTTCACCTTCTTC	268330	100526	AAGCACTAGTTTTCTTTTGT
179157	11353	AAAGACTTCAGATCAGCACC	223744	55940	CAGACAACCTTCACCTTCTT	268331	100527	TAAGCACTAGTTTTCTTTTG
179158	11354	CAAAGACTTCAGATCAGCAC	223745	55941	CCAGACAACCTTCACCTTCT	268332	100528	ATAAGCACTAGTTTTCTTTT
179159	11355	CCAAAGACTTCAGATCAGCA	223746	55942	CCCAGACAACCTTCACCTTC	268333	100529	AATAAGCACTAGTTTTCTTT
179160	11356	ACCAAAGACTTCAGATCAGC	223747	55943	GCCCAGACAACCTTCACCTT	268334	100530	GAATAAGCACTAGTTTTCTT
179161	11357	CACCAAAGACTTCAGATCAG	223748	55944	GGCCCAGACAACCTTCACCT	268335	100531	CGAATAAGCACTAGTTTTCT
179162	11358	CCACCAAAGACTTCAGATCA	223749	55945	GGGCCCAGACAACCTTCACC	268336	100532	ACGAATAAGCACTAGTTTTC
179163	11359	CCCACCAAAGACTTCAGATC	223750	55946	GGGGCCCAGACAACCTTCAC	268337	100533	GACGAATAAGCACTAGTTTT
179164	11360	GCCCACCAAAGACTTCAGAT	223751	55947	AGGGGCCCAGACAACCTTCA	268338	100534	TGACGAATAAGCACTAGTTT
179165	11361	AGCCCACCAAAGACTTCAGA	223752	55948	CAGGGGCCCAGACAACCTTC	268339	100535	GTGACGAATAAGCACTAGTT
179166	11362	CAGCCCACCAAAGACTTCAG	223753	55949	GCAGGGGCCCAGACAACCTT	268340	100536	AGTGACGAATAAGCACTAGT
179167	11363	TCAGCCCACCAAAGACTTCA	223754	55950	GGCAGGGGCCCAGACAACCT	268341	100537	CAGTGACGAATAAGCACTAG
179168	11364	GTCAGCCCACCAAAGACTTC	223755	55951	TGGCAGGGGCCCAGACAACC	268342	100538	CCAGTGACGAATAAGCACTA
179169	11365	AGTCAGCCCACCAAAGACTT	223756	55952	CTGGCAGGGGCCCAGACAAC	268343	100539	GCCAGTGACGAATAAGCACT
179170	11366	AAGTCAGCCCACCAAAGACT	223757	55953	CCTGGCAGGGGCCCAGACAA	268344	100540	GGCCAGTGACGAATAAGCAC
179171	11367	AAAGTCAGCCCACCAAAGAC	223758	55954	GCCTGGCAGGGGCCCAGACA	268345	100541	TGGCCAGTGACGAATAAGCA
179172	11368	TAAAGTCAGCCCACCAAAGA	223759	55955	AGCCTGGCAGGGGCCCAGAC	268346	100542	TTGGCCAGTGACGAATAAGC
179173	11369	CTAAAGTCAGCCCACCAAAG	223760	55956	GAGCCTGGCAGGGGCCCAGA	268347	100543	CTTGGCCAGTGACGAATAAG
179174	11370	GCTAAAGTCAGCCCACCAAA	223761	55957	GGAGCCTGGCAGGGGCCCAG	268348	100544	GCTTGGCCAGTGACGAATAA
179175	11371	GGCTAAAGTCAGCCCACCAA	223762	55958	AGGAGCCTGGCAGGGGCCCA	268349	100545	AGCTTGGCCAGTGACGAATA
179176	11372	AGGCTAAAGTCAGCCCACCA	223763	55959	AAGGAGCCTGGCAGGGGCCC	268350	100546	CAGCTTGGCCAGTGACGAAT
179177	11373	CAGGCTAAAGTCAGCCCACC	223764	55960	GAAGGAGCCTGGCAGGGGCC	268351	100547	GCAGCTTGGCCAGTGACGAA
179178	11374	TCAGGCTAAAGTCAGCCCAC	223765	55961	GGAAGGAGCCTGGCAGGGGC	268352	100548	GGCAGCTTGGCCAGTGACGA

179179	11375	GTCAGGCTAAAGTCAGCCCA	223766	55962	AGGAAGGAGCCTGGCAGGGG	268353	100549	GGGCAGCTTGGCCAGTGACG
179180	11376	GGTCAGGCTAAAGTCAGCCC	223767	55963	GAGGAAGGAGCCTGGCAGGG	268354	100550	TGGGCAGCTTGGCCAGTGAC
179181	11377	AGGTCAGGCTAAAGTCAGCC	223768	55964	CGAGGAAGGAGCCTGGCAGG	268355	100551	ATGGGCAGCTTGGCCAGTGA
179182	11378	CAGGTCAGGCTAAAGTCAGC	223769	55965	CCGAGGAAGGAGCCTGGCAG	268356	100552	AATGGGCAGCTTGGCCAGTG
179183	11379	TCAGGTCAGGCTAAAGTCAG	223770	55966	GCCGAGGAAGGAGCCTGGCA	268357	100553	CAATGGGCAGCTTGGCCAGT
179184	11380	TTCAGGTCAGGCTAAAGTCA	223771	55967	GGCCGAGGAAGGAGCCTGGC	268358	100554	CCAATGGGCAGCTTGGCCAG
179185	11381	TTTCAGGTCAGGCTAAAGTC	223772	55968	TGGCCGAGGAAGGAGCCTGG	268359	100555	GCCAATGGGCAGCTTGGCCA
179186	11382	ATTTCAGGTCAGGCTAAAGT	223773	55969	GTGGCCGAGGAAGGAGCCTG	268360	100556	AGCCAATGGGCAGCTTGGCC
179187	11383	TATTTCAGGTCAGGCTAAAG	223774	55970	CGTGGCCGAGGAAGGAGCCT	268361	100557	TAGCCAATGGGCAGCTTGGC
179188	11384	CTATTTCAGGTCAGGCTAAA	223775	55971	GCGTGGCCGAGGAAGGAGCC	268362	100558	GTAGCCAATGGGCAGCTTGG
179189	11385	ACTATTTCAGGTCAGGCTAA	223776	55972	TGCGTGGCCGAGGAAGGAGC	268363	100559	TGTAGCCAATGGGCAGCTTG
179190	11386	TACTATTTCAGGTCAGGCTA	223777	55973	GTGCGTGGCCGAGGAAGGAG	268364	100560	ATGTAGCCAATGGGCAGCTT
179191	11387	ATACTATTTCAGGTCAGGCT	223778	55974	AGTGCGTGGCCGAGGAAGGA	268365	100561	CATGTAGCCAATGGGCAGCT
179192	11388	TATACTATTTCAGGTCAGGC	223779	55975	GAGTGCGTGGCCGAGGAAGG	268366	100562	CCATGTAGCCAATGGGCAGC
179193	11389	CTATACTATTTCAGGTCAGG	223780	55976	GGAGTGCGTGGCCGAGGAAG	268367	100563	CCCATGTAGCCAATGGGCAG
179194	11390	GCTATACTATTTCAGGTCAG	223781	55977	GGGAGTGCGTGGCCGAGGAA	268368	100564	ACCCATGTAGCCAATGGGCA
179195	11391	AGCTATACTATTTCAGGTCA	223782	55978	GGGGAGTGCGTGGCCGAGGA	268369	100565	CACCCATGTAGCCAATGGGC
179196	11392	CAGCTATACTATTTCAGGTC	223783	55979	AGGGGAGTGCGTGGCCGAGG	268370	100566	GCACCCATGTAGCCAATGGG
179197	11393	GCAGCTATACTATTTCAGGT	223784	55980	AAGGGGAGTGCGTGGCCGAG	268371	100567	AGCACCCATGTAGCCAATGG
179198	11394	AGCAGCTATACTATTTCAGG	223785	55981	GAAGGGGAGTGCGTGGCCGA	268372	100568	AAGCACCCATGTAGCCAATG
179199	11395	CAGCAGCTATACTATTTCAG	223786	55982	GGAAGGGGAGTGCGTGGCCG	268373	100569	GAAGCACCCATGTAGCCAAT
179200	11396	GCAGCAGCTATACTATTTCA	223787	55983	AGGAAGGGGAGTGCGTGGCC	268374	100570	TGAAGCACCCATGTAGCCAA
179201	11397	GGCAGCAGCTATACTATTTC	223788	55984	CAGGAAGGGGAGTGCGTGGC	268375	100571	TTGAAGCACCCATGTAGCCA
179202	11398	TGGCAGCAGCTATACTATTT	223789	55985	GCAGGAAGGGGAGTGCGTGG	268376	100572	TTTGAAGCACCCATGTAGCC
179203	11399	GTGGCAGCAGCTATACTATT	223790	55986	TGCAGGAAGGGGAGTGCGTG	268377	100573	CTTTGAAGCACCCATGTAGC
179204	11400	GGTGGCAGCAGCTATACTAT	223791	55987	GTGCAGGAAGGGGAGTGCGT	268378	100574	TCTTTGAAGCACCCATGTAG
179205	11401	AGGTGGCAGCAGCTATACTA	223792	55988	TGTGCAGGAAGGGGAGTGCG	268379	100575	CTCTTTGAAGCACCCATGTA
179206	11402	CAGGTGGCAGCAGCTATACT	223793	55989	GTGTGCAGGAAGGGGAGTGC	268380	100576	GCTCTTTGAAGCACCCATGT
179207	11403	CCAGGTGGCAGCAGCTATAC	223794	55990	TGTGTGCAGGAAGGGGAGTG	268381	100577	AGCTCTTTGAAGCACCCATG
179208	11404	GCCAGGTGGCAGCAGCTATA	223795	55991	GTGTGTGCAGGAAGGGGAGT	268382	100578	CAGCTCTTTGAAGCACCCAT
179209	11405	AGCCAGGTGGCAGCAGCTAT	223796	55992	TGTGTGTGCAGGAAGGGGAG	268383	100579	GCAGCTCTTTGAAGCACCCA
179210	11406	GAGCCAGGTGGCAGCAGCTA	223797	55993	GTGTGTGTGCAGGAAGGGGA	268384	100580	GGCAGCTCTTTGAAGCACCC
179211	11407	GGAGCCAGGTGGCAGCAGCT	223798	55994	GGTGTGTGTGCAGGAAGGGG	268385	100581	GGGCAGCTCTTTGAAGCACC
179212	11408	GGGAGCCAGGTGGCAGCAGC	223799	55995	GGGTGTGTGTGCAGGAAGGG	268386	100582	AGGGCAGCTCTTTGAAGCAC
179213	11409	AGGGAGCCAGGTGGCAGCAG	223800	55996	AGGGTGTGTGTGCAGGAAGG	268387	100583	AAGGGCAGCTCTTTGAAGCA
179214	11410	AAGGGAGCCAGGTGGCAGCA	223801	55997	AAGGGTGTGTGTGCAGGAAG	268388	100584	GAAGGGCAGCTCTTTGAAGC
179215	11411	TAAGGGAGCCAGGTGGCAGC	223802	55998	GAAGGGTGTGTGTGCAGGAA	268389	100585	AGAAGGGCAGCTCTTTGAAG
179216	11412	CTAAGGGAGCCAGGTGGCAG	223803	55999	AGAAGGGTGTGTGTGCAGGA	268390	100586	GAGAAGGGCAGCTCTTTGAA
179217	11413	GCTAAGGGAGCCAGGTGGCA	223804	56000	GAGAAGGGTGTGTGTGCAGG	268391	100587	GGAGAAGGGCAGCTCTTTGA
179218	11414	CGCTAAGGGAGCCAGGTGGC	223805	56001	GGAGAAGGGTGTGTGTGCAG	268392	100588	TGGAGAAGGGCAGCTCTTTG
179219	11415	ACGCTAAGGGAGCCAGGTGG	223806	56002	GGGAGAAGGGTGTGTGTGCA	268393	100589	CTGGAGAAGGGCAGCTCTTT
179220	11416	GACGCTAAGGGAGCCAGGTG	223807	56003	AGGGAGAAGGGTGTGTGTGC	268394	100590	CCTGGAGAAGGGCAGCTCTT
179221	11417	TGACGCTAAGGGAGCCAGGT	223808	56004	GAGGGAGAAGGGTGTGTGTG	268395	100591	ACCTGGAGAAGGGCAGCTCT
179222	11418	CTGACGCTAAGGGAGCCAGG	223809	56005	GGAGGGAGAAGGGTGTGTGT	268396	100592	GACCTGGAGAAGGGCAGCTC
179223	11419	ACTGACGCTAAGGGAGCCAG	223810	56006	TGGAGGGAGAAGGGTGTGTG	268397	100593	AGACCTGGAGAAGGGCAGCT
179224	11420	GACTGACGCTAAGGGAGCCA	223811	56007	GTGGAGGGAGAAGGGTGTGT	268398	100594	CAGACCTGGAGAAGGGCAGC
179225	11421	TGACTGACGCTAAGGGAGCC	223812	56008	GGTGGAGGGAGAAGGGTGTG	268399	100595	CCAGACCTGGAGAAGGGCAG
179226	11422	CTGACTGACGCTAAGGGAGC	223813	56009	GGGTGGAGGGAGAAGGGTGT	268400	100596	GCCAGACCTGGAGAAGGGCA
179227	11423	TCTGACTGACGCTAAGGGAG	223814	56010	GGGGTGGAGGGAGAAGGGTG	268401	100597	GGCCAGACCTGGAGAAGGGC
179228	11424	GTCTGACTGACGCTAAGGGA	223815	56011	TGGGGTGGAGGGAGAAGGGT	268402	100598	TGGCCAGACCTGGAGAAGGG
179229	11425	CGTCTGACTGACGCTAAGGG	223816	56012	ATGGGGTGGAGGGAGAAGGG	268403	100599	CTGGCCAGACCTGGAGAAGG
179230	11426	CCGTCTGACTGACGCTAAGG	223817	56013	GATGGGGTGGAGGGAGAAGG	268404	100600	GCTGGCCAGACCTGGAGAAG
179231	11427	ACCGTCTGACTGACGCTAAG	223818	56014	AGATGGGGTGGAGGGAGAAG	268405	100601	TGCTGGCCAGACCTGGAGAA
179232	11428	CACCGTCTGACTGACGCTAA	223819	56015	GAGATGGGGTGGAGGGAGAA	268406	100602	CTGCTGGCCAGACCTGGAGA
179233	11429	GCACCGTCTGACTGACGCTA	223820	56016	GGAGATGGGGTGGAGGGAGA	268407	100603	CCTGCTGGCCAGACCTGGAG
179234	11430	TGCACCGTCTGACTGACGCT	223821	56017	TGGAGATGGGGTGGAGGGAG	268408	100604	ACCTGCTGGCCAGACCTGGA
179235	11431	CTGCACCGTCTGACTGACGC	223822	56018	ATGGAGATGGGGTGGAGGGA	268409	100605	TACCTGCTGGCCAGACCTGG
179236	11432	GCTGCACCGTCTGACTGACG	223823	56019	AATGGAGATGGGGTGGAGGG	268410	100606	ATACCTGCTGGCCAGACCTG
179237	11433	AGCTGCACCGTCTGACTGAC	223824	56020	CAATGGAGATGGGGTGGAGG	268411	100607	CATACCTGCTGGCCAGACCT
179238	11434	CAGCTGCACCGTCTGACTGA	223825	56021	ACAATGGAGATGGGGTGGAG	268412	100608	ACATACCTGCTGGCCAGACC
179239	11435	CCAGCTGCACCGTCTGACTG	223826	56022	AACAATGGAGATGGGGTGGA	268413	100609	CACATACCTGCTGGCCAGAC
179240	11436	ACCAGCTGCACCGTCTGACT	223827	56023	CAACAATGGAGATGGGGTGG	268414	100610	ACACATACCTGCTGGCCAGA
179241	11437	AACCAGCTGCACCGTCTGAC	223828	56024	ACAACAATGGAGATGGGGTG	268415	100611	AACACATACCTGCTGGCCAG
179242	11438	GAACCAGCTGCACCGTCTGA	223829	56025	GACAACAATGGAGATGGGGT	268416	100612	TAACACATACCTGCTGGCCA
179243	11439	GGAACCAGCTGCACCGTCTG	223830	56026	TGACAACAATGGAGATGGGG	268417	100613	GTAACACATACCTGCTGGCC
179244	11440	AGGAACCAGCTGCACCGTCT	223831	56027	CTGACAACAATGGAGATGGG	268418	100614	TGTAACACATACCTGCTGGC
179245	11441	TAGGAACCAGCTGCACCGTC	223832	56028	TCTGACAACAATGGAGATGG	268419	100615	CTGTAACACATACCTGCTGG
179246	11442	CTAGGAACCAGCTGCACCGT	223833	56029	TTCTGACAACAATGGAGATG	268420	100616	GCTGTAACACATACCTGCTG
179247	11443	CCTAGGAACCAGCTGCACCG	223834	56030	TTTCTGACAACAATGGAGAT	268421	100617	TGCTGTAACACATACCTGCT
179248	11444	CCCTAGGAACCAGCTGCACC	223835	56031	TTTTCTGACAACAATGGAGA	268422	100618	TTGCTGTAACACATACCTGC
179249	11445	CCCCTAGGAACCAGCTGCAC	223836	56032	CTTTTCTGACAACAATGGAG	268423	100619	TTTGCTGTAACACATACCTG
179250	11446	ACCCCTAGGAACCAGCTGCA	223837	56033	ACTTTTCTGACAACAATGGA	268424	100620	ATTTGCTGTAACACATACCT

179251	11447	CACCCCTAGGAACCAGCTGC	223838	56034	GACTTTTCTGACAACAATGG	268425	100621	CATTTGCTGTAACACATACC
179252	11448	TCACCCCTAGGAACCAGCTG	223839	56035	TGACTTTTCTGACAACAATG	268426	100622	GCATTTGCTGTAACACATAC
179253	11449	CTCACCCCTAGGAACCAGCT	223840	56036	GTGACTTTTCTGACAACAAT	268427	100623	GGCATTTGCTGTAACACATA
179254	11450	CCTCACCCCTAGGAACCAGC	223841	56037	TGTGACTTTTCTGACAACAA	268428	100624	AGGCATTTGCTGTAACACAT
179255	11451	CCCTCACCCCTAGGAACCAG	223842	56038	TTGTGACTTTTCTGACAACA	268429	100625	CAGGCATTTGCTGTAACACA
179256	11452	GCCCTCACCCCTAGGAACCA	223843	56039	ATTGTGACTTTTCTGACAAC	268430	100626	CCAGGCATTTGCTGTAACAC
179257	11453	AGCCCTCACCCCTAGGAACC	223844	56040	TATTGTGACTTTTCTGACAA	268431	100627	CCCAGGCATTTGCTGTAACA
179258	11454	CAGCCCTCACCCCTAGGAAC	223845	56041	TTATTGTGACTTTTCTGACA	268432	100628	CCCCAGGCATTTGCTGTAAC
179259	11455	TCAGCCCTCACCCCTAGGAA	223846	56042	TTTATTGTGACTTTTCTGAC	268433	100629	GCCCCAGGCATTTGCTGTAA
179260	11456	CTCAGCCCTCACCCCTAGGA	223847	56043	TTTTATTGTGACTTTTCTGA	268434	100630	TGCCCCAGGCATTTGCTGTA
179261	11457	GCTCAGCCCTCACCCCTAGG	223848	56044	TTTTTATTGTGACTTTTCTG	268435	100631	CTGCCCCAGGCATTTGCTGT
179262	11458	GGCTCAGCCCTCACCCCTAG	223849	56045	CTTTTTATTGTGACTTTTCT	268436	100632	GCTGCCCCAGGCATTTGCTG
179263	11459	TGGCTCAGCCCTCACCCCTA	223850	56046	CCTTTTTATTGTGACTTTTC	268437	100633	CGCTGCCCCAGGCATTTGCT
179264	11460	CTGGCTCAGCCCTCACCCCT	223851	56047	ACCTTTTTATTGTGACTTTT	268438	100634	CCGCTGCCCCAGGCATTTGC
179265	11461	GCTGGCTCAGCCCTCACCCC	223852	56048	GACCTTTTTATTGTGACTTT	268439	100635	GCCGCTGCCCCAGGCATTTG
179266	11462	TGCTGGCTCAGCCCTCACCC	223853	56049	GGACCTTTTTATTGTGACTT	268440	100636	TGCCGCTGCCCCAGGCATTT
179267	11463	CTGCTGGCTCAGCCCTCACC	223854	56050	TGGACCTTTTTATTGTGACT	268441	100637	CTGCCGCTGCCCCAGGCATT
179268	11464	CCTGCTGGCTCAGCCCTCAC	223855	56051	ATGGACCTTTTTATTGTGAC	268442	100638	CCTGCCGCTGCCCCAGGCAT
179269	11465	CCCTGCTGGCTCAGCCCTCA	223856	56052	TATGGACCTTTTTATTGTGA	268443	100639	CCCTGCCGCTGCCCCAGGCA
179270	11466	ACCCTGCTGGCTCAGCCCTC	223857	56053	ATATGGACCTTTTTATTGTG	268444	100640	CCCCTGCCGCTGCCCCAGGC
179271	11467	GACCCTGCTGGCTCAGCCCT	223858	56054	AATATGGACCTTTTTATTGT	268445	100641	GCCCCTGCCGCTGCCCCAGG
179272	11468	GGACCCTGCTGGCTCAGCCC	223859	56055	CAATATGGACCTTTTTATTG	268446	100642	TGCCCCTGCCGCTGCCCCAG
179273	11469	CGGACCCTGCTGGCTCAGCC	223860	56056	ACAATATGGACCTTTTTATT	268447	100643	ATGCCCCTGCCGCTGCCCCA
179274	11470	ACGGACCCTGCTGGCTCAGC	223861	56057	GACAATATGGACCTTTTTAT	268448	100644	AATGCCCCTGCCGCTGCCCC
179275	11471	CACGGACCCTGCTGGCTCAG	223862	56058	AGACAATATGGACCTTTTTA	268449	100645	CAATGCCCCTGCCGCTGCCC
179276	11472	GCACGGACCCTGCTGGCTCA	223863	56059	TAGACAATATGGACCTTTTT	268450	100646	GCAATGCCCCTGCCGCTGCC
179277	11473	GGCACGGACCCTGCTGGCTC	223864	56060	CTAGACAATATGGACCTTTT	268451	100647	AGCAATGCCCCTGCCGCTGC
179278	11474	GGGCACGGACCCTGCTGGCT	223865	56061	ACTAGACAATATGGACCTTT	268452	100648	CAGCAATGCCCCTGCCGCTG
179279	11475	TGGGCACGGACCCTGCTGGC	223866	56062	AACTAGACAATATGGACCTT	268453	100649	GCAGCAATGCCCCTGCCGCT
179280	11476	CTGGGCACGGACCCTGCTGG	223867	56063	GAACTAGACAATATGGACCT	268454	100650	CGCAGCAATGCCCCTGCCGC
179281	11477	CCTGGGCACGGACCCTGCTG	223868	56064	GGAACTAGACAATATGGACC	268455	100651	CCGCAGCAATGCCCCTGCCG
179282	11478	TCCTGGGCACGGACCCTGCT	223869	56065	GGGAACTAGACAATATGGAC	268456	100652	CCCGCAGCAATGCCCCTGCC
179283	11479	CTCCTGGGCACGGACCCTGC	223870	56066	TGGGAACTAGACAATATGGA	268457	100653	TCCCGCAGCAATGCCCCTGC
179284	11480	CCTCCTGGGCACGGACCCTG	223871	56067	ATGGGAACTAGACAATATGG	268458	100654	TTCCCGCAGCAATGCCCCTG
179285	11481	CCCTCCTGGGCACGGACCCT	223872	56068	TATGGGAACTAGACAATATG	268459	100655	CTTCCCGCAGCAATGCCCCT
179286	11482	TCCCTCCTGGGCACGGACCC	223873	56069	GTATGGGAACTAGACAATAT	268460	100656	GCTTCCCGCAGCAATGCCCC
179287	11483	ATCCCTCCTGGGCACGGACC	223874	56070	AGTATGGGAACTAGACAATA	268461	100657	AGCTTCCCGCAGCAATGCCC
179288	11484	CATCCCTCCTGGGCACGGAC	223875	56071	AAGTATGGGAACTAGACAAT	268462	100658	AAGCTTCCCGCAGCAATGCC
179289	11485	GCATCCCTCCTGGGCACGGA	223876	56072	AAAGTATGGGAACTAGACAA	268463	100659	GAAGCTTCCCGCAGCAATGC
179290	11486	TGCATCCCTCCTGGGCACGG	223877	56073	AAAAGTATGGGAACTAGACA	268464	100660	AGAAGCTTCCCGCAGCAATG
179291	11487	ATGCATCCCTCCTGGGCACG	223878	56074	TAAAAGTATGGGAACTAGAC	268465	100661	CAGAAGCTTCCCGCAGCAAT
179292	11488	CATGCATCCCTCCTGGGCAC	223879	56075	TTAAAAGTATGGGAACTAGA	268466	100662	CCAGAAGCTTCCCGCAGCAA
179293	11489	CCATGCATCCCTCCTGGGCA	223880	56076	ATTAAAAGTATGGGAACTAG	268467	100663	TCCAGAAGCTTCCCGCAGCA
179294	11490	CCCATGCATCCCTCCTGGGC	223881	56077	AATTAAAAGTATGGGAACTA	268468	100664	GTCCAGAAGCTTCCCGCAGC
179295	11491	ACCCATGCATCCCTCCTGGG	223882	56078	AAATTAAAAGTATGGGAACT	268469	100665	AGTCCAGAAGCTTCCCGCAG
179296	11492	CACCCATGCATCCCTCCTGG	223883	56079	AAAATTAAAAGTATGGGAAC	268470	100666	AAGTCCAGAAGCTTCCCGCA
179297	11493	CCACCCATGCATCCCTCCTG	223884	56080	AAAAATTAAAAGTATGGGAA	268471	100667	CAAGTCCAGAAGCTTCCCGC
179298	11494	GCCACCCATGCATCCCTCCT	223885	56081	TAAAAATTAAAAGTATGGGA	268472	100668	GCAAGTCCAGAAGCTTCCCG
179299	11495	GGCCACCCATGCATCCCTCC	223886	56082	TTAAAAATTAAAAGTATGGG	268473	100669	TGCAAGTCCAGAAGCTTCCC
179300	11496	TGGCCACCCATGCATCCCTC	223887	56083	TTTAAAAATTAAAAGTATGG	268474	100670	CTGCAAGTCCAGAAGCTTCC
179301	11497	GTGGCCACCCATGCATCCCT	223888	56084	TTTTAAAAATTAAAAGTATG	268475	100671	CCTGCAAGTCCAGAAGCTTC
179302	11498	TGTGGCCACCCATGCATCCC	223889	56085	ATTTTAAAAATTAAAAGTAT	268476	100672	TCCTGCAAGTCCAGAAGCTT
179303	11499	CTGTGGCCACCCATGCATCC	223890	56086	AATTTTAAAAATTAAAAGTA	268477	100673	TTCCTGCAAGTCCAGAAGCT
179304	11500	GCTGTGGCCACCCATGCATC	223891	56087	AAATTTTAAAAATTAAAAGT	268478	100674	TTTCCTGCAAGTCCAGAAGC
179305	11501	GGCTGTGGCCACCCATGCAT	223892	56088	AAAATTTTAAAAATTAAAAG	268479	100675	CTTTCCTGCAAGTCCAGAAG
179306	11502	GGGCTGTGGCCACCCATGCA	223893	56089	TAAAATTTTAAAAATTAAAA	268480	100676	GCTTTCCTGCAAGTCCAGAA
179307	11503	TGGGCTGTGGCCACCCATGC	223894	56090	ATAAAATTTTAAAAATTAAA	268481	100677	AGCTTTCCTGCAAGTCCAGA
179308	11504	CTGGGCTGTGGCCACCCATG	223895	56091	AATAAAATTTTAAAAATTAA	268482	100678	TAGCTTTCCTGCAAGTCCAG
179309	11505	GCTGGGCTGTGGCCACCCAT	223896	56092	AAATAAAATTTTAAAAATTA	268483	100679	TTAGCTTTCCTGCAAGTCCA
179310	11506	GGCTGGGCTGTGGCCACCCA	223897	56093	TAAATAAAATTTTAAAAATT	268484	100680	CTTAGCTTTCCTGCAAGTCC
179311	11507	AGGCTGGGCTGTGGCCACCC	223898	56094	ATAAATAAAATTTTAAAAAT	268485	100681	ACTTAGCTTTCCTGCAAGTC
179312	11508	CAGGCTGGGCTGTGGCCACC	223899	56095	AATAAATAAAATTTTAAAAA	268486	100682	AACTTAGCTTTCCTGCAAGT
179313	11509	GCAGGCTGGGCTGTGGCCAC	223900	56096	AAATAAATAAAATTTTAAAA	268487	100683	GAACTTAGCTTTCCTGCAAG
179314	11510	TGCAGGCTGGGCTGTGGCCA	223901	56097	TAAATAAATAAAATTTTAAA	268488	100684	AGAACTTAGCTTTCCTGCAA
179315	11511	GTGCAGGCTGGGCTGTGGCC	223902	56098	ATAAATAAATAAAATTTTAA	268489	100685	GAGAACTTAGCTTTCCTGCA
179316	11512	AGTGCAGGCTGGGCTGTGGC	223903	56099	AATAAATAAATAAAATTTTA	268490	100686	TGAGAACTTAGCTTTCCTGC
179317	11513	CAGTGCAGGCTGGGCTGTGG	223904	56100	AAATAAATAAATAAAATTTT	268491	100687	CTGAGAACTTAGCTTTCCTG
179318	11514	TCAGTGCAGGCTGGGCTGTG	223905	56101	TAAATAAATAAATAAAATTT	268492	100688	TCTGAGAACTTAGCTTTCCT
179319	11515	ATCAGTGCAGGCTGGGCTGT	223906	56102	ATAAATAAATAAATAAAATT	268493	100689	GTCTGAGAACTTAGCTTTCC
179320	11516	GATCAGTGCAGGCTGGGCTG	223907	56103	AATAAATAAATAAATAAAAT	268494	100690	AGTCTGAGAACTTAGCTTTC
179321	11517	AGATCAGTGCAGGCTGGGCT	223908	56104	AAATAAATAAATAAATAAAA	268495	100691	CAGTCTGAGAACTTAGCTTT
179322	11518	AAGATCAGTGCAGGCTGGGC	223909	56105	TAAATAAATAAATAAATAAA	268496	100692	GCAGTCTGAGAACTTAGCTT

179323	11519	CAAGATCAGTGCAGGCTGGG	223910	56106	ATAAATAAATAAATAAATAA	268497	100693	TGCAGTCTGAGAACTTAGCT
179324	11520	ACAAGATCAGTGCAGGCTGG	223911	56107	CATAAATAAATAAATAAATA	268498	100694	CTGCAGTCTGAGAACTTAGC
179325	11521	GACAAGATCAGTGCAGGCTG	223912	56108	ACATAAATAAATAAATAAAT	268499	100695	CCTGCAGTCTGAGAACTTAG
179326	11522	AGACAAGATCAGTGCAGGCT	223913	56109	TACATAAATAAATAAATAAA	268500	100696	CCCTGCAGTCTGAGAACTTA
179327	11523	CAGACAAGATCAGTGCAGGC	223914	56110	ATACATAAATAAATAAATAA	268501	100697	CCCCTGCAGTCTGAGAACTT
179328	11524	ACAGACAAGATCAGTGCAGG	223915	56111	AATACATAAATAAATAAATA	268502	100698	TCCCCTGCAGTCTGAGAACT
179329	11525	GACAGACAAGATCAGTGCAG	223916	56112	AAATACATAAATAAATAAAT	268503	100699	CTCCCCTGCAGTCTGAGAAC
179330	11526	GGACAGACAAGATCAGTGCA	223917	56113	AAAATACATAAATAAATAAA	268504	100700	GCTCCCCTGCAGTCTGAGAA
179331	11527	GGGACAGACAAGATCAGTGC	223918	56114	AAAAATACATAAATAAATAA	268505	100701	AGCTCCCCTGCAGTCTGAGA
179332	11528	GGGGACAGACAAGATCAGTG	223919	56115	AAAAAATACATAAATAAATA	268506	100702	TAGCTCCCCTGCAGTCTGAG
179333	11529	AGGGGACAGACAAGATCAGT	223920	56116	CAAAAAATACATAAATAAAT	268507	100703	TTAGCTCCCCTGCAGTCTGA
179334	11530	AAGGGGACAGACAAGATCAG	223921	56117	TCAAAAAATACATAAATAAA	268508	100704	CTTAGCTCCCCTGCAGTCTG
179335	11531	GAAGGGGACAGACAAGATCA	223922	56118	CTCAAAAAATACATAAATAA	268509	100705	GCTTAGCTCCCCTGCAGTCT
179336	11532	AGAAGGGGACAGACAAGATC	223923	56119	TCTCAAAAAATACATAAATA	268510	100706	TGCTTAGCTCCCCTGCAGTC
179337	11533	AAGAAGGGGACAGACAAGAT	223924	56120	GTCTCAAAAAATACATAAAT	268511	100707	GTGCTTAGCTCCCCTGCAGT
179338	11534	AAAGAAGGGGACAGACAAGA	223925	56121	TGTCTCAAAAAATACATAAA	268512	100708	TGTGCTTAGCTCCCCTGCAG
179339	11535	CAAAGAAGGGGACAGACAAG	223926	56122	CTGTCTCAAAAAATACATAA	268513	100709	GTGTGCTTAGCTCCCCTGCA
179340	11536	CCAAAGAAGGGGACAGACAA	223927	56123	TCTGTCTCAAAAAATACATA	268514	100710	GGTGTGCTTAGCTCCCCTGC
179341	11537	TCCAAAGAAGGGGACAGACA	223928	56124	CTCTGTCTCAAAAAATACAT	268515	100711	AGGTGTGCTTAGCTCCCCTG
179342	11538	TTCCAAAGAAGGGGACAGAC	223929	56125	ACTCTGTCTCAAAAAATACA	268516	100712	GAGGTGTGCTTAGCTCCCCT
179343	11539	CTTCCAAAGAAGGGGACAGA	223930	56126	GACTCTGTCTCAAAAAATAC	268517	100713	CGAGGTGTGCTTAGCTCCCC
179344	11540	CCTTCCAAAGAAGGGGACAG	223931	56127	AGACTCTGTCTCAAAAAATA	268518	100714	CCGAGGTGTGCTTAGCTCCC
179345	11541	TCCTTCCAAAGAAGGGGACA	223932	56128	AAGACTCTGTCTCAAAAAAT	268519	100715	GCCGAGGTGTGCTTAGCTCC
179346	11542	TTCCTTCCAAAGAAGGGGAC	223933	56129	TAAGACTCTGTCTCAAAAAA	268520	100716	TGCCGAGGTGTGCTTAGCTC
179347	11543	CTTCCTTCCAAAGAAGGGGA	223934	56130	TTAAGACTCTGTCTCAAAAA	268521	100717	GTGCCGAGGTGTGCTTAGCT
179348	11544	CCTTCCTTCCAAAGAAGGGG	223935	56131	GTTAAGACTCTGTCTCAAAA	268522	100718	TGTGCCGAGGTGTGCTTAGC
179349	11545	TCCTTCCTTCCAAAGAAGGG	223936	56132	GGTTAAGACTCTGTCTCAAA	268523	100719	CTGTGCCGAGGTGTGCTTAG
179350	11546	CTCCTTCCTTCCAAAGAAGG	223937	56133	GGGTTAAGACTCTGTCTCAA	268524	100720	CCTGTGCCGAGGTGTGCTTA
179351	11547	GCTCCTTCCTTCCAAAGAAG	223938	56134	TGGGTTAAGACTCTGTCTCA	268525	100721	CCCTGTGCCGAGGTGTGCTT
179352	11548	GGCTCCTTCCTTCCAAAGAA	223939	56135	CTGGGTTAAGACTCTGTCTC	268526	100722	ACCCTGTGCCGAGGTGTGCT
179353	11549	GGGCTCCTTCCTTCCAAAGA	223940	56136	CCTGGGTTAAGACTCTGTCT	268527	100723	CACCCTGTGCCGAGGTGTGC
179354	11550	GGGGCTCCTTCCTTCCAAAG	223941	56137	GCCTGGGTTAAGACTCTGTC	268528	100724	TCACCCTGTGCCGAGGTGTG
179355	11551	TGGGGCTCCTTCCTTCCAAA	223942	56138	AGCCTGGGTTAAGACTCTGT	268529	100725	CTCACCCTGTGCCGAGGTGT
179356	11552	TTGGGGCTCCTTCCTTCCAA	223943	56139	CAGCCTGGGTTAAGACTCTG	268530	100726	CCTCACCCTGTGCCGAGGTG
179357	11553	TTTGGGGCTCCTTCCTTCCA	223944	56140	CCAGCCTGGGTTAAGACTCT	268531	100727	GCCTCACCCTGTGCCGAGGT
179358	11554	GTTTGGGGCTCCTTCCTTCC	223945	56141	TCCAGCCTGGGTTAAGACTC	268532	100728	GGCCTCACCCTGTGCCGAGG
179359	11555	GGTTTGGGGCTCCTTCCTTC	223946	56142	CTCCAGCCTGGGTTAAGACT	268533	100729	AGGCCTCACCCTGTGCCGAG
179360	11556	TGGTTTGGGGCTCCTTCCTT	223947	56143	ACTCCAGCCTGGGTTAAGAC	268534	100730	CAGGCCTCACCCTGTGCCGA
179361	11557	CTGGTTTGGGGCTCCTTCCT	223948	56144	AACTCCAGCCTGGGTTAAGA	268535	100731	GCAGGCCTCACCCTGTGCCG
179362	11558	CCTGGTTTGGGGCTCCTTCC	223949	56145	GAACTCCAGCCTGGGTTAAG	268536	100732	CGCAGGCCTCACCCTGTGCC
179363	11559	CCCTGGTTTGGGGCTCCTTC	223950	56146	TGAACTCCAGCCTGGGTTAA	268537	100733	CCGCAGGCCTCACCCTGTGC
179364	11560	ACCCTGGTTTGGGGCTCCTT	223951	56147	CTGAACTCCAGCCTGGGTTA	268538	100734	ACCGCAGGCCTCACCCTGTG
179365	11561	CACCCTGGTTTGGGGCTCCT	223952	56148	ACTGAACTCCAGCCTGGGTT	268539	100735	AACCGCAGGCCTCACCCTGT
179366	11562	GCACCCTGGTTTGGGGCTCC	223953	56149	CACTGAACTCCAGCCTGGGT	268540	100736	GAACCGCAGGCCTCACCCTG
179367	11563	TGCACCCTGGTTTGGGGCTC	223954	56150	CCACTGAACTCCAGCCTGGG	268541	100737	AGAACCGCAGGCCTCACCCT
179368	11564	TTGCACCCTGGTTTGGGGCT	223955	56151	GCCACTGAACTCCAGCCTGG	268542	100738	GAGAACCGCAGGCCTCACCC
179369	11565	CTTGCACCCTGGTTTGGGGC	223956	56152	TGCCACTGAACTCCAGCCTG	268543	100739	TGAGAACCGCAGGCCTCACC
179370	11566	TCTTGCACCCTGGTTTGGGG	223957	56153	ATGCCACTGAACTCCAGCCT	268544	100740	CTGAGAACCGCAGGCCTCAC
179371	11567	GTCTTGCACCCTGGTTTGGG	223958	56154	CATGCCACTGAACTCCAGCC	268545	100741	TCTGAGAACCGCAGGCCTCA
179372	11568	TGTCTTGCACCCTGGTTTGG	223959	56155	TCATGCCACTGAACTCCAGC	268546	100742	GTCTGAGAACCGCAGGCCTC
179373	11569	CTGTCTTGCACCCTGGTTTG	223960	56156	ATCATGCCACTGAACTCCAG	268547	100743	AGTCTGAGAACCGCAGGCCT
179374	11570	ACTGTCTTGCACCCTGGTTT	223961	56157	GATCATGCCACTGAACTCCA	268548	100744	AAGTCTGAGAACCGCAGGCC
179375	11571	CACTGTCTTGCACCCTGGTT	223962	56158	AGATCATGCCACTGAACTCC	268549	100745	GAAGTCTGAGAACCGCAGGC
179376	11572	CCACTGTCTTGCACCCTGGT	223963	56159	TAGATCATGCCACTGAACTC	268550	100746	TGAAGTCTGAGAACCGCAGG
179377	11573	CCCACTGTCTTGCACCCTGG	223964	56160	CTAGATCATGCCACTGAACT	268551	100747	CTGAAGTCTGAGAACCGCAG
179378	11574	ACCCACTGTCTTGCACCCTG	223965	56161	CCTAGATCATGCCACTGAAC	268552	100748	ACTGAAGTCTGAGAACCGCA
179379	11575	CACCCACTGTCTTGCACCCT	223966	56162	GCCTAGATCATGCCACTGAA	268553	100749	GACTGAAGTCTGAGAACCGC
179380	11576	CCACCCACTGTCTTGCACCC	223967	56163	AGCCTAGATCATGCCACTGA	268554	100750	AGACTGAAGTCTGAGAACCG
179381	11577	CCCACCCACTGTCTTGCACC	223968	56164	GAGCCTAGATCATGCCACTG	268555	100751	AAGACTGAAGTCTGAGAACC
179382	11578	CCCCACCCACTGTCTTGCAC	223969	56165	TGAGCCTAGATCATGCCACT	268556	100752	AAAGACTGAAGTCTGAGAAC
179383	11579	CCCCCACCCACTGTCTTGCA	223970	56166	GTGAGCCTAGATCATGCCAC	268557	100753	CAAAGACTGAAGTCTGAGAA
179384	11580	ACCCCCACCCACTGTCTTGC	223971	56167	AGTGAGCCTAGATCATGCCA	268558	100754	ACAAAGACTGAAGTCTGAGA
179385	11581	CACCCCCACCCACTGTCTTG	223972	56168	CAGTGAGCCTAGATCATGCC	268559	100755	CACAAAGACTGAAGTCTGAG
179386	11582	GCACCCCCACCCACTGTCTT	223973	56169	GCAGTGAGCCTAGATCATGC	268560	100756	CCACAAAGACTGAAGTCTGA
179387	11583	GGCACCCCCACCCACTGTCT	223974	56170	TGCAGTGAGCCTAGATCATG	268561	100757	TCCACAAAGACTGAAGTCTG
179388	11584	AGGCACCCCCACCCACTGTC	223975	56171	TTGCAGTGAGCCTAGATCAT	268562	100758	CTCCACAAAGACTGAAGTCT
179389	11585	AAGGCACCCCCACCCACTGT	223976	56172	GTTGCAGTGAGCCTAGATCA	268563	100759	GCTCCACAAAGACTGAAGTC
179390	11586	CAAGGCACCCCCACCCACTG	223977	56173	GGTTGCAGTGAGCCTAGATC	268564	100760	AGCTCCACAAAGACTGAAGT
179391	11587	TCAAGGCACCCCCACCCACT	223978	56174	AGGTTGCAGTGAGCCTAGAT	268565	100761	AAGCTCCACAAAGACTGAAG
179392	11588	CTCAAGGCACCCCCACCCAC	223979	56175	GAGGTTGCAGTGAGCCTAGA	268566	100762	CAAGCTCCACAAAGACTGAA
179393	11589	GCTCAAGGCACCCCCACCCA	223980	56176	AGAGGTTGCAGTGAGCCTAG	268567	100763	TCAAGCTCCACAAAGACTGA
179394	11590	TGCTCAAGGCACCCCCACCC	223981	56177	GAGAGGTTGCAGTGAGCCTA	268568	100764	CTCAAGCTCCACAAAGACTG

179395	11591	ATGCTCAAGGCACCCCCACC	223982	56178	GGAGAGGTTGCAGTGAGCCT	268569	100765	TCTCAAGCTCCACAAAGACT
179396	11592	CATGCTCAAGGCACCCCCAC	223983	56179	GGGAGAGGTTGCAGTGAGCC	268570	100766	TTCTCAAGCTCCACAAAGAC
179397	11593	TCATGCTCAAGGCACCCCCA	223984	56180	AGGGAGAGGTTGCAGTGAGC	268571	100767	TTTCTCAAGCTCCACAAAGA
179398	11594	GTCATGCTCAAGGCACCCCC	223985	56181	GAGGGAGAGGTTGCAGTGAG	268572	100768	TTTTCTCAAGCTCCACAAAG
179399	11595	GGTCATGCTCAAGGCACCCC	223986	56182	GGAGGGAGAGGTTGCAGTGA	268573	100769	TTTTTCTCAAGCTCCACAAA
179400	11596	AGGTCATGCTCAAGGCACCC	223987	56183	AGGAGGGAGAGGTTGCAGTG	268574	100770	ATTTTTCTCAAGCTCCACAA
179401	11597	GAGGTCATGCTCAAGGCACC	223988	56184	CAGGAGGGAGAGGTTGCAGT	268575	100771	CATTTTTCTCAAGCTCCACA
179402	11598	TGAGGTCATGCTCAAGGCAC	223989	56185	CCAGGAGGGAGAGGTTGCAG	268576	100772	TCATTTTTCTCAAGCTCCAC
179403	11599	TTGAGGTCATGCTCAAGGCA	223990	56186	CCCAGGAGGGAGAGGTTGCA	268577	100773	CTCATTTTTCTCAAGCTCCA
179404	11600	CTTGAGGTCATGCTCAAGGC	223991	56187	ACCCAGGAGGGAGAGGTTGC	268578	100774	CCTCATTTTTCTCAAGCTCC
179405	11601	ACTTGAGGTCATGCTCAAGG	223992	56188	AACCCAGGAGGGAGAGGTTG	268579	100775	GCCTCATTTTTCTCAAGCTC
179406	11602	CACTTGAGGTCATGCTCAAG	223993	56189	GAACCCAGGAGGGAGAGGTT	268580	100776	AGCCTCATTTTTCTCAAGCT
179407	11603	TCACTTGAGGTCATGCTCAA	223994	56190	TGAACCCAGGAGGGAGAGGT	268581	100777	AAGCCTCATTTTTCTCAAGC
179408	11604	ATCACTTGAGGTCATGCTCA	223995	56191	TTGAACCCAGGAGGGAGAGG	268582	100778	AAAGCCTCATTTTTCTCAAG
179409	11605	AATCACTTGAGGTCATGCTC	223996	56192	CTTGAACCCAGGAGGGAGAG	268583	100779	CAAAGCCTCATTTTTCTCAA
179410	11606	AAATCACTTGAGGTCATGCT	223997	56193	ACTTGAACCCAGGAGGGAGA	268584	100780	GCAAAGCCTCATTTTTCTCA
179411	11607	GAAATCACTTGAGGTCATGC	223998	56194	CACTTGAACCCAGGAGGGAG	268585	100781	TGCAAAGCCTCATTTTTCTC
179412	11608	GGAAATCACTTGAGGTCATG	223999	56195	TCACTTGAACCCAGGAGGGA	268586	100782	CTGCAAAGCCTCATTTTTCT
179413	11609	TGGAAATCACTTGAGGTCAT	224000	56196	ATCACTTGAACCCAGGAGGG	268587	100783	CCTGCAAAGCCTCATTTTTC
179414	11610	CTGGAAATCACTTGAGGTCA	224001	56197	AATCACTTGAACCCAGGAGG	268588	100784	ACCTGCAAAGCCTCATTTTT
179415	11611	GCTGGAAATCACTTGAGGTC	224002	56198	GAATCACTTGAACCCAGGAG	268589	100785	GACCTGCAAAGCCTCATTTT
179416	11612	GGCTGGAAATCACTTGAGGT	224003	56199	AGAATCACTTGAACCCAGGA	268590	100786	GGACCTGCAAAGCCTCATTT
179417	11613	GGGCTGGAAATCACTTGAGG	224004	56200	GAGAATCACTTGAACCCAGG	268591	100787	GGGACCTGCAAAGCCTCATT
179418	11614	GGGGCTGGAAATCACTTGAG	224005	56201	TGAGAATCACTTGAACCCAG	268592	100788	TGGGACCTGCAAAGCCTCAT
179419	11615	AGGGGCTGGAAATCACTTGA	224006	56202	ATGAGAATCACTTGAACCCA	268593	100789	GTGGGACCTGCAAAGCCTCA
179420	11616	CAGGGGCTGGAAATCACTTG	224007	56203	CATGAGAATCACTTGAACCC	268594	100790	GGTGGGACCTGCAAAGCCTC
179421	11617	GCAGGGGCTGGAAATCACTT	224008	56204	GCATGAGAATCACTTGAACC	268595	100791	GGGTGGGACCTGCAAAGCCT
179422	11618	GGCAGGGGCTGGAAATCACT	224009	56205	GGCATGAGAATCACTTGAAC	268596	100792	GGGGTGGGACCTGCAAAGCC
179423	11619	TGGCAGGGGCTGGAAATCAC	224010	56206	AGGCATGAGAATCACTTGAA	268597	100793	AGGGGTGGGACCTGCAAAGC
179424	11620	CTGGCAGGGGCTGGAAATCA	224011	56207	GAGGCATGAGAATCACTTGA	268598	100794	TAGGGGTGGGACCTGCAAAG
179425	11621	ACTGGCAGGGGCTGGAAATC	224012	56208	TGAGGCATGAGAATCACTTG	268599	100795	CTAGGGGTGGGACCTGCAAA
179426	11622	CACTGGCAGGGGCTGGAAAT	224013	56209	CTGAGGCATGAGAATCACTT	268600	100796	TCTAGGGGTGGGACCTGCAA
179427	11623	GCACTGGCAGGGGCTGGAAA	224014	56210	GCTGAGGCATGAGAATCACT	268601	100797	CTCTAGGGGTGGGACCTGCA
179428	11624	AGCACTGGCAGGGGCTGGAA	224015	56211	GGCTGAGGCATGAGAATCAC	268602	100798	TCTCTAGGGGTGGGACCTGC
179429	11625	CAGCACTGGCAGGGGCTGGA	224016	56212	AGGCTGAGGCATGAGAATCA	268603	100799	ATCTCTAGGGGTGGGACCTG
179430	11626	TCAGCACTGGCAGGGGCTGG	224017	56213	GAGGCTGAGGCATGAGAATC	268604	100800	AATCTCTAGGGGTGGGACCT
179431	11627	GTCAGCACTGGCAGGGGCTG	224018	56214	GGAGGCTGAGGCATGAGAAT	268605	100801	GAATCTCTAGGGGTGGGACC
179432	11628	AGTCAGCACTGGCAGGGGCT	224019	56215	GGGAGGCTGAGGCATGAGAA	268606	100802	AGAATCTCTAGGGGTGGGAC
179433	11629	AAGTCAGCACTGGCAGGGGC	224020	56216	CGGGAGGCTGAGGCATGAGA	268607	100803	CAGAATCTCTAGGGGTGGGA
179434	11630	GAAGTCAGCACTGGCAGGGG	224021	56217	TCGGGAGGCTGAGGCATGAG	268608	100804	GCAGAATCTCTAGGGGTGGG
179435	11631	AGAAGTCAGCACTGGCAGGG	224022	56218	CTCGGGAGGCTGAGGCATGA	268609	100805	AGCAGAATCTCTAGGGGTGG
179436	11632	GAGAAGTCAGCACTGGCAGG	224023	56219	ACTCGGGAGGCTGAGGCATG	268610	100806	GAGCAGAATCTCTAGGGGTG
179437	11633	AGAGAAGTCAGCACTGGCAG	224024	56220	TACTCGGGAGGCTGAGGCAT	268611	100807	AGAGCAGAATCTCTAGGGGT
179438	11634	CAGAGAAGTCAGCACTGGCA	224025	56221	CTACTCGGGAGGCTGAGGCA	268612	100808	TAGAGCAGAATCTCTAGGGG
179439	11635	CCAGAGAAGTCAGCACTGGC	224026	56222	GCTACTCGGGAGGCTGAGGC	268613	100809	ATAGAGCAGAATCTCTAGGG
179440	11636	CCCAGAGAAGTCAGCACTGG	224027	56223	AGCTACTCGGGAGGCTGAGG	268614	100810	GATAGAGCAGAATCTCTAGG
179441	11637	CCCCAGAGAAGTCAGCACTG	224028	56224	CAGCTACTCGGGAGGCTGAG	268615	100811	GGATAGAGCAGAATCTCTAG
179442	11638	TCCCCAGAGAAGTCAGCACT	224029	56225	TCAGCTACTCGGGAGGCTGA	268616	100812	TGGATAGAGCAGAATCTCTA
179443	11639	TTCCCCAGAGAAGTCAGCAC	224030	56226	CTCAGCTACTCGGGAGGCTG	268617	100813	GTGGATAGAGCAGAATCTCT
179444	11640	CTTCCCCAGAGAAGTCAGCA	224031	56227	TCTCAGCTACTCGGGAGGCT	268618	100814	AGTGGATAGAGCAGAATCTC
179445	11641	CCTTCCCCAGAGAAGTCAGC	224032	56228	ATCTCAGCTACTCGGGAGGC	268619	100815	GAGTGGATAGAGCAGAATCT
179446	11642	CCCTTCCCCAGAGAAGTCAG	224033	56229	AATCTCAGCTACTCGGGAGG	268620	100816	AGAGTGGATAGAGCAGAATC
179447	11643	GCCCTTCCCCAGAGAAGTCA	224034	56230	TAATCTCAGCTACTCGGGAG	268621	100817	AAGAGTGGATAGAGCAGAAT
179448	11644	AGCCCTTCCCCAGAGAAGTC	224035	56231	GTAATCTCAGCTACTCGGGA	268622	100818	CAAGAGTGGATAGAGCAGAA
179449	11645	CAGCCCTTCCCCAGAGAAGT	224036	56232	TGTAATCTCAGCTACTCGGG	268623	100819	TCAAGAGTGGATAGAGCAGA
179450	11646	CCAGCCCTTCCCCAGAGAAG	224037	56233	CTGTAATCTCAGCTACTCGG	268624	100820	TTCAAGAGTGGATAGAGCAG
179451	11647	CCCAGCCCTTCCCCAGAGAA	224038	56234	TCTGTAATCTCAGCTACTCG	268625	100821	CTTCAAGAGTGGATAGAGCA
179452	11648	TCCCAGCCCTTCCCCAGAGA	224039	56235	ATCTGTAATCTCAGCTACTC	268626	100822	CCTTCAAGAGTGGATAGAGC
179453	11649	GTCCCAGCCCTTCCCCAGAG	224040	56236	TATCTGTAATCTCAGCTACT	268627	100823	CCCTTCAAGAGTGGATAGAG
179454	11650	AGTCCCAGCCCTTCCCCAGA	224041	56237	ATATCTGTAATCTCAGCTAC	268628	100824	CCCCTTCAAGAGTGGATAGA
179455	11651	AAGTCCCAGCCCTTCCCCAG	224042	56238	CATATCTGTAATCTCAGCTA	268629	100825	TCCCCTTCAAGAGTGGATAG
179456	11652	GAAGTCCCAGCCCTTCCCCA	224043	56239	ACATATCTGTAATCTCAGCT	268630	100826	ATCCCCTTCAAGAGTGGATA
179457	11653	GGAAGTCCCAGCCCTTCCCC	224044	56240	CACATATCTGTAATCTCAGC	268631	100827	GATCCCCTTCAAGAGTGGAT
179458	11654	AGGAAGTCCCAGCCCTTCCC	224045	56241	GCACATATCTGTAATCTCAG	268632	100828	CGATCCCCTTCAAGAGTGGA
179459	11655	AAGGAAGTCCCAGCCCTTCC	224046	56242	GGCACATATCTGTAATCTCA	268633	100829	TCGATCCCCTTCAAGAGTGG
179460	11656	GAAGGAAGTCCCAGCCCTTC	224047	56243	TGGCACATATCTGTAATCTC	268634	100830	CTCGATCCCCTTCAAGAGTG
179461	11657	AGAAGGAAGTCCCAGCCCTT	224048	56244	GTGGCACATATCTGTAATCT	268635	100831	TCTCGATCCCCTTCAAGAGT
179462	11658	CAGAAGGAAGTCCCAGCCCT	224049	56245	AGTGGCACATATCTGTAATC	268636	100832	TTCTCGATCCCCTTCAAGAG
179463	11659	CCAGAAGGAAGTCCCAGCCC	224050	56246	TAGTGGCACATATCTGTAAT	268637	100833	TTTCTCGATCCCCTTCAAGA
179464	11660	CCCAGAAGGAAGTCCCAGCC	224051	56247	ATAGTGGCACATATCTGTAA	268638	100834	ATTTCTCGATCCCCTTCAAG
179465	11661	GCCCAGAAGGAAGTCCCAGC	224052	56248	CATAGTGGCACATATCTGTA	268639	100835	AATTTCTCGATCCCCTTCAA
179466	11662	AGCCCAGAAGGAAGTCCCAG	224053	56249	GCATAGTGGCACATATCTGT	268640	100836	AAATTTCTCGATCCCCTTCA

179467	11663	GAGCCCAGAAGGAAGTCCCA	224054	56250	GGCATAGTGGCACATATCTG	268641	100837	CAAATTTCTCGATCCCCTTC
179468	11664	TGAGCCCAGAAGGAAGTCCC	224055	56251	GGGCATAGTGGCACATATCT	268642	100838	GCAAATTTCTCGATCCCCTT
179469	11665	TTGAGCCCAGAAGGAAGTCC	224056	56252	TGGGCATAGTGGCACATATC	268643	100839	TGCAAATTTCTCGATCCCCT
179470	11666	CTTGAGCCCAGAAGGAAGTC	224057	56253	CTGGGCATAGTGGCACATAT	268644	100840	ATGCAAATTTCTCGATCCCC
179471	11667	ACTTGAGCCCAGAAGGAAGT	224058	56254	GCTGGGCATAGTGGCACATA	268645	100841	AATGCAAATTTCTCGATCCC
179472	11668	GACTTGAGCCCAGAAGGAAG	224059	56255	AGCTGGGCATAGTGGCACAT	268646	100842	AAATGCAAATTTCTCGATCC
179473	11669	TGACTTGAGCCCAGAAGGAA	224060	56256	TAGCTGGGCATAGTGGCACA	268647	100843	AAAATGCAAATTTCTCGATC
179474	11670	GTGACTTGAGCCCAGAAGGA	224061	56257	TTAGCTGGGCATAGTGGCAC	268648	100844	CAAAATGCAAATTTCTCGAT
179475	11671	CGTGACTTGAGCCCAGAAGG	224062	56258	ATTAGCTGGGCATAGTGGCA	268649	100845	GCAAAATGCAAATTTCTCGA
179476	11672	TCGTGACTTGAGCCCAGAAG	224063	56259	AATTAGCTGGGCATAGTGGC	268650	100846	TGCAAAATGCAAATTTCTCG
179477	11673	GTCGTGACTTGAGCCCAGAA	224064	56260	AAATTAGCTGGGCATAGTGG	268651	100847	TTGCAAAATGCAAATTTCTC
179478	11674	GGTCGTGACTTGAGCCCAGA	224065	56261	AAAATTAGCTGGGCATAGTG	268652	100848	GTTGCAAAATGCAAATTTCT
179479	11675	GGGTCGTGACTTGAGCCCAG	224066	56262	AAAAATTAGCTGGGCATAGT	268653	100849	AGTTGCAAAATGCAAATTTC
179480	11676	AGGGTCGTGACTTGAGCCCA	224067	56263	CAAAAATTAGCTGGGCATAG	268654	100850	GAGTTGCAAAATGCAAATTT
179481	11677	AAGGGTCGTGACTTGAGCCC	224068	56264	ACAAAAATTAGCTGGGCATA	268655	100851	GGAGTTGCAAAATGCAAATT
179482	11678	CAAGGGTCGTGACTTGAGCC	224069	56265	TACAAAAATTAGCTGGGCAT	268656	100852	GGGAGTTGCAAAATGCAAAT
179483	11679	CCAAGGGTCGTGACTTGAGC	224070	56266	ATACAAAAATTAGCTGGGCA	268657	100853	TGGGAGTTGCAAAATGCAAA
179484	11680	TCCAAGGGTCGTGACTTGAG	224071	56267	AATACAAAAATTAGCTGGGC	268658	100854	GTGGGAGTTGCAAAATGCAA
179485	11681	ATCCAAGGGTCGTGACTTGA	224072	56268	AAATACAAAAATTAGCTGGG	268659	100855	AGTGGGAGTTGCAAAATGCA
179486	11682	CATCCAAGGGTCGTGACTTG	224073	56269	AAAATACAAAAATTAGCTGG	268660	100856	AAGTGGGAGTTGCAAAATGC
179487	11683	CCATCCAAGGGTCGTGACTT	224074	56270	AAAAATACAAAAATTAGCTG	268661	100857	AAAGTGGGAGTTGCAAAATG
179488	11684	TCCATCCAAGGGTCGTGACT	224075	56271	TAAAAATACAAAAATTAGCT	268662	100858	GAAAGTGGGAGTTGCAAAAT
179489	11685	TTCCATCCAAGGGTCGTGAC	224076	56272	CTAAAAATACAAAAATTAGC	268663	100859	GGAAAGTGGGAGTTGCAAAA
179490	11686	ATTCCATCCAAGGGTCGTGA	224077	56273	ACTAAAAATACAAAAATTAG	268664	100860	AGGAAAGTGGGAGTTGCAAA
179491	11687	AATTCCATCCAAGGGTCGTG	224078	56274	TACTAAAAATACAAAAATTA	268665	100861	GAGGAAAGTGGGAGTTGCAA
179492	11688	AAATTCCATCCAAGGGTCGT	224079	56275	CTACTAAAAATACAAAAATT	268666	100862	GGAGGAAAGTGGGAGTTGCA
179493	11689	GAAATTCCATCCAAGGGTCG	224080	56276	TCTACTAAAAATACAAAAAT	268667	100863	AGGAGGAAAGTGGGAGTTGC
179494	11690	GGAAATTCCATCCAAGGGTC	224081	56277	CTCTACTAAAAATACAAAAA	268668	100864	AAGGAGGAAAGTGGGAGTTG
179495	11691	AGGAAATTCCATCCAAGGGT	224082	56278	TCTCTACTAAAAATACAAAA	268669	100865	CAAGGAGGAAAGTGGGAGTT
179496	11692	CAGGAAATTCCATCCAAGGG	224083	56279	GTCTCTACTAAAAATACAAA	268670	100866	TCAAGGAGGAAAGTGGGAGT
179497	11693	CCAGGAAATTCCATCCAAGG	224084	56280	CGTCTCTACTAAAAATACAA	268671	100867	TTCAAGGAGGAAAGTGGGAG
179498	11694	CCCAGGAAATTCCATCCAAG	224085	56281	CCGTCTCTACTAAAAATACA	268672	100868	TTTCAAGGAGGAAAGTGGGA
179499	11695	TCCCAGGAAATTCCATCCAA	224086	56282	CCCGTCTCTACTAAAAATAC	268673	100869	CTTTCAAGGAGGAAAGTGGG
179500	11696	CTCCCAGGAAATTCCATCCA	224087	56283	CCCCGTCTCTACTAAAAATA	268674	100870	GCTTTCAAGGAGGAAAGTGG
179501	11697	GCTCCCAGGAAATTCCATCC	224088	56284	ACCCCGTCTCTACTAAAAAT	268675	100871	AGCTTTCAAGGAGGAAAGTG
179502	11698	AGCTCCCAGGAAATTCCATC	224089	56285	AACCCCGTCTCTACTAAAAA	268676	100872	GAGCTTTCAAGGAGGAAAGT
179503	11699	AAGCTCCCAGGAAATTCCAT	224090	56286	AAACCCCGTCTCTACTAAAA	268677	100873	GGAGCTTTCAAGGAGGAAAG
179504	11700	AAAGCTCCCAGGAAATTCCA	224091	56287	GAAACCCCGTCTCTACTAAA	268678	100874	CGGAGCTTTCAAGGAGGAAA
179505	11701	AAAAGCTCCCAGGAAATTCC	224092	56288	TGAAACCCCGTCTCTACTAA	268679	100875	CCGGAGCTTTCAAGGAGGAA
179506	11702	GAAAAGCTCCCAGGAAATTC	224093	56289	GTGAAACCCCGTCTCTACTA	268680	100876	TCCGGAGCTTTCAAGGAGGA
179507	11703	AGAAAAGCTCCCAGGAAATT	224094	56290	GGTGAAACCCCGTCTCTACT	268681	100877	CTCCGGAGCTTTCAAGGAGG
179508	11704	CAGAAAAGCTCCCAGGAAAT	224095	56291	TGGTGAAACCCCGTCTCTAC	268682	100878	TCTCCGGAGCTTTCAAGGAG
179509	11705	ACAGAAAAGCTCCCAGGAAA	224096	56292	ATGGTGAAACCCCGTCTCTA	268683	100879	ATCTCCGGAGCTTTCAAGGA
179510	11706	AACAGAAAAGCTCCCAGGAA	224097	56293	CATGGTGAAACCCCGTCTCT	268684	100880	AATCTCCGGAGCTTTCAAGG
179511	11707	AAACAGAAAAGCTCCCAGGA	224098	56294	ACATGGTGAAACCCCGTCTC	268685	100881	GAATCTCCGGAGCTTTCAAG
179512	11708	AAAACAGAAAAGCTCCCAGG	224099	56295	AACATGGTGAAACCCCGTCT	268686	100882	AGAATCTCCGGAGCTTTCAA
179513	11709	AAAAACAGAAAAGCTCCCAG	224100	56296	CAACATGGTGAAACCCCGTC	268687	100883	CAGAATCTCCGGAGCTTTCA
179514	11710	AAAAAACAGAAAAGCTCCCA	224101	56297	CCAACATGGTGAAACCCCGT	268688	100884	TCAGAATCTCCGGAGCTTTC
179515	11711	GAAAAAACAGAAAAGCTCCC	224102	56298	GCCAACATGGTGAAACCCCG	268689	100885	GTCAGAATCTCCGGAGCTTT
179516	11712	AGAAAAAACAGAAAAGCTCC	224103	56299	GGCCAACATGGTGAAACCCC	268690	100886	CGTCAGAATCTCCGGAGCTT
179517	11713	CAGAAAAAACAGAAAAGCTC	224104	56300	TGGCCAACATGGTGAAACCC	268691	100887	GCGTCAGAATCTCCGGAGCT
179518	11714	CCAGAAAAAACAGAAAAGCT	224105	56301	CTGGCCAACATGGTGAAACC	268692	100888	TGCGTCAGAATCTCCGGAGC
179519	11715	TCCAGAAAAAACAGAAAAGC	224106	56302	CCTGGCCAACATGGTGAAAC	268693	100889	CTGCGTCAGAATCTCCGGAG
179520	11716	CTCCAGAAAAAACAGAAAAG	224107	56303	GCCTGGCCAACATGGTGAAA	268694	100890	CCTGCGTCAGAATCTCCGGA
179521	11717	ACTCCAGAAAAAACAGAAAA	224108	56304	AGCCTGGCCAACATGGTGAA	268695	100891	CCCTGCGTCAGAATCTCCGG
179522	11718	AACTCCAGAAAAAACAGAAA	224109	56305	CAGCCTGGCCAACATGGTGA	268696	100892	ACCCTGCGTCAGAATCTCCG
179523	11719	AAACTCCAGAAAAAACAGAA	224110	56306	CCAGCCTGGCCAACATGGTG	268697	100893	AACCCTGCGTCAGAATCTCC
179524	11720	AAAACTCCAGAAAAAACAGA	224111	56307	ACCAGCCTGGCCAACATGGT	268698	100894	GAACCCTGCGTCAGAATCTC
179525	11721	GAAAACTCCAGAAAAAACAG	224112	56308	GACCAGCCTGGCCAACATGG	268699	100895	GGAACCCTGCGTCAGAATCT
179526	11722	TGAAAACTCCAGAAAAAACA	224113	56309	AGACCAGCCTGGCCAACATG	268700	100896	CGGAACCCTGCGTCAGAATC
179527	11723	CTGAAAACTCCAGAAAAAAC	224114	56310	GAGACCAGCCTGGCCAACAT	268701	100897	ACGGAACCCTGCGTCAGAAT
179528	11724	ACTGAAAACTCCAGAAAAAA	224115	56311	CGAGACCAGCCTGGCCAACA	268702	100898	CACGGAACCCTGCGTCAGAA
179529	11725	AACTGAAAACTCCAGAAAAA	224116	56312	TCGAGACCAGCCTGGCCAAC	268703	100899	CCACGGAACCCTGCGTCAGA
179530	11726	AAACTGAAAACTCCAGAAAA	224117	56313	TTCGAGACCAGCCTGGCCAA	268704	100900	CCCACGGAACCCTGCGTCAG
179531	11727	AAAACTGAAAACTCCAGAAA	224118	56314	GTTCGAGACCAGCCTGGCCA	268705	100901	GCCCACGGAACCCTGCGTCA
179532	11728	AAAAACTGAAAACTCCAGAA	224119	56315	AGTTCGAGACCAGCCTGGCC	268706	100902	GGCCCACGGAACCCTGCGTC
179533	11729	AAAAAACTGAAAACTCCAGA	224120	56316	GAGTTCGAGACCAGCCTGGC	268707	100903	TGGCCCACGGAACCCTGCGT
179534	11730	GAAAAAACTGAAAACTCCAG	224121	56317	GGAGTTCGAGACCAGCCTGG	268708	100904	GTGGCCCACGGAACCCTGCG
179535	11731	GGAAAAAACTGAAAACTCCA	224122	56318	AGGAGTTCGAGACCAGCCTG	268709	100905	TGTGGCCCACGGAACCCTGC
179536	11732	AGGAAAAAACTGAAAACTCC	224123	56319	CAGGAGTTCGAGACCAGCCT	268710	100906	GTGTGGCCCACGGAACCCTG
179537	11733	TAGGAAAAAACTGAAAACTC	224124	56320	CCAGGAGTTCGAGACCAGCC	268711	100907	AGTGTGGCCCACGGAACCCT
179538	11734	TTAGGAAAAAACTGAAAACT	224125	56321	GCCAGGAGTTCGAGACCAGC	268712	100908	AAGTGTGGCCCACGGAACCC

179539	11735	GTTAGGAAAAAACTGAAAAC	224126	56322	GGCCAGGAGTTCGAGACCAG	268713	100909	AAAGTGTGGCCCACGGAACC
179540	11736	GGTTAGGAAAAAACTGAAAA	224127	56323	AGGCCAGGAGTTCGAGACCA	268714	100910	CAAAGTGTGGCCCACGGAAC
179541	11737	TGGTTAGGAAAAAACTGAAA	224128	56324	GAGGCCAGGAGTTCGAGACC	268715	100911	CCAAAGTGTGGCCCACGGAA
179542	11738	CTGGTTAGGAAAAAACTGAA	224129	56325	TGAGGCCAGGAGTTCGAGAC	268716	100912	TCCAAAGTGTGGCCCACGGA
179543	11739	TCTGGTTAGGAAAAAACTGA	224130	56326	TTGAGGCCAGGAGTTCGAGA	268717	100913	TTCCAAAGTGTGGCCCACGG
179544	11740	GTCTGGTTAGGAAAAAACTG	224131	56327	CTTGAGGCCAGGAGTTCGAG	268718	100914	TTTCCAAAGTGTGGCCCACG
179545	11741	TGTCTGGTTAGGAAAAAACT	224132	56328	ACTTGAGGCCAGGAGTTCGA	268719	100915	TTTTCCAAAGTGTGGCCCAC
179546	11742	CTGTCTGGTTAGGAAAAAAC	224133	56329	CACTTGAGGCCAGGAGTTCG	268720	100916	ATTTTCCAAAGTGTGGCCCA
179547	11743	CCTGTCTGGTTAGGAAAAAA	224134	56330	TCACTTGAGGCCAGGAGTTC	268721	100917	TATTTTCCAAAGTGTGGCCC
179548	11744	CCCTGTCTGGTTAGGAAAAA	224135	56331	ATCACTTGAGGCCAGGAGTT	268722	100918	GTATTTTCCAAAGTGTGGCC
179549	11745	TCCCTGTCTGGTTAGGAAAA	224136	56332	GATCACTTGAGGCCAGGAGT	268723	100919	TGTATTTTCCAAAGTGTGGC
179550	11746	GTCCCTGTCTGGTTAGGAAA	224137	56333	AGATCACTTGAGGCCAGGAG	268724	100920	CTGTATTTTCCAAAGTGTGG
179551	11747	AGTCCCTGTCTGGTTAGGAA	224138	56334	CAGATCACTTGAGGCCAGGA	268725	100921	TCTGTATTTTCCAAAGTGTG
179552	11748	AAGTCCCTGTCTGGTTAGGA	224139	56335	GCAGATCACTTGAGGCCAGG	268726	100922	GTCTGTATTTTCCAAAGTGT
179553	11749	CAAGTCCCTGTCTGGTTAGG	224140	56336	GGCAGATCACTTGAGGCCAG	268727	100923	GGTCTGTATTTTCCAAAGTG
179554	11750	CCAAGTCCCTGTCTGGTTAG	224141	56337	AGGCAGATCACTTGAGGCCA	268728	100924	GGGTCTGTATTTTCCAAAGT
179555	11751	ACCAAGTCCCTGTCTGGTTA	224142	56338	CAGGCAGATCACTTGAGGCC	268729	100925	TGGGTCTGTATTTTCCAAAG
179556	11752	TACCAAGTCCCTGTCTGGTT	224143	56339	GCAGGCAGATCACTTGAGGC	268730	100926	ATGGGTCTGTATTTTCCAAA
179557	11753	GTACCAAGTCCCTGTCTGGT	224144	56340	GGCAGGCAGATCACTTGAGG	268731	100927	CATGGGTCTGTATTTTCCAA
179558	11754	TGTACCAAGTCCCTGTCTGG	224145	56341	AGGCAGGCAGATCACTTGAG	268732	100928	TCATGGGTCTGTATTTTCCA
179559	11755	CTGTACCAAGTCCCTGTCTG	224146	56342	CAGGCAGGCAGATCACTTGA	268733	100929	CTCATGGGTCTGTATTTTCC
179560	11756	TCTGTACCAAGTCCCTGTCT	224147	56343	TCAGGCAGGCAGATCACTTG	268734	100930	TCTCATGGGTCTGTATTTTC
179561	11757	TTCTGTACCAAGTCCCTGTC	224148	56344	CTCAGGCAGGCAGATCACTT	268735	100931	ATCTCATGGGTCTGTATTTT
179562	11758	ATTCTGTACCAAGTCCCTGT	224149	56345	GCTCAGGCAGGCAGATCACT	268736	100932	TATCTCATGGGTCTGTATTT
179563	11759	GATTCTGTACCAAGTCCCTG	224150	56346	GGCTCAGGCAGGCAGATCAC	268737	100933	CTATCTCATGGGTCTGTATT
179564	11760	AGATTCTGTACCAAGTCCCT	224151	56347	AGGCTCAGGCAGGCAGATCA	268738	100934	TCTATCTCATGGGTCTGTAT
179565	11761	GAGATTCTGTACCAAGTCCC	224152	56348	GAGGCTCAGGCAGGCAGATC	268739	100935	TTCTATCTCATGGGTCTGTA
179566	11762	TGAGATTCTGTACCAAGTCC	224153	56349	GGAGGCTCAGGCAGGCAGAT	268740	100936	ATTCTATCTCATGGGTCTGT
179567	11763	ATGAGATTCTGTACCAAGTC	224154	56350	CGGAGGCTCAGGCAGGCAGA	268741	100937	TATTCTATCTCATGGGTCTG
179568	11764	TATGAGATTCTGTACCAAGT	224155	56351	CCGGAGGCTCAGGCAGGCAG	268742	100938	GTATTCTATCTCATGGGTCT
179569	11765	ATATGAGATTCTGTACCAAG	224156	56352	TCCGGAGGCTCAGGCAGGCA	268743	100939	GGTATTCTATCTCATGGGTC
179570	11766	AATATGAGATTCTGTACCAA	224157	56353	TTCCGGAGGCTCAGGCAGGC	268744	100940	TGGTATTCTATCTCATGGGT
179571	11767	GAATATGAGATTCTGTACCA	224158	56354	CTTCCGGAGGCTCAGGCAGG	268745	100941	CTGGTATTCTATCTCATGGG
179572	11768	AGAATATGAGATTCTGTACC	224159	56355	ACTTCCGGAGGCTCAGGCAG	268746	100942	TCTGGTATTCTATCTCATGG
179573	11769	TAGAATATGAGATTCTGTAC	224160	56356	CACTTCCGGAGGCTCAGGCA	268747	100943	GTCTGGTATTCTATCTCATG
179574	11770	TTAGAATATGAGATTCTGTA	224161	56357	GCACTTCCGGAGGCTCAGGC	268748	100944	AGTCTGGTATTCTATCTCAT
179575	11771	ATTAGAATATGAGATTCTGT	224162	56358	AGCACTTCCGGAGGCTCAGG	268749	100945	CAGTCTGGTATTCTATCTCA
179576	11772	AATTAGAATATGAGATTCTG	224163	56359	CAGCACTTCCGGAGGCTCAG	268750	100946	ACAGTCTGGTATTCTATCTC
179577	11773	TAATTAGAATATGAGATTCT	224164	56360	CCAGCACTTCCGGAGGCTCA	268751	100947	AACAGTCTGGTATTCTATCT
179578	11774	ATAATTAGAATATGAGATTC	224165	56361	CCCAGCACTTCCGGAGGCTC	268752	100948	CAACAGTCTGGTATTCTATC
179579	11775	CATAATTAGAATATGAGATT	224166	56362	TCCCAGCACTTCCGGAGGCT	268753	100949	TCAACAGTCTGGTATTCTAT
179580	11776	GCATAATTAGAATATGAGAT	224167	56363	ATCCCAGCACTTCCGGAGGC	268754	100950	TTCAACAGTCTGGTATTCTA
179581	11777	GGCATAATTAGAATATGAGA	224168	56364	AATCCCAGCACTTCCGGAGG	268755	100951	CTTCAACAGTCTGGTATTCT
179582	11778	AGGCATAATTAGAATATGAG	224169	56365	AAATCCCAGCACTTCCGGAG	268756	100952	ACTTCAACAGTCTGGTATTC
179583	11779	TAGGCATAATTAGAATATGA	224170	56366	GAAATCCCAGCACTTCCGGA	268757	100953	CACTTCAACAGTCTGGTATT
179584	11780	CTAGGCATAATTAGAATATG	224171	56367	TGAAATCCCAGCACTTCCGG	268758	100954	ACACTTCAACAGTCTGGTAT
179585	11781	CCTAGGCATAATTAGAATAT	224172	56368	CTGAAATCCCAGCACTTCCG	268759	100955	TACACTTCAACAGTCTGGTA
179586	11782	TCCTAGGCATAATTAGAATA	224173	56369	CCTGAAATCCCAGCACTTCC	268760	100956	TTACACTTCAACAGTCTGGT
179587	11783	CTCCTAGGCATAATTAGAAT	224174	56370	ACCTGAAATCCCAGCACTTC	268761	100957	GTTACACTTCAACAGTCTGG
179588	11784	GCTCCTAGGCATAATTAGAA	224175	56371	CACCTGAAATCCCAGCACTT	268762	100958	CGTTACACTTCAACAGTCTG
179589	11785	TGCTCCTAGGCATAATTAGA	224176	56372	ACACCTGAAATCCCAGCACT	268763	100959	CCGTTACACTTCAACAGTCT
179590	11786	CTGCTCCTAGGCATAATTAG	224177	56373	CACACCTGAAATCCCAGCAC	268764	100960	CCCGTTACACTTCAACAGTC
179591	11787	GCTGCTCCTAGGCATAATTA	224178	56374	TCACACCTGAAATCCCAGCA	268765	100961	CCCCGTTACACTTCAACAGT
179592	11788	GGCTGCTCCTAGGCATAATT	224179	56375	CTCACACCTGAAATCCCAGC	268766	100962	CCCCCGTTACACTTCAACAG
179593	11789	AGGCTGCTCCTAGGCATAAT	224180	56376	GCTCACACCTGAAATCCCAG	268767	100963	GCCCCCGTTACACTTCAACA
179594	11790	GAGGCTGCTCCTAGGCATAA	224181	56377	GGCTCACACCTGAAATCCCA	268768	100964	GGCCCCCGTTACACTTCAAC
179595	11791	AGAGGCTGCTCCTAGGCATA	224182	56378	TGGCTCACACCTGAAATCCC	268769	100965	AGGCCCCCGTTACACTTCAA
179596	11792	GAGAGGCTGCTCCTAGGCAT	224183	56379	GTGGCTCACACCTGAAATCC	268770	100966	CAGGCCCCCGTTACACTTCA
179597	11793	GGAGAGGCTGCTCCTAGGCA	224184	56380	GGTGGCTCACACCTGAAATC	268771	100967	CCAGGCCCCCGTTACACTTC
179598	11794	GGGAGAGGCTGCTCCTAGGC	224185	56381	CGGTGGCTCACACCTGAAAT	268772	100968	CCCAGGCCCCCGTTACACTT
179599	11795	GGGGAGAGGCTGCTCCTAGG	224186	56382	GCGGTGGCTCACACCTGAAA	268773	100969	TCCCAGGCCCCCGTTACACT
179600	11796	TGGGGAGAGGCTGCTCCTAG	224187	56383	TGCGGTGGCTCACACCTGAA	268774	100970	TTCCCAGGCCCCCGTTACAC
179601	11797	GTGGGGAGAGGCTGCTCCTA	224188	56384	GTGCGGTGGCTCACACCTGA	268775	100971	CTTCCCAGGCCCCCGTTACA
179602	11798	GGTGGGGAGAGGCTGCTCCT	224189	56385	AGTGCGGTGGCTCACACCTG	268776	100972	ACTTCCCAGGCCCCCGTTAC
179603	11799	TGGTGGGGAGAGGCTGCTCC	224190	56386	GAGTGCGGTGGCTCACACCT	268777	100973	CACTTCCCAGGCCCCCGTTA
179604	11800	GTGGTGGGGAGAGGCTGCTC	224191	56387	CGAGTGCGGTGGCTCACACC	268778	100974	GCACTTCCCAGGCCCCCGTT
179605	11801	AGTGGTGGGGAGAGGCTGCT	224192	56388	CCGAGTGCGGTGGCTCACAC	268779	100975	TGCACTTCCCAGGCCCCCGT
179606	11802	GAGTGGTGGGGAGAGGCTGC	224193	56389	GCCGAGTGCGGTGGCTCACA	268780	100976	CTGCACTTCCCAGGCCCCCG
179607	11803	TGAGTGGTGGGGAGAGGCTG	224194	56390	AGCCGAGTGCGGTGGCTCAC	268781	100977	ACTGCACTTCCCAGGCCCCC
179608	11804	GTGAGTGGTGGGGAGAGGCT	224195	56391	GAGCCGAGTGCGGTGGCTCA	268782	100978	TACTGCACTTCCCAGGCCCC
179609	11805	TGTGAGTGGTGGGGAGAGGC	224196	56392	GGAGCCGAGTGCGGTGGCTC	268783	100979	TTACTGCACTTCCCAGGCCC
179610	11806	CTGTGAGTGGTGGGGAGAGG	224197	56393	TGGAGCCGAGTGCGGTGGCT	268784	100980	GTTACTGCACTTCCCAGGCC

179611	11807	ACTGTGAGTGGTGGGGAGAG	224198	56394	GTGGAGCCGAGTGCGGTGGC	268785	100981	TGTTACTGCACTTCCCAGGC
179612	11808	CACTGTGAGTGGTGGGGAGA	224199	56395	TGTGGAGCCGAGTGCGGTGG	268786	100982	CTGTTACTGCACTTCCCAGG
179613	11809	ACACTGTGAGTGGTGGGGAG	224200	56396	GTGTGGAGCCGAGTGCGGTG	268787	100983	TCTGTTACTGCACTTCCCAG
179614	11810	AACACTGTGAGTGGTGGGGA	224201	56397	AGTGTGGAGCCGAGTGCGGT	268788	100984	TTCTGTTACTGCACTTCCCA
179615	11811	AAACACTGTGAGTGGTGGGG	224202	56398	AAGTGTGGAGCCGAGTGCGG	268789	100985	CTTCTGTTACTGCACTTCCC
179616	11812	TAAACACTGTGAGTGGTGGG	224203	56399	AAAGTGTGGAGCCGAGTGCG	268790	100986	GCTTCTGTTACTGCACTTCC
179617	11813	CTAAACACTGTGAGTGGTGG	224204	56400	AAAAGTGTGGAGCCGAGTGC	268791	100987	TGCTTCTGTTACTGCACTTC
179618	11814	GCTAAACACTGTGAGTGGTG	224205	56401	GAAAAGTGTGGAGCCGAGTG	268792	100988	TTGCTTCTGTTACTGCACTT
179619	11815	TGCTAAACACTGTGAGTGGT	224206	56402	TGAAAAGTGTGGAGCCGAGT	268793	100989	CTTGCTTCTGTTACTGCACT
179620	11816	ATGCTAAACACTGTGAGTGG	224207	56403	GTGAAAAGTGTGGAGCCGAG	268794	100990	ACTTGCTTCTGTTACTGCAC
179621	11817	CATGCTAAACACTGTGAGTG	224208	56404	AGTGAAAAGTGTGGAGCCGA	268795	100991	AACTTGCTTCTGTTACTGCA
179622	11818	ACATGCTAAACACTGTGAGT	224209	56405	AAGTGAAAAGTGTGGAGCCG	268796	100992	AAACTTGCTTCTGTTACTGC
179623	11819	CACATGCTAAACACTGTGAG	224210	56406	TAAGTGAAAAGTGTGGAGCC	268797	100993	CAAACTTGCTTCTGTTACTG
179624	11820	TCACATGCTAAACACTGTGA	224211	56407	ATAAGTGAAAAGTGTGGAGC	268798	100994	TCAAACTTGCTTCTGTTACT
179625	11821	GTCACATGCTAAACACTGTG	224212	56408	AATAAGTGAAAAGTGTGGAG	268799	100995	CTCAAACTTGCTTCTGTTAC
179626	11822	TGTCACATGCTAAACACTGT	224213	56409	TAATAAGTGAAAAGTGTGGA	268800	100996	CCTCAAACTTGCTTCTGTTA
179627	11823	CTGTCACATGCTAAACACTG	224214	56410	TTAATAAGTGAAAAGTGTGG	268801	100997	CCCTCAAACTTGCTTCTGTT
179628	11824	CCTGTCACATGCTAAACACT	224215	56411	TTTAATAAGTGAAAAGTGTG	268802	100998	ACCCTCAAACTTGCTTCTGT
179629	11825	TCCTGTCACATGCTAAACAC	224216	56412	TTTTAATAAGTGAAAAGTGT	268803	100999	TACCCTCAAACTTGCTTCTG
179630	11826	TTCCTGTCACATGCTAAACA	224217	56413	CTTTTAATAAGTGAAAAGTG	268804	101000	TTACCCTCAAACTTGCTTCT
179631	11827	ATTCCTGTCACATGCTAAAC	224218	56414	TCTTTTAATAAGTGAAAAGT	268805	101001	TTTACCCTCAAACTTGCTTC
179632	11828	GATTCCTGTCACATGCTAAA	224219	56415	GTCTTTTAATAAGTGAAAAG	268806	101002	CTTTACCCTCAAACTTGCTT
179633	11829	CGATTCCTGTCACATGCTAA	224220	56416	AGTCTTTTAATAAGTGAAAA	268807	101003	CCTTTACCCTCAAACTTGCT
179634	11830	TCGATTCCTGTCACATGCTA	224221	56417	CAGTCTTTTAATAAGTGAAA	268808	101004	TCCTTTACCCTCAAACTTGC
179635	11831	ATCGATTCCTGTCACATGCT	224222	56418	ACAGTCTTTTAATAAGTGAA	268809	101005	GTCCTTTACCCTCAAACTTG
179636	11832	AATCGATTCCTGTCACATGC	224223	56419	CACAGTCTTTTAATAAGTGA	268810	101006	TGTCCTTTACCCTCAAACTT
179637	11833	TAATCGATTCCTGTCACATG	224224	56420	CCACAGTCTTTTAATAAGTG	268811	101007	GTGTCCTTTACCCTCAAACT
179638	11834	TTAATCGATTCCTGTCACAT	224225	56421	ACCACAGTCTTTTAATAAGT	268812	101008	GGTGTCCTTTACCCTCAAAC
179639	11835	CTTAATCGATTCCTGTCACA	224226	56422	CACCACAGTCTTTTAATAAG	268813	101009	GGGTGTCCTTTACCCTCAAA
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179641	11837	GCCTTAATCGATTCCTGTCA	224228	56424	GACACCACAGTCTTTTAATA	268815	101011	CTGGGTGTCCTTTACCCTCA
179642	11838	TGCCTTAATCGATTCCTGTC	224229	56425	GGACACCACAGTCTTTTAAT	268816	101012	TCTGGGTGTCCTTTACCCTC
179643	11839	ATGCCTTAATCGATTCCTGT	224230	56426	TGGACACCACAGTCTTTTAA	268817	101013	CTCTGGGTGTCCTTTACCCT
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179645	11841	TCATGCCTTAATCGATTCCT	224232	56428	GATGGACACCACAGTCTTTT	268819	101015	TCCTCTGGGTGTCCTTTACC
179646	11842	CTCATGCCTTAATCGATTCC	224233	56429	TGATGGACACCACAGTCTTT	268820	101016	CTCCTCTGGGTGTCCTTTAC
179647	11843	ACTCATGCCTTAATCGATTC	224234	56430	TTGATGGACACCACAGTCTT	268821	101017	CCTCCTCTGGGTGTCCTTTA
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179652	11848	TAATCACTCATGCCTTAATC	224239	56435	ATCCATTGATGGACACCACA	268826	101022	CCCTCCCTCCTCTGGGTGTC
179653	11849	TTAATCACTCATGCCTTAAT	224240	56436	CATCCATTGATGGACACCAC	268827	101023	TCCCTCCCTCCTCTGGGTGT
179654	11850	TTTAATCACTCATGCCTTAA	224241	56437	TCATCCATTGATGGACACCA	268828	101024	GTCCCTCCCTCCTCTGGGTG
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179661	11857	GCTTTAATTTAATCACTCAT	224248	56444	TATTCATTCATCCATTGATG	268835	101031	AGATGCTGTCCCTCCCTCCT
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179663	11859	TGGCTTTAATTTAATCACTC	224250	56446	TTTATTCATTCATCCATTGA	268837	101033	GCAGATGCTGTCCCTCCCTC
179664	11860	CTGGCTTTAATTTAATCACT	224251	56447	GTTTATTCATTCATCCATTG	268838	101034	TGCAGATGCTGTCCCTCCCT
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179666	11862	GCCTGGCTTTAATTTAATCA	224253	56449	TGGTTTATTCATTCATCCAT	268840	101036	CATGCAGATGCTGTCCCTCC
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179670	11866	CAATGCCTGGCTTTAATTTA	224257	56453	ACATTGGTTTATTCATTCAT	268844	101040	TCTCCATGCAGATGCTGTCC
179671	11867	TCAATGCCTGGCTTTAATTT	224258	56454	CACATTGGTTTATTCATTCA	268845	101041	CTCTCCATGCAGATGCTGTC
179672	11868	GTCAATGCCTGGCTTTAATT	224259	56455	CCACATTGGTTTATTCATTC	268846	101042	CCTCTCCATGCAGATGCTGT
179673	11869	AGTCAATGCCTGGCTTTAAT	224260	56456	TCCACATTGGTTTATTCATT	268847	101043	TCCTCTCCATGCAGATGCTG
179674	11870	AAGTCAATGCCTGGCTTTAA	224261	56457	GTCCACATTGGTTTATTCAT	268848	101044	CTCCTCTCCATGCAGATGCT
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179676	11872	CCAAGTCAATGCCTGGCTTT	224263	56459	TAGTCCACATTGGTTTATTC	268850	101046	TTCTCCTCTCCATGCAGATG
179677	11873	TCCAAGTCAATGCCTGGCTT	224264	56460	ATAGTCCACATTGGTTTATT	268851	101047	CTTCTCCTCTCCATGCAGAT
179678	11874	ATCCAAGTCAATGCCTGGCT	224265	56461	GATAGTCCACATTGGTTTAT	268852	101048	TCTTCTCCTCTCCATGCAGA
179679	11875	CATCCAAGTCAATGCCTGGC	224266	56462	GGATAGTCCACATTGGTTTA	268853	101049	CTCTTCTCCTCTCCATGCAG
179680	11876	CCATCCAAGTCAATGCCTGG	224267	56463	GGGATAGTCCACATTGGTTT	268854	101050	TCTCTTCTCCTCTCCATGCA
179681	11877	ACCATCCAAGTCAATGCCTG	224268	56464	AGGGATAGTCCACATTGGTT	268855	101051	GTCTCTTCTCCTCTCCATGC
179682	11878	CACCATCCAAGTCAATGCCT	224269	56465	GAGGGATAGTCCACATTGGT	268856	101052	GGTCTCTTCTCCTCTCCATG

179683	11879	ACACCATCCAAGTCAATGCC	224270	56466	GGAGGGATAGTCCACATTGG	268857	101053	GGGTCTCTTCTCCTCTCCAT
179684	11880	TACACCATCCAAGTCAATGC	224271	56467	GGGAGGGATAGTCCACATTG	268858	101054	GGGGTCTCTTCTCCTCTCCA
179685	11881	TTACACCATCCAAGTCAATG	224272	56468	TGGGAGGGATAGTCCACATT	268859	101055	GGGGGTCTCTTCTCCTCTCC
179686	11882	ATTACACCATCCAAGTCAAT	224273	56469	ATGGGAGGGATAGTCCACAT	268860	101056	GGGGGGTCTCTTCTCCTCTC
179687	11883	TATTACACCATCCAAGTCAA	224274	56470	AATGGGAGGGATAGTCCACA	268861	101057	TGGGGGGTCTCTTCTCCTCT
179688	11884	ATATTACACCATCCAAGTCA	224275	56471	TAATGGGAGGGATAGTCCAC	268862	101058	CTGGGGGGTCTCTTCTCCTC
179689	11885	AATATTACACCATCCAAGTC	224276	56472	GTAATGGGAGGGATAGTCCA	268863	101059	GCTGGGGGGTCTCTTCTCCT
179690	11886	GAATATTACACCATCCAAGT	224277	56473	GGTAATGGGAGGGATAGTCC	268864	101060	TGCTGGGGGGTCTCTTCTCC
179691	11887	AGAATATTACACCATCCAAG	224278	56474	GGGTAATGGGAGGGATAGTC	268865	101061	CTGCTGGGGGGTCTCTTCTC
179692	11888	CAGAATATTACACCATCCAA	224279	56475	TGGGTAATGGGAGGGATAGT	268866	101062	GCTGCTGGGGGGTCTCTTCT
179693	11889	TCAGAATATTACACCATCCA	224280	56476	TTGGGTAATGGGAGGGATAG	268867	101063	AGCTGCTGGGGGGTCTCTTC
179694	11890	GTCAGAATATTACACCATCC	224281	56477	CTTGGGTAATGGGAGGGATA	268868	101064	AAGCTGCTGGGGGGTCTCTT
179695	11891	TGTCAGAATATTACACCATC	224282	56478	CCTTGGGTAATGGGAGGGAT	268869	101065	GAAGCTGCTGGGGGGTCTCT
179696	11892	ATGTCAGAATATTACACCAT	224283	56479	TCCTTGGGTAATGGGAGGGA	268870	101066	GGAAGCTGCTGGGGGGTCTC
179697	11893	GATGTCAGAATATTACACCA	224284	56480	TTCCTTGGGTAATGGGAGGG	268871	101067	TGGAAGCTGCTGGGGGGTCT
179698	11894	AGATGTCAGAATATTACACC	224285	56481	ATTCCTTGGGTAATGGGAGG	268872	101068	CTGGAAGCTGCTGGGGGGTC
179699	11895	CAGATGTCAGAATATTACAC	224286	56482	CATTCCTTGGGTAATGGGAG	268873	101069	CCTGGAAGCTGCTGGGGGGT
179700	11896	ACAGATGTCAGAATATTACA	224287	56483	TCATTCCTTGGGTAATGGGA	268874	101070	CCCTGGAAGCTGCTGGGGGG
179701	11897	AACAGATGTCAGAATATTAC	224288	56484	TTCATTCCTTGGGTAATGGG	268875	101071	ACCCTGGAAGCTGCTGGGGG
179702	11898	AAACAGATGTCAGAATATTA	224289	56485	CTTCATTCCTTGGGTAATGG	268876	101072	CACCCTGGAAGCTGCTGGGG
179703	11899	CAAACAGATGTCAGAATATT	224290	56486	GCTTCATTCCTTGGGTAATG	268877	101073	ACACCCTGGAAGCTGCTGGG
179704	11900	CCAAACAGATGTCAGAATAT	224291	56487	TGCTTCATTCCTTGGGTAAT	268878	101074	AACACCCTGGAAGCTGCTGG
179705	11901	ACCAAACAGATGTCAGAATA	224292	56488	GTGCTTCATTCCTTGGGTAA	268879	101075	CAACACCCTGGAAGCTGCTG
179706	11902	CACCAAACAGATGTCAGAAT	224293	56489	CGTGCTTCATTCCTTGGGTA	268880	101076	CCAACACCCTGGAAGCTGCT
179707	11903	ACACCAAACAGATGTCAGAA	224294	56490	CCGTGCTTCATTCCTTGGGT	268881	101077	TCCAACACCCTGGAAGCTGC
179708	11904	GACACCAAACAGATGTCAGA	224295	56491	TCCGTGCTTCATTCCTTGGG	268882	101078	TTCCAACACCCTGGAAGCTG
179709	11905	TGACACCAAACAGATGTCAG	224296	56492	CTCCGTGCTTCATTCCTTGG	268883	101079	CTTCCAACACCCTGGAAGCT
179710	11906	TTGACACCAAACAGATGTCA	224297	56493	GCTCCGTGCTTCATTCCTTG	268884	101080	CCTTCCAACACCCTGGAAGC
179711	11907	TTTGACACCAAACAGATGTC	224298	56494	GGCTCCGTGCTTCATTCCTT	268885	101081	CCCTTCCAACACCCTGGAAG
179712	11908	CTTTGACACCAAACAGATGT	224299	56495	CGGCTCCGTGCTTCATTCCT	268886	101082	ACCCTTCCAACACCCTGGAA
179713	11909	CCTTTGACACCAAACAGATG	224300	56496	ACGGCTCCGTGCTTCATTCC	268887	101083	CACCCTTCCAACACCCTGGA
179714	11910	GCCTTTGACACCAAACAGAT	224301	56497	CACGGCTCCGTGCTTCATTC	268888	101084	GCACCCTTCCAACACCCTGG
179715	11911	TGCCTTTGACACCAAACAGA	224302	56498	GCACGGCTCCGTGCTTCATT	268889	101085	CGCACCCTTCCAACACCCTG
179716	11912	GTGCCTTTGACACCAAACAG	224303	56499	GGCACGGCTCCGTGCTTCAT	268890	101086	GCGCACCCTTCCAACACCCT
179717	11913	CGTGCCTTTGACACCAAACA	224304	56500	TGGCACGGCTCCGTGCTTCA	268891	101087	AGCGCACCCTTCCAACACCC
179718	11914	CCGTGCCTTTGACACCAAAC	224305	56501	TTGGCACGGCTCCGTGCTTC	268892	101088	TAGCGCACCCTTCCAACACC
179719	11915	CCCGTGCCTTTGACACCAAA	224306	56502	CTTGGCACGGCTCCGTGCTT	268893	101089	CTAGCGCACCCTTCCAACAC
179720	11916	CCCCGTGCCTTTGACACCAA	224307	56503	TCTTGGCACGGCTCCGTGCT	268894	101090	ACTAGCGCACCCTTCCAACA
179721	11917	GCCCCGTGCCTTTGACACCA	224308	56504	ATCTTGGCACGGCTCCGTGC	268895	101091	TACTAGCGCACCCTTCCAAC
179722	11918	TGCCCCGTGCCTTTGACACC	224309	56505	GATCTTGGCACGGCTCCGTG	268896	101092	TTACTAGCGCACCCTTCCAA
179723	11919	CTGCCCCGTGCCTTTGACAC	224310	56506	AGATCTTGGCACGGCTCCGT	268897	101093	GTTACTAGCGCACCCTTCCA
179724	11920	CCTGCCCCGTGCCTTTGACA	224311	56507	CAGATCTTGGCACGGCTCCG	268898	101094	AGTTACTAGCGCACCCTTCC
179725	11921	GCCTGCCCCGTGCCTTTGAC	224312	56508	CCAGATCTTGGCACGGCTCC	268899	101095	CAGTTACTAGCGCACCCTTC
179726	11922	CGCCTGCCCCGTGCCTTTGA	224313	56509	TCCAGATCTTGGCACGGCTC	268900	101096	GCAGTTACTAGCGCACCCTT
179727	11923	GCGCCTGCCCCGTGCCTTTG	224314	56510	ATCCAGATCTTGGCACGGCT	268901	101097	AGCAGTTACTAGCGCACCCT
179728	11924	CGCGCCTGCCCCGTGCCTTT	224315	56511	AATCCAGATCTTGGCACGGC	268902	101098	TAGCAGTTACTAGCGCACCC
179729	11925	ACGCGCCTGCCCCGTGCCTT	224316	56512	GAATCCAGATCTTGGCACGG	268903	101099	ATAGCAGTTACTAGCGCACC
179730	11926	AACGCGCCTGCCCCGTGCCT	224317	56513	TGAATCCAGATCTTGGCACG	268904	101100	CATAGCAGTTACTAGCGCAC
179731	11927	TAACGCGCCTGCCCCGTGCC	224318	56514	GTGAATCCAGATCTTGGCAC	268905	101101	GCATAGCAGTTACTAGCGCA
179732	11928	TTAACGCGCCTGCCCCGTGC	224319	56515	TGTGAATCCAGATCTTGGCA	268906	101102	TGCATAGCAGTTACTAGCGC
179733	11929	ATTAACGCGCCTGCCCCGTG	224320	56516	CTGTGAATCCAGATCTTGGC	268907	101103	ATGCATAGCAGTTACTAGCG
179734	11930	AATTAACGCGCCTGCCCCGT	224321	56517	ACTGTGAATCCAGATCTTGG	268908	101104	CATGCATAGCAGTTACTAGC
179735	11931	CAATTAACGCGCCTGCCCCG	224322	56518	CACTGTGAATCCAGATCTTG	268909	101105	CCATGCATAGCAGTTACTAG
179736	11932	TCAATTAACGCGCCTGCCCC	224323	56519	TCACTGTGAATCCAGATCTT	268910	101106	GCCATGCATAGCAGTTACTA
179737	11933	TTCAATTAACGCGCCTGCCC	224324	56520	TTCACTGTGAATCCAGATCT	268911	101107	TGCCATGCATAGCAGTTACT
179738	11934	GTTCAATTAACGCGCCTGCC	224325	56521	TTTCACTGTGAATCCAGATC	268912	101108	CTGCCATGCATAGCAGTTAC
179739	11935	AGTTCAATTAACGCGCCTGC	224326	56522	CTTTCACTGTGAATCCAGAT	268913	101109	CCTGCCATGCATAGCAGTTA
179740	11936	CAGTTCAATTAACGCGCCTG	224327	56523	TCTTTCACTGTGAATCCAGA	268914	101110	ACCTGCCATGCATAGCAGTT
179741	11937	GCAGTTCAATTAACGCGCCT	224328	56524	TTCTTTCACTGTGAATCCAG	268915	101111	CACCTGCCATGCATAGCAGT
179742	11938	AGCAGTTCAATTAACGCGCC	224329	56525	CTTCTTTCACTGTGAATCCA	268916	101112	CCACCTGCCATGCATAGCAG
179743	11939	AAGCAGTTCAATTAACGCGC	224330	56526	GCTTCTTTCACTGTGAATCC	268917	101113	CCCACCTGCCATGCATAGCA
179744	11940	CAAGCAGTTCAATTAACGCG	224331	56527	GGCTTCTTTCACTGTGAATC	268918	101114	CCCCACCTGCCATGCATAGC
179745	11941	GCAAGCAGTTCAATTAACGC	224332	56528	TGGCTTCTTTCACTGTGAAT	268919	101115	TCCCCACCTGCCATGCATAG
179746	11942	TGCAAGCAGTTCAATTAACG	224333	56529	CTGGCTTCTTTCACTGTGAA	268920	101116	TTCCCCACCTGCCATGCATA
179747	11943	GTGCAAGCAGTTCAATTAAC	224334	56530	ACTGGCTTCTTTCACTGTGA	268921	101117	GTTCCCCACCTGCCATGCAT
179748	11944	GGTGCAAGCAGTTCAATTAA	224335	56531	GACTGGCTTCTTTCACTGTG	268922	101118	AGTTCCCCACCTGCCATGCA
179749	11945	AGGTGCAAGCAGTTCAATTA	224336	56532	TGACTGGCTTCTTTCACTGT	268923	101119	CAGTTCCCCACCTGCCATGC
179750	11946	CAGGTGCAAGCAGTTCAATT	224337	56533	GTGACTGGCTTCTTTCACTG	268924	101120	ACAGTTCCCCACCTGCCATG
179751	11947	CCAGGTGCAAGCAGTTCAAT	224338	56534	GGTGACTGGCTTCTTTCACT	268925	101121	TACAGTTCCCCACCTGCCAT
179752	11948	GCCAGGTGCAAGCAGTTCAA	224339	56535	TGGTGACTGGCTTCTTTCAC	268926	101122	GTACAGTTCCCCACCTGCCA
179753	11949	TGCCAGGTGCAAGCAGTTCA	224340	56536	TTGGTGACTGGCTTCTTTCA	268927	101123	CGTACAGTTCCCCACCTGCC
179754	11950	ATGCCAGGTGCAAGCAGTTC	224341	56537	TTTGGTGACTGGCTTCTTTC	268928	101124	ACGTACAGTTCCCCACCTGC

179755	11951	AATGCCAGGTGCAAGCAGTT	224342	56538	TTTTGGTGACTGGCTTCTTT	268929	101125	GACGTACAGTTCCCCACCTG
179756	11952	AAATGCCAGGTGCAAGCAGT	224343	56539	CTTTTGGTGACTGGCTTCTT	268930	101126	TGACGTACAGTTCCCCACCT
179757	11953	CAAATGCCAGGTGCAAGCAG	224344	56540	GCTTTTGGTGACTGGCTTCT	268931	101127	CTGACGTACAGTTCCCCACC
179758	11954	TCAAATGCCAGGTGCAAGCA	224345	56541	GGCTTTTGGTGACTGGCTTC	268932	101128	CCTGACGTACAGTTCCCCAC
179759	11955	TTCAAATGCCAGGTGCAAGC	224346	56542	TGGCTTTTGGTGACTGGCTT	268933	101129	CCCTGACGTACAGTTCCCCA
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179761	11957	AATTCAAATGCCAGGTGCAA	224348	56544	CGTGGCTTTTGGTGACTGGC	268935	101131	TGCCCTGACGTACAGTTCCC
179762	11958	CAATTCAAATGCCAGGTGCA	224349	56545	ACGTGGCTTTTGGTGACTGG	268936	101132	GTGCCCTGACGTACAGTTCC
179763	11959	TCAATTCAAATGCCAGGTGC	224350	56546	CACGTGGCTTTTGGTGACTG	268937	101133	TGTGCCCTGACGTACAGTTC
179764	11960	CTCAATTCAAATGCCAGGTG	224351	56547	GCACGTGGCTTTTGGTGACT	268938	101134	CTGTGCCCTGACGTACAGTT
179765	11961	GCTCAATTCAAATGCCAGGT	224352	56548	AGCACGTGGCTTTTGGTGAC	268939	101135	GCTGTGCCCTGACGTACAGT
179766	11962	GGCTCAATTCAAATGCCAGG	224353	56549	CAGCACGTGGCTTTTGGTGA	268940	101136	TGCTGTGCCCTGACGTACAG
179767	11963	TGGCTCAATTCAAATGCCAG	224354	56550	ACAGCACGTGGCTTTTGGTG	268941	101137	CTGCTGTGCCCTGACGTACA
179768	11964	CTGGCTCAATTCAAATGCCA	224355	56551	CACAGCACGTGGCTTTTGGT	268942	101138	GCTGCTGTGCCCTGACGTAC
179769	11965	TCTGGCTCAATTCAAATGCC	224356	56552	ACACAGCACGTGGCTTTTGG	268943	101139	TGCTGCTGTGCCCTGACGTA
179770	11966	CTCTGGCTCAATTCAAATGC	224357	56553	CACACAGCACGTGGCTTTTG	268944	101140	ATGCTGCTGTGCCCTGACGT
179771	11967	GCTCTGGCTCAATTCAAATG	224358	56554	TCACACAGCACGTGGCTTTT	268945	101141	CATGCTGCTGTGCCCTGACG
179772	11968	CGCTCTGGCTCAATTCAAAT	224359	56555	GTCACACAGCACGTGGCTTT	268946	101142	TCATGCTGCTGTGCCCTGAC
179773	11969	CCGCTCTGGCTCAATTCAAA	224360	56556	AGTCACACAGCACGTGGCTT	268947	101143	TTCATGCTGCTGTGCCCTGA
179774	11970	CCCGCTCTGGCTCAATTCAA	224361	56557	AAGTCACACAGCACGTGGCT	268948	101144	CTTCATGCTGCTGTGCCCTG
179775	11971	CCCCGCTCTGGCTCAATTCA	224362	56558	GAAGTCACACAGCACGTGGC	268949	101145	GCTTCATGCTGCTGTGCCCT
179776	11972	GCCCCGCTCTGGCTCAATTC	224363	56559	GGAAGTCACACAGCACGTGG	268950	101146	CGCTTCATGCTGCTGTGCCC
179777	11973	AGCCCCGCTCTGGCTCAATT	224364	56560	GGGAAGTCACACAGCACGTG	268951	101147	CCGCTTCATGCTGCTGTGCC
179778	11974	TAGCCCCGCTCTGGCTCAAT	224365	56561	AGGGAAGTCACACAGCACGT	268952	101148	ACCGCTTCATGCTGCTGTGC
179779	11975	TTAGCCCCGCTCTGGCTCAA	224366	56562	AAGGGAAGTCACACAGCACG	268953	101149	TACCGCTTCATGCTGCTGTG
179780	11976	TTTAGCCCCGCTCTGGCTCA	224367	56563	TAAGGGAAGTCACACAGCAC	268954	101150	ATACCGCTTCATGCTGCTGT
179781	11977	CTTTAGCCCCGCTCTGGCTC	224368	56564	ATAAGGGAAGTCACACAGCA	268955	101151	CATACCGCTTCATGCTGCTG
179782	11978	ACTTTAGCCCCGCTCTGGCT	224369	56565	TATAAGGGAAGTCACACAGC	268956	101152	CCATACCGCTTCATGCTGCT
179783	11979	GACTTTAGCCCCGCTCTGGC	224370	56566	GTATAAGGGAAGTCACACAG	268957	101153	GCCATACCGCTTCATGCTGC
179784	11980	TGACTTTAGCCCCGCTCTGG	224371	56567	CGTATAAGGGAAGTCACACA	268958	101154	AGCCATACCGCTTCATGCTG
179785	11981	CTGACTTTAGCCCCGCTCTG	224372	56568	TCGTATAAGGGAAGTCACAC	268959	101155	GAGCCATACCGCTTCATGCT
179786	11982	ACTGACTTTAGCCCCGCTCT	224373	56569	TTCGTATAAGGGAAGTCACA	268960	101156	CGAGCCATACCGCTTCATGC
179787	11983	AACTGACTTTAGCCCCGCTC	224374	56570	TTTCGTATAAGGGAAGTCAC	268961	101157	ACGAGCCATACCGCTTCATG
179788	11984	AAACTGACTTTAGCCCCGCT	224375	56571	ATTTCGTATAAGGGAAGTCA	268962	101158	CACGAGCCATACCGCTTCAT
179789	11985	CAAACTGACTTTAGCCCCGC	224376	56572	TATTTCGTATAAGGGAAGTC	268963	101159	ACACGAGCCATACCGCTTCA
179790	11986	GCAAACTGACTTTAGCCCCG	224377	56573	ATATTTCGTATAAGGGAAGT	268964	101160	CACACGAGCCATACCGCTTC
179791	11987	GGCAAACTGACTTTAGCCCC	224378	56574	GATATTTCGTATAAGGGAAG	268965	101161	CCACACGAGCCATACCGCTT
179792	11988	AGGCAAACTGACTTTAGCCC	224379	56575	GGATATTTCGTATAAGGGAA	268966	101162	TCCACACGAGCCATACCGCT
179793	11989	AAGGCAAACTGACTTTAGCC	224380	56576	TGGATATTTCGTATAAGGGA	268967	101163	GTCCACACGAGCCATACCGC
179794	11990	GAAGGCAAACTGACTTTAGC	224381	56577	CTGGATATTTCGTATAAGGG	268968	101164	TGTCCACACGAGCCATACCG
179795	11991	TGAAGGCAAACTGACTTTAG	224382	56578	TCTGGATATTTCGTATAAGG	268969	101165	CTGTCCACACGAGCCATACC
179796	11992	GTGAAGGCAAACTGACTTTA	224383	56579	TTCTGGATATTTCGTATAAG	268970	101166	GCTGTCCACACGAGCCATAC
179797	11993	GGTGAAGGCAAACTGACTTT	224384	56580	CTTCTGGATATTTCGTATAA	268971	101167	AGCTGTCCACACGAGCCATA
179798	11994	GGGTGAAGGCAAACTGACTT	224385	56581	TCTTCTGGATATTTCGTATA	268972	101168	TAGCTGTCCACACGAGCCAT
179799	11995	AGGGTGAAGGCAAACTGACT	224386	56582	CTCTTCTGGATATTTCGTAT	268973	101169	CTAGCTGTCCACACGAGCCA
179800	11996	CAGGGTGAAGGCAAACTGAC	224387	56583	TCTCTTCTGGATATTTCGTA	268974	101170	CCTAGCTGTCCACACGAGCC
179801	11997	ACAGGGTGAAGGCAAACTGA	224388	56584	ATCTCTTCTGGATATTTCGT	268975	101171	CCCTAGCTGTCCACACGAGC
179802	11998	TACAGGGTGAAGGCAAACTG	224389	56585	TATCTCTTCTGGATATTTCG	268976	101172	TCCCTAGCTGTCCACACGAG
179803	11999	TTACAGGGTGAAGGCAAACT	224390	56586	GTATCTCTTCTGGATATTTC	268977	101173	GTCCCTAGCTGTCCACACGA
179804	12000	TTTACAGGGTGAAGGCAAAC	224391	56587	TGTATCTCTTCTGGATATTT	268978	101174	TGTCCCTAGCTGTCCACACG
179805	12001	ATTTACAGGGTGAAGGCAAA	224392	56588	ATGTATCTCTTCTGGATATT	268979	101175	CTGTCCCTAGCTGTCCACAC
179806	12002	CATTTACAGGGTGAAGGCAA	224393	56589	GATGTATCTCTTCTGGATAT	268980	101176	CCTGTCCCTAGCTGTCCACA
179807	12003	CCATTTACAGGGTGAAGGCA	224394	56590	GGATGTATCTCTTCTGGATA	268981	101177	GCCTGTCCCTAGCTGTCCAC
179808	12004	TCCATTTACAGGGTGAAGGC	224395	56591	TGGATGTATCTCTTCTGGAT	268982	101178	TGCCTGTCCCTAGCTGTCCA
179809	12005	CTCCATTTACAGGGTGAAGG	224396	56592	ATGGATGTATCTCTTCTGGA	268983	101179	CTGCCTGTCCCTAGCTGTCC
179810	12006	CCTCCATTTACAGGGTGAAG	224397	56593	CATGGATGTATCTCTTCTGG	268984	101180	CCTGCCTGTCCCTAGCTGTC
179811	12007	CCCTCCATTTACAGGGTGAA	224398	56594	CCATGGATGTATCTCTTCTG	268985	101181	GCCTGCCTGTCCCTAGCTGT
179812	12008	ACCCTCCATTTACAGGGTGA	224399	56595	ACCATGGATGTATCTCTTCT	268986	101182	CGCCTGCCTGTCCCTAGCTG
179813	12009	AACCCTCCATTTACAGGGTG	224400	56596	CACCATGGATGTATCTCTTC	268987	101183	ACGCCTGCCTGTCCCTAGCT
179814	12010	AAACCCTCCATTTACAGGGT	224401	56597	TCACCATGGATGTATCTCTT	268988	101184	CACGCCTGCCTGTCCCTAGC
179815	12011	GAAACCCTCCATTTACAGGG	224402	56598	GTCACCATGGATGTATCTCT	268989	101185	CCACGCCTGCCTGTCCCTAG
179816	12012	AGAAACCCTCCATTTACAGG	224403	56599	TGTCACCATGGATGTATCTC	268990	101186	TCCACGCCTGCCTGTCCCTA
179817	12013	GAGAAACCCTCCATTTACAG	224404	56600	CTGTCACCATGGATGTATCT	268991	101187	CTCCACGCCTGCCTGTCCCT
179818	12014	GGAGAAACCCTCCATTTACA	224405	56601	TCTGTCACCATGGATGTATC	268992	101188	GCTCCACGCCTGCCTGTCCC
179819	12015	CGGAGAAACCCTCCATTTAC	224406	56602	TTCTGTCACCATGGATGTAT	268993	101189	TGCTCCACGCCTGCCTGTCC
179820	12016	CCGGAGAAACCCTCCATTTA	224407	56603	TTTCTGTCACCATGGATGTA	268994	101190	CTGCTCCACGCCTGCCTGTC
179821	12017	TCCGGAGAAACCCTCCATTT	224408	56604	CTTTCTGTCACCATGGATGT	268995	101191	CCTGCTCCACGCCTGCCTGT
179822	12018	CTCCGGAGAAACCCTCCATT	224409	56605	ACTTTCTGTCACCATGGATG	268996	101192	GCCTGCTCCACGCCTGCCTG
179823	12019	GCTCCGGAGAAACCCTCCAT	224410	56606	TACTTTCTGTCACCATGGAT	268997	101193	TGCCTGCTCCACGCCTGCCT
179824	12020	CGCTCCGGAGAAACCCTCCA	224411	56607	CTACTTTCTGTCACCATGGA	268998	101194	ATGCCTGCTCCACGCCTGCC
179825	12021	ACGCTCCGGAGAAACCCTCC	224412	56608	TCTACTTTCTGTCACCATGG	268999	101195	GATGCCTGCTCCACGCCTGC
179826	12022	CACGCTCCGGAGAAACCCTC	224413	56609	ATCTACTTTCTGTCACCATG	269000	101196	GGATGCCTGCTCCACGCCTG

179827	12023	CCACGCTCCGGAGAAACCCT	224414	56610	CATCTACTTTCTGTCACCAT	269001	101197	AGGATGCCTGCTCCACGCCT
179828	12024	TCCACGCTCCGGAGAAACCC	224415	56611	TCATCTACTTTCTGTCACCA	269002	101198	CAGGATGCCTGCTCCACGCC
179829	12025	ATCCACGCTCCGGAGAAACC	224416	56612	CTCATCTACTTTCTGTCACC	269003	101199	ACAGGATGCCTGCTCCACGC
179830	12026	CATCCACGCTCCGGAGAAAC	224417	56613	GCTCATCTACTTTCTGTCAC	269004	101200	AACAGGATGCCTGCTCCACG
179831	12027	CCATCCACGCTCCGGAGAAA	224418	56614	TGCTCATCTACTTTCTGTCA	269005	101201	GAACAGGATGCCTGCTCCAC
179832	12028	ACCATCCACGCTCCGGAGAA	224419	56615	CTGCTCATCTACTTTCTGTC	269006	101202	AGAACAGGATGCCTGCTCCA
179833	12029	CACCATCCACGCTCCGGAGA	224420	56616	GCTGCTCATCTACTTTCTGT	269007	101203	CAGAACAGGATGCCTGCTCC
179834	12030	CCACCATCCACGCTCCGGAG	224421	56617	AGCTGCTCATCTACTTTCTG	269008	101204	TCAGAACAGGATGCCTGCTC
179835	12031	CCCACCATCCACGCTCCGGA	224422	56618	CAGCTGCTCATCTACTTTCT	269009	101205	TTCAGAACAGGATGCCTGCT
179836	12032	TCCCACCATCCACGCTCCGG	224423	56619	CCAGCTGCTCATCTACTTTC	269010	101206	CTTCAGAACAGGATGCCTGC
179837	12033	CTCCCACCATCCACGCTCCG	224424	56620	CCCAGCTGCTCATCTACTTT	269011	101207	CCTTCAGAACAGGATGCCTG
179838	12034	CCTCCCACCATCCACGCTCC	224425	56621	CCCCAGCTGCTCATCTACTT	269012	101208	GCCTTCAGAACAGGATGCCT
179839	12035	ACCTCCCACCATCCACGCTC	224426	56622	TCCCCAGCTGCTCATCTACT	269013	101209	GGCCTTCAGAACAGGATGCC
179840	12036	TACCTCCCACCATCCACGCT	224427	56623	GTCCCCAGCTGCTCATCTAC	269014	101210	TGGCCTTCAGAACAGGATGC
179841	12037	ATACCTCCCACCATCCACGC	224428	56624	AGTCCCCAGCTGCTCATCTA	269015	101211	TTGGCCTTCAGAACAGGATG
179842	12038	AATACCTCCCACCATCCACG	224429	56625	CAGTCCCCAGCTGCTCATCT	269016	101212	TTTGGCCTTCAGAACAGGAT
179843	12039	AAATACCTCCCACCATCCAC	224430	56626	CCAGTCCCCAGCTGCTCATC	269017	101213	ATTTGGCCTTCAGAACAGGA
179844	12040	GAAATACCTCCCACCATCCA	224431	56627	GCCAGTCCCCAGCTGCTCAT	269018	101214	GATTTGGCCTTCAGAACAGG
179845	12041	TGAAATACCTCCCACCATCC	224432	56628	CGCCAGTCCCCAGCTGCTCA	269019	101215	GGATTTGGCCTTCAGAACAG
179846	12042	CTGAAATACCTCCCACCATC	224433	56629	TCGCCAGTCCCCAGCTGCTC	269020	101216	GGGATTTGGCCTTCAGAACA
179847	12043	CCTGAAATACCTCCCACCAT	224434	56630	TTCGCCAGTCCCCAGCTGCT	269021	101217	TGGGATTTGGCCTTCAGAAC
179848	12044	CCCTGAAATACCTCCCACCA	224435	56631	CTTCGCCAGTCCCCAGCTGC	269022	101218	GTGGGATTTGGCCTTCAGAA
179849	12045	ACCCTGAAATACCTCCCACC	224436	56632	CCTTCGCCAGTCCCCAGCTG	269023	101219	TGTGGGATTTGGCCTTCAGA
179850	12046	CACCCTGAAATACCTCCCAC	224437	56633	CCCTTCGCCAGTCCCCAGCT	269024	101220	CTGTGGGATTTGGCCTTCAG
179851	12047	ACACCCTGAAATACCTCCCA	224438	56634	CCCCTTCGCCAGTCCCCAGC	269025	101221	TCTGTGGGATTTGGCCTTCA
179852	12048	TACACCCTGAAATACCTCCC	224439	56635	TCCCCTTCGCCAGTCCCCAG	269026	101222	CTCTGTGGGATTTGGCCTTC
179853	12049	ATACACCCTGAAATACCTCC	224440	56636	CTCCCCTTCGCCAGTCCCCA	269027	101223	CCTCTGTGGGATTTGGCCTT
179854	12050	CATACACCCTGAAATACCTC	224441	56637	TCTCCCCTTCGCCAGTCCCC	269028	101224	TCCTCTGTGGGATTTGGCCT
179855	12051	GCATACACCCTGAAATACCT	224442	56638	TTCTCCCCTTCGCCAGTCCC	269029	101225	CTCCTCTGTGGGATTTGGCC
179856	12052	TGCATACACCCTGAAATACC	224443	56639	CTTCTCCCCTTCGCCAGTCC	269030	101226	GCTCCTCTGTGGGATTTGGC
179857	12053	ATGCATACACCCTGAAATAC	224444	56640	CCTTCTCCCCTTCGCCAGTC	269031	101227	GGCTCCTCTGTGGGATTTGG
179858	12054	TATGCATACACCCTGAAATA	224445	56641	CCCTTCTCCCCTTCGCCAGT	269032	101228	TGGCTCCTCTGTGGGATTTG
179859	12055	TTATGCATACACCCTGAAAT	224446	56642	CCCCTTCTCCCCTTCGCCAG	269033	101229	CTGGCTCCTCTGTGGGATTT
179860	12056	GTTATGCATACACCCTGAAA	224447	56643	CCCCCTTCTCCCCTTCGCCA	269034	101230	CCTGGCTCCTCTGTGGGATT
179861	12057	GGTTATGCATACACCCTGAA	224448	56644	TCCCCCTTCTCCCCTTCGCC	269035	101231	CCCTGGCTCCTCTGTGGGAT
179862	12058	GGGTTATGCATACACCCTGA	224449	56645	CTCCCCCTTCTCCCCTTCGC	269036	101232	ACCCTGGCTCCTCTGTGGGA
179863	12059	GGGGTTATGCATACACCCTG	224450	56646	GCTCCCCCTTCTCCCCTTCG	269037	101233	CACCCTGGCTCCTCTGTGGG
179864	12060	GGGGGTTATGCATACACCCT	224451	56647	TGCTCCCCCTTCTCCCCTTC	269038	101234	GCACCCTGGCTCCTCTGTGG
179865	12061	TGGGGGTTATGCATACACCC	224452	56648	CTGCTCCCCCTTCTCCCCTT	269039	101235	AGCACCCTGGCTCCTCTGTG
179866	12062	GTGGGGGTTATGCATACACC	224453	56649	GCTGCTCCCCCTTCTCCCCT	269040	101236	CAGCACCCTGGCTCCTCTGT
179867	12063	GGTGGGGGTTATGCATACAC	224454	56650	AGCTGCTCCCCCTTCTCCCC	269041	101237	CCAGCACCCTGGCTCCTCTG
179868	12064	GGGTGGGGGTTATGCATACA	224455	56651	CAGCTGCTCCCCCTTCTCCC	269042	101238	GCCAGCACCCTGGCTCCTCT
179869	12065	AGGGTGGGGGTTATGCATAC	224456	56652	ACAGCTGCTCCCCCTTCTCC	269043	101239	TGCCAGCACCCTGGCTCCTC
179870	12066	CAGGGTGGGGGTTATGCATA	224457	56653	GACAGCTGCTCCCCCTTCTC	269044	101240	CTGCCAGCACCCTGGCTCCT
179871	12067	TCAGGGTGGGGGTTATGCAT	224458	56654	AGACAGCTGCTCCCCCTTCT	269045	101241	CCTGCCAGCACCCTGGCTCC
179872	12068	GTCAGGGTGGGGGTTATGCA	224459	56655	TAGACAGCTGCTCCCCCTTC	269046	101242	TCCTGCCAGCACCCTGGCTC
179873	12069	TGTCAGGGTGGGGGTTATGC	224460	56656	ATAGACAGCTGCTCCCCCTT	269047	101243	CTCCTGCCAGCACCCTGGCT
179874	12070	TTGTCAGGGTGGGGGTTATG	224461	56657	CATAGACAGCTGCTCCCCCT	269048	101244	GCTCCTGCCAGCACCCTGGC
179875	12071	ATTGTCAGGGTGGGGGTTAT	224462	56658	TCATAGACAGCTGCTCCCCC	269049	101245	GGCTCCTGCCAGCACCCTGG
179876	12072	CATTGTCAGGGTGGGGGTTA	224463	56659	CTCATAGACAGCTGCTCCCC	269050	101246	GGGCTCCTGCCAGCACCCTG
179877	12073	CCATTGTCAGGGTGGGGGTT	224464	56660	CCTCATAGACAGCTGCTCCC	269051	101247	AGGGCTCCTGCCAGCACCCT
179878	12074	GCCATTGTCAGGGTGGGGGT	224465	56661	ACCTCATAGACAGCTGCTCC	269052	101248	CAGGGCTCCTGCCAGCACCC
179879	12075	GGCCATTGTCAGGGTGGGGG	224466	56662	GACCTCATAGACAGCTGCTC	269053	101249	TCAGGGCTCCTGCCAGCACC
179880	12076	GGGCCATTGTCAGGGTGGGG	224467	56663	GGACCTCATAGACAGCTGCT	269054	101250	TTCAGGGCTCCTGCCAGCAC
179881	12077	TGGGCCATTGTCAGGGTGGG	224468	56664	TGGACCTCATAGACAGCTGC	269055	101251	GTTCAGGGCTCCTGCCAGCA
179882	12078	ATGGGCCATTGTCAGGGTGG	224469	56665	CTGGACCTCATAGACAGCTG	269056	101252	AGTTCAGGGCTCCTGCCAGC
179883	12079	GATGGGCCATTGTCAGGGTG	224470	56666	GCTGGACCTCATAGACAGCT	269057	101253	TAGTTCAGGGCTCCTGCCAG
179884	12080	AGATGGGCCATTGTCAGGGT	224471	56667	GGCTGGACCTCATAGACAGC	269058	101254	CTAGTTCAGGGCTCCTGCCA
179885	12081	GAGATGGGCCATTGTCAGGG	224472	56668	AGGCTGGACCTCATAGACAG	269059	101255	GCTAGTTCAGGGCTCCTGCC
179886	12082	AGAGATGGGCCATTGTCAGG	224473	56669	AAGGCTGGACCTCATAGACA	269060	101256	GGCTAGTTCAGGGCTCCTGC
179887	12083	AAGAGATGGGCCATTGTCAG	224474	56670	AAAGGCTGGACCTCATAGAC	269061	101257	CGGCTAGTTCAGGGCTCCTG
179888	12084	GAAGAGATGGGCCATTGTCA	224475	56671	GAAAGGCTGGACCTCATAGA	269062	101258	TCGGCTAGTTCAGGGCTCCT
179889	12085	AGAAGAGATGGGCCATTGTC	224476	56672	AGAAAGGCTGGACCTCATAG	269063	101259	TTCGGCTAGTTCAGGGCTCC
179890	12086	GAGAAGAGATGGGCCATTGT	224477	56673	AAGAAAGGCTGGACCTCATA	269064	101260	GTTCGGCTAGTTCAGGGCTC
179891	12087	GGAGAAGAGATGGGCCATTG	224478	56674	GAAGAAAGGCTGGACCTCAT	269065	101261	TGTTCGGCTAGTTCAGGGCT
179892	12088	TGGAGAAGAGATGGGCCATT	224479	56675	AGAAGAAAGGCTGGACCTCA	269066	101262	CTGTTCGGCTAGTTCAGGGC
179893	12089	CTGGAGAAGAGATGGGCCAT	224480	56676	CAGAAGAAAGGCTGGACCTC	269067	101263	GCTGTTCGGCTAGTTCAGGG
179894	12090	GCTGGAGAAGAGATGGGCCA	224481	56677	CCAGAAGAAAGGCTGGACCT	269068	101264	AGCTGTTCGGCTAGTTCAGG
179895	12091	CGCTGGAGAAGAGATGGGCC	224482	56678	CCCAGAAGAAAGGCTGGACC	269069	101265	CAGCTGTTCGGCTAGTTCAG
179896	12092	ACGCTGGAGAAGAGATGGGC	224483	56679	ACCCAGAAGAAAGGCTGGAC	269070	101266	TCAGCTGTTCGGCTAGTTCA
179897	12093	CACGCTGGAGAAGAGATGGG	224484	56680	AACCCAGAAGAAAGGCTGGA	269071	101267	TTCAGCTGTTCGGCTAGTTC
179898	12094	CCACGCTGGAGAAGAGATGG	224485	56681	AAACCCAGAAGAAAGGCTGG	269072	101268	GTTCAGCTGTTCGGCTAGTT

179899	12095	GCCACGCTGGAGAAGAGATG	224486	56682	CAAACCCAGAAGAAAGGCTG	269073	101269	TGTTCAGCTGTTCGGCTAGT
179900	12096	GGCCACGCTGGAGAAGAGAT	224487	56683	CCAAACCCAGAAGAAAGGCT	269074	101270	CTGTTCAGCTGTTCGGCTAG
179901	12097	TGGCCACGCTGGAGAAGAGA	224488	56684	ACCAAACCCAGAAGAAAGGC	269075	101271	GCTGTTCAGCTGTTCGGCTA
179902	12098	CTGGCCACGCTGGAGAAGAG	224489	56685	CACCAAACCCAGAAGAAAGG	269076	101272	AGCTGTTCAGCTGTTCGGCT
179903	12099	CCTGGCCACGCTGGAGAAGA	224490	56686	TCACCAAACCCAGAAGAAAG	269077	101273	CAGCTGTTCAGCTGTTCGGC
179904	12100	ACCTGGCCACGCTGGAGAAG	224491	56687	CTCACCAAACCCAGAAGAAA	269078	101274	TCAGCTGTTCAGCTGTTCGG
179905	12101	AACCTGGCCACGCTGGAGAA	224492	56688	TCTCACCAAACCCAGAAGAA	269079	101275	TTCAGCTGTTCAGCTGTTCG
179906	12102	AAACCTGGCCACGCTGGAGA	224493	56689	TTCTCACCAAACCCAGAAGA	269080	101276	GTTCAGCTGTTCAGCTGTTC
179907	12103	CAAACCTGGCCACGCTGGAG	224494	56690	ATTCTCACCAAACCCAGAAG	269081	101277	TGTTCAGCTGTTCAGCTGTT
179908	12104	TCAAACCTGGCCACGCTGGA	224495	56691	CATTCTCACCAAACCCAGAA	269082	101278	ATGTTCAGCTGTTCAGCTGT
179909	12105	CTCAAACCTGGCCACGCTGG	224496	56692	ACATTCTCACCAAACCCAGA	269083	101279	AATGTTCAGCTGTTCAGCTG
179910	12106	ACTCAAACCTGGCCACGCTG	224497	56693	AACATTCTCACCAAACCCAG	269084	101280	GAATGTTCAGCTGTTCAGCT
179911	12107	CACTCAAACCTGGCCACGCT	224498	56694	AAACATTCTCACCAAACCCA	269085	101281	TGAATGTTCAGCTGTTCAGC
179912	12108	GCACTCAAACCTGGCCACGC	224499	56695	AAAACATTCTCACCAAACCC	269086	101282	GTGAATGTTCAGCTGTTCAG
179913	12109	GGCACTCAAACCTGGCCACG	224500	56696	CAAAACATTCTCACCAAACC	269087	101283	GGTGAATGTTCAGCTGTTCA
179914	12110	TGGCACTCAAACCTGGCCAC	224501	56697	CCAAAACATTCTCACCAAAC	269088	101284	GGGTGAATGTTCAGCTGTTC
179915	12111	CTGGCACTCAAACCTGGCCA	224502	56698	TCCAAAACATTCTCACCAAA	269089	101285	AGGGTGAATGTTCAGCTGTT
179916	12112	ACTGGCACTCAAACCTGGCC	224503	56699	TTCCAAAACATTCTCACCAA	269090	101286	CAGGGTGAATGTTCAGCTGT
179917	12113	GACTGGCACTCAAACCTGGC	224504	56700	GTTCCAAAACATTCTCACCA	269091	101287	ACAGGGTGAATGTTCAGCTG
179918	12114	GGACTGGCACTCAAACCTGG	224505	56701	AGTTCCAAAACATTCTCACC	269092	101288	CACAGGGTGAATGTTCAGCT
179919	12115	AGGACTGGCACTCAAACCTG	224506	56702	TAGTTCCAAAACATTCTCAC	269093	101289	CCACAGGGTGAATGTTCAGC
179920	12116	CAGGACTGGCACTCAAACCT	224507	56703	CTAGTTCCAAAACATTCTCA	269094	101290	CCCACAGGGTGAATGTTCAG
179921	12117	CCAGGACTGGCACTCAAACC	224508	56704	TCTAGTTCCAAAACATTCTC	269095	101291	CCCCACAGGGTGAATGTTCA
179922	12118	CCCAGGACTGGCACTCAAAC	224509	56705	ATCTAGTTCCAAAACATTCT	269096	101292	TCCCCACAGGGTGAATGTTC
179923	12119	ACCCAGGACTGGCACTCAAA	224510	56706	TATCTAGTTCCAAAACATTC	269097	101293	TTCCCCACAGGGTGAATGTT
179924	12120	CACCCAGGACTGGCACTCAA	224511	56707	CTATCTAGTTCCAAAACATT	269098	101294	TTTCCCCACAGGGTGAATGT
179925	12121	ACACCCAGGACTGGCACTCA	224512	56708	TCTATCTAGTTCCAAAACAT	269099	101295	CTTTCCCCACAGGGTGAATG
179926	12122	GACACCCAGGACTGGCACTC	224513	56709	CTCTATCTAGTTCCAAAACA	269100	101296	CCTTTCCCCACAGGGTGAAT
179927	12123	GGACACCCAGGACTGGCACT	224514	56710	CCTCTATCTAGTTCCAAAAC	269101	101297	CCCTTTCCCCACAGGGTGAA
179928	12124	TGGACACCCAGGACTGGCAC	224515	56711	ACCTCTATCTAGTTCCAAAA	269102	101298	ACCCTTTCCCCACAGGGTGA
179929	12125	CTGGACACCCAGGACTGGCA	224516	56712	CACCTCTATCTAGTTCCAAA	269103	101299	GACCCTTTCCCCACAGGGTG
179930	12126	ACTGGACACCCAGGACTGGC	224517	56713	TCACCTCTATCTAGTTCCAA	269104	101300	TGACCCTTTCCCCACAGGGT
179931	12127	CACTGGACACCCAGGACTGG	224518	56714	ATCACCTCTATCTAGTTCCA	269105	101301	CTGACCCTTTCCCCACAGGG
179932	12128	CCACTGGACACCCAGGACTG	224519	56715	TATCACCTCTATCTAGTTCC	269106	101302	TCTGACCCTTTCCCCACAGG
179933	12129	GCCACTGGACACCCAGGACT	224520	56716	CTATCACCTCTATCTAGTTC	269107	101303	TTCTGACCCTTTCCCCACAG
179934	12130	GGCCACTGGACACCCAGGAC	224521	56717	ACTATCACCTCTATCTAGTT	269108	101304	CTTCTGACCCTTTCCCCACA
179935	12131	GGGCCACTGGACACCCAGGA	224522	56718	AACTATCACCTCTATCTAGT	269109	101305	GCTTCTGACCCTTTCCCCAC
179936	12132	GGGGCCACTGGACACCCAGG	224523	56719	CAACTATCACCTCTATCTAG	269110	101306	CGCTTCTGACCCTTTCCCCA
179937	12133	TGGGGCCACTGGACACCCAG	224524	56720	ACAACTATCACCTCTATCTA	269111	101307	ACGCTTCTGACCCTTTCCCC
179938	12134	ATGGGGCCACTGGACACCCA	224525	56721	TACAACTATCACCTCTATCT	269112	101308	GACGCTTCTGACCCTTTCCC
179939	12135	TATGGGGCCACTGGACACCC	224526	56722	GTACAACTATCACCTCTATC	269113	101309	GGACGCTTCTGACCCTTTCC
179940	12136	CTATGGGGCCACTGGACACC	224527	56723	TGTACAACTATCACCTCTAT	269114	101310	TGGACGCTTCTGACCCTTTC
179941	12137	GCTATGGGGCCACTGGACAC	224528	56724	TTGTACAACTATCACCTCTA	269115	101311	CTGGACGCTTCTGACCCTTT
179942	12138	GGCTATGGGGCCACTGGACA	224529	56725	GTTGTACAACTATCACCTCT	269116	101312	CCTGGACGCTTCTGACCCTT
179943	12139	AGGCTATGGGGCCACTGGAC	224530	56726	TGTTGTACAACTATCACCTC	269117	101313	GCCTGGACGCTTCTGACCCT
179944	12140	AAGGCTATGGGGCCACTGGA	224531	56727	ATGTTGTACAACTATCACCT	269118	101314	AGCCTGGACGCTTCTGACCC
179945	12141	CAAGGCTATGGGGCCACTGG	224532	56728	AATGTTGTACAACTATCACC	269119	101315	AAGCCTGGACGCTTCTGACC
179946	12142	GCAAGGCTATGGGGCCACTG	224533	56729	CAATGTTGTACAACTATCAC	269120	101316	CAAGCCTGGACGCTTCTGAC
179947	12143	CGCAAGGCTATGGGGCCACT	224534	56730	ACAATGTTGTACAACTATCA	269121	101317	TCAAGCCTGGACGCTTCTGA
179948	12144	ACGCAAGGCTATGGGGCCAC	224535	56731	CACAATGTTGTACAACTATC	269122	101318	CTCAAGCCTGGACGCTTCTG
179949	12145	AACGCAAGGCTATGGGGCCA	224536	56732	TCACAATGTTGTACAACTAT	269123	101319	CCTCAAGCCTGGACGCTTCT
179950	12146	AAACGCAAGGCTATGGGGCC	224537	56733	TTCACAATGTTGTACAACTA	269124	101320	CCCTCAAGCCTGGACGCTTC
179951	12147	AAAACGCAAGGCTATGGGGC	224538	56734	ATTCACAATGTTGTACAACT	269125	101321	GCCCTCAAGCCTGGACGCTT
179952	12148	TAAAACGCAAGGCTATGGGG	224539	56735	CATTCACAATGTTGTACAAC	269126	101322	TGCCCTCAAGCCTGGACGCT
179953	12149	CTAAAACGCAAGGCTATGGG	224540	56736	ACATTCACAATGTTGTACAA	269127	101323	GTGCCCTCAAGCCTGGACGC
179954	12150	ACTAAAACGCAAGGCTATGG	224541	56737	TACATTCACAATGTTGTACA	269128	101324	TGTGCCCTCAAGCCTGGACG
179955	12151	TACTAAAACGCAAGGCTATG	224542	56738	GTACATTCACAATGTTGTAC	269129	101325	CTGTGCCCTCAAGCCTGGAC
179956	12152	TTACTAAAACGCAAGGCTAT	224543	56739	AGTACATTCACAATGTTGTA	269130	101326	GCTGTGCCCTCAAGCCTGGA
179957	12153	TTTACTAAAACGCAAGGCTA	224544	56740	TAGTACATTCACAATGTTGT	269131	101327	AGCTGTGCCCTCAAGCCTGG
179958	12154	TTTTACTAAAACGCAAGGCT	224545	56741	TTAGTACATTCACAATGTTG	269132	101328	CAGCTGTGCCCTCAAGCCTG
179959	12155	ATTTTACTAAAACGCAAGGC	224546	56742	TTTAGTACATTCACAATGTT	269133	101329	CCAGCTGTGCCCTCAAGCCT
179960	12156	CATTTTACTAAAACGCAAGG	224547	56743	ATTTAGTACATTCACAATGT	269134	101330	CCCAGCTGTGCCCTCAAGCC
179961	12157	GCATTTTACTAAAACGCAAG	224548	56744	CATTTAGTACATTCACAATG	269135	101331	ACCCAGCTGTGCCCTCAAGC
179962	12158	AGCATTTTACTAAAACGCAA	224549	56745	GCATTTAGTACATTCACAAT	269136	101332	GACCCAGCTGTGCCCTCAAG
179963	12159	CAGCATTTTACTAAAACGCA	224550	56746	GGCATTTAGTACATTCACAA	269137	101333	AGACCCAGCTGTGCCCTCAA
179964	12160	GCAGCATTTTACTAAAACGC	224551	56747	TGGCATTTAGTACATTCACA	269138	101334	GAGACCCAGCTGTGCCCTCA
179965	12161	GGCAGCATTTTACTAAAACG	224552	56748	GTGGCATTTAGTACATTCAC	269139	101335	CGAGACCCAGCTGTGCCCTC
179966	12162	GGGCAGCATTTTACTAAAAC	224553	56749	AGTGGCATTTAGTACATTCA	269140	101336	ACGAGACCCAGCTGTGCCCT
179967	12163	GGGGCAGCATTTTACTAAAA	224554	56750	CAGTGGCATTTAGTACATTC	269141	101337	GACGAGACCCAGCTGTGCCC
179968	12164	GGGGGCAGCATTTTACTAAA	224555	56751	TCAGTGGCATTTAGTACATT	269142	101338	TGACGAGACCCAGCTGTGCC
179969	12165	TGGGGGCAGCATTTTACTAA	224556	56752	TTCAGTGGCATTTAGTACAT	269143	101339	GTGACGAGACCCAGCTGTGC
179970	12166	ATGGGGGCAGCATTTTACTA	224557	56753	ATTCAGTGGCATTTAGTACA	269144	101340	AGTGACGAGACCCAGCTGTG

179971	12167	AATGGGGGCAGCATTTTACT	224558	56754	GATTCAGTGGCATTTAGTAC	269145	101341	CAGTGACGAGACCCAGCTGT
179972	12168	TAATGGGGGCAGCATTTTAC	224559	56755	TGATTCAGTGGCATTTAGTA	269146	101342	GCAGTGACGAGACCCAGCTG
179973	12169	GTAATGGGGGCAGCATTTTA	224560	56756	ATGATTCAGTGGCATTTAGT	269147	101343	TGCAGTGACGAGACCCAGCT
179974	12170	GGTAATGGGGGCAGCATTTT	224561	56757	AATGATTCAGTGGCATTTAG	269148	101344	ATGCAGTGACGAGACCCAGC
179975	12171	TGGTAATGGGGGCAGCATTT	224562	56758	GAATGATTCAGTGGCATTTA	269149	101345	GATGCAGTGACGAGACCCAG
179976	12172	GTGGTAATGGGGGCAGCATT	224563	56759	TGAATGATTCAGTGGCATTT	269150	101346	TGATGCAGTGACGAGACCCA
179977	12173	GGTGGTAATGGGGGCAGCAT	224564	56760	ATGAATGATTCAGTGGCATT	269151	101347	GTGATGCAGTGACGAGACCC
179978	12174	AGGTGGTAATGGGGGCAGCA	224565	56761	AATGAATGATTCAGTGGCAT	269152	101348	GGTGATGCAGTGACGAGACC
179979	12175	CAGGTGGTAATGGGGGCAGC	224566	56762	AAATGAATGATTCAGTGGCA	269153	101349	GGGTGATGCAGTGACGAGAC
179980	12176	CCAGGTGGTAATGGGGGCAG	224567	56763	AAAATGAATGATTCAGTGGC	269154	101350	AGGGTGATGCAGTGACGAGA
179981	12177	ACCAGGTGGTAATGGGGGCA	224568	56764	TAAAATGAATGATTCAGTGG	269155	101351	AAGGGTGATGCAGTGACGAG
179982	12178	GACCAGGTGGTAATGGGGGC	224569	56765	TTAAAATGAATGATTCAGTG	269156	101352	TAAGGGTGATGCAGTGACGA
179983	12179	AGACCAGGTGGTAATGGGGG	224570	56766	TTTAAAATGAATGATTCAGT	269157	101353	ATAAGGGTGATGCAGTGACG
179984	12180	CAGACCAGGTGGTAATGGGG	224571	56767	ATTTAAAATGAATGATTCAG	269158	101354	AATAAGGGTGATGCAGTGAC
179985	12181	ACAGACCAGGTGGTAATGGG	224572	56768	GATTTAAAATGAATGATTCA	269159	101355	AAATAAGGGTGATGCAGTGA
179986	12182	CACAGACCAGGTGGTAATGG	224573	56769	CGATTTAAAATGAATGATTC	269160	101356	TAAATAAGGGTGATGCAGTG
179987	12183	GCACAGACCAGGTGGTAATG	224574	56770	ACGATTTAAAATGAATGATT	269161	101357	CTAAATAAGGGTGATGCAGT
179988	12184	TGCACAGACCAGGTGGTAAT	224575	56771	AACGATTTAAAATGAATGAT	269162	101358	CCTAAATAAGGGTGATGCAG
179989	12185	GTGCACAGACCAGGTGGTAA	224576	56772	GAACGATTTAAAATGAATGA	269163	101359	TCCTAAATAAGGGTGATGCA
179990	12186	AGTGCACAGACCAGGTGGTA	224577	56773	AGAACGATTTAAAATGAATG	269164	101360	ATCCTAAATAAGGGTGATGC
179991	12187	AAGTGCACAGACCAGGTGGT	224578	56774	AAGAACGATTTAAAATGAAT	269165	101361	TATCCTAAATAAGGGTGATG
179992	12188	GAAGTGCACAGACCAGGTGG	224579	56775	AAAGAACGATTTAAAATGAA	269166	101362	TTATCCTAAATAAGGGTGAT
179993	12189	CGAAGTGCACAGACCAGGTG	224580	56776	TAAAGAACGATTTAAAATGA	269167	101363	TTTATCCTAAATAAGGGTGA
179994	12190	CCGAAGTGCACAGACCAGGT	224581	56777	GTAAAGAACGATTTAAAATG	269168	101364	CTTTATCCTAAATAAGGGTG
179995	12191	ACCGAAGTGCACAGACCAGG	224582	56778	CGTAAAGAACGATTTAAAAT	269169	101365	CCTTTATCCTAAATAAGGGT
179996	12192	GACCGAAGTGCACAGACCAG	224583	56779	ACGTAAAGAACGATTTAAAA	269170	101366	GCCTTTATCCTAAATAAGGG
179997	12193	TGACCGAAGTGCACAGACCA	224584	56780	AACGTAAAGAACGATTTAAA	269171	101367	GGCCTTTATCCTAAATAAGG
179998	12194	GTGACCGAAGTGCACAGACC	224585	56781	CAACGTAAAGAACGATTTAA	269172	101368	GGGCCTTTATCCTAAATAAG
179999	12195	AGTGACCGAAGTGCACAGAC	224586	56782	GCAACGTAAAGAACGATTTA	269173	101369	AGGGCCTTTATCCTAAATAA
180000	12196	CAGTGACCGAAGTGCACAGA	224587	56783	TGCAACGTAAAGAACGATTT	269174	101370	CAGGGCCTTTATCCTAAATA
180001	12197	CCAGTGACCGAAGTGCACAG	224588	56784	ATGCAACGTAAAGAACGATT	269175	101371	TCAGGGCCTTTATCCTAAAT
180002	12198	TCCAGTGACCGAAGTGCACA	224589	56785	CATGCAACGTAAAGAACGAT	269176	101372	TTCAGGGCCTTTATCCTAAA
180003	12199	TTCCAGTGACCGAAGTGCAC	224590	56786	TCATGCAACGTAAAGAACGA	269177	101373	CTTCAGGGCCTTTATCCTAA
180004	12200	ATTCCAGTGACCGAAGTGCA	224591	56787	TTCATGCAACGTAAAGAACG	269178	101374	TCTTCAGGGCCTTTATCCTA
180005	12201	AATTCCAGTGACCGAAGTGC	224592	56788	ATTCATGCAACGTAAAGAAC	269179	101375	TTCTTCAGGGCCTTTATCCT
180006	12202	AAATTCCAGTGACCGAAGTG	224593	56789	AATTCATGCAACGTAAAGAA	269180	101376	ATTCTTCAGGGCCTTTATCC
180007	12203	CAAATTCCAGTGACCGAAGT	224594	56790	AAATTCATGCAACGTAAAGA	269181	101377	AATTCTTCAGGGCCTTTATC
180008	12204	GCAAATTCCAGTGACCGAAG	224595	56791	AAAATTCATGCAACGTAAAG	269182	101378	CAATTCTTCAGGGCCTTTAT
180009	12205	GGCAAATTCCAGTGACCGAA	224596	56792	TAAAATTCATGCAACGTAAA	269183	101379	ACAATTCTTCAGGGCCTTTA
180010	12206	TGGCAAATTCCAGTGACCGA	224597	56793	TTAAAATTCATGCAACGTAA	269184	101380	TACAATTCTTCAGGGCCTTT
180011	12207	ATGGCAAATTCCAGTGACCG	224598	56794	CTTAAAATTCATGCAACGTA	269185	101381	ATACAATTCTTCAGGGCCTT
180012	12208	GATGGCAAATTCCAGTGACC	224599	56795	ACTTAAAATTCATGCAACGT	269186	101382	AATACAATTCTTCAGGGCCT
180013	12209	AGATGGCAAATTCCAGTGAC	224600	56796	GACTTAAAATTCATGCAACG	269187	101383	TAATACAATTCTTCAGGGCC
180014	12210	AAGATGGCAAATTCCAGTGA	224601	56797	TGACTTAAAATTCATGCAAC	269188	101384	CTAATACAATTCTTCAGGGC
180015	12211	GAAGATGGCAAATTCCAGTG	224602	56798	TTGACTTAAAATTCATGCAA	269189	101385	TCTAATACAATTCTTCAGGG
180016	12212	GGAAGATGGCAAATTCCAGT	224603	56799	ATTGACTTAAAATTCATGCA	269190	101386	CTCTAATACAATTCTTCAGG
180017	12213	TGGAAGATGGCAAATTCCAG	224604	56800	GATTGACTTAAAATTCATGC	269191	101387	CCTCTAATACAATTCTTCAG
180018	12214	CTGGAAGATGGCAAATTCCA	224605	56801	TGATTGACTTAAAATTCATG	269192	101388	ACCTCTAATACAATTCTTCA
180019	12215	ACTGGAAGATGGCAAATTCC	224606	56802	TTGATTGACTTAAAATTCAT	269193	101389	AACCTCTAATACAATTCTTC
180020	12216	GACTGGAAGATGGCAAATTC	224607	56803	TTTGATTGACTTAAAATTCA	269194	101390	CAACCTCTAATACAATTCTT
180021	12217	GGACTGGAAGATGGCAAATT	224608	56804	TTTTGATTGACTTAAAATTC	269195	101391	CCAACCTCTAATACAATTCT
180022	12218	GGGACTGGAAGATGGCAAAT	224609	56805	TTTTTGATTGACTTAAAATT	269196	101392	GCCAACCTCTAATACAATTC
180023	12219	CGGGACTGGAAGATGGCAAA	224610	56806	GTTTTTGATTGACTTAAAAT	269197	101393	TGCCAACCTCTAATACAATT
180024	12220	TCGGGACTGGAAGATGGCAA	224611	56807	TGTTTTTGATTGACTTAAAA	269198	101394	TTGCCAACCTCTAATACAAT
180025	12221	TTCGGGACTGGAAGATGGCA	224612	56808	CTGTTTTTGATTGACTTAAA	269199	101395	TTTGCCAACCTCTAATACAA
180026	12222	ATTCGGGACTGGAAGATGGC	224613	56809	ACTGTTTTTGATTGACTTAA	269200	101396	CTTTGCCAACCTCTAATACA
180027	12223	CATTCGGGACTGGAAGATGG	224614	56810	AACTGTTTTTGATTGACTTA	269201	101397	GCTTTGCCAACCTCTAATAC
180028	12224	ACATTCGGGACTGGAAGATG	224615	56811	CAACTGTTTTTGATTGACTT	269202	101398	TGCTTTGCCAACCTCTAATA
180029	12225	CACATTCGGGACTGGAAGAT	224616	56812	ACAACTGTTTTTGATTGACT	269203	101399	ATGCTTTGCCAACCTCTAAT
180030	12226	CCACATTCGGGACTGGAAGA	224617	56813	AACAACTGTTTTTGATTGAC	269204	101400	TATGCTTTGCCAACCTCTAA
180031	12227	GCCACATTCGGGACTGGAAG	224618	56814	AAACAACTGTTTTTGATTGA	269205	101401	ATATGCTTTGCCAACCTCTA
180032	12228	TGCCACATTCGGGACTGGAA	224619	56815	CAAACAACTGTTTTTGATTG	269206	101402	GATATGCTTTGCCAACCTCT
180033	12229	TTGCCACATTCGGGACTGGA	224620	56816	TCAAACAACTGTTTTTGATT	269207	101403	AGATATGCTTTGCCAACCTC
180034	12230	CTTGCCACATTCGGGACTGG	224621	56817	TTCAAACAACTGTTTTTGAT	269208	101404	TAGATATGCTTTGCCAACCT
180035	12231	GCTTGCCACATTCGGGACTG	224622	56818	TTTCAAACAACTGTTTTTGA	269209	101405	GTAGATATGCTTTGCCAACC
180036	12232	GGCTTGCCACATTCGGGACT	224623	56819	TTTTCAAACAACTGTTTTTG	269210	101406	GGTAGATATGCTTTGCCAAC
180037	12233	TGGCTTGCCACATTCGGGAC	224624	56820	CTTTTCAAACAACTGTTTTT	269211	101407	TGGTAGATATGCTTTGCCAA
180038	12234	ATGGCTTGCCACATTCGGGA	224625	56821	TCTTTTCAAACAACTGTTTT	269212	101408	GTGGTAGATATGCTTTGCCA
180039	12235	CATGGCTTGCCACATTCGGG	224626	56822	CTCTTTTCAAACAACTGTTT	269213	101409	GGTGGTAGATATGCTTTGCC
180040	12236	CCATGGCTTGCCACATTCGG	224627	56823	TCTCTTTTCAAACAACTGTT	269214	101410	AGGTGGTAGATATGCTTTGC
180041	12237	TCCATGGCTTGCCACATTCG	224628	56824	TTCTCTTTTCAAACAACTGT	269215	101411	GAGGTGGTAGATATGCTTTG
180042	12238	CTCCATGGCTTGCCACATTC	224629	56825	TTTCTCTTTTCAAACAACTG	269216	101412	GGAGGTGGTAGATATGCTTT

180043	12239	GCTCCATGGCTTGCCACATT	224630	56826	TTTTCTCTTTTCAAACAACT	269217	101413	AGGAGGTGGTAGATATGCTT
180044	12240	GGCTCCATGGCTTGCCACAT	224631	56827	CTTTTCTCTTTTCAAACAAC	269218	101414	CAGGAGGTGGTAGATATGCT
180045	12241	AGGCTCCATGGCTTGCCACA	224632	56828	GCTTTTCTCTTTTCAAACAA	269219	101415	CCAGGAGGTGGTAGATATGC
180046	12242	AAGGCTCCATGGCTTGCCAC	224633	56829	GGCTTTTCTCTTTTCAAACA	269220	101416	TCCAGGAGGTGGTAGATATG
180047	12243	TAAGGCTCCATGGCTTGCCA	224634	56830	AGGCTTTTCTCTTTTCAAAC	269221	101417	CTCCAGGAGGTGGTAGATAT
180048	12244	TTAAGGCTCCATGGCTTGCC	224635	56831	TAGGCTTTTCTCTTTTCAAA	269222	101418	GCTCCAGGAGGTGGTAGATA
180049	12245	CTTAAGGCTCCATGGCTTGC	224636	56832	ATAGGCTTTTCTCTTTTCAA	269223	101419	GGCTCCAGGAGGTGGTAGAT
180050	12246	GCTTAAGGCTCCATGGCTTG	224637	56833	CATAGGCTTTTCTCTTTTCA	269224	101420	TGGCTCCAGGAGGTGGTAGA
180051	12247	AGCTTAAGGCTCCATGGCTT	224638	56834	CCATAGGCTTTTCTCTTTTC	269225	101421	GTGGCTCCAGGAGGTGGTAG
180052	12248	GAGCTTAAGGCTCCATGGCT	224639	56835	CCCATAGGCTTTTCTCTTTT	269226	101422	CGTGGCTCCAGGAGGTGGTA
180053	12249	AGAGCTTAAGGCTCCATGGC	224640	56836	ACCCATAGGCTTTTCTCTTT	269227	101423	GCGTGGCTCCAGGAGGTGGT
180054	12250	AAGAGCTTAAGGCTCCATGG	224641	56837	TACCCATAGGCTTTTCTCTT	269228	101424	AGCGTGGCTCCAGGAGGTGG
180055	12251	GAAGAGCTTAAGGCTCCATG	224642	56838	CTACCCATAGGCTTTTCTCT	269229	101425	CAGCGTGGCTCCAGGAGGTG
180056	12252	AGAAGAGCTTAAGGCTCCAT	224643	56839	GCTACCCATAGGCTTTTCTC	269230	101426	CCAGCGTGGCTCCAGGAGGT
180057	12253	GAGAAGAGCTTAAGGCTCCA	224644	56840	CGCTACCCATAGGCTTTTCT	269231	101427	GCCAGCGTGGCTCCAGGAGG
180058	12254	GGAGAAGAGCTTAAGGCTCC	224645	56841	CCGCTACCCATAGGCTTTTC	269232	101428	GGCCAGCGTGGCTCCAGGAG
180059	12255	GGGAGAAGAGCTTAAGGCTC	224646	56842	GCCGCTACCCATAGGCTTTT	269233	101429	CGGCCAGCGTGGCTCCAGGA
180060	12256	AGGGAGAAGAGCTTAAGGCT	224647	56843	TGCCGCTACCCATAGGCTTT	269234	101430	GCGGCCAGCGTGGCTCCAGG
180061	12257	GAGGGAGAAGAGCTTAAGGC	224648	56844	CTGCCGCTACCCATAGGCTT	269235	101431	TGCGGCCAGCGTGGCTCCAG
180062	12258	GGAGGGAGAAGAGCTTAAGG	224649	56845	GCTGCCGCTACCCATAGGCT	269236	101432	CTGCGGCCAGCGTGGCTCCA
180063	12259	TGGAGGGAGAAGAGCTTAAG	224650	56846	TGCTGCCGCTACCCATAGGC	269237	101433	CCTGCGGCCAGCGTGGCTCC
180064	12260	GTGGAGGGAGAAGAGCTTAA	224651	56847	CTGCTGCCGCTACCCATAGG	269238	101434	CCCTGCGGCCAGCGTGGCTC
180065	12261	TGTGGAGGGAGAAGAGCTTA	224652	56848	ACTGCTGCCGCTACCCATAG	269239	101435	TCCCTGCGGCCAGCGTGGCT
180066	12262	ATGTGGAGGGAGAAGAGCTT	224653	56849	CACTGCTGCCGCTACCCATA	269240	101436	ATCCCTGCGGCCAGCGTGGC
180067	12263	GATGTGGAGGGAGAAGAGCT	224654	56850	TCACTGCTGCCGCTACCCAT	269241	101437	AATCCCTGCGGCCAGCGTGG
180068	12264	GGATGTGGAGGGAGAAGAGC	224655	56851	ATCACTGCTGCCGCTACCCA	269242	101438	TAATCCCTGCGGCCAGCGTG
180069	12265	AGGATGTGGAGGGAGAAGAG	224656	56852	AATCACTGCTGCCGCTACCC	269243	101439	ATAATCCCTGCGGCCAGCGT
180070	12266	CAGGATGTGGAGGGAGAAGA	224657	56853	CAATCACTGCTGCCGCTACC	269244	101440	TATAATCCCTGCGGCCAGCG
180071	12267	CCAGGATGTGGAGGGAGAAG	224658	56854	CCAATCACTGCTGCCGCTAC	269245	101441	TTATAATCCCTGCGGCCAGC
180072	12268	TCCAGGATGTGGAGGGAGAA	224659	56855	TCCAATCACTGCTGCCGCTA	269246	101442	ATTATAATCCCTGCGGCCAG
180073	12269	TTCCAGGATGTGGAGGGAGA	224660	56856	ATCCAATCACTGCTGCCGCT	269247	101443	AATTATAATCCCTGCGGCCA
180074	12270	GTTCCAGGATGTGGAGGGAG	224661	56857	AATCCAATCACTGCTGCCGC	269248	101444	TAATTATAATCCCTGCGGCC
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180077	12273	TCTGTTCCAGGATGTGGAGG	224664	56860	ATAAATCCAATCACTGCTGC	269251	101447	AAATAATTATAATCCCTGCG
180078	12274	GTCTGTTCCAGGATGTGGAG	224665	56861	CATAAATCCAATCACTGCTG	269252	101448	GAAATAATTATAATCCCTGC
180079	12275	GGTCTGTTCCAGGATGTGGA	224666	56862	TCATAAATCCAATCACTGCT	269253	101449	GGAAATAATTATAATCCCTG
180080	12276	GGGTCTGTTCCAGGATGTGG	224667	56863	ATCATAAATCCAATCACTGC	269254	101450	TGGAAATAATTATAATCCCT
180081	12277	CGGGTCTGTTCCAGGATGTG	224668	56864	AATCATAAATCCAATCACTG	269255	101451	ATGGAAATAATTATAATCCC
180082	12278	GCGGGTCTGTTCCAGGATGT	224669	56865	GAATCATAAATCCAATCACT	269256	101452	AATGGAAATAATTATAATCC
180083	12279	GGCGGGTCTGTTCCAGGATG	224670	56866	CGAATCATAAATCCAATCAC	269257	101453	AAATGGAAATAATTATAATC
180084	12280	TGGCGGGTCTGTTCCAGGAT	224671	56867	TCGAATCATAAATCCAATCA	269258	101454	AAAATGGAAATAATTATAAT
180085	12281	CTGGCGGGTCTGTTCCAGGA	224672	56868	ATCGAATCATAAATCCAATC	269259	101455	GAAAATGGAAATAATTATAA
180086	12282	ACTGGCGGGTCTGTTCCAGG	224673	56869	AATCGAATCATAAATCCAAT	269260	101456	TGAAAATGGAAATAATTATA
180087	12283	AACTGGCGGGTCTGTTCCAG	224674	56870	GAATCGAATCATAAATCCAA	269261	101457	TTGAAAATGGAAATAATTAT
180088	12284	AAACTGGCGGGTCTGTTCCA	224675	56871	GGAATCGAATCATAAATCCA	269262	101458	TTTGAAAATGGAAATAATTA
180089	12285	GAAACTGGCGGGTCTGTTCC	224676	56872	TGGAATCGAATCATAAATCC	269263	101459	ATTTGAAAATGGAAATAATT
180090	12286	AGAAACTGGCGGGTCTGTTC	224677	56873	ATGGAATCGAATCATAAATC	269264	101460	AATTTGAAAATGGAAATAAT
180091	12287	AAGAAACTGGCGGGTCTGTT	224678	56874	CATGGAATCGAATCATAAAT	269265	101461	TAATTTGAAAATGGAAATAA
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180093	12289	GGAAGAAACTGGCGGGTCTG	224680	56876	GCCATGGAATCGAATCATAA	269267	101463	CTTAATTTGAAAATGGAAAT
180094	12290	TGGAAGAAACTGGCGGGTCT	224681	56877	AGCCATGGAATCGAATCATA	269268	101464	CCTTAATTTGAAAATGGAAA
180095	12291	CTGGAAGAAACTGGCGGGTC	224682	56878	GAGCCATGGAATCGAATCAT	269269	101465	GCCTTAATTTGAAAATGGAA
180096	12292	CCTGGAAGAAACTGGCGGGT	224683	56879	TGAGCCATGGAATCGAATCA	269270	101466	GGCCTTAATTTGAAAATGGA
180097	12293	GCCTGGAAGAAACTGGCGGG	224684	56880	ATGAGCCATGGAATCGAATC	269271	101467	AGGCCTTAATTTGAAAATGG
180098	12294	TGCCTGGAAGAAACTGGCGG	224685	56881	GATGAGCCATGGAATCGAAT	269272	101468	GAGGCCTTAATTTGAAAATG
180099	12295	ATGCCTGGAAGAAACTGGCG	224686	56882	GGATGAGCCATGGAATCGAA	269273	101469	AGAGGCCTTAATTTGAAAAT
180100	12296	AATGCCTGGAAGAAACTGGC	224687	56883	GGGATGAGCCATGGAATCGA	269274	101470	CAGAGGCCTTAATTTGAAAA
180101	12297	CAATGCCTGGAAGAAACTGG	224688	56884	AGGGATGAGCCATGGAATCG	269275	101471	TCAGAGGCCTTAATTTGAAA
180102	12298	GCAATGCCTGGAAGAAACTG	224689	56885	GAGGGATGAGCCATGGAATC	269276	101472	CTCAGAGGCCTTAATTTGAA
180103	12299	GGCAATGCCTGGAAGAAACT	224690	56886	GGAGGGATGAGCCATGGAAT	269277	101473	GCTCAGAGGCCTTAATTTGA
180104	12300	AGGCAATGCCTGGAAGAAAC	224691	56887	GGGAGGGATGAGCCATGGAA	269278	101474	AGCTCAGAGGCCTTAATTTG
180105	12301	GAGGCAATGCCTGGAAGAAA	224692	56888	GGGGAGGGATGAGCCATGGA	269279	101475	GAGCTCAGAGGCCTTAATTT
180106	12302	TGAGGCAATGCCTGGAAGAA	224693	56889	AGGGGAGGGATGAGCCATGG	269280	101476	TGAGCTCAGAGGCCTTAATT
180107	12303	CTGAGGCAATGCCTGGAAGA	224694	56890	CAGGGGAGGGATGAGCCATG	269281	101477	CTGAGCTCAGAGGCCTTAAT
180108	12304	ACTGAGGCAATGCCTGGAAG	224695	56891	GCAGGGGAGGGATGAGCCAT	269282	101478	TCTGAGCTCAGAGGCCTTAA
180109	12305	AACTGAGGCAATGCCTGGAA	224696	56892	GGCAGGGGAGGGATGAGCCA	269283	101479	CTCTGAGCTCAGAGGCCTTA
180110	12306	AAACTGAGGCAATGCCTGGA	224697	56893	AGGCAGGGGAGGGATGAGCC	269284	101480	TCTCTGAGCTCAGAGGCCTT
180111	12307	CAAACTGAGGCAATGCCTGG	224698	56894	GAGGCAGGGGAGGGATGAGC	269285	101481	CTCTCTGAGCTCAGAGGCCT
180112	12308	GCAAACTGAGGCAATGCCTG	224699	56895	TGAGGCAGGGGAGGGATGAG	269286	101482	CCTCTCTGAGCTCAGAGGCC
180113	12309	GGCAAACTGAGGCAATGCCT	224700	56896	GTGAGGCAGGGGAGGGATGA	269287	101483	CCCTCTCTGAGCTCAGAGGC
180114	12310	GGGCAAACTGAGGCAATGCC	224701	56897	GGTGAGGCAGGGGAGGGATG	269288	101484	CCCCTCTCTGAGCTCAGAGG

180115	12311	GGGGCAAACTGAGGCAATGC	224702	56898	GGGTGAGGCAGGGGAGGGAT	269289	101485	TCCCCTCTCTGAGCTCAGAG
180116	12312	AGGGGCAAACTGAGGCAATG	224703	56899	GGGGTGAGGCAGGGGAGGGA	269290	101486	TTCCCCTCTCTGAGCTCAGA
180117	12313	GAGGGGCAAACTGAGGCAAT	224704	56900	GGGGGTGAGGCAGGGGAGGG	269291	101487	CTTCCCCTCTCTGAGCTCAG
180118	12314	AGAGGGGCAAACTGAGGCAA	224705	56901	AGGGGGTGAGGCAGGGGAGG	269292	101488	ACTTCCCCTCTCTGAGCTCA
180119	12315	CAGAGGGGCAAACTGAGGCA	224706	56902	GAGGGGGTGAGGCAGGGGAG	269293	101489	AACTTCCCCTCTCTGAGCTC
180120	12316	ACAGAGGGGCAAACTGAGGC	224707	56903	CGAGGGGGTGAGGCAGGGGA	269294	101490	TAACTTCCCCTCTCTGAGCT
180121	12317	AACAGAGGGGCAAACTGAGG	224708	56904	GCGAGGGGGTGAGGCAGGGG	269295	101491	GTAACTTCCCCTCTCTGAGC
180122	12318	AAACAGAGGGGCAAACTGAG	224709	56905	GGCGAGGGGGTGAGGCAGGG	269296	101492	AGTAACTTCCCCTCTCTGAG
180123	12319	GAAACAGAGGGGCAAACTGA	224710	56906	GGGCGAGGGGGTGAGGCAGG	269297	101493	AAGTAACTTCCCCTCTCTGA
180124	12320	GGAAACAGAGGGGCAAACTG	224711	56907	AGGGCGAGGGGGTGAGGCAG	269298	101494	CAAGTAACTTCCCCTCTCTG
180125	12321	TGGAAACAGAGGGGCAAACT	224712	56908	GAGGGCGAGGGGGTGAGGCA	269299	101495	ACAAGTAACTTCCCCTCTCT
180126	12322	CTGGAAACAGAGGGGCAAAC	224713	56909	GGAGGGCGAGGGGGTGAGGC	269300	101496	GACAAGTAACTTCCCCTCTC
180127	12323	ACTGGAAACAGAGGGGCAAA	224714	56910	CGGAGGGCGAGGGGGTGAGG	269301	101497	AGACAAGTAACTTCCCCTCT
180128	12324	GACTGGAAACAGAGGGGCAA	224715	56911	TCGGAGGGCGAGGGGGTGAG	269302	101498	CAGACAAGTAACTTCCCCTC
180129	12325	TGACTGGAAACAGAGGGGCA	224716	56912	GTCGGAGGGCGAGGGGGTGA	269303	101499	TCAGACAAGTAACTTCCCCT
180130	12326	GTGACTGGAAACAGAGGGGC	224717	56913	CGTCGGAGGGCGAGGGGGTG	269304	101500	CTCAGACAAGTAACTTCCCC
180131	12327	TGTGACTGGAAACAGAGGGG	224718	56914	ACGTCGGAGGGCGAGGGGGT	269305	101501	CCTCAGACAAGTAACTTCCC
180132	12328	GTGTGACTGGAAACAGAGGG	224719	56915	GACGTCGGAGGGCGAGGGGG	269306	101502	GCCTCAGACAAGTAACTTCC
180133	12329	AGTGTGACTGGAAACAGAGG	224720	56916	AGACGTCGGAGGGCGAGGGG	269307	101503	GGCCTCAGACAAGTAACTTC
180134	12330	GAGTGTGACTGGAAACAGAG	224721	56917	AAGACGTCGGAGGGCGAGGG	269308	101504	TGGCCTCAGACAAGTAACTT
180135	12331	AGAGTGTGACTGGAAACAGA	224722	56918	GAAGACGTCGGAGGGCGAGG	269309	101505	GTGGCCTCAGACAAGTAACT
180136	12332	GAGAGTGTGACTGGAAACAG	224723	56919	AGAAGACGTCGGAGGGCGAG	269310	101506	TGTGGCCTCAGACAAGTAAC
180137	12333	TGAGAGTGTGACTGGAAACA	224724	56920	AAGAAGACGTCGGAGGGCGA	269311	101507	GTGTGGCCTCAGACAAGTAA
180138	12334	GTGAGAGTGTGACTGGAAAC	224725	56921	GAAGAAGACGTCGGAGGGCG	269312	101508	TGTGTGGCCTCAGACAAGTA
180139	12335	GGTGAGAGTGTGACTGGAAA	224726	56922	AGAAGAAGACGTCGGAGGGC	269313	101509	CTGTGTGGCCTCAGACAAGT
180140	12336	TGGTGAGAGTGTGACTGGAA	224727	56923	AAGAAGAAGACGTCGGAGGG	269314	101510	GCTGTGTGGCCTCAGACAAG
180141	12337	CTGGTGAGAGTGTGACTGGA	224728	56924	AAAGAAGAAGACGTCGGAGG	269315	101511	AGCTGTGTGGCCTCAGACAA
180142	12338	GCTGGTGAGAGTGTGACTGG	224729	56925	AAAAGAAGAAGACGTCGGAG	269316	101512	AAGCTGTGTGGCCTCAGACA
180143	12339	CGCTGGTGAGAGTGTGACTG	224730	56926	TAAAAGAAGAAGACGTCGGA	269317	101513	CAAGCTGTGTGGCCTCAGAC
180144	12340	TCGCTGGTGAGAGTGTGACT	224731	56927	GTAAAAGAAGAAGACGTCGG	269318	101514	ACAAGCTGTGTGGCCTCAGA
180145	12341	ATCGCTGGTGAGAGTGTGAC	224732	56928	AGTAAAAGAAGAAGACGTCG	269319	101515	AACAAGCTGTGTGGCCTCAG
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180147	12343	TTATCGCTGGTGAGAGTGTG	224734	56930	AGAGTAAAAGAAGAAGACGT	269321	101517	CCAACAAGCTGTGTGGCCTC
180148	12344	TTTATCGCTGGTGAGAGTGT	224735	56931	CAGAGTAAAAGAAGAAGACG	269322	101518	TCCAACAAGCTGTGTGGCCT
180149	12345	TTTTATCGCTGGTGAGAGTG	224736	56932	TCAGAGTAAAAGAAGAAGAC	269323	101519	CTCCAACAAGCTGTGTGGCC
180150	12346	ATTTTATCGCTGGTGAGAGT	224737	56933	TTCAGAGTAAAAGAAGAAGA	269324	101520	GCTCCAACAAGCTGTGTGGC
180151	12347	CATTTTATCGCTGGTGAGAG	224738	56934	GTTCAGAGTAAAAGAAGAAG	269325	101521	GGCTCCAACAAGCTGTGTGG
180152	12348	TCATTTTATCGCTGGTGAGA	224739	56935	AGTTCAGAGTAAAAGAAGAA	269326	101522	GGGCTCCAACAAGCTGTGTG
180153	12349	ATCATTTTATCGCTGGTGAG	224740	56936	CAGTTCAGAGTAAAAGAAGA	269327	101523	TGGGCTCCAACAAGCTGTGT
180154	12350	AATCATTTTATCGCTGGTGA	224741	56937	ACAGTTCAGAGTAAAAGAAG	269328	101524	ATGGGCTCCAACAAGCTGTG
180155	12351	AAATCATTTTATCGCTGGTG	224742	56938	AACAGTTCAGAGTAAAAGAA	269329	101525	GATGGGCTCCAACAAGCTGT
180156	12352	AAAATCATTTTATCGCTGGT	224743	56939	TAACAGTTCAGAGTAAAAGA	269330	101526	AGATGGGCTCCAACAAGCTG
180157	12353	TAAAATCATTTTATCGCTGG	224744	56940	ATAACAGTTCAGAGTAAAAG	269331	101527	GAGATGGGCTCCAACAAGCT
180158	12354	CTAAAATCATTTTATCGCTG	224745	56941	GATAACAGTTCAGAGTAAAA	269332	101528	AGAGATGGGCTCCAACAAGC
180159	12355	TCTAAAATCATTTTATCGCT	224746	56942	AGATAACAGTTCAGAGTAAA	269333	101529	AAGAGATGGGCTCCAACAAG
180160	12356	GTCTAAAATCATTTTATCGC	224747	56943	AAGATAACAGTTCAGAGTAA	269334	101530	CAAGAGATGGGCTCCAACAA
180161	12357	GGTCTAAAATCATTTTATCG	224748	56944	AAAGATAACAGTTCAGAGTA	269335	101531	TCAAGAGATGGGCTCCAACA
180162	12358	AGGTCTAAAATCATTTTATC	224749	56945	CAAAGATAACAGTTCAGAGT	269336	101532	GTCAAGAGATGGGCTCCAAC
180163	12359	AAGGTCTAAAATCATTTTAT	224750	56946	ACAAAGATAACAGTTCAGAG	269337	101533	GGTCAAGAGATGGGCTCCAA
180164	12360	TAAGGTCTAAAATCATTTTA	224751	56947	AACAAAGATAACAGTTCAGA	269338	101534	GGGTCAAGAGATGGGCTCCA
180165	12361	ATAAGGTCTAAAATCATTTT	224752	56948	GAACAAAGATAACAGTTCAG	269339	101535	TGGGTCAAGAGATGGGCTCC
180166	12362	GATAAGGTCTAAAATCATTT	224753	56949	AGAACAAAGATAACAGTTCA	269340	101536	TTGGGTCAAGAGATGGGCTC
180167	12363	TGATAAGGTCTAAAATCATT	224754	56950	GAGAACAAAGATAACAGTTC	269341	101537	TTTGGGTCAAGAGATGGGCT
180168	12364	ATGATAAGGTCTAAAATCAT	224755	56951	TGAGAACAAAGATAACAGTT	269342	101538	CTTTGGGTCAAGAGATGGGC
180169	12365	GATGATAAGGTCTAAAATCA	224756	56952	ATGAGAACAAAGATAACAGT	269343	101539	TCTTTGGGTCAAGAGATGGG
180170	12366	AGATGATAAGGTCTAAAATC	224757	56953	GATGAGAACAAAGATAACAG	269344	101540	GTCTTTGGGTCAAGAGATGG
180171	12367	GAGATGATAAGGTCTAAAAT	224758	56954	AGATGAGAACAAAGATAACA	269345	101541	AGTCTTTGGGTCAAGAGATG
180172	12368	TGAGATGATAAGGTCTAAAA	224759	56955	GAGATGAGAACAAAGATAAC	269346	101542	CAGTCTTTGGGTCAAGAGAT
180173	12369	GTGAGATGATAAGGTCTAAA	224760	56956	AGAGATGAGAACAAAGATAA	269347	101543	ACAGTCTTTGGGTCAAGAGA
180174	12370	GGTGAGATGATAAGGTCTAA	224761	56957	GAGAGATGAGAACAAAGATA	269348	101544	CACAGTCTTTGGGTCAAGAG
180175	12371	GGGTGAGATGATAAGGTCTA	224762	56958	AGAGAGATGAGAACAAAGAT	269349	101545	CCACAGTCTTTGGGTCAAGA
180176	12372	AGGGTGAGATGATAAGGTCT	224763	56959	GAGAGAGATGAGAACAAAGA	269350	101546	TCCACAGTCTTTGGGTCAAG
180177	12373	GAGGGTGAGATGATAAGGTC	224764	56960	AGAGAGAGATGAGAACAAAG	269351	101547	CTCCACAGTCTTTGGGTCAA
180178	12374	CGAGGGTGAGATGATAAGGT	224765	56961	GAGAGAGAGATGAGAACAAA	269352	101548	GCTCCACAGTCTTTGGGTCA
180179	12375	CCGAGGGTGAGATGATAAGG	224766	56962	AGAGAGAGAGATGAGAACAA	269353	101549	GGCTCCACAGTCTTTGGGTC
180180	12376	TCCGAGGGTGAGATGATAAG	224767	56963	GAGAGAGAGAGATGAGAACA	269354	101550	CGGCTCCACAGTCTTTGGGT
180181	12377	ATCCGAGGGTGAGATGATAA	224768	56964	AGAGAGAGAGAGATGAGAAC	269355	101551	TCGGCTCCACAGTCTTTGGG
180182	12378	GATCCGAGGGTGAGATGATA	224769	56965	GAGAGAGAGAGAGATGAGAA	269356	101552	CTCGGCTCCACAGTCTTTGG
180183	12379	GGATCCGAGGGTGAGATGAT	224770	56966	AGAGAGAGAGAGAGATGAGA	269357	101553	ACTCGGCTCCACAGTCTTTG
180184	12380	AGGATCCGAGGGTGAGATGA	224771	56967	GAGAGAGAGAGAGAGATGAG	269358	101554	AACTCGGCTCCACAGTCTTT
180185	12381	AAGGATCCGAGGGTGAGATG	224772	56968	AGAGAGAGAGAGAGAGATGA	269359	101555	CAACTCGGCTCCACAGTCTT
180186	12382	TAAGGATCCGAGGGTGAGAT	224773	56969	GAGAGAGAGAGAGAGAGATG	269360	101556	CCAACTCGGCTCCACAGTCT

180187	12383	ATAAGGATCCGAGGGTGAGA	224774	56970	TGAGAGAGAGAGAGAGAGAT	269361	101557	GCCAACTCGGCTCCACAGTC
180188	12384	CATAAGGATCCGAGGGTGAG	224775	56971	TTGAGAGAGAGAGAGAGAGA	269362	101558	GGCCAACTCGGCTCCACAGT
180189	12385	CCATAAGGATCCGAGGGTGA	224776	56972	GTTGAGAGAGAGAGAGAGAG	269363	101559	TGGCCAACTCGGCTCCACAG
180190	12386	TCCATAAGGATCCGAGGGTG	224777	56973	GGTTGAGAGAGAGAGAGAGA	269364	101560	GTGGCCAACTCGGCTCCACA
180191	12387	TTCCATAAGGATCCGAGGGT	224778	56974	GGGTTGAGAGAGAGAGAGAG	269365	101561	GGTGGCCAACTCGGCTCCAC
180192	12388	TTTCCATAAGGATCCGAGGG	224779	56975	AGGGTTGAGAGAGAGAGAGA	269366	101562	AGGTGGCCAACTCGGCTCCA
180193	12389	GTTTCCATAAGGATCCGAGG	224780	56976	CAGGGTTGAGAGAGAGAGAG	269367	101563	GAGGTGGCCAACTCGGCTCC
180194	12390	TGTTTCCATAAGGATCCGAG	224781	56977	GCAGGGTTGAGAGAGAGAGA	269368	101564	AGAGGTGGCCAACTCGGCTC
180195	12391	TTGTTTCCATAAGGATCCGA	224782	56978	TGCAGGGTTGAGAGAGAGAG	269369	101565	GAGAGGTGGCCAACTCGGCT
180196	12392	ATTGTTTCCATAAGGATCCG	224783	56979	CTGCAGGGTTGAGAGAGAGA	269370	101566	AGAGAGGTGGCCAACTCGGC
180197	12393	TATTGTTTCCATAAGGATCC	224784	56980	TCTGCAGGGTTGAGAGAGAG	269371	101567	CAGAGAGGTGGCCAACTCGG
180198	12394	TTATTGTTTCCATAAGGATC	224785	56981	GTCTGCAGGGTTGAGAGAGA	269372	101568	CCAGAGAGGTGGCCAACTCG
180199	12395	ATTATTGTTTCCATAAGGAT	224786	56982	TGTCTGCAGGGTTGAGAGAG	269373	101569	CCCAGAGAGGTGGCCAACTC
180200	12396	CATTATTGTTTCCATAAGGA	224787	56983	GTGTCTGCAGGGTTGAGAGA	269374	101570	TCCCAGAGAGGTGGCCAACT
180201	12397	TCATTATTGTTTCCATAAGG	224788	56984	AGTGTCTGCAGGGTTGAGAG	269375	101571	CTCCCAGAGAGGTGGCCAAC
180202	12398	CTCATTATTGTTTCCATAAG	224789	56985	AAGTGTCTGCAGGGTTGAGA	269376	101572	GCTCCCAGAGAGGTGGCCAA
180203	12399	ACTCATTATTGTTTCCATAA	224790	56986	AAAGTGTCTGCAGGGTTGAG	269377	101573	CGCTCCCAGAGAGGTGGCCA
180204	12400	AACTCATTATTGTTTCCATA	224791	56987	AAAAGTGTCTGCAGGGTTGA	269378	101574	CCGCTCCCAGAGAGGTGGCC
180205	12401	CAACTCATTATTGTTTCCAT	224792	56988	GAAAAGTGTCTGCAGGGTTG	269379	101575	CCCGCTCCCAGAGAGGTGGC
180206	12402	ACAACTCATTATTGTTTCCA	224793	56989	GGAAAAGTGTCTGCAGGGTT	269380	101576	ACCCGCTCCCAGAGAGGTGG
180207	12403	AACAACTCATTATTGTTTCC	224794	56990	GGGAAAAGTGTCTGCAGGGT	269381	101577	TACCCGCTCCCAGAGAGGTG
180208	12404	GAACAACTCATTATTGTTTC	224795	56991	AGGGAAAAGTGTCTGCAGGG	269382	101578	ATACCCGCTCCCAGAGAGGT
180209	12405	GGAACAACTCATTATTGTTT	224796	56992	AAGGGAAAAGTGTCTGCAGG	269383	101579	AATACCCGCTCCCAGAGAGG
180210	12406	GGGAACAACTCATTATTGTT	224797	56993	AAAGGGAAAAGTGTCTGCAG	269384	101580	CAATACCCGCTCCCAGAGAG
180211	12407	AGGGAACAACTCATTATTGT	224798	56994	GAAAGGGAAAAGTGTCTGCA	269385	101581	CCAATACCCGCTCCCAGAGA
180212	12408	CAGGGAACAACTCATTATTG	224799	56995	AGAAAGGGAAAAGTGTCTGC	269386	101582	TCCAATACCCGCTCCCAGAG
180213	12409	ACAGGGAACAACTCATTATT	224800	56996	AAGAAAGGGAAAAGTGTCTG	269387	101583	ATCCAATACCCGCTCCCAGA
180214	12410	AACAGGGAACAACTCATTAT	224801	56997	AAAGAAAGGGAAAAGTGTCT	269388	101584	CATCCAATACCCGCTCCCAG
180215	12411	AAACAGGGAACAACTCATTA	224802	56998	CAAAGAAAGGGAAAAGTGTC	269389	101585	CCATCCAATACCCGCTCCCA
180216	12412	GAAACAGGGAACAACTCATT	224803	56999	ACAAAGAAAGGGAAAAGTGT	269390	101586	ACCATCCAATACCCGCTCCC
180217	12413	TGAAACAGGGAACAACTCAT	224804	57000	GACAAAGAAAGGGAAAAGTG	269391	101587	CACCATCCAATACCCGCTCC
180218	12414	TTGAAACAGGGAACAACTCA	224805	57001	AGACAAAGAAAGGGAAAAGT	269392	101588	CCACCATCCAATACCCGCTC
180219	12415	ATTGAAACAGGGAACAACTC	224806	57002	CAGACAAAGAAAGGGAAAAG	269393	101589	ACCACCATCCAATACCCGCT
180220	12416	AATTGAAACAGGGAACAACT	224807	57003	GCAGACAAAGAAAGGGAAAA	269394	101590	AACCACCATCCAATACCCGC
180221	12417	GAATTGAAACAGGGAACAAC	224808	57004	GGCAGACAAAGAAAGGGAAA	269395	101591	CAACCACCATCCAATACCCG
180222	12418	GGAATTGAAACAGGGAACAA	224809	57005	GGGCAGACAAAGAAAGGGAA	269396	101592	TCAACCACCATCCAATACCC
180223	12419	TGGAATTGAAACAGGGAACA	224810	57006	GGGGCAGACAAAGAAAGGGA	269397	101593	ATCAACCACCATCCAATACC
180224	12420	TTGGAATTGAAACAGGGAAC	224811	57007	GGGGGCAGACAAAGAAAGGG	269398	101594	CATCAACCACCATCCAATAC
180225	12421	TTTGGAATTGAAACAGGGAA	224812	57008	TGGGGGCAGACAAAGAAAGG	269399	101595	CCATCAACCACCATCCAATA
180226	12422	TTTTGGAATTGAAACAGGGA	224813	57009	GTGGGGGCAGACAAAGAAAG	269400	101596	ACCATCAACCACCATCCAAT
180227	12423	ATTTTGGAATTGAAACAGGG	224814	57010	GGTGGGGGCAGACAAAGAAA	269401	101597	AACCATCAACCACCATCCAA
180228	12424	AATTTTGGAATTGAAACAGG	224815	57011	GGGTGGGGGCAGACAAAGAA	269402	101598	AAACCATCAACCACCATCCA
180229	12425	GAATTTTGGAATTGAAACAG	224816	57012	AGGGTGGGGGCAGACAAAGA	269403	101599	AAAACCATCAACCACCATCC
180230	12426	TGAATTTTGGAATTGAAACA	224817	57013	GAGGGTGGGGGCAGACAAAG	269404	101600	GAAAACCATCAACCACCATC
180231	12427	ATGAATTTTGGAATTGAAAC	224818	57014	GGAGGGTGGGGGCAGACAAA	269405	101601	GGAAAACCATCAACCACCAT
180232	12428	TATGAATTTTGGAATTGAAA	224819	57015	TGGAGGGTGGGGGCAGACAA	269406	101602	TGGAAAACCATCAACCACCA
180233	12429	ATATGAATTTTGGAATTGAA	224820	57016	CTGGAGGGTGGGGGCAGACA	269407	101603	ATGGAAAACCATCAACCACC
180234	12430	GATATGAATTTTGGAATTGA	224821	57017	TCTGGAGGGTGGGGGCAGAC	269408	101604	AATGGAAAACCATCAACCAC
180235	12431	GGATATGAATTTTGGAATTG	224822	57018	ATCTGGAGGGTGGGGGCAGA	269409	101605	CAATGGAAAACCATCAACCA
180236	12432	TGGATATGAATTTTGGAATT	224823	57019	AATCTGGAGGGTGGGGGCAG	269410	101606	GCAATGGAAAACCATCAACC
180237	12433	TTGGATATGAATTTTGGAAT	224824	57020	AAATCTGGAGGGTGGGGGCA	269411	101607	AGCAATGGAAAACCATCAAC
180238	12434	ATTGGATATGAATTTTGGAA	224825	57021	GAAATCTGGAGGGTGGGGGC	269412	101608	AAGCAATGGAAAACCATCAA
180239	12435	GATTGGATATGAATTTTGGA	224826	57022	GGAAATCTGGAGGGTGGGGG	269413	101609	AAAGCAATGGAAAACCATCA
180240	12436	GGATTGGATATGAATTTTGG	224827	57023	CGGAAATCTGGAGGGTGGGG	269414	101610	GAAAGCAATGGAAAACCATC
180241	12437	CGGATTGGATATGAATTTTG	224828	57024	ACGGAAATCTGGAGGGTGGG	269415	101611	GGAAAGCAATGGAAAACCAT
180242	12438	ACGGATTGGATATGAATTTT	224829	57025	CACGGAAATCTGGAGGGTGG	269416	101612	AGGAAAGCAATGGAAAACCA
180243	12439	AACGGATTGGATATGAATTT	224830	57026	ACACGGAAATCTGGAGGGTG	269417	101613	CAGGAAAGCAATGGAAAACC
180244	12440	AAACGGATTGGATATGAATT	224831	57027	GACACGGAAATCTGGAGGGT	269418	101614	CCAGGAAAGCAATGGAAAAC
180245	12441	AAAACGGATTGGATATGAAT	224832	57028	AGACACGGAAATCTGGAGGG	269419	101615	CCCAGGAAAGCAATGGAAAA
180246	12442	CAAAACGGATTGGATATGAA	224833	57029	GAGACACGGAAATCTGGAGG	269420	101616	TCCCAGGAAAGCAATGGAAA
180247	12443	GCAAAACGGATTGGATATGA	224834	57030	GGAGACACGGAAATCTGGAG	269421	101617	TTCCCAGGAAAGCAATGGAA
180248	12444	TGCAAAACGGATTGGATATG	224835	57031	TGGAGACACGGAAATCTGGA	269422	101618	TTTCCCAGGAAAGCAATGGA
180249	12445	ATGCAAAACGGATTGGATAT	224836	57032	CTGGAGACACGGAAATCTGG	269423	101619	CTTTCCCAGGAAAGCAATGG
180250	12446	CATGCAAAACGGATTGGATA	224837	57033	ACTGGAGACACGGAAATCTG	269424	101620	CCTTTCCCAGGAAAGCAATG
180251	12447	GCATGCAAAACGGATTGGAT	224838	57034	CACTGGAGACACGGAAATCT	269425	101621	CCCTTTCCCAGGAAAGCAAT
180252	12448	GGCATGCAAAACGGATTGGA	224839	57035	ACACTGGAGACACGGAAATC	269426	101622	CCCCTTTCCCAGGAAAGCAA
180253	12449	TGGCATGCAAAACGGATTGG	224840	57036	GACACTGGAGACACGGAAAT	269427	101623	ACCCCTTTCCCAGGAAAGCA
180254	12450	ATGGCATGCAAAACGGATTG	224841	57037	AGACACTGGAGACACGGAAA	269428	101624	CACCCCTTTCCCAGGAAAGC
180255	12451	AATGGCATGCAAAACGGATT	224842	57038	GAGACACTGGAGACACGGAA	269429	101625	ACACCCCTTTCCCAGGAAAG
180256	12452	CAATGGCATGCAAAACGGAT	224843	57039	GGAGACACTGGAGACACGGA	269430	101626	GACACCCCTTTCCCAGGAAA
180257	12453	GCAATGGCATGCAAAACGGA	224844	57040	GGGAGACACTGGAGACACGG	269431	101627	AGACACCCCTTTCCCAGGAA
180258	12454	GGCAATGGCATGCAAAACGG	224845	57041	AGGGAGACACTGGAGACACG	269432	101628	GAGACACCCCTTTCCCAGGA

180259	12455	TGGCAATGGCATGCAAAACG	224846	57042	TAGGGAGACACTGGAGACAC	269433	101629	AGAGACACCCCTTTCCCAGG
180260	12456	TTGGCAATGGCATGCAAAAC	224847	57043	GTAGGGAGACACTGGAGACA	269434	101630	CAGAGACACCCCTTTCCCAG
180261	12457	TTTGGCAATGGCATGCAAAA	224848	57044	CGTAGGGAGACACTGGAGAC	269435	101631	ACAGAGACACCCCTTTCCCA
180262	12458	ATTTGGCAATGGCATGCAAA	224849	57045	TCGTAGGGAGACACTGGAGA	269436	101632	GACAGAGACACCCCTTTCCC
180263	12459	AATTTGGCAATGGCATGCAA	224850	57046	CTCGTAGGGAGACACTGGAG	269437	101633	GGACAGAGACACCCCTTTCC
180264	12460	GAATTTGGCAATGGCATGCA	224851	57047	CCTCGTAGGGAGACACTGGA	269438	101634	GGGACAGAGACACCCCTTTC
180265	12461	GGAATTTGGCAATGGCATGC	224852	57048	GCCTCGTAGGGAGACACTGG	269439	101635	AGGGACAGAGACACCCCTTT
180266	12462	AGGAATTTGGCAATGGCATG	224853	57049	TGCCTCGTAGGGAGACACTG	269440	101636	TAGGGACAGAGACACCCCTT
180267	12463	GAGGAATTTGGCAATGGCAT	224854	57050	ATGCCTCGTAGGGAGACACT	269441	101637	TTAGGGACAGAGACACCCCT
180268	12464	GGAGGAATTTGGCAATGGCA	224855	57051	CATGCCTCGTAGGGAGACAC	269442	101638	CTTAGGGACAGAGACACCCC
180269	12465	GGGAGGAATTTGGCAATGGC	224856	57052	TCATGCCTCGTAGGGAGACA	269443	101639	GCTTAGGGACAGAGACACCC
180270	12466	TGGGAGGAATTTGGCAATGG	224857	57053	TTCATGCCTCGTAGGGAGAC	269444	101640	TGCTTAGGGACAGAGACACC
180271	12467	CTGGGAGGAATTTGGCAATG	224858	57054	ATTCATGCCTCGTAGGGAGA	269445	101641	TTGCTTAGGGACAGAGACAC
180272	12468	TCTGGGAGGAATTTGGCAAT	224859	57055	AATTCATGCCTCGTAGGGAG	269446	101642	TTTGCTTAGGGACAGAGACA
180273	12469	CTCTGGGAGGAATTTGGCAA	224860	57056	CAATTCATGCCTCGTAGGGA	269447	101643	TTTTGCTTAGGGACAGAGAC
180274	12470	GCTCTGGGAGGAATTTGGCA	224861	57057	TCAATTCATGCCTCGTAGGG	269448	101644	TTTTTGCTTAGGGACAGAGA
180275	12471	TGCTCTGGGAGGAATTTGGC	224862	57058	CTCAATTCATGCCTCGTAGG	269449	101645	CTTTTTGCTTAGGGACAGAG
180276	12472	TTGCTCTGGGAGGAATTTGG	224863	57059	TCTCAATTCATGCCTCGTAG	269450	101646	CCTTTTTGCTTAGGGACAGA
180277	12473	GTTGCTCTGGGAGGAATTTG	224864	57060	GTCTCAATTCATGCCTCGTA	269451	101647	GCCTTTTTGCTTAGGGACAG
180278	12474	GGTTGCTCTGGGAGGAATTT	224865	57061	AGTCTCAATTCATGCCTCGT	269452	101648	TGCCTTTTTGCTTAGGGACA
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180281	12477	CGGGGTTGCTCTGGGAGGAA	224868	57064	CCCAGTCTCAATTCATGCCT	269455	101651	CCCTGCCTTTTTGCTTAGGG
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180283	12479	GACGGGGTTGCTCTGGGAGG	224870	57066	CTCCCAGTCTCAATTCATGC	269457	101653	CTCCCTGCCTTTTTGCTTAG
180284	12480	TGACGGGGTTGCTCTGGGAG	224871	57067	CCTCCCAGTCTCAATTCATG	269458	101654	CCTCCCTGCCTTTTTGCTTA
180285	12481	GTGACGGGGTTGCTCTGGGA	224872	57068	CCCTCCCAGTCTCAATTCAT	269459	101655	TCCTCCCTGCCTTTTTGCTT
180286	12482	GGTGACGGGGTTGCTCTGGG	224873	57069	ACCCTCCCAGTCTCAATTCA	269460	101656	TTCCTCCCTGCCTTTTTGCT
180287	12483	AGGTGACGGGGTTGCTCTGG	224874	57070	CACCCTCCCAGTCTCAATTC	269461	101657	CTTCCTCCCTGCCTTTTTGC
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180289	12485	GCAGGTGACGGGGTTGCTCT	224876	57072	CACACCCTCCCAGTCTCAAT	269463	101659	CTCTTCCTCCCTGCCTTTTT
180290	12486	GGCAGGTGACGGGGTTGCTC	224877	57073	TCACACCCTCCCAGTCTCAA	269464	101660	TCTCTTCCTCCCTGCCTTTT
180291	12487	GGGCAGGTGACGGGGTTGCT	224878	57074	ATCACACCCTCCCAGTCTCA	269465	101661	ATCTCTTCCTCCCTGCCTTT
180292	12488	AGGGCAGGTGACGGGGTTGC	224879	57075	AATCACACCCTCCCAGTCTC	269466	101662	CATCTCTTCCTCCCTGCCTT
180293	12489	CAGGGCAGGTGACGGGGTTG	224880	57076	GAATCACACCCTCCCAGTCT	269467	101663	GCATCTCTTCCTCCCTGCCT
180294	12490	CCAGGGCAGGTGACGGGGTT	224881	57077	AGAATCACACCCTCCCAGTC	269468	101664	AGCATCTCTTCCTCCCTGCC
180295	12491	GCCAGGGCAGGTGACGGGGT	224882	57078	CAGAATCACACCCTCCCAGT	269469	101665	AAGCATCTCTTCCTCCCTGC
180296	12492	GGCCAGGGCAGGTGACGGGG	224883	57079	TCAGAATCACACCCTCCCAG	269470	101666	GAAGCATCTCTTCCTCCCTG
180297	12493	GGGCCAGGGCAGGTGACGGG	224884	57080	TTCAGAATCACACCCTCCCA	269471	101667	GGAAGCATCTCTTCCTCCCT
180298	12494	AGGGCCAGGGCAGGTGACGG	224885	57081	CTTCAGAATCACACCCTCCC	269472	101668	GGGAAGCATCTCTTCCTCCC
180299	12495	GAGGGCCAGGGCAGGTGACG	224886	57082	TCTTCAGAATCACACCCTCC	269473	101669	GGGGAAGCATCTCTTCCTCC
180300	12496	AGAGGGCCAGGGCAGGTGAC	224887	57083	TTCTTCAGAATCACACCCTC	269474	101670	TGGGGAAGCATCTCTTCCTC
180301	12497	GAGAGGGCCAGGGCAGGTGA	224888	57084	CTTCTTCAGAATCACACCCT	269475	101671	CTGGGGAAGCATCTCTTCCT
180302	12498	GGAGAGGGCCAGGGCAGGTG	224889	57085	CCTTCTTCAGAATCACACCC	269476	101672	CCTGGGGAAGCATCTCTTCC
180303	12499	TGGAGAGGGCCAGGGCAGGT	224890	57086	GCCTTCTTCAGAATCACACC	269477	101673	CCCTGGGGAAGCATCTCTTC
180304	12500	TTGGAGAGGGCCAGGGCAGG	224891	57087	TGCCTTCTTCAGAATCACAC	269478	101674	GCCCTGGGGAAGCATCTCTT
180305	12501	CTTGGAGAGGGCCAGGGCAG	224892	57088	GTGCCTTCTTCAGAATCACA	269479	101675	TGCCCTGGGGAAGCATCTCT
180306	12502	ACTTGGAGAGGGCCAGGGCA	224893	57089	GGTGCCTTCTTCAGAATCAC	269480	101676	CTGCCCTGGGGAAGCATCTC
180307	12503	CACTTGGAGAGGGCCAGGGC	224894	57090	TGGTGCCTTCTTCAGAATCA	269481	101677	GCTGCCCTGGGGAAGCATCT
180308	12504	ACACTTGGAGAGGGCCAGGG	224895	57091	TTGGTGCCTTCTTCAGAATC	269482	101678	GGCTGCCCTGGGGAAGCATC
180309	12505	CACACTTGGAGAGGGCCAGG	224896	57092	GTTGGTGCCTTCTTCAGAAT	269483	101679	CGGCTGCCCTGGGGAAGCAT
180310	12506	CCACACTTGGAGAGGGCCAG	224897	57093	TGTTGGTGCCTTCTTCAGAA	269484	101680	ACGGCTGCCCTGGGGAAGCA
180311	12507	ACCACACTTGGAGAGGGCCA	224898	57094	CTGTTGGTGCCTTCTTCAGA	269485	101681	GACGGCTGCCCTGGGGAAGC
180312	12508	GACCACACTTGGAGAGGGCC	224899	57095	ACTGTTGGTGCCTTCTTCAG	269486	101682	AGACGGCTGCCCTGGGGAAG
180313	12509	GGACCACACTTGGAGAGGGC	224900	57096	CACTGTTGGTGCCTTCTTCA	269487	101683	CAGACGGCTGCCCTGGGGAA
180314	12510	AGGACCACACTTGGAGAGGG	224901	57097	TCACTGTTGGTGCCTTCTTC	269488	101684	GCAGACGGCTGCCCTGGGGA
180315	12511	CAGGACCACACTTGGAGAGG	224902	57098	GTCACTGTTGGTGCCTTCTT	269489	101685	AGCAGACGGCTGCCCTGGGG
180316	12512	GCAGGACCACACTTGGAGAG	224903	57099	AGTCACTGTTGGTGCCTTCT	269490	101686	CAGCAGACGGCTGCCCTGGG
180317	12513	GGCAGGACCACACTTGGAGA	224904	57100	GAGTCACTGTTGGTGCCTTC	269491	101687	ACAGCAGACGGCTGCCCTGG
180318	12514	TGGCAGGACCACACTTGGAG	224905	57101	TGAGTCACTGTTGGTGCCTT	269492	101688	TACAGCAGACGGCTGCCCTG
180319	12515	ATGGCAGGACCACACTTGGA	224906	57102	CTGAGTCACTGTTGGTGCCT	269493	101689	CTACAGCAGACGGCTGCCCT
180320	12516	CATGGCAGGACCACACTTGG	224907	57103	GCTGAGTCACTGTTGGTGCC	269494	101690	GCTACAGCAGACGGCTGCCC
180321	12517	CCATGGCAGGACCACACTTG	224908	57104	AGCTGAGTCACTGTTGGTGC	269495	101691	AGCTACAGCAGACGGCTGCC
180322	12518	CCCATGGCAGGACCACACTT	224909	57105	TAGCTGAGTCACTGTTGGTG	269496	101692	CAGCTACAGCAGACGGCTGC
180323	12519	GCCCATGGCAGGACCACACT	224910	57106	CTAGCTGAGTCACTGTTGGT	269497	101693	GCAGCTACAGCAGACGGCTG
180324	12520	TGCCCATGGCAGGACCACAC	224911	57107	GCTAGCTGAGTCACTGTTGG	269498	101694	CGCAGCTACAGCAGACGGCT
180325	12521	ATGCCCATGGCAGGACCACA	224912	57108	GGCTAGCTGAGTCACTGTTG	269499	101695	GCGCAGCTACAGCAGACGGC
180326	12522	GATGCCCATGGCAGGACCAC	224913	57109	GGGCTAGCTGAGTCACTGTT	269500	101696	AGCGCAGCTACAGCAGACGG
180327	12523	CGATGCCCATGGCAGGACCA	224914	57110	GGGGCTAGCTGAGTCACTGT	269501	101697	AAGCGCAGCTACAGCAGACG
180328	12524	GCGATGCCCATGGCAGGACC	224915	57111	AGGGGCTAGCTGAGTCACTG	269502	101698	GAAGCGCAGCTACAGCAGAC
180329	12525	GGCGATGCCCATGGCAGGAC	224916	57112	AAGGGGCTAGCTGAGTCACT	269503	101699	GGAAGCGCAGCTACAGCAGA
180330	12526	AGGCGATGCCCATGGCAGGA	224917	57113	GAAGGGGCTAGCTGAGTCAC	269504	101700	TGGAAGCGCAGCTACAGCAG

180331	12527	CAGGCGATGCCCATGGCAGG	224918	57114	GGAAGGGGCTAGCTGAGTCA	269505	101701	TTGGAAGCGCAGCTACAGCA
180332	12528	GCAGGCGATGCCCATGGCAG	224919	57115	GGGAAGGGGCTAGCTGAGTC	269506	101702	GTTGGAAGCGCAGCTACAGC
180333	12529	AGCAGGCGATGCCCATGGCA	224920	57116	GGGGAAGGGGCTAGCTGAGT	269507	101703	GGTTGGAAGCGCAGCTACAG
180334	12530	TAGCAGGCGATGCCCATGGC	224921	57117	GGGGGAAGGGGCTAGCTGAG	269508	101704	AGGTTGGAAGCGCAGCTACA
180335	12531	TTAGCAGGCGATGCCCATGG	224922	57118	TGGGGGAAGGGGCTAGCTGA	269509	101705	CAGGTTGGAAGCGCAGCTAC
180336	12532	CTTAGCAGGCGATGCCCATG	224923	57119	GTGGGGGAAGGGGCTAGCTG	269510	101706	CCAGGTTGGAAGCGCAGCTA
180337	12533	GCTTAGCAGGCGATGCCCAT	224924	57120	GGTGGGGGAAGGGGCTAGCT	269511	101707	GCCAGGTTGGAAGCGCAGCT
180338	12534	GGCTTAGCAGGCGATGCCCA	224925	57121	GGGTGGGGGAAGGGGCTAGC	269512	101708	AGCCAGGTTGGAAGCGCAGC
180339	12535	TGGCTTAGCAGGCGATGCCC	224926	57122	GGGGTGGGGGAAGGGGCTAG	269513	101709	AAGCCAGGTTGGAAGCGCAG
180340	12536	TTGGCTTAGCAGGCGATGCC	224927	57123	CGGGGTGGGGGAAGGGGCTA	269514	101710	GAAGCCAGGTTGGAAGCGCA
180341	12537	CTTGGCTTAGCAGGCGATGC	224928	57124	GCGGGGTGGGGGAAGGGGCT	269515	101711	GGAAGCCAGGTTGGAAGCGC
180342	12538	GCTTGGCTTAGCAGGCGATG	224929	57125	GGCGGGGTGGGGGAAGGGGC	269516	101712	TGGAAGCCAGGTTGGAAGCG
180343	12539	AGCTTGGCTTAGCAGGCGAT	224930	57126	GGGCGGGGTGGGGGAAGGGG	269517	101713	GTGGAAGCCAGGTTGGAAGC
180344	12540	CAGCTTGGCTTAGCAGGCGA	224931	57127	GGGGCGGGGTGGGGGAAGGG	269518	101714	GGTGGAAGCCAGGTTGGAAG
180345	12541	CCAGCTTGGCTTAGCAGGCG	224932	57128	GGGGGCGGGGTGGGGGAAGG	269519	101715	AGGTGGAAGCCAGGTTGGAA
180346	12542	GCCAGCTTGGCTTAGCAGGC	224933	57129	GGGGGGCGGGGTGGGGGAAG	269520	101716	CAGGTGGAAGCCAGGTTGGA
180347	12543	GGCCAGCTTGGCTTAGCAGG	224934	57130	CGGGGGGCGGGGTGGGGGAA	269521	101717	GCAGGTGGAAGCCAGGTTGG
180348	12544	AGGCCAGCTTGGCTTAGCAG	224935	57131	CCGGGGGGCGGGGTGGGGGA	269522	101718	GGCAGGTGGAAGCCAGGTTG
180349	12545	GAGGCCAGCTTGGCTTAGCA	224936	57132	CCCGGGGGGCGGGGTGGGGG	269523	101719	AGGCAGGTGGAAGCCAGGTT
180350	12546	CGAGGCCAGCTTGGCTTAGC	224937	57133	GCCCGGGGGGCGGGGTGGGG	269524	101720	TAGGCAGGTGGAAGCCAGGT
180351	12547	TCGAGGCCAGCTTGGCTTAG	224938	57134	GGCCCGGGGGGCGGGGTGGG	269525	101721	TTAGGCAGGTGGAAGCCAGG
180352	12548	CTCGAGGCCAGCTTGGCTTA	224939	57135	AGGCCCGGGGGGCGGGGTGG	269526	101722	GTTAGGCAGGTGGAAGCCAG
180353	12549	GCTCGAGGCCAGCTTGGCTT	224940	57136	GAGGCCCGGGGGGCGGGGTG	269527	101723	GGTTAGGCAGGTGGAAGCCA
180354	12550	AGCTCGAGGCCAGCTTGGCT	224941	57137	TGAGGCCCGGGGGGCGGGGT	269528	101724	GGGTTAGGCAGGTGGAAGCC
180355	12551	CAGCTCGAGGCCAGCTTGGC	224942	57138	TTGAGGCCCGGGGGGCGGGG	269529	101725	TGGGTTAGGCAGGTGGAAGC
180356	12552	GCAGCTCGAGGCCAGCTTGG	224943	57139	ATTGAGGCCCGGGGGGCGGG	269530	101726	CTGGGTTAGGCAGGTGGAAG
180357	12553	GGCAGCTCGAGGCCAGCTTG	224944	57140	AATTGAGGCCCGGGGGGCGG	269531	101727	ACTGGGTTAGGCAGGTGGAA
180358	12554	AGGCAGCTCGAGGCCAGCTT	224945	57141	AAATTGAGGCCCGGGGGGCG	269532	101728	CACTGGGTTAGGCAGGTGGA
180359	12555	CAGGCAGCTCGAGGCCAGCT	224946	57142	TAAATTGAGGCCCGGGGGGC	269533	101729	CCACTGGGTTAGGCAGGTGG
180360	12556	GCAGGCAGCTCGAGGCCAGC	224947	57143	CTAAATTGAGGCCCGGGGGG	269534	101730	ACCACTGGGTTAGGCAGGTG
180361	12557	GGCAGGCAGCTCGAGGCCAG	224948	57144	GCTAAATTGAGGCCCGGGGG	269535	101731	CACCACTGGGTTAGGCAGGT
180362	12558	GGGCAGGCAGCTCGAGGCCA	224949	57145	AGCTAAATTGAGGCCCGGGG	269536	101732	TCACCACTGGGTTAGGCAGG
180363	12559	CGGGCAGGCAGCTCGAGGCC	224950	57146	TAGCTAAATTGAGGCCCGGG	269537	101733	CTCACCACTGGGTTAGGCAG
180364	12560	CCGGGCAGGCAGCTCGAGGC	224951	57147	TTAGCTAAATTGAGGCCCGG	269538	101734	GCTCACCACTGGGTTAGGCA
180365	12561	CCCGGGCAGGCAGCTCGAGG	224952	57148	TTTAGCTAAATTGAGGCCCG	269539	101735	GGCTCACCACTGGGTTAGGC
180366	12562	ACCCGGGCAGGCAGCTCGAG	224953	57149	TTTTAGCTAAATTGAGGCCC	269540	101736	AGGCTCACCACTGGGTTAGG
180367	12563	GACCCGGGCAGGCAGCTCGA	224954	57150	TTTTTAGCTAAATTGAGGCC	269541	101737	CAGGCTCACCACTGGGTTAG
180368	12564	GGACCCGGGCAGGCAGCTCG	224955	57151	TTTTTTAGCTAAATTGAGGC	269542	101738	CCAGGCTCACCACTGGGTTA
180369	12565	GGGACCCGGGCAGGCAGCTC	224956	57152	GTTTTTTAGCTAAATTGAGG	269543	101739	CCCAGGCTCACCACTGGGTT
180370	12566	GGGGACCCGGGCAGGCAGCT	224957	57153	GGTTTTTTAGCTAAATTGAG	269544	101740	TCCCAGGCTCACCACTGGGT
180371	12567	TGGGGACCCGGGCAGGCAGC	224958	57154	TGGTTTTTTAGCTAAATTGA	269545	101741	TTCCCAGGCTCACCACTGGG
180372	12568	GTGGGGACCCGGGCAGGCAG	224959	57155	GTGGTTTTTTAGCTAAATTG	269546	101742	ATTCCCAGGCTCACCACTGG
180373	12569	TGTGGGGACCCGGGCAGGCA	224960	57156	TGTGGTTTTTTAGCTAAATT	269547	101743	CATTCCCAGGCTCACCACTG
180374	12570	GTGTGGGGACCCGGGCAGGC	224961	57157	CTGTGGTTTTTTAGCTAAAT	269548	101744	CCATTCCCAGGCTCACCACT
180375	12571	GGTGTGGGGACCCGGGCAGG	224962	57158	CCTGTGGTTTTTTAGCTAAA	269549	101745	TCCATTCCCAGGCTCACCAC
180376	12572	AGGTGTGGGGACCCGGGCAG	224963	57159	CCCTGTGGTTTTTTAGCTAA	269550	101746	GTCCATTCCCAGGCTCACCA
180377	12573	AAGGTGTGGGGACCCGGGCA	224964	57160	TCCCTGTGGTTTTTTAGCTA	269551	101747	GGTCCATTCCCAGGCTCACC
180378	12574	CAAGGTGTGGGGACCCGGGC	224965	57161	GTCCCTGTGGTTTTTTAGCT	269552	101748	GGGTCCATTCCCAGGCTCAC
180379	12575	CCAAGGTGTGGGGACCCGGG	224966	57162	CGTCCCTGTGGTTTTTTAGC	269553	101749	TGGGTCCATTCCCAGGCTCA
180380	12576	GCCAAGGTGTGGGGACCCGG	224967	57163	CCGTCCCTGTGGTTTTTTAG	269554	101750	GTGGGTCCATTCCCAGGCTC
180381	12577	AGCCAAGGTGTGGGGACCCG	224968	57164	TCCGTCCCTGTGGTTTTTTA	269555	101751	CGTGGGTCCATTCCCAGGCT
180382	12578	GAGCCAAGGTGTGGGGACCC	224969	57165	GTCCGTCCCTGTGGTTTTTT	269556	101752	CCGTGGGTCCATTCCCAGGC
180383	12579	TGAGCCAAGGTGTGGGGACC	224970	57166	AGTCCGTCCCTGTGGTTTTT	269557	101753	CCCGTGGGTCCATTCCCAGG
180384	12580	GTGAGCCAAGGTGTGGGGAC	224971	57167	GAGTCCGTCCCTGTGGTTTT	269558	101754	TCCCGTGGGTCCATTCCCAG
180385	12581	GGTGAGCCAAGGTGTGGGGA	224972	57168	TGAGTCCGTCCCTGTGGTTT	269559	101755	GTCCCGTGGGTCCATTCCCA
180386	12582	AGGTGAGCCAAGGTGTGGGG	224973	57169	CTGAGTCCGTCCCTGTGGTT	269560	101756	TGTCCCGTGGGTCCATTCCC
180387	12583	GAGGTGAGCCAAGGTGTGGG	224974	57170	CCTGAGTCCGTCCCTGTGGT	269561	101757	CTGTCCCGTGGGTCCATTCC
180388	12584	GGAGGTGAGCCAAGGTGTGG	224975	57171	TCCTGAGTCCGTCCCTGTGG	269562	101758	CCTGTCCCGTGGGTCCATTC
180389	12585	GGGAGGTGAGCCAAGGTGTG	224976	57172	CTCCTGAGTCCGTCCCTGTG	269563	101759	GCCTGTCCCGTGGGTCCATT
180390	12586	AGGGAGGTGAGCCAAGGTGT	224977	57173	CCTCCTGAGTCCGTCCCTGT	269564	101760	TGCCTGTCCCGTGGGTCCAT
180391	12587	CAGGGAGGTGAGCCAAGGTG	224978	57174	GCCTCCTGAGTCCGTCCCTG	269565	101761	CTGCCTGTCCCGTGGGTCCA
180392	12588	GCAGGGAGGTGAGCCAAGGT	224979	57175	TGCCTCCTGAGTCCGTCCCT	269566	101762	GCTGCCTGTCCCGTGGGTCC
180393	12589	GGCAGGGAGGTGAGCCAAGG	224980	57176	TTGCCTCCTGAGTCCGTCCC	269567	101763	GGCTGCCTGTCCCGTGGGTC
180394	12590	GGGCAGGGAGGTGAGCCAAG	224981	57177	ATTGCCTCCTGAGTCCGTCC	269568	101764	GGGCTGCCTGTCCCGTGGGT
180395	12591	TGGGCAGGGAGGTGAGCCAA	224982	57178	TATTGCCTCCTGAGTCCGTC	269569	101765	GGGGCTGCCTGTCCCGTGGG
180396	12592	CTGGGCAGGGAGGTGAGCCA	224983	57179	GTATTGCCTCCTGAGTCCGT	269570	101766	GGGGGCTGCCTGTCCCGTGG
180397	12593	ACTGGGCAGGGAGGTGAGCC	224984	57180	GGTATTGCCTCCTGAGTCCG	269571	101767	TGGGGGCTGCCTGTCCCGTG
180398	12594	GACTGGGCAGGGAGGTGAGC	224985	57181	AGGTATTGCCTCCTGAGTCC	269572	101768	CTGGGGGCTGCCTGTCCCGT
180399	12595	GGACTGGGCAGGGAGGTGAG	224986	57182	AAGGTATTGCCTCCTGAGTC	269573	101769	CCTGGGGGCTGCCTGTCCCG
180400	12596	GGGACTGGGCAGGGAGGTGA	224987	57183	AAAGGTATTGCCTCCTGAGT	269574	101770	CCCTGGGGGCTGCCTGTCCC
180401	12597	CGGGACTGGGCAGGGAGGTG	224988	57184	GAAAGGTATTGCCTCCTGAG	269575	101771	GCCCTGGGGGCTGCCTGTCC
180402	12598	GCGGGACTGGGCAGGGAGGT	224989	57185	GGAAAGGTATTGCCTCCTGA	269576	101772	GGCCCTGGGGGCTGCCTGTC

180403	12599	GGCGGGACTGGGCAGGGAGG	224990	57186	TGGAAAGGTATTGCCTCCTG	269577	101773	AGGCCCTGGGGGCTGCCTGT
180404	12600	AGGCGGGACTGGGCAGGGAG	224991	57187	TTGGAAAGGTATTGCCTCCT	269578	101774	AAGGCCCTGGGGGCTGCCTG
180405	12601	GAGGCGGGACTGGGCAGGGA	224992	57188	CTTGGAAAGGTATTGCCTCC	269579	101775	AAAGGCCCTGGGGGCTGCCT
180406	12602	GGAGGCGGGACTGGGCAGGG	224993	57189	CCTTGGAAAGGTATTGCCTC	269580	101776	AAAAGGCCCTGGGGGCTGCC
180407	12603	AGGAGGCGGGACTGGGCAGG	224994	57190	CCCTTGGAAAGGTATTGCCT	269581	101777	GAAAAGGCCCTGGGGGCTGC
180408	12604	CAGGAGGCGGGACTGGGCAG	224995	57191	ACCCTTGGAAAGGTATTGCC	269582	101778	AGAAAAGGCCCTGGGGGCTG
180409	12605	GCAGGAGGCGGGACTGGGCA	224996	57192	GACCCTTGGAAAGGTATTGC	269583	101779	CAGAAAAGGCCCTGGGGGCT
180410	12606	GGCAGGAGGCGGGACTGGGC	224997	57193	GGACCCTTGGAAAGGTATTG	269584	101780	TCAGAAAAGGCCCTGGGGGC
180411	12607	TGGCAGGAGGCGGGACTGGG	224998	57194	GGGACCCTTGGAAAGGTATT	269585	101781	GTCAGAAAAGGCCCTGGGGG
180412	12608	CTGGCAGGAGGCGGGACTGG	224999	57195	AGGGACCCTTGGAAAGGTAT	269586	101782	GGTCAGAAAAGGCCCTGGGG
180413	12609	GCTGGCAGGAGGCGGGACTG	225000	57196	TAGGGACCCTTGGAAAGGTA	269587	101783	GGGTCAGAAAAGGCCCTGGG
180414	12610	GGCTGGCAGGAGGCGGGACT	225001	57197	TTAGGGACCCTTGGAAAGGT	269588	101784	GGGGTCAGAAAAGGCCCTGG
180415	12611	AGGCTGGCAGGAGGCGGGAC	225002	57198	TTTAGGGACCCTTGGAAAGG	269589	101785	TGGGGTCAGAAAAGGCCCTG
180416	12612	CAGGCTGGCAGGAGGCGGGA	225003	57199	TTTTAGGGACCCTTGGAAAG	269590	101786	GTGGGGTCAGAAAAGGCCCT
180417	12613	GCAGGCTGGCAGGAGGCGGG	225004	57200	TTTTTAGGGACCCTTGGAAA	269591	101787	GGTGGGGTCAGAAAAGGCCC
180418	12614	GGCAGGCTGGCAGGAGGCGG	225005	57201	TTTTTTAGGGACCCTTGGAA	269592	101788	GGGTGGGGTCAGAAAAGGCC
180419	12615	GGGCAGGCTGGCAGGAGGCG	225006	57202	ATTTTTTAGGGACCCTTGGA	269593	101789	TGGGTGGGGTCAGAAAAGGC
180420	12616	AGGGCAGGCTGGCAGGAGGC	225007	57203	CATTTTTTAGGGACCCTTGG	269594	101790	GTGGGTGGGGTCAGAAAAGG
180421	12617	CAGGGCAGGCTGGCAGGAGG	225008	57204	ACATTTTTTAGGGACCCTTG	269595	101791	AGTGGGTGGGGTCAGAAAAG
180422	12618	ACAGGGCAGGCTGGCAGGAG	225009	57205	GACATTTTTTAGGGACCCTT	269596	101792	GAGTGGGTGGGGTCAGAAAA
180423	12619	CACAGGGCAGGCTGGCAGGA	225010	57206	GGACATTTTTTAGGGACCCT	269597	101793	CGAGTGGGTGGGGTCAGAAA
180424	12620	CCACAGGGCAGGCTGGCAGG	225011	57207	GGGACATTTTTTAGGGACCC	269598	101794	TCGAGTGGGTGGGGTCAGAA
180425	12621	GCCACAGGGCAGGCTGGCAG	225012	57208	TGGGACATTTTTTAGGGACC	269599	101795	CTCGAGTGGGTGGGGTCAGA
180426	12622	AGCCACAGGGCAGGCTGGCA	225013	57209	ATGGGACATTTTTTAGGGAC	269600	101796	ACTCGAGTGGGTGGGGTCAG
180427	12623	GAGCCACAGGGCAGGCTGGC	225014	57210	AATGGGACATTTTTTAGGGA	269601	101797	GACTCGAGTGGGTGGGGTCA
180428	12624	GGAGCCACAGGGCAGGCTGG	225015	57211	AAATGGGACATTTTTTAGGG	269602	101798	GGACTCGAGTGGGTGGGGTC
180429	12625	AGGAGCCACAGGGCAGGCTG	225016	57212	AAAATGGGACATTTTTTAGG	269603	101799	AGGACTCGAGTGGGTGGGGT
180430	12626	AAGGAGCCACAGGGCAGGCT	225017	57213	TAAAATGGGACATTTTTTAG	269604	101800	CAGGACTCGAGTGGGTGGGG
180431	12627	GAAGGAGCCACAGGGCAGGC	225018	57214	CTAAAATGGGACATTTTTTA	269605	101801	CCAGGACTCGAGTGGGTGGG
180432	12628	TGAAGGAGCCACAGGGCAGG	225019	57215	ACTAAAATGGGACATTTTTT	269606	101802	GCCAGGACTCGAGTGGGTGG
180433	12629	ATGAAGGAGCCACAGGGCAG	225020	57216	CACTAAAATGGGACATTTTT	269607	101803	AGCCAGGACTCGAGTGGGTG
180434	12630	TATGAAGGAGCCACAGGGCA	225021	57217	ACACTAAAATGGGACATTTT	269608	101804	AAGCCAGGACTCGAGTGGGT
180435	12631	CTATGAAGGAGCCACAGGGC	225022	57218	GACACTAAAATGGGACATTT	269609	101805	GAAGCCAGGACTCGAGTGGG
180436	12632	TCTATGAAGGAGCCACAGGG	225023	57219	GGACACTAAAATGGGACATT	269610	101806	TGAAGCCAGGACTCGAGTGG
180437	12633	ATCTATGAAGGAGCCACAGG	225024	57220	TGGACACTAAAATGGGACAT	269611	101807	GTGAAGCCAGGACTCGAGTG
180438	12634	CATCTATGAAGGAGCCACAG	225025	57221	CTGGACACTAAAATGGGACA	269612	101808	AGTGAAGCCAGGACTCGAGT
180439	12635	GCATCTATGAAGGAGCCACA	225026	57222	CCTGGACACTAAAATGGGAC	269613	101809	GAGTGAAGCCAGGACTCGAG
180440	12636	GGCATCTATGAAGGAGCCAC	225027	57223	ACCTGGACACTAAAATGGGA	269614	101810	GGAGTGAAGCCAGGACTCGA
180441	12637	CGGCATCTATGAAGGAGCCA	225028	57224	AACCTGGACACTAAAATGGG	269615	101811	GGGAGTGAAGCCAGGACTCG
180442	12638	ACGGCATCTATGAAGGAGCC	225029	57225	AAACCTGGACACTAAAATGG	269616	101812	AGGGAGTGAAGCCAGGACTC
180443	12639	CACGGCATCTATGAAGGAGC	225030	57226	GAAACCTGGACACTAAAATG	269617	101813	AAGGGAGTGAAGCCAGGACT
180444	12640	GCACGGCATCTATGAAGGAG	225031	57227	TGAAACCTGGACACTAAAAT	269618	101814	GAAGGGAGTGAAGCCAGGAC
180445	12641	AGCACGGCATCTATGAAGGA	225032	57228	GTGAAACCTGGACACTAAAA	269619	101815	GGAAGGGAGTGAAGCCAGGA
180446	12642	GAGCACGGCATCTATGAAGG	225033	57229	AGTGAAACCTGGACACTAAA	269620	101816	AGGAAGGGAGTGAAGCCAGG
180447	12643	AGAGCACGGCATCTATGAAG	225034	57230	GAGTGAAACCTGGACACTAA	269621	101817	AAGGAAGGGAGTGAAGCCAG
180448	12644	AAGAGCACGGCATCTATGAA	225035	57231	TGAGTGAAACCTGGACACTA	269622	101818	GAAGGAAGGGAGTGAAGCCA
180449	12645	AAAGAGCACGGCATCTATGA	225036	57232	TTGAGTGAAACCTGGACACT	269623	101819	GGAAGGAAGGGAGTGAAGCC
180450	12646	GAAAGAGCACGGCATCTATG	225037	57233	GTTGAGTGAAACCTGGACAC	269624	101820	AGGAAGGAAGGGAGTGAAGC
180451	12647	AGAAAGAGCACGGCATCTAT	225038	57234	AGTTGAGTGAAACCTGGACA	269625	101821	AAGGAAGGAAGGGAGTGAAG
180452	12648	CAGAAAGAGCACGGCATCTA	225039	57235	AAGTTGAGTGAAACCTGGAC	269626	101822	GAAGGAAGGAAGGGAGTGAA
180453	12649	GCAGAAAGAGCACGGCATCT	225040	57236	AAAGTTGAGTGAAACCTGGA	269627	101823	GGAAGGAAGGAAGGGAGTGA
180454	12650	GGCAGAAAGAGCACGGCATC	225041	57237	TAAAGTTGAGTGAAACCTGG	269628	101824	GGGAAGGAAGGAAGGGAGTG
180455	12651	GGGCAGAAAGAGCACGGCAT	225042	57238	CTAAAGTTGAGTGAAACCTG	269629	101825	TGGGAAGGAAGGAAGGGAGT
180456	12652	GGGGCAGAAAGAGCACGGCA	225043	57239	ACTAAAGTTGAGTGAAACCT	269630	101826	CTGGGAAGGAAGGAAGGGAG
180457	12653	AGGGGCAGAAAGAGCACGGC	225044	57240	CACTAAAGTTGAGTGAAACC	269631	101827	CCTGGGAAGGAAGGAAGGGA
180458	12654	AAGGGGCAGAAAGAGCACGG	225045	57241	GCACTAAAGTTGAGTGAAAC	269632	101828	ACCTGGGAAGGAAGGAAGGG
180459	12655	CAAGGGGCAGAAAGAGCACG	225046	57242	GGCACTAAAGTTGAGTGAAA	269633	101829	CACCTGGGAAGGAAGGAAGG
180460	12656	GCAAGGGGCAGAAAGAGCAC	225047	57243	AGGCACTAAAGTTGAGTGAA	269634	101830	TCACCTGGGAAGGAAGGAAG
180461	12657	AGCAAGGGGCAGAAAGAGCA	225048	57244	GAGGCACTAAAGTTGAGTGA	269635	101831	TTCACCTGGGAAGGAAGGAA
180462	12658	GAGCAAGGGGCAGAAAGAGC	225049	57245	GGAGGCACTAAAGTTGAGTG	269636	101832	GTTCACCTGGGAAGGAAGGA
180463	12659	TGAGCAAGGGGCAGAAAGAG	225050	57246	GGGAGGCACTAAAGTTGAGT	269637	101833	GGTTCACCTGGGAAGGAAGG
180464	12660	GTGAGCAAGGGGCAGAAAGA	225051	57247	GGGGAGGCACTAAAGTTGAG	269638	101834	AGGTTCACCTGGGAAGGAAG
180465	12661	GGTGAGCAAGGGGCAGAAAG	225052	57248	AGGGGAGGCACTAAAGTTGA	269639	101835	GAGGTTCACCTGGGAAGGAA
180466	12662	GGGTGAGCAAGGGGCAGAAA	225053	57249	TAGGGGAGGCACTAAAGTTG	269640	101836	GGAGGTTCACCTGGGAAGGA
180467	12663	TGGGTGAGCAAGGGGCAGAA	225054	57250	TTAGGGGAGGCACTAAAGTT	269641	101837	TGGAGGTTCACCTGGGAAGG
180468	12664	ATGGGTGAGCAAGGGGCAGA	225055	57251	TTTAGGGGAGGCACTAAAGT	269642	101838	TTGGAGGTTCACCTGGGAAG
180469	12665	CATGGGTGAGCAAGGGGCAG	225056	57252	TTTTAGGGGAGGCACTAAAG	269643	101839	TTTGGAGGTTCACCTGGGAA
180470	12666	CCATGGGTGAGCAAGGGGCA	225057	57253	ATTTTAGGGGAGGCACTAAA	269644	101840	TTTTGGAGGTTCACCTGGGA
180471	12667	GCCATGGGTGAGCAAGGGGC	225058	57254	CATTTTAGGGGAGGCACTAA	269645	101841	ATTTTGGAGGTTCACCTGGG
180472	12668	TGCCATGGGTGAGCAAGGGG	225059	57255	ACATTTTAGGGGAGGCACTA	269646	101842	GATTTTGGAGGTTCACCTGG
180473	12669	CTGCCATGGGTGAGCAAGGG	225060	57256	CACATTTTAGGGGAGGCACT	269647	101843	TGATTTTGGAGGTTCACCTG
180474	12670	GCTGCCATGGGTGAGCAAGG	225061	57257	ACACATTTTAGGGGAGGCAC	269648	101844	CTGATTTTGGAGGTTCACCT

180475	12671	GGCTGCCATGGGTGAGCAAG	225062	57258	AACACATTTTAGGGGAGGCA	269649	101845	CCTGATTTTGGAGGTTCACC
180476	12672	AGGCTGCCATGGGTGAGCAA	225063	57259	GAACACATTTTAGGGGAGGC	269650	101846	CCCTGATTTTGGAGGTTCAC
180477	12673	AAGGCTGCCATGGGTGAGCA	225064	57260	GGAACACATTTTAGGGGAGG	269651	101847	CCCCTGATTTTGGAGGTTCA
180478	12674	CAAGGCTGCCATGGGTGAGC	225065	57261	AGGAACACATTTTAGGGGAG	269652	101848	TCCCCTGATTTTGGAGGTTC
180479	12675	GCAAGGCTGCCATGGGTGAG	225066	57262	AAGGAACACATTTTAGGGGA	269653	101849	ATCCCCTGATTTTGGAGGTT
180480	12676	GGCAAGGCTGCCATGGGTGA	225067	57263	TAAGGAACACATTTTAGGGG	269654	101850	GATCCCCTGATTTTGGAGGT
180481	12677	GGGCAAGGCTGCCATGGGTG	225068	57264	GTAAGGAACACATTTTAGGG	269655	101851	CGATCCCCTGATTTTGGAGG
180482	12678	GGGGCAAGGCTGCCATGGGT	225069	57265	GGTAAGGAACACATTTTAGG	269656	101852	GCGATCCCCTGATTTTGGAG
180483	12679	AGGGGCAAGGCTGCCATGGG	225070	57266	AGGTAAGGAACACATTTTAG	269657	101853	TGCGATCCCCTGATTTTGGA
180484	12680	GAGGGGCAAGGCTGCCATGG	225071	57267	GAGGTAAGGAACACATTTTA	269658	101854	CTGCGATCCCCTGATTTTGG
180485	12681	AGAGGGGCAAGGCTGCCATG	225072	57268	GGAGGTAAGGAACACATTTT	269659	101855	GCTGCGATCCCCTGATTTTG
180486	12682	GAGAGGGGCAAGGCTGCCAT	225073	57269	GGGAGGTAAGGAACACATTT	269660	101856	CGCTGCGATCCCCTGATTTT
180487	12683	AGAGAGGGGCAAGGCTGCCA	225074	57270	TGGGAGGTAAGGAACACATT	269661	101857	CCGCTGCGATCCCCTGATTT
180488	12684	GAGAGAGGGGCAAGGCTGCC	225075	57271	GTGGGAGGTAAGGAACACAT	269662	101858	GCCGCTGCGATCCCCTGATT
180489	12685	GGAGAGAGGGGCAAGGCTGC	225076	57272	GGTGGGAGGTAAGGAACACA	269663	101859	AGCCGCTGCGATCCCCTGAT
180490	12686	GGGAGAGAGGGGCAAGGCTG	225077	57273	GGGTGGGAGGTAAGGAACAC	269664	101860	TAGCCGCTGCGATCCCCTGA
180491	12687	AGGGAGAGAGGGGCAAGGCT	225078	57274	GGGGTGGGAGGTAAGGAACA	269665	101861	GTAGCCGCTGCGATCCCCTG
180492	12688	CAGGGAGAGAGGGGCAAGGC	225079	57275	TGGGGTGGGAGGTAAGGAAC	269666	101862	TGTAGCCGCTGCGATCCCCT
180493	12689	GCAGGGAGAGAGGGGCAAGG	225080	57276	GTGGGGTGGGAGGTAAGGAA	269667	101863	CTGTAGCCGCTGCGATCCCC
180494	12690	GGCAGGGAGAGAGGGGCAAG	225081	57277	AGTGGGGTGGGAGGTAAGGA	269668	101864	GCTGTAGCCGCTGCGATCCC
180495	12691	GGGCAGGGAGAGAGGGGCAA	225082	57278	CAGTGGGGTGGGAGGTAAGG	269669	101865	TGCTGTAGCCGCTGCGATCC
180496	12692	GGGGCAGGGAGAGAGGGGCA	225083	57279	GCAGTGGGGTGGGAGGTAAG	269670	101866	CTGCTGTAGCCGCTGCGATC
180497	12693	TGGGGCAGGGAGAGAGGGGC	225084	57280	TGCAGTGGGGTGGGAGGTAA	269671	101867	GCTGCTGTAGCCGCTGCGAT
180498	12694	GTGGGGCAGGGAGAGAGGGG	225085	57281	ATGCAGTGGGGTGGGAGGTA	269672	101868	GGCTGCTGTAGCCGCTGCGA
180499	12695	GGTGGGGCAGGGAGAGAGGG	225086	57282	GATGCAGTGGGGTGGGAGGT	269673	101869	GGGCTGCTGTAGCCGCTGCG
180500	12696	GGGTGGGGCAGGGAGAGAGG	225087	57283	AGATGCAGTGGGGTGGGAGG	269674	101870	GGGGCTGCTGTAGCCGCTGC
180501	12697	GGGGTGGGGCAGGGAGAGAG	225088	57284	TAGATGCAGTGGGGTGGGAG	269675	101871	CGGGGCTGCTGTAGCCGCTG
180502	12698	GGGGGTGGGGCAGGGAGAGA	225089	57285	TTAGATGCAGTGGGGTGGGA	269676	101872	CCGGGGCTGCTGTAGCCGCT
180503	12699	AGGGGGTGGGGCAGGGAGAG	225090	57286	CTTAGATGCAGTGGGGTGGG	269677	101873	GCCGGGGCTGCTGTAGCCGC
180504	12700	TAGGGGGTGGGGCAGGGAGA	225091	57287	ACTTAGATGCAGTGGGGTGG	269678	101874	AGCCGGGGCTGCTGTAGCCG
180505	12701	ATAGGGGGTGGGGCAGGGAG	225092	57288	GACTTAGATGCAGTGGGGTG	269679	101875	GAGCCGGGGCTGCTGTAGCC
180506	12702	AATAGGGGGTGGGGCAGGGA	225093	57289	TGACTTAGATGCAGTGGGGT	269680	101876	GGAGCCGGGGCTGCTGTAGC
180507	12703	AAATAGGGGGTGGGGCAGGG	225094	57290	GTGACTTAGATGCAGTGGGG	269681	101877	GGGAGCCGGGGCTGCTGTAG
180508	12704	TAAATAGGGGGTGGGGCAGG	225095	57291	AGTGACTTAGATGCAGTGGG	269682	101878	GGGGAGCCGGGGCTGCTGTA
180509	12705	TTAAATAGGGGGTGGGGCAG	225096	57292	CAGTGACTTAGATGCAGTGG	269683	101879	TGGGGAGCCGGGGCTGCTGT
180510	12706	TTTAAATAGGGGGTGGGGCA	225097	57293	GCAGTGACTTAGATGCAGTG	269684	101880	CTGGGGAGCCGGGGCTGCTG
180511	12707	ATTTAAATAGGGGGTGGGGC	225098	57294	GGCAGTGACTTAGATGCAGT	269685	101881	CCTGGGGAGCCGGGGCTGCT
180512	12708	AATTTAAATAGGGGGTGGGG	225099	57295	AGGCAGTGACTTAGATGCAG	269686	101882	GCCTGGGGAGCCGGGGCTGC
180513	12709	CAATTTAAATAGGGGGTGGG	225100	57296	CAGGCAGTGACTTAGATGCA	269687	101883	TGCCTGGGGAGCCGGGGCTG
180514	12710	TCAATTTAAATAGGGGGTGG	225101	57297	TCAGGCAGTGACTTAGATGC	269688	101884	GTGCCTGGGGAGCCGGGGCT
180515	12711	GTCAATTTAAATAGGGGGTG	225102	57298	CTCAGGCAGTGACTTAGATG	269689	101885	AGTGCCTGGGGAGCCGGGGC
180516	12712	GGTCAATTTAAATAGGGGGT	225103	57299	TCTCAGGCAGTGACTTAGAT	269690	101886	GAGTGCCTGGGGAGCCGGGG
180517	12713	AGGTCAATTTAAATAGGGGG	225104	57300	TTCTCAGGCAGTGACTTAGA	269691	101887	GGAGTGCCTGGGGAGCCGGG
180518	12714	CAGGTCAATTTAAATAGGGG	225105	57301	TTTCTCAGGCAGTGACTTAG	269692	101888	GGGAGTGCCTGGGGAGCCGG
180519	12715	TCAGGTCAATTTAAATAGGG	225106	57302	TTTTCTCAGGCAGTGACTTA	269693	101889	CGGGAGTGCCTGGGGAGCCG
180520	12716	GTCAGGTCAATTTAAATAGG	225107	57303	GTTTTCTCAGGCAGTGACTT	269694	101890	CCGGGAGTGCCTGGGGAGCC
180521	12717	GGTCAGGTCAATTTAAATAG	225108	57304	TGTTTTCTCAGGCAGTGACT	269695	101891	GCCGGGAGTGCCTGGGGAGC
180522	12718	AGGTCAGGTCAATTTAAATA	225109	57305	CTGTTTTCTCAGGCAGTGAC	269696	101892	TGCCGGGAGTGCCTGGGGAG
180523	12719	AAGGTCAGGTCAATTTAAAT	225110	57306	CCTGTTTTCTCAGGCAGTGA	269697	101893	CTGCCGGGAGTGCCTGGGGA
180524	12720	GAAGGTCAGGTCAATTTAAA	225111	57307	TCCTGTTTTCTCAGGCAGTG	269698	101894	GCTGCCGGGAGTGCCTGGGG
180525	12721	GGAAGGTCAGGTCAATTTAA	225112	57308	ATCCTGTTTTCTCAGGCAGT	269699	101895	GGCTGCCGGGAGTGCCTGGG
180526	12722	AGGAAGGTCAGGTCAATTTA	225113	57309	AATCCTGTTTTCTCAGGCAG	269700	101896	CGGCTGCCGGGAGTGCCTGG
180527	12723	GAGGAAGGTCAGGTCAATTT	225114	57310	CAATCCTGTTTTCTCAGGCA	269701	101897	GCGGCTGCCGGGAGTGCCTG
180528	12724	TGAGGAAGGTCAGGTCAATT	225115	57311	TCAATCCTGTTTTCTCAGGC	269702	101898	AGCGGCTGCCGGGAGTGCCT
180529	12725	CTGAGGAAGGTCAGGTCAAT	225116	57312	CTCAATCCTGTTTTCTCAGG	269703	101899	GAGCGGCTGCCGGGAGTGCC
180530	12726	ACTGAGGAAGGTCAGGTCAA	225117	57313	CCTCAATCCTGTTTTCTCAG	269704	101900	GGAGCGGCTGCCGGGAGTGC
180531	12727	CACTGAGGAAGGTCAGGTCA	225118	57314	TCCTCAATCCTGTTTTCTCA	269705	101901	GGGAGCGGCTGCCGGGAGTG
180532	12728	ACACTGAGGAAGGTCAGGTC	225119	57315	TTCCTCAATCCTGTTTTCTC	269706	101902	CGGGAGCGGCTGCCGGGAGT
180533	12729	GACACTGAGGAAGGTCAGGT	225120	57316	TTTCCTCAATCCTGTTTTCT	269707	101903	GCGGGAGCGGCTGCCGGGAG
180534	12730	GGACACTGAGGAAGGTCAGG	225121	57317	CTTTCCTCAATCCTGTTTTC	269708	101904	TGCGGGAGCGGCTGCCGGGA
180535	12731	TGGACACTGAGGAAGGTCAG	225122	57318	CCTTTCCTCAATCCTGTTTT	269709	101905	GTGCGGGAGCGGCTGCCGGG
180536	12732	ATGGACACTGAGGAAGGTCA	225123	57319	TCCTTTCCTCAATCCTGTTT	269710	101906	GGTGCGGGAGCGGCTGCCGG
180537	12733	GATGGACACTGAGGAAGGTC	225124	57320	CTCCTTTCCTCAATCCTGTT	269711	101907	GGGTGCGGGAGCGGCTGCCG
180538	12734	AGATGGACACTGAGGAAGGT	225125	57321	TCTCCTTTCCTCAATCCTGT	269712	101908	GGGGTGCGGGAGCGGCTGCC
180539	12735	AAGATGGACACTGAGGAAGG	225126	57322	TTCTCCTTTCCTCAATCCTG	269713	101909	CGGGGTGCGGGAGCGGCTGC
180540	12736	GAAGATGGACACTGAGGAAG	225127	57323	TTTCTCCTTTCCTCAATCCT	269714	101910	ACGGGGTGCGGGAGCGGCTG
180541	12737	GGAAGATGGACACTGAGGAA	225128	57324	CTTTCTCCTTTCCTCAATCC	269715	101911	GACGGGGTGCGGGAGCGGCT
180542	12738	GGGAAGATGGACACTGAGGA	225129	57325	CCTTTCTCCTTTCCTCAATC	269716	101912	GGACGGGGTGCGGGAGCGGC
180543	12739	GGGGAAGATGGACACTGAGG	225130	57326	TCCTTTCTCCTTTCCTCAAT	269717	101913	GGGACGGGGTGCGGGAGCGG
180544	12740	CGGGGAAGATGGACACTGAG	225131	57327	TTCCTTTCTCCTTTCCTCAA	269718	101914	AGGGACGGGGTGCGGGAGCG
180545	12741	TCGGGGAAGATGGACACTGA	225132	57328	CTTCCTTTCTCCTTTCCTCA	269719	101915	AAGGGACGGGGTGCGGGAGC
180546	12742	TTCGGGGAAGATGGACACTG	225133	57329	TCTTCCTTTCTCCTTTCCTC	269720	101916	GAAGGGACGGGGTGCGGGAG

180547	12743	CTTCGGGGAAGATGGACACT	225134	57330	CTCTTCCTTTCTCCTTTCCT	269721	101917	GGAAGGGACGGGGTGCGGGA
180548	12744	GCTTCGGGGAAGATGGACAC	225135	57331	TCTCTTCCTTTCTCCTTTCC	269722	101918	TGGAAGGGACGGGGTGCGGG
180549	12745	AGCTTCGGGGAAGATGGACA	225136	57332	CTCTCTTCCTTTCTCCTTTC	269723	101919	TTGGAAGGGACGGGGTGCGG
180550	12746	AAGCTTCGGGGAAGATGGAC	225137	57333	TCTCTCTTCCTTTCTCCTTT	269724	101920	GTTGGAAGGGACGGGGTGCG
180551	12747	AAAGCTTCGGGGAAGATGGA	225138	57334	CTCTCTCTTCCTTTCTCCTT	269725	101921	GGTTGGAAGGGACGGGGTGC
180552	12748	GAAAGCTTCGGGGAAGATGG	225139	57335	TCTCTCTCTTCCTTTCTCCT	269726	101922	GGGTTGGAAGGGACGGGGTG
180553	12749	GGAAAGCTTCGGGGAAGATG	225140	57336	CTCTCTCTCTTCCTTTCTCC	269727	101923	GGGGTTGGAAGGGACGGGGT
180554	12750	GGGAAAGCTTCGGGGAAGAT	225141	57337	TCTCTCTCTCTTCCTTTCTC	269728	101924	TGGGGTTGGAAGGGACGGGG
180555	12751	GGGGAAAGCTTCGGGGAAGA	225142	57338	CTCTCTCTCTCTTCCTTTCT	269729	101925	GTGGGGTTGGAAGGGACGGG
180556	12752	TGGGGAAAGCTTCGGGGAAG	225143	57339	TCTCTCTCTCTCTTCCTTTC	269730	101926	GGTGGGGTTGGAAGGGACGG
180557	12753	CTGGGGAAAGCTTCGGGGAA	225144	57340	CTCTCTCTCTCTCTTCCTTT	269731	101927	GGGTGGGGTTGGAAGGGACG
180558	12754	GCTGGGGAAAGCTTCGGGGA	225145	57341	CCTCTCTCTCTCTCTTCCTT	269732	101928	TGGGTGGGGTTGGAAGGGAC
180559	12755	GGCTGGGGAAAGCTTCGGGG	225146	57342	TCCTCTCTCTCTCTCTTCCT	269733	101929	GTGGGTGGGGTTGGAAGGGA
180560	12756	AGGCTGGGGAAAGCTTCGGG	225147	57343	CTCCTCTCTCTCTCTCTTCC	269734	101930	GGTGGGTGGGGTTGGAAGGG
180561	12757	AAGGCTGGGGAAAGCTTCGG	225148	57344	CCTCCTCTCTCTCTCTCTTC	269735	101931	GGGTGGGTGGGGTTGGAAGG
180562	12758	CAAGGCTGGGGAAAGCTTCG	225149	57345	TCCTCCTCTCTCTCTCTCTT	269736	101932	CGGGTGGGTGGGGTTGGAAG
180563	12759	CCAAGGCTGGGGAAAGCTTC	225150	57346	CTCCTCCTCTCTCTCTCTCT	269737	101933	CCGGGTGGGTGGGGTTGGAA
180564	12760	GCCAAGGCTGGGGAAAGCTT	225151	57347	TCTCCTCCTCTCTCTCTCTC	269738	101934	CCCGGGTGGGTGGGGTTGGA
180565	12761	TGCCAAGGCTGGGGAAAGCT	225152	57348	CTCTCCTCCTCTCTCTCTCT	269739	101935	TCCCGGGTGGGTGGGGTTGG
180566	12762	GTGCCAAGGCTGGGGAAAGC	225153	57349	TCTCTCCTCCTCTCTCTCTC	269740	101936	CTCCCGGGTGGGTGGGGTTG
180567	12763	AGTGCCAAGGCTGGGGAAAG	225154	57350	CTCTCTCCTCCTCTCTCTCT	269741	101937	GCTCCCGGGTGGGTGGGGTT
180568	12764	GAGTGCCAAGGCTGGGGAAA	225155	57351	TCTCTCTCCTCCTCTCTCTC	269742	101938	GGCTCCCGGGTGGGTGGGGT
180569	12765	TGAGTGCCAAGGCTGGGGAA	225156	57352	CTCTCTCTCCTCCTCTCTCT	269743	101939	GGGCTCCCGGGTGGGTGGGG
180570	12766	TTGAGTGCCAAGGCTGGGGA	225157	57353	TCTCTCTCTCCTCCTCTCTC	269744	101940	TGGGCTCCCGGGTGGGTGGG
180571	12767	CTTGAGTGCCAAGGCTGGGG	225158	57354	CTCTCTCTCTCCTCCTCTCT	269745	101941	TTGGGCTCCCGGGTGGGTGG
180572	12768	CCTTGAGTGCCAAGGCTGGG	225159	57355	TCTCTCTCTCTCCTCCTCTC	269746	101942	CTTGGGCTCCCGGGTGGGTG
180573	12769	ACCTTGAGTGCCAAGGCTGG	225160	57356	CTCTCTCTCTCTCCTCCTCT	269747	101943	TCTTGGGCTCCCGGGTGGGT
180574	12770	GACCTTGAGTGCCAAGGCTG	225161	57357	TCTCTCTCTCTCTCCTCCTC	269748	101944	TTCTTGGGCTCCCGGGTGGG
180575	12771	GGACCTTGAGTGCCAAGGCT	225162	57358	CTCTCTCTCTCTCTCCTCCT	269749	101945	CTTCTTGGGCTCCCGGGTGG
180576	12772	TGGACCTTGAGTGCCAAGGC	225163	57359	CCTCTCTCTCTCTCTCCTCC	269750	101946	CCTTCTTGGGCTCCCGGGTG
180577	12773	CTGGACCTTGAGTGCCAAGG	225164	57360	CCCTCTCTCTCTCTCTCCTC	269751	101947	ACCTTCTTGGGCTCCCGGGT
180578	12774	TCTGGACCTTGAGTGCCAAG	225165	57361	TCCCTCTCTCTCTCTCTCCT	269752	101948	CACCTTCTTGGGCTCCCGGG
180579	12775	CTCTGGACCTTGAGTGCCAA	225166	57362	CTCCCTCTCTCTCTCTCTCC	269753	101949	CCACCTTCTTGGGCTCCCGG
180580	12776	CCTCTGGACCTTGAGTGCCA	225167	57363	CCTCCCTCTCTCTCTCTCTC	269754	101950	GCCACCTTCTTGGGCTCCCG
180581	12777	GCCTCTGGACCTTGAGTGCC	225168	57364	TCCTCCCTCTCTCTCTCTCT	269755	101951	TGCCACCTTCTTGGGCTCCC
180582	12778	AGCCTCTGGACCTTGAGTGC	225169	57365	TTCCTCCCTCTCTCTCTCTC	269756	101952	CTGCCACCTTCTTGGGCTCC
180583	12779	TAGCCTCTGGACCTTGAGTG	225170	57366	CTTCCTCCCTCTCTCTCTCT	269757	101953	ACTGCCACCTTCTTGGGCTC
180584	12780	GTAGCCTCTGGACCTTGAGT	225171	57367	CCTTCCTCCCTCTCTCTCTC	269758	101954	CACTGCCACCTTCTTGGGCT
180585	12781	CGTAGCCTCTGGACCTTGAG	225172	57368	GCCTTCCTCCCTCTCTCTCT	269759	101955	CCACTGCCACCTTCTTGGGC
180586	12782	GCGTAGCCTCTGGACCTTGA	225173	57369	AGCCTTCCTCCCTCTCTCTC	269760	101956	ACCACTGCCACCTTCTTGGG
180587	12783	CGCGTAGCCTCTGGACCTTG	225174	57370	CAGCCTTCCTCCCTCTCTCT	269761	101957	GACCACTGCCACCTTCTTGG
180588	12784	ACGCGTAGCCTCTGGACCTT	225175	57371	TCAGCCTTCCTCCCTCTCTC	269762	101958	GGACCACTGCCACCTTCTTG
180589	12785	AACGCGTAGCCTCTGGACCT	225176	57372	ATCAGCCTTCCTCCCTCTCT	269763	101959	CGGACCACTGCCACCTTCTT
180590	12786	AAACGCGTAGCCTCTGGACC	225177	57373	CATCAGCCTTCCTCCCTCTC	269764	101960	ACGGACCACTGCCACCTTCT
180591	12787	GAAACGCGTAGCCTCTGGAC	225178	57374	CCATCAGCCTTCCTCCCTCT	269765	101961	TACGGACCACTGCCACCTTC
180592	12788	GGAAACGCGTAGCCTCTGGA	225179	57375	TCCATCAGCCTTCCTCCCTC	269766	101962	GTACGGACCACTGCCACCTT
180593	12789	AGGAAACGCGTAGCCTCTGG	225180	57376	ATCCATCAGCCTTCCTCCCT	269767	101963	AGTACGGACCACTGCCACCT
180594	12790	GAGGAAACGCGTAGCCTCTG	225181	57377	AATCCATCAGCCTTCCTCCC	269768	101964	GAGTACGGACCACTGCCACC
180595	12791	AGAGGAAACGCGTAGCCTCT	225182	57378	AAATCCATCAGCCTTCCTCC	269769	101965	GGAGTACGGACCACTGCCAC
180596	12792	GAGAGGAAACGCGTAGCCTC	225183	57379	TAAATCCATCAGCCTTCCTC	269770	101966	TGGAGTACGGACCACTGCCA
180597	12793	TGAGAGGAAACGCGTAGCCT	225184	57380	CTAAATCCATCAGCCTTCCT	269771	101967	GTGGAGTACGGACCACTGCC
180598	12794	GTGAGAGGAAACGCGTAGCC	225185	57381	TCTAAATCCATCAGCCTTCC	269772	101968	GGTGGAGTACGGACCACTGC
180599	12795	GGTGAGAGGAAACGCGTAGC	225186	57382	TTCTAAATCCATCAGCCTTC	269773	101969	GGGTGGAGTACGGACCACTG
180600	12796	AGGTGAGAGGAAACGCGTAG	225187	57383	TTTCTAAATCCATCAGCCTT	269774	101970	TGGGTGGAGTACGGACCACT
180601	12797	CAGGTGAGAGGAAACGCGTA	225188	57384	TTTTCTAAATCCATCAGCCT	269775	101971	TTGGGTGGAGTACGGACCAC
180602	12798	ACAGGTGAGAGGAAACGCGT	225189	57385	CTTTTCTAAATCCATCAGCC	269776	101972	CTTGGGTGGAGTACGGACCA
180603	12799	CACAGGTGAGAGGAAACGCG	225190	57386	TCTTTTCTAAATCCATCAGC	269777	101973	ACTTGGGTGGAGTACGGACC
180604	12800	CCACAGGTGAGAGGAAACGC	225191	57387	TTCTTTTCTAAATCCATCAG	269778	101974	GACTTGGGTGGAGTACGGAC
180605	12801	GCCACAGGTGAGAGGAAACG	225192	57388	CTTCTTTTCTAAATCCATCA	269779	101975	CGACTTGGGTGGAGTACGGA
180606	12802	TGCCACAGGTGAGAGGAAAC	225193	57389	TCTTCTTTTCTAAATCCATC	269780	101976	GCGACTTGGGTGGAGTACGG
180607	12803	CTGCCACAGGTGAGAGGAAA	225194	57390	TTCTTCTTTTCTAAATCCAT	269781	101977	GGCGACTTGGGTGGAGTACG
180608	12804	GCTGCCACAGGTGAGAGGAA	225195	57391	TTTCTTCTTTTCTAAATCCA	269782	101978	CGGCGACTTGGGTGGAGTAC
180609	12805	CGCTGCCACAGGTGAGAGGA	225196	57392	TTTTCTTCTTTTCTAAATCC	269783	101979	ACGGCGACTTGGGTGGAGTA
180610	12806	GCGCTGCCACAGGTGAGAGG	225197	57393	GTTTTCTTCTTTTCTAAATC	269784	101980	GACGGCGACTTGGGTGGAGT
180611	12807	GGCGCTGCCACAGGTGAGAG	225198	57394	TGTTTTCTTCTTTTCTAAAT	269785	101981	AGACGGCGACTTGGGTGGAG
180612	12808	CGGCGCTGCCACAGGTGAGA	225199	57395	TTGTTTTCTTCTTTTCTAAA	269786	101982	AAGACGGCGACTTGGGTGGA
180613	12809	ACGGCGCTGCCACAGGTGAG	225200	57396	CTTGTTTTCTTCTTTTCTAA	269787	101983	GAAGACGGCGACTTGGGTGG
180614	12810	CACGGCGCTGCCACAGGTGA	225201	57397	ACTTGTTTTCTTCTTTTCTA	269788	101984	GGAAGACGGCGACTTGGGTG
180615	12811	GCACGGCGCTGCCACAGGTG	225202	57398	CACTTGTTTTCTTCTTTTCT	269789	101985	CGGAAGACGGCGACTTGGGT
180616	12812	AGCACGGCGCTGCCACAGGT	225203	57399	CCACTTGTTTTCTTCTTTTC	269790	101986	GCGGAAGACGGCGACTTGGG
180617	12813	GAGCACGGCGCTGCCACAGG	225204	57400	ACCACTTGTTTTCTTCTTTT	269791	101987	GGCGGAAGACGGCGACTTGG
180618	12814	GGAGCACGGCGCTGCCACAG	225205	57401	GACCACTTGTTTTCTTCTTT	269792	101988	TGGCGGAAGACGGCGACTTG

180619	12815	GGGAGCACGGCGCTGCCACA	225206	57402	AGACCACTTGTTTTCTTCTT	269793	101989	TTGGCGGAAGACGGCGACTT
180620	12816	GGGGAGCACGGCGCTGCCAC	225207	57403	CAGACCACTTGTTTTCTTCT	269794	101990	CTTGGCGGAAGACGGCGACT
180621	12817	TGGGGAGCACGGCGCTGCCA	225208	57404	TCAGACCACTTGTTTTCTTC	269795	101991	TCTTGGCGGAAGACGGCGAC
180622	12818	CTGGGGAGCACGGCGCTGCC	225209	57405	CTCAGACCACTTGTTTTCTT	269796	101992	CTCTTGGCGGAAGACGGCGA
180623	12819	ACTGGGGAGCACGGCGCTGC	225210	57406	CCTCAGACCACTTGTTTTCT	269797	101993	GCTCTTGGCGGAAGACGGCG
180624	12820	CACTGGGGAGCACGGCGCTG	225211	57407	TCCTCAGACCACTTGTTTTC	269798	101994	GGCTCTTGGCGGAAGACGGC
180625	12821	GCACTGGGGAGCACGGCGCT	225212	57408	TTCCTCAGACCACTTGTTTT	269799	101995	CGGCTCTTGGCGGAAGACGG
180626	12822	GGCACTGGGGAGCACGGCGC	225213	57409	TTTCCTCAGACCACTTGTTT	269800	101996	GCGGCTCTTGGCGGAAGACG
180627	12823	AGGCACTGGGGAGCACGGCG	225214	57410	TTTTCCTCAGACCACTTGTT	269801	101997	GGCGGCTCTTGGCGGAAGAC
180628	12824	GAGGCACTGGGGAGCACGGC	225215	57411	GTTTTCCTCAGACCACTTGT	269802	101998	AGGCGGCTCTTGGCGGAAGA
180629	12825	TGAGGCACTGGGGAGCACGG	225216	57412	TGTTTTCCTCAGACCACTTG	269803	101999	CAGGCGGCTCTTGGCGGAAG
180630	12826	GTGAGGCACTGGGGAGCACG	225217	57413	CTGTTTTCCTCAGACCACTT	269804	102000	GCAGGCGGCTCTTGGCGGAA
180631	12827	TGTGAGGCACTGGGGAGCAC	225218	57414	GCTGTTTTCCTCAGACCACT	269805	102001	TGCAGGCGGCTCTTGGCGGA
180632	12828	CTGTGAGGCACTGGGGAGCA	225219	57415	GGCTGTTTTCCTCAGACCAC	269806	102002	CTGCAGGCGGCTCTTGGCGG
180633	12829	ACTGTGAGGCACTGGGGAGC	225220	57416	AGGCTGTTTTCCTCAGACCA	269807	102003	TCTGCAGGCGGCTCTTGGCG
180634	12830	AACTGTGAGGCACTGGGGAG	225221	57417	AAGGCTGTTTTCCTCAGACC	269808	102004	GTCTGCAGGCGGCTCTTGGC
180635	12831	AAACTGTGAGGCACTGGGGA	225222	57418	CAAGGCTGTTTTCCTCAGAC	269809	102005	TGTCTGCAGGCGGCTCTTGG
180636	12832	GAAACTGTGAGGCACTGGGG	225223	57419	CCAAGGCTGTTTTCCTCAGA	269810	102006	CTGTCTGCAGGCGGCTCTTG
180637	12833	GGAAACTGTGAGGCACTGGG	225224	57420	ACCAAGGCTGTTTTCCTCAG	269811	102007	GCTGTCTGCAGGCGGCTCTT
180638	12834	AGGAAACTGTGAGGCACTGG	225225	57421	CACCAAGGCTGTTTTCCTCA	269812	102008	GGCTGTCTGCAGGCGGCTCT
180639	12835	AAGGAAACTGTGAGGCACTG	225226	57422	ACACCAAGGCTGTTTTCCTC	269813	102009	GGGCTGTCTGCAGGCGGCTC
180640	12836	GAAGGAAACTGTGAGGCACT	225227	57423	CACACCAAGGCTGTTTTCCT	269814	102010	GGGGCTGTCTGCAGGCGGCT
180641	12837	AGAAGGAAACTGTGAGGCAC	225228	57424	ACACACCAAGGCTGTTTTCC	269815	102011	GGGGGCTGTCTGCAGGCGGC
180642	12838	AAGAAGGAAACTGTGAGGCA	225229	57425	AACACACCAAGGCTGTTTTC	269816	102012	CGGGGGCTGTCTGCAGGCGG
180643	12839	CAAGAAGGAAACTGTGAGGC	225230	57426	AAACACACCAAGGCTGTTTT	269817	102013	ACGGGGGCTGTCTGCAGGCG
180644	12840	GCAAGAAGGAAACTGTGAGG	225231	57427	TAAACACACCAAGGCTGTTT	269818	102014	CACGGGGGCTGTCTGCAGGC
180645	12841	GGCAAGAAGGAAACTGTGAG	225232	57428	ATAAACACACCAAGGCTGTT	269819	102015	GCACGGGGGCTGTCTGCAGG
180646	12842	GGGCAAGAAGGAAACTGTGA	225233	57429	AATAAACACACCAAGGCTGT	269820	102016	GGCACGGGGGCTGTCTGCAG
180647	12843	GGGGCAAGAAGGAAACTGTG	225234	57430	AAATAAACACACCAAGGCTG	269821	102017	GGGCACGGGGGCTGTCTGCA
180648	12844	GGGGGCAAGAAGGAAACTGT	225235	57431	AAAATAAACACACCAAGGCT	269822	102018	TGGGCACGGGGGCTGTCTGC
180649	12845	CGGGGGCAAGAAGGAAACTG	225236	57432	GAAAATAAACACACCAAGGC	269823	102019	ATGGGCACGGGGGCTGTCTG
180650	12846	GCGGGGGCAAGAAGGAAACT	225237	57433	GGAAAATAAACACACCAAGG	269824	102020	CATGGGCACGGGGGCTGTCT
180651	12847	AGCGGGGGCAAGAAGGAAAC	225238	57434	AGGAAAATAAACACACCAAG	269825	102021	GCATGGGCACGGGGGCTGTC
180652	12848	AAGCGGGGGCAAGAAGGAAA	225239	57435	CAGGAAAATAAACACACCAA	269826	102022	GGCATGGGCACGGGGGCTGT
180653	12849	GAAGCGGGGGCAAGAAGGAA	225240	57436	ACAGGAAAATAAACACACCA	269827	102023	TGGCATGGGCACGGGGGCTG
180654	12850	GGAAGCGGGGGCAAGAAGGA	225241	57437	GACAGGAAAATAAACACACC	269828	102024	CTGGCATGGGCACGGGGGCT
180655	12851	AGGAAGCGGGGGCAAGAAGG	225242	57438	AGACAGGAAAATAAACACAC	269829	102025	TCTGGCATGGGCACGGGGGC
180656	12852	CAGGAAGCGGGGGCAAGAAG	225243	57439	CAGACAGGAAAATAAACACA	269830	102026	GTCTGGCATGGGCACGGGGG
180657	12853	ACAGGAAGCGGGGGCAAGAA	225244	57440	ACAGACAGGAAAATAAACAC	269831	102027	GGTCTGGCATGGGCACGGGG
180658	12854	CACAGGAAGCGGGGGCAAGA	225245	57441	CACAGACAGGAAAATAAACA	269832	102028	AGGTCTGGCATGGGCACGGG
180659	12855	ACACAGGAAGCGGGGGCAAG	225246	57442	ACACAGACAGGAAAATAAAC	269833	102029	CAGGTCTGGCATGGGCACGG
180660	12856	TACACAGGAAGCGGGGGCAA	225247	57443	TACACAGACAGGAAAATAAA	269834	102030	TCAGGTCTGGCATGGGCACG
180661	12857	CTACACAGGAAGCGGGGGCA	225248	57444	ATACACAGACAGGAAAATAA	269835	102031	TTCAGGTCTGGCATGGGCAC
180662	12858	CCTACACAGGAAGCGGGGGC	225249	57445	GATACACAGACAGGAAAATA	269836	102032	CTTCAGGTCTGGCATGGGCA
180663	12859	TCCTACACAGGAAGCGGGGG	225250	57446	CGATACACAGACAGGAAAAT	269837	102033	TCTTCAGGTCTGGCATGGGC
180664	12860	GTCCTACACAGGAAGCGGGG	225251	57447	GCGATACACAGACAGGAAAA	269838	102034	TTCTTCAGGTCTGGCATGGG
180665	12861	AGTCCTACACAGGAAGCGGG	225252	57448	AGCGATACACAGACAGGAAA	269839	102035	ATTCTTCAGGTCTGGCATGG
180666	12862	GAGTCCTACACAGGAAGCGG	225253	57449	AAGCGATACACAGACAGGAA	269840	102036	CATTCTTCAGGTCTGGCATG
180667	12863	TGAGTCCTACACAGGAAGCG	225254	57450	GAAGCGATACACAGACAGGA	269841	102037	ACATTCTTCAGGTCTGGCAT
180668	12864	ATGAGTCCTACACAGGAAGC	225255	57451	AGAAGCGATACACAGACAGG	269842	102038	GACATTCTTCAGGTCTGGCA
180669	12865	GATGAGTCCTACACAGGAAG	225256	57452	GAGAAGCGATACACAGACAG	269843	102039	TGACATTCTTCAGGTCTGGC
180670	12866	AGATGAGTCCTACACAGGAA	225257	57453	CGAGAAGCGATACACAGACA	269844	102040	TTGACATTCTTCAGGTCTGG
180671	12867	CAGATGAGTCCTACACAGGA	225258	57454	CCGAGAAGCGATACACAGAC	269845	102041	CTTGACATTCTTCAGGTCTG
180672	12868	GCAGATGAGTCCTACACAGG	225259	57455	GCCGAGAAGCGATACACAGA	269846	102042	ACTTGACATTCTTCAGGTCT
180673	12869	GGCAGATGAGTCCTACACAG	225260	57456	GGCCGAGAAGCGATACACAG	269847	102043	GACTTGACATTCTTCAGGTC
180674	12870	GGGCAGATGAGTCCTACACA	225261	57457	AGGCCGAGAAGCGATACACA	269848	102044	GGACTTGACATTCTTCAGGT
180675	12871	TGGGCAGATGAGTCCTACAC	225262	57458	AAGGCCGAGAAGCGATACAC	269849	102045	TGGACTTGACATTCTTCAGG
180676	12872	GTGGGCAGATGAGTCCTACA	225263	57459	AAAGGCCGAGAAGCGATACA	269850	102046	TTGGACTTGACATTCTTCAG
180677	12873	TGTGGGCAGATGAGTCCTAC	225264	57460	AAAAGGCCGAGAAGCGATAC	269851	102047	CTTGGACTTGACATTCTTCA
180678	12874	CTGTGGGCAGATGAGTCCTA	225265	57461	CAAAAGGCCGAGAAGCGATA	269852	102048	TCTTGGACTTGACATTCTTC
180679	12875	CCTGTGGGCAGATGAGTCCT	225266	57462	CCAAAAGGCCGAGAAGCGAT	269853	102049	ATCTTGGACTTGACATTCTT
180680	12876	ACCTGTGGGCAGATGAGTCC	225267	57463	GCCAAAAGGCCGAGAAGCGA	269854	102050	GATCTTGGACTTGACATTCT
180681	12877	AACCTGTGGGCAGATGAGTC	225268	57464	AGCCAAAAGGCCGAGAAGCG	269855	102051	CGATCTTGGACTTGACATTC
180682	12878	CAACCTGTGGGCAGATGAGT	225269	57465	TAGCCAAAAGGCCGAGAAGC	269856	102052	CCGATCTTGGACTTGACATT
180683	12879	GCAACCTGTGGGCAGATGAG	225270	57466	TTAGCCAAAAGGCCGAGAAG	269857	102053	GCCGATCTTGGACTTGACAT
180684	12880	TGCAACCTGTGGGCAGATGA	225271	57467	CTTAGCCAAAAGGCCGAGAA	269858	102054	AGCCGATCTTGGACTTGACA
180685	12881	GTGCAACCTGTGGGCAGATG	225272	57468	TCTTAGCCAAAAGGCCGAGA	269859	102055	GAGCCGATCTTGGACTTGAC
180686	12882	CGTGCAACCTGTGGGCAGAT	225273	57469	ATCTTAGCCAAAAGGCCGAG	269860	102056	GGAGCCGATCTTGGACTTGA
180687	12883	ACGTGCAACCTGTGGGCAGA	225274	57470	GATCTTAGCCAAAAGGCCGA	269861	102057	TGGAGCCGATCTTGGACTTG
180688	12884	GACGTGCAACCTGTGGGCAG	225275	57471	TGATCTTAGCCAAAAGGCCG	269862	102058	GTGGAGCCGATCTTGGACTT
180689	12885	GGACGTGCAACCTGTGGGCA	225276	57472	TTGATCTTAGCCAAAAGGCC	269863	102059	AGTGGAGCCGATCTTGGACT
180690	12886	AGGACGTGCAACCTGTGGGC	225277	57473	CTTGATCTTAGCCAAAAGGC	269864	102060	CAGTGGAGCCGATCTTGGAC

180691	12887	CAGGACGTGCAACCTGTGGG	225278	57474	ACTTGATCTTAGCCAAAAGG	269865	102061	TCAGTGGAGCCGATCTTGGA
180692	12888	ACAGGACGTGCAACCTGTGG	225279	57475	CACTTGATCTTAGCCAAAAG	269866	102062	CTCAGTGGAGCCGATCTTGG
180693	12889	CACAGGACGTGCAACCTGTG	225280	57476	ACACTTGATCTTAGCCAAAA	269867	102063	TCTCAGTGGAGCCGATCTTG
180694	12890	TCACAGGACGTGCAACCTGT	225281	57477	TACACTTGATCTTAGCCAAA	269868	102064	TTCTCAGTGGAGCCGATCTT
180695	12891	CTCACAGGACGTGCAACCTG	225282	57478	ATACACTTGATCTTAGCCAA	269869	102065	GTTCTCAGTGGAGCCGATCT
180696	12892	CCTCACAGGACGTGCAACCT	225283	57479	AATACACTTGATCTTAGCCA	269870	102066	GGTTCTCAGTGGAGCCGATC
180697	12893	CCCTCACAGGACGTGCAACC	225284	57480	AAATACACTTGATCTTAGCC	269871	102067	AGGTTCTCAGTGGAGCCGAT
180698	12894	GCCCTCACAGGACGTGCAAC	225285	57481	AAAATACACTTGATCTTAGC	269872	102068	CAGGTTCTCAGTGGAGCCGA
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180700	12896	TTGCCCTCACAGGACGTGCA	225287	57483	GGAAAATACACTTGATCTTA	269874	102070	TTCAGGTTCTCAGTGGAGCC
180701	12897	CTTGCCCTCACAGGACGTGC	225288	57484	AGGAAAATACACTTGATCTT	269875	102071	CTTCAGGTTCTCAGTGGAGC
180702	12898	CCTTGCCCTCACAGGACGTG	225289	57485	CAGGAAAATACACTTGATCT	269876	102072	GCTTCAGGTTCTCAGTGGAG
180703	12899	TCCTTGCCCTCACAGGACGT	225290	57486	ACAGGAAAATACACTTGATC	269877	102073	TGCTTCAGGTTCTCAGTGGA
180704	12900	GTCCTTGCCCTCACAGGACG	225291	57487	GACAGGAAAATACACTTGAT	269878	102074	GTGCTTCAGGTTCTCAGTGG
180705	12901	AGTCCTTGCCCTCACAGGAC	225292	57488	AGACAGGAAAATACACTTGA	269879	102075	GGTGCTTCAGGTTCTCAGTG
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180707	12903	ACAGTCCTTGCCCTCACAGG	225294	57490	ACAGACAGGAAAATACACTT	269881	102077	CTGGTGCTTCAGGTTCTCAG
180708	12904	CACAGTCCTTGCCCTCACAG	225295	57491	CACAGACAGGAAAATACACT	269882	102078	GCTGGTGCTTCAGGTTCTCA
180709	12905	ACACAGTCCTTGCCCTCACA	225296	57492	ACACAGACAGGAAAATACAC	269883	102079	GGCTGGTGCTTCAGGTTCTC
180710	12906	GACACAGTCCTTGCCCTCAC	225297	57493	CACACAGACAGGAAAATACA	269884	102080	CGGCTGGTGCTTCAGGTTCT
180711	12907	AGACACAGTCCTTGCCCTCA	225298	57494	ACACACAGACAGGAAAATAC	269885	102081	CCGGCTGGTGCTTCAGGTTC
180712	12908	AAGACACAGTCCTTGCCCTC	225299	57495	GACACACAGACAGGAAAATA	269886	102082	CCCGGCTGGTGCTTCAGGTT
180713	12909	TAAGACACAGTCCTTGCCCT	225300	57496	AGACACACAGACAGGAAAAT	269887	102083	TCCCGGCTGGTGCTTCAGGT
180714	12910	ATAAGACACAGTCCTTGCCC	225301	57497	GAGACACACAGACAGGAAAA	269888	102084	CTCCCGGCTGGTGCTTCAGG
180715	12911	CATAAGACACAGTCCTTGCC	225302	57498	CGAGACACACAGACAGGAAA	269889	102085	CCTCCCGGCTGGTGCTTCAG
180716	12912	ACATAAGACACAGTCCTTGC	225303	57499	GCGAGACACACAGACAGGAA	269890	102086	GCCTCCCGGCTGGTGCTTCA
180717	12913	CACATAAGACACAGTCCTTG	225304	57500	AGCGAGACACACAGACAGGA	269891	102087	CGCCTCCCGGCTGGTGCTTC
180718	12914	TCACATAAGACACAGTCCTT	225305	57501	AAGCGAGACACACAGACAGG	269892	102088	CCGCCTCCCGGCTGGTGCTT
180719	12915	GTCACATAAGACACAGTCCT	225306	57502	TAAGCGAGACACACAGACAG	269893	102089	CCCGCCTCCCGGCTGGTGCT
180720	12916	AGTCACATAAGACACAGTCC	225307	57503	CTAAGCGAGACACACAGACA	269894	102090	TCCCGCCTCCCGGCTGGTGC
180721	12917	AAGTCACATAAGACACAGTC	225308	57504	TCTAAGCGAGACACACAGAC	269895	102091	TTCCCGCCTCCCGGCTGGTG
180722	12918	AAAGTCACATAAGACACAGT	225309	57505	ATCTAAGCGAGACACACAGA	269896	102092	CTTCCCGCCTCCCGGCTGGT
180723	12919	GAAAGTCACATAAGACACAG	225310	57506	AATCTAAGCGAGACACACAG	269897	102093	CCTTCCCGCCTCCCGGCTGG
180724	12920	GGAAAGTCACATAAGACACA	225311	57507	TAATCTAAGCGAGACACACA	269898	102094	ACCTTCCCGCCTCCCGGCTG
180725	12921	AGGAAAGTCACATAAGACAC	225312	57508	GTAATCTAAGCGAGACACAC	269899	102095	CACCTTCCCGCCTCCCGGCT
180726	12922	AAGGAAAGTCACATAAGACA	225313	57509	TGTAATCTAAGCGAGACACA	269900	102096	TCACCTTCCCGCCTCCCGGC
180727	12923	GAAGGAAAGTCACATAAGAC	225314	57510	CTGTAATCTAAGCGAGACAC	269901	102097	CTCACCTTCCCGCCTCCCGG
180728	12924	AGAAGGAAAGTCACATAAGA	225315	57511	CCTGTAATCTAAGCGAGACA	269902	102098	TCTCACCTTCCCGCCTCCCG
180729	12925	GAGAAGGAAAGTCACATAAG	225316	57512	CCCTGTAATCTAAGCGAGAC	269903	102099	CTCTCACCTTCCCGCCTCCC
180730	12926	GGAGAAGGAAAGTCACATAA	225317	57513	TCCCTGTAATCTAAGCGAGA	269904	102100	ACTCTCACCTTCCCGCCTCC
180731	12927	TGGAGAAGGAAAGTCACATA	225318	57514	ATCCCTGTAATCTAAGCGAG	269905	102101	CACTCTCACCTTCCCGCCTC
180732	12928	CTGGAGAAGGAAAGTCACAT	225319	57515	GATCCCTGTAATCTAAGCGA	269906	102102	CCACTCTCACCTTCCCGCCT
180733	12929	ACTGGAGAAGGAAAGTCACA	225320	57516	AGATCCCTGTAATCTAAGCG	269907	102103	GCCACTCTCACCTTCCCGCC
180734	12930	GACTGGAGAAGGAAAGTCAC	225321	57517	CAGATCCCTGTAATCTAAGC	269908	102104	AGCCACTCTCACCTTCCCGC
180735	12931	TGACTGGAGAAGGAAAGTCA	225322	57518	ACAGATCCCTGTAATCTAAG	269909	102105	CAGCCACTCTCACCTTCCCG
180736	12932	GTGACTGGAGAAGGAAAGTC	225323	57519	CACAGATCCCTGTAATCTAA	269910	102106	CCAGCCACTCTCACCTTCCC
180737	12933	TGTGACTGGAGAAGGAAAGT	225324	57520	CCACAGATCCCTGTAATCTA	269911	102107	GCCAGCCACTCTCACCTTCC
180738	12934	CTGTGACTGGAGAAGGAAAG	225325	57521	CCCACAGATCCCTGTAATCT	269912	102108	AGCCAGCCACTCTCACCTTC
180739	12935	TCTGTGACTGGAGAAGGAAA	225326	57522	ACCCACAGATCCCTGTAATC	269913	102109	CAGCCAGCCACTCTCACCTT
180740	12936	CTCTGTGACTGGAGAAGGAA	225327	57523	CACCCACAGATCCCTGTAAT	269914	102110	GCAGCCAGCCACTCTCACCT
180741	12937	GCTCTGTGACTGGAGAAGGA	225328	57524	TCACCCACAGATCCCTGTAA	269915	102111	CGCAGCCAGCCACTCTCACC
180742	12938	AGCTCTGTGACTGGAGAAGG	225329	57525	ATCACCCACAGATCCCTGTA	269916	102112	GCGCAGCCAGCCACTCTCAC
180743	12939	CAGCTCTGTGACTGGAGAAG	225330	57526	CATCACCCACAGATCCCTGT	269917	102113	CGCGCAGCCAGCCACTCTCA
180744	12940	CCAGCTCTGTGACTGGAGAA	225331	57527	TCATCACCCACAGATCCCTG	269918	102114	ACGCGCAGCCAGCCACTCTC
180745	12941	CCCAGCTCTGTGACTGGAGA	225332	57528	GTCATCACCCACAGATCCCT	269919	102115	CACGCGCAGCCAGCCACTCT
180746	12942	GCCCAGCTCTGTGACTGGAG	225333	57529	TGTCATCACCCACAGATCCC	269920	102116	CCACGCGCAGCCAGCCACTC
180747	12943	TGCCCAGCTCTGTGACTGGA	225334	57530	GTGTCATCACCCACAGATCC	269921	102117	TCCACGCGCAGCCAGCCACT
180748	12944	GTGCCCAGCTCTGTGACTGG	225335	57531	CGTGTCATCACCCACAGATC	269922	102118	CTCCACGCGCAGCCAGCCAC
180749	12945	TGTGCCCAGCTCTGTGACTG	225336	57532	ACGTGTCATCACCCACAGAT	269923	102119	CCTCCACGCGCAGCCAGCCA
180750	12946	ATGTGCCCAGCTCTGTGACT	225337	57533	GACGTGTCATCACCCACAGA	269924	102120	ACCTCCACGCGCAGCCAGCC
180751	12947	TATGTGCCCAGCTCTGTGAC	225338	57534	AGACGTGTCATCACCCACAG	269925	102121	CACCTCCACGCGCAGCCAGC
180752	12948	CTATGTGCCCAGCTCTGTGA	225339	57535	CAGACGTGTCATCACCCACA	269926	102122	ACACCTCCACGCGCAGCCAG
180753	12949	TCTATGTGCCCAGCTCTGTG	225340	57536	CCAGACGTGTCATCACCCAC	269927	102123	CACACCTCCACGCGCAGCCA
180754	12950	ATCTATGTGCCCAGCTCTGT	225341	57537	ACCAGACGTGTCATCACCCA	269928	102124	CCACACCTCCACGCGCAGCC
180755	12951	TATCTATGTGCCCAGCTCTG	225342	57538	GACCAGACGTGTCATCACCC	269929	102125	CCCACACCTCCACGCGCAGC
180756	12952	CTATCTATGTGCCCAGCTCT	225343	57539	GGACCAGACGTGTCATCACC	269930	102126	CCCCACACCTCCACGCGCAG
180757	12953	GCTATCTATGTGCCCAGCTC	225344	57540	TGGACCAGACGTGTCATCAC	269931	102127	CCCCCACACCTCCACGCGCA
180758	12954	AGCTATCTATGTGCCCAGCT	225345	57541	CTGGACCAGACGTGTCATCA	269932	102128	CCCCCCACACCTCCACGCGC
180759	12955	GAGCTATCTATGTGCCCAGC	225346	57542	CCTGGACCAGACGTGTCATC	269933	102129	GCCCCCCACACCTCCACGCG
180760	12956	TGAGCTATCTATGTGCCCAG	225347	57543	GCCTGGACCAGACGTGTCAT	269934	102130	AGCCCCCCACACCTCCACGC
180761	12957	TTGAGCTATCTATGTGCCCA	225348	57544	AGCCTGGACCAGACGTGTCA	269935	102131	CAGCCCCCCACACCTCCACG
180762	12958	TTTGAGCTATCTATGTGCCC	225349	57545	CAGCCTGGACCAGACGTGTC	269936	102132	GCAGCCCCCCACACCTCCAC

180763	12959	TTTTGAGCTATCTATGTGCC	225350	57546	GCAGCCTGGACCAGACGTGT	269937	102133	CGCAGCCCCCCACACCTCCA
180764	12960	GTTTTGAGCTATCTATGTGC	225351	57547	CGCAGCCTGGACCAGACGTG	269938	102134	GCGCAGCCCCCCACACCTCC
180765	12961	GGTTTTGAGCTATCTATGTG	225352	57548	ACGCAGCCTGGACCAGACGT	269939	102135	GGCGCAGCCCCCCACACCTC
180766	12962	GGGTTTTGAGCTATCTATGT	225353	57549	TACGCAGCCTGGACCAGACG	269940	102136	AGGCGCAGCCCCCCACACCT
180767	12963	AGGGTTTTGAGCTATCTATG	225354	57550	CTACGCAGCCTGGACCAGAC	269941	102137	CAGGCGCAGCCCCCCACACC
180768	12964	GAGGGTTTTGAGCTATCTAT	225355	57551	ACTACGCAGCCTGGACCAGA	269942	102138	CCAGGCGCAGCCCCCCACAC
180769	12965	AGAGGGTTTTGAGCTATCTA	225356	57552	GACTACGCAGCCTGGACCAG	269943	102139	TCCAGGCGCAGCCCCCCACA
180770	12966	AAGAGGGTTTTGAGCTATCT	225357	57553	TGACTACGCAGCCTGGACCA	269944	102140	CTCCAGGCGCAGCCCCCCAC
180771	12967	AAAGAGGGTTTTGAGCTATC	225358	57554	GTGACTACGCAGCCTGGACC	269945	102141	CCTCCAGGCGCAGCCCCCCA
180772	12968	TAAAGAGGGTTTTGAGCTAT	225359	57555	GGTGACTACGCAGCCTGGAC	269946	102142	CCCTCCAGGCGCAGCCCCCC
180773	12969	ATAAAGAGGGTTTTGAGCTA	225360	57556	AGGTGACTACGCAGCCTGGA	269947	102143	CCCCTCCAGGCGCAGCCCCC
180774	12970	AATAAAGAGGGTTTTGAGCT	225361	57557	GAGGTGACTACGCAGCCTGG	269948	102144	ACCCCTCCAGGCGCAGCCCC
180775	12971	TAATAAAGAGGGTTTTGAGC	225362	57558	TGAGGTGACTACGCAGCCTG	269949	102145	TACCCCTCCAGGCGCAGCCC
180776	12972	TTAATAAAGAGGGTTTTGAG	225363	57559	TTGAGGTGACTACGCAGCCT	269950	102146	CTACCCCTCCAGGCGCAGCC
180777	12973	GTTAATAAAGAGGGTTTTGA	225364	57560	CTTGAGGTGACTACGCAGCC	269951	102147	CCTACCCCTCCAGGCGCAGC
180778	12974	TGTTAATAAAGAGGGTTTTG	225365	57561	CCTTGAGGTGACTACGCAGC	269952	102148	CCCTACCCCTCCAGGCGCAG
180779	12975	GTGTTAATAAAGAGGGTTTT	225366	57562	CCCTTGAGGTGACTACGCAG	269953	102149	GCCCTACCCCTCCAGGCGCA
180780	12976	TGTGTTAATAAAGAGGGTTT	225367	57563	GCCCTTGAGGTGACTACGCA	269954	102150	AGCCCTACCCCTCCAGGCGC
180781	12977	CTGTGTTAATAAAGAGGGTT	225368	57564	TGCCCTTGAGGTGACTACGC	269955	102151	CAGCCCTACCCCTCCAGGCG
180782	12978	ACTGTGTTAATAAAGAGGGT	225369	57565	ATGCCCTTGAGGTGACTACG	269956	102152	ACAGCCCTACCCCTCCAGGC
180783	12979	AACTGTGTTAATAAAGAGGG	225370	57566	CATGCCCTTGAGGTGACTAC	269957	102153	CACAGCCCTACCCCTCCAGG
180784	12980	CAACTGTGTTAATAAAGAGG	225371	57567	GCATGCCCTTGAGGTGACTA	269958	102154	GCACAGCCCTACCCCTCCAG
180785	12981	CCAACTGTGTTAATAAAGAG	225372	57568	AGCATGCCCTTGAGGTGACT	269959	102155	GGCACAGCCCTACCCCTCCA
180786	12982	TCCAACTGTGTTAATAAAGA	225373	57569	AAGCATGCCCTTGAGGTGAC	269960	102156	AGGCACAGCCCTACCCCTCC
180787	12983	ATCCAACTGTGTTAATAAAG	225374	57570	TAAGCATGCCCTTGAGGTGA	269961	102157	CAGGCACAGCCCTACCCCTC
180788	12984	CATCCAACTGTGTTAATAAA	225375	57571	ATAAGCATGCCCTTGAGGTG	269962	102158	CCAGGCACAGCCCTACCCCT
180789	12985	ACATCCAACTGTGTTAATAA	225376	57572	AATAAGCATGCCCTTGAGGT	269963	102159	TCCAGGCACAGCCCTACCCC
180790	12986	AACATCCAACTGTGTTAATA	225377	57573	CAATAAGCATGCCCTTGAGG	269964	102160	TTCCAGGCACAGCCCTACCC
180791	12987	CAACATCCAACTGTGTTAAT	225378	57574	TCAATAAGCATGCCCTTGAG	269965	102161	CTTCCAGGCACAGCCCTACC
180792	12988	TCAACATCCAACTGTGTTAA	225379	57575	ATCAATAAGCATGCCCTTGA	269966	102162	CCTTCCAGGCACAGCCCTAC
180793	12989	CTCAACATCCAACTGTGTTA	225380	57576	CATCAATAAGCATGCCCTTG	269967	102163	CCCTTCCAGGCACAGCCCTA
180794	12990	TCTCAACATCCAACTGTGTT	225381	57577	ACATCAATAAGCATGCCCTT	269968	102164	ACCCTTCCAGGCACAGCCCT
180795	12991	TTCTCAACATCCAACTGTGT	225382	57578	CACATCAATAAGCATGCCCT	269969	102165	TACCCTTCCAGGCACAGCCC
180796	12992	TTTCTCAACATCCAACTGTG	225383	57579	ACACATCAATAAGCATGCCC	269970	102166	CTACCCTTCCAGGCACAGCC
180797	12993	ATTTCTCAACATCCAACTGT	225384	57580	AACACATCAATAAGCATGCC	269971	102167	CCTACCCTTCCAGGCACAGC
180798	12994	GATTTCTCAACATCCAACTG	225385	57581	AAACACATCAATAAGCATGC	269972	102168	CCCTACCCTTCCAGGCACAG
180799	12995	TGATTTCTCAACATCCAACT	225386	57582	AAAACACATCAATAAGCATG	269973	102169	GCCCTACCCTTCCAGGCACA
180800	12996	TTGATTTCTCAACATCCAAC	225387	57583	AAAAACACATCAATAAGCAT	269974	102170	AGCCCTACCCTTCCAGGCAC
180801	12997	TTTGATTTCTCAACATCCAA	225388	57584	GAAAAACACATCAATAAGCA	269975	102171	CAGCCCTACCCTTCCAGGCA
180802	12998	GTTTGATTTCTCAACATCCA	225389	57585	TGAAAAACACATCAATAAGC	269976	102172	GCAGCCCTACCCTTCCAGGC
180803	12999	TGTTTGATTTCTCAACATCC	225390	57586	TTGAAAAACACATCAATAAG	269977	102173	CGCAGCCCTACCCTTCCAGG
180804	13000	CTGTTTGATTTCTCAACATC	225391	57587	ATTGAAAAACACATCAATAA	269978	102174	GCGCAGCCCTACCCTTCCAG
180805	13001	CCTGTTTGATTTCTCAACAT	225392	57588	AATTGAAAAACACATCAATA	269979	102175	GGCGCAGCCCTACCCTTCCA
180806	13002	GCCTGTTTGATTTCTCAACA	225393	57589	GAATTGAAAAACACATCAAT	269980	102176	AGGCGCAGCCCTACCCTTCC
180807	13003	GGCCTGTTTGATTTCTCAAC	225394	57590	TGAATTGAAAAACACATCAA	269981	102177	CAGGCGCAGCCCTACCCTTC
180808	13004	TGGCCTGTTTGATTTCTCAA	225395	57591	GTGAATTGAAAAACACATCA	269982	102178	CCAGGCGCAGCCCTACCCTT
180809	13005	TTGGCCTGTTTGATTTCTCA	225396	57592	AGTGAATTGAAAAACACATC	269983	102179	TCCAGGCGCAGCCCTACCCT
180810	13006	ATTGGCCTGTTTGATTTCTC	225397	57593	TAGTGAATTGAAAAACACAT	269984	102180	CTCCAGGCGCAGCCCTACCC
180811	13007	CATTGGCCTGTTTGATTTCT	225398	57594	ATAGTGAATTGAAAAACACA	269985	102181	CCTCCAGGCGCAGCCCTACC
180812	13008	ACATTGGCCTGTTTGATTTC	225399	57595	GATAGTGAATTGAAAAACAC	269986	102182	ACCTCCAGGCGCAGCCCTAC
180813	13009	GACATTGGCCTGTTTGATTT	225400	57596	AGATAGTGAATTGAAAAACA	269987	102183	CACCTCCAGGCGCAGCCCTA
180814	13010	TGACATTGGCCTGTTTGATT	225401	57597	AAGATAGTGAATTGAAAAAC	269988	102184	GCACCTCCAGGCGCAGCCCT
180815	13011	TTGACATTGGCCTGTTTGAT	225402	57598	AAAGATAGTGAATTGAAAAA	269989	102185	CGCACCTCCAGGCGCAGCCC
180816	13012	TTTGACATTGGCCTGTTTGA	225403	57599	CAAAGATAGTGAATTGAAAA	269990	102186	GCGCACCTCCAGGCGCAGCC
180817	13013	ATTTGACATTGGCCTGTTTG	225404	57600	GCAAAGATAGTGAATTGAAA	269991	102187	CGCGCACCTCCAGGCGCAGC
180818	13014	CATTTGACATTGGCCTGTTT	225405	57601	TGCAAAGATAGTGAATTGAA	269992	102188	CCGCGCACCTCCAGGCGCAG
180819	13015	TCATTTGACATTGGCCTGTT	225406	57602	ATGCAAAGATAGTGAATTGA	269993	102189	ACCGCGCACCTCCAGGCGCA
180820	13016	CTCATTTGACATTGGCCTGT	225407	57603	CATGCAAAGATAGTGAATTG	269994	102190	AACCGCGCACCTCCAGGCGC
180821	13017	GCTCATTTGACATTGGCCTG	225408	57604	CCATGCAAAGATAGTGAATT	269995	102191	CAACCGCGCACCTCCAGGCG
180822	13018	AGCTCATTTGACATTGGCCT	225409	57605	CCCATGCAAAGATAGTGAAT	269996	102192	TCAACCGCGCACCTCCAGGC
180823	13019	GAGCTCATTTGACATTGGCC	225410	57606	TCCCATGCAAAGATAGTGAA	269997	102193	CTCAACCGCGCACCTCCAGG
180824	13020	AGAGCTCATTTGACATTGGC	225411	57607	CTCCCATGCAAAGATAGTGA	269998	102194	GCTCAACCGCGCACCTCCAG
180825	13021	GAGAGCTCATTTGACATTGG	225412	57608	ACTCCCATGCAAAGATAGTG	269999	102195	CGCTCAACCGCGCACCTCCA
180826	13022	GGAGAGCTCATTTGACATTG	225413	57609	GACTCCCATGCAAAGATAGT	270000	102196	ACGCTCAACCGCGCACCTCC
180827	13023	AGGAGAGCTCATTTGACATT	225414	57610	GGACTCCCATGCAAAGATAG	270001	102197	CACGCTCAACCGCGCACCTC
180828	13024	AAGGAGAGCTCATTTGACAT	225415	57611	GGGACTCCCATGCAAAGATA	270002	102198	CCACGCTCAACCGCGCACCT
180829	13025	TAAGGAGAGCTCATTTGACA	225416	57612	TGGGACTCCCATGCAAAGAT	270003	102199	TCCACGCTCAACCGCGCACC
180830	13026	ATAAGGAGAGCTCATTTGAC	225417	57613	CTGGGACTCCCATGCAAAGA	270004	102200	CTCCACGCTCAACCGCGCAC
180831	13027	AATAAGGAGAGCTCATTTGA	225418	57614	CCTGGGACTCCCATGCAAAG	270005	102201	ACTCCACGCTCAACCGCGCA
180832	13028	AAATAAGGAGAGCTCATTTG	225419	57615	GCCTGGGACTCCCATGCAAA	270006	102202	GACTCCACGCTCAACCGCGC
180833	13029	TAAATAAGGAGAGCTCATTT	225420	57616	GGCCTGGGACTCCCATGCAA	270007	102203	CGACTCCACGCTCAACCGCG
180834	13030	TTAAATAAGGAGAGCTCATT	225421	57617	TGGCCTGGGACTCCCATGCA	270008	102204	ACGACTCCACGCTCAACCGC

180835	13031	TTTAAATAAGGAGAGCTCAT	225422	57618	TTGGCCTGGGACTCCCATGC	270009	102205	CACGACTCCACGCTCAACCG
180836	13032	ATTTAAATAAGGAGAGCTCA	225423	57619	CTTGGCCTGGGACTCCCATG	270010	102206	CCACGACTCCACGCTCAACC
180837	13033	GATTTAAATAAGGAGAGCTC	225424	57620	TCTTGGCCTGGGACTCCCAT	270011	102207	CCCACGACTCCACGCTCAAC
180838	13034	TGATTTAAATAAGGAGAGCT	225425	57621	CTCTTGGCCTGGGACTCCCA	270012	102208	TCCCACGACTCCACGCTCAA
180839	13035	TTGATTTAAATAAGGAGAGC	225426	57622	CCTCTTGGCCTGGGACTCCC	270013	102209	GTCCCACGACTCCACGCTCA
180840	13036	CTTGATTTAAATAAGGAGAG	225427	57623	GCCTCTTGGCCTGGGACTCC	270014	102210	AGTCCCACGACTCCACGCTC
180841	13037	ACTTGATTTAAATAAGGAGA	225428	57624	TGCCTCTTGGCCTGGGACTC	270015	102211	CAGTCCCACGACTCCACGCT
180842	13038	GACTTGATTTAAATAAGGAG	225429	57625	GTGCCTCTTGGCCTGGGACT	270016	102212	ACAGTCCCACGACTCCACGC
180843	13039	TGACTTGATTTAAATAAGGA	225430	57626	TGTGCCTCTTGGCCTGGGAC	270017	102213	CACAGTCCCACGACTCCACG
180844	13040	CTGACTTGATTTAAATAAGG	225431	57627	CTGTGCCTCTTGGCCTGGGA	270018	102214	GCACAGTCCCACGACTCCAC
180845	13041	ACTGACTTGATTTAAATAAG	225432	57628	GCTGTGCCTCTTGGCCTGGG	270019	102215	TGCACAGTCCCACGACTCCA
180846	13042	AACTGACTTGATTTAAATAA	225433	57629	AGCTGTGCCTCTTGGCCTGG	270020	102216	ATGCACAGTCCCACGACTCC
180847	13043	GAACTGACTTGATTTAAATA	225434	57630	CAGCTGTGCCTCTTGGCCTG	270021	102217	CATGCACAGTCCCACGACTC
180848	13044	AGAACTGACTTGATTTAAAT	225435	57631	GCAGCTGTGCCTCTTGGCCT	270022	102218	CCATGCACAGTCCCACGACT
180849	13045	GAGAACTGACTTGATTTAAA	225436	57632	CGCAGCTGTGCCTCTTGGCC	270023	102219	TCCATGCACAGTCCCACGAC
180850	13046	GGAGAACTGACTTGATTTAA	225437	57633	GCGCAGCTGTGCCTCTTGGC	270024	102220	CTCCATGCACAGTCCCACGA
180851	13047	TGGAGAACTGACTTGATTTA	225438	57634	GGCGCAGCTGTGCCTCTTGG	270025	102221	CCTCCATGCACAGTCCCACG
180852	13048	GTGGAGAACTGACTTGATTT	225439	57635	TGGCGCAGCTGTGCCTCTTG	270026	102222	ACCTCCATGCACAGTCCCAC
180853	13049	GGTGGAGAACTGACTTGATT	225440	57636	ATGGCGCAGCTGTGCCTCTT	270027	102223	CACCTCCATGCACAGTCCCA
180854	13050	AGGTGGAGAACTGACTTGAT	225441	57637	AATGGCGCAGCTGTGCCTCT	270028	102224	ACACCTCCATGCACAGTCCC
180855	13051	GAGGTGGAGAACTGACTTGA	225442	57638	AAATGGCGCAGCTGTGCCTC	270029	102225	CACACCTCCATGCACAGTCC
180856	13052	GGAGGTGGAGAACTGACTTG	225443	57639	CAAATGGCGCAGCTGTGCCT	270030	102226	CCACACCTCCATGCACAGTC
180857	13053	AGGAGGTGGAGAACTGACTT	225444	57640	ACAAATGGCGCAGCTGTGCC	270031	102227	CCCACACCTCCATGCACAGT
180858	13054	TAGGAGGTGGAGAACTGACT	225445	57641	GACAAATGGCGCAGCTGTGC	270032	102228	CCCCACACCTCCATGCACAG
180859	13055	CTAGGAGGTGGAGAACTGAC	225446	57642	AGACAAATGGCGCAGCTGTG	270033	102229	GCCCCACACCTCCATGCACA
180860	13056	GCTAGGAGGTGGAGAACTGA	225447	57643	CAGACAAATGGCGCAGCTGT	270034	102230	AGCCCCACACCTCCATGCAC
180861	13057	TGCTAGGAGGTGGAGAACTG	225448	57644	ACAGACAAATGGCGCAGCTG	270035	102231	GAGCCCCACACCTCCATGCA
180862	13058	GTGCTAGGAGGTGGAGAACT	225449	57645	AACAGACAAATGGCGCAGCT	270036	102232	GGAGCCCCACACCTCCATGC
180863	13059	AGTGCTAGGAGGTGGAGAAC	225450	57646	CAACAGACAAATGGCGCAGC	270037	102233	GGGAGCCCCACACCTCCATG
180864	13060	GAGTGCTAGGAGGTGGAGAA	225451	57647	CCAACAGACAAATGGCGCAG	270038	102234	GGGGAGCCCCACACCTCCAT
180865	13061	TGAGTGCTAGGAGGTGGAGA	225452	57648	ACCAACAGACAAATGGCGCA	270039	102235	CGGGGAGCCCCACACCTCCA
180866	13062	CTGAGTGCTAGGAGGTGGAG	225453	57649	AACCAACAGACAAATGGCGC	270040	102236	GCGGGGAGCCCCACACCTCC
180867	13063	ACTGAGTGCTAGGAGGTGGA	225454	57650	AAACCAACAGACAAATGGCG	270041	102237	TGCGGGGAGCCCCACACCTC
180868	13064	AACTGAGTGCTAGGAGGTGG	225455	57651	TAAACCAACAGACAAATGGC	270042	102238	GTGCGGGGAGCCCCACACCT
180869	13065	GAACTGAGTGCTAGGAGGTG	225456	57652	CTAAACCAACAGACAAATGG	270043	102239	GGTGCGGGGAGCCCCACACC
180870	13066	GGAACTGAGTGCTAGGAGGT	225457	57653	TCTAAACCAACAGACAAATG	270044	102240	AGGTGCGGGGAGCCCCACAC
180871	13067	TGGAACTGAGTGCTAGGAGG	225458	57654	ATCTAAACCAACAGACAAAT	270045	102241	CAGGTGCGGGGAGCCCCACA
180872	13068	CTGGAACTGAGTGCTAGGAG	225459	57655	TATCTAAACCAACAGACAAA	270046	102242	TCAGGTGCGGGGAGCCCCAC
180873	13069	ACTGGAACTGAGTGCTAGGA	225460	57656	ATATCTAAACCAACAGACAA	270047	102243	CTCAGGTGCGGGGAGCCCCA
180874	13070	TACTGGAACTGAGTGCTAGG	225461	57657	GATATCTAAACCAACAGACA	270048	102244	GCTCAGGTGCGGGGAGCCCC
180875	13071	GTACTGGAACTGAGTGCTAG	225462	57658	GGATATCTAAACCAACAGAC	270049	102245	TGCTCAGGTGCGGGGAGCCC
180876	13072	AGTACTGGAACTGAGTGCTA	225463	57659	AGGATATCTAAACCAACAGA	270050	102246	GTGCTCAGGTGCGGGGAGCC
180877	13073	GAGTACTGGAACTGAGTGCT	225464	57660	AAGGATATCTAAACCAACAG	270051	102247	GGTGCTCAGGTGCGGGGAGC
180878	13074	AGAGTACTGGAACTGAGTGC	225465	57661	AAAGGATATCTAAACCAACA	270052	102248	GGGTGCTCAGGTGCGGGGAG
180879	13075	TAGAGTACTGGAACTGAGTG	225466	57662	TAAAGGATATCTAAACCAAC	270053	102249	GGGGTGCTCAGGTGCGGGGA
180880	13076	ATAGAGTACTGGAACTGAGT	225467	57663	ATAAAGGATATCTAAACCAA	270054	102250	GGGGGTGCTCAGGTGCGGGG
180881	13077	TATAGAGTACTGGAACTGAG	225468	57664	GATAAAGGATATCTAAACCA	270055	102251	CGGGGGTGCTCAGGTGCGGG
180882	13078	ATATAGAGTACTGGAACTGA	225469	57665	GGATAAAGGATATCTAAACC	270056	102252	GCGGGGGTGCTCAGGTGCGG
180883	13079	TATATAGAGTACTGGAACTG	225470	57666	TGGATAAAGGATATCTAAAC	270057	102253	TGCGGGGGTGCTCAGGTGCG
180884	13080	GTATATAGAGTACTGGAACT	225471	57667	CTGGATAAAGGATATCTAAA	270058	102254	ATGCGGGGGTGCTCAGGTGC
180885	13081	TGTATATAGAGTACTGGAAC	225472	57668	ACTGGATAAAGGATATCTAA	270059	102255	TATGCGGGGGTGCTCAGGTG
180886	13082	ATGTATATAGAGTACTGGAA	225473	57669	AACTGGATAAAGGATATCTA	270060	102256	TTATGCGGGGGTGCTCAGGT
180887	13083	CATGTATATAGAGTACTGGA	225474	57670	GAACTGGATAAAGGATATCT	270061	102257	GTTATGCGGGGGTGCTCAGG
180888	13084	CCATGTATATAGAGTACTGG	225475	57671	AGAACTGGATAAAGGATATC	270062	102258	TGTTATGCGGGGGTGCTCAG
180889	13085	TCCATGTATATAGAGTACTG	225476	57672	AAGAACTGGATAAAGGATAT	270063	102259	GTGTTATGCGGGGGTGCTCA
180890	13086	TTCCATGTATATAGAGTACT	225477	57673	GAAGAACTGGATAAAGGATA	270064	102260	GGTGTTATGCGGGGGTGCTC
180891	13087	TTTCCATGTATATAGAGTAC	225478	57674	GGAAGAACTGGATAAAGGAT	270065	102261	GGGTGTTATGCGGGGGTGCT
180892	13088	ATTTCCATGTATATAGAGTA	225479	57675	TGGAAGAACTGGATAAAGGA	270066	102262	GGGGTGTTATGCGGGGGTGC
180893	13089	TATTTCCATGTATATAGAGT	225480	57676	CTGGAAGAACTGGATAAAGG	270067	102263	TGGGGTGTTATGCGGGGGTG
180894	13090	TTATTTCCATGTATATAGAG	225481	57677	TCTGGAAGAACTGGATAAAG	270068	102264	CTGGGGTGTTATGCGGGGGT
180895	13091	ATTATTTCCATGTATATAGA	225482	57678	CTCTGGAAGAACTGGATAAA	270069	102265	ACTGGGGTGTTATGCGGGGG
180896	13092	TATTATTTCCATGTATATAG	225483	57679	TCTCTGGAAGAACTGGATAA	270070	102266	GACTGGGGTGTTATGCGGGG
180897	13093	TTATTATTTCCATGTATATA	225484	57680	TTCTCTGGAAGAACTGGATA	270071	102267	GGACTGGGGTGTTATGCGGG
180898	13094	TTTATTATTTCCATGTATAT	225485	57681	TTTCTCTGGAAGAACTGGAT	270072	102268	GGGACTGGGGTGTTATGCGG
180899	13095	TTTTATTATTTCCATGTATA	225486	57682	ATTTCTCTGGAAGAACTGGA	270073	102269	GGGGACTGGGGTGTTATGCG
180900	13096	TTTTTATTATTTCCATGTAT	225487	57683	GATTTCTCTGGAAGAACTGG	270074	102270	AGGGGACTGGGGTGTTATGC
180901	13097	TTTTTTATTATTTCCATGTA	225488	57684	TGATTTCTCTGGAAGAACTG	270075	102271	GAGGGGACTGGGGTGTTATG
180902	13098	GTTTTTTATTATTTCCATGT	225489	57685	ATGATTTCTCTGGAAGAACT	270076	102272	AGAGGGGACTGGGGTGTTAT
180903	13099	TGTTTTTTATTATTTCCATG	225490	57686	GATGATTTCTCTGGAAGAAC	270077	102273	CAGAGGGGACTGGGGTGTTA
180904	13100	GTGTTTTTTATTATTTCCAT	225491	57687	GGATGATTTCTCTGGAAGAA	270078	102274	CCAGAGGGGACTGGGGTGTT
180905	13101	TGTGTTTTTTATTATTTCCA	225492	57688	AGGATGATTTCTCTGGAAGA	270079	102275	TCCAGAGGGGACTGGGGTGT
180906	13102	ATGTGTTTTTTATTATTTCC	225493	57689	CAGGATGATTTCTCTGGAAG	270080	102276	GTCCAGAGGGGACTGGGGTG

180907	13103	AATGTGTTTTTTATTATTTC	225494	57690	GCAGGATGATTTCTCTGGAA	270081	102277	GGTCCAGAGGGGACTGGGGT
180908	13104	AAATGTGTTTTTTATTATTT	225495	57691	GGCAGGATGATTTCTCTGGA	270082	102278	GGGTCCAGAGGGGACTGGGG
180909	13105	GAAATGTGTTTTTTATTATT	225496	57692	GGGCAGGATGATTTCTCTGG	270083	102279	AGGGTCCAGAGGGGACTGGG
180910	13106	GGAAATGTGTTTTTTATTAT	225497	57693	AGGGCAGGATGATTTCTCTG	270084	102280	GAGGGTCCAGAGGGGACTGG
180911	13107	AGGAAATGTGTTTTTTATTA	225498	57694	AAGGGCAGGATGATTTCTCT	270085	102281	AGAGGGTCCAGAGGGGACTG
180912	13108	AAGGAAATGTGTTTTTTATT	225499	57695	GAAGGGCAGGATGATTTCTC	270086	102282	AAGAGGGTCCAGAGGGGACT
180913	13109	AAAGGAAATGTGTTTTTTAT	225500	57696	AGAAGGGCAGGATGATTTCT	270087	102283	GAAGAGGGTCCAGAGGGGAC
180914	13110	CAAAGGAAATGTGTTTTTTA	225501	57697	CAGAAGGGCAGGATGATTTC	270088	102284	TGAAGAGGGTCCAGAGGGGA
180915	13111	TCAAAGGAAATGTGTTTTTT	225502	57698	CCAGAAGGGCAGGATGATTT	270089	102285	TTGAAGAGGGTCCAGAGGGG
180916	13112	TTCAAAGGAAATGTGTTTTT	225503	57699	TCCAGAAGGGCAGGATGATT	270090	102286	CTTGAAGAGGGTCCAGAGGG
180917	13113	TTTCAAAGGAAATGTGTTTT	225504	57700	CTCCAGAAGGGCAGGATGAT	270091	102287	CCTTGAAGAGGGTCCAGAGG
180918	13114	GTTTCAAAGGAAATGTGTTT	225505	57701	CCTCCAGAAGGGCAGGATGA	270092	102288	TCCTTGAAGAGGGTCCAGAG
180919	13115	TGTTTCAAAGGAAATGTGTT	225506	57702	TCCTCCAGAAGGGCAGGATG	270093	102289	TTCCTTGAAGAGGGTCCAGA
180920	13116	ATGTTTCAAAGGAAATGTGT	225507	57703	CTCCTCCAGAAGGGCAGGAT	270094	102290	CTTCCTTGAAGAGGGTCCAG
180921	13117	AATGTTTCAAAGGAAATGTG	225508	57704	CCTCCTCCAGAAGGGCAGGA	270095	102291	ACTTCCTTGAAGAGGGTCCA
180922	13118	GAATGTTTCAAAGGAAATGT	225509	57705	ACCTCCTCCAGAAGGGCAGG	270096	102292	AACTTCCTTGAAGAGGGTCC
180923	13119	AGAATGTTTCAAAGGAAATG	225510	57706	CACCTCCTCCAGAAGGGCAG	270097	102293	GAACTTCCTTGAAGAGGGTC
180924	13120	TAGAATGTTTCAAAGGAAAT	225511	57707	CCACCTCCTCCAGAAGGGCA	270098	102294	TGAACTTCCTTGAAGAGGGT
180925	13121	ATAGAATGTTTCAAAGGAAA	225512	57708	CCCACCTCCTCCAGAAGGGC	270099	102295	CTGAACTTCCTTGAAGAGGG
180926	13122	TATAGAATGTTTCAAAGGAA	225513	57709	GCCCACCTCCTCCAGAAGGG	270100	102296	ACTGAACTTCCTTGAAGAGG
180927	13123	TTATAGAATGTTTCAAAGGA	225514	57710	TGCCCACCTCCTCCAGAAGG	270101	102297	AACTGAACTTCCTTGAAGAG
180928	13124	ATTATAGAATGTTTCAAAGG	225515	57711	CTGCCCACCTCCTCCAGAAG	270102	102298	GAACTGAACTTCCTTGAAGA
180929	13125	GATTATAGAATGTTTCAAAG	225516	57712	GCTGCCCACCTCCTCCAGAA	270103	102299	AGAACTGAACTTCCTTGAAG
180930	13126	CGATTATAGAATGTTTCAAA	225517	57713	TGCTGCCCACCTCCTCCAGA	270104	102300	AAGAACTGAACTTCCTTGAA
180931	13127	ACGATTATAGAATGTTTCAA	225518	57714	CTGCTGCCCACCTCCTCCAG	270105	102301	AAAGAACTGAACTTCCTTGA
180932	13128	AACGATTATAGAATGTTTCA	225519	57715	CCTGCTGCCCACCTCCTCCA	270106	102302	TAAAGAACTGAACTTCCTTG
180933	13129	GAACGATTATAGAATGTTTC	225520	57716	CCCTGCTGCCCACCTCCTCC	270107	102303	ATAAAGAACTGAACTTCCTT
180934	13130	GGAACGATTATAGAATGTTT	225521	57717	CCCCTGCTGCCCACCTCCTC	270108	102304	AATAAAGAACTGAACTTCCT
180935	13131	AGGAACGATTATAGAATGTT	225522	57718	ACCCCTGCTGCCCACCTCCT	270109	102305	CAATAAAGAACTGAACTTCC
180936	13132	AAGGAACGATTATAGAATGT	225523	57719	GACCCCTGCTGCCCACCTCC	270110	102306	CCAATAAAGAACTGAACTTC
180937	13133	AAAGGAACGATTATAGAATG	225524	57720	TGACCCCTGCTGCCCACCTC	270111	102307	CCCAATAAAGAACTGAACTT
180938	13134	CAAAGGAACGATTATAGAAT	225525	57721	CTGACCCCTGCTGCCCACCT	270112	102308	GCCCAATAAAGAACTGAACT
180939	13135	GCAAAGGAACGATTATAGAA	225526	57722	TCTGACCCCTGCTGCCCACC	270113	102309	AGCCCAATAAAGAACTGAAC
180940	13136	GGCAAAGGAACGATTATAGA	225527	57723	CTCTGACCCCTGCTGCCCAC	270114	102310	GAGCCCAATAAAGAACTGAA
180941	13137	GGGCAAAGGAACGATTATAG	225528	57724	TCTCTGACCCCTGCTGCCCA	270115	102311	AGAGCCCAATAAAGAACTGA
180942	13138	AGGGCAAAGGAACGATTATA	225529	57725	ATCTCTGACCCCTGCTGCCC	270116	102312	GAGAGCCCAATAAAGAACTG
180943	13139	TAGGGCAAAGGAACGATTAT	225530	57726	CATCTCTGACCCCTGCTGCC	270117	102313	GGAGAGCCCAATAAAGAACT
180944	13140	GTAGGGCAAAGGAACGATTA	225531	57727	CCATCTCTGACCCCTGCTGC	270118	102314	TGGAGAGCCCAATAAAGAAC
180945	13141	AGTAGGGCAAAGGAACGATT	225532	57728	CCCATCTCTGACCCCTGCTG	270119	102315	GTGGAGAGCCCAATAAAGAA
180946	13142	AAGTAGGGCAAAGGAACGAT	225533	57729	TCCCATCTCTGACCCCTGCT	270120	102316	AGTGGAGAGCCCAATAAAGA
180947	13143	GAAGTAGGGCAAAGGAACGA	225534	57730	CTCCCATCTCTGACCCCTGC	270121	102317	TAGTGGAGAGCCCAATAAAG
180948	13144	TGAAGTAGGGCAAAGGAACG	225535	57731	CCTCCCATCTCTGACCCCTG	270122	102318	GTAGTGGAGAGCCCAATAAA
180949	13145	CTGAAGTAGGGCAAAGGAAC	225536	57732	CCCTCCCATCTCTGACCCCT	270123	102319	TGTAGTGGAGAGCCCAATAA
180950	13146	TCTGAAGTAGGGCAAAGGAA	225537	57733	TCCCTCCCATCTCTGACCCC	270124	102320	GTGTAGTGGAGAGCCCAATA
180951	13147	GTCTGAAGTAGGGCAAAGGA	225538	57734	TTCCCTCCCATCTCTGACCC	270125	102321	AGTGTAGTGGAGAGCCCAAT
180952	13148	GGTCTGAAGTAGGGCAAAGG	225539	57735	TTTCCCTCCCATCTCTGACC	270126	102322	CAGTGTAGTGGAGAGCCCAA
180953	13149	TGGTCTGAAGTAGGGCAAAG	225540	57736	CTTTCCCTCCCATCTCTGAC	270127	102323	ACAGTGTAGTGGAGAGCCCA
180954	13150	TTGGTCTGAAGTAGGGCAAA	225541	57737	CCTTTCCCTCCCATCTCTGA	270128	102324	CACAGTGTAGTGGAGAGCCC
180955	13151	GTTGGTCTGAAGTAGGGCAA	225542	57738	TCCTTTCCCTCCCATCTCTG	270129	102325	TCACAGTGTAGTGGAGAGCC
180956	13152	AGTTGGTCTGAAGTAGGGCA	225543	57739	TTCCTTTCCCTCCCATCTCT	270130	102326	CTCACAGTGTAGTGGAGAGC
180957	13153	AAGTTGGTCTGAAGTAGGGC	225544	57740	CTTCCTTTCCCTCCCATCTC	270131	102327	ACTCACAGTGTAGTGGAGAG
180958	13154	TAAGTTGGTCTGAAGTAGGG	225545	57741	CCTTCCTTTCCCTCCCATCT	270132	102328	CACTCACAGTGTAGTGGAGA
180959	13155	TTAAGTTGGTCTGAAGTAGG	225546	57742	TCCTTCCTTTCCCTCCCATC	270133	102329	GCACTCACAGTGTAGTGGAG
180960	13156	GTTAAGTTGGTCTGAAGTAG	225547	57743	CTCCTTCCTTTCCCTCCCAT	270134	102330	GGCACTCACAGTGTAGTGGA
180961	13157	CGTTAAGTTGGTCTGAAGTA	225548	57744	GCTCCTTCCTTTCCCTCCCA	270135	102331	GGGCACTCACAGTGTAGTGG
180962	13158	GCGTTAAGTTGGTCTGAAGT	225549	57745	GGCTCCTTCCTTTCCCTCCC	270136	102332	AGGGCACTCACAGTGTAGTG
180963	13159	TGCGTTAAGTTGGTCTGAAG	225550	57746	TGGCTCCTTCCTTTCCCTCC	270137	102333	GAGGGCACTCACAGTGTAGT
180964	13160	GTGCGTTAAGTTGGTCTGAA	225551	57747	CTGGCTCCTTCCTTTCCCTC	270138	102334	GGAGGGCACTCACAGTGTAG
180965	13161	AGTGCGTTAAGTTGGTCTGA	225552	57748	CCTGGCTCCTTCCTTTCCCT	270139	102335	AGGAGGGCACTCACAGTGTA
180966	13162	GAGTGCGTTAAGTTGGTCTG	225553	57749	ACCTGGCTCCTTCCTTTCCC	270140	102336	GAGGAGGGCACTCACAGTGT
180967	13163	GGAGTGCGTTAAGTTGGTCT	225554	57750	GACCTGGCTCCTTCCTTTCC	270141	102337	TGAGGAGGGCACTCACAGTG
180968	13164	GGGAGTGCGTTAAGTTGGTC	225555	57751	GGACCTGGCTCCTTCCTTTC	270142	102338	CTGAGGAGGGCACTCACAGT
180969	13165	GGGGAGTGCGTTAAGTTGGT	225556	57752	AGGACCTGGCTCCTTCCTTT	270143	102339	CCTGAGGAGGGCACTCACAG
180970	13166	TGGGGAGTGCGTTAAGTTGG	225557	57753	AAGGACCTGGCTCCTTCCTT	270144	102340	GCCTGAGGAGGGCACTCACA
180971	13167	ATGGGGAGTGCGTTAAGTTG	225558	57754	CAAGGACCTGGCTCCTTCCT	270145	102341	CGCCTGAGGAGGGCACTCAC
180972	13168	AATGGGGAGTGCGTTAAGTT	225559	57755	CCAAGGACCTGGCTCCTTCC	270146	102342	TCGCCTGAGGAGGGCACTCA
180973	13169	CAATGGGGAGTGCGTTAAGT	225560	57756	GCCAAGGACCTGGCTCCTTC	270147	102343	CTCGCCTGAGGAGGGCACTC
180974	13170	CCAATGGGGAGTGCGTTAAG	225561	57757	AGCCAAGGACCTGGCTCCTT	270148	102344	TCTCGCCTGAGGAGGGCACT
180975	13171	ACCAATGGGGAGTGCGTTAA	225562	57758	TAGCCAAGGACCTGGCTCCT	270149	102345	CTCTCGCCTGAGGAGGGCAC
180976	13172	GACCAATGGGGAGTGCGTTA	225563	57759	CTAGCCAAGGACCTGGCTCC	270150	102346	TCTCTCGCCTGAGGAGGGCA
180977	13173	GGACCAATGGGGAGTGCGTT	225564	57760	CCTAGCCAAGGACCTGGCTC	270151	102347	TTCTCTCGCCTGAGGAGGGC
180978	13174	TGGACCAATGGGGAGTGCGT	225565	57761	TCCTAGCCAAGGACCTGGCT	270152	102348	GTTCTCTCGCCTGAGGAGGG

180979	13175	TTGGACCAATGGGGAGTGCG	225566	57762	ATCCTAGCCAAGGACCTGGC	270153	102349	CGTTCTCTCGCCTGAGGAGG
180980	13176	TTTGGACCAATGGGGAGTGC	225567	57763	CATCCTAGCCAAGGACCTGG	270154	102350	ACGTTCTCTCGCCTGAGGAG
180981	13177	ATTTGGACCAATGGGGAGTG	225568	57764	GCATCCTAGCCAAGGACCTG	270155	102351	AACGTTCTCTCGCCTGAGGA
180982	13178	CATTTGGACCAATGGGGAGT	225569	57765	GGCATCCTAGCCAAGGACCT	270156	102352	GAACGTTCTCTCGCCTGAGG
180983	13179	TCATTTGGACCAATGGGGAG	225570	57766	TGGCATCCTAGCCAAGGACC	270157	102353	AGAACGTTCTCTCGCCTGAG
180984	13180	CTCATTTGGACCAATGGGGA	225571	57767	CTGGCATCCTAGCCAAGGAC	270158	102354	CAGAACGTTCTCTCGCCTGA
180985	13181	ACTCATTTGGACCAATGGGG	225572	57768	CCTGGCATCCTAGCCAAGGA	270159	102355	CCAGAACGTTCTCTCGCCTG
180986	13182	AACTCATTTGGACCAATGGG	225573	57769	CCCTGGCATCCTAGCCAAGG	270160	102356	GCCAGAACGTTCTCTCGCCT
180987	13183	AAACTCATTTGGACCAATGG	225574	57770	ACCCTGGCATCCTAGCCAAG	270161	102357	AGCCAGAACGTTCTCTCGCC
180988	13184	AAAACTCATTTGGACCAATG	225575	57771	GACCCTGGCATCCTAGCCAA	270162	102358	GAGCCAGAACGTTCTCTCGC
180989	13185	CAAAACTCATTTGGACCAAT	225576	57772	GGACCCTGGCATCCTAGCCA	270163	102359	AGAGCCAGAACGTTCTCTCG
180990	13186	GCAAAACTCATTTGGACCAA	225577	57773	GGGACCCTGGCATCCTAGCC	270164	102360	AAGAGCCAGAACGTTCTCTC
180991	13187	AGCAAAACTCATTTGGACCA	225578	57774	GGGGACCCTGGCATCCTAGC	270165	102361	GAAGAGCCAGAACGTTCTCT
180992	13188	TAGCAAAACTCATTTGGACC	225579	57775	AGGGGACCCTGGCATCCTAG	270166	102362	AGAAGAGCCAGAACGTTCTC
180993	13189	ATAGCAAAACTCATTTGGAC	225580	57776	CAGGGGACCCTGGCATCCTA	270167	102363	GAGAAGAGCCAGAACGTTCT
180994	13190	TATAGCAAAACTCATTTGGA	225581	57777	GCAGGGGACCCTGGCATCCT	270168	102364	AGAGAAGAGCCAGAACGTTC
180995	13191	GTATAGCAAAACTCATTTGG	225582	57778	GGCAGGGGACCCTGGCATCC	270169	102365	AAGAGAAGAGCCAGAACGTT
180996	13192	CGTATAGCAAAACTCATTTG	225583	57779	AGGCAGGGGACCCTGGCATC	270170	102366	CAAGAGAAGAGCCAGAACGT
180997	13193	TCGTATAGCAAAACTCATTT	225584	57780	GAGGCAGGGGACCCTGGCAT	270171	102367	GCAAGAGAAGAGCCAGAACG
180998	13194	TTCGTATAGCAAAACTCATT	225585	57781	AGAGGCAGGGGACCCTGGCA	270172	102368	GGCAAGAGAAGAGCCAGAAC
180999	13195	CTTCGTATAGCAAAACTCAT	225586	57782	GAGAGGCAGGGGACCCTGGC	270173	102369	GGGCAAGAGAAGAGCCAGAA
181000	13196	TCTTCGTATAGCAAAACTCA	225587	57783	TGAGAGGCAGGGGACCCTGG	270174	102370	GGGGCAAGAGAAGAGCCAGA
181001	13197	ATCTTCGTATAGCAAAACTC	225588	57784	GTGAGAGGCAGGGGACCCTG	270175	102371	AGGGGCAAGAGAAGAGCCAG
181002	13198	CATCTTCGTATAGCAAAACT	225589	57785	GGTGAGAGGCAGGGGACCCT	270176	102372	AAGGGGCAAGAGAAGAGCCA
181003	13199	GCATCTTCGTATAGCAAAAC	225590	57786	AGGTGAGAGGCAGGGGACCC	270177	102373	GAAGGGGCAAGAGAAGAGCC
181004	13200	AGCATCTTCGTATAGCAAAA	225591	57787	CAGGTGAGAGGCAGGGGACC	270178	102374	TGAAGGGGCAAGAGAAGAGC
181005	13201	CAGCATCTTCGTATAGCAAA	225592	57788	CCAGGTGAGAGGCAGGGGAC	270179	102375	CTGAAGGGGCAAGAGAAGAG
181006	13202	TCAGCATCTTCGTATAGCAA	225593	57789	GCCAGGTGAGAGGCAGGGGA	270180	102376	GCTGAAGGGGCAAGAGAAGA
181007	13203	ATCAGCATCTTCGTATAGCA	225594	57790	GGCCAGGTGAGAGGCAGGGG	270181	102377	GGCTGAAGGGGCAAGAGAAG
181008	13204	TATCAGCATCTTCGTATAGC	225595	57791	AGGCCAGGTGAGAGGCAGGG	270182	102378	GGGCTGAAGGGGCAAGAGAA
181009	13205	TTATCAGCATCTTCGTATAG	225596	57792	CAGGCCAGGTGAGAGGCAGG	270183	102379	GGGGCTGAAGGGGCAAGAGA
181010	13206	ATTATCAGCATCTTCGTATA	225597	57793	CCAGGCCAGGTGAGAGGCAG	270184	102380	AGGGGCTGAAGGGGCAAGAG
181011	13207	TATTATCAGCATCTTCGTAT	225598	57794	CCCAGGCCAGGTGAGAGGCA	270185	102381	CAGGGGCTGAAGGGGCAAGA
181012	13208	TTATTATCAGCATCTTCGTA	225599	57795	GCCCAGGCCAGGTGAGAGGC	270186	102382	ACAGGGGCTGAAGGGGCAAG
181013	13209	ATTATTATCAGCATCTTCGT	225600	57796	AGCCCAGGCCAGGTGAGAGG	270187	102383	AACAGGGGCTGAAGGGGCAA
181014	13210	TATTATTATCAGCATCTTCG	225601	57797	CAGCCCAGGCCAGGTGAGAG	270188	102384	TAACAGGGGCTGAAGGGGCA
181015	13211	CTATTATTATCAGCATCTTC	225602	57798	CCAGCCCAGGCCAGGTGAGA	270189	102385	TTAACAGGGGCTGAAGGGGC
181016	13212	GCTATTATTATCAGCATCTT	225603	57799	TCCAGCCCAGGCCAGGTGAG	270190	102386	ATTAACAGGGGCTGAAGGGG
181017	13213	TGCTATTATTATCAGCATCT	225604	57800	CTCCAGCCCAGGCCAGGTGA	270191	102387	GATTAACAGGGGCTGAAGGG
181018	13214	CTGCTATTATTATCAGCATC	225605	57801	CCTCCAGCCCAGGCCAGGTG	270192	102388	CGATTAACAGGGGCTGAAGG
181019	13215	GCTGCTATTATTATCAGCAT	225606	57802	GCCTCCAGCCCAGGCCAGGT	270193	102389	CCGATTAACAGGGGCTGAAG
181020	13216	TGCTGCTATTATTATCAGCA	225607	57803	GGCCTCCAGCCCAGGCCAGG	270194	102390	TCCGATTAACAGGGGCTGAA
181021	13217	CTGCTGCTATTATTATCAGC	225608	57804	AGGCCTCCAGCCCAGGCCAG	270195	102391	GTCCGATTAACAGGGGCTGA
181022	13218	ACTGCTGCTATTATTATCAG	225609	57805	GAGGCCTCCAGCCCAGGCCA	270196	102392	TGTCCGATTAACAGGGGCTG
181023	13219	CACTGCTGCTATTATTATCA	225610	57806	GGAGGCCTCCAGCCCAGGCC	270197	102393	CTGTCCGATTAACAGGGGCT
181024	13220	CCACTGCTGCTATTATTATC	225611	57807	AGGAGGCCTCCAGCCCAGGC	270198	102394	TCTGTCCGATTAACAGGGGC
181025	13221	TCCACTGCTGCTATTATTAT	225612	57808	CAGGAGGCCTCCAGCCCAGG	270199	102395	CTCTGTCCGATTAACAGGGG
181026	13222	ATCCACTGCTGCTATTATTA	225613	57809	GCAGGAGGCCTCCAGCCCAG	270200	102396	TCTCTGTCCGATTAACAGGG
181027	13223	AATCCACTGCTGCTATTATT	225614	57810	AGCAGGAGGCCTCCAGCCCA	270201	102397	ATCTCTGTCCGATTAACAGG
181028	13224	TAATCCACTGCTGCTATTAT	225615	57811	CAGCAGGAGGCCTCCAGCCC	270202	102398	CATCTCTGTCCGATTAACAG
181029	13225	ATAATCCACTGCTGCTATTA	225616	57812	ACAGCAGGAGGCCTCCAGCC	270203	102399	CCATCTCTGTCCGATTAACA
181030	13226	AATAATCCACTGCTGCTATT	225617	57813	GACAGCAGGAGGCCTCCAGC	270204	102400	GCCATCTCTGTCCGATTAAC
181031	13227	GAATAATCCACTGCTGCTAT	225618	57814	GGACAGCAGGAGGCCTCCAG	270205	102401	TGCCATCTCTGTCCGATTAA
181032	13228	AGAATAATCCACTGCTGCTA	225619	57815	AGGACAGCAGGAGGCCTCCA	270206	102402	CTGCCATCTCTGTCCGATTA
181033	13229	CAGAATAATCCACTGCTGCT	225620	57816	CAGGACAGCAGGAGGCCTCC	270207	102403	CCTGCCATCTCTGTCCGATT
181034	13230	GCAGAATAATCCACTGCTGC	225621	57817	ACAGGACAGCAGGAGGCCTC	270208	102404	CCCTGCCATCTCTGTCCGAT
181035	13231	AGCAGAATAATCCACTGCTG	225622	57818	GACAGGACAGCAGGAGGCCT	270209	102405	GCCCTGCCATCTCTGTCCGA
181036	13232	TAGCAGAATAATCCACTGCT	225623	57819	TGACAGGACAGCAGGAGGCC	270210	102406	AGCCCTGCCATCTCTGTCCG
181037	13233	TTAGCAGAATAATCCACTGC	225624	57820	GTGACAGGACAGCAGGAGGC	270211	102407	CAGCCCTGCCATCTCTGTCC
181038	13234	TTTAGCAGAATAATCCACTG	225625	57821	AGTGACAGGACAGCAGGAGG	270212	102408	ACAGCCCTGCCATCTCTGTC
181039	13235	TTTTAGCAGAATAATCCACT	225626	57822	CAGTGACAGGACAGCAGGAG	270213	102409	CACAGCCCTGCCATCTCTGT
181040	13236	GTTTTAGCAGAATAATCCAC	225627	57823	TCAGTGACAGGACAGCAGGA	270214	102410	ACACAGCCCTGCCATCTCTG
181041	13237	GGTTTTAGCAGAATAATCCA	225628	57824	ATCAGTGACAGGACAGCAGG	270215	102411	GACACAGCCCTGCCATCTCT
181042	13238	TGGTTTTAGCAGAATAATCC	225629	57825	GATCAGTGACAGGACAGCAG	270216	102412	AGACACAGCCCTGCCATCTC
181043	13239	ATGGTTTTAGCAGAATAATC	225630	57826	TGATCAGTGACAGGACAGCA	270217	102413	GAGACACAGCCCTGCCATCT
181044	13240	AATGGTTTTAGCAGAATAAT	225631	57827	GTGATCAGTGACAGGACAGC	270218	102414	GGAGACACAGCCCTGCCATC
181045	13241	CAATGGTTTTAGCAGAATAA	225632	57828	AGTGATCAGTGACAGGACAG	270219	102415	TGGAGACACAGCCCTGCCAT
181046	13242	GCAATGGTTTTAGCAGAATA	225633	57829	TAGTGATCAGTGACAGGACA	270220	102416	GTGGAGACACAGCCCTGCCA
181047	13243	GGCAATGGTTTTAGCAGAAT	225634	57830	GTAGTGATCAGTGACAGGAC	270221	102417	CGTGGAGACACAGCCCTGCC
181048	13244	AGGCAATGGTTTTAGCAGAA	225635	57831	GGTAGTGATCAGTGACAGGA	270222	102418	CCGTGGAGACACAGCCCTGC
181049	13245	GAGGCAATGGTTTTAGCAGA	225636	57832	GGGTAGTGATCAGTGACAGG	270223	102419	GCCGTGGAGACACAGCCCTG
181050	13246	CGAGGCAATGGTTTTAGCAG	225637	57833	GGGGTAGTGATCAGTGACAG	270224	102420	GGCCGTGGAGACACAGCCCT

181051	13247	ACGAGGCAATGGTTTTAGCA	225638	57834	CGGGGTAGTGATCAGTGACA	270225	102421	CGGCCGTGGAGACACAGCCC
181052	13248	AACGAGGCAATGGTTTTAGC	225639	57835	GCGGGGTAGTGATCAGTGAC	270226	102422	CCGGCCGTGGAGACACAGCC
181053	13249	TAACGAGGCAATGGTTTTAG	225640	57836	GGCGGGGTAGTGATCAGTGA	270227	102423	TCCGGCCGTGGAGACACAGC
181054	13250	TTAACGAGGCAATGGTTTTA	225641	57837	GGGCGGGGTAGTGATCAGTG	270228	102424	CTCCGGCCGTGGAGACACAG
181055	13251	ATTAACGAGGCAATGGTTTT	225642	57838	GGGGCGGGGTAGTGATCAGT	270229	102425	CCTCCGGCCGTGGAGACACA
181056	13252	GATTAACGAGGCAATGGTTT	225643	57839	TGGGGCGGGGTAGTGATCAG	270230	102426	GCCTCCGGCCGTGGAGACAC
181057	13253	GGATTAACGAGGCAATGGTT	225644	57840	CTGGGGCGGGGTAGTGATCA	270231	102427	AGCCTCCGGCCGTGGAGACA
181058	13254	AGGATTAACGAGGCAATGGT	225645	57841	GCTGGGGCGGGGTAGTGATC	270232	102428	GAGCCTCCGGCCGTGGAGAC
181059	13255	GAGGATTAACGAGGCAATGG	225646	57842	GGCTGGGGCGGGGTAGTGAT	270233	102429	AGAGCCTCCGGCCGTGGAGA
181060	13256	TGAGGATTAACGAGGCAATG	225647	57843	AGGCTGGGGCGGGGTAGTGA	270234	102430	GAGAGCCTCCGGCCGTGGAG
181061	13257	CTGAGGATTAACGAGGCAAT	225648	57844	GAGGCTGGGGCGGGGTAGTG	270235	102431	TGAGAGCCTCCGGCCGTGGA
181062	13258	ACTGAGGATTAACGAGGCAA	225649	57845	GGAGGCTGGGGCGGGGTAGT	270236	102432	ATGAGAGCCTCCGGCCGTGG
181063	13259	GACTGAGGATTAACGAGGCA	225650	57846	AGGAGGCTGGGGCGGGGTAG	270237	102433	TATGAGAGCCTCCGGCCGTG
181064	13260	GGACTGAGGATTAACGAGGC	225651	57847	CAGGAGGCTGGGGCGGGGTA	270238	102434	CTATGAGAGCCTCCGGCCGT
181065	13261	GGGACTGAGGATTAACGAGG	225652	57848	TCAGGAGGCTGGGGCGGGGT	270239	102435	ACTATGAGAGCCTCCGGCCG
181066	13262	CGGGACTGAGGATTAACGAG	225653	57849	CTCAGGAGGCTGGGGCGGGG	270240	102436	GACTATGAGAGCCTCCGGCC
181067	13263	TCGGGACTGAGGATTAACGA	225654	57850	ACTCAGGAGGCTGGGGCGGG	270241	102437	TGACTATGAGAGCCTCCGGC
181068	13264	CTCGGGACTGAGGATTAACG	225655	57851	AACTCAGGAGGCTGGGGCGG	270242	102438	CTGACTATGAGAGCCTCCGG
181069	13265	CCTCGGGACTGAGGATTAAC	225656	57852	TAACTCAGGAGGCTGGGGCG	270243	102439	CCTGACTATGAGAGCCTCCG
181070	13266	ACCTCGGGACTGAGGATTAA	225657	57853	CTAACTCAGGAGGCTGGGGC	270244	102440	CCCTGACTATGAGAGCCTCC
181071	13267	CACCTCGGGACTGAGGATTA	225658	57854	TCTAACTCAGGAGGCTGGGG	270245	102441	GCCCTGACTATGAGAGCCTC
181072	13268	CCACCTCGGGACTGAGGATT	225659	57855	TTCTAACTCAGGAGGCTGGG	270246	102442	TGCCCTGACTATGAGAGCCT
181073	13269	CCCACCTCGGGACTGAGGAT	225660	57856	CTTCTAACTCAGGAGGCTGG	270247	102443	GTGCCCTGACTATGAGAGCC
181074	13270	CCCCACCTCGGGACTGAGGA	225661	57857	TCTTCTAACTCAGGAGGCTG	270248	102444	GGTGCCCTGACTATGAGAGC
181075	13271	TCCCCACCTCGGGACTGAGG	225662	57858	GTCTTCTAACTCAGGAGGCT	270249	102445	GGGTGCCCTGACTATGAGAG
181076	13272	ATCCCCACCTCGGGACTGAG	225663	57859	TGTCTTCTAACTCAGGAGGC	270250	102446	TGGGTGCCCTGACTATGAGA
181077	13273	AATCCCCACCTCGGGACTGA	225664	57860	GTGTCTTCTAACTCAGGAGG	270251	102447	GTGGGTGCCCTGACTATGAG
181078	13274	TAATCCCCACCTCGGGACTG	225665	57861	TGTGTCTTCTAACTCAGGAG	270252	102448	TGTGGGTGCCCTGACTATGA
181079	13275	ATAATCCCCACCTCGGGACT	225666	57862	CTGTGTCTTCTAACTCAGGA	270253	102449	CTGTGGGTGCCCTGACTATG
181080	13276	AATAATCCCCACCTCGGGAC	225667	57863	CCTGTGTCTTCTAACTCAGG	270254	102450	GCTGTGGGTGCCCTGACTAT
181081	13277	TAATAATCCCCACCTCGGGA	225668	57864	GCCTGTGTCTTCTAACTCAG	270255	102451	CGCTGTGGGTGCCCTGACTA
181082	13278	ATAATAATCCCCACCTCGGG	225669	57865	AGCCTGTGTCTTCTAACTCA	270256	102452	CCGCTGTGGGTGCCCTGACT
181083	13279	GATAATAATCCCCACCTCGG	225670	57866	TAGCCTGTGTCTTCTAACTC	270257	102453	ACCGCTGTGGGTGCCCTGAC
181084	13280	GGATAATAATCCCCACCTCG	225671	57867	TTAGCCTGTGTCTTCTAACT	270258	102454	AACCGCTGTGGGTGCCCTGA
181085	13281	AGGATAATAATCCCCACCTC	225672	57868	TTTAGCCTGTGTCTTCTAAC	270259	102455	GAACCGCTGTGGGTGCCCTG
181086	13282	GAGGATAATAATCCCCACCT	225673	57869	CTTTAGCCTGTGTCTTCTAA	270260	102456	GGAACCGCTGTGGGTGCCCT
181087	13283	TGAGGATAATAATCCCCACC	225674	57870	ACTTTAGCCTGTGTCTTCTA	270261	102457	GGGAACCGCTGTGGGTGCCC
181088	13284	ATGAGGATAATAATCCCCAC	225675	57871	TACTTTAGCCTGTGTCTTCT	270262	102458	GGGGAACCGCTGTGGGTGCC
181089	13285	AATGAGGATAATAATCCCCA	225676	57872	CTACTTTAGCCTGTGTCTTC	270263	102459	TGGGGAACCGCTGTGGGTGC
181090	13286	AAATGAGGATAATAATCCCC	225677	57873	TCTACTTTAGCCTGTGTCTT	270264	102460	GTGGGGAACCGCTGTGGGTG
181091	13287	AAAATGAGGATAATAATCCC	225678	57874	CTCTACTTTAGCCTGTGTCT	270265	102461	GGTGGGGAACCGCTGTGGGT
181092	13288	CAAAATGAGGATAATAATCC	225679	57875	ACTCTACTTTAGCCTGTGTC	270266	102462	AGGTGGGGAACCGCTGTGGG
181093	13289	GCAAAATGAGGATAATAATC	225680	57876	TACTCTACTTTAGCCTGTGT	270267	102463	CAGGTGGGGAACCGCTGTGG
181094	13290	TGCAAAATGAGGATAATAAT	225681	57877	ATACTCTACTTTAGCCTGTG	270268	102464	GCAGGTGGGGAACCGCTGTG
181095	13291	CTGCAAAATGAGGATAATAA	225682	57878	AATACTCTACTTTAGCCTGT	270269	102465	GGCAGGTGGGGAACCGCTGT
181096	13292	TCTGCAAAATGAGGATAATA	225683	57879	AAATACTCTACTTTAGCCTG	270270	102466	AGGCAGGTGGGGAACCGCTG
181097	13293	CTCTGCAAAATGAGGATAAT	225684	57880	GAAATACTCTACTTTAGCCT	270271	102467	AAGGCAGGTGGGGAACCGCT
181098	13294	TCTCTGCAAAATGAGGATAA	225685	57881	AGAAATACTCTACTTTAGCC	270272	102468	GAAGGCAGGTGGGGAACCGC
181099	13295	TTCTCTGCAAAATGAGGATA	225686	57882	AAGAAATACTCTACTTTAGC	270273	102469	AGAAGGCAGGTGGGGAACCG
181100	13296	CTTCTCTGCAAAATGAGGAT	225687	57883	GAAGAAATACTCTACTTTAG	270274	102470	CAGAAGGCAGGTGGGGAACC
181101	13297	GCTTCTCTGCAAAATGAGGA	225688	57884	TGAAGAAATACTCTACTTTA	270275	102471	CCAGAAGGCAGGTGGGGAAC
181102	13298	TGCTTCTCTGCAAAATGAGG	225689	57885	ATGAAGAAATACTCTACTTT	270276	102472	CCCAGAAGGCAGGTGGGGAA
181103	13299	TTGCTTCTCTGCAAAATGAG	225690	57886	AATGAAGAAATACTCTACTT	270277	102473	GCCCAGAAGGCAGGTGGGGA
181104	13300	TTTGCTTCTCTGCAAAATGA	225691	57887	CAATGAAGAAATACTCTACT	270278	102474	TGCCCAGAAGGCAGGTGGGG
181105	13301	GTTTGCTTCTCTGCAAAATG	225692	57888	TCAATGAAGAAATACTCTAC	270279	102475	CTGCCCAGAAGGCAGGTGGG
181106	13302	AGTTTGCTTCTCTGCAAAAT	225693	57889	TTCAATGAAGAAATACTCTA	270280	102476	TCTGCCCAGAAGGCAGGTGG
181107	13303	CAGTTTGCTTCTCTGCAAAA	225694	57890	TTTCAATGAAGAAATACTCT	270281	102477	TTCTGCCCAGAAGGCAGGTG
181108	13304	TCAGTTTGCTTCTCTGCAAA	225695	57891	TTTTCAATGAAGAAATACTC	270282	102478	ATTCTGCCCAGAAGGCAGGT
181109	13305	CTCAGTTTGCTTCTCTGCAA	225696	57892	TTTTTCAATGAAGAAATACT	270283	102479	TATTCTGCCCAGAAGGCAGG
181110	13306	TCTCAGTTTGCTTCTCTGCA	225697	57893	GTTTTTCAATGAAGAAATAC	270284	102480	GTATTCTGCCCAGAAGGCAG
181111	13307	GTCTCAGTTTGCTTCTCTGC	225698	57894	GGTTTTTCAATGAAGAAATA	270285	102481	TGTATTCTGCCCAGAAGGCA
181112	13308	AGTCTCAGTTTGCTTCTCTG	225699	57895	GGGTTTTTCAATGAAGAAAT	270286	102482	GTGTATTCTGCCCAGAAGGC
181113	13309	GAGTCTCAGTTTGCTTCTCT	225700	57896	TGGGTTTTTCAATGAAGAAA	270287	102483	AGTGTATTCTGCCCAGAAGG
181114	13310	TGAGTCTCAGTTTGCTTCTC	225701	57897	ATGGGTTTTTCAATGAAGAA	270288	102484	CAGTGTATTCTGCCCAGAAG
181115	13311	CTGAGTCTCAGTTTGCTTCT	225702	57898	TATGGGTTTTTCAATGAAGA	270289	102485	GCAGTGTATTCTGCCCAGAA
181116	13312	TCTGAGTCTCAGTTTGCTTC	225703	57899	GTATGGGTTTTTCAATGAAG	270290	102486	GGCAGTGTATTCTGCCCAGA
181117	13313	CTCTGAGTCTCAGTTTGCTT	225704	57900	TGTATGGGTTTTTCAATGAA	270291	102487	TGGCAGTGTATTCTGCCCAG
181118	13314	TCTCTGAGTCTCAGTTTGCT	225705	57901	TTGTATGGGTTTTTCAATGA	270292	102488	GTGGCAGTGTATTCTGCCCA
181119	13315	ATCTCTGAGTCTCAGTTTGC	225706	57902	TTTGTATGGGTTTTTCAATG	270293	102489	GGTGGCAGTGTATTCTGCCC
181120	13316	AATCTCTGAGTCTCAGTTTG	225707	57903	TTTTGTATGGGTTTTTCAAT	270294	102490	GGGTGGCAGTGTATTCTGCC
181121	13317	AAATCTCTGAGTCTCAGTTT	225708	57904	ATTTTGTATGGGTTTTTCAA	270295	102491	TGGGTGGCAGTGTATTCTGC
181122	13318	GAAATCTCTGAGTCTCAGTT	225709	57905	TATTTTGTATGGGTTTTTCA	270296	102492	ATGGGTGGCAGTGTATTCTG

181123	13319	TGAAATCTCTGAGTCTCAGT	225710	57906	TTATTTTGTATGGGTTTTTC	270297	102493	TATGGGTGGCAGTGTATTCT
181124	13320	GTGAAATCTCTGAGTCTCAG	225711	57907	TTTATTTTGTATGGGTTTTT	270298	102494	CTATGGGTGGCAGTGTATTC
181125	13321	TGTGAAATCTCTGAGTCTCA	225712	57908	CTTTATTTTGTATGGGTTTT	270299	102495	CCTATGGGTGGCAGTGTATT
181126	13322	CTGTGAAATCTCTGAGTCTC	225713	57909	CCTTTATTTTGTATGGGTTT	270300	102496	ACCTATGGGTGGCAGTGTAT
181127	13323	GCTGTGAAATCTCTGAGTCT	225714	57910	ACCTTTATTTTGTATGGGTT	270301	102497	GACCTATGGGTGGCAGTGTA
181128	13324	AGCTGTGAAATCTCTGAGTC	225715	57911	AACCTTTATTTTGTATGGGT	270302	102498	TGACCTATGGGTGGCAGTGT
181129	13325	CAGCTGTGAAATCTCTGAGT	225716	57912	GAACCTTTATTTTGTATGGG	270303	102499	CTGACCTATGGGTGGCAGTG
181130	13326	CCAGCTGTGAAATCTCTGAG	225717	57913	TGAACCTTTATTTTGTATGG	270304	102500	GCTGACCTATGGGTGGCAGT
181131	13327	CCCAGCTGTGAAATCTCTGA	225718	57914	ATGAACCTTTATTTTGTATG	270305	102501	TGCTGACCTATGGGTGGCAG
181132	13328	CCCCAGCTGTGAAATCTCTG	225719	57915	TATGAACCTTTATTTTGTAT	270306	102502	ATGCTGACCTATGGGTGGCA
181133	13329	TCCCCAGCTGTGAAATCTCT	225720	57916	TTATGAACCTTTATTTTGTA	270307	102503	GATGCTGACCTATGGGTGGC
181134	13330	CTCCCCAGCTGTGAAATCTC	225721	57917	TTTATGAACCTTTATTTTGT	270308	102504	AGATGCTGACCTATGGGTGG
181135	13331	CCTCCCCAGCTGTGAAATCT	225722	57918	TTTTATGAACCTTTATTTTG	270309	102505	GAGATGCTGACCTATGGGTG
181136	13332	CCCTCCCCAGCTGTGAAATC	225723	57919	TTTTTATGAACCTTTATTTT	270310	102506	GGAGATGCTGACCTATGGGT
181137	13333	TCCCTCCCCAGCTGTGAAAT	225724	57920	TTTTTTATGAACCTTTATTT	270311	102507	TGGAGATGCTGACCTATGGG
181138	13334	CTCCCTCCCCAGCTGTGAAA	225725	57921	ATTTTTTATGAACCTTTATT	270312	102508	GTGGAGATGCTGACCTATGG
181139	13335	GCTCCCTCCCCAGCTGTGAA	225726	57922	TATTTTTTATGAACCTTTAT	270313	102509	AGTGGAGATGCTGACCTATG
181140	13336	GGCTCCCTCCCCAGCTGTGA	225727	57923	TTATTTTTTATGAACCTTTA	270314	102510	GAGTGGAGATGCTGACCTAT
181141	13337	TGGCTCCCTCCCCAGCTGTG	225728	57924	TTTATTTTTTATGAACCTTT	270315	102511	CGAGTGGAGATGCTGACCTA
181142	13338	CTGGCTCCCTCCCCAGCTGT	225729	57925	TTTTATTTTTTATGAACCTT	270316	102512	ACGAGTGGAGATGCTGACCT
181143	13339	GCTGGCTCCCTCCCCAGCTG	225730	57926	TTTTTATTTTTTATGAACCT	270317	102513	CACGAGTGGAGATGCTGACC
181144	13340	AGCTGGCTCCCTCCCCAGCT	225731	57927	ATTTTTATTTTTTATGAACC	270318	102514	CCACGAGTGGAGATGCTGAC
181145	13341	GAGCTGGCTCCCTCCCCAGC	225732	57928	AATTTTTATTTTTTATGAAC	270319	102515	CCCACGAGTGGAGATGCTGA
181146	13342	TGAGCTGGCTCCCTCCCCAG	225733	57929	AAATTTTTATTTTTTATGAA	270320	102516	GCCCACGAGTGGAGATGCTG
181147	13343	ATGAGCTGGCTCCCTCCCCA	225734	57930	TAAATTTTTATTTTTTATGA	270321	102517	GGCCCACGAGTGGAGATGCT
181148	13344	GATGAGCTGGCTCCCTCCCC	225735	57931	CTAAATTTTTATTTTTTATG	270322	102518	TGGCCCACGAGTGGAGATGC
181149	13345	GGATGAGCTGGCTCCCTCCC	225736	57932	TCTAAATTTTTATTTTTTAT	270323	102519	ATGGCCCACGAGTGGAGATG
181150	13346	GGGATGAGCTGGCTCCCTCC	225737	57933	GTCTAAATTTTTATTTTTTA	270324	102520	GATGGCCCACGAGTGGAGAT
181151	13347	AGGGATGAGCTGGCTCCCTC	225738	57934	AGTCTAAATTTTTATTTTTT	270325	102521	AGATGGCCCACGAGTGGAGA
181152	13348	GAGGGATGAGCTGGCTCCCT	225739	57935	CAGTCTAAATTTTTATTTTT	270326	102522	CAGATGGCCCACGAGTGGAG
181153	13349	AGAGGGATGAGCTGGCTCCC	225740	57936	CCAGTCTAAATTTTTATTTT	270327	102523	GCAGATGGCCCACGAGTGGA
181154	13350	CAGAGGGATGAGCTGGCTCC	225741	57937	CCCAGTCTAAATTTTTATTT	270328	102524	AGCAGATGGCCCACGAGTGG
181155	13351	ACAGAGGGATGAGCTGGCTC	225742	57938	ACCCAGTCTAAATTTTTATT	270329	102525	AAGCAGATGGCCCACGAGTG
181156	13352	GACAGAGGGATGAGCTGGCT	225743	57939	CACCCAGTCTAAATTTTTAT	270330	102526	TAAGCAGATGGCCCACGAGT
181157	13353	GGACAGAGGGATGAGCTGGC	225744	57940	GCACCCAGTCTAAATTTTTA	270331	102527	CTAAGCAGATGGCCCACGAG
181158	13354	TGGACAGAGGGATGAGCTGG	225745	57941	AGCACCCAGTCTAAATTTTT	270332	102528	CCTAAGCAGATGGCCCACGA
181159	13355	CTGGACAGAGGGATGAGCTG	225746	57942	CAGCACCCAGTCTAAATTTT	270333	102529	ACCTAAGCAGATGGCCCACG
181160	13356	CCTGGACAGAGGGATGAGCT	225747	57943	ACAGCACCCAGTCTAAATTT	270334	102530	AACCTAAGCAGATGGCCCAC
181161	13357	GCCTGGACAGAGGGATGAGC	225748	57944	CACAGCACCCAGTCTAAATT	270335	102531	CAACCTAAGCAGATGGCCCA
181162	13358	GGCCTGGACAGAGGGATGAG	225749	57945	CCACAGCACCCAGTCTAAAT	270336	102532	CCAACCTAAGCAGATGGCCC
181163	13359	GGGCCTGGACAGAGGGATGA	225750	57946	GCCACAGCACCCAGTCTAAA	270337	102533	CCCAACCTAAGCAGATGGCC
181164	13360	TGGGCCTGGACAGAGGGATG	225751	57947	AGCCACAGCACCCAGTCTAA	270338	102534	ACCCAACCTAAGCAGATGGC
181165	13361	TTGGGCCTGGACAGAGGGAT	225752	57948	GAGCCACAGCACCCAGTCTA	270339	102535	AACCCAACCTAAGCAGATGG
181166	13362	CTTGGGCCTGGACAGAGGGA	225753	57949	TGAGCCACAGCACCCAGTCT	270340	102536	GAACCCAACCTAAGCAGATG
181167	13363	GCTTGGGCCTGGACAGAGGG	225754	57950	GTGAGCCACAGCACCCAGTC	270341	102537	GGAACCCAACCTAAGCAGAT
181168	13364	AGCTTGGGCCTGGACAGAGG	225755	57951	TGTGAGCCACAGCACCCAGT	270342	102538	AGGAACCCAACCTAAGCAGA
181169	13365	GAGCTTGGGCCTGGACAGAG	225756	57952	GTGTGAGCCACAGCACCCAG	270343	102539	GAGGAACCCAACCTAAGCAG
181170	13366	AGAGCTTGGGCCTGGACAGA	225757	57953	GGTGTGAGCCACAGCACCCA	270344	102540	AGAGGAACCCAACCTAAGCA
181171	13367	GAGAGCTTGGGCCTGGACAG	225758	57954	AGGTGTGAGCCACAGCACCC	270345	102541	CAGAGGAACCCAACCTAAGC
181172	13368	AGAGAGCTTGGGCCTGGACA	225759	57955	CAGGTGTGAGCCACAGCACC	270346	102542	CCAGAGGAACCCAACCTAAG
181173	13369	GAGAGAGCTTGGGCCTGGAC	225760	57956	ACAGGTGTGAGCCACAGCAC	270347	102543	TCCAGAGGAACCCAACCTAA
181174	13370	GGAGAGAGCTTGGGCCTGGA	225761	57957	CACAGGTGTGAGCCACAGCA	270348	102544	ATCCAGAGGAACCCAACCTA
181175	13371	GGGAGAGAGCTTGGGCCTGG	225762	57958	TCACAGGTGTGAGCCACAGC	270349	102545	AATCCAGAGGAACCCAACCT
181176	13372	CGGGAGAGAGCTTGGGCCTG	225763	57959	ATCACAGGTGTGAGCCACAG	270350	102546	GAATCCAGAGGAACCCAACC
181177	13373	GCGGGAGAGAGCTTGGGCCT	225764	57960	GATCACAGGTGTGAGCCACA	270351	102547	AGAATCCAGAGGAACCCAAC
181178	13374	AGCGGGAGAGAGCTTGGGCC	225765	57961	GGATCACAGGTGTGAGCCAC	270352	102548	CAGAATCCAGAGGAACCCAA
181179	13375	AAGCGGGAGAGAGCTTGGGC	225766	57962	GGGATCACAGGTGTGAGCCA	270353	102549	CCAGAATCCAGAGGAACCCA
181180	13376	CAAGCGGGAGAGAGCTTGGG	225767	57963	TGGGATCACAGGTGTGAGCC	270354	102550	CCCAGAATCCAGAGGAACCC
181181	13377	GCAAGCGGGAGAGAGCTTGG	225768	57964	CTGGGATCACAGGTGTGAGC	270355	102551	CCCCAGAATCCAGAGGAACC
181182	13378	GGCAAGCGGGAGAGAGCTTG	225769	57965	GCTGGGATCACAGGTGTGAG	270356	102552	TCCCCAGAATCCAGAGGAAC
181183	13379	AGGCAAGCGGGAGAGAGCTT	225770	57966	TGCTGGGATCACAGGTGTGA	270357	102553	CTCCCCAGAATCCAGAGGAA
181184	13380	AAGGCAAGCGGGAGAGAGCT	225771	57967	GTGCTGGGATCACAGGTGTG	270358	102554	TCTCCCCAGAATCCAGAGGA
181185	13381	GAAGGCAAGCGGGAGAGAGC	225772	57968	AGTGCTGGGATCACAGGTGT	270359	102555	ATCTCCCCAGAATCCAGAGG
181186	13382	GGAAGGCAAGCGGGAGAGAG	225773	57969	AAGTGCTGGGATCACAGGTG	270360	102556	AATCTCCCCAGAATCCAGAG
181187	13383	AGGAAGGCAAGCGGGAGAGA	225774	57970	AAAGTGCTGGGATCACAGGT	270361	102557	CAATCTCCCCAGAATCCAGA
181188	13384	CAGGAAGGCAAGCGGGAGAG	225775	57971	CAAAGTGCTGGGATCACAGG	270362	102558	CCAATCTCCCCAGAATCCAG
181189	13385	GCAGGAAGGCAAGCGGGAGA	225776	57972	CCAAAGTGCTGGGATCACAG	270363	102559	CCCAATCTCCCCAGAATCCA
181190	13386	GGCAGGAAGGCAAGCGGGAG	225777	57973	CCCAAAGTGCTGGGATCACA	270364	102560	CCCCAATCTCCCCAGAATCC
181191	13387	AGGCAGGAAGGCAAGCGGGA	225778	57974	TCCCAAAGTGCTGGGATCAC	270365	102561	CCCCCAATCTCCCCAGAATC
181192	13388	GAGGCAGGAAGGCAAGCGGG	225779	57975	CTCCCAAAGTGCTGGGATCA	270366	102562	ACCCCCAATCTCCCCAGAAT
181193	13389	AGAGGCAGGAAGGCAAGCGG	225780	57976	CCTCCCAAAGTGCTGGGATC	270367	102563	AACCCCCAATCTCCCCAGAA
181194	13390	CAGAGGCAGGAAGGCAAGCG	225781	57977	GCCTCCCAAAGTGCTGGGAT	270368	102564	GAACCCCCAATCTCCCCAGA

181195	13391	GCAGAGGCAGGAAGGCAAGC	225782	57978	GGCCTCCCAAAGTGCTGGGA	270369	102565	AGAACCCCCAATCTCCCCAG
181196	13392	TGCAGAGGCAGGAAGGCAAG	225783	57979	TGGCCTCCCAAAGTGCTGGG	270370	102566	CAGAACCCCCAATCTCCCCA
181197	13393	TTGCAGAGGCAGGAAGGCAA	225784	57980	TTGGCCTCCCAAAGTGCTGG	270371	102567	ACAGAACCCCCAATCTCCCC
181198	13394	GTTGCAGAGGCAGGAAGGCA	225785	57981	CTTGGCCTCCCAAAGTGCTG	270372	102568	AACAGAACCCCCAATCTCCC
181199	13395	GGTTGCAGAGGCAGGAAGGC	225786	57982	CCTTGGCCTCCCAAAGTGCT	270373	102569	AAACAGAACCCCCAATCTCC
181200	13396	AGGTTGCAGAGGCAGGAAGG	225787	57983	GCCTTGGCCTCCCAAAGTGC	270374	102570	AAAACAGAACCCCCAATCTC
181201	13397	GAGGTTGCAGAGGCAGGAAG	225788	57984	TGCCTTGGCCTCCCAAAGTG	270375	102571	CAAAACAGAACCCCCAATCT
181202	13398	TGAGGTTGCAGAGGCAGGAA	225789	57985	CTGCCTTGGCCTCCCAAAGT	270376	102572	TCAAAACAGAACCCCCAATC
181203	13399	CTGAGGTTGCAGAGGCAGGA	225790	57986	CCTGCCTTGGCCTCCCAAAG	270377	102573	ATCAAAACAGAACCCCCAAT
181204	13400	TCTGAGGTTGCAGAGGCAGG	225791	57987	ACCTGCCTTGGCCTCCCAAA	270378	102574	GATCAAAACAGAACCCCCAA
181205	13401	CTCTGAGGTTGCAGAGGCAG	225792	57988	CACCTGCCTTGGCCTCCCAA	270379	102575	TGATCAAAACAGAACCCCCA
181206	13402	GCTCTGAGGTTGCAGAGGCA	225793	57989	CCACCTGCCTTGGCCTCCCA	270380	102576	CTGATCAAAACAGAACCCCC
181207	13403	TGCTCTGAGGTTGCAGAGGC	225794	57990	TCCACCTGCCTTGGCCTCCC	270381	102577	GCTGATCAAAACAGAACCCC
181208	13404	ATGCTCTGAGGTTGCAGAGG	225795	57991	ATCCACCTGCCTTGGCCTCC	270382	102578	AGCTGATCAAAACAGAACCC
181209	13405	GATGCTCTGAGGTTGCAGAG	225796	57992	GATCCACCTGCCTTGGCCTC	270383	102579	CAGCTGATCAAAACAGAACC
181210	13406	GGATGCTCTGAGGTTGCAGA	225797	57993	CGATCCACCTGCCTTGGCCT	270384	102580	TCAGCTGATCAAAACAGAAC
181211	13407	GGGATGCTCTGAGGTTGCAG	225798	57994	GCGATCCACCTGCCTTGGCC	270385	102581	ATCAGCTGATCAAAACAGAA
181212	13408	GGGGATGCTCTGAGGTTGCA	225799	57995	AGCGATCCACCTGCCTTGGC	270386	102582	AATCAGCTGATCAAAACAGA
181213	13409	GGGGGATGCTCTGAGGTTGC	225800	57996	AAGCGATCCACCTGCCTTGG	270387	102583	GAATCAGCTGATCAAAACAG
181214	13410	TGGGGGATGCTCTGAGGTTG	225801	57997	CAAGCGATCCACCTGCCTTG	270388	102584	AGAATCAGCTGATCAAAACA
181215	13411	ATGGGGGATGCTCTGAGGTT	225802	57998	TCAAGCGATCCACCTGCCTT	270389	102585	AAGAATCAGCTGATCAAAAC
181216	13412	GATGGGGGATGCTCTGAGGT	225803	57999	CTCAAGCGATCCACCTGCCT	270390	102586	GAAGAATCAGCTGATCAAAA
181217	13413	AGATGGGGGATGCTCTGAGG	225804	58000	GCTCAAGCGATCCACCTGCC	270391	102587	AGAAGAATCAGCTGATCAAA
181218	13414	CAGATGGGGGATGCTCTGAG	225805	58001	GGCTCAAGCGATCCACCTGC	270392	102588	CAGAAGAATCAGCTGATCAA
181219	13415	CCAGATGGGGGATGCTCTGA	225806	58002	GGGCTCAAGCGATCCACCTG	270393	102589	CCAGAAGAATCAGCTGATCA
181220	13416	ACCAGATGGGGGATGCTCTG	225807	58003	AGGGCTCAAGCGATCCACCT	270394	102590	CCCAGAAGAATCAGCTGATC
181221	13417	AACCAGATGGGGGATGCTCT	225808	58004	CAGGGCTCAAGCGATCCACC	270395	102591	TCCCAGAAGAATCAGCTGAT
181222	13418	GAACCAGATGGGGGATGCTC	225809	58005	CCAGGGCTCAAGCGATCCAC	270396	102592	CTCCCAGAAGAATCAGCTGA
181223	13419	AGAACCAGATGGGGGATGCT	225810	58006	CCCAGGGCTCAAGCGATCCA	270397	102593	GCTCCCAGAAGAATCAGCTG
181224	13420	TAGAACCAGATGGGGGATGC	225811	58007	CCCCAGGGCTCAAGCGATCC	270398	102594	TGCTCCCAGAAGAATCAGCT
181225	13421	GTAGAACCAGATGGGGGATG	225812	58008	ACCCCAGGGCTCAAGCGATC	270399	102595	TTGCTCCCAGAAGAATCAGC
181226	13422	AGTAGAACCAGATGGGGGAT	225813	58009	AACCCCAGGGCTCAAGCGAT	270400	102596	CTTGCTCCCAGAAGAATCAG
181227	13423	CAGTAGAACCAGATGGGGGA	225814	58010	GAACCCCAGGGCTCAAGCGA	270401	102597	ACTTGCTCCCAGAAGAATCA
181228	13424	GCAGTAGAACCAGATGGGGG	225815	58011	TGAACCCCAGGGCTCAAGCG	270402	102598	CACTTGCTCCCAGAAGAATC
181229	13425	GGCAGTAGAACCAGATGGGG	225816	58012	ATGAACCCCAGGGCTCAAGC	270403	102599	CCACTTGCTCCCAGAAGAAT
181230	13426	AGGCAGTAGAACCAGATGGG	225817	58013	CATGAACCCCAGGGCTCAAG	270404	102600	CCCACTTGCTCCCAGAAGAA
181231	13427	CAGGCAGTAGAACCAGATGG	225818	58014	TCATGAACCCCAGGGCTCAA	270405	102601	ACCCACTTGCTCCCAGAAGA
181232	13428	ACAGGCAGTAGAACCAGATG	225819	58015	GTCATGAACCCCAGGGCTCA	270406	102602	CACCCACTTGCTCCCAGAAG
181233	13429	CACAGGCAGTAGAACCAGAT	225820	58016	GGTCATGAACCCCAGGGCTC	270407	102603	GCACCCACTTGCTCCCAGAA
181234	13430	GCACAGGCAGTAGAACCAGA	225821	58017	TGGTCATGAACCCCAGGGCT	270408	102604	AGCACCCACTTGCTCCCAGA
181235	13431	AGCACAGGCAGTAGAACCAG	225822	58018	CTGGTCATGAACCCCAGGGC	270409	102605	GAGCACCCACTTGCTCCCAG
181236	13432	TAGCACAGGCAGTAGAACCA	225823	58019	GCTGGTCATGAACCCCAGGG	270410	102606	CGAGCACCCACTTGCTCCCA
181237	13433	CTAGCACAGGCAGTAGAACC	225824	58020	GGCTGGTCATGAACCCCAGG	270411	102607	GCGAGCACCCACTTGCTCCC
181238	13434	ACTAGCACAGGCAGTAGAAC	225825	58021	AGGCTGGTCATGAACCCCAG	270412	102608	CGCGAGCACCCACTTGCTCC
181239	13435	GACTAGCACAGGCAGTAGAA	225826	58022	CAGGCTGGTCATGAACCCCA	270413	102609	TCGCGAGCACCCACTTGCTC
181240	13436	CGACTAGCACAGGCAGTAGA	225827	58023	CCAGGCTGGTCATGAACCCC	270414	102610	CTCGCGAGCACCCACTTGCT
181241	13437	ACGACTAGCACAGGCAGTAG	225828	58024	CCCAGGCTGGTCATGAACCC	270415	102611	GCTCGCGAGCACCCACTTGC
181242	13438	CACGACTAGCACAGGCAGTA	225829	58025	GCCCAGGCTGGTCATGAACC	270416	102612	AGCTCGCGAGCACCCACTTG
181243	13439	GCACGACTAGCACAGGCAGT	225830	58026	TGCCCAGGCTGGTCATGAAC	270417	102613	GAGCTCGCGAGCACCCACTT
181244	13440	TGCACGACTAGCACAGGCAG	225831	58027	TTGCCCAGGCTGGTCATGAA	270418	102614	AGAGCTCGCGAGCACCCACT
181245	13441	CTGCACGACTAGCACAGGCA	225832	58028	GTTGCCCAGGCTGGTCATGA	270419	102615	GAGAGCTCGCGAGCACCCAC
181246	13442	CCTGCACGACTAGCACAGGC	225833	58029	TGTTGCCCAGGCTGGTCATG	270420	102616	GGAGAGCTCGCGAGCACCCA
181247	13443	TCCTGCACGACTAGCACAGG	225834	58030	ATGTTGCCCAGGCTGGTCAT	270421	102617	TGGAGAGCTCGCGAGCACCC
181248	13444	CTCCTGCACGACTAGCACAG	225835	58031	TATGTTGCCCAGGCTGGTCA	270422	102618	CTGGAGAGCTCGCGAGCACC
181249	13445	GCTCCTGCACGACTAGCACA	225836	58032	CTATGTTGCCCAGGCTGGTC	270423	102619	GCTGGAGAGCTCGCGAGCAC
181250	13446	GGCTCCTGCACGACTAGCAC	225837	58033	ACTATGTTGCCCAGGCTGGT	270424	102620	AGCTGGAGAGCTCGCGAGCA
181251	13447	TGGCTCCTGCACGACTAGCA	225838	58034	CACTATGTTGCCCAGGCTGG	270425	102621	AAGCTGGAGAGCTCGCGAGC
181252	13448	TTGGCTCCTGCACGACTAGC	225839	58035	TCACTATGTTGCCCAGGCTG	270426	102622	GAAGCTGGAGAGCTCGCGAG
181253	13449	TTTGGCTCCTGCACGACTAG	225840	58036	TTCACTATGTTGCCCAGGCT	270427	102623	GGAAGCTGGAGAGCTCGCGA
181254	13450	TTTTGGCTCCTGCACGACTA	225841	58037	TTTCACTATGTTGCCCAGGC	270428	102624	AGGAAGCTGGAGAGCTCGCG
181255	13451	CTTTTGGCTCCTGCACGACT	225842	58038	GTTTCACTATGTTGCCCAGG	270429	102625	TAGGAAGCTGGAGAGCTCGC
181256	13452	TCTTTTGGCTCCTGCACGAC	225843	58039	GGTTTCACTATGTTGCCCAG	270430	102626	TTAGGAAGCTGGAGAGCTCG
181257	13453	GTCTTTTGGCTCCTGCACGA	225844	58040	GGGTTTCACTATGTTGCCCA	270431	102627	TTTAGGAAGCTGGAGAGCTC
181258	13454	TGTCTTTTGGCTCCTGCACG	225845	58041	GGGGTTTCACTATGTTGCCC	270432	102628	CTTTAGGAAGCTGGAGAGCT
181259	13455	GTGTCTTTTGGCTCCTGCAC	225846	58042	TGGGGTTTCACTATGTTGCC	270433	102629	CCTTTAGGAAGCTGGAGAGC
181260	13456	CGTGTCTTTTGGCTCCTGCA	225847	58043	ATGGGGTTTCACTATGTTGC	270434	102630	ACCTTTAGGAAGCTGGAGAG
181261	13457	ACGTGTCTTTTGGCTCCTGC	225848	58044	GATGGGGTTTCACTATGTTG	270435	102631	CACCTTTAGGAAGCTGGAGA
181262	13458	GACGTGTCTTTTGGCTCCTG	225849	58045	AGATGGGGTTTCACTATGTT	270436	102632	CCACCTTTAGGAAGCTGGAG
181263	13459	AGACGTGTCTTTTGGCTCCT	225850	58046	GAGATGGGGTTTCACTATGT	270437	102633	TCCACCTTTAGGAAGCTGGA
181264	13460	AAGACGTGTCTTTTGGCTCC	225851	58047	AGAGATGGGGTTTCACTATG	270438	102634	CTCCACCTTTAGGAAGCTGG
181265	13461	AAAGACGTGTCTTTTGGCTC	225852	58048	TAGAGATGGGGTTTCACTAT	270439	102635	TCTCCACCTTTAGGAAGCTG
181266	13462	TAAAGACGTGTCTTTTGGCT	225853	58049	GTAGAGATGGGGTTTCACTA	270440	102636	TTCTCCACCTTTAGGAAGCT

181267	13463	CTAAAGACGTGTCTTTTGGC	225854	58050	TGTAGAGATGGGGTTTCACT	270441	102637	CTTCTCCACCTTTAGGAAGC
181268	13464	ACTAAAGACGTGTCTTTTGG	225855	58051	TTGTAGAGATGGGGTTTCAC	270442	102638	GCTTCTCCACCTTTAGGAAG
181269	13465	CACTAAAGACGTGTCTTTTG	225856	58052	TTTGTAGAGATGGGGTTTCA	270443	102639	TGCTTCTCCACCTTTAGGAA
181270	13466	GCACTAAAGACGTGTCTTTT	225857	58053	TTTTGTAGAGATGGGGTTTC	270444	102640	GTGCTTCTCCACCTTTAGGA
181271	13467	AGCACTAAAGACGTGTCTTT	225858	58054	TTTTTGTAGAGATGGGGTTT	270445	102641	TGTGCTTCTCCACCTTTAGG
181272	13468	TAGCACTAAAGACGTGTCTT	225859	58055	TTTTTTGTAGAGATGGGGTT	270446	102642	CTGTGCTTCTCCACCTTTAG
181273	13469	TTAGCACTAAAGACGTGTCT	225860	58056	ATTTTTTGTAGAGATGGGGT	270447	102643	TCTGTGCTTCTCCACCTTTA
181274	13470	CTTAGCACTAAAGACGTGTC	225861	58057	TATTTTTTGTAGAGATGGGG	270448	102644	GTCTGTGCTTCTCCACCTTT
181275	13471	CCTTAGCACTAAAGACGTGT	225862	58058	GTATTTTTTGTAGAGATGGG	270449	102645	AGTCTGTGCTTCTCCACCTT
181276	13472	TCCTTAGCACTAAAGACGTG	225863	58059	TGTATTTTTTGTAGAGATGG	270450	102646	AAGTCTGTGCTTCTCCACCT
181277	13473	GTCCTTAGCACTAAAGACGT	225864	58060	TTGTATTTTTTGTAGAGATG	270451	102647	GAAGTCTGTGCTTCTCCACC
181278	13474	AGTCCTTAGCACTAAAGACG	225865	58061	TTTGTATTTTTTGTAGAGAT	270452	102648	CGAAGTCTGTGCTTCTCCAC
181279	13475	CAGTCCTTAGCACTAAAGAC	225866	58062	TTTTGTATTTTTTGTAGAGA	270453	102649	CCGAAGTCTGTGCTTCTCCA
181280	13476	CCAGTCCTTAGCACTAAAGA	225867	58063	TTTTTGTATTTTTTGTAGAG	270454	102650	CCCGAAGTCTGTGCTTCTCC
181281	13477	TCCAGTCCTTAGCACTAAAG	225868	58064	TTTTTTGTATTTTTTGTAGA	270455	102651	CCCCGAAGTCTGTGCTTCTC
181282	13478	CTCCAGTCCTTAGCACTAAA	225869	58065	ATTTTTTGTATTTTTTGTAG	270456	102652	CCCCCGAAGTCTGTGCTTCT
181283	13479	TCTCCAGTCCTTAGCACTAA	225870	58066	AATTTTTTGTATTTTTTGTA	270457	102653	GCCCCCGAAGTCTGTGCTTC
181284	13480	TTCTCCAGTCCTTAGCACTA	225871	58067	TAATTTTTTGTATTTTTTGT	270458	102654	GGCCCCCGAAGTCTGTGCTT
181285	13481	CTTCTCCAGTCCTTAGCACT	225872	58068	CTAATTTTTTGTATTTTTTG	270459	102655	AGGCCCCCGAAGTCTGTGCT
181286	13482	GCTTCTCCAGTCCTTAGCAC	225873	58069	GCTAATTTTTTGTATTTTTT	270460	102656	CAGGCCCCCGAAGTCTGTGC
181287	13483	GGCTTCTCCAGTCCTTAGCA	225874	58070	GGCTAATTTTTTGTATTTTT	270461	102657	CCAGGCCCCCGAAGTCTGTG
181288	13484	TGGCTTCTCCAGTCCTTAGC	225875	58071	TGGCTAATTTTTTGTATTTT	270462	102658	GCCAGGCCCCCGAAGTCTGT
181289	13485	ATGGCTTCTCCAGTCCTTAG	225876	58072	CTGGCTAATTTTTTGTATTT	270463	102659	GGCCAGGCCCCCGAAGTCTG
181290	13486	CATGGCTTCTCCAGTCCTTA	225877	58073	CCTGGCTAATTTTTTGTATT	270464	102660	AGGCCAGGCCCCCGAAGTCT
181291	13487	GCATGGCTTCTCCAGTCCTT	225878	58074	GCCTGGCTAATTTTTTGTAT	270465	102661	CAGGCCAGGCCCCCGAAGTC
181292	13488	GGCATGGCTTCTCCAGTCCT	225879	58075	TGCCTGGCTAATTTTTTGTA	270466	102662	CCAGGCCAGGCCCCCGAAGT
181293	13489	GGGCATGGCTTCTCCAGTCC	225880	58076	ATGCCTGGCTAATTTTTTGT	270467	102663	TCCAGGCCAGGCCCCCGAAG
181294	13490	AGGGCATGGCTTCTCCAGTC	225881	58077	CATGCCTGGCTAATTTTTTG	270468	102664	ATCCAGGCCAGGCCCCCGAA
181295	13491	GAGGGCATGGCTTCTCCAGT	225882	58078	CCATGCCTGGCTAATTTTTT	270469	102665	GATCCAGGCCAGGCCCCCGA
181296	13492	GGAGGGCATGGCTTCTCCAG	225883	58079	ACCATGCCTGGCTAATTTTT	270470	102666	GGATCCAGGCCAGGCCCCCG
181297	13493	TGGAGGGCATGGCTTCTCCA	225884	58080	CACCATGCCTGGCTAATTTT	270471	102667	GGGATCCAGGCCAGGCCCCC
181298	13494	CTGGAGGGCATGGCTTCTCC	225885	58081	CCACCATGCCTGGCTAATTT	270472	102668	AGGGATCCAGGCCAGGCCCC
181299	13495	GCTGGAGGGCATGGCTTCTC	225886	58082	ACCACCATGCCTGGCTAATT	270473	102669	AAGGGATCCAGGCCAGGCCC
181300	13496	GGCTGGAGGGCATGGCTTCT	225887	58083	CACCACCATGCCTGGCTAAT	270474	102670	AAAGGGATCCAGGCCAGGCC
181301	13497	AGGCTGGAGGGCATGGCTTC	225888	58084	GCACCACCATGCCTGGCTAA	270475	102671	GAAAGGGATCCAGGCCAGGC
181302	13498	GAGGCTGGAGGGCATGGCTT	225889	58085	TGCACCACCATGCCTGGCTA	270476	102672	GGAAAGGGATCCAGGCCAGG
181303	13499	AGAGGCTGGAGGGCATGGCT	225890	58086	ATGCACCACCATGCCTGGCT	270477	102673	GGGAAAGGGATCCAGGCCAG
181304	13500	CAGAGGCTGGAGGGCATGGC	225891	58087	TATGCACCACCATGCCTGGC	270478	102674	GGGGAAAGGGATCCAGGCCA
181305	13501	ACAGAGGCTGGAGGGCATGG	225892	58088	GTATGCACCACCATGCCTGG	270479	102675	TGGGGAAAGGGATCCAGGCC
181306	13502	CACAGAGGCTGGAGGGCATG	225893	58089	GGTATGCACCACCATGCCTG	270480	102676	ATGGGGAAAGGGATCCAGGC
181307	13503	TCACAGAGGCTGGAGGGCAT	225894	58090	AGGTATGCACCACCATGCCT	270481	102677	AATGGGGAAAGGGATCCAGG
181308	13504	TTCACAGAGGCTGGAGGGCA	225895	58091	CAGGTATGCACCACCATGCC	270482	102678	GAATGGGGAAAGGGATCCAG
181309	13505	ATTCACAGAGGCTGGAGGGC	225896	58092	ACAGGTATGCACCACCATGC	270483	102679	GGAATGGGGAAAGGGATCCA
181310	13506	CATTCACAGAGGCTGGAGGG	225897	58093	CACAGGTATGCACCACCATG	270484	102680	AGGAATGGGGAAAGGGATCC
181311	13507	CCATTCACAGAGGCTGGAGG	225898	58094	CCACAGGTATGCACCACCAT	270485	102681	CAGGAATGGGGAAAGGGATC
181312	13508	CCCATTCACAGAGGCTGGAG	225899	58095	ACCACAGGTATGCACCACCA	270486	102682	ACAGGAATGGGGAAAGGGAT
181313	13509	ACCCATTCACAGAGGCTGGA	225900	58096	GACCACAGGTATGCACCACC	270487	102683	GACAGGAATGGGGAAAGGGA
181314	13510	GACCCATTCACAGAGGCTGG	225901	58097	GGACCACAGGTATGCACCAC	270488	102684	GGACAGGAATGGGGAAAGGG
181315	13511	TGACCCATTCACAGAGGCTG	225902	58098	GGGACCACAGGTATGCACCA	270489	102685	GGGACAGGAATGGGGAAAGG
181316	13512	ATGACCCATTCACAGAGGCT	225903	58099	TGGGACCACAGGTATGCACC	270490	102686	AGGGACAGGAATGGGGAAAG
181317	13513	TATGACCCATTCACAGAGGC	225904	58100	CTGGGACCACAGGTATGCAC	270491	102687	CAGGGACAGGAATGGGGAAA
181318	13514	ATATGACCCATTCACAGAGG	225905	58101	GCTGGGACCACAGGTATGCA	270492	102688	ACAGGGACAGGAATGGGGAA
181319	13515	CATATGACCCATTCACAGAG	225906	58102	AGCTGGGACCACAGGTATGC	270493	102689	CACAGGGACAGGAATGGGGA
181320	13516	ACATATGACCCATTCACAGA	225907	58103	AAGCTGGGACCACAGGTATG	270494	102690	GCACAGGGACAGGAATGGGG
181321	13517	TACATATGACCCATTCACAG	225908	58104	GAAGCTGGGACCACAGGTAT	270495	102691	GGCACAGGGACAGGAATGGG
181322	13518	TTACATATGACCCATTCACA	225909	58105	AGAAGCTGGGACCACAGGTA	270496	102692	GGGCACAGGGACAGGAATGG
181323	13519	GTTACATATGACCCATTCAC	225910	58106	GAGAAGCTGGGACCACAGGT	270497	102693	GGGGCACAGGGACAGGAATG
181324	13520	TGTTACATATGACCCATTCA	225911	58107	TGAGAAGCTGGGACCACAGG	270498	102694	AGGGGCACAGGGACAGGAAT
181325	13521	ATGTTACATATGACCCATTC	225912	58108	CTGAGAAGCTGGGACCACAG	270499	102695	GAGGGGCACAGGGACAGGAA
181326	13522	CATGTTACATATGACCCATT	225913	58109	GCTGAGAAGCTGGGACCACA	270500	102696	CGAGGGGCACAGGGACAGGA
181327	13523	TCATGTTACATATGACCCAT	225914	58110	GGCTGAGAAGCTGGGACCAC	270501	102697	ACGAGGGGCACAGGGACAGG
181328	13524	CTCATGTTACATATGACCCA	225915	58111	AGGCTGAGAAGCTGGGACCA	270502	102698	GACGAGGGGCACAGGGACAG
181329	13525	GCTCATGTTACATATGACCC	225916	58112	TAGGCTGAGAAGCTGGGACC	270503	102699	AGACGAGGGGCACAGGGACA
181330	13526	GGCTCATGTTACATATGACC	225917	58113	ATAGGCTGAGAAGCTGGGAC	270504	102700	CAGACGAGGGGCACAGGGAC
181331	13527	AGGCTCATGTTACATATGAC	225918	58114	CATAGGCTGAGAAGCTGGGA	270505	102701	CCAGACGAGGGGCACAGGGA
181332	13528	CAGGCTCATGTTACATATGA	225919	58115	CCATAGGCTGAGAAGCTGGG	270506	102702	CCCAGACGAGGGGCACAGGG
181333	13529	CCAGGCTCATGTTACATATG	225920	58116	TCCATAGGCTGAGAAGCTGG	270507	102703	ACCCAGACGAGGGGCACAGG
181334	13530	TCCAGGCTCATGTTACATAT	225921	58117	GTCCATAGGCTGAGAAGCTG	270508	102704	CACCCAGACGAGGGGCACAG
181335	13531	CTCCAGGCTCATGTTACATA	225922	58118	GGTCCATAGGCTGAGAAGCT	270509	102705	GCACCCAGACGAGGGGCACA
181336	13532	TCTCCAGGCTCATGTTACAT	225923	58119	GGGTCCATAGGCTGAGAAGC	270510	102706	CGCACCCAGACGAGGGGCAC
181337	13533	TTCTCCAGGCTCATGTTACA	225924	58120	TGGGTCCATAGGCTGAGAAG	270511	102707	ACGCACCCAGACGAGGGGCA
181338	13534	TTTCTCCAGGCTCATGTTAC	225925	58121	GTGGGTCCATAGGCTGAGAA	270512	102708	AACGCACCCAGACGAGGGGC

181339	13535	ATTTCTCCAGGCTCATGTTA	225926	58122	TGTGGGTCCATAGGCTGAGA	270513	102709	TAACGCACCCAGACGAGGGG
181340	13536	AATTTCTCCAGGCTCATGTT	225927	58123	ATGTGGGTCCATAGGCTGAG	270514	102710	CTAACGCACCCAGACGAGGG
181341	13537	TAATTTCTCCAGGCTCATGT	225928	58124	TATGTGGGTCCATAGGCTGA	270515	102711	CCTAACGCACCCAGACGAGG
181342	13538	ATAATTTCTCCAGGCTCATG	225929	58125	CTATGTGGGTCCATAGGCTG	270516	102712	CCCTAACGCACCCAGACGAG
181343	13539	AATAATTTCTCCAGGCTCAT	225930	58126	TCTATGTGGGTCCATAGGCT	270517	102713	GCCCTAACGCACCCAGACGA
181344	13540	AAATAATTTCTCCAGGCTCA	225931	58127	TTCTATGTGGGTCCATAGGC	270518	102714	AGCCCTAACGCACCCAGACG
181345	13541	CAAATAATTTCTCCAGGCTC	225932	58128	ATTCTATGTGGGTCCATAGG	270519	102715	CAGCCCTAACGCACCCAGAC
181346	13542	TCAAATAATTTCTCCAGGCT	225933	58129	TATTCTATGTGGGTCCATAG	270520	102716	TCAGCCCTAACGCACCCAGA
181347	13543	TTCAAATAATTTCTCCAGGC	225934	58130	GTATTCTATGTGGGTCCATA	270521	102717	GTCAGCCCTAACGCACCCAG
181348	13544	TTTCAAATAATTTCTCCAGG	225935	58131	TGTATTCTATGTGGGTCCAT	270522	102718	TGTCAGCCCTAACGCACCCA
181349	13545	GTTTCAAATAATTTCTCCAG	225936	58132	TTGTATTCTATGTGGGTCCA	270523	102719	ATGTCAGCCCTAACGCACCC
181350	13546	GGTTTCAAATAATTTCTCCA	225937	58133	ATTGTATTCTATGTGGGTCC	270524	102720	TATGTCAGCCCTAACGCACC
181351	13547	TGGTTTCAAATAATTTCTCC	225938	58134	CATTGTATTCTATGTGGGTC	270525	102721	GTATGTCAGCCCTAACGCAC
181352	13548	TTGGTTTCAAATAATTTCTC	225939	58135	ACATTGTATTCTATGTGGGT	270526	102722	TGTATGTCAGCCCTAACGCA
181353	13549	TTTGGTTTCAAATAATTTCT	225940	58136	GACATTGTATTCTATGTGGG	270527	102723	TTGTATGTCAGCCCTAACGC
181354	13550	CTTTGGTTTCAAATAATTTC	225941	58137	TGACATTGTATTCTATGTGG	270528	102724	TTTGTATGTCAGCCCTAACG
181355	13551	CCTTTGGTTTCAAATAATTT	225942	58138	CTGACATTGTATTCTATGTG	270529	102725	CTTTGTATGTCAGCCCTAAC
181356	13552	GCCTTTGGTTTCAAATAATT	225943	58139	GCTGACATTGTATTCTATGT	270530	102726	GCTTTGTATGTCAGCCCTAA
181357	13553	TGCCTTTGGTTTCAAATAAT	225944	58140	TGCTGACATTGTATTCTATG	270531	102727	TGCTTTGTATGTCAGCCCTA
181358	13554	TTGCCTTTGGTTTCAAATAA	225945	58141	ATGCTGACATTGTATTCTAT	270532	102728	GTGCTTTGTATGTCAGCCCT
181359	13555	CTTGCCTTTGGTTTCAAATA	225946	58142	TATGCTGACATTGTATTCTA	270533	102729	GGTGCTTTGTATGTCAGCCC
181360	13556	GCTTGCCTTTGGTTTCAAAT	225947	58143	TTATGCTGACATTGTATTCT	270534	102730	TGGTGCTTTGTATGTCAGCC
181361	13557	GGCTTGCCTTTGGTTTCAAA	225948	58144	CTTATGCTGACATTGTATTC	270535	102731	GTGGTGCTTTGTATGTCAGC
181362	13558	AGGCTTGCCTTTGGTTTCAA	225949	58145	TCTTATGCTGACATTGTATT	270536	102732	TGTGGTGCTTTGTATGTCAG
181363	13559	GAGGCTTGCCTTTGGTTTCA	225950	58146	TTCTTATGCTGACATTGTAT	270537	102733	CTGTGGTGCTTTGTATGTCA
181364	13560	AGAGGCTTGCCTTTGGTTTC	225951	58147	CTTCTTATGCTGACATTGTA	270538	102734	ACTGTGGTGCTTTGTATGTC
181365	13561	TAGAGGCTTGCCTTTGGTTT	225952	58148	CCTTCTTATGCTGACATTGT	270539	102735	CACTGTGGTGCTTTGTATGT
181366	13562	TTAGAGGCTTGCCTTTGGTT	225953	58149	CCCTTCTTATGCTGACATTG	270540	102736	TCACTGTGGTGCTTTGTATG
181367	13563	TTTAGAGGCTTGCCTTTGGT	225954	58150	TCCCTTCTTATGCTGACATT	270541	102737	TTCACTGTGGTGCTTTGTAT
181368	13564	GTTTAGAGGCTTGCCTTTGG	225955	58151	CTCCCTTCTTATGCTGACAT	270542	102738	TTTCACTGTGGTGCTTTGTA
181369	13565	GGTTTAGAGGCTTGCCTTTG	225956	58152	GCTCCCTTCTTATGCTGACA	270543	102739	CTTTCACTGTGGTGCTTTGT
181370	13566	TGGTTTAGAGGCTTGCCTTT	225957	58153	GGCTCCCTTCTTATGCTGAC	270544	102740	TCTTTCACTGTGGTGCTTTG
181371	13567	CTGGTTTAGAGGCTTGCCTT	225958	58154	GGGCTCCCTTCTTATGCTGA	270545	102741	TTCTTTCACTGTGGTGCTTT
181372	13568	CCTGGTTTAGAGGCTTGCCT	225959	58155	AGGGCTCCCTTCTTATGCTG	270546	102742	GTTCTTTCACTGTGGTGCTT
181373	13569	GCCTGGTTTAGAGGCTTGCC	225960	58156	CAGGGCTCCCTTCTTATGCT	270547	102743	TGTTCTTTCACTGTGGTGCT
181374	13570	AGCCTGGTTTAGAGGCTTGC	225961	58157	CCAGGGCTCCCTTCTTATGC	270548	102744	CTGTTCTTTCACTGTGGTGC
181375	13571	CAGCCTGGTTTAGAGGCTTG	225962	58158	CCCAGGGCTCCCTTCTTATG	270549	102745	GCTGTTCTTTCACTGTGGTG
181376	13572	GCAGCCTGGTTTAGAGGCTT	225963	58159	CCCCAGGGCTCCCTTCTTAT	270550	102746	TGCTGTTCTTTCACTGTGGT
181377	13573	AGCAGCCTGGTTTAGAGGCT	225964	58160	ACCCCAGGGCTCCCTTCTTA	270551	102747	CTGCTGTTCTTTCACTGTGG
181378	13574	CAGCAGCCTGGTTTAGAGGC	225965	58161	GACCCCAGGGCTCCCTTCTT	270552	102748	ACTGCTGTTCTTTCACTGTG
181379	13575	GCAGCAGCCTGGTTTAGAGG	225966	58162	TGACCCCAGGGCTCCCTTCT	270553	102749	TACTGCTGTTCTTTCACTGT
181380	13576	AGCAGCAGCCTGGTTTAGAG	225967	58163	GTGACCCCAGGGCTCCCTTC	270554	102750	ATACTGCTGTTCTTTCACTG
181381	13577	AAGCAGCAGCCTGGTTTAGA	225968	58164	GGTGACCCCAGGGCTCCCTT	270555	102751	CATACTGCTGTTCTTTCACT
181382	13578	GAAGCAGCAGCCTGGTTTAG	225969	58165	TGGTGACCCCAGGGCTCCCT	270556	102752	GCATACTGCTGTTCTTTCAC
181383	13579	TGAAGCAGCAGCCTGGTTTA	225970	58166	TTGGTGACCCCAGGGCTCCC	270557	102753	GGCATACTGCTGTTCTTTCA
181384	13580	ATGAAGCAGCAGCCTGGTTT	225971	58167	TTTGGTGACCCCAGGGCTCC	270558	102754	AGGCATACTGCTGTTCTTTC
181385	13581	CATGAAGCAGCAGCCTGGTT	225972	58168	ATTTGGTGACCCCAGGGCTC	270559	102755	GAGGCATACTGCTGTTCTTT
181386	13582	CCATGAAGCAGCAGCCTGGT	225973	58169	CATTTGGTGACCCCAGGGCT	270560	102756	GGAGGCATACTGCTGTTCTT
181387	13583	GCCATGAAGCAGCAGCCTGG	225974	58170	CCATTTGGTGACCCCAGGGC	270561	102757	AGGAGGCATACTGCTGTTCT
181388	13584	CGCCATGAAGCAGCAGCCTG	225975	58171	ACCATTTGGTGACCCCAGGG	270562	102758	GAGGAGGCATACTGCTGTTC
181389	13585	GCGCCATGAAGCAGCAGCCT	225976	58172	AACCATTTGGTGACCCCAGG	270563	102759	TGAGGAGGCATACTGCTGTT
181390	13586	GGCGCCATGAAGCAGCAGCC	225977	58173	AAACCATTTGGTGACCCCAG	270564	102760	GTGAGGAGGCATACTGCTGT
181391	13587	CGGCGCCATGAAGCAGCAGC	225978	58174	CAAACCATTTGGTGACCCCA	270565	102761	AGTGAGGAGGCATACTGCTG
181392	13588	CCGGCGCCATGAAGCAGCAG	225979	58175	CCAAACCATTTGGTGACCCC	270566	102762	TAGTGAGGAGGCATACTGCT
181393	13589	ACCGGCGCCATGAAGCAGCA	225980	58176	CCCAAACCATTTGGTGACCC	270567	102763	CTAGTGAGGAGGCATACTGC
181394	13590	CACCGGCGCCATGAAGCAGC	225981	58177	GCCCAAACCATTTGGTGACC	270568	102764	GCTAGTGAGGAGGCATACTG
181395	13591	TCACCGGCGCCATGAAGCAG	225982	58178	CGCCCAAACCATTTGGTGAC	270569	102765	GGCTAGTGAGGAGGCATACT
181396	13592	GTCACCGGCGCCATGAAGCA	225983	58179	CCGCCCAAACCATTTGGTGA	270570	102766	TGGCTAGTGAGGAGGCATAC
181397	13593	CGTCACCGGCGCCATGAAGC	225984	58180	GCCGCCCAAACCATTTGGTG	270571	102767	CTGGCTAGTGAGGAGGCATA
181398	13594	CCGTCACCGGCGCCATGAAG	225985	58181	TGCCGCCCAAACCATTTGGT	270572	102768	CCTGGCTAGTGAGGAGGCAT
181399	13595	GCCGTCACCGGCGCCATGAA	225986	58182	TTGCCGCCCAAACCATTTGG	270573	102769	ACCTGGCTAGTGAGGAGGCA
181400	13596	TGCCGTCACCGGCGCCATGA	225987	58183	TTTGCCGCCCAAACCATTTG	270574	102770	CACCTGGCTAGTGAGGAGGC
181401	13597	CTGCCGTCACCGGCGCCATG	225988	58184	CTTTGCCGCCCAAACCATTT	270575	102771	ACACCTGGCTAGTGAGGAGG
181402	13598	TCTGCCGTCACCGGCGCCAT	225989	58185	TCTTTGCCGCCCAAACCATT	270576	102772	CACACCTGGCTAGTGAGGAG
181403	13599	TTCTGCCGTCACCGGCGCCA	225990	58186	TTCTTTGCCGCCCAAACCAT	270577	102773	CCACACCTGGCTAGTGAGGA
181404	13600	GTTCTGCCGTCACCGGCGCC	225991	58187	GTTCTTTGCCGCCCAAACCA	270578	102774	CCCACACCTGGCTAGTGAGG
181405	13601	GGTTCTGCCGTCACCGGCGC	225992	58188	GGTTCTTTGCCGCCCAAACC	270579	102775	GCCCACACCTGGCTAGTGAG
181406	13602	TGGTTCTGCCGTCACCGGCG	225993	58189	AGGTTCTTTGCCGCCCAAAC	270580	102776	CGCCCACACCTGGCTAGTGA
181407	13603	TTGGTTCTGCCGTCACCGGC	225994	58190	CAGGTTCTTTGCCGCCCAAA	270581	102777	CCGCCCACACCTGGCTAGTG
181408	13604	TTTGGTTCTGCCGTCACCGG	225995	58191	TCAGGTTCTTTGCCGCCCAA	270582	102778	CCCGCCCACACCTGGCTAGT
181409	13605	ATTTGGTTCTGCCGTCACCG	225996	58192	TTCAGGTTCTTTGCCGCCCA	270583	102779	ACCCGCCCACACCTGGCTAG
181410	13606	AATTTGGTTCTGCCGTCACC	225997	58193	CTTCAGGTTCTTTGCCGCCC	270584	102780	CACCCGCCCACACCTGGCTA

181411	13607	AAATTTGGTTCTGCCGTCAC	225998	58194	CCTTCAGGTTCTTTGCCGCC	270585	102781	CCACCCGCCCACACCTGGCT
181412	13608	TAAATTTGGTTCTGCCGTCA	225999	58195	ACCTTCAGGTTCTTTGCCGC	270586	102782	CCCACCCGCCCACACCTGGC
181413	13609	CTAAATTTGGTTCTGCCGTC	226000	58196	AACCTTCAGGTTCTTTGCCG	270587	102783	ACCCACCCGCCCACACCTGG
181414	13610	ACTAAATTTGGTTCTGCCGT	226001	58197	CAACCTTCAGGTTCTTTGCC	270588	102784	AACCCACCCGCCCACACCTG
181415	13611	CACTAAATTTGGTTCTGCCG	226002	58198	TCAACCTTCAGGTTCTTTGC	270589	102785	AAACCCACCCGCCCACACCT
181416	13612	GCACTAAATTTGGTTCTGCC	226003	58199	CTCAACCTTCAGGTTCTTTG	270590	102786	GAAACCCACCCGCCCACACC
181417	13613	AGCACTAAATTTGGTTCTGC	226004	58200	TCTCAACCTTCAGGTTCTTT	270591	102787	AGAAACCCACCCGCCCACAC
181418	13614	CAGCACTAAATTTGGTTCTG	226005	58201	CTCTCAACCTTCAGGTTCTT	270592	102788	AAGAAACCCACCCGCCCACA
181419	13615	ACAGCACTAAATTTGGTTCT	226006	58202	TCTCTCAACCTTCAGGTTCT	270593	102789	GAAGAAACCCACCCGCCCAC
181420	13616	CACAGCACTAAATTTGGTTC	226007	58203	TTCTCTCAACCTTCAGGTTC	270594	102790	GGAAGAAACCCACCCGCCCA
181421	13617	CCACAGCACTAAATTTGGTT	226008	58204	CTTCTCTCAACCTTCAGGTT	270595	102791	TGGAAGAAACCCACCCGCCC
181422	13618	CCCACAGCACTAAATTTGGT	226009	58205	ACTTCTCTCAACCTTCAGGT	270596	102792	TTGGAAGAAACCCACCCGCC
181423	13619	GCCCACAGCACTAAATTTGG	226010	58206	CACTTCTCTCAACCTTCAGG	270597	102793	CTTGGAAGAAACCCACCCGC
181424	13620	TGCCCACAGCACTAAATTTG	226011	58207	CCACTTCTCTCAACCTTCAG	270598	102794	CCTTGGAAGAAACCCACCCG
181425	13621	CTGCCCACAGCACTAAATTT	226012	58208	GCCACTTCTCTCAACCTTCA	270599	102795	GCCTTGGAAGAAACCCACCC
181426	13622	CCTGCCCACAGCACTAAATT	226013	58209	AGCCACTTCTCTCAACCTTC	270600	102796	GGCCTTGGAAGAAACCCACC
181427	13623	ACCTGCCCACAGCACTAAAT	226014	58210	AAGCCACTTCTCTCAACCTT	270601	102797	AGGCCTTGGAAGAAACCCAC
181428	13624	GACCTGCCCACAGCACTAAA	226015	58211	CAAGCCACTTCTCTCAACCT	270602	102798	GAGGCCTTGGAAGAAACCCA
181429	13625	GGACCTGCCCACAGCACTAA	226016	58212	CCAAGCCACTTCTCTCAACC	270603	102799	AGAGGCCTTGGAAGAAACCC
181430	13626	TGGACCTGCCCACAGCACTA	226017	58213	ACCAAGCCACTTCTCTCAAC	270604	102800	GAGAGGCCTTGGAAGAAACC
181431	13627	GTGGACCTGCCCACAGCACT	226018	58214	AACCAAGCCACTTCTCTCAA	270605	102801	AGAGAGGCCTTGGAAGAAAC
181432	13628	TGTGGACCTGCCCACAGCAC	226019	58215	TAACCAAGCCACTTCTCTCA	270606	102802	CAGAGAGGCCTTGGAAGAAA
181433	13629	GTGTGGACCTGCCCACAGCA	226020	58216	GTAACCAAGCCACTTCTCTC	270607	102803	ACAGAGAGGCCTTGGAAGAA
181434	13630	AGTGTGGACCTGCCCACAGC	226021	58217	GGTAACCAAGCCACTTCTCT	270608	102804	CACAGAGAGGCCTTGGAAGA
181435	13631	AAGTGTGGACCTGCCCACAG	226022	58218	GGGTAACCAAGCCACTTCTC	270609	102805	CCACAGAGAGGCCTTGGAAG
181436	13632	TAAGTGTGGACCTGCCCACA	226023	58219	TGGGTAACCAAGCCACTTCT	270610	102806	GCCACAGAGAGGCCTTGGAA
181437	13633	ATAAGTGTGGACCTGCCCAC	226024	58220	CTGGGTAACCAAGCCACTTC	270611	102807	GGCCACAGAGAGGCCTTGGA
181438	13634	GATAAGTGTGGACCTGCCCA	226025	58221	GCTGGGTAACCAAGCCACTT	270612	102808	CGGCCACAGAGAGGCCTTGG
181439	13635	TGATAAGTGTGGACCTGCCC	226026	58222	AGCTGGGTAACCAAGCCACT	270613	102809	ACGGCCACAGAGAGGCCTTG
181440	13636	TTGATAAGTGTGGACCTGCC	226027	58223	CAGCTGGGTAACCAAGCCAC	270614	102810	CACGGCCACAGAGAGGCCTT
181441	13637	TTTGATAAGTGTGGACCTGC	226028	58224	ACAGCTGGGTAACCAAGCCA	270615	102811	CCACGGCCACAGAGAGGCCT
181442	13638	ATTTGATAAGTGTGGACCTG	226029	58225	AACAGCTGGGTAACCAAGCC	270616	102812	CCCACGGCCACAGAGAGGCC
181443	13639	TATTTGATAAGTGTGGACCT	226030	58226	CAACAGCTGGGTAACCAAGC	270617	102813	ACCCACGGCCACAGAGAGGC
181444	13640	CTATTTGATAAGTGTGGACC	226031	58227	CCAACAGCTGGGTAACCAAG	270618	102814	TACCCACGGCCACAGAGAGG
181445	13641	TCTATTTGATAAGTGTGGAC	226032	58228	TCCAACAGCTGGGTAACCAA	270619	102815	CTACCCACGGCCACAGAGAG
181446	13642	CTCTATTTGATAAGTGTGGA	226033	58229	ATCCAACAGCTGGGTAACCA	270620	102816	GCTACCCACGGCCACAGAGA
181447	13643	TCTCTATTTGATAAGTGTGG	226034	58230	CATCCAACAGCTGGGTAACC	270621	102817	GGCTACCCACGGCCACAGAG
181448	13644	TTCTCTATTTGATAAGTGTG	226035	58231	ACATCCAACAGCTGGGTAAC	270622	102818	TGGCTACCCACGGCCACAGA
181449	13645	CTTCTCTATTTGATAAGTGT	226036	58232	CACATCCAACAGCTGGGTAA	270623	102819	GTGGCTACCCACGGCCACAG
181450	13646	GCTTCTCTATTTGATAAGTG	226037	58233	TCACATCCAACAGCTGGGTA	270624	102820	GGTGGCTACCCACGGCCACA
181451	13647	AGCTTCTCTATTTGATAAGT	226038	58234	CTCACATCCAACAGCTGGGT	270625	102821	AGGTGGCTACCCACGGCCAC
181452	13648	GAGCTTCTCTATTTGATAAG	226039	58235	TCTCACATCCAACAGCTGGG	270626	102822	GAGGTGGCTACCCACGGCCA
181453	13649	TGAGCTTCTCTATTTGATAA	226040	58236	GTCTCACATCCAACAGCTGG	270627	102823	AGAGGTGGCTACCCACGGCC
181454	13650	ATGAGCTTCTCTATTTGATA	226041	58237	GGTCTCACATCCAACAGCTG	270628	102824	CAGAGGTGGCTACCCACGGC
181455	13651	AATGAGCTTCTCTATTTGAT	226042	58238	AGGTCTCACATCCAACAGCT	270629	102825	ACAGAGGTGGCTACCCACGG
181456	13652	AAATGAGCTTCTCTATTTGA	226043	58239	CAGGTCTCACATCCAACAGC	270630	102826	GACAGAGGTGGCTACCCACG
181457	13653	AAAATGAGCTTCTCTATTTG	226044	58240	CCAGGTCTCACATCCAACAG	270631	102827	GGACAGAGGTGGCTACCCAC
181458	13654	AAAAATGAGCTTCTCTATTT	226045	58241	GCCAGGTCTCACATCCAACA	270632	102828	AGGACAGAGGTGGCTACCCA
181459	13655	GAAAAATGAGCTTCTCTATT	226046	58242	GGCCAGGTCTCACATCCAAC	270633	102829	CAGGACAGAGGTGGCTACCC
181460	13656	AGAAAAATGAGCTTCTCTAT	226047	58243	TGGCCAGGTCTCACATCCAA	270634	102830	GCAGGACAGAGGTGGCTACC
181461	13657	AAGAAAAATGAGCTTCTCTA	226048	58244	GTGGCCAGGTCTCACATCCA	270635	102831	TGCAGGACAGAGGTGGCTAC
181462	13658	GAAGAAAAATGAGCTTCTCT	226049	58245	AGTGGCCAGGTCTCACATCC	270636	102832	GTGCAGGACAGAGGTGGCTA
181463	13659	GGAAGAAAAATGAGCTTCTC	226050	58246	CAGTGGCCAGGTCTCACATC	270637	102833	GGTGCAGGACAGAGGTGGCT
181464	13660	CGGAAGAAAAATGAGCTTCT	226051	58247	GCAGTGGCCAGGTCTCACAT	270638	102834	CGGTGCAGGACAGAGGTGGC
181465	13661	CCGGAAGAAAAATGAGCTTC	226052	58248	AGCAGTGGCCAGGTCTCACA	270639	102835	GCGGTGCAGGACAGAGGTGG
181466	13662	GCCGGAAGAAAAATGAGCTT	226053	58249	AAGCAGTGGCCAGGTCTCAC	270640	102836	AGCGGTGCAGGACAGAGGTG
181467	13663	AGCCGGAAGAAAAATGAGCT	226054	58250	GAAGCAGTGGCCAGGTCTCA	270641	102837	CAGCGGTGCAGGACAGAGGT
181468	13664	GAGCCGGAAGAAAAATGAGC	226055	58251	AGAAGCAGTGGCCAGGTCTC	270642	102838	GCAGCGGTGCAGGACAGAGG
181469	13665	TGAGCCGGAAGAAAAATGAG	226056	58252	AAGAAGCAGTGGCCAGGTCT	270643	102839	TGCAGCGGTGCAGGACAGAG
181470	13666	GTGAGCCGGAAGAAAAATGA	226057	58253	GAAGAAGCAGTGGCCAGGTC	270644	102840	CTGCAGCGGTGCAGGACAGA
181471	13667	TGTGAGCCGGAAGAAAAATG	226058	58254	GGAAGAAGCAGTGGCCAGGT	270645	102841	ACTGCAGCGGTGCAGGACAG
181472	13668	ATGTGAGCCGGAAGAAAAAT	226059	58255	TGGAAGAAGCAGTGGCCAGG	270646	102842	GACTGCAGCGGTGCAGGACA
181473	13669	GATGTGAGCCGGAAGAAAAA	226060	58256	ATGGAAGAAGCAGTGGCCAG	270647	102843	AGACTGCAGCGGTGCAGGAC
181474	13670	TGATGTGAGCCGGAAGAAAA	226061	58257	TATGGAAGAAGCAGTGGCCA	270648	102844	AAGACTGCAGCGGTGCAGGA
181475	13671	TTGATGTGAGCCGGAAGAAA	226062	58258	GTATGGAAGAAGCAGTGGCC	270649	102845	GAAGACTGCAGCGGTGCAGG
181476	13672	CTTGATGTGAGCCGGAAGAA	226063	58259	GGTATGGAAGAAGCAGTGGC	270650	102846	GGAAGACTGCAGCGGTGCAG
181477	13673	GCTTGATGTGAGCCGGAAGA	226064	58260	GGGTATGGAAGAAGCAGTGG	270651	102847	GGGAAGACTGCAGCGGTGCA
181478	13674	TGCTTGATGTGAGCCGGAAG	226065	58261	AGGGTATGGAAGAAGCAGTG	270652	102848	AGGGAAGACTGCAGCGGTGC
181479	13675	ATGCTTGATGTGAGCCGGAA	226066	58262	TAGGGTATGGAAGAAGCAGT	270653	102849	GAGGGAAGACTGCAGCGGTG
181480	13676	CATGCTTGATGTGAGCCGGA	226067	58263	CTAGGGTATGGAAGAAGCAG	270654	102850	AGAGGGAAGACTGCAGCGGT
181481	13677	TCATGCTTGATGTGAGCCGG	226068	58264	TCTAGGGTATGGAAGAAGCA	270655	102851	CAGAGGGAAGACTGCAGCGG
181482	13678	TTCATGCTTGATGTGAGCCG	226069	58265	GTCTAGGGTATGGAAGAAGC	270656	102852	ACAGAGGGAAGACTGCAGCG

181483	13679	TTTCATGCTTGATGTGAGCC	226070	58266	GGTCTAGGGTATGGAAGAAG	270657	102853	CACAGAGGGAAGACTGCAGC
181484	13680	TTTTCATGCTTGATGTGAGC	226071	58267	AGGTCTAGGGTATGGAAGAA	270658	102854	ACACAGAGGGAAGACTGCAG
181485	13681	TTTTTCATGCTTGATGTGAG	226072	58268	CAGGTCTAGGGTATGGAAGA	270659	102855	CACACAGAGGGAAGACTGCA
181486	13682	ATTTTTCATGCTTGATGTGA	226073	58269	GCAGGTCTAGGGTATGGAAG	270660	102856	ACACACAGAGGGAAGACTGC
181487	13683	CATTTTTCATGCTTGATGTG	226074	58270	TGCAGGTCTAGGGTATGGAA	270661	102857	CACACACAGAGGGAAGACTG
181488	13684	ACATTTTTCATGCTTGATGT	226075	58271	GTGCAGGTCTAGGGTATGGA	270662	102858	GCACACACAGAGGGAAGACT
181489	13685	AACATTTTTCATGCTTGATG	226076	58272	GGTGCAGGTCTAGGGTATGG	270663	102859	AGCACACACAGAGGGAAGAC
181490	13686	GAACATTTTTCATGCTTGAT	226077	58273	GGGTGCAGGTCTAGGGTATG	270664	102860	GAGCACACACAGAGGGAAGA
181491	13687	TGAACATTTTTCATGCTTGA	226078	58274	AGGGTGCAGGTCTAGGGTAT	270665	102861	GGAGCACACACAGAGGGAAG
181492	13688	GTGAACATTTTTCATGCTTG	226079	58275	CAGGGTGCAGGTCTAGGGTA	270666	102862	AGGAGCACACACAGAGGGAA
181493	13689	TGTGAACATTTTTCATGCTT	226080	58276	TCAGGGTGCAGGTCTAGGGT	270667	102863	CAGGAGCACACACAGAGGGA
181494	13690	GTGTGAACATTTTTCATGCT	226081	58277	GTCAGGGTGCAGGTCTAGGG	270668	102864	CCAGGAGCACACACAGAGGG
181495	13691	TGTGTGAACATTTTTCATGC	226082	58278	TGTCAGGGTGCAGGTCTAGG	270669	102865	ACCAGGAGCACACACAGAGG
181496	13692	ATGTGTGAACATTTTTCATG	226083	58279	ATGTCAGGGTGCAGGTCTAG	270670	102866	TACCAGGAGCACACACAGAG
181497	13693	TATGTGTGAACATTTTTCAT	226084	58280	GATGTCAGGGTGCAGGTCTA	270671	102867	CTACCAGGAGCACACACAGA
181498	13694	GTATGTGTGAACATTTTTCA	226085	58281	AGATGTCAGGGTGCAGGTCT	270672	102868	GCTACCAGGAGCACACACAG
181499	13695	GGTATGTGTGAACATTTTTC	226086	58282	GAGATGTCAGGGTGCAGGTC	270673	102869	AGCTACCAGGAGCACACACA
181500	13696	GGGTATGTGTGAACATTTTT	226087	58283	TGAGATGTCAGGGTGCAGGT	270674	102870	GAGCTACCAGGAGCACACAC
181501	13697	GGGGTATGTGTGAACATTTT	226088	58284	TTGAGATGTCAGGGTGCAGG	270675	102871	AGAGCTACCAGGAGCACACA
181502	13698	GGGGGTATGTGTGAACATTT	226089	58285	CTTGAGATGTCAGGGTGCAG	270676	102872	CAGAGCTACCAGGAGCACAC
181503	13699	GGGGGGTATGTGTGAACATT	226090	58286	ACTTGAGATGTCAGGGTGCA	270677	102873	GCAGAGCTACCAGGAGCACA
181504	13700	TGGGGGGTATGTGTGAACAT	226091	58287	TACTTGAGATGTCAGGGTGC	270678	102874	CGCAGAGCTACCAGGAGCAC
181505	13701	GTGGGGGGTATGTGTGAACA	226092	58288	TTACTTGAGATGTCAGGGTG	270679	102875	GCGCAGAGCTACCAGGAGCA
181506	13702	TGTGGGGGGTATGTGTGAAC	226093	58289	TTTACTTGAGATGTCAGGGT	270680	102876	TGCGCAGAGCTACCAGGAGC
181507	13703	GTGTGGGGGGTATGTGTGAA	226094	58290	TTTTACTTGAGATGTCAGGG	270681	102877	ATGCGCAGAGCTACCAGGAG
181508	13704	TGTGTGGGGGGTATGTGTGA	226095	58291	TTTTTACTTGAGATGTCAGG	270682	102878	CATGCGCAGAGCTACCAGGA
181509	13705	GTGTGTGGGGGGTATGTGTG	226096	58292	CTTTTTACTTGAGATGTCAG	270683	102879	GCATGCGCAGAGCTACCAGG
181510	13706	TGTGTGTGGGGGGTATGTGT	226097	58293	ACTTTTTACTTGAGATGTCA	270684	102880	AGCATGCGCAGAGCTACCAG
181511	13707	GTGTGTGTGGGGGGTATGTG	226098	58294	AACTTTTTACTTGAGATGTC	270685	102881	GAGCATGCGCAGAGCTACCA
181512	13708	TGTGTGTGTGGGGGGTATGT	226099	58295	CAACTTTTTACTTGAGATGT	270686	102882	TGAGCATGCGCAGAGCTACC
181513	13709	ATGTGTGTGTGGGGGGTATG	226100	58296	CCAACTTTTTACTTGAGATG	270687	102883	ATGAGCATGCGCAGAGCTAC
181514	13710	CATGTGTGTGTGGGGGGTAT	226101	58297	CCCAACTTTTTACTTGAGAT	270688	102884	GATGAGCATGCGCAGAGCTA
181515	13711	GCATGTGTGTGTGGGGGGTA	226102	58298	CCCCAACTTTTTACTTGAGA	270689	102885	AGATGAGCATGCGCAGAGCT
181516	13712	AGCATGTGTGTGTGGGGGGT	226103	58299	CCCCCAACTTTTTACTTGAG	270690	102886	AAGATGAGCATGCGCAGAGC
181517	13713	AAGCATGTGTGTGTGGGGGG	226104	58300	TCCCCCAACTTTTTACTTGA	270691	102887	GAAGATGAGCATGCGCAGAG
181518	13714	AAAGCATGTGTGTGTGGGGG	226105	58301	ATCCCCCAACTTTTTACTTG	270692	102888	AGAAGATGAGCATGCGCAGA
181519	13715	GAAAGCATGTGTGTGTGGGG	226106	58302	CATCCCCCAACTTTTTACTT	270693	102889	AAGAAGATGAGCATGCGCAG
181520	13716	GGAAAGCATGTGTGTGTGGG	226107	58303	ACATCCCCCAACTTTTTACT	270694	102890	TAAGAAGATGAGCATGCGCA
181521	13717	CGGAAAGCATGTGTGTGTGG	226108	58304	AACATCCCCCAACTTTTTAC	270695	102891	ATAAGAAGATGAGCATGCGC
181522	13718	CCGGAAAGCATGTGTGTGTG	226109	58305	AAACATCCCCCAACTTTTTA	270696	102892	TATAAGAAGATGAGCATGCG
181523	13719	TCCGGAAAGCATGTGTGTGT	226110	58306	AAAACATCCCCCAACTTTTT	270697	102893	TTATAAGAAGATGAGCATGC
181524	13720	CTCCGGAAAGCATGTGTGTG	226111	58307	TAAAACATCCCCCAACTTTT	270698	102894	CTTATAAGAAGATGAGCATG
181525	13721	CCTCCGGAAAGCATGTGTGT	226112	58308	ATAAAACATCCCCCAACTTT	270699	102895	TCTTATAAGAAGATGAGCAT
181526	13722	CCCTCCGGAAAGCATGTGTG	226113	58309	CATAAAACATCCCCCAACTT	270700	102896	TTCTTATAAGAAGATGAGCA
181527	13723	CCCCTCCGGAAAGCATGTGT	226114	58310	CCATAAAACATCCCCCAACT	270701	102897	GTTCTTATAAGAAGATGAGC
181528	13724	ACCCCTCCGGAAAGCATGTG	226115	58311	ACCATAAAACATCCCCCAAC	270702	102898	TGTTCTTATAAGAAGATGAG
181529	13725	GACCCCTCCGGAAAGCATGT	226116	58312	GACCATAAAACATCCCCCAA	270703	102899	GTGTTCTTATAAGAAGATGA
181530	13726	GGACCCCTCCGGAAAGCATG	226117	58313	GGACCATAAAACATCCCCCA	270704	102900	GGTGTTCTTATAAGAAGATG
181531	13727	TGGACCCCTCCGGAAAGCAT	226118	58314	TGGACCATAAAACATCCCCC	270705	102901	TGGTGTTCTTATAAGAAGAT
181532	13728	ATGGACCCCTCCGGAAAGCA	226119	58315	CTGGACCATAAAACATCCCC	270706	102902	ATGGTGTTCTTATAAGAAGA
181533	13729	CATGGACCCCTCCGGAAAGC	226120	58316	CCTGGACCATAAAACATCCC	270707	102903	CATGGTGTTCTTATAAGAAG
181534	13730	ACATGGACCCCTCCGGAAAG	226121	58317	TCCTGGACCATAAAACATCC	270708	102904	CCATGGTGTTCTTATAAGAA
181535	13731	CACATGGACCCCTCCGGAAA	226122	58318	ATCCTGGACCATAAAACATC	270709	102905	GCCATGGTGTTCTTATAAGA
181536	13732	CCACATGGACCCCTCCGGAA	226123	58319	CATCCTGGACCATAAAACAT	270710	102906	TGCCATGGTGTTCTTATAAG
181537	13733	GCCACATGGACCCCTCCGGA	226124	58320	TCATCCTGGACCATAAAACA	270711	102907	CTGCCATGGTGTTCTTATAA
181538	13734	AGCCACATGGACCCCTCCGG	226125	58321	TTCATCCTGGACCATAAAAC	270712	102908	GCTGCCATGGTGTTCTTATA
181539	13735	TAGCCACATGGACCCCTCCG	226126	58322	CTTCATCCTGGACCATAAAA	270713	102909	AGCTGCCATGGTGTTCTTAT
181540	13736	CTAGCCACATGGACCCCTCC	226127	58323	CCTTCATCCTGGACCATAAA	270714	102910	CAGCTGCCATGGTGTTCTTA
181541	13737	TCTAGCCACATGGACCCCTC	226128	58324	TCCTTCATCCTGGACCATAA	270715	102911	CCAGCTGCCATGGTGTTCTT
181542	13738	CTCTAGCCACATGGACCCCT	226129	58325	TTCCTTCATCCTGGACCATA	270716	102912	CCCAGCTGCCATGGTGTTCT
181543	13739	CCTCTAGCCACATGGACCCC	226130	58326	CTTCCTTCATCCTGGACCAT	270717	102913	GCCCAGCTGCCATGGTGTTC
181544	13740	GCCTCTAGCCACATGGACCC	226131	58327	CCTTCCTTCATCCTGGACCA	270718	102914	CGCCCAGCTGCCATGGTGTT
181545	13741	AGCCTCTAGCCACATGGACC	226132	58328	CCCTTCCTTCATCCTGGACC	270719	102915	ACGCCCAGCTGCCATGGTGT
181546	13742	CAGCCTCTAGCCACATGGAC	226133	58329	GCCCTTCCTTCATCCTGGAC	270720	102916	TACGCCCAGCTGCCATGGTG
181547	13743	CCAGCCTCTAGCCACATGGA	226134	58330	TGCCCTTCCTTCATCCTGGA	270721	102917	CTACGCCCAGCTGCCATGGT
181548	13744	TCCAGCCTCTAGCCACATGG	226135	58331	CTGCCCTTCCTTCATCCTGG	270722	102918	ACTACGCCCAGCTGCCATGG
181549	13745	TTCCAGCCTCTAGCCACATG	226136	58332	ACTGCCCTTCCTTCATCCTG	270723	102919	CACTACGCCCAGCTGCCATG
181550	13746	CTTCCAGCCTCTAGCCACAT	226137	58333	CACTGCCCTTCCTTCATCCT	270724	102920	CCACTACGCCCAGCTGCCAT
181551	13747	TCTTCCAGCCTCTAGCCACA	226138	58334	TCACTGCCCTTCCTTCATCC	270725	102921	GCCACTACGCCCAGCTGCCA
181552	13748	ATCTTCCAGCCTCTAGCCAC	226139	58335	CTCACTGCCCTTCCTTCATC	270726	102922	AGCCACTACGCCCAGCTGCC
181553	13749	CATCTTCCAGCCTCTAGCCA	226140	58336	CCTCACTGCCCTTCCTTCAT	270727	102923	GAGCCACTACGCCCAGCTGC
181554	13750	ACATCTTCCAGCCTCTAGCC	226141	58337	CCCTCACTGCCCTTCCTTCA	270728	102924	TGAGCCACTACGCCCAGCTG

181555	13751	CACATCTTCCAGCCTCTAGC	226142	58338	CCCCTCACTGCCCTTCCTTC	270729	102925	GTGAGCCACTACGCCCAGCT
181556	13752	CCACATCTTCCAGCCTCTAG	226143	58339	GCCCCTCACTGCCCTTCCTT	270730	102926	CGTGAGCCACTACGCCCAGC
181557	13753	TCCACATCTTCCAGCCTCTA	226144	58340	TGCCCCTCACTGCCCTTCCT	270731	102927	GCGTGAGCCACTACGCCCAG
181558	13754	ATCCACATCTTCCAGCCTCT	226145	58341	CTGCCCCTCACTGCCCTTCC	270732	102928	GGCGTGAGCCACTACGCCCA
181559	13755	CATCCACATCTTCCAGCCTC	226146	58342	GCTGCCCCTCACTGCCCTTC	270733	102929	AGGCGTGAGCCACTACGCCC
181560	13756	TCATCCACATCTTCCAGCCT	226147	58343	CGCTGCCCCTCACTGCCCTT	270734	102930	TAGGCGTGAGCCACTACGCC
181561	13757	CTCATCCACATCTTCCAGCC	226148	58344	CCGCTGCCCCTCACTGCCCT	270735	102931	ATAGGCGTGAGCCACTACGC
181562	13758	TCTCATCCACATCTTCCAGC	226149	58345	TCCGCTGCCCCTCACTGCCC	270736	102932	TATAGGCGTGAGCCACTACG
181563	13759	CTCTCATCCACATCTTCCAG	226150	58346	CTCCGCTGCCCCTCACTGCC	270737	102933	TTATAGGCGTGAGCCACTAC
181564	13760	CCTCTCATCCACATCTTCCA	226151	58347	GCTCCGCTGCCCCTCACTGC	270738	102934	ATTATAGGCGTGAGCCACTA
181565	13761	TCCTCTCATCCACATCTTCC	226152	58348	TGCTCCGCTGCCCCTCACTG	270739	102935	GATTATAGGCGTGAGCCACT
181566	13762	CTCCTCTCATCCACATCTTC	226153	58349	ATGCTCCGCTGCCCCTCACT	270740	102936	GGATTATAGGCGTGAGCCAC
181567	13763	GCTCCTCTCATCCACATCTT	226154	58350	GATGCTCCGCTGCCCCTCAC	270741	102937	GGGATTATAGGCGTGAGCCA
181568	13764	GGCTCCTCTCATCCACATCT	226155	58351	TGATGCTCCGCTGCCCCTCA	270742	102938	TGGGATTATAGGCGTGAGCC
181569	13765	AGGCTCCTCTCATCCACATC	226156	58352	GTGATGCTCCGCTGCCCCTC	270743	102939	CTGGGATTATAGGCGTGAGC
181570	13766	CAGGCTCCTCTCATCCACAT	226157	58353	AGTGATGCTCCGCTGCCCCT	270744	102940	GCTGGGATTATAGGCGTGAG
181571	13767	CCAGGCTCCTCTCATCCACA	226158	58354	AAGTGATGCTCCGCTGCCCC	270745	102941	TGCTGGGATTATAGGCGTGA
181572	13768	GCCAGGCTCCTCTCATCCAC	226159	58355	AAAGTGATGCTCCGCTGCCC	270746	102942	GTGCTGGGATTATAGGCGTG
181573	13769	TGCCAGGCTCCTCTCATCCA	226160	58356	CAAAGTGATGCTCCGCTGCC	270747	102943	AGTGCTGGGATTATAGGCGT
181574	13770	CTGCCAGGCTCCTCTCATCC	226161	58357	GCAAAGTGATGCTCCGCTGC	270748	102944	AAGTGCTGGGATTATAGGCG
181575	13771	CCTGCCAGGCTCCTCTCATC	226162	58358	TGCAAAGTGATGCTCCGCTG	270749	102945	AAAGTGCTGGGATTATAGGC
181576	13772	ACCTGCCAGGCTCCTCTCAT	226163	58359	ATGCAAAGTGATGCTCCGCT	270750	102946	CAAAGTGCTGGGATTATAGG
181577	13773	TACCTGCCAGGCTCCTCTCA	226164	58360	AATGCAAAGTGATGCTCCGC	270751	102947	CCAAAGTGCTGGGATTATAG
181578	13774	TTACCTGCCAGGCTCCTCTC	226165	58361	AAATGCAAAGTGATGCTCCG	270752	102948	CCCAAAGTGCTGGGATTATA
181579	13775	CTTACCTGCCAGGCTCCTCT	226166	58362	GAAATGCAAAGTGATGCTCC	270753	102949	TCCCAAAGTGCTGGGATTAT
181580	13776	GCTTACCTGCCAGGCTCCTC	226167	58363	AGAAATGCAAAGTGATGCTC	270754	102950	CTCCCAAAGTGCTGGGATTA
181581	13777	GGCTTACCTGCCAGGCTCCT	226168	58364	CAGAAATGCAAAGTGATGCT	270755	102951	CCTCCCAAAGTGCTGGGATT
181582	13778	GGGCTTACCTGCCAGGCTCC	226169	58365	ACAGAAATGCAAAGTGATGC	270756	102952	GCCTCCCAAAGTGCTGGGAT
181583	13779	TGGGCTTACCTGCCAGGCTC	226170	58366	GACAGAAATGCAAAGTGATG	270757	102953	AGCCTCCCAAAGTGCTGGGA
181584	13780	CTGGGCTTACCTGCCAGGCT	226171	58367	AGACAGAAATGCAAAGTGAT	270758	102954	CAGCCTCCCAAAGTGCTGGG
181585	13781	CCTGGGCTTACCTGCCAGGC	226172	58368	CAGACAGAAATGCAAAGTGA	270759	102955	TCAGCCTCCCAAAGTGCTGG
181586	13782	CCCTGGGCTTACCTGCCAGG	226173	58369	GCAGACAGAAATGCAAAGTG	270760	102956	CTCAGCCTCCCAAAGTGCTG
181587	13783	TCCCTGGGCTTACCTGCCAG	226174	58370	GGCAGACAGAAATGCAAAGT	270761	102957	CCTCAGCCTCCCAAAGTGCT
181588	13784	TTCCCTGGGCTTACCTGCCA	226175	58371	AGGCAGACAGAAATGCAAAG	270762	102958	GCCTCAGCCTCCCAAAGTGC
181589	13785	CTTCCCTGGGCTTACCTGCC	226176	58372	GAGGCAGACAGAAATGCAAA	270763	102959	TGCCTCAGCCTCCCAAAGTG
181590	13786	TCTTCCCTGGGCTTACCTGC	226177	58373	AGAGGCAGACAGAAATGCAA	270764	102960	CTGCCTCAGCCTCCCAAAGT
181591	13787	ATCTTCCCTGGGCTTACCTG	226178	58374	AAGAGGCAGACAGAAATGCA	270765	102961	CCTGCCTCAGCCTCCCAAAG
181592	13788	CATCTTCCCTGGGCTTACCT	226179	58375	TAAGAGGCAGACAGAAATGC	270766	102962	GCCTGCCTCAGCCTCCCAAA
181593	13789	TCATCTTCCCTGGGCTTACC	226180	58376	GTAAGAGGCAGACAGAAATG	270767	102963	TGCCTGCCTCAGCCTCCCAA
181594	13790	GTCATCTTCCCTGGGCTTAC	226181	58377	AGTAAGAGGCAGACAGAAAT	270768	102964	CTGCCTGCCTCAGCCTCCCA
181595	13791	TGTCATCTTCCCTGGGCTTA	226182	58378	CAGTAAGAGGCAGACAGAAA	270769	102965	TCTGCCTGCCTCAGCCTCCC
181596	13792	ATGTCATCTTCCCTGGGCTT	226183	58379	CCAGTAAGAGGCAGACAGAA	270770	102966	ATCTGCCTGCCTCAGCCTCC
181597	13793	AATGTCATCTTCCCTGGGCT	226184	58380	GCCAGTAAGAGGCAGACAGA	270771	102967	GATCTGCCTGCCTCAGCCTC
181598	13794	GAATGTCATCTTCCCTGGGC	226185	58381	AGCCAGTAAGAGGCAGACAG	270772	102968	TGATCTGCCTGCCTCAGCCT
181599	13795	TGAATGTCATCTTCCCTGGG	226186	58382	CAGCCAGTAAGAGGCAGACA	270773	102969	GTGATCTGCCTGCCTCAGCC
181600	13796	CTGAATGTCATCTTCCCTGG	226187	58383	ACAGCCAGTAAGAGGCAGAC	270774	102970	CGTGATCTGCCTGCCTCAGC
181601	13797	GCTGAATGTCATCTTCCCTG	226188	58384	CACAGCCAGTAAGAGGCAGA	270775	102971	TCGTGATCTGCCTGCCTCAG
181602	13798	AGCTGAATGTCATCTTCCCT	226189	58385	ACACAGCCAGTAAGAGGCAG	270776	102972	CTCGTGATCTGCCTGCCTCA
181603	13799	AAGCTGAATGTCATCTTCCC	226190	58386	CACACAGCCAGTAAGAGGCA	270777	102973	CCTCGTGATCTGCCTGCCTC
181604	13800	GAAGCTGAATGTCATCTTCC	226191	58387	TCACACAGCCAGTAAGAGGC	270778	102974	ACCTCGTGATCTGCCTGCCT
181605	13801	GGAAGCTGAATGTCATCTTC	226192	58388	GTCACACAGCCAGTAAGAGG	270779	102975	GACCTCGTGATCTGCCTGCC
181606	13802	GGGAAGCTGAATGTCATCTT	226193	58389	GGTCACACAGCCAGTAAGAG	270780	102976	TGACCTCGTGATCTGCCTGC
181607	13803	TGGGAAGCTGAATGTCATCT	226194	58390	AGGTCACACAGCCAGTAAGA	270781	102977	CTGACCTCGTGATCTGCCTG
181608	13804	CTGGGAAGCTGAATGTCATC	226195	58391	CAGGTCACACAGCCAGTAAG	270782	102978	CCTGACCTCGTGATCTGCCT
181609	13805	TCTGGGAAGCTGAATGTCAT	226196	58392	CCAGGTCACACAGCCAGTAA	270783	102979	TCCTGACCTCGTGATCTGCC
181610	13806	GTCTGGGAAGCTGAATGTCA	226197	58393	CCCAGGTCACACAGCCAGTA	270784	102980	CTCCTGACCTCGTGATCTGC
181611	13807	TGTCTGGGAAGCTGAATGTC	226198	58394	CCCCAGGTCACACAGCCAGT	270785	102981	ACTCCTGACCTCGTGATCTG
181612	13808	CTGTCTGGGAAGCTGAATGT	226199	58395	GCCCCAGGTCACACAGCCAG	270786	102982	AACTCCTGACCTCGTGATCT
181613	13809	GCTGTCTGGGAAGCTGAATG	226200	58396	TGCCCCAGGTCACACAGCCA	270787	102983	GAACTCCTGACCTCGTGATC
181614	13810	TGCTGTCTGGGAAGCTGAAT	226201	58397	CTGCCCCAGGTCACACAGCC	270788	102984	CGAACTCCTGACCTCGTGAT
181615	13811	ATGCTGTCTGGGAAGCTGAA	226202	58398	CCTGCCCCAGGTCACACAGC	270789	102985	TCGAACTCCTGACCTCGTGA
181616	13812	GATGCTGTCTGGGAAGCTGA	226203	58399	ACCTGCCCCAGGTCACACAG	270790	102986	CTCGAACTCCTGACCTCGTG
181617	13813	AGATGCTGTCTGGGAAGCTG	226204	58400	TACCTGCCCCAGGTCACACA	270791	102987	TCTCGAACTCCTGACCTCGT
181618	13814	TAGATGCTGTCTGGGAAGCT	226205	58401	TTACCTGCCCCAGGTCACAC	270792	102988	GTCTCGAACTCCTGACCTCG
181619	13815	GTAGATGCTGTCTGGGAAGC	226206	58402	GTTACCTGCCCCAGGTCACA	270793	102989	GGTCTCGAACTCCTGACCTC
181620	13816	TGTAGATGCTGTCTGGGAAG	226207	58403	AGTTACCTGCCCCAGGTCAC	270794	102990	TGGTCTCGAACTCCTGACCT
181621	13817	CTGTAGATGCTGTCTGGGAA	226208	58404	AAGTTACCTGCCCCAGGTCA	270795	102991	TTGGTCTCGAACTCCTGACC
181622	13818	CCTGTAGATGCTGTCTGGGA	226209	58405	GAAGTTACCTGCCCCAGGTC	270796	102992	GTTGGTCTCGAACTCCTGAC
181623	13819	CCCTGTAGATGCTGTCTGGG	226210	58406	GGAAGTTACCTGCCCCAGGT	270797	102993	GGTTGGTCTCGAACTCCTGA
181624	13820	TCCCTGTAGATGCTGTCTGG	226211	58407	GGGAAGTTACCTGCCCCAGG	270798	102994	AGGTTGGTCTCGAACTCCTG
181625	13821	CTCCCTGTAGATGCTGTCTG	226212	58408	TGGGAAGTTACCTGCCCCAG	270799	102995	CAGGTTGGTCTCGAACTCCT
181626	13822	TCTCCCTGTAGATGCTGTCT	226213	58409	CTGGGAAGTTACCTGCCCCA	270800	102996	TCAGGTTGGTCTCGAACTCC

181627	13823	TTCTCCCTGTAGATGCTGTC	226214	58410	TCTGGGAAGTTACCTGCCCC	270801	102997	GTCAGGTTGGTCTCGAACTC
181628	13824	TTTCTCCCTGTAGATGCTGT	226215	58411	GTCTGGGAAGTTACCTGCCC	270802	102998	GGTCAGGTTGGTCTCGAACT
181629	13825	ATTTCTCCCTGTAGATGCTG	226216	58412	AGTCTGGGAAGTTACCTGCC	270803	102999	TGGTCAGGTTGGTCTCGAAC
181630	13826	AATTTCTCCCTGTAGATGCT	226217	58413	GAGTCTGGGAAGTTACCTGC	270804	103000	TTGGTCAGGTTGGTCTCGAA
181631	13827	AAATTTCTCCCTGTAGATGC	226218	58414	GGAGTCTGGGAAGTTACCTG	270805	103001	GTTGGTCAGGTTGGTCTCGA
181632	13828	TAAATTTCTCCCTGTAGATG	226219	58415	AGGAGTCTGGGAAGTTACCT	270806	103002	TGTTGGTCAGGTTGGTCTCG
181633	13829	TTAAATTTCTCCCTGTAGAT	226220	58416	CAGGAGTCTGGGAAGTTACC	270807	103003	CTGTTGGTCAGGTTGGTCTC
181634	13830	ATTAAATTTCTCCCTGTAGA	226221	58417	CCAGGAGTCTGGGAAGTTAC	270808	103004	CCTGTTGGTCAGGTTGGTCT
181635	13831	AATTAAATTTCTCCCTGTAG	226222	58418	CCCAGGAGTCTGGGAAGTTA	270809	103005	CCCTGTTGGTCAGGTTGGTC
181636	13832	TAATTAAATTTCTCCCTGTA	226223	58419	TCCCAGGAGTCTGGGAAGTT	270810	103006	ACCCTGTTGGTCAGGTTGGT
181637	13833	TTAATTAAATTTCTCCCTGT	226224	58420	TTCCCAGGAGTCTGGGAAGT	270811	103007	CACCCTGTTGGTCAGGTTGG
181638	13834	TTTAATTAAATTTCTCCCTG	226225	58421	ATTCCCAGGAGTCTGGGAAG	270812	103008	TCACCCTGTTGGTCAGGTTG
181639	13835	TTTTAATTAAATTTCTCCCT	226226	58422	GATTCCCAGGAGTCTGGGAA	270813	103009	TTCACCCTGTTGGTCAGGTT
181640	13836	CTTTTAATTAAATTTCTCCC	226227	58423	TGATTCCCAGGAGTCTGGGA	270814	103010	TTTCACCCTGTTGGTCAGGT
181641	13837	ACTTTTAATTAAATTTCTCC	226228	58424	ATGATTCCCAGGAGTCTGGG	270815	103011	GTTTCACCCTGTTGGTCAGG
181642	13838	CACTTTTAATTAAATTTCTC	226229	58425	TATGATTCCCAGGAGTCTGG	270816	103012	GGTTTCACCCTGTTGGTCAG
181643	13839	CCACTTTTAATTAAATTTCT	226230	58426	TTATGATTCCCAGGAGTCTG	270817	103013	AGGTTTCACCCTGTTGGTCA
181644	13840	CCCACTTTTAATTAAATTTC	226231	58427	GTTATGATTCCCAGGAGTCT	270818	103014	GAGGTTTCACCCTGTTGGTC
181645	13841	CCCCACTTTTAATTAAATTT	226232	58428	TGTTATGATTCCCAGGAGTC	270819	103015	CGAGGTTTCACCCTGTTGGT
181646	13842	GCCCCACTTTTAATTAAATT	226233	58429	GTGTTATGATTCCCAGGAGT	270820	103016	ACGAGGTTTCACCCTGTTGG
181647	13843	CGCCCCACTTTTAATTAAAT	226234	58430	GGTGTTATGATTCCCAGGAG	270821	103017	GACGAGGTTTCACCCTGTTG
181648	13844	CCGCCCCACTTTTAATTAAA	226235	58431	AGGTGTTATGATTCCCAGGA	270822	103018	AGACGAGGTTTCACCCTGTT
181649	13845	ACCGCCCCACTTTTAATTAA	226236	58432	TAGGTGTTATGATTCCCAGG	270823	103019	GAGACGAGGTTTCACCCTGT
181650	13846	AACCGCCCCACTTTTAATTA	226237	58433	ATAGGTGTTATGATTCCCAG	270824	103020	AGAGACGAGGTTTCACCCTG
181651	13847	AAACCGCCCCACTTTTAATT	226238	58434	CATAGGTGTTATGATTCCCA	270825	103021	TAGAGACGAGGTTTCACCCT
181652	13848	GAAACCGCCCCACTTTTAAT	226239	58435	TCATAGGTGTTATGATTCCC	270826	103022	GTAGAGACGAGGTTTCACCC
181653	13849	GGAAACCGCCCCACTTTTAA	226240	58436	ATCATAGGTGTTATGATTCC	270827	103023	AGTAGAGACGAGGTTTCACC
181654	13850	GGGAAACCGCCCCACTTTTA	226241	58437	CATCATAGGTGTTATGATTC	270828	103024	TAGTAGAGACGAGGTTTCAC
181655	13851	AGGGAAACCGCCCCACTTTT	226242	58438	TCATCATAGGTGTTATGATT	270829	103025	TTAGTAGAGACGAGGTTTCA
181656	13852	CAGGGAAACCGCCCCACTTT	226243	58439	ATCATCATAGGTGTTATGAT	270830	103026	TTTAGTAGAGACGAGGTTTC
181657	13853	TCAGGGAAACCGCCCCACTT	226244	58440	CATCATCATAGGTGTTATGA	270831	103027	TTTTAGTAGAGACGAGGTTT
181658	13854	CTCAGGGAAACCGCCCCACT	226245	58441	TCATCATCATAGGTGTTATG	270832	103028	TTTTTAGTAGAGACGAGGTT
181659	13855	GCTCAGGGAAACCGCCCCAC	226246	58442	ATCATCATCATAGGTGTTAT	270833	103029	ATTTTTAGTAGAGACGAGGT
181660	13856	TGCTCAGGGAAACCGCCCCA	226247	58443	CATCATCATCATAGGTGTTA	270834	103030	TATTTTTAGTAGAGACGAGG
181661	13857	TTGCTCAGGGAAACCGCCCC	226248	58444	TCATCATCATCATAGGTGTT	270835	103031	GTATTTTTAGTAGAGACGAG
181662	13858	CTTGCTCAGGGAAACCGCCC	226249	58445	ATCATCATCATCATAGGTGT	270836	103032	TGTATTTTTAGTAGAGACGA
181663	13859	CCTTGCTCAGGGAAACCGCC	226250	58446	CATCATCATCATCATAGGTG	270837	103033	TTGTATTTTTAGTAGAGACG
181664	13860	GCCTTGCTCAGGGAAACCGC	226251	58447	TCATCATCATCATCATAGGT	270838	103034	TTTGTATTTTTAGTAGAGAC
181665	13861	TGCCTTGCTCAGGGAAACCG	226252	58448	ATCATCATCATCATCATAGG	270839	103035	TTTTGTATTTTTAGTAGAGA
181666	13862	CTGCCTTGCTCAGGGAAACC	226253	58449	CATCATCATCATCATCATAG	270840	103036	TTTTTGTATTTTTAGTAGAG
181667	13863	TCTGCCTTGCTCAGGGAAAC	226254	58450	TCATCATCATCATCATCATA	270841	103037	ATTTTTGTATTTTTAGTAGA
181668	13864	GTCTGCCTTGCTCAGGGAAA	226255	58451	ATCATCATCATCATCATCAT	270842	103038	TATTTTTGTATTTTTAGTAG
181669	13865	TGTCTGCCTTGCTCAGGGAA	226256	58452	CATCATCATCATCATCATCA	270843	103039	GTATTTTTGTATTTTTAGTA
181670	13866	TTGTCTGCCTTGCTCAGGGA	226257	58453	TCATCATCATCATCATCATC	270844	103040	GGTATTTTTGTATTTTTAGT
181671	13867	TTTGTCTGCCTTGCTCAGGG	226258	58454	ATCATCATCATCATCATCAT	270845	103041	AGGTATTTTTGTATTTTTAG
181672	13868	CTTTGTCTGCCTTGCTCAGG	226259	58455	CATCATCATCATCATCATCA	270846	103042	CAGGTATTTTTGTATTTTTA
181673	13869	ACTTTGTCTGCCTTGCTCAG	226260	58456	TCATCATCATCATCATCATC	270847	103043	CCAGGTATTTTTGTATTTTT
181674	13870	GACTTTGTCTGCCTTGCTCA	226261	58457	ATCATCATCATCATCATCAT	270848	103044	CCCAGGTATTTTTGTATTTT
181675	13871	TGACTTTGTCTGCCTTGCTC	226262	58458	CATCATCATCATCATCATCA	270849	103045	GCCCAGGTATTTTTGTATTT
181676	13872	CTGACTTTGTCTGCCTTGCT	226263	58459	TCATCATCATCATCATCATC	270850	103046	CGCCCAGGTATTTTTGTATT
181677	13873	GCTGACTTTGTCTGCCTTGC	226264	58460	ATCATCATCATCATCATCAT	270851	103047	ACGCCCAGGTATTTTTGTAT
181678	13874	GGCTGACTTTGTCTGCCTTG	226265	58461	CATCATCATCATCATCATCA	270852	103048	CACGCCCAGGTATTTTTGTA
181679	13875	GGGCTGACTTTGTCTGCCTT	226266	58462	TCATCATCATCATCATCATC	270853	103049	CCACGCCCAGGTATTTTTGT
181680	13876	AGGGCTGACTTTGTCTGCCT	226267	58463	GTCATCATCATCATCATCAT	270854	103050	ACCACGCCCAGGTATTTTTG
181681	13877	GAGGGCTGACTTTGTCTGCC	226268	58464	TGTCATCATCATCATCATCA	270855	103051	CACCACGCCCAGGTATTTTT
181682	13878	AGAGGGCTGACTTTGTCTGC	226269	58465	GTGTCATCATCATCATCATC	270856	103052	CCACCACGCCCAGGTATTTT
181683	13879	TAGAGGGCTGACTTTGTCTG	226270	58466	GGTGTCATCATCATCATCAT	270857	103053	ACCACCACGCCCAGGTATTT
181684	13880	GTAGAGGGCTGACTTTGTCT	226271	58467	AGGTGTCATCATCATCATCA	270858	103054	CACCACCACGCCCAGGTATT
181685	13881	AGTAGAGGGCTGACTTTGTC	226272	58468	TAGGTGTCATCATCATCATC	270859	103055	CCACCACCACGCCCAGGTAT
181686	13882	CAGTAGAGGGCTGACTTTGT	226273	58469	GTAGGTGTCATCATCATCAT	270860	103056	ACCACCACCACGCCCAGGTA
181687	13883	ACAGTAGAGGGCTGACTTTG	226274	58470	GGTAGGTGTCATCATCATCA	270861	103057	CACCACCACCACGCCCAGGT
181688	13884	AACAGTAGAGGGCTGACTTT	226275	58471	AGGTAGGTGTCATCATCATC	270862	103058	GCACCACCACCACGCCCAGG
181689	13885	TAACAGTAGAGGGCTGACTT	226276	58472	GAGGTAGGTGTCATCATCAT	270863	103059	CGCACCACCACCACGCCCAG
181690	13886	TTAACAGTAGAGGGCTGACT	226277	58473	TGAGGTAGGTGTCATCATCA	270864	103060	GCGCACCACCACCACGCCCA
181691	13887	CTTAACAGTAGAGGGCTGAC	226278	58474	TTGAGGTAGGTGTCATCATC	270865	103061	CGCGCACCACCACCACGCCC
181692	13888	TCTTAACAGTAGAGGGCTGA	226279	58475	CTTGAGGTAGGTGTCATCAT	270866	103062	GCGCGCACCACCACCACGCC
181693	13889	TTCTTAACAGTAGAGGGCTG	226280	58476	CCTTGAGGTAGGTGTCATCA	270867	103063	GGCGCGCACCACCACCACGC
181694	13890	TTTCTTAACAGTAGAGGGCT	226281	58477	TCCTTGAGGTAGGTGTCATC	270868	103064	AGGCGCGCACCACCACCACG
181695	13891	TTTTCTTAACAGTAGAGGGC	226282	58478	ATCCTTGAGGTAGGTGTCAT	270869	103065	TAGGCGCGCACCACCACCAC
181696	13892	TTTTTCTTAACAGTAGAGGG	226283	58479	AATCCTTGAGGTAGGTGTCA	270870	103066	ATAGGCGCGCACCACCACCA
181697	13893	CTTTTTCTTAACAGTAGAGG	226284	58480	CAATCCTTGAGGTAGGTGTC	270871	103067	TATAGGCGCGCACCACCACC
181698	13894	CCTTTTTCTTAACAGTAGAG	226285	58481	GCAATCCTTGAGGTAGGTGT	270872	103068	TTATAGGCGCGCACCACCAC

181699	13895	CCCTTTTTCTTAACAGTAGA	226286	58482	GGCAATCCTTGAGGTAGGTG	270873	103069	ATTATAGGCGCGCACCACCA
181700	13896	ACCCTTTTTCTTAACAGTAG	226287	58483	GGGCAATCCTTGAGGTAGGT	270874	103070	GATTATAGGCGCGCACCACC
181701	13897	GACCCTTTTTCTTAACAGTA	226288	58484	AGGGCAATCCTTGAGGTAGG	270875	103071	GGATTATAGGCGCGCACCAC
181702	13898	TGACCCTTTTTCTTAACAGT	226289	58485	CAGGGCAATCCTTGAGGTAG	270876	103072	GGGATTATAGGCGCGCACCA
181703	13899	GTGACCCTTTTTCTTAACAG	226290	58486	TCAGGGCAATCCTTGAGGTA	270877	103073	TGGGATTATAGGCGCGCACC
181704	13900	TGTGACCCTTTTTCTTAACA	226291	58487	TTCAGGGCAATCCTTGAGGT	270878	103074	CTGGGATTATAGGCGCGCAC
181705	13901	CTGTGACCCTTTTTCTTAAC	226292	58488	CTTCAGGGCAATCCTTGAGG	270879	103075	GCTGGGATTATAGGCGCGCA
181706	13902	ACTGTGACCCTTTTTCTTAA	226293	58489	CCTTCAGGGCAATCCTTGAG	270880	103076	AGCTGGGATTATAGGCGCGC
181707	13903	CACTGTGACCCTTTTTCTTA	226294	58490	CCCTTCAGGGCAATCCTTGA	270881	103077	TAGCTGGGATTATAGGCGCG
181708	13904	TCACTGTGACCCTTTTTCTT	226295	58491	ACCCTTCAGGGCAATCCTTG	270882	103078	GTAGCTGGGATTATAGGCGC
181709	13905	CTCACTGTGACCCTTTTTCT	226296	58492	GACCCTTCAGGGCAATCCTT	270883	103079	AGTAGCTGGGATTATAGGCG
181710	13906	TCTCACTGTGACCCTTTTTC	226297	58493	TGACCCTTCAGGGCAATCCT	270884	103080	GAGTAGCTGGGATTATAGGC
181711	13907	CTCTCACTGTGACCCTTTTT	226298	58494	GTGACCCTTCAGGGCAATCC	270885	103081	TGAGTAGCTGGGATTATAGG
181712	13908	CCTCTCACTGTGACCCTTTT	226299	58495	TGTGACCCTTCAGGGCAATC	270886	103082	CTGAGTAGCTGGGATTATAG
181713	13909	CCCTCTCACTGTGACCCTTT	226300	58496	CTGTGACCCTTCAGGGCAAT	270887	103083	CCTGAGTAGCTGGGATTATA
181714	13910	CCCCTCTCACTGTGACCCTT	226301	58497	TCTGTGACCCTTCAGGGCAA	270888	103084	TCCTGAGTAGCTGGGATTAT
181715	13911	TCCCCTCTCACTGTGACCCT	226302	58498	CTCTGTGACCCTTCAGGGCA	270889	103085	CTCCTGAGTAGCTGGGATTA
181716	13912	CTCCCCTCTCACTGTGACCC	226303	58499	TCTCTGTGACCCTTCAGGGC	270890	103086	CCTCCTGAGTAGCTGGGATT
181717	13913	CCTCCCCTCTCACTGTGACC	226304	58500	ATCTCTGTGACCCTTCAGGG	270891	103087	GCCTCCTGAGTAGCTGGGAT
181718	13914	ACCTCCCCTCTCACTGTGAC	226305	58501	CATCTCTGTGACCCTTCAGG	270892	103088	AGCCTCCTGAGTAGCTGGGA
181719	13915	CACCTCCCCTCTCACTGTGA	226306	58502	GCATCTCTGTGACCCTTCAG	270893	103089	CAGCCTCCTGAGTAGCTGGG
181720	13916	TCACCTCCCCTCTCACTGTG	226307	58503	GGCATCTCTGTGACCCTTCA	270894	103090	TCAGCCTCCTGAGTAGCTGG
181721	13917	CTCACCTCCCCTCTCACTGT	226308	58504	AGGCATCTCTGTGACCCTTC	270895	103091	CTCAGCCTCCTGAGTAGCTG
181722	13918	CCTCACCTCCCCTCTCACTG	226309	58505	CAGGCATCTCTGTGACCCTT	270896	103092	CCTCAGCCTCCTGAGTAGCT
181723	13919	TCCTCACCTCCCCTCTCACT	226310	58506	GCAGGCATCTCTGTGACCCT	270897	103093	GCCTCAGCCTCCTGAGTAGC
181724	13920	CTCCTCACCTCCCCTCTCAC	226311	58507	TGCAGGCATCTCTGTGACCC	270898	103094	TGCCTCAGCCTCCTGAGTAG
181725	13921	TCTCCTCACCTCCCCTCTCA	226312	58508	TTGCAGGCATCTCTGTGACC	270899	103095	CTGCCTCAGCCTCCTGAGTA
181726	13922	GTCTCCTCACCTCCCCTCTC	226313	58509	CTTGCAGGCATCTCTGTGAC	270900	103096	CCTGCCTCAGCCTCCTGAGT
181727	13923	AGTCTCCTCACCTCCCCTCT	226314	58510	CCTTGCAGGCATCTCTGTGA	270901	103097	TCCTGCCTCAGCCTCCTGAG
181728	13924	CAGTCTCCTCACCTCCCCTC	226315	58511	GCCTTGCAGGCATCTCTGTG	270902	103098	CTCCTGCCTCAGCCTCCTGA
181729	13925	TCAGTCTCCTCACCTCCCCT	226316	58512	TGCCTTGCAGGCATCTCTGT	270903	103099	TCTCCTGCCTCAGCCTCCTG
181730	13926	CTCAGTCTCCTCACCTCCCC	226317	58513	GTGCCTTGCAGGCATCTCTG	270904	103100	TTCTCCTGCCTCAGCCTCCT
181731	13927	ACTCAGTCTCCTCACCTCCC	226318	58514	GGTGCCTTGCAGGCATCTCT	270905	103101	ATTCTCCTGCCTCAGCCTCC
181732	13928	GACTCAGTCTCCTCACCTCC	226319	58515	AGGTGCCTTGCAGGCATCTC	270906	103102	GATTCTCCTGCCTCAGCCTC
181733	13929	AGACTCAGTCTCCTCACCTC	226320	58516	CAGGTGCCTTGCAGGCATCT	270907	103103	CGATTCTCCTGCCTCAGCCT
181734	13930	CAGACTCAGTCTCCTCACCT	226321	58517	GCAGGTGCCTTGCAGGCATC	270908	103104	GCGATTCTCCTGCCTCAGCC
181735	13931	ACAGACTCAGTCTCCTCACC	226322	58518	TGCAGGTGCCTTGCAGGCAT	270909	103105	AGCGATTCTCCTGCCTCAGC
181736	13932	TACAGACTCAGTCTCCTCAC	226323	58519	ATGCAGGTGCCTTGCAGGCA	270910	103106	AAGCGATTCTCCTGCCTCAG
181737	13933	ATACAGACTCAGTCTCCTCA	226324	58520	CATGCAGGTGCCTTGCAGGC	270911	103107	CAAGCGATTCTCCTGCCTCA
181738	13934	AATACAGACTCAGTCTCCTC	226325	58521	CCATGCAGGTGCCTTGCAGG	270912	103108	TCAAGCGATTCTCCTGCCTC
181739	13935	AAATACAGACTCAGTCTCCT	226326	58522	TCCATGCAGGTGCCTTGCAG	270913	103109	TTCAAGCGATTCTCCTGCCT
181740	13936	AAAATACAGACTCAGTCTCC	226327	58523	CTCCATGCAGGTGCCTTGCA	270914	103110	GTTCAAGCGATTCTCCTGCC
181741	13937	GAAAATACAGACTCAGTCTC	226328	58524	GCTCCATGCAGGTGCCTTGC	270915	103111	GGTTCAAGCGATTCTCCTGC
181742	13938	AGAAAATACAGACTCAGTCT	226329	58525	TGCTCCATGCAGGTGCCTTG	270916	103112	GGGTTCAAGCGATTCTCCTG
181743	13939	TAGAAAATACAGACTCAGTC	226330	58526	TTGCTCCATGCAGGTGCCTT	270917	103113	TGGGTTCAAGCGATTCTCCT
181744	13940	CTAGAAAATACAGACTCAGT	226331	58527	CTTGCTCCATGCAGGTGCCT	270918	103114	CTGGGTTCAAGCGATTCTCC
181745	13941	ACTAGAAAATACAGACTCAG	226332	58528	GCTTGCTCCATGCAGGTGCC	270919	103115	CCTGGGTTCAAGCGATTCTC
181746	13942	GACTAGAAAATACAGACTCA	226333	58529	CGCTTGCTCCATGCAGGTGC	270920	103116	TCCTGGGTTCAAGCGATTCT
181747	13943	AGACTAGAAAATACAGACTC	226334	58530	GCGCTTGCTCCATGCAGGTG	270921	103117	CTCCTGGGTTCAAGCGATTC
181748	13944	CAGACTAGAAAATACAGACT	226335	58531	GGCGCTTGCTCCATGCAGGT	270922	103118	CCTCCTGGGTTCAAGCGATT
181749	13945	ACAGACTAGAAAATACAGAC	226336	58532	GGGCGCTTGCTCCATGCAGG	270923	103119	GCCTCCTGGGTTCAAGCGAT
181750	13946	AACAGACTAGAAAATACAGA	226337	58533	GGGGCGCTTGCTCCATGCAG	270924	103120	TGCCTCCTGGGTTCAAGCGA
181751	13947	CAACAGACTAGAAAATACAG	226338	58534	AGGGGCGCTTGCTCCATGCA	270925	103121	CTGCCTCCTGGGTTCAAGCG
181752	13948	CCAACAGACTAGAAAATACA	226339	58535	AAGGGGCGCTTGCTCCATGC	270926	103122	TCTGCCTCCTGGGTTCAAGC
181753	13949	CCCAACAGACTAGAAAATAC	226340	58536	GAAGGGGCGCTTGCTCCATG	270927	103123	CTCTGCCTCCTGGGTTCAAG
181754	13950	GCCCAACAGACTAGAAAATA	226341	58537	AGAAGGGGCGCTTGCTCCAT	270928	103124	CCTCTGCCTCCTGGGTTCAA
181755	13951	AGCCCAACAGACTAGAAAAT	226342	58538	GAGAAGGGGCGCTTGCTCCA	270929	103125	ACCTCTGCCTCCTGGGTTCA
181756	13952	TAGCCCAACAGACTAGAAAA	226343	58539	AGAGAAGGGGCGCTTGCTCC	270930	103126	AACCTCTGCCTCCTGGGTTC
181757	13953	GTAGCCCAACAGACTAGAAA	226344	58540	CAGAGAAGGGGCGCTTGCTC	270931	103127	CAACCTCTGCCTCCTGGGTT
181758	13954	TGTAGCCCAACAGACTAGAA	226345	58541	CCAGAGAAGGGGCGCTTGCT	270932	103128	GCAACCTCTGCCTCCTGGGT
181759	13955	GTGTAGCCCAACAGACTAGA	226346	58542	GCCAGAGAAGGGGCGCTTGC	270933	103129	TGCAACCTCTGCCTCCTGGG
181760	13956	AGTGTAGCCCAACAGACTAG	226347	58543	TGCCAGAGAAGGGGCGCTTG	270934	103130	CTGCAACCTCTGCCTCCTGG
181761	13957	TAGTGTAGCCCAACAGACTA	226348	58544	CTGCCAGAGAAGGGGCGCTT	270935	103131	ACTGCAACCTCTGCCTCCTG
181762	13958	GTAGTGTAGCCCAACAGACT	226349	58545	CCTGCCAGAGAAGGGGCGCT	270936	103132	CACTGCAACCTCTGCCTCCT
181763	13959	GGTAGTGTAGCCCAACAGAC	226350	58546	ACCTGCCAGAGAAGGGGCGC	270937	103133	TCACTGCAACCTCTGCCTCC
181764	13960	AGGTAGTGTAGCCCAACAGA	226351	58547	CACCTGCCAGAGAAGGGGCG	270938	103134	CTCACTGCAACCTCTGCCTC
181765	13961	CAGGTAGTGTAGCCCAACAG	226352	58548	GCACCTGCCAGAGAAGGGGC	270939	103135	GCTCACTGCAACCTCTGCCT
181766	13962	TCAGGTAGTGTAGCCCAACA	226353	58549	AGCACCTGCCAGAGAAGGGG	270940	103136	GGCTCACTGCAACCTCTGCC
181767	13963	ATCAGGTAGTGTAGCCCAAC	226354	58550	CAGCACCTGCCAGAGAAGGG	270941	103137	CGGCTCACTGCAACCTCTGC
181768	13964	GATCAGGTAGTGTAGCCCAA	226355	58551	CCAGCACCTGCCAGAGAAGG	270942	103138	TCGGCTCACTGCAACCTCTG
181769	13965	GGATCAGGTAGTGTAGCCCA	226356	58552	CCCAGCACCTGCCAGAGAAG	270943	103139	CTCGGCTCACTGCAACCTCT
181770	13966	GGGATCAGGTAGTGTAGCCC	226357	58553	ACCCAGCACCTGCCAGAGAA	270944	103140	TCTCGGCTCACTGCAACCTC

181771	13967	GGGGATCAGGTAGTGTAGCC	226358	58554	CACCCAGCACCTGCCAGAGA	270945	103141	ATCTCGGCTCACTGCAACCT
181772	13968	GGGGGATCAGGTAGTGTAGC	226359	58555	TCACCCAGCACCTGCCAGAG	270946	103142	TATCTCGGCTCACTGCAACC
181773	13969	AGGGGGATCAGGTAGTGTAG	226360	58556	CTCACCCAGCACCTGCCAGA	270947	103143	CTATCTCGGCTCACTGCAAC
181774	13970	AAGGGGGATCAGGTAGTGTA	226361	58557	GCTCACCCAGCACCTGCCAG	270948	103144	ACTATCTCGGCTCACTGCAA
181775	13971	GAAGGGGGATCAGGTAGTGT	226362	58558	TGCTCACCCAGCACCTGCCA	270949	103145	CACTATCTCGGCTCACTGCA
181776	13972	GGAAGGGGGATCAGGTAGTG	226363	58559	GTGCTCACCCAGCACCTGCC	270950	103146	GCACTATCTCGGCTCACTGC
181777	13973	AGGAAGGGGGATCAGGTAGT	226364	58560	AGTGCTCACCCAGCACCTGC	270951	103147	GGCACTATCTCGGCTCACTG
181778	13974	GAGGAAGGGGGATCAGGTAG	226365	58561	TAGTGCTCACCCAGCACCTG	270952	103148	TGGCACTATCTCGGCTCACT
181779	13975	TGAGGAAGGGGGATCAGGTA	226366	58562	GTAGTGCTCACCCAGCACCT	270953	103149	GTGGCACTATCTCGGCTCAC
181780	13976	TTGAGGAAGGGGGATCAGGT	226367	58563	GGTAGTGCTCACCCAGCACC	270954	103150	AGTGGCACTATCTCGGCTCA
181781	13977	TTTGAGGAAGGGGGATCAGG	226368	58564	AGGTAGTGCTCACCCAGCAC	270955	103151	CAGTGGCACTATCTCGGCTC
181782	13978	TTTTGAGGAAGGGGGATCAG	226369	58565	CAGGTAGTGCTCACCCAGCA	270956	103152	GCAGTGGCACTATCTCGGCT
181783	13979	TTTTTGAGGAAGGGGGATCA	226370	58566	GCAGGTAGTGCTCACCCAGC	270957	103153	TGCAGTGGCACTATCTCGGC
181784	13980	ATTTTTGAGGAAGGGGGATC	226371	58567	AGCAGGTAGTGCTCACCCAG	270958	103154	GTGCAGTGGCACTATCTCGG
181785	13981	GATTTTTGAGGAAGGGGGAT	226372	58568	CAGCAGGTAGTGCTCACCCA	270959	103155	AGTGCAGTGGCACTATCTCG
181786	13982	GGATTTTTGAGGAAGGGGGA	226373	58569	GCAGCAGGTAGTGCTCACCC	270960	103156	GAGTGCAGTGGCACTATCTC
181787	13983	TGGATTTTTGAGGAAGGGGG	226374	58570	GGCAGCAGGTAGTGCTCACC	270961	103157	GGAGTGCAGTGGCACTATCT
181788	13984	GTGGATTTTTGAGGAAGGGG	226375	58571	TGGCAGCAGGTAGTGCTCAC	270962	103158	TGGAGTGCAGTGGCACTATC
181789	13985	AGTGGATTTTTGAGGAAGGG	226376	58572	CTGGCAGCAGGTAGTGCTCA	270963	103159	CTGGAGTGCAGTGGCACTAT
181790	13986	AAGTGGATTTTTGAGGAAGG	226377	58573	CCTGGCAGCAGGTAGTGCTC	270964	103160	ACTGGAGTGCAGTGGCACTA
181791	13987	AAAGTGGATTTTTGAGGAAG	226378	58574	GCCTGGCAGCAGGTAGTGCT	270965	103161	AACTGGAGTGCAGTGGCACT
181792	13988	TAAAGTGGATTTTTGAGGAA	226379	58575	GGCCTGGCAGCAGGTAGTGC	270966	103162	AAACTGGAGTGCAGTGGCAC
181793	13989	GTAAAGTGGATTTTTGAGGA	226380	58576	GGGCCTGGCAGCAGGTAGTG	270967	103163	CAAACTGGAGTGCAGTGGCA
181794	13990	AGTAAAGTGGATTTTTGAGG	226381	58577	AGGGCCTGGCAGCAGGTAGT	270968	103164	TCAAACTGGAGTGCAGTGGC
181795	13991	AAGTAAAGTGGATTTTTGAG	226382	58578	CAGGGCCTGGCAGCAGGTAG	270969	103165	CTCAAACTGGAGTGCAGTGG
181796	13992	AAAGTAAAGTGGATTTTTGA	226383	58579	CCAGGGCCTGGCAGCAGGTA	270970	103166	GCTCAAACTGGAGTGCAGTG
181797	13993	GAAAGTAAAGTGGATTTTTG	226384	58580	CCCAGGGCCTGGCAGCAGGT	270971	103167	TGCTCAAACTGGAGTGCAGT
181798	13994	GGAAAGTAAAGTGGATTTTT	226385	58581	CCCCAGGGCCTGGCAGCAGG	270972	103168	TTGCTCAAACTGGAGTGCAG
181799	13995	GGGAAAGTAAAGTGGATTTT	226386	58582	GCCCCAGGGCCTGGCAGCAG	270973	103169	GTTGCTCAAACTGGAGTGCA
181800	13996	GGGGAAAGTAAAGTGGATTT	226387	58583	AGCCCCAGGGCCTGGCAGCA	270974	103170	TGTTGCTCAAACTGGAGTGC
181801	13997	TGGGGAAAGTAAAGTGGATT	226388	58584	TAGCCCCAGGGCCTGGCAGC	270975	103171	CTGTTGCTCAAACTGGAGTG
181802	13998	ATGGGGAAAGTAAAGTGGAT	226389	58585	ATAGCCCCAGGGCCTGGCAG	270976	103172	TCTGTTGCTCAAACTGGAGT
181803	13999	CATGGGGAAAGTAAAGTGGA	226390	58586	CATAGCCCCAGGGCCTGGCA	270977	103173	CTCTGTTGCTCAAACTGGAG
181804	14000	ACATGGGGAAAGTAAAGTGG	226391	58587	CCATAGCCCCAGGGCCTGGC	270978	103174	GCTCTGTTGCTCAAACTGGA
181805	14001	GACATGGGGAAAGTAAAGTG	226392	58588	GCCATAGCCCCAGGGCCTGG	270979	103175	CGCTCTGTTGCTCAAACTGG
181806	14002	AGACATGGGGAAAGTAAAGT	226393	58589	TGCCATAGCCCCAGGGCCTG	270980	103176	TCGCTCTGTTGCTCAAACTG
181807	14003	TAGACATGGGGAAAGTAAAG	226394	58590	GTGCCATAGCCCCAGGGCCT	270981	103177	CTCGCTCTGTTGCTCAAACT
181808	14004	GTAGACATGGGGAAAGTAAA	226395	58591	AGTGCCATAGCCCCAGGGCC	270982	103178	TCTCGCTCTGTTGCTCAAAC
181809	14005	TGTAGACATGGGGAAAGTAA	226396	58592	CAGTGCCATAGCCCCAGGGC	270983	103179	GTCTCGCTCTGTTGCTCAAA
181810	14006	GTGTAGACATGGGGAAAGTA	226397	58593	GCAGTGCCATAGCCCCAGGG	270984	103180	AGTCTCGCTCTGTTGCTCAA
181811	14007	GGTGTAGACATGGGGAAAGT	226398	58594	CGCAGTGCCATAGCCCCAGG	270985	103181	GAGTCTCGCTCTGTTGCTCA
181812	14008	TGGTGTAGACATGGGGAAAG	226399	58595	ACGCAGTGCCATAGCCCCAG	270986	103182	AGAGTCTCGCTCTGTTGCTC
181813	14009	TTGGTGTAGACATGGGGAAA	226400	58596	CACGCAGTGCCATAGCCCCA	270987	103183	CAGAGTCTCGCTCTGTTGCT
181814	14010	ATTGGTGTAGACATGGGGAA	226401	58597	TCACGCAGTGCCATAGCCCC	270988	103184	ACAGAGTCTCGCTCTGTTGC
181815	14011	CATTGGTGTAGACATGGGGA	226402	58598	GTCACGCAGTGCCATAGCCC	270989	103185	GACAGAGTCTCGCTCTGTTG
181816	14012	ACATTGGTGTAGACATGGGG	226403	58599	GGTCACGCAGTGCCATAGCC	270990	103186	AGACAGAGTCTCGCTCTGTT
181817	14013	CACATTGGTGTAGACATGGG	226404	58600	GGGTCACGCAGTGCCATAGC	270991	103187	GAGACAGAGTCTCGCTCTGT
181818	14014	CCACATTGGTGTAGACATGG	226405	58601	AGGGTCACGCAGTGCCATAG	270992	103188	TGAGACAGAGTCTCGCTCTG
181819	14015	ACCACATTGGTGTAGACATG	226406	58602	CAGGGTCACGCAGTGCCATA	270993	103189	TTGAGACAGAGTCTCGCTCT
181820	14016	AACCACATTGGTGTAGACAT	226407	58603	GCAGGGTCACGCAGTGCCAT	270994	103190	TTTGAGACAGAGTCTCGCTC
181821	14017	GAACCACATTGGTGTAGACA	226408	58604	TGCAGGGTCACGCAGTGCCA	270995	103191	TTTTGAGACAGAGTCTCGCT
181822	14018	TGAACCACATTGGTGTAGAC	226409	58605	TTGCAGGGTCACGCAGTGCC	270996	103192	GTTTTGAGACAGAGTCTCGC
181823	14019	GTGAACCACATTGGTGTAGA	226410	58606	CTTGCAGGGTCACGCAGTGC	270997	103193	TGTTTTGAGACAGAGTCTCG
181824	14020	TGTGAACCACATTGGTGTAG	226411	58607	ACTTGCAGGGTCACGCAGTG	270998	103194	TTGTTTTGAGACAGAGTCTC
181825	14021	GTGTGAACCACATTGGTGTA	226412	58608	GACTTGCAGGGTCACGCAGT	270999	103195	TTTGTTTTGAGACAGAGTCT
181826	14022	AGTGTGAACCACATTGGTGT	226413	58609	GGACTTGCAGGGTCACGCAG	271000	103196	TTTTGTTTTGAGACAGAGTC
181827	14023	GAGTGTGAACCACATTGGTG	226414	58610	AGGACTTGCAGGGTCACGCA	271001	103197	ATTTTGTTTTGAGACAGAGT
181828	14024	AGAGTGTGAACCACATTGGT	226415	58611	TAGGACTTGCAGGGTCACGC	271002	103198	TATTTTGTTTTGAGACAGAG
181829	14025	CAGAGTGTGAACCACATTGG	226416	58612	GTAGGACTTGCAGGGTCACG	271003	103199	TTATTTTGTTTTGAGACAGA
181830	14026	CCAGAGTGTGAACCACATTG	226417	58613	GGTAGGACTTGCAGGGTCAC	271004	103200	TTTATTTTGTTTTGAGACAG
181831	14027	CCCAGAGTGTGAACCACATT	226418	58614	AGGTAGGACTTGCAGGGTCA	271005	103201	TTTTATTTTGTTTTGAGACA
181832	14028	TCCCAGAGTGTGAACCACAT	226419	58615	CAGGTAGGACTTGCAGGGTC	271006	103202	GTTTTATTTTGTTTTGAGAC
181833	14029	GTCCCAGAGTGTGAACCACA	226420	58616	CCAGGTAGGACTTGCAGGGT	271007	103203	TGTTTTATTTTGTTTTGAGA
181834	14030	GGTCCCAGAGTGTGAACCAC	226421	58617	GCCAGGTAGGACTTGCAGGG	271008	103204	TTGTTTTATTTTGTTTTGAG
181835	14031	TGGTCCCAGAGTGTGAACCA	226422	58618	CGCCAGGTAGGACTTGCAGG	271009	103205	TTTGTTTTATTTTGTTTTGA
181836	14032	CTGGTCCCAGAGTGTGAACC	226423	58619	TCGCCAGGTAGGACTTGCAG	271010	103206	GTTTGTTTTATTTTGTTTTG
181837	14033	CCTGGTCCCAGAGTGTGAAC	226424	58620	TTCGCCAGGTAGGACTTGCA	271011	103207	GGTTTGTTTTATTTTGTTTT
181838	14034	TCCTGGTCCCAGAGTGTGAA	226425	58621	CTTCGCCAGGTAGGACTTGC	271012	103208	TGGTTTGTTTTATTTTGTTT
181839	14035	TTCCTGGTCCCAGAGTGTGA	226426	58622	GCTTCGCCAGGTAGGACTTG	271013	103209	TTGGTTTGTTTTATTTTGTT
181840	14036	TTTCCTGGTCCCAGAGTGTG	226427	58623	AGCTTCGCCAGGTAGGACTT	271014	103210	TTTGGTTTGTTTTATTTTGT
181841	14037	TTTTCCTGGTCCCAGAGTGT	226428	58624	CAGCTTCGCCAGGTAGGACT	271015	103211	TTTTGGTTTGTTTTATTTTG
181842	14038	CTTTTCCTGGTCCCAGAGTG	226429	58625	ACAGCTTCGCCAGGTAGGAC	271016	103212	TTTTTGGTTTGTTTTATTTT

181843	14039	CCTTTTCCTGGTCCCAGAGT	226430	58626	GACAGCTTCGCCAGGTAGGA	271017	103213	TTTTTTGGTTTGTTTTATTT
181844	14040	CCCTTTTCCTGGTCCCAGAG	226431	58627	CGACAGCTTCGCCAGGTAGG	271018	103214	TTTTTTTGGTTTGTTTTATT
181845	14041	CCCCTTTTCCTGGTCCCAGA	226432	58628	ACGACAGCTTCGCCAGGTAG	271019	103215	GTTTTTTTGGTTTGTTTTAT
181846	14042	CCCCCTTTTCCTGGTCCCAG	226433	58629	AACGACAGCTTCGCCAGGTA	271020	103216	GGTTTTTTTGGTTTGTTTTA
181847	14043	TCCCCCTTTTCCTGGTCCCA	226434	58630	GAACGACAGCTTCGCCAGGT	271021	103217	GGGTTTTTTTGGTTTGTTTT
181848	14044	CTCCCCCTTTTCCTGGTCCC	226435	58631	AGAACGACAGCTTCGCCAGG	271022	103218	TGGGTTTTTTTGGTTTGTTT
181849	14045	ACTCCCCCTTTTCCTGGTCC	226436	58632	AAGAACGACAGCTTCGCCAG	271023	103219	GTGGGTTTTTTTGGTTTGTT
181850	14046	CACTCCCCCTTTTCCTGGTC	226437	58633	CAAGAACGACAGCTTCGCCA	271024	103220	GGTGGGTTTTTTTGGTTTGT
181851	14047	TCACTCCCCCTTTTCCTGGT	226438	58634	ACAAGAACGACAGCTTCGCC	271025	103221	TGGTGGGTTTTTTTGGTTTG
181852	14048	ATCACTCCCCCTTTTCCTGG	226439	58635	CACAAGAACGACAGCTTCGC	271026	103222	ATGGTGGGTTTTTTTGGTTT
181853	14049	CATCACTCCCCCTTTTCCTG	226440	58636	GCACAAGAACGACAGCTTCG	271027	103223	CATGGTGGGTTTTTTTGGTT
181854	14050	CCATCACTCCCCCTTTTCCT	226441	58637	AGCACAAGAACGACAGCTTC	271028	103224	CCATGGTGGGTTTTTTTGGT
181855	14051	CCCATCACTCCCCCTTTTCC	226442	58638	GAGCACAAGAACGACAGCTT	271029	103225	GCCATGGTGGGTTTTTTTGG
181856	14052	CCCCATCACTCCCCCTTTTC	226443	58639	TGAGCACAAGAACGACAGCT	271030	103226	AGCCATGGTGGGTTTTTTTG
181857	14053	TCCCCATCACTCCCCCTTTT	226444	58640	CTGAGCACAAGAACGACAGC	271031	103227	AAGCCATGGTGGGTTTTTTT
181858	14054	TTCCCCATCACTCCCCCTTT	226445	58641	ACTGAGCACAAGAACGACAG	271032	103228	TAAGCCATGGTGGGTTTTTT
181859	14055	GTTCCCCATCACTCCCCCTT	226446	58642	GACTGAGCACAAGAACGACA	271033	103229	CTAAGCCATGGTGGGTTTTT
181860	14056	TGTTCCCCATCACTCCCCCT	226447	58643	TGACTGAGCACAAGAACGAC	271034	103230	CCTAAGCCATGGTGGGTTTT
181861	14057	CTGTTCCCCATCACTCCCCC	226448	58644	CTGACTGAGCACAAGAACGA	271035	103231	CCCTAAGCCATGGTGGGTTT
181862	14058	TCTGTTCCCCATCACTCCCC	226449	58645	ACTGACTGAGCACAAGAACG	271036	103232	GCCCTAAGCCATGGTGGGTT
181863	14059	CTCTGTTCCCCATCACTCCC	226450	58646	CACTGACTGAGCACAAGAAC	271037	103233	GGCCCTAAGCCATGGTGGGT
181864	14060	TCTCTGTTCCCCATCACTCC	226451	58647	ACACTGACTGAGCACAAGAA	271038	103234	GGGCCCTAAGCCATGGTGGG
181865	14061	TTCTCTGTTCCCCATCACTC	226452	58648	AACACTGACTGAGCACAAGA	271039	103235	TGGGCCCTAAGCCATGGTGG
181866	14062	CTTCTCTGTTCCCCATCACT	226453	58649	CAACACTGACTGAGCACAAG	271040	103236	CTGGGCCCTAAGCCATGGTG
181867	14063	CCTTCTCTGTTCCCCATCAC	226454	58650	CCAACACTGACTGAGCACAA	271041	103237	GCTGGGCCCTAAGCCATGGT
181868	14064	CCCTTCTCTGTTCCCCATCA	226455	58651	ACCAACACTGACTGAGCACA	271042	103238	GGCTGGGCCCTAAGCCATGG
181869	14065	TCCCTTCTCTGTTCCCCATC	226456	58652	AACCAACACTGACTGAGCAC	271043	103239	AGGCTGGGCCCTAAGCCATG
181870	14066	CTCCCTTCTCTGTTCCCCAT	226457	58653	CAACCAACACTGACTGAGCA	271044	103240	CAGGCTGGGCCCTAAGCCAT
181871	14067	CCTCCCTTCTCTGTTCCCCA	226458	58654	ACAACCAACACTGACTGAGC	271045	103241	TCAGGCTGGGCCCTAAGCCA
181872	14068	TCCTCCCTTCTCTGTTCCCC	226459	58655	TACAACCAACACTGACTGAG	271046	103242	ATCAGGCTGGGCCCTAAGCC
181873	14069	CTCCTCCCTTCTCTGTTCCC	226460	58656	TTACAACCAACACTGACTGA	271047	103243	CATCAGGCTGGGCCCTAAGC
181874	14070	GCTCCTCCCTTCTCTGTTCC	226461	58657	CTTACAACCAACACTGACTG	271048	103244	TCATCAGGCTGGGCCCTAAG
181875	14071	AGCTCCTCCCTTCTCTGTTC	226462	58658	TCTTACAACCAACACTGACT	271049	103245	GTCATCAGGCTGGGCCCTAA
181876	14072	GAGCTCCTCCCTTCTCTGTT	226463	58659	GTCTTACAACCAACACTGAC	271050	103246	GGTCATCAGGCTGGGCCCTA
181877	14073	TGAGCTCCTCCCTTCTCTGT	226464	58660	AGTCTTACAACCAACACTGA	271051	103247	AGGTCATCAGGCTGGGCCCT
181878	14074	GTGAGCTCCTCCCTTCTCTG	226465	58661	CAGTCTTACAACCAACACTG	271052	103248	GAGGTCATCAGGCTGGGCCC
181879	14075	TGTGAGCTCCTCCCTTCTCT	226466	58662	TCAGTCTTACAACCAACACT	271053	103249	TGAGGTCATCAGGCTGGGCC
181880	14076	GTGTGAGCTCCTCCCTTCTC	226467	58663	CTCAGTCTTACAACCAACAC	271054	103250	ATGAGGTCATCAGGCTGGGC
181881	14077	TGTGTGAGCTCCTCCCTTCT	226468	58664	TCTCAGTCTTACAACCAACA	271055	103251	AATGAGGTCATCAGGCTGGG
181882	14078	CTGTGTGAGCTCCTCCCTTC	226469	58665	TTCTCAGTCTTACAACCAAC	271056	103252	AAATGAGGTCATCAGGCTGG
181883	14079	GCTGTGTGAGCTCCTCCCTT	226470	58666	CTTCTCAGTCTTACAACCAA	271057	103253	AAAATGAGGTCATCAGGCTG
181884	14080	AGCTGTGTGAGCTCCTCCCT	226471	58667	TCTTCTCAGTCTTACAACCA	271058	103254	AAAAATGAGGTCATCAGGCT
181885	14081	CAGCTGTGTGAGCTCCTCCC	226472	58668	CTCTTCTCAGTCTTACAACC	271059	103255	GAAAAATGAGGTCATCAGGC
181886	14082	TCAGCTGTGTGAGCTCCTCC	226473	58669	ACTCTTCTCAGTCTTACAAC	271060	103256	TGAAAAATGAGGTCATCAGG
181887	14083	CTCAGCTGTGTGAGCTCCTC	226474	58670	GACTCTTCTCAGTCTTACAA	271061	103257	GTGAAAAATGAGGTCATCAG
181888	14084	CCTCAGCTGTGTGAGCTCCT	226475	58671	TGACTCTTCTCAGTCTTACA	271062	103258	AGTGAAAAATGAGGTCATCA
181889	14085	GCCTCAGCTGTGTGAGCTCC	226476	58672	GTGACTCTTCTCAGTCTTAC	271063	103259	AAGTGAAAAATGAGGTCATC
181890	14086	AGCCTCAGCTGTGTGAGCTC	226477	58673	AGTGACTCTTCTCAGTCTTA	271064	103260	TAAGTGAAAAATGAGGTCAT
181891	14087	CAGCCTCAGCTGTGTGAGCT	226478	58674	AAGTGACTCTTCTCAGTCTT	271065	103261	CTAAGTGAAAAATGAGGTCA
181892	14088	CCAGCCTCAGCTGTGTGAGC	226479	58675	GAAGTGACTCTTCTCAGTCT	271066	103262	ACTAAGTGAAAAATGAGGTC
181893	14089	CCCAGCCTCAGCTGTGTGAG	226480	58676	TGAAGTGACTCTTCTCAGTC	271067	103263	GACTAAGTGAAAAATGAGGT
181894	14090	CCCCAGCCTCAGCTGTGTGA	226481	58677	ATGAAGTGACTCTTCTCAGT	271068	103264	TGACTAAGTGAAAAATGAGG
181895	14091	ACCCCAGCCTCAGCTGTGTG	226482	58678	AATGAAGTGACTCTTCTCAG	271069	103265	GTGACTAAGTGAAAAATGAG
181896	14092	AACCCCAGCCTCAGCTGTGT	226483	58679	AAATGAAGTGACTCTTCTCA	271070	103266	GGTGACTAAGTGAAAAATGA
181897	14093	TAACCCCAGCCTCAGCTGTG	226484	58680	AAAATGAAGTGACTCTTCTC	271071	103267	AGGTGACTAAGTGAAAAATG
181898	14094	ATAACCCCAGCCTCAGCTGT	226485	58681	CAAAATGAAGTGACTCTTCT	271072	103268	GAGGTGACTAAGTGAAAAAT
181899	14095	CATAACCCCAGCCTCAGCTG	226486	58682	GCAAAATGAAGTGACTCTTC	271073	103269	AGAGGTGACTAAGTGAAAAA
181900	14096	GCATAACCCCAGCCTCAGCT	226487	58683	AGCAAAATGAAGTGACTCTT	271074	103270	GAGAGGTGACTAAGTGAAAA
181901	14097	TGCATAACCCCAGCCTCAGC	226488	58684	GAGCAAAATGAAGTGACTCT	271075	103271	AGAGAGGTGACTAAGTGAAA
181902	14098	ATGCATAACCCCAGCCTCAG	226489	58685	AGAGCAAAATGAAGTGACTC	271076	103272	TAGAGAGGTGACTAAGTGAA
181903	14099	TATGCATAACCCCAGCCTCA	226490	58686	GAGAGCAAAATGAAGTGACT	271077	103273	TTAGAGAGGTGACTAAGTGA
181904	14100	ATATGCATAACCCCAGCCTC	226491	58687	GGAGAGCAAAATGAAGTGAC	271078	103274	TTTAGAGAGGTGACTAAGTG
181905	14101	GATATGCATAACCCCAGCCT	226492	58688	TGGAGAGCAAAATGAAGTGA	271079	103275	CTTTAGAGAGGTGACTAAGT
181906	14102	CGATATGCATAACCCCAGCC	226493	58689	CTGGAGAGCAAAATGAAGTG	271080	103276	CCTTTAGAGAGGTGACTAAG
181907	14103	TCGATATGCATAACCCCAGC	226494	58690	CCTGGAGAGCAAAATGAAGT	271081	103277	GCCTTTAGAGAGGTGACTAA
181908	14104	TTCGATATGCATAACCCCAG	226495	58691	CCCTGGAGAGCAAAATGAAG	271082	103278	GGCCTTTAGAGAGGTGACTA
181909	14105	ATTCGATATGCATAACCCCA	226496	58692	TCCCTGGAGAGCAAAATGAA	271083	103279	GGGCCTTTAGAGAGGTGACT
181910	14106	AATTCGATATGCATAACCCC	226497	58693	GTCCCTGGAGAGCAAAATGA	271084	103280	AGGGCCTTTAGAGAGGTGAC
181911	14107	TAATTCGATATGCATAACCC	226498	58694	TGTCCCTGGAGAGCAAAATG	271085	103281	CAGGGCCTTTAGAGAGGTGA
181912	14108	GTAATTCGATATGCATAACC	226499	58695	ATGTCCCTGGAGAGCAAAAT	271086	103282	ACAGGGCCTTTAGAGAGGTG
181913	14109	AGTAATTCGATATGCATAAC	226500	58696	GATGTCCCTGGAGAGCAAAA	271087	103283	GACAGGGCCTTTAGAGAGGT
181914	14110	AAGTAATTCGATATGCATAA	226501	58697	AGATGTCCCTGGAGAGCAAA	271088	103284	AGACAGGGCCTTTAGAGAGG

181915	14111	TAAGTAATTCGATATGCATA	226502	58698	AAGATGTCCCTGGAGAGCAA	271089	103285	GAGACAGGGCCTTTAGAGAG
181916	14112	CTAAGTAATTCGATATGCAT	226503	58699	AAAGATGTCCCTGGAGAGCA	271090	103286	GGAGACAGGGCCTTTAGAGA
181917	14113	TCTAAGTAATTCGATATGCA	226504	58700	GAAAGATGTCCCTGGAGAGC	271091	103287	TGGAGACAGGGCCTTTAGAG
181918	14114	TTCTAAGTAATTCGATATGC	226505	58701	AGAAAGATGTCCCTGGAGAG	271092	103288	TTGGAGACAGGGCCTTTAGA
181919	14115	ATTCTAAGTAATTCGATATG	226506	58702	CAGAAAGATGTCCCTGGAGA	271093	103289	TTTGGAGACAGGGCCTTTAG
181920	14116	AATTCTAAGTAATTCGATAT	226507	58703	CCAGAAAGATGTCCCTGGAG	271094	103290	ATTTGGAGACAGGGCCTTTA
181921	14117	AAATTCTAAGTAATTCGATA	226508	58704	CCCAGAAAGATGTCCCTGGA	271095	103291	TATTTGGAGACAGGGCCTTT
181922	14118	CAAATTCTAAGTAATTCGAT	226509	58705	ACCCAGAAAGATGTCCCTGG	271096	103292	CTATTTGGAGACAGGGCCTT
181923	14119	GCAAATTCTAAGTAATTCGA	226510	58706	GACCCAGAAAGATGTCCCTG	271097	103293	TCTATTTGGAGACAGGGCCT
181924	14120	TGCAAATTCTAAGTAATTCG	226511	58707	GGACCCAGAAAGATGTCCCT	271098	103294	CTCTATTTGGAGACAGGGCC
181925	14121	TTGCAAATTCTAAGTAATTC	226512	58708	AGGACCCAGAAAGATGTCCC	271099	103295	ACTCTATTTGGAGACAGGGC
181926	14122	GTTGCAAATTCTAAGTAATT	226513	58709	TAGGACCCAGAAAGATGTCC	271100	103296	GACTCTATTTGGAGACAGGG
181927	14123	GGTTGCAAATTCTAAGTAAT	226514	58710	ATAGGACCCAGAAAGATGTC	271101	103297	TGACTCTATTTGGAGACAGG
181928	14124	AGGTTGCAAATTCTAAGTAA	226515	58711	AATAGGACCCAGAAAGATGT	271102	103298	GTGACTCTATTTGGAGACAG
181929	14125	GAGGTTGCAAATTCTAAGTA	226516	58712	AAATAGGACCCAGAAAGATG	271103	103299	TGTGACTCTATTTGGAGACA
181930	14126	TGAGGTTGCAAATTCTAAGT	226517	58713	AAAATAGGACCCAGAAAGAT	271104	103300	ATGTGACTCTATTTGGAGAC
181931	14127	GTGAGGTTGCAAATTCTAAG	226518	58714	GAAAATAGGACCCAGAAAGA	271105	103301	AATGTGACTCTATTTGGAGA
181932	14128	TGTGAGGTTGCAAATTCTAA	226519	58715	AGAAAATAGGACCCAGAAAG	271106	103302	GAATGTGACTCTATTTGGAG
181933	14129	CTGTGAGGTTGCAAATTCTA	226520	58716	CAGAAAATAGGACCCAGAAA	271107	103303	AGAATGTGACTCTATTTGGA
181934	14130	CCTGTGAGGTTGCAAATTCT	226521	58717	GCAGAAAATAGGACCCAGAA	271108	103304	TAGAATGTGACTCTATTTGG
181935	14131	CCCTGTGAGGTTGCAAATTC	226522	58718	GGCAGAAAATAGGACCCAGA	271109	103305	TTAGAATGTGACTCTATTTG
181936	14132	ACCCTGTGAGGTTGCAAATT	226523	58719	AGGCAGAAAATAGGACCCAG	271110	103306	CTTAGAATGTGACTCTATTT
181937	14133	TACCCTGTGAGGTTGCAAAT	226524	58720	TAGGCAGAAAATAGGACCCA	271111	103307	CCTTAGAATGTGACTCTATT
181938	14134	GTACCCTGTGAGGTTGCAAA	226525	58721	ATAGGCAGAAAATAGGACCC	271112	103308	ACCTTAGAATGTGACTCTAT
181939	14135	AGTACCCTGTGAGGTTGCAA	226526	58722	CATAGGCAGAAAATAGGACC	271113	103309	TACCTTAGAATGTGACTCTA
181940	14136	AAGTACCCTGTGAGGTTGCA	226527	58723	ACATAGGCAGAAAATAGGAC	271114	103310	GTACCTTAGAATGTGACTCT
181941	14137	AAAGTACCCTGTGAGGTTGC	226528	58724	GACATAGGCAGAAAATAGGA	271115	103311	CGTACCTTAGAATGTGACTC
181942	14138	GAAAGTACCCTGTGAGGTTG	226529	58725	TGACATAGGCAGAAAATAGG	271116	103312	CCGTACCTTAGAATGTGACT
181943	14139	TGAAAGTACCCTGTGAGGTT	226530	58726	TTGACATAGGCAGAAAATAG	271117	103313	CCCGTACCTTAGAATGTGAC
181944	14140	ATGAAAGTACCCTGTGAGGT	226531	58727	CTTGACATAGGCAGAAAATA	271118	103314	CCCCGTACCTTAGAATGTGA
181945	14141	CATGAAAGTACCCTGTGAGG	226532	58728	ACTTGACATAGGCAGAAAAT	271119	103315	CCCCCGTACCTTAGAATGTG
181946	14142	CCATGAAAGTACCCTGTGAG	226533	58729	TACTTGACATAGGCAGAAAA	271120	103316	ACCCCCGTACCTTAGAATGT
181947	14143	GCCATGAAAGTACCCTGTGA	226534	58730	CTACTTGACATAGGCAGAAA	271121	103317	CACCCCCGTACCTTAGAATG
181948	14144	CGCCATGAAAGTACCCTGTG	226535	58731	GCTACTTGACATAGGCAGAA	271122	103318	ACACCCCCGTACCTTAGAAT
181949	14145	ACGCCATGAAAGTACCCTGT	226536	58732	CGCTACTTGACATAGGCAGA	271123	103319	AACACCCCCGTACCTTAGAA
181950	14146	AACGCCATGAAAGTACCCTG	226537	58733	GCGCTACTTGACATAGGCAG	271124	103320	CAACACCCCCGTACCTTAGA
181951	14147	CAACGCCATGAAAGTACCCT	226538	58734	GGCGCTACTTGACATAGGCA	271125	103321	CCAACACCCCCGTACCTTAG
181952	14148	TCAACGCCATGAAAGTACCC	226539	58735	AGGCGCTACTTGACATAGGC	271126	103322	CCCAACACCCCCGTACCTTA
181953	14149	TTCAACGCCATGAAAGTACC	226540	58736	GAGGCGCTACTTGACATAGG	271127	103323	CCCCAACACCCCCGTACCTT
181954	14150	TTTCAACGCCATGAAAGTAC	226541	58737	TGAGGCGCTACTTGACATAG	271128	103324	TCCCCAACACCCCCGTACCT
181955	14151	ATTTCAACGCCATGAAAGTA	226542	58738	TTGAGGCGCTACTTGACATA	271129	103325	CTCCCCAACACCCCCGTACC
181956	14152	TATTTCAACGCCATGAAAGT	226543	58739	CTTGAGGCGCTACTTGACAT	271130	103326	CCTCCCCAACACCCCCGTAC
181957	14153	GTATTTCAACGCCATGAAAG	226544	58740	CCTTGAGGCGCTACTTGACA	271131	103327	CCCTCCCCAACACCCCCGTA
181958	14154	TGTATTTCAACGCCATGAAA	226545	58741	TCCTTGAGGCGCTACTTGAC	271132	103328	CCCCTCCCCAACACCCCCGT
181959	14155	GTGTATTTCAACGCCATGAA	226546	58742	ATCCTTGAGGCGCTACTTGA	271133	103329	CCCCCTCCCCAACACCCCCG
181960	14156	AGTGTATTTCAACGCCATGA	226547	58743	CATCCTTGAGGCGCTACTTG	271134	103330	CCCCCCTCCCCAACACCCCC
181961	14157	AAGTGTATTTCAACGCCATG	226548	58744	GCATCCTTGAGGCGCTACTT	271135	103331	ACCCCCCTCCCCAACACCCC
181962	14158	GAAGTGTATTTCAACGCCAT	226549	58745	AGCATCCTTGAGGCGCTACT	271136	103332	AACCCCCCTCCCCAACACCC
181963	14159	GGAAGTGTATTTCAACGCCA	226550	58746	GAGCATCCTTGAGGCGCTAC	271137	103333	TAACCCCCCTCCCCAACACC
181964	14160	GGGAAGTGTATTTCAACGCC	226551	58747	GGAGCATCCTTGAGGCGCTA	271138	103334	CTAACCCCCCTCCCCAACAC
181965	14161	TGGGAAGTGTATTTCAACGC	226552	58748	AGGAGCATCCTTGAGGCGCT	271139	103335	CCTAACCCCCCTCCCCAACA
181966	14162	GTGGGAAGTGTATTTCAACG	226553	58749	CAGGAGCATCCTTGAGGCGC	271140	103336	CCCTAACCCCCCTCCCCAAC
181967	14163	TGTGGGAAGTGTATTTCAAC	226554	58750	TCAGGAGCATCCTTGAGGCG	271141	103337	GCCCTAACCCCCCTCCCCAA
181968	14164	CTGTGGGAAGTGTATTTCAA	226555	58751	TTCAGGAGCATCCTTGAGGC	271142	103338	AGCCCTAACCCCCCTCCCCA
181969	14165	GCTGTGGGAAGTGTATTTCA	226556	58752	TTTCAGGAGCATCCTTGAGG	271143	103339	AAGCCCTAACCCCCCTCCCC
181970	14166	GGCTGTGGGAAGTGTATTTC	226557	58753	TTTTCAGGAGCATCCTTGAG	271144	103340	GAAGCCCTAACCCCCCTCCC
181971	14167	TGGCTGTGGGAAGTGTATTT	226558	58754	ATTTTCAGGAGCATCCTTGA	271145	103341	TGAAGCCCTAACCCCCCTCC
181972	14168	GTGGCTGTGGGAAGTGTATT	226559	58755	CATTTTCAGGAGCATCCTTG	271146	103342	TTGAAGCCCTAACCCCCCTC
181973	14169	GGTGGCTGTGGGAAGTGTAT	226560	58756	CCATTTTCAGGAGCATCCTT	271147	103343	GTTGAAGCCCTAACCCCCCT
181974	14170	GGGTGGCTGTGGGAAGTGTA	226561	58757	CCCATTTTCAGGAGCATCCT	271148	103344	TGTTGAAGCCCTAACCCCCC
181975	14171	AGGGTGGCTGTGGGAAGTGT	226562	58758	GCCCATTTTCAGGAGCATCC	271149	103345	ATGTTGAAGCCCTAACCCCC
181976	14172	GAGGGTGGCTGTGGGAAGTG	226563	58759	AGCCCATTTTCAGGAGCATC	271150	103346	CATGTTGAAGCCCTAACCCC
181977	14173	GGAGGGTGGCTGTGGGAAGT	226564	58760	AAGCCCATTTTCAGGAGCAT	271151	103347	ACATGTTGAAGCCCTAACCC
181978	14174	GGGAGGGTGGCTGTGGGAAG	226565	58761	CAAGCCCATTTTCAGGAGCA	271152	103348	CACATGTTGAAGCCCTAACC
181979	14175	AGGGAGGGTGGCTGTGGGAA	226566	58762	ACAAGCCCATTTTCAGGAGC	271153	103349	TCACATGTTGAAGCCCTAAC
181980	14176	GAGGGAGGGTGGCTGTGGGA	226567	58763	GACAAGCCCATTTTCAGGAG	271154	103350	TTCACATGTTGAAGCCCTAA
181981	14177	AGAGGGAGGGTGGCTGTGGG	226568	58764	AGACAAGCCCATTTTCAGGA	271155	103351	ATTCACATGTTGAAGCCCTA
181982	14178	TAGAGGGAGGGTGGCTGTGG	226569	58765	AAGACAAGCCCATTTTCAGG	271156	103352	AATTCACATGTTGAAGCCCT
181983	14179	TTAGAGGGAGGGTGGCTGTG	226570	58766	AAAGACAAGCCCATTTTCAG	271157	103353	AAATTCACATGTTGAAGCCC
181984	14180	GTTAGAGGGAGGGTGGCTGT	226571	58767	GAAAGACAAGCCCATTTTCA	271158	103354	CAAATTCACATGTTGAAGCC
181985	14181	AGTTAGAGGGAGGGTGGCTG	226572	58768	AGAAAGACAAGCCCATTTTC	271159	103355	GCAAATTCACATGTTGAAGC
181986	14182	TAGTTAGAGGGAGGGTGGCT	226573	58769	AAGAAAGACAAGCCCATTTT	271160	103356	CGCAAATTCACATGTTGAAG

181987	14183	TTAGTTAGAGGGAGGGTGGC	226574	58770	TAAGAAAGACAAGCCCATTT	271161	103357	CCGCAAATTCACATGTTGAA
181988	14184	TTTAGTTAGAGGGAGGGTGG	226575	58771	TTAAGAAAGACAAGCCCATT	271162	103358	CCCGCAAATTCACATGTTGA
181989	14185	TTTTAGTTAGAGGGAGGGTG	226576	58772	GTTAAGAAAGACAAGCCCAT	271163	103359	CCCCGCAAATTCACATGTTG
181990	14186	CTTTTAGTTAGAGGGAGGGT	226577	58773	TGTTAAGAAAGACAAGCCCA	271164	103360	TCCCCGCAAATTCACATGTT
181991	14187	GCTTTTAGTTAGAGGGAGGG	226578	58774	ATGTTAAGAAAGACAAGCCC	271165	103361	GTCCCCGCAAATTCACATGT
181992	14188	TGCTTTTAGTTAGAGGGAGG	226579	58775	CATGTTAAGAAAGACAAGCC	271166	103362	GGTCCCCGCAAATTCACATG
181993	14189	TTGCTTTTAGTTAGAGGGAG	226580	58776	CCATGTTAAGAAAGACAAGC	271167	103363	TGGTCCCCGCAAATTCACAT
181994	14190	CTTGCTTTTAGTTAGAGGGA	226581	58777	GCCATGTTAAGAAAGACAAG	271168	103364	GTGGTCCCCGCAAATTCACA
181995	14191	TCTTGCTTTTAGTTAGAGGG	226582	58778	TGCCATGTTAAGAAAGACAA	271169	103365	TGTGGTCCCCGCAAATTCAC
181996	14192	CTCTTGCTTTTAGTTAGAGG	226583	58779	CTGCCATGTTAAGAAAGACA	271170	103366	TTGTGGTCCCCGCAAATTCA
181997	14193	ACTCTTGCTTTTAGTTAGAG	226584	58780	CCTGCCATGTTAAGAAAGAC	271171	103367	ATTGTGGTCCCCGCAAATTC
181998	14194	GACTCTTGCTTTTAGTTAGA	226585	58781	ACCTGCCATGTTAAGAAAGA	271172	103368	AATTGTGGTCCCCGCAAATT
181999	14195	TGACTCTTGCTTTTAGTTAG	226586	58782	TACCTGCCATGTTAAGAAAG	271173	103369	GAATTGTGGTCCCCGCAAAT
182000	14196	ATGACTCTTGCTTTTAGTTA	226587	58783	CTACCTGCCATGTTAAGAAA	271174	103370	TGAATTGTGGTCCCCGCAAA
182001	14197	AATGACTCTTGCTTTTAGTT	226588	58784	CCTACCTGCCATGTTAAGAA	271175	103371	CTGAATTGTGGTCCCCGCAA
182002	14198	AAATGACTCTTGCTTTTAGT	226589	58785	ACCTACCTGCCATGTTAAGA	271176	103372	GCTGAATTGTGGTCCCCGCA
182003	14199	GAAATGACTCTTGCTTTTAG	226590	58786	GACCTACCTGCCATGTTAAG	271177	103373	GGCTGAATTGTGGTCCCCGC
182004	14200	AGAAATGACTCTTGCTTTTA	226591	58787	GGACCTACCTGCCATGTTAA	271178	103374	GGGCTGAATTGTGGTCCCCG
182005	14201	GAGAAATGACTCTTGCTTTT	226592	58788	GGGACCTACCTGCCATGTTA	271179	103375	TGGGCTGAATTGTGGTCCCC
182006	14202	TGAGAAATGACTCTTGCTTT	226593	58789	TGGGACCTACCTGCCATGTT	271180	103376	CTGGGCTGAATTGTGGTCCC
182007	14203	CTGAGAAATGACTCTTGCTT	226594	58790	TTGGGACCTACCTGCCATGT	271181	103377	CCTGGGCTGAATTGTGGTCC
182008	14204	ACTGAGAAATGACTCTTGCT	226595	58791	TTTGGGACCTACCTGCCATG	271182	103378	TCCTGGGCTGAATTGTGGTC
182009	14205	AACTGAGAAATGACTCTTGC	226596	58792	CTTTGGGACCTACCTGCCAT	271183	103379	GTCCTGGGCTGAATTGTGGT
182010	14206	GAACTGAGAAATGACTCTTG	226597	58793	GCTTTGGGACCTACCTGCCA	271184	103380	GGTCCTGGGCTGAATTGTGG
182011	14207	AGAACTGAGAAATGACTCTT	226598	58794	TGCTTTGGGACCTACCTGCC	271185	103381	GGGTCCTGGGCTGAATTGTG
182012	14208	CAGAACTGAGAAATGACTCT	226599	58795	ATGCTTTGGGACCTACCTGC	271186	103382	GGGGTCCTGGGCTGAATTGT
182013	14209	CCAGAACTGAGAAATGACTC	226600	58796	AATGCTTTGGGACCTACCTG	271187	103383	CGGGGTCCTGGGCTGAATTG
182014	14210	ACCAGAACTGAGAAATGACT	226601	58797	TAATGCTTTGGGACCTACCT	271188	103384	GCGGGGTCCTGGGCTGAATT
182015	14211	GACCAGAACTGAGAAATGAC	226602	58798	CTAATGCTTTGGGACCTACC	271189	103385	AGCGGGGTCCTGGGCTGAAT
182016	14212	AGACCAGAACTGAGAAATGA	226603	58799	GCTAATGCTTTGGGACCTAC	271190	103386	GAGCGGGGTCCTGGGCTGAA
182017	14213	AAGACCAGAACTGAGAAATG	226604	58800	TGCTAATGCTTTGGGACCTA	271191	103387	GGAGCGGGGTCCTGGGCTGA
182018	14214	CAAGACCAGAACTGAGAAAT	226605	58801	ATGCTAATGCTTTGGGACCT	271192	103388	GGGAGCGGGGTCCTGGGCTG
182019	14215	GCAAGACCAGAACTGAGAAA	226606	58802	CATGCTAATGCTTTGGGACC	271193	103389	CGGGAGCGGGGTCCTGGGCT
182020	14216	GGCAAGACCAGAACTGAGAA	226607	58803	CCATGCTAATGCTTTGGGAC	271194	103390	GCGGGAGCGGGGTCCTGGGC
182021	14217	AGGCAAGACCAGAACTGAGA	226608	58804	CCCATGCTAATGCTTTGGGA	271195	103391	GGCGGGAGCGGGGTCCTGGG
182022	14218	GAGGCAAGACCAGAACTGAG	226609	58805	CCCCATGCTAATGCTTTGGG	271196	103392	TGGCGGGAGCGGGGTCCTGG
182023	14219	GGAGGCAAGACCAGAACTGA	226610	58806	GCCCCATGCTAATGCTTTGG	271197	103393	GTGGCGGGAGCGGGGTCCTG
182024	14220	GGGAGGCAAGACCAGAACTG	226611	58807	TGCCCCATGCTAATGCTTTG	271198	103394	GGTGGCGGGAGCGGGGTCCT
182025	14221	TGGGAGGCAAGACCAGAACT	226612	58808	CTGCCCCATGCTAATGCTTT	271199	103395	GGGTGGCGGGAGCGGGGTCC
182026	14222	GTGGGAGGCAAGACCAGAAC	226613	58809	GCTGCCCCATGCTAATGCTT	271200	103396	TGGGTGGCGGGAGCGGGGTC
182027	14223	CGTGGGAGGCAAGACCAGAA	226614	58810	AGCTGCCCCATGCTAATGCT	271201	103397	CTGGGTGGCGGGAGCGGGGT
182028	14224	ACGTGGGAGGCAAGACCAGA	226615	58811	CAGCTGCCCCATGCTAATGC	271202	103398	GCTGGGTGGCGGGAGCGGGG
182029	14225	AACGTGGGAGGCAAGACCAG	226616	58812	TCAGCTGCCCCATGCTAATG	271203	103399	TGCTGGGTGGCGGGAGCGGG
182030	14226	GAACGTGGGAGGCAAGACCA	226617	58813	GTCAGCTGCCCCATGCTAAT	271204	103400	GTGCTGGGTGGCGGGAGCGG
182031	14227	AGAACGTGGGAGGCAAGACC	226618	58814	GGTCAGCTGCCCCATGCTAA	271205	103401	AGTGCTGGGTGGCGGGAGCG
182032	14228	GAGAACGTGGGAGGCAAGAC	226619	58815	AGGTCAGCTGCCCCATGCTA	271206	103402	CAGTGCTGGGTGGCGGGAGC
182033	14229	GGAGAACGTGGGAGGCAAGA	226620	58816	TAGGTCAGCTGCCCCATGCT	271207	103403	CCAGTGCTGGGTGGCGGGAG
182034	14230	AGGAGAACGTGGGAGGCAAG	226621	58817	CTAGGTCAGCTGCCCCATGC	271208	103404	CCCAGTGCTGGGTGGCGGGA
182035	14231	GAGGAGAACGTGGGAGGCAA	226622	58818	GCTAGGTCAGCTGCCCCATG	271209	103405	CCCCAGTGCTGGGTGGCGGG
182036	14232	GGAGGAGAACGTGGGAGGCA	226623	58819	GGCTAGGTCAGCTGCCCCAT	271210	103406	TCCCCAGTGCTGGGTGGCGG
182037	14233	TGGAGGAGAACGTGGGAGGC	226624	58820	GGGCTAGGTCAGCTGCCCCA	271211	103407	CTCCCCAGTGCTGGGTGGCG
182038	14234	GTGGAGGAGAACGTGGGAGG	226625	58821	TGGGCTAGGTCAGCTGCCCC	271212	103408	GCTCCCCAGTGCTGGGTGGC
182039	14235	TGTGGAGGAGAACGTGGGAG	226626	58822	CTGGGCTAGGTCAGCTGCCC	271213	103409	AGCTCCCCAGTGCTGGGTGG
182040	14236	ATGTGGAGGAGAACGTGGGA	226627	58823	GCTGGGCTAGGTCAGCTGCC	271214	103410	CAGCTCCCCAGTGCTGGGTG
182041	14237	AATGTGGAGGAGAACGTGGG	226628	58824	GGCTGGGCTAGGTCAGCTGC	271215	103411	CCAGCTCCCCAGTGCTGGGT
182042	14238	AAATGTGGAGGAGAACGTGG	226629	58825	TGGCTGGGCTAGGTCAGCTG	271216	103412	CCCAGCTCCCCAGTGCTGGG
182043	14239	TAAATGTGGAGGAGAACGTG	226630	58826	TTGGCTGGGCTAGGTCAGCT	271217	103413	CCCCAGCTCCCCAGTGCTGG
182044	14240	TTAAATGTGGAGGAGAACGT	226631	58827	ATTGGCTGGGCTAGGTCAGC	271218	103414	TCCCCAGCTCCCCAGTGCTG
182045	14241	CTTAAATGTGGAGGAGAACG	226632	58828	CATTGGCTGGGCTAGGTCAG	271219	103415	TTCCCCAGCTCCCCAGTGCT
182046	14242	TCTTAAATGTGGAGGAGAAC	226633	58829	GCATTGGCTGGGCTAGGTCA	271220	103416	CTTCCCCAGCTCCCCAGTGC
182047	14243	TTCTTAAATGTGGAGGAGAA	226634	58830	TGCATTGGCTGGGCTAGGTC	271221	103417	CCTTCCCCAGCTCCCCAGTG
182048	14244	TTTCTTAAATGTGGAGGAGA	226635	58831	CTGCATTGGCTGGGCTAGGT	271222	103418	CCCTTCCCCAGCTCCCCAGT
182049	14245	TTTTCTTAAATGTGGAGGAG	226636	58832	ACTGCATTGGCTGGGCTAGG	271223	103419	ACCCTTCCCCAGCTCCCCAG
182050	14246	ATTTTCTTAAATGTGGAGGA	226637	58833	CACTGCATTGGCTGGGCTAG	271224	103420	CACCCTTCCCCAGCTCCCCA
182051	14247	GATTTTCTTAAATGTGGAGG	226638	58834	GCACTGCATTGGCTGGGCTA	271225	103421	TCACCCTTCCCCAGCTCCCC
182052	14248	GGATTTTCTTAAATGTGGAG	226639	58835	TGCACTGCATTGGCTGGGCT	271226	103422	TTCACCCTTCCCCAGCTCCC
182053	14249	TGGATTTTCTTAAATGTGGA	226640	58836	CTGCACTGCATTGGCTGGGC	271227	103423	CTTCACCCTTCCCCAGCTCC
182054	14250	GTGGATTTTCTTAAATGTGG	226641	58837	ACTGCACTGCATTGGCTGGG	271228	103424	TCTTCACCCTTCCCCAGCTC
182055	14251	GGTGGATTTTCTTAAATGTG	226642	58838	CACTGCACTGCATTGGCTGG	271229	103425	CTCTTCACCCTTCCCCAGCT
182056	14252	TGGTGGATTTTCTTAAATGT	226643	58839	TCACTGCACTGCATTGGCTG	271230	103426	CCTCTTCACCCTTCCCCAGC
182057	14253	CTGGTGGATTTTCTTAAATG	226644	58840	GTCACTGCACTGCATTGGCT	271231	103427	TCCTCTTCACCCTTCCCCAG
182058	14254	GCTGGTGGATTTTCTTAAAT	226645	58841	AGTCACTGCACTGCATTGGC	271232	103428	CTCCTCTTCACCCTTCCCCA

182059	14255	AGCTGGTGGATTTTCTTAAA	226646	58842	GAGTCACTGCACTGCATTGG	271233	103429	CCTCCTCTTCACCCTTCCCC
182060	14256	TAGCTGGTGGATTTTCTTAA	226647	58843	AGAGTCACTGCACTGCATTG	271234	103430	GCCTCCTCTTCACCCTTCCC
182061	14257	GTAGCTGGTGGATTTTCTTA	226648	58844	AAGAGTCACTGCACTGCATT	271235	103431	AGCCTCCTCTTCACCCTTCC
182062	14258	TGTAGCTGGTGGATTTTCTT	226649	58845	CAAGAGTCACTGCACTGCAT	271236	103432	CAGCCTCCTCTTCACCCTTC
182063	14259	TTGTAGCTGGTGGATTTTCT	226650	58846	GCAAGAGTCACTGCACTGCA	271237	103433	CCAGCCTCCTCTTCACCCTT
182064	14260	TTTGTAGCTGGTGGATTTTC	226651	58847	TGCAAGAGTCACTGCACTGC	271238	103434	CCCAGCCTCCTCTTCACCCT
182065	14261	CTTTGTAGCTGGTGGATTTT	226652	58848	TTGCAAGAGTCACTGCACTG	271239	103435	CCCCAGCCTCCTCTTCACCC
182066	14262	ACTTTGTAGCTGGTGGATTT	226653	58849	GTTGCAAGAGTCACTGCACT	271240	103436	CCCCCAGCCTCCTCTTCACC
182067	14263	CACTTTGTAGCTGGTGGATT	226654	58850	GGTTGCAAGAGTCACTGCAC	271241	103437	ACCCCCAGCCTCCTCTTCAC
182068	14264	TCACTTTGTAGCTGGTGGAT	226655	58851	CGGTTGCAAGAGTCACTGCA	271242	103438	CACCCCCAGCCTCCTCTTCA
182069	14265	TTCACTTTGTAGCTGGTGGA	226656	58852	TCGGTTGCAAGAGTCACTGC	271243	103439	TCACCCCCAGCCTCCTCTTC
182070	14266	CTTCACTTTGTAGCTGGTGG	226657	58853	CTCGGTTGCAAGAGTCACTG	271244	103440	CTCACCCCCAGCCTCCTCTT
182071	14267	TCTTCACTTTGTAGCTGGTG	226658	58854	ACTCGGTTGCAAGAGTCACT	271245	103441	TCTCACCCCCAGCCTCCTCT
182072	14268	ATCTTCACTTTGTAGCTGGT	226659	58855	GACTCGGTTGCAAGAGTCAC	271246	103442	TTCTCACCCCCAGCCTCCTC
182073	14269	TATCTTCACTTTGTAGCTGG	226660	58856	AGACTCGGTTGCAAGAGTCA	271247	103443	CTTCTCACCCCCAGCCTCCT
182074	14270	GTATCTTCACTTTGTAGCTG	226661	58857	TAGACTCGGTTGCAAGAGTC	271248	103444	CCTTCTCACCCCCAGCCTCC
182075	14271	GGTATCTTCACTTTGTAGCT	226662	58858	TTAGACTCGGTTGCAAGAGT	271249	103445	TCCTTCTCACCCCCAGCCTC
182076	14272	TGGTATCTTCACTTTGTAGC	226663	58859	ATTAGACTCGGTTGCAAGAG	271250	103446	GTCCTTCTCACCCCCAGCCT
182077	14273	ATGGTATCTTCACTTTGTAG	226664	58860	GATTAGACTCGGTTGCAAGA	271251	103447	GGTCCTTCTCACCCCCAGCC
182078	14274	TATGGTATCTTCACTTTGTA	226665	58861	TGATTAGACTCGGTTGCAAG	271252	103448	TGGTCCTTCTCACCCCCAGC
182079	14275	ATATGGTATCTTCACTTTGT	226666	58862	CTGATTAGACTCGGTTGCAA	271253	103449	GTGGTCCTTCTCACCCCCAG
182080	14276	CATATGGTATCTTCACTTTG	226667	58863	TCTGATTAGACTCGGTTGCA	271254	103450	TGTGGTCCTTCTCACCCCCA
182081	14277	ACATATGGTATCTTCACTTT	226668	58864	TTCTGATTAGACTCGGTTGC	271255	103451	CTGTGGTCCTTCTCACCCCC
182082	14278	CACATATGGTATCTTCACTT	226669	58865	CTTCTGATTAGACTCGGTTG	271256	103452	GCTGTGGTCCTTCTCACCCC
182083	14279	TCACATATGGTATCTTCACT	226670	58866	CCTTCTGATTAGACTCGGTT	271257	103453	AGCTGTGGTCCTTCTCACCC
182084	14280	ATCACATATGGTATCTTCAC	226671	58867	ACCTTCTGATTAGACTCGGT	271258	103454	GAGCTGTGGTCCTTCTCACC
182085	14281	TATCACATATGGTATCTTCA	226672	58868	GACCTTCTGATTAGACTCGG	271259	103455	TGAGCTGTGGTCCTTCTCAC
182086	14282	ATATCACATATGGTATCTTC	226673	58869	GGACCTTCTGATTAGACTCG	271260	103456	GTGAGCTGTGGTCCTTCTCA
182087	14283	GATATCACATATGGTATCTT	226674	58870	TGGACCTTCTGATTAGACTC	271261	103457	AGTGAGCTGTGGTCCTTCTC
182088	14284	GGATATCACATATGGTATCT	226675	58871	ATGGACCTTCTGATTAGACT	271262	103458	GAGTGAGCTGTGGTCCTTCT
182089	14285	GGGATATCACATATGGTATC	226676	58872	CATGGACCTTCTGATTAGAC	271263	103459	AGAGTGAGCTGTGGTCCTTC
182090	14286	TGGGATATCACATATGGTAT	226677	58873	TCATGGACCTTCTGATTAGA	271264	103460	CAGAGTGAGCTGTGGTCCTT
182091	14287	GTGGGATATCACATATGGTA	226678	58874	TTCATGGACCTTCTGATTAG	271265	103461	TCAGAGTGAGCTGTGGTCCT
182092	14288	GGTGGGATATCACATATGGT	226679	58875	GTTCATGGACCTTCTGATTA	271266	103462	CTCAGAGTGAGCTGTGGTCC
182093	14289	GGGTGGGATATCACATATGG	226680	58876	GGTTCATGGACCTTCTGATT	271267	103463	CCTCAGAGTGAGCTGTGGTC
182094	14290	AGGGTGGGATATCACATATG	226681	58877	AGGTTCATGGACCTTCTGAT	271268	103464	GCCTCAGAGTGAGCTGTGGT
182095	14291	TAGGGTGGGATATCACATAT	226682	58878	TAGGTTCATGGACCTTCTGA	271269	103465	AGCCTCAGAGTGAGCTGTGG
182096	14292	CTAGGGTGGGATATCACATA	226683	58879	GTAGGTTCATGGACCTTCTG	271270	103466	CAGCCTCAGAGTGAGCTGTG
182097	14293	ACTAGGGTGGGATATCACAT	226684	58880	CGTAGGTTCATGGACCTTCT	271271	103467	GCAGCCTCAGAGTGAGCTGT
182098	14294	AACTAGGGTGGGATATCACA	226685	58881	TCGTAGGTTCATGGACCTTC	271272	103468	TGCAGCCTCAGAGTGAGCTG
182099	14295	AAACTAGGGTGGGATATCAC	226686	58882	CTCGTAGGTTCATGGACCTT	271273	103469	CTGCAGCCTCAGAGTGAGCT
182100	14296	GAAACTAGGGTGGGATATCA	226687	58883	GCTCGTAGGTTCATGGACCT	271274	103470	TCTGCAGCCTCAGAGTGAGC
182101	14297	AGAAACTAGGGTGGGATATC	226688	58884	TGCTCGTAGGTTCATGGACC	271275	103471	ATCTGCAGCCTCAGAGTGAG
182102	14298	CAGAAACTAGGGTGGGATAT	226689	58885	ATGCTCGTAGGTTCATGGAC	271276	103472	CATCTGCAGCCTCAGAGTGA
182103	14299	ACAGAAACTAGGGTGGGATA	226690	58886	AATGCTCGTAGGTTCATGGA	271277	103473	ACATCTGCAGCCTCAGAGTG
182104	14300	AACAGAAACTAGGGTGGGAT	226691	58887	AAATGCTCGTAGGTTCATGG	271278	103474	CACATCTGCAGCCTCAGAGT
182105	14301	AAACAGAAACTAGGGTGGGA	226692	58888	GAAATGCTCGTAGGTTCATG	271279	103475	GCACATCTGCAGCCTCAGAG
182106	14302	AAAACAGAAACTAGGGTGGG	226693	58889	GGAAATGCTCGTAGGTTCAT	271280	103476	AGCACATCTGCAGCCTCAGA
182107	14303	TAAAACAGAAACTAGGGTGG	226694	58890	AGGAAATGCTCGTAGGTTCA	271281	103477	CAGCACATCTGCAGCCTCAG
182108	14304	ATAAAACAGAAACTAGGGTG	226695	58891	CAGGAAATGCTCGTAGGTTC	271282	103478	CCAGCACATCTGCAGCCTCA
182109	14305	GATAAAACAGAAACTAGGGT	226696	58892	ACAGGAAATGCTCGTAGGTT	271283	103479	CCCAGCACATCTGCAGCCTC
182110	14306	TGATAAAACAGAAACTAGGG	226697	58893	GACAGGAAATGCTCGTAGGT	271284	103480	GCCCAGCACATCTGCAGCCT
182111	14307	CTGATAAAACAGAAACTAGG	226698	58894	GGACAGGAAATGCTCGTAGG	271285	103481	GGCCCAGCACATCTGCAGCC
182112	14308	CCTGATAAAACAGAAACTAG	226699	58895	GGGACAGGAAATGCTCGTAG	271286	103482	AGGCCCAGCACATCTGCAGC
182113	14309	CCCTGATAAAACAGAAACTA	226700	58896	TGGGACAGGAAATGCTCGTA	271287	103483	AAGGCCCAGCACATCTGCAG
182114	14310	ACCCTGATAAAACAGAAACT	226701	58897	CTGGGACAGGAAATGCTCGT	271288	103484	GAAGGCCCAGCACATCTGCA
182115	14311	AACCCTGATAAAACAGAAAC	226702	58898	CCTGGGACAGGAAATGCTCG	271289	103485	AGAAGGCCCAGCACATCTGC
182116	14312	AAACCCTGATAAAACAGAAA	226703	58899	TCCTGGGACAGGAAATGCTC	271290	103486	CAGAAGGCCCAGCACATCTG
182117	14313	CAAACCCTGATAAAACAGAA	226704	58900	ATCCTGGGACAGGAAATGCT	271291	103487	CCAGAAGGCCCAGCACATCT
182118	14314	CCAAACCCTGATAAAACAGA	226705	58901	GATCCTGGGACAGGAAATGC	271292	103488	CCCAGAAGGCCCAGCACATC
182119	14315	TCCAAACCCTGATAAAACAG	226706	58902	TGATCCTGGGACAGGAAATG	271293	103489	GCCCAGAAGGCCCAGCACAT
182120	14316	CTCCAAACCCTGATAAAACA	226707	58903	CTGATCCTGGGACAGGAAAT	271294	103490	TGCCCAGAAGGCCCAGCACA
182121	14317	GCTCCAAACCCTGATAAAAC	226708	58904	CCTGATCCTGGGACAGGAAA	271295	103491	GTGCCCAGAAGGCCCAGCAC
182122	14318	TGCTCCAAACCCTGATAAAA	226709	58905	CCCTGATCCTGGGACAGGAA	271296	103492	AGTGCCCAGAAGGCCCAGCA
182123	14319	CTGCTCCAAACCCTGATAAA	226710	58906	ACCCTGATCCTGGGACAGGA	271297	103493	CAGTGCCCAGAAGGCCCAGC
182124	14320	CCTGCTCCAAACCCTGATAA	226711	58907	CACCCTGATCCTGGGACAGG	271298	103494	CCAGTGCCCAGAAGGCCCAG
182125	14321	ACCTGCTCCAAACCCTGATA	226712	58908	CCACCCTGATCCTGGGACAG	271299	103495	CCCAGTGCCCAGAAGGCCCA
182126	14322	CACCTGCTCCAAACCCTGAT	226713	58909	TCCACCCTGATCCTGGGACA	271300	103496	GCCCAGTGCCCAGAAGGCCC
182127	14323	CCACCTGCTCCAAACCCTGA	226714	58910	CTCCACCCTGATCCTGGGAC	271301	103497	GGCCCAGTGCCCAGAAGGCC
182128	14324	TCCACCTGCTCCAAACCCTG	226715	58911	CCTCCACCCTGATCCTGGGA	271302	103498	AGGCCCAGTGCCCAGAAGGC
182129	14325	CTCCACCTGCTCCAAACCCT	226716	58912	GCCTCCACCCTGATCCTGGG	271303	103499	GAGGCCCAGTGCCCAGAAGG
182130	14326	GCTCCACCTGCTCCAAACCC	226717	58913	AGCCTCCACCCTGATCCTGG	271304	103500	CGAGGCCCAGTGCCCAGAAG

182131	14327	TGCTCCACCTGCTCCAAACC	226718	58914	CAGCCTCCACCCTGATCCTG	271305	103501	CCGAGGCCCAGTGCCCAGAA
182132	14328	CTGCTCCACCTGCTCCAAAC	226719	58915	TCAGCCTCCACCCTGATCCT	271306	103502	CCCGAGGCCCAGTGCCCAGA
182133	14329	CCTGCTCCACCTGCTCCAAA	226720	58916	CTCAGCCTCCACCCTGATCC	271307	103503	CCCCGAGGCCCAGTGCCCAG
182134	14330	GCCTGCTCCACCTGCTCCAA	226721	58917	GCTCAGCCTCCACCCTGATC	271308	103504	TCCCCGAGGCCCAGTGCCCA
182135	14331	TGCCTGCTCCACCTGCTCCA	226722	58918	GGCTCAGCCTCCACCCTGAT	271309	103505	CTCCCCGAGGCCCAGTGCCC
182136	14332	CTGCCTGCTCCACCTGCTCC	226723	58919	AGGCTCAGCCTCCACCCTGA	271310	103506	GCTCCCCGAGGCCCAGTGCC
182137	14333	TCTGCCTGCTCCACCTGCTC	226724	58920	GAGGCTCAGCCTCCACCCTG	271311	103507	AGCTCCCCGAGGCCCAGTGC
182138	14334	CTCTGCCTGCTCCACCTGCT	226725	58921	GGAGGCTCAGCCTCCACCCT	271312	103508	TAGCTCCCCGAGGCCCAGTG
182139	14335	CCTCTGCCTGCTCCACCTGC	226726	58922	GGGAGGCTCAGCCTCCACCC	271313	103509	CTAGCTCCCCGAGGCCCAGT
182140	14336	CCCTCTGCCTGCTCCACCTG	226727	58923	AGGGAGGCTCAGCCTCCACC	271314	103510	CCTAGCTCCCCGAGGCCCAG
182141	14337	TCCCTCTGCCTGCTCCACCT	226728	58924	CAGGGAGGCTCAGCCTCCAC	271315	103511	CCCTAGCTCCCCGAGGCCCA
182142	14338	ATCCCTCTGCCTGCTCCACC	226729	58925	GCAGGGAGGCTCAGCCTCCA	271316	103512	CCCCTAGCTCCCCGAGGCCC
182143	14339	GATCCCTCTGCCTGCTCCAC	226730	58926	AGCAGGGAGGCTCAGCCTCC	271317	103513	CCCCCTAGCTCCCCGAGGCC
182144	14340	TGATCCCTCTGCCTGCTCCA	226731	58927	AAGCAGGGAGGCTCAGCCTC	271318	103514	GCCCCCTAGCTCCCCGAGGC
182145	14341	ATGATCCCTCTGCCTGCTCC	226732	58928	TAAGCAGGGAGGCTCAGCCT	271319	103515	AGCCCCCTAGCTCCCCGAGG
182146	14342	AATGATCCCTCTGCCTGCTC	226733	58929	CTAAGCAGGGAGGCTCAGCC	271320	103516	AAGCCCCCTAGCTCCCCGAG
182147	14343	AAATGATCCCTCTGCCTGCT	226734	58930	TCTAAGCAGGGAGGCTCAGC	271321	103517	AAAGCCCCCTAGCTCCCCGA
182148	14344	GAAATGATCCCTCTGCCTGC	226735	58931	CTCTAAGCAGGGAGGCTCAG	271322	103518	GAAAGCCCCCTAGCTCCCCG
182149	14345	TGAAATGATCCCTCTGCCTG	226736	58932	TCTCTAAGCAGGGAGGCTCA	271323	103519	AGAAAGCCCCCTAGCTCCCC
182150	14346	CTGAAATGATCCCTCTGCCT	226737	58933	ATCTCTAAGCAGGGAGGCTC	271324	103520	CAGAAAGCCCCCTAGCTCCC
182151	14347	GCTGAAATGATCCCTCTGCC	226738	58934	AATCTCTAAGCAGGGAGGCT	271325	103521	CCAGAAAGCCCCCTAGCTCC
182152	14348	GGCTGAAATGATCCCTCTGC	226739	58935	GAATCTCTAAGCAGGGAGGC	271326	103522	TCCAGAAAGCCCCCTAGCTC
182153	14349	AGGCTGAAATGATCCCTCTG	226740	58936	AGAATCTCTAAGCAGGGAGG	271327	103523	TTCCAGAAAGCCCCCTAGCT
182154	14350	TAGGCTGAAATGATCCCTCT	226741	58937	AAGAATCTCTAAGCAGGGAG	271328	103524	GTTCCAGAAAGCCCCCTAGC
182155	14351	ATAGGCTGAAATGATCCCTC	226742	58938	GAAGAATCTCTAAGCAGGGA	271329	103525	GGTTCCAGAAAGCCCCCTAG
182156	14352	TATAGGCTGAAATGATCCCT	226743	58939	GGAAGAATCTCTAAGCAGGG	271330	103526	GGGTTCCAGAAAGCCCCCTA
182157	14353	TTATAGGCTGAAATGATCCC	226744	58940	GGGAAGAATCTCTAAGCAGG	271331	103527	AGGGTTCCAGAAAGCCCCCT
182158	14354	TTTATAGGCTGAAATGATCC	226745	58941	TGGGAAGAATCTCTAAGCAG	271332	103528	CAGGGTTCCAGAAAGCCCCC
182159	14355	ATTTATAGGCTGAAATGATC	226746	58942	ATGGGAAGAATCTCTAAGCA	271333	103529	CCAGGGTTCCAGAAAGCCCC
182160	14356	AATTTATAGGCTGAAATGAT	226747	58943	CATGGGAAGAATCTCTAAGC	271334	103530	CCCAGGGTTCCAGAAAGCCC
182161	14357	CAATTTATAGGCTGAAATGA	226748	58944	GCATGGGAAGAATCTCTAAG	271335	103531	GCCCAGGGTTCCAGAAAGCC
182162	14358	ACAATTTATAGGCTGAAATG	226749	58945	TGCATGGGAAGAATCTCTAA	271336	103532	GGCCCAGGGTTCCAGAAAGC
182163	14359	TACAATTTATAGGCTGAAAT	226750	58946	ATGCATGGGAAGAATCTCTA	271337	103533	AGGCCCAGGGTTCCAGAAAG
182164	14360	ATACAATTTATAGGCTGAAA	226751	58947	AATGCATGGGAAGAATCTCT	271338	103534	CAGGCCCAGGGTTCCAGAAA
182165	14361	AATACAATTTATAGGCTGAA	226752	58948	GAATGCATGGGAAGAATCTC	271339	103535	GCAGGCCCAGGGTTCCAGAA
182166	14362	TAATACAATTTATAGGCTGA	226753	58949	GGAATGCATGGGAAGAATCT	271340	103536	CGCAGGCCCAGGGTTCCAGA
182167	14363	TTAATACAATTTATAGGCTG	226754	58950	TGGAATGCATGGGAAGAATC	271341	103537	ACGCAGGCCCAGGGTTCCAG
182168	14364	CTTAATACAATTTATAGGCT	226755	58951	GTGGAATGCATGGGAAGAAT	271342	103538	CACGCAGGCCCAGGGTTCCA
182169	14365	CCTTAATACAATTTATAGGC	226756	58952	AGTGGAATGCATGGGAAGAA	271343	103539	ACACGCAGGCCCAGGGTTCC
182170	14366	CCCTTAATACAATTTATAGG	226757	58953	AAGTGGAATGCATGGGAAGA	271344	103540	GACACGCAGGCCCAGGGTTC
182171	14367	ACCCTTAATACAATTTATAG	226758	58954	AAAGTGGAATGCATGGGAAG	271345	103541	TGACACGCAGGCCCAGGGTT
182172	14368	CACCCTTAATACAATTTATA	226759	58955	AAAAGTGGAATGCATGGGAA	271346	103542	CTGACACGCAGGCCCAGGGT
182173	14369	TCACCCTTAATACAATTTAT	226760	58956	AAAAAGTGGAATGCATGGGA	271347	103543	GCTGACACGCAGGCCCAGGG
182174	14370	CTCACCCTTAATACAATTTA	226761	58957	AAAAAAGTGGAATGCATGGG	271348	103544	AGCTGACACGCAGGCCCAGG
182175	14371	ACTCACCCTTAATACAATTT	226762	58958	GAAAAAAGTGGAATGCATGG	271349	103545	AAGCTGACACGCAGGCCCAG
182176	14372	TACTCACCCTTAATACAATT	226763	58959	GGAAAAAAGTGGAATGCATG	271350	103546	CAAGCTGACACGCAGGCCCA
182177	14373	GTACTCACCCTTAATACAAT	226764	58960	GGGAAAAAAGTGGAATGCAT	271351	103547	GCAAGCTGACACGCAGGCCC
182178	14374	AGTACTCACCCTTAATACAA	226765	58961	GGGGAAAAAAGTGGAATGCA	271352	103548	GGCAAGCTGACACGCAGGCC
182179	14375	CAGTACTCACCCTTAATACA	226766	58962	TGGGGAAAAAAGTGGAATGC	271353	103549	AGGCAAGCTGACACGCAGGC
182180	14376	TCAGTACTCACCCTTAATAC	226767	58963	TTGGGGAAAAAAGTGGAATG	271354	103550	GAGGCAAGCTGACACGCAGG
182181	14377	CTCAGTACTCACCCTTAATA	226768	58964	TTTGGGGAAAAAAGTGGAAT	271355	103551	GGAGGCAAGCTGACACGCAG
182182	14378	ACTCAGTACTCACCCTTAAT	226769	58965	TTTTGGGGAAAAAAGTGGAA	271356	103552	GGGAGGCAAGCTGACACGCA
182183	14379	GACTCAGTACTCACCCTTAA	226770	58966	CTTTTGGGGAAAAAAGTGGA	271357	103553	GGGGAGGCAAGCTGACACGC
182184	14380	TGACTCAGTACTCACCCTTA	226771	58967	TCTTTTGGGGAAAAAAGTGG	271358	103554	GGGGGAGGCAAGCTGACACG
182185	14381	ATGACTCAGTACTCACCCTT	226772	58968	TTCTTTTGGGGAAAAAAGTG	271359	103555	TGGGGGAGGCAAGCTGACAC
182186	14382	AATGACTCAGTACTCACCCT	226773	58969	TTTCTTTTGGGGAAAAAAGT	271360	103556	GTGGGGGAGGCAAGCTGACA
182187	14383	GAATGACTCAGTACTCACCC	226774	58970	TTTTCTTTTGGGGAAAAAAG	271361	103557	CGTGGGGGAGGCAAGCTGAC
182188	14384	AGAATGACTCAGTACTCACC	226775	58971	ATTTTCTTTTGGGGAAAAAA	271362	103558	GCGTGGGGGAGGCAAGCTGA
182189	14385	AAGAATGACTCAGTACTCAC	226776	58972	TATTTTCTTTTGGGGAAAAA	271363	103559	TGCGTGGGGGAGGCAAGCTG
182190	14386	GAAGAATGACTCAGTACTCA	226777	58973	ATATTTTCTTTTGGGGAAAA	271364	103560	CTGCGTGGGGGAGGCAAGCT
182191	14387	TGAAGAATGACTCAGTACTC	226778	58974	AATATTTTCTTTTGGGGAAA	271365	103561	CCTGCGTGGGGGAGGCAAGC
182192	14388	TTGAAGAATGACTCAGTACT	226779	58975	CAATATTTTCTTTTGGGGAA	271366	103562	GCCTGCGTGGGGGAGGCAAG
182193	14389	CTTGAAGAATGACTCAGTAC	226780	58976	TCAATATTTTCTTTTGGGGA	271367	103563	CGCCTGCGTGGGGGAGGCAA
182194	14390	TCTTGAAGAATGACTCAGTA	226781	58977	GTCAATATTTTCTTTTGGGG	271368	103564	GCGCCTGCGTGGGGGAGGCA
182195	14391	TTCTTGAAGAATGACTCAGT	226782	58978	GGTCAATATTTTCTTTTGGG	271369	103565	AGCGCCTGCGTGGGGGAGGC
182196	14392	TTTCTTGAAGAATGACTCAG	226783	58979	GGGTCAATATTTTCTTTTGG	271370	103566	GAGCGCCTGCGTGGGGGAGG
182197	14393	TTTTCTTGAAGAATGACTCA	226784	58980	AGGGTCAATATTTTCTTTTG	271371	103567	AGAGCGCCTGCGTGGGGGAG
182198	14394	CTTTTCTTGAAGAATGACTC	226785	58981	AAGGGTCAATATTTTCTTTT	271372	103568	GAGAGCGCCTGCGTGGGGGA
182199	14395	ACTTTTCTTGAAGAATGACT	226786	58982	CAAGGGTCAATATTTTCTTT	271373	103569	GGAGAGCGCCTGCGTGGGGG
182200	14396	AACTTTTCTTGAAGAATGAC	226787	58983	TCAAGGGTCAATATTTTCTT	271374	103570	TGGAGAGCGCCTGCGTGGGG
182201	14397	AAACTTTTCTTGAAGAATGA	226788	58984	CTCAAGGGTCAATATTTTCT	271375	103571	GTGGAGAGCGCCTGCGTGGG
182202	14398	AAAACTTTTCTTGAAGAATG	226789	58985	TCTCAAGGGTCAATATTTTC	271376	103572	TGTGGAGAGCGCCTGCGTGG

182203	14399	TAAAACTTTTCTTGAAGAAT	226790	58986	CTCTCAAGGGTCAATATTTT	271377	103573	GTGTGGAGAGCGCCTGCGTG
182204	14400	CTAAAACTTTTCTTGAAGAA	226791	58987	CCTCTCAAGGGTCAATATTT	271378	103574	GGTGTGGAGAGCGCCTGCGT
182205	14401	TCTAAAACTTTTCTTGAAGA	226792	58988	GCCTCTCAAGGGTCAATATT	271379	103575	TGGTGTGGAGAGCGCCTGCG
182206	14402	TTCTAAAACTTTTCTTGAAG	226793	58989	TGCCTCTCAAGGGTCAATAT	271380	103576	ATGGTGTGGAGAGCGCCTGC
182207	14403	CTTCTAAAACTTTTCTTGAA	226794	58990	GTGCCTCTCAAGGGTCAATA	271381	103577	AATGGTGTGGAGAGCGCCTG
182208	14404	GCTTCTAAAACTTTTCTTGA	226795	58991	TGTGCCTCTCAAGGGTCAAT	271382	103578	CAATGGTGTGGAGAGCGCCT
182209	14405	TGCTTCTAAAACTTTTCTTG	226796	58992	GTGTGCCTCTCAAGGGTCAA	271383	103579	TCAATGGTGTGGAGAGCGCC
182210	14406	ATGCTTCTAAAACTTTTCTT	226797	58993	TGTGTGCCTCTCAAGGGTCA	271384	103580	TTCAATGGTGTGGAGAGCGC
182211	14407	GATGCTTCTAAAACTTTTCT	226798	58994	CTGTGTGCCTCTCAAGGGTC	271385	103581	CTTCAATGGTGTGGAGAGCG
182212	14408	GGATGCTTCTAAAACTTTTC	226799	58995	ACTGTGTGCCTCTCAAGGGT	271386	103582	ACTTCAATGGTGTGGAGAGC
182213	14409	TGGATGCTTCTAAAACTTTT	226800	58996	AACTGTGTGCCTCTCAAGGG	271387	103583	AACTTCAATGGTGTGGAGAG
182214	14410	TTGGATGCTTCTAAAACTTT	226801	58997	AAACTGTGTGCCTCTCAAGG	271388	103584	GAACTTCAATGGTGTGGAGA
182215	14411	TTTGGATGCTTCTAAAACTT	226802	58998	TAAACTGTGTGCCTCTCAAG	271389	103585	AGAACTTCAATGGTGTGGAG
182216	14412	TTTTGGATGCTTCTAAAACT	226803	58999	ATAAACTGTGTGCCTCTCAA	271390	103586	AAGAACTTCAATGGTGTGGA
182217	14413	GTTTTGGATGCTTCTAAAAC	226804	59000	AATAAACTGTGTGCCTCTCA	271391	103587	TAAGAACTTCAATGGTGTGG
182218	14414	AGTTTTGGATGCTTCTAAAA	226805	59001	AAATAAACTGTGTGCCTCTC	271392	103588	ATAAGAACTTCAATGGTGTG
182219	14415	CAGTTTTGGATGCTTCTAAA	226806	59002	TAAATAAACTGTGTGCCTCT	271393	103589	GATAAGAACTTCAATGGTGT
182220	14416	TCAGTTTTGGATGCTTCTAA	226807	59003	ATAAATAAACTGTGTGCCTC	271394	103590	TGATAAGAACTTCAATGGTG
182221	14417	TTCAGTTTTGGATGCTTCTA	226808	59004	AATAAATAAACTGTGTGCCT	271395	103591	GTGATAAGAACTTCAATGGT
182222	14418	CTTCAGTTTTGGATGCTTCT	226809	59005	AAATAAATAAACTGTGTGCC	271396	103592	AGTGATAAGAACTTCAATGG
182223	14419	CCTTCAGTTTTGGATGCTTC	226810	59006	AAAATAAATAAACTGTGTGC	271397	103593	AAGTGATAAGAACTTCAATG
182224	14420	CCCTTCAGTTTTGGATGCTT	226811	59007	CAAAATAAATAAACTGTGTG	271398	103594	CAAGTGATAAGAACTTCAAT
182225	14421	ACCCTTCAGTTTTGGATGCT	226812	59008	GCAAAATAAATAAACTGTGT	271399	103595	CCAAGTGATAAGAACTTCAA
182226	14422	CACCCTTCAGTTTTGGATGC	226813	59009	TGCAAAATAAATAAACTGTG	271400	103596	CCCAAGTGATAAGAACTTCA
182227	14423	CCACCCTTCAGTTTTGGATG	226814	59010	ATGCAAAATAAATAAACTGT	271401	103597	ACCCAAGTGATAAGAACTTC
182228	14424	TCCACCCTTCAGTTTTGGAT	226815	59011	TATGCAAAATAAATAAACTG	271402	103598	GACCCAAGTGATAAGAACTT
182229	14425	CTCCACCCTTCAGTTTTGGA	226816	59012	CTATGCAAAATAAATAAACT	271403	103599	AGACCCAAGTGATAAGAACT
182230	14426	GCTCCACCCTTCAGTTTTGG	226817	59013	ACTATGCAAAATAAATAAAC	271404	103600	CAGACCCAAGTGATAAGAAC
182231	14427	GGCTCCACCCTTCAGTTTTG	226818	59014	TACTATGCAAAATAAATAAA	271405	103601	TCAGACCCAAGTGATAAGAA
182232	14428	TGGCTCCACCCTTCAGTTTT	226819	59015	TTACTATGCAAAATAAATAA	271406	103602	CTCAGACCCAAGTGATAAGA
182233	14429	GTGGCTCCACCCTTCAGTTT	226820	59016	TTTACTATGCAAAATAAATA	271407	103603	GCTCAGACCCAAGTGATAAG
182234	14430	GGTGGCTCCACCCTTCAGTT	226821	59017	ATTTACTATGCAAAATAAAT	271408	103604	GGCTCAGACCCAAGTGATAA
182235	14431	AGGTGGCTCCACCCTTCAGT	226822	59018	TATTTACTATGCAAAATAAA	271409	103605	AGGCTCAGACCCAAGTGATA
182236	14432	CAGGTGGCTCCACCCTTCAG	226823	59019	CTATTTACTATGCAAAATAA	271410	103606	CAGGCTCAGACCCAAGTGAT
182237	14433	CCAGGTGGCTCCACCCTTCA	226824	59020	ACTATTTACTATGCAAAATA	271411	103607	CCAGGCTCAGACCCAAGTGA
182238	14434	TCCAGGTGGCTCCACCCTTC	226825	59021	TACTATTTACTATGCAAAAT	271412	103608	CCCAGGCTCAGACCCAAGTG
182239	14435	CTCCAGGTGGCTCCACCCTT	226826	59022	CTACTATTTACTATGCAAAA	271413	103609	CCCCAGGCTCAGACCCAAGT
182240	14436	TCTCCAGGTGGCTCCACCCT	226827	59023	GCTACTATTTACTATGCAAA	271414	103610	GCCCCAGGCTCAGACCCAAG
182241	14437	GTCTCCAGGTGGCTCCACCC	226828	59024	GGCTACTATTTACTATGCAA	271415	103611	TGCCCCAGGCTCAGACCCAA
182242	14438	TGTCTCCAGGTGGCTCCACC	226829	59025	AGGCTACTATTTACTATGCA	271416	103612	ATGCCCCAGGCTCAGACCCA
182243	14439	CTGTCTCCAGGTGGCTCCAC	226830	59026	CAGGCTACTATTTACTATGC	271417	103613	AATGCCCCAGGCTCAGACCC
182244	14440	ACTGTCTCCAGGTGGCTCCA	226831	59027	ACAGGCTACTATTTACTATG	271418	103614	AAATGCCCCAGGCTCAGACC
182245	14441	TACTGTCTCCAGGTGGCTCC	226832	59028	TACAGGCTACTATTTACTAT	271419	103615	CAAATGCCCCAGGCTCAGAC
182246	14442	ATACTGTCTCCAGGTGGCTC	226833	59029	ATACAGGCTACTATTTACTA	271420	103616	CCAAATGCCCCAGGCTCAGA
182247	14443	GATACTGTCTCCAGGTGGCT	226834	59030	AATACAGGCTACTATTTACT	271421	103617	TCCAAATGCCCCAGGCTCAG
182248	14444	TGATACTGTCTCCAGGTGGC	226835	59031	AAATACAGGCTACTATTTAC	271422	103618	GTCCAAATGCCCCAGGCTCA
182249	14445	ATGATACTGTCTCCAGGTGG	226836	59032	AAAATACAGGCTACTATTTA	271423	103619	CGTCCAAATGCCCCAGGCTC
182250	14446	GATGATACTGTCTCCAGGTG	226837	59033	TAAAATACAGGCTACTATTT	271424	103620	CCGTCCAAATGCCCCAGGCT
182251	14447	TGATGATACTGTCTCCAGGT	226838	59034	TTAAAATACAGGCTACTATT	271425	103621	TCCGTCCAAATGCCCCAGGC
182252	14448	CTGATGATACTGTCTCCAGG	226839	59035	CTTAAAATACAGGCTACTAT	271426	103622	CTCCGTCCAAATGCCCCAGG
182253	14449	ACTGATGATACTGTCTCCAG	226840	59036	CCTTAAAATACAGGCTACTA	271427	103623	CCTCCGTCCAAATGCCCCAG
182254	14450	GACTGATGATACTGTCTCCA	226841	59037	TCCTTAAAATACAGGCTACT	271428	103624	CCCTCCGTCCAAATGCCCCA
182255	14451	GGACTGATGATACTGTCTCC	226842	59038	ATCCTTAAAATACAGGCTAC	271429	103625	ACCCTCCGTCCAAATGCCCC
182256	14452	AGGACTGATGATACTGTCTC	226843	59039	CATCCTTAAAATACAGGCTA	271430	103626	CACCCTCCGTCCAAATGCCC
182257	14453	CAGGACTGATGATACTGTCT	226844	59040	TCATCCTTAAAATACAGGCT	271431	103627	CCACCCTCCGTCCAAATGCC
182258	14454	CCAGGACTGATGATACTGTC	226845	59041	CTCATCCTTAAAATACAGGC	271432	103628	GCCACCCTCCGTCCAAATGC
182259	14455	GCCAGGACTGATGATACTGT	226846	59042	ACTCATCCTTAAAATACAGG	271433	103629	GGCCACCCTCCGTCCAAATG
182260	14456	GGCCAGGACTGATGATACTG	226847	59043	AACTCATCCTTAAAATACAG	271434	103630	TGGCCACCCTCCGTCCAAAT
182261	14457	GGGCCAGGACTGATGATACT	226848	59044	CAACTCATCCTTAAAATACA	271435	103631	GTGGCCACCCTCCGTCCAAA
182262	14458	GGGGCCAGGACTGATGATAC	226849	59045	TCAACTCATCCTTAAAATAC	271436	103632	GGTGGCCACCCTCCGTCCAA
182263	14459	CGGGGCCAGGACTGATGATA	226850	59046	ATCAACTCATCCTTAAAATA	271437	103633	TGGTGGCCACCCTCCGTCCA
182264	14460	TCGGGGCCAGGACTGATGAT	226851	59047	AATCAACTCATCCTTAAAAT	271438	103634	CTGGTGGCCACCCTCCGTCC
182265	14461	CTCGGGGCCAGGACTGATGA	226852	59048	AAATCAACTCATCCTTAAAA	271439	103635	ACTGGTGGCCACCCTCCGTC
182266	14462	GCTCGGGGCCAGGACTGATG	226853	59049	GAAATCAACTCATCCTTAAA	271440	103636	CACTGGTGGCCACCCTCCGT
182267	14463	TGCTCGGGGCCAGGACTGAT	226854	59050	AGAAATCAACTCATCCTTAA	271441	103637	GCACTGGTGGCCACCCTCCG
182268	14464	ATGCTCGGGGCCAGGACTGA	226855	59051	CAGAAATCAACTCATCCTTA	271442	103638	TGCACTGGTGGCCACCCTCC
182269	14465	CATGCTCGGGGCCAGGACTG	226856	59052	GCAGAAATCAACTCATCCTT	271443	103639	GTGCACTGGTGGCCACCCTC
182270	14466	CCATGCTCGGGGCCAGGACT	226857	59053	TGCAGAAATCAACTCATCCT	271444	103640	TGTGCACTGGTGGCCACCCT
182271	14467	GCCATGCTCGGGGCCAGGAC	226858	59054	ATGCAGAAATCAACTCATCC	271445	103641	ATGTGCACTGGTGGCCACCC
182272	14468	GGCCATGCTCGGGGCCAGGA	226859	59055	GATGCAGAAATCAACTCATC	271446	103642	CATGTGCACTGGTGGCCACC
182273	14469	AGGCCATGCTCGGGGCCAGG	226860	59056	TGATGCAGAAATCAACTCAT	271447	103643	CCATGTGCACTGGTGGCCAC
182274	14470	CAGGCCATGCTCGGGGCCAG	226861	59057	CTGATGCAGAAATCAACTCA	271448	103644	CCCATGTGCACTGGTGGCCA

182275	14471	GCAGGCCATGCTCGGGGCCA	226862	59058	GCTGATGCAGAAATCAACTC	271449	103645	GCCCATGTGCACTGGTGGCC
182276	14472	TGCAGGCCATGCTCGGGGCC	226863	59059	GGCTGATGCAGAAATCAACT	271450	103646	TGCCCATGTGCACTGGTGGC
182277	14473	ATGCAGGCCATGCTCGGGGC	226864	59060	GGGCTGATGCAGAAATCAAC	271451	103647	GTGCCCATGTGCACTGGTGG
182278	14474	TATGCAGGCCATGCTCGGGG	226865	59061	GGGGCTGATGCAGAAATCAA	271452	103648	GGTGCCCATGTGCACTGGTG
182279	14475	CTATGCAGGCCATGCTCGGG	226866	59062	AGGGGCTGATGCAGAAATCA	271453	103649	AGGTGCCCATGTGCACTGGT
182280	14476	CCTATGCAGGCCATGCTCGG	226867	59063	CAGGGGCTGATGCAGAAATC	271454	103650	AAGGTGCCCATGTGCACTGG
182281	14477	GCCTATGCAGGCCATGCTCG	226868	59064	ACAGGGGCTGATGCAGAAAT	271455	103651	CAAGGTGCCCATGTGCACTG
182282	14478	GGCCTATGCAGGCCATGCTC	226869	59065	TACAGGGGCTGATGCAGAAA	271456	103652	GCAAGGTGCCCATGTGCACT
182283	14479	GGGCCTATGCAGGCCATGCT	226870	59066	CTACAGGGGCTGATGCAGAA	271457	103653	GGCAAGGTGCCCATGTGCAC
182284	14480	GGGGCCTATGCAGGCCATGC	226871	59067	CCTACAGGGGCTGATGCAGA	271458	103654	AGGCAAGGTGCCCATGTGCA
182285	14481	GGGGGCCTATGCAGGCCATG	226872	59068	ACCTACAGGGGCTGATGCAG	271459	103655	GAGGCAAGGTGCCCATGTGC
182286	14482	TGGGGGCCTATGCAGGCCAT	226873	59069	GACCTACAGGGGCTGATGCA	271460	103656	TGAGGCAAGGTGCCCATGTG
182287	14483	ATGGGGGCCTATGCAGGCCA	226874	59070	TGACCTACAGGGGCTGATGC	271461	103657	TTGAGGCAAGGTGCCCATGT
182288	14484	CATGGGGGCCTATGCAGGCC	226875	59071	ATGACCTACAGGGGCTGATG	271462	103658	TTTGAGGCAAGGTGCCCATG
182289	14485	CCATGGGGGCCTATGCAGGC	226876	59072	GATGACCTACAGGGGCTGAT	271463	103659	GTTTGAGGCAAGGTGCCCAT
182290	14486	TCCATGGGGGCCTATGCAGG	226877	59073	TGATGACCTACAGGGGCTGA	271464	103660	GGTTTGAGGCAAGGTGCCCA
182291	14487	ATCCATGGGGGCCTATGCAG	226878	59074	CTGATGACCTACAGGGGCTG	271465	103661	GGGTTTGAGGCAAGGTGCCC
182292	14488	GATCCATGGGGGCCTATGCA	226879	59075	GCTGATGACCTACAGGGGCT	271466	103662	AGGGTTTGAGGCAAGGTGCC
182293	14489	GGATCCATGGGGGCCTATGC	226880	59076	GGCTGATGACCTACAGGGGC	271467	103663	CAGGGTTTGAGGCAAGGTGC
182294	14490	GGGATCCATGGGGGCCTATG	226881	59077	AGGCTGATGACCTACAGGGG	271468	103664	GCAGGGTTTGAGGCAAGGTG
182295	14491	TGGGATCCATGGGGGCCTAT	226882	59078	AAGGCTGATGACCTACAGGG	271469	103665	GGCAGGGTTTGAGGCAAGGT
182296	14492	CTGGGATCCATGGGGGCCTA	226883	59079	GAAGGCTGATGACCTACAGG	271470	103666	TGGCAGGGTTTGAGGCAAGG
182297	14493	GCTGGGATCCATGGGGGCCT	226884	59080	AGAAGGCTGATGACCTACAG	271471	103667	GTGGCAGGGTTTGAGGCAAG
182298	14494	CGCTGGGATCCATGGGGGCC	226885	59081	TAGAAGGCTGATGACCTACA	271472	103668	GGTGGCAGGGTTTGAGGCAA
182299	14495	CCGCTGGGATCCATGGGGGC	226886	59082	ATAGAAGGCTGATGACCTAC	271473	103669	AGGTGGCAGGGTTTGAGGCA
182300	14496	CCCGCTGGGATCCATGGGGG	226887	59083	AATAGAAGGCTGATGACCTA	271474	103670	GAGGTGGCAGGGTTTGAGGC
182301	14497	TCCCGCTGGGATCCATGGGG	226888	59084	CAATAGAAGGCTGATGACCT	271475	103671	GGAGGTGGCAGGGTTTGAGG
182302	14498	CTCCCGCTGGGATCCATGGG	226889	59085	CCAATAGAAGGCTGATGACC	271476	103672	GGGAGGTGGCAGGGTTTGAG
182303	14499	GCTCCCGCTGGGATCCATGG	226890	59086	ACCAATAGAAGGCTGATGAC	271477	103673	GGGGAGGTGGCAGGGTTTGA
182304	14500	AGCTCCCGCTGGGATCCATG	226891	59087	CACCAATAGAAGGCTGATGA	271478	103674	GGGGGAGGTGGCAGGGTTTG
182305	14501	CAGCTCCCGCTGGGATCCAT	226892	59088	GCACCAATAGAAGGCTGATG	271479	103675	GGGGGGAGGTGGCAGGGTTT
182306	14502	GCAGCTCCCGCTGGGATCCA	226893	59089	TGCACCAATAGAAGGCTGAT	271480	103676	TGGGGGGAGGTGGCAGGGTT
182307	14503	TGCAGCTCCCGCTGGGATCC	226894	59090	ATGCACCAATAGAAGGCTGA	271481	103677	GTGGGGGGAGGTGGCAGGGT
182308	14504	CTGCAGCTCCCGCTGGGATC	226895	59091	GATGCACCAATAGAAGGCTG	271482	103678	GGTGGGGGGAGGTGGCAGGG
182309	14505	TCTGCAGCTCCCGCTGGGAT	226896	59092	AGATGCACCAATAGAAGGCT	271483	103679	GGGTGGGGGGAGGTGGCAGG
182310	14506	CTCTGCAGCTCCCGCTGGGA	226897	59093	CAGATGCACCAATAGAAGGC	271484	103680	TGGGTGGGGGGAGGTGGCAG
182311	14507	ACTCTGCAGCTCCCGCTGGG	226898	59094	TCAGATGCACCAATAGAAGG	271485	103681	CTGGGTGGGGGGAGGTGGCA
182312	14508	CACTCTGCAGCTCCCGCTGG	226899	59095	GTCAGATGCACCAATAGAAG	271486	103682	CCTGGGTGGGGGGAGGTGGC
182313	14509	GCACTCTGCAGCTCCCGCTG	226900	59096	AGTCAGATGCACCAATAGAA	271487	103683	TCCTGGGTGGGGGGAGGTGG
182314	14510	CGCACTCTGCAGCTCCCGCT	226901	59097	GAGTCAGATGCACCAATAGA	271488	103684	ATCCTGGGTGGGGGGAGGTG
182315	14511	CCGCACTCTGCAGCTCCCGC	226902	59098	AGAGTCAGATGCACCAATAG	271489	103685	GATCCTGGGTGGGGGGAGGT
182316	14512	CCCGCACTCTGCAGCTCCCG	226903	59099	GAGAGTCAGATGCACCAATA	271490	103686	GGATCCTGGGTGGGGGGAGG
182317	14513	GCCCGCACTCTGCAGCTCCC	226904	59100	AGAGAGTCAGATGCACCAAT	271491	103687	GGGATCCTGGGTGGGGGGAG
182318	14514	TGCCCGCACTCTGCAGCTCC	226905	59101	GAGAGAGTCAGATGCACCAA	271492	103688	GGGGATCCTGGGTGGGGGGA
182319	14515	GTGCCCGCACTCTGCAGCTC	226906	59102	AGAGAGAGTCAGATGCACCA	271493	103689	GGGGGATCCTGGGTGGGGGG
182320	14516	GGTGCCCGCACTCTGCAGCT	226907	59103	TAGAGAGAGTCAGATGCACC	271494	103690	GGGGGGATCCTGGGTGGGGG
182321	14517	AGGTGCCCGCACTCTGCAGC	226908	59104	CTAGAGAGAGTCAGATGCAC	271495	103691	AGGGGGGATCCTGGGTGGGG
182322	14518	AAGGTGCCCGCACTCTGCAG	226909	59105	GCTAGAGAGAGTCAGATGCA	271496	103692	CAGGGGGGATCCTGGGTGGG
182323	14519	CAAGGTGCCCGCACTCTGCA	226910	59106	GGCTAGAGAGAGTCAGATGC	271497	103693	GCAGGGGGGATCCTGGGTGG
182324	14520	CCAAGGTGCCCGCACTCTGC	226911	59107	GGGCTAGAGAGAGTCAGATG	271498	103694	GGCAGGGGGGATCCTGGGTG
182325	14521	GCCAAGGTGCCCGCACTCTG	226912	59108	AGGGCTAGAGAGAGTCAGAT	271499	103695	GGGCAGGGGGGATCCTGGGT
182326	14522	TGCCAAGGTGCCCGCACTCT	226913	59109	CAGGGCTAGAGAGAGTCAGA	271500	103696	GGGGCAGGGGGGATCCTGGG
182327	14523	GTGCCAAGGTGCCCGCACTC	226914	59110	GCAGGGCTAGAGAGAGTCAG	271501	103697	GGGGGCAGGGGGGATCCTGG
182328	14524	TGTGCCAAGGTGCCCGCACT	226915	59111	TGCAGGGCTAGAGAGAGTCA	271502	103698	CGGGGGCAGGGGGGATCCTG
182329	14525	GTGTGCCAAGGTGCCCGCAC	226916	59112	CTGCAGGGCTAGAGAGAGTC	271503	103699	TCGGGGGCAGGGGGGATCCT
182330	14526	TGTGTGCCAAGGTGCCCGCA	226917	59113	CCTGCAGGGCTAGAGAGAGT	271504	103700	TTCGGGGGCAGGGGGGATCC
182331	14527	CTGTGTGCCAAGGTGCCCGC	226918	59114	CCCTGCAGGGCTAGAGAGAG	271505	103701	GTTCGGGGGCAGGGGGGATC
182332	14528	GCTGTGTGCCAAGGTGCCCG	226919	59115	TCCCTGCAGGGCTAGAGAGA	271506	103702	TGTTCGGGGGCAGGGGGGAT
182333	14529	GGCTGTGTGCCAAGGTGCCC	226920	59116	ATCCCTGCAGGGCTAGAGAG	271507	103703	TTGTTCGGGGGCAGGGGGGA
182334	14530	GGGCTGTGTGCCAAGGTGCC	226921	59117	CATCCCTGCAGGGCTAGAGA	271508	103704	CTTGTTCGGGGGCAGGGGGG
182335	14531	AGGGCTGTGTGCCAAGGTGC	226922	59118	CCATCCCTGCAGGGCTAGAG	271509	103705	GCTTGTTCGGGGGCAGGGGG
182336	14532	CAGGGCTGTGTGCCAAGGTG	226923	59119	ACCATCCCTGCAGGGCTAGA	271510	103706	AGCTTGTTCGGGGGCAGGGG
182337	14533	TCAGGGCTGTGTGCCAAGGT	226924	59120	CCACCATCCCTGCAGGGCTAG	271511	103707	AAGCTTGTTCGGGGGCAGGG
182338	14534	CTCAGGGCTGTGTGCCAAGG	226925	59121	CCACCATCCCTGCAGGGCTA	271512	103708	CAAGCTTGTTCGGGGGCAGG
182339	14535	ACTCAGGGCTGTGTGCCAAG	226926	59122	TCCACCATCCCTGCAGGGCT	271513	103709	ACAAGCTTGTTCGGGGGCAG
182340	14536	CACTCAGGGCTGTGTGCCAA	226927	59123	CTCCACCATCCCTGCAGGGC	271514	103710	CACAAGCTTGTTCGGGGGCA
182341	14537	GCACTCAGGGCTGTGTGCCA	226928	59124	CCTCCACCATCCCTGCAGGG	271515	103711	TCACAAGCTTGTTCGGGGGC
182342	14538	TGCACTCAGGGCTGTGTGCC	226929	59125	CCCTCCACCATCCCTGCAGG	271516	103712	CTCACAAGCTTGTTCGGGGG
182343	14539	TTGCACTCAGGGCTGTGTGC	226930	59126	CCCCTCCACCATCCCTGCAG	271517	103713	ACTCACAAGCTTGTTCGGGG
182344	14540	TTTGCACTCAGGGCTGTGTG	226931	59127	CCCCCTCCACCATCCCTGCA	271518	103714	CACTCACAAGCTTGTTCGGG
182345	14541	TTTTGCACTCAGGGCTGTGT	226932	59128	TCCCCCTCCACCATCCCTGC	271519	103715	GCACTCACAAGCTTGTTCGG
182346	14542	ATTTTGCACTCAGGGCTGTG	226933	59129	CTCCCCCTCCACCATCCCTG	271520	103716	TGCACTCACAAGCTTGTTCG

182347	14543	AATTTTGCACTCAGGGCTGT	226934	59130	CCTCCCCCTCCACCATCCCT	271521	103717	CTGCACTCACAAGCTTGTTC
182348	14544	TAATTTTGCACTCAGGGCTG	226935	59131	CCCTCCCCCTCCACCATCCC	271522	103718	ACTGCACTCACAAGCTTGTT
182349	14545	CTAATTTTGCACTCAGGGCT	226936	59132	CCCCTCCCCCTCCACCATCC	271523	103719	CACTGCACTCACAAGCTTGT
182350	14546	CCTAATTTTGCACTCAGGGC	226937	59133	TCCCCTCCCCCTCCACCATC	271524	103720	ACACTGCACTCACAAGCTTG
182351	14547	TCCTAATTTTGCACTCAGGG	226938	59134	TTCCCCTCCCCCTCCACCAT	271525	103721	GACACTGCACTCACAAGCTT
182352	14548	CTCCTAATTTTGCACTCAGG	226939	59135	CTTCCCCTCCCCCTCCACCA	271526	103722	TGACACTGCACTCACAAGCT
182353	14549	GCTCCTAATTTTGCACTCAG	226940	59136	CCTTCCCCTCCCCCTCCACC	271527	103723	GTGACACTGCACTCACAAGC
182354	14550	AGCTCCTAATTTTGCACTCA	226941	59137	TCCTTCCCCTCCCCCTCCAC	271528	103724	TGTGACACTGCACTCACAAG
182355	14551	CAGCTCCTAATTTTGCACTC	226942	59138	CTCCTTCCCCTCCCCCTCCA	271529	103725	ATGTGACACTGCACTCACAA
182356	14552	CCAGCTCCTAATTTTGCACT	226943	59139	CCTCCTTCCCCTCCCCCTCC	271530	103726	GATGTGACACTGCACTCACA
182357	14553	CCCAGCTCCTAATTTTGCAC	226944	59140	CCCTCCTTCCCCTCCCCCTC	271531	103727	GGATGTGACACTGCACTCAC
182358	14554	GCCCAGCTCCTAATTTTGCA	226945	59141	TCCCTCCTTCCCCTCCCCCT	271532	103728	GGGATGTGACACTGCACTCA
182359	14555	TGCCCAGCTCCTAATTTTGC	226946	59142	ATCCCTCCTTCCCCTCCCCC	271533	103729	TGGGATGTGACACTGCACTC
182360	14556	CTGCCCAGCTCCTAATTTTG	226947	59143	GATCCCTCCTTCCCCTCCCC	271534	103730	ATGGGATGTGACACTGCACT
182361	14557	TCTGCCCAGCTCCTAATTTT	226948	59144	AGATCCCTCCTTCCCCTCCC	271535	103731	GATGGGATGTGACACTGCAC
182362	14558	CTCTGCCCAGCTCCTAATTT	226949	59145	AAGATCCCTCCTTCCCCTCC	271536	103732	CGATGGGATGTGACACTGCA
182363	14559	CCTCTGCCCAGCTCCTAATT	226950	59146	AAAGATCCCTCCTTCCCCTC	271537	103733	CCGATGGGATGTGACACTGC
182364	14560	CCCTCTGCCCAGCTCCTAAT	226951	59147	TAAAGATCCCTCCTTCCCCT	271538	103734	CCCGATGGGATGTGACACTG
182365	14561	GCCCTCTGCCCAGCTCCTAA	226952	59148	ATAAAGATCCCTCCTTCCCC	271539	103735	TCCCGATGGGATGTGACACT
182366	14562	TGCCCTCTGCCCAGCTCCTA	226953	59149	AATAAAGATCCCTCCTTCCC	271540	103736	ATCCCGATGGGATGTGACAC
182367	14563	ATGCCCTCTGCCCAGCTCCT	226954	59150	CAATAAAGATCCCTCCTTCC	271541	103737	CATCCCGATGGGATGTGACA
182368	14564	GATGCCCTCTGCCCAGCTCC	226955	59151	CCAATAAAGATCCCTCCTTC	271542	103738	CCATCCCGATGGGATGTGAC
182369	14565	AGATGCCCTCTGCCCAGCTC	226956	59152	TCCAATAAAGATCCCTCCTT	271543	103739	TCCATCCCGATGGGATGTGA
182370	14566	GAGATGCCCTCTGCCCAGCT	226957	59153	TTCCAATAAAGATCCCTCCT	271544	103740	TTCCATCCCGATGGGATGTG
182371	14567	AGAGATGCCCTCTGCCCAGC	226958	59154	TTTCCAATAAAGATCCCTCC	271545	103741	TTTCCATCCCGATGGGATGT
182372	14568	GAGAGATGCCCTCTGCCCAG	226959	59155	GTTTCCAATAAAGATCCCTC	271546	103742	ATTTCCATCCCGATGGGATG
182373	14569	AGAGAGATGCCCTCTGCCCA	226960	59156	GGTTTCCAATAAAGATCCCT	271547	103743	CATTTCCATCCCGATGGGAT
182374	14570	CAGAGAGATGCCCTCTGCCC	226961	59157	TGGTTTCCAATAAAGATCCC	271548	103744	CCATTTCCATCCCGATGGGA
182375	14571	ACAGAGAGATGCCCTCTGCC	226962	59158	CTGGTTTCCAATAAAGATCC	271549	103745	TCCATTTCCATCCCGATGGG
182376	14572	GACAGAGAGATGCCCTCTGC	226963	59159	CCTGGTTTCCAATAAAGATC	271550	103746	GTCCATTTCCATCCCGATGG
182377	14573	CGACAGAGAGATGCCCTCTG	226964	59160	TCCTGGTTTCCAATAAAGAT	271551	103747	CGTCCATTTCCATCCCGATG
182378	14574	GCGACAGAGAGATGCCCTCT	226965	59161	GTCCTGGTTTCCAATAAAGA	271552	103748	CCGTCCATTTCCATCCCGAT
182379	14575	GGCGACAGAGAGATGCCCTC	226966	59162	TGTCCTGGTTTCCAATAAAG	271553	103749	ACCGTCCATTTCCATCCCGA
182380	14576	TGGCGACAGAGAGATGCCCT	226967	59163	CTGTCCTGGTTTCCAATAAA	271554	103750	GACCGTCCATTTCCATCCCG
182381	14577	ATGGCGACAGAGAGATGCCC	226968	59164	ACTGTCCTGGTTTCCAATAA	271555	103751	CGACCGTCCATTTCCATCCC
182382	14578	AATGGCGACAGAGAGATGCC	226969	59165	CACTGTCCTGGTTTCCAATA	271556	103752	CCGACCGTCCATTTCCATCC
182383	14579	CAATGGCGACAGAGAGATGC	226970	59166	TCACTGTCCTGGTTTCCAAT	271557	103753	CCCGACCGTCCATTTCCATC
182384	14580	CCAATGGCGACAGAGAGATG	226971	59167	CTCACTGTCCTGGTTTCCAA	271558	103754	ACCCGACCGTCCATTTCCAT
182385	14581	CCCAATGGCGACAGAGAGAT	226972	59168	TCTCACTGTCCTGGTTTCCA	271559	103755	AACCCGACCGTCCATTTCCA
182386	14582	GCCCAATGGCGACAGAGAGA	226973	59169	GTCTCACTGTCCTGGTTTCC	271560	103756	TAACCCGACCGTCCATTTCC
182387	14583	TGCCCAATGGCGACAGAGAG	226974	59170	AGTCTCACTGTCCTGGTTTC	271561	103757	TTAACCCGACCGTCCATTTC
182388	14584	CTGCCCAATGGCGACAGAGA	226975	59171	GAGTCTCACTGTCCTGGTTT	271562	103758	TTTAACCCGACCGTCCATTT
182389	14585	GCTGCCCAATGGCGACAGAG	226976	59172	TGAGTCTCACTGTCCTGGTT	271563	103759	TTTTAACCCGACCGTCCATT
182390	14586	GGCTGCCCAATGGCGACAGA	226977	59173	ATGAGTCTCACTGTCCTGGT	271564	103760	CTTTTAACCCGACCGTCCAT
182391	14587	GGGCTGCCCAATGGCGACAG	226978	59174	AATGAGTCTCACTGTCCTGG	271565	103761	CCTTTTAACCCGACCGTCCA
182392	14588	TGGGCTGCCCAATGGCGACA	226979	59175	CAATGAGTCTCACTGTCCTG	271566	103762	CCCTTTTAACCCGACCGTCC
182393	14589	CTGGGCTGCCCAATGGCGAC	226980	59176	GCAATGAGTCTCACTGTCCT	271567	103763	TCCCTTTTAACCCGACCGTC
182394	14590	CCTGGGCTGCCCAATGGCGA	226981	59177	GGCAATGAGTCTCACTGTCC	271568	103764	GTCCCTTTTAACCCGACCGT
182395	14591	CCCTGGGCTGCCCAATGGCG	226982	59178	GGGCAATGAGTCTCACTGTC	271569	103765	CGTCCCTTTTAACCCGACCG
182396	14592	GCCCTGGGCTGCCCAATGGC	226983	59179	AGGGCAATGAGTCTCACTGT	271570	103766	GCGTCCCTTTTAACCCGACC
182397	14593	TGCCCTGGGCTGCCCAATGG	226984	59180	CAGGGCAATGAGTCTCACTG	271571	103767	TGCGTCCCTTTTAACCCGAC
182398	14594	GTGCCCTGGGCTGCCCAATG	226985	59181	ACAGGGCAATGAGTCTCACT	271572	103768	ATGCGTCCCTTTTAACCCGA
182399	14595	TGTGCCCTGGGCTGCCCAAT	226986	59182	GACAGGGCAATGAGTCTCAC	271573	103769	CATGCGTCCCTTTTAACCCG
182400	14596	GTGTGCCCTGGGCTGCCCAA	226987	59183	TGACAGGGCAATGAGTCTCA	271574	103770	ACATGCGTCCCTTTTAACCC
182401	14597	AGTGTGCCCTGGGCTGCCCA	226988	59184	ATGACAGGGCAATGAGTCTC	271575	103771	CACATGCGTCCCTTTTAACC
182402	14598	CAGTGTGCCCTGGGCTGCCC	226989	59185	GATGACAGGGCAATGAGTCT	271576	103772	ACACATGCGTCCCTTTTAAC
182403	14599	CCAGTGTGCCCTGGGCTGCC	226990	59186	AGATGACAGGGCAATGAGTC	271577	103773	TACACATGCGTCCCTTTTAA
182404	14600	ACCAGTGTGCCCTGGGCTGC	226991	59187	CAGATGACAGGGCAATGAGT	271578	103774	CTACACATGCGTCCCTTTTA
182405	14601	GACCAGTGTGCCCTGGGCTG	226992	59188	GCAGATGACAGGGCAATGAG	271579	103775	TCTACACATGCGTCCCTTTT
182406	14602	TGACCAGTGTGCCCTGGGCT	226993	59189	AGCAGATGACAGGGCAATGA	271580	103776	GTCTACACATGCGTCCCTTT
182407	14603	ATGACCAGTGTGCCCTGGGC	226994	59190	GAGCAGATGACAGGGCAATG	271581	103777	GGTCTACACATGCGTCCCTT
182408	14604	TATGACCAGTGTGCCCTGGG	226995	59191	AGAGCAGATGACAGGGCAAT	271582	103778	GGGTCTACACATGCGTCCCT
182409	14605	CTATGACCAGTGTGCCCTGG	226996	59192	CAGAGCAGATGACAGGGCAA	271583	103779	AGGGTCTACACATGCGTCCC
182410	14606	GCTATGACCAGTGTGCCCTG	226997	59193	ACAGAGCAGATGACAGGGCA	271584	103780	CAGGGTCTACACATGCGTCC
182411	14607	GGCTATGACCAGTGTGCCCT	226998	59194	CACAGAGCAGATGACAGGGC	271585	103781	GCAGGGTCTACACATGCGTC
182412	14608	AGGCTATGACCAGTGTGCCC	226999	59195	CCACAGAGCAGATGACAGGG	271586	103782	GGCAGGGTCTACACATGCGT
182413	14609	AAGGCTATGACCAGTGTGCC	227000	59196	ACCACAGAGCAGATGACAGG	271587	103783	AGGCAGGGTCTACACATGCG
182414	14610	TAAGGCTATGACCAGTGTGC	227001	59197	CACCACAGAGCAGATGACAG	271588	103784	GAGGCAGGGTCTACACATGC
182415	14611	CTAAGGCTATGACCAGTGTG	227002	59198	GCACCACAGAGCAGATGACA	271589	103785	AGAGGCAGGGTCTACACATG
182416	14612	TCTAAGGCTATGACCAGTGT	227003	59199	AGCACCACAGAGCAGATGAC	271590	103786	CAGAGGCAGGGTCTACACAT
182417	14613	GTCTAAGGCTATGACCAGTG	227004	59200	CAGCACCACAGAGCAGATGA	271591	103787	ACAGAGGCAGGGTCTACACA
182418	14614	GGTCTAAGGCTATGACCAGT	227005	59201	TCAGCACCACAGAGCAGATG	271592	103788	CACAGAGGCAGGGTCTACAC

182419	14615	TGGTCTAAGGCTATGACCAG	227006	59202	TTCAGCACCACAGAGCAGAT	271593	103789	GCACAGAGGCAGGGTCTACA
182420	14616	GTGGTCTAAGGCTATGACCA	227007	59203	ATTCAGCACCACAGAGCAGA	271594	103790	TGCACAGAGGCAGGGTCTAC
182421	14617	CGTGGTCTAAGGCTATGACC	227008	59204	CATTCAGCACCACAGAGCAG	271595	103791	ATGCACAGAGGCAGGGTCTA
182422	14618	TCGTGGTCTAAGGCTATGAC	227009	59205	TCATTCAGCACCACAGAGCA	271596	103792	GATGCACAGAGGCAGGGTCT
182423	14619	TTCGTGGTCTAAGGCTATGA	227010	59206	CTCATTCAGCACCACAGAGC	271597	103793	TGATGCACAGAGGCAGGGTC
182424	14620	GTTCGTGGTCTAAGGCTATG	227011	59207	CCTCATTCAGCACCACAGAG	271598	103794	CTGATGCACAGAGGCAGGGT
182425	14621	TGTTCGTGGTCTAAGGCTAT	227012	59208	GCCTCATTCAGCACCACAGA	271599	103795	CCTGATGCACAGAGGCAGGG
182426	14622	GTGTTCGTGGTCTAAGGCTA	227013	59209	TGCCTCATTCAGCACCACAG	271600	103796	GCCTGATGCACAGAGGCAGG
182427	14623	GGTGTTCGTGGTCTAAGGCT	227014	59210	CTGCCTCATTCAGCACCACA	271601	103797	GGCCTGATGCACAGAGGCAG
182428	14624	GGGTGTTCGTGGTCTAAGGC	227015	59211	GCTGCCTCATTCAGCACCAC	271602	103798	AGGCCTGATGCACAGAGGCA
182429	14625	AGGGTGTTCGTGGTCTAAGG	227016	59212	GGCTGCCTCATTCAGCACCA	271603	103799	GAGGCCTGATGCACAGAGGC
182430	14626	CAGGGTGTTCGTGGTCTAAG	227017	59213	GGGCTGCCTCATTCAGCACC	271604	103800	AGAGGCCTGATGCACAGAGG
182431	14627	ACAGGGTGTTCGTGGTCTAA	227018	59214	TGGGCTGCCTCATTCAGCAC	271605	103801	AAGAGGCCTGATGCACAGAG
182432	14628	CACAGGGTGTTCGTGGTCTA	227019	59215	TTGGGCTGCCTCATTCAGCA	271606	103802	AAAGAGGCCTGATGCACAGA
182433	14629	GCACAGGGTGTTCGTGGTCT	227020	59216	GTTGGGCTGCCTCATTCAGC	271607	103803	AAAAGAGGCCTGATGCACAG
182434	14630	GGCACAGGGTGTTCGTGGTC	227021	59217	TGTTGGGCTGCCTCATTCAG	271608	103804	CAAAAGAGGCCTGATGCACA
182435	14631	GGGCACAGGGTGTTCGTGGT	227022	59218	CTGTTGGGCTGCCTCATTCA	271609	103805	TCAAAAGAGGCCTGATGCAC
182436	14632	CGGGCACAGGGTGTTCGTGG	227023	59219	TCTGTTGGGCTGCCTCATTC	271610	103806	CTCAAAAGAGGCCTGATGCA
182437	14633	CCGGGCACAGGGTGTTCGTG	227024	59220	CTCTGTTGGGCTGCCTCATT	271611	103807	TCTCAAAAGAGGCCTGATGC
182438	14634	CCCGGGCACAGGGTGTTCGT	227025	59221	TCTCTGTTGGGCTGCCTCAT	271612	103808	CTCTCAAAAGAGGCCTGATG
182439	14635	CCCCGGGCACAGGGTGTTCG	227026	59222	TTCTCTGTTGGGCTGCCTCA	271613	103809	ACTCTCAAAAGAGGCCTGAT
182440	14636	CCCCCGGGCACAGGGTGTTC	227027	59223	TTTCTCTGTTGGGCTGCCTC	271614	103810	GACTCTCAAAAGAGGCCTGA
182441	14637	TCCCCCGGGCACAGGGTGTT	227028	59224	ATTTCTCTGTTGGGCTGCCT	271615	103811	GGACTCTCAAAAGAGGCCTG
182442	14638	GTCCCCCGGGCACAGGGTGT	227029	59225	TATTTCTCTGTTGGGCTGCC	271616	103812	GGGACTCTCAAAAGAGGCCT
182443	14639	TGTCCCCCGGGCACAGGGTG	227030	59226	GTATTTCTCTGTTGGGCTGC	271617	103813	AGGGACTCTCAAAAGAGGCC
182444	14640	CTGTCCCCCGGGCACAGGGT	227031	59227	GGTATTTCTCTGTTGGGCTG	271618	103814	CAGGGACTCTCAAAAGAGGC
182445	14641	TCTGTCCCCCGGGCACAGGG	227032	59228	GGGTATTTCTCTGTTGGGCT	271619	103815	GCAGGGACTCTCAAAAGAGG
182446	14642	ATCTGTCCCCCGGGCACAGG	227033	59229	AGGGTATTTCTCTGTTGGGC	271620	103816	CGCAGGGACTCTCAAAAGAG
182447	14643	CATCTGTCCCCCGGGCACAG	227034	59230	CAGGGTATTTCTCTGTTGGG	271621	103817	ACGCAGGGACTCTCAAAAGA
182448	14644	GCATCTGTCCCCCGGGCACA	227035	59231	TCAGGGTATTTCTCTGTTGG	271622	103818	CACGCAGGGACTCTCAAAAG
182449	14645	TGCATCTGTCCCCCGGGCAC	227036	59232	CTCAGGGTATTTCTCTGTTG	271623	103819	GCACGCAGGGACTCTCAAAA
182450	14646	TTGCATCTGTCCCCCGGGCA	227037	59233	GCTCAGGGTATTTCTCTGTT	271624	103820	GGCACGCAGGGACTCTCAAA
182451	14647	GTTGCATCTGTCCCCCGGGC	227038	59234	CGCTCAGGGTATTTCTCTGT	271625	103821	TGGCACGCAGGGACTCTCAA
182452	14648	GGTTGCATCTGTCCCCCGGG	227039	59235	TCGCTCAGGGTATTTCTCTG	271626	103822	CTGGCACGCAGGGACTCTCA
182453	14649	TGGTTGCATCTGTCCCCCGG	227040	59236	CTCGCTCAGGGTATTTCTCT	271627	103823	CCTGGCACGCAGGGACTCTC
182454	14650	CTGGTTGCATCTGTCCCCCG	227041	59237	GCTCGCTCAGGGTATTTCTC	271628	103824	GCCTGGCACGCAGGGACTCT
182455	14651	ACTGGTTGCATCTGTCCCCC	227042	59238	TGCTCGCTCAGGGTATTTCT	271629	103825	CGCCTGGCACGCAGGGACTC
182456	14652	CACTGGTTGCATCTGTCCCC	227043	59239	ATGCTCGCTCAGGGTATTTC	271630	103826	CCGCCTGGCACGCAGGGACT
182457	14653	ACACTGGTTGCATCTGTCCC	227044	59240	GATGCTCGCTCAGGGTATTT	271631	103827	ACCGCCTGGCACGCAGGGAC
182458	14654	CACACTGGTTGCATCTGTCC	227045	59241	GGATGCTCGCTCAGGGTATT	271632	103828	CACCGCCTGGCACGCAGGGA
182459	14655	GCACACTGGTTGCATCTGTC	227046	59242	GGGATGCTCGCTCAGGGTAT	271633	103829	GCACCGCCTGGCACGCAGGG
182460	14656	GGCACACTGGTTGCATCTGT	227047	59243	GGGGATGCTCGCTCAGGGTA	271634	103830	TGCACCGCCTGGCACGCAGG
182461	14657	GGGCACACTGGTTGCATCTG	227048	59244	TGGGGATGCTCGCTCAGGGT	271635	103831	GTGCACCGCCTGGCACGCAG
182462	14658	AGGGCACACTGGTTGCATCT	227049	59245	CTGGGGATGCTCGCTCAGGG	271636	103832	TGTGCACCGCCTGGCACGCA
182463	14659	CAGGGCACACTGGTTGCATC	227050	59246	GCTGGGGATGCTCGCTCAGG	271637	103833	CTGTGCACCGCCTGGCACGC
182464	14660	CCAGGGCACACTGGTTGCAT	227051	59247	GGCTGGGGATGCTCGCTCAG	271638	103834	TCTGTGCACCGCCTGGCACG
182465	14661	CCCAGGGCACACTGGTTGCA	227052	59248	AGGCTGGGGATGCTCGCTCA	271639	103835	CTCTGTGCACCGCCTGGCAC
182466	14662	GCCCAGGGCACACTGGTTGC	227053	59249	GAGGCTGGGGATGCTCGCTC	271640	103836	CCTCTGTGCACCGCCTGGCA
182467	14663	AGCCCAGGGCACACTGGTTG	227054	59250	GGAGGCTGGGGATGCTCGCT	271641	103837	ACCTCTGTGCACCGCCTGGC
182468	14664	CAGCCCAGGGCACACTGGTT	227055	59251	TGGAGGCTGGGGATGCTCGC	271642	103838	CACCTCTGTGCACCGCCTGG
182469	14665	GCAGCCCAGGGCACACTGGT	227056	59252	TTGGAGGCTGGGGATGCTCG	271643	103839	CCACCTCTGTGCACCGCCTG
182470	14666	GGCAGCCCAGGGCACACTGG	227057	59253	TTTGGAGGCTGGGGATGCTC	271644	103840	TCCACCTCTGTGCACCGCCT
182471	14667	GGGCAGCCCAGGGCACACTG	227058	59254	TTTTGGAGGCTGGGGATGCT	271645	103841	CTCCACCTCTGTGCACCGCC
182472	14668	TGGGCAGCCCAGGGCACACT	227059	59255	GTTTTGGAGGCTGGGGATGC	271646	103842	TCTCCACCTCTGTGCACCGC
182473	14669	TTGGGCAGCCCAGGGCACAC	227060	59256	TGTTTTGGAGGCTGGGGATG	271647	103843	TTCTCCACCTCTGTGCACCG
182474	14670	ATTGGGCAGCCCAGGGCACA	227061	59257	CTGTTTTGGAGGCTGGGGAT	271648	103844	CTTCTCCACCTCTGTGCACC
182475	14671	CATTGGGCAGCCCAGGGCAC	227062	59258	ACTGTTTTGGAGGCTGGGGA	271649	103845	TCTTCTCCACCTCTGTGCAC
182476	14672	CCATTGGGCAGCCCAGGGCA	227063	59259	CACTGTTTTGGAGGCTGGGG	271650	103846	GTCTTCTCCACCTCTGTGCA
182477	14673	GCCATTGGGCAGCCCAGGGC	227064	59260	CCACTGTTTTGGAGGCTGGG	271651	103847	AGTCTTCTCCACCTCTGTGC
182478	14674	TGCCATTGGGCAGCCCAGGG	227065	59261	GCCACTGTTTTGGAGGCTGG	271652	103848	GAGTCTTCTCCACCTCTGTG
182479	14675	TTGCCATTGGGCAGCCCAGG	227066	59262	CGCCACTGTTTTGGAGGCTG	271653	103849	CGAGTCTTCTCCACCTCTGT
182480	14676	GTTGCCATTGGGCAGCCCAG	227067	59263	GCGCCACTGTTTTGGAGGCT	271654	103850	CCGAGTCTTCTCCACCTCTG
182481	14677	TGTTGCCATTGGGCAGCCCA	227068	59264	TGCGCCACTGTTTTGGAGGC	271655	103851	GCCGAGTCTTCTCCACCTCT
182482	14678	CTGTTGCCATTGGGCAGCCC	227069	59265	ATGCGCCACTGTTTTGGAGG	271656	103852	AGCCGAGTCTTCTCCACCTC
182483	14679	TCTGTTGCCATTGGGCAGCC	227070	59266	AATGCGCCACTGTTTTGGAG	271657	103853	CAGCCGAGTCTTCTCCACCT
182484	14680	CTCTGTTGCCATTGGGCAGC	227071	59267	CAATGCGCCACTGTTTTGGA	271658	103854	ACAGCCGAGTCTTCTCCACC
182485	14681	TCTCTGTTGCCATTGGGCAG	227072	59268	GCAATGCGCCACTGTTTTGG	271659	103855	CACAGCCGAGTCTTCTCCAC
182486	14682	CTCTCTGTTGCCATTGGGCA	227073	59269	GGCAATGCGCCACTGTTTTG	271660	103856	GCACAGCCGAGTCTTCTCCA
182487	14683	TCTCTCTGTTGCCATTGGGC	227074	59270	GGGCAATGCGCCACTGTTTT	271661	103857	GGCACAGCCGAGTCTTCTCC
182488	14684	ATCTCTCTGTTGCCATTGGG	227075	59271	AGGGCAATGCGCCACTGTTT	271662	103858	GGGCACAGCCGAGTCTTCTC
182489	14685	GATCTCTCTGTTGCCATTGG	227076	59272	CAGGGCAATGCGCCACTGTT	271663	103859	GGGGCACAGCCGAGTCTTCT
182490	14686	CGATCTCTCTGTTGCCATTG	227077	59273	TCAGGGCAATGCGCCACTGT	271664	103860	TGGGGCACAGCCGAGTCTTC

182491	14687	TCGATCTCTCTGTTGCCATT	227078	59274	CTCAGGGCAATGCGCCACTG	271665	103861	CTGGGGCACAGCCGAGTCTT
182492	14688	GTCGATCTCTCTGTTGCCAT	227079	59275	ACTCAGGGCAATGCGCCACT	271666	103862	TCTGGGGCACAGCCGAGTCT
182493	14689	TGTCGATCTCTCTGTTGCCA	227080	59276	GACTCAGGGCAATGCGCCAC	271667	103863	CTCTGGGGCACAGCCGAGTC
182494	14690	GTGTCGATCTCTCTGTTGCC	227081	59277	GGACTCAGGGCAATGCGCCA	271668	103864	GCTCTGGGGCACAGCCGAGT
182495	14691	GGTGTCGATCTCTCTGTTGC	227082	59278	AGGACTCAGGGCAATGCGCC	271669	103865	TGCTCTGGGGCACAGCCGAG
182496	14692	AGGTGTCGATCTCTCTGTTG	227083	59279	CAGGACTCAGGGCAATGCGC	271670	103866	GTGCTCTGGGGCACAGCCGA
182497	14693	CAGGTGTCGATCTCTCTGTT	227084	59280	CCAGGACTCAGGGCAATGCG	271671	103867	GGTGCTCTGGGGCACAGCCG
182498	14694	CCAGGTGTCGATCTCTCTGT	227085	59281	CCCAGGACTCAGGGCAATGC	271672	103868	AGGTGCTCTGGGGCACAGCC
182499	14695	TCCAGGTGTCGATCTCTCTG	227086	59282	TCCCAGGACTCAGGGCAATG	271673	103869	GAGGTGCTCTGGGGCACAGC
182500	14696	GTCCAGGTGTCGATCTCTCT	227087	59283	TTCCCAGGACTCAGGGCAAT	271674	103870	GGAGGTGCTCTGGGGCACAG
182501	14697	GGTCCAGGTGTCGATCTCTC	227088	59284	ATTCCCAGGACTCAGGGCAA	271675	103871	AGGAGGTGCTCTGGGGCACA
182502	14698	GGGTCCAGGTGTCGATCTCT	227089	59285	CATTCCCAGGACTCAGGGCA	271676	103872	GAGGAGGTGCTCTGGGGCAC
182503	14699	GGGGTCCAGGTGTCGATCTC	227090	59286	TCATTCCCAGGACTCAGGGC	271677	103873	AGAGGAGGTGCTCTGGGGCA
182504	14700	TGGGGTCCAGGTGTCGATCT	227091	59287	GTCATTCCCAGGACTCAGGG	271678	103874	GAGAGGAGGTGCTCTGGGGC
182505	14701	ATGGGGTCCAGGTGTCGATC	227092	59288	GGTCATTCCCAGGACTCAGG	271679	103875	TGAGAGGAGGTGCTCTGGGG
182506	14702	CATGGGGTCCAGGTGTCGAT	227093	59289	AGGTCATTCCCAGGACTCAG	271680	103876	ATGAGAGGAGGTGCTCTGGG
182507	14703	ACATGGGGTCCAGGTGTCGA	227094	59290	AAGGTCATTCCCAGGACTCA	271681	103877	GATGAGAGGAGGTGCTCTGG
182508	14704	GACATGGGGTCCAGGTGTCG	227095	59291	AAAGGTCATTCCCAGGACTC	271682	103878	CGATGAGAGGAGGTGCTCTG
182509	14705	TGACATGGGGTCCAGGTGTC	227096	59292	CAAAGGTCATTCCCAGGACT	271683	103879	TCGATGAGAGGAGGTGCTCT
182510	14706	GTGACATGGGGTCCAGGTGT	227097	59293	TCAAAGGTCATTCCCAGGAC	271684	103880	CTCGATGAGAGGAGGTGCTC
182511	14707	CGTGACATGGGGTCCAGGTG	227098	59294	ATCAAAGGTCATTCCCAGGA	271685	103881	CCTCGATGAGAGGAGGTGCT
182512	14708	CCGTGACATGGGGTCCAGGT	227099	59295	AATCAAAGGTCATTCCCAGG	271686	103882	TCCTCGATGAGAGGAGGTGC
182513	14709	CCCGTGACATGGGGTCCAGG	227100	59296	GAATCAAAGGTCATTCCCAG	271687	103883	TTCCTCGATGAGAGGAGGTG
182514	14710	CCCCGTGACATGGGGTCCAG	227101	59297	AGAATCAAAGGTCATTCCCA	271688	103884	TTTCCTCGATGAGAGGAGGT
182515	14711	TCCCCGTGACATGGGGTCCA	227102	59298	GAGAATCAAAGGTCATTCCC	271689	103885	CTTTCCTCGATGAGAGGAGG
182516	14712	GTCCCCGTGACATGGGGTCC	227103	59299	GGAGAATCAAAGGTCATTCC	271690	103886	CCTTTCCTCGATGAGAGGAG
182517	14713	AGTCCCCGTGACATGGGGTC	227104	59300	AGGAGAATCAAAGGTCATTC	271691	103887	TCCTTTCCTCGATGAGAGGA
182518	14714	GAGTCCCCGTGACATGGGGT	227105	59301	CAGGAGAATCAAAGGTCATT	271692	103888	GTCCTTTCCTCGATGAGAGG
182519	14715	GGAGTCCCCGTGACATGGGG	227106	59302	GCAGGAGAATCAAAGGTCAT	271693	103889	TGTCCTTTCCTCGATGAGAG
182520	14716	TGGAGTCCCCGTGACATGGG	227107	59303	AGCAGGAGAATCAAAGGTCA	271694	103890	CTGTCCTTTCCTCGATGAGA
182521	14717	GTGGAGTCCCCGTGACATGG	227108	59304	GAGCAGGAGAATCAAAGGTC	271695	103891	TCTGTCCTTTCCTCGATGAG
182522	14718	AGTGGAGTCCCCGTGACATG	227109	59305	GGAGCAGGAGAATCAAAGGT	271696	103892	GTCTGTCCTTTCCTCGATGA
182523	14719	TAGTGGAGTCCCCGTGACAT	227110	59306	AGGAGCAGGAGAATCAAAGG	271697	103893	TGTCTGTCCTTTCCTCGATG
182524	14720	GTAGTGGAGTCCCCGTGACA	227111	59307	CAGGAGCAGGAGAATCAAAG	271698	103894	CTGTCTGTCCTTTCCTCGAT
182525	14721	AGTAGTGGAGTCCCCGTGAC	227112	59308	TCAGGAGCAGGAGAATCAAA	271699	103895	ACTGTCTGTCCTTTCCTCGA
182526	14722	TAGTAGTGGAGTCCCCGTGA	227113	59309	GTCAGGAGCAGGAGAATCAA	271700	103896	CACTGTCTGTCCTTTCCTCG
182527	14723	TTAGTAGTGGAGTCCCCGTG	227114	59310	AGTCAGGAGCAGGAGAATCA	271701	103897	CCACTGTCTGTCCTTTCCTC
182528	14724	CTTAGTAGTGGAGTCCCCGT	227115	59311	AAGTCAGGAGCAGGAGAATC	271702	103898	GCCACTGTCTGTCCTTTCCT
182529	14725	CCTTAGTAGTGGAGTCCCCG	227116	59312	CAAGTCAGGAGCAGGAGAAT	271703	103899	AGCCACTGTCTGTCCTTTCC
182530	14726	GCCTTAGTAGTGGAGTCCCC	227117	59313	CCAAGTCAGGAGCAGGAGAA	271704	103900	GAGCCACTGTCTGTCCTTTC
182531	14727	AGCCTTAGTAGTGGAGTCCC	227118	59314	TCCAAGTCAGGAGCAGGAGA	271705	103901	GGAGCCACTGTCTGTCCTTT
182532	14728	GAGCCTTAGTAGTGGAGTCC	227119	59315	TTCCAAGTCAGGAGCAGGAG	271706	103902	GGGAGCCACTGTCTGTCCTT
182533	14729	GGAGCCTTAGTAGTGGAGTC	227120	59316	GTTCCAAGTCAGGAGCAGGA	271707	103903	GGGGAGCCACTGTCTGTCCT
182534	14730	AGGAGCCTTAGTAGTGGAGT	227121	59317	GGTTCCAAGTCAGGAGCAGG	271708	103904	AGGGGAGCCACTGTCTGTCC
182535	14731	TAGGAGCCTTAGTAGTGGAG	227122	59318	GGGTTCCAAGTCAGGAGCAG	271709	103905	CAGGGGAGCCACTGTCTGTC
182536	14732	TTAGGAGCCTTAGTAGTGGA	227123	59319	TGGGTTCCAAGTCAGGAGCA	271710	103906	ACAGGGGAGCCACTGTCTGT
182537	14733	CTTAGGAGCCTTAGTAGTGG	227124	59320	ATGGGTTCCAAGTCAGGAGC	271711	103907	CACAGGGGAGCCACTGTCTG
182538	14734	TCTTAGGAGCCTTAGTAGTG	227125	59321	CATGGGTTCCAAGTCAGGAG	271712	103908	CCACAGGGGAGCCACTGTCT
182539	14735	GTCTTAGGAGCCTTAGTAGT	227126	59322	CCATGGGTTCCAAGTCAGGA	271713	103909	GCCACAGGGGAGCCACTGTC
182540	14736	AGTCTTAGGAGCCTTAGTAG	227127	59323	TCCATGGGTTCCAAGTCAGG	271714	103910	AGCCACAGGGGAGCCACTGT
182541	14737	CAGTCTTAGGAGCCTTAGTA	227128	59324	TTCCATGGGTTCCAAGTCAG	271715	103911	CAGCCACAGGGGAGCCACTG
182542	14738	GCAGTCTTAGGAGCCTTAGT	227129	59325	TTTCCATGGGTTCCAAGTCA	271716	103912	ACAGCCACAGGGGAGCCACT
182543	14739	GGCAGTCTTAGGAGCCTTAG	227130	59326	GTTTCCATGGGTTCCAAGTC	271717	103913	CACAGCCACAGGGGAGCCAC
182544	14740	TGGCAGTCTTAGGAGCCTTA	227131	59327	GGTTTCCATGGGTTCCAAGT	271718	103914	CCACAGCCACAGGGGAGCCA
182545	14741	GTGGCAGTCTTAGGAGCCTT	227132	59328	AGGTTTCCATGGGTTCCAAG	271719	103915	CCCACAGCCACAGGGGAGCC
182546	14742	GGTGGCAGTCTTAGGAGCCT	227133	59329	GAGGTTTCCATGGGTTCCAA	271720	103916	CCCCACAGCCACAGGGGAGC
182547	14743	AGGTGGCAGTCTTAGGAGCC	227134	59330	AGAGGTTTCCATGGGTTCCA	271721	103917	TCCCCACAGCCACAGGGGAG
182548	14744	AAGGTGGCAGTCTTAGGAGC	227135	59331	TAGAGGTTTCCATGGGTTCC	271722	103918	GTCCCCACAGCCACAGGGGA
182549	14745	GAAGGTGGCAGTCTTAGGAG	227136	59332	CTAGAGGTTTCCATGGGTTC	271723	103919	TGTCCCCACAGCCACAGGGG
182550	14746	GGAAGGTGGCAGTCTTAGGA	227137	59333	TCTAGAGGTTTCCATGGGTT	271724	103920	TTGTCCCCACAGCCACAGGG
182551	14747	TGGAAGGTGGCAGTCTTAGG	227138	59334	TTCTAGAGGTTTCCATGGGT	271725	103921	CTTGTCCCCACAGCCACAGG
182552	14748	CTGGAAGGTGGCAGTCTTAG	227139	59335	CTTCTAGAGGTTTCCATGGG	271726	103922	CCTTGTCCCCACAGCCACAG
182553	14749	ACTGGAAGGTGGCAGTCTTA	227140	59336	GCTTCTAGAGGTTTCCATGG	271727	103923	CCCTTGTCCCCACAGCCACA
182554	14750	CACTGGAAGGTGGCAGTCTT	227141	59337	TGCTTCTAGAGGTTTCCATG	271728	103924	GCCCTTGTCCCCACAGCCAC
182555	14751	CCACTGGAAGGTGGCAGTCT	227142	59338	CTGCTTCTAGAGGTTTCCAT	271729	103925	TGCCCTTGTCCCCACAGCCA
182556	14752	CCCACTGGAAGGTGGCAGTC	227143	59339	GCTGCTTCTAGAGGTTTCCA	271730	103926	CTGCCCTTGTCCCCACAGCC
182557	14753	TCCCACTGGAAGGTGGCAGT	227144	59340	AGCTGCTTCTAGAGGTTTCC	271731	103927	TCTGCCCTTGTCCCCACAGC
182558	14754	ATCCCACTGGAAGGTGGCAG	227145	59341	CAGCTGCTTCTAGAGGTTTC	271732	103928	CTCTGCCCTTGTCCCCACAG
182559	14755	TATCCCACTGGAAGGTGGCA	227146	59342	TCAGCTGCTTCTAGAGGTTT	271733	103929	GCTCTGCCCTTGTCCCCACA
182560	14756	TTATCCCACTGGAAGGTGGC	227147	59343	CTCAGCTGCTTCTAGAGGTT	271734	103930	AGCTCTGCCCTTGTCCCCAC
182561	14757	CTTATCCCACTGGAAGGTGG	227148	59344	CCTCAGCTGCTTCTAGAGGT	271735	103931	GAGCTCTGCCCTTGTCCCCA
182562	14758	GCTTATCCCACTGGAAGGTG	227149	59345	TCCTCAGCTGCTTCTAGAGG	271736	103932	GGAGCTCTGCCCTTGTCCCC

182563	14759	GGCTTATCCCACTGGAAGGT	227150	59346	TTCCTCAGCTGCTTCTAGAG	271737	103933	GGGAGCTCTGCCCTTGTCCC
182564	14760	GGGCTTATCCCACTGGAAGG	227151	59347	TTTCCTCAGCTGCTTCTAGA	271738	103934	AGGGAGCTCTGCCCTTGTCC
182565	14761	AGGGCTTATCCCACTGGAAG	227152	59348	TTTTCCTCAGCTGCTTCTAG	271739	103935	CAGGGAGCTCTGCCCTTGTC
182566	14762	CAGGGCTTATCCCACTGGAA	227153	59349	GTTTTCCTCAGCTGCTTCTA	271740	103936	CCAGGGAGCTCTGCCCTTGT
182567	14763	GCAGGGCTTATCCCACTGGA	227154	59350	GGTTTTCCTCAGCTGCTTCT	271741	103937	TCCAGGGAGCTCTGCCCTTG
182568	14764	GGCAGGGCTTATCCCACTGG	227155	59351	GGGTTTTCCTCAGCTGCTTC	271742	103938	TTCCAGGGAGCTCTGCCCTT
182569	14765	AGGCAGGGCTTATCCCACTG	227156	59352	TGGGTTTTCCTCAGCTGCTT	271743	103939	GTTCCAGGGAGCTCTGCCCT
182570	14766	GAGGCAGGGCTTATCCCACT	227157	59353	TTGGGTTTTCCTCAGCTGCT	271744	103940	TGTTCCAGGGAGCTCTGCCC
182571	14767	GGAGGCAGGGCTTATCCCAC	227158	59354	GTTGGGTTTTCCTCAGCTGC	271745	103941	GTGTTCCAGGGAGCTCTGCC
182572	14768	AGGAGGCAGGGCTTATCCCA	227159	59355	TGTTGGGTTTTCCTCAGCTG	271746	103942	TGTGTTCCAGGGAGCTCTGC
182573	14769	TAGGAGGCAGGGCTTATCCC	227160	59356	ATGTTGGGTTTTCCTCAGCT	271747	103943	CTGTGTTCCAGGGAGCTCTG
182574	14770	GTAGGAGGCAGGGCTTATCC	227161	59357	CATGTTGGGTTTTCCTCAGC	271748	103944	CCTGTGTTCCAGGGAGCTCT
182575	14771	AGTAGGAGGCAGGGCTTATC	227162	59358	TCATGTTGGGTTTTCCTCAG	271749	103945	TCCTGTGTTCCAGGGAGCTC
182576	14772	CAGTAGGAGGCAGGGCTTAT	227163	59359	TTCATGTTGGGTTTTCCTCA	271750	103946	CTCCTGTGTTCCAGGGAGCT
182577	14773	CCAGTAGGAGGCAGGGCTTA	227164	59360	TTTCATGTTGGGTTTTCCTC	271751	103947	CCTCCTGTGTTCCAGGGAGC
182578	14774	CCCAGTAGGAGGCAGGGCTT	227165	59361	TTTTCATGTTGGGTTTTCCT	271752	103948	CCCTCCTGTGTTCCAGGGAG
182579	14775	GCCCAGTAGGAGGCAGGGCT	227166	59362	CTTTTCATGTTGGGTTTTCC	271753	103949	TCCCTCCTGTGTTCCAGGGA
182580	14776	GGCCCAGTAGGAGGCAGGGC	227167	59363	GCTTTTCATGTTGGGTTTTC	271754	103950	CTCCCTCCTGTGTTCCAGGG
182581	14777	GGGCCCAGTAGGAGGCAGGG	227168	59364	TGCTTTTCATGTTGGGTTTT	271755	103951	CCTCCCTCCTGTGTTCCAGG
182582	14778	TGGGCCCAGTAGGAGGCAGG	227169	59365	CTGCTTTTCATGTTGGGTTT	271756	103952	CCCTCCCTCCTGTGTTCCAG
182583	14779	GTGGGCCCAGTAGGAGGCAG	227170	59366	TCTGCTTTTCATGTTGGGTT	271757	103953	TCCCTCCCTCCTGTGTTCCA
182584	14780	TGTGGGCCCAGTAGGAGGCA	227171	59367	TTCTGCTTTTCATGTTGGGT	271758	103954	TTCCCTCCCTCCTGTGTTCC
182585	14781	TTGTGGGCCCAGTAGGAGGC	227172	59368	GTTCTGCTTTTCATGTTGGG	271759	103955	CTTCCCTCCCTCCTGTGTTC
182586	14782	ATTGTGGGCCCAGTAGGAGG	227173	59369	AGTTCTGCTTTTCATGTTGG	271760	103956	CCTTCCCTCCCTCCTGTGTT
182587	14783	CATTGTGGGCCCAGTAGGAG	227174	59370	GAGTTCTGCTTTTCATGTTG	271761	103957	TCCTTCCCTCCCTCCTGTGT
182588	14784	ACATTGTGGGCCCAGTAGGA	227175	59371	GGAGTTCTGCTTTTCATGTT	271762	103958	TTCCTTCCCTCCCTCCTGTG
182589	14785	CACATTGTGGGCCCAGTAGG	227176	59372	TGGAGTTCTGCTTTTCATGT	271763	103959	CTTCCTTCCCTCCCTCCTGT
182590	14786	GCACATTGTGGGCCCAGTAG	227177	59373	GTGGAGTTCTGCTTTTCATG	271764	103960	TCTTCCTTCCCTCCCTCCTG
182591	14787	TGCACATTGTGGGCCCAGTA	227178	59374	TGTGGAGTTCTGCTTTTCAT	271765	103961	CTCTTCCTTCCCTCCCTCCT
182592	14788	CTGCACATTGTGGGCCCAGT	227179	59375	GTGTGGAGTTCTGCTTTTCA	271766	103962	TCTCTTCCTTCCCTCCCTCC
182593	14789	TCTGCACATTGTGGGCCCAG	227180	59376	AGTGTGGAGTTCTGCTTTTC	271767	103963	TTCTCTTCCTTCCCTCCCTC
182594	14790	CTCTGCACATTGTGGGCCCA	227181	59377	CAGTGTGGAGTTCTGCTTTT	271768	103964	GTTCTCTTCCTTCCCTCCCT
182595	14791	TCTCTGCACATTGTGGGCCC	227182	59378	TCAGTGTGGAGTTCTGCTTT	271769	103965	TGTTCTCTTCCTTCCCTCCC
182596	14792	TTCTCTGCACATTGTGGGCC	227183	59379	CTCAGTGTGGAGTTCTGCTT	271770	103966	ATGTTCTCTTCCTTCCCTCC
182597	14793	GTTCTCTGCACATTGTGGGC	227184	59380	TCTCAGTGTGGAGTTCTGCT	271771	103967	GATGTTCTCTTCCTTCCCTC
182598	14794	TGTTCTCTGCACATTGTGGG	227185	59381	TTCTCAGTGTGGAGTTCTGC	271772	103968	AGATGTTCTCTTCCTTCCCT
182599	14795	GTGTTCTCTGCACATTGTGG	227186	59382	ATTCTCAGTGTGGAGTTCTG	271773	103969	GAGATGTTCTCTTCCTTCCC
182600	14796	AGTGTTCTCTGCACATTGTG	227187	59383	TATTCTCAGTGTGGAGTTCT	271774	103970	TGAGATGTTCTCTTCCTTCC
182601	14797	AAGTGTTCTCTGCACATTGT	227188	59384	ATATTCTCAGTGTGGAGTTC	271775	103971	CTGAGATGTTCTCTTCCTTC
182602	14798	CAAGTGTTCTCTGCACATTG	227189	59385	TATATTCTCAGTGTGGAGTT	271776	103972	TCTGAGATGTTCTCTTCCTT
182603	14799	CCAAGTGTTCTCTGCACATT	227190	59386	CTATATTCTCAGTGTGGAGT	271777	103973	TTCTGAGATGTTCTCTTCCT
182604	14800	CCCAAGTGTTCTCTGCACAT	227191	59387	CCTATATTCTCAGTGTGGAG	271778	103974	ATTCTGAGATGTTCTCTTCC
182605	14801	TCCCAAGTGTTCTCTGCACA	227192	59388	TCCTATATTCTCAGTGTGGA	271779	103975	GATTCTGAGATGTTCTCTTC
182606	14802	GTCCCAAGTGTTCTCTGCAC	227193	59389	CTCCTATATTCTCAGTGTGG	271780	103976	AGATTCTGAGATGTTCTCTT
182607	14803	AGTCCCAAGTGTTCTCTGCA	227194	59390	CCTCCTATATTCTCAGTGTG	271781	103977	GAGATTCTGAGATGTTCTCT
182608	14804	TAGTCCCAAGTGTTCTCTGC	227195	59391	ACCTCCTATATTCTCAGTGT	271782	103978	GGAGATTCTGAGATGTTCTC
182609	14805	GTAGTCCCAAGTGTTCTCTG	227196	59392	CACCTCCTATATTCTCAGTG	271783	103979	GGGAGATTCTGAGATGTTCT
182610	14806	GGTAGTCCCAAGTGTTCTCT	227197	59393	TCACCTCCTATATTCTCAGT	271784	103980	AGGGAGATTCTGAGATGTTC
182611	14807	AGGTAGTCCCAAGTGTTCTC	227198	59394	ATCACCTCCTATATTCTCAG	271785	103981	GAGGGAGATTCTGAGATGTT
182612	14808	CAGGTAGTCCCAAGTGTTCT	227199	59395	GATCACCTCCTATATTCTCA	271786	103982	GGAGGGAGATTCTGAGATGT
182613	14809	CCAGGTAGTCCCAAGTGTTC	227200	59396	CGATCACCTCCTATATTCTC	271787	103983	AGGAGGGAGATTCTGAGATG
182614	14810	GCCAGGTAGTCCCAAGTGTT	227201	59397	CCGATCACCTCCTATATTCT	271788	103984	CAGGAGGGAGATTCTGAGAT
182615	14811	AGCCAGGTAGTCCCAAGTGT	227202	59398	TCCGATCACCTCCTATATTC	271789	103985	TCAGGAGGGAGATTCTGAGA
182616	14812	AAGCCAGGTAGTCCCAAGTG	227203	59399	TTCCGATCACCTCCTATATT	271790	103986	ATCAGGAGGGAGATTCTGAG
182617	14813	AAAGCCAGGTAGTCCCAAGT	227204	59400	GTTCCGATCACCTCCTATAT	271791	103987	CATCAGGAGGGAGATTCTGA
182618	14814	GAAAGCCAGGTAGTCCCAAG	227205	59401	TGTTCCGATCACCTCCTATA	271792	103988	CCATCAGGAGGGAGATTCTG
182619	14815	AGAAAGCCAGGTAGTCCCAA	227206	59402	ATGTTCCGATCACCTCCTAT	271793	103989	GCCATCAGGAGGGAGATTCT
182620	14816	CAGAAAGCCAGGTAGTCCCA	227207	59403	TATGTTCCGATCACCTCCTA	271794	103990	TGCCATCAGGAGGGAGATTC
182621	14817	CCAGAAAGCCAGGTAGTCCC	227208	59404	GTATGTTCCGATCACCTCCT	271795	103991	TTGCCATCAGGAGGGAGATT
182622	14818	TCCAGAAAGCCAGGTAGTCC	227209	59405	TGTATGTTCCGATCACCTCC	271796	103992	TTTGCCATCAGGAGGGAGAT
182623	14819	ATCCAGAAAGCCAGGTAGTC	227210	59406	TTGTATGTTCCGATCACCTC	271797	103993	GTTTGCCATCAGGAGGGAGA
182624	14820	TATCCAGAAAGCCAGGTAGT	227211	59407	ATTGTATGTTCCGATCACCT	271798	103994	CGTTTGCCATCAGGAGGGAG
182625	14821	GTATCCAGAAAGCCAGGTAG	227212	59408	CATTGTATGTTCCGATCACC	271799	103995	TCGTTTGCCATCAGGAGGGA
182626	14822	TGTATCCAGAAAGCCAGGTA	227213	59409	TCATTGTATGTTCCGATCAC	271800	103996	ATCGTTTGCCATCAGGAGGG
182627	14823	GTGTATCCAGAAAGCCAGGT	227214	59410	ATCATTGTATGTTCCGATCA	271801	103997	GATCGTTTGCCATCAGGAGG
182628	14824	TGTGTATCCAGAAAGCCAGG	227215	59411	AATCATTGTATGTTCCGATC	271802	103998	GGATCGTTTGCCATCAGGAG
182629	14825	TTGTGTATCCAGAAAGCCAG	227216	59412	GAATCATTGTATGTTCCGAT	271803	103999	CGGATCGTTTGCCATCAGGA
182630	14826	TTTGTGTATCCAGAAAGCCA	227217	59413	AGAATCATTGTATGTTCCGA	271804	104000	CCGGATCGTTTGCCATCAGG
182631	14827	ATTTGTGTATCCAGAAAGCC	227218	59414	AAGAATCATTGTATGTTCCG	271805	104001	CCCGGATCGTTTGCCATCAG
182632	14828	TATTTGTGTATCCAGAAAGC	227219	59415	CAAGAATCATTGTATGTTCC	271806	104002	ACCCGGATCGTTTGCCATCA
182633	14829	ATATTTGTGTATCCAGAAAG	227220	59416	GCAAGAATCATTGTATGTTC	271807	104003	AACCCGGATCGTTTGCCATC
182634	14830	AATATTTGTGTATCCAGAAA	227221	59417	AGCAAGAATCATTGTATGTT	271808	104004	TAACCCGGATCGTTTGCCAT

182635	14831	CAATATTTGTGTATCCAGAA	227222	59418	TAGCAAGAATCATTGTATGT	271809	104005	TTAACCCGGATCGTTTGCCA
182636	14832	TCAATATTTGTGTATCCAGA	227223	59419	TTAGCAAGAATCATTGTATG	271810	104006	TTTAACCCGGATCGTTTGCC
182637	14833	ATCAATATTTGTGTATCCAG	227224	59420	CTTAGCAAGAATCATTGTAT	271811	104007	ATTTAACCCGGATCGTTTGC
182638	14834	GATCAATATTTGTGTATCCA	227225	59421	TCTTAGCAAGAATCATTGTA	271812	104008	AATTTAACCCGGATCGTTTG
182639	14835	GGATCAATATTTGTGTATCC	227226	59422	GTCTTAGCAAGAATCATTGT	271813	104009	TAATTTAACCCGGATCGTTT
182640	14836	TGGATCAATATTTGTGTATC	227227	59423	GGTCTTAGCAAGAATCATTG	271814	104010	TTAATTTAACCCGGATCGTT
182641	14837	TTGGATCAATATTTGTGTAT	227228	59424	CGGTCTTAGCAAGAATCATT	271815	104011	CTTAATTTAACCCGGATCGT
182642	14838	ATTGGATCAATATTTGTGTA	227229	59425	TCGGTCTTAGCAAGAATCAT	271816	104012	CCTTAATTTAACCCGGATCG
182643	14839	GATTGGATCAATATTTGTGT	227230	59426	ATCGGTCTTAGCAAGAATCA	271817	104013	ACCTTAATTTAACCCGGATC
182644	14840	AGATTGGATCAATATTTGTG	227231	59427	AATCGGTCTTAGCAAGAATC	271818	104014	GACCTTAATTTAACCCGGAT
182645	14841	CAGATTGGATCAATATTTGT	227232	59428	GAATCGGTCTTAGCAAGAAT	271819	104015	GGACCTTAATTTAACCCGGA
182646	14842	CCAGATTGGATCAATATTTG	227233	59429	TGAATCGGTCTTAGCAAGAA	271820	104016	CGGACCTTAATTTAACCCGG
182647	14843	TCCAGATTGGATCAATATTT	227234	59430	GTGAATCGGTCTTAGCAAGA	271821	104017	CCGGACCTTAATTTAACCCG
182648	14844	GTCCAGATTGGATCAATATT	227235	59431	TGTGAATCGGTCTTAGCAAG	271822	104018	GCCGGACCTTAATTTAACCC
182649	14845	AGTCCAGATTGGATCAATAT	227236	59432	CTGTGAATCGGTCTTAGCAA	271823	104019	GGCCGGACCTTAATTTAACC
182650	14846	TAGTCCAGATTGGATCAATA	227237	59433	ACTGTGAATCGGTCTTAGCA	271824	104020	AGGCCGGACCTTAATTTAAC
182651	14847	TTAGTCCAGATTGGATCAAT	227238	59434	AACTGTGAATCGGTCTTAGC	271825	104021	AAGGCCGGACCTTAATTTAA
182652	14848	ATTAGTCCAGATTGGATCAA	227239	59435	AAACTGTGAATCGGTCTTAG	271826	104022	AAAGGCCGGACCTTAATTTA
182653	14849	AATTAGTCCAGATTGGATCA	227240	59436	AAAACTGTGAATCGGTCTTA	271827	104023	AAAAGGCCGGACCTTAATTT
182654	14850	TAATTAGTCCAGATTGGATC	227241	59437	AAAAACTGTGAATCGGTCTT	271828	104024	GAAAAGGCCGGACCTTAATT
182655	14851	CTAATTAGTCCAGATTGGAT	227242	59438	GAAAAACTGTGAATCGGTCT	271829	104025	GGAAAAGGCCGGACCTTAAT
182656	14852	TCTAATTAGTCCAGATTGGA	227243	59439	AGAAAAACTGTGAATCGGTC	271830	104026	AGGAAAAGGCCGGACCTTAA
182657	14853	TTCTAATTAGTCCAGATTGG	227244	59440	AAGAAAAACTGTGAATCGGT	271831	104027	CAGGAAAAGGCCGGACCTTA
182658	14854	CTTCTAATTAGTCCAGATTG	227245	59441	AAAGAAAAACTGTGAATCGG	271832	104028	GCAGGAAAAGGCCGGACCTT
182659	14855	CCTTCTAATTAGTCCAGATT	227246	59442	AAAAGAAAAACTGTGAATCG	271833	104029	AGCAGGAAAAGGCCGGACCT
182660	14856	ACCTTCTAATTAGTCCAGAT	227247	59443	AAAAAGAAAAACTGTGAATC	271834	104030	GAGCAGGAAAAGGCCGGACC
182661	14857	GACCTTCTAATTAGTCCAGA	227248	59444	AAAAAAGAAAAACTGTGAAT	271835	104031	TGAGCAGGAAAAGGCCGGAC
182662	14858	TGACCTTCTAATTAGTCCAG	227249	59445	AAAAAAAGAAAAACTGTGAA	271836	104032	CTGAGCAGGAAAAGGCCGGA
182663	14859	CTGACCTTCTAATTAGTCCA	227250	59446	AAAAAAAAGAAAAACTGTGA	271837	104033	CCTGAGCAGGAAAAGGCCGG
182664	14860	ACTGACCTTCTAATTAGTCC	227251	59447	GAAAAAAAAGAAAAACTGTG	271838	104034	GCCTGAGCAGGAAAAGGCCG
182665	14861	GACTGACCTTCTAATTAGTC	227252	59448	CGAAAAAAAAGAAAAACTGT	271839	104035	TGCCTGAGCAGGAAAAGGCC
182666	14862	GGACTGACCTTCTAATTAGT	227253	59449	TCGAAAAAAAAGAAAAACTG	271840	104036	ATGCCTGAGCAGGAAAAGGC
182667	14863	GGGACTGACCTTCTAATTAG	227254	59450	ATCGAAAAAAAAGAAAAACT	271841	104037	CATGCCTGAGCAGGAAAAGG
182668	14864	TGGGACTGACCTTCTAATTA	227255	59451	GATCGAAAAAAAAGAAAAAC	271842	104038	ACATGCCTGAGCAGGAAAAG
182669	14865	TTGGGACTGACCTTCTAATT	227256	59452	CGATCGAAAAAAAAGAAAAA	271843	104039	CACATGCCTGAGCAGGAAAA
182670	14866	ATTGGGACTGACCTTCTAAT	227257	59453	TCGATCGAAAAAAAAGAAAA	271844	104040	CCACATGCCTGAGCAGGAAA
182671	14867	TATTGGGACTGACCTTCTAA	227258	59454	TTCGATCGAAAAAAAAGAAA	271845	104041	TCCACATGCCTGAGCAGGAA
182672	14868	TTATTGGGACTGACCTTCTA	227259	59455	CTTCGATCGAAAAAAAAGAA	271846	104042	CTCCACATGCCTGAGCAGGA
182673	14869	GTTATTGGGACTGACCTTCT	227260	59456	TCTTCGATCGAAAAAAAAGA	271847	104043	GCTCCACATGCCTGAGCAGG
182674	14870	TGTTATTGGGACTGACCTTC	227261	59457	TTCTTCGATCGAAAAAAAAG	271848	104044	AGCTCCACATGCCTGAGCAG
182675	14871	TTGTTATTGGGACTGACCTT	227262	59458	TTTCTTCGATCGAAAAAAAA	271849	104045	AAGCTCCACATGCCTGAGCA
182676	14872	TTTGTTATTGGGACTGACCT	227263	59459	ATTTCTTCGATCGAAAAAAA	271850	104046	CAAGCTCCACATGCCTGAGC
182677	14873	ATTTGTTATTGGGACTGACC	227264	59460	TATTTCTTCGATCGAAAAAA	271851	104047	ACAAGCTCCACATGCCTGAG
182678	14874	GATTTGTTATTGGGACTGAC	227265	59461	GTATTTCTTCGATCGAAAAA	271852	104048	TACAAGCTCCACATGCCTGA
182679	14875	CGATTTGTTATTGGGACTGA	227266	59462	AGTATTTCTTCGATCGAAAA	271853	104049	CTACAAGCTCCACATGCCTG
182680	14876	TCGATTTGTTATTGGGACTG	227267	59463	CAGTATTTCTTCGATCGAAA	271854	104050	ACTACAAGCTCCACATGCCT
182681	14877	TTCGATTTGTTATTGGGACT	227268	59464	CCAGTATTTCTTCGATCGAA	271855	104051	CACTACAAGCTCCACATGCC
182682	14878	CTTCGATTTGTTATTGGGAC	227269	59465	TCCAGTATTTCTTCGATCGA	271856	104052	CCACTACAAGCTCCACATGC
182683	14879	ACTTCGATTTGTTATTGGGA	227270	59466	CTCCAGTATTTCTTCGATCG	271857	104053	TCCACTACAAGCTCCACATG
182684	14880	GACTTCGATTTGTTATTGGG	227271	59467	TCTCCAGTATTTCTTCGATC	271858	104054	TTCCACTACAAGCTCCACAT
182685	14881	TGACTTCGATTTGTTATTGG	227272	59468	TTCTCCAGTATTTCTTCGAT	271859	104055	CTTCCACTACAAGCTCCACA
182686	14882	CTGACTTCGATTTGTTATTG	227273	59469	CTTCTCCAGTATTTCTTCGA	271860	104056	TCTTCCACTACAAGCTCCAC
182687	14883	GCTGACTTCGATTTGTTATT	227274	59470	GCTTCTCCAGTATTTCTTCG	271861	104057	CTCTTCCACTACAAGCTCCA
182688	14884	AGCTGACTTCGATTTGTTAT	227275	59471	GGCTTCTCCAGTATTTCTTC	271862	104058	CCTCTTCCACTACAAGCTCC
182689	14885	CAGCTGACTTCGATTTGTTA	227276	59472	AGGCTTCTCCAGTATTTCTT	271863	104059	GCCTCTTCCACTACAAGCTC
182690	14886	CCAGCTGACTTCGATTTGTT	227277	59473	TAGGCTTCTCCAGTATTTCT	271864	104060	AGCCTCTTCCACTACAAGCT
182691	14887	CCCAGCTGACTTCGATTTGT	227278	59474	TTAGGCTTCTCCAGTATTTC	271865	104061	GAGCCTCTTCCACTACAAGC
182692	14888	GCCCAGCTGACTTCGATTTG	227279	59475	TTTAGGCTTCTCCAGTATTT	271866	104062	AGAGCCTCTTCCACTACAAG
182693	14889	CGCCCAGCTGACTTCGATTT	227280	59476	CTTTAGGCTTCTCCAGTATT	271867	104063	GAGAGCCTCTTCCACTACAA
182694	14890	ACGCCCAGCTGACTTCGATT	227281	59477	TCTTTAGGCTTCTCCAGTAT	271868	104064	AGAGAGCCTCTTCCACTACA
182695	14891	CACGCCCAGCTGACTTCGAT	227282	59478	TTCTTTAGGCTTCTCCAGTA	271869	104065	CAGAGAGCCTCTTCCACTAC
182696	14892	TCACGCCCAGCTGACTTCGA	227283	59479	CTTCTTTAGGCTTCTCCAGT	271870	104066	CCAGAGAGCCTCTTCCACTA
182697	14893	ATCACGCCCAGCTGACTTCG	227284	59480	CCTTCTTTAGGCTTCTCCAG	271871	104067	TCCAGAGAGCCTCTTCCACT
182698	14894	CATCACGCCCAGCTGACTTC	227285	59481	TCCTTCTTTAGGCTTCTCCA	271872	104068	GTCCAGAGAGCCTCTTCCAC
182699	14895	CCATCACGCCCAGCTGACTT	227286	59482	CTCCTTCTTTAGGCTTCTCC	271873	104069	GGTCCAGAGAGCCTCTTCCA
182700	14896	GCCATCACGCCCAGCTGACT	227287	59483	ACTCCTTCTTTAGGCTTCTC	271874	104070	GGGTCCAGAGAGCCTCTTCC
182701	14897	AGCCATCACGCCCAGCTGAC	227288	59484	GACTCCTTCTTTAGGCTTCT	271875	104071	AGGGTCCAGAGAGCCTCTTC
182702	14898	GAGCCATCACGCCCAGCTGA	227289	59485	AGACTCCTTCTTTAGGCTTC	271876	104072	GAGGGTCCAGAGAGCCTCTT
182703	14899	TGAGCCATCACGCCCAGCTG	227290	59486	TAGACTCCTTCTTTAGGCTT	271877	104073	TGAGGGTCCAGAGAGCCTCT
182704	14900	GTGAGCCATCACGCCCAGCT	227291	59487	TTAGACTCCTTCTTTAGGCT	271878	104074	ATGAGGGTCCAGAGAGCCTC
182705	14901	AGTGAGCCATCACGCCCAGC	227292	59488	TTTAGACTCCTTCTTTAGGC	271879	104075	GATGAGGGTCCAGAGAGCCT
182706	14902	GAGTGAGCCATCACGCCCAG	227293	59489	TTTTAGACTCCTTCTTTAGG	271880	104076	GGATGAGGGTCCAGAGAGCC

182707	14903	GGAGTGAGCCATCACGCCCA	227294	59490	TTTTTAGACTCCTTCTTTAG	271881	104077	TGGATGAGGGTCCAGAGAGC
182708	14904	AGGAGTGAGCCATCACGCCC	227295	59491	GTTTTTAGACTCCTTCTTTA	271882	104078	GTGGATGAGGGTCCAGAGAG
182709	14905	TAGGAGTGAGCCATCACGCC	227296	59492	AGTTTTTAGACTCCTTCTTT	271883	104079	GGTGGATGAGGGTCCAGAGA
182710	14906	ATAGGAGTGAGCCATCACGC	227297	59493	GAGTTTTTAGACTCCTTCTT	271884	104080	TGGTGGATGAGGGTCCAGAG
182711	14907	TATAGGAGTGAGCCATCACG	227298	59494	AGAGTTTTTAGACTCCTTCT	271885	104081	GTGGTGGATGAGGGTCCAGA
182712	14908	TTATAGGAGTGAGCCATCAC	227299	59495	CAGAGTTTTTAGACTCCTTC	271886	104082	TGTGGTGGATGAGGGTCCAG
182713	14909	ATTATAGGAGTGAGCCATCA	227300	59496	CCAGAGTTTTTAGACTCCTT	271887	104083	CTGTGGTGGATGAGGGTCCA
182714	14910	GATTATAGGAGTGAGCCATC	227301	59497	GCCAGAGTTTTTAGACTCCT	271888	104084	ACTGTGGTGGATGAGGGTCC
182715	14911	GGATTATAGGAGTGAGCCAT	227302	59498	TGCCAGAGTTTTTAGACTCC	271889	104085	CACTGTGGTGGATGAGGGTC
182716	14912	GGGATTATAGGAGTGAGCCA	227303	59499	GTGCCAGAGTTTTTAGACTC	271890	104086	CCACTGTGGTGGATGAGGGT
182717	14913	TGGGATTATAGGAGTGAGCC	227304	59500	CGTGCCAGAGTTTTTAGACT	271891	104087	GCCACTGTGGTGGATGAGGG
182718	14914	CTGGGATTATAGGAGTGAGC	227305	59501	ACGTGCCAGAGTTTTTAGAC	271892	104088	GGCCACTGTGGTGGATGAGG
182719	14915	GCTGGGATTATAGGAGTGAG	227306	59502	CACGTGCCAGAGTTTTTAGA	271893	104089	AGGCCACTGTGGTGGATGAG
182720	14916	TGCTGGGATTATAGGAGTGA	227307	59503	CCACGTGCCAGAGTTTTTAG	271894	104090	CAGGCCACTGTGGTGGATGA
182721	14917	GTGCTGGGATTATAGGAGTG	227308	59504	CCCACGTGCCAGAGTTTTTA	271895	104091	CCAGGCCACTGTGGTGGATG
182722	14918	AGTGCTGGGATTATAGGAGT	227309	59505	GCCCACGTGCCAGAGTTTTT	271896	104092	ACCAGGCCACTGTGGTGGAT
182723	14919	AAGTGCTGGGATTATAGGAG	227310	59506	GGCCCACGTGCCAGAGTTTT	271897	104093	AACCAGGCCACTGTGGTGGA
182724	14920	AAAGTGCTGGGATTATAGGA	227311	59507	TGGCCCACGTGCCAGAGTTT	271898	104094	TAACCAGGCCACTGTGGTGG
182725	14921	CAAAGTGCTGGGATTATAGG	227312	59508	TTGGCCCACGTGCCAGAGTT	271899	104095	CTAACCAGGCCACTGTGGTG
182726	14922	CCAAAGTGCTGGGATTATAG	227313	59509	TTTGGCCCACGTGCCAGAGT	271900	104096	TCTAACCAGGCCACTGTGGT
182727	14923	CCCAAAGTGCTGGGATTATA	227314	59510	TTTTGGCCCACGTGCCAGAG	271901	104097	CTCTAACCAGGCCACTGTGG
182728	14924	TCCCAAAGTGCTGGGATTAT	227315	59511	GTTTTGGCCCACGTGCCAGA	271902	104098	TCTCTAACCAGGCCACTGTG
182729	14925	CTCCCAAAGTGCTGGGATTA	227316	59512	AGTTTTGGCCCACGTGCCAG	271903	104099	GTCTCTAACCAGGCCACTGT
182730	14926	CCTCCCAAAGTGCTGGGATT	227317	59513	CAGTTTTGGCCCACGTGCCA	271904	104100	GGTCTCTAACCAGGCCACTG
182731	14927	GCCTCCCAAAGTGCTGGGAT	227318	59514	ACAGTTTTGGCCCACGTGCC	271905	104101	AGGTCTCTAACCAGGCCACT
182732	14928	AGCCTCCCAAAGTGCTGGGA	227319	59515	GACAGTTTTGGCCCACGTGC	271906	104102	AAGGTCTCTAACCAGGCCAC
182733	14929	CAGCCTCCCAAAGTGCTGGG	227320	59516	GGACAGTTTTGGCCCACGTG	271907	104103	CAAGGTCTCTAACCAGGCCA
182734	14930	TCAGCCTCCCAAAGTGCTGG	227321	59517	AGGACAGTTTTGGCCCACGT	271908	104104	CCAAGGTCTCTAACCAGGCC
182735	14931	CTCAGCCTCCCAAAGTGCTG	227322	59518	AAGGACAGTTTTGGCCCACG	271909	104105	CCCAAGGTCTCTAACCAGGC
182736	14932	CCTCAGCCTCCCAAAGTGCT	227323	59519	CAAGGACAGTTTTGGCCCAC	271910	104106	CCCCAAGGTCTCTAACCAGG
182737	14933	ACCTCAGCCTCCCAAAGTGC	227324	59520	TCAAGGACAGTTTTGGCCCA	271911	104107	TCCCCAAGGTCTCTAACCAG
182738	14934	CACCTCAGCCTCCCAAAGTG	227325	59521	CTCAAGGACAGTTTTGGCCC	271912	104108	TTCCCCAAGGTCTCTAACCA
182739	14935	CCACCTCAGCCTCCCAAAGT	227326	59522	GCTCAAGGACAGTTTTGGCC	271913	104109	TTTCCCCAAGGTCTCTAACC
182740	14936	CCCACCTCAGCCTCCCAAAG	227327	59523	AGCTCAAGGACAGTTTTGGC	271914	104110	ATTTCCCCAAGGTCTCTAAC
182741	14937	GCCCACCTCAGCCTCCCAAA	227328	59524	TAGCTCAAGGACAGTTTTGG	271915	104111	TATTTCCCCAAGGTCTCTAA
182742	14938	TGCCCACCTCAGCCTCCCAA	227329	59525	TTAGCTCAAGGACAGTTTTG	271916	104112	TTATTTCCCCAAGGTCTCTA
182743	14939	CTGCCCACCTCAGCCTCCCA	227330	59526	CTTAGCTCAAGGACAGTTTT	271917	104113	GTTATTTCCCCAAGGTCTCT
182744	14940	TCTGCCCACCTCAGCCTCCC	227331	59527	TCTTAGCTCAAGGACAGTTT	271918	104114	AGTTATTTCCCCAAGGTCTC
182745	14941	ATCTGCCCACCTCAGCCTCC	227332	59528	TTCTTAGCTCAAGGACAGTT	271919	104115	GAGTTATTTCCCCAAGGTCT
182746	14942	GATCTGCCCACCTCAGCCTC	227333	59529	ATTCTTAGCTCAAGGACAGT	271920	104116	TGAGTTATTTCCCCAAGGTC
182747	14943	TGATCTGCCCACCTCAGCCT	227334	59530	CATTCTTAGCTCAAGGACAG	271921	104117	GTGAGTTATTTCCCCAAGGT
182748	14944	ATGATCTGCCCACCTCAGCC	227335	59531	TCATTCTTAGCTCAAGGACA	271922	104118	TGTGAGTTATTTCCCCAAGG
182749	14945	AATGATCTGCCCACCTCAGC	227336	59532	ATCATTCTTAGCTCAAGGAC	271923	104119	CTGTGAGTTATTTCCCCAAG
182750	14946	AAATGATCTGCCCACCTCAG	227337	59533	AATCATTCTTAGCTCAAGGA	271924	104120	CCTGTGAGTTATTTCCCCAA
182751	14947	CAAATGATCTGCCCACCTCA	227338	59534	AAATCATTCTTAGCTCAAGG	271925	104121	ACCTGTGAGTTATTTCCCCA
182752	14948	TCAAATGATCTGCCCACCTC	227339	59535	AAAATCATTCTTAGCTCAAG	271926	104122	CACCTGTGAGTTATTTCCCC
182753	14949	TTCAAATGATCTGCCCACCT	227340	59536	GAAAATCATTCTTAGCTCAA	271927	104123	TCACCTGTGAGTTATTTCCC
182754	14950	CTTCAAATGATCTGCCCACC	227341	59537	TGAAAATCATTCTTAGCTCA	271928	104124	GTCACCTGTGAGTTATTTCC
182755	14951	GCTTCAAATGATCTGCCCAC	227342	59538	GTGAAAATCATTCTTAGCTC	271929	104125	GGTCACCTGTGAGTTATTTC
182756	14952	GGCTTCAAATGATCTGCCCA	227343	59539	TGTGAAAATCATTCTTAGCT	271930	104126	GGGTCACCTGTGAGTTATTT
182757	14953	TGGCTTCAAATGATCTGCCC	227344	59540	ATGTGAAAATCATTCTTAGC	271931	104127	TGGGTCACCTGTGAGTTATT
182758	14954	CTGGCTTCAAATGATCTGCC	227345	59541	AATGTGAAAATCATTCTTAG	271932	104128	CTGGGTCACCTGTGAGTTAT
182759	14955	TCTGGCTTCAAATGATCTGC	227346	59542	AAATGTGAAAATCATTCTTA	271933	104129	CCTGGGTCACCTGTGAGTTA
182760	14956	TTCTGGCTTCAAATGATCTG	227347	59543	AAAATGTGAAAATCATTCTT	271934	104130	CCCTGGGTCACCTGTGAGTT
182761	14957	CTTCTGGCTTCAAATGATCT	227348	59544	AAAAATGTGAAAATCATTCT	271935	104131	GCCCTGGGTCACCTGTGAGT
182762	14958	ACTTCTGGCTTCAAATGATC	227349	59545	TAAAAATGTGAAAATCATTC	271936	104132	GGCCCTGGGTCACCTGTGAG
182763	14959	AACTTCTGGCTTCAAATGAT	227350	59546	TTAAAAATGTGAAAATCATT	271937	104133	AGGCCCTGGGTCACCTGTGA
182764	14960	GAACTTCTGGCTTCAAATGA	227351	59547	CTTAAAAATGTGAAAATCAT	271938	104134	GAGGCCCTGGGTCACCTGTG
182765	14961	TGAACTTCTGGCTTCAAATG	227352	59548	ACTTAAAAATGTGAAAATCA	271939	104135	AGAGGCCCTGGGTCACCTGT
182766	14962	TTGAACTTCTGGCTTCAAAT	227353	59549	CACTTAAAAATGTGAAAATC	271940	104136	CAGAGGCCCTGGGTCACCTG
182767	14963	CTTGAACTTCTGGCTTCAAA	227354	59550	CCACTTAAAAATGTGAAAAT	271941	104137	ACAGAGGCCCTGGGTCACCT
182768	14964	TCTTGAACTTCTGGCTTCAA	227355	59551	ACCACTTAAAAATGTGAAAA	271942	104138	GACAGAGGCCCTGGGTCACC
182769	14965	GTCTTGAACTTCTGGCTTCA	227356	59552	AACCACTTAAAAATGTGAAA	271943	104139	GGACAGAGGCCCTGGGTCAC
182770	14966	GGTCTTGAACTTCTGGCTTC	227357	59553	CAACCACTTAAAAATGTGAA	271944	104140	AGGACAGAGGCCCTGGGTCA
182771	14967	TGGTCTTGAACTTCTGGCTT	227358	59554	TCAACCACTTAAAAATGTGA	271945	104141	CAGGACAGAGGCCCTGGGTC
182772	14968	CTGGTCTTGAACTTCTGGCT	227359	59555	TTCAACCACTTAAAAATGTG	271946	104142	ACAGGACAGAGGCCCTGGGT
182773	14969	GCTGGTCTTGAACTTCTGGC	227360	59556	TTTCAACCACTTAAAAATGT	271947	104143	TACAGGACAGAGGCCCTGGG
182774	14970	GGCTGGTCTTGAACTTCTGG	227361	59557	TTTTCAACCACTTAAAAATG	271948	104144	GTACAGGACAGAGGCCCTGG
182775	14971	AGGCTGGTCTTGAACTTCTG	227362	59558	TTTTTCAACCACTTAAAAAT	271949	104145	GGTACAGGACAGAGGCCCTG
182776	14972	CAGGCTGGTCTTGAACTTCT	227363	59559	ATTTTTCAACCACTTAAAAA	271950	104146	CGGTACAGGACAGAGGCCCT
182777	14973	CCAGGCTGGTCTTGAACTTC	227364	59560	CATTTTTCAACCACTTAAAA	271951	104147	GCGGTACAGGACAGAGGCCC
182778	14974	CCCAGGCTGGTCTTGAACTT	227365	59561	TCATTTTTCAACCACTTAAA	271952	104148	TGCGGTACAGGACAGAGGCC

182779	14975	GCCCAGGCTGGTCTTGAACT	227366	59562	TTCATTTTTCAACCACTTAA	271953	104149	CTGCGGTACAGGACAGAGGC
182780	14976	TGCCCAGGCTGGTCTTGAAC	227367	59563	TTTCATTTTTCAACCACTTA	271954	104150	GCTGCGGTACAGGACAGAGG
182781	14977	TTGCCCAGGCTGGTCTTGAA	227368	59564	ATTTCATTTTTCAACCACTT	271955	104151	AGCTGCGGTACAGGACAGAG
182782	14978	GTTGCCCAGGCTGGTCTTGA	227369	59565	TATTTCATTTTTCAACCACT	271956	104152	CAGCTGCGGTACAGGACAGA
182783	14979	TGTTGCCCAGGCTGGTCTTG	227370	59566	TTATTTCATTTTTCAACCAC	271957	104153	TCAGCTGCGGTACAGGACAG
182784	14980	ATGTTGCCCAGGCTGGTCTT	227371	59567	TTTATTTCATTTTTCAACCA	271958	104154	CTCAGCTGCGGTACAGGACA
182785	14981	TATGTTGCCCAGGCTGGTCT	227372	59568	TTTTATTTCATTTTTCAACC	271959	104155	CCTCAGCTGCGGTACAGGAC
182786	14982	CTATGTTGCCCAGGCTGGTC	227373	59569	ATTTTATTTCATTTTTCAAC	271960	104156	CCCTCAGCTGCGGTACAGGA
182787	14983	GCTATGTTGCCCAGGCTGGT	227374	59570	TATTTTATTTCATTTTTCAA	271961	104157	TCCCTCAGCTGCGGTACAGG
182788	14984	TGCTATGTTGCCCAGGCTGG	227375	59571	TTATTTTATTTCATTTTTCA	271962	104158	TTCCCTCAGCTGCGGTACAG
182789	14985	TTGCTATGTTGCCCAGGCTG	227376	59572	CTTATTTTATTTCATTTTTC	271963	104159	TTTCCCTCAGCTGCGGTACA
182790	14986	TTTGCTATGTTGCCCAGGCT	227377	59573	TCTTATTTTATTTCATTTTT	271964	104160	GTTTCCCTCAGCTGCGGTAC
182791	14987	TTTTGCTATGTTGCCCAGGC	227378	59574	ATCTTATTTTATTTCATTTT	271965	104161	AGTTTCCCTCAGCTGCGGTA
182792	14988	GTTTTGCTATGTTGCCCAGG	227379	59575	CATCTTATTTTATTTCATTT	271966	104162	CAGTTTCCCTCAGCTGCGGT
182793	14989	GGTTTTGCTATGTTGCCCAG	227380	59576	TCATCTTATTTTATTTCATT	271967	104163	ACAGTTTCCCTCAGCTGCGG
182794	14990	GGGTTTTGCTATGTTGCCCA	227381	59577	ATCATCTTATTTTATTTCAT	271968	104164	GACAGTTTCCCTCAGCTGCG
182795	14991	AGGGTTTTGCTATGTTGCCC	227382	59578	CATCATCTTATTTTATTTCA	271969	104165	GGACAGTTTCCCTCAGCTGC
182796	14992	CAGGGTTTTGCTATGTTGCC	227383	59579	ACATCATCTTATTTTATTTC	271970	104166	AGGACAGTTTCCCTCAGCTG
182797	14993	ACAGGGTTTTGCTATGTTGC	227384	59580	AACATCATCTTATTTTATTT	271971	104167	CAGGACAGTTTCCCTCAGCT
182798	14994	GACAGGGTTTTGCTATGTTG	227385	59581	AAACATCATCTTATTTTATT	271972	104168	GCAGGACAGTTTCCCTCAGC
182799	14995	AGACAGGGTTTTGCTATGTT	227386	59582	AAAACATCATCTTATTTTAT	271973	104169	CGCAGGACAGTTTCCCTCAG
182800	14996	GAGACAGGGTTTTGCTATGT	227387	59583	CAAAACATCATCTTATTTTA	271974	104170	GCGCAGGACAGTTTCCCTCA
182801	14997	AGAGACAGGGTTTTGCTATG	227388	59584	ACAAAACATCATCTTATTTT	271975	104171	AGCGCAGGACAGTTTCCCTC
182802	14998	TAGAGACAGGGTTTTGCTAT	227389	59585	CACAAAACATCATCTTATTT	271976	104172	AAGCGCAGGACAGTTTCCCT
182803	14999	GTAGAGACAGGGTTTTGCTA	227390	59586	TCACAAAACATCATCTTATT	271977	104173	GAAGCGCAGGACAGTTTCCC
182804	15000	AGTAGAGACAGGGTTTTGCT	227391	59587	GTCACAAAACATCATCTTAT	271978	104174	GGAAGCGCAGGACAGTTTCC
182805	15001	TAGTAGAGACAGGGTTTTGC	227392	59588	TGTCACAAAACATCATCTTA	271979	104175	TGGAAGCGCAGGACAGTTTC
182806	15002	TTAGTAGAGACAGGGTTTTG	227393	59589	GTGTCACAAAACATCATCTT	271980	104176	GTGGAAGCGCAGGACAGTTT
182807	15003	TTTAGTAGAGACAGGGTTTT	227394	59590	TGTGTCACAAAACATCATCT	271981	104177	AGTGGAAGCGCAGGACAGTT
182808	15004	TTTTAGTAGAGACAGGGTTT	227395	59591	ATGTGTCACAAAACATCATC	271982	104178	CAGTGGAAGCGCAGGACAGT
182809	15005	TTTTTAGTAGAGACAGGGTT	227396	59592	CATGTGTCACAAAACATCAT	271983	104179	CCAGTGGAAGCGCAGGACAG
182810	15006	ATTTTTAGTAGAGACAGGGT	227397	59593	TCATGTGTCACAAAACATCA	271984	104180	CCCAGTGGAAGCGCAGGACA
182811	15007	TATTTTTAGTAGAGACAGGG	227398	59594	TTCATGTGTCACAAAACATC	271985	104181	CCCCAGTGGAAGCGCAGGAC
182812	15008	GTATTTTTAGTAGAGACAGG	227399	59595	TTTCATGTGTCACAAAACAT	271986	104182	TCCCCAGTGGAAGCGCAGGA
182813	15009	TGTATTTTTAGTAGAGACAG	227400	59596	CTTTCATGTGTCACAAAACA	271987	104183	GTCCCCAGTGGAAGCGCAGG
182814	15010	TTGTATTTTTAGTAGAGACA	227401	59597	GCTTTCATGTGTCACAAAAC	271988	104184	TGTCCCCAGTGGAAGCGCAG
182815	15011	TTTGTATTTTTAGTAGAGAC	227402	59598	AGCTTTCATGTGTCACAAAA	271989	104185	TTGTCCCCAGTGGAAGCGCA
182816	15012	ATTTGTATTTTTAGTAGAGA	227403	59599	TAGCTTTCATGTGTCACAAA	271990	104186	ATTGTCCCCAGTGGAAGCGC
182817	15013	TATTTGTATTTTTAGTAGAG	227404	59600	ATAGCTTTCATGTGTCACAA	271991	104187	CATTGTCCCCAGTGGAAGCG
182818	15014	TTATTTGTATTTTTAGTAGA	227405	59601	CATAGCTTTCATGTGTCACA	271992	104188	GCATTGTCCCCAGTGGAAGC
182819	15015	ATTATTTGTATTTTTAGTAG	227406	59602	CCATAGCTTTCATGTGTCAC	271993	104189	CGCATTGTCCCCAGTGGAAG
182820	15016	AATTATTTGTATTTTTAGTA	227407	59603	CCCATAGCTTTCATGTGTCA	271994	104190	GCGCATTGTCCCCAGTGGAA
182821	15017	TAATTATTTGTATTTTTAGT	227408	59604	TCCCATAGCTTTCATGTGTC	271995	104191	AGCGCATTGTCCCCAGTGGA
182822	15018	CTAATTATTTGTATTTTTAG	227409	59605	TTCCCATAGCTTTCATGTGT	271996	104192	GAGCGCATTGTCCCCAGTGG
182823	15019	CCTAATTATTTGTATTTTTA	227410	59606	TTTCCCATAGCTTTCATGTG	271997	104193	GGAGCGCATTGTCCCCAGTG
182824	15020	GCCTAATTATTTGTATTTTT	227411	59607	ATTTCCCATAGCTTTCATGT	271998	104194	GGGAGCGCATTGTCCCCAGT
182825	15021	AGCCTAATTATTTGTATTTT	227412	59608	AATTTCCCATAGCTTTCATG	271999	104195	AGGGAGCGCATTGTCCCCAG
182826	15022	CAGCCTAATTATTTGTATTT	227413	59609	GAATTTCCCATAGCTTTCAT	272000	104196	GAGGGAGCGCATTGTCCCCA
182827	15023	CCAGCCTAATTATTTGTATT	227414	59610	TGAATTTCCCATAGCTTTCA	272001	104197	CGAGGGAGCGCATTGTCCCC
182828	15024	CCCAGCCTAATTATTTGTAT	227415	59611	TTGAATTTCCCATAGCTTTC	272002	104198	ACGAGGGAGCGCATTGTCCC
182829	15025	ACCCAGCCTAATTATTTGTA	227416	59612	TTTGAATTTCCCATAGCTTT	272003	104199	GACGAGGGAGCGCATTGTCC
182830	15026	CACCCAGCCTAATTATTTGT	227417	59613	ATTTGAATTTCCCATAGCTT	272004	104200	AGACGAGGGAGCGCATTGTC
182831	15027	ACACCCAGCCTAATTATTTG	227418	59614	AATTTGAATTTCCCATAGCT	272005	104201	GAGACGAGGGAGCGCATTGT
182832	15028	CACACCCAGCCTAATTATTT	227419	59615	GAATTTGAATTTCCCATAGC	272006	104202	GGAGACGAGGGAGCGCATTG
182833	15029	CCACACCCAGCCTAATTATT	227420	59616	AGAATTTGAATTTCCCATAG	272007	104203	TGGAGACGAGGGAGCGCATT
182834	15030	ACCACACCCAGCCTAATTAT	227421	59617	TAGAATTTGAATTTCCCATA	272008	104204	CTGGAGACGAGGGAGCGCAT
182835	15031	CACCACACCCAGCCTAATTA	227422	59618	TTAGAATTTGAATTTCCCAT	272009	104205	TCTGGAGACGAGGGAGCGCA
182836	15032	CCACCACACCCAGCCTAATT	227423	59619	ATTAGAATTTGAATTTCCCA	272010	104206	GTCTGGAGACGAGGGAGCGC
182837	15033	GCCACCACACCCAGCCTAAT	227424	59620	TATTAGAATTTGAATTTCCC	272011	104207	AGTCTGGAGACGAGGGAGCG
182838	15034	AGCCACCACACCCAGCCTAA	227425	59621	ATATTAGAATTTGAATTTCC	272012	104208	AAGTCTGGAGACGAGGGAGC
182839	15035	GAGCCACCACACCCAGCCTA	227426	59622	GATATTAGAATTTGAATTTC	272013	104209	AAAGTCTGGAGACGAGGGAG
182840	15036	TGAGCCACCACACCCAGCCT	227427	59623	AGATATTAGAATTTGAATTT	272014	104210	GAAAGTCTGGAGACGAGGGA
182841	15037	ATGAGCCACCACACCCAGCC	227428	59624	TAGATATTAGAATTTGAATT	272015	104211	GGAAAGTCTGGAGACGAGGG
182842	15038	CATGAGCCACCACACCCAGC	227429	59625	ATAGATATTAGAATTTGAAT	272016	104212	TGGAAAGTCTGGAGACGAGG
182843	15039	GCATGAGCCACCACACCCAG	227430	59626	TATAGATATTAGAATTTGAA	272017	104213	CTGGAAAGTCTGGAGACGAG
182844	15040	GGCATGAGCCACCACACCCA	227431	59627	TTATAGATATTAGAATTTGA	272018	104214	ACTGGAAAGTCTGGAGACGA
182845	15041	AGGCATGAGCCACCACACCC	227432	59628	TTTATAGATATTAGAATTTG	272019	104215	GACTGGAAAGTCTGGAGACG
182846	15042	CAGGCATGAGCCACCACACC	227433	59629	ATTTATAGATATTAGAATTT	272020	104216	GGACTGGAAAGTCTGGAGAC
182847	15043	ACAGGCATGAGCCACCACAC	227434	59630	TATTTATAGATATTAGAATT	272021	104217	AGGACTGGAAAGTCTGGAGA
182848	15044	TACAGGCATGAGCCACCACA	227435	59631	CTATTTATAGATATTAGAAT	272022	104218	GAGGACTGGAAAGTCTGGAG
182849	15045	TTACAGGCATGAGCCACCAC	227436	59632	ACTATTTATAGATATTAGAA	272023	104219	TGAGGACTGGAAAGTCTGGA
182850	15046	ATTACAGGCATGAGCCACCA	227437	59633	CACTATTTATAGATATTAGA	272024	104220	ATGAGGACTGGAAAGTCTGG

182851	15047	GATTACAGGCATGAGCCACC	227438	59634	ACACTATTTATAGATATTAG	272025	104221	AATGAGGACTGGAAAGTCTG
182852	15048	GGATTACAGGCATGAGCCAC	227439	59635	AACACTATTTATAGATATTA	272026	104222	GAATGAGGACTGGAAAGTCT
182853	15049	GGGATTACAGGCATGAGCCA	227440	59636	AAACACTATTTATAGATATT	272027	104223	CGAATGAGGACTGGAAAGTC
182854	15050	TGGGATTACAGGCATGAGCC	227441	59637	AAAACACTATTTATAGATAT	272028	104224	CCGAATGAGGACTGGAAAGT
182855	15051	TTGGGATTACAGGCATGAGC	227442	59638	TAAAACACTATTTATAGATA	272029	104225	ACCGAATGAGGACTGGAAAG
182856	15052	GTTGGGATTACAGGCATGAG	227443	59639	ATAAAACACTATTTATAGAT	272030	104226	AACCGAATGAGGACTGGAAA
182857	15053	TGTTGGGATTACAGGCATGA	227444	59640	GATAAAACACTATTTATAGA	272031	104227	GAACCGAATGAGGACTGGAA
182858	15054	CTGTTGGGATTACAGGCATG	227445	59641	TGATAAAACACTATTTATAG	272032	104228	AGAACCGAATGAGGACTGGA
182859	15055	ACTGTTGGGATTACAGGCAT	227446	59642	CTGATAAAACACTATTTATA	272033	104229	GAGAACCGAATGAGGACTGG
182860	15056	AACTGTTGGGATTACAGGCA	227447	59643	TCTGATAAAACACTATTTAT	272034	104230	CGAGAACCGAATGAGGACTG
182861	15057	AAACTGTTGGGATTACAGGC	227448	59644	TTCTGATAAAACACTATTTA	272035	104231	TCGAGAACCGAATGAGGACT
182862	15058	CAAACTGTTGGGATTACAGG	227449	59645	GTTCTGATAAAACACTATTT	272036	104232	TTCGAGAACCGAATGAGGAC
182863	15059	CCAAACTGTTGGGATTACAG	227450	59646	TGTTCTGATAAAACACTATT	272037	104233	TTTCGAGAACCGAATGAGGA
182864	15060	CCCAAACTGTTGGGATTACA	227451	59647	GTGTTCTGATAAAACACTAT	272038	104234	CTTTCGAGAACCGAATGAGG
182865	15061	TCCCAAACTGTTGGGATTAC	227452	59648	TGTGTTCTGATAAAACACTA	272039	104235	ACTTTCGAGAACCGAATGAG
182866	15062	CTCCCAAACTGTTGGGATTA	227453	59649	CTGTGTTCTGATAAAACACT	272040	104236	GACTTTCGAGAACCGAATGA
182867	15063	CCTCCCAAACTGTTGGGATT	227454	59650	ACTGTGTTCTGATAAAACAC	272041	104237	CGACTTTCGAGAACCGAATG
182868	15064	GCCTCCCAAACTGTTGGGAT	227455	59651	GACTGTGTTCTGATAAAACA	272042	104238	GCGACTTTCGAGAACCGAAT
182869	15065	AGCCTCCCAAACTGTTGGGA	227456	59652	TGACTGTGTTCTGATAAAAC	272043	104239	GGCGACTTTCGAGAACCGAA
182870	15066	CAGCCTCCCAAACTGTTGGG	227457	59653	ATGACTGTGTTCTGATAAAA	272044	104240	AGGCGACTTTCGAGAACCGA
182871	15067	TCAGCCTCCCAAACTGTTGG	227458	59654	CATGACTGTGTTCTGATAAA	272045	104241	GAGGCGACTTTCGAGAACCG
182872	15068	CTCAGCCTCCCAAACTGTTG	227459	59655	GCATGACTGTGTTCTGATAA	272046	104242	GGAGGCGACTTTCGAGAACC
182873	15069	CCTCAGCCTCCCAAACTGTT	227460	59656	AGCATGACTGTGTTCTGATA	272047	104243	TGGAGGCGACTTTCGAGAAC
182874	15070	GCCTCAGCCTCCCAAACTGT	227461	59657	GAGCATGACTGTGTTCTGAT	272048	104244	CTGGAGGCGACTTTCGAGAA
182875	15071	TGCCTCAGCCTCCCAAACTG	227462	59658	TGAGCATGACTGTGTTCTGA	272049	104245	TCTGGAGGCGACTTTCGAGA
182876	15072	CTGCCTCAGCCTCCCAAACT	227463	59659	ATGAGCATGACTGTGTTCTG	272050	104246	TTCTGGAGGCGACTTTCGAG
182877	15073	CCTGCCTCAGCCTCCCAAAC	227464	59660	AATGAGCATGACTGTGTTCT	272051	104247	CTTCTGGAGGCGACTTTCGA
182878	15074	ACCTGCCTCAGCCTCCCAAA	227465	59661	AAATGAGCATGACTGTGTTC	272052	104248	GCTTCTGGAGGCGACTTTCG
182879	15075	CACCTGCCTCAGCCTCCCAA	227466	59662	TAAATGAGCATGACTGTGTT	272053	104249	GGCTTCTGGAGGCGACTTTC
182880	15076	CCACCTGCCTCAGCCTCCCA	227467	59663	ATAAATGAGCATGACTGTGT	272054	104250	GGGCTTCTGGAGGCGACTTT
182881	15077	ACCACCTGCCTCAGCCTCCC	227468	59664	AATAAATGAGCATGACTGTG	272055	104251	GGGGCTTCTGGAGGCGACTT
182882	15078	GACCACCTGCCTCAGCCTCC	227469	59665	AAATAAATGAGCATGACTGT	272056	104252	TGGGGCTTCTGGAGGCGACT
182883	15079	TGACCACCTGCCTCAGCCTC	227470	59666	TAAATAAATGAGCATGACTG	272057	104253	ATGGGGCTTCTGGAGGCGAC
182884	15080	GTGACCACCTGCCTCAGCCT	227471	59667	ATAAATAAATGAGCATGACT	272058	104254	GATGGGGCTTCTGGAGGCGA
182885	15081	GGTGACCACCTGCCTCAGCC	227472	59668	CATAAATAAATGAGCATGAC	272059	104255	AGATGGGGCTTCTGGAGGCG
182886	15082	AGGTGACCACCTGCCTCAGC	227473	59669	GCATAAATAAATGAGCATGA	272060	104256	AAGATGGGGCTTCTGGAGGC
182887	15083	CAGGTGACCACCTGCCTCAG	227474	59670	AGCATAAATAAATGAGCATG	272061	104257	CAAGATGGGGCTTCTGGAGG
182888	15084	TCAGGTGACCACCTGCCTCA	227475	59671	GAGCATAAATAAATGAGCAT	272062	104258	CCAAGATGGGGCTTCTGGAG
182889	15085	CTCAGGTGACCACCTGCCTC	227476	59672	CGAGCATAAATAAATGAGCA	272063	104259	CCCAAGATGGGGCTTCTGGA
182890	15086	CCTCAGGTGACCACCTGCCT	227477	59673	TCGAGCATAAATAAATGAGC	272064	104260	TCCCAAGATGGGGCTTCTGG
182891	15087	ACCTCAGGTGACCACCTGCC	227478	59674	ATCGAGCATAAATAAATGAG	272065	104261	GTCCCAAGATGGGGCTTCTG
182892	15088	GACCTCAGGTGACCACCTGC	227479	59675	CATCGAGCATAAATAAATGA	272066	104262	GGTCCCAAGATGGGGCTTCT
182893	15089	TGACCTCAGGTGACCACCTG	227480	59676	CCATCGAGCATAAATAAATG	272067	104263	TGGTCCCAAGATGGGGCTTC
182894	15090	CTGACCTCAGGTGACCACCT	227481	59677	GCCATCGAGCATAAATAAAT	272068	104264	GTGGTCCCAAGATGGGGCTT
182895	15091	CCTGACCTCAGGTGACCACC	227482	59678	AGCCATCGAGCATAAATAAA	272069	104265	GGTGGTCCCAAGATGGGGCT
182896	15092	TCCTGACCTCAGGTGACCAC	227483	59679	CAGCCATCGAGCATAAATAA	272070	104266	CGGTGGTCCCAAGATGGGGC
182897	15093	CTCCTGACCTCAGGTGACCA	227484	59680	GCAGCCATCGAGCATAAATA	272071	104267	ACGGTGGTCCCAAGATGGGG
182898	15094	ACTCCTGACCTCAGGTGACC	227485	59681	AGCAGCCATCGAGCATAAAT	272072	104268	CACGGTGGTCCCAAGATGGG
182899	15095	AACTCCTGACCTCAGGTGAC	227486	59682	AAGCAGCCATCGAGCATAAA	272073	104269	TCACGGTGGTCCCAAGATGG
182900	15096	AAACTCCTGACCTCAGGTGA	227487	59683	AAAGCAGCCATCGAGCATAA	272074	104270	GTCACGGTGGTCCCAAGATG
182901	15097	CAAACTCCTGACCTCAGGTG	227488	59684	GAAAGCAGCCATCGAGCATA	272075	104271	AGTCACGGTGGTCCCAAGAT
182902	15098	TCAAACTCCTGACCTCAGGT	227489	59685	GGAAAGCAGCCATCGAGCAT	272076	104272	AAGTCACGGTGGTCCCAAGA
182903	15099	CTCAAACTCCTGACCTCAGG	227490	59686	GGGAAAGCAGCCATCGAGCA	272077	104273	AAAGTCACGGTGGTCCCAAG
182904	15100	TCTCAAACTCCTGACCTCAG	227491	59687	CGGGAAAGCAGCCATCGAGC	272078	104274	GAAAGTCACGGTGGTCCCAA
182905	15101	GTCTCAAACTCCTGACCTCA	227492	59688	GCGGGAAAGCAGCCATCGAG	272079	104275	TGAAAGTCACGGTGGTCCCA
182906	15102	GGTCTCAAACTCCTGACCTC	227493	59689	AGCGGGAAAGCAGCCATCGA	272080	104276	ATGAAAGTCACGGTGGTCCC
182907	15103	TGGTCTCAAACTCCTGACCT	227494	59690	TAGCGGGAAAGCAGCCATCG	272081	104277	AATGAAAGTCACGGTGGTCC
182908	15104	CTGGTCTCAAACTCCTGACC	227495	59691	GTAGCGGGAAAGCAGCCATC	272082	104278	GAATGAAAGTCACGGTGGTC
182909	15105	GCTGGTCTCAAACTCCTGAC	227496	59692	TGTAGCGGGAAAGCAGCCAT	272083	104279	AGAATGAAAGTCACGGTGGT
182910	15106	GGCTGGTCTCAAACTCCTGA	227497	59693	TTGTAGCGGGAAAGCAGCCA	272084	104280	GAGAATGAAAGTCACGGTGG
182911	15107	AGGCTGGTCTCAAACTCCTG	227498	59694	ATTGTAGCGGGAAAGCAGCC	272085	104281	GGAGAATGAAAGTCACGGTG
182912	15108	CAGGCTGGTCTCAAACTCCT	227499	59695	AATTGTAGCGGGAAAGCAGC	272086	104282	TGGAGAATGAAAGTCACGGT
182913	15109	CCAGGCTGGTCTCAAACTCC	227500	59696	TAATTGTAGCGGGAAAGCAG	272087	104283	CTGGAGAATGAAAGTCACGG
182914	15110	GCCAGGCTGGTCTCAAACTC	227501	59697	GTAATTGTAGCGGGAAAGCA	272088	104284	CCTGGAGAATGAAAGTCACG
182915	15111	GGCCAGGCTGGTCTCAAACT	227502	59698	CGTAATTGTAGCGGGAAAGC	272089	104285	CCCTGGAGAATGAAAGTCAC
182916	15112	TGGCCAGGCTGGTCTCAAAC	227503	59699	ACGTAATTGTAGCGGGAAAG	272090	104286	ACCCTGGAGAATGAAAGTCA
182917	15113	TTGGCCAGGCTGGTCTCAAA	227504	59700	AACGTAATTGTAGCGGGAAA	272091	104287	CACCCTGGAGAATGAAAGTC
182918	15114	GTTGGCCAGGCTGGTCTCAA	227505	59701	CAACGTAATTGTAGCGGGAA	272092	104288	GCACCCTGGAGAATGAAAGT
182919	15115	TGTTGGCCAGGCTGGTCTCA	227506	59702	TCAACGTAATTGTAGCGGGA	272093	104289	GGCACCCTGGAGAATGAAAG
182920	15116	CTGTTGGCCAGGCTGGTCTC	227507	59703	CTCAACGTAATTGTAGCGGG	272094	104290	AGGCACCCTGGAGAATGAAA
182921	15117	CCTGTTGGCCAGGCTGGTCT	227508	59704	GCTCAACGTAATTGTAGCGG	272095	104291	CAGGCACCCTGGAGAATGAA
182922	15118	CCCTGTTGGCCAGGCTGGTC	227509	59705	TGCTCAACGTAATTGTAGCG	272096	104292	CCAGGCACCCTGGAGAATGA

182923	15119	ACCCTGTTGGCCAGGCTGGT	227510	59706	CTGCTCAACGTAATTGTAGC	272097	104293	GCCAGGCACCCTGGAGAATG
182924	15120	CACCCTGTTGGCCAGGCTGG	227511	59707	ACTGCTCAACGTAATTGTAG	272098	104294	GGCCAGGCACCCTGGAGAAT
182925	15121	TCACCCTGTTGGCCAGGCTG	227512	59708	AACTGCTCAACGTAATTGTA	272099	104295	AGGCCAGGCACCCTGGAGAA
182926	15122	TTCACCCTGTTGGCCAGGCT	227513	59709	TAACTGCTCAACGTAATTGT	272100	104296	AAGGCCAGGCACCCTGGAGA
182927	15123	TTTCACCCTGTTGGCCAGGC	227514	59710	GTAACTGCTCAACGTAATTG	272101	104297	CAAGGCCAGGCACCCTGGAG
182928	15124	GTTTCACCCTGTTGGCCAGG	227515	59711	TGTAACTGCTCAACGTAATT	272102	104298	CCAAGGCCAGGCACCCTGGA
182929	15125	GGTTTCACCCTGTTGGCCAG	227516	59712	TTGTAACTGCTCAACGTAAT	272103	104299	ACCAAGGCCAGGCACCCTGG
182930	15126	GGGTTTCACCCTGTTGGCCA	227517	59713	GTTGTAACTGCTCAACGTAA	272104	104300	CACCAAGGCCAGGCACCCTG
182931	15127	GGGGTTTCACCCTGTTGGCC	227518	59714	TGTTGTAACTGCTCAACGTA	272105	104301	GCACCAAGGCCAGGCACCCT
182932	15128	CGGGGTTTCACCCTGTTGGC	227519	59715	CTGTTGTAACTGCTCAACGT	272106	104302	AGCACCAAGGCCAGGCACCC
182933	15129	ACGGGGTTTCACCCTGTTGG	227520	59716	TCTGTTGTAACTGCTCAACG	272107	104303	CAGCACCAAGGCCAGGCACC
182934	15130	CACGGGGTTTCACCCTGTTG	227521	59717	CTCTGTTGTAACTGCTCAAC	272108	104304	GCAGCACCAAGGCCAGGCAC
182935	15131	ACACGGGGTTTCACCCTGTT	227522	59718	TCTCTGTTGTAACTGCTCAA	272109	104305	GGCAGCACCAAGGCCAGGCA
182936	15132	GACACGGGGTTTCACCCTGT	227523	59719	GTCTCTGTTGTAACTGCTCA	272110	104306	GGGCAGCACCAAGGCCAGGC
182937	15133	AGACACGGGGTTTCACCCTG	227524	59720	GGTCTCTGTTGTAACTGCTC	272111	104307	TGGGCAGCACCAAGGCCAGG
182938	15134	TAGACACGGGGTTTCACCCT	227525	59721	TGGTCTCTGTTGTAACTGCT	272112	104308	TTGGGCAGCACCAAGGCCAG
182939	15135	GTAGACACGGGGTTTCACCC	227526	59722	GTGGTCTCTGTTGTAACTGC	272113	104309	CTTGGGCAGCACCAAGGCCA
182940	15136	AGTAGACACGGGGTTTCACC	227527	59723	CGTGGTCTCTGTTGTAACTG	272114	104310	TCTTGGGCAGCACCAAGGCC
182941	15137	TAGTAGACACGGGGTTTCAC	227528	59724	ACGTGGTCTCTGTTGTAACT	272115	104311	GTCTTGGGCAGCACCAAGGC
182942	15138	TTAGTAGACACGGGGTTTCA	227529	59725	CACGTGGTCTCTGTTGTAAC	272116	104312	GGTCTTGGGCAGCACCAAGG
182943	15139	TTTAGTAGACACGGGGTTTC	227530	59726	CCACGTGGTCTCTGTTGTAA	272117	104313	GGGTCTTGGGCAGCACCAAG
182944	15140	TTTTAGTAGACACGGGGTTT	227531	59727	GCCACGTGGTCTCTGTTGTA	272118	104314	GGGGTCTTGGGCAGCACCAA
182945	15141	TTTTTAGTAGACACGGGGTT	227532	59728	GGCCACGTGGTCTCTGTTGT	272119	104315	TGGGGTCTTGGGCAGCACCA
182946	15142	GTTTTTAGTAGACACGGGGT	227533	59729	GGGCCACGTGGTCTCTGTTG	272120	104316	CTGGGGTCTTGGGCAGCACC
182947	15143	TGTTTTTAGTAGACACGGGG	227534	59730	TGGGCCACGTGGTCTCTGTT	272121	104317	TCTGGGGTCTTGGGCAGCAC
182948	15144	ATGTTTTTAGTAGACACGGG	227535	59731	GTGGGCCACGTGGTCTCTGT	272122	104318	CTCTGGGGTCTTGGGCAGCA
182949	15145	TATGTTTTTAGTAGACACGG	227536	59732	TGTGGGCCACGTGGTCTCTG	272123	104319	CCTCTGGGGTCTTGGGCAGC
182950	15146	TTATGTTTTTAGTAGACACG	227537	59733	TTGTGGGCCACGTGGTCTCT	272124	104320	CCCTCTGGGGTCTTGGGCAG
182951	15147	TTTATGTTTTTAGTAGACAC	227538	59734	TTTGTGGGCCACGTGGTCTC	272125	104321	CCCCTCTGGGGTCTTGGGCA
182952	15148	TTTTATGTTTTTAGTAGACA	227539	59735	CTTTGTGGGCCACGTGGTCT	272126	104322	GCCCCTCTGGGGTCTTGGGC
182953	15149	TTTTTATGTTTTTAGTAGAC	227540	59736	GCTTTGTGGGCCACGTGGTC	272127	104323	GGCCCCTCTGGGGTCTTGGG
182954	15150	ATTTTTATGTTTTTAGTAGA	227541	59737	GGCTTTGTGGGCCACGTGGT	272128	104324	GGGCCCCTCTGGGGTCTTGG
182955	15151	AATTTTTATGTTTTTAGTAG	227542	59738	AGGCTTTGTGGGCCACGTGG	272129	104325	AGGGCCCCTCTGGGGTCTTG
182956	15152	TAATTTTTATGTTTTTAGTA	227543	59739	AAGGCTTTGTGGGCCACGTG	272130	104326	GAGGGCCCCTCTGGGGTCTT
182957	15153	CTAATTTTTATGTTTTTAGT	227544	59740	TAAGGCTTTGTGGGCCACGT	272131	104327	TGAGGGCCCCTCTGGGGTCT
182958	15154	GCTAATTTTTATGTTTTTAG	227545	59741	GTAAGGCTTTGTGGGCCACG	272132	104328	GTGAGGGCCCCTCTGGGGTC
182959	15155	GGCTAATTTTTATGTTTTTA	227546	59742	TGTAAGGCTTTGTGGGCCAC	272133	104329	AGTGAGGGCCCCTCTGGGGT
182960	15156	TGGCTAATTTTTATGTTTTT	227547	59743	TTGTAAGGCTTTGTGGGCCA	272134	104330	CAGTGAGGGCCCCTCTGGGG
182961	15157	TTGGCTAATTTTTATGTTTT	227548	59744	ATTGTAAGGCTTTGTGGGCC	272135	104331	CCAGTGAGGGCCCCTCTGGG
182962	15158	CTTGGCTAATTTTTATGTTT	227549	59745	TATTGTAAGGCTTTGTGGGC	272136	104332	GCCAGTGAGGGCCCCTCTGG
182963	15159	GCTTGGCTAATTTTTATGTT	227550	59746	ATATTGTAAGGCTTTGTGGG	272137	104333	GGCCAGTGAGGGCCCCTCTG
182964	15160	TGCTTGGCTAATTTTTATGT	227551	59747	AATATTGTAAGGCTTTGTGG	272138	104334	AGGCCAGTGAGGGCCCCTCT
182965	15161	ATGCTTGGCTAATTTTTATG	227552	59748	AAATATTGTAAGGCTTTGTG	272139	104335	AAGGCCAGTGAGGGCCCCTC
182966	15162	CATGCTTGGCTAATTTTTAT	227553	59749	TAAATATTGTAAGGCTTTGT	272140	104336	AAAGGCCAGTGAGGGCCCCT
182967	15163	TCATGCTTGGCTAATTTTTA	227554	59750	GTAAATATTGTAAGGCTTTG	272141	104337	GAAAGGCCAGTGAGGGCCCC
182968	15164	ATCATGCTTGGCTAATTTTT	227555	59751	AGTAAATATTGTAAGGCTTT	272142	104338	GGAAAGGCCAGTGAGGGCCC
182969	15165	CATCATGCTTGGCTAATTTT	227556	59752	TAGTAAATATTGTAAGGCTT	272143	104339	AGGAAAGGCCAGTGAGGGCC
182970	15166	CCATCATGCTTGGCTAATTT	227557	59753	ATAGTAAATATTGTAAGGCT	272144	104340	CAGGAAAGGCCAGTGAGGGC
182971	15167	GCCATCATGCTTGGCTAATT	227558	59754	GATAGTAAATATTGTAAGGC	272145	104341	GCAGGAAAGGCCAGTGAGGG
182972	15168	TGCCATCATGCTTGGCTAAT	227559	59755	AGATAGTAAATATTGTAAGG	272146	104342	GGCAGGAAAGGCCAGTGAGG
182973	15169	ATGCCATCATGCTTGGCTAA	227560	59756	CAGATAGTAAATATTGTAAG	272147	104343	AGGCAGGAAAGGCCAGTGAG
182974	15170	CATGCCATCATGCTTGGCTA	227561	59757	CCAGATAGTAAATATTGTAA	272148	104344	AAGGCAGGAAAGGCCAGTGA
182975	15171	ACATGCCATCATGCTTGGCT	227562	59758	GCCAGATAGTAAATATTGTA	272149	104345	AAAGGCAGGAAAGGCCAGTG
182976	15172	CACATGCCATCATGCTTGGC	227563	59759	GGCCAGATAGTAAATATTGT	272150	104346	AAAAGGCAGGAAAGGCCAGT
182977	15173	GCACATGCCATCATGCTTGG	227564	59760	GGGCCAGATAGTAAATATTG	272151	104347	GAAAAGGCAGGAAAGGCCAG
182978	15174	GGCACATGCCATCATGCTTG	227565	59761	AGGGCCAGATAGTAAATATT	272152	104348	AGAAAAGGCAGGAAAGGCCA
182979	15175	AGGCACATGCCATCATGCTT	227566	59762	AAGGGCCAGATAGTAAATAT	272153	104349	GAGAAAAGGCAGGAAAGGCC
182980	15176	TAGGCACATGCCATCATGCT	227567	59763	AAAGGGCCAGATAGTAAATA	272154	104350	GGAGAAAAGGCAGGAAAGGC
182981	15177	ATAGGCACATGCCATCATGC	227568	59764	GAAAGGGCCAGATAGTAAAT	272155	104351	GGGAGAAAAGGCAGGAAAGG
182982	15178	TATAGGCACATGCCATCATG	227569	59765	GGAAAGGGCCAGATAGTAAA	272156	104352	TGGGAGAAAAGGCAGGAAAG
182983	15179	TTATAGGCACATGCCATCAT	227570	59766	TGGAAAGGGCCAGATAGTAA	272157	104353	ATGGGAGAAAAGGCAGGAAA
182984	15180	ATTATAGGCACATGCCATCA	227571	59767	CTGGAAAGGGCCAGATAGTA	272158	104354	AATGGGAGAAAAGGCAGGAA
182985	15181	GATTATAGGCACATGCCATC	227572	59768	TCTGGAAAGGGCCAGATAGT	272159	104355	CAATGGGAGAAAAGGCAGGA
182986	15182	GGATTATAGGCACATGCCAT	227573	59769	TTCTGGAAAGGGCCAGATAG	272160	104356	GCAATGGGAGAAAAGGCAGG
182987	15183	AGGATTATAGGCACATGCCA	227574	59770	TTTCTGGAAAGGGCCAGATA	272161	104357	GGCAATGGGAGAAAAGGCAG
182988	15184	CAGGATTATAGGCACATGCC	227575	59771	TTTTCTGGAAAGGGCCAGAT	272162	104358	GGGCAATGGGAGAAAAGGCA
182989	15185	CCAGGATTATAGGCACATGC	227576	59772	TTTTTCTGGAAAGGGCCAGA	272163	104359	TGGGCAATGGGAGAAAAGGC
182990	15186	GCCAGGATTATAGGCACATG	227577	59773	TTTTTTCTGGAAAGGGCCAG	272164	104360	GTGGGCAATGGGAGAAAAGG
182991	15187	AGCCAGGATTATAGGCACAT	227578	59774	TTTTTTTCTGGAAAGGGCCA	272165	104361	GGTGGGCAATGGGAGAAAAG
182992	15188	TAGCCAGGATTATAGGCACA	227579	59775	ATTTTTTTCTGGAAAGGGCC	272166	104362	GGGTGGGCAATGGGAGAAAA
182993	15189	GTAGCCAGGATTATAGGCAC	227580	59776	CATTTTTTTCTGGAAAGGGC	272167	104363	TGGGTGGGCAATGGGAGAAA
182994	15190	AGTAGCCAGGATTATAGGCA	227581	59777	ACATTTTTTTCTGGAAAGGG	272168	104364	ATGGGTGGGCAATGGGAGAA

182995	15191	TAGTAGCCAGGATTATAGGC	227582	59778	CACATTTTTTTCTGGAAAGG	272169	104365	CATGGGTGGGCAATGGGAGA
182996	15192	CTAGTAGCCAGGATTATAGG	227583	59779	GCACATTTTTTTCTGGAAAG	272170	104366	GCATGGGTGGGCAATGGGAG
182997	15193	CCTAGTAGCCAGGATTATAG	227584	59780	GGCACATTTTTTTCTGGAAA	272171	104367	TGCATGGGTGGGCAATGGGA
182998	15194	CCCTAGTAGCCAGGATTATA	227585	59781	CGGCACATTTTTTTCTGGAA	272172	104368	GTGCATGGGTGGGCAATGGG
182999	15195	TCCCTAGTAGCCAGGATTAT	227586	59782	TCGGCACATTTTTTTCTGGA	272173	104369	GGTGCATGGGTGGGCAATGG
183000	15196	CTCCCTAGTAGCCAGGATTA	227587	59783	GTCGGCACATTTTTTTCTGG	272174	104370	GGGTGCATGGGTGGGCAATG
183001	15197	CCTCCCTAGTAGCCAGGATT	227588	59784	AGTCGGCACATTTTTTTCTG	272175	104371	GGGGTGCATGGGTGGGCAAT
183002	15198	GCCTCCCTAGTAGCCAGGAT	227589	59785	GAGTCGGCACATTTTTTTCT	272176	104372	GGGGGTGCATGGGTGGGCAA
183003	15199	AGCCTCCCTAGTAGCCAGGA	227590	59786	AGAGTCGGCACATTTTTTTC	272177	104373	TGGGGGTGCATGGGTGGGCA
183004	15200	CAGCCTCCCTAGTAGCCAGG	227591	59787	AAGAGTCGGCACATTTTTTT	272178	104374	ATGGGGGTGCATGGGTGGGC
183005	15201	TCAGCCTCCCTAGTAGCCAG	227592	59788	CAAGAGTCGGCACATTTTTT	272179	104375	GATGGGGGTGCATGGGTGGG
183006	15202	CTCAGCCTCCCTAGTAGCCA	227593	59789	TCAAGAGTCGGCACATTTTT	272180	104376	GGATGGGGGTGCATGGGTGG
183007	15203	TCTCAGCCTCCCTAGTAGCC	227594	59790	GTCAAGAGTCGGCACATTTT	272181	104377	AGGATGGGGGTGCATGGGTG
183008	15204	GTCTCAGCCTCCCTAGTAGC	227595	59791	GGTCAAGAGTCGGCACATTT	272182	104378	CAGGATGGGGGTGCATGGGT
183009	15205	TGTCTCAGCCTCCCTAGTAG	227596	59792	AGGTCAAGAGTCGGCACATT	272183	104379	GCAGGATGGGGGTGCATGGG
183010	15206	CTGTCTCAGCCTCCCTAGTA	227597	59793	AAGGTCAAGAGTCGGCACAT	272184	104380	AGCAGGATGGGGGTGCATGG
183011	15207	CCTGTCTCAGCCTCCCTAGT	227598	59794	TAAGGTCAAGAGTCGGCACA	272185	104381	GAGCAGGATGGGGGTGCATG
183012	15208	TCCTGTCTCAGCCTCCCTAG	227599	59795	TTAAGGTCAAGAGTCGGCAC	272186	104382	GGAGCAGGATGGGGGTGCAT
183013	15209	CTCCTGTCTCAGCCTCCCTA	227600	59796	GTTAAGGTCAAGAGTCGGCA	272187	104383	TGGAGCAGGATGGGGGTGCA
183014	15210	TCTCCTGTCTCAGCCTCCCT	227601	59797	GGTTAAGGTCAAGAGTCGGC	272188	104384	CTGGAGCAGGATGGGGGTGC
183015	15211	CTCTCCTGTCTCAGCCTCCC	227602	59798	AGGTTAAGGTCAAGAGTCGG	272189	104385	GCTGGAGCAGGATGGGGGTG
183016	15212	TCTCTCCTGTCTCAGCCTCC	227603	59799	GAGGTTAAGGTCAAGAGTCG	272190	104386	TGCTGGAGCAGGATGGGGGT
183017	15213	TTCTCTCCTGTCTCAGCCTC	227604	59800	TGAGGTTAAGGTCAAGAGTC	272191	104387	GTGCTGGAGCAGGATGGGGG
183018	15214	ATTCTCTCCTGTCTCAGCCT	227605	59801	CTGAGGTTAAGGTCAAGAGT	272192	104388	GGTGCTGGAGCAGGATGGGG
183019	15215	GATTCTCTCCTGTCTCAGCC	227606	59802	GCTGAGGTTAAGGTCAAGAG	272193	104389	GGGTGCTGGAGCAGGATGGG
183020	15216	CGATTCTCTCCTGTCTCAGC	227607	59803	TGCTGAGGTTAAGGTCAAGA	272194	104390	TGGGTGCTGGAGCAGGATGG
183021	15217	GCGATTCTCTCCTGTCTCAG	227608	59804	TTGCTGAGGTTAAGGTCAAG	272195	104391	CTGGGTGCTGGAGCAGGATG
183022	15218	AGCGATTCTCTCCTGTCTCA	227609	59805	ATTGCTGAGGTTAAGGTCAA	272196	104392	TCTGGGTGCTGGAGCAGGAT
183023	15219	AAGCGATTCTCTCCTGTCTC	227610	59806	AATTGCTGAGGTTAAGGTCA	272197	104393	GTCTGGGTGCTGGAGCAGGA
183024	15220	CAAGCGATTCTCTCCTGTCT	227611	59807	AAATTGCTGAGGTTAAGGTC	272198	104394	AGTCTGGGTGCTGGAGCAGG
183025	15221	TCAAGCGATTCTCTCCTGTC	227612	59808	CAAATTGCTGAGGTTAAGGT	272199	104395	CAGTCTGGGTGCTGGAGCAG
183026	15222	TTCAAGCGATTCTCTCCTGT	227613	59809	CCAAATTGCTGAGGTTAAGG	272200	104396	GCAGTCTGGGTGCTGGAGCA
183027	15223	ATTCAAGCGATTCTCTCCTG	227614	59810	CCCAAATTGCTGAGGTTAAG	272201	104397	GGCAGTCTGGGTGCTGGAGC
183028	15224	GATTCAAGCGATTCTCTCCT	227615	59811	TCCCAAATTGCTGAGGTTAA	272202	104398	TGGCAGTCTGGGTGCTGGAG
183029	15225	GGATTCAAGCGATTCTCTCC	227616	59812	CTCCCAAATTGCTGAGGTTA	272203	104399	ATGGCAGTCTGGGTGCTGGA
183030	15226	TGGATTCAAGCGATTCTCTC	227617	59813	CCTCCCAAATTGCTGAGGTT	272204	104400	GATGGCAGTCTGGGTGCTGG
183031	15227	CTGGATTCAAGCGATTCTCT	227618	59814	GCCTCCCAAATTGCTGAGGT	272205	104401	GGATGGCAGTCTGGGTGCTG
183032	15228	CCTGGATTCAAGCGATTCTC	227619	59815	GGCCTCCCAAATTGCTGAGG	272206	104402	TGGATGGCAGTCTGGGTGCT
183033	15229	TCCTGGATTCAAGCGATTCT	227620	59816	CGGCCTCCCAAATTGCTGAG	272207	104403	CTGGATGGCAGTCTGGGTGC
183034	15230	CTCCTGGATTCAAGCGATTC	227621	59817	TCGGCCTCCCAAATTGCTGA	272208	104404	CCTGGATGGCAGTCTGGGTG
183035	15231	CCTCCTGGATTCAAGCGATT	227622	59818	CTCGGCCTCCCAAATTGCTG	272209	104405	TCCTGGATGGCAGTCTGGGT
183036	15232	ACCTCCTGGATTCAAGCGAT	227623	59819	CCTCGGCCTCCCAAATTGCT	272210	104406	ATCCTGGATGGCAGTCTGGG
183037	15233	CACCTCCTGGATTCAAGCGA	227624	59820	GCCTCGGCCTCCCAAATTGC	272211	104407	GATCCTGGATGGCAGTCTGG
183038	15234	CCACCTCCTGGATTCAAGCG	227625	59821	TGCCTCGGCCTCCCAAATTG	272212	104408	AGATCCTGGATGGCAGTCTG
183039	15235	ACCACCTCCTGGATTCAAGC	227626	59822	CTGCCTCGGCCTCCCAAATT	272213	104409	GAGATCCTGGATGGCAGTCT
183040	15236	AACCACCTCCTGGATTCAAG	227627	59823	CCTGCCTCGGCCTCCCAAAT	272214	104410	GGAGATCCTGGATGGCAGTC
183041	15237	CAACCACCTCCTGGATTCAA	227628	59824	GCCTGCCTCGGCCTCCCAAA	272215	104411	AGGAGATCCTGGATGGCAGT
183042	15238	GCAACCACCTCCTGGATTCA	227629	59825	CGCCTGCCTCGGCCTCCCAA	272216	104412	GAGGAGATCCTGGATGGCAG
183043	15239	TGCAACCACCTCCTGGATTC	227630	59826	CCGCCTGCCTCGGCCTCCCA	272217	104413	TGAGGAGATCCTGGATGGCA
183044	15240	CTGCAACCACCTCCTGGATT	227631	59827	TCCGCCTGCCTCGGCCTCCC	272218	104414	TTGAGGAGATCCTGGATGGC
183045	15241	ACTGCAACCACCTCCTGGAT	227632	59828	ATCCGCCTGCCTCGGCCTCC	272219	104415	CTTGAGGAGATCCTGGATGG
183046	15242	CACTGCAACCACCTCCTGGA	227633	59829	GATCCGCCTGCCTCGGCCTC	272220	104416	ACTTGAGGAGATCCTGGATG
183047	15243	TCACTGCAACCACCTCCTGG	227634	59830	CGATCCGCCTGCCTCGGCCT	272221	104417	GACTTGAGGAGATCCTGGAT
183048	15244	CTCACTGCAACCACCTCCTG	227635	59831	GCGATCCGCCTGCCTCGGCC	272222	104418	TGACTTGAGGAGATCCTGGA
183049	15245	GCTCACTGCAACCACCTCCT	227636	59832	AGCGATCCGCCTGCCTCGGC	272223	104419	GTGACTTGAGGAGATCCTGG
183050	15246	AGCTCACTGCAACCACCTCC	227637	59833	AAGCGATCCGCCTGCCTCGG	272224	104420	TGTGACTTGAGGAGATCCTG
183051	15247	CAGCTCACTGCAACCACCTC	227638	59834	CAAGCGATCCGCCTGCCTCG	272225	104421	ATGTGACTTGAGGAGATCCT
183052	15248	TCAGCTCACTGCAACCACCT	227639	59835	TCAAGCGATCCGCCTGCCTC	272226	104422	TATGTGACTTGAGGAGATCC
183053	15249	CTCAGCTCACTGCAACCACC	227640	59836	CTCAAGCGATCCGCCTGCCT	272227	104423	TTATGTGACTTGAGGAGATC
183054	15250	TCTCAGCTCACTGCAACCAC	227641	59837	GCTCAAGCGATCCGCCTGCC	272228	104424	GTTATGTGACTTGAGGAGAT
183055	15251	ATCTCAGCTCACTGCAACCA	227642	59838	AGCTCAAGCGATCCGCCTGC	272229	104425	TGTTATGTGACTTGAGGAGA
183056	15252	CATCTCAGCTCACTGCAACC	227643	59839	GAGCTCAAGCGATCCGCCTG	272230	104426	TTGTTATGTGACTTGAGGAG
183057	15253	CCATCTCAGCTCACTGCAAC	227644	59840	AGAGCTCAAGCGATCCGCCT	272231	104427	CTTGTTATGTGACTTGAGGA
183058	15254	ACCATCTCAGCTCACTGCAA	227645	59841	CAGAGCTCAAGCGATCCGCC	272232	104428	GCTTGTTATGTGACTTGAGG
183059	15255	CACCATCTCAGCTCACTGCA	227646	59842	CCAGAGCTCAAGCGATCCGC	272233	104429	TGCTTGTTATGTGACTTGAG
183060	15256	GCACCATCTCAGCTCACTGC	227647	59843	TCCAGAGCTCAAGCGATCCG	272234	104430	CTGCTTGTTATGTGACTTGA
183061	15257	GGCACCATCTCAGCTCACTG	227648	59844	CTCCAGAGCTCAAGCGATCC	272235	104431	GCTGCTTGTTATGTGACTTG
183062	15258	TGGCACCATCTCAGCTCACT	227649	59845	ACTCCAGAGCTCAAGCGATC	272236	104432	TGCTGCTTGTTATGTGACTT
183063	15259	GTGGCACCATCTCAGCTCAC	227650	59846	AACTCCAGAGCTCAAGCGAT	272237	104433	GTGCTGCTTGTTATGTGACT
183064	15260	AGTGGCACCATCTCAGCTCA	227651	59847	GAACTCCAGAGCTCAAGCGA	272238	104434	GGTGCTGCTTGTTATGTGAC
183065	15261	CAGTGGCACCATCTCAGCTC	227652	59848	TGAACTCCAGAGCTCAAGCG	272239	104435	GGGTGCTGCTTGTTATGTGA
183066	15262	GCAGTGGCACCATCTCAGCT	227653	59849	ATGAACTCCAGAGCTCAAGC	272240	104436	TGGGTGCTGCTTGTTATGTG

183067	15263	TGCAGTGGCACCATCTCAGC	227654	59850	CATGAACTCCAGAGCTCAAG	272241	104437	GTGGGTGCTGCTTGTTATGT
183068	15264	GTGCAGTGGCACCATCTCAG	227655	59851	TCATGAACTCCAGAGCTCAA	272242	104438	TGTGGGTGCTGCTTGTTATG
183069	15265	AGTGCAGTGGCACCATCTCA	227656	59852	GTCATGAACTCCAGAGCTCA	272243	104439	TTGTGGGTGCTGCTTGTTAT
183070	15266	GAGTGCAGTGGCACCATCTC	227657	59853	GGTCATGAACTCCAGAGCTC	272244	104440	CTTGTGGGTGCTGCTTGTTA
183071	15267	GGAGTGCAGTGGCACCATCT	227658	59854	TGGTCATGAACTCCAGAGCT	272245	104441	CCTTGTGGGTGCTGCTTGTT
183072	15268	TGGAGTGCAGTGGCACCATC	227659	59855	CTGGTCATGAACTCCAGAGC	272246	104442	ACCTTGTGGGTGCTGCTTGT
183073	15269	CTGGAGTGCAGTGGCACCAT	227660	59856	GCTGGTCATGAACTCCAGAG	272247	104443	CACCTTGTGGGTGCTGCTTG
183074	15270	GCTGGAGTGCAGTGGCACCA	227661	59857	GGCTGGTCATGAACTCCAGA	272248	104444	GCACCTTGTGGGTGCTGCTT
183075	15271	GGCTGGAGTGCAGTGGCACC	227662	59858	AGGCTGGTCATGAACTCCAG	272249	104445	AGCACCTTGTGGGTGCTGCT
183076	15272	AGGCTGGAGTGCAGTGGCAC	227663	59859	CAGGCTGGTCATGAACTCCA	272250	104446	GAGCACCTTGTGGGTGCTGC
183077	15273	CAGGCTGGAGTGCAGTGGCA	227664	59860	CCAGGCTGGTCATGAACTCC	272251	104447	GGAGCACCTTGTGGGTGCTG
183078	15274	CCAGGCTGGAGTGCAGTGGC	227665	59861	CCCAGGCTGGTCATGAACTC	272252	104448	GGGAGCACCTTGTGGGTGCT
183079	15275	ACCAGGCTGGAGTGCAGTGG	227666	59862	GCCCAGGCTGGTCATGAACT	272253	104449	AGGGAGCACCTTGTGGGTGC
183080	15276	AACCAGGCTGGAGTGCAGTG	227667	59863	TGCCCAGGCTGGTCATGAAC	272254	104450	AAGGGAGCACCTTGTGGGTG
183081	15277	CAACCAGGCTGGAGTGCAGT	227668	59864	TTGCCCAGGCTGGTCATGAA	272255	104451	GAAGGGAGCACCTTGTGGGT
183082	15278	TCAACCAGGCTGGAGTGCAG	227669	59865	GTTGCCCAGGCTGGTCATGA	272256	104452	GGAAGGGAGCACCTTGTGGG
183083	15279	GTCAACCAGGCTGGAGTGCA	227670	59866	TGTTGCCCAGGCTGGTCATG	272257	104453	GGGAAGGGAGCACCTTGTGG
183084	15280	TGTCAACCAGGCTGGAGTGC	227671	59867	ATGTTGCCCAGGCTGGTCAT	272258	104454	GGGGAAGGGAGCACCTTGTG
183085	15281	CTGTCAACCAGGCTGGAGTG	227672	59868	TATGTTGCCCAGGCTGGTCA	272259	104455	GGGGGAAGGGAGCACCTTGT
183086	15282	TCTGTCAACCAGGCTGGAGT	227673	59869	CTATGTTGCCCAGGCTGGTC	272260	104456	AGGGGGAAGGGAGCACCTTG
183087	15283	CTCTGTCAACCAGGCTGGAG	227674	59870	ACTATGTTGCCCAGGCTGGT	272261	104457	TAGGGGGAAGGGAGCACCTT
183088	15284	GCTCTGTCAACCAGGCTGGA	227675	59871	TACTATGTTGCCCAGGCTGG	272262	104458	CTAGGGGGAAGGGAGCACCT
183089	15285	TGCTCTGTCAACCAGGCTGG	227676	59872	TTACTATGTTGCCCAGGCTG	272263	104459	GCTAGGGGGAAGGGAGCACC
183090	15286	TTGCTCTGTCAACCAGGCTG	227677	59873	CTTACTATGTTGCCCAGGCT	272264	104460	GGCTAGGGGGAAGGGAGCAC
183091	15287	CTTGCTCTGTCAACCAGGCT	227678	59874	TCTTACTATGTTGCCCAGGC	272265	104461	AGGCTAGGGGGAAGGGAGCA
183092	15288	TCTTGCTCTGTCAACCAGGC	227679	59875	GTCTTACTATGTTGCCCAGG	272266	104462	CAGGCTAGGGGGAAGGGAGC
183093	15289	GTCTTGCTCTGTCAACCAGG	227680	59876	AGTCTTACTATGTTGCCCAG	272267	104463	TCAGGCTAGGGGGAAGGGAG
183094	15290	AGTCTTGCTCTGTCAACCAG	227681	59877	GAGTCTTACTATGTTGCCCA	272268	104464	TTCAGGCTAGGGGGAAGGGA
183095	15291	GAGTCTTGCTCTGTCAACCA	227682	59878	GGAGTCTTACTATGTTGCCC	272269	104465	ATTCAGGCTAGGGGGAAGGG
183096	15292	AGAGTCTTGCTCTGTCAACC	227683	59879	TGGAGTCTTACTATGTTGCC	272270	104466	GATTCAGGCTAGGGGGAAGG
183097	15293	CAGAGTCTTGCTCTGTCAAC	227684	59880	ATGGAGTCTTACTATGTTGC	272271	104467	AGATTCAGGCTAGGGGGAAG
183098	15294	ACAGAGTCTTGCTCTGTCAA	227685	59881	GATGGAGTCTTACTATGTTG	272272	104468	CAGATTCAGGCTAGGGGGAA
183099	15295	GACAGAGTCTTGCTCTGTCA	227686	59882	AGATGGAGTCTTACTATGTT	272273	104469	GCAGATTCAGGCTAGGGGGA
183100	15296	AGACAGAGTCTTGCTCTGTC	227687	59883	GAGATGGAGTCTTACTATGT	272274	104470	AGCAGATTCAGGCTAGGGGG
183101	15297	GAGACAGAGTCTTGCTCTGT	227688	59884	AGAGATGGAGTCTTACTATG	272275	104471	CAGCAGATTCAGGCTAGGGG
183102	15298	TGAGACAGAGTCTTGCTCTG	227689	59885	TAGAGATGGAGTCTTACTAT	272276	104472	GCAGCAGATTCAGGCTAGGG
183103	15299	TTGAGACAGAGTCTTGCTCT	227690	59886	GTAGAGATGGAGTCTTACTA	272277	104473	AGCAGCAGATTCAGGCTAGG
183104	15300	TTTGAGACAGAGTCTTGCTC	227691	59887	TGTAGAGATGGAGTCTTACT	272278	104474	GAGCAGCAGATTCAGGCTAG
183105	15301	TTTTGAGACAGAGTCTTGCT	227692	59888	TTGTAGAGATGGAGTCTTAC	272279	104475	GGAGCAGCAGATTCAGGCTA
183106	15302	TTTTTGAGACAGAGTCTTGC	227693	59889	TTTGTAGAGATGGAGTCTTA	272280	104476	GGGAGCAGCAGATTCAGGCT
183107	15303	TTTTTTGAGACAGAGTCTTG	227694	59890	TTTTGTAGAGATGGAGTCTT	272281	104477	GGGGAGCAGCAGATTCAGGC
183108	15304	TTTTTTTGAGACAGAGTCTT	227695	59891	TTTTTGTAGAGATGGAGTCT	272282	104478	CGGGGAGCAGCAGATTCAGG
183109	15305	TTTTTTTTGAGACAGAGTCT	227696	59892	TTTTTTGTAGAGATGGAGTC	272283	104479	ACGGGGAGCAGCAGATTCAG
183110	15306	TTTTTTTTTGAGACAGAGTC	227697	59893	ATTTTTTGTAGAGATGGAGT	272284	104480	GACGGGGAGCAGCAGATTCA
183111	15307	TTTTTTTTTTGAGACAGAGT	227698	59894	TATTTTTTGTAGAGATGGAG	272285	104481	AGACGGGGAGCAGCAGATTC
183112	15308	TTTTTTTTTTTGAGACAGAG	227699	59895	GTATTTTTTGTAGAGATGGA	272286	104482	CAGACGGGGAGCAGCAGATT
183113	15309	TTTTTTTTTTTTGAGACAGA	227700	59896	TGTATTTTTTGTAGAGATGG	272287	104483	CCAGACGGGGAGCAGCAGAT
183114	15310	TTTTTTTTTTTTTGAGACAG	227701	59897	TTGTATTTTTTGTAGAGATG	272288	104484	CCCAGACGGGGAGCAGCAGA
183115	15311	TTTTTTTTTTTTTTGAGACA	227702	59898	TTTGTATTTTTTGTAGAGAT	272289	104485	CCCCAGACGGGGAGCAGCAG
183116	15312	TTTTTTTTTTTTTTTGAGAC	227703	59899	TTTTGTATTTTTTGTAGAGA	272290	104486	ACCCCAGACGGGGAGCAGCA
183117	15313	TTTTTTTTTTTTTTTTGAGA	227704	59900	GTTTTGTATTTTTTGTAGAG	272291	104487	AACCCCAGACGGGGAGCAGC
183118	15314	TTTTTTTTTTTTTTTTTGAG	227705	59901	TGTTTTGTATTTTTTGTAGA	272292	104488	GAACCCCAGACGGGGAGCAG
183119	15315	TTTTTTTTTTTTTTTTTTGA	227706	59902	ATGTTTTGTATTTTTTGTAG	272293	104489	GGAACCCCAGACGGGGAGCA
183120	15316	TTTTTTTTTTTTTTTTTTTG	227707	59903	AATGTTTTGTATTTTTTGTA	272294	104490	GGGAACCCCAGACGGGGAGC
183121	15317	TTTTTTTTTTTTTTTTTTTT	227708	59904	TAATGTTTTGTATTTTTTGT	272295	104491	GGGGAACCCCAGACGGGGAG
183122	15318	TTTTTTTTTTTTTTTTTTTT	227709	59905	CTAATGTTTTGTATTTTTTG	272296	104492	CGGGGAACCCCAGACGGGGA
183123	15319	TTTTTTTTTTTTTTTTTTTT	227710	59906	GCTAATGTTTTGTATTTTTT	272297	104493	GCGGGGAACCCCAGACGGGG
183124	15320	TTTTTTTTTTTTTTTTTTTT	227711	59907	GGCTAATGTTTTGTATTTTT	272298	104494	GGCGGGGAACCCCAGACGGG
183125	15321	TTTTTTTTTTTTTTTTTTTT	227712	59908	TGGCTAATGTTTTGTATTTT	272299	104495	GGGCGGGGAACCCCAGACGG
183126	15322	CTTTTTTTTTTTTTTTTTTT	227713	59909	CTGGCTAATGTTTTGTATTT	272300	104496	TGGGCGGGGAACCCCAGACG
183127	15323	GCTTTTTTTTTTTTTTTTTT	227714	59910	CCTGGCTAATGTTTTGTATT	272301	104497	ATGGGCGGGGAACCCCAGAC
183128	15324	GGCTTTTTTTTTTTTTTTTT	227715	59911	GCCTGGCTAATGTTTTGTAT	272302	104498	CATGGGCGGGGAACCCCAGA
183129	15325	TGGCTTTTTTTTTTTTTTTT	227716	59912	TGCCTGGCTAATGTTTTGTA	272303	104499	GCATGGGCGGGGAACCCCAG
183130	15326	ATGGCTTTTTTTTTTTTTTT	227717	59913	ATGCCTGGCTAATGTTTTGT	272304	104500	TGCATGGGCGGGGAACCCCA
183131	15327	CATGGCTTTTTTTTTTTTTT	227718	59914	CATGCCTGGCTAATGTTTTG	272305	104501	GTGCATGGGCGGGGAACCCC
183132	15328	GCATGGCTTTTTTTTTTTTT	227719	59915	CCATGCCTGGCTAATGTTTT	272306	104502	GGTGCATGGGCGGGGAACCC
183133	15329	GGCATGGCTTTTTTTTTTTT	227720	59916	ACCATGCCTGGCTAATGTTT	272307	104503	AGGTGCATGGGCGGGGAACC
183134	15330	AGGCATGGCTTTTTTTTTTT	227721	59917	CACCATGCCTGGCTAATGTT	272308	104504	GAGGTGCATGGGCGGGGAAC
183135	15331	CAGGCATGGCTTTTTTTTTT	227722	59918	CCACCATGCCTGGCTAATGT	272309	104505	AGAGGTGCATGGGCGGGGAA
183136	15332	CCAGGCATGGCTTTTTTTTT	227723	59919	ACCACCATGCCTGGCTAATG	272310	104506	CAGAGGTGCATGGGCGGGGA
183137	15333	ACCAGGCATGGCTTTTTTTT	227724	59920	CACCACCATGCCTGGCTAAT	272311	104507	CCAGAGGTGCATGGGCGGGG
183138	15334	CACCAGGCATGGCTTTTTTT	227725	59921	GCACCACCATGCCTGGCTAA	272312	104508	CCCAGAGGTGCATGGGCGGG

183139	15335	CCACCAGGCATGGCTTTTTT	227726	59922	TGCACCACCATGCCTGGCTA	272313	104509	CCCCAGAGGTGCATGGGCGG
183140	15336	TCCACCAGGCATGGCTTTTT	227727	59923	GTGCACCACCATGCCTGGCT	272314	104510	CCCCCAGAGGTGCATGGGCG
183141	15337	CTCCACCAGGCATGGCTTTT	227728	59924	TGTGCACCACCATGCCTGGC	272315	104511	GCCCCCAGAGGTGCATGGGC
183142	15338	GCTCCACCAGGCATGGCTTT	227729	59925	GTGTGCACCACCATGCCTGG	272316	104512	GGCCCCCAGAGGTGCATGGG
183143	15339	TGCTCCACCAGGCATGGCTT	227730	59926	GGTGTGCACCACCATGCCTG	272317	104513	GGGCCCCCAGAGGTGCATGG
183144	15340	GTGCTCCACCAGGCATGGCT	227731	59927	AGGTGTGCACCACCATGCCT	272318	104514	GGGGCCCCCAGAGGTGCATG
183145	15341	AGTGCTCCACCAGGCATGGC	227732	59928	CAGGTGTGCACCACCATGCC	272319	104515	AGGGGCCCCCAGAGGTGCAT
183146	15342	TAGTGCTCCACCAGGCATGG	227733	59929	ACAGGTGTGCACCACCATGC	272320	104516	CAGGGGCCCCCAGAGGTGCA
183147	15343	GTAGTGCTCCACCAGGCATG	227734	59930	CACAGGTGTGCACCACCATG	272321	104517	CCAGGGGCCCCCAGAGGTGC
183148	15344	CGTAGTGCTCCACCAGGCAT	227735	59931	CCACAGGTGTGCACCACCAT	272322	104518	CCCAGGGGCCCCCAGAGGTG
183149	15345	ACGTAGTGCTCCACCAGGCA	227736	59932	ACCACAGGTGTGCACCACCA	272323	104519	ACCCAGGGGCCCCCAGAGGT
183150	15346	CACGTAGTGCTCCACCAGGC	227737	59933	GACCACAGGTGTGCACCACC	272324	104520	AACCCAGGGGCCCCCAGAGG
183151	15347	ACACGTAGTGCTCCACCAGG	227738	59934	GGACCACAGGTGTGCACCAC	272325	104521	GAACCCAGGGGCCCCCAGAG
183152	15348	TACACGTAGTGCTCCACCAG	227739	59935	AGGACCACAGGTGTGCACCA	272326	104522	AGAACCCAGGGGCCCCCAGA
183153	15349	TTACACGTAGTGCTCCACCA	227740	59936	TAGGACCACAGGTGTGCACC	272327	104523	CAGAACCCAGGGGCCCCCAG
183154	15350	ATTACACGTAGTGCTCCACC	227741	59937	CTAGGACCACAGGTGTGCAC	272328	104524	GCAGAACCCAGGGGCCCCCA
183155	15351	GATTACACGTAGTGCTCCAC	227742	59938	GCTAGGACCACAGGTGTGCA	272329	104525	GGCAGAACCCAGGGGCCCCC
183156	15352	AGATTACACGTAGTGCTCCA	227743	59939	GGCTAGGACCACAGGTGTGC	272330	104526	TGGCAGAACCCAGGGGCCCC
183157	15353	GAGATTACACGTAGTGCTCC	227744	59940	TGGCTAGGACCACAGGTGTG	272331	104527	ATGGCAGAACCCAGGGGCCC
183158	15354	TGAGATTACACGTAGTGCTC	227745	59941	GTGGCTAGGACCACAGGTGT	272332	104528	TATGGCAGAACCCAGGGGCC
183159	15355	CTGAGATTACACGTAGTGCT	227746	59942	AGTGGCTAGGACCACAGGTG	272333	104529	GTATGGCAGAACCCAGGGGC
183160	15356	GCTGAGATTACACGTAGTGC	227747	59943	GAGTGGCTAGGACCACAGGT	272334	104530	GGTATGGCAGAACCCAGGGG
183161	15357	AGCTGAGATTACACGTAGTG	227748	59944	CGAGTGGCTAGGACCACAGG	272335	104531	GGGTATGGCAGAACCCAGGG
183162	15358	TAGCTGAGATTACACGTAGT	227749	59945	CCGAGTGGCTAGGACCACAG	272336	104532	AGGGTATGGCAGAACCCAGG
183163	15359	ATAGCTGAGATTACACGTAG	227750	59946	CCCGAGTGGCTAGGACCACA	272337	104533	CAGGGTATGGCAGAACCCAG
183164	15360	AATAGCTGAGATTACACGTA	227751	59947	TCCCGAGTGGCTAGGACCAC	272338	104534	GCAGGGTATGGCAGAACCCA
183165	15361	AAATAGCTGAGATTACACGT	227752	59948	CTCCCGAGTGGCTAGGACCA	272339	104535	GGCAGGGTATGGCAGAACCC
183166	15362	CAAATAGCTGAGATTACACG	227753	59949	TCTCCCGAGTGGCTAGGACC	272340	104536	GGGCAGGGTATGGCAGAACC
183167	15363	CCAAATAGCTGAGATTACAC	227754	59950	GTCTCCCGAGTGGCTAGGAC	272341	104537	AGGGCAGGGTATGGCAGAAC
183168	15364	CCCAAATAGCTGAGATTACA	227755	59951	AGTCTCCCGAGTGGCTAGGA	272342	104538	CAGGGCAGGGTATGGCAGAA
183169	15365	TCCCAAATAGCTGAGATTAC	227756	59952	CAGTCTCCCGAGTGGCTAGG	272343	104539	ACAGGGCAGGGTATGGCAGA
183170	15366	CTCCCAAATAGCTGAGATTA	227757	59953	TCAGTCTCCCGAGTGGCTAG	272344	104540	CACAGGGCAGGGTATGGCAG
183171	15367	CCTCCCAAATAGCTGAGATT	227758	59954	CTCAGTCTCCCGAGTGGCTA	272345	104541	ACACAGGGCAGGGTATGGCA
183172	15368	GCCTCCCAAATAGCTGAGAT	227759	59955	CCTCAGTCTCCCGAGTGGCT	272346	104542	GACACAGGGCAGGGTATGGC
183173	15369	AGCCTCCCAAATAGCTGAGA	227760	59956	ACCTCAGTCTCCCGAGTGGC	272347	104543	GGACACAGGGCAGGGTATGG
183174	15370	CAGCCTCCCAAATAGCTGAG	227761	59957	CACCTCAGTCTCCCGAGTGG	272348	104544	GGGACACAGGGCAGGGTATG
183175	15371	TCAGCCTCCCAAATAGCTGA	227762	59958	CCACCTCAGTCTCCCGAGTG	272349	104545	TGGGACACAGGGCAGGGTAT
183176	15372	CTCAGCCTCCCAAATAGCTG	227763	59959	CCCACCTCAGTCTCCCGAGT	272350	104546	ATGGGACACAGGGCAGGGTA
183177	15373	CCTCAGCCTCCCAAATAGCT	227764	59960	TCCCACCTCAGTCTCCCGAG	272351	104547	CATGGGACACAGGGCAGGGT
183178	15374	GCCTCAGCCTCCCAAATAGC	227765	59961	CTCCCACCTCAGTCTCCCGA	272352	104548	CCATGGGACACAGGGCAGGG
183179	15375	TGCCTCAGCCTCCCAAATAG	227766	59962	CCTCCCACCTCAGTCTCCCG	272353	104549	ACCATGGGACACAGGGCAGG
183180	15376	GTGCCTCAGCCTCCCAAATA	227767	59963	TCCTCCCACCTCAGTCTCCC	272354	104550	CACCATGGGACACAGGGCAG
183181	15377	CGTGCCTCAGCCTCCCAAAT	227768	59964	ATCCTCCCACCTCAGTCTCC	272355	104551	CCACCATGGGACACAGGGCA
183182	15378	TCGTGCCTCAGCCTCCCAAA	227769	59965	GATCCTCCCACCTCAGTCTC	272356	104552	CCCACCATGGGACACAGGGC
183183	15379	CTCGTGCCTCAGCCTCCCAA	227770	59966	CGATCCTCCCACCTCAGTCT	272357	104553	CCCCACCATGGGACACAGGG
183184	15380	TCTCGTGCCTCAGCCTCCCA	227771	59967	GCGATCCTCCCACCTCAGTC	272358	104554	TCCCCACCATGGGACACAGG
183185	15381	TTCTCGTGCCTCAGCCTCCC	227772	59968	GGCGATCCTCCCACCTCAGT	272359	104555	TTCCCCACCATGGGACACAG
183186	15382	ATTCTCGTGCCTCAGCCTCC	227773	59969	AGGCGATCCTCCCACCTCAG	272360	104556	ATTCCCCACCATGGGACACA
183187	15383	GATTCTCGTGCCTCAGCCTC	227774	59970	CAGGCGATCCTCCCACCTCA	272361	104557	CATTCCCCACCATGGGACAC
183188	15384	TGATTCTCGTGCCTCAGCCT	227775	59971	TCAGGCGATCCTCCCACCTC	272362	104558	ACATTCCCCACCATGGGACA
183189	15385	GTGATTCTCGTGCCTCAGCC	227776	59972	CTCAGGCGATCCTCCCACCT	272363	104559	GACATTCCCCACCATGGGAC
183190	15386	AGTGATTCTCGTGCCTCAGC	227777	59973	GCTCAGGCGATCCTCCCACC	272364	104560	GGACATTCCCCACCATGGGA
183191	15387	AAGTGATTCTCGTGCCTCAG	227778	59974	GGCTCAGGCGATCCTCCCAC	272365	104561	AGGACATTCCCCACCATGGG
183192	15388	CAAGTGATTCTCGTGCCTCA	227779	59975	GGGCTCAGGCGATCCTCCCA	272366	104562	AAGGACATTCCCCACCATGG
183193	15389	TCAAGTGATTCTCGTGCCTC	227780	59976	TGGGCTCAGGCGATCCTCCC	272367	104563	GAAGGACATTCCCCACCATG
183194	15390	TTCAAGTGATTCTCGTGCCT	227781	59977	CTGGGCTCAGGCGATCCTCC	272368	104564	AGAAGGACATTCCCCACCAT
183195	15391	GTTCAAGTGATTCTCGTGCC	227782	59978	CCTGGGCTCAGGCGATCCTC	272369	104565	GAGAAGGACATTCCCCACCA
183196	15392	GGTTCAAGTGATTCTCGTGC	227783	59979	TCCTGGGCTCAGGCGATCCT	272370	104566	AGAGAAGGACATTCCCCACC
183197	15393	AGGTTCAAGTGATTCTCGTG	227784	59980	TTCCTGGGCTCAGGCGATCC	272371	104567	GAGAGAAGGACATTCCCCAC
183198	15394	CAGGTTCAAGTGATTCTCGT	227785	59981	CTTCCTGGGCTCAGGCGATC	272372	104568	GGAGAGAAGGACATTCCCCA
183199	15395	CCAGGTTCAAGTGATTCTCG	227786	59982	ACTTCCTGGGCTCAGGCGAT	272373	104569	AGGAGAGAAGGACATTCCCC
183200	15396	CCCAGGTTCAAGTGATTCTC	227787	59983	GACTTCCTGGGCTCAGGCGA	272374	104570	AAGGAGAGAAGGACATTCCC
183201	15397	TCCCAGGTTCAAGTGATTCT	227788	59984	CGACTTCCTGGGCTCAGGCG	272375	104571	TAAGGAGAGAAGGACATTCC
183202	15398	CTCCCAGGTTCAAGTGATTC	227789	59985	TCGACTTCCTGGGCTCAGGC	272376	104572	ATAAGGAGAGAAGGACATTC
183203	15399	CCTCCCAGGTTCAAGTGATT	227790	59986	CTCGACTTCCTGGGCTCAGG	272377	104573	GATAAGGAGAGAAGGACATT
183204	15400	GCCTCCCAGGTTCAAGTGAT	227791	59987	CCTCGACTTCCTGGGCTCAG	272378	104574	AGATAAGGAGAGAAGGACAT
183205	15401	TGCCTCCCAGGTTCAAGTGA	227792	59988	GCCTCGACTTCCTGGGCTCA	272379	104575	GAGATAAGGAGAGAAGGACA
183206	15402	CTGCCTCCCAGGTTCAAGTG	227793	59989	AGCCTCGACTTCCTGGGCTC	272380	104576	AGAGATAAGGAGAGAAGGAC
183207	15403	ACTGCCTCCCAGGTTCAAGT	227794	59990	CAGCCTCGACTTCCTGGGCT	272381	104577	AAGAGATAAGGAGAGAAGGA
183208	15404	CACTGCCTCCCAGGTTCAAG	227795	59991	GCAGCCTCGACTTCCTGGGC	272382	104578	GAAGAGATAAGGAGAGAAGG
183209	15405	CCACTGCCTCCCAGGTTCAA	227796	59992	TGCAGCCTCGACTTCCTGGG	272383	104579	GGAAGAGATAAGGAGAGAAG
183210	15406	ACCACTGCCTCCCAGGTTCA	227797	59993	CTGCAGCCTCGACTTCCTGG	272384	104580	GGGAAGAGATAAGGAGAGAA

183211	15407	AACCACTGCCTCCCAGGTTC	227798	59994	ACTGCAGCCTCGACTTCCTG	272385	104581	AGGGAAGAGATAAGGAGAGA
183212	15408	CAACCACTGCCTCCCAGGTT	227799	59995	CACTGCAGCCTCGACTTCCT	272386	104582	AAGGGAAGAGATAAGGAGAG
183213	15409	GCAACCACTGCCTCCCAGGT	227800	59996	TCACTGCAGCCTCGACTTCC	272387	104583	GAAGGGAAGAGATAAGGAGA
183214	15410	TGCAACCACTGCCTCCCAGG	227801	59997	CTCACTGCAGCCTCGACTTC	272388	104584	GGAAGGGAAGAGATAAGGAG
183215	15411	CTGCAACCACTGCCTCCCAG	227802	59998	GCTCACTGCAGCCTCGACTT	272389	104585	GGGAAGGGAAGAGATAAGGA
183216	15412	ACTGCAACCACTGCCTCCCA	227803	59999	AGCTCACTGCAGCCTCGACT	272390	104586	AGGGAAGGGAAGAGATAAGG
183217	15413	CACTGCAACCACTGCCTCCC	227804	60000	CAGCTCACTGCAGCCTCGAC	272391	104587	AAGGGAAGGGAAGAGATAAG
183218	15414	TCACTGCAACCACTGCCTCC	227805	60001	ACAGCTCACTGCAGCCTCGA	272392	104588	TAAGGGAAGGGAAGAGATAA
183219	15415	CTCACTGCAACCACTGCCTC	227806	60002	CACAGCTCACTGCAGCCTCG	272393	104589	TTAAGGGAAGGGAAGAGATA
183220	15416	GCTCACTGCAACCACTGCCT	227807	60003	TCACAGCTCACTGCAGCCTC	272394	104590	TTTAAGGGAAGGGAAGAGAT
183221	15417	AGCTCACTGCAACCACTGCC	227808	60004	ATCACAGCTCACTGCAGCCT	272395	104591	ATTTAAGGGAAGGGAAGAGA
183222	15418	CAGCTCACTGCAACCACTGC	227809	60005	CATCACAGCTCACTGCAGCC	272396	104592	GATTTAAGGGAAGGGAAGAG
183223	15419	TCAGCTCACTGCAACCACTG	227810	60006	CCATCACAGCTCACTGCAGC	272397	104593	GGATTTAAGGGAAGGGAAGA
183224	15420	CTCAGCTCACTGCAACCACT	227811	60007	GCCATCACAGCTCACTGCAG	272398	104594	TGGATTTAAGGGAAGGGAAG
183225	15421	TCTCAGCTCACTGCAACCAC	227812	60008	TGCCATCACAGCTCACTGCA	272399	104595	TTGGATTTAAGGGAAGGGAA
183226	15422	ATCTCAGCTCACTGCAACCA	227813	60009	GTGCCATCACAGCTCACTGC	272400	104596	CTTGGATTTAAGGGAAGGGA
183227	15423	GATCTCAGCTCACTGCAACC	227814	60010	GGTGCCATCACAGCTCACTG	272401	104597	ACTTGGATTTAAGGGAAGGG
183228	15424	CGATCTCAGCTCACTGCAAC	227815	60011	TGGTGCCATCACAGCTCACT	272402	104598	AACTTGGATTTAAGGGAAGG
183229	15425	GCGATCTCAGCTCACTGCAA	227816	60012	GTGGTGCCATCACAGCTCAC	272403	104599	GAACTTGGATTTAAGGGAAG
183230	15426	CGCGATCTCAGCTCACTGCA	227817	60013	AGTGGTGCCATCACAGCTCA	272404	104600	TGAACTTGGATTTAAGGGAA
183231	15427	GCGCGATCTCAGCTCACTGC	227818	60014	CAGTGGTGCCATCACAGCTC	272405	104601	CTGAACTTGGATTTAAGGGA
183232	15428	GGCGCGATCTCAGCTCACTG	227819	60015	GCAGTGGTGCCATCACAGCT	272406	104602	ACTGAACTTGGATTTAAGGG
183233	15429	TGGCGCGATCTCAGCTCACT	227820	60016	TGCAGTGGTGCCATCACAGC	272407	104603	AACTGAACTTGGATTTAAGG
183234	15430	GTGGCGCGATCTCAGCTCAC	227821	60017	GTGCAGTGGTGCCATCACAG	272408	104604	CAACTGAACTTGGATTTAAG
183235	15431	AGTGGCGCGATCTCAGCTCA	227822	60018	GGTGCAGTGGTGCCATCACA	272409	104605	GCAACTGAACTTGGATTTAA
183236	15432	CAGTGGCGCGATCTCAGCTC	227823	60019	AGGTGCAGTGGTGCCATCAC	272410	104606	GGCAACTGAACTTGGATTTA
183237	15433	GCAGTGGCGCGATCTCAGCT	227824	60020	GAGGTGCAGTGGTGCCATCA	272411	104607	TGGCAACTGAACTTGGATTT
183238	15434	TGCAGTGGCGCGATCTCAGC	227825	60021	TGAGGTGCAGTGGTGCCATC	272412	104608	ATGGCAACTGAACTTGGATT
183239	15435	GTGCAGTGGCGCGATCTCAG	227826	60022	CTGAGGTGCAGTGGTGCCAT	272413	104609	GATGGCAACTGAACTTGGAT
183240	15436	AGTGCAGTGGCGCGATCTCA	227827	60023	GCTGAGGTGCAGTGGTGCCA	272414	104610	AGATGGCAACTGAACTTGGA
183241	15437	GAGTGCAGTGGCGCGATCTC	227828	60024	GGCTGAGGTGCAGTGGTGCC	272415	104611	GAGATGGCAACTGAACTTGG
183242	15438	GGAGTGCAGTGGCGCGATCT	227829	60025	AGGCTGAGGTGCAGTGGTGC	272416	104612	GGAGATGGCAACTGAACTTG
183243	15439	TGGAGTGCAGTGGCGCGATC	227830	60026	CAGGCTGAGGTGCAGTGGTG	272417	104613	AGGAGATGGCAACTGAACTT
183244	15440	CTGGAGTGCAGTGGCGCGAT	227831	60027	CCAGGCTGAGGTGCAGTGGT	272418	104614	GAGGAGATGGCAACTGAACT
183245	15441	GCTGGAGTGCAGTGGCGCGA	227832	60028	CCCAGGCTGAGGTGCAGTGG	272419	104615	GGAGGAGATGGCAACTGAAC
183246	15442	GGCTGGAGTGCAGTGGCGCG	227833	60029	GCCCAGGCTGAGGTGCAGTG	272420	104616	TGGAGGAGATGGCAACTGAA
183247	15443	AGGCTGGAGTGCAGTGGCGC	227834	60030	CGCCCAGGCTGAGGTGCAGT	272421	104617	CTGGAGGAGATGGCAACTGA
183248	15444	CAGGCTGGAGTGCAGTGGCG	227835	60031	TCGCCCAGGCTGAGGTGCAG	272422	104618	CCTGGAGGAGATGGCAACTG
183249	15445	CCAGGCTGGAGTGCAGTGGC	227836	60032	GTCGCCCAGGCTGAGGTGCA	272423	104619	TCCTGGAGGAGATGGCAACT
183250	15446	CCCAGGCTGGAGTGCAGTGG	227837	60033	TGTCGCCCAGGCTGAGGTGC	272424	104620	TTCCTGGAGGAGATGGCAAC
183251	15447	GCCCAGGCTGGAGTGCAGTG	227838	60034	CTGTCGCCCAGGCTGAGGTG	272425	104621	CTTCCTGGAGGAGATGGCAA
183252	15448	CGCCCAGGCTGGAGTGCAGT	227839	60035	TCTGTCGCCCAGGCTGAGGT	272426	104622	ACTTCCTGGAGGAGATGGCA
183253	15449	TCGCCCAGGCTGGAGTGCAG	227840	60036	CTCTGTCGCCCAGGCTGAGG	272427	104623	GACTTCCTGGAGGAGATGGC
183254	15450	GTCGCCCAGGCTGGAGTGCA	227841	60037	GCTCTGTCGCCCAGGCTGAG	272428	104624	AGACTTCCTGGAGGAGATGG
183255	15451	TGTCGCCCAGGCTGGAGTGC	227842	60038	TGCTCTGTCGCCCAGGCTGA	272429	104625	AAGACTTCCTGGAGGAGATG
183256	15452	CTGTCGCCCAGGCTGGAGTG	227843	60039	TTGCTCTGTCGCCCAGGCTG	272430	104626	GAAGACTTCCTGGAGGAGAT
183257	15453	TCTGTCGCCCAGGCTGGAGT	227844	60040	CTTGCTCTGTCGCCCAGGCT	272431	104627	GGAAGACTTCCTGGAGGAGA
183258	15454	CTCTGTCGCCCAGGCTGGAG	227845	60041	TCTTGCTCTGTCGCCCAGGC	272432	104628	AGGAAGACTTCCTGGAGGAG
183259	15455	ACTCTGTCGCCCAGGCTGGA	227846	60042	GTCTTGCTCTGTCGCCCAGG	272433	104629	CAGGAAGACTTCCTGGAGGA
183260	15456	CACTCTGTCGCCCAGGCTGG	227847	60043	GGTCTTGCTCTGTCGCCCAG	272434	104630	CCAGGAAGACTTCCTGGAGG
183261	15457	TCACTCTGTCGCCCAGGCTG	227848	60044	AGGTCTTGCTCTGTCGCCCA	272435	104631	TCCAGGAAGACTTCCTGGAG
183262	15458	CTCACTCTGTCGCCCAGGCT	227849	60045	AAGGTCTTGCTCTGTCGCCC	272436	104632	ATCCAGGAAGACTTCCTGGA
183263	15459	ACTCACTCTGTCGCCCAGGC	227850	60046	CAAGGTCTTGCTCTGTCGCC	272437	104633	AATCCAGGAAGACTTCCTGG
183264	15460	CACTCACTCTGTCGCCCAGG	227851	60047	ACAAGGTCTTGCTCTGTCGC	272438	104634	GAATCCAGGAAGACTTCCTG
183265	15461	TCACTCACTCTGTCGCCCAG	227852	60048	GACAAGGTCTTGCTCTGTCG	272439	104635	GGAATCCAGGAAGACTTCCT
183266	15462	CTCACTCACTCTGTCGCCCA	227853	60049	AGACAAGGTCTTGCTCTGTC	272440	104636	GGGAATCCAGGAAGACTTCC
183267	15463	TCTCACTCACTCTGTCGCCC	227854	60050	GAGACAAGGTCTTGCTCTGT	272441	104637	GGGGAATCCAGGAAGACTTC
183268	15464	GTCTCACTCACTCTGTCGCC	227855	60051	GGAGACAAGGTCTTGCTCTG	272442	104638	AGGGGAATCCAGGAAGACTT
183269	15465	AGTCTCACTCACTCTGTCGC	227856	60052	TGGAGACAAGGTCTTGCTCT	272443	104639	GAGGGGAATCCAGGAAGACT
183270	15466	GAGTCTCACTCACTCTGTCG	227857	60053	TTGGAGACAAGGTCTTGCTC	272444	104640	AGAGGGGAATCCAGGAAGAC
183271	15467	GGAGTCTCACTCACTCTGTC	227858	60054	TTTGGAGACAAGGTCTTGCT	272445	104641	GAGAGGGGAATCCAGGAAGA
183272	15468	TGGAGTCTCACTCACTCTGT	227859	60055	ATTTGGAGACAAGGTCTTGC	272446	104642	AGAGAGGGGAATCCAGGAAG
183273	15469	ATGGAGTCTCACTCACTCTG	227860	60056	TATTTGGAGACAAGGTCTTG	272447	104643	GAGAGAGGGGAATCCAGGAA
183274	15470	AATGGAGTCTCACTCACTCT	227861	60057	TTATTTGGAGACAAGGTCTT	272448	104644	AGAGAGAGGGGAATCCAGGA
183275	15471	AAATGGAGTCTCACTCACTC	227862	60058	TTTATTTGGAGACAAGGTCT	272449	104645	AAGAGAGAGGGGAATCCAGG
183276	15472	GAAATGGAGTCTCACTCACT	227863	60059	ATTTATTTGGAGACAAGGTC	272450	104646	GAAGAGAGAGGGGAATCCAG
183277	15473	TGAAATGGAGTCTCACTCAC	227864	60060	TATTTATTTGGAGACAAGGT	272451	104647	AGAAGAGAGAGGGGAATCCA
183278	15474	TTGAAATGGAGTCTCACTCA	227865	60061	TTATTTATTTGGAGACAAGG	272452	104648	AAGAAGAGAGAGGGGAATCC
183279	15475	TTTGAAATGGAGTCTCACTC	227866	60062	TTTATTTATTTGGAGACAAG	272453	104649	TAAGAAGAGAGAGGGGAATC
183280	15476	TTTTGAAATGGAGTCTCACT	227867	60063	ATTTATTTATTTGGAGACAA	272454	104650	TTAAGAAGAGAGAGGGGAAT
183281	15477	TTTTTGAAATGGAGTCTCAC	227868	60064	TATTTATTTATTTGGAGACA	272455	104651	TTTAAGAAGAGAGAGGGGAA
183282	15478	TTTTTTGAAATGGAGTCTCA	227869	60065	TTATTTATTTATTTGGAGAC	272456	104652	CTTTAAGAAGAGAGAGGGGA

183283	15479	TTTTTTTGAAATGGAGTCTC	227870	60066	ATTATTTATTTATTTGGAGA	272457	104653	GCTTTAAGAAGAGAGAGGGG
183284	15480	ATTTTTTTGAAATGGAGTCT	227871	60067	CATTATTTATTTATTTGGAG	272458	104654	GGCTTTAAGAAGAGAGAGGG
183285	15481	TATTTTTTTGAAATGGAGTC	227872	60068	GCATTATTTATTTATTTGGA	272459	104655	GGGCTTTAAGAAGAGAGAGG
183286	15482	TTATTTTTTTGAAATGGAGT	227873	60069	TGCATTATTTATTTATTTGG	272460	104656	GGGGCTTTAAGAAGAGAGAG
183287	15483	ATTATTTTTTTGAAATGGAG	227874	60070	TTGCATTATTTATTTATTTG	272461	104657	AGGGGCTTTAAGAAGAGAGA
183288	15484	TATTATTTTTTTGAAATGGA	227875	60071	TTTGCATTATTTATTTATTT	272462	104658	CAGGGGCTTTAAGAAGAGAG
183289	15485	TTATTATTTTTTTGAAATGG	227876	60072	CTTTGCATTATTTATTTATT	272463	104659	ACAGGGGCTTTAAGAAGAGA
183290	15486	TTTATTATTTTTTTGAAATG	227877	60073	ACTTTGCATTATTTATTTAT	272464	104660	TACAGGGGCTTTAAGAAGAG
183291	15487	ATTTATTATTTTTTTGAAAT	227878	60074	TACTTTGCATTATTTATTTA	272465	104661	TTACAGGGGCTTTAAGAAGA
183292	15488	GATTTATTATTTTTTTGAAA	227879	60075	TTACTTTGCATTATTTATTT	272466	104662	TTTACAGGGGCTTTAAGAAG
183293	15489	AGATTTATTATTTTTTTGAA	227880	60076	TTTACTTTGCATTATTTATT	272467	104663	GTTTACAGGGGCTTTAAGAA
183294	15490	CAGATTTATTATTTTTTTGA	227881	60077	TTTTACTTTGCATTATTTAT	272468	104664	AGTTTACAGGGGCTTTAAGA
183295	15491	TCAGATTTATTATTTTTTTG	227882	60078	ATTTTACTTTGCATTATTTA	272469	104665	GAGTTTACAGGGGCTTTAAG
183296	15492	CTCAGATTTATTATTTTTTT	227883	60079	TATTTTACTTTGCATTATTT	272470	104666	AGAGTTTACAGGGGCTTTAA
183297	15493	ACTCAGATTTATTATTTTTT	227884	60080	TTATTTTACTTTGCATTATT	272471	104667	CAGAGTTTACAGGGGCTTTA
183298	15494	GACTCAGATTTATTATTTTT	227885	60081	TTTATTTTACTTTGCATTAT	272472	104668	TCAGAGTTTACAGGGGCTTT
183299	15495	TGACTCAGATTTATTATTTT	227886	60082	ATTTATTTTACTTTGCATTA	272473	104669	GTCAGAGTTTACAGGGGCTT
183300	15496	GTGACTCAGATTTATTATTT	227887	60083	TATTTATTTTACTTTGCATT	272474	104670	GGTCAGAGTTTACAGGGGCT
183301	15497	AGTGACTCAGATTTATTATT	227888	60084	TTATTTATTTTACTTTGCAT	272475	104671	TGGTCAGAGTTTACAGGGGC
183302	15498	AAGTGACTCAGATTTATTAT	227889	60085	TTTATTTATTTTACTTTGCA	272476	104672	GTGGTCAGAGTTTACAGGGG
183303	15499	AAAGTGACTCAGATTTATTA	227890	60086	TTTTATTTATTTTACTTTGC	272477	104673	TGTGGTCAGAGTTTACAGGG
183304	15500	TAAAGTGACTCAGATTTATT	227891	60087	GTTTTATTTATTTTACTTTG	272478	104674	GTGTGGTCAGAGTTTACAGG
183305	15501	TTAAAGTGACTCAGATTTAT	227892	60088	GGTTTTATTTATTTTACTTT	272479	104675	AGTGTGGTCAGAGTTTACAG
183306	15502	ATTAAAGTGACTCAGATTTA	227893	60089	TGGTTTTATTTATTTTACTT	272480	104676	CAGTGTGGTCAGAGTTTACA
183307	15503	TATTAAAGTGACTCAGATTT	227894	60090	ATGGTTTTATTTATTTTACT	272481	104677	TCAGTGTGGTCAGAGTTTAC
183308	15504	ATATTAAAGTGACTCAGATT	227895	60091	TATGGTTTTATTTATTTTAC	272482	104678	CTCAGTGTGGTCAGAGTTTA
183309	15505	AATATTAAAGTGACTCAGAT	227896	60092	ATATGGTTTTATTTATTTTA	272483	104679	GCTCAGTGTGGTCAGAGTTT
183310	15506	CAATATTAAAGTGACTCAGA	227897	60093	TATATGGTTTTATTTATTTT	272484	104680	TGCTCAGTGTGGTCAGAGTT
183311	15507	ACAATATTAAAGTGACTCAG	227898	60094	TTATATGGTTTTATTTATTT	272485	104681	ATGCTCAGTGTGGTCAGAGT
183312	15508	AACAATATTAAAGTGACTCA	227899	60095	TTTATATGGTTTTATTTATT	272486	104682	CATGCTCAGTGTGGTCAGAG
183313	15509	TAACAATATTAAAGTGACTC	227900	60096	TTTTATATGGTTTTATTTAT	272487	104683	ACATGCTCAGTGTGGTCAGA
183314	15510	ATAACAATATTAAAGTGACT	227901	60097	TTTTTATATGGTTTTATTTA	272488	104684	CACATGCTCAGTGTGGTCAG
183315	15511	AATAACAATATTAAAGTGAC	227902	60098	CTTTTTATATGGTTTTATTT	272489	104685	ACACATGCTCAGTGTGGTCA
183316	15512	AAATAACAATATTAAAGTGA	227903	60099	CCTTTTTATATGGTTTTATT	272490	104686	GACACATGCTCAGTGTGGTC
183317	15513	CAAATAACAATATTAAAGTG	227904	60100	TCCTTTTTATATGGTTTTAT	272491	104687	AGACACATGCTCAGTGTGGT
183318	15514	CCAAATAACAATATTAAAGT	227905	60101	TTCCTTTTTATATGGTTTTA	272492	104688	CAGACACATGCTCAGTGTGG
183319	15515	TCCAAATAACAATATTAAAG	227906	60102	ATTCCTTTTTATATGGTTTT	272493	104689	GCAGACACATGCTCAGTGTG
183320	15516	ATCCAAATAACAATATTAAA	227907	60103	GATTCCTTTTTATATGGTTT	272494	104690	AGCAGACACATGCTCAGTGT
183321	15517	CATCCAAATAACAATATTAA	227908	60104	TGATTCCTTTTTATATGGTT	272495	104691	CAGCAGACACATGCTCAGTG
183322	15518	ACATCCAAATAACAATATTA	227909	60105	TTGATTCCTTTTTATATGGT	272496	104692	GCAGCAGACACATGCTCAGT
183323	15519	GACATCCAAATAACAATATT	227910	60106	ATTGATTCCTTTTTATATGG	272497	104693	AGCAGCAGACACATGCTCAG
183324	15520	TGACATCCAAATAACAATAT	227911	60107	AATTGATTCCTTTTTATATG	272498	104694	GAGCAGCAGACACATGCTCA
183325	15521	TTGACATCCAAATAACAATA	227912	60108	AAATTGATTCCTTTTTATAT	272499	104695	GGAGCAGCAGACACATGCTC
183326	15522	GTTGACATCCAAATAACAAT	227913	60109	TAAATTGATTCCTTTTTATA	272500	104696	GGGAGCAGCAGACACATGCT
183327	15523	GGTTGACATCCAAATAACAA	227914	60110	TTAAATTGATTCCTTTTTAT	272501	104697	AGGGAGCAGCAGACACATGC
183328	15524	AGGTTGACATCCAAATAACA	227915	60111	TTTAAATTGATTCCTTTTTA	272502	104698	TAGGGAGCAGCAGACACATG
183329	15525	GAGGTTGACATCCAAATAAC	227916	60112	TTTTAAATTGATTCCTTTTT	272503	104699	CTAGGGAGCAGCAGACACAT
183330	15526	AGAGGTTGACATCCAAATAA	227917	60113	ATTTTAAATTGATTCCTTTT	272504	104700	ACTAGGGAGCAGCAGACACA
183331	15527	TAGAGGTTGACATCCAAATA	227918	60114	AATTTTAAATTGATTCCTTT	272505	104701	GACTAGGGAGCAGCAGACAC
183332	15528	CTAGAGGTTGACATCCAAAT	227919	60115	TAATTTTAAATTGATTCCTT	272506	104702	AGACTAGGGAGCAGCAGACA
183333	15529	CCTAGAGGTTGACATCCAAA	227920	60116	ATAATTTTAAATTGATTCCT	272507	104703	CAGACTAGGGAGCAGCAGAC
183334	15530	ACCTAGAGGTTGACATCCAA	227921	60117	TATAATTTTAAATTGATTCC	272508	104704	CCAGACTAGGGAGCAGCAGA
183335	15531	CACCTAGAGGTTGACATCCA	227922	60118	TTATAATTTTAAATTGATTC	272509	104705	CCCAGACTAGGGAGCAGCAG
183336	15532	ACACCTAGAGGTTGACATCC	227923	60119	ATTATAATTTTAAATTGATT	272510	104706	GCCCAGACTAGGGAGCAGCA
183337	15533	AACACCTAGAGGTTGACATC	227924	60120	CATTATAATTTTAAATTGAT	272511	104707	GGCCCAGACTAGGGAGCAGC
183338	15534	AAACACCTAGAGGTTGACAT	227925	60121	TCATTATAATTTTAAATTGA	272512	104708	TGGCCCAGACTAGGGAGCAG
183339	15535	CAAACACCTAGAGGTTGACA	227926	60122	TTCATTATAATTTTAAATTG	272513	104709	ATGGCCCAGACTAGGGAGCA
183340	15536	TCAAACACCTAGAGGTTGAC	227927	60123	TTTCATTATAATTTTAAATT	272514	104710	CATGGCCCAGACTAGGGAGC
183341	15537	CTCAAACACCTAGAGGTTGA	227928	60124	CTTTCATTATAATTTTAAAT	272515	104711	TCATGGCCCAGACTAGGGAG
183342	15538	TCTCAAACACCTAGAGGTTG	227929	60125	GCTTTCATTATAATTTTAAA	272516	104712	CTCATGGCCCAGACTAGGGA
183343	15539	GTCTCAAACACCTAGAGGTT	227930	60126	AGCTTTCATTATAATTTTAA	272517	104713	ACTCATGGCCCAGACTAGGG
183344	15540	TGTCTCAAACACCTAGAGGT	227931	60127	CAGCTTTCATTATAATTTTA	272518	104714	CACTCATGGCCCAGACTAGG
183345	15541	CTGTCTCAAACACCTAGAGG	227932	60128	CCAGCTTTCATTATAATTTT	272519	104715	TCACTCATGGCCCAGACTAG
183346	15542	CCTGTCTCAAACACCTAGAG	227933	60129	GCCAGCTTTCATTATAATTT	272520	104716	CTCACTCATGGCCCAGACTA
183347	15543	TCCTGTCTCAAACACCTAGA	227934	60130	GGCCAGCTTTCATTATAATT	272521	104717	CCTCACTCATGGCCCAGACT
183348	15544	CTCCTGTCTCAAACACCTAG	227935	60131	CGGCCAGCTTTCATTATAAT	272522	104718	CCCTCACTCATGGCCCAGAC
183349	15545	TCTCCTGTCTCAAACACCTA	227936	60132	CCGGCCAGCTTTCATTATAA	272523	104719	ACCCTCACTCATGGCCCAGA
183350	15546	CTCTCCTGTCTCAAACACCT	227937	60133	CCCGGCCAGCTTTCATTATA	272524	104720	CACCCTCACTCATGGCCCAG
183351	15547	ACTCTCCTGTCTCAAACACC	227938	60134	GCCCGGCCAGCTTTCATTAT	272525	104721	CCACCCTCACTCATGGCCCA
183352	15548	CACTCTCCTGTCTCAAACAC	227939	60135	TGCCCGGCCAGCTTTCATTA	272526	104722	TCCACCCTCACTCATGGCCC
183353	15549	TCACTCTCCTGTCTCAAACA	227940	60136	ATGCCCGGCCAGCTTTCATT	272527	104723	CTCCACCCTCACTCATGGCC
183354	15550	ATCACTCTCCTGTCTCAAAC	227941	60137	CATGCCCGGCCAGCTTTCAT	272528	104724	CCTCCACCCTCACTCATGGC

183355	15551	TATCACTCTCCTGTCTCAAA	227942	60138	CCATGCCCGGCCAGCTTTCA	272529	104725	GCCTCCACCCTCACTCATGG
183356	15552	ATATCACTCTCCTGTCTCAA	227943	60139	ACCATGCCCGGCCAGCTTTC	272530	104726	GGCCTCCACCCTCACTCATG
183357	15553	CATATCACTCTCCTGTCTCA	227944	60140	CACCATGCCCGGCCAGCTTT	272531	104727	TGGCCTCCACCCTCACTCAT
183358	15554	CCATATCACTCTCCTGTCTC	227945	60141	CCACCATGCCCGGCCAGCTT	272532	104728	TTGGCCTCCACCCTCACTCA
183359	15555	CCCATATCACTCTCCTGTCT	227946	60142	GCCACCATGCCCGGCCAGCT	272533	104729	CTTGGCCTCCACCCTCACTC
183360	15556	CCCCATATCACTCTCCTGTC	227947	60143	AGCCACCATGCCCGGCCAGC	272534	104730	ACTTGGCCTCCACCCTCACT
183361	15557	CCCCCATATCACTCTCCTGT	227948	60144	GAGCCACCATGCCCGGCCAG	272535	104731	GACTTGGCCTCCACCCTCAC
183362	15558	GCCCCCATATCACTCTCCTG	227949	60145	TGAGCCACCATGCCCGGCCA	272536	104732	AGACTTGGCCTCCACCCTCA
183363	15559	TGCCCCCATATCACTCTCCT	227950	60146	GTGAGCCACCATGCCCGGCC	272537	104733	GAGACTTGGCCTCCACCCTC
183364	15560	GTGCCCCCATATCACTCTCC	227951	60147	CGTGAGCCACCATGCCCGGC	272538	104734	TGAGACTTGGCCTCCACCCT
183365	15561	AGTGCCCCCATATCACTCTC	227952	60148	GCGTGAGCCACCATGCCCGG	272539	104735	ATGAGACTTGGCCTCCACCC
183366	15562	CAGTGCCCCCATATCACTCT	227953	60149	GGCGTGAGCCACCATGCCCG	272540	104736	CATGAGACTTGGCCTCCACC
183367	15563	CCAGTGCCCCCATATCACTC	227954	60150	AGGCGTGAGCCACCATGCCC	272541	104737	GCATGAGACTTGGCCTCCAC
183368	15564	TCCAGTGCCCCCATATCACT	227955	60151	CAGGCGTGAGCCACCATGCC	272542	104738	TGCATGAGACTTGGCCTCCA
183369	15565	TTCCAGTGCCCCCATATCAC	227956	60152	ACAGGCGTGAGCCACCATGC	272543	104739	ATGCATGAGACTTGGCCTCC
183370	15566	TTTCCAGTGCCCCCATATCA	227957	60153	TACAGGCGTGAGCCACCATG	272544	104740	AATGCATGAGACTTGGCCTC
183371	15567	GTTTCCAGTGCCCCCATATC	227958	60154	TTACAGGCGTGAGCCACCAT	272545	104741	AAATGCATGAGACTTGGCCT
183372	15568	TGTTTCCAGTGCCCCCATAT	227959	60155	ATTACAGGCGTGAGCCACCA	272546	104742	AAAATGCATGAGACTTGGCC
183373	15569	GTGTTTCCAGTGCCCCCATA	227960	60156	GATTACAGGCGTGAGCCACC	272547	104743	AAAAATGCATGAGACTTGGC
183374	15570	TGTGTTTCCAGTGCCCCCAT	227961	60157	GGATTACAGGCGTGAGCCAC	272548	104744	CAAAAATGCATGAGACTTGG
183375	15571	GTGTGTTTCCAGTGCCCCCA	227962	60158	GGGATTACAGGCGTGAGCCA	272549	104745	GCAAAAATGCATGAGACTTG
183376	15572	TGTGTGTTTCCAGTGCCCCC	227963	60159	TGGGATTACAGGCGTGAGCC	272550	104746	TGCAAAAATGCATGAGACTT
183377	15573	CTGTGTGTTTCCAGTGCCCC	227964	60160	CTGGGATTACAGGCGTGAGC	272551	104747	CTGCAAAAATGCATGAGACT
183378	15574	CCTGTGTGTTTCCAGTGCCC	227965	60161	GCTGGGATTACAGGCGTGAG	272552	104748	GCTGCAAAAATGCATGAGAC
183379	15575	GCCTGTGTGTTTCCAGTGCC	227966	60162	TGCTGGGATTACAGGCGTGA	272553	104749	GGCTGCAAAAATGCATGAGA
183380	15576	TGCCTGTGTGTTTCCAGTGC	227967	60163	GTGCTGGGATTACAGGCGTG	272554	104750	GGGCTGCAAAAATGCATGAG
183381	15577	GTGCCTGTGTGTTTCCAGTG	227968	60164	AGTGCTGGGATTACAGGCGT	272555	104751	GGGGCTGCAAAAATGCATGA
183382	15578	CGTGCCTGTGTGTTTCCAGT	227969	60165	AAGTGCTGGGATTACAGGCG	272556	104752	GGGGGCTGCAAAAATGCATG
183383	15579	CCGTGCCTGTGTGTTTCCAG	227970	60166	AAAGTGCTGGGATTACAGGC	272557	104753	TGGGGGCTGCAAAAATGCAT
183384	15580	CCCGTGCCTGTGTGTTTCCA	227971	60167	CAAAGTGCTGGGATTACAGG	272558	104754	GTGGGGGCTGCAAAAATGCA
183385	15581	CCCCGTGCCTGTGTGTTTCC	227972	60168	CCAAAGTGCTGGGATTACAG	272559	104755	TGTGGGGGCTGCAAAAATGC
183386	15582	ACCCCGTGCCTGTGTGTTTC	227973	60169	CCCAAAGTGCTGGGATTACA	272560	104756	TTGTGGGGGCTGCAAAAATG
183387	15583	CACCCCGTGCCTGTGTGTTT	227974	60170	TCCCAAAGTGCTGGGATTAC	272561	104757	CTTGTGGGGGCTGCAAAAAT
183388	15584	ACACCCCGTGCCTGTGTGTT	227975	60171	CTCCCAAAGTGCTGGGATTA	272562	104758	TCTTGTGGGGGCTGCAAAAA
183389	15585	GACACCCCGTGCCTGTGTGT	227976	60172	CCTCCCAAAGTGCTGGGATT	272563	104759	GTCTTGTGGGGGCTGCAAAA
183390	15586	GGACACCCCGTGCCTGTGTG	227977	60173	GCCTCCCAAAGTGCTGGGAT	272564	104760	AGTCTTGTGGGGGCTGCAAA
183391	15587	AGGACACCCCGTGCCTGTGT	227978	60174	AGCCTCCCAAAGTGCTGGGA	272565	104761	CAGTCTTGTGGGGGCTGCAA
183392	15588	GAGGACACCCCGTGCCTGTG	227979	60175	CAGCCTCCCAAAGTGCTGGG	272566	104762	ACAGTCTTGTGGGGGCTGCA
183393	15589	TGAGGACACCCCGTGCCTGT	227980	60176	TCAGCCTCCCAAAGTGCTGG	272567	104763	CACAGTCTTGTGGGGGCTGC
183394	15590	GTGAGGACACCCCGTGCCTG	227981	60177	CTCAGCCTCCCAAAGTGCTG	272568	104764	GCACAGTCTTGTGGGGGCTG
183395	15591	TGTGAGGACACCCCGTGCCT	227982	60178	CCTCAGCCTCCCAAAGTGCT	272569	104765	TGCACAGTCTTGTGGGGGCT
183396	15592	GTGTGAGGACACCCCGTGCC	227983	60179	ACCTCAGCCTCCCAAAGTGC	272570	104766	CTGCACAGTCTTGTGGGGGC
183397	15593	AGTGTGAGGACACCCCGTGC	227984	60180	CACCTCAGCCTCCCAAAGTG	272571	104767	CCTGCACAGTCTTGTGGGGG
183398	15594	AAGTGTGAGGACACCCCGTG	227985	60181	CCACCTCAGCCTCCCAAAGT	272572	104768	ACCTGCACAGTCTTGTGGGG
183399	15595	CAAGTGTGAGGACACCCCGT	227986	60182	CCCACCTCAGCCTCCCAAAG	272573	104769	CACCTGCACAGTCTTGTGGG
183400	15596	CCAAGTGTGAGGACACCCCG	227987	60183	ACCCACCTCAGCCTCCCAAA	272574	104770	CCACCTGCACAGTCTTGTGG
183401	15597	CCCAAGTGTGAGGACACCCC	227988	60184	CACCCACCTCAGCCTCCCAA	272575	104771	GCCACCTGCACAGTCTTGTG
183402	15598	ACCCAAGTGTGAGGACACCC	227989	60185	CCACCCACCTCAGCCTCCCA	272576	104772	GGCCACCTGCACAGTCTTGT
183403	15599	TACCCAAGTGTGAGGACACC	227990	60186	TCCACCCACCTCAGCCTCCC	272577	104773	CGGCCACCTGCACAGTCTTG
183404	15600	CTACCCAAGTGTGAGGACAC	227991	60187	ATCCACCCACCTCAGCCTCC	272578	104774	CCGGCCACCTGCACAGTCTT
183405	15601	GCTACCCAAGTGTGAGGACA	227992	60188	GATCCACCCACCTCAGCCTC	272579	104775	GCCGGCCACCTGCACAGTCT
183406	15602	GGCTACCCAAGTGTGAGGAC	227993	60189	TGATCCACCCACCTCAGCCT	272580	104776	GGCCGGCCACCTGCACAGTC
183407	15603	GGGCTACCCAAGTGTGAGGA	227994	60190	GTGATCCACCCACCTCAGCC	272581	104777	GGGCCGGCCACCTGCACAGT
183408	15604	TGGGCTACCCAAGTGTGAGG	227995	60191	CGTGATCCACCCACCTCAGC	272582	104778	AGGGCCGGCCACCTGCACAG
183409	15605	GTGGGCTACCCAAGTGTGAG	227996	60192	TCGTGATCCACCCACCTCAG	272583	104779	GAGGGCCGGCCACCTGCACA
183410	15606	TGTGGGCTACCCAAGTGTGA	227997	60193	CTCGTGATCCACCCACCTCA	272584	104780	TGAGGGCCGGCCACCTGCAC
183411	15607	GTGTGGGCTACCCAAGTGTG	227998	60194	CCTCGTGATCCACCCACCTC	272585	104781	ATGAGGGCCGGCCACCTGCA
183412	15608	CGTGTGGGCTACCCAAGTGT	227999	60195	GCCTCGTGATCCACCCACCT	272586	104782	AATGAGGGCCGGCCACCTGC
183413	15609	TCGTGTGGGCTACCCAAGTG	228000	60196	GGCCTCGTGATCCACCCACC	272587	104783	CAATGAGGGCCGGCCACCTG
183414	15610	ATCGTGTGGGCTACCCAAGT	228001	60197	TGGCCTCGTGATCCACCCAC	272588	104784	TCAATGAGGGCCGGCCACCT
183415	15611	CATCGTGTGGGCTACCCAAG	228002	60198	CTGGCCTCGTGATCCACCCA	272589	104785	TTCAATGAGGGCCGGCCACC
183416	15612	ACATCGTGTGGGCTACCCAA	228003	60199	CCTGGCCTCGTGATCCACCC	272590	104786	ATTCAATGAGGGCCGGCCAC
183417	15613	CACATCGTGTGGGCTACCCA	228004	60200	TCCTGGCCTCGTGATCCACC	272591	104787	CATTCAATGAGGGCCGGCCA
183418	15614	TCACATCGTGTGGGCTACCC	228005	60201	CTCCTGGCCTCGTGATCCAC	272592	104788	GCATTCAATGAGGGCCGGCC
183419	15615	ATCACATCGTGTGGGCTACC	228006	60202	TCTCCTGGCCTCGTGATCCA	272593	104789	CGCATTCAATGAGGGCCGGC
183420	15616	AATCACATCGTGTGGGCTAC	228007	60203	ATCTCCTGGCCTCGTGATCC	272594	104790	CCGCATTCAATGAGGGCCGG
183421	15617	AAATCACATCGTGTGGGCTA	228008	60204	GATCTCCTGGCCTCGTGATC	272595	104791	CCCGCATTCAATGAGGGCCG
183422	15618	GAAATCACATCGTGTGGGCT	228009	60205	CGATCTCCTGGCCTCGTGAT	272596	104792	CCCCGCATTCAATGAGGGCC
183423	15619	TGAAATCACATCGTGTGGGC	228010	60206	TCGATCTCCTGGCCTCGTGA	272597	104793	ACCCCGCATTCAATGAGGGC
183424	15620	CTGAAATCACATCGTGTGGG	228011	60207	CTCGATCTCCTGGCCTCGTG	272598	104794	AACCCCGCATTCAATGAGGG
183425	15621	CCTGAAATCACATCGTGTGG	228012	60208	TCTCGATCTCCTGGCCTCGT	272599	104795	TAACCCCGCATTCAATGAGG
183426	15622	CCCTGAAATCACATCGTGTG	228013	60209	GTCTCGATCTCCTGGCCTCG	272600	104796	TTAACCCCGCATTCAATGAG

183427	15623	ACCCTGAAATCACATCGTGT	228014	60210	GGTCTCGATCTCCTGGCCTC	272601	104797	ATTAACCCCGCATTCAATGA
183428	15624	CACCCTGAAATCACATCGTG	228015	60211	TGGTCTCGATCTCCTGGCCT	272602	104798	AATTAACCCCGCATTCAATG
183429	15625	GCACCCTGAAATCACATCGT	228016	60212	ATGGTCTCGATCTCCTGGCC	272603	104799	AAATTAACCCCGCATTCAAT
183430	15626	AGCACCCTGAAATCACATCG	228017	60213	GATGGTCTCGATCTCCTGGC	272604	104800	TAAATTAACCCCGCATTCAA
183431	15627	CAGCACCCTGAAATCACATC	228018	60214	AGATGGTCTCGATCTCCTGG	272605	104801	TTAAATTAACCCCGCATTCA
183432	15628	CCAGCACCCTGAAATCACAT	228019	60215	AAGATGGTCTCGATCTCCTG	272606	104802	GTTAAATTAACCCCGCATTC
183433	15629	CCCAGCACCCTGAAATCACA	228020	60216	CAAGATGGTCTCGATCTCCT	272607	104803	AGTTAAATTAACCCCGCATT
183434	15630	TCCCAGCACCCTGAAATCAC	228021	60217	CCAAGATGGTCTCGATCTCC	272608	104804	GAGTTAAATTAACCCCGCAT
183435	15631	CTCCCAGCACCCTGAAATCA	228022	60218	GCCAAGATGGTCTCGATCTC	272609	104805	TGAGTTAAATTAACCCCGCA
183436	15632	CCTCCCAGCACCCTGAAATC	228023	60219	AGCCAAGATGGTCTCGATCT	272610	104806	CTGAGTTAAATTAACCCCGC
183437	15633	ACCTCCCAGCACCCTGAAAT	228024	60220	TAGCCAAGATGGTCTCGATC	272611	104807	GCTGAGTTAAATTAACCCCG
183438	15634	GACCTCCCAGCACCCTGAAA	228025	60221	TTAGCCAAGATGGTCTCGAT	272612	104808	GGCTGAGTTAAATTAACCCC
183439	15635	GGACCTCCCAGCACCCTGAA	228026	60222	GTTAGCCAAGATGGTCTCGA	272613	104809	AGGCTGAGTTAAATTAACCC
183440	15636	GGGACCTCCCAGCACCCTGA	228027	60223	TGTTAGCCAAGATGGTCTCG	272614	104810	GAGGCTGAGTTAAATTAACC
183441	15637	GGGGACCTCCCAGCACCCTG	228028	60224	GTGTTAGCCAAGATGGTCTC	272615	104811	AGAGGCTGAGTTAAATTAAC
183442	15638	GGGGGACCTCCCAGCACCCT	228029	60225	CGTGTTAGCCAAGATGGTCT	272616	104812	CAGAGGCTGAGTTAAATTAA
183443	15639	GGGGGGACCTCCCAGCACCC	228030	60226	CCGTGTTAGCCAAGATGGTC	272617	104813	ACAGAGGCTGAGTTAAATTA
183444	15640	TGGGGGGACCTCCCAGCACC	228031	60227	ACCGTGTTAGCCAAGATGGT	272618	104814	CACAGAGGCTGAGTTAAATT
183445	15641	GTGGGGGGACCTCCCAGCAC	228032	60228	CACCGTGTTAGCCAAGATGG	272619	104815	ACACAGAGGCTGAGTTAAAT
183446	15642	AGTGGGGGGACCTCCCAGCA	228033	60229	TCACCGTGTTAGCCAAGATG	272620	104816	CACACAGAGGCTGAGTTAAA
183447	15643	GAGTGGGGGGACCTCCCAGC	228034	60230	TTCACCGTGTTAGCCAAGAT	272621	104817	TCACACAGAGGCTGAGTTAA
183448	15644	GGAGTGGGGGGACCTCCCAG	228035	60231	TTTCACCGTGTTAGCCAAGA	272622	104818	CTCACACAGAGGCTGAGTTA
183449	15645	GGGAGTGGGGGGACCTCCCA	228036	60232	GTTTCACCGTGTTAGCCAAG	272623	104819	ACTCACACAGAGGCTGAGTT
183450	15646	GGGGAGTGGGGGGACCTCCC	228037	60233	GGTTTCACCGTGTTAGCCAA	272624	104820	CACTCACACAGAGGCTGAGT
183451	15647	TGGGGAGTGGGGGGACCTCC	228038	60234	GGGTTTCACCGTGTTAGCCA	272625	104821	CCACTCACACAGAGGCTGAG
183452	15648	TTGGGGAGTGGGGGGACCTC	228039	60235	GGGGTTTCACCGTGTTAGCC	272626	104822	TCCACTCACACAGAGGCTGA
183453	15649	TTTGGGGAGTGGGGGGACCT	228040	60236	CGGGGTTTCACCGTGTTAGC	272627	104823	ATCCACTCACACAGAGGCTG
183454	15650	ATTTGGGGAGTGGGGGGACC	228041	60237	ACGGGGTTTCACCGTGTTAG	272628	104824	CATCCACTCACACAGAGGCT
183455	15651	AATTTGGGGAGTGGGGGGAC	228042	60238	GACGGGGTTTCACCGTGTTA	272629	104825	TCATCCACTCACACAGAGGC
183456	15652	TAATTTGGGGAGTGGGGGGA	228043	60239	AGACGGGGTTTCACCGTGTT	272630	104826	ATCATCCACTCACACAGAGG
183457	15653	GTAATTTGGGGAGTGGGGGG	228044	60240	GAGACGGGGTTTCACCGTGT	272631	104827	AATCATCCACTCACACAGAG
183458	15654	AGTAATTTGGGGAGTGGGGG	228045	60241	AGAGACGGGGTTTCACCGTG	272632	104828	GAATCATCCACTCACACAGA
183459	15655	TAGTAATTTGGGGAGTGGGG	228046	60242	TAGAGACGGGGTTTCACCGT	272633	104829	TGAATCATCCACTCACACAG
183460	15656	TTAGTAATTTGGGGAGTGGG	228047	60243	GTAGAGACGGGGTTTCACCG	272634	104830	CTGAATCATCCACTCACACA
183461	15657	GTTAGTAATTTGGGGAGTGG	228048	60244	AGTAGAGACGGGGTTTCACC	272635	104831	CCTGAATCATCCACTCACAC
183462	15658	TGTTAGTAATTTGGGGAGTG	228049	60245	TAGTAGAGACGGGGTTTCAC	272636	104832	ACCTGAATCATCCACTCACA
183463	15659	TTGTTAGTAATTTGGGGAGT	228050	60246	TTAGTAGAGACGGGGTTTCA	272637	104833	AACCTGAATCATCCACTCAC
183464	15660	CTTGTTAGTAATTTGGGGAG	228051	60247	TTTAGTAGAGACGGGGTTTC	272638	104834	CAACCTGAATCATCCACTCA
183465	15661	ACTTGTTAGTAATTTGGGGA	228052	60248	TTTTAGTAGAGACGGGGTTT	272639	104835	GCAACCTGAATCATCCACTC
183466	15662	CACTTGTTAGTAATTTGGGG	228053	60249	TTTTTAGTAGAGACGGGGTT	272640	104836	GGCAACCTGAATCATCCACT
183467	15663	CCACTTGTTAGTAATTTGGG	228054	60250	ATTTTTAGTAGAGACGGGGT	272641	104837	TGGCAACCTGAATCATCCAC
183468	15664	TCCACTTGTTAGTAATTTGG	228055	60251	TATTTTTAGTAGAGACGGGG	272642	104838	CTGGCAACCTGAATCATCCA
183469	15665	ATCCACTTGTTAGTAATTTG	228056	60252	GTATTTTTAGTAGAGACGGG	272643	104839	TCTGGCAACCTGAATCATCC
183470	15666	TATCCACTTGTTAGTAATTT	228057	60253	TGTATTTTTAGTAGAGACGG	272644	104840	CTCTGGCAACCTGAATCATC
183471	15667	CTATCCACTTGTTAGTAATT	228058	60254	TTGTATTTTTAGTAGAGACG	272645	104841	TCTCTGGCAACCTGAATCAT
183472	15668	ACTATCCACTTGTTAGTAAT	228059	60255	TTTGTATTTTTAGTAGAGAC	272646	104842	GTCTCTGGCAACCTGAATCA
183473	15669	TACTATCCACTTGTTAGTAA	228060	60256	TTTTGTATTTTTAGTAGAGA	272647	104843	TGTCTCTGGCAACCTGAATC
183474	15670	GTACTATCCACTTGTTAGTA	228061	60257	TTTTTGTATTTTTAGTAGAG	272648	104844	CTGTCTCTGGCAACCTGAAT
183475	15671	AGTACTATCCACTTGTTAGT	228062	60258	TTTTTTGTATTTTTAGTAGA	272649	104845	TCTGTCTCTGGCAACCTGAA
183476	15672	AAGTACTATCCACTTGTTAG	228063	60259	TTTTTTTGTATTTTTAGTAG	272650	104846	TTCTGTCTCTGGCAACCTGA
183477	15673	AAAGTACTATCCACTTGTTA	228064	60260	TTTTTTTTGTATTTTTAGTA	272651	104847	GTTCTGTCTCTGGCAACCTG
183478	15674	TAAAGTACTATCCACTTGTT	228065	60261	TTTTTTTTTGTATTTTTAGT	272652	104848	GGTTCTGTCTCTGGCAACCT
183479	15675	GTAAAGTACTATCCACTTGT	228066	60262	TTTTTTTTTTGTATTTTTAG	272653	104849	GGGTTCTGTCTCTGGCAACC
183480	15676	TGTAAAGTACTATCCACTTG	228067	60263	ATTTTTTTTTTGTATTTTTA	272654	104850	AGGGTTCTGTCTCTGGCAAC
183481	15677	CTGTAAAGTACTATCCACTT	228068	60264	AATTTTTTTTTTGTATTTTT	272655	104851	GAGGGTTCTGTCTCTGGCAA
183482	15678	ACTGTAAAGTACTATCCACT	228069	60265	TAATTTTTTTTTTGTATTTT	272656	104852	TGAGGGTTCTGTCTCTGGCA
183483	15679	AACTGTAAAGTACTATCCAC	228070	60266	CTAATTTTTTTTTTGTATTT	272657	104853	CTGAGGGTTCTGTCTCTGGC
183484	15680	AAACTGTAAAGTACTATCCA	228071	60267	GCTAATTTTTTTTTTGTATT	272658	104854	GCTGAGGGTTCTGTCTCTGG
183485	15681	TAAACTGTAAAGTACTATCC	228072	60268	GGCTAATTTTTTTTTTGTAT	272659	104855	AGCTGAGGGTTCTGTCTCTG
183486	15682	ATAAACTGTAAAGTACTATC	228073	60269	CGGCTAATTTTTTTTTTGTA	272660	104856	AAGCTGAGGGTTCTGTCTCT
183487	15683	TATAAACTGTAAAGTACTAT	228074	60270	CCGGCTAATTTTTTTTTTGT	272661	104857	TAAGCTGAGGGTTCTGTCTC
183488	15684	ATATAAACTGTAAAGTACTA	228075	60271	CCCGGCTAATTTTTTTTTTG	272662	104858	CTAAGCTGAGGGTTCTGTCT
183489	15685	CATATAAACTGTAAAGTACT	228076	60272	GCCCGGCTAATTTTTTTTTT	272663	104859	GCTAAGCTGAGGGTTCTGTC
183490	15686	TCATATAAACTGTAAAGTAC	228077	60273	TGCCCGGCTAATTTTTTTTT	272664	104860	TGCTAAGCTGAGGGTTCTGT
183491	15687	ATCATATAAACTGTAAAGTA	228078	60274	GTGCCCGGCTAATTTTTTTT	272665	104861	ATGCTAAGCTGAGGGTTCTG
183492	15688	GATCATATAAACTGTAAAGT	228079	60275	TGTGCCCGGCTAATTTTTTT	272666	104862	CATGCTAAGCTGAGGGTTCT
183493	15689	AGATCATATAAACTGTAAAG	228080	60276	CTGTGCCCGGCTAATTTTTT	272667	104863	CCATGCTAAGCTGAGGGTTC
183494	15690	GAGATCATATAAACTGTAAA	228081	60277	ACTGTGCCCGGCTAATTTTT	272668	104864	CCCATGCTAAGCTGAGGGTT
183495	15691	TGAGATCATATAAACTGTAA	228082	60278	CACTGTGCCCGGCTAATTTT	272669	104865	TCCCATGCTAAGCTGAGGGT
183496	15692	ATGAGATCATATAAACTGTA	228083	60279	CCACTGTGCCCGGCTAATTT	272670	104866	TTCCCATGCTAAGCTGAGGG
183497	15693	AATGAGATCATATAAACTGT	228084	60280	GCCACTGTGCCCGGCTAATT	272671	104867	CTTCCCATGCTAAGCTGAGG
183498	15694	AAATGAGATCATATAAACTG	228085	60281	CGCCACTGTGCCCGGCTAAT	272672	104868	ACTTCCCATGCTAAGCTGAG

183499	15695	CAAATGAGATCATATAAACT	228086	60282	CCGCCACTGTGCCCGGCTAA	272673	104869	TACTTCCCATGCTAAGCTGA
183500	15696	TCAAATGAGATCATATAAAC	228087	60283	CCCGCCACTGTGCCCGGCTA	272674	104870	CTACTTCCCATGCTAAGCTG
183501	15697	ATCAAATGAGATCATATAAA	228088	60284	GCCCGCCACTGTGCCCGGCT	272675	104871	GCTACTTCCCATGCTAAGCT
183502	15698	AATCAAATGAGATCATATAA	228089	60285	CGCCCGCCACTGTGCCCGGC	272676	104872	AGCTACTTCCCATGCTAAGC
183503	15699	GAATCAAATGAGATCATATA	228090	60286	GCGCCCGCCACTGTGCCCGG	272677	104873	AAGCTACTTCCCATGCTAAG
183504	15700	AGAATCAAATGAGATCATAT	228091	60287	GGCGCCCGCCACTGTGCCCG	272678	104874	GAAGCTACTTCCCATGCTAA
183505	15701	AAGAATCAAATGAGATCATA	228092	60288	AGGCGCCCGCCACTGTGCCC	272679	104875	GGAAGCTACTTCCCATGCTA
183506	15702	TAAGAATCAAATGAGATCAT	228093	60289	CAGGCGCCCGCCACTGTGCC	272680	104876	GGGAAGCTACTTCCCATGCT
183507	15703	TTAAGAATCAAATGAGATCA	228094	60290	ACAGGCGCCCGCCACTGTGC	272681	104877	AGGGAAGCTACTTCCCATGC
183508	15704	GTTAAGAATCAAATGAGATC	228095	60291	TACAGGCGCCCGCCACTGTG	272682	104878	CAGGGAAGCTACTTCCCATG
183509	15705	TGTTAAGAATCAAATGAGAT	228096	60292	CTACAGGCGCCCGCCACTGT	272683	104879	ACAGGGAAGCTACTTCCCAT
183510	15706	ATGTTAAGAATCAAATGAGA	228097	60293	ACTACAGGCGCCCGCCACTG	272684	104880	AACAGGGAAGCTACTTCCCA
183511	15707	CATGTTAAGAATCAAATGAG	228098	60294	GACTACAGGCGCCCGCCACT	272685	104881	CAACAGGGAAGCTACTTCCC
183512	15708	TCATGTTAAGAATCAAATGA	228099	60295	GGACTACAGGCGCCCGCCAC	272686	104882	TCAACAGGGAAGCTACTTCC
183513	15709	CTCATGTTAAGAATCAAATG	228100	60296	GGGACTACAGGCGCCCGCCA	272687	104883	GTCAACAGGGAAGCTACTTC
183514	15710	GCTCATGTTAAGAATCAAAT	228101	60297	TGGGACTACAGGCGCCCGCC	272688	104884	GGTCAACAGGGAAGCTACTT
183515	15711	GGCTCATGTTAAGAATCAAA	228102	60298	CTGGGACTACAGGCGCCCGC	272689	104885	GGGTCAACAGGGAAGCTACT
183516	15712	AGGCTCATGTTAAGAATCAA	228103	60299	GCTGGGACTACAGGCGCCCG	272690	104886	AGGGTCAACAGGGAAGCTAC
183517	15713	CAGGCTCATGTTAAGAATCA	228104	60300	AGCTGGGACTACAGGCGCCC	272691	104887	CAGGGTCAACAGGGAAGCTA
183518	15714	ACAGGCTCATGTTAAGAATC	228105	60301	TAGCTGGGACTACAGGCGCC	272692	104888	TCAGGGTCAACAGGGAAGCT
183519	15715	CACAGGCTCATGTTAAGAAT	228106	60302	GTAGCTGGGACTACAGGCGC	272693	104889	CTCAGGGTCAACAGGGAAGC
183520	15716	TCACAGGCTCATGTTAAGAA	228107	60303	AGTAGCTGGGACTACAGGCG	272694	104890	ACTCAGGGTCAACAGGGAAG
183521	15717	CTCACAGGCTCATGTTAAGA	228108	60304	GAGTAGCTGGGACTACAGGC	272695	104891	AACTCAGGGTCAACAGGGAA
183522	15718	ACTCACAGGCTCATGTTAAG	228109	60305	CGAGTAGCTGGGACTACAGG	272696	104892	GAACTCAGGGTCAACAGGGA
183523	15719	CACTCACAGGCTCATGTTAA	228110	60306	CCGAGTAGCTGGGACTACAG	272697	104893	TGAACTCAGGGTCAACAGGG
183524	15720	TCACTCACAGGCTCATGTTA	228111	60307	CCCGAGTAGCTGGGACTACA	272698	104894	ATGAACTCAGGGTCAACAGG
183525	15721	TTCACTCACAGGCTCATGTT	228112	60308	TCCCGAGTAGCTGGGACTAC	272699	104895	GATGAACTCAGGGTCAACAG
183526	15722	TTTCACTCACAGGCTCATGT	228113	60309	CTCCCGAGTAGCTGGGACTA	272700	104896	AGATGAACTCAGGGTCAACA
183527	15723	TTTTCACTCACAGGCTCATG	228114	60310	CCTCCCGAGTAGCTGGGACT	272701	104897	CAGATGAACTCAGGGTCAAC
183528	15724	TTTTTCACTCACAGGCTCAT	228115	60311	GCCTCCCGAGTAGCTGGGAC	272702	104898	TCAGATGAACTCAGGGTCAA
183529	15725	ATTTTTCACTCACAGGCTCA	228116	60312	AGCCTCCCGAGTAGCTGGGA	272703	104899	CTCAGATGAACTCAGGGTCA
183530	15726	AATTTTTCACTCACAGGCTC	228117	60313	CAGCCTCCCGAGTAGCTGGG	272704	104900	CCTCAGATGAACTCAGGGTC
183531	15727	GAATTTTTCACTCACAGGCT	228118	60314	TCAGCCTCCCGAGTAGCTGG	272705	104901	ACCTCAGATGAACTCAGGGT
183532	15728	GGAATTTTTCACTCACAGGC	228119	60315	CTCAGCCTCCCGAGTAGCTG	272706	104902	AACCTCAGATGAACTCAGGG
183533	15729	AGGAATTTTTCACTCACAGG	228120	60316	CCTCAGCCTCCCGAGTAGCT	272707	104903	CAACCTCAGATGAACTCAGG
183534	15730	AAGGAATTTTTCACTCACAG	228121	60317	GCCTCAGCCTCCCGAGTAGC	272708	104904	CCAACCTCAGATGAACTCAG
183535	15731	GAAGGAATTTTTCACTCACA	228122	60318	TGCCTCAGCCTCCCGAGTAG	272709	104905	GCCAACCTCAGATGAACTCA
183536	15732	GGAAGGAATTTTTCACTCAC	228123	60319	CTGCCTCAGCCTCCCGAGTA	272710	104906	AGCCAACCTCAGATGAACTC
183537	15733	GGGAAGGAATTTTTCACTCA	228124	60320	CCTGCCTCAGCCTCCCGAGT	272711	104907	AAGCCAACCTCAGATGAACT
183538	15734	GGGGAAGGAATTTTTCACTC	228125	60321	TCCTGCCTCAGCCTCCCGAG	272712	104908	CAAGCCAACCTCAGATGAAC
183539	15735	AGGGGAAGGAATTTTTCACT	228126	60322	CTCCTGCCTCAGCCTCCCGA	272713	104909	CCAAGCCAACCTCAGATGAA
183540	15736	GAGGGGAAGGAATTTTTCAC	228127	60323	TCTCCTGCCTCAGCCTCCCG	272714	104910	TCCAAGCCAACCTCAGATGA
183541	15737	AGAGGGGAAGGAATTTTTCA	228128	60324	TTCTCCTGCCTCAGCCTCCC	272715	104911	TTCCAAGCCAACCTCAGATG
183542	15738	AAGAGGGGAAGGAATTTTTC	228129	60325	ATTCTCCTGCCTCAGCCTCC	272716	104912	CTTCCAAGCCAACCTCAGAT
183543	15739	GAAGAGGGGAAGGAATTTTT	228130	60326	CATTCTCCTGCCTCAGCCTC	272717	104913	CCTTCCAAGCCAACCTCAGA
183544	15740	AGAAGAGGGGAAGGAATTTT	228131	60327	ACATTCTCCTGCCTCAGCCT	272718	104914	ACCTTCCAAGCCAACCTCAG
183545	15741	TAGAAGAGGGGAAGGAATTT	228132	60328	GACATTCTCCTGCCTCAGCC	272719	104915	CACCTTCCAAGCCAACCTCA
183546	15742	GTAGAAGAGGGGAAGGAATT	228133	60329	AGACATTCTCCTGCCTCAGC	272720	104916	ACACCTTCCAAGCCAACCTC
183547	15743	TGTAGAAGAGGGGAAGGAAT	228134	60330	AAGACATTCTCCTGCCTCAG	272721	104917	CACACCTTCCAAGCCAACCT
183548	15744	CTGTAGAAGAGGGGAAGGAA	228135	60331	CAAGACATTCTCCTGCCTCA	272722	104918	CCACACCTTCCAAGCCAACC
183549	15745	TCTGTAGAAGAGGGGAAGGA	228136	60332	TCAAGACATTCTCCTGCCTC	272723	104919	CCCACACCTTCCAAGCCAAC
183550	15746	ATCTGTAGAAGAGGGGAAGG	228137	60333	TTCAAGACATTCTCCTGCCT	272724	104920	GCCCACACCTTCCAAGCCAA
183551	15747	AATCTGTAGAAGAGGGGAAG	228138	60334	GTTCAAGACATTCTCCTGCC	272725	104921	TGCCCACACCTTCCAAGCCA
183552	15748	TAATCTGTAGAAGAGGGGAA	228139	60335	GGTTCAAGACATTCTCCTGC	272726	104922	GTGCCCACACCTTCCAAGCC
183553	15749	CTAATCTGTAGAAGAGGGGA	228140	60336	GGGTTCAAGACATTCTCCTG	272727	104923	GGTGCCCACACCTTCCAAGC
183554	15750	CCTAATCTGTAGAAGAGGGG	228141	60337	CGGGTTCAAGACATTCTCCT	272728	104924	TGGTGCCCACACCTTCCAAG
183555	15751	TCCTAATCTGTAGAAGAGGG	228142	60338	CCGGGTTCAAGACATTCTCC	272729	104925	ATGGTGCCCACACCTTCCAA
183556	15752	GTCCTAATCTGTAGAAGAGG	228143	60339	CCCGGGTTCAAGACATTCTC	272730	104926	AATGGTGCCCACACCTTCCA
183557	15753	CGTCCTAATCTGTAGAAGAG	228144	60340	TCCCGGGTTCAAGACATTCT	272731	104927	AAATGGTGCCCACACCTTCC
183558	15754	ACGTCCTAATCTGTAGAAGA	228145	60341	CTCCCGGGTTCAAGACATTC	272732	104928	CAAATGGTGCCCACACCTTC
183559	15755	AACGTCCTAATCTGTAGAAG	228146	60342	CCTCCCGGGTTCAAGACATT	272733	104929	CCAAATGGTGCCCACACCTT
183560	15756	CAACGTCCTAATCTGTAGAA	228147	60343	ACCTCCCGGGTTCAAGACAT	272734	104930	GCCAAATGGTGCCCACACCT
183561	15757	TCAACGTCCTAATCTGTAGA	228148	60344	CACCTCCCGGGTTCAAGACA	272735	104931	GGCCAAATGGTGCCCACACC
183562	15758	CTCAACGTCCTAATCTGTAG	228149	60345	CCACCTCCCGGGTTCAAGAC	272736	104932	GGGCCAAATGGTGCCCACAC
183563	15759	TCTCAACGTCCTAATCTGTA	228150	60346	TCCACCTCCCGGGTTCAAGA	272737	104933	TGGGCCAAATGGTGCCCACA
183564	15760	ATCTCAACGTCCTAATCTGT	228151	60347	CTCCACCTCCCGGGTTCAAG	272738	104934	CTGGGCCAAATGGTGCCCAC
183565	15761	AATCTCAACGTCCTAATCTG	228152	60348	GCTCCACCTCCCGGGTTCAA	272739	104935	ACTGGGCCAAATGGTGCCCA
183566	15762	GAATCTCAACGTCCTAATCT	228153	60349	AGCTCCACCTCCCGGGTTCA	272740	104936	AACTGGGCCAAATGGTGCCC
183567	15763	TGAATCTCAACGTCCTAATC	228154	60350	AAGCTCCACCTCCCGGGTTC	272741	104937	GAACTGGGCCAAATGGTGCC
183568	15764	CTGAATCTCAACGTCCTAAT	228155	60351	CAAGCTCCACCTCCCGGGTT	272742	104938	AGAACTGGGCCAAATGGTGC
183569	15765	CCTGAATCTCAACGTCCTAA	228156	60352	GCAAGCTCCACCTCCCGGGT	272743	104939	AAGAACTGGGCCAAATGGTG
183570	15766	CCCTGAATCTCAACGTCCTA	228157	60353	TGCAAGCTCCACCTCCCGGG	272744	104940	TAAGAACTGGGCCAAATGGT

183571	15767	TCCCTGAATCTCAACGTCCT	228158	60354	CTGCAAGCTCCACCTCCCGG	272745	104941	GTAAGAACTGGGCCAAATGG
183572	15768	CTCCCTGAATCTCAACGTCC	228159	60355	ACTGCAAGCTCCACCTCCCG	272746	104942	TGTAAGAACTGGGCCAAATG
183573	15769	CCTCCCTGAATCTCAACGTC	228160	60356	CACTGCAAGCTCCACCTCCC	272747	104943	CTGTAAGAACTGGGCCAAAT
183574	15770	ACCTCCCTGAATCTCAACGT	228161	60357	TCACTGCAAGCTCCACCTCC	272748	104944	GCTGTAAGAACTGGGCCAAA
183575	15771	AACCTCCCTGAATCTCAACG	228162	60358	CTCACTGCAAGCTCCACCTC	272749	104945	AGCTGTAAGAACTGGGCCAA
183576	15772	GAACCTCCCTGAATCTCAAC	228163	60359	GCTCACTGCAAGCTCCACCT	272750	104946	GAGCTGTAAGAACTGGGCCA
183577	15773	TGAACCTCCCTGAATCTCAA	228164	60360	GGCTCACTGCAAGCTCCACC	272751	104947	AGAGCTGTAAGAACTGGGCC
183578	15774	CTGAACCTCCCTGAATCTCA	228165	60361	CGGCTCACTGCAAGCTCCAC	272752	104948	CAGAGCTGTAAGAACTGGGC
183579	15775	TCTGAACCTCCCTGAATCTC	228166	60362	TCGGCTCACTGCAAGCTCCA	272753	104949	TCAGAGCTGTAAGAACTGGG
183580	15776	CTCTGAACCTCCCTGAATCT	228167	60363	CTCGGCTCACTGCAAGCTCC	272754	104950	TTCAGAGCTGTAAGAACTGG
183581	15777	CCTCTGAACCTCCCTGAATC	228168	60364	TCTCGGCTCACTGCAAGCTC	272755	104951	CTTCAGAGCTGTAAGAACTG
183582	15778	CCCTCTGAACCTCCCTGAAT	228169	60365	ATCTCGGCTCACTGCAAGCT	272756	104952	TCTTCAGAGCTGTAAGAACT
183583	15779	TCCCTCTGAACCTCCCTGAA	228170	60366	GATCTCGGCTCACTGCAAGC	272757	104953	CTCTTCAGAGCTGTAAGAAC
183584	15780	ATCCCTCTGAACCTCCCTGA	228171	60367	CGATCTCGGCTCACTGCAAG	272758	104954	TCTCTTCAGAGCTGTAAGAA
183585	15781	AATCCCTCTGAACCTCCCTG	228172	60368	ACGATCTCGGCTCACTGCAA	272759	104955	CTCTCTTCAGAGCTGTAAGA
183586	15782	GAATCCCTCTGAACCTCCCT	228173	60369	CACGATCTCGGCTCACTGCA	272760	104956	GCTCTCTTCAGAGCTGTAAG
183587	15783	TGAATCCCTCTGAACCTCCC	228174	60370	GCACGATCTCGGCTCACTGC	272761	104957	TGCTCTCTTCAGAGCTGTAA
183588	15784	CTGAATCCCTCTGAACCTCC	228175	60371	GGCACGATCTCGGCTCACTG	272762	104958	CTGCTCTCTTCAGAGCTGTA
183589	15785	CCTGAATCCCTCTGAACCTC	228176	60372	TGGCACGATCTCGGCTCACT	272763	104959	GCTGCTCTCTTCAGAGCTGT
183590	15786	CCCTGAATCCCTCTGAACCT	228177	60373	GTGGCACGATCTCGGCTCAC	272764	104960	TGCTGCTCTCTTCAGAGCTG
183591	15787	TCCCTGAATCCCTCTGAACC	228178	60374	AGTGGCACGATCTCGGCTCA	272765	104961	CTGCTGCTCTCTTCAGAGCT
183592	15788	TTCCCTGAATCCCTCTGAAC	228179	60375	AAGTGGCACGATCTCGGCTC	272766	104962	CCTGCTGCTCTCTTCAGAGC
183593	15789	CTTCCCTGAATCCCTCTGAA	228180	60376	CAAGTGGCACGATCTCGGCT	272767	104963	TCCTGCTGCTCTCTTCAGAG
183594	15790	ACTTCCCTGAATCCCTCTGA	228181	60377	GCAAGTGGCACGATCTCGGC	272768	104964	TTCCTGCTGCTCTCTTCAGA
183595	15791	GACTTCCCTGAATCCCTCTG	228182	60378	TGCAAGTGGCACGATCTCGG	272769	104965	ATTCCTGCTGCTCTCTTCAG
183596	15792	TGACTTCCCTGAATCCCTCT	228183	60379	CTGCAAGTGGCACGATCTCG	272770	104966	CATTCCTGCTGCTCTCTTCA
183597	15793	TTGACTTCCCTGAATCCCTC	228184	60380	ACTGCAAGTGGCACGATCTC	272771	104967	CCATTCCTGCTGCTCTCTTC
183598	15794	CTTGACTTCCCTGAATCCCT	228185	60381	GACTGCAAGTGGCACGATCT	272772	104968	CCCATTCCTGCTGCTCTCTT
183599	15795	ACTTGACTTCCCTGAATCCC	228186	60382	GGACTGCAAGTGGCACGATC	272773	104969	CCCCATTCCTGCTGCTCTCT
183600	15796	CACTTGACTTCCCTGAATCC	228187	60383	TGGACTGCAAGTGGCACGAT	272774	104970	GCCCCATTCCTGCTGCTCTC
183601	15797	CCACTTGACTTCCCTGAATC	228188	60384	CTGGACTGCAAGTGGCACGA	272775	104971	AGCCCCATTCCTGCTGCTCT
183602	15798	GCCACTTGACTTCCCTGAAT	228189	60385	GCTGGACTGCAAGTGGCACG	272776	104972	CAGCCCCATTCCTGCTGCTC
183603	15799	TGCCACTTGACTTCCCTGAA	228190	60386	GGCTGGACTGCAAGTGGCAC	272777	104973	TCAGCCCCATTCCTGCTGCT
183604	15800	GTGCCACTTGACTTCCCTGA	228191	60387	AGGCTGGACTGCAAGTGGCA	272778	104974	CTCAGCCCCATTCCTGCTGC
183605	15801	GGTGCCACTTGACTTCCCTG	228192	60388	CAGGCTGGACTGCAAGTGGC	272779	104975	GCTCAGCCCCATTCCTGCTG
183606	15802	AGGTGCCACTTGACTTCCCT	228193	60389	CCAGGCTGGACTGCAAGTGG	272780	104976	TGCTCAGCCCCATTCCTGCT
183607	15803	CAGGTGCCACTTGACTTCCC	228194	60390	CCCAGGCTGGACTGCAAGTG	272781	104977	CTGCTCAGCCCCATTCCTGC
183608	15804	CCAGGTGCCACTTGACTTCC	228195	60391	GCCCAGGCTGGACTGCAAGT	272782	104978	CCTGCTCAGCCCCATTCCTG
183609	15805	TCCAGGTGCCACTTGACTTC	228196	60392	CGCCCAGGCTGGACTGCAAG	272783	104979	CCCTGCTCAGCCCCATTCCT
183610	15806	CTCCAGGTGCCACTTGACTT	228197	60393	TCGCCCAGGCTGGACTGCAA	272784	104980	TCCCTGCTCAGCCCCATTCC
183611	15807	ACTCCAGGTGCCACTTGACT	228198	60394	TTCGCCCAGGCTGGACTGCA	272785	104981	TTCCCTGCTCAGCCCCATTC
183612	15808	GACTCCAGGTGCCACTTGAC	228199	60395	TTTCGCCCAGGCTGGACTGC	272786	104982	CTTCCCTGCTCAGCCCCATT
183613	15809	GGACTCCAGGTGCCACTTGA	228200	60396	CTTTCGCCCAGGCTGGACTG	272787	104983	TCTTCCCTGCTCAGCCCCAT
183614	15810	GGGACTCCAGGTGCCACTTG	228201	60397	TCTTTCGCCCAGGCTGGACT	272788	104984	GTCTTCCCTGCTCAGCCCCA
183615	15811	CGGGACTCCAGGTGCCACTT	228202	60398	CTCTTTCGCCCAGGCTGGAC	272789	104985	TGTCTTCCCTGCTCAGCCCC
183616	15812	ACGGGACTCCAGGTGCCACT	228203	60399	GCTCTTTCGCCCAGGCTGGA	272790	104986	TTGTCTTCCCTGCTCAGCCC
183617	15813	CACGGGACTCCAGGTGCCAC	228204	60400	CGCTCTTTCGCCCAGGCTGG	272791	104987	GTTGTCTTCCCTGCTCAGCC
183618	15814	CCACGGGACTCCAGGTGCCA	228205	60401	TCGCTCTTTCGCCCAGGCTG	272792	104988	AGTTGTCTTCCCTGCTCAGC
183619	15815	GCCACGGGACTCCAGGTGCC	228206	60402	CTCGCTCTTTCGCCCAGGCT	272793	104989	AAGTTGTCTTCCCTGCTCAG
183620	15816	AGCCACGGGACTCCAGGTGC	228207	60403	TCTCGCTCTTTCGCCCAGGC	272794	104990	AAAGTTGTCTTCCCTGCTCA
183621	15817	TAGCCACGGGACTCCAGGTG	228208	60404	GTCTCGCTCTTTCGCCCAGG	272795	104991	GAAAGTTGTCTTCCCTGCTC
183622	15818	TTAGCCACGGGACTCCAGGT	228209	60405	AGTCTCGCTCTTTCGCCCAG	272796	104992	GGAAAGTTGTCTTCCCTGCT
183623	15819	ATTAGCCACGGGACTCCAGG	228210	60406	GAGTCTCGCTCTTTCGCCCA	272797	104993	TGGAAAGTTGTCTTCCCTGC
183624	15820	AATTAGCCACGGGACTCCAG	228211	60407	GGAGTCTCGCTCTTTCGCCC	272798	104994	ATGGAAAGTTGTCTTCCCTG
183625	15821	AAATTAGCCACGGGACTCCA	228212	60408	CGGAGTCTCGCTCTTTCGCC	272799	104995	AATGGAAAGTTGTCTTCCCT
183626	15822	CAAATTAGCCACGGGACTCC	228213	60409	ACGGAGTCTCGCTCTTTCGC	272800	104996	CAATGGAAAGTTGTCTTCCC
183627	15823	TCAAATTAGCCACGGGACTC	228214	60410	GACGGAGTCTCGCTCTTTCG	272801	104997	TCAATGGAAAGTTGTCTTCC
183628	15824	CTCAAATTAGCCACGGGACT	228215	60411	AGACGGAGTCTCGCTCTTTC	272802	104998	TTCAATGGAAAGTTGTCTTC
183629	15825	CCTCAAATTAGCCACGGGAC	228216	60412	GAGACGGAGTCTCGCTCTTT	272803	104999	CTTCAATGGAAAGTTGTCTT
183630	15826	GCCTCAAATTAGCCACGGGA	228217	60413	TGAGACGGAGTCTCGCTCTT	272804	105000	CCTTCAATGGAAAGTTGTCT
183631	15827	GGCCTCAAATTAGCCACGGG	228218	60414	TTGAGACGGAGTCTCGCTCT	272805	105001	GCCTTCAATGGAAAGTTGTC
183632	15828	CGGCCTCAAATTAGCCACGG	228219	60415	TTTGAGACGGAGTCTCGCTC	272806	105002	GGCCTTCAATGGAAAGTTGT
183633	15829	CCGGCCTCAAATTAGCCACG	228220	60416	TTTTGAGACGGAGTCTCGCT	272807	105003	GGGCCTTCAATGGAAAGTTG
183634	15830	ACCGGCCTCAAATTAGCCAC	228221	60417	TTTTTGAGACGGAGTCTCGC	272808	105004	GGGGCCTTCAATGGAAAGTT
183635	15831	TACCGGCCTCAAATTAGCCA	228222	60418	GTTTTTGAGACGGAGTCTCG	272809	105005	AGGGGCCTTCAATGGAAAGT
183636	15832	CTACCGGCCTCAAATTAGCC	228223	60419	TGTTTTTGAGACGGAGTCTC	272810	105006	AAGGGGCCTTCAATGGAAAG
183637	15833	CCTACCGGCCTCAAATTAGC	228224	60420	TTGTTTTTGAGACGGAGTCT	272811	105007	AAAGGGGCCTTCAATGGAAA
183638	15834	CCCTACCGGCCTCAAATTAG	228225	60421	TTTGTTTTTGAGACGGAGTC	272812	105008	GAAAGGGGCCTTCAATGGAA
183639	15835	CCCCTACCGGCCTCAAATTA	228226	60422	TTTTGTTTTTGAGACGGAGT	272813	105009	TGAAAGGGGCCTTCAATGGA
183640	15836	TCCCCTACCGGCCTCAAATT	228227	60423	TTTTTGTTTTTGAGACGGAG	272814	105010	CTGAAAGGGGCCTTCAATGG
183641	15837	ATCCCCTACCGGCCTCAAAT	228228	60424	GTTTTTGTTTTTGAGACGGA	272815	105011	CCTGAAAGGGGCCTTCAATG
183642	15838	AATCCCCTACCGGCCTCAAA	228229	60425	TGTTTTTGTTTTTGAGACGG	272816	105012	CCCTGAAAGGGGCCTTCAAT

183643	15839	GAATCCCCTACCGGCCTCAA	228230	60426	TTGTTTTTGTTTTTGAGACG	272817	105013	GCCCTGAAAGGGGCCTTCAA
183644	15840	CGAATCCCCTACCGGCCTCA	228231	60427	TTTGTTTTTGTTTTTGAGAC	272818	105014	GGCCCTGAAAGGGGCCTTCA
183645	15841	TCGAATCCCCTACCGGCCTC	228232	60428	TTTTGTTTTTGTTTTTGAGA	272819	105015	TGGCCCTGAAAGGGGCCTTC
183646	15842	TTCGAATCCCCTACCGGCCT	228233	60429	TTTTTGTTTTTGTTTTTGAG	272820	105016	CTGGCCCTGAAAGGGGCCTT
183647	15843	GTTCGAATCCCCTACCGGCC	228234	60430	GTTTTTGTTTTTGTTTTTGA	272821	105017	TCTGGCCCTGAAAGGGGCCT
183648	15844	GGTTCGAATCCCCTACCGGC	228235	60431	TGTTTTTGTTTTTGTTTTTG	272822	105018	TTCTGGCCCTGAAAGGGGCC
183649	15845	GGGTTCGAATCCCCTACCGG	228236	60432	TTGTTTTTGTTTTTGTTTTT	272823	105019	GTTCTGGCCCTGAAAGGGGC
183650	15846	TGGGTTCGAATCCCCTACCG	228237	60433	TTTGTTTTTGTTTTTGTTTT	272824	105020	AGTTCTGGCCCTGAAAGGGG
183651	15847	CTGGGTTCGAATCCCCTACC	228238	60434	TTTTGTTTTTGTTTTTGTTT	272825	105021	CAGTTCTGGCCCTGAAAGGG
183652	15848	CCTGGGTTCGAATCCCCTAC	228239	60435	TTTTTGTTTTTGTTTTTGTT	272826	105022	ACAGTTCTGGCCCTGAAAGG
183653	15849	TCCTGGGTTCGAATCCCCTA	228240	60436	GTTTTTGTTTTTGTTTTTGT	272827	105023	GACAGTTCTGGCCCTGAAAG
183654	15850	ATCCTGGGTTCGAATCCCCT	228241	60437	TGTTTTTGTTTTTGTTTTTG	272828	105024	GGACAGTTCTGGCCCTGAAA
183655	15851	AATCCTGGGTTCGAATCCCC	228242	60438	TTGTTTTTGTTTTTGTTTTT	272829	105025	GGGACAGTTCTGGCCCTGAA
183656	15852	AAATCCTGGGTTCGAATCCC	228243	60439	TTTGTTTTTGTTTTTGTTTT	272830	105026	AGGGACAGTTCTGGCCCTGA
183657	15853	CAAATCCTGGGTTCGAATCC	228244	60440	TTTTGTTTTTGTTTTTGTTT	272831	105027	GAGGGACAGTTCTGGCCCTG
183658	15854	ACAAATCCTGGGTTCGAATC	228245	60441	TTTTTGTTTTTGTTTTTGTT	272832	105028	GGAGGGACAGTTCTGGCCCT
183659	15855	CACAAATCCTGGGTTCGAAT	228246	60442	TTTTTTGTTTTTGTTTTTGT	272833	105029	GGGAGGGACAGTTCTGGCCC
183660	15856	GCACAAATCCTGGGTTCGAA	228247	60443	TTTTTTTGTTTTTGTTTTTG	272834	105030	TGGGAGGGACAGTTCTGGCC
183661	15857	AGCACAAATCCTGGGTTCGA	228248	60444	TTTTTTTTGTTTTTGTTTTT	272835	105031	GTGGGAGGGACAGTTCTGGC
183662	15858	AAGCACAAATCCTGGGTTCG	228249	60445	TTTTTTTTTGTTTTTGTTTT	272836	105032	GGTGGGAGGGACAGTTCTGG
183663	15859	GAAGCACAAATCCTGGGTTC	228250	60446	ATTTTTTTTTGTTTTTGTTT	272837	105033	GGGTGGGAGGGACAGTTCTG
183664	15860	AGAAGCACAAATCCTGGGTT	228251	60447	AATTTTTTTTTGTTTTTGTT	272838	105034	AGGGTGGGAGGGACAGTTCT
183665	15861	AAGAAGCACAAATCCTGGGT	228252	60448	TAATTTTTTTTTGTTTTTGT	272839	105035	CAGGGTGGGAGGGACAGTTC
183666	15862	TAAGAAGCACAAATCCTGGG	228253	60449	ATAATTTTTTTTTGTTTTTG	272840	105036	GCAGGGTGGGAGGGACAGTT
183667	15863	ATAAGAAGCACAAATCCTGG	228254	60450	TATAATTTTTTTTTGTTTTT	272841	105037	TGCAGGGTGGGAGGGACAGT
183668	15864	CATAAGAAGCACAAATCCTG	228255	60451	TTATAATTTTTTTTTGTTTT	272842	105038	CTGCAGGGTGGGAGGGACAG
183669	15865	GCATAAGAAGCACAAATCCT	228256	60452	ATTATAATTTTTTTTTGTTT	272843	105039	GCTGCAGGGTGGGAGGGACA
183670	15866	GGCATAAGAAGCACAAATCC	228257	60453	CATTATAATTTTTTTTTGTT	272844	105040	AGCTGCAGGGTGGGAGGGAC
183671	15867	AGGCATAAGAAGCACAAATC	228258	60454	TCATTATAATTTTTTTTTGT	272845	105041	CAGCTGCAGGGTGGGAGGGA
183672	15868	CAGGCATAAGAAGCACAAAT	228259	60455	TTCATTATAATTTTTTTTTG	272846	105042	GCAGCTGCAGGGTGGGAGGG
183673	15869	CCAGGCATAAGAAGCACAAA	228260	60456	TTTCATTATAATTTTTTTTT	272847	105043	GGCAGCTGCAGGGTGGGAGG
183674	15870	CCCAGGCATAAGAAGCACAA	228261	60457	CTTTCATTATAATTTTTTTT	272848	105044	GGGCAGCTGCAGGGTGGGAG
183675	15871	GCCCAGGCATAAGAAGCACA	228262	60458	GCTTTCATTATAATTTTTTT	272849	105045	AGGGCAGCTGCAGGGTGGGA
183676	15872	AGCCCAGGCATAAGAAGCAC	228263	60459	GGCTTTCATTATAATTTTTT	272850	105046	CAGGGCAGCTGCAGGGTGGG
183677	15873	AAGCCCAGGCATAAGAAGCA	228264	60460	TGGCTTTCATTATAATTTTT	272851	105047	GCAGGGCAGCTGCAGGGTGG
183678	15874	GAAGCCCAGGCATAAGAAGC	228265	60461	TTGGCTTTCATTATAATTTT	272852	105048	GGCAGGGCAGCTGCAGGGTG
183679	15875	AGAAGCCCAGGCATAAGAAG	228266	60462	CTTGGCTTTCATTATAATTT	272853	105049	AGGCAGGGCAGCTGCAGGGT
183680	15876	CAGAAGCCCAGGCATAAGAA	228267	60463	CCTTGGCTTTCATTATAATT	272854	105050	GAGGCAGGGCAGCTGCAGGG
183681	15877	GCAGAAGCCCAGGCATAAGA	228268	60464	CCCTTGGCTTTCATTATAAT	272855	105051	AGAGGCAGGGCAGCTGCAGG
183682	15878	AGCAGAAGCCCAGGCATAAG	228269	60465	CCCCTTGGCTTTCATTATAA	272856	105052	CAGAGGCAGGGCAGCTGCAG
183683	15879	GAGCAGAAGCCCAGGCATAA	228270	60466	GCCCCTTGGCTTTCATTATA	272857	105053	GCAGAGGCAGGGCAGCTGCA
183684	15880	GGAGCAGAAGCCCAGGCATA	228271	60467	TGCCCCTTGGCTTTCATTAT	272858	105054	GGCAGAGGCAGGGCAGCTGC
183685	15881	GGGAGCAGAAGCCCAGGCAT	228272	60468	ATGCCCCTTGGCTTTCATTA	272859	105055	GGGCAGAGGCAGGGCAGCTG
183686	15882	AGGGAGCAGAAGCCCAGGCA	228273	60469	TATGCCCCTTGGCTTTCATT	272860	105056	TGGGCAGAGGCAGGGCAGCT
183687	15883	CAGGGAGCAGAAGCCCAGGC	228274	60470	CTATGCCCCTTGGCTTTCAT	272861	105057	ATGGGCAGAGGCAGGGCAGC
183688	15884	CCAGGGAGCAGAAGCCCAGG	228275	60471	ACTATGCCCCTTGGCTTTCA	272862	105058	CATGGGCAGAGGCAGGGCAG
183689	15885	CCCAGGGAGCAGAAGCCCAG	228276	60472	TACTATGCCCCTTGGCTTTC	272863	105059	TCATGGGCAGAGGCAGGGCA
183690	15886	CCCCAGGGAGCAGAAGCCCA	228277	60473	CTACTATGCCCCTTGGCTTT	272864	105060	CTCATGGGCAGAGGCAGGGC
183691	15887	GCCCCAGGGAGCAGAAGCCC	228278	60474	TCTACTATGCCCCTTGGCTT	272865	105061	CCTCATGGGCAGAGGCAGGG
183692	15888	TGCCCCAGGGAGCAGAAGCC	228279	60475	TTCTACTATGCCCCTTGGCT	272866	105062	CCCTCATGGGCAGAGGCAGG
183693	15889	ATGCCCCAGGGAGCAGAAGC	228280	60476	GTTCTACTATGCCCCTTGGC	272867	105063	CCCCTCATGGGCAGAGGCAG
183694	15890	CATGCCCCAGGGAGCAGAAG	228281	60477	TGTTCTACTATGCCCCTTGG	272868	105064	ACCCCTCATGGGCAGAGGCA
183695	15891	CCATGCCCCAGGGAGCAGAA	228282	60478	TTGTTCTACTATGCCCCTTG	272869	105065	CACCCCTCATGGGCAGAGGC
183696	15892	ACCATGCCCCAGGGAGCAGA	228283	60479	TTTGTTCTACTATGCCCCTT	272870	105066	TCACCCCTCATGGGCAGAGG
183697	15893	GACCATGCCCCAGGGAGCAG	228284	60480	ATTTGTTCTACTATGCCCCT	272871	105067	CTCACCCCTCATGGGCAGAG
183698	15894	AGACCATGCCCCAGGGAGCA	228285	60481	AATTTGTTCTACTATGCCCC	272872	105068	TCTCACCCCTCATGGGCAGA
183699	15895	AAGACCATGCCCCAGGGAGC	228286	60482	AAATTTGTTCTACTATGCCC	272873	105069	CTCTCACCCCTCATGGGCAG
183700	15896	GAAGACCATGCCCCAGGGAG	228287	60483	AAAATTTGTTCTACTATGCC	272874	105070	ACTCTCACCCCTCATGGGCA
183701	15897	GGAAGACCATGCCCCAGGGA	228288	60484	GAAAATTTGTTCTACTATGC	272875	105071	GACTCTCACCCCTCATGGGC
183702	15898	GGGAAGACCATGCCCCAGGG	228289	60485	AGAAAATTTGTTCTACTATG	272876	105072	TGACTCTCACCCCTCATGGG
183703	15899	GGGGAAGACCATGCCCCAGG	228290	60486	TAGAAAATTTGTTCTACTAT	272877	105073	CTGACTCTCACCCCTCATGG
183704	15900	GGGGGAAGACCATGCCCCAG	228291	60487	CTAGAAAATTTGTTCTACTA	272878	105074	CCTGACTCTCACCCCTCATG
183705	15901	AGGGGGAAGACCATGCCCCA	228292	60488	TCTAGAAAATTTGTTCTACT	272879	105075	GCCTGACTCTCACCCCTCAT
183706	15902	TAGGGGGAAGACCATGCCCC	228293	60489	CTCTAGAAAATTTGTTCTAC	272880	105076	CGCCTGACTCTCACCCCTCA
183707	15903	CTAGGGGGAAGACCATGCCC	228294	60490	GCTCTAGAAAATTTGTTCTA	272881	105077	TCGCCTGACTCTCACCCCTC
183708	15904	GCTAGGGGGAAGACCATGCC	228295	60491	AGCTCTAGAAAATTTGTTCT	272882	105078	GTCGCCTGACTCTCACCCCT
183709	15905	AGCTAGGGGGAAGACCATGC	228296	60492	GAGCTCTAGAAAATTTGTTC	272883	105079	GGTCGCCTGACTCTCACCCC
183710	15906	AAGCTAGGGGGAAGACCATG	228297	60493	TGAGCTCTAGAAAATTTGTT	272884	105080	AGGTCGCCTGACTCTCACCC
183711	15907	AAAGCTAGGGGGAAGACCAT	228298	60494	ATGAGCTCTAGAAAATTTGT	272885	105081	GAGGTCGCCTGACTCTCACC
183712	15908	GAAAGCTAGGGGGAAGACCA	228299	60495	AATGAGCTCTAGAAAATTTG	272886	105082	TGAGGTCGCCTGACTCTCAC
183713	15909	GGAAAGCTAGGGGGAAGACC	228300	60496	TAATGAGCTCTAGAAAATTT	272887	105083	ATGAGGTCGCCTGACTCTCA
183714	15910	GGGAAAGCTAGGGGGAAGAC	228301	60497	TTAATGAGCTCTAGAAAATT	272888	105084	CATGAGGTCGCCTGACTCTC

183715	15911	TGGGAAAGCTAGGGGGAAGA	228302	60498	CTTAATGAGCTCTAGAAAAT	272889	105085	GCATGAGGTCGCCTGACTCT
183716	15912	ATGGGAAAGCTAGGGGGAAG	228303	60499	ACTTAATGAGCTCTAGAAAA	272890	105086	GGCATGAGGTCGCCTGACTC
183717	15913	AATGGGAAAGCTAGGGGGAA	228304	60500	GACTTAATGAGCTCTAGAAA	272891	105087	TGGCATGAGGTCGCCTGACT
183718	15914	GAATGGGAAAGCTAGGGGGA	228305	60501	TGACTTAATGAGCTCTAGAA	272892	105088	TTGGCATGAGGTCGCCTGAC
183719	15915	TGAATGGGAAAGCTAGGGGG	228306	60502	TTGACTTAATGAGCTCTAGA	272893	105089	CTTGGCATGAGGTCGCCTGA
183720	15916	GTGAATGGGAAAGCTAGGGG	228307	60503	TTTGACTTAATGAGCTCTAG	272894	105090	ACTTGGCATGAGGTCGCCTG
183721	15917	AGTGAATGGGAAAGCTAGGG	228308	60504	ATTTGACTTAATGAGCTCTA	272895	105091	CACTTGGCATGAGGTCGCCT
183722	15918	CAGTGAATGGGAAAGCTAGG	228309	60505	CATTTGACTTAATGAGCTCT	272896	105092	ACACTTGGCATGAGGTCGCC
183723	15919	GCAGTGAATGGGAAAGCTAG	228310	60506	TCATTTGACTTAATGAGCTC	272897	105093	TACACTTGGCATGAGGTCGC
183724	15920	AGCAGTGAATGGGAAAGCTA	228311	60507	CTCATTTGACTTAATGAGCT	272898	105094	CTACACTTGGCATGAGGTCG
183725	15921	AAGCAGTGAATGGGAAAGCT	228312	60508	ACTCATTTGACTTAATGAGC	272899	105095	TCTACACTTGGCATGAGGTC
183726	15922	AAAGCAGTGAATGGGAAAGC	228313	60509	GACTCATTTGACTTAATGAG	272900	105096	TTCTACACTTGGCATGAGGT
183727	15923	TAAAGCAGTGAATGGGAAAG	228314	60510	TGACTCATTTGACTTAATGA	272901	105097	TTTCTACACTTGGCATGAGG
183728	15924	CTAAAGCAGTGAATGGGAAA	228315	60511	GTGACTCATTTGACTTAATG	272902	105098	CTTTCTACACTTGGCATGAG
183729	15925	GCTAAAGCAGTGAATGGGAA	228316	60512	GGTGACTCATTTGACTTAAT	272903	105099	CCTTTCTACACTTGGCATGA
183730	15926	GGCTAAAGCAGTGAATGGGA	228317	60513	TGGTGACTCATTTGACTTAA	272904	105100	CCCTTTCTACACTTGGCATG
183731	15927	AGGCTAAAGCAGTGAATGGG	228318	60514	CTGGTGACTCATTTGACTTA	272905	105101	CCCCTTTCTACACTTGGCAT
183732	15928	TAGGCTAAAGCAGTGAATGG	228319	60515	ACTGGTGACTCATTTGACTT	272906	105102	GCCCCTTTCTACACTTGGCA
183733	15929	CTAGGCTAAAGCAGTGAATG	228320	60516	AACTGGTGACTCATTTGACT	272907	105103	TGCCCCTTTCTACACTTGGC
183734	15930	CCTAGGCTAAAGCAGTGAAT	228321	60517	TAACTGGTGACTCATTTGAC	272908	105104	CTGCCCCTTTCTACACTTGG
183735	15931	CCCTAGGCTAAAGCAGTGAA	228322	60518	CTAACTGGTGACTCATTTGA	272909	105105	TCTGCCCCTTTCTACACTTG
183736	15932	CCCCTAGGCTAAAGCAGTGA	228323	60519	ACTAACTGGTGACTCATTTG	272910	105106	ATCTGCCCCTTTCTACACTT
183737	15933	ACCCCTAGGCTAAAGCAGTG	228324	60520	TACTAACTGGTGACTCATTT	272911	105107	CATCTGCCCCTTTCTACACT
183738	15934	GACCCCTAGGCTAAAGCAGT	228325	60521	TTACTAACTGGTGACTCATT	272912	105108	CCATCTGCCCCTTTCTACAC
183739	15935	GGACCCCTAGGCTAAAGCAG	228326	60522	TTTACTAACTGGTGACTCAT	272913	105109	CCCATCTGCCCCTTTCTACA
183740	15936	AGGACCCCTAGGCTAAAGCA	228327	60523	TTTTACTAACTGGTGACTCA	272914	105110	TCCCATCTGCCCCTTTCTAC
183741	15937	TAGGACCCCTAGGCTAAAGC	228328	60524	GTTTTACTAACTGGTGACTC	272915	105111	CTCCCATCTGCCCCTTTCTA
183742	15938	GTAGGACCCCTAGGCTAAAG	228329	60525	CGTTTTACTAACTGGTGACT	272916	105112	GCTCCCATCTGCCCCTTTCT
183743	15939	GGTAGGACCCCTAGGCTAAA	228330	60526	GCGTTTTACTAACTGGTGAC	272917	105113	GGCTCCCATCTGCCCCTTTC
183744	15940	GGGTAGGACCCCTAGGCTAA	228331	60527	TGCGTTTTACTAACTGGTGA	272918	105114	GGGCTCCCATCTGCCCCTTT
183745	15941	AGGGTAGGACCCCTAGGCTA	228332	60528	CTGCGTTTTACTAACTGGTG	272919	105115	GGGGCTCCCATCTGCCCCTT
183746	15942	AAGGGTAGGACCCCTAGGCT	228333	60529	ACTGCGTTTTACTAACTGGT	272920	105116	TGGGGCTCCCATCTGCCCCT
183747	15943	AAAGGGTAGGACCCCTAGGC	228334	60530	GACTGCGTTTTACTAACTGG	272921	105117	CTGGGGCTCCCATCTGCCCC
183748	15944	TAAAGGGTAGGACCCCTAGG	228335	60531	TGACTGCGTTTTACTAACTG	272922	105118	CCTGGGGCTCCCATCTGCCC
183749	15945	ATAAAGGGTAGGACCCCTAG	228336	60532	GTGACTGCGTTTTACTAACT	272923	105119	ACCTGGGGCTCCCATCTGCC
183750	15946	AATAAAGGGTAGGACCCCTA	228337	60533	CGTGACTGCGTTTTACTAAC	272924	105120	AACCTGGGGCTCCCATCTGC
183751	15947	TAATAAAGGGTAGGACCCCT	228338	60534	CCGTGACTGCGTTTTACTAA	272925	105121	TAACCTGGGGCTCCCATCTG
183752	15948	TTAATAAAGGGTAGGACCCC	228339	60535	CCCGTGACTGCGTTTTACTA	272926	105122	ATAACCTGGGGCTCCCATCT
183753	15949	TTTAATAAAGGGTAGGACCC	228340	60536	CCCCGTGACTGCGTTTTACT	272927	105123	CATAACCTGGGGCTCCCATC
183754	15950	GTTTAATAAAGGGTAGGACC	228341	60537	TCCCCGTGACTGCGTTTTAC	272928	105124	TCATAACCTGGGGCTCCCAT
183755	15951	AGTTTAATAAAGGGTAGGAC	228342	60538	TTCCCCGTGACTGCGTTTTA	272929	105125	GTCATAACCTGGGGCTCCCA
183756	15952	CAGTTTAATAAAGGGTAGGA	228343	60539	CTTCCCCGTGACTGCGTTTT	272930	105126	CGTCATAACCTGGGGCTCCC
183757	15953	GCAGTTTAATAAAGGGTAGG	228344	60540	TCTTCCCCGTGACTGCGTTT	272931	105127	ACGTCATAACCTGGGGCTCC
183758	15954	GGCAGTTTAATAAAGGGTAG	228345	60541	CTCTTCCCCGTGACTGCGTT	272932	105128	GACGTCATAACCTGGGGCTC
183759	15955	TGGCAGTTTAATAAAGGGTA	228346	60542	TCTCTTCCCCGTGACTGCGT	272933	105129	TGACGTCATAACCTGGGGCT
183760	15956	CTGGCAGTTTAATAAAGGGT	228347	60543	CTCTCTTCCCCGTGACTGCG	272934	105130	GTGACGTCATAACCTGGGGC
183761	15957	ACTGGCAGTTTAATAAAGGG	228348	60544	CCTCTCTTCCCCGTGACTGC	272935	105131	GGTGACGTCATAACCTGGGG
183762	15958	CACTGGCAGTTTAATAAAGG	228349	60545	CCCTCTCTTCCCCGTGACTG	272936	105132	TGGTGACGTCATAACCTGGG
183763	15959	GCACTGGCAGTTTAATAAAG	228350	60546	GCCCTCTCTTCCCCGTGACT	272937	105133	ATGGTGACGTCATAACCTGG
183764	15960	GGCACTGGCAGTTTAATAAA	228351	60547	TGCCCTCTCTTCCCCGTGAC	272938	105134	CATGGTGACGTCATAACCTG
183765	15961	AGGCACTGGCAGTTTAATAA	228352	60548	CTGCCCTCTCTTCCCCGTGA	272939	105135	GCATGGTGACGTCATAACCT
183766	15962	GAGGCACTGGCAGTTTAATA	228353	60549	CCTGCCCTCTCTTCCCCGTG	272940	105136	AGCATGGTGACGTCATAACC
183767	15963	TGAGGCACTGGCAGTTTAAT	228354	60550	TCCTGCCCTCTCTTCCCCGT	272941	105137	CAGCATGGTGACGTCATAAC
183768	15964	GTGAGGCACTGGCAGTTTAA	228355	60551	ATCCTGCCCTCTCTTCCCCG	272942	105138	CCAGCATGGTGACGTCATAA
183769	15965	AGTGAGGCACTGGCAGTTTA	228356	60552	AATCCTGCCCTCTCTTCCCC	272943	105139	CCCAGCATGGTGACGTCATA
183770	15966	CAGTGAGGCACTGGCAGTTT	228357	60553	GAATCCTGCCCTCTCTTCCC	272944	105140	ACCCAGCATGGTGACGTCAT
183771	15967	GCAGTGAGGCACTGGCAGTT	228358	60554	AGAATCCTGCCCTCTCTTCC	272945	105141	CACCCAGCATGGTGACGTCA
183772	15968	AGCAGTGAGGCACTGGCAGT	228359	60555	AAGAATCCTGCCCTCTCTTC	272946	105142	CCACCCAGCATGGTGACGTC
183773	15969	AAGCAGTGAGGCACTGGCAG	228360	60556	AAAGAATCCTGCCCTCTCTT	272947	105143	TCCACCCAGCATGGTGACGT
183774	15970	AAAGCAGTGAGGCACTGGCA	228361	60557	CAAAGAATCCTGCCCTCTCT	272948	105144	CTCCACCCAGCATGGTGACG
183775	15971	AAAAGCAGTGAGGCACTGGC	228362	60558	TCAAAGAATCCTGCCCTCTC	272949	105145	CCTCCACCCAGCATGGTGAC
183776	15972	GAAAAGCAGTGAGGCACTGG	228363	60559	TTCAAAGAATCCTGCCCTCT	272950	105146	GCCTCCACCCAGCATGGTGA
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183778	15974	GAGAAAAGCAGTGAGGCACT	228365	60561	GCTTCAAAGAATCCTGCCCT	272952	105148	CTGCCTCCACCCAGCATGGT
183779	15975	GGAGAAAAGCAGTGAGGCAC	228366	60562	TGCTTCAAAGAATCCTGCCC	272953	105149	GCTGCCTCCACCCAGCATGG
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183781	15977	GGGGAGAAAAGCAGTGAGGC	228368	60564	GCTGCTTCAAAGAATCCTGC	272955	105151	GTGCTGCCTCCACCCAGCAT
183782	15978	GGGGGAGAAAAGCAGTGAGG	228369	60565	CGCTGCTTCAAAGAATCCTG	272956	105152	CGTGCTGCCTCCACCCAGCA
183783	15979	TGGGGGAGAAAAGCAGTGAG	228370	60566	CCGCTGCTTCAAAGAATCCT	272957	105153	ACGTGCTGCCTCCACCCAGC
183784	15980	TTGGGGGAGAAAAGCAGTGA	228371	60567	GCCGCTGCTTCAAAGAATCC	272958	105154	GACGTGCTGCCTCCACCCAG
183785	15981	TTTGGGGGAGAAAAGCAGTG	228372	60568	AGCCGCTGCTTCAAAGAATC	272959	105155	GGACGTGCTGCCTCCACCCA
183786	15982	CTTTGGGGGAGAAAAGCAGT	228373	60569	GAGCCGCTGCTTCAAAGAAT	272960	105156	TGGACGTGCTGCCTCCACCC

183787	15983	TCTTTGGGGGAGAAAAGCAG	228374	60570	AGAGCCGCTGCTTCAAAGAA	272961	105157	TTGGACGTGCTGCCTCCACC
183788	15984	GTCTTTGGGGGAGAAAAGCA	228375	60571	GAGAGCCGCTGCTTCAAAGA	272962	105158	TTTGGACGTGCTGCCTCCAC
183789	15985	TGTCTTTGGGGGAGAAAAGC	228376	60572	GGAGAGCCGCTGCTTCAAAG	272963	105159	ATTTGGACGTGCTGCCTCCA
183790	15986	TTGTCTTTGGGGGAGAAAAG	228377	60573	AGGAGAGCCGCTGCTTCAAA	272964	105160	GATTTGGACGTGCTGCCTCC
183791	15987	TTTGTCTTTGGGGGAGAAAA	228378	60574	TAGGAGAGCCGCTGCTTCAA	272965	105161	AGATTTGGACGTGCTGCCTC
183792	15988	TTTTGTCTTTGGGGGAGAAA	228379	60575	TTAGGAGAGCCGCTGCTTCA	272966	105162	TAGATTTGGACGTGCTGCCT
183793	15989	TTTTTGTCTTTGGGGGAGAA	228380	60576	TTTAGGAGAGCCGCTGCTTC	272967	105163	GTAGATTTGGACGTGCTGCC
183794	15990	TTTTTTGTCTTTGGGGGAGA	228381	60577	TTTTAGGAGAGCCGCTGCTT	272968	105164	AGTAGATTTGGACGTGCTGC
183795	15991	TTTTTTTGTCTTTGGGGGAG	228382	60578	TTTTTAGGAGAGCCGCTGCT	272969	105165	TAGTAGATTTGGACGTGCTG
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183797	15993	TTTTTTTTTGTCTTTGGGGG	228384	60580	TGTTTTTAGGAGAGCCGCTG	272971	105167	TTTAGTAGATTTGGACGTGC
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183800	15996	CACTTTTTTTTTGTCTTTGG	228387	60583	GGTTGTTTTTAGGAGAGCCG	272974	105170	CCCTTTAGTAGATTTGGACG
183801	15997	ACACTTTTTTTTTGTCTTTG	228388	60584	GGGTTGTTTTTAGGAGAGCC	272975	105171	ACCCTTTAGTAGATTTGGAC
183802	15998	AACACTTTTTTTTTGTCTTT	228389	60585	TGGGTTGTTTTTAGGAGAGC	272976	105172	AACCCTTTAGTAGATTTGGA
183803	15999	AAACACTTTTTTTTTGTCTT	228390	60586	GTGGGTTGTTTTTAGGAGAG	272977	105173	TAACCCTTTAGTAGATTTGG
183804	16000	AAAACACTTTTTTTTTGTCT	228391	60587	GGTGGGTTGTTTTTAGGAGA	272978	105174	TTAACCCTTTAGTAGATTTG
183805	16001	AAAAACACTTTTTTTTTGTC	228392	60588	GGGTGGGTTGTTTTTAGGAG	272979	105175	TTTAACCCTTTAGTAGATTT
183806	16002	CAAAAACACTTTTTTTTTGT	228393	60589	AGGGTGGGTTGTTTTTAGGA	272980	105176	CTTTAACCCTTTAGTAGATT
183807	16003	GCAAAAACACTTTTTTTTTG	228394	60590	AAGGGTGGGTTGTTTTTAGG	272981	105177	CCTTTAACCCTTTAGTAGAT
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183810	16006	AAAGCAAAAACACTTTTTTT	228397	60593	GACAAGGGTGGGTTGTTTTT	272984	105180	TCTCCTTTAACCCTTTAGTA
183811	16007	AAAAGCAAAAACACTTTTTT	228398	60594	GGACAAGGGTGGGTTGTTTT	272985	105181	TTCTCCTTTAACCCTTTAGT
183812	16008	CAAAAGCAAAAACACTTTTT	228399	60595	TGGACAAGGGTGGGTTGTTT	272986	105182	TTTCTCCTTTAACCCTTTAG
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183814	16010	AACAAAAGCAAAAACACTTT	228401	60597	GCTGGACAAGGGTGGGTTGT	272988	105184	CCTTTCTCCTTTAACCCTTT
183815	16011	AAACAAAAGCAAAAACACTT	228402	60598	AGCTGGACAAGGGTGGGTTG	272989	105185	CCCTTTCTCCTTTAACCCTT
183816	16012	AAAACAAAAGCAAAAACACT	228403	60599	CAGCTGGACAAGGGTGGGTT	272990	105186	ACCCTTTCTCCTTTAACCCT
183817	16013	CAAAACAAAAGCAAAAACAC	228404	60600	GCAGCTGGACAAGGGTGGGT	272991	105187	CACCCTTTCTCCTTTAACCC
183818	16014	ACAAAACAAAAGCAAAAACA	228405	60601	GGCAGCTGGACAAGGGTGGG	272992	105188	TCACCCTTTCTCCTTTAACC
183819	16015	AACAAAACAAAAGCAAAAAC	228406	60602	AGGCAGCTGGACAAGGGTGG	272993	105189	GTCACCCTTTCTCCTTTAAC
183820	16016	AAACAAAACAAAAGCAAAAA	228407	60603	AAGGCAGCTGGACAAGGGTG	272994	105190	AGTCACCCTTTCTCCTTTAA
183821	16017	AAAACAAAACAAAAGCAAAA	228408	60604	GAAGGCAGCTGGACAAGGGT	272995	105191	AAGTCACCCTTTCTCCTTTA
183822	16018	AAAAACAAAACAAAAGCAAA	228409	60605	GGAAGGCAGCTGGACAAGGG	272996	105192	CAAGTCACCCTTTCTCCTTT
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183825	16021	ATGAAAAACAAAACAAAAGC	228412	60608	GAGGGAAGGCAGCTGGACAA	272999	105195	AGTCAAGTCACCCTTTCTCC
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183827	16023	CCATGAAAAACAAAACAAAA	228414	60610	AGGAGGGAAGGCAGCTGGAC	273001	105197	AAAGTCAAGTCACCCTTTCT
183828	16024	CCCATGAAAAACAAAACAAA	228415	60611	CAGGAGGGAAGGCAGCTGGA	273002	105198	AAAAGTCAAGTCACCCTTTC
183829	16025	GCCCATGAAAAACAAAACAA	228416	60612	TCAGGAGGGAAGGCAGCTGG	273003	105199	GAAAAGTCAAGTCACCCTTT
183830	16026	TGCCCATGAAAAACAAAACA	228417	60613	CTCAGGAGGGAAGGCAGCTG	273004	105200	AGAAAAGTCAAGTCACCCTT
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183832	16028	TCTGCCCATGAAAAACAAAA	228419	60615	CCCTCAGGAGGGAAGGCAGC	273006	105202	CAAGAAAAGTCAAGTCACCC
183833	16029	CTCTGCCCATGAAAAACAAA	228420	60616	ACCCTCAGGAGGGAAGGCAG	273007	105203	TCAAGAAAAGTCAAGTCACC
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183837	16033	AGGTCTCTGCCCATGAAAAA	228424	60620	GAACACCCTCAGGAGGGAAG	273011	105207	TATCTCAAGAAAAGTCAAGT
183838	16034	CAGGTCTCTGCCCATGAAAA	228425	60621	GGAACACCCTCAGGAGGGAA	273012	105208	ATATCTCAAGAAAAGTCAAG
183839	16035	CCAGGTCTCTGCCCATGAAA	228426	60622	GGGAACACCCTCAGGAGGGA	273013	105209	AATATCTCAAGAAAAGTCAA
183840	16036	TCCAGGTCTCTGCCCATGAA	228427	60623	AGGGAACACCCTCAGGAGGG	273014	105210	AAATATCTCAAGAAAAGTCA
183841	16037	TTCCAGGTCTCTGCCCATGA	228428	60624	AAGGGAACACCCTCAGGAGG	273015	105211	AAAATATCTCAAGAAAAGTC
183842	16038	ATTCCAGGTCTCTGCCCATG	228429	60625	AAAGGGAACACCCTCAGGAG	273016	105212	CAAAATATCTCAAGAAAAGT
183843	16039	AATTCCAGGTCTCTGCCCAT	228430	60626	CAAAGGGAACACCCTCAGGA	273017	105213	CCAAAATATCTCAAGAAAAG
183844	16040	AAATTCCAGGTCTCTGCCCA	228431	60627	TCAAAGGGAACACCCTCAGG	273018	105214	CCCAAAATATCTCAAGAAAA
183845	16041	GAAATTCCAGGTCTCTGCCC	228432	60628	GTCAAAGGGAACACCCTCAG	273019	105215	CCCCAAAATATCTCAAGAAA
183846	16042	TGAAATTCCAGGTCTCTGCC	228433	60629	AGTCAAAGGGAACACCCTCA	273020	105216	CCCCCAAAATATCTCAAGAA
183847	16043	CTGAAATTCCAGGTCTCTGC	228434	60630	CAGTCAAAGGGAACACCCTC	273021	105217	TCCCCCAAAATATCTCAAGA
183848	16044	GCTGAAATTCCAGGTCTCTG	228435	60631	ACAGTCAAAGGGAACACCCT	273022	105218	GTCCCCCAAAATATCTCAAG
183849	16045	AGCTGAAATTCCAGGTCTCT	228436	60632	CACAGTCAAAGGGAACACCC	273023	105219	CGTCCCCCAAAATATCTCAA
183850	16046	AAGCTGAAATTCCAGGTCTC	228437	60633	ACACAGTCAAAGGGAACACC	273024	105220	TCGTCCCCCAAAATATCTCA
183851	16047	CAAGCTGAAATTCCAGGTCT	228438	60634	CACACAGTCAAAGGGAACAC	273025	105221	TTCGTCCCCCAAAATATCTC
183852	16048	TCAAGCTGAAATTCCAGGTC	228439	60635	TCACACAGTCAAAGGGAACA	273026	105222	CTTCGTCCCCCAAAATATCT
183853	16049	CTCAAGCTGAAATTCCAGGT	228440	60636	GTCACACAGTCAAAGGGAAC	273027	105223	ACTTCGTCCCCCAAAATATC
183854	16050	TCTCAAGCTGAAATTCCAGG	228441	60637	GGTCACACAGTCAAAGGGAA	273028	105224	CACTTCGTCCCCCAAAATAT
183855	16051	TTCTCAAGCTGAAATTCCAG	228442	60638	GGGTCACACAGTCAAAGGGA	273029	105225	ACACTTCGTCCCCCAAAATA
183856	16052	ATTCTCAAGCTGAAATTCCA	228443	60639	GGGGTCACACAGTCAAAGGG	273030	105226	CACACTTCGTCCCCCAAAAT
183857	16053	AATTCTCAAGCTGAAATTCC	228444	60640	GGGGGTCACACAGTCAAAGG	273031	105227	CCACACTTCGTCCCCCAAAA
183858	16054	AAATTCTCAAGCTGAAATTC	228445	60641	TGGGGGTCACACAGTCAAAG	273032	105228	TCCACACTTCGTCCCCCAAA

183859	16055	CAAATTCTCAAGCTGAAATT	228446	60642	ATGGGGGTCACACAGTCAAA	273033	105229	TTCCACACTTCGTCCCCCAA
183860	16056	ACAAATTCTCAAGCTGAAAT	228447	60643	GATGGGGGTCACACAGTCAA	273034	105230	TTTCCACACTTCGTCCCCCA
183861	16057	CACAAATTCTCAAGCTGAAA	228448	60644	GGATGGGGGTCACACAGTCA	273035	105231	TTTTCCACACTTCGTCCCCC
183862	16058	GCACAAATTCTCAAGCTGAA	228449	60645	GGGATGGGGGTCACACAGTC	273036	105232	CTTTTCCACACTTCGTCCCC
183863	16059	GGCACAAATTCTCAAGCTGA	228450	60646	GGGGATGGGGGTCACACAGT	273037	105233	ACTTTTCCACACTTCGTCCC
183864	16060	TGGCACAAATTCTCAAGCTG	228451	60647	AGGGGATGGGGGTCACACAG	273038	105234	CACTTTTCCACACTTCGTCC
183865	16061	ATGGCACAAATTCTCAAGCT	228452	60648	TAGGGGATGGGGGTCACACA	273039	105235	CCACTTTTCCACACTTCGTC
183866	16062	TATGGCACAAATTCTCAAGC	228453	60649	ATAGGGGATGGGGGTCACAC	273040	105236	GCCACTTTTCCACACTTCGT
183867	16063	ATATGGCACAAATTCTCAAG	228454	60650	AATAGGGGATGGGGGTCACA	273041	105237	TGCCACTTTTCCACACTTCG
183868	16064	CATATGGCACAAATTCTCAA	228455	60651	AAATAGGGGATGGGGGTCAC	273042	105238	CTGCCACTTTTCCACACTTC
183869	16065	TCATATGGCACAAATTCTCA	228456	60652	GAAATAGGGGATGGGGGTCA	273043	105239	TCTGCCACTTTTCCACACTT
183870	16066	ATCATATGGCACAAATTCTC	228457	60653	GGAAATAGGGGATGGGGGTC	273044	105240	CTCTGCCACTTTTCCACACT
183871	16067	TATCATATGGCACAAATTCT	228458	60654	GGGAAATAGGGGATGGGGGT	273045	105241	CCTCTGCCACTTTTCCACAC
183872	16068	TTATCATATGGCACAAATTC	228459	60655	TGGGAAATAGGGGATGGGGG	273046	105242	TCCTCTGCCACTTTTCCACA
183873	16069	TTTATCATATGGCACAAATT	228460	60656	TTGGGAAATAGGGGATGGGG	273047	105243	GTCCTCTGCCACTTTTCCAC
183874	16070	ATTTATCATATGGCACAAAT	228461	60657	GTTGGGAAATAGGGGATGGG	273048	105244	TGTCCTCTGCCACTTTTCCA
183875	16071	TATTTATCATATGGCACAAA	228462	60658	GGTTGGGAAATAGGGGATGG	273049	105245	GTGTCCTCTGCCACTTTTCC
183876	16072	TTATTTATCATATGGCACAA	228463	60659	CGGTTGGGAAATAGGGGATG	273050	105246	TGTGTCCTCTGCCACTTTTC
183877	16073	TTTATTTATCATATGGCACA	228464	60660	ACGGTTGGGAAATAGGGGAT	273051	105247	CTGTGTCCTCTGCCACTTTT
183878	16074	ATTTATTTATCATATGGCAC	228465	60661	GACGGTTGGGAAATAGGGGA	273052	105248	ACTGTGTCCTCTGCCACTTT
183879	16075	GATTTATTTATCATATGGCA	228466	60662	GGACGGTTGGGAAATAGGGG	273053	105249	GACTGTGTCCTCTGCCACTT
183880	16076	TGATTTATTTATCATATGGC	228467	60663	TGGACGGTTGGGAAATAGGG	273054	105250	TGACTGTGTCCTCTGCCACT
183881	16077	TTGATTTATTTATCATATGG	228468	60664	TTGGACGGTTGGGAAATAGG	273055	105251	GTGACTGTGTCCTCTGCCAC
183882	16078	GTTGATTTATTTATCATATG	228469	60665	CTTGGACGGTTGGGAAATAG	273056	105252	TGTGACTGTGTCCTCTGCCA
183883	16079	TGTTGATTTATTTATCATAT	228470	60666	GCTTGGACGGTTGGGAAATA	273057	105253	CTGTGACTGTGTCCTCTGCC
183884	16080	CTGTTGATTTATTTATCATA	228471	60667	GGCTTGGACGGTTGGGAAAT	273058	105254	GCTGTGACTGTGTCCTCTGC
183885	16081	TCTGTTGATTTATTTATCAT	228472	60668	GGGCTTGGACGGTTGGGAAA	273059	105255	GGCTGTGACTGTGTCCTCTG
183886	16082	ATCTGTTGATTTATTTATCA	228473	60669	TGGGCTTGGACGGTTGGGAA	273060	105256	AGGCTGTGACTGTGTCCTCT
183887	16083	CATCTGTTGATTTATTTATC	228474	60670	GTGGGCTTGGACGGTTGGGA	273061	105257	GAGGCTGTGACTGTGTCCTC
183888	16084	CCATCTGTTGATTTATTTAT	228475	60671	GGTGGGCTTGGACGGTTGGG	273062	105258	GGAGGCTGTGACTGTGTCCT
183889	16085	GCCATCTGTTGATTTATTTA	228476	60672	AGGTGGGCTTGGACGGTTGG	273063	105259	GGGAGGCTGTGACTGTGTCC
183890	16086	AGCCATCTGTTGATTTATTT	228477	60673	GAGGTGGGCTTGGACGGTTG	273064	105260	AGGGAGGCTGTGACTGTGTC
183891	16087	AAGCCATCTGTTGATTTATT	228478	60674	AGAGGTGGGCTTGGACGGTT	273065	105261	AAGGGAGGCTGTGACTGTGT
183892	16088	AAAGCCATCTGTTGATTTAT	228479	60675	TAGAGGTGGGCTTGGACGGT	273066	105262	TAAGGGAGGCTGTGACTGTG
183893	16089	AAAAGCCATCTGTTGATTTA	228480	60676	CTAGAGGTGGGCTTGGACGG	273067	105263	TTAAGGGAGGCTGTGACTGT
183894	16090	AAAAAGCCATCTGTTGATTT	228481	60677	GCTAGAGGTGGGCTTGGACG	273068	105264	TTTAAGGGAGGCTGTGACTG
183895	16091	GAAAAAGCCATCTGTTGATT	228482	60678	TGCTAGAGGTGGGCTTGGAC	273069	105265	ATTTAAGGGAGGCTGTGACT
183896	16092	GGAAAAAGCCATCTGTTGAT	228483	60679	ATGCTAGAGGTGGGCTTGGA	273070	105266	CATTTAAGGGAGGCTGTGAC
183897	16093	AGGAAAAAGCCATCTGTTGA	228484	60680	TATGCTAGAGGTGGGCTTGG	273071	105267	GCATTTAAGGGAGGCTGTGA
183898	16094	AAGGAAAAAGCCATCTGTTG	228485	60681	TTATGCTAGAGGTGGGCTTG	273072	105268	GGCATTTAAGGGAGGCTGTG
183899	16095	TAAGGAAAAAGCCATCTGTT	228486	60682	ATTATGCTAGAGGTGGGCTT	273073	105269	TGGCATTTAAGGGAGGCTGT
183900	16096	TTAAGGAAAAAGCCATCTGT	228487	60683	TATTATGCTAGAGGTGGGCT	273074	105270	CTGGCATTTAAGGGAGGCTG
183901	16097	TTTAAGGAAAAAGCCATCTG	228488	60684	GTATTATGCTAGAGGTGGGC	273075	105271	CCTGGCATTTAAGGGAGGCT
183902	16098	TTTTAAGGAAAAAGCCATCT	228489	60685	CGTATTATGCTAGAGGTGGG	273076	105272	TCCTGGCATTTAAGGGAGGC
183903	16099	TTTTTAAGGAAAAAGCCATC	228490	60686	TCGTATTATGCTAGAGGTGG	273077	105273	TTCCTGGCATTTAAGGGAGG
183904	16100	TTTTTTAAGGAAAAAGCCAT	228491	60687	CTCGTATTATGCTAGAGGTG	273078	105274	TTTCCTGGCATTTAAGGGAG
183905	16101	TTTTTTTAAGGAAAAAGCCA	228492	60688	GCTCGTATTATGCTAGAGGT	273079	105275	CTTTCCTGGCATTTAAGGGA
183906	16102	TTTTTTTTAAGGAAAAAGCC	228493	60689	AGCTCGTATTATGCTAGAGG	273080	105276	GCTTTCCTGGCATTTAAGGG
183907	16103	TTTTTTTTTAAGGAAAAAGC	228494	60690	AAGCTCGTATTATGCTAGAG	273081	105277	GGCTTTCCTGGCATTTAAGG
183908	16104	TTTTTTTTTTAAGGAAAAAG	228495	60691	AAAGCTCGTATTATGCTAGA	273082	105278	AGGCTTTCCTGGCATTTAAG
183909	16105	TTTTTTTTTTTAAGGAAAAA	228496	60692	AAAAGCTCGTATTATGCTAG	273083	105279	TAGGCTTTCCTGGCATTTAA
183910	16106	TTTTTTTTTTTTAAGGAAAA	228497	60693	TAAAAGCTCGTATTATGCTA	273084	105280	CTAGGCTTTCCTGGCATTTA
183911	16107	TTTTTTTTTTTTTAAGGAAA	228498	60694	TTAAAAGCTCGTATTATGCT	273085	105281	TCTAGGCTTTCCTGGCATTT
183912	16108	TTTTTTTTTTTTTTAAGGAA	228499	60695	ATTAAAAGCTCGTATTATGC	273086	105282	TTCTAGGCTTTCCTGGCATT
183913	16109	TTTTTTTTTTTTTTTAAGGA	228500	60696	GATTAAAAGCTCGTATTATG	273087	105283	TTTCTAGGCTTTCCTGGCAT
183914	16110	TTTTTTTTTTTTTTTTAAGG	228501	60697	GGATTAAAAGCTCGTATTAT	273088	105284	TTTTCTAGGCTTTCCTGGCA
183915	16111	TTTTTTTTTTTTTTTTTAAG	228502	60698	GGGATTAAAAGCTCGTATTA	273089	105285	TTTTTCTAGGCTTTCCTGGC
183916	16112	TTTTTTTTTTTTTTTTTTAA	228503	60699	AGGGATTAAAAGCTCGTATT	273090	105286	ATTTTTCTAGGCTTTCCTGG
183917	16113	TTTTTTTTTTTTTTTTTTA	228504	60700	GAGGGATTAAAAGCTCGTAT	273091	105287	AATTTTTCTAGGCTTTCCTG
183918	16114	TTTTTTTTTTTTTTTTTTT	228505	60701	AGAGGGATTAAAAGCTCGTA	273092	105288	CAATTTTTCTAGGCTTTCCT
183919	16115	GTTTTTTTTTTTTTTTTTT	228506	60702	GAGAGGGATTAAAAGCTCGT	273093	105289	ACAATTTTTCTAGGCTTTCC
183920	16116	AGTTTTTTTTTTTTTTTTT	228507	60703	GGAGAGGGATTAAAAGCTCG	273094	105290	GACAATTTTTCTAGGCTTTC
183921	16117	TAGTTTTTTTTTTTTTTTT	228508	60704	GGGAGAGGGATTAAAAGCTC	273095	105291	AGACAATTTTTCTAGGCTTT
183922	16118	TTAGTTTTTTTTTTTTTTT	228509	60705	AGGGAGAGGGATTAAAAGCT	273096	105292	CAGACAATTTTTCTAGGCTT
183923	16119	CTTAGTTTTTTTTTTTTTT	228510	60706	CAGGGAGAGGGATTAAAAGC	273097	105293	TCAGACAATTTTTCTAGGCT
183924	16120	TCTTAGTTTTTTTTTTTTT	228511	60707	TCAGGGAGAGGGATTAAAAG	273098	105294	TTCAGACAATTTTTCTAGGC
183925	16121	ATCTTAGTTTTTTTTTTTT	228512	60708	GTCAGGGAGAGGGATTAAAA	273099	105295	TTTCAGACAATTTTTCTAGG
183926	16122	CATCTTAGTTTTTTTTTTT	228513	60709	GGTCAGGGAGAGGGATTAAA	273100	105296	GTTTCAGACAATTTTTCTAG
183927	16123	ACATCTTAGTTTTTTTTTT	228514	60710	GGGTCAGGGAGAGGGATTAA	273101	105297	AGTTTCAGACAATTTTTCTA
183928	16124	TACATCTTAGTTTTTTTTT	228515	60711	GGGGTCAGGGAGAGGGATTA	273102	105298	TAGTTTCAGACAATTTTTCT
183929	16125	ATACATCTTAGTTTTTTTT	228516	60712	TGGGGTCAGGGAGAGGGATT	273103	105299	TTAGTTTCAGACAATTTTTC
183930	16126	AATACATCTTAGTTTTTTT	228517	60713	TTGGGGTCAGGGAGAGGGAT	273104	105300	TTTAGTTTCAGACAATTTTT

183931	16127	AAATACATCTTAGTTTTTTT	228518	60714	GTTGGGGTCAGGGAGAGGGA	273105	105301	GTTTAGTTTCAGACAATTTT
183932	16128	CAAATACATCTTAGTTTTTT	228519	60715	GGTTGGGGTCAGGGAGAGGG	273106	105302	GGTTTAGTTTCAGACAATTT
183933	16129	GCAAATACATCTTAGTTTTT	228520	60716	GGGTTGGGGTCAGGGAGAGG	273107	105303	AGGTTTAGTTTCAGACAATT
183934	16130	TGCAAATACATCTTAGTTTT	228521	60717	CGGGTTGGGGTCAGGGAGAG	273108	105304	GAGGTTTAGTTTCAGACAAT
183935	16131	CTGCAAATACATCTTAGTTT	228522	60718	TCGGGTTGGGGTCAGGGAGA	273109	105305	TGAGGTTTAGTTTCAGACAA
183936	16132	ACTGCAAATACATCTTAGTT	228523	60719	ATCGGGTTGGGGTCAGGGAG	273110	105306	CTGAGGTTTAGTTTCAGACA
183937	16133	CACTGCAAATACATCTTAGT	228524	60720	AATCGGGTTGGGGTCAGGGA	273111	105307	GCTGAGGTTTAGTTTCAGAC
183938	16134	TCACTGCAAATACATCTTAG	228525	60721	AAATCGGGTTGGGGTCAGGG	273112	105308	GGCTGAGGTTTAGTTTCAGA
183939	16135	CTCACTGCAAATACATCTTA	228526	60722	AAAATCGGGTTGGGGTCAGG	273113	105309	TGGCTGAGGTTTAGTTTCAG
183940	16136	CCTCACTGCAAATACATCTT	228527	60723	CAAAATCGGGTTGGGGTCAG	273114	105310	ATGGCTGAGGTTTAGTTTCA
183941	16137	GCCTCACTGCAAATACATCT	228528	60724	TCAAAATCGGGTTGGGGTCA	273115	105311	TATGGCTGAGGTTTAGTTTC
183942	16138	TGCCTCACTGCAAATACATC	228529	60725	TTCAAAATCGGGTTGGGGTC	273116	105312	TTATGGCTGAGGTTTAGTTT
183943	16139	ATGCCTCACTGCAAATACAT	228530	60726	CTTCAAAATCGGGTTGGGGT	273117	105313	GTTATGGCTGAGGTTTAGTT
183944	16140	TATGCCTCACTGCAAATACA	228531	60727	GCTTCAAAATCGGGTTGGGG	273118	105314	TGTTATGGCTGAGGTTTAGT
183945	16141	TTATGCCTCACTGCAAATAC	228532	60728	GGCTTCAAAATCGGGTTGGG	273119	105315	TTGTTATGGCTGAGGTTTAG
183946	16142	ATTATGCCTCACTGCAAATA	228533	60729	GGGCTTCAAAATCGGGTTGG	273120	105316	TTTGTTATGGCTGAGGTTTA
183947	16143	AATTATGCCTCACTGCAAAT	228534	60730	TGGGCTTCAAAATCGGGTTG	273121	105317	CTTTGTTATGGCTGAGGTTT
183948	16144	AAATTATGCCTCACTGCAAA	228535	60731	CTGGGCTTCAAAATCGGGTT	273122	105318	TCTTTGTTATGGCTGAGGTT
183949	16145	CAAATTATGCCTCACTGCAA	228536	60732	ACTGGGCTTCAAAATCGGGT	273123	105319	GTCTTTGTTATGGCTGAGGT
183950	16146	ACAAATTATGCCTCACTGCA	228537	60733	GACTGGGCTTCAAAATCGGG	273124	105320	GGTCTTTGTTATGGCTGAGG
183951	16147	TACAAATTATGCCTCACTGC	228538	60734	AGACTGGGCTTCAAAATCGG	273125	105321	TGGTCTTTGTTATGGCTGAG
183952	16148	GTACAAATTATGCCTCACTG	228539	60735	TAGACTGGGCTTCAAAATCG	273126	105322	TTGGTCTTTGTTATGGCTGA
183953	16149	GGTACAAATTATGCCTCACT	228540	60736	CTAGACTGGGCTTCAAAATC	273127	105323	GTTGGTCTTTGTTATGGCTG
183954	16150	TGGTACAAATTATGCCTCAC	228541	60737	ACTAGACTGGGCTTCAAAAT	273128	105324	TGTTGGTCTTTGTTATGGCT
183955	16151	TTGGTACAAATTATGCCTCA	228542	60738	TACTAGACTGGGCTTCAAAA	273129	105325	GTGTTGGTCTTTGTTATGGC
183956	16152	TTTGGTACAAATTATGCCTC	228543	60739	ATACTAGACTGGGCTTCAAA	273130	105326	TGTGTTGGTCTTTGTTATGG
183957	16153	TTTTGGTACAAATTATGCCT	228544	60740	AATACTAGACTGGGCTTCAA	273131	105327	ATGTGTTGGTCTTTGTTATG
183958	16154	TTTTTGGTACAAATTATGCC	228545	60741	AAATACTAGACTGGGCTTCA	273132	105328	CATGTGTTGGTCTTTGTTAT
183959	16155	CTTTTTGGTACAAATTATGC	228546	60742	AAAATACTAGACTGGGCTTC	273133	105329	TCATGTGTTGGTCTTTGTTA
183960	16156	ACTTTTTGGTACAAATTATG	228547	60743	GAAAATACTAGACTGGGCTT	273134	105330	TTCATGTGTTGGTCTTTGTT
183961	16157	CACTTTTTGGTACAAATTAT	228548	60744	AGAAAATACTAGACTGGGCT	273135	105331	ATTCATGTGTTGGTCTTTGT
183962	16158	GCACTTTTTGGTACAAATTA	228549	60745	GAGAAAATACTAGACTGGGC	273136	105332	GATTCATGTGTTGGTCTTTG
183963	16159	AGCACTTTTTGGTACAAATT	228550	60746	TGAGAAAATACTAGACTGGG	273137	105333	AGATTCATGTGTTGGTCTTT
183964	16160	GAGCACTTTTTGGTACAAAT	228551	60747	TTGAGAAAATACTAGACTGG	273138	105334	GAGATTCATGTGTTGGTCTT
183965	16161	TGAGCACTTTTTGGTACAAA	228552	60748	TTTGAGAAAATACTAGACTG	273139	105335	GGAGATTCATGTGTTGGTCT
183966	16162	GTGAGCACTTTTTGGTACAA	228553	60749	ATTTGAGAAAATACTAGACT	273140	105336	TGGAGATTCATGTGTTGGTC
183967	16163	GGTGAGCACTTTTTGGTACA	228554	60750	TATTTGAGAAAATACTAGAC	273141	105337	CTGGAGATTCATGTGTTGGT
183968	16164	TGGTGAGCACTTTTTGGTAC	228555	60751	GTATTTGAGAAAATACTAGA	273142	105338	CCTGGAGATTCATGTGTTGG
183969	16165	GTGGTGAGCACTTTTTGGTA	228556	60752	TGTATTTGAGAAAATACTAG	273143	105339	TCCTGGAGATTCATGTGTTG
183970	16166	TGTGGTGAGCACTTTTTGGT	228557	60753	GTGTATTTGAGAAAATACTA	273144	105340	TTCCTGGAGATTCATGTGTT
183971	16167	GTGTGGTGAGCACTTTTTGG	228558	60754	AGTGTATTTGAGAAAATACT	273145	105341	TTTCCTGGAGATTCATGTGT
183972	16168	AGTGTGGTGAGCACTTTTTG	228559	60755	AAGTGTATTTGAGAAAATAC	273146	105342	TTTTCCTGGAGATTCATGTG
183973	16169	CAGTGTGGTGAGCACTTTTT	228560	60756	GAAGTGTATTTGAGAAAATA	273147	105343	TTTTTCCTGGAGATTCATGT
183974	16170	ACAGTGTGGTGAGCACTTTT	228561	60757	AGAAGTGTATTTGAGAAAAT	273148	105344	TTTTTTCCTGGAGATTCATG
183975	16171	TACAGTGTGGTGAGCACTTT	228562	60758	AAGAAGTGTATTTGAGAAAA	273149	105345	CTTTTTTCCTGGAGATTCAT
183976	16172	CTACAGTGTGGTGAGCACTT	228563	60759	CAAGAAGTGTATTTGAGAAA	273150	105346	TCTTTTTTCCTGGAGATTCA
183977	16173	ACTACAGTGTGGTGAGCACT	228564	60760	CCAAGAAGTGTATTTGAGAA	273151	105347	TTCTTTTTTCCTGGAGATTC
183978	16174	GACTACAGTGTGGTGAGCAC	228565	60761	GCCAAGAAGTGTATTTGAGA	273152	105348	TTTCTTTTTTCCTGGAGATT
183979	16175	TGACTACAGTGTGGTGAGCA	228566	60762	AGCCAAGAAGTGTATTTGAG	273153	105349	TTTTCTTTTTTCCTGGAGAT
183980	16176	ATGACTACAGTGTGGTGAGC	228567	60763	GAGCCAAGAAGTGTATTTGA	273154	105350	TTTTTCTTTTTTCCTGGAGA
183981	16177	CATGACTACAGTGTGGTGAG	228568	60764	GGAGCCAAGAAGTGTATTTG	273155	105351	CTTTTTCTTTTTTCCTGGAG
183982	16178	CCATGACTACAGTGTGGTGA	228569	60765	TGGAGCCAAGAAGTGTATTT	273156	105352	TCTTTTTCTTTTTTCCTGGA
183983	16179	CCCATGACTACAGTGTGGTG	228570	60766	ATGGAGCCAAGAAGTGTATT	273157	105353	TTCTTTTTCTTTTTTCCTGG
183984	16180	CCCCATGACTACAGTGTGGT	228571	60767	AATGGAGCCAAGAAGTGTAT	273158	105354	TTTCTTTTTCTTTTTTCCTG
183985	16181	CCCCCATGACTACAGTGTGG	228572	60768	GAATGGAGCCAAGAAGTGTA	273159	105355	TTTTCTTTTTCTTTTTTCCT
183986	16182	GCCCCCATGACTACAGTGTG	228573	60769	GGAATGGAGCCAAGAAGTGT	273160	105356	TTTTTCTTTTTCTTTTTTCC
183987	16183	TGCCCCCATGACTACAGTGT	228574	60770	AGGAATGGAGCCAAGAAGTG	273161	105357	ATTTTTCTTTTTCTTTTTTC
183988	16184	CTGCCCCCATGACTACAGTG	228575	60771	AAGGAATGGAGCCAAGAAGT	273162	105358	CATTTTTCTTTTTCTTTTTT
183989	16185	CCTGCCCCCATGACTACAGT	228576	60772	GAAGGAATGGAGCCAAGAAG	273163	105359	ACATTTTTCTTTTTCTTTTT
183990	16186	TCCTGCCCCCATGACTACAG	228577	60773	GGAAGGAATGGAGCCAAGAA	273164	105360	GACATTTTTCTTTTTCTTTT
183991	16187	CTCCTGCCCCCATGACTACA	228578	60774	AGGAAGGAATGGAGCCAAGA	273165	105361	TGACATTTTTCTTTTTCTTT
183992	16188	CCTCCTGCCCCCATGACTAC	228579	60775	AAGGAAGGAATGGAGCCAAG	273166	105362	ATGACATTTTTCTTTTTCTT
183993	16189	GCCTCCTGCCCCCATGACTA	228580	60776	AAAGGAAGGAATGGAGCCAA	273167	105363	TATGACATTTTTCTTTTTCT
183994	16190	TGCCTCCTGCCCCCATGACT	228581	60777	GAAAGGAAGGAATGGAGCCA	273168	105364	GTATGACATTTTTCTTTTTC
183995	16191	CTGCCTCCTGCCCCCATGAC	228582	60778	GGAAAGGAAGGAATGGAGCC	273169	105365	TGTATGACATTTTTCTTTTT
183996	16192	GCTGCCTCCTGCCCCCATGA	228583	60779	TGGAAAGGAAGGAATGGAGC	273170	105366	CTGTATGACATTTTTCTTTT
183997	16193	GGCTGCCTCCTGCCCCCATG	228584	60780	ATGGAAAGGAAGGAATGGAG	273171	105367	CCTGTATGACATTTTTCTTT
183998	16194	CGGCTGCCTCCTGCCCCCAT	228585	60781	GATGGAAAGGAAGGAATGGA	273172	105368	CCCTGTATGACATTTTTCTT
183999	16195	GCGGCTGCCTCCTGCCCCCA	228586	60782	TGATGGAAAGGAAGGAATGG	273173	105369	ACCCTGTATGACATTTTTCT
184000	16196	CGCGGCTGCCTCCTGCCCCC	228587	60783	GTGATGGAAAGGAAGGAATG	273174	105370	GACCCTGTATGACATTTTTC
184001	16197	CCGCGGCTGCCTCCTGCCCC	228588	60784	GGTGATGGAAAGGAAGGAAT	273175	105371	GGACCCTGTATGACATTTTT
184002	16198	CCCGCGGCTGCCTCCTGCCC	228589	60785	AGGTGATGGAAAGGAAGGAA	273176	105372	TGGACCCTGTATGACATTTT

184003	16199	ACCCGCGGCTGCCTCCTGCC	228590	60786	GAGGTGATGGAAAGGAAGGA	273177	105373	ATGGACCCTGTATGACATTT
184004	16200	CACCCGCGGCTGCCTCCTGC	228591	60787	AGAGGTGATGGAAAGGAAGG	273178	105374	CATGGACCCTGTATGACATT
184005	16201	TCACCCGCGGCTGCCTCCTG	228592	60788	CAGAGGTGATGGAAAGGAAG	273179	105375	GCATGGACCCTGTATGACAT
184006	16202	TTCACCCGCGGCTGCCTCCT	228593	60789	GCAGAGGTGATGGAAAGGAA	273180	105376	TGCATGGACCCTGTATGACA
184007	16203	CTTCACCCGCGGCTGCCTCC	228594	60790	GGCAGAGGTGATGGAAAGGA	273181	105377	GTGCATGGACCCTGTATGAC
184008	16204	CCTTCACCCGCGGCTGCCTC	228595	60791	AGGCAGAGGTGATGGAAAGG	273182	105378	TGTGCATGGACCCTGTATGA
184009	16205	CCCTTCACCCGCGGCTGCCT	228596	60792	AAGGCAGAGGTGATGGAAAG	273183	105379	TTGTGCATGGACCCTGTATG
184010	16206	TCCCTTCACCCGCGGCTGCC	228597	60793	AAAGGCAGAGGTGATGGAAA	273184	105380	CTTGTGCATGGACCCTGTAT
184011	16207	CTCCCTTCACCCGCGGCTGC	228598	60794	AAAAGGCAGAGGTGATGGAA	273185	105381	TCTTGTGCATGGACCCTGTA
184012	16208	TCTCCCTTCACCCGCGGCTG	228599	60795	GAAAAGGCAGAGGTGATGGA	273186	105382	CTCTTGTGCATGGACCCTGT
184013	16209	TTCTCCCTTCACCCGCGGCT	228600	60796	TGAAAAGGCAGAGGTGATGG	273187	105383	GCTCTTGTGCATGGACCCTG
184014	16210	TTTCTCCCTTCACCCGCGGC	228601	60797	GTGAAAAGGCAGAGGTGATG	273188	105384	GGCTCTTGTGCATGGACCCT
184015	16211	ATTTCTCCCTTCACCCGCGG	228602	60798	AGTGAAAAGGCAGAGGTGAT	273189	105385	AGGCTCTTGTGCATGGACCC
184016	16212	GATTTCTCCCTTCACCCGCG	228603	60799	CAGTGAAAAGGCAGAGGTGA	273190	105386	AAGGCTCTTGTGCATGGACC
184017	16213	AGATTTCTCCCTTCACCCGC	228604	60800	GCAGTGAAAAGGCAGAGGTG	273191	105387	AAAGGCTCTTGTGCATGGAC
184018	16214	AAGATTTCTCCCTTCACCCG	228605	60801	TGCAGTGAAAAGGCAGAGGT	273192	105388	TAAAGGCTCTTGTGCATGGA
184019	16215	CAAGATTTCTCCCTTCACCC	228606	60802	ATGCAGTGAAAAGGCAGAGG	273193	105389	TTAAAGGCTCTTGTGCATGG
184020	16216	CCAAGATTTCTCCCTTCACC	228607	60803	CATGCAGTGAAAAGGCAGAG	273194	105390	TTTAAAGGCTCTTGTGCATG
184021	16217	TCCAAGATTTCTCCCTTCAC	228608	60804	GCATGCAGTGAAAAGGCAGA	273195	105391	TTTTAAAGGCTCTTGTGCAT
184022	16218	CTCCAAGATTTCTCCCTTCA	228609	60805	AGCATGCAGTGAAAAGGCAG	273196	105392	ATTTTAAAGGCTCTTGTGCA
184023	16219	ACTCCAAGATTTCTCCCTTC	228610	60806	AAGCATGCAGTGAAAAGGCA	273197	105393	CATTTTAAAGGCTCTTGTGC
184024	16220	GACTCCAAGATTTCTCCCTT	228611	60807	CAAGCATGCAGTGAAAAGGC	273198	105394	TCATTTTAAAGGCTCTTGTG
184025	16221	GGACTCCAAGATTTCTCCCT	228612	60808	CCAAGCATGCAGTGAAAAGG	273199	105395	GTCATTTTAAAGGCTCTTGT
184026	16222	TGGACTCCAAGATTTCTCCC	228613	60809	TCCAAGCATGCAGTGAAAAG	273200	105396	GGTCATTTTAAAGGCTCTTG
184027	16223	CTGGACTCCAAGATTTCTCC	228614	60810	GTCCAAGCATGCAGTGAAAA	273201	105397	GGGTCATTTTAAAGGCTCTT
184028	16224	CCTGGACTCCAAGATTTCTC	228615	60811	GGTCCAAGCATGCAGTGAAA	273202	105398	CGGGTCATTTTAAAGGCTCT
184029	16225	GCCTGGACTCCAAGATTTCT	228616	60812	TGGTCCAAGCATGCAGTGAA	273203	105399	GCGGGTCATTTTAAAGGCTC
184030	16226	TGCCTGGACTCCAAGATTTC	228617	60813	GTGGTCCAAGCATGCAGTGA	273204	105400	AGCGGGTCATTTTAAAGGCT
184031	16227	CTGCCTGGACTCCAAGATTT	228618	60814	AGTGGTCCAAGCATGCAGTG	273205	105401	CAGCGGGTCATTTTAAAGGC
184032	16228	GCTGCCTGGACTCCAAGATT	228619	60815	CAGTGGTCCAAGCATGCAGT	273206	105402	TCAGCGGGTCATTTTAAAGG
184033	16229	GGCTGCCTGGACTCCAAGAT	228620	60816	GCAGTGGTCCAAGCATGCAG	273207	105403	TTCAGCGGGTCATTTTAAAG
184034	16230	GGGCTGCCTGGACTCCAAGA	228621	60817	TGCAGTGGTCCAAGCATGCA	273208	105404	CTTCAGCGGGTCATTTTAAA
184035	16231	GGGGCTGCCTGGACTCCAAG	228622	60818	CTGCAGTGGTCCAAGCATGC	273209	105405	CCTTCAGCGGGTCATTTTAA
184036	16232	GGGGGCTGCCTGGACTCCAA	228623	60819	ACTGCAGTGGTCCAAGCATG	273210	105406	CCCTTCAGCGGGTCATTTTA
184037	16233	AGGGGGCTGCCTGGACTCCA	228624	60820	GACTGCAGTGGTCCAAGCAT	273211	105407	ACCCTTCAGCGGGTCATTTT
184038	16234	AAGGGGGCTGCCTGGACTCC	228625	60821	TGACTGCAGTGGTCCAAGCA	273212	105408	CACCCTTCAGCGGGTCATTT
184039	16235	GAAGGGGGCTGCCTGGACTC	228626	60822	CTGACTGCAGTGGTCCAAGC	273213	105409	ACACCCTTCAGCGGGTCATT
184040	16236	AGAAGGGGGCTGCCTGGACT	228627	60823	GCTGACTGCAGTGGTCCAAG	273214	105410	GACACCCTTCAGCGGGTCAT
184041	16237	CAGAAGGGGGCTGCCTGGAC	228628	60824	AGCTGACTGCAGTGGTCCAA	273215	105411	TGACACCCTTCAGCGGGTCA
184042	16238	CCAGAAGGGGGCTGCCTGGA	228629	60825	GAGCTGACTGCAGTGGTCCA	273216	105412	CTGACACCCTTCAGCGGGTC
184043	16239	CCCAGAAGGGGGCTGCCTGG	228630	60826	GGAGCTGACTGCAGTGGTCC	273217	105413	CCTGACACCCTTCAGCGGGT
184044	16240	GCCCAGAAGGGGGCTGCCTG	228631	60827	GGGAGCTGACTGCAGTGGTC	273218	105414	GCCTGACACCCTTCAGCGGG
184045	16241	AGCCCAGAAGGGGGCTGCCT	228632	60828	AGGGAGCTGACTGCAGTGGT	273219	105415	GGCCTGACACCCTTCAGCGG
184046	16242	CAGCCCAGAAGGGGGCTGCC	228633	60829	TAGGGAGCTGACTGCAGTGG	273220	105416	AGGCCTGACACCCTTCAGCG
184047	16243	TCAGCCCAGAAGGGGGCTGC	228634	60830	ATAGGGAGCTGACTGCAGTG	273221	105417	GAGGCCTGACACCCTTCAGC
184048	16244	TTCAGCCCAGAAGGGGGCTG	228635	60831	CATAGGGAGCTGACTGCAGT	273222	105418	GGAGGCCTGACACCCTTCAG
184049	16245	GTTCAGCCCAGAAGGGGGCT	228636	60832	TCATAGGGAGCTGACTGCAG	273223	105419	AGGAGGCCTGACACCCTTCA
184050	16246	AGTTCAGCCCAGAAGGGGGC	228637	60833	TTCATAGGGAGCTGACTGCA	273224	105420	GAGGAGGCCTGACACCCTTC
184051	16247	CAGTTCAGCCCAGAAGGGGG	228638	60834	GTTCATAGGGAGCTGACTGC	273225	105421	GGAGGAGGCCTGACACCCTT
184052	16248	CCAGTTCAGCCCAGAAGGGG	228639	60835	TGTTCATAGGGAGCTGACTG	273226	105422	AGGAGGAGGCCTGACACCCT
184053	16249	CCCAGTTCAGCCCAGAAGGG	228640	60836	CTGTTCATAGGGAGCTGACT	273227	105423	GAGGAGGAGGCCTGACACCC
184054	16250	CCCCAGTTCAGCCCAGAAGG	228641	60837	ACTGTTCATAGGGAGCTGAC	273228	105424	GGAGGAGGAGGCCTGACACC
184055	16251	TCCCCAGTTCAGCCCAGAAG	228642	60838	AACTGTTCATAGGGAGCTGA	273229	105425	AGGAGGAGGAGGCCTGACAC
184056	16252	CTCCCCAGTTCAGCCCAGAA	228643	60839	CAACTGTTCATAGGGAGCTG	273230	105426	CAGGAGGAGGAGGCCTGACA
184057	16253	GCTCCCCAGTTCAGCCCAGA	228644	60840	GCAACTGTTCATAGGGAGCT	273231	105427	CCAGGAGGAGGAGGCCTGAC
184058	16254	AGCTCCCCAGTTCAGCCCAG	228645	60841	AGCAACTGTTCATAGGGAGC	273232	105428	TCCAGGAGGAGGAGGCCTGA
184059	16255	CAGCTCCCCAGTTCAGCCCA	228646	60842	GAGCAACTGTTCATAGGGAG	273233	105429	GTCCAGGAGGAGGAGGCCTG
184060	16256	CCAGCTCCCCAGTTCAGCCC	228647	60843	AGAGCAACTGTTCATAGGGA	273234	105430	AGTCCAGGAGGAGGAGGCCT
184061	16257	CCCAGCTCCCCAGTTCAGCC	228648	60844	GAGAGCAACTGTTCATAGGG	273235	105431	CAGTCCAGGAGGAGGAGGCC
184062	16258	CCCCAGCTCCCCAGTTCAGC	228649	60845	AGAGAGCAACTGTTCATAGG	273236	105432	CCAGTCCAGGAGGAGGAGGC
184063	16259	CCCCCAGCTCCCCAGTTCAG	228650	60846	TAGAGAGCAACTGTTCATAG	273237	105433	GCCAGTCCAGGAGGAGGAGG
184064	16260	ACCCCCAGCTCCCCAGTTCA	228651	60847	GTAGAGAGCAACTGTTCATA	273238	105434	GGCCAGTCCAGGAGGAGGAG
184065	16261	CACCCCCAGCTCCCCAGTTC	228652	60848	GGTAGAGAGCAACTGTTCAT	273239	105435	AGGCCAGTCCAGGAGGAGGA
184066	16262	GCACCCCCAGCTCCCCAGTT	228653	60849	GGGTAGAGAGCAACTGTTCA	273240	105436	CAGGCCAGTCCAGGAGGAGG
184067	16263	AGCACCCCCAGCTCCCCAGT	228654	60850	TGGGTAGAGAGCAACTGTTC	273241	105437	TCAGGCCAGTCCAGGAGGAG
184068	16264	CAGCACCCCCAGCTCCCCAG	228655	60851	ATGGGTAGAGAGCAACTGTT	273242	105438	TTCAGGCCAGTCCAGGAGGA
184069	16265	GCAGCACCCCCAGCTCCCCA	228656	60852	GATGGGTAGAGAGCAACTGT	273243	105439	CTTCAGGCCAGTCCAGGAGG
184070	16266	GGCAGCACCCCCAGCTCCCC	228657	60853	GGATGGGTAGAGAGCAACTG	273244	105440	CCTTCAGGCCAGTCCAGGAG
184071	16267	TGGCAGCACCCCCAGCTCCC	228658	60854	TGGATGGGTAGAGAGCAACT	273245	105441	GCCTTCAGGCCAGTCCAGGA
184072	16268	CTGGCAGCACCCCCAGCTCC	228659	60855	TTGGATGGGTAGAGAGCAAC	273246	105442	AGCCTTCAGGCCAGTCCAGG
184073	16269	GCTGGCAGCACCCCCAGCTC	228660	60856	ATTGGATGGGTAGAGAGCAA	273247	105443	GAGCCTTCAGGCCAGTCCAG
184074	16270	GGCTGGCAGCACCCCCAGCT	228661	60857	GATTGGATGGGTAGAGAGCA	273248	105444	GGAGCCTTCAGGCCAGTCCA

184075	16271	GGGCTGGCAGCACCCCCAGC	228662	60858	CGATTGGATGGGTAGAGAGC	273249	105445	TGGAGCCTTCAGGCCAGTCC
184076	16272	AGGGCTGGCAGCACCCCCAG	228663	60859	CCGATTGGATGGGTAGAGAG	273250	105446	GTGGAGCCTTCAGGCCAGTC
184077	16273	CAGGGCTGGCAGCACCCCCA	228664	60860	GCCGATTGGATGGGTAGAGA	273251	105447	CGTGGAGCCTTCAGGCCAGT
184078	16274	GCAGGGCTGGCAGCACCCCC	228665	60861	GGCCGATTGGATGGGTAGAG	273252	105448	TCGTGGAGCCTTCAGGCCAG
184079	16275	GGCAGGGCTGGCAGCACCCC	228666	60862	GGGCCGATTGGATGGGTAGA	273253	105449	CTCGTGGAGCCTTCAGGCCA
184080	16276	TGGCAGGGCTGGCAGCACCC	228667	60863	GGGGCCGATTGGATGGGTAG	273254	105450	GCTCGTGGAGCCTTCAGGCC
184081	16277	CTGGCAGGGCTGGCAGCACC	228668	60864	CGGGGCCGATTGGATGGGTA	273255	105451	AGCTCGTGGAGCCTTCAGGC
184082	16278	CCTGGCAGGGCTGGCAGCAC	228669	60865	GCGGGGCCGATTGGATGGGT	273256	105452	AAGCTCGTGGAGCCTTCAGG
184083	16279	ACCTGGCAGGGCTGGCAGCA	228670	60866	GGCGGGGCCGATTGGATGGG	273257	105453	AAAGCTCGTGGAGCCTTCAG
184084	16280	AACCTGGCAGGGCTGGCAGC	228671	60867	AGGCGGGGCCGATTGGATGG	273258	105454	AAAAGCTCGTGGAGCCTTCA
184085	16281	GAACCTGGCAGGGCTGGCAG	228672	60868	CAGGCGGGGCCGATTGGATG	273259	105455	CAAAAGCTCGTGGAGCCTTC
184086	16282	AGAACCTGGCAGGGCTGGCA	228673	60869	GCAGGCGGGGCCGATTGGAT	273260	105456	GCAAAAGCTCGTGGAGCCTT
184087	16283	GAGAACCTGGCAGGGCTGGC	228674	60870	AGCAGGCGGGGCCGATTGGA	273261	105457	AGCAAAAGCTCGTGGAGCCT
184088	16284	GGAGAACCTGGCAGGGCTGG	228675	60871	CAGCAGGCGGGGCCGATTGG	273262	105458	CAGCAAAAGCTCGTGGAGCC
184089	16285	AGGAGAACCTGGCAGGGCTG	228676	60872	GCAGCAGGCGGGGCCGATTG	273263	105459	TCAGCAAAAGCTCGTGGAGC
184090	16286	TAGGAGAACCTGGCAGGGCT	228677	60873	AGCAGCAGGCGGGGCCGATT	273264	105460	CTCAGCAAAAGCTCGTGGAG
184091	16287	CTAGGAGAACCTGGCAGGGC	228678	60874	CAGCAGCAGGCGGGGCCGAT	273265	105461	TCTCAGCAAAAGCTCGTGGA
184092	16288	CCTAGGAGAACCTGGCAGGG	228679	60875	GCAGCAGCAGGCGGGGCCGA	273266	105462	GTCTCAGCAAAAGCTCGTGG
184093	16289	TCCTAGGAGAACCTGGCAGG	228680	60876	GGCAGCAGCAGGCGGGGCCG	273267	105463	GGTCTCAGCAAAAGCTCGTG
184094	16290	CTCCTAGGAGAACCTGGCAG	228681	60877	TGGCAGCAGCAGGCGGGGCC	273268	105464	AGGTCTCAGCAAAAGCTCGT
184095	16291	CCTCCTAGGAGAACCTGGCA	228682	60878	TTGGCAGCAGCAGGCGGGGC	273269	105465	AAGGTCTCAGCAAAAGCTCG
184096	16292	GCCTCCTAGGAGAACCTGGC	228683	60879	TTTGGCAGCAGCAGGCGGGG	273270	105466	AAAGGTCTCAGCAAAAGCTC
184097	16293	CGCCTCCTAGGAGAACCTGG	228684	60880	ATTTGGCAGCAGCAGGCGGG	273271	105467	CAAAGGTCTCAGCAAAAGCT
184098	16294	CCGCCTCCTAGGAGAACCTG	228685	60881	AATTTGGCAGCAGCAGGCGG	273272	105468	CCAAAGGTCTCAGCAAAAGC
184099	16295	GCCGCCTCCTAGGAGAACCT	228686	60882	GAATTTGGCAGCAGCAGGCG	273273	105469	CCCAAAGGTCTCAGCAAAAG
184100	16296	TGCCGCCTCCTAGGAGAACC	228687	60883	TGAATTTGGCAGCAGCAGGC	273274	105470	ACCCAAAGGTCTCAGCAAAA
184101	16297	CTGCCGCCTCCTAGGAGAAC	228688	60884	GTGAATTTGGCAGCAGCAGG	273275	105471	GACCCAAAGGTCTCAGCAAA
184102	16298	GCTGCCGCCTCCTAGGAGAA	228689	60885	GGTGAATTTGGCAGCAGCAG	273276	105472	GGACCCAAAGGTCTCAGCAA
184103	16299	AGCTGCCGCCTCCTAGGAGA	228690	60886	CGGTGAATTTGGCAGCAGCA	273277	105473	GGGACCCAAAGGTCTCAGCA
184104	16300	GAGCTGCCGCCTCCTAGGAG	228691	60887	TCGGTGAATTTGGCAGCAGC	273278	105474	AGGGACCCAAAGGTCTCAGC
184105	16301	TGAGCTGCCGCCTCCTAGGA	228692	60888	CTCGGTGAATTTGGCAGCAG	273279	105475	CAGGGACCCAAAGGTCTCAG
184106	16302	ATGAGCTGCCGCCTCCTAGG	228693	60889	CCTCGGTGAATTTGGCAGCA	273280	105476	ACAGGGACCCAAAGGTCTCA
184107	16303	TATGAGCTGCCGCCTCCTAG	228694	60890	CCCTCGGTGAATTTGGCAGC	273281	105477	CACAGGGACCCAAAGGTCTC
184108	16304	ATATGAGCTGCCGCCTCCTA	228695	60891	GCCCTCGGTGAATTTGGCAG	273282	105478	CCACAGGGACCCAAAGGTCT
184109	16305	CATATGAGCTGCCGCCTCCT	228696	60892	TGCCCTCGGTGAATTTGGCA	273283	105479	GCCACAGGGACCCAAAGGTC
184110	16306	CCATATGAGCTGCCGCCTCC	228697	60893	GTGCCCTCGGTGAATTTGGC	273284	105480	GGCCACAGGGACCCAAAGGT
184111	16307	GCCATATGAGCTGCCGCCTC	228698	60894	GGTGCCCTCGGTGAATTTGG	273285	105481	AGGCCACAGGGACCCAAAGG
184112	16308	AGCCATATGAGCTGCCGCCT	228699	60895	AGGTGCCCTCGGTGAATTTG	273286	105482	GAGGCCACAGGGACCCAAAG
184113	16309	CAGCCATATGAGCTGCCGCC	228700	60896	GAGGTGCCCTCGGTGAATTT	273287	105483	TGAGGCCACAGGGACCCAAA
184114	16310	ACAGCCATATGAGCTGCCGC	228701	60897	AGAGGTGCCCTCGGTGAATT	273288	105484	ATGAGGCCACAGGGACCCAA
184115	16311	CACAGCCATATGAGCTGCCG	228702	60898	CAGAGGTGCCCTCGGTGAAT	273289	105485	CATGAGGCCACAGGGACCCA
184116	16312	CCACAGCCATATGAGCTGCC	228703	60899	ACAGAGGTGCCCTCGGTGAA	273290	105486	ACATGAGGCCACAGGGACCC
184117	16313	CCCACAGCCATATGAGCTGC	228704	60900	CACAGAGGTGCCCTCGGTGA	273291	105487	TACATGAGGCCACAGGGACC
184118	16314	TCCCACAGCCATATGAGCTG	228705	60901	CCACAGAGGTGCCCTCGGTG	273292	105488	CTACATGAGGCCACAGGGAC
184119	16315	CTCCCACAGCCATATGAGCT	228706	60902	ACCACAGAGGTGCCCTCGGT	273293	105489	ACTACATGAGGCCACAGGGA
184120	16316	CCTCCCACAGCCATATGAGC	228707	60903	CACCACAGAGGTGCCCTCGG	273294	105490	TACTACATGAGGCCACAGGG
184121	16317	TCCTCCCACAGCCATATGAG	228708	60904	GCACCACAGAGGTGCCCTCG	273295	105491	GTACTACATGAGGCCACAGG
184122	16318	CTCCTCCCACAGCCATATGA	228709	60905	AGCACCACAGAGGTGCCCTC	273296	105492	GGTACTACATGAGGCCACAG
184123	16319	CCTCCTCCCACAGCCATATG	228710	60906	CAGCACCACAGAGGTGCCCT	273297	105493	GGGTACTACATGAGGCCACA
184124	16320	GCCTCCTCCCACAGCCATAT	228711	60907	GCAGCACCACAGAGGTGCCC	273298	105494	TGGGTACTACATGAGGCCAC
184125	16321	TGCCTCCTCCCACAGCCATA	228712	60908	GGCAGCACCACAGAGGTGCC	273299	105495	CTGGGTACTACATGAGGCCA
184126	16322	CTGCCTCCTCCCACAGCCAT	228713	60909	AGGCAGCACCACAGAGGTGC	273300	105496	ACTGGGTACTACATGAGGCC
184127	16323	TCTGCCTCCTCCCACAGCCA	228714	60910	CAGGCAGCACCACAGAGGTG	273301	105497	TACTGGGTACTACATGAGGC
184128	16324	CTCTGCCTCCTCCCACAGCC	228715	60911	ACAGGCAGCACCACAGAGGT	273302	105498	ATACTGGGTACTACATGAGG
184129	16325	CCTCTGCCTCCTCCCACAGC	228716	60912	CACAGGCAGCACCACAGAGG	273303	105499	CATACTGGGTACTACATGAG
184130	16326	CCCTCTGCCTCCTCCCACAG	228717	60913	CCACAGGCAGCACCACAGAG	273304	105500	GCATACTGGGTACTACATGA
184131	16327	TCCCTCTGCCTCCTCCCACA	228718	60914	TCCACAGGCAGCACCACAGA	273305	105501	TGCATACTGGGTACTACATG
184132	16328	CTCCCTCTGCCTCCTCCCAC	228719	60915	GTCCACAGGCAGCACCACAG	273306	105502	CTGCATACTGGGTACTACAT
184133	16329	GCTCCCTCTGCCTCCTCCCA	228720	60916	TGTCCACAGGCAGCACCACA	273307	105503	ACTGCATACTGGGTACTACA
184134	16330	GGCTCCCTCTGCCTCCTCCC	228721	60917	TTGTCCACAGGCAGCACCAC	273308	105504	TACTGCATACTGGGTACTAC
184135	16331	AGGCTCCCTCTGCCTCCTCC	228722	60918	TTTGTCCACAGGCAGCACCA	273309	105505	TTACTGCATACTGGGTACTA
184136	16332	GAGGCTCCCTCTGCCTCCTC	228723	60919	CTTTGTCCACAGGCAGCACC	273310	105506	CTTACTGCATACTGGGTACT
184137	16333	TGAGGCTCCCTCTGCCTCCT	228724	60920	ACTTTGTCCACAGGCAGCAC	273311	105507	ACTTACTGCATACTGGGTAC
184138	16334	ATGAGGCTCCCTCTGCCTCC	228725	60921	GACTTTGTCCACAGGCAGCA	273312	105508	CACTTACTGCATACTGGGTA
184139	16335	TATGAGGCTCCCTCTGCCTC	228726	60922	GGACTTTGTCCACAGGCAGC	273313	105509	GCACTTACTGCATACTGGGT
184140	16336	ATATGAGGCTCCCTCTGCCT	228727	60923	TGGACTTTGTCCACAGGCAG	273314	105510	AGCACTTACTGCATACTGGG
184141	16337	CATATGAGGCTCCCTCTGCC	228728	60924	TTGGACTTTGTCCACAGGCA	273315	105511	GAGCACTTACTGCATACTGG
184142	16338	GCATATGAGGCTCCCTCTGC	228729	60925	CTTGGACTTTGTCCACAGGC	273316	105512	TGAGCACTTACTGCATACTG
184143	16339	TGCATATGAGGCTCCCTCTG	228730	60926	GCTTGGACTTTGTCCACAGG	273317	105513	TTGAGCACTTACTGCATACT
184144	16340	GTGCATATGAGGCTCCCTCT	228731	60927	GGCTTGGACTTTGTCCACAG	273318	105514	ATTGAGCACTTACTGCATAC
184145	16341	GGTGCATATGAGGCTCCCTC	228732	60928	TGGCTTGGACTTTGTCCACA	273319	105515	TATTGAGCACTTACTGCATA
184146	16342	GGGTGCATATGAGGCTCCCT	228733	60929	CTGGCTTGGACTTTGTCCAC	273320	105516	TTATTGAGCACTTACTGCAT

184147	16343	TGGGTGCATATGAGGCTCCC	228734	60930	GCTGGCTTGGACTTTGTCCA	273321	105517	TTTATTGAGCACTTACTGCA
184148	16344	GTGGGTGCATATGAGGCTCC	228735	60931	GGCTGGCTTGGACTTTGTCC	273322	105518	ATTTATTGAGCACTTACTGC
184149	16345	TGTGGGTGCATATGAGGCTC	228736	60932	TGGCTGGCTTGGACTTTGTC	273323	105519	CATTTATTGAGCACTTACTG
184150	16346	ATGTGGGTGCATATGAGGCT	228737	60933	GTGGCTGGCTTGGACTTTGT	273324	105520	ACATTTATTGAGCACTTACT
184151	16347	AATGTGGGTGCATATGAGGC	228738	60934	GGTGGCTGGCTTGGACTTTG	273325	105521	AACATTTATTGAGCACTTAC
184152	16348	AAATGTGGGTGCATATGAGG	228739	60935	AGGTGGCTGGCTTGGACTTT	273326	105522	AAACATTTATTGAGCACTTA
184153	16349	GAAATGTGGGTGCATATGAG	228740	60936	GAGGTGGCTGGCTTGGACTT	273327	105523	CAAACATTTATTGAGCACTT
184154	16350	GGAAATGTGGGTGCATATGA	228741	60937	TGAGGTGGCTGGCTTGGACT	273328	105524	CCAAACATTTATTGAGCACT
184155	16351	TGGAAATGTGGGTGCATATG	228742	60938	GTGAGGTGGCTGGCTTGGAC	273329	105525	GCCAAACATTTATTGAGCAC
184156	16352	CTGGAAATGTGGGTGCATAT	228743	60939	GGTGAGGTGGCTGGCTTGGA	273330	105526	AGCCAAACATTTATTGAGCA
184157	16353	CCTGGAAATGTGGGTGCATA	228744	60940	GGGTGAGGTGGCTGGCTTGG	273331	105527	TAGCCAAACATTTATTGAGC
184158	16354	CCCTGGAAATGTGGGTGCAT	228745	60941	TGGGTGAGGTGGCTGGCTTG	273332	105528	GTAGCCAAACATTTATTGAG
184159	16355	TCCCTGGAAATGTGGGTGCA	228746	60942	GTGGGTGAGGTGGCTGGCTT	273333	105529	TGTAGCCAAACATTTATTGA
184160	16356	ATCCCTGGAAATGTGGGTGC	228747	60943	GGTGGGTGAGGTGGCTGGCT	273334	105530	TTGTAGCCAAACATTTATTG
184161	16357	GATCCCTGGAAATGTGGGTG	228748	60944	AGGTGGGTGAGGTGGCTGGC	273335	105531	TTTGTAGCCAAACATTTATT
184162	16358	AGATCCCTGGAAATGTGGGT	228749	60945	TAGGTGGGTGAGGTGGCTGG	273336	105532	TTTTGTAGCCAAACATTTAT
184163	16359	TAGATCCCTGGAAATGTGGG	228750	60946	GTAGGTGGGTGAGGTGGCTG	273337	105533	CTTTTGTAGCCAAACATTTA
184164	16360	CTAGATCCCTGGAAATGTGG	228751	60947	TGTAGGTGGGTGAGGTGGCT	273338	105534	TCTTTTGTAGCCAAACATTT
184165	16361	TCTAGATCCCTGGAAATGTG	228752	60948	CTGTAGGTGGGTGAGGTGGC	273339	105535	CTCTTTTGTAGCCAAACATT
184166	16362	TTCTAGATCCCTGGAAATGT	228753	60949	CCTGTAGGTGGGTGAGGTGG	273340	105536	CCTCTTTTGTAGCCAAACAT
184167	16363	CTTCTAGATCCCTGGAAATG	228754	60950	ACCTGTAGGTGGGTGAGGTG	273341	105537	GCCTCTTTTGTAGCCAAACA
184168	16364	TCTTCTAGATCCCTGGAAAT	228755	60951	CACCTGTAGGTGGGTGAGGT	273342	105538	TGCCTCTTTTGTAGCCAAAC
184169	16365	GTCTTCTAGATCCCTGGAAA	228756	60952	TCACCTGTAGGTGGGTGAGG	273343	105539	TTGCCTCTTTTGTAGCCAAA
184170	16366	TGTCTTCTAGATCCCTGGAA	228757	60953	CTCACCTGTAGGTGGGTGAG	273344	105540	TTTGCCTCTTTTGTAGCCAA
184171	16367	CTGTCTTCTAGATCCCTGGA	228758	60954	ACTCACCTGTAGGTGGGTGA	273345	105541	CTTTGCCTCTTTTGTAGCCA
184172	16368	TCTGTCTTCTAGATCCCTGG	228759	60955	CACTCACCTGTAGGTGGGTG	273346	105542	GCTTTGCCTCTTTTGTAGCC
184173	16369	TTCTGTCTTCTAGATCCCTG	228760	60956	CCACTCACCTGTAGGTGGGT	273347	105543	AGCTTTGCCTCTTTTGTAGC
184174	16370	CTTCTGTCTTCTAGATCCCT	228761	60957	CCCACTCACCTGTAGGTGGG	273348	105544	CAGCTTTGCCTCTTTTGTAG
184175	16371	CCTTCTGTCTTCTAGATCCC	228762	60958	CCCCACTCACCTGTAGGTGG	273349	105545	CCAGCTTTGCCTCTTTTGTA
184176	16372	TCCTTCTGTCTTCTAGATCC	228763	60959	TCCCCACTCACCTGTAGGTG	273350	105546	GCCAGCTTTGCCTCTTTTGT
184177	16373	CTCCTTCTGTCTTCTAGATC	228764	60960	CTCCCCACTCACCTGTAGGT	273351	105547	CGCCAGCTTTGCCTCTTTTG
184178	16374	CCTCCTTCTGTCTTCTAGAT	228765	60961	GCTCCCCACTCACCTGTAGG	273352	105548	CCGCCAGCTTTGCCTCTTTT
184179	16375	TCCTCCTTCTGTCTTCTAGA	228766	60962	TGCTCCCCACTCACCTGTAG	273353	105549	TCCGCCAGCTTTGCCTCTTT
184180	16376	TTCCTCCTTCTGTCTTCTAG	228767	60963	CTGCTCCCCACTCACCTGTA	273354	105550	CTCCGCCAGCTTTGCCTCTT
184181	16377	TTTCCTCCTTCTGTCTTCTA	228768	60964	GCTGCTCCCCACTCACCTGT	273355	105551	ACTCCGCCAGCTTTGCCTCT
184182	16378	TTTTCCTCCTTCTGTCTTCT	228769	60965	GGCTGCTCCCCACTCACCTG	273356	105552	GACTCCGCCAGCTTTGCCTC
184183	16379	GTTTTCCTCCTTCTGTCTTC	228770	60966	TGGCTGCTCCCCACTCACCT	273357	105553	AGACTCCGCCAGCTTTGCCT
184184	16380	GGTTTTCCTCCTTCTGTCTT	228771	60967	CTGGCTGCTCCCCACTCACC	273358	105554	CAGACTCCGCCAGCTTTGCC
184185	16381	TGGTTTTCCTCCTTCTGTCT	228772	60968	GCTGGCTGCTCCCCACTCAC	273359	105555	TCAGACTCCGCCAGCTTTGC
184186	16382	GTGGTTTTCCTCCTTCTGTC	228773	60969	CGCTGGCTGCTCCCCACTCA	273360	105556	TTCAGACTCCGCCAGCTTTG
184187	16383	GGTGGTTTTCCTCCTTCTGT	228774	60970	ACGCTGGCTGCTCCCCACTC	273361	105557	CTTCAGACTCCGCCAGCTTT
184188	16384	TGGTGGTTTTCCTCCTTCTG	228775	60971	CACGCTGGCTGCTCCCCACT	273362	105558	TCTTCAGACTCCGCCAGCTT
184189	16385	ATGGTGGTTTTCCTCCTTCT	228776	60972	ACACGCTGGCTGCTCCCCAC	273363	105559	TTCTTCAGACTCCGCCAGCT
184190	16386	GATGGTGGTTTTCCTCCTTC	228777	60973	GACACGCTGGCTGCTCCCCA	273364	105560	ATTCTTCAGACTCCGCCAGC
184191	16387	TGATGGTGGTTTTCCTCCTT	228778	60974	GGACACGCTGGCTGCTCCCC	273365	105561	GATTCTTCAGACTCCGCCAG
184192	16388	ATGATGGTGGTTTTCCTCCT	228779	60975	TGGACACGCTGGCTGCTCCC	273366	105562	GGATTCTTCAGACTCCGCCA
184193	16389	CATGATGGTGGTTTTCCTCC	228780	60976	CTGGACACGCTGGCTGCTCC	273367	105563	GGGATTCTTCAGACTCCGCC
184194	16390	ACATGATGGTGGTTTTCCTC	228781	60977	ACTGGACACGCTGGCTGCTC	273368	105564	AGGGATTCTTCAGACTCCGC
184195	16391	AACATGATGGTGGTTTTCCT	228782	60978	CACTGGACACGCTGGCTGCT	273369	105565	GAGGGATTCTTCAGACTCCG
184196	16392	TAACATGATGGTGGTTTTCC	228783	60979	CCACTGGACACGCTGGCTGC	273370	105566	TGAGGGATTCTTCAGACTCC
184197	16393	TTAACATGATGGTGGTTTTC	228784	60980	ACCACTGGACACGCTGGCTG	273371	105567	TTGAGGGATTCTTCAGACTC
184198	16394	TTTAACATGATGGTGGTTTT	228785	60981	AACCACTGGACACGCTGGCT	273372	105568	GTTGAGGGATTCTTCAGACT
184199	16395	CTTTAACATGATGGTGGTTT	228786	60982	AAACCACTGGACACGCTGGC	273373	105569	GGTTGAGGGATTCTTCAGAC
184200	16396	GCTTTAACATGATGGTGGTT	228787	60983	TAAACCACTGGACACGCTGG	273374	105570	CGGTTGAGGGATTCTTCAGA
184201	16397	TGCTTTAACATGATGGTGGT	228788	60984	GTAAACCACTGGACACGCTG	273375	105571	ACGGTTGAGGGATTCTTCAG
184202	16398	CTGCTTTAACATGATGGTGG	228789	60985	GGTAAACCACTGGACACGCT	273376	105572	CACGGTTGAGGGATTCTTCA
184203	16399	TCTGCTTTAACATGATGGTG	228790	60986	GGGTAAACCACTGGACACGC	273377	105573	GCACGGTTGAGGGATTCTTC
184204	16400	GTCTGCTTTAACATGATGGT	228791	60987	GGGGTAAACCACTGGACACG	273378	105574	GGCACGGTTGAGGGATTCTT
184205	16401	TGTCTGCTTTAACATGATGG	228792	60988	TGGGGTAAACCACTGGACAC	273379	105575	CGGCACGGTTGAGGGATTCT
184206	16402	CTGTCTGCTTTAACATGATG	228793	60989	ATGGGGTAAACCACTGGACA	273380	105576	CCGGCACGGTTGAGGGATTC
184207	16403	ACTGTCTGCTTTAACATGAT	228794	60990	GATGGGGTAAACCACTGGAC	273381	105577	TCCGGCACGGTTGAGGGATT
184208	16404	AACTGTCTGCTTTAACATGA	228795	60991	CGATGGGGTAAACCACTGGA	273382	105578	TTCCGGCACGGTTGAGGGAT
184209	16405	TAACTGTCTGCTTTAACATG	228796	60992	GCGATGGGGTAAACCACTGG	273383	105579	GTTCCGGCACGGTTGAGGGA
184210	16406	CTAACTGTCTGCTTTAACAT	228797	60993	GGCGATGGGGTAAACCACTG	273384	105580	TGTTCCGGCACGGTTGAGGG
184211	16407	CCTAACTGTCTGCTTTAACA	228798	60994	TGGCGATGGGGTAAACCACT	273385	105581	CTGTTCCGGCACGGTTGAGG
184212	16408	ACCTAACTGTCTGCTTTAAC	228799	60995	GTGGCGATGGGGTAAACCAC	273386	105582	TCTGTTCCGGCACGGTTGAG
184213	16409	TACCTAACTGTCTGCTTTAA	228800	60996	TGTGGCGATGGGGTAAACCA	273387	105583	ATCTGTTCCGGCACGGTTGA
184214	16410	TTACCTAACTGTCTGCTTTA	228801	60997	CTGTGGCGATGGGGTAAACC	273388	105584	CATCTGTTCCGGCACGGTTG
184215	16411	GTTACCTAACTGTCTGCTTT	228802	60998	TCTGTGGCGATGGGGTAAAC	273389	105585	GCATCTGTTCCGGCACGGTT
184216	16412	TGTTACCTAACTGTCTGCTT	228803	60999	GTCTGTGGCGATGGGGTAAA	273390	105586	AGCATCTGTTCCGGCACGGT
184217	16413	GTGTTACCTAACTGTCTGCT	228804	61000	AGTCTGTGGCGATGGGGTAA	273391	105587	TAGCATCTGTTCCGGCACGG
184218	16414	TGTGTTACCTAACTGTCTGC	228805	61001	AAGTCTGTGGCGATGGGGTA	273392	105588	TTAGCATCTGTTCCGGCACG

184219	16415	ATGTGTTACCTAACTGTCTG	228806	61002	CAAGTCTGTGGCGATGGGGT	273393	105589	GTTAGCATCTGTTCCGGCAC
184220	16416	GATGTGTTACCTAACTGTCT	228807	61003	CCAAGTCTGTGGCGATGGGG	273394	105590	TGTTAGCATCTGTTCCGGCA
184221	16417	GGATGTGTTACCTAACTGTC	228808	61004	ACCAAGTCTGTGGCGATGGG	273395	105591	GTGTTAGCATCTGTTCCGGC
184222	16418	AGGATGTGTTACCTAACTGT	228809	61005	CACCAAGTCTGTGGCGATGG	273396	105592	GGTGTTAGCATCTGTTCCGG
184223	16419	CAGGATGTGTTACCTAACTG	228810	61006	TCACCAAGTCTGTGGCGATG	273397	105593	TGGTGTTAGCATCTGTTCCG
184224	16420	ACAGGATGTGTTACCTAACT	228811	61007	ATCACCAAGTCTGTGGCGAT	273398	105594	TTGGTGTTAGCATCTGTTCC
184225	16421	TACAGGATGTGTTACCTAAC	228812	61008	CATCACCAAGTCTGTGGCGA	273399	105595	TTTGGTGTTAGCATCTGTTC
184226	16422	TTACAGGATGTGTTACCTAA	228813	61009	ACATCACCAAGTCTGTGGCG	273400	105596	CTTTGGTGTTAGCATCTGTT
184227	16423	ATTACAGGATGTGTTACCTA	228814	61010	CACATCACCAAGTCTGTGGC	273401	105597	CCTTTGGTGTTAGCATCTGT
184228	16424	TATTACAGGATGTGTTACCT	228815	61011	ACACATCACCAAGTCTGTGG	273402	105598	CCCTTTGGTGTTAGCATCTG
184229	16425	GTATTACAGGATGTGTTACC	228816	61012	GACACATCACCAAGTCTGTG	273403	105599	TCCCTTTGGTGTTAGCATCT
184230	16426	TGTATTACAGGATGTGTTAC	228817	61013	CGACACATCACCAAGTCTGT	273404	105600	TTCCCTTTGGTGTTAGCATC
184231	16427	TTGTATTACAGGATGTGTTA	228818	61014	TCGACACATCACCAAGTCTG	273405	105601	TTTCCCTTTGGTGTTAGCAT
184232	16428	CTTGTATTACAGGATGTGTT	228819	61015	ATCGACACATCACCAAGTCT	273406	105602	TTTTCCCTTTGGTGTTAGCA
184233	16429	ACTTGTATTACAGGATGTGT	228820	61016	CATCGACACATCACCAAGTC	273407	105603	CTTTTCCCTTTGGTGTTAGC
184234	16430	AACTTGTATTACAGGATGTG	228821	61017	ACATCGACACATCACCAAGT	273408	105604	TCTTTTCCCTTTGGTGTTAG
184235	16431	TAACTTGTATTACAGGATGT	228822	61018	CACATCGACACATCACCAAG	273409	105605	CTCTTTTCCCTTTGGTGTTA
184236	16432	ATAACTTGTATTACAGGATG	228823	61019	GCACATCGACACATCACCAA	273410	105606	GCTCTTTTCCCTTTGGTGTT
184237	16433	AATAACTTGTATTACAGGAT	228824	61020	TGCACATCGACACATCACCA	273411	105607	TGCTCTTTTCCCTTTGGTGT
184238	16434	AAATAACTTGTATTACAGGA	228825	61021	CTGCACATCGACACATCACC	273412	105608	CTGCTCTTTTCCCTTTGGTG
184239	16435	AAAATAACTTGTATTACAGG	228826	61022	TCTGCACATCGACACATCAC	273413	105609	CCTGCTCTTTTCCCTTTGGT
184240	16436	AAAAATAACTTGTATTACAG	228827	61023	CTCTGCACATCGACACATCA	273414	105610	TCCTGCTCTTTTCCCTTTGG
184241	16437	AAAAAATAACTTGTATTACA	228828	61024	TCTCTGCACATCGACACATC	273415	105611	CTCCTGCTCTTTTCCCTTTG
184242	16438	GAAAAAATAACTTGTATTAC	228829	61025	TTCTCTGCACATCGACACAT	273416	105612	GCTCCTGCTCTTTTCCCTTT
184243	16439	GGAAAAAATAACTTGTATTA	228830	61026	CTTCTCTGCACATCGACACA	273417	105613	GGCTCCTGCTCTTTTCCCTT
184244	16440	TGGAAAAAATAACTTGTATT	228831	61027	CCTTCTCTGCACATCGACAC	273418	105614	TGGCTCCTGCTCTTTTCCCT
184245	16441	GTGGAAAAAATAACTTGTAT	228832	61028	CCCTTCTCTGCACATCGACA	273419	105615	TTGGCTCCTGCTCTTTTCCC
184246	16442	TGTGGAAAAAATAACTTGTA	228833	61029	CCCCTTCTCTGCACATCGAC	273420	105616	CTTGGCTCCTGCTCTTTTCC
184247	16443	ATGTGGAAAAAATAACTTGT	228834	61030	ACCCCTTCTCTGCACATCGA	273421	105617	ACTTGGCTCCTGCTCTTTTC
184248	16444	GATGTGGAAAAAATAACTTG	228835	61031	CACCCCTTCTCTGCACATCG	273422	105618	GACTTGGCTCCTGCTCTTTT
184249	16445	AGATGTGGAAAAAATAACTT	228836	61032	ACACCCCTTCTCTGCACATC	273423	105619	TGACTTGGCTCCTGCTCTTT
184250	16446	TAGATGTGGAAAAAATAACT	228837	61033	AACACCCCTTCTCTGCACAT	273424	105620	GTGACTTGGCTCCTGCTCTT
184251	16447	TTAGATGTGGAAAAAATAAC	228838	61034	CAACACCCCTTCTCTGCACA	273425	105621	CGTGACTTGGCTCCTGCTCT
184252	16448	TTTAGATGTGGAAAAAATAA	228839	61035	CCAACACCCCTTCTCTGCAC	273426	105622	ACGTGACTTGGCTCCTGCTC
184253	16449	CTTTAGATGTGGAAAAAATA	228840	61036	GCCAACACCCCTTCTCTGCA	273427	105623	AACGTGACTTGGCTCCTGCT
184254	16450	CCTTTAGATGTGGAAAAAAT	228841	61037	TGCCAACACCCCTTCTCTGC	273428	105624	AAACGTGACTTGGCTCCTGC
184255	16451	GCCTTTAGATGTGGAAAAAA	228842	61038	CTGCCAACACCCCTTCTCTG	273429	105625	CAAACGTGACTTGGCTCCTG
184256	16452	AGCCTTTAGATGTGGAAAAA	228843	61039	GCTGCCAACACCCCTTCTCT	273430	105626	CCAAACGTGACTTGGCTCCT
184257	16453	TAGCCTTTAGATGTGGAAAA	228844	61040	GGCTGCCAACACCCCTTCTC	273431	105627	CCCAAACGTGACTTGGCTCC
184258	16454	TTAGCCTTTAGATGTGGAAA	228845	61041	TGGCTGCCAACACCCCTTCT	273432	105628	TCCCAAACGTGACTTGGCTC
184259	16455	TTTAGCCTTTAGATGTGGAA	228846	61042	GTGGCTGCCAACACCCCTTC	273433	105629	TTCCCAAACGTGACTTGGCT
184260	16456	TTTTAGCCTTTAGATGTGGA	228847	61043	TGTGGCTGCCAACACCCCTT	273434	105630	GTTCCCAAACGTGACTTGGC
184261	16457	TTTTTAGCCTTTAGATGTGG	228848	61044	TTGTGGCTGCCAACACCCCT	273435	105631	GGTTCCCAAACGTGACTTGG
184262	16458	ATTTTTAGCCTTTAGATGTG	228849	61045	GTTGTGGCTGCCAACACCCC	273436	105632	AGGTTCCCAAACGTGACTTG
184263	16459	TATTTTTAGCCTTTAGATGT	228850	61046	TGTTGTGGCTGCCAACACCC	273437	105633	CAGGTTCCCAAACGTGACTT
184264	16460	CTATTTTTAGCCTTTAGATG	228851	61047	GTGTTGTGGCTGCCAACACC	273438	105634	GCAGGTTCCCAAACGTGACT
184265	16461	ACTATTTTTAGCCTTTAGAT	228852	61048	TGTGTTGTGGCTGCCAACAC	273439	105635	TGCAGGTTCCCAAACGTGAC
184266	16462	AACTATTTTTAGCCTTTAGA	228853	61049	TTGTGTTGTGGCTGCCAACA	273440	105636	CTGCAGGTTCCCAAACGTGA
184267	16463	CAACTATTTTTAGCCTTTAG	228854	61050	CTTGTGTTGTGGCTGCCAAC	273441	105637	TCTGCAGGTTCCCAAACGTG
184268	16464	ACAACTATTTTTAGCCTTTA	228855	61051	GCTTGTGTTGTGGCTGCCAA	273442	105638	CTCTGCAGGTTCCCAAACGT
184269	16465	AACAACTATTTTTAGCCTTT	228856	61052	TGCTTGTGTTGTGGCTGCCA	273443	105639	CCTCTGCAGGTTCCCAAACG
184270	16466	TAACAACTATTTTTAGCCTT	228857	61053	TTGCTTGTGTTGTGGCTGCC	273444	105640	GCCTCTGCAGGTTCCCAAAC
184271	16467	CTAACAACTATTTTTAGCCT	228858	61054	GTTGCTTGTGTTGTGGCTGC	273445	105641	AGCCTCTGCAGGTTCCCAAA
184272	16468	TCTAACAACTATTTTTAGCC	228859	61055	GGTTGCTTGTGTTGTGGCTG	273446	105642	CAGCCTCTGCAGGTTCCCAA
184273	16469	TTCTAACAACTATTTTTAGC	228860	61056	GGGTTGCTTGTGTTGTGGCT	273447	105643	TCAGCCTCTGCAGGTTCCCA
184274	16470	ATTCTAACAACTATTTTTAG	228861	61057	GGGGTTGCTTGTGTTGTGGC	273448	105644	TTCAGCCTCTGCAGGTTCCC
184275	16471	AATTCTAACAACTATTTTTA	228862	61058	CGGGGTTGCTTGTGTTGTGG	273449	105645	TTTCAGCCTCTGCAGGTTCC
184276	16472	AAATTCTAACAACTATTTTT	228863	61059	GCGGGGTTGCTTGTGTTGTG	273450	105646	TTTTCAGCCTCTGCAGGTTC
184277	16473	TAAATTCTAACAACTATTTT	228864	61060	GGCGGGGTTGCTTGTGTTGT	273451	105647	GTTTTCAGCCTCTGCAGGTT
184278	16474	TTAAATTCTAACAACTATTT	228865	61061	GGGCGGGGTTGCTTGTGTTG	273452	105648	AGTTTTCAGCCTCTGCAGGT
184279	16475	TTTAAATTCTAACAACTATT	228866	61062	GGGGCGGGGTTGCTTGTGTT	273453	105649	CAGTTTTCAGCCTCTGCAGG
184280	16476	CTTTAAATTCTAACAACTAT	228867	61063	TGGGGCGGGGTTGCTTGTGT	273454	105650	GCAGTTTTCAGCCTCTGCAG
184281	16477	TCTTTAAATTCTAACAACTA	228868	61064	ATGGGGCGGGGTTGCTTGTG	273455	105651	GGCAGTTTTCAGCCTCTGCA
184282	16478	ATCTTTAAATTCTAACAACT	228869	61065	CATGGGGCGGGGTTGCTTGT	273456	105652	CGGCAGTTTTCAGCCTCTGC
184283	16479	TATCTTTAAATTCTAACAAC	228870	61066	ACATGGGGCGGGGTTGCTTG	273457	105653	GCGGCAGTTTTCAGCCTCTG
184284	16480	TTATCTTTAAATTCTAACAA	228871	61067	CACATGGGGCGGGGTTGCTT	273458	105654	TGCGGCAGTTTTCAGCCTCT
184285	16481	ATTATCTTTAAATTCTAACA	228872	61068	TCACATGGGGCGGGGTTGCT	273459	105655	CTGCGGCAGTTTTCAGCCTC
184286	16482	AATTATCTTTAAATTCTAAC	228873	61069	CTCACATGGGGCGGGGTTGC	273460	105656	TCTGCGGCAGTTTTCAGCCT
184287	16483	CAATTATCTTTAAATTCTAA	228874	61070	TCTCACATGGGGCGGGGTTG	273461	105657	ATCTGCGGCAGTTTTCAGCC
184288	16484	CCAATTATCTTTAAATTCTA	228875	61071	ATCTCACATGGGGCGGGGTT	273462	105658	AATCTGCGGCAGTTTTCAGC
184289	16485	ACCAATTATCTTTAAATTCT	228876	61072	GATCTCACATGGGGCGGGGT	273463	105659	CAATCTGCGGCAGTTTTCAG
184290	16486	TACCAATTATCTTTAAATTC	228877	61073	AGATCTCACATGGGGCGGGG	273464	105660	GCAATCTGCGGCAGTTTTCA

184291	16487	TTACCAATTATCTTTAAATT	228878	61074	TAGATCTCACATGGGGCGGG	273465	105661	AGCAATCTGCGGCAGTTTTC
184292	16488	TTTACCAATTATCTTTAAAT	228879	61075	TTAGATCTCACATGGGGCGG	273466	105662	CAGCAATCTGCGGCAGTTTT
184293	16489	ATTTACCAATTATCTTTAAA	228880	61076	CTTAGATCTCACATGGGGCG	273467	105663	GCAGCAATCTGCGGCAGTTT
184294	16490	CATTTACCAATTATCTTTAA	228881	61077	TCTTAGATCTCACATGGGGC	273468	105664	TGCAGCAATCTGCGGCAGTT
184295	16491	TCATTTACCAATTATCTTTA	228882	61078	ATCTTAGATCTCACATGGGG	273469	105665	TTGCAGCAATCTGCGGCAGT
184296	16492	CTCATTTACCAATTATCTTT	228883	61079	CATCTTAGATCTCACATGGG	273470	105666	TTTGCAGCAATCTGCGGCAG
184297	16493	ACTCATTTACCAATTATCTT	228884	61080	CCATCTTAGATCTCACATGG	273471	105667	ATTTGCAGCAATCTGCGGCA
184298	16494	AACTCATTTACCAATTATCT	228885	61081	CCCATCTTAGATCTCACATG	273472	105668	GATTTGCAGCAATCTGCGGC
184299	16495	AAACTCATTTACCAATTATC	228886	61082	GCCCATCTTAGATCTCACAT	273473	105669	TGATTTGCAGCAATCTGCGG
184300	16496	GAAACTCATTTACCAATTAT	228887	61083	CGCCCATCTTAGATCTCACA	273474	105670	ATGATTTGCAGCAATCTGCG
184301	16497	AGAAACTCATTTACCAATTA	228888	61084	ACGCCCATCTTAGATCTCAC	273475	105671	AATGATTTGCAGCAATCTGC
184302	16498	TAGAAACTCATTTACCAATT	228889	61085	CACGCCCATCTTAGATCTCA	273476	105672	CAATGATTTGCAGCAATCTG
184303	16499	ATAGAAACTCATTTACCAAT	228890	61086	GCACGCCCATCTTAGATCTC	273477	105673	CCAATGATTTGCAGCAATCT
184304	16500	GATAGAAACTCATTTACCAA	228891	61087	AGCACGCCCATCTTAGATCT	273478	105674	CCCAATGATTTGCAGCAATC
184305	16501	GGATAGAAACTCATTTACCA	228892	61088	CAGCACGCCCATCTTAGATC	273479	105675	CCCCAATGATTTGCAGCAAT
184306	16502	AGGATAGAAACTCATTTACC	228893	61089	CCAGCACGCCCATCTTAGAT	273480	105676	CCCCCAATGATTTGCAGCAA
184307	16503	AAGGATAGAAACTCATTTAC	228894	61090	CCCAGCACGCCCATCTTAGA	273481	105677	TCCCCCAATGATTTGCAGCA
184308	16504	GAAGGATAGAAACTCATTTA	228895	61091	TCCCAGCACGCCCATCTTAG	273482	105678	TTCCCCCAATGATTTGCAGC
184309	16505	AGAAGGATAGAAACTCATTT	228896	61092	CTCCCAGCACGCCCATCTTA	273483	105679	TTTCCCCCAATGATTTGCAG
184310	16506	TAGAAGGATAGAAACTCATT	228897	61093	GCTCCCAGCACGCCCATCTT	273484	105680	TTTTCCCCCAATGATTTGCA
184311	16507	CTAGAAGGATAGAAACTCAT	228898	61094	GGCTCCCAGCACGCCCATCT	273485	105681	TTTTTCCCCCAATGATTTGC
184312	16508	ACTAGAAGGATAGAAACTCA	228899	61095	TGGCTCCCAGCACGCCCATC	273486	105682	GTTTTTCCCCCAATGATTTG
184313	16509	AACTAGAAGGATAGAAACTC	228900	61096	GTGGCTCCCAGCACGCCCAT	273487	105683	CGTTTTTCCCCCAATGATTT
184314	16510	AAACTAGAAGGATAGAAACT	228901	61097	GGTGGCTCCCAGCACGCCCA	273488	105684	CCGTTTTTCCCCCAATGATT
184315	16511	GAAACTAGAAGGATAGAAAC	228902	61098	AGGTGGCTCCCAGCACGCCC	273489	105685	TCCGTTTTTCCCCCAATGAT
184316	16512	TGAAACTAGAAGGATAGAAA	228903	61099	GAGGTGGCTCCCAGCACGCC	273490	105686	TTCCGTTTTTCCCCCAATGA
184317	16513	GTGAAACTAGAAGGATAGAA	228904	61100	AGAGGTGGCTCCCAGCACGC	273491	105687	TTTCCGTTTTTCCCCCAATG
184318	16514	TGTGAAACTAGAAGGATAGA	228905	61101	CAGAGGTGGCTCCCAGCACG	273492	105688	TTTTCCGTTTTTCCCCCAAT
184319	16515	ATGTGAAACTAGAAGGATAG	228906	61102	TCAGAGGTGGCTCCCAGCAC	273493	105689	GTTTTCCGTTTTTCCCCCAA
184320	16516	GATGTGAAACTAGAAGGATA	228907	61103	CTCAGAGGTGGCTCCCAGCA	273494	105690	CGTTTTCCGTTTTTCCCCCA
184321	16517	TGATGTGAAACTAGAAGGAT	228908	61104	TCTCAGAGGTGGCTCCCAGC	273495	105691	ACGTTTTCCGTTTTTCCCCC
184322	16518	TTGATGTGAAACTAGAAGGA	228909	61105	TTCTCAGAGGTGGCTCCCAG	273496	105692	GACGTTTTCCGTTTTTCCCC
184323	16519	TTTGATGTGAAACTAGAAGG	228910	61106	ATTCTCAGAGGTGGCTCCCA	273497	105693	AGACGTTTTCCGTTTTTCCC
184324	16520	ATTTGATGTGAAACTAGAAG	228911	61107	GATTCTCAGAGGTGGCTCCC	273498	105694	CAGACGTTTTCCGTTTTTCC
184325	16521	CATTTGATGTGAAACTAGAA	228912	61108	GGATTCTCAGAGGTGGCTCC	273499	105695	ACAGACGTTTTCCGTTTTTC
184326	16522	CCATTTGATGTGAAACTAGA	228913	61109	TGGATTCTCAGAGGTGGCTC	273500	105696	AACAGACGTTTTCCGTTTTT
184327	16523	TCCATTTGATGTGAAACTAG	228914	61110	TTGGATTCTCAGAGGTGGCT	273501	105697	AAACAGACGTTTTCCGTTTT
184328	16524	TTCCATTTGATGTGAAACTA	228915	61111	GTTGGATTCTCAGAGGTGGC	273502	105698	AAAACAGACGTTTTCCGTTT
184329	16525	ATTCCATTTGATGTGAAACT	228916	61112	TGTTGGATTCTCAGAGGTGG	273503	105699	GAAAACAGACGTTTTCCGTT
184330	16526	GATTCCATTTGATGTGAAAC	228917	61113	CTGTTGGATTCTCAGAGGTG	273504	105700	GGAAAACAGACGTTTTCCGT
184331	16527	TGATTCCATTTGATGTGAAA	228918	61114	TCTGTTGGATTCTCAGAGGT	273505	105701	GGGAAAACAGACGTTTTCCG
184332	16528	ATGATTCCATTTGATGTGAA	228919	61115	TTCTGTTGGATTCTCAGAGG	273506	105702	GGGGAAAACAGACGTTTTCC
184333	16529	CATGATTCCATTTGATGTGA	228920	61116	CTTCTGTTGGATTCTCAGAG	273507	105703	AGGGGAAAACAGACGTTTTC
184334	16530	GCATGATTCCATTTGATGTG	228921	61117	CCTTCTGTTGGATTCTCAGA	273508	105704	AAGGGGAAAACAGACGTTTT
184335	16531	AGCATGATTCCATTTGATGT	228922	61118	GCCTTCTGTTGGATTCTCAG	273509	105705	AAAGGGGAAAACAGACGTTT
184336	16532	CAGCATGATTCCATTTGATG	228923	61119	TGCCTTCTGTTGGATTCTCA	273510	105706	CAAAGGGGAAAACAGACGTT
184337	16533	GCAGCATGATTCCATTTGAT	228924	61120	CTGCCTTCTGTTGGATTCTC	273511	105707	ACAAAGGGGAAAACAGACGT
184338	16534	GGCAGCATGATTCCATTTGA	228925	61121	TCTGCCTTCTGTTGGATTCT	273512	105708	CACAAAGGGGAAAACAGACG
184339	16535	AGGCAGCATGATTCCATTTG	228926	61122	CTCTGCCTTCTGTTGGATTC	273513	105709	GCACAAAGGGGAAAACAGAC
184340	16536	AAGGCAGCATGATTCCATTT	228927	61123	CCTCTGCCTTCTGTTGGATT	273514	105710	AGCACAAAGGGGAAAACAGA
184341	16537	GAAGGCAGCATGATTCCATT	228928	61124	CCCTCTGCCTTCTGTTGGAT	273515	105711	AAGCACAAAGGGGAAAACAG
184342	16538	TGAAGGCAGCATGATTCCAT	228929	61125	CCCCTCTGCCTTCTGTTGGA	273516	105712	AAAGCACAAAGGGGAAAACA
184343	16539	GTGAAGGCAGCATGATTCCA	228930	61126	TCCCCTCTGCCTTCTGTTGG	273517	105713	AAAAGCACAAAGGGGAAAAC
184344	16540	TGTGAAGGCAGCATGATTCC	228931	61127	CTCCCCTCTGCCTTCTGTTG	273518	105714	GAAAAGCACAAAGGGGAAAA
184345	16541	ATGTGAAGGCAGCATGATTC	228932	61128	TCTCCCCTCTGCCTTCTGTT	273519	105715	AGAAAAGCACAAAGGGGAAA
184346	16542	GATGTGAAGGCAGCATGATT	228933	61129	TTCTCCCCTCTGCCTTCTGT	273520	105716	GAGAAAAGCACAAAGGGGAA
184347	16543	TGATGTGAAGGCAGCATGAT	228934	61130	GTTCTCCCCTCTGCCTTCTG	273521	105717	AGAGAAAAGCACAAAGGGGA
184348	16544	GTGATGTGAAGGCAGCATGA	228935	61131	CGTTCTCCCCTCTGCCTTCT	273522	105718	CAGAGAAAAGCACAAAGGGG
184349	16545	AGTGATGTGAAGGCAGCATG	228936	61132	CCGTTCTCCCCTCTGCCTTC	273523	105719	ACAGAGAAAAGCACAAAGGG
184350	16546	TAGTGATGTGAAGGCAGCAT	228937	61133	GCCGTTCTCCCCTCTGCCTT	273524	105720	AACAGAGAAAAGCACAAAGG
184351	16547	CTAGTGATGTGAAGGCAGCA	228938	61134	AGCCGTTCTCCCCTCTGCCT	273525	105721	AAACAGAGAAAAGCACAAAG
184352	16548	ACTAGTGATGTGAAGGCAGC	228939	61135	GAGCCGTTCTCCCCTCTGCC	273526	105722	AAAACAGAGAAAAGCACAAA
184353	16549	CACTAGTGATGTGAAGGCAG	228940	61136	TGAGCCGTTCTCCCCTCTGC	273527	105723	GAAAACAGAGAAAAGCACAA
184354	16550	GCACTAGTGATGTGAAGGCA	228941	61137	GTGAGCCGTTCTCCCCTCTG	273528	105724	AGAAAACAGAGAAAAGCACA
184355	16551	GGCACTAGTGATGTGAAGGC	228942	61138	TGTGAGCCGTTCTCCCCTCT	273529	105725	AAGAAAACAGAGAAAAGCAC
184356	16552	GGGCACTAGTGATGTGAAGG	228943	61139	GTGTGAGCCGTTCTCCCCTC	273530	105726	GAAGAAAACAGAGAAAAGCA
184357	16553	CGGGCACTAGTGATGTGAAG	228944	61140	CGTGTGAGCCGTTCTCCCCT	273531	105727	AGAAGAAAACAGAGAAAAGC
184358	16554	ACGGGCACTAGTGATGTGAA	228945	61141	CCGTGTGAGCCGTTCTCCCC	273532	105728	AAGAAGAAAACAGAGAAAAG
184359	16555	AACGGGCACTAGTGATGTGA	228946	61142	GCCGTGTGAGCCGTTCTCCC	273533	105729	AAAGAAGAAAACAGAGAAAA
184360	16556	TAACGGGCACTAGTGATGTG	228947	61143	TGCCGTGTGAGCCGTTCTCC	273534	105730	CAAAGAAGAAAACAGAGAAA
184361	16557	ATAACGGGCACTAGTGATGT	228948	61144	GTGCCGTGTGAGCCGTTCTC	273535	105731	ACAAAGAAGAAAACAGAGAA
184362	16558	AATAACGGGCACTAGTGATG	228949	61145	TGTGCCGTGTGAGCCGTTCT	273536	105732	CACAAAGAAGAAAACAGAGA

184363	16559	AAATAACGGGCACTAGTGAT	228950	61146	TTGTGCCGTGTGAGCCGTTC	273537	105733	GCACAAAGAAGAAAACAGAG
184364	16560	CAAATAACGGGCACTAGTGA	228951	61147	TTTGTGCCGTGTGAGCCGTT	273538	105734	AGCACAAAGAAGAAAACAGA
184365	16561	ACAAATAACGGGCACTAGTG	228952	61148	GTTTGTGCCGTGTGAGCCGT	273539	105735	AAGCACAAAGAAGAAAACAG
184366	16562	CACAAATAACGGGCACTAGT	228953	61149	TGTTTGTGCCGTGTGAGCCG	273540	105736	AAAGCACAAAGAAGAAAACA
184367	16563	ACACAAATAACGGGCACTAG	228954	61150	GTGTTTGTGCCGTGTGAGCC	273541	105737	AAAAGCACAAAGAAGAAAAC
184368	16564	AACACAAATAACGGGCACTA	228955	61151	AGTGTTTGTGCCGTGTGAGC	273542	105738	GAAAAGCACAAAGAAGAAAA
184369	16565	AAACACAAATAACGGGCACT	228956	61152	GAGTGTTTGTGCCGTGTGAG	273543	105739	AGAAAAGCACAAAGAAGAAA
184370	16566	TAAACACAAATAACGGGCAC	228957	61153	GGAGTGTTTGTGCCGTGTGA	273544	105740	GAGAAAAGCACAAAGAAGAA
184371	16567	TTAAACACAAATAACGGGCA	228958	61154	AGGAGTGTTTGTGCCGTGTG	273545	105741	AGAGAAAAGCACAAAGAAGA
184372	16568	ATTAAACACAAATAACGGGC	228959	61155	AAGGAGTGTTTGTGCCGTGT	273546	105742	CAGAGAAAAGCACAAAGAAG
184373	16569	AATTAAACACAAATAACGGG	228960	61156	GAAGGAGTGTTTGTGCCGTG	273547	105743	ACAGAGAAAAGCACAAAGAA
184374	16570	AAATTAAACACAAATAACGG	228961	61157	GGAAGGAGTGTTTGTGCCGT	273548	105744	AACAGAGAAAAGCACAAAGA
184375	16571	GAAATTAAACACAAATAACG	228962	61158	AGGAAGGAGTGTTTGTGCCG	273549	105745	AAACAGAGAAAAGCACAAAG
184376	16572	GGAAATTAAACACAAATAAC	228963	61159	AAGGAAGGAGTGTTTGTGCC	273550	105746	AAAACAGAGAAAAGCACAAA
184377	16573	TGGAAATTAAACACAAATAA	228964	61160	AAAGGAAGGAGTGTTTGTGC	273551	105747	GAAAACAGAGAAAAGCACAA
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184380	16576	TTGTGGAAATTAAACACAAA	228967	61163	AAAAAAGGAAGGAGTGTTTG	273554	105750	CCTGAAAACAGAGAAAAGCA
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184383	16579	ACATTGTGGAAATTAAACAC	228970	61166	AAAAAAAAAGGAAGGAGTGT	273557	105753	AATCCTGAAAACAGAGAAAA
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184385	16581	CAACATTGTGGAAATTAAAC	228972	61168	AAAAAAAAAAAGGAAGGAGT	273559	105755	CAAATCCTGAAAACAGAGAA
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184390	16586	TTAGACAACATTGTGGAAAT	228977	61173	AAAGAAAAAAAAAAAAGGAA	273564	105760	TGTAGCAAATCCTGAAAACA
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184392	16588	AATTAGACAACATTGTGGAA	228979	61175	AAAAAGAAAAAAAAAAAAGG	273566	105762	ACTGTAGCAAATCCTGAAAA
184393	16589	GAATTAGACAACATTGTGGA	228980	61176	GAAAAAGAAAAAAAAAAAAG	273567	105763	CACTGTAGCAAATCCTGAAA
184394	16590	GGAATTAGACAACATTGTGG	228981	61177	GGAAAAAGAAAAAAAAAAAA	273568	105764	TCACTGTAGCAAATCCTGAA
184395	16591	TGGAATTAGACAACATTGTG	228982	61178	AGGAAAAAGAAAAAAAAAAA	273569	105765	TTCACTGTAGCAAATCCTGA
184396	16592	GTGGAATTAGACAACATTGT	228983	61179	AAGGAAAAAGAAAAAAAAAA	273570	105766	GTTCACTGTAGCAAATCCTG
184397	16593	AGTGGAATTAGACAACATTG	228984	61180	AAAGGAAAAAGAAAAAAAAA	273571	105767	TGTTCACTGTAGCAAATCCT
184398	16594	GAGTGGAATTAGACAACATT	228985	61181	AAAAGGAAAAAGAAAAAAAA	273572	105768	ATGTTCACTGTAGCAAATCC
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184405	16601	GCCCAAAGAGTGGAATTAGA	228992	61188	CCTTTCAAAAAGGAAAAAGA	273579	105775	GCAATCTATGTTCACTGTAG
184406	16602	AGCCCAAAGAGTGGAATTAG	228993	61189	TCCTTTCAAAAAGGAAAAAG	273580	105776	AGCAATCTATGTTCACTGTA
184407	16603	AAGCCCAAAGAGTGGAATTA	228994	61190	CTCCTTTCAAAAAGGAAAAA	273581	105777	AAGCAATCTATGTTCACTGT
184408	16604	GAAGCCCAAAGAGTGGAATT	228995	61191	ACTCCTTTCAAAAAGGAAAA	273582	105778	AAAGCAATCTATGTTCACTG
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184412	16608	TGGGGAAGCCCAAAGAGTGG	228999	61195	TGAGACTCCTTTCAAAAAGG	273586	105782	CCCCAAAGCAATCTATGTTC
184413	16609	CTGGGGAAGCCCAAAGAGTG	229000	61196	GTGAGACTCCTTTCAAAAAG	273587	105783	GCCCCAAAGCAATCTATGTT
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184417	16613	ATCCCTGGGGAAGCCCAAAG	229004	61200	TAGAGTGAGACTCCTTTCAA	273591	105787	TGGGGCCCCAAAGCAATCTA
184418	16614	GATCCCTGGGGAAGCCCAAA	229005	61201	ATAGAGTGAGACTCCTTTCA	273592	105788	TTGGGGCCCCAAAGCAATCT
184419	16615	GGATCCCTGGGGAAGCCCAA	229006	61202	AATAGAGTGAGACTCCTTTC	273593	105789	TTTGGGGCCCCAAAGCAATC
184420	16616	TGGATCCCTGGGGAAGCCCA	229007	61203	CAATAGAGTGAGACTCCTTT	273594	105790	ATTTGGGGCCCCAAAGCAAT
184421	16617	CTGGATCCCTGGGGAAGCCC	229008	61204	GCAATAGAGTGAGACTCCTT	273595	105791	CATTTGGGGCCCCAAAGCAA
184422	16618	GCTGGATCCCTGGGGAAGCC	229009	61205	GGCAATAGAGTGAGACTCCT	273596	105792	CCATTTGGGGCCCCAAAGCA
184423	16619	GGCTGGATCCCTGGGGAAGC	229010	61206	GGGCAATAGAGTGAGACTCC	273597	105793	TCCATTTGGGGCCCCAAAGC
184424	16620	AGGCTGGATCCCTGGGGAAG	229011	61207	TGGGCAATAGAGTGAGACTC	273598	105794	TTCCATTTGGGGCCCCAAAG
184425	16621	GAGGCTGGATCCCTGGGGAA	229012	61208	CTGGGCAATAGAGTGAGACT	273599	105795	ATTCCATTTGGGGCCCCAAA
184426	16622	GGAGGCTGGATCCCTGGGGA	229013	61209	CCTGGGCAATAGAGTGAGAC	273600	105796	AATTCCATTTGGGGCCCCAA
184427	16623	GGGAGGCTGGATCCCTGGGG	229014	61210	GCCTGGGCAATAGAGTGAGA	273601	105797	TAATTCCATTTGGGGCCCCA
184428	16624	AGGGAGGCTGGATCCCTGGG	229015	61211	TGCCTGGGCAATAGAGTGAG	273602	105798	ATAATTCCATTTGGGGCCCC
184429	16625	GAGGGAGGCTGGATCCCTGG	229016	61212	CTGCCTGGGCAATAGAGTGA	273603	105799	AATAATTCCATTTGGGGCCC
184430	16626	TGAGGGAGGCTGGATCCCTG	229017	61213	CCTGCCTGGGCAATAGAGTG	273604	105800	AAATAATTCCATTTGGGGCC
184431	16627	GTGAGGGAGGCTGGATCCCT	229018	61214	TCCTGCCTGGGCAATAGAGT	273605	105801	AAAATAATTCCATTTGGGGC
184432	16628	AGTGAGGGAGGCTGGATCCC	229019	61215	CTCCTGCCTGGGCAATAGAG	273606	105802	CAAAATAATTCCATTTGGGG
184433	16629	GAGTGAGGGAGGCTGGATCC	229020	61216	ACTCCTGCCTGGGCAATAGA	273607	105803	TCAAAATAATTCCATTTGGG
184434	16630	CGAGTGAGGGAGGCTGGATC	229021	61217	CACTCCTGCCTGGGCAATAG	273608	105804	TTCAAAATAATTCCATTTGG

184435	16631	GCGAGTGAGGGAGGCTGGAT	229022	61218	GCACTCCTGCCTGGGCAATA	273609	105805	TTTCAAAATAATTCCATTTG
184436	16632	GGCGAGTGAGGGAGGCTGGA	229023	61219	TGCACTCCTGCCTGGGCAAT	273610	105806	CTTTCAAAATAATTCCATTT
184437	16633	GGGCGAGTGAGGGAGGCTGG	229024	61220	CTGCACTCCTGCCTGGGCAA	273611	105807	CCTTTCAAAATAATTCCATT
184438	16634	TGGGCGAGTGAGGGAGGCTG	229025	61221	ACTGCACTCCTGCCTGGGCA	273612	105808	TCCTTTCAAAATAATTCCAT
184439	16635	ATGGGCGAGTGAGGGAGGCT	229026	61222	CACTGCACTCCTGCCTGGGC	273613	105809	TTCCTTTCAAAATAATTCCA
184440	16636	GATGGGCGAGTGAGGGAGGC	229027	61223	CCACTGCACTCCTGCCTGGG	273614	105810	TTTCCTTTCAAAATAATTCC
184441	16637	CGATGGGCGAGTGAGGGAGG	229028	61224	ACCACTGCACTCCTGCCTGG	273615	105811	TTTTCCTTTCAAAATAATTC
184442	16638	GCGATGGGCGAGTGAGGGAG	229029	61225	CACCACTGCACTCCTGCCTG	273616	105812	ATTTTCCTTTCAAAATAATT
184443	16639	TGCGATGGGCGAGTGAGGGA	229030	61226	GCACCACTGCACTCCTGCCT	273617	105813	CATTTTCCTTTCAAAATAAT
184444	16640	CTGCGATGGGCGAGTGAGGG	229031	61227	TGCACCACTGCACTCCTGCC	273618	105814	GCATTTTCCTTTCAAAATAA
184445	16641	CCTGCGATGGGCGAGTGAGG	229032	61228	TTGCACCACTGCACTCCTGC	273619	105815	TGCATTTTCCTTTCAAAATA
184446	16642	CCCTGCGATGGGCGAGTGAG	229033	61229	ATTGCACCACTGCACTCCTG	273620	105816	CTGCATTTTCCTTTCAAAAT
184447	16643	TCCCTGCGATGGGCGAGTGA	229034	61230	GATTGCACCACTGCACTCCT	273621	105817	TCTGCATTTTCCTTTCAAAA
184448	16644	CTCCCTGCGATGGGCGAGTG	229035	61231	AGATTGCACCACTGCACTCC	273622	105818	ATCTGCATTTTCCTTTCAAA
184449	16645	TCTCCCTGCGATGGGCGAGT	229036	61232	GAGATTGCACCACTGCACTC	273623	105819	TATCTGCATTTTCCTTTCAA
184450	16646	ATCTCCCTGCGATGGGCGAG	229037	61233	TGAGATTGCACCACTGCACT	273624	105820	TTATCTGCATTTTCCTTTCA
184451	16647	CATCTCCCTGCGATGGGCGA	229038	61234	CTGAGATTGCACCACTGCAC	273625	105821	ATTATCTGCATTTTCCTTTC
184452	16648	GCATCTCCCTGCGATGGGCG	229039	61235	GCTGAGATTGCACCACTGCA	273626	105822	GATTATCTGCATTTTCCTTT
184453	16649	AGCATCTCCCTGCGATGGGC	229040	61236	AGCTGAGATTGCACCACTGC	273627	105823	TGATTATCTGCATTTTCCTT
184454	16650	AAGCATCTCCCTGCGATGGG	229041	61237	GAGCTGAGATTGCACCACTG	273628	105824	CTGATTATCTGCATTTTCCT
184455	16651	AAAGCATCTCCCTGCGATGG	229042	61238	TGAGCTGAGATTGCACCACT	273629	105825	CCTGATTATCTGCATTTTCC
184456	16652	TAAAGCATCTCCCTGCGATG	229043	61239	GTGAGCTGAGATTGCACCAC	273630	105826	ACCTGATTATCTGCATTTTC
184457	16653	ATAAAGCATCTCCCTGCGAT	229044	61240	AGTGAGCTGAGATTGCACCA	273631	105827	CACCTGATTATCTGCATTTT
184458	16654	AATAAAGCATCTCCCTGCGA	229045	61241	CAGTGAGCTGAGATTGCACC	273632	105828	CCACCTGATTATCTGCATTT
184459	16655	GAATAAAGCATCTCCCTGCG	229046	61242	GCAGTGAGCTGAGATTGCAC	273633	105829	GCCACCTGATTATCTGCATT
184460	16656	TGAATAAAGCATCTCCCTGC	229047	61243	TGCAGTGAGCTGAGATTGCA	273634	105830	GGCCACCTGATTATCTGCAT
184461	16657	ATGAATAAAGCATCTCCCTG	229048	61244	TTGCAGTGAGCTGAGATTGC	273635	105831	CGGCCACCTGATTATCTGCA
184462	16658	GATGAATAAAGCATCTCCCT	229049	61245	GTTGCAGTGAGCTGAGATTG	273636	105832	GCGGCCACCTGATTATCTGC
184463	16659	AGATGAATAAAGCATCTCCC	229050	61246	GGTTGCAGTGAGCTGAGATT	273637	105833	TGCGGCCACCTGATTATCTG
184464	16660	AAGATGAATAAAGCATCTCC	229051	61247	AGGTTGCAGTGAGCTGAGAT	273638	105834	GTGCGGCCACCTGATTATCT
184465	16661	AAAGATGAATAAAGCATCTC	229052	61248	GAGGTTGCAGTGAGCTGAGA	273639	105835	AGTGCGGCCACCTGATTATC
184466	16662	CAAAGATGAATAAAGCATCT	229053	61249	GGAGGTTGCAGTGAGCTGAG	273640	105836	CAGTGCGGCCACCTGATTAT
184467	16663	ACAAAGATGAATAAAGCATC	229054	61250	CGGAGGTTGCAGTGAGCTGA	273641	105837	CCAGTGCGGCCACCTGATTA
184468	16664	CACAAAGATGAATAAAGCAT	229055	61251	GCGGAGGTTGCAGTGAGCTG	273642	105838	TCCAGTGCGGCCACCTGATT
184469	16665	ACACAAAGATGAATAAAGCA	229056	61252	GGCGGAGGTTGCAGTGAGCT	273643	105839	CTCCAGTGCGGCCACCTGAT
184470	16666	GACACAAAGATGAATAAAGC	229057	61253	AGGCGGAGGTTGCAGTGAGC	273644	105840	GCTCCAGTGCGGCCACCTGA
184471	16667	AGACACAAAGATGAATAAAG	229058	61254	GAGGCGGAGGTTGCAGTGAG	273645	105841	TGCTCCAGTGCGGCCACCTG
184472	16668	AAGACACAAAGATGAATAAA	229059	61255	GGAGGCGGAGGTTGCAGTGA	273646	105842	GTGCTCCAGTGCGGCCACCT
184473	16669	GAAGACACAAAGATGAATAA	229060	61256	AGGAGGCGGAGGTTGCAGTG	273647	105843	GGTGCTCCAGTGCGGCCACC
184474	16670	AGAAGACACAAAGATGAATA	229061	61257	TAGGAGGCGGAGGTTGCAGT	273648	105844	TGGTGCTCCAGTGCGGCCAC
184475	16671	CAGAAGACACAAAGATGAAT	229062	61258	CTAGGAGGCGGAGGTTGCAG	273649	105845	CTGGTGCTCCAGTGCGGCCA
184476	16672	ACAGAAGACACAAAGATGAA	229063	61259	CCTAGGAGGCGGAGGTTGCA	273650	105846	GCTGGTGCTCCAGTGCGGCC
184477	16673	CACAGAAGACACAAAGATGA	229064	61260	ACCTAGGAGGCGGAGGTTGC	273651	105847	AGCTGGTGCTCCAGTGCGGC
184478	16674	GCACAGAAGACACAAAGATG	229065	61261	AACCTAGGAGGCGGAGGTTG	273652	105848	CAGCTGGTGCTCCAGTGCGG
184479	16675	GGCACAGAAGACACAAAGAT	229066	61262	GAACCTAGGAGGCGGAGGTT	273653	105849	CCAGCTGGTGCTCCAGTGCG
184480	16676	CGGCACAGAAGACACAAAGA	229067	61263	TGAACCTAGGAGGCGGAGGT	273654	105850	CCCAGCTGGTGCTCCAGTGC
184481	16677	CCGGCACAGAAGACACAAAG	229068	61264	TTGAACCTAGGAGGCGGAGG	273655	105851	ACCCAGCTGGTGCTCCAGTG
184482	16678	CCCGGCACAGAAGACACAAA	229069	61265	CTTGAACCTAGGAGGCGGAG	273656	105852	TACCCAGCTGGTGCTCCAGT
184483	16679	GCCCGGCACAGAAGACACAA	229070	61266	GCTTGAACCTAGGAGGCGGA	273657	105853	CTACCCAGCTGGTGCTCCAG
184484	16680	TGCCCGGCACAGAAGACACA	229071	61267	CGCTTGAACCTAGGAGGCGG	273658	105854	CCTACCCAGCTGGTGCTCCA
184485	16681	ATGCCCGGCACAGAAGACAC	229072	61268	TCGCTTGAACCTAGGAGGCG	273659	105855	CCCTACCCAGCTGGTGCTCC
184486	16682	TATGCCCGGCACAGAAGACA	229073	61269	ATCGCTTGAACCTAGGAGGC	273660	105856	CCCCTACCCAGCTGGTGCTC
184487	16683	CTATGCCCGGCACAGAAGAC	229074	61270	AATCGCTTGAACCTAGGAGG	273661	105857	ACCCCTACCCAGCTGGTGCT
184488	16684	GCTATGCCCGGCACAGAAGA	229075	61271	GAATCGCTTGAACCTAGGAG	273662	105858	TACCCCTACCCAGCTGGTGC
184489	16685	CGCTATGCCCGGCACAGAAG	229076	61272	AGAATCGCTTGAACCTAGGA	273663	105859	CTACCCCTACCCAGCTGGTG
184490	16686	GCGCTATGCCCGGCACAGAA	229077	61273	GAGAATCGCTTGAACCTAGG	273664	105860	TCTACCCCTACCCAGCTGGT
184491	16687	TGCGCTATGCCCGGCACAGA	229078	61274	GGAGAATCGCTTGAACCTAG	273665	105861	CTCTACCCCTACCCAGCTGG
184492	16688	ATGCGCTATGCCCGGCACAG	229079	61275	TGGAGAATCGCTTGAACCTA	273666	105862	TCTCTACCCCTACCCAGCTG
184493	16689	CATGCGCTATGCCCGGCACA	229080	61276	CTGGAGAATCGCTTGAACCT	273667	105863	ATCTCTACCCCTACCCAGCT
184494	16690	CCATGCGCTATGCCCGGCAC	229081	61277	GCTGGAGAATCGCTTGAACC	273668	105864	AATCTCTACCCCTACCCAGC
184495	16691	GCCATGCGCTATGCCCGGCA	229082	61278	GGCTGGAGAATCGCTTGAAC	273669	105865	CAATCTCTACCCCTACCCAG
184496	16692	TGCCATGCGCTATGCCCGGC	229083	61279	AGGCTGGAGAATCGCTTGAA	273670	105866	GCAATCTCTACCCCTACCCA
184497	16693	GTGCCATGCGCTATGCCCGG	229084	61280	GAGGCTGGAGAATCGCTTGA	273671	105867	TGCAATCTCTACCCCTACCC
184498	16694	TGTGCCATGCGCTATGCCCG	229085	61281	TGAGGCTGGAGAATCGCTTG	273672	105868	CTGCAATCTCTACCCCTACC
184499	16695	CTGTGCCATGCGCTATGCCC	229086	61282	CTGAGGCTGGAGAATCGCTT	273673	105869	CCTGCAATCTCTACCCCTAC
184500	16696	TCTGTGCCATGCGCTATGCC	229087	61283	GCTGAGGCTGGAGAATCGCT	273674	105870	GCCTGCAATCTCTACCCCTA
184501	16697	TTCTGTGCCATGCGCTATGC	229088	61284	AGCTGAGGCTGGAGAATCGC	273675	105871	TGCCTGCAATCTCTACCCCT
184502	16698	ATTCTGTGCCATGCGCTATG	229089	61285	AAGCTGAGGCTGGAGAATCG	273676	105872	TTGCCTGCAATCTCTACCCC
184503	16699	TATTCTGTGCCATGCGCTAT	229090	61286	GAAGCTGAGGCTGGAGAATC	273677	105873	CTTGCCTGCAATCTCTACCC
184504	16700	TTATTCTGTGCCATGCGCTA	229091	61287	GGAAGCTGAGGCTGGAGAAT	273678	105874	CCTTGCCTGCAATCTCTACC
184505	16701	CTTATTCTGTGCCATGCGCT	229092	61288	GGGAAGCTGAGGCTGGAGAA	273679	105875	TCCTTGCCTGCAATCTCTAC
184506	16702	GCTTATTCTGTGCCATGCGC	229093	61289	TGGGAAGCTGAGGCTGGAGA	273680	105876	CTCCTTGCCTGCAATCTCTA

184507	16703	TGCTTATTCTGTGCCATGCG	229094	61290	TTGGGAAGCTGAGGCTGGAG	273681	105877	CCTCCTTGCCTGCAATCTCT
184508	16704	GTGCTTATTCTGTGCCATGC	229095	61291	CTTGGGAAGCTGAGGCTGGA	273682	105878	TCCTCCTTGCCTGCAATCTC
184509	16705	AGTGCTTATTCTGTGCCATG	229096	61292	ACTTGGGAAGCTGAGGCTGG	273683	105879	CTCCTCCTTGCCTGCAATCT
184510	16706	GAGTGCTTATTCTGTGCCAT	229097	61293	TACTTGGGAAGCTGAGGCTG	273684	105880	CCTCCTCCTTGCCTGCAATC
184511	16707	TGAGTGCTTATTCTGTGCCA	229098	61294	CTACTTGGGAAGCTGAGGCT	273685	105881	TCCTCCTCCTTGCCTGCAAT
184512	16708	CTGAGTGCTTATTCTGTGCC	229099	61295	GCTACTTGGGAAGCTGAGGC	273686	105882	CTCCTCCTCCTTGCCTGCAA
184513	16709	ACTGAGTGCTTATTCTGTGC	229100	61296	AGCTACTTGGGAAGCTGAGG	273687	105883	GCTCCTCCTCCTTGCCTGCA
184514	16710	TACTGAGTGCTTATTCTGTG	229101	61297	CAGCTACTTGGGAAGCTGAG	273688	105884	AGCTCCTCCTCCTTGCCTGC
184515	16711	TTACTGAGTGCTTATTCTGT	229102	61298	CCAGCTACTTGGGAAGCTGA	273689	105885	CAGCTCCTCCTCCTTGCCTG
184516	16712	ATTACTGAGTGCTTATTCTG	229103	61299	CCCAGCTACTTGGGAAGCTG	273690	105886	CCAGCTCCTCCTCCTTGCCT
184517	16713	AATTACTGAGTGCTTATTCT	229104	61300	TCCCAGCTACTTGGGAAGCT	273691	105887	CCCAGCTCCTCCTCCTTGCC
184518	16714	CAATTACTGAGTGCTTATTC	229105	61301	ATCCCAGCTACTTGGGAAGC	273692	105888	ACCCAGCTCCTCCTCCTTGC
184519	16715	TCAATTACTGAGTGCTTATT	229106	61302	AATCCCAGCTACTTGGGAAG	273693	105889	CACCCAGCTCCTCCTCCTTG
184520	16716	ATCAATTACTGAGTGCTTAT	229107	61303	TAATCCCAGCTACTTGGGAA	273694	105890	CCACCCAGCTCCTCCTCCTT
184521	16717	AATCAATTACTGAGTGCTTA	229108	61304	GTAATCCCAGCTACTTGGGA	273695	105891	CCCACCCAGCTCCTCCTCCT
184522	16718	GAATCAATTACTGAGTGCTT	229109	61305	TGTAATCCCAGCTACTTGGG	273696	105892	CCCCACCCAGCTCCTCCTCC
184523	16719	TGAATCAATTACTGAGTGCT	229110	61306	CTGTAATCCCAGCTACTTGG	273697	105893	ACCCCACCCAGCTCCTCCTC
184524	16720	GTGAATCAATTACTGAGTGC	229111	61307	CCTGTAATCCCAGCTACTTG	273698	105894	CACCCCACCCAGCTCCTCCT
184525	16721	CGTGAATCAATTACTGAGTG	229112	61308	ACCTGTAATCCCAGCTACTT	273699	105895	GCACCCCACCCAGCTCCTCC
184526	16722	TCGTGAATCAATTACTGAGT	229113	61309	TACCTGTAATCCCAGCTACT	273700	105896	GGCACCCCACCCAGCTCCTC
184527	16723	CTCGTGAATCAATTACTGAG	229114	61310	GTACCTGTAATCCCAGCTAC	273701	105897	TGGCACCCCACCCAGCTCCT
184528	16724	ACTCGTGAATCAATTACTGA	229115	61311	TGTACCTGTAATCCCAGCTA	273702	105898	CTGGCACCCCACCCAGCTCC
184529	16725	CACTCGTGAATCAATTACTG	229116	61312	GTGTACCTGTAATCCCAGCT	273703	105899	CCTGGCACCCCACCCAGCTC
184530	16726	TCACTCGTGAATCAATTACT	229117	61313	AGTGTACCTGTAATCCCAGC	273704	105900	GCCTGGCACCCCACCCAGCT
184531	16727	TTCACTCGTGAATCAATTAC	229118	61314	GAGTGTACCTGTAATCCCAG	273705	105901	TGCCTGGCACCCCACCCAGC
184532	16728	ATTCACTCGTGAATCAATTA	229119	61315	GGAGTGTACCTGTAATCCCA	273706	105902	CTGCCTGGCACCCCACCCAG
184533	16729	TATTCACTCGTGAATCAATT	229120	61316	TGGAGTGTACCTGTAATCCC	273707	105903	CCTGCCTGGCACCCCACCCA
184534	16730	TTATTCACTCGTGAATCAAT	229121	61317	GTGGAGTGTACCTGTAATCC	273708	105904	TCCTGCCTGGCACCCCACCC
184535	16731	TTTATTCACTCGTGAATCAA	229122	61318	GGTGGAGTGTACCTGTAATC	273709	105905	TTCCTGCCTGGCACCCCACC
184536	16732	ATTTATTCACTCGTGAATCA	229123	61319	TGGTGGAGTGTACCTGTAAT	273710	105906	CTTCCTGCCTGGCACCCCAC
184537	16733	CATTTATTCACTCGTGAATC	229124	61320	ATGGTGGAGTGTACCTGTAA	273711	105907	TCTTCCTGCCTGGCACCCCA
184538	16734	CCATTTATTCACTCGTGAAT	229125	61321	CATGGTGGAGTGTACCTGTA	273712	105908	CTCTTCCTGCCTGGCACCCC
184539	16735	TCCATTTATTCACTCGTGAA	229126	61322	GCATGGTGGAGTGTACCTGT	273713	105909	GCTCTTCCTGCCTGGCACCC
184540	16736	ATCCATTTATTCACTCGTGA	229127	61323	GGCATGGTGGAGTGTACCTG	273714	105910	GGCTCTTCCTGCCTGGCACC
184541	16737	CATCCATTTATTCACTCGTG	229128	61324	GGGCATGGTGGAGTGTACCT	273715	105911	GGGCTCTTCCTGCCTGGCAC
184542	16738	TCATCCATTTATTCACTCGT	229129	61325	CGGGCATGGTGGAGTGTACC	273716	105912	CGGGCTCTTCCTGCCTGGCA
184543	16739	CTCATCCATTTATTCACTCG	229130	61326	CCGGGCATGGTGGAGTGTAC	273717	105913	ACGGGCTCTTCCTGCCTGGC
184544	16740	ACTCATCCATTTATTCACTC	229131	61327	GCCGGGCATGGTGGAGTGTA	273718	105914	TACGGGCTCTTCCTGCCTGG
184545	16741	CACTCATCCATTTATTCACT	229132	61328	AGCCGGGCATGGTGGAGTGT	273719	105915	CTACGGGCTCTTCCTGCCTG
184546	16742	CCACTCATCCATTTATTCAC	229133	61329	TAGCCGGGCATGGTGGAGTG	273720	105916	CCTACGGGCTCTTCCTGCCT
184547	16743	CCCACTCATCCATTTATTCA	229134	61330	TTAGCCGGGCATGGTGGAGT	273721	105917	GCCTACGGGCTCTTCCTGCC
184548	16744	ACCCACTCATCCATTTATTC	229135	61331	ATTAGCCGGGCATGGTGGAG	273722	105918	GGCCTACGGGCTCTTCCTGC
184549	16745	CACCCACTCATCCATTTATT	229136	61332	AATTAGCCGGGCATGGTGGA	273723	105919	GGGCCTACGGGCTCTTCCTG
184550	16746	TCACCCACTCATCCATTTAT	229137	61333	AAATTAGCCGGGCATGGTGG	273724	105920	GGGGCCTACGGGCTCTTCCT
184551	16747	CTCACCCACTCATCCATTTA	229138	61334	AAAATTAGCCGGGCATGGTG	273725	105921	CGGGGCCTACGGGCTCTTCC
184552	16748	ACTCACCCACTCATCCATTT	229139	61335	AAAAATTAGCCGGGCATGGT	273726	105922	GCGGGGCCTACGGGCTCTTC
184553	16749	AACTCACCCACTCATCCATT	229140	61336	CAAAAATTAGCCGGGCATGG	273727	105923	GGCGGGGCCTACGGGCTCTT
184554	16750	GAACTCACCCACTCATCCAT	229141	61337	ACAAAAATTAGCCGGGCATG	273728	105924	CGGCGGGGCCTACGGGCTCT
184555	16751	TGAACTCACCCACTCATCCA	229142	61338	CACAAAAATTAGCCGGGCAT	273729	105925	TCGGCGGGGCCTACGGGCTC
184556	16752	TTGAACTCACCCACTCATCC	229143	61339	ACACAAAAATTAGCCGGGCA	273730	105926	ATCGGCGGGGCCTACGGGCT
184557	16753	ATTGAACTCACCCACTCATC	229144	61340	AACACAAAAATTAGCCGGGC	273731	105927	GATCGGCGGGGCCTACGGGC
184558	16754	TATTGAACTCACCCACTCAT	229145	61341	AAACACAAAAATTAGCCGGG	273732	105928	AGATCGGCGGGGCCTACGGG
184559	16755	ATATTGAACTCACCCACTCA	229146	61342	AAAACACAAAAATTAGCCGG	273733	105929	AAGATCGGCGGGGCCTACGG
184560	16756	AATATTGAACTCACCCACTC	229147	61343	AAAAACACAAAAATTAGCCG	273734	105930	CAAGATCGGCGGGGCCTACG
184561	16757	CAATATTGAACTCACCCACT	229148	61344	TAAAAACACAAAAATTAGCC	273735	105931	ACAAGATCGGCGGGGCCTAC
184562	16758	TCAATATTGAACTCACCCAC	229149	61345	CTAAAAACACAAAAATTAGC	273736	105932	CACAAGATCGGCGGGGCCTA
184563	16759	GTCAATATTGAACTCACCCA	229150	61346	ACTAAAAACACAAAAATTAG	273737	105933	CCACAAGATCGGCGGGGCCT
184564	16760	AGTCAATATTGAACTCACCC	229151	61347	TACTAAAAACACAAAAATTA	273738	105934	CCCACAAGATCGGCGGGGCC
184565	16761	TAGTCAATATTGAACTCACC	229152	61348	CTACTAAAAACACAAAAATT	273739	105935	TCCCACAAGATCGGCGGGGC
184566	16762	GTAGTCAATATTGAACTCAC	229153	61349	TCTACTAAAAACACAAAAAT	273740	105936	CTCCCACAAGATCGGCGGGG
184567	16763	TGTAGTCAATATTGAACTCA	229154	61350	CTCTACTAAAAACACAAAAA	273741	105937	ACTCCCACAAGATCGGCGGG
184568	16764	TTGTAGTCAATATTGAACTC	229155	61351	TCTCTACTAAAAACACAAAA	273742	105938	GACTCCCACAAGATCGGCGG
184569	16765	TTTGTAGTCAATATTGAACT	229156	61352	GTCTCTACTAAAAACACAAA	273743	105939	CGACTCCCACAAGATCGGCG
184570	16766	TTTTGTAGTCAATATTGAAC	229157	61353	CGTCTCTACTAAAAACACAA	273744	105940	ACGACTCCCACAAGATCGGC
184571	16767	TTTTTGTAGTCAATATTGAA	229158	61354	CCGTCTCTACTAAAAACACA	273745	105941	CACGACTCCCACAAGATCGG
184572	16768	GTTTTTGTAGTCAATATTGA	229159	61355	CCCGTCTCTACTAAAAACAC	273746	105942	CCACGACTCCCACAAGATCG
184573	16769	GGTTTTTGTAGTCAATATTG	229160	61356	CCCCGTCTCTACTAAAAACA	273747	105943	CCCACGACTCCCACAAGATC
184574	16770	GGGTTTTTGTAGTCAATATT	229161	61357	ACCCCGTCTCTACTAAAAAC	273748	105944	ACCCACGACTCCCACAAGAT
184575	16771	AGGGTTTTTGTAGTCAATAT	229162	61358	AACCCCGTCTCTACTAAAAA	273749	105945	CACCCACGACTCCCACAAGA
184576	16772	TAGGGTTTTTGTAGTCAATA	229163	61359	AAACCCCGTCTCTACTAAAA	273750	105946	CCACCCACGACTCCCACAAG
184577	16773	TTAGGGTTTTTGTAGTCAAT	229164	61360	GAAACCCCGTCTCTACTAAA	273751	105947	GCCACCCACGACTCCCACAA
184578	16774	CTTAGGGTTTTTGTAGTCAA	229165	61361	GGAAACCCCGTCTCTACTAA	273752	105948	TGCCACCCACGACTCCCACA

184579	16775	CCTTAGGGTTTTTGTAGTCA	229166	61362	GGGAAACCCCGTCTCTACTA	273753	105949	CTGCCACCCACGACTCCCAC
184580	16776	GCCTTAGGGTTTTTGTAGTC	229167	61363	AGGGAAACCCCGTCTCTACT	273754	105950	ACTGCCACCCACGACTCCCA
184581	16777	GGCCTTAGGGTTTTTGTAGT	229168	61364	TAGGGAAACCCCGTCTCTAC	273755	105951	CACTGCCACCCACGACTCCC
184582	16778	TGGCCTTAGGGTTTTTGTAG	229169	61365	ATAGGGAAACCCCGTCTCTA	273756	105952	ACACTGCCACCCACGACTCC
184583	16779	GTGGCCTTAGGGTTTTTGTA	229170	61366	CATAGGGAAACCCCGTCTCT	273757	105953	AACACTGCCACCCACGACTC
184584	16780	TGTGGCCTTAGGGTTTTTGT	229171	61367	ACATAGGGAAACCCCGTCTC	273758	105954	GAACACTGCCACCCACGACT
184585	16781	GTGTGGCCTTAGGGTTTTTG	229172	61368	AACATAGGGAAACCCCGTCT	273759	105955	GGAACACTGCCACCCACGAC
184586	16782	AGTGTGGCCTTAGGGTTTTT	229173	61369	CAACATAGGGAAACCCCGTC	273760	105956	GGGAACACTGCCACCCACGA
184587	16783	CAGTGTGGCCTTAGGGTTTT	229174	61370	CCAACATAGGGAAACCCCGT	273761	105957	AGGGAACACTGCCACCCACG
184588	16784	CCAGTGTGGCCTTAGGGTTT	229175	61371	GCCAACATAGGGAAACCCCG	273762	105958	GAGGGAACACTGCCACCCAC
184589	16785	ACCAGTGTGGCCTTAGGGTT	229176	61372	GGCCAACATAGGGAAACCCC	273763	105959	GGAGGGAACACTGCCACCCA
184590	16786	CACCAGTGTGGCCTTAGGGT	229177	61373	TGGCCAACATAGGGAAACCC	273764	105960	TGGAGGGAACACTGCCACCC
184591	16787	TCACCAGTGTGGCCTTAGGG	229178	61374	CTGGCCAACATAGGGAAACC	273765	105961	CTGGAGGGAACACTGCCACC
184592	16788	CTCACCAGTGTGGCCTTAGG	229179	61375	CCTGGCCAACATAGGGAAAC	273766	105962	TCTGGAGGGAACACTGCCAC
184593	16789	ACTCACCAGTGTGGCCTTAG	229180	61376	GCCTGGCCAACATAGGGAAA	273767	105963	GTCTGGAGGGAACACTGCCA
184594	16790	CACTCACCAGTGTGGCCTTA	229181	61377	AGCCTGGCCAACATAGGGAA	273768	105964	AGTCTGGAGGGAACACTGCC
184595	16791	CCACTCACCAGTGTGGCCTT	229182	61378	CAGCCTGGCCAACATAGGGA	273769	105965	CAGTCTGGAGGGAACACTGC
184596	16792	GCCACTCACCAGTGTGGCCT	229183	61379	CCAGCCTGGCCAACATAGGG	273770	105966	ACAGTCTGGAGGGAACACTG
184597	16793	AGCCACTCACCAGTGTGGCC	229184	61380	ACCAGCCTGGCCAACATAGG	273771	105967	TACAGTCTGGAGGGAACACT
184598	16794	CAGCCACTCACCAGTGTGGC	229185	61381	GACCAGCCTGGCCAACATAG	273772	105968	TTACAGTCTGGAGGGAACAC
184599	16795	GCAGCCACTCACCAGTGTGG	229186	61382	AGACCAGCCTGGCCAACATA	273773	105969	TTTACAGTCTGGAGGGAACA
184600	16796	CGCAGCCACTCACCAGTGTG	229187	61383	AAGACCAGCCTGGCCAACAT	273774	105970	TTTTACAGTCTGGAGGGAAC
184601	16797	GCGCAGCCACTCACCAGTGT	229188	61384	CAAGACCAGCCTGGCCAACA	273775	105971	CTTTTACAGTCTGGAGGGAA
184602	16798	GGCGCAGCCACTCACCAGTG	229189	61385	TCAAGACCAGCCTGGCCAAC	273776	105972	CCTTTTACAGTCTGGAGGGA
184603	16799	AGGCGCAGCCACTCACCAGT	229190	61386	CTCAAGACCAGCCTGGCCAA	273777	105973	CCCTTTTACAGTCTGGAGGG
184604	16800	CAGGCGCAGCCACTCACCAG	229191	61387	GCTCAAGACCAGCCTGGCCA	273778	105974	TCCCTTTTACAGTCTGGAGG
184605	16801	ACAGGCGCAGCCACTCACCA	229192	61388	AGCTCAAGACCAGCCTGGCC	273779	105975	CTCCCTTTTACAGTCTGGAG
184606	16802	TACAGGCGCAGCCACTCACC	229193	61389	GAGCTCAAGACCAGCCTGGC	273780	105976	GCTCCCTTTTACAGTCTGGA
184607	16803	CTACAGGCGCAGCCACTCAC	229194	61390	GGAGCTCAAGACCAGCCTGG	273781	105977	TGCTCCCTTTTACAGTCTGG
184608	16804	ACTACAGGCGCAGCCACTCA	229195	61391	AGGAGCTCAAGACCAGCCTG	273782	105978	GTGCTCCCTTTTACAGTCTG
184609	16805	GACTACAGGCGCAGCCACTC	229196	61392	CAGGAGCTCAAGACCAGCCT	273783	105979	GGTGCTCCCTTTTACAGTCT
184610	16806	GGACTACAGGCGCAGCCACT	229197	61393	TCAGGAGCTCAAGACCAGCC	273784	105980	AGGTGCTCCCTTTTACAGTC
184611	16807	GGGACTACAGGCGCAGCCAC	229198	61394	GTCAGGAGCTCAAGACCAGC	273785	105981	CAGGTGCTCCCTTTTACAGT
184612	16808	TGGGACTACAGGCGCAGCCA	229199	61395	GGTCAGGAGCTCAAGACCAG	273786	105982	CCAGGTGCTCCCTTTTACAG
184613	16809	CTGGGACTACAGGCGCAGCC	229200	61396	AGGTCAGGAGCTCAAGACCA	273787	105983	GCCAGGTGCTCCCTTTTACA
184614	16810	GCTGGGACTACAGGCGCAGC	229201	61397	GAGGTCAGGAGCTCAAGACC	273788	105984	CGCCAGGTGCTCCCTTTTAC
184615	16811	AGCTGGGACTACAGGCGCAG	229202	61398	TGAGGTCAGGAGCTCAAGAC	273789	105985	CCGCCAGGTGCTCCCTTTTA
184616	16812	CAGCTGGGACTACAGGCGCA	229203	61399	CTGAGGTCAGGAGCTCAAGA	273790	105986	CCCGCCAGGTGCTCCCTTTT
184617	16813	GCAGCTGGGACTACAGGCGC	229204	61400	CCTGAGGTCAGGAGCTCAAG	273791	105987	TCCCGCCAGGTGCTCCCTTT
184618	16814	AGCAGCTGGGACTACAGGCG	229205	61401	ACCTGAGGTCAGGAGCTCAA	273792	105988	TTCCCGCCAGGTGCTCCCTT
184619	16815	CAGCAGCTGGGACTACAGGC	229206	61402	CACCTGAGGTCAGGAGCTCA	273793	105989	CTTCCCGCCAGGTGCTCCCT
184620	16816	CCAGCAGCTGGGACTACAGG	229207	61403	TCACCTGAGGTCAGGAGCTC	273794	105990	TCTTCCCGCCAGGTGCTCCC
184621	16817	CCCAGCAGCTGGGACTACAG	229208	61404	ATCACCTGAGGTCAGGAGCT	273795	105991	CTCTTCCCGCCAGGTGCTCC
184622	16818	CCCCAGCAGCTGGGACTACA	229209	61405	GATCACCTGAGGTCAGGAGC	273796	105992	CCTCTTCCCGCCAGGTGCTC
184623	16819	TCCCCAGCAGCTGGGACTAC	229210	61406	AGATCACCTGAGGTCAGGAG	273797	105993	CCCTCTTCCCGCCAGGTGCT
184624	16820	TTCCCCAGCAGCTGGGACTA	229211	61407	CAGATCACCTGAGGTCAGGA	273798	105994	TCCCTCTTCCCGCCAGGTGC
184625	16821	ATTCCCCAGCAGCTGGGACT	229212	61408	GCAGATCACCTGAGGTCAGG	273799	105995	TTCCCTCTTCCCGCCAGGTG
184626	16822	GATTCCCCAGCAGCTGGGAC	229213	61409	GGCAGATCACCTGAGGTCAG	273800	105996	ATTCCCTCTTCCCGCCAGGT
184627	16823	AGATTCCCCAGCAGCTGGGA	229214	61410	AGGCAGATCACCTGAGGTCA	273801	105997	AATTCCCTCTTCCCGCCAGG
184628	16824	CAGATTCCCCAGCAGCTGGG	229215	61411	CAGGCAGATCACCTGAGGTC	273802	105998	GAATTCCCTCTTCCCGCCAG
184629	16825	TCAGATTCCCCAGCAGCTGG	229216	61412	GCAGGCAGATCACCTGAGGT	273803	105999	AGAATTCCCTCTTCCCGCCA
184630	16826	CTCAGATTCCCCAGCAGCTG	229217	61413	GGCAGGCAGATCACCTGAGG	273804	106000	AAGAATTCCCTCTTCCCGCC
184631	16827	CCTCAGATTCCCCAGCAGCT	229218	61414	AGGCAGGCAGATCACCTGAG	273805	106001	AAAGAATTCCCTCTTCCCGC
184632	16828	GCCTCAGATTCCCCAGCAGC	229219	61415	AAGGCAGGCAGATCACCTGA	273806	106002	AAAAGAATTCCCTCTTCCCG
184633	16829	TGCCTCAGATTCCCCAGCAG	229220	61416	CAAGGCAGGCAGATCACCTG	273807	106003	TAAAAGAATTCCCTCTTCCC
184634	16830	CTGCCTCAGATTCCCCAGCA	229221	61417	CCAAGGCAGGCAGATCACCT	273808	106004	TTAAAAGAATTCCCTCTTCC
184635	16831	CCTGCCTCAGATTCCCCAGC	229222	61418	GCCAAGGCAGGCAGATCACC	273809	106005	TTTAAAAGAATTCCCTCTTC
184636	16832	TCCTGCCTCAGATTCCCCAG	229223	61419	GGCCAAGGCAGGCAGATCAC	273810	106006	GTTTAAAAGAATTCCCTCTT
184637	16833	CTCCTGCCTCAGATTCCCCA	229224	61420	AGGCCAAGGCAGGCAGATCA	273811	106007	TGTTTAAAAGAATTCCCTCT
184638	16834	CCTCCTGCCTCAGATTCCCC	229225	61421	GAGGCCAAGGCAGGCAGATC	273812	106008	ATGTTTAAAAGAATTCCCTC
184639	16835	TCCTCCTGCCTCAGATTCCC	229226	61422	GGAGGCCAAGGCAGGCAGAT	273813	106009	GATGTTTAAAAGAATTCCCT
184640	16836	ATCCTCCTGCCTCAGATTCC	229227	61423	GGGAGGCCAAGGCAGGCAGA	273814	106010	TGATGTTTAAAAGAATTCCC
184641	16837	GATCCTCCTGCCTCAGATTC	229228	61424	TGGGAGGCCAAGGCAGGCAG	273815	106011	ATGATGTTTAAAAGAATTCC
184642	16838	AGATCCTCCTGCCTCAGATT	229229	61425	TTGGGAGGCCAAGGCAGGCA	273816	106012	AATGATGTTTAAAAGAATTC
184643	16839	GAGATCCTCCTGCCTCAGAT	229230	61426	TTTGGGAGGCCAAGGCAGGC	273817	106013	GAATGATGTTTAAAAGAATT
184644	16840	AGAGATCCTCCTGCCTCAGA	229231	61427	CTTTGGGAGGCCAAGGCAGG	273818	106014	GGAATGATGTTTAAAAGAAT
184645	16841	AAGAGATCCTCCTGCCTCAG	229232	61428	ACTTTGGGAGGCCAAGGCAG	273819	106015	TGGAATGATGTTTAAAAGAA
184646	16842	CAAGAGATCCTCCTGCCTCA	229233	61429	CACTTTGGGAGGCCAAGGCA	273820	106016	CTGGAATGATGTTTAAAAGA
184647	16843	TCAAGAGATCCTCCTGCCTC	229234	61430	GCACTTTGGGAGGCCAAGGC	273821	106017	ACTGGAATGATGTTTAAAAG
184648	16844	CTCAAGAGATCCTCCTGCCT	229235	61431	AGCACTTTGGGAGGCCAAGG	273822	106018	CACTGGAATGATGTTTAAAA
184649	16845	GCTCAAGAGATCCTCCTGCC	229236	61432	CAGCACTTTGGGAGGCCAAG	273823	106019	GCACTGGAATGATGTTTAAA
184650	16846	GGCTCAAGAGATCCTCCTGC	229237	61433	CCAGCACTTTGGGAGGCCAA	273824	106020	GGCACTGGAATGATGTTTAA

184651	16847	GGGCTCAAGAGATCCTCCTG	229238	61434	CCCAGCACTTTGGGAGGCCA	273825	106021	GGGCACTGGAATGATGTTTA
184652	16848	TGGGCTCAAGAGATCCTCCT	229239	61435	TCCCAGCACTTTGGGAGGCC	273826	106022	CGGGCACTGGAATGATGTTT
184653	16849	CTGGGCTCAAGAGATCCTCC	229240	61436	ATCCCAGCACTTTGGGAGGC	273827	106023	TCGGGCACTGGAATGATGTT
184654	16850	CCTGGGCTCAAGAGATCCTC	229241	61437	AATCCCAGCACTTTGGGAGG	273828	106024	CTCGGGCACTGGAATGATGT
184655	16851	TCCTGGGCTCAAGAGATCCT	229242	61438	TAATCCCAGCACTTTGGGAG	273829	106025	GCTCGGGCACTGGAATGATG
184656	16852	CTCCTGGGCTCAAGAGATCC	229243	61439	GTAATCCCAGCACTTTGGGA	273830	106026	GGCTCGGGCACTGGAATGAT
184657	16853	ACTCCTGGGCTCAAGAGATC	229244	61440	TGTAATCCCAGCACTTTGGG	273831	106027	AGGCTCGGGCACTGGAATGA
184658	16854	AACTCCTGGGCTCAAGAGAT	229245	61441	CTGTAATCCCAGCACTTTGG	273832	106028	GAGGCTCGGGCACTGGAATG
184659	16855	AAACTCCTGGGCTCAAGAGA	229246	61442	CCTGTAATCCCAGCACTTTG	273833	106029	GGAGGCTCGGGCACTGGAAT
184660	16856	CAAACTCCTGGGCTCAAGAG	229247	61443	ACCTGTAATCCCAGCACTTT	273834	106030	AGGAGGCTCGGGCACTGGAA
184661	16857	TCAAACTCCTGGGCTCAAGA	229248	61444	CACCTGTAATCCCAGCACTT	273835	106031	CAGGAGGCTCGGGCACTGGA
184662	16858	TTCAAACTCCTGGGCTCAAG	229249	61445	ACACCTGTAATCCCAGCACT	273836	106032	CCAGGAGGCTCGGGCACTGG
184663	16859	TTTCAAACTCCTGGGCTCAA	229250	61446	CACACCTGTAATCCCAGCAC	273837	106033	TCCAGGAGGCTCGGGCACTG
184664	16860	GTTTCAAACTCCTGGGCTCA	229251	61447	TCACACCTGTAATCCCAGCA	273838	106034	GTCCAGGAGGCTCGGGCACT
184665	16861	AGTTTCAAACTCCTGGGCTC	229252	61448	CTCACACCTGTAATCCCAGC	273839	106035	GGTCCAGGAGGCTCGGGCAC
184666	16862	TAGTTTCAAACTCCTGGGCT	229253	61449	GCTCACACCTGTAATCCCAG	273840	106036	AGGTCCAGGAGGCTCGGGCA
184667	16863	CTAGTTTCAAACTCCTGGGC	229254	61450	GGCTCACACCTGTAATCCCA	273841	106037	CAGGTCCAGGAGGCTCGGGC
184668	16864	GCTAGTTTCAAACTCCTGGG	229255	61451	TGGCTCACACCTGTAATCCC	273842	106038	ACAGGTCCAGGAGGCTCGGG
184669	16865	GGCTAGTTTCAAACTCCTGG	229256	61452	ATGGCTCACACCTGTAATCC	273843	106039	AACAGGTCCAGGAGGCTCGG
184670	16866	AGGCTAGTTTCAAACTCCTG	229257	61453	CATGGCTCACACCTGTAATC	273844	106040	CAACAGGTCCAGGAGGCTCG
184671	16867	CAGGCTAGTTTCAAACTCCT	229258	61454	CCATGGCTCACACCTGTAAT	273845	106041	ACAACAGGTCCAGGAGGCTC
184672	16868	CCAGGCTAGTTTCAAACTCC	229259	61455	CCCATGGCTCACACCTGTAA	273846	106042	GACAACAGGTCCAGGAGGCT
184673	16869	CCCAGGCTAGTTTCAAACTC	229260	61456	CCCCATGGCTCACACCTGTA	273847	106043	TGACAACAGGTCCAGGAGGC
184674	16870	GCCCAGGCTAGTTTCAAACT	229261	61457	GCCCCATGGCTCACACCTGT	273848	106044	ATGACAACAGGTCCAGGAGG
184675	16871	CGCCCAGGCTAGTTTCAAAC	229262	61458	GGCCCCATGGCTCACACCTG	273849	106045	GATGACAACAGGTCCAGGAG
184676	16872	TCGCCCAGGCTAGTTTCAAA	229263	61459	AGGCCCCATGGCTCACACCT	273850	106046	AGATGACAACAGGTCCAGGA
184677	16873	ATCGCCCAGGCTAGTTTCAA	229264	61460	TAGGCCCCATGGCTCACACC	273851	106047	AAGATGACAACAGGTCCAGG
184678	16874	TATCGCCCAGGCTAGTTTCA	229265	61461	CTAGGCCCCATGGCTCACAC	273852	106048	CAAGATGACAACAGGTCCAG
184679	16875	ATATCGCCCAGGCTAGTTTC	229266	61462	GCTAGGCCCCATGGCTCACA	273853	106049	TCAAGATGACAACAGGTCCA
184680	16876	TATATCGCCCAGGCTAGTTT	229267	61463	GGCTAGGCCCCATGGCTCAC	273854	106050	CTCAAGATGACAACAGGTCC
184681	16877	CTATATCGCCCAGGCTAGTT	229268	61464	AGGCTAGGCCCCATGGCTCA	273855	106051	CCTCAAGATGACAACAGGTC
184682	16878	GCTATATCGCCCAGGCTAGT	229269	61465	GAGGCTAGGCCCCATGGCTC	273856	106052	ACCTCAAGATGACAACAGGT
184683	16879	CGCTATATCGCCCAGGCTAG	229270	61466	GGAGGCTAGGCCCCATGGCT	273857	106053	CACCTCAAGATGACAACAGG
184684	16880	TCGCTATATCGCCCAGGCTA	229271	61467	AGGAGGCTAGGCCCCATGGC	273858	106054	CCACCTCAAGATGACAACAG
184685	16881	CTCGCTATATCGCCCAGGCT	229272	61468	AAGGAGGCTAGGCCCCATGG	273859	106055	CCCACCTCAAGATGACAACA
184686	16882	TCTCGCTATATCGCCCAGGC	229273	61469	GAAGGAGGCTAGGCCCCATG	273860	106056	GCCCACCTCAAGATGACAAC
184687	16883	TTCTCGCTATATCGCCCAGG	229274	61470	GGAAGGAGGCTAGGCCCCAT	273861	106057	GGCCCACCTCAAGATGACAA
184688	16884	GTTCTCGCTATATCGCCCAG	229275	61471	TGGAAGGAGGCTAGGCCCCA	273862	106058	AGGCCCACCTCAAGATGACA
184689	16885	GGTTCTCGCTATATCGCCCA	229276	61472	ATGGAAGGAGGCTAGGCCCC	273863	106059	GAGGCCCACCTCAAGATGAC
184690	16886	AGGTTCTCGCTATATCGCCC	229277	61473	AATGGAAGGAGGCTAGGCCC	273864	106060	GGAGGCCCACCTCAAGATGA
184691	16887	CAGGTTCTCGCTATATCGCC	229278	61474	AAATGGAAGGAGGCTAGGCC	273865	106061	GGGAGGCCCACCTCAAGATG
184692	16888	ACAGGTTCTCGCTATATCGC	229279	61475	TAAATGGAAGGAGGCTAGGC	273866	106062	GGGGAGGCCCACCTCAAGAT
184693	16889	GACAGGTTCTCGCTATATCG	229280	61476	TTAAATGGAAGGAGGCTAGG	273867	106063	AGGGGAGGCCCACCTCAAGA
184694	16890	AGACAGGTTCTCGCTATATC	229281	61477	TTTAAATGGAAGGAGGCTAG	273868	106064	CAGGGGAGGCCCACCTCAAG
184695	16891	GAGACAGGTTCTCGCTATAT	229282	61478	ATTTAAATGGAAGGAGGCTA	273869	106065	CCAGGGGAGGCCCACCTCAA
184696	16892	TGAGACAGGTTCTCGCTATA	229283	61479	CATTTAAATGGAAGGAGGCT	273870	106066	CCCAGGGGAGGCCCACCTCA
184697	16893	TTGAGACAGGTTCTCGCTAT	229284	61480	ACATTTAAATGGAAGGAGGC	273871	106067	ACCCAGGGGAGGCCCACCTC
184698	16894	TTTGAGACAGGTTCTCGCTA	229285	61481	TACATTTAAATGGAAGGAGG	273872	106068	CACCCAGGGGAGGCCCACCT
184699	16895	ATTTGAGACAGGTTCTCGCT	229286	61482	ATACATTTAAATGGAAGGAG	273873	106069	TCACCCAGGGGAGGCCCACC
184700	16896	CATTTGAGACAGGTTCTCGC	229287	61483	CATACATTTAAATGGAAGGA	273874	106070	GTCACCCAGGGGAGGCCCAC
184701	16897	TCATTTGAGACAGGTTCTCG	229288	61484	GCATACATTTAAATGGAAGG	273875	106071	AGTCACCCAGGGGAGGCCCA
184702	16898	GTCATTTGAGACAGGTTCTC	229289	61485	GGCATACATTTAAATGGAAG	273876	106072	GAGTCACCCAGGGGAGGCCC
184703	16899	TGTCATTTGAGACAGGTTCT	229290	61486	AGGCATACATTTAAATGGAA	273877	106073	AGAGTCACCCAGGGGAGGCC
184704	16900	TTGTCATTTGAGACAGGTTC	229291	61487	TAGGCATACATTTAAATGGA	273878	106074	TAGAGTCACCCAGGGGAGGC
184705	16901	TTTGTCATTTGAGACAGGTT	229292	61488	TTAGGCATACATTTAAATGG	273879	106075	CTAGAGTCACCCAGGGGAGG
184706	16902	TTTTGTCATTTGAGACAGGT	229293	61489	ATTAGGCATACATTTAAATG	273880	106076	ACTAGAGTCACCCAGGGGAG
184707	16903	TTTTTGTCATTTGAGACAGG	229294	61490	AATTAGGCATACATTTAAAT	273881	106077	CACTAGAGTCACCCAGGGGA
184708	16904	GTTTTTGTCATTTGAGACAG	229295	61491	AAATTAGGCATACATTTAAA	273882	106078	ACACTAGAGTCACCCAGGGG
184709	16905	TGTTTTTGTCATTTGAGACA	229296	61492	CAAATTAGGCATACATTTAA	273883	106079	CACACTAGAGTCACCCAGGG
184710	16906	CTGTTTTTGTCATTTGAGAC	229297	61493	GCAAATTAGGCATACATTTA	273884	106080	GCACACTAGAGTCACCCAGG
184711	16907	CCTGTTTTTGTCATTTGAGA	229298	61494	GGCAAATTAGGCATACATTT	273885	106081	TGCACACTAGAGTCACCCAG
184712	16908	CCCTGTTTTTGTCATTTGAG	229299	61495	GGGCAAATTAGGCATACATT	273886	106082	CTGCACACTAGAGTCACCCA
184713	16909	GCCCTGTTTTTGTCATTTGA	229300	61496	TGGGCAAATTAGGCATACAT	273887	106083	GCTGCACACTAGAGTCACCC
184714	16910	GGCCCTGTTTTTGTCATTTG	229301	61497	ATGGGCAAATTAGGCATACA	273888	106084	GGCTGCACACTAGAGTCACC
184715	16911	TGGCCCTGTTTTTGTCATTT	229302	61498	AATGGGCAAATTAGGCATAC	273889	106085	AGGCTGCACACTAGAGTCAC
184716	16912	CTGGCCCTGTTTTTGTCATT	229303	61499	CAATGGGCAAATTAGGCATA	273890	106086	CAGGCTGCACACTAGAGTCA
184717	16913	CCTGGCCCTGTTTTTGTCAT	229304	61500	TCAATGGGCAAATTAGGCAT	273891	106087	CCAGGCTGCACACTAGAGTC
184718	16914	ACCTGGCCCTGTTTTTGTCA	229305	61501	CTCAATGGGCAAATTAGGCA	273892	106088	GCCAGGCTGCACACTAGAGT
184719	16915	CACCTGGCCCTGTTTTTGTC	229306	61502	TCTCAATGGGCAAATTAGGC	273893	106089	AGCCAGGCTGCACACTAGAG
184720	16916	GCACCTGGCCCTGTTTTTGT	229307	61503	TTCTCAATGGGCAAATTAGG	273894	106090	CAGCCAGGCTGCACACTAGA
184721	16917	TGCACCTGGCCCTGTTTTTG	229308	61504	GTTCTCAATGGGCAAATTAG	273895	106091	TCAGCCAGGCTGCACACTAG
184722	16918	CTGCACCTGGCCCTGTTTTT	229309	61505	CGTTCTCAATGGGCAAATTA	273896	106092	CTCAGCCAGGCTGCACACTA

184723	16919	ACTGCACCTGGCCCTGTTTT	229310	61506	CCGTTCTCAATGGGCAAATT	273897	106093	TCTCAGCCAGGCTGCACACT
184724	16920	CACTGCACCTGGCCCTGTTT	229311	61507	GCCGTTCTCAATGGGCAAAT	273898	106094	GTCTCAGCCAGGCTGCACAC
184725	16921	CCACTGCACCTGGCCCTGTT	229312	61508	AGCCGTTCTCAATGGGCAAA	273899	106095	AGTCTCAGCCAGGCTGCACA
184726	16922	GCCACTGCACCTGGCCCTGT	229313	61509	CAGCCGTTCTCAATGGGCAA	273900	106096	GAGTCTCAGCCAGGCTGCAC
184727	16923	AGCCACTGCACCTGGCCCTG	229314	61510	TCAGCCGTTCTCAATGGGCA	273901	106097	TGAGTCTCAGCCAGGCTGCA
184728	16924	GAGCCACTGCACCTGGCCCT	229315	61511	CTCAGCCGTTCTCAATGGGC	273902	106098	CTGAGTCTCAGCCAGGCTGC
184729	16925	TGAGCCACTGCACCTGGCCC	229316	61512	TCTCAGCCGTTCTCAATGGG	273903	106099	ACTGAGTCTCAGCCAGGCTG
184730	16926	GTGAGCCACTGCACCTGGCC	229317	61513	GTCTCAGCCGTTCTCAATGG	273904	106100	CACTGAGTCTCAGCCAGGCT
184731	16927	CGTGAGCCACTGCACCTGGC	229318	61514	CGTCTCAGCCGTTCTCAATG	273905	106101	CCACTGAGTCTCAGCCAGGC
184732	16928	GCGTGAGCCACTGCACCTGG	229319	61515	GCGTCTCAGCCGTTCTCAAT	273906	106102	GCCACTGAGTCTCAGCCAGG
184733	16929	GGCGTGAGCCACTGCACCTG	229320	61516	TGCGTCTCAGCCGTTCTCAA	273907	106103	GGCCACTGAGTCTCAGCCAG
184734	16930	AGGCGTGAGCCACTGCACCT	229321	61517	ATGCGTCTCAGCCGTTCTCA	273908	106104	GGGCCACTGAGTCTCAGCCA
184735	16931	CAGGCGTGAGCCACTGCACC	229322	61518	AATGCGTCTCAGCCGTTCTC	273909	106105	AGGGCCACTGAGTCTCAGCC
184736	16932	CCAGGCGTGAGCCACTGCAC	229323	61519	AAATGCGTCTCAGCCGTTCT	273910	106106	CAGGGCCACTGAGTCTCAGC
184737	16933	TCCAGGCGTGAGCCACTGCA	229324	61520	AAAATGCGTCTCAGCCGTTC	273911	106107	CCAGGGCCACTGAGTCTCAG
184738	16934	TTCCAGGCGTGAGCCACTGC	229325	61521	TAAAATGCGTCTCAGCCGTT	273912	106108	CCCAGGGCCACTGAGTCTCA
184739	16935	ATTCCAGGCGTGAGCCACTG	229326	61522	TTAAAATGCGTCTCAGCCGT	273913	106109	ACCCAGGGCCACTGAGTCTC
184740	16936	GATTCCAGGCGTGAGCCACT	229327	61523	CTTAAAATGCGTCTCAGCCG	273914	106110	AACCCAGGGCCACTGAGTCT
184741	16937	GGATTCCAGGCGTGAGCCAC	229328	61524	ACTTAAAATGCGTCTCAGCC	273915	106111	GAACCCAGGGCCACTGAGTC
184742	16938	GGGATTCCAGGCGTGAGCCA	229329	61525	CACTTAAAATGCGTCTCAGC	273916	106112	AGAACCCAGGGCCACTGAGT
184743	16939	TGGGATTCCAGGCGTGAGCC	229330	61526	CCACTTAAAATGCGTCTCAG	273917	106113	AAGAACCCAGGGCCACTGAG
184744	16940	CTGGGATTCCAGGCGTGAGC	229331	61527	GCCACTTAAAATGCGTCTCA	273918	106114	TAAGAACCCAGGGCCACTGA
184745	16941	GCTGGGATTCCAGGCGTGAG	229332	61528	GGCCACTTAAAATGCGTCTC	273919	106115	GTAAGAACCCAGGGCCACTG
184746	16942	TGCTGGGATTCCAGGCGTGA	229333	61529	TGGCCACTTAAAATGCGTCT	273920	106116	AGTAAGAACCCAGGGCCACT
184747	16943	GTGCTGGGATTCCAGGCGTG	229334	61530	CTGGCCACTTAAAATGCGTC	273921	106117	CAGTAAGAACCCAGGGCCAC
184748	16944	AGTGCTGGGATTCCAGGCGT	229335	61531	CCTGGCCACTTAAAATGCGT	273922	106118	GCAGTAAGAACCCAGGGCCA
184749	16945	AAGTGCTGGGATTCCAGGCG	229336	61532	CCCTGGCCACTTAAAATGCG	273923	106119	AGCAGTAAGAACCCAGGGCC
184750	16946	AAAGTGCTGGGATTCCAGGC	229337	61533	ACCCTGGCCACTTAAAATGC	273924	106120	CAGCAGTAAGAACCCAGGGC
184751	16947	TAAAGTGCTGGGATTCCAGG	229338	61534	GACCCTGGCCACTTAAAATG	273925	106121	TCAGCAGTAAGAACCCAGGG
184752	16948	CTAAAGTGCTGGGATTCCAG	229339	61535	AGACCCTGGCCACTTAAAAT	273926	106122	GTCAGCAGTAAGAACCCAGG
184753	16949	CCTAAAGTGCTGGGATTCCA	229340	61536	TAGACCCTGGCCACTTAAAA	273927	106123	TGTCAGCAGTAAGAACCCAG
184754	16950	TCCTAAAGTGCTGGGATTCC	229341	61537	GTAGACCCTGGCCACTTAAA	273928	106124	GTGTCAGCAGTAAGAACCCA
184755	16951	CTCCTAAAGTGCTGGGATTC	229342	61538	AGTAGACCCTGGCCACTTAA	273929	106125	GGTGTCAGCAGTAAGAACCC
184756	16952	CCTCCTAAAGTGCTGGGATT	229343	61539	AAGTAGACCCTGGCCACTTA	273930	106126	AGGTGTCAGCAGTAAGAACC
184757	16953	GCCTCCTAAAGTGCTGGGAT	229344	61540	TAAGTAGACCCTGGCCACTT	273931	106127	TAGGTGTCAGCAGTAAGAAC
184758	16954	GGCCTCCTAAAGTGCTGGGA	229345	61541	CTAAGTAGACCCTGGCCACT	273932	106128	GTAGGTGTCAGCAGTAAGAA
184759	16955	TGGCCTCCTAAAGTGCTGGG	229346	61542	TCTAAGTAGACCCTGGCCAC	273933	106129	GGTAGGTGTCAGCAGTAAGA
184760	16956	TTGGCCTCCTAAAGTGCTGG	229347	61543	CTCTAAGTAGACCCTGGCCA	273934	106130	GGGTAGGTGTCAGCAGTAAG
184761	16957	CTTGGCCTCCTAAAGTGCTG	229348	61544	ACTCTAAGTAGACCCTGGCC	273935	106131	AGGGTAGGTGTCAGCAGTAA
184762	16958	TCTTGGCCTCCTAAAGTGCT	229349	61545	AACTCTAAGTAGACCCTGGC	273936	106132	GAGGGTAGGTGTCAGCAGTA
184763	16959	ATCTTGGCCTCCTAAAGTGC	229350	61546	TAACTCTAAGTAGACCCTGG	273937	106133	TGAGGGTAGGTGTCAGCAGT
184764	16960	CATCTTGGCCTCCTAAAGTG	229351	61547	CTAACTCTAAGTAGACCCTG	273938	106134	TTGAGGGTAGGTGTCAGCAG
184765	16961	CCATCTTGGCCTCCTAAAGT	229352	61548	ACTAACTCTAAGTAGACCCT	273939	106135	GTTGAGGGTAGGTGTCAGCA
184766	16962	CCCATCTTGGCCTCCTAAAG	229353	61549	CACTAACTCTAAGTAGACCC	273940	106136	GGTTGAGGGTAGGTGTCAGC
184767	16963	TCCCATCTTGGCCTCCTAAA	229354	61550	GCACTAACTCTAAGTAGACC	273941	106137	AGGTTGAGGGTAGGTGTCAG
184768	16964	CTCCCATCTTGGCCTCCTAA	229355	61551	AGCACTAACTCTAAGTAGAC	273942	106138	GAGGTTGAGGGTAGGTGTCA
184769	16965	CCTCCCATCTTGGCCTCCTA	229356	61552	GAGCACTAACTCTAAGTAGA	273943	106139	TGAGGTTGAGGGTAGGTGTC
184770	16966	TCCTCCCATCTTGGCCTCCT	229357	61553	TGAGCACTAACTCTAAGTAG	273944	106140	TTGAGGTTGAGGGTAGGTGT
184771	16967	ATCCTCCCATCTTGGCCTCC	229358	61554	ATGAGCACTAACTCTAAGTA	273945	106141	GTTGAGGTTGAGGGTAGGTG
184772	16968	GATCCTCCCATCTTGGCCTC	229359	61555	CATGAGCACTAACTCTAAGT	273946	106142	GGTTGAGGTTGAGGGTAGGT
184773	16969	TGATCCTCCCATCTTGGCCT	229360	61556	TCATGAGCACTAACTCTAAG	273947	106143	TGGTTGAGGTTGAGGGTAGG
184774	16970	GTGATCCTCCCATCTTGGCC	229361	61557	GTCATGAGCACTAACTCTAA	273948	106144	GTGGTTGAGGTTGAGGGTAG
184775	16971	AGTGATCCTCCCATCTTGGC	229362	61558	GGTCATGAGCACTAACTCTA	273949	106145	AGTGGTTGAGGTTGAGGGTA
184776	16972	AAGTGATCCTCCCATCTTGG	229363	61559	TGGTCATGAGCACTAACTCT	273950	106146	CAGTGGTTGAGGTTGAGGGT
184777	16973	CAAGTGATCCTCCCATCTTG	229364	61560	CTGGTCATGAGCACTAACTC	273951	106147	GCAGTGGTTGAGGTTGAGGG
184778	16974	TCAAGTGATCCTCCCATCTT	229365	61561	CCTGGTCATGAGCACTAACT	273952	106148	CGCAGTGGTTGAGGTTGAGG
184779	16975	CTCAAGTGATCCTCCCATCT	229366	61562	GCCTGGTCATGAGCACTAAC	273953	106149	CCGCAGTGGTTGAGGTTGAG
184780	16976	CCTCAAGTGATCCTCCCATC	229367	61563	GGCCTGGTCATGAGCACTAA	273954	106150	GCCGCAGTGGTTGAGGTTGA
184781	16977	GCCTCAAGTGATCCTCCCAT	229368	61564	GGGCCTGGTCATGAGCACTA	273955	106151	GGCCGCAGTGGTTGAGGTTG
184782	16978	GGCCTCAAGTGATCCTCCCA	229369	61565	TGGGCCTGGTCATGAGCACT	273956	106152	AGGCCGCAGTGGTTGAGGTT
184783	16979	TGGCCTCAAGTGATCCTCCC	229370	61566	CTGGGCCTGGTCATGAGCAC	273957	106153	GAGGCCGCAGTGGTTGAGGT
184784	16980	CTGGCCTCAAGTGATCCTCC	229371	61567	CCTGGGCCTGGTCATGAGCA	273958	106154	GGAGGCCGCAGTGGTTGAGG
184785	16981	CCTGGCCTCAAGTGATCCTC	229372	61568	ACCTGGGCCTGGTCATGAGC	273959	106155	AGGAGGCCGCAGTGGTTGAG
184786	16982	TCCTGGCCTCAAGTGATCCT	229373	61569	GACCTGGGCCTGGTCATGAG	273960	106156	CAGGAGGCCGCAGTGGTTGA
184787	16983	CTCCTGGCCTCAAGTGATCC	229374	61570	TGACCTGGGCCTGGTCATGA	273961	106157	ACAGGAGGCCGCAGTGGTTG
184788	16984	ACTCCTGGCCTCAAGTGATC	229375	61571	TTGACCTGGGCCTGGTCATG	273962	106158	CACAGGAGGCCGCAGTGGTT
184789	16985	GACTCCTGGCCTCAAGTGAT	229376	61572	CTTGACCTGGGCCTGGTCAT	273963	106159	GCACAGGAGGCCGCAGTGGT
184790	16986	GGACTCCTGGCCTCAAGTGA	229377	61573	GCTTGACCTGGGCCTGGTCA	273964	106160	TGCACAGGAGGCCGCAGTGG
184791	16987	CGGACTCCTGGCCTCAAGTG	229378	61574	GGCTTGACCTGGGCCTGGTC	273965	106161	GTGCACAGGAGGCCGCAGTG
184792	16988	TCGGACTCCTGGCCTCAAGT	229379	61575	AGGCTTGACCTGGGCCTGGT	273966	106162	GGTGCACAGGAGGCCGCAGT
184793	16989	CTCGGACTCCTGGCCTCAAG	229380	61576	CAGGCTTGACCTGGGCCTGG	273967	106163	GGGTGCACAGGAGGCCGCAG
184794	16990	TCTCGGACTCCTGGCCTCAA	229381	61577	CCAGGCTTGACCTGGGCCTG	273968	106164	AGGGTGCACAGGAGGCCGCA

184795	16991	GTCTCGGACTCCTGGCCTCA	229382	61578	GCCAGGCTTGACCTGGGCCT	273969	106165	CAGGGTGCACAGGAGGCCGC
184796	16992	GGTCTCGGACTCCTGGCCTC	229383	61579	AGCCAGGCTTGACCTGGGCC	273970	106166	TCAGGGTGCACAGGAGGCCG
184797	16993	TGGTCTCGGACTCCTGGCCT	229384	61580	CAGCCAGGCTTGACCTGGGC	273971	106167	ATCAGGGTGCACAGGAGGCC
184798	16994	CTGGTCTCGGACTCCTGGCC	229385	61581	CCAGCCAGGCTTGACCTGGG	273972	106168	GATCAGGGTGCACAGGAGGC
184799	16995	GCTGGTCTCGGACTCCTGGC	229386	61582	GCCAGCCAGGCTTGACCTGG	273973	106169	GGATCAGGGTGCACAGGAGG
184800	16996	GGCTGGTCTCGGACTCCTGG	229387	61583	GGCCAGCCAGGCTTGACCTG	273974	106170	TGGATCAGGGTGCACAGGAG
184801	16997	AGGCTGGTCTCGGACTCCTG	229388	61584	TGGCCAGCCAGGCTTGACCT	273975	106171	CTGGATCAGGGTGCACAGGA
184802	16998	CAGGCTGGTCTCGGACTCCT	229389	61585	CTGGCCAGCCAGGCTTGACC	273976	106172	ACTGGATCAGGGTGCACAGG
184803	16999	CCAGGCTGGTCTCGGACTCC	229390	61586	TCTGGCCAGCCAGGCTTGAC	273977	106173	CACTGGATCAGGGTGCACAG
184804	17000	CCCAGGCTGGTCTCGGACTC	229391	61587	ATCTGGCCAGCCAGGCTTGA	273978	106174	CCACTGGATCAGGGTGCACA
184805	17001	GCCCAGGCTGGTCTCGGACT	229392	61588	CATCTGGCCAGCCAGGCTTG	273979	106175	GCCACTGGATCAGGGTGCAC
184806	17002	TGCCCAGGCTGGTCTCGGAC	229393	61589	CCATCTGGCCAGCCAGGCTT	273980	106176	AGCCACTGGATCAGGGTGCA
184807	17003	TTGCCCAGGCTGGTCTCGGA	229394	61590	ACCATCTGGCCAGCCAGGCT	273981	106177	GAGCCACTGGATCAGGGTGC
184808	17004	GTTGCCCAGGCTGGTCTCGG	229395	61591	CACCATCTGGCCAGCCAGGC	273982	106178	TGAGCCACTGGATCAGGGTG
184809	17005	TGTTGCCCAGGCTGGTCTCG	229396	61592	GCACCATCTGGCCAGCCAGG	273983	106179	ATGAGCCACTGGATCAGGGT
184810	17006	ATGTTGCCCAGGCTGGTCTC	229397	61593	GGCACCATCTGGCCAGCCAG	273984	106180	AATGAGCCACTGGATCAGGG
184811	17007	TATGTTGCCCAGGCTGGTCT	229398	61594	AGGCACCATCTGGCCAGCCA	273985	106181	AAATGAGCCACTGGATCAGG
184812	17008	CTATGTTGCCCAGGCTGGTC	229399	61595	AAGGCACCATCTGGCCAGCC	273986	106182	AAAATGAGCCACTGGATCAG
184813	17009	CCTATGTTGCCCAGGCTGGT	229400	61596	AAAGGCACCATCTGGCCAGC	273987	106183	GAAAATGAGCCACTGGATCA
184814	17010	CCCTATGTTGCCCAGGCTGG	229401	61597	CAAAGGCACCATCTGGCCAG	273988	106184	GGAAAATGAGCCACTGGATC
184815	17011	TCCCTATGTTGCCCAGGCTG	229402	61598	TCAAAGGCACCATCTGGCCA	273989	106185	TGGAAAATGAGCCACTGGAT
184816	17012	CTCCCTATGTTGCCCAGGCT	229403	61599	GTCAAAGGCACCATCTGGCC	273990	106186	GTGGAAAATGAGCCACTGGA
184817	17013	TCTCCCTATGTTGCCCAGGC	229404	61600	GGTCAAAGGCACCATCTGGC	273991	106187	AGTGGAAAATGAGCCACTGG
184818	17014	GTCTCCCTATGTTGCCCAGG	229405	61601	AGGTCAAAGGCACCATCTGG	273992	106188	AAGTGGAAAATGAGCCACTG
184819	17015	GGTCTCCCTATGTTGCCCAG	229406	61602	CAGGTCAAAGGCACCATCTG	273993	106189	AAAGTGGAAAATGAGCCACT
184820	17016	GGGTCTCCCTATGTTGCCCA	229407	61603	GCAGGTCAAAGGCACCATCT	273994	106190	GAAAGTGGAAAATGAGCCAC
184821	17017	AGGGTCTCCCTATGTTGCCC	229408	61604	AGCAGGTCAAAGGCACCATC	273995	106191	TGAAAGTGGAAAATGAGCCA
184822	17018	CAGGGTCTCCCTATGTTGCC	229409	61605	GAGCAGGTCAAAGGCACCAT	273996	106192	CTGAAAGTGGAAAATGAGCC
184823	17019	ACAGGGTCTCCCTATGTTGC	229410	61606	AGAGCAGGTCAAAGGCACCA	273997	106193	ACTGAAAGTGGAAAATGAGC
184824	17020	GACAGGGTCTCCCTATGTTG	229411	61607	CAGAGCAGGTCAAAGGCACC	273998	106194	GACTGAAAGTGGAAAATGAG
184825	17021	AGACAGGGTCTCCCTATGTT	229412	61608	ACAGAGCAGGTCAAAGGCAC	273999	106195	GGACTGAAAGTGGAAAATGA
184826	17022	GAGACAGGGTCTCCCTATGT	229413	61609	GACAGAGCAGGTCAAAGGCA	274000	106196	GGGACTGAAAGTGGAAAATG
184827	17023	AGAGACAGGGTCTCCCTATG	229414	61610	AGACAGAGCAGGTCAAAGGC	274001	106197	TGGGACTGAAAGTGGAAAAT
184828	17024	TAGAGACAGGGTCTCCCTAT	229415	61611	GAGACAGAGCAGGTCAAAGG	274002	106198	CTGGGACTGAAAGTGGAAAA
184829	17025	GTAGAGACAGGGTCTCCCTA	229416	61612	AGAGACAGAGCAGGTCAAAG	274003	106199	GCTGGGACTGAAAGTGGAAA
184830	17026	TGTAGAGACAGGGTCTCCCT	229417	61613	CAGAGACAGAGCAGGTCAAA	274004	106200	AGCTGGGACTGAAAGTGGAA
184831	17027	TTGTAGAGACAGGGTCTCCC	229418	61614	ACAGAGACAGAGCAGGTCAA	274005	106201	GAGCTGGGACTGAAAGTGGA
184832	17028	TTTGTAGAGACAGGGTCTCC	229419	61615	CACAGAGACAGAGCAGGTCA	274006	106202	AGAGCTGGGACTGAAAGTGG
184833	17029	TTTTGTAGAGACAGGGTCTC	229420	61616	GCACAGAGACAGAGCAGGTC	274007	106203	TAGAGCTGGGACTGAAAGTG
184834	17030	TTTTTGTAGAGACAGGGTCT	229421	61617	TGCACAGAGACAGAGCAGGT	274008	106204	ATAGAGCTGGGACTGAAAGT
184835	17031	TTTTTTGTAGAGACAGGGTC	229422	61618	TTGCACAGAGACAGAGCAGG	274009	106205	GATAGAGCTGGGACTGAAAG
184836	17032	ATTTTTTGTAGAGACAGGGT	229423	61619	TTTGCACAGAGACAGAGCAG	274010	106206	GGATAGAGCTGGGACTGAAA
184837	17033	AATTTTTTGTAGAGACAGGG	229424	61620	CTTTGCACAGAGACAGAGCA	274011	106207	GGGATAGAGCTGGGACTGAA
184838	17034	AAATTTTTTGTAGAGACAGG	229425	61621	CCTTTGCACAGAGACAGAGC	274012	106208	AGGGATAGAGCTGGGACTGA
184839	17035	AAAATTTTTTGTAGAGACAG	229426	61622	TCCTTTGCACAGAGACAGAG	274013	106209	TAGGGATAGAGCTGGGACTG
184840	17036	AAAAATTTTTTGTAGAGACA	229427	61623	TTCCTTTGCACAGAGACAGA	274014	106210	ATAGGGATAGAGCTGGGACT
184841	17037	AAAAAATTTTTTGTAGAGAC	229428	61624	ATTCCTTTGCACAGAGACAG	274015	106211	AATAGGGATAGAGCTGGGAC
184842	17038	TAAAAAATTTTTTGTAGAGA	229429	61625	CATTCCTTTGCACAGAGACA	274016	106212	AAATAGGGATAGAGCTGGGA
184843	17039	TTAAAAAATTTTTTGTAGAG	229430	61626	TCATTCCTTTGCACAGAGAC	274017	106213	CAAATAGGGATAGAGCTGGG
184844	17040	TTTAAAAAATTTTTTGTAGA	229431	61627	CTCATTCCTTTGCACAGAGA	274018	106214	GCAAATAGGGATAGAGCTGG
184845	17041	TTTTAAAAAATTTTTTGTAG	229432	61628	GCTCATTCCTTTGCACAGAG	274019	106215	TGCAAATAGGGATAGAGCTG
184846	17042	TTTTTAAAAAATTTTTTGTA	229433	61629	AGCTCATTCCTTTGCACAGA	274020	106216	CTGCAAATAGGGATAGAGCT
184847	17043	ATTTTTAAAAAATTTTTTGT	229434	61630	CAGCTCATTCCTTTGCACAG	274021	106217	ACTGCAAATAGGGATAGAGC
184848	17044	AATTTTTAAAAAATTTTTTG	229435	61631	TCAGCTCATTCCTTTGCACA	274022	106218	AACTGCAAATAGGGATAGAG
184849	17045	TAATTTTTAAAAAATTTTTT	229436	61632	TTCAGCTCATTCCTTTGCAC	274023	106219	AAACTGCAAATAGGGATAGA
184850	17046	CTAATTTTTAAAAAATTTTT	229437	61633	CTTCAGCTCATTCCTTTGCA	274024	106220	GAAACTGCAAATAGGGATAG
184851	17047	GCTAATTTTTAAAAAATTTT	229438	61634	CCTTCAGCTCATTCCTTTGC	274025	106221	GGAAACTGCAAATAGGGATA
184852	17048	AGCTAATTTTTAAAAAATTT	229439	61635	TCCTTCAGCTCATTCCTTTG	274026	106222	TGGAAACTGCAAATAGGGAT
184853	17049	CAGCTAATTTTTAAAAAATT	229440	61636	ATCCTTCAGCTCATTCCTTT	274027	106223	TTGGAAACTGCAAATAGGGA
184854	17050	CCAGCTAATTTTTAAAAAAT	229441	61637	CATCCTTCAGCTCATTCCTT	274028	106224	CTTGGAAACTGCAAATAGGG
184855	17051	CCCAGCTAATTTTTAAAAAA	229442	61638	CCATCCTTCAGCTCATTCCT	274029	106225	ACTTGGAAACTGCAAATAGG
184856	17052	GCCCAGCTAATTTTTAAAAA	229443	61639	CCCATCCTTCAGCTCATTCC	274030	106226	CACTTGGAAACTGCAAATAG
184857	17053	TGCCCAGCTAATTTTTAAAA	229444	61640	CCCCATCCTTCAGCTCATTC	274031	106227	GCACTTGGAAACTGCAAATA
184858	17054	ATGCCCAGCTAATTTTTAAA	229445	61641	CCCCCATCCTTCAGCTCATT	274032	106228	GGCACTTGGAAACTGCAAAT
184859	17055	CATGCCCAGCTAATTTTTAA	229446	61642	ACCCCCATCCTTCAGCTCAT	274033	106229	AGGCACTTGGAAACTGCAAA
184860	17056	CCATGCCCAGCTAATTTTTA	229447	61643	CACCCCCATCCTTCAGCTCA	274034	106230	CAGGCACTTGGAAACTGCAA
184861	17057	GCCATGCCCAGCTAATTTTT	229448	61644	GCACCCCCATCCTTCAGCTC	274035	106231	CCAGGCACTTGGAAACTGCA
184862	17058	CGCCATGCCCAGCTAATTTT	229449	61645	TGCACCCCCATCCTTCAGCT	274036	106232	ACCAGGCACTTGGAAACTGC
184863	17059	CCGCCATGCCCAGCTAATTT	229450	61646	CTGCACCCCCATCCTTCAGC	274037	106233	GACCAGGCACTTGGAAACTG
184864	17060	ACCGCCATGCCCAGCTAATT	229451	61647	ACTGCACCCCCATCCTTCAG	274038	106234	GGACCAGGCACTTGGAAACT
184865	17061	CACCGCCATGCCCAGCTAAT	229452	61648	CACTGCACCCCCATCCTTCA	274039	106235	AGGACCAGGCACTTGGAAAC
184866	17062	ACACCGCCATGCCCAGCTAA	229453	61649	ACACTGCACCCCCATCCTTC	274040	106236	GAGGACCAGGCACTTGGAAA

184867	17063	CACACCGCCATGCCCAGCTA	229454	61650	CACACTGCACCCCCATCCTT	274041	106237	TGAGGACCAGGCACTTGGAA
184868	17064	GCACACCGCCATGCCCAGCT	229455	61651	ACACACTGCACCCCCATCCT	274042	106238	CTGAGGACCAGGCACTTGGA
184869	17065	CGCACACCGCCATGCCCAGC	229456	61652	CACACACTGCACCCCCATCC	274043	106239	ACTGAGGACCAGGCACTTGG
184870	17066	GCGCACACCGCCATGCCCAG	229457	61653	CCACACACTGCACCCCCATC	274044	106240	GACTGAGGACCAGGCACTTG
184871	17067	AGCGCACACCGCCATGCCCA	229458	61654	CCCACACACTGCACCCCCAT	274045	106241	TGACTGAGGACCAGGCACTT
184872	17068	AAGCGCACACCGCCATGCCC	229459	61655	GCCCACACACTGCACCCCCA	274046	106242	CTGACTGAGGACCAGGCACT
184873	17069	CAAGCGCACACCGCCATGCC	229460	61656	TGCCCACACACTGCACCCCC	274047	106243	GCTGACTGAGGACCAGGCAC
184874	17070	ACAAGCGCACACCGCCATGC	229461	61657	CTGCCCACACACTGCACCCC	274048	106244	AGCTGACTGAGGACCAGGCA
184875	17071	TACAAGCGCACACCGCCATG	229462	61658	ACTGCCCACACACTGCACCC	274049	106245	GAGCTGACTGAGGACCAGGC
184876	17072	CTACAAGCGCACACCGCCAT	229463	61659	CACTGCCCACACACTGCACC	274050	106246	TGAGCTGACTGAGGACCAGG
184877	17073	ACTACAAGCGCACACCGCCA	229464	61660	CCACTGCCCACACACTGCAC	274051	106247	CTGAGCTGACTGAGGACCAG
184878	17074	GACTACAAGCGCACACCGCC	229465	61661	CCCACTGCCCACACACTGCA	274052	106248	TCTGAGCTGACTGAGGACCA
184879	17075	GGACTACAAGCGCACACCGC	229466	61662	GCCCACTGCCCACACACTGC	274053	106249	GTCTGAGCTGACTGAGGACC
184880	17076	GGGACTACAAGCGCACACCG	229467	61663	AGCCCACTGCCCACACACTG	274054	106250	GGTCTGAGCTGACTGAGGAC
184881	17077	TGGGACTACAAGCGCACACC	229468	61664	CAGCCCACTGCCCACACACT	274055	106251	GGGTCTGAGCTGACTGAGGA
184882	17078	CTGGGACTACAAGCGCACAC	229469	61665	CCAGCCCACTGCCCACACAC	274056	106252	TGGGTCTGAGCTGACTGAGG
184883	17079	GCTGGGACTACAAGCGCACA	229470	61666	CCCAGCCCACTGCCCACACA	274057	106253	CTGGGTCTGAGCTGACTGAG
184884	17080	AGCTGGGACTACAAGCGCAC	229471	61667	CCCCAGCCCACTGCCCACAC	274058	106254	GCTGGGTCTGAGCTGACTGA
184885	17081	TAGCTGGGACTACAAGCGCA	229472	61668	GCCCCAGCCCACTGCCCACA	274059	106255	GGCTGGGTCTGAGCTGACTG
184886	17082	GTAGCTGGGACTACAAGCGC	229473	61669	AGCCCCAGCCCACTGCCCAC	274060	106256	TGGCTGGGTCTGAGCTGACT
184887	17083	AGTAGCTGGGACTACAAGCG	229474	61670	CAGCCCCAGCCCACTGCCCA	274061	106257	CTGGCTGGGTCTGAGCTGAC
184888	17084	GAGTAGCTGGGACTACAAGC	229475	61671	CCAGCCCCAGCCCACTGCCC	274062	106258	CCTGGCTGGGTCTGAGCTGA
184889	17085	TGAGTAGCTGGGACTACAAG	229476	61672	GCCAGCCCCAGCCCACTGCC	274063	106259	GCCTGGCTGGGTCTGAGCTG
184890	17086	CTGAGTAGCTGGGACTACAA	229477	61673	TGCCAGCCCCAGCCCACTGC	274064	106260	GGCCTGGCTGGGTCTGAGCT
184891	17087	CCTGAGTAGCTGGGACTACA	229478	61674	CTGCCAGCCCCAGCCCACTG	274065	106261	TGGCCTGGCTGGGTCTGAGC
184892	17088	TCCTGAGTAGCTGGGACTAC	229479	61675	CCTGCCAGCCCCAGCCCACT	274066	106262	CTGGCCTGGCTGGGTCTGAG
184893	17089	CTCCTGAGTAGCTGGGACTA	229480	61676	TCCTGCCAGCCCCAGCCCAC	274067	106263	GCTGGCCTGGCTGGGTCTGA
184894	17090	CCTCCTGAGTAGCTGGGACT	229481	61677	GTCCTGCCAGCCCCAGCCCA	274068	106264	GGCTGGCCTGGCTGGGTCTG
184895	17091	GCCTCCTGAGTAGCTGGGAC	229482	61678	AGTCCTGCCAGCCCCAGCCC	274069	106265	GGGCTGGCCTGGCTGGGTCT
184896	17092	AGCCTCCTGAGTAGCTGGGA	229483	61679	GAGTCCTGCCAGCCCCAGCC	274070	106266	GGGGCTGGCCTGGCTGGGTC
184897	17093	CAGCCTCCTGAGTAGCTGGG	229484	61680	TGAGTCCTGCCAGCCCCAGC	274071	106267	AGGGGCTGGCCTGGCTGGGT
184898	17094	TCAGCCTCCTGAGTAGCTGG	229485	61681	CTGAGTCCTGCCAGCCCCAG	274072	106268	CAGGGGCTGGCCTGGCTGGG
184899	17095	CTCAGCCTCCTGAGTAGCTG	229486	61682	ACTGAGTCCTGCCAGCCCCA	274073	106269	CCAGGGGCTGGCCTGGCTGG
184900	17096	CCTCAGCCTCCTGAGTAGCT	229487	61683	CACTGAGTCCTGCCAGCCCC	274074	106270	ACCAGGGGCTGGCCTGGCTG
184901	17097	GCCTCAGCCTCCTGAGTAGC	229488	61684	TCACTGAGTCCTGCCAGCCC	274075	106271	AACCAGGGGCTGGCCTGGCT
184902	17098	TGCCTCAGCCTCCTGAGTAG	229489	61685	GTCACTGAGTCCTGCCAGCC	274076	106272	GAACCAGGGGCTGGCCTGGC
184903	17099	CTGCCTCAGCCTCCTGAGTA	229490	61686	AGTCACTGAGTCCTGCCAGC	274077	106273	GGAACCAGGGGCTGGCCTGG
184904	17100	CCTGCCTCAGCCTCCTGAGT	229491	61687	TAGTCACTGAGTCCTGCCAG	274078	106274	GGGAACCAGGGGCTGGCCTG
184905	17101	TCCTGCCTCAGCCTCCTGAG	229492	61688	TTAGTCACTGAGTCCTGCCA	274079	106275	TGGGAACCAGGGGCTGGCCT
184906	17102	CTCCTGCCTCAGCCTCCTGA	229493	61689	CTTAGTCACTGAGTCCTGCC	274080	106276	GTGGGAACCAGGGGCTGGCC
184907	17103	CCTCCTGCCTCAGCCTCCTG	229494	61690	CCTTAGTCACTGAGTCCTGC	274081	106277	TGTGGGAACCAGGGGCTGGC
184908	17104	TCCTCCTGCCTCAGCCTCCT	229495	61691	CCCTTAGTCACTGAGTCCTG	274082	106278	ATGTGGGAACCAGGGGCTGG
184909	17105	ATCCTCCTGCCTCAGCCTCC	229496	61692	TCCCTTAGTCACTGAGTCCT	274083	106279	GATGTGGGAACCAGGGGCTG
184910	17106	GATCCTCCTGCCTCAGCCTC	229497	61693	TTCCCTTAGTCACTGAGTCC	274084	106280	GGATGTGGGAACCAGGGGCT
184911	17107	TGATCCTCCTGCCTCAGCCT	229498	61694	CTTCCCTTAGTCACTGAGTC	274085	106281	GGGATGTGGGAACCAGGGGC
184912	17108	GTGATCCTCCTGCCTCAGCC	229499	61695	TCTTCCCTTAGTCACTGAGT	274086	106282	GGGGATGTGGGAACCAGGGG
184913	17109	AGTGATCCTCCTGCCTCAGC	229500	61696	CTCTTCCCTTAGTCACTGAG	274087	106283	AGGGGATGTGGGAACCAGGG
184914	17110	AAGTGATCCTCCTGCCTCAG	229501	61697	TCTCTTCCCTTAGTCACTGA	274088	106284	AAGGGGATGTGGGAACCAGG
184915	17111	CAAGTGATCCTCCTGCCTCA	229502	61698	TTCTCTTCCCTTAGTCACTG	274089	106285	AAAGGGGATGTGGGAACCAG
184916	17112	TCAAGTGATCCTCCTGCCTC	229503	61699	GTTCTCTTCCCTTAGTCACT	274090	106286	CAAAGGGGATGTGGGAACCA
184917	17113	CTCAAGTGATCCTCCTGCCT	229504	61700	AGTTCTCTTCCCTTAGTCAC	274091	106287	GCAAAGGGGATGTGGGAACC
184918	17114	GCTCAAGTGATCCTCCTGCC	229505	61701	AAGTTCTCTTCCCTTAGTCA	274092	106288	GGCAAAGGGGATGTGGGAAC
184919	17115	GGCTCAAGTGATCCTCCTGC	229506	61702	AAAGTTCTCTTCCCTTAGTC	274093	106289	TGGCAAAGGGGATGTGGGAA
184920	17116	GGGCTCAAGTGATCCTCCTG	229507	61703	GAAAGTTCTCTTCCCTTAGT	274094	106290	TTGGCAAAGGGGATGTGGGA
184921	17117	TGGGCTCAAGTGATCCTCCT	229508	61704	GGAAAGTTCTCTTCCCTTAG	274095	106291	CTTGGCAAAGGGGATGTGGG
184922	17118	CTGGGCTCAAGTGATCCTCC	229509	61705	AGGAAAGTTCTCTTCCCTTA	274096	106292	GCTTGGCAAAGGGGATGTGG
184923	17119	CCTGGGCTCAAGTGATCCTC	229510	61706	GAGGAAAGTTCTCTTCCCTT	274097	106293	AGCTTGGCAAAGGGGATGTG
184924	17120	TCCTGGGCTCAAGTGATCCT	229511	61707	TGAGGAAAGTTCTCTTCCCT	274098	106294	GAGCTTGGCAAAGGGGATGT
184925	17121	TTCCTGGGCTCAAGTGATCC	229512	61708	GTGAGGAAAGTTCTCTTCCC	274099	106295	TGAGCTTGGCAAAGGGGATG
184926	17122	TTTCCTGGGCTCAAGTGATC	229513	61709	AGTGAGGAAAGTTCTCTTCC	274100	106296	ATGAGCTTGGCAAAGGGGAT
184927	17123	ATTTCCTGGGCTCAAGTGAT	229514	61710	TAGTGAGGAAAGTTCTCTTC	274101	106297	GATGAGCTTGGCAAAGGGGA
184928	17124	AATTTCCTGGGCTCAAGTGA	229515	61711	GTAGTGAGGAAAGTTCTCTT	274102	106298	GGATGAGCTTGGCAAAGGGG
184929	17125	CAATTTCCTGGGCTCAAGTG	229516	61712	GGTAGTGAGGAAAGTTCTCT	274103	106299	GGGATGAGCTTGGCAAAGGG
184930	17126	TCAATTTCCTGGGCTCAAGT	229517	61713	TGGTAGTGAGGAAAGTTCTC	274104	106300	GGGGATGAGCTTGGCAAAGG
184931	17127	CTCAATTTCCTGGGCTCAAG	229518	61714	CTGGTAGTGAGGAAAGTTCT	274105	106301	CGGGGATGAGCTTGGCAAAG
184932	17128	CCTCAATTTCCTGGGCTCAA	229519	61715	GCTGGTAGTGAGGAAAGTTC	274106	106302	GCGGGGATGAGCTTGGCAAA
184933	17129	GCCTCAATTTCCTGGGCTCA	229520	61716	GGCTGGTAGTGAGGAAAGTT	274107	106303	GGCGGGGATGAGCTTGGCAA
184934	17130	AGCCTCAATTTCCTGGGCTC	229521	61717	AGGCTGGTAGTGAGGAAAGT	274108	106304	GGGCGGGGATGAGCTTGGCA
184935	17131	CAGCCTCAATTTCCTGGGCT	229522	61718	CAGGCTGGTAGTGAGGAAAG	274109	106305	AGGGCGGGGATGAGCTTGGC
184936	17132	GCAGCCTCAATTTCCTGGGC	229523	61719	ACAGGCTGGTAGTGAGGAAA	274110	106306	CAGGGCGGGGATGAGCTTGG
184937	17133	TGCAGCCTCAATTTCCTGGG	229524	61720	GACAGGCTGGTAGTGAGGAA	274111	106307	ACAGGGCGGGGATGAGCTTG
184938	17134	CTGCAGCCTCAATTTCCTGG	229525	61721	AGACAGGCTGGTAGTGAGGA	274112	106308	AACAGGGCGGGGATGAGCTT

184939	17135	GCTGCAGCCTCAATTTCCTG	229526	61722	AAGACAGGCTGGTAGTGAGG	274113	106309	AAACAGGGCGGGGATGAGCT
184940	17136	CGCTGCAGCCTCAATTTCCT	229527	61723	AAAGACAGGCTGGTAGTGAG	274114	106310	CAAACAGGGCGGGGATGAGC
184941	17137	TCGCTGCAGCCTCAATTTCC	229528	61724	AAAAGACAGGCTGGTAGTGA	274115	106311	CCAAACAGGGCGGGGATGAG
184942	17138	CTCGCTGCAGCCTCAATTTC	229529	61725	GAAAAGACAGGCTGGTAGTG	274116	106312	GCCAAACAGGGCGGGGATGA
184943	17139	GCTCGCTGCAGCCTCAATTT	229530	61726	TGAAAAGACAGGCTGGTAGT	274117	106313	GGCCAAACAGGGCGGGGATG
184944	17140	GGCTCGCTGCAGCCTCAATT	229531	61727	CTGAAAAGACAGGCTGGTAG	274118	106314	AGGCCAAACAGGGCGGGGAT
184945	17141	TGGCTCGCTGCAGCCTCAAT	229532	61728	CCTGAAAAGACAGGCTGGTA	274119	106315	CAGGCCAAACAGGGCGGGGA
184946	17142	ATGGCTCGCTGCAGCCTCAA	229533	61729	CCCTGAAAAGACAGGCTGGT	274120	106316	GCAGGCCAAACAGGGCGGGG
184947	17143	CATGGCTCGCTGCAGCCTCA	229534	61730	GCCCTGAAAAGACAGGCTGG	274121	106317	CGCAGGCCAAACAGGGCGGG
184948	17144	TCATGGCTCGCTGCAGCCTC	229535	61731	TGCCCTGAAAAGACAGGCTG	274122	106318	CCGCAGGCCAAACAGGGCGG
184949	17145	ATCATGGCTCGCTGCAGCCT	229536	61732	GTGCCCTGAAAAGACAGGCT	274123	106319	CCCGCAGGCCAAACAGGGCG
184950	17146	CATCATGGCTCGCTGCAGCC	229537	61733	GGTGCCCTGAAAAGACAGGC	274124	106320	TCCCGCAGGCCAAACAGGGC
184951	17147	CCATCATGGCTCGCTGCAGC	229538	61734	CGGTGCCCTGAAAAGACAGG	274125	106321	CTCCCGCAGGCCAAACAGGG
184952	17148	GCCATCATGGCTCGCTGCAG	229539	61735	GCGGTGCCCTGAAAAGACAG	274126	106322	ACTCCCGCAGGCCAAACAGG
184953	17149	TGCCATCATGGCTCGCTGCA	229540	61736	CGCGGTGCCCTGAAAAGACA	274127	106323	CACTCCCGCAGGCCAAACAG
184954	17150	GTGCCATCATGGCTCGCTGC	229541	61737	CCGCGGTGCCCTGAAAAGAC	274128	106324	CCACTCCCGCAGGCCAAACA
184955	17151	GGTGCCATCATGGCTCGCTG	229542	61738	CCCGCGGTGCCCTGAAAAGA	274129	106325	CCCACTCCCGCAGGCCAAAC
184956	17152	TGGTGCCATCATGGCTCGCT	229543	61739	CCCCGCGGTGCCCTGAAAAG	274130	106326	TCCCACTCCCGCAGGCCAAA
184957	17153	GTGGTGCCATCATGGCTCGC	229544	61740	CCCCCGCGGTGCCCTGAAAA	274131	106327	CTCCCACTCCCGCAGGCCAA
184958	17154	AGTGGTGCCATCATGGCTCG	229545	61741	CCCCCCGCGGTGCCCTGAAA	274132	106328	ACTCCCACTCCCGCAGGCCA
184959	17155	CAGTGGTGCCATCATGGCTC	229546	61742	GCCCCCCGCGGTGCCCTGAA	274133	106329	CACTCCCACTCCCGCAGGCC
184960	17156	GCAGTGGTGCCATCATGGCT	229547	61743	AGCCCCCCGCGGTGCCCTGA	274134	106330	ACACTCCCACTCCCGCAGGC
184961	17157	TGCAGTGGTGCCATCATGGC	229548	61744	AAGCCCCCCGCGGTGCCCTG	274135	106331	CACACTCCCACTCCCGCAGG
184962	17158	GTGCAGTGGTGCCATCATGG	229549	61745	AAAGCCCCCCGCGGTGCCCT	274136	106332	ACACACTCCCACTCCCGCAG
184963	17159	AGTGCAGTGGTGCCATCATG	229550	61746	CAAAGCCCCCCGCGGTGCCC	274137	106333	GACACACTCCCACTCCCGCA
184964	17160	CAGTGCAGTGGTGCCATCAT	229551	61747	CCAAAGCCCCCCGCGGTGCC	274138	106334	GGACACACTCCCACTCCCGC
184965	17161	GCAGTGCAGTGGTGCCATCA	229552	61748	CCCAAAGCCCCCCGCGGTGC	274139	106335	TGGACACACTCCCACTCCCG
184966	17162	TGCAGTGCAGTGGTGCCATC	229553	61749	TCCCAAAGCCCCCCGCGGTG	274140	106336	CTGGACACACTCCCACTCCC
184967	17163	CTGCAGTGCAGTGGTGCCAT	229554	61750	GTCCCAAAGCCCCCCGCGGT	274141	106337	TCTGGACACACTCCCACTCC
184968	17164	GCTGCAGTGCAGTGGTGCCA	229555	61751	AGTCCCAAAGCCCCCCGCGG	274142	106338	GTCTGGACACACTCCCACTC
184969	17165	GGCTGCAGTGCAGTGGTGCC	229556	61752	AAGTCCCAAAGCCCCCCGCG	274143	106339	TGTCTGGACACACTCCCACT
184970	17166	AGGCTGCAGTGCAGTGGTGC	229557	61753	CAAGTCCCAAAGCCCCCCGC	274144	106340	GTGTCTGGACACACTCCCAC
184971	17167	CAGGCTGCAGTGCAGTGGTG	229558	61754	CCAAGTCCCAAAGCCCCCCG	274145	106341	TGTGTCTGGACACACTCCCA
184972	17168	CCAGGCTGCAGTGCAGTGGT	229559	61755	ACCAAGTCCCAAAGCCCCCC	274146	106342	CTGTGTCTGGACACACTCCC
184973	17169	CCCAGGCTGCAGTGCAGTGG	229560	61756	CACCAAGTCCCAAAGCCCCC	274147	106343	TCTGTGTCTGGACACACTCC
184974	17170	GCCCAGGCTGCAGTGCAGTG	229561	61757	TCACCAAGTCCCAAAGCCCC	274148	106344	CTCTGTGTCTGGACACACTC
184975	17171	CGCCCAGGCTGCAGTGCAGT	229562	61758	ATCACCAAGTCCCAAAGCCC	274149	106345	TCTCTGTGTCTGGACACACT
184976	17172	ACGCCCAGGCTGCAGTGCAG	229563	61759	CATCACCAAGTCCCAAAGCC	274150	106346	GTCTCTGTGTCTGGACACAC
184977	17173	GACGCCCAGGCTGCAGTGCA	229564	61760	TCATCACCAAGTCCCAAAGC	274151	106347	TGTCTCTGTGTCTGGACACA
184978	17174	TGACGCCCAGGCTGCAGTGC	229565	61761	TTCATCACCAAGTCCCAAAG	274152	106348	TTGTCTCTGTGTCTGGACAC
184979	17175	CTGACGCCCAGGCTGCAGTG	229566	61762	GTTCATCACCAAGTCCCAAA	274153	106349	TTTGTCTCTGTGTCTGGACA
184980	17176	TCTGACGCCCAGGCTGCAGT	229567	61763	TGTTCATCACCAAGTCCCAA	274154	106350	CTTTGTCTCTGTGTCTGGAC
184981	17177	TTCTGACGCCCAGGCTGCAG	229568	61764	GTGTTCATCACCAAGTCCCA	274155	106351	CCTTTGTCTCTGTGTCTGGA
184982	17178	GTTCTGACGCCCAGGCTGCA	229569	61765	TGTGTTCATCACCAAGTCCC	274156	106352	TCCTTTGTCTCTGTGTCTGG
184983	17179	CGTTCTGACGCCCAGGCTGC	229570	61766	CTGTGTTCATCACCAAGTCC	274157	106353	GTCCTTTGTCTCTGTGTCTG
184984	17180	TCGTTCTGACGCCCAGGCTG	229571	61767	GCTGTGTTCATCACCAAGTC	274158	106354	GGTCCTTTGTCTCTGTGTCT
184985	17181	CTCGTTCTGACGCCCAGGCT	229572	61768	TGCTGTGTTCATCACCAAGT	274159	106355	TGGTCCTTTGTCTCTGTGTC
184986	17182	TCTCGTTCTGACGCCCAGGC	229573	61769	GTGCTGTGTTCATCACCAAG	274160	106356	CTGGTCCTTTGTCTCTGTGT
184987	17183	GTCTCGTTCTGACGCCCAGG	229574	61770	TGTGCTGTGTTCATCACCAA	274161	106357	GCTGGTCCTTTGTCTCTGTG
184988	17184	GGTCTCGTTCTGACGCCCAG	229575	61771	CTGTGCTGTGTTCATCACCA	274162	106358	AGCTGGTCCTTTGTCTCTGT
184989	17185	AGGTCTCGTTCTGACGCCCA	229576	61772	TCTGTGCTGTGTTCATCACC	274163	106359	AAGCTGGTCCTTTGTCTCTG
184990	17186	CAGGTCTCGTTCTGACGCCC	229577	61773	CTCTGTGCTGTGTTCATCAC	274164	106360	AAAGCTGGTCCTTTGTCTCT
184991	17187	GCAGGTCTCGTTCTGACGCC	229578	61774	TCTCTGTGCTGTGTTCATCA	274165	106361	AAAAGCTGGTCCTTTGTCTC
184992	17188	AGCAGGTCTCGTTCTGACGC	229579	61775	CTCTCTGTGCTGTGTTCATC	274166	106362	TAAAAGCTGGTCCTTTGTCT
184993	17189	GAGCAGGTCTCGTTCTGACG	229580	61776	GCTCTCTGTGCTGTGTTCAT	274167	106363	TTAAAAGCTGGTCCTTTGTC
184994	17190	AGAGCAGGTCTCGTTCTGAC	229581	61777	AGCTCTCTGTGCTGTGTTCA	274168	106364	TTTAAAAGCTGGTCCTTTGT
184995	17191	GAGAGCAGGTCTCGTTCTGA	229582	61778	CAGCTCTCTGTGCTGTGTTC	274169	106365	TTTTAAAAGCTGGTCCTTTG
184996	17192	TGAGAGCAGGTCTCGTTCTG	229583	61779	ACAGCTCTCTGTGCTGTGTT	274170	106366	GTTTTAAAAGCTGGTCCTTT
184997	17193	TTGAGAGCAGGTCTCGTTCT	229584	61780	GACAGCTCTCTGTGCTGTGT	274171	106367	TGTTTTAAAAGCTGGTCCTT
184998	17194	TTTGAGAGCAGGTCTCGTTC	229585	61781	GGACAGCTCTCTGTGCTGTG	274172	106368	ATGTTTTAAAAGCTGGTCCT
184999	17195	TTTTGAGAGCAGGTCTCGTT	229586	61782	TGGACAGCTCTCTGTGCTGT	274173	106369	AATGTTTTAAAAGCTGGTCC
185000	17196	TTTTTGAGAGCAGGTCTCGT	229587	61783	CTGGACAGCTCTCTGTGCTG	274174	106370	AAATGTTTTAAAAGCTGGTC
185001	17197	TTTTTTGAGAGCAGGTCTCG	229588	61784	GCTGGACAGCTCTCTGTGCT	274175	106371	AAAATGTTTTAAAAGCTGGT
185002	17198	TTTTTTTGAGAGCAGGTCTC	229589	61785	TGCTGGACAGCTCTCTGTGC	274176	106372	CAAAATGTTTTAAAAGCTGG
185003	17199	GTTTTTTTGAGAGCAGGTCT	229590	61786	ATGCTGGACAGCTCTCTGTG	274177	106373	ACAAAATGTTTTAAAAGCTG
185004	17200	TGTTTTTTTGAGAGCAGGTC	229591	61787	CATGCTGGACAGCTCTCTGT	274178	106374	AACAAAATGTTTTAAAAGCT
185005	17201	TTGTTTTTTTGAGAGCAGGT	229592	61788	GCATGCTGGACAGCTCTCTG	274179	106375	CAACAAAATGTTTTAAAAGC
185006	17202	TTTGTTTTTTTGAGAGCAGG	229593	61789	CGCATGCTGGACAGCTCTCT	274180	106376	CCAACAAAATGTTTTAAAAG
185007	17203	GTTTGTTTTTTTGAGAGCAG	229594	61790	CCGCATGCTGGACAGCTCTC	274181	106377	CCCAACAAAATGTTTTAAAA
185008	17204	TGTTTGTTTTTTTGAGAGCA	229595	61791	CCCGCATGCTGGACAGCTCT	274182	106378	CCCCAACAAAATGTTTTAAA
185009	17205	TTGTTTGTTTTTTTGAGAGC	229596	61792	ACCCGCATGCTGGACAGCTC	274183	106379	GCCCCAACAAAATGTTTTAA
185010	17206	TTTGTTTGTTTTTTTGAGAG	229597	61793	GACCCGCATGCTGGACAGCT	274184	106380	GGCCCCAACAAAATGTTTTA

185011	17207	GTTTGTTTGTTTTTTTGAGA	229598	61794	GGACCCGCATGCTGGACAGC	274185	106381	TGGCCCCAACAAAATGTTTT
185012	17208	TGTTTGTTTGTTTTTTGAG	229599	61795	GGGACCCGCATGCTGGACAG	274186	106382	CTGGCCCCAACAAAATGTTT
185013	17209	TTGTTTGTTTGTTTTTTTGA	229600	61796	AGGGACCCGCATGCTGGACA	274187	106383	CCTGGCCCCAACAAAATGTT
185014	17210	GTTGTTTGTTTGTTTTTTTG	229601	61797	CAGGGACCCGCATGCTGGAC	274188	106384	ACCTGGCCCCAACAAAATGT
185015	17211	TGTTGTTTGTTTGTTTTTTT	229602	61798	CCAGGGACCCGCATGCTGGA	274189	106385	CACCTGGCCCCAACAAAATG
185016	17212	TTGTTGTTTGTTTGTTTTTT	229603	61799	GCCAGGGACCCGCATGCTGG	274190	106386	ACACCTGGCCCCAACAAAAT
185017	17213	TTTGTTGTTTGTTTGTTTTT	229604	61800	AGCCAGGGACCCGCATGCTG	274191	106387	CACACCTGGCCCCAACAAAA
185018	17214	TTTTGTTGTTTGTTTGTTTT	229605	61801	AAGCCAGGGACCCGCATGCT	274192	106388	CCACACCTGGCCCCAACAAA
185019	17215	TTTTTGTTGTTTGTTTGTTT	229606	61802	GAAGCCAGGGACCCGCATGC	274193	106389	ACCACACCTGGCCCCAACAA
185020	17216	TTTTTTGTTGTTTGTTTGTT	229607	61803	AGAAGCCAGGGACCCGCATG	274194	106390	CACCACACCTGGCCCCAACA
185021	17217	TTTTTTTGTTGTTTGTTTGT	229608	61804	GAGAAGCCAGGGACCCGCAT	274195	106391	CCACCACACCTGGCCCCAAC
185022	17218	TTTTTTTTGTTGTTTGTTTG	229609	61805	TGAGAAGCCAGGGACCCGCA	274196	106392	GCCACCACACCTGGCCCCAA
185023	17219	TTTTTTTTTGTTGTTTGTTT	229610	61806	GTGAGAAGCCAGGGACCCGC	274197	106393	AGCCACCACACCTGGCCCCA
185024	17220	CTTTTTTTTTGTTGTTTGTT	229611	61807	TGTGAGAAGCCAGGGACCCG	274198	106394	GAGCCACCACACCTGGCCCC
185025	17221	CCTTTTTTTTTGTTGTTTGT	229612	61808	GTGTGAGAAGCCAGGGACCC	274199	106395	TGAGCCACCACACCTGGCCC
185026	17222	GCCTTTTTTTTTGTTGTTTG	229613	61809	AGTGTGAGAAGCCAGGGACC	274200	106396	GTGAGCCACCACACCTGGCC
185027	17223	AGCCTTTTTTTTTGTTGTTT	229614	61810	AAGTGTGAGAAGCCAGGGAC	274201	106397	TGTGAGCCACCACACCTGGC
185028	17224	AAGCCTTTTTTTTTGTTGTT	229615	61811	GAAGTGTGAGAAGCCAGGGA	274202	106398	GTGTGAGCCACCACACCTGG
185029	17225	AAAGCCTTTTTTTTTGTTGT	229616	61812	GGAAGTGTGAGAAGCCAGGG	274203	106399	GGTGTGAGCCACCACACCTG
185030	17226	GAAAGCCTTTTTTTTTGTTG	229617	61813	GGGAAGTGTGAGAAGCCAGG	274204	106400	AGGTGTGAGCCACCACACCT
185031	17227	AGAAAGCCTTTTTTTTTGTT	229618	61814	TGGGAAGTGTGAGAAGCCAG	274205	106401	TAGGTGTGAGCCACCACACC
185032	17228	AAGAAAGCCTTTTTTTTTGT	229619	61815	CTGGGAAGTGTGAGAAGCCA	274206	106402	TTAGGTGTGAGCCACCACAC
185033	17229	TAAGAAAGCCTTTTTTTTTG	229620	61816	CCTGGGAAGTGTGAGAAGCC	274207	106403	ATTAGGTGTGAGCCACCACA
185034	17230	TTAAGAAAGCCTTTTTTTTT	229621	61817	GCCTGGGAAGTGTGAGAAGC	274208	106404	GATTAGGTGTGAGCCACCAC
185035	17231	TTTAAGAAAGCCTTTTTTTT	229622	61818	AGCCTGGGAAGTGTGAGAAG	274209	106405	GGATTAGGTGTGAGCCACCA
185036	17232	CTTTAAGAAAGCCTTTTTTT	229623	61819	GAGCCTGGGAAGTGTGAGAA	274210	106406	GGGATTAGGTGTGAGCCACC
185037	17233	TCTTTAAGAAAGCCTTTTTT	229624	61820	GGAGCCTGGGAAGTGTGAGA	274211	106407	TGGGATTAGGTGTGAGCCAC
185038	17234	CTCTTTAAGAAAGCCTTTTT	229625	61821	AGGAGCCTGGGAAGTGTGAG	274212	106408	TTGGGATTAGGTGTGAGCCA
185039	17235	TCTCTTTAAGAAAGCCTTTT	229626	61822	AAGGAGCCTGGGAAGTGTGA	274213	106409	GTTGGGATTAGGTGTGAGCC
185040	17236	GTCTCTTTAAGAAAGCCTTT	229627	61823	GAAGGAGCCTGGGAAGTGTG	274214	106410	TGTTGGGATTAGGTGTGAGC
185041	17237	AGTCTCTTTAAGAAAGCCTT	229628	61824	TGAAGGAGCCTGGGAAGTGT	274215	106411	GTGTTGGGATTAGGTGTGAG
185042	17238	AAGTCTCTTTAAGAAAGCCT	229629	61825	CTGAAGGAGCCTGGGAAGTG	274216	106412	GGTGTTGGGATTAGGTGTGA
185043	17239	CAAGTCTCTTTAAGAAAGCC	229630	61826	TCTGAAGGAGCCTGGGAAGT	274217	106413	AGGTGTTGGGATTAGGTGTG
185044	17240	TCAAGTCTCTTTAAGAAAGC	229631	61827	CTCTGAAGGAGCCTGGGAAG	274218	106414	CAGGTGTTGGGATTAGGTGT
185045	17241	CTCAAGTCTCTTTAAGAAAG	229632	61828	CCTCTGAAGGAGCCTGGGAA	274219	106415	CCAGGTGTTGGGATTAGGTG
185046	17242	TCTCAAGTCTCTTTAAGAAA	229633	61829	GCCTCTGAAGGAGCCTGGGA	274220	106416	CCCAGGTGTTGGGATTAGGT
185047	17243	TTCTCAAGTCTCTTTAAGAA	229634	61830	AGCCTCTGAAGGAGCCTGGG	274221	106417	CCCCAGGTGTTGGGATTAGG
185048	17244	GTTCTCAAGTCTCTTTAAGA	229635	61831	GAGCCTCTGAAGGAGCCTGG	274222	106418	TCCCCAGGTGTTGGGATTAG
185049	17245	TGTTCTCAAGTCTCTTTAAG	229636	61832	AGAGCCTCTGAAGGAGCCTG	274223	106419	CTCCCCAGGTGTTGGGATTA
185050	17246	CTGTTCTCAAGTCTCTTTAA	229637	61833	GAGAGCCTCTGAAGGAGCCT	274224	106420	CCTCCCCAGGTGTTGGGATT
185051	17247	TCTGTTCTCAAGTCTCTTTA	229638	61834	AGAGAGCCTCTGAAGGAGCC	274225	106421	GCCTCCCCAGGTGTTGGGAT
185052	17248	TTCTGTTCTCAAGTCTCTTT	229639	61835	GAGAGAGCCTCTGAAGGAGC	274226	106422	GGCCTCCCCAGGTGTTGGGA
185053	17249	TTTCTGTTCTCAAGTCTCTT	229640	61836	GGAGAGAGCCTCTGAAGGAG	274227	106423	TGGCCTCCCCAGGTGTTGGG
185054	17250	CTTTCTGTTCTCAAGTCTCT	229641	61837	TGGAGAGAGCCTCTGAAGGA	274228	106424	TTGGCCTCCCCAGGTGTTGG
185055	17251	CCTTTCTGTTCTCAAGTCTC	229642	61838	TTGGAGAGAGCCTCTGAAGG	274229	106425	CTTGGCCTCCCCAGGTGTTG
185056	17252	CCCTTTCTGTTCTCAAGTCT	229643	61839	TTTGGAGAGAGCCTCTGAAG	274230	106426	CCTTGGCCTCCCCAGGTGTT
185057	17253	CCCCTTTCTGTTCTCAAGTC	229644	61840	CTTTGGAGAGAGCCTCTGAA	274231	106427	GCCTTGGCCTCCCCAGGTGT
185058	17254	TCCCCTTTCTGTTCTCAAGT	229645	61841	CCTTTGGAGAGAGCCTCTGA	274232	106428	TGCCTTGGCCTCCCCAGGTG
185059	17255	TTCCCCTTTCTGTTCTCAAG	229646	61842	CCCTTTGGAGAGAGCCTCTG	274233	106429	CTGCCTTGGCCTCCCCAGGT
185060	17256	GTTCCCCTTTCTGTTCTCAA	229647	61843	TCCCTTTGGAGAGAGCCTCT	274234	106430	TCTGCCTTGGCCTCCCCAGG
185061	17257	TGTTCCCCTTTCTGTTCTCA	229648	61844	CTCCCTTTGGAGAGAGCCTC	274235	106431	TTCTGCCTTGGCCTCCCCAG
185062	17258	CTGTTCCCCTTTCTGTTCTC	229649	61845	GCTCCCTTTGGAGAGAGCCT	274236	106432	CTTCTGCCTTGGCCTCCCCA
185063	17259	TCTGTTCCCCTTTCTGTTCT	229650	61846	AGCTCCCTTTGGAGAGAGCC	274237	106433	CCTTCTGCCTTGGCCTCCCC
185064	17260	ATCTGTTCCCCTTTCTGTTC	229651	61847	CAGCTCCCTTTGGAGAGAGC	274238	106434	TCCTTCTGCCTTGGCCTCCC
185065	17261	TATCTGTTCCCCTTTCTGTT	229652	61848	GCAGCTCCCTTTGGAGAGAG	274239	106435	ATCCTTCTGCCTTGGCCTCC
185066	17262	GTATCTGTTCCCCTTTCTGT	229653	61849	AGCAGCTCCCTTTGGAGAGA	274240	106436	GATCCTTCTGCCTTGGCCTC
185067	17263	TGTATCTGTTCCCCTTTCTG	229654	61850	GAGCAGCTCCCTTTGGAGAG	274241	106437	TGATCCTTCTGCCTTGGCCT
185068	17264	ATGTATCTGTTCCCCTTTCT	229655	61851	AGAGCAGCTCCCTTTGGAGA	274242	106438	GTGATCCTTCTGCCTTGGCC
185069	17265	TATGTATCTGTTCCCCTTTC	229656	61852	GAGAGCAGCTCCCTTTGGAG	274243	106439	AGTGATCCTTCTGCCTTGGC
185070	17266	TTATGTATCTGTTCCCCTTT	229657	61853	AGAGAGCAGCTCCCTTTGGA	274244	106440	AAGTGATCCTTCTGCCTTGG
185071	17267	GTTATGTATCTGTTCCCCTT	229658	61854	GAGAGAGCAGCTCCCTTTGG	274245	106441	CAAGTGATCCTTCTGCCTTG
185072	17268	AGTTATGTATCTGTTCCCCT	229659	61855	AGAGAGAGCAGCTCCCTTTG	274246	106442	TCAAGTGATCCTTCTGCCTT
185073	17269	AAGTTATGTATCTGTTCCCC	229660	61856	TAGAGAGAGCAGCTCCCTTT	274247	106443	CTCAAGTGATCCTTCTGCCT
185074	17270	TAAGTTATGTATCTGTTCCC	229661	61857	CTAGAGAGAGCAGCTCCCTT	274248	106444	ACTCAAGTGATCCTTCTGCC
185075	17271	ATAAGTTATGTATCTGTTCC	229662	61858	TCTAGAGAGAGCAGCTCCCT	274249	106445	GACTCAAGTGATCCTTCTGC
185076	17272	TATAAGTTATGTATCTGTTC	229663	61859	TTCTAGAGAGAGCAGCTCCC	274250	106446	GGACTCAAGTGATCCTTCTG
185077	17273	ATATAAGTTATGTATCTGTT	229664	61860	GTTCTAGAGAGAGCAGCTCC	274251	106447	TGGACTCAAGTGATCCTTCT
185078	17274	TATATAAGTTATGTATCTGT	229665	61861	GGTTCTAGAGAGAGCAGCTC	274252	106448	CTGGACTCAAGTGATCCTTC
185079	17275	ATATATAAGTTATGTATCTG	229666	61862	GGGTTCTAGAGAGAGCAGCT	274253	106449	CCTGGACTCAAGTGATCCTT
185080	17276	AATATATAAGTTATGTATCT	229667	61863	TGGGTTCTAGAGAGAGCAGC	274254	106450	TCCTGGACTCAAGTGATCCT
185081	17277	AAATATATAAGTTATGTATC	229668	61864	ATGGGTTCTAGAGAGAGCAG	274255	106451	CTCCTGGACTCAAGTGATCC
185082	17278	TAAATATATAAGTTATGTAT	229669	61865	CATGGGTTCTAGAGAGAGCA	274256	106452	ACTCCTGGACTCAAGTGATC

185083	17279	ATAAATATATAAGTTATGTA	229670	61866	TCATGGGTTCTAGAGAGAGC	274257	106453	AACTCCTGGACTCAAGTGAT
185084	17280	AATAAATATATAAGTTATGT	229671	61867	TTCATGGGTTCTAGAGAGAG	274258	106454	GAACTCCTGGACTCAAGTGA
185085	17281	AAATAAATATATAAGTTATG	229672	61868	ATTCATGGGTTCTAGAGAGA	274259	106455	TGAACTCCTGGACTCAAGTG
185086	17282	CAAATAAATATATAAGTTAT	229673	61869	AATTCATGGGTTCTAGAGAG	274260	106456	TTGAACTCCTGGACTCAAGT
185087	17283	ACAAATAAATATATAAGTTA	229674	61870	AAATTCATGGGTTCTAGAGA	274261	106457	CTTGAACTCCTGGACTCAAG
185088	17284	AACAAATAAATATATAAGTT	229675	61871	CAAATTCATGGGTTCTAGAG	274262	106458	TCTTGAACTCCTGGACTCAA
185089	17285	GAACAAATAAATATATAAGT	229676	61872	CCAAATTCATGGGTTCTAGA	274263	106459	GTCTTGAACTCCTGGACTCA
185090	17286	TGAACAAATAAATATATAAG	229677	61873	TCCAAATTCATGGGTTCTAG	274264	106460	GGTCTTGAACTCCTGGACTC
185091	17287	ATGAACAAATAAATATATAA	229678	61874	TTCCAAATTCATGGGTTCTA	274265	106461	TGGTCTTGAACTCCTGGACT
185092	17288	GATGAACAAATAAATATATA	229679	61875	ATTCCAAATTCATGGGTTCT	274266	106462	CTGGTCTTGAACTCCTGGAC
185093	17289	AGATGAACAAATAAATATAT	229680	61876	TATTCCAAATTCATGGGTTC	274267	106463	GCTGGTCTTGAACTCCTGGA
185094	17290	AAGATGAACAAATAAATATA	229681	61877	ATATTCCAAATTCATGGGTT	274268	106464	GGCTGGTCTTGAACTCCTGG
185095	17291	AAAGATGAACAAATAAATAT	229682	61878	TATATTCCAAATTCATGGGT	274269	106465	AGGCTGGTCTTGAACTCCTG
185096	17292	GAAAGATGAACAAATAAATA	229683	61879	CTATATTCCAAATTCATGGG	274270	106466	CAGGCTGGTCTTGAACTCCT
185097	17293	GGAAAGATGAACAAATAAAT	229684	61880	CCTATATTCCAAATTCATGG	274271	106467	CCAGGCTGGTCTTGAACTCC
185098	17294	TGGAAAGATGAACAAATAAA	229685	61881	GCCTATATTCCAAATTCATG	274272	106468	CCCAGGCTGGTCTTGAACTC
185099	17295	GTGGAAAGATGAACAAATAA	229686	61882	TGCCTATATTCCAAATTCAT	274273	106469	GCCCAGGCTGGTCTTGAACT
185100	17296	GGTGGAAAGATGAACAAATA	229687	61883	TTGCCTATATTCCAAATTCA	274274	106470	TGCCCAGGCTGGTCTTGAAC
185101	17297	AGGTGGAAAGATGAACAAAT	229688	61884	GTTGCCTATATTCCAAATTC	274275	106471	TTGCCCAGGCTGGTCTTGAA
185102	17298	AAGGTGGAAAGATGAACAAA	229689	61885	GGTTGCCTATATTCCAAATT	274276	106472	GTTGCCCAGGCTGGTCTTGA
185103	17299	GAAGGTGGAAAGATGAACAA	229690	61886	TGGTTGCCTATATTCCAAAT	274277	106473	TGTTGCCCAGGCTGGTCTTG
185104	17300	GGAAGGTGGAAAGATGAACA	229691	61887	GTGGTTGCCTATATTCCAAA	274278	106474	ATGTTGCCCAGGCTGGTCTT
185105	17301	AGGAAGGTGGAAAGATGAAC	229692	61888	AGTGGTTGCCTATATTCCAA	274279	106475	TATGTTGCCCAGGCTGGTCT
185106	17302	CAGGAAGGTGGAAAGATGAA	229693	61889	CAGTGGTTGCCTATATTCCA	274280	106476	CTATGTTGCCCAGGCTGGTC
185107	17303	CCAGGAAGGTGGAAAGATGA	229694	61890	GCAGTGGTTGCCTATATTCC	274281	106477	CCTATGTTGCCCAGGCTGGT
185108	17304	TCCAGGAAGGTGGAAAGATG	229695	61891	TGCAGTGGTTGCCTATATTC	274282	106478	CCCTATGTTGCCCAGGCTGG
185109	17305	CTCCAGGAAGGTGGAAAGAT	229696	61892	ATGCAGTGGTTGCCTATATT	274283	106479	TCCCTATGTTGCCCAGGCTG
185110	17306	CCTCCAGGAAGGTGGAAAGA	229697	61893	AATGCAGTGGTTGCCTATAT	274284	106480	CTCCCTATGTTGCCCAGGCT
185111	17307	CCCTCCAGGAAGGTGGAAAG	229698	61894	CAATGCAGTGGTTGCCTATA	274285	106481	TCTCCCTATGTTGCCCAGGC
185112	17308	ACCCTCCAGGAAGGTGGAAA	229699	61895	CCAATGCAGTGGTTGCCTAT	274286	106482	GTCTCCCTATGTTGCCCAGG
185113	17309	CACCCTCCAGGAAGGTGGAA	229700	61896	CCCAATGCAGTGGTTGCCTA	274287	106483	GGTCTCCCTATGTTGCCCAG
185114	17310	CCACCCTCCAGGAAGGTGGA	229701	61897	CCCCAATGCAGTGGTTGCCT	274288	106484	GGGTCTCCCTATGTTGCCCA
185115	17311	TCCACCCTCCAGGAAGGTGG	229702	61898	TCCCCAATGCAGTGGTTGCC	274289	106485	AGGGTCTCCCTATGTTGCCC
185116	17312	CTCCACCCTCCAGGAAGGTG	229703	61899	GTCCCCAATGCAGTGGTTGC	274290	106486	CAGGGTCTCCCTATGTTGCC
185117	17313	CCTCCACCCTCCAGGAAGGT	229704	61900	GGTCCCCAATGCAGTGGTTG	274291	106487	ACAGGGTCTCCCTATGTTGC
185118	17314	CCCTCCACCCTCCAGGAAGG	229705	61901	TGGTCCCCAATGCAGTGGTT	274292	106488	GACAGGGTCTCCCTATGTTG
185119	17315	CCCCTCCACCCTCCAGGAAG	229706	61902	GTGGTCCCCAATGCAGTGGT	274293	106489	AGACAGGGTCTCCCTATGTT
185120	17316	TCCCCTCCACCCTCCAGGAA	229707	61903	AGTGGTCCCCAATGCAGTGG	274294	106490	GAGACAGGGTCTCCCTATGT
185121	17317	TTCCCCTCCACCCTCCAGGA	229708	61904	CAGTGGTCCCCAATGCAGTG	274295	106491	AGAGACAGGGTCTCCCTATG
185122	17318	GTTCCCCTCCACCCTCCAGG	229709	61905	TCAGTGGTCCCCAATGCAGT	274296	106492	TAGAGACAGGGTCTCCCTAT
185123	17319	TGTTCCCCTCCACCCTCCAG	229710	61906	GTCAGTGGTCCCCAATGCAG	274297	106493	GTAGAGACAGGGTCTCCCTA
185124	17320	CTGTTCCCCTCCACCCTCCA	229711	61907	GGTCAGTGGTCCCCAATGCA	274298	106494	TGTAGAGACAGGGTCTCCCT
185125	17321	CCTGTTCCCCTCCACCCTCC	229712	61908	AGGTCAGTGGTCCCCAATGC	274299	106495	TTGTAGAGACAGGGTCTCCC
185126	17322	ACCTGTTCCCCTCCACCCTC	229713	61909	GAGGTCAGTGGTCCCCAATG	274300	106496	ATTGTAGAGACAGGGTCTCC
185127	17323	GACCTGTTCCCCTCCACCCT	229714	61910	TGAGGTCAGTGGTCCCCAAT	274301	106497	AATTGTAGAGACAGGGTCTC
185128	17324	AGACCTGTTCCCCTCCACCC	229715	61911	TTGAGGTCAGTGGTCCCCAA	274302	106498	AAATTGTAGAGACAGGGTCT
185129	17325	CAGACCTGTTCCCCTCCACC	229716	61912	TTTGAGGTCAGTGGTCCCCA	274303	106499	AAAATTGTAGAGACAGGGTC
185130	17326	ACAGACCTGTTCCCCTCCAC	229717	61913	GTTTGAGGTCAGTGGTCCCC	274304	106500	AAAAATTGTAGAGACAGGGT
185131	17327	TACAGACCTGTTCCCCTCCA	229718	61914	TGTTTGAGGTCAGTGGTCCC	274305	106501	AAAAAATTGTAGAGACAGGG
185132	17328	ATACAGACCTGTTCCCCTCC	229719	61915	ATGTTTGAGGTCAGTGGTCC	274306	106502	AAAAAAATTGTAGAGACAGG
185133	17329	AATACAGACCTGTTCCCCTC	229720	61916	TATGTTTGAGGTCAGTGGTC	274307	106503	AAAAAAAATTGTAGAGACAG
185134	17330	AAATACAGACCTGTTCCCCT	229721	61917	CTATGTTTGAGGTCAGTGGT	274308	106504	AAAAAAAAATTGTAGAGACA
185135	17331	CAAATACAGACCTGTTCCCC	229722	61918	TCTATGTTTGAGGTCAGTGG	274309	106505	AAAAAAAAAATTGTAGAGAC
185136	17332	CCAAATACAGACCTGTTCCC	229723	61919	CTCTATGTTTGAGGTCAGTG	274310	106506	TAAAAAAAAAATTGTAGAGA
185137	17333	TCCAAATACAGACCTGTTCC	229724	61920	TCTCTATGTTTGAGGTCAGT	274311	106507	TTAAAAAAAAAATTGTAGAG
185138	17334	CTCCAAATACAGACCTGTTC	229725	61921	GTCTCTATGTTTGAGGTCAG	274312	106508	ATTAAAAAAAAAATTGTAGA
185139	17335	ACTCCAAATACAGACCTGTT	229726	61922	GGTCTCTATGTTTGAGGTCA	274313	106509	AATTAAAAAAAAAATTGTAG
185140	17336	AACTCCAAATACAGACCTGT	229727	61923	TGGTCTCTATGTTTGAGGTC	274314	106510	TAATTAAAAAAAAAATTGTA
185141	17337	AAACTCCAAATACAGACCTG	229728	61924	CTGGTCTCTATGTTTGAGGT	274315	106511	CTAATTAAAAAAAAAATTGT
185142	17338	AAAACTCCAAATACAGACCT	229729	61925	TCTGGTCTCTATGTTTGAGG	274316	106512	GCTAATTAAAAAAAAAATTG
185143	17339	CAAAACTCCAAATACAGACC	229730	61926	CTCTGGTCTCTATGTTTGAG	274317	106513	AGCTAATTAAAAAAAAAATT
185144	17340	TCAAAACTCCAAATACAGAC	229731	61927	GCTCTGGTCTCTATGTTTGA	274318	106514	CAGCTAATTAAAAAAAAAAT
185145	17341	TTCAAAACTCCAAATACAGA	229732	61928	TGCTCTGGTCTCTATGTTTG	274319	106515	CCAGCTAATTAAAAAAAAAA
185146	17342	ATTCAAAACTCCAAATACAG	229733	61929	TTGCTCTGGTCTCTATGTTT	274320	106516	CCCAGCTAATTAAAAAAAAA
185147	17343	CATTCAAAACTCCAAATACA	229734	61930	TTTGCTCTGGTCTCTATGTT	274321	106517	GCCCAGCTAATTAAAAAAAA
185148	17344	GCATTCAAAACTCCAAATAC	229735	61931	ATTTGCTCTGGTCTCTATGT	274322	106518	GGCCCAGCTAATTAAAAAAA
185149	17345	AGCATTCAAAACTCCAAATA	229736	61932	CATTTGCTCTGGTCTCTATG	274323	106519	AGGCCCAGCTAATTAAAAAA
185150	17346	TAGCATTCAAAACTCCAAAT	229737	61933	CCATTTGCTCTGGTCTCTAT	274324	106520	CAGGCCCAGCTAATTAAAAA
185151	17347	TTAGCATTCAAAACTCCAAA	229738	61934	CCCATTTGCTCTGGTCTCTA	274325	106521	ACAGGCCCAGCTAATTAAAA
185152	17348	TTTAGCATTCAAAACTCCAA	229739	61935	CCCCATTTGCTCTGGTCTCT	274326	106522	AACAGGCCCAGCTAATTAAA
185153	17349	TTTTAGCATTCAAAACTCCA	229740	61936	GCCCCATTTGCTCTGGTCTC	274327	106523	CAACAGGCCCAGCTAATTAA
185154	17350	CTTTTAGCATTCAAAACTCC	229741	61937	AGCCCCATTTGCTCTGGTCT	274328	106524	CCAACAGGCCCAGCTAATTA

185155	17351	ACTTTTAGCATTCAAAACTC	229742	61938	GAGCCCCATTTGCTCTGGTC	274329	106525	GCCAACAGGCCCAGCTAATT
185156	17352	CACTTTTAGCATTCAAAACT	229743	61939	TGAGCCCCATTTGCTCTGGT	274330	106526	TGCCAACAGGCCCAGCTAAT
185157	17353	CCACTTTTAGCATTCAAAAC	229744	61940	ATGAGCCCCATTTGCTCTGG	274331	106527	GTGCCAACAGGCCCAGCTAA
185158	17354	CCCACTTTTAGCATTCAAAA	229745	61941	GATGAGCCCCATTTGCTCTG	274332	106528	AGTGCCAACAGGCCCAGCTA
185159	17355	TCCCACTTTTAGCATTCAAA	229746	61942	TGATGAGCCCCATTTGCTCT	274333	106529	GAGTGCCAACAGGCCCAGCT
185160	17356	TTCCCACTTTTAGCATTCAA	229747	61943	GTGATGAGCCCCATTTGCTC	274334	106530	AGAGTGCCAACAGGCCCAGC
185161	17357	ATTCCCACTTTTAGCATTCA	229748	61944	CGTGATGAGCCCCATTTGCT	274335	106531	GAGAGTGCCAACAGGCCCAG
185162	17358	TATTCCCACTTTTAGCATTC	229749	61945	ACGTGATGAGCCCCATTTGC	274336	106532	GGAGAGTGCCAACAGGCCCA
185163	17359	GTATTCCCACTTTTAGCATT	229750	61946	CACGTGATGAGCCCCATTTG	274337	106533	AGGAGAGTGCCAACAGGCCC
185164	17360	TGTATTCCCACTTTTAGCAT	229751	61947	TCACGTGATGAGCCCCATTT	274338	106534	CAGGAGAGTGCCAACAGGCC
185165	17361	ATGTATTCCCACTTTTAGCA	229752	61948	TTCACGTGATGAGCCCCATT	274339	106535	ACAGGAGAGTGCCAACAGGC
185166	17362	CATGTATTCCCACTTTTAGC	229753	61949	TTTCACGTGATGAGCCCCAT	274340	106536	TACAGGAGAGTGCCAACAGG
185167	17363	ACATGTATTCCCACTTTTAG	229754	61950	GTTTCACGTGATGAGCCCCA	274341	106537	CTACAGGAGAGTGCCAACAG
185168	17364	TACATGTATTCCCACTTTTA	229755	61951	AGTTTCACGTGATGAGCCCC	274342	106538	ACTACAGGAGAGTGCCAACA
185169	17365	GTACATGTATTCCCACTTTT	229756	61952	GAGTTTCACGTGATGAGCCC	274343	106539	AACTACAGGAGAGTGCCAAC
185170	17366	AGTACATGTATTCCCACTTT	229757	61953	TGAGTTTCACGTGATGAGCC	274344	106540	GAACTACAGGAGAGTGCCAA
185171	17367	CAGTACATGTATTCCCACTT	229758	61954	ATGAGTTTCACGTGATGAGC	274345	106541	GGAACTACAGGAGAGTGCCA
185172	17368	ACAGTACATGTATTCCCACT	229759	61955	GATGAGTTTCACGTGATGAG	274346	106542	TGGAACTACAGGAGAGTGCC
185173	17369	AACAGTACATGTATTCCCAC	229760	61956	AGATGAGTTTCACGTGATGA	274347	106543	CTGGAACTACAGGAGAGTGC
185174	17370	AAACAGTACATGTATTCCCA	229761	61957	CAGATGAGTTTCACGTGATG	274348	106544	GCTGGAACTACAGGAGAGTG
185175	17371	CAAACAGTACATGTATTCCC	229762	61958	CCAGATGAGTTTCACGTGAT	274349	106545	AGCTGGAACTACAGGAGAGT
185176	17372	GCAAACAGTACATGTATTCC	229763	61959	TCCAGATGAGTTTCACGTGA	274350	106546	TAGCTGGAACTACAGGAGAG
185177	17373	GGCAAACAGTACATGTATTC	229764	61960	TTCCAGATGAGTTTCACGTG	274351	106547	GTAGCTGGAACTACAGGAGA
185178	17374	TGGCAAACAGTACATGTATT	229765	61961	GTTCCAGATGAGTTTCACGT	274352	106548	AGTAGCTGGAACTACAGGAG
185179	17375	ATGGCAAACAGTACATGTAT	229766	61962	AGTTCCAGATGAGTTTCACG	274353	106549	GAGTAGCTGGAACTACAGGA
185180	17376	CATGGCAAACAGTACATGTA	229767	61963	GAGTTCCAGATGAGTTTCAC	274354	106550	AGAGTAGCTGGAACTACAGG
185181	17377	TCATGGCAAACAGTACATGT	229768	61964	AGAGTTCCAGATGAGTTTCA	274355	106551	TAGAGTAGCTGGAACTACAG
185182	17378	ATCATGGCAAACAGTACATG	229769	61965	TAGAGTTCCAGATGAGTTTC	274356	106552	CTAGAGTAGCTGGAACTACA
185183	17379	GATCATGGCAAACAGTACAT	229770	61966	CTAGAGTTCCAGATGAGTTT	274357	106553	TCTAGAGTAGCTGGAACTAC
185184	17380	AGATCATGGCAAACAGTACA	229771	61967	GCTAGAGTTCCAGATGAGTT	274358	106554	CTCTAGAGTAGCTGGAACTA
185185	17381	CAGATCATGGCAAACAGTAC	229772	61968	TGCTAGAGTTCCAGATGAGT	274359	106555	CCTCTAGAGTAGCTGGAACT
185186	17382	ACAGATCATGGCAAACAGTA	229773	61969	CTGCTAGAGTTCCAGATGAG	274360	106556	GCCTCTAGAGTAGCTGGAAC
185187	17383	AACAGATCATGGCAAACAGT	229774	61970	CCTGCTAGAGTTCCAGATGA	274361	106557	AGCCTCTAGAGTAGCTGGAA
185188	17384	GAACAGATCATGGCAAACAG	229775	61971	ACCTGCTAGAGTTCCAGATG	274362	106558	CAGCCTCTAGAGTAGCTGGA
185189	17385	TGAACAGATCATGGCAAACA	229776	61972	AACCTGCTAGAGTTCCAGAT	274363	106559	TCAGCCTCTAGAGTAGCTGG
185190	17386	TTGAACAGATCATGGCAAAC	229777	61973	GAACCTGCTAGAGTTCCAGA	274364	106560	CTCAGCCTCTAGAGTAGCTG
185191	17387	TTTGAACAGATCATGGCAAA	229778	61974	AGAACCTGCTAGAGTTCCAG	274365	106561	CCTCAGCCTCTAGAGTAGCT
185192	17388	TTTTGAACAGATCATGGCAA	229779	61975	AAGAACCTGCTAGAGTTCCA	274366	106562	ACCTCAGCCTCTAGAGTAGC
185193	17389	CTTTTGAACAGATCATGGCA	229780	61976	AAAGAACCTGCTAGAGTTCC	274367	106563	CACCTCAGCCTCTAGAGTAG
185194	17390	ACTTTTGAACAGATCATGGC	229781	61977	AAAAGAACCTGCTAGAGTTC	274368	106564	CCACCTCAGCCTCTAGAGTA
185195	17391	AACTTTTGAACAGATCATGG	229782	61978	TAAAAGAACCTGCTAGAGTT	274369	106565	CCCACCTCAGCCTCTAGAGT
185196	17392	TAACTTTTGAACAGATCATG	229783	61979	ATAAAAGAACCTGCTAGAGT	274370	106566	TCCCACCTCAGCCTCTAGAG
185197	17393	TTAACTTTTGAACAGATCAT	229784	61980	TATAAAAGAACCTGCTAGAG	274371	106567	CTCCCACCTCAGCCTCTAGA
185198	17394	CTTAACTTTTGAACAGATCA	229785	61981	ATATAAAAGAACCTGCTAGA	274372	106568	CCTCCCACCTCAGCCTCTAG
185199	17395	GCTTAACTTTTGAACAGATC	229786	61982	TATATAAAAGAACCTGCTAG	274373	106569	TCCTCCCACCTCAGCCTCTA
185200	17396	GGCTTAACTTTTGAACAGAT	229787	61983	ATATATAAAAGAACCTGCTA	274374	106570	GTCCTCCCACCTCAGCCTCT
185201	17397	TGGCTTAACTTTTGAACAGA	229788	61984	TATATATAAAAGAACCTGCT	274375	106571	AGTCCTCCCACCTCAGCCTC
185202	17398	TTGGCTTAACTTTTGAACAG	229789	61985	ATATATATAAAAGAACCTGC	274376	106572	CAGTCCTCCCACCTCAGCCT
185203	17399	TTTGGCTTAACTTTTGAACA	229790	61986	TATATATATAAAAGAACCTG	274377	106573	GCAGTCCTCCCACCTCAGCC
185204	17400	ATTTGGCTTAACTTTTGAAC	229791	61987	ATATATATATAAAAGAACCT	274378	106574	AGCAGTCCTCCCACCTCAGC
185205	17401	CATTTGGCTTAACTTTTGAA	229792	61988	TATATATATATAAAAGAACC	274379	106575	AAGCAGTCCTCCCACCTCAG
185206	17402	GCATTTGGCTTAACTTTTGA	229793	61989	ATATATATATATAAAAGAAC	274380	106576	CAAGCAGTCCTCCCACCTCA
185207	17403	GGCATTTGGCTTAACTTTTG	229794	61990	TATATATATATATAAAAGAA	274381	106577	TCAAGCAGTCCTCCCACCTC
185208	17404	AGGCATTTGGCTTAACTTTT	229795	61991	ATATATATATATATAAAAGA	274382	106578	CTCAAGCAGTCCTCCCACCT
185209	17405	AAGGCATTTGGCTTAACTTT	229796	61992	TATATATATATATATAAAAG	274383	106579	GCTCAAGCAGTCCTCCCACC
185210	17406	TAAGGCATTTGGCTTAACTT	229797	61993	ATATATATATATATATAAAA	274384	106580	GGCTCAAGCAGTCCTCCCAC
185211	17407	CTAAGGCATTTGGCTTAACT	229798	61994	TATATATATATATATATAAA	274385	106581	AGGCTCAAGCAGTCCTCCCA
185212	17408	TCTAAGGCATTTGGCTTAAC	229799	61995	ATATATATATATATATATAA	274386	106582	CAGGCTCAAGCAGTCCTCCC
185213	17409	ATCTAAGGCATTTGGCTTAA	229800	61996	TATATATATATATATATATA	274387	106583	CCAGGCTCAAGCAGTCCTCC
185214	17410	AATCTAAGGCATTTGGCTTA	229801	61997	ATATATATATATATATATAT	274388	106584	CCCAGGCTCAAGCAGTCCTC
185215	17411	GAATCTAAGGCATTTGGCTT	229802	61998	TATATATATATATATATATA	274389	106585	TCCCAGGCTCAAGCAGTCCT
185216	17412	AGAATCTAAGGCATTTGGCT	229803	61999	ATATATATATATATATATAT	274390	106586	CTCCCAGGCTCAAGCAGTCC
185217	17413	GAGAATCTAAGGCATTTGGC	229804	62000	TATATATATATATATATATA	274391	106587	CCTCCCAGGCTCAAGCAGTC
185218	17414	GGAGAATCTAAGGCATTTGG	229805	62001	ATATATATATATATATATAT	274392	106588	ACCTCCCAGGCTCAAGCAGT
185219	17415	AGGAGAATCTAAGGCATTTG	229806	62002	TATATATATATATATATATA	274393	106589	GACCTCCCAGGCTCAAGCAG
185220	17416	CAGGAGAATCTAAGGCATTT	229807	62003	ATATATATATATATATATAT	274394	106590	TGACCTCCCAGGCTCAAGCA
185221	17417	TCAGGAGAATCTAAGGCATT	229808	62004	TATATATATATATATATATA	274395	106591	CTGACCTCCCAGGCTCAAGC
185222	17418	TTCAGGAGAATCTAAGGCAT	229809	62005	ATATATATATATATATATAT	274396	106592	CCTGACCTCCCAGGCTCAAG
185223	17419	TTTCAGGAGAATCTAAGGCA	229810	62006	TATATATATATATATATATA	274397	106593	CCCTGACCTCCCAGGCTCAA
185224	17420	TTTTCAGGAGAATCTAAGGC	229811	62007	ATATATATATATATATATAT	274398	106594	GCCCTGACCTCCCAGGCTCA
185225	17421	GTTTTCAGGAGAATCTAAGG	229812	62008	TATATATATATATATATATA	274399	106595	AGCCCTGACCTCCCAGGCTC
185226	17422	AGTTTTCAGGAGAATCTAAG	229813	62009	ATATATATATATATATATAT	274400	106596	CAGCCCTGACCTCCCAGGCT

185227	17423	CAGTTTTCAGGAGAATCTAA	229814	62010	TATATATATATATATATATA	274401	106597	GCAGCCCTGACCTCCCAGGC
185228	17424	CCAGTTTTCAGGAGAATCTA	229815	62011	ATATATATATATATATATAT	274402	106598	TGCAGCCCTGACCTCCCAGG
185229	17425	TCCAGTTTTCAGGAGAATCT	229816	62012	TATATATATATATATATATA	274403	106599	TTGCAGCCCTGACCTCCCAG
185230	17426	TTCCAGTTTTCAGGAGAATC	229817	62013	ATATATATATATATATATAT	274404	106600	ATTGCAGCCCTGACCTCCCA
185231	17427	ATTCCAGTTTTCAGGAGAAT	229818	62014	TATATATATATATATATATA	274405	106601	CATTGCAGCCCTGACCTCCC
185232	17428	CATTCCAGTTTTCAGGAGAA	229819	62015	ATATATATATATATATATAT	274406	106602	TCATTGCAGCCCTGACCTCC
185233	17429	GCATTCCAGTTTTCAGGAGA	229820	62016	TATATATATATATATATATA	274407	106603	CTCATTGCAGCCCTGACCTC
185234	17430	GGCATTCCAGTTTTCAGGAG	229821	62017	ATATATATATATATATATAT	274408	106604	GCTCATTGCAGCCCTGACCT
185235	17431	TGGCATTCCAGTTTTCAGGA	229822	62018	TATATATATATATATATATA	274409	106605	GGCTCATTGCAGCCCTGACC
185236	17432	GTGGCATTCCAGTTTTCAGG	229823	62019	ATATATATATATATATATAT	274410	106606	TGGCTCATTGCAGCCCTGAC
185237	17433	AGTGGCATTCCAGTTTTCAG	229824	62020	TATATATATATATATATATA	274411	106607	ATGGCTCATTGCAGCCCTGA
185238	17434	CAGTGGCATTCCAGTTTTCA	229825	62021	ATATATATATATATATATAT	274412	106608	CATGGCTCATTGCAGCCCTG
185239	17435	ACAGTGGCATTCCAGTTTTC	229826	62022	TATATATATATATATATATA	274413	106609	ACATGGCTCATTGCAGCCCT
185240	17436	TACAGTGGCATTCCAGTTTT	229827	62023	ATATATATATATATATATAT	274414	106610	AACATGGCTCATTGCAGCCC
185241	17437	TTACAGTGGCATTCCAGTTT	229828	62024	TATATATATATATATATATA	274415	106611	GAACATGGCTCATTGCAGCC
185242	17438	TTTACAGTGGCATTCCAGTT	229829	62025	ATATATATATATATATATAT	274416	106612	TGAACATGGCTCATTGCAGC
185243	17439	GTTTACAGTGGCATTCCAGT	229830	62026	TATATATATATATATATATA	274417	106613	GTGAACATGGCTCATTGCAG
185244	17440	AGTTTACAGTGGCATTCCAG	229831	62027	ATATATATATATATATATAT	274418	106614	TGTGAACATGGCTCATTGCA
185245	17441	TAGTTTACAGTGGCATTCCA	229832	62028	TATATATATATATATATATA	274419	106615	GTGTGAACATGGCTCATTGC
185246	17442	ATAGTTTACAGTGGCATTCC	229833	62029	ATATATATATATATATATAT	274420	106616	GGTGTGAACATGGCTCATTG
185247	17443	TATAGTTTACAGTGGCATTC	229834	62030	AATATATATATATATATATA	274421	106617	TGGTGTGAACATGGCTCATT
185248	17444	TTATAGTTTACAGTGGCATT	229835	62031	AAATATATATATATATATAT	274422	106618	GTGGTGTGAACATGGCTCAT
185249	17445	CTTATAGTTTACAGTGGCAT	229836	62032	AAAATATATATATATATATA	274423	106619	AGTGGTGTGAACATGGCTCA
185250	17446	GCTTATAGTTTACAGTGGCA	229837	62033	AAAAATATATATATATATAT	274424	106620	CAGTGGTGTGAACATGGCTC
185251	17447	GGCTTATAGTTTACAGTGGC	229838	62034	AAAAAATATATATATATATA	274425	106621	TCAGTGGTGTGAACATGGCT
185252	17448	GGGCTTATAGTTTACAGTGG	229839	62035	TAAAAAATATATATATATAT	274426	106622	TTCAGTGGTGTGAACATGGC
185253	17449	GGGGCTTATAGTTTACAGTG	229840	62036	ATAAAAAATATATATATATA	274427	106623	GTTCAGTGGTGTGAACATGG
185254	17450	TGGGGCTTATAGTTTACAGT	229841	62037	AATAAAAAATATATATATAT	274428	106624	CGTTCAGTGGTGTGAACATG
185255	17451	GTGGGGCTTATAGTTTACAG	229842	62038	TAATAAAAAATATATATATA	274429	106625	GCGTTCAGTGGTGTGAACAT
185256	17452	AGTGGGGCTTATAGTTTACA	229843	62039	ATAATAAAAAATATATATAT	274430	106626	GGCGTTCAGTGGTGTGAACA
185257	17453	AAGTGGGGCTTATAGTTTAC	229844	62040	AATAATAAAAAATATATATA	274431	106627	TGGCGTTCAGTGGTGTGAAC
185258	17454	GAAGTGGGGCTTATAGTTTA	229845	62041	TAATAATAAAAAATATATAT	274432	106628	CTGGCGTTCAGTGGTGTGAA
185259	17455	TGAAGTGGGGCTTATAGTTT	229846	62042	ATAATAATAAAAAATATATA	274433	106629	GCTGGCGTTCAGTGGTGTGA
185260	17456	TTGAAGTGGGGCTTATAGTT	229847	62043	TATAATAATAAAAAATATAT	274434	106630	GGCTGGCGTTCAGTGGTGTG
185261	17457	TTTGAAGTGGGGCTTATAGT	229848	62044	GTATAATAATAAAAAATATA	274435	106631	AGGCTGGCGTTCAGTGGTGT
185262	17458	CTTTGAAGTGGGGCTTATAG	229849	62045	AGTATAATAATAAAAAATAT	274436	106632	CAGGCTGGCGTTCAGTGGTG
185263	17459	TCTTTGAAGTGGGGCTTATA	229850	62046	AAGTATAATAATAAAAAATA	274437	106633	CCAGGCTGGCGTTCAGTGGT
185264	17460	ATCTTTGAAGTGGGGCTTAT	229851	62047	AAAGTATAATAATAAAAAAT	274438	106634	CCCAGGCTGGCGTTCAGTGG
185265	17461	TATCTTTGAAGTGGGGCTTA	229852	62048	TAAAGTATAATAATAAAAAA	274439	106635	GCCCAGGCTGGCGTTCAGTG
185266	17462	TTATCTTTGAAGTGGGGCTT	229853	62049	TTAAAGTATAATAATAAAAA	274440	106636	CGCCCAGGCTGGCGTTCAGT
185267	17463	TTTATCTTTGAAGTGGGGCT	229854	62050	CTTAAAGTATAATAATAAAA	274441	106637	TCGCCCAGGCTGGCGTTCAG
185268	17464	TTTTATCTTTGAAGTGGGGC	229855	62051	ACTTAAAGTATAATAATAAA	274442	106638	CTCGCCCAGGCTGGCGTTCA
185269	17465	CTTTTATCTTTGAAGTGGGG	229856	62052	AACTTAAAGTATAATAATAA	274443	106639	TCTCGCCCAGGCTGGCGTTC
185270	17466	TCTTTTATCTTTGAAGTGGG	229857	62053	GAACTTAAAGTATAATAATA	274444	106640	GTCTCGCCCAGGCTGGCGTT
185271	17467	ATCTTTTATCTTTGAAGTGG	229858	62054	AGAACTTAAAGTATAATAAT	274445	106641	GGTCTCGCCCAGGCTGGCGT
185272	17468	GATCTTTTATCTTTGAAGTG	229859	62055	TAGAACTTAAAGTATAATAA	274446	106642	GGGTCTCGCCCAGGCTGGCG
185273	17469	AGATCTTTTATCTTTGAAGT	229860	62056	CTAGAACTTAAAGTATAATA	274447	106643	AGGGTCTCGCCCAGGCTGGC
185274	17470	AAGATCTTTTATCTTTGAAG	229861	62057	CCTAGAACTTAAAGTATAAT	274448	106644	CAGGGTCTCGCCCAGGCTGG
185275	17471	CAAGATCTTTTATCTTTGAA	229862	62058	CCCTAGAACTTAAAGTATAA	274449	106645	ACAGGGTCTCGCCCAGGCTG
185276	17472	TCAAGATCTTTTATCTTTGA	229863	62059	ACCCTAGAACTTAAAGTATA	274450	106646	TACAGGGTCTCGCCCAGGCT
185277	17473	ATCAAGATCTTTTATCTTTG	229864	62060	TACCCTAGAACTTAAAGTAT	274451	106647	ATACAGGGTCTCGCCCAGGC
185278	17474	CATCAAGATCTTTTATCTTT	229865	62061	GTACCCTAGAACTTAAAGTA	274452	106648	GATACAGGGTCTCGCCCAGG
185279	17475	TCATCAAGATCTTTTATCTT	229866	62062	TGTACCCTAGAACTTAAAGT	274453	106649	TGATACAGGGTCTCGCCCAG
185280	17476	TTCATCAAGATCTTTTATCT	229867	62063	ATGTACCCTAGAACTTAAAG	274454	106650	TTGATACAGGGTCTCGCCCA
185281	17477	GTTCATCAAGATCTTTTATC	229868	62064	CATGTACCCTAGAACTTAAA	274455	106651	TTTGATACAGGGTCTCGCCC
185282	17478	TGTTCATCAAGATCTTTTAT	229869	62065	ACATGTACCCTAGAACTTAA	274456	106652	TTTTGATACAGGGTCTCGCC
185283	17479	CTGTTCATCAAGATCTTTTA	229870	62066	CACATGTACCCTAGAACTTA	274457	106653	TTTTTGATACAGGGTCTCGC
185284	17480	CCTGTTCATCAAGATCTTTT	229871	62067	GCACATGTACCCTAGAACTT	274458	106654	TTTTTTGATACAGGGTCTCG
185285	17481	CCCTGTTCATCAAGATCTTT	229872	62068	TGCACATGTACCCTAGAACT	274459	106655	CTTTTTTGATACAGGGTCTC
185286	17482	GCCCTGTTCATCAAGATCTT	229873	62069	GTGCACATGTACCCTAGAAC	274460	106656	ACTTTTTTGATACAGGGTCT
185287	17483	AGCCCTGTTCATCAAGATCT	229874	62070	TGTGCACATGTACCCTAGAA	274461	106657	TACTTTTTTGATACAGGGTC
185288	17484	CAGCCCTGTTCATCAAGATC	229875	62071	TTGTGCACATGTACCCTAGA	274462	106658	TTACTTTTTTGATACAGGGT
185289	17485	CCAGCCCTGTTCATCAAGAT	229876	62072	GTTGTGCACATGTACCCTAG	274463	106659	TTTACTTTTTTGATACAGGG
185290	17486	CCCAGCCCTGTTCATCAAGA	229877	62073	TGTTGTGCACATGTACCCTA	274464	106660	CTTTACTTTTTTGATACAGG
185291	17487	ACCCAGCCCTGTTCATCAAG	229878	62074	ATGTTGTGCACATGTACCCT	274465	106661	ACTTTACTTTTTTGATACAG
185292	17488	GACCCAGCCCTGTTCATCAA	229879	62075	CATGTTGTGCACATGTACCC	274466	106662	TACTTTACTTTTTTGATACA
185293	17489	AGACCCAGCCCTGTTCATCA	229880	62076	GCATGTTGTGCACATGTACC	274467	106663	TTACTTTACTTTTTTGATAC
185294	17490	CAGACCCAGCCCTGTTCATC	229881	62077	TGCATGTTGTGCACATGTAC	274468	106664	TTTACTTTACTTTTTTGATA
185295	17491	ACAGACCCAGCCCTGTTCAT	229882	62078	CTGCATGTTGTGCACATGTA	274469	106665	TTTTACTTTACTTTTTTGAT
185296	17492	CACAGACCCAGCCCTGTTCA	229883	62079	CCTGCATGTTGTGCACATGT	274470	106666	ATTTTACTTTACTTTTTTGA
185297	17493	CCACAGACCCAGCCCTGTTC	229884	62080	ACCTGCATGTTGTGCACATG	274471	106667	CATTTTACTTTACTTTTTTG
185298	17494	TCCACAGACCCAGCCCTGTT	229885	62081	AACCTGCATGTTGTGCACAT	274472	106668	TCATTTTACTTTACTTTTTT

185299	17495	GTCCACAGACCCAGCCCTGT	229886	62082	AAACCTGCATGTTGTGCACA	274473	106669	TTCATTTTACTTTACTTTTT
185300	17496	AGTCCACAGACCCAGCCCTG	229887	62083	CAAACCTGCATGTTGTGCAC	274474	106670	ATTCATTTTACTTTACTTTT
185301	17497	CAGTCCACAGACCCAGCCCT	229888	62084	ACAAACCTGCATGTTGTGCA	274475	106671	GATTCATTTTACTTTACTTT
185302	17498	CCAGTCCACAGACCCAGCCC	229889	62085	AACAAACCTGCATGTTGTGC	274476	106672	GGATTCATTTTACTTTACTT
185303	17499	CCCAGTCCACAGACCCAGCC	229890	62086	TAACAAACCTGCATGTTGTG	274477	106673	AGGATTCATTTTACTTTACT
185304	17500	GCCCAGTCCACAGACCCAGC	229891	62087	GTAACAAACCTGCATGTTGT	274478	106674	CAGGATTCATTTTACTTTAC
185305	17501	GGCCCAGTCCACAGACCCAG	229892	62088	TGTAACAAACCTGCATGTTG	274479	106675	ACAGGATTCATTTTACTTTA
185306	17502	AGGCCCAGTCCACAGACCCA	229893	62089	ATGTAACAAACCTGCATGTT	274480	106676	TACAGGATTCATTTTACTTT
185307	17503	GAGGCCCAGTCCACAGACCC	229894	62090	TATGTAACAAACCTGCATGT	274481	106677	GTACAGGATTCATTTTACTT
185308	17504	AGAGGCCCAGTCCACAGACC	229895	62091	ATATGTAACAAACCTGCATG	274482	106678	CGTACAGGATTCATTTTACT
185309	17505	GAGAGGCCCAGTCCACAGAC	229896	62092	CATATGTAACAAACCTGCAT	274483	106679	ACGTACAGGATTCATTTTAC
185310	17506	GGAGAGGCCCAGTCCACAGA	229897	62093	ACATATGTAACAAACCTGCA	274484	106680	AACGTACAGGATTCATTTTA
185311	17507	GGGAGAGGCCCAGTCCACAG	229898	62094	TACATATGTAACAAACCTGC	274485	106681	TAACGTACAGGATTCATTTT
185312	17508	GGGGAGAGGCCCAGTCCACA	229899	62095	ATACATATGTAACAAACCTG	274486	106682	ATAACGTACAGGATTCATTT
185313	17509	TGGGGAGAGGCCCAGTCCAC	229900	62096	TATACATATGTAACAAACCT	274487	106683	TATAACGTACAGGATTCATT
185314	17510	GTGGGGAGAGGCCCAGTCCA	229901	62097	GTATACATATGTAACAAACC	274488	106684	ATATAACGTACAGGATTCAT
185315	17511	GGTGGGGAGAGGCCCAGTCC	229902	62098	TGTATACATATGTAACAAAC	274489	106685	AATATAACGTACAGGATTCA
185316	17512	TGGTGGGGAGAGGCCCAGTC	229903	62099	ATGTATACATATGTAACAAA	274490	106686	TAATATAACGTACAGGATTC
185317	17513	GTGGTGGGGAGAGGCCCAGT	229904	62100	CATGTATACATATGTAACAA	274491	106687	TTAATATAACGTACAGGATT
185318	17514	TGTGGTGGGGAGAGGCCCAG	229905	62101	ACATGTATACATATGTAACA	274492	106688	CTTAATATAACGTACAGGAT
185319	17515	GTGTGGTGGGGAGAGGCCCA	229906	62102	CACATGTATACATATGTAAC	274493	106689	CCTTAATATAACGTACAGGA
185320	17516	TGTGTGGTGGGGAGAGGCCC	229907	62103	GCACATGTATACATATGTAA	274494	106690	ACCTTAATATAACGTACAGG
185321	17517	TTGTGTGGTGGGGAGAGGCC	229908	62104	GGCACATGTATACATATGTA	274495	106691	CACCTTAATATAACGTACAG
185322	17518	CTTGTGTGGTGGGGAGAGGC	229909	62105	TGGCACATGTATACATATGT	274496	106692	GCACCTTAATATAACGTACA
185323	17519	CCTTGTGTGGTGGGGAGAGG	229910	62106	ATGGCACATGTATACATATG	274497	106693	GGCACCTTAATATAACGTAC
185324	17520	TCCTTGTGTGGTGGGGAGAG	229911	62107	CATGGCACATGTATACATAT	274498	106694	GGGCACCTTAATATAACGTA
185325	17521	TTCCTTGTGTGGTGGGGAGA	229912	62108	ACATGGCACATGTATACATA	274499	106695	GGGGCACCTTAATATAACGT
185326	17522	CTTCCTTGTGTGGTGGGGAG	229913	62109	AACATGGCACATGTATACAT	274500	106696	TGGGGCACCTTAATATAACG
185327	17523	CCTTCCTTGTGTGGTGGGGA	229914	62110	CAACATGGCACATGTATACA	274501	106697	TTGGGGCACCTTAATATAAC
185328	17524	CCCTTCCTTGTGTGGTGGGG	229915	62111	CCAACATGGCACATGTATAC	274502	106698	TTTGGGGCACCTTAATATAA
185329	17525	ACCCTTCCTTGTGTGGTGGG	229916	62112	ACCAACATGGCACATGTATA	274503	106699	ATTTGGGGCACCTTAATATA
185330	17526	CACCCTTCCTTGTGTGGTGG	229917	62113	CACCAACATGGCACATGTAT	274504	106700	AATTTGGGGCACCTTAATAT
185331	17527	CCACCCTTCCTTGTGTGGTG	229918	62114	ACACCAACATGGCACATGTA	274505	106701	CAATTTGGGGCACCTTAATA
185332	17528	ACCACCCTTCCTTGTGTGGT	229919	62115	CACACCAACATGGCACATGT	274506	106702	ACAATTTGGGGCACCTTAAT
185333	17529	CACCACCCTTCCTTGTGTGG	229920	62116	GCACACCAACATGGCACATG	274507	106703	TACAATTTGGGGCACCTTAA
185334	17530	GCACCACCCTTCCTTGTGTG	229921	62117	AGCACACCAACATGGCACAT	274508	106704	GTACAATTTGGGGCACCTTA
185335	17531	GGCACCACCCTTCCTTGTGT	229922	62118	CAGCACACCAACATGGCACA	274509	106705	AGTACAATTTGGGGCACCTT
185336	17532	TGGCACCACCCTTCCTTGTG	229923	62119	GCAGCACACCAACATGGCAC	274510	106706	AAGTACAATTTGGGGCACCT
185337	17533	CTGGCACCACCCTTCCTTGT	229924	62120	TGCAGCACACCAACATGGCA	274511	106707	TAAGTACAATTTGGGGCACC
185338	17534	ACTGGCACCACCCTTCCTTG	229925	62121	GTGCAGCACACCAACATGGC	274512	106708	CTAAGTACAATTTGGGGCAC
185339	17535	AACTGGCACCACCCTTCCTT	229926	62122	GGTGCAGCACACCAACATGG	274513	106709	TCTAAGTACAATTTGGGGCA
185340	17536	CAACTGGCACCACCCTTCCT	229927	62123	GGGTGCAGCACACCAACATG	274514	106710	TTCTAAGTACAATTTGGGGC
185341	17537	TCAACTGGCACCACCCTTCC	229928	62124	TGGGTGCAGCACACCAACAT	274515	106711	CTTCTAAGTACAATTTGGGG
185342	17538	TTCAACTGGCACCACCCTTC	229929	62125	ATGGGTGCAGCACACCAACA	274516	106712	CCTTCTAAGTACAATTTGGG
185343	17539	CTTCAACTGGCACCACCCTT	229930	62126	AATGGGTGCAGCACACCAAC	274517	106713	TCCTTCTAAGTACAATTTGG
185344	17540	CCTTCAACTGGCACCACCCT	229931	62127	TAATGGGTGCAGCACACCAA	274518	106714	ATCCTTCTAAGTACAATTTG
185345	17541	TCCTTCAACTGGCACCACCC	229932	62128	TTAATGGGTGCAGCACACCA	274519	106715	AATCCTTCTAAGTACAATTT
185346	17542	TTCCTTCAACTGGCACCACC	229933	62129	ATTAATGGGTGCAGCACACC	274520	106716	AAATCCTTCTAAGTACAATT
185347	17543	TTTCCTTCAACTGGCACCAC	229934	62130	AATTAATGGGTGCAGCACAC	274521	106717	GAAATCCTTCTAAGTACAAT
185348	17544	TTTTCCTTCAACTGGCACCA	229935	62131	GAATTAATGGGTGCAGCACA	274522	106718	TGAAATCCTTCTAAGTACAA
185349	17545	ATTTTCCTTCAACTGGCACC	229936	62132	TGAATTAATGGGTGCAGCAC	274523	106719	ATGAAATCCTTCTAAGTACA
185350	17546	GATTTTCCTTCAACTGGCAC	229937	62133	ATGAATTAATGGGTGCAGCA	274524	106720	TATGAAATCCTTCTAAGTAC
185351	17547	TGATTTTCCTTCAACTGGCA	229938	62134	GATGAATTAATGGGTGCAGC	274525	106721	CTATGAAATCCTTCTAAGTA
185352	17548	GTGATTTTCCTTCAACTGGC	229939	62135	TGATGAATTAATGGGTGCAG	274526	106722	ACTATGAAATCCTTCTAAGT
185353	17549	AGTGATTTTCCTTCAACTGG	229940	62136	ATGATGAATTAATGGGTGCA	274527	106723	AACTATGAAATCCTTCTAAG
185354	17550	AAGTGATTTTCCTTCAACTG	229941	62137	AATGATGAATTAATGGGTGC	274528	106724	AAACTATGAAATCCTTCTAA
185355	17551	TAAGTGATTTTCCTTCAACT	229942	62138	AAATGATGAATTAATGGGTG	274529	106725	AAAACTATGAAATCCTTCTA
185356	17552	TTAAGTGATTTTCCTTCAAC	229943	62139	TAAATGATGAATTAATGGGT	274530	106726	TAAAACTATGAAATCCTTCT
185357	17553	TTTAAGTGATTTTCCTTCAA	229944	62140	GTAAATGATGAATTAATGGG	274531	106727	TTAAAACTATGAAATCCTTC
185358	17554	ATTTAAGTGATTTTCCTTCA	229945	62141	TGTAAATGATGAATTAATGG	274532	106728	TTTAAAACTATGAAATCCTT
185359	17555	GATTTAAGTGATTTTCCTTC	229946	62142	ATGTAAATGATGAATTAATG	274533	106729	ATTTAAAACTATGAAATCCT
185360	17556	GGATTTAAGTGATTTTCCTT	229947	62143	AATGTAAATGATGAATTAAT	274534	106730	TATTTAAAACTATGAAATCC
185361	17557	AGGATTTAAGTGATTTTCCT	229948	62144	TAATGTAAATGATGAATTAA	274535	106731	GTATTTAAAACTATGAAATC
185362	17558	AAGGATTTAAGTGATTTTCC	229949	62145	CTAATGTAAATGATGAATTA	274536	106732	AGTATTTAAAACTATGAAAT
185363	17559	CAAGGATTTAAGTGATTTTC	229950	62146	CCTAATGTAAATGATGAATT	274537	106733	AAGTATTTAAAACTATGAAA
185364	17560	GCAAGGATTTAAGTGATTTT	229951	62147	ACCTAATGTAAATGATGAAT	274538	106734	AAAGTATTTAAAACTATGAA
185365	17561	AGCAAGGATTTAAGTGATTT	229952	62148	TACCTAATGTAAATGATGAA	274539	106735	AAAAGTATTTAAAACTATGA
185366	17562	CAGCAAGGATTTAAGTGATT	229953	62149	ATACCTAATGTAAATGATGA	274540	106736	CAAAAGTATTTAAAACTATG
185367	17563	ACAGCAAGGATTTAAGTGAT	229954	62150	TATACCTAATGTAAATGATG	274541	106737	ACAAAAGTATTTAAAACTAT
185368	17564	GACAGCAAGGATTTAAGTGA	229955	62151	ATATACCTAATGTAAATGAT	274542	106738	AACAAAAGTATTTAAAACTA
185369	17565	AGACAGCAAGGATTTAAGTG	229956	62152	GATATACCTAATGTAAATGA	274543	106739	TAACAAAAGTATTTAAAACT
185370	17566	GAGACAGCAAGGATTTAAGT	229957	62153	AGATATACCTAATGTAAATG	274544	106740	ATAACAAAAGTATTTAAAAC

185371	17567	GGAGACAGCAAGGATTTAAG	229958	62154	GAGATATACCTAATGTAAAT	274545	106741	AATAACAAAAGTATTTAAAA
185372	17568	AGGAGACAGCAAGGATTTAA	229959	62155	GGAGATATACCTAATGTAAA	274546	106742	AAATAACAAAAGTATTTAAA
185373	17569	TAGGAGACAGCAAGGATTTA	229960	62156	AGGAGATATACCTAATGTAA	274547	106743	TAAATAACAAAAGTATTTAA
185374	17570	TTAGGAGACAGCAAGGATTT	229961	62157	TAGGAGATATACCTAATGTA	274548	106744	TTAAATAACAAAAGTATTTA
185375	17571	ATTAGGAGACAGCAAGGATT	229962	62158	TTAGGAGATATACCTAATGT	274549	106745	TTTAAATAACAAAAGTATTT
185376	17572	TATTAGGAGACAGCAAGGAT	229963	62159	ATTAGGAGATATACCTAATG	274550	106746	TTTTAAATAACAAAAGTATT
185377	17573	TTATTAGGAGACAGCAAGGA	229964	62160	CATTAGGAGATATACCTAAT	274551	106747	TTTTTAAATAACAAAAGTAT
185378	17574	CTTATTAGGAGACAGCAAGG	229965	62161	GCATTAGGAGATATACCTAA	274552	106748	TTTTTTAAATAACAAAAGTA
185379	17575	CCTTATTAGGAGACAGCAAG	229966	62162	AGCATTAGGAGATATACCTA	274553	106749	ATTTTTTAAATAACAAAAGT
185380	17576	ACCTTATTAGGAGACAGCAA	229967	62163	TAGCATTAGGAGATATACCT	274554	106750	AATTTTTTAAATAACAAAAG
185381	17577	CACCTTATTAGGAGACAGCA	229968	62164	ATAGCATTAGGAGATATACC	274555	106751	TAATTTTTTAAATAACAAAA
185382	17578	ACACCTTATTAGGAGACAGC	229969	62165	GATAGCATTAGGAGATATAC	274556	106752	TTAATTTTTTAAATAACAAA
185383	17579	CACACCTTATTAGGAGACAG	229970	62166	GGATAGCATTAGGAGATATA	274557	106753	TTTAATTTTTTAAATAACAA
185384	17580	CCACACCTTATTAGGAGACA	229971	62167	GGGATAGCATTAGGAGATAT	274558	106754	ATTTAATTTTTTAAATAACA
185385	17581	ACCACACCTTATTAGGAGAC	229972	62168	AGGGATAGCATTAGGAGATA	274559	106755	CATTTAATTTTTTAAATAAC
185386	17582	GACCACACCTTATTAGGAGA	229973	62169	GAGGGATAGCATTAGGAGAT	274560	106756	TCATTTAATTTTTTAAATAA
185387	17583	GGACCACACCTTATTAGGAG	229974	62170	GGAGGGATAGCATTAGGAGA	274561	106757	GTCATTTAATTTTTTAAATA
185388	17584	GGGACCACACCTTATTAGGA	229975	62171	GGGAGGGATAGCATTAGGAG	274562	106758	AGTCATTTAATTTTTTAAAT
185389	17585	TGGGACCACACCTTATTAGG	229976	62172	GGGGAGGGATAGCATTAGGA	274563	106759	CAGTCATTTAATTTTTTAAA
185390	17586	CTGGGACCACACCTTATTAG	229977	62173	TGGGGAGGGATAGCATTAGG	274564	106760	GCAGTCATTTAATTTTTTAA
185391	17587	CCTGGGACCACACCTTATTA	229978	62174	GTGGGGAGGGATAGCATTAG	274565	106761	TGCAGTCATTTAATTTTTTA
185392	17588	ACCTGGGACCACACCTTATT	229979	62175	AGTGGGGAGGGATAGCATTA	274566	106762	CTGCAGTCATTTAATTTTTT
185393	17589	TACCTGGGACCACACCTTAT	229980	62176	GAGTGGGGAGGGATAGCATT	274567	106763	GCTGCAGTCATTTAATTTTT
185394	17590	CTACCTGGGACCACACCTTA	229981	62177	GGAGTGGGGAGGGATAGCAT	274568	106764	TGCTGCAGTCATTTAATTTT
185395	17591	CCTACCTGGGACCACACCTT	229982	62178	GGGAGTGGGGAGGGATAGCA	274569	106765	ATGCTGCAGTCATTTAATTT
185396	17592	CCCTACCTGGGACCACACCT	229983	62179	GGGGAGTGGGGAGGGATAGC	274570	106766	TATGCTGCAGTCATTTAATT
185397	17593	GCCCTACCTGGGACCACACC	229984	62180	GGGGGAGTGGGGAGGGATAG	274571	106767	ATATGCTGCAGTCATTTAAT
185398	17594	AGCCCTACCTGGGACCACAC	229985	62181	GGGGGGAGTGGGGAGGGATA	274572	106768	TATATGCTGCAGTCATTTAA
185399	17595	CAGCCCTACCTGGGACCACA	229986	62182	TGGGGGGAGTGGGGAGGGAT	274573	106769	TTATATGCTGCAGTCATTTA
185400	17596	ACAGCCCTACCTGGGACCAC	229987	62183	GTGGGGGGAGTGGGGAGGGA	274574	106770	TTTATATGCTGCAGTCATTT
185401	17597	GACAGCCCTACCTGGGACCA	229988	62184	GGTGGGGGGAGTGGGGAGGG	274575	106771	ATTTATATGCTGCAGTCATT
185402	17598	TGACAGCCCTACCTGGGACC	229989	62185	GGGTGGGGGGAGTGGGGAGG	274576	106772	AATTTATATGCTGCAGTCAT
185403	17599	CTGACAGCCCTACCTGGGAC	229990	62186	GGGGTGGGGGGAGTGGGGAG	274577	106773	TAATTTATATGCTGCAGTCA
185404	17600	TCTGACAGCCCTACCTGGGA	229991	62187	TGGGGTGGGGGGAGTGGGGA	274578	106774	CTAATTTATATGCTGCAGTC
185405	17601	TTCTGACAGCCCTACCTGGG	229992	62188	GTGGGGTGGGGGGAGTGGGG	274579	106775	CCTAATTTATATGCTGCAGT
185406	17602	ATTCTGACAGCCCTACCTGG	229993	62189	TGTGGGGTGGGGGGAGTGGG	274580	106776	ACCTAATTTATATGCTGCAG
185407	17603	AATTCTGACAGCCCTACCTG	229994	62190	TTGTGGGGTGGGGGGAGTGG	274581	106777	AACCTAATTTATATGCTGCA
185408	17604	TAATTCTGACAGCCCTACCT	229995	62191	GTTGTGGGGTGGGGGGAGTG	274582	106778	GAACCTAATTTATATGCTGC
185409	17605	CTAATTCTGACAGCCCTACC	229996	62192	TGTTGTGGGGTGGGGGGAGT	274583	106779	AGAACCTAATTTATATGCTG
185410	17606	GCTAATTCTGACAGCCCTAC	229997	62193	CTGTTGTGGGGTGGGGGGAG	274584	106780	AAGAACCTAATTTATATGCT
185411	17607	TGCTAATTCTGACAGCCCTA	229998	62194	CCTGTTGTGGGGTGGGGGGA	274585	106781	TAAGAACCTAATTTATATGC
185412	17608	TTGCTAATTCTGACAGCCCT	229999	62195	GCCTGTTGTGGGGTGGGGGG	274586	106782	TTAAGAACCTAATTTATATG
185413	17609	TTTGCTAATTCTGACAGCCC	230000	62196	GGCCTGTTGTGGGGTGGGGG	274587	106783	ATTAAGAACCTAATTTATAT
185414	17610	ATTTGCTAATTCTGACAGCC	230001	62197	GGGCCTGTTGTGGGGTGGGG	274588	106784	CATTAAGAACCTAATTTATA
185415	17611	AATTTGCTAATTCTGACAGC	230002	62198	GGGGCCTGTTGTGGGGTGGG	274589	106785	CCATTAAGAACCTAATTTAT
185416	17612	TAATTTGCTAATTCTGACAG	230003	62199	TGGGGCCTGTTGTGGGGTGG	274590	106786	TCCATTAAGAACCTAATTTA
185417	17613	TTAATTTGCTAATTCTGACA	230004	62200	CTGGGGCCTGTTGTGGGGTG	274591	106787	CTCCATTAAGAACCTAATTT
185418	17614	TTTAATTTGCTAATTCTGAC	230005	62201	ACTGGGGCCTGTTGTGGGGT	274592	106788	CCTCCATTAAGAACCTAATT
185419	17615	TTTTAATTTGCTAATTCTGA	230006	62202	CACTGGGGCCTGTTGTGGGG	274593	106789	CCCTCCATTAAGAACCTAAT
185420	17616	GTTTTAATTTGCTAATTCTG	230007	62203	ACACTGGGGCCTGTTGTGGG	274594	106790	CCCCTCCATTAAGAACCTAA
185421	17617	TGTTTTAATTTGCTAATTCT	230008	62204	CACACTGGGGCCTGTTGTGG	274595	106791	TCCCCTCCATTAAGAACCTA
185422	17618	GTGTTTTAATTTGCTAATTC	230009	62205	ACACACTGGGGCCTGTTGTG	274596	106792	TTCCCCTCCATTAAGAACCT
185423	17619	TGTGTTTTAATTTGCTAATT	230010	62206	CACACACTGGGGCCTGTTGT	274597	106793	TTTCCCCTCCATTAAGAACC
185424	17620	CTGTGTTTTAATTTGCTAAT	230011	62207	TCACACACTGGGGCCTGTTG	274598	106794	TTTTCCCCTCCATTAAGAAC
185425	17621	CCTGTGTTTTAATTTGCTAA	230012	62208	ATCACACACTGGGGCCTGTT	274599	106795	TTTTTCCCCTCCATTAAGAA
185426	17622	CCCTGTGTTTTAATTTGCTA	230013	62209	CATCACACACTGGGGCCTGT	274600	106796	CTTTTTCCCCTCCATTAAGA
185427	17623	GCCCTGTGTTTTAATTTGCT	230014	62210	ACATCACACACTGGGGCCTG	274601	106797	TCTTTTTCCCCTCCATTAAG
185428	17624	TGCCCTGTGTTTTAATTTGC	230015	62211	AACATCACACACTGGGGCCT	274602	106798	CTCTTTTTCCCCTCCATTAA
185429	17625	ATGCCCTGTGTTTTAATTTG	230016	62212	GAACATCACACACTGGGGCC	274603	106799	ACTCTTTTTCCCCTCCATTA
185430	17626	GATGCCCTGTGTTTTAATTT	230017	62213	GGAACATCACACACTGGGGC	274604	106800	TACTCTTTTTCCCCTCCATT
185431	17627	AGATGCCCTGTGTTTTAATT	230018	62214	GGGAACATCACACACTGGGG	274605	106801	GTACTCTTTTTCCCCTCCAT
185432	17628	CAGATGCCCTGTGTTTTAAT	230019	62215	GGGGAACATCACACACTGGG	274606	106802	TGTACTCTTTTTCCCCTCCA
185433	17629	ACAGATGCCCTGTGTTTTAA	230020	62216	AGGGGAACATCACACACTGG	274607	106803	TTGTACTCTTTTTCCCCTCC
185434	17630	CACAGATGCCCTGTGTTTTA	230021	62217	AAGGGGAACATCACACACTG	274608	106804	CTTGTACTCTTTTTCCCCTC
185435	17631	TCACAGATGCCCTGTGTTTT	230022	62218	GAAGGGGAACATCACACACT	274609	106805	TCTTGTACTCTTTTTCCCCT
185436	17632	TTCACAGATGCCCTGTGTTT	230023	62219	GGAAGGGGAACATCACACAC	274610	106806	TTCTTGTACTCTTTTTCCCC
185437	17633	TTTCACAGATGCCCTGTGTT	230024	62220	AGGAAGGGGAACATCACACA	274611	106807	TTTCTTGTACTCTTTTTCCC
185438	17634	TTTTCACAGATGCCCTGTGT	230025	62221	CAGGAAGGGGAACATCACAC	274612	106808	TTTTCTTGTACTCTTTTTCC
185439	17635	ATTTTCACAGATGCCCTGTG	230026	62222	ACAGGAAGGGGAACATCACA	274613	106809	CTTTTCTTGTACTCTTTTTC
185440	17636	AATTTTCACAGATGCCCTGT	230027	62223	CACAGGAAGGGGAACATCAC	274614	106810	TCTTTTCTTGTACTCTTTTT
185441	17637	TAATTTTCACAGATGCCCTG	230028	62224	ACACAGGAAGGGGAACATCA	274615	106811	TTCTTTTCTTGTACTCTTTT
185442	17638	CTAATTTTCACAGATGCCCT	230029	62225	GACACAGGAAGGGGAACATC	274616	106812	TTTCTTTTCTTGTACTCTTT

185443	17639	TCTAATTTTCACAGATGCCC	230030	62226	GGACACAGGAAGGGGAACAT	274617	106813	ATTTCTTTTCTTGTACTCTT
185444	17640	TTCTAATTTTCACAGATGCC	230031	62227	TGGACACAGGAAGGGGAACA	274618	106814	TATTTCTTTTCTTGTACTCT
185445	17641	ATTCTAATTTTCACAGATGC	230032	62228	TTGGACACAGGAAGGGGAAC	274619	106815	TTATTTCTTTTCTTGTACTC
185446	17642	AATTCTAATTTTCACAGATG	230033	62229	CTTGGACACAGGAAGGGGAA	274620	106816	CTTATTTCTTTTCTTGTACT
185447	17643	AAATTCTAATTTTCACAGAT	230034	62230	ACTTGGACACAGGAAGGGGA	274621	106817	TCTTATTTCTTTTCTTGTAC
185448	17644	GAAATTCTAATTTTCACAGA	230035	62231	CACTTGGACACAGGAAGGGG	274622	106818	TTCTTATTTCTTTTCTTGTA
185449	17645	TGAAATTCTAATTTTCACAG	230036	62232	ACACTTGGACACAGGAAGGG	274623	106819	ATTCTTATTTCTTTTCTTGT
185450	17646	CTGAAATTCTAATTTTCACA	230037	62233	AACACTTGGACACAGGAAGG	274624	106820	GATTCTTATTTCTTTTCTTG
185451	17647	TCTGAAATTCTAATTTTCAC	230038	62234	GAACACTTGGACACAGGAAG	274625	106821	AGATTCTTATTTCTTTTCTT
185452	17648	ATCTGAAATTCTAATTTTCA	230039	62235	AGAACACTTGGACACAGGAA	274626	106822	TAGATTCTTATTTCTTTTCT
185453	17649	TATCTGAAATTCTAATTTTC	230040	62236	GAGAACACTTGGACACAGGA	274627	106823	CTAGATTCTTATTTCTTTTC
185454	17650	TTATCTGAAATTCTAATTTT	230041	62237	TGAGAACACTTGGACACAGG	274628	106824	TCTAGATTCTTATTTCTTTT
185455	17651	GTTATCTGAAATTCTAATTT	230042	62238	ATGAGAACACTTGGACACAG	274629	106825	TTCTAGATTCTTATTTCTTT
185456	17652	TGTTATCTGAAATTCTAATT	230043	62239	AATGAGAACACTTGGACACA	274630	106826	TTTCTAGATTCTTATTTCTT
185457	17653	TTGTTATCTGAAATTCTAAT	230044	62240	CAATGAGAACACTTGGACAC	274631	106827	GTTTCTAGATTCTTATTTCT
185458	17654	GTTGTTATCTGAAATTCTAA	230045	62241	ACAATGAGAACACTTGGACA	274632	106828	TGTTTCTAGATTCTTATTTC
185459	17655	TGTTGTTATCTGAAATTCTA	230046	62242	AACAATGAGAACACTTGGAC	274633	106829	TTGTTTCTAGATTCTTATTT
185460	17656	TTGTTGTTATCTGAAATTCT	230047	62243	GAACAATGAGAACACTTGGA	274634	106830	TTTGTTTCTAGATTCTTATT
185461	17657	TTTGTTGTTATCTGAAATTC	230048	62244	TGAACAATGAGAACACTTGG	274635	106831	CTTTGTTTCTAGATTCTTAT
185462	17658	ATTTGTTGTTATCTGAAATT	230049	62245	TTGAACAATGAGAACACTTG	274636	106832	TCTTTGTTTCTAGATTCTTA
185463	17659	TATTTGTTGTTATCTGAAAT	230050	62246	ATTGAACAATGAGAACACTT	274637	106833	ATCTTTGTTTCTAGATTCTT
185464	17660	TTATTTGTTGTTATCTGAAA	230051	62247	AATTGAACAATGAGAACACT	274638	106834	TATCTTTGTTTCTAGATTCT
185465	17661	ATTATTTGTTGTTATCTGAA	230052	62248	GAATTGAACAATGAGAACAC	274639	106835	TTATCTTTGTTTCTAGATTC
185466	17662	AATTATTTGTTGTTATCTGA	230053	62249	GGAATTGAACAATGAGAACA	274640	106836	CTTATCTTTGTTTCTAGATT
185467	17663	CAATTATTTGTTGTTATCTG	230054	62250	GGGAATTGAACAATGAGAAC	274641	106837	TCTTATCTTTGTTTCTAGAT
185468	17664	CCAATTATTTGTTGTTATCT	230055	62251	TGGGAATTGAACAATGAGAA	274642	106838	CTCTTATCTTTGTTTCTAGA
185469	17665	GCCAATTATTTGTTGTTATC	230056	62252	GTGGGAATTGAACAATGAGA	274643	106839	GCTCTTATCTTTGTTTCTAG
185470	17666	TGCCAATTATTTGTTGTTAT	230057	62253	GGTGGGAATTGAACAATGAG	274644	106840	TGCTCTTATCTTTGTTTCTA
185471	17667	ATGCCAATTATTTGTTGTTA	230058	62254	AGGTGGGAATTGAACAATGA	274645	106841	CTGCTCTTATCTTTGTTTCT
185472	17668	TATGCCAATTATTTGTTGTT	230059	62255	TAGGTGGGAATTGAACAATG	274646	106842	TCTGCTCTTATCTTTGTTTC
185473	17669	CTATGCCAATTATTTGTTGT	230060	62256	GTAGGTGGGAATTGAACAAT	274647	106843	TTCTGCTCTTATCTTTGTTT
185474	17670	CCTATGCCAATTATTTGTTG	230061	62257	CGTAGGTGGGAATTGAACAA	274648	106844	TTTCTGCTCTTATCTTTGTT
185475	17671	GCCTATGCCAATTATTTGTT	230062	62258	TCGTAGGTGGGAATTGAACA	274649	106845	ATTTCTGCTCTTATCTTTGT
185476	17672	AGCCTATGCCAATTATTTGT	230063	62259	CTCGTAGGTGGGAATTGAAC	274650	106846	TATTTCTGCTCTTATCTTTG
185477	17673	CAGCCTATGCCAATTATTTG	230064	62260	ACTCGTAGGTGGGAATTGAA	274651	106847	TTATTTCTGCTCTTATCTTT
185478	17674	GCAGCCTATGCCAATTATTT	230065	62261	CACTCGTAGGTGGGAATTGA	274652	106848	TTTATTTCTGCTCTTATCTT
185479	17675	TGCAGCCTATGCCAATTATT	230066	62262	TCACTCGTAGGTGGGAATTG	274653	106849	GTTTATTTCTGCTCTTATCT
185480	17676	ATGCAGCCTATGCCAATTAT	230067	62263	CTCACTCGTAGGTGGGAATT	274654	106850	GGTTTATTTCTGCTCTTATC
185481	17677	TATGCAGCCTATGCCAATTA	230068	62264	TCTCACTCGTAGGTGGGAAT	274655	106851	TGGTTTATTTCTGCTCTTAT
185482	17678	TTATGCAGCCTATGCCAATT	230069	62265	TTCTCACTCGTAGGTGGGAA	274656	106852	CTGGTTTATTTCTGCTCTTA
185483	17679	ATTATGCAGCCTATGCCAAT	230070	62266	GTTCTCACTCGTAGGTGGGA	274657	106853	TCTGGTTTATTTCTGCTCTT
185484	17680	CATTATGCAGCCTATGCCAA	230071	62267	TGTTCTCACTCGTAGGTGGG	274658	106854	TTCTGGTTTATTTCTGCTCT
185485	17681	ACATTATGCAGCCTATGCCA	230072	62268	ATGTTCTCACTCGTAGGTGG	274659	106855	TTTCTGGTTTATTTCTGCTC
185486	17682	GACATTATGCAGCCTATGCC	230073	62269	CATGTTCTCACTCGTAGGTG	274660	106856	TTTTCTGGTTTATTTCTGCT
185487	17683	GGACATTATGCAGCCTATGC	230074	62270	GCATGTTCTCACTCGTAGGT	274661	106857	GTTTTCTGGTTTATTTCTGC
185488	17684	GGGACATTATGCAGCCTATG	230075	62271	AGCATGTTCTCACTCGTAGG	274662	106858	TGTTTTCTGGTTTATTTCTG
185489	17685	AGGGACATTATGCAGCCTAT	230076	62272	CAGCATGTTCTCACTCGTAG	274663	106859	GTGTTTTCTGGTTTATTTCT
185490	17686	GAGGGACATTATGCAGCCTA	230077	62273	ACAGCATGTTCTCACTCGTA	274664	106860	TGTGTTTTCTGGTTTATTTC
185491	17687	TGAGGGACATTATGCAGCCT	230078	62274	CACAGCATGTTCTCACTCGT	274665	106861	TTGTGTTTTCTGGTTTATTT
185492	17688	TTGAGGGACATTATGCAGCC	230079	62275	ACACAGCATGTTCTCACTCG	274666	106862	GTTGTGTTTTCTGGTTTATT
185493	17689	TTTGAGGGACATTATGCAGC	230080	62276	AACACAGCATGTTCTCACTC	274667	106863	GGTTGTGTTTTCTGGTTTAT
185494	17690	CTTTGAGGGACATTATGCAG	230081	62277	AAACACAGCATGTTCTCACT	274668	106864	AGGTTGTGTTTTCTGGTTTA
185495	17691	TCTTTGAGGGACATTATGCA	230082	62278	CAAACACAGCATGTTCTCAC	274669	106865	AAGGTTGTGTTTTCTGGTTT
185496	17692	ATCTTTGAGGGACATTATGC	230083	62279	CCAAACACAGCATGTTCTCA	274670	106866	CAAGGTTGTGTTTTCTGGTT
185497	17693	TATCTTTGAGGGACATTATG	230084	62280	ACCAAACACAGCATGTTCTC	274671	106867	GCAAGGTTGTGTTTTCTGGT
185498	17694	ATATCTTTGAGGGACATTAT	230085	62281	AACCAAACACAGCATGTTCT	274672	106868	TGCAAGGTTGTGTTTTCTGG
185499	17695	GATATCTTTGAGGGACATTA	230086	62282	AAACCAAACACAGCATGTTC	274673	106869	GTGCAAGGTTGTGTTTTCTG
185500	17696	TGATATCTTTGAGGGACATT	230087	62283	AAAACCAAACACAGCATGTT	274674	106870	AGTGCAAGGTTGTGTTTTCT
185501	17697	CTGATATCTTTGAGGGACAT	230088	62284	AAAAACCAAACACAGCATGT	274675	106871	GAGTGCAAGGTTGTGTTTTC
185502	17698	CCTGATATCTTTGAGGGACA	230089	62285	AAAAAACCAAACACAGCATG	274676	106872	GGAGTGCAAGGTTGTGTTTT
185503	17699	ACCTGATATCTTTGAGGGAC	230090	62286	AAAAAAACCAAACACAGCAT	274677	106873	AGGAGTGCAAGGTTGTGTTT
185504	17700	GACCTGATATCTTTGAGGGA	230091	62287	CAAAAAAACCAAACACAGCA	274678	106874	TAGGAGTGCAAGGTTGTGTT
185505	17701	GGACCTGATATCTTTGAGGG	230092	62288	ACAAAAAAACCAAACACAGC	274679	106875	TTAGGAGTGCAAGGTTGTGT
185506	17702	AGGACCTGATATCTTTGAGG	230093	62289	GACAAAAAAACCAAACACAG	274680	106876	GTTAGGAGTGCAAGGTTGTG
185507	17703	TAGGACCTGATATCTTTGAG	230094	62290	GGACAAAAAAACCAAACACA	274681	106877	AGTTAGGAGTGCAAGGTTGT
185508	17704	TTAGGACCTGATATCTTTGA	230095	62291	AGGACAAAAAAACCAAACAC	274682	106878	AAGTTAGGAGTGCAAGGTTG
185509	17705	ATTAGGACCTGATATCTTTG	230096	62292	AAGGACAAAAAAACCAAACA	274683	106879	TAAGTTAGGAGTGCAAGGTT
185510	17706	GATTAGGACCTGATATCTTT	230097	62293	CAAGGACAAAAAAACCAAAC	274684	106880	TTAAGTTAGGAGTGCAAGGT
185511	17707	AGATTAGGACCTGATATCTT	230098	62294	GCAAGGACAAAAAAACCAAA	274685	106881	TTTAAGTTAGGAGTGCAAGG
185512	17708	GAGATTAGGACCTGATATCT	230099	62295	CGCAAGGACAAAAAAACCAA	274686	106882	TTTTAAGTTAGGAGTGCAAG
185513	17709	GGAGATTAGGACCTGATATC	230100	62296	TCGCAAGGACAAAAAAACCA	274687	106883	TTTTTAAGTTAGGAGTGCAA
185514	17710	TGGAGATTAGGACCTGATAT	230101	62297	ATCGCAAGGACAAAAAAACC	274688	106884	TTTTTTAAGTTAGGAGTGCA

185515	17711	CTGGAGATTAGGACCTGATA	230102	62298	TATCGCAAGGACAAAAAAAC	274689	106885	TTTTTTTAAGTTAGGAGTGC
185516	17712	TCTGGAGATTAGGACCTGAT	230103	62299	CTATCGCAAGGACAAAAAAA	274690	106886	TTTTTTTTAAGTTAGGAGTG
185517	17713	TTCTGGAGATTAGGACCTGA	230104	62300	ACTATCGCAAGGACAAAAAA	274691	106887	TTTTTTTTTAAGTTAGGAGT
185518	17714	GTTCTGGAGATTAGGACCTG	230105	62301	AACTATCGCAAGGACAAAAA	274692	106888	TTTTTTTTTTAAGTTAGGAG
185519	17715	GGTTCTGGAGATTAGGACCT	230106	62302	AAACTATCGCAAGGACAAAA	274693	106889	TTTTTTTTTTTAAGTTAGGA
185520	17716	AGGTTCTGGAGATTAGGACC	230107	62303	CAAACTATCGCAAGGACAAA	274694	106890	ATTTTTTTTTTTAAGTTAGG
185521	17717	CAGGTTCTGGAGATTAGGAC	230108	62304	GCAAACTATCGCAAGGACAA	274695	106891	CATTTTTTTTTTTAAGTTAG
185522	17718	ACAGGTTCTGGAGATTAGGA	230109	62305	AGCAAACTATCGCAAGGACA	274696	106892	TCATTTTTTTTTTTAAGTTA
185523	17719	TACAGGTTCTGGAGATTAGG	230110	62306	CAGCAAACTATCGCAAGGAC	274697	106893	TTCATTTTTTTTTTTAAGTT
185524	17720	TTACAGGTTCTGGAGATTAG	230111	62307	TCAGCAAACTATCGCAAGGA	274698	106894	CTTCATTTTTTTTTTTAAGT
185525	17721	TTTACAGGTTCTGGAGATTA	230112	62308	CTCAGCAAACTATCGCAAGG	274699	106895	TCTTCATTTTTTTTTTTAAG
185526	17722	ATTTACAGGTTCTGGAGATT	230113	62309	TCTCAGCAAACTATCGCAAG	274700	106896	TTCTTCATTTTTTTTTTTAA
185527	17723	CATTTACAGGTTCTGGAGAT	230114	62310	TTCTCAGCAAACTATCGCAA	274701	106897	TTTCTTCATTTTTTTTTTTA
185528	17724	ACATTTACAGGTTCTGGAGA	230115	62311	ATTCTCAGCAAACTATCGCA	274702	106898	TTTTCTTCATTTTTTTTTTT
185529	17725	CACATTTACAGGTTCTGGAG	230116	62312	CATTCTCAGCAAACTATCGC	274703	106899	GTTTTCTTCATTTTTTTTTT
185530	17726	TCACATTTACAGGTTCTGGA	230117	62313	TCATTCTCAGCAAACTATCG	274704	106900	TGTTTTCTTCATTTTTTTTT
185531	17727	ATCACATTTACAGGTTCTGG	230118	62314	ATCATTCTCAGCAAACTATC	274705	106901	GTGTTTTCTTCATTTTTTTT
185532	17728	GATCACATTTACAGGTTCTG	230119	62315	CATCATTCTCAGCAAACTAT	274706	106902	TGTGTTTTCTTCATTTTTTT
185533	17729	AGATCACATTTACAGGTTCT	230120	62316	CCATCATTCTCAGCAAACTA	274707	106903	TTGTGTTTTCTTCATTTTTT
185534	17730	AAGATCACATTTACAGGTTC	230121	62317	ACCATCATTCTCAGCAAACT	274708	106904	GTTGTGTTTTCTTCATTTTT
185535	17731	TAAGATCACATTTACAGGTT	230122	62318	AACCATCATTCTCAGCAAAC	274709	106905	GGTTGTGTTTTCTTCATTTT
185536	17732	ATAAGATCACATTTACAGGT	230123	62319	AAACCATCATTCTCAGCAAA	274710	106906	TGGTTGTGTTTTCTTCATTT
185537	17733	AATAAGATCACATTTACAGG	230124	62320	GAAACCATCATTCTCAGCAA	274711	106907	CTGGTTGTGTTTTCTTCATT
185538	17734	AAATAAGATCACATTTACAG	230125	62321	GGAAACCATCATTCTCAGCA	274712	106908	ACTGGTTGTGTTTTCTTCAT
185539	17735	CAAATAAGATCACATTTACA	230126	62322	TGGAAACCATCATTCTCAGC	274713	106909	TACTGGTTGTGTTTTCTTCA
185540	17736	CCAAATAAGATCACATTTAC	230127	62323	CTGGAAACCATCATTCTCAG	274714	106910	TTACTGGTTGTGTTTTCTTC
185541	17737	TCCAAATAAGATCACATTTA	230128	62324	GCTGGAAACCATCATTCTCA	274715	106911	TTTACTGGTTGTGTTTTCTT
185542	17738	TTCCAAATAAGATCACATTT	230129	62325	AGCTGGAAACCATCATTCTC	274716	106912	TTTTACTGGTTGTGTTTTCT
185543	17739	TTTCCAAATAAGATCACATT	230130	62326	AAGCTGGAAACCATCATTCT	274717	106913	GTTTTACTGGTTGTGTTTTC
185544	17740	TTTTCCAAATAAGATCACAT	230131	62327	GAAGCTGGAAACCATCATTC	274718	106914	TGTTTTACTGGTTGTGTTTT
185545	17741	CTTTTCCAAATAAGATCACA	230132	62328	TGAAGCTGGAAACCATCATT	274719	106915	TTGTTTTACTGGTTGTGTTT
185546	17742	CCTTTTCCAAATAAGATCAC	230133	62329	ATGAAGCTGGAAACCATCAT	274720	106916	GTTGTTTTACTGGTTGTGTT
185547	17743	CCCTTTTCCAAATAAGATCA	230134	62330	GATGAAGCTGGAAACCATCA	274721	106917	TGTTGTTTTACTGGTTGTGT
185548	17744	CCCCTTTTCCAAATAAGATC	230135	62331	GGATGAAGCTGGAAACCATC	274722	106918	ATGTTGTTTTACTGGTTGTG
185549	17745	ACCCCTTTTCCAAATAAGAT	230136	62332	TGGATGAAGCTGGAAACCAT	274723	106919	TATGTTGTTTTACTGGTTGT
185550	17746	GACCCCTTTTCCAAATAAGA	230137	62333	ATGGATGAAGCTGGAAACCA	274724	106920	ATATGTTGTTTTACTGGTTG
185551	17747	AGACCCCTTTTCCAAATAAG	230138	62334	CATGGATGAAGCTGGAAACC	274725	106921	TATATGTTGTTTTACTGGTT
185552	17748	AAGACCCCTTTTCCAAATAA	230139	62335	ACATGGATGAAGCTGGAAAC	274726	106922	TTATATGTTGTTTTACTGGT
185553	17749	AAAGACCCCTTTTCCAAATA	230140	62336	GACATGGATGAAGCTGGAAA	274727	106923	GTTATATGTTGTTTTACTGG
185554	17750	CAAAGACCCCTTTTCCAAAT	230141	62337	GGACATGGATGAAGCTGGAA	274728	106924	TGTTATATGTTGTTTTACTG
185555	17751	ACAAAGACCCCTTTTCCAAA	230142	62338	GGGACATGGATGAAGCTGGA	274729	106925	CTGTTATATGTTGTTTTACT
185556	17752	TACAAAGACCCCTTTTCCAA	230143	62339	AGGGACATGGATGAAGCTGG	274730	106926	GCTGTTATATGTTGTTTTAC
185557	17753	CTACAAAGACCCCTTTTCCA	230144	62340	TAGGGACATGGATGAAGCTG	274731	106927	TGCTGTTATATGTTGTTTTA
185558	17754	TCTACAAAGACCCCTTTTCC	230145	62341	GTAGGGACATGGATGAAGCT	274732	106928	ATGCTGTTATATGTTGTTTT
185559	17755	ATCTACAAAGACCCCTTTTC	230146	62342	TGTAGGGACATGGATGAAGC	274733	106929	AATGCTGTTATATGTTGTTT
185560	17756	CATCTACAAAGACCCCTTTT	230147	62343	TTGTAGGGACATGGATGAAG	274734	106930	TAATGCTGTTATATGTTGTT
185561	17757	ACATCTACAAAGACCCCTTT	230148	62344	TTTGTAGGGACATGGATGAA	274735	106931	TTAATGCTGTTATATGTTGT
185562	17758	CACATCTACAAAGACCCCTT	230149	62345	CTTTGTAGGGACATGGATGA	274736	106932	CTTAATGCTGTTATATGTTG
185563	17759	CCACATCTACAAAGACCCCT	230150	62346	CCTTTGTAGGGACATGGATG	274737	106933	TCTTAATGCTGTTATATGTT
185564	17760	ACCACATCTACAAAGACCCC	230151	62347	TCCTTTGTAGGGACATGGAT	274738	106934	CTCTTAATGCTGTTATATGT
185565	17761	AACCACATCTACAAAGACCC	230152	62348	GTCCTTTGTAGGGACATGGA	274739	106935	GCTCTTAATGCTGTTATATG
185566	17762	TAACCACATCTACAAAGACC	230153	62349	TGTCCTTTGTAGGGACATGG	274740	106936	AGCTCTTAATGCTGTTATAT
185567	17763	TTAACCACATCTACAAAGAC	230154	62350	ATGTCCTTTGTAGGGACATG	274741	106937	CAGCTCTTAATGCTGTTATA
185568	17764	TTTAACCACATCTACAAAGA	230155	62351	CATGTCCTTTGTAGGGACAT	274742	106938	CCAGCTCTTAATGCTGTTAT
185569	17765	ATTTAACCACATCTACAAAG	230156	62352	TCATGTCCTTTGTAGGGACA	274743	106939	GCCAGCTCTTAATGCTGTTA
185570	17766	AATTTAACCACATCTACAAA	230157	62353	TTCATGTCCTTTGTAGGGAC	274744	106940	AGCCAGCTCTTAATGCTGTT
185571	17767	TAATTTAACCACATCTACAA	230158	62354	GTTCATGTCCTTTGTAGGGA	274745	106941	GAGCCAGCTCTTAATGCTGT
185572	17768	TTAATTTAACCACATCTACA	230159	62355	AGTTCATGTCCTTTGTAGGG	274746	106942	GGAGCCAGCTCTTAATGCTG
185573	17769	CTTAATTTAACCACATCTAC	230160	62356	GAGTTCATGTCCTTTGTAGG	274747	106943	AGGAGCCAGCTCTTAATGCT
185574	17770	CCTTAATTTAACCACATCTA	230161	62357	TGAGTTCATGTCCTTTGTAG	274748	106944	CAGGAGCCAGCTCTTAATGC
185575	17771	TCCTTAATTTAACCACATCT	230162	62358	ATGAGTTCATGTCCTTTGTA	274749	106945	CCAGGAGCCAGCTCTTAATG
185576	17772	ATCCTTAATTTAACCACATC	230163	62359	GATGAGTTCATGTCCTTTGT	274750	106946	GCCAGGAGCCAGCTCTTAAT
185577	17773	AATCCTTAATTTAACCACAT	230164	62360	TGATGAGTTCATGTCCTTTG	274751	106947	AGCCAGGAGCCAGCTCTTAA
185578	17774	AAATCCTTAATTTAACCACA	230165	62361	ATGATGAGTTCATGTCCTTT	274752	106948	CAGCCAGGAGCCAGCTCTTA
185579	17775	AAAATCCTTAATTTAACCAC	230166	62362	AATGATGAGTTCATGTCCTT	274753	106949	CCAGCCAGGAGCCAGCTCTT
185580	17776	CAAAATCCTTAATTTAACCA	230167	62363	AAATGATGAGTTCATGTCCT	274754	106950	CCCAGCCAGGAGCCAGCTCT
185581	17777	TCAAAATCCTTAATTTAACC	230168	62364	AAAATGATGAGTTCATGTCC	274755	106951	GCCCAGCCAGGAGCCAGCTC
185582	17778	CTCAAAATCCTTAATTTAAC	230169	62365	AAAAATGATGAGTTCATGTC	274756	106952	CGCCCAGCCAGGAGCCAGCT
185583	17779	TCTCAAAATCCTTAATTTAA	230170	62366	AAAAAATGATGAGTTCATGT	274757	106953	GCGCCCAGCCAGGAGCCAGC
185584	17780	ATCTCAAAATCCTTAATTTA	230171	62367	TAAAAAATGATGAGTTCATG	274758	106954	CGCGCCCAGCCAGGAGCCAG
185585	17781	CATCTCAAAATCCTTAATTT	230172	62368	ATAAAAAATGATGAGTTCAT	274759	106955	CCGCGCCCAGCCAGGAGCCA
185586	17782	CCATCTCAAAATCCTTAATT	230173	62369	CATAAAAAATGATGAGTTCA	274760	106956	ACCGCGCCCAGCCAGGAGCC

185587	17783	CCCATCTCAAAATCCTTAAT	230174	62370	CCATAAAAAATGATGAGTTC	274761	106957	CACCGCGCCCAGCCAGGAGC
185588	17784	CCCCATCTCAAAATCCTTAA	230175	62371	GCCATAAAAAATGATGAGTT	274762	106958	CCACCGCGCCCAGCCAGGAG
185589	17785	CCCCCATCTCAAAATCCTTA	230176	62372	AGCCATAAAAAATGATGAGT	274763	106959	GCCACCGCGCCCAGCCAGGA
185590	17786	CCCCCCATCTCAAAATCCTT	230177	62373	CAGCCATAAAAAATGATGAG	274764	106960	CGCCACCGCGCCCAGCCAGG
185591	17787	TCCCCCCATCTCAAAATCCT	230178	62374	GCAGCCATAAAAAATGATGA	274765	106961	GCGCCACCGCGCCCAGCCAG
185592	17788	ATCCCCCCATCTCAAAATCC	230179	62375	TGCAGCCATAAAAAATGATG	274766	106962	TGCGCCACCGCGCCCAGCCA
185593	17789	AATCCCCCCATCTCAAAATC	230180	62376	ATGCAGCCATAAAAAATGAT	274767	106963	ATGCGCCACCGCGCCCAGCC
185594	17790	TAATCCCCCCATCTCAAAAT	230181	62377	TATGCAGCCATAAAAAATGA	274768	106964	CATGCGCCACCGCGCCCAGC
185595	17791	ATAATCCCCCCATCTCAAAA	230182	62378	CTATGCAGCCATAAAAAATG	274769	106965	GCATGCGCCACCGCGCCCAG
185596	17792	GATAATCCCCCCATCTCAAA	230183	62379	ACTATGCAGCCATAAAAAAT	274770	106966	GGCATGCGCCACCGCGCCCA
185597	17793	GGATAATCCCCCCATCTCAA	230184	62380	TACTATGCAGCCATAAAAAA	274771	106967	AGGCATGCGCCACCGCGCCC
185598	17794	AGGATAATCCCCCCATCTCA	230185	62381	ATACTATGCAGCCATAAAAA	274772	106968	CAGGCATGCGCCACCGCGCC
185599	17795	CAGGATAATCCCCCCATCTC	230186	62382	AATACTATGCAGCCATAAAA	274773	106969	ACAGGCATGCGCCACCGCGC
185600	17796	ACAGGATAATCCCCCCATCT	230187	62383	GAATACTATGCAGCCATAAA	274774	106970	TACAGGCATGCGCCACCGCG
185601	17797	TACAGGATAATCCCCCCATC	230188	62384	GGAATACTATGCAGCCATAA	274775	106971	TTACAGGCATGCGCCACCGC
185602	17798	ATACAGGATAATCCCCCCAT	230189	62385	TGGAATACTATGCAGCCATA	274776	106972	ATTACAGGCATGCGCCACCG
185603	17799	AATACAGGATAATCCCCCCA	230190	62386	ATGGAATACTATGCAGCCAT	274777	106973	GATTACAGGCATGCGCCACC
185604	17800	TAATACAGGATAATCCCCCC	230191	62387	CATGGAATACTATGCAGCCA	274778	106974	GGATTACAGGCATGCGCCAC
185605	17801	ATAATACAGGATAATCCCCC	230192	62388	CCATGGAATACTATGCAGCC	274779	106975	GGGATTACAGGCATGCGCCA
185606	17802	GATAATACAGGATAATCCCC	230193	62389	ACCATGGAATACTATGCAGC	274780	106976	TGGGATTACAGGCATGCGCC
185607	17803	AGATAATACAGGATAATCCC	230194	62390	CACCATGGAATACTATGCAG	274781	106977	TTGGGATTACAGGCATGCGC
185608	17804	TAGATAATACAGGATAATCC	230195	62391	ACACCATGGAATACTATGCA	274782	106978	GTTGGGATTACAGGCATGCG
185609	17805	CTAGATAATACAGGATAATC	230196	62392	TACACCATGGAATACTATGC	274783	106979	TGTTGGGATTACAGGCATGC
185610	17806	CCTAGATAATACAGGATAAT	230197	62393	ATACACCATGGAATACTATG	274784	106980	GTGTTGGGATTACAGGCATG
185611	17807	ACCTAGATAATACAGGATAA	230198	62394	TATACACCATGGAATACTAT	274785	106981	AGTGTTGGGATTACAGGCAT
185612	17808	TACCTAGATAATACAGGATA	230199	62395	ATATACACCATGGAATACTA	274786	106982	AAGTGTTGGGATTACAGGCA
185613	17809	CTACCTAGATAATACAGGAT	230200	62396	CATATACACCATGGAATACT	274787	106983	AAAGTGTTGGGATTACAGGC
185614	17810	CCTACCTAGATAATACAGGA	230201	62397	ACATATACACCATGGAATAC	274788	106984	CAAAGTGTTGGGATTACAGG
185615	17811	ACCTACCTAGATAATACAGG	230202	62398	CACATATACACCATGGAATA	274789	106985	CCAAAGTGTTGGGATTACAG
185616	17812	GACCTACCTAGATAATACAG	230203	62399	GCACATATACACCATGGAAT	274790	106986	CCCAAAGTGTTGGGATTACA
185617	17813	GGACCTACCTAGATAATACA	230204	62400	GGCACATATACACCATGGAA	274791	106987	TCCCAAAGTGTTGGGATTAC
185618	17814	AGGACCTACCTAGATAATAC	230205	62401	TGGCACATATACACCATGGA	274792	106988	CTCCCAAAGTGTTGGGATTA
185619	17815	TAGGACCTACCTAGATAATA	230206	62402	GTGGCACATATACACCATGG	274793	106989	CCTCCCAAAGTGTTGGGATT
185620	17816	TTAGGACCTACCTAGATAAT	230207	62403	TGTGGCACATATACACCATG	274794	106990	GCCTCCCAAAGTGTTGGGAT
185621	17817	TTTAGGACCTACCTAGATAA	230208	62404	ATGTGGCACATATACACCAT	274795	106991	GGCCTCCCAAAGTGTTGGGA
185622	17818	ATTTAGGACCTACCTAGATA	230209	62405	AATGTGGCACATATACACCA	274796	106992	CGGCCTCCCAAAGTGTTGGG
185623	17819	CATTTAGGACCTACCTAGAT	230210	62406	AAATGTGGCACATATACACC	274797	106993	TCGGCCTCCCAAAGTGTTGG
185624	17820	GCATTTAGGACCTACCTAGA	230211	62407	AAAATGTGGCACATATACAC	274798	106994	ATCGGCCTCCCAAAGTGTTG
185625	17821	TGCATTTAGGACCTACCTAG	230212	62408	GAAAATGTGGCACATATACA	274799	106995	CATCGGCCTCCCAAAGTGTT
185626	17822	CTGCATTTAGGACCTACCTA	230213	62409	AGAAAATGTGGCACATATAC	274800	106996	GCATCGGCCTCCCAAAGTGT
185627	17823	ACTGCATTTAGGACCTACCT	230214	62410	AAGAAAATGTGGCACATATA	274801	106997	AGCATCGGCCTCCCAAAGTG
185628	17824	GACTGCATTTAGGACCTACC	230215	62411	TAAGAAAATGTGGCACATAT	274802	106998	CAGCATCGGCCTCCCAAAGT
185629	17825	TGACTGCATTTAGGACCTAC	230216	62412	TTAAGAAAATGTGGCACATA	274803	106999	CCAGCATCGGCCTCCCAAAG
185630	17826	GTGACTGCATTTAGGACCTA	230217	62413	ATTAAGAAAATGTGGCACAT	274804	107000	TCCAGCATCGGCCTCCCAAA
185631	17827	TGTGACTGCATTTAGGACCT	230218	62414	GATTAAGAAAATGTGGCACA	274805	107001	CTCCAGCATCGGCCTCCCAA
185632	17828	GTGTGACTGCATTTAGGACC	230219	62415	GGATTAAGAAAATGTGGCAC	274806	107002	CCTCCAGCATCGGCCTCCCA
185633	17829	AGTGTGACTGCATTTAGGAC	230220	62416	TGGATTAAGAAAATGTGGCA	274807	107003	TCCTCCAGCATCGGCCTCCC
185634	17830	GAGTGTGACTGCATTTAGGA	230221	62417	CTGGATTAAGAAAATGTGGC	274808	107004	ATCCTCCAGCATCGGCCTCC
185635	17831	TGAGTGTGACTGCATTTAGG	230222	62418	ACTGGATTAAGAAAATGTGG	274809	107005	GATCCTCCAGCATCGGCCTC
185636	17832	ATGAGTGTGACTGCATTTAG	230223	62419	GACTGGATTAAGAAAATGTG	274810	107006	TGATCCTCCAGCATCGGCCT
185637	17833	GATGAGTGTGACTGCATTTA	230224	62420	AGACTGGATTAAGAAAATGT	274811	107007	GTGATCCTCCAGCATCGGCC
185638	17834	GGATGAGTGTGACTGCATTT	230225	62421	TAGACTGGATTAAGAAAATG	274812	107008	AGTGATCCTCCAGCATCGGC
185639	17835	AGGATGAGTGTGACTGCATT	230226	62422	ATAGACTGGATTAAGAAAAT	274813	107009	AAGTGATCCTCCAGCATCGG
185640	17836	AAGGATGAGTGTGACTGCAT	230227	62423	GATAGACTGGATTAAGAAAA	274814	107010	CAAGTGATCCTCCAGCATCG
185641	17837	CAAGGATGAGTGTGACTGCA	230228	62424	TGATAGACTGGATTAAGAAA	274815	107011	TCAAGTGATCCTCCAGCATC
185642	17838	ACAAGGATGAGTGTGACTGC	230229	62425	ATGATAGACTGGATTAAGAA	274816	107012	CTCAAGTGATCCTCCAGCAT
185643	17839	TACAAGGATGAGTGTGACTG	230230	62426	AATGATAGACTGGATTAAGA	274817	107013	TCTCAAGTGATCCTCCAGCA
185644	17840	TTACAAGGATGAGTGTGACT	230231	62427	CAATGATAGACTGGATTAAG	274818	107014	GTCTCAAGTGATCCTCCAGC
185645	17841	CTTACAAGGATGAGTGTGAC	230232	62428	ACAATGATAGACTGGATTAA	274819	107015	GGTCTCAAGTGATCCTCCAG
185646	17842	TCTTACAAGGATGAGTGTGA	230233	62429	AACAATGATAGACTGGATTA	274820	107016	TGGTCTCAAGTGATCCTCCA
185647	17843	CTCTTACAAGGATGAGTGTG	230234	62430	CAACAATGATAGACTGGATT	274821	107017	CTGGTCTCAAGTGATCCTCC
185648	17844	CCTCTTACAAGGATGAGTGT	230235	62431	CCAACAATGATAGACTGGAT	274822	107018	CCTGGTCTCAAGTGATCCTC
185649	17845	TCCTCTTACAAGGATGAGTG	230236	62432	TCCAACAATGATAGACTGGA	274823	107019	TCCTGGTCTCAAGTGATCCT
185650	17846	TTCCTCTTACAAGGATGAGT	230237	62433	GTCCAACAATGATAGACTGG	274824	107020	CTCCTGGTCTCAAGTGATCC
185651	17847	CTTCCTCTTACAAGGATGAG	230238	62434	TGTCCAACAATGATAGACTG	274825	107021	ACTCCTGGTCTCAAGTGATC
185652	17848	CCTTCCTCTTACAAGGATGA	230239	62435	ATGTCCAACAATGATAGACT	274826	107022	AACTCCTGGTCTCAAGTGAT
185653	17849	TCCTTCCTCTTACAAGGATG	230240	62436	AATGTCCAACAATGATAGAC	274827	107023	GAACTCCTGGTCTCAAGTGA
185654	17850	TTCCTTCCTCTTACAAGGAT	230241	62437	AAATGTCCAACAATGATAGA	274828	107024	TGAACTCCTGGTCTCAAGTG
185655	17851	CTTCCTTCCTCTTACAAGGA	230242	62438	CAAATGTCCAACAATGATAG	274829	107025	TTGAACTCCTGGTCTCAAGT
185656	17852	TCTTCCTTCCTCTTACAAGG	230243	62439	CCAAATGTCCAACAATGATA	274830	107026	CTTGAACTCCTGGTCTCAAG
185657	17853	CTCTTCCTTCCTCTTACAAG	230244	62440	CCCAAATGTCCAACAATGAT	274831	107027	CCTTGAACTCCTGGTCTCAA
185658	17854	TCTCTTCCTTCCTCTTACAA	230245	62441	ACCCAAATGTCCAACAATGA	274832	107028	ACCTTGAACTCCTGGTCTCA

185659	17855	CTCTCTTCCTTCCTCTTACA	230246	62442	AACCCAAATGTCCAACAATG	274833	107029	AACCTTGAACTCCTGGTCTC
185660	17856	TCTCTCTTCCTTCCTCTTAC	230247	62443	CAACCCAAATGTCCAACAAT	274834	107030	CAACCTTGAACTCCTGGTCT
185661	17857	CTCTCTCTTCCTTCCTCTTA	230248	62444	CCAACCCAAATGTCCAACAA	274835	107031	GCAACCTTGAACTCCTGGTC
185662	17858	TCTCTCTCTTCCTTCCTCTT	230249	62445	ACCAACCCAAATGTCCAACA	274836	107032	TGCAACCTTGAACTCCTGGT
185663	17859	ATCTCTCTCTTCCTTCCTCT	230250	62446	AACCAACCCAAATGTCCAAC	274837	107033	CTGCAACCTTGAACTCCTGG
185664	17860	CATCTCTCTCTTCCTTCCTC	230251	62447	GAACCAACCCAAATGTCCAA	274838	107034	ACTGCAACCTTGAACTCCTG
185665	17861	CCATCTCTCTCTTCCTTCCT	230252	62448	GGAACCAACCCAAATGTCCA	274839	107035	CACTGCAACCTTGAACTCCT
185666	17862	TCCATCTCTCTCTTCCTTCC	230253	62449	TGGAACCAACCCAAATGTCC	274840	107036	TCACTGCAACCTTGAACTCC
185667	17863	TTCCATCTCTCTCTTCCTTC	230254	62450	TTGGAACCAACCCAAATGTC	274841	107037	CTCACTGCAACCTTGAACTC
185668	17864	TTTCCATCTCTCTCTTCCTT	230255	62451	CTTGGAACCAACCCAAATGT	274842	107038	GCTCACTGCAACCTTGAACT
185669	17865	TTTTCCATCTCTCTCTTCCT	230256	62452	ACTTGGAACCAACCCAAATG	274843	107039	AGCTCACTGCAACCTTGAAC
185670	17866	GTTTTCCATCTCTCTCTTCC	230257	62453	GACTTGGAACCAACCCAAAT	274844	107040	TAGCTCACTGCAACCTTGAA
185671	17867	TGTTTTCCATCTCTCTCTTC	230258	62454	AGACTTGGAACCAACCCAAA	274845	107041	ATAGCTCACTGCAACCTTGA
185672	17868	GTGTTTTCCATCTCTCTCTT	230259	62455	AAGACTTGGAACCAACCCAA	274846	107042	CATAGCTCACTGCAACCTTG
185673	17869	TGTGTTTTCCATCTCTCTCT	230260	62456	AAAGACTTGGAACCAACCCA	274847	107043	TCATAGCTCACTGCAACCTT
185674	17870	CTGTGTTTTCCATCTCTCTC	230261	62457	CAAAGACTTGGAACCAACCC	274848	107044	ATCATAGCTCACTGCAACCT
185675	17871	TCTGTGTTTTCCATCTCTCT	230262	62458	GCAAAGACTTGGAACCAACC	274849	107045	GATCATAGCTCACTGCAACC
185676	17872	TTCTGTGTTTTCCATCTCTC	230263	62459	AGCAAAGACTTGGAACCAAC	274850	107046	TGATCATAGCTCACTGCAAC
185677	17873	CTTCTGTGTTTTCCATCTCT	230264	62460	TAGCAAAGACTTGGAACCAA	274851	107047	ATGATCATAGCTCACTGCAA
185678	17874	TCTTCTGTGTTTTCCATCTC	230265	62461	ATAGCAAAGACTTGGAACCA	274852	107048	TATGATCATAGCTCACTGCA
185679	17875	CTCTTCTGTGTTTTCCATCT	230266	62462	AATAGCAAAGACTTGGAACC	274853	107049	GTATGATCATAGCTCACTGC
185680	17876	TCTCTTCTGTGTTTTCCATC	230267	62463	CAATAGCAAAGACTTGGAAC	274854	107050	GGTATGATCATAGCTCACTG
185681	17877	TTCTCTTCTGTGTTTTCCAT	230268	62464	ACAATAGCAAAGACTTGGAA	274855	107051	TGGTATGATCATAGCTCACT
185682	17878	CTTCTCTTCTGTGTTTTCCA	230269	62465	CACAATAGCAAAGACTTGGA	274856	107052	GTGGTATGATCATAGCTCAC
185683	17879	TCTTCTCTTCTGTGTTTTCC	230270	62466	TCACAATAGCAAAGACTTGG	274857	107053	AGTGGTATGATCATAGCTCA
185684	17880	GTCTTCTCTTCTGTGTTTTC	230271	62467	TTCACAATAGCAAAGACTTG	274858	107054	TAGTGGTATGATCATAGCTC
185685	17881	TGTCTTCTCTTCTGTGTTTT	230272	62468	ATTCACAATAGCAAAGACTT	274859	107055	GTAGTGGTATGATCATAGCT
185686	17882	TTGTCTTCTCTTCTGTGTTT	230273	62469	TATTCACAATAGCAAAGACT	274860	107056	TGTAGTGGTATGATCATAGC
185687	17883	ATTGTCTTCTCTTCTGTGTT	230274	62470	CTATTCACAATAGCAAAGAC	274861	107057	GTGTAGTGGTATGATCATAG
185688	17884	CATTGTCTTCTCTTCTGTGT	230275	62471	ACTATTCACAATAGCAAAGA	274862	107058	GGTGTAGTGGTATGATCATA
185689	17885	ACATTGTCTTCTCTTCTGTG	230276	62472	CACTATTCACAATAGCAAAG	274863	107059	GGGTGTAGTGGTATGATCAT
185690	17886	CACATTGTCTTCTCTTCTGT	230277	62473	GCACTATTCACAATAGCAAA	274864	107060	AGGGTGTAGTGGTATGATCA
185691	17887	CCACATTGTCTTCTCTTCTG	230278	62474	GGCACTATTCACAATAGCAA	274865	107061	TAGGGTGTAGTGGTATGATC
185692	17888	ACCACATTGTCTTCTCTTCT	230279	62475	CGGCACTATTCACAATAGCA	274866	107062	CTAGGGTGTAGTGGTATGAT
185693	17889	CACCACATTGTCTTCTCTTC	230280	62476	GCGGCACTATTCACAATAGC	274867	107063	GCTAGGGTGTAGTGGTATGA
185694	17890	TCACCACATTGTCTTCTCTT	230281	62477	TGCGGCACTATTCACAATAG	274868	107064	GGCTAGGGTGTAGTGGTATG
185695	17891	ATCACCACATTGTCTTCTCT	230282	62478	TTGCGGCACTATTCACAATA	274869	107065	AGGCTAGGGTGTAGTGGTAT
185696	17892	CATCACCACATTGTCTTCTC	230283	62479	ATTGCGGCACTATTCACAAT	274870	107066	CAGGCTAGGGTGTAGTGGTA
185697	17893	CCATCACCACATTGTCTTCT	230284	62480	TATTGCGGCACTATTCACAA	274871	107067	CCAGGCTAGGGTGTAGTGGT
185698	17894	TCCATCACCACATTGTCTTC	230285	62481	TTATTGCGGCACTATTCACA	274872	107068	CCCAGGCTAGGGTGTAGTGG
185699	17895	CTCCATCACCACATTGTCTT	230286	62482	TTTATTGCGGCACTATTCAC	274873	107069	GCCCAGGCTAGGGTGTAGTG
185700	17896	CCTCCATCACCACATTGTCT	230287	62483	GTTTATTGCGGCACTATTCA	274874	107070	TGCCCAGGCTAGGGTGTAGT
185701	17897	GCCTCCATCACCACATTGTC	230288	62484	TGTTTATTGCGGCACTATTC	274875	107071	TTGCCCAGGCTAGGGTGTAG
185702	17898	TGCCTCCATCACCACATTGT	230289	62485	ATGTTTATTGCGGCACTATT	274876	107072	GTTGCCCAGGCTAGGGTGTA
185703	17899	CTGCCTCCATCACCACATTG	230290	62486	TATGTTTATTGCGGCACTAT	274877	107073	TGTTGCCCAGGCTAGGGTGT
185704	17900	TCTGCCTCCATCACCACATT	230291	62487	GTATGTTTATTGCGGCACTA	274878	107074	GTGTTGCCCAGGCTAGGGTG
185705	17901	CTCTGCCTCCATCACCACAT	230292	62488	CGTATGTTTATTGCGGCACT	274879	107075	TGTGTTGCCCAGGCTAGGGT
185706	17902	TCTCTGCCTCCATCACCACA	230293	62489	ACGTATGTTTATTGCGGCAC	274880	107076	CTGTGTTGCCCAGGCTAGGG
185707	17903	ATCTCTGCCTCCATCACCAC	230294	62490	CACGTATGTTTATTGCGGCA	274881	107077	ACTGTGTTGCCCAGGCTAGG
185708	17904	AATCTCTGCCTCCATCACCA	230295	62491	ACACGTATGTTTATTGCGGC	274882	107078	CACTGTGTTGCCCAGGCTAG
185709	17905	CAATCTCTGCCTCCATCACC	230296	62492	CACACGTATGTTTATTGCGG	274883	107079	TCACTGTGTTGCCCAGGCTA
185710	17906	CCAATCTCTGCCTCCATCAC	230297	62493	GCACACGTATGTTTATTGCG	274884	107080	CTCACTGTGTTGCCCAGGCT
185711	17907	TCCAATCTCTGCCTCCATCA	230298	62494	TGCACACGTATGTTTATTGC	274885	107081	TCTCACTGTGTTGCCCAGGC
185712	17908	CTCCAATCTCTGCCTCCATC	230299	62495	ATGCACACGTATGTTTATTG	274886	107082	GTCTCACTGTGTTGCCCAGG
185713	17909	ACTCCAATCTCTGCCTCCAT	230300	62496	CATGCACACGTATGTTTATT	274887	107083	AGTCTCACTGTGTTGCCCAG
185714	17910	CACTCCAATCTCTGCCTCCA	230301	62497	ACATGCACACGTATGTTTAT	274888	107084	CAGTCTCACTGTGTTGCCCA
185715	17911	TCACTCCAATCTCTGCCTCC	230302	62498	CACATGCACACGTATGTTTA	274889	107085	TCAGTCTCACTGTGTTGCCC
185716	17912	CTCACTCCAATCTCTGCCTC	230303	62499	ACACATGCACACGTATGTTT	274890	107086	CTCAGTCTCACTGTGTTGCC
185717	17913	CCTCACTCCAATCTCTGCCT	230304	62500	GACACATGCACACGTATGTT	274891	107087	TCTCAGTCTCACTGTGTTGC
185718	17914	ACCTCACTCCAATCTCTGCC	230305	62501	AGACACATGCACACGTATGT	274892	107088	GTCTCAGTCTCACTGTGTTG
185719	17915	CACCTCACTCCAATCTCTGC	230306	62502	AAGACACATGCACACGTATG	274893	107089	AGTCTCAGTCTCACTGTGTT
185720	17916	CCACCTCACTCCAATCTCTG	230307	62503	AAAGACACATGCACACGTAT	274894	107090	GAGTCTCAGTCTCACTGTGT
185721	17917	GCCACCTCACTCCAATCTCT	230308	62504	TAAAGACACATGCACACGTA	274895	107091	AGAGTCTCAGTCTCACTGTG
185722	17918	GGCCACCTCACTCCAATCTC	230309	62505	ATAAAGACACATGCACACGT	274896	107092	TAGAGTCTCAGTCTCACTGT
185723	17919	TGGCCACCTCACTCCAATCT	230310	62506	TATAAAGACACATGCACACG	274897	107093	ATAGAGTCTCAGTCTCACTG
185724	17920	GTGGCCACCTCACTCCAATC	230311	62507	TTATAAAGACACATGCACAC	274898	107094	AATAGAGTCTCAGTCTCACT
185725	17921	TGTGGCCACCTCACTCCAAT	230312	62508	GTTATAAAGACACATGCACA	274899	107095	TAATAGAGTCTCAGTCTCAC
185726	17922	TTGTGGCCACCTCACTCCAA	230313	62509	TGTTATAAAGACACATGCAC	274900	107096	TTAATAGAGTCTCAGTCTCA
185727	17923	CTTGTGGCCACCTCACTCCA	230314	62510	CTGTTATAAAGACACATGCA	274901	107097	TTTAATAGAGTCTCAGTCTC
185728	17924	GCTTGTGGCCACCTCACTCC	230315	62511	GCTGTTATAAAGACACATGC	274902	107098	TTTTAATAGAGTCTCAGTCT
185729	17925	GGCTTGTGGCCACCTCACTC	230316	62512	TGCTGTTATAAAGACACATG	274903	107099	TTTTTAATAGAGTCTCAGTC
185730	17926	TGGCTTGTGGCCACCTCACT	230317	62513	ATGCTGTTATAAAGACACAT	274904	107100	TTTTTTAATAGAGTCTCAGT

185731	17927	TTGGCTTGTGGCCACCTCAC	230318	62514	CATGCTGTTATAAAGACACA	274905	107101	TTTTTTTAATAGAGTCTCAG
185732	17928	CTTGGCTTGTGGCCACCTCA	230319	62515	TCATGCTGTTATAAAGACAC	274906	107102	TTTTTTTTAATAGAGTCTCA
185733	17929	CCTTGGCTTGTGGCCACCTC	230320	62516	ATCATGCTGTTATAAAGACA	274907	107103	TTTTTTTTTAATAGAGTCTC
185734	17930	TCCTTGGCTTGTGGCCACCT	230321	62517	AATCATGCTGTTATAAAGAC	274908	107104	TTTTTTTTTAATAGAGTCT
185735	17931	GTCCTTGGCTTGTGGCCACC	230322	62518	AAATCATGCTGTTATAAAGA	274909	107105	ATTTTTTTTTTAATAGAGTC
185736	17932	AGTCCTTGGCTTGTGGCCAC	230323	62519	TAAATCATGCTGTTATAAAG	274910	107106	CATTTTTTTTTTAATAGAGT
185737	17933	CAGTCCTTGGCTTGTGGCCA	230324	62520	ATAAATCATGCTGTTATAAA	274911	107107	GCATTTTTTTTTTAATAGAG
185738	17934	GCAGTCCTTGGCTTGTGGCC	230325	62521	TATAAATCATGCTGTTATAA	274912	107108	AGCATTTTTTTTTTAATAGA
185739	17935	AGCAGTCCTTGGCTTGTGGC	230326	62522	ATATAAATCATGCTGTTATA	274913	107109	CAGCATTTTTTTTTTAATAG
185740	17936	CAGCAGTCCTTGGCTTGTGG	230327	62523	AATATAAATCATGCTGTTAT	274914	107110	CCAGCATTTTTTTTTTAATA
185741	17937	CCAGCAGTCCTTGGCTTGTG	230328	62524	GAATATAAATCATGCTGTTA	274915	107111	ACCAGCATTTTTTTTTTAAT
185742	17938	GCCAGCAGTCCTTGGCTTGT	230329	62525	GGAATATAAATCATGCTGTT	274916	107112	AACCAGCATTTTTTTTTTAA
185743	17939	TGCCAGCAGTCCTTGGCTTG	230330	62526	AGGAATATAAATCATGCTGT	274917	107113	GAACCAGCATTTTTTTTTTA
185744	17940	CTGCCAGCAGTCCTTGGCTT	230331	62527	AAGGAATATAAATCATGCTG	274918	107114	GGAACCAGCATTTTTTTTTT
185745	17941	GCTGCCAGCAGTCCTTGGCT	230332	62528	AAAGGAATATAAATCATGCT	274919	107115	AGGAACCAGCATTTTTTTTT
185746	17942	AGCTGCCAGCAGTCCTTGGC	230333	62529	CAAAGGAATATAAATCATGC	274920	107116	AAGGAACCAGCATTTTTTTT
185747	17943	TAGCTGCCAGCAGTCCTTGG	230334	62530	CCAAAGGAATATAAATCATG	274921	107117	GAAGGAACCAGCATTTTTTT
185748	17944	GTAGCTGCCAGCAGTCCTTG	230335	62531	ACCAAAGGAATATAAATCAT	274922	107118	GGAAGGAACCAGCATTTTTT
185749	17945	GGTAGCTGCCAGCAGTCCTT	230336	62532	AACCAAAGGAATATAAATCA	274923	107119	AGGAAGGAACCAGCATTTTT
185750	17946	TGGTAGCTGCCAGCAGTCCT	230337	62533	TAACCAAAGGAATATAAATC	274924	107120	AAGGAAGGAACCAGCATTTT
185751	17947	CTGGTAGCTGCCAGCAGTCC	230338	62534	ATAACCAAAGGAATATAAAT	274925	107121	TAAGGAAGGAACCAGCATTT
185752	17948	GCTGGTAGCTGCCAGCAGTC	230339	62535	TATAACCAAAGGAATATAAA	274926	107122	ATAAGGAAGGAACCAGCATT
185753	17949	TGCTGGTAGCTGCCAGCAGT	230340	62536	ATATAACCAAAGGAATATAA	274927	107123	AATAAGGAAGGAACCAGCAT
185754	17950	CTGCTGGTAGCTGCCAGCAG	230341	62537	TATATAACCAAAGGAATATA	274928	107124	AAATAAGGAAGGAACCAGCA
185755	17951	GCTGCTGGTAGCTGCCAGCA	230342	62538	GTATATAACCAAAGGAATAT	274929	107125	GAAATAAGGAAGGAACCAGC
185756	17952	GGCTGCTGGTAGCTGCCAGC	230343	62539	GGTATATAACCAAAGGAATA	274930	107126	TGAAATAAGGAAGGAACCAG
185757	17953	TGGCTGCTGGTAGCTGCCAG	230344	62540	GGGTATATAACCAAAGGAAT	274931	107127	ATGAAATAAGGAAGGAACCA
185758	17954	CTGGCTGCTGGTAGCTGCCA	230345	62541	TGGGTATATAACCAAAGGAA	274932	107128	AATGAAATAAGGAAGGAACC
185759	17955	TCTGGCTGCTGGTAGCTGCC	230346	62542	CTGGGTATATAACCAAAGGA	274933	107129	GAATGAAATAAGGAAGGAAC
185760	17956	TTCTGGCTGCTGGTAGCTGC	230347	62543	ACTGGGTATATAACCAAAGG	274934	107130	GGAATGAAATAAGGAAGGAA
185761	17957	TTTCTGGCTGCTGGTAGCTG	230348	62544	TACTGGGTATATAACCAAAG	274935	107131	AGGAATGAAATAAGGAAGGA
185762	17958	TTTTCTGGCTGCTGGTAGCT	230349	62545	TTACTGGGTATATAACCAAA	274936	107132	AAGGAATGAAATAAGGAAGG
185763	17959	CTTTTCTGGCTGCTGGTAGC	230350	62546	ATTACTGGGTATATAACCAA	274937	107133	AAAGGAATGAAATAAGGAAG
185764	17960	ACTTTTCTGGCTGCTGGTAG	230351	62547	CATTACTGGGTATATAACCA	274938	107134	TAAAGGAATGAAATAAGGAA
185765	17961	GACTTTTCTGGCTGCTGGTA	230352	62548	TCATTACTGGGTATATAACC	274939	107135	ATAAAGGAATGAAATAAGGA
185766	17962	GGACTTTTCTGGCTGCTGGT	230353	62549	CTCATTACTGGGTATATAAC	274940	107136	AATAAAGGAATGAAATAAGG
185767	17963	TGGACTTTTCTGGCTGCTGG	230354	62550	TCTCATTACTGGGTATATAA	274941	107137	GAATAAAGGAATGAAATAAG
185768	17964	CTGGACTTTTCTGGCTGCTG	230355	62551	ATCTCATTACTGGGTATATA	274942	107138	TGAATAAAGGAATGAAATAA
185769	17965	CCTGGACTTTTCTGGCTGCT	230356	62552	CATCTCATTACTGGGTATAT	274943	107139	ATGAATAAAGGAATGAAATA
185770	17966	TCCTGGACTTTTCTGGCTGC	230357	62553	CCATCTCATTACTGGGTATA	274944	107140	AATGAATAAAGGAATGAAAT
185771	17967	TTCCTGGACTTTTCTGGCTG	230358	62554	GCCATCTCATTACTGGGTAT	274945	107141	GAATGAATAAAGGAATGAAA
185772	17968	GTTCCTGGACTTTTCTGGCT	230359	62555	AGCCATCTCATTACTGGGTA	274946	107142	TGAATGAATAAAGGAATGAA
185773	17969	GGTTCCTGGACTTTTCTGGC	230360	62556	CAGCCATCTCATTACTGGGT	274947	107143	ATGAATGAATAAAGGAATGA
185774	17970	TGGTTCCTGGACTTTTCTGG	230361	62557	CCAGCCATCTCATTACTGGG	274948	107144	AATGAATGAATAAAGGAATG
185775	17971	TTGGTTCCTGGACTTTTCTG	230362	62558	CCCAGCCATCTCATTACTGG	274949	107145	GAATGAATGAATAAAGGAAT
185776	17972	ATTGGTTCCTGGACTTTTCT	230363	62559	ACCCAGCCATCTCATTACTG	274950	107146	TGAATGAATGAATAAAGGAA
185777	17973	AATTGGTTCCTGGACTTTTC	230364	62560	GACCCAGCCATCTCATTACT	274951	107147	CTGAATGAATGAATAAAGGA
185778	17974	GAATTGGTTCCTGGACTTTT	230365	62561	TGACCCAGCCATCTCATTAC	274952	107148	TCTGAATGAATGAATAAAGG
185779	17975	AGAATTGGTTCCTGGACTTT	230366	62562	TTGACCCAGCCATCTCATTA	274953	107149	GTCTGAATGAATGAATAAAG
185780	17976	GAGAATTGGTTCCTGGACTT	230367	62563	TTTGACCCAGCCATCTCATT	274954	107150	TGTCTGAATGAATGAATAAA
185781	17977	AGAGAATTGGTTCCTGGACT	230368	62564	ATTTGACCCAGCCATCTCAT	274955	107151	TTGTCTGAATGAATGAATAA
185782	17978	GAGAGAATTGGTTCCTGGAC	230369	62565	CATTTGACCCAGCCATCTCA	274956	107152	GTTGTCTGAATGAATGAATA
185783	17979	AGAGAGAATTGGTTCCTGGA	230370	62566	CCATTTGACCCAGCCATCTC	274957	107153	TGTTGTCTGAATGAATGAAT
185784	17980	AAGAGAGAATTGGTTCCTGG	230371	62567	ACCATTTGACCCAGCCATCT	274958	107154	ATGTTGTCTGAATGAATGAA
185785	17981	CAAGAGAGAATTGGTTCCTG	230372	62568	TACCATTTGACCCAGCCATC	274959	107155	AATGTTGTCTGAATGAATGA
185786	17982	CCAAGAGAGAATTGGTTCCT	230373	62569	ATACCATTTGACCCAGCCAT	274960	107156	AAATGTTGTCTGAATGAATG
185787	17983	TCCAAGAGAGAATTGGTTCC	230374	62570	AATACCATTTGACCCAGCCA	274961	107157	TAAATGTTGTCTGAATGAAT
185788	17984	CTCCAAGAGAGAATTGGTTC	230375	62571	AAATACCATTTGACCCAGCC	274962	107158	ATAAATGTTGTCTGAATGAA
185789	17985	GCTCCAAGAGAGAATTGGTT	230376	62572	GAAATACCATTTGACCCAGC	274963	107159	CATAAATGTTGTCTGAATGA
185790	17986	AGCTCCAAGAGAGAATTGGT	230377	62573	AGAAATACCATTTGACCCAG	274964	107160	CCATAAATGTTGTCTGAATG
185791	17987	GAGCTCCAAGAGAGAATTGG	230378	62574	TAGAAATACCATTTGACCCA	274965	107161	CCCATAAATGTTGTCTGAAT
185792	17988	GGAGCTCCAAGAGAGAATTG	230379	62575	CTAGAAATACCATTTGACCC	274966	107162	CCCCATAAATGTTGTCTGAA
185793	17989	TGGAGCTCCAAGAGAGAATT	230380	62576	ACTAGAAATACCATTTGACC	274967	107163	GCCCCATAAATGTTGTCTGA
185794	17990	CTGGAGCTCCAAGAGAGAAT	230381	62577	AACTAGAAATACCATTTGAC	274968	107164	TGCCCCATAAATGTTGTCTG
185795	17991	TCTGGAGCTCCAAGAGAGAA	230382	62578	GAACTAGAAATACCATTTGA	274969	107165	GTGCCCCATAAATGTTGTCT
185796	17992	CTCTGGAGCTCCAAGAGAGA	230383	62579	AGAACTAGAAATACCATTTG	274970	107166	AGTGCCCCATAAATGTTGTC
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185798	17994	CCCTCTGGAGCTCCAAGAGA	230385	62581	CTAGAACTAGAAATACCATT	274972	107168	GAAGTGCCCCATAAATGTTG
185799	17995	TCCCTCTGGAGCTCCAAGAG	230386	62582	TCTAGAACTAGAAATACCAT	274973	107169	AGAAGTGCCCCATAAATGTT
185800	17996	CTCCCTCTGGAGCTCCAAGA	230387	62583	ATCTAGAACTAGAAATACCA	274974	107170	CAGAAGTGCCCCATAAATGT
185801	17997	ACTCCCTCTGGAGCTCCAAG	230388	62584	GATCTAGAACTAGAAATACC	274975	107171	TCAGAAGTGCCCCATAAATG
185802	17998	CACTCCCTCTGGAGCTCCAA	230389	62585	GGATCTAGAACTAGAAATAC	274976	107172	CTCAGAAGTGCCCCATAAAT

185803	17999	ACACTCCCTCTGGAGCTCCA	230390	62586	GGGATCTAGAACTAGAAATA	274977	107173	GCTCAGAAGTGCCCCATAAA
185804	18000	CACACTCCCTCTGGAGCTCC	230391	62587	AGGGATCTAGAACTAGAAAT	274978	107174	TGCTCAGAAGTGCCCCATAA
185805	18001	CCACACTCCCTCTGGAGCTC	230392	62588	CAGGGATCTAGAACTAGAAA	274979	107175	GTGCTCAGAAGTGCCCCATA
185806	18002	GCCACACTCCCTCTGGAGCT	230393	62589	TCAGGGATCTAGAACTAGAA	274980	107176	GGTGCTCAGAAGTGCCCCAT
185807	18003	GGCCACACTCCCTCTGGAGC	230394	62590	CTCAGGGATCTAGAACTAGA	274981	107177	TGGTGCTCAGAAGTGCCCCA
185808	18004	GGGCCACACTCCCTCTGGAG	230395	62591	CCTCAGGGATCTAGAACTAG	274982	107178	CTGGTGCTCAGAAGTGCCCC
185809	18005	AGGGCCACACTCCCTCTGGA	230396	62592	TCCTCAGGGATCTAGAACTA	274983	107179	CCTGGTGCTCAGAAGTGCCC
185810	18006	CAGGGCCACACTCCCTCTGG	230397	62593	TTCCTCAGGGATCTAGAACT	274984	107180	GCCTGGTGCTCAGAAGTGCC
185811	18007	GCAGGGCCACACTCCCTCTG	230398	62594	ATTCCTCAGGGATCTAGAAC	274985	107181	AGCCTGGTGCTCAGAAGTGC
185812	18008	AGCAGGGCCACACTCCCTCT	230399	62595	GATTCCTCAGGGATCTAGAA	274986	107182	GAGCCTGGTGCTCAGAAGTG
185813	18009	CAGCAGGGCCACACTCCCTC	230400	62596	CGATTCCTCAGGGATCTAGA	274987	107183	AGAGCCTGGTGCTCAGAAGT
185814	18010	TCAGCAGGGCCACACTCCCT	230401	62597	GCGATTCCTCAGGGATCTAG	274988	107184	CAGAGCCTGGTGCTCAGAAG
185815	18011	GTCAGCAGGGCCACACTCCC	230402	62598	GGCGATTCCTCAGGGATCTA	274989	107185	ACAGAGCCTGGTGCTCAGAA
185816	18012	TGTCAGCAGGGCCACACTCC	230403	62599	TGGCGATTCCTCAGGGATCT	274990	107186	CACAGAGCCTGGTGCTCAGA
185817	18013	GTGTCAGCAGGGCCACACTC	230404	62600	GTGGCGATTCCTCAGGGATC	274991	107187	GCACAGAGCCTGGTGCTCAG
185818	18014	GGTGTCAGCAGGGCCACACT	230405	62601	TGTGGCGATTCCTCAGGGAT	274992	107188	AGCACAGAGCCTGGTGCTCA
185819	18015	AGGTGTCAGCAGGGCCACAC	230406	62602	GTGTGGCGATTCCTCAGGGA	274993	107189	TAGCACAGAGCCTGGTGCTC
185820	18016	AAGGTGTCAGCAGGGCCACA	230407	62603	AGTGTGGCGATTCCTCAGGG	274994	107190	TTAGCACAGAGCCTGGTGCT
185821	18017	TAAGGTGTCAGCAGGGCCAC	230408	62604	CAGTGTGGCGATTCCTCAGG	274995	107191	CTTAGCACAGAGCCTGGTGC
185822	18018	CTAAGGTGTCAGCAGGGCCA	230409	62605	ACAGTGTGGCGATTCCTCAG	274996	107192	TCTTAGCACAGAGCCTGGTG
185823	18019	GCTAAGGTGTCAGCAGGGCC	230410	62606	GACAGTGTGGCGATTCCTCA	274997	107193	CTCTTAGCACAGAGCCTGGT
185824	18020	AGCTAAGGTGTCAGCAGGGC	230411	62607	AGACAGTGTGGCGATTCCTC	274998	107194	GCTCTTAGCACAGAGCCTGG
185825	18021	AAGCTAAGGTGTCAGCAGGG	230412	62608	AAGACAGTGTGGCGATTCCT	274999	107195	AGCTCTTAGCACAGAGCCTG
185826	18022	GAAGCTAAGGTGTCAGCAGG	230413	62609	GAAGACAGTGTGGCGATTCC	275000	107196	AAGCTCTTAGCACAGAGCCT
185827	18023	TGAAGCTAAGGTGTCAGCAG	230414	62610	GGAAGACAGTGTGGCGATTC	275001	107197	AAAGCTCTTAGCACAGAGCC
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185830	18026	GGTTGAAGCTAAGGTGTCAG	230417	62613	TGTGGAAGACAGTGTGGCGA	275004	107200	GCAAAAGCTCTTAGCACAGA
185831	18027	AGGTTGAAGCTAAGGTGTCA	230418	62614	TTGTGGAAGACAGTGTGGCG	275005	107201	GGCAAAAGCTCTTAGCACAG
185832	18028	TAGGTTGAAGCTAAGGTGTC	230419	62615	ATTGTGGAAGACAGTGTGGC	275006	107202	GGGCAAAAGCTCTTAGCACA
185833	18029	CTAGGTTGAAGCTAAGGTGT	230420	62616	CATTGTGGAAGACAGTGTGG	275007	107203	GGGGCAAAAGCTCTTAGCAC
185834	18030	ACTAGGTTGAAGCTAAGGTG	230421	62617	CCATTGTGGAAGACAGTGTG	275008	107204	GGGGGCAAAAGCTCTTAGCA
185835	18031	CACTAGGTTGAAGCTAAGGT	230422	62618	ACCATTGTGGAAGACAGTGT	275009	107205	TGGGGGCAAAAGCTCTTAGC
185836	18032	TCACTAGGTTGAAGCTAAGG	230423	62619	AACCATTGTGGAAGACAGTG	275010	107206	CTGGGGGCAAAAGCTCTTAG
185837	18033	ATCACTAGGTTGAAGCTAAG	230424	62620	CAACCATTGTGGAAGACAGT	275011	107207	CCTGGGGGCAAAAGCTCTTA
185838	18034	GATCACTAGGTTGAAGCTAA	230425	62621	TCAACCATTGTGGAAGACAG	275012	107208	CCCTGGGGGCAAAAGCTCTT
185839	18035	GGATCACTAGGTTGAAGCTA	230426	62622	TTCAACCATTGTGGAAGACA	275013	107209	ACCCTGGGGGCAAAAGCTCT
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185842	18038	TCAGGATCACTAGGTTGAAG	230429	62625	TAGTTCAACCATTGTGGAAG	275016	107212	TGGACCCTGGGGGCAAAAGC
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185844	18040	AATCAGGATCACTAGGTTGA	230431	62627	ACTAGTTCAACCATTGTGGA	275018	107214	CCTGGACCCTGGGGGCAAAA
185845	18041	AAATCAGGATCACTAGGTTG	230432	62628	AACTAGTTCAACCATTGTGG	275019	107215	GCCTGGACCCTGGGGGCAAA
185846	18042	AAAATCAGGATCACTAGGTT	230433	62629	AAACTAGTTCAACCATTGTG	275020	107216	GGCCTGGACCCTGGGGGCAA
185847	18043	CAAAATCAGGATCACTAGGT	230434	62630	TAAACTAGTTCAACCATTGT	275021	107217	TGGCCTGGACCCTGGGGGCA
185848	18044	CCAAAATCAGGATCACTAGG	230435	62631	GTAAACTAGTTCAACCATTG	275022	107218	CTGGCCTGGACCCTGGGGGC
185849	18045	TCCAAAATCAGGATCACTAG	230436	62632	TGTAAACTAGTTCAACCATT	275023	107219	CCTGGCCTGGACCCTGGGGG
185850	18046	GTCCAAAATCAGGATCACTA	230437	62633	CTGTAAACTAGTTCAACCAT	275024	107220	CCCTGGCCTGGACCCTGGGG
185851	18047	AGTCCAAAATCAGGATCACT	230438	62634	ACTGTAAACTAGTTCAACCA	275025	107221	CCCCTGGCCTGGACCCTGGG
185852	18048	AAGTCCAAAATCAGGATCAC	230439	62635	GACTGTAAACTAGTTCAACC	275026	107222	TCCCCTGGCCTGGACCCTGG
185853	18049	AAAGTCCAAAATCAGGATCA	230440	62636	GGACTGTAAACTAGTTCAAC	275027	107223	GTCCCCTGGCCTGGACCCTG
185854	18050	CAAAGTCCAAAATCAGGATC	230441	62637	AGGACTGTAAACTAGTTCAA	275028	107224	TGTCCCCTGGCCTGGACCCT
185855	18051	CCAAAGTCCAAAATCAGGAT	230442	62638	TAGGACTGTAAACTAGTTCA	275029	107225	CTGTCCCCTGGCCTGGACCC
185856	18052	GCCAAAGTCCAAAATCAGGA	230443	62639	GTAGGACTGTAAACTAGTTC	275030	107226	CCTGTCCCCTGGCCTGGACC
185857	18053	GGCCAAAGTCCAAAATCAGG	230444	62640	GGTAGGACTGTAAACTAGTT	275031	107227	CCCTGTCCCCTGGCCTGGAC
185858	18054	AGGCCAAAGTCCAAAATCAG	230445	62641	TGGTAGGACTGTAAACTAGT	275032	107228	CCCCTGTCCCCTGGCCTGGA
185859	18055	AAGGCCAAAGTCCAAAATCA	230446	62642	TTGGTAGGACTGTAAACTAG	275033	107229	GCCCCTGTCCCCTGGCCTGG
185860	18056	GAAGGCCAAAGTCCAAAATC	230447	62643	GTTGGTAGGACTGTAAACTA	275034	107230	TGCCCCTGTCCCCTGGCCTG
185861	18057	TGAAGGCCAAAGTCCAAAAT	230448	62644	TGTTGGTAGGACTGTAAACT	275035	107231	CTGCCCCTGTCCCCTGGCCT
185862	18058	CTGAAGGCCAAAGTCCAAAA	230449	62645	CTGTTGGTAGGACTGTAAAC	275036	107232	CCTGCCCCTGTCCCCTGGCC
185863	18059	TCTGAAGGCCAAAGTCCAAA	230450	62646	ACTGTTGGTAGGACTGTAAA	275037	107233	ACCTGCCCCTGTCCCCTGGC
185864	18060	TTCTGAAGGCCAAAGTCCAA	230451	62647	CACTGTTGGTAGGACTGTAA	275038	107234	CACCTGCCCCTGTCCCCTGG
185865	18061	CTTCTGAAGGCCAAAGTCCA	230452	62648	ACACTGTTGGTAGGACTGTA	275039	107235	TCACCTGCCCCTGTCCCCTG
185866	18062	ACTTCTGAAGGCCAAAGTCC	230453	62649	TACACTGTTGGTAGGACTGT	275040	107236	CTCACCTGCCCCTGTCCCCT
185867	18063	CACTTCTGAAGGCCAAAGTC	230454	62650	TTACACTGTTGGTAGGACTG	275041	107237	GCTCACCTGCCCCTGTCCCC
185868	18064	ACACTTCTGAAGGCCAAAGT	230455	62651	TTTACACTGTTGGTAGGACT	275042	107238	TGCTCACCTGCCCCTGTCCC
185869	18065	CACACTTCTGAAGGCCAAAG	230456	62652	TTTTACACTGTTGGTAGGAC	275043	107239	CTGCTCACCTGCCCCTGTCC
185870	18066	TCACACTTCTGAAGGCCAAA	230457	62653	CTTTTACACTGTTGGTAGGA	275044	107240	TCTGCTCACCTGCCCCTGTC
185871	18067	CTCACACTTCTGAAGGCCAA	230458	62654	ACTTTTACACTGTTGGTAGG	275045	107241	CTCTGCTCACCTGCCCCTGT
185872	18068	CCTCACACTTCTGAAGGCCA	230459	62655	CACTTTTACACTGTTGGTAG	275046	107242	TCTCTGCTCACCTGCCCCTG
185873	18069	CCCTCACACTTCTGAAGGCC	230460	62656	ACACTTTTACACTGTTGGTA	275047	107243	TTCTCTGCTCACCTGCCCCT
185874	18070	TCCCTCACACTTCTGAAGGC	230461	62657	AACACTTTTACACTGTTGGT	275048	107244	TTTCTCTGCTCACCTGCCCC

185875	18071	TTCCCTCACACTTCTGAAGG	230462	62658	GAACACTTTTACACTGTTGG	275049	107245	GTTTCTCTGCTCACCTGCCC
185876	18072	ATTCCCTCACACTTCTGAAG	230463	62659	GGAACACTTTTACACTGTTG	275050	107246	TGTTTCTCTGCTCACCTGCC
185877	18073	CATTCCCTCACACTTCTGAA	230464	62660	AGGAACACTTTTACACTGTT	275051	107247	CTGTTTCTCTGCTCACCTGC
185878	18074	TCATTCCCTCACACTTCTGA	230465	62661	TAGGAACACTTTTACACTGT	275052	107248	CCTGTTTCTCTGCTCACCTG
185879	18075	TTCATTCCCTCACACTTCTG	230466	62662	ATAGGAACACTTTTACACTG	275053	107249	CCCTGTTTCTCTGCTCACCT
185880	18076	ATTCATTCCCTCACACTTCT	230467	62663	AATAGGAACACTTTTACACT	275054	107250	GCCCTGTTTCTCTGCTCACC
185881	18077	TATTCATTCCCTCACACTTC	230468	62664	AAATAGGAACACTTTTACAC	275055	107251	GGCCCTGTTTCTCTGCTCAC
185882	18078	ATATTCATTCCCTCACACTT	230469	62665	GAAATAGGAACACTTTTACA	275056	107252	TGGCCCTGTTTCTCTGCTCA
185883	18079	GATATTCATTCCCTCACACT	230470	62666	AGAAATAGGAACACTTTTAC	275057	107253	CTGGCCCTGTTTCTCTGCTC
185884	18080	AGATATTCATTCCCTCACAC	230471	62667	GAGAAATAGGAACACTTTTA	275058	107254	ACTGGCCCTGTTTCTCTGCT
185885	18081	CAGATATTCATTCCCTCACA	230472	62668	GGAGAAATAGGAACACTTTT	275059	107255	GACTGGCCCTGTTTCTCTGC
185886	18082	ACAGATATTCATTCCCTCAC	230473	62669	TGGAGAAATAGGAACACTTT	275060	107256	TGACTGGCCCTGTTTCTCTG
185887	18083	AACAGATATTCATTCCCTCA	230474	62670	GTGGAGAAATAGGAACACTT	275061	107257	GTGACTGGCCCTGTTTCTCT
185888	18084	CAACAGATATTCATTCCCTC	230475	62671	TGTGGAGAAATAGGAACACT	275062	107258	TGTGACTGGCCCTGTTTCTC
185889	18085	ACAACAGATATTCATTCCCT	230476	62672	ATGTGGAGAAATAGGAACAC	275063	107259	CTGTGACTGGCCCTGTTTCT
185890	18086	AACAACAGATATTCATTCCC	230477	62673	GATGTGGAGAAATAGGAACA	275064	107260	GCTGTGACTGGCCCTGTTTC
185891	18087	AAACAACAGATATTCATTCC	230478	62674	GGATGTGGAGAAATAGGAAC	275065	107261	TGCTGTGACTGGCCCTGTTT
185892	18088	AAAACAACAGATATTCATTC	230479	62675	AGGATGTGGAGAAATAGGAA	275066	107262	CTGCTGTGACTGGCCCTGTT
185893	18089	TAAAACAACAGATATTCATT	230480	62676	GAGGATGTGGAGAAATAGGA	275067	107263	GCTGCTGTGACTGGCCCTGT
185894	18090	TTAAAACAACAGATATTCAT	230481	62677	AGAGGATGTGGAGAAATAGG	275068	107264	TGCTGCTGTGACTGGCCCTG
185895	18091	CTTAAAACAACAGATATTCA	230482	62678	GAGAGGATGTGGAGAAATAG	275069	107265	CTGCTGCTGTGACTGGCCCT
185896	18092	GCTTAAAACAACAGATATTC	230483	62679	GGAGAGGATGTGGAGAAATA	275070	107266	CCTGCTGCTGTGACTGGCCC
185897	18093	GGCTTAAAACAACAGATATT	230484	62680	TGGAGAGGATGTGGAGAAAT	275071	107267	TCCTGCTGCTGTGACTGGCC
185898	18094	TGGCTTAAAACAACAGATAT	230485	62681	CTGGAGAGGATGTGGAGAAA	275072	107268	CTCCTGCTGCTGTGACTGGC
185899	18095	GTGGCTTAAAACAACAGATA	230486	62682	GCTGGAGAGGATGTGGAGAA	275073	107269	CCTCCTGCTGCTGTGACTGG
185900	18096	GGTGGCTTAAAACAACAGAT	230487	62683	TGCTGGAGAGGATGTGGAGA	275074	107270	TCCTCCTGCTGCTGTGACTG
185901	18097	TGGTGGCTTAAAACAACAGA	230488	62684	CTGCTGGAGAGGATGTGGAG	275075	107271	TTCCTCCTGCTGCTGTGACT
185902	18098	TTGGTGGCTTAAAACAACAG	230489	62685	GCTGCTGGAGAGGATGTGGA	275076	107272	ATTCCTCCTGCTGCTGTGAC
185903	18099	CTTGGTGGCTTAAAACAACA	230490	62686	AGCTGCTGGAGAGGATGTGG	275077	107273	CATTCCTCCTGCTGCTGTGA
185904	18100	ACTTGGTGGCTTAAAACAAC	230491	62687	CAGCTGCTGGAGAGGATGTG	275078	107274	ACATTCCTCCTGCTGCTGTG
185905	18101	AACTTGGTGGCTTAAAACAA	230492	62688	ACAGCTGCTGGAGAGGATGT	275079	107275	TACATTCCTCCTGCTGCTGT
185906	18102	AAACTTGGTGGCTTAAAACA	230493	62689	AACAGCTGCTGGAGAGGATG	275080	107276	CTACATTCCTCCTGCTGCTG
185907	18103	TAAACTTGGTGGCTTAAAAC	230494	62690	CAACAGCTGCTGGAGAGGAT	275081	107277	CCTACATTCCTCCTGCTGCT
185908	18104	ATAAACTTGGTGGCTTAAAA	230495	62691	ACAACAGCTGCTGGAGAGGA	275082	107278	TCCTACATTCCTCCTGCTGC
185909	18105	CATAAACTTGGTGGCTTAAA	230496	62692	AACAACAGCTGCTGGAGAGG	275083	107279	ATCCTACATTCCTCCTGCTG
185910	18106	CCATAAACTTGGTGGCTTAA	230497	62693	AAACAACAGCTGCTGGAGAG	275084	107280	CATCCTACATTCCTCCTGCT
185911	18107	ACCATAAACTTGGTGGCTTA	230498	62694	GAAACAACAGCTGCTGGAGA	275085	107281	CCATCCTACATTCCTCCTGC
185912	18108	GACCATAAACTTGGTGGCTT	230499	62695	GGAAACAACAGCTGCTGGAG	275086	107282	TCCATCCTACATTCCTCCTG
185913	18109	TGACCATAAACTTGGTGGCT	230500	62696	AGGAAACAACAGCTGCTGGA	275087	107283	CTCCATCCTACATTCCTCCT
185914	18110	ATGACCATAAACTTGGTGGC	230501	62697	CAGGAAACAACAGCTGCTGG	275088	107284	TCTCCATCCTACATTCCTCC
185915	18111	AATGACCATAAACTTGGTGG	230502	62698	TCAGGAAACAACAGCTGCTG	275089	107285	CTCTCCATCCTACATTCCTC
185916	18112	AAATGACCATAAACTTGGTG	230503	62699	GTCAGGAAACAACAGCTGCT	275090	107286	GCTCTCCATCCTACATTCCT
185917	18113	GAAATGACCATAAACTTGGT	230504	62700	AGTCAGGAAACAACAGCTGC	275091	107287	AGCTCTCCATCCTACATTCC
185918	18114	GGAAATGACCATAAACTTGG	230505	62701	AAGTCAGGAAACAACAGCTG	275092	107288	AAGCTCTCCATCCTACATTC
185919	18115	AGGAAATGACCATAAACTTG	230506	62702	AAAGTCAGGAAACAACAGCT	275093	107289	CAAGCTCTCCATCCTACATT
185920	18116	TAGGAAATGACCATAAACTT	230507	62703	AAAAGTCAGGAAACAACAGC	275094	107290	CCAAGCTCTCCATCCTACAT
185921	18117	GTAGGAAATGACCATAAACT	230508	62704	AAAAAGTCAGGAAACAACAG	275095	107291	GCCAAGCTCTCCATCCTACA
185922	18118	TGTAGGAAATGACCATAAAC	230509	62705	TAAAAAGTCAGGAAACAACA	275096	107292	GGCCAAGCTCTCCATCCTAC
185923	18119	CTGTAGGAAATGACCATAAA	230510	62706	TTAAAAAGTCAGGAAACAAC	275097	107293	TGGCCAAGCTCTCCATCCTA
185924	18120	GCTGTAGGAAATGACCATAA	230511	62707	ATTAAAAAGTCAGGAAACAA	275098	107294	CTGGCCAAGCTCTCCATCCT
185925	18121	TGCTGTAGGAAATGACCATA	230512	62708	CATTAAAAAGTCAGGAAACA	275099	107295	CCTGGCCAAGCTCTCCATCC
185926	18122	CTGCTGTAGGAAATGACCAT	230513	62709	TCATTAAAAAGTCAGGAAAC	275100	107296	GCCTGGCCAAGCTCTCCATC
185927	18123	GCTGCTGTAGGAAATGACCA	230514	62710	ATCATTAAAAAGTCAGGAAA	275101	107297	TGCCTGGCCAAGCTCTCCAT
185928	18124	GGCTGCTGTAGGAAATGACC	230515	62711	GATCATTAAAAAGTCAGGAA	275102	107298	TTGCCTGGCCAAGCTCTCCA
185929	18125	TGGCTGCTGTAGGAAATGAC	230516	62712	CGATCATTAAAAAGTCAGGA	275103	107299	CTTGCCTGGCCAAGCTCTCC
185930	18126	GTGGCTGCTGTAGGAAATGA	230517	62713	GCGATCATTAAAAAGTCAGG	275104	107300	CCTTGCCTGGCCAAGCTCTC
185931	18127	TGTGGCTGCTGTAGGAAATG	230518	62714	GGCGATCATTAAAAAGTCAG	275105	107301	TCCTTGCCTGGCCAAGCTCT
185932	18128	CTGTGGCTGCTGTAGGAAAT	230519	62715	TGGCGATCATTAAAAAGTCA	275106	107302	GTCCTTGCCTGGCCAAGCTC
185933	18129	CCTGTGGCTGCTGTAGGAAA	230520	62716	ATGGCGATCATTAAAAAGTC	275107	107303	TGTCCTTGCCTGGCCAAGCT
185934	18130	TCCTGTGGCTGCTGTAGGAA	230521	62717	AATGGCGATCATTAAAAAGT	275108	107304	ATGTCCTTGCCTGGCCAAGC
185935	18131	TTCCTGTGGCTGCTGTAGGA	230522	62718	GAATGGCGATCATTAAAAAG	275109	107305	CATGTCCTTGCCTGGCCAAG
185936	18132	ATTCCTGTGGCTGCTGTAGG	230523	62719	AGAATGGCGATCATTAAAAA	275110	107306	GCATGTCCTTGCCTGGCCAA
185937	18133	GATTCCTGTGGCTGCTGTAG	230524	62720	TAGAATGGCGATCATTAAAA	275111	107307	TGCATGTCCTTGCCTGGCCA
185938	18134	TGATTCCTGTGGCTGCTGTA	230525	62721	TTAGAATGGCGATCATTAAA	275112	107308	CTGCATGTCCTTGCCTGGCC
185939	18135	TTGATTCCTGTGGCTGCTGT	230526	62722	GTTAGAATGGCGATCATTAA	275113	107309	CCTGCATGTCCTTGCCTGGC
185940	18136	TTTGATTCCTGTGGCTGCTG	230527	62723	AGTTAGAATGGCGATCATTA	275114	107310	CCCTGCATGTCCTTGCCTGG
185941	18137	TTTTGATTCCTGTGGCTGCT	230528	62724	CAGTTAGAATGGCGATCATT	275115	107311	CCCCTGCATGTCCTTGCCTG
185942	18138	TTTTTGATTCCTGTGGCTGC	230529	62725	CCAGTTAGAATGGCGATCAT	275116	107312	CCCCCTGCATGTCCTTGCCT
185943	18139	GTTTTTGATTCCTGTGGCTG	230530	62726	ACCAGTTAGAATGGCGATCA	275117	107313	TCCCCCTGCATGTCCTTGCC
185944	18140	TGTTTTTGATTCCTGTGGCT	230531	62727	CACCAGTTAGAATGGCGATC	275118	107314	CTCCCCCTGCATGTCCTTGC
185945	18141	CTGTTTTTGATTCCTGTGGC	230532	62728	ACACCAGTTAGAATGGCGAT	275119	107315	GCTCCCCCTGCATGTCCTTG
185946	18142	ACTGTTTTTGATTCCTGTGG	230533	62729	CACACCAGTTAGAATGGCGA	275120	107316	TGCTCCCCCTGCATGTCCTT

185947	18143	TACTGTTTTTGATTCCTGTG	230534	62730	TCACACCAGTTAGAATGGCG	275121	107317	CTGCTCCCCCTGCATGTCCT
185948	18144	TTACTGTTTTTGATTCCTGT	230535	62731	CTCACACCAGTTAGAATGGC	275122	107318	GCTGCTCCCCCTGCATGTCC
185949	18145	CTTACTGTTTTTGATTCCTG	230536	62732	TCTCACACCAGTTAGAATGG	275123	107319	GGCTGCTCCCCCTGCATGTC
185950	18146	ACTTACTGTTTTTGATTCCT	230537	62733	ATCTCACACCAGTTAGAATG	275124	107320	AGGCTGCTCCCCCTGCATGT
185951	18147	TACTTACTGTTTTTGATTCC	230538	62734	CATCTCACACCAGTTAGAAT	275125	107321	CAGGCTGCTCCCCCTGCATG
185952	18148	ATACTTACTGTTTTTGATTC	230539	62735	ACATCTCACACCAGTTAGAA	275126	107322	GCAGGCTGCTCCCCCTGCAT
185953	18149	CATACTTACTGTTTTTGATT	230540	62736	AACATCTCACACCAGTTAGA	275127	107323	TGCAGGCTGCTCCCCCTGCA
185954	18150	ACATACTTACTGTTTTTGAT	230541	62737	TAACATCTCACACCAGTTAG	275128	107324	GTGCAGGCTGCTCCCCCTGC
185955	18151	GACATACTTACTGTTTTTGA	230542	62738	ATAACATCTCACACCAGTTA	275129	107325	TGTGCAGGCTGCTCCCCCTG
185956	18152	GGACATACTTACTGTTTTTG	230543	62739	GATAACATCTCACACCAGTT	275130	107326	TTGTGCAGGCTGCTCCCCCT
185957	18153	GGGACATACTTACTGTTTTT	230544	62740	AGATAACATCTCACACCAGT	275131	107327	CTTGTGCAGGCTGCTCCCCC
185958	18154	TGGGACATACTTACTGTTTT	230545	62741	GAGATAACATCTCACACCAG	275132	107328	ACTTGTGCAGGCTGCTCCCC
185959	18155	ATGGGACATACTTACTGTTT	230546	62742	TGAGATAACATCTCACACCA	275133	107329	GACTTGTGCAGGCTGCTCCC
185960	18156	CATGGGACATACTTACTGTT	230547	62743	ATGAGATAACATCTCACACC	275134	107330	TGACTTGTGCAGGCTGCTCC
185961	18157	GCATGGGACATACTTACTGT	230548	62744	CATGAGATAACATCTCACAC	275135	107331	CTGACTTGTGCAGGCTGCTC
185962	18158	TGCATGGGACATACTTACTG	230549	62745	CCATGAGATAACATCTCACA	275136	107332	GCTGACTTGTGCAGGCTGCT
185963	18159	TTGCATGGGACATACTTACT	230550	62746	ACCATGAGATAACATCTCAC	275137	107333	TGCTGACTTGTGCAGGCTGC
185964	18160	ATTGCATGGGACATACTTAC	230551	62747	CACCATGAGATAACATCTCA	275138	107334	TTGCTGACTTGTGCAGGCTG
185965	18161	CATTGCATGGGACATACTTA	230552	62748	CCACCATGAGATAACATCTC	275139	107335	CTTGCTGACTTGTGCAGGCT
185966	18162	ACATTGCATGGGACATACTT	230553	62749	ACCACCATGAGATAACATCT	275140	107336	GCTTGCTGACTTGTGCAGGC
185967	18163	AACATTGCATGGGACATACT	230554	62750	AACCACCATGAGATAACATC	275141	107337	GGCTTGCTGACTTGTGCAGG
185968	18164	AAACATTGCATGGGACATAC	230555	62751	AAACCACCATGAGATAACAT	275142	107338	TGGCTTGCTGACTTGTGCAG
185969	18165	CAAACATTGCATGGGACATA	230556	62752	AAAACCACCATGAGATAACA	275143	107339	CTGGCTTGCTGACTTGTGCA
185970	18166	ACAAACATTGCATGGGACAT	230557	62753	CAAAACCACCATGAGATAAC	275144	107340	TCTGGCTTGCTGACTTGTGC
185971	18167	CACAAACATTGCATGGGACA	230558	62754	TCAAAACCACCATGAGATAA	275145	107341	CTCTGGCTTGCTGACTTGTG
185972	18168	TCACAAACATTGCATGGGAC	230559	62755	ATCAAAACCACCATGAGATA	275146	107342	TCTCTGGCTTGCTGACTTGT
185973	18169	GTCACAAACATTGCATGGGA	230560	62756	AATCAAAACCACCATGAGAT	275147	107343	TTCTCTGGCTTGCTGACTTG
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185975	18171	GTGTCACAAACATTGCATGG	230562	62758	CAAATCAAAACCACCATGAG	275149	107345	TCTTCTCTGGCTTGCTGACT
185976	18172	TGTGTCACAAACATTGCATG	230563	62759	GCAAATCAAAACCACCATGA	275150	107346	GTCTTCTCTGGCTTGCTGAC
185977	18173	GTGTGTCACAAACATTGCAT	230564	62760	TGCAAATCAAAACCACCATG	275151	107347	TGTCTTCTCTGGCTTGCTGA
185978	18174	TGTGTGTCACAAACATTGCA	230565	62761	ATGCAAATCAAAACCACCAT	275152	107348	CTGTCTTCTCTGGCTTGCTG
185979	18175	GTGTGTGTCACAAACATTGC	230566	62762	AATGCAAATCAAAACCACCA	275153	107349	CCTGTCTTCTCTGGCTTGCT
185980	18176	GGTGTGTGTCACAAACATTG	230567	62763	AAATGCAAATCAAAACCACC	275154	107350	GCCTGTCTTCTCTGGCTTGC
185981	18177	TGGTGTGTGTCACAAACATT	230568	62764	GAAATGCAAATCAAAACCAC	275155	107351	TGCCTGTCTTCTCTGGCTTG
185982	18178	TTGGTGTGTGTCACAAACAT	230569	62765	AGAAATGCAAATCAAAACCA	275156	107352	CTGCCTGTCTTCTCTGGCTT
185983	18179	TTTGGTGTGTGTCACAAACA	230570	62766	GAGAAATGCAAATCAAAACC	275157	107353	TCTGCCTGTCTTCTCTGGCT
185984	18180	TTTTGGTGTGTGTCACAAAC	230571	62767	AGAGAAATGCAAATCAAAAC	275158	107354	GTCTGCCTGTCTTCTCTGGC
185985	18181	TTTTTGGTGTGTGTCACAAA	230572	62768	CAGAGAAATGCAAATCAAAA	275159	107355	GGTCTGCCTGTCTTCTCTGG
185986	18182	ATTTTTGGTGTGTGTCACAA	230573	62769	TCAGAGAAATGCAAATCAAA	275160	107356	GGGTCTGCCTGTCTTCTCTG
185987	18183	TATTTTTGGTGTGTGTCACA	230574	62770	ATCAGAGAAATGCAAATCAA	275161	107357	AGGGTCTGCCTGTCTTCTCT
185988	18184	ATATTTTTGGTGTGTGTCAC	230575	62771	CATCAGAGAAATGCAAATCA	275162	107358	AAGGGTCTGCCTGTCTTCTC
185989	18185	AATATTTTTGGTGTGTGTCA	230576	62772	CCATCAGAGAAATGCAAATC	275163	107359	CAAGGGTCTGCCTGTCTTCT
185990	18186	TAATATTTTTGGTGTGTGTC	230577	62773	GCCATCAGAGAAATGCAAAT	275164	107360	ACAAGGGTCTGCCTGTCTTC
185991	18187	GTAATATTTTTGGTGTGTGT	230578	62774	GGCCATCAGAGAAATGCAAA	275165	107361	AACAAGGGTCTGCCTGTCTT
185992	18188	AGTAATATTTTTGGTGTGTG	230579	62775	TGGCCATCAGAGAAATGCAA	275166	107362	AAACAAGGGTCTGCCTGTCT
185993	18189	AAGTAATATTTTTGGTGTGT	230580	62776	CTGGCCATCAGAGAAATGCA	275167	107363	CAAACAAGGGTCTGCCTGTC
185994	18190	CAAGTAATATTTTTGGTGTG	230581	62777	ACTGGCCATCAGAGAAATGC	275168	107364	CCAAACAAGGGTCTGCCTGT
185995	18191	ACAAGTAATATTTTTGGTGT	230582	62778	CACTGGCCATCAGAGAAATG	275169	107365	CCCAAACAAGGGTCTGCCTG
185996	18192	AACAAGTAATATTTTTGGTG	230583	62779	TCACTGGCCATCAGAGAAAT	275170	107366	TCCCAAACAAGGGTCTGCCT
185997	18193	CAACAAGTAATATTTTTGGT	230584	62780	ATCACTGGCCATCAGAGAAA	275171	107367	GTCCCAAACAAGGGTCTGCC
185998	18194	ACAACAAGTAATATTTTTGG	230585	62781	CATCACTGGCCATCAGAGAA	275172	107368	GGTCCCAAACAAGGGTCTGC
185999	18195	AACAACAAGTAATATTTTTG	230586	62782	TCATCACTGGCCATCAGAGA	275173	107369	AGGTCCCAAACAAGGGTCTG
186000	18196	GAACAACAAGTAATATTTTT	230587	62783	ATCATCACTGGCCATCAGAG	275174	107370	CAGGTCCCAAACAAGGGTCT
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186002	18198	GTGAACAACAAGTAATATTT	230589	62785	TCATCATCACTGGCCATCAG	275176	107372	AACAGGTCCCAAACAAGGGT
186003	18199	GGTGAACAACAAGTAATATT	230590	62786	CTCATCATCACTGGCCATCA	275177	107373	GAACAGGTCCCAAACAAGGG
186004	18200	AGGTGAACAACAAGTAATAT	230591	62787	GCTCATCATCACTGGCCATC	275178	107374	TGAACAGGTCCCAAACAAGG
186005	18201	CAGGTGAACAACAAGTAATA	230592	62788	TGCTCATCATCACTGGCCAT	275179	107375	CTGAACAGGTCCCAAACAAG
186006	18202	TCAGGTGAACAACAAGTAAT	230593	62789	ATGCTCATCATCACTGGCCA	275180	107376	ACTGAACAGGTCCCAAACAA
186007	18203	TTCAGGTGAACAACAAGTAA	230594	62790	AATGCTCATCATCACTGGCC	275181	107377	CACTGAACAGGTCCCAAACA
186008	18204	TTTCAGGTGAACAACAAGTA	230595	62791	AAATGCTCATCATCACTGGC	275182	107378	CCACTGAACAGGTCCCAAAC
186009	18205	ATTTCAGGTGAACAACAAGT	230596	62792	AAAATGCTCATCATCACTGG	275183	107379	GCCACTGAACAGGTCCCAAA
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186011	18207	GAATTTCAGGTGAACAACAA	230598	62794	AAAAAATGCTCATCATCACT	275185	107381	AGGCCACTGAACAGGTCCCA
186012	18208	TGAATTTCAGGTGAACAACA	230599	62795	GAAAAAATGCTCATCATCAC	275186	107382	AAGGCCACTGAACAGGTCCC
186013	18209	TTGAATTTCAGGTGAACAAC	230600	62796	TGAAAAAATGCTCATCATCA	275187	107383	AAAGGCCACTGAACAGGTCC
186014	18210	TTTGAATTTCAGGTGAACAA	230601	62797	GTGAAAAAATGCTCATCATC	275188	107384	CAAAGGCCACTGAACAGGTC
186015	18211	ATTTGAATTTCAGGTGAACA	230602	62798	CGTGAAAAAATGCTCATCAT	275189	107385	TCAAAGGCCACTGAACAGGT
186016	18212	AATTTGAATTTCAGGTGAAC	230603	62799	ACGTGAAAAAATGCTCATCA	275190	107386	TTCAAAGGCCACTGAACAGG
186017	18213	AAATTTGAATTTCAGGTGAA	230604	62800	CACGTGAAAAAATGCTCATC	275191	107387	TTTCAAAGGCCACTGAACAG
186018	18214	TAAATTTGAATTTCAGGTGA	230605	62801	ACACGTGAAAAAATGCTCAT	275192	107388	CTTTCAAAGGCCACTGAACA

186019	18215	TTAAATTTGAATTTCAGGTG	230606	62802	GACACGTGAAAAAATGCTCA	275193	107389	CCTTTCAAAGGCCACTGAAC
186020	18216	GTTAAATTTGAATTTCAGGT	230607	62803	AGACACGTGAAAAAATGCTC	275194	107390	TCCTTTCAAAGGCCACTGAA
186021	18217	AGTTAAATTTGAATTTCAGG	230608	62804	CAGACACGTGAAAAAATGCT	275195	107391	GTCCTTTCAAAGGCCACTGA
186022	18218	CAGTTAAATTTGAATTTCAG	230609	62805	ACAGACACGTGAAAAAATGC	275196	107392	TGTCCTTTCAAAGGCCACTG
186023	18219	CCAGTTAAATTTGAATTTCA	230610	62806	AACAGACACGTGAAAAAATG	275197	107393	CTGTCCTTTCAAAGGCCACT
186024	18220	CCCAGTTAAATTTGAATTTC	230611	62807	CAACAGACACGTGAAAAAAT	275198	107394	GCTGTCCTTTCAAAGGCCAC
186025	18221	ACCCAGTTAAATTTGAATTT	230612	62808	CCAACAGACACGTGAAAAAA	275199	107395	GGCTGTCCTTTCAAAGGCCA
186026	18222	GACCCAGTTAAATTTGAATT	230613	62809	GCCAACAGACACGTGAAAAA	275200	107396	GGGCTGTCCTTTCAAAGGCC
186027	18223	AGACCCAGTTAAATTTGAAT	230614	62810	CGCCAACAGACACGTGAAAA	275201	107397	GGGGCTGTCCTTTCAAAGGC
186028	18224	GAGACCCAGTTAAATTTGAA	230615	62811	TCGCCAACAGACACGTGAAA	275202	107398	GGGGGCTGTCCTTTCAAAGG
186029	18225	GGAGACCCAGTTAAATTTGA	230616	62812	TTCGCCAACAGACACGTGAA	275203	107399	TGGGGGCTGTCCTTTCAAAG
186030	18226	AGGAGACCCAGTTAAATTTG	230617	62813	GTTCGCCAACAGACACGTGA	275204	107400	GTGGGGGCTGTCCTTTCAAA
186031	18227	CAGGAGACCCAGTTAAATTT	230618	62814	AGTTCGCCAACAGACACGTG	275205	107401	GGTGGGGGCTGTCCTTTCAA
186032	18228	ACAGGAGACCCAGTTAAATT	230619	62815	GAGTTCGCCAACAGACACGT	275206	107402	GGGTGGGGGCTGTCCTTTCA
186033	18229	TACAGGAGACCCAGTTAAAT	230620	62816	AGAGTTCGCCAACAGACACG	275207	107403	CGGGTGGGGGCTGTCCTTTC
186034	18230	ATACAGGAGACCCAGTTAAA	230621	62817	TAGAGTTCGCCAACAGACAC	275208	107404	CCGGGTGGGGGCTGTCCTTT
186035	18231	AATACAGGAGACCCAGTTAA	230622	62818	CTAGAGTTCGCCAACAGACA	275209	107405	TCCGGGTGGGGGCTGTCCTT
186036	18232	AAATACAGGAGACCCAGTTA	230623	62819	GCTAGAGTTCGCCAACAGAC	275210	107406	CTCCGGGTGGGGGCTGTCCT
186037	18233	AAAATACAGGAGACCCAGTT	230624	62820	TGCTAGAGTTCGCCAACAGA	275211	107407	ACTCCGGGTGGGGGCTGTCC
186038	18234	TAAAATACAGGAGACCCAGT	230625	62821	CTGCTAGAGTTCGCCAACAG	275212	107408	CACTCCGGGTGGGGGCTGTC
186039	18235	ATAAAATACAGGAGACCCAG	230626	62822	GCTGCTAGAGTTCGCCAACA	275213	107409	GCACTCCGGGTGGGGGCTGT
186040	18236	AATAAAATACAGGAGACCCA	230627	62823	AGCTGCTAGAGTTCGCCAAC	275214	107410	AGCACTCCGGGTGGGGGCTG
186041	18237	AAATAAAATACAGGAGACCC	230628	62824	AAGCTGCTAGAGTTCGCCAA	275215	107411	CAGCACTCCGGGTGGGGGCT
186042	18238	CAAATAAAATACAGGAGACC	230629	62825	GAAGCTGCTAGAGTTCGCCA	275216	107412	CCAGCACTCCGGGTGGGGGC
186043	18239	CCAAATAAAATACAGGAGAC	230630	62826	AGAAGCTGCTAGAGTTCGCC	275217	107413	CCCAGCACTCCGGGTGGGGG
186044	18240	GCCAAATAAAATACAGGAGA	230631	62827	AAGAAGCTGCTAGAGTTCGC	275218	107414	ACCCAGCACTCCGGGTGGGG
186045	18241	GGCCAAATAAAATACAGGAG	230632	62828	AAAGAAGCTGCTAGAGTTCG	275219	107415	CACCCAGCACTCCGGGTGGG
186046	18242	TGGCCAAATAAAATACAGGA	230633	62829	AAAAGAAGCTGCTAGAGTTC	275220	107416	GCACCCAGCACTCCGGGTGG
186047	18243	TTGGCCAAATAAAATACAGG	230634	62830	GAAAAGAAGCTGCTAGAGTT	275221	107417	TGCACCCAGCACTCCGGGTG
186048	18244	GTTGGCCAAATAAAATACAG	230635	62831	TGAAAAGAAGCTGCTAGAGT	275222	107418	CTGCACCCAGCACTCCGGGT
186049	18245	GGTTGGCCAAATAAAATACA	230636	62832	GTGAAAAGAAGCTGCTAGAG	275223	107419	CCTGCACCCAGCACTCCGGG
186050	18246	AGGTTGGCCAAATAAAATAC	230637	62833	TGTGAAAAGAAGCTGCTAGA	275224	107420	TCCTGCACCCAGCACTCCGG
186051	18247	TAGGTTGGCCAAATAAAATA	230638	62834	TTGTGAAAAGAAGCTGCTAG	275225	107421	CTCCTGCACCCAGCACTCCG
186052	18248	CTAGGTTGGCCAAATAAAAT	230639	62835	CTTGTGAAAAGAAGCTGCTA	275226	107422	GCTCCTGCACCCAGCACTCC
186053	18249	ACTAGGTTGGCCAAATAAAA	230640	62836	ACTTGTGAAAAGAAGCTGCT	275227	107423	AGCTCCTGCACCCAGCACTC
186054	18250	AACTAGGTTGGCCAAATAAA	230641	62837	AACTTGTGAAAAGAAGCTGC	275228	107424	CAGCTCCTGCACCCAGCACT
186055	18251	GAACTAGGTTGGCCAAATAA	230642	62838	GAACTTGTGAAAAGAAGCTG	275229	107425	TCAGCTCCTGCACCCAGCAC
186056	18252	GGAACTAGGTTGGCCAAATA	230643	62839	TGAACTTGTGAAAAGAAGCT	275230	107426	TTCAGCTCCTGCACCCAGCA
186057	18253	GGGAACTAGGTTGGCCAAAT	230644	62840	ATGAACTTGTGAAAAGAAGC	275231	107427	CTTCAGCTCCTGCACCCAGC
186058	18254	TGGGAACTAGGTTGGCCAAA	230645	62841	CATGAACTTGTGAAAAGAAG	275232	107428	CCTTCAGCTCCTGCACCCAG
186059	18255	CTGGGAACTAGGTTGGCCAA	230646	62842	CCATGAACTTGTGAAAAGAA	275233	107429	TCCTTCAGCTCCTGCACCCA
186060	18256	CCTGGGAACTAGGTTGGCCA	230647	62843	TCCATGAACTTGTGAAAAGA	275234	107430	CTCCTTCAGCTCCTGCACCC
186061	18257	GCCTGGGAACTAGGTTGGCC	230648	62844	CTCCATGAACTTGTGAAAAG	275235	107431	CCTCCTTCAGCTCCTGCACC
186062	18258	GGCCTGGGAACTAGGTTGGC	230649	62845	TCTCCATGAACTTGTGAAAA	275236	107432	TCCTCCTTCAGCTCCTGCAC
186063	18259	GGGCCTGGGAACTAGGTTGG	230650	62846	CTCTCCATGAACTTGTGAAA	275237	107433	ATCCTCCTTCAGCTCCTGCA
186064	18260	TGGGCCTGGGAACTAGGTTG	230651	62847	TCTCTCCATGAACTTGTGAA	275238	107434	TATCCTCCTTCAGCTCCTGC
186065	18261	TTGGGCCTGGGAACTAGGTT	230652	62848	CTCTCTCCATGAACTTGTGA	275239	107435	CTATCCTCCTTCAGCTCCTG
186066	18262	TTTGGGCCTGGGAACTAGGT	230653	62849	CCTCTCTCCATGAACTTGTG	275240	107436	ACTATCCTCCTTCAGCTCCT
186067	18263	CTTTGGGCCTGGGAACTAGG	230654	62850	ACCTCTCTCCATGAACTTGT	275241	107437	CACTATCCTCCTTCAGCTCC
186068	18264	TCTTTGGGCCTGGGAACTAG	230655	62851	AACCTCTCTCCATGAACTTG	275242	107438	CCACTATCCTCCTTCAGCTC
186069	18265	TTCTTTGGGCCTGGGAACTA	230656	62852	AAACCTCTCTCCATGAACTT	275243	107439	TCCACTATCCTCCTTCAGCT
186070	18266	TTTCTTTGGGCCTGGGAACT	230657	62853	GAAACCTCTCTCCATGAACT	275244	107440	TTCCACTATCCTCCTTCAGC
186071	18267	CTTTCTTTGGGCCTGGGAAC	230658	62854	GGAAACCTCTCTCCATGAAC	275245	107441	GTTCCACTATCCTCCTTCAG
186072	18268	TCTTTCTTTGGGCCTGGGAA	230659	62855	GGGAAACCTCTCTCCATGAA	275246	107442	TGTTCCACTATCCTCCTTCA
186073	18269	CTCTTTCTTTGGGCCTGGGA	230660	62856	TGGGAAACCTCTCTCCATGA	275247	107443	GTGTTCCACTATCCTCCTTC
186074	18270	CCTCTTTCTTTGGGCCTGGG	230661	62857	GTGGGAAACCTCTCTCCATG	275248	107444	AGTGTTCCACTATCCTCCTT
186075	18271	GCCTCTTTCTTTGGGCCTGG	230662	62858	AGTGGGAAACCTCTCTCCAT	275249	107445	CAGTGTTCCACTATCCTCCT
186076	18272	AGCCTCTTTCTTTGGGCCTG	230663	62859	CAGTGGGAAACCTCTCTCCA	275250	107446	GCAGTGTTCCACTATCCTCC
186077	18273	AAGCCTCTTTCTTTGGGCCT	230664	62860	TCAGTGGGAAACCTCTCTCC	275251	107447	TGCAGTGTTCCACTATCCTC
186078	18274	AAAGCCTCTTTCTTTGGGCC	230665	62861	CTCAGTGGGAAACCTCTCTC	275252	107448	TTGCAGTGTTCCACTATCCT
186079	18275	AAAAGCCTCTTTCTTTGGGC	230666	62862	CCTCAGTGGGAAACCTCTCT	275253	107449	GTTGCAGTGTTCCACTATCC
186080	18276	CAAAAGCCTCTTTCTTTGGG	230667	62863	CCCTCAGTGGGAAACCTCTC	275254	107450	CGTTGCAGTGTTCCACTATC
186081	18277	TCAAAAGCCTCTTTCTTTGG	230668	62864	TCCCTCAGTGGGAAACCTCT	275255	107451	ACGTTGCAGTGTTCCACTAT
186082	18278	TTCAAAAGCCTCTTTCTTTG	230669	62865	TTCCCTCAGTGGGAAACCTC	275256	107452	CACGTTGCAGTGTTCCACTA
186083	18279	TTTCAAAAGCCTCTTTCTTT	230670	62866	ATTCCCTCAGTGGGAAACCT	275257	107453	CCACGTTGCAGTGTTCCACT
186084	18280	ATTTCAAAAGCCTCTTTCTT	230671	62867	GATTCCCTCAGTGGGAAACC	275258	107454	TCCACGTTGCAGTGTTCCAC
186085	18281	AATTTCAAAAGCCTCTTTCT	230672	62868	TGATTCCCTCAGTGGGAAAC	275259	107455	CTCCACGTTGCAGTGTTCCA
186086	18282	AAATTTCAAAAGCCTCTTTC	230673	62869	GTGATTCCCTCAGTGGGAAA	275260	107456	GCTCCACGTTGCAGTGTTCC
186087	18283	CAAATTTCAAAAGCCTCTTT	230674	62870	TGTGATTCCCTCAGTGGGAA	275261	107457	AGCTCCACGTTGCAGTGTTC
186088	18284	GCAAATTTCAAAAGCCTCTT	230675	62871	ATGTGATTCCCTCAGTGGGA	275262	107458	GAGCTCCACGTTGCAGTGTT
186089	18285	TGCAAATTTCAAAAGCCTCT	230676	62872	GATGTGATTCCCTCAGTGGG	275263	107459	AGAGCTCCACGTTGCAGTGT
186090	18286	TTGCAAATTTCAAAAGCCTC	230677	62873	AGATGTGATTCCCTCAGTGG	275264	107460	AAGAGCTCCACGTTGCAGTG

186091	18287	CTTGCAAATTTCAAAAGCCT	230678	62874	CAGATGTGATTCCCTCAGTG	275265	107461	GAAGAGCTCCACGTTGCAGT
186092	18288	TCTTGCAAATTTCAAAAGCC	230679	62875	ACAGATGTGATTCCCTCAGT	275266	107462	TGAAGAGCTCCACGTTGCAG
186093	18289	TTCTTGCAAATTTCAAAAGC	230680	62876	GACAGATGTGATTCCCTCAG	275267	107463	CTGAAGAGCTCCACGTTGCA
186094	18290	TTTCTTGCAAATTTCAAAAG	230681	62877	AGACAGATGTGATTCCCTCA	275268	107464	TCTGAAGAGCTCCACGTTGC
186095	18291	CTTTCTTGCAAATTTCAAAA	230682	62878	CAGACAGATGTGATTCCCTC	275269	107465	CTCTGAAGAGCTCCACGTTG
186096	18292	GCTTTCTTGCAAATTTCAAA	230683	62879	TCAGACAGATGTGATTCCCT	275270	107466	GCTCTGAAGAGCTCCACGTT
186097	18293	AGCTTTCTTGCAAATTTCAA	230684	62880	ATCAGACAGATGTGATTCCC	275271	107467	TGCTCTGAAGAGCTCCACGT
186098	18294	CAGCTTTCTTGCAAATTTCA	230685	62881	GATCAGACAGATGTGATTCC	275272	107468	TTGCTCTGAAGAGCTCCACG
186099	18295	CCAGCTTTCTTGCAAATTTC	230686	62882	TGATCAGACAGATGTGATTC	275273	107469	TTTGCTCTGAAGAGCTCCAC
186100	18296	ACCAGCTTTCTTGCAAATTT	230687	62883	TTGATCAGACAGATGTGATT	275274	107470	TTTTGCTCTGAAGAGCTCCA
186101	18297	AACCAGCTTTCTTGCAAATT	230688	62884	TTTGATCAGACAGATGTGAT	275275	107471	CTTTTGCTCTGAAGAGCTCC
186102	18298	CAACCAGCTTTCTTGCAAAT	230689	62885	TTTTGATCAGACAGATGTGA	275276	107472	GCTTTTGCTCTGAAGAGCTC
186103	18299	CCAACCAGCTTTCTTGCAAA	230690	62886	CTTTTGATCAGACAGATGTG	275277	107473	TGCTTTTGCTCTGAAGAGCT
186104	18300	TCCAACCAGCTTTCTTGCAA	230691	62887	TCTTTTGATCAGACAGATGT	275278	107474	TTGCTTTTGCTCTGAAGAGC
186105	18301	CTCCAACCAGCTTTCTTGCA	230692	62888	CTCTTTTGATCAGACAGATG	275279	107475	TTTGCTTTTGCTCTGAAGAG
186106	18302	GCTCCAACCAGCTTTCTTGC	230693	62889	CCTCTTTTGATCAGACAGAT	275280	107476	TTTTGCTTTTGCTCTGAAGA
186107	18303	AGCTCCAACCAGCTTTCTTG	230694	62890	GCCTCTTTTGATCAGACAGA	275281	107477	ATTTTGCTTTTGCTCTGAAG
186108	18304	CAGCTCCAACCAGCTTTCTT	230695	62891	AGCCTCTTTTGATCAGACAG	275282	107478	TATTTTGCTTTTGCTCTGAA
186109	18305	ACAGCTCCAACCAGCTTTCT	230696	62892	AAGCCTCTTTTGATCAGACA	275283	107479	TTATTTTGCTTTTGCTCTGA
186110	18306	GACAGCTCCAACCAGCTTTC	230697	62893	CAAGCCTCTTTTGATCAGAC	275284	107480	TTTATTTTGCTTTTGCTCTG
186111	18307	TGACAGCTCCAACCAGCTTT	230698	62894	CCAAGCCTCTTTTGATCAGA	275285	107481	GTTTATTTTGCTTTTGCTCT
186112	18308	CTGACAGCTCCAACCAGCTT	230699	62895	CCCAAGCCTCTTTTGATCAG	275286	107482	TGTTTATTTTGCTTTTGCTC
186113	18309	TCTGACAGCTCCAACCAGCT	230700	62896	TCCCAAGCCTCTTTTGATCA	275287	107483	TTGTTTATTTTGCTTTTGCT
186114	18310	TTCTGACAGCTCCAACCAGC	230701	62897	TTCCCAAGCCTCTTTTGATC	275288	107484	GTTGTTTATTTTGCTTTTGC
186115	18311	TTTCTGACAGCTCCAACCAG	230702	62898	TTTCCCAAGCCTCTTTTGAT	275289	107485	AGTTGTTTATTTTGCTTTTG
186116	18312	CTTTCTGACAGCTCCAACCA	230703	62899	ATTTCCCAAGCCTCTTTTGA	275290	107486	CAGTTGTTTATTTTGCTTTT
186117	18313	ACTTTCTGACAGCTCCAACC	230704	62900	CATTTCCCAAGCCTCTTTTG	275291	107487	CCAGTTGTTTATTTTGCTTT
186118	18314	CACTTTCTGACAGCTCCAAC	230705	62901	CCATTTCCCAAGCCTCTTTT	275292	107488	TCCAGTTGTTTATTTTGCTT
186119	18315	CCACTTTCTGACAGCTCCAA	230706	62902	GCCATTTCCCAAGCCTCTTT	275293	107489	CTCCAGTTGTTTATTTTGCT
186120	18316	TCCACTTTCTGACAGCTCCA	230707	62903	AGCCATTTCCCAAGCCTCTT	275294	107490	CCTCCAGTTGTTTATTTTGC
186121	18317	GTCCACTTTCTGACAGCTCC	230708	62904	GAGCCATTTCCCAAGCCTCT	275295	107491	GCCTCCAGTTGTTTATTTTG
186122	18318	AGTCCACTTTCTGACAGCTC	230709	62905	AGAGCCATTTCCCAAGCCTC	275296	107492	TGCCTCCAGTTGTTTATTTT
186123	18319	AAGTCCACTTTCTGACAGCT	230710	62906	GAGAGCCATTTCCCAAGCCT	275297	107493	CTGCCTCCAGTTGTTTATTT
186124	18320	AAAGTCCACTTTCTGACAGC	230711	62907	GGAGAGCCATTTCCCAAGCC	275298	107494	GCTGCCTCCAGTTGTTTATT
186125	18321	CAAAGTCCACTTTCTGACAG	230712	62908	AGGAGAGCCATTTCCCAAGC	275299	107495	AGCTGCCTCCAGTTGTTTAT
186126	18322	ACAAAGTCCACTTTCTGACA	230713	62909	CAGGAGAGCCATTTCCCAAG	275300	107496	CAGCTGCCTCCAGTTGTTTA
186127	18323	TACAAAGTCCACTTTCTGAC	230714	62910	ACAGGAGAGCCATTTCCCAA	275301	107497	CCAGCTGCCTCCAGTTGTTT
186128	18324	TTACAAAGTCCACTTTCTGA	230715	62911	AACAGGAGAGCCATTTCCCA	275302	107498	CCCAGCTGCCTCCAGTTGTT
186129	18325	TTTACAAAGTCCACTTTCTG	230716	62912	GAACAGGAGAGCCATTTCCC	275303	107499	CCCCAGCTGCCTCCAGTTGT
186130	18326	GTTTACAAAGTCCACTTTCT	230717	62913	TGAACAGGAGAGCCATTTCC	275304	107500	GCCCCAGCTGCCTCCAGTTG
186131	18327	TGTTTACAAAGTCCACTTTC	230718	62914	ATGAACAGGAGAGCCATTTC	275305	107501	TGCCCCAGCTGCCTCCAGTT
186132	18328	GTGTTTACAAAGTCCACTTT	230719	62915	AATGAACAGGAGAGCCATTT	275306	107502	CTGCCCCAGCTGCCTCCAGT
186133	18329	TGTGTTTACAAAGTCCACTT	230720	62916	GAATGAACAGGAGAGCCATT	275307	107503	GCTGCCCCAGCTGCCTCCAG
186134	18330	CTGTGTTTACAAAGTCCACT	230721	62917	GGAATGAACAGGAGAGCCAT	275308	107504	TGCTGCCCCAGCTGCCTCCA
186135	18331	ACTGTGTTTACAAAGTCCAC	230722	62918	GGGAATGAACAGGAGAGCCA	275309	107505	CTGCTGCCCCAGCTGCCTCC
186136	18332	TACTGTGTTTACAAAGTCCA	230723	62919	AGGGAATGAACAGGAGAGCC	275310	107506	TCTGCTGCCCCAGCTGCCTC
186137	18333	GTACTGTGTTTACAAAGTCC	230724	62920	CAGGGAATGAACAGGAGAGC	275311	107507	CTCTGCTGCCCCAGCTGCCT
186138	18334	GGTACTGTGTTTACAAAGTC	230725	62921	TCAGGGAATGAACAGGAGAG	275312	107508	CCTCTGCTGCCCCAGCTGCC
186139	18335	TGGTACTGTGTTTACAAAGT	230726	62922	TTCAGGGAATGAACAGGAGA	275313	107509	CCCTCTGCTGCCCCAGCTGC
186140	18336	GTGGTACTGTGTTTACAAAG	230727	62923	TTTCAGGGAATGAACAGGAG	275314	107510	ACCCTCTGCTGCCCCAGCTG
186141	18337	GGTGGTACTGTGTTTACAAA	230728	62924	TTTTCAGGGAATGAACAGGA	275315	107511	CACCCTCTGCTGCCCCAGCT
186142	18338	CGGTGGTACTGTGTTTACAA	230729	62925	GTTTTCAGGGAATGAACAGG	275316	107512	ACACCCTCTGCTGCCCCAGC
186143	18339	TCGGTGGTACTGTGTTTACA	230730	62926	GGTTTTCAGGGAATGAACAG	275317	107513	CACACCCTCTGCTGCCCCAG
186144	18340	TTCGGTGGTACTGTGTTTAC	230731	62927	AGGTTTTCAGGGAATGAACA	275318	107514	ACACACCCTCTGCTGCCCCA
186145	18341	GTTCGGTGGTACTGTGTTTA	230732	62928	GAGGTTTTCAGGGAATGAAC	275319	107515	CACACACCCTCTGCTGCCCC
186146	18342	GGTTCGGTGGTACTGTGTTT	230733	62929	AGAGGTTTTCAGGGAATGAA	275320	107516	ACACACACCCTCTGCTGCCC
186147	18343	TGGTTCGGTGGTACTGTGTT	230734	62930	CAGAGGTTTTCAGGGAATGA	275321	107517	AACACACACCCTCTGCTGCC
186148	18344	TTGGTTCGGTGGTACTGTGT	230735	62931	TCAGAGGTTTTCAGGGAATG	275322	107518	GAACACACACCCTCTGCTGC
186149	18345	ATTGGTTCGGTGGTACTGTG	230736	62932	ATCAGAGGTTTTCAGGGAAT	275323	107519	TGAACACACACCCTCTGCTG
186150	18346	AATTGGTTCGGTGGTACTGT	230737	62933	CATCAGAGGTTTTCAGGGAA	275324	107520	CTGAACACACACCCTCTGCT
186151	18347	AAATTGGTTCGGTGGTACTG	230738	62934	CCATCAGAGGTTTTCAGGGA	275325	107521	GCTGAACACACACCCTCTGC
186152	18348	CAAATTGGTTCGGTGGTACT	230739	62935	TCCATCAGAGGTTTTCAGGG	275326	107522	TGCTGAACACACACCCTCTG
186153	18349	TCAAATTGGTTCGGTGGTAC	230740	62936	TTCCATCAGAGGTTTTCAGG	275327	107523	GTGCTGAACACACACCCTCT
186154	18350	TTCAAATTGGTTCGGTGGTA	230741	62937	GTTCCATCAGAGGTTTTCAG	275328	107524	AGTGCTGAACACACACCCTC
186155	18351	GTTCAAATTGGTTCGGTGGT	230742	62938	GGTTCCATCAGAGGTTTTCA	275329	107525	TAGTGCTGAACACACACCCT
186156	18352	AGTTCAAATTGGTTCGGTGG	230743	62939	TGGTTCCATCAGAGGTTTTC	275330	107526	TTAGTGCTGAACACACACCC
186157	18353	CAGTTCAAATTGGTTCGGTG	230744	62940	GTGGTTCCATCAGAGGTTTT	275331	107527	CTTAGTGCTGAACACACACC
186158	18354	ACAGTTCAAATTGGTTCGGT	230745	62941	AGTGGTTCCATCAGAGGTTT	275332	107528	CCTTAGTGCTGAACACACAC
186159	18355	TACAGTTCAAATTGGTTCGG	230746	62942	CAGTGGTTCCATCAGAGGTT	275333	107529	CCCTTAGTGCTGAACACACA
186160	18356	GTACAGTTCAAATTGGTTCG	230747	62943	GCAGTGGTTCCATCAGAGGT	275334	107530	CCCCTTAGTGCTGAACACAC
186161	18357	AGTACAGTTCAAATTGGTTC	230748	62944	GGCAGTGGTTCCATCAGAGG	275335	107531	ACCCCTTAGTGCTGAACACA
186162	18358	TAGTACAGTTCAAATTGGTT	230749	62945	TGGCAGTGGTTCCATCAGAG	275336	107532	CACCCCTTAGTGCTGAACAC

186163	18359	GTAGTACAGTTCAAATTGGT	230750	62946	GTGGCAGTGGTTCCATCAGA	275337	107533	ACACCCCTTAGTGCTGAACA
186164	18360	GGTAGTACAGTTCAAATTGG	230751	62947	AGTGGCAGTGGTTCCATCAG	275338	107534	CACACCCCTTAGTGCTGAAC
186165	18361	AGGTAGTACAGTTCAAATTG	230752	62948	CAGTGGCAGTGGTTCCATCA	275339	107535	TCACACCCCTTAGTGCTGAA
186166	18362	GAGGTAGTACAGTTCAAATT	230753	62949	ACAGTGGCAGTGGTTCCATC	275340	107536	TTCACACCCCTTAGTGCTGA
186167	18363	AGAGGTAGTACAGTTCAAAT	230754	62950	CACAGTGGCAGTGGTTCCAT	275341	107537	CTTCACACCCCTTAGTGCTG
186168	18364	TAGAGGTAGTACAGTTCAAA	230755	62951	CCACAGTGGCAGTGGTTCCA	275342	107538	GCTTCACACCCCTTAGTGCT
186169	18365	CTAGAGGTAGTACAGTTCAA	230756	62952	GCCACAGTGGCAGTGGTTCC	275343	107539	AGCTTCACACCCCTTAGTGC
186170	18366	TCTAGAGGTAGTACAGTTCA	230757	62953	TGCCACAGTGGCAGTGGTTC	275344	107540	AAGCTTCACACCCCTTAGTG
186171	18367	GTCTAGAGGTAGTACAGTTC	230758	62954	CTGCCACAGTGGCAGTGGTT	275345	107541	CAAGCTTCACACCCCTTAGT
186172	18368	TGTCTAGAGGTAGTACAGTT	230759	62955	GCTGCCACAGTGGCAGTGGT	275346	107542	TCAAGCTTCACACCCCTTAG
186173	18369	TTGTCTAGAGGTAGTACAGT	230760	62956	GGCTGCCACAGTGGCAGTGG	275347	107543	CTCAAGCTTCACACCCCTTA
186174	18370	TTTGTCTAGAGGTAGTACAG	230761	62957	GGGCTGCCACAGTGGCAGTG	275348	107544	GCTCAAGCTTCACACCCCTT
186175	18371	TTTTGTCTAGAGGTAGTACA	230762	62958	GGGGCTGCCACAGTGGCAGT	275349	107545	CGCTCAAGCTTCACACCCCT
186176	18372	CTTTTGTCTAGAGGTAGTAC	230763	62959	TGGGGCTGCCACAGTGGCAG	275350	107546	GCGCTCAAGCTTCACACCCC
186177	18373	TCTTTTGTCTAGAGGTAGTA	230764	62960	CTGGGGCTGCCACAGTGGCA	275351	107547	AGCGCTCAAGCTTCACACCC
186178	18374	CTCTTTTGTCTAGAGGTAGT	230765	62961	GCTGGGGCTGCCACAGTGGC	275352	107548	TAGCGCTCAAGCTTCACACC
186179	18375	TCTCTTTTGTCTAGAGGTAG	230766	62962	TGCTGGGGCTGCCACAGTGG	275353	107549	CTAGCGCTCAAGCTTCACAC
186180	18376	CTCTCTTTTGTCTAGAGGTA	230767	62963	GTGCTGGGGCTGCCACAGTG	275354	107550	CCTAGCGCTCAAGCTTCACA
186181	18377	CCTCTCTTTTGTCTAGAGGT	230768	62964	AGTGCTGGGGCTGCCACAGT	275355	107551	TCCTAGCGCTCAAGCTTCAC
186182	18378	CCCTCTCTTTTGTCTAGAGG	230769	62965	CAGTGCTGGGGCTGCCACAG	275356	107552	CTCCTAGCGCTCAAGCTTCA
186183	18379	GCCCTCTCTTTTGTCTAGAG	230770	62966	CCAGTGCTGGGGCTGCCACA	275357	107553	TCTCCTAGCGCTCAAGCTTC
186184	18380	TGCCCTCTCTTTTGTCTAGA	230771	62967	GCCAGTGCTGGGGCTGCCAC	275358	107554	CTCTCCTAGCGCTCAAGCTT
186185	18381	CTGCCCTCTCTTTTGTCTAG	230772	62968	TGCCAGTGCTGGGGCTGCCA	275359	107555	ACTCTCCTAGCGCTCAAGCT
186186	18382	ACTGCCCTCTCTTTTGTCTA	230773	62969	GTGCCAGTGCTGGGGCTGCC	275360	107556	AACTCTCCTAGCGCTCAAGC
186187	18383	GACTGCCCTCTCTTTTGTCT	230774	62970	GGTGCCAGTGCTGGGGCTGC	275361	107557	GAACTCTCCTAGCGCTCAAG
186188	18384	TGACTGCCCTCTCTTTTGTC	230775	62971	GGGTGCCAGTGCTGGGGCTG	275362	107558	TGAACTCTCCTAGCGCTCAA
186189	18385	CTGACTGCCCTCTCTTTTGT	230776	62972	GGGGTGCCAGTGCTGGGGCT	275363	107559	GTGAACTCTCCTAGCGCTCA
186190	18386	TCTGACTGCCCTCTCTTTTG	230777	62973	TGGGGTGCCAGTGCTGGGGC	275364	107560	TGTGAACTCTCCTAGCGCTC
186191	18387	GTCTGACTGCCCTCTCTTTT	230778	62974	CTGGGGTGCCAGTGCTGGGG	275365	107561	GTGTGAACTCTCCTAGCGCT
186192	18388	TGTCTGACTGCCCTCTCTTT	230779	62975	GCTGGGGTGCCAGTGCTGGG	275366	107562	AGTGTGAACTCTCCTAGCGC
186193	18389	CTGTCTGACTGCCCTCTCTT	230780	62976	GGCTGGGGTGCCAGTGCTGG	275367	107563	CAGTGTGAACTCTCCTAGCG
186194	18390	ACTGTCTGACTGCCCTCTCT	230781	62977	TGGCTGGGGTGCCAGTGCTG	275368	107564	CCAGTGTGAACTCTCCTAGC
186195	18391	AACTGTCTGACTGCCCTCTC	230782	62978	ATGGCTGGGGTGCCAGTGCT	275369	107565	GCCAGTGTGAACTCTCCTAG
186196	18392	CAACTGTCTGACTGCCCTCT	230783	62979	CATGGCTGGGGTGCCAGTGC	275370	107566	TGCCAGTGTGAACTCTCCTA
186197	18393	ACAACTGTCTGACTGCCCTC	230784	62980	TCATGGCTGGGGTGCCAGTG	275371	107567	CTGCCAGTGTGAACTCTCCT
186198	18394	AACAACTGTCTGACTGCCCT	230785	62981	ATCATGGCTGGGGTGCCAGT	275372	107568	TCTGCCAGTGTGAACTCTCC
186199	18395	GAACAACTGTCTGACTGCCC	230786	62982	AATCATGGCTGGGGTGCCAG	275373	107569	TTCTGCCAGTGTGAACTCTC
186200	18396	CGAACAACTGTCTGACTGCC	230787	62983	CAATCATGGCTGGGGTGCCA	275374	107570	CTTCTGCCAGTGTGAACTCT
186201	18397	ACGAACAACTGTCTGACTGC	230788	62984	CCAATCATGGCTGGGGTGCC	275375	107571	TCTTCTGCCAGTGTGAACTC
186202	18398	CACGAACAACTGTCTGACTG	230789	62985	ACCAATCATGGCTGGGGTGC	275376	107572	CTCTTCTGCCAGTGTGAACT
186203	18399	TCACGAACAACTGTCTGACT	230790	62986	CACCAATCATGGCTGGGGTG	275377	107573	TCTCTTCTGCCAGTGTGAAC
186204	18400	ATCACGAACAACTGTCTGAC	230791	62987	GCACCAATCATGGCTGGGGT	275378	107574	CTCTCTTCTGCCAGTGTGAA
186205	18401	AATCACGAACAACTGTCTGA	230792	62988	GGCACCAATCATGGCTGGGG	275379	107575	CCTCTCTTCTGCCAGTGTGA
186206	18402	AAATCACGAACAACTGTCTG	230793	62989	GGGCACCAATCATGGCTGGG	275380	107576	ACCTCTCTTCTGCCAGTGTG
186207	18403	GAAATCACGAACAACTGTCT	230794	62990	GGGGCACCAATCATGGCTGG	275381	107577	AACCTCTCTTCTGCCAGTGT
186208	18404	AGAAATCACGAACAACTGTC	230795	62991	TGGGGCACCAATCATGGCTG	275382	107578	CAACCTCTCTTCTGCCAGTG
186209	18405	AAGAAATCACGAACAACTGT	230796	62992	CTGGGGCACCAATCATGGCT	275383	107579	CCAACCTCTCTTCTGCCAGT
186210	18406	GAAGAAATCACGAACAACTG	230797	62993	GCTGGGGCACCAATCATGGC	275384	107580	CCCAACCTCTCTTCTGCCAG
186211	18407	AGAAGAAATCACGAACAACT	230798	62994	GGCTGGGGCACCAATCATGG	275385	107581	CCCCAACCTCTCTTCTGCCA
186212	18408	AAGAAGAAATCACGAACAAC	230799	62995	TGGCTGGGGCACCAATCATG	275386	107582	GCCCCAACCTCTCTTCTGCC
186213	18409	AAAGAAGAAATCACGAACAA	230800	62996	GTGGCTGGGGCACCAATCAT	275387	107583	TGCCCCAACCTCTCTTCTGC
186214	18410	GAAAGAAGAAATCACGAACA	230801	62997	TGTGGCTGGGGCACCAATCA	275388	107584	CTGCCCCAACCTCTCTTCTG
186215	18411	TGAAAGAAGAAATCACGAAC	230802	62998	ATGTGGCTGGGGCACCAATC	275389	107585	GCTGCCCCAACCTCTCTTCT
186216	18412	TTGAAAGAAGAAATCACGAA	230803	62999	GATGTGGCTGGGGCACCAAT	275390	107586	AGCTGCCCCAACCTCTCTTC
186217	18413	GTTGAAAGAAGAAATCACGA	230804	63000	AGATGTGGCTGGGGCACCAA	275391	107587	CAGCTGCCCCAACCTCTCTT
186218	18414	TGTTGAAAGAAGAAATCACG	230805	63001	GAGATGTGGCTGGGGCACCA	275392	107588	GCAGCTGCCCCAACCTCTCT
186219	18415	CTGTTGAAAGAAGAAATCAC	230806	63002	AGAGATGTGGCTGGGGCACC	275393	107589	TGCAGCTGCCCCAACCTCTC
186220	18416	ACTGTTGAAAGAAGAAATCA	230807	63003	CAGAGATGTGGCTGGGGCAC	275394	107590	TTGCAGCTGCCCCAACCTCT
186221	18417	GACTGTTGAAAGAAGAAATC	230808	63004	GCAGAGATGTGGCTGGGGCA	275395	107591	CTTGCAGCTGCCCCAACCTC
186222	18418	TGACTGTTGAAAGAAGAAAT	230809	63005	AGCAGAGATGTGGCTGGGGC	275396	107592	GCTTGCAGCTGCCCCAACCT
186223	18419	ATGACTGTTGAAAGAAGAAA	230810	63006	CAGCAGAGATGTGGCTGGGG	275397	107593	GGCTTGCAGCTGCCCCAACC
186224	18420	AATGACTGTTGAAAGAAGAA	230811	63007	ACAGCAGAGATGTGGCTGGG	275398	107594	AGGCTTGCAGCTGCCCCAAC
186225	18421	AAATGACTGTTGAAAGAAGA	230812	63008	CACAGCAGAGATGTGGCTGG	275399	107595	GAGGCTTGCAGCTGCCCCAA
186226	18422	CAAATGACTGTTGAAAGAAG	230813	63009	TCACAGCAGAGATGTGGCTG	275400	107596	AGAGGCTTGCAGCTGCCCCA
186227	18423	TCAAATGACTGTTGAAAGAA	230814	63010	CTCACAGCAGAGATGTGGCT	275401	107597	CAGAGGCTTGCAGCTGCCCC
186228	18424	CTCAAATGACTGTTGAAAGA	230815	63011	GCTCACAGCAGAGATGTGGC	275402	107598	CCAGAGGCTTGCAGCTGCCC
186229	18425	GCTCAAATGACTGTTGAAAG	230816	63012	GGCTCACAGCAGAGATGTGG	275403	107599	TCCAGAGGCTTGCAGCTGCC
186230	18426	TGCTCAAATGACTGTTGAAA	230817	63013	GGGCTCACAGCAGAGATGTG	275404	107600	GTCCAGAGGCTTGCAGCTGC
186231	18427	GTGCTCAAATGACTGTTGAA	230818	63014	GGGGCTCACAGCAGAGATGT	275405	107601	TGTCCAGAGGCTTGCAGCTG
186232	18428	AGTGCTCAAATGACTGTTGA	230819	63015	TGGGGCTCACAGCAGAGATG	275406	107602	ATGTCCAGAGGCTTGCAGCT
186233	18429	AAGTGCTCAAATGACTGTTG	230820	63016	CTGGGGCTCACAGCAGAGAT	275407	107603	GATGTCCAGAGGCTTGCAGC
186234	18430	TAAGTGCTCAAATGACTGTT	230821	63017	TCTGGGGCTCACAGCAGAGA	275408	107604	CGATGTCCAGAGGCTTGCAG

186235	18431	GTAAGTGCTCAAATGACTGT	230822	63018	CTCTGGGGCTCACAGCAGAG	275409	107605	GCGATGTCCAGAGGCTTGCA
186236	18432	AGTAAGTGCTCAAATGACTG	230823	63019	GCTCTGGGGCTCACAGCAGA	275410	107606	GGCGATGTCCAGAGGCTTGC
186237	18433	TAGTAAGTGCTCAAATGACT	230824	63020	GGCTCTGGGGCTCACAGCAG	275411	107607	GGGCGATGTCCAGAGGCTTG
186238	18434	GTAGTAAGTGCTCAAATGAC	230825	63021	GGGCTCTGGGGCTCACAGCA	275412	107608	CGGGCGATGTCCAGAGGCTT
186239	18435	TGTAGTAAGTGCTCAAATGA	230826	63022	AGGGCTCTGGGGCTCACAGC	275413	107609	TCGGGCGATGTCCAGAGGCT
186240	18436	TTGTAGTAAGTGCTCAAATG	230827	63023	CAGGGCTCTGGGGCTCACAG	275414	107610	GTCGGGCGATGTCCAGAGGC
186241	18437	TTTGTAGTAAGTGCTCAAAT	230828	63024	CCAGGGCTCTGGGGCTCACA	275415	107611	TGTCGGGCGATGTCCAGAGG
186242	18438	TTTTGTAGTAAGTGCTCAAA	230829	63025	ACCAGGGCTCTGGGGCTCAC	275416	107612	CTGTCGGGCGATGTCCAGAG
186243	18439	GTTTTGTAGTAAGTGCTCAA	230830	63026	AACCAGGGCTCTGGGGCTCA	275417	107613	CCTGTCGGGCGATGTCCAGA
186244	18440	TGTTTTGTAGTAAGTGCTCA	230831	63027	TAACCAGGGCTCTGGGGCTC	275418	107614	TCCTGTCGGGCGATGTCCAG
186245	18441	CTGTTTTGTAGTAAGTGCTC	230832	63028	TTAACCAGGGCTCTGGGGCT	275419	107615	GTCCTGTCGGGCGATGTCCA
186246	18442	TCTGTTTTGTAGTAAGTGCT	230833	63029	ATTAACCAGGGCTCTGGGGC	275420	107616	TGTCCTGTCGGGCGATGTCC
186247	18443	TTCTGTTTTGTAGTAAGTGC	230834	63030	AATTAACCAGGGCTCTGGGG	275421	107617	CTGTCCTGTCGGGCGATGTC
186248	18444	CTTCTGTTTTGTAGTAAGTG	230835	63031	TAATTAACCAGGGCTCTGGG	275422	107618	TCTGTCCTGTCGGGCGATGT
186249	18445	GCTTCTGTTTTGTAGTAAGT	230836	63032	TTAATTAACCAGGGCTCTGG	275423	107619	CTCTGTCCTGTCGGGCGATG
186250	18446	AGCTTCTGTTTTGTAGTAAG	230837	63033	ATTAATTAACCAGGGCTCTG	275424	107620	CCTCTGTCCTGTCGGGCGAT
186251	18447	TAGCTTCTGTTTTGTAGTAA	230838	63034	GATTAATTAACCAGGGCTCT	275425	107621	CCCTCTGTCCTGTCGGGCGA
186252	18448	ATAGCTTCTGTTTTGTAGTA	230839	63035	TGATTAATTAACCAGGGCTC	275426	107622	ACCCTCTGTCCTGTCGGGCG
186253	18449	CATAGCTTCTGTTTTGTAGT	230840	63036	ATGATTAATTAACCAGGGCT	275427	107623	CACCCTCTGTCCTGTCGGGC
186254	18450	ACATAGCTTCTGTTTTGTAG	230841	63037	GATGATTAATTAACCAGGGC	275428	107624	CCACCCTCTGTCCTGTCGGG
186255	18451	CACATAGCTTCTGTTTTGTA	230842	63038	GGATGATTAATTAACCAGGG	275429	107625	ACCACCCTCTGTCCTGTCGG
186256	18452	ACACATAGCTTCTGTTTTGT	230843	63039	TGGATGATTAATTAACCAGG	275430	107626	CACCACCCTCTGTCCTGTCG
186257	18453	TACACATAGCTTCTGTTTTG	230844	63040	GTGGATGATTAATTAACCAG	275431	107627	CCACCACCCTCTGTCCTGTC
186258	18454	TTACACATAGCTTCTGTTTT	230845	63041	CGTGGATGATTAATTAACCA	275432	107628	TCCACCACCCTCTGTCCTGT
186259	18455	CTTACACATAGCTTCTGTTT	230846	63042	ACGTGGATGATTAATTAACC	275433	107629	GTCCACCACCCTCTGTCCTG
186260	18456	CCTTACACATAGCTTCTGTT	230847	63043	CACGTGGATGATTAATTAAC	275434	107630	CGTCCACCACCCTCTGTCCT
186261	18457	CCCTTACACATAGCTTCTGT	230848	63044	ACACGTGGATGATTAATTAA	275435	107631	CCGTCCACCACCCTCTGTCC
186262	18458	ACCCTTACACATAGCTTCTG	230849	63045	AACACGTGGATGATTAATTA	275436	107632	ACCGTCCACCACCCTCTGTC
186263	18459	CACCCTTACACATAGCTTCT	230850	63046	CAACACGTGGATGATTAATT	275437	107633	CACCGTCCACCACCCTCTGT
186264	18460	CCACCCTTACACATAGCTTC	230851	63047	TCAACACGTGGATGATTAAT	275438	107634	CCACCGTCCACCACCCTCTG
186265	18461	TCCACCCTTACACATAGCTT	230852	63048	ATCAACACGTGGATGATTAA	275439	107635	GCCACCGTCCACCACCCTCT
186266	18462	CTCCACCCTTACACATAGCT	230853	63049	CATCAACACGTGGATGATTA	275440	107636	GGCCACCGTCCACCACCCTC
186267	18463	CCTCCACCCTTACACATAGC	230854	63050	CCATCAACACGTGGATGATT	275441	107637	GGGCCACCGTCCACCACCCT
186268	18464	GCCTCCACCCTTACACATAG	230855	63051	CCCATCAACACGTGGATGAT	275442	107638	AGGGCCACCGTCCACCACCC
186269	18465	CGCCTCCACCCTTACACATA	230856	63052	CCCCATCAACACGTGGATGA	275443	107639	CAGGGCCACCGTCCACCACC
186270	18466	ACGCCTCCACCCTTACACAT	230857	63053	TCCCCATCAACACGTGGATG	275444	107640	TCAGGGCCACCGTCCACCAC
186271	18467	AACGCCTCCACCCTTACACA	230858	63054	CTCCCCATCAACACGTGGAT	275445	107641	TTCAGGGCCACCGTCCACCA
186272	18468	TAACGCCTCCACCCTTACAC	230859	63055	TCTCCCCATCAACACGTGGA	275446	107642	CTTCAGGGCCACCGTCCACC
186273	18469	CTAACGCCTCCACCCTTACA	230860	63056	CTCTCCCCATCAACACGTGG	275447	107643	TCTTCAGGGCCACCGTCCAC
186274	18470	GCTAACGCCTCCACCCTTAC	230861	63057	CCTCTCCCCATCAACACGTG	275448	107644	CTCTTCAGGGCCACCGTCCA
186275	18471	AGCTAACGCCTCCACCCTTA	230862	63058	GCCTCTCCCCATCAACACGT	275449	107645	TCTCTTCAGGGCCACCGTCC
186276	18472	CAGCTAACGCCTCCACCCTT	230863	63059	GGCCTCTCCCCATCAACACG	275450	107646	CTCTCTTCAGGGCCACCGTC
186277	18473	ACAGCTAACGCCTCCACCCT	230864	63060	GGGCCTCTCCCCATCAACAC	275451	107647	CCTCTCTTCAGGGCCACCGT
186278	18474	AACAGCTAACGCCTCCACCC	230865	63061	TGGGCCTCTCCCCATCAACA	275452	107648	GCCTCTCTTCAGGGCCACCG
186279	18475	TAACAGCTAACGCCTCCACC	230866	63062	ATGGGCCTCTCCCCATCAAC	275453	107649	AGCCTCTCTTCAGGGCCACC
186280	18476	TTAACAGCTAACGCCTCCAC	230867	63063	AATGGGCCTCTCCCCATCAA	275454	107650	GAGCCTCTCTTCAGGGCCAC
186281	18477	ATTAACAGCTAACGCCTCCA	230868	63064	GAATGGGCCTCTCCCCATCA	275455	107651	TGAGCCTCTCTTCAGGGCCA
186282	18478	GATTAACAGCTAACGCCTCC	230869	63065	TGAATGGGCCTCTCCCCATC	275456	107652	CTGAGCCTCTCTTCAGGGCC
186283	18479	TGATTAACAGCTAACGCCTC	230870	63066	GTGAATGGGCCTCTCCCCAT	275457	107653	ACTGAGCCTCTCTTCAGGGC
186284	18480	CTGATTAACAGCTAACGCCT	230871	63067	TGTGAATGGGCCTCTCCCCA	275458	107654	AACTGAGCCTCTCTTCAGGG
186285	18481	CCTGATTAACAGCTAACGCC	230872	63068	TTGTGAATGGGCCTCTCCCC	275459	107655	GAACTGAGCCTCTCTTCAGG
186286	18482	TCCTGATTAACAGCTAACGC	230873	63069	TTTGTGAATGGGCCTCTCCC	275460	107656	TGAACTGAGCCTCTCTTCAG
186287	18483	GTCCTGATTAACAGCTAACG	230874	63070	TTTTGTGAATGGGCCTCTCC	275461	107657	CTGAACTGAGCCTCTCTTCA
186288	18484	GGTCCTGATTAACAGCTAAC	230875	63071	CTTTTGTGAATGGGCCTCTC	275462	107658	GCTGAACTGAGCCTCTCTTC
186289	18485	AGGTCCTGATTAACAGCTAA	230876	63072	GCTTTTGTGAATGGGCCTCT	275463	107659	AGCTGAACTGAGCCTCTCTT
186290	18486	GAGGTCCTGATTAACAGCTA	230877	63073	CGCTTTTGTGAATGGGCCTC	275464	107660	CAGCTGAACTGAGCCTCTCT
186291	18487	GGAGGTCCTGATTAACAGCT	230878	63074	TCGCTTTTGTGAATGGGCCT	275465	107661	CCAGCTGAACTGAGCCTCTC
186292	18488	TGGAGGTCCTGATTAACAGC	230879	63075	GTCGCTTTTGTGAATGGGCC	275466	107662	GCCAGCTGAACTGAGCCTCT
186293	18489	CTGGAGGTCCTGATTAACAG	230880	63076	TGTCGCTTTTGTGAATGGGC	275467	107663	TGCCAGCTGAACTGAGCCTC
186294	18490	CCTGGAGGTCCTGATTAACA	230881	63077	ATGTCGCTTTTGTGAATGGG	275468	107664	CTGCCAGCTGAACTGAGCCT
186295	18491	GCCTGGAGGTCCTGATTAAC	230882	63078	TATGTCGCTTTTGTGAATGG	275469	107665	ACTGCCAGCTGAACTGAGCC
186296	18492	AGCCTGGAGGTCCTGATTAA	230883	63079	TTATGTCGCTTTTGTGAATG	275470	107666	CACTGCCAGCTGAACTGAGC
186297	18493	TAGCCTGGAGGTCCTGATTA	230884	63080	TTTATGTCGCTTTTGTGAAT	275471	107667	CCACTGCCAGCTGAACTGAG
186298	18494	TTAGCCTGGAGGTCCTGATT	230885	63081	CTTTATGTCGCTTTTGTGAA	275472	107668	GCCACTGCCAGCTGAACTGA
186299	18495	CTTAGCCTGGAGGTCCTGAT	230886	63082	GCTTTATGTCGCTTTTGTGA	275473	107669	GGCCACTGCCAGCTGAACTG
186300	18496	ACTTAGCCTGGAGGTCCTGA	230887	63083	GGCTTTATGTCGCTTTTGTG	275474	107670	CGGCCACTGCCAGCTGAACT
186301	18497	AACTTAGCCTGGAGGTCCTG	230888	63084	GGGCTTTATGTCGCTTTTGT	275475	107671	ACGGCCACTGCCAGCTGAAC
186302	18498	AAACTTAGCCTGGAGGTCCT	230889	63085	TGGGCTTTATGTCGCTTTTG	275476	107672	CACGGCCACTGCCAGCTGAA
186303	18499	GAAACTTAGCCTGGAGGTCC	230890	63086	CTGGGCTTTATGTCGCTTTT	275477	107673	CCACGGCCACTGCCAGCTGA
186304	18500	AGAAACTTAGCCTGGAGGTC	230891	63087	CCTGGGCTTTATGTCGCTTT	275478	107674	CCCACGGCCACTGCCAGCTG
186305	18501	CAGAAACTTAGCCTGGAGGT	230892	63088	CCCTGGGCTTTATGTCGCTT	275479	107675	TCCCACGGCCACTGCCAGCT
186306	18502	ACAGAAACTTAGCCTGGAGG	230893	63089	TCCCTGGGCTTTATGTCGCT	275480	107676	CTCCCACGGCCACTGCCAGC

186307	18503	TACAGAAACTTAGCCTGGAG	230894	63090	CTCCCTGGGCTTTATGTCGC	275481	107677	ACTCCCACGGCCACTGCCAG
186308	18504	ATACAGAAACTTAGCCTGGA	230895	63091	TCTCCCTGGGCTTTATGTCG	275482	107678	CACTCCCACGGCCACTGCCA
186309	18505	AATACAGAAACTTAGCCTGG	230896	63092	GTCTCCCTGGGCTTTATGTC	275483	107679	GCACTCCCACGGCCACTGCC
186310	18506	TAATACAGAAACTTAGCCTG	230897	63093	CGTCTCCCTGGGCTTTATGT	275484	107680	AGCACTCCCACGGCCACTGC
186311	18507	CTAATACAGAAACTTAGCCT	230898	63094	ACGTCTCCCTGGGCTTTATG	275485	107681	CAGCACTCCCACGGCCACTG
186312	18508	ACTAATACAGAAACTTAGCC	230899	63095	CACGTCTCCCTGGGCTTTAT	275486	107682	TCAGCACTCCCACGGCCACT
186313	18509	GACTAATACAGAAACTTAGC	230900	63096	CCACGTCTCCCTGGGCTTTA	275487	107683	TTCAGCACTCCCACGGCCAC
186314	18510	GGACTAATACAGAAACTTAG	230901	63097	GCCACGTCTCCCTGGGCTTT	275488	107684	CTTCAGCACTCCCACGGCCA
186315	18511	CGGACTAATACAGAAACTTA	230902	63098	GGCCACGTCTCCCTGGGCTT	275489	107685	GCTTCAGCACTCCCACGGCC
186316	18512	ACGGACTAATACAGAAACTT	230903	63099	CGGCCACGTCTCCCTGGGCT	275490	107686	TGCTTCAGCACTCCCACGGC
186317	18513	AACGGACTAATACAGAAACT	230904	63100	ACGGCCACGTCTCCCTGGGC	275491	107687	CTGCTTCAGCACTCCCACGG
186318	18514	AAACGGACTAATACAGAAAC	230905	63101	CACGGCCACGTCTCCCTGGG	275492	107688	CCTGCTTCAGCACTCCCACG
186319	18515	AAAACGGACTAATACAGAAA	230906	63102	CCACGGCCACGTCTCCCTGG	275493	107689	GCCTGCTTCAGCACTCCCAC
186320	18516	GAAAACGGACTAATACAGAA	230907	63103	GCCACGGCCACGTCTCCCTG	275494	107690	TGCCTGCTTCAGCACTCCCA
186321	18517	TGAAAACGGACTAATACAGA	230908	63104	TGCCACGGCCACGTCTCCCT	275495	107691	CTGCCTGCTTCAGCACTCCC
186322	18518	GTGAAAACGGACTAATACAG	230909	63105	TTGCCACGGCCACGTCTCCC	275496	107692	CCTGCCTGCTTCAGCACTCC
186323	18519	CGTGAAAACGGACTAATACA	230910	63106	CTTGCCACGGCCACGTCTCC	275497	107693	GCCTGCCTGCTTCAGCACTC
186324	18520	GCGTGAAAACGGACTAATAC	230911	63107	TCTTGCCACGGCCACGTCTC	275498	107694	AGCCTGCCTGCTTCAGCACT
186325	18521	AGCGTGAAAACGGACTAATA	230912	63108	TTCTTGCCACGGCCACGTCT	275499	107695	CAGCCTGCCTGCTTCAGCAC
186326	18522	CAGCGTGAAAACGGACTAAT	230913	63109	CTTCTTGCCACGGCCACGTC	275500	107696	ACAGCCTGCCTGCTTCAGCA
186327	18523	GCAGCGTGAAAACGGACTAA	230914	63110	CCTTCTTGCCACGGCCACGT	275501	107697	GACAGCCTGCCTGCTTCAGC
186328	18524	AGCAGCGTGAAAACGGACTA	230915	63111	CCCTTCTTGCCACGGCCACG	275502	107698	CGACAGCCTGCCTGCTTCAG
186329	18525	CAGCAGCGTGAAAACGGACT	230916	63112	ACCCTTCTTGCCACGGCCAC	275503	107699	CCGACAGCCTGCCTGCTTCA
186330	18526	TCAGCAGCGTGAAAACGGAC	230917	63113	CACCCTTCTTGCCACGGCCA	275504	107700	GCCGACAGCCTGCCTGCTTC
186331	18527	ATCAGCAGCGTGAAAACGGA	230918	63114	ACACCCTTCTTGCCACGGCC	275505	107701	TGCCGACAGCCTGCCTGCTT
186332	18528	TATCAGCAGCGTGAAAACGG	230919	63115	CACACCCTTCTTGCCACGGC	275506	107702	ATGCCGACAGCCTGCCTGCT
186333	18529	TTATCAGCAGCGTGAAAACG	230920	63116	CCACACCCTTCTTGCCACGG	275507	107703	GATGCCGACAGCCTGCCTGC
186334	18530	TTTATCAGCAGCGTGAAAAC	230921	63117	CCCACACCCTTCTTGCCACG	275508	107704	AGATGCCGACAGCCTGCCTG
186335	18531	CTTTATCAGCAGCGTGAAAA	230922	63118	TCCCACACCCTTCTTGCCAC	275509	107705	CAGATGCCGACAGCCTGCCT
186336	18532	TCTTTATCAGCAGCGTGAAA	230923	63119	GTCCCACACCCTTCTTGCCA	275510	107706	GCAGATGCCGACAGCCTGCC
186337	18533	GTCTTTATCAGCAGCGTGAA	230924	63120	AGTCCCACACCCTTCTTGCC	275511	107707	AGCAGATGCCGACAGCCTGC
186338	18534	TGTCTTTATCAGCAGCGTGA	230925	63121	TAGTCCCACACCCTTCTTGC	275512	107708	CAGCAGATGCCGACAGCCTG
186339	18535	ATGTCTTTATCAGCAGCGTG	230926	63122	GTAGTCCCACACCCTTCTTG	275513	107709	CCAGCAGATGCCGACAGCCT
186340	18536	TATGTCTTTATCAGCAGCGT	230927	63123	TGTAGTCCCACACCCTTCTT	275514	107710	CCCAGCAGATGCCGACAGCC
186341	18537	GTATGTCTTTATCAGCAGCG	230928	63124	ATGTAGTCCCACACCCTTCT	275515	107711	CCCCAGCAGATGCCGACAGC
186342	18538	GGTATGTCTTTATCAGCAGC	230929	63125	AATGTAGTCCCACACCCTTC	275516	107712	TCCCCAGCAGATGCCGACAG
186343	18539	GGGTATGTCTTTATCAGCAG	230930	63126	GAATGTAGTCCCACACCCTT	275517	107713	GTCCCCAGCAGATGCCGACA
186344	18540	CGGGTATGTCTTTATCAGCA	230931	63127	GGAATGTAGTCCCACACCCT	275518	107714	CGTCCCCAGCAGATGCCGAC
186345	18541	TCGGGTATGTCTTTATCAGC	230932	63128	CGGAATGTAGTCCCACACCC	275519	107715	CCGTCCCCAGCAGATGCCGA
186346	18542	CTCGGGTATGTCTTTATCAG	230933	63129	GCGGAATGTAGTCCCACACC	275520	107716	ACCGTCCCCAGCAGATGCCG
186347	18543	TCTCGGGTATGTCTTTATCA	230934	63130	GGCGGAATGTAGTCCCACAC	275521	107717	AACCGTCCCCAGCAGATGCC
186348	18544	GTCTCGGGTATGTCTTTATC	230935	63131	GGGCGGAATGTAGTCCCACA	275522	107718	TAACCGTCCCCAGCAGATGC
186349	18545	AGTCTCGGGTATGTCTTTAT	230936	63132	GGGGCGGAATGTAGTCCCAC	275523	107719	TTAACCGTCCCCAGCAGATG
186350	18546	CAGTCTCGGGTATGTCTTTA	230937	63133	GGGGGCGGAATGTAGTCCCA	275524	107720	CTTAACCGTCCCCAGCAGAT
186351	18547	CCAGTCTCGGGTATGTCTTT	230938	63134	TGGGGGCGGAATGTAGTCCC	275525	107721	GCTTAACCGTCCCCAGCAGA
186352	18548	CCCAGTCTCGGGTATGTCTT	230939	63135	TTGGGGGCGGAATGTAGTCC	275526	107722	TGCTTAACCGTCCCCAGCAG
186353	18549	CCCCAGTCTCGGGTATGTCT	230940	63136	GTTGGGGGCGGAATGTAGTC	275527	107723	CTGCTTAACCGTCCCCAGCA
186354	18550	TCCCCAGTCTCGGGTATGTC	230941	63137	AGTTGGGGGCGGAATGTAGT	275528	107724	CCTGCTTAACCGTCCCCAGC
186355	18551	TTCCCCAGTCTCGGGTATGT	230942	63138	CAGTTGGGGGCGGAATGTAG	275529	107725	CCCTGCTTAACCGTCCCCAG
186356	18552	ATTCCCCAGTCTCGGGTATG	230943	63139	TCAGTTGGGGGCGGAATGTA	275530	107726	CCCCTGCTTAACCGTCCCCA
186357	18553	AATTCCCCAGTCTCGGGTAT	230944	63140	CTCAGTTGGGGGCGGAATGT	275531	107727	ACCCCTGCTTAACCGTCCCC
186358	18554	AAATTCCCCAGTCTCGGGTA	230945	63141	TCTCAGTTGGGGGCGGAATG	275532	107728	CACCCCTGCTTAACCGTCCC
186359	18555	TAAATTCCCCAGTCTCGGGT	230946	63142	CTCTCAGTTGGGGGCGGAAT	275533	107729	TCACCCCTGCTTAACCGTCC
186360	18556	GTAAATTCCCCAGTCTCGGG	230947	63143	TCTCTCAGTTGGGGGCGGAA	275534	107730	CTCACCCCTGCTTAACCGTC
186361	18557	TGTAAATTCCCCAGTCTCGG	230948	63144	ATCTCTCAGTTGGGGGCGGA	275535	107731	CCTCACCCCTGCTTAACCGT
186362	18558	TTGTAAATTCCCCAGTCTCG	230949	63145	AATCTCTCAGTTGGGGGCGG	275536	107732	CCCTCACCCCTGCTTAACCG
186363	18559	TTTGTAAATTCCCCAGTCTC	230950	63146	GAATCTCTCAGTTGGGGGCG	275537	107733	GCCCTCACCCCTGCTTAACC
186364	18560	TTTTGTAAATTCCCCAGTCT	230951	63147	TGAATCTCTCAGTTGGGGGC	275538	107734	GGCCCTCACCCCTGCTTAAC
186365	18561	CTTTTGTAAATTCCCCAGTC	230952	63148	CTGAATCTCTCAGTTGGGGG	275539	107735	GGGCCCTCACCCCTGCTTAA
186366	18562	TCTTTTGTAAATTCCCCAGT	230953	63149	TCTGAATCTCTCAGTTGGGG	275540	107736	TGGGCCCTCACCCCTGCTTA
186367	18563	TTCTTTTGTAAATTCCCCAG	230954	63150	TTCTGAATCTCTCAGTTGGG	275541	107737	CTGGGCCCTCACCCCTGCTT
186368	18564	TTTCTTTTGTAAATTCCCCA	230955	63151	TTTCTGAATCTCTCAGTTGG	275542	107738	GCTGGGCCCTCACCCCTGCT
186369	18565	CTTTCTTTTGTAAATTCCCC	230956	63152	GTTTCTGAATCTCTCAGTTG	275543	107739	GGCTGGGCCCTCACCCCTGC
186370	18566	TCTTTCTTTTGTAAATTCCC	230957	63153	GGTTTCTGAATCTCTCAGTT	275544	107740	AGGCTGGGCCCTCACCCCTG
186371	18567	CTCTTTCTTTTGTAAATTCC	230958	63154	TGGTTTCTGAATCTCTCAGT	275545	107741	GAGGCTGGGCCCTCACCCCT
186372	18568	CCTCTTTCTTTTGTAAATTC	230959	63155	CTGGTTTCTGAATCTCTCAG	275546	107742	TGAGGCTGGGCCCTCACCCC
186373	18569	ACCTCTTTCTTTTGTAAATT	230960	63156	TCTGGTTTCTGAATCTCTCA	275547	107743	CTGAGGCTGGGCCCTCACCC
186374	18570	AACCTCTTTCTTTTGTAAAT	230961	63157	TTCTGGTTTCTGAATCTCTC	275548	107744	GCTGAGGCTGGGCCCTCACC
186375	18571	AAACCTCTTTCTTTTGTAAA	230962	63158	TTTCTGGTTTCTGAATCTCT	275549	107745	TGCTGAGGCTGGGCCCTCAC
186376	18572	TAAACCTCTTTCTTTTGTAA	230963	63159	TTTTCTGGTTTCTGAATCTC	275550	107746	CTGCTGAGGCTGGGCCCTCA
186377	18573	TTAAACCTCTTTCTTTTGTA	230964	63160	TTTTTCTGGTTTCTGAATCT	275551	107747	GCTGCTGAGGCTGGGCCCTC
186378	18574	ATTAAACCTCTTTCTTTTGT	230965	63161	TTTTTTCTGGTTTCTGAATC	275552	107748	GGCTGCTGAGGCTGGGCCCT

186379	18575	AATTAAACCTCTTTCTTTTG	230966	63162	TTTTTTTCTGGTTTCTGAAT	275553	107749	GGGCTGCTGAGGCTGGGCCC
186380	18576	CAATTAAACCTCTTTCTTTT	230967	63163	ATTTTTTTCTGGTTTCTGAA	275554	107750	AGGGCTGCTGAGGCTGGGCC
186381	18577	CCAATTAAACCTCTTTCTTT	230968	63164	CATTTTTTTCTGGTTTCTGA	275555	107751	AAGGGCTGCTGAGGCTGGGC
186382	18578	TCCAATTAAACCTCTTTCTT	230969	63165	CCATTTTTTTCTGGTTTCTG	275556	107752	GAAGGGCTGCTGAGGCTGGG
186383	18579	GTCCAATTAAACCTCTTTCT	230970	63166	TCCATTTTTTTCTGGTTTCT	275557	107753	AGAAGGGCTGCTGAGGCTGG
186384	18580	AGTCCAATTAAACCTCTTTC	230971	63167	TTCCATTTTTTTCTGGTTTC	275558	107754	AAGAAGGGCTGCTGAGGCTG
186385	18581	AAGTCCAATTAAACCTCTTT	230972	63168	TTTCCATTTTTTTCTGGTTT	275559	107755	CAAGAAGGGCTGCTGAGGCT
186386	18582	TAAGTCCAATTAAACCTCTT	230973	63169	TTTTCCATTTTTTTCTGGTT	275560	107756	CCAAGAAGGGCTGCTGAGGC
186387	18583	GTAAGTCCAATTAAACCTCT	230974	63170	TTTTTCCATTTTTTTCTGGT	275561	107757	CCCAAGAAGGGCTGCTGAGG
186388	18584	TGTAAGTCCAATTAAACCTC	230975	63171	GTTTTTCCATTTTTTTCTGG	275562	107758	CCCCAAGAAGGGCTGCTGAG
186389	18585	CTGTAAGTCCAATTAAACCT	230976	63172	TGTTTTTCCATTTTTTTCTG	275563	107759	CCCCCAAGAAGGGCTGCTGA
186390	18586	ACTGTAAGTCCAATTAAACC	230977	63173	ATGTTTTTCCATTTTTTTCT	275564	107760	CCCCCCAAGAAGGGCTGCTG
186391	18587	AACTGTAAGTCCAATTAAAC	230978	63174	TATGTTTTTCCATTTTTTTC	275565	107761	ACCCCCCAAGAAGGGCTGCT
186392	18588	GAACTGTAAGTCCAATTAAA	230979	63175	GTATGTTTTTCCATTTTTTT	275566	107762	GACCCCCCAAGAAGGGCTGC
186393	18589	GGAACTGTAAGTCCAATTAA	230980	63176	AGTATGTTTTTCCATTTTTT	275567	107763	CGACCCCCCAAGAAGGGCTG
186394	18590	TGGAACTGTAAGTCCAATTA	230981	63177	CAGTATGTTTTTCCATTTTT	275568	107764	GCGACCCCCCAAGAAGGGCT
186395	18591	TTGGAACTGTAAGTCCAATT	230982	63178	ACAGTATGTTTTTCCATTTT	275569	107765	AGCGACCCCCCAAGAAGGGC
186396	18592	CTTGGAACTGTAAGTCCAAT	230983	63179	CACAGTATGTTTTTCCATTT	275570	107766	CAGCGACCCCCCAAGAAGGG
186397	18593	ACTTGGAACTGTAAGTCCAA	230984	63180	GCACAGTATGTTTTTCCATT	275571	107767	CCAGCGACCCCCCAAGAAGG
186398	18594	CACTTGGAACTGTAAGTCCA	230985	63181	AGCACAGTATGTTTTTCCAT	275572	107768	CCCAGCGACCCCCCAAGAAG
186399	18595	CCACTTGGAACTGTAAGTCC	230986	63182	GAGCACAGTATGTTTTTCCA	275573	107769	TCCCAGCGACCCCCCAAGAA
186400	18596	GCCACTTGGAACTGTAAGTC	230987	63183	AGAGCACAGTATGTTTTTCC	275574	107770	TTCCCAGCGACCCCCCAAGA
186401	18597	AGCCACTTGGAACTGTAAGT	230988	63184	AAGAGCACAGTATGTTTTTC	275575	107771	TTTCCCAGCGACCCCCCAAG
186402	18598	CAGCCACTTGGAACTGTAAG	230989	63185	CAAGAGCACAGTATGTTTTT	275576	107772	GTTTCCCAGCGACCCCCCAA
186403	18599	CCAGCCACTTGGAACTGTAA	230990	63186	CCAAGAGCACAGTATGTTTT	275577	107773	TGTTTCCCAGCGACCCCCCA
186404	18600	CCCAGCCACTTGGAACTGTA	230991	63187	CCCAAGAGCACAGTATGTTT	275578	107774	ATGTTTCCCAGCGACCCCCC
186405	18601	CCCCAGCCACTTGGAACTGT	230992	63188	ACCCAAGAGCACAGTATGTT	275579	107775	TATGTTTCCCAGCGACCCCC
186406	18602	TCCCCAGCCACTTGGAACTG	230993	63189	CACCCAAGAGCACAGTATGT	275580	107776	CTATGTTTCCCAGCGACCCC
186407	18603	TTCCCCAGCCACTTGGAACT	230994	63190	CCACCCAAGAGCACAGTATG	275581	107777	TCTATGTTTCCCAGCGACCC
186408	18604	CTTCCCCAGCCACTTGGAAC	230995	63191	CCCACCCAAGAGCACAGTAT	275582	107778	CTCTATGTTTCCCAGCGACC
186409	18605	GCTTCCCCAGCCACTTGGAA	230996	63192	TCCCACCCAAGAGCACAGTA	275583	107779	CCTCTATGTTTCCCAGCGAC
186410	18606	GGCTTCCCCAGCCACTTGGA	230997	63193	TTCCCACCCAAGAGCACAGT	275584	107780	TCCTCTATGTTTCCCAGCGA
186411	18607	AGGCTTCCCCAGCCACTTGG	230998	63194	TTTCCCACCCAAGAGCACAG	275585	107781	CTCCTCTATGTTTCCCAGCG
186412	18608	GAGGCTTCCCCAGCCACTTG	230999	63195	TTTTCCCACCCAAGAGCACA	275586	107782	TCTCCTCTATGTTTCCCAGC
186413	18609	TGAGGCTTCCCCAGCCACTT	231000	63196	GTTTTCCCACCCAAGAGCAC	275587	107783	TTCTCCTCTATGTTTCCCAG
186414	18610	GTGAGGCTTCCCCAGCCACT	231001	63197	AGTTTTCCCACCCAAGAGCA	275588	107784	GTTCTCCTCTATGTTTCCCA
186415	18611	TGTGAGGCTTCCCCAGCCAC	231002	63198	TAGTTTTCCCACCCAAGAGC	275589	107785	AGTTCTCCTCTATGTTTCCC
186416	18612	TTGTGAGGCTTCCCCAGCCA	231003	63199	TTAGTTTTCCCACCCAAGAG	275590	107786	CAGTTCTCCTCTATGTTTCC
186417	18613	ATTGTGAGGCTTCCCCAGCC	231004	63200	TTTAGTTTTCCCACCCAAGA	275591	107787	TCAGTTCTCCTCTATGTTTC
186418	18614	GATTGTGAGGCTTCCCCAGC	231005	63201	ATTTAGTTTTCCCACCCAAG	275592	107788	TTCAGTTCTCCTCTATGTTT
186419	18615	TGATTGTGAGGCTTCCCCAG	231006	63202	TATTTAGTTTTCCCACCCAA	275593	107789	CTTCAGTTCTCCTCTATGTT
186420	18616	ATGATTGTGAGGCTTCCCCA	231007	63203	ATATTTAGTTTTCCCACCCA	275594	107790	TCTTCAGTTCTCCTCTATGT
186421	18617	CATGATTGTGAGGCTTCCCC	231008	63204	GATATTTAGTTTTCCCACCC	275595	107791	TTCTTCAGTTCTCCTCTATG
186422	18618	CCATGATTGTGAGGCTTCCC	231009	63205	TGATATTTAGTTTTCCCACC	275596	107792	CTTCTTCAGTTCTCCTCTAT
186423	18619	GCCATGATTGTGAGGCTTCC	231010	63206	ATGATATTTAGTTTTCCCAC	275597	107793	GCTTCTTCAGTTCTCCTCTA
186424	18620	TGCCATGATTGTGAGGCTTC	231011	63207	CATGATATTTAGTTTTCCCA	275598	107794	TGCTTCTTCAGTTCTCCTCT
186425	18621	CTGCCATGATTGTGAGGCTT	231012	63208	TCATGATATTTAGTTTTCCC	275599	107795	CTGCTTCTTCAGTTCTCCTC
186426	18622	TCTGCCATGATTGTGAGGCT	231013	63209	TTCATGATATTTAGTTTTCC	275600	107796	CCTGCTTCTTCAGTTCTCCT
186427	18623	TTCTGCCATGATTGTGAGGC	231014	63210	CTTCATGATATTTAGTTTTC	275601	107797	CCCTGCTTCTTCAGTTCTCC
186428	18624	CTTCTGCCATGATTGTGAGG	231015	63211	CCTTCATGATATTTAGTTTT	275602	107798	TCCCTGCTTCTTCAGTTCTC
186429	18625	CCTTCTGCCATGATTGTGAG	231016	63212	CCCTTCATGATATTTAGTTT	275603	107799	CTCCCTGCTTCTTCAGTTCT
186430	18626	GCCTTCTGCCATGATTGTGA	231017	63213	TCCCTTCATGATATTTAGTT	275604	107800	ACTCCCTGCTTCTTCAGTTC
186431	18627	TGCCTTCTGCCATGATTGTG	231018	63214	CTCCCTTCATGATATTTAGT	275605	107801	GACTCCCTGCTTCTTCAGTT
186432	18628	TTGCCTTCTGCCATGATTGT	231019	63215	GCTCCCTTCATGATATTTAG	275606	107802	GGACTCCCTGCTTCTTCAGT
186433	18629	CTTGCCTTCTGCCATGATTG	231020	63216	TGCTCCCTTCATGATATTTA	275607	107803	GGGACTCCCTGCTTCTTCAG
186434	18630	CCTTGCCTTCTGCCATGATT	231021	63217	TTGCTCCCTTCATGATATTT	275608	107804	TGGGACTCCCTGCTTCTTCA
186435	18631	TCCTTGCCTTCTGCCATGAT	231022	63218	ATTGCTCCCTTCATGATATT	275609	107805	CTGGGACTCCCTGCTTCTTC
186436	18632	CTCCTTGCCTTCTGCCATGA	231023	63219	AATTGCTCCCTTCATGATAT	275610	107806	CCTGGGACTCCCTGCTTCTT
186437	18633	CCTCCTTGCCTTCTGCCATG	231024	63220	AAATTGCTCCCTTCATGATA	275611	107807	CCCTGGGACTCCCTGCTTCT
186438	18634	TCCTCCTTGCCTTCTGCCAT	231025	63221	AAAATTGCTCCCTTCATGAT	275612	107808	ACCCTGGGACTCCCTGCTTC
186439	18635	CTCCTCCTTGCCTTCTGCCA	231026	63222	AAAAATTGCTCCCTTCATGA	275613	107809	GACCCTGGGACTCCCTGCTT
186440	18636	GCTCCTCCTTGCCTTCTGCC	231027	63223	TAAAAATTGCTCCCTTCATG	275614	107810	GGACCCTGGGACTCCCTGCT
186441	18637	TGCTCCTCCTTGCCTTCTGC	231028	63224	ATAAAAATTGCTCCCTTCAT	275615	107811	TGGACCCTGGGACTCCCTGC
186442	18638	TTGCTCCTCCTTGCCTTCTG	231029	63225	TATAAAAATTGCTCCCTTCA	275616	107812	ATGGACCCTGGGACTCCCTG
186443	18639	CTTGCTCCTCCTTGCCTTCT	231030	63226	CTATAAAAATTGCTCCCTTC	275617	107813	CATGGACCCTGGGACTCCCT
186444	18640	GCTTGCTCCTCCTTGCCTTC	231031	63227	ACTATAAAAATTGCTCCCTT	275618	107814	GCATGGACCCTGGGACTCCC
186445	18641	GGCTTGCTCCTCCTTGCCTT	231032	63228	AACTATAAAAATTGCTCCCT	275619	107815	TGCATGGACCCTGGGACTCC
186446	18642	TGGCTTGCTCCTCCTTGCCT	231033	63229	AAACTATAAAAATTGCTCCC	275620	107816	CTGCATGGACCCTGGGACTC
186447	18643	GTGGCTTGCTCCTCCTTGCC	231034	63230	AAAACTATAAAAATTGCTCC	275621	107817	CCTGCATGGACCCTGGGACT
186448	18644	TGTGGCTTGCTCCTCCTTGC	231035	63231	CAAAACTATAAAAATTGCTC	275622	107818	CCCTGCATGGACCCTGGGAC
186449	18645	ATGTGGCTTGCTCCTCCTTG	231036	63232	CCAAAACTATAAAAATTGCT	275623	107819	GCCCTGCATGGACCCTGGGA
186450	18646	GATGTGGCTTGCTCCTCCTT	231037	63233	GCCAAAACTATAAAAATTGC	275624	107820	CGCCCTGCATGGACCCTGGG

186451	18647	AGATGTGGCTTGCTCCTCCT	231038	63234	GGCCAAAACTATAAAAATTG	275625	107821	TCGCCCTGCATGGACCCTGG
186452	18648	AAGATGTGGCTTGCTCCTCC	231039	63235	AGGCCAAAACTATAAAAATT	275626	107822	CTCGCCCTGCATGGACCCTG
186453	18649	TAAGATGTGGCTTGCTCCTC	231040	63236	TAGGCCAAAACTATAAAAAT	275627	107823	TCTCGCCCTGCATGGACCCT
186454	18650	GTAAGATGTGGCTTGCTCCT	231041	63237	ATAGGCCAAAACTATAAAAA	275628	107824	CTCTCGCCCTGCATGGACCC
186455	18651	TGTAAGATGTGGCTTGCTCC	231042	63238	TATAGGCCAAAACTATAAAA	275629	107825	TCTCTCGCCCTGCATGGACC
186456	18652	ATGTAAGATGTGGCTTGCTC	231043	63239	TTATAGGCCAAAACTATAAA	275630	107826	CTCTCTCGCCCTGCATGGAC
186457	18653	CATGTAAGATGTGGCTTGCT	231044	63240	ATTATAGGCCAAAACTATAA	275631	107827	TCTCTCTCGCCCTGCATGGA
186458	18654	CCATGTAAGATGTGGCTTGC	231045	63241	TATTATAGGCCAAAACTATA	275632	107828	TTCTCTCTCGCCCTGCATGG
186459	18655	TCCATGTAAGATGTGGCTTG	231046	63242	GTATTATAGGCCAAAACTAT	275633	107829	CTTCTCTCTCGCCCTGCATG
186460	18656	ATCCATGTAAGATGTGGCTT	231047	63243	TGTATTATAGGCCAAAACTA	275634	107830	ACTTCTCTCTCGCCCTGCAT
186461	18657	CATCCATGTAAGATGTGGCT	231048	63244	TTGTATTATAGGCCAAAACT	275635	107831	AACTTCTCTCTCGCCCTGCA
186462	18658	CCATCCATGTAAGATGTGGC	231049	63245	ATTGTATTATAGGCCAAAAC	275636	107832	CAACTTCTCTCTCGCCCTGC
186463	18659	GCCATCCATGTAAGATGTGG	231050	63246	AATTGTATTATAGGCCAAAA	275637	107833	GCAACTTCTCTCTCGCCCTG
186464	18660	TGCCATCCATGTAAGATGTG	231051	63247	GAATTGTATTATAGGCCAAA	275638	107834	AGCAACTTCTCTCTCGCCCT
186465	18661	CTGCCATCCATGTAAGATGT	231052	63248	GGAATTGTATTATAGGCCAA	275639	107835	GAGCAACTTCTCTCTCGCCC
186466	18662	GCTGCCATCCATGTAAGATG	231053	63249	TGGAATTGTATTATAGGCCA	275640	107836	TGAGCAACTTCTCTCTCGCC
186467	18663	TGCTGCCATCCATGTAAGAT	231054	63250	CTGGAATTGTATTATAGGCC	275641	107837	ATGAGCAACTTCTCTCTCGC
186468	18664	CTGCTGCCATCCATGTAAGA	231055	63251	GCTGGAATTGTATTATAGGC	275642	107838	CATGAGCAACTTCTCTCTCG
186469	18665	TCTGCTGCCATCCATGTAAG	231056	63252	GGCTGGAATTGTATTATAGG	275643	107839	ACATGAGCAACTTCTCTCTC
186470	18666	GTCTGCTGCCATCCATGTAA	231057	63253	CGGCTGGAATTGTATTATAG	275644	107840	CACATGAGCAACTTCTCTCT
186471	18667	TGTCTGCTGCCATCCATGTA	231058	63254	TCGGCTGGAATTGTATTATA	275645	107841	CCACATGAGCAACTTCTCTC
186472	18668	CTGTCTGCTGCCATCCATGT	231059	63255	TTCGGCTGGAATTGTATTAT	275646	107842	CCCACATGAGCAACTTCTCT
186473	18669	TCTGTCTGCTGCCATCCATG	231060	63256	TTTCGGCTGGAATTGTATTA	275647	107843	CCCCACATGAGCAACTTCTC
186474	18670	GTCTGTCTGCTGCCATCCAT	231061	63257	ATTTCGGCTGGAATTGTATT	275648	107844	GCCCCACATGAGCAACTTCT
186475	18671	TGTCTGTCTGCTGCCATCCA	231062	63258	GATTTCGGCTGGAATTGTAT	275649	107845	GGCCCCACATGAGCAACTTC
186476	18672	CTGTCTGTCTGCTGCCATCC	231063	63259	GGATTTCGGCTGGAATTGTA	275650	107846	GGGCCCCACATGAGCAACTT
186477	18673	CCTGTCTGTCTGCTGCCATC	231064	63260	GGGATTTCGGCTGGAATTGT	275651	107847	TGGGCCCCACATGAGCAACT
186478	18674	CCCTGTCTGTCTGCTGCCAT	231065	63261	TGGGATTTCGGCTGGAATTG	275652	107848	CTGGGCCCCACATGAGCAAC
186479	18675	TCCCTGTCTGTCTGCTGCCA	231066	63262	CTGGGATTTCGGCTGGAATT	275653	107849	CCTGGGCCCCACATGAGCAA
186480	18676	CTCCCTGTCTGTCTGCTGCC	231067	63263	ACTGGGATTTCGGCTGGAAT	275654	107850	GCCTGGGCCCCACATGAGCA
186481	18677	TCTCCCTGTCTGTCTGCTGC	231068	63264	CACTGGGATTTCGGCTGGAA	275655	107851	AGCCTGGGCCCCACATGAGC
186482	18678	CTCTCCCTGTCTGTCTGCTG	231069	63265	CCACTGGGATTTCGGCTGGA	275656	107852	CAGCCTGGGCCCCACATGAG
186483	18679	TCTCTCCCTGTCTGTCTGCT	231070	63266	TCCACTGGGATTTCGGCTGG	275657	107853	GCAGCCTGGGCCCCACATGA
186484	18680	CTCTCTCCCTGTCTGTCTGC	231071	63267	TTCCACTGGGATTTCGGCTG	275658	107854	TGCAGCCTGGGCCCCACATG
186485	18681	TCTCTCTCCCTGTCTGTCTG	231072	63268	GTTCCACTGGGATTTCGGCT	275659	107855	CTGCAGCCTGGGCCCCACAT
186486	18682	CTCTCTCTCCCTGTCTGTCT	231073	63269	AGTTCCACTGGGATTTCGGC	275660	107856	CCTGCAGCCTGGGCCCCACA
186487	18683	GCTCTCTCTCCCTGTCTGTC	231074	63270	AAGTTCCACTGGGATTTCGG	275661	107857	TCCTGCAGCCTGGGCCCCAC
186488	18684	AGCTCTCTCTCCCTGTCTGT	231075	63271	AAAGTTCCACTGGGATTTCG	275662	107858	ATCCTGCAGCCTGGGCCCCA
186489	18685	AAGCTCTCTCTCCCTGTCTG	231076	63272	CAAAGTTCCACTGGGATTTC	275663	107859	GATCCTGCAGCCTGGGCCCC
186490	18686	CAAGCTCTCTCTCCCTGTCT	231077	63273	TCAAAGTTCCACTGGGATTT	275664	107860	TGATCCTGCAGCCTGGGCCC
186491	18687	ACAAGCTCTCTCTCCCTGTC	231078	63274	CTCAAAGTTCCACTGGGATT	275665	107861	CTGATCCTGCAGCCTGGGCC
186492	18688	CACAAGCTCTCTCTCCCTGT	231079	63275	TCTCAAAGTTCCACTGGGAT	275666	107862	CCTGATCCTGCAGCCTGGGC
186493	18689	GCACAAGCTCTCTCTCCCTG	231080	63276	TTCTCAAAGTTCCACTGGGA	275667	107863	TCCTGATCCTGCAGCCTGGG
186494	18690	TGCACAAGCTCTCTCTCCCT	231081	63277	ATTCTCAAAGTTCCACTGGG	275668	107864	CTCCTGATCCTGCAGCCTGG
186495	18691	CTGCACAAGCTCTCTCTCCC	231082	63278	AATTCTCAAAGTTCCACTGG	275669	107865	TCTCCTGATCCTGCAGCCTG
186496	18692	CCTGCACAAGCTCTCTCTCC	231083	63279	AAATTCTCAAAGTTCCACTG	275670	107866	TTCTCCTGATCCTGCAGCCT
186497	18693	CCCTGCACAAGCTCTCTCTC	231084	63280	CAAATTCTCAAAGTTCCACT	275671	107867	GTTCTCCTGATCCTGCAGCC
186498	18694	CCCCTGCACAAGCTCTCTCT	231085	63281	GCAAATTCTCAAAGTTCCAC	275672	107868	AGTTCTCCTGATCCTGCAGC
186499	18695	TCCCCTGCACAAGCTCTCTC	231086	63282	TGCAAATTCTCAAAGTTCCA	275673	107869	CAGTTCTCCTGATCCTGCAG
186500	18696	TTCCCCTGCACAAGCTCTCT	231087	63283	CTGCAAATTCTCAAAGTTCC	275674	107870	CCAGTTCTCCTGATCCTGCA
186501	18697	GTTCCCCTGCACAAGCTCTC	231088	63284	CCTGCAAATTCTCAAAGTTC	275675	107871	CCCAGTTCTCCTGATCCTGC
186502	18698	AGTTCCCCTGCACAAGCTCT	231089	63285	TCCTGCAAATTCTCAAAGTT	275676	107872	CCCCAGTTCTCCTGATCCTG
186503	18699	GAGTTCCCCTGCACAAGCTC	231090	63286	TTCCTGCAAATTCTCAAAGT	275677	107873	TCCCCAGTTCTCCTGATCCT
186504	18700	GGAGTTCCCCTGCACAAGCT	231091	63287	TTTCCTGCAAATTCTCAAAG	275678	107874	GTCCCCAGTTCTCCTGATCC
186505	18701	AGGAGTTCCCCTGCACAAGC	231092	63288	TTTTCCTGCAAATTCTCAAA	275679	107875	GGTCCCCAGTTCTCCTGATC
186506	18702	GAGGAGTTCCCCTGCACAAG	231093	63289	TTTTTCCTGCAAATTCTCAA	275680	107876	GGGTCCCCAGTTCTCCTGAT
186507	18703	AGAGGAGTTCCCCTGCACAA	231094	63290	TTTTTTCCTGCAAATTCTCA	275681	107877	AGGGTCCCCAGTTCTCCTGA
186508	18704	AAGAGGAGTTCCCCTGCACA	231095	63291	TTTTTTTCCTGCAAATTCTC	275682	107878	CAGGGTCCCCAGTTCTCCTG
186509	18705	AAAGAGGAGTTCCCCTGCAC	231096	63292	TTTTTTTTCCTGCAAATTCT	275683	107879	ACAGGGTCCCCAGTTCTCCT
186510	18706	AAAAGAGGAGTTCCCCTGCA	231097	63293	TTTTTTTTTCCTGCAAATTC	275684	107880	CACAGGGTCCCCAGTTCTCC
186511	18707	AAAAAGAGGAGTTCCCCTGC	231098	63294	TTTTTTTTTTCCTGCAAATT	275685	107881	TCACAGGGTCCCCAGTTCTC
186512	18708	TAAAAAGAGGAGTTCCCCTG	231099	63295	TTTTTTTTTTTCCTGCAAAT	275686	107882	GTCACAGGGTCCCCAGTTCT
186513	18709	TTAAAAAGAGGAGTTCCCCT	231100	63296	ATTTTTTTTTTTCCTGCAAA	275687	107883	AGTCACAGGGTCCCCAGTTC
186514	18710	TTTAAAAAGAGGAGTTCCCC	231101	63297	CATTTTTTTTTTTCCTGCAA	275688	107884	CAGTCACAGGGTCCCCAGTT
186515	18711	TTTTAAAAAGAGGAGTTCCC	231102	63298	ACATTTTTTTTTTTCCTGCA	275689	107885	GCAGTCACAGGGTCCCCAGT
186516	18712	GTTTTAAAAAGAGGAGTTCC	231103	63299	GACATTTTTTTTTTTCCTGC	275690	107886	GGCAGTCACAGGGTCCCCAG
186517	18713	GGTTTTAAAAAGAGGAGTTC	231104	63300	AGACATTTTTTTTTTTCCTG	275691	107887	TGGCAGTCACAGGGTCCCCA
186518	18714	TGGTTTTAAAAAGAGGAGTT	231105	63301	TAGACATTTTTTTTTTTCCT	275692	107888	CTGGCAGTCACAGGGTCCCC
186519	18715	ATGGTTTTAAAAAGAGGAGT	231106	63302	TTAGACATTTTTTTTTTTCC	275693	107889	GCTGGCAGTCACAGGGTCCC
186520	18716	GATGGTTTTAAAAAGAGGAG	231107	63303	TTTAGACATTTTTTTTTTTC	275694	107890	CGCTGGCAGTCACAGGGTCC
186521	18717	TGATGGTTTTAAAAAGAGGA	231108	63304	CTTTAGACATTTTTTTTTTT	275695	107891	CCGCTGGCAGTCACAGGGTC
186522	18718	CTGATGGTTTTAAAAAGAGG	231109	63305	ACTTTAGACATTTTTTTTTT	275696	107892	CCCGCTGGCAGTCACAGGGT

186523	18719	TCTGATGGTTTTAAAAAGAG	231110	63306	TACTTTAGACATTTTTTTT	275697	107893	CCCCGCTGGCAGTCACAGGG
186524	18720	ATCTGATGGTTTTAAAAAGA	231111	63307	GTACTTTAGACATTTTTTT	275698	107894	TCCCCGCTGGCAGTCACAGG
186525	18721	GATCTGATGGTTTTAAAAAG	231112	63308	TGTACTTTAGACATTTTTT	275699	107895	CTCCCCGCTGGCAGTCACAG
186526	18722	AGATCTGATGGTTTTAAAAA	231113	63309	ATGTACTTTAGACATTTTTT	275700	107896	TCTCCCCGCTGGCAGTCACA
186527	18723	GAGATCTGATGGTTTTAAAA	231114	63310	GATGTACTTTAGACATTTTT	275701	107897	TTCTCCCCGCTGGCAGTCAC
186528	18724	CGAGATCTGATGGTTTTAAA	231115	63311	AGATGTACTTTAGACATTTT	275702	107898	CTTCTCCCCGCTGGCAGTCA
186529	18725	ACGAGATCTGATGGTTTTAA	231116	63312	CAGATGTACTTTAGACATTT	275703	107899	CCTTCTCCCCGCTGGCAGTC
186530	18726	AACGAGATCTGATGGTTTTA	231117	63313	CCAGATGTACTTTAGACATT	275704	107900	CCCTTCTCCCCGCTGGCAGT
186531	18727	TAACGAGATCTGATGGTTTT	231118	63314	TCCAGATGTACTTTAGACAT	275705	107901	CCCCTTCTCCCCGCTGGCAG
186532	18728	CTAACGAGATCTGATGGTTT	231119	63315	TTCCAGATGTACTTTAGACA	275706	107902	CCCCCTTCTCCCCGCTGGCA
186533	18729	TCTAACGAGATCTGATGGTT	231120	63316	CTTCCAGATGTACTTTAGAC	275707	107903	ACCCCCTTCTCCCCGCTGGC
186534	18730	GTCTAACGAGATCTGATGGT	231121	63317	TCTTCCAGATGTACTTTAGA	275708	107904	CACCCCCTTCTCCCCGCTGG
186535	18731	AGTCTAACGAGATCTGATGG	231122	63318	GTCTTCCAGATGTACTTTAG	275709	107905	ACACCCCCTTCTCCCCGCTG
186536	18732	AAGTCTAACGAGATCTGATG	231123	63319	TGTCTTCCAGATGTACTTTA	275710	107906	CACACCCCCTTCTCCCCGCT
186537	18733	TAAGTCTAACGAGATCTGAT	231124	63320	TTGTCTTCCAGATGTACTTT	275711	107907	GCACACCCCCTTCTCCCCGC
186538	18734	ATAAGTCTAACGAGATCTGA	231125	63321	TTTGTCTTCCAGATGTACTT	275712	107908	TGCACACCCCCTTCTCCCCG
186539	18735	AATAAGTCTAACGAGATCTG	231126	63322	GTTTGTCTTCCAGATGTACT	275713	107909	CTGCACACCCCCTTCTCCCC
186540	18736	GAATAAGTCTAACGAGATCT	231127	63323	AGTTTGTCTTCCAGATGTAC	275714	107910	CCTGCACACCCCCTTCTCCC
186541	18737	TGAATAAGTCTAACGAGATC	231128	63324	AAGTTTGTCTTCCAGATGTA	275715	107911	TCCTGCACACCCCCTTCTCC
186542	18738	GTGAATAAGTCTAACGAGAT	231129	63325	TAAGTTTGTCTTCCAGATGT	275716	107912	ATCCTGCACACCCCCTTCTC
186543	18739	AGTGAATAAGTCTAACGAGA	231130	63326	GTAAGTTTGTCTTCCAGATG	275717	107913	GATCCTGCACACCCCCTTCT
186544	18740	TAGTGAATAAGTCTAACGAG	231131	63327	TGTAAGTTTGTCTTCCAGAT	275718	107914	TGATCCTGCACACCCCCTTC
186545	18741	ATAGTGAATAAGTCTAACGA	231132	63328	TTGTAAGTTTGTCTTCCAGA	275719	107915	ATGATCCTGCACACCCCCTT
186546	18742	GATAGTGAATAAGTCTAACG	231133	63329	CTTGTAAGTTTGTCTTCCAG	275720	107916	CATGATCCTGCACACCCCCT
186547	18743	TGATAGTGAATAAGTCTAAC	231134	63330	TCTTGTAAGTTTGTCTTCCA	275721	107917	GCATGATCCTGCACACCCCC
186548	18744	TTGATAGTGAATAAGTCTAA	231135	63331	TTCTTGTAAGTTTGTCTTCC	275722	107918	GGCATGATCCTGCACACCCC
186549	18745	CTTGATAGTGAATAAGTCTA	231136	63332	CTTCTTGTAAGTTTGTCTTC	275723	107919	GGGCATGATCCTGCACACCC
186550	18746	TCTTGATAGTGAATAAGTCT	231137	63333	CCTTCTTGTAAGTTTGTCTT	275724	107920	TGGGCATGATCCTGCACACC
186551	18747	CTCTTGATAGTGAATAAGTC	231138	63334	ACCTTCTTGTAAGTTTGTCT	275725	107921	CTGGGCATGATCCTGCACAC
186552	18748	TCTCTTGATAGTGAATAAGT	231139	63335	GACCTTCTTGTAAGTTTGTC	275726	107922	CCTGGGCATGATCCTGCACA
186553	18749	TTCTCTTGATAGTGAATAAG	231140	63336	TGACCTTCTTGTAAGTTTGT	275727	107923	CCCTGGGCATGATCCTGCAC
186554	18750	GTTCTCTTGATAGTGAATAA	231141	63337	TTGACCTTCTTGTAAGTTTG	275728	107924	TCCCTGGGCATGATCCTGCA
186555	18751	TGTTCTCTTGATAGTGAATA	231142	63338	TTTGACCTTCTTGTAAGTTT	275729	107925	TTCCCTGGGCATGATCCTGC
186556	18752	CTGTTCTCTTGATAGTGAAT	231143	63339	ATTTGACCTTCTTGTAAGTT	275730	107926	CTTCCCTGGGCATGATCCTG
186557	18753	GCTGTTCTCTTGATAGTGAA	231144	63340	TATTTGACCTTCTTGTAAGT	275731	107927	CCTTCCCTGGGCATGATCCT
186558	18754	TGCTGTTCTCTTGATAGTGA	231145	63341	TTATTTGACCTTCTTGTAAG	275732	107928	CCCTTCCCTGGGCATGATCC
186559	18755	GTGCTGTTCTCTTGATAGTG	231146	63342	ATTATTTGACCTTCTTGTAA	275733	107929	GCCCTTCCCTGGGCATGATC
186560	18756	TGTGCTGTTCTCTTGATAGT	231147	63343	AATTATTTGACCTTCTTGTA	275734	107930	GGCCCTTCCCTGGGCATGAT
186561	18757	CTGTGCTGTTCTCTTGATAG	231148	63344	AAATTATTTGACCTTCTTGT	275735	107931	GGGCCCTTCCCTGGGCATGA
186562	18758	TCTGTGCTGTTCTCTTGATA	231149	63345	AAAATTATTTGACCTTCTTG	275736	107932	TGGGCCCTTCCCTGGGCATG
186563	18759	TTCTGTGCTGTTCTCTTGAT	231150	63346	CAAAATTATTTGACCTTCTT	275737	107933	CTGGGCCCTTCCCTGGGCAT
186564	18760	TTTCTGTGCTGTTCTCTTGA	231151	63347	TCAAAATTATTTGACCTTCT	275738	107934	CCTGGGCCCTTCCCTGGGCA
186565	18761	TTTTCTGTGCTGTTCTCTTG	231152	63348	TTCAAAATTATTTGACCTTC	275739	107935	CCCTGGGCCCTTCCCTGGGC
186566	18762	CTTTTCTGTGCTGTTCTCTT	231153	63349	TTTCAAAATTATTTGACCTT	275740	107936	CCCCTGGGCCCTTCCCTGGG
186567	18763	TCTTTTCTGTGCTGTTCTCT	231154	63350	TTTTCAAAATTATTTGACCT	275741	107937	GCCCCTGGGCCCTTCCCTGG
186568	18764	GTCTTTTCTGTGCTGTTCTC	231155	63351	TTTTTCAAAATTATTTGACC	275742	107938	GGCCCCTGGGCCCTTCCCTG
186569	18765	GGTCTTTTCTGTGCTGTTCT	231156	63352	CTTTTTCAAAATTATTTGAC	275743	107939	GGGCCCCTGGGCCCTTCCCT
186570	18766	AGGTCTTTTCTGTGCTGTTC	231157	63353	TCTTTTTCAAAATTATTTGA	275744	107940	TGGGCCCCTGGGCCCTTCCC
186571	18767	CAGGTCTTTTCTGTGCTGTT	231158	63354	TTCTTTTTCAAAATTATTTG	275745	107941	TTGGGCCCCTGGGCCCTTCC
186572	18768	GCAGGTCTTTTCTGTGCTGT	231159	63355	TTTCTTTTTCAAAATTATTT	275746	107942	CTTGGGCCCCTGGGCCCTTC
186573	18769	GGCAGGTCTTTTCTGTGCTG	231160	63356	TTTTCTTTTTCAAAATTATT	275747	107943	GCTTGGGCCCCTGGGCCCTT
186574	18770	GGGCAGGTCTTTTCTGTGCT	231161	63357	ATTTTCTTTTTCAAAATTAT	275748	107944	TGCTTGGGCCCCTGGGCCCT
186575	18771	GGGGCAGGTCTTTTCTGTGC	231162	63358	CATTTTCTTTTTCAAAATTA	275749	107945	ATGCTTGGGCCCCTGGGCCC
186576	18772	GGGGGCAGGTCTTTTCTGTG	231163	63359	TCATTTTCTTTTTCAAAATT	275750	107946	CATGCTTGGGCCCCTGGGCC
186577	18773	TGGGGGCAGGTCTTTTCTGT	231164	63360	ATCATTTTCTTTTTCAAAAT	275751	107947	CCATGCTTGGGCCCCTGGGC
186578	18774	ATGGGGGCAGGTCTTTTCTG	231165	63361	TATCATTTTCTTTTTCAAAA	275752	107948	CCCATGCTTGGGCCCCTGGG
186579	18775	CATGGGGGCAGGTCTTTTCT	231166	63362	ATATCATTTTCTTTTTCAAA	275753	107949	CCCCATGCTTGGGCCCCTGG
186580	18776	TCATGGGGGCAGGTCTTTTC	231167	63363	GATATCATTTTCTTTTTCAA	275754	107950	CCCCCATGCTTGGGCCCCTG
186581	18777	ATCATGGGGGCAGGTCTTTT	231168	63364	AGATATCATTTTCTTTTTCA	275755	107951	CCCCCCATGCTTGGGCCCCT
186582	18778	AATCATGGGGGCAGGTCTTT	231169	63365	TAGATATCATTTTCTTTTTC	275756	107952	CCCCCCCATGCTTGGGCCCC
186583	18779	GAATCATGGGGGCAGGTCTT	231170	63366	TTAGATATCATTTTCTTTTT	275757	107953	GCCCCCCCATGCTTGGGCCC
186584	18780	TGAATCATGGGGGCAGGTCT	231171	63367	CTTAGATATCATTTTCTTTT	275758	107954	GGCCCCCCCATGCTTGGGCC
186585	18781	CTGAATCATGGGGGCAGGTC	231172	63368	GCTTAGATATCATTTTCTTT	275759	107955	AGGCCCCCCCATGCTTGGGC
186586	18782	ACTGAATCATGGGGGCAGGT	231173	63369	GGCTTAGATATCATTTTCTT	275760	107956	CAGGCCCCCCCATGCTTGGG
186587	18783	AACTGAATCATGGGGGCAGG	231174	63370	GGGCTTAGATATCATTTTCT	275761	107957	CCAGGCCCCCCCATGCTTGG
186588	18784	TAACTGAATCATGGGGGCAG	231175	63371	TGGGCTTAGATATCATTTTC	275762	107958	ACCAGGCCCCCCCATGCTTG
186589	18785	GTAACTGAATCATGGGGGCA	231176	63372	GTGGGCTTAGATATCATTTT	275763	107959	AACCAGGCCCCCCCATGCTT
186590	18786	AGTAACTGAATCATGGGGGC	231177	63373	GGTGGGCTTAGATATCATTT	275764	107960	CAACCAGGCCCCCCCATGCT
186591	18787	AAGTAACTGAATCATGGGGG	231178	63374	AGGTGGGCTTAGATATCATT	275765	107961	CCAACCAGGCCCCCCCATGC
186592	18788	GAAGTAACTGAATCATGGGG	231179	63375	TAGGTGGGCTTAGATATCAT	275766	107962	GCCAACCAGGCCCCCCCATG
186593	18789	GGAAGTAACTGAATCATGGG	231180	63376	CTAGGTGGGCTTAGATATCA	275767	107963	AGCCAACCAGGCCCCCCCAT
186594	18790	GGGAAGTAACTGAATCATGG	231181	63377	TCTAGGTGGGCTTAGATATC	275768	107964	GAGCCAACCAGGCCCCCCCA

186595	18791	TGGGAAGTAACTGAATCATG	231182	63378	CTCTAGGTGGGCTTAGATAT	275769	107965	AGAGCCAACCAGGCCCCCCC
186596	18792	GTGGGAAGTAACTGAATCAT	231183	63379	TCTCTAGGTGGGCTTAGATA	275770	107966	CAGAGCCAACCAGGCCCCCC
186597	18793	GGTGGGAAGTAACTGAATCA	231184	63380	TTCTCTAGGTGGGCTTAGAT	275771	107967	TCAGAGCCAACCAGGCCCCC
186598	18794	TGGTGGGAAGTAACTGAATC	231185	63381	ATTCTCTAGGTGGGCTTAGA	275772	107968	CTCAGAGCCAACCAGGCCCC
186599	18795	CTGGTGGGAAGTAACTGAAT	231186	63382	TATTCTCTAGGTGGGCTTAG	275773	107969	TCTCAGAGCCAACCAGGCCC
186600	18796	TCTGGTGGGAAGTAACTGAA	231187	63383	TTATTCTCTAGGTGGGCTTA	275774	107970	TTCTCAGAGCCAACCAGGCC
186601	18797	ATCTGGTGGGAAGTAACTGA	231188	63384	CTTATTCTCTAGGTGGGCTT	275775	107971	CTTCTCAGAGCCAACCAGGC
186602	18798	GATCTGGTGGGAAGTAACTG	231189	63385	TCTTATTCTCTAGGTGGGCT	275776	107972	TCTTCTCAGAGCCAACCAGG
186603	18799	GGATCTGGTGGGAAGTAACT	231190	63386	GTCTTATTCTCTAGGTGGGC	275777	107973	ATCTTCTCAGAGCCAACCAG
186604	18800	GGGATCTGGTGGGAAGTAAC	231191	63387	AGTCTTATTCTCTAGGTGGG	275778	107974	CATCTTCTCAGAGCCAACCA
186605	18801	AGGGATCTGGTGGGAAGTAA	231192	63388	AAGTCTTATTCTCTAGGTGG	275779	107975	CCATCTTCTCAGAGCCAACC
186606	18802	GAGGGATCTGGTGGGAAGTA	231193	63389	CAAGTCTTATTCTCTAGGTG	275780	107976	TCCATCTTCTCAGAGCCAAC
186607	18803	GGAGGGATCTGGTGGGAAGT	231194	63390	TCAAGTCTTATTCTCTAGGT	275781	107977	CTCCATCTTCTCAGAGCCAA
186608	18804	GGGAGGGATCTGGTGGGAAG	231195	63391	CTCAAGTCTTATTCTCTAGG	275782	107978	GCTCCATCTTCTCAGAGCCA
186609	18805	TGGGAGGGATCTGGTGGGAA	231196	63392	TCTCAAGTCTTATTCTCTAG	275783	107979	AGCTCCATCTTCTCAGAGCC
186610	18806	GTGGGAGGGATCTGGTGGGA	231197	63393	ATCTCAAGTCTTATTCTCTA	275784	107980	TAGCTCCATCTTCTCAGAGC
186611	18807	TGTGGGAGGGATCTGGTGGG	231198	63394	GATCTCAAGTCTTATTCTCT	275785	107981	TTAGCTCCATCTTCTCAGAG
186612	18808	TTGTGGGAGGGATCTGGTGG	231199	63395	GGATCTCAAGTCTTATTCTC	275786	107982	TTTAGCTCCATCTTCTCAGA
186613	18809	GTTGTGGGAGGGATCTGGTG	231200	63396	TGGATCTCAAGTCTTATTCT	275787	107983	CTTTAGCTCCATCTTCTCAG
186614	18810	TGTTGTGGGAGGGATCTGGT	231201	63397	TTGGATCTCAAGTCTTATTC	275788	107984	ACTTTAGCTCCATCTTCTCA
186615	18811	ATGTTGTGGGAGGGATCTGG	231202	63398	TTTGGATCTCAAGTCTTATT	275789	107985	GACTTTAGCTCCATCTTCTC
186616	18812	CATGTTGTGGGAGGGATCTG	231203	63399	CTTTGGATCTCAAGTCTTAT	275790	107986	TGACTTTAGCTCCATCTTCT
186617	18813	ACATGTTGTGGGAGGGATCT	231204	63400	GCTTTGGATCTCAAGTCTTA	275791	107987	GTGACTTTAGCTCCATCTTC
186618	18814	CACATGTTGTGGGAGGGATC	231205	63401	AGCTTTGGATCTCAAGTCTT	275792	107988	AGTGACTTTAGCTCCATCTT
186619	18815	CCACATGTTGTGGGAGGGAT	231206	63402	TAGCTTTGGATCTCAAGTCT	275793	107989	AAGTGACTTTAGCTCCATCT
186620	18816	CCCACATGTTGTGGGAGGGA	231207	63403	TTAGCTTTGGATCTCAAGTC	275794	107990	AAAGTGACTTTAGCTCCATC
186621	18817	TCCCACATGTTGTGGGAGGG	231208	63404	TTTAGCTTTGGATCTCAAGT	275795	107991	GAAAGTGACTTTAGCTCCAT
186622	18818	TTCCCACATGTTGTGGGAGG	231209	63405	ATTTAGCTTTGGATCTCAAG	275796	107992	AGAAAGTGACTTTAGCTCCA
186623	18819	ATTCCCACATGTTGTGGGAG	231210	63406	GATTTAGCTTTGGATCTCAA	275797	107993	GAGAAAGTGACTTTAGCTCC
186624	18820	AATTCCCACATGTTGTGGGA	231211	63407	TGATTTAGCTTTGGATCTCA	275798	107994	CGAGAAAGTGACTTTAGCTC
186625	18821	GAATTCCCACATGTTGTGGG	231212	63408	CTGATTTAGCTTTGGATCTC	275799	107995	CCGAGAAAGTGACTTTAGCT
186626	18822	TGAATTCCCACATGTTGTGG	231213	63409	CCTGATTTAGCTTTGGATCT	275800	107996	TCCGAGAAAGTGACTTTAGC
186627	18823	TTGAATTCCCACATGTTGTG	231214	63410	TCCTGATTTAGCTTTGGATC	275801	107997	CTCCGAGAAAGTGACTTTAG
186628	18824	CTTGAATTCCCACATGTTGT	231215	63411	CTCCTGATTTAGCTTTGGAT	275802	107998	CCTCCGAGAAAGTGACTTTA
186629	18825	TCTTGAATTCCCACATGTTG	231216	63412	CCTCCTGATTTAGCTTTGGA	275803	107999	TCCTCCGAGAAAGTGACTTT
186630	18826	ATCTTGAATTCCCACATGTT	231217	63413	GCCTCCTGATTTAGCTTTGG	275804	108000	ATCCTCCGAGAAAGTGACTT
186631	18827	CATCTTGAATTCCCACATGT	231218	63414	AGCCTCCTGATTTAGCTTTG	275805	108001	CATCCTCCGAGAAAGTGACT
186632	18828	TCATCTTGAATTCCCACATG	231219	63415	GAGCCTCCTGATTTAGCTTT	275806	108002	ACATCCTCCGAGAAAGTGAC
186633	18829	CTCATCTTGAATTCCCACAT	231220	63416	AGAGCCTCCTGATTTAGCTT	275807	108003	GACATCCTCCGAGAAAGTGA
186634	18830	TCTCATCTTGAATTCCCACA	231221	63417	TAGAGCCTCCTGATTTAGCT	275808	108004	GGACATCCTCCGAGAAAGTG
186635	18831	ATCTCATCTTGAATTCCCAC	231222	63418	CTAGAGCCTCCTGATTTAGC	275809	108005	TGGACATCCTCCGAGAAAGT
186636	18832	AATCTCATCTTGAATTCCCA	231223	63419	GCTAGAGCCTCCTGATTTAG	275810	108006	CTGGACATCCTCCGAGAAAG
186637	18833	AAATCTCATCTTGAATTCCC	231224	63420	TGCTAGAGCCTCCTGATTTA	275811	108007	CCTGGACATCCTCCGAGAAA
186638	18834	CAAATCTCATCTTGAATTCC	231225	63421	TTGCTAGAGCCTCCTGATTT	275812	108008	GCCTGGACATCCTCCGAGAA
186639	18835	ACAAATCTCATCTTGAATTC	231226	63422	TTTGCTAGAGCCTCCTGATT	275813	108009	GGCCTGGACATCCTCCGAGA
186640	18836	AACAAATCTCATCTTGAATT	231227	63423	TTTTGCTAGAGCCTCCTGAT	275814	108010	TGGCCTGGACATCCTCCGAG
186641	18837	TAACAAATCTCATCTTGAAT	231228	63424	ATTTTGCTAGAGCCTCCTGA	275815	108011	TTGGCCTGGACATCCTCCGA
186642	18838	GTAACAAATCTCATCTTGAA	231229	63425	AATTTTGCTAGAGCCTCCTG	275816	108012	ATTGGCCTGGACATCCTCCG
186643	18839	GGTAACAAATCTCATCTTGA	231230	63426	CAATTTTGCTAGAGCCTCCT	275817	108013	TATTGGCCTGGACATCCTCC
186644	18840	TGGTAACAAATCTCATCTTG	231231	63427	TCAATTTTGCTAGAGCCTCC	275818	108014	CTATTGGCCTGGACATCCTC
186645	18841	ATGGTAACAAATCTCATCTT	231232	63428	GTCAATTTTGCTAGAGCCTC	275819	108015	ACTATTGGCCTGGACATCCT
186646	18842	TATGGTAACAAATCTCATCT	231233	63429	TGTCAATTTTGCTAGAGCCT	275820	108016	AACTATTGGCCTGGACATCC
186647	18843	ATATGGTAACAAATCTCATC	231234	63430	CTGTCAATTTTGCTAGAGCC	275821	108017	CAACTATTGGCCTGGACATC
186648	18844	GATATGGTAACAAATCTCAT	231235	63431	TCTGTCAATTTTGCTAGAGC	275822	108018	CCAACTATTGGCCTGGACAT
186649	18845	TGATATGGTAACAAATCTCA	231236	63432	ATCTGTCAATTTTGCTAGAG	275823	108019	CCCAACTATTGGCCTGGACA
186650	18846	CTGATATGGTAACAAATCTC	231237	63433	TATCTGTCAATTTTGCTAGA	275824	108020	TCCCAACTATTGGCCTGGAC
186651	18847	ACTGATATGGTAACAAATCT	231238	63434	TTATCTGTCAATTTTGCTAG	275825	108021	ATCCCAACTATTGGCCTGGA
186652	18848	AACTGATATGGTAACAAATC	231239	63435	CTTATCTGTCAATTTTGCTA	275826	108022	CATCCCAACTATTGGCCTGG
186653	18849	TAACTGATATGGTAACAAAT	231240	63436	GCTTATCTGTCAATTTTGCT	275827	108023	ACATCCCAACTATTGGCCTG
186654	18850	GTAACTGATATGGTAACAAA	231241	63437	TGCTTATCTGTCAATTTTGC	275828	108024	CACATCCCAACTATTGGCCT
186655	18851	GGTAACTGATATGGTAACAA	231242	63438	CTGCTTATCTGTCAATTTTG	275829	108025	TCACATCCCAACTATTGGCC
186656	18852	TGGTAACTGATATGGTAACA	231243	63439	CCTGCTTATCTGTCAATTTT	275830	108026	TTCACATCCCAACTATTGGC
186657	18853	TTGGTAACTGATATGGTAAC	231244	63440	TCCTGCTTATCTGTCAATTT	275831	108027	CTTCACATCCCAACTATTGG
186658	18854	GTTGGTAACTGATATGGTAA	231245	63441	GTCCTGCTTATCTGTCAATT	275832	108028	TCTTCACATCCCAACTATTG
186659	18855	GGTTGGTAACTGATATGGTA	231246	63442	TGTCCTGCTTATCTGTCAAT	275833	108029	GTCTTCACATCCCAACTATT
186660	18856	GGGTTGGTAACTGATATGGT	231247	63443	CTGTCCTGCTTATCTGTCAA	275834	108030	CGTCTTCACATCCCAACTAT
186661	18857	AGGGTTGGTAACTGATATGG	231248	63444	TCTGTCCTGCTTATCTGTCA	275835	108031	ACGTCTTCACATCCCAACTA
186662	18858	AAGGGTTGGTAACTGATATG	231249	63445	CTCTGTCCTGCTTATCTGTC	275836	108032	CACGTCTTCACATCCCAACT
186663	18859	GAAGGGTTGGTAACTGATAT	231250	63446	ACTCTGTCCTGCTTATCTGT	275837	108033	TCACGTCTTCACATCCCAAC
186664	18860	GGAAGGGTTGGTAACTGATA	231251	63447	CACTCTGTCCTGCTTATCTG	275838	108034	TTCACGTCTTCACATCCCAA
186665	18861	TGGAAGGGTTGGTAACTGAT	231252	63448	GCACTCTGTCCTGCTTATCT	275839	108035	CTTCACGTCTTCACATCCCA
186666	18862	CTGGAAGGGTTGGTAACTGA	231253	63449	TGCACTCTGTCCTGCTTATC	275840	108036	GCTTCACGTCTTCACATCCC

186667	18863	TCTGGAAGGGTTGGTAACTG	231254	63450	ATGCACTCTGTCCTGCTTAT	275841	108037	TGCTTCACGTCTTCACATCC
186668	18864	ATCTGGAAGGGTTGGTAACT	231255	63451	CATGCACTCTGTCCTGCTTA	275842	108038	CTGCTTCACGTCTTCACATC
186669	18865	TATCTGGAAGGGTTGGTAAC	231256	63452	CCATGCACTCTGTCCTGCTT	275843	108039	GCTGCTTCACGTCTTCACAT
186670	18866	TTATCTGGAAGGGTTGGTAA	231257	63453	ACCATGCACTCTGTCCTGCT	275844	108040	TGCTGCTTCACGTCTTCACA
186671	18867	TTTATCTGGAAGGGTTGGTA	231258	63454	CACCATGCACTCTGTCCTGC	275845	108041	GTGCTGCTTCACGTCTTCAC
186672	18868	ATTTATCTGGAAGGGTTGGT	231259	63455	GCACCATGCACTCTGTCCTG	275846	108042	TGTGCTGCTTCACGTCTTCA
186673	18869	GATTTATCTGGAAGGGTTGG	231260	63456	TGCACCATGCACTCTGTCCT	275847	108043	CTGTGCTGCTTCACGTCTTC
186674	18870	TGATTTATCTGGAAGGGTTG	231261	63457	ATGCACCATGCACTCTGTCC	275848	108044	TCTGTGCTGCTTCACGTCTT
186675	18871	GTGATTTATCTGGAAGGGTT	231262	63458	AATGCACCATGCACTCTGTC	275849	108045	CTCTGTGCTGCTTCACGTCT
186676	18872	CGTGATTTATCTGGAAGGGT	231263	63459	GAATGCACCATGCACTCTGT	275850	108046	GCTCTGTGCTGCTTCACGTC
186677	18873	ACGTGATTTATCTGGAAGGG	231264	63460	TGAATGCACCATGCACTCTG	275851	108047	GGCTCTGTGCTGCTTCACGT
186678	18874	CACGTGATTTATCTGGAAGG	231265	63461	GTGAATGCACCATGCACTCT	275852	108048	AGGCTCTGTGCTGCTTCACG
186679	18875	TCACGTGATTTATCTGGAAG	231266	63462	GGTGAATGCACCATGCACTC	275853	108049	CAGGCTCTGTGCTGCTTCAC
186680	18876	TTCACGTGATTTATCTGGAA	231267	63463	AGGTGAATGCACCATGCACT	275854	108050	CCAGGCTCTGTGCTGCTTCA
186681	18877	TTTCACGTGATTTATCTGGA	231268	63464	CAGGTGAATGCACCATGCAC	275855	108051	TCCAGGCTCTGTGCTGCTTC
186682	18878	ATTTCACGTGATTTATCTGG	231269	63465	CCAGGTGAATGCACCATGCA	275856	108052	TTCCAGGCTCTGTGCTGCTT
186683	18879	TATTTCACGTGATTTATCTG	231270	63466	CCCAGGTGAATGCACCATGC	275857	108053	CTTCCAGGCTCTGTGCTGCT
186684	18880	ATATTTCACGTGATTTATCT	231271	63467	CCCCAGGTGAATGCACCATG	275858	108054	GCTTCCAGGCTCTGTGCTGC
186685	18881	GATATTTCACGTGATTTATC	231272	63468	TCCCCAGGTGAATGCACCAT	275859	108055	GGCTTCCAGGCTCTGTGCTG
186686	18882	CGATATTTCACGTGATTTAT	231273	63469	TTCCCCAGGTGAATGCACCA	275860	108056	GGGCTTCCAGGCTCTGTGCT
186687	18883	GCGATATTTCACGTGATTTA	231274	63470	CTTCCCCAGGTGAATGCACC	275861	108057	TGGGCTTCCAGGCTCTGTGC
186688	18884	GGCGATATTTCACGTGATTT	231275	63471	TCTTCCCCAGGTGAATGCAC	275862	108058	CTGGGCTTCCAGGCTCTGTG
186689	18885	TGGCGATATTTCACGTGATT	231276	63472	CTCTTCCCCAGGTGAATGCA	275863	108059	CCTGGGCTTCCAGGCTCTGT
186690	18886	ATGGCGATATTTCACGTGAT	231277	63473	CCTCTTCCCCAGGTGAATGC	275864	108060	TCCTGGGCTTCCAGGCTCTG
186691	18887	AATGGCGATATTTCACGTGA	231278	63474	CCCTCTTCCCCAGGTGAATG	275865	108061	ATCCTGGGCTTCCAGGCTCT
186692	18888	TAATGGCGATATTTCACGTG	231279	63475	GCCCTCTTCCCCAGGTGAAT	275866	108062	CATCCTGGGCTTCCAGGCTC
186693	18889	TTAATGGCGATATTTCACGT	231280	63476	TGCCCTCTTCCCCAGGTGAA	275867	108063	CCATCCTGGGCTTCCAGGCT
186694	18890	GTTAATGGCGATATTTCACG	231281	63477	CTGCCCTCTTCCCCAGGTGA	275868	108064	TCCATCCTGGGCTTCCAGGC
186695	18891	TGTTAATGGCGATATTTCAC	231282	63478	TCTGCCCTCTTCCCCAGGTG	275869	108065	GTCCATCCTGGGCTTCCAGG
186696	18892	CTGTTAATGGCGATATTTCA	231283	63479	ATCTGCCCTCTTCCCCAGGT	275870	108066	TGTCCATCCTGGGCTTCCAG
186697	18893	TCTGTTAATGGCGATATTTC	231284	63480	AATCTGCCCTCTTCCCCAGG	275871	108067	CTGTCCATCCTGGGCTTCCA
186698	18894	CTCTGTTAATGGCGATATTT	231285	63481	CAATCTGCCCTCTTCCCCAG	275872	108068	TCTGTCCATCCTGGGCTTCC
186699	18895	ACTCTGTTAATGGCGATATT	231286	63482	CCAATCTGCCCTCTTCCCCA	275873	108069	TTCTGTCCATCCTGGGCTTC
186700	18896	CACTCTGTTAATGGCGATAT	231287	63483	ACCAATCTGCCCTCTTCCCC	275874	108070	TTTCTGTCCATCCTGGGCTT
186701	18897	TCACTCTGTTAATGGCGATA	231288	63484	GACCAATCTGCCCTCTTCCC	275875	108071	GTTTCTGTCCATCCTGGGCT
186702	18898	CTCACTCTGTTAATGGCGAT	231289	63485	AGACCAATCTGCCCTCTTCC	275876	108072	GGTTTCTGTCCATCCTGGGC
186703	18899	GCTCACTCTGTTAATGGCGA	231290	63486	TAGACCAATCTGCCCTCTTC	275877	108073	AGGTTTCTGTCCATCCTGGG
186704	18900	AGCTCACTCTGTTAATGGCG	231291	63487	GTAGACCAATCTGCCCTCTT	275878	108074	TAGGTTTCTGTCCATCCTGG
186705	18901	GAGCTCACTCTGTTAATGGC	231292	63488	TGTAGACCAATCTGCCCTCT	275879	108075	GTAGGTTTCTGTCCATCCTG
186706	18902	TGAGCTCACTCTGTTAATGG	231293	63489	TTGTAGACCAATCTGCCCTC	275880	108076	GGTAGGTTTCTGTCCATCCT
186707	18903	CTGAGCTCACTCTGTTAATG	231294	63490	TTTGTAGACCAATCTGCCCT	275881	108077	AGGTAGGTTTCTGTCCATCC
186708	18904	CCTGAGCTCACTCTGTTAAT	231295	63491	ATTTGTAGACCAATCTGCCC	275882	108078	CAGGTAGGTTTCTGTCCATC
186709	18905	ACCTGAGCTCACTCTGTTAA	231296	63492	TATTTGTAGACCAATCTGCC	275883	108079	TCAGGTAGGTTTCTGTCCAT
186710	18906	CACCTGAGCTCACTCTGTTA	231297	63493	CTATTTGTAGACCAATCTGC	275884	108080	CTCAGGTAGGTTTCTGTCCA
186711	18907	CCACCTGAGCTCACTCTGTT	231298	63494	CCTATTTGTAGACCAATCTG	275885	108081	GCTCAGGTAGGTTTCTGTCC
186712	18908	ACCACCTGAGCTCACTCTGT	231299	63495	GCCTATTTGTAGACCAATCT	275886	108082	TGCTCAGGTAGGTTTCTGTC
186713	18909	AACCACCTGAGCTCACTCTG	231300	63496	GGCCTATTTGTAGACCAATC	275887	108083	CTGCTCAGGTAGGTTTCTGT
186714	18910	GAACCACCTGAGCTCACTCT	231301	63497	AGGCCTATTTGTAGACCAAT	275888	108084	ACTGCTCAGGTAGGTTTCTG
186715	18911	AGAACCACCTGAGCTCACTC	231302	63498	CAGGCCTATTTGTAGACCAA	275889	108085	CACTGCTCAGGTAGGTTTCT
186716	18912	AAGAACCACCTGAGCTCACT	231303	63499	CCAGGCCTATTTGTAGACCA	275890	108086	CCACTGCTCAGGTAGGTTTC
186717	18913	GAAGAACCACCTGAGCTCAC	231304	63500	CCCAGGCCTATTTGTAGACC	275891	108087	CCCACTGCTCAGGTAGGTTT
186718	18914	TGAAGAACCACCTGAGCTCA	231305	63501	ACCCAGGCCTATTTGTAGAC	275892	108088	CCCCACTGCTCAGGTAGGTT
186719	18915	CTGAAGAACCACCTGAGCTC	231306	63502	GACCCAGGCCTATTTGTAGA	275893	108089	GCCCCACTGCTCAGGTAGGT
186720	18916	ACTGAAGAACCACCTGAGCT	231307	63503	GGACCCAGGCCTATTTGTAG	275894	108090	AGCCCCACTGCTCAGGTAGG
186721	18917	CACTGAAGAACCACCTGAGC	231308	63504	TGGACCCAGGCCTATTTGTA	275895	108091	AAGCCCCACTGCTCAGGTAG
186722	18918	GCACTGAAGAACCACCTGAG	231309	63505	GTGGACCCAGGCCTATTTGT	275896	108092	AAAGCCCCACTGCTCAGGTA
186723	18919	TGCACTGAAGAACCACCTGA	231310	63506	AGTGGACCCAGGCCTATTTG	275897	108093	CAAAGCCCCACTGCTCAGGT
186724	18920	ATGCACTGAAGAACCACCTG	231311	63507	CAGTGGACCCAGGCCTATTT	275898	108094	TCAAAGCCCCACTGCTCAGG
186725	18921	AATGCACTGAAGAACCACCT	231312	63508	TCAGTGGACCCAGGCCTATT	275899	108095	TTCAAAGCCCCACTGCTCAG
186726	18922	AAATGCACTGAAGAACCACC	231313	63509	GTCAGTGGACCCAGGCCTAT	275900	108096	TTTCAAAGCCCCACTGCTCA
186727	18923	GAAATGCACTGAAGAACCAC	231314	63510	AGTCAGTGGACCCAGGCCTA	275901	108097	CTTTCAAAGCCCCACTGCTC
186728	18924	AGAAATGCACTGAAGAACCA	231315	63511	AAGTCAGTGGACCCAGGCCT	275902	108098	GCTTTCAAAGCCCCACTGCT
186729	18925	CAGAAATGCACTGAAGAACC	231316	63512	AAAGTCAGTGGACCCAGGCC	275903	108099	GGCTTTCAAAGCCCCACTGC
186730	18926	TCAGAAATGCACTGAAGAAC	231317	63513	TAAAGTCAGTGGACCCAGGC	275904	108100	AGGCTTTCAAAGCCCCACTG
186731	18927	ATCAGAAATGCACTGAAGAA	231318	63514	CTAAAGTCAGTGGACCCAGG	275905	108101	AAGGCTTTCAAAGCCCCACT
186732	18928	TATCAGAAATGCACTGAAGA	231319	63515	GCTAAAGTCAGTGGACCCAG	275906	108102	CAAGGCTTTCAAAGCCCCAC
186733	18929	GTATCAGAAATGCACTGAAG	231320	63516	AGCTAAAGTCAGTGGACCCA	275907	108103	CCAAGGCTTTCAAAGCCCCA
186734	18930	GGTATCAGAAATGCACTGAA	231321	63517	CAGCTAAAGTCAGTGGACCC	275908	108104	CCCAAGGCTTTCAAAGCCCC
186735	18931	AGGTATCAGAAATGCACTGA	231322	63518	ACAGCTAAAGTCAGTGGACC	275909	108105	CCCCAAGGCTTTCAAAGCCC
186736	18932	CAGGTATCAGAAATGCACTG	231323	63519	AACAGCTAAAGTCAGTGGAC	275910	108106	GCCCCAAGGCTTTCAAAGCC
186737	18933	TCAGGTATCAGAAATGCACT	231324	63520	TAACAGCTAAAGTCAGTGGA	275911	108107	CGCCCCAAGGCTTTCAAAGC
186738	18934	TTCAGGTATCAGAAATGCAC	231325	63521	ATAACAGCTAAAGTCAGTGG	275912	108108	CCGCCCCAAGGCTTTCAAAG

186739	18935	GTTCAGGTATCAGAAATGCA	231326	63522	TATAACAGCTAAAGTCAGTG	275913	108109	CCCGCCCCAAGGCTTTCAAA
186740	18936	GGTTCAGGTATCAGAAATGC	231327	63523	ATATAACAGCTAAAGTCAGT	275914	108110	CCCCGCCCCAAGGCTTTCAA
186741	18937	AGGTTCAGGTATCAGAAATG	231328	63524	AATATAACAGCTAAAGTCAG	275915	108111	CCCCCGCCCCAAGGCTTTCA
186742	18938	AAGGTTCAGGTATCAGAAAT	231329	63525	AAATATAACAGCTAAAGTCA	275916	108112	CCCCCCGCCCCAAGGCTTTC
186743	18939	GAAGGTTCAGGTATCAGAAA	231330	63526	CAAATATAACAGCTAAAGTC	275917	108113	ACCCCCCGCCCCAAGGCTTT
186744	18940	GGAAGGTTCAGGTATCAGAA	231331	63527	CCAAATATAACAGCTAAAGT	275918	108114	CACCCCCCGCCCCAAGGCTT
186745	18941	GGGAAGGTTCAGGTATCAGA	231332	63528	CCCAAATATAACAGCTAAAG	275919	108115	GCACCCCCCGCCCCAAGGCT
186746	18942	AGGGAAGGTTCAGGTATCAG	231333	63529	CCCCAAATATAACAGCTAAA	275920	108116	TGCACCCCCCGCCCCAAGGC
186747	18943	CAGGGAAGGTTCAGGTATCA	231334	63530	TCCCCAAATATAACAGCTAA	275921	108117	TTGCACCCCCCGCCCCAAGG
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186750	18946	TCCCAGGGAAGGTTCAGGTA	231337	63533	TTCTCCCCAAATATAACAGC	275924	108120	ATATTGCACCCCCCGCCCCA
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186754	18950	AAATTCCCAGGGAAGGTTCA	231341	63537	AAGTTTCTCCCCAAATATAA	275928	108124	TTGAATATTGCACCCCCCGC
186755	18951	GAAATTCCCAGGGAAGGTTC	231342	63538	AAAGTTTCTCCCCAAATATA	275929	108125	CTTGAATATTGCACCCCCCG
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186758	18954	TGTGAAATTCCCAGGGAAGG	231345	63541	TGAAAAGTTTCTCCCCAAAT	275932	108128	CATCTTGAATATTGCACCCC
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186762	18958	GGTCTGTGAAATTCCCAGGG	231349	63545	AGGTTGAAAAGTTTCTCCCC	275936	108132	TGGCCATCTTGAATATTGCA
186763	18959	TGGTCTGTGAAATTCCCAGG	231350	63546	GAGGTTGAAAAGTTTCTCCC	275937	108133	GTGGCCATCTTGAATATTGC
186764	18960	ATGGTCTGTGAAATTCCCAG	231351	63547	TGAGGTTGAAAAGTTTCTCC	275938	108134	TGTGGCCATCTTGAATATTG
186765	18961	GATGGTCTGTGAAATTCCCA	231352	63548	GTGAGGTTGAAAAGTTTCTC	275939	108135	TTGTGGCCATCTTGAATATT
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186767	18963	CTGATGGTCTGTGAAATTCC	231354	63550	GAGTGAGGTTGAAAAGTTTC	275941	108137	TCTTGTGGCCATCTTGAATA
186768	18964	CCTGATGGTCTGTGAAATTC	231355	63551	GGAGTGAGGTTGAAAAGTTT	275942	108138	ATCTTGTGGCCATCTTGAAT
186769	18965	GCCTGATGGTCTGTGAAATT	231356	63552	TGGAGTGAGGTTGAAAAGTT	275943	108139	CATCTTGTGGCCATCTTGAA
186770	18966	AGCCTGATGGTCTGTGAAAT	231357	63553	ATGGAGTGAGGTTGAAAAGT	275944	108140	CCATCTTGTGGCCATCTTGA
186771	18967	GAGCCTGATGGTCTGTGAAA	231358	63554	GATGGAGTGAGGTTGAAAAG	275945	108141	GCCATCTTGTGGCCATCTTG
186772	18968	AGAGCCTGATGGTCTGTGAA	231359	63555	AGATGGAGTGAGGTTGAAAA	275946	108142	TGCCATCTTGTGGCCATCTT
186773	18969	GAGAGCCTGATGGTCTGTGA	231360	63556	AAGATGGAGTGAGGTTGAAA	275947	108143	TTGCCATCTTGTGGCCATCT
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186792	18988	ATCCTGCTATCAAAGGGTGG	231379	63575	CTGGAATATTTTTAGGTTTA	275966	108162	AGAAAGTTACAGCATTCTAT
186793	18989	TATCCTGCTATCAAAGGGTG	231380	63576	TCTGGAATATTTTTAGGTTT	275967	108163	AAGAAAGTTACAGCATTCTA
186794	18990	CTATCCTGCTATCAAAGGGT	231381	63577	ATCTGGAATATTTTTAGGTT	275968	108164	CAAGAAAGTTACAGCATTCT
186795	18991	GCTATCCTGCTATCAAAGGG	231382	63578	CATCTGGAATATTTTTAGGT	275969	108165	CCAAGAAAGTTACAGCATTC
186796	18992	TGCTATCCTGCTATCAAAGG	231383	63579	TCATCTGGAATATTTTTAGG	275970	108166	ACCAAGAAAGTTACAGCATT
186797	18993	CTGCTATCCTGCTATCAAAG	231384	63580	TTCATCTGGAATATTTTTAG	275971	108167	AACCAAGAAAGTTACAGCAT
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186799	18995	CCCTGCTATCCTGCTATCAA	231386	63582	AATTCATCTGGAATATTTTT	275973	108169	AGAACCAAGAAAGTTACAGC
186800	18996	GCCCTGCTATCCTGCTATCA	231387	63583	TAATTCATCTGGAATATTTT	275974	108170	CAGAACCAAGAAAGTTACAG
186801	18997	GGCCCTGCTATCCTGCTATC	231388	63584	TTAATTCATCTGGAATATTT	275975	108171	CCAGAACCAAGAAAGTTACA
186802	18998	GGGCCCTGCTATCCTGCTAT	231389	63585	ATTAATTCATCTGGAATATT	275976	108172	CCCAGAACCAAGAAAGTTAC
186803	18999	TGGGCCCTGCTATCCTGCTA	231390	63586	TATTAATTCATCTGGAATAT	275977	108173	GCCCAGAACCAAGAAAGTTA
186804	19000	CTGGGCCCTGCTATCCTGCT	231391	63587	TTATTAATTCATCTGGAATA	275978	108174	GGCCCAGAACCAAGAAAGTT
186805	19001	CCTGGGCCCTGCTATCCTGC	231392	63588	TTTATTAATTCATCTGGAAT	275979	108175	CGGCCCAGAACCAAGAAAGT
186806	19002	ACCTGGGCCCTGCTATCCTG	231393	63589	ATTTATTAATTCATCTGGAA	275980	108176	GCGGCCCAGAACCAAGAAAG
186807	19003	AACCTGGGCCCTGCTATCCT	231394	63590	TATTTATTAATTCATCTGGA	275981	108177	TGCGGCCCAGAACCAAGAAA
186808	19004	GAACCTGGGCCCTGCTATCC	231395	63591	ATATTTATTAATTCATCTGG	275982	108178	CTGCGGCCCAGAACCAAGAA
186809	19005	AGAACCTGGGCCCTGCTATC	231396	63592	TATATTTATTAATTCATCTG	275983	108179	GCTGCGGCCCAGAACCAAGA
186810	19006	CAGAACCTGGGCCCTGCTAT	231397	63593	TTATATTTATTAATTCATCT	275984	108180	GGCTGCGGCCCAGAACCAAG

186811	19007	GCAGAACCTGGGCCCTGCTA	231398	63594	TTTATATTTATTAATTCATC	275985	108181	AGGCTGCGGCCCAGAACCAA
186812	19008	TGCAGAACCTGGGCCCTGCT	231399	63595	TTTTATATTTATTAATTCAT	275986	108182	CAGGCTGCGGCCCAGAACCA
186813	19009	CTGCAGAACCTGGGCCCTGC	231400	63596	TTTTTATATTTATTAATTCA	275987	108183	CCAGGCTGCGGCCCAGAACC
186814	19010	CCTGCAGAACCTGGGCCCTG	231401	63597	TTTTTTATATTTATTAATTC	275988	108184	CCCAGGCTGCGGCCCAGAAC
186815	19011	TCCTGCAGAACCTGGGCCCT	231402	63598	ATTTTTTATATTTATTAATT	275989	108185	ACCCAGGCTGCGGCCCAGAA
186816	19012	CTCCTGCAGAACCTGGGCCC	231403	63599	AATTTTTTATATTTATTAAT	275990	108186	CACCCAGGCTGCGGCCCAGA
186817	19013	CCTCCTGCAGAACCTGGGCC	231404	63600	TAATTTTTTATATTTATTAA	275991	108187	CCACCCAGGCTGCGGCCCAG
186818	19014	TCCTCCTGCAGAACCTGGGC	231405	63601	CTAATTTTTTATATTTATTA	275992	108188	GCCACCCAGGCTGCGGCCCA
186819	19015	CTCCTCCTGCAGAACCTGGG	231406	63602	TCTAATTTTTTATATTTATT	275993	108189	AGCCACCCAGGCTGCGGCCC
186820	19016	TCTCCTCCTGCAGAACCTGG	231407	63603	GTCTAATTTTTTATATTTAT	275994	108190	CAGCCACCCAGGCTGCGGCC
186821	19017	ATCTCCTCCTGCAGAACCTG	231408	63604	GGTCTAATTTTTTATATTTA	275995	108191	GCAGCCACCCAGGCTGCGGC
186822	19018	CATCTCCTCCTGCAGAACCT	231409	63605	TGGTCTAATTTTTTATATTT	275996	108192	AGCAGCCACCCAGGCTGCGG
186823	19019	ACATCTCCTCCTGCAGAACC	231410	63606	GTGGTCTAATTTTTTATATT	275997	108193	AAGCAGCCACCCAGGCTGCG
186824	19020	AACATCTCCTCCTGCAGAAC	231411	63607	AGTGGTCTAATTTTTTATAT	275998	108194	GAAGCAGCCACCCAGGCTGC
186825	19021	TAACATCTCCTCCTGCAGAA	231412	63608	TAGTGGTCTAATTTTTTATA	275999	108195	GGAAGCAGCCACCCAGGCTG
186826	19022	GTAACATCTCCTCCTGCAGA	231413	63609	TTAGTGGTCTAATTTTTTAT	276000	108196	AGGAAGCAGCCACCCAGGCT
186827	19023	GGTAACATCTCCTCCTGCAG	231414	63610	TTTAGTGGTCTAATTTTTTA	276001	108197	AAGGAAGCAGCCACCCAGGC
186828	19024	TGGTAACATCTCCTCCTGCA	231415	63611	TTTTAGTGGTCTAATTTTTT	276002	108198	GAAGGAAGCAGCCACCCAGG
186829	19025	GTGGTAACATCTCCTCCTGC	231416	63612	TTTTTAGTGGTCTAATTTTT	276003	108199	GGAAGGAAGCAGCCACCCAG
186830	19026	TGTGGTAACATCTCCTCCTG	231417	63613	ATTTTTAGTGGTCTAATTTT	276004	108200	GGGAAGGAAGCAGCCACCCA
186831	19027	CTGTGGTAACATCTCCTCCT	231418	63614	CATTTTTAGTGGTCTAATTT	276005	108201	AGGGAAGGAAGCAGCCACCC
186832	19028	CCTGTGGTAACATCTCCTCC	231419	63615	ACATTTTTAGTGGTCTAATT	276006	108202	CAGGGAAGGAAGCAGCCACC
186833	19029	GCCTGTGGTAACATCTCCTC	231420	63616	TACATTTTTAGTGGTCTAAT	276007	108203	ACAGGGAAGGAAGCAGCCAC
186834	19030	GGCCTGTGGTAACATCTCCT	231421	63617	CTACATTTTTAGTGGTCTAA	276008	108204	CACAGGGAAGGAAGCAGCCA
186835	19031	AGGCCTGTGGTAACATCTCC	231422	63618	TCTACATTTTTAGTGGTCTA	276009	108205	ACACAGGGAAGGAAGCAGCC
186836	19032	CAGGCCTGTGGTAACATCTC	231423	63619	TTCTACATTTTTAGTGGTCT	276010	108206	CACACAGGGAAGGAAGCAGC
186837	19033	TCAGGCCTGTGGTAACATCT	231424	63620	CTTCTACATTTTTAGTGGTC	276011	108207	ACACACAGGGAAGGAAGCAG
186838	19034	TTCAGGCCTGTGGTAACATC	231425	63621	TCTTCTACATTTTTAGTGGT	276012	108208	TACACACAGGGAAGGAAGCA
186839	19035	TTTCAGGCCTGTGGTAACAT	231426	63622	TTCTTCTACATTTTTAGTGG	276013	108209	ATACACACAGGGAAGGAAGC
186840	19036	CTTTCAGGCCTGTGGTAACA	231427	63623	TTTCTTCTACATTTTTAGTG	276014	108210	AATACACACAGGGAAGGAAG
186841	19037	CCTTTCAGGCCTGTGGTAAC	231428	63624	TTTTCTTCTACATTTTTAGT	276015	108211	CAATACACACAGGGAAGGAA
186842	19038	CCCTTTCAGGCCTGTGGTAA	231429	63625	ATTTTCTTCTACATTTTTAG	276016	108212	TCAATACACACAGGGAAGGA
186843	19039	TCCCTTTCAGGCCTGTGGTA	231430	63626	CATTTTCTTCTACATTTTTA	276017	108213	ATCAATACACACAGGGAAGG
186844	19040	CTCCCTTTCAGGCCTGTGGT	231431	63627	CCATTTTCTTCTACATTTTT	276018	108214	AATCAATACACACAGGGAAG
186845	19041	CCTCCCTTTCAGGCCTGTGG	231432	63628	TCCATTTTCTTCTACATTTT	276019	108215	AAATCAATACACACAGGGAA
186846	19042	CCCTCCCTTTCAGGCCTGTG	231433	63629	ATCCATTTTCTTCTACATTT	276020	108216	CAAATCAATACACACAGGGA
186847	19043	TCCCTCCCTTTCAGGCCTGT	231434	63630	CATCCATTTTCTTCTACATT	276021	108217	ACAAATCAATACACACAGGG
186848	19044	CTCCCTCCCTTTCAGGCCTG	231435	63631	TCATCCATTTTCTTCTACAT	276022	108218	AACAAATCAATACACACAGG
186849	19045	CCTCCCTCCCTTTCAGGCCT	231436	63632	ATCATCCATTTTCTTCTACA	276023	108219	AAACAAATCAATACACACAG
186850	19046	CCCTCCCTCCCTTTCAGGCC	231437	63633	GATCATCCATTTTCTTCTAC	276024	108220	GAAACAAATCAATACACACA
186851	19047	CCCCTCCCTCCCTTTCAGGC	231438	63634	AGATCATCCATTTTCTTCTA	276025	108221	AGAAACAAATCAATACACAC
186852	19048	GCCCCTCCCTCCCTTTCAGG	231439	63635	AAGATCATCCATTTTCTTCT	276026	108222	GAGAAACAAATCAATACACA
186853	19049	TGCCCCTCCCTCCCTTTCAG	231440	63636	AAAGATCATCCATTTTCTTC	276027	108223	AGAGAAACAAATCAATACAC
186854	19050	CTGCCCCTCCCTCCCTTTCA	231441	63637	GAAAGATCATCCATTTTCTT	276028	108224	AAGAGAAACAAATCAATACA
186855	19051	TCTGCCCCTCCCTCCCTTTC	231442	63638	AGAAAGATCATCCATTTTCT	276029	108225	AAAGAGAAACAAATCAATAC
186856	19052	ATCTGCCCCTCCCTCCCTTT	231443	63639	TAGAAAGATCATCCATTTTC	276030	108226	AAAAGAGAAACAAATCAATA
186857	19053	CATCTGCCCCTCCCTCCCTT	231444	63640	ATAGAAAGATCATCCATTTT	276031	108227	AAAAAGAGAAACAAATCAAT
186858	19054	GCATCTGCCCCTCCCTCCCT	231445	63641	TATAGAAAGATCATCCATTT	276032	108228	AAAAAAGAGAAACAAATCAA
186859	19055	AGCATCTGCCCCTCCCTCCC	231446	63642	GTATAGAAAGATCATCCATT	276033	108229	CAAAAAAGAGAAACAAATCA
186860	19056	TAGCATCTGCCCCTCCCTCC	231447	63643	GGTATAGAAAGATCATCCAT	276034	108230	TCAAAAAAGAGAAACAAATC
186861	19057	GTAGCATCTGCCCCTCCCTC	231448	63644	TGGTATAGAAAGATCATCCA	276035	108231	CTCAAAAAAGAGAAACAAAT
186862	19058	TGTAGCATCTGCCCCTCCCT	231449	63645	ATGGTATAGAAAGATCATCC	276036	108232	TCTCAAAAAAGAGAAACAAA
186863	19059	CTGTAGCATCTGCCCCTCCC	231450	63646	TATGGTATAGAAAGATCATC	276037	108233	GTCTCAAAAAAGAGAAACAA
186864	19060	CCTGTAGCATCTGCCCCTCC	231451	63647	CTATGGTATAGAAAGATCAT	276038	108234	TGTCTCAAAAAAGAGAAACA
186865	19061	TCCTGTAGCATCTGCCCCTC	231452	63648	TCTATGGTATAGAAAGATCA	276039	108235	CTGTCTCAAAAAAGAGAAAC
186866	19062	TTCCTGTAGCATCTGCCCCT	231453	63649	CTCTATGGTATAGAAAGATC	276040	108236	TCTGTCTCAAAAAAGAGAAA
186867	19063	CTTCCTGTAGCATCTGCCCC	231454	63650	GCTCTATGGTATAGAAAGAT	276041	108237	CTCTGTCTCAAAAAAGAGAA
186868	19064	TCTTCCTGTAGCATCTGCCC	231455	63651	TGCTCTATGGTATAGAAAGA	276042	108238	ACTCTGTCTCAAAAAAGAGA
186869	19065	ATCTTCCTGTAGCATCTGCC	231456	63652	TTGCTCTATGGTATAGAAAG	276043	108239	GACTCTGTCTCAAAAAAGAG
186870	19066	CATCTTCCTGTAGCATCTGC	231457	63653	ATTGCTCTATGGTATAGAAA	276044	108240	AGACTCTGTCTCAAAAAAGA
186871	19067	GCATCTTCCTGTAGCATCTG	231458	63654	CATTGCTCTATGGTATAGAA	276045	108241	AAGACTCTGTCTCAAAAAAG
186872	19068	AGCATCTTCCTGTAGCATCT	231459	63655	CCATTGCTCTATGGTATAGA	276046	108242	CAAGACTCTGTCTCAAAAAA
186873	19069	CAGCATCTTCCTGTAGCATC	231460	63656	TCCATTGCTCTATGGTATAG	276047	108243	GCAAGACTCTGTCTCAAAAA
186874	19070	CCAGCATCTTCCTGTAGCAT	231461	63657	TTCCATTGCTCTATGGTATA	276048	108244	AGCAAGACTCTGTCTCAAAA
186875	19071	GCCAGCATCTTCCTGTAGCA	231462	63658	ATTCCATTGCTCTATGGTAT	276049	108245	CAGCAAGACTCTGTCTCAAA
186876	19072	AGCCAGCATCTTCCTGTAGC	231463	63659	TATTCCATTGCTCTATGGTA	276050	108246	CCAGCAAGACTCTGTCTCAA
186877	19073	GAGCCAGCATCTTCCTGTAG	231464	63660	TTATTCCATTGCTCTATGGT	276051	108247	CCCAGCAAGACTCTGTCTCA
186878	19074	AGAGCCAGCATCTTCCTGTA	231465	63661	TTTATTCCATTGCTCTATGG	276052	108248	ACCCAGCAAGACTCTGTCTC
186879	19075	CAGAGCCAGCATCTTCCTGT	231466	63662	ATTTATTCCATTGCTCTATG	276053	108249	AACCCAGCAAGACTCTGTCT
186880	19076	CCAGAGCCAGCATCTTCCTG	231467	63663	GATTTATTCCATTGCTCTAT	276054	108250	CAACCCAGCAAGACTCTGTC
186881	19077	TCCAGAGCCAGCATCTTCCT	231468	63664	TGATTTATTCCATTGCTCTA	276055	108251	GCAACCCAGCAAGACTCTGT
186882	19078	ATCCAGAGCCAGCATCTTCC	231469	63665	GTGATTTATTCCATTGCTCT	276056	108252	GGCAACCCAGCAAGACTCTG

186883	19079	AATCCAGAGCCAGCATCTTC	231470	63666	TGTGATTTATTCCATTGCTC	276057	108253	GGGCAACCCAGCAAGACTCT
186884	19080	GAATCCAGAGCCAGCATCTT	231471	63667	TTGTGATTTATTCCATTGCT	276058	108254	TGGGCAACCCAGCAAGACTC
186885	19081	CGAATCCAGAGCCAGCATCT	231472	63668	TTTGTGATTTATTCCATTGC	276059	108255	CTGGGCAACCCAGCAAGACT
186886	19082	GCGAATCCAGAGCCAGCATC	231473	63669	CTTTGTGATTTATTCCATTG	276060	108256	CCTGGGCAACCCAGCAAGAC
186887	19083	AGCGAATCCAGAGCCAGCAT	231474	63670	CCTTTGTGATTTATTCCATT	276061	108257	GCCTGGGCAACCCAGCAAGA
186888	19084	CAGCGAATCCAGAGCCAGCA	231475	63671	TCCTTTGTGATTTATTCCAT	276062	108258	AGCCTGGGCAACCCAGCAAG
186889	19085	CCAGCGAATCCAGAGCCAGC	231476	63672	TTCCTTTGTGATTTATTCCA	276063	108259	CAGCCTGGGCAACCCAGCAA
186890	19086	TCCAGCGAATCCAGAGCCAG	231477	63673	TTTCCTTTGTGATTTATTCC	276064	108260	CCAGCCTGGGCAACCCAGCA
186891	19087	CTCCAGCGAATCCAGAGCCA	231478	63674	TTTTCCTTTGTGATTTATTC	276065	108261	TCCAGCCTGGGCAACCCAGC
186892	19088	CCTCCAGCGAATCCAGAGCC	231479	63675	GTTTTCCTTTGTGATTTATT	276066	108262	CTCCAGCCTGGGCAACCCAG
186893	19089	TCCTCCAGCGAATCCAGAGC	231480	63676	TGTTTTCCTTTGTGATTTAT	276067	108263	ACTCCAGCCTGGGCAACCCA
186894	19090	CTCCTCCAGCGAATCCAGAG	231481	63677	CTGTTTTCCTTTGTGATTTA	276068	108264	CACTCCAGCCTGGGCAACCC
186895	19091	GCTCCTCCAGCGAATCCAGA	231482	63678	TCTGTTTTCCTTTGTGATTT	276069	108265	GCACTCCAGCCTGGGCAACC
186896	19092	AGCTCCTCCAGCGAATCCAG	231483	63679	ATCTGTTTTCCTTTGTGATT	276070	108266	TGCACTCCAGCCTGGGCAAC
186897	19093	AAGCTCCTCCAGCGAATCCA	231484	63680	AATCTGTTTTCCTTTGTGAT	276071	108267	CTGCACTCCAGCCTGGGCAA
186898	19094	AAAGCTCCTCCAGCGAATCC	231485	63681	AAATCTGTTTTCCTTTGTGA	276072	108268	ACTGCACTCCAGCCTGGGCA
186899	19095	GAAAGCTCCTCCAGCGAATC	231486	63682	CAAATCTGTTTTCCTTTGTG	276073	108269	CACTGCACTCCAGCCTGGGC
186900	19096	TGAAAGCTCCTCCAGCGAAT	231487	63683	TCAAATCTGTTTTCCTTTGT	276074	108270	CCACTGCACTCCAGCCTGGG
186901	19097	TTGAAAGCTCCTCCAGCGAA	231488	63684	GTCAAATCTGTTTTCCTTTG	276075	108271	ACCACTGCACTCCAGCCTGG
186902	19098	CTTGAAAGCTCCTCCAGCGA	231489	63685	AGTCAAATCTGTTTTCCTTT	276076	108272	CACCACTGCACTCCAGCCTG
186903	19099	CCTTGAAAGCTCCTCCAGCG	231490	63686	TAGTCAAATCTGTTTTCCTT	276077	108273	GCACCACTGCACTCCAGCCT
186904	19100	CCCTTGAAAGCTCCTCCAGC	231491	63687	ATAGTCAAATCTGTTTTCCT	276078	108274	CGCACCACTGCACTCCAGCC
186905	19101	TCCCTTGAAAGCTCCTCCAG	231492	63688	TATAGTCAAATCTGTTTTCC	276079	108275	TCGCACCACTGCACTCCAGC
186906	19102	TTCCCTTGAAAGCTCCTCCA	231493	63689	ATATAGTCAAATCTGTTTTC	276080	108276	ATCGCACCACTGCACTCCAG
186907	19103	CTTCCCTTGAAAGCTCCTCC	231494	63690	TATATAGTCAAATCTGTTTT	276081	108277	GATCGCACCACTGCACTCCA
186908	19104	ACTTCCCTTGAAAGCTCCTC	231495	63691	TTATATAGTCAAATCTGTTT	276082	108278	TGATCGCACCACTGCACTCC
186909	19105	TACTTCCCTTGAAAGCTCCT	231496	63692	TTTATATAGTCAAATCTGTT	276083	108279	ATGATCGCACCACTGCACTC
186910	19106	CTACTTCCCTTGAAAGCTCC	231497	63693	TTTTATATAGTCAAATCTGT	276084	108280	TATGATCGCACCACTGCACT
186911	19107	TCTACTTCCCTTGAAAGCTC	231498	63694	GTTTTATATAGTCAAATCTG	276085	108281	CTATGATCGCACCACTGCAC
186912	19108	ATCTACTTCCCTTGAAAGCT	231499	63695	AGTTTTATATAGTCAAATCT	276086	108282	GCTATGATCGCACCACTGCA
186913	19109	TATCTACTTCCCTTGAAAGC	231500	63696	AAGTTTTATATAGTCAAATC	276087	108283	AGCTATGATCGCACCACTGC
186914	19110	GTATCTACTTCCCTTGAAAG	231501	63697	TAAGTTTTATATAGTCAAAT	276088	108284	GAGCTATGATCGCACCACTG
186915	19111	TGTATCTACTTCCCTTGAAA	231502	63698	TTAAGTTTTATATAGTCAAA	276089	108285	TGAGCTATGATCGCACCACT
186916	19112	GTGTATCTACTTCCCTTGAA	231503	63699	TTTAAGTTTTATATAGTCAA	276090	108286	GTGAGCTATGATCGCACCAC
186917	19113	TGTGTATCTACTTCCCTTGA	231504	63700	GTTTAAGTTTTATATAGTCA	276091	108287	AGTGAGCTATGATCGCACCA
186918	19114	GTGTGTATCTACTTCCCTTG	231505	63701	GGTTTAAGTTTTATATAGTC	276092	108288	CAGTGAGCTATGATCGCACC
186919	19115	AGTGTGTATCTACTTCCCTT	231506	63702	GGGTTTAAGTTTTATATAGT	276093	108289	GCAGTGAGCTATGATCGCAC
186920	19116	CAGTGTGTATCTACTTCCCT	231507	63703	AGGGTTTAAGTTTTATATAG	276094	108290	TGCAGTGAGCTATGATCGCA
186921	19117	ACAGTGTGTATCTACTTCCC	231508	63704	CAGGGTTTAAGTTTTATATA	276095	108291	CTGCAGTGAGCTATGATCGC
186922	19118	GACAGTGTGTATCTACTTCC	231509	63705	GCAGGGTTTAAGTTTTATAT	276096	108292	GCTGCAGTGAGCTATGATCG
186923	19119	AGACAGTGTGTATCTACTTC	231510	63706	GGCAGGGTTTAAGTTTTATA	276097	108293	GGCTGCAGTGAGCTATGATC
186924	19120	GAGACAGTGTGTATCTACTT	231511	63707	GGGCAGGGTTTAAGTTTTAT	276098	108294	AGGCTGCAGTGAGCTATGAT
186925	19121	GGAGACAGTGTGTATCTACT	231512	63708	TGGGCAGGGTTTAAGTTTTA	276099	108295	AAGGCTGCAGTGAGCTATGA
186926	19122	TGGAGACAGTGTGTATCTAC	231513	63709	ATGGGCAGGGTTTAAGTTTT	276100	108296	CAAGGCTGCAGTGAGCTATG
186927	19123	ATGGAGACAGTGTGTATCTA	231514	63710	GATGGGCAGGGTTTAAGTTT	276101	108297	TCAAGGCTGCAGTGAGCTAT
186928	19124	GATGGAGACAGTGTGTATCT	231515	63711	TGATGGGCAGGGTTTAAGTT	276102	108298	TTCAAGGCTGCAGTGAGCTA
186929	19125	TGATGGAGACAGTGTGTATC	231516	63712	TTGATGGGCAGGGTTTAAGT	276103	108299	CTTCAAGGCTGCAGTGAGCT
186930	19126	ATGATGGAGACAGTGTGTAT	231517	63713	TTTGATGGGCAGGGTTTAAG	276104	108300	ACTTCAAGGCTGCAGTGAGC
186931	19127	AATGATGGAGACAGTGTGTA	231518	63714	TTTTGATGGGCAGGGTTTAA	276105	108301	GACTTCAAGGCTGCAGTGAG
186932	19128	AAATGATGGAGACAGTGTGT	231519	63715	TTTTTGATGGGCAGGGTTTA	276106	108302	GGACTTCAAGGCTGCAGTGA
186933	19129	GAAATGATGGAGACAGTGTG	231520	63716	GTTTTTGATGGGCAGGGTTT	276107	108303	AGGACTTCAAGGCTGCAGTG
186934	19130	TGAAATGATGGAGACAGTGT	231521	63717	GGTTTTTGATGGGCAGGGTT	276108	108304	CAGGACTTCAAGGCTGCAGT
186935	19131	ATGAAATGATGGAGACAGTG	231522	63718	TGGTTTTTGATGGGCAGGGT	276109	108305	TCAGGACTTCAAGGCTGCAG
186936	19132	CATGAAATGATGGAGACAGT	231523	63719	ATGGTTTTTGATGGGCAGGG	276110	108306	CTCAGGACTTCAAGGCTGCA
186937	19133	ACATGAAATGATGGAGACAG	231524	63720	GATGGTTTTTGATGGGCAGG	276111	108307	GCTCAGGACTTCAAGGCTGC
186938	19134	GACATGAAATGATGGAGACA	231525	63721	TGATGGTTTTTGATGGGCAG	276112	108308	AGCTCAGGACTTCAAGGCTG
186939	19135	GGACATGAAATGATGGAGAC	231526	63722	CTGATGGTTTTTGATGGGCA	276113	108309	GAGCTCAGGACTTCAAGGCT
186940	19136	TGGACATGAAATGATGGAGA	231527	63723	TCTGATGGTTTTTGATGGGC	276114	108310	TGAGCTCAGGACTTCAAGGC
186941	19137	ATGGACATGAAATGATGGAG	231528	63724	TTCTGATGGTTTTTGATGGG	276115	108311	TTGAGCTCAGGACTTCAAGG
186942	19138	GATGGACATGAAATGATGGA	231529	63725	TTTCTGATGGTTTTTGATGG	276116	108312	CTTGAGCTCAGGACTTCAAG
186943	19139	TGATGGACATGAAATGATGG	231530	63726	GTTTCTGATGGTTTTTGATG	276117	108313	TCTTGAGCTCAGGACTTCAA
186944	19140	GTGATGGACATGAAATGATG	231531	63727	GGTTTCTGATGGTTTTTGAT	276118	108314	CTCTTGAGCTCAGGACTTCA
186945	19141	TGTGATGGACATGAAATGAT	231532	63728	TGGTTTCTGATGGTTTTTGA	276119	108315	TCTCTTGAGCTCAGGACTTC
186946	19142	GTGTGATGGACATGAAATGA	231533	63729	TTGGTTTCTGATGGTTTTTG	276120	108316	ATCTCTTGAGCTCAGGACTT
186947	19143	AGTGTGATGGACATGAAATG	231534	63730	TTTGGTTTCTGATGGTTTTT	276121	108317	GATCTCTTGAGCTCAGGACT
186948	19144	GAGTGTGATGGACATGAAAT	231535	63731	TTTTGGTTTCTGATGGTTTT	276122	108318	GGATCTCTTGAGCTCAGGAC
186949	19145	AGAGTGTGATGGACATGAAA	231536	63732	ATTTTGGTTTCTGATGGTTT	276123	108319	AGGATCTCTTGAGCTCAGGA
186950	19146	TAGAGTGTGATGGACATGAA	231537	63733	TATTTTGGTTTCTGATGGTT	276124	108320	AAGGATCTCTTGAGCTCAGG
186951	19147	TTAGAGTGTGATGGACATGA	231538	63734	TTATTTTGGTTTCTGATGGT	276125	108321	GAAGGATCTCTTGAGCTCAG
186952	19148	TTTAGAGTGTGATGGACATG	231539	63735	TTTATTTTGGTTTCTGATGG	276126	108322	GGAAGGATCTCTTGAGCTCA
186953	19149	TTTTAGAGTGTGATGGACAT	231540	63736	TTTTATTTTGGTTTCTGATG	276127	108323	TGGAAGGATCTCTTGAGCTC
186954	19150	ATTTTAGAGTGTGATGGACA	231541	63737	CTTTTATTTTGGTTTCTGAT	276128	108324	GTGGAAGGATCTCTTGAGCT

186955	19151	CATTTTAGAGTGTGATGGAC	231542	63738	CCTTTTATTTTGGTTTCTGA	276129	108325	GGTGGAAGGATCTCTTGAGC
186956	19152	GCATTTTAGAGTGTGATGGA	231543	63739	GCCTTTTATTTTGGTTTCTG	276130	108326	AGGTGGAAGGATCTCTTGAG
186957	19153	AGCATTTTAGAGTGTGATGG	231544	63740	TGCCTTTTATTTTGGTTTCT	276131	108327	GAGGTGGAAGGATCTCTTGA
186958	19154	AAGCATTTTAGAGTGTGATG	231545	63741	TTGCCTTTTATTTTGGTTTC	276132	108328	TGAGGTGGAAGGATCTCTTG
186959	19155	AAAGCATTTTAGAGTGTGAT	231546	63742	GTTGCCTTTTATTTTGGTTT	276133	108329	CTGAGGTGGAAGGATCTCTT
186960	19156	CAAAGCATTTTAGAGTGTGA	231547	63743	GGTTGCCTTTTATTTTGGTT	276134	108330	GCTGAGGTGGAAGGATCTCT
186961	19157	CCAAAGCATTTTAGAGTGTG	231548	63744	TGGTTGCCTTTTATTTTGGT	276135	108331	GGCTGAGGTGGAAGGATCTC
186962	19158	TCCAAAGCATTTTAGAGTGT	231549	63745	TTGGTTGCCTTTTATTTTGG	276136	108332	AGGCTGAGGTGGAAGGATCT
186963	19159	GTCCAAAGCATTTTAGAGTG	231550	63746	GTTGGTTGCCTTTTATTTTG	276137	108333	GAGGCTGAGGTGGAAGGATC
186964	19160	TGTCCAAAGCATTTTAGAGT	231551	63747	AGTTGGTTGCCTTTTATTTT	276138	108334	GGAGGCTGAGGTGGAAGGAT
186965	19161	TTGTCCAAAGCATTTTAGAG	231552	63748	CAGTTGGTTGCCTTTTATTT	276139	108335	AGGAGGCTGAGGTGGAAGGA
186966	19162	CTTGTCCAAAGCATTTTAGA	231553	63749	CCAGTTGGTTGCCTTTTATT	276140	108336	CAGGAGGCTGAGGTGGAAGG
186967	19163	TCTTGTCCAAAGCATTTTAG	231554	63750	TCCAGTTGGTTGCCTTTTAT	276141	108337	TCAGGAGGCTGAGGTGGAAG
186968	19164	TTCTTGTCCAAAGCATTTTA	231555	63751	CTCCAGTTGGTTGCCTTTTA	276142	108338	CTCAGGAGGCTGAGGTGGAA
186969	19165	CTTCTTGTCCAAAGCATTTT	231556	63752	TCTCCAGTTGGTTGCCTTTT	276143	108339	ACTCAGGAGGCTGAGGTGGA
186970	19166	GCTTCTTGTCCAAAGCATTT	231557	63753	TTCTCCAGTTGGTTGCCTTT	276144	108340	TACTCAGGAGGCTGAGGTGG
186971	19167	TGCTTCTTGTCCAAAGCATT	231558	63754	CTTCTCCAGTTGGTTGCCTT	276145	108341	CTACTCAGGAGGCTGAGGTG
186972	19168	TTGCTTCTTGTCCAAAGCAT	231559	63755	TCTTCTCCAGTTGGTTGCCT	276146	108342	ACTACTCAGGAGGCTGAGGT
186973	19169	TTTGCTTCTTGTCCAAAGCA	231560	63756	ATCTTCTCCAGTTGGTTGCC	276147	108343	AACTACTCAGGAGGCTGAGG
186974	19170	ATTTGCTTCTTGTCCAAAGC	231561	63757	TATCTTCTCCAGTTGGTTGC	276148	108344	CAACTACTCAGGAGGCTGAG
186975	19171	CATTTGCTTCTTGTCCAAAG	231562	63758	CTATCTTCTCCAGTTGGTTG	276149	108345	CCAACTACTCAGGAGGCTGA
186976	19172	ACATTTGCTTCTTGTCCAAA	231563	63759	ACTATCTTCTCCAGTTGGTT	276150	108346	CCCAACTACTCAGGAGGCTG
186977	19173	AACATTTGCTTCTTGTCCAA	231564	63760	AACTATCTTCTCCAGTTGGT	276151	108347	TCCCAACTACTCAGGAGGCT
186978	19174	TAACATTTGCTTCTTGTCCA	231565	63761	CAACTATCTTCTCCAGTTGG	276152	108348	GTCCCAACTACTCAGGAGGC
186979	19175	TTAACATTTGCTTCTTGTCC	231566	63762	GCAACTATCTTCTCCAGTTG	276153	108349	GGTCCCAACTACTCAGGAGG
186980	19176	TTTAACATTTGCTTCTTGTC	231567	63763	GGCAACTATCTTCTCCAGTT	276154	108350	TGGTCCCAACTACTCAGGAG
186981	19177	CTTTAACATTTGCTTCTTGT	231568	63764	TGGCAACTATCTTCTCCAGT	276155	108351	GTGGTCCCAACTACTCAGGA
186982	19178	TCTTTAACATTTGCTTCTTG	231569	63765	GTGGCAACTATCTTCTCCAG	276156	108352	TGTGGTCCCAACTACTCAGG
186983	19179	GTCTTTAACATTTGCTTCTT	231570	63766	TGTGGCAACTATCTTCTCCA	276157	108353	CTGTGGTCCCAACTACTCAG
186984	19180	TGTCTTTAACATTTGCTTCT	231571	63767	TTGTGGCAACTATCTTCTCC	276158	108354	CCTGTGGTCCCAACTACTCA
186985	19181	TTGTCTTTAACATTTGCTTC	231572	63768	TTTGTGGCAACTATCTTCTC	276159	108355	GCCTGTGGTCCCAACTACTC
186986	19182	TTTGTCTTTAACATTTGCTT	231573	63769	ATTTGTGGCAACTATCTTCT	276160	108356	AGCCTGTGGTCCCAACTACT
186987	19183	ATTTGTCTTTAACATTTGCT	231574	63770	TATTTGTGGCAACTATCTTC	276161	108357	AAGCCTGTGGTCCCAACTAC
186988	19184	CATTTGTCTTTAACATTTGC	231575	63771	ATATTTGTGGCAACTATCTT	276162	108358	CAAGCCTGTGGTCCCAACTA
186989	19185	ACATTTGTCTTTAACATTTG	231576	63772	CATATTTGTGGCAACTATCT	276163	108359	GCAAGCCTGTGGTCCCAACT
186990	19186	CACATTTGTCTTTAACATTT	231577	63773	TCATATTTGTGGCAACTATC	276164	108360	TGCAAGCCTGTGGTCCCAAC
186991	19187	CCACATTTGTCTTTAACATT	231578	63774	ATCATATTTGTGGCAACTAT	276165	108361	GTGCAAGCCTGTGGTCCCAA
186992	19188	GCCACATTTGTCTTTAACAT	231579	63775	GATCATATTTGTGGCAACTA	276166	108362	GGTGCAAGCCTGTGGTCCCA
186993	19189	GGCCACATTTGTCTTTAACA	231580	63776	TGATCATATTTGTGGCAACT	276167	108363	TGGTGCAAGCCTGTGGTCCC
186994	19190	GGGCCACATTTGTCTTTAAC	231581	63777	TTGATCATATTTGTGGCAAC	276168	108364	GTGGTGCAAGCCTGTGGTCC
186995	19191	TGGGCCACATTTGTCTTTAA	231582	63778	CTTGATCATATTTGTGGCAA	276169	108365	TGTGGTGCAAGCCTGTGGTC
186996	19192	ATGGGCCACATTTGTCTTTA	231583	63779	CCTTGATCATATTTGTGGCA	276170	108366	CTGTGGTGCAAGCCTGTGGT
186997	19193	AATGGGCCACATTTGTCTTT	231584	63780	CCCTTGATCATATTTGTGGC	276171	108367	ACTGTGGTGCAAGCCTGTGG
186998	19194	AAATGGGCCACATTTGTCTT	231585	63781	ACCCTTGATCATATTTGTGG	276172	108368	CACTGTGGTGCAAGCCTGTG
186999	19195	AAAATGGGCCACATTTGTCT	231586	63782	AACCCTTGATCATATTTGTG	276173	108369	GCACTGTGGTGCAAGCCTGT
187000	19196	GAAAATGGGCCACATTTGTC	231587	63783	TAACCCTTGATCATATTTGT	276174	108370	GGCACTGTGGTGCAAGCCTG
187001	19197	GGAAAATGGGCCACATTTGT	231588	63784	TTAACCCTTGATCATATTTG	276175	108371	GGGCACTGTGGTGCAAGCCT
187002	19198	AGGAAAATGGGCCACATTTG	231589	63785	ATTAACCCTTGATCATATTT	276176	108372	TGGGCACTGTGGTGCAAGCC
187003	19199	CAGGAAAATGGGCCACATTT	231590	63786	CATTAACCCTTGATCATATT	276177	108373	TTGGGCACTGTGGTGCAAGC
187004	19200	ACAGGAAAATGGGCCACATT	231591	63787	ACATTAACCCTTGATCATAT	276178	108374	GTTGGGCACTGTGGTGCAAG
187005	19201	TACAGGAAAATGGGCCACAT	231592	63788	AACATTAACCCTTGATCATA	276179	108375	AGTTGGGCACTGTGGTGCAA
187006	19202	GTACAGGAAAATGGGCCACA	231593	63789	TAACATTAACCCTTGATCAT	276180	108376	TAGTTGGGCACTGTGGTGCA
187007	19203	TGTACAGGAAAATGGGCCAC	231594	63790	ATAACATTAACCCTTGATCA	276181	108377	TTAGTTGGGCACTGTGGTGC
187008	19204	TTGTACAGGAAAATGGGCCA	231595	63791	AATAACATTAACCCTTGATC	276182	108378	ATTAGTTGGGCACTGTGGTG
187009	19205	TTTGTACAGGAAAATGGGCC	231596	63792	GAATAACATTAACCCTTGAT	276183	108379	AATTAGTTGGGCACTGTGGT
187010	19206	CTTTGTACAGGAAAATGGGC	231597	63793	TGAATAACATTAACCCTTGA	276184	108380	AAATTAGTTGGGCACTGTGG
187011	19207	TCTTTGTACAGGAAAATGGG	231598	63794	ATGAATAACATTAACCCTTG	276185	108381	GAAATTAGTTGGGCACTGTG
187012	19208	CTCTTTGTACAGGAAAATGG	231599	63795	TATGAATAACATTAACCCTT	276186	108382	AGAAATTAGTTGGGCACTGT
187013	19209	CCTCTTTGTACAGGAAAATG	231600	63796	TTATGAATAACATTAACCCT	276187	108383	AAGAAATTAGTTGGGCACTG
187014	19210	CCCTCTTTGTACAGGAAAAT	231601	63797	TTTATGAATAACATTAACCC	276188	108384	TAAGAAATTAGTTGGGCACT
187015	19211	GCCCTCTTTGTACAGGAAAA	231602	63798	ATTTATGAATAACATTAACC	276189	108385	ATAAGAAATTAGTTGGGCAC
187016	19212	AGCCCTCTTTGTACAGGAAA	231603	63799	AATTTATGAATAACATTAAC	276190	108386	TATAAGAAATTAGTTGGGCA
187017	19213	CAGCCCTCTTTGTACAGGAA	231604	63800	TAATTTATGAATAACATTAA	276191	108387	ATATAAGAAATTAGTTGGGC
187018	19214	GCAGCCCTCTTTGTACAGGA	231605	63801	TTAATTTATGAATAACATTA	276192	108388	AATATAAGAAATTAGTTGGG
187019	19215	AGCAGCCCTCTTTGTACAGG	231606	63802	CTTAATTTATGAATAACATT	276193	108389	AAATATAAGAAATTAGTTGG
187020	19216	GAGCAGCCCTCTTTGTACAG	231607	63803	TCTTAATTTATGAATAACAT	276194	108390	AAAATATAAGAAATTAGTTG
187021	19217	GGAGCAGCCCTCTTTGTACA	231608	63804	CTCTTAATTTATGAATAACA	276195	108391	AAAAATATAAGAAATTAGTT
187022	19218	GGGAGCAGCCCTCTTTGTAC	231609	63805	GCTCTTAATTTATGAATAAC	276196	108392	AAAAAATATAAGAAATTAGT
187023	19219	TGGGAGCAGCCCTCTTTGTA	231610	63806	GGCTCTTAATTTATGAATAA	276197	108393	CAAAAAATATAAGAAATTAG
187024	19220	ATGGGAGCAGCCCTCTTTGT	231611	63807	GGGCTCTTAATTTATGAATA	276198	108394	ACAAAAAATATAAGAAATTA
187025	19221	CATGGGAGCAGCCCTCTTTG	231612	63808	TGGGCTCTTAATTTATGAAT	276199	108395	TACAAAAAATATAAGAAATT
187026	19222	GCATGGGAGCAGCCCTCTTT	231613	63809	GTGGGCTCTTAATTTATGAA	276200	108396	CTACAAAAAATATAAGAAAT

187027	19223	GGCATGGGAGCAGCCCTCTT	231614	63810	TGTGGGCTCTTAATTTATGA	276201	108397	TCTACAAAAAATATAAGAAA
187028	19224	TGGCATGGGAGCAGCCCTCT	231615	63811	GTGTGGGCTCTTAATTTATG	276202	108398	CTCTACAAAAAATATAAGAA
187029	19225	CTGGCATGGGAGCAGCCCTC	231616	63812	TGTGTGGGCTCTTAATTTAT	276203	108399	TCTCTACAAAAAATATAAGA
187030	19226	CCTGGCATGGGAGCAGCCCT	231617	63813	TTGTGTGGGCTCTTAATTTA	276204	108400	ATCTCTACAAAAAATATAAG
187031	19227	GCCTGGCATGGGAGCAGCCC	231618	63814	CTTGTGTGGGCTCTTAATTT	276205	108401	CATCTCTACAAAAAATATAA
187032	19228	AGCCTGGCATGGGAGCAGCC	231619	63815	ACTTGTGTGGGCTCTTAATT	276206	108402	CCATCTCTACAAAAAATATA
187033	19229	TAGCCTGGCATGGGAGCAGC	231620	63816	GACTTGTGTGGGCTCTTAAT	276207	108403	CCCATCTCTACAAAAAATAT
187034	19230	ATAGCCTGGCATGGGAGCAG	231621	63817	TGACTTGTGTGGGCTCTTAA	276208	108404	CCCCATCTCTACAAAAAATA
187035	19231	AATAGCCTGGCATGGGAGCA	231622	63818	ATGACTTGTGTGGGCTCTTA	276209	108405	ACCCCATCTCTACAAAAAAT
187036	19232	CAATAGCCTGGCATGGGAGC	231623	63819	AATGACTTGTGTGGGCTCTT	276210	108406	AACCCCATCTCTACAAAAAA
187037	19233	CCAATAGCCTGGCATGGGAG	231624	63820	TAATGACTTGTGTGGGCTCT	276211	108407	AAACCCCATCTCTACAAAAA
187038	19234	GCCAATAGCCTGGCATGGGA	231625	63821	CTAATGACTTGTGTGGGCTC	276212	108408	GAAACCCCATCTCTACAAAA
187039	19235	TGCCAATAGCCTGGCATGGG	231626	63822	TCTAATGACTTGTGTGGGCT	276213	108409	TGAAACCCCATCTCTACAAA
187040	19236	GTGCCAATAGCCTGGCATGG	231627	63823	TTCTAATGACTTGTGTGGGC	276214	108410	GTGAAACCCCATCTCTACAA
187041	19237	AGTGCCAATAGCCTGGCATG	231628	63824	ATTCTAATGACTTGTGTGGG	276215	108411	AGTGAAACCCCATCTCTACA
187042	19238	CAGTGCCAATAGCCTGGCAT	231629	63825	TATTCTAATGACTTGTGTGG	276216	108412	CAGTGAAACCCCATCTCTAC
187043	19239	CCAGTGCCAATAGCCTGGCA	231630	63826	TTATTCTAATGACTTGTGTG	276217	108413	ACAGTGAAACCCCATCTCTA
187044	19240	ACCAGTGCCAATAGCCTGGC	231631	63827	CTTATTCTAATGACTTGTGT	276218	108414	CACAGTGAAACCCCATCTCT
187045	19241	CACCAGTGCCAATAGCCTGG	231632	63828	GCTTATTCTAATGACTTGTG	276219	108415	ACACAGTGAAACCCCATCTC
187046	19242	CCACCAGTGCCAATAGCCTG	231633	63829	TGCTTATTCTAATGACTTGT	276220	108416	GACACAGTGAAACCCCATCT
187047	19243	CCCACCAGTGCCAATAGCCT	231634	63830	GTGCTTATTCTAATGACTTG	276221	108417	CGACACAGTGAAACCCCATC
187048	19244	GCCCACCAGTGCCAATAGCC	231635	63831	AGTGCTTATTCTAATGACTT	276222	108418	GCGACACAGTGAAACCCCAT
187049	19245	TGCCCACCAGTGCCAATAGC	231636	63832	CAGTGCTTATTCTAATGACT	276223	108419	GGCGACACAGTGAAACCCCA
187050	19246	ATGCCCACCAGTGCCAATAG	231637	63833	TCAGTGCTTATTCTAATGAC	276224	108420	GGGCGACACAGTGAAACCCC
187051	19247	CATGCCCACCAGTGCCAATA	231638	63834	CTCAGTGCTTATTCTAATGA	276225	108421	TGGGCGACACAGTGAAACCC
187052	19248	TCATGCCCACCAGTGCCAAT	231639	63835	TCTCAGTGCTTATTCTAATG	276226	108422	CTGGGCGACACAGTGAAACC
187053	19249	CTCATGCCCACCAGTGCCAA	231640	63836	GTCTCAGTGCTTATTCTAAT	276227	108423	CCTGGGCGACACAGTGAAAC
187054	19250	CCTCATGCCCACCAGTGCCA	231641	63837	GGTCTCAGTGCTTATTCTAA	276228	108424	TCCTGGGCGACACAGTGAAA
187055	19251	GCCTCATGCCCACCAGTGCC	231642	63838	AGGTCTCAGTGCTTATTCTA	276229	108425	ATCCTGGGCGACACAGTGAA
187056	19252	AGCCTCATGCCCACCAGTGC	231643	63839	CAGGTCTCAGTGCTTATTCT	276230	108426	CATCCTGGGCGACACAGTGA
187057	19253	AAGCCTCATGCCCACCAGTG	231644	63840	TCAGGTCTCAGTGCTTATTC	276231	108427	CCATCCTGGGCGACACAGTG
187058	19254	GAAGCCTCATGCCCACCAGT	231645	63841	TTCAGGTCTCAGTGCTTATT	276232	108428	ACCATCCTGGGCGACACAGT
187059	19255	AGAAGCCTCATGCCCACCAG	231646	63842	GTTCAGGTCTCAGTGCTTAT	276233	108429	GACCATCCTGGGCGACACAG
187060	19256	GAGAAGCCTCATGCCCACCA	231647	63843	TGTTCAGGTCTCAGTGCTTA	276234	108430	AGACCATCCTGGGCGACACA
187061	19257	AGAGAAGCCTCATGCCCACC	231648	63844	CTGTTCAGGTCTCAGTGCTT	276235	108431	AAGACCATCCTGGGCGACAC
187062	19258	CAGAGAAGCCTCATGCCCAC	231649	63845	TCTGTTCAGGTCTCAGTGCT	276236	108432	CAAGACCATCCTGGGCGACA
187063	19259	GCAGAGAAGCCTCATGCCCA	231650	63846	GTCTGTTCAGGTCTCAGTGC	276237	108433	TCAAGACCATCCTGGGCGAC
187064	19260	AGCAGAGAAGCCTCATGCCC	231651	63847	TGTCTGTTCAGGTCTCAGTG	276238	108434	TTCAAGACCATCCTGGGCGA
187065	19261	CAGCAGAGAAGCCTCATGCC	231652	63848	TTGTCTGTTCAGGTCTCAGT	276239	108435	GTTCAAGACCATCCTGGGCG
187066	19262	GCAGCAGAGAAGCCTCATGC	231653	63849	CTTGTCTGTTCAGGTCTCAG	276240	108436	AGTTCAAGACCATCCTGGGC
187067	19263	GGCAGCAGAGAAGCCTCATG	231654	63850	GCTTGTCTGTTCAGGTCTCA	276241	108437	GAGTTCAAGACCATCCTGGG
187068	19264	GGGCAGCAGAGAAGCCTCAT	231655	63851	TGCTTGTCTGTTCAGGTCTC	276242	108438	GGAGTTCAAGACCATCCTGG
187069	19265	AGGGCAGCAGAGAAGCCTCA	231656	63852	TTGCTTGTCTGTTCAGGTCT	276243	108439	AGGAGTTCAAGACCATCCTG
187070	19266	CAGGGCAGCAGAGAAGCCTC	231657	63853	TTTGCTTGTCTGTTCAGGTC	276244	108440	CAGGAGTTCAAGACCATCCT
187071	19267	CCAGGGCAGCAGAGAAGCCT	231658	63854	TTTTGCTTGTCTGTTCAGGT	276245	108441	CCAGGAGTTCAAGACCATCC
187072	19268	GCCAGGGCAGCAGAGAAGCC	231659	63855	TTTTTGCTTGTCTGTTCAGG	276246	108442	CCCAGGAGTTCAAGACCATC
187073	19269	GGCCAGGGCAGCAGAGAAGC	231660	63856	CTTTTTGCTTGTCTGTTCAG	276247	108443	GCCCAGGAGTTCAAGACCAT
187074	19270	CGGCCAGGGCAGCAGAGAAG	231661	63857	TCTTTTTGCTTGTCTGTTCA	276248	108444	AGCCCAGGAGTTCAAGACCA
187075	19271	CCGGCCAGGGCAGCAGAGAA	231662	63858	TTCTTTTTGCTTGTCTGTTC	276249	108445	GAGCCCAGGAGTTCAAGACC
187076	19272	CCCGGCCAGGGCAGCAGAGA	231663	63859	ATTCTTTTTGCTTGTCTGTT	276250	108446	TGAGCCCAGGAGTTCAAGAC
187077	19273	CCCCGGCCAGGGCAGCAGAG	231664	63860	CATTCTTTTTGCTTGTCTGT	276251	108447	TTGAGCCCAGGAGTTCAAGA
187078	19274	CCCCCGGCCAGGGCAGCAGA	231665	63861	TCATTCTTTTTGCTTGTCTG	276252	108448	CTTGAGCCCAGGAGTTCAAG
187079	19275	CCCCCCGGCCAGGGCAGCAG	231666	63862	CTCATTCTTTTTGCTTGTCT	276253	108449	ACTTGAGCCCAGGAGTTCAA
187080	19276	ACCCCCCGGCCAGGGCAGCA	231667	63863	TCTCATTCTTTTTGCTTGTC	276254	108450	CACTTGAGCCCAGGAGTTCA
187081	19277	AACCCCCCGGCCAGGGCAGC	231668	63864	CTCTCATTCTTTTTGCTTGT	276255	108451	TCACTTGAGCCCAGGAGTTC
187082	19278	GAACCCCCCGGCCAGGGCAG	231669	63865	ACTCTCATTCTTTTTGCTTG	276256	108452	ATCACTTGAGCCCAGGAGTT
187083	19279	AGAACCCCCCGGCCAGGGCA	231670	63866	CACTCTCATTCTTTTTGCTT	276257	108453	GATCACTTGAGCCCAGGAGT
187084	19280	GAGAACCCCCCGGCCAGGGC	231671	63867	CCACTCTCATTCTTTTTGCT	276258	108454	GGATCACTTGAGCCCAGGAG
187085	19281	AGAGAACCCCCCGGCCAGGG	231672	63868	CCCACTCTCATTCTTTTTGC	276259	108455	AGGATCACTTGAGCCCAGGA
187086	19282	GAGAGAACCCCCCGGCCAGG	231673	63869	ACCCACTCTCATTCTTTTTG	276260	108456	GAGGATCACTTGAGCCCAGG
187087	19283	TGAGAGAACCCCCCGGCCAG	231674	63870	GACCCACTCTCATTCTTTTT	276261	108457	GGAGGATCACTTGAGCCCAG
187088	19284	GTGAGAGAACCCCCCGGCCA	231675	63871	CGACCCACTCTCATTCTTTT	276262	108458	AGGAGGATCACTTGAGCCCA
187089	19285	AGTGAGAGAACCCCCCGGCC	231676	63872	CCGACCCACTCTCATTCTTT	276263	108459	CAGGAGGATCACTTGAGCCC
187090	19286	GAGTGAGAGAACCCCCCGGC	231677	63873	GCCGACCCACTCTCATTCTT	276264	108460	GCAGGAGGATCACTTGAGCC
187091	19287	TGAGTGAGAGAACCCCCCGG	231678	63874	CGCCGACCCACTCTCATTCT	276265	108461	GGCAGGAGGATCACTTGAGC
187092	19288	GTGAGTGAGAGAACCCCCCG	231679	63875	GCGCCGACCCACTCTCATTC	276266	108462	AGGCAGGAGGATCACTTGAG
187093	19289	GGTGAGTGAGAGAACCCCCC	231680	63876	CGCGCCGACCCACTCTCATT	276267	108463	GAGGCAGGAGGATCACTTGA
187094	19290	TGGTGAGTGAGAGAACCCCC	231681	63877	CCGCGCCGACCCACTCTCAT	276268	108464	TGAGGCAGGAGGATCACTTG
187095	19291	ATGGTGAGTGAGAGAACCCC	231682	63878	GCCGCGCCGACCCACTCTCA	276269	108465	CTGAGGCAGGAGGATCACTT
187096	19292	AATGGTGAGTGAGAGAACCC	231683	63879	CGCCGCGCCGACCCACTCTC	276270	108466	GCTGAGGCAGGAGGATCACT
187097	19293	CAATGGTGAGTGAGAGAACC	231684	63880	CCGCCGCGCCGACCCACTCT	276271	108467	GGCTGAGGCAGGAGGATCAC
187098	19294	CCAATGGTGAGTGAGAGAAC	231685	63881	GCCGCCGCGCCGACCCACTC	276272	108468	AGGCTGAGGCAGGAGGATCA

187099	19295	GCCAATGGTGAGTGAGAGAA	231686	63882	AGCCGCCGCGCCGACCCACT	276273	108469	GAGGCTGAGGCAGGAGGATC
187100	19296	AGCCAATGGTGAGTGAGAGA	231687	63883	GAGCCGCCGCGCCGACCCAC	276274	108470	CGAGGCTGAGGCAGGAGGAT
187101	19297	GAGCCAATGGTGAGTGAGAG	231688	63884	TGAGCCGCCGCGCCGACCCA	276275	108471	GCGAGGCTGAGGCAGGAGGA
187102	19298	AGAGCCAATGGTGAGTGAGA	231689	63885	ATGAGCCGCCGCGCCGACCC	276276	108472	TGCGAGGCTGAGGCAGGAGG
187103	19299	GAGAGCCAATGGTGAGTGAG	231690	63886	CATGAGCCGCCGCGCCGACC	276277	108473	TTGCGAGGCTGAGGCAGGAG
187104	19300	AGAGAGCCAATGGTGAGTGA	231691	63887	GCATGAGCCGCCGCGCCGAC	276278	108474	TTTGCGAGGCTGAGGCAGGA
187105	19301	CAGAGAGCCAATGGTGAGTG	231692	63888	GGCATGAGCCGCCGCGCCGA	276279	108475	ATTTGCGAGGCTGAGGCAGG
187106	19302	TCAGAGAGCCAATGGTGAGT	231693	63889	AGGCATGAGCCGCCGCGCCG	276280	108476	AATTTGCGAGGCTGAGGCAG
187107	19303	GTCAGAGAGCCAATGGTGAG	231694	63890	CAGGCATGAGCCGCCGCGCC	276281	108477	CAATTTGCGAGGCTGAGGCA
187108	19304	TGTCAGAGAGCCAATGGTGA	231695	63891	ACAGGCATGAGCCGCCGCGC	276282	108478	GCAATTTGCGAGGCTGAGGC
187109	19305	GTGTCAGAGAGCCAATGGTG	231696	63892	TACAGGCATGAGCCGCCGCG	276283	108479	AGCAATTTGCGAGGCTGAGG
187110	19306	GGTGTCAGAGAGCCAATGGT	231697	63893	TTACAGGCATGAGCCGCCGC	276284	108480	CAGCAATTTGCGAGGCTGAG
187111	19307	AGGTGTCAGAGAGCCAATGG	231698	63894	ATTACAGGCATGAGCCGCCG	276285	108481	CCAGCAATTTGCGAGGCTGA
187112	19308	CAGGTGTCAGAGAGCCAATG	231699	63895	GATTACAGGCATGAGCCGCC	276286	108482	CCCAGCAATTTGCGAGGCTG
187113	19309	CCAGGTGTCAGAGAGCCAAT	231700	63896	GGATTACAGGCATGAGCCGC	276287	108483	TCCCAGCAATTTGCGAGGCT
187114	19310	TCCAGGTGTCAGAGAGCCAA	231701	63897	GGGATTACAGGCATGAGCCG	276288	108484	ATCCCAGCAATTTGCGAGGC
187115	19311	CTCCAGGTGTCAGAGAGCCA	231702	63898	TGGGATTACAGGCATGAGCC	276289	108485	AATCCCAGCAATTTGCGAGG
187116	19312	TCTCCAGGTGTCAGAGAGCC	231703	63899	CTGGGATTACAGGCATGAGC	276290	108486	TAATCCCAGCAATTTGCGAG
187117	19313	CTCTCCAGGTGTCAGAGAGC	231704	63900	GCTGGGATTACAGGCATGAG	276291	108487	GTAATCCCAGCAATTTGCGA
187118	19314	TCTCTCCAGGTGTCAGAGAG	231705	63901	TGCTGGGATTACAGGCATGA	276292	108488	TGTAATCCCAGCAATTTGCG
187119	19315	GTCTCTCCAGGTGTCAGAGA	231706	63902	GTGCTGGGATTACAGGCATG	276293	108489	CTGTAATCCCAGCAATTTGC
187120	19316	GGTCTCTCCAGGTGTCAGAG	231707	63903	AGTGCTGGGATTACAGGCAT	276294	108490	CCTGTAATCCCAGCAATTTG
187121	19317	TGGTCTCTCCAGGTGTCAGA	231708	63904	AAGTGCTGGGATTACAGGCA	276295	108491	ACCTGTAATCCCAGCAATTT
187122	19318	GTGGTCTCTCCAGGTGTCAG	231709	63905	AAAGTGCTGGGATTACAGGC	276296	108492	CACCTGTAATCCCAGCAATT
187123	19319	GGTGGTCTCTCCAGGTGTCA	231710	63906	CAAAGTGCTGGGATTACAGG	276297	108493	ACACCTGTAATCCCAGCAAT
187124	19320	TGGTGGTCTCTCCAGGTGTC	231711	63907	CCAAAGTGCTGGGATTACAG	276298	108494	CACACCTGTAATCCCAGCAA
187125	19321	GTGGTGGTCTCTCCAGGTGT	231712	63908	TCCAAAGTGCTGGGATTACA	276299	108495	TCACACCTGTAATCCCAGCA
187126	19322	GGTGGTGGTCTCTCCAGGTG	231713	63909	TTCCAAAGTGCTGGGATTAC	276300	108496	CTCACACCTGTAATCCCAGC
187127	19323	GGGTGGTGGTCTCTCCAGGT	231714	63910	CTTCCAAAGTGCTGGGATTA	276301	108497	GCTCACACCTGTAATCCCAG
187128	19324	AGGGTGGTGGTCTCTCCAGG	231715	63911	CCTTCCAAAGTGCTGGGATT	276302	108498	GGCTCACACCTGTAATCCCA
187129	19325	AAGGGTGGTGGTCTCTCCAG	231716	63912	GCCTTCCAAAGTGCTGGGAT	276303	108499	TGGCTCACACCTGTAATCCC
187130	19326	CAAGGGTGGTGGTCTCTCCA	231717	63913	AGCCTTCCAAAGTGCTGGGA	276304	108500	GTGGCTCACACCTGTAATCC
187131	19327	CCAAGGGTGGTGGTCTCTCC	231718	63914	CAGCCTTCCAAAGTGCTGGG	276305	108501	GGTGGCTCACACCTGTAATC
187132	19328	CCCAAGGGTGGTGGTCTCTC	231719	63915	TCAGCCTTCCAAAGTGCTGG	276306	108502	TGGTGGCTCACACCTGTAAT
187133	19329	GCCCAAGGGTGGTGGTCTCT	231720	63916	TTCAGCCTTCCAAAGTGCTG	276307	108503	ATGGTGGCTCACACCTGTAA
187134	19330	AGCCCAAGGGTGGTGGTCTC	231721	63917	CTTCAGCCTTCCAAAGTGCT	276308	108504	CATGGTGGCTCACACCTGTA
187135	19331	AAGCCCAAGGGTGGTGGTCT	231722	63918	GCTTCAGCCTTCCAAAGTGC	276309	108505	GCATGGTGGCTCACACCTGT
187136	19332	AAAGCCCAAGGGTGGTGGTC	231723	63919	TGCTTCAGCCTTCCAAAGTG	276310	108506	GGCATGGTGGCTCACACCTG
187137	19333	GAAAGCCCAAGGGTGGTGGT	231724	63920	CTGCTTCAGCCTTCCAAAGT	276311	108507	GGGCATGGTGGCTCACACCT
187138	19334	TGAAAGCCCAAGGGTGGTGG	231725	63921	CCTGCTTCAGCCTTCCAAAG	276312	108508	CGGGCATGGTGGCTCACACC
187139	19335	ATGAAAGCCCAAGGGTGGTG	231726	63922	GCCTGCTTCAGCCTTCCAAA	276313	108509	TCGGGCATGGTGGCTCACAC
187140	19336	CATGAAAGCCCAAGGGTGGT	231727	63923	CGCCTGCTTCAGCCTTCCAA	276314	108510	GTCGGGCATGGTGGCTCACA
187141	19337	TCATGAAAGCCCAAGGGTGG	231728	63924	CCGCCTGCTTCAGCCTTCCA	276315	108511	GGTCGGGCATGGTGGCTCAC
187142	19338	ATCATGAAAGCCCAAGGGTG	231729	63925	TCCGCCTGCTTCAGCCTTCC	276316	108512	AGGTCGGGCATGGTGGCTCA
187143	19339	CATCATGAAAGCCCAAGGGT	231730	63926	ATCCGCCTGCTTCAGCCTTC	276317	108513	AAGGTCGGGCATGGTGGCTC
187144	19340	GCATCATGAAAGCCCAAGGG	231731	63927	GATCCGCCTGCTTCAGCCTT	276318	108514	GAAGGTCGGGCATGGTGGCT
187145	19341	AGCATCATGAAAGCCCAAGG	231732	63928	TGATCCGCCTGCTTCAGCCT	276319	108515	AGAAGGTCGGGCATGGTGGC
187146	19342	GAGCATCATGAAAGCCCAAG	231733	63929	GTGATCCGCCTGCTTCAGCC	276320	108516	GAGAAGGTCGGGCATGGTGG
187147	19343	TGAGCATCATGAAAGCCCAA	231734	63930	AGTGATCCGCCTGCTTCAGC	276321	108517	AGAGAAGGTCGGGCATGGTG
187148	19344	GTGAGCATCATGAAAGCCCA	231735	63931	AAGTGATCCGCCTGCTTCAG	276322	108518	AAGAGAAGGTCGGGCATGGT
187149	19345	TGTGAGCATCATGAAAGCCC	231736	63932	CAAGTGATCCGCCTGCTTCA	276323	108519	AAAGAGAAGGTCGGGCATGG
187150	19346	CTGTGAGCATCATGAAAGCC	231737	63933	TCAAGTGATCCGCCTGCTTC	276324	108520	AAAAGAGAAGGTCGGGCATG
187151	19347	TCTGTGAGCATCATGAAAGC	231738	63934	ATCAAGTGATCCGCCTGCTT	276325	108521	AAAAAGAGAAGGTCGGGCAT
187152	19348	TTCTGTGAGCATCATGAAAG	231739	63935	GATCAAGTGATCCGCCTGCT	276326	108522	TAAAAAGAGAAGGTCGGGCA
187153	19349	ATTCTGTGAGCATCATGAAA	231740	63936	GGATCAAGTGATCCGCCTGC	276327	108523	TTAAAAAGAGAAGGTCGGGC
187154	19350	GATTCTGTGAGCATCATGAA	231741	63937	GGGATCAAGTGATCCGCCTG	276328	108524	CTTAAAAAGAGAAGGTCGGG
187155	19351	GGATTCTGTGAGCATCATGA	231742	63938	TGGGATCAAGTGATCCGCCT	276329	108525	CCTTAAAAAGAGAAGGTCGG
187156	19352	TGGATTCTGTGAGCATCATG	231743	63939	CTGGGATCAAGTGATCCGCC	276330	108526	CCCTTAAAAAGAGAAGGTCG
187157	19353	GTGGATTCTGTGAGCATCAT	231744	63940	CCTGGGATCAAGTGATCCGC	276331	108527	GCCCTTAAAAAGAGAAGGTC
187158	19354	TGTGGATTCTGTGAGCATCA	231745	63941	TCCTGGGATCAAGTGATCCG	276332	108528	CGCCCTTAAAAAGAGAAGGT
187159	19355	GTGTGGATTCTGTGAGCATC	231746	63942	CTCCTGGGATCAAGTGATCC	276333	108529	ACGCCCTTAAAAAGAGAAGG
187160	19356	AGTGTGGATTCTGTGAGCAT	231747	63943	ACTCCTGGGATCAAGTGATC	276334	108530	CACGCCCTTAAAAAGAGAAG
187161	19357	CAGTGTGGATTCTGTGAGCA	231748	63944	AACTCCTGGGATCAAGTGAT	276335	108531	ACACGCCCTTAAAAAGAGAA
187162	19358	ACAGTGTGGATTCTGTGAGC	231749	63945	GAACTCCTGGGATCAAGTGA	276336	108532	CACACGCCCTTAAAAAGAGA
187163	19359	AACAGTGTGGATTCTGTGAG	231750	63946	GGAACTCCTGGGATCAAGTG	276337	108533	ACACACGCCCTTAAAAAGAG
187164	19360	CAACAGTGTGGATTCTGTGA	231751	63947	TGGAACTCCTGGGATCAAGT	276338	108534	CACACACGCCCTTAAAAAGA
187165	19361	CCAACAGTGTGGATTCTGTG	231752	63948	TTGGAACTCCTGGGATCAAG	276339	108535	ACACACACGCCCTTAAAAAG
187166	19362	TCCAACAGTGTGGATTCTGT	231753	63949	GTTGGAACTCCTGGGATCAA	276340	108536	CACACACACGCCCTTAAAAA
187167	19363	CTCCAACAGTGTGGATTCTG	231754	63950	TGTTGGAACTCCTGGGATCA	276341	108537	ACACACACACGCCCTTAAAA
187168	19364	GCTCCAACAGTGTGGATTCT	231755	63951	GTGTTGGAACTCCTGGGATC	276342	108538	CACACACACACGCCCTTAAA
187169	19365	AGCTCCAACAGTGTGGATTC	231756	63952	GGTGTTGGAACTCCTGGGAT	276343	108539	ACACACACACACGCCCTTAA
187170	19366	AAGCTCCAACAGTGTGGATT	231757	63953	TGGTGTTGGAACTCCTGGGA	276344	108540	CACACACACACACGCCCTTA

187171	19367	AAAGCTCCAACAGTGTGGAT	231758	63954	CTGGTGTTGGAACTCCTGGG	276345	108541	ACACACACACACACGCCCTT
187172	19368	TAAAGCTCCAACAGTGTGGA	231759	63955	GCTGGTGTTGGAACTCCTGG	276346	108542	CACACACACACACACGCCCT
187173	19369	TTAAAGCTCCAACAGTGTGG	231760	63956	GGCTGGTGTTGGAACTCCTG	276347	108543	ACACACACACACACACGCCC
187174	19370	CTTAAAGCTCCAACAGTGTG	231761	63957	AGGCTGGTGTTGGAACTCCT	276348	108544	CACACACACACACACACGCC
187175	19371	CCTTAAAGCTCCAACAGTGT	231762	63958	CAGGCTGGTGTTGGAACTCC	276349	108545	ACACACACACACACACACGC
187176	19372	TCCTTAAAGCTCCAACAGTG	231763	63959	TCAGGCTGGTGTTGGAACTC	276350	108546	CACACACACACACACACACG
187177	19373	CTCCTTAAAGCTCCAACAGT	231764	63960	CTCAGGCTGGTGTTGGAACT	276351	108547	ACACACACACACACACACAC
187178	19374	GCTCCTTAAAGCTCCAACAG	231765	63961	GCTCAGGCTGGTGTTGGAAC	276352	108548	CACACACACACACACACACA
187179	19375	GGCTCCTTAAAGCTCCAACA	231766	63962	TGCTCAGGCTGGTGTTGGAA	276353	108549	ACACACACACACACACACAC
187180	19376	AGGCTCCTTAAAGCTCCAAC	231767	63963	TTGCTCAGGCTGGTGTTGGA	276354	108550	CACACACACACACACACACA
187181	19377	CAGGCTCCTTAAAGCTCCAA	231768	63964	GTTGCTCAGGCTGGTGTTGG	276355	108551	CCACACACACACACACACAC
187182	19378	CCAGGCTCCTTAAAGCTCCA	231769	63965	TGTTGCTCAGGCTGGTGTTG	276356	108552	CCCACACACACACACACACA
187183	19379	TCCAGGCTCCTTAAAGCTCC	231770	63966	ATGTTGCTCAGGCTGGTGTT	276357	108553	GCCCACACACACACACACAC
187184	19380	ATCCAGGCTCCTTAAAGCTC	231771	63967	CATGTTGCTCAGGCTGGTGT	276358	108554	CGCCCACACACACACACACA
187185	19381	GATCCAGGCTCCTTAAAGCT	231772	63968	CCATGTTGCTCAGGCTGGTG	276359	108555	GCGCCCACACACACACACAC
187186	19382	TGATCCAGGCTCCTTAAAGC	231773	63969	ACCATGTTGCTCAGGCTGGT	276360	108556	TGCGCCCACACACACACACA
187187	19383	TTGATCCAGGCTCCTTAAAG	231774	63970	CACCATGTTGCTCAGGCTGG	276361	108557	GTGCGCCCACACACACACAC
187188	19384	GTTGATCCAGGCTCCTTAAA	231775	63971	TCACCATGTTGCTCAGGCTG	276362	108558	AGTGCGCCCACACACACACA
187189	19385	AGTTGATCCAGGCTCCTTAA	231776	63972	TTCACCATGTTGCTCAGGCT	276363	108559	GAGTGCGCCCACACACACAC
187190	19386	CAGTTGATCCAGGCTCCTTA	231777	63973	TTTCACCATGTTGCTCAGGC	276364	108560	AGAGTGCGCCCACACACACA
187191	19387	CCAGTTGATCCAGGCTCCTT	231778	63974	GTTTCACCATGTTGCTCAGG	276365	108561	GAGAGTGCGCCCACACACAC
187192	19388	TCCAGTTGATCCAGGCTCCT	231779	63975	GGTTTCACCATGTTGCTCAG	276366	108562	CGAGAGTGCGCCCACACACA
187193	19389	TTCCAGTTGATCCAGGCTCC	231780	63976	GGGTTTCACCATGTTGCTCA	276367	108563	ACGAGAGTGCGCCCACACAC
187194	19390	GTTCCAGTTGATCCAGGCTC	231781	63977	AGGGTTTCACCATGTTGCTC	276368	108564	GACGAGAGTGCGCCCACACA
187195	19391	TGTTCCAGTTGATCCAGGCT	231782	63978	CAGGGTTTCACCATGTTGCT	276369	108565	AGACGAGAGTGCGCCCACAC
187196	19392	CTGTTCCAGTTGATCCAGGC	231783	63979	GCAGGGTTTCACCATGTTGC	276370	108566	AAGACGAGAGTGCGCCCACA
187197	19393	CCTGTTCCAGTTGATCCAGG	231784	63980	GGCAGGGTTTCACCATGTTG	276371	108567	GAAGACGAGAGTGCGCCCAC
187198	19394	GCCTGTTCCAGTTGATCCAG	231785	63981	AGGCAGGGTTTCACCATGTT	276372	108568	TGAAGACGAGAGTGCGCCCA
187199	19395	TGCCTGTTCCAGTTGATCCA	231786	63982	GAGGCAGGGTTTCACCATGT	276373	108569	GTGAAGACGAGAGTGCGCCC
187200	19396	CTGCCTGTTCCAGTTGATCC	231787	63983	AGAGGCAGGGTTTCACCATG	276374	108570	GGTGAAGACGAGAGTGCGCC
187201	19397	CCTGCCTGTTCCAGTTGATC	231788	63984	TAGAGGCAGGGTTTCACCAT	276375	108571	AGGTGAAGACGAGAGTGCGC
187202	19398	CCCTGCCTGTTCCAGTTGAT	231789	63985	GTAGAGGCAGGGTTTCACCA	276376	108572	AAGGTGAAGACGAGAGTGCG
187203	19399	TCCCTGCCTGTTCCAGTTGA	231790	63986	TGTAGAGGCAGGGTTTCACC	276377	108573	GAAGGTGAAGACGAGAGTGC
187204	19400	CTCCCTGCCTGTTCCAGTTG	231791	63987	TTGTAGAGGCAGGGTTTCAC	276378	108574	GGAAGGTGAAGACGAGAGTG
187205	19401	ACTCCCTGCCTGTTCCAGTT	231792	63988	TTTGTAGAGGCAGGGTTTCA	276379	108575	GGGAAGGTGAAGACGAGAGT
187206	19402	TACTCCCTGCCTGTTCCAGT	231793	63989	TTTTGTAGAGGCAGGGTTTC	276380	108576	GGGGAAGGTGAAGACGAGAG
187207	19403	GTACTCCCTGCCTGTTCCAG	231794	63990	CTTTTGTAGAGGCAGGGTTT	276381	108577	GGGGGAAGGTGAAGACGAGA
187208	19404	AGTACTCCCTGCCTGTTCCA	231795	63991	ACTTTTGTAGAGGCAGGGTT	276382	108578	TGGGGGAAGGTGAAGACGAG
187209	19405	TAGTACTCCCTGCCTGTTCC	231796	63992	GACTTTTGTAGAGGCAGGGT	276383	108579	CTGGGGGAAGGTGAAGACGA
187210	19406	CTAGTACTCCCTGCCTGTTC	231797	63993	TGACTTTTGTAGAGGCAGGG	276384	108580	GCTGGGGGAAGGTGAAGACG
187211	19407	CCTAGTACTCCCTGCCTGTT	231798	63994	ATGACTTTTGTAGAGGCAGG	276385	108581	GGCTGGGGGAAGGTGAAGAC
187212	19408	TCCTAGTACTCCCTGCCTGT	231799	63995	TATGACTTTTGTAGAGGCAG	276386	108582	AGGCTGGGGGAAGGTGAAGA
187213	19409	GTCCTAGTACTCCCTGCCTG	231800	63996	TTATGACTTTTGTAGAGGCA	276387	108583	AAGGCTGGGGGAAGGTGAAG
187214	19410	TGTCCTAGTACTCCCTGCCT	231801	63997	TTTATGACTTTTGTAGAGGC	276388	108584	CAAGGCTGGGGGAAGGTGAA
187215	19411	CTGTCCTAGTACTCCCTGCC	231802	63998	ATTTATGACTTTTGTAGAGG	276389	108585	GCAAGGCTGGGGGAAGGTGA
187216	19412	GCTGTCCTAGTACTCCCTGC	231803	63999	TATTTATGACTTTTGTAGAG	276390	108586	AGCAAGGCTGGGGGAAGGTG
187217	19413	GGCTGTCCTAGTACTCCCTG	231804	64000	ATATTTATGACTTTTGTAGA	276391	108587	GAGCAAGGCTGGGGGAAGGT
187218	19414	GGGCTGTCCTAGTACTCCCT	231805	64001	AATATTTATGACTTTTGTAG	276392	108588	AGAGCAAGGCTGGGGGAAGG
187219	19415	TGGGCTGTCCTAGTACTCCC	231806	64002	TAATATTTATGACTTTTGTA	276393	108589	CAGAGCAAGGCTGGGGGAAG
187220	19416	CTGGGCTGTCCTAGTACTCC	231807	64003	CTAATATTTATGACTTTTGT	276394	108590	ACAGAGCAAGGCTGGGGGAA
187221	19417	GCTGGGCTGTCCTAGTACTC	231808	64004	GCTAATATTTATGACTTTTG	276395	108591	GACAGAGCAAGGCTGGGGGA
187222	19418	TGCTGGGCTGTCCTAGTACT	231809	64005	GGCTAATATTTATGACTTTT	276396	108592	AGACAGAGCAAGGCTGGGGG
187223	19419	ATGCTGGGCTGTCCTAGTAC	231810	64006	CGGCTAATATTTATGACTTT	276397	108593	GAGACAGAGCAAGGCTGGGG
187224	19420	AATGCTGGGCTGTCCTAGTA	231811	64007	CCGGCTAATATTTATGACTT	276398	108594	AGAGACAGAGCAAGGCTGGG
187225	19421	CAATGCTGGGCTGTCCTAGT	231812	64008	CCCGGCTAATATTTATGACT	276399	108595	TAGAGACAGAGCAAGGCTGG
187226	19422	GCAATGCTGGGCTGTCCTAG	231813	64009	ACCCGGCTAATATTTATGAC	276400	108596	GTAGAGACAGAGCAAGGCTG
187227	19423	GGCAATGCTGGGCTGTCCTA	231814	64010	CACCCGGCTAATATTTATGA	276401	108597	GGTAGAGACAGAGCAAGGCT
187228	19424	GGGCAATGCTGGGCTGTCCT	231815	64011	ACACCCGGCTAATATTTATG	276402	108598	GGGTAGAGACAGAGCAAGGC
187229	19425	GGGGCAATGCTGGGCTGTCC	231816	64012	CACACCCGGCTAATATTTAT	276403	108599	TGGGTAGAGACAGAGCAAGG
187230	19426	TGGGGCAATGCTGGGCTGTC	231817	64013	TCACACCCGGCTAATATTTA	276404	108600	CTGGGTAGAGACAGAGCAAG
187231	19427	TTGGGGCAATGCTGGGCTGT	231818	64014	ATCACACCCGGCTAATATTT	276405	108601	ACTGGGTAGAGACAGAGCAA
187232	19428	TTTGGGGCAATGCTGGGCTG	231819	64015	CATCACACCCGGCTAATATT	276406	108602	GACTGGGTAGAGACAGAGCA
187233	19429	TTTTGGGGCAATGCTGGGCT	231820	64016	CCATCACACCCGGCTAATAT	276407	108603	TGACTGGGTAGAGACAGAGC
187234	19430	ATTTTGGGGCAATGCTGGGC	231821	64017	GCCATCACACCCGGCTAATA	276408	108604	GTGACTGGGTAGAGACAGAG
187235	19431	TATTTTGGGGCAATGCTGGG	231822	64018	TGCCATCACACCCGGCTAAT	276409	108605	GGTGACTGGGTAGAGACAGA
187236	19432	ATATTTTGGGGCAATGCTGG	231823	64019	GTGCCATCACACCCGGCTAA	276410	108606	AGGTGACTGGGTAGAGACAG
187237	19433	GATATTTTGGGGCAATGCTG	231824	64020	TGTGCCATCACACCCGGCTA	276411	108607	GAGGTGACTGGGTAGAGACA
187238	19434	GGATATTTTGGGGCAATGCT	231825	64021	GTGTGCCATCACACCCGGCT	276412	108608	AGAGGTGACTGGGTAGAGAC
187239	19435	TGGATATTTTGGGGCAATGC	231826	64022	CGTGTGCCATCACACCCGGC	276413	108609	CAGAGGTGACTGGGTAGAGA
187240	19436	CTGGATATTTTGGGGCAATG	231827	64023	GCGTGTGCCATCACACCCGG	276414	108610	GCAGAGGTGACTGGGTAGAG
187241	19437	CCTGGATATTTTGGGGCAAT	231828	64024	GGCGTGTGCCATCACACCCG	276415	108611	GGCAGAGGTGACTGGGTAGA
187242	19438	GCCTGGATATTTTGGGGCAA	231829	64025	AGGCGTGTGCCATCACACCC	276416	108612	GGGCAGAGGTGACTGGGTAG

187243	19439	GGCCTGGATATTTTGGGGCA	231830	64026	CAGGCGTGTGCCATCACACC	276417	108613	TGGGCAGAGGTGACTGGGTA
187244	19440	AGGCCTGGATATTTTGGGGC	231831	64027	ACAGGCGTGTGCCATCACAC	276418	108614	ATGGGCAGAGGTGACTGGGT
187245	19441	CAGGCCTGGATATTTTGGGG	231832	64028	TACAGGCGTGTGCCATCACA	276419	108615	GATGGGCAGAGGTGACTGGG
187246	19442	TCAGGCCTGGATATTTTGGG	231833	64029	CTACAGGCGTGTGCCATCAC	276420	108616	AGATGGGCAGAGGTGACTGG
187247	19443	ATCAGGCCTGGATATTTTGG	231834	64030	ACTACAGGCGTGTGCCATCA	276421	108617	GAGATGGGCAGAGGTGACTG
187248	19444	TATCAGGCCTGGATATTTTG	231835	64031	GACTACAGGCGTGTGCCATC	276422	108618	AGAGATGGGCAGAGGTGACT
187249	19445	TTATCAGGCCTGGATATTTT	231836	64032	GGACTACAGGCGTGTGCCAT	276423	108619	GAGAGATGGGCAGAGGTGAC
187250	19446	TTTATCAGGCCTGGATATTT	231837	64033	GGGACTACAGGCGTGTGCCA	276424	108620	GGAGAGATGGGCAGAGGTGA
187251	19447	TTTTATCAGGCCTGGATATT	231838	64034	TGGGACTACAGGCGTGTGCC	276425	108621	CGGAGAGATGGGCAGAGGTG
187252	19448	CTTTTATCAGGCCTGGATAT	231839	64035	CTGGGACTACAGGCGTGTGC	276426	108622	TCGGAGAGATGGGCAGAGGT
187253	19449	TCTTTTATCAGGCCTGGATA	231840	64036	GCTGGGACTACAGGCGTGTG	276427	108623	ATCGGAGAGATGGGCAGAGG
187254	19450	CTCTTTTATCAGGCCTGGAT	231841	64037	AGCTGGGACTACAGGCGTGT	276428	108624	GATCGGAGAGATGGGCAGAG
187255	19451	TCTCTTTTATCAGGCCTGGA	231842	64038	TAGCTGGGACTACAGGCGTG	276429	108625	AGATCGGAGAGATGGGCAGA
187256	19452	TTCTCTTTTATCAGGCCTGG	231843	64039	GTAGCTGGGACTACAGGCGT	276430	108626	CAGATCGGAGAGATGGGCAG
187257	19453	TTTCTCTTTTATCAGGCCTG	231844	64040	AGTAGCTGGGACTACAGGCG	276431	108627	ACAGATCGGAGAGATGGGCA
187258	19454	TTTTCTCTTTTATCAGGCCT	231845	64041	GAGTAGCTGGGACTACAGGC	276432	108628	AACAGATCGGAGAGATGGGC
187259	19455	TTTTTCTCTTTTATCAGGCC	231846	64042	TGAGTAGCTGGGACTACAGG	276433	108629	AAACAGATCGGAGAGATGGG
187260	19456	GTTTTTCTCTTTTATCAGGC	231847	64043	CTGAGTAGCTGGGACTACAG	276434	108630	GAAACAGATCGGAGAGATGG
187261	19457	TGTTTTTCTCTTTTATCAGG	231848	64044	CCTGAGTAGCTGGGACTACA	276435	108631	AGAAACAGATCGGAGAGATG
187262	19458	CTGTTTTTCTCTTTTATCAG	231849	64045	TCCTGAGTAGCTGGGACTAC	276436	108632	GAGAAACAGATCGGAGAGAT
187263	19459	CCTGTTTTTCTCTTTTATCA	231850	64046	CTCCTGAGTAGCTGGGACTA	276437	108633	AGAGAAACAGATCGGAGAGA
187264	19460	ACCTGTTTTTCTCTTTTATC	231851	64047	CCTCCTGAGTAGCTGGGACT	276438	108634	GAGAGAAACAGATCGGAGAG
187265	19461	TACCTGTTTTTCTCTTTTAT	231852	64048	GCCTCCTGAGTAGCTGGGAC	276439	108635	AGAGAGAAACAGATCGGAGA
187266	19462	CTACCTGTTTTTCTCTTTTA	231853	64049	AGCCTCCTGAGTAGCTGGGA	276440	108636	GAGAGAGAAACAGATCGGAG
187267	19463	GCTACCTGTTTTTCTCTTTT	231854	64050	CAGCCTCCTGAGTAGCTGGG	276441	108637	GGAGAGAGAAACAGATCGGA
187268	19464	AGCTACCTGTTTTTCTCTTT	231855	64051	TCAGCCTCCTGAGTAGCTGG	276442	108638	AGGAGAGAGAAACAGATCGG
187269	19465	GAGCTACCTGTTTTTCTCTT	231856	64052	CTCAGCCTCCTGAGTAGCTG	276443	108639	AAGGAGAGAGAAACAGATCG
187270	19466	TGAGCTACCTGTTTTTCTCT	231857	64053	CCTCAGCCTCCTGAGTAGCT	276444	108640	AAAGGAGAGAGAAACAGATC
187271	19467	GTGAGCTACCTGTTTTTCTC	231858	64054	ACCTCAGCCTCCTGAGTAGC	276445	108641	AAAAGGAGAGAGAAACAGAT
187272	19468	TGTGAGCTACCTGTTTTTCT	231859	64055	CACCTCAGCCTCCTGAGTAG	276446	108642	TAAAAGGAGAGAGAAACAGA
187273	19469	CTGTGAGCTACCTGTTTTTC	231860	64056	CCACCTCAGCCTCCTGAGTA	276447	108643	GTAAAAGGAGAGAGAAACAG
187274	19470	CCTGTGAGCTACCTGTTTTT	231861	64057	CCCACCTCAGCCTCCTGAGT	276448	108644	GGTAAAAGGAGAGAGAAACA
187275	19471	TCCTGTGAGCTACCTGTTTT	231862	64058	ACCCACCTCAGCCTCCTGAG	276449	108645	GGGTAAAAGGAGAGAGAAAC
187276	19472	TTCCTGTGAGCTACCTGTTT	231863	64059	CACCCACCTCAGCCTCCTGA	276450	108646	GGGGTAAAAGGAGAGAGAAA
187277	19473	TTTCCTGTGAGCTACCTGTT	231864	64060	CCACCCACCTCAGCCTCCTG	276451	108647	AGGGGTAAAAGGAGAGAGAA
187278	19474	TTTTCCTGTGAGCTACCTGT	231865	64061	TCCACCCACCTCAGCCTCCT	276452	108648	GAGGGGTAAAAGGAGAGAGA
187279	19475	CTTTTCCTGTGAGCTACCTG	231866	64062	ATCCACCCACCTCAGCCTCC	276453	108649	AGAGGGGTAAAAGGAGAGAG
187280	19476	CCTTTTCCTGTGAGCTACCT	231867	64063	GATCCACCCACCTCAGCCTC	276454	108650	AAGAGGGGTAAAAGGAGAGA
187281	19477	TCCTTTTCCTGTGAGCTACC	231868	64064	TGATCCACCCACCTCAGCCT	276455	108651	AAAGAGGGGTAAAAGGAGAG
187282	19478	ATCCTTTTCCTGTGAGCTAC	231869	64065	GTGATCCACCCACCTCAGCC	276456	108652	GAAAGAGGGGTAAAAGGAGA
187283	19479	TATCCTTTTCCTGTGAGCTA	231870	64066	AGTGATCCACCCACCTCAGC	276457	108653	GGAAAGAGGGGTAAAAGGAG
187284	19480	TTATCCTTTTCCTGTGAGCT	231871	64067	AAGTGATCCACCCACCTCAG	276458	108654	AGGAAAGAGGGGTAAAAGGA
187285	19481	TTTATCCTTTTCCTGTGAGC	231872	64068	CAAGTGATCCACCCACCTCA	276459	108655	GAGGAAAGAGGGGTAAAAGG
187286	19482	TTTTATCCTTTTCCTGTGAG	231873	64069	TCAAGTGATCCACCCACCTC	276460	108656	GGAGGAAAGAGGGGTAAAAG
187287	19483	TTTTTATCCTTTTCCTGTGA	231874	64070	CTCAAGTGATCCACCCACCT	276461	108657	GGGAGGAAAGAGGGGTAAAA
187288	19484	TTTTTTATCCTTTTCCTGTG	231875	64071	GCTCAAGTGATCCACCCACC	276462	108658	AGGGAGGAAAGAGGGGTAAA
187289	19485	TTTTTTTATCCTTTTCCTGT	231876	64072	GGCTCAAGTGATCCACCCAC	276463	108659	GAGGGAGGAAAGAGGGGTAA
187290	19486	CTTTTTTTATCCTTTTCCTG	231877	64073	GGGCTCAAGTGATCCACCCA	276464	108660	GGAGGGAGGAAAGAGGGGTA
187291	19487	CCTTTTTTTATCCTTTTCCT	231878	64074	CGGGCTCAAGTGATCCACCC	276465	108661	AGGAGGGAGGAAAGAGGGGT
187292	19488	TCCTTTTTTTTATCCTTTTCC	231879	64075	CCGGGCTCAAGTGATCCACC	276466	108662	GAGGAGGGAGGAAAGAGGGG
187293	19489	CTCCTTTTTTTTATCCTTTTC	231880	64076	CCCGGGCTCAAGTGATCCAC	276467	108663	TGAGGAGGGAGGAAAGAGGG
187294	19490	CCTCCTTTTTTTTATCCTTTT	231881	64077	TCCCGGGCTCAAGTGATCCA	276468	108664	ATGAGGAGGGAGGAAAGAGG
187295	19491	TCCTCCTTTTTTTTATCCTTT	231882	64078	CTCCCGGGCTCAAGTGATCC	276469	108665	TATGAGGAGGGAGGAAAGAG
187296	19492	CTCCTCCTTTTTTTTATCCTT	231883	64079	CCTCCCGGGCTCAAGTGATC	276470	108666	GTATGAGGAGGGAGGAAAGA
187297	19493	CCTCCTCCTTTTTTTTATCCT	231884	64080	ACCTCCCGGGCTCAAGTGAT	276471	108667	TGTATGAGGAGGGAGGAAAG
187298	19494	CCCTCCTCCTTTTTTTTATCC	231885	64081	TACCTCCCGGGCTCAAGTGA	276472	108668	GTGTATGAGGAGGGAGGAAA
187299	19495	TCCCTCCTCCTTTTTTTTATC	231886	64082	CTACCTCCCGGGCTCAAGTG	276473	108669	GGTGTATGAGGAGGGAGGAA
187300	19496	ATCCCTCCTCCTTTTTTTAT	231887	64083	TCTACCTCCCGGGCTCAAGT	276474	108670	TGGTGTATGAGGAGGGAGGA
187301	19497	AATCCCTCCTCCTTTTTTTA	231888	64084	CTCTACCTCCCGGGCTCAAG	276475	108671	GTGGTGTATGAGGAGGGAGG
187302	19498	AAATCCCTCCTCCTTTTTTT	231889	64085	ACTCTACCTCCCGGGCTCAA	276476	108672	AGTGGTGTATGAGGAGGGAG
187303	19499	TAAATCCCTCCTCCTTTTTT	231890	64086	GACTCTACCTCCCGGGCTCA	276477	108673	CAGTGGTGTATGAGGAGGGA
187304	19500	TTAAATCCCTCCTCCTTTTT	231891	64087	AGACTCTACCTCCCGGGCTC	276478	108674	TCAGTGGTGTATGAGGAGGG
187305	19501	GTTAAATCCCTCCTCCTTTT	231892	64088	CAGACTCTACCTCCCGGGCT	276479	108675	GTCAGTGGTGTATGAGGAGG
187306	19502	TGTTAAATCCCTCCTCCTTT	231893	64089	GCAGACTCTACCTCCCGGGC	276480	108676	GGTCAGTGGTGTATGAGGAG
187307	19503	ATGTTAAATCCCTCCTCCTT	231894	64090	TGCAGACTCTACCTCCCGGG	276481	108677	TGGTCAGTGGTGTATGAGGA
187308	19504	CATGTTAAATCCCTCCTCCT	231895	64091	CTGCAGACTCTACCTCCCGG	276482	108678	ATGGTCAGTGGTGTATGAGG
187309	19505	TCATGTTAAATCCCTCCTCC	231896	64092	ACTGCAGACTCTACCTCCCG	276483	108679	AATGGTCAGTGGTGTATGAG
187310	19506	TTCATGTTAAATCCCTCCTC	231897	64093	CACTGCAGACTCTACCTCCC	276484	108680	TAATGGTCAGTGGTGTATGA
187311	19507	TTTCATGTTAAATCCCTCCT	231898	64094	TCACTGCAGACTCTACCTCC	276485	108681	ATAATGGTCAGTGGTGTATG
187312	19508	TTTTCATGTTAAATCCCTCC	231899	64095	CTCACTGCAGACTCTACCTC	276486	108682	TATAATGGTCAGTGGTGTAT
187313	19509	CTTTTCATGTTAAATCCCTC	231900	64096	GCTCACTGCAGACTCTACCT	276487	108683	CTATAATGGTCAGTGGTGTA
187314	19510	CCTTTTCATGTTAAATCCCT	231901	64097	GGCTCACTGCAGACTCTACC	276488	108684	TCTATAATGGTCAGTGGTGT

187315	19511	ACCTTTTCATGTTAAATCCC	231902	64098	TGGCTCACTGCAGACTCTAC	276489	108685	CTCTATAATGGTCAGTGGTG
187316	19512	CACCTTTTCATGTTAAATCC	231903	64099	TTGGCTCACTGCAGACTCTA	276490	108686	TCTCTATAATGGTCAGTGGT
187317	19513	GCACCTTTTCATGTTAAATC	231904	64100	CTTGGCTCACTGCAGACTCT	276491	108687	TTCTCTATAATGGTCAGTGG
187318	19514	AGCACCTTTTCATGTTAAAT	231905	64101	TCTTGGCTCACTGCAGACTC	276492	108688	GTTCTCTATAATGGTCAGTG
187319	19515	AAGCACCTTTTCATGTTAAA	231906	64102	ATCTTGGCTCACTGCAGACT	276493	108689	AGTTCTCTATAATGGTCAGT
187320	19516	CAAGCACCTTTTCATGTTAA	231907	64103	GATCTTGGCTCACTGCAGAC	276494	108690	CAGTTCTCTATAATGGTCAG
187321	19517	TCAAGCACCTTTTCATGTTA	231908	64104	TGATCTTGGCTCACTGCAGA	276495	108691	TCAGTTCTCTATAATGGTCA
187322	19518	ATCAAGCACCTTTTCATGTT	231909	64105	GTGATCTTGGCTCACTGCAG	276496	108692	CTCAGTTCTCTATAATGGTC
187323	19519	GATCAAGCACCTTTTCATGT	231910	64106	TGTGATCTTGGCTCACTGCA	276497	108693	ACTCAGTTCTCTATAATGGT
187324	19520	AGATCAAGCACCTTTTCATG	231911	64107	GTGTGATCTTGGCTCACTGC	276498	108694	TACTCAGTTCTCTATAATGG
187325	19521	GAGATCAAGCACCTTTTCAT	231912	64108	GGTGTGATCTTGGCTCACTG	276499	108695	ATACTCAGTTCTCTATAATG
187326	19522	GGAGATCAAGCACCTTTTCA	231913	64109	CGGTGTGATCTTGGCTCACT	276500	108696	AATACTCAGTTCTCTATAAT
187327	19523	GGGAGATCAAGCACCTTTTC	231914	64110	GCGGTGTGATCTTGGCTCAC	276501	108697	GAATACTCAGTTCTCTATAA
187328	19524	AGGGAGATCAAGCACCTTTT	231915	64111	AGCGGTGTGATCTTGGCTCA	276502	108698	AGAATACTCAGTTCTCTATA
187329	19525	GAGGGAGATCAAGCACCTTT	231916	64112	CAGCGGTGTGATCTTGGCTC	276503	108699	TAGAATACTCAGTTCTCTAT
187330	19526	TGAGGGAGATCAAGCACCTT	231917	64113	GCAGCGGTGTGATCTTGGCT	276504	108700	TTAGAATACTCAGTTCTCTA
187331	19527	ATGAGGGAGATCAAGCACCT	231918	64114	TGCAGCGGTGTGATCTTGGC	276505	108701	TTTAGAATACTCAGTTCTCT
187332	19528	TATGAGGGAGATCAAGCACC	231919	64115	GTGCAGCGGTGTGATCTTGG	276506	108702	TTTTAGAATACTCAGTTCTC
187333	19529	TTATGAGGGAGATCAAGCAC	231920	64116	AGTGCAGCGGTGTGATCTTG	276507	108703	TTTTTAGAATACTCAGTTCT
187334	19530	ATTATGAGGGAGATCAAGCA	231921	64117	GAGTGCAGCGGTGTGATCTT	276508	108704	ATTTTTAGAATACTCAGTTC
187335	19531	TATTATGAGGGAGATCAAGC	231922	64118	GGAGTGCAGCGGTGTGATCT	276509	108705	TATTTTTAGAATACTCAGTT
187336	19532	TTATTATGAGGGAGATCAAG	231923	64119	TGGAGTGCAGCGGTGTGATC	276510	108706	GTATTTTTAGAATACTCAGT
187337	19533	TTTATTATGAGGGAGATCAA	231924	64120	CTGGAGTGCAGCGGTGTGAT	276511	108707	TGTATTTTTAGAATACTCAG
187338	19534	TTTTATTATGAGGGAGATCA	231925	64121	GCTGGAGTGCAGCGGTGTGA	276512	108708	ATGTATTTTTAGAATACTCA
187339	19535	TTTTTATTATGAGGGAGATC	231926	64122	AGCTGGAGTGCAGCGGTGTG	276513	108709	AATGTATTTTTAGAATACTC
187340	19536	CTTTTTATTATGAGGGAGAT	231927	64123	CAGCTGGAGTGCAGCGGTGT	276514	108710	AAATGTATTTTTAGAATACT
187341	19537	TCTTTTTATTATGAGGGAGA	231928	64124	CCAGCTGGAGTGCAGCGGTG	276515	108711	AAAATGTATTTTTAGAATAC
187342	19538	GTCTTTTTATTATGAGGGAG	231929	64125	TCCAGCTGGAGTGCAGCGGT	276516	108712	TAAAATGTATTTTTAGAATA
187343	19539	AGTCTTTTTATTATGAGGGA	231930	64126	CTCCAGCTGGAGTGCAGCGG	276517	108713	ATAAAATGTATTTTTAGAAT
187344	19540	CAGTCTTTTTATTATGAGGG	231931	64127	GCTCCAGCTGGAGTGCAGCG	276518	108714	AATAAAATGTATTTTTAGAA
187345	19541	GCAGTCTTTTTATTATGAGG	231932	64128	TGCTCCAGCTGGAGTGCAGC	276519	108715	AAATAAAATGTATTTTTAGA
187346	19542	AGCAGTCTTTTTATTATGAG	231933	64129	TTGCTCCAGCTGGAGTGCAG	276520	108716	TAAATAAAATGTATTTTTAG
187347	19543	CAGCAGTCTTTTTATTATGA	231934	64130	GTTGCTCCAGCTGGAGTGCA	276521	108717	ATAAATAAAATGTATTTTTA
187348	19544	TCAGCAGTCTTTTTATTATG	231935	64131	TGTTGCTCCAGCTGGAGTGC	276522	108718	AATAAATAAAATGTATTTTT
187349	19545	ATCAGCAGTCTTTTTATTAT	231936	64132	CTGTTGCTCCAGCTGGAGTG	276523	108719	AAATAAATAAAATGTATTTT
187350	19546	AATCAGCAGTCTTTTTATTA	231937	64133	TCTGTTGCTCCAGCTGGAGT	276524	108720	TAAATAAATAAAATGTATTT
187351	19547	GAATCAGCAGTCTTTTTATT	231938	64134	CTCTGTTGCTCCAGCTGGAG	276525	108721	ATAAATAAATAAAATGTATT
187352	19548	GGAATCAGCAGTCTTTTTAT	231939	64135	ACTCTGTTGCTCCAGCTGGA	276526	108722	AATAAATAAATAAAATGTAT
187353	19549	TGGAATCAGCAGTCTTTTTA	231940	64136	CACTCTGTTGCTCCAGCTGG	276527	108723	AAATAAATAAATAAAATGTA
187354	19550	ATGGAATCAGCAGTCTTTTT	231941	64137	TCACTCTGTTGCTCCAGCTG	276528	108724	AAAATAAATAAATAAAATGT
187355	19551	GATGGAATCAGCAGTCTTTT	231942	64138	CTCACTCTGTTGCTCCAGCT	276529	108725	CAAAATAAATAAATAAAATG
187356	19552	GGATGGAATCAGCAGTCTTT	231943	64139	TCTCACTCTGTTGCTCCAGC	276530	108726	TCAAAATAAATAAATAAAAT
187357	19553	TGGATGGAATCAGCAGTCTT	231944	64140	GTCTCACTCTGTTGCTCCAG	276531	108727	CTCAAAATAAATAAATAAAA
187358	19554	CTGGATGGAATCAGCAGTCT	231945	64141	GGTCTCACTCTGTTGCTCCA	276532	108728	TCTCAAAATAAATAAATAAA
187359	19555	CCTGGATGGAATCAGCAGTC	231946	64142	GGGTCTCACTCTGTTGCTCC	276533	108729	GTCTCAAAATAAATAAATAA
187360	19556	GCCTGGATGGAATCAGCAGT	231947	64143	AGGGTCTCACTCTGTTGCTC	276534	108730	TGTCTCAAAATAAATAAATA
187361	19557	TGCCTGGATGGAATCAGCAG	231948	64144	CAGGGTCTCACTCTGTTGCT	276535	108731	CTGTCTCAAAATAAATAAAT
187362	19558	TTGCCTGGATGGAATCAGCA	231949	64145	TCAGGGTCTCACTCTGTTGC	276536	108732	TCTGTCTCAAAATAAATAAA
187363	19559	CTTGCCTGGATGGAATCAGC	231950	64146	GTCAGGGTCTCACTCTGTTG	276537	108733	CTCTGTCTCAAAATAAATAA
187364	19560	ACTTGCCTGGATGGAATCAG	231951	64147	AGTCAGGGTCTCACTCTGTT	276538	108734	ACTCTGTCTCAAAATAAATA
187365	19561	CACTTGCCTGGATGGAATCA	231952	64148	AAGTCAGGGTCTCACTCTGT	276539	108735	GACTCTGTCTCAAAATAAAT
187366	19562	TCACTTGCCTGGATGGAATC	231953	64149	TAAGTCAGGGTCTCACTCTG	276540	108736	AGACTCTGTCTCAAAATAAA
187367	19563	GTCACTTGCCTGGATGGAAT	231954	64150	TTAAGTCAGGGTCTCACTCT	276541	108737	GAGACTCTGTCTCAAAATAA
187368	19564	TGTCACTTGCCTGGATGGAA	231955	64151	TTTAAGTCAGGGTCTCACTC	276542	108738	TGAGACTCTGTCTCAAAATA
187369	19565	CTGTCACTTGCCTGGATGGA	231956	64152	TTTTAAGTCAGGGTCTCACT	276543	108739	GTGAGACTCTGTCTCAAAAT
187370	19566	TCTGTCACTTGCCTGGATGG	231957	64153	CTTTTAAGTCAGGGTCTCAC	276544	108740	AGTGAGACTCTGTCTCAAAA
187371	19567	TTCTGTCACTTGCCTGGATG	231958	64154	TCTTTTAAGTCAGGGTCTCA	276545	108741	GAGTGAGACTCTGTCTCAAA
187372	19568	TTTCTGTCACTTGCCTGGAT	231959	64155	TTCTTTTAAGTCAGGGTCTC	276546	108742	AGAGTGAGACTCTGTCTCAA
187373	19569	TTTTCTGTCACTTGCCTGGA	231960	64156	TTTCTTTTAAGTCAGGGTCT	276547	108743	CAGAGTGAGACTCTGTCTCA
187374	19570	TTTTTCTGTCACTTGCCTGG	231961	64157	TTTTCTTTTAAGTCAGGGTC	276548	108744	ACAGAGTGAGACTCTGTCTC
187375	19571	TTTTTTCTGTCACTTGCCTG	231962	64158	TTTTTCTTTTAAGTCAGGGT	276549	108745	GACAGAGTGAGACTCTGTCT
187376	19572	TTTTTTTCTGTCACTTGCCT	231963	64159	TTTTTTCTTTTAAGTCAGGG	276550	108746	TGACAGAGTGAGACTCTGTC
187377	19573	TTTTTTTTCTGTCACTTGCC	231964	64160	TTTTTTTCTTTTAAGTCAGG	276551	108747	GTGACAGAGTGAGACTCTGT
187378	19574	TTTTTTTTTCTGTCACTTGC	231965	64161	TTTTTTTTCTTTTAAGTCAG	276552	108748	GGTGACAGAGTGAGACTCTG
187379	19575	TTTTTTTTTTCTGTCACTTG	231966	64162	TTTTTTTTTCTTTTAAGTCA	276553	108749	GGGTGACAGAGTGAGACTCT
187380	19576	TTTTTTTTTTTCTGTCACTT	231967	64163	TTTTTTTTTTCTTTTAAGTC	276554	108750	TGGGTGACAGAGTGAGACTC
187381	19577	ATTTTTTTTTTTCTGTCACT	231968	64164	TTTTTTTTTTTCTTTTAAGT	276555	108751	CTGGGTGACAGAGTGAGACT
187382	19578	AATTTTTTTTTTTCTGTCAC	231969	64165	TTTTTTTTTTTTCTTTTAAG	276556	108752	CCTGGGTGACAGAGTGAGAC
187383	19579	TAATTTTTTTTTTTCTGTCA	231970	64166	TTTTTTTTTTTTTCTTTTAA	276557	108753	GCCTGGGTGACAGAGTGAGA
187384	19580	TTAATTTTTTTTTTTCTGTC	231971	64167	TTTTTTTTTTTTTTCTTTTA	276558	108754	AGCCTGGGTGACAGAGTGAG
187385	19581	ATTAATTTTTTTTTTTCTGT	231972	64168	TTTTTTTTTTTTTTTCTTTT	276559	108755	CAGCCTGGGTGACAGAGTGA
187386	19582	AATTAATTTTTTTTTTTCTG	231973	64169	CTTTTTTTTTTTTTTTCTTT	276560	108756	CCAGCCTGGGTGACAGAGTG

187387	19583	AAATTAATTTTTTTTTTTCT	231974	64170	TCTTTTTTTTTTTTTTTCTT	276561	108757	TCCAGCCTGGGTGACAGAGT
187388	19584	TAAATTAATTTTTTTTTTTC	231975	64171	CTCTTTTTTTTTTTTTTTCT	276562	108758	CTCCAGCCTGGGTGACAGAG
187389	19585	TTAAATTAATTTTTTTTTTT	231976	64172	CCTCTTTTTTTTTTTTTTTC	276563	108759	ACTCCAGCCTGGGTGACAGA
187390	19586	TTTAAATTAATTTTTTTTTT	231977	64173	TCCTCTTTTTTTTTTTTTTT	276564	108760	CACTCCAGCCTGGGTGACAG
187391	19587	TTTTAAATTAATTTTTTTTT	231978	64174	CTCCTCTTTTTTTTTTTTTT	276565	108761	GCACTCCAGCCTGGGTGACA
187392	19588	TTTTTAAATTAATTTTTTTT	231979	64175	TCTCCTCTTTTTTTTTTTTT	276566	108762	TGCACTCCAGCCTGGGTGAC
187393	19589	CTTTTTAAATTAATTTTTTT	231980	64176	TTCTCCTCTTTTTTTTTTTT	276567	108763	CTGCACTCCAGCCTGGGTGA
187394	19590	TCTTTTTAAATTAATTTTTT	231981	64177	TTTCTCCTCTTTTTTTTTTT	276568	108764	ACTGCACTCCAGCCTGGGTG
187395	19591	GTCTTTTTAAATTAATTTTT	231982	64178	TTTTCTCCTCTTTTTTTTTT	276569	108765	CACTGCACTCCAGCCTGGGT
187396	19592	AGTCTTTTTAAATTAATTTT	231983	64179	TTTTTCTCCTCTTTTTTTTT	276570	108766	CCACTGCACTCCAGCCTGGG
187397	19593	CAGTCTTTTTAAATTAATTT	231984	64180	ATTTTTCTCCTCTTTTTTTT	276571	108767	ACCACTGCACTCCAGCCTGG
187398	19594	GCAGTCTTTTTAAATTAATT	231985	64181	CATTTTTCTCCTCTTTTTTT	276572	108768	CACCACTGCACTCCAGCCTG
187399	19595	AGCAGTCTTTTTAAATTAAT	231986	64182	GCATTTTTCTCCTCTTTTTT	276573	108769	GCACCACTGCACTCCAGCCT
187400	19596	CAGCAGTCTTTTTAAATTAA	231987	64183	AGCATTTTTCTCCTCTTTTT	276574	108770	TGCACCACTGCACTCCAGCC
187401	19597	TCAGCAGTCTTTTTAAATTA	231988	64184	CAGCATTTTTCTCCTCTTTT	276575	108771	TTGCACCACTGCACTCCAGC
187402	19598	ATCAGCAGTCTTTTTAAATT	231989	64185	TCAGCATTTTTCTCCTCTTT	276576	108772	ATTGCACCACTGCACTCCAG
187403	19599	TATCAGCAGTCTTTTTAAAT	231990	64186	ATCAGCATTTTTCTCCTCTT	276577	108773	GATTGCACCACTGCACTCCA
187404	19600	TTATCAGCAGTCTTTTTAAA	231991	64187	GATCAGCATTTTTCTCCTCT	276578	108774	AGATTGCACCACTGCACTCC
187405	19601	TTTATCAGCAGTCTTTTTAA	231992	64188	AGATCAGCATTTTTCTCCTC	276579	108775	GAGATTGCACCACTGCACTC
187406	19602	TTTTATCAGCAGTCTTTTTA	231993	64189	GAGATCAGCATTTTTCTCCT	276580	108776	CGAGATTGCACCACTGCACT
187407	19603	GTTTTATCAGCAGTCTTTTT	231994	64190	TGAGATCAGCATTTTTCTCC	276581	108777	CCGAGATTGCACCACTGCAC
187408	19604	GGTTTTATCAGCAGTCTTTT	231995	64191	GTGAGATCAGCATTTTTCTC	276582	108778	GCCGAGATTGCACCACTGCA
187409	19605	TGGTTTTATCAGCAGTCTTT	231996	64192	AGTGAGATCAGCATTTTTCT	276583	108779	AGCCGAGATTGCACCACTGC
187410	19606	GTGGTTTTATCAGCAGTCTT	231997	64193	TAGTGAGATCAGCATTTTTC	276584	108780	GAGCCGAGATTGCACCACTG
187411	19607	TGTGGTTTTATCAGCAGTCT	231998	64194	CTAGTGAGATCAGCATTTTT	276585	108781	TGAGCCGAGATTGCACCACT
187412	19608	CTGTGGTTTTATCAGCAGTC	231999	64195	ACTAGTGAGATCAGCATTTT	276586	108782	GTGAGCCGAGATTGCACCAC
187413	19609	GCTGTGGTTTTATCAGCAGT	232000	64196	TACTAGTGAGATCAGCATTT	276587	108783	AGTGAGCCGAGATTGCACCA
187414	19610	CGCTGTGGTTTTATCAGCAG	232001	64197	TTACTAGTGAGATCAGCATT	276588	108784	CAGTGAGCCGAGATTGCACC
187415	19611	TCGCTGTGGTTTTATCAGCA	232002	64198	ATTACTAGTGAGATCAGCAT	276589	108785	GCAGTGAGCCGAGATTGCAC
187416	19612	CTCGCTGTGGTTTTATCAGC	232003	64199	AATTACTAGTGAGATCAGCA	276590	108786	TGCAGTGAGCCGAGATTGCA
187417	19613	TCTCGCTGTGGTTTTATCAG	232004	64200	TAATTACTAGTGAGATCAGC	276591	108787	TTGCAGTGAGCCGAGATTGC
187418	19614	GTCTCGCTGTGGTTTTATCA	232005	64201	TTAATTACTAGTGAGATCAG	276592	108788	GTTGCAGTGAGCCGAGATTG
187419	19615	TGTCTCGCTGTGGTTTTATC	232006	64202	TTTAATTACTAGTGAGATCA	276593	108789	GGTTGCAGTGAGCCGAGATT
187420	19616	GTGTCTCGCTGTGGTTTTAT	232007	64203	TTTTAATTACTAGTGAGATC	276594	108790	AGGTTGCAGTGAGCCGAGAT
187421	19617	AGTGTCTCGCTGTGGTTTTA	232008	64204	GTTTTAATTACTAGTGAGAT	276595	108791	GAGGTTGCAGTGAGCCGAGA
187422	19618	CAGTGTCTCGCTGTGGTTTT	232009	64205	TGTTTTAATTACTAGTGAGA	276596	108792	GGAGGTTGCAGTGAGCCGAG
187423	19619	GCAGTGTCTCGCTGTGGTTT	232010	64206	ATGTTTTAATTACTAGTGAG	276597	108793	CGGAGGTTGCAGTGAGCCGA
187424	19620	AGCAGTGTCTCGCTGTGGTT	232011	64207	GATGTTTTAATTACTAGTGA	276598	108794	GCGGAGGTTGCAGTGAGCCG
187425	19621	CAGCAGTGTCTCGCTGTGGT	232012	64208	TGATGTTTTAATTACTAGTG	276599	108795	GGCGGAGGTTGCAGTGAGCC
187426	19622	GCAGCAGTGTCTCGCTGTGG	232013	64209	CTGATGTTTTAATTACTAGT	276600	108796	AGGCGGAGGTTGCAGTGAGC
187427	19623	AGCAGCAGTGTCTCGCTGTG	232014	64210	CCTGATGTTTTAATTACTAG	276601	108797	GAGGCGGAGGTTGCAGTGAG
187428	19624	GAGCAGCAGTGTCTCGCTGT	232015	64211	GCCTGATGTTTTAATTACTA	276602	108798	GGAGGCGGAGGTTGCAGTGA
187429	19625	TGAGCAGCAGTGTCTCGCTG	232016	64212	GGCCTGATGTTTTAATTACT	276603	108799	GGGAGGCGGAGGTTGCAGTG
187430	19626	CTGAGCAGCAGTGTCTCGCT	232017	64213	TGGCCTGATGTTTTAATTAC	276604	108800	TGGGAGGCGGAGGTTGCAGT
187431	19627	CCTGAGCAGCAGTGTCTCGC	232018	64214	CTGGCCTGATGTTTTAATTA	276605	108801	CTGGGAGGCGGAGGTTGCAG
187432	19628	CCCTGAGCAGCAGTGTCTCG	232019	64215	CCTGGCCTGATGTTTTAATT	276606	108802	CCTGGGAGGCGGAGGTTGCA
187433	19629	TCCCTGAGCAGCAGTGTCTC	232020	64216	GCCTGGCCTGATGTTTTAAT	276607	108803	ACCTGGGAGGCGGAGGTTGC
187434	19630	ATCCCTGAGCAGCAGTGTCT	232021	64217	CGCCTGGCCTGATGTTTTAA	276608	108804	AACCTGGGAGGCGGAGGTTG
187435	19631	GATCCCTGAGCAGCAGTGTC	232022	64218	GCGCCTGGCCTGATGTTTTA	276609	108805	CAACCTGGGAGGCGGAGGTT
187436	19632	AGATCCCTGAGCAGCAGTGT	232023	64219	TGCGCCTGGCCTGATGTTTT	276610	108806	TCAACCTGGGAGGCGGAGGT
187437	19633	CAGATCCCTGAGCAGCAGTG	232024	64220	CTGCGCCTGGCCTGATGTTT	276611	108807	TTCAACCTGGGAGGCGGAGG
187438	19634	TCAGATCCCTGAGCAGCAGT	232025	64221	ACTGCGCCTGGCCTGATGTT	276612	108808	CTTCAACCTGGGAGGCGGAG
187439	19635	CTCAGATCCCTGAGCAGCAG	232026	64222	CACTGCGCCTGGCCTGATGT	276613	108809	GCTTCAACCTGGGAGGCGGA
187440	19636	CCTCAGATCCCTGAGCAGCA	232027	64223	CCACTGCGCCTGGCCTGATG	276614	108810	TGCTTCAACCTGGGAGGCGG
187441	19637	CCCTCAGATCCCTGAGCAGC	232028	64224	GCCACTGCGCCTGGCCTGAT	276615	108811	TTGCTTCAACCTGGGAGGCG
187442	19638	ACCCTCAGATCCCTGAGCAG	232029	64225	AGCCACTGCGCCTGGCCTGA	276616	108812	GTTGCTTCAACCTGGGAGGC
187443	19639	CACCCTCAGATCCCTGAGCA	232030	64226	GAGCCACTGCGCCTGGCCTG	276617	108813	AGTTGCTTCAACCTGGGAGG
187444	19640	ACACCCTCAGATCCCTGAGC	232031	64227	TGAGCCACTGCGCCTGGCCT	276618	108814	GAGTTGCTTCAACCTGGGAG
187445	19641	CACACCCTCAGATCCCTGAG	232032	64228	GTGAGCCACTGCGCCTGGCC	276619	108815	AGAGTTGCTTCAACCTGGGA
187446	19642	CCACACCCTCAGATCCCTGA	232033	64229	TGTGAGCCACTGCGCCTGGC	276620	108816	GAGAGTTGCTTCAACCTGGG
187447	19643	CCCACACCCTCAGATCCCTG	232034	64230	GTGTGAGCCACTGCGCCTGG	276621	108817	GGAGAGTTGCTTCAACCTGG
187448	19644	GCCCACACCCTCAGATCCCT	232035	64231	GGTGTGAGCCACTGCGCCTG	276622	108818	AGGAGAGTTGCTTCAACCTG
187449	19645	TGCCCACACCCTCAGATCCC	232036	64232	AGGTGTGAGCCACTGCGCCT	276623	108819	CAGGAGAGTTGCTTCAACCT
187450	19646	CTGCCCACACCCTCAGATCC	232037	64233	AAGGTGTGAGCCACTGCGCC	276624	108820	GCAGGAGAGTTGCTTCAACC
187451	19647	GCTGCCCACACCCTCAGATC	232038	64234	AAAGGTGTGAGCCACTGCGC	276625	108821	GGCAGGAGAGTTGCTTCAAC
187452	19648	GGCTGCCCACACCCTCAGAT	232039	64235	TAAAGGTGTGAGCCACTGCG	276626	108822	AGGCAGGAGAGTTGCTTCAA
187453	19649	TGGCTGCCCACACCCTCAGA	232040	64236	TTAAAGGTGTGAGCCACTGC	276627	108823	GAGGCAGGAGAGTTGCTTCA
187454	19650	CTGGCTGCCCACACCCTCAG	232041	64237	ATTAAAGGTGTGAGCCACTG	276628	108824	TGAGGCAGGAGAGTTGCTTC
187455	19651	CCTGGCTGCCCACACCCTCA	232042	64238	GATTAAAGGTGTGAGCCACT	276629	108825	CTGAGGCAGGAGAGTTGCTT
187456	19652	GCCTGGCTGCCCACACCCTC	232043	64239	GGATTAAAGGTGTGAGCCAC	276630	108826	GCTGAGGCAGGAGAGTTGCT
187457	19653	AGCCTGGCTGCCCACACCCT	232044	64240	GGGATTAAAGGTGTGAGCCA	276631	108827	GGCTGAGGCAGGAGAGTTGC
187458	19654	CAGCCTGGCTGCCCACACCC	232045	64241	TGGGATTAAAGGTGTGAGCC	276632	108828	AGGCTGAGGCAGGAGAGTTG

187459	19655	GCAGCCTGGCTGCCCACACC	232046	64242	CTGGGATTAAAGGTGTGAGC	276633	108829	GAGGCTGAGGCAGGAGAGTT
187460	19656	GGCAGCCTGGCTGCCCACAC	232047	64243	GCTGGGATTAAAGGTGTGAG	276634	108830	GGAGGCTGAGGCAGGAGAGT
187461	19657	TGGCAGCCTGGCTGCCCACA	232048	64244	TGCTGGGATTAAAGGTGTGA	276635	108831	GGGAGGCTGAGGCAGGAGAG
187462	19658	GTGGCAGCCTGGCTGCCCAC	232049	64245	GTGCTGGGATTAAAGGTGTG	276636	108832	AGGGAGGCTGAGGCAGGAGA
187463	19659	CGTGGCAGCCTGGCTGCCCA	232050	64246	AGTGCTGGGATTAAAGGTGT	276637	108833	TAGGGAGGCTGAGGCAGGAG
187464	19660	GCGTGGCAGCCTGGCTGCCC	232051	64247	GAGTGCTGGGATTAAAGGTG	276638	108834	CTAGGGAGGCTGAGGCAGGA
187465	19661	TGCGTGGCAGCCTGGCTGCC	232052	64248	AGAGTGCTGGGATTAAAGGT	276639	108835	ACTAGGGAGGCTGAGGCAGG
187466	19662	ATGCGTGGCAGCCTGGCTGC	232053	64249	CAGAGTGCTGGGATTAAAGG	276640	108836	TACTAGGGAGGCTGAGGCAG
187467	19663	GATGCGTGGCAGCCTGGCTG	232054	64250	CCAGAGTGCTGGGATTAAAG	276641	108837	CTACTAGGGAGGCTGAGGCA
187468	19664	TGATGCGTGGCAGCCTGGCT	232055	64251	CCCAGAGTGCTGGGATTAAA	276642	108838	GCTACTAGGGAGGCTGAGGC
187469	19665	ATGATGCGTGGCAGCCTGGC	232056	64252	TCCCAGAGTGCTGGGATTAA	276643	108839	AGCTACTAGGGAGGCTGAGG
187470	19666	CATGATGCGTGGCAGCCTGG	232057	64253	CTCCCAGAGTGCTGGGATTA	276644	108840	CAGCTACTAGGGAGGCTGAG
187471	19667	CCATGATGCGTGGCAGCCTG	232058	64254	CCTCCCAGAGTGCTGGGATT	276645	108841	CCAGCTACTAGGGAGGCTGA
187472	19668	CCCATGATGCGTGGCAGCCT	232059	64255	GCCTCCCAGAGTGCTGGGAT	276646	108842	CCCAGCTACTAGGGAGGCTG
187473	19669	ACCCATGATGCGTGGCAGCC	232060	64256	AGCCTCCCAGAGTGCTGGGA	276647	108843	TCCCAGCTACTAGGGAGGCT
187474	19670	GACCCATGATGCGTGGCAGC	232061	64257	CAGCCTCCCAGAGTGCTGGG	276648	108844	ATCCCAGCTACTAGGGAGGC
187475	19671	CGACCCATGATGCGTGGCAG	232062	64258	TCAGCCTCCCAGAGTGCTGG	276649	108845	AATCCCAGCTACTAGGGAGG
187476	19672	CCGACCCATGATGCGTGGCA	232063	64259	CTCAGCCTCCCAGAGTGCTG	276650	108846	TAATCCCAGCTACTAGGGAG
187477	19673	TCCGACCCATGATGCGTGGC	232064	64260	CCTCAGCCTCCCAGAGTGCT	276651	108847	GTAATCCCAGCTACTAGGGA
187478	19674	CTCCGACCCATGATGCGTGG	232065	64261	GCCTCAGCCTCCCAGAGTGC	276652	108848	TGTAATCCCAGCTACTAGGG
187479	19675	TCTCCGACCCATGATGCGTG	232066	64262	TGCCTCAGCCTCCCAGAGTG	276653	108849	TTGTAATCCCAGCTACTAGG
187480	19676	CTCTCCGACCCATGATGCGT	232067	64263	CTGCCTCAGCCTCCCAGAGT	276654	108850	CTTGTAATCCCAGCTACTAG
187481	19677	CCTCTCCGACCCATGATGCG	232068	64264	CCTGCCTCAGCCTCCCAGAG	276655	108851	GCTTGTAATCCCAGCTACTA
187482	19678	TCCTCTCCGACCCATGATGC	232069	64265	GCCTGCCTCAGCCTCCCAGA	276656	108852	TGCTTGTAATCCCAGCTACT
187483	19679	TTCCTCTCCGACCCATGATG	232070	64266	TGCCTGCCTCAGCCTCCCAG	276657	108853	GTGCTTGTAATCCCAGCTAC
187484	19680	CTTCCTCTCCGACCCATGAT	232071	64267	CTGCCTGCCTCAGCCTCCCA	276658	108854	TGTGCTTGTAATCCCAGCTA
187485	19681	TCTTCCTCTCCGACCCATGA	232072	64268	TCTGCCTGCCTCAGCCTCCC	276659	108855	GTGTGCTTGTAATCCCAGCT
187486	19682	GTCTTCCTCTCCGACCCATG	232073	64269	ATCTGCCTGCCTCAGCCTCC	276660	108856	TGTGTGCTTGTAATCCCAGC
187487	19683	GGTCTTCCTCTCCGACCCAT	232074	64270	GATCTGCCTGCCTCAGCCTC	276661	108857	GTGTGTGCTTGTAATCCCAG
187488	19684	TGGTCTTCCTCTCCGACCCA	232075	64271	TGATCTGCCTGCCTCAGCCT	276662	108858	GGTGTGTGCTTGTAATCCCA
187489	19685	GTGGTCTTCCTCTCCGACCC	232076	64272	GTGATCTGCCTGCCTCAGCC	276663	108859	TGGTGTGTGCTTGTAATCCC
187490	19686	TGTGGTCTTCCTCTCCGACC	232077	64273	AGTGATCTGCCTGCCTCAGC	276664	108860	GTGGTGTGTGCTTGTAATCC
187491	19687	GTGTGGTCTTCCTCTCCGAC	232078	64274	AAGTGATCTGCCTGCCTCAG	276665	108861	GGTGGTGTGTGCTTGTAATC
187492	19688	GGTGTGGTCTTCCTCTCCGA	232079	64275	CAAGTGATCTGCCTGCCTCA	276666	108862	TGGTGGTGTGTGCTTGTAAT
187493	19689	GGGTGTGGTCTTCCTCTCCG	232080	64276	TCAAGTGATCTGCCTGCCTC	276667	108863	ATGGTGGTGTGTGCTTGTAA
187494	19690	GGGGTGTGGTCTTCCTCTCC	232081	64277	CTCAAGTGATCTGCCTGCCT	276668	108864	CATGGTGGTGTGTGCTTGTA
187495	19691	AGGGGTGTGGTCTTCCTCTC	232082	64278	TCTCAAGTGATCTGCCTGCC	276669	108865	GCATGGTGGTGTGTGCTTGT
187496	19692	CAGGGGTGTGGTCTTCCTCT	232083	64279	ATCTCAAGTGATCTGCCTGC	276670	108866	GGCATGGTGGTGTGTGCTTG
187497	19693	CCAGGGGTGTGGTCTTCCTC	232084	64280	GATCTCAAGTGATCTGCCTG	276671	108867	AGGCATGGTGGTGTGTGCTT
187498	19694	TCCAGGGGTGTGGTCTTCCT	232085	64281	TGATCTCAAGTGATCTGCCT	276672	108868	TAGGCATGGTGGTGTGTGCT
187499	19695	CTCCAGGGGTGTGGTCTTCC	232086	64282	CTGATCTCAAGTGATCTGCC	276673	108869	CTAGGCATGGTGGTGTGTGC
187500	19696	GCTCCAGGGGTGTGGTCTTC	232087	64283	CCTGATCTCAAGTGATCTGC	276674	108870	GCTAGGCATGGTGGTGTGTG
187501	19697	TGCTCCAGGGGTGTGGTCTT	232088	64284	TCCTGATCTCAAGTGATCTG	276675	108871	TGCTAGGCATGGTGGTGTGT
187502	19698	CTGCTCCAGGGGTGTGGTCT	232089	64285	CTCCTGATCTCAAGTGATCT	276676	108872	TTGCTAGGCATGGTGGTGTG
187503	19699	TCTGCTCCAGGGGTGTGGTC	232090	64286	ACTCCTGATCTCAAGTGATC	276677	108873	TTTGCTAGGCATGGTGGTGT
187504	19700	CTCTGCTCCAGGGGTGTGGT	232091	64287	AACTCCTGATCTCAAGTGAT	276678	108874	ATTTGCTAGGCATGGTGGTG
187505	19701	CCTCTGCTCCAGGGGTGTGG	232092	64288	GAACTCCTGATCTCAAGTGA	276679	108875	AATTTGCTAGGCATGGTGGT
187506	19702	CCCTCTGCTCCAGGGGTGTG	232093	64289	AGAACTCCTGATCTCAAGTG	276680	108876	AAATTTGCTAGGCATGGTGG
187507	19703	GCCCTCTGCTCCAGGGGTGT	232094	64290	TAGAACTCCTGATCTCAAGT	276681	108877	AAAATTTGCTAGGCATGGTG
187508	19704	CGCCCTCTGCTCCAGGGGTG	232095	64291	CTAGAACTCCTGATCTCAAG	276682	108878	AAAAATTTGCTAGGCATGGT
187509	19705	CCGCCCTCTGCTCCAGGGGT	232096	64292	TCTAGAACTCCTGATCTCAA	276683	108879	TAAAAATTTGCTAGGCATGG
187510	19706	GCCGCCCTCTGCTCCAGGGG	232097	64293	GTCTAGAACTCCTGATCTCA	276684	108880	ATAAAAATTTGCTAGGCATG
187511	19707	AGCCGCCCTCTGCTCCAGGG	232098	64294	GGTCTAGAACTCCTGATCTC	276685	108881	TATAAAAATTTGCTAGGCAT
187512	19708	CAGCCGCCCTCTGCTCCAGG	232099	64295	TGGTCTAGAACTCCTGATCT	276686	108882	ATATAAAAATTTGCTAGGCA
187513	19709	TCAGCCGCCCTCTGCTCCAG	232100	64296	CTGGTCTAGAACTCCTGATC	276687	108883	AATATAAAAATTTGCTAGGC
187514	19710	ATCAGCCGCCCTCTGCTCCA	232101	64297	GCTGGTCTAGAACTCCTGAT	276688	108884	AAATATAAAAATTTGCTAGG
187515	19711	GATCAGCCGCCCTCTGCTCC	232102	64298	AGCTGGTCTAGAACTCCTGA	276689	108885	AAAATATAAAAATTTGCTAG
187516	19712	AGATCAGCCGCCCTCTGCTC	232103	64299	AAGCTGGTCTAGAACTCCTG	276690	108886	AAAAATATAAAAATTTGCTA
187517	19713	CAGATCAGCCGCCCTCTGCT	232104	64300	CAAGCTGGTCTAGAACTCCT	276691	108887	TAAAAATATAAAAATTTGCT
187518	19714	ACAGATCAGCCGCCCTCTGC	232105	64301	CCAAGCTGGTCTAGAACTCC	276692	108888	CTAAAAATATAAAAATTTGC
187519	19715	GACAGATCAGCCGCCCTCTG	232106	64302	GCCAAGCTGGTCTAGAACTC	276693	108889	ACTAAAAATATAAAAATTTG
187520	19716	TGACAGATCAGCCGCCCTCT	232107	64303	GGCCAAGCTGGTCTAGAACT	276694	108890	TACTAAAAATATAAAAATTT
187521	19717	CTGACAGATCAGCCGCCCTC	232108	64304	TGGCCAAGCTGGTCTAGAAC	276695	108891	CTACTAAAAATATAAAAATT
187522	19718	TCTGACAGATCAGCCGCCCT	232109	64305	TTGGCCAAGCTGGTCTAGAA	276696	108892	TCTACTAAAAATATAAAAAT
187523	19719	ATCTGACAGATCAGCCGCCC	232110	64306	GTTGGCCAAGCTGGTCTAGA	276697	108893	CTCTACTAAAAATATAAAAA
187524	19720	CATCTGACAGATCAGCCGCC	232111	64307	TGTTGGCCAAGCTGGTCTAG	276698	108894	CCTCTACTAAAAATATAAAA
187525	19721	GCATCTGACAGATCAGCCGC	232112	64308	ATGTTGGCCAAGCTGGTCTA	276699	108895	TCCTCTACTAAAAATATAAA
187526	19722	GGCATCTGACAGATCAGCCG	232113	64309	CATGTTGGCCAAGCTGGTCT	276700	108896	CTCCTCTACTAAAAATATAA
187527	19723	GGGCATCTGACAGATCAGCC	232114	64310	CCATGTTGGCCAAGCTGGTC	276701	108897	CCTCCTCTACTAAAAATATA
187528	19724	AGGGCATCTGACAGATCAGC	232115	64311	ACCATGTTGGCCAAGCTGGT	276702	108898	CCCTCCTCTACTAAAAATAT
187529	19725	AAGGGCATCTGACAGATCAG	232116	64312	CACCATGTTGGCCAAGCTGG	276703	108899	CCCCTCCTCTACTAAAAATA
187530	19726	AAAGGGCATCTGACAGATCA	232117	64313	TCACCATGTTGGCCAAGCTG	276704	108900	ACCCCTCCTCTACTAAAAAT

187531	19727	CAAAGGGCATCTGACAGATC	232118	64314	TTCACCATGTTGGCCAAGCT	276705	108901	CACCCCTCCTCTACTAAAAA
187532	19728	TCAAAGGGCATCTGACAGAT	232119	64315	TTTCACCATGTTGGCCAAGC	276706	108902	ACACCCCTCCTCTACTAAAA
187533	19729	GTCAAAGGGCATCTGACAGA	232120	64316	ATTTCACCATGTTGGCCAAG	276707	108903	GACACCCCTCCTCTACTAAA
187534	19730	TGTCAAAGGGCATCTGACAG	232121	64317	GATTTCACCATGTTGGCCAA	276708	108904	TGACACCCCTCCTCTACTAA
187535	19731	CTGTCAAAGGGCATCTGACA	232122	64318	GGATTTCACCATGTTGGCCA	276709	108905	GTGACACCCCTCCTCTACTA
187536	19732	GCTGTCAAAGGGCATCTGAC	232123	64319	GGGATTTCACCATGTTGGCC	276710	108906	GGTGACACCCCTCCTCTACT
187537	19733	TGCTGTCAAAGGGCATCTGA	232124	64320	CGGGATTTCACCATGTTGGC	276711	108907	TGGTGACACCCCTCCTCTAC
187538	19734	GTGCTGTCAAAGGGCATCTG	232125	64321	ACGGGATTTCACCATGTTGG	276712	108908	ATGGTGACACCCCTCCTCTA
187539	19735	GGTGCTGTCAAAGGGCATCT	232126	64322	GACGGGATTTCACCATGTTG	276713	108909	CATGGTGACACCCCTCCTCT
187540	19736	AGGTGCTGTCAAAGGGCATC	232127	64323	AGACGGGATTTCACCATGTT	276714	108910	ACATGGTGACACCCCTCCTC
187541	19737	GAGGTGCTGTCAAAGGGCAT	232128	64324	GAGACGGGATTTCACCATGT	276715	108911	AACATGGTGACACCCCTCCT
187542	19738	TGAGGTGCTGTCAAAGGGCA	232129	64325	AGAGACGGGATTTCACCATG	276716	108912	AAACATGGTGACACCCCTCC
187543	19739	CTGAGGTGCTGTCAAAGGGC	232130	64326	TAGAGACGGGATTTCACCAT	276717	108913	CAAACATGGTGACACCCCTC
187544	19740	GCTGAGGTGCTGTCAAAGGG	232131	64327	GTAGAGACGGGATTTCACCA	276718	108914	GCAAACATGGTGACACCCCT
187545	19741	AGCTGAGGTGCTGTCAAAGG	232132	64328	TGTAGAGACGGGATTTCACC	276719	108915	GGCAAACATGGTGACACCCC
187546	19742	AAGCTGAGGTGCTGTCAAAG	232133	64329	TTGTAGAGACGGGATTTCAC	276720	108916	TGGCAAACATGGTGACACCC
187547	19743	GAAGCTGAGGTGCTGTCAAA	232134	64330	TTTGTAGAGACGGGATTTCA	276721	108917	TTGGCAAACATGGTGACACC
187548	19744	GGAAGCTGAGGTGCTGTCAA	232135	64331	TTTTGTAGAGACGGGATTTC	276722	108918	CTTGGCAAACATGGTGACAC
187549	19745	TGGAAGCTGAGGTGCTGTCA	232136	64332	TTTTTGTAGAGACGGGATTT	276723	108919	GCTTGGCAAACATGGTGACA
187550	19746	TTGGAAGCTGAGGTGCTGTC	232137	64333	TTTTTTGTAGAGACGGGATT	276724	108920	AGCTTGGCAAACATGGTGAC
187551	19747	CTTGGAAGCTGAGGTGCTGT	232138	64334	ATTTTTTGTAGAGACGGGAT	276725	108921	CAGCTTGGCAAACATGGTGA
187552	19748	TCTTGGAAGCTGAGGTGCTG	232139	64335	TATTTTTTGTAGAGACGGGA	276726	108922	CCAGCTTGGCAAACATGGTG
187553	19749	TTCTTGGAAGCTGAGGTGCT	232140	64336	GTATTTTTTGTAGAGACGGG	276727	108923	ACCAGCTTGGCAAACATGGT
187554	19750	ATTCTTGGAAGCTGAGGTGC	232141	64337	TGTATTTTTTGTAGAGACGG	276728	108924	GACCAGCTTGGCAAACATGG
187555	19751	AATTCTTGGAAGCTGAGGTG	232142	64338	TTGTATTTTTTGTAGAGACG	276729	108925	AGACCAGCTTGGCAAACATG
187556	19752	TAATTCTTGGAAGCTGAGGT	232143	64339	TTTGTATTTTTTGTAGAGAC	276730	108926	GAGACCAGCTTGGCAAACAT
187557	19753	TTAATTCTTGGAAGCTGAGG	232144	64340	TTTTGTATTTTTTGTAGAGA	276731	108927	TGAGACCAGCTTGGCAAACA
187558	19754	GTTAATTCTTGGAAGCTGAG	232145	64341	TTTTTGTATTTTTTGTAGAG	276732	108928	TTGAGACCAGCTTGGCAAAC
187559	19755	GGTTAATTCTTGGAAGCTGA	232146	64342	ATTTTTGTATTTTTTGTAGA	276733	108929	TTTGAGACCAGCTTGGCAAA
187560	19756	GGGTTAATTCTTGGAAGCTG	232147	64343	AATTTTTGTATTTTTTGTAG	276734	108930	GTTTGAGACCAGCTTGGCAA
187561	19757	AGGGTTAATTCTTGGAAGCT	232148	64344	GAATTTTTGTATTTTTTGTA	276735	108931	AGTTTGAGACCAGCTTGGCA
187562	19758	AAGGGTTAATTCTTGGAAGC	232149	64345	CGAATTTTTGTATTTTTTGT	276736	108932	GAGTTTGAGACCAGCTTGGC
187563	19759	AAAGGGTTAATTCTTGGAAG	232150	64346	GCGAATTTTTGTATTTTTTG	276737	108933	GGAGTTTGAGACCAGCTTGG
187564	19760	GAAAGGGTTAATTCTTGGAA	232151	64347	GGCGAATTTTTGTATTTTTT	276738	108934	AGGAGTTTGAGACCAGCTTG
187565	19761	AGAAAGGGTTAATTCTTGGA	232152	64348	TGGCGAATTTTTGTATTTTT	276739	108935	CAGGAGTTTGAGACCAGCTT
187566	19762	TAGAAAGGGTTAATTCTTGG	232153	64349	TTGGCGAATTTTTGTATTTT	276740	108936	CCAGGAGTTTGAGACCAGCT
187567	19763	ATAGAAAGGGTTAATTCTTG	232154	64350	CTTGGCGAATTTTTGTATTT	276741	108937	GCCAGGAGTTTGAGACCAGC
187568	19764	CATAGAAAGGGTTAATTCTT	232155	64351	GCTTGGCGAATTTTTGTATT	276742	108938	GGCCAGGAGTTTGAGACCAG
187569	19765	ACATAGAAAGGGTTAATTCT	232156	64352	CGCTTGGCGAATTTTTGTAT	276743	108939	AGGCCAGGAGTTTGAGACCA
187570	19766	CACATAGAAAGGGTTAATTC	232157	64353	ACGCTTGGCGAATTTTTGTA	276744	108940	GAGGCCAGGAGTTTGAGACC
187571	19767	TCACATAGAAAGGGTTAATT	232158	64354	CACGCTTGGCGAATTTTTGT	276745	108941	TGAGGCCAGGAGTTTGAGAC
187572	19768	CTCACATAGAAAGGGTTAAT	232159	64355	CCACGCTTGGCGAATTTTTG	276746	108942	CTGAGGCCAGGAGTTTGAGA
187573	19769	GCTCACATAGAAAGGGTTAA	232160	64356	ACCACGCTTGGCGAATTTTT	276747	108943	CCTGAGGCCAGGAGTTTGAG
187574	19770	TGCTCACATAGAAAGGGTTA	232161	64357	CACCACGCTTGGCGAATTTT	276748	108944	ACCTGAGGCCAGGAGTTTGA
187575	19771	CTGCTCACATAGAAAGGGTT	232162	64358	CCACCACGCTTGGCGAATTT	276749	108945	CACCTGAGGCCAGGAGTTTG
187576	19772	TCTGCTCACATAGAAAGGGT	232163	64359	GCCACCACGCTTGGCGAATT	276750	108946	TCACCTGAGGCCAGGAGTTT
187577	19773	CTCTGCTCACATAGAAAGGG	232164	64360	TGCCACCACGCTTGGCGAAT	276751	108947	ATCACCTGAGGCCAGGAGTT
187578	19774	CCTCTGCTCACATAGAAAGG	232165	64361	GTGCCACCACGCTTGGCGAA	276752	108948	GATCACCTGAGGCCAGGAGT
187579	19775	GCCTCTGCTCACATAGAAAG	232166	64362	TGTGCCACCACGCTTGGCGA	276753	108949	AGATCACCTGAGGCCAGGAG
187580	19776	TGCCTCTGCTCACATAGAAA	232167	64363	ATGTGCCACCACGCTTGGCG	276754	108950	CAGATCACCTGAGGCCAGGA
187581	19777	ATGCCTCTGCTCACATAGAA	232168	64364	CATGTGCCACCACGCTTGGC	276755	108951	GCAGATCACCTGAGGCCAGG
187582	19778	GATGCCTCTGCTCACATAGA	232169	64365	GCATGTGCCACCACGCTTGG	276756	108952	GGCAGATCACCTGAGGCCAG
187583	19779	GGATGCCTCTGCTCACATAG	232170	64366	GGCATGTGCCACCACGCTTG	276757	108953	AGGCAGATCACCTGAGGCCA
187584	19780	TGGATGCCTCTGCTCACATA	232171	64367	AGGCATGTGCCACCACGCTT	276758	108954	TAGGCAGATCACCTGAGGCC
187585	19781	ATGGATGCCTCTGCTCACAT	232172	64368	CAGGCATGTGCCACCACGCT	276759	108955	GTAGGCAGATCACCTGAGGC
187586	19782	CATGGATGCCTCTGCTCACA	232173	64369	ACAGGCATGTGCCACCACGC	276760	108956	GGTAGGCAGATCACCTGAGG
187587	19783	CCATGGATGCCTCTGCTCAC	232174	64370	CACAGGCATGTGCCACCACG	276761	108957	AGGTAGGCAGATCACCTGAG
187588	19784	CCCATGGATGCCTCTGCTCA	232175	64371	TCACAGGCATGTGCCACCAC	276762	108958	AAGGTAGGCAGATCACCTGA
187589	19785	CCCCATGGATGCCTCTGCTC	232176	64372	ATCACAGGCATGTGCCACCA	276763	108959	CAAGGTAGGCAGATCACCTG
187590	19786	CCCCCATGGATGCCTCTGCT	232177	64373	GATCACAGGCATGTGCCACC	276764	108960	CCAAGGTAGGCAGATCACCT
187591	19787	CCCCCCATGGATGCCTCTGC	232178	64374	GGATCACAGGCATGTGCCAC	276765	108961	ACCAAGGTAGGCAGATCACC
187592	19788	TCCCCCCATGGATGCCTCTG	232179	64375	GGGATCACAGGCATGTGCCA	276766	108962	GACCAAGGTAGGCAGATCAC
187593	19789	GTCCCCCCATGGATGCCTCT	232180	64376	TGGGATCACAGGCATGTGCC	276767	108963	AGACCAAGGTAGGCAGATCA
187594	19790	TGTCCCCCCATGGATGCCTC	232181	64377	CTGGGATCACAGGCATGTGC	276768	108964	GAGACCAAGGTAGGCAGATC
187595	19791	GTGTCCCCCCATGGATGCCT	232182	64378	GCTGGGATCACAGGCATGTG	276769	108965	GGAGACCAAGGTAGGCAGAT
187596	19792	TGTGTCCCCCCATGGATGCC	232183	64379	AGCTGGGATCACAGGCATGT	276770	108966	GGGAGACCAAGGTAGGCAGA
187597	19793	GTGTGTCCCCCCATGGATGC	232184	64380	TAGCTGGGATCACAGGCATG	276771	108967	TGGGAGACCAAGGTAGGCAG
187598	19794	AGTGTGTCCCCCCATGGATG	232185	64381	GTAGCTGGGATCACAGGCAT	276772	108968	TTGGGAGACCAAGGTAGGCA
187599	19795	CAGTGTGTCCCCCCATGGAT	232186	64382	AGTAGCTGGGATCACAGGCA	276773	108969	TTTGGGAGACCAAGGTAGGC
187600	19796	CCAGTGTGTCCCCCCATGGA	232187	64383	GAGTAGCTGGGATCACAGGC	276774	108970	CTTTGGGAGACCAAGGTAGG
187601	19797	ACCAGTGTGTCCCCCCATGG	232188	64384	CGAGTAGCTGGGATCACAGG	276775	108971	ACTTTGGGAGACCAAGGTAG
187602	19798	CACCAGTGTGTCCCCCCATG	232189	64385	CCGAGTAGCTGGGATCACAG	276776	108972	CACTTTGGGAGACCAAGGTA

187603	19799	TCACCAGTGTGTCCCCCCAT	232190	64386	CCCGAGTAGCTGGGATCACA	276777	108973	GCACTTTGGGAGACCAAGGT
187604	19800	TTCACCAGTGTGTCCCCCCA	232191	64387	TCCCGAGTAGCTGGGATCAC	276778	108974	AGCACTTTGGGAGACCAAGG
187605	19801	ATTCACCAGTGTGTCCCCCC	232192	64388	CTCCCGAGTAGCTGGGATCA	276779	108975	CAGCACTTTGGGAGACCAAG
187606	19802	GATTCACCAGTGTGTCCCCC	232193	64389	CCTCCCGAGTAGCTGGGATC	276780	108976	CCAGCACTTTGGGAGACCAA
187607	19803	TGATTCACCAGTGTGTCCCC	232194	64390	GCCTCCCGAGTAGCTGGGAT	276781	108977	CCCAGCACTTTGGGAGACCA
187608	19804	ATGATTCACCAGTGTGTCCC	232195	64391	AGCCTCCCGAGTAGCTGGGA	276782	108978	TCCCAGCACTTTGGGAGACC
187609	19805	GATGATTCACCAGTGTGTCC	232196	64392	CAGCCTCCCGAGTAGCTGGG	276783	108979	ATCCCAGCACTTTGGGAGAC
187610	19806	AGATGATTCACCAGTGTGTC	232197	64393	TCAGCCTCCCGAGTAGCTGG	276784	108980	AATCCCAGCACTTTGGGAGA
187611	19807	CAGATGATTCACCAGTGTGT	232198	64394	CTCAGCCTCCCGAGTAGCTG	276785	108981	TAATCCCAGCACTTTGGGAG
187612	19808	ACAGATGATTCACCAGTGTG	232199	64395	TCTCAGCCTCCCGAGTAGCT	276786	108982	GTAATCCCAGCACTTTGGGA
187613	19809	AACAGATGATTCACCAGTGT	232200	64396	GTCTCAGCCTCCCGAGTAGC	276787	108983	TGTAATCCCAGCACTTTGGG
187614	19810	TAACAGATGATTCACCAGTG	232201	64397	TGTCTCAGCCTCCCGAGTAG	276788	108984	CTGTAATCCCAGCACTTTGG
187615	19811	ATAACAGATGATTCACCAGT	232202	64398	CTGTCTCAGCCTCCCGAGTA	276789	108985	CCTGTAATCCCAGCACTTTG
187616	19812	CATAACAGATGATTCACCAG	232203	64399	CCTGTCTCAGCCTCCCGAGT	276790	108986	ACCTGTAATCCCAGCACTTT
187617	19813	ACATAACAGATGATTCACCA	232204	64400	TCCTGTCTCAGCCTCCCGAG	276791	108987	CACCTGTAATCCCAGCACTT
187618	19814	TACATAACAGATGATTCACC	232205	64401	CTCCTGTCTCAGCCTCCCGA	276792	108988	ACACCTGTAATCCCAGCACT
187619	19815	CTACATAACAGATGATTCAC	232206	64402	TCTCCTGTCTCAGCCTCCCG	276793	108989	CACACCTGTAATCCCAGCAC
187620	19816	TCTACATAACAGATGATTCA	232207	64403	TTCTCCTGTCTCAGCCTCCC	276794	108990	TCACACCTGTAATCCCAGCA
187621	19817	TTCTACATAACAGATGATTC	232208	64404	ATTCTCCTGTCTCAGCCTCC	276795	108991	CTCACACCTGTAATCCCAGC
187622	19818	CTTCTACATAACAGATGATT	232209	64405	AATTCTCCTGTCTCAGCCTC	276796	108992	GCTCACACCTGTAATCCCAG
187623	19819	ACTTCTACATAACAGATGAT	232210	64406	CAATTCTCCTGTCTCAGCCT	276797	108993	GGCTCACACCTGTAATCCCA
187624	19820	GACTTCTACATAACAGATGA	232211	64407	GCAATTCTCCTGTCTCAGCC	276798	108994	TGGCTCACACCTGTAATCCC
187625	19821	AGACTTCTACATAACAGATG	232212	64408	AGCAATTCTCCTGTCTCAGC	276799	108995	GTGGCTCACACCTGTAATCC
187626	19822	CAGACTTCTACATAACAGAT	232213	64409	AAGCAATTCTCCTGTCTCAG	276800	108996	GGTGGCTCACACCTGTAATC
187627	19823	CCAGACTTCTACATAACAGA	232214	64410	CAAGCAATTCTCCTGTCTCA	276801	108997	TGGTGGCTCACACCTGTAAT
187628	19824	TCCAGACTTCTACATAACAG	232215	64411	TCAAGCAATTCTCCTGTCTC	276802	108998	GTGGTGGCTCACACCTGTAA
187629	19825	TTCCAGACTTCTACATAACA	232216	64412	TTCAAGCAATTCTCCTGTCT	276803	108999	CGTGGTGGCTCACACCTGTA
187630	19826	TTTCCAGACTTCTACATAAC	232217	64413	GTTCAAGCAATTCTCCTGTC	276804	109000	GCGTGGTGGCTCACACCTGT
187631	19827	TTTTCCAGACTTCTACATAA	232218	64414	TGTTCAAGCAATTCTCCTGT	276805	109001	GGCGTGGTGGCTCACACCTG
187632	19828	GTTTTCCAGACTTCTACATA	232219	64415	GTGTTCAAGCAATTCTCCTG	276806	109002	AGGCGTGGTGGCTCACACCT
187633	19829	TGTTTTCCAGACTTCTACAT	232220	64416	CGTGTTCAAGCAATTCTCCT	276807	109003	CAGGCGTGGTGGCTCACACC
187634	19830	ATGTTTTCCAGACTTCTACA	232221	64417	CCGTGTTCAAGCAATTCTCC	276808	109004	GCAGGCGTGGTGGCTCACAC
187635	19831	GATGTTTTCCAGACTTCTAC	232222	64418	CCCGTGTTCAAGCAATTCTC	276809	109005	GGCAGGCGTGGTGGCTCACA
187636	19832	TGATGTTTTCCAGACTTCTA	232223	64419	TCCCGTGTTCAAGCAATTCT	276810	109006	GGGCAGGCGTGGTGGCTCAC
187637	19833	CTGATGTTTTCCAGACTTCT	232224	64420	CTCCCGTGTTCAAGCAATTC	276811	109007	AGGGCAGGCGTGGTGGCTCA
187638	19834	CCTGATGTTTTCCAGACTTC	232225	64421	CCTCCCGTGTTCAAGCAATT	276812	109008	AAGGGCAGGCGTGGTGGCTC
187639	19835	TCCTGATGTTTTCCAGACTT	232226	64422	GCCTCCCGTGTTCAAGCAAT	276813	109009	TAAGGGCAGGCGTGGTGGCT
187640	19836	ATCCTGATGTTTTCCAGACT	232227	64423	TGCCTCCCGTGTTCAAGCAA	276814	109010	TTAAGGGCAGGCGTGGTGGC
187641	19837	CATCCTGATGTTTTCCAGAC	232228	64424	CTGCCTCCCGTGTTCAAGCA	276815	109011	TTTAAGGGCAGGCGTGGTGG
187642	19838	CCATCCTGATGTTTTCCAGA	232229	64425	TCTGCCTCCCGTGTTCAAGC	276816	109012	TTTTAAGGGCAGGCGTGGTG
187643	19839	TCCATCCTGATGTTTTCCAG	232230	64426	CTCTGCCTCCCGTGTTCAAG	276817	109013	TTTTTAAGGGCAGGCGTGGT
187644	19840	TTCCATCCTGATGTTTTCCA	232231	64427	CCTCTGCCTCCCGTGTTCAA	276818	109014	ATTTTTAAGGGCAGGCGTGG
187645	19841	GTTCCATCCTGATGTTTTCC	232232	64428	ACCTCTGCCTCCCGTGTTCA	276819	109015	TATTTTTAAGGGCAGGCGTG
187646	19842	AGTTCCATCCTGATGTTTTC	232233	64429	AACCTCTGCCTCCCGTGTTC	276820	109016	GTATTTTTAAGGGCAGGCGT
187647	19843	CAGTTCCATCCTGATGTTTT	232234	64430	CAACCTCTGCCTCCCGTGTT	276821	109017	TGTATTTTTAAGGGCAGGCG
187648	19844	CCAGTTCCATCCTGATGTTT	232235	64431	GCAACCTCTGCCTCCCGTGT	276822	109018	ATGTATTTTTAAGGGCAGGC
187649	19845	ACCAGTTCCATCCTGATGTT	232236	64432	TGCAACCTCTGCCTCCCGTG	276823	109019	AATGTATTTTTAAGGGCAGG
187650	19846	CACCAGTTCCATCCTGATGT	232237	64433	CTGCAACCTCTGCCTCCCGT	276824	109020	TAATGTATTTTTAAGGGCAG
187651	19847	TCACCAGTTCCATCCTGATG	232238	64434	ACTGCAACCTCTGCCTCCCG	276825	109021	ATAATGTATTTTTAAGGGCA
187652	19848	TTCACCAGTTCCATCCTGAT	232239	64435	TACTGCAACCTCTGCCTCCC	276826	109022	TATAATGTATTTTTAAGGGC
187653	19849	TTTCACCAGTTCCATCCTGA	232240	64436	TTACTGCAACCTCTGCCTCC	276827	109023	ATATAATGTATTTTTAAGGG
187654	19850	ATTTCACCAGTTCCATCCTG	232241	64437	CTTACTGCAACCTCTGCCTC	276828	109024	AATATAATGTATTTTTAAGG
187655	19851	TATTTCACCAGTTCCATCCT	232242	64438	GCTTACTGCAACCTCTGCCT	276829	109025	AAATATAATGTATTTTTAAG
187656	19852	TTATTTCACCAGTTCCATCC	232243	64439	AGCTTACTGCAACCTCTGCC	276830	109026	TAAATATAATGTATTTTTAA
187657	19853	CTTATTTCACCAGTTCCATC	232244	64440	CAGCTTACTGCAACCTCTGC	276831	109027	TTAAATATAATGTATTTTTA
187658	19854	ACTTATTTCACCAGTTCCAT	232245	64441	TCAGCTTACTGCAACCTCTG	276832	109028	ATTAAATATAATGTATTTTT
187659	19855	CACTTATTTCACCAGTTCCA	232246	64442	CTCAGCTTACTGCAACCTCT	276833	109029	TATTAAATATAATGTATTTT
187660	19856	ACACTTATTTCACCAGTTCC	232247	64443	TCTCAGCTTACTGCAACCTC	276834	109030	CTATTAAATATAATGTATTT
187661	19857	CACACTTATTTCACCAGTTC	232248	64444	ATCTCAGCTTACTGCAACCT	276835	109031	GCTATTAAATATAATGTATT
187662	19858	CCACACTTATTTCACCAGTT	232249	64445	GATCTCAGCTTACTGCAACC	276836	109032	TGCTATTAAATATAATGTAT
187663	19859	GCCACACTTATTTCACCAGT	232250	64446	CGATCTCAGCTTACTGCAAC	276837	109033	TTGCTATTAAATATAATGTA
187664	19860	GGCCACACTTATTTCACCAG	232251	64447	ACGATCTCAGCTTACTGCAA	276838	109034	TTTGCTATTAAATATAATGT
187665	19861	AGGCCACACTTATTTCACCA	232252	64448	TACGATCTCAGCTTACTGCA	276839	109035	CTTTGCTATTAAATATAATG
187666	19862	GAGGCCACACTTATTTCACC	232253	64449	GTACGATCTCAGCTTACTGC	276840	109036	GCTTTGCTATTAAATATAAT
187667	19863	AGAGGCCACACTTATTTCAC	232254	64450	GGTACGATCTCAGCTTACTG	276841	109037	GGCTTTGCTATTAAATATAA
187668	19864	CAGAGGCCACACTTATTTCA	232255	64451	TGGTACGATCTCAGCTTACT	276842	109038	GGGCTTTGCTATTAAATATA
187669	19865	TCAGAGGCCACACTTATTTC	232256	64452	ATGGTACGATCTCAGCTTAC	276843	109039	GGGGCTTTGCTATTAAATAT
187670	19866	GTCAGAGGCCACACTTATTT	232257	64453	AATGGTACGATCTCAGCTTA	276844	109040	TGGGGCTTTGCTATTAAATA
187671	19867	CGTCAGAGGCCACACTTATT	232258	64454	GAATGGTACGATCTCAGCTT	276845	109041	CTGGGGCTTTGCTATTAAAT
187672	19868	CCGTCAGAGGCCACACTTAT	232259	64455	GGAATGGTACGATCTCAGCT	276846	109042	ACTGGGGCTTTGCTATTAAA
187673	19869	TCCGTCAGAGGCCACACTTA	232260	64456	TGGAATGGTACGATCTCAGC	276847	109043	AACTGGGGCTTTGCTATTAA
187674	19870	TTCCGTCAGAGGCCACACTT	232261	64457	CTGGAATGGTACGATCTCAG	276848	109044	CAACTGGGGCTTTGCTATTA

187675	19871	ATTCCGTCAGAGGCCACACT	232262	64458	ACTGGAATGGTACGATCTCA	276849	109045	ACAACTGGGGCTTTGCTATT
187676	19872	CATTCCGTCAGAGGCCACAC	232263	64459	GACTGGAATGGTACGATCTC	276850	109046	GACAACTGGGGCTTTGCTAT
187677	19873	CCATTCCGTCAGAGGCCACA	232264	64460	GGACTGGAATGGTACGATCT	276851	109047	TGACAACTGGGGCTTTGCTA
187678	19874	TCCATTCCGTCAGAGGCCAC	232265	64461	TGGACTGGAATGGTACGATC	276852	109048	GTGACAACTGGGGCTTTGCT
187679	19875	CTCCATTCCGTCAGAGGCCA	232266	64462	CTGGACTGGAATGGTACGAT	276853	109049	AGTGACAACTGGGGCTTTGC
187680	19876	GCTCCATTCCGTCAGAGGCC	232267	64463	GCTGGACTGGAATGGTACGA	276854	109050	AAGTGACAACTGGGGCTTTG
187681	19877	CGCTCCATTCCGTCAGAGGC	232268	64464	GGCTGGACTGGAATGGTACG	276855	109051	AAAGTGACAACTGGGGCTTT
187682	19878	CCGCTCCATTCCGTCAGAGG	232269	64465	AGGCTGGACTGGAATGGTAC	276856	109052	TAAAGTGACAACTGGGGCTT
187683	19879	ACCGCTCCATTCCGTCAGAG	232270	64466	CAGGCTGGACTGGAATGGTA	276857	109053	TTAAAGTGACAACTGGGGCT
187684	19880	GACCGCTCCATTCCGTCAGA	232271	64467	CCAGGCTGGACTGGAATGGT	276858	109054	TTTAAAGTGACAACTGGGGC
187685	19881	GGACCGCTCCATTCCGTCAG	232272	64468	CCCAGGCTGGACTGGAATGG	276859	109055	TTTTAAAGTGACAACTGGGG
187686	19882	CGGACCGCTCCATTCCGTCA	232273	64469	GCCCAGGCTGGACTGGAATG	276860	109056	TTTTTAAAGTGACAACTGGG
187687	19883	ACGGACCGCTCCATTCCGTC	232274	64470	AGCCCAGGCTGGACTGGAAT	276861	109057	CTTTTTAAAGTGACAACTGG
187688	19884	GACGGACCGCTCCATTCCGT	232275	64471	TAGCCCAGGCTGGACTGGAA	276862	109058	GCTTTTTAAAGTGACAACTG
187689	19885	AGACGGACCGCTCCATTCCG	232276	64472	GTAGCCCAGGCTGGACTGGA	276863	109059	TGCTTTTTAAAGTGACAACT
187690	19886	CAGACGGACCGCTCCATTCC	232277	64473	TGTAGCCCAGGCTGGACTGG	276864	109060	ATGCTTTTTAAAGTGACAAC
187691	19887	GCAGACGGACCGCTCCATTC	232278	64474	CTGTAGCCCAGGCTGGACTG	276865	109061	GATGCTTTTTAAAGTGACAA
187692	19888	TGCAGACGGACCGCTCCATT	232279	64475	TCTGTAGCCCAGGCTGGACT	276866	109062	AGATGCTTTTTAAAGTGACA
187693	19889	GTGCAGACGGACCGCTCCAT	232280	64476	CTCTGTAGCCCAGGCTGGAC	276867	109063	TAGATGCTTTTTAAAGTGAC
187694	19890	AGTGCAGACGGACCGCTCCA	232281	64477	GCTCTGTAGCCCAGGCTGGA	276868	109064	ATAGATGCTTTTTAAAGTGA
187695	19891	CAGTGCAGACGGACCGCTCC	232282	64478	CGCTCTGTAGCCCAGGCTGG	276869	109065	CATAGATGCTTTTTAAAGTG
187696	19892	GCAGTGCAGACGGACCGCTC	232283	64479	TCGCTCTGTAGCCCAGGCTG	276870	109066	ACATAGATGCTTTTTAAAGT
187697	19893	AGCAGTGCAGACGGACCGCT	232284	64480	CTCGCTCTGTAGCCCAGGCT	276871	109067	TACATAGATGCTTTTTAAAG
187698	19894	CAGCAGTGCAGACGGACCGC	232285	64481	TCTCGCTCTGTAGCCCAGGC	276872	109068	CTACATAGATGCTTTTTAAA
187699	19895	GCAGCAGTGCAGACGGACCG	232286	64482	GTCTCGCTCTGTAGCCCAGG	276873	109069	TCTACATAGATGCTTTTTAA
187700	19896	CGCAGCAGTGCAGACGGACC	232287	64483	AGTCTCGCTCTGTAGCCCAG	276874	109070	TTCTACATAGATGCTTTTTA
187701	19897	CCGCAGCAGTGCAGACGGAC	232288	64484	GAGTCTCGCTCTGTAGCCCA	276875	109071	GTTCTACATAGATGCTTTTT
187702	19898	CCCGCAGCAGTGCAGACGGA	232289	64485	AGAGTCTCGCTCTGTAGCCC	276876	109072	TGTTCTACATAGATGCTTTT
187703	19899	ACCCGCAGCAGTGCAGACGG	232290	64486	CAGAGTCTCGCTCTGTAGCC	276877	109073	ATGTTCTACATAGATGCTTT
187704	19900	CACCCGCAGCAGTGCAGACG	232291	64487	ACAGAGTCTCGCTCTGTAGC	276878	109074	AATGTTCTACATAGATGCTT
187705	19901	GCACCCGCAGCAGTGCAGAC	232292	64488	GACAGAGTCTCGCTCTGTAG	276879	109075	AAATGTTCTACATAGATGCT
187706	19902	GGCACCCGCAGCAGTGCAGA	232293	64489	GGACAGAGTCTCGCTCTGTA	276880	109076	TAAATGTTCTACATAGATGC
187707	19903	GGGCACCCGCAGCAGTGCAG	232294	64490	GGGACAGAGTCTCGCTCTGT	276881	109077	ATAAATGTTCTACATAGATG
187708	19904	GGGGCACCCGCAGCAGTGCA	232295	64491	TGGGACAGAGTCTCGCTCTG	276882	109078	CATAAATGTTCTACATAGAT
187709	19905	AGGGGCACCCGCAGCAGTGC	232296	64492	CTGGGACAGAGTCTCGCTCT	276883	109079	ACATAAATGTTCTACATAGA
187710	19906	GAGGGGCACCCGCAGCAGTG	232297	64493	TCTGGGACAGAGTCTCGCTC	276884	109080	CACATAAATGTTCTACATAG
187711	19907	TGAGGGGCACCCGCAGCAGT	232298	64494	TTCTGGGACAGAGTCTCGCT	276885	109081	CCACATAAATGTTCTACATA
187712	19908	CTGAGGGGCACCCGCAGCAG	232299	64495	TTTCTGGGACAGAGTCTCGC	276886	109082	TCCACATAAATGTTCTACAT
187713	19909	TCTGAGGGGCACCCGCAGCA	232300	64496	TTTTCTGGGACAGAGTCTCG	276887	109083	TTCCACATAAATGTTCTACA
187714	19910	ATCTGAGGGGCACCCGCAGC	232301	64497	TTTTTCTGGGACAGAGTCTC	276888	109084	ATTCCACATAAATGTTCTAC
187715	19911	GATCTGAGGGGCACCCGCAG	232302	64498	TTTTTTCTGGGACAGAGTCT	276889	109085	TATTCCACATAAATGTTCTA
187716	19912	GGATCTGAGGGGCACCCGCA	232303	64499	ATTTTTTCTGGGACAGAGTC	276890	109086	TTATTCCACATAAATGTTCT
187717	19913	AGGATCTGAGGGGCACCCGC	232304	64500	AATTTTTTCTGGGACAGAGT	276891	109087	TTTATTCCACATAAATGTTC
187718	19914	CAGGATCTGAGGGGCACCCG	232305	64501	TAATTTTTTCTGGGACAGAG	276892	109088	ATTTATTCCACATAAATGTT
187719	19915	ACAGGATCTGAGGGGCACCC	232306	64502	TTAATTTTTTCTGGGACAGA	276893	109089	TATTTATTCCACATAAATGT
187720	19916	CACAGGATCTGAGGGGCACC	232307	64503	TTTAATTTTTTCTGGGACAG	276894	109090	GTATTTATTCCACATAAATG
187721	19917	CCACAGGATCTGAGGGGCAC	232308	64504	TTTTAATTTTTTCTGGGACA	276895	109091	TGTATTTATTCCACATAAAT
187722	19918	CCCACAGGATCTGAGGGGCA	232309	64505	GTTTTAATTTTTTCTGGGAC	276896	109092	CTGTATTTATTCCACATAAA
187723	19919	ACCCACAGGATCTGAGGGGC	232310	64506	TGTTTTAATTTTTTCTGGGA	276897	109093	ACTGTATTTATTCCACATAA
187724	19920	GACCCACAGGATCTGAGGGG	232311	64507	ATGTTTTAATTTTTTCTGGG	276898	109094	CACTGTATTTATTCCACATA
187725	19921	TGACCCACAGGATCTGAGGG	232312	64508	GATGTTTTAATTTTTTCTGG	276899	109095	TCACTGTATTTATTCCACAT
187726	19922	CTGACCCACAGGATCTGAGG	232313	64509	TGATGTTTTAATTTTTTCTG	276900	109096	TTCACTGTATTTATTCCACA
187727	19923	ACTGACCCACAGGATCTGAG	232314	64510	GTGATGTTTTAATTTTTTCT	276901	109097	ATTCACTGTATTTATTCCAC
187728	19924	CACTGACCCACAGGATCTGA	232315	64511	TGTGATGTTTTAATTTTTTC	276902	109098	AATTCACTGTATTTATTCCA
187729	19925	TCACTGACCCACAGGATCTG	232316	64512	ATGTGATGTTTTAATTTTTT	276903	109099	AAATTCACTGTATTTATTCC
187730	19926	CTCACTGACCCACAGGATCT	232317	64513	TATGTGATGTTTTAATTTTT	276904	109100	CAAATTCACTGTATTTATTC
187731	19927	TCTCACTGACCCACAGGATC	232318	64514	ATATGTGATGTTTTAATTTT	276905	109101	ACAAATTCACTGTATTTATT
187732	19928	TTCTCACTGACCCACAGGAT	232319	64515	AATATGTGATGTTTTAATTT	276906	109102	TACAAATTCACTGTATTTAT
187733	19929	TTTCTCACTGACCCACAGGA	232320	64516	AAATATGTGATGTTTTAATT	276907	109103	GTACAAATTCACTGTATTTA
187734	19930	TTTTCTCACTGACCCACAGG	232321	64517	TAAATATGTGATGTTTTAAT	276908	109104	CGTACAAATTCACTGTATTT
187735	19931	CTTTTCTCACTGACCCACAG	232322	64518	TTAAATATGTGATGTTTTAA	276909	109105	ACGTACAAATTCACTGTATT
187736	19932	GCTTTTCTCACTGACCCACA	232323	64519	TTTAAATATGTGATGTTTTA	276910	109106	CACGTACAAATTCACTGTAT
187737	19933	TGCTTTTCTCACTGACCCAC	232324	64520	GTTTAAATATGTGATGTTTT	276911	109107	CCACGTACAAATTCACTGTA
187738	19934	CTGCTTTTCTCACTGACCCA	232325	64521	TGTTTAAATATGTGATGTTT	276912	109108	TCCACGTACAAATTCACTGT
187739	19935	ACTGCTTTTCTCACTGACCC	232326	64522	TTGTTTAAATATGTGATGTT	276913	109109	TTCCACGTACAAATTCACTG
187740	19936	CACTGCTTTTCTCACTGACC	232327	64523	GTTGTTTAAATATGTGATGT	276914	109110	ATTCCACGTACAAATTCACT
187741	19937	TCACTGCTTTTCTCACTGAC	232328	64524	AGTTGTTTAAATATGTGATG	276915	109111	GATTCCACGTACAAATTCAC
187742	19938	CTCACTGCTTTTCTCACTGA	232329	64525	GAGTTGTTTAAATATGTGAT	276916	109112	CGATTCCACGTACAAATTCA
187743	19939	CCTCACTGCTTTTCTCACTG	232330	64526	AGAGTTGTTTAAATATGTGA	276917	109113	ACGATTCCACGTACAAATTC
187744	19940	TCCTCACTGCTTTTCTCACT	232331	64527	TAGAGTTGTTTAAATATGTG	276918	109114	AACGATTCCACGTACAAATT
187745	19941	TTCCTCACTGCTTTTCTCAC	232332	64528	CTAGAGTTGTTTAAATATGT	276919	109115	AAACGATTCCACGTACAAAT
187746	19942	GTTCCTCACTGCTTTTCTCA	232333	64529	CCTAGAGTTGTTTAAATATG	276920	109116	CAAACGATTCCACGTACAAA

187747	19943	TGTTCCTCACTGCTTTTCTC	232334	64530	TCCTAGAGTTGTTTAAATAT	276921	109117	GCAAACGATTCCACGTACAA
187748	19944	TTGTTCCTCACTGCTTTTCT	232335	64531	ATCCTAGAGTTGTTTAAATA	276922	109118	GGCAAACGATTCCACGTACA
187749	19945	CTTGTTCCTCACTGCTTTTC	232336	64532	TATCCTAGAGTTGTTTAAAT	276923	109119	AGGCAAACGATTCCACGTAC
187750	19946	CCTTGTTCCTCACTGCTTTT	232337	64533	ATATCCTAGAGTTGTTTAAA	276924	109120	GAGGCAAACGATTCCACGTA
187751	19947	GCCTTGTTCCTCACTGCTTT	232338	64534	GATATCCTAGAGTTGTTTAA	276925	109121	AGAGGCAAACGATTCCACGT
187752	19948	TGCCTTGTTCCTCACTGCTT	232339	64535	TGATATCCTAGAGTTGTTTA	276926	109122	GAGAGGCAAACGATTCCACG
187753	19949	CTGCCTTGTTCCTCACTGCT	232340	64536	ATGATATCCTAGAGTTGTTT	276927	109123	GGAGAGGCAAACGATTCCAC
187754	19950	CCTGCCTTGTTCCTCACTGC	232341	64537	AATGATATCCTAGAGTTGTT	276928	109124	AGGAGAGGCAAACGATTCCA
187755	19951	ACCTGCCTTGTTCCTCACTG	232342	64538	AAATGATATCCTAGAGTTGT	276929	109125	GAGGAGAGGCAAACGATTCC
187756	19952	TACCTGCCTTGTTCCTCACT	232343	64539	TAAATGATATCCTAGAGTTG	276930	109126	TGAGGAGAGGCAAACGATTC
187757	19953	GTACCTGCCTTGTTCCTCAC	232344	64540	TTAAATGATATCCTAGAGTT	276931	109127	TTGAGGAGAGGCAAACGATT
187758	19954	AGTACCTGCCTTGTTCCTCA	232345	64541	TTTAAATGATATCCTAGAGT	276932	109128	ATTGAGGAGAGGCAAACGAT
187759	19955	CAGTACCTGCCTTGTTCCTC	232346	64542	TTTTAAATGATATCCTAGAG	276933	109129	GATTGAGGAGAGGCAAACGA
187760	19956	ACAGTACCTGCCTTGTTCCT	232347	64543	TTTTTAAATGATATCCTAGA	276934	109130	TGATTGAGGAGAGGCAAACG
187761	19957	CACAGTACCTGCCTTGTTCC	232348	64544	TTTTTTAAATGATATCCTAG	276935	109131	CTGATTGAGGAGAGGCAAAC
187762	19958	ACACAGTACCTGCCTTGTTC	232349	64545	TTTTTTTAAATGATATCCTA	276936	109132	CCTGATTGAGGAGAGGCAAA
187763	19959	TACACAGTACCTGCCTTGTT	232350	64546	GTTTTTTTAAATGATATCCT	276937	109133	CCCTGATTGAGGAGAGGCAA
187764	19960	GTACACAGTACCTGCCTTGT	232351	64547	TGTTTTTTTAAATGATATCC	276938	109134	GCCCTGATTGAGGAGAGGCA
187765	19961	AGTACACAGTACCTGCCTTG	232352	64548	ATGTTTTTTTAAATGATATC	276939	109135	GGCCCTGATTGAGGAGAGGC
187766	19962	CAGTACACAGTACCTGCCTT	232353	64549	AATGTTTTTTTAAATGATAT	276940	109136	TGGCCCTGATTGAGGAGAGG
187767	19963	ACAGTACACAGTACCTGCCT	232354	64550	TAATGTTTTTTTAAATGATA	276941	109137	CTGGCCCTGATTGAGGAGAG
187768	19964	GACAGTACACAGTACCTGCC	232355	64551	TTAATGTTTTTTTAAATGAT	276942	109138	CCTGGCCCTGATTGAGGAGA
187769	19965	GGACAGTACACAGTACCTGC	232356	64552	ATTAATGTTTTTTTAAATGA	276943	109139	CCCTGGCCCTGATTGAGGAG
187770	19966	AGGACAGTACACAGTACCTG	232357	64553	TATTAATGTTTTTTTAAATG	276944	109140	TCCCTGGCCCTGATTGAGGA
187771	19967	GAGGACAGTACACAGTACCT	232358	64554	CTATTAATGTTTTTTTAAAT	276945	109141	ATCCCTGGCCCTGATTGAGG
187772	19968	AGAGGACAGTACACAGTACC	232359	64555	TCTATTAATGTTTTTTTAAA	276946	109142	CATCCCTGGCCCTGATTGAG
187773	19969	CAGAGGACAGTACACAGTAC	232360	64556	GTCTATTAATGTTTTTTTAA	276947	109143	GCATCCCTGGCCCTGATTGA
187774	19970	GCAGAGGACAGTACACAGTA	232361	64557	AGTCTATTAATGTTTTTTTA	276948	109144	TGCATCCCTGGCCCTGATTG
187775	19971	CGCAGAGGACAGTACACAGT	232362	64558	CAGTCTATTAATGTTTTTTT	276949	109145	CTGCATCCCTGGCCCTGATT
187776	19972	ACGCAGAGGACAGTACACAG	232363	64559	ACAGTCTATTAATGTTTTTT	276950	109146	CCTGCATCCCTGGCCCTGAT
187777	19973	CACGCAGAGGACAGTACACA	232364	64560	AACAGTCTATTAATGTTTTT	276951	109147	ACCTGCATCCCTGGCCCTGA
187778	19974	GCACGCAGAGGACAGTACAC	232365	64561	AAACAGTCTATTAATGTTTT	276952	109148	CACCTGCATCCCTGGCCCTG
187779	19975	TGCACGCAGAGGACAGTACA	232366	64562	AAAACAGTCTATTAATGTTT	276953	109149	TCACCTGCATCCCTGGCCCT
187780	19976	TTGCACGCAGAGGACAGTAC	232367	64563	AAAAACAGTCTATTAATGTT	276954	109150	CTCACCTGCATCCCTGGCCC
187781	19977	CTTGCACGCAGAGGACAGTA	232368	64564	AAAAAACAGTCTATTAATGT	276955	109151	GCTCACCTGCATCCCTGGCC
187782	19978	CCTTGCACGCAGAGGACAGT	232369	64565	TAAAAAACAGTCTATTAATG	276956	109152	AGCTCACCTGCATCCCTGGC
187783	19979	TCCTTGCACGCAGAGGACAG	232370	64566	CTAAAAAACAGTCTATTAAT	276957	109153	AAGCTCACCTGCATCCCTGG
187784	19980	TTCCTTGCACGCAGAGGACA	232371	64567	TCTAAAAAACAGTCTATTAA	276958	109154	CAAGCTCACCTGCATCCCTG
187785	19981	CTTCCTTGCACGCAGAGGAC	232372	64568	CTCTAAAAAACAGTCTATTA	276959	109155	CCAAGCTCACCTGCATCCCT
187786	19982	CCTTCCTTGCACGCAGAGGA	232373	64569	GCTCTAAAAAACAGTCTATT	276960	109156	CCCAAGCTCACCTGCATCCC
187787	19983	GCCTTCCTTGCACGCAGAGG	232374	64570	TGCTCTAAAAAACAGTCTAT	276961	109157	GCCCAAGCTCACCTGCATCC
187788	19984	GGCCTTCCTTGCACGCAGAG	232375	64571	GTGCTCTAAAAAACAGTCTA	276962	109158	AGCCCAAGCTCACCTGCATC
187789	19985	TGGCCTTCCTTGCACGCAGA	232376	64572	AGTGCTCTAAAAAACAGTCT	276963	109159	CAGCCCAAGCTCACCTGCAT
187790	19986	CTGGCCTTCCTTGCACGCAG	232377	64573	AAGTGCTCTAAAAAACAGTC	276964	109160	TCAGCCCAAGCTCACCTGCA
187791	19987	GCTGGCCTTCCTTGCACGCA	232378	64574	AAAGTGCTCTAAAAAACAGT	276965	109161	CTCAGCCCAAGCTCACCTGC
187792	19988	CGCTGGCCTTCCTTGCACGC	232379	64575	AAAAGTGCTCTAAAAAACAG	276966	109162	TCTCAGCCCAAGCTCACCTG
187793	19989	GCGCTGGCCTTCCTTGCACG	232380	64576	TAAAAGTGCTCTAAAAAACA	276967	109163	ATCTCAGCCCAAGCTCACCT
187794	19990	TGCGCTGGCCTTCCTTGCAC	232381	64577	CTAAAAGTGCTCTAAAAAAC	276968	109164	CATCTCAGCCCAAGCTCACC
187795	19991	ATGCGCTGGCCTTCCTTGCA	232382	64578	CCTAAAAGTGCTCTAAAAAA	276969	109165	ACATCTCAGCCCAAGCTCAC
187796	19992	CATGCGCTGGCCTTCCTTGC	232383	64579	ACCTAAAAGTGCTCTAAAAA	276970	109166	GACATCTCAGCCCAAGCTCA
187797	19993	GCATGCGCTGGCCTTCCTTG	232384	64580	AACCTAAAAGTGCTCTAAAA	276971	109167	TGACATCTCAGCCCAAGCTC
187798	19994	TGCATGCGCTGGCCTTCCTT	232385	64581	GAACCTAAAAGTGCTCTAAA	276972	109168	CTGACATCTCAGCCCAAGCT
187799	19995	TTGCATGCGCTGGCCTTCCT	232386	64582	TGAACCTAAAAGTGCTCTAA	276973	109169	TCTGACATCTCAGCCCAAGC
187800	19996	GTTGCATGCGCTGGCCTTCC	232387	64583	GTGAACCTAAAAGTGCTCTA	276974	109170	GTCTGACATCTCAGCCCAAG
187801	19997	TGTTGCATGCGCTGGCCTTC	232388	64584	TGTGAACCTAAAAGTGCTCT	276975	109171	GGTCTGACATCTCAGCCCAA
187802	19998	CTGTTGCATGCGCTGGCCTT	232389	64585	CTGTGAACCTAAAAGTGCTC	276976	109172	GGGTCTGACATCTCAGCCCA
187803	19999	TCTGTTGCATGCGCTGGCCT	232390	64586	ACTGTGAACCTAAAAGTGCT	276977	109173	GGGGTCTGACATCTCAGCCC
187804	20000	CTCTGTTGCATGCGCTGGCC	232391	64587	CACTGTGAACCTAAAAGTGC	276978	109174	TGGGGTCTGACATCTCAGCC
187805	20001	ACTCTGTTGCATGCGCTGGC	232392	64588	TCACTGTGAACCTAAAAGTG	276979	109175	GTGGGGTCTGACATCTCAGC
187806	20002	GACTCTGTTGCATGCGCTGG	232393	64589	TTCACTGTGAACCTAAAAGT	276980	109176	TGTGGGGTCTGACATCTCAG
187807	20003	GGACTCTGTTGCATGCGCTG	232394	64590	TTTCACTGTGAACCTAAAAG	276981	109177	CTGTGGGGTCTGACATCTCA
187808	20004	TGGACTCTGTTGCATGCGCT	232395	64591	GTTTCACTGTGAACCTAAAA	276982	109178	ACTGTGGGGTCTGACATCTC
187809	20005	GTGGACTCTGTTGCATGCGC	232396	64592	AGTTTCACTGTGAACCTAAA	276983	109179	TACTGTGGGGTCTGACATCT
187810	20006	TGTGGACTCTGTTGCATGCG	232397	64593	CAGTTTCACTGTGAACCTAA	276984	109180	TTACTGTGGGGTCTGACATC
187811	20007	GTGTGGACTCTGTTGCATGC	232398	64594	TCAGTTTCACTGTGAACCTA	276985	109181	CTTACTGTGGGGTCTGACAT
187812	20008	TGTGTGGACTCTGTTGCATG	232399	64595	CTCAGTTTCACTGTGAACCT	276986	109182	ACTTACTGTGGGGTCTGACA
187813	20009	CTGTGTGGACTCTGTTGCAT	232400	64596	ACTCAGTTTCACTGTGAACC	276987	109183	CACTTACTGTGGGGTCTGAC
187814	20010	TCTGTGTGGACTCTGTTGCA	232401	64597	CACTCAGTTTCACTGTGAAC	276988	109184	CCACTTACTGTGGGGTCTGA
187815	20011	GTCTGTGTGGACTCTGTTGC	232402	64598	CCACTCAGTTTCACTGTGAA	276989	109185	CCCACTTACTGTGGGGTCTG
187816	20012	TGTCTGTGTGGACTCTGTTG	232403	64599	TCCACTCAGTTTCACTGTGA	276990	109186	CCCCACTTACTGTGGGGTCT
187817	20013	ATGTCTGTGTGGACTCTGTT	232404	64600	TTCCACTCAGTTTCACTGTG	276991	109187	CCCCCACTTACTGTGGGGTC
187818	20014	TATGTCTGTGTGGACTCTGT	232405	64601	CTTCCACTCAGTTTCACTGT	276992	109188	CCCCCCACTTACTGTGGGGT

187819	20015	CTATGTCTGTGTGGACTCTG	232406	64602	CCTTCCACTCAGTTTCACTG	276993	109189	GCCCCCCACTTACTGTGGGG
187820	20016	GCTATGTCTGTGTGGACTCT	232407	64603	ACCTTCCACTCAGTTTCACT	276994	109190	TGCCCCCCACTTACTGTGGG
187821	20017	GGCTATGTCTGTGTGGACTC	232408	64604	TACCTTCCACTCAGTTTCAC	276995	109191	CTGCCCCCCACTTACTGTGG
187822	20018	AGGCTATGTCTGTGTGGACT	232409	64605	GTACCTTCCACTCAGTTTCA	276996	109192	TCTGCCCCCCACTTACTGTG
187823	20019	TAGGCTATGTCTGTGTGGAC	232410	64606	TGTACCTTCCACTCAGTTTC	276997	109193	CTCTGCCCCCCACTTACTGT
187824	20020	TTAGGCTATGTCTGTGTGGA	232411	64607	CTGTACCTTCCACTCAGTTT	276998	109194	GCTCTGCCCCCCACTTACTG
187825	20021	GTTAGGCTATGTCTGTGTGG	232412	64608	TCTGTACCTTCCACTCAGTT	276999	109195	GGCTCTGCCCCCCACTTACT
187826	20022	AGTTAGGCTATGTCTGTGTG	232413	64609	CTCTGTACCTTCCACTCAGT	277000	109196	TGGCTCTGCCCCCCACTTAC
187827	20023	GAGTTAGGCTATGTCTGTGT	232414	64610	TCTCTGTACCTTCCACTCAG	277001	109197	CTGGCTCTGCCCCCCACTTA
187828	20024	AGAGTTAGGCTATGTCTGTG	232415	64611	GTCTCTGTACCTTCCACTCA	277002	109198	CCTGGCTCTGCCCCCCACTT
187829	20025	CAGAGTTAGGCTATGTCTGT	232416	64612	AGTCTCTGTACCTTCCACTC	277003	109199	GCCTGGCTCTGCCCCCCACT
187830	20026	CCAGAGTTAGGCTATGTCTG	232417	64613	AAGTCTCTGTACCTTCCACT	277004	109200	AGCCTGGCTCTGCCCCCCAC
187831	20027	TCCAGAGTTAGGCTATGTCT	232418	64614	GAAGTCTCTGTACCTTCCAC	277005	109201	CAGCCTGGCTCTGCCCCCCA
187832	20028	TTCCAGAGTTAGGCTATGTC	232419	64615	GGAAGTCTCTGTACCTTCCA	277006	109202	CCAGCCTGGCTCTGCCCCCC
187833	20029	CTTCCAGAGTTAGGCTATGT	232420	64616	GGGAAGTCTCTGTACCTTCC	277007	109203	CCCAGCCTGGCTCTGCCCCC
187834	20030	CCTTCCAGAGTTAGGCTATG	232421	64617	CGGGAAGTCTCTGTACCTTC	277008	109204	TCCCAGCCTGGCTCTGCCCC
187835	20031	TCCTTCCAGAGTTAGGCTAT	232422	64618	ACGGGAAGTCTCTGTACCTT	277009	109205	GTCCCAGCCTGGCTCTGCCC
187836	20032	TTCCTTCCAGAGTTAGGCTA	232423	64619	TACGGGAAGTCTCTGTACCT	277010	109206	GGTCCCAGCCTGGCTCTGCC
187837	20033	CTTCCTTCCAGAGTTAGGCT	232424	64620	ATACGGGAAGTCTCTGTACC	277011	109207	GGGTCCCAGCCTGGCTCTGC
187838	20034	TCTTCCTTCCAGAGTTAGGC	232425	64621	CATACGGGAAGTCTCTGTAC	277012	109208	AGGGTCCCAGCCTGGCTCTG
187839	20035	TTCTTCCTTCCAGAGTTAGG	232426	64622	ACATACGGGAAGTCTCTGTA	277013	109209	GAGGGTCCCAGCCTGGCTCT
187840	20036	ATTCTTCCTTCCAGAGTTAG	232427	64623	AACATACGGGAAGTCTCTGT	277014	109210	GGAGGGTCCCAGCCTGGCTC
187841	20037	CATTCTTCCTTCCAGAGTTA	232428	64624	GAACATACGGGAAGTCTCTG	277015	109211	AGGAGGGTCCCAGCCTGGCT
187842	20038	TCATTCTTCCTTCCAGAGTT	232429	64625	GGAACATACGGGAAGTCTCT	277016	109212	GAGGAGGGTCCCAGCCTGGC
187843	20039	CTCATTCTTCCTTCCAGAGT	232430	64626	GGGAACATACGGGAAGTCTC	277017	109213	AGAGGAGGGTCCCAGCCTGG
187844	20040	TCTCATTCTTCCTTCCAGAG	232431	64627	AGGGAACATACGGGAAGTCT	277018	109214	TAGAGGAGGGTCCCAGCCTG
187845	20041	TTCTCATTCTTCCTTCCAGA	232432	64628	CAGGGAACATACGGGAAGTC	277019	109215	CTAGAGGAGGGTCCCAGCCT
187846	20042	ATTCTCATTCTTCCTTCCAG	232433	64629	GCAGGGAACATACGGGAAGT	277020	109216	CCTAGAGGAGGGTCCCAGCC
187847	20043	CATTCTCATTCTTCCTTCCA	232434	64630	GGCAGGGAACATACGGGAAG	277021	109217	TCCTAGAGGAGGGTCCCAGC
187848	20044	GCATTCTCATTCTTCCTTCC	232435	64631	GGGCAGGGAACATACGGGAA	277022	109218	GTCCTAGAGGAGGGTCCCAG
187849	20045	TGCATTCTCATTCTTCCTTC	232436	64632	AGGGCAGGGAACATACGGGA	277023	109219	TGTCCTAGAGGAGGGTCCCA
187850	20046	CTGCATTCTCATTCTTCCTT	232437	64633	GAGGGCAGGGAACATACGGG	277024	109220	CTGTCCTAGAGGAGGGTCCC
187851	20047	ACTGCATTCTCATTCTTCCT	232438	64634	GGAGGGCAGGGAACATACGG	277025	109221	GCTGTCCTAGAGGAGGGTCC
187852	20048	AACTGCATTCTCATTCTTCC	232439	64635	TGGAGGGCAGGGAACATACG	277026	109222	AGCTGTCCTAGAGGAGGGTC
187853	20049	AAACTGCATTCTCATTCTTC	232440	64636	GTGGAGGGCAGGGAACATAC	277027	109223	GAGCTGTCCTAGAGGAGGGT
187854	20050	GAAACTGCATTCTCATTCTT	232441	64637	CGTGGAGGGCAGGGAACATA	277028	109224	AGAGCTGTCCTAGAGGAGGG
187855	20051	TGAAACTGCATTCTCATTCT	232442	64638	ACGTGGAGGGCAGGGAACAT	277029	109225	CAGAGCTGTCCTAGAGGAGG
187856	20052	CTGAAACTGCATTCTCATTC	232443	64639	TACGTGGAGGGCAGGGAACA	277030	109226	ACAGAGCTGTCCTAGAGGAG
187857	20053	ACTGAAACTGCATTCTCATT	232444	64640	GTACGTGGAGGGCAGGGAAC	277031	109227	TACAGAGCTGTCCTAGAGGA
187858	20054	CACTGAAACTGCATTCTCAT	232445	64641	TGTACGTGGAGGGCAGGGAA	277032	109228	TTACAGAGCTGTCCTAGAGG
187859	20055	CCACTGAAACTGCATTCTCA	232446	64642	CTGTACGTGGAGGGCAGGGA	277033	109229	GTTACAGAGCTGTCCTAGAG
187860	20056	ACCACTGAAACTGCATTCTC	232447	64643	GCTGTACGTGGAGGGCAGGG	277034	109230	AGTTACAGAGCTGTCCTAGA
187861	20057	CACCACTGAAACTGCATTCT	232448	64644	GGCTGTACGTGGAGGGCAGG	277035	109231	GAGTTACAGAGCTGTCCTAG
187862	20058	CCACCACTGAAACTGCATTC	232449	64645	AGGCTGTACGTGGAGGGCAG	277036	109232	AGAGTTACAGAGCTGTCCTA
187863	20059	GCCACCACTGAAACTGCATT	232450	64646	GAGGCTGTACGTGGAGGGCA	277037	109233	CAGAGTTACAGAGCTGTCCT
187864	20060	GGCCACCACTGAAACTGCAT	232451	64647	GGAGGCTGTACGTGGAGGGC	277038	109234	TCAGAGTTACAGAGCTGTCC
187865	20061	AGGCCACCACTGAAACTGCA	232452	64648	GGGAGGCTGTACGTGGAGGG	277039	109235	CTCAGAGTTACAGAGCTGTC
187866	20062	GAGGCCACCACTGAAACTGC	232453	64649	GGGGAGGCTGTACGTGGAGG	277040	109236	TCTCAGAGTTACAGAGCTGT
187867	20063	AGAGGCCACCACTGAAACTG	232454	64650	GGGGGAGGCTGTACGTGGAG	277041	109237	GTCTCAGAGTTACAGAGCTG
187868	20064	CAGAGGCCACCACTGAAACT	232455	64651	TGGGGGAGGCTGTACGTGGA	277042	109238	GGTCTCAGAGTTACAGAGCT
187869	20065	CCAGAGGCCACCACTGAAAC	232456	64652	GTGGGGGAGGCTGTACGTGG	277043	109239	GGGTCTCAGAGTTACAGAGC
187870	20066	ACCAGAGGCCACCACTGAAA	232457	64653	AGTGGGGGAGGCTGTACGTG	277044	109240	AGGGTCTCAGAGTTACAGAG
187871	20067	CACCAGAGGCCACCACTGAA	232458	64654	CAGTGGGGGAGGCTGTACGT	277045	109241	GAGGGTCTCAGAGTTACAGA
187872	20068	CCACCAGAGGCCACCACTGA	232459	64655	GCAGTGGGGGAGGCTGTACG	277046	109242	GGAGGGTCTCAGAGTTACAG
187873	20069	CCCACCAGAGGCCACCACTG	232460	64656	GGCAGTGGGGGAGGCTGTAC	277047	109243	TGGAGGGTCTCAGAGTTACA
187874	20070	CCCCACCAGAGGCCACCACT	232461	64657	TGGCAGTGGGGGAGGCTGTA	277048	109244	CTGGAGGGTCTCAGAGTTAC
187875	20071	TCCCCACCAGAGGCCACCAC	232462	64658	TTGGCAGTGGGGGAGGCTGT	277049	109245	CCTGGAGGGTCTCAGAGTTA
187876	20072	CTCCCCACCAGAGGCCACCA	232463	64659	GTTGGCAGTGGGGGAGGCTG	277050	109246	GCCTGGAGGGTCTCAGAGTT
187877	20073	TCTCCCCACCAGAGGCCACC	232464	64660	CGTTGGCAGTGGGGGAGGCT	277051	109247	TGCCTGGAGGGTCTCAGAGT
187878	20074	TTCTCCCCACCAGAGGCCAC	232465	64661	ACGTTGGCAGTGGGGGAGGC	277052	109248	ATGCCTGGAGGGTCTCAGAG
187879	20075	TTTCTCCCCACCAGAGGCCA	232466	64662	GACGTTGGCAGTGGGGGAGG	277053	109249	GATGCCTGGAGGGTCTCAGA
187880	20076	GTTTCTCCCCACCAGAGGCC	232467	64663	GGACGTTGGCAGTGGGGGAG	277054	109250	AGATGCCTGGAGGGTCTCAG
187881	20077	AGTTTCTCCCCACCAGAGGC	232468	64664	AGGACGTTGGCAGTGGGGGA	277055	109251	AAGATGCCTGGAGGGTCTCA
187882	20078	CAGTTTCTCCCCACCAGAGG	232469	64665	CAGGACGTTGGCAGTGGGGG	277056	109252	AAAGATGCCTGGAGGGTCTC
187883	20079	CCAGTTTCTCCCCACCAGAG	232470	64666	GCAGGACGTTGGCAGTGGGG	277057	109253	AAAAGATGCCTGGAGGGTCT
187884	20080	CCCAGTTTCTCCCCACCAGA	232471	64667	TGCAGGACGTTGGCAGTGGG	277058	109254	GAAAAGATGCCTGGAGGGTC
187885	20081	ACCCAGTTTCTCCCCACCAG	232472	64668	GTGCAGGACGTTGGCAGTGG	277059	109255	GGAAAAGATGCCTGGAGGGT
187886	20082	CACCCAGTTTCTCCCCACCA	232473	64669	GGTGCAGGACGTTGGCAGTG	277060	109256	AGGAAAAGATGCCTGGAGGG
187887	20083	TCACCCAGTTTCTCCCCACC	232474	64670	TGGTGCAGGACGTTGGCAGT	277061	109257	CAGGAAAAGATGCCTGGAGG
187888	20084	TTCACCCAGTTTCTCCCCAC	232475	64671	CTGGTGCAGGACGTTGGCAG	277062	109258	ACAGGAAAAGATGCCTGGAG
187889	20085	CTTCACCCAGTTTCTCCCCA	232476	64672	TCTGGTGCAGGACGTTGGCA	277063	109259	TACAGGAAAAGATGCCTGGA
187890	20086	CCTTCACCCAGTTTCTCCCC	232477	64673	CTCTGGTGCAGGACGTTGGC	277064	109260	GTACAGGAAAAGATGCCTGG

187891	20087	CCCTTCACCCAGTTTCTCCC	232478	64674	ACTCTGGTGCAGGACGTTGG	277065	109261	GGTACAGGAAAAGATGCCTG
187892	20088	TCCCTTCACCCAGTTTCTCC	232479	64675	CACTCTGGTGCAGGACGTTG	277066	109262	AGGTACAGGAAAAGATGCCT
187893	20089	CTCCCTTCACCCAGTTTCTC	232480	64676	CCACTCTGGTGCAGGACGTT	277067	109263	GAGGTACAGGAAAAGATGCC
187894	20090	TCTCCCTTCACCCAGTTTCT	232481	64677	ACCACTCTGGTGCAGGACGT	277068	109264	TGAGGTACAGGAAAAGATGC
187895	20091	ATCTCCCTTCACCCAGTTTC	232482	64678	TACCACTCTGGTGCAGGACG	277069	109265	CTGAGGTACAGGAAAAGATG
187896	20092	CATCTCCCTTCACCCAGTTT	232483	64679	GTACCACTCTGGTGCAGGAC	277070	109266	ACTGAGGTACAGGAAAAGAT
187897	20093	ACATCTCCCTTCACCCAGTT	232484	64680	TGTACCACTCTGGTGCAGGA	277071	109267	CACTGAGGTACAGGAAAAGA
187898	20094	GACATCTCCCTTCACCCAGT	232485	64681	GTGTACCACTCTGGTGCAGG	277072	109268	GCACTGAGGTACAGGAAAAG
187899	20095	TGACATCTCCCTTCACCCAG	232486	64682	AGTGTACCACTCTGGTGCAG	277073	109269	AGCACTGAGGTACAGGAAAA
187900	20096	ATGACATCTCCCTTCACCCA	232487	64683	AAGTGTACCACTCTGGTGCA	277074	109270	AAGCACTGAGGTACAGGAAA
187901	20097	AATGACATCTCCCTTCACCC	232488	64684	CAAGTGTACCACTCTGGTGC	277075	109271	GAAGCACTGAGGTACAGGAA
187902	20098	AAATGACATCTCCCTTCACC	232489	64685	ACAAGTGTACCACTCTGGTG	277076	109272	AGAAGCACTGAGGTACAGGA
187903	20099	GAAATGACATCTCCCTTCAC	232490	64686	AACAAGTGTACCACTCTGGT	277077	109273	CAGAAGCACTGAGGTACAGG
187904	20100	GGAAATGACATCTCCCTTCA	232491	64687	TAACAAGTGTACCACTCTGG	277078	109274	TCAGAAGCACTGAGGTACAG
187905	20101	TGGAAATGACATCTCCCTTC	232492	64688	GTAACAAGTGTACCACTCTG	277079	109275	TTCAGAAGCACTGAGGTACA
187906	20102	ATGGAAATGACATCTCCCTT	232493	64689	TGTAACAAGTGTACCACTCT	277080	109276	TTTCAGAAGCACTGAGGTAC
187907	20103	AATGGAAATGACATCTCCCT	232494	64690	TTGTAACAAGTGTACCACTC	277081	109277	TTTTCAGAAGCACTGAGGTA
187908	20104	AAATGGAAATGACATCTCCC	232495	64691	GTTGTAACAAGTGTACCACT	277082	109278	TTTTTCAGAAGCACTGAGGT
187909	20105	GAAATGGAAATGACATCTCC	232496	64692	GGTTGTAACAAGTGTACCAC	277083	109279	ATTTTTCAGAAGCACTGAGG
187910	20106	AGAAATGGAAATGACATCTC	232497	64693	TGGTTGTAACAAGTGTACCA	277084	109280	GATTTTTCAGAAGCACTGAG
187911	20107	GAGAAATGGAAATGACATCT	232498	64694	TTGGTTGTAACAAGTGTACC	277085	109281	AGATTTTTCAGAAGCACTGA
187912	20108	AGAGAAATGGAAATGACATC	232499	64695	ATTGGTTGTAACAAGTGTAC	277086	109282	CAGATTTTTCAGAAGCACTG
187913	20109	TAGAGAAATGGAAATGACAT	232500	64696	CATTGGTTGTAACAAGTGTA	277087	109283	ACAGATTTTTCAGAAGCACT
187914	20110	GTAGAGAAATGGAAATGACA	232501	64697	TCATTGGTTGTAACAAGTGT	277088	109284	CACAGATTTTTCAGAAGCAC
187915	20111	AGTAGAGAAATGGAAATGAC	232502	64698	TTCATTGGTTGTAACAAGTG	277089	109285	ACACAGATTTTTCAGAAGCA
187916	20112	TAGTAGAGAAATGGAAATGA	232503	64699	ATTCATTGGTTGTAACAAGT	277090	109286	CACACAGATTTTTCAGAAGC
187917	20113	ATAGTAGAGAAATGGAAATG	232504	64700	GATTCATTGGTTGTAACAAG	277091	109287	TCACACAGATTTTTCAGAAG
187918	20114	AATAGTAGAGAAATGGAAAT	232505	64701	GGATTCATTGGTTGTAACAA	277092	109288	TTCACACAGATTTTTCAGAA
187919	20115	TAATAGTAGAGAAATGGAAA	232506	64702	AGGATTCATTGGTTGTAACA	277093	109289	ATTCACACAGATTTTTCAGA
187920	20116	TTAATAGTAGAGAAATGGAA	232507	64703	GAGGATTCATTGGTTGTAAC	277094	109290	GATTCACACAGATTTTTCAG
187921	20117	ATTAATAGTAGAGAAATGGA	232508	64704	TGAGGATTCATTGGTTGTAA	277095	109291	TGATTCACACAGATTTTTCA
187922	20118	AATTAATAGTAGAGAAATGG	232509	64705	ATGAGGATTCATTGGTTGTA	277096	109292	TTGATTCACACAGATTTTTC
187923	20119	AAATTAATAGTAGAGAAATG	232510	64706	AATGAGGATTCATTGGTTGT	277097	109293	TTTGATTCACACAGATTTTT
187924	20120	AAAATTAATAGTAGAGAAAT	232511	64707	TAATGAGGATTCATTGGTTG	277098	109294	ATTTGATTCACACAGATTTT
187925	20121	CAAAATTAATAGTAGAGAAA	232512	64708	TTAATGAGGATTCATTGGTT	277099	109295	GATTTGATTCACACAGATTT
187926	20122	ACAAAATTAATAGTAGAGAA	232513	64709	GTTAATGAGGATTCATTGGT	277100	109296	TGATTTGATTCACACAGATT
187927	20123	TACAAAATTAATAGTAGAGA	232514	64710	TGTTAATGAGGATTCATTGG	277101	109297	ATGATTTGATTCACACAGAT
187928	20124	ATACAAAATTAATAGTAGAG	232515	64711	ATGTTAATGAGGATTCATTG	277102	109298	AATGATTTGATTCACACAGA
187929	20125	AATACAAAATTAATAGTAGA	232516	64712	TATGTTAATGAGGATTCATT	277103	109299	AAATGATTTGATTCACACAG
187930	20126	TAATACAAAATTAATAGTAG	232517	64713	ATATGTTAATGAGGATTCAT	277104	109300	AAAATGATTTGATTCACACA
187931	20127	GTAATACAAAATTAATAGTA	232518	64714	GATATGTTAATGAGGATTCA	277105	109301	TAAAATGATTTGATTCACAC
187932	20128	GGTAATACAAAATTAATAGT	232519	64715	TGATATGTTAATGAGGATTC	277106	109302	TTAAAATGATTTGATTCACA
187933	20129	TGGTAATACAAAATTAATAG	232520	64716	ATGATATGTTAATGAGGATT	277107	109303	TTTAAAATGATTTGATTCAC
187934	20130	ATGGTAATACAAAATTAATA	232521	64717	AATGATATGTTAATGAGGAT	277108	109304	CTTTAAAATGATTTGATTCA
187935	20131	CATGGTAATACAAAATTAAT	232522	64718	TAATGATATGTTAATGAGGA	277109	109305	CCTTTAAAATGATTTGATTC
187936	20132	GCATGGTAATACAAAATTAA	232523	64719	ATAATGATATGTTAATGAGG	277110	109306	TCCTTTAAAATGATTTGATT
187937	20133	AGCATGGTAATACAAAATTA	232524	64720	GATAATGATATGTTAATGAG	277111	109307	CTCCTTTAAAATGATTTGAT
187938	20134	AAGCATGGTAATACAAAATT	232525	64721	TGATAATGATATGTTAATGA	277112	109308	GCTCCTTTAAAATGATTTGA
187939	20135	TAAGCATGGTAATACAAAAT	232526	64722	GTGATAATGATATGTTAATG	277113	109309	AGCTCCTTTAAAATGATTTG
187940	20136	TTAAGCATGGTAATACAAAA	232527	64723	GGTGATAATGATATGTTAAT	277114	109310	AAGCTCCTTTAAAATGATTT
187941	20137	TTTAAGCATGGTAATACAAA	232528	64724	GGGTGATAATGATATGTTAA	277115	109311	CAAGCTCCTTTAAAATGATT
187942	20138	ATTTAAGCATGGTAATACAA	232529	64725	TGGGTGATAATGATATGTTA	277116	109312	CCAAGCTCCTTTAAAATGAT
187943	20139	CATTTAAGCATGGTAATACA	232530	64726	TTGGGTGATAATGATATGTT	277117	109313	CCCAAGCTCCTTTAAAATGA
187944	20140	ACATTTAAGCATGGTAATAC	232531	64727	CTTGGGTGATAATGATATGT	277118	109314	ACCCAAGCTCCTTTAAAATG
187945	20141	AACATTTAAGCATGGTAATA	232532	64728	ACTTGGGTGATAATGATATG	277119	109315	AACCCAAGCTCCTTTAAAAT
187946	20142	TAACATTTAAGCATGGTAAT	232533	64729	AACTTGGGTGATAATGATAT	277120	109316	GAACCCAAGCTCCTTTAAAA
187947	20143	GTAACATTTAAGCATGGTAA	232534	64730	GAACTTGGGTGATAATGATA	277121	109317	TGAACCCAAGCTCCTTTAAA
187948	20144	AGTAACATTTAAGCATGGTA	232535	64731	TGAACTTGGGTGATAATGAT	277122	109318	ATGAACCCAAGCTCCTTTAA
187949	20145	AAGTAACATTTAAGCATGGT	232536	64732	ATGAACTTGGGTGATAATGA	277123	109319	GATGAACCCAAGCTCCTTTA
187950	20146	AAAGTAACATTTAAGCATGG	232537	64733	TATGAACTTGGGTGATAATG	277124	109320	TGATGAACCCAAGCTCCTTT
187951	20147	AAAAGTAACATTTAAGCATG	232538	64734	CTATGAACTTGGGTGATAAT	277125	109321	GTGATGAACCCAAGCTCCTT
187952	20148	AAAAAGTAACATTTAAGCAT	232539	64735	ACTATGAACTTGGGTGATAA	277126	109322	AGTGATGAACCCAAGCTCCT
187953	20149	TAAAAAGTAACATTTAAGCA	232540	64736	AACTATGAACTTGGGTGATA	277127	109323	CAGTGATGAACCCAAGCTCC
187954	20150	GTAAAAAGTAACATTTAAGC	232541	64737	AAACTATGAACTTGGGTGAT	277128	109324	ACAGTGATGAACCCAAGCTC
187955	20151	GGTAAAAAGTAACATTTAAG	232542	64738	TAAACTATGAACTTGGGTGA	277129	109325	AACAGTGATGAACCCAAGCT
187956	20152	AGGTAAAAAGTAACATTTAA	232543	64739	GTAAACTATGAACTTGGGTG	277130	109326	AAACAGTGATGAACCCAAGC
187957	20153	AAGGTAAAAAGTAACATTTA	232544	64740	TGTAAACTATGAACTTGGGT	277131	109327	TAAACAGTGATGAACCCAAG
187958	20154	AAAGGTAAAAAGTAACATTT	232545	64741	ATGTAAACTATGAACTTGGG	277132	109328	TTAAACAGTGATGAACCCAA
187959	20155	AAAAGGTAAAAAGTAACATT	232546	64742	AATGTAAACTATGAACTTGG	277133	109329	TTTAAACAGTGATGAACCCA
187960	20156	AAAAAGGTAAAAAGTAACAT	232547	64743	TAATGTAAACTATGAACTTG	277134	109330	CTTTAAACAGTGATGAACCC
187961	20157	AAAAAAGGTAAAAAGTAACA	232548	64744	CTAATGTAAACTATGAACTT	277135	109331	CCTTTAAACAGTGATGAACC
187962	20158	AAAAAAAGGTAAAAAGTAAC	232549	64745	ACTAATGTAAACTATGAACT	277136	109332	TCCTTTAAACAGTGATGAAC

187963	20159	AAAAAAAAGGTAAAAAGTAA	232550	64746	TACTAATGTAAACTATGAAC	277137	109333	GTCCTTTAAACAGTGATGAA
187964	20160	AAAAAAAAGGTAAAAAGTA	232551	64747	TTACTAATGTAAACTATGAA	277138	109334	TGTCCTTTAAACAGTGATGA
187965	20161	AAAAAAAAAGGTAAAAAGT	232552	64748	TTTACTAATGTAAACTATGA	277139	109335	CTGTCCTTTAAACAGTGATG
187966	20162	AAAAAAAAAAGGTAAAAAG	232553	64749	TTTTACTAATGTAAACTATG	277140	109336	ACTGTCCTTTAAACAGTGAT
187967	20163	AAAAAAAAAAAGGTAAAAA	232554	64750	GTTTTACTAATGTAAACTAT	277141	109337	CACTGTCCTTTAAACAGTGA
187968	20164	AAAAAAAAAAAAGGTAAAA	232555	64751	TGTTTTACTAATGTAAACTA	277142	109338	ACACTGTCCTTTAAACAGTG
187969	20165	AAAAAAAAAAAAAGGTAAA	232556	64752	ATGTTTTACTAATGTAAACT	277143	109339	TACACTGTCCTTTAAACAGT
187970	20166	AAAAAAAAAAAAAAGGTAA	232557	64753	GATGTTTTACTAATGTAAAC	277144	109340	TTACACTGTCCTTTAAACAG
187971	20167	CAAAAAAAAAAAAAAGGTA	232558	64754	TGATGTTTTACTAATGTAAA	277145	109341	TTTACACTGTCCTTTAAACA
187972	20168	TCAAAAAAAAAAAAAAGGT	232559	64755	ATGATGTTTTACTAATGTAA	277146	109342	ATTTACACTGTCCTTTAAAC
187973	20169	CTCAAAAAAAAAAAAAAGG	232560	64756	GATGATGTTTTACTAATGTA	277147	109343	TATTTACACTGTCCTTTAAA
187974	20170	TCTCAAAAAAAAAAAAAAG	232561	64757	AGATGATGTTTTACTAATGT	277148	109344	TTATTTACACTGTCCTTTAA
187975	20171	GTCTCAAAAAAAAAAAAAA	232562	64758	AAGATGATGTTTTACTAATG	277149	109345	ATTATTTACACTGTCCTTTA
187976	20172	TGTCTCAAAAAAAAAAAAA	232563	64759	AAAGATGATGTTTTACTAAT	277150	109346	AATTATTTACACTGTCCTTT
187977	20173	CTGTCTCAAAAAAAAAAAA	232564	64760	GAAAGATGATGTTTTACTAA	277151	109347	GAATTATTTACACTGTCCTT
187978	20174	CCTGTCTCAAAAAAAAAAA	232565	64761	TGAAAGATGATGTTTTACTA	277152	109348	AGAATTATTTACACTGTCCT
187979	20175	CCCTGTCTCAAAAAAAAAA	232566	64762	ATGAAAGATGATGTTTTACT	277153	109349	CAGAATTATTTACACTGTCC
187980	20176	ACCCTGTCTCAAAAAAAAA	232567	64763	GATGAAAGATGATGTTTTAC	277154	109350	TCAGAATTATTTACACTGTC
187981	20177	GACCCTGTCTCAAAAAAAA	232568	64764	AGATGAAAGATGATGTTTTA	277155	109351	TTCAGAATTATTTACACTGT
187982	20178	AGACCCTGTCTCAAAAAAA	232569	64765	TAGATGAAAGATGATGTTTT	277156	109352	CTTCAGAATTATTTACACTG
187983	20179	GAGACCCTGTCTCAAAAAA	232570	64766	ATAGATGAAAGATGATGTTT	277157	109353	CCTTCAGAATTATTTACACT
187984	20180	AGAGACCCTGTCTCAAAAA	232571	64767	TATAGATGAAAGATGATGTT	277158	109354	ACCTTCAGAATTATTTACAC
187985	20181	GAGAGACCCTGTCTCAAAA	232572	64768	TTATAGATGAAAGATGATGT	277159	109355	CACCTTCAGAATTATTTACA
187986	20182	AGAGAGACCCTGTCTCAAAA	232573	64769	CTTATAGATGAAAGATGATG	277160	109356	TCACCTTCAGAATTATTTAC
187987	20183	GAGAGAGACCCTGTCTCAAA	232574	64770	GCTTATAGATGAAAGATGAT	277161	109357	GTCACCTTCAGAATTATTTA
187988	20184	AGAGAGAGACCCTGTCTCAA	232575	64771	TGCTTATAGATGAAAGATGA	277162	109358	AGTCACCTTCAGAATTATTT
187989	20185	CAGAGAGAGACCCTGTCTCA	232576	64772	GTGCTTATAGATGAAAGATG	277163	109359	GAGTCACCTTCAGAATTATT
187990	20186	ACAGAGAGAGACCCTGTCTC	232577	64773	TGTGCTTATAGATGAAAGAT	277164	109360	AGAGTCACCTTCAGAATTAT
187991	20187	AACAGAGAGAGACCCTGTCT	232578	64774	TTGTGCTTATAGATGAAAGA	277165	109361	TAGAGTCACCTTCAGAATTA
187992	20188	CAACAGAGAGAGACCCTGTC	232579	64775	TTTGTGCTTATAGATGAAAG	277166	109362	GTAGAGTCACCTTCAGAATT
187993	20189	GCAACAGAGAGAGACCCTGT	232580	64776	TTTTGTGCTTATAGATGAAA	277167	109363	GGTAGAGTCACCTTCAGAAT
187994	20190	GGCAACAGAGAGAGACCCTG	232581	64777	TTTTTGTGCTTATAGATGAA	277168	109364	GGGTAGAGTCACCTTCAGAA
187995	20191	GGGCAACAGAGAGAGACCCT	232582	64778	ATTTTTGTGCTTATAGATGA	277169	109365	AGGGTAGAGTCACCTTCAGA
187996	20192	TGGGCAACAGAGAGAGACCC	232583	64779	AATTTTTGTGCTTATAGATG	277170	109366	CAGGGTAGAGTCACCTTCAG
187997	20193	CTGGGCAACAGAGAGAGACC	232584	64780	AAATTTTTGTGCTTATAGAT	277171	109367	ACAGGGTAGAGTCACCTTCA
187998	20194	CCTGGGCAACAGAGAGAGAC	232585	64781	AAAATTTTTGTGCTTATAGA	277172	109368	AACAGGGTAGAGTCACCTTC
187999	20195	GCCTGGGCAACAGAGAGAGA	232586	64782	AAAAATTTTTGTGCTTATAG	277173	109369	TAACAGGGTAGAGTCACCTT
188000	20196	TGCCTGGGCAACAGAGAGAG	232587	64783	AAAAAATTTTTGTGCTTATA	277174	109370	ATAACAGGGTAGAGTCACCT
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188002	20198	CCTGCCTGGGCAACAGAGAG	232589	64785	CCAAAAAATTTTTGTGCTTA	277176	109372	AAATAACAGGGTAGAGTCAC
188003	20199	TCCTGCCTGGGCAACAGAGA	232590	64786	GCCAAAAAATTTTTGTGCTT	277177	109373	CAAATAACAGGGTAGAGTCA
188004	20200	CTCCTGCCTGGGCAACAGAG	232591	64787	TGCCAAAAAATTTTTGTGCT	277178	109374	TCAAATAACAGGGTAGAGTC
188005	20201	ACTCCTGCCTGGGCAACAGA	232592	64788	ATGCCAAAAAATTTTTGTGC	277179	109375	ATCAAATAACAGGGTAGAGT
188006	20202	CACTCCTGCCTGGGCAACAG	232593	64789	AATGCCAAAAAATTTTTGTG	277180	109376	GATCAAATAACAGGGTAGAG
188007	20203	GCACTCCTGCCTGGGCAACA	232594	64790	AAATGCCAAAAAATTTTTGT	277181	109377	AGATCAAATAACAGGGTAGA
188008	20204	TGCACTCCTGCCTGGGCAAC	232595	64791	TAAATGCCAAAAAATTTTTG	277182	109378	GAGATCAAATAACAGGGTAG
188009	20205	CTGCACTCCTGCCTGGGCAA	232596	64792	ATAAATGCCAAAAAATTTTT	277183	109379	AGAGATCAAATAACAGGGTA
188010	20206	ACTGCACTCCTGCCTGGGCA	232597	64793	AATAAATGCCAAAAAATTTT	277184	109380	AAGAGATCAAATAACAGGGT
188011	20207	CACTGCACTCCTGCCTGGGC	232598	64794	AAATAAATGCCAAAAAATTT	277185	109381	GAAGAGATCAAATAACAGGG
188012	20208	CCACTGCACTCCTGCCTGGG	232599	64795	TAAATAAATGCCAAAAAATT	277186	109382	AGAAGAGATCAAATAACAGG
188013	20209	ACCACTGCACTCCTGCCTGG	232600	64796	CTAAATAAATGCCAAAAAAT	277187	109383	AAGAAGAGATCAAATAACAG
188014	20210	TACCACTGCACTCCTGCCTG	232601	64797	CCTAAATAAATGCCAAAAAA	277188	109384	AAAGAAGAGATCAAATAACA
188015	20211	GTACCACTGCACTCCTGCCT	232602	64798	ACCTAAATAAATGCCAAAAA	277189	109385	CAAAGAAGAGATCAAATAAC
188016	20212	TGTACCACTGCACTCCTGCC	232603	64799	CACCTAAATAAATGCCAAAA	277190	109386	CCAAAGAAGAGATCAAATAA
188017	20213	TTGTACCACTGCACTCCTGC	232604	64800	ACACCTAAATAAATGCCAAA	277191	109387	GCCAAAGAAGAGATCAAATA
188018	20214	ATTGTACCACTGCACTCCTG	232605	64801	TACACCTAAATAAATGCCAA	277192	109388	GGCCAAAGAAGAGATCAAAT
188019	20215	GATTGTACCACTGCACTCCT	232606	64802	ATACACCTAAATAAATGCCA	277193	109389	TGGCCAAAGAAGAGATCAAA
188020	20216	TGATTGTACCACTGCACTCC	232607	64803	CATACACCTAAATAAATGCC	277194	109390	CTGGCCAAAGAAGAGATCAA
188021	20217	ATGATTGTACCACTGCACTC	232608	64804	TCATACACCTAAATAAATGC	277195	109391	GCTGGCCAAAGAAGAGATCA
188022	20218	CATGATTGTACCACTGCACT	232609	64805	ATCATACACCTAAATAAATG	277196	109392	AGCTGGCCAAAGAAGAGATC
188023	20219	CCATGATTGTACCACTGCAC	232610	64806	AATCATACACCTAAATAAAT	277197	109393	CAGCTGGCCAAAGAAGAGAT
188024	20220	ACCATGATTGTACCACTGCA	232611	64807	TAATCATACACCTAAATAAA	277198	109394	TCAGCTGGCCAAAGAAGAGA
188025	20221	AACCATGATTGTACCACTGC	232612	64808	TTAATCATACACCTAAATAA	277199	109395	GTCAGCTGGCCAAAGAAGAG
188026	20222	GAACCATGATTGTACCACTG	232613	64809	GTTAATCATACACCTAAATA	277200	109396	AGTCAGCTGGCCAAAGAAGA
188027	20223	TGAACCATGATTGTACCACT	232614	64810	AGTTAATCATACACCTAAAT	277201	109397	AAGTCAGCTGGCCAAAGAAG
188028	20224	GTGAACCATGATTGTACCAC	232615	64811	GAGTTAATCATACACCTAAA	277202	109398	TAAGTCAGCTGGCCAAAGAA
188029	20225	AGTGAACCATGATTGTACCA	232616	64812	TGAGTTAATCATACACCTAA	277203	109399	TTAAGTCAGCTGGCCAAAGA
188030	20226	CAGTGAACCATGATTGTACC	232617	64813	CTGAGTTAATCATACACCTA	277204	109400	GTTAAGTCAGCTGGCCAAAG
188031	20227	GCAGTGAACCATGATTGTAC	232618	64814	ACTGAGTTAATCATACACCT	277205	109401	TGTTAAGTCAGCTGGCCAAA
188032	20228	TGCAGTGAACCATGATTGTA	232619	64815	CACTGAGTTAATCATACACC	277206	109402	CTGTTAAGTCAGCTGGCCAA
188033	20229	CTGCAGTGAACCATGATTGT	232620	64816	ACACTGAGTTAATCATACAC	277207	109403	CCTGTTAAGTCAGCTGGCCA
188034	20230	GCTGCAGTGAACCATGATTG	232621	64817	AACACTGAGTTAATCATACA	277208	109404	TCCTGTTAAGTCAGCTGGCC

188035	20231	GGCTGCAGTGAACCATGATT	232622	64818	CAACACTGAGTTAATCATAC	277209	109405	GTCCTGTTAAGTCAGCTGGC
188036	20232	AGGCTGCAGTGAACCATGAT	232623	64819	TCAACACTGAGTTAATCATA	277210	109406	TGTCCTGTTAAGTCAGCTGG
188037	20233	CAGGCTGCAGTGAACCATGA	232624	64820	GTCAACACTGAGTTAATCAT	277211	109407	ATGTCCTGTTAAGTCAGCTG
188038	20234	TCAGGCTGCAGTGAACCATG	232625	64821	TGTCAACACTGAGTTAATCA	277212	109408	TATGTCCTGTTAAGTCAGCT
188039	20235	TTCAGGCTGCAGTGAACCAT	232626	64822	TTGTCAACACTGAGTTAATC	277213	109409	CTATGTCCTGTTAAGTCAGC
188040	20236	GTTCAGGCTGCAGTGAACCA	232627	64823	CTTGTCAACACTGAGTTAAT	277214	109410	TCTATGTCCTGTTAAGTCAG
188041	20237	GGTTCAGGCTGCAGTGAACC	232628	64824	TCTTGTCAACACTGAGTTAA	277215	109411	GTCTATGTCCTGTTAAGTCA
188042	20238	AGGTTCAGGCTGCAGTGAAC	232629	64825	GTCTTGTCAACACTGAGTTA	277216	109412	TGTCTATGTCCTGTTAAGTC
188043	20239	GAGGTTCAGGCTGCAGTGAA	232630	64826	AGTCTTGTCAACACTGAGTT	277217	109413	CTGTCTATGTCCTGTTAAGT
188044	20240	GGAGGTTCAGGCTGCAGTGA	232631	64827	GAGTCTTGTCAACACTGAGT	277218	109414	CCTGTCTATGTCCTGTTAAG
188045	20241	GGGAGGTTCAGGCTGCAGTG	232632	64828	TGAGTCTTGTCAACACTGAG	277219	109415	ACCTGTCTATGTCCTGTTAA
188046	20242	TGGGAGGTTCAGGCTGCAGT	232633	64829	GTGAGTCTTGTCAACACTGA	277220	109416	AACCTGTCTATGTCCTGTTA
188047	20243	CTGGGAGGTTCAGGCTGCAG	232634	64830	TGTGAGTCTTGTCAACACTG	277221	109417	AAACCTGTCTATGTCCTGTT
188048	20244	CCTGGGAGGTTCAGGCTGCA	232635	64831	GTGTGAGTCTTGTCAACACT	277222	109418	AAAACCTGTCTATGTCCTGT
188049	20245	GCCTGGGAGGTTCAGGCTGC	232636	64832	AGTGTGAGTCTTGTCAACAC	277223	109419	GAAAACCTGTCTATGTCCTG
188050	20246	AGCCTGGGAGGTTCAGGCTG	232637	64833	AAGTGTGAGTCTTGTCAACA	277224	109420	GGAAAACCTGTCTATGTCCT
188051	20247	GAGCCTGGGAGGTTCAGGCT	232638	64834	GAAGTGTGAGTCTTGTCAAC	277225	109421	AGGAAAACCTGTCTATGTCC
188052	20248	TGAGCCTGGGAGGTTCAGGC	232639	64835	TGAAGTGTGAGTCTTGTCAA	277226	109422	CAGGAAAACCTGTCTATGTC
188053	20249	TTGAGCCTGGGAGGTTCAGG	232640	64836	ATGAAGTGTGAGTCTTGTCA	277227	109423	ACAGGAAAACCTGTCTATGT
188054	20250	CTTGAGCCTGGGAGGTTCAG	232641	64837	TATGAAGTGTGAGTCTTGTC	277228	109424	CACAGGAAAACCTGTCTATG
188055	20251	GCTTGAGCCTGGGAGGTTCA	232642	64838	GTATGAAGTGTGAGTCTTGT	277229	109425	ACACAGGAAAACCTGTCTAT
188056	20252	TGCTTGAGCCTGGGAGGTTC	232643	64839	GGTATGAAGTGTGAGTCTTG	277230	109426	GACACAGGAAAACCTGTCTA
188057	20253	TTGCTTGAGCCTGGGAGGTT	232644	64840	GGGTATGAAGTGTGAGTCTT	277231	109427	TGACACAGGAAAACCTGTCT
188058	20254	ATTGCTTGAGCCTGGGAGGT	232645	64841	TGGGTATGAAGTGTGAGTCT	277232	109428	CTGACACAGGAAAACCTGTC
188059	20255	GATTGCTTGAGCCTGGGAGG	232646	64842	GTGGGTATGAAGTGTGAGTC	277233	109429	ACTGACACAGGAAAACCTGT
188060	20256	GGATTGCTTGAGCCTGGGAG	232647	64843	AGTGGGTATGAAGTGTGAGT	277234	109430	AACTGACACAGGAAAACCTG
188061	20257	AGGATTGCTTGAGCCTGGGA	232648	64844	AAGTGGGTATGAAGTGTGAG	277235	109431	GAACTGACACAGGAAAACCT
188062	20258	GAGGATTGCTTGAGCCTGGG	232649	64845	CAAGTGGGTATGAAGTGTGA	277236	109432	GGAACTGACACAGGAAAACC
188063	20259	GGAGGATTGCTTGAGCCTGG	232650	64846	GCAAGTGGGTATGAAGTGTG	277237	109433	AGGAACTGACACAGGAAAAC
188064	20260	GGGAGGATTGCTTGAGCCTG	232651	64847	TGCAAGTGGGTATGAAGTGT	277238	109434	TAGGAACTGACACAGGAAAA
188065	20261	TGGGAGGATTGCTTGAGCCT	232652	64848	GTGCAAGTGGGTATGAAGTG	277239	109435	TTAGGAACTGACACAGGAAA
188066	20262	GTGGGAGGATTGCTTGAGCC	232653	64849	AGTGCAAGTGGGTATGAAGT	277240	109436	CTTAGGAACTGACACAGGAA
188067	20263	GGTGGGAGGATTGCTTGAGC	232654	64850	CAGTGCAAGTGGGTATGAAG	277241	109437	GCTTAGGAACTGACACAGGA
188068	20264	AGGTGGGAGGATTGCTTGAG	232655	64851	GCAGTGCAAGTGGGTATGAA	277242	109438	AGCTTAGGAACTGACACAGG
188069	20265	GAGGTGGGAGGATTGCTTGA	232656	64852	TGCAGTGCAAGTGGGTATGA	277243	109439	CAGCTTAGGAACTGACACAG
188070	20266	TGAGGTGGGAGGATTGCTTG	232657	64853	ATGCAGTGCAAGTGGGTATG	277244	109440	TCAGCTTAGGAACTGACACA
188071	20267	CTGAGGTGGGAGGATTGCTT	232658	64854	GATGCAGTGCAAGTGGGTAT	277245	109441	ATCAGCTTAGGAACTGACAC
188072	20268	GCTGAGGTGGGAGGATTGCT	232659	64855	AGATGCAGTGCAAGTGGGTA	277246	109442	GATCAGCTTAGGAACTGACA
188073	20269	GGCTGAGGTGGGAGGATTGC	232660	64856	CAGATGCAGTGCAAGTGGGT	277247	109443	TGATCAGCTTAGGAACTGAC
188074	20270	AGGCTGAGGTGGGAGGATTG	232661	64857	TCAGATGCAGTGCAAGTGGG	277248	109444	GTGATCAGCTTAGGAACTGA
188075	20271	GAGGCTGAGGTGGGAGGATT	232662	64858	CTCAGATGCAGTGCAAGTGG	277249	109445	GGTGATCAGCTTAGGAACTG
188076	20272	GGAGGCTGAGGTGGGAGGAT	232663	64859	TCTCAGATGCAGTGCAAGTG	277250	109446	AGGTGATCAGCTTAGGAACT
188077	20273	AGGAGGCTGAGGTGGGAGGA	232664	64860	TTCTCAGATGCAGTGCAAGT	277251	109447	AAGGTGATCAGCTTAGGAAC
188078	20274	CAGGAGGCTGAGGTGGGAGG	232665	64861	CTTCTCAGATGCAGTGCAAG	277252	109448	CAAGGTGATCAGCTTAGGAA
188079	20275	TCAGGAGGCTGAGGTGGGAG	232666	64862	GCTTCTCAGATGCAGTGCAA	277253	109449	CCAAGGTGATCAGCTTAGGA
188080	20276	CTCAGGAGGCTGAGGTGGGA	232667	64863	TGCTTCTCAGATGCAGTGCA	277254	109450	TCCAAGGTGATCAGCTTAGG
188081	20277	ACTCAGGAGGCTGAGGTGGG	232668	64864	TTGCTTCTCAGATGCAGTGC	277255	109451	GTCCAAGGTGATCAGCTTAG
188082	20278	TACTCAGGAGGCTGAGGTGG	232669	64865	ATTGCTTCTCAGATGCAGTG	277256	109452	AGTCCAAGGTGATCAGCTTA
188083	20279	CTACTCAGGAGGCTGAGGTG	232670	64866	AATTGCTTCTCAGATGCAGT	277257	109453	AAGTCCAAGGTGATCAGCTT
188084	20280	GCTACTCAGGAGGCTGAGGT	232671	64867	CAATTGCTTCTCAGATGCAG	277258	109454	CAAGTCCAAGGTGATCAGCT
188085	20281	AGCTACTCAGGAGGCTGAGG	232672	64868	CCAATTGCTTCTCAGATGCA	277259	109455	TCAAGTCCAAGGTGATCAGC
188086	20282	CAGCTACTCAGGAGGCTGAG	232673	64869	ACCAATTGCTTCTCAGATGC	277260	109456	TTCAAGTCCAAGGTGATCAG
188087	20283	CCAGCTACTCAGGAGGCTGA	232674	64870	CACCAATTGCTTCTCAGATG	277261	109457	CTTCAAGTCCAAGGTGATCA
188088	20284	CCCAGCTACTCAGGAGGCTG	232675	64871	ACACCAATTGCTTCTCAGAT	277262	109458	TCTTCAAGTCCAAGGTGATC
188089	20285	TCCCAGCTACTCAGGAGGCT	232676	64872	GACACCAATTGCTTCTCAGA	277263	109459	CTCTTCAAGTCCAAGGTGAT
188090	20286	GTCCCAGCTACTCAGGAGGC	232677	64873	AGACACCAATTGCTTCTCAG	277264	109460	CCTCTTCAAGTCCAAGGTGA
188091	20287	AGTCCCAGCTACTCAGGAGG	232678	64874	TAGACACCAATTGCTTCTCA	277265	109461	TCCTCTTCAAGTCCAAGGTG
188092	20288	TAGTCCCAGCTACTCAGGAG	232679	64875	GTAGACACCAATTGCTTCTC	277266	109462	CTCCTCTTCAAGTCCAAGGT
188093	20289	ATAGTCCCAGCTACTCAGGA	232680	64876	TGTAGACACCAATTGCTTCT	277267	109463	CCTCCTCTTCAAGTCCAAGG
188094	20290	TATAGTCCCAGCTACTCAGG	232681	64877	CTGTAGACACCAATTGCTTC	277268	109464	GCCTCCTCTTCAAGTCCAAG
188095	20291	CTATAGTCCCAGCTACTCAG	232682	64878	GCTGTAGACACCAATTGCTT	277269	109465	AGCCTCCTCTTCAAGTCCAA
188096	20292	CCTATAGTCCCAGCTACTCA	232683	64879	GGCTGTAGACACCAATTGCT	277270	109466	AAGCCTCCTCTTCAAGTCCA
188097	20293	GCCTATAGTCCCAGCTACTC	232684	64880	CGGCTGTAGACACCAATTGC	277271	109467	CAAGCCTCCTCTTCAAGTCC
188098	20294	TGCCTATAGTCCCAGCTACT	232685	64881	GCGGCTGTAGACACCAATTG	277272	109468	ACAAGCCTCCTCTTCAAGTC
188099	20295	GTGCCTATAGTCCCAGCTAC	232686	64882	AGCGGCTGTAGACACCAATT	277273	109469	CACAAGCCTCCTCTTCAAGT
188100	20296	CGTGCCTATAGTCCCAGCTA	232687	64883	TAGCGGCTGTAGACACCAAT	277274	109470	ACACAAGCCTCCTCTTCAAG
188101	20297	GCGTGCCTATAGTCCCAGCT	232688	64884	GTAGCGGCTGTAGACACCAA	277275	109471	CACACAAGCCTCCTCTTCAA
188102	20298	TGCGTGCCTATAGTCCCAGC	232689	64885	TGTAGCGGCTGTAGACACCA	277276	109472	CCACACAAGCCTCCTCTTCA
188103	20299	ATGCGTGCCTATAGTCCCAG	232690	64886	GTGTAGCGGCTGTAGACACC	277277	109473	CCCACACAAGCCTCCTCTTC
188104	20300	TATGCGTGCCTATAGTCCCA	232691	64887	GGTGTAGCGGCTGTAGACAC	277278	109474	GCCCACACAAGCCTCCTCTT
188105	20301	GTATGCGTGCCTATAGTCCC	232692	64888	GGGTGTAGCGGCTGTAGACA	277279	109475	TGCCCACACAAGCCTCCTCT
188106	20302	GGTATGCGTGCCTATAGTCC	232693	64889	AGGGTGTAGCGGCTGTAGAC	277280	109476	ATGCCCACACAAGCCTCCTC

188107	20303	TGGTATGCGTGCCTATAGTC	232694	64890	GAGGGTGTAGCGGCTGTAGA	277281	109477	GATGCCCACACAAGCCTCCT
188108	20304	GTGGTATGCGTGCCTATAGT	232695	64891	TGAGGGTGTAGCGGCTGTAG	277282	109478	GGATGCCCACACAAGCCTCC
188109	20305	GGTGGTATGCGTGCCTATAG	232696	64892	TTGAGGGTGTAGCGGCTGTA	277283	109479	TGGATGCCCACACAAGCCTC
188110	20306	CGGTGGTATGCGTGCCTATA	232697	64893	GTTGAGGGTGTAGCGGCTGT	277284	109480	CTGGATGCCCACACAAGCCT
188111	20307	ACGGTGGTATGCGTGCCTAT	232698	64894	TGTTGAGGGTGTAGCGGCTG	277285	109481	ACTGGATGCCCACACAAGCC
188112	20308	CACGGTGGTATGCGTGCCTA	232699	64895	TTGTTGAGGGTGTAGCGGCT	277286	109482	CACTGGATGCCCACACAAGC
188113	20309	GCACGGTGGTATGCGTGCCT	232700	64896	CTTGTTGAGGGTGTAGCGGC	277287	109483	GCACTGGATGCCCACACAAG
188114	20310	GGCACGGTGGTATGCGTGCC	232701	64897	GCTTGTTGAGGGTGTAGCGG	277288	109484	GGCACTGGATGCCCACACAA
188115	20311	GGGCACGGTGGTATGCGTGC	232702	64898	GGCTTGTTGAGGGTGTAGCG	277289	109485	GGGCACTGGATGCCCACACA
188116	20312	TGGGCACGGTGGTATGCGTG	232703	64899	GGGCTTGTTGAGGGTGTAGC	277290	109486	TGGGCACTGGATGCCCACAC
188117	20313	CTGGGCACGGTGGTATGCGT	232704	64900	CGGGCTTGTTGAGGGTGTAG	277291	109487	GTGGGCACTGGATGCCCACA
188118	20314	GCTGGGCACGGTGGTATGCG	232705	64901	TCGGGCTTGTTGAGGGTGTA	277292	109488	GGTGGGCACTGGATGCCCAC
188119	20315	AGCTGGGCACGGTGGTATGC	232706	64902	ATCGGGCTTGTTGAGGGTGT	277293	109489	GGGTGGGCACTGGATGCCCA
188120	20316	TAGCTGGGCACGGTGGTATG	232707	64903	GATCGGGCTTGTTGAGGGTG	277294	109490	GGGGTGGGCACTGGATGCCC
188121	20317	ATAGCTGGGCACGGTGGTAT	232708	64904	AGATCGGGCTTGTTGAGGGT	277295	109491	CGGGGTGGGCACTGGATGCC
188122	20318	AATAGCTGGGCACGGTGGTA	232709	64905	AAGATCGGGCTTGTTGAGGG	277296	109492	CCGGGGTGGGCACTGGATGC
188123	20319	AAATAGCTGGGCACGGTGGT	232710	64906	CAAGATCGGGCTTGTTGAGG	277297	109493	CCCGGGGTGGGCACTGGATG
188124	20320	AAAATAGCTGGGCACGGTGG	232711	64907	ACAAGATCGGGCTTGTTGAG	277298	109494	ACCCGGGGTGGGCACTGGAT
188125	20321	AAAAATAGCTGGGCACGGTG	232712	64908	AACAAGATCGGGCTTGTTGA	277299	109495	AACCCGGGGTGGGCACTGGA
188126	20322	AAAAAATAGCTGGGCACGGT	232713	64909	AAACAAGATCGGGCTTGTTG	277300	109496	TAACCCGGGGTGGGCACTGG
188127	20323	AAAAAAATAGCTGGGCACGG	232714	64910	CAAACAAGATCGGGCTTGTT	277301	109497	TTAACCCGGGGTGGGCACTG
188128	20324	AAAAAAAATAGCTGGGCACG	232715	64911	TCAAACAAGATCGGGCTTGT	277302	109498	TTTAACCCGGGGTGGGCACT
188129	20325	TAAAAAAAATAGCTGGGCAC	232716	64912	TTCAAACAAGATCGGGCTTG	277303	109499	GTTTAACCCGGGGTGGGCAC
188130	20326	TTAAAAAAAATAGCTGGGCA	232717	64913	TTTCAAACAAGATCGGGCTT	277304	109500	AGTTTAACCCGGGGTGGGCA
188131	20327	ATTAAAAAAAATAGCTGGGC	232718	64914	TTTTCAAACAAGATCGGGCT	277305	109501	GAGTTTAACCCGGGGTGGGC
188132	20328	GATTAAAAAAAATAGCTGGG	232719	64915	CTTTTCAAACAAGATCGGGC	277306	109502	GGAGTTTAACCCGGGGTGGG
188133	20329	TGATTAAAAAAAATAGCTGG	232720	64916	GCTTTTCAAACAAGATCGGG	277307	109503	GGGAGTTTAACCCGGGGTGG
188134	20330	TTGATTAAAAAAAATAGCTG	232721	64917	TGCTTTTCAAACAAGATCGG	277308	109504	TGGGAGTTTAACCCGGGGTG
188135	20331	CTTGATTAAAAAAAATAGCT	232722	64918	TTGCTTTTCAAACAAGATCG	277309	109505	CTGGGAGTTTAACCCGGGGT
188136	20332	TCTTGATTAAAAAAAATAGC	232723	64919	ATTGCTTTTCAAACAAGATC	277310	109506	GCTGGGAGTTTAACCCGGGG
188137	20333	ATCTTGATTAAAAAAAATAG	232724	64920	AATTGCTTTTCAAACAAGAT	277311	109507	TGCTGGGAGTTTAACCCGGG
188138	20334	CATCTTGATTAAAAAAAATA	232725	64921	CAATTGCTTTTCAAACAAGA	277312	109508	CTGCTGGGAGTTTAACCCGG
188139	20335	CCATCTTGATTAAAAAAAAT	232726	64922	CCAATTGCTTTTCAAACAAG	277313	109509	TCTGCTGGGAGTTTAACCCG
188140	20336	TCCATCTTGATTAAAAAAAA	232727	64923	ACCAATTGCTTTTCAAACAA	277314	109510	CTCTGCTGGGAGTTTAACCC
188141	20337	CTCCATCTTGATTAAAAAAA	232728	64924	CACCAATTGCTTTTCAAACA	277315	109511	ACTCTGCTGGGAGTTTAACC
188142	20338	ACTCCATCTTGATTAAAAAA	232729	64925	TCACCAATTGCTTTTCAAAC	277316	109512	TACTCTGCTGGGAGTTTAAC
188143	20339	AACTCCATCTTGATTAAAAA	232730	64926	ATCACCAATTGCTTTTCAAA	277317	109513	ATACTCTGCTGGGAGTTTAA
188144	20340	AAACTCCATCTTGATTAAAA	232731	64927	CATCACCAATTGCTTTTCAA	277318	109514	AATACTCTGCTGGGAGTTTA
188145	20341	AAAACTCCATCTTGATTAAA	232732	64928	GCATCACCAATTGCTTTTCA	277319	109515	CAATACTCTGCTGGGAGTTT
188146	20342	AAAAACTCCATCTTGATTAA	232733	64929	AGCATCACCAATTGCTTTTC	277320	109516	GCAATACTCTGCTGGGAGTT
188147	20343	GAAAAACTCCATCTTGATTA	232734	64930	AAGCATCACCAATTGCTTTT	277321	109517	TGCAATACTCTGCTGGGAGT
188148	20344	AGAAAAACTCCATCTTGATT	232735	64931	GAAGCATCACCAATTGCTTT	277322	109518	GTGCAATACTCTGCTGGGAG
188149	20345	TAGAAAAACTCCATCTTGAT	232736	64932	AGAAGCATCACCAATTGCTT	277323	109519	AGTGCAATACTCTGCTGGGA
188150	20346	ATAGAAAAACTCCATCTTGA	232737	64933	GAGAAGCATCACCAATTGCT	277324	109520	CAGTGCAATACTCTGCTGGG
188151	20347	CATAGAAAAACTCCATCTTG	232738	64934	TGAGAAGCATCACCAATTGC	277325	109521	CCAGTGCAATACTCTGCTGG
188152	20348	ACATAGAAAAACTCCATCTT	232739	64935	TTGAGAAGCATCACCAATTG	277326	109522	CCCAGTGCAATACTCTGCTG
188153	20349	AACATAGAAAAACTCCATCT	232740	64936	TTTGAGAAGCATCACCAATT	277327	109523	GCCCAGTGCAATACTCTGCT
188154	20350	CAACATAGAAAAACTCCATC	232741	64937	TTTTGAGAAGCATCACCAAT	277328	109524	AGCCCAGTGCAATACTCTGC
188155	20351	GCAACATAGAAAAACTCCAT	232742	64938	ATTTTGAGAAGCATCACCAA	277329	109525	AAGCCCAGTGCAATACTCTG
188156	20352	GGCAACATAGAAAAACTCCA	232743	64939	AATTTTGAGAAGCATCACCA	277330	109526	CAAGCCCAGTGCAATACTCT
188157	20353	GGGCAACATAGAAAAACTCC	232744	64940	GAATTTTGAGAAGCATCACC	277331	109527	GCAAGCCCAGTGCAATACTC
188158	20354	TGGGCAACATAGAAAAACTC	232745	64941	AGAATTTTGAGAAGCATCAC	277332	109528	AGCAAGCCCAGTGCAATACT
188159	20355	CTGGGCAACATAGAAAAACT	232746	64942	TAGAATTTTGAGAAGCATCA	277333	109529	CAGCAAGCCCAGTGCAATAC
188160	20356	CCTGGGCAACATAGAAAAAC	232747	64943	ATAGAATTTTGAGAAGCATC	277334	109530	TCAGCAAGCCCAGTGCAATA
188161	20357	GCCTGGGCAACATAGAAAAA	232748	64944	CATAGAATTTTGAGAAGCAT	277335	109531	CTCAGCAAGCCCAGTGCAAT
188162	20358	AGCCTGGGCAACATAGAAAA	232749	64945	CCATAGAATTTTGAGAAGCA	277336	109532	GCTCAGCAAGCCCAGTGCAA
188163	20359	CAGCCTGGGCAACATAGAAA	232750	64946	TCCATAGAATTTTGAGAAGC	277337	109533	GGCTCAGCAAGCCCAGTGCA
188164	20360	CCAGCCTGGGCAACATAGAA	232751	64947	GTCCATAGAATTTTGAGAAG	277338	109534	AGGCTCAGCAAGCCCAGTGC
188165	20361	ACCAGCCTGGGCAACATAGA	232752	64948	TGTCCATAGAATTTTGAGAA	277339	109535	CAGGCTCAGCAAGCCCAGTG
188166	20362	GACCAGCCTGGGCAACATAG	232753	64949	TTGTCCATAGAATTTTGAGA	277340	109536	CCAGGCTCAGCAAGCCCAGT
188167	20363	AGACCAGCCTGGGCAACATA	232754	64950	TTTGTCCATAGAATTTTGAG	277341	109537	ACCAGGCTCAGCAAGCCCAG
188168	20364	GAGACCAGCCTGGGCAACAT	232755	64951	CTTTGTCCATAGAATTTTGA	277342	109538	CACCAGGCTCAGCAAGCCCA
188169	20365	TGAGACCAGCCTGGGCAACA	232756	64952	ACTTTGTCCATAGAATTTTG	277343	109539	TCACCAGGCTCAGCAAGCCC
188170	20366	TTGAGACCAGCCTGGGCAAC	232757	64953	GACTTTGTCCATAGAATTTT	277344	109540	CTCACCAGGCTCAGCAAGCC
188171	20367	CTTGAGACCAGCCTGGGCAA	232758	64954	TGACTTTGTCCATAGAATTT	277345	109541	CCTCACCAGGCTCAGCAAGC
188172	20368	GCTTGAGACCAGCCTGGGCA	232759	64955	CTGACTTTGTCCATAGAATT	277346	109542	GCCTCACCAGGCTCAGCAAG
188173	20369	AGCTTGAGACCAGCCTGGGC	232760	64956	GCTGACTTTGTCCATAGAAT	277347	109543	TGCCTCACCAGGCTCAGCAA
188174	20370	GAGCTTGAGACCAGCCTGGG	232761	64957	GGCTGACTTTGTCCATAGAA	277348	109544	TTGCCTCACCAGGCTCAGCA
188175	20371	GGAGCTTGAGACCAGCCTGG	232762	64958	CGGCTGACTTTGTCCATAGA	277349	109545	TTTGCCTCACCAGGCTCAGC
188176	20372	AGGAGCTTGAGACCAGCCTG	232763	64959	CCGGCTGACTTTGTCCATAG	277350	109546	CTTTGCCTCACCAGGCTCAG
188177	20373	CAGGAGCTTGAGACCAGCCT	232764	64960	CCCGGCTGACTTTGTCCATA	277351	109547	GCTTTGCCTCACCAGGCTCA
188178	20374	CCAGGAGCTTGAGACCAGCC	232765	64961	GCCCGGCTGACTTTGTCCAT	277352	109548	TGCTTTGCCTCACCAGGCTC

188179	20375	TCCAGGAGCTTGAGACCAGC	232766	64962	TGCCCGGCTGACTTTGTCCA	277353	109549	GTGCTTTGCCTCACCAGGCT
188180	20376	GTCCAGGAGCTTGAGACCAG	232767	64963	ATGCCCGGCTGACTTTGTCC	277354	109550	TGTGCTTTGCCTCACCAGGC
188181	20377	AGTCCAGGAGCTTGAGACCA	232768	64964	CATGCCCGGCTGACTTTGTC	277355	109551	CTGTGCTTTGCCTCACCAGG
188182	20378	GAGTCCAGGAGCTTGAGACC	232769	64965	CCATGCCCGGCTGACTTTGT	277356	109552	GCTGTGCTTTGCCTCACCAG
188183	20379	TGAGTCCAGGAGCTTGAGAC	232770	64966	ACCATGCCCGGCTGACTTTG	277357	109553	TGCTGTGCTTTGCCTCACCA
188184	20380	TTGAGTCCAGGAGCTTGAGA	232771	64967	CACCATGCCCGGCTGACTTT	277358	109554	GTGCTGTGCTTTGCCTCACC
188185	20381	CTTGAGTCCAGGAGCTTGAG	232772	64968	CCACCATGCCCGGCTGACTT	277359	109555	TGTGCTGTGCTTTGCCTCAC
188186	20382	GCTTGAGTCCAGGAGCTTGA	232773	64969	GCCACCATGCCCGGCTGACT	277360	109556	CTGTGCTGTGCTTTGCCTCA
188187	20383	TGCTTGAGTCCAGGAGCTTG	232774	64970	AGCCACCATGCCCGGCTGAC	277361	109557	GCTGTGCTGTGCTTTGCCTC
188188	20384	TTGCTTGAGTCCAGGAGCTT	232775	64971	GAGCCACCATGCCCGGCTGA	277362	109558	CGCTGTGCTGTGCTTTGCCT
188189	20385	ATTGCTTGAGTCCAGGAGCT	232776	64972	TGAGCCACCATGCCCGGCTG	277363	109559	TCGCTGTGCTGTGCTTTGCC
188190	20386	GATTGCTTGAGTCCAGGAGC	232777	64973	ATGAGCCACCATGCCCGGCT	277364	109560	CTCGCTGTGCTGTGCTTTGC
188191	20387	GGATTGCTTGAGTCCAGGAG	232778	64974	CATGAGCCACCATGCCCGGC	277365	109561	GCTCGCTGTGCTGTGCTTTG
188192	20388	AGGATTGCTTGAGTCCAGGA	232779	64975	GCATGAGCCACCATGCCCGG	277366	109562	TGCTCGCTGTGCTGTGCTTT
188193	20389	GAGGATTGCTTGAGTCCAGG	232780	64976	GGCATGAGCCACCATGCCCG	277367	109563	GTGCTCGCTGTGCTGTGCTT
188194	20390	GGAGGATTGCTTGAGTCCAG	232781	64977	AGGCATGAGCCACCATGCCC	277368	109564	GGTGCTCGCTGTGCTGTGCT
188195	20391	AGGAGGATTGCTTGAGTCCA	232782	64978	CAGGCATGAGCCACCATGCC	277369	109565	TGGTGCTCGCTGTGCTGTGC
188196	20392	CAGGAGGATTGCTTGAGTCC	232783	64979	ACAGGCATGAGCCACCATGC	277370	109566	CTGGTGCTCGCTGTGCTGTG
188197	20393	GCAGGAGGATTGCTTGAGTC	232784	64980	TACAGGCATGAGCCACCATG	277371	109567	CCTGGTGCTCGCTGTGCTGT
188198	20394	GGCAGGAGGATTGCTTGAGT	232785	64981	TTACAGGCATGAGCCACCAT	277372	109568	GCCTGGTGCTCGCTGTGCTG
188199	20395	AGGCAGGAGGATTGCTTGAG	232786	64982	ATTACAGGCATGAGCCACCA	277373	109569	TGCCTGGTGCTCGCTGTGCT
188200	20396	GAGGCAGGAGGATTGCTTGA	232787	64983	GATTACAGGCATGAGCCACC	277374	109570	CTGCCTGGTGCTCGCTGTGC
188201	20397	TGAGGCAGGAGGATTGCTTG	232788	64984	GGATTACAGGCATGAGCCAC	277375	109571	ACTGCCTGGTGCTCGCTGTG
188202	20398	CTGAGGCAGGAGGATTGCTT	232789	64985	GGGATTACAGGCATGAGCCA	277376	109572	CACTGCCTGGTGCTCGCTGT
188203	20399	GCTGAGGCAGGAGGATTGCT	232790	64986	AGGGATTACAGGCATGAGCC	277377	109573	GCACTGCCTGGTGCTCGCTG
188204	20400	GGCTGAGGCAGGAGGATTGC	232791	64987	TAGGGATTACAGGCATGAGC	277378	109574	AGCACTGCCTGGTGCTCGCT
188205	20401	AGGCTGAGGCAGGAGGATTG	232792	64988	TTAGGGATTACAGGCATGAG	277379	109575	CAGCACTGCCTGGTGCTCGC
188206	20402	GAGGCTGAGGCAGGAGGATT	232793	64989	TTTAGGGATTACAGGCATGA	277380	109576	CCAGCACTGCCTGGTGCTCG
188207	20403	GGAGGCTGAGGCAGGAGGAT	232794	64990	GTTTAGGGATTACAGGCATG	277381	109577	TCCAGCACTGCCTGGTGCTC
188208	20404	GGGAGGCTGAGGCAGGAGGA	232795	64991	AGTTTAGGGATTACAGGCAT	277382	109578	CTCCAGCACTGCCTGGTGCT
188209	20405	TGGGAGGCTGAGGCAGGAGG	232796	64992	AAGTTTAGGGATTACAGGCA	277383	109579	TCTCCAGCACTGCCTGGTGC
188210	20406	TTGGGAGGCTGAGGCAGGAG	232797	64993	AAAGTTTAGGGATTACAGGC	277384	109580	GTCTCCAGCACTGCCTGGTG
188211	20407	TTTGGGAGGCTGAGGCAGGA	232798	64994	CAAAGTTTAGGGATTACAGG	277385	109581	TGTCTCCAGCACTGCCTGGT
188212	20408	CTTTGGGAGGCTGAGGCAGG	232799	64995	CCAAAGTTTAGGGATTACAG	277386	109582	CTGTCTCCAGCACTGCCTGG
188213	20409	CCTTTGGGAGGCTGAGGCAG	232800	64996	CCCAAAGTTTAGGGATTACA	277387	109583	CCTGTCTCCAGCACTGCCTG
188214	20410	CCCTTTGGGAGGCTGAGGCA	232801	64997	TCCCAAAGTTTAGGGATTAC	277388	109584	GCCTGTCTCCAGCACTGCCT
188215	20411	GCCCTTTGGGAGGCTGAGGC	232802	64998	CTCCCAAAGTTTAGGGATTA	277389	109585	GGCCTGTCTCCAGCACTGCC
188216	20412	AGCCCTTTGGGAGGCTGAGG	232803	64999	CCTCCCAAAGTTTAGGGATT	277390	109586	TGGCCTGTCTCCAGCACTGC
188217	20413	CAGCCCTTTGGGAGGCTGAG	232804	65000	GCCTCCCAAAGTTTAGGGAT	277391	109587	TTGGCCTGTCTCCAGCACTG
188218	20414	TCAGCCCTTTGGGAGGCTGA	232805	65001	GGCCTCCCAAAGTTTAGGGA	277392	109588	CTTGGCCTGTCTCCAGCACT
188219	20415	CTCAGCCCTTTGGGAGGCTG	232806	65002	CGGCCTCCCAAAGTTTAGGG	277393	109589	ACTTGGCCTGTCTCCAGCAC
188220	20416	TCTCAGCCCTTTGGGAGGCT	232807	65003	TCGGCCTCCCAAAGTTTAGG	277394	109590	GACTTGGCCTGTCTCCAGCA
188221	20417	ATCTCAGCCCTTTGGGAGGC	232808	65004	CTCGGCCTCCCAAAGTTTAG	277395	109591	AGACTTGGCCTGTCTCCAGC
188222	20418	AATCTCAGCCCTTTGGGAGG	232809	65005	CCTCGGCCTCCCAAAGTTTA	277396	109592	CAGACTTGGCCTGTCTCCAG
188223	20419	TAATCTCAGCCCTTTGGGAG	232810	65006	GCCTCGGCCTCCCAAAGTTT	277397	109593	CCAGACTTGGCCTGTCTCCA
188224	20420	TTAATCTCAGCCCTTTGGGA	232811	65007	TGCCTCGGCCTCCCAAAGTT	277398	109594	CCCAGACTTGGCCTGTCTCC
188225	20421	TTTAATCTCAGCCCTTTGGG	232812	65008	CTGCCTCGGCCTCCCAAAGT	277399	109595	GCCCAGACTTGGCCTGTCTC
188226	20422	TTTTAATCTCAGCCCTTTGG	232813	65009	CCTGCCTCGGCCTCCCAAAG	277400	109596	GGCCCAGACTTGGCCTGTCT
188227	20423	GTTTTAATCTCAGCCCTTTG	232814	65010	GCCTGCCTCGGCCTCCCAAA	277401	109597	TGGCCCAGACTTGGCCTGTC
188228	20424	CGTTTTAATCTCAGCCCTTT	232815	65011	TGCCTGCCTCGGCCTCCCAA	277402	109598	CTGGCCCAGACTTGGCCTGT
188229	20425	ACGTTTTAATCTCAGCCCTT	232816	65012	CTGCCTGCCTCGGCCTCCCA	277403	109599	GCTGGCCCAGACTTGGCCTG
188230	20426	CACGTTTTAATCTCAGCCCT	232817	65013	TCTGCCTGCCTCGGCCTCCC	277404	109600	GGCTGGCCCAGACTTGGCCT
188231	20427	TCACGTTTTAATCTCAGCCC	232818	65014	ATCTGCCTGCCTCGGCCTCC	277405	109601	AGGCTGGCCCAGACTTGGCC
188232	20428	CTCACGTTTTAATCTCAGCC	232819	65015	GATCTGCCTGCCTCGGCCTC	277406	109602	CAGGCTGGCCCAGACTTGGC
188233	20429	ACTCACGTTTTAATCTCAGC	232820	65016	TGATCTGCCTGCCTCGGCCT	277407	109603	CCAGGCTGGCCCAGACTTGG
188234	20430	GACTCACGTTTTAATCTCAG	232821	65017	GTGATCTGCCTGCCTCGGCC	277408	109604	CCCAGGCTGGCCCAGACTTG
188235	20431	TGACTCACGTTTTAATCTCA	232822	65018	GGTGATCTGCCTGCCTCGGC	277409	109605	TCCCAGGCTGGCCCAGACTT
188236	20432	GTGACTCACGTTTTAATCTC	232823	65019	AGGTGATCTGCCTGCCTCGG	277410	109606	CTCCCAGGCTGGCCCAGACT
188237	20433	GGTGACTCACGTTTTAATCT	232824	65020	CAGGTGATCTGCCTGCCTCG	277411	109607	GCTCCCAGGCTGGCCCAGAC
188238	20434	GGGTGACTCACGTTTTAATC	232825	65021	TCAGGTGATCTGCCTGCCTC	277412	109608	GGCTCCCAGGCTGGCCCAGA
188239	20435	AGGGTGACTCACGTTTTAAT	232826	65022	CTCAGGTGATCTGCCTGCCT	277413	109609	TGGCTCCCAGGCTGGCCCAG
188240	20436	CAGGGTGACTCACGTTTTAA	232827	65023	CCTCAGGTGATCTGCCTGCC	277414	109610	TTGGCTCCCAGGCTGGCCCA
188241	20437	GCAGGGTGACTCACGTTTTA	232828	65024	ACCTCAGGTGATCTGCCTGC	277415	109611	GTTGGCTCCCAGGCTGGCCC
188242	20438	GGCAGGGTGACTCACGTTTT	232829	65025	GACCTCAGGTGATCTGCCTG	277416	109612	AGTTGGCTCCCAGGCTGGCC
188243	20439	GGGCAGGGTGACTCACGTTT	232830	65026	AGACCTCAGGTGATCTGCCT	277417	109613	CAGTTGGCTCCCAGGCTGGC
188244	20440	TGGGCAGGGTGACTCACGTT	232831	65027	CAGACCTCAGGTGATCTGCC	277418	109614	ACAGTTGGCTCCCAGGCTGG
188245	20441	CTGGGCAGGGTGACTCACGT	232832	65028	CCAGACCTCAGGTGATCTGC	277419	109615	CACAGTTGGCTCCCAGGCTG
188246	20442	GCTGGGCAGGGTGACTCACG	232833	65029	ACCAGACCTCAGGTGATCTG	277420	109616	TCACAGTTGGCTCCCAGGCT
188247	20443	GGCTGGGCAGGGTGACTCAC	232834	65030	CACCAGACCTCAGGTGATCT	277421	109617	CTCACAGTTGGCTCCCAGGC
188248	20444	TGGCTGGGCAGGGTGACTCA	232835	65031	TCACCAGACCTCAGGTGATC	277422	109618	CCTCACAGTTGGCTCCCAGG
188249	20445	TTGGCTGGGCAGGGTGACTC	232836	65032	TTCACCAGACCTCAGGTGAT	277423	109619	GCCTCACAGTTGGCTCCCAG
188250	20446	ATTGGCTGGGCAGGGTGACT	232837	65033	TTTCACCAGACCTCAGGTGA	277424	109620	TGCCTCACAGTTGGCTCCCA

188251	20447	AATTGGCTGGGCAGGGTGAC	232838	65034	GTTTCACCAGACCTCAGGTG	277425	109621	GTGCCTCACAGTTGGCTCCC
188252	20448	CAATTGGCTGGGCAGGGTGA	232839	65035	GGTTTCACCAGACCTCAGGT	277426	109622	CGTGCCTCACAGTTGGCTCC
188253	20449	GCAATTGGCTGGGCAGGGTG	232840	65036	GGGTTTCACCAGACCTCAGG	277427	109623	CCGTGCCTCACAGTTGGCTC
188254	20450	AGCAATTGGCTGGGCAGGGT	232841	65037	AGGGTTTCACCAGACCTCAG	277428	109624	TCCGTGCCTCACAGTTGGCT
188255	20451	AAGCAATTGGCTGGGCAGGG	232842	65038	CAGGGTTTCACCAGACCTCA	277429	109625	GTCCGTGCCTCACAGTTGGC
188256	20452	AAAGCAATTGGCTGGGCAGG	232843	65039	ACAGGGTTTCACCAGACCTC	277430	109626	CGTCCGTGCCTCACAGTTGG
188257	20453	AAAAGCAATTGGCTGGGCAG	232844	65040	GACAGGGTTTCACCAGACCT	277431	109627	CCGTCCGTGCCTCACAGTTG
188258	20454	AAAAAGCAATTGGCTGGGCA	232845	65041	AGACAGGGTTTCACCAGACC	277432	109628	CCCGTCCGTGCCTCACAGTT
188259	20455	TAAAAAGCAATTGGCTGGGC	232846	65042	GAGACAGGGTTTCACCAGAC	277433	109629	CCCCGTCCGTGCCTCACAGT
188260	20456	TTAAAAAGCAATTGGCTGGG	232847	65043	AGAGACAGGGTTTCACCAGA	277434	109630	GCCCCGTCCGTGCCTCACAG
188261	20457	TTTAAAAAGCAATTGGCTGG	232848	65044	TAGAGACAGGGTTTCACCAG	277435	109631	AGCCCCGTCCGTGCCTCACA
188262	20458	TTTTAAAAAGCAATTGGCTG	232849	65045	GTAGAGACAGGGTTTCACCA	277436	109632	CAGCCCCGTCCGTGCCTCAC
188263	20459	TTTTTAAAAAGCAATTGGCT	232850	65046	AGTAGAGACAGGGTTTCACC	277437	109633	ACAGCCCCGTCCGTGCCTCA
188264	20460	TTTTTTAAAAAGCAATTGGC	232851	65047	TAGTAGAGACAGGGTTTCAC	277438	109634	CACAGCCCCGTCCGTGCCTC
188265	20461	CTTTTTTAAAAAGCAATTGG	232852	65048	TTAGTAGAGACAGGGTTTCA	277439	109635	CCACAGCCCCGTCCGTGCCT
188266	20462	TCTTTTTTAAAAAGCAATTG	232853	65049	TTTAGTAGAGACAGGGTTTC	277440	109636	CCCACAGCCCCGTCCGTGCC
188267	20463	ATCTTTTTTAAAAAGCAATT	232854	65050	TTTTAGTAGAGACAGGGTTT	277441	109637	CCCCACAGCCCCGTCCGTGC
188268	20464	AATCTTTTTTAAAAAGCAAT	232855	65051	TTTTTAGTAGAGACAGGGTT	277442	109638	GCCCCACAGCCCCGTCCGTG
188269	20465	TAATCTTTTTTAAAAAGCAA	232856	65052	ATTTTTAGTAGAGACAGGGT	277443	109639	AGCCCCACAGCCCCGTCCGT
188270	20466	TTAATCTTTTTTAAAAAGCA	232857	65053	CATTTTTAGTAGAGACAGGG	277444	109640	CAGCCCCACAGCCCCGTCCG
188271	20467	TTTAATCTTTTTTAAAAAGC	232858	65054	GCATTTTTAGTAGAGACAGG	277445	109641	ACAGCCCCACAGCCCCGTCC
188272	20468	ATTTAATCTTTTTTAAAAAG	232859	65055	TGCATTTTTAGTAGAGACAG	277446	109642	CACAGCCCCACAGCCCCGTC
188273	20469	CATTTAATCTTTTTTAAAAA	232860	65056	TTGCATTTTTAGTAGAGACA	277447	109643	CCACAGCCCCACAGCCCCGT
188274	20470	GCATTTAATCTTTTTTAAAA	232861	65057	TTTGCATTTTTAGTAGAGAC	277448	109644	CCCACAGCCCCACAGCCCCG
188275	20471	TGCATTTAATCTTTTTTAAA	232862	65058	TTTTGCATTTTTAGTAGAGA	277449	109645	CCCCACAGCCCCACAGCCCC
188276	20472	ATGCATTTAATCTTTTTTAA	232863	65059	TTTTTGCATTTTTAGTAGAG	277450	109646	GCCCCACAGCCCCACAGCCC
188277	20473	CATGCATTTAATCTTTTTTA	232864	65060	ATTTTTGCATTTTTAGTAGA	277451	109647	AGCCCCACAGCCCCACAGCC
188278	20474	ACATGCATTTAATCTTTTTT	232865	65061	AATTTTTGCATTTTTAGTAG	277452	109648	CAGCCCCACAGCCCCACAGC
188279	20475	TACATGCATTTAATCTTTTT	232866	65062	TAATTTTTGCATTTTTAGTA	277453	109649	GCAGCCCCACAGCCCCACAG
188280	20476	ATACATGCATTTAATCTTTT	232867	65063	GTAATTTTTGCATTTTTAGT	277454	109650	TGCAGCCCCACAGCCCCACA
188281	20477	TATACATGCATTTAATCTTT	232868	65064	GGTAATTTTTGCATTTTTAG	277455	109651	CTGCAGCCCCACAGCCCCAC
188282	20478	GTATACATGCATTTAATCTT	232869	65065	GGGTAATTTTTGCATTTTTA	277456	109652	CCTGCAGCCCCACAGCCCCA
188283	20479	CGTATACATGCATTTAATCT	232870	65066	TGGGTAATTTTTGCATTTTT	277457	109653	GCCTGCAGCCCCACAGCCCC
188284	20480	GCGTATACATGCATTTAATC	232871	65067	CTGGGTAATTTTTGCATTTT	277458	109654	AGCCTGCAGCCCCACAGCCC
188285	20481	AGCGTATACATGCATTTAAT	232872	65068	CCTGGGTAATTTTTGCATTT	277459	109655	AAGCCTGCAGCCCCACAGCC
188286	20482	GAGCGTATACATGCATTTAA	232873	65069	GCCTGGGTAATTTTTGCATT	277460	109656	CAAGCCTGCAGCCCCACAGC
188287	20483	TGAGCGTATACATGCATTTA	232874	65070	TGCCTGGGTAATTTTTGCAT	277461	109657	CCAAGCCTGCAGCCCCACAG
188288	20484	CTGAGCGTATACATGCATTT	232875	65071	ATGCCTGGGTAATTTTTGCA	277462	109658	CCCAAGCCTGCAGCCCCACA
188289	20485	CCTGAGCGTATACATGCATT	232876	65072	CATGCCTGGGTAATTTTTGC	277463	109659	CCCCAAGCCTGCAGCCCCAC
188290	20486	GCCTGAGCGTATACATGCAT	232877	65073	CCATGCCTGGGTAATTTTTG	277464	109660	GCCCCAAGCCTGCAGCCCCA
188291	20487	TGCCTGAGCGTATACATGCA	232878	65074	ACCATGCCTGGGTAATTTTT	277465	109661	GGCCCCAAGCCTGCAGCCCC
188292	20488	ATGCCTGAGCGTATACATGC	232879	65075	CACCATGCCTGGGTAATTTT	277466	109662	TGGCCCCAAGCCTGCAGCCC
188293	20489	GATGCCTGAGCGTATACATG	232880	65076	CCACCATGCCTGGGTAATTT	277467	109663	CTGGCCCCAAGCCTGCAGCC
188294	20490	TGATGCCTGAGCGTATACAT	232881	65077	GCCACCATGCCTGGGTAATT	277468	109664	CCTGGCCCCAAGCCTGCAGC
188295	20491	CTGATGCCTGAGCGTATACA	232882	65078	AGCCACCATGCCTGGGTAAT	277469	109665	CCCTGGCCCCAAGCCTGCAG
188296	20492	GCTGATGCCTGAGCGTATAC	232883	65079	CAGCCACCATGCCTGGGTAA	277470	109666	TCCCTGGCCCCAAGCCTGCA
188297	20493	TGCTGATGCCTGAGCGTATA	232884	65080	CCAGCCACCATGCCTGGGTA	277471	109667	CTCCCTGGCCCCAAGCCTGC
188298	20494	GTGCTGATGCCTGAGCGTAT	232885	65081	CCCAGCCACCATGCCTGGGT	277472	109668	CCTCCCTGGCCCCAAGCCTG
188299	20495	TGTGCTGATGCCTGAGCGTA	232886	65082	CCCCAGCCACCATGCCTGGG	277473	109669	CCCTCCCTGGCCCCAAGCCT
188300	20496	GTGTGCTGATGCCTGAGCGT	232887	65083	GCCCCAGCCACCATGCCTGG	277474	109670	TCCCTCCCTGGCCCCAAGCC
188301	20497	AGTGTGCTGATGCCTGAGCG	232888	65084	GGCCCCAGCCACCATGCCTG	277475	109671	CTCCCTCCCTGGCCCCAAGC
188302	20498	AAGTGTGCTGATGCCTGAGC	232889	65085	AGGCCCCAGCCACCATGCCT	277476	109672	CCTCCCTCCCTGGCCCCAAG
188303	20499	CAAGTGTGCTGATGCCTGAG	232890	65086	CAGGCCCCAGCCACCATGCC	277477	109673	CCCTCCCTCCCTGGCCCCAA
188304	20500	CCAAGTGTGCTGATGCCTGA	232891	65087	ACAGGCCCCAGCCACCATGC	277478	109674	GCCCTCCCTCCCTGGCCCCA
188305	20501	TCCAAGTGTGCTGATGCCTG	232892	65088	TACAGGCCCCAGCCACCATG	277479	109675	AGCCCTCCCTCCCTGGCCCC
188306	20502	TTCCAAGTGTGCTGATGCCT	232893	65089	TTACAGGCCCCAGCCACCAT	277480	109676	CAGCCCTCCCTCCCTGGCCC
188307	20503	TTTCCAAGTGTGCTGATGCC	232894	65090	ATTACAGGCCCCAGCCACCA	277481	109677	CCAGCCCTCCCTCCCTGGCC
188308	20504	CTTTCCAAGTGTGCTGATGC	232895	65091	GATTACAGGCCCCAGCCACC	277482	109678	CCCAGCCCTCCCTCCCTGGC
188309	20505	CCTTTCCAAGTGTGCTGATG	232896	65092	GGATTACAGGCCCCAGCCAC	277483	109679	GCCCAGCCCTCCCTCCCTGG
188310	20506	TCCTTTCCAAGTGTGCTGAT	232897	65093	GGGATTACAGGCCCCAGCCA	277484	109680	AGCCCAGCCCTCCCTCCCTG
188311	20507	ATCCTTTCCAAGTGTGCTGA	232898	65094	TGGGATTACAGGCCCCAGCC	277485	109681	GAGCCCAGCCCTCCCTCCCT
188312	20508	CATCCTTTCCAAGTGTGCTG	232899	65095	CTGGGATTACAGGCCCCAGC	277486	109682	AGAGCCCAGCCCTCCCTCCC
188313	20509	TCATCCTTTCCAAGTGTGCT	232900	65096	GCTGGGATTACAGGCCCCAG	277487	109683	AAGAGCCCAGCCCTCCCTCC
188314	20510	TTCATCCTTTCCAAGTGTGC	232901	65097	AGCTGGGATTACAGGCCCCA	277488	109684	AAAGAGCCCAGCCCTCCCTC
188315	20511	TTTCATCCTTTCCAAGTGTG	232902	65098	TAGCTGGGATTACAGGCCCC	277489	109685	CAAAGAGCCCAGCCCTCCCT
188316	20512	TTTTCATCCTTTCCAAGTGT	232903	65099	GTAGCTGGGATTACAGGCCC	277490	109686	CCAAAGAGCCCAGCCCTCCC
188317	20513	ATTTTCATCCTTTCCAAGTG	232904	65100	AGTAGCTGGGATTACAGGCC	277491	109687	TCCAAAGAGCCCAGCCCTCC
188318	20514	TATTTTCATCCTTTCCAAGT	232905	65101	GAGTAGCTGGGATTACAGGC	277492	109688	TTCCAAAGAGCCCAGCCCTC
188319	20515	ATATTTTCATCCTTTCCAAG	232906	65102	CGAGTAGCTGGGATTACAGG	277493	109689	GTTCCAAAGAGCCCAGCCCT
188320	20516	GATATTTTCATCCTTTCCAA	232907	65103	CCGAGTAGCTGGGATTACAG	277494	109690	TGTTCCAAAGAGCCCAGCCC
188321	20517	GGATATTTTCATCCTTTCCA	232908	65104	CCCGAGTAGCTGGGATTACA	277495	109691	CTGTTCCAAAGAGCCCAGCC
188322	20518	CGGATATTTTCATCCTTTCC	232909	65105	TCCCGAGTAGCTGGGATTAC	277496	109692	GCTGTTCCAAAGAGCCCAGC

188323	20519	CCGGATATTTTCATCCTTTC	232910	65106	CTCCCGAGTAGCTGGGATTA	277497	109693	GGCTGTTCCAAAGAGCCCAG
188324	20520	TCCGGATATTTTCATCCTTT	232911	65107	CCTCCCGAGTAGCTGGGATT	277498	109694	AGGCTGTTCCAAAGAGCCCA
188325	20521	TTCCGGATATTTTCATCCTT	232912	65108	GCCTCCCGAGTAGCTGGGAT	277499	109695	AAGGCTGTTCCAAAGAGCCC
188326	20522	CTTCCGGATATTTTCATCCT	232913	65109	AGCCTCCCGAGTAGCTGGGA	277500	109696	CAAGGCTGTTCCAAAGAGCC
188327	20523	TCTTCCGGATATTTTCATCC	232914	65110	CAGCCTCCCGAGTAGCTGGG	277501	109697	TCAAGGCTGTTCCAAAGAGC
188328	20524	TTCTTCCGGATATTTTCATC	232915	65111	TCAGCCTCCCGAGTAGCTGG	277502	109698	CTCAAGGCTGTTCCAAAGAG
188329	20525	CTTCTTCCGGATATTTTCAT	232916	65112	CTCAGCCTCCCGAGTAGCTG	277503	109699	TCTCAAGGCTGTTCCAAAGA
188330	20526	CCTTCTTCCGGATATTTTCA	232917	65113	CCTCAGCCTCCCGAGTAGCT	277504	109700	CTCTCAAGGCTGTTCCAAAG
188331	20527	CCCTTCTTCCGGATATTTTC	232918	65114	GCCTCAGCCTCCCGAGTAGC	277505	109701	TCTCTCAAGGCTGTTCCAAA
188332	20528	ACCCTTCTTCCGGATATTTT	232919	65115	TGCCTCAGCCTCCCGAGTAG	277506	109702	TTCTCTCAAGGCTGTTCCAA
188333	20529	AACCCTTCTTCCGGATATTT	232920	65116	CTGCCTCAGCCTCCCGAGTA	277507	109703	GTTCTCTCAAGGCTGTTCCA
188334	20530	GAACCCTTCTTCCGGATATT	232921	65117	CCTGCCTCAGCCTCCCGAGT	277508	109704	AGTTCTCTCAAGGCTGTTCC
188335	20531	AGAACCCTTCTTCCGGATAT	232922	65118	TCCTGCCTCAGCCTCCCGAG	277509	109705	CAGTTCTCTCAAGGCTGTTC
188336	20532	AAGAACCCTTCTTCCGGATA	232923	65119	CTCCTGCCTCAGCCTCCCGA	277510	109706	TCAGTTCTCTCAAGGCTGTT
188337	20533	AAAGAACCCTTCTTCCGGAT	232924	65120	TCTCCTGCCTCAGCCTCCCG	277511	109707	TTCAGTTCTCTCAAGGCTGT
188338	20534	AAAAGAACCCTTCTTCCGGA	232925	65121	TTCTCCTGCCTCAGCCTCCC	277512	109708	GTTCAGTTCTCTCAAGGCTG
188339	20535	TAAAAGAACCCTTCTTCCGG	232926	65122	ATTCTCCTGCCTCAGCCTCC	277513	109709	GGTTCAGTTCTCTCAAGGCT
188340	20536	TTAAAAGAACCCTTCTTCCG	232927	65123	GATTCTCCTGCCTCAGCCTC	277514	109710	GGGTTCAGTTCTCTCAAGGC
188341	20537	TTTAAAAGAACCCTTCTTCC	232928	65124	CGATTCTCCTGCCTCAGCCT	277515	109711	TGGGTTCAGTTCTCTCAAGG
188342	20538	TTTTAAAAGAACCCTTCTTC	232929	65125	GCGATTCTCCTGCCTCAGCC	277516	109712	TTGGGTTCAGTTCTCTCAAG
188343	20539	CTTTTAAAAGAACCCTTCTT	232930	65126	AGCGATTCTCCTGCCTCAGC	277517	109713	TTTGGGTTCAGTTCTCTCAA
188344	20540	CCTTTTAAAAGAACCCTTCT	232931	65127	AAGCGATTCTCCTGCCTCAG	277518	109714	GTTTGGGTTCAGTTCTCTCA
188345	20541	GCCTTTTAAAAGAACCCTTC	232932	65128	CAAGCGATTCTCCTGCCTCA	277519	109715	TGTTTGGGTTCAGTTCTCTC
188346	20542	AGCCTTTTAAAAGAACCCTT	232933	65129	TCAAGCGATTCTCCTGCCTC	277520	109716	TTGTTTGGGTTCAGTTCTCT
188347	20543	GAGCCTTTTAAAAGAACCCT	232934	65130	TTCAAGCGATTCTCCTGCCT	277521	109717	TTTGTTTGGGTTCAGTTCTC
188348	20544	GGAGCCTTTTAAAAGAACCC	232935	65131	CTTCAAGCGATTCTCCTGCC	277522	109718	TTTTGTTTGGGTTCAGTTCT
188349	20545	AGGAGCCTTTTAAAAGAACC	232936	65132	GCTTCAAGCGATTCTCCTGC	277523	109719	GTTTTGTTTGGGTTCAGTTC
188350	20546	GAGGAGCCTTTTAAAAGAAC	232937	65133	TGCTTCAAGCGATTCTCCTG	277524	109720	GGTTTTGTTTGGGTTCAGTT
188351	20547	TGAGGAGCCTTTTAAAAGAA	232938	65134	TTGCTTCAAGCGATTCTCCT	277525	109721	TGGTTTTGTTTGGGTTCAGT
188352	20548	TTGAGGAGCCTTTTAAAAGA	232939	65135	CTTGCTTCAAGCGATTCTCC	277526	109722	CTGGTTTTGTTTGGGTTCAG
188353	20549	CTTGAGGAGCCTTTTAAAAG	232940	65136	CCTTGCTTCAAGCGATTCTC	277527	109723	TCTGGTTTTGTTTGGGTTCA
188354	20550	ACTTGAGGAGCCTTTTAAAA	232941	65137	TCCTTGCTTCAAGCGATTCT	277528	109724	ATCTGGTTTTGTTTGGGTTC
188355	20551	CACTTGAGGAGCCTTTTAAA	232942	65138	CTCCTTGCTTCAAGCGATTC	277529	109725	GATCTGGTTTTGTTTGGGTT
188356	20552	TCACTTGAGGAGCCTTTTAA	232943	65139	CCTCCTTGCTTCAAGCGATT	277530	109726	TGATCTGGTTTTGTTTGGGT
188357	20553	ATCACTTGAGGAGCCTTTTA	232944	65140	GCCTCCTTGCTTCAAGCGAT	277531	109727	TTGATCTGGTTTTGTTTGGG
188358	20554	CATCACTTGAGGAGCCTTTT	232945	65141	CGCCTCCTTGCTTCAAGCGA	277532	109728	CTTGATCTGGTTTTGTTTGG
188359	20555	GCATCACTTGAGGAGCCTTT	232946	65142	CCGCCTCCTTGCTTCAAGCG	277533	109729	CCTTGATCTGGTTTTGTTTG
188360	20556	AGCATCACTTGAGGAGCCTT	232947	65143	TCCGCCTCCTTGCTTCAAGC	277534	109730	ACCTTGATCTGGTTTTGTTT
188361	20557	CAGCATCACTTGAGGAGCCT	232948	65144	CTCCGCCTCCTTGCTTCAAG	277535	109731	GACCTTGATCTGGTTTTGTT
188362	20558	CCAGCATCACTTGAGGAGCC	232949	65145	CCTCCGCCTCCTTGCTTCAA	277536	109732	AGACCTTGATCTGGTTTTGT
188363	20559	GCCAGCATCACTTGAGGAGC	232950	65146	ACCTCCGCCTCCTTGCTTCA	277537	109733	TAGACCTTGATCTGGTTTTG
188364	20560	TGCCAGCATCACTTGAGGAG	232951	65147	AACCTCCGCCTCCTTGCTTC	277538	109734	CTAGACCTTGATCTGGTTTT
188365	20561	CTGCCAGCATCACTTGAGGA	232952	65148	AAACCTCCGCCTCCTTGCTT	277539	109735	ACTAGACCTTGATCTGGTTT
188366	20562	CCTGCCAGCATCACTTGAGG	232953	65149	GAAACCTCCGCCTCCTTGCT	277540	109736	CACTAGACCTTGATCTGGTT
188367	20563	GCCTGCCAGCATCACTTGAG	232954	65150	TGAAACCTCCGCCTCCTTGC	277541	109737	TCACTAGACCTTGATCTGGT
188368	20564	TGCCTGCCAGCATCACTTGA	232955	65151	CTGAAACCTCCGCCTCCTTG	277542	109738	CTCACTAGACCTTGATCTGG
188369	20565	ATGCCTGCCAGCATCACTTG	232956	65152	ACTGAAACCTCCGCCTCCTT	277543	109739	TCTCACTAGACCTTGATCTG
188370	20566	CATGCCTGCCAGCATCACTT	232957	65153	CACTGAAACCTCCGCCTCCT	277544	109740	CTCTCACTAGACCTTGATCT
188371	20567	TCATGCCTGCCAGCATCACT	232958	65154	TCACTGAAACCTCCGCCTCC	277545	109741	GCTCTCACTAGACCTTGATC
188372	20568	GTCATGCCTGCCAGCATCAC	232959	65155	CTCACTGAAACCTCCGCCTC	277546	109742	AGCTCTCACTAGACCTTGAT
188373	20569	CGTCATGCCTGCCAGCATCA	232960	65156	GCTCACTGAAACCTCCGCCT	277547	109743	AAGCTCTCACTAGACCTTGA
188374	20570	TCGTCATGCCTGCCAGCATC	232961	65157	GGCTCACTGAAACCTCCGCC	277548	109744	TAAGCTCTCACTAGACCTTG
188375	20571	TTCGTCATGCCTGCCAGCAT	232962	65158	TGGCTCACTGAAACCTCCGC	277549	109745	CTAAGCTCTCACTAGACCTT
188376	20572	ATTCGTCATGCCTGCCAGCA	232963	65159	TTGGCTCACTGAAACCTCCG	277550	109746	CCTAAGCTCTCACTAGACCT
188377	20573	CATTCGTCATGCCTGCCAGC	232964	65160	CTTGGCTCACTGAAACCTCC	277551	109747	CCCTAAGCTCTCACTAGACC
188378	20574	ACATTCGTCATGCCTGCCAG	232965	65161	TCTTGGCTCACTGAAACCTC	277552	109748	GCCCTAAGCTCTCACTAGAC
188379	20575	GACATTCGTCATGCCTGCCA	232966	65162	ATCTTGGCTCACTGAAACCT	277553	109749	AGCCCTAAGCTCTCACTAGA
188380	20576	GGACATTCGTCATGCCTGCC	232967	65163	AATCTTGGCTCACTGAAACC	277554	109750	CAGCCCTAAGCTCTCACTAG
188381	20577	GGGACATTCGTCATGCCTGC	232968	65164	CAATCTTGGCTCACTGAAAC	277555	109751	GCAGCCCTAAGCTCTCACTA
188382	20578	AGGGACATTCGTCATGCCTG	232969	65165	GCAATCTTGGCTCACTGAAA	277556	109752	AGCAGCCCTAAGCTCTCACT
188383	20579	CAGGGACATTCGTCATGCCT	232970	65166	TGCAATCTTGGCTCACTGAA	277557	109753	AAGCAGCCCTAAGCTCTCAC
188384	20580	CCAGGGACATTCGTCATGCC	232971	65167	GTGCAATCTTGGCTCACTGA	277558	109754	AAAGCAGCCCTAAGCTCTCA
188385	20581	ACCAGGGACATTCGTCATGC	232972	65168	GGTGCAATCTTGGCTCACTG	277559	109755	CAAAGCAGCCCTAAGCTCTC
188386	20582	GACCAGGGACATTCGTCATG	232973	65169	TGGTGCAATCTTGGCTCACT	277560	109756	CCAAAGCAGCCCTAAGCTCT
188387	20583	TGACCAGGGACATTCGTCAT	232974	65170	GTGGTGCAATCTTGGCTCAC	277561	109757	CCCAAAGCAGCCCTAAGCTC
188388	20584	GTGACCAGGGACATTCGTCA	232975	65171	AGTGGTGCAATCTTGGCTCA	277562	109758	ACCCAAAGCAGCCCTAAGCT
188389	20585	TGTGACCAGGGACATTCGTC	232976	65172	CAGTGGTGCAATCTTGGCTC	277563	109759	CACCCAAAGCAGCCCTAAGC
188390	20586	TTGTGACCAGGGACATTCGT	232977	65173	GCAGTGGTGCAATCTTGGCT	277564	109760	GCACCCAAAGCAGCCCTAAG
188391	20587	TTTGTGACCAGGGACATTCG	232978	65174	TGCAGTGGTGCAATCTTGGC	277565	109761	AGCACCCAAAGCAGCCCTAA
188392	20588	TTTTGTGACCAGGGACATTC	232979	65175	GTGCAGTGGTGCAATCTTGG	277566	109762	GAGCACCCAAAGCAGCCCTA
188393	20589	CTTTTGTGACCAGGGACATT	232980	65176	AGTGCAGTGGTGCAATCTTG	277567	109763	GGAGCACCCAAAGCAGCCCT
188394	20590	GCTTTTGTGACCAGGGACAT	232981	65177	GAGTGCAGTGGTGCAATCTT	277568	109764	TGGAGCACCCAAAGCAGCCC

188395	20591	AGCTTTTGTGACCAGGGACA	232982	65178	GGAGTGCAGTGGTGCAATCT	277569	109765	CTGGAGCACCCAAAGCAGCC
188396	20592	GAGCTTTTGTGACCAGGGAC	232983	65179	TGGAGTGCAGTGGTGCAATC	277570	109766	CCTGGAGCACCCAAAGCAGC
188397	20593	AGAGCTTTTGTGACCAGGGA	232984	65180	CTGGAGTGCAGTGGTGCAAT	277571	109767	TCCTGGAGCACCCAAAGCAG
188398	20594	CAGAGCTTTTGTGACCAGGG	232985	65181	GCTGGAGTGCAGTGGTGCAA	277572	109768	TTCCTGGAGCACCCAAAGCA
188399	20595	TCAGAGCTTTTGTGACCAGG	232986	65182	GGCTGGAGTGCAGTGGTGCA	277573	109769	TTTCCTGGAGCACCCAAAGC
188400	20596	ATCAGAGCTTTTGTGACCAG	232987	65183	AGGCTGGAGTGCAGTGGTGC	277574	109770	ATTTCCTGGAGCACCCAAAG
188401	20597	GATCAGAGCTTTTGTGACCA	232988	65184	CAGGCTGGAGTGCAGTGGTG	277575	109771	AATTTCCTGGAGCACCCAAA
188402	20598	AGATCAGAGCTTTTGTGACC	232989	65185	CCAGGCTGGAGTGCAGTGGT	277576	109772	CAATTTCCTGGAGCACCCAA
188403	20599	CAGATCAGAGCTTTTGTGAC	232990	65186	CCCAGGCTGGAGTGCAGTGG	277577	109773	TCAATTTCCTGGAGCACCCA
188404	20600	CCAGATCAGAGCTTTTGTGA	232991	65187	ACCCAGGCTGGAGTGCAGTG	277578	109774	ATCAATTTCCTGGAGCACCC
188405	20601	GCCAGATCAGAGCTTTTGTG	232992	65188	CACCCAGGCTGGAGTGCAGT	277579	109775	AATCAATTTCCTGGAGCACC
188406	20602	GGCCAGATCAGAGCTTTTGT	232993	65189	TCACCCAGGCTGGAGTGCAG	277580	109776	TAATCAATTTCCTGGAGCAC
188407	20603	AGGCCAGATCAGAGCTTTTG	232994	65190	GTCACCCAGGCTGGAGTGCA	277581	109777	TTAATCAATTTCCTGGAGCA
188408	20604	TAGGCCAGATCAGAGCTTTT	232995	65191	TGTCACCCAGGCTGGAGTGC	277582	109778	TTTAATCAATTTCCTGGAGC
188409	20605	TTAGGCCAGATCAGAGCTTT	232996	65192	TTGTCACCCAGGCTGGAGTG	277583	109779	GTTTAATCAATTTCCTGGAG
188410	20606	GTTAGGCCAGATCAGAGCTT	232997	65193	CTTGTCACCCAGGCTGGAGT	277584	109780	GGTTTAATCAATTTCCTGGA
188411	20607	GGTTAGGCCAGATCAGAGCT	232998	65194	TCTTGTCACCCAGGCTGGAG	277585	109781	TGGTTTAATCAATTTCCTGG
188412	20608	GGGTTAGGCCAGATCAGAGC	232999	65195	CTCTTGTCACCCAGGCTGGA	277586	109782	TTGGTTTAATCAATTTCCTG
188413	20609	AGGGTTAGGCCAGATCAGAG	233000	65196	ACTCTTGTCACCCAGGCTGG	277587	109783	CTTGGTTTAATCAATTTCCT
188414	20610	CAGGGTTAGGCCAGATCAGA	233001	65197	CACTCTTGTCACCCAGGCTG	277588	109784	ACTTGGTTTAATCAATTTCC
188415	20611	ACAGGGTTAGGCCAGATCAG	233002	65198	TCACTCTTGTCACCCAGGCT	277589	109785	CACTTGGTTTAATCAATTTC
188416	20612	GACAGGGTTAGGCCAGATCA	233003	65199	TTCACTCTTGTCACCCAGGC	277590	109786	CCACTTGGTTTAATCAATTT
188417	20613	TGACAGGGTTAGGCCAGATC	233004	65200	TTTCACTCTTGTCACCCAGG	277591	109787	TCCACTTGGTTTAATCAATT
188418	20614	ATGACAGGGTTAGGCCAGAT	233005	65201	GTTTCACTCTTGTCACCCAG	277592	109788	GTCCACTTGGTTTAATCAAT
188419	20615	CATGACAGGGTTAGGCCAGA	233006	65202	AGTTTCACTCTTGTCACCCA	277593	109789	TGTCCACTTGGTTTAATCAA
188420	20616	ACATGACAGGGTTAGGCCAG	233007	65203	GAGTTTCACTCTTGTCACCC	277594	109790	GTGTCCACTTGGTTTAATCA
188421	20617	AACATGACAGGGTTAGGCCA	233008	65204	GGAGTTTCACTCTTGTCACC	277595	109791	TGTGTCCACTTGGTTTAATC
188422	20618	TAACATGACAGGGTTAGGCC	233009	65205	TGGAGTTTCACTCTTGTCAC	277596	109792	GTGTGTCCACTTGGTTTAAT
188423	20619	CTAACATGACAGGGTTAGGC	233010	65206	ATGGAGTTTCACTCTTGTCA	277597	109793	TGTGTGTCCACTTGGTTTAA
188424	20620	TCTAACATGACAGGGTTAGG	233011	65207	GATGGAGTTTCACTCTTGTC	277598	109794	GTGTGTGTCCACTTGGTTTA
188425	20621	CTCTAACATGACAGGGTTAG	233012	65208	AGATGGAGTTTCACTCTTGT	277599	109795	GGTGTGTGTCCACTTGGTTT
188426	20622	TCTCTAACATGACAGGGTTA	233013	65209	TAGATGGAGTTTCACTCTTG	277600	109796	GGGTGTGTGTCCACTTGGTT
188427	20623	GTCTCTAACATGACAGGGTT	233014	65210	TTAGATGGAGTTTCACTCTT	277601	109797	GGGGTGTGTGTCCACTTGGT
188428	20624	AGTCTCTAACATGACAGGGT	233015	65211	TTTAGATGGAGTTTCACTCT	277602	109798	GGGGGTGTGTGTCCACTTGG
188429	20625	CAGTCTCTAACATGACAGGG	233016	65212	TTTTAGATGGAGTTTCACTC	277603	109799	TGGGGGTGTGTGTCCACTTG
188430	20626	CCAGTCTCTAACATGACAGG	233017	65213	TTTTTAGATGGAGTTTCACT	277604	109800	CTGGGGGTGTGTGTCCACTT
188431	20627	TCCAGTCTCTAACATGACAG	233018	65214	TTTTTTAGATGGAGTTTCAC	277605	109801	GCTGGGGGTGTGTGTCCACT
188432	20628	CTCCAGTCTCTAACATGACA	233019	65215	TTTTTTTAGATGGAGTTTCA	277606	109802	GGCTGGGGGTGTGTGTCCAC
188433	20629	ACTCCAGTCTCTAACATGAC	233020	65216	TTTTTTTTAGATGGAGTTTC	277607	109803	GGGCTGGGGGTGTGTGTCCA
188434	20630	CACTCCAGTCTCTAACATGA	233021	65217	TTTTTTTTTAGATGGAGTTT	277608	109804	GGGGCTGGGGGTGTGTGTCC
188435	20631	GCACTCCAGTCTCTAACATG	233022	65218	TTTTTTTTTTAGATGGAGTT	277609	109805	TGGGGCTGGGGGTGTGTGTC
188436	20632	CGCACTCCAGTCTCTAACAT	233023	65219	TTTTTTTTTTTAGATGGAGT	277610	109806	GTGGGGCTGGGGGTGTGTGT
188437	20633	ACGCACTCCAGTCTCTAACA	233024	65220	TTTTTTTTTTTTAGATGGAG	277611	109807	GGTGGGGCTGGGGGTGTGTG
188438	20634	CACGCACTCCAGTCTCTAAC	233025	65221	ATTTTTTTTTTTTAGATGGA	277612	109808	AGGTGGGGCTGGGGGTGTGT
188439	20635	ACACGCACTCCAGTCTCTAA	233026	65222	AATTTTTTTTTTTTAGATGG	277613	109809	GAGGTGGGGCTGGGGGTGTG
188440	20636	CACACGCACTCCAGTCTCTA	233027	65223	TAATTTTTTTTTTTTAGATG	277614	109810	TGAGGTGGGGCTGGGGGTGT
188441	20637	ACACACGCACTCCAGTCTCT	233028	65224	ATAATTTTTTTTTTTTAGAT	277615	109811	GTGAGGTGGGGCTGGGGGTG
188442	20638	CACACACGCACTCCAGTCTC	233029	65225	CATAATTTTTTTTTTTTAGA	277616	109812	GGTGAGGTGGGGCTGGGGGT
188443	20639	ACACACACGCACTCCAGTCT	233030	65226	CCATAATTTTTTTTTTTTAG	277617	109813	TGGTGAGGTGGGGCTGGGGG
188444	20640	CACACACACGCACTCCAGTC	233031	65227	TCCATAATTTTTTTTTTTTA	277618	109814	GTGGTGAGGTGGGGCTGGGG
188445	20641	GCACACACACGCACTCCAGT	233032	65228	GTCCATAATTTTTTTTTTT	277619	109815	TGTGGTGAGGTGGGGCTGGG
188446	20642	CGCACACACACGCACTCCAG	233033	65229	TGTCCATAATTTTTTTTTT	277620	109816	CTGTGGTGAGGTGGGGCTGG
188447	20643	GCGCACACACACGCACTCCA	233034	65230	TTGTCCATAATTTTTTTTT	277621	109817	GCTGTGGTGAGGTGGGGCTG
188448	20644	CGCGCACACACACGCACTCC	233035	65231	TTTGTCCATAATTTTTTTT	277622	109818	GGCTGTGGTGAGGTGGGGCT
188449	20645	GCGCGCACACACACGCACTC	233036	65232	CTTTGTCCATAATTTTTTT	277623	109819	AGGCTGTGGTGAGGTGGGGC
188450	20646	TGCGCGCACACACACGCACT	233037	65233	ACTTTGTCCATAATTTTTT	277624	109820	GAGGCTGTGGTGAGGTGGGG
188451	20647	TTGCGCGCACACACACGCAC	233038	65234	AACTTTGTCCATAATTTTT	277625	109821	AGAGGCTGTGGTGAGGTGGG
188452	20648	TTTGCGCGCACACACACGCA	233039	65235	AAACTTTGTCCATAATTTT	277626	109822	GAGAGGCTGTGGTGAGGTGG
188453	20649	CTTTGCGCGCACACACACGC	233040	65236	AAAACTTTGTCCATAATTT	277627	109823	GGAGAGGCTGTGGTGAGGTG
188454	20650	ACTTTGCGCGCACACACACG	233041	65237	AAAAACTTTGTCCATAATT	277628	109824	AGGAGAGGCTGTGGTGAGGT
188455	20651	CACTTTGCGCGCACACACAC	233042	65238	GAAAAACTTTGTCCATAATT	277629	109825	AAGGAGAGGCTGTGGTGAGG
188456	20652	ACACTTTGCGCGCACACACA	233043	65239	TGAAAAACTTTGTCCATAAT	277630	109826	GAAGGAGAGGCTGTGGTGAG
188457	20653	CACACTTTGCGCGCACACAC	233044	65240	TTGAAAAACTTTGTCCATAA	277631	109827	TGAAGGAGAGGCTGTGGTGA
188458	20654	CCACACTTTGCGCGCACACA	233045	65241	TTTGAAAAACTTTGTCCATA	277632	109828	CTGAAGGAGAGGCTGTGGTG
188459	20655	CCCACACTTTGCGCGCACAC	233046	65242	TTTTGAAAAACTTTGTCCAT	277633	109829	CCTGAAGGAGAGGCTGTGGT
188460	20656	CCCCACACTTTGCGCGCACA	233047	65243	TTTTTGAAAAACTTTGTCCA	277634	109830	CCCTGAAGGAGAGGCTGTGG
188461	20657	CCCCCACACTTTGCGCGCAC	233048	65244	CTTTTTGAAAAACTTTGTCC	277635	109831	ACCCTGAAGGAGAGGCTGTG
188462	20658	CCCCCCACACTTTGCGCGCA	233049	65245	TCTTTTTGAAAAACTTTGTC	277636	109832	GACCCTGAAGGAGAGGCTGT
188463	20659	TCCCCCCACACTTTGCGCGC	233050	65246	ATCTTTTTGAAAAACTTTGT	277637	109833	TGACCCTGAAGGAGAGGCTG
188464	20660	ATCCCCCCACACTTTGCGCG	233051	65247	TATCTTTTTGAAAAACTTTG	277638	109834	TTGACCCTGAAGGAGAGGCT
188465	20661	CATCCCCCCACACTTTGCGC	233052	65248	ATATCTTTTTGAAAAACTTT	277639	109835	TTTGACCCTGAAGGAGAGGC
188466	20662	CCATCCCCCCACACTTTGCG	233053	65249	AATATCTTTTTGAAAAACTT	277640	109836	GTTTGACCCTGAAGGAGAGG

188467	20663	CCCATCCCCCCACACTTTGC	233054	65250	AAATATCTTTTTGAAAAACT	277641	109837	AGTTTGACCCTGAAGGAGAG
188468	20664	CCCCATCCCCCCACACTTTG	233055	65251	TAAATATCTTTTTGAAAAAC	277642	109838	GAGTTTGACCCTGAAGGAGA
188469	20665	CCCCCATCCCCCCACACTTT	233056	65252	TTAAATATCTTTTTGAAAAA	277643	109839	AGAGTTTGACCCTGAAGGAG
188470	20666	ACCCCCATCCCCCCACACTT	233057	65253	ATTAAATATCTTTTTGAAAA	277644	109840	CAGAGTTTGACCCTGAAGGA
188471	20667	CACCCCCATCCCCCCACACT	233058	65254	CATTAAATATCTTTTTGAAA	277645	109841	TCAGAGTTTGACCCTGAAGG
188472	20668	TCACCCCCATCCCCCCACAC	233059	65255	GCATTAAATATCTTTTTGAA	277646	109842	GTCAGAGTTTGACCCTGAAG
188473	20669	CTCACCCCCATCCCCCCACA	233060	65256	TGCATTAAATATCTTTTTGA	277647	109843	GGTCAGAGTTTGACCCTGAA
188474	20670	ACTCACCCCCATCCCCCCAC	233061	65257	TTGCATTAAATATCTTTTTG	277648	109844	TGGTCAGAGTTTGACCCTGA
188475	20671	CACTCACCCCCATCCCCCCA	233062	65258	GTTGCATTAAATATCTTTTT	277649	109845	GTGGTCAGAGTTTGACCCTG
188476	20672	ACACTCACCCCCATCCCCCC	233063	65259	AGTTGCATTAAATATCTTTT	277650	109846	TGTGGTCAGAGTTTGACCCT
188477	20673	CACACTCACCCCCATCCCCC	233064	65260	AAGTTGCATTAAATATCTTT	277651	109847	CTGTGGTCAGAGTTTGACCC
188478	20674	ACACACTCACCCCCATCCCC	233065	65261	AAAGTTGCATTAAATATCTT	277652	109848	TCTGTGGTCAGAGTTTGACC
188479	20675	CACACACTCACCCCCATCCC	233066	65262	TAAAGTTGCATTAAATATCT	277653	109849	GTCTGTGGTCAGAGTTTGAC
188480	20676	ACACACACTCACCCCCATCC	233067	65263	ATAAAGTTGCATTAAATATC	277654	109850	TGTCTGTGGTCAGAGTTTGA
188481	20677	CACACACACTCACCCCCATC	233068	65264	AATAAAGTTGCATTAAATAT	277655	109851	ATGTCTGTGGTCAGAGTTTG
188482	20678	CCACACACACTCACCCCCAT	233069	65265	AAATAAAGTTGCATTAAATA	277656	109852	AATGTCTGTGGTCAGAGTTT
188483	20679	ACCACACACACTCACCCCCA	233070	65266	CAAATAAAGTTGCATTAAAT	277657	109853	AAATGTCTGTGGTCAGAGTT
188484	20680	CACCACACACACTCACCCCC	233071	65267	ACAAATAAAGTTGCATTAAA	277658	109854	GAAATGTCTGTGGTCAGAGT
188485	20681	ACACCACACACACTCACCCC	233072	65268	TACAAATAAAGTTGCATTAA	277659	109855	AGAAATGTCTGTGGTCAGAG
188486	20682	CACACCACACACACTCACCC	233073	65269	TTACAAATAAAGTTGCATTA	277660	109856	GAGAAATGTCTGTGGTCAGA
188487	20683	ACACACCACACACACTCACC	233074	65270	ATTACAAATAAAGTTGCATT	277661	109857	GGAGAAATGTCTGTGGTCAG
188488	20684	TACACACCACACACACTCAC	233075	65271	TATTACAAATAAAGTTGCAT	277662	109858	GGGAGAAATGTCTGTGGTCA
188489	20685	TTACACACCACACACACTCA	233076	65272	ATATTACAAATAAAGTTGCA	277663	109859	GGGGAGAAATGTCTGTGGTC
188490	20686	CTTACACACCACACACACTC	233077	65273	AATATTACAAATAAAGTTGC	277664	109860	AGGGGAGAAATGTCTGTGGT
188491	20687	GCTTACACACCACACACACT	233078	65274	CAATATTACAAATAAAGTTG	277665	109861	CAGGGGAGAAATGTCTGTGG
188492	20688	TGCTTACACACCACACACAC	233079	65275	CCAATATTACAAATAAAGTT	277666	109862	TCAGGGGAGAAATGTCTGTG
188493	20689	ATGCTTACACACCACACACA	233080	65276	TCCAATATTACAAATAAAGT	277667	109863	GTCAGGGGAGAAATGTCTGT
188494	20690	CATGCTTACACACCACACAC	233081	65277	TTCCAATATTACAAATAAAG	277668	109864	AGTCAGGGGAGAAATGTCTG
188495	20691	TCATGCTTACACACCACACA	233082	65278	GTTCCAATATTACAAATAAA	277669	109865	TAGTCAGGGGAGAAATGTCT
188496	20692	CTCATGCTTACACACCACAC	233083	65279	TGTTCCAATATTACAAATAA	277670	109866	CTAGTCAGGGGAGAAATGTC
188497	20693	ACTCATGCTTACACACCACA	233084	65280	ATGTTCCAATATTACAAATA	277671	109867	CCTAGTCAGGGGAGAAATGT
188498	20694	CACTCATGCTTACACACCAC	233085	65281	GATGTTCCAATATTACAAAT	277672	109868	TCCTAGTCAGGGGAGAAATG
188499	20695	ACACTCATGCTTACACACCA	233086	65282	AGATGTTCCAATATTACAAA	277673	109869	CTCCTAGTCAGGGGAGAAAT
188500	20696	CACACTCATGCTTACACACC	233087	65283	CAGATGTTCCAATATTACAA	277674	109870	ACTCCTAGTCAGGGGAGAAA
188501	20697	ACACACTCATGCTTACACAC	233088	65284	TCAGATGTTCCAATATTACA	277675	109871	AACTCCTAGTCAGGGGAGAA
188502	20698	TACACACTCATGCTTACACA	233089	65285	CTCAGATGTTCCAATATTAC	277676	109872	GAACTCCTAGTCAGGGGAGA
188503	20699	ATACACACTCATGCTTACAC	233090	65286	CCTCAGATGTTCCAATATTA	277677	109873	GGAACTCCTAGTCAGGGGAG
188504	20700	CATACACACTCATGCTTACA	233091	65287	GCCTCAGATGTTCCAATATT	277678	109874	GGGAACTCCTAGTCAGGGGA
188505	20701	ACATACACACTCATGCTTAC	233092	65288	GGCCTCAGATGTTCCAATAT	277679	109875	AGGGAACTCCTAGTCAGGGG
188506	20702	CACATACACACTCATGCTTA	233093	65289	TGGCCTCAGATGTTCCAATA	277680	109876	CAGGGAACTCCTAGTCAGGG
188507	20703	ACACATACACACTCATGCTT	233094	65290	ATGGCCTCAGATGTTCCAAT	277681	109877	CCAGGGAACTCCTAGTCAGG
188508	20704	CACACATACACACTCATGCT	233095	65291	AATGGCCTCAGATGTTCCAA	277682	109878	TCCAGGGAACTCCTAGTCAG
188509	20705	ACACACATACACACTCATGC	233096	65292	AAATGGCCTCAGATGTTCCA	277683	109879	ATCCAGGGAACTCCTAGTCA
188510	20706	CACACACATACACACTCATG	233097	65293	GAAATGGCCTCAGATGTTCC	277684	109880	GATCCAGGGAACTCCTAGTC
188511	20707	CCACACACATACACACTCAT	233098	65294	TGAAATGGCCTCAGATGTTC	277685	109881	TGATCCAGGGAACTCCTAGT
188512	20708	ACCACACACATACACACTCA	233099	65295	CTGAAATGGCCTCAGATGTT	277686	109882	TTGATCCAGGGAACTCCTAG
188513	20709	CACCACACACATACACACTC	233100	65296	ACTGAAATGGCCTCAGATGT	277687	109883	TTTGATCCAGGGAACTCCTA
188514	20710	ACACCACACACATACACACT	233101	65297	CACTGAAATGGCCTCAGATG	277688	109884	TTTTGATCCAGGGAACTCCT
188515	20711	CACACCACACACATACACAC	233102	65298	GCACTGAAATGGCCTCAGAT	277689	109885	ATTTTGATCCAGGGAACTCC
188516	20712	CCACACCACACACATACACA	233103	65299	AGCACTGAAATGGCCTCAGA	277690	109886	AATTTTGATCCAGGGAACTC
188517	20713	CCCACACCACACACATACAC	233104	65300	TAGCACTGAAATGGCCTCAG	277691	109887	CAATTTTGATCCAGGGAACT
188518	20714	CCCCACACCACACACATACA	233105	65301	TTAGCACTGAAATGGCCTCA	277692	109888	CCAATTTTGATCCAGGGAAC
188519	20715	CCCCCACACCACACACATAC	233106	65302	GTTAGCACTGAAATGGCCTC	277693	109889	CCCAATTTTGATCCAGGGAA
188520	20716	ACCCCCACACCACACACATA	233107	65303	AGTTAGCACTGAAATGGCCT	277694	109890	TCCCAATTTTGATCCAGGGA
188521	20717	CACCCCCACACCACACACAT	233108	65304	TAGTTAGCACTGAAATGGCC	277695	109891	CTCCCAATTTTGATCCAGGG
188522	20718	ACACCCCCACACCACACACA	233109	65305	ATAGTTAGCACTGAAATGGC	277696	109892	GCTCCCAATTTTGATCCAGG
188523	20719	CACACCCCCACACCACACAC	233110	65306	AATAGTTAGCACTGAAATGG	277697	109893	AGCTCCCAATTTTGATCCAG
188524	20720	ACACACCCCCACACCACACA	233111	65307	TAATAGTTAGCACTGAAATG	277698	109894	AAGCTCCCAATTTTGATCCA
188525	20721	CACACACCCCCACACCACAC	233112	65308	CTAATAGTTAGCACTGAAAT	277699	109895	CAAGCTCCCAATTTTGATCC
188526	20722	GCACACACCCCCACACCACA	233113	65309	CCTAATAGTTAGCACTGAAA	277700	109896	GCAAGCTCCCAATTTTGATC
188527	20723	AGCACACACCCCCACACCAC	233114	65310	CCCTAATAGTTAGCACTGAA	277701	109897	TGCAAGCTCCCAATTTTGAT
188528	20724	CAGCACACACCCCCACACCA	233115	65311	CCCCTAATAGTTAGCACTGA	277702	109898	TTGCAAGCTCCCAATTTTGA
188529	20725	ACAGCACACACCCCCACACC	233116	65312	TCCCCTAATAGTTAGCACTG	277703	109899	GTTGCAAGCTCCCAATTTTG
188530	20726	CACAGCACACACCCCCACAC	233117	65313	ATCCCCTAATAGTTAGCACT	277704	109900	TGTTGCAAGCTCCCAATTTT
188531	20727	ACACAGCACACACCCCCACA	233118	65314	CATCCCCTAATAGTTAGCAC	277705	109901	GTGTTGCAAGCTCCCAATTT
188532	20728	CACACAGCACACACCCCCAC	233119	65315	CCATCCCCTAATAGTTAGCA	277706	109902	TGTGTTGCAAGCTCCCAATT
188533	20729	TCACACAGCACACACCCCCA	233120	65316	ACCATCCCCTAATAGTTAGC	277707	109903	ATGTGTTGCAAGCTCCCAAT
188534	20730	CTCACACAGCACACACCCCC	233121	65317	AACCATCCCCTAATAGTTAG	277708	109904	GATGTGTTGCAAGCTCCCAA
188535	20731	GCTCACACAGCACACACCCC	233122	65318	TAACCATCCCCTAATAGTTA	277709	109905	CGATGTGTTGCAAGCTCCCA
188536	20732	CGCTCACACAGCACACACCC	233123	65319	CTAACCATCCCCTAATAGTT	277710	109906	ACGATGTGTTGCAAGCTCCC
188537	20733	ACGCTCACACAGCACACACC	233124	65320	CCTAACCATCCCCTAATAGT	277711	109907	AACGATGTGTTGCAAGCTCC
188538	20734	CACGCTCACACAGCACACAC	233125	65321	TCCTAACCATCCCCTAATAG	277712	109908	GAACGATGTGTTGCAAGCTC

188539	20735	ACACGCTCACACAGCACACA	233126	65322	TTCCTAACCATCCCCTAATA	277713	109909	AGAACGATGTGTTGCAAGCT
188540	20736	CACACGCTCACACAGCACAC	233127	65323	TTTCCTAACCATCCCCTAAT	277714	109910	GAGAACGATGTGTTGCAAGC
188541	20737	ACACACGCTCACACAGCACA	233128	65324	TTTTCCTAACCATCCCCTAA	277715	109911	AGAGAACGATGTGTTGCAAG
188542	20738	CACACACGCTCACACAGCAC	233129	65325	ATTTTCCTAACCATCCCCTA	277716	109912	GAGAGAACGATGTGTTGCAA
188543	20739	TCACACACGCTCACACAGCA	233130	65326	TATTTTCCTAACCATCCCCT	277717	109913	GGAGAGAACGATGTGTTGCA
188544	20740	CTCACACACGCTCACACAGC	233131	65327	ATATTTTCCTAACCATCCCC	277718	109914	GGGAGAGAACGATGTGTTGC
188545	20741	ACTCACACACGCTCACACAG	233132	65328	CATATTTTCCTAACCATCCC	277719	109915	AGGGAGAGAACGATGTGTTG
188546	20742	GACTCACACACGCTCACACA	233133	65329	CCATATTTTCCTAACCATCC	277720	109916	AAGGGAGAGAACGATGTGTT
188547	20743	AGACTCACACACGCTCACAC	233134	65330	ACCATATTTTCCTAACCATC	277721	109917	CAAGGGAGAGAACGATGTGT
188548	20744	CAGACTCACACACGCTCACA	233135	65331	TACCATATTTTCCTAACCAT	277722	109918	TCAAGGGAGAGAACGATGTG
188549	20745	ACAGACTCACACACGCTCAC	233136	65332	GTACCATATTTTCCTAACCA	277723	109919	ATCAAGGGAGAGAACGATGT
188550	20746	CACAGACTCACACACGCTCA	233137	65333	TGTACCATATTTTCCTAACC	277724	109920	CATCAAGGGAGAGAACGATG
188551	20747	ACACAGACTCACACACGCTC	233138	65334	ATGTACCATATTTTCCTAAC	277725	109921	CCATCAAGGGAGAGAACGAT
188552	20748	CACACAGACTCACACACGCT	233139	65335	TATGTACCATATTTTCCTAA	277726	109922	ACCATCAAGGGAGAGAACGA
188553	20749	ACACACAGACTCACACACGC	233140	65336	ATATGTACCATATTTTCCTA	277727	109923	AACCATCAAGGGAGAGAACG
188554	20750	CACACACAGACTCACACACG	233141	65337	CATATGTACCATATTTTCCT	277728	109924	AAACCATCAAGGGAGAGAAC
188555	20751	ACACACACAGACTCACACAC	233142	65338	ACATATGTACCATATTTTCC	277729	109925	AAAACCATCAAGGGAGAGAA
188556	20752	TACACACACAGACTCACACA	233143	65339	CACATATGTACCATATTTTC	277730	109926	AAAAACCATCAAGGGAGAGA
188557	20753	CTACACACACAGACTCACAC	233144	65340	CCACATATGTACCATATTTT	277731	109927	CAAAAACCATCAAGGGAGAG
188558	20754	ACTACACACACAGACTCACA	233145	65341	TCCACATATGTACCATATTT	277732	109928	ACAAAAACCATCAAGGGAGA
188559	20755	CACTACACACACAGACTCAC	233146	65342	TTCCACATATGTACCATATT	277733	109929	GACAAAAACCATCAAGGGAG
188560	20756	ACACTACACACACAGACTCA	233147	65343	TTTCCACATATGTACCATAT	277734	109930	TGACAAAAACCATCAAGGGA
188561	20757	CACACTACACACACAGACTC	233148	65344	CTTTCCACATATGTACCATA	277735	109931	CTGACAAAAACCATCAAGGG
188562	20758	ACACACTACACACACAGACT	233149	65345	CCTTTCCACATATGTACCAT	277736	109932	ACTGACAAAAACCATCAAGG
188563	20759	CACACACTACACACACAGAC	233150	65346	TCCTTTCCACATATGTACCA	277737	109933	CACTGACAAAAACCATCAAG
188564	20760	ACACACACTACACACACAGA	233151	65347	TTCCTTTCCACATATGTACC	277738	109934	ACACTGACAAAAACCATCAA
188565	20761	CACACACACTACACACACAG	233152	65348	GTTCCTTTCCACATATGTAC	277739	109935	GACACTGACAAAAACCATCA
188566	20762	ACACACACACTACACACACA	233153	65349	TGTTCCTTTCCACATATGTA	277740	109936	AGACACTGACAAAAACCATC
188567	20763	CACACACACACTACACACAC	233154	65350	ATGTTCCTTTCCACATATGT	277741	109937	TAGACACTGACAAAAACCAT
188568	20764	TCACACACACACTACACACA	233155	65351	AATGTTCCTTTCCACATATG	277742	109938	ATAGACACTGACAAAAACCA
188569	20765	TTCACACACACACTACACAC	233156	65352	AAATGTTCCTTTCCACATAT	277743	109939	GATAGACACTGACAAAAACC
188570	20766	CTTCACACACACACTACACA	233157	65353	CAAATGTTCCTTTCCACATA	277744	109940	GGATAGACACTGACAAAAAC
188571	20767	ACTTCACACACACACTACAC	233158	65354	CCAAATGTTCCTTTCCACAT	277745	109941	TGGATAGACACTGACAAAAA
188572	20768	TACTTCACACACACACTACA	233159	65355	ACCAAATGTTCCTTTCCACA	277746	109942	CTGGATAGACACTGACAAAA
188573	20769	ATACTTCACACACACACTAC	233160	65356	TACCAAATGTTCCTTTCCAC	277747	109943	TCTGGATAGACACTGACAAA
188574	20770	CATACTTCACACACACACTA	233161	65357	CTACCAAATGTTCCTTTCCA	277748	109944	CTCTGGATAGACACTGACAA
188575	20771	ACATACTTCACACACACACT	233162	65358	ACTACCAAATGTTCCTTTCC	277749	109945	GCTCTGGATAGACACTGACA
188576	20772	CACATACTTCACACACACAC	233163	65359	AACTACCAAATGTTCCTTTC	277750	109946	AGCTCTGGATAGACACTGAC
188577	20773	CCACATACTTCACACACACA	233164	65360	TAACTACCAAATGTTCCTTT	277751	109947	CAGCTCTGGATAGACACTGA
188578	20774	ACCACATACTTCACACACAC	233165	65361	CTAACTACCAAATGTTCCTT	277752	109948	TCAGCTCTGGATAGACACTG
188579	20775	CACCACATACTTCACACACA	233166	65362	ACTAACTACCAAATGTTCCT	277753	109949	TTCAGCTCTGGATAGACACT
188580	20776	ACACCACATACTTCACACAC	233167	65363	CACTAACTACCAAATGTTCC	277754	109950	CTTCAGCTCTGGATAGACAC
188581	20777	CACACCACATACTTCACACA	233168	65364	GCACTAACTACCAAATGTTC	277755	109951	ACTTCAGCTCTGGATAGACA
188582	20778	ACACACCACATACTTCACAC	233169	65365	GGCACTAACTACCAAATGTT	277756	109952	CACTTCAGCTCTGGATAGAC
188583	20779	TACACACCACATACTTCACA	233170	65366	GGGCACTAACTACCAAATGT	277757	109953	ACACTTCAGCTCTGGATAGA
188584	20780	ATACACACCACATACTTCAC	233171	65367	GGGGCACTAACTACCAAATG	277758	109954	TACACTTCAGCTCTGGATAG
188585	20781	CATACACACCACATACTTCA	233172	65368	AGGGGCACTAACTACCAAAT	277759	109955	TTACACTTCAGCTCTGGATA
188586	20782	ACATACACACCACATACTTC	233173	65369	CAGGGGCACTAACTACCAAA	277760	109956	ATTACACTTCAGCTCTGGAT
188587	20783	CACATACACACCACATACTT	233174	65370	TCAGGGGCACTAACTACCAA	277761	109957	TATTACACTTCAGCTCTGGA
188588	20784	ACACATACACACCACATACT	233175	65371	ATCAGGGGCACTAACTACCA	277762	109958	ATATTACACTTCAGCTCTGG
188589	20785	CACACATACACACCACATAC	233176	65372	CATCAGGGGCACTAACTACC	277763	109959	TATATTACACTTCAGCTCTG
188590	20786	TCACACATACACACCACATA	233177	65373	ACATCAGGGGCACTAACTAC	277764	109960	ATATATTACACTTCAGCTCT
188591	20787	GTCACACATACACACCACAT	233178	65374	AACATCAGGGGCACTAACTA	277765	109961	TATATATTACACTTCAGCTC
188592	20788	CGTCACACATACACACCACA	233179	65375	AAACATCAGGGGCACTAACT	277766	109962	ATATATATTACACTTCAGCT
188593	20789	ACGTCACACATACACACCAC	233180	65376	TAAACATCAGGGGCACTAAC	277767	109963	CATATATATTACACTTCAGC
188594	20790	CACGTCACACATACACACCA	233181	65377	GTAAACATCAGGGGCACTAA	277768	109964	ACATATATATTACACTTCAG
188595	20791	TCACGTCACACATACACACC	233182	65378	TGTAAACATCAGGGGCACTA	277769	109965	AACATATATATTACACTTCA
188596	20792	CTCACGTCACACATACACAC	233183	65379	TTGTAAACATCAGGGGCACT	277770	109966	TAACATATATATTACACTTC
188597	20793	CCTCACGTCACACATACACA	233184	65380	TTTGTAAACATCAGGGGCAC	277771	109967	GTAACATATATATTACACTT
188598	20794	ACCTCACGTCACACATACAC	233185	65381	CTTTGTAAACATCAGGGGCA	277772	109968	AGTAACATATATATTACACT
188599	20795	CACCTCACGTCACACATACA	233186	65382	CCTTTGTAAACATCAGGGGC	277773	109969	CAGTAACATATATATTACAC
188600	20796	ACACCTCACGTCACACATAC	233187	65383	GCCTTTGTAAACATCAGGGG	277774	109970	ACAGTAACATATATATTACA
188601	20797	CACACCTCACGTCACACATA	233188	65384	AGCCTTTGTAAACATCAGGG	277775	109971	TACAGTAACATATATATTAC
188602	20798	ACACACCTCACGTCACACAT	233189	65385	AAGCCTTTGTAAACATCAGG	277776	109972	CTACAGTAACATATATATTA
188603	20799	CACACACCTCACGTCACACA	233190	65386	AAAGCCTTTGTAAACATCAG	277777	109973	GCTACAGTAACATATATATT
188604	20800	ACACACACCTCACGTCACAC	233191	65387	AAAAGCCTTTGTAAACATCA	277778	109974	AGCTACAGTAACATATATAT
188605	20801	CACACACACCTCACGTCACA	233192	65388	TAAAAGCCTTTGTAAACATC	277779	109975	CAGCTACAGTAACATATATA
188606	20802	CCACACACACCTCACGTCAC	233193	65389	CTAAAAGCCTTTGTAAACAT	277780	109976	TCAGCTACAGTAACATATAT
188607	20803	ACCACACACACCTCACGTCA	233194	65390	ACTAAAAGCCTTTGTAAACA	277781	109977	CTCAGCTACAGTAACATATA
188608	20804	CACCACACACACCTCACGTC	233195	65391	CACTAAAAGCCTTTGTAAAC	277782	109978	TCTCAGCTACAGTAACATAT
188609	20805	ACACCACACACACCTCACGT	233196	65392	TCACTAAAAGCCTTTGTAAA	277783	109979	TTCTCAGCTACAGTAACATA
188610	20806	CACACCACACACACCTCACG	233197	65393	GTCACTAAAAGCCTTTGTAA	277784	109980	TTTCTCAGCTACAGTAACAT

188611	20807	ACACACCACACACACCTCAC	233198	65394	GGTCACTAAAAGCCTTTGTA	277785	109981	ATTTCTCAGCTACAGTAACA
188612	20808	CACACACCACACACACCTCA	233199	65395	TGGTCACTAAAAGCCTTTGT	277786	109982	AATTTCTCAGCTACAGTAAC
188613	20809	TCACACACCACACACACCTC	233200	65396	TTGGTCACTAAAAGCCTTTG	277787	109983	TAATTTCTCAGCTACAGTAA
188614	20810	CTCACACACCACACACACCT	233201	65397	GTTGGTCACTAAAAGCCTTT	277788	109984	TTAATTTCTCAGCTACAGTA
188615	20811	ACTCACACACCACACACACC	233202	65398	TGTTGGTCACTAAAAGCCTT	277789	109985	TTTAATTTCTCAGCTACAGT
188616	20812	AACTCACACACCACACACAC	233203	65399	TTGTTGGTCACTAAAAGCCT	277790	109986	ATTTAATTTCTCAGCTACAG
188617	20813	CAACTCACACACCACACACA	233204	65400	TTTGTTGGTCACTAAAAGCC	277791	109987	AATTTAATTTCTCAGCTACA
188618	20814	ACAACTCACACACCACACAC	233205	65401	ATTTGTTGGTCACTAAAAGC	277792	109988	AAATTTAATTTCTCAGCTAC
188619	20815	CACAACTCACACACCACACA	233206	65402	CATTTGTTGGTCACTAAAAG	277793	109989	GAAATTTAATTTCTCAGCTA
188620	20816	ACACAACTCACACACCACAC	233207	65403	GCATTTGTTGGTCACTAAAA	277794	109990	TGAAATTTAATTTCTCAGCT
188621	20817	TACACAACTCACACACCACA	233208	65404	AGCATTTGTTGGTCACTAAA	277795	109991	CTGAAATTTAATTTCTCAGC
188622	20818	ATACACAACTCACACACCAC	233209	65405	GAGCATTTGTTGGTCACTAA	277796	109992	CCTGAAATTTAATTTCTCAG
188623	20819	CATACACAACTCACACACCA	233210	65406	TGAGCATTTGTTGGTCACTA	277797	109993	TCCTGAAATTTAATTTCTCA
188624	20820	CCATACACAACTCACACACC	233211	65407	ATGAGCATTTGTTGGTCACT	277798	109994	ATCCTGAAATTTAATTTCTC
188625	20821	ACCATACACAACTCACACAC	233212	65408	CATGAGCATTTGTTGGTCAC	277799	109995	AATCCTGAAATTTAATTTCT
188626	20822	CACCATACACAACTCACACA	233213	65409	GCATGAGCATTTGTTGGTCA	277800	109996	GAATCCTGAAATTTAATTTC
188627	20823	ACACCATACACAACTCACAC	233214	65410	AGCATGAGCATTTGTTGGTC	277801	109997	AGAATCCTGAAATTTAATTT
188628	20824	CACACCATACACAACTCACA	233215	65411	TAGCATGAGCATTTGTTGGT	277802	109998	CAGAATCCTGAAATTTAATT
188629	20825	ACACACCATACACAACTCAC	233216	65412	ATAGCATGAGCATTTGTTGG	277803	109999	TCAGAATCCTGAAATTTAAT
188630	20826	CACACACCATACACAACTCA	233217	65413	TATAGCATGAGCATTTGTTG	277804	110000	ATCAGAATCCTGAAATTTAA
188631	20827	GCACACACCATACACAACTC	233218	65414	TTATAGCATGAGCATTTGTT	277805	110001	AATCAGAATCCTGAAATTTA
188632	20828	TGCACACACCATACACAACT	233219	65415	ATTATAGCATGAGCATTTGT	277806	110002	AAATCAGAATCCTGAAATTT
188633	20829	ATGCACACACCATACACAAC	233220	65416	GATTATAGCATGAGCATTTG	277807	110003	GAAATCAGAATCCTGAAATT
188634	20830	CATGCACACACCATACACAA	233221	65417	AGATTATAGCATGAGCATTT	277808	110004	TGAAATCAGAATCCTGAAAT
188635	20831	TCATGCACACACCATACACA	233222	65418	AAGATTATAGCATGAGCATT	277809	110005	ATGAAATCAGAATCCTGAAA
188636	20832	CTCATGCACACACCATACAC	233223	65419	TAAGATTATAGCATGAGCAT	277810	110006	TATGAAATCAGAATCCTGAA
188637	20833	GCTCATGCACACACCATACA	233224	65420	ATAAGATTATAGCATGAGCA	277811	110007	TTATGAAATCAGAATCCTGA
188638	20834	TGCTCATGCACACACCATAC	233225	65421	CATAAGATTATAGCATGAGC	277812	110008	ATTATGAAATCAGAATCCTG
188639	20835	ATGCTCATGCACACACCATA	233226	65422	ACATAAGATTATAGCATGAG	277813	110009	CATTATGAAATCAGAATCCT
188640	20836	CATGCTCATGCACACACCAT	233227	65423	CACATAAGATTATAGCATGA	277814	110010	TCATTATGAAATCAGAATCC
188641	20837	ACATGCTCATGCACACACCA	233228	65424	TCACATAAGATTATAGCATG	277815	110011	GTCATTATGAAATCAGAATC
188642	20838	CACATGCTCATGCACACACC	233229	65425	TTCACATAAGATTATAGCAT	277816	110012	TGTCATTATGAAATCAGAAT
188643	20839	ACACATGCTCATGCACACAC	233230	65426	TTTCACATAAGATTATAGCA	277817	110013	TTGTCATTATGAAATCAGAA
188644	20840	CACACATGCTCATGCACACA	233231	65427	TTTTCACATAAGATTATAGC	277818	110014	GTTGTCATTATGAAATCAGA
188645	20841	ACACACATGCTCATGCACAC	233232	65428	TTTTTCACATAAGATTATAG	277819	110015	GGTTGTCATTATGAAATCAG
188646	20842	CACACACATGCTCATGCACA	233233	65429	TTTTTTCACATAAGATTATA	277820	110016	TGGTTGTCATTATGAAATCA
188647	20843	CCACACACATGCTCATGCAC	233234	65430	CTTTTTTCACATAAGATTAT	277821	110017	ATGGTTGTCATTATGAAATC
188648	20844	CCCACACACATGCTCATGCA	233235	65431	GCTTTTTTCACATAAGATTA	277822	110018	AATGGTTGTCATTATGAAAT
188649	20845	GCCCACACACATGCTCATGC	233236	65432	TGCTTTTTTCACATAAGATT	277823	110019	GAATGGTTGTCATTATGAAA
188650	20846	TGCCCACACACATGCTCATG	233237	65433	TTGCTTTTTTCACATAAGAT	277824	110020	GGAATGGTTGTCATTATGAA
188651	20847	ATGCCCACACACATGCTCAT	233238	65434	CTTGCTTTTTTCACATAAGA	277825	110021	AGGAATGGTTGTCATTATGA
188652	20848	CATGCCCACACACATGCTCA	233239	65435	ACTTGCTTTTTTCACATAAG	277826	110022	GAGGAATGGTTGTCATTATG
188653	20849	ACATGCCCACACACATGCTC	233240	65436	TACTTGCTTTTTTCACATAA	277827	110023	AGAGGAATGGTTGTCATTAT
188654	20850	CACATGCCCACACACATGCT	233241	65437	CTACTTGCTTTTTTCACATA	277828	110024	AAGAGGAATGGTTGTCATTA
188655	20851	TCACATGCCCACACACATGC	233242	65438	GCTACTTGCTTTTTTCACAT	277829	110025	AAAGAGGAATGGTTGTCATT
188656	20852	ATCACATGCCCACACACATG	233243	65439	TGCTACTTGCTTTTTTCACA	277830	110026	AAAAGAGGAATGGTTGTCAT
188657	20853	CATCACATGCCCACACACAT	233244	65440	ATGCTACTTGCTTTTTTCAC	277831	110027	GAAAAGAGGAATGGTTGTCA
188658	20854	ACATCACATGCCCACACACA	233245	65441	TATGCTACTTGCTTTTTTCA	277832	110028	AGAAAAGAGGAATGGTTGTC
188659	20855	CACATCACATGCCCACACAC	233246	65442	TTATGCTACTTGCTTTTTTC	277833	110029	GAGAAAAGAGGAATGGTTGT
188660	20856	ACACATCACATGCCCACACA	233247	65443	ATTATGCTACTTGCTTTTTT	277834	110030	AGAGAAAAGAGGAATGGTTG
188661	20857	CACACATCACATGCCCACAC	233248	65444	AATTATGCTACTTGCTTTTT	277835	110031	GAGAGAAAAGAGGAATGGTT
188662	20858	ACACACATCACATGCCCACA	233249	65445	CAATTATGCTACTTGCTTTT	277836	110032	GGAGAGAAAAGAGGAATGGT
188663	20859	CACACACATCACATGCCCAC	233250	65446	GCAATTATGCTACTTGCTTT	277837	110033	GGGAGAGAAAAGAGGAATGG
188664	20860	ACACACACATCACATGCCCA	233251	65447	TGCAATTATGCTACTTGCTT	277838	110034	AGGGAGAGAAAAGAGGAATG
188665	20861	CACACACACATCACATGCCC	233252	65448	TTGCAATTATGCTACTTGCT	277839	110035	AAGGGAGAGAAAAGAGGAAT
188666	20862	CCACACACACATCACATGCC	233253	65449	GTTGCAATTATGCTACTTGC	277840	110036	GAAGGGAGAGAAAAGAGGAA
188667	20863	ACCACACACACATCACATGC	233254	65450	AGTTGCAATTATGCTACTTG	277841	110037	AGAAGGGAGAGAAAAGAGGA
188668	20864	CACCACACACACATCACATG	233255	65451	TAGTTGCAATTATGCTACTT	277842	110038	CAGAAGGGAGAGAAAAGAGG
188669	20865	ACACCACACACACATCACAT	233256	65452	ATAGTTGCAATTATGCTACT	277843	110039	ACAGAAGGGAGAGAAAAGAG
188670	20866	CACACCACACACACATCACA	233257	65453	TATAGTTGCAATTATGCTAC	277844	110040	TACAGAAGGGAGAGAAAAGA
188671	20867	ACACACCACACACACATCAC	233258	65454	ATATAGTTGCAATTATGCTA	277845	110041	TTACAGAAGGGAGAGAAAAG
188672	20868	TACACACCACACACACATCA	233259	65455	AATATAGTTGCAATTATGCT	277846	110042	TTTACAGAAGGGAGAGAAAA
188673	20869	TTACACACCACACACACATC	233260	65456	AAATATAGTTGCAATTATGC	277847	110043	ATTTACAGAAGGGAGAGAAA
188674	20870	CTTACACACCACACACACAT	233261	65457	AAAATATAGTTGCAATTATG	277848	110044	GATTTACAGAAGGGAGAGAA
188675	20871	GCTTACACACCACACACACA	233262	65458	AAAAATATAGTTGCAATTAT	277849	110045	AGATTTACAGAAGGGAGAGA
188676	20872	TGCTTACACACCACACACAC	233263	65459	TAAAAATATAGTTGCAATTA	277850	110046	TAGATTTACAGAAGGGAGAG
188677	20873	ATGCTTACACACCACACACA	233264	65460	TTAAAAATATAGTTGCAATT	277851	110047	TTAGATTTACAGAAGGGAGA
188678	20874	CATGCTTACACACCACACAC	233265	65461	ATTAAAAATATAGTTGCAAT	277852	110048	CTTAGATTTACAGAAGGGAG
188679	20875	ACATGCTTACACACCACACA	233266	65462	CATTAAAAATATAGTTGCAA	277853	110049	TCTTAGATTTACAGAAGGGA
188680	20876	CACATGCTTACACACCACAC	233267	65463	GCATTAAAAATATAGTTGCA	277854	110050	ATCTTAGATTTACAGAAGGG
188681	20877	ACACATGCTTACACACCACA	233268	65464	TGCATTAAAAATATAGTTGC	277855	110051	AATCTTAGATTTACAGAAGG
188682	20878	CACACATGCTTACACACCAC	233269	65465	ATGCATTAAAAATATAGTTG	277856	110052	GAATCTTAGATTTACAGAAG

188683	20879	TCACACATGCTTACACACCA	233270	65466	TATGCATTAAAAATATAGTT	277857	110053	AGAATCTTAGATTTACAGAA
188684	20880	CTCACACATGCTTACACACC	233271	65467	CTATGCATTAAAAATATAGT	277858	110054	TAGAATCTTAGATTTACAGA
188685	20881	ACTCACACATGCTTACACAC	233272	65468	TCTATGCATTAAAAATATAG	277859	110055	ATAGAATCTTAGATTTACAG
188686	20882	CACTCACACATGCTTACACA	233273	65469	TTCTATGCATTAAAAATATA	277860	110056	TATAGAATCTTAGATTTACA
188687	20883	ACACTCACACATGCTTACAC	233274	65470	ATTCTATGCATTAAAAATAT	277861	110057	TTATAGAATCTTAGATTTAC
188688	20884	CACACTCACACATGCTTACA	233275	65471	TATTCTATGCATTAAAAATA	277862	110058	TTTATAGAATCTTAGATTTA
188689	20885	ACACACTCACACATGCTTAC	233276	65472	TTATTCTATGCATTAAAAAT	277863	110059	GTTTATAGAATCTTAGATTT
188690	20886	TACACACTCACACATGCTTA	233277	65473	TTTATTCTATGCATTAAAAA	277864	110060	CGTTTATAGAATCTTAGATT
188691	20887	ATACACACTCACACATGCTT	233278	65474	TTTTATTCTATGCATTAAAA	277865	110061	CCGTTTATAGAATCTTAGAT
188692	20888	CATACACACTCACACATGCT	233279	65475	CTTTTATTCTATGCATTAAA	277866	110062	ACCGTTTATAGAATCTTAGA
188693	20889	ACATACACACTCACACATGC	233280	65476	CCTTTTATTCTATGCATTAA	277867	110063	CACCGTTTATAGAATCTTAG
188694	20890	AACATACACACTCACACATG	233281	65477	GCCTTTTATTCTATGCATTA	277868	110064	ACACCGTTTATAGAATCTTA
188695	20891	AAACATACACACTCACACAT	233282	65478	AGCCTTTTATTCTATGCATT	277869	110065	AACACCGTTTATAGAATCTT
188696	20892	CAAACATACACACTCACACA	233283	65479	TAGCCTTTTATTCTATGCAT	277870	110066	CAACACCGTTTATAGAATCT
188697	20893	TCAAACATACACACTCACAC	233284	65480	CTAGCCTTTTATTCTATGCA	277871	110067	TCAACACCGTTTATAGAATC
188698	20894	CTCAAACATACACACTCACA	233285	65481	TCTAGCCTTTTATTCTATGC	277872	110068	GTCAACACCGTTTATAGAAT
188699	20895	GCTCAAACATACACACTCAC	233286	65482	TTCTAGCCTTTTATTCTATG	277873	110069	AGTCAACACCGTTTATAGAA
188700	20896	TGCTCAAACATACACACTCA	233287	65483	CTTCTAGCCTTTTATTCTAT	277874	110070	AAGTCAACACCGTTTATAGA
188701	20897	ATGCTCAAACATACACACTC	233288	65484	CCTTCTAGCCTTTTATTCTA	277875	110071	TAAGTCAACACCGTTTATAG
188702	20898	CATGCTCAAACATACACACT	233289	65485	TCCTTCTAGCCTTTTATTCT	277876	110072	TTAAGTCAACACCGTTTATA
188703	20899	ACATGCTCAAACATACACAC	233290	65486	TTCCTTCTAGCCTTTTATTC	277877	110073	ATTAAGTCAACACCGTTTAT
188704	20900	CACATGCTCAAACATACACA	233291	65487	TTTCCTTCTAGCCTTTTATT	277878	110074	CATTAAGTCAACACCGTTTA
188705	20901	ACACATGCTCAAACATACAC	233292	65488	ATTTCCTTCTAGCCTTTTAT	277879	110075	ACATTAAGTCAACACCGTTT
188706	20902	CACACATGCTCAAACATACA	233293	65489	TATTTCCTTCTAGCCTTTTA	277880	110076	CACATTAAGTCAACACCGTT
188707	20903	CCACACATGCTCAAACATAC	233294	65490	ATATTTCCTTCTAGCCTTTT	277881	110077	TCACATTAAGTCAACACCGT
188708	20904	ACCACACATGCTCAAACATA	233295	65491	GATATTTCCTTCTAGCCTTT	277882	110078	GTCACATTAAGTCAACACCG
188709	20905	CACCACACATGCTCAAACAT	233296	65492	TGATATTTCCTTCTAGCCTT	277883	110079	TGTCACATTAAGTCAACACC
188710	20906	ACACCACACATGCTCAAACA	233297	65493	GTGATATTTCCTTCTAGCCT	277884	110080	TTGTCACATTAAGTCAACAC
188711	20907	CACACCACACATGCTCAAAC	233298	65494	TGTGATATTTCCTTCTAGCC	277885	110081	ATTGTCACATTAAGTCAACA
188712	20908	ACACACCACACATGCTCAAA	233299	65495	CTGTGATATTTCCTTCTAGC	277886	110082	AATTGTCACATTAAGTCAAC
188713	20909	AACACACCACACATGCTCAA	233300	65496	TCTGTGATATTTCCTTCTAG	277887	110083	CAATTGTCACATTAAGTCAA
188714	20910	CAACACACCACACATGCTCA	233301	65497	ATCTGTGATATTTCCTTCTA	277888	110084	CCAATTGTCACATTAAGTCA
188715	20911	ACAACACACCACACATGCTC	233302	65498	GATCTGTGATATTTCCTTCT	277889	110085	GCCAATTGTCACATTAAGTC
188716	20912	CACAACACACCACACATGCT	233303	65499	GGATCTGTGATATTTCCTTC	277890	110086	TGCCAATTGTCACATTAAGT
188717	20913	TCACAACACACCACACATGC	233304	65500	AGGATCTGTGATATTTCCTT	277891	110087	CTGCCAATTGTCACATTAAG
188718	20914	ATCACAACACACCACACATG	233305	65501	AAGGATCTGTGATATTTCCT	277892	110088	ACTGCCAATTGTCACATTAA
188719	20915	TATCACAACACACCACACAT	233306	65502	CAAGGATCTGTGATATTTCC	277893	110089	TACTGCCAATTGTCACATTA
188720	20916	ATATCACAACACACCACACA	233307	65503	TCAAGGATCTGTGATATTTC	277894	110090	CTACTGCCAATTGTCACATT
188721	20917	CATATCACAACACACCACAC	233308	65504	GTCAAGGATCTGTGATATTT	277895	110091	ACTACTGCCAATTGTCACAT
188722	20918	ACATATCACAACACACCACA	233309	65505	TGTCAAGGATCTGTGATATT	277896	110092	AACTACTGCCAATTGTCACA
188723	20919	CACATATCACAACACACCAC	233310	65506	ATGTCAAGGATCTGTGATAT	277897	110093	GAACTACTGCCAATTGTCAC
188724	20920	ACACATATCACAACACACCA	233311	65507	TATGTCAAGGATCTGTGATA	277898	110094	TGAACTACTGCCAATTGTCA
188725	20921	CACACATATCACAACACACC	233312	65508	GTATGTCAAGGATCTGTGAT	277899	110095	CTGAACTACTGCCAATTGTC
188726	20922	ACACACATATCACAACACAC	233313	65509	TGTATGTCAAGGATCTGTGA	277900	110096	CCTGAACTACTGCCAATTGT
188727	20923	CACACACATATCACAACACA	233314	65510	ATGTATGTCAAGGATCTGTG	277901	110097	ACCTGAACTACTGCCAATTG
188728	20924	CCACACACATATCACAACAC	233315	65511	AATGTATGTCAAGGATCTGT	277902	110098	GACCTGAACTACTGCCAATT
188729	20925	ACCACACACATATCACAACA	233316	65512	GAATGTATGTCAAGGATCTG	277903	110099	AGACCTGAACTACTGCCAAT
188730	20926	CACCACACACATATCACAAC	233317	65513	GGAATGTATGTCAAGGATCT	277904	110100	CAGACCTGAACTACTGCCAA
188731	20927	ACACCACACACATATCACAA	233318	65514	GGGAATGTATGTCAAGGATC	277905	110101	GCAGACCTGAACTACTGCCA
188732	20928	CACACCACACACATATCACA	233319	65515	TGGGAATGTATGTCAAGGAT	277906	110102	AGCAGACCTGAACTACTGCC
188733	20929	ACACACCACACACATATCAC	233320	65516	TTGGGAATGTATGTCAAGGA	277907	110103	AAGCAGACCTGAACTACTGC
188734	20930	CACACACCACACACATATCA	233321	65517	TTTGGGAATGTATGTCAAGG	277908	110104	AAAGCAGACCTGAACTACTG
188735	20931	TCACACACCACACACATATC	233322	65518	GTTTGGGAATGTATGTCAAG	277909	110105	CAAAGCAGACCTGAACTACT
188736	20932	CTCACACACCACACACATAT	233323	65519	GGTTTGGGAATGTATGTCAA	277910	110106	ACAAAGCAGACCTGAACTAC
188737	20933	GCTCACACACCACACACATA	233324	65520	AGGTTTGGGAATGTATGTCA	277911	110107	TACAAAGCAGACCTGAACTA
188738	20934	TGCTCACACACCACACACAT	233325	65521	AAGGTTTGGGAATGTATGTC	277912	110108	TTACAAAGCAGACCTGAACT
188739	20935	ATGCTCACACACCACACACA	233326	65522	AAAGGTTTGGGAATGTATGT	277913	110109	TTTACAAAGCAGACCTGAAC
188740	20936	CATGCTCACACACCACACAC	233327	65523	CAAAGGTTTGGGAATGTATG	277914	110110	ATTTACAAAGCAGACCTGAA
188741	20937	ACATGCTCACACACCACACA	233328	65524	ACAAAGGTTTGGGAATGTAT	277915	110111	TATTTACAAAGCAGACCTGA
188742	20938	CACATGCTCACACACCACAC	233329	65525	TACAAAGGTTTGGGAATGTA	277916	110112	GTATTTACAAAGCAGACCTG
188743	20939	ACACATGCTCACACACCACA	233330	65526	TTACAAAGGTTTGGGAATGT	277917	110113	GGTATTTACAAAGCAGACCT
188744	20940	CACACATGCTCACACACCAC	233331	65527	TTTACAAAGGTTTGGGAATG	277918	110114	GGGTATTTACAAAGCAGACC
188745	20941	ACACACATGCTCACACACCA	233332	65528	ATTTACAAAGGTTTGGGAAT	277919	110115	AGGGTATTTACAAAGCAGAC
188746	20942	CACACACATGCTCACACACC	233333	65529	GATTTACAAAGGTTTGGGAA	277920	110116	AAGGGTATTTACAAAGCAGA
188747	20943	ACACACACATGCTCACACAC	233334	65530	GGATTTACAAAGGTTTGGGA	277921	110117	CAAGGGTATTTACAAAGCAG
188748	20944	CACACACACATGCTCACACA	233335	65531	CGGATTTACAAAGGTTTGGG	277922	110118	ACAAGGGTATTTACAAAGCA
188749	20945	TCACACACACATGCTCACAC	233336	65532	GCGGATTTACAAAGGTTTGG	277923	110119	CACAAGGGTATTTACAAAGC
188750	20946	ATCACACACACATGCTCACA	233337	65533	CGCGGATTTACAAAGGTTTG	277924	110120	ACACAAGGGTATTTACAAAG
188751	20947	CATCACACACACATGCTCAC	233338	65534	CCGCGGATTTACAAAGGTTT	277925	110121	GACACAAGGGTATTTACAAA
188752	20948	ACATCACACACACATGCTCA	233339	65535	TCCGCGGATTTACAAAGGTT	277926	110122	AGACACAAGGGTATTTACAA
188753	20949	CACATCACACACACATGCTC	233340	65536	ATCCGCGGATTTACAAAGGT	277927	110123	TAGACACAAGGGTATTTACA
188754	20950	ACACATCACACACACATGCT	233341	65537	AATCCGCGGATTTACAAAGG	277928	110124	ATAGACACAAGGGTATTTAC

188755	20951	GACACATCACACACACATGC	233342	65538	GAATCCGCGGATTTACAAAG	277929	110125	AATAGACACAAGGGTATTTA
188756	20952	AGACACATCACACACACATG	233343	65539	TGAATCCGCGGATTTACAAA	277930	110126	CAATAGACACAAGGGTATTT
188757	20953	CAGACACATCACACACACAT	233344	65540	ATGAATCCGCGGATTTACAA	277931	110127	ACAATAGACACAAGGGTATT
188758	20954	ACAGACACATCACACACACA	233345	65541	CATGAATCCGCGGATTTACA	277932	110128	TACAATAGACACAAGGGTAT
188759	20955	CACAGACACATCACACACAC	233346	65542	TCATGAATCCGCGGATTTAC	277933	110129	TTACAATAGACACAAGGGTA
188760	20956	ACACAGACACATCACACACA	233347	65543	TTCATGAATCCGCGGATTTA	277934	110130	TTTACAATAGACACAAGGGT
188761	20957	CACACAGACACATCACACAC	233348	65544	TTTCATGAATCCGCGGATTT	277935	110131	TTTTACAATAGACACAAGGG
188762	20958	ACACACAGACACATCACACA	233349	65545	TTTTCATGAATCCGCGGATT	277936	110132	ATTTTACAATAGACACAAGG
188763	20959	CACACACAGACACATCACAC	233350	65546	GTTTTCATGAATCCGCGGAT	277937	110133	GATTTTACAATAGACACAAG
188764	20960	CCACACACAGACACATCACA	233351	65547	TGTTTTCATGAATCCGCGGA	277938	110134	AGATTTTACAATAGACACAA
188765	20961	ACCACACACAGACACATCAC	233352	65548	CTGTTTTCATGAATCCGCGG	277939	110135	GAGATTTTACAATAGACACA
188766	20962	CACCACACACAGACACATCA	233353	65549	TCTGTTTTCATGAATCCGCG	277940	110136	TGAGATTTTACAATAGACAC
188767	20963	ACACCACACACAGACACATC	233354	65550	GTCTGTTTTCATGAATCCGC	277941	110137	GTGAGATTTTACAATAGACA
188768	20964	CACACCACACACAGACACAT	233355	65551	TGTCTGTTTTCATGAATCCG	277942	110138	TGTGAGATTTTACAATAGAC
188769	20965	ACACACCACACACAGACACA	233356	65552	GTGTCTGTTTTCATGAATCC	277943	110139	TTGTGAGATTTTACAATAGA
188770	20966	CACACACCACACACAGACAC	233357	65553	TGTGTCTGTTTTCATGAATC	277944	110140	TTTGTGAGATTTTACAATAG
188771	20967	ACACACACCACACACAGACA	233358	65554	ATGTGTCTGTTTTCATGAAT	277945	110141	CTTTGTGAGATTTTACAATA
188772	20968	CACACACACCACACACAGAC	233359	65555	AATGTGTCTGTTTTCATGAA	277946	110142	CCTTTGTGAGATTTTACAAT
188773	20969	TCACACACACCACACACAGA	233360	65556	AAATGTGTCTGTTTTCATGA	277947	110143	GCCTTTGTGAGATTTTACAA
188774	20970	CTCACACACACCACACACAG	233361	65557	CAAATGTGTCTGTTTTCATG	277948	110144	AGCCTTTGTGAGATTTTACA
188775	20971	GCTCACACACACCACACACA	233362	65558	GCAAATGTGTCTGTTTTCAT	277949	110145	AAGCCTTTGTGAGATTTTAC
188776	20972	TGCTCACACACACCACACAC	233363	65559	TGCAAATGTGTCTGTTTTCA	277950	110146	CAAGCCTTTGTGAGATTTTA
188777	20973	ATGCTCACACACACCACACA	233364	65560	GTGCAAATGTGTCTGTTTTC	277951	110147	ACAAGCCTTTGTGAGATTTT
188778	20974	CATGCTCACACACACCACAC	233365	65561	TGTGCAAATGTGTCTGTTTT	277952	110148	AACAAGCCTTTGTGAGATTT
188779	20975	ACATGCTCACACACACCACA	233366	65562	TTGTGCAAATGTGTCTGTTT	277953	110149	CAACAAGCCTTTGTGAGATT
188780	20976	CACATGCTCACACACACCAC	233367	65563	CTTGTGCAAATGTGTCTGTT	277954	110150	GCAACAAGCCTTTGTGAGAT
188781	20977	ACACATGCTCACACACACCA	233368	65564	ACTTGTGCAAATGTGTCTGT	277955	110151	GGCAACAAGCCTTTGTGAGA
188782	20978	CACACATGCTCACACACACC	233369	65565	CACTTGTGCAAATGTGTCTG	277956	110152	AGGCAACAAGCCTTTGTGAG
188783	20979	ACACACATGCTCACACACAC	233370	65566	GCACTTGTGCAAATGTGTCT	277957	110153	AAGGCAACAAGCCTTTGTGA
188784	20980	AACACACATGCTCACACACA	233371	65567	GGCACTTGTGCAAATGTGTC	277958	110154	AAAGGCAACAAGCCTTTGTG
188785	20981	CAACACACATGCTCACACAC	233372	65568	AGGCACTTGTGCAAATGTGT	277959	110155	AAAAGGCAACAAGCCTTTGT
188786	20982	ACAACACACATGCTCACACA	233373	65569	CAGGCACTTGTGCAAATGTG	277960	110156	AAAAAGGCAACAAGCCTTTG
188787	20983	CACAACACACATGCTCACAC	233374	65570	TCAGGCACTTGTGCAAATGT	277961	110157	AAAAAAGGCAACAAGCCTTT
188788	20984	ACACAACACACATGCTCACA	233375	65571	ATCAGGCACTTGTGCAAATG	277962	110158	CAAAAAAGGCAACAAGCCTT
188789	20985	CACACAACACACATGCTCAC	233376	65572	GATCAGGCACTTGTGCAAAT	277963	110159	ACAAAAAAGGCAACAAGCCT
188790	20986	ACACACAACACACATGCTCA	233377	65573	AGATCAGGCACTTGTGCAAA	277964	110160	CACAAAAAAGGCAACAAGCC
188791	20987	CACACACAACACACATGCTC	233378	65574	AAGATCAGGCACTTGTGCAA	277965	110161	CCACAAAAAAGGCAACAAGC
188792	20988	ACACACACAACACACATGCT	233379	65575	AAAGATCAGGCACTTGTGCA	277966	110162	CCCACAAAAAAGGCAACAAG
188793	20989	CACACACACAACACACATGC	233380	65576	AAAAGATCAGGCACTTGTGC	277967	110163	CCCCACAAAAAAGGCAACAA
188794	20990	CCACACACACAACACACATG	233381	65577	GAAAAGATCAGGCACTTGTG	277968	110164	ACCCCACAAAAAAGGCAACA
188795	20991	ACCACACACACAACACACAT	233382	65578	AGAAAAGATCAGGCACTTGT	277969	110165	AACCCCACAAAAAAGGCAAC
188796	20992	CACCACACACACAACACACA	233383	65579	CAGAAAAGATCAGGCACTTG	277970	110166	TAACCCCACAAAAAAGGCAA
188797	20993	GCACCACACACACAACACAC	233384	65580	ACAGAAAAGATCAGGCACTT	277971	110167	CTAACCCCACAAAAAAGGCA
188798	20994	TGCACCACACACACAACACA	233385	65581	AACAGAAAAGATCAGGCACT	277972	110168	TCTAACCCCACAAAAAAGGC
188799	20995	ATGCACCACACACACAACAC	233386	65582	TAACAGAAAAGATCAGGCAC	277973	110169	TTCTAACCCCACAAAAAAGG
188800	20996	CATGCACCACACACACAACA	233387	65583	ATAACAGAAAAGATCAGGCA	277974	110170	GTTCTAACCCCACAAAAAAG
188801	20997	ACATGCACCACACACACAAC	233388	65584	TATAACAGAAAAGATCAGGC	277975	110171	TGTTCTAACCCCACAAAAAA
188802	20998	CACATGCACCACACACACAA	233389	65585	GTATAACAGAAAAGATCAGG	277976	110172	TTGTTCTAACCCCACAAAAA
188803	20999	ACACATGCACCACACACACA	233390	65586	TGTATAACAGAAAAGATCAG	277977	110173	CTTGTTCTAACCCCACAAAA
188804	21000	CACACATGCACCACACACAC	233391	65587	ATGTATAACAGAAAAGATCA	277978	110174	TCTTGTTCTAACCCCACAAA
188805	21001	ACACACATGCACCACACACA	233392	65588	AATGTATAACAGAAAAGATC	277979	110175	TTCTTGTTCTAACCCCACAA
188806	21002	CACACACATGCACCACACAC	233393	65589	GAATGTATAACAGAAAAGAT	277980	110176	TTTCTTGTTCTAACCCCACA
188807	21003	CCACACACATGCACCACACA	233394	65590	TGAATGTATAACAGAAAAGA	277981	110177	TTTTCTTGTTCTAACCCCAC
188808	21004	GCCACACACATGCACCACAC	233395	65591	ATGAATGTATAACAGAAAAG	277982	110178	TTTTTCTTGTTCTAACCCCA
188809	21005	CGCCACACACATGCACCACA	233396	65592	AATGAATGTATAACAGAAAA	277983	110179	CTTTTTCTTGTTCTAACCCC
188810	21006	ACGCCACACACATGCACCAC	233397	65593	TAATGAATGTATAACAGAAA	277984	110180	GCTTTTTCTTGTTCTAACCC
188811	21007	CACGCCACACACATGCACCA	233398	65594	CTAATGAATGTATAACAGAA	277985	110181	GGCTTTTTCTTGTTCTAACC
188812	21008	ACACGCCACACACATGCACC	233399	65595	TCTAATGAATGTATAACAGA	277986	110182	TGGCTTTTTCTTGTTCTAAC
188813	21009	CACACGCCACACACATGCAC	233400	65596	TTCTAATGAATGTATAACAG	277987	110183	GTGGCTTTTTCTTGTTCTAA
188814	21010	TCACACGCCACACACATGCA	233401	65597	CTTCTAATGAATGTATAACA	277988	110184	TGTGGCTTTTTCTTGTTCTA
188815	21011	CTCACACGCCACACACATGC	233402	65598	ACTTCTAATGAATGTATAAC	277989	110185	ATGTGGCTTTTTCTTGTTCT
188816	21012	GCTCACACGCCACACACATG	233403	65599	GACTTCTAATGAATGTATAA	277990	110186	CATGTGGCTTTTTCTTGTTC
188817	21013	CGCTCACACGCCACACACAT	233404	65600	TGACTTCTAATGAATGTATA	277991	110187	CCATGTGGCTTTTTCTTGTT
188818	21014	ACGCTCACACGCCACACACA	233405	65601	TTGACTTCTAATGAATGTAT	277992	110188	TCCATGTGGCTTTTTCTTGT
188819	21015	CACGCTCACACGCCACACAC	233406	65602	CTTGACTTCTAATGAATGTA	277993	110189	TTCCATGTGGCTTTTTCTTG
188820	21016	ACACGCTCACACGCCACACA	233407	65603	GCTTGACTTCTAATGAATGT	277994	110190	TTTCCATGTGGCTTTTTCTT
188821	21017	CACACGCTCACACGCCACAC	233408	65604	GGCTTGACTTCTAATGAATG	277995	110191	TTTTCCATGTGGCTTTTTCT
188822	21018	ACACACGCTCACACGCCACA	233409	65605	GGGCTTGACTTCTAATGAAT	277996	110192	TTTTTCCATGTGGCTTTTTC
188823	21019	CACACACGCTCACACGCCAC	233410	65606	AGGGCTTGACTTCTAATGAA	277997	110193	TTTTTTCCATGTGGCTTTTT
188824	21020	ACACACACGCTCACACGCCA	233411	65607	CAGGGCTTGACTTCTAATGA	277998	110194	TTTTTTTCCATGTGGCTTTT
188825	21021	CACACACACGCTCACACGCC	233412	65608	CCAGGGCTTGACTTCTAATG	277999	110195	TTTTTTTTCCATGTGGCTTT
188826	21022	GCACACACACGCTCACACGC	233413	65609	ACCAGGGCTTGACTTCTAAT	278000	110196	ATTTTTTTTCCATGTGGCTT

188827	21023	TGCACACACACGCTCACACG	233414	65610	CACCAGGGCTTGACTTCTAA	278001	110197	AATTTTTTTTCCATGTGGCT
188828	21024	ATGCACACACACGCTCACAC	233415	65611	GCACCAGGGCTTGACTTCTA	278002	110198	AAATTTTTTTTCCATGTGGC
188829	21025	AATGCACACACACGCTCACA	233416	65612	GGCACCAGGGCTTGACTTCT	278003	110199	GAAATTTTTTTTCCATGTGG
188830	21026	CAATGCACACACACGCTCAC	233417	65613	TGGCACCAGGGCTTGACTTC	278004	110200	AGAAATTTTTTTTCCATGTG
188831	21027	ACAATGCACACACACGCTCA	233418	65614	GTGGCACCAGGGCTTGACTT	278005	110201	AAGAAATTTTTTTTCCATGT
188832	21028	CACAATGCACACACACGCTC	233419	65615	TGTGGCACCAGGGCTTGACT	278006	110202	AAAGAAATTTTTTTTCCATG
188833	21029	ACACAATGCACACACACGCT	233420	65616	TTGTGGCACCAGGGCTTGAC	278007	110203	AAAAGAAATTTTTTTTCCAT
188834	21030	GACACAATGCACACACACGC	233421	65617	TTTGTGGCACCAGGGCTTGA	278008	110204	AAAAAGAAATTTTTTTTCCA
188835	21031	AGACACAATGCACACACACG	233422	65618	CTTTGTGGCACCAGGGCTTG	278009	110205	AAAAAAGAAATTTTTTTTCC
188836	21032	CAGACACAATGCACACACAC	233423	65619	ACTTTGTGGCACCAGGGCTT	278010	110206	CAAAAAAGAAATTTTTTTTC
188837	21033	ACAGACACAATGCACACACA	233424	65620	TACTTTGTGGCACCAGGGCT	278011	110207	ACAAAAAAGAAATTTTTTTT
188838	21034	CACAGACACAATGCACACAC	233425	65621	ATACTTTGTGGCACCAGGGC	278012	110208	AACAAAAAAGAAATTTTTTT
188839	21035	TCACAGACACAATGCACACA	233426	65622	GATACTTTGTGGCACCAGGG	278013	110209	AAACAAAAAAGAAATTTTTT
188840	21036	CTCACAGACACAATGCACAC	233427	65623	AGATACTTTGTGGCACCAGG	278014	110210	AAAACAAAAAAGAAATTTTT
188841	21037	GCTCACAGACACAATGCACA	233428	65624	CAGATACTTTGTGGCACCAG	278015	110211	AAAAACAAAAAAGAAATTTT
188842	21038	TGCTCACAGACACAATGCAC	233429	65625	GCAGATACTTTGTGGCACCA	278016	110212	AAAAAACAAAAAAGAAATTT
188843	21039	ATGCTCACAGACACAATGCA	233430	65626	GGCAGATACTTTGTGGCACC	278017	110213	AAAAAAACAAAAAAGAAATT
188844	21040	CATGCTCACAGACACAATGC	233431	65627	AGGCAGATACTTTGTGGCAC	278018	110214	CAAAAAAACAAAAAAGAAAT
188845	21041	ACATGCTCACAGACACAATG	233432	65628	AAGGCAGATACTTTGTGGCA	278019	110215	ACAAAAAAACAAAAAAGAAA
188846	21042	CACATGCTCACAGACACAAT	233433	65629	AAAGGCAGATACTTTGTGGC	278020	110216	AACAAAAAAACAAAAAAGAA
188847	21043	ACACATGCTCACAGACACAA	233434	65630	AAAAGGCAGATACTTTGTGG	278021	110217	AAACAAAAAAACAAAAAAGA
188848	21044	CACACATGCTCACAGACACA	233435	65631	GAAAAGGCAGATACTTTGTG	278022	110218	CAAACAAAAAAACAAAAAAG
188849	21045	TCACACATGCTCACAGACAC	233436	65632	TGAAAAGGCAGATACTTTGT	278023	110219	GCAAACAAAAAAACAAAAAA
188850	21046	CTCACACATGCTCACAGACA	233437	65633	TTGAAAAGGCAGATACTTTG	278024	110220	AGCAAACAAAAAAACAAAAA
188851	21047	ACTCACACATGCTCACAGAC	233438	65634	TTTGAAAAGGCAGATACTTT	278025	110221	AAGCAAACAAAAAAACAAAA
188852	21048	CACTCACACATGCTCACAGA	233439	65635	ATTTGAAAAGGCAGATACTT	278026	110222	CAAGCAAACAAAAAAACAAA
188853	21049	ACACTCACACATGCTCACAG	233440	65636	CATTTGAAAAGGCAGATACT	278027	110223	ACAAGCAAACAAAAAAACAA
188854	21050	CACACTCACACATGCTCACA	233441	65637	ACATTTGAAAAGGCAGATAC	278028	110224	AACAAGCAAACAAAAAAACA
188855	21051	ACACACTCACACATGCTCAC	233442	65638	CACATTTGAAAAGGCAGATA	278029	110225	AAACAAGCAAACAAAAAAAC
188856	21052	CACACACTCACACATGCTCA	233443	65639	TCACATTTGAAAAGGCAGAT	278030	110226	AAAACAAGCAAACAAAAAAA
188857	21053	ACACACACTCACACATGCTC	233444	65640	ATCACATTTGAAAAGGCAGA	278031	110227	AAAAACAAGCAAACAAAAAA
188858	21054	CACACACACTCACACATGCT	233445	65641	GATCACATTTGAAAAGGCAG	278032	110228	AAAAAACAAGCAAACAAAAA
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188860	21056	CACACACACACTCACACATG	233447	65643	CTGATCACATTTGAAAAGGC	278034	110230	CAAAAAAACAAGCAAACAAA
188861	21057	ACACACACACACTCACACAT	233448	65644	TCTGATCACATTTGAAAAGG	278035	110231	TCAAAAAAACAAGCAAACAA
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188865	21061	CTGAACACACACACACTCAC	233452	65648	ACATTCTGATCACATTTGAA	278039	110235	TGTCTCAAAAAAACAAGCAA
188866	21062	GCTGAACACACACACACTCA	233453	65649	AACATTCTGATCACATTTGA	278040	110236	CTGTCTCAAAAAAACAAGCA
188867	21063	TGCTGAACACACACACACTC	233454	65650	GAACATTCTGATCACATTTG	278041	110237	TCTGTCTCAAAAAAACAAGC
188868	21064	ATGCTGAACACACACACACT	233455	65651	AGAACATTCTGATCACATTT	278042	110238	CTCTGTCTCAAAAAAACAAG
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188871	21067	TATATGCTGAACACACACAC	233458	65654	AAGAGAACATTCTGATCACA	278045	110241	AAACTCTGTCTCAAAAAAAC
188872	21068	ATATATGCTGAACACACACA	233459	65655	AAAGAGAACATTCTGATCAC	278046	110242	GAAACTCTGTCTCAAAAAAA
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188874	21070	TTATATATGCTGAACACACA	233461	65657	CAAAAGAGAACATTCTGATC	278048	110244	GTGAAACTCTGTCTCAAAAA
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188876	21072	CCTTATATATGCTGAACACA	233463	65659	AGCAAAAGAGAACATTCTGA	278050	110246	GAGTGAAACTCTGTCTCAAA
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188878	21074	TGCCTTATATATGCTGAACA	233465	65661	GAAGCAAAAGAGAACATTCT	278052	110248	CAGAGTGAAACTCTGTCTCA
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188880	21076	CATGCCTTATATATGCTGAA	233467	65663	TTGAAGCAAAAGAGAACATT	278054	110250	GACAGAGTGAAACTCTGTCT
188881	21077	ACATGCCTTATATATGCTGA	233468	65664	CTTGAAGCAAAAGAGAACAT	278055	110251	CGACAGAGTGAAACTCTGTC
188882	21078	TACATGCCTTATATATGCTG	233469	65665	CCTTGAAGCAAAAGAGAACA	278056	110252	GCGACAGAGTGAAACTCTGT
188883	21079	TTACATGCCTTATATATGCT	233470	65666	GCCTTGAAGCAAAAGAGAAC	278057	110253	GGCGACAGAGTGAAACTCTG
188884	21080	GTTACATGCCTTATATATGC	233471	65667	GGCCTTGAAGCAAAAGAGAA	278058	110254	GGGCGACAGAGTGAAACTCT
188885	21081	AGTTACATGCCTTATATATG	233472	65668	TGGCCTTGAAGCAAAAGAGA	278059	110255	TGGGCGACAGAGTGAAACTC
188886	21082	CAGTTACATGCCTTATATAT	233473	65669	ATGGCCTTGAAGCAAAAGAG	278060	110256	CTGGGCGACAGAGTGAAACT
188887	21083	TCAGTTACATGCCTTATATA	233474	65670	AATGGCCTTGAAGCAAAAGA	278061	110257	CCTGGGCGACAGAGTGAAAC
188888	21084	TTCAGTTACATGCCTTATAT	233475	65671	AAATGGCCTTGAAGCAAAAG	278062	110258	GCCTGGGCGACAGAGTGAAA
188889	21085	GTTCAGTTACATGCCTTATA	233476	65672	AAAATGGCCTTGAAGCAAAA	278063	110259	AGCCTGGGCGACAGAGTGAA
188890	21086	TGTTCAGTTACATGCCTTAT	233477	65673	AAAAATGGCCTTGAAGCAAA	278064	110260	CAGCCTGGGCGACAGAGTGA
188891	21087	GTGTTCAGTTACATGCCTTA	233478	65674	GAAAAATGGCCTTGAAGCAA	278065	110261	CCAGCCTGGGCGACAGAGTG
188892	21088	TGTGTTCAGTTACATGCCTT	233479	65675	TGAAAAATGGCCTTGAAGCA	278066	110262	TCCAGCCTGGGCGACAGAGT
188893	21089	CTGTGTTCAGTTACATGCCT	233480	65676	GTGAAAAATGGCCTTGAAGC	278067	110263	CTCCAGCCTGGGCGACAGAG
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188896	21092	GTGCTGTGTTCAGTTACATG	233483	65679	TTCGTGAAAAATGGCCTTGA	278070	110266	GCACTCCAGCCTGGGCGACA
188897	21093	AGTGCTGTGTTCAGTTACAT	233484	65680	CTTCGTGAAAAATGGCCTTG	278071	110267	TGCACTCCAGCCTGGGCGAC
188898	21094	AAGTGCTGTGTTCAGTTACA	233485	65681	GCTTCGTGAAAAATGGCCTT	278072	110268	CTGCACTCCAGCCTGGGCGA

188899	21095	AAAGTGCTGTGTTCAGTTAC	233486	65682	TGCTTCGTGAAAAATGGCCT	278073	110269	ACTGCACTCCAGCCTGGGCG
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188901	21097	CTAAAGTGCTGTGTTCAGTT	233488	65684	ACTGCTTCGTGAAAAATGGC	278075	110271	CCACTGCACTCCAGCCTGGG
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188903	21099	CTCTAAAGTGCTGTGTTCAG	233490	65686	CCACTGCTTCGTGAAAAATG	278077	110273	CACCACTGCACTCCAGCCTG
188904	21100	CCTCTAAAGTGCTGTGTTCA	233491	65687	GCCACTGCTTCGTGAAAAAT	278078	110274	GCACCACTGCACTCCAGCCT
188905	21101	CCCTCTAAAGTGCTGTGTTC	233492	65688	TGCCACTGCTTCGTGAAAAA	278079	110275	CGCACCACTGCACTCCAGCC
188906	21102	GCCCTCTAAAGTGCTGTGTT	233493	65689	ATGCCACTGCTTCGTGAAAA	278080	110276	TCGCACCACTGCACTCCAGC
188907	21103	AGCCCTCTAAAGTGCTGTGT	233494	65690	AATGCCACTGCTTCGTGAAA	278081	110277	ATCGCACCACTGCACTCCAG
188908	21104	GAGCCCTCTAAAGTGCTGTG	233495	65691	AAATGCCACTGCTTCGTGAA	278082	110278	GATCGCACCACTGCACTCCA
188909	21105	AGAGCCCTCTAAAGTGCTGT	233496	65692	AAAATGCCACTGCTTCGTGA	278083	110279	AGATCGCACCACTGCACTCC
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188911	21107	GGAGAGCCCTCTAAAGTGCT	233498	65694	CAAAAATGCCACTGCTTCGT	278085	110281	GGAGATCGCACCACTGCACT
188912	21108	AGGAGAGCCCTCTAAAGTGC	233499	65695	GCAAAAATGCCACTGCTTCG	278086	110282	CGGAGATCGCACCACTGCAC
188913	21109	CAGGAGAGCCCTCTAAAGTG	233500	65696	GGCAAAAATGCCACTGCTTC	278087	110283	GCGGAGATCGCACCACTGCA
188914	21110	CCAGGAGAGCCCTCTAAAGT	233501	65697	AGGCAAAAATGCCACTGCTT	278088	110284	GGCGGAGATCGCACCACTGC
188915	21111	TCCAGGAGAGCCCTCTAAAG	233502	65698	GAGGCAAAAATGCCACTGCT	278089	110285	GGGCGGAGATCGCACCACTG
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188918	21114	GACTCCAGGAGAGCCCTCTA	233505	65701	GAAGAGGCAAAAATGCCACT	278092	110288	AGTGGGCGGAGATCGCACCA
188919	21115	TGACTCCAGGAGAGCCCTCT	233506	65702	TGAAGAGGCAAAAATGCCAC	278093	110289	CAGTGGGCGGAGATCGCACC
188920	21116	CTGACTCCAGGAGAGCCCTC	233507	65703	ATGAAGAGGCAAAAATGCCA	278094	110290	GCAGTGGGCGGAGATCGCAC
188921	21117	TCTGACTCCAGGAGAGCCCT	233508	65704	GATGAAGAGGCAAAAATGCC	278095	110291	TGCAGTGGGCGGAGATCGCA
188922	21118	CTCTGACTCCAGGAGAGCCC	233509	65705	TGATGAAGAGGCAAAAATGC	278096	110292	TTGCAGTGGGCGGAGATCGC
188923	21119	CCTCTGACTCCAGGAGAGCC	233510	65706	CTGATGAAGAGGCAAAAATG	278097	110293	CTTGCAGTGGGCGGAGATCG
188924	21120	CCCTCTGACTCCAGGAGAGC	233511	65707	TCTGATGAAGAGGCAAAAAT	278098	110294	GCTTGCAGTGGGCGGAGATC
188925	21121	CCCCTCTGACTCCAGGAGAG	233512	65708	CTCTGATGAAGAGGCAAAAA	278099	110295	AGCTTGCAGTGGGCGGAGAT
188926	21122	CCCCCTCTGACTCCAGGAGA	233513	65709	ACTCTGATGAAGAGGCAAAA	278100	110296	GAGCTTGCAGTGGGCGGAGA
188927	21123	ACCCCCTCTGACTCCAGGAG	233514	65710	GACTCTGATGAAGAGGCAAA	278101	110297	GGAGCTTGCAGTGGGCGGAG
188928	21124	CACCCCCTCTGACTCCAGGA	233515	65711	TGACTCTGATGAAGAGGCAA	278102	110298	TGGAGCTTGCAGTGGGCGGA
188929	21125	CCACCCCCTCTGACTCCAGG	233516	65712	GTGACTCTGATGAAGAGGCA	278103	110299	GTGGAGCTTGCAGTGGGCGG
188930	21126	CCCACCCCCTCTGACTCCAG	233517	65713	GGTGACTCTGATGAAGAGGC	278104	110300	GGTGGAGCTTGCAGTGGGCG
188931	21127	ACCCACCCCCTCTGACTCCA	233518	65714	CGGTGACTCTGATGAAGAGG	278105	110301	AGGTGGAGCTTGCAGTGGGC
188932	21128	TACCCACCCCCTCTGACTCC	233519	65715	ACGGTGACTCTGATGAAGAG	278106	110302	GAGGTGGAGCTTGCAGTGGG
188933	21129	CTACCCACCCCCTCTGACTC	233520	65716	CACGGTGACTCTGATGAAGA	278107	110303	GGAGGTGGAGCTTGCAGTGG
188934	21130	CCTACCCACCCCCTCTGACT	233521	65717	ACACGGTGACTCTGATGAAG	278108	110304	GGGAGGTGGAGCTTGCAGTG
188935	21131	TCCTACCCACCCCCTCTGAC	233522	65718	CACACGGTGACTCTGATGAA	278109	110305	CGGGAGGTGGAGCTTGCAGT
188936	21132	CTCCTACCCACCCCCTCTGA	233523	65719	GCACACGGTGACTCTGATGA	278110	110306	CCGGGAGGTGGAGCTTGCAG
188937	21133	CCTCCTACCCACCCCCTCTG	233524	65720	GGCACACGGTGACTCTGATG	278111	110307	CCCGGGAGGTGGAGCTTGCA
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188940	21136	TCTCCTCCTACCCACCCCCT	233527	65723	CAGGGCACACGGTGACTCTG	278114	110310	GAACCCGGGAGGTGGAGCTT
188941	21137	TTCTCCTCCTACCCACCCCC	233528	65724	CCAGGGCACACGGTGACTCT	278115	110311	TGAACCCGGGAGGTGGAGCT
188942	21138	CTTCTCCTCCTACCCACCCC	233529	65725	TCCAGGGCACACGGTGACTC	278116	110312	ATGAACCCGGGAGGTGGAGC
188943	21139	CCTTCTCCTCCTACCCACCC	233530	65726	CTCCAGGGCACACGGTGACT	278117	110313	CATGAACCCGGGAGGTGGAG
188944	21140	CCCTTCTCCTCCTACCCACC	233531	65727	CCTCCAGGGCACACGGTGAC	278118	110314	GCATGAACCCGGGAGGTGGA
188945	21141	TCCCTTCTCCTCCTACCCAC	233532	65728	TCCTCCAGGGCACACGGTGA	278119	110315	AGCATGAACCCGGGAGGTGG
188946	21142	CTCCCTTCTCCTCCTACCCA	233533	65729	GTCCTCCAGGGCACACGGTG	278120	110316	TAGCATGAACCCGGGAGGTG
188947	21143	CCTCCCTTCTCCTCCTACCC	233534	65730	AGTCCTCCAGGGCACACGGT	278121	110317	ATAGCATGAACCCGGGAGGT
188948	21144	ACCTCCCTTCTCCTCCTACC	233535	65731	CAGTCCTCCAGGGCACACGG	278122	110318	AATAGCATGAACCCGGGAGG
188949	21145	CACCTCCCTTCTCCTCCTAC	233536	65732	TCAGTCCTCCAGGGCACACG	278123	110319	GAATAGCATGAACCCGGGAG
188950	21146	CCACCTCCCTTCTCCTCCTA	233537	65733	CTCAGTCCTCCAGGGCACAC	278124	110320	AGAATAGCATGAACCCGGGA
188951	21147	CCCACCTCCCTTCTCCTCCT	233538	65734	TCTCAGTCCTCCAGGGCACA	278125	110321	GAGAATAGCATGAACCCGGG
188952	21148	GCCCACCTCCCTTCTCCTCC	233539	65735	TTCTCAGTCCTCCAGGGCAC	278126	110322	GGAGAATAGCATGAACCCGG
188953	21149	AGCCCACCTCCCTTCTCCTC	233540	65736	GTTCTCAGTCCTCCAGGGCA	278127	110323	AGGAGAATAGCATGAACCCG
188954	21150	TAGCCCACCTCCCTTCTCCT	233541	65737	TGTTCTCAGTCCTCCAGGGC	278128	110324	CAGGAGAATAGCATGAACCC
188955	21151	CTAGCCCACCTCCCTTCTCC	233542	65738	CTGTTCTCAGTCCTCCAGGG	278129	110325	ACAGGAGAATAGCATGAACC
188956	21152	ACTAGCCCACCTCCCTTCTC	233543	65739	GCTGTTCTCAGTCCTCCAGG	278130	110326	GACAGGAGAATAGCATGAAC
188957	21153	CACTAGCCCACCTCCCTTCT	233544	65740	TGCTGTTCTCAGTCCTCCAG	278131	110327	AGACAGGAGAATAGCATGAA
188958	21154	ACACTAGCCCACCTCCCTTC	233545	65741	CTGCTGTTCTCAGTCCTCCA	278132	110328	GAGACAGGAGAATAGCATGA
188959	21155	CACACTAGCCCACCTCCCTT	233546	65742	TCTGCTGTTCTCAGTCCTCC	278133	110329	TGAGACAGGAGAATAGCATG
188960	21156	GCACACTAGCCCACCTCCCT	233547	65743	CTCTGCTGTTCTCAGTCCTC	278134	110330	CTGAGACAGGAGAATAGCAT
188961	21157	AGCACACTAGCCCACCTCCC	233548	65744	GCTCTGCTGTTCTCAGTCCT	278135	110331	GCTGAGACAGGAGAATAGCA
188962	21158	CAGCACACTAGCCCACCTCC	233549	65745	GGCTCTGCTGTTCTCAGTCC	278136	110332	GGCTGAGACAGGAGAATAGC
188963	21159	TCAGCACACTAGCCCACCTC	233550	65746	CGGCTCTGCTGTTCTCAGTC	278137	110333	AGGCTGAGACAGGAGAATAG
188964	21160	TTCAGCACACTAGCCCACCT	233551	65747	ACGGCTCTGCTGTTCTCAGT	278138	110334	GAGGCTGAGACAGGAGAATA
188965	21161	CTTCAGCACACTAGCCCACC	233552	65748	AACGGCTCTGCTGTTCTCAG	278139	110335	GGAGGCTGAGACAGGAGAAT
188966	21162	ACTTCAGCACACTAGCCCAC	233553	65749	AAACGGCTCTGCTGTTCTCA	278140	110336	GGGAGGCTGAGACAGGAGAA
188967	21163	TACTTCAGCACACTAGCCCA	233554	65750	AAAACGGCTCTGCTGTTCTC	278141	110337	TGGGAGGCTGAGACAGGAGA
188968	21164	ATACTTCAGCACACTAGCCC	233555	65751	TAAAACGGCTCTGCTGTTCT	278142	110338	TTGGGAGGCTGAGACAGGAG
188969	21165	GATACTTCAGCACACTAGCC	233556	65752	CTAAAACGGCTCTGCTGTTC	278143	110339	CTTGGGAGGCTGAGACAGGA
188970	21166	AGATACTTCAGCACACTAGC	233557	65753	CCTAAAACGGCTCTGCTGTT	278144	110340	ACTTGGGAGGCTGAGACAGG

188971	21167	TAGATACTTCAGCACACTAG	233558	65754	TCCTAAAACGGCTCTGCTGT	278145	110341	TACTTGGGAGGCTGAGACAG
188972	21168	GTAGATACTTCAGCACACTA	233559	65755	ATCCTAAAACGGCTCTGCTG	278146	110342	CTACTTGGGAGGCTGAGACA
188973	21169	AGTAGATACTTCAGCACACT	233560	65756	CATCCTAAAACGGCTCTGCT	278147	110343	GCTACTTGGGAGGCTGAGAC
188974	21170	GAGTAGATACTTCAGCACAC	233561	65757	CCATCCTAAAACGGCTCTGC	278148	110344	AGCTACTTGGGAGGCTGAGA
188975	21171	GGAGTAGATACTTCAGCACA	233562	65758	CCCATCCTAAAACGGCTCTG	278149	110345	CAGCTACTTGGGAGGCTGAG
188976	21172	AGGAGTAGATACTTCAGCAC	233563	65759	TCCCATCCTAAAACGGCTCT	278150	110346	CCAGCTACTTGGGAGGCTGA
188977	21173	AAGGAGTAGATACTTCAGCA	233564	65760	GTCCCATCCTAAAACGGCTC	278151	110347	CCCAGCTACTTGGGAGGCTG
188978	21174	CAAGGAGTAGATACTTCAGC	233565	65761	TGTCCCATCCTAAAACGGCT	278152	110348	TCCCAGCTACTTGGGAGGCT
188979	21175	ACAAGGAGTAGATACTTCAG	233566	65762	CTGTCCCATCCTAAAACGGC	278153	110349	GTCCCAGCTACTTGGGAGGC
188980	21176	GACAAGGAGTAGATACTTCA	233567	65763	CCTGTCCCATCCTAAAACGG	278154	110350	AGTCCCAGCTACTTGGGAGG
188981	21177	TGACAAGGAGTAGATACTTC	233568	65764	CCCTGTCCCATCCTAAAACG	278155	110351	CAGTCCCAGCTACTTGGGAG
188982	21178	ATGACAAGGAGTAGATACTT	233569	65765	GCCCTGTCCCATCCTAAAAC	278156	110352	GCAGTCCCAGCTACTTGGGA
188983	21179	TATGACAAGGAGTAGATACT	233570	65766	TGCCCTGTCCCATCCTAAAA	278157	110353	TGCAGTCCCAGCTACTTGGG
188984	21180	CTATGACAAGGAGTAGATAC	233571	65767	CTGCCCTGTCCCATCCTAAA	278158	110354	CTGCAGTCCCAGCTACTTGG
188985	21181	ACTATGACAAGGAGTAGATA	233572	65768	GCTGCCCTGTCCCATCCTAA	278159	110355	CCTGCAGTCCCAGCTACTTG
188986	21182	GACTATGACAAGGAGTAGAT	233573	65769	GGCTGCCCTGTCCCATCCTA	278160	110356	ACCTGCAGTCCCAGCTACTT
188987	21183	AGACTATGACAAGGAGTAGA	233574	65770	TGGCTGCCCTGTCCCATCCT	278161	110357	CACCTGCAGTCCCAGCTACT
188988	21184	CAGACTATGACAAGGAGTAG	233575	65771	CTGGCTGCCCTGTCCCATCC	278162	110358	GCACCTGCAGTCCCAGCTAC
188989	21185	ACAGACTATGACAAGGAGTA	233576	65772	CCTGGCTGCCCTGTCCCATC	278163	110359	GGCACCTGCAGTCCCAGCTA
188990	21186	CACAGACTATGACAAGGAGT	233577	65773	TCCTGGCTGCCCTGTCCCAT	278164	110360	GGGCACCTGCAGTCCCAGCT
188991	21187	TCACAGACTATGACAAGGAG	233578	65774	CTCCTGGCTGCCCTGTCCCA	278165	110361	CGGGCACCTGCAGTCCCAGC
188992	21188	GTCACAGACTATGACAAGGA	233579	65775	CCTCCTGGCTGCCCTGTCCC	278166	110362	GCGGGCACCTGCAGTCCCAG
188993	21189	TGTCACAGACTATGACAAGG	233580	65776	TCCTCCTGGCTGCCCTGTCC	278167	110363	GGCGGGCACCTGCAGTCCCA
188994	21190	TTGTCACAGACTATGACAAG	233581	65777	ATCCTCCTGGCTGCCCTGTC	278168	110364	TGGCGGGCACCTGCAGTCCC
188995	21191	GTTGTCACAGACTATGACAA	233582	65778	AATCCTCCTGGCTGCCCTGT	278169	110365	GTGGCGGGCACCTGCAGTCC
188996	21192	GGTTGTCACAGACTATGACA	233583	65779	CAATCCTCCTGGCTGCCCTG	278170	110366	GGTGGCGGGCACCTGCAGTC
188997	21193	GGGTTGTCACAGACTATGAC	233584	65780	CCAATCCTCCTGGCTGCCCT	278171	110367	TGGTGGCGGGCACCTGCAGT
188998	21194	TGGGTTGTCACAGACTATGA	233585	65781	CCCAATCCTCCTGGCTGCCC	278172	110368	GTGGTGGCGGGCACCTGCAG
188999	21195	CTGGGTTGTCACAGACTATG	233586	65782	GCCCAATCCTCCTGGCTGCC	278173	110369	TGTGGTGGCGGGCACCTGCA
189000	21196	TCTGGGTTGTCACAGACTAT	233587	65783	AGCCCAATCCTCCTGGCTGC	278174	110370	GTGTGGTGGCGGGCACCTGC
189001	21197	GTCTGGGTTGTCACAGACTA	233588	65784	GAGCCCAATCCTCCTGGCTG	278175	110371	GGTGTGGTGGCGGGCACCTG
189002	21198	AGTCTGGGTTGTCACAGACT	233589	65785	TGAGCCCAATCCTCCTGGCT	278176	110372	AGGTGTGGTGGCGGGCACCT
189003	21199	TAGTCTGGGTTGTCACAGAC	233590	65786	GTGAGCCCAATCCTCCTGGC	278177	110373	CAGGTGTGGTGGCGGGCACC
189004	21200	CTAGTCTGGGTTGTCACAGA	233591	65787	AGTGAGCCCAATCCTCCTGG	278178	110374	CCAGGTGTGGTGGCGGGCAC
189005	21201	GCTAGTCTGGGTTGTCACAG	233592	65788	GAGTGAGCCCAATCCTCCTG	278179	110375	GCCAGGTGTGGTGGCGGGCA
189006	21202	GGCTAGTCTGGGTTGTCACA	233593	65789	GGAGTGAGCCCAATCCTCCT	278180	110376	AGCCAGGTGTGGTGGCGGGC
189007	21203	GGGCTAGTCTGGGTTGTCAC	233594	65790	GGGAGTGAGCCCAATCCTCC	278181	110377	TAGCCAGGTGTGGTGGCGGG
189008	21204	TGGGCTAGTCTGGGTTGTCA	233595	65791	AGGGAGTGAGCCCAATCCTC	278182	110378	TTAGCCAGGTGTGGTGGCGG
189009	21205	ATGGGCTAGTCTGGGTTGTC	233596	65792	TAGGGAGTGAGCCCAATCCT	278183	110379	ATTAGCCAGGTGTGGTGGCG
189010	21206	CATGGGCTAGTCTGGGTTGT	233597	65793	GTAGGGAGTGAGCCCAATCC	278184	110380	AATTAGCCAGGTGTGGTGGC
189011	21207	TCATGGGCTAGTCTGGGTTG	233598	65794	AGTAGGGAGTGAGCCCAATC	278185	110381	AAATTAGCCAGGTGTGGTGG
189012	21208	CTCATGGGCTAGTCTGGGTT	233599	65795	CAGTAGGGAGTGAGCCCAAT	278186	110382	AAAATTAGCCAGGTGTGGTG
189013	21209	GCTCATGGGCTAGTCTGGGT	233600	65796	TCAGTAGGGAGTGAGCCCAA	278187	110383	AAAAATTAGCCAGGTGTGGT
189014	21210	GGCTCATGGGCTAGTCTGGG	233601	65797	CTCAGTAGGGAGTGAGCCCA	278188	110384	AAAAAATTAGCCAGGTGTGG
189015	21211	TGGCTCATGGGCTAGTCTGG	233602	65798	ACTCAGTAGGGAGTGAGCCC	278189	110385	AAAAAAATTAGCCAGGTGTG
189016	21212	GTGGCTCATGGGCTAGTCTG	233603	65799	CACTCAGTAGGGAGTGAGCC	278190	110386	CAAAAAAATTAGCCAGGTGT
189017	21213	GGTGGCTCATGGGCTAGTCT	233604	65800	GCACTCAGTAGGGAGTGAGC	278191	110387	ACAAAAAAATTAGCCAGGTG
189018	21214	GGGTGGCTCATGGGCTAGTC	233605	65801	GGCACTCAGTAGGGAGTGAG	278192	110388	TACAAAAAAATTAGCCAGGT
189019	21215	AGGGTGGCTCATGGGCTAGT	233606	65802	AGGCACTCAGTAGGGAGTGA	278193	110389	ATACAAAAAAATTAGCCAGG
189020	21216	CAGGGTGGCTCATGGGCTAG	233607	65803	GAGGCACTCAGTAGGGAGTG	278194	110390	AATACAAAAAAATTAGCCAG
189021	21217	ACAGGGTGGCTCATGGGCTA	233608	65804	TGAGGCACTCAGTAGGGAGT	278195	110391	AAATACAAAAAAATTAGCCA
189022	21218	AACAGGGTGGCTCATGGGCT	233609	65805	GTGAGGCACTCAGTAGGGAG	278196	110392	AAAATACAAAAAAATTAGCC
189023	21219	GAACAGGGTGGCTCATGGGC	233610	65806	AGTGAGGCACTCAGTAGGGA	278197	110393	AAAAATACAAAAAAATTAGC
189024	21220	GGAACAGGGTGGCTCATGGG	233611	65807	GAGTGAGGCACTCAGTAGGG	278198	110394	TAAAAATACAAAAAAATTAG
189025	21221	GGGAACAGGGTGGCTCATGG	233612	65808	GGAGTGAGGCACTCAGTAGG	278199	110395	CTAAAAATACAAAAAAATTA
189026	21222	AGGGAACAGGGTGGCTCATG	233613	65809	GGGAGTGAGGCACTCAGTAG	278200	110396	ACTAAAAATACAAAAAAATT
189027	21223	CAGGGAACAGGGTGGCTCAT	233614	65810	CGGGAGTGAGGCACTCAGTA	278201	110397	TACTAAAAATACAAAAAAAT
189028	21224	GCAGGGAACAGGGTGGCTCA	233615	65811	ACGGGAGTGAGGCACTCAGT	278202	110398	CTACTAAAAATACAAAAAAA
189029	21225	TGCAGGGAACAGGGTGGCTC	233616	65812	TACGGGAGTGAGGCACTCAG	278203	110399	TCTACTAAAAATACAAAAAA
189030	21226	ATGCAGGGAACAGGGTGGCT	233617	65813	GTACGGGAGTGAGGCACTCA	278204	110400	CTCTACTAAAAATACAAAAA
189031	21227	AATGCAGGGAACAGGGTGGC	233618	65814	TGTACGGGAGTGAGGCACTC	278205	110401	TCTCTACTAAAAATACAAAA
189032	21228	AAATGCAGGGAACAGGGTGG	233619	65815	CTGTACGGGAGTGAGGCACT	278206	110402	GTCTCTACTAAAAATACAAA
189033	21229	GAAATGCAGGGAACAGGGTG	233620	65816	GCTGTACGGGAGTGAGGCAC	278207	110403	CGTCTCTACTAAAAATACAA
189034	21230	GGAAATGCAGGGAACAGGGT	233621	65817	GGCTGTACGGGAGTGAGGCA	278208	110404	CCGTCTCTACTAAAAATACA
189035	21231	TGGAAATGCAGGGAACAGGG	233622	65818	GGGCTGTACGGGAGTGAGGC	278209	110405	CCCGTCTCTACTAAAAATAC
189036	21232	TTGGAAATGCAGGGAACAGG	233623	65819	GGGGCTGTACGGGAGTGAGG	278210	110406	CCCCGTCTCTACTAAAAATA
189037	21233	ATTGGAAATGCAGGGAACAG	233624	65820	GGGGGCTGTACGGGAGTGAG	278211	110407	ACCCCGTCTCTACTAAAAAT
189038	21234	CATTGGAAATGCAGGGAACA	233625	65821	TGGGGGCTGTACGGGAGTGA	278212	110408	AACCCCGTCTCTACTAAAAA
189039	21235	TCATTGGAAATGCAGGGAAC	233626	65822	ATGGGGGCTGTACGGGAGTG	278213	110409	AAACCCCGTCTCTACTAAAA
189040	21236	CTCATTGGAAATGCAGGGAA	233627	65823	TATGGGGGCTGTACGGGAGT	278214	110410	GAAACCCCGTCTCTACTAAA
189041	21237	TCTCATTGGAAATGCAGGGA	233628	65824	CTATGGGGGCTGTACGGGAG	278215	110411	TGAAACCCCGTCTCTACTAA
189042	21238	GTCTCATTGGAAATGCAGGG	233629	65825	TCTATGGGGGCTGTACGGGA	278216	110412	GTGAAACCCCGTCTCTACTA

189043	21239	GGTCTCATTGGAAATGCAGG	233630	65826	CTCTATGGGGGCTGTACGGG	278217	110413	GGTGAAACCCCGTCTCTACT
189044	21240	AGGTCTCATTGGAAATGCAG	233631	65827	CCTCTATGGGGGCTGTACGG	278218	110414	CGGTGAAACCCCGTCTCTAC
189045	21241	GAGGTCTCATTGGAAATGCA	233632	65828	TCCTCTATGGGGGCTGTACG	278219	110415	ACGGTGAAACCCCGTCTCTA
189046	21242	CGAGGTCTCATTGGAAATGC	233633	65829	TTCCTCTATGGGGGCTGTAC	278220	110416	CACGGTGAAACCCCGTCTCT
189047	21243	CCGAGGTCTCATTGGAAATG	233634	65830	CTTCCTCTATGGGGGCTGTA	278221	110417	ACACGGTGAAACCCCGTCTC
189048	21244	ACCGAGGTCTCATTGGAAAT	233635	65831	TCTTCCTCTATGGGGGCTGT	278222	110418	AACACGGTGAAACCCCGTCT
189049	21245	CACCGAGGTCTCATTGGAAA	233636	65832	CTCTTCCTCTATGGGGGCTG	278223	110419	TAACACGGTGAAACCCCGTC
189050	21246	CCACCGAGGTCTCATTGGAA	233637	65833	CCTCTTCCTCTATGGGGGCT	278224	110420	CTAACACGGTGAAACCCCGT
189051	21247	TCCACCGAGGTCTCATTGGA	233638	65834	CCCTCTTCCTCTATGGGGGC	278225	110421	GCTAACACGGTGAAACCCCG
189052	21248	GTCCACCGAGGTCTCATTGG	233639	65835	CCCCTCTTCCTCTATGGGGG	278226	110422	GGCTAACACGGTGAAACCCC
189053	21249	TGTCCACCGAGGTCTCATTG	233640	65836	ACCCCTCTTCCTCTATGGGG	278227	110423	TGGCTAACACGGTGAAACCC
189054	21250	ATGTCCACCGAGGTCTCATT	233641	65837	AACCCCTCTTCCTCTATGGG	278228	110424	CTGGCTAACACGGTGAAACC
189055	21251	CATGTCCACCGAGGTCTCAT	233642	65838	GAACCCCTCTTCCTCTATGG	278229	110425	CCTGGCTAACACGGTGAAAC
189056	21252	ACATGTCCACCGAGGTCTCA	233643	65839	TGAACCCCTCTTCCTCTATG	278230	110426	TCCTGGCTAACACGGTGAAA
189057	21253	AACATGTCCACCGAGGTCTC	233644	65840	TTGAACCCCTCTTCCTCTAT	278231	110427	ATCCTGGCTAACACGGTGAA
189058	21254	GAACATGTCCACCGAGGTCT	233645	65841	TTTGAACCCCTCTTCCTCTA	278232	110428	CATCCTGGCTAACACGGTGA
189059	21255	GGAACATGTCCACCGAGGTC	233646	65842	ATTTGAACCCCTCTTCCTCT	278233	110429	CCATCCTGGCTAACACGGTG
189060	21256	GGGAACATGTCCACCGAGGT	233647	65843	AATTTGAACCCCTCTTCCTC	278234	110430	ACCATCCTGGCTAACACGGT
189061	21257	AGGGAACATGTCCACCGAGG	233648	65844	AAATTTGAACCCCTCTTCCT	278235	110431	GACCATCCTGGCTAACACGG
189062	21258	CAGGGAACATGTCCACCGAG	233649	65845	TAAATTTGAACCCCTCTTCC	278236	110432	AGACCATCCTGGCTAACACG
189063	21259	TCAGGGAACATGTCCACCGA	233650	65846	ATAAATTTGAACCCCTCTTC	278237	110433	GAGACCATCCTGGCTAACAC
189064	21260	CTCAGGGAACATGTCCACCG	233651	65847	AATAAATTTGAACCCCTCTT	278238	110434	TGAGACCATCCTGGCTAACA
189065	21261	CCTCAGGGAACATGTCCACC	233652	65848	GAATAAATTTGAACCCCTCT	278239	110435	TTGAGACCATCCTGGCTAAC
189066	21262	ACCTCAGGGAACATGTCCAC	233653	65849	GGAATAAATTTGAACCCCTC	278240	110436	ATTGAGACCATCCTGGCTAA
189067	21263	CACCTCAGGGAACATGTCCA	233654	65850	AGGAATAAATTTGAACCCCT	278241	110437	GATTGAGACCATCCTGGCTA
189068	21264	TCACCTCAGGGAACATGTCC	233655	65851	GAGGAATAAATTTGAACCCC	278242	110438	AGATTGAGACCATCCTGGCT
189069	21265	CTCACCTCAGGGAACATGTC	233656	65852	TGAGGAATAAATTTGAACCC	278243	110439	GAGATTGAGACCATCCTGGC
189070	21266	CCTCACCTCAGGGAACATGT	233657	65853	CTGAGGAATAAATTTGAACC	278244	110440	GGAGATTGAGACCATCCTGG
189071	21267	GCCTCACCTCAGGGAACATG	233658	65854	GCTGAGGAATAAATTTGAAC	278245	110441	AGGAGATTGAGACCATCCTG
189072	21268	AGCCTCACCTCAGGGAACAT	233659	65855	GGCTGAGGAATAAATTTGAA	278246	110442	CAGGAGATTGAGACCATCCT
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189075	21271	GTCAGCCTCACCTCAGGGAA	233662	65858	TCTGGCTGAGGAATAAATTT	278249	110445	GGTCAGGAGATTGAGACCAT
189076	21272	AGTCAGCCTCACCTCAGGGA	233663	65859	ATCTGGCTGAGGAATAAATT	278250	110446	AGGTCAGGAGATTGAGACCA
189077	21273	CAGTCAGCCTCACCTCAGGG	233664	65860	CATCTGGCTGAGGAATAAAT	278251	110447	GAGGTCAGGAGATTGAGACC
189078	21274	TCAGTCAGCCTCACCTCAGG	233665	65861	CCATCTGGCTGAGGAATAAA	278252	110448	CGAGGTCAGGAGATTGAGAC
189079	21275	ATCAGTCAGCCTCACCTCAG	233666	65862	GCCATCTGGCTGAGGAATAA	278253	110449	ACGAGGTCAGGAGATTGAGA
189080	21276	CATCAGTCAGCCTCACCTCA	233667	65863	TGCCATCTGGCTGAGGAATA	278254	110450	GACGAGGTCAGGAGATTGAG
189081	21277	ACATCAGTCAGCCTCACCTC	233668	65864	ATGCCATCTGGCTGAGGAAT	278255	110451	TGACGAGGTCAGGAGATTGA
189082	21278	GACATCAGTCAGCCTCACCT	233669	65865	CATGCCATCTGGCTGAGGAA	278256	110452	ATGACGAGGTCAGGAGATTG
189083	21279	TGACATCAGTCAGCCTCACC	233670	65866	ACATGCCATCTGGCTGAGGA	278257	110453	GATGACGAGGTCAGGAGATT
189084	21280	ATGACATCAGTCAGCCTCAC	233671	65867	CACATGCCATCTGGCTGAGG	278258	110454	AGATGACGAGGTCAGGAGAT
189085	21281	AATGACATCAGTCAGCCTCA	233672	65868	GCACATGCCATCTGGCTGAG	278259	110455	CAGATGACGAGGTCAGGAGA
189086	21282	AAATGACATCAGTCAGCCTC	233673	65869	GGCACATGCCATCTGGCTGA	278260	110456	GCAGATGACGAGGTCAGGAG
189087	21283	CAAATGACATCAGTCAGCCT	233674	65870	CGGCACATGCCATCTGGCTG	278261	110457	GGCAGATGACGAGGTCAGGA
189088	21284	TCAAATGACATCAGTCAGCC	233675	65871	GCGGCACATGCCATCTGGCT	278262	110458	AGGCAGATGACGAGGTCAGG
189089	21285	GTCAAATGACATCAGTCAGC	233676	65872	GGCGGCACATGCCATCTGGC	278263	110459	CAGGCAGATGACGAGGTCAG
189090	21286	CGTCAAATGACATCAGTCAG	233677	65873	AGGCGGCACATGCCATCTGG	278264	110460	GCAGGCAGATGACGAGGTCA
189091	21287	TCGTCAAATGACATCAGTCA	233678	65874	CAGGCGGCACATGCCATCTG	278265	110461	GGCAGGCAGATGACGAGGTC
189092	21288	ATCGTCAAATGACATCAGTC	233679	65875	ACAGGCGGCACATGCCATCT	278266	110462	AGGCAGGCAGATGACGAGGT
189093	21289	GATCGTCAAATGACATCAGT	233680	65876	GACAGGCGGCACATGCCATC	278267	110463	GAGGCAGGCAGATGACGAGG
189094	21290	AGATCGTCAAATGACATCAG	233681	65877	GGACAGGCGGCACATGCCAT	278268	110464	CGAGGCAGGCAGATGACGAG
189095	21291	AAGATCGTCAAATGACATCA	233682	65878	AGGACAGGCGGCACATGCCA	278269	110465	CCGAGGCAGGCAGATGACGA
189096	21292	CAAGATCGTCAAATGACATC	233683	65879	CAGGACAGGCGGCACATGCC	278270	110466	GCCGAGGCAGGCAGATGACG
189097	21293	TCAAGATCGTCAAATGACAT	233684	65880	CCAGGACAGGCGGCACATGC	278271	110467	GGCCGAGGCAGGCAGATGAC
189098	21294	ATCAAGATCGTCAAATGACA	233685	65881	TCCAGGACAGGCGGCACATG	278272	110468	AGGCCGAGGCAGGCAGATGA
189099	21295	CATCAAGATCGTCAAATGAC	233686	65882	TTCCAGGACAGGCGGCACAT	278273	110469	GAGGCCGAGGCAGGCAGATG
189100	21296	GCATCAAGATCGTCAAATGA	233687	65883	ATTCCAGGACAGGCGGCACA	278274	110470	GGAGGCCGAGGCAGGCAGAT
189101	21297	GGCATCAAGATCGTCAAATG	233688	65884	AATTCCAGGACAGGCGGCAC	278275	110471	GGGAGGCCGAGGCAGGCAGA
189102	21298	TGGCATCAAGATCGTCAAAT	233689	65885	AAATTCCAGGACAGGCGGCA	278276	110472	TGGGAGGCCGAGGCAGGCAG
189103	21299	TTGGCATCAAGATCGTCAAA	233690	65886	GAAATTCCAGGACAGGCGGC	278277	110473	TTGGGAGGCCGAGGCAGGCA
189104	21300	TTTGGCATCAAGATCGTCAA	233691	65887	TGAAATTCCAGGACAGGCGG	278278	110474	TTTGGGAGGCCGAGGCAGGC
189105	21301	ATTTGGCATCAAGATCGTCA	233692	65888	GTGAAATTCCAGGACAGGCG	278279	110475	CTTTGGGAGGCCGAGGCAGG
189106	21302	GATTTGGCATCAAGATCGTC	233693	65889	TGTGAAATTCCAGGACAGGC	278280	110476	ACTTTGGGAGGCCGAGGCAG
189107	21303	GGATTTGGCATCAAGATCGT	233694	65890	ATGTGAAATTCCAGGACAGG	278281	110477	CACTTTGGGAGGCCGAGGCA
189108	21304	AGGATTTGGCATCAAGATCG	233695	65891	GATGTGAAATTCCAGGACAG	278282	110478	GCACTTTGGGAGGCCGAGGC
189109	21305	AAGGATTTGGCATCAAGATC	233696	65892	TGATGTGAAATTCCAGGACA	278283	110479	AGCACTTTGGGAGGCCGAGG
189110	21306	AAAGGATTTGGCATCAAGAT	233697	65893	GTGATGTGAAATTCCAGGAC	278284	110480	CAGCACTTTGGGAGGCCGAG
189111	21307	AAAAGGATTTGGCATCAAGA	233698	65894	AGTGATGTGAAATTCCAGGA	278285	110481	TCAGCACTTTGGGAGGCCGA
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189113	21309	ATAAAAGGATTTGGCATCAA	233700	65896	TAAGTGATGTGAAATTCCAG	278287	110483	TCTCAGCACTTTGGGAGGCC
189114	21310	TATAAAAGGATTTGGCATCA	233701	65897	ATAAGTGATGTGAAATTCCA	278288	110484	ATCTCAGCACTTTGGGAGGC

189115	21311	ATATAAAAGGATTTGGCATC	233702	65898	CATAAGTGATGTGAAATTCC	278289	110485	AATCTCAGCACTTTGGGAGG
189116	21312	GATATAAAAGGATTTGGCAT	233703	65899	TCATAAGTGATGTGAAATTC	278290	110486	TAATCTCAGCACTTTGGGAG
189117	21313	TGATATAAAAGGATTTGGCA	233704	65900	ATCATAAGTGATGTGAAATT	278291	110487	GTAATCTCAGCACTTTGGGA
189118	21314	TTGATATAAAAGGATTTGGC	233705	65901	CATCATAAGTGATGTGAAAT	278292	110488	TGTAATCTCAGCACTTTGGG
189119	21315	TTTGATATAAAAGGATTTGG	233706	65902	CCATCATAAGTGATGTGAAA	278293	110489	CTGTAATCTCAGCACTTTGG
189120	21316	TTTTGATATAAAAGGATTTG	233707	65903	TCCATCATAAGTGATGTGAA	278294	110490	CCTGTAATCTCAGCACTTTG
189121	21317	TTTTTGATATAAAAGGATTT	233708	65904	GTCCATCATAAGTGATGTGA	278295	110491	GCCTGTAATCTCAGCACTTT
189122	21318	GTTTTTGATATAAAAGGATT	233709	65905	GGTCCATCATAAGTGATGTG	278296	110492	CGCCTGTAATCTCAGCACTT
189123	21319	TGTTTTTGATATAAAAGGAT	233710	65906	TGGTCCATCATAAGTGATGT	278297	110493	ACGCCTGTAATCTCAGCACT
189124	21320	TTGTTTTTGATATAAAAGGA	233711	65907	TTGGTCCATCATAAGTGATG	278298	110494	CACGCCTGTAATCTCAGCAC
189125	21321	GTTGTTTTTGATATAAAAGG	233712	65908	TTTGGTCCATCATAAGTGAT	278299	110495	TCACGCCTGTAATCTCAGCA
189126	21322	GGTTGTTTTTGATATAAAAG	233713	65909	TTTTGGTCCATCATAAGTGA	278300	110496	CTCACGCCTGTAATCTCAGC
189127	21323	TGGTTGTTTTTGATATAAAA	233714	65910	ATTTTGGTCCATCATAAGTG	278301	110497	GCTCACGCCTGTAATCTCAG
189128	21324	CTGGTTGTTTTTGATATAAA	233715	65911	AATTTTGGTCCATCATAAGT	278302	110498	GGCTCACGCCTGTAATCTCA
189129	21325	TCTGGTTGTTTTTGATATAA	233716	65912	GAATTTTGGTCCATCATAAG	278303	110499	TGGCTCACGCCTGTAATCTC
189130	21326	TTCTGGTTGTTTTTGATATA	233717	65913	GGAATTTTGGTCCATCATAA	278304	110500	GTGGCTCACGCCTGTAATCT
189131	21327	GTTCTGGTTGTTTTTGATAT	233718	65914	TGGAATTTTGGTCCATCATA	278305	110501	GGTGGCTCACGCCTGTAATC
189132	21328	TGTTCTGGTTGTTTTTGATA	233719	65915	TTGGAATTTTGGTCCATCAT	278306	110502	CGGTGGCTCACGCCTGTAAT
189133	21329	GTGTTCTGGTTGTTTTTGAT	233720	65916	TTTGGAATTTTGGTCCATCA	278307	110503	ACGGTGGCTCACGCCTGTAA
189134	21330	AGTGTTCTGGTTGTTTTTGA	233721	65917	TTTTGGAATTTTGGTCCATC	278308	110504	CACGGTGGCTCACGCCTGTA
189135	21331	GAGTGTTCTGGTTGTTTTTG	233722	65918	CTTTTGGAATTTTGGTCCAT	278309	110505	GCACGGTGGCTCACGCCTGT
189136	21332	AGAGTGTTCTGGTTGTTTTT	233723	65919	GCTTTTGGAATTTTGGTCCA	278310	110506	GGCACGGTGGCTCACGCCTG
189137	21333	GAGAGTGTTCTGGTTGTTTT	233724	65920	AGCTTTTGGAATTTTGGTCC	278311	110507	GGGCACGGTGGCTCACGCCT
189138	21334	AGAGAGTGTTCTGGTTGTTT	233725	65921	CAGCTTTTGGAATTTTGGTC	278312	110508	CGGGCACGGTGGCTCACGCC
189139	21335	AAGAGAGTGTTCTGGTTGTT	233726	65922	TCAGCTTTTGGAATTTTGGT	278313	110509	CCGGGCACGGTGGCTCACGC
189140	21336	AAAGAGAGTGTTCTGGTTGT	233727	65923	TTCAGCTTTTGGAATTTTGG	278314	110510	GCCGGGCACGGTGGCTCACG
189141	21337	AAAAGAGAGTGTTCTGGTTG	233728	65924	ATTCAGCTTTTGGAATTTTG	278315	110511	GGCCGGGCACGGTGGCTCAC
189142	21338	GAAAAGAGAGTGTTCTGGTT	233729	65925	GATTCAGCTTTTGGAATTTT	278316	110512	TGGCCGGGCACGGTGGCTCA
189143	21339	AGAAAAGAGAGTGTTCTGGT	233730	65926	GGATTCAGCTTTTGGAATTT	278317	110513	CTGGCCGGGCACGGTGGCTC
189144	21340	GAGAAAAGAGAGTGTTCTGG	233731	65927	TGGATTCAGCTTTTGGAATT	278318	110514	TCTGGCCGGGCACGGTGGCT
189145	21341	AGAGAAAAGAGAGTGTTCTG	233732	65928	ATGGATTCAGCTTTTGGAAT	278319	110515	TTCTGGCCGGGCACGGTGGC
189146	21342	AAGAGAAAAGAGAGTGTTCT	233733	65929	CATGGATTCAGCTTTTGGAA	278320	110516	TTTCTGGCCGGGCACGGTGG
189147	21343	TAAGAGAAAAGAGAGTGTTC	233734	65930	TCATGGATTCAGCTTTTGGA	278321	110517	TTTTCTGGCCGGGCACGGTG
189148	21344	CTAAGAGAAAAGAGAGTGTT	233735	65931	ATCATGGATTCAGCTTTTGG	278322	110518	TTTTTCTGGCCGGGCACGGT
189149	21345	ACTAAGAGAAAAGAGAGTGT	233736	65932	AATCATGGATTCAGCTTTTG	278323	110519	TTTTTTCTGGCCGGGCACGG
189150	21346	CACTAAGAGAAAAGAGAGTG	233737	65933	CAATCATGGATTCAGCTTTT	278324	110520	TTTTTTTCTGGCCGGGCACG
189151	21347	GCACTAAGAGAAAAGAGAGT	233738	65934	ACAATCATGGATTCAGCTTT	278325	110521	GTTTTTTTCTGGCCGGGCAC
189152	21348	AGCACTAAGAGAAAAGAGAG	233739	65935	GACAATCATGGATTCAGCTT	278326	110522	TGTTTTTTTCTGGCCGGGCA
189153	21349	AAGCACTAAGAGAAAAGAGA	233740	65936	TGACAATCATGGATTCAGCT	278327	110523	ATGTTTTTTTCTGGCCGGGC
189154	21350	AAAGCACTAAGAGAAAAGAG	233741	65937	TTGACAATCATGGATTCAGC	278328	110524	AATGTTTTTTTCTGGCCGGG
189155	21351	GAAAGCACTAAGAGAAAAGA	233742	65938	TTTGACAATCATGGATTCAG	278329	110525	AAATGTTTTTTTCTGGCCGG
189156	21352	TGAAAGCACTAAGAGAAAAG	233743	65939	CTTTGACAATCATGGATTCA	278330	110526	GAAATGTTTTTTTCTGGCCG
189157	21353	GTGAAAGCACTAAGAGAAAA	233744	65940	ACTTTGACAATCATGGATTC	278331	110527	AGAAATGTTTTTTTCTGGCC
189158	21354	GGTGAAAGCACTAAGAGAAA	233745	65941	GACTTTGACAATCATGGATT	278332	110528	TAGAAATGTTTTTTTCTGGC
189159	21355	GGGTGAAAGCACTAAGAGAA	233746	65942	AGACTTTGACAATCATGGAT	278333	110529	TTAGAAATGTTTTTTTCTGG
189160	21356	TGGGTGAAAGCACTAAGAGA	233747	65943	CAGACTTTGACAATCATGGA	278334	110530	CTTAGAAATGTTTTTTTCTG
189161	21357	CTGGGTGAAAGCACTAAGAG	233748	65944	CCAGACTTTGACAATCATGG	278335	110531	ACTTAGAAATGTTTTTTTCT
189162	21358	TCTGGGTGAAAGCACTAAGA	233749	65945	ACCAGACTTTGACAATCATG	278336	110532	TACTTAGAAATGTTTTTTTC
189163	21359	ATCTGGGTGAAAGCACTAAG	233750	65946	TACCAGACTTTGACAATCAT	278337	110533	ATACTTAGAAATGTTTTTTT
189164	21360	CATCTGGGTGAAAGCACTAA	233751	65947	ATACCAGACTTTGACAATCA	278338	110534	CATACTTAGAAATGTTTTTT
189165	21361	TCATCTGGGTGAAAGCACTA	233752	65948	CATACCAGACTTTGACAATC	278339	110535	ACATACTTAGAAATGTTTTT
189166	21362	GTCATCTGGGTGAAAGCACT	233753	65949	CCATACCAGACTTTGACAAT	278340	110536	CACATACTTAGAAATGTTTT
189167	21363	GGTCATCTGGGTGAAAGCAC	233754	65950	GCCATACCAGACTTTGACAA	278341	110537	CCACATACTTAGAAATGTTT
189168	21364	TGGTCATCTGGGTGAAAGCA	233755	65951	TGCCATACCAGACTTTGACA	278342	110538	GCCACATACTTAGAAATGTT
189169	21365	GTGGTCATCTGGGTGAAAGC	233756	65952	CTGCCATACCAGACTTTGAC	278343	110539	TGCCACATACTTAGAAATGT
189170	21366	TGTGGTCATCTGGGTGAAAG	233757	65953	CCTGCCATACCAGACTTTGA	278344	110540	CTGCCACATACTTAGAAATG
189171	21367	ATGTGGTCATCTGGGTGAAA	233758	65954	TCCTGCCATACCAGACTTTG	278345	110541	TCTGCCACATACTTAGAAAT
189172	21368	AATGTGGTCATCTGGGTGAA	233759	65955	ATCCTGCCATACCAGACTTT	278346	110542	ATCTGCCACATACTTAGAAA
189173	21369	AAATGTGGTCATCTGGGTGA	233760	65956	CATCCTGCCATACCAGACTT	278347	110543	TATCTGCCACATACTTAGAA
189174	21370	GAAATGTGGTCATCTGGGTG	233761	65957	ACATCCTGCCATACCAGACT	278348	110544	GTATCTGCCACATACTTAGA
189175	21371	TGAAATGTGGTCATCTGGGT	233762	65958	GACATCCTGCCATACCAGAC	278349	110545	AGTATCTGCCACATACTTAG
189176	21372	ATGAAATGTGGTCATCTGGG	233763	65959	TGACATCCTGCCATACCAGA	278350	110546	CAGTATCTGCCACATACTTA
189177	21373	GATGAAATGTGGTCATCTGG	233764	65960	TTGACATCCTGCCATACCAG	278351	110547	TCAGTATCTGCCACATACTT
189178	21374	GGATGAAATGTGGTCATCTG	233765	65961	GTTGACATCCTGCCATACCA	278352	110548	TTCAGTATCTGCCACATACT
189179	21375	AGGATGAAATGTGGTCATCT	233766	65962	TGTTGACATCCTGCCATACC	278353	110549	ATTCAGTATCTGCCACATAC
189180	21376	GAGGATGAAATGTGGTCATC	233767	65963	CTGTTGACATCCTGCCATAC	278354	110550	AATTCAGTATCTGCCACATA
189181	21377	GGAGGATGAAATGTGGTCAT	233768	65964	ACTGTTGACATCCTGCCATA	278355	110551	TAATTCAGTATCTGCCACAT
189182	21378	GGGAGGATGAAATGTGGTCA	233769	65965	TACTGTTGACATCCTGCCAT	278356	110552	ATAATTCAGTATCTGCCACA
189183	21379	TGGGAGGATGAAATGTGGTC	233770	65966	TTACTGTTGACATCCTGCCA	278357	110553	AATAATTCAGTATCTGCCAC
189184	21380	CTGGGAGGATGAAATGTGGT	233771	65967	ATTACTGTTGACATCCTGCC	278358	110554	CAATAATTCAGTATCTGCCA
189185	21381	GCTGGGAGGATGAAATGTGG	233772	65968	GATTACTGTTGACATCCTGC	278359	110555	GCAATAATTCAGTATCTGCC
189186	21382	GGCTGGGAGGATGAAATGTG	233773	65969	CGATTACTGTTGACATCCTG	278360	110556	AGCAATAATTCAGTATCTGC

189187	21383	TGGCTGGGAGGATGAAATGT	233774	65970	ACGATTACTGTTGACATCCT	278361	110557	AAGCAATAATTCAGTATCTG
189188	21384	GTGGCTGGGAGGATGAAATG	233775	65971	AACGATTACTGTTGACATCC	278362	110558	TAAGCAATAATTCAGTATCT
189189	21385	AGTGGCTGGGAGGATGAAAT	233776	65972	AAACGATTACTGTTGACATC	278363	110559	TTAAGCAATAATTCAGTATC
189190	21386	GAGTGGCTGGGAGGATGAAA	233777	65973	GAAACGATTACTGTTGACAT	278364	110560	ATTAAGCAATAATTCAGTAT
189191	21387	AGAGTGGCTGGGAGGATGAA	233778	65974	AGAAACGATTACTGTTGACA	278365	110561	CATTAAGCAATAATTCAGTA
189192	21388	CAGAGTGGCTGGGAGGATGA	233779	65975	CAGAAACGATTACTGTTGAC	278366	110562	ACATTAAGCAATAATTCAGT
189193	21389	CCAGAGTGGCTGGGAGGATG	233780	65976	CCAGAAACGATTACTGTTGA	278367	110563	GACATTAAGCAATAATTCAG
189194	21390	CCCAGAGTGGCTGGGAGGAT	233781	65977	CCCAGAAACGATTACTGTTG	278368	110564	GGACATTAAGCAATAATTCA
189195	21391	GCCCAGAGTGGCTGGGAGGA	233782	65978	GCCCAGAAACGATTACTGTT	278369	110565	AGGACATTAAGCAATAATTC
189196	21392	GGCCCAGAGTGGCTGGGAGG	233783	65979	TGCCCAGAAACGATTACTGT	278370	110566	AAGGACATTAAGCAATAATT
189197	21393	TGGCCCAGAGTGGCTGGGAG	233784	65980	CTGCCCAGAAACGATTACTG	278371	110567	AAAGGACATTAAGCAATAAT
189198	21394	CTGGCCCAGAGTGGCTGGGA	233785	65981	TCTGCCCAGAAACGATTACT	278372	110568	CAAAGGACATTAAGCAATAA
189199	21395	CCTGGCCCAGAGTGGCTGGG	233786	65982	CTCTGCCCAGAAACGATTAC	278373	110569	TCAAAGGACATTAAGCAATA
189200	21396	ACCTGGCCCAGAGTGGCTGG	233787	65983	CCTCTGCCCAGAAACGATTA	278374	110570	ATCAAAGGACATTAAGCAAT
189201	21397	CACCTGGCCCAGAGTGGCTG	233788	65984	CCCTCTGCCCAGAAACGATT	278375	110571	AATCAAAGGACATTAAGCAA
189202	21398	CCACCTGGCCCAGAGTGGCT	233789	65985	TCCCTCTGCCCAGAAACGAT	278376	110572	GAATCAAAGGACATTAAGCA
189203	21399	GCCACCTGGCCCAGAGTGGC	233790	65986	ATCCCTCTGCCCAGAAACGA	278377	110573	TGAATCAAAGGACATTAAGC
189204	21400	TGCCACCTGGCCCAGAGTGG	233791	65987	CATCCCTCTGCCCAGAAACG	278378	110574	ATGAATCAAAGGACATTAAG
189205	21401	GTGCCACCTGGCCCAGAGTG	233792	65988	TCATCCCTCTGCCCAGAAAC	278379	110575	AATGAATCAAAGGACATTAA
189206	21402	AGTGCCACCTGGCCCAGAGT	233793	65989	ATCATCCCTCTGCCCAGAAA	278380	110576	AAATGAATCAAAGGACATTA
189207	21403	CAGTGCCACCTGGCCCAGAG	233794	65990	AATCATCCCTCTGCCCAGAA	278381	110577	CAAATGAATCAAAGGACATT
189208	21404	GCAGTGCCACCTGGCCCAGA	233795	65991	AAATCATCCCTCTGCCCAGA	278382	110578	ACAAATGAATCAAAGGACAT
189209	21405	AGCAGTGCCACCTGGCCCAG	233796	65992	AAAATCATCCCTCTGCCCAG	278383	110579	AACAAATGAATCAAAGGACA
189210	21406	CAGCAGTGCCACCTGGCCCA	233797	65993	GAAAATCATCCCTCTGCCCA	278384	110580	AAACAAATGAATCAAAGGAC
189211	21407	CCAGCAGTGCCACCTGGCCC	233798	65994	AGAAAATCATCCCTCTGCCC	278385	110581	TAAACAAATGAATCAAAGGA
189212	21408	ACCAGCAGTGCCACCTGGCC	233799	65995	GAGAAAATCATCCCTCTGCC	278386	110582	TTAAACAAATGAATCAAAGG
189213	21409	AACCAGCAGTGCCACCTGGC	233800	65996	AGAGAAAATCATCCCTCTGC	278387	110583	ATTAAACAAATGAATCAAAG
189214	21410	AAACCAGCAGTGCCACCTGG	233801	65997	AAGAGAAAATCATCCCTCTG	278388	110584	AATTAAACAAATGAATCAAA
189215	21411	CAAACCAGCAGTGCCACCTG	233802	65998	GAAGAGAAAATCATCCCTCT	278389	110585	AAATTAAACAAATGAATCAA
189216	21412	TCAAACCAGCAGTGCCACCT	233803	65999	GGAAGAGAAAATCATCCCTC	278390	110586	GAAATTAAACAAATGAATCA
189217	21413	TTCAAACCAGCAGTGCCACC	233804	66000	GGGAAGAGAAAATCATCCCT	278391	110587	AGAAATTAAACAAATGAATC
189218	21414	TTTCAAACCAGCAGTGCCAC	233805	66001	TGGGAAGAGAAAATCATCCC	278392	110588	AAGAAATTAAACAAATGAAT
189219	21415	CTTTCAAACCAGCAGTGCCA	233806	66002	ATGGGAAGAGAAAATCATCC	278393	110589	AAAGAAATTAAACAAATGAA
189220	21416	CCTTTCAAACCAGCAGTGCC	233807	66003	GATGGGAAGAGAAAATCATC	278394	110590	TAAAGAAATTAAACAAATGA
189221	21417	CCCTTTCAAACCAGCAGTGC	233808	66004	AGATGGGAAGAGAAAATCAT	278395	110591	TTAAAGAAATTAAACAAATG
189222	21418	TCCCTTTCAAACCAGCAGTG	233809	66005	AAGATGGGAAGAGAAAATCA	278396	110592	ATTAAAGAAATTAAACAAAT
189223	21419	CTCCCTTTCAAACCAGCAGT	233810	66006	CAAGATGGGAAGAGAAAATC	278397	110593	CATTAAAGAAATTAAACAAA
189224	21420	CCTCCCTTTCAAACCAGCAG	233811	66007	GCAAGATGGGAAGAGAAAAT	278398	110594	CCATTAAAGAAATTAAACAA
189225	21421	ACCTCCCTTTCAAACCAGCA	233812	66008	AGCAAGATGGGAAGAGAAAA	278399	110595	TCCATTAAAGAAATTAAACA
189226	21422	GACCTCCCTTTCAAACCAGC	233813	66009	AAGCAAGATGGGAAGAGAAA	278400	110596	ATCCATTAAAGAAATTAAAC
189227	21423	AGACCTCCCTTTCAAACCAG	233814	66010	AAAGCAAGATGGGAAGAGAA	278401	110597	AATCCATTAAAGAAATTAAA
189228	21424	GAGACCTCCCTTTCAAACCA	233815	66011	CAAAGCAAGATGGGAAGAGA	278402	110598	TAATCCATTAAAGAAATTAA
189229	21425	GGAGACCTCCCTTTCAAACC	233816	66012	ACAAAGCAAGATGGGAAGAG	278403	110599	CTAATCCATTAAAGAAATTA
189230	21426	GGGAGACCTCCCTTTCAAAC	233817	66013	TACAAAGCAAGATGGGAAGA	278404	110600	ACTAATCCATTAAAGAAATT
189231	21427	GGGGAGACCTCCCTTTCAAA	233818	66014	ATACAAAGCAAGATGGGAAG	278405	110601	TACTAATCCATTAAAGAAAT
189232	21428	AGGGGAGACCTCCCTTTCAA	233819	66015	TATACAAAGCAAGATGGGAA	278406	110602	GTACTAATCCATTAAAGAAA
189233	21429	CAGGGGAGACCTCCCTTTCA	233820	66016	TTATACAAAGCAAGATGGGA	278407	110603	TGTACTAATCCATTAAAGAA
189234	21430	CCAGGGGAGACCTCCCTTTC	233821	66017	TTTATACAAAGCAAGATGGG	278408	110604	CTGTACTAATCCATTAAAGA
189235	21431	TCCAGGGGAGACCTCCCTTT	233822	66018	ATTTATACAAAGCAAGATGG	278409	110605	TCTGTACTAATCCATTAAAG
189236	21432	CTCCAGGGGAGACCTCCCTT	233823	66019	TATTTATACAAAGCAAGATG	278410	110606	TTCTGTACTAATCCATTAAA
189237	21433	ACTCCAGGGGAGACCTCCCT	233824	66020	GTATTTATACAAAGCAAGAT	278411	110607	TTTCTGTACTAATCCATTAA
189238	21434	TACTCCAGGGGAGACCTCCC	233825	66021	TGTATTTATACAAAGCAAGA	278412	110608	TTTTCTGTACTAATCCATTA
189239	21435	TTACTCCAGGGGAGACCTCC	233826	66022	ATGTATTTATACAAAGCAAG	278413	110609	GTTTTCTGTACTAATCCATT
189240	21436	GTTACTCCAGGGGAGACCTC	233827	66023	AATGTATTTATACAAAGCAA	278414	110610	TGTTTTCTGTACTAATCCAT
189241	21437	AGTTACTCCAGGGGAGACCT	233828	66024	AAATGTATTTATACAAAGCA	278415	110611	TTGTTTTCTGTACTAATCCA
189242	21438	AAGTTACTCCAGGGGAGACC	233829	66025	AAAATGTATTTATACAAAGC	278416	110612	TTTGTTTTCTGTACTAATCC
189243	21439	GAAGTTACTCCAGGGGAGAC	233830	66026	GAAAATGTATTTATACAAAG	278417	110613	CTTTGTTTTCTGTACTAATC
189244	21440	GGAAGTTACTCCAGGGGAGA	233831	66027	AGAAAATGTATTTATACAAA	278418	110614	ACTTTGTTTTCTGTACTAAT
189245	21441	CGGAAGTTACTCCAGGGGAG	233832	66028	TAGAAAATGTATTTATACAA	278419	110615	AACTTTGTTTTCTGTACTAA
189246	21442	ACGGAAGTTACTCCAGGGGA	233833	66029	ATAGAAAATGTATTTATACA	278420	110616	GAACTTTGTTTTCTGTACTA
189247	21443	CACGGAAGTTACTCCAGGGG	233834	66030	TATAGAAAATGTATTTATAC	278421	110617	AGAACTTTGTTTTCTGTACT
189248	21444	CCACGGAAGTTACTCCAGGG	233835	66031	TTATAGAAAATGTATTTATA	278422	110618	GAGAACTTTGTTTTCTGTAC
189249	21445	CCCACGGAAGTTACTCCAGG	233836	66032	ATTATAGAAAATGTATTTAT	278423	110619	AGAGAACTTTGTTTTCTGTA
189250	21446	GCCCACGGAAGTTACTCCAG	233837	66033	TATTATAGAAAATGTATTTA	278424	110620	AAGAGAACTTTGTTTTCTGT
189251	21447	CGCCCACGGAAGTTACTCCA	233838	66034	TTATTATAGAAAATGTATTT	278425	110621	GAAGAGAACTTTGTTTTCTG
189252	21448	CCGCCCACGGAAGTTACTCC	233839	66035	CTTATTATAGAAAATGTATT	278426	110622	GGAAGAGAACTTTGTTTTCT
189253	21449	TCCGCCCACGGAAGTTACTC	233840	66036	CCTTATTATAGAAAATGTAT	278427	110623	AGGAAGAGAACTTTGTTTTC
189254	21450	ATCCGCCCACGGAAGTTACT	233841	66037	ACCTTATTATAGAAAATGTA	278428	110624	AAGGAAGAGAACTTTGTTTT
189255	21451	AATCCGCCCACGGAAGTTAC	233842	66038	AACCTTATTATAGAAAATGT	278429	110625	CAAGGAAGAGAACTTTGTTT
189256	21452	GAATCCGCCCACGGAAGTTA	233843	66039	CAACCTTATTATAGAAAATG	278430	110626	TCAAGGAAGAGAACTTTGTT
189257	21453	TGAATCCGCCCACGGAAGTT	233844	66040	ACAACCTTATTATAGAAAAT	278431	110627	TTCAAGGAAGAGAACTTTGT
189258	21454	GTGAATCCGCCCACGGAAGT	233845	66041	TACAACCTTATTATAGAAAA	278432	110628	TTTCAAGGAAGAGAACTTTG

189259	21455	TGTGAATCCGCCCACGGAAG	233846	66042	ATACAACCTTATTATAGAAA	278433	110629	TTTTCAAGGAAGAGAACTTT
189260	21456	GTGTGAATCCGCCCACGGAA	233847	66043	AATACAACCTTATTATAGAA	278434	110630	TTTTTCAAGGAAGAGAACTT
189261	21457	GGTGTGAATCCGCCCACGGA	233848	66044	TAATACAACCTTATTATAGA	278435	110631	GTTTTTCAAGGAAGAGAACT
189262	21458	GGGTGTGAATCCGCCCACGG	233849	66045	GTAATACAACCTTATTATAG	278436	110632	AGTTTTTCAAGGAAGAGAAC
189263	21459	AGGGTGTGAATCCGCCCACG	233850	66046	AGTAATACAACCTTATTATA	278437	110633	CAGTTTTTCAAGGAAGAGAA
189264	21460	CAGGGTGTGAATCCGCCCAC	233851	66047	AAGTAATACAACCTTATTAT	278438	110634	CCAGTTTTTCAAGGAAGAGA
189265	21461	GCAGGGTGTGAATCCGCCCA	233852	66048	AAAGTAATACAACCTTATTA	278439	110635	ACCAGTTTTTCAAGGAAGAG
189266	21462	GGCAGGGTGTGAATCCGCCC	233853	66049	AAAAGTAATACAACCTTATT	278440	110636	TACCAGTTTTTCAAGGAAGA
189267	21463	GGGCAGGGTGTGAATCCGCC	233854	66050	GAAAAGTAATACAACCTTAT	278441	110637	TTACCAGTTTTTCAAGGAAG
189268	21464	TGGGCAGGGTGTGAATCCGC	233855	66051	AGAAAAGTAATACAACCTTA	278442	110638	CTTACCAGTTTTTCAAGGAA
189269	21465	GTGGGCAGGGTGTGAATCCG	233856	66052	GAGAAAAGTAATACAACCTT	278443	110639	ACTTACCAGTTTTTCAAGGA
189270	21466	TGTGGGCAGGGTGTGAATCC	233857	66053	TGAGAAAAGTAATACAACCT	278444	110640	AACTTACCAGTTTTTCAAGG
189271	21467	CTGTGGGCAGGGTGTGAATC	233858	66054	ATGAGAAAAGTAATACAACC	278445	110641	AAACTTACCAGTTTTTCAAG
189272	21468	ACTGTGGGCAGGGTGTGAAT	233859	66055	GATGAGAAAAGTAATACAAC	278446	110642	AAAACTTACCAGTTTTTCAA
189273	21469	GACTGTGGGCAGGGTGTGAA	233860	66056	TGATGAGAAAAGTAATACAA	278447	110643	GAAAACTTACCAGTTTTTCA
189274	21470	GGACTGTGGGCAGGGTGTGA	233861	66057	TTGATGAGAAAAGTAATACA	278448	110644	AGAAAACTTACCAGTTTTTC
189275	21471	AGGACTGTGGGCAGGGTGTG	233862	66058	CTTGATGAGAAAAGTAATAC	278449	110645	AAGAAAACTTACCAGTTTTT
189276	21472	CAGGACTGTGGGCAGGGTGT	233863	66059	TCTTGATGAGAAAAGTAATA	278450	110646	AAAGAAAACTTACCAGTTTT
189277	21473	ACAGGACTGTGGGCAGGGTG	233864	66060	TTCTTGATGAGAAAAGTAAT	278451	110647	CAAAGAAAACTTACCAGTTT
189278	21474	GACAGGACTGTGGGCAGGGT	233865	66061	TTTCTTGATGAGAAAAGTAA	278452	110648	ACAAAGAAAACTTACCAGTT
189279	21475	GGACAGGACTGTGGGCAGGG	233866	66062	ATTTCTTGATGAGAAAAGTA	278453	110649	GACAAAGAAAACTTACCAGT
189280	21476	GGGACAGGACTGTGGGCAGG	233867	66063	TATTTCTTGATGAGAAAAGT	278454	110650	TGACAAAGAAAACTTACCAG
189281	21477	TGGGACAGGACTGTGGGCAG	233868	66064	CTATTTCTTGATGAGAAAAG	278455	110651	CTGACAAAGAAAACTTACCA
189282	21478	CTGGGACAGGACTGTGGGCA	233869	66065	GCTATTTCTTGATGAGAAAA	278456	110652	TCTGACAAAGAAAACTTACC
189283	21479	ACTGGGACAGGACTGTGGGC	233870	66066	TGCTATTTCTTGATGAGAAA	278457	110653	ATCTGACAAAGAAAACTTAC
189284	21480	GACTGGGACAGGACTGTGGG	233871	66067	TTGCTATTTCTTGATGAGAA	278458	110654	TATCTGACAAAGAAAACTTA
189285	21481	TGACTGGGACAGGACTGTGG	233872	66068	TTTGCTATTTCTTGATGAGA	278459	110655	TTATCTGACAAAGAAAACTT
189286	21482	CTGACTGGGACAGGACTGTG	233873	66069	CTTTGCTATTTCTTGATGAG	278460	110656	CTTATCTGACAAAGAAAACT
189287	21483	GCTGACTGGGACAGGACTGT	233874	66070	ACTTTGCTATTTCTTGATGA	278461	110657	CCTTATCTGACAAAGAAAAC
189288	21484	GGCTGACTGGGACAGGACTG	233875	66071	TACTTTGCTATTTCTTGATG	278462	110658	TCCTTATCTGACAAAGAAAA
189289	21485	GGGCTGACTGGGACAGGACT	233876	66072	GTACTTTGCTATTTCTTGAT	278463	110659	CTCCTTATCTGACAAAGAAA
189290	21486	TGGGCTGACTGGGACAGGAC	233877	66073	AGTACTTTGCTATTTCTTGA	278464	110660	TCTCCTTATCTGACAAAGAA
189291	21487	GTGGGCTGACTGGGACAGGA	233878	66074	CAGTACTTTGCTATTTCTTG	278465	110661	CTCTCCTTATCTGACAAAGA
189292	21488	GGTGGGCTGACTGGGACAGG	233879	66075	ACAGTACTTTGCTATTTCTT	278466	110662	ACTCTCCTTATCTGACAAAG
189293	21489	TGGTGGGCTGACTGGGACAG	233880	66076	AACAGTACTTTGCTATTTCT	278467	110663	AACTCTCCTTATCTGACAAA
189294	21490	ATGGTGGGCTGACTGGGACA	233881	66077	AAACAGTACTTTGCTATTTC	278468	110664	TAACTCTCCTTATCTGACAA
189295	21491	CATGGTGGGCTGACTGGGAC	233882	66078	AAAACAGTACTTTGCTATTT	278469	110665	TTAACTCTCCTTATCTGACA
189296	21492	CCATGGTGGGCTGACTGGGA	233883	66079	TAAAACAGTACTTTGCTATT	278470	110666	TTTAACTCTCCTTATCTGAC
189297	21493	ACCATGGTGGGCTGACTGGG	233884	66080	GTAAAACAGTACTTTGCTAT	278471	110667	ATTTAACTCTCCTTATCTGA
189298	21494	CACCATGGTGGGCTGACTGG	233885	66081	AGTAAAACAGTACTTTGCTA	278472	110668	TATTTAACTCTCCTTATCTG
189299	21495	CCACCATGGTGGGCTGACTG	233886	66082	GAGTAAAACAGTACTTTGCT	278473	110669	TTATTTAACTCTCCTTATCT
189300	21496	ACCACCATGGTGGGCTGACT	233887	66083	TGAGTAAAACAGTACTTTGC	278474	110670	GTTATTTAACTCTCCTTATC
189301	21497	GACCACCATGGTGGGCTGAC	233888	66084	TTGAGTAAAACAGTACTTTG	278475	110671	GGTTATTTAACTCTCCTTAT
189302	21498	AGACCACCATGGTGGGCTGA	233889	66085	TTTGAGTAAAACAGTACTTT	278476	110672	GGGTTATTTAACTCTCCTTA
189303	21499	GAGACCACCATGGTGGGCTG	233890	66086	TTTTGAGTAAAACAGTACTT	278477	110673	TGGGTTATTTAACTCTCCTT
189304	21500	GGAGACCACCATGGTGGGCT	233891	66087	ATTTTGAGTAAAACAGTACT	278478	110674	ATGGGTTATTTAACTCTCCT
189305	21501	CGGAGACCACCATGGTGGGC	233892	66088	TATTTTGAGTAAAACAGTAC	278479	110675	CATGGGTTATTTAACTCTCC
189306	21502	CCGGAGACCACCATGGTGGG	233893	66089	ATATTTTGAGTAAAACAGTA	278480	110676	TCATGGGTTATTTAACTCTC
189307	21503	ACCGGAGACCACCATGGTGG	233894	66090	CATATTTTGAGTAAAACAGT	278481	110677	GTCATGGGTTATTTAACTCT
189308	21504	AACCGGAGACCACCATGGTG	233895	66091	TCATATTTTGAGTAAAACAG	278482	110678	TGTCATGGGTTATTTAACTC
189309	21505	GAACCGGAGACCACCATGGT	233896	66092	TTCATATTTTGAGTAAAACA	278483	110679	ATGTCATGGGTTATTTAACT
189310	21506	GGAACCGGAGACCACCATGG	233897	66093	ATTCATATTTTGAGTAAAAC	278484	110680	AATGTCATGGGTTATTTAAC
189311	21507	AGGAACCGGAGACCACCATG	233898	66094	TATTCATATTTTGAGTAAAA	278485	110681	AAATGTCATGGGTTATTTAA
189312	21508	GAGGAACCGGAGACCACCAT	233899	66095	CTATTCATATTTTGAGTAAA	278486	110682	GAAATGTCATGGGTTATTTA
189313	21509	GGAGGAACCGGAGACCACCA	233900	66096	TCTATTCATATTTTGAGTAA	278487	110683	GGAAATGTCATGGGTTATTT
189314	21510	TGGAGGAACCGGAGACCACC	233901	66097	CTCTATTCATATTTTGAGTA	278488	110684	GGGAAATGTCATGGGTTATT
189315	21511	CTGGAGGAACCGGAGACCAC	233902	66098	GCTCTATTCATATTTTGAGT	278489	110685	AGGGAAATGTCATGGGTTAT
189316	21512	TCTGGAGGAACCGGAGACCA	233903	66099	GGCTCTATTCATATTTTGAG	278490	110686	AAGGGAAATGTCATGGGTTA
189317	21513	TTCTGGAGGAACCGGAGACC	233904	66100	TGGCTCTATTCATATTTTGA	278491	110687	AAAGGGAAATGTCATGGGTT
189318	21514	ATTCTGGAGGAACCGGAGAC	233905	66101	CTGGCTCTATTCATATTTTG	278492	110688	AAAAGGGAAATGTCATGGGT
189319	21515	AATTCTGGAGGAACCGGAGA	233906	66102	CCTGGCTCTATTCATATTTT	278493	110689	AAAAAGGGAAATGTCATGGG
189320	21516	GAATTCTGGAGGAACCGGAG	233907	66103	GCCTGGCTCTATTCATATTT	278494	110690	CAAAAAGGGAAATGTCATGG
189321	21517	GGAATTCTGGAGGAACCGGA	233908	66104	TGCCTGGCTCTATTCATATT	278495	110691	GCAAAAAGGGAAATGTCATG
189322	21518	GGGAATTCTGGAGGAACCGG	233909	66105	ATGCCTGGCTCTATTCATAT	278496	110692	GGCAAAAAGGGAAATGTCAT
189323	21519	CGGGAATTCTGGAGGAACCG	233910	66106	CATGCCTGGCTCTATTCATA	278497	110693	AGGCAAAAAGGGAAATGTCA
189324	21520	GCGGGAATTCTGGAGGAACC	233911	66107	CCATGCCTGGCTCTATTCAT	278498	110694	GAGGCAAAAAGGGAAATGTC
189325	21521	AGCGGGAATTCTGGAGGAAC	233912	66108	ACCATGCCTGGCTCTATTCA	278499	110695	CGAGGCAAAAAGGGAAATGT
189326	21522	AAGCGGGAATTCTGGAGGAA	233913	66109	CACCATGCCTGGCTCTATTC	278500	110696	CCGAGGCAAAAAGGGAAATG
189327	21523	AAAGCGGGAATTCTGGAGGA	233914	66110	CCACCATGCCTGGCTCTATT	278501	110697	GCCGAGGCAAAAAGGGAAAT
189328	21524	AAAAGCGGGAATTCTGGAGG	233915	66111	GCCACCATGCCTGGCTCTAT	278502	110698	AGCCGAGGCAAAAAGGGAAA
189329	21525	GAAAAGCGGGAATTCTGGAG	233916	66112	TGCCACCATGCCTGGCTCTA	278503	110699	AAGCCGAGGCAAAAAGGGAA
189330	21526	TGAAAAGCGGGAATTCTGGA	233917	66113	CTGCCACCATGCCTGGCTCT	278504	110700	GAAGCCGAGGCAAAAAGGGA

189331	21527	CTGAAAAGCGGGAATTCTGG	233918	66114	GCTGCCACCATGCCTGGCTC	278505	110701	GGAAGCCGAGGCAAAAAGGG
189332	21528	GCTGAAAAGCGGGAATTCTG	233919	66115	AGCTGCCACCATGCCTGGCT	278506	110702	TGGAAGCCGAGGCAAAAAGG
189333	21529	AGCTGAAAAGCGGGAATTCT	233920	66116	AAGCTGCCACCATGCCTGGC	278507	110703	CTGGAAGCCGAGGCAAAAAG
189334	21530	GAGCTGAAAAGCGGGAATTC	233921	66117	TAAGCTGCCACCATGCCTGG	278508	110704	CCTGGAAGCCGAGGCAAAAA
189335	21531	TGAGCTGAAAAGCGGGAATT	233922	66118	ATAAGCTGCCACCATGCCTG	278509	110705	TCCTGGAAGCCGAGGCAAAA
189336	21532	ATGAGCTGAAAAGCGGGAAT	233923	66119	CATAAGCTGCCACCATGCCT	278510	110706	TTCCTGGAAGCCGAGGCAAA
189337	21533	GATGAGCTGAAAAGCGGGAA	233924	66120	GCATAAGCTGCCACCATGCC	278511	110707	CTTCCTGGAAGCCGAGGCAA
189338	21534	GGATGAGCTGAAAAGCGGGA	233925	66121	GGCATAAGCTGCCACCATGC	278512	110708	GCTTCCTGGAAGCCGAGGCA
189339	21535	GGGATGAGCTGAAAAGCGGG	233926	66122	AGGCATAAGCTGCCACCATG	278513	110709	AGCTTCCTGGAAGCCGAGGC
189340	21536	GGGGATGAGCTGAAAAGCGG	233927	66123	CAGGCATAAGCTGCCACCAT	278514	110710	GAGCTTCCTGGAAGCCGAGG
189341	21537	TGGGGATGAGCTGAAAAGCG	233928	66124	ACAGGCATAAGCTGCCACCA	278515	110711	TGAGCTTCCTGGAAGCCGAG
189342	21538	GTGGGGATGAGCTGAAAAGC	233929	66125	TACAGGCATAAGCTGCCACC	278516	110712	TTGAGCTTCCTGGAAGCCGA
189343	21539	TGTGGGGATGAGCTGAAAAG	233930	66126	TTACAGGCATAAGCTGCCAC	278517	110713	TTTGAGCTTCCTGGAAGCCG
189344	21540	ATGTGGGGATGAGCTGAAAA	233931	66127	ATTACAGGCATAAGCTGCCA	278518	110714	CTTTGAGCTTCCTGGAAGCC
189345	21541	AATGTGGGGATGAGCTGAAA	233932	66128	GATTACAGGCATAAGCTGCC	278519	110715	ACTTTGAGCTTCCTGGAAGC
189346	21542	GAATGTGGGGATGAGCTGAA	233933	66129	GGATTACAGGCATAAGCTGC	278520	110716	AACTTTGAGCTTCCTGGAAG
189347	21543	GGAATGTGGGGATGAGCTGA	233934	66130	GGGATTACAGGCATAAGCTG	278521	110717	TAACTTTGAGCTTCCTGGAA
189348	21544	GGGAATGTGGGGATGAGCTG	233935	66131	TGGGATTACAGGCATAAGCT	278522	110718	TTAACTTTGAGCTTCCTGGA
189349	21545	CGGGAATGTGGGGATGAGCT	233936	66132	TTGGGATTACAGGCATAAGC	278523	110719	TTTAACTTTGAGCTTCCTGG
189350	21546	CCGGGAATGTGGGGATGAGC	233937	66133	GTTGGGATTACAGGCATAAG	278524	110720	ATTTAACTTTGAGCTTCCTG
189351	21547	TCCGGGAATGTGGGGATGAG	233938	66134	TGTTGGGATTACAGGCATAA	278525	110721	CATTTAACTTTGAGCTTCCT
189352	21548	CTCCGGGAATGTGGGGATGA	233939	66135	GTGTTGGGATTACAGGCATA	278526	110722	ACATTTAACTTTGAGCTTCC
189353	21549	CCTCCGGGAATGTGGGGATG	233940	66136	AGTGTTGGGATTACAGGCAT	278527	110723	TACATTTAACTTTGAGCTTC
189354	21550	CCCTCCGGGAATGTGGGGAT	233941	66137	AAGTGTTGGGATTACAGGCA	278528	110724	TTACATTTAACTTTGAGCTT
189355	21551	TCCCTCCGGGAATGTGGGGA	233942	66138	AAAGTGTTGGGATTACAGGC	278529	110725	ATTACATTTAACTTTGAGCT
189356	21552	GTCCCTCCGGGAATGTGGGG	233943	66139	CAAAGTGTTGGGATTACAGG	278530	110726	CATTACATTTAACTTTGAGC
189357	21553	AGTCCCTCCGGGAATGTGGG	233944	66140	TCAAAGTGTTGGGATTACAG	278531	110727	TCATTACATTTAACTTTGAG
189358	21554	CAGTCCCTCCGGGAATGTGG	233945	66141	CTCAAAGTGTTGGGATTACA	278532	110728	ATCATTACATTTAACTTTGA
189359	21555	TCAGTCCCTCCGGGAATGTG	233946	66142	TCTCAAAGTGTTGGGATTAC	278533	110729	GATCATTACATTTAACTTTG
189360	21556	CTCAGTCCCTCCGGGAATGT	233947	66143	CTCTCAAAGTGTTGGGATTA	278534	110730	TGATCATTACATTTAACTTT
189361	21557	TCTCAGTCCCTCCGGGAATG	233948	66144	CCTCTCAAAGTGTTGGGATT	278535	110731	GTGATCATTACATTTAACTT
189362	21558	CTCTCAGTCCCTCCGGGAAT	233949	66145	GCCTCTCAAAGTGTTGGGAT	278536	110732	AGTGATCATTACATTTAACT
189363	21559	GCTCTCAGTCCCTCCGGGAA	233950	66146	CGCCTCTCAAAGTGTTGGGA	278537	110733	GAGTGATCATTACATTTAAC
189364	21560	CGCTCTCAGTCCCTCCGGGA	233951	66147	CCGCCTCTCAAAGTGTTGGG	278538	110734	AGAGTGATCATTACATTTAA
189365	21561	GCGCTCTCAGTCCCTCCGGG	233952	66148	TCCGCCTCTCAAAGTGTTGG	278539	110735	AAGAGTGATCATTACATTTA
189366	21562	TGCGCTCTCAGTCCCTCCGG	233953	66149	ATCCGCCTCTCAAAGTGTTG	278540	110736	CAAGAGTGATCATTACATTT
189367	21563	CTGCGCTCTCAGTCCCTCCG	233954	66150	TATCCGCCTCTCAAAGTGTT	278541	110737	ACAAGAGTGATCATTACATT
189368	21564	GCTGCGCTCTCAGTCCCTCC	233955	66151	ATATCCGCCTCTCAAAGTGT	278542	110738	TACAAGAGTGATCATTACAT
189369	21565	GGCTGCGCTCTCAGTCCCTC	233956	66152	CATATCCGCCTCTCAAAGTG	278543	110739	TTACAAGAGTGATCATTACA
189370	21566	GGGCTGCGCTCTCAGTCCCT	233957	66153	CCATATCCGCCTCTCAAAGT	278544	110740	ATTACAAGAGTGATCATTAC
189371	21567	GGGGCTGCGCTCTCAGTCCC	233958	66154	CCCATATCCGCCTCTCAAAG	278545	110741	AATTACAAGAGTGATCATTA
189372	21568	TGGGGCTGCGCTCTCAGTCC	233959	66155	TCCCATATCCGCCTCTCAAA	278546	110742	TAATTACAAGAGTGATCATT
189373	21569	CTGGGGCTGCGCTCTCAGTC	233960	66156	CTCCCATATCCGCCTCTCAA	278547	110743	ATAATTACAAGAGTGATCAT
189374	21570	CCTGGGGCTGCGCTCTCAGT	233961	66157	CCTCCCATATCCGCCTCTCA	278548	110744	GATAATTACAAGAGTGATCA
189375	21571	CCCTGGGGCTGCGCTCTCAG	233962	66158	TCCTCCCATATCCGCCTCTC	278549	110745	TGATAATTACAAGAGTGATC
189376	21572	GCCCTGGGGCTGCGCTCTCA	233963	66159	ATCCTCCCATATCCGCCTCT	278550	110746	CTGATAATTACAAGAGTGAT
189377	21573	GGCCCTGGGGCTGCGCTCTC	233964	66160	GATCCTCCCATATCCGCCTC	278551	110747	ACTGATAATTACAAGAGTGA
189378	21574	GGGCCCTGGGGCTGCGCTCT	233965	66161	TGATCCTCCCATATCCGCCT	278552	110748	CACTGATAATTACAAGAGTG
189379	21575	AGGGCCCTGGGGCTGCGCTC	233966	66162	GTGATCCTCCCATATCCGCC	278553	110749	ACACTGATAATTACAAGAGT
189380	21576	CAGGGCCCTGGGGCTGCGCT	233967	66163	AGTGATCCTCCCATATCCGC	278554	110750	AACACTGATAATTACAAGAG
189381	21577	GCAGGGCCCTGGGGCTGCGC	233968	66164	AAGTGATCCTCCCATATCCG	278555	110751	CAACACTGATAATTACAAGA
189382	21578	AGCAGGGCCCTGGGGCTGCG	233969	66165	AAAGTGATCCTCCCATATCC	278556	110752	TCAACACTGATAATTACAAG
189383	21579	GAGCAGGGCCCTGGGGCTGC	233970	66166	TAAAGTGATCCTCCCATATC	278557	110753	ATCAACACTGATAATTACAA
189384	21580	AGAGCAGGGCCCTGGGGCTG	233971	66167	CTAAAGTGATCCTCCCATAT	278558	110754	CATCAACACTGATAATTACA
189385	21581	AAGAGCAGGGCCCTGGGGCT	233972	66168	GCTAAAGTGATCCTCCCATA	278559	110755	GCATCAACACTGATAATTAC
189386	21582	AAAGAGCAGGGCCCTGGGGC	233973	66169	GGCTAAAGTGATCCTCCCAT	278560	110756	GGCATCAACACTGATAATTA
189387	21583	CAAAGAGCAGGGCCCTGGGG	233974	66170	GGGCTAAAGTGATCCTCCCA	278561	110757	GGGCATCAACACTGATAATT
189388	21584	CCAAAGAGCAGGGCCCTGGG	233975	66171	TGGGCTAAAGTGATCCTCCC	278562	110758	AGGGCATCAACACTGATAAT
189389	21585	CCCAAAGAGCAGGGCCCTGG	233976	66172	CTGGGCTAAAGTGATCCTCC	278563	110759	AAGGGCATCAACACTGATAA
189390	21586	CCCCAAAGAGCAGGGCCCTG	233977	66173	CCTGGGCTAAAGTGATCCTC	278564	110760	GAAGGGCATCAACACTGATA
189391	21587	CCCCCAAAGAGCAGGGCCCT	233978	66174	TCCTGGGCTAAAGTGATCCT	278565	110761	GGAAGGGCATCAACACTGAT
189392	21588	GCCCCCAAAGAGCAGGGCCC	233979	66175	CTCCTGGGCTAAAGTGATCC	278566	110762	GGGAAGGGCATCAACACTGA
189393	21589	GGCCCCCAAAGAGCAGGGCC	233980	66176	ACTCCTGGGCTAAAGTGATC	278567	110763	AGGGAAGGGCATCAACACTG
189394	21590	CGGCCCCCAAAGAGCAGGGC	233981	66177	AACTCCTGGGCTAAAGTGAT	278568	110764	AAGGGAAGGGCATCAACACT
189395	21591	ACGGCCCCCAAAGAGCAGGG	233982	66178	AAACTCCTGGGCTAAAGTGA	278569	110765	GAAGGGAAGGGCATCAACAC
189396	21592	GACGGCCCCCAAAGAGCAGG	233983	66179	CAAACTCCTGGGCTAAAGTG	278570	110766	AGAAGGGAAGGGCATCAACA
189397	21593	AGACGGCCCCCAAAGAGCAG	233984	66180	TCAAACTCCTGGGCTAAAGT	278571	110767	AAGAAGGGAAGGGCATCAAC
189398	21594	GAGACGGCCCCCAAAGAGCA	233985	66181	CTCAAACTCCTGGGCTAAAG	278572	110768	GAAGAAGGGAAGGGCATCAA
189399	21595	AGAGACGGCCCCCAAAGAGC	233986	66182	TCTCAAACTCCTGGGCTAAA	278573	110769	AGAAGAAGGGAAGGGCATCA
189400	21596	TAGAGACGGCCCCCAAAGAG	233987	66183	GTCTCAAACTCCTGGGCTAA	278574	110770	TAGAAGAAGGGAAGGGCATC
189401	21597	GTAGAGACGGCCCCCAAAGA	233988	66184	GGTCTCAAACTCCTGGGCTA	278575	110771	TTAGAAGAAGGGAAGGGCAT
189402	21598	TGTAGAGACGGCCCCCAAAG	233989	66185	TGGTCTCAAACTCCTGGGCT	278576	110772	ATTAGAAGAAGGGAAGGGCA

189403	21599	GTGTAGAGACGGCCCCCAAA	233990	66186	CTGGTCTCAAACTCCTGGGC	278577	110773	CATTAGAAGAAGGGAAGGGC
189404	21600	GGTGTAGAGACGGCCCCCAA	233991	66187	GCTGGTCTCAAACTCCTGGG	278578	110774	ACATTAGAAGAAGGGAAGGG
189405	21601	GGGTGTAGAGACGGCCCCCA	233992	66188	GGCTGGTCTCAAACTCCTGG	278579	110775	AACATTAGAAGAAGGGAAGG
189406	21602	TGGGTGTAGAGACGGCCCCC	233993	66189	AGGCTGGTCTCAAACTCCTG	278580	110776	TAACATTAGAAGAAGGGAAG
189407	21603	CTGGGTGTAGAGACGGCCCC	233994	66190	CAGGCTGGTCTCAAACTCCT	278581	110777	GTAACATTAGAAGAAGGGAA
189408	21604	TCTGGGTGTAGAGACGGCCC	233995	66191	CCAGGCTGGTCTCAAACTCC	278582	110778	AGTAACATTAGAAGAAGGGA
189409	21605	CTCTGGGTGTAGAGACGGCC	233996	66192	CCCAGGCTGGTCTCAAACTC	278583	110779	GAGTAACATTAGAAGAAGGG
189410	21606	TCTCTGGGTGTAGAGACGGC	233997	66193	GCCCAGGCTGGTCTCAAACT	278584	110780	AGAGTAACATTAGAAGAAGG
189411	21607	TTCTCTGGGTGTAGAGACGG	233998	66194	TGCCCAGGCTGGTCTCAAAC	278585	110781	AAGAGTAACATTAGAAGAAG
189412	21608	CTTCTCTGGGTGTAGAGACG	233999	66195	TTGCCCAGGCTGGTCTCAAA	278586	110782	AAAGAGTAACATTAGAAGAA
189413	21609	GCTTCTCTGGGTGTAGAGAC	234000	66196	GTTGCCCAGGCTGGTCTCAA	278587	110783	TAAAGAGTAACATTAGAAGA
189414	21610	TGCTTCTCTGGGTGTAGAGA	234001	66197	TGTTGCCCAGGCTGGTCTCA	278588	110784	GTAAAGAGTAACATTAGAAG
189415	21611	CTGCTTCTCTGGGTGTAGAG	234002	66198	ATGTTGCCCAGGCTGGTCTC	278589	110785	TGTAAAGAGTAACATTAGAA
189416	21612	GCTGCTTCTCTGGGTGTAGA	234003	66199	TATGTTGCCCAGGCTGGTCT	278590	110786	ATGTAAAGAGTAACATTAGA
189417	21613	TGCTGCTTCTCTGGGTGTAG	234004	66200	CTATGTTGCCCAGGCTGGTC	278591	110787	AATGTAAAGAGTAACATTAG
189418	21614	TTGCTGCTTCTCTGGGTGTA	234005	66201	ACTATGTTGCCCAGGCTGGT	278592	110788	AAATGTAAAGAGTAACATTA
189419	21615	CTTGCTGCTTCTCTGGGTGT	234006	66202	CACTATGTTGCCCAGGCTGG	278593	110789	AAAATGTAAAGAGTAACATT
189420	21616	CCTTGCTGCTTCTCTGGGTG	234007	66203	TCACTATGTTGCCCAGGCTG	278594	110790	GAAAATGTAAAGAGTAACAT
189421	21617	GCCTTGCTGCTTCTCTGGGT	234008	66204	CTCACTATGTTGCCCAGGCT	278595	110791	GGAAAATGTAAAGAGTAACA
189422	21618	TGCCTTGCTGCTTCTCTGGG	234009	66205	TCTCACTATGTTGCCCAGGC	278596	110792	AGGAAAATGTAAAGAGTAAC
189423	21619	ATGCCTTGCTGCTTCTCTGG	234010	66206	GTCTCACTATGTTGCCCAGG	278597	110793	CAGGAAAATGTAAAGAGTAA
189424	21620	AATGCCTTGCTGCTTCTCTG	234011	66207	GGTCTCACTATGTTGCCCAG	278598	110794	GCAGGAAAATGTAAAGAGTA
189425	21621	GAATGCCTTGCTGCTTCTCT	234012	66208	GGGTCTCACTATGTTGCCCA	278599	110795	AGCAGGAAAATGTAAAGAGT
189426	21622	GGAATGCCTTGCTGCTTCTC	234013	66209	GGGGTCTCACTATGTTGCCC	278600	110796	AAGCAGGAAAATGTAAAGAG
189427	21623	AGGAATGCCTTGCTGCTTCT	234014	66210	GGGGGTCTCACTATGTTGCC	278601	110797	AAAGCAGGAAAATGTAAAGA
189428	21624	TAGGAATGCCTTGCTGCTTC	234015	66211	CGGGGGTCTCACTATGTTGC	278602	110798	TAAAGCAGGAAAATGTAAAG
189429	21625	CTAGGAATGCCTTGCTGCTT	234016	66212	ACGGGGGTCTCACTATGTTG	278603	110799	ATAAAGCAGGAAAATGTAAA
189430	21626	CCTAGGAATGCCTTGCTGCT	234017	66213	GACGGGGGTCTCACTATGTT	278604	110800	AATAAAGCAGGAAAATGTAA
189431	21627	ACCTAGGAATGCCTTGCTGC	234018	66214	GGACGGGGGTCTCACTATGT	278605	110801	TAATAAAGCAGGAAAATGTA
189432	21628	AACCTAGGAATGCCTTGCTG	234019	66215	GGGACGGGGGTCTCACTATG	278606	110802	ATAATAAAGCAGGAAAATGT
189433	21629	AAACCTAGGAATGCCTTGCT	234020	66216	GGGGACGGGGGTCTCACTAT	278607	110803	AATAATAAAGCAGGAAAATG
189434	21630	GAAACCTAGGAATGCCTTGC	234021	66217	TGGGGACGGGGGTCTCACTA	278608	110804	CAATAATAAAGCAGGAAAAT
189435	21631	AGAAACCTAGGAATGCCTTG	234022	66218	GTGGGGACGGGGGTCTCACT	278609	110805	ACAATAATAAAGCAGGAAAA
189436	21632	GAGAAACCTAGGAATGCCTT	234023	66219	AGTGGGGACGGGGGTCTCAC	278610	110806	CACAATAATAAAGCAGGAAA
189437	21633	AGAGAAACCTAGGAATGCCT	234024	66220	GAGTGGGGACGGGGGTCTCA	278611	110807	ACACAATAATAAAGCAGGAA
189438	21634	AAGAGAAACCTAGGAATGCC	234025	66221	GGAGTGGGGACGGGGGTCTC	278612	110808	CACACAATAATAAAGCAGGA
189439	21635	AAAGAGAAACCTAGGAATGC	234026	66222	GGGAGTGGGGACGGGGGTCT	278613	110809	ACACACAATAATAAAGCAGG
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189441	21637	TGAAAGAGAAACCTAGGAAT	234028	66224	GGGGGAGTGGGGACGGGGGT	278615	110811	ACACACACAATAATAAAGCA
189442	21638	CTGAAAGAGAAACCTAGGAA	234029	66225	TGGGGGAGTGGGGACGGGGG	278616	110812	AACACACACAATAATAAAGC
189443	21639	TCTGAAAGAGAAACCTAGGA	234030	66226	TTGGGGGAGTGGGGACGGGG	278617	110813	AAACACACACAATAATAAAG
189444	21640	ATCTGAAAGAGAAACCTAGG	234031	66227	TTTGGGGGAGTGGGGACGGG	278618	110814	AAAACACACACAATAATAAA
189445	21641	CATCTGAAAGAGAAACCTAG	234032	66228	CTTTGGGGGAGTGGGGACGG	278619	110815	GAAAACACACACAATAATAA
189446	21642	GCATCTGAAAGAGAAACCTA	234033	66229	TCTTTGGGGGAGTGGGGACG	278620	110816	AGAAAACACACACAATAATA
189447	21643	TGCATCTGAAAGAGAAACCT	234034	66230	TTCTTTGGGGGAGTGGGGAC	278621	110817	TAGAAAACACACACAATAAT
189448	21644	CTGCATCTGAAAGAGAAACC	234035	66231	TTTCTTTGGGGGAGTGGGGA	278622	110818	TTAGAAAACACACACAATAA
189449	21645	TCTGCATCTGAAAGAGAAAC	234036	66232	TTTTCTTTGGGGGAGTGGGG	278623	110819	ATTAGAAAACACACACAATA
189450	21646	TTCTGCATCTGAAAGAGAAA	234037	66233	GTTTTCTTTGGGGGAGTGGG	278624	110820	AATTAGAAAACACACACAAT
189451	21647	GTTCTGCATCTGAAAGAGAA	234038	66234	GGTTTTCTTTGGGGGAGTGG	278625	110821	GAATTAGAAAACACACACAA
189452	21648	AGTTCTGCATCTGAAAGAGA	234039	66235	GGGTTTTCTTTGGGGGAGTG	278626	110822	AGAATTAGAAAACACACACA
189453	21649	AAGTTCTGCATCTGAAAGAG	234040	66236	TGGGTTTTCTTTGGGGGAGT	278627	110823	TAGAATTAGAAAACACACAC
189454	21650	GAAGTTCTGCATCTGAAAGA	234041	66237	GTGGGTTTTCTTTGGGGGAG	278628	110824	TTAGAATTAGAAAACACACA
189455	21651	TGAAGTTCTGCATCTGAAAG	234042	66238	TGTGGGTTTTCTTTGGGGGA	278629	110825	CTTAGAATTAGAAAACACAC
189456	21652	CTGAAGTTCTGCATCTGAAA	234043	66239	TTGTGGGTTTTCTTTGGGGG	278630	110826	GCTTAGAATTAGAAAACACA
189457	21653	ACTGAAGTTCTGCATCTGAA	234044	66240	TTTGTGGGTTTTCTTTGGGG	278631	110827	AGCTTAGAATTAGAAAACAC
189458	21654	CACTGAAGTTCTGCATCTGA	234045	66241	CTTTGTGGGTTTTCTTTGGG	278632	110828	CAGCTTAGAATTAGAAAACA
189459	21655	ACACTGAAGTTCTGCATCTG	234046	66242	GCTTTGTGGGTTTTCTTTGG	278633	110829	ACAGCTTAGAATTAGAAAAC
189460	21656	AACACTGAAGTTCTGCATCT	234047	66243	TGCTTTGTGGGTTTTCTTTG	278634	110830	AACAGCTTAGAATTAGAAAA
189461	21657	GAACACTGAAGTTCTGCATC	234048	66244	ATGCTTTGTGGGTTTTCTTT	278635	110831	GAACAGCTTAGAATTAGAAA
189462	21658	TGAACACTGAAGTTCTGCAT	234049	66245	AATGCTTTGTGGGTTTTCTT	278636	110832	GGAACAGCTTAGAATTAGAA
189463	21659	CTGAACACTGAAGTTCTGCA	234050	66246	AAATGCTTTGTGGGTTTTCT	278637	110833	GGGAACAGCTTAGAATTAGA
189464	21660	TCTGAACACTGAAGTTCTGC	234051	66247	TAAATGCTTTGTGGGTTTTC	278638	110834	TGGGAACAGCTTAGAATTAG
189465	21661	CTCTGAACACTGAAGTTCTG	234052	66248	ATAAATGCTTTGTGGGTTTT	278639	110835	GTGGGAACAGCTTAGAATTA
189466	21662	TCTCTGAACACTGAAGTTCT	234053	66249	GATAAATGCTTTGTGGGTTT	278640	110836	AGTGGGAACAGCTTAGAATT
189467	21663	ATCTCTGAACACTGAAGTTC	234054	66250	GGATAAATGCTTTGTGGGTT	278641	110837	GAGTGGGAACAGCTTAGAAT
189468	21664	CATCTCTGAACACTGAAGTT	234055	66251	AGGATAAATGCTTTGTGGGT	278642	110838	GGAGTGGGAACAGCTTAGAA
189469	21665	ACATCTCTGAACACTGAAGT	234056	66252	CAGGATAAATGCTTTGTGGG	278643	110839	AGGAGTGGGAACAGCTTAGA
189470	21666	AACATCTCTGAACACTGAAG	234057	66253	CCAGGATAAATGCTTTGTGG	278644	110840	AAGGAGTGGGAACAGCTTAG
189471	21667	GAACATCTCTGAACACTGAA	234058	66254	TCCAGGATAAATGCTTTGTG	278645	110841	AAAGGAGTGGGAACAGCTTA
189472	21668	GGAACATCTCTGAACACTGA	234059	66255	ATCCAGGATAAATGCTTTGT	278646	110842	GAAAGGAGTGGGAACAGCTT
189473	21669	GGGAACATCTCTGAACACTG	234060	66256	AATCCAGGATAAATGCTTTG	278647	110843	AGAAAGGAGTGGGAACAGCT
189474	21670	TGGGAACATCTCTGAACACT	234061	66257	TAATCCAGGATAAATGCTTT	278648	110844	CAGAAAGGAGTGGGAACAGC

189475	21671	GTGGGAACATCTCTGAACAC	234062	66258	ATAATCCAGGATAAATGCTT	278649	110845	TCAGAAAGGAGTGGGAACAG
189476	21672	AGTGGGAACATCTCTGAACA	234063	66259	AATAATCCAGGATAAATGCT	278650	110846	TTCAGAAAGGAGTGGGAACA
189477	21673	CAGTGGGAACATCTCTGAAC	234064	66260	GAATAATCCAGGATAAATGC	278651	110847	TTTCAGAAAGGAGTGGGAAC
189478	21674	CCAGTGGGAACATCTCTGAA	234065	66261	TGAATAATCCAGGATAAATG	278652	110848	CTTTCAGAAAGGAGTGGGAA
189479	21675	ACCAGTGGGAACATCTCTGA	234066	66262	GTGAATAATCCAGGATAAAT	278653	110849	GCTTTCAGAAAGGAGTGGGA
189480	21676	GACCAGTGGGAACATCTCTG	234067	66263	TGTGAATAATCCAGGATAAA	278654	110850	TGCTTTCAGAAAGGAGTGGG
189481	21677	GGACCAGTGGGAACATCTCT	234068	66264	CTGTGAATAATCCAGGATAA	278655	110851	CTGCTTTCAGAAAGGAGTGG
189482	21678	AGGACCAGTGGGAACATCTC	234069	66265	CCTGTGAATAATCCAGGATA	278656	110852	CCTGCTTTCAGAAAGGAGTG
189483	21679	CAGGACCAGTGGGAACATCT	234070	66266	CCCTGTGAATAATCCAGGAT	278657	110853	GCCTGCTTTCAGAAAGGAGT
189484	21680	TCAGGACCAGTGGGAACATC	234071	66267	CCCCTGTGAATAATCCAGGA	278658	110854	TGCCTGCTTTCAGAAAGGAG
189485	21681	CTCAGGACCAGTGGGAACAT	234072	66268	GCCCCTGTGAATAATCCAGG	278659	110855	TTGCCTGCTTTCAGAAAGGA
189486	21682	TCTCAGGACCAGTGGGAACA	234073	66269	GGCCCCTGTGAATAATCCAG	278660	110856	TTTGCCTGCTTTCAGAAAGG
189487	21683	CTCTCAGGACCAGTGGGAAC	234074	66270	TGGCCCCTGTGAATAATCCA	278661	110857	ATTTGCCTGCTTTCAGAAAG
189488	21684	CCTCTCAGGACCAGTGGGAA	234075	66271	TTGGCCCCTGTGAATAATCC	278662	110858	GATTTGCCTGCTTTCAGAAA
189489	21685	CCCTCTCAGGACCAGTGGGA	234076	66272	TTTGGCCCCTGTGAATAATC	278663	110859	AGATTTGCCTGCTTTCAGAA
189490	21686	GCCCTCTCAGGACCAGTGGG	234077	66273	TTTTGGCCCCTGTGAATAAT	278664	110860	AAGATTTGCCTGCTTTCAGA
189491	21687	AGCCCTCTCAGGACCAGTGG	234078	66274	TTTTTGGCCCCTGTGAATAA	278665	110861	GAAGATTTGCCTGCTTTCAG
189492	21688	GAGCCCTCTCAGGACCAGTG	234079	66275	TTTTTTGGCCCCTGTGAATA	278666	110862	AGAAGATTTGCCTGCTTTCA
189493	21689	TGAGCCCTCTCAGGACCAGT	234080	66276	TTTTTTTGGCCCCTGTGAAT	278667	110863	TAGAAGATTTGCCTGCTTTC
189494	21690	CTGAGCCCTCTCAGGACCAG	234081	66277	TTTTTTTTGGCCCCTGTGAA	278668	110864	TTAGAAGATTTGCCTGCTTT
189495	21691	ACTGAGCCCTCTCAGGACCA	234082	66278	TTTTTTTTTGGCCCCTGTGA	278669	110865	CTTAGAAGATTTGCCTGCTT
189496	21692	AACTGAGCCCTCTCAGGACC	234083	66279	TTTTTTTTTTGGCCCCTGTG	278670	110866	GCTTAGAAGATTTGCCTGCT
189497	21693	GAACTGAGCCCTCTCAGGAC	234084	66280	TTTTTTTTTTTGGCCCCTGT	278671	110867	GGCTTAGAAGATTTGCCTGC
189498	21694	TGAACTGAGCCCTCTCAGGA	234085	66281	TTTTTTTTTTTTGGCCCCTG	278672	110868	AGGCTTAGAAGATTTGCCTG
189499	21695	CTGAACTGAGCCCTCTCAGG	234086	66282	TTTTTTTTTTTTTGGCCCCT	278673	110869	AAGGCTTAGAAGATTTGCCT
189500	21696	GCTGAACTGAGCCCTCTCAG	234087	66283	TTTTTTTTTTTTTTGGCCCC	278674	110870	TAAGGCTTAGAAGATTTGCC
189501	21697	AGCTGAACTGAGCCCTCTCA	234088	66284	TTTTTTTTTTTTTTTGGCCC	278675	110871	ATAAGGCTTAGAAGATTTGC
189502	21698	AAGCTGAACTGAGCCCTCTC	234089	66285	TTTTTTTTTTTTTTTTGGCC	278676	110872	GATAAGGCTTAGAAGATTTG
189503	21699	AAAGCTGAACTGAGCCCTCT	234090	66286	TTTTTTTTTTTTTTTTTGGC	278677	110873	GGATAAGGCTTAGAAGATTT
189504	21700	TAAAGCTGAACTGAGCCCTC	234091	66287	ATTTTTTTTTTTTTTTTGG	278678	110874	TGGATAAGGCTTAGAAGATT
189505	21701	TTAAAGCTGAACTGAGCCCT	234092	66288	AATTTTTTTTTTTTTTTTG	278679	110875	GTGGATAAGGCTTAGAAGAT
189506	21702	ATTAAAGCTGAACTGAGCCC	234093	66289	GAATTTTTTTTTTTTTTTT	278680	110876	AGTGGATAAGGCTTAGAAGA
189507	21703	CATTAAAGCTGAACTGAGCC	234094	66290	TGAATTTTTTTTTTTTTTT	278681	110877	CAGTGGATAAGGCTTAGAAG
189508	21704	TCATTAAAGCTGAACTGAGC	234095	66291	CTGAATTTTTTTTTTTTTT	278682	110878	TCAGTGGATAAGGCTTAGAA
189509	21705	GTCATTAAAGCTGAACTGAG	234096	66292	CCTGAATTTTTTTTTTTTT	278683	110879	TTCAGTGGATAAGGCTTAGA
189510	21706	AGTCATTAAAGCTGAACTGA	234097	66293	GCCTGAATTTTTTTTTTTT	278684	110880	TTTCAGTGGATAAGGCTTAG
189511	21707	CAGTCATTAAAGCTGAACTG	234098	66294	GGCCTGAATTTTTTTTTTT	278685	110881	TTTTCAGTGGATAAGGCTTA
189512	21708	GCAGTCATTAAAGCTGAACT	234099	66295	AGGCCTGAATTTTTTTTTT	278686	110882	CTTTTCAGTGGATAAGGCTT
189513	21709	CGCAGTCATTAAAGCTGAAC	234100	66296	GAGGCCTGAATTTTTTTTT	278687	110883	ACTTTTCAGTGGATAAGGCT
189514	21710	GCGCAGTCATTAAAGCTGAA	234101	66297	GGAGGCCTGAATTTTTTTT	278688	110884	AACTTTTCAGTGGATAAGGC
189515	21711	AGCGCAGTCATTAAAGCTGA	234102	66298	AGGAGGCCTGAATTTTTTT	278689	110885	TAACTTTTCAGTGGATAAGG
189516	21712	CAGCGCAGTCATTAAAGCTG	234103	66299	TAGGAGGCCTGAATTTTTT	278690	110886	ATAACTTTTCAGTGGATAAG
189517	21713	ACAGCGCAGTCATTAAAGCT	234104	66300	ATAGGAGGCCTGAATTTTT	278691	110887	CATAACTTTTCAGTGGATAA
189518	21714	AACAGCGCAGTCATTAAAGC	234105	66301	TATAGGAGGCCTGAATTTT	278692	110888	TCATAACTTTTCAGTGGATA
189519	21715	CAACAGCGCAGTCATTAAAG	234106	66302	CTATAGGAGGCCTGAATTT	278693	110889	TTCATAACTTTTCAGTGGAT
189520	21716	GCAACAGCGCAGTCATTAAA	234107	66303	GCTATAGGAGGCCTGAATT	278694	110890	ATTCATAACTTTTCAGTGGA
189521	21717	CGCAACAGCGCAGTCATTAA	234108	66304	GGCTATAGGAGGCCTGAAT	278695	110891	TATTCATAACTTTTCAGTGG
189522	21718	ACGCAACAGCGCAGTCATTA	234109	66305	TGGCTATAGGAGGCCTGAA	278696	110892	TTATTCATAACTTTTCAGTG
189523	21719	CACGCAACAGCGCAGTCATT	234110	66306	ATGGCTATAGGAGGCCTGA	278697	110893	TTTATTCATAACTTTTCAGT
189524	21720	ACACGCAACAGCGCAGTCAT	234111	66307	CATGGCTATAGGAGGCCTGA	278698	110894	TTTTATTCATAACTTTTCAG
189525	21721	CACACGCAACAGCGCAGTCA	234112	66308	TCATGGCTATAGGAGGCCTG	278699	110895	TTTTTATTCATAACTTTTCA
189526	21722	GCACACGCAACAGCGCAGTC	234113	66309	CTCATGGCTATAGGAGGCCT	278700	110896	TTTTTTATTCATAACTTTTC
189527	21723	AGCACACGCAACAGCGCAGT	234114	66310	GCTCATGGCTATAGGAGGCC	278701	110897	ATTTTTTATTCATAACTTTT
189528	21724	GAGCACACGCAACAGCGCAG	234115	66311	AGCTCATGGCTATAGGAGGC	278702	110898	CATTTTTTATTCATAACTTT
189529	21725	AGAGCACACGCAACAGCGCA	234116	66312	TAGCTCATGGCTATAGGAGG	278703	110899	TCATTTTTTATTCATAACTT
189530	21726	CAGAGCACACGCAACAGCGC	234117	66313	GTAGCTCATGGCTATAGGAG	278704	110900	ATCATTTTTTATTCATAACT
189531	21727	GCAGAGCACACGCAACAGCG	234118	66314	CGTAGCTCATGGCTATAGGA	278705	110901	GATCATTTTTTATTCATAAC
189532	21728	TGCAGAGCACACGCAACAGC	234119	66315	TCGTAGCTCATGGCTATAGG	278706	110902	CGATCATTTTTTATTCATAA
189533	21729	CTGCAGAGCACACGCAACAG	234120	66316	TTCGTAGCTCATGGCTATAG	278707	110903	ACGATCATTTTTTATTCATA
189534	21730	TCTGCAGAGCACACGCAACA	234121	66317	ATTCGTAGCTCATGGCTATA	278708	110904	GACGATCATTTTTTATTCAT
189535	21731	CTCTGCAGAGCACACGCAAC	234122	66318	TATTCGTAGCTCATGGCTAT	278709	110905	TGACGATCATTTTTTATTCA
189536	21732	CCTCTGCAGAGCACACGCAA	234123	66319	ATATTCGTAGCTCATGGCTA	278710	110906	TTGACGATCATTTTTTATTC
189537	21733	CCCTCTGCAGAGCACACGCA	234124	66320	CATATTCGTAGCTCATGGCT	278711	110907	CTTGACGATCATTTTTTATT
189538	21734	GCCCTCTGCAGAGCACACGC	234125	66321	TCATATTCGTAGCTCATGGC	278712	110908	GCTTGACGATCATTTTTTAT
189539	21735	CGCCCTCTGCAGAGCACACG	234126	66322	TTCATATTCGTAGCTCATGG	278713	110909	GGCTTGACGATCATTTTTTA
189540	21736	CCGCCCTCTGCAGAGCACAC	234127	66323	TTTCATATTCGTAGCTCATG	278714	110910	AGGCTTGACGATCATTTTTT
189541	21737	CCCGCCCTCTGCAGAGCACA	234128	66324	TTTTCATATTCGTAGCTCAT	278715	110911	TAGGCTTGACGATCATTTTT
189542	21738	ACCCGCCCTCTGCAGAGCAC	234129	66325	ATTTTCATATTCGTAGCTCA	278716	110912	GTAGGCTTGACGATCATTTT
189543	21739	CACCCGCCCTCTGCAGAGCA	234130	66326	TATTTTCATATTCGTAGCTC	278717	110913	TGTAGGCTTGACGATCATTT
189544	21740	CCACCCGCCCTCTGCAGAGC	234131	66327	ATATTTTCATATTCGTAGCT	278718	110914	CTGTAGGCTTGACGATCATT
189545	21741	GCCACCCGCCCTCTGCAGAG	234132	66328	CATATTTTCATATTCGTAGC	278719	110915	CCTGTAGGCTTGACGATCAT
189546	21742	GGCCACCCGCCCTCTGCAGA	234133	66329	GCATATTTTCATATTCGTAG	278720	110916	ACCTGTAGGCTTGACGATCA

189547	21743	GGGCCACCCGCCCTCTGCAG	234134	66330	TGCATATTTTCATATTCGTA	278721	110917	CACCTGTAGGCTTGACGATC
189548	21744	TGGGCCACCCGCCCTCTGCA	234135	66331	TTGCATATTTTCATATTCGT	278722	110918	GCACCTGTAGGCTTGACGAT
189549	21745	CTGGGCCACCCGCCCTCTGC	234136	66332	TTTGCATATTTTCATATTCG	278723	110919	AGCACCTGTAGGCTTGACGA
189550	21746	GCTGGGCCACCCGCCCTCTG	234137	66333	ATTTGCATATTTTCATATTC	278724	110920	CAGCACCTGTAGGCTTGACG
189551	21747	CGCTGGGCCACCCGCCCTCT	234138	66334	CATTTGCATATTTTCATATT	278725	110921	TCAGCACCTGTAGGCTTGAC
189552	21748	ACGCTGGGCCACCCGCCCTC	234139	66335	ACATTTGCATATTTTCATAT	278726	110922	CTCAGCACCTGTAGGCTTGA
189553	21749	CACGCTGGGCCACCCGCCCT	234140	66336	CACATTTGCATATTTTCATA	278727	110923	CCTCAGCACCTGTAGGCTTG
189554	21750	CCACGCTGGGCCACCCGCCC	234141	66337	ACACATTTGCATATTTTCAT	278728	110924	GCCTCAGCACCTGTAGGCTT
189555	21751	GCCACGCTGGGCCACCCGCC	234142	66338	TACACATTTGCATATTTTCA	278729	110925	AGCCTCAGCACCTGTAGGCT
189556	21752	AGCCACGCTGGGCCACCCGC	234143	66339	TTACACATTTGCATATTTTC	278730	110926	TAGCCTCAGCACCTGTAGGC
189557	21753	CAGCCACGCTGGGCCACCCG	234144	66340	CTTACACATTTGCATATTTT	278731	110927	GTAGCCTCAGCACCTGTAGG
189558	21754	TCAGCCACGCTGGGCCACCC	234145	66341	TCTTACACATTTGCATATTT	278732	110928	AGTAGCCTCAGCACCTGTAG
189559	21755	GTCAGCCACGCTGGGCCACC	234146	66342	TTCTTACACATTTGCATATT	278733	110929	GAGTAGCCTCAGCACCTGTA
189560	21756	AGTCAGCCACGCTGGGCCAC	234147	66343	TTTCTTACACATTTGCATAT	278734	110930	GGAGTAGCCTCAGCACCTGT
189561	21757	CAGTCAGCCACGCTGGGCCA	234148	66344	TTTTCTTACACATTTGCATA	278735	110931	TGGAGTAGCCTCAGCACCTG
189562	21758	GCAGTCAGCCACGCTGGGCC	234149	66345	CTTTTCTTACACATTTGCAT	278736	110932	CTGGAGTAGCCTCAGCACCT
189563	21759	TGCAGTCAGCCACGCTGGGC	234150	66346	GCTTTTCTTACACATTTGCA	278737	110933	TCTGGAGTAGCCTCAGCACC
189564	21760	CTGCAGTCAGCCACGCTGGG	234151	66347	GGCTTTTCTTACACATTTGC	278738	110934	CTCTGGAGTAGCCTCAGCAC
189565	21761	ACTGCAGTCAGCCACGCTGG	234152	66348	TGGCTTTTCTTACACATTTG	278739	110935	CCTCTGGAGTAGCCTCAGCA
189566	21762	AACTGCAGTCAGCCACGCTG	234153	66349	CTGGCTTTTCTTACACATTT	278740	110936	GCCTCTGGAGTAGCCTCAGC
189567	21763	AAACTGCAGTCAGCCACGCT	234154	66350	GCTGGCTTTTCTTACACATT	278741	110937	AGCCTCTGGAGTAGCCTCAG
189568	21764	AAAACTGCAGTCAGCCACGC	234155	66351	TGCTGGCTTTTCTTACACAT	278742	110938	CAGCCTCTGGAGTAGCCTCA
189569	21765	GAAAACTGCAGTCAGCCACG	234156	66352	GTGCTGGCTTTTCTTACACA	278743	110939	TCAGCCTCTGGAGTAGCCTC
189570	21766	GGAAAACTGCAGTCAGCCAC	234157	66353	TGTGCTGGCTTTTCTTACAC	278744	110940	CTCAGCCTCTGGAGTAGCCT
189571	21767	AGGAAAACTGCAGTCAGCCA	234158	66354	ATGTGCTGGCTTTTCTTACA	278745	110941	CCTCAGCCTCTGGAGTAGCC
189572	21768	CAGGAAAACTGCAGTCAGCC	234159	66355	GATGTGCTGGCTTTTCTTAC	278746	110942	GCCTCAGCCTCTGGAGTAGC
189573	21769	TCAGGAAAACTGCAGTCAGC	234160	66356	GGATGTGCTGGCTTTTCTTA	278747	110943	GGCCTCAGCCTCTGGAGTAG
189574	21770	GTCAGGAAAACTGCAGTCAG	234161	66357	CGGATGTGCTGGCTTTTCTT	278748	110944	TGGCCTCAGCCTCTGGAGTA
189575	21771	CGTCAGGAAAACTGCAGTCA	234162	66358	TCGGATGTGCTGGCTTTTCT	278749	110945	CTGGCCTCAGCCTCTGGAGT
189576	21772	ACGTCAGGAAAACTGCAGTC	234163	66359	ATCGGATGTGCTGGCTTTTC	278750	110946	TCTGGCCTCAGCCTCTGGAG
189577	21773	CACGTCAGGAAAACTGCAGT	234164	66360	AATCGGATGTGCTGGCTTTT	278751	110947	CTCTGGCCTCAGCCTCTGGA
189578	21774	CCACGTCAGGAAAACTGCAG	234165	66361	AAATCGGATGTGCTGGCTTT	278752	110948	CCTCTGGCCTCAGCCTCTGG
189579	21775	TCCACGTCAGGAAAACTGCA	234166	66362	AAAATCGGATGTGCTGGCTT	278753	110949	TCCTCTGGCCTCAGCCTCTG
189580	21776	CTCCACGTCAGGAAAACTGC	234167	66363	AAAAATCGGATGTGCTGGCT	278754	110950	GTCCTCTGGCCTCAGCCTCT
189581	21777	GCTCCACGTCAGGAAAACTG	234168	66364	TAAAAATCGGATGTGCTGGC	278755	110951	GGTCCTCTGGCCTCAGCCTC
189582	21778	GGCTCCACGTCAGGAAAACT	234169	66365	GTAAAAATCGGATGTGCTGG	278756	110952	TGGTCCTCTGGCCTCAGCCT
189583	21779	GGGCTCCACGTCAGGAAAAC	234170	66366	AGTAAAAATCGGATGTGCTG	278757	110953	GTGGTCCTCTGGCCTCAGCC
189584	21780	CGGGCTCCACGTCAGGAAAA	234171	66367	AAGTAAAAATCGGATGTGCT	278758	110954	AGTGGTCCTCTGGCCTCAGC
189585	21781	TCGGGCTCCACGTCAGGAAA	234172	66368	AAAGTAAAAATCGGATGTGC	278759	110955	AAGTGGTCCTCTGGCCTCAG
189586	21782	CTCGGGCTCCACGTCAGGAA	234173	66369	AAAAGTAAAAATCGGATGTG	278760	110956	CAAGTGGTCCTCTGGCCTCA
189587	21783	GCTCGGGCTCCACGTCAGGA	234174	66370	TAAAAGTAAAAATCGGATGT	278761	110957	TCAAGTGGTCCTCTGGCCTC
189588	21784	GGCTCGGGCTCCACGTCAGG	234175	66371	GTAAAAGTAAAAATCGGATG	278762	110958	CTCAAGTGGTCCTCTGGCCT
189589	21785	AGGCTCGGGCTCCACGTCAG	234176	66372	AGTAAAAGTAAAAATCGGAT	278763	110959	GCTCAAGTGGTCCTCTGGCC
189590	21786	CAGGCTCGGGCTCCACGTCA	234177	66373	AAGTAAAAGTAAAAATCGGA	278764	110960	GGCTCAAGTGGTCCTCTGGC
189591	21787	GCAGGCTCGGGCTCCACGTC	234178	66374	AAAGTAAAAGTAAAAATCGG	278765	110961	GGGCTCAAGTGGTCCTCTGG
189592	21788	GGCAGGCTCGGGCTCCACGT	234179	66375	GAAAGTAAAAGTAAAAATCG	278766	110962	TGGGCTCAAGTGGTCCTCTG
189593	21789	GGGCAGGCTCGGGCTCCACG	234180	66376	TGAAAGTAAAAGTAAAAATC	278767	110963	CTGGGCTCAAGTGGTCCTCT
189594	21790	GGGGCAGGCTCGGGCTCCAC	234181	66377	GTGAAAGTAAAAGTAAAAAT	278768	110964	CCTGGGCTCAAGTGGTCCTC
189595	21791	CGGGGCAGGCTCGGGCTCCA	234182	66378	TGTGAAAGTAAAAGTAAAAA	278769	110965	TCCTGGGCTCAAGTGGTCCT
189596	21792	GCGGGGCAGGCTCGGGCTCC	234183	66379	GTGTGAAAGTAAAAGTAAAA	278770	110966	TTCCTGGGCTCAAGTGGTCC
189597	21793	AGCGGGGCAGGCTCGGGCTC	234184	66380	GGTGTGAAAGTAAAAGTAAA	278771	110967	ATTCCTGGGCTCAAGTGGTC
189598	21794	CAGCGGGGCAGGCTCGGGCT	234185	66381	AGGTGTGAAAGTAAAAGTAA	278772	110968	AATTCCTGGGCTCAAGTGGT
189599	21795	ACAGCGGGGCAGGCTCGGGC	234186	66382	GAGGTGTGAAAGTAAAAGTA	278773	110969	AAATTCCTGGGCTCAAGTGG
189600	21796	AACAGCGGGGCAGGCTCGGG	234187	66383	AGAGGTGTGAAAGTAAAAGT	278774	110970	CAAATTCCTGGGCTCAAGTG
189601	21797	AAACAGCGGGGCAGGCTCGG	234188	66384	CAGAGGTGTGAAAGTAAAAG	278775	110971	TCAAATTCCTGGGCTCAAGT
189602	21798	TAAACAGCGGGGCAGGCTCG	234189	66385	ACAGAGGTGTGAAAGTAAAA	278776	110972	CTCAAATTCCTGGGCTCAAG
189603	21799	ATAAACAGCGGGGCAGGCTC	234190	66386	GACAGAGGTGTGAAAGTAAA	278777	110973	TCTCAAATTCCTGGGCTCAA
189604	21800	AATAAACAGCGGGGCAGGCT	234191	66387	GGACAGAGGTGTGAAAGTAA	278778	110974	GTCTCAAATTCCTGGGCTCA
189605	21801	TAATAAACAGCGGGGCAGGC	234192	66388	TGGACAGAGGTGTGAAAGTA	278779	110975	GGTCTCAAATTCCTGGGCTC
189606	21802	TTAATAAACAGCGGGGCAGG	234193	66389	GTGGACAGAGGTGTGAAAGT	278780	110976	AGGTCTCAAATTCCTGGGCT
189607	21803	ATTAATAAACAGCGGGGCAG	234194	66390	GGTGGACAGAGGTGTGAAAG	278781	110977	CAGGTCTCAAATTCCTGGGC
189608	21804	AATTAATAAACAGCGGGGCA	234195	66391	TGGTGGACAGAGGTGTGAAA	278782	110978	CCAGGTCTCAAATTCCTGGG
189609	21805	TAATTAATAAACAGCGGGGC	234196	66392	ATGGTGGACAGAGGTGTGAA	278783	110979	CCCAGGTCTCAAATTCCTGG
189610	21806	TTAATTAATAAACAGCGGGG	234197	66393	CATGGTGGACAGAGGTGTGA	278784	110980	GCCCAGGTCTCAAATTCCTG
189611	21807	CTTAATTAATAAACAGCGGG	234198	66394	ACATGGTGGACAGAGGTGTG	278785	110981	AGCCCAGGTCTCAAATTCCT
189612	21808	CCTTAATTAATAAACAGCGG	234199	66395	AACATGGTGGACAGAGGTGT	278786	110982	CAGCCCAGGTCTCAAATTCC
189613	21809	TCCTTAATTAATAAACAGCG	234200	66396	GAACATGGTGGACAGAGGTG	278787	110983	CCAGCCCAGGTCTCAAATTC
189614	21810	ATCCTTAATTAATAAACAGC	234201	66397	GGAACATGGTGGACAGAGGT	278788	110984	CCCAGCCCAGGTCTCAAATT
189615	21811	GATCCTTAATTAATAAACAG	234202	66398	TGGAACATGGTGGACAGAGG	278789	110985	GCCCAGCCCAGGTCTCAAAT
189616	21812	TGATCCTTAATTAATAAACA	234203	66399	TTGGAACATGGTGGACAGAG	278790	110986	TGCCCAGCCCAGGTCTCAAA
189617	21813	GTGATCCTTAATTAATAAAC	234204	66400	CTTGGAACATGGTGGACAGA	278791	110987	CTGCCCAGCCCAGGTCTCAA
189618	21814	AGTGATCCTTAATTAATAAA	234205	66401	TCTTGGAACATGGTGGACAG	278792	110988	GCTGCCCAGCCCAGGTCTCA

189619	21815	GAGTGATCCTTAATTAATAA	234206	66402	CTCTTGGAACATGGTGGACA	278793	110989	TGCTGCCCAGCCCAGGTCTC
189620	21816	AGAGTGATCCTTAATTAATA	234207	66403	TCTCTTGGAACATGGTGGAC	278794	110990	ATGCTGCCCAGCCCAGGTCT
189621	21817	CAGAGTGATCCTTAATTAAT	234208	66404	TTCTCTTGGAACATGGTGGA	278795	110991	TATGCTGCCCAGCCCAGGTC
189622	21818	GCAGAGTGATCCTTAATTAA	234209	66405	CTTCTCTTGGAACATGGTGG	278796	110992	CTATGCTGCCCAGCCCAGGT
189623	21819	AGCAGAGTGATCCTTAATTA	234210	66406	TCTTCTCTTGGAACATGGTG	278797	110993	GCTATGCTGCCCAGCCCAGG
189624	21820	AAGCAGAGTGATCCTTAATT	234211	66407	TTCTTCTCTTGGAACATGGT	278798	110994	TGCTATGCTGCCCAGCCCAG
189625	21821	CAAGCAGAGTGATCCTTAAT	234212	66408	TTTCTTCTCTTGGAACATGG	278799	110995	TTGCTATGCTGCCCAGCCCA
189626	21822	GCAAGCAGAGTGATCCTTAA	234213	66409	GTTTCTTCTCTTGGAACATG	278800	110996	CTTGCTATGCTGCCCAGCCC
189627	21823	TGCAAGCAGAGTGATCCTTA	234214	66410	AGTTTCTTCTCTTGGAACAT	278801	110997	TCTTGCTATGCTGCCCAGCC
189628	21824	CTGCAAGCAGAGTGATCCTT	234215	66411	AAGTTTCTTCTCTTGGAACA	278802	110998	GTCTTGCTATGCTGCCCAGC
189629	21825	TCTGCAAGCAGAGTGATCCT	234216	66412	CAAGTTTCTTCTCTTGGAAC	278803	110999	AGTCTTGCTATGCTGCCCAG
189630	21826	TTCTGCAAGCAGAGTGATCC	234217	66413	CCAAGTTTCTTCTCTTGGAA	278804	111000	GAGTCTTGCTATGCTGCCCA
189631	21827	GTTCTGCAAGCAGAGTGATC	234218	66414	ACCAAGTTTCTTCTCTTGGA	278805	111001	AGAGTCTTGCTATGCTGCCC
189632	21828	GGTTCTGCAAGCAGAGTGAT	234219	66415	GACCAAGTTTCTTCTCTTGG	278806	111002	TAGAGTCTTGCTATGCTGCC
189633	21829	GGGTTCTGCAAGCAGAGTGA	234220	66416	TGACCAAGTTTCTTCTCTTG	278807	111003	ATAGAGTCTTGCTATGCTGC
189634	21830	AGGGTTCTGCAAGCAGAGTG	234221	66417	ATGACCAAGTTTCTTCTCTT	278808	111004	GATAGAGTCTTGCTATGCTG
189635	21831	CAGGGTTCTGCAAGCAGAGT	234222	66418	AATGACCAAGTTTCTTCTCT	278809	111005	AGATAGAGTCTTGCTATGCT
189636	21832	TCAGGGTTCTGCAAGCAGAG	234223	66419	CAATGACCAAGTTTCTTCTC	278810	111006	GAGATAGAGTCTTGCTATGC
189637	21833	TTCAGGGTTCTGCAAGCAGA	234224	66420	TCAATGACCAAGTTTCTTCT	278811	111007	GGAGATAGAGTCTTGCTATG
189638	21834	GTTCAGGGTTCTGCAAGCAG	234225	66421	TTCAATGACCAAGTTTCTTC	278812	111008	TGGAGATAGAGTCTTGCTAT
189639	21835	AGTTCAGGGTTCTGCAAGCA	234226	66422	TTTCAATGACCAAGTTTCTT	278813	111009	ATGGAGATAGAGTCTTGCTA
189640	21836	GAGTTCAGGGTTCTGCAAGC	234227	66423	CTTTCAATGACCAAGTTTCT	278814	111010	AATGGAGATAGAGTCTTGCT
189641	21837	GGAGTTCAGGGTTCTGCAAG	234228	66424	CCTTTCAATGACCAAGTTTC	278815	111011	TAATGGAGATAGAGTCTTGC
189642	21838	GGGAGTTCAGGGTTCTGCAA	234229	66425	TCCTTTCAATGACCAAGTTT	278816	111012	TTAATGGAGATAGAGTCTTG
189643	21839	GGGGAGTTCAGGGTTCTGCA	234230	66426	TTCCTTTCAATGACCAAGTT	278817	111013	TTTAATGGAGATAGAGTCTT
189644	21840	TGGGGAGTTCAGGGTTCTGC	234231	66427	ATTCCTTTCAATGACCAAGT	278818	111014	TTTTAATGGAGATAGAGTCT
189645	21841	CTGGGGAGTTCAGGGTTCTG	234232	66428	TATTCCTTTCAATGACCAAG	278819	111015	GTTTTAATGGAGATAGAGTC
189646	21842	TCTGGGGAGTTCAGGGTTCT	234233	66429	CTATTCCTTTCAATGACCAA	278820	111016	AGTTTTAATGGAGATAGAGT
189647	21843	TTCTGGGGAGTTCAGGGTTC	234234	66430	TCTATTCCTTTCAATGACCA	278821	111017	TAGTTTTAATGGAGATAGAG
189648	21844	GTTCTGGGGAGTTCAGGGTT	234235	66431	ATCTATTCCTTTCAATGACC	278822	111018	ATAGTTTTAATGGAGATAGA
189649	21845	AGTTCTGGGGAGTTCAGGGT	234236	66432	GATCTATTCCTTTCAATGAC	278823	111019	AATAGTTTTAATGGAGATAG
189650	21846	CAGTTCTGGGGAGTTCAGGG	234237	66433	TGATCTATTCCTTTCAATGA	278824	111020	AAATAGTTTTAATGGAGATA
189651	21847	ACAGTTCTGGGGAGTTCAGG	234238	66434	TTGATCTATTCCTTTCAATG	278825	111021	AAAATAGTTTTAATGGAGAT
189652	21848	CACAGTTCTGGGGAGTTCAG	234239	66435	TTTGATCTATTCCTTTCAAT	278826	111022	AAAAATAGTTTTAATGGAGA
189653	21849	TCACAGTTCTGGGGAGTTCA	234240	66436	ATTTGATCTATTCCTTTCAA	278827	111023	AAAAAATAGTTTTAATGGAG
189654	21850	CTCACAGTTCTGGGGAGTTC	234241	66437	GATTTGATCTATTCCTTTCA	278828	111024	AAAAAAATAGTTTTAATGGA
189655	21851	CCTCACAGTTCTGGGGAGTT	234242	66438	GGATTTGATCTATTCCTTTC	278829	111025	AAAAAAAATAGTTTTAATGG
189656	21852	ACCTCACAGTTCTGGGGAGT	234243	66439	TGGATTTGATCTATTCCTTT	278830	111026	AAAAAAAAATAGTTTTAATG
189657	21853	CACCTCACAGTTCTGGGGAG	234244	66440	TTGGATTTGATCTATTCCTT	278831	111027	TAAAAAAAAATAGTTTTAAT
189658	21854	CCACCTCACAGTTCTGGGGA	234245	66441	TTTGGATTTGATCTATTCCT	278832	111028	ATAAAAAAAAATAGTTTTAA
189659	21855	CCCACCTCACAGTTCTGGGG	234246	66442	CTTTGGATTTGATCTATTCC	278833	111029	AATAAAAAAAAATAGTTTTA
189660	21856	TCCCACCTCACAGTTCTGGG	234247	66443	TCTTTGGATTTGATCTATTC	278834	111030	AAATAAAAAAAAATAGTTTT
189661	21857	CTCCCACCTCACAGTTCTGG	234248	66444	TTCTTTGGATTTGATCTATT	278835	111031	TAAATAAAAAAAAATAGTTT
189662	21858	TCTCCCACCTCACAGTTCTG	234249	66445	GTTCTTTGGATTTGATCTAT	278836	111032	TTAAATAAAAAAAAATAGTT
189663	21859	TTCTCCCACCTCACAGTTCT	234250	66446	TGTTCTTTGGATTTGATCTA	278837	111033	TTTAAATAAAAAAAAATAGT
189664	21860	GTTCTCCCACCTCACAGTTC	234251	66447	TTGTTCTTTGGATTTGATCT	278838	111034	TTTTAAATAAAAAAAAATAG
189665	21861	GGTTCTCCCACCTCACAGTT	234252	66448	TTTGTTCTTTGGATTTGATC	278839	111035	TTTTTAAATAAAAAAAAATA
189666	21862	GGGTTCTCCCACCTCACAGT	234253	66449	TTTTGTTCTTTGGATTTGAT	278840	111036	TTTTTTAAATAAAAAAAAAT
189667	21863	GGGGTTCTCCCACCTCACAG	234254	66450	GTTTTGTTCTTTGGATTTGA	278841	111037	ATTTTTTAAATAAAAAAAAA
189668	21864	CGGGGTTCTCCCACCTCACA	234255	66451	GGTTTTGTTCTTTGGATTTG	278842	111038	TATTTTTTAAATAAAAAAAA
189669	21865	TCGGGGTTCTCCCACCTCAC	234256	66452	TGGTTTTGTTCTTTGGATTT	278843	111039	TTATTTTTTAAATAAAAAAA
189670	21866	CTCGGGGTTCTCCCACCTCA	234257	66453	GTGGTTTTGTTCTTTGGATT	278844	111040	ATTATTTTTTAAATAAAAAA
189671	21867	TCTCGGGGTTCTCCCACCTC	234258	66454	AGTGGTTTTGTTCTTTGGAT	278845	111041	GATTATTTTTTAAATAAAAA
189672	21868	CTCTCGGGGTTCTCCCACCT	234259	66455	CAGTGGTTTTGTTCTTTGGA	278846	111042	GGATTATTTTTTAAATAAAA
189673	21869	CCTCTCGGGGTTCTCCCACC	234260	66456	ACAGTGGTTTTGTTCTTTGG	278847	111043	CGGATTATTTTTTAAATAAA
189674	21870	GCCTCTCGGGGTTCTCCCAC	234261	66457	CACAGTGGTTTTGTTCTTTG	278848	111044	GCGGATTATTTTTTAAATAA
189675	21871	GGCCTCTCGGGGTTCTCCCA	234262	66458	GCACAGTGGTTTTGTTCTTT	278849	111045	TGCGGATTATTTTTTAAATA
189676	21872	TGGCCTCTCGGGGTTCTCCC	234263	66459	AGCACAGTGGTTTTGTTCTT	278850	111046	TTGCGGATTATTTTTTAAAT
189677	21873	GTGGCCTCTCGGGGTTCTCC	234264	66460	GAGCACAGTGGTTTTGTTCT	278851	111047	TTTGCGGATTATTTTTTAAA
189678	21874	GGTGGCCTCTCGGGGTTCTC	234265	66461	TGAGCACAGTGGTTTTGTTC	278852	111048	CTTTGCGGATTATTTTTTAA
189679	21875	AGGTGGCCTCTCGGGGTTCT	234266	66462	ATGAGCACAGTGGTTTTGTT	278853	111049	TCTTTGCGGATTATTTTTTA
189680	21876	CAGGTGGCCTCTCGGGGTTC	234267	66463	AATGAGCACAGTGGTTTTGT	278854	111050	TTCTTTGCGGATTATTTTTT
189681	21877	CCAGGTGGCCTCTCGGGGTT	234268	66464	TAATGAGCACAGTGGTTTTG	278855	111051	CTTCTTTGCGGATTATTTTT
189682	21878	GCCAGGTGGCCTCTCGGGGT	234269	66465	TTAATGAGCACAGTGGTTTT	278856	111052	CCTTCTTTGCGGATTATTTT
189683	21879	GGCCAGGTGGCCTCTCGGGG	234270	66466	TTTAATGAGCACAGTGGTTT	278857	111053	TCCTTCTTTGCGGATTATTT
189684	21880	GGGCCAGGTGGCCTCTCGGG	234271	66467	GTTTAATGAGCACAGTGGTT	278858	111054	CTCCTTCTTTGCGGATTATT
189685	21881	GGGGCCAGGTGGCCTCTCGG	234272	66468	AGTTTAATGAGCACAGTGGT	278859	111055	ACTCCTTCTTTGCGGATTAT
189686	21882	TGGGGCCAGGTGGCCTCTCG	234273	66469	AAGTTTAATGAGCACAGTGG	278860	111056	AACTCCTTCTTTGCGGATTA
189687	21883	GTGGGGCCAGGTGGCCTCTC	234274	66470	GAAGTTTAATGAGCACAGTG	278861	111057	AAACTCCTTCTTTGCGGATT
189688	21884	AGTGGGGCCAGGTGGCCTCT	234275	66471	AGAAGTTTAATGAGCACAGT	278862	111058	TAAACTCCTTCTTTGCGGAT
189689	21885	AAGTGGGGCCAGGTGGCCTC	234276	66472	AAGAAGTTTAATGAGCACAG	278863	111059	ATAAACTCCTTCTTTGCGGA
189690	21886	GAAGTGGGGCCAGGTGGCCT	234277	66473	TAAGAAGTTTAATGAGCACA	278864	111060	CATAAACTCCTTCTTTGCGG

189691	21887	GGAAGTGGGGCCAGGTGGCC	234278	66474	CTAAGAAGTTTAATGAGCAC	278865	111061	ACATAAACTCCTTCTTTGCG
189692	21888	GGGAAGTGGGGCCAGGTGGC	234279	66475	ACTAAGAAGTTTAATGAGCA	278866	111062	CACATAAACTCCTTCTTTGC
189693	21889	TGGGAAGTGGGGCCAGGTGG	234280	66476	CACTAAGAAGTTTAATGAGC	278867	111063	CCACATAAACTCCTTCTTTG
189694	21890	GTGGGAAGTGGGGCCAGGTG	234281	66477	ACACTAAGAAGTTTAATGAG	278868	111064	CCCACATAAACTCCTTCTTT
189695	21891	GGTGGGAAGTGGGGCCAGGT	234282	66478	AACACTAAGAAGTTTAATGA	278869	111065	TCCCACATAAACTCCTTCTT
189696	21892	AGGTGGGAAGTGGGGCCAGG	234283	66479	GAACACTAAGAAGTTTAATG	278870	111066	ATCCCACATAAACTCCTTCT
189697	21893	CAGGTGGGAAGTGGGGCCAG	234284	66480	TGAACACTAAGAAGTTTAAT	278871	111067	AATCCCACATAAACTCCTTC
189698	21894	GCAGGTGGGAAGTGGGGCCA	234285	66481	GTGAACACTAAGAAGTTTAA	278872	111068	GAATCCCACATAAACTCCTT
189699	21895	AGCAGGTGGGAAGTGGGGCC	234286	66482	TGTGAACACTAAGAAGTTTA	278873	111069	GGAATCCCACATAAACTCCT
189700	21896	CAGCAGGTGGGAAGTGGGGC	234287	66483	TTGTGAACACTAAGAAGTTT	278874	111070	AGGAATCCCACATAAACTCC
189701	21897	GCAGCAGGTGGGAAGTGGGG	234288	66484	TTTGTGAACACTAAGAAGTT	278875	111071	AAGGAATCCCACATAAACTC
189702	21898	GGCAGCAGGTGGGAAGTGGG	234289	66485	CTTTGTGAACACTAAGAAGT	278876	111072	TAAGGAATCCCACATAAACT
189703	21899	GGGCAGCAGGTGGGAAGTGG	234290	66486	GCTTTGTGAACACTAAGAAG	278877	111073	TTAAGGAATCCCACATAAAC
189704	21900	TGGGCAGCAGGTGGGAAGTG	234291	66487	AGCTTTGTGAACACTAAGAA	278878	111074	TTTAAGGAATCCCACATAAA
189705	21901	TTGGGCAGCAGGTGGGAAGT	234292	66488	AAGCTTTGTGAACACTAAGA	278879	111075	TTTTAAGGAATCCCACATAA
189706	21902	TTTGGGCAGCAGGTGGGAAG	234293	66489	AAAGCTTTGTGAACACTAAG	278880	111076	ATTTTAAGGAATCCCACATA
189707	21903	GTTTGGGCAGCAGGTGGGAA	234294	66490	TAAAGCTTTGTGAACACTAA	278881	111077	GATTTTAAGGAATCCCACAT
189708	21904	GGTTTGGGCAGCAGGTGGGA	234295	66491	CTAAAGCTTTGTGAACACTA	278882	111078	CGATTTTAAGGAATCCCACA
189709	21905	GGGTTTGGGCAGCAGGTGGG	234296	66492	GCTAAAGCTTTGTGAACACT	278883	111079	CCGATTTTAAGGAATCCCAC
189710	21906	GGGGTTTGGGCAGCAGGTGG	234297	66493	AGCTAAAGCTTTGTGAACAC	278884	111080	TCCGATTTTAAGGAATCCCA
189711	21907	GGGGGTTTGGGCAGCAGGTG	234298	66494	CAGCTAAAGCTTTGTGAACA	278885	111081	CTCCGATTTTAAGGAATCCC
189712	21908	AGGGGGTTTGGGCAGCAGGT	234299	66495	GCAGCTAAAGCTTTGTGAAC	278886	111082	CCTCCGATTTTAAGGAATCC
189713	21909	GAGGGGGTTTGGGCAGCAGG	234300	66496	TGCAGCTAAAGCTTTGTGAA	278887	111083	CCCTCCGATTTTAAGGAATC
189714	21910	AGAGGGGGTTTGGGCAGCAG	234301	66497	CTGCAGCTAAAGCTTTGTGA	278888	111084	ACCCTCCGATTTTAAGGAAT
189715	21911	GAGAGGGGGTTTGGGCAGCA	234302	66498	CCTGCAGCTAAAGCTTTGTG	278889	111085	CACCCTCCGATTTTAAGGAA
189716	21912	AGAGAGGGGGTTTGGGCAGC	234303	66499	ACCTGCAGCTAAAGCTTTGT	278890	111086	CCACCCTCCGATTTTAAGGA
189717	21913	CAGAGAGGGGGTTTGGGCAG	234304	66500	AACCTGCAGCTAAAGCTTTG	278891	111087	GCCACCCTCCGATTTTAAGG
189718	21914	GCAGAGAGGGGGTTTGGGCA	234305	66501	CAACCTGCAGCTAAAGCTTT	278892	111088	TGCCACCCTCCGATTTTAAG
189719	21915	GGCAGAGAGGGGGTTTGGGC	234306	66502	TCAACCTGCAGCTAAAGCTT	278893	111089	ATGCCACCCTCCGATTTTAA
189720	21916	AGGCAGAGAGGGGGTTTGGG	234307	66503	TTCAACCTGCAGCTAAAGCT	278894	111090	CATGCCACCCTCCGATTTTA
189721	21917	AAGGCAGAGAGGGGGTTTGG	234308	66504	ATTCAACCTGCAGCTAAAGC	278895	111091	TCATGCCACCCTCCGATTTT
189722	21918	GAAGGCAGAGAGGGGGTTTG	234309	66505	CATTCAACCTGCAGCTAAAG	278896	111092	TTCATGCCACCCTCCGATTT
189723	21919	GGAAGGCAGAGAGGGGGTTT	234310	66506	CCATTCAACCTGCAGCTAAA	278897	111093	ATTCATGCCACCCTCCGATT
189724	21920	AGGAAGGCAGAGAGGGGGTT	234311	66507	CCCATTCAACCTGCAGCTAA	278898	111094	AATTCATGCCACCCTCCGAT
189725	21921	CAGGAAGGCAGAGAGGGGGT	234312	66508	CCCCATTCAACCTGCAGCTA	278899	111095	CAATTCATGCCACCCTCCGA
189726	21922	TCAGGAAGGCAGAGAGGGGG	234313	66509	GCCCCATTCAACCTGCAGCT	278900	111096	TCAATTCATGCCACCCTCCG
189727	21923	GTCAGGAAGGCAGAGAGGGG	234314	66510	TGCCCCATTCAACCTGCAGC	278901	111097	ATCAATTCATGCCACCCTCC
189728	21924	TGTCAGGAAGGCAGAGAGGG	234315	66511	TTGCCCCATTCAACCTGCAG	278902	111098	AATCAATTCATGCCACCCTC
189729	21925	CTGTCAGGAAGGCAGAGAGG	234316	66512	GTTGCCCCATTCAACCTGCA	278903	111099	GAATCAATTCATGCCACCCT
189730	21926	ACTGTCAGGAAGGCAGAGAG	234317	66513	GGTTGCCCCATTCAACCTGC	278904	111100	TGAATCAATTCATGCCACCC
189731	21927	GACTGTCAGGAAGGCAGAGA	234318	66514	GGGTTGCCCCATTCAACCTG	278905	111101	TTGAATCAATTCATGCCACC
189732	21928	TGACTGTCAGGAAGGCAGAG	234319	66515	CGGGTTGCCCCATTCAACCT	278906	111102	TTTGAATCAATTCATGCCAC
189733	21929	GTGACTGTCAGGAAGGCAGA	234320	66516	TCGGGTTGCCCCATTCAACC	278907	111103	CTTTGAATCAATTCATGCCA
189734	21930	GGTGACTGTCAGGAAGGCAG	234321	66517	TTCGGGTTGCCCCATTCAAC	278908	111104	TCTTTGAATCAATTCATGCC
189735	21931	GGGTGACTGTCAGGAAGGCA	234322	66518	ATTCGGGTTGCCCCATTCAA	278909	111105	GTCTTTGAATCAATTCATGC
189736	21932	GGGGTGACTGTCAGGAAGGC	234323	66519	AATTCGGGTTGCCCCATTCA	278910	111106	AGTCTTTGAATCAATTCATG
189737	21933	TGGGGTGACTGTCAGGAAGG	234324	66520	CAATTCGGGTTGCCCCATTC	278911	111107	AAGTCTTTGAATCAATTCAT
189738	21934	TTGGGGTGACTGTCAGGAAG	234325	66521	CCAATTCGGGTTGCCCCATT	278912	111108	CAAGTCTTTGAATCAATTCA
189739	21935	GTTGGGGTGACTGTCAGGAA	234326	66522	GCCAATTCGGGTTGCCCCAT	278913	111109	ACAAGTCTTTGAATCAATTC
189740	21936	AGTTGGGGTGACTGTCAGGA	234327	66523	AGCCAATTCGGGTTGCCCCA	278914	111110	CACAAGTCTTTGAATCAATT
189741	21937	GAGTTGGGGTGACTGTCAGG	234328	66524	CAGCCAATTCGGGTTGCCCC	278915	111111	GCACAAGTCTTTGAATCAAT
189742	21938	GGAGTTGGGGTGACTGTCAG	234329	66525	CCAGCCAATTCGGGTTGCCC	278916	111112	TGCACAAGTCTTTGAATCAA
189743	21939	GGGAGTTGGGGTGACTGTCA	234330	66526	GCCAGCCAATTCGGGTTGCC	278917	111113	CTGCACAAGTCTTTGAATCA
189744	21940	TGGGAGTTGGGGTGACTGTC	234331	66527	AGCCAGCCAATTCGGGTTGC	278918	111114	TCTGCACAAGTCTTTGAATC
189745	21941	CTGGGAGTTGGGGTGACTGT	234332	66528	GAGCCAGCCAATTCGGGTTG	278919	111115	CTCTGCACAAGTCTTTGAAT
189746	21942	ACTGGGAGTTGGGGTGACTG	234333	66529	TGAGCCAGCCAATTCGGGTT	278920	111116	CCTCTGCACAAGTCTTTGAA
189747	21943	CACTGGGAGTTGGGGTGACT	234334	66530	GTGAGCCAGCCAATTCGGGT	278921	111117	CCCTCTGCACAAGTCTTTGA
189748	21944	TCACTGGGAGTTGGGGTGAC	234335	66531	GGTGAGCCAGCCAATTCGGG	278922	111118	GCCCTCTGCACAAGTCTTTG
189749	21945	ATCACTGGGAGTTGGGGTGA	234336	66532	AGGTGAGCCAGCCAATTCGG	278923	111119	CGCCCTCTGCACAAGTCTTT
189750	21946	GATCACTGGGAGTTGGGGTG	234337	66533	CAGGTGAGCCAGCCAATTCG	278924	111120	TCGCCCTCTGCACAAGTCTT
189751	21947	GGATCACTGGGAGTTGGGGT	234338	66534	CCAGGTGAGCCAGCCAATTC	278925	111121	GTCGCCCTCTGCACAAGTCT
189752	21948	GGGATCACTGGGAGTTGGGG	234339	66535	CCCAGGTGAGCCAGCCAATT	278926	111122	TGTCGCCCTCTGCACAAGTC
189753	21949	GGGGATCACTGGGAGTTGGG	234340	66536	GCCCAGGTGAGCCAGCCAAT	278927	111123	CTGTCGCCCTCTGCACAAGT
189754	21950	TGGGGATCACTGGGAGTTGG	234341	66537	AGCCCAGGTGAGCCAGCCAA	278928	111124	ACTGTCGCCCTCTGCACAAG
189755	21951	ATGGGGATCACTGGGAGTTG	234342	66538	CAGCCCAGGTGAGCCAGCCA	278929	111125	CACTGTCGCCCTCTGCACAA
189756	21952	GATGGGGATCACTGGGAGTT	234343	66539	GCAGCCCAGGTGAGCCAGCC	278930	111126	TCACTGTCGCCCTCTGCACA
189757	21953	TGATGGGGATCACTGGGAGT	234344	66540	TGCAGCCCAGGTGAGCCAGC	278931	111127	GTCACTGTCGCCCTCTGCAC
189758	21954	TTGATGGGGATCACTGGGAG	234345	66541	CTGCAGCCCAGGTGAGCCAG	278932	111128	AGTCACTGTCGCCCTCTGCA
189759	21955	GTTGATGGGGATCACTGGGA	234346	66542	CCTGCAGCCCAGGTGAGCCA	278933	111129	GAGTCACTGTCGCCCTCTGC
189760	21956	GGTTGATGGGGATCACTGGG	234347	66543	CCCTGCAGCCCAGGTGAGCC	278934	111130	GGAGTCACTGTCGCCCTCTG
189761	21957	TGGTTGATGGGGATCACTGG	234348	66544	TCCCTGCAGCCCAGGTGAGC	278935	111131	AGGAGTCACTGTCGCCCTCT
189762	21958	ATGGTTGATGGGGATCACTG	234349	66545	CTCCCTGCAGCCCAGGTGAG	278936	111132	AAGGAGTCACTGTCGCCCTC

189763	21959	GATGGTTGATGGGGATCACT	234350	66546	GCTCCCTGCAGCCCAGGTGA	278937	111133	CAAGGAGTCACTGTCGCCCT
189764	21960	AGATGGTTGATGGGGATCAC	234351	66547	TGCTCCCTGCAGCCCAGGTG	278938	111134	TCAAGGAGTCACTGTCGCCC
189765	21961	CAGATGGTTGATGGGGATCA	234352	66548	CTGCTCCCTGCAGCCCAGGT	278939	111135	CTCAAGGAGTCACTGTCGCC
189766	21962	TCAGATGGTTGATGGGGATC	234353	66549	TCTGCTCCCTGCAGCCCAGG	278940	111136	TCTCAAGGAGTCACTGTCGC
189767	21963	GTCAGATGGTTGATGGGGAT	234354	66550	CTCTGCTCCCTGCAGCCCAG	278941	111137	TTCTCAAGGAGTCACTGTCG
189768	21964	TGTCAGATGGTTGATGGGGA	234355	66551	TCTCTGCTCCCTGCAGCCCA	278942	111138	CTTCTCAAGGAGTCACTGTC
189769	21965	TTGTCAGATGGTTGATGGGG	234356	66552	ATCTCTGCTCCCTGCAGCCC	278943	111139	GCTTCTCAAGGAGTCACTGT
189770	21966	CTTGTCAGATGGTTGATGGG	234357	66553	GATCTCTGCTCCCTGCAGCC	278944	111140	TGCTTCTCAAGGAGTCACTG
189771	21967	CCTTGTCAGATGGTTGATGG	234358	66554	CGATCTCTGCTCCCTGCAGC	278945	111141	CTGCTTCTCAAGGAGTCACT
189772	21968	CCCTTGTCAGATGGTTGATG	234359	66555	GCGATCTCTGCTCCCTGCAG	278946	111142	ACTGCTTCTCAAGGAGTCAC
189773	21969	CCCCTTGTCAGATGGTTGAT	234360	66556	CGCGATCTCTGCTCCCTGCA	278947	111143	CACTGCTTCTCAAGGAGTCA
189774	21970	TCCCCTTGTCAGATGGTTGA	234361	66557	TCGCGATCTCTGCTCCCTGC	278948	111144	ACACTGCTTCTCAAGGAGTC
189775	21971	GTCCCCTTGTCAGATGGTTG	234362	66558	GTCGCGATCTCTGCTCCCTG	278949	111145	CACACTGCTTCTCAAGGAGT
189776	21972	AGTCCCCTTGTCAGATGGTT	234363	66559	TGTCGCGATCTCTGCTCCCT	278950	111146	TCACACTGCTTCTCAAGGAG
189777	21973	CAGTCCCCTTGTCAGATGGT	234364	66560	GTGTCGCGATCTCTGCTCCC	278951	111147	CTCACACTGCTTCTCAAGGA
189778	21974	TCAGTCCCCTTGTCAGATGG	234365	66561	AGTGTCGCGATCTCTGCTCC	278952	111148	TCTCACACTGCTTCTCAAGG
189779	21975	CTCAGTCCCCTTGTCAGATG	234366	66562	CAGTGTCGCGATCTCTGCTC	278953	111149	TTCTCACACTGCTTCTCAAG
189780	21976	TCTCAGTCCCCTTGTCAGAT	234367	66563	GCAGTGTCGCGATCTCTGCT	278954	111150	TTTCTCACACTGCTTCTCAA
189781	21977	CTCTCAGTCCCCTTGTCAGA	234368	66564	TGCAGTGTCGCGATCTCTGC	278955	111151	CTTTCTCACACTGCTTCTCA
189782	21978	CCTCTCAGTCCCCTTGTCAG	234369	66565	GTGCAGTGTCGCGATCTCTG	278956	111152	GCTTTCTCACACTGCTTCTC
189783	21979	CCCTCTCAGTCCCCTTGTCA	234370	66566	AGTGCAGTGTCGCGATCTCT	278957	111153	GGCTTTCTCACACTGCTTCT
189784	21980	TCCCTCTCAGTCCCCTTGTC	234371	66567	GAGTGCAGTGTCGCGATCTC	278958	111154	AGGCTTTCTCACACTGCTTC
189785	21981	TTCCCTCTCAGTCCCCTTGT	234372	66568	GGAGTGCAGTGTCGCGATCT	278959	111155	CAGGCTTTCTCACACTGCTT
189786	21982	CTTCCCTCTCAGTCCCCTTG	234373	66569	TGGAGTGCAGTGTCGCGATC	278960	111156	ACAGGCTTTCTCACACTGCT
189787	21983	TCTTCCCTCTCAGTCCCCTT	234374	66570	CTGGAGTGCAGTGTCGCGAT	278961	111157	GACAGGCTTTCTCACACTGC
189788	21984	CTCTTCCCTCTCAGTCCCCT	234375	66571	GCTGGAGTGCAGTGTCGCGA	278962	111158	GGACAGGCTTTCTCACACTG
189789	21985	TCTCTTCCCTCTCAGTCCCC	234376	66572	GGCTGGAGTGCAGTGTCGCG	278963	111159	GGGACAGGCTTTCTCACACT
189790	21986	TTCTCTTCCCTCTCAGTCCC	234377	66573	AGGCTGGAGTGCAGTGTCGC	278964	111160	TGGGACAGGCTTTCTCACAC
189791	21987	TTTCTCTTCCCTCTCAGTCC	234378	66574	CAGGCTGGAGTGCAGTGTCG	278965	111161	GTGGGACAGGCTTTCTCACA
189792	21988	CTTTCTCTTCCCTCTCAGTC	234379	66575	CCAGGCTGGAGTGCAGTGTC	278966	111162	GGTGGGACAGGCTTTCTCAC
189793	21989	CCTTTCTCTTCCCTCTCAGT	234380	66576	CCCAGGCTGGAGTGCAGTGT	278967	111163	AGGTGGGACAGGCTTTCTCA
189794	21990	TCCTTTCTCTTCCCTCTCAG	234381	66577	GCCCAGGCTGGAGTGCAGTG	278968	111164	GAGGTGGGACAGGCTTTCTC
189795	21991	CTCCTTTCTCTTCCCTCTCA	234382	66578	TGCCCAGGCTGGAGTGCAGT	278969	111165	GGAGGTGGGACAGGCTTTCT
189796	21992	CCTCCTTTCTCTTCCCTCTC	234383	66579	TTGCCCAGGCTGGAGTGCAG	278970	111166	AGGAGGTGGGACAGGCTTTC
189797	21993	CCCTCCTTTCTCTTCCCTCT	234384	66580	GTTGCCCAGGCTGGAGTGCA	278971	111167	AAGGAGGTGGGACAGGCTTT
189798	21994	CCCCTCCTTTCTCTTCCCTC	234385	66581	TGTTGCCCAGGCTGGAGTGC	278972	111168	GAAGGAGGTGGGACAGGCTT
189799	21995	GCCCCTCCTTTCTCTTCCCT	234386	66582	TTGTTGCCCAGGCTGGAGTG	278973	111169	GGAAGGAGGTGGGACAGGCT
189800	21996	GGCCCCTCCTTTCTCTTCCC	234387	66583	TTTGTTGCCCAGGCTGGAGT	278974	111170	CGGAAGGAGGTGGGACAGGC
189801	21997	GGGCCCCTCCTTTCTCTTCC	234388	66584	CTTTGTTGCCCAGGCTGGAG	278975	111171	GCGGAAGGAGGTGGGACAGG
189802	21998	TGGGCCCCTCCTTTCTCTTC	234389	66585	GCTTTGTTGCCCAGGCTGGA	278976	111172	TGCGGAAGGAGGTGGGACAG
189803	21999	TTGGGCCCCTCCTTTCTCTT	234390	66586	CGCTTTGTTGCCCAGGCTGG	278977	111173	CTGCGGAAGGAGGTGGGACA
189804	22000	TTTGGGCCCCTCCTTTCTCT	234391	66587	TCGCTTTGTTGCCCAGGCTG	278978	111174	GCTGCGGAAGGAGGTGGGAC
189805	22001	CTTTGGGCCCCTCCTTTCTC	234392	66588	CTCGCTTTGTTGCCCAGGCT	278979	111175	AGCTGCGGAAGGAGGTGGGA
189806	22002	TCTTTGGGCCCCTCCTTTCT	234393	66589	TCTCGCTTTGTTGCCCAGGC	278980	111176	GAGCTGCGGAAGGAGGTGGG
189807	22003	CTCTTTGGGCCCCTCCTTTC	234394	66590	GTCTCGCTTTGTTGCCCAGG	278981	111177	GGAGCTGCGGAAGGAGGTGG
189808	22004	CCTCTTTGGGCCCCTCCTTT	234395	66591	AGTCTCGCTTTGTTGCCCAG	278982	111178	TGGAGCTGCGGAAGGAGGTG
189809	22005	TCCTCTTTGGGCCCCTCCTT	234396	66592	GAGTCTCGCTTTGTTGCCCA	278983	111179	CTGGAGCTGCGGAAGGAGGT
189810	22006	TTCCTCTTTGGGCCCCTCCT	234397	66593	AGAGTCTCGCTTTGTTGCCC	278984	111180	GCTGGAGCTGCGGAAGGAGG
189811	22007	CTTCCTCTTTGGGCCCCTCC	234398	66594	TAGAGTCTCGCTTTGTTGCC	278985	111181	GGCTGGAGCTGCGGAAGGAG
189812	22008	CCTTCCTCTTTGGGCCCCTC	234399	66595	ATAGAGTCTCGCTTTGTTGC	278986	111182	AGGCTGGAGCTGCGGAAGGA
189813	22009	ACCTTCCTCTTTGGGCCCCT	234400	66596	GATAGAGTCTCGCTTTGTTG	278987	111183	CAGGCTGGAGCTGCGGAAGG
189814	22010	TACCTTCCTCTTTGGGCCCC	234401	66597	AGATAGAGTCTCGCTTTGTT	278988	111184	CCAGGCTGGAGCTGCGGAAG
189815	22011	TTACCTTCCTCTTTGGGCCC	234402	66598	GAGATAGAGTCTCGCTTTGT	278989	111185	CCCAGGCTGGAGCTGCGGAA
189816	22012	TTTACCTTCCTCTTTGGGCC	234403	66599	TGAGATAGAGTCTCGCTTTG	278990	111186	GCCCAGGCTGGAGCTGCGGA
189817	22013	TTTTACCTTCCTCTTTGGGC	234404	66600	TTGAGATAGAGTCTCGCTTT	278991	111187	AGCCCAGGCTGGAGCTGCGG
189818	22014	GTTTTACCTTCCTCTTTGGG	234405	66601	TTTGAGATAGAGTCTCGCTT	278992	111188	CAGCCCAGGCTGGAGCTGCG
189819	22015	AGTTTTACCTTCCTCTTTGG	234406	66602	TTTTGAGATAGAGTCTCGCT	278993	111189	TCAGCCCAGGCTGGAGCTGC
189820	22016	CAGTTTTACCTTCCTCTTTG	234407	66603	TTTTTGAGATAGAGTCTCGC	278994	111190	CTCAGCCCAGGCTGGAGCTG
189821	22017	ACAGTTTTACCTTCCTCTTT	234408	66604	TTTTTTGAGATAGAGTCTCG	278995	111191	CCTCAGCCCAGGCTGGAGCT
189822	22018	GACAGTTTTACCTTCCTCTT	234409	66605	TTTTTTTGAGATAGAGTCTC	278996	111192	GCCTCAGCCCAGGCTGGAGC
189823	22019	CGACAGTTTTACCTTCCTCT	234410	66606	TTTTTTTTGAGATAGAGTCT	278997	111193	TGCCTCAGCCCAGGCTGGAG
189824	22020	CCGACAGTTTTACCTTCCTC	234411	66607	TTTTTTTTTGAGATAGAGTC	278998	111194	GTGCCTCAGCCCAGGCTGGA
189825	22021	CCCGACAGTTTTACCTTCCT	234412	66608	TTTTTTTTTTGAGATAGAGT	278999	111195	AGTGCCTCAGCCCAGGCTGG
189826	22022	TCCCGACAGTTTTACCTTCC	234413	66609	TTTTTTTTTTTGAGATAGAG	279000	111196	CAGTGCCTCAGCCCAGGCTG
189827	22023	TTCCCGACAGTTTTACCTTC	234414	66610	TTTTTTTTTTTTGAGATAGA	279001	111197	ACAGTGCCTCAGCCCAGGCT
189828	22024	GTTCCCGACAGTTTTACCTT	234415	66611	CTTTTTTTTTTTTGAGATAG	279002	111198	GACAGTGCCTCAGCCCAGGC
189829	22025	TGTTCCCGACAGTTTTACCT	234416	66612	ACTTTTTTTTTTTTGAGATA	279003	111199	TGACAGTGCCTCAGCCCAGG
189830	22026	CTGTTCCCGACAGTTTTACC	234417	66613	AACTTTTTTTTTTTTGAGAT	279004	111200	GTGACAGTGCCTCAGCCCAG
189831	22027	GCTGTTCCCGACAGTTTTAC	234418	66614	GAACTTTTTTTTTTTTGAGA	279005	111201	TGTGACAGTGCCTCAGCCCA
189832	22028	GGCTGTTCCCGACAGTTTTA	234419	66615	TGAACTTTTTTTTTTTTGAG	279006	111202	CTGTGACAGTGCCTCAGCCC
189833	22029	GGGCTGTTCCCGACAGTTTT	234420	66616	ATGAACTTTTTTTTTTTTGA	279007	111203	ACTGTGACAGTGCCTCAGCC
189834	22030	GGGGCTGTTCCCGACAGTTT	234421	66617	TATGAACTTTTTTTTTTTTG	279008	111204	CACTGTGACAGTGCCTCAGC

189835	22031	GGGGGCTGTTCCCGACAGTT	234422	66618	TTATGAACTTTTTTTTTTT	279009	111205	ACACTGTGACAGTGCCTCAG
189836	22032	TGGGGGCTGTTCCCGACAGT	234423	66619	TTTATGAACTTTTTTTTTT	279010	111206	GACACTGTGACAGTGCCTCA
189837	22033	TTGGGGGCTGTTCCCGACAG	234424	66620	ATTTATGAACTTTTTTTTT	279011	111207	AGACACTGTGACAGTGCCTC
189838	22034	TTTGGGGGCTGTTCCCGACA	234425	66621	AATTTATGAACTTTTTTTT	279012	111208	GAGACACTGTGACAGTGCCT
189839	22035	ATTTGGGGGCTGTTCCCGAC	234426	66622	GAATTTATGAACTTTTTTT	279013	111209	GGAGACACTGTGACAGTGCC
189840	22036	CATTTGGGGGCTGTTCCCGA	234427	66623	TGAATTTATGAACTTTTTT	279014	111210	AGGAGACACTGTGACAGTGC
189841	22037	ACATTTGGGGGCTGTTCCCG	234428	66624	TTGAATTTATGAACTTTTT	279015	111211	AAGGAGACACTGTGACAGTG
189842	22038	CACATTTGGGGGCTGTTCCC	234429	66625	TTTGAATTTATGAACTTTT	279016	111212	CAAGGAGACACTGTGACAGT
189843	22039	ACACATTTGGGGGCTGTTCC	234430	66626	CTTTGAATTTATGAACTTT	279017	111213	GCAAGGAGACACTGTGACAG
189844	22040	CACACATTTGGGGGCTGTTC	234431	66627	ACTTTGAATTTATGAACTT	279018	111214	AGCAAGGAGACACTGTGACA
189845	22041	TCACACATTTGGGGGCTGTT	234432	66628	AACTTTGAATTTATGAACTT	279019	111215	CAGCAAGGAGACACTGTGAC
189846	22042	GTCACACATTTGGGGGCTGT	234433	66629	TAACTTTGAATTTATGAACT	279020	111216	CCAGCAAGGAGACACTGTGA
189847	22043	TGTCACACATTTGGGGGCTG	234434	66630	ATAACTTTGAATTTATGAAC	279021	111217	GCCAGCAAGGAGACACTGTG
189848	22044	CTGTCACACATTTGGGGGCT	234435	66631	CATAACTTTGAATTTATGAA	279022	111218	TGCCAGCAAGGAGACACTGT
189849	22045	GCTGTCACACATTTGGGGGC	234436	66632	TCATAACTTTGAATTTATGA	279023	111219	CTGCCAGCAAGGAGACACTG
189850	22046	GGCTGTCACACATTTGGGGG	234437	66633	TTCATAACTTTGAATTTATG	279024	111220	CCTGCCAGCAAGGAGACACT
189851	22047	AGGCTGTCACACATTTGGGG	234438	66634	ATTCATAACTTTGAATTTAT	279025	111221	TCCTGCCAGCAAGGAGACAC
189852	22048	AAGGCTGTCACACATTTGGG	234439	66635	AATTCATAACTTTGAATTTA	279026	111222	CTCCTGCCAGCAAGGAGACA
189853	22049	GAAGGCTGTCACACATTTGG	234440	66636	TAATTCATAACTTTGAATTT	279027	111223	TCTCCTGCCAGCAAGGAGAC
189854	22050	TGAAGGCTGTCACACATTTG	234441	66637	ATAATTCATAACTTTGAATT	279028	111224	CTCTCCTGCCAGCAAGGAGA
189855	22051	CTGAAGGCTGTCACACATTT	234442	66638	AATAATTCATAACTTTGAAT	279029	111225	TCTCTCCTGCCAGCAAGGAG
189856	22052	ACTGAAGGCTGTCACACATT	234443	66639	AAATAATTCATAACTTTGAA	279030	111226	TTCTCTCCTGCCAGCAAGGA
189857	22053	CACTGAAGGCTGTCACACAT	234444	66640	AAAATAATTCATAACTTTGA	279031	111227	ATTCTCTCCTGCCAGCAAGG
189858	22054	CCACTGAAGGCTGTCACACA	234445	66641	AAAAATAATTCATAACTTTG	279032	111228	AATTCTCTCCTGCCAGCAAG
189859	22055	TCCACTGAAGGCTGTCACAC	234446	66642	TAAAAATAATTCATAACTTT	279033	111229	AAATTCTCTCCTGCCAGCAA
189860	22056	CTCCACTGAAGGCTGTCACA	234447	66643	TTAAAAATAATTCATAACTT	279034	111230	GAAATTCTCTCCTGCCAGCA
189861	22057	ACTCCACTGAAGGCTGTCAC	234448	66644	TTTAAAAATAATTCATAACT	279035	111231	TGAAATTCTCTCCTGCCAGC
189862	22058	AACTCCACTGAAGGCTGTCA	234449	66645	TTTTAAAAATAATTCATAAC	279036	111232	TTGAAATTCTCTCCTGCCAG
189863	22059	CAACTCCACTGAAGGCTGTC	234450	66646	ATTTTAAAAATAATTCATAA	279037	111233	GTTGAAATTCTCTCCTGCCA
189864	22060	GCAACTCCACTGAAGGCTGT	234451	66647	TATTTTAAAAATAATTCATA	279038	111234	TGTTGAAATTCTCTCCTGCC
189865	22061	GGCAACTCCACTGAAGGCTG	234452	66648	TTATTTTAAAAATAATTCAT	279039	111235	ATGTTGAAATTCTCTCCTGC
189866	22062	GGGCAACTCCACTGAAGGCT	234453	66649	ATTATTTTAAAAATAATTCA	279040	111236	AATGTTGAAATTCTCTCCTG
189867	22063	TGGGCAACTCCACTGAAGGC	234454	66650	TATTATTTTAAAAATAATTC	279041	111237	GAATGTTGAAATTCTCTCCT
189868	22064	GTGGGCAACTCCACTGAAGG	234455	66651	TTATTATTTTAAAAATAATT	279042	111238	TGAATGTTGAAATTCTCTCC
189869	22065	AGTGGGCAACTCCACTGAAG	234456	66652	ATTATTATTTTAAAAATAAT	279043	111239	GTGAATGTTGAAATTCTCTC
189870	22066	AAGTGGGCAACTCCACTGAA	234457	66653	TATTATTATTTTAAAAATAA	279044	111240	GGTGAATGTTGAAATTCTCT
189871	22067	AAAGTGGGCAACTCCACTGA	234458	66654	TTATTATTATTTTAAAAATA	279045	111241	TGGTGAATGTTGAAATTCTC
189872	22068	GAAAGTGGGCAACTCCACTG	234459	66655	ATTATTATTATTTTAAAAAT	279046	111242	TTGGTGAATGTTGAAATTCT
189873	22069	GGAAAGTGGGCAACTCCACT	234460	66656	AATTATTATTATTTTAAAAA	279047	111243	TTTGGTGAATGTTGAAATTC
189874	22070	GGGAAAGTGGGCAACTCCAC	234461	66657	AAATTATTATTATTTTAAAA	279048	111244	TTTTGGTGAATGTTGAAATT
189875	22071	AGGGAAAGTGGGCAACTCCA	234462	66658	TAAATTATTATTATTTTAAA	279049	111245	TTTTTGGTGAATGTTGAAAT
189876	22072	AAGGGAAAGTGGGCAACTCC	234463	66659	GTAAATTATTATTATTTTAA	279050	111246	CTTTTTGGTGAATGTTGAAA
189877	22073	AAAGGGAAAGTGGGCAACTC	234464	66660	TGTAAATTATTATTATTTTA	279051	111247	ACTTTTTGGTGAATGTTGAA
189878	22074	AAAAGGGAAAGTGGGCAACT	234465	66661	TTGTAAATTATTATTATTTT	279052	111248	TACTTTTTGGTGAATGTTGA
189879	22075	GAAAAGGGAAAGTGGGCAAC	234466	66662	ATTGTAAATTATTATTATTT	279053	111249	CTACTTTTTGGTGAATGTTG
189880	22076	AGAAAAGGGAAAGTGGGCAA	234467	66663	TATTGTAAATTATTATTATT	279054	111250	ACTACTTTTTGGTGAATGTT
189881	22077	GAGAAAAGGGAAAGTGGGCA	234468	66664	TTATTGTAAATTATTATTAT	279055	111251	TACTACTTTTTGGTGAATGT
189882	22078	GGAGAAAAGGGAAAGTGGGC	234469	66665	TTTATTGTAAATTATTATTA	279056	111252	ATACTACTTTTTGGTGAATG
189883	22079	AGGAGAAAAGGGAAAGTGGG	234470	66666	CTTTATTGTAAATTATTATT	279057	111253	AATACTACTTTTTGGTGAAT
189884	22080	GAGGAGAAAAGGGAAAGTGG	234471	66667	TCTTTATTGTAAATTATTAT	279058	111254	CAATACTACTTTTTGGTGAA
189885	22081	GGAGGAGAAAAGGGAAAGTG	234472	66668	ATCTTTATTGTAAATTATTA	279059	111255	ACAATACTACTTTTTGGTGA
189886	22082	GGGAGGAGAAAAGGGAAAGT	234473	66669	CATCTTTATTGTAAATTATT	279060	111256	AACAATACTACTTTTTGGTG
189887	22083	AGGGAGGAGAAAAGGGAAAG	234474	66670	TCATCTTTATTGTAAATTAT	279061	111257	AAACAATACTACTTTTTGGT
189888	22084	CAGGGAGGAGAAAAGGGAAA	234475	66671	CTCATCTTTATTGTAAATTA	279062	111258	AAAACAATACTACTTTTTGG
189889	22085	GCAGGGAGGAGAAAAGGGAA	234476	66672	CCTCATCTTTATTGTAAATT	279063	111259	AAAAACAATACTACTTTTTG
189890	22086	TGCAGGGAGGAGAAAAGGGA	234477	66673	TCCTCATCTTTATTGTAAAT	279064	111260	TAAAAACAATACTACTTTTT
189891	22087	CTGCAGGGAGGAGAAAAGGG	234478	66674	GTCCTCATCTTTATTGTAAA	279065	111261	ATAAAAACAATACTACTTTT
189892	22088	CCTGCAGGGAGGAGAAAAGG	234479	66675	TGTCCTCATCTTTATTGTAA	279066	111262	AATAAAAACAATACTACTTT
189893	22089	TCCTGCAGGGAGGAGAAAAG	234480	66676	TTGTCCTCATCTTTATTGTA	279067	111263	TAATAAAAACAATACTACTT
189894	22090	GTCCTGCAGGGAGGAGAAAA	234481	66677	TTTGTCCTCATCTTTATTGT	279068	111264	CTAATAAAAACAATACTACT
189895	22091	GGTCCTGCAGGGAGGAGAAA	234482	66678	CTTTGTCCTCATCTTTATTG	279069	111265	CCTAATAAAAACAATACTAC
189896	22092	AGGTCCTGCAGGGAGGAGAA	234483	66679	ACTTTGTCCTCATCTTTATT	279070	111266	ACCTAATAAAAACAATACTA
189897	22093	GAGGTCCTGCAGGGAGGAGA	234484	66680	CACTTTGTCCTCATCTTTAT	279071	111267	AACCTAATAAAAACAATACT
189898	22094	GGAGGTCCTGCAGGGAGGAG	234485	66681	ACACTTTGTCCTCATCTTTA	279072	111268	AAACCTAATAAAAACAATAC
189899	22095	GGGAGGTCCTGCAGGGAGGA	234486	66682	CACACTTTGTCCTCATCTTT	279073	111269	TAAACCTAATAAAAACAATA
189900	22096	AGGGAGGTCCTGCAGGGAGG	234487	66683	TCACACTTTGTCCTCATCTT	279074	111270	ATAAACCTAATAAAAACAAT
189901	22097	AAGGGAGGTCCTGCAGGGAG	234488	66684	CTCACACTTTGTCCTCATCT	279075	111271	CATAAACCTAATAAAAACAA
189902	22098	GAAGGGAGGTCCTGCAGGGA	234489	66685	ACTCACACTTTGTCCTCATC	279076	111272	TCATAAACCTAATAAAAACA
189903	22099	AGAAGGGAGGTCCTGCAGGG	234490	66686	TACTCACACTTTGTCCTCAT	279077	111273	CTCATAAACCTAATAAAAAC
189904	22100	GAGAAGGGAGGTCCTGCAGG	234491	66687	TTACTCACACTTTGTCCTCA	279078	111274	CCTCATAAACCTAATAAAAA
189905	22101	GGAGAAGGGAGGTCCTGCAG	234492	66688	TTTACTCACACTTTGTCCTC	279079	111275	GCCTCATAAACCTAATAAAA
189906	22102	GGGAGAAGGGAGGTCCTGCA	234493	66689	ATTTACTCACACTTTGTCCT	279080	111276	AGCCTCATAAACCTAATAAA

189907	22103	GGGGAGAAGGGAGGTCCTGC	234494	66690	CATTTACTCACACTTTGTCC	279081	111277	CAGCCTCATAAACCTAATAA
189908	22104	TGGGGAGAAGGGAGGTCCTG	234495	66691	CCATTTACTCACACTTTGTC	279082	111278	ACAGCCTCATAAACCTAATA
189909	22105	CTGGGGAGAAGGGAGGTCCT	234496	66692	ACCATTTACTCACACTTTGT	279083	111279	TACAGCCTCATAAACCTAAT
189910	22106	ACTGGGGAGAAGGGAGGTCC	234497	66693	CACCATTTACTCACACTTTG	279084	111280	CTACAGCCTCATAAACCTAA
189911	22107	GACTGGGGAGAAGGGAGGTC	234498	66694	CCACCATTTACTCACACTTT	279085	111281	GCTACAGCCTCATAAACCTA
189912	22108	GGACTGGGGAGAAGGGAGGT	234499	66695	ACCACCATTTACTCACACTT	279086	111282	GGCTACAGCCTCATAAACCT
189913	22109	AGGACTGGGGAGAAGGGAGG	234500	66696	AACCACCATTTACTCACACT	279087	111283	AGGCTACAGCCTCATAAACC
189914	22110	GAGGACTGGGGAGAAGGGAG	234501	66697	AAACCACCATTTACTCACAC	279088	111284	AAGGCTACAGCCTCATAAAC
189915	22111	GGAGGACTGGGGAGAAGGGA	234502	66698	GAAACCACCATTTACTCACA	279089	111285	CAAGGCTACAGCCTCATAAA
189916	22112	GGGAGGACTGGGGAGAAGGG	234503	66699	AGAAACCACCATTTACTCAC	279090	111286	TCAAGGCTACAGCCTCATAA
189917	22113	GGGGAGGACTGGGGAGAAGG	234504	66700	TAGAAACCACCATTTACTCA	279091	111287	CTCAAGGCTACAGCCTCATA
189918	22114	TGGGGAGGACTGGGGAGAAG	234505	66701	ATAGAAACCACCATTTACTC	279092	111288	CCTCAAGGCTACAGCCTCAT
189919	22115	TTGGGGAGGACTGGGGAGAA	234506	66702	GATAGAAACCACCATTTACT	279093	111289	TCCTCAAGGCTACAGCCTCA
189920	22116	GTTGGGGAGGACTGGGGAGA	234507	66703	GGATAGAAACCACCATTTAC	279094	111290	GTCCTCAAGGCTACAGCCTC
189921	22117	AGTTGGGGAGGACTGGGGAG	234508	66704	TGGATAGAAACCACCATTTA	279095	111291	TGTCCTCAAGGCTACAGCCT
189922	22118	AAGTTGGGGAGGACTGGGGA	234509	66705	CTGGATAGAAACCACCATTT	279096	111292	CTGTCCTCAAGGCTACAGCC
189923	22119	GAAGTTGGGGAGGACTGGGG	234510	66706	GCTGGATAGAAACCACCATT	279097	111293	GCTGTCCTCAAGGCTACAGC
189924	22120	AGAAGTTGGGGAGGACTGGG	234511	66707	AGCTGGATAGAAACCACCAT	279098	111294	GGCTGTCCTCAAGGCTACAG
189925	22121	CAGAAGTTGGGGAGGACTGG	234512	66708	GAGCTGGATAGAAACCACCA	279099	111295	GGGCTGTCCTCAAGGCTACA
189926	22122	TCAGAAGTTGGGGAGGACTG	234513	66709	AGAGCTGGATAGAAACCACC	279100	111296	TGGGCTGTCCTCAAGGCTAC
189927	22123	CTCAGAAGTTGGGGAGGACT	234514	66710	CAGAGCTGGATAGAAACCAC	279101	111297	CTGGGCTGTCCTCAAGGCTA
189928	22124	CCTCAGAAGTTGGGGAGGAC	234515	66711	ACAGAGCTGGATAGAAACCA	279102	111298	CCTGGGCTGTCCTCAAGGCT
189929	22125	ACCTCAGAAGTTGGGGAGGA	234516	66712	AACAGAGCTGGATAGAAACC	279103	111299	TCCTGGGCTGTCCTCAAGGC
189930	22126	AACCTCAGAAGTTGGGGAGG	234517	66713	CAACAGAGCTGGATAGAAAC	279104	111300	GTCCTGGGCTGTCCTCAAGG
189931	22127	TAACCTCAGAAGTTGGGGAG	234518	66714	TCAACAGAGCTGGATAGAAA	279105	111301	TGTCCTGGGCTGTCCTCAAG
189932	22128	GTAACCTCAGAAGTTGGGGA	234519	66715	CTCAACAGAGCTGGATAGAA	279106	111302	TTGTCCTGGGCTGTCCTCAA
189933	22129	TGTAACCTCAGAAGTTGGGG	234520	66716	GCTCAACAGAGCTGGATAGA	279107	111303	GTTGTCCTGGGCTGTCCTCA
189934	22130	ATGTAACCTCAGAAGTTGGG	234521	66717	AGCTCAACAGAGCTGGATAG	279108	111304	AGTTGTCCTGGGCTGTCCTC
189935	22131	AATGTAACCTCAGAAGTTGG	234522	66718	CAGCTCAACAGAGCTGGATA	279109	111305	AAGTTGTCCTGGGCTGTCCT
189936	22132	CAATGTAACCTCAGAAGTTG	234523	66719	TCAGCTCAACAGAGCTGGAT	279110	111306	AAAGTTGTCCTGGGCTGTCC
189937	22133	TCAATGTAACCTCAGAAGTT	234524	66720	TTCAGCTCAACAGAGCTGGA	279111	111307	CAAAGTTGTCCTGGGCTGTC
189938	22134	CTCAATGTAACCTCAGAAGT	234525	66721	CTTCAGCTCAACAGAGCTGG	279112	111308	ACAAAGTTGTCCTGGGCTGT
189939	22135	TCTCAATGTAACCTCAGAAG	234526	66722	ACTTCAGCTCAACAGAGCTG	279113	111309	AACAAAGTTGTCCTGGGCTG
189940	22136	TTCTCAATGTAACCTCAGAA	234527	66723	CACTTCAGCTCAACAGAGCT	279114	111310	CAACAAAGTTGTCCTGGGCT
189941	22137	TTTCTCAATGTAACCTCAGA	234528	66724	CCACTTCAGCTCAACAGAGC	279115	111311	ACAACAAAGTTGTCCTGGGC
189942	22138	TTTTCTCAATGTAACCTCAG	234529	66725	GCCACTTCAGCTCAACAGAG	279116	111312	GACAACAAAGTTGTCCTGGG
189943	22139	CTTTTCTCAATGTAACCTCA	234530	66726	TGCCACTTCAGCTCAACAGA	279117	111313	TGACAACAAAGTTGTCCTGG
189944	22140	ACTTTTCTCAATGTAACCTC	234531	66727	ATGCCACTTCAGCTCAACAG	279118	111314	GTGACAACAAAGTTGTCCTG
189945	22141	GACTTTTCTCAATGTAACCT	234532	66728	GATGCCACTTCAGCTCAACA	279119	111315	TGTGACAACAAAGTTGTCCT
189946	22142	AGACTTTTCTCAATGTAACC	234533	66729	AGATGCCACTTCAGCTCAAC	279120	111316	ATGTGACAACAAAGTTGTCC
189947	22143	CAGACTTTTCTCAATGTAAC	234534	66730	GAGATGCCACTTCAGCTCAA	279121	111317	TATGTGACAACAAAGTTGTC
189948	22144	GCAGACTTTTCTCAATGTAA	234535	66731	GGAGATGCCACTTCAGCTCA	279122	111318	CTATGTGACAACAAAGTTGT
189949	22145	TGCAGACTTTTCTCAATGTA	234536	66732	GGGAGATGCCACTTCAGCTC	279123	111319	TCTATGTGACAACAAAGTTG
189950	22146	CTGCAGACTTTTCTCAATGT	234537	66733	AGGGAGATGCCACTTCAGCT	279124	111320	ATCTATGTGACAACAAAGTT
189951	22147	TCTGCAGACTTTTCTCAATG	234538	66734	CAGGGAGATGCCACTTCAGC	279125	111321	TATCTATGTGACAACAAAGT
189952	22148	CTCTGCAGACTTTTCTCAAT	234539	66735	GCAGGGAGATGCCACTTCAG	279126	111322	CTATCTATGTGACAACAAAG
189953	22149	TCTCTGCAGACTTTTCTCAA	234540	66736	AGCAGGGAGATGCCACTTCA	279127	111323	GCTATCTATGTGACAACAAA
189954	22150	CTCTCTGCAGACTTTTCTCA	234541	66737	CAGCAGGGAGATGCCACTTC	279128	111324	GGCTATCTATGTGACAACAA
189955	22151	CCTCTCTGCAGACTTTTCTC	234542	66738	CCAGCAGGGAGATGCCACTT	279129	111325	AGGCTATCTATGTGACAACA
189956	22152	ACCTCTCTGCAGACTTTTCT	234543	66739	CCCAGCAGGGAGATGCCACT	279130	111326	CAGGCTATCTATGTGACAAC
189957	22153	CACCTCTCTGCAGACTTTTC	234544	66740	CCCCAGCAGGGAGATGCCAC	279131	111327	ACAGGCTATCTATGTGACAA
189958	22154	GCACCTCTCTGCAGACTTTT	234545	66741	GCCCCAGCAGGGAGATGCCA	279132	111328	CACAGGCTATCTATGTGACA
189959	22155	GGCACCTCTCTGCAGACTTT	234546	66742	AGCCCCAGCAGGGAGATGCC	279133	111329	CCACAGGCTATCTATGTGAC
189960	22156	TGGCACCTCTCTGCAGACTT	234547	66743	AAGCCCCAGCAGGGAGATGC	279134	111330	GCCACAGGCTATCTATGTGA
189961	22157	CTGGCACCTCTCTGCAGACT	234548	66744	AAAGCCCCAGCAGGGAGATG	279135	111331	AGCCACAGGCTATCTATGTG
189962	22158	GCTGGCACCTCTCTGCAGAC	234549	66745	AAAAGCCCCAGCAGGGAGAT	279136	111332	TAGCCACAGGCTATCTATGT
189963	22159	TGCTGGCACCTCTCTGCAGA	234550	66746	CAAAAGCCCCAGCAGGGAGA	279137	111333	GTAGCCACAGGCTATCTATG
189964	22160	ATGCTGGCACCTCTCTGCAG	234551	66747	CCAAAAGCCCCAGCAGGGAG	279138	111334	TGTAGCCACAGGCTATCTAT
189965	22161	GATGCTGGCACCTCTCTGCA	234552	66748	CCCAAAAGCCCCAGCAGGGA	279139	111335	TTGTAGCCACAGGCTATCTA
189966	22162	TGATGCTGGCACCTCTCTGC	234553	66749	CCCCAAAAGCCCCAGCAGGG	279140	111336	TTTGTAGCCACAGGCTATCT
189967	22163	GTGATGCTGGCACCTCTCTG	234554	66750	TCCCCAAAAGCCCCAGCAGG	279141	111337	GTTTGTAGCCACAGGCTATC
189968	22164	TGTGATGCTGGCACCTCTCT	234555	66751	TTCCCCAAAAGCCCCAGCAG	279142	111338	AGTTTGTAGCCACAGGCTAT
189969	22165	TTGTGATGCTGGCACCTCTC	234556	66752	CTTCCCCAAAAGCCCCAGCA	279143	111339	GAGTTTGTAGCCACAGGCTA
189970	22166	CTTGTGATGCTGGCACCTCT	234557	66753	TCTTCCCCAAAAGCCCCAGC	279144	111340	AGAGTTTGTAGCCACAGGCT
189971	22167	CCTTGTGATGCTGGCACCTC	234558	66754	TTCTTCCCCAAAAGCCCCAG	279145	111341	CAGAGTTTGTAGCCACAGGC
189972	22168	ACCTTGTGATGCTGGCACCT	234559	66755	CTTCTTCCCCAAAAGCCCCA	279146	111342	TCAGAGTTTGTAGCCACAGG
189973	22169	CACCTTGTGATGCTGGCACC	234560	66756	CCTTCTTCCCCAAAAGCCCC	279147	111343	CTCAGAGTTTGTAGCCACAG
189974	22170	ACACCTTGTGATGCTGGCAC	234561	66757	CCCTTCTTCCCCAAAAGCCC	279148	111344	TCTCAGAGTTTGTAGCCACA
189975	22171	AACACCTTGTGATGCTGGCA	234562	66758	ACCCTTCTTCCCCAAAAGCC	279149	111345	ATCTCAGAGTTTGTAGCCAC
189976	22172	TAACACCTTGTGATGCTGGC	234563	66759	CACCCTTCTTCCCCAAAAGC	279150	111346	GATCTCAGAGTTTGTAGCCA
189977	22173	TTAACACCTTGTGATGCTGG	234564	66760	ACACCCTTCTTCCCCAAAAG	279151	111347	AGATCTCAGAGTTTGTAGCC
189978	22174	CTTAACACCTTGTGATGCTG	234565	66761	CACACCCTTCTTCCCCAAAA	279152	111348	TAGATCTCAGAGTTTGTAGC

189979	22175	CCTTAACACCTTGTGATGCT	234566	66762	ACACACCCTTCTTCCCCAAA	279153	111349	CTAGATCTCAGAGTTTGTAG
189980	22176	TCCTTAACACCTTGTGATGC	234567	66763	CACACACCCTTCTTCCCCAA	279154	111350	TCTAGATCTCAGAGTTTGTA
189981	22177	GTCCTTAACACCTTGTGATG	234568	66764	ACACACACCCTTCTTCCCCA	279155	111351	ATCTAGATCTCAGAGTTTGT
189982	22178	GGTCCTTAACACCTTGTGAT	234569	66765	AACACACACCCTTCTTCCCC	279156	111352	AATCTAGATCTCAGAGTTTG
189983	22179	TGGTCCTTAACACCTTGTGA	234570	66766	CAACACACACCCTTCTTCCC	279157	111353	GAATCTAGATCTCAGAGTTT
189984	22180	GTGGTCCTTAACACCTTGTG	234571	66767	GCAACACACACCCTTCTTCC	279158	111354	AGAATCTAGATCTCAGAGTT
189985	22181	CGTGGTCCTTAACACCTTGT	234572	66768	AGCAACACACACCCTTCTTC	279159	111355	AAGAATCTAGATCTCAGAGT
189986	22182	TCGTGGTCCTTAACACCTTG	234573	66769	GAGCAACACACACCCTTCTT	279160	111356	GAAGAATCTAGATCTCAGAG
189987	22183	CTCGTGGTCCTTAACACCTT	234574	66770	AGAGCAACACACACCCTTCT	279161	111357	AGAAGAATCTAGATCTCAGA
189988	22184	ACTCGTGGTCCTTAACACCT	234575	66771	AAGAGCAACACACACCCTTC	279162	111358	CAGAAGAATCTAGATCTCAG
189989	22185	AACTCGTGGTCCTTAACACC	234576	66772	GAAGAGCAACACACACCCTT	279163	111359	ACAGAAGAATCTAGATCTCA
189990	22186	AAACTCGTGGTCCTTAACAC	234577	66773	TGAAGAGCAACACACACCCT	279164	111360	CACAGAAGAATCTAGATCTC
189991	22187	CAAACTCGTGGTCCTTAACA	234578	66774	CTGAAGAGCAACACACACCC	279165	111361	CCACAGAAGAATCTAGATCT
189992	22188	CCAAACTCGTGGTCCTTAAC	234579	66775	TCTGAAGAGCAACACACACC	279166	111362	GCCACAGAAGAATCTAGATC
189993	22189	GCCAAACTCGTGGTCCTTAA	234580	66776	ATCTGAAGAGCAACACACAC	279167	111363	AGCCACAGAAGAATCTAGAT
189994	22190	TGCCAAACTCGTGGTCCTTA	234581	66777	GATCTGAAGAGCAACACACA	279168	111364	CAGCCACAGAAGAATCTAGA
189995	22191	ATGCCAAACTCGTGGTCCTT	234582	66778	GGATCTGAAGAGCAACACAC	279169	111365	GCAGCCACAGAAGAATCTAG
189996	22192	AATGCCAAACTCGTGGTCCT	234583	66779	GGGATCTGAAGAGCAACACA	279170	111366	AGCAGCCACAGAAGAATCTA
189997	22193	AAATGCCAAACTCGTGGTCC	234584	66780	TGGGATCTGAAGAGCAACAC	279171	111367	AAGCAGCCACAGAAGAATCT
189998	22194	AAAATGCCAAACTCGTGGTC	234585	66781	TTGGGATCTGAAGAGCAACA	279172	111368	GAAGCAGCCACAGAAGAATC
189999	22195	TAAAATGCCAAACTCGTGGT	234586	66782	CTTGGGATCTGAAGAGCAAC	279173	111369	AGAAGCAGCCACAGAAGAAT
190000	22196	TTAAAATGCCAAACTCGTGG	234587	66783	GCTTGGGATCTGAAGAGCAA	279174	111370	CAGAAGCAGCCACAGAAGAA
190001	22197	GTTAAAATGCCAAACTCGTG	234588	66784	GGCTTGGGATCTGAAGAGCA	279175	111371	TCAGAAGCAGCCACAGAAGA
190002	22198	TGTTAAAATGCCAAACTCGT	234589	66785	AGGCTTGGGATCTGAAGAGC	279176	111372	GTCAGAAGCAGCCACAGAAG
190003	22199	CTGTTAAAATGCCAAACTCG	234590	66786	GAGGCTTGGGATCTGAAGAG	279177	111373	GGTCAGAAGCAGCCACAGAA
190004	22200	TCTGTTAAAATGCCAAACTC	234591	66787	TGAGGCTTGGGATCTGAAGA	279178	111374	AGGTCAGAAGCAGCCACAGA
190005	22201	ATCTGTTAAAATGCCAAACT	234592	66788	ATGAGGCTTGGGATCTGAAG	279179	111375	CAGGTCAGAAGCAGCCACAG
190006	22202	CATCTGTTAAAATGCCAAAC	234593	66789	CATGAGGCTTGGGATCTGAA	279180	111376	TCAGGTCAGAAGCAGCCACA
190007	22203	GCATCTGTTAAAATGCCAAA	234594	66790	GCATGAGGCTTGGGATCTGA	279181	111377	CTCAGGTCAGAAGCAGCCAC
190008	22204	GGCATCTGTTAAAATGCCAA	234595	66791	GGCATGAGGCTTGGGATCTG	279182	111378	TCTCAGGTCAGAAGCAGCCA
190009	22205	TGGCATCTGTTAAAATGCCA	234596	66792	GGGCATGAGGCTTGGGATCT	279183	111379	TTCTCAGGTCAGAAGCAGCC
190010	22206	CTGGCATCTGTTAAAATGCC	234597	66793	GGGGCATGAGGCTTGGGATC	279184	111380	TTTCTCAGGTCAGAAGCAGC
190011	22207	TCTGGCATCTGTTAAAATGC	234598	66794	AGGGGCATGAGGCTTGGGAT	279185	111381	CTTTCTCAGGTCAGAAGCAG
190012	22208	CTCTGGCATCTGTTAAAATG	234599	66795	TAGGGGCATGAGGCTTGGGA	279186	111382	ACTTTCTCAGGTCAGAAGCA
190013	22209	GCTCTGGCATCTGTTAAAAT	234600	66796	GTAGGGGCATGAGGCTTGGG	279187	111383	AACTTTCTCAGGTCAGAAGC
190014	22210	GGCTCTGGCATCTGTTAAAA	234601	66797	AGTAGGGGCATGAGGCTTGG	279188	111384	CAACTTTCTCAGGTCAGAAG
190015	22211	TGGCTCTGGCATCTGTTAAA	234602	66798	CAGTAGGGGCATGAGGCTTG	279189	111385	GCAACTTTCTCAGGTCAGAA
190016	22212	GTGGCTCTGGCATCTGTTAA	234603	66799	CCAGTAGGGGCATGAGGCTT	279190	111386	CGCAACTTTCTCAGGTCAGA
190017	22213	AGTGGCTCTGGCATCTGTTA	234604	66800	CCCAGTAGGGGCATGAGGCT	279191	111387	CCGCAACTTTCTCAGGTCAG
190018	22214	AAGTGGCTCTGGCATCTGTT	234605	66801	GCCCAGTAGGGGCATGAGGC	279192	111388	TCCGCAACTTTCTCAGGTCA
190019	22215	CAAGTGGCTCTGGCATCTGT	234606	66802	GGCCCAGTAGGGGCATGAGG	279193	111389	TTCCGCAACTTTCTCAGGTC
190020	22216	TCAAGTGGCTCTGGCATCTG	234607	66803	GGGCCCAGTAGGGGCATGAG	279194	111390	GTTCCGCAACTTTCTCAGGT
190021	22217	CTCAAGTGGCTCTGGCATCT	234608	66804	AGGGCCCAGTAGGGGCATGA	279195	111391	GGTTCCGCAACTTTCTCAGG
190022	22218	TCTCAAGTGGCTCTGGCATC	234609	66805	CAGGGCCCAGTAGGGGCATG	279196	111392	AGGTTCCGCAACTTTCTCAG
190023	22219	TTCTCAAGTGGCTCTGGCAT	234610	66806	ACAGGGCCCAGTAGGGGCAT	279197	111393	GAGGTTCCGCAACTTTCTCA
190024	22220	TTTCTCAAGTGGCTCTGGCA	234611	66807	CACAGGGCCCAGTAGGGGCA	279198	111394	TGAGGTTCCGCAACTTTCTC
190025	22221	ATTTCTCAAGTGGCTCTGGC	234612	66808	CCACAGGGCCCAGTAGGGGC	279199	111395	CTGAGGTTCCGCAACTTTCT
190026	22222	CATTTCTCAAGTGGCTCTGG	234613	66809	CCCACAGGGCCCAGTAGGGG	279200	111396	GCTGAGGTTCCGCAACTTTC
190027	22223	ACATTTCTCAAGTGGCTCTG	234614	66810	CCCCACAGGGCCCAGTAGGG	279201	111397	CGCTGAGGTTCCGCAACTTT
190028	22224	CACATTTCTCAAGTGGCTCT	234615	66811	ACCCCACAGGGCCCAGTAGG	279202	111398	TCGCTGAGGTTCCGCAACTT
190029	22225	CCACATTTCTCAAGTGGCTC	234616	66812	CACCCCACAGGGCCCAGTAG	279203	111399	CTCGCTGAGGTTCCGCAACT
190030	22226	ACCACATTTCTCAAGTGGCT	234617	66813	GCACCCCACAGGGCCCAGTA	279204	111400	GCTCGCTGAGGTTCCGCAAC
190031	22227	TACCACATTTCTCAAGTGGC	234618	66814	AGCACCCCACAGGGCCCAGT	279205	111401	GGCTCGCTGAGGTTCCGCAA
190032	22228	TTACCACATTTCTCAAGTGG	234619	66815	AAGCACCCCACAGGGCCCAG	279206	111402	AGGCTCGCTGAGGTTCCGCA
190033	22229	GTTACCACATTTCTCAAGTG	234620	66816	GAAGCACCCCACAGGGCCCA	279207	111403	GAGGCTCGCTGAGGTTCCGC
190034	22230	AGTTACCACATTTCTCAAGT	234621	66817	AGAAGCACCCCACAGGGCCC	279208	111404	TGAGGCTCGCTGAGGTTCCG
190035	22231	TAGTTACCACATTTCTCAAG	234622	66818	GAGAAGCACCCCACAGGGCC	279209	111405	GTGAGGCTCGCTGAGGTTCC
190036	22232	TTAGTTACCACATTTCTCAA	234623	66819	TGAGAAGCACCCCACAGGGC	279210	111406	TGTGAGGCTCGCTGAGGTTC
190037	22233	CTTAGTTACCACATTTCTCA	234624	66820	CTGAGAAGCACCCCACAGGG	279211	111407	ATGTGAGGCTCGCTGAGGTT
190038	22234	GCTTAGTTACCACATTTCTC	234625	66821	GCTGAGAAGCACCCCACAGG	279212	111408	CATGTGAGGCTCGCTGAGGT
190039	22235	GGCTTAGTTACCACATTTCT	234626	66822	GGCTGAGAAGCACCCCACAG	279213	111409	CCATGTGAGGCTCGCTGAGG
190040	22236	GGGCTTAGTTACCACATTTC	234627	66823	GGGCTGAGAAGCACCCCACA	279214	111410	GCCATGTGAGGCTCGCTGAG
190041	22237	TGGGCTTAGTTACCACATTT	234628	66824	TGGGCTGAGAAGCACCCCAC	279215	111411	GGCCATGTGAGGCTCGCTGA
190042	22238	CTGGGCTTAGTTACCACATT	234629	66825	GTGGGCTGAGAAGCACCCCA	279216	111412	AGGCCATGTGAGGCTCGCTG
190043	22239	TCTGGGCTTAGTTACCACAT	234630	66826	GGTGGGCTGAGAAGCACCCC	279217	111413	GAGGCCATGTGAGGCTCGCT
190044	22240	CTCTGGGCTTAGTTACCACA	234631	66827	TGGTGGGCTGAGAAGCACCC	279218	111414	GGAGGCCATGTGAGGCTCGC
190045	22241	TCTCTGGGCTTAGTTACCAC	234632	66828	CTGGTGGGCTGAGAAGCACC	279219	111415	AGGAGGCCATGTGAGGCTCG
190046	22242	CTCTCTGGGCTTAGTTACCA	234633	66829	CCTGGTGGGCTGAGAAGCAC	279220	111416	AAGGAGGCCATGTGAGGCTC
190047	22243	CCTCTCTGGGCTTAGTTACC	234634	66830	TCCTGGTGGGCTGAGAAGCA	279221	111417	CAAGGAGGCCATGTGAGGCT
190048	22244	ACCTCTCTGGGCTTAGTTAC	234635	66831	CTCCTGGTGGGCTGAGAAGC	279222	111418	ACAAGGAGGCCATGTGAGGC
190049	22245	TACCTCTCTGGGCTTAGTTA	234636	66832	TCTCCTGGTGGGCTGAGAAG	279223	111419	GACAAGGAGGCCATGTGAGG
190050	22246	GTACCTCTCTGGGCTTAGTT	234637	66833	CTCTCCTGGTGGGCTGAGAA	279224	111420	GGACAAGGAGGCCATGTGAG

190051	22247	TGTACCTCTCTGGGCTTAGT	234638	66834	GCTCTCCTGGTGGGCTGAGA	279225	111421	AGGACAAGGAGGCCATGTGA
190052	22248	CTGTACCTCTCTGGGCTTAG	234639	66835	GGCTCTCCTGGTGGGCTGAG	279226	111422	AAGGACAAGGAGGCCATGTG
190053	22249	ACTGTACCTCTCTGGGCTTA	234640	66836	TGGCTCTCCTGGTGGGCTGA	279227	111423	TAAGGACAAGGAGGCCATGT
190054	22250	AACTGTACCTCTCTGGGCTT	234641	66837	GTGGCTCTCCTGGTGGGCTG	279228	111424	TTAAGGACAAGGAGGCCATG
190055	22251	TAACTGTACCTCTCTGGGCT	234642	66838	GGTGGCTCTCCTGGTGGGCT	279229	111425	GTTAAGGACAAGGAGGCCAT
190056	22252	TTAACTGTACCTCTCTGGGC	234643	66839	CGGTGGCTCTCCTGGTGGGC	279230	111426	CGTTAAGGACAAGGAGGCCA
190057	22253	GTTAACTGTACCTCTCTGGG	234644	66840	ACGGTGGCTCTCCTGGTGGG	279231	111427	ACGTTAAGGACAAGGAGGCC
190058	22254	GGTTAACTGTACCTCTCTGG	234645	66841	AACGGTGGCTCTCCTGGTGG	279232	111428	CACGTTAAGGACAAGGAGGC
190059	22255	AGGTTAACTGTACCTCTCTG	234646	66842	CAACGGTGGCTCTCCTGGTG	279233	111429	CCACGTTAAGGACAAGGAGG
190060	22256	GAGGTTAACTGTACCTCTCT	234647	66843	CCAACGGTGGCTCTCCTGGT	279234	111430	CCCACGTTAAGGACAAGGAG
190061	22257	GGAGGTTAACTGTACCTCTC	234648	66844	TCCAACGGTGGCTCTCCTGG	279235	111431	CCCCACGTTAAGGACAAGGA
190062	22258	GGGAGGTTAACTGTACCTCT	234649	66845	TTCCAACGGTGGCTCTCCTG	279236	111432	TCCCCACGTTAAGGACAAGG
190063	22259	GGGGAGGTTAACTGTACCTC	234650	66846	GTTCCAACGGTGGCTCTCCT	279237	111433	GTCCCCACGTTAAGGACAAG
190064	22260	TGGGGAGGTTAACTGTACCT	234651	66847	TGTTCCAACGGTGGCTCTCC	279238	111434	CGTCCCCACGTTAAGGACAA
190065	22261	CTGGGGAGGTTAACTGTACC	234652	66848	GTGTTCCAACGGTGGCTCTC	279239	111435	CCGTCCCCACGTTAAGGACA
190066	22262	TCTGGGGAGGTTAACTGTAC	234653	66849	TGTGTTCCAACGGTGGCTCT	279240	111436	ACCGTCCCCACGTTAAGGAC
190067	22263	CTCTGGGGAGGTTAACTGTA	234654	66850	GTGTGTTCCAACGGTGGCTC	279241	111437	CACCGTCCCCACGTTAAGGA
190068	22264	ACTCTGGGGAGGTTAACTGT	234655	66851	TGTGTGTTCCAACGGTGGCT	279242	111438	CCACCGTCCCCACGTTAAGG
190069	22265	GACTCTGGGGAGGTTAACTG	234656	66852	GTGTGTGTTCCAACGGTGGC	279243	111439	CCCACCGTCCCCACGTTAAG
190070	22266	TGACTCTGGGGAGGTTAACT	234657	66853	CGTGTGTGTTCCAACGGTGG	279244	111440	GCCCACCGTCCCCACGTTAA
190071	22267	GTGACTCTGGGGAGGTTAAC	234658	66854	ACGTGTGTGTTCCAACGGTG	279245	111441	TGCCCACCGTCCCCACGTTA
190072	22268	TGTGACTCTGGGGAGGTTAA	234659	66855	CACGTGTGTGTTCCAACGGT	279246	111442	TTGCCCACCGTCCCCACGTT
190073	22269	GTGTGACTCTGGGGAGGTTA	234660	66856	CCACGTGTGTGTTCCAACGG	279247	111443	CTTGCCCACCGTCCCCACGT
190074	22270	TGTGTGACTCTGGGGAGGTT	234661	66857	CCCACGTGTGTGTTCCAACG	279248	111444	TCTTGCCCACCGTCCCCACG
190075	22271	CTGTGTGACTCTGGGGAGGT	234662	66858	CCCCACGTGTGTGTTCCAAC	279249	111445	TTCTTGCCCACCGTCCCCAC
190076	22272	GCTGTGTGACTCTGGGGAGG	234663	66859	CCCCCACGTGTGTGTTCCAA	279250	111446	TTTCTTGCCCACCGTCCCCA
190077	22273	TGCTGTGTGACTCTGGGGAG	234664	66860	TCCCCCACGTGTGTGTTCCA	279251	111447	CTTTCTTGCCCACCGTCCCC
190078	22274	CTGCTGTGTGACTCTGGGGA	234665	66861	GTCCCCCACGTGTGTGTTCC	279252	111448	CCTTTCTTGCCCACCGTCCC
190079	22275	CCTGCTGTGTGACTCTGGGG	234666	66862	GGTCCCCCACGTGTGTGTTC	279253	111449	ACCTTTCTTGCCCACCGTCC
190080	22276	ACCTGCTGTGTGACTCTGGG	234667	66863	AGGTCCCCCACGTGTGTGTT	279254	111450	CACCTTTCTTGCCCACCGTC
190081	22277	AACCTGCTGTGTGACTCTGG	234668	66864	CAGGTCCCCCACGTGTGTGT	279255	111451	TCACCTTTCTTGCCCACCGT
190082	22278	GAACCTGCTGTGTGACTCTG	234669	66865	CCAGGTCCCCCACGTGTGTG	279256	111452	ATCACCTTTCTTGCCCACCG
190083	22279	TGAACCTGCTGTGTGACTCT	234670	66866	ACCAGGTCCCCCACGTGTGT	279257	111453	CATCACCTTTCTTGCCCACC
190084	22280	ATGAACCTGCTGTGTGACTC	234671	66867	CACCAGGTCCCCCACGTGTG	279258	111454	ACATCACCTTTCTTGCCCAC
190085	22281	CATGAACCTGCTGTGTGACT	234672	66868	CCACCAGGTCCCCCACGTGT	279259	111455	CACATCACCTTTCTTGCCCA
190086	22282	CCATGAACCTGCTGTGTGAC	234673	66869	CCCACCAGGTCCCCCACGTG	279260	111456	CCACATCACCTTTCTTGCCC
190087	22283	GCCATGAACCTGCTGTGTGA	234674	66870	ACCCACCAGGTCCCCCACGT	279261	111457	GCCACATCACCTTTCTTGCC
190088	22284	TGCCATGAACCTGCTGTGTG	234675	66871	CACCCACCAGGTCCCCCACG	279262	111458	TGCCACATCACCTTTCTTGC
190089	22285	TTGCCATGAACCTGCTGTGT	234676	66872	GCACCCACCAGGTCCCCCAC	279263	111459	GTGCCACATCACCTTTCTTG
190090	22286	TTTGCCATGAACCTGCTGTG	234677	66873	GGCACCCACCAGGTCCCCCA	279264	111460	AGTGCCACATCACCTTTCTT
190091	22287	CTTTGCCATGAACCTGCTGT	234678	66874	CGGCACCCACCAGGTCCCCC	279265	111461	TAGTGCCACATCACCTTTCT
190092	22288	GCTTTGCCATGAACCTGCTG	234679	66875	CCGGCACCCACCAGGTCCCC	279266	111462	CTAGTGCCACATCACCTTTC
190093	22289	AGCTTTGCCATGAACCTGCT	234680	66876	ACCGGCACCCACCAGGTCCC	279267	111463	TCTAGTGCCACATCACCTTT
190094	22290	CAGCTTTGCCATGAACCTGC	234681	66877	CACCGGCACCCACCAGGTCC	279268	111464	CTCTAGTGCCACATCACCTT
190095	22291	CCAGCTTTGCCATGAACCTG	234682	66878	ACACCGGCACCCACCAGGTC	279269	111465	TCTCTAGTGCCACATCACCT
190096	22292	TCCAGCTTTGCCATGAACCT	234683	66879	CACACCGGCACCCACCAGGT	279270	111466	ATCTCTAGTGCCACATCACC
190097	22293	GTCCAGCTTTGCCATGAACC	234684	66880	CCACACCGGCACCCACCAGG	279271	111467	AATCTCTAGTGCCACATCAC
190098	22294	AGTCCAGCTTTGCCATGAAC	234685	66881	ACCACACCGGCACCCACCAG	279272	111468	AAATCTCTAGTGCCACATCA
190099	22295	TAGTCCAGCTTTGCCATGAA	234686	66882	CACCACACCGGCACCCACCA	279273	111469	TAAATCTCTAGTGCCACATC
190100	22296	CTAGTCCAGCTTTGCCATGA	234687	66883	TCACCACACCGGCACCCACC	279274	111470	ATAAATCTCTAGTGCCACAT
190101	22297	GCTAGTCCAGCTTTGCCATG	234688	66884	TTCACCACACCGGCACCCAC	279275	111471	GATAAATCTCTAGTGCCACA
190102	22298	TGCTAGTCCAGCTTTGCCAT	234689	66885	ATTCACCACACCGGCACCCA	279276	111472	GGATAAATCTCTAGTGCCAC
190103	22299	GTGCTAGTCCAGCTTTGCCA	234690	66886	CATTCACCACACCGGCACCC	279277	111473	TGGATAAATCTCTAGTGCCA
190104	22300	TGTGCTAGTCCAGCTTTGCC	234691	66887	CCATTCACCACACCGGCACC	279278	111474	ATGGATAAATCTCTAGTGCC
190105	22301	CTGTGCTAGTCCAGCTTTGC	234692	66888	CCCATTCACCACACCGGCAC	279279	111475	GATGGATAAATCTCTAGTGC
190106	22302	CCTGTGCTAGTCCAGCTTTG	234693	66889	CCCCATTCACCACACCGGCA	279280	111476	AGATGGATAAATCTCTAGTG
190107	22303	ACCTGTGCTAGTCCAGCTTT	234694	66890	CCCCCATTCACCACACCGGC	279281	111477	GAGATGGATAAATCTCTAGT
190108	22304	CACCTGTGCTAGTCCAGCTT	234695	66891	GCCCCCATTCACCACACCGG	279282	111478	AGAGATGGATAAATCTCTAG
190109	22305	ACACCTGTGCTAGTCCAGCT	234696	66892	GGCCCCCATTCACCACACCG	279283	111479	TAGAGATGGATAAATCTCTA
190110	22306	GACACCTGTGCTAGTCCAGC	234697	66893	TGGCCCCCATTCACCACACC	279284	111480	TTAGAGATGGATAAATCTCT
190111	22307	GGACACCTGTGCTAGTCCAG	234698	66894	GTGGCCCCCATTCACCACAC	279285	111481	TTTAGAGATGGATAAATCTC
190112	22308	AGGACACCTGTGCTAGTCCA	234699	66895	TGTGGCCCCCATTCACCACA	279286	111482	CTTTAGAGATGGATAAATCT
190113	22309	AAGGACACCTGTGCTAGTCC	234700	66896	CTGTGGCCCCCATTCACCAC	279287	111483	CCTTTAGAGATGGATAAATC
190114	22310	GAAGGACACCTGTGCTAGTC	234701	66897	GCTGTGGCCCCCATTCACCA	279288	111484	TCCTTTAGAGATGGATAAAT
190115	22311	GGAAGGACACCTGTGCTAGT	234702	66898	GGCTGTGGCCCCCATTCACC	279289	111485	CTCCTTTAGAGATGGATAAA
190116	22312	GGGAAGGACACCTGTGCTAG	234703	66899	AGGCTGTGGCCCCCATTCAC	279290	111486	CCTCCTTTAGAGATGGATAA
190117	22313	GGGGAAGGACACCTGTGCTA	234704	66900	CAGGCTGTGGCCCCCATTCA	279291	111487	TCCTCCTTTAGAGATGGATA
190118	22314	AGGGGAAGGACACCTGTGCT	234705	66901	TCAGGCTGTGGCCCCCATTC	279292	111488	CTCCTCCTTTAGAGATGGAT
190119	22315	CAGGGGAAGGACACCTGTGC	234706	66902	GTCAGGCTGTGGCCCCCATT	279293	111489	ACTCCTCCTTTAGAGATGGA
190120	22316	GCAGGGGAAGGACACCTGTG	234707	66903	AGTCAGGCTGTGGCCCCCAT	279294	111490	CACTCCTCCTTTAGAGATGG
190121	22317	TGCAGGGGAAGGACACCTGT	234708	66904	GAGTCAGGCTGTGGCCCCCA	279295	111491	CCACTCCTCCTTTAGAGATG
190122	22318	CTGCAGGGGAAGGACACCTG	234709	66905	GGAGTCAGGCTGTGGCCCCC	279296	111492	TCCACTCCTCCTTTAGAGAT

190123	22319	TCTGCAGGGGAAGGACACCT	234710	66906	TGGAGTCAGGCTGTGGCCCC	279297	111493	ATCCACTCCTCCTTTAGAGA
190124	22320	ATCTGCAGGGGAAGGACACC	234711	66907	CTGGAGTCAGGCTGTGGCCC	279298	111494	AATCCACTCCTCCTTTAGAG
190125	22321	GATCTGCAGGGGAAGGACAC	234712	66908	CCTGGAGTCAGGCTGTGGCC	279299	111495	CAATCCACTCCTCCTTTAGA
190126	22322	GGATCTGCAGGGGAAGGACA	234713	66909	TCCTGGAGTCAGGCTGTGGC	279300	111496	ACAATCCACTCCTCCTTTAG
190127	22323	GGGATCTGCAGGGGAAGGAC	234714	66910	TTCCTGGAGTCAGGCTGTGG	279301	111497	TACAATCCACTCCTCCTTTA
190128	22324	GGGGATCTGCAGGGGAAGGA	234715	66911	CTTCCTGGAGTCAGGCTGTG	279302	111498	GTACAATCCACTCCTCCTTT
190129	22325	AGGGGATCTGCAGGGGAAGG	234716	66912	GCTTCCTGGAGTCAGGCTGT	279303	111499	TGTACAATCCACTCCTCCTT
190130	22326	AAGGGGATCTGCAGGGGAAG	234717	66913	GGCTTCCTGGAGTCAGGCTG	279304	111500	ATGTACAATCCACTCCTCCT
190131	22327	GAAGGGGATCTGCAGGGGAA	234718	66914	TGGCTTCCTGGAGTCAGGCT	279305	111501	AATGTACAATCCACTCCTCC
190132	22328	AGAAGGGGATCTGCAGGGGA	234719	66915	CTGGCTTCCTGGAGTCAGGC	279306	111502	CAATGTACAATCCACTCCTC
190133	22329	CAGAAGGGGATCTGCAGGGG	234720	66916	GCTGGCTTCCTGGAGTCAGG	279307	111503	TCAATGTACAATCCACTCCT
190134	22330	ACAGAAGGGGATCTGCAGGG	234721	66917	TGCTGGCTTCCTGGAGTCAG	279308	111504	TTCAATGTACAATCCACTCC
190135	22331	CACAGAAGGGGATCTGCAGG	234722	66918	TTGCTGGCTTCCTGGAGTCA	279309	111505	TTTCAATGTACAATCCACTC
190136	22332	GCACAGAAGGGGATCTGCAG	234723	66919	TTTGCTGGCTTCCTGGAGTC	279310	111506	GTTTCAATGTACAATCCACT
190137	22333	GGCACAGAAGGGGATCTGCA	234724	66920	GTTTGCTGGCTTCCTGGAGT	279311	111507	TGTTTCAATGTACAATCCAC
190138	22334	GGGCACAGAAGGGGATCTGC	234725	66921	AGTTTGCTGGCTTCCTGGAG	279312	111508	GTGTTTCAATGTACAATCCA
190139	22335	GGGGCACAGAAGGGGATCTG	234726	66922	GAGTTTGCTGGCTTCCTGGA	279313	111509	GGTGTTTCAATGTACAATCC
190140	22336	TGGGGCACAGAAGGGGATCT	234727	66923	CGAGTTTGCTGGCTTCCTGG	279314	111510	TGGTGTTTCAATGTACAATC
190141	22337	GTGGGGCACAGAAGGGGATC	234728	66924	CCGAGTTTGCTGGCTTCCTG	279315	111511	CTGGTGTTTCAATGTACAAT
190142	22338	TGTGGGGCACAGAAGGGGAT	234729	66925	TCCGAGTTTGCTGGCTTCCT	279316	111512	TCTGGTGTTTCAATGTACAA
190143	22339	ATGTGGGGCACAGAAGGGGA	234730	66926	CTCCGAGTTTGCTGGCTTCC	279317	111513	CTCTGGTGTTTCAATGTACA
190144	22340	GATGTGGGGCACAGAAGGGG	234731	66927	GCTCCGAGTTTGCTGGCTTC	279318	111514	TCTCTGGTGTTTCAATGTAC
190145	22341	TGATGTGGGGCACAGAAGGG	234732	66928	AGCTCCGAGTTTGCTGGCTT	279319	111515	TTCTCTGGTGTTTCAATGTA
190146	22342	GTGATGTGGGGCACAGAAGG	234733	66929	CAGCTCCGAGTTTGCTGGCT	279320	111516	CTTCTCTGGTGTTTCAATGT
190147	22343	GGTGATGTGGGGCACAGAAG	234734	66930	CCAGCTCCGAGTTTGCTGGC	279321	111517	CCTTCTCTGGTGTTTCAATG
190148	22344	AGGTGATGTGGGGCACAGAA	234735	66931	TCCAGCTCCGAGTTTGCTGG	279322	111518	TCCTTCTCTGGTGTTTCAAT
190149	22345	GAGGTGATGTGGGGCACAGA	234736	66932	CTCCAGCTCCGAGTTTGCTG	279323	111519	TTCCTTCTCTGGTGTTTCAA
190150	22346	GGAGGTGATGTGGGGCACAG	234737	66933	CCTCCAGCTCCGAGTTTGCT	279324	111520	ATTCCTTCTCTGGTGTTTCA
190151	22347	GGGAGGTGATGTGGGGCACA	234738	66934	TCCTCCAGCTCCGAGTTTGC	279325	111521	AATTCCTTCTCTGGTGTTTC
190152	22348	AGGGAGGTGATGTGGGGCAC	234739	66935	CTCCTCCAGCTCCGAGTTTG	279326	111522	TAATTCCTTCTCTGGTGTTT
190153	22349	GAGGGAGGTGATGTGGGGCA	234740	66936	ACTCCTCCAGCTCCGAGTTT	279327	111523	GTAATTCCTTCTCTGGTGTT
190154	22350	GGAGGGAGGTGATGTGGGGC	234741	66937	GACTCCTCCAGCTCCGAGTT	279328	111524	TGTAATTCCTTCTCTGGTGT
190155	22351	TGGAGGGAGGTGATGTGGGG	234742	66938	TGACTCCTCCAGCTCCGAGT	279329	111525	TTGTAATTCCTTCTCTGGTG
190156	22352	CTGGAGGGAGGTGATGTGGG	234743	66939	CTGACTCCTCCAGCTCCGAG	279330	111526	TTTGTAATTCCTTCTCTGGT
190157	22353	ACTGGAGGGAGGTGATGTGG	234744	66940	CCTGACTCCTCCAGCTCCGA	279331	111527	CTTTGTAATTCCTTCTCTGG
190158	22354	CACTGGAGGGAGGTGATGTG	234745	66941	TCCTGACTCCTCCAGCTCCG	279332	111528	CCTTTGTAATTCCTTCTCTG
190159	22355	ACACTGGAGGGAGGTGATGT	234746	66942	GTCCTGACTCCTCCAGCTCC	279333	111529	TCCTTTGTAATTCCTTCTCT
190160	22356	GACACTGGAGGGAGGTGATG	234747	66943	TGTCCTGACTCCTCCAGCTC	279334	111530	TTCCTTTGTAATTCCTTCTC
190161	22357	AGACACTGGAGGGAGGTGAT	234748	66944	GTGTCCTGACTCCTCCAGCT	279335	111531	CTTCCTTTGTAATTCCTTCT
190162	22358	CAGACACTGGAGGGAGGTGA	234749	66945	GGTGTCCTGACTCCTCCAGC	279336	111532	TCTTCCTTTGTAATTCCTTC
190163	22359	CCAGACACTGGAGGGAGGTG	234750	66946	GGGTGTCCTGACTCCTCCAG	279337	111533	TTCTTCCTTTGTAATTCCTT
190164	22360	CCCAGACACTGGAGGGAGGT	234751	66947	GGGGTGTCCTGACTCCTCCA	279338	111534	ATTCTTCCTTTGTAATTCCT
190165	22361	GCCCAGACACTGGAGGGAGG	234752	66948	GGGGGTGTCCTGACTCCTCC	279339	111535	AATTCTTCCTTTGTAATTCC
190166	22362	GGCCCAGACACTGGAGGGAG	234753	66949	CGGGGGTGTCCTGACTCCTC	279340	111536	AAATTCTTCCTTTGTAATTC
190167	22363	TGGCCCAGACACTGGAGGGA	234754	66950	TCGGGGGTGTCCTGACTCCT	279341	111537	CAAATTCTTCCTTTGTAATT
190168	22364	GTGGCCCAGACACTGGAGGG	234755	66951	ATCGGGGGTGTCCTGACTCC	279342	111538	TCAAATTCTTCCTTTGTAAT
190169	22365	GGTGGCCCAGACACTGGAGG	234756	66952	CATCGGGGGTGTCCTGACTC	279343	111539	CTCAAATTCTTCCTTTGTAA
190170	22366	AGGTGGCCCAGACACTGGAG	234757	66953	TCATCGGGGGTGTCCTGACT	279344	111540	ACTCAAATTCTTCCTTTGTA
190171	22367	CAGGTGGCCCAGACACTGGA	234758	66954	CTCATCGGGGGTGTCCTGAC	279345	111541	TACTCAAATTCTTCCTTTGT
190172	22368	CCAGGTGGCCCAGACACTGG	234759	66955	ACTCATCGGGGGTGTCCTGA	279346	111542	ATACTCAAATTCTTCCTTTG
190173	22369	TCCAGGTGGCCCAGACACTG	234760	66956	GACTCATCGGGGGTGTCCTG	279347	111543	GATACTCAAATTCTTCCTTT
190174	22370	CTCCAGGTGGCCCAGACACT	234761	66957	TGACTCATCGGGGGTGTCCT	279348	111544	AGATACTCAAATTCTTCCTT
190175	22371	TCTCCAGGTGGCCCAGACAC	234762	66958	TTGACTCATCGGGGGTGTCC	279349	111545	TAGATACTCAAATTCTTCCT
190176	22372	ATCTCCAGGTGGCCCAGACA	234763	66959	CTTGACTCATCGGGGGTGTC	279350	111546	TTAGATACTCAAATTCTTCC
190177	22373	CATCTCCAGGTGGCCCAGAC	234764	66960	TCTTGACTCATCGGGGGTGT	279351	111547	TTTAGATACTCAAATTCTTC
190178	22374	CCATCTCCAGGTGGCCCAGA	234765	66961	CTCTTGACTCATCGGGGGTG	279352	111548	TTTTAGATACTCAAATTCTT
190179	22375	CCCATCTCCAGGTGGCCCAG	234766	66962	ACTCTTGACTCATCGGGGGT	279353	111549	TTTTTAGATACTCAAATTCT
190180	22376	GCCCATCTCCAGGTGGCCCA	234767	66963	AACTCTTGACTCATCGGGGG	279354	111550	ATTTTTAGATACTCAAATTC
190181	22377	GGCCCATCTCCAGGTGGCCC	234768	66964	CAACTCTTGACTCATCGGGG	279355	111551	CATTTTTAGATACTCAAATT
190182	22378	GGGCCCATCTCCAGGTGGCC	234769	66965	CCAACTCTTGACTCATCGGG	279356	111552	ACATTTTTAGATACTCAAAT
190183	22379	AGGGCCCATCTCCAGGTGGC	234770	66966	ACCAACTCTTGACTCATCGG	279357	111553	TACATTTTTAGATACTCAAA
190184	22380	GAGGGCCCATCTCCAGGTGG	234771	66967	AACCAACTCTTGACTCATCG	279358	111554	CTACATTTTTAGATACTCAA
190185	22381	TGAGGGCCCATCTCCAGGTG	234772	66968	AAACCAACTCTTGACTCATC	279359	111555	CCTACATTTTTAGATACTCA
190186	22382	CTGAGGGCCCATCTCCAGGT	234773	66969	AAAACCAACTCTTGACTCAT	279360	111556	ACCTACATTTTTAGATACTC
190187	22383	TCTGAGGGCCCATCTCCAGG	234774	66970	CAAAACCAACTCTTGACTCA	279361	111557	GACCTACATTTTTAGATACT
190188	22384	GTCTGAGGGCCCATCTCCAG	234775	66971	GCAAAACCAACTCTTGACTC	279362	111558	TGACCTACATTTTTAGATAC
190189	22385	AGTCTGAGGGCCCATCTCCA	234776	66972	AGCAAAACCAACTCTTGACT	279363	111559	CTGACCTACATTTTTAGATA
190190	22386	GAGTCTGAGGGCCCATCTCC	234777	66973	CAGCAAAACCAACTCTTGAC	279364	111560	CCTGACCTACATTTTTAGAT
190191	22387	TGAGTCTGAGGGCCCATCTC	234778	66974	GCAGCAAAACCAACTCTTGA	279365	111561	GCCTGACCTACATTTTTAGA
190192	22388	GTGAGTCTGAGGGCCCATCT	234779	66975	GGCAGCAAAACCAACTCTTG	279366	111562	CGCCTGACCTACATTTTTAG
190193	22389	GGTGAGTCTGAGGGCCCATC	234780	66976	TGGCAGCAAAACCAACTCTT	279367	111563	GCGCCTGACCTACATTTTTA
190194	22390	GGGTGAGTCTGAGGGCCCAT	234781	66977	CTGGCAGCAAAACCAACTCT	279368	111564	AGCGCCTGACCTACATTTTT

190195	22391	CGGGTGAGTCTGAGGGCCCA	234782	66978	ACTGGCAGCAAAACCAACTC	279369	111565	GAGCGCCTGACCTACATTTT
190196	22392	CCGGGTGAGTCTGAGGGCCC	234783	66979	AACTGGCAGCAAAACCAACT	279370	111566	GGAGCGCCTGACCTACATTT
190197	22393	GCCGGGTGAGTCTGAGGGCC	234784	66980	CAACTGGCAGCAAAACCAAC	279371	111567	AGGAGCGCCTGACCTACATT
190198	22394	GGCCGGGTGAGTCTGAGGGC	234785	66981	TCAACTGGCAGCAAAACCAA	279372	111568	CAGGAGCGCCTGACCTACAT
190199	22395	TGGCCGGGTGAGTCTGAGGG	234786	66982	GTCAACTGGCAGCAAAACCA	279373	111569	ACAGGAGCGCCTGACCTACA
190200	22396	CTGGCCGGGTGAGTCTGAGG	234787	66983	TGTCAACTGGCAGCAAAACC	279374	111570	CACAGGAGCGCCTGACCTAC
190201	22397	TCTGGCCGGGTGAGTCTGAG	234788	66984	ATGTCAACTGGCAGCAAAAC	279375	111571	ACACAGGAGCGCCTGACCTA
190202	22398	CTCTGGCCGGGTGAGTCTGA	234789	66985	GATGTCAACTGGCAGCAAAA	279376	111572	AACACAGGAGCGCCTGACCT
190203	22399	CCTCTGGCCGGGTGAGTCTG	234790	66986	AGATGTCAACTGGCAGCAAA	279377	111573	CAACACAGGAGCGCCTGACC
190204	22400	ACCTCTGGCCGGGTGAGTCT	234791	66987	CAGATGTCAACTGGCAGCAA	279378	111574	TCAACACAGGAGCGCCTGAC
190205	22401	CACCTCTGGCCGGGTGAGTC	234792	66988	TCAGATGTCAACTGGCAGCA	279379	111575	ATCAACACAGGAGCGCCTGA
190206	22402	GCACCTCTGGCCGGGTGAGT	234793	66989	ATCAGATGTCAACTGGCAGC	279380	111576	AATCAACACAGGAGCGCCTG
190207	22403	GGCACCTCTGGCCGGGTGAG	234794	66990	AATCAGATGTCAACTGGCAG	279381	111577	CAATCAACACAGGAGCGCCT
190208	22404	TGGCACCTCTGGCCGGGTGA	234795	66991	CAATCAGATGTCAACTGGCA	279382	111578	GCAATCAACACAGGAGCGCC
190209	22405	ATGGCACCTCTGGCCGGGTG	234796	66992	TCAATCAGATGTCAACTGGC	279383	111579	TGCAATCAACACAGGAGCGC
190210	22406	GATGGCACCTCTGGCCGGGT	234797	66993	TTCAATCAGATGTCAACTGG	279384	111580	CTGCAATCAACACAGGAGCG
190211	22407	AGATGGCACCTCTGGCCGGG	234798	66994	GTTCAATCAGATGTCAACTG	279385	111581	CCTGCAATCAACACAGGAGC
190212	22408	GAGATGGCACCTCTGGCCGG	234799	66995	GGTTCAATCAGATGTCAACT	279386	111582	CCCTGCAATCAACACAGGAG
190213	22409	TGAGATGGCACCTCTGGCCG	234800	66996	TGGTTCAATCAGATGTCAAC	279387	111583	GCCCTGCAATCAACACAGGA
190214	22410	ATGAGATGGCACCTCTGGCC	234801	66997	ATGGTTCAATCAGATGTCAA	279388	111584	AGCCCTGCAATCAACACAGG
190215	22411	CATGAGATGGCACCTCTGGC	234802	66998	GATGGTTCAATCAGATGTCA	279389	111585	TAGCCCTGCAATCAACACAG
190216	22412	CCATGAGATGGCACCTCTGG	234803	66999	AGATGGTTCAATCAGATGTC	279390	111586	ATAGCCCTGCAATCAACACA
190217	22413	CCCATGAGATGGCACCTCTG	234804	67000	GAGATGGTTCAATCAGATGT	279391	111587	AATAGCCCTGCAATCAACAC
190218	22414	TCCCATGAGATGGCACCTCT	234805	67001	AGAGATGGTTCAATCAGATG	279392	111588	GAATAGCCCTGCAATCAACA
190219	22415	CTCCCATGAGATGGCACCTC	234806	67002	AAGAGATGGTTCAATCAGAT	279393	111589	TGAATAGCCCTGCAATCAAC
190220	22416	TCTCCCATGAGATGGCACCT	234807	67003	GAAGAGATGGTTCAATCAGA	279394	111590	GTGAATAGCCCTGCAATCAA
190221	22417	CTCTCCCATGAGATGGCACC	234808	67004	TGAAGAGATGGTTCAATCAG	279395	111591	TGTGAATAGCCCTGCAATCA
190222	22418	CCTCTCCCATGAGATGGCAC	234809	67005	GTGAAGAGATGGTTCAATCA	279396	111592	TTGTGAATAGCCCTGCAATC
190223	22419	ACCTCTCCCATGAGATGGCA	234810	67006	AGTGAAGAGATGGTTCAATC	279397	111593	ATTGTGAATAGCCCTGCAAT
190224	22420	GACCTCTCCCATGAGATGGC	234811	67007	AAGTGAAGAGATGGTTCAAT	279398	111594	TATTGTGAATAGCCCTGCAA
190225	22421	AGACCTCTCCCATGAGATGG	234812	67008	GAAGTGAAGAGATGGTTCAA	279399	111595	CTATTGTGAATAGCCCTGCA
190226	22422	CAGACCTCTCCCATGAGATG	234813	67009	AGAAGTGAAGAGATGGTTCA	279400	111596	GCTATTGTGAATAGCCCTGC
190227	22423	CCAGACCTCTCCCATGAGAT	234814	67010	GAGAAGTGAAGAGATGGTTC	279401	111597	GGCTATTGTGAATAGCCCTG
190228	22424	GCCAGACCTCTCCCATGAGA	234815	67011	GGAGAAGTGAAGAGATGGTT	279402	111598	TGGCTATTGTGAATAGCCCT
190229	22425	GGCCAGACCTCTCCCATGAG	234816	67012	CGGAGAAGTGAAGAGATGGT	279403	111599	TTGGCTATTGTGAATAGCCC
190230	22426	TGGCCAGACCTCTCCCATGA	234817	67013	ACGGAGAAGTGAAGAGATGG	279404	111600	CTTGGCTATTGTGAATAGCC
190231	22427	CTGGCCAGACCTCTCCCATG	234818	67014	CACGGAGAAGTGAAGAGATG	279405	111601	TCTTGGCTATTGTGAATAGC
190232	22428	CCTGGCCAGACCTCTCCCAT	234819	67015	GCACGGAGAAGTGAAGAGAT	279406	111602	ATCTTGGCTATTGTGAATAG
190233	22429	TCCTGGCCAGACCTCTCCCA	234820	67016	GGCACGGAGAAGTGAAGAGA	279407	111603	AATCTTGGCTATTGTGAATA
190234	22430	TTCCTGGCCAGACCTCTCCC	234821	67017	AGGCACGGAGAAGTGAAGAG	279408	111604	AAATCTTGGCTATTGTGAAT
190235	22431	CTTCCTGGCCAGACCTCTCC	234822	67018	GAGGCACGGAGAAGTGAAGA	279409	111605	CAAATCTTGGCTATTGTGAA
190236	22432	GCTTCCTGGCCAGACCTCTC	234823	67019	TGAGGCACGGAGAAGTGAAG	279410	111606	CCAAATCTTGGCTATTGTGA
190237	22433	TGCTTCCTGGCCAGACCTCT	234824	67020	GTGAGGCACGGAGAAGTGAA	279411	111607	TCCAAATCTTGGCTATTGTG
190238	22434	ATGCTTCCTGGCCAGACCTC	234825	67021	AGTGAGGCACGGAGAAGTGA	279412	111608	TTCCAAATCTTGGCTATTGT
190239	22435	GATGCTTCCTGGCCAGACCT	234826	67022	AAGTGAGGCACGGAGAAGTG	279413	111609	CTTCCAAATCTTGGCTATTG
190240	22436	CGATGCTTCCTGGCCAGACC	234827	67023	AAAGTGAGGCACGGAGAAGT	279414	111610	GCTTCCAAATCTTGGCTATT
190241	22437	TCGATGCTTCCTGGCCAGAC	234828	67024	GAAAGTGAGGCACGGAGAAG	279415	111611	TGCTTCCAAATCTTGGCTAT
190242	22438	ATCGATGCTTCCTGGCCAGA	234829	67025	GGAAAGTGAGGCACGGAGAA	279416	111612	TTGCTTCCAAATCTTGGCTA
190243	22439	TATCGATGCTTCCTGGCCAG	234830	67026	AGGAAAGTGAGGCACGGAGA	279417	111613	GTTGCTTCCAAATCTTGGCT
190244	22440	ATATCGATGCTTCCTGGCCA	234831	67027	AAGGAAAGTGAGGCACGGAG	279418	111614	GGTTGCTTCCAAATCTTGGC
190245	22441	AATATCGATGCTTCCTGGCC	234832	67028	TAAGGAAAGTGAGGCACGGA	279419	111615	GGGTTGCTTCCAAATCTTGG
190246	22442	AAATATCGATGCTTCCTGGC	234833	67029	GTAAGGAAAGTGAGGCACGG	279420	111616	TGGGTTGCTTCCAAATCTTG
190247	22443	CAAATATCGATGCTTCCTGG	234834	67030	GGTAAGGAAAGTGAGGCACG	279421	111617	TTGGGTTGCTTCCAAATCTT
190248	22444	TCAAATATCGATGCTTCCTG	234835	67031	TGGTAAGGAAAGTGAGGCAC	279422	111618	CTTGGGTTGCTTCCAAATCT
190249	22445	CTCAAATATCGATGCTTCCT	234836	67032	CTGGTAAGGAAAGTGAGGCA	279423	111619	ACTTGGGTTGCTTCCAAATC
190250	22446	TCTCAAATATCGATGCTTCC	234837	67033	TCTGGTAAGGAAAGTGAGGC	279424	111620	CACTTGGGTTGCTTCCAAAT
190251	22447	ATCTCAAATATCGATGCTTC	234838	67034	GTCTGGTAAGGAAAGTGAGG	279425	111621	ACACTTGGGTTGCTTCCAAA
190252	22448	GATCTCAAATATCGATGCTT	234839	67035	TGTCTGGTAAGGAAAGTGAG	279426	111622	GACACTTGGGTTGCTTCCAA
190253	22449	GGATCTCAAATATCGATGCT	234840	67036	CTGTCTGGTAAGGAAAGTGA	279427	111623	GGACACTTGGGTTGCTTCCA
190254	22450	GGGATCTCAAATATCGATGC	234841	67037	CCTGTCTGGTAAGGAAAGTG	279428	111624	TGGACACTTGGGTTGCTTCC
190255	22451	TGGGATCTCAAATATCGATG	234842	67038	GCCTGTCTGGTAAGGAAAGT	279429	111625	ATGGACACTTGGGTTGCTTC
190256	22452	TTGGGATCTCAAATATCGAT	234843	67039	AGCCTGTCTGGTAAGGAAAG	279430	111626	GATGGACACTTGGGTTGCTT
190257	22453	CTTGGGATCTCAAATATCGA	234844	67040	GAGCCTGTCTGGTAAGGAAA	279431	111627	TGATGGACACTTGGGTTGCT
190258	22454	TCTTGGGATCTCAAATATCG	234845	67041	AGAGCCTGTCTGGTAAGGAA	279432	111628	TTGATGGACACTTGGGTTGC
190259	22455	TTCTTGGGATCTCAAATATC	234846	67042	CAGAGCCTGTCTGGTAAGGA	279433	111629	GTTGATGGACACTTGGGTTG
190260	22456	TTTCTTGGGATCTCAAATAT	234847	67043	GCAGAGCCTGTCTGGTAAGG	279434	111630	TGTTGATGGACACTTGGGTT
190261	22457	ATTTCTTGGGATCTCAAATA	234848	67044	AGCAGAGCCTGTCTGGTAAG	279435	111631	CTGTTGATGGACACTTGGGT
190262	22458	CATTTCTTGGGATCTCAAAT	234849	67045	CAGCAGAGCCTGTCTGGTAA	279436	111632	TCTGTTGATGGACACTTGGG
190263	22459	TCATTTCTTGGGATCTCAAA	234850	67046	TCAGCAGAGCCTGTCTGGTA	279437	111633	GTCTGTTGATGGACACTTGG
190264	22460	TTCATTTCTTGGGATCTCAA	234851	67047	ATCAGCAGAGCCTGTCTGGT	279438	111634	TGTCTGTTGATGGACACTTG
190265	22461	CTTCATTTCTTGGGATCTCA	234852	67048	CATCAGCAGAGCCTGTCTGG	279439	111635	TTGTCTGTTGATGGACACTT
190266	22462	TCTTCATTTCTTGGGATCTC	234853	67049	GCATCAGCAGAGCCTGTCTG	279440	111636	TTTGTCTGTTGATGGACACT

190267	22463	GTCTTCATTTCTTGGGATCT	234854	67050	AGCATCAGCAGAGCCTGTCT	279441	111637	ATTTGTCTGTTGATGGACAC
190268	22464	AGTCTTCATTTCTTGGGATC	234855	67051	CAGCATCAGCAGAGCCTGTC	279442	111638	CATTTGTCTGTTGATGGACA
190269	22465	AAGTCTTCATTTCTTGGGAT	234856	67052	ACAGCATCAGCAGAGCCTGT	279443	111639	CCATTTGTCTGTTGATGGAC
190270	22466	CAAGTCTTCATTTCTTGGGA	234857	67053	GACAGCATCAGCAGAGCCTG	279444	111640	TCCATTTGTCTGTTGATGGA
190271	22467	CCAAGTCTTCATTTCTTGGG	234858	67054	GGACAGCATCAGCAGAGCCT	279445	111641	ATCCATTTGTCTGTTGATGG
190272	22468	GCCAAGTCTTCATTTCTTGG	234859	67055	GGGACAGCATCAGCAGAGCC	279446	111642	TATCCATTTGTCTGTTGATG
190273	22469	GGCCAAGTCTTCATTTCTTG	234860	67056	AGGGACAGCATCAGCAGAGC	279447	111643	TTATCCATTTGTCTGTTGAT
190274	22470	AGGCCAAGTCTTCATTTCTT	234861	67057	GAGGGACAGCATCAGCAGAG	279448	111644	TTTATCCATTTGTCTGTTGA
190275	22471	CAGGCCAAGTCTTCATTTCT	234862	67058	AGAGGGACAGCATCAGCAGA	279449	111645	CTTTATCCATTTGTCTGTTG
190276	22472	ACAGGCCAAGTCTTCATTTC	234863	67059	GAGAGGGACAGCATCAGCAG	279450	111646	TCTTTATCCATTTGTCTGTT
190277	22473	GACAGGCCAAGTCTTCATTT	234864	67060	GGAGAGGGACAGCATCAGCA	279451	111647	TTCTTTATCCATTTGTCTGT
190278	22474	TGACAGGCCAAGTCTTCATT	234865	67061	AGGAGAGGGACAGCATCAGC	279452	111648	TTTCTTTATCCATTTGTCTG
190279	22475	CTGACAGGCCAAGTCTTCAT	234866	67062	CAGGAGAGGGACAGCATCAG	279453	111649	TTTTCTTTATCCATTTGTCT
190280	22476	TCTGACAGGCCAAGTCTTCA	234867	67063	ACAGGAGAGGGACAGCATCA	279454	111650	ATTTTCTTTATCCATTTGTC
190281	22477	ATCTGACAGGCCAAGTCTTC	234868	67064	AACAGGAGAGGGACAGCATC	279455	111651	CATTTTCTTTATCCATTTGT
190282	22478	CATCTGACAGGCCAAGTCTT	234869	67065	GAACAGGAGAGGGACAGCAT	279456	111652	ACATTTTCTTTATCCATTTG
190283	22479	TCATCTGACAGGCCAAGTCT	234870	67066	TGAACAGGAGAGGGACAGCA	279457	111653	CACATTTTCTTTATCCATTT
190284	22480	GTCATCTGACAGGCCAAGTC	234871	67067	CTGAACAGGAGAGGGACAGC	279458	111654	CCACATTTTCTTTATCCATT
190285	22481	TGTCATCTGACAGGCCAAGT	234872	67068	ACTGAACAGGAGAGGGACAG	279459	111655	ACCACATTTTCTTTATCCAT
190286	22482	CTGTCATCTGACAGGCCAAG	234873	67069	GACTGAACAGGAGAGGGACA	279460	111656	CACCACATTTTCTTTATCCA
190287	22483	TCTGTCATCTGACAGGCCAA	234874	67070	CGACTGAACAGGAGAGGGAC	279461	111657	GCACCACATTTTCTTTATCC
190288	22484	GTCTGTCATCTGACAGGCCA	234875	67071	ACGACTGAACAGGAGAGGGA	279462	111658	TGCACCACATTTTCTTTATC
190289	22485	AGTCTGTCATCTGACAGGCC	234876	67072	CACGACTGAACAGGAGAGGG	279463	111659	ATGCACCACATTTTCTTTAT
190290	22486	AAGTCTGTCATCTGACAGGC	234877	67073	GCACGACTGAACAGGAGAGG	279464	111660	TATGCACCACATTTTCTTTA
190291	22487	GAAGTCTGTCATCTGACAGG	234878	67074	GGCACGACTGAACAGGAGAG	279465	111661	ATATGCACCACATTTTCTTT
190292	22488	CGAAGTCTGTCATCTGACAG	234879	67075	GGGCACGACTGAACAGGAGA	279466	111662	TATATGCACCACATTTTCTT
190293	22489	CCGAAGTCTGTCATCTGACA	234880	67076	AGGGCACGACTGAACAGGAG	279467	111663	GTATATGCACCACATTTTCT
190294	22490	ACCGAAGTCTGTCATCTGAC	234881	67077	GAGGGCACGACTGAACAGGA	279468	111664	TGTATATGCACCACATTTTC
190295	22491	GACCGAAGTCTGTCATCTGA	234882	67078	TGAGGGCACGACTGAACAGG	279469	111665	GTGTATATGCACCACATTTT
190296	22492	TGACCGAAGTCTGTCATCTG	234883	67079	GTGAGGGCACGACTGAACAG	279470	111666	TGTGTATATGCACCACATTT
190297	22493	ATGACCGAAGTCTGTCATCT	234884	67080	GGTGAGGGCACGACTGAACA	279471	111667	TTGTGTATATGCACCACATT
190298	22494	CATGACCGAAGTCTGTCATC	234885	67081	CGGTGAGGGCACGACTGAAC	279472	111668	ATTGTGTATATGCACCACAT
190299	22495	CCATGACCGAAGTCTGTCAT	234886	67082	ACGGTGAGGGCACGACTGAA	279473	111669	CATTGTGTATATGCACCACA
190300	22496	CCCATGACCGAAGTCTGTCA	234887	67083	AACGGTGAGGGCACGACTGA	279474	111670	CCATTGTGTATATGCACCAC
190301	22497	TCCCATGACCGAAGTCTGTC	234888	67084	TAACGGTGAGGGCACGACTG	279475	111671	TCCATTGTGTATATGCACCA
190302	22498	TTCCCATGACCGAAGTCTGT	234889	67085	TTAACGGTGAGGGCACGACT	279476	111672	TTCCATTGTGTATATGCACC
190303	22499	GTTCCCATGACCGAAGTCTG	234890	67086	TTTAACGGTGAGGGCACGAC	279477	111673	ATTCCATTGTGTATATGCAC
190304	22500	TGTTCCCATGACCGAAGTCT	234891	67087	CTTTAACGGTGAGGGCACGA	279478	111674	TATTCCATTGTGTATATGCA
190305	22501	GTGTTCCCATGACCGAAGTC	234892	67088	TCTTTAACGGTGAGGGCACG	279479	111675	GTATTCCATTGTGTATATGC
190306	22502	CGTGTTCCCATGACCGAAGT	234893	67089	CTCTTTAACGGTGAGGGCAC	279480	111676	AGTATTCCATTGTGTATATG
190307	22503	ACGTGTTCCCATGACCGAAG	234894	67090	TCTCTTTAACGGTGAGGGCA	279481	111677	TAGTATTCCATTGTGTATAT
190308	22504	CACGTGTTCCCATGACCGAA	234895	67091	TTCTCTTTAACGGTGAGGGC	279482	111678	ATAGTATTCCATTGTGTATA
190309	22505	TCACGTGTTCCCATGACCGA	234896	67092	TTTCTCTTTAACGGTGAGGG	279483	111679	AATAGTATTCCATTGTGTAT
190310	22506	ATCACGTGTTCCCATGACCG	234897	67093	CTTTCTCTTTAACGGTGAGG	279484	111680	GAATAGTATTCCATTGTGTA
190311	22507	GATCACGTGTTCCCATGACC	234898	67094	TCTTTCTCTTTAACGGTGAG	279485	111681	TGAATAGTATTCCATTGTGT
190312	22508	AGATCACGTGTTCCCATGAC	234899	67095	CTCTTTCTCTTTAACGGTGA	279486	111682	CTGAATAGTATTCCATTGTG
190313	22509	CAGATCACGTGTTCCCATGA	234900	67096	GCTCTTTCTCTTTAACGGTG	279487	111683	GCTGAATAGTATTCCATTGT
190314	22510	ACAGATCACGTGTTCCCATG	234901	67097	TGCTCTTTCTCTTTAACGGT	279488	111684	GGCTGAATAGTATTCCATTG
190315	22511	AACAGATCACGTGTTCCCAT	234902	67098	TTGCTCTTTCTCTTTAACGG	279489	111685	TGGCTGAATAGTATTCCATT
190316	22512	AAACAGATCACGTGTTCCCA	234903	67099	TTTGCTCTTTCTCTTTAACG	279490	111686	ATGGCTGAATAGTATTCCAT
190317	22513	AAAACAGATCACGTGTTCCC	234904	67100	GTTTGCTCTTTCTCTTTAAC	279491	111687	CATGGCTGAATAGTATTCCA
190318	22514	TAAAACAGATCACGTGTTCC	234905	67101	AGTTTGCTCTTTCTCTTTAA	279492	111688	TCATGGCTGAATAGTATTCC
190319	22515	GTAAAACAGATCACGTGTTC	234906	67102	CAGTTTGCTCTTTCTCTTTA	279493	111689	TTCATGGCTGAATAGTATTC
190320	22516	TGTAAAACAGATCACGTGTT	234907	67103	GCAGTTTGCTCTTTCTCTTT	279494	111690	TTTCATGGCTGAATAGTATT
190321	22517	GTGTAAAACAGATCACGTGT	234908	67104	AGCAGTTTGCTCTTTCTCTT	279495	111691	TTTTCATGGCTGAATAGTAT
190322	22518	TGTGTAAAACAGATCACGTG	234909	67105	CAGCAGTTTGCTCTTTCTCT	279496	111692	TTTTTCATGGCTGAATAGTA
190323	22519	ATGTGTAAAACAGATCACGT	234910	67106	CCAGCAGTTTGCTCTTTCTC	279497	111693	CTTTTTCATGGCTGAATAGT
190324	22520	CATGTGTAAAACAGATCACG	234911	67107	CCCAGCAGTTTGCTCTTTCT	279498	111694	TCTTTTTCATGGCTGAATAG
190325	22521	GCATGTGTAAAACAGATCAC	234912	67108	GCCCAGCAGTTTGCTCTTTC	279499	111695	TTCTTTTTCATGGCTGAATA
190326	22522	CGCATGTGTAAAACAGATCA	234913	67109	TGCCCAGCAGTTTGCTCTTT	279500	111696	ATTCTTTTTCATGGCTGAAT
190327	22523	ACGCATGTGTAAAACAGATC	234914	67110	CTGCCCAGCAGTTTGCTCTT	279501	111697	CATTCTTTTTCATGGCTGAA
190328	22524	GACGCATGTGTAAAACAGAT	234915	67111	GCTGCCCAGCAGTTTGCTCT	279502	111698	TCATTCTTTTTCATGGCTGA
190329	22525	GGACGCATGTGTAAAACAGA	234916	67112	TGCTGCCCAGCAGTTTGCTC	279503	111699	CTCATTCTTTTTCATGGCTG
190330	22526	GGGACGCATGTGTAAAACAG	234917	67113	CTGCTGCCCAGCAGTTTGCT	279504	111700	TCTCATTCTTTTTCATGGCT
190331	22527	GGGGACGCATGTGTAAAACA	234918	67114	GCTGCTGCCCAGCAGTTTGC	279505	111701	TTCTCATTCTTTTTCATGGC
190332	22528	AGGGGACGCATGTGTAAAAC	234919	67115	TGCTGCTGCCCAGCAGTTTG	279506	111702	ATTCTCATTCTTTTTCATGG
190333	22529	GAGGGGACGCATGTGTAAAA	234920	67116	ATGCTGCTGCCCAGCAGTTT	279507	111703	GATTCTCATTCTTTTTCATG
190334	22530	TGAGGGGACGCATGTGTAAA	234921	67117	AATGCTGCTGCCCAGCAGTT	279508	111704	AGATTCTCATTCTTTTTCAT
190335	22531	CTGAGGGGACGCATGTGTAA	234922	67118	CAATGCTGCTGCCCAGCAGT	279509	111705	CAGATTCTCATTCTTTTTCA
190336	22532	GCTGAGGGGACGCATGTGTA	234923	67119	TCAATGCTGCTGCCCAGCAG	279510	111706	ACAGATTCTCATTCTTTTTC
190337	22533	TGCTGAGGGGACGCATGTGT	234924	67120	ATCAATGCTGCTGCCCAGCA	279511	111707	GACAGATTCTCATTCTTTTT
190338	22534	CTGCTGAGGGGACGCATGTG	234925	67121	AATCAATGCTGCTGCCCAGC	279512	111708	TGACAGATTCTCATTCTTTT

190339	22535	GCTGCTGAGGGGACGCATGT	234926	67122	AAATCAATGCTGCTGCCCAG	279513	111709	ATGACAGATTCTCATTCTTT
190340	22536	TGCTGCTGAGGGGACGCATG	234927	67123	AAAATCAATGCTGCTGCCCA	279514	111710	AATGACAGATTCTCATTCTT
190341	22537	CTGCTGCTGAGGGGACGCAT	234928	67124	AAAAATCAATGCTGCTGCCC	279515	111711	AAATGACAGATTCTCATTCT
190342	22538	GCTGCTGCTGAGGGGACGCA	234929	67125	AAAAAATCAATGCTGCTGCC	279516	111712	CAAATGACAGATTCTCATTC
190343	22539	AGCTGCTGCTGAGGGGACGC	234930	67126	AAAAAAATCAATGCTGCTGC	279517	111713	TCAAATGACAGATTCTCATT
190344	22540	AAGCTGCTGCTGAGGGGACG	234931	67127	TAAAAAAATCAATGCTGCTG	279518	111714	TTCAAATGACAGATTCTCAT
190345	22541	AAAGCTGCTGCTGAGGGGAC	234932	67128	TTAAAAAAATCAATGCTGCT	279519	111715	TTTCAAATGACAGATTCTCA
190346	22542	GAAAGCTGCTGCTGAGGGGA	234933	67129	ATTAAAAAAATCAATGCTGC	279520	111716	GTTTCAAATGACAGATTCTC
190347	22543	GGAAAGCTGCTGCTGAGGGG	234934	67130	CATTAAAAAAATCAATGCTG	279521	111717	TGTTTCAAATGACAGATTCT
190348	22544	TGGAAAGCTGCTGCTGAGGG	234935	67131	TCATTAAAAAAATCAATGCT	279522	111718	TTGTTTCAAATGACAGATTC
190349	22545	CTGGAAAGCTGCTGCTGAGG	234936	67132	TTCATTAAAAAAATCAATGC	279523	111719	GTTGTTTCAAATGACAGATT
190350	22546	TCTGGAAAGCTGCTGCTGAG	234937	67133	CTTCATTAAAAAAATCAATG	279524	111720	TGTTGTTTCAAATGACAGAT
190351	22547	TTCTGGAAAGCTGCTGCTGA	234938	67134	ACTTCATTAAAAAAATCAAT	279525	111721	ATGTTGTTTCAAATGACAGA
190352	22548	GTTCTGGAAAGCTGCTGCTG	234939	67135	CACTTCATTAAAAAAATCAA	279526	111722	CATGTTGTTTCAAATGACAG
190353	22549	TGTTCTGGAAAGCTGCTGCT	234940	67136	CCACTTCATTAAAAAAATCA	279527	111723	CCATGTTGTTTCAAATGACA
190354	22550	ATGTTCTGGAAAGCTGCTGC	234941	67137	TCCACTTCATTAAAAAAATC	279528	111724	TCCATGTTGTTTCAAATGAC
190355	22551	AATGTTCTGGAAAGCTGCTG	234942	67138	TTCCACTTCATTAAAAAAAT	279529	111725	ATCCATGTTGTTTCAAATGA
190356	22552	GAATGTTCTGGAAAGCTGCT	234943	67139	TTTCCACTTCATTAAAAAAA	279530	111726	CATCCATGTTGTTTCAAATG
190357	22553	GGAATGTTCTGGAAAGCTGC	234944	67140	CTTTCCACTTCATTAAAAAA	279531	111727	CCATCCATGTTGTTTCAAAT
190358	22554	GGGAATGTTCTGGAAAGCTG	234945	67141	TCTTTCCACTTCATTAAAAA	279532	111728	TCCATCCATGTTGTTTCAAA
190359	22555	TGGGAATGTTCTGGAAAGCT	234946	67142	CTCTTTCCACTTCATTAAAA	279533	111729	TTCCATCCATGTTGTTTCAA
190360	22556	GTGGGAATGTTCTGGAAAGC	234947	67143	TCTCTTTCCACTTCATTAAA	279534	111730	GTTCCATCCATGTTGTTTCA
190361	22557	AGTGGGAATGTTCTGGAAAG	234948	67144	CTCTCTTTCCACTTCATTAA	279535	111731	AGTTCCATCCATGTTGTTTC
190362	22558	AAGTGGGAATGTTCTGGAAA	234949	67145	GCTCTCTTTCCACTTCATTA	279536	111732	CAGTTCCATCCATGTTGTTT
190363	22559	AAAGTGGGAATGTTCTGGAA	234950	67146	AGCTCTCTTTCCACTTCATT	279537	111733	CCAGTTCCATCCATGTTGTT
190364	22560	GAAAGTGGGAATGTTCTGGA	234951	67147	CAGCTCTCTTTCCACTTCAT	279538	111734	TCCAGTTCCATCCATGTTGT
190365	22561	AGAAAGTGGGAATGTTCTGG	234952	67148	CCAGCTCTCTTTCCACTTCA	279539	111735	CTCCAGTTCCATCCATGTTG
190366	22562	AAGAAAGTGGGAATGTTCTG	234953	67149	CCCAGCTCTCTTTCCACTTC	279540	111736	CCTCCAGTTCCATCCATGTT
190367	22563	GAAGAAAGTGGGAATGTTCT	234954	67150	TCCCAGCTCTCTTTCCACTT	279541	111737	TCCTCCAGTTCCATCCATGT
190368	22564	AGAAGAAAGTGGGAATGTTC	234955	67151	TTCCCAGCTCTCTTTCCACT	279542	111738	GTCCTCCAGTTCCATCCATG
190369	22565	CAGAAGAAAGTGGGAATGTT	234956	67152	ATTCCCAGCTCTCTTTCCAC	279543	111739	TGTCCTCCAGTTCCATCCAT
190370	22566	ACAGAAGAAAGTGGGAATGT	234957	67153	TATTCCCAGCTCTCTTTCCA	279544	111740	ATGTCCTCCAGTTCCATCCA
190371	22567	TACAGAAGAAAGTGGGAATG	234958	67154	TTATTCCCAGCTCTCTTTCC	279545	111741	AATGTCCTCCAGTTCCATCC
190372	22568	CTACAGAAGAAAGTGGGAAT	234959	67155	GTTATTCCCAGCTCTCTTTC	279546	111742	TAATGTCCTCCAGTTCCATC
190373	22569	ACTACAGAAGAAAGTGGGAA	234960	67156	TGTTATTCCCAGCTCTCTTT	279547	111743	ATAATGTCCTCCAGTTCCAT
190374	22570	CACTACAGAAGAAAGTGGGA	234961	67157	TTGTTATTCCCAGCTCTCTT	279548	111744	CATAATGTCCTCCAGTTCCA
190375	22571	TCACTACAGAAGAAAGTGGG	234962	67158	CTTGTTATTCCCAGCTCTCT	279549	111745	ACATAATGTCCTCCAGTTCC
190376	22572	CTCACTACAGAAGAAAGTGG	234963	67159	ACTTGTTATTCCCAGCTCTC	279550	111746	AACATAATGTCCTCCAGTTC
190377	22573	TCTCACTACAGAAGAAAGTG	234964	67160	GACTTGTTATTCCCAGCTCT	279551	111747	TAACATAATGTCCTCCAGTT
190378	22574	TTCTCACTACAGAAGAAAGT	234965	67161	CGACTTGTTATTCCCAGCTC	279552	111748	TTAACATAATGTCCTCCAGT
190379	22575	CTTCTCACTACAGAAGAAAG	234966	67162	CCGACTTGTTATTCCCAGCT	279553	111749	CTTAACATAATGTCCTCCAG
190380	22576	TCTTCTCACTACAGAAGAAA	234967	67163	CCCGACTTGTTATTCCCAGC	279554	111750	ACTTAACATAATGTCCTCCA
190381	22577	TTCTTCTCACTACAGAAGAA	234968	67164	GCCCGACTTGTTATTCCCAG	279555	111751	CACTTAACATAATGTCCTCC
190382	22578	GTTCTTCTCACTACAGAAGA	234969	67165	GGCCCGACTTGTTATTCCCA	279556	111752	TCACTTAACATAATGTCCTC
190383	22579	AGTTCTTCTCACTACAGAAG	234970	67166	GGGCCCGACTTGTTATTCCC	279557	111753	TTCACTTAACATAATGTCCT
190384	22580	GAGTTCTTCTCACTACAGAA	234971	67167	TGGGCCCGACTTGTTATTCC	279558	111754	TTTCACTTAACATAATGTCC
190385	22581	AGAGTTCTTCTCACTACAGA	234972	67168	GTGGGCCCGACTTGTTATTC	279559	111755	ATTTCACTTAACATAATGTC
190386	22582	AAGAGTTCTTCTCACTACAG	234973	67169	GGTGGGCCCGACTTGTTATT	279560	111756	TATTTCACTTAACATAATGT
190387	22583	AAAGAGTTCTTCTCACTACA	234974	67170	AGGTGGGCCCGACTTGTTAT	279561	111757	TTATTTCACTTAACATAATG
190388	22584	GAAAGAGTTCTTCTCACTAC	234975	67171	GAGGTGGGCCCGACTTGTTA	279562	111758	CTTATTTCACTTAACATAAT
190389	22585	GGAAAGAGTTCTTCTCACTA	234976	67172	TGAGGTGGGCCCGACTTGTT	279563	111759	GCTTATTTCACTTAACATAA
190390	22586	GGGAAAGAGTTCTTCTCACT	234977	67173	GTGAGGTGGGCCCGACTTGT	279564	111760	GGCTTATTTCACTTAACATA
190391	22587	AGGGAAAGAGTTCTTCTCAC	234978	67174	GGTGAGGTGGGCCCGACTTG	279565	111761	TGGCTTATTTCACTTAACAT
190392	22588	CAGGGAAAGAGTTCTTCTCA	234979	67175	AGGTGAGGTGGGCCCGACTT	279566	111762	CTGGCTTATTTCACTTAACA
190393	22589	GCAGGGAAAGAGTTCTTCTC	234980	67176	CAGGTGAGGTGGGCCCGACT	279567	111763	TCTGGCTTATTTCACTTAAC
190394	22590	TGCAGGGAAAGAGTTCTTCT	234981	67177	GCAGGTGAGGTGGGCCCGAC	279568	111764	GTCTGGCTTATTTCACTTAA
190395	22591	CTGCAGGGAAAGAGTTCTTC	234982	67178	GGCAGGTGAGGTGGGCCCGA	279569	111765	TGTCTGGCTTATTTCACTTA
190396	22592	GCTGCAGGGAAAGAGTTCTT	234983	67179	AGGCAGGTGAGGTGGGCCCG	279570	111766	CTGTCTGGCTTATTTCACTT
190397	22593	GGCTGCAGGGAAAGAGTTCT	234984	67180	GAGGCAGGTGAGGTGGGCCC	279571	111767	TCTGTCTGGCTTATTTCACT
190398	22594	AGGCTGCAGGGAAAGAGTTC	234985	67181	TGAGGCAGGTGAGGTGGGCC	279572	111768	TTCTGTCTGGCTTATTTCAC
190399	22595	GAGGCTGCAGGGAAAGAGTT	234986	67182	GTGAGGCAGGTGAGGTGGGC	279573	111769	CTTCTGTCTGGCTTATTTCA
190400	22596	GGAGGCTGCAGGGAAAGAGT	234987	67183	GGTGAGGCAGGTGAGGTGGG	279574	111770	CCTTCTGTCTGGCTTATTTC
190401	22597	AGGAGGCTGCAGGGAAAGAG	234988	67184	AGGTGAGGCAGGTGAGGTGG	279575	111771	TCCTTCTGTCTGGCTTATTT
190402	22598	CAGGAGGCTGCAGGGAAAGA	234989	67185	CAGGTGAGGCAGGTGAGGTG	279576	111772	GTCCTTCTGTCTGGCTTATT
190403	22599	GCAGGAGGCTGCAGGGAAAG	234990	67186	CCAGGTGAGGCAGGTGAGGT	279577	111773	TGTCCTTCTGTCTGGCTTAT
190404	22600	GGCAGGAGGCTGCAGGGAAA	234991	67187	ACCAGGTGAGGCAGGTGAGG	279578	111774	CTGTCCTTCTGTCTGGCTTA
190405	22601	GGGCAGGAGGCTGCAGGGAA	234992	67188	CACCAGGTGAGGCAGGTGAG	279579	111775	TCTGTCCTTCTGTCTGGCTT
190406	22602	TGGGCAGGAGGCTGCAGGGA	234993	67189	CCACCAGGTGAGGCAGGTGA	279580	111776	GTCTGTCCTTCTGTCTGGCT
190407	22603	TTGGGCAGGAGGCTGCAGGG	234994	67190	CCCACCAGGTGAGGCAGGTG	279581	111777	AGTCTGTCCTTCTGTCTGGC
190408	22604	GTTGGGCAGGAGGCTGCAGG	234995	67191	ACCCACCAGGTGAGGCAGGT	279582	111778	AAGTCTGTCCTTCTGTCTGG
190409	22605	AGTTGGGCAGGAGGCTGCAG	234996	67192	AACCCACCAGGTGAGGCAGG	279583	111779	GAAGTCTGTCCTTCTGTCTG
190410	22606	GAGTTGGGCAGGAGGCTGCA	234997	67193	AAACCCACCAGGTGAGGCAG	279584	111780	TGAAGTCTGTCCTTCTGTCT

190411	22607	GGAGTTGGGCAGGAGGCTGC	234998	67194	TAAACCCACCAGGTGAGGCA	279585	111781	GTGAAGTCTGTCCTTCTGTC
190412	22608	AGGAGTTGGGCAGGAGGCTG	234999	67195	ATAAACCCACCAGGTGAGGC	279586	111782	TGTGAAGTCTGTCCTTCTGT
190413	22609	GAGGAGTTGGGCAGGAGGCT	235000	67196	AATAAACCCACCAGGTGAGG	279587	111783	ATGTGAAGTCTGTCCTTCTG
190414	22610	GGAGGAGTTGGGCAGGAGGC	235001	67197	AAATAAACCCACCAGGTGAG	279588	111784	CATGTGAAGTCTGTCCTTCT
190415	22611	AGGAGGAGTTGGGCAGGAGG	235002	67198	CAAATAAACCCACCAGGTGA	279589	111785	ACATGTGAAGTCTGTCCTTC
190416	22612	AAGGAGGAGTTGGGCAGGAG	235003	67199	ACAAATAAACCCACCAGGTG	279590	111786	AACATGTGAAGTCTGTCCTT
190417	22613	GAAGGAGGAGTTGGGCAGGA	235004	67200	AACAAATAAACCCACCAGGT	279591	111787	GAACATGTGAAGTCTGTCCT
190418	22614	TGAAGGAGGAGTTGGGCAGG	235005	67201	AAACAAATAAACCCACCAGG	279592	111788	AGAACATGTGAAGTCTGTCC
190419	22615	CTGAAGGAGGAGTTGGGCAG	235006	67202	AAAACAAATAAACCCACCAG	279593	111789	GAGAACATGTGAAGTCTGTC
190420	22616	ACTGAAGGAGGAGTTGGGCA	235007	67203	CAAAACAAATAAACCCACCA	279594	111790	TGAGAACATGTGAAGTCTGT
190421	22617	CACTGAAGGAGGAGTTGGGC	235008	67204	ACAAAACAAATAAACCCACC	279595	111791	GTGAGAACATGTGAAGTCTG
190422	22618	ACACTGAAGGAGGAGTTGGG	235009	67205	AACAAAACAAATAAACCCAC	279596	111792	TGTGAGAACATGTGAAGTCT
190423	22619	GACACTGAAGGAGGAGTTGG	235010	67206	AAACAAAACAAATAAACCCA	279597	111793	GTGTGAGAACATGTGAAGTC
190424	22620	AGACACTGAAGGAGGAGTTG	235011	67207	AAAACAAAACAAATAAACCC	279598	111794	TGTGTGAGAACATGTGAAGT
190425	22621	AAGACACTGAAGGAGGAGTT	235012	67208	AAAAACAAAACAAATAAACC	279599	111795	ATGTGTGAGAACATGTGAAG
190426	22622	AAAGACACTGAAGGAGGAGT	235013	67209	AAAAAACAAAACAAATAAAC	279600	111796	AATGTGTGAGAACATGTGAA
190427	22623	CAAAGACACTGAAGGAGGAG	235014	67210	AAAAAAACAAAACAAATAAA	279601	111797	AAATGTGTGAGAACATGTGA
190428	22624	GCAAAGACACTGAAGGAGGA	235015	67211	AAAAAAAACAAAACAAATAA	279602	111798	CAAATGTGTGAGAACATGTG
190429	22625	AGCAAAGACACTGAAGGAGG	235016	67212	AAAAAAAAACAAAACAAATA	279603	111799	ACAAATGTGTGAGAACATGT
190430	22626	AAGCAAAGACACTGAAGGAG	235017	67213	AAAAAAAAAACAAAACAAAT	279604	111800	CACAAATGTGTGAGAACATG
190431	22627	GAAGCAAAGACACTGAAGGA	235018	67214	AAAAAAAAAAACAAAACAAA	279605	111801	CCACAAATGTGTGAGAACAT
190432	22628	TGAAGCAAAGACACTGAAGG	235019	67215	AAAAAAAAAAAACAAAACAA	279606	111802	CCCACAAATGTGTGAGAACA
190433	22629	CTGAAGCAAAGACACTGAAG	235020	67216	AAAAAAAAAAAAACAAAACA	279607	111803	TCCCACAAATGTGTGAGAAC
190434	22630	ACTGAAGCAAAGACACTGAA	235021	67217	CAAAAAAAAAAAAACAAAAC	279608	111804	CTCCCACAAATGTGTGAGAA
190435	22631	CACTGAAGCAAAGACACTGA	235022	67218	ACAAAAAAAAAAAAACAAAA	279609	111805	GCTCCCACAAATGTGTGAGA
190436	22632	ACACTGAAGCAAAGACACTG	235023	67219	AACAAAAAAAAAAAAACAAA	279610	111806	AGCTCCCACAAATGTGTGAG
190437	22633	GACACTGAAGCAAAGACACT	235024	67220	AAACAAAAAAAAAAAAACAA	279611	111807	TAGCTCCCACAAATGTGTGA
190438	22634	AGACACTGAAGCAAAGACAC	235025	67221	AAAACAAAAAAAAAAAAACA	279612	111808	TTAGCTCCCACAAATGTGTG
190439	22635	AAGACACTGAAGCAAAGACA	235026	67222	CAAAACAAAAAAAAAAAAAC	279613	111809	TTTAGCTCCCACAAATGTGT
190440	22636	AAAGACACTGAAGCAAAGAC	235027	67223	TCAAAACAAAAAAAAAAAAA	279614	111810	TTTTAGCTCCCACAAATGTG
190441	22637	CAAAGACACTGAAGCAAAGA	235028	67224	CTCAAAACAAAAAAAAAAAA	279615	111811	TTTTTAGCTCCCACAAATGT
190442	22638	TCAAAGACACTGAAGCAAAG	235029	67225	TCTCAAAACAAAAAAAAAAA	279616	111812	ATTTTTAGCTCCCACAAATG
190443	22639	ATCAAAGACACTGAAGCAAA	235030	67226	GTCTCAAAACAAAAAAAAAA	279617	111813	AATTTTTAGCTCCCACAAAT
190444	22640	TATCAAAGACACTGAAGCAA	235031	67227	TGTCTCAAAACAAAAAAAAA	279618	111814	TAATTTTTAGCTCCCACAAA
190445	22641	TTATCAAAGACACTGAAGCA	235032	67228	CTGTCTCAAAACAAAAAAAA	279619	111815	TTAATTTTTAGCTCCCACAA
190446	22642	TTTATCAAAGACACTGAAGC	235033	67229	TCTGTCTCAAAACAAAAAAA	279620	111816	TTTAATTTTTAGCTCCCACA
190447	22643	GTTTATCAAAGACACTGAAG	235034	67230	CTCTGTCTCAAAACAAAAAA	279621	111817	GTTTAATTTTTAGCTCCCAC
190448	22644	GGTTTATCAAAGACACTGAA	235035	67231	ACTCTGTCTCAAAACAAAAA	279622	111818	AGTTTAATTTTTAGCTCCCA
190449	22645	TGGTTTATCAAAGACACTGA	235036	67232	AACTCTGTCTCAAAACAAAA	279623	111819	GAGTTTAATTTTTAGCTCCC
190450	22646	ATGGTTTATCAAAGACACTG	235037	67233	AAACTCTGTCTCAAAACAAA	279624	111820	TGAGTTTAATTTTTAGCTCC
190451	22647	AATGGTTTATCAAAGACACT	235038	67234	GAAACTCTGTCTCAAAACAA	279625	111821	ATGAGTTTAATTTTTAGCTC
190452	22648	GAATGGTTTATCAAAGACAC	235039	67235	TGAAACTCTGTCTCAAAACA	279626	111822	CATGAGTTTAATTTTTAGCT
190453	22649	AGAATGGTTTATCAAAGACA	235040	67236	GTGAAACTCTGTCTCAAAAC	279627	111823	CCATGAGTTTAATTTTTAGC
190454	22650	CAGAATGGTTTATCAAAGAC	235041	67237	GGTGAAACTCTGTCTCAAAA	279628	111824	TCCATGAGTTTAATTTTTAG
190455	22651	GCAGAATGGTTTATCAAAGA	235042	67238	GGGTGAAACTCTGTCTCAAA	279629	111825	CTCCATGAGTTTAATTTTTA
190456	22652	AGCAGAATGGTTTATCAAAG	235043	67239	AGGGTGAAACTCTGTCTCAA	279630	111826	TCTCCATGAGTTTAATTTTT
190457	22653	AAGCAGAATGGTTTATCAAA	235044	67240	CAGGGTGAAACTCTGTCTCA	279631	111827	ATCTCCATGAGTTTAATTTT
190458	22654	AAAGCAGAATGGTTTATCAA	235045	67241	ACAGGGTGAAACTCTGTCTC	279632	111828	TATCTCCATGAGTTTAATTT
190459	22655	CAAAGCAGAATGGTTTATCA	235046	67242	GACAGGGTGAAACTCTGTCT	279633	111829	CTATCTCCATGAGTTTAATT
190460	22656	GCAAAGCAGAATGGTTTATC	235047	67243	TGACAGGGTGAAACTCTGTC	279634	111830	TCTATCTCCATGAGTTTAAT
190461	22657	TGCAAAGCAGAATGGTTTAT	235048	67244	GTGACAGGGTGAAACTCTGT	279635	111831	CTCTATCTCCATGAGTTTAA
190462	22658	CTGCAAAGCAGAATGGTTTA	235049	67245	GGTGACAGGGTGAAACTCTG	279636	111832	TCTCTATCTCCATGAGTTTA
190463	22659	TCTGCAAAGCAGAATGGTTT	235050	67246	GGGTGACAGGGTGAAACTCT	279637	111833	CTCTCTATCTCCATGAGTTT
190464	22660	CTCTGCAAAGCAGAATGGTT	235051	67247	TGGGTGACAGGGTGAAACTC	279638	111834	ACTCTCTATCTCCATGAGTT
190465	22661	ACTCTGCAAAGCAGAATGGT	235052	67248	CTGGGTGACAGGGTGAAACT	279639	111835	TACTCTCTATCTCCATGAGT
190466	22662	CACTCTGCAAAGCAGAATGG	235053	67249	CCTGGGTGACAGGGTGAAAC	279640	111836	CTACTCTCTATCTCCATGAG
190467	22663	GCACTCTGCAAAGCAGAATG	235054	67250	GCCTGGGTGACAGGGTGAAA	279641	111837	TCTACTCTCTATCTCCATGA
190468	22664	CGCACTCTGCAAAGCAGAAT	235055	67251	AGCCTGGGTGACAGGGTGAA	279642	111838	TTCTACTCTCTATCTCCATG
190469	22665	TCGCACTCTGCAAAGCAGAA	235056	67252	CAGCCTGGGTGACAGGGTGA	279643	111839	CTTCTACTCTCTATCTCCAT
190470	22666	CTCGCACTCTGCAAAGCAGA	235057	67253	CCAGCCTGGGTGACAGGGTG	279644	111840	CCTTCTACTCTCTATCTCCA
190471	22667	GCTCGCACTCTGCAAAGCAG	235058	67254	TCCAGCCTGGGTGACAGGGT	279645	111841	TCCTTCTACTCTCTATCTCC
190472	22668	AGCTCGCACTCTGCAAAGCA	235059	67255	CTCCAGCCTGGGTGACAGGG	279646	111842	ATCCTTCTACTCTCTATCTC
190473	22669	GAGCTCGCACTCTGCAAAGC	235060	67256	ACTCCAGCCTGGGTGACAGG	279647	111843	CATCCTTCTACTCTCTATCT
190474	22670	AGAGCTCGCACTCTGCAAAG	235061	67257	CACTCCAGCCTGGGTGACAG	279648	111844	CCATCCTTCTACTCTCTATC
190475	22671	CAGAGCTCGCACTCTGCAAA	235062	67258	GCACTCCAGCCTGGGTGACA	279649	111845	ACCATCCTTCTACTCTCTAT
190476	22672	GCAGAGCTCGCACTCTGCAA	235063	67259	TGCACTCCAGCCTGGGTGAC	279650	111846	AACCATCCTTCTACTCTCTA
190477	22673	GGCAGAGCTCGCACTCTGCA	235064	67260	CTGCACTCCAGCCTGGGTGA	279651	111847	TAACCATCCTTCTACTCTCT
190478	22674	AGGCAGAGCTCGCACTCTGC	235065	67261	ACTGCACTCCAGCCTGGGTG	279652	111848	GTAACCATCCTTCTACTCTC
190479	22675	AAGGCAGAGCTCGCACTCTG	235066	67262	CACTGCACTCCAGCCTGGGT	279653	111849	GGTAACCATCCTTCTACTCT
190480	22676	CAAGGCAGAGCTCGCACTCT	235067	67263	CCACTGCACTCCAGCCTGGG	279654	111850	TGGTAACCATCCTTCTACTC
190481	22677	GCAAGGCAGAGCTCGCACTC	235068	67264	ACCACTGCACTCCAGCCTGG	279655	111851	CTGGTAACCATCCTTCTACT
190482	22678	TGCAAGGCAGAGCTCGCACT	235069	67265	CACCACTGCACTCCAGCCTG	279656	111852	TCTGGTAACCATCCTTCTAC

190483	22679	CTGCAAGGCAGAGCTCGCAC	235070	67266	ACACCACTGCACTCCAGCCT	279657	111853	CTCTGGTAACCATCCTTCTA
190484	22680	CCTGCAAGGCAGAGCTCGCA	235071	67267	TACACCACTGCACTCCAGCC	279658	111854	CCTCTGGTAACCATCCTTCT
190485	22681	CCCTGCAAGGCAGAGCTCGC	235072	67268	TTACACCACTGCACTCCAGC	279659	111855	GCCTCTGGTAACCATCCTTC
190486	22682	ACCCTGCAAGGCAGAGCTCG	235073	67269	ATTACACCACTGCACTCCAG	279660	111856	AGCCTCTGGTAACCATCCTT
190487	22683	AACCCTGCAAGGCAGAGCTC	235074	67270	GATTACACCACTGCACTCCA	279661	111857	CAGCCTCTGGTAACCATCCT
190488	22684	GAACCCTGCAAGGCAGAGCT	235075	67271	AGATTACACCACTGCACTCC	279662	111858	TCAGCCTCTGGTAACCATCC
190489	22685	CGAACCCTGCAAGGCAGAGC	235076	67272	GAGATTACACCACTGCACTC	279663	111859	CTCAGCCTCTGGTAACCATC
190490	22686	GCGAACCCTGCAAGGCAGAG	235077	67273	TGAGATTACACCACTGCACT	279664	111860	CCTCAGCCTCTGGTAACCAT
190491	22687	TGCGAACCCTGCAAGGCAGA	235078	67274	CTGAGATTACACCACTGCAC	279665	111861	TCCTCAGCCTCTGGTAACCA
190492	22688	ATGCGAACCCTGCAAGGCAG	235079	67275	GCTGAGATTACACCACTGCA	279666	111862	CTCCTCAGCCTCTGGTAACC
190493	22689	GATGCGAACCCTGCAAGGCA	235080	67276	AGCTGAGATTACACCACTGC	279667	111863	CCTCCTCAGCCTCTGGTAAC
190494	22690	AGATGCGAACCCTGCAAGGC	235081	67277	GAGCTGAGATTACACCACTG	279668	111864	CCCTCCTCAGCCTCTGGTAA
190495	22691	CAGATGCGAACCCTGCAAGG	235082	67278	TGAGCTGAGATTACACCACT	279669	111865	ACCCTCCTCAGCCTCTGGTA
190496	22692	GCAGATGCGAACCCTGCAAG	235083	67279	GTGAGCTGAGATTACACCAC	279670	111866	CACCCTCCTCAGCCTCTGGT
190497	22693	GGCAGATGCGAACCCTGCAA	235084	67280	AGTGAGCTGAGATTACACCA	279671	111867	CCACCCTCCTCAGCCTCTGG
190498	22694	AGGCAGATGCGAACCCTGCA	235085	67281	CAGTGAGCTGAGATTACACC	279672	111868	TCCACCCTCCTCAGCCTCTG
190499	22695	CAGGCAGATGCGAACCCTGC	235086	67282	GCAGTGAGCTGAGATTACAC	279673	111869	CTCCACCCTCCTCAGCCTCT
190500	22696	ACAGGCAGATGCGAACCCTG	235087	67283	TGCAGTGAGCTGAGATTACA	279674	111870	CCTCCACCCTCCTCAGCCTC
190501	22697	CACAGGCAGATGCGAACCCT	235088	67284	TTGCAGTGAGCTGAGATTAC	279675	111871	CCCTCCACCCTCCTCAGCCT
190502	22698	GCACAGGCAGATGCGAACCC	235089	67285	GTTGCAGTGAGCTGAGATTA	279676	111872	CCCCTCCACCCTCCTCAGCC
190503	22699	AGCACAGGCAGATGCGAACC	235090	67286	GGTTGCAGTGAGCTGAGATT	279677	111873	TCCCCTCCACCCTCCTCAGC
190504	22700	CAGCACAGGCAGATGCGAAC	235091	67287	AGGTTGCAGTGAGCTGAGAT	279678	111874	CTCCCCTCCACCCTCCTCAG
190505	22701	TCAGCACAGGCAGATGCGAA	235092	67288	GAGGTTGCAGTGAGCTGAGA	279679	111875	GCTCCCCTCCACCCTCCTCA
190506	22702	CTCAGCACAGGCAGATGCGA	235093	67289	GGAGGTTGCAGTGAGCTGAG	279680	111876	TGCTCCCCTCCACCCTCCTC
190507	22703	ACTCAGCACAGGCAGATGCG	235094	67290	TGGAGGTTGCAGTGAGCTGA	279681	111877	CTGCTCCCCTCCACCCTCCT
190508	22704	TACTCAGCACAGGCAGATGC	235095	67291	GTGGAGGTTGCAGTGAGCTG	279682	111878	CCTGCTCCCCTCCACCCTCC
190509	22705	TTACTCAGCACAGGCAGATG	235096	67292	GGTGGAGGTTGCAGTGAGCT	279683	111879	CCCTGCTCCCCTCCACCCTC
190510	22706	GTTACTCAGCACAGGCAGAT	235097	67293	AGGTGGAGGTTGCAGTGAGC	279684	111880	TCCCTGCTCCCCTCCACCCT
190511	22707	GGTTACTCAGCACAGGCAGA	235098	67294	CAGGTGGAGGTTGCAGTGAG	279685	111881	CTCCCTGCTCCCCTCCACCC
190512	22708	TGGTTACTCAGCACAGGCAG	235099	67295	GCAGGTGGAGGTTGCAGTGA	279686	111882	TCTCCCTGCTCCCCTCCACC
190513	22709	TTGGTTACTCAGCACAGGCA	235100	67296	GGCAGGTGGAGGTTGCAGTG	279687	111883	TTCTCCCTGCTCCCCTCCAC
190514	22710	GTTGGTTACTCAGCACAGGC	235101	67297	TGGCAGGTGGAGGTTGCAGT	279688	111884	TTTCTCCCTGCTCCCCTCCA
190515	22711	CGTTGGTTACTCAGCACAGG	235102	67298	CTGGCAGGTGGAGGTTGCAG	279689	111885	CTTTCTCCCTGCTCCCCTCC
190516	22712	GCGTTGGTTACTCAGCACAG	235103	67299	CCTGGCAGGTGGAGGTTGCA	279690	111886	ACTTTCTCCCTGCTCCCCTC
190517	22713	AGCGTTGGTTACTCAGCACA	235104	67300	ACCTGGCAGGTGGAGGTTGC	279691	111887	TACTTTCTCCCTGCTCCCCT
190518	22714	TAGCGTTGGTTACTCAGCAC	235105	67301	AACCTGGCAGGTGGAGGTTG	279692	111888	CTACTTTCTCCCTGCTCCCC
190519	22715	TTAGCGTTGGTTACTCAGCA	235106	67302	GAACCTGGCAGGTGGAGGTT	279693	111889	CCTACTTTCTCCCTGCTCCC
190520	22716	CTTAGCGTTGGTTACTCAGC	235107	67303	TGAACCTGGCAGGTGGAGGT	279694	111890	CCCTACTTTCTCCCTGCTCC
190521	22717	CCTTAGCGTTGGTTACTCAG	235108	67304	TTGAACCTGGCAGGTGGAGG	279695	111891	TCCCTACTTTCTCCCTGCTC
190522	22718	ACCTTAGCGTTGGTTACTCA	235109	67305	ATTGAACCTGGCAGGTGGAG	279696	111892	ATCCCTACTTTCTCCCTGCT
190523	22719	GACCTTAGCGTTGGTTACTC	235110	67306	AATTGAACCTGGCAGGTGGA	279697	111893	CATCCCTACTTTCTCCCTGC
190524	22720	CGACCTTAGCGTTGGTTACT	235111	67307	CAATTGAACCTGGCAGGTGG	279698	111894	CCATCCCTACTTTCTCCCTG
190525	22721	TCGACCTTAGCGTTGGTTAC	235112	67308	TCAATTGAACCTGGCAGGTG	279699	111895	ACCATCCCTACTTTCTCCCT
190526	22722	CTCGACCTTAGCGTTGGTTA	235113	67309	ATCAATTGAACCTGGCAGGT	279700	111896	AACCATCCCTACTTTCTCCC
190527	22723	ACTCGACCTTAGCGTTGGTT	235114	67310	AATCAATTGAACCTGGCAGG	279701	111897	TAACCATCCCTACTTTCTCC
190528	22724	CACTCGACCTTAGCGTTGGT	235115	67311	GAATCAATTGAACCTGGCAG	279702	111898	TTAACCATCCCTACTTTCTC
190529	22725	CCACTCGACCTTAGCGTTGG	235116	67312	AGAATCAATTGAACCTGGCA	279703	111899	ATTAACCATCCCTACTTTCT
190530	22726	ACCACTCGACCTTAGCGTTG	235117	67313	GAGAATCAATTGAACCTGGC	279704	111900	CATTAACCATCCCTACTTTC
190531	22727	GACCACTCGACCTTAGCGTT	235118	67314	GGAGAATCAATTGAACCTGG	279705	111901	CCATTAACCATCCCTACTTT
190532	22728	CGACCACTCGACCTTAGCGT	235119	67315	AGGAGAATCAATTGAACCTG	279706	111902	CCCATTAACCATCCCTACTT
190533	22729	CCGACCACTCGACCTTAGCG	235120	67316	CAGGAGAATCAATTGAACCT	279707	111903	ACCCATTAACCATCCCTACT
190534	22730	ACCGACCACTCGACCTTAGC	235121	67317	GCAGGAGAATCAATTGAACC	279708	111904	TACCCATTAACCATCCCTAC
190535	22731	GACCGACCACTCGACCTTAG	235122	67318	GGCAGGAGAATCAATTGAAC	279709	111905	GTACCCATTAACCATCCCTA
190536	22732	TGACCGACCACTCGACCTTA	235123	67319	AGGCAGGAGAATCAATTGAA	279710	111906	TGTACCCATTAACCATCCCT
190537	22733	GTGACCGACCACTCGACCTT	235124	67320	GAGGCAGGAGAATCAATTGA	279711	111907	TTGTACCCATTAACCATCCC
190538	22734	GGTGACCGACCACTCGACCT	235125	67321	TGAGGCAGGAGAATCAATTG	279712	111908	TTTGTACCCATTAACCATCC
190539	22735	AGGTGACCGACCACTCGACC	235126	67322	CTGAGGCAGGAGAATCAATT	279713	111909	TTTTGTACCCATTAACCATC
190540	22736	GAGGTGACCGACCACTCGAC	235127	67323	GCTGAGGCAGGAGAATCAAT	279714	111910	TTTTTGTACCCATTAACCAT
190541	22737	AGAGGTGACCGACCACTCGA	235128	67324	GGCTGAGGCAGGAGAATCAA	279715	111911	GTTTTTGTACCCATTAACCA
190542	22738	GAGAGGTGACCGACCACTCG	235129	67325	AGGCTGAGGCAGGAGAATCA	279716	111912	CGTTTTTGTACCCATTAACC
190543	22739	TGAGAGGTGACCGACCACTC	235130	67326	GAGGCTGAGGCAGGAGAATC	279717	111913	ACGTTTTTGTACCCATTAAC
190544	22740	ATGAGAGGTGACCGACCACT	235131	67327	GGAGGCTGAGGCAGGAGAAT	279718	111914	TACGTTTTTGTACCCATTAA
190545	22741	TATGAGAGGTGACCGACCAC	235132	67328	GGGAGGCTGAGGCAGGAGAA	279719	111915	CTACGTTTTTGTACCCATTA
190546	22742	TTATGAGAGGTGACCGACCA	235133	67329	GGGGAGGCTGAGGCAGGAGA	279720	111916	ACTACGTTTTTGTACCCATT
190547	22743	CTTATGAGAGGTGACCGACC	235134	67330	TGGGGAGGCTGAGGCAGGAG	279721	111917	AACTACGTTTTTGTACCCAT
190548	22744	TCTTATGAGAGGTGACCGAC	235135	67331	CTGGGGAGGCTGAGGCAGGA	279722	111918	TAACTACGTTTTTGTACCCA
190549	22745	CTCTTATGAGAGGTGACCGA	235136	67332	ACTGGGGAGGCTGAGGCAGG	279723	111919	CTAACTACGTTTTTGTACCC
190550	22746	GCTCTTATGAGAGGTGACCG	235137	67333	TACTGGGGAGGCTGAGGCAG	279724	111920	GCTAACTACGTTTTTGTACC
190551	22747	AGCTCTTATGAGAGGTGACC	235138	67334	CTACTGGGGAGGCTGAGGCA	279725	111921	TGCTAACTACGTTTTTGTAC
190552	22748	TAGCTCTTATGAGAGGTGAC	235139	67335	GCTACTGGGGAGGCTGAGGC	279726	111922	ATGCTAACTACGTTTTTGTA
190553	22749	CTAGCTCTTATGAGAGGTGA	235140	67336	AGCTACTGGGGAGGCTGAGG	279727	111923	CATGCTAACTACGTTTTTGT
190554	22750	CCTAGCTCTTATGAGAGGTG	235141	67337	CAGCTACTGGGGAGGCTGAG	279728	111924	GCATGCTAACTACGTTTTTG

190555	22751	CCCTAGCTCTTATGAGAGGT	235142	67338	CCAGCTACTGGGGAGGCTGA	279729	111925	TGCATGCTAACTACGTTTTT
190556	22752	ACCCTAGCTCTTATGAGAGG	235143	67339	CCCAGCTACTGGGGAGGCTG	279730	111926	ATGCATGCTAACTACGTTTT
190557	22753	AACCCTAGCTCTTATGAGAG	235144	67340	TCCCAGCTACTGGGGAGGCT	279731	111927	TATGCATGCTAACTACGTTT
190558	22754	CAACCCTAGCTCTTATGAGA	235145	67341	ATCCCAGCTACTGGGGAGGC	279732	111928	CTATGCATGCTAACTACGTT
190559	22755	ACAACCCTAGCTCTTATGAG	235146	67342	AATCCCAGCTACTGGGGAGG	279733	111929	TCTATGCATGCTAACTACGT
190560	22756	GACAACCCTAGCTCTTATGA	235147	67343	TAATCCCAGCTACTGGGGAG	279734	111930	ATCTATGCATGCTAACTACG
190561	22757	AGACAACCCTAGCTCTTATG	235148	67344	GTAATCCCAGCTACTGGGGA	279735	111931	GATCTATGCATGCTAACTAC
190562	22758	GAGACAACCCTAGCTCTTAT	235149	67345	TGTAATCCCAGCTACTGGGG	279736	111932	AGATCTATGCATGCTAACTA
190563	22759	TGAGACAACCCTAGCTCTTA	235150	67346	CTGTAATCCCAGCTACTGGG	279737	111933	TAGATCTATGCATGCTAACT
190564	22760	ATGAGACAACCCTAGCTCTT	235151	67347	CCTGTAATCCCAGCTACTGG	279738	111934	CTAGATCTATGCATGCTAAC
190565	22761	CATGAGACAACCCTAGCTCT	235152	67348	GCCTGTAATCCCAGCTACTG	279739	111935	ACTAGATCTATGCATGCTAA
190566	22762	GCATGAGACAACCCTAGCTC	235153	67349	TGCCTGTAATCCCAGCTACT	279740	111936	TACTAGATCTATGCATGCTA
190567	22763	AGCATGAGACAACCCTAGCT	235154	67350	GTGCCTGTAATCCCAGCTAC	279741	111937	ATACTAGATCTATGCATGCT
190568	22764	CAGCATGAGACAACCCTAGC	235155	67351	GGTGCCTGTAATCCCAGCTA	279742	111938	AATACTAGATCTATGCATGC
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190570	22766	ATCAGCATGAGACAACCCTA	235157	67353	CAGGTGCCTGTAATCCCAGC	279744	111940	CCAATACTAGATCTATGCAT
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190574	22770	AGTCATCAGCATGAGACAAC	235161	67357	GTGGCAGGTGCCTGTAATCC	279748	111944	CTATCCAATACTAGATCTAT
190575	22771	TAGTCATCAGCATGAGACAA	235162	67358	TGTGGCAGGTGCCTGTAATC	279749	111945	GCTATCCAATACTAGATCTA
190576	22772	CTAGTCATCAGCATGAGACA	235163	67359	ATGTGGCAGGTGCCTGTAAT	279750	111946	TGCTATCCAATACTAGATCT
190577	22773	CCTAGTCATCAGCATGAGAC	235164	67360	CATGTGGCAGGTGCCTGTAA	279751	111947	GTGCTATCCAATACTAGATC
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190579	22775	GTCCTAGTCATCAGCATGAG	235166	67362	GGCATGTGGCAGGTGCCTGT	279753	111949	CTGTGCTATCCAATACTAGA
190580	22776	AGTCCTAGTCATCAGCATGA	235167	67363	AGGCATGTGGCAGGTGCCTG	279754	111950	GCTGTGCTATCCAATACTAG
190581	22777	AAGTCCTAGTCATCAGCATG	235168	67364	CAGGCATGTGGCAGGTGCCT	279755	111951	TGCTGTGCTATCCAATACTA
190582	22778	CAAGTCCTAGTCATCAGCAT	235169	67365	CCAGGCATGTGGCAGGTGCC	279756	111952	CTGCTGTGCTATCCAATACT
190583	22779	GCAAGTCCTAGTCATCAGCA	235170	67366	GCCAGGCATGTGGCAGGTGC	279757	111953	CCTGCTGTGCTATCCAATAC
190584	22780	GGCAAGTCCTAGTCATCAGC	235171	67367	AGCCAGGCATGTGGCAGGTG	279758	111954	CCCTGCTGTGCTATCCAATA
190585	22781	GGGCAAGTCCTAGTCATCAG	235172	67368	TAGCCAGGCATGTGGCAGGT	279759	111955	ACCCTGCTGTGCTATCCAAT
190586	22782	AGGGCAAGTCCTAGTCATCA	235173	67369	TTAGCCAGGCATGTGGCAGG	279760	111956	CACCCTGCTGTGCTATCCAA
190587	22783	GAGGGCAAGTCCTAGTCATC	235174	67370	ATTAGCCAGGCATGTGGCAG	279761	111957	TCACCCTGCTGTGCTATCCA
190588	22784	TGAGGGCAAGTCCTAGTCAT	235175	67371	AATTAGCCAGGCATGTGGCA	279762	111958	GTCACCCTGCTGTGCTATCC
190589	22785	TTGAGGGCAAGTCCTAGTCA	235176	67372	TAATTAGCCAGGCATGTGGC	279763	111959	CGTCACCCTGCTGTGCTATC
190590	22786	CTTGAGGGCAAGTCCTAGTC	235177	67373	ATAATTAGCCAGGCATGTGG	279764	111960	TCGTCACCCTGCTGTGCTAT
190591	22787	CCTTGAGGGCAAGTCCTAGT	235178	67374	AATAATTAGCCAGGCATGTG	279765	111961	GTCGTCACCCTGCTGTGCTA
190592	22788	TCCTTGAGGGCAAGTCCTAG	235179	67375	CAATAATTAGCCAGGCATGT	279766	111962	TGTCGTCACCCTGCTGTGCT
190593	22789	CTCCTTGAGGGCAAGTCCTA	235180	67376	ACAATAATTAGCCAGGCATG	279767	111963	CTGTCGTCACCCTGCTGTGC
190594	22790	TCTCCTTGAGGGCAAGTCCT	235181	67377	TACAATAATTAGCCAGGCAT	279768	111964	GCTGTCGTCACCCTGCTGTG
190595	22791	TTCTCCTTGAGGGCAAGTCC	235182	67378	ATACAATAATTAGCCAGGCA	279769	111965	GGCTGTCGTCACCCTGCTGT
190596	22792	TTTCTCCTTGAGGGCAAGTC	235183	67379	AATACAATAATTAGCCAGGC	279770	111966	TGGCTGTCGTCACCCTGCTG
190597	22793	TTTTCTCCTTGAGGGCAAGT	235184	67380	AAATACAATAATTAGCCAGG	279771	111967	TTGGCTGTCGTCACCCTGCT
190598	22794	TTTTTCTCCTTGAGGGCAAG	235185	67381	AAAATACAATAATTAGCCAG	279772	111968	GTTGGCTGTCGTCACCCTGC
190599	22795	ATTTTTCTCCTTGAGGGCAA	235186	67382	AAAAATACAATAATTAGCCA	279773	111969	TGTTGGCTGTCGTCACCCTG
190600	22796	TATTTTTCTCCTTGAGGGCA	235187	67383	TAAAAATACAATAATTAGCC	279774	111970	CTGTTGGCTGTCGTCACCCT
190601	22797	TTATTTTTCTCCTTGAGGGC	235188	67384	CTAAAAATACAATAATTAGC	279775	111971	ACTGTTGGCTGTCGTCACCC
190602	22798	TTTATTTTTCTCCTTGAGGG	235189	67385	ACTAAAAATACAATAATTAG	279776	111972	TACTGTTGGCTGTCGTCACC
190603	22799	ATTTATTTTTCTCCTTGAGG	235190	67386	TACTAAAAATACAATAATTA	279777	111973	TTACTGTTGGCTGTCGTCAC
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190605	22801	TGATTTATTTTTCTCCTTGA	235192	67388	TCTACTAAAAATACAATAAT	279779	111975	AATTACTGTTGGCTGTCGTC
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190607	22803	TTTGATTTATTTTTCTCCTT	235194	67390	TCTCTACTAAAAATACAATA	279781	111977	TAAATTACTGTTGGCTGTCG
190608	22804	TTTTGATTTATTTTTCTCCT	235195	67391	ATCTCTACTAAAAATACAAT	279782	111978	ATAAATTACTGTTGGCTGTC
190609	22805	GTTTTGATTTATTTTTCTCC	235196	67392	CATCTCTACTAAAAATACAA	279783	111979	TATAAATTACTGTTGGCTGT
190610	22806	TGTTTTGATTTATTTTTCTC	235197	67393	CCATCTCTACTAAAAATACA	279784	111980	CTATAAATTACTGTTGGCTG
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190613	22809	TTTTGTTTTGATTTATTTTT	235200	67396	ACCCCATCTCTACTAAAAAT	279787	111983	GTACTATAAATTACTGTTGG
190614	22810	CTTTTGTTTTGATTTATTTT	235201	67397	AACCCCATCTCTACTAAAAA	279788	111984	TGTACTATAAATTACTGTTG
190615	22811	GCTTTTGTTTTGATTTATTT	235202	67398	AAACCCCATCTCTACTAAAA	279789	111985	ATGTACTATAAATTACTGTT
190616	22812	TGCTTTTGTTTTGATTTATT	235203	67399	AAAACCCCATCTCTACTAAA	279790	111986	AATGTACTATAAATTACTGT
190617	22813	TTGCTTTTGTTTTGATTTAT	235204	67400	TAAAACCCCATCTCTACTAA	279791	111987	AAATGTACTATAAATTACTG
190618	22814	TTTGCTTTTGTTTTGATTTA	235205	67401	GTAAAACCCCATCTCTACTA	279792	111988	TAAATGTACTATAAATTACT
190619	22815	TTTTGCTTTTGTTTTGATTT	235206	67402	GGTAAAACCCCATCTCTACT	279793	111989	TTAAATGTACTATAAATTAC
190620	22816	TTTTTGCTTTTGTTTTGATT	235207	67403	TGGTAAAACCCCATCTCTAC	279794	111990	TTTAAATGTACTATAAATTA
190621	22817	GTTTTTGCTTTTGTTTTGAT	235208	67404	ATGGTAAAACCCCATCTCTA	279795	111991	TTTTAAATGTACTATAAATT
190622	22818	TGTTTTTGCTTTTGTTTTGA	235209	67405	CATGGTAAAACCCCATCTCT	279796	111992	TTTTTAAATGTACTATAAAT
190623	22819	CTGTTTTTGCTTTTGTTTTG	235210	67406	ACATGGTAAAACCCCATCTC	279797	111993	GTTTTTAAATGTACTATAAA
190624	22820	GCTGTTTTTGCTTTTGTTTT	235211	67407	AACATGGTAAAACCCCATCT	279798	111994	TGTTTTTAAATGTACTATAA
190625	22821	TGCTGTTTTTGCTTTTGTTT	235212	67408	CAACATGGTAAAACCCCATC	279799	111995	TTGTTTTTAAATGTACTATA
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190629	22825	TGTTTGCTGTTTTTGCTTTT	235216	67412	TGGCCAACATGGTAAAACCC	279803	111999	TTAGTTGTTTTTAAATGTAC
190630	22826	ATGTTTGCTGTTTTTGCTTT	235217	67413	CTGGCCAACATGGTAAAACC	279804	112000	TTTAGTTGTTTTTAAATGTA
190631	22827	CATGTTTGCTGTTTTTGCTT	235218	67414	CCTGGCCAACATGGTAAAAC	279805	112001	TTTTAGTTGTTTTTAAATGT
190632	22828	GCATGTTTGCTGTTTTTGCT	235219	67415	GCCTGGCCAACATGGTAAAA	279806	112002	CTTTTAGTTGTTTTTAAATG
190633	22829	TGCATGTTTGCTGTTTTTGC	235220	67416	AGCCTGGCCAACATGGTAAA	279807	112003	TCTTTTAGTTGTTTTTAAAT
190634	22830	ATGCATGTTTGCTGTTTTTG	235221	67417	CAGCCTGGCCAACATGGTAA	279808	112004	CTCTTTTAGTTGTTTTTAAA
190635	22831	GATGCATGTTTGCTGTTTTT	235222	67418	CCAGCCTGGCCAACATGGTA	279809	112005	ACTCTTTTAGTTGTTTTTAA
190636	22832	AGATGCATGTTTGCTGTTTT	235223	67419	ACCAGCCTGGCCAACATGGT	279810	112006	CACTCTTTTAGTTGTTTTTA
190637	22833	GAGATGCATGTTTGCTGTTT	235224	67420	GACCAGCCTGGCCAACATGG	279811	112007	ACACTCTTTTAGTTGTTTTT
190638	22834	AGAGATGCATGTTTGCTGTT	235225	67421	AGACCAGCCTGGCCAACATG	279812	112008	TACACTCTTTTAGTTGTTTT
190639	22835	AAGAGATGCATGTTTGCTGT	235226	67422	GAGACCAGCCTGGCCAACAT	279813	112009	TTACACTCTTTTAGTTGTTT
190640	22836	TAAGAGATGCATGTTTGCTG	235227	67423	CGAGACCAGCCTGGCCAACA	279814	112010	ATTACACTCTTTTAGTTGTT
190641	22837	TTAAGAGATGCATGTTTGCT	235228	67424	TCGAGACCAGCCTGGCCAAC	279815	112011	AATTACACTCTTTTAGTTGT
190642	22838	TTTAAGAGATGCATGTTTGC	235229	67425	ATCGAGACCAGCCTGGCCAA	279816	112012	CAATTACACTCTTTTAGTTG
190643	22839	CTTTAAGAGATGCATGTTTG	235230	67426	GATCGAGACCAGCCTGGCCA	279817	112013	CCAATTACACTCTTTTAGTT
190644	22840	TCTTTAAGAGATGCATGTTT	235231	67427	GGATCGAGACCAGCCTGGCC	279818	112014	TCCAATTACACTCTTTTAGT
190645	22841	TTCTTTAAGAGATGCATGTT	235232	67428	GGGATCGAGACCAGCCTGGC	279819	112015	GTCCAATTACACTCTTTTAG
190646	22842	CTTCTTTAAGAGATGCATGT	235233	67429	GGGGATCGAGACCAGCCTGG	279820	112016	AGTCCAATTACACTCTTTTA
190647	22843	CCTTCTTTAAGAGATGCATG	235234	67430	AGGGGATCGAGACCAGCCTG	279821	112017	CAGTCCAATTACACTCTTTT
190648	22844	GCCTTCTTTAAGAGATGCAT	235235	67431	CAGGGGATCGAGACCAGCCT	279822	112018	CCAGTCCAATTACACTCTTT
190649	22845	AGCCTTCTTTAAGAGATGCA	235236	67432	TCAGGGGATCGAGACCAGCC	279823	112019	GCCAGTCCAATTACACTCTT
190650	22846	GAGCCTTCTTTAAGAGATGC	235237	67433	GTCAGGGGATCGAGACCAGC	279824	112020	AGCCAGTCCAATTACACTCT
190651	22847	AGAGCCTTCTTTAAGAGATG	235238	67434	GGTCAGGGGATCGAGACCAG	279825	112021	TAGCCAGTCCAATTACACTC
190652	22848	CAGAGCCTTCTTTAAGAGAT	235239	67435	AGGTCAGGGGATCGAGACCA	279826	112022	TTAGCCAGTCCAATTACACT
190653	22849	TCAGAGCCTTCTTTAAGAGA	235240	67436	GAGGTCAGGGGATCGAGACC	279827	112023	GTTAGCCAGTCCAATTACAC
190654	22850	CTCAGAGCCTTCTTTAAGAG	235241	67437	TGAGGTCAGGGGATCGAGAC	279828	112024	TGTTAGCCAGTCCAATTACA
190655	22851	ACTCAGAGCCTTCTTTAAGA	235242	67438	CTGAGGTCAGGGGATCGAGA	279829	112025	ATGTTAGCCAGTCCAATTAC
190656	22852	GACTCAGAGCCTTCTTTAAG	235243	67439	CCTGAGGTCAGGGGATCGAG	279830	112026	CATGTTAGCCAGTCCAATTA
190657	22853	GGACTCAGAGCCTTCTTTAA	235244	67440	ACCTGAGGTCAGGGGATCGA	279831	112027	CCATGTTAGCCAGTCCAATT
190658	22854	TGGACTCAGAGCCTTCTTTA	235245	67441	CACCTGAGGTCAGGGGATCG	279832	112028	ACCATGTTAGCCAGTCCAAT
190659	22855	CTGGACTCAGAGCCTTCTTT	235246	67442	TCACCTGAGGTCAGGGGATC	279833	112029	CACCATGTTAGCCAGTCCAA
190660	22856	CCTGGACTCAGAGCCTTCTT	235247	67443	ATCACCTGAGGTCAGGGGAT	279834	112030	TCACCATGTTAGCCAGTCCA
190661	22857	ACCTGGACTCAGAGCCTTCT	235248	67444	GATCACCTGAGGTCAGGGGA	279835	112031	TTCACCATGTTAGCCAGTCC
190662	22858	TACCTGGACTCAGAGCCTTC	235249	67445	GGATCACCTGAGGTCAGGGG	279836	112032	TTTCACCATGTTAGCCAGTC
190663	22859	TTACCTGGACTCAGAGCCTT	235250	67446	TGGATCACCTGAGGTCAGGG	279837	112033	GTTTCACCATGTTAGCCAGT
190664	22860	TTTACCTGGACTCAGAGCCT	235251	67447	GTGGATCACCTGAGGTCAGG	279838	112034	GGTTTCACCATGTTAGCCAG
190665	22861	ATTTACCTGGACTCAGAGCC	235252	67448	GGTGGATCACCTGAGGTCAG	279839	112035	GGGTTTCACCATGTTAGCCA
190666	22862	AATTTACCTGGACTCAGAGC	235253	67449	GGGTGGATCACCTGAGGTCA	279840	112036	GGGGTTTCACCATGTTAGCC
190667	22863	AAATTTACCTGGACTCAGAG	235254	67450	TGGGTGGATCACCTGAGGTC	279841	112037	CGGGGTTTCACCATGTTAGC
190668	22864	GAAATTTACCTGGACTCAGA	235255	67451	GTGGGTGGATCACCTGAGGT	279842	112038	ACGGGGTTTCACCATGTTAG
190669	22865	GGAAATTTACCTGGACTCAG	235256	67452	GGTGGGTGGATCACCTGAGG	279843	112039	GACGGGGTTTCACCATGTTA
190670	22866	AGGAAATTTACCTGGACTCA	235257	67453	AGGTGGGTGGATCACCTGAG	279844	112040	AGACGGGGTTTCACCATGTT
190671	22867	AAGGAAATTTACCTGGACTC	235258	67454	GAGGTGGGTGGATCACCTGA	279845	112041	GAGACGGGGTTTCACCATGT
190672	22868	GAAGGAAATTTACCTGGACT	235259	67455	CGAGGTGGGTGGATCACCTG	279846	112042	AGAGACGGGGTTTCACCATG
190673	22869	GGAAGGAAATTTACCTGGAC	235260	67456	CCGAGGTGGGTGGATCACCT	279847	112043	TAGAGACGGGGTTTCACCAT
190674	22870	TGGAAGGAAATTTACCTGGA	235261	67457	GCCGAGGTGGGTGGATCACC	279848	112044	GTAGAGACGGGGTTTCACCA
190675	22871	GTGGAAGGAAATTTACCTGG	235262	67458	GGCCGAGGTGGGTGGATCAC	279849	112045	AGTAGAGACGGGGTTTCACC
190676	22872	AGTGGAAGGAAATTTACCTG	235263	67459	AGGCCGAGGTGGGTGGATCA	279850	112046	TAGTAGAGACGGGGTTTCAC
190677	22873	CAGTGGAAGGAAATTTACCT	235264	67460	GAGGCCGAGGTGGGTGGATC	279851	112047	TTAGTAGAGACGGGGTTTCA
190678	22874	TCAGTGGAAGGAAATTTACC	235265	67461	GGAGGCCGAGGTGGGTGGAT	279852	112048	TTTAGTAGAGACGGGGTTTC
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190681	22877	GCTTCAGTGGAAGGAAATTT	235268	67464	TTGGGAGGCCGAGGTGGGTG	279855	112051	ATTTTTAGTAGAGACGGGGT
190682	22878	TGCTTCAGTGGAAGGAAATT	235269	67465	TTTGGGAGGCCGAGGTGGGT	279856	112052	TATTTTTAGTAGAGACGGGG
190683	22879	CTGCTTCAGTGGAAGGAAAT	235270	67466	CTTTGGGAGGCCGAGGTGGG	279857	112053	GTATTTTTAGTAGAGACGGG
190684	22880	GCTGCTTCAGTGGAAGGAAA	235271	67467	ACTTTGGGAGGCCGAGGTGG	279858	112054	TGTATTTTTAGTAGAGACGG
190685	22881	GGCTGCTTCAGTGGAAGGAA	235272	67468	CACTTTGGGAGGCCGAGGTG	279859	112055	TTGTATTTTTAGTAGAGACG
190686	22882	TGGCTGCTTCAGTGGAAGGA	235273	67469	GCACTTTGGGAGGCCGAGGT	279860	112056	TTTGTATTTTTAGTAGAGAC
190687	22883	CTGGCTGCTTCAGTGGAAGG	235274	67470	AGCACTTTGGGAGGCCGAGG	279861	112057	TTTTGTATTTTTAGTAGAGA
190688	22884	CCTGGCTGCTTCAGTGGAAG	235275	67471	CAGCACTTTGGGAGGCCGAG	279862	112058	TTTTTGTATTTTTAGTAGAG
190689	22885	GCCTGGCTGCTTCAGTGGAA	235276	67472	TCAGCACTTTGGGAGGCCGA	279863	112059	ATTTTTGTATTTTTAGTAGA
190690	22886	AGCCTGGCTGCTTCAGTGGA	235277	67473	CTCAGCACTTTGGGAGGCCG	279864	112060	AATTTTTGTATTTTTAGTAG
190691	22887	CAGCCTGGCTGCTTCAGTGG	235278	67474	TCTCAGCACTTTGGGAGGCC	279865	112061	TAATTTTTGTATTTTTAGTA
190692	22888	TCAGCCTGGCTGCTTCAGTG	235279	67475	ATCTCAGCACTTTGGGAGGC	279866	112062	CTAATTTTTGTATTTTTAGT
190693	22889	TTCAGCCTGGCTGCTTCAGT	235280	67476	GATCTCAGCACTTTGGGAGG	279867	112063	GCTAATTTTTGTATTTTTAG
190694	22890	ATTCAGCCTGGCTGCTTCAG	235281	67477	TGATCTCAGCACTTTGGGAG	279868	112064	AGCTAATTTTTGTATTTTTA
190695	22891	AATTCAGCCTGGCTGCTTCA	235282	67478	GTGATCTCAGCACTTTGGGA	279869	112065	CAGCTAATTTTTGTATTTTT
190696	22892	GAATTCAGCCTGGCTGCTTC	235283	67479	TGTGATCTCAGCACTTTGGG	279870	112066	CCAGCTAATTTTTGTATTTT
190697	22893	CGAATTCAGCCTGGCTGCTT	235284	67480	CTGTGATCTCAGCACTTTGG	279871	112067	CCCAGCTAATTTTTGTATTT
190698	22894	TCGAATTCAGCCTGGCTGCT	235285	67481	CCTGTGATCTCAGCACTTTG	279872	112068	GCCCAGCTAATTTTTGTATT

190699	22895	TTCGAATTCAGCCTGGCTGC	235286	67482	GCCTGTGATCTCAGCACTTT	279873	112069	TGCCCAGCTAATTTTTGTAT
190700	22896	ATTCGAATTCAGCCTGGCTG	235287	67483	CGCCTGTGATCTCAGCACTT	279874	112070	ATGCCCAGCTAATTTTTGTA
190701	22897	AATTCGAATTCAGCCTGGCT	235288	67484	ACGCCTGTGATCTCAGCACT	279875	112071	CATGCCCAGCTAATTTTTGT
190702	22898	TAATTCGAATTCAGCCTGGC	235289	67485	CACGCCTGTGATCTCAGCAC	279876	112072	CCATGCCCAGCTAATTTTTG
190703	22899	ATAATTCGAATTCAGCCTGG	235290	67486	TCACGCCTGTGATCTCAGCA	279877	112073	ACCATGCCCAGCTAATTTTT
190704	22900	GATAATTCGAATTCAGCCTG	235291	67487	CTCACGCCTGTGATCTCAGC	279878	112074	CACCATGCCCAGCTAATTTT
190705	22901	AGATAATTCGAATTCAGCCT	235292	67488	GCTCACGCCTGTGATCTCAG	279879	112075	CCACCATGCCCAGCTAATTT
190706	22902	AAGATAATTCGAATTCAGCC	235293	67489	GGCTCACGCCTGTGATCTCA	279880	112076	GCCACCATGCCCAGCTAATT
190707	22903	AAAGATAATTCGAATTCAGC	235294	67490	TGGCTCACGCCTGTGATCTC	279881	112077	AGCCACCATGCCCAGCTAAT
190708	22904	CAAAGATAATTCGAATTCAG	235295	67491	GTGGCTCACGCCTGTGATCT	279882	112078	GAGCCACCATGCCCAGCTAA
190709	22905	GCAAAGATAATTCGAATTCA	235296	67492	GGTGGCTCACGCCTGTGATC	279883	112079	TGAGCCACCATGCCCAGCTA
190710	22906	GGCAAAGATAATTCGAATTC	235297	67493	TGGTGGCTCACGCCTGTGAT	279884	112080	GTGAGCCACCATGCCCAGCT
190711	22907	GGGCAAAGATAATTCGAATT	235298	67494	ATGGTGGCTCACGCCTGTGA	279885	112081	CGTGAGCCACCATGCCCAGC
190712	22908	GGGGCAAAGATAATTCGAAT	235299	67495	CATGGTGGCTCACGCCTGTG	279886	112082	GCGTGAGCCACCATGCCCAG
190713	22909	AGGGGCAAAGATAATTCGAA	235300	67496	GCATGGTGGCTCACGCCTGT	279887	112083	GGCGTGAGCCACCATGCCCA
190714	22910	CAGGGGCAAAGATAATTCGA	235301	67497	GGCATGGTGGCTCACGCCTG	279888	112084	AGGCGTGAGCCACCATGCCC
190715	22911	GCAGGGGCAAAGATAATTCG	235302	67498	AGGCATGGTGGCTCACGCCT	279889	112085	CAGGCGTGAGCCACCATGCC
190716	22912	AGCAGGGGCAAAGATAATTC	235303	67499	CAGGCATGGTGGCTCACGCC	279890	112086	ACAGGCGTGAGCCACCATGC
190717	22913	AAGCAGGGGCAAAGATAATT	235304	67500	CCAGGCATGGTGGCTCACGC	279891	112087	TACAGGCGTGAGCCACCATG
190718	22914	TAAGCAGGGGCAAAGATAAT	235305	67501	GCCAGGCATGGTGGCTCACG	279892	112088	TTACAGGCGTGAGCCACCAT
190719	22915	TTAAGCAGGGGCAAAGATAA	235306	67502	GGCCAGGCATGGTGGCTCAC	279893	112089	ATTACAGGCGTGAGCCACCA
190720	22916	TTTAAGCAGGGGCAAAGATA	235307	67503	CGGCCAGGCATGGTGGCTCA	279894	112090	GATTACAGGCGTGAGCCACC
190721	22917	TTTTAAGCAGGGGCAAAGAT	235308	67504	ACGGCCAGGCATGGTGGCTC	279895	112091	GGATTACAGGCGTGAGCCAC
190722	22918	TTTTTAAGCAGGGGCAAAGA	235309	67505	GACGGCCAGGCATGGTGGCT	279896	112092	GGGATTACAGGCGTGAGCCA
190723	22919	GTTTTTAAGCAGGGGCAAAG	235310	67506	TGACGGCCAGGCATGGTGGC	279897	112093	TGGGATTACAGGCGTGAGCC
190724	22920	AGTTTTTAAGCAGGGGCAAA	235311	67507	GTGACGGCCAGGCATGGTGG	279898	112094	CTGGGATTACAGGCGTGAGC
190725	22921	TAGTTTTTAAGCAGGGGCAA	235312	67508	GGTGACGGCCAGGCATGGTG	279899	112095	GCTGGGATTACAGGCGTGAG
190726	22922	TTAGTTTTTAAGCAGGGGCA	235313	67509	AGGTGACGGCCAGGCATGGT	279900	112096	TGCTGGGATTACAGGCGTGA
190727	22923	ATTAGTTTTTAAGCAGGGGC	235314	67510	CAGGTGACGGCCAGGCATGG	279901	112097	GTGCTGGGATTACAGGCGTG
190728	22924	CATTAGTTTTTAAGCAGGGG	235315	67511	CCAGGTGACGGCCAGGCATG	279902	112098	AGTGCTGGGATTACAGGCGT
190729	22925	GCATTAGTTTTTAAGCAGGG	235316	67512	ACCAGGTGACGGCCAGGCAT	279903	112099	AAGTGCTGGGATTACAGGCG
190730	22926	TGCATTAGTTTTTAAGCAGG	235317	67513	CACCAGGTGACGGCCAGGCA	279904	112100	AAAGTGCTGGGATTACAGGC
190731	22927	TTGCATTAGTTTTTAAGCAG	235318	67514	CCACCAGGTGACGGCCAGGC	279905	112101	CAAAGTGCTGGGATTACAGG
190732	22928	TTTGCATTAGTTTTTAAGCA	235319	67515	ACCACCAGGTGACGGCCAGG	279906	112102	CCAAAGTGCTGGGATTACAG
190733	22929	ATTTGCATTAGTTTTTAAGC	235320	67516	CACCACCAGGTGACGGCCAG	279907	112103	CCCAAAGTGCTGGGATTACA
190734	22930	AATTTGCATTAGTTTTTAAG	235321	67517	ACACCACCAGGTGACGGCCA	279908	112104	TCCCAAAGTGCTGGGATTAC
190735	22931	AAATTTGCATTAGTTTTTAA	235322	67518	AACACCACCAGGTGACGGCC	279909	112105	CTCCCAAAGTGCTGGGATTA
190736	22932	AAAATTTGCATTAGTTTTTA	235323	67519	CAACACCACCAGGTGACGGC	279910	112106	CCTCCCAAAGTGCTGGGATT
190737	22933	GAAAATTTGCATTAGTTTTT	235324	67520	TCAACACCACCAGGTGACGG	279911	112107	GCCTCCCAAAGTGCTGGGAT
190738	22934	GGAAAATTTGCATTAGTTTT	235325	67521	TTCAACACCACCAGGTGACG	279912	112108	GGCCTCCCAAAGTGCTGGGA
190739	22935	AGGAAAATTTGCATTAGTTT	235326	67522	ATTCAACACCACCAGGTGAC	279913	112109	CGGCCTCCCAAAGTGCTGGG
190740	22936	TAGGAAAATTTGCATTAGTT	235327	67523	TATTCAACACCACCAGGTGA	279914	112110	TCGGCCTCCCAAAGTGCTGG
190741	22937	CTAGGAAAATTTGCATTAGT	235328	67524	ATATTCAACACCACCAGGTG	279915	112111	CTCGGCCTCCCAAAGTGCTG
190742	22938	TCTAGGAAAATTTGCATTAG	235329	67525	CATATTCAACACCACCAGGT	279916	112112	CCTCGGCCTCCCAAAGTGCT
190743	22939	CTCTAGGAAAATTTGCATTA	235330	67526	TCATATTCAACACCACCAGG	279917	112113	GCCTCGGCCTCCCAAAGTGC
190744	22940	TCTCTAGGAAAATTTGCATT	235331	67527	TTCATATTCAACACCACCAG	279918	112114	CGCCTCGGCCTCCCAAAGTG
190745	22941	TTCTCTAGGAAAATTTGCAT	235332	67528	GTTCATATTCAACACCACCA	279919	112115	CCGCCTCGGCCTCCCAAAGT
190746	22942	ATTCTCTAGGAAAATTTGCA	235333	67529	AGTTCATATTCAACACCACC	279920	112116	CCCGCCTCGGCCTCCCAAAG
190747	22943	TATTCTCTAGGAAAATTTGC	235334	67530	CAGTTCATATTCAACACCAC	279921	112117	GCCCGCCTCGGCCTCCCAAA
190748	22944	ATATTCTCTAGGAAAATTTG	235335	67531	GCAGTTCATATTCAACACCA	279922	112118	GGCCCGCCTCGGCCTCCCAA
190749	22945	GATATTCTCTAGGAAAATTT	235336	67532	AGCAGTTCATATTCAACACC	279923	112119	CGGCCCGCCTCGGCCTCCCA
190750	22946	GGATATTCTCTAGGAAAATT	235337	67533	CAGCAGTTCATATTCAACAC	279924	112120	TCGGCCCGCCTCGGCCTCCC
190751	22947	TGGATATTCTCTAGGAAAAT	235338	67534	GCAGCAGTTCATATTCAACA	279925	112121	ATCGGCCCGCCTCGGCCTCC
190752	22948	GTGGATATTCTCTAGGAAAA	235339	67535	CGCAGCAGTTCATATTCAAC	279926	112122	GATCGGCCCGCCTCGGCCTC
190753	22949	AGTGGATATTCTCTAGGAAA	235340	67536	CCGCAGCAGTTCATATTCAA	279927	112123	TGATCGGCCCGCCTCGGCCT
190754	22950	TAGTGGATATTCTCTAGGAA	235341	67537	ACCGCAGCAGTTCATATTCA	279928	112124	GTGATCGGCCCGCCTCGGCC
190755	22951	TTAGTGGATATTCTCTAGGA	235342	67538	CACCGCAGCAGTTCATATTC	279929	112125	CGTGATCGGCCCGCCTCGGC
190756	22952	ATTAGTGGATATTCTCTAGG	235343	67539	ACACCGCAGCAGTTCATATT	279930	112126	TCGTGATCGGCCCGCCTCGG
190757	22953	AATTAGTGGATATTCTCTAG	235344	67540	AACACCGCAGCAGTTCATAT	279931	112127	CTCGTGATCGGCCCGCCTCG
190758	22954	GAATTAGTGGATATTCTCTA	235345	67541	CAACACCGCAGCAGTTCATA	279932	112128	CCTCGTGATCGGCCCGCCTC
190759	22955	GGAATTAGTGGATATTCTCT	235346	67542	CCAACACCGCAGCAGTTCAT	279933	112129	ACCTCGTGATCGGCCCGCCT
190760	22956	AGGAATTAGTGGATATTCTC	235347	67543	ACCAACACCGCAGCAGTTCA	279934	112130	GACCTCGTGATCGGCCCGCC
190761	22957	CAGGAATTAGTGGATATTCT	235348	67544	TACCAACACCGCAGCAGTTC	279935	112131	TGACCTCGTGATCGGCCCGC
190762	22958	CCAGGAATTAGTGGATATTC	235349	67545	TTACCAACACCGCAGCAGTT	279936	112132	CTGACCTCGTGATCGGCCCG
190763	22959	TCCAGGAATTAGTGGATATT	235350	67546	TTTACCAACACCGCAGCAGT	279937	112133	CCTGACCTCGTGATCGGCCC
190764	22960	CTCCAGGAATTAGTGGATAT	235351	67547	ATTTACCAACACCGCAGCAG	279938	112134	TCCTGACCTCGTGATCGGCC
190765	22961	CCTCCAGGAATTAGTGGATA	235352	67548	AATTTACCAACACCGCAGCA	279939	112135	CTCCTGACCTCGTGATCGGC
190766	22962	CCCTCCAGGAATTAGTGGAT	235353	67549	TAATTTACCAACACCGCAGC	279940	112136	TCTCCTGACCTCGTGATCGG
190767	22963	CCCCTCCAGGAATTAGTGGA	235354	67550	TTAATTTACCAACACCGCAG	279941	112137	ATCTCCTGACCTCGTGATCG
190768	22964	CCCCCTCCAGGAATTAGTGG	235355	67551	CTTAATTTACCAACACCGCA	279942	112138	GATCTCCTGACCTCGTGATC
190769	22965	GCCCCCTCCAGGAATTAGTG	235356	67552	GCTTAATTTACCAACACCGC	279943	112139	CGATCTCCTGACCTCGTGAT
190770	22966	TGCCCCCTCCAGGAATTAGT	235357	67553	TGCTTAATTTACCAACACCG	279944	112140	TCGATCTCCTGACCTCGTGA

190771	22967	ATGCCCCCTCCAGGAATTAG	235358	67554	TTGCTTAATTTACCAACACC	279945	112141	CTCGATCTCCTGACCTCGTG
190772	22968	CATGCCCCCTCCAGGAATTA	235359	67555	CTTGCTTAATTTACCAACAC	279946	112142	TCTCGATCTCCTGACCTCGT
190773	22969	CCATGCCCCCTCCAGGAATT	235360	67556	GCTTGCTTAATTTACCAACA	279947	112143	GTCTCGATCTCCTGACCTCG
190774	22970	CCCATGCCCCCTCCAGGAAT	235361	67557	TGCTTGCTTAATTTACCAAC	279948	112144	GGTCTCGATCTCCTGACCTC
190775	22971	GCCCATGCCCCCTCCAGGAA	235362	67558	CTGCTTGCTTAATTTACCAA	279949	112145	TGGTCTCGATCTCCTGACCT
190776	22972	TGCCCATGCCCCCTCCAGGA	235363	67559	TCTGCTTGCTTAATTTACCA	279950	112146	ATGGTCTCGATCTCCTGACC
190777	22973	ATGCCCATGCCCCCTCCAGG	235364	67560	ATCTGCTTGCTTAATTTACC	279951	112147	GATGGTCTCGATCTCCTGAC
190778	22974	AATGCCCATGCCCCCTCCAG	235365	67561	TATCTGCTTGCTTAATTTAC	279952	112148	GGATGGTCTCGATCTCCTGA
190779	22975	GAATGCCCATGCCCCCTCCA	235366	67562	CTATCTGCTTGCTTAATTTA	279953	112149	AGGATGGTCTCGATCTCCTG
190780	22976	GGAATGCCCATGCCCCCTCC	235367	67563	TCTATCTGCTTGCTTAATTT	279954	112150	TAGGATGGTCTCGATCTCCT
190781	22977	AGGAATGCCCATGCCCCCTC	235368	67564	ATCTATCTGCTTGCTTAATT	279955	112151	CTAGGATGGTCTCGATCTCC
190782	22978	CAGGAATGCCCATGCCCCCT	235369	67565	CATCTATCTGCTTGCTTAAT	279956	112152	GCTAGGATGGTCTCGATCTC
190783	22979	TCAGGAATGCCCATGCCCCC	235370	67566	ACATCTATCTGCTTGCTTAA	279957	112153	AGCTAGGATGGTCTCGATCT
190784	22980	ATCAGGAATGCCCATGCCCC	235371	67567	TACATCTATCTGCTTGCTTA	279958	112154	TAGCTAGGATGGTCTCGATC
190785	22981	CATCAGGAATGCCCATGCCC	235372	67568	TTACATCTATCTGCTTGCTT	279959	112155	TTAGCTAGGATGGTCTCGAT
190786	22982	GCATCAGGAATGCCCATGCC	235373	67569	TTTACATCTATCTGCTTGCT	279960	112156	GTTAGCTAGGATGGTCTCGA
190787	22983	GGCATCAGGAATGCCCATGC	235374	67570	ATTTACATCTATCTGCTTGC	279961	112157	TGTTAGCTAGGATGGTCTCG
190788	22984	GGGCATCAGGAATGCCCATG	235375	67571	TATTTACATCTATCTGCTTG	279962	112158	ATGTTAGCTAGGATGGTCTC
190789	22985	TGGGCATCAGGAATGCCCAT	235376	67572	TTATTTACATCTATCTGCTT	279963	112159	CATGTTAGCTAGGATGGTCT
190790	22986	ATGGGCATCAGGAATGCCCA	235377	67573	GTTATTTACATCTATCTGCT	279964	112160	CCATGTTAGCTAGGATGGTC
190791	22987	CATGGGCATCAGGAATGCCC	235378	67574	CGTTATTTACATCTATCTGC	279965	112161	ACCATGTTAGCTAGGATGGT
190792	22988	TCATGGGCATCAGGAATGCC	235379	67575	GCGTTATTTACATCTATCTG	279966	112162	CACCATGTTAGCTAGGATGG
190793	22989	CTCATGGGCATCAGGAATGC	235380	67576	AGCGTTATTTACATCTATCT	279967	112163	TCACCATGTTAGCTAGGATG
190794	22990	TCTCATGGGCATCAGGAATG	235381	67577	AAGCGTTATTTACATCTATC	279968	112164	TTCACCATGTTAGCTAGGAT
190795	22991	CTCTCATGGGCATCAGGAAT	235382	67578	CAAGCGTTATTTACATCTAT	279969	112165	TTTCACCATGTTAGCTAGGA
190796	22992	CCTCTCATGGGCATCAGGAA	235383	67579	CCAAGCGTTATTTACATCTA	279970	112166	GTTTCACCATGTTAGCTAGG
190797	22993	TCCTCTCATGGGCATCAGGA	235384	67580	CCCAAGCGTTATTTACATCT	279971	112167	GGTTTCACCATGTTAGCTAG
190798	22994	GTCCTCTCATGGGCATCAGG	235385	67581	GCCCAAGCGTTATTTACATC	279972	112168	GGGTTTCACCATGTTAGCTA
190799	22995	GGTCCTCTCATGGGCATCAG	235386	67582	TGCCCAAGCGTTATTTACAT	279973	112169	GGGGTTTCACCATGTTAGCT
190800	22996	TGGTCCTCTCATGGGCATCA	235387	67583	CTGCCCAAGCGTTATTTACA	279974	112170	CGGGGTTTCACCATGTTAGC
190801	22997	ATGGTCCTCTCATGGGCATC	235388	67584	CCTGCCCAAGCGTTATTTAC	279975	112171	ACGGGGTTTCACCATGTTAG
190802	22998	AATGGTCCTCTCATGGGCAT	235389	67585	TCCTGCCCAAGCGTTATTTA	279976	112172	GACGGGGTTTCACCATGTTA
190803	22999	AAATGGTCCTCTCATGGGCA	235390	67586	TTCCTGCCCAAGCGTTATTT	279977	112173	AGACGGGGTTTCACCATGTT
190804	23000	CAAATGGTCCTCTCATGGGC	235391	67587	ATTCCTGCCCAAGCGTTATT	279978	112174	GAGACGGGGTTTCACCATGT
190805	23001	GCAAATGGTCCTCTCATGGG	235392	67588	TATTCCTGCCCAAGCGTTAT	279979	112175	AGAGACGGGGTTTCACCATG
190806	23002	AGCAAATGGTCCTCTCATGG	235393	67589	ATATTCCTGCCCAAGCGTTA	279980	112176	TAGAGACGGGGTTTCACCAT
190807	23003	GAGCAAATGGTCCTCTCATG	235394	67590	CATATTCCTGCCCAAGCGTT	279981	112177	GTAGAGACGGGGTTTCACCA
190808	23004	AGAGCAAATGGTCCTCTCAT	235395	67591	CCATATTCCTGCCCAAGCGT	279982	112178	AGTAGAGACGGGGTTTCACC
190809	23005	AAGAGCAAATGGTCCTCTCA	235396	67592	TCCATATTCCTGCCCAAGCG	279983	112179	TAGTAGAGACGGGGTTTCAC
190810	23006	GAAGAGCAAATGGTCCTCTC	235397	67593	CTCCATATTCCTGCCCAAGC	279984	112180	GTAGTAGAGACGGGGTTTCA
190811	23007	GGAAGAGCAAATGGTCCTCT	235398	67594	GCTCCATATTCCTGCCCAAG	279985	112181	TGTAGTAGAGACGGGGTTTC
190812	23008	GGGAAGAGCAAATGGTCCTC	235399	67595	TGCTCCATATTCCTGCCCAA	279986	112182	TTGTAGTAGAGACGGGGTTT
190813	23009	AGGGAAGAGCAAATGGTCCT	235400	67596	GTGCTCCATATTCCTGCCCA	279987	112183	TTTGTAGTAGAGACGGGGTT
190814	23010	GAGGGAAGAGCAAATGGTCC	235401	67597	CGTGCTCCATATTCCTGCCC	279988	112184	ATTTGTAGTAGAGACGGGGT
190815	23011	TGAGGGAAGAGCAAATGGTC	235402	67598	CCGTGCTCCATATTCCTGCC	279989	112185	TATTTGTAGTAGAGACGGGG
190816	23012	CTGAGGGAAGAGCAAATGGT	235403	67599	CCCGTGCTCCATATTCCTGC	279990	112186	GTATTTGTAGTAGAGACGGG
190817	23013	ACTGAGGGAAGAGCAAATGG	235404	67600	TCCCGTGCTCCATATTCCTG	279991	112187	TGTATTTGTAGTAGAGACGG
190818	23014	TACTGAGGGAAGAGCAAATG	235405	67601	ATCCCGTGCTCCATATTCCT	279992	112188	TTGTATTTGTAGTAGAGACG
190819	23015	ATACTGAGGGAAGAGCAAAT	235406	67602	CATCCCGTGCTCCATATTCC	279993	112189	TTTGTATTTGTAGTAGAGAC
190820	23016	CATACTGAGGGAAGAGCAAA	235407	67603	TCATCCCGTGCTCCATATTC	279994	112190	TTTTGTATTTGTAGTAGAGA
190821	23017	GCATACTGAGGGAAGAGCAA	235408	67604	CTCATCCCGTGCTCCATATT	279995	112191	TTTTTGTATTTGTAGTAGAG
190822	23018	AGCATACTGAGGGAAGAGCA	235409	67605	CCTCATCCCGTGCTCCATAT	279996	112192	TTTTTTGTATTTGTAGTAGA
190823	23019	TAGCATACTGAGGGAAGAGC	235410	67606	TCCTCATCCCGTGCTCCATA	279997	112193	TTTTTTTGTATTTGTAGTAG
190824	23020	TTAGCATACTGAGGGAAGAG	235411	67607	ATCCTCATCCCGTGCTCCAT	279998	112194	TTTTTTTTGTATTTGTAGTA
190825	23021	TTTAGCATACTGAGGGAAGA	235412	67608	CATCCTCATCCCGTGCTCCA	279999	112195	CTTTTTTTTGTATTTGTAGT
190826	23022	ATTTAGCATACTGAGGGAAG	235413	67609	CCATCCTCATCCCGTGCTCC	280000	112196	TCTTTTTTTTGTATTTGTAG
190827	23023	TATTTAGCATACTGAGGGAA	235414	67610	CCCATCCTCATCCCGTGCTC	280001	112197	TTCTTTTTTTTGTATTTGTA
190828	23024	TTATTTAGCATACTGAGGGA	235415	67611	GCCCATCCTCATCCCGTGCT	280002	112198	TTTCTTTTTTTTGTATTTGT
190829	23025	GTTATTTAGCATACTGAGGG	235416	67612	CGCCCATCCTCATCCCGTGC	280003	112199	TTTTCTTTTTTTTGTATTTG
190830	23026	TGTTATTTAGCATACTGAGG	235417	67613	CCGCCCATCCTCATCCCGTG	280004	112200	TTTTTCTTTTTTTTGTATTT
190831	23027	CTGTTATTTAGCATACTGAG	235418	67614	GCCGCCCATCCTCATCCCGT	280005	112201	TTTTTCTTTTTTTTGTATT
190832	23028	TCTGTTATTTAGCATACTGA	235419	67615	GGCCGCCCATCCTCATCCCG	280006	112202	ATTTTTTCTTTTTTTTGTAT
190833	23029	TTCTGTTATTTAGCATACTG	235420	67616	TGGCCGCCCATCCTCATCCC	280007	112203	AATTTTTTCTTTTTTTTGTA
190834	23030	CTTCTGTTATTTAGCATACT	235421	67617	TTGGCCGCCCATCCTCATCC	280008	112204	TAATTTTTTCTTTTTTTTGT
190835	23031	GCTTCTGTTATTTAGCATAC	235422	67618	GTTGGCCGCCCATCCTCATC	280009	112205	CTAATTTTTTCTTTTTTTTG
190836	23032	CGCTTCTGTTATTTAGCATA	235423	67619	AGTTGGCCGCCCATCCTCAT	280010	112206	GCTAATTTTTTCTTTTTTTT
190837	23033	TCGCTTCTGTTATTTAGCAT	235424	67620	CAGTTGGCCGCCCATCCTCA	280011	112207	GGCTAATTTTTTCTTTTTTT
190838	23034	GTCGCTTCTGTTATTTAGCA	235425	67621	ACAGTTGGCCGCCCATCCTC	280012	112208	CGGCTAATTTTTTCTTTTTT
190839	23035	TGTCGCTTCTGTTATTTAGC	235426	67622	AACAGTTGGCCGCCCATCCT	280013	112209	CCGGCTAATTTTTTCTTTTT
190840	23036	ATGTCGCTTCTGTTATTTAG	235427	67623	TAACAGTTGGCCGCCCATCC	280014	112210	CCCGGCTAATTTTTTCTTTT
190841	23037	AATGTCGCTTCTGTTATTTA	235428	67624	CTAACAGTTGGCCGCCCATC	280015	112211	GCCCGGCTAATTTTTTCTTT
190842	23038	AAATGTCGCTTCTGTTATTT	235429	67625	TCTAACAGTTGGCCGCCCAT	280016	112212	TGCCCGGCTAATTTTTTCTT

190843	23039	CAAATGTCGCTTCTGTTATT	235430	67626	CTCTAACAGTTGGCCGCCCA	280017	112213	ATGCCCGGCTAATTTTTTCT
190844	23040	ACAAATGTCGCTTCTGTTAT	235431	67627	TCTCTAACAGTTGGCCGCCC	280018	112214	CATGCCCGGCTAATTTTTTC
190845	23041	AACAAATGTCGCTTCTGTTA	235432	67628	CTCTCTAACAGTTGGCCGCC	280019	112215	CCATGCCCGGCTAATTTTTT
190846	23042	CAACAAATGTCGCTTCTGTT	235433	67629	CCTCTCTAACAGTTGGCCGC	280020	112216	ACCATGCCCGGCTAATTTTT
190847	23043	GCAACAAATGTCGCTTCTGT	235434	67630	CCCTCTCTAACAGTTGGCCG	280021	112217	CACCATGCCCGGCTAATTTT
190848	23044	AGCAACAAATGTCGCTTCTG	235435	67631	ACCCTCTCTAACAGTTGGCC	280022	112218	CCACCATGCCCGGCTAATTT
190849	23045	CAGCAACAAATGTCGCTTCT	235436	67632	TACCCTCTCTAACAGTTGGC	280023	112219	ACCACCATGCCCGGCTAATT
190850	23046	CCAGCAACAAATGTCGCTTC	235437	67633	CTACCCTCTCTAACAGTTGG	280024	112220	CACCACCATGCCCGGCTAAT
190851	23047	TCCAGCAACAAATGTCGCTT	235438	67634	GCTACCCTCTCTAACAGTTG	280025	112221	CCACCACCATGCCCGGCTAA
190852	23048	TTCCAGCAACAAATGTCGCT	235439	67635	TGCTACCCTCTCTAACAGTT	280026	112222	CCCACCACCATGCCCGGCTA
190853	23049	TTTCCAGCAACAAATGTCGC	235440	67636	CTGCTACCCTCTCTAACAGT	280027	112223	GCCCACCACCATGCCCGGCT
190854	23050	CTTTCCAGCAACAAATGTCG	235441	67637	CCTGCTACCCTCTCTAACAG	280028	112224	CGCCCACCACCATGCCCGGC
190855	23051	ACTTTCCAGCAACAAATGTC	235442	67638	CCCTGCTACCCTCTCTAACA	280029	112225	GCGCCCACCACCATGCCCGG
190856	23052	TACTTTCCAGCAACAAATGT	235443	67639	TCCCTGCTACCCTCTCTAAC	280030	112226	GGCGCCCACCACCATGCCCG
190857	23053	ATACTTTCCAGCAACAAATG	235444	67640	CTCCCTGCTACCCTCTCTAA	280031	112227	AGGCGCCCACCACCATGCCC
190858	23054	GATACTTTCCAGCAACAAAT	235445	67641	CCTCCCTGCTACCCTCTCTA	280032	112228	CAGGCGCCCACCACCATGCC
190859	23055	TGATACTTTCCAGCAACAAA	235446	67642	GCCTCCCTGCTACCCTCTCT	280033	112229	ACAGGCGCCCACCACCATGC
190860	23056	CTGATACTTTCCAGCAACAA	235447	67643	AGCCTCCCTGCTACCCTCTC	280034	112230	TACAGGCGCCCACCACCATG
190861	23057	ACTGATACTTTCCAGCAACA	235448	67644	CAGCCTCCCTGCTACCCTCT	280035	112231	CTACAGGCGCCCACCACCAT
190862	23058	CACTGATACTTTCCAGCAAC	235449	67645	TCAGCCTCCCTGCTACCCTC	280036	112232	ACTACAGGCGCCCACCACCA
190863	23059	TCACTGATACTTTCCAGCAA	235450	67646	CTCAGCCTCCCTGCTACCCT	280037	112233	GACTACAGGCGCCCACCACC
190864	23060	TTCACTGATACTTTCCAGCA	235451	67647	TCTCAGCCTCCCTGCTACCC	280038	112234	GGACTACAGGCGCCCACCAC
190865	23061	CTTCACTGATACTTTCCAGC	235452	67648	ATCTCAGCCTCCCTGCTACC	280039	112235	GGGACTACAGGCGCCCACCA
190866	23062	ACTTCACTGATACTTTCCAG	235453	67649	GATCTCAGCCTCCCTGCTAC	280040	112236	TGGGACTACAGGCGCCCACC
190867	23063	AACTTCACTGATACTTTCCA	235454	67650	AGATCTCAGCCTCCCTGCTA	280041	112237	CTGGGACTACAGGCGCCCAC
190868	23064	TAACTTCACTGATACTTTCC	235455	67651	CAGATCTCAGCCTCCCTGCT	280042	112238	GCTGGGACTACAGGCGCCCA
190869	23065	TTAACTTCACTGATACTTTC	235456	67652	GCAGATCTCAGCCTCCCTGC	280043	112239	AGCTGGGACTACAGGCGCCC
190870	23066	ATTAACTTCACTGATACTTT	235457	67653	GGCAGATCTCAGCCTCCCTG	280044	112240	TAGCTGGGACTACAGGCGCC
190871	23067	TATTAACTTCACTGATACTT	235458	67654	AGGCAGATCTCAGCCTCCCT	280045	112241	GTAGCTGGGACTACAGGCGC
190872	23068	TTATTAACTTCACTGATACT	235459	67655	CAGGCAGATCTCAGCCTCCC	280046	112242	AGTAGCTGGGACTACAGGCG
190873	23069	CTTATTAACTTCACTGATAC	235460	67656	GCAGGCAGATCTCAGCCTCC	280047	112243	GAGTAGCTGGGACTACAGGC
190874	23070	CCTTATTAACTTCACTGATA	235461	67657	GGCAGGCAGATCTCAGCCTC	280048	112244	CGAGTAGCTGGGACTACAGG
190875	23071	ACCTTATTAACTTCACTGAT	235462	67658	TGGCAGGCAGATCTCAGCCT	280049	112245	CCGAGTAGCTGGGACTACAG
190876	23072	AACCTTATTAACTTCACTGA	235463	67659	ATGGCAGGCAGATCTCAGCC	280050	112246	CCCGAGTAGCTGGGACTACA
190877	23073	AAACCTTATTAACTTCACTG	235464	67660	CATGGCAGGCAGATCTCAGC	280051	112247	TCCCGAGTAGCTGGGACTAC
190878	23074	AAAACCTTATTAACTTCACT	235465	67661	TCATGGCAGGCAGATCTCAG	280052	112248	CTCCCGAGTAGCTGGGACTA
190879	23075	AAAAACCTTATTAACTTCAC	235466	67662	TTCATGGCAGGCAGATCTCA	280053	112249	CCTCCCGAGTAGCTGGGACT
190880	23076	GAAAAACCTTATTAACTTCA	235467	67663	GTTCATGGCAGGCAGATCTC	280054	112250	GCCTCCCGAGTAGCTGGGAC
190881	23077	AGAAAAACCTTATTAACTTC	235468	67664	AGTTCATGGCAGGCAGATCT	280055	112251	AGCCTCCCGAGTAGCTGGGA
190882	23078	AAGAAAAACCTTATTAACTT	235469	67665	CAGTTCATGGCAGGCAGATC	280056	112252	CAGCCTCCCGAGTAGCTGGG
190883	23079	CAAGAAAAACCTTATTAACT	235470	67666	CCAGTTCATGGCAGGCAGAT	280057	112253	TCAGCCTCCCGAGTAGCTGG
190884	23080	GCAAGAAAAACCTTATTAAC	235471	67667	CCCAGTTCATGGCAGGCAGA	280058	112254	CTCAGCCTCCCGAGTAGCTG
190885	23081	GGCAAGAAAAACCTTATTAA	235472	67668	TCCCAGTTCATGGCAGGCAG	280059	112255	CCTCAGCCTCCCGAGTAGCT
190886	23082	GGGCAAGAAAAACCTTATTA	235473	67669	CTCCCAGTTCATGGCAGGCA	280060	112256	GCCTCAGCCTCCCGAGTAGC
190887	23083	TGGGCAAGAAAAACCTTATT	235474	67670	CCTCCCAGTTCATGGCAGGC	280061	112257	TGCCTCAGCCTCCCGAGTAG
190888	23084	CTGGGCAAGAAAAACCTTAT	235475	67671	TCCTCCCAGTTCATGGCAGG	280062	112258	CTGCCTCAGCCTCCCGAGTA
190889	23085	CCTGGGCAAGAAAAACCTTA	235476	67672	CTCCTCCCAGTTCATGGCAG	280063	112259	CCTGCCTCAGCCTCCCGAGT
190890	23086	CCCTGGGCAAGAAAAACCTT	235477	67673	TCTCCTCCCAGTTCATGGCA	280064	112260	TCCTGCCTCAGCCTCCCGAG
190891	23087	ACCCTGGGCAAGAAAAACCT	235478	67674	CTCTCCTCCCAGTTCATGGC	280065	112261	CTCCTGCCTCAGCCTCCCGA
190892	23088	CACCCTGGGCAAGAAAAACC	235479	67675	CCTCTCCTCCCAGTTCATGG	280066	112262	TCTCCTGCCTCAGCCTCCCG
190893	23089	TCACCCTGGGCAAGAAAAAC	235480	67676	GCCTCTCCTCCCAGTTCATG	280067	112263	TTCTCCTGCCTCAGCCTCCC
190894	23090	CTCACCCTGGGCAAGAAAAA	235481	67677	AGCCTCTCCTCCCAGTTCAT	280068	112264	ATTCTCCTGCCTCAGCCTCC
190895	23091	CCTCACCCTGGGCAAGAAAA	235482	67678	GAGCCTCTCCTCCCAGTTCA	280069	112265	CATTCTCCTGCCTCAGCCTC
190896	23092	CCCTCACCCTGGGCAAGAAA	235483	67679	GGAGCCTCTCCTCCCAGTTC	280070	112266	CCATTCTCCTGCCTCAGCCT
190897	23093	TCCCTCACCCTGGGCAAGAA	235484	67680	AGGAGCCTCTCCTCCCAGTT	280071	112267	GCCATTCTCCTGCCTCAGCC
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190899	23095	GTTCCCTCACCCTGGGCAAG	235486	67682	AGAGGAGCCTCTCCTCCCAG	280073	112269	ACGCCATTCTCCTGCCTCAG
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190901	23097	CTGTTCCCTCACCCTGGGCA	235488	67684	AGAGAGGAGCCTCTCCTCCC	280075	112271	TCACGCCATTCTCCTGCCTC
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190904	23100	GAACTGTTCCCTCACCCTGG	235491	67687	GAGAGAGAGGAGCCTCTCCT	280078	112274	GGTTCACGCCATTCTCCTGC
190905	23101	GGAACTGTTCCCTCACCCTG	235492	67688	AGAGAGAGAGGAGCCTCTCC	280079	112275	GGGTTCACGCCATTCTCCTG
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190907	23103	TGGGAACTGTTCCCTCACCC	235494	67690	GAAGAGAGAGAGGAGCCTCT	280081	112277	CCGGGTTCACGCCATTCTCC
190908	23104	TTGGGAACTGTTCCCTCACC	235495	67691	TGAAGAGAGAGAGGAGCCTC	280082	112278	CCCGGGTTCACGCCATTCTC
190909	23105	ATTGGGAACTGTTCCCTCAC	235496	67692	GTGAAGAGAGAGAGGAGCCT	280083	112279	TCCCGGGTTCACGCCATTCT
190910	23106	CATTGGGAACTGTTCCCTCA	235497	67693	GGTGAAGAGAGAGAGGAGCC	280084	112280	CTCCCGGGTTCACGCCATTC
190911	23107	TCATTGGGAACTGTTCCCTC	235498	67694	GGGTGAAGAGAGAGAGGAGC	280085	112281	CCTCCCGGGTTCACGCCATT
190912	23108	GTCATTGGGAACTGTTCCCT	235499	67695	GGGGTGAAGAGAGAGAGGAG	280086	112282	GCCTCCCGGGTTCACGCCAT
190913	23109	TGTCATTGGGAACTGTTCCC	235500	67696	GGGGGTGAAGAGAGAGAGGA	280087	112283	CGCCTCCCGGGTTCACGCCA
190914	23110	TTGTCATTGGGAACTGTTCC	235501	67697	TGGGGGTGAAGAGAGAGAGG	280088	112284	CCGCCTCCCGGGTTCACGCC

190915	23111	TTTGTCATTGGGAACTGTTC	235502	67698	GTGGGGGTGAAGAGAGAGAG	280089	112285	TCCGCCTCCCGGGTTCACGC
190916	23112	ATTTGTCATTGGGAACTGTT	235503	67699	AGTGGGGGTGAAGAGAGAGA	280090	112286	CTCCGCCTCCCGGGTTCACG
190917	23113	CATTTGTCATTGGGAACTGT	235504	67700	GAGTGGGGGTGAAGAGAGAG	280091	112287	GCTCCGCCTCCCGGGTTCAC
190918	23114	GCATTTGTCATTGGGAACTG	235505	67701	AGAGTGGGGGTGAAGAGAGA	280092	112288	AGCTCCGCCTCCCGGGTTCA
190919	23115	AGCATTTGTCATTGGGAACT	235506	67702	CAGAGTGGGGGTGAAGAGAG	280093	112289	AAGCTCCGCCTCCCGGGTTC
190920	23116	CAGCATTTGTCATTGGGAAC	235507	67703	GCAGAGTGGGGGTGAAGAGA	280094	112290	CAAGCTCCGCCTCCCGGGTT
190921	23117	ACAGCATTTGTCATTGGGAA	235508	67704	GGCAGAGTGGGGGTGAAGAG	280095	112291	GCAAGCTCCGCCTCCCGGGT
190922	23118	TACAGCATTTGTCATTGGGA	235509	67705	GGGCAGAGTGGGGGTGAAGA	280096	112292	TGCAAGCTCCGCCTCCCGGG
190923	23119	ATACAGCATTTGTCATTGGG	235510	67706	GGGGCAGAGTGGGGGTGAAG	280097	112293	CTGCAAGCTCCGCCTCCCGG
190924	23120	CATACAGCATTTGTCATTGG	235511	67707	GGGGGCAGAGTGGGGGTGAA	280098	112294	ACTGCAAGCTCCGCCTCCCG
190925	23121	CCATACAGCATTTGTCATTG	235512	67708	GGGGGGCAGAGTGGGGGTGA	280099	112295	CACTGCAAGCTCCGCCTCCC
190926	23122	CCCATACAGCATTTGTCATT	235513	67709	TGGGGGGCAGAGTGGGGGTG	280100	112296	TCACTGCAAGCTCCGCCTCC
190927	23123	TCCCATACAGCATTTGTCAT	235514	67710	TTGGGGGGCAGAGTGGGGGT	280101	112297	CTCACTGCAAGCTCCGCCTC
190928	23124	TTCCCATACAGCATTTGTCA	235515	67711	GTTGGGGGGCAGAGTGGGGG	280102	112298	GCTCACTGCAAGCTCCGCCT
190929	23125	CTTCCCATACAGCATTTGTC	235516	67712	TGTTGGGGGGCAGAGTGGGG	280103	112299	GGCTCACTGCAAGCTCCGCC
190930	23126	CCTTCCCATACAGCATTTGT	235517	67713	GTGTTGGGGGGCAGAGTGGG	280104	112300	CGGCTCACTGCAAGCTCCGC
190931	23127	CCCTTCCCATACAGCATTTG	235518	67714	AGTGTTGGGGGGCAGAGTGG	280105	112301	TCGGCTCACTGCAAGCTCCG
190932	23128	CCCCTTCCCATACAGCATTT	235519	67715	GAGTGTTGGGGGGCAGAGTG	280106	112302	CTCGGCTCACTGCAAGCTCC
190933	23129	GCCCCTTCCCATACAGCATT	235520	67716	GGAGTGTTGGGGGGCAGAGT	280107	112303	TCTCGGCTCACTGCAAGCTC
190934	23130	AGCCCCTTCCCATACAGCAT	235521	67717	AGGAGTGTTGGGGGGCAGAG	280108	112304	ATCTCGGCTCACTGCAAGCT
190935	23131	CAGCCCCTTCCCATACAGCA	235522	67718	GAGGAGTGTTGGGGGGCAGA	280109	112305	GATCTCGGCTCACTGCAAGC
190936	23132	ACAGCCCCTTCCCATACAGC	235523	67719	TGAGGAGTGTTGGGGGGCAG	280110	112306	CGATCTCGGCTCACTGCAAG
190937	23133	TACAGCCCCTTCCCATACAG	235524	67720	CTGAGGAGTGTTGGGGGGCA	280111	112307	GCGATCTCGGCTCACTGCAA
190938	23134	CTACAGCCCCTTCCCATACA	235525	67721	TCTGAGGAGTGTTGGGGGGC	280112	112308	CGCGATCTCGGCTCACTGCA
190939	23135	TCTACAGCCCCTTCCCATAC	235526	67722	TTCTGAGGAGTGTTGGGGGG	280113	112309	GCGCGATCTCGGCTCACTGC
190940	23136	TTCTACAGCCCCTTCCCATA	235527	67723	GTTCTGAGGAGTGTTGGGGG	280114	112310	GGCGCGATCTCGGCTCACTG
190941	23137	GTTCTACAGCCCCTTCCCAT	235528	67724	AGTTCTGAGGAGTGTTGGGG	280115	112311	TGGCGCGATCTCGGCTCACT
190942	23138	AGTTCTACAGCCCCTTCCCA	235529	67725	AAGTTCTGAGGAGTGTTGGG	280116	112312	GTGGCGCGATCTCGGCTCAC
190943	23139	CAGTTCTACAGCCCCTTCCC	235530	67726	TAAGTTCTGAGGAGTGTTGG	280117	112313	AGTGGCGCGATCTCGGCTCA
190944	23140	GCAGTTCTACAGCCCCTTCC	235531	67727	ATAAGTTCTGAGGAGTGTTG	280118	112314	CAGTGGCGCGATCTCGGCTC
190945	23141	GGCAGTTCTACAGCCCCTTC	235532	67728	GATAAGTTCTGAGGAGTGTT	280119	112315	GCAGTGGCGCGATCTCGGCT
190946	23142	TGGCAGTTCTACAGCCCCTT	235533	67729	GGATAAGTTCTGAGGAGTGT	280120	112316	TGCAGTGGCGCGATCTCGGC
190947	23143	CTGGCAGTTCTACAGCCCCT	235534	67730	AGGATAAGTTCTGAGGAGTG	280121	112317	GTGCAGTGGCGCGATCTCGG
190948	23144	GCTGGCAGTTCTACAGCCCC	235535	67731	GAGGATAAGTTCTGAGGAGT	280122	112318	AGTGCAGTGGCGCGATCTCG
190949	23145	GGCTGGCAGTTCTACAGCCC	235536	67732	AGAGGATAAGTTCTGAGGAG	280123	112319	GAGTGCAGTGGCGCGATCTC
190950	23146	GGGCTGGCAGTTCTACAGCC	235537	67733	GAGAGGATAAGTTCTGAGGA	280124	112320	GGAGTGCAGTGGCGCGATCT
190951	23147	GGGGCTGGCAGTTCTACAGC	235538	67734	GGAGAGGATAAGTTCTGAGG	280125	112321	TGGAGTGCAGTGGCGCGATC
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190953	23149	AAGGGGCTGGCAGTTCTACA	235540	67736	GAGGAGAGGATAAGTTCTGA	280127	112323	GCTGGAGTGCAGTGGCGCGA
190954	23150	AAAGGGGCTGGCAGTTCTAC	235541	67737	AGAGGAGAGGATAAGTTCTG	280128	112324	GGCTGGAGTGCAGTGGCGCG
190955	23151	CAAAGGGGCTGGCAGTTCTA	235542	67738	AAGAGGAGAGGATAAGTTCT	280129	112325	AGGCTGGAGTGCAGTGGCGC
190956	23152	CCAAAGGGGCTGGCAGTTCT	235543	67739	GAAGAGGAGAGGATAAGTTC	280130	112326	CAGGCTGGAGTGCAGTGGCG
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190959	23155	GGACCAAAGGGGCTGGCAGT	235546	67742	AAAGAAGAGGAGAGGATAAG	280133	112329	GCCCAGGCTGGAGTGCAGTG
190960	23156	TGGACCAAAGGGGCTGGCAG	235547	67743	GAAAGAAGAGGAGAGGATAA	280134	112330	CGCCCAGGCTGGAGTGCAGT
190961	23157	ATGGACCAAAGGGGCTGGCA	235548	67744	GGAAAGAAGAGGAGAGGATA	280135	112331	TCGCCCAGGCTGGAGTGCAG
190962	23158	GATGGACCAAAGGGGCTGGC	235549	67745	GGGAAAGAAGAGGAGAGGAT	280136	112332	GTCGCCCAGGCTGGAGTGCA
190963	23159	GGATGGACCAAAGGGGCTGG	235550	67746	GGGGAAAGAAGAGGAGAGGA	280137	112333	TGTCGCCCAGGCTGGAGTGC
190964	23160	CGGATGGACCAAAGGGGCTG	235551	67747	TGGGGAAAGAAGAGGAGAGG	280138	112334	TTGTCGCCCAGGCTGGAGTG
190965	23161	ACGGATGGACCAAAGGGGCT	235552	67748	CTGGGGAAAGAAGAGGAGAG	280139	112335	CTTGTCGCCCAGGCTGGAGT
190966	23162	TACGGATGGACCAAAGGGGC	235553	67749	CCTGGGGAAAGAAGAGGAGA	280140	112336	CCTTGTCGCCCAGGCTGGAG
190967	23163	TTACGGATGGACCAAAGGGG	235554	67750	ACCTGGGGAAAGAAGAGGAG	280141	112337	GCCTTGTCGCCCAGGCTGGA
190968	23164	TTTACGGATGGACCAAAGGG	235555	67751	CACCTGGGGAAAGAAGAGGA	280142	112338	TGCCTTGTCGCCCAGGCTGG
190969	23165	CTTTACGGATGGACCAAAGG	235556	67752	TCACCTGGGGAAAGAAGAGG	280143	112339	TTGCCTTGTCGCCCAGGCTG
190970	23166	ACTTTACGGATGGACCAAAG	235557	67753	TTCACCTGGGGAAAGAAGAG	280144	112340	CTTGCCTTGTCGCCCAGGCT
190971	23167	CACTTTACGGATGGACCAAA	235558	67754	GTTCACCTGGGGAAAGAAGA	280145	112341	TCTTGCCTTGTCGCCCAGGC
190972	23168	TCACTTTACGGATGGACCAA	235559	67755	AGTTCACCTGGGGAAAGAAG	280146	112342	ATCTTGCCTTGTCGCCCAGG
190973	23169	TTCACTTTACGGATGGACCA	235560	67756	AAGTTCACCTGGGGAAAGAA	280147	112343	AATCTTGCCTTGTCGCCCAG
190974	23170	GTTCACTTTACGGATGGACC	235561	67757	AAAGTTCACCTGGGGAAAGA	280148	112344	GAATCTTGCCTTGTCGCCCA
190975	23171	AGTTCACTTTACGGATGGAC	235562	67758	CAAAGTTCACCTGGGGAAAG	280149	112345	AGAATCTTGCCTTGTCGCCC
190976	23172	GAGTTCACTTTACGGATGGA	235563	67759	TCAAAGTTCACCTGGGGAAA	280150	112346	TAGAATCTTGCCTTGTCGCC
190977	23173	AGAGTTCACTTTACGGATGG	235564	67760	TTCAAAGTTCACCTGGGGAA	280151	112347	ATAGAATCTTGCCTTGTCGC
190978	23174	CAGAGTTCACTTTACGGATG	235565	67761	GTTCAAAGTTCACCTGGGGA	280152	112348	GATAGAATCTTGCCTTGTCG
190979	23175	ACAGAGTTCACTTTACGGAT	235566	67762	GGTTCAAAGTTCACCTGGGG	280153	112349	AGATAGAATCTTGCCTTGTC
190980	23176	CACAGAGTTCACTTTACGGA	235567	67763	TGGTTCAAAGTTCACCTGGG	280154	112350	GAGATAGAATCTTGCCTTGT
190981	23177	CCACAGAGTTCACTTTACGG	235568	67764	CTGGTTCAAAGTTCACCTGG	280155	112351	TGAGATAGAATCTTGCCTTG
190982	23178	TCCACAGAGTTCACTTTACG	235569	67765	CCTGGTTCAAAGTTCACCTG	280156	112352	TTGAGATAGAATCTTGCCTT
190983	23179	ATCCACAGAGTTCACTTTAC	235570	67766	TCCTGGTTCAAAGTTCACCT	280157	112353	TTTGAGATAGAATCTTGCCT
190984	23180	GATCCACAGAGTTCACTTTA	235571	67767	ATCCTGGTTCAAAGTTCACC	280158	112354	TTTTGAGATAGAATCTTGCC
190985	23181	GGATCCACAGAGTTCACTTT	235572	67768	CATCCTGGTTCAAAGTTCAC	280159	112355	TTTTTGAGATAGAATCTTGC
190986	23182	AGGATCCACAGAGTTCACTT	235573	67769	CCATCCTGGTTCAAAGTTCA	280160	112356	TTTTTTGAGATAGAATCTTG

190987	23183	CAGGATCCACAGAGTTCACT	235574	67770	GCCATCCTGGTTCAAAGTTC	280161	112357	TTTTTTTGAGATAGAATCTT
190988	23184	CCAGGATCCACAGAGTTCAC	235575	67771	AGCCATCCTGGTTCAAAGTT	280162	112358	ATTTTTTTGAGATAGAATCT
190989	23185	TCCAGGATCCACAGAGTTCA	235576	67772	CAGCCATCCTGGTTCAAAGT	280163	112359	TATTTTTTTGAGATAGAATC
190990	23186	CTCCAGGATCCACAGAGTTC	235577	67773	TCAGCCATCCTGGTTCAAAG	280164	112360	TTATTTTTTTGAGATAGAAT
190991	23187	CCTCCAGGATCCACAGAGTT	235578	67774	CTCAGCCATCCTGGTTCAAA	280165	112361	TTTATTTTTTTGAGATAGAA
190992	23188	TCCTCCAGGATCCACAGAGT	235579	67775	GCTCAGCCATCCTGGTTCAA	280166	112362	TTTTATTTTTTTGAGATAGA
190993	23189	ATCCTCCAGGATCCACAGAG	235580	67776	GGCTCAGCCATCCTGGTTCA	280167	112363	TTTTTATTTTTTTGAGATAG
190994	23190	AATCCTCCAGGATCCACAGA	235581	67777	GGGCTCAGCCATCCTGGTTC	280168	112364	ATTTTTATTTTTTTGAGATA
190995	23191	GAATCCTCCAGGATCCACAG	235582	67778	GGGGCTCAGCCATCCTGGTT	280169	112365	TATTTTTATTTTTTTGAGAT
190996	23192	GGAATCCTCCAGGATCCACA	235583	67779	CGGGGCTCAGCCATCCTGGT	280170	112366	TTATTTTTATTTTTTTGAGA
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190998	23194	CTGGAATCCTCCAGGATCCA	235585	67781	GGCGGGGCTCAGCCATCCTG	280172	112368	TTTTATTTTTATTTTTTTGA
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191000	23196	CGCTGGAATCCTCCAGGATC	235587	67783	CTGGCGGGGCTCAGCCATCC	280174	112370	TATTTTATTTTTATTTTTTT
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191002	23198	GACGCTGGAATCCTCCAGGA	235589	67785	TCCTGGCGGGGCTCAGCCAT	280176	112372	TTTATTTTATTTTTATTTTT
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191004	23200	AAGACGCTGGAATCCTCCAG	235591	67787	ACTCCTGGCGGGGCTCAGCC	280178	112374	ATTTTATTTTATTTTTATTT
191005	23201	AAAGACGCTGGAATCCTCCA	235592	67788	AACTCCTGGCGGGGCTCAGC	280179	112375	TATTTTATTTTATTTTTATT
191006	23202	AAAAGACGCTGGAATCCTCC	235593	67789	GAACTCCTGGCGGGGCTCAG	280180	112376	TTATTTTATTTTATTTTTAT
191007	23203	AAAAAGACGCTGGAATCCTC	235594	67790	CGAACTCCTGGCGGGGCTCA	280181	112377	TTTATTTTATTTTATTTTTA
191008	23204	AAAAAAGACGCTGGAATCCT	235595	67791	TCGAACTCCTGGCGGGGCTC	280182	112378	TTTTATTTTATTTTATTTTT
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191015	23211	AAAAAAAAAAAAAGACGCTG	235602	67798	CATCACTTCGAACTCCTGGC	280189	112385	TTTATTATTTTATTTTATTT
191016	23212	GAAAAAAAAAAAAAGACGCT	235603	67799	CCATCACTTCGAACTCCTGG	280190	112386	TTTTATTATTTTATTTTATT
191017	23213	AGAAAAAAAAAAAAAGACGC	235604	67800	TCCATCACTTCGAACTCCTG	280191	112387	ATTTTATTATTTTATTTTAT
191018	23214	AAGAAAAAAAAAAAAAGACG	235605	67801	TTCCATCACTTCGAACTCCT	280192	112388	TATTTTATTATTTTATTTTA
191019	23215	AAAGAAAAAAAAAAAAAGAC	235606	67802	CTTCCATCACTTCGAACTCC	280193	112389	TTATTTTATTATTTTATTTT
191020	23216	AAAAGAAAAAAAAAAAAAGA	235607	67803	TCTTCCATCACTTCGAACTC	280194	112390	TTTATTTTATTATTTTATTT
191021	23217	AAAAAGAAAAAAAAAAAAAG	235608	67804	ATCTTCCATCACTTCGAACT	280195	112391	TTTTATTTTATTATTTTATT
191022	23218	AAAAAAGAAAAAAAAAAAAA	235609	67805	GATCTTCCATCACTTCGAAC	280196	112392	ATTTTATTTTATTATTTTAT
191023	23219	AAAAAAAGAAAAAAAAAAAA	235610	67806	TGATCTTCCATCACTTCGAA	280197	112393	TATTTTATTTTATTATTTTA
191024	23220	AAAAAAAAGAAAAAAAAAAA	235611	67807	GTGATCTTCCATCACTTCGA	280198	112394	TTATTTTATTTTATTATTTT
191025	23221	AAAAAAAAAGAAAAAAAAAA	235612	67808	CGTGATCTTCCATCACTTCG	280199	112395	TTTATTTTATTTTATTATTT
191026	23222	TAAAAAAAAAGAAAAAAAAA	235613	67809	GCGTGATCTTCCATCACTTC	280200	112396	TTTTATTTTATTTTATTATT
191027	23223	TTAAAAAAAAAGAAAAAAAA	235614	67810	AGCGTGATCTTCCATCACTT	280201	112397	ATTTTATTTTATTTTATTAT
191028	23224	CTTAAAAAAAAAGAAAAAAA	235615	67811	CAGCGTGATCTTCCATCACT	280202	112398	TATTTTATTTTATTTTATTA
191029	23225	TCTTAAAAAAAAAGAAAAAA	235616	67812	CCAGCGTGATCTTCCATCAC	280203	112399	TTATTTTATTTTATTTTATT
191030	23226	GTCTTAAAAAAAAAGAAAAA	235617	67813	CCCAGCGTGATCTTCCATCA	280204	112400	TTTATTTTATTTTATTTTAT
191031	23227	TGTCTTAAAAAAAAAGAAAA	235618	67814	TCCCAGCGTGATCTTCCATC	280205	112401	TTTTATTTTATTTTATTTTA
191032	23228	CTGTCTTAAAAAAAAAGAAA	235619	67815	GTCCCAGCGTGATCTTCCAT	280206	112402	ATTTTATTTTATTTTATTTT
191033	23229	TCTGTCTTAAAAAAAAAGAA	235620	67816	CGTCCCAGCGTGATCTTCCA	280207	112403	TATTTTATTTTATTTTATTT
191034	23230	CTCTGTCTTAAAAAAAAAGA	235621	67817	ACGTCCCAGCGTGATCTTCC	280208	112404	TTATTTTATTTTATTTTATT
191035	23231	GCTCTGTCTTAAAAAAAAAG	235622	67818	TACGTCCCAGCGTGATCTTC	280209	112405	TTTATTTTATTTTATTTTAT
191036	23232	GGCTCTGTCTTAAAAAAAAA	235623	67819	GTACGTCCCAGCGTGATCTT	280210	112406	TTTTATTTTATTTTATTTTA
191037	23233	AGGCTCTGTCTTAAAAAAAA	235624	67820	CGTACGTCCCAGCGTGATCT	280211	112407	ATTTTATTTTATTTTATTTT
191038	23234	AAGGCTCTGTCTTAAAAAAA	235625	67821	CCGTACGTCCCAGCGTGATC	280212	112408	TATTTTATTTTATTTTATTT
191039	23235	CAAGGCTCTGTCTTAAAAAA	235626	67822	CCCGTACGTCCCAGCGTGAT	280213	112409	TTATTTTATTTTATTTTATT
191040	23236	GCAAGGCTCTGTCTTAAAAA	235627	67823	ACCCGTACGTCCCAGCGTGA	280214	112410	TTTATTTTATTTTATTTTAT
191041	23237	AGCAAGGCTCTGTCTTAAAA	235628	67824	AACCCGTACGTCCCAGCGTG	280215	112411	ATTTATTTTATTTTATTTTA
191042	23238	CAGCAAGGCTCTGTCTTAAA	235629	67825	CAACCCGTACGTCCCAGCGT	280216	112412	TATTTATTTTATTTTATTTT
191043	23239	ACAGCAAGGCTCTGTCTTAA	235630	67826	CCAACCCGTACGTCCCAGCG	280217	112413	TTATTTATTTTATTTTATTT
191044	23240	GACAGCAAGGCTCTGTCTTA	235631	67827	CCCAACCCGTACGTCCCAGC	280218	112414	TTTATTTATTTTATTTTATT
191045	23241	TGACAGCAAGGCTCTGTCTT	235632	67828	CCCCAACCCGTACGTCCCAG	280219	112415	TTTTATTTATTTTATTTTAT
191046	23242	GTGACAGCAAGGCTCTGTCT	235633	67829	CCCCCAACCCGTACGTCCCA	280220	112416	ATTTTATTTATTTTATTTTA
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191049	23245	TGGGTGACAGCAAGGCTCTG	235636	67832	TGTCCCCCAACCCGTACGTC	280223	112419	TTTATTTTATTTTATTTTAT
191050	23246	CTGGGTGACAGCAAGGCTCT	235637	67833	CTGTCCCCCAACCCGTACGT	280224	112420	TTTTATTTTATTTTATTTTAT
191051	23247	CCTGGGTGACAGCAAGGCTC	235638	67834	CCTGTCCCCCAACCCGTACG	280225	112421	ATTTTATTTTATTTATTTTA
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191054	23250	CAGCCTGGGTGACAGCAAGG	235641	67837	TTTCCTGTCCCCCAACCCGT	280228	112424	TTTATTTTATTTTATTTATT
191055	23251	CCAGCCTGGGTGACAGCAAG	235642	67838	CTTTCCTGTCCCCCAACCCG	280229	112425	TTTTATTTTATTTTATTTAT
191056	23252	TCCAGCCTGGGTGACAGCAA	235643	67839	TCTTTCCTGTCCCCCAACCC	280230	112426	ATTTTATTTTATTTTATTTA
191057	23253	CTCCAGCCTGGGTGACAGCA	235644	67840	ATCTTTCCTGTCCCCCAACC	280231	112427	CATTTTATTTTATTTTATTT
191058	23254	ACTCCAGCCTGGGTGACAGC	235645	67841	GATCTTTCCTGTCCCCCAAC	280232	112428	ACATTTTATTTTATTTTATT

191059	23255	CACTCCAGCCTGGGTGACAG	235646	67842	TGATCTTTCCTGTCCCCCAA	280233	112429	TACATTTTATTTTATTTTAT
191060	23256	GCACTCCAGCCTGGGTGACA	235647	67843	CTGATCTTTCCTGTCCCCCA	280234	112430	ATACATTTTATTTTATTTTA
191061	23257	TGCACTCCAGCCTGGGTGAC	235648	67844	CCTGATCTTTCCTGTCCCCC	280235	112431	TATACATTTTATTTTATTTT
191062	23258	CTGCACTCCAGCCTGGGTGA	235649	67845	CCCTGATCTTTCCTGTCCCC	280236	112432	TTATACATTTTATTTTATTT
191063	23259	ACTGCACTCCAGCCTGGGTG	235650	67846	CCCCTGATCTTTCCTGTCCC	280237	112433	ATTATACATTTTATTTTATT
191064	23260	CACTGCACTCCAGCCTGGGT	235651	67847	CCCCCTGATCTTTCCTGTCC	280238	112434	AATTATACATTTTATTTTAT
191065	23261	CCACTGCACTCCAGCCTGGG	235652	67848	CCCCCCTGATCTTTCCTGTC	280239	112435	CAATTATACATTTTATTTTA
191066	23262	GCCACTGCACTCCAGCCTGG	235653	67849	GCCCCCCTGATCTTTCCTGT	280240	112436	CCAATTATACATTTTATTTT
191067	23263	TGCCACTGCACTCCAGCCTG	235654	67850	AGCCCCCCTGATCTTTCCTG	280241	112437	TCCAATTATACATTTTATTT
191068	23264	GTGCCACTGCACTCCAGCCT	235655	67851	TAGCCCCCCTGATCTTTCCT	280242	112438	TTCCAATTATACATTTTATT
191069	23265	CGTGCCACTGCACTCCAGCC	235656	67852	GTAGCCCCCCTGATCTTTCC	280243	112439	ATTCCAATTATACATTTTAT
191070	23266	TCGTGCCACTGCACTCCAGC	235657	67853	TGTAGCCCCCCTGATCTTTC	280244	112440	CATTCCAATTATACATTTTA
191071	23267	ATCGTGCCACTGCACTCCAG	235658	67854	GTGTAGCCCCCCTGATCTTT	280245	112441	ACATTCCAATTATACATTTT
191072	23268	GATCGTGCCACTGCACTCCA	235659	67855	GGTGTAGCCCCCCTGATCTT	280246	112442	AACATTCCAATTATACATTT
191073	23269	AGATCGTGCCACTGCACTCC	235660	67856	TGGTGTAGCCCCCCTGATCT	280247	112443	AAACATTCCAATTATACATT
191074	23270	GAGATCGTGCCACTGCACTC	235661	67857	ATGGTGTAGCCCCCCTGATC	280248	112444	TAAACATTCCAATTATACAT
191075	23271	TGAGATCGTGCCACTGCACT	235662	67858	CATGGTGTAGCCCCCCTGAT	280249	112445	ATAAACATTCCAATTATACA
191076	23272	CTGAGATCGTGCCACTGCAC	235663	67859	GCATGGTGTAGCCCCCCTGA	280250	112446	TATAAACATTCCAATTATAC
191077	23273	ACTGAGATCGTGCCACTGCA	235664	67860	TGCATGGTGTAGCCCCCCTG	280251	112447	TTATAAACATTCCAATTATA
191078	23274	AACTGAGATCGTGCCACTGC	235665	67861	GTGCATGGTGTAGCCCCCCT	280252	112448	GTTATAAACATTCCAATTAT
191079	23275	GAACTGAGATCGTGCCACTG	235666	67862	GGTGCATGGTGTAGCCCCCC	280253	112449	TGTTATAAACATTCCAATTA
191080	23276	TGAACTGAGATCGTGCCACT	235667	67863	TGGTGCATGGTGTAGCCCCC	280254	112450	GTGTTATAAACATTCCAATT
191081	23277	GTGAACTGAGATCGTGCCAC	235668	67864	TTGGTGCATGGTGTAGCCCC	280255	112451	TGTGTTATAAACATTCCAAT
191082	23278	AGTGAACTGAGATCGTGCCA	235669	67865	CTTGGTGCATGGTGTAGCCC	280256	112452	TTGTGTTATAAACATTCCAA
191083	23279	CAGTGAACTGAGATCGTGCC	235670	67866	TCTTGGTGCATGGTGTAGCC	280257	112453	CTTGTGTTATAAACATTCCA
191084	23280	GCAGTGAACTGAGATCGTGC	235671	67867	GTCTTGGTGCATGGTGTAGC	280258	112454	TCTTGTGTTATAAACATTCC
191085	23281	TGCAGTGAACTGAGATCGTG	235672	67868	GGTCTTGGTGCATGGTGTAG	280259	112455	TTCTTGTGTTATAAACATTC
191086	23282	TTGCAGTGAACTGAGATCGT	235673	67869	TGGTCTTGGTGCATGGTGTA	280260	112456	TTTCTTGTGTTATAAACATT
191087	23283	GTTGCAGTGAACTGAGATCG	235674	67870	TTGGTCTTGGTGCATGGTGT	280261	112457	ATTTCTTGTGTTATAAACAT
191088	23284	GGTTGCAGTGAACTGAGATC	235675	67871	CTTGGTCTTGGTGCATGGTG	280262	112458	CATTTCTTGTGTTATAAACA
191089	23285	AGGTTGCAGTGAACTGAGAT	235676	67872	TCTTGGTCTTGGTGCATGGT	280263	112459	TCATTTCTTGTGTTATAAAC
191090	23286	GAGGTTGCAGTGAACTGAGA	235677	67873	CTCTTGGTCTTGGTGCATGG	280264	112460	ATCATTTCTTGTGTTATAAA
191091	23287	GGAGGTTGCAGTGAACTGAG	235678	67874	CCTCTTGGTCTTGGTGCATG	280265	112461	TATCATTTCTTGTGTTATAA
191092	23288	CGGAGGTTGCAGTGAACTGA	235679	67875	CCCTCTTGGTCTTGGTGCAT	280266	112462	TTATCATTTCTTGTGTTATA
191093	23289	GCGGAGGTTGCAGTGAACTG	235680	67876	ACCCTCTTGGTCTTGGTGCA	280267	112463	TTTATCATTTCTTGTGTTAT
191094	23290	GGCGGAGGTTGCAGTGAACT	235681	67877	CACCCTCTTGGTCTTGGTGC	280268	112464	ATTTATCATTTCTTGTGTTA
191095	23291	AGGCGGAGGTTGCAGTGAAC	235682	67878	TCACCCTCTTGGTCTTGGTG	280269	112465	CATTTATCATTTCTTGTGTT
191096	23292	GAGGCGGAGGTTGCAGTGAA	235683	67879	GTCACCCTCTTGGTCTTGGT	280270	112466	GCATTTATCATTTCTTGTGT
191097	23293	GGAGGCGGAGGTTGCAGTGA	235684	67880	TGTCACCCTCTTGGTCTTGG	280271	112467	AGCATTTATCATTTCTTGTG
191098	23294	GGGAGGCGGAGGTTGCAGTG	235685	67881	GTGTCACCCTCTTGGTCTTG	280272	112468	AAGCATTTATCATTTCTTGT
191099	23295	CGGGAGGCGGAGGTTGCAGT	235686	67882	CGTGTCACCCTCTTGGTCTT	280273	112469	CAAGCATTTATCATTTCTTG
191100	23296	CCGGGAGGCGGAGGTTGCAG	235687	67883	CCGTGTCACCCTCTTGGTCT	280274	112470	TCAAGCATTTATCATTTCTT
191101	23297	CCCGGGAGGCGGAGGTTGCA	235688	67884	TCCGTGTCACCCTCTTGGTC	280275	112471	CTCAAGCATTTATCATTTCT
191102	23298	ACCCGGGAGGCGGAGGTTGC	235689	67885	GTCCGTGTCACCCTCTTGGT	280276	112472	CCTCAAGCATTTATCATTTC
191103	23299	AACCCGGGAGGCGGAGGTTG	235690	67886	CGTCCGTGTCACCCTCTTGG	280277	112473	ACCTCAAGCATTTATCATTT
191104	23300	GAACCCGGGAGGCGGAGGTT	235691	67887	GCGTCCGTGTCACCCTCTTG	280278	112474	CACCTCAAGCATTTATCATT
191105	23301	TGAACCCGGGAGGCGGAGGT	235692	67888	AGCGTCCGTGTCACCCTCTT	280279	112475	TCACCTCAAGCATTTATCAT
191106	23302	TTGAACCCGGGAGGCGGAGG	235693	67889	CAGCGTCCGTGTCACCCTCT	280280	112476	ATCACCTCAAGCATTTATCA
191107	23303	CTTGAACCCGGGAGGCGGAG	235694	67890	CCAGCGTCCGTGTCACCCTC	280281	112477	TATCACCTCAAGCATTTATC
191108	23304	GCTTGAACCCGGGAGGCGGA	235695	67891	GCCAGCGTCCGTGTCACCCT	280282	112478	CTATCACCTCAAGCATTTAT
191109	23305	CGCTTGAACCCGGGAGGCGG	235696	67892	GGCCAGCGTCCGTGTCACCC	280283	112479	TCTATCACCTCAAGCATTTA
191110	23306	TCGCTTGAACCCGGGAGGCG	235697	67893	AGGCCAGCGTCCGTGTCACC	280284	112480	ATCTATCACCTCAAGCATTT
191111	23307	ATCGCTTGAACCCGGGAGGC	235698	67894	CAGGCCAGCGTCCGTGTCAC	280285	112481	TATCTATCACCTCAAGCATT
191112	23308	AATCGCTTGAACCCGGGAGG	235699	67895	TCAGGCCAGCGTCCGTGTCA	280286	112482	GTATCTATCACCTCAAGCAT
191113	23309	GAATCGCTTGAACCCGGGAG	235700	67896	TTCAGGCCAGCGTCCGTGTC	280287	112483	GGTATCTATCACCTCAAGCA
191114	23310	AGAATCGCTTGAACCCGGGA	235701	67897	TTTCAGGCCAGCGTCCGTGT	280288	112484	GGGTATCTATCACCTCAAGC
191115	23311	GAGAATCGCTTGAACCCGGG	235702	67898	CTTTCAGGCCAGCGTCCGTG	280289	112485	GGGGTATCTATCACCTCAAG
191116	23312	TGAGAATCGCTTGAACCCGG	235703	67899	CCTTTCAGGCCAGCGTCCGT	280290	112486	TGGGGTATCTATCACCTCAA
191117	23313	ATGAGAATCGCTTGAACCCG	235704	67900	ACCTTTCAGGCCAGCGTCCG	280291	112487	ATGGGGTATCTATCACCTCA
191118	23314	CATGAGAATCGCTTGAACCC	235705	67901	AACCTTTCAGGCCAGCGTCC	280292	112488	AATGGGGTATCTATCACCTC
191119	23315	ACATGAGAATCGCTTGAACC	235706	67902	TAACCTTTCAGGCCAGCGTC	280293	112489	GAATGGGGTATCTATCACCT
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191121	23317	AGACATGAGAATCGCTTGAA	235708	67904	ACTAACCTTTCAGGCCAGCG	280295	112491	GTGAATGGGGTATCTATCAC
191122	23318	GAGACATGAGAATCGCTTGA	235709	67905	CACTAACCTTTCAGGCCAGC	280296	112492	GGTGAATGGGGTATCTATCA
191123	23319	CGAGACATGAGAATCGCTTG	235710	67906	CCACTAACCTTTCAGGCCAG	280297	112493	CGGTGAATGGGGTATCTATC
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191125	23321	GCCGAGACATGAGAATCGCT	235712	67908	GTCCACTAACCTTTCAGGCC	280299	112495	CACGGTGAATGGGGTATCTA
191126	23322	GGCCGAGACATGAGAATCGC	235713	67909	TGTCCACTAACCTTTCAGGC	280300	112496	TCACGGTGAATGGGGTATCT
191127	23323	AGGCCGAGACATGAGAATCG	235714	67910	CTGTCCACTAACCTTTCAGG	280301	112497	ATCACGGTGAATGGGGTATC
191128	23324	GAGGCCGAGACATGAGAATC	235715	67911	GCTGTCCACTAACCTTTCAG	280302	112498	CATCACGGTGAATGGGGTAT
191129	23325	GGAGGCCGAGACATGAGAAT	235716	67912	GGCTGTCCACTAACCTTTCA	280303	112499	ACATCACGGTGAATGGGGTA
191130	23326	GGGAGGCCGAGACATGAGAA	235717	67913	TGGCTGTCCACTAACCTTTC	280304	112500	CACATCACGGTGAATGGGGT

191131	23327	CGGGAGGCCGAGACATGAGA	235718	67914	ATGGCTGTCCACTAACCTTT	280305	112501	TCACATCACGGTGAATGGGG
191132	23328	TCGGGAGGCCGAGACATGAG	235719	67915	CATGGCTGTCCACTAACCTT	280306	112502	ATCACATCACGGTGAATGGG
191133	23329	CTCGGGAGGCCGAGACATGA	235720	67916	GCATGGCTGTCCACTAACCT	280307	112503	AATCACATCACGGTGAATGG
191134	23330	GCTCGGGAGGCCGAGACATG	235721	67917	TGCATGGCTGTCCACTAACC	280308	112504	TAATCACATCACGGTGAATG
191135	23331	TGCTCGGGAGGCCGAGACAT	235722	67918	GTGCATGGCTGTCCACTAAC	280309	112505	ATAATCACATCACGGTGAAT
191136	23332	CTGCTCGGGAGGCCGAGACA	235723	67919	TGTGCATGGCTGTCCACTAA	280310	112506	AATAATCACATCACGGTGAA
191137	23333	GCTGCTCGGGAGGCCGAGAC	235724	67920	CTGTGCATGGCTGTCCACTA	280311	112507	CAATAATCACATCACGGTGA
191138	23334	TGCTGCTCGGGAGGCCGAGA	235725	67921	GCTGTGCATGGCTGTCCACT	280312	112508	GCAATAATCACATCACGGTG
191139	23335	TTGCTGCTCGGGAGGCCGAG	235726	67922	TGCTGTGCATGGCTGTCCAC	280313	112509	TGCAATAATCACATCACGGT
191140	23336	CTTGCTGCTCGGGAGGCCGA	235727	67923	CTGCTGTGCATGGCTGTCCA	280314	112510	GTGCAATAATCACATCACGG
191141	23337	TCTTGCTGCTCGGGAGGCCG	235728	67924	CCTGCTGTGCATGGCTGTCC	280315	112511	TGTGCAATAATCACATCACG
191142	23338	GTCTTGCTGCTCGGGAGGCC	235729	67925	GCCTGCTGTGCATGGCTGTC	280316	112512	TTGTGCAATAATCACATCAC
191143	23339	AGTCTTGCTGCTCGGGAGGC	235730	67926	GGCCTGCTGTGCATGGCTGT	280317	112513	ATTGTGCAATAATCACATCA
191144	23340	TAGTCTTGCTGCTCGGGAGG	235731	67927	GGGCCTGCTGTGCATGGCTG	280318	112514	CATTGTGCAATAATCACATC
191145	23341	GTAGTCTTGCTGCTCGGGAG	235732	67928	TGGGCCTGCTGTGCATGGCT	280319	112515	ACATTGTGCAATAATCACAT
191146	23342	TGTAGTCTTGCTGCTCGGGA	235733	67929	CTGGGCCTGCTGTGCATGGC	280320	112516	TACATTGTGCAATAATCACA
191147	23343	CTGTAGTCTTGCTGCTCGGG	235734	67930	TCTGGGCCTGCTGTGCATGG	280321	112517	ATACATTGTGCAATAATCAC
191148	23344	CCTGTAGTCTTGCTGCTCGG	235735	67931	ATCTGGGCCTGCTGTGCATG	280322	112518	CATACATTGTGCAATAATCA
191149	23345	ACCTGTAGTCTTGCTGCTCG	235736	67932	GATCTGGGCCTGCTGTGCAT	280323	112519	ACATACATTGTGCAATAATC
191150	23346	CACCTGTAGTCTTGCTGCTC	235737	67933	TGATCTGGGCCTGCTGTGCA	280324	112520	GACATACATTGTGCAATAAT
191151	23347	GCACCTGTAGTCTTGCTGCT	235738	67934	GTGATCTGGGCCTGCTGTGC	280325	112521	AGACATACATTGTGCAATAA
191152	23348	CGCACCTGTAGTCTTGCTGC	235739	67935	AGTGATCTGGGCCTGCTGTG	280326	112522	CAGACATACATTGTGCAATA
191153	23349	GCGCACCTGTAGTCTTGCTG	235740	67936	CAGTGATCTGGGCCTGCTGT	280327	112523	ACAGACATACATTGTGCAAT
191154	23350	TGCGCACCTGTAGTCTTGCT	235741	67937	GCAGTGATCTGGGCCTGCTG	280328	112524	TACAGACATACATTGTGCAA
191155	23351	GTGCGCACCTGTAGTCTTGC	235742	67938	TGCAGTGATCTGGGCCTGCT	280329	112525	ATACAGACATACATTGTGCA
191156	23352	GGTGCGCACCTGTAGTCTTG	235743	67939	TTGCAGTGATCTGGGCCTGC	280330	112526	GATACAGACATACATTGTGC
191157	23353	TGGTGCGCACCTGTAGTCTT	235744	67940	CTTGCAGTGATCTGGGCCTG	280331	112527	AGATACAGACATACATTGTG
191158	23354	GTGGTGCGCACCTGTAGTCT	235745	67941	GCTTGCAGTGATCTGGGCCT	280332	112528	TAGATACAGACATACATTGT
191159	23355	GGTGGTGCGCACCTGTAGTC	235746	67942	GGCTTGCAGTGATCTGGGCC	280333	112529	TTAGATACAGACATACATTG
191160	23356	TGGTGGTGCGCACCTGTAGT	235747	67943	TGGCTTGCAGTGATCTGGGC	280334	112530	TTTAGATACAGACATACATT
191161	23357	ATGGTGGTGCGCACCTGTAG	235748	67944	TTGGCTTGCAGTGATCTGGG	280335	112531	ATTTAGATACAGACATACAT
191162	23358	CATGGTGGTGCGCACCTGTA	235749	67945	CTTGGCTTGCAGTGATCTGG	280336	112532	TATTTAGATACAGACATACA
191163	23359	GCATGGTGGTGCGCACCTGT	235750	67946	CCTTGGCTTGCAGTGATCTG	280337	112533	ATATTTAGATACAGACATAC
191164	23360	GGCATGGTGGTGCGCACCTG	235751	67947	CCCTTGGCTTGCAGTGATCT	280338	112534	GATATTTAGATACAGACATA
191165	23361	GGGCATGGTGGTGCGCACCT	235752	67948	CCCCTTGGCTTGCAGTGATC	280339	112535	AGATATTTAGATACAGACAT
191166	23362	CGGGCATGGTGGTGCGCACC	235753	67949	ACCCCTTGGCTTGCAGTGAT	280340	112536	GAGATATTTAGATACAGACA
191167	23363	TCGGGCATGGTGGTGCGCAC	235754	67950	CACCCCTTGGCTTGCAGTGA	280341	112537	TGAGATATTTAGATACAGAC
191168	23364	GTCGGGCATGGTGGTGCGCA	235755	67951	CCACCCCTTGGCTTGCAGTG	280342	112538	ATGAGATATTTAGATACAGA
191169	23365	AGTCGGGCATGGTGGTGCGC	235756	67952	GCCACCCCTTGGCTTGCAGT	280343	112539	CATGAGATATTTAGATACAG
191170	23366	TAGTCGGGCATGGTGGTGCG	235757	67953	CGCCACCCCTTGGCTTGCAG	280344	112540	ACATGAGATATTTAGATACA
191171	23367	TTAGTCGGGCATGGTGGTGC	235758	67954	CCGCCACCCCTTGGCTTGCA	280345	112541	TACATGAGATATTTAGATAC
191172	23368	ATTAGTCGGGCATGGTGGTG	235759	67955	CCCGCCACCCCTTGGCTTGC	280346	112542	GTACATGAGATATTTAGATA
191173	23369	AATTAGTCGGGCATGGTGGT	235760	67956	TCCCGCCACCCCTTGGCTTG	280347	112543	GGTACATGAGATATTTAGAT
191174	23370	AAATTAGTCGGGCATGGTGG	235761	67957	TTCCCGCCACCCCTTGGCTT	280348	112544	GGGTACATGAGATATTTAGA
191175	23371	AAAATTAGTCGGGCATGGTG	235762	67958	GTTCCCGCCACCCCTTGGCT	280349	112545	GGGGTACATGAGATATTTAG
191176	23372	AAAAATTAGTCGGGCATGGT	235763	67959	TGTTCCCGCCACCCCTTGGC	280350	112546	TGGGGTACATGAGATATTTA
191177	23373	CAAAAATTAGTCGGGCATGG	235764	67960	CTGTTCCCGCCACCCCTTGG	280351	112547	GTGGGGTACATGAGATATTT
191178	23374	ACAAAAATTAGTCGGGCATG	235765	67961	ACTGTTCCCGCCACCCCTTG	280352	112548	TGTGGGGTACATGAGATATT
191179	23375	TACAAAAATTAGTCGGGCAT	235766	67962	AACTGTTCCCGCCACCCCTT	280353	112549	TTGTGGGGTACATGAGATAT
191180	23376	ATACAAAAATTAGTCGGGCA	235767	67963	AAACTGTTCCCGCCACCCCT	280354	112550	CTTGTGGGGTACATGAGATA
191181	23377	AATACAAAAATTAGTCGGGC	235768	67964	CAAACTGTTCCCGCCACCCC	280355	112551	ACTTGTGGGGTACATGAGAT
191182	23378	TAATACAAAAATTAGTCGGG	235769	67965	GCAAACTGTTCCCGCCACCC	280356	112552	TACTTGTGGGGTACATGAGA
191183	23379	ATAATACAAAAATTAGTCGG	235770	67966	TGCAAACTGTTCCCGCCACC	280357	112553	ATACTTGTGGGGTACATGAG
191184	23380	AATAATACAAAAATTAGTCG	235771	67967	ATGCAAACTGTTCCCGCCAC	280358	112554	TATACTTGTGGGGTACATGA
191185	23381	TAATAATACAAAAATTAGTC	235772	67968	GATGCAAACTGTTCCCGCCA	280359	112555	ATATACTTGTGGGGTACATG
191186	23382	CTAATAATACAAAAATTAGT	235773	67969	GGATGCAAACTGTTCCCGCC	280360	112556	TATATACTTGTGGGGTACAT
191187	23383	ACTAATAATACAAAAATTAG	235774	67970	TGGATGCAAACTGTTCCCGC	280361	112557	GTATATACTTGTGGGGTACA
191188	23384	TACTAATAATACAAAAATTA	235775	67971	CTGGATGCAAACTGTTCCCG	280362	112558	TGTATATACTTGTGGGGTAC
191189	23385	CTACTAATAATACAAAAATT	235776	67972	TCTGGATGCAAACTGTTCCC	280363	112559	GTGTATATACTTGTGGGGTA
191190	23386	TCTACTAATAATACAAAAAT	235777	67973	TTCTGGATGCAAACTGTTCC	280364	112560	GGTGTATATACTTGTGGGGT
191191	23387	CTCTACTAATAATACAAAAA	235778	67974	ATTCTGGATGCAAACTGTTC	280365	112561	AGGTGTATATACTTGTGGGG
191192	23388	TCTCTACTAATAATACAAAA	235779	67975	AATTCTGGATGCAAACTGTT	280366	112562	TAGGTGTATATACTTGTGGG
191193	23389	GTCTCTACTAATAATACAAA	235780	67976	CAATTCTGGATGCAAACTGT	280367	112563	GTAGGTGTATATACTTGTGG
191194	23390	CGTCTCTACTAATAATACAA	235781	67977	GCAATTCTGGATGCAAACTG	280368	112564	AGTAGGTGTATATACTTGTG
191195	23391	CCGTCTCTACTAATAATACA	235782	67978	TGCAATTCTGGATGCAAACT	280369	112565	TAGTAGGTGTATATACTTGT
191196	23392	CCCGTCTCTACTAATAATAC	235783	67979	TTGCAATTCTGGATGCAAAC	280370	112566	ATAGTAGGTGTATATACTTG
191197	23393	CCCCGTCTCTACTAATAATA	235784	67980	TTTGCAATTCTGGATGCAAA	280371	112567	CATAGTAGGTGTATATACTT
191198	23394	CCCCCGTCTCTACTAATAAT	235785	67981	CTTTGCAATTCTGGATGCAA	280372	112568	ACATAGTAGGTGTATATACT
191199	23395	ACCCCCGTCTCTACTAATAA	235786	67982	TCTTTGCAATTCTGGATGCA	280373	112569	TACATAGTAGGTGTATATAC
191200	23396	AACCCCCGTCTCTACTAATA	235787	67983	TTCTTTGCAATTCTGGATGC	280374	112570	GTACATAGTAGGTGTATATA
191201	23397	AAACCCCCGTCTCTACTAAT	235788	67984	TTTCTTTGCAATTCTGGATG	280375	112571	GGTACATAGTAGGTGTATAT
191202	23398	GAAACCCCCGTCTCTACTAA	235789	67985	ATTTCTTTGCAATTCTGGAT	280376	112572	GGGTACATAGTAGGTGTATA

191203	23399	TGAAACCCCCGTCTCTACTA	235790	67986	AATTTCTTTGCAATTCTGGA	280377	112573	TGGGTACATAGTAGGTGTAT
191204	23400	GTGAAACCCCCGTCTCTACT	235791	67987	AAATTTCTTTGCAATTCTGG	280378	112574	ATGGGTACATAGTAGGTGTA
191205	23401	AGTGAAACCCCCGTCTCTAC	235792	67988	AAAATTTCTTTGCAATTCTG	280379	112575	TATGGGTACATAGTAGGTGT
191206	23402	GAGTGAAACCCCCGTCTCTA	235793	67989	TAAAATTTCTTTGCAATTCT	280380	112576	ATATGGGTACATAGTAGGTG
191207	23403	AGAGTGAAACCCCCGTCTCT	235794	67990	TTAAAATTTCTTTGCAATTC	280381	112577	TATATGGGTACATAGTAGGT
191208	23404	CAGAGTGAAACCCCCGTCTC	235795	67991	TTTAAAATTTCTTTGCAATT	280382	112578	TTATATGGGTACATAGTAGG
191209	23405	ACAGAGTGAAACCCCCGTCT	235796	67992	ATTTAAAATTTCTTTGCAAT	280383	112579	TTTATATGGGTACATAGTAG
191210	23406	AACAGAGTGAAACCCCCGTC	235797	67993	TATTTAAAATTTCTTTGCAA	280384	112580	ATTTATATGGGTACATAGTA
191211	23407	CAACAGAGTGAAACCCCCGT	235798	67994	GTATTTAAAATTTCTTTGCA	280385	112581	AATTTATATGGGTACATAGT
191212	23408	CCAACAGAGTGAAACCCCCG	235799	67995	TGTATTTAAAATTTCTTTGC	280386	112582	AAATTTATATGGGTACATAG
191213	23409	GCCAACAGAGTGAAACCCCC	235800	67996	ATGTATTTAAAATTTCTTTG	280387	112583	TAAATTTATATGGGTACATA
191214	23410	GGCCAACAGAGTGAAACCCC	235801	67997	AATGTATTTAAAATTTCTTT	280388	112584	TTAAATTTATATGGGTACAT
191215	23411	TGGCCAACAGAGTGAAACCC	235802	67998	TAATGTATTTAAAATTTCTT	280389	112585	TTTAAATTTATATGGGTACA
191216	23412	CTGGCCAACAGAGTGAAACC	235803	67999	ATAATGTATTTAAAATTTCT	280390	112586	TTTTAAATTTATATGGGTAC
191217	23413	CCTGGCCAACAGAGTGAAAC	235804	68000	AATAATGTATTTAAAATTTC	280391	112587	ATTTTAAATTTATATGGGTA
191218	23414	GCCTGGCCAACAGAGTGAAA	235805	68001	CAATAATGTATTTAAAATTT	280392	112588	AATTTTAAATTTATATGGGT
191219	23415	AGCCTGGCCAACAGAGTGAA	235806	68002	ACAATAATGTATTTAAAATT	280393	112589	TAATTTTAAATTTATATGGG
191220	23416	CAGCCTGGCCAACAGAGTGA	235807	68003	GACAATAATGTATTTAAAAT	280394	112590	TTAATTTTAAATTTATATGG
191221	23417	CCAGCCTGGCCAACAGAGTG	235808	68004	AGACAATAATGTATTTAAAA	280395	112591	TTTAATTTTAAATTTATATG
191222	23418	ACCAGCCTGGCCAACAGAGT	235809	68005	AAGACAATAATGTATTTAAA	280396	112592	TTTTAATTTTAAATTTATAT
191223	23419	GACCAGCCTGGCCAACAGAG	235810	68006	TAAGACAATAATGTATTTAA	280397	112593	TTTTTAATTTTAAATTTATA
191224	23420	AGACCAGCCTGGCCAACAGA	235811	68007	CTAAGACAATAATGTATTTA	280398	112594	TTTTTTAATTTTAAATTTAT
191225	23421	GAGACCAGCCTGGCCAACAG	235812	68008	TCTAAGACAATAATGTATTT	280399	112595	ATTTTTTAATTTTAAATTTA
191226	23422	TGAGACCAGCCTGGCCAACA	235813	68009	GTCTAAGACAATAATGTATT	280400	112596	AATTTTTTAATTTTAAATTT
191227	23423	TTGAGACCAGCCTGGCCAAC	235814	68010	AGTCTAAGACAATAATGTAT	280401	112597	TAATTTTTTAATTTTAAATT
191228	23424	TTTGAGACCAGCCTGGCCAA	235815	68011	CAGTCTAAGACAATAATGTA	280402	112598	ATAATTTTTTAATTTTAAAT
191229	23425	GTTTGAGACCAGCCTGGCCA	235816	68012	ACAGTCTAAGACAATAATGT	280403	112599	TATAATTTTTTAATTTTAAA
191230	23426	AGTTTGAGACCAGCCTGGCC	235817	68013	GACAGTCTAAGACAATAATG	280404	112600	TTATAATTTTTTAATTTTAA
191231	23427	GAGTTTGAGACCAGCCTGGC	235818	68014	TGACAGTCTAAGACAATAAT	280405	112601	TTTATAATTTTTTAATTTTA
191232	23428	GGAGTTTGAGACCAGCCTGG	235819	68015	CTGACAGTCTAAGACAATAA	280406	112602	TTTTATAATTTTTTAATTTT
191233	23429	AGGAGTTTGAGACCAGCCTG	235820	68016	ACTGACAGTCTAAGACAATA	280407	112603	GTTTTATAATTTTTTAATTT
191234	23430	CAGGAGTTTGAGACCAGCCT	235821	68017	TACTGACAGTCTAAGACAAT	280408	112604	TGTTTTATAATTTTTTAATT
191235	23431	TCAGGAGTTTGAGACCAGCC	235822	68018	TTACTGACAGTCTAAGACAA	280409	112605	TTGTTTTATAATTTTTTAAT
191236	23432	GTCAGGAGTTTGAGACCAGC	235823	68019	TTTACTGACAGTCTAAGACA	280410	112606	TTTGTTTTATAATTTTTTAA
191237	23433	GGTCAGGAGTTTGAGACCAG	235824	68020	CTTTACTGACAGTCTAAGAC	280411	112607	TTTTGTTTTATAATTTTTTA
191238	23434	AGGTCAGGAGTTTGAGACCA	235825	68021	ACTTTACTGACAGTCTAAGA	280412	112608	TTTTTGTTTTATAATTTTTT
191239	23435	GAGGTCAGGAGTTTGAGACC	235826	68022	TACTTTACTGACAGTCTAAG	280413	112609	ATTTTTGTTTTATAATTTTT
191240	23436	TGAGGTCAGGAGTTTGAGAC	235827	68023	TTACTTTACTGACAGTCTAA	280414	112610	TATTTTTGTTTTATAATTTT
191241	23437	CTGAGGTCAGGAGTTTGAGA	235828	68024	TTTACTTTACTGACAGTCTA	280415	112611	TTATTTTTGTTTTATAATTT
191242	23438	CCTGAGGTCAGGAGTTTGAG	235829	68025	CTTTACTTTACTGACAGTCT	280416	112612	TTTATTTTTGTTTTATAATT
191243	23439	ACCTGAGGTCAGGAGTTTGA	235830	68026	GCTTTACTTTACTGACAGTC	280417	112613	ATTTATTTTTGTTTTATAAT
191244	23440	CACCTGAGGTCAGGAGTTTG	235831	68027	GGCTTTACTTTACTGACAGT	280418	112614	TATTTATTTTTGTTTTATAA
191245	23441	TCACCTGAGGTCAGGAGTTT	235832	68028	AGGCTTTACTTTACTGACAG	280419	112615	TTATTTATTTTTGTTTTATA
191246	23442	ATCACCTGAGGTCAGGAGTT	235833	68029	GAGGCTTTACTTTACTGACA	280420	112616	CTTATTTATTTTTGTTTTAT
191247	23443	GATCACCTGAGGTCAGGAGT	235834	68030	TGAGGCTTTACTTTACTGAC	280421	112617	ACTTATTTATTTTTGTTTTA
191248	23444	GGATCACCTGAGGTCAGGAG	235835	68031	ATGAGGCTTTACTTTACTGA	280422	112618	TACTTATTTATTTTTGTTTT
191249	23445	TGGATCACCTGAGGTCAGGA	235836	68032	AATGAGGCTTTACTTTACTG	280423	112619	TTACTTATTTATTTTTGTTT
191250	23446	GTGGATCACCTGAGGTCAGG	235837	68033	TAATGAGGCTTTACTTTACT	280424	112620	TTTACTTATTTATTTTTGTT
191251	23447	GGTGGATCACCTGAGGTCAG	235838	68034	TTAATGAGGCTTTACTTTAC	280425	112621	ATTTACTTATTTATTTTTGT
191252	23448	GGGTGGATCACCTGAGGTCA	235839	68035	ATTAATGAGGCTTTACTTTA	280426	112622	AATTTACTTATTTATTTTTG
191253	23449	CGGGTGGATCACCTGAGGTC	235840	68036	AATTAATGAGGCTTTACTTT	280427	112623	TAATTTACTTATTTATTTTT
191254	23450	GCGGGTGGATCACCTGAGGT	235841	68037	AAATTAATGAGGCTTTACTT	280428	112624	TTAATTTACTTATTTATTTT
191255	23451	GGCGGGTGGATCACCTGAGG	235842	68038	CAAATTAATGAGGCTTTACT	280429	112625	TTTAATTTACTTATTTATTT
191256	23452	AGGCGGGTGGATCACCTGAG	235843	68039	TCAAATTAATGAGGCTTTAC	280430	112626	TTTTAATTTACTTATTTATT
191257	23453	GAGGCGGGTGGATCACCTGA	235844	68040	CTCAAATTAATGAGGCTTTA	280431	112627	ATTTTAATTTACTTATTTAT
191258	23454	TGAGGCGGGTGGATCACCTG	235845	68041	ACTCAAATTAATGAGGCTTT	280432	112628	CATTTTAATTTACTTATTTA
191259	23455	CTGAGGCGGGTGGATCACCT	235846	68042	CACTCAAATTAATGAGGCTT	280433	112629	ACATTTTAATTTACTTATTT
191260	23456	GCTGAGGCGGGTGGATCACC	235847	68043	CCACTCAAATTAATGAGGCT	280434	112630	TACATTTTAATTTACTTATT
191261	23457	GGCTGAGGCGGGTGGATCAC	235848	68044	CCCACTCAAATTAATGAGGC	280435	112631	CTACATTTTAATTTACTTAT
191262	23458	AGGCTGAGGCGGGTGGATCA	235849	68045	GCCCACTCAAATTAATGAGG	280436	112632	CCTACATTTTAATTTACTTA
191263	23459	GAGGCTGAGGCGGGTGGATC	235850	68046	GGCCCACTCAAATTAATGAG	280437	112633	GCCTACATTTTAATTTACTT
191264	23460	GGAGGCTGAGGCGGGTGGAT	235851	68047	TGGCCCACTCAAATTAATGA	280438	112634	AGCCTACATTTTAATTTACT
191265	23461	GGGAGGCTGAGGCGGGTGGA	235852	68048	TTGGCCCACTCAAATTAATG	280439	112635	CAGCCTACATTTTAATTTAC
191266	23462	TGGGAGGCTGAGGCGGGTGG	235853	68049	CTTGGCCCACTCAAATTAAT	280440	112636	CCAGCCTACATTTTAATTTA
191267	23463	TTGGGAGGCTGAGGCGGGTG	235854	68050	TCTTGGCCCACTCAAATTAA	280441	112637	TCCAGCCTACATTTTAATTT
191268	23464	TTTGGGAGGCTGAGGCGGGT	235855	68051	ATCTTGGCCCACTCAAATTA	280442	112638	GTCCAGCCTACATTTTAATT
191269	23465	CTTTGGGAGGCTGAGGCGGG	235856	68052	TATCTTGGCCCACTCAAATT	280443	112639	TGTCCAGCCTACATTTTAAT
191270	23466	ACTTTGGGAGGCTGAGGCGG	235857	68053	TTATCTTGGCCCACTCAAAT	280444	112640	GTGTCCAGCCTACATTTTAA
191271	23467	CACTTTGGGAGGCTGAGGCG	235858	68054	GTTATCTTGGCCCACTCAAA	280445	112641	GGTGTCCAGCCTACATTTTA
191272	23468	GCACTTTGGGAGGCTGAGGC	235859	68055	AGTTATCTTGGCCCACTCAA	280446	112642	CGGTGTCCAGCCTACATTTT
191273	23469	AGCACTTTGGGAGGCTGAGG	235860	68056	GAGTTATCTTGGCCCACTCA	280447	112643	ACGGTGTCCAGCCTACATTT
191274	23470	CAGCACTTTGGGAGGCTGAG	235861	68057	TGAGTTATCTTGGCCCACTC	280448	112644	CACGGTGTCCAGCCTACATT

191275	23471	CCAGCACTTTGGGAGGCTGA	235862	68058	TTGAGTTATCTTGGCCCACT	280449	112645	CCACGGTGTCCAGCCTACAT
191276	23472	CCCAGCACTTTGGGAGGCTG	235863	68059	CTTGAGTTATCTTGGCCCAC	280450	112646	ACCACGGTGTCCAGCCTACA
191277	23473	TCCCAGCACTTTGGGAGGCT	235864	68060	GCTTGAGTTATCTTGGCCCA	280451	112647	AACCACGGTGTCCAGCCTAC
191278	23474	ATCCCAGCACTTTGGGAGGC	235865	68061	TGCTTGAGTTATCTTGGCCC	280452	112648	GAACCACGGTGTCCAGCCTA
191279	23475	AATCCCAGCACTTTGGGAGG	235866	68062	CTGCTTGAGTTATCTTGGCC	280453	112649	TGAACCACGGTGTCCAGCCT
191280	23476	TAATCCCAGCACTTTGGGAG	235867	68063	ACTGCTTGAGTTATCTTGGC	280454	112650	GTGAACCACGGTGTCCAGCC
191281	23477	GTAATCCCAGCACTTTGGGA	235868	68064	CACTGCTTGAGTTATCTTGG	280455	112651	CGTGAACCACGGTGTCCAGC
191282	23478	TGTAATCCCAGCACTTTGGG	235869	68065	TCACTGCTTGAGTTATCTTG	280456	112652	GCGTGAACCACGGTGTCCAG
191283	23479	CTGTAATCCCAGCACTTTGG	235870	68066	CTCACTGCTTGAGTTATCTT	280457	112653	GGCGTGAACCACGGTGTCCA
191284	23480	CCTGTAATCCCAGCACTTTG	235871	68067	TCTCACTGCTTGAGTTATCT	280458	112654	AGGCGTGAACCACGGTGTCC
191285	23481	GCCTGTAATCCCAGCACTTT	235872	68068	ATCTCACTGCTTGAGTTATC	280459	112655	CAGGCGTGAACCACGGTGTC
191286	23482	TGCCTGTAATCCCAGCACTT	235873	68069	TATCTCACTGCTTGAGTTAT	280460	112656	ACAGGCGTGAACCACGGTGT
191287	23483	ATGCCTGTAATCCCAGCACT	235874	68070	TTATCTCACTGCTTGAGTTA	280461	112657	TACAGGCGTGAACCACGGTG
191288	23484	CATGCCTGTAATCCCAGCAC	235875	68071	ATTATCTCACTGCTTGAGTT	280462	112658	TTACAGGCGTGAACCACGGT
191289	23485	TCATGCCTGTAATCCCAGCA	235876	68072	CATTATCTCACTGCTTGAGT	280463	112659	ATTACAGGCGTGAACCACGG
191290	23486	CTCATGCCTGTAATCCCAGC	235877	68073	CCATTATCTCACTGCTTGAG	280464	112660	GATTACAGGCGTGAACCACG
191291	23487	GCTCATGCCTGTAATCCCAG	235878	68074	GCCATTATCTCACTGCTTGA	280465	112661	GGATTACAGGCGTGAACCAC
191292	23488	GGCTCATGCCTGTAATCCCA	235879	68075	GGCCATTATCTCACTGCTTG	280466	112662	GGGATTACAGGCGTGAACCA
191293	23489	TGGCTCATGCCTGTAATCCC	235880	68076	TGGCCATTATCTCACTGCTT	280467	112663	TGGGATTACAGGCGTGAACC
191294	23490	GTGGCTCATGCCTGTAATCC	235881	68077	CTGGCCATTATCTCACTGCT	280468	112664	CTGGGATTACAGGCGTGAAC
191295	23491	GGTGGCTCATGCCTGTAATC	235882	68078	TCTGGCCATTATCTCACTGC	280469	112665	ACTGGGATTACAGGCGTGAA
191296	23492	TGGTGGCTCATGCCTGTAAT	235883	68079	GTCTGGCCATTATCTCACTG	280470	112666	CACTGGGATTACAGGCGTGA
191297	23493	ATGGTGGCTCATGCCTGTAA	235884	68080	TGTCTGGCCATTATCTCACT	280471	112667	GCACTGGGATTACAGGCGTG
191298	23494	CATGGTGGCTCATGCCTGTA	235885	68081	GTGTCTGGCCATTATCTCAC	280472	112668	AGCACTGGGATTACAGGCGT
191299	23495	GCATGGTGGCTCATGCCTGT	235886	68082	CGTGTCTGGCCATTATCTCA	280473	112669	AAGCACTGGGATTACAGGCG
191300	23496	GGCATGGTGGCTCATGCCTG	235887	68083	CCGTGTCTGGCCATTATCTC	280474	112670	AAAGCACTGGGATTACAGGC
191301	23497	GGGCATGGTGGCTCATGCCT	235888	68084	ACCGTGTCTGGCCATTATCT	280475	112671	CAAAGCACTGGGATTACAGG
191302	23498	TGGGCATGGTGGCTCATGCC	235889	68085	CACCGTGTCTGGCCATTATC	280476	112672	ACAAAGCACTGGGATTACAG
191303	23499	CTGGGCATGGTGGCTCATGC	235890	68086	CCACCGTGTCTGGCCATTAT	280477	112673	CACAAAGCACTGGGATTACA
191304	23500	GCTGGGCATGGTGGCTCATG	235891	68087	GCCACCGTGTCTGGCCATTA	280478	112674	TCACAAAGCACTGGGATTAC
191305	23501	GGCTGGGCATGGTGGCTCAT	235892	68088	AGCCACCGTGTCTGGCCATT	280479	112675	CTCACAAAGCACTGGGATTA
191306	23502	TGGCTGGGCATGGTGGCTCA	235893	68089	GAGCCACCGTGTCTGGCCAT	280480	112676	CCTCACAAAGCACTGGGATT
191307	23503	CTGGCTGGGCATGGTGGCTC	235894	68090	TGAGCCACCGTGTCTGGCCA	280481	112677	GCCTCACAAAGCACTGGGAT
191308	23504	GCTGGCTGGGCATGGTGGCT	235895	68091	GTGAGCCACCGTGTCTGGCC	280482	112678	AGCCTCACAAAGCACTGGGA
191309	23505	TGCTGGCTGGGCATGGTGGC	235896	68092	CGTGAGCCACCGTGTCTGGC	280483	112679	CAGCCTCACAAAGCACTGGG
191310	23506	ATGCTGGCTGGGCATGGTGG	235897	68093	GCGTGAGCCACCGTGTCTGG	280484	112680	TCAGCCTCACAAAGCACTGG
191311	23507	GATGCTGGCTGGGCATGGTG	235898	68094	GGCGTGAGCCACCGTGTCTG	280485	112681	CTCAGCCTCACAAAGCACTG
191312	23508	AGATGCTGGCTGGGCATGGT	235899	68095	AGGCGTGAGCCACCGTGTCT	280486	112682	CCTCAGCCTCACAAAGCACT
191313	23509	AAGATGCTGGCTGGGCATGG	235900	68096	CAGGCGTGAGCCACCGTGTC	280487	112683	ACCTCAGCCTCACAAAGCAC
191314	23510	AAAGATGCTGGCTGGGCATG	235901	68097	ACAGGCGTGAGCCACCGTGT	280488	112684	CACCTCAGCCTCACAAAGCA
191315	23511	GAAAGATGCTGGCTGGGCAT	235902	68098	TACAGGCGTGAGCCACCGTG	280489	112685	TCACCTCAGCCTCACAAAGC
191316	23512	TGAAAGATGCTGGCTGGGCA	235903	68099	TTACAGGCGTGAGCCACCGT	280490	112686	CTCACCTCAGCCTCACAAAG
191317	23513	ATGAAAGATGCTGGCTGGGC	235904	68100	ATTACAGGCGTGAGCCACCG	280491	112687	TCTCACCTCAGCCTCACAAA
191318	23514	AATGAAAGATGCTGGCTGGG	235905	68101	GATTACAGGCGTGAGCCACC	280492	112688	CTCTCACCTCAGCCTCACAA
191319	23515	AAATGAAAGATGCTGGCTGG	235906	68102	GGATTACAGGCGTGAGCCAC	280493	112689	TCTCTCACCTCAGCCTCACA
191320	23516	AAAATGAAAGATGCTGGCTG	235907	68103	GGGATTACAGGCGTGAGCCA	280494	112690	TTCTCTCACCTCAGCCTCAC
191321	23517	AAAAATGAAAGATGCTGGCT	235908	68104	TGGGATTACAGGCGTGAGCC	280495	112691	ATTCTCTCACCTCAGCCTCA
191322	23518	GAAAAATGAAAGATGCTGGC	235909	68105	CTGGGATTACAGGCGTGAGC	280496	112692	GATTCTCTCACCTCAGCCTC
191323	23519	AGAAAAATGAAAGATGCTGG	235910	68106	GCTGGGATTACAGGCGTGAG	280497	112693	TGATTCTCTCACCTCAGCCT
191324	23520	CAGAAAAATGAAAGATGCTG	235911	68107	TGCTGGGATTACAGGCGTGA	280498	112694	GTGATTCTCTCACCTCAGCC
191325	23521	ACAGAAAAATGAAAGATGCT	235912	68108	GTGCTGGGATTACAGGCGTG	280499	112695	AGTGATTCTCTCACCTCAGC
191326	23522	GACAGAAAAATGAAAGATGC	235913	68109	AGTGCTGGGATTACAGGCGT	280500	112696	AAGTGATTCTCTCACCTCAG
191327	23523	AGACAGAAAAATGAAAGATG	235914	68110	AAGTGCTGGGATTACAGGCG	280501	112697	CAAGTGATTCTCTCACCTCA
191328	23524	CAGACAGAAAAATGAAAGAT	235915	68111	AAAGTGCTGGGATTACAGGC	280502	112698	TCAAGTGATTCTCTCACCTC
191329	23525	GCAGACAGAAAAATGAAAGA	235916	68112	CAAAGTGCTGGGATTACAGG	280503	112699	CTCAAGTGATTCTCTCACCT
191330	23526	AGCAGACAGAAAAATGAAAG	235917	68113	CCAAAGTGCTGGGATTACAG	280504	112700	GCTCAAGTGATTCTCTCACC
191331	23527	AAGCAGACAGAAAAATGAAA	235918	68114	TCCAAAGTGCTGGGATTACA	280505	112701	GGCTCAAGTGATTCTCTCAC
191332	23528	AAAGCAGACAGAAAAATGAA	235919	68115	TTCCAAAGTGCTGGGATTAC	280506	112702	GGGCTCAAGTGATTCTCTCA
191333	23529	CAAAGCAGACAGAAAAATGA	235920	68116	CTTCCAAAGTGCTGGGATTA	280507	112703	TGGGCTCAAGTGATTCTCTC
191334	23530	CCAAAGCAGACAGAAAAATG	235921	68117	CCTTCCAAAGTGCTGGGATT	280508	112704	CTGGGCTCAAGTGATTCTCT
191335	23531	GCCAAAGCAGACAGAAAAAT	235922	68118	GCCTTCCAAAGTGCTGGGAT	280509	112705	CCTGGGCTCAAGTGATTCTC
191336	23532	GGCCAAAGCAGACAGAAAAA	235923	68119	GGCCTTCCAAAGTGCTGGGA	280510	112706	TCCTGGGCTCAAGTGATTCT
191337	23533	GGGCCAAAGCAGACAGAAAA	235924	68120	GGGCCTTCCAAAGTGCTGGG	280511	112707	CTCCTGGGCTCAAGTGATTC
191338	23534	AGGGCCAAAGCAGACAGAAA	235925	68121	TGGGCCTTCCAAAGTGCTGG	280512	112708	ACTCCTGGGCTCAAGTGATT
191339	23535	AAGGGCCAAAGCAGACAGAA	235926	68122	CTGGGCCTTCCAAAGTGCTG	280513	112709	AACTCCTGGGCTCAAGTGAT
191340	23536	AAAGGGCCAAAGCAGACAGA	235927	68123	CCTGGGCCTTCCAAAGTGCT	280514	112710	AAACTCCTGGGCTCAAGTGA
191341	23537	GAAAGGGCCAAAGCAGACAG	235928	68124	GCCTGGGCCTTCCAAAGTGC	280515	112711	CAAACTCCTGGGCTCAAGTG
191342	23538	GGAAAGGGCCAAAGCAGACA	235929	68125	TGCCTGGGCCTTCCAAAGTG	280516	112712	TCAAACTCCTGGGCTCAAGT
191343	23539	AGGAAAGGGCCAAAGCAGAC	235930	68126	CTGCCTGGGCCTTCCAAAGT	280517	112713	CTCAAACTCCTGGGCTCAAG
191344	23540	GAGGAAAGGGCCAAAGCAGA	235931	68127	CCTGCCTGGGCCTTCCAAAG	280518	112714	TCTCAAACTCCTGGGCTCAA
191345	23541	AGAGGAAAGGGCCAAAGCAG	235932	68128	TCCTGCCTGGGCCTTCCAAA	280519	112715	GTCTCAAACTCCTGGGCTCA
191346	23542	GAGAGGAAAGGGCCAAAGCA	235933	68129	CTCCTGCCTGGGCCTTCCAA	280520	112716	GGTCTCAAACTCCTGGGCTC

191347	23543	AGAGAGGAAAGGGCCAAAGC	235934	68130	CCTCCTGCCTGGGCCTTCCA	280521	112717	CGGTCTCAAACTCCTGGGCT
191348	23544	GAGAGAGGAAAGGGCCAAAG	235935	68131	TCCTCCTGCCTGGGCCTTCC	280522	112718	CCGGTCTCAAACTCCTGGGC
191349	23545	TGAGAGAGGAAAGGGCCAAA	235936	68132	ATCCTCCTGCCTGGGCCTTC	280523	112719	GCCGGTCTCAAACTCCTGGG
191350	23546	GTGAGAGAGGAAAGGGCCAA	235937	68133	GATCCTCCTGCCTGGGCCTT	280524	112720	GGCCGGTCTCAAACTCCTGG
191351	23547	AGTGAGAGAGGAAAGGGCCA	235938	68134	GGATCCTCCTGCCTGGGCCT	280525	112721	AGGCCGGTCTCAAACTCCTG
191352	23548	CAGTGAGAGAGGAAAGGGCC	235939	68135	GGGATCCTCCTGCCTGGGCC	280526	112722	CAGGCCGGTCTCAAACTCCT
191353	23549	ACAGTGAGAGAGGAAAGGGC	235940	68136	AGGGATCCTCCTGCCTGGGC	280527	112723	CCAGGCCGGTCTCAAACTCC
191354	23550	GACAGTGAGAGAGGAAAGGG	235941	68137	AAGGGATCCTCCTGCCTGGG	280528	112724	CCCAGGCCGGTCTCAAACTC
191355	23551	AGACAGTGAGAGAGGAAAGG	235942	68138	CAAGGGATCCTCCTGCCTGG	280529	112725	ACCCAGGCCGGTCTCAAACT
191356	23552	AAGACAGTGAGAGAGGAAAG	235943	68139	TCAAGGGATCCTCCTGCCTG	280530	112726	CACCCAGGCCGGTCTCAAAC
191357	23553	GAAGACAGTGAGAGAGGAAA	235944	68140	CTCAAGGGATCCTCCTGCCT	280531	112727	TCACCCAGGCCGGTCTCAAA
191358	23554	GGAAGACAGTGAGAGAGGAA	235945	68141	CCTCAAGGGATCCTCCTGCC	280532	112728	GTCACCCAGGCCGGTCTCAA
191359	23555	AGGAAGACAGTGAGAGAGGA	235946	68142	GCCTCAAGGGATCCTCCTGC	280533	112729	TGTCACCCAGGCCGGTCTCA
191360	23556	AAGGAAGACAGTGAGAGAGG	235947	68143	GGCCTCAAGGGATCCTCCTG	280534	112730	ATGTCACCCAGGCCGGTCTC
191361	23557	AAAGGAAGACAGTGAGAGAG	235948	68144	TGGCCTCAAGGGATCCTCCT	280535	112731	TATGTCACCCAGGCCGGTCT
191362	23558	AAAAGGAAGACAGTGAGAGA	235949	68145	CTGGCCTCAAGGGATCCTCC	280536	112732	CTATGTCACCCAGGCCGGTC
191363	23559	GAAAAGGAAGACAGTGAGAG	235950	68146	CCTGGCCTCAAGGGATCCTC	280537	112733	GCTATGTCACCCAGGCCGGT
191364	23560	GGAAAAGGAAGACAGTGAGA	235951	68147	TCCTGGCCTCAAGGGATCCT	280538	112734	CGCTATGTCACCCAGGCCGG
191365	23561	TGGAAAAGGAAGACAGTGAG	235952	68148	TTCCTGGCCTCAAGGGATCC	280539	112735	TCGCTATGTCACCCAGGCCG
191366	23562	ATGGAAAAGGAAGACAGTGA	235953	68149	ATTCCTGGCCTCAAGGGATC	280540	112736	CTCGCTATGTCACCCAGGCC
191367	23563	AATGGAAAAGGAAGACAGTG	235954	68150	AATTCCTGGCCTCAAGGGAT	280541	112737	TCTCGCTATGTCACCCAGGC
191368	23564	AAATGGAAAAGGAAGACAGT	235955	68151	AAATTCCTGGCCTCAAGGGA	280542	112738	GTCTCGCTATGTCACCCAGG
191369	23565	GAAATGGAAAAGGAAGACAG	235956	68152	CAAATTCCTGGCCTCAAGGG	280543	112739	GGTCTCGCTATGTCACCCAG
191370	23566	GGAAATGGAAAAGGAAGACA	235957	68153	TCAAATTCCTGGCCTCAAGG	280544	112740	GGGTCTCGCTATGTCACCCA
191371	23567	TGGAAATGGAAAAGGAAGAC	235958	68154	CTCAAATTCCTGGCCTCAAG	280545	112741	GGGGTCTCGCTATGTCACCC
191372	23568	TTGGAAATGGAAAAGGAAGA	235959	68155	TCTCAAATTCCTGGCCTCAA	280546	112742	TGGGGTCTCGCTATGTCACC
191373	23569	TTTGGAAATGGAAAAGGAAG	235960	68156	GTCTCAAATTCCTGGCCTCA	280547	112743	ATGGGGTCTCGCTATGTCAC
191374	23570	CTTTGGAAATGGAAAAGGAA	235961	68157	GGTCTCAAATTCCTGGCCTC	280548	112744	GATGGGGTCTCGCTATGTCA
191375	23571	ACTTTGGAAATGGAAAAGGA	235962	68158	CGGTCTCAAATTCCTGGCCT	280549	112745	TGATGGGGTCTCGCTATGTC
191376	23572	GACTTTGGAAATGGAAAAGG	235963	68159	CCGGTCTCAAATTCCTGGCC	280550	112746	ATGATGGGGTCTCGCTATGT
191377	23573	TGACTTTGGAAATGGAAAAG	235964	68160	GCCGGTCTCAAATTCCTGGC	280551	112747	GATGATGGGGTCTCGCTATG
191378	23574	CTGACTTTGGAAATGGAAAA	235965	68161	GGCCGGTCTCAAATTCCTGG	280552	112748	TGATGATGGGGTCTCGCTAT
191379	23575	ACTGACTTTGGAAATGGAAA	235966	68162	AGGCCGGTCTCAAATTCCTG	280553	112749	GTGATGATGGGGTCTCGCTA
191380	23576	GACTGACTTTGGAAATGGAA	235967	68163	CAGGCCGGTCTCAAATTCCT	280554	112750	TGTGATGATGGGGTCTCGCT
191381	23577	GGACTGACTTTGGAAATGGA	235968	68164	CCAGGCCGGTCTCAAATTCC	280555	112751	TTGTGATGATGGGGTCTCGC
191382	23578	TGGACTGACTTTGGAAATGG	235969	68165	CCCAGGCCGGTCTCAAATTC	280556	112752	TTTGTGATGATGGGGTCTCG
191383	23579	ATGGACTGACTTTGGAAATG	235970	68166	GCCCAGGCCGGTCTCAAATT	280557	112753	CTTTGTGATGATGGGGTCTC
191384	23580	GATGGACTGACTTTGGAAAT	235971	68167	TGCCCAGGCCGGTCTCAAAT	280558	112754	TCTTTGTGATGATGGGGTCT
191385	23581	AGATGGACTGACTTTGGAAA	235972	68168	TTGCCCAGGCCGGTCTCAAA	280559	112755	TTCTTTGTGATGATGGGGTC
191386	23582	GAGATGGACTGACTTTGGAA	235973	68169	GTTGCCCAGGCCGGTCTCAA	280560	112756	ATTCTTTGTGATGATGGGGT
191387	23583	TGAGATGGACTGACTTTGGA	235974	68170	TGTTGCCCAGGCCGGTCTCA	280561	112757	AATTCTTTGTGATGATGGGG
191388	23584	GTGAGATGGACTGACTTTGG	235975	68171	ATGTTGCCCAGGCCGGTCTC	280562	112758	AAATTCTTTGTGATGATGGG
191389	23585	AGTGAGATGGACTGACTTTG	235976	68172	TATGTTGCCCAGGCCGGTCT	280563	112759	AAAATTCTTTGTGATGATGG
191390	23586	TAGTGAGATGGACTGACTTT	235977	68173	CTATGTTGCCCAGGCCGGTC	280564	112760	AAAAATTCTTTGTGATGATG
191391	23587	ATAGTGAGATGGACTGACTT	235978	68174	GCTATGTTGCCCAGGCCGGT	280565	112761	TAAAAATTCTTTGTGATGAT
191392	23588	AATAGTGAGATGGACTGACT	235979	68175	TGCTATGTTGCCCAGGCCGG	280566	112762	TTAAAAATTCTTTGTGATGA
191393	23589	TAATAGTGAGATGGACTGAC	235980	68176	TTGCTATGTTGCCCAGGCCG	280567	112763	TTTAAAAATTCTTTGTGATG
191394	23590	CTAATAGTGAGATGGACTGA	235981	68177	CTTGCTATGTTGCCCAGGCC	280568	112764	TTTTAAAAATTCTTTGTGAT
191395	23591	GCTAATAGTGAGATGGACTG	235982	68178	TCTTGCTATGTTGCCCAGGC	280569	112765	TTTTTAAAAATTCTTTGTGA
191396	23592	TGCTAATAGTGAGATGGACT	235983	68179	GTCTTGCTATGTTGCCCAGG	280570	112766	ATTTTTAAAAATTCTTTGTG
191397	23593	GTGCTAATAGTGAGATGGAC	235984	68180	GGTCTTGCTATGTTGCCCAG	280571	112767	AATTTTTAAAAATTCTTTGT
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191400	23596	TTTGTGCTAATAGTGAGATG	235987	68183	CGGGGTCTTGCTATGTTGCC	280574	112770	GCTAATTTTTAAAAATTCTT
191401	23597	TTTTGTGCTAATAGTGAGAT	235988	68184	ACGGGGTCTTGCTATGTTGC	280575	112771	AGCTAATTTTTAAAAATTCT
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191403	23599	GTTTTTGTGCTAATAGTGAG	235990	68186	AGACGGGGTCTTGCTATGTT	280577	112773	CCAGCTAATTTTTAAAAATT
191404	23600	AGTTTTTGTGCTAATAGTGA	235991	68187	GAGACGGGGTCTTGCTATGT	280578	112774	CCCAGCTAATTTTTAAAAAT
191405	23601	CAGTTTTTGTGCTAATAGTG	235992	68188	AGAGACGGGGTCTTGCTATG	280579	112775	GCCCAGCTAATTTTTAAAAA
191406	23602	GCAGTTTTTGTGCTAATAGT	235993	68189	TAGAGACGGGGTCTTGCTAT	280580	112776	CGCCCAGCTAATTTTTAAAA
191407	23603	AGCAGTTTTTGTGCTAATAG	235994	68190	TTAGAGACGGGGTCTTGCTA	280581	112777	ACGCCCAGCTAATTTTTAAA
191408	23604	TAGCAGTTTTTGTGCTAATA	235995	68191	TTTAGAGACGGGGTCTTGCT	280582	112778	CACGCCCAGCTAATTTTTAA
191409	23605	CTAGCAGTTTTTGTGCTAAT	235996	68192	TTTTAGAGACGGGGTCTTGC	280583	112779	CCACGCCCAGCTAATTTTTA
191410	23606	TCTAGCAGTTTTTGTGCTAA	235997	68193	ATTTTAGAGACGGGGTCTTG	280584	112780	ACCACGCCCAGCTAATTTTT
191411	23607	CTCTAGCAGTTTTTGTGCTA	235998	68194	TATTTTAGAGACGGGGTCTT	280585	112781	TACCACGCCCAGCTAATTTT
191412	23608	GCTCTAGCAGTTTTTGTGCT	235999	68195	TTATTTTAGAGACGGGGTCT	280586	112782	CTACCACGCCCAGCTAATTT
191413	23609	CGCTCTAGCAGTTTTTGTGC	236000	68196	ATTATTTTAGAGACGGGGTC	280587	112783	GCTACCACGCCCAGCTAATT
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191415	23611	AGCGCTCTAGCAGTTTTTGT	236002	68198	AAATTATTTTAGAGACGGGG	280589	112785	GTGCTACCACGCCCAGCTAA
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191417	23613	CAAGCGCTCTAGCAGTTTTT	236004	68200	TTAAATTATTTTAGAGACGG	280591	112787	ATGTGCTACCACGCCCAGCT
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191419	23615	GACAAGCGCTCTAGCAGTTT	236006	68202	TTTTAAATTATTTTAGAGAC	280593	112789	GTATGTGCTACCACGCCCAG
191420	23616	TGACAAGCGCTCTAGCAGTT	236007	68203	TTTTTAAATTATTTTAGAGA	280594	112790	GGTATGTGCTACCACGCCCA
191421	23617	ATGACAAGCGCTCTAGCAGT	236008	68204	ATTTTTAAATTATTTTAGAG	280595	112791	CGGTATGTGCTACCACGCCC
191422	23618	AATGACAAGCGCTCTAGCAG	236009	68205	AATTTTTAAATTATTTTAGA	280596	112792	CCGGTATGTGCTACCACGCC
191423	23619	CAATGACAAGCGCTCTAGCA	236010	68206	TAATTTTTAAATTATTTTAG	280597	112793	ACCGGTATGTGCTACCACGC
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191425	23621	ACCAATGACAAGCGCTCTAG	236012	68208	GCTAATTTTTAAATTATTTT	280599	112795	CTACCGGTATGTGCTACCAC
191426	23622	GACCAATGACAAGCGCTCTA	236013	68209	GGCTAATTTTTAAATTATTT	280600	112796	ACTACCGGTATGTGCTACCA
191427	23623	TGACCAATGACAAGCGCTCT	236014	68210	TGGCTAATTTTTAAATTATT	280601	112797	AACTACCGGTATGTGCTACC
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191429	23625	GATGACCAATGACAAGCGCT	236016	68212	CCTGGCTAATTTTTAAATTA	280603	112799	GGAACTACCGGTATGTGCTA
191430	23626	AGATGACCAATGACAAGCGC	236017	68213	ACCTGGCTAATTTTTAAATT	280604	112800	TGGAACTACCGGTATGTGCT
191431	23627	GAGATGACCAATGACAAGCG	236018	68214	CACCTGGCTAATTTTTAAAT	280605	112801	CTGGAACTACCGGTATGTGC
191432	23628	AGAGATGACCAATGACAAGC	236019	68215	ACACCTGGCTAATTTTTAAA	280606	112802	GCTGGAACTACCGGTATGTG
191433	23629	GAGAGATGACCAATGACAAG	236020	68216	AACACCTGGCTAATTTTTAA	280607	112803	AGCTGGAACTACCGGTATGT
191434	23630	GGAGAGATGACCAATGACAA	236021	68217	CAACACCTGGCTAATTTTTA	280608	112804	TAGCTGGAACTACCGGTATG
191435	23631	GGGAGAGATGACCAATGACA	236022	68218	ACAACACCTGGCTAATTTTT	280609	112805	GTAGCTGGAACTACCGGTAT
191436	23632	AGGGAGAGATGACCAATGAC	236023	68219	CACAACACCTGGCTAATTTT	280610	112806	AGTAGCTGGAACTACCGGTA
191437	23633	CAGGGAGAGATGACCAATGA	236024	68220	CCACAACACCTGGCTAATTT	280611	112807	AAGTAGCTGGAACTACCGGT
191438	23634	GCAGGGAGAGATGACCAATG	236025	68221	ACCACAACACCTGGCTAATT	280612	112808	CAAGTAGCTGGAACTACCGG
191439	23635	TGCAGGGAGAGATGACCAAT	236026	68222	CACCACAACACCTGGCTAAT	280613	112809	CCAAGTAGCTGGAACTACCG
191440	23636	GTGCAGGGAGAGATGACCAA	236027	68223	GCACCACAACACCTGGCTAA	280614	112810	CCCAAGTAGCTGGAACTACC
191441	23637	GGTGCAGGGAGAGATGACCA	236028	68224	TGCACCACAACACCTGGCTA	280615	112811	TCCCAAGTAGCTGGAACTAC
191442	23638	AGGTGCAGGGAGAGATGACC	236029	68225	ATGCACCACAACACCTGGCT	280616	112812	CTCCCAAGTAGCTGGAACTA
191443	23639	CAGGTGCAGGGAGAGATGAC	236030	68226	CATGCACCACAACACCTGGC	280617	112813	TCTCCCAAGTAGCTGGAACT
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191445	23641	GCCAGGTGCAGGGAGAGATG	236032	68228	GACATGCACCACAACACCTG	280619	112815	GGTCTCCCAAGTAGCTGGAA
191446	23642	AGCCAGGTGCAGGGAGAGAT	236033	68229	AGACATGCACCACAACACCT	280620	112816	CGGTCTCCCAAGTAGCTGGA
191447	23643	CAGCCAGGTGCAGGGAGAGA	236034	68230	TAGACATGCACCACAACACC	280621	112817	TCGGTCTCCCAAGTAGCTGG
191448	23644	CCAGCCAGGTGCAGGGAGAG	236035	68231	ATAGACATGCACCACAACAC	280622	112818	CTCGGTCTCCCAAGTAGCTG
191449	23645	ACCAGCCAGGTGCAGGGAGA	236036	68232	TATAGACATGCACCACAACA	280623	112819	CCTCGGTCTCCCAAGTAGCT
191450	23646	GACCAGCCAGGTGCAGGGAG	236037	68233	CTATAGACATGCACCACAAC	280624	112820	GCCTCGGTCTCCCAAGTAGC
191451	23647	AGACCAGCCAGGTGCAGGGA	236038	68234	ACTATAGACATGCACCACAA	280625	112821	TGCCTCGGTCTCCCAAGTAG
191452	23648	CAGACCAGCCAGGTGCAGGG	236039	68235	GACTATAGACATGCACCACA	280626	112822	CTGCCTCGGTCTCCCAAGTA
191453	23649	ACAGACCAGCCAGGTGCAGG	236040	68236	GGACTATAGACATGCACCAC	280627	112823	CCTGCCTCGGTCTCCCAAGT
191454	23650	AACAGACCAGCCAGGTGCAG	236041	68237	AGGACTATAGACATGCACCA	280628	112824	TCCTGCCTCGGTCTCCCAAG
191455	23651	GAACAGACCAGCCAGGTGCA	236042	68238	TAGGACTATAGACATGCACC	280629	112825	CTCCTGCCTCGGTCTCCCAA
191456	23652	AGAACAGACCAGCCAGGTGC	236043	68239	CTAGGACTATAGACATGCAC	280630	112826	CCTCCTGCCTCGGTCTCCCA
191457	23653	AAGAACAGACCAGCCAGGTG	236044	68240	GCTAGGACTATAGACATGCA	280631	112827	TCCTCCTGCCTCGGTCTCCC
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191459	23655	CCAAGAACAGACCAGCCAGG	236046	68242	TAGCTAGGACTATAGACATG	280633	112829	AATCCTCCTGCCTCGGTCTC
191460	23656	GCCAAGAACAGACCAGCCAG	236047	68243	GTAGCTAGGACTATAGACAT	280634	112830	CAATCCTCCTGCCTCGGTCT
191461	23657	GGCCAAGAACAGACCAGCCA	236048	68244	AGTAGCTAGGACTATAGACA	280635	112831	GCAATCCTCCTGCCTCGGTC
191462	23658	TGGCCAAGAACAGACCAGCC	236049	68245	GAGTAGCTAGGACTATAGAC	280636	112832	AGCAATCCTCCTGCCTCGGT
191463	23659	GTGGCCAAGAACAGACCAGC	236050	68246	TGAGTAGCTAGGACTATAGA	280637	112833	AAGCAATCCTCCTGCCTCGG
191464	23660	AGTGGCCAAGAACAGACCAG	236051	68247	CTGAGTAGCTAGGACTATAG	280638	112834	CAAGCAATCCTCCTGCCTCG
191465	23661	CAGTGGCCAAGAACAGACCA	236052	68248	CCTGAGTAGCTAGGACTATA	280639	112835	TCAAGCAATCCTCCTGCCTC
191466	23662	TCAGTGGCCAAGAACAGACC	236053	68249	TCCTGAGTAGCTAGGACTAT	280640	112836	CTCAAGCAATCCTCCTGCCT
191467	23663	TTCAGTGGCCAAGAACAGAC	236054	68250	ATCCTGAGTAGCTAGGACTA	280641	112837	GCTCAAGCAATCCTCCTGCC
191468	23664	CTTCAGTGGCCAAGAACAGA	236055	68251	CATCCTGAGTAGCTAGGACT	280642	112838	GGCTCAAGCAATCCTCCTGC
191469	23665	GCTTCAGTGGCCAAGAACAG	236056	68252	GCATCCTGAGTAGCTAGGAC	280643	112839	GGGCTCAAGCAATCCTCCTG
191470	23666	CGCTTCAGTGGCCAAGAACA	236057	68253	AGCATCCTGAGTAGCTAGGA	280644	112840	TGGGCTCAAGCAATCCTCCT
191471	23667	ACGCTTCAGTGGCCAAGAAC	236058	68254	CAGCATCCTGAGTAGCTAGG	280645	112841	CTGGGCTCAAGCAATCCTCC
191472	23668	AACGCTTCAGTGGCCAAGAA	236059	68255	TCAGCATCCTGAGTAGCTAG	280646	112842	CCTGGGCTCAAGCAATCCTC
191473	23669	AAACGCTTCAGTGGCCAAGA	236060	68256	CTCAGCATCCTGAGTAGCTA	280647	112843	TCCTGGGCTCAAGCAATCCT
191474	23670	GAAACGCTTCAGTGGCCAAG	236061	68257	CCTCAGCATCCTGAGTAGCT	280648	112844	CTCCTGGGCTCAAGCAATCC
191475	23671	GGAAACGCTTCAGTGGCCAA	236062	68258	GCCTCAGCATCCTGAGTAGC	280649	112845	ACTCCTGGGCTCAAGCAATC
191476	23672	GGGAAACGCTTCAGTGGCCA	236063	68259	TGCCTCAGCATCCTGAGTAG	280650	112846	AACTCCTGGGCTCAAGCAAT
191477	23673	GGGGAAACGCTTCAGTGGCC	236064	68260	CTGCCTCAGCATCCTGAGTA	280651	112847	AAACTCCTGGGCTCAAGCAA
191478	23674	GGGGGAAACGCTTCAGTGGC	236065	68261	TCTGCCTCAGCATCCTGAGT	280652	112848	TAAACTCCTGGGCTCAAGCA
191479	23675	TGGGGGAAACGCTTCAGTGG	236066	68262	TTCTGCCTCAGCATCCTGAG	280653	112849	TTAAACTCCTGGGCTCAAGC
191480	23676	CTGGGGGAAACGCTTCAGTG	236067	68263	CTTCTGCCTCAGCATCCTGA	280654	112850	CTTAAACTCCTGGGCTCAAG
191481	23677	GCTGGGGGAAACGCTTCAGT	236068	68264	CCTTCTGCCTCAGCATCCTG	280655	112851	CCTTAAACTCCTGGGCTCAA
191482	23678	AGCTGGGGGAAACGCTTCAG	236069	68265	TCCTTCTGCCTCAGCATCCT	280656	112852	GCCTTAAACTCCTGGGCTCA
191483	23679	CAGCTGGGGGAAACGCTTCA	236070	68266	ATCCTTCTGCCTCAGCATCC	280657	112853	AGCCTTAAACTCCTGGGCTC
191484	23680	ACAGCTGGGGGAAACGCTTC	236071	68267	GATCCTTCTGCCTCAGCATC	280658	112854	CAGCCTTAAACTCCTGGGCT
191485	23681	AACAGCTGGGGGAAACGCTT	236072	68268	TGATCCTTCTGCCTCAGCAT	280659	112855	GCAGCCTTAAACTCCTGGGC
191486	23682	CAACAGCTGGGGGAAACGCT	236073	68269	GTGATCCTTCTGCCTCAGCA	280660	112856	TGCAGCCTTAAACTCCTGGG
191487	23683	GCAACAGCTGGGGGAAACGC	236074	68270	AGTGATCCTTCTGCCTCAGC	280661	112857	CTGCAGCCTTAAACTCCTGG
191488	23684	AGCAACAGCTGGGGGAAACG	236075	68271	AAGTGATCCTTCTGCCTCAG	280662	112858	ACTGCAGCCTTAAACTCCTG
191489	23685	AAGCAACAGCTGGGGGAAAC	236076	68272	CAAGTGATCCTTCTGCCTCA	280663	112859	CACTGCAGCCTTAAACTCCT
191490	23686	AAAGCAACAGCTGGGGGAAA	236077	68273	TCAAGTGATCCTTCTGCCTC	280664	112860	TCACTGCAGCCTTAAACTCC

191491	23687	TAAAGCAACAGCTGGGGGAA	236078	68274	CTCAAGTGATCCTTCTGCCT	280665	112861	CTCACTGCAGCCTTAAACTC
191492	23688	TTAAAGCAACAGCTGGGGGA	236079	68275	GCTCAAGTGATCCTTCTGCC	280666	112862	GCTCACTGCAGCCTTAAACT
191493	23689	ATTAAAGCAACAGCTGGGGG	236080	68276	GGCTCAAGTGATCCTTCTGC	280667	112863	AGCTCACTGCAGCCTTAAAC
191494	23690	GATTAAAGCAACAGCTGGGG	236081	68277	GGGCTCAAGTGATCCTTCTG	280668	112864	TAGCTCACTGCAGCCTTAAA
191495	23691	TGATTAAAGCAACAGCTGGG	236082	68278	TGGGCTCAAGTGATCCTTCT	280669	112865	GTAGCTCACTGCAGCCTTAA
191496	23692	ATGATTAAAGCAACAGCTGG	236083	68279	CTGGGCTCAAGTGATCCTTC	280670	112866	CGTAGCTCACTGCAGCCTTA
191497	23693	AATGATTAAAGCAACAGCTG	236084	68280	CCTGGGCTCAAGTGATCCTT	280671	112867	TCGTAGCTCACTGCAGCCTT
191498	23694	AAATGATTAAAGCAACAGCT	236085	68281	TCCTGGGCTCAAGTGATCCT	280672	112868	ATCGTAGCTCACTGCAGCCT
191499	23695	AAAATGATTAAAGCAACAGC	236086	68282	CTCCTGGGCTCAAGTGATCC	280673	112869	CATCGTAGCTCACTGCAGCC
191500	23696	TAAAATGATTAAAGCAACAG	236087	68283	ACTCCTGGGCTCAAGTGATC	280674	112870	CCATCGTAGCTCACTGCAGC
191501	23697	ATAAAATGATTAAAGCAACA	236088	68284	AACTCCTGGGCTCAAGTGAT	280675	112871	GCCATCGTAGCTCACTGCAG
191502	23698	AATAAAATGATTAAAGCAAC	236089	68285	GAACTCCTGGGCTCAAGTGA	280676	112872	CGCCATCGTAGCTCACTGCA
191503	23699	CAATAAAATGATTAAAGCAA	236090	68286	TGAACTCCTGGGCTCAAGTG	280677	112873	GCGCCATCGTAGCTCACTGC
191504	23700	ACAATAAAATGATTAAAGCA	236091	68287	TTGAACTCCTGGGCTCAAGT	280678	112874	GGCGCCATCGTAGCTCACTG
191505	23701	AACAATAAAATGATTAAAGC	236092	68288	CTTGAACTCCTGGGCTCAAG	280679	112875	TGGCGCCATCGTAGCTCACT
191506	23702	TAACAATAAAATGATTAAAG	236093	68289	CCTTGAACTCCTGGGCTCAA	280680	112876	GTGGCGCCATCGTAGCTCAC
191507	23703	ATAACAATAAAATGATTAAA	236094	68290	ACCTTGAACTCCTGGGCTCA	280681	112877	AGTGGCGCCATCGTAGCTCA
191508	23704	AATAACAATAAAATGATTAA	236095	68291	AACCTTGAACTCCTGGGCTC	280682	112878	CAGTGGCGCCATCGTAGCTC
191509	23705	TAATAACAATAAAATGATTA	236096	68292	CAACCTTGAACTCCTGGGCT	280683	112879	GCAGTGGCGCCATCGTAGCT
191510	23706	ATAATAACAATAAAATGATT	236097	68293	GCAACCTTGAACTCCTGGGC	280684	112880	TGCAGTGGCGCCATCGTAGC
191511	23707	CATAATAACAATAAAATGAT	236098	68294	TGCAACCTTGAACTCCTGGG	280685	112881	ATGCAGTGGCGCCATCGTAG
191512	23708	GCATAATAACAATAAAATGA	236099	68295	CTGCAACCTTGAACTCCTGG	280686	112882	AATGCAGTGGCGCCATCGTA
191513	23709	GGCATAATAACAATAAAATG	236100	68296	ACTGCAACCTTGAACTCCTG	280687	112883	GAATGCAGTGGCGCCATCGT
191514	23710	AGGCATAATAACAATAAAAT	236101	68297	TACTGCAACCTTGAACTCCT	280688	112884	GGAATGCAGTGGCGCCATCG
191515	23711	AAGGCATAATAACAATAAAA	236102	68298	TTACTGCAACCTTGAACTCC	280689	112885	TGGAATGCAGTGGCGCCATC
191516	23712	TAAGGCATAATAACAATAAA	236103	68299	CTTACTGCAACCTTGAACTC	280690	112886	CTGGAATGCAGTGGCGCCAT
191517	23713	GTAAGGCATAATAACAATAA	236104	68300	GCTTACTGCAACCTTGAACT	280691	112887	GCTGGAATGCAGTGGCGCCA
191518	23714	AGTAAGGCATAATAACAATA	236105	68301	AGCTTACTGCAACCTTGAAC	280692	112888	GGCTGGAATGCAGTGGCGCC
191519	23715	AAGTAAGGCATAATAACAAT	236106	68302	CAGCTTACTGCAACCTTGAA	280693	112889	AGGCTGGAATGCAGTGGCGC
191520	23716	TAAGTAAGGCATAATAACAA	236107	68303	ACAGCTTACTGCAACCTTGA	280694	112890	CAGGCTGGAATGCAGTGGCG
191521	23717	TTAAGTAAGGCATAATAACA	236108	68304	CACAGCTTACTGCAACCTTG	280695	112891	CCAGGCTGGAATGCAGTGGC
191522	23718	CTTAAGTAAGGCATAATAAC	236109	68305	TCACAGCTTACTGCAACCTT	280696	112892	CCCAGGCTGGAATGCAGTGG
191523	23719	TCTTAAGTAAGGCATAATAA	236110	68306	ATCACAGCTTACTGCAACCT	280697	112893	ACCCAGGCTGGAATGCAGTG
191524	23720	TTCTTAAGTAAGGCATAATA	236111	68307	AATCACAGCTTACTGCAACC	280698	112894	CACCCAGGCTGGAATGCAGT
191525	23721	TTTCTTAAGTAAGGCATAAT	236112	68308	TAATCACAGCTTACTGCAAC	280699	112895	TCACCCAGGCTGGAATGCAG
191526	23722	ATTTCTTAAGTAAGGCATAA	236113	68309	ATAATCACAGCTTACTGCAA	280700	112896	GTCACCCAGGCTGGAATGCA
191527	23723	CATTTCTTAAGTAAGGCATA	236114	68310	TATAATCACAGCTTACTGCA	280701	112897	TGTCACCCAGGCTGGAATGC
191528	23724	CCATTTCTTAAGTAAGGCAT	236115	68311	TTATAATCACAGCTTACTGC	280702	112898	CTGTCACCCAGGCTGGAATG
191529	23725	TCCATTTCTTAAGTAAGGCA	236116	68312	TTTATAATCACAGCTTACTG	280703	112899	TCTGTCACCCAGGCTGGAAT
191530	23726	ATCCATTTCTTAAGTAAGGC	236117	68313	TTTTATAATCACAGCTTACT	280704	112900	CTCTGTCACCCAGGCTGGAA
191531	23727	TATCCATTTCTTAAGTAAGG	236118	68314	GTTTTATAATCACAGCTTAC	280705	112901	ACTCTGTCACCCAGGCTGGA
191532	23728	ATATCCATTTCTTAAGTAAG	236119	68315	AGTTTTATAATCACAGCTTA	280706	112902	CACTCTGTCACCCAGGCTGG
191533	23729	CATATCCATTTCTTAAGTAA	236120	68316	CAGTTTTATAATCACAGCTT	280707	112903	TCACTCTGTCACCCAGGCTG
191534	23730	TCATATCCATTTCTTAAGTA	236121	68317	GCAGTTTTATAATCACAGCT	280708	112904	CTCACTCTGTCACCCAGGCT
191535	23731	CTCATATCCATTTCTTAAGT	236122	68318	TGCAGTTTTATAATCACAGC	280709	112905	TCTCACTCTGTCACCCAGGC
191536	23732	TCTCATATCCATTTCTTAAG	236123	68319	GTGCAGTTTTATAATCACAG	280710	112906	CTCTCACTCTGTCACCCAGG
191537	23733	ATCTCATATCCATTTCTTAA	236124	68320	AGTGCAGTTTTATAATCACA	280711	112907	GCTCTCACTCTGTCACCCAG
191538	23734	CATCTCATATCCATTTCTTA	236125	68321	GAGTGCAGTTTTATAATCAC	280712	112908	AGCTCTCACTCTGTCACCCA
191539	23735	GCATCTCATATCCATTTCTT	236126	68322	GGAGTGCAGTTTTATAATCA	280713	112909	AAGCTCTCACTCTGTCACCC
191540	23736	TGCATCTCATATCCATTTCT	236127	68323	TGGAGTGCAGTTTTATAATC	280714	112910	CAAGCTCTCACTCTGTCACC
191541	23737	ATGCATCTCATATCCATTTC	236128	68324	CTGGAGTGCAGTTTTATAAT	280715	112911	ACAAGCTCTCACTCTGTCAC
191542	23738	AATGCATCTCATATCCATTT	236129	68325	GCTGGAGTGCAGTTTTATAA	280716	112912	GACAAGCTCTCACTCTGTCA
191543	23739	AAATGCATCTCATATCCATT	236130	68326	GGCTGGAGTGCAGTTTTATA	280717	112913	AGACAAGCTCTCACTCTGTC
191544	23740	TAAATGCATCTCATATCCAT	236131	68327	AGGCTGGAGTGCAGTTTTAT	280718	112914	GAGACAAGCTCTCACTCTGT
191545	23741	GTAAATGCATCTCATATCCA	236132	68328	CAGGCTGGAGTGCAGTTTTA	280719	112915	AGAGACAAGCTCTCACTCTG
191546	23742	GGTAAATGCATCTCATATCC	236133	68329	TCAGGCTGGAGTGCAGTTTT	280720	112916	TAGAGACAAGCTCTCACTCT
191547	23743	AGGTAAATGCATCTCATATC	236134	68330	CTCAGGCTGGAGTGCAGTTT	280721	112917	ATAGAGACAAGCTCTCACTC
191548	23744	CAGGTAAATGCATCTCATAT	236135	68331	GCTCAGGCTGGAGTGCAGTT	280722	112918	AATAGAGACAAGCTCTCACT
191549	23745	ACAGGTAAATGCATCTCATA	236136	68332	TGCTCAGGCTGGAGTGCAGT	280723	112919	AAATAGAGACAAGCTCTCAC
191550	23746	GACAGGTAAATGCATCTCAT	236137	68333	TTGCTCAGGCTGGAGTGCAG	280724	112920	AAAATAGAGACAAGCTCTCA
191551	23747	AGACAGGTAAATGCATCTCA	236138	68334	GTTGCTCAGGCTGGAGTGCA	280725	112921	TAAAATAGAGACAAGCTCTC
191552	23748	GAGACAGGTAAATGCATCTC	236139	68335	TGTTGCTCAGGCTGGAGTGC	280726	112922	TTAAAATAGAGACAAGCTCT
191553	23749	AGAGACAGGTAAATGCATCT	236140	68336	CTGTTGCTCAGGCTGGAGTG	280727	112923	TTTAAAATAGAGACAAGCTC
191554	23750	AAGAGACAGGTAAATGCATC	236141	68337	TCTGTTGCTCAGGCTGGAGT	280728	112924	TTTTAAAATAGAGACAAGCT
191555	23751	GAAGAGACAGGTAAATGCAT	236142	68338	CTCTGTTGCTCAGGCTGGAG	280729	112925	TTTTTAAAATAGAGACAAGC
191556	23752	GGAAGAGACAGGTAAATGCA	236143	68339	GCTCTGTTGCTCAGGCTGGA	280730	112926	ATTTTTAAAATAGAGACAAG
191557	23753	AGGAAGAGACAGGTAAATGC	236144	68340	TGCTCTGTTGCTCAGGCTGG	280731	112927	TATTTTTAAAATAGAGACAA
191558	23754	CAGGAAGAGACAGGTAAATG	236145	68341	TTGCTCTGTTGCTCAGGCTG	280732	112928	TTATTTTTAAAATAGAGACA
191559	23755	GCAGGAAGAGACAGGTAAAT	236146	68342	CTTGCTCTGTTGCTCAGGCT	280733	112929	ATTATTTTTAAAATAGAGAC
191560	23756	GGCAGGAAGAGACAGGTAAA	236147	68343	TCTTGCTCTGTTGCTCAGGC	280734	112930	TATTATTTTTAAAATAGAGA
191561	23757	TGGCAGGAAGAGACAGGTAA	236148	68344	GTCTTGCTCTGTTGCTCAGG	280735	112931	TTATTATTTTTAAAATAGAG
191562	23758	GTGGCAGGAAGAGACAGGTA	236149	68345	GGTCTTGCTCTGTTGCTCAG	280736	112932	TTTATTATTTTTAAAATAGA

191563	23759	AGTGGCAGGAAGAGACAGGT	236150	68346	GGGTCTTGCTCTGTTGCTCA	280737	112933	TTTTATTATTTTTAAAATAG
191564	23760	GAGTGGCAGGAAGAGACAGG	236151	68347	AGGGTCTTGCTCTGTTGCTC	280738	112934	TTTTTATTATTTTTAAAATA
191565	23761	AGAGTGGCAGGAAGAGACAG	236152	68348	CAGGGTCTTGCTCTGTTGCT	280739	112935	CTTTTTATTATTTTTAAAAT
191566	23762	CAGAGTGGCAGGAAGAGACA	236153	68349	ACAGGGTCTTGCTCTGTTGC	280740	112936	TCTTTTTATTATTTTTAAAA
191567	23763	GCAGAGTGGCAGGAAGAGAC	236154	68350	GACAGGGTCTTGCTCTGTTG	280741	112937	TTCTTTTTATTATTTTTAAA
191568	23764	TGCAGAGTGGCAGGAAGAGA	236155	68351	TGACAGGGTCTTGCTCTGTT	280742	112938	ATTCTTTTTATTATTTTTAA
191569	23765	CTGCAGAGTGGCAGGAAGAG	236156	68352	TTGACAGGGTCTTGCTCTGT	280743	112939	TATTCTTTTTATTATTTTTA
191570	23766	TCTGCAGAGTGGCAGGAAGA	236157	68353	TTTGACAGGGTCTTGCTCTG	280744	112940	TTATTCTTTTTATTATTTTT
191571	23767	CTCTGCAGAGTGGCAGGAAG	236158	68354	TTTTGACAGGGTCTTGCTCT	280745	112941	TTTATTCTTTTTATTATTTT
191572	23768	GCTCTGCAGAGTGGCAGGAA	236159	68355	TTTTTGACAGGGTCTTGCTC	280746	112942	ATTTATTCTTTTTATTATTT
191573	23769	GGCTCTGCAGAGTGGCAGGA	236160	68356	TTTTTTGACAGGGTCTTGCT	280747	112943	TATTTATTCTTTTTATTATT
191574	23770	TGGCTCTGCAGAGTGGCAGG	236161	68357	TTTTTTTGACAGGGTCTTGC	280748	112944	TTATTTATTCTTTTTATTAT
191575	23771	CTGGCTCTGCAGAGTGGCAG	236162	68358	TTTTTTTTGACAGGGTCTTG	280749	112945	TTTATTTATTCTTTTTATTA
191576	23772	ACTGGCTCTGCAGAGTGGCA	236163	68359	TTTTTTTTTGACAGGGTCTT	280750	112946	TTTTATTTATTCTTTTTATT
191577	23773	TACTGGCTCTGCAGAGTGGC	236164	68360	TTTTTTTTTTGACAGGGTCT	280751	112947	TTTTTATTTATTCTTTTTAT
191578	23774	TTACTGGCTCTGCAGAGTGG	236165	68361	CTTTTTTTTTTGACAGGGTC	280752	112948	ATTTTTATTTATTCTTTTTA
191579	23775	CTTACTGGCTCTGCAGAGTG	236166	68362	TCTTTTTTTTTTGACAGGGT	280753	112949	TATTTTTATTTATTCTTTTT
191580	23776	TCTTACTGGCTCTGCAGAGT	236167	68363	TTCTTTTTTTTTTGACAGGG	280754	112950	TTATTTTTATTTATTCTTTT
191581	23777	ATCTTACTGGCTCTGCAGAG	236168	68364	TTTCTTTTTTTTTTGACAGG	280755	112951	TTTATTTTTATTTATTCTTT
191582	23778	CATCTTACTGGCTCTGCAGA	236169	68365	TTTTCTTTTTTTTTTGACAG	280756	112952	ATTTATTTTTATTTATTCTT
191583	23779	ACATCTTACTGGCTCTGCAG	236170	68366	CTTTTCTTTTTTTTTTGACA	280757	112953	AATTTATTTTTATTTATTCT
191584	23780	CACATCTTACTGGCTCTGCA	236171	68367	TCTTTTCTTTTTTTTTTGAC	280758	112954	TAATTTATTTTTATTTATTC
191585	23781	CCACATCTTACTGGCTCTGC	236172	68368	TTCTTTTCTTTTTTTTTTGA	280759	112955	TTAATTTATTTTTATTTATT
191586	23782	ACCACATCTTACTGGCTCTG	236173	68369	TTTCTTTTCTTTTTTTTTTG	280760	112956	TTTAATTTATTTTTATTTAT
191587	23783	CACCACATCTTACTGGCTCT	236174	68370	TTTTCTTTTCTTTTTTTTTT	280761	112957	TTTTAATTTATTTTTATTTA
191588	23784	CCACCACATCTTACTGGCTC	236175	68371	TTTTTCTTTTCTTTTTTTTT	280762	112958	ATTTTAATTTATTTTTATTT
191589	23785	TCCACCACATCTTACTGGCT	236176	68372	TTTTTTCTTTTCTTTTTTTT	280763	112959	CATTTTAATTTATTTTTATT
191590	23786	TTCCACCACATCTTACTGGC	236177	68373	CTTTTTTCTTTTCTTTTTTT	280764	112960	ACATTTTAATTTATTTTTAT
191591	23787	TTTCCACCACATCTTACTGG	236178	68374	TCTTTTTTCTTTTCTTTTTT	280765	112961	TACATTTTAATTTATTTTTA
191592	23788	CTTTCCACCACATCTTACTG	236179	68375	TTCTTTTTTCTTTTCTTTTT	280766	112962	TTACATTTTAATTTATTTTT
191593	23789	CCTTTCCACCACATCTTACT	236180	68376	TTTCTTTTTTCTTTTCTTTT	280767	112963	TTTACATTTTAATTTATTTT
191594	23790	CCCTTTCCACCACATCTTAC	236181	68377	CTTTCTTTTTTCTTTTCTTT	280768	112964	ATTTACATTTTAATTTATTT
191595	23791	GCCCTTTCCACCACATCTTA	236182	68378	TCTTTCTTTTTTCTTTTCTT	280769	112965	TATTTACATTTTAATTTATT
191596	23792	GGCCCTTTCCACCACATCTT	236183	68379	TTCTTTCTTTTTTCTTTTCT	280770	112966	ATATTTACATTTTAATTTAT
191597	23793	GGGCCCTTTCCACCACATCT	236184	68380	TTTCTTTCTTTTTTCTTTTC	280771	112967	CATATTTACATTTTAATTTA
191598	23794	TGGGCCCTTTCCACCACATC	236185	68381	CTTTCTTTCTTTTTTCTTTT	280772	112968	ACATATTTACATTTTAATTT
191599	23795	CTGGGCCCTTTCCACCACAT	236186	68382	TCTTTCTTTCTTTTTTCTTT	280773	112969	CACATATTTACATTTTAATT
191600	23796	CCTGGGCCCTTTCCACCACA	236187	68383	TTCTTTCTTTCTTTTTTCTT	280774	112970	GCACATATTTACATTTTAAT
191601	23797	GCCTGGGCCCTTTCCACCAC	236188	68384	TTTCTTTCTTTCTTTTTTCT	280775	112971	TGCACATATTTACATTTTAA
191602	23798	AGCCTGGGCCCTTTCCACCA	236189	68385	ATTTCTTTCTTTCTTTTTTC	280776	112972	ATGCACATATTTACATTTTA
191603	23799	AAGCCTGGGCCCTTTCCACC	236190	68386	AATTTCTTTCTTTCTTTTTT	280777	112973	CATGCACATATTTACATTTT
191604	23800	AAAGCCTGGGCCCTTTCCAC	236191	68387	AAATTTCTTTCTTTCTTTTT	280778	112974	ACATGCACATATTTACATTT
191605	23801	CAAAGCCTGGGCCCTTTCCA	236192	68388	TAAATTTCTTTCTTTCTTTT	280779	112975	AACATGCACATATTTACATT
191606	23802	CCAAAGCCTGGGCCCTTTCC	236193	68389	GTAAATTTCTTTCTTTCTTT	280780	112976	TAACATGCACATATTTACAT
191607	23803	TCCAAAGCCTGGGCCCTTTC	236194	68390	GGTAAATTTCTTTCTTTCTT	280781	112977	CTAACATGCACATATTTACA
191608	23804	CTCCAAAGCCTGGGCCCTTT	236195	68391	AGGTAAATTTCTTTCTTTCT	280782	112978	TCTAACATGCACATATTTAC
191609	23805	CCTCCAAAGCCTGGGCCCTT	236196	68392	AAGGTAAATTTCTTTCTTTC	280783	112979	TTCTAACATGCACATATTTA
191610	23806	TCCTCCAAAGCCTGGGCCCT	236197	68393	CAAGGTAAATTTCTTTCTTT	280784	112980	TTTCTAACATGCACATATTT
191611	23807	CTCCTCCAAAGCCTGGGCCC	236198	68394	TCAAGGTAAATTTCTTTCTT	280785	112981	TTTTCTAACATGCACATATT
191612	23808	CCTCCTCCAAAGCCTGGGCC	236199	68395	CTCAAGGTAAATTTCTTTCT	280786	112982	TTTTTCTAACATGCACATAT
191613	23809	CCCTCCTCCAAAGCCTGGGC	236200	68396	ACTCAAGGTAAATTTCTTTC	280787	112983	TTTTTTCTAACATGCACATA
191614	23810	GCCCTCCTCCAAAGCCTGGG	236201	68397	AACTCAAGGTAAATTTCTTT	280788	112984	ATTTTTTCTAACATGCACAT
191615	23811	AGCCCTCCTCCAAAGCCTGG	236202	68398	TAACTCAAGGTAAATTTCTT	280789	112985	TATTTTTTCTAACATGCACA
191616	23812	CAGCCCTCCTCCAAAGCCTG	236203	68399	GTAACTCAAGGTAAATTTCT	280790	112986	GTATTTTTTCTAACATGCAC
191617	23813	CCAGCCCTCCTCCAAAGCCT	236204	68400	GGTAACTCAAGGTAAATTTC	280791	112987	TGTATTTTTTCTAACATGCA
191618	23814	GCCAGCCCTCCTCCAAAGCC	236205	68401	GGGTAACTCAAGGTAAATTT	280792	112988	GTGTATTTTTTCTAACATGC
191619	23815	AGCCAGCCCTCCTCCAAAGC	236206	68402	TGGGTAACTCAAGGTAAATT	280793	112989	GGTGTATTTTTTCTAACATG
191620	23816	CAGCCAGCCCTCCTCCAAAG	236207	68403	GTGGGTAACTCAAGGTAAAT	280794	112990	GGGTGTATTTTTTCTAACAT
191621	23817	CCAGCCAGCCCTCCTCCAAA	236208	68404	TGTGGGTAACTCAAGGTAAA	280795	112991	TGGGTGTATTTTTTCTAACA
191622	23818	CCCAGCCAGCCCTCCTCCAA	236209	68405	ATGTGGGTAACTCAAGGTAA	280796	112992	ATGGGTGTATTTTTTCTAAC
191623	23819	CCCCAGCCAGCCCTCCTCCA	236210	68406	CATGTGGGTAACTCAAGGTA	280797	112993	GATGGGTGTATTTTTTCTAA
191624	23820	ACCCCAGCCAGCCCTCCTCC	236211	68407	TCATGTGGGTAACTCAAGGT	280798	112994	TGATGGGTGTATTTTTTCTA
191625	23821	AACCCCAGCCAGCCCTCCTC	236212	68408	CTCATGTGGGTAACTCAAGG	280799	112995	CTGATGGGTGTATTTTTTCT
191626	23822	CAACCCCAGCCAGCCCTCCT	236213	68409	ACTCATGTGGGTAACTCAAG	280800	112996	GCTGATGGGTGTATTTTTTC
191627	23823	CCAACCCCAGCCAGCCCTCC	236214	68410	CACTCATGTGGGTAACTCAA	280801	112997	TGCTGATGGGTGTATTTTTT
191628	23824	TCCAACCCCAGCCAGCCCTC	236215	68411	TCACTCATGTGGGTAACTCA	280802	112998	TTGCTGATGGGTGTATTTTT
191629	23825	ATCCAACCCCAGCCAGCCCT	236216	68412	TTCACTCATGTGGGTAACTC	280803	112999	TTTGCTGATGGGTGTATTTT
191630	23826	GATCCAACCCCAGCCAGCCC	236217	68413	ATTCACTCATGTGGGTAACT	280804	113000	TTTTGCTGATGGGTGTATTT
191631	23827	AGATCCAACCCCAGCCAGCC	236218	68414	CATTCACTCATGTGGGTAAC	280805	113001	TTTTTGCTGATGGGTGTATT
191632	23828	AAGATCCAACCCCAGCCAGC	236219	68415	ACATTCACTCATGTGGGTAA	280806	113002	CTTTTTGCTGATGGGTGTAT
191633	23829	CAAGATCCAACCCCAGCCAG	236220	68416	TACATTCACTCATGTGGGTA	280807	113003	CCTTTTTGCTGATGGGTGTA
191634	23830	CCAAGATCCAACCCCAGCCA	236221	68417	CTACATTCACTCATGTGGGT	280808	113004	CCCTTTTTGCTGATGGGTGT

191635	23831	GCCAAGATCCAACCCCAGCC	236222	68418	CCTACATTCACTCATGTGGG	280809	113005	CCCCTTTTTGCTGATGGGTG
191636	23832	AGCCAAGATCCAACCCCAGC	236223	68419	CCCTACATTCACTCATGTGG	280810	113006	CCCCCTTTTTGCTGATGGGT
191637	23833	CAGCCAAGATCCAACCCCAG	236224	68420	TCCCTACATTCACTCATGTG	280811	113007	ACCCCCTTTTTGCTGATGGG
191638	23834	GCAGCCAAGATCCAACCCCA	236225	68421	GTCCCTACATTCACTCATGT	280812	113008	TACCCCCTTTTTGCTGATGG
191639	23835	GGCAGCCAAGATCCAACCCC	236226	68422	TGTCCCTACATTCACTCATG	280813	113009	TTACCCCCTTTTTGCTGATG
191640	23836	GGGCAGCCAAGATCCAACCC	236227	68423	CTGTCCCTACATTCACTCAT	280814	113010	TTTACCCCCTTTTTGCTGAT
191641	23837	GGGGCAGCCAAGATCCAACC	236228	68424	TCTGTCCCTACATTCACTCA	280815	113011	CTTTACCCCCTTTTTGCTGA
191642	23838	GGGGGCAGCCAAGATCCAAC	236229	68425	CTCTGTCCCTACATTCACTC	280816	113012	CCTTTACCCCCTTTTTGCTG
191643	23839	AGGGGGCAGCCAAGATCCAA	236230	68426	TCTCTGTCCCTACATTCACT	280817	113013	TCCTTTACCCCCTTTTTGCT
191644	23840	TAGGGGGCAGCCAAGATCCA	236231	68427	ATCTCTGTCCCTACATTCAC	280818	113014	CTCCTTTACCCCCTTTTTGC
191645	23841	GTAGGGGGCAGCCAAGATCC	236232	68428	AATCTCTGTCCCTACATTCA	280819	113015	GCTCCTTTACCCCCTTTTTG
191646	23842	AGTAGGGGGCAGCCAAGATC	236233	68429	AAATCTCTGTCCCTACATTC	280820	113016	CGCTCCTTTACCCCCTTTTT
191647	23843	TAGTAGGGGGCAGCCAAGAT	236234	68430	AAAATCTCTGTCCCTACATT	280821	113017	TCGCTCCTTTACCCCCTTTT
191648	23844	CTAGTAGGGGGCAGCCAAGA	236235	68431	TAAAATCTCTGTCCCTACAT	280822	113018	ATCGCTCCTTTACCCCCTTT
191649	23845	GCTAGTAGGGGGCAGCCAAG	236236	68432	CTAAAATCTCTGTCCCTACA	280823	113019	AATCGCTCCTTTACCCCCTT
191650	23846	AGCTAGTAGGGGGCAGCCAA	236237	68433	CCTAAAATCTCTGTCCCTAC	280824	113020	AAATCGCTCCTTTACCCCCT
191651	23847	CAGCTAGTAGGGGGCAGCCA	236238	68434	CCCTAAAATCTCTGTCCCTA	280825	113021	GAAATCGCTCCTTTACCCCC
191652	23848	ACAGCTAGTAGGGGGCAGCC	236239	68435	GCCCTAAAATCTCTGTCCCT	280826	113022	TGAAATCGCTCCTTTACCCC
191653	23849	CACAGCTAGTAGGGGGCAGC	236240	68436	GGCCCTAAAATCTCTGTCCC	280827	113023	CTGAAATCGCTCCTTTACCC
191654	23850	ACACAGCTAGTAGGGGGCAG	236241	68437	AGGCCCTAAAATCTCTGTCC	280828	113024	ACTGAAATCGCTCCTTTACC
191655	23851	CACACAGCTAGTAGGGGGCA	236242	68438	AAGGCCCTAAAATCTCTGTC	280829	113025	GACTGAAATCGCTCCTTTAC
191656	23852	TCACACAGCTAGTAGGGGGC	236243	68439	TAAGGCCCTAAAATCTCTGT	280830	113026	TGACTGAAATCGCTCCTTTA
191657	23853	GTCACACAGCTAGTAGGGGG	236244	68440	TTAAGGCCCTAAAATCTCTG	280831	113027	ATGACTGAAATCGCTCCTTT
191658	23854	GGTCACACAGCTAGTAGGGG	236245	68441	GTTAAGGCCCTAAAATCTCT	280832	113028	TATGACTGAAATCGCTCCTT
191659	23855	AGGTCACACAGCTAGTAGGG	236246	68442	TGTTAAGGCCCTAAAATCTC	280833	113029	TTATGACTGAAATCGCTCCT
191660	23856	AAGGTCACACAGCTAGTAGG	236247	68443	TTGTTAAGGCCCTAAAATCT	280834	113030	ATTATGACTGAAATCGCTCC
191661	23857	CAAGGTCACACAGCTAGTAG	236248	68444	ATTGTTAAGGCCCTAAAATC	280835	113031	AATTATGACTGAAATCGCTC
191662	23858	CCAAGGTCACACAGCTAGTA	236249	68445	GATTGTTAAGGCCCTAAAAT	280836	113032	CAATTATGACTGAAATCGCT
191663	23859	CCCAAGGTCACACAGCTAGT	236250	68446	AGATTGTTAAGGCCCTAAAA	280837	113033	CCAATTATGACTGAAATCGC
191664	23860	ACCCAAGGTCACACAGCTAG	236251	68447	GAGATTGTTAAGGCCCTAAA	280838	113034	TCCAATTATGACTGAAATCG
191665	23861	TACCCAAGGTCACACAGCTA	236252	68448	AGAGATTGTTAAGGCCCTAA	280839	113035	CTCCAATTATGACTGAAATC
191666	23862	TTACCCAAGGTCACACAGCT	236253	68449	GAGAGATTGTTAAGGCCCTA	280840	113036	TCTCCAATTATGACTGAAAT
191667	23863	CTTACCCAAGGTCACACAGC	236254	68450	TGAGAGATTGTTAAGGCCCT	280841	113037	CTCTCCAATTATGACTGAAA
191668	23864	ACTTACCCAAGGTCACACAG	236255	68451	TTGAGAGATTGTTAAGGCCC	280842	113038	TCTCTCCAATTATGACTGAA
191669	23865	TACTTACCCAAGGTCACACA	236256	68452	TTTGAGAGATTGTTAAGGCC	280843	113039	ATCTCTCCAATTATGACTGA
191670	23866	CTACTTACCCAAGGTCACAC	236257	68453	ATTTGAGAGATTGTTAAGGC	280844	113040	CATCTCTCCAATTATGACTG
191671	23867	GCTACTTACCCAAGGTCACA	236258	68454	TATTTGAGAGATTGTTAAGG	280845	113041	GCATCTCTCCAATTATGACT
191672	23868	AGCTACTTACCCAAGGTCAC	236259	68455	GTATTTGAGAGATTGTTAAG	280846	113042	TGCATCTCTCCAATTATGAC
191673	23869	CAGCTACTTACCCAAGGTCA	236260	68456	TGTATTTGAGAGATTGTTAA	280847	113043	CTGCATCTCTCCAATTATGA
191674	23870	CCAGCTACTTACCCAAGGTC	236261	68457	CTGTATTTGAGAGATTGTTA	280848	113044	TCTGCATCTCTCCAATTATG
191675	23871	TCCAGCTACTTACCCAAGGT	236262	68458	CCTGTATTTGAGAGATTGTT	280849	113045	TTCTGCATCTCTCCAATTAT
191676	23872	GTCCAGCTACTTACCCAAGG	236263	68459	CCCTGTATTTGAGAGATTGT	280850	113046	ATTCTGCATCTCTCCAATTA
191677	23873	GGTCCAGCTACTTACCCAAG	236264	68460	ACCCTGTATTTGAGAGATTG	280851	113047	TATTCTGCATCTCTCCAATT
191678	23874	AGGTCCAGCTACTTACCCAA	236265	68461	TACCCTGTATTTGAGAGATT	280852	113048	TTATTCTGCATCTCTCCAAT
191679	23875	GAGGTCCAGCTACTTACCCA	236266	68462	GTACCCTGTATTTGAGAGAT	280853	113049	CTTATTCTGCATCTCTCCAA
191680	23876	AGAGGTCCAGCTACTTACCC	236267	68463	AGTACCCTGTATTTGAGAGA	280854	113050	GCTTATTCTGCATCTCTCCA
191681	23877	GAGAGGTCCAGCTACTTACC	236268	68464	AAGTACCCTGTATTTGAGAG	280855	113051	GGCTTATTCTGCATCTCTCC
191682	23878	AGAGAGGTCCAGCTACTTAC	236269	68465	AAAGTACCCTGTATTTGAGA	280856	113052	TGGCTTATTCTGCATCTCTC
191683	23879	CAGAGAGGTCCAGCTACTTA	236270	68466	AAAAGTACCCTGTATTTGAG	280857	113053	CTGGCTTATTCTGCATCTCT
191684	23880	TCAGAGAGGTCCAGCTACTT	236271	68467	AAAAAGTACCCTGTATTTGA	280858	113054	GCTGGCTTATTCTGCATCTC
191685	23881	CTCAGAGAGGTCCAGCTACT	236272	68468	CAAAAAGTACCCTGTATTTG	280859	113055	TGCTGGCTTATTCTGCATCT
191686	23882	GCTCAGAGAGGTCCAGCTAC	236273	68469	TCAAAAAGTACCCTGTATTT	280860	113056	TTGCTGGCTTATTCTGCATC
191687	23883	GGCTCAGAGAGGTCCAGCTA	236274	68470	CTCAAAAAGTACCCTGTATT	280861	113057	ATTGCTGGCTTATTCTGCAT
191688	23884	AGGCTCAGAGAGGTCCAGCT	236275	68471	CCTCAAAAAGTACCCTGTAT	280862	113058	CATTGCTGGCTTATTCTGCA
191689	23885	CAGGCTCAGAGAGGTCCAGC	236276	68472	GCCTCAAAAAGTACCCTGTA	280863	113059	GCATTGCTGGCTTATTCTGC
191690	23886	CCAGGCTCAGAGAGGTCCAG	236277	68473	TGCCTCAAAAAGTACCCTGT	280864	113060	TGCATTGCTGGCTTATTCTG
191691	23887	ACCAGGCTCAGAGAGGTCCA	236278	68474	ATGCCTCAAAAAGTACCCTG	280865	113061	CTGCATTGCTGGCTTATTCT
191692	23888	AACCAGGCTCAGAGAGGTCC	236279	68475	AATGCCTCAAAAAGTACCCT	280866	113062	ACTGCATTGCTGGCTTATTC
191693	23889	GAACCAGGCTCAGAGAGGTC	236280	68476	TAATGCCTCAAAAAGTACCC	280867	113063	AACTGCATTGCTGGCTTATT
191694	23890	CGAACCAGGCTCAGAGAGGT	236281	68477	CTAATGCCTCAAAAAGTACC	280868	113064	AAACTGCATTGCTGGCTTAT
191695	23891	CCGAACCAGGCTCAGAGAGG	236282	68478	GCTAATGCCTCAAAAAGTAC	280869	113065	GAAACTGCATTGCTGGCTTA
191696	23892	TCCGAACCAGGCTCAGAGAG	236283	68479	GGCTAATGCCTCAAAAAGTA	280870	113066	AGAAACTGCATTGCTGGCTT
191697	23893	TTCCGAACCAGGCTCAGAGA	236284	68480	TGGCTAATGCCTCAAAAAGT	280871	113067	AAGAAACTGCATTGCTGGCT
191698	23894	ATTCCGAACCAGGCTCAGAG	236285	68481	GTGGCTAATGCCTCAAAAAG	280872	113068	AAAGAAACTGCATTGCTGGC
191699	23895	GATTCCGAACCAGGCTCAGA	236286	68482	TGTGGCTAATGCCTCAAAAA	280873	113069	AAAAGAAACTGCATTGCTGG
191700	23896	TGATTCCGAACCAGGCTCAG	236287	68483	GTGTGGCTAATGCCTCAAAA	280874	113070	TAAAAGAAACTGCATTGCTG
191701	23897	ATGATTCCGAACCAGGCTCA	236288	68484	GGTGTGGCTAATGCCTCAAA	280875	113071	ATAAAAGAAACTGCATTGCT
191702	23898	TATGATTCCGAACCAGGCTC	236289	68485	AGGTGTGGCTAATGCCTCAA	280876	113072	AATAAAAGAAACTGCATTGC
191703	23899	CTATGATTCCGAACCAGGCT	236290	68486	CAGGTGTGGCTAATGCCTCA	280877	113073	AAATAAAAGAAACTGCATTG
191704	23900	GCTATGATTCCGAACCAGGC	236291	68487	ACAGGTGTGGCTAATGCCTC	280878	113074	AAAATAAAAGAAACTGCATT
191705	23901	TGCTATGATTCCGAACCAGG	236292	68488	AACAGGTGTGGCTAATGCCT	280879	113075	CAAAATAAAAGAAACTGCAT
191706	23902	GTGCTATGATTCCGAACCAG	236293	68489	TAACAGGTGTGGCTAATGCC	280880	113076	CCAAAATAAAAGAAACTGCA

191707	23903	GGTGCTATGATTCCGAACCA	236294	68490	CTAACAGGTGTGGCTAATGC	280881	113077	ACCAAAATAAAAGAAACTGC
191708	23904	AGGTGCTATGATTCCGAACC	236295	68491	GCTAACAGGTGTGGCTAATG	280882	113078	GACCAAAATAAAAGAAACTG
191709	23905	GAGGTGCTATGATTCCGAAC	236296	68492	AGCTAACAGGTGTGGCTAAT	280883	113079	TGACCAAAATAAAAGAAACT
191710	23906	AGAGGTGCTATGATTCCGAA	236297	68493	AAGCTAACAGGTGTGGCTAA	280884	113080	TTGACCAAAATAAAAGAAAC
191711	23907	GAGAGGTGCTATGATTCCGA	236298	68494	TAAGCTAACAGGTGTGGCTA	280885	113081	TTTGACCAAAATAAAAGAAA
191712	23908	AGAGAGGTGCTATGATTCCG	236299	68495	ATAAGCTAACAGGTGTGGCT	280886	113082	TTTTGACCAAAATAAAAGAA
191713	23909	AAGAGAGGTGCTATGATTCC	236300	68496	TATAAGCTAACAGGTGTGGC	280887	113083	TTTTTGACCAAAATAAAAGA
191714	23910	AAAGAGAGGTGCTATGATTC	236301	68497	TTATAAGCTAACAGGTGTGG	280888	113084	TTTTTTGACCAAAATAAAAG
191715	23911	GAAAGAGAGGTGCTATGATT	236302	68498	TTTATAAGCTAACAGGTGTG	280889	113085	TTTTTTTGACCAAAATAAAA
191716	23912	TGAAAGAGAGGTGCTATGAT	236303	68499	ATTTATAAGCTAACAGGTGT	280890	113086	TTTTTTTTGACCAAAATAAA
191717	23913	CTGAAAGAGAGGTGCTATGA	236304	68500	GATTTATAAGCTAACAGGTG	280891	113087	ATTTTTTTTGACCAAAATAA
191718	23914	CCTGAAAGAGAGGTGCTATG	236305	68501	TGATTTATAAGCTAACAGGT	280892	113088	TATTTTTTTTGACCAAAATA
191719	23915	CCCTGAAAGAGAGGTGCTAT	236306	68502	CTGATTTATAAGCTAACAGG	280893	113089	TTATTTTTTTTGACCAAAAT
191720	23916	GCCCTGAAAGAGAGGTGCTA	236307	68503	ACTGATTTATAAGCTAACAG	280894	113090	CTTATTTTTTTTGACCAAAA
191721	23917	AGCCCTGAAAGAGAGGTGCT	236308	68504	CACTGATTTATAAGCTAACA	280895	113091	GCTTATTTTTTTTGACCAAA
191722	23918	CAGCCCTGAAAGAGAGGTGC	236309	68505	CCACTGATTTATAAGCTAAC	280896	113092	TGCTTATTTTTTTTGACCAA
191723	23919	GCAGCCCTGAAAGAGAGGTG	236310	68506	ACCACTGATTTATAAGCTAA	280897	113093	TTGCTTATTTTTTTTGACCA
191724	23920	AGCAGCCCTGAAAGAGAGGT	236311	68507	TACCACTGATTTATAAGCTA	280898	113094	TTTGCTTATTTTTTTTGACC
191725	23921	CAGCAGCCCTGAAAGAGAGG	236312	68508	ATACCACTGATTTATAAGCT	280899	113095	TTTTGCTTATTTTTTTTGAC
191726	23922	ACAGCAGCCCTGAAAGAGAG	236313	68509	AATACCACTGATTTATAAGC	280900	113096	GTTTTGCTTATTTTTTTTGA
191727	23923	TACAGCAGCCCTGAAAGAGA	236314	68510	CAATACCACTGATTTATAAG	280901	113097	TGTTTTGCTTATTTTTTTTG
191728	23924	TTACAGCAGCCCTGAAAGAG	236315	68511	TCAATACCACTGATTTATAA	280902	113098	TTGTTTTGCTTATTTTTTTT
191729	23925	CTTACAGCAGCCCTGAAAGA	236316	68512	ATCAATACCACTGATTTATA	280903	113099	ATTGTTTTGCTTATTTTTTT
191730	23926	CCTTACAGCAGCCCTGAAAG	236317	68513	AATCAATACCACTGATTTAT	280904	113100	CATTGTTTTGCTTATTTTTT
191731	23927	TCCTTACAGCAGCCCTGAAA	236318	68514	TAATCAATACCACTGATTTA	280905	113101	ACATTGTTTTGCTTATTTTT
191732	23928	TTCCTTACAGCAGCCCTGAA	236319	68515	CTAATCAATACCACTGATTT	280906	113102	AACATTGTTTTGCTTATTTT
191733	23929	ATTCCTTACAGCAGCCCTGA	236320	68516	GCTAATCAATACCACTGATT	280907	113103	CAACATTGTTTTGCTTATTT
191734	23930	TATTCCTTACAGCAGCCCTG	236321	68517	TGCTAATCAATACCACTGAT	280908	113104	ACAACATTGTTTTGCTTATT
191735	23931	CTATTCCTTACAGCAGCCCT	236322	68518	ATGCTAATCAATACCACTGA	280909	113105	TACAACATTGTTTTGCTTAT
191736	23932	GCTATTCCTTACAGCAGCCC	236323	68519	CATGCTAATCAATACCACTG	280910	113106	TTACAACATTGTTTTGCTTA
191737	23933	TGCTATTCCTTACAGCAGCC	236324	68520	ACATGCTAATCAATACCACT	280911	113107	TTTACAACATTGTTTTGCTT
191738	23934	CTGCTATTCCTTACAGCAGC	236325	68521	TACATGCTAATCAATACCAC	280912	113108	GTTTACAACATTGTTTTGCT
191739	23935	ACTGCTATTCCTTACAGCAG	236326	68522	TTACATGCTAATCAATACCA	280913	113109	TGTTTACAACATTGTTTTGC
191740	23936	CACTGCTATTCCTTACAGCA	236327	68523	TTTACATGCTAATCAATACC	280914	113110	GTGTTTACAACATTGTTTTG
191741	23937	CCACTGCTATTCCTTACAGC	236328	68524	TTTTACATGCTAATCAATAC	280915	113111	GGTGTTTACAACATTGTTTT
191742	23938	ACCACTGCTATTCCTTACAG	236329	68525	ATTTTACATGCTAATCAATA	280916	113112	GGGTGTTTACAACATTGTTT
191743	23939	CACCACTGCTATTCCTTACA	236330	68526	TATTTTACATGCTAATCAAT	280917	113113	TGGGTGTTTACAACATTGTT
191744	23940	ACACCACTGCTATTCCTTAC	236331	68527	ATATTTTACATGCTAATCAA	280918	113114	CTGGGTGTTTACAACATTGT
191745	23941	CACACCACTGCTATTCCTTA	236332	68528	CATATTTTACATGCTAATCA	280919	113115	ACTGGGTGTTTACAACATTG
191746	23942	ACACACCACTGCTATTCCTT	236333	68529	ACATATTTTACATGCTAATC	280920	113116	CACTGGGTGTTTACAACATT
191747	23943	TACACACCACTGCTATTCCT	236334	68530	CACATATTTTACATGCTAAT	280921	113117	GCACTGGGTGTTTACAACAT
191748	23944	ATACACACCACTGCTATTCC	236335	68531	TCACATATTTTACATGCTAA	280922	113118	AGCACTGGGTGTTTACAACA
191749	23945	TATACACACCACTGCTATTC	236336	68532	GTCACATATTTTACATGCTA	280923	113119	CAGCACTGGGTGTTTACAAC
191750	23946	TTATACACACCACTGCTATT	236337	68533	AGTCACATATTTTACATGCT	280924	113120	CCAGCACTGGGTGTTTACAA
191751	23947	TTTATACACACCACTGCTAT	236338	68534	AAGTCACATATTTTACATGC	280925	113121	GCCAGCACTGGGTGTTTACA
191752	23948	CTTTATACACACCACTGCTA	236339	68535	AAAGTCACATATTTTACATG	280926	113122	TGCCAGCACTGGGTGTTTAC
191753	23949	GCTTTATACACACCACTGCT	236340	68536	TAAAGTCACATATTTTACAT	280927	113123	CTGCCAGCACTGGGTGTTTA
191754	23950	TGCTTTATACACACCACTGC	236341	68537	TTAAAGTCACATATTTTACA	280928	113124	GCTGCCAGCACTGGGTGTTT
191755	23951	CTGCTTTATACACACCACTG	236342	68538	TTTAAAGTCACATATTTTAC	280929	113125	TGCTGCCAGCACTGGGTGTT
191756	23952	TCTGCTTTATACACACCACT	236343	68539	GTTTAAAGTCACATATTTTA	280930	113126	TTGCTGCCAGCACTGGGTGT
191757	23953	CTCTGCTTTATACACACCAC	236344	68540	TGTTTAAAGTCACATATTTT	280931	113127	ATTGCTGCCAGCACTGGGTG
191758	23954	GCTCTGCTTTATACACACCA	236345	68541	ATGTTTAAAGTCACATATTT	280932	113128	CATTGCTGCCAGCACTGGGT
191759	23955	CGCTCTGCTTTATACACACC	236346	68542	AATGTTTAAAGTCACATATT	280933	113129	ACATTGCTGCCAGCACTGGG
191760	23956	GCGCTCTGCTTTATACACAC	236347	68543	CAATGTTTAAAGTCACATAT	280934	113130	CACATTGCTGCCAGCACTGG
191761	23957	TGCGCTCTGCTTTATACACA	236348	68544	GCAATGTTTAAAGTCACATA	280935	113131	CCACATTGCTGCCAGCACTG
191762	23958	GTGCGCTCTGCTTTATACAC	236349	68545	AGCAATGTTTAAAGTCACAT	280936	113132	ACCACATTGCTGCCAGCACT
191763	23959	TGTGCGCTCTGCTTTATACA	236350	68546	AAGCAATGTTTAAAGTCACA	280937	113133	CACCACATTGCTGCCAGCAC
191764	23960	CTGTGCGCTCTGCTTTATAC	236351	68547	AAAGCAATGTTTAAAGTCAC	280938	113134	TCACCACATTGCTGCCAGCA
191765	23961	GCTGTGCGCTCTGCTTTATA	236352	68548	AAAAGCAATGTTTAAAGTCA	280939	113135	CTCACCACATTGCTGCCAGC
191766	23962	GGCTGTGCGCTCTGCTTTAT	236353	68549	AAAAAGCAATGTTTAAAGTC	280940	113136	CCTCACCACATTGCTGCCAG
191767	23963	TGGCTGTGCGCTCTGCTTTA	236354	68550	TAAAAAGCAATGTTTAAAGT	280941	113137	GCCTCACCACATTGCTGCCA
191768	23964	CTGGCTGTGCGCTCTGCTTT	236355	68551	ATAAAAAGCAATGTTTAAAG	280942	113138	AGCCTCACCACATTGCTGCC
191769	23965	GCTGGCTGTGCGCTCTGCTT	236356	68552	GATAAAAAGCAATGTTTAAA	280943	113139	CAGCCTCACCACATTGCTGC
191770	23966	TGCTGGCTGTGCGCTCTGCT	236357	68553	AGATAAAAAGCAATGTTTAA	280944	113140	CCAGCCTCACCACATTGCTG
191771	23967	TTGCTGGCTGTGCGCTCTGC	236358	68554	GAGATAAAAAGCAATGTTTA	280945	113141	GCCAGCCTCACCACATTGCT
191772	23968	GTTGCTGGCTGTGCGCTCTG	236359	68555	AGAGATAAAAAGCAATGTTT	280946	113142	AGCCAGCCTCACCACATTGC
191773	23969	AGTTGCTGGCTGTGCGCTCT	236360	68556	AAGAGATAAAAAGCAATGTT	280947	113143	GAGCCAGCCTCACCACATTG
191774	23970	CAGTTGCTGGCTGTGCGCTC	236361	68557	TAAGAGATAAAAAGCAATGT	280948	113144	AGAGCCAGCCTCACCACATT
191775	23971	CCAGTTGCTGGCTGTGCGCT	236362	68558	GTAAGAGATAAAAAGCAATG	280949	113145	GAGAGCCAGCCTCACCACAT
191776	23972	GCCAGTTGCTGGCTGTGCGC	236363	68559	AGTAAGAGATAAAAAGCAAT	280950	113146	AGAGAGCCAGCCTCACCACA
191777	23973	GGCCAGTTGCTGGCTGTGCG	236364	68560	AAGTAAGAGATAAAAAGCAA	280951	113147	GAGAGAGCCAGCCTCACCAC
191778	23974	GGGCCAGTTGCTGGCTGTGC	236365	68561	TAAGTAAGAGATAAAAAGCA	280952	113148	TGAGAGAGCCAGCCTCACCA

191779	23975	GGGGCCAGTTGCTGGCTGTG	236366	68562	CTAAGTAAGAGATAAAAAGC	280953	113149	GTGAGAGAGCCAGCCTCACC
191780	23976	AGGGGCCAGTTGCTGGCTGT	236367	68563	TCTAAGTAAGAGATAAAAAG	280954	113150	GGTGAGAGAGCCAGCCTCAC
191781	23977	TAGGGGCCAGTTGCTGGCTG	236368	68564	ATCTAAGTAAGAGATAAAAA	280955	113151	TGGTGAGAGAGCCAGCCTCA
191782	23978	CTAGGGGCCAGTTGCTGGCT	236369	68565	GATCTAAGTAAGAGATAAAA	280956	113152	CTGGTGAGAGAGCCAGCCTC
191783	23979	GCTAGGGGCCAGTTGCTGGC	236370	68566	TGATCTAAGTAAGAGATAAA	280957	113153	CCTGGTGAGAGAGCCAGCCT
191784	23980	GGCTAGGGGCCAGTTGCTGG	236371	68567	CTGATCTAAGTAAGAGATAA	280958	113154	CCCTGGTGAGAGAGCCAGCC
191785	23981	TGGCTAGGGGCCAGTTGCTG	236372	68568	CCTGATCTAAGTAAGAGATA	280959	113155	GCCCTGGTGAGAGAGCCAGC
191786	23982	GTGGCTAGGGGCCAGTTGCT	236373	68569	GCCTGATCTAAGTAAGAGAT	280960	113156	AGCCCTGGTGAGAGAGCCAG
191787	23983	TGTGGCTAGGGGCCAGTTGC	236374	68570	GGCCTGATCTAAGTAAGAGA	280961	113157	GAGCCCTGGTGAGAGAGCCA
191788	23984	GTGTGGCTAGGGGCCAGTTG	236375	68571	AGGCCTGATCTAAGTAAGAG	280962	113158	TGAGCCCTGGTGAGAGAGCC
191789	23985	AGTGTGGCTAGGGGCCAGTT	236376	68572	CAGGCCTGATCTAAGTAAGA	280963	113159	GTGAGCCCTGGTGAGAGAGC
191790	23986	CAGTGTGGCTAGGGGCCAGT	236377	68573	TCAGGCCTGATCTAAGTAAG	280964	113160	TGTGAGCCCTGGTGAGAGAG
191791	23987	GCAGTGTGGCTAGGGGCCAG	236378	68574	CTCAGGCCTGATCTAAGTAA	280965	113161	CTGTGAGCCCTGGTGAGAGA
191792	23988	AGCAGTGTGGCTAGGGGCCA	236379	68575	ACTCAGGCCTGATCTAAGTA	280966	113162	CCTGTGAGCCCTGGTGAGAG
191793	23989	CAGCAGTGTGGCTAGGGGCC	236380	68576	CACTCAGGCCTGATCTAAGT	280967	113163	CCCTGTGAGCCCTGGTGAGA
191794	23990	TCAGCAGTGTGGCTAGGGGC	236381	68577	CCACTCAGGCCTGATCTAAG	280968	113164	TCCCTGTGAGCCCTGGTGAG
191795	23991	CTCAGCAGTGTGGCTAGGGG	236382	68578	GCCACTCAGGCCTGATCTAA	280969	113165	TTCCCTGTGAGCCCTGGTGA
191796	23992	GCTCAGCAGTGTGGCTAGGG	236383	68579	GGCCACTCAGGCCTGATCTA	280970	113166	TTTCCCTGTGAGCCCTGGTG
191797	23993	TGCTCAGCAGTGTGGCTAGG	236384	68580	AGGCCACTCAGGCCTGATCT	280971	113167	TTTTCCCTGTGAGCCCTGGT
191798	23994	GTGCTCAGCAGTGTGGCTAG	236385	68581	GAGGCCACTCAGGCCTGATC	280972	113168	GTTTTCCCTGTGAGCCCTGG
191799	23995	GGTGCTCAGCAGTGTGGCTA	236386	68582	AGAGGCCACTCAGGCCTGAT	280973	113169	AGTTTTCCCTGTGAGCCCTG
191800	23996	AGGTGCTCAGCAGTGTGGCT	236387	68583	GAGAGGCCACTCAGGCCTGA	280974	113170	GAGTTTTCCCTGTGAGCCCT
191801	23997	TAGGTGCTCAGCAGTGTGGC	236388	68584	AGAGAGGCCACTCAGGCCTG	280975	113171	TGAGTTTTCCCTGTGAGCCC
191802	23998	GTAGGTGCTCAGCAGTGTGG	236389	68585	AAGAGAGGCCACTCAGGCCT	280976	113172	ATGAGTTTTCCCTGTGAGCC
191803	23999	AGTAGGTGCTCAGCAGTGTG	236390	68586	AAAGAGAGGCCACTCAGGCC	280977	113173	CATGAGTTTTCCCTGTGAGC
191804	24000	CAGTAGGTGCTCAGCAGTGT	236391	68587	TAAAGAGAGGCCACTCAGGC	280978	113174	GCATGAGTTTTCCCTGTGAG
191805	24001	ACAGTAGGTGCTCAGCAGTG	236392	68588	CTAAAGAGAGGCCACTCAGG	280979	113175	TGCATGAGTTTTCCCTGTGA
191806	24002	CACAGTAGGTGCTCAGCAGT	236393	68589	GCTAAAGAGAGGCCACTCAG	280980	113176	TTGCATGAGTTTTCCCTGTG
191807	24003	TCACAGTAGGTGCTCAGCAG	236394	68590	TGCTAAAGAGAGGCCACTCA	280981	113177	GTTGCATGAGTTTTCCCTGT
191808	24004	ATCACAGTAGGTGCTCAGCA	236395	68591	TTGCTAAAGAGAGGCCACTC	280982	113178	GGTTGCATGAGTTTTCCCTG
191809	24005	TATCACAGTAGGTGCTCAGC	236396	68592	CTTGCTAAAGAGAGGCCACT	280983	113179	GGGTTGCATGAGTTTTCCCT
191810	24006	TTATCACAGTAGGTGCTCAG	236397	68593	TCTTGCTAAAGAGAGGCCAC	280984	113180	AGGGTTGCATGAGTTTTCCC
191811	24007	CTTATCACAGTAGGTGCTCA	236398	68594	CTCTTGCTAAAGAGAGGCCA	280985	113181	AAGGGTTGCATGAGTTTTCC
191812	24008	GCTTATCACAGTAGGTGCTC	236399	68595	ACTCTTGCTAAAGAGAGGCC	280986	113182	AAAGGGTTGCATGAGTTTTC
191813	24009	AGCTTATCACAGTAGGTGCT	236400	68596	AACTCTTGCTAAAGAGAGGC	280987	113183	AAAAGGGTTGCATGAGTTTT
191814	24010	CAGCTTATCACAGTAGGTGC	236401	68597	CAACTCTTGCTAAAGAGAGG	280988	113184	TAAAAGGGTTGCATGAGTTT
191815	24011	GCAGCTTATCACAGTAGGTG	236402	68598	CCAACTCTTGCTAAAGAGAG	280989	113185	CTAAAAGGGTTGCATGAGTT
191816	24012	GGCAGCTTATCACAGTAGGT	236403	68599	ACCAACTCTTGCTAAAGAGA	280990	113186	TCTAAAAGGGTTGCATGAGT
191817	24013	TGGCAGCTTATCACAGTAGG	236404	68600	AACCAACTCTTGCTAAAGAG	280991	113187	TTCTAAAAGGGTTGCATGAG
191818	24014	ATGGCAGCTTATCACAGTAG	236405	68601	TAACCAACTCTTGCTAAAGA	280992	113188	TTTCTAAAAGGGTTGCATGA
191819	24015	AATGGCAGCTTATCACAGTA	236406	68602	CTAACCAACTCTTGCTAAAG	280993	113189	CTTTCTAAAAGGGTTGCATG
191820	24016	CAATGGCAGCTTATCACAGT	236407	68603	GCTAACCAACTCTTGCTAAA	280994	113190	GCTTTCTAAAAGGGTTGCAT
191821	24017	ACAATGGCAGCTTATCACAG	236408	68604	GGCTAACCAACTCTTGCTAA	280995	113191	GGCTTTCTAAAAGGGTTGCA
191822	24018	CACAATGGCAGCTTATCACA	236409	68605	GGGCTAACCAACTCTTGCTA	280996	113192	TGGCTTTCTAAAAGGGTTGC
191823	24019	CCACAATGGCAGCTTATCAC	236410	68606	AGGGCTAACCAACTCTTGCT	280997	113193	ATGGCTTTCTAAAAGGGTTG
191824	24020	ACCACAATGGCAGCTTATCA	236411	68607	CAGGGCTAACCAACTCTTGC	280998	113194	CATGGCTTTCTAAAAGGGTT
191825	24021	CACCACAATGGCAGCTTATC	236412	68608	CCAGGGCTAACCAACTCTTG	280999	113195	ACATGGCTTTCTAAAAGGGT
191826	24022	ACACCACAATGGCAGCTTAT	236413	68609	CCCAGGGCTAACCAACTCTT	281000	113196	CACATGGCTTTCTAAAAGGG
191827	24023	CACACCACAATGGCAGCTTA	236414	68610	TCCCAGGGCTAACCAACTCT	281001	113197	CCACATGGCTTTCTAAAAGG
191828	24024	ACACACCACAATGGCAGCTT	236415	68611	ATCCCAGGGCTAACCAACTC	281002	113198	TCCACATGGCTTTCTAAAAG
191829	24025	CACACACCACAATGGCAGCT	236416	68612	AATCCCAGGGCTAACCAACT	281003	113199	CTCCACATGGCTTTCTAAAA
191830	24026	TCACACACCACAATGGCAGC	236417	68613	GAATCCCAGGGCTAACCAAC	281004	113200	TCTCCACATGGCTTTCTAAA
191831	24027	TTCACACACCACAATGGCAG	236418	68614	AGAATCCCAGGGCTAACCAA	281005	113201	CTCTCCACATGGCTTTCTAA
191832	24028	CTTCACACACCACAATGGCA	236419	68615	AAGAATCCCAGGGCTAACCA	281006	113202	ACTCTCCACATGGCTTTCTA
191833	24029	GCTTCACACACCACAATGGC	236420	68616	TAAGAATCCCAGGGCTAACC	281007	113203	AACTCTCCACATGGCTTTCT
191834	24030	TGCTTCACACACCACAATGG	236421	68617	GTAAGAATCCCAGGGCTAAC	281008	113204	CAACTCTCCACATGGCTTTC
191835	24031	TTGCTTCACACACCACAATG	236422	68618	AGTAAGAATCCCAGGGCTAA	281009	113205	ACAACTCTCCACATGGCTTT
191836	24032	TTTGCTTCACACACCACAAT	236423	68619	CAGTAAGAATCCCAGGGCTA	281010	113206	TACAACTCTCCACATGGCTT
191837	24033	CTTTGCTTCACACACCACAA	236424	68620	ACAGTAAGAATCCCAGGGCT	281011	113207	GTACAACTCTCCACATGGCT
191838	24034	CCTTTGCTTCACACACCACA	236425	68621	TACAGTAAGAATCCCAGGGC	281012	113208	GGTACAACTCTCCACATGGC
191839	24035	CCCTTTGCTTCACACACCAC	236426	68622	CTACAGTAAGAATCCCAGGG	281013	113209	CGGTACAACTCTCCACATGG
191840	24036	CCCCTTTGCTTCACACACCA	236427	68623	GCTACAGTAAGAATCCCAGG	281014	113210	TCGGTACAACTCTCCACATG
191841	24037	TCCCCTTTGCTTCACACACC	236428	68624	GGCTACAGTAAGAATCCCAG	281015	113211	CTCGGTACAACTCTCCACAT
191842	24038	TTCCCCTTTGCTTCACACAC	236429	68625	TGGCTACAGTAAGAATCCCA	281016	113212	TCTCGGTACAACTCTCCACA
191843	24039	TTTCCCCTTTGCTTCACACA	236430	68626	GTGGCTACAGTAAGAATCCC	281017	113213	CTCTCGGTACAACTCTCCAC
191844	24040	GTTTCCCCTTTGCTTCACAC	236431	68627	TGTGGCTACAGTAAGAATCC	281018	113214	CCTCTCGGTACAACTCTCCA
191845	24041	TGTTTCCCCTTTGCTTCACA	236432	68628	ATGTGGCTACAGTAAGAATC	281019	113215	ACCTCTCGGTACAACTCTCC
191846	24042	ATGTTTCCCCTTTGCTTCAC	236433	68629	AATGTGGCTACAGTAAGAAT	281020	113216	AACCTCTCGGTACAACTCTC
191847	24043	CATGTTTCCCCTTTGCTTCA	236434	68630	TAATGTGGCTACAGTAAGAA	281021	113217	AAACCTCTCGGTACAACTCT
191848	24044	GCATGTTTCCCCTTTGCTTC	236435	68631	TTAATGTGGCTACAGTAAGA	281022	113218	AAAACCTCTCGGTACAACTC
191849	24045	GGCATGTTTCCCCTTTGCTT	236436	68632	ATTAATGTGGCTACAGTAAG	281023	113219	TAAAACCTCTCGGTACAACT
191850	24046	AGGCATGTTTCCCCTTTGCT	236437	68633	TATTAATGTGGCTACAGTAA	281024	113220	CTAAAACCTCTCGGTACAAC

191851	24047	CAGGCATGTTTCCCCTTTGC	236438	68634	TTATTAATGTGGCTACAGTA	281025	113221	TCTAAAACCTCTCGGTACAA
191852	24048	GCAGGCATGTTTCCCCTTTG	236439	68635	TTTATTAATGTGGCTACAGT	281026	113222	TTCTAAAACCTCTCGGTACA
191853	24049	AGCAGGCATGTTTCCCCTTT	236440	68636	GTTTATTAATGTGGCTACAG	281027	113223	ATTCTAAAACCTCTCGGTAC
191854	24050	CAGCAGGCATGTTTCCCCTT	236441	68637	TGTTTATTAATGTGGCTACA	281028	113224	TATTCTAAAACCTCTCGGTA
191855	24051	ACAGCAGGCATGTTTCCCCT	236442	68638	TTGTTTATTAATGTGGCTAC	281029	113225	ATATTCTAAAACCTCTCGGT
191856	24052	TACAGCAGGCATGTTTCCCC	236443	68639	GTTGTTTATTAATGTGGCTA	281030	113226	AATATTCTAAAACCTCTCGG
191857	24053	CTACAGCAGGCATGTTTCCC	236444	68640	TGTTGTTTATTAATGTGGCT	281031	113227	AAATATTCTAAAACCTCTCG
191858	24054	ACTACAGCAGGCATGTTTCC	236445	68641	ATGTTGTTTATTAATGTGGC	281032	113228	TAAATATTCTAAAACCTCTC
191859	24055	CACTACAGCAGGCATGTTTC	236446	68642	GATGTTGTTTATTAATGTGG	281033	113229	ATAAATATTCTAAAACCTCT
191860	24056	TCACTACAGCAGGCATGTTT	236447	68643	CGATGTTGTTTATTAATGTG	281034	113230	TATAAATATTCTAAAACCTC
191861	24057	CTCACTACAGCAGGCATGTT	236448	68644	TCGATGTTGTTTATTAATGT	281035	113231	TTATAAATATTCTAAAACCT
191862	24058	GCTCACTACAGCAGGCATGT	236449	68645	GTCGATGTTGTTTATTAATG	281036	113232	GTTATAAATATTCTAAAACC
191863	24059	AGCTCACTACAGCAGGCATG	236450	68646	AGTCGATGTTGTTTATTAAT	281037	113233	AGTTATAAATATTCTAAAAC
191864	24060	AAGCTCACTACAGCAGGCAT	236451	68647	AAGTCGATGTTGTTTATTAA	281038	113234	AAGTTATAAATATTCTAAAA
191865	24061	GAAGCTCACTACAGCAGGCA	236452	68648	GAAGTCGATGTTGTTTATTA	281039	113235	AAAGTTATAAATATTCTAAA
191866	24062	GGAAGCTCACTACAGCAGGC	236453	68649	AGAAGTCGATGTTGTTTATT	281040	113236	CAAAGTTATAAATATTCTAA
191867	24063	AGGAAGCTCACTACAGCAGG	236454	68650	TAGAAGTCGATGTTGTTTAT	281041	113237	TCAAAGTTATAAATATTCTA
191868	24064	CAGGAAGCTCACTACAGCAG	236455	68651	TTAGAAGTCGATGTTGTTTA	281042	113238	GTCAAAGTTATAAATATTCT
191869	24065	ACAGGAAGCTCACTACAGCA	236456	68652	TTTAGAAGTCGATGTTGTTT	281043	113239	GGTCAAAGTTATAAATATTC
191870	24066	TACAGGAAGCTCACTACAGC	236457	68653	GTTTAGAAGTCGATGTTGTT	281044	113240	GGGTCAAAGTTATAAATATT
191871	24067	CTACAGGAAGCTCACTACAG	236458	68654	TGTTTAGAAGTCGATGTTGT	281045	113241	TGGGTCAAAGTTATAAATAT
191872	24068	CCTACAGGAAGCTCACTACA	236459	68655	ATGTTTAGAAGTCGATGTTG	281046	113242	CTGGGTCAAAGTTATAAATA
191873	24069	CCCTACAGGAAGCTCACTAC	236460	68656	AATGTTTAGAAGTCGATGTT	281047	113243	TCTGGGTCAAAGTTATAAAT
191874	24070	GCCCTACAGGAAGCTCACTA	236461	68657	GAATGTTTAGAAGTCGATGT	281048	113244	TTCTGGGTCAAAGTTATAAA
191875	24071	TGCCCTACAGGAAGCTCACT	236462	68658	AGAATGTTTAGAAGTCGATG	281049	113245	TTTCTGGGTCAAAGTTATAA
191876	24072	CTGCCCTACAGGAAGCTCAC	236463	68659	TAGAATGTTTAGAAGTCGAT	281050	113246	ATTTCTGGGTCAAAGTTATA
191877	24073	CCTGCCCTACAGGAAGCTCA	236464	68660	ATAGAATGTTTAGAAGTCGA	281051	113247	AATTTCTGGGTCAAAGTTAT
191878	24074	ACCTGCCCTACAGGAAGCTC	236465	68661	TATAGAATGTTTAGAAGTCG	281052	113248	GAATTTCTGGGTCAAAGTTA
191879	24075	AACCTGCCCTACAGGAAGCT	236466	68662	TTATAGAATGTTTAGAAGTC	281053	113249	AGAATTTCTGGGTCAAAGTT
191880	24076	CAACCTGCCCTACAGGAAGC	236467	68663	ATTATAGAATGTTTAGAAGT	281054	113250	TAGAATTTCTGGGTCAAAGT
191881	24077	ACAACCTGCCCTACAGGAAG	236468	68664	TATTATAGAATGTTTAGAAG	281055	113251	ATAGAATTTCTGGGTCAAAG
191882	24078	TACAACCTGCCCTACAGGAA	236469	68665	GTATTATAGAATGTTTAGAA	281056	113252	AATAGAATTTCTGGGTCAAA
191883	24079	CTACAACCTGCCCTACAGGA	236470	68666	GGTATTATAGAATGTTTAGA	281057	113253	GAATAGAATTTCTGGGTCAA
191884	24080	TCTACAACCTGCCCTACAGG	236471	68667	TGGTATTATAGAATGTTTAG	281058	113254	AGAATAGAATTTCTGGGTCA
191885	24081	TTCTACAACCTGCCCTACAG	236472	68668	ATGGTATTATAGAATGTTTA	281059	113255	TAGAATAGAATTTCTGGGTC
191886	24082	GTTCTACAACCTGCCCTACA	236473	68669	GATGGTATTATAGAATGTTT	281060	113256	CTAGAATAGAATTTCTGGGT
191887	24083	GGTTCTACAACCTGCCCTAC	236474	68670	AGATGGTATTATAGAATGTT	281061	113257	CCTAGAATAGAATTTCTGGG
191888	24084	TGGTTCTACAACCTGCCCTA	236475	68671	AAGATGGTATTATAGAATGT	281062	113258	TCCTAGAATAGAATTTCTGG
191889	24085	CTGGTTCTACAACCTGCCCT	236476	68672	AAAGATGGTATTATAGAATG	281063	113259	GTCCTAGAATAGAATTTCTG
191890	24086	TCTGGTTCTACAACCTGCCC	236477	68673	AAAAGATGGTATTATAGAAT	281064	113260	AGTCCTAGAATAGAATTTCT
191891	24087	CTCTGGTTCTACAACCTGCC	236478	68674	CAAAAGATGGTATTATAGAA	281065	113261	GAGTCCTAGAATAGAATTTC
191892	24088	CCTCTGGTTCTACAACCTGC	236479	68675	CCAAAAGATGGTATTATAGA	281066	113262	AGAGTCCTAGAATAGAATTT
191893	24089	ACCTCTGGTTCTACAACCTG	236480	68676	GCCAAAAGATGGTATTATAG	281067	113263	CAGAGTCCTAGAATAGAATT
191894	24090	CACCTCTGGTTCTACAACCT	236481	68677	GGCCAAAAGATGGTATTATA	281068	113264	ACAGAGTCCTAGAATAGAAT
191895	24091	CCACCTCTGGTTCTACAACC	236482	68678	TGGCCAAAAGATGGTATTAT	281069	113265	CACAGAGTCCTAGAATAGAA
191896	24092	CCCACCTCTGGTTCTACAAC	236483	68679	TTGGCCAAAAGATGGTATTA	281070	113266	ACACAGAGTCCTAGAATAGA
191897	24093	ACCCACCTCTGGTTCTACAA	236484	68680	TTTGGCCAAAAGATGGTATT	281071	113267	AACACAGAGTCCTAGAATAG
191898	24094	AACCCACCTCTGGTTCTACA	236485	68681	ATTTGGCCAAAAGATGGTAT	281072	113268	TAACACAGAGTCCTAGAATA
191899	24095	GAACCCACCTCTGGTTCTAC	236486	68682	AATTTGGCCAAAAGATGGTA	281073	113269	ATAACACAGAGTCCTAGAAT
191900	24096	GGAACCCACCTCTGGTTCTA	236487	68683	CAATTTGGCCAAAAGATGGT	281074	113270	CATAACACAGAGTCCTAGAA
191901	24097	TGGAACCCACCTCTGGTTCT	236488	68684	TCAATTTGGCCAAAAGATGG	281075	113271	TCATAACACAGAGTCCTAGA
191902	24098	TTGGAACCCACCTCTGGTTC	236489	68685	GTCAATTTGGCCAAAAGATG	281076	113272	TTCATAACACAGAGTCCTAG
191903	24099	CTTGGAACCCACCTCTGGTT	236490	68686	AGTCAATTTGGCCAAAAGAT	281077	113273	TTTCATAACACAGAGTCCTA
191904	24100	CCTTGGAACCCACCTCTGGT	236491	68687	AAGTCAATTTGGCCAAAAGA	281078	113274	TTTTCATAACACAGAGTCCT
191905	24101	ACCTTGGAACCCACCTCTGG	236492	68688	GAAGTCAATTTGGCCAAAAG	281079	113275	ATTTTCATAACACAGAGTCC
191906	24102	AACCTTGGAACCCACCTCTG	236493	68689	CGAAGTCAATTTGGCCAAAA	281080	113276	TATTTTCATAACACAGAGTC
191907	24103	TAACCTTGGAACCCACCTCT	236494	68690	GCGAAGTCAATTTGGCCAAA	281081	113277	TTATTTTCATAACACAGAGT
191908	24104	GTAACCTTGGAACCCACCTC	236495	68691	GGCGAAGTCAATTTGGCCAA	281082	113278	GTTATTTTCATAACACAGAG
191909	24105	TGTAACCTTGGAACCCACCT	236496	68692	AGGCGAAGTCAATTTGGCCA	281083	113279	GGTTATTTTCATAACACAGA
191910	24106	TTGTAACCTTGGAACCCACC	236497	68693	GAGGCGAAGTCAATTTGGCC	281084	113280	GGGTTATTTTCATAACACAG
191911	24107	TTTGTAACCTTGGAACCCAC	236498	68694	AGAGGCGAAGTCAATTTGGC	281085	113281	TGGGTTATTTTCATAACACA
191912	24108	CTTTGTAACCTTGGAACCCA	236499	68695	AAGAGGCGAAGTCAATTTGG	281086	113282	ATGGGTTATTTTCATAACAC
191913	24109	CCTTTGTAACCTTGGAACCC	236500	68696	GAAGAGGCGAAGTCAATTTG	281087	113283	GATGGGTTATTTTCATAACA
191914	24110	CCCTTTGTAACCTTGGAACC	236501	68697	GGAAGAGGCGAAGTCAATTT	281088	113284	TGATGGGTTATTTTCATAAC
191915	24111	TCCCTTTGTAACCTTGGAAC	236502	68698	AGGAAGAGGCGAAGTCAATT	281089	113285	ATGATGGGTTATTTTCATAA
191916	24112	GTCCCTTTGTAACCTTGGAA	236503	68699	GAGGAAGAGGCGAAGTCAAT	281090	113286	TATGATGGGTTATTTTCATA
191917	24113	AGTCCCTTTGTAACCTTGGA	236504	68700	AGAGGAAGAGGCGAAGTCAA	281091	113287	ATATGATGGGTTATTTTCAT
191918	24114	GAGTCCCTTTGTAACCTTGG	236505	68701	GAGAGGAAGAGGCGAAGTCA	281092	113288	CATATGATGGGTTATTTTCA
191919	24115	AGAGTCCCTTTGTAACCTTG	236506	68702	AGAGAGGAAGAGGCGAAGTC	281093	113289	CCATATGATGGGTTATTTTC
191920	24116	AAGAGTCCCTTTGTAACCTT	236507	68703	GAGAGAGGAAGAGGCGAAGT	281094	113290	TCCATATGATGGGTTATTTT
191921	24117	TAAGAGTCCCTTTGTAACCT	236508	68704	AGAGAGAGGAAGAGGCGAAG	281095	113291	TTCCATATGATGGGTTATTT
191922	24118	CTAAGAGTCCCTTTGTAACC	236509	68705	AAGAGAGAGGAAGAGGCGAA	281096	113292	TTTCCATATGATGGGTTATT

191923	24119	ACTAAGAGTCCCTTTGTAAC	236510	68706	AAAGAGAGAGGAAGAGGCGA	281097	113293	TTTTCCATATGATGGGTTAT
191924	24120	CACTAAGAGTCCCTTTGTAA	236511	68707	GAAAGAGAGAGGAAGAGGCG	281098	113294	TTTTTCCATATGATGGGTTA
191925	24121	ACACTAAGAGTCCCTTTGTA	236512	68708	GGAAAGAGAGAGGAAGAGGC	281099	113295	CTTTTTCCATATGATGGGTT
191926	24122	TACACTAAGAGTCCCTTTGT	236513	68709	TGGAAAGAGAGAGGAAGAGG	281100	113296	GCTTTTTCCATATGATGGGT
191927	24123	ATACACTAAGAGTCCCTTTG	236514	68710	TTGGAAAGAGAGAGGAAGAG	281101	113297	AGCTTTTTCCATATGATGGG
191928	24124	AATACACTAAGAGTCCCTTT	236515	68711	TTTGGAAAGAGAGAGGAAGA	281102	113298	GAGCTTTTTCCATATGATGG
191929	24125	TAATACACTAAGAGTCCCTT	236516	68712	ATTTGGAAAGAGAGAGGAAG	281103	113299	GGAGCTTTTTCCATATGATG
191930	24126	CTAATACACTAAGAGTCCCT	236517	68713	CATTTGGAAAGAGAGAGGAA	281104	113300	AGGAGCTTTTTCCATATGAT
191931	24127	ACTAATACACTAAGAGTCCC	236518	68714	TCATTTGGAAAGAGAGAGGA	281105	113301	AAGGAGCTTTTTCCATATGA
191932	24128	GACTAATACACTAAGAGTCC	236519	68715	TTCATTTGGAAAGAGAGAGG	281106	113302	AAAGGAGCTTTTTCCATATG
191933	24129	AGACTAATACACTAAGAGTC	236520	68716	TTTCATTTGGAAAGAGAGAG	281107	113303	GAAAGGAGCTTTTTCCATAT
191934	24130	CAGACTAATACACTAAGAGT	236521	68717	ATTTCATTTGGAAAGAGAGA	281108	113304	TGAAAGGAGCTTTTTCCATA
191935	24131	ACAGACTAATACACTAAGAG	236522	68718	CATTTCATTTGGAAAGAGAG	281109	113305	CTGAAAGGAGCTTTTTCCAT
191936	24132	AACAGACTAATACACTAAGA	236523	68719	ACATTTCATTTGGAAAGAGA	281110	113306	TCTGAAAGGAGCTTTTTCCA
191937	24133	GAACAGACTAATACACTAAG	236524	68720	CACATTTCATTTGGAAAGAG	281111	113307	TTCTGAAAGGAGCTTTTTCC
191938	24134	AGAACAGACTAATACACTAA	236525	68721	ACACATTTCATTTGGAAAGA	281112	113308	TTTCTGAAAGGAGCTTTTTC
191939	24135	GAGAACAGACTAATACACTA	236526	68722	AACACATTTCATTTGGAAAG	281113	113309	CTTTCTGAAAGGAGCTTTTT
191940	24136	TGAGAACAGACTAATACACT	236527	68723	AAACACATTTCATTTGGAAA	281114	113310	TCTTTCTGAAAGGAGCTTTT
191941	24137	GTGAGAACAGACTAATACAC	236528	68724	GAAACACATTTCATTTGGAA	281115	113311	CTCTTTCTGAAAGGAGCTTT
191942	24138	TGTGAGAACAGACTAATACA	236529	68725	TGAAACACATTTCATTTGGA	281116	113312	CCTCTTTCTGAAAGGAGCTT
191943	24139	ATGTGAGAACAGACTAATAC	236530	68726	ATGAAACACATTTCATTTGG	281117	113313	ACCTCTTTCTGAAAGGAGCT
191944	24140	AATGTGAGAACAGACTAATA	236531	68727	AATGAAACACATTTCATTTG	281118	113314	AACCTCTTTCTGAAAGGAGC
191945	24141	TAATGTGAGAACAGACTAAT	236532	68728	AAATGAAACACATTTCATTT	281119	113315	GAACCTCTTTCTGAAAGGAG
191946	24142	GTAATGTGAGAACAGACTAA	236533	68729	GAAATGAAACACATTTCATT	281120	113316	TGAACCTCTTTCTGAAAGGA
191947	24143	AGTAATGTGAGAACAGACTA	236534	68730	TGAAATGAAACACATTTCAT	281121	113317	ATGAACCTCTTTCTGAAAGG
191948	24144	TAGTAATGTGAGAACAGACT	236535	68731	GTGAAATGAAACACATTTCA	281122	113318	CATGAACCTCTTTCTGAAAG
191949	24145	ATAGTAATGTGAGAACAGAC	236536	68732	AGTGAAATGAAACACATTTC	281123	113319	CCATGAACCTCTTTCTGAAA
191950	24146	TATAGTAATGTGAGAACAGA	236537	68733	CAGTGAAATGAAACACATTT	281124	113320	CCCATGAACCTCTTTCTGAA
191951	24147	TTATAGTAATGTGAGAACAG	236538	68734	ACAGTGAAATGAAACACATT	281125	113321	TCCCATGAACCTCTTTCTGA
191952	24148	TTTATAGTAATGTGAGAACA	236539	68735	GACAGTGAAATGAAACACAT	281126	113322	CTCCCATGAACCTCTTTCTG
191953	24149	CTTTATAGTAATGTGAGAAC	236540	68736	TGACAGTGAAATGAAACACA	281127	113323	CCTCCCATGAACCTCTTTCT
191954	24150	TCTTTATAGTAATGTGAGAA	236541	68737	CTGACAGTGAAATGAAACAC	281128	113324	GCCTCCCATGAACCTCTTTC
191955	24151	GTCTTTATAGTAATGTGAGA	236542	68738	TCTGACAGTGAAATGAAACA	281129	113325	AGCCTCCCATGAACCTCTTT
191956	24152	GGTCTTTATAGTAATGTGAG	236543	68739	GTCTGACAGTGAAATGAAAC	281130	113326	CAGCCTCCCATGAACCTCTT
191957	24153	AGGTCTTTATAGTAATGTGA	236544	68740	GGTCTGACAGTGAAATGAAA	281131	113327	ACAGCCTCCCATGAACCTCT
191958	24154	TAGGTCTTTATAGTAATGTG	236545	68741	TGGTCTGACAGTGAAATGAA	281132	113328	AACAGCCTCCCATGAACCTC
191959	24155	GTAGGTCTTTATAGTAATGT	236546	68742	GTGGTCTGACAGTGAAATGA	281133	113329	AAACAGCCTCCCATGAACCT
191960	24156	GGTAGGTCTTTATAGTAATG	236547	68743	TGTGGTCTGACAGTGAAATG	281134	113330	CAAACAGCCTCCCATGAACC
191961	24157	AGGTAGGTCTTTATAGTAAT	236548	68744	ATGTGGTCTGACAGTGAAAT	281135	113331	ACAAACAGCCTCCCATGAAC
191962	24158	CAGGTAGGTCTTTATAGTAA	236549	68745	CATGTGGTCTGACAGTGAAA	281136	113332	TACAAACAGCCTCCCATGAA
191963	24159	TCAGGTAGGTCTTTATAGTA	236550	68746	CCATGTGGTCTGACAGTGAA	281137	113333	ATACAAACAGCCTCCCATGA
191964	24160	CTCAGGTAGGTCTTTATAGT	236551	68747	ACCATGTGGTCTGACAGTGA	281138	113334	AATACAAACAGCCTCCCATG
191965	24161	TCTCAGGTAGGTCTTTATAG	236552	68748	AACCATGTGGTCTGACAGTG	281139	113335	AAATACAAACAGCCTCCCAT
191966	24162	GTCTCAGGTAGGTCTTTATA	236553	68749	CAACCATGTGGTCTGACAGT	281140	113336	AAAATACAAACAGCCTCCCA
191967	24163	AGTCTCAGGTAGGTCTTTAT	236554	68750	CCAACCATGTGGTCTGACAG	281141	113337	AAAAATACAAACAGCCTCCC
191968	24164	CAGTCTCAGGTAGGTCTTTA	236555	68751	CCCAACCATGTGGTCTGACA	281142	113338	AAAAAATACAAACAGCCTCC
191969	24165	CCAGTCTCAGGTAGGTCTTT	236556	68752	CCCCAACCATGTGGTCTGAC	281143	113339	AAAAAAATACAAACAGCCTC
191970	24166	TCCAGTCTCAGGTAGGTCTT	236557	68753	TCCCCAACCATGTGGTCTGA	281144	113340	AAAAAAAATACAAACAGCCT
191971	24167	ATCCAGTCTCAGGTAGGTCT	236558	68754	GTCCCCAACCATGTGGTCTG	281145	113341	AAAAAAAAATACAAACAGCC
191972	24168	GATCCAGTCTCAGGTAGGTC	236559	68755	GGTCCCCAACCATGTGGTCT	281146	113342	AAAAAAAAAATACAAACAGC
191973	24169	TGATCCAGTCTCAGGTAGGT	236560	68756	GGGTCCCCAACCATGTGGTC	281147	113343	GAAAAAAAAAATACAAACAG
191974	24170	ATGATCCAGTCTCAGGTAGG	236561	68757	GGGGTCCCCAACCATGTGGT	281148	113344	AGAAAAAAAAAATACAAACA
191975	24171	AATGATCCAGTCTCAGGTAG	236562	68758	TGGGGTCCCCAACCATGTGG	281149	113345	AAGAAAAAAAAAATACAAAC
191976	24172	AAATGATCCAGTCTCAGGTA	236563	68759	GTGGGGTCCCCAACCATGTG	281150	113346	AAAGAAAAAAAAAATACAAA
191977	24173	TAAATGATCCAGTCTCAGGT	236564	68760	TGTGGGGTCCCCAACCATGT	281151	113347	CAAAGAAAAAAAAAATACAA
191978	24174	ATAAATGATCCAGTCTCAGG	236565	68761	CTGTGGGGTCCCCAACCATG	281152	113348	GCAAAGAAAAAAAAAATACA
191979	24175	TATAAATGATCCAGTCTCAG	236566	68762	TCTGTGGGGTCCCCAACCAT	281153	113349	TGCAAAGAAAAAAAAAATAC
191980	24176	TTATAAATGATCCAGTCTCA	236567	68763	CTCTGTGGGGTCCCCAACCA	281154	113350	ATGCAAAGAAAAAAAAAATA
191981	24177	TTTATAAATGATCCAGTCTC	236568	68764	GCTCTGTGGGGTCCCCAACC	281155	113351	GATGCAAAGAAAAAAAAAAT
191982	24178	CTTTATAAATGATCCAGTCT	236569	68765	TGCTCTGTGGGGTCCCCAAC	281156	113352	TGATGCAAAGAAAAAAAAAA
191983	24179	TCTTTATAAATGATCCAGTC	236570	68766	GTGCTCTGTGGGGTCCCCAA	281157	113353	TTGATGCAAAGAAAAAAAAA
191984	24180	TTCTTTATAAATGATCCAGT	236571	68767	TGTGCTCTGTGGGGTCCCCA	281158	113354	TTTGATGCAAAGAAAAAAAA
191985	24181	TTTCTTTATAAATGATCCAG	236572	68768	GTGTGCTCTGTGGGGTCCCC	281159	113355	ATTTGATGCAAAGAAAAAAA
191986	24182	TTTTCTTTATAAATGATCCA	236573	68769	TGTGTGCTCTGTGGGGTCCC	281160	113356	GATTTGATGCAAAGAAAAAA
191987	24183	CTTTTCTTTATAAATGATCC	236574	68770	CTGTGTGCTCTGTGGGGTCC	281161	113357	GGATTTGATGCAAAGAAAAA
191988	24184	TCTTTTCTTTATAAATGATC	236575	68771	GCTGTGTGCTCTGTGGGGTC	281162	113358	TGGATTTGATGCAAAGAAAA
191989	24185	CTCTTTTCTTTATAAATGAT	236576	68772	GGCTGTGTGCTCTGTGGGGT	281163	113359	CTGGATTTGATGCAAAGAAA
191990	24186	CCTCTTTTCTTTATAAATGA	236577	68773	GGGCTGTGTGCTCTGTGGGG	281164	113360	GCTGGATTTGATGCAAAGAA
191991	24187	ACCTCTTTTCTTTATAAATG	236578	68774	AGGGCTGTGTGCTCTGTGGG	281165	113361	AGCTGGATTTGATGCAAAGA
191992	24188	AACCTCTTTTCTTTATAAAT	236579	68775	GAGGGCTGTGTGCTCTGTGG	281166	113362	GAGCTGGATTTGATGCAAAG
191993	24189	AAACCTCTTTTCTTTATAAA	236580	68776	GGAGGGCTGTGTGCTCTGTG	281167	113363	GGAGCTGGATTTGATGCAAA
191994	24190	TAAACCTCTTTTCTTTATAA	236581	68777	GGGAGGGCTGTGTGCTCTGT	281168	113364	AGGAGCTGGATTTGATGCAA

191995	24191	TTAAACCTCTTTTCTTTATA	236582	68778	AGGGAGGGCTGTGTGCTCTG	281169	113365	CAGGAGCTGGATTTGATGCA
191996	24192	ATTAAACCTCTTTTCTTTAT	236583	68779	GAGGGAGGGCTGTGTGCTCT	281170	113366	GCAGGAGCTGGATTTGATGC
191997	24193	AATTAAACCTCTTTTCTTTA	236584	68780	AGAGGGAGGGCTGTGTGCTC	281171	113367	TGCAGGAGCTGGATTTGATG
191998	24194	CAATTAAACCTCTTTTCTTT	236585	68781	CAGAGGGAGGGCTGTGTGCT	281172	113368	CTGCAGGAGCTGGATTTGAT
191999	24195	CCAATTAAACCTCTTTTCTT	236586	68782	GCAGAGGGAGGGCTGTGTGC	281173	113369	CCTGCAGGAGCTGGATTTGA
192000	24196	GCCAATTAAACCTCTTTTCT	236587	68783	GGCAGAGGGAGGGCTGTGTG	281174	113370	TCCTGCAGGAGCTGGATTTG
192001	24197	AGCCAATTAAACCTCTTTTC	236588	68784	AGGCAGAGGGAGGGCTGTGT	281175	113371	GTCCTGCAGGAGCTGGATTT
192002	24198	GAGCCAATTAAACCTCTTTT	236589	68785	AAGGCAGAGGGAGGGCTGTG	281176	113372	AGTCCTGCAGGAGCTGGATT
192003	24199	TGAGCCAATTAAACCTCTTT	236590	68786	GAAGGCAGAGGGAGGGCTGT	281177	113373	CAGTCCTGCAGGAGCTGGAT
192004	24200	GTGAGCCAATTAAACCTCTT	236591	68787	GGAAGGCAGAGGGAGGGCTG	281178	113374	ACAGTCCTGCAGGAGCTGGA
192005	24201	TGTGAGCCAATTAAACCTCT	236592	68788	GGGAAGGCAGAGGGAGGGCT	281179	113375	AACAGTCCTGCAGGAGCTGG
192006	24202	ATGTGAGCCAATTAAACCTC	236593	68789	TGGGAAGGCAGAGGGAGGGC	281180	113376	AAACAGTCCTGCAGGAGCTG
192007	24203	AATGTGAGCCAATTAAACCT	236594	68790	ATGGGAAGGCAGAGGGAGGG	281181	113377	CAAACAGTCCTGCAGGAGCT
192008	24204	CAATGTGAGCCAATTAAACC	236595	68791	CATGGGAAGGCAGAGGGAGG	281182	113378	ACAAACAGTCCTGCAGGAGC
192009	24205	CCAATGTGAGCCAATTAAAC	236596	68792	GCATGGGAAGGCAGAGGGAG	281183	113379	TACAAACAGTCCTGCAGGAG
192010	24206	GCCAATGTGAGCCAATTAAA	236597	68793	AGCATGGGAAGGCAGAGGGA	281184	113380	ATACAAACAGTCCTGCAGGA
192011	24207	AGCCAATGTGAGCCAATTAA	236598	68794	CAGCATGGGAAGGCAGAGGG	281185	113381	AATACAAACAGTCCTGCAGG
192012	24208	CAGCCAATGTGAGCCAATTA	236599	68795	CCAGCATGGGAAGGCAGAGG	281186	113382	TAATACAAACAGTCCTGCAG
192013	24209	CCAGCCAATGTGAGCCAATT	236600	68796	GCCAGCATGGGAAGGCAGAG	281187	113383	ATAATACAAACAGTCCTGCA
192014	24210	CCCAGCCAATGTGAGCCAAT	236601	68797	GGCCAGCATGGGAAGGCAGA	281188	113384	AATAATACAAACAGTCCTGC
192015	24211	ACCCAGCCAATGTGAGCCAA	236602	68798	GGGCCAGCATGGGAAGGCAG	281189	113385	CAATAATACAAACAGTCCTG
192016	24212	CACCCAGCCAATGTGAGCCA	236603	68799	AGGGCCAGCATGGGAAGGCA	281190	113386	TCAATAATACAAACAGTCCT
192017	24213	GCACCCAGCCAATGTGAGCC	236604	68800	AAGGGCCAGCATGGGAAGGC	281191	113387	TTCAATAATACAAACAGTCC
192018	24214	CGCACCCAGCCAATGTGAGC	236605	68801	GAAGGGCCAGCATGGGAAGG	281192	113388	CTTCAATAATACAAACAGTC
192019	24215	CCGCACCCAGCCAATGTGAG	236606	68802	TGAAGGGCCAGCATGGGAAG	281193	113389	ACTTCAATAATACAAACAGT
192020	24216	ACCGCACCCAGCCAATGTGA	236607	68803	GTGAAGGGCCAGCATGGGAA	281194	113390	TACTTCAATAATACAAACAG
192021	24217	CACCGCACCCAGCCAATGTG	236608	68804	GGTGAAGGGCCAGCATGGGA	281195	113391	GTACTTCAATAATACAAACA
192022	24218	CCACCGCACCCAGCCAATGT	236609	68805	GGGTGAAGGGCCAGCATGGG	281196	113392	TGTACTTCAATAATACAAAC
192023	24219	GCCACCGCACCCAGCCAATG	236610	68806	TGGGTGAAGGGCCAGCATGG	281197	113393	TTGTACTTCAATAATACAAA
192024	24220	AGCCACCGCACCCAGCCAAT	236611	68807	GTGGGTGAAGGGCCAGCATG	281198	113394	TTTGTACTTCAATAATACAA
192025	24221	GAGCCACCGCACCCAGCCAA	236612	68808	AGTGGGTGAAGGGCCAGCAT	281199	113395	CTTTGTACTTCAATAATACA
192026	24222	TGAGCCACCGCACCCAGCCA	236613	68809	CAGTGGGTGAAGGGCCAGCA	281200	113396	ACTTTGTACTTCAATAATAC
192027	24223	GTGAGCCACCGCACCCAGCC	236614	68810	GCAGTGGGTGAAGGGCCAGC	281201	113397	CACTTTGTACTTCAATAATA
192028	24224	CGTGAGCCACCGCACCCAGC	236615	68811	AGCAGTGGGTGAAGGGCCAG	281202	113398	CCACTTTGTACTTCAATAAT
192029	24225	GCGTGAGCCACCGCACCCAG	236616	68812	CAGCAGTGGGTGAAGGGCCA	281203	113399	TCCACTTTGTACTTCAATAA
192030	24226	GGCGTGAGCCACCGCACCCA	236617	68813	CCAGCAGTGGGTGAAGGGCC	281204	113400	TTCCACTTTGTACTTCAATA
192031	24227	AGGCGTGAGCCACCGCACCC	236618	68814	TCCAGCAGTGGGTGAAGGGC	281205	113401	ATTCCACTTTGTACTTCAAT
192032	24228	CAGGCGTGAGCCACCGCACC	236619	68815	CTCCAGCAGTGGGTGAAGGG	281206	113402	GATTCCACTTTGTACTTCAA
192033	24229	ACAGGCGTGAGCCACCGCAC	236620	68816	ACTCCAGCAGTGGGTGAAGG	281207	113403	TGATTCCACTTTGTACTTCA
192034	24230	TACAGGCGTGAGCCACCGCA	236621	68817	CACTCCAGCAGTGGGTGAAG	281208	113404	TTGATTCCACTTTGTACTTC
192035	24231	TTACAGGCGTGAGCCACCGC	236622	68818	GCACTCCAGCAGTGGGTGAA	281209	113405	ATTGATTCCACTTTGTACTT
192036	24232	ATTACAGGCGTGAGCCACCG	236623	68819	GGCACTCCAGCAGTGGGTGA	281210	113406	TATTGATTCCACTTTGTACT
192037	24233	GATTACAGGCGTGAGCCACC	236624	68820	TGGCACTCCAGCAGTGGGTG	281211	113407	GTATTGATTCCACTTTGTAC
192038	24234	GGATTACAGGCGTGAGCCAC	236625	68821	CTGGCACTCCAGCAGTGGGT	281212	113408	TGTATTGATTCCACTTTGTA
192039	24235	GGGATTACAGGCGTGAGCCA	236626	68822	CCTGGCACTCCAGCAGTGGG	281213	113409	TTGTATTGATTCCACTTTGT
192040	24236	TGGGATTACAGGCGTGAGCC	236627	68823	ACCTGGCACTCCAGCAGTGG	281214	113410	TTTGTATTGATTCCACTTTG
192041	24237	CTGGGATTACAGGCGTGAGC	236628	68824	AACCTGGCACTCCAGCAGTG	281215	113411	ATTTGTATTGATTCCACTTT
192042	24238	GCTGGGATTACAGGCGTGAG	236629	68825	CAACCTGGCACTCCAGCAGT	281216	113412	CATTTGTATTGATTCCACTT
192043	24239	TGCTGGGATTACAGGCGTGA	236630	68826	CCAACCTGGCACTCCAGCAG	281217	113413	ACATTTGTATTGATTCCACT
192044	24240	ATGCTGGGATTACAGGCGTG	236631	68827	ACCAACCTGGCACTCCAGCA	281218	113414	AACATTTGTATTGATTCCAC
192045	24241	AATGCTGGGATTACAGGCGT	236632	68828	GACCAACCTGGCACTCCAGC	281219	113415	CAACATTTGTATTGATTCCA
192046	24242	AAATGCTGGGATTACAGGCG	236633	68829	GGACCAACCTGGCACTCCAG	281220	113416	CCAACATTTGTATTGATTCC
192047	24243	AAAATGCTGGGATTACAGGC	236634	68830	TGGACCAACCTGGCACTCCA	281221	113417	TCCAACATTTGTATTGATTC
192048	24244	CAAAATGCTGGGATTACAGG	236635	68831	TTGGACCAACCTGGCACTCC	281222	113418	ATCCAACATTTGTATTGATT
192049	24245	CCAAAATGCTGGGATTACAG	236636	68832	CTTGGACCAACCTGGCACTC	281223	113419	TATCCAACATTTGTATTGAT
192050	24246	CCCAAAATGCTGGGATTACA	236637	68833	CCTTGGACCAACCTGGCACT	281224	113420	CTATCCAACATTTGTATTGA
192051	24247	TCCCAAAATGCTGGGATTAC	236638	68834	CCCTTGGACCAACCTGGCAC	281225	113421	GCTATCCAACATTTGTATTG
192052	24248	CTCCCAAAATGCTGGGATTA	236639	68835	ACCCTTGGACCAACCTGGCA	281226	113422	TGCTATCCAACATTTGTATT
192053	24249	CCTCCCAAAATGCTGGGATT	236640	68836	AACCCTTGGACCAACCTGGC	281227	113423	CTGCTATCCAACATTTGTAT
192054	24250	GCCTCCCAAAATGCTGGGAT	236641	68837	CAACCCTTGGACCAACCTGG	281228	113424	CCTGCTATCCAACATTTGTA
192055	24251	GGCCTCCCAAAATGCTGGGA	236642	68838	CCAACCCTTGGACCAACCTG	281229	113425	CCCTGCTATCCAACATTTGT
192056	24252	TGGCCTCCCAAAATGCTGGG	236643	68839	TCCAACCCTTGGACCAACCT	281230	113426	CCCCTGCTATCCAACATTTG
192057	24253	TTGGCCTCCCAAAATGCTGG	236644	68840	GTCCAACCCTTGGACCAACC	281231	113427	TCCCCTGCTATCCAACATTT
192058	24254	CTTGGCCTCCCAAAATGCTG	236645	68841	GGTCCAACCCTTGGACCAAC	281232	113428	TTCCCCTGCTATCCAACATT
192059	24255	CCTTGGCCTCCCAAAATGCT	236646	68842	TGGTCCAACCCTTGGACCAA	281233	113429	GTTCCCCTGCTATCCAACAT
192060	24256	GCCTTGGCCTCCCAAAATGC	236647	68843	TTGGTCCAACCCTTGGACCA	281234	113430	TGTTCCCCTGCTATCCAACA
192061	24257	GGCCTTGGCCTCCCAAAATG	236648	68844	CTTGGTCCAACCCTTGGACC	281235	113431	TTGTTCCCCTGCTATCCAAC
192062	24258	CGGCCTTGGCCTCCCAAAAT	236649	68845	ACTTGGTCCAACCCTTGGAC	281236	113432	ATTGTTCCCCTGCTATCCAA
192063	24259	CCGGCCTTGGCCTCCCAAAA	236650	68846	AACTTGGTCCAACCCTTGGA	281237	113433	TATTGTTCCCCTGCTATCCA
192064	24260	GCCGGCCTTGGCCTCCCAAA	236651	68847	CAACTTGGTCCAACCCTTGG	281238	113434	ATATTGTTCCCCTGCTATCC
192065	24261	CGCCGGCCTTGGCCTCCCAA	236652	68848	ACAACTTGGTCCAACCCTTG	281239	113435	AATATTGTTCCCCTGCTATC
192066	24262	CCGCCGGCCTTGGCCTCCCA	236653	68849	GACAACTTGGTCCAACCCTT	281240	113436	GAATATTGTTCCCCTGCTAT

192067	24263	TCCGCCGGCCTTGGCCTCCC	236654	68850	AGACAACTTGGTCCAACCCT	281241	113437	TGAATATTGTTCCCCTGCTA
192068	24264	ATCCGCCGGCCTTGGCCTCC	236655	68851	CAGACAACTTGGTCCAACCC	281242	113438	GTGAATATTGTTCCCCTGCT
192069	24265	GATCCGCCGGCCTTGGCCTC	236656	68852	TCAGACAACTTGGTCCAACC	281243	113439	TGTGAATATTGTTCCCCTGC
192070	24266	TGATCCGCCGGCCTTGGCCT	236657	68853	CTCAGACAACTTGGTCCAAC	281244	113440	TTGTGAATATTGTTCCCCTG
192071	24267	GTGATCCGCCGGCCTTGGCC	236658	68854	CCTCAGACAACTTGGTCCAA	281245	113441	TTTGTGAATATTGTTCCCCT
192072	24268	AGTGATCCGCCGGCCTTGGC	236659	68855	ACCTCAGACAACTTGGTCCA	281246	113442	TTTTGTGAATATTGTTCCCC
192073	24269	AAGTGATCCGCCGGCCTTGG	236660	68856	AACCTCAGACAACTTGGTCC	281247	113443	ATTTTGTGAATATTGTTCCC
192074	24270	CAAGTGATCCGCCGGCCTTG	236661	68857	CAACCTCAGACAACTTGGTC	281248	113444	CATTTTGTGAATATTGTTCC
192075	24271	TCAAGTGATCCGCCGGCCTT	236662	68858	ACAACCTCAGACAACTTGGT	281249	113445	CCATTTTGTGAATATTGTTC
192076	24272	CTCAAGTGATCCGCCGGCCT	236663	68859	GACAACCTCAGACAACTTGG	281250	113446	TCCATTTTGTGAATATTGTT
192077	24273	CCTCAAGTGATCCGCCGGCC	236664	68860	AGACAACCTCAGACAACTTG	281251	113447	TTCCATTTTGTGAATATTGT
192078	24274	ACCTCAAGTGATCCGCCGGC	236665	68861	GAGACAACCTCAGACAACTT	281252	113448	ATTCCATTTTGTGAATATTG
192079	24275	GACCTCAAGTGATCCGCCGG	236666	68862	TGAGACAACCTCAGACAACT	281253	113449	CATTCCATTTTGTGAATATT
192080	24276	TGACCTCAAGTGATCCGCCG	236667	68863	TTGAGACAACCTCAGACAAC	281254	113450	CCATTCCATTTTGTGAATAT
192081	24277	CTGACCTCAAGTGATCCGCC	236668	68864	CTTGAGACAACCTCAGACAA	281255	113451	CCCATTCCATTTTGTGAATA
192082	24278	CCTGACCTCAAGTGATCCGC	236669	68865	CCTTGAGACAACCTCAGACA	281256	113452	TCCCATTCCATTTTGTGAAT
192083	24279	TCCTGACCTCAAGTGATCCG	236670	68866	ACCTTGAGACAACCTCAGAC	281257	113453	GTCCCATTCCATTTTGTGAA
192084	24280	TTCCTGACCTCAAGTGATCC	236671	68867	AACCTTGAGACAACCTCAGA	281258	113454	TGTCCCATTCCATTTTGTGA
192085	24281	ATTCCTGACCTCAAGTGATC	236672	68868	CAACCTTGAGACAACCTCAG	281259	113455	ATGTCCCATTCCATTTTGTG
192086	24282	AATTCCTGACCTCAAGTGAT	236673	68869	CCAACCTTGAGACAACCTCA	281260	113456	TATGTCCCATTCCATTTTGT
192087	24283	AAATTCCTGACCTCAAGTGA	236674	68870	ACCAACCTTGAGACAACCTC	281261	113457	CTATGTCCCATTCCATTTTG
192088	24284	CAAATTCCTGACCTCAAGTG	236675	68871	GACCAACCTTGAGACAACCT	281262	113458	ACTATGTCCCATTCCATTTT
192089	24285	TCAAATTCCTGACCTCAAGT	236676	68872	CGACCAACCTTGAGACAACC	281263	113459	TACTATGTCCCATTCCATTT
192090	24286	CTCAAATTCCTGACCTCAAG	236677	68873	TCGACCAACCTTGAGACAAC	281264	113460	ATACTATGTCCCATTCCATT
192091	24287	TCTCAAATTCCTGACCTCAA	236678	68874	CTCGACCAACCTTGAGACAA	281265	113461	AATACTATGTCCCATTCCAT
192092	24288	GTCTCAAATTCCTGACCTCA	236679	68875	CCTCGACCAACCTTGAGACA	281266	113462	TAATACTATGTCCCATTCCA
192093	24289	GGTCTCAAATTCCTGACCTC	236680	68876	GCCTCGACCAACCTTGAGAC	281267	113463	TTAATACTATGTCCCATTCC
192094	24290	TGGTCTCAAATTCCTGACCT	236681	68877	AGCCTCGACCAACCTTGAGA	281268	113464	TTTAATACTATGTCCCATTC
192095	24291	CTGGTCTCAAATTCCTGACC	236682	68878	CAGCCTCGACCAACCTTGAG	281269	113465	GTTTAATACTATGTCCCATT
192096	24292	GCTGGTCTCAAATTCCTGAC	236683	68879	ACAGCCTCGACCAACCTTGA	281270	113466	TGTTTAATACTATGTCCCAT
192097	24293	GGCTGGTCTCAAATTCCTGA	236684	68880	GACAGCCTCGACCAACCTTG	281271	113467	ATGTTTAATACTATGTCCCA
192098	24294	AGGCTGGTCTCAAATTCCTG	236685	68881	AGACAGCCTCGACCAACCTT	281272	113468	TATGTTTAATACTATGTCCC
192099	24295	CAGGCTGGTCTCAAATTCCT	236686	68882	GAGACAGCCTCGACCAACCT	281273	113469	CTATGTTTAATACTATGTCC
192100	24296	CCAGGCTGGTCTCAAATTCC	236687	68883	GGAGACAGCCTCGACCAACC	281274	113470	ACTATGTTTAATACTATGTC
192101	24297	GCCAGGCTGGTCTCAAATTC	236688	68884	CGGAGACAGCCTCGACCAAC	281275	113471	CACTATGTTTAATACTATGT
192102	24298	GGCCAGGCTGGTCTCAAATT	236689	68885	GCGGAGACAGCCTCGACCAA	281276	113472	GCACTATGTTTAATACTATG
192103	24299	TGGCCAGGCTGGTCTCAAAT	236690	68886	CGCGGAGACAGCCTCGACCA	281277	113473	AGCACTATGTTTAATACTAT
192104	24300	TTGGCCAGGCTGGTCTCAAA	236691	68887	GCGCGGAGACAGCCTCGACC	281278	113474	AAGCACTATGTTTAATACTA
192105	24301	GTTGGCCAGGCTGGTCTCAA	236692	68888	AGCGCGGAGACAGCCTCGAC	281279	113475	GAAGCACTATGTTTAATACT
192106	24302	TGTTGGCCAGGCTGGTCTCA	236693	68889	CAGCGCGGAGACAGCCTCGA	281280	113476	AGAAGCACTATGTTTAATAC
192107	24303	ATGTTGGCCAGGCTGGTCTC	236694	68890	CCAGCGCGGAGACAGCCTCG	281281	113477	CAGAAGCACTATGTTTAATA
192108	24304	CATGTTGGCCAGGCTGGTCT	236695	68891	CCCAGCGCGGAGACAGCCTC	281282	113478	TCAGAAGCACTATGTTTAAT
192109	24305	CCATGTTGGCCAGGCTGGTC	236696	68892	ACCCAGCGCGGAGACAGCCT	281283	113479	ATCAGAAGCACTATGTTTAA
192110	24306	ACCATGTTGGCCAGGCTGGT	236697	68893	AACCCAGCGCGGAGACAGCC	281284	113480	CATCAGAAGCACTATGTTTA
192111	24307	CACCATGTTGGCCAGGCTGG	236698	68894	CAACCCAGCGCGGAGACAGC	281285	113481	TCATCAGAAGCACTATGTTT
192112	24308	TCACCATGTTGGCCAGGCTG	236699	68895	ACAACCCAGCGCGGAGACAG	281286	113482	GTCATCAGAAGCACTATGTT
192113	24309	TTCACCATGTTGGCCAGGCT	236700	68896	CACAACCCAGCGCGGAGACA	281287	113483	GGTCATCAGAAGCACTATGT
192114	24310	TTTCACCATGTTGGCCAGGC	236701	68897	GCACAACCCAGCGCGGAGAC	281288	113484	CGGTCATCAGAAGCACTATG
192115	24311	GTTTCACCATGTTGGCCAGG	236702	68898	AGCACAACCCAGCGCGGAGA	281289	113485	ACGGTCATCAGAAGCACTAT
192116	24312	GGTTTCACCATGTTGGCCAG	236703	68899	TAGCACAACCCAGCGCGGAG	281290	113486	TACGGTCATCAGAAGCACTA
192117	24313	GGGTTTCACCATGTTGGCCA	236704	68900	GTAGCACAACCCAGCGCGGA	281291	113487	CTACGGTCATCAGAAGCACT
192118	24314	AGGGTTTCACCATGTTGGCC	236705	68901	TGTAGCACAACCCAGCGCGG	281292	113488	TCTACGGTCATCAGAAGCAC
192119	24315	CAGGGTTTCACCATGTTGGC	236706	68902	TTGTAGCACAACCCAGCGCG	281293	113489	GTCTACGGTCATCAGAAGCA
192120	24316	ACAGGGTTTCACCATGTTGG	236707	68903	CTTGTAGCACAACCCAGCGC	281294	113490	GGTCTACGGTCATCAGAAGC
192121	24317	GACAGGGTTTCACCATGTTG	236708	68904	CCTTGTAGCACAACCCAGCG	281295	113491	TGGTCTACGGTCATCAGAAG
192122	24318	AGACAGGGTTTCACCATGTT	236709	68905	TCCTTGTAGCACAACCCAGC	281296	113492	ATGGTCTACGGTCATCAGAA
192123	24319	GAGACAGGGTTTCACCATGT	236710	68906	CTCCTTGTAGCACAACCCAG	281297	113493	TATGGTCTACGGTCATCAGA
192124	24320	AGAGACAGGGTTTCACCATG	236711	68907	GCTCCTTGTAGCACAACCCA	281298	113494	CTATGGTCTACGGTCATCAG
192125	24321	AAGAGACAGGGTTTCACCAT	236712	68908	GGCTCCTTGTAGCACAACCC	281299	113495	TCTATGGTCTACGGTCATCA
192126	24322	GAAGAGACAGGGTTTCACCA	236713	68909	GGGCTCCTTGTAGCACAACC	281300	113496	GTCTATGGTCTACGGTCATC
192127	24323	AGAAGAGACAGGGTTTCACC	236714	68910	AGGGCTCCTTGTAGCACAAC	281301	113497	TGTCTATGGTCTACGGTCAT
192128	24324	TAGAAGAGACAGGGTTTCAC	236715	68911	AAGGGCTCCTTGTAGCACAA	281302	113498	TTGTCTATGGTCTACGGTCA
192129	24325	TTAGAAGAGACAGGGTTTCA	236716	68912	GAAGGGCTCCTTGTAGCACA	281303	113499	ATTGTCTATGGTCTACGGTC
192130	24326	TTTAGAAGAGACAGGGTTTC	236717	68913	AGAAGGGCTCCTTGTAGCAC	281304	113500	CATTGTCTATGGTCTACGGT
192131	24327	TTTTAGAAGAGACAGGGTTT	236718	68914	AAGAAGGGCTCCTTGTAGCA	281305	113501	GCATTGTCTATGGTCTACGG
192132	24328	ATTTTAGAAGAGACAGGGTT	236719	68915	AAAGAAGGGCTCCTTGTAGC	281306	113502	AGCATTGTCTATGGTCTACG
192133	24329	TATTTTAGAAGAGACAGGGT	236720	68916	GAAAGAAGGGCTCCTTGTAG	281307	113503	AAGCATTGTCTATGGTCTAC
192134	24330	TTATTTTAGAAGAGACAGGG	236721	68917	GGAAAGAAGGGCTCCTTGTA	281308	113504	TAAGCATTGTCTATGGTCTA
192135	24331	TTTATTTTAGAAGAGACAGG	236722	68918	TGGAAAGAAGGGCTCCTTGT	281309	113505	CTAAGCATTGTCTATGGTCT
192136	24332	TTTTATTTTAGAAGAGACAG	236723	68919	ATGGAAAGAAGGGCTCCTTG	281310	113506	CCTAAGCATTGTCTATGGTC
192137	24333	ATTTTATTTTAGAAGAGACA	236724	68920	CATGGAAAGAAGGGCTCCTT	281311	113507	TCCTAAGCATTGTCTATGGT
192138	24334	TATTTTATTTTAGAAGAGAC	236725	68921	CCATGGAAAGAAGGGCTCCT	281312	113508	ATCCTAAGCATTGTCTATGG

192139	24335	GTATTTTATTTTAGAAGAGA	236726	68922	CCCATGGAAAGAAGGGCTCC	281313	113509	TATCCTAAGCATTGTCTATG
192140	24336	TGTATTTTATTTTAGAAGAG	236727	68923	ACCCATGGAAAGAAGGGCTC	281314	113510	ATATCCTAAGCATTGTCTAT
192141	24337	TTGTATTTTATTTTAGAAGA	236728	68924	CACCCATGGAAAGAAGGGCT	281315	113511	CATATCCTAAGCATTGTCTA
192142	24338	TTTGTATTTTATTTTAGAAG	236729	68925	ACACCCATGGAAAGAAGGGC	281316	113512	TCATATCCTAAGCATTGTCT
192143	24339	TTTTGTATTTTATTTTAGAA	236730	68926	CACACCCATGGAAAGAAGGG	281317	113513	ATCATATCCTAAGCATTGTC
192144	24340	TTTTTGTATTTTATTTTAGA	236731	68927	CCACACCCATGGAAAGAAGG	281318	113514	TATCATATCCTAAGCATTGT
192145	24341	ATTTTTGTATTTTATTTTAG	236732	68928	GCCACACCCATGGAAAGAAG	281319	113515	ATATCATATCCTAAGCATTG
192146	24342	AATTTTTGTATTTTATTTTA	236733	68929	AGCCACACCCATGGAAAGAA	281320	113516	GATATCATATCCTAAGCATT
192147	24343	TAATTTTTGTATTTTATTTT	236734	68930	CAGCCACACCCATGGAAAGA	281321	113517	TGATATCATATCCTAAGCAT
192148	24344	CTAATTTTTGTATTTTATTT	236735	68931	CCAGCCACACCCATGGAAAG	281322	113518	GTGATATCATATCCTAAGCA
192149	24345	GCTAATTTTTGTATTTTATT	236736	68932	GCCAGCCACACCCATGGAAA	281323	113519	AGTGATATCATATCCTAAGC
192150	24346	AGCTAATTTTTGTATTTTAT	236737	68933	TGCCAGCCACACCCATGGAA	281324	113520	AAGTGATATCATATCCTAAG
192151	24347	CAGCTAATTTTTGTATTTTA	236738	68934	CTGCCAGCCACACCCATGGA	281325	113521	GAAGTGATATCATATCCTAA
192152	24348	CCAGCTAATTTTTGTATTTT	236739	68935	ACTGCCAGCCACACCCATGG	281326	113522	AGAAGTGATATCATATCCTA
192153	24349	GCCAGCTAATTTTTGTATTT	236740	68936	CACTGCCAGCCACACCCATG	281327	113523	AAGAAGTGATATCATATCCT
192154	24350	GGCCAGCTAATTTTTGTATT	236741	68937	TCACTGCCAGCCACACCCAT	281328	113524	AAAGAAGTGATATCATATCC
192155	24351	TGGCCAGCTAATTTTTGTAT	236742	68938	CTCACTGCCAGCCACACCCA	281329	113525	AAAAGAAGTGATATCATATC
192156	24352	ATGGCCAGCTAATTTTTGTA	236743	68939	ACTCACTGCCAGCCACACCC	281330	113526	CAAAAGAAGTGATATCATAT
192157	24353	CATGGCCAGCTAATTTTTGT	236744	68940	CACTCACTGCCAGCCACACC	281331	113527	ACAAAAGAAGTGATATCATA
192158	24354	CCATGGCCAGCTAATTTTTG	236745	68941	GCACTCACTGCCAGCCACAC	281332	113528	AACAAAAGAAGTGATATCAT
192159	24355	ACCATGGCCAGCTAATTTTT	236746	68942	AGCACTCACTGCCAGCCACA	281333	113529	CAACAAAAGAAGTGATATCA
192160	24356	CACCATGGCCAGCTAATTTT	236747	68943	GAGCACTCACTGCCAGCCAC	281334	113530	ACAACAAAAGAAGTGATATC
192161	24357	CCACCATGGCCAGCTAATTT	236748	68944	TGAGCACTCACTGCCAGCCA	281335	113531	AACAACAAAAGAAGTGATAT
192162	24358	ACCACCATGGCCAGCTAATT	236749	68945	GTGAGCACTCACTGCCAGCC	281336	113532	AAACAACAAAAGAAGTGATA
192163	24359	CACCACCATGGCCAGCTAAT	236750	68946	TGTGAGCACTCACTGCCAGC	281337	113533	AAAACAACAAAAGAAGTGAT
192164	24360	ACACCACCATGGCCAGCTAA	236751	68947	CTGTGAGCACTCACTGCCAG	281338	113534	AAAAACAACAAAAGAAGTGA
192165	24361	CACACCACCATGGCCAGCTA	236752	68948	GCTGTGAGCACTCACTGCCA	281339	113535	AAAAAACAACAAAAGAAGTG
192166	24362	GCACACCACCATGGCCAGCT	236753	68949	TGCTGTGAGCACTCACTGCC	281340	113536	CAAAAAACAACAAAAGAAGT
192167	24363	CGCACACCACCATGGCCAGC	236754	68950	TTGCTGTGAGCACTCACTGC	281341	113537	ACAAAAAACAACAAAAGAAG
192168	24364	GCGCACACCACCATGGCCAG	236755	68951	GTTGCTGTGAGCACTCACTG	281342	113538	TACAAAAAACAACAAAAGAA
192169	24365	GGCGCACACCACCATGGCCA	236756	68952	TGTTGCTGTGAGCACTCACT	281343	113539	ATACAAAAAACAACAAAAGA
192170	24366	AGGCGCACACCACCATGGCC	236757	68953	CTGTTGCTGTGAGCACTCAC	281344	113540	AATACAAAAAACAACAAAAG
192171	24367	CAGGCGCACACCACCATGGC	236758	68954	GCTGTTGCTGTGAGCACTCA	281345	113541	AAATACAAAAAACAACAAAA
192172	24368	CCAGGCGCACACCACCATGG	236759	68955	GGCTGTTGCTGTGAGCACTC	281346	113542	AAAATACAAAAAACAACAAA
192173	24369	TCCAGGCGCACACCACCATG	236760	68956	GGGCTGTTGCTGTGAGCACT	281347	113543	CAAAATACAAAAAACAACAA
192174	24370	TTCCAGGCGCACACCACCAT	236761	68957	TGGGCTGTTGCTGTGAGCAC	281348	113544	TCAAAATACAAAAAACAACA
192175	24371	ATTCCAGGCGCACACCACCA	236762	68958	GTGGGCTGTTGCTGTGAGCA	281349	113545	CTCAAAATACAAAAAACAAC
192176	24372	GATTCCAGGCGCACACCACC	236763	68959	TGTGGGCTGTTGCTGTGAGC	281350	113546	TCTCAAAATACAAAAAACAA
192177	24373	GGATTCCAGGCGCACACCAC	236764	68960	CTGTGGGCTGTTGCTGTGAG	281351	113547	GTCTCAAAATACAAAAAACA
192178	24374	GGGATTCCAGGCGCACACCA	236765	68961	ACTGTGGGCTGTTGCTGTGA	281352	113548	CGTCTCAAAATACAAAAAAC
192179	24375	TGGGATTCCAGGCGCACACC	236766	68962	CACTGTGGGCTGTTGCTGTG	281353	113549	TCGTCTCAAAATACAAAAAA
192180	24376	CTGGGATTCCAGGCGCACAC	236767	68963	GCACTGTGGGCTGTTGCTGT	281354	113550	TTCGTCTCAAAATACAAAAA
192181	24377	GCTGGGATTCCAGGCGCACA	236768	68964	TGCACTGTGGGCTGTTGCTG	281355	113551	CTTCGTCTCAAAATACAAAA
192182	24378	AGCTGGGATTCCAGGCGCAC	236769	68965	CTGCACTGTGGGCTGTTGCT	281356	113552	ACTTCGTCTCAAAATACAAA
192183	24379	TAGCTGGGATTCCAGGCGCA	236770	68966	GCTGCACTGTGGGCTGTTGC	281357	113553	GACTTCGTCTCAAAATACAA
192184	24380	GTAGCTGGGATTCCAGGCGC	236771	68967	GGCTGCACTGTGGGCTGTTG	281358	113554	AGACTTCGTCTCAAAATACA
192185	24381	AGTAGCTGGGATTCCAGGCG	236772	68968	GGGCTGCACTGTGGGCTGTT	281359	113555	GAGACTTCGTCTCAAAATAC
192186	24382	GAGTAGCTGGGATTCCAGGC	236773	68969	CGGGCTGCACTGTGGGCTGT	281360	113556	TGAGACTTCGTCTCAAAATA
192187	24383	TGAGTAGCTGGGATTCCAGG	236774	68970	TCGGGCTGCACTGTGGGCTG	281361	113557	ATGAGACTTCGTCTCAAAAT
192188	24384	CTGAGTAGCTGGGATTCCAG	236775	68971	CTCGGGCTGCACTGTGGGCT	281362	113558	AATGAGACTTCGTCTCAAAA
192189	24385	CCTGAGTAGCTGGGATTCCA	236776	68972	CCTCGGGCTGCACTGTGGGC	281363	113559	GAATGAGACTTCGTCTCAAA
192190	24386	TCCTGAGTAGCTGGGATTCC	236777	68973	CCCTCGGGCTGCACTGTGGG	281364	113560	AGAATGAGACTTCGTCTCAA
192191	24387	CTCCTGAGTAGCTGGGATTC	236778	68974	GCCCTCGGGCTGCACTGTGG	281365	113561	CAGAATGAGACTTCGTCTCA
192192	24388	CCTCCTGAGTAGCTGGGATT	236779	68975	TGCCCTCGGGCTGCACTGTG	281366	113562	ACAGAATGAGACTTCGTCTC
192193	24389	GCCTCCTGAGTAGCTGGGAT	236780	68976	CTGCCCTCGGGCTGCACTGT	281367	113563	GACAGAATGAGACTTCGTCT
192194	24390	AGCCTCCTGAGTAGCTGGGA	236781	68977	CCTGCCCTCGGGCTGCACTG	281368	113564	TGACAGAATGAGACTTCGTC
192195	24391	CAGCCTCCTGAGTAGCTGGG	236782	68978	TCCTGCCCTCGGGCTGCACT	281369	113565	GTGACAGAATGAGACTTCGT
192196	24392	TCAGCCTCCTGAGTAGCTGG	236783	68979	ATCCTGCCCTCGGGCTGCAC	281370	113566	GGTGACAGAATGAGACTTCG
192197	24393	CTCAGCCTCCTGAGTAGCTG	236784	68980	CATCCTGCCCTCGGGCTGCA	281371	113567	GGGTGACAGAATGAGACTTC
192198	24394	CCTCAGCCTCCTGAGTAGCT	236785	68981	CCATCCTGCCCTCGGGCTGC	281372	113568	TGGGTGACAGAATGAGACTT
192199	24395	ACCTCAGCCTCCTGAGTAGC	236786	68982	TCCATCCTGCCCTCGGGCTG	281373	113569	CTGGGTGACAGAATGAGACT
192200	24396	CACCTCAGCCTCCTGAGTAG	236787	68983	GTCCATCCTGCCCTCGGGCT	281374	113570	CCTGGGTGACAGAATGAGAC
192201	24397	CCACCTCAGCCTCCTGAGTA	236788	68984	AGTCCATCCTGCCCTCGGGC	281375	113571	GCCTGGGTGACAGAATGAGA
192202	24398	TCCACCTCAGCCTCCTGAGT	236789	68985	GAGTCCATCCTGCCCTCGGG	281376	113572	AGCCTGGGTGACAGAATGAG
192203	24399	TTCCACCTCAGCCTCCTGAG	236790	68986	TGAGTCCATCCTGCCCTCGG	281377	113573	CAGCCTGGGTGACAGAATGA
192204	24400	CTTCCACCTCAGCCTCCTGA	236791	68987	CTGAGTCCATCCTGCCCTCG	281378	113574	CCAGCCTGGGTGACAGAATG
192205	24401	TCTTCCACCTCAGCCTCCTG	236792	68988	ACTGAGTCCATCCTGCCCTC	281379	113575	TCCAGCCTGGGTGACAGAAT
192206	24402	TTCTTCCACCTCAGCCTCCT	236793	68989	GACTGAGTCCATCCTGCCCT	281380	113576	CTCCAGCCTGGGTGACAGAA
192207	24403	ATTCTTCCACCTCAGCCTCC	236794	68990	GGACTGAGTCCATCCTGCCC	281381	113577	ACTCCAGCCTGGGTGACAGA
192208	24404	AATTCTTCCACCTCAGCCTC	236795	68991	GGGACTGAGTCCATCCTGCC	281382	113578	AACTCCAGCCTGGGTGACAG
192209	24405	CAATTCTTCCACCTCAGCCT	236796	68992	AGGGACTGAGTCCATCCTGC	281383	113579	GAACTCCAGCCTGGGTGACA
192210	24406	GCAATTCTTCCACCTCAGCC	236797	68993	CAGGGACTGAGTCCATCCTG	281384	113580	TGAACTCCAGCCTGGGTGAC

192211	24407	AGCAATTCTTCCACCTCAGC	236798	68994	GCAGGGACTGAGTCCATCCT	281385	113581	CTGAACTCCAGCCTGGGTGA
192212	24408	AAGCAATTCTTCCACCTCAG	236799	68995	GGCAGGGACTGAGTCCATCC	281386	113582	ACTGAACTCCAGCCTGGGTG
192213	24409	CAAGCAATTCTTCCACCTCA	236800	68996	AGGCAGGGACTGAGTCCATC	281387	113583	CACTGAACTCCAGCCTGGGT
192214	24410	TCAAGCAATTCTTCCACCTC	236801	68997	GAGGCAGGGACTGAGTCCAT	281388	113584	CCACTGAACTCCAGCCTGGG
192215	24411	CTCAAGCAATTCTTCCACCT	236802	68998	GGAGGCAGGGACTGAGTCCA	281389	113585	GCCACTGAACTCCAGCCTGG
192216	24412	GCTCAAGCAATTCTTCCACC	236803	68999	TGGAGGCAGGGACTGAGTCC	281390	113586	CGCCACTGAACTCCAGCCTG
192217	24413	GGCTCAAGCAATTCTTCCAC	236804	69000	ATGGAGGCAGGGACTGAGTC	281391	113587	GCGCCACTGAACTCCAGCCT
192218	24414	GGGCTCAAGCAATTCTTCCA	236805	69001	TATGGAGGCAGGGACTGAGT	281392	113588	GGCGCCACTGAACTCCAGCC
192219	24415	CGGGCTCAAGCAATTCTTCC	236806	69002	GTATGGAGGCAGGGACTGAG	281393	113589	TGGCGCCACTGAACTCCAGC
192220	24416	CCGGGCTCAAGCAATTCTTC	236807	69003	GGTATGGAGGCAGGGACTGA	281394	113590	ATGGCGCCACTGAACTCCAG
192221	24417	CCCGGGCTCAAGCAATTCTT	236808	69004	GGGTATGGAGGCAGGGACTG	281395	113591	GATGGCGCCACTGAACTCCA
192222	24418	TCCCGGGCTCAAGCAATTCT	236809	69005	TGGGTATGGAGGCAGGGACT	281396	113592	AGATGGCGCCACTGAACTCC
192223	24419	CTCCCGGGCTCAAGCAATTC	236810	69006	ATGGGTATGGAGGCAGGGAC	281397	113593	GAGATGGCGCCACTGAACTC
192224	24420	CCTCCCGGGCTCAAGCAATT	236811	69007	AATGGGTATGGAGGCAGGGA	281398	113594	TGAGATGGCGCCACTGAACT
192225	24421	ACCTCCCGGGCTCAAGCAAT	236812	69008	AAATGGGTATGGAGGCAGGG	281399	113595	CTGAGATGGCGCCACTGAAC
192226	24422	CACCTCCCGGGCTCAAGCAA	236813	69009	GAAATGGGTATGGAGGCAGG	281400	113596	GCTGAGATGGCGCCACTGAA
192227	24423	CCACCTCCCGGGCTCAAGCA	236814	69010	AGAAATGGGTATGGAGGCAG	281401	113597	AGCTGAGATGGCGCCACTGA
192228	24424	TCCACCTCCCGGGCTCAAGC	236815	69011	TAGAAATGGGTATGGAGGCA	281402	113598	GAGCTGAGATGGCGCCACTG
192229	24425	CTCCACCTCCCGGGCTCAAG	236816	69012	TTAGAAATGGGTATGGAGGC	281403	113599	TGAGCTGAGATGGCGCCACT
192230	24426	CCTCCACCTCCCGGGCTCAA	236817	69013	CTTAGAAATGGGTATGGAGG	281404	113600	GTGAGCTGAGATGGCGCCAC
192231	24427	ACCTCCACCTCCCGGGCTCA	236818	69014	CCTTAGAAATGGGTATGGAG	281405	113601	AGTGAGCTGAGATGGCGCCA
192232	24428	AACCTCCACCTCCCGGGCTC	236819	69015	TCCTTAGAAATGGGTATGGA	281406	113602	CAGTGAGCTGAGATGGCGCC
192233	24429	CAACCTCCACCTCCCGGGCT	236820	69016	CTCCTTAGAAATGGGTATGG	281407	113603	GCAGTGAGCTGAGATGGCGC
192234	24430	GCAACCTCCACCTCCCGGGC	236821	69017	CCTCCTTAGAAATGGGTATG	281408	113604	TGCAGTGAGCTGAGATGGCG
192235	24431	TGCAACCTCCACCTCCCGGG	236822	69018	GCCTCCTTAGAAATGGGTAT	281409	113605	TTGCAGTGAGCTGAGATGGC
192236	24432	CTGCAACCTCCACCTCCCGG	236823	69019	TGCCTCCTTAGAAATGGGTA	281410	113606	GTTGCAGTGAGCTGAGATGG
192237	24433	ACTGCAACCTCCACCTCCCG	236824	69020	TTGCCTCCTTAGAAATGGGT	281411	113607	GGTTGCAGTGAGCTGAGATG
192238	24434	CACTGCAACCTCCACCTCCC	236825	69021	TTTGCCTCCTTAGAAATGGG	281412	113608	AGGTTGCAGTGAGCTGAGAT
192239	24435	TCACTGCAACCTCCACCTCC	236826	69022	TTTTGCCTCCTTAGAAATGG	281413	113609	GAGGTTGCAGTGAGCTGAGA
192240	24436	CTCACTGCAACCTCCACCTC	236827	69023	ATTTTGCCTCCTTAGAAATG	281414	113610	GGAGGTTGCAGTGAGCTGAG
192241	24437	GCTCACTGCAACCTCCACCT	236828	69024	CATTTTGCCTCCTTAGAAAT	281415	113611	TGGAGGTTGCAGTGAGCTGA
192242	24438	GGCTCACTGCAACCTCCACC	236829	69025	CCATTTTGCCTCCTTAGAAA	281416	113612	ATGGAGGTTGCAGTGAGCTG
192243	24439	TGGCTCACTGCAACCTCCAC	236830	69026	GCCATTTTGCCTCCTTAGAA	281417	113613	GATGGAGGTTGCAGTGAGCT
192244	24440	TTGGCTCACTGCAACCTCCA	236831	69027	TGCCATTTTGCCTCCTTAGA	281418	113614	AGATGGAGGTTGCAGTGAGC
192245	24441	CTTGGCTCACTGCAACCTCC	236832	69028	TTGCCATTTTGCCTCCTTAG	281419	113615	GAGATGGAGGTTGCAGTGAG
192246	24442	TCTTGGCTCACTGCAACCTC	236833	69029	TTTGCCATTTTGCCTCCTTA	281420	113616	GGAGATGGAGGTTGCAGTGA
192247	24443	ATCTTGGCTCACTGCAACCT	236834	69030	GTTTGCCATTTTGCCTCCTT	281421	113617	GGGAGATGGAGGTTGCAGTG
192248	24444	GATCTTGGCTCACTGCAACC	236835	69031	TGTTTGCCATTTTGCCTCCT	281422	113618	CGGGAGATGGAGGTTGCAGT
192249	24445	CGATCTTGGCTCACTGCAAC	236836	69032	GTGTTTGCCATTTTGCCTCC	281423	113619	CCGGGAGATGGAGGTTGCAG
192250	24446	GCGATCTTGGCTCACTGCAA	236837	69033	AGTGTTTGCCATTTTGCCTC	281424	113620	CCCGGGAGATGGAGGTTGCA
192251	24447	GGCGATCTTGGCTCACTGCA	236838	69034	GAGTGTTTGCCATTTTGCCT	281425	113621	ACCCGGGAGATGGAGGTTGC
192252	24448	GGGCGATCTTGGCTCACTGC	236839	69035	AGAGTGTTTGCCATTTTGCC	281426	113622	AACCCGGGAGATGGAGGTTG
192253	24449	GGGGCGATCTTGGCTCACTG	236840	69036	TAGAGTGTTTGCCATTTTGC	281427	113623	GAACCCGGGAGATGGAGGTT
192254	24450	TGGGGCGATCTTGGCTCACT	236841	69037	GTAGAGTGTTTGCCATTTTG	281428	113624	TGAACCCGGGAGATGGAGGT
192255	24451	GTGGGGCGATCTTGGCTCAC	236842	69038	AGTAGAGTGTTTGCCATTTT	281429	113625	TTGAACCCGGGAGATGGAGG
192256	24452	AGTGGGGCGATCTTGGCTCA	236843	69039	AAGTAGAGTGTTTGCCATTT	281430	113626	CTTGAACCCGGGAGATGGAG
192257	24453	CAGTGGGGCGATCTTGGCTC	236844	69040	AAAGTAGAGTGTTTGCCATT	281431	113627	GCTTGAACCCGGGAGATGGA
192258	24454	GCAGTGGGGCGATCTTGGCT	236845	69041	AAAAGTAGAGTGTTTGCCAT	281432	113628	AGCTTGAACCCGGGAGATGG
192259	24455	TGCAGTGGGGCGATCTTGGC	236846	69042	GAAAAGTAGAGTGTTTGCCA	281433	113629	TAGCTTGAACCCGGGAGATG
192260	24456	GTGCAGTGGGGCGATCTTGG	236847	69043	AGAAAAGTAGAGTGTTTGCC	281434	113630	ATAGCTTGAACCCGGGAGAT
192261	24457	AGTGCAGTGGGGCGATCTTG	236848	69044	GAGAAAAGTAGAGTGTTTGC	281435	113631	AATAGCTTGAACCCGGGAGA
192262	24458	GAGTGCAGTGGGGCGATCTT	236849	69045	AGAGAAAAGTAGAGTGTTTG	281436	113632	GAATAGCTTGAACCCGGGAG
192263	24459	AGAGTGCAGTGGGGCGATCT	236850	69046	AAGAGAAAAGTAGAGTGTTT	281437	113633	AGAATAGCTTGAACCCGGGA
192264	24460	TAGAGTGCAGTGGGGCGATC	236851	69047	AAAGAGAAAAGTAGAGTGTT	281438	113634	GAGAATAGCTTGAACCCGGG
192265	24461	CTAGAGTGCAGTGGGGCGAT	236852	69048	AAAAGAGAAAAGTAGAGTGT	281439	113635	GGAGAATAGCTTGAACCCGG
192266	24462	GCTAGAGTGCAGTGGGGCGA	236853	69049	TAAAAGAGAAAAGTAGAGTG	281440	113636	AGGAGAATAGCTTGAACCCG
192267	24463	GGCTAGAGTGCAGTGGGGCG	236854	69050	TTAAAAGAGAAAAGTAGAGT	281441	113637	AAGGAGAATAGCTTGAACCC
192268	24464	AGGCTAGAGTGCAGTGGGGC	236855	69051	ATTAAAAGAGAAAAGTAGAG	281442	113638	GAAGGAGAATAGCTTGAACC
192269	24465	CAGGCTAGAGTGCAGTGGGG	236856	69052	CATTAAAAGAGAAAAGTAGA	281443	113639	GGAAGGAGAATAGCTTGAAC
192270	24466	CCAGGCTAGAGTGCAGTGGG	236857	69053	GCATTAAAAGAGAAAAGTAG	281444	113640	AGGAAGGAGAATAGCTTGAA
192271	24467	CCCAGGCTAGAGTGCAGTGG	236858	69054	AGCATTAAAAGAGAAAAGTA	281445	113641	GAGGAAGGAGAATAGCTTGA
192272	24468	GCCCAGGCTAGAGTGCAGTG	236859	69055	TAGCATTAAAAGAGAAAAGT	281446	113642	TGAGGAAGGAGAATAGCTTG
192273	24469	TGCCCAGGCTAGAGTGCAGT	236860	69056	TTAGCATTAAAAGAGAAAAG	281447	113643	TTGAGGAAGGAGAATAGCTT
192274	24470	CTGCCCAGGCTAGAGTGCAG	236861	69057	TTTAGCATTAAAAGAGAAAA	281448	113644	GTTGAGGAAGGAGAATAGCT
192275	24471	GCTGCCCAGGCTAGAGTGCA	236862	69058	TTTTAGCATTAAAAGAGAAA	281449	113645	GGTTGAGGAAGGAGAATAGC
192276	24472	TGCTGCCCAGGCTAGAGTGC	236863	69059	TTTTTAGCATTAAAAGAGAA	281450	113646	AGGTTGAGGAAGGAGAATAG
192277	24473	CTGCTGCCCAGGCTAGAGTG	236864	69060	ATTTTTAGCATTAAAAGAGA	281451	113647	GAGGTTGAGGAAGGAGAATA
192278	24474	TCTGCTGCCCAGGCTAGAGT	236865	69061	TATTTTTAGCATTAAAAGAG	281452	113648	GGAGGTTGAGGAAGGAGAAT
192279	24475	GTCTGCTGCCCAGGCTAGAG	236866	69062	TTATTTTTAGCATTAAAAGA	281453	113649	GGGAGGTTGAGGAAGGAGAA
192280	24476	AGTCTGCTGCCCAGGCTAGA	236867	69063	CTTATTTTTAGCATTAAAAG	281454	113650	CGGGAGGTTGAGGAAGGAGA
192281	24477	CAGTCTGCTGCCCAGGCTAG	236868	69064	TCTTATTTTTAGCATTAAAA	281455	113651	TCGGGAGGTTGAGGAAGGAG
192282	24478	TCAGTCTGCTGCCCAGGCTA	236869	69065	TTCTTATTTTTAGCATTAAA	281456	113652	CTCGGGAGGTTGAGGAAGGA

192283	24479	CTCAGTCTGCTGCCCAGGCT	236870	69066	TTTCTTATTTTTAGCATTAA	281457	113653	ACTCGGGAGGTTGAGGAAGG
192284	24480	TCTCAGTCTGCTGCCCAGGC	236871	69067	TTTTCTTATTTTTAGCATTA	281458	113654	TACTCGGGAGGTTGAGGAAG
192285	24481	GTCTCAGTCTGCTGCCCAGG	236872	69068	GTTTTCTTATTTTTAGCATT	281459	113655	CTACTCGGGAGGTTGAGGAA
192286	24482	AGTCTCAGTCTGCTGCCCAG	236873	69069	TGTTTTCTTATTTTTAGCAT	281460	113656	GCTACTCGGGAGGTTGAGGA
192287	24483	GAGTCTCAGTCTGCTGCCCA	236874	69070	GTGTTTTCTTATTTTTAGCA	281461	113657	AGCTACTCGGGAGGTTGAGG
192288	24484	AGAGTCTCAGTCTGCTGCCC	236875	69071	GGTGTTTTCTTATTTTTAGC	281462	113658	CAGCTACTCGGGAGGTTGAG
192289	24485	CAGAGTCTCAGTCTGCTGCC	236876	69072	AGGTGTTTTCTTATTTTTAG	281463	113659	CCAGCTACTCGGGAGGTTGA
192290	24486	ACAGAGTCTCAGTCTGCTGC	236877	69073	AAGGTGTTTTCTTATTTTTA	281464	113660	CCCAGCTACTCGGGAGGTTG
192291	24487	GACAGAGTCTCAGTCTGCTG	236878	69074	CAAGGTGTTTTCTTATTTTT	281465	113661	ACCCAGCTACTCGGGAGGTT
192292	24488	AGACAGAGTCTCAGTCTGCT	236879	69075	GCAAGGTGTTTTCTTATTTT	281466	113662	AACCCAGCTACTCGGGAGGT
192293	24489	GAGACAGAGTCTCAGTCTGC	236880	69076	TGCAAGGTGTTTTCTTATTT	281467	113663	CAACCCAGCTACTCGGGAGG
192294	24490	TGAGACAGAGTCTCAGTCTG	236881	69077	CTGCAAGGTGTTTTCTTATT	281468	113664	GCAACCCAGCTACTCGGGAG
192295	24491	TTGAGACAGAGTCTCAGTCT	236882	69078	GCTGCAAGGTGTTTTCTTAT	281469	113665	CGCAACCCAGCTACTCGGGA
192296	24492	ATTGAGACAGAGTCTCAGTC	236883	69079	GGCTGCAAGGTGTTTTCTTA	281470	113666	GCGCAACCCAGCTACTCGGG
192297	24493	TATTGAGACAGAGTCTCAGT	236884	69080	GGGCTGCAAGGTGTTTTCTT	281471	113667	TGCGCAACCCAGCTACTCGG
192298	24494	TTATTGAGACAGAGTCTCAG	236885	69081	TGGGCTGCAAGGTGTTTTCT	281472	113668	GTGCGCAACCCAGCTACTCG
192299	24495	TTTATTGAGACAGAGTCTCA	236886	69082	CTGGGCTGCAAGGTGTTTTC	281473	113669	GGTGCGCAACCCAGCTACTC
192300	24496	TTTTATTGAGACAGAGTCTC	236887	69083	CCTGGGCTGCAAGGTGTTTT	281474	113670	TGGTGCGCAACCCAGCTACT
192301	24497	TTTTTATTGAGACAGAGTCT	236888	69084	CCCTGGGCTGCAAGGTGTTT	281475	113671	GTGGTGCGCAACCCAGCTAC
192302	24498	TTTTTTATTGAGACAGAGTC	236889	69085	ACCCTGGGCTGCAAGGTGTT	281476	113672	GGTGGTGCGCAACCCAGCTA
192303	24499	TTTTTTTATTGAGACAGAGT	236890	69086	TACCCTGGGCTGCAAGGTGT	281477	113673	TGGTGGTGCGCAACCCAGCT
192304	24500	TTTTTTTTATTGAGACAGAG	236891	69087	ATACCCTGGGCTGCAAGGTG	281478	113674	ATGGTGGTGCGCAACCCAGC
192305	24501	TTTTTTTTTATTGAGACAGA	236892	69088	CATACCCTGGGCTGCAAGGT	281479	113675	CATGGTGGTGCGCAACCCAG
192306	24502	TTTTTTTTTTATTGAGACAG	236893	69089	CCATACCCTGGGCTGCAAGG	281480	113676	GCATGGTGGTGCGCAACCCA
192307	24503	TTTTTTTTTTTATTGAGACA	236894	69090	CCCATACCCTGGGCTGCAAG	281481	113677	GGCATGGTGGTGCGCAACCC
192308	24504	TTTTTTTTTTTTATTGAGAC	236895	69091	ACCCATACCCTGGGCTGCAA	281482	113678	AGGCATGGTGGTGCGCAACC
192309	24505	TTTTTTTTTTTTTATTGAGA	236896	69092	TACCCATACCCTGGGCTGCA	281483	113679	CAGGCATGGTGGTGCGCAAC
192310	24506	TTTTTTTTTTTTTTATTGAG	236897	69093	CTACCCATACCCTGGGCTGC	281484	113680	CCAGGCATGGTGGTGCGCAA
192311	24507	TTTTTTTTTTTTTTTATTGA	236898	69094	ACTACCCATACCCTGGGCTG	281485	113681	GCCAGGCATGGTGGTGCGCA
192312	24508	CTTTTTTTTTTTTTTATTG	236899	69095	CACTACCCATACCCTGGGCT	281486	113682	AGCCAGGCATGGTGGTGCGC
192313	24509	TCTTTTTTTTTTTTTTATT	236900	69096	GCACTACCCATACCCTGGGC	281487	113683	TAGCCAGGCATGGTGGTGCG
192314	24510	TTCTTTTTTTTTTTTTTAT	236901	69097	TGCACTACCCATACCCTGGG	281488	113684	TTAGCCAGGCATGGTGGTGC
192315	24511	TTTCTTTTTTTTTTTTTTA	236902	69098	ATGCACTACCCATACCCTGG	281489	113685	GTTAGCCAGGCATGGTGGTG
192316	24512	TTTTCTTTTTTTTTTTTTT	236903	69099	CATGCACTACCCATACCCTG	281490	113686	AGTTAGCCAGGCATGGTGGT
192317	24513	CTTTTCTTTTTTTTTTTTT	236904	69100	CCATGCACTACCCATACCCT	281491	113687	AAGTTAGCCAGGCATGGTGG
192318	24514	TCTTTTCTTTTTTTTTTTT	236905	69101	TCCATGCACTACCCATACCC	281492	113688	AAAGTTAGCCAGGCATGGTG
192319	24515	TTCTTTTCTTTTTTTTTTT	236906	69102	TTCCATGCACTACCCATACC	281493	113689	AAAAGTTAGCCAGGCATGGT
192320	24516	TTTCTTTTCTTTTTTTTTT	236907	69103	CTTCCATGCACTACCCATAC	281494	113690	CAAAAGTTAGCCAGGCATGG
192321	24517	TTTTCTTTTCTTTTTTTTT	236908	69104	GCTTCCATGCACTACCCATA	281495	113691	ACAAAAGTTAGCCAGGCATG
192322	24518	TTTTTCTTTTCTTTTTTTT	236909	69105	GGCTTCCATGCACTACCCAT	281496	113692	TACAAAAGTTAGCCAGGCAT
192323	24519	CTTTTTCTTTTCTTTTTTT	236910	69106	CGGCTTCCATGCACTACCCA	281497	113693	ATACAAAAGTTAGCCAGGCA
192324	24520	TCTTTTTCTTTTCTTTTTT	236911	69107	ACGGCTTCCATGCACTACCC	281498	113694	AATACAAAAGTTAGCCAGGC
192325	24521	TTCTTTTTCTTTTCTTTTT	236912	69108	CACGGCTTCCATGCACTACC	281499	113695	AAATACAAAAGTTAGCCAGG
192326	24522	ATTCTTTTTCTTTTCTTTT	236913	69109	CCACGGCTTCCATGCACTAC	281500	113696	AAAATACAAAAGTTAGCCAG
192327	24523	AATTCTTTTTCTTTTCTTTT	236914	69110	TCCACGGCTTCCATGCACTA	281501	113697	AAAAATACAAAAGTTAGCCA
192328	24524	CAATTCTTTTTCTTTTCTTT	236915	69111	CTCCACGGCTTCCATGCACT	281502	113698	TAAAAATACAAAAGTTAGCC
192329	24525	GCAATTCTTTTTCTTTTCTT	236916	69112	ACTCCACGGCTTCCATGCAC	281503	113699	CTAAAAATACAAAAGTTAGC
192330	24526	TGCAATTCTTTTTCTTTTCT	236917	69113	AACTCCACGGCTTCCATGCA	281504	113700	ACTAAAAATACAAAAGTTAG
192331	24527	TTGCAATTCTTTTTCTTTTC	236918	69114	CAACTCCACGGCTTCCATGC	281505	113701	TACTAAAAATACAAAAGTTA
192332	24528	CTTGCAATTCTTTTTCTTTT	236919	69115	ACAACTCCACGGCTTCCATG	281506	113702	GTACTAAAAATACAAAAGTT
192333	24529	TCTTGCAATTCTTTTTCTTT	236920	69116	CACAACTCCACGGCTTCCAT	281507	113703	TGTACTAAAAATACAAAAGT
192334	24530	TTCTTGCAATTCTTTTTCTT	236921	69117	TCACAACTCCACGGCTTCCA	281508	113704	CTGTACTAAAAATACAAAAG
192335	24531	TTTCTTGCAATTCTTTTTCT	236922	69118	CTCACAACTCCACGGCTTCC	281509	113705	TCTGTACTAAAAATACAAAA
192336	24532	ATTTCTTGCAATTCTTTTTC	236923	69119	CCTCACAACTCCACGGCTTC	281510	113706	GTCTGTACTAAAAATACAAA
192337	24533	TATTTCTTGCAATTCTTTTT	236924	69120	ACCTCACAACTCCACGGCTT	281511	113707	CGTCTGTACTAAAAATACAA
192338	24534	TTATTTCTTGCAATTCTTTT	236925	69121	CACCTCACAACTCCACGGCT	281512	113708	CCGTCTGTACTAAAAATACA
192339	24535	TTTATTTCTTGCAATTCTTT	236926	69122	CCACCTCACAACTCCACGGC	281513	113709	CCCGTCTGTACTAAAAATAC
192340	24536	ATTTATTTCTTGCAATTCTT	236927	69123	CCCACCTCACAACTCCACGG	281514	113710	CCCCGTCTGTACTAAAAATA
192341	24537	AATTTATTTCTTGCAATTCT	236928	69124	TCCCACCTCACAACTCCACG	281515	113711	ACCCCGTCTGTACTAAAAAT
192342	24538	TAATTTATTTCTTGCAATTC	236929	69125	TTCCCACCTCACAACTCCAC	281516	113712	AACCCCGTCTGTACTAAAAA
192343	24539	ATAATTTATTTCTTGCAATT	236930	69126	CTTCCCACCTCACAACTCCA	281517	113713	AAACCCCGTCTGTACTAAAA
192344	24540	AATAATTTATTTCTTGCAAT	236931	69127	ACTTCCCACCTCACAACTCC	281518	113714	GAAACCCCGTCTGTACTAAA
192345	24541	CAATAATTTATTTCTTGCAA	236932	69128	CACTTCCCACCTCACAACTC	281519	113715	TGAAACCCCGTCTGTACTAA
192346	24542	ACAATAATTTATTTCTTGCA	236933	69129	TCACTTCCCACCTCACAACT	281520	113716	GTGAAACCCCGTCTGTACTA
192347	24543	AACAATAATTTATTTCTTGC	236934	69130	GTCACTTCCCACCTCACAAC	281521	113717	GGTGAAACCCCGTCTGTACT
192348	24544	AAACAATAATTTATTTCTTG	236935	69131	GGTCACTTCCCACCTCACAA	281522	113718	TGGTGAAACCCCGTCTGTAC
192349	24545	TAAACAATAATTTATTTCTT	236936	69132	AGGTCACTTCCCACCTCACA	281523	113719	GTGGTGAAACCCCGTCTGTA
192350	24546	ATAAACAATAATTTATTTCT	236937	69133	GAGGTCACTTCCCACCTCAC	281524	113720	CGTGGTGAAACCCCGTCTGT
192351	24547	CATAAACAATAATTTATTTC	236938	69134	AGAGGTCACTTCCCACCTCA	281525	113721	ACGTGGTGAAACCCCGTCTG
192352	24548	TCATAAACAATAATTTATTT	236939	69135	CAGAGGTCACTTCCCACCTC	281526	113722	AACGTGGTGAAACCCCGTCT
192353	24549	CTCATAAACAATAATTTATT	236940	69136	GCAGAGGTCACTTCCCACCT	281527	113723	CAACGTGGTGAAACCCCGTC
192354	24550	GCTCATAAACAATAATTTAT	236941	69137	AGCAGAGGTCACTTCCCACC	281528	113724	CCAACGTGGTGAAACCCCGT

192355	24551	AGCTCATAAACAATAATTTA	236942	69138	CAGCAGAGGTCACTTCCCAC	281529	113725	GCCAACGTGGTGAAACCCCG
192356	24552	TAGCTCATAAACAATAATTT	236943	69139	CCAGCAGAGGTCACTTCCCA	281530	113726	GGCCAACGTGGTGAAACCCC
192357	24553	ATAGCTCATAAACAATAATT	236944	69140	TCCAGCAGAGGTCACTTCCC	281531	113727	TGGCCAACGTGGTGAAACCC
192358	24554	TATAGCTCATAAACAATAAT	236945	69141	ATCCAGCAGAGGTCACTTCC	281532	113728	CTGGCCAACGTGGTGAAACC
192359	24555	ATATAGCTCATAAACAATAA	236946	69142	TATCCAGCAGAGGTCACTTC	281533	113729	CCTGGCCAACGTGGTGAAAC
192360	24556	CATATAGCTCATAAACAATA	236947	69143	ATATCCAGCAGAGGTCACTT	281534	113730	GCCTGGCCAACGTGGTGAAA
192361	24557	CCATATAGCTCATAAACAAT	236948	69144	CATATCCAGCAGAGGTCACT	281535	113731	AGCCTGGCCAACGTGGTGAA
192362	24558	ACCATATAGCTCATAAACAA	236949	69145	ACATATCCAGCAGAGGTCAC	281536	113732	CAGCCTGGCCAACGTGGTGA
192363	24559	GACCATATAGCTCATAAACA	236950	69146	GACATATCCAGCAGAGGTCA	281537	113733	GCAGCCTGGCCAACGTGGTG
192364	24560	AGACCATATAGCTCATAAAC	236951	69147	AGACATATCCAGCAGAGGTC	281538	113734	AGCAGCCTGGCCAACGTGGT
192365	24561	CAGACCATATAGCTCATAAA	236952	69148	TAGACATATCCAGCAGAGGT	281539	113735	GAGCAGCCTGGCCAACGTGG
192366	24562	ACAGACCATATAGCTCATAA	236953	69149	ATAGACATATCCAGCAGAGG	281540	113736	AGAGCAGCCTGGCCAACGTG
192367	24563	CACAGACCATATAGCTCATA	236954	69150	AATAGACATATCCAGCAGAG	281541	113737	AAGAGCAGCCTGGCCAACGT
192368	24564	CCACAGACCATATAGCTCAT	236955	69151	GAATAGACATATCCAGCAGA	281542	113738	CAAGAGCAGCCTGGCCAACG
192369	24565	ACCACAGACCATATAGCTCA	236956	69152	TGAATAGACATATCCAGCAG	281543	113739	TCAAGAGCAGCCTGGCCAAC
192370	24566	TACCACAGACCATATAGCTC	236957	69153	CTGAATAGACATATCCAGCA	281544	113740	TTCAAGAGCAGCCTGGCCAA
192371	24567	GTACCACAGACCATATAGCT	236958	69154	CCTGAATAGACATATCCAGC	281545	113741	GTTCAAGAGCAGCCTGGCCA
192372	24568	GGTACCACAGACCATATAGC	236959	69155	TCCTGAATAGACATATCCAG	281546	113742	AGTTCAAGAGCAGCCTGGCC
192373	24569	AGGTACCACAGACCATATAG	236960	69156	TTCCTGAATAGACATATCCA	281547	113743	GAGTTCAAGAGCAGCCTGGC
192374	24570	AAGGTACCACAGACCATATA	236961	69157	CTTCCTGAATAGACATATCC	281548	113744	GGAGTTCAAGAGCAGCCTGG
192375	24571	CAAGGTACCACAGACCATAT	236962	69158	TCTTCCTGAATAGACATATC	281549	113745	AGGAGTTCAAGAGCAGCCTG
192376	24572	ACAAGGTACCACAGACCATA	236963	69159	ATCTTCCTGAATAGACATAT	281550	113746	CAGGAGTTCAAGAGCAGCCT
192377	24573	AACAAGGTACCACAGACCAT	236964	69160	AATCTTCCTGAATAGACATA	281551	113747	TCAGGAGTTCAAGAGCAGCC
192378	24574	CAACAAGGTACCACAGACCA	236965	69161	CAATCTTCCTGAATAGACAT	281552	113748	GTCAGGAGTTCAAGAGCAGC
192379	24575	ACAACAAGGTACCACAGACC	236966	69162	GCAATCTTCCTGAATAGACA	281553	113749	CGTCAGGAGTTCAAGAGCAG
192380	24576	CACAACAAGGTACCACAGAC	236967	69163	AGCAATCTTCCTGAATAGAC	281554	113750	ACGTCAGGAGTTCAAGAGCA
192381	24577	CCACAACAAGGTACCACAGA	236968	69164	CAGCAATCTTCCTGAATAGA	281555	113751	GACGTCAGGAGTTCAAGAGC
192382	24578	CCCACAACAAGGTACCACAG	236969	69165	CCAGCAATCTTCCTGAATAG	281556	113752	TGACGTCAGGAGTTCAAGAG
192383	24579	TCCCACAACAAGGTACCACA	236970	69166	TCCAGCAATCTTCCTGAATA	281557	113753	CTGACGTCAGGAGTTCAAGA
192384	24580	GTCCCACAACAAGGTACCAC	236971	69167	CTCCAGCAATCTTCCTGAAT	281558	113754	CCTGACGTCAGGAGTTCAAG
192385	24581	AGTCCCACAACAAGGTACCA	236972	69168	ACTCCAGCAATCTTCCTGAA	281559	113755	ACCTGACGTCAGGAGTTCAA
192386	24582	CAGTCCCACAACAAGGTACC	236973	69169	CACTCCAGCAATCTTCCTGA	281560	113756	CACCTGACGTCAGGAGTTCA
192387	24583	CCAGTCCCACAACAAGGTAC	236974	69170	CCACTCCAGCAATCTTCCTG	281561	113757	TCACCTGACGTCAGGAGTTC
192388	24584	CCCAGTCCCACAACAAGGTA	236975	69171	CCCACTCCAGCAATCTTCCT	281562	113758	ATCACCTGACGTCAGGAGTT
192389	24585	TCCCAGTCCCACAACAAGGT	236976	69172	ACCCACTCCAGCAATCTTCC	281563	113759	GATCACCTGACGTCAGGAGT
192390	24586	CTCCCAGTCCCACAACAAGG	236977	69173	CACCCACTCCAGCAATCTTC	281564	113760	GGATCACCTGACGTCAGGAG
192391	24587	ACTCCCAGTCCCACAACAAG	236978	69174	CCACCCACTCCAGCAATCTT	281565	113761	TGGATCACCTGACGTCAGGA
192392	24588	GACTCCCAGTCCCACAACAA	236979	69175	CCCACCCACTCCAGCAATCT	281566	113762	GTGGATCACCTGACGTCAGG
192393	24589	AGACTCCCAGTCCCACAACA	236980	69176	CCCCACCCACTCCAGCAATC	281567	113763	GGTGGATCACCTGACGTCAG
192394	24590	AAGACTCCCAGTCCCACAAC	236981	69177	ACCCCACCCACTCCAGCAAT	281568	113764	TGGTGGATCACCTGACGTCA
192395	24591	CAAGACTCCCAGTCCCACAA	236982	69178	GACCCCACCCACTCCAGCAA	281569	113765	CTGGTGGATCACCTGACGTC
192396	24592	CCAAGACTCCCAGTCCCACA	236983	69179	AGACCCCACCCACTCCAGCA	281570	113766	GCTGGTGGATCACCTGACGT
192397	24593	GCCAAGACTCCCAGTCCCAC	236984	69180	GAGACCCCACCCACTCCAGC	281571	113767	GGCTGGTGGATCACCTGACG
192398	24594	CGCCAAGACTCCCAGTCCCA	236985	69181	AGAGACCCCACCCACTCCAG	281572	113768	AGGCTGGTGGATCACCTGAC
192399	24595	ACGCCAAGACTCCCAGTCCC	236986	69182	CAGAGACCCCACCCACTCCA	281573	113769	AAGGCTGGTGGATCACCTGA
192400	24596	GACGCCAAGACTCCCAGTCC	236987	69183	CCAGAGACCCCACCCACTCC	281574	113770	CAAGGCTGGTGGATCACCTG
192401	24597	AGACGCCAAGACTCCCAGTC	236988	69184	CCCAGAGACCCCACCCACTC	281575	113771	TCAAGGCTGGTGGATCACCT
192402	24598	GAGACGCCAAGACTCCCAGT	236989	69185	TCCCAGAGACCCCACCCACT	281576	113772	GTCAAGGCTGGTGGATCACC
192403	24599	GGAGACGCCAAGACTCCCAG	236990	69186	CTCCCAGAGACCCCACCCAC	281577	113773	GGTCAAGGCTGGTGGATCAC
192404	24600	GGGAGACGCCAAGACTCCCA	236991	69187	CCTCCCAGAGACCCCACCCA	281578	113774	AGGTCAAGGCTGGTGGATCA
192405	24601	AGGGAGACGCCAAGACTCCC	236992	69188	ACCTCCCAGAGACCCCACCC	281579	113775	GAGGTCAAGGCTGGTGGATC
192406	24602	CAGGGAGACGCCAAGACTCC	236993	69189	GACCTCCCAGAGACCCCACC	281580	113776	GGAGGTCAAGGCTGGTGGAT
192407	24603	TCAGGGAGACGCCAAGACTC	236994	69190	GGACCTCCCAGAGACCCCAC	281581	113777	GGGAGGTCAAGGCTGGTGGA
192408	24604	GTCAGGGAGACGCCAAGACT	236995	69191	GGGACCTCCCAGAGACCCCA	281582	113778	TGGGAGGTCAAGGCTGGTGG
192409	24605	GGTCAGGGAGACGCCAAGAC	236996	69192	GGGGACCTCCCAGAGACCCC	281583	113779	TTGGGAGGTCAAGGCTGGTG
192410	24606	GGGTCAGGGAGACGCCAAGA	236997	69193	AGGGGACCTCCCAGAGACCC	281584	113780	TTTGGGAGGTCAAGGCTGGT
192411	24607	AGGGTCAGGGAGACGCCAAG	236998	69194	CAGGGGACCTCCCAGAGACC	281585	113781	CTTTGGGAGGTCAAGGCTGG
192412	24608	CAGGGTCAGGGAGACGCCAA	236999	69195	TCAGGGGACCTCCCAGAGAC	281586	113782	ACTTTGGGAGGTCAAGGCTG
192413	24609	GCAGGGTCAGGGAGACGCCA	237000	69196	CTCAGGGGACCTCCCAGAGA	281587	113783	CACTTTGGGAGGTCAAGGCT
192414	24610	GGCAGGGTCAGGGAGACGCC	237001	69197	ACTCAGGGGACCTCCCAGAG	281588	113784	GCACTTTGGGAGGTCAAGGC
192415	24611	AGGCAGGGTCAGGGAGACGC	237002	69198	CACTCAGGGGACCTCCCAGA	281589	113785	AGCACTTTGGGAGGTCAAGG
192416	24612	CAGGCAGGGTCAGGGAGACG	237003	69199	ACACTCAGGGGACCTCCCAG	281590	113786	TAGCACTTTGGGAGGTCAAG
192417	24613	ACAGGCAGGGTCAGGGAGAC	237004	69200	CACACTCAGGGGACCTCCCA	281591	113787	CTAGCACTTTGGGAGGTCAA
192418	24614	AACAGGCAGGGTCAGGGAGA	237005	69201	CCACACTCAGGGGACCTCCC	281592	113788	CCTAGCACTTTGGGAGGTCA
192419	24615	CAACAGGCAGGGTCAGGGAG	237006	69202	CCCACACTCAGGGGACCTCC	281593	113789	TCCTAGCACTTTGGGAGGTC
192420	24616	GCAACAGGCAGGGTCAGGGA	237007	69203	TCCCACACTCAGGGGACCTC	281594	113790	ATCCTAGCACTTTGGGAGGT
192421	24617	AGCAACAGGCAGGGTCAGGG	237008	69204	TTCCCACACTCAGGGGACCT	281595	113791	AATCCTAGCACTTTGGGAGG
192422	24618	CAGCAACAGGCAGGGTCAGG	237009	69205	CTTCCCACACTCAGGGGACC	281596	113792	TAATCCTAGCACTTTGGGAG
192423	24619	GCAGCAACAGGCAGGGTCAG	237010	69206	GCTTCCCACACTCAGGGGAC	281597	113793	GTAATCCTAGCACTTTGGGA
192424	24620	TGCAGCAACAGGCAGGGTCA	237011	69207	AGCTTCCCACACTCAGGGGA	281598	113794	TGTAATCCTAGCACTTTGGG
192425	24621	CTGCAGCAACAGGCAGGGTC	237012	69208	CAGCTTCCCACACTCAGGGG	281599	113795	CTGTAATCCTAGCACTTTGG
192426	24622	GCTGCAGCAACAGGCAGGGT	237013	69209	CCAGCTTCCCACACTCAGGG	281600	113796	CCTGTAATCCTAGCACTTTG

192427	24623	TGCTGCAGCAACAGGCAGGG	237014	69210	CCCAGCTTCCCACACTCAGG	281601	113797	TCCTGTAATCCTAGCACTTT
192428	24624	GTGCTGCAGCAACAGGCAGG	237015	69211	TCCCAGCTTCCCACACTCAG	281602	113798	CTCCTGTAATCCTAGCACTT
192429	24625	GGTGCTGCAGCAACAGGCAG	237016	69212	GTCCCAGCTTCCCACACTCA	281603	113799	GCTCCTGTAATCCTAGCACT
192430	24626	CGGTGCTGCAGCAACAGGCA	237017	69213	GGTCCCAGCTTCCCACACTC	281604	113800	GGCTCCTGTAATCCTAGCAC
192431	24627	GCGGTGCTGCAGCAACAGGC	237018	69214	TGGTCCCAGCTTCCCACACT	281605	113801	TGGCTCCTGTAATCCTAGCA
192432	24628	AGCGGTGCTGCAGCAACAGG	237019	69215	GTGGTCCCAGCTTCCCACAC	281606	113802	GTGGCTCCTGTAATCCTAGC
192433	24629	GAGCGGTGCTGCAGCAACAG	237020	69216	GGTGGTCCCAGCTTCCCACA	281607	113803	AGTGGCTCCTGTAATCCTAG
192434	24630	TGAGCGGTGCTGCAGCAACA	237021	69217	TGGTGGTCCCAGCTTCCCAC	281608	113804	CAGTGGCTCCTGTAATCCTA
192435	24631	CTGAGCGGTGCTGCAGCAAC	237022	69218	CTGGTGGTCCCAGCTTCCCA	281609	113805	ACAGTGGCTCCTGTAATCCT
192436	24632	GCTGAGCGGTGCTGCAGCAA	237023	69219	GCTGGTGGTCCCAGCTTCCC	281610	113806	TACAGTGGCTCCTGTAATCC
192437	24633	GGCTGAGCGGTGCTGCAGCA	237024	69220	AGCTGGTGGTCCCAGCTTCC	281611	113807	GTACAGTGGCTCCTGTAATC
192438	24634	GGGCTGAGCGGTGCTGCAGC	237025	69221	AAGCTGGTGGTCCCAGCTTC	281612	113808	GGTACAGTGGCTCCTGTAAT
192439	24635	AGGGCTGAGCGGTGCTGCAG	237026	69222	AAAGCTGGTGGTCCCAGCTT	281613	113809	GGGTACAGTGGCTCCTGTAA
192440	24636	CAGGGCTGAGCGGTGCTGCA	237027	69223	GAAAGCTGGTGGTCCCAGCT	281614	113810	TGGGTACAGTGGCTCCTGTA
192441	24637	GCAGGGCTGAGCGGTGCTGC	237028	69224	AGAAAGCTGGTGGTCCCAGC	281615	113811	CTGGGTACAGTGGCTCCTGT
192442	24638	GGCAGGGCTGAGCGGTGCTG	237029	69225	GAGAAAGCTGGTGGTCCCAG	281616	113812	GCTGGGTACAGTGGCTCCTG
192443	24639	AGGCAGGGCTGAGCGGTGCT	237030	69226	CGAGAAAGCTGGTGGTCCCA	281617	113813	GGCTGGGTACAGTGGCTCCT
192444	24640	CAGGCAGGGCTGAGCGGTGC	237031	69227	GCGAGAAAGCTGGTGGTCCC	281618	113814	AGGCTGGGTACAGTGGCTCC
192445	24641	GCAGGCAGGGCTGAGCGGTG	237032	69228	TGCGAGAAAGCTGGTGGTCC	281619	113815	TAGGCTGGGTACAGTGGCTC
192446	24642	AGCAGGCAGGGCTGAGCGGT	237033	69229	GTGCGAGAAAGCTGGTGGTC	281620	113816	CTAGGCTGGGTACAGTGGCT
192447	24643	GAGCAGGCAGGGCTGAGCGG	237034	69230	TGTGCGAGAAAGCTGGTGGT	281621	113817	CCTAGGCTGGGTACAGTGGC
192448	24644	GGAGCAGGCAGGGCTGAGCG	237035	69231	CTGTGCGAGAAAGCTGGTGG	281622	113818	TCCTAGGCTGGGTACAGTGG
192449	24645	GGGAGCAGGCAGGGCTGAGC	237036	69232	CCTGTGCGAGAAAGCTGGTG	281623	113819	ATCCTAGGCTGGGTACAGTG
192450	24646	AGGGAGCAGGCAGGGCTGAG	237037	69233	CCCTGTGCGAGAAAGCTGGT	281624	113820	TATCCTAGGCTGGGTACAGT
192451	24647	TAGGGAGCAGGCAGGGCTGA	237038	69234	TCCCTGTGCGAGAAAGCTGG	281625	113821	ATATCCTAGGCTGGGTACAG
192452	24648	GTAGGGAGCAGGCAGGGCTG	237039	69235	CTCCCTGTGCGAGAAAGCTG	281626	113822	CATATCCTAGGCTGGGTACA
192453	24649	GGTAGGGAGCAGGCAGGGCT	237040	69236	ACTCCCTGTGCGAGAAAGCT	281627	113823	TCATATCCTAGGCTGGGTAC
192454	24650	AGGTAGGGAGCAGGCAGGGC	237041	69237	CACTCCCTGTGCGAGAAAGC	281628	113824	ATCATATCCTAGGCTGGGTA
192455	24651	CAGGTAGGGAGCAGGCAGGG	237042	69238	CCACTCCCTGTGCGAGAAAG	281629	113825	TATCATATCCTAGGCTGGGT
192456	24652	GCAGGTAGGGAGCAGGCAGG	237043	69239	GCCACTCCCTGTGCGAGAAA	281630	113826	ATATCATATCCTAGGCTGGG
192457	24653	GGCAGGTAGGGAGCAGGCAG	237044	69240	GGCCACTCCCTGTGCGAGAA	281631	113827	GATATCATATCCTAGGCTGG
192458	24654	AGGCAGGTAGGGAGCAGGCA	237045	69241	TGGCCACTCCCTGTGCGAGA	281632	113828	TGATATCATATCCTAGGCTG
192459	24655	GAGGCAGGTAGGGAGCAGGC	237046	69242	ATGGCCACTCCCTGTGCGAG	281633	113829	GTGATATCATATCCTAGGCT
192460	24656	GGAGGCAGGTAGGGAGCAGG	237047	69243	GATGGCCACTCCCTGTGCGA	281634	113830	AGTGATATCATATCCTAGGC
192461	24657	GGGAGGCAGGTAGGGAGCAG	237048	69244	GGATGGCCACTCCCTGTGCG	281635	113831	AAGTGATATCATATCCTAGG
192462	24658	GGGGAGGCAGGTAGGGAGCA	237049	69245	GGGATGGCCACTCCCTGTGC	281636	113832	GAAGTGATATCATATCCTAG
192463	24659	AGGGGAGGCAGGTAGGGAGC	237050	69246	TGGGATGGCCACTCCCTGTG	281637	113833	AGAAGTGATATCATATCCTA
192464	24660	GAGGGGAGGCAGGTAGGGAG	237051	69247	CTGGGATGGCCACTCCCTGT	281638	113834	AAGAAGTGATATCATATCCT
192465	24661	CGAGGGGAGGCAGGTAGGGA	237052	69248	GCTGGGATGGCCACTCCCTG	281639	113835	TAAGAAGTGATATCATATCC
192466	24662	CCGAGGGGAGGCAGGTAGGG	237053	69249	AGCTGGGATGGCCACTCCCT	281640	113836	CTAAGAAGTGATATCATATC
192467	24663	GCCGAGGGGAGGCAGGTAGG	237054	69250	AAGCTGGGATGGCCACTCCC	281641	113837	TCTAAGAAGTGATATCATAT
192468	24664	GGCCGAGGGGAGGCAGGTAG	237055	69251	CAAGCTGGGATGGCCACTCC	281642	113838	CTCTAAGAAGTGATATCATA
192469	24665	AGGCCGAGGGGAGGCAGGTA	237056	69252	CCAAGCTGGGATGGCCACTC	281643	113839	GCTCTAAGAAGTGATATCAT
192470	24666	GAGGCCGAGGGGAGGCAGGT	237057	69253	TCCAAGCTGGGATGGCCACT	281644	113840	TGCTCTAAGAAGTGATATCA
192471	24667	AGAGGCCGAGGGGAGGCAGG	237058	69254	CTCCAAGCTGGGATGGCCAC	281645	113841	TTGCTCTAAGAAGTGATATC
192472	24668	GAGAGGCCGAGGGGAGGCAG	237059	69255	TCTCCAAGCTGGGATGGCCA	281646	113842	CTTGCTCTAAGAAGTGATAT
192473	24669	GGAGAGGCCGAGGGGAGGCA	237060	69256	CTCTCCAAGCTGGGATGGCC	281647	113843	TCTTGCTCTAAGAAGTGATA
192474	24670	AGGAGAGGCCGAGGGGAGGC	237061	69257	CCTCTCCAAGCTGGGATGGC	281648	113844	ATCTTGCTCTAAGAAGTGAT
192475	24671	CAGGAGAGGCCGAGGGGAGG	237062	69258	ACCTCTCCAAGCTGGGATGG	281649	113845	TATCTTGCTCTAAGAAGTGA
192476	24672	GCAGGAGAGGCCGAGGGGAG	237063	69259	AACCTCTCCAAGCTGGGATG	281650	113846	GTATCTTGCTCTAAGAAGTG
192477	24673	GGCAGGAGAGGCCGAGGGGA	237064	69260	GAACCTCTCCAAGCTGGGAT	281651	113847	TGTATCTTGCTCTAAGAAGT
192478	24674	AGGCAGGAGAGGCCGAGGGG	237065	69261	GGAACCTCTCCAAGCTGGGA	281652	113848	TTGTATCTTGCTCTAAGAAG
192479	24675	GAGGCAGGAGAGGCCGAGGG	237066	69262	TGGAACCTCTCCAAGCTGGG	281653	113849	TTTGTATCTTGCTCTAAGAA
192480	24676	GGAGGCAGGAGAGGCCGAGG	237067	69263	CTGGAACCTCTCCAAGCTGG	281654	113850	TTTTGTATCTTGCTCTAAGA
192481	24677	TGGAGGCAGGAGAGGCCGAG	237068	69264	CCTGGAACCTCTCCAAGCTG	281655	113851	ATTTTGTATCTTGCTCTAAG
192482	24678	GTGGAGGCAGGAGAGGCCGA	237069	69265	TCCTGGAACCTCTCCAAGCT	281656	113852	AATTTTGTATCTTGCTCTAA
192483	24679	GGTGGAGGCAGGAGAGGCCG	237070	69266	GTCCTGGAACCTCTCCAAGC	281657	113853	CAATTTTGTATCTTGCTCTA
192484	24680	CGGTGGAGGCAGGAGAGGCC	237071	69267	AGTCCTGGAACCTCTCCAAG	281658	113854	GCAATTTTGTATCTTGCTCT
192485	24681	CCGGTGGAGGCAGGAGAGGC	237072	69268	CAGTCCTGGAACCTCTCCAA	281659	113855	TGCAATTTTGTATCTTGCTC
192486	24682	CCCGGTGGAGGCAGGAGAGG	237073	69269	CCAGTCCTGGAACCTCTCCA	281660	113856	ATGCAATTTTGTATCTTGCT
192487	24683	GCCCGGTGGAGGCAGGAGAG	237074	69270	ACCAGTCCTGGAACCTCTCC	281661	113857	CATGCAATTTTGTATCTTGC
192488	24684	GGCCCGGTGGAGGCAGGAGA	237075	69271	AACCAGTCCTGGAACCTCTC	281662	113858	ACATGCAATTTTGTATCTTG
192489	24685	GGGCCCGGTGGAGGCAGGAG	237076	69272	CAACCAGTCCTGGAACCTCT	281663	113859	CACATGCAATTTTGTATCTT
192490	24686	GGGGCCCGGTGGAGGCAGGA	237077	69273	CCAACCAGTCCTGGAACCTC	281664	113860	GCACATGCAATTTTGTATCT
192491	24687	AGGGGCCCGGTGGAGGCAGG	237078	69274	CCCAACCAGTCCTGGAACCT	281665	113861	TGCACATGCAATTTTGTATC
192492	24688	CAGGGGCCCGGTGGAGGCAG	237079	69275	TCCCAACCAGTCCTGGAACC	281666	113862	GTGCACATGCAATTTTGTAT
192493	24689	CCAGGGGCCCGGTGGAGGCA	237080	69276	CTCCCAACCAGTCCTGGAAC	281667	113863	TGTGCACATGCAATTTTGTA
192494	24690	ACCAGGGGCCCGGTGGAGGC	237081	69277	CCTCCCAACCAGTCCTGGAA	281668	113864	TTGTGCACATGCAATTTTGT
192495	24691	CACCAGGGGCCCGGTGGAGG	237082	69278	GCCTCCCAACCAGTCCTGGA	281669	113865	ATTGTGCACATGCAATTTTG
192496	24692	GCACCAGGGGCCCGGTGGAG	237083	69279	TGCCTCCCAACCAGTCCTGG	281670	113866	TATTGTGCACATGCAATTTT
192497	24693	GGCACCAGGGGCCCGGTGGA	237084	69280	GTGCCTCCCAACCAGTCCTG	281671	113867	TTATTGTGCACATGCAATTT
192498	24694	AGGCACCAGGGGCCCGGTGG	237085	69281	CGTGCCTCCCAACCAGTCCT	281672	113868	ATTATTGTGCACATGCAATT

192499	24695	GAGGCACCAGGGGCCCGGTG	237086	69282	ACGTGCCTCCCAACCAGTCC	281673	113869	AATTATTGTGCACATGCAAT
192500	24696	GGAGGCACCAGGGGCCCGGT	237087	69283	AACGTGCCTCCCAACCAGTC	281674	113870	GAATTATTGTGCACATGCAA
192501	24697	AGGAGGCACCAGGGGCCCGG	237088	69284	AAACGTGCCTCCCAACCAGT	281675	113871	AGAATTATTGTGCACATGCA
192502	24698	GAGGAGGCACCAGGGGCCCG	237089	69285	GAAACGTGCCTCCCAACCAG	281676	113872	TAGAATTATTGTGCACATGC
192503	24699	AGAGGAGGCACCAGGGGCCC	237090	69286	TGAAACGTGCCTCCCAACCA	281677	113873	GTAGAATTATTGTGCACATG
192504	24700	TAGAGGAGGCACCAGGGGCC	237091	69287	CTGAAACGTGCCTCCCAACC	281678	113874	GGTAGAATTATTGTGCACAT
192505	24701	CTAGAGGAGGCACCAGGGGC	237092	69288	TCTGAAACGTGCCTCCCAAC	281679	113875	TGGTAGAATTATTGTGCACA
192506	24702	TCTAGAGGAGGCACCAGGGG	237093	69289	ATCTGAAACGTGCCTCCCAA	281680	113876	TTGGTAGAATTATTGTGCAC
192507	24703	CTCTAGAGGAGGCACCAGGG	237094	69290	AATCTGAAACGTGCCTCCCA	281681	113877	CTTGGTAGAATTATTGTGCA
192508	24704	TCTCTAGAGGAGGCACCAGG	237095	69291	AAATCTGAAACGTGCCTCCC	281682	113878	ACTTGGTAGAATTATTGTGC
192509	24705	GTCTCTAGAGGAGGCACCAG	237096	69292	GAAATCTGAAACGTGCCTCC	281683	113879	TACTTGGTAGAATTATTGTG
192510	24706	TGTCTCTAGAGGAGGCACCA	237097	69293	AGAAATCTGAAACGTGCCTC	281684	113880	ATACTTGGTAGAATTATTGT
192511	24707	CTGTCTCTAGAGGAGGCACC	237098	69294	TAGAAATCTGAAACGTGCCT	281685	113881	TATACTTGGTAGAATTATTG
192512	24708	ACTGTCTCTAGAGGAGGCAC	237099	69295	ATAGAAATCTGAAACGTGCC	281686	113882	CTATACTTGGTAGAATTATT
192513	24709	GACTGTCTCTAGAGGAGGCA	237100	69296	GATAGAAATCTGAAACGTGC	281687	113883	CCTATACTTGGTAGAATTAT
192514	24710	GGACTGTCTCTAGAGGAGGC	237101	69297	AGATAGAAATCTGAAACGTG	281688	113884	ACCTATACTTGGTAGAATTA
192515	24711	AGGACTGTCTCTAGAGGAGG	237102	69298	CAGATAGAAATCTGAAACGT	281689	113885	TACCTATACTTGGTAGAATT
192516	24712	GAGGACTGTCTCTAGAGGAG	237103	69299	ACAGATAGAAATCTGAAACG	281690	113886	ATACCTATACTTGGTAGAAT
192517	24713	GGAGGACTGTCTCTAGAGGA	237104	69300	AACAGATAGAAATCTGAAAC	281691	113887	TATACCTATACTTGGTAGAA
192518	24714	AGGAGGACTGTCTCTAGAGG	237105	69301	CAACAGATAGAAATCTGAAA	281692	113888	GTATACCTATACTTGGTAGA
192519	24715	CAGGAGGACTGTCTCTAGAG	237106	69302	TCAACAGATAGAAATCTGAA	281693	113889	TGTATACCTATACTTGGTAG
192520	24716	CCAGGAGGACTGTCTCTAGA	237107	69303	TTCAACAGATAGAAATCTGA	281694	113890	CTGTATACCTATACTTGGTA
192521	24717	CCCAGGAGGACTGTCTCTAG	237108	69304	ATTCAACAGATAGAAATCTG	281695	113891	CCTGTATACCTATACTTGGT
192522	24718	TCCCAGGAGGACTGTCTCTA	237109	69305	GATTCAACAGATAGAAATCT	281696	113892	CCCTGTATACCTATACTTGG
192523	24719	GTCCCAGGAGGACTGTCTCT	237110	69306	TGATTCAACAGATAGAAATC	281697	113893	CCCCTGTATACCTATACTTG
192524	24720	GGTCCCAGGAGGACTGTCTC	237111	69307	CTGATTCAACAGATAGAAAT	281698	113894	ACCCCTGTATACCTATACTT
192525	24721	CGGTCCCAGGAGGACTGTCT	237112	69308	GCTGATTCAACAGATAGAAA	281699	113895	TACCCCTGTATACCTATACT
192526	24722	TCGGTCCCAGGAGGACTGTC	237113	69309	CGCTGATTCAACAGATAGAA	281700	113896	CTACCCCTGTATACCTATAC
192527	24723	ATCGGTCCCAGGAGGACTGT	237114	69310	TCGCTGATTCAACAGATAGA	281701	113897	ACTACCCCTGTATACCTATA
192528	24724	AATCGGTCCCAGGAGGACTG	237115	69311	TTCGCTGATTCAACAGATAG	281702	113898	AACTACCCCTGTATACCTAT
192529	24725	CAATCGGTCCCAGGAGGACT	237116	69312	CTTCGCTGATTCAACAGATA	281703	113899	TAACTACCCCTGTATACCTA
192530	24726	ACAATCGGTCCCAGGAGGAC	237117	69313	TCTTCGCTGATTCAACAGAT	281704	113900	ATAACTACCCCTGTATACCT
192531	24727	CACAATCGGTCCCAGGAGGA	237118	69314	ATCTTCGCTGATTCAACAGA	281705	113901	TATAACTACCCCTGTATACC
192532	24728	ACACAATCGGTCCCAGGAGG	237119	69315	TATCTTCGCTGATTCAACAG	281706	113902	ATATAACTACCCCTGTATAC
192533	24729	AACACAATCGGTCCCAGGAG	237120	69316	ATATCTTCGCTGATTCAACA	281707	113903	TATATAACTACCCCTGTATA
192534	24730	GAACACAATCGGTCCCAGGA	237121	69317	AATATCTTCGCTGATTCAAC	281708	113904	ATATATAACTACCCCTGTAT
192535	24731	AGAACACAATCGGTCCCAGG	237122	69318	CAATATCTTCGCTGATTCAA	281709	113905	TATATATAACTACCCCTGTA
192536	24732	GAGAACACAATCGGTCCCAG	237123	69319	CCAATATCTTCGCTGATTCA	281710	113906	TTATATATAACTACCCCTGT
192537	24733	TGAGAACACAATCGGTCCCA	237124	69320	TCCAATATCTTCGCTGATTC	281711	113907	TTTATATATAACTACCCCTG
192538	24734	GTGAGAACACAATCGGTCCC	237125	69321	ATCCAATATCTTCGCTGATT	281712	113908	ATTTATATATAACTACCCCT
192539	24735	AGTGAGAACACAATCGGTCC	237126	69322	AATCCAATATCTTCGCTGAT	281713	113909	CATTTATATATAACTACCCC
192540	24736	AAGTGAGAACACAATCGGTC	237127	69323	TAATCCAATATCTTCGCTGA	281714	113910	TCATTTATATATAACTACCC
192541	24737	TAAGTGAGAACACAATCGGT	237128	69324	ATAATCCAATATCTTCGCTG	281715	113911	CTCATTTATATATAACTACC
192542	24738	GTAAGTGAGAACACAATCGG	237129	69325	CATAATCCAATATCTTCGCT	281716	113912	TCTCATTTATATATAACTAC
192543	24739	TGTAAGTGAGAACACAATCG	237130	69326	TCATAATCCAATATCTTCGC	281717	113913	GTCTCATTTATATATAACTA
192544	24740	GTGTAAGTGAGAACACAATC	237131	69327	CTCATAATCCAATATCTTCG	281718	113914	AGTCTCATTTATATATAACT
192545	24741	CGTGTAAGTGAGAACACAAT	237132	69328	CCTCATAATCCAATATCTTC	281719	113915	AAGTCTCATTTATATATAAC
192546	24742	TCGTGTAAGTGAGAACACAA	237133	69329	TCCTCATAATCCAATATCTT	281720	113916	GAAGTCTCATTTATATATAA
192547	24743	CTCGTGTAAGTGAGAACACA	237134	69330	TTCCTCATAATCCAATATCT	281721	113917	TGAAGTCTCATTTATATATA
192548	24744	CCTCGTGTAAGTGAGAACAC	237135	69331	ATTCCTCATAATCCAATATC	281722	113918	TTGAAGTCTCATTTATATAT
192549	24745	GCCTCGTGTAAGTGAGAACA	237136	69332	AATTCCTCATAATCCAATAT	281723	113919	CTTGAAGTCTCATTTATATA
192550	24746	TGCCTCGTGTAAGTGAGAAC	237137	69333	AAATTCCTCATAATCCAATA	281724	113920	CCTTGAAGTCTCATTTATAT
192551	24747	ATGCCTCGTGTAAGTGAGAA	237138	69334	CAAATTCCTCATAATCCAAT	281725	113921	TCCTTGAAGTCTCATTTATA
192552	24748	GATGCCTCGTGTAAGTGAGA	237139	69335	CCAAATTCCTCATAATCCAA	281726	113922	TTCCTTGAAGTCTCATTTAT
192553	24749	GGATGCCTCGTGTAAGTGAG	237140	69336	CCCAAATTCCTCATAATCCA	281727	113923	TTTCCTTGAAGTCTCATTTA
192554	24750	TGGATGCCTCGTGTAAGTGA	237141	69337	TCCCAAATTCCTCATAATCC	281728	113924	ATTTCCTTGAAGTCTCATTT
192555	24751	CTGGATGCCTCGTGTAAGTG	237142	69338	TTCCCAAATTCCTCATAATC	281729	113925	TATTTCCTTGAAGTCTCATT
192556	24752	CCTGGATGCCTCGTGTAAGT	237143	69339	ATTCCCAAATTCCTCATAAT	281730	113926	GTATTTCCTTGAAGTCTCAT
192557	24753	TCCTGGATGCCTCGTGTAAG	237144	69340	AATTCCCAAATTCCTCATAA	281731	113927	TGTATTTCCTTGAAGTCTCA
192558	24754	GTCCTGGATGCCTCGTGTAA	237145	69341	TAATTCCCAAATTCCTCATA	281732	113928	TTGTATTTCCTTGAAGTCTC
192559	24755	AGTCCTGGATGCCTCGTGTA	237146	69342	CTAATTCCCAAATTCCTCAT	281733	113929	GTTGTATTTCCTTGAAGTCT
192560	24756	TAGTCCTGGATGCCTCGTGT	237147	69343	CCTAATTCCCAAATTCCTCA	281734	113930	TGTTGTATTTCCTTGAAGTC
192561	24757	GTAGTCCTGGATGCCTCGTG	237148	69344	TCCTAATTCCCAAATTCCTC	281735	113931	TTGTTGTATTTCCTTGAAGT
192562	24758	TGTAGTCCTGGATGCCTCGT	237149	69345	TTCCTAATTCCCAAATTCCT	281736	113932	TTTGTTGTATTTCCTTGAAG
192563	24759	CTGTAGTCCTGGATGCCTCG	237150	69346	TTTCCTAATTCCCAAATTCC	281737	113933	TTTTGTTGTATTTCCTTGAA
192564	24760	TCTGTAGTCCTGGATGCCTC	237151	69347	CTTTCCTAATTCCCAAATTC	281738	113934	ATTTTGTTGTATTTCCTTGA
192565	24761	ATCTGTAGTCCTGGATGCCT	237152	69348	ACTTTCCTAATTCCCAAATT	281739	113935	CATTTTGTTGTATTTCCTTG
192566	24762	TATCTGTAGTCCTGGATGCC	237153	69349	CACTTTCCTAATTCCCAAAT	281740	113936	GCATTTTGTTGTATTTCCTT
192567	24763	TTATCTGTAGTCCTGGATGC	237154	69350	CCACTTTCCTAATTCCCAAA	281741	113937	TGCATTTTGTTGTATTTCCT
192568	24764	GTTATCTGTAGTCCTGGATG	237155	69351	CCCACTTTCCTAATTCCCAA	281742	113938	TTGCATTTTGTTGTATTTCC
192569	24765	GGTTATCTGTAGTCCTGGAT	237156	69352	ACCCACTTTCCTAATTCCCA	281743	113939	ATTGCATTTTGTTGTATTTC
192570	24766	TGGTTATCTGTAGTCCTGGA	237157	69353	CACCCACTTTCCTAATTCCC	281744	113940	GATTGCATTTTGTTGTATTT

192571	24767	CTGGTTATCTGTAGTCCTGG	237158	69354	GCACCCACTTTCCTAATTCC	281745	113941	CGATTGCATTTTGTTGTATT
192572	24768	TCTGGTTATCTGTAGTCCTG	237159	69355	TGCACCCACTTTCCTAATTC	281746	113942	ACGATTGCATTTTGTTGTAT
192573	24769	CTCTGGTTATCTGTAGTCCT	237160	69356	CTGCACCCACTTTCCTAATT	281747	113943	CACGATTGCATTTTGTTGTA
192574	24770	CCTCTGGTTATCTGTAGTCC	237161	69357	CCTGCACCCACTTTCCTAAT	281748	113944	TCACGATTGCATTTTGTTGT
192575	24771	TCCTCTGGTTATCTGTAGTC	237162	69358	ACCTGCACCCACTTTCCTAA	281749	113945	ATCACGATTGCATTTTGTTG
192576	24772	TTCCTCTGGTTATCTGTAGT	237163	69359	CACCTGCACCCACTTTCCTA	281750	113946	AATCACGATTGCATTTTGTT
192577	24773	CTTCCTCTGGTTATCTGTAG	237164	69360	CCACCTGCACCCACTTTCCT	281751	113947	CAATCACGATTGCATTTTGT
192578	24774	CCTTCCTCTGGTTATCTGTA	237165	69361	CCCACCTGCACCCACTTTCC	281752	113948	ACAATCACGATTGCATTTTG
192579	24775	CCCTTCCTCTGGTTATCTGT	237166	69362	ACCCACCTGCACCCACTTTC	281753	113949	CACAATCACGATTGCATTTT
192580	24776	CCCCTTCCTCTGGTTATCTG	237167	69363	AACCCACCTGCACCCACTTT	281754	113950	ACACAATCACGATTGCATTT
192581	24777	GCCCCTTCCTCTGGTTATCT	237168	69364	CAACCCACCTGCACCCACTT	281755	113951	AACACAATCACGATTGCATT
192582	24778	CGCCCCTTCCTCTGGTTATC	237169	69365	CCAACCCACCTGCACCCACT	281756	113952	TAACACAATCACGATTGCAT
192583	24779	GCGCCCCTTCCTCTGGTTAT	237170	69366	CCCAACCCACCTGCACCCAC	281757	113953	CTAACACAATCACGATTGCA
192584	24780	GGCGCCCCTTCCTCTGGTTA	237171	69367	CCCCAACCCACCTGCACCCA	281758	113954	CCTAACACAATCACGATTGC
192585	24781	GGGCGCCCCTTCCTCTGGTT	237172	69368	CCCCCAACCCACCTGCACCC	281759	113955	CCCTAACACAATCACGATTG
192586	24782	GGGGCGCCCCTTCCTCTGGT	237173	69369	ACCCCCAACCCACCTGCACC	281760	113956	ACCCTAACACAATCACGATT
192587	24783	GGGGGCGCCCCTTCCTCTGG	237174	69370	TACCCCCAACCCACCTGCAC	281761	113957	CACCCTAACACAATCACGAT
192588	24784	GGGGGGCGCCCCTTCCTCTG	237175	69371	CTACCCCCAACCCACCTGCA	281762	113958	CCACCCTAACACAATCACGA
192589	24785	GGGGGGGCGCCCCTTCCTCT	237176	69372	CCTACCCCCAACCCACCTGC	281763	113959	ACCACCCTAACACAATCACG
192590	24786	GGGGGGGGCGCCCCTTCCTC	237177	69373	ACCTACCCCCAACCCACCTG	281764	113960	TACCACCCTAACACAATCAC
192591	24787	CGGGGGGGGCGCCCCTTCCT	237178	69374	CACCTACCCCCAACCCACCT	281765	113961	TTACCACCCTAACACAATCA
192592	24788	GCGGGGGGGGCGCCCCTTCC	237179	69375	TCACCTACCCCCAACCCACC	281766	113962	CTTACCACCCTAACACAATC
192593	24789	GGCGGGGGGGGCGCCCCTTC	237180	69376	TTCACCTACCCCCAACCCAC	281767	113963	TCTTACCACCCTAACACAAT
192594	24790	AGGCGGGGGGGGGCGCCCCTT	237181	69377	CTTCACCTACCCCCAACCCA	281768	113964	TTCTTACCACCCTAACACAA
192595	24791	CAGGCGGGGGGGGCGCCCCT	237182	69378	CCTTCACCTACCCCCAACCC	281769	113965	TTTCTTACCACCCTAACACA
192596	24792	GCAGGCGGGGGGGGCGCCCC	237183	69379	TCCTTCACCTACCCCCAACC	281770	113966	TTTTCTTACCACCCTAACAC
192597	24793	GGCAGGCGGGGGGGGCGCCC	237184	69380	TTCCTTCACCTACCCCCAAC	281771	113967	GTTTTCTTACCACCCTAACA
192598	24794	GGGCAGGCGGGGGGGGCGCC	237185	69381	CTTCCTTCACCTACCCCCAA	281772	113968	CGTTTTCTTACCACCCTAAC
192599	24795	AGGGCAGGCGGGGGGGGCGC	237186	69382	TCTTCCTTCACCTACCCCCA	281773	113969	CCGTTTTCTTACCACCCTAA
192600	24796	GAGGGCAGGCGGGGGGGGCG	237187	69383	GTCTTCCTTCACCTACCCCC	281774	113970	ACCGTTTTCTTACCACCCTA
192601	24797	GGAGGGCAGGCGGGGGGGGC	237188	69384	TGTCTTCCTTCACCTACCCC	281775	113971	AACCGTTTTCTTACCACCCT
192602	24798	AGGAGGGCAGGCGGGGGGGG	237189	69385	ATGTCTTCCTTCACCTACCC	281776	113972	AAACCGTTTTCTTACCACCC
192603	24799	GAGGAGGGCAGGCGGGGGGG	237190	69386	CATGTCTTCCTTCACCTACC	281777	113973	AAAACCGTTTTCTTACCACC
192604	24800	GGAGGAGGGCAGGCGGGGGG	237191	69387	CCATGTCTTCCTTCACCTAC	281778	113974	AAAAACCGTTTTCTTACCAC
192605	24801	GGGAGGAGGGCAGGCGGGGG	237192	69388	CCCATGTCTTCCTTCACCTA	281779	113975	CAAAAACCGTTTTCTTACCA
192606	24802	AGGGAGGAGGGCAGGCGGGG	237193	69389	GCCCATGTCTTCCTTCACCT	281780	113976	GCAAAAACCGTTTTCTTACC
192607	24803	CAGGGAGGAGGGCAGGCGGG	237194	69390	CGCCCATGTCTTCCTTCACC	281781	113977	AGCAAAAACCGTTTTCTTAC
192608	24804	CCAGGGAGGAGGGCAGGCGG	237195	69391	ACGCCCATGTCTTCCTTCAC	281782	113978	AAGCAAAAACCGTTTTCTTA
192609	24805	GCCAGGGAGGAGGGCAGGCG	237196	69392	TACGCCCATGTCTTCCTTCA	281783	113979	AAAGCAAAAACCGTTTTCTT
192610	24806	TGCCAGGGAGGAGGGCAGGC	237197	69393	ATACGCCCATGTCTTCCTTC	281784	113980	CAAAGCAAAAACCGTTTTCT
192611	24807	ATGCCAGGGAGGAGGGCAGG	237198	69394	AATACGCCCATGTCTTCCTT	281785	113981	TCAAAGCAAAAACCGTTTTC
192612	24808	GATGCCAGGGAGGAGGGCAG	237199	69395	CAATACGCCCATGTCTTCCT	281786	113982	ATCAAAGCAAAAACCGTTTT
192613	24809	GGATGCCAGGGAGGAGGGCA	237200	69396	CCAATACGCCCATGTCTTCC	281787	113983	CATCAAAGCAAAAACCGTTT
192614	24810	AGGATGCCAGGGAGGAGGGC	237201	69397	CCCAATACGCCCATGTCTTC	281788	113984	TCATCAAAGCAAAAACCGTT
192615	24811	GAGGATGCCAGGGAGGAGGG	237202	69398	CCCCAATACGCCCATGTCTT	281789	113985	CTCATCAAAGCAAAAACCGT
192616	24812	TGAGGATGCCAGGGAGGAGG	237203	69399	CCCCCAATACGCCCATGTCT	281790	113986	GCTCATCAAAGCAAAAACCG
192617	24813	GTGAGGATGCCAGGGAGGAG	237204	69400	TCCCCCAATACGCCCATGTC	281791	113987	AGCTCATCAAAGCAAAAACC
192618	24814	CGTGAGGATGCCAGGGAGGA	237205	69401	CTCCCCCAATACGCCCATGT	281792	113988	GAGCTCATCAAAGCAAAAAC
192619	24815	GCGTGAGGATGCCAGGGAGG	237206	69402	GCTCCCCCAATACGCCCATG	281793	113989	AGAGCTCATCAAAGCAAAAA
192620	24816	AGCGTGAGGATGCCAGGGAG	237207	69403	TGCTCCCCCAATACGCCCAT	281794	113990	CAGAGCTCATCAAAGCAAAA
192621	24817	CAGCGTGAGGATGCCAGGGA	237208	69404	CTGCTCCCCCAATACGCCCA	281795	113991	ACAGAGCTCATCAAAGCAAA
192622	24818	GCAGCGTGAGGATGCCAGGG	237209	69405	CCTGCTCCCCCAATACGCCC	281796	113992	AACAGAGCTCATCAAAGCAA
192623	24819	TGCAGCGTGAGGATGCCAGG	237210	69406	CCCTGCTCCCCCAATACGCC	281797	113993	AAACAGAGCTCATCAAAGCA
192624	24820	CTGCAGCGTGAGGATGCCAG	237211	69407	CCCCTGCTCCCCCAATACGC	281798	113994	AAAACAGAGCTCATCAAAGC
192625	24821	TCTGCAGCGTGAGGATGCCA	237212	69408	GCCCCTGCTCCCCCAATACG	281799	113995	AAAAACAGAGCTCATCAAAG
192626	24822	CTCTGCAGCGTGAGGATGCC	237213	69409	AGCCCCTGCTCCCCCAATAC	281800	113996	AAAAAACAGAGCTCATCAAA
192627	24823	CCTCTGCAGCGTGAGGATGC	237214	69410	CAGCCCCTGCTCCCCCAATA	281801	113997	TAAAAAACAGAGCTCATCAA
192628	24824	ACCTCTGCAGCGTGAGGATG	237215	69411	GCAGCCCCTGCTCCCCCAAT	281802	113998	TTAAAAAACAGAGCTCATCA
192629	24825	GACCTCTGCAGCGTGAGGAT	237216	69412	AGCAGCCCCTGCTCCCCCAA	281803	113999	TTTAAAAAACAGAGCTCATC
192630	24826	TGACCTCTGCAGCGTGAGGA	237217	69413	GAGCAGCCCCTGCTCCCCCA	281804	114000	TTTTAAAAAACAGAGCTCAT
192631	24827	CTGACCTCTGCAGCGTGAGG	237218	69414	TGAGCAGCCCCTGCTCCCCC	281805	114001	ATTTTAAAAAACAGAGCTCA
192632	24828	TCTGACCTCTGCAGCGTGAG	237219	69415	CTGAGCAGCCCCTGCTCCCC	281806	114002	GATTTTAAAAAACAGAGCTC
192633	24829	CTCTGACCTCTGCAGCGTGA	237220	69416	TCTGAGCAGCCCCTGCTCCC	281807	114003	CGATTTTAAAAAACAGAGCT
192634	24830	GCTCTGACCTCTGCAGCGTG	237221	69417	CTCTGAGCAGCCCCTGCTCC	281808	114004	ACGATTTTAAAAAACAGAGC
192635	24831	GGCTCTGACCTCTGCAGCGT	237222	69418	CCTCTGAGCAGCCCCTGCTC	281809	114005	AACGATTTTAAAAAACAGAG
192636	24832	AGGCTCTGACCTCTGCAGCG	237223	69419	ACCTCTGAGCAGCCCCTGCT	281810	114006	TAACGATTTTAAAAAACAGA
192637	24833	GAGGCTCTGACCTCTGCAGC	237224	69420	CACCTCTGAGCAGCCCCTGC	281811	114007	ATAACGATTTTAAAAAACAG
192638	24834	TGAGGCTCTGACCTCTGCAG	237225	69421	ACACCTCTGAGCAGCCCCTG	281812	114008	TATAACGATTTTAAAAAACA
192639	24835	ATGAGGCTCTGACCTCTGCA	237226	69422	AACACCTCTGAGCAGCCCCT	281813	114009	ATATAACGATTTTAAAAAAC
192640	24836	GATGAGGCTCTGACCTCTGC	237227	69423	GAACACCTCTGAGCAGCCCC	281814	114010	AATATAACGATTTTAAAAAA
192641	24837	GGATGAGGCTCTGACCTCTG	237228	69424	GGAACACCTCTGAGCAGCCC	281815	114011	AAATATAACGATTTTAAAAA
192642	24838	GGGATGAGGCTCTGACCTCT	237229	69425	TGGAACACCTCTGAGCAGCC	281816	114012	AAAATATAACGATTTTAAAA

192643	24839	TGGGATGAGGCTCTGACCTC	237230	69426	CTGGAACACCTCTGAGCAGC	281817	114013	GAAAATATAACGATTTTAAA
192644	24840	CTGGGATGAGGCTCTGACCT	237231	69427	TCTGGAACACCTCTGAGCAG	281818	114014	AGAAAATATAACGATTTTAA
192645	24841	GCTGGGATGAGGCTCTGACC	237232	69428	TTCTGGAACACCTCTGAGCA	281819	114015	TAGAAAATATAACGATTTTA
192646	24842	GGCTGGGATGAGGCTCTGAC	237233	69429	CTTCTGGAACACCTCTGAGC	281820	114016	TTAGAAAATATAACGATTTT
192647	24843	GGGCTGGGATGAGGCTCTGA	237234	69430	GCTTCTGGAACACCTCTGAG	281821	114017	ATTAGAAAATATAACGATTT
192648	24844	GGGGCTGGGATGAGGCTCTG	237235	69431	AGCTTCTGGAACACCTCTGA	281822	114018	TATTAGAAAATATAACGATT
192649	24845	AGGGGCTGGGATGAGGCTCT	237236	69432	GAGCTTCTGGAACACCTCTG	281823	114019	TTATTAGAAAATATAACGAT
192650	24846	AAGGGGCTGGGATGAGGCTC	237237	69433	AGAGCTTCTGGAACACCTCT	281824	114020	TTTATTAGAAAATATAACGA
192651	24847	TAAGGGGCTGGGATGAGGCT	237238	69434	CAGAGCTTCTGGAACACCTC	281825	114021	TTTTATTAGAAAATATAACG
192652	24848	GTAAGGGGCTGGGATGAGGC	237239	69435	CCAGAGCTTCTGGAACACCT	281826	114022	TTTTTATTAGAAAATATAAC
192653	24849	GGTAAGGGGCTGGGATGAGG	237240	69436	CCCAGAGCTTCTGGAACACC	281827	114023	ATTTTTATTAGAAAATATAA
192654	24850	AGGTAAGGGGCTGGGATGAG	237241	69437	ACCCAGAGCTTCTGGAACAC	281828	114024	TATTTTTATTAGAAAATATA
192655	24851	CAGGTAAGGGGCTGGGATGA	237242	69438	CACCCAGAGCTTCTGGAACA	281829	114025	GTATTTTTATTAGAAAATAT
192656	24852	GCAGGTAAGGGGCTGGGATG	237243	69439	TCACCCAGAGCTTCTGGAAC	281830	114026	TGTATTTTTATTAGAAAATA
192657	24853	GGCAGGTAAGGGGCTGGGAT	237244	69440	CTCACCCAGAGCTTCTGGAA	281831	114027	ATGTATTTTTATTAGAAAAT
192658	24854	GGGCAGGTAAGGGGCTGGGA	237245	69441	CCTCACCCAGAGCTTCTGGA	281832	114028	TATGTATTTTTATTAGAAAA
192659	24855	GGGGCAGGTAAGGGGCTGGG	237246	69442	TCCTCACCCAGAGCTTCTGG	281833	114029	CTATGTATTTTTATTAGAAA
192660	24856	AGGGGCAGGTAAGGGGCTGG	237247	69443	CTCCTCACCCAGAGCTTCTG	281834	114030	ACTATGTATTTTTATTAGAA
192661	24857	TAGGGGCAGGTAAGGGGCTG	237248	69444	CCTCCTCACCCAGAGCTTCT	281835	114031	GACTATGTATTTTTATTAGA
192662	24858	GTAGGGGCAGGTAAGGGGCT	237249	69445	ACCTCCTCACCCAGAGCTTC	281836	114032	AGACTATGTATTTTTATTAG
192663	24859	AGTAGGGGCAGGTAAGGGGC	237250	69446	CACCTCCTCACCCAGAGCTT	281837	114033	AAGACTATGTATTTTTATTA
192664	24860	GAGTAGGGGCAGGTAAGGGG	237251	69447	TCACCTCCTCACCCAGAGCT	281838	114034	AAAGACTATGTATTTTTATT
192665	24861	AGAGTAGGGGCAGGTAAGGG	237252	69448	CTCACCTCCTCACCCAGAGC	281839	114035	AAAAGACTATGTATTTTTAT
192666	24862	CAGAGTAGGGGCAGGTAAGG	237253	69449	TCTCACCTCCTCACCCAGAG	281840	114036	CAAAAGACTATGTATTTTTA
192667	24863	ACAGAGTAGGGGCAGGTAAG	237254	69450	CTCTCACCTCCTCACCCAGA	281841	114037	TCAAAAGACTATGTATTTTT
192668	24864	CACAGAGTAGGGGCAGGTAA	237255	69451	CCTCTCACCTCCTCACCCAG	281842	114038	TTCAAAAGACTATGTATTTT
192669	24865	CCACAGAGTAGGGGCAGGTA	237256	69452	CCCTCTCACCTCCTCACCCA	281843	114039	CTTCAAAAGACTATGTATTT
192670	24866	TCCACAGAGTAGGGGCAGGT	237257	69453	TCCCTCTCACCTCCTCACCC	281844	114040	CCTTCAAAAGACTATGTATT
192671	24867	CTCCACAGAGTAGGGGCAGG	237258	69454	GTCCCTCTCACCTCCTCACC	281845	114041	TCCTTCAAAAGACTATGTAT
192672	24868	TCTCCACAGAGTAGGGGCAG	237259	69455	GGTCCCTCTCACCTCCTCAC	281846	114042	TTCCTTCAAAAGACTATGTA
192673	24869	TTCTCCACAGAGTAGGGGCA	237260	69456	CGGTCCCTCTCACCTCCTCA	281847	114043	GTTCCTTCAAAAGACTATGT
192674	24870	GTTCTCCACAGAGTAGGGGC	237261	69457	CCGGTCCCTCTCACCTCCTC	281848	114044	TGTTCCTTCAAAAGACTATG
192675	24871	GGTTCTCCACAGAGTAGGGG	237262	69458	CCCGGTCCCTCTCACCTCCT	281849	114045	ATGTTCCTTCAAAAGACTAT
192676	24872	CGGTTCTCCACAGAGTAGGG	237263	69459	CCCCGGTCCCTCTCACCTCC	281850	114046	TATGTTCCTTCAAAAGACTA
192677	24873	ACGGTTCTCCACAGAGTAGG	237264	69460	TCCCCGGTCCCTCTCACCTC	281851	114047	TTATGTTCCTTCAAAAGACT
192678	24874	CACGGTTCTCCACAGAGTAG	237265	69461	TTCCCCGGTCCCTCTCACCT	281852	114048	TTTATGTTCCTTCAAAAGAC
192679	24875	CCACGGTTCTCCACAGAGTA	237266	69462	ATTCCCCGGTCCCTCTCACC	281853	114049	TTTTATGTTCCTTCAAAAGA
192680	24876	ACCACGGTTCTCCACAGAGT	237267	69463	CATTCCCCGGTCCCTCTCAC	281854	114050	CTTTTATGTTCCTTCAAAAG
192681	24877	GACCACGGTTCTCCACAGAG	237268	69464	GCATTCCCCGGTCCCTCTCA	281855	114051	TCTTTTATGTTCCTTCAAAA
192682	24878	TGACCACGGTTCTCCACAGA	237269	69465	TGCATTCCCCGGTCCCTCTC	281856	114052	ATCTTTTATGTTCCTTCAAA
192683	24879	CTGACCACGGTTCTCCACAG	237270	69466	CTGCATTCCCCGGTCCCTCT	281857	114053	AATCTTTTATGTTCCTTCAA
192684	24880	ACTGACCACGGTTCTCCACA	237271	69467	GCTGCATTCCCCGGTCCCTC	281858	114054	TAATCTTTTATGTTCCTTCA
192685	24881	AACTGACCACGGTTCTCCAC	237272	69468	AGCTGCATTCCCCGGTCCCT	281859	114055	ATAATCTTTTATGTTCCTTC
192686	24882	GAACTGACCACGGTTCTCCA	237273	69469	GAGCTGCATTCCCCGGTCCC	281860	114056	CATAATCTTTTATGTTCCTT
192687	24883	CGAACTGACCACGGTTCTCC	237274	69470	CGAGCTGCATTCCCCGGTCC	281861	114057	TCATAATCTTTTATGTTCCT
192688	24884	GCGAACTGACCACGGTTCTC	237275	69471	CCGAGCTGCATTCCCCGGTC	281862	114058	TTCATAATCTTTTATGTTCC
192689	24885	GGCGAACTGACCACGGTTCT	237276	69472	GCCGAGCTGCATTCCCCGGT	281863	114059	CTTCATAATCTTTTATGTTC
192690	24886	TGGCGAACTGACCACGGTTC	237277	69473	GGCCGAGCTGCATTCCCCGG	281864	114060	TCTTCATAATCTTTTATGTT
192691	24887	CTGGCGAACTGACCACGGTT	237278	69474	GGGCCGAGCTGCATTCCCCG	281865	114061	TTCTTCATAATCTTTTATGT
192692	24888	CCTGGCGAACTGACCACGGT	237279	69475	TGGGCCGAGCTGCATTCCCC	281866	114062	TTTCTTCATAATCTTTTATG
192693	24889	GCCTGGCGAACTGACCACGG	237280	69476	CTGGGCCGAGCTGCATTCCC	281867	114063	ATTTCTTCATAATCTTTTAT
192694	24890	GGCCTGGCGAACTGACCACG	237281	69477	GCTGGGCCGAGCTGCATTCC	281868	114064	CATTTCTTCATAATCTTTTA
192695	24891	CGGCCTGGCGAACTGACCAC	237282	69478	GGCTGGGCCGAGCTGCATTC	281869	114065	TCATTTCTTCATAATCTTTT
192696	24892	CCGGCCTGGCGAACTGACCA	237283	69479	AGGCTGGGCCGAGCTGCATT	281870	114066	CTCATTTCTTCATAATCTTT
192697	24893	TCCGGCCTGGCGAACTGACC	237284	69480	GAGGCTGGGCCGAGCTGCAT	281871	114067	ACTCATTTCTTCATAATCTT
192698	24894	ATCCGGCCTGGCGAACTGAC	237285	69481	GGAGGCTGGGCCGAGCTGCA	281872	114068	AACTCATTTCTTCATAATCT
192699	24895	GATCCGGCCTGGCGAACTGA	237286	69482	GGGAGGCTGGGCCGAGCTGC	281873	114069	TAACTCATTTCTTCATAATC
192700	24896	GGATCCGGCCTGGCGAACTG	237287	69483	AGGGAGGCTGGGCCGAGCTG	281874	114070	CTAACTCATTTCTTCATAAT
192701	24897	TGGATCCGGCCTGGCGAACT	237288	69484	CAGGGAGGCTGGGCCGAGCT	281875	114071	TCTAACTCATTTCTTCATAA
192702	24898	GTGGATCCGGCCTGGCGAAC	237289	69485	GCAGGGAGGCTGGGCCGAGC	281876	114072	ATCTAACTCATTTCTTCATA
192703	24899	CGTGGATCCGGCCTGGCGAA	237290	69486	GGCAGGGAGGCTGGGCCGAG	281877	114073	TATCTAACTCATTTCTTCAT
192704	24900	TCGTGGATCCGGCCTGGCGA	237291	69487	AGGCAGGGAGGCTGGGCCGA	281878	114074	ATATCTAACTCATTTCTTCA
192705	24901	TTCGTGGATCCGGCCTGGCG	237292	69488	CAGGCAGGGAGGCTGGGCCG	281879	114075	AATATCTAACTCATTTCTTC
192706	24902	GTTCGTGGATCCGGCCTGGC	237293	69489	TCAGGCAGGGAGGCTGGGCC	281880	114076	CAATATCTAACTCATTTCTT
192707	24903	CGTTCGTGGATCCGGCCTGG	237294	69490	CTCAGGCAGGGAGGCTGGGC	281881	114077	TCAATATCTAACTCATTTCT
192708	24904	CCGTTCGTGGATCCGGCCTG	237295	69491	CCTCAGGCAGGGAGGCTGGG	281882	114078	ATCAATATCTAACTCATTTC
192709	24905	GCCGTTCGTGGATCCGGCCT	237296	69492	ACCTCAGGCAGGGAGGCTGG	281883	114079	AATCAATATCTAACTCATTT
192710	24906	GGCCGTTCGTGGATCCGGCC	237297	69493	GACCTCAGGCAGGGAGGCTG	281884	114080	GAATCAATATCTAACTCATT
192711	24907	AGGCCGTTCGTGGATCCGGC	237298	69494	TGACCTCAGGCAGGGAGGCT	281885	114081	GGAATCAATATCTAACTCAT
192712	24908	AAGGCCGTTCGTGGATCCGG	237299	69495	CTGACCTCAGGCAGGGAGGC	281886	114082	AGGAATCAATATCTAACTCA
192713	24909	CAAGGCCGTTCGTGGATCCG	237300	69496	GCTGACCTCAGGCAGGGAGG	281887	114083	TAGGAATCAATATCTAACTC
192714	24910	ACAAGGCCGTTCGTGGATCC	237301	69497	GGCTGACCTCAGGCAGGGAG	281888	114084	ATAGGAATCAATATCTAACT

192715	24911	CACAAGGCCGTTCGTGGATC	237302	69498	TGGCTGACCTCAGGCAGGGA	281889	114085	AATAGGAATCAATATCTAAC
192716	24912	CCACAAGGCCGTTCGTGGAT	237303	69499	ATGGCTGACCTCAGGCAGGG	281890	114086	CAATAGGAATCAATATCTAA
192717	24913	TCCACAAGGCCGTTCGTGGA	237304	69500	GATGGCTGACCTCAGGCAGG	281891	114087	TCAATAGGAATCAATATCTA
192718	24914	TTCCACAAGGCCGTTCGTGG	237305	69501	TGATGGCTGACCTCAGGCAG	281892	114088	TTCAATAGGAATCAATATCT
192719	24915	CTTCCACAAGGCCGTTCGTG	237306	69502	GTGATGGCTGACCTCAGGCA	281893	114089	CTTCAATAGGAATCAATATC
192720	24916	TCTTCCACAAGGCCGTTCGT	237307	69503	CGTGATGGCTGACCTCAGGC	281894	114090	TCTTCAATAGGAATCAATAT
192721	24917	ATCTTCCACAAGGCCGTTCG	237308	69504	ACGTGATGGCTGACCTCAGG	281895	114091	ATCTTCAATAGGAATCAATA
192722	24918	CATCTTCCACAAGGCCGTTC	237309	69505	CACGTGATGGCTGACCTCAG	281896	114092	AATCTTCAATAGGAATCAAT
192723	24919	CCATCTTCCACAAGGCCGTT	237310	69506	CCACGTGATGGCTGACCTCA	281897	114093	GAATCTTCAATAGGAATCAA
192724	24920	ACCATCTTCCACAAGGCCGT	237311	69507	ACCACGTGATGGCTGACCTC	281898	114094	TGAATCTTCAATAGGAATCA
192725	24921	CACCATCTTCCACAAGGCCG	237312	69508	CACCACGTGATGGCTGACCT	281899	114095	CTGAATCTTCAATAGGAATC
192726	24922	TCACCATCTTCCACAAGGCC	237313	69509	TCACCACGTGATGGCTGACC	281900	114096	TCTGAATCTTCAATAGGAAT
192727	24923	CTCACCATCTTCCACAAGGC	237314	69510	ATCACCACGTGATGGCTGAC	281901	114097	GTCTGAATCTTCAATAGGAA
192728	24924	GCTCACCATCTTCCACAAGG	237315	69511	CATCACCACGTGATGGCTGA	281902	114098	TGTCTGAATCTTCAATAGGA
192729	24925	AGCTCACCATCTTCCACAAG	237316	69512	CCATCACCACGTGATGGCTG	281903	114099	TTGTCTGAATCTTCAATAGG
192730	24926	GAGCTCACCATCTTCCACAA	237317	69513	GCCATCACCACGTGATGGCT	281904	114100	CTTGTCTGAATCTTCAATAG
192731	24927	TGAGCTCACCATCTTCCACA	237318	69514	TGCCATCACCACGTGATGGC	281905	114101	ACTTGTCTGAATCTTCAATA
192732	24928	GTGAGCTCACCATCTTCCAC	237319	69515	TTGCCATCACCACGTGATGG	281906	114102	TACTTGTCTGAATCTTCAAT
192733	24929	TGTGAGCTCACCATCTTCCA	237320	69516	CTTGCCATCACCACGTGATG	281907	114103	TTACTTGTCTGAATCTTCAA
192734	24930	GTGTGAGCTCACCATCTTCC	237321	69517	TCTTGCCATCACCACGTGAT	281908	114104	TTTACTTGTCTGAATCTTCA
192735	24931	GGTGTGAGCTCACCATCTTC	237322	69518	ATCTTGCCATCACCACGTGA	281909	114105	TTTTACTTGTCTGAATCTTC
192736	24932	GGGTGTGAGCTCACCATCTT	237323	69519	CATCTTGCCATCACCACGTG	281910	114106	ATTTTACTTGTCTGAATCTT
192737	24933	TGGGTGTGAGCTCACCATCT	237324	69520	CCATCTTGCCATCACCACGT	281911	114107	AATTTTACTTGTCTGAATCT
192738	24934	CTGGGTGTGAGCTCACCATC	237325	69521	TCCATCTTGCCATCACCACG	281912	114108	TAATTTTACTTGTCTGAATC
192739	24935	TCTGGGTGTGAGCTCACCAT	237326	69522	TTCCATCTTGCCATCACCAC	281913	114109	TTAATTTTACTTGTCTGAAT
192740	24936	CTCTGGGTGTGAGCTCACCA	237327	69523	TTTCCATCTTGCCATCACCA	281914	114110	CTTAATTTTACTTGTCTGAA
192741	24937	GCTCTGGGTGTGAGCTCACC	237328	69524	ATTTCCATCTTGCCATCACC	281915	114111	CCTTAATTTTACTTGTCTGA
192742	24938	AGCTCTGGGTGTGAGCTCAC	237329	69525	CATTTCCATCTTGCCATCAC	281916	114112	CCCTTAATTTTACTTGTCTG
192743	24939	CAGCTCTGGGTGTGAGCTCA	237330	69526	ACATTTCCATCTTGCCATCA	281917	114113	CCCCTTAATTTTACTTGTCT
192744	24940	CCAGCTCTGGGTGTGAGCTC	237331	69527	CACATTTCCATCTTGCCATC	281918	114114	TCCCCTTAATTTTACTTGTC
192745	24941	GCCAGCTCTGGGTGTGAGCT	237332	69528	GCACATTTCCATCTTGCCAT	281919	114115	TTCCCCTTAATTTTACTTGT
192746	24942	AGCCAGCTCTGGGTGTGAGC	237333	69529	AGCACATTTCCATCTTGCCA	281920	114116	TTTCCCCTTAATTTTACTTG
192747	24943	GAGCCAGCTCTGGGTGTGAG	237334	69530	AAGCACATTTCCATCTTGCC	281921	114117	TTTTCCCCTTAATTTTACTT
192748	24944	GGAGCCAGCTCTGGGTGTGA	237335	69531	AAAGCACATTTCCATCTTGC	281922	114118	TTTTTCCCCTTAATTTTACT
192749	24945	CGGAGCCAGCTCTGGGTGTG	237336	69532	GAAAGCACATTTCCATCTTG	281923	114119	TTTTTTCCCCTTAATTTTAC
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192754	24950	GTCATCGGAGCCAGCTCTGG	237341	69537	AGTCAGAAAGCACATTTCCA	281928	114124	CCGTTTTTTTTCCCCTTAAT
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192756	24952	GGGTCATCGGAGCCAGCTCT	237343	69539	GCAGTCAGAAAGCACATTTC	281930	114126	TCCCGTTTTTTTTCCCCTTA
192757	24953	AGGGTCATCGGAGCCAGCTC	237344	69540	AGCAGTCAGAAAGCACATTT	281931	114127	ATCCCGTTTTTTTTCCCCTT
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192759	24955	ACAGGGTCATCGGAGCCAGC	237346	69542	GGAGCAGTCAGAAAGCACAT	281933	114129	TCATCCCGTTTTTTTTCCCC
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192761	24957	AGACAGGGTCATCGGAGCCA	237348	69544	CTGGAGCAGTCAGAAAGCAC	281935	114131	GTTCATCCCGTTTTTTTTCC
192762	24958	GAGACAGGGTCATCGGAGCC	237349	69545	GCTGGAGCAGTCAGAAAGCA	281936	114132	GGTTCATCCCGTTTTTTTTC
192763	24959	GGAGACAGGGTCATCGGAGC	237350	69546	GGCTGGAGCAGTCAGAAAGC	281937	114133	TGGTTCATCCCGTTTTTTTT
192764	24960	AGGAGACAGGGTCATCGGAG	237351	69547	TGGCTGGAGCAGTCAGAAAG	281938	114134	CTGGTTCATCCCGTTTTTTT
192765	24961	AAGGAGACAGGGTCATCGGA	237352	69548	CTGGCTGGAGCAGTCAGAAA	281939	114135	TCTGGTTCATCCCGTTTTTT
192766	24962	AAAGGAGACAGGGTCATCGG	237353	69549	ACTGGCTGGAGCAGTCAGAA	281940	114136	TTCTGGTTCATCCCGTTTTT
192767	24963	TAAAGGAGACAGGGTCATCG	237354	69550	CACTGGCTGGAGCAGTCAGA	281941	114137	CTTCTGGTTCATCCCGTTTT
192768	24964	GTAAAGGAGACAGGGTCATC	237355	69551	GCACTGGCTGGAGCAGTCAG	281942	114138	ACTTCTGGTTCATCCCGTTT
192769	24965	TGTAAAGGAGACAGGGTCAT	237356	69552	AGCACTGGCTGGAGCAGTCA	281943	114139	GACTTCTGGTTCATCCCGTT
192770	24966	ATGTAAAGGAGACAGGGTCA	237357	69553	CAGCACTGGCTGGAGCAGTC	281944	114140	TGACTTCTGGTTCATCCCGT
192771	24967	CATGTAAAGGAGACAGGGTC	237358	69554	GCAGCACTGGCTGGAGCAGT	281945	114141	CTGACTTCTGGTTCATCCCG
192772	24968	ACATGTAAAGGAGACAGGGT	237359	69555	GGCAGCACTGGCTGGAGCAG	281946	114142	CCTGACTTCTGGTTCATCCC
192773	24969	AACATGTAAAGGAGACAGGG	237360	69556	TGGCAGCACTGGCTGGAGCA	281947	114143	GCCTGACTTCTGGTTCATCC
192774	24970	AAACATGTAAAGGAGACAGG	237361	69557	CTGGCAGCACTGGCTGGAGC	281948	114144	AGCCTGACTTCTGGTTCATC
192775	24971	GAAACATGTAAAGGAGACAG	237362	69558	TCTGGCAGCACTGGCTGGAG	281949	114145	CAGCCTGACTTCTGGTTCAT
192776	24972	AGAAACATGTAAAGGAGACA	237363	69559	ATCTGGCAGCACTGGCTGGA	281950	114146	CCAGCCTGACTTCTGGTTCA
192777	24973	TAGAAACATGTAAAGGAGAC	237364	69560	AATCTGGCAGCACTGGCTGG	281951	114147	TCCAGCCTGACTTCTGGTTC
192778	24974	GTAGAAACATGTAAAGGAGA	237365	69561	GAATCTGGCAGCACTGGCTG	281952	114148	CTCCAGCCTGACTTCTGGTT
192779	24975	GGTAGAAACATGTAAAGGAG	237366	69562	TGAATCTGGCAGCACTGGCT	281953	114149	ACTCCAGCCTGACTTCTGGT
192780	24976	AGGTAGAAACATGTAAAGGA	237367	69563	CTGAATCTGGCAGCACTGGC	281954	114150	AACTCCAGCCTGACTTCTGG
192781	24977	AAGGTAGAAACATGTAAAGG	237368	69564	GCTGAATCTGGCAGCACTGG	281955	114151	GAACTCCAGCCTGACTTCTG
192782	24978	GAAGGTAGAAACATGTAAAG	237369	69565	AGCTGAATCTGGCAGCACTG	281956	114152	GGAACTCCAGCCTGACTTCT
192783	24979	GGAAGGTAGAAACATGTAAA	237370	69566	GAGCTGAATCTGGCAGCACT	281957	114153	TGGAACTCCAGCCTGACTTC
192784	24980	GGGAAGGTAGAAACATGTAA	237371	69567	GGAGCTGAATCTGGCAGCAC	281958	114154	TTGGAACTCCAGCCTGACTT
192785	24981	GGGGAAGGTAGAAACATGTA	237372	69568	GGGAGCTGAATCTGGCAGCA	281959	114155	GTTGGAACTCCAGCCTGACT
192786	24982	AGGGGAAGGTAGAAACATGT	237373	69569	GGGGAGCTGAATCTGGCAGC	281960	114156	GGTTGGAACTCCAGCCTGAC

192787	24983	GAGGGGAAGGTAGAAACATG	237374	69570	TGGGGAGCTGAATCTGGCAG	281961	114157	GGGTTGGAACTCCAGCCTGA
192788	24984	GGAGGGGAAGGTAGAAACAT	237375	69571	CTGGGGAGCTGAATCTGGCA	281962	114158	GGGGTTGGAACTCCAGCCTG
192789	24985	GGGAGGGGAAGGTAGAAACA	237376	69572	CCTGGGGAGCTGAATCTGGC	281963	114159	TGGGGTTGGAACTCCAGCCT
192790	24986	AGGGAGGGGAAGGTAGAAAC	237377	69573	CCCTGGGGAGCTGAATCTGG	281964	114160	CTGGGGTTGGAACTCCAGCC
192791	24987	TAGGGAGGGGAAGGTAGAAA	237378	69574	TCCCTGGGGAGCTGAATCTG	281965	114161	TCTGGGGTTGGAACTCCAGC
192792	24988	GTAGGGAGGGGAAGGTAGAA	237379	69575	CTCCCTGGGGAGCTGAATCT	281966	114162	ATCTGGGGTTGGAACTCCAG
192793	24989	GGTAGGGAGGGGAAGGTAGA	237380	69576	CCTCCCTGGGGAGCTGAATC	281967	114163	GATCTGGGGTTGGAACTCCA
192794	24990	AGGTAGGGAGGGGAAGGTAG	237381	69577	CCCTCCCTGGGGAGCTGAAT	281968	114164	GGATCTGGGGTTGGAACTCC
192795	24991	AAGGTAGGGAGGGGAAGGTA	237382	69578	GCCCTCCCTGGGGAGCTGAA	281969	114165	CGGATCTGGGGTTGGAACTC
192796	24992	GAAGGTAGGGAGGGGAAGGT	237383	69579	TGCCCTCCCTGGGGAGCTGA	281970	114166	TCGGATCTGGGGTTGGAACT
192797	24993	GGAAGGTAGGGAGGGGAAGG	237384	69580	GTGCCCTCCCTGGGGAGCTG	281971	114167	GTCGGATCTGGGGTTGGAAC
192798	24994	GGGAAGGTAGGGAGGGGAAG	237385	69581	GGTGCCCTCCCTGGGGAGCT	281972	114168	TGTCGGATCTGGGGTTGGAA
192799	24995	GGGGAAGGTAGGGAGGGGAA	237386	69582	AGGTGCCCTCCCTGGGGAGC	281973	114169	CTGTCGGATCTGGGGTTGGA
192800	24996	GGGGGAAGGTAGGGAGGGGA	237387	69583	CAGGTGCCCTCCCTGGGGAG	281974	114170	GCTGTCGGATCTGGGGTTGG
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192804	25000	CAGTGGGGGAAGGTAGGGAG	237391	69587	CTCTCAGGTGCCCTCCCTGG	281978	114174	CTGGGCTGTCGGATCTGGGG
192805	25001	GCAGTGGGGGAAGGTAGGGA	237392	69588	CCTCTCAGGTGCCCTCCCTG	281979	114175	CCTGGGCTGTCGGATCTGGG
192806	25002	AGCAGTGGGGGAAGGTAGGG	237393	69589	GCCTCTCAGGTGCCCTCCCT	281980	114176	GCCTGGGCTGTCGGATCTGG
192807	25003	CAGCAGTGGGGGAAGGTAGG	237394	69590	AGCCTCTCAGGTGCCCTCCC	281981	114177	AGCCTGGGCTGTCGGATCTG
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192811	25007	CGCCCAGCAGTGGGGGAAGG	237398	69594	TTGGAGCCTCTCAGGTGCCC	281985	114181	CATCAGCCTGGGCTGTCGGA
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192813	25009	TGCGCCCAGCAGTGGGGGAA	237400	69596	GCTTGGAGCCTCTCAGGTGC	281987	114183	CCCATCAGCCTGGGCTGTCG
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192818	25014	CACTCTGCGCCCAGCAGTGG	237405	69601	TCCTGGCTTGGAGCCTCTCA	281992	114188	GAGGCCCCATCAGCCTGGGC
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192823	25019	GCCTCCACTCTGCGCCCAGC	237410	69606	AGATCTCCTGGCTTGGAGCC	281997	114193	CCCTGGAGGCCCCATCAGCC
192824	25020	TGCCTCCACTCTGCGCCCAG	237411	69607	CAGATCTCCTGGCTTGGAGC	281998	114194	GCCCTGGAGGCCCCATCAGC
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192826	25022	TCTGCCTCCACTCTGCGCCC	237413	69609	AACAGATCTCCTGGCTTGGA	282000	114196	CTGCCCTGGAGGCCCCATCA
192827	25023	ATCTGCCTCCACTCTGCGCC	237414	69610	AAACAGATCTCCTGGCTTGG	282001	114197	ACTGCCCTGGAGGCCCCATC
192828	25024	CATCTGCCTCCACTCTGCGC	237415	69611	AAAACAGATCTCCTGGCTTG	282002	114198	CACTGCCCTGGAGGCCCCAT
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192830	25026	CTCATCTGCCTCCACTCTGC	237417	69613	AGAAAACAGATCTCCTGGCT	282004	114200	ACCACTGCCCTGGAGGCCCC
192831	25027	CCTCATCTGCCTCCACTCTG	237418	69614	GAGAAAACAGATCTCCTGGC	282005	114201	AACCACTGCCCTGGAGGCCC
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192833	25029	AACCTCATCTGCCTCCACTC	237420	69616	AGGAGAAAACAGATCTCCTG	282007	114203	GAAACCACTGCCCTGGAGGC
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192835	25031	TAAACCTCATCTGCCTCCAC	237422	69618	AAAGGAGAAAACAGATCTCC	282009	114205	TGGAAACCACTGCCCTGGAG
192836	25032	TTAAACCTCATCTGCCTCCA	237423	69619	CAAAGGAGAAAACAGATCTC	282010	114206	GTGGAAACCACTGCCCTGGA
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192838	25034	CTTTAAACCTCATCTGCCTC	237425	69621	AACAAAGGAGAAAACAGATC	282012	114208	GGGTGGAAACCACTGCCCTG
192839	25035	GCTTTAAACCTCATCTGCCT	237426	69622	AAACAAAGGAGAAAACAGAT	282013	114209	TGGGTGGAAACCACTGCCCT
192840	25036	AGCTTTAAACCTCATCTGCC	237427	69623	AAAACAAAGGAGAAAACAGA	282014	114210	CTGGGTGGAAACCACTGCCC
192841	25037	GAGCTTTAAACCTCATCTGC	237428	69624	CAAAACAAAGGAGAAAACAG	282015	114211	GCTGGGTGGAAACCACTGCC
192842	25038	TGAGCTTTAAACCTCATCTG	237429	69625	ACAAAACAAAGGAGAAAACA	282016	114212	TGCTGGGTGGAAACCACTGC
192843	25039	CTGAGCTTTAAACCTCATCT	237430	69626	AACAAAACAAAGGAGAAAAC	282017	114213	ATGCTGGGTGGAAACCACTG
192844	25040	TCTGAGCTTTAAACCTCATC	237431	69627	AAACAAAACAAAGGAGAAAA	282018	114214	AATGCTGGGTGGAAACCACT
192845	25041	TTCTGAGCTTTAAACCTCAT	237432	69628	AAAACAAAACAAAGGAGAAA	282019	114215	GAATGCTGGGTGGAAACCAC
192846	25042	CTTCTGAGCTTTAAACCTCA	237433	69629	AAAAACAAAACAAAGGAGAA	282020	114216	AGAATGCTGGGTGGAAACCA
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192852	25048	TAAGCCCTTCTGAGCTTTAA	237439	69635	ACAAAAAAAAACAAAACAAA	282026	114222	CTTTTGAGAATGCTGGGTGG
192853	25049	TTAAGCCCTTCTGAGCTTTA	237440	69636	AACAAAAAAAAACAAAACAA	282027	114223	TCTTTTGAGAATGCTGGGTG
192854	25050	TTTAAGCCCTTCTGAGCTTT	237441	69637	AAACAAAAAAAAACAAAACA	282028	114224	CTCTTTTGAGAATGCTGGGT
192855	25051	GTTTAAGCCCTTCTGAGCTT	237442	69638	AAAACAAAAAAAAACAAAAC	282029	114225	GCTCTTTTGAGAATGCTGGG
192856	25052	CGTTTAAGCCCTTCTGAGCT	237443	69639	CAAAACAAAAAAAAACAAAA	282030	114226	GGCTCTTTTGAGAATGCTGG
192857	25053	CCGTTTAAGCCCTTCTGAGC	237444	69640	ACAAAACAAAAAAAAACAAA	282031	114227	TGGCTCTTTTGAGAATGCTG
192858	25054	CCCGTTTAAGCCCTTCTGAG	237445	69641	AACAAAACAAAAAAAAACAA	282032	114228	GTGGCTCTTTTGAGAATGCT

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192861	25057	CAACCCGTTTAAGCCCTTCT	237448	69644	CAAAACAAAACAAAAAAAA	282035	114231	TCAGTGGCTCTTTTGAGAAT
192862	25058	CCAACCCGTTTAAGCCCTTC	237449	69645	ACAAAACAAAACAAAAAAA	282036	114232	CTCAGTGGCTCTTTTGAGAA
192863	25059	CCCAACCCGTTTAAGCCCTT	237450	69646	AACAAAACAAAACAAAAAA	282037	114233	CCTCAGTGGCTCTTTTGAGA
192864	25060	CCCCAACCCGTTTAAGCCCT	237451	69647	AAACAAAACAAAACAAAAA	282038	114234	ACCTCAGTGGCTCTTTTGAG
192865	25061	GCCCCAACCCGTTTAAGCCC	237452	69648	AAAACAAAACAAAACAAAA	282039	114235	GACCTCAGTGGCTCTTTTGA
192866	25062	CGCCCCAACCCGTTTAAGCC	237453	69649	TAAAACAAAACAAAACAAA	282040	114236	AGACCTCAGTGGCTCTTTTG
192867	25063	GCGCCCCAACCCGTTTAAGC	237454	69650	ATAAAACAAAACAAAACAA	282041	114237	GAGACCTCAGTGGCTCTTTT
192868	25064	TGCGCCCCAACCCGTTTAAG	237455	69651	AATAAAACAAAACAAAACA	282042	114238	TGAGACCTCAGTGGCTCTTT
192869	25065	CTGCGCCCCAACCCGTTTAA	237456	69652	TAATAAAACAAAACAAAAC	282043	114239	CTGAGACCTCAGTGGCTCTT
192870	25066	ACTGCGCCCCAACCCGTTTA	237457	69653	ATAATAAAACAAAACAAAC	282044	114240	ACTGAGACCTCAGTGGCTCT
192871	25067	CACTGCGCCCCAACCCGTTT	237458	69654	TATAATAAAACAAAACAAA	282045	114241	CACTGAGACCTCAGTGGCTC
192872	25068	CCACTGCGCCCCAACCCGTT	237459	69655	GTATAATAAAACAAAACAA	282046	114242	GCACTGAGACCTCAGTGGCT
192873	25069	GCCACTGCGCCCCAACCCGT	237460	69656	AGTATAATAAAACAAAACA	282047	114243	GGCACTGAGACCTCAGTGGC
192874	25070	AGCCACTGCGCCCCAACCCG	237461	69657	AAGTATAATAAAACAAAAC	282048	114244	TGGCACTGAGACCTCAGTGG
192875	25071	GAGCCACTGCGCCCCAACCC	237462	69658	AAAGTATAATAAAACAAAA	282049	114245	ATGGCACTGAGACCTCAGTG
192876	25072	TGAGCCACTGCGCCCCAACC	237463	69659	TAAAGTATAATAAAACAAA	282050	114246	AATGGCACTGAGACCTCAGT
192877	25073	ATGAGCCACTGCGCCCCAAC	237464	69660	TTAAAGTATAATAAAACAA	282051	114247	AAATGGCACTGAGACCTCAG
192878	25074	CATGAGCCACTGCGCCCCAA	237465	69661	CTTAAAGTATAATAAAACAA	282052	114248	AAAATGGCACTGAGACCTCA
192879	25075	GCATGAGCCACTGCGCCCCA	237466	69662	ACTTAAAGTATAATAAAACA	282053	114249	GAAAATGGCACTGAGACCTC
192880	25076	GGCATGAGCCACTGCGCCCC	237467	69663	AACTTAAAGTATAATAAAAC	282054	114250	TGAAAATGGCACTGAGACCT
192881	25077	AGGCATGAGCCACTGCGCCC	237468	69664	GAACTTAAAGTATAATAAAA	282055	114251	TTGAAAATGGCACTGAGACC
192882	25078	CAGGCATGAGCCACTGCGCC	237469	69665	AGAACTTAAAGTATAATAAA	282056	114252	CTTGAAAATGGCACTGAGAC
192883	25079	ACAGGCATGAGCCACTGCGC	237470	69666	TAGAACTTAAAGTATAATAA	282057	114253	TCTTGAAAATGGCACTGAGA
192884	25080	TACAGGCATGAGCCACTGCG	237471	69667	CTAGAACTTAAAGTATAATA	282058	114254	ATCTTGAAAATGGCACTGAG
192885	25081	TTACAGGCATGAGCCACTGC	237472	69668	CCTAGAACTTAAAGTATAAT	282059	114255	AATCTTGAAAATGGCACTGA
192886	25082	ATTACAGGCATGAGCCACTG	237473	69669	CCCTAGAACTTAAAGTATAA	282060	114256	AAATCTTGAAAATGGCACTG
192887	25083	GATTACAGGCATGAGCCACT	237474	69670	ACCCTAGAACTTAAAGTATA	282061	114257	GAAATCTTGAAAATGGCACT
192888	25084	GGATTACAGGCATGAGCCAC	237475	69671	TACCCTAGAACTTAAAGTAT	282062	114258	CGAAATCTTGAAAATGGCAC
192889	25085	GGGATTACAGGCATGAGCCA	237476	69672	GTACCCTAGAACTTAAAGTA	282063	114259	CCGAAATCTTGAAAATGGCA
192890	25086	CGGGATTACAGGCATGAGCC	237477	69673	TGTACCCTAGAACTTAAAGT	282064	114260	TCCGAAATCTTGAAAATGGC
192891	25087	CCGGGATTACAGGCATGAGC	237478	69674	ATGTACCCTAGAACTTAAAG	282065	114261	TTCCGAAATCTTGAAAATGG
192892	25088	GCCGGGATTACAGGCATGAG	237479	69675	CATGTACCCTAGAACTTAAA	282066	114262	CTTCCGAAATCTTGAAAATG
192893	25089	TGCCGGGATTACAGGCATGA	237480	69676	ACATGTACCCTAGAACTTAA	282067	114263	GCTTCCGAAATCTTGAAAAT
192894	25090	GTGCCGGGATTACAGGCATG	237481	69677	CACATGTACCCTAGAACTTA	282068	114264	CGCTTCCGAAATCTTGAAAA
192895	25091	AGTGCCGGGATTACAGGCAT	237482	69678	GCACATGTACCCTAGAACTT	282069	114265	CCGCTTCCGAAATCTTGAAA
192896	25092	AAGTGCCGGGATTACAGGCA	237483	69679	TGCACATGTACCCTAGAACT	282070	114266	GCCGCTTCCGAAATCTTGAA
192897	25093	AAAGTGCCGGGATTACAGGC	237484	69680	GTGCACATGTACCCTAGAAC	282071	114267	GGCCGCTTCCGAAATCTTGA
192898	25094	CAAAGTGCCGGGATTACAGG	237485	69681	TGTGCACATGTACCCTAGAA	282072	114268	AGGCCGCTTCCGAAATCTTG
192899	25095	CCAAAGTGCCGGGATTACAG	237486	69682	TTGTGCACATGTACCCTAGA	282073	114269	CAGGCCGCTTCCGAAATCTT
192900	25096	CCCAAAGTGCCGGGATTACA	237487	69683	GTTGTGCACATGTACCCTAG	282074	114270	CCAGGCCGCTTCCGAAATCT
192901	25097	TCCCAAAGTGCCGGGATTAC	237488	69684	CGTTGTGCACATGTACCCTA	282075	114271	CCCAGGCCGCTTCCGAAATC
192902	25098	CTCCCAAAGTGCCGGGATTA	237489	69685	ACGTTGTGCACATGTACCCT	282076	114272	GCCCAGGCCGCTTCCGAAAT
192903	25099	CCTCCCAAAGTGCCGGGATT	237490	69686	CACGTTGTGCACATGTACCC	282077	114273	TGCCCAGGCCGCTTCCGAAA
192904	25100	GCCTCCCAAAGTGCCGGGAT	237491	69687	GCACGTTGTGCACATGTACC	282078	114274	GTGCCCAGGCCGCTTCCGAA
192905	25101	GGCCTCCCAAAGTGCCGGGA	237492	69688	TGCACGTTGTGCACATGTAC	282079	114275	CGTGCCCAGGCCGCTTCCGA
192906	25102	TGGCCTCCCAAAGTGCCGGG	237493	69689	CTGCACGTTGTGCACATGTA	282080	114276	CCGTGCCCAGGCCGCTTCCG
192907	25103	TTGGCCTCCCAAAGTGCCGG	237494	69690	CCTGCACGTTGTGCACATGT	282081	114277	GCCGTGCCCAGGCCGCTTCC
192908	25104	CTTGGCCTCCCAAAGTGCCG	237495	69691	ACCTGCACGTTGTGCACATG	282082	114278	AGCCGTGCCCAGGCCGCTTC
192909	25105	CCTTGGCCTCCCAAAGTGCC	237496	69692	AACCTGCACGTTGTGCACAT	282083	114279	CAGCCGTGCCCAGGCCGCTT
192910	25106	GCCTTGGCCTCCCAAAGTGC	237497	69693	AAACCTGCACGTTGTGCACA	282084	114280	CCAGCCGTGCCCAGGCCGCT
192911	25107	TGCCTTGGCCTCCCAAAGTG	237498	69694	CAAACCTGCACGTTGTGCAC	282085	114281	ACCAGCCGTGCCCAGGCCGC
192912	25108	CTGCCTTGGCCTCCCAAAGT	237499	69695	ACAAACCTGCACGTTGTGCA	282086	114282	GACCAGCCGTGCCCAGGCCG
192913	25109	TCTGCCTTGGCCTCCCAAAG	237500	69696	AACAAACCTGCACGTTGTGC	282087	114283	GGACCAGCCGTGCCCAGGCC
192914	25110	CTCTGCCTTGGCCTCCCAAA	237501	69697	TAACAAACCTGCACGTTGTG	282088	114284	AGGACCAGCCGTGCCCAGGC
192915	25111	CCTCTGCCTTGGCCTCCCAA	237502	69698	GTAACAAACCTGCACGTTGT	282089	114285	AAGGACCAGCCGTGCCCAGG
192916	25112	TCCTCTGCCTTGGCCTCCCA	237503	69699	TGTAACAAACCTGCACGTTG	282090	114286	GAAGGACCAGCCGTGCCCAG
192917	25113	ATCCTCTGCCTTGGCCTCCC	237504	69700	ATGTAACAAACCTGCACGTT	282091	114287	TGAAGGACCAGCCGTGCCCA
192918	25114	GATCCTCTGCCTTGGCCTCC	237505	69701	TATGTAACAAACCTGCACGT	282092	114288	GTGAAGGACCAGCCGTGCCC
192919	25115	TGATCCTCTGCCTTGGCCTC	237506	69702	ATATGTAACAAACCTGCACG	282093	114289	AGTGAAGGACCAGCCGTGCC
192920	25116	GTGATCCTCTGCCTTGGCCT	237507	69703	CATATGTAACAAACCTGCAC	282094	114290	CAGTGAAGGACCAGCCGTGC
192921	25117	AGTGATCCTCTGCCTTGGCC	237508	69704	ACATATGTAACAAACCTGCA	282095	114291	CCAGTGAAGGACCAGCCGTG
192922	25118	AAGTGATCCTCTGCCTTGGC	237509	69705	TACATATGTAACAAACCTGC	282096	114292	CCCAGTGAAGGACCAGCCGT
192923	25119	CAAGTGATCCTCTGCCTTGG	237510	69706	ATACATATGTAACAAACCTG	282097	114293	TCCCAGTGAAGGACCAGCCG
192924	25120	TCAAGTGATCCTCTGCCTTG	237511	69707	TATACATATGTAACAAACCT	282098	114294	ATCCCAGTGAAGGACCAGCC
192925	25121	CTCAAGTGATCCTCTGCCTT	237512	69708	GTATACATATGTAACAAACC	282099	114295	GATCCCAGTGAAGGACCAGC
192926	25122	GCTCAAGTGATCCTCTGCCT	237513	69709	TGTATACATATGTAACAAAC	282100	114296	TGATCCCAGTGAAGGACCAG
192927	25123	GGCTCAAGTGATCCTCTGCC	237514	69710	ATGTATACATATGTAACAAA	282101	114297	GTGATCCCAGTGAAGGACCA
192928	25124	GGGCTCAAGTGATCCTCTGC	237515	69711	CATGTATACATATGTAACAA	282102	114298	GGTGATCCCAGTGAAGGACC
192929	25125	TGGGCTCAAGTGATCCTCTG	237516	69712	ACATGTATACATATGTAACA	282103	114299	TGGTGATCCCAGTGAAGGAC
192930	25126	CTGGGCTCAAGTGATCCTCT	237517	69713	CACATGTATACATATGTAAC	282104	114300	GTGGTGATCCCAGTGAAGGA

192931	25127	CCTGGGCTCAAGTGATCCTC	237518	69714	GCACATGTATACATATGTAA	282105	114301	AGTGGTGATCCCAGTGAAGG
192932	25128	TCCTGGGCTCAAGTGATCCT	237519	69715	GGCACATGTATACATATGTA	282106	114302	AAGTGGTGATCCCAGTGAAG
192933	25129	CTCCTGGGCTCAAGTGATCC	237520	69716	TGGCACATGTATACATATGT	282107	114303	CAAGTGGTGATCCCAGTGAA
192934	25130	ACTCCTGGGCTCAAGTGATC	237521	69717	ATGGCACATGTATACATATG	282108	114304	CCAAGTGGTGATCCCAGTGA
192935	25131	AACTCCTGGGCTCAAGTGAT	237522	69718	CATGGCACATGTATACATAT	282109	114305	GCCAAGTGGTGATCCCAGTG
192936	25132	GAACTCCTGGGCTCAAGTGA	237523	69719	ACATGGCACATGTATACATA	282110	114306	TGCCAAGTGGTGATCCCAGT
192937	25133	CGAACTCCTGGGCTCAAGTG	237524	69720	AACATGGCACATGTATACAT	282111	114307	TTGCCAAGTGGTGATCCCAG
192938	25134	TCGAACTCCTGGGCTCAAGT	237525	69721	CAACATGGCACATGTATACA	282112	114308	ATTGCCAAGTGGTGATCCCA
192939	25135	CTCGAACTCCTGGGCTCAAG	237526	69722	CCAACATGGCACATGTATAC	282113	114309	AATTGCCAAGTGGTGATCCC
192940	25136	TCTCGAACTCCTGGGCTCAA	237527	69723	ACCAACATGGCACATGTATA	282114	114310	TAATTGCCAAGTGGTGATCC
192941	25137	GTCTCGAACTCCTGGGCTCA	237528	69724	CACCAACATGGCACATGTAT	282115	114311	ATAATTGCCAAGTGGTGATC
192942	25138	GGTCTCGAACTCCTGGGCTC	237529	69725	ACACCAACATGGCACATGTA	282116	114312	AATAATTGCCAAGTGGTGAT
192943	25139	TGGTCTCGAACTCCTGGGCT	237530	69726	CACACCAACATGGCACATGT	282117	114313	AAATAATTGCCAAGTGGTGA
192944	25140	TTGGTCTCGAACTCCTGGGC	237531	69727	GCACACCAACATGGCACATG	282118	114314	TAAATAATTGCCAAGTGGTG
192945	25141	GTTGGTCTCGAACTCCTGGG	237532	69728	AGCACACCAACATGGCACAT	282119	114315	GTAAATAATTGCCAAGTGGT
192946	25142	GGTTGGTCTCGAACTCCTGG	237533	69729	CAGCACACCAACATGGCACA	282120	114316	TGTAAATAATTGCCAAGTGG
192947	25143	AGGTTGGTCTCGAACTCCTG	237534	69730	GCAGCACACCAACATGGCAC	282121	114317	GTGTAAATAATTGCCAAGTG
192948	25144	CAGGTTGGTCTCGAACTCCT	237535	69731	TGCAGCACACCAACATGGCA	282122	114318	GGTGTAAATAATTGCCAAGT
192949	25145	TCAGGTTGGTCTCGAACTCC	237536	69732	GTGCAGCACACCAACATGGC	282123	114319	AGGTGTAAATAATTGCCAAG
192950	25146	CTCAGGTTGGTCTCGAACTC	237537	69733	GGTGCAGCACACCAACATGG	282124	114320	CAGGTGTAAATAATTGCCAA
192951	25147	GCTCAGGTTGGTCTCGAACT	237538	69734	GGGTGCAGCACACCAACATG	282125	114321	TCAGGTGTAAATAATTGCCA
192952	25148	TGCTCAGGTTGGTCTCGAAC	237539	69735	TGGGTGCAGCACACCAACAT	282126	114322	CTCAGGTGTAAATAATTGCC
192953	25149	TTGCTCAGGTTGGTCTCGAA	237540	69736	ATGGGTGCAGCACACCAACA	282127	114323	TCTCAGGTGTAAATAATTGC
192954	25150	GTTGCTCAGGTTGGTCTCGA	237541	69737	GATGGGTGCAGCACACCAAC	282128	114324	GTCTCAGGTGTAAATAATTG
192955	25151	TGTTGCTCAGGTTGGTCTCG	237542	69738	TGATGGGTGCAGCACACCAA	282129	114325	CGTCTCAGGTGTAAATAATT
192956	25152	ATGTTGCTCAGGTTGGTCTC	237543	69739	TTGATGGGTGCAGCACACCA	282130	114326	TCGTCTCAGGTGTAAATAAT
192957	25153	TATGTTGCTCAGGTTGGTCT	237544	69740	GTTGATGGGTGCAGCACACC	282131	114327	TTCGTCTCAGGTGTAAATAA
192958	25154	CTATGTTGCTCAGGTTGGTC	237545	69741	AGTTGATGGGTGCAGCACAC	282132	114328	ATTCGTCTCAGGTGTAAATA
192959	25155	ACTATGTTGCTCAGGTTGGT	237546	69742	AAGTTGATGGGTGCAGCACA	282133	114329	TATTCGTCTCAGGTGTAAAT
192960	25156	CACTATGTTGCTCAGGTTGG	237547	69743	CAAGTTGATGGGTGCAGCAC	282134	114330	TTATTCGTCTCAGGTGTAAA
192961	25157	TCACTATGTTGCTCAGGTTG	237548	69744	ACAAGTTGATGGGTGCAGCA	282135	114331	TTTATTCGTCTCAGGTGTAA
192962	25158	CTCACTATGTTGCTCAGGTT	237549	69745	GACAAGTTGATGGGTGCAGC	282136	114332	TTTTATTCGTCTCAGGTGTA
192963	25159	TCTCACTATGTTGCTCAGGT	237550	69746	TGACAAGTTGATGGGTGCAG	282137	114333	TTTTTATTCGTCTCAGGTGT
192964	25160	GTCTCACTATGTTGCTCAGG	237551	69747	ATGACAAGTTGATGGGTGCA	282138	114334	GTTTTTATTCGTCTCAGGTG
192965	25161	GGTCTCACTATGTTGCTCAG	237552	69748	AATGACAAGTTGATGGGTGC	282139	114335	GGTTTTTATTCGTCTCAGGT
192966	25162	CGGTCTCACTATGTTGCTCA	237553	69749	AAATGACAAGTTGATGGGTG	282140	114336	TGGTTTTTATTCGTCTCAGG
192967	25163	GCGGTCTCACTATGTTGCTC	237554	69750	TAAATGACAAGTTGATGGGT	282141	114337	CTGGTTTTTATTCGTCTCAG
192968	25164	CGCGGTCTCACTATGTTGCT	237555	69751	GTAAATGACAAGTTGATGGG	282142	114338	TCTGGTTTTTATTCGTCTCA
192969	25165	ACGCGGTCTCACTATGTTGC	237556	69752	TGTAAATGACAAGTTGATGG	282143	114339	CTCTGGTTTTTATTCGTCTC
192970	25166	GACGCGGTCTCACTATGTTG	237557	69753	ATGTAAATGACAAGTTGATG	282144	114340	ACTCTGGTTTTTATTCGTCT
192971	25167	AGACGCGGTCTCACTATGTT	237558	69754	AATGTAAATGACAAGTTGAT	282145	114341	CACTCTGGTTTTTATTCGTC
192972	25168	GAGACGCGGTCTCACTATGT	237559	69755	TAATGTAAATGACAAGTTGA	282146	114342	GCACTCTGGTTTTTATTCGT
192973	25169	AGAGACGCGGTCTCACTATG	237560	69756	CTAATGTAAATGACAAGTTG	282147	114343	AGCACTCTGGTTTTTATTCG
192974	25170	TAGAGACGCGGTCTCACTAT	237561	69757	CCTAATGTAAATGACAAGTT	282148	114344	CAGCACTCTGGTTTTTATTC
192975	25171	GTAGAGACGCGGTCTCACTA	237562	69758	ACCTAATGTAAATGACAAGT	282149	114345	TCAGCACTCTGGTTTTTATT
192976	25172	TGTAGAGACGCGGTCTCACT	237563	69759	TACCTAATGTAAATGACAAG	282150	114346	CTCAGCACTCTGGTTTTTAT
192977	25173	TTGTAGAGACGCGGTCTCAC	237564	69760	ATACCTAATGTAAATGACAA	282151	114347	TCTCAGCACTCTGGTTTTTA
192978	25174	TTTGTAGAGACGCGGTCTCA	237565	69761	TATACCTAATGTAAATGACA	282152	114348	ATCTCAGCACTCTGGTTTTT
192979	25175	TTTTGTAGAGACGCGGTCTC	237566	69762	ATATACCTAATGTAAATGAC	282153	114349	AATCTCAGCACTCTGGTTTT
192980	25176	TTTTTGTAGAGACGCGGTCT	237567	69763	GATATACCTAATGTAAATGA	282154	114350	TAATCTCAGCACTCTGGTTT
192981	25177	TTTTTTGTAGAGACGCGGTC	237568	69764	AGATATACCTAATGTAAATG	282155	114351	GTAATCTCAGCACTCTGGTT
192982	25178	ATTTTTTGTAGAGACGCGGT	237569	69765	GAGATATACCTAATGTAAAT	282156	114352	TGTAATCTCAGCACTCTGGT
192983	25179	TATTTTTTGTAGAGACGCGG	237570	69766	GGAGATATACCTAATGTAAA	282157	114353	CTGTAATCTCAGCACTCTGG
192984	25180	TTATTTTTTGTAGAGACGCG	237571	69767	AGGAGATATACCTAATGTAA	282158	114354	CCTGTAATCTCAGCACTCTG
192985	25181	TTTATTTTTTGTAGAGACGC	237572	69768	TAGGAGATATACCTAATGTA	282159	114355	GCCTGTAATCTCAGCACTCT
192986	25182	TTTTATTTTTTGTAGAGACG	237573	69769	TTAGGAGATATACCTAATGT	282160	114356	TGCCTGTAATCTCAGCACTC
192987	25183	ATTTTATTTTTTGTAGAGAC	237574	69770	ATTAGGAGATATACCTAATG	282161	114357	ATGCCTGTAATCTCAGCACT
192988	25184	TATTTTATTTTTTGTAGAGA	237575	69771	CATTAGGAGATATACCTAAT	282162	114358	CATGCCTGTAATCTCAGCAC
192989	25185	TTATTTTATTTTTTGTAGAG	237576	69772	GCATTAGGAGATATACCTAA	282163	114359	CCATGCCTGTAATCTCAGCA
192990	25186	TTTATTTTATTTTTTGTAGA	237577	69773	AGCATTAGGAGATATACCTA	282164	114360	ACCATGCCTGTAATCTCAGC
192991	25187	ATTTATTTTATTTTTTGTAG	237578	69774	TAGCATTAGGAGATATACCT	282165	114361	CACCATGCCTGTAATCTCAG
192992	25188	TATTTATTTTATTTTTTGTA	237579	69775	ATAGCATTAGGAGATATACC	282166	114362	CCACCATGCCTGTAATCTCA
192993	25189	TTATTTATTTTATTTTTTGT	237580	69776	GATAGCATTAGGAGATATAC	282167	114363	GCCACCATGCCTGTAATCTC
192994	25190	TTTATTTATTTTATTTTTTG	237581	69777	GGATAGCATTAGGAGATATA	282168	114364	AGCCACCATGCCTGTAATCT
192995	25191	TTTTATTTATTTTATTTTTT	237582	69778	GGGATAGCATTAGGAGATAT	282169	114365	AAGCCACCATGCCTGTAATC
192996	25192	ATTTTATTTATTTTATTTTT	237583	69779	AGGGATAGCATTAGGAGATA	282170	114366	TAAGCCACCATGCCTGTAAT
192997	25193	AATTTTATTTATTTTATTTT	237584	69780	GAGGGATAGCATTAGGAGAT	282171	114367	GTAAGCCACCATGCCTGTAA
192998	25194	TAATTTTATTTATTTTATTT	237585	69781	GGAGGGATAGCATTAGGAGA	282172	114368	CGTAAGCCACCATGCCTGTA
192999	25195	CTAATTTTATTTATTTTATT	237586	69782	GGGAGGGATAGCATTAGGAG	282173	114369	GCGTAAGCCACCATGCCTGT
193000	25196	GCTAATTTTATTTATTTTAT	237587	69783	GGGGAGGGATAGCATTAGGA	282174	114370	AGCGTAAGCCACCATGCCTG
193001	25197	AGCTAATTTTATTTATTTTA	237588	69784	GGGGGAGGGATAGCATTAGG	282175	114371	AAGCGTAAGCCACCATGCCT
193002	25198	AAGCTAATTTTATTTATTTT	237589	69785	GGGGGGAGGGATAGCATTAG	282176	114372	CAAGCGTAAGCCACCATGCC

193003	25199	AAAGCTAATTTTATTTATTT	237590	69786	AGGGGGGAGGGATAGCATTA	282177	114373	ACAAGCGTAAGCCACCATGC
193004	25200	CAAAGCTAATTTTATTTATT	237591	69787	GAGGGGGGAGGGATAGCATT	282178	114374	TACAAGCGTAAGCCACCATG
193005	25201	GCAAAGCTAATTTTATTTAT	237592	69788	GGAGGGGGGAGGGATAGCAT	282179	114375	TTACAAGCGTAAGCCACCAT
193006	25202	TGCAAAGCTAATTTTATTTA	237593	69789	GGGAGGGGGGAGGGATAGCA	282180	114376	ATTACAAGCGTAAGCCACCA
193007	25203	CTGCAAAGCTAATTTTATTT	237594	69790	GGGGAGGGGGGAGGGATAGC	282181	114377	GATTACAAGCGTAAGCCACC
193008	25204	CCTGCAAAGCTAATTTTATT	237595	69791	GGGGGAGGGGGGAGGGATAG	282182	114378	CGATTACAAGCGTAAGCCAC
193009	25205	CCCTGCAAAGCTAATTTTAT	237596	69792	GGGGGGAGGGGGGAGGGATA	282183	114379	CCGATTACAAGCGTAAGCCA
193010	25206	ACCCTGCAAAGCTAATTTTA	237597	69793	TGGGGGGAGGGGGGAGGGAT	282184	114380	GCCGATTACAAGCGTAAGCC
193011	25207	CACCCTGCAAAGCTAATTTT	237598	69794	GTGGGGGGAGGGGGGAGGGA	282185	114381	AGCCGATTACAAGCGTAAGC
193012	25208	CCACCCTGCAAAGCTAATTT	237599	69795	GGTGGGGGGGAGGGGGGAGGG	282186	114382	AAGCCGATTACAAGCGTAAG
193013	25209	GCCACCCTGCAAAGCTAATT	237600	69796	GGGTGGGGGGGAGGGGGGAGG	282187	114383	AAAGCCGATTACAAGCGTAA
193014	25210	TGCCACCCTGCAAAGCTAAT	237601	69797	GGGGTGGGGGGAGGGGGGAG	282188	114384	CAAAGCCGATTACAAGCGTA
193015	25211	ATGCCACCCTGCAAAGCTAA	237602	69798	GGGGGTGGGGGGAGGGGGGA	282189	114385	CCAAAGCCGATTACAAGCGT
193016	25212	CATGCCACCCTGCAAAGCTA	237603	69799	AGGGGGTGGGGGGAGGGGGG	282190	114386	CCCAAAGCCGATTACAAGCG
193017	25213	GCATGCCACCCTGCAAAGCT	237604	69800	CAGGGGGTGGGGGGAGGGGG	282191	114387	TCCCAAAGCCGATTACAAGC
193018	25214	TGCATGCCACCCTGCAAAGC	237605	69801	ACAGGGGGTGGGGGGAGGGG	282192	114388	TTCCCAAAGCCGATTACAAG
193019	25215	GTGCATGCCACCCTGCAAAG	237606	69802	AACAGGGGGTGGGGGGAGGG	282193	114389	CTTCCCAAAGCCGATTACAA
193020	25216	GGTGCATGCCACCCTGCAAA	237607	69803	AAACAGGGGGTGGGGGGAGG	282194	114390	GCTTCCCAAAGCCGATTACA
193021	25217	AGGTGCATGCCACCCTGCAA	237608	69804	AAAACAGGGGGTGGGGGGAG	282195	114391	GGCTTCCCAAAGCCGATTAC
193022	25218	CAGGTGCATGCCACCCTGCA	237609	69805	GAAAACAGGGGGTGGGGGGA	282196	114392	CGGCTTCCCAAAGCCGATTA
193023	25219	GCAGGTGCATGCCACCCTGC	237610	69806	AGAAAACAGGGGGTGGGGGG	282197	114393	TCGGCTTCCCAAAGCCGATT
193024	25220	TGCAGGTGCATGCCACCCTG	237611	69807	GAGAAAACAGGGGGTGGGGG	282198	114394	CTCGGCTTCCCAAAGCCGAT
193025	25221	CTGCAGGTGCATGCCACCCT	237612	69808	GGAGAAAACAGGGGGTGGGG	282199	114395	CCTCGGCTTCCCAAAGCCGA
193026	25222	ACTGCAGGTGCATGCCACCC	237613	69809	AGGAGAAAACAGGGGGTGGG	282200	114396	ACCTCGGCTTCCCAAAGCCG
193027	25223	GACTGCAGGTGCATGCCACC	237614	69810	AAGGAGAAAACAGGGGGTGG	282201	114397	CACCTCGGCTTCCCAAAGCC
193028	25224	GGACTGCAGGTGCATGCCAC	237615	69811	AAAGGAGAAAACAGGGGGTG	282202	114398	CCACCTCGGCTTCCCAAAGC
193029	25225	GGGACTGCAGGTGCATGCCA	237616	69812	CAAAGGAGAAAACAGGGGGT	282203	114399	CCCACCTCGGCTTCCCAAAG
193030	25226	AGGGACTGCAGGTGCATGCC	237617	69813	TCAAAGGAGAAAACAGGGGG	282204	114400	GCCCACCTCGGCTTCCCAAA
193031	25227	CAGGGACTGCAGGTGCATGC	237618	69814	TTCAAAGGAGAAAACAGGGG	282205	114401	AGCCCACCTCGGCTTCCCAA
193032	25228	GCAGGGACTGCAGGTGCATG	237619	69815	ATTCAAAGGAGAAAACAGGG	282206	114402	CAGCCCACCTCGGCTTCCCA
193033	25229	AGCAGGGACTGCAGGTGCAT	237620	69816	GATTCAAAGGAGAAAACAGG	282207	114403	TCAGCCCACCTCGGCTTCCC
193034	25230	TAGCAGGGACTGCAGGTGCA	237621	69817	GGATTCAAAGGAGAAAACAG	282208	114404	ATCAGCCCACCTCGGCTTCC
193035	25231	GTAGCAGGGACTGCAGGTGC	237622	69818	AGGATTCAAAGGAGAAAACA	282209	114405	AATCAGCCCACCTCGGCTTC
193036	25232	AGTAGCAGGGACTGCAGGTG	237623	69819	AAGGATTCAAAGGAGAAAAC	282210	114406	CAATCAGCCCACCTCGGCTT
193037	25233	GAGTAGCAGGGACTGCAGGT	237624	69820	GAAGGATTCAAAGGAGAAAA	282211	114407	GCAATCAGCCCACCTCGGCT
193038	25234	TGAGTAGCAGGGACTGCAGG	237625	69821	AGAAGGATTCAAAGGAGAAA	282212	114408	AGCAATCAGCCCACCTCGGC
193039	25235	CTGAGTAGCAGGGACTGCAG	237626	69822	AAGAAGGATTCAAAGGAGAA	282213	114409	AAGCAATCAGCCCACCTCGG
193040	25236	TCTGAGTAGCAGGGACTGCA	237627	69823	TAAGAAGGATTCAAAGGAGA	282214	114410	CAAGCAATCAGCCCACCTCG
193041	25237	TTCTGAGTAGCAGGGACTGC	237628	69824	CTAAGAAGGATTCAAAGGAG	282215	114411	TCAAGCAATCAGCCCACCTC
193042	25238	CTTCTGAGTAGCAGGGACTG	237629	69825	TCTAAGAAGGATTCAAAGGA	282216	114412	CTCAAGCAATCAGCCCACCT
193043	25239	CCTTCTGAGTAGCAGGGACT	237630	69826	CTCTAAGAAGGATTCAAAGG	282217	114413	GCTCAAGCAATCAGCCCACC
193044	25240	GCCTTCTGAGTAGCAGGGAC	237631	69827	CCTCTAAGAAGGATTCAAAG	282218	114414	GGCTCAAGCAATCAGCCCAC
193045	25241	AGCCTTCTGAGTAGCAGGGA	237632	69828	GCCTCTAAGAAGGATTCAAA	282219	114415	GGGCTCAAGCAATCAGCCCA
193046	25242	CAGCCTTCTGAGTAGCAGGG	237633	69829	GGCCTCTAAGAAGGATTCAA	282220	114416	TGGGCTCAAGCAATCAGCCC
193047	25243	TCAGCCTTCTGAGTAGCAGG	237634	69830	CGGCCTCTAAGAAGGATTCA	282221	114417	CTGGGCTCAAGCAATCAGCC
193048	25244	CTCAGCCTTCTGAGTAGCAG	237635	69831	CCGGCCTCTAAGAAGGATTC	282222	114418	CCTGGGCTCAAGCAATCAGC
193049	25245	CCTCAGCCTTCTGAGTAGCA	237636	69832	CCCGGCCTCTAAGAAGGATT	282223	114419	TCCTGGGCTCAAGCAATCAG
193050	25246	ACCTCAGCCTTCTGAGTAGC	237637	69833	GCCCGGCCTCTAAGAAGGAT	282224	114420	CTCCTGGGCTCAAGCAATCA
193051	25247	CACCTCAGCCTTCTGAGTAG	237638	69834	CGCCCGGCCTCTAAGAAGGA	282225	114421	ACTCCTGGGCTCAAGCAATC
193052	25248	CCACCTCAGCCTTCTGAGTA	237639	69835	GCGCCCGGCCTCTAAGAAGG	282226	114422	AACTCCTGGGCTCAAGCAAT
193053	25249	CCCACCTCAGCCTTCTGAGT	237640	69836	CGCGCCCGGCCTCTAAGAAG	282227	114423	AAACTCCTGGGCTCAAGCAA
193054	25250	TCCCACCTCAGCCTTCTGAG	237641	69837	CCGCGCCCGGCCTCTAAGAA	282228	114424	GAAACTCCTGGGCTCAAGCA
193055	25251	CTCCCACCTCAGCCTTCTGA	237642	69838	ACCGCGCCCGGCCTCTAAGA	282229	114425	TGAAACTCCTGGGCTCAAGC
193056	25252	CCTCCCACCTCAGCCTTCTG	237643	69839	CACCGCGCCCGGCCTCTAAG	282230	114426	TTGAAACTCCTGGGCTCAAG
193057	25253	TCCTCCCACCTCAGCCTTCT	237644	69840	CCACCGCGCCCGGCCTCTAA	282231	114427	TTTGAAACTCCTGGGCTCAA
193058	25254	ATCCTCCCACCTCAGCCTTC	237645	69841	GCCACCGCGCCCGGCCTCTA	282232	114428	GTTTGAAACTCCTGGGCTCA
193059	25255	GATCCTCCCACCTCAGCCTT	237646	69842	AGCCACCGCGCCCGGCCTCT	282233	114429	AGTTTGAAACTCCTGGGCTC
193060	25256	CGATCCTCCCACCTCAGCCT	237647	69843	GAGCCACCGCGCCCGGCCTC	282234	114430	TAGTTTGAAACTCCTGGGCT
193061	25257	GCGATCCTCCCACCTCAGCC	237648	69844	TGAGCCACCGCGCCCGGCCT	282235	114431	ATAGTTTGAAACTCCTGGGC
193062	25258	AGCGATCCTCCCACCTCAGC	237649	69845	GTGAGCCACCGCGCCCGGCC	282236	114432	GATAGTTTGAAACTCCTGGG
193063	25259	AAGCGATCCTCCCACCTCAG	237650	69846	CGTGAGCCACCGCGCCCGGC	282237	114433	GGATAGTTTGAAACTCCTGG
193064	25260	CAAGCGATCCTCCCACCTCA	237651	69847	GCGTGAGCCACCGCGCCCGG	282238	114434	AGGATAGTTTGAAACTCCTG
193065	25261	ACAAGCGATCCTCCCACCTC	237652	69848	GGCGTGAGCCACCGCGCCCG	282239	114435	CAGGATAGTTTGAAACTCCT
193066	25262	CACAAGCGATCCTCCCACCT	237653	69849	AGGCGTGAGCCACCGCGCCC	282240	114436	CCAGGATAGTTTGAAACTCC
193067	25263	GCACAAGCGATCCTCCCACC	237654	69850	CAGGCGTGAGCCACCGCGCC	282241	114437	TCCAGGATAGTTTGAAACTC
193068	25264	GGCACAAGCGATCCTCCCAC	237655	69851	ACAGGCGTGAGCCACCGCGC	282242	114438	GTCCAGGATAGTTTGAAACT
193069	25265	GGGCACAAGCGATCCTCCCA	237656	69852	TACAGGCGTGAGCCACCGCG	282243	114439	TGTCCAGGATAGTTTGAAAC
193070	25266	TGGGCACAAGCGATCCTCCC	237657	69853	TTACAGGCGTGAGCCACCGC	282244	114440	TTGTCCAGGATAGTTTGAAA
193071	25267	CTGGGCACAAGCGATCCTCC	237658	69854	ATTACAGGCGTGAGCCACCG	282245	114441	GTTGTCCAGGATAGTTTGAA
193072	25268	CCTGGGCACAAGCGATCCTC	237659	69855	GATTACAGGCGTGAGCCACC	282246	114442	TGTTGTCCAGGATAGTTTGA
193073	25269	TCCTGGGCACAAGCGATCCT	237660	69856	GGATTACAGGCGTGAGCCAC	282247	114443	ATGTTGTCCAGGATAGTTTG
193074	25270	CTCCTGGGCACAAGCGATCC	237661	69857	GGGATTACAGGCGTGAGCCA	282248	114444	TATGTTGTCCAGGATAGTTT

193075	25271	ACTCCTGGGCACAAGCGATC	237662	69858	TGGGATTACAGGCGTGAGCC	282249	114445	CTATGTTGTCCAGGATAGTT
193076	25272	AACTCCTGGGCACAAGCGAT	237663	69859	CTGGGATTACAGGCGTGAGC	282250	114446	GCTATGTTGTCCAGGATAGT
193077	25273	AAACTCCTGGGCACAAGCGA	237664	69860	GCTGGGATTACAGGCGTGAG	282251	114447	TGCTATGTTGTCCAGGATAG
193078	25274	CAAACTCCTGGGCACAAGCG	237665	69861	TGCTGGGATTACAGGCGTGA	282252	114448	ATGCTATGTTGTCCAGGATA
193079	25275	TCAAACTCCTGGGCACAAGC	237666	69862	GTGCTGGGATTACAGGCGTG	282253	114449	CATGCTATGTTGTCCAGGAT
193080	25276	CTCAAACTCCTGGGCACAAG	237667	69863	AGTGCTGGGATTACAGGCGT	282254	114450	TCATGCTATGTTGTCCAGGA
193081	25277	CCTCAAACTCCTGGGCACAA	237668	69864	AAGTGCTGGGATTACAGGCG	282255	114451	GTCATGCTATGTTGTCCAGG
193082	25278	GCCTCAAACTCCTGGGCACA	237669	69865	AAAGTGCTGGGATTACAGGC	282256	114452	GGTCATGCTATGTTGTCCAG
193083	25279	AGCCTCAAACTCCTGGGCAC	237670	69866	CAAAGTGCTGGGATTACAGG	282257	114453	AGGTCATGCTATGTTGTCCA
193084	25280	CAGCCTCAAACTCCTGGGCA	237671	69867	CCAAAGTGCTGGGATTACAG	282258	114454	GAGGTCATGCTATGTTGTCC
193085	25281	GCAGCCTCAAACTCCTGGGC	237672	69868	CCCAAAGTGCTGGGATTACA	282259	114455	CGAGGTCATGCTATGTTGTC
193086	25282	TGCAGCCTCAAACTCCTGGG	237673	69869	TCCCAAAGTGCTGGGATTAC	282260	114456	ACGAGGTCATGCTATGTTGT
193087	25283	CTGCAGCCTCAAACTCCTGG	237674	69870	CTCCCAAAGTGCTGGGATTA	282261	114457	GACGAGGTCATGCTATGTTG
193088	25284	ACTGCAGCCTCAAACTCCTG	237675	69871	CCTCCCAAAGTGCTGGGATT	282262	114458	AGACGAGGTCATGCTATGTT
193089	25285	CACTGCAGCCTCAAACTCCT	237676	69872	GCCTCCCAAAGTGCTGGGAT	282263	114459	GAGACGAGGTCATGCTATGT
193090	25286	TCACTGCAGCCTCAAACTCC	237677	69873	AGCCTCCCAAAGTGCTGGGA	282264	114460	AGAGACGAGGTCATGCTATG
193091	25287	CTCACTGCAGCCTCAAACTC	237678	69874	CAGCCTCCCAAAGTGCTGGG	282265	114461	TAGAGACGAGGTCATGCTAT
193092	25288	GCTCACTGCAGCCTCAAACT	237679	69875	GCAGCCTCCCAAAGTGCTGG	282266	114462	GTAGAGACGAGGTCATGCTA
193093	25289	AGCTCACTGCAGCCTCAAAC	237680	69876	CGCAGCCTCCCAAAGTGCTG	282267	114463	TGTAGAGACGAGGTCATGCT
193094	25290	TAGCTCACTGCAGCCTCAAA	237681	69877	CCGCAGCCTCCCAAAGTGCT	282268	114464	TTGTAGAGACGAGGTCATGC
193095	25291	ATAGCTCACTGCAGCCTCAA	237682	69878	GCCGCAGCCTCCCAAAGTGC	282269	114465	TTTGTAGAGACGAGGTCATG
193096	25292	CATAGCTCACTGCAGCCTCA	237683	69879	TGCCGCAGCCTCCCAAAGTG	282270	114466	TTTTGTAGAGACGAGGTCAT
193097	25293	GCATAGCTCACTGCAGCCTC	237684	69880	CTGCCGCAGCCTCCCAAAGT	282271	114467	TTTTTGTAGAGACGAGGTCA
193098	25294	AGCATAGCTCACTGCAGCCT	237685	69881	CCTGCCGCAGCCTCCCAAAG	282272	114468	TTTTTTGTAGAGACGAGGTC
193099	25295	CAGCATAGCTCACTGCAGCC	237686	69882	TCCTGCCGCAGCCTCCCAAA	282273	114469	ATTTTTTGTAGAGACGAGGT
193100	25296	CCAGCATAGCTCACTGCAGC	237687	69883	CTCCTGCCGCAGCCTCCCAA	282274	114470	TATTTTTTGTAGAGACGAGG
193101	25297	GCCAGCATAGCTCACTGCAG	237688	69884	CCTCCTGCCGCAGCCTCCCA	282275	114471	GTATTTTTTGTAGAGACGAG
193102	25298	TGCCAGCATAGCTCACTGCA	237689	69885	TCCTCCTGCCGCAGCCTCCC	282276	114472	TGTATTTTTTGTAGAGACGA
193103	25299	GTGCCAGCATAGCTCACTGC	237690	69886	ATCCTCCTGCCGCAGCCTCC	282277	114473	TTGTATTTTTTGTAGAGACG
193104	25300	GGTGCCAGCATAGCTCACTG	237691	69887	AATCCTCCTGCCGCAGCCTC	282278	114474	TTTGTATTTTTTGTAGAGAC
193105	25301	TGGTGCCAGCATAGCTCACT	237692	69888	CAATCCTCCTGCCGCAGCCT	282279	114475	TTTTGTATTTTTTGTAGAGA
193106	25302	GTGGTGCCAGCATAGCTCAC	237693	69889	GCAATCCTCCTGCCGCAGCC	282280	114476	TTTTTGTATTTTTTGTAGAG
193107	25303	TGTGGTGCCAGCATAGCTCA	237694	69890	AGCAATCCTCCTGCCGCAGC	282281	114477	TTTTTTGTATTTTTTGTAGA
193108	25304	CTGTGGTGCCAGCATAGCTC	237695	69891	AAGCAATCCTCCTGCCGCAG	282282	114478	ATTTTTTGTATTTTTTGTAG
193109	25305	GCTGTGGTGCCAGCATAGCT	237696	69892	CAAGCAATCCTCCTGCCGCA	282283	114479	AATTTTTTGTATTTTTTGTA
193110	25306	TGCTGTGGTGCCAGCATAGC	237697	69893	TCAAGCAATCCTCCTGCCGC	282284	114480	AAATTTTTTGTATTTTTTGT
193111	25307	GTGCTGTGGTGCCAGCATAG	237698	69894	CTCAAGCAATCCTCCTGCCG	282285	114481	CAAATTTTTTGTATTTTTTG
193112	25308	AGTGCTGTGGTGCCAGCATA	237699	69895	GCTCAAGCAATCCTCCTGCC	282286	114482	GCAAATTTTTTGTATTTTTT
193113	25309	GAGTGCTGTGGTGCCAGCAT	237700	69896	GGCTCAAGCAATCCTCCTGC	282287	114483	GGCAAATTTTTTGTATTTTT
193114	25310	GGAGTGCTGTGGTGCCAGCA	237701	69897	GGGCTCAAGCAATCCTCCTG	282288	114484	TGGCAAATTTTTTGTATTTT
193115	25311	TGGAGTGCTGTGGTGCCAGC	237702	69898	TGGGCTCAAGCAATCCTCCT	282289	114485	CTGGCAAATTTTTTGTATTT
193116	25312	CTGGAGTGCTGTGGTGCCAG	237703	69899	CTGGGCTCAAGCAATCCTCC	282290	114486	CCTGGCAAATTTTTTGTATT
193117	25313	GCTGGAGTGCTGTGGTGCCA	237704	69900	CCTGGGCTCAAGCAATCCTC	282291	114487	ACCTGGCAAATTTTTTGTAT
193118	25314	GGCTGGAGTGCTGTGGTGCC	237705	69901	TCCTGGGCTCAAGCAATCCT	282292	114488	CACCTGGCAAATTTTTTGTA
193119	25315	AGGCTGGAGTGCTGTGGTGC	237706	69902	CTCCTGGGCTCAAGCAATCC	282293	114489	ACACCTGGCAAATTTTTTGT
193120	25316	CAGGCTGGAGTGCTGTGGTG	237707	69903	ACTCCTGGGCTCAAGCAATC	282294	114490	CACACCTGGCAAATTTTTTG
193121	25317	TCAGGCTGGAGTGCTGTGGT	237708	69904	AACTCCTGGGCTCAAGCAAT	282295	114491	CCACACCTGGCAAATTTTTT
193122	25318	CTCAGGCTGGAGTGCTGTGG	237709	69905	GAACTCCTGGGCTCAAGCAA	282296	114492	ACCACACCTGGCAAATTTTT
193123	25319	ACTCAGGCTGGAGTGCTGTG	237710	69906	GGAACTCCTGGGCTCAAGCA	282297	114493	CACCACACCTGGCAAATTTT
193124	25320	TACTCAGGCTGGAGTGCTGT	237711	69907	TGGAACTCCTGGGCTCAAGC	282298	114494	CCACCACACCTGGCAAATTT
193125	25321	TTACTCAGGCTGGAGTGCTG	237712	69908	CTGGAACTCCTGGGCTCAAG	282299	114495	GCCACCACACCTGGCAAATT
193126	25322	GTTACTCAGGCTGGAGTGCT	237713	69909	TCTGGAACTCCTGGGCTCAA	282300	114496	TGCCACCACACCTGGCAAAT
193127	25323	TGTTACTCAGGCTGGAGTGC	237714	69910	GTCTGGAACTCCTGGGCTCA	282301	114497	ATGCCACCACACCTGGCAAA
193128	25324	CTGTTACTCAGGCTGGAGTG	237715	69911	GGTCTGGAACTCCTGGGCTC	282302	114498	CATGCCACCACACCTGGCAA
193129	25325	TCTGTTACTCAGGCTGGAGT	237716	69912	TGGTCTGGAACTCCTGGGCT	282303	114499	ACATGCCACCACACCTGGCA
193130	25326	TTCTGTTACTCAGGCTGGAG	237717	69913	CTGGTCTGGAACTCCTGGGC	282304	114500	CACATGCCACCACACCTGGC
193131	25327	ATTCTGTTACTCAGGCTGGA	237718	69914	GCTGGTCTGGAACTCCTGGG	282305	114501	GCACATGCCACCACACCTGG
193132	25328	CATTCTGTTACTCAGGCTGG	237719	69915	GGCTGGTCTGGAACTCCTGG	282306	114502	GGCACATGCCACCACACCTG
193133	25329	TCATTCTGTTACTCAGGCTG	237720	69916	AGGCTGGTCTGGAACTCCTG	282307	114503	AGGCACATGCCACCACACCT
193134	25330	CTCATTCTGTTACTCAGGCT	237721	69917	CAGGCTGGTCTGGAACTCCT	282308	114504	CAGGCACATGCCACCACACC
193135	25331	TCTCATTCTGTTACTCAGGC	237722	69918	CCAGGCTGGTCTGGAACTCC	282309	114505	ACAGGCACATGCCACCACAC
193136	25332	ATCTCATTCTGTTACTCAGG	237723	69919	CCCAGGCTGGTCTGGAACTC	282310	114506	CACAGGCACATGCCACCACA
193137	25333	GATCTCATTCTGTTACTCAG	237724	69920	GCCCAGGCTGGTCTGGAACT	282311	114507	CCACAGGCACATGCCACCAC
193138	25334	GGATCTCATTCTGTTACTCA	237725	69921	TGCCCAGGCTGGTCTGGAAC	282312	114508	ACCACAGGCACATGCCACCA
193139	25335	AGGATCTCATTCTGTTACTC	237726	69922	TTGCCCAGGCTGGTCTGGAA	282313	114509	GACCACAGGCACATGCCACC
193140	25336	CAGGATCTCATTCTGTTACT	237727	69923	GTTGCCCAGGCTGGTCTGGA	282314	114510	GGACCACAGGCACATGCCAC
193141	25337	ACAGGATCTCATTCTGTTAC	237728	69924	TGTTGCCCAGGCTGGTCTGG	282315	114511	GGGACCACAGGCACATGCCA
193142	25338	GACAGGATCTCATTCTGTTA	237729	69925	ATGTTGCCCAGGCTGGTCTG	282316	114512	TGGGACCACAGGCACATGCC
193143	25339	AGACAGGATCTCATTCTGTT	237730	69926	TATGTTGCCCAGGCTGGTCT	282317	114513	CTGGGACCACAGGCACATGC
193144	25340	GAGACAGGATCTCATTCTGT	237731	69927	CTATGTTGCCCAGGCTGGTC	282318	114514	GCTGGGACCACAGGCACATG
193145	25341	TGAGACAGGATCTCATTCTG	237732	69928	ACTATGTTGCCCAGGCTGGT	282319	114515	AGCTGGGACCACAGGCACAT
193146	25342	TTGAGACAGGATCTCATTCT	237733	69929	CACTATGTTGCCCAGGCTGG	282320	114516	TAGCTGGGACCACAGGCACA

193147	25343	TTTGAGACAGGATCTCATTC	237734	69930	TCACTATGTTGCCCAGGCTG	282321	114517	GTAGCTGGGACCACAGGCAC
193148	25344	TTTTGAGACAGGATCTCATT	237735	69931	CTCACTATGTTGCCCAGGCT	282322	114518	AGTAGCTGGGACCACAGGCA
193149	25345	GTTTTGAGACAGGATCTCAT	237736	69932	TCTCACTATGTTGCCCAGGC	282323	114519	AAGTAGCTGGGACCACAGGC
193150	25346	TGTTTTGAGACAGGATCTCA	237737	69933	GTCTCACTATGTTGCCCAGG	282324	114520	CAAGTAGCTGGGACCACAGG
193151	25347	TTGTTTTGAGACAGGATCTC	237738	69934	GGTCTCACTATGTTGCCCAG	282325	114521	CCAAGTAGCTGGGACCACAG
193152	25348	TTTGTTTTGAGACAGGATCT	237739	69935	AGGTCTCACTATGTTGCCCA	282326	114522	CCCAAGTAGCTGGGACCACA
193153	25349	GTTTGTTTTGAGACAGGATC	237740	69936	GAGGTCTCACTATGTTGCCC	282327	114523	TCCCAAGTAGCTGGGACCAC
193154	25350	TGTTTGTTTTGAGACAGGAT	237741	69937	CGAGGTCTCACTATGTTGCC	282328	114524	CTCCCAAGTAGCTGGGACCA
193155	25351	TTGTTTGTTTTGAGACAGGA	237742	69938	ACGAGGTCTCACTATGTTGC	282329	114525	CCTCCCAAGTAGCTGGGACC
193156	25352	TTTGTTTGTTTTGAGACAGG	237743	69939	GACGAGGTCTCACTATGTTG	282330	114526	GCCTCCCAAGTAGCTGGGAC
193157	25353	GTTTGTTTGTTTTGAGACAG	237744	69940	AGACGAGGTCTCACTATGTT	282331	114527	AGCCTCCCAAGTAGCTGGGA
193158	25354	TGTTTGTTTGTTTTGAGACA	237745	69941	GAGACGAGGTCTCACTATGT	282332	114528	CAGCCTCCCAAGTAGCTGGG
193159	25355	TTGTTTGTTTGTTTTGAGAC	237746	69942	AGAGACGAGGTCTCACTATG	282333	114529	TCAGCCTCCCAAGTAGCTGG
193160	25356	TTTGTTTGTTTGTTTTGAGA	237747	69943	TAGAGACGAGGTCTCACTAT	282334	114530	TTCAGCCTCCCAAGTAGCTG
193161	25357	GTTTGTTTGTTTGTTTTGAG	237748	69944	GTAGAGACGAGGTCTCACTA	282335	114531	CTTCAGCCTCCCAAGTAGCT
193162	25358	TGTTTGTTTGTTTGTTTTGA	237749	69945	TGTAGAGACGAGGTCTCACT	282336	114532	ACTTCAGCCTCCCAAGTAGC
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193164	25360	TTTGTTTGTTTGTTTGTTTT	237751	69947	TCTGTAGAGACGAGGTCTCA	282338	114534	CTACTTCAGCCTCCCAAGTA
193165	25361	GTTTGTTTGTTTGTTTGTTT	237752	69948	ATCTGTAGAGACGAGGTCTC	282339	114535	CCTACTTCAGCCTCCCAAGT
193166	25362	TGTTTGTTTGTTTGTTTGTT	237753	69949	TATCTGTAGAGACGAGGTCT	282340	114536	TCCTACTTCAGCCTCCCAAG
193167	25363	TTGTTTGTTTGTTTGTTTGT	237754	69950	TTATCTGTAGAGACGAGGTC	282341	114537	CTCCTACTTCAGCCTCCCAA
193168	25364	TTTGTTTGTTTGTTTGTTTG	237755	69951	ATTATCTGTAGAGACGAGGT	282342	114538	TCTCCTACTTCAGCCTCCCA
193169	25365	TTTTGTTTGTTTGTTTGTTT	237756	69952	TATTATCTGTAGAGACGAGG	282343	114539	TTCTCCTACTTCAGCCTCCC
193170	25366	CTTTTGTTTGTTTGTTTGTT	237757	69953	TTATTATCTGTAGAGACGAG	282344	114540	ATTCTCCTACTTCAGCCTCC
193171	25367	TCTTTTGTTTGTTTGTTTGT	237758	69954	ATTATTATCTGTAGAGACGA	282345	114541	GATTCTCCTACTTCAGCCTC
193172	25368	TTCTTTTGTTTGTTTGTTTG	237759	69955	AATTATTATCTGTAGAGACG	282346	114542	GGATTCTCCTACTTCAGCCT
193173	25369	CTTCTTTTGTTTGTTTGTTT	237760	69956	AAATTATTATCTGTAGAGAC	282347	114543	GGGATTCTCCTACTTCAGCC
193174	25370	CCTTCTTTTGTTTGTTTGTT	237761	69957	AAAATTATTATCTGTAGAGA	282348	114544	GGGGATTCTCCTACTTCAGC
193175	25371	GCCTTCTTTTGTTTGTTTGT	237762	69958	TAAAATTATTATCTGTAGAG	282349	114545	AGGGGATTCTCCTACTTCAG
193176	25372	AGCCTTCTTTTGTTTGTTTG	237763	69959	TTAAAATTATTATCTGTAGA	282350	114546	CAGGGGATTCTCCTACTTCA
193177	25373	AAGCCTTCTTTTGTTTGTTT	237764	69960	TTTAAAATTATTATCTGTAG	282351	114547	TCAGGGGATTCTCCTACTTC
193178	25374	TAAGCCTTCTTTTGTTTGTT	237765	69961	TTTTAAAATTATTATCTGTA	282352	114548	CTCAGGGGATTCTCCTACTT
193179	25375	TTAAGCCTTCTTTTGTTTGT	237766	69962	TTTTTAAAATTATTATCTGT	282353	114549	GCTCAGGGGATTCTCCTACT
193180	25376	TTTAAGCCTTCTTTTGTTTG	237767	69963	ATTTTTAAAATTATTATCTG	282354	114550	GGCTCAGGGGATTCTCCTAC
193181	25377	CTTTAAGCCTTCTTTTGTTT	237768	69964	AATTTTTAAAATTATTATCT	282355	114551	GGGCTCAGGGGATTCTCCTA
193182	25378	CCTTTAAGCCTTCTTTTGTT	237769	69965	TAATTTTTAAAATTATTATC	282356	114552	AGGGCTCAGGGGATTCTCCT
193183	25379	CCCTTTAAGCCTTCTTTTGT	237770	69966	ATAATTTTTAAAATTATTAT	282357	114553	CAGGGCTCAGGGGATTCTCC
193184	25380	CCCCTTTAAGCCTTCTTTTG	237771	69967	GATAATTTTTAAAATTATTA	282358	114554	CCAGGGCTCAGGGGATTCTC
193185	25381	CCCCCTTTAAGCCTTCTTTT	237772	69968	GGATAATTTTTAAAATTATT	282359	114555	CCCAGGGCTCAGGGGATTCT
193186	25382	GCCCCCTTTAAGCCTTCTTT	237773	69969	CGGATAATTTTTAAAATTAT	282360	114556	TCCCAGGGCTCAGGGGATTC
193187	25383	AGCCCCCTTTAAGCCTTCTT	237774	69970	CCGGATAATTTTTAAAATTA	282361	114557	TTCCCAGGGCTCAGGGGATT
193188	25384	GAGCCCCCTTTAAGCCTTCT	237775	69971	CCCGGATAATTTTTAAAATT	282362	114558	CTTCCCAGGGCTCAGGGGAT
193189	25385	GGAGCCCCCTTTAAGCCTTC	237776	69972	GCCCGGATAATTTTTAAAAT	282363	114559	ACTTCCCAGGGCTCAGGGGA
193190	25386	TGGAGCCCCCTTTAAGCCTT	237777	69973	TGCCCGGATAATTTTTAAAA	282364	114560	GACTTCCCAGGGCTCAGGGG
193191	25387	CTGGAGCCCCCTTTAAGCCT	237778	69974	ATGCCCGGATAATTTTTAAA	282365	114561	CGACTTCCCAGGGCTCAGGG
193192	25388	CCTGGAGCCCCCTTTAAGCC	237779	69975	TATGCCCGGATAATTTTTAA	282366	114562	TCGACTTCCCAGGGCTCAGG
193193	25389	ACCTGGAGCCCCCTTTAAGC	237780	69976	CTATGCCCGGATAATTTTTA	282367	114563	CTCGACTTCCCAGGGCTCAG
193194	25390	CACCTGGAGCCCCCTTTAAG	237781	69977	ACTATGCCCGGATAATTTTT	282368	114564	CCTCGACTTCCCAGGGCTCA
193195	25391	CCACCTGGAGCCCCCTTTAA	237782	69978	CACTATGCCCGGATAATTTT	282369	114565	GCCTCGACTTCCCAGGGCTC
193196	25392	CCCACCTGGAGCCCCCTTTA	237783	69979	CCACTATGCCCGGATAATTT	282370	114566	AGCCTCGACTTCCCAGGGCT
193197	25393	GCCCACCTGGAGCCCCCTTT	237784	69980	GCCACTATGCCCGGATAATT	282371	114567	CAGCCTCGACTTCCCAGGGC
193198	25394	AGCCCACCTGGAGCCCCCTT	237785	69981	TGCCACTATGCCCGGATAAT	282372	114568	GCAGCCTCGACTTCCCAGGG
193199	25395	AAGCCCACCTGGAGCCCCCT	237786	69982	ATGCCACTATGCCCGGATAA	282373	114569	TGCAGCCTCGACTTCCCAGG
193200	25396	CAAGCCCACCTGGAGCCCCC	237787	69983	CATGCCACTATGCCCGGATA	282374	114570	GTGCAGCCTCGACTTCCCAG
193201	25397	CCAAGCCCACCTGGAGCCCC	237788	69984	GCATGCCACTATGCCCGGAT	282375	114571	AGTGCAGCCTCGACTTCCCA
193202	25398	GCCAAGCCCACCTGGAGCCC	237789	69985	TGCATGCCACTATGCCCGGA	282376	114572	CAGTGCAGCCTCGACTTCCC
193203	25399	TGCCAAGCCCACCTGGAGCC	237790	69986	GTGCATGCCACTATGCCCGG	282377	114573	TCAGTGCAGCCTCGACTTCC
193204	25400	CTGCCAAGCCCACCTGGAGC	237791	69987	GGTGCATGCCACTATGCCCG	282378	114574	CTCAGTGCAGCCTCGACTTC
193205	25401	GCTGCCAAGCCCACCTGGAG	237792	69988	AGGTGCATGCCACTATGCCC	282379	114575	GCTCAGTGCAGCCTCGACTT
193206	25402	TGCTGCCAAGCCCACCTGGA	237793	69989	TAGGTGCATGCCACTATGCC	282380	114576	GGCTCAGTGCAGCCTCGACT
193207	25403	GTGCTGCCAAGCCCACCTGG	237794	69990	ATAGGTGCATGCCACTATGC	282381	114577	CGGCTCAGTGCAGCCTCGAC
193208	25404	TGTGCTGCCAAGCCCACCTG	237795	69991	TATAGGTGCATGCCACTATG	282382	114578	ACGGCTCAGTGCAGCCTCGA
193209	25405	TTGTGCTGCCAAGCCCACCT	237796	69992	CTATAGGTGCATGCCACTAT	282383	114579	CACGGCTCAGTGCAGCCTCG
193210	25406	TTTGTGCTGCCAAGCCCACC	237797	69993	ACTATAGGTGCATGCCACTA	282384	114580	TCACGGCTCAGTGCAGCCTC
193211	25407	CTTTGTGCTGCCAAGCCCAC	237798	69994	GACTATAGGTGCATGCCACT	282385	114581	ATCACGGCTCAGTGCAGCCT
193212	25408	GCTTTGTGCTGCCAAGCCCA	237799	69995	GGACTATAGGTGCATGCCAC	282386	114582	CATCACGGCTCAGTGCAGCC
193213	25409	AGCTTTGTGCTGCCAAGCCC	237800	69996	GGGACTATAGGTGCATGCCA	282387	114583	CCATCACGGCTCAGTGCAGC
193214	25410	TAGCTTTGTGCTGCCAAGCC	237801	69997	TGGGACTATAGGTGCATGCC	282388	114584	ACCATCACGGCTCAGTGCAG
193215	25411	ATAGCTTTGTGCTGCCAAGC	237802	69998	CTGGGACTATAGGTGCATGC	282389	114585	CACCATCACGGCTCAGTGCA
193216	25412	CATAGCTTTGTGCTGCCAAG	237803	69999	GCTGGGACTATAGGTGCATG	282390	114586	ACACCATCACGGCTCAGTGC
193217	25413	TCATAGCTTTGTGCTGCCAA	237804	70000	AGCTGGGACTATAGGTGCAT	282391	114587	GACACCATCACGGCTCAGTG
193218	25414	TTCATAGCTTTGTGCTGCCA	237805	70001	TAGCTGGGACTATAGGTGCA	282392	114588	TGACACCATCACGGCTCAGT

193219	25415	CTTCATAGCTTTGTGCTGCC	237806	70002	GTAGCTGGGACTATAGGTGC	282393	114589	GTGACACCATCACGGCTCAG
193220	25416	ACTTCATAGCTTTGTGCTGC	237807	70003	AGTAGCTGGGACTATAGGTG	282394	114590	AGTGACACCATCACGGCTCA
193221	25417	AACTTCATAGCTTTGTGCTG	237808	70004	GAGTAGCTGGGACTATAGGT	282395	114591	CAGTGACACCATCACGGCTC
193222	25418	GAACTTCATAGCTTTGTGCT	237809	70005	TGAGTAGCTGGGACTATAGG	282396	114592	GCAGTGACACCATCACGGCT
193223	25419	AGAACTTCATAGCTTTGTGC	237810	70006	TTGAGTAGCTGGGACTATAG	282397	114593	TGCAGTGACACCATCACGGC
193224	25420	TAGAACTTCATAGCTTTGTG	237811	70007	CTTGAGTAGCTGGGACTATA	282398	114594	GTGCAGTGACACCATCACGG
193225	25421	ATAGAACTTCATAGCTTTGT	237812	70008	TCTTGAGTAGCTGGGACTAT	282399	114595	AGTGCAGTGACACCATCACG
193226	25422	GATAGAACTTCATAGCTTTG	237813	70009	CTCTTGAGTAGCTGGGACTA	282400	114596	GAGTGCAGTGACACCATCAC
193227	25423	AGATAGAACTTCATAGCTTT	237814	70010	CCTCTTGAGTAGCTGGGACT	282401	114597	GGAGTGCAGTGACACCATCA
193228	25424	AAGATAGAACTTCATAGCTT	237815	70011	GCCTCTTGAGTAGCTGGGAC	282402	114598	TGGAGTGCAGTGACACCATC
193229	25425	TAAGATAGAACTTCATAGCT	237816	70012	TGCCTCTTGAGTAGCTGGGA	282403	114599	CTGGAGTGCAGTGACACCAT
193230	25426	CTAAGATAGAACTTCATAGC	237817	70013	CTGCCTCTTGAGTAGCTGGG	282404	114600	GCTGGAGTGCAGTGACACCA
193231	25427	TCTAAGATAGAACTTCATAG	237818	70014	TCTGCCTCTTGAGTAGCTGG	282405	114601	GGCTGGAGTGCAGTGACACC
193232	25428	GTCTAAGATAGAACTTCATA	237819	70015	CTCTGCCTCTTGAGTAGCTG	282406	114602	AGGCTGGAGTGCAGTGACAC
193233	25429	TGTCTAAGATAGAACTTCAT	237820	70016	CCTCTGCCTCTTGAGTAGCT	282407	114603	CAGGCTGGAGTGCAGTGACA
193234	25430	GTGTCTAAGATAGAACTTCA	237821	70017	GCCTCTGCCTCTTGAGTAGC	282408	114604	CCAGGCTGGAGTGCAGTGAC
193235	25431	TGTGTCTAAGATAGAACTTC	237822	70018	TGCCTCTGCCTCTTGAGTAG	282409	114605	CCCAGGCTGGAGTGCAGTGA
193236	25432	TTGTGTCTAAGATAGAACTT	237823	70019	CTGCCTCTGCCTCTTGAGTA	282410	114606	ACCCAGGCTGGAGTGCAGTG
193237	25433	CTTGTGTCTAAGATAGAACT	237824	70020	CCTGCCTCTGCCTCTTGAGT	282411	114607	CACCCAGGCTGGAGTGCAGT
193238	25434	ACTTGTGTCTAAGATAGAAC	237825	70021	TCCTGCCTCTGCCTCTTGAG	282412	114608	TCACCCAGGCTGGAGTGCAG
193239	25435	AACTTGTGTCTAAGATAGAA	237826	70022	CTCCTGCCTCTGCCTCTTGA	282413	114609	GTCACCCAGGCTGGAGTGCA
193240	25436	GAACTTGTGTCTAAGATAGA	237827	70023	CCTCCTGCCTCTGCCTCTTG	282414	114610	TGTCACCCAGGCTGGAGTGC
193241	25437	AGAACTTGTGTCTAAGATAG	237828	70024	TCCTCCTGCCTCTGCCTCTT	282415	114611	TTGTCACCCAGGCTGGAGTG
193242	25438	CAGAACTTGTGTCTAAGATA	237829	70025	ATCCTCCTGCCTCTGCCTCT	282416	114612	TTTGTCACCCAGGCTGGAGT
193243	25439	ACAGAACTTGTGTCTAAGAT	237830	70026	GATCCTCCTGCCTCTGCCTC	282417	114613	CTTTGTCACCCAGGCTGGAG
193244	25440	AACAGAACTTGTGTCTAAGA	237831	70027	TGATCCTCCTGCCTCTGCCT	282418	114614	ACTTTGTCACCCAGGCTGGA
193245	25441	TAACAGAACTTGTGTCTAAG	237832	70028	GTGATCCTCCTGCCTCTGCC	282419	114615	CACTTTGTCACCCAGGCTGG
193246	25442	GTAACAGAACTTGTGTCTAA	237833	70029	AGTGATCCTCCTGCCTCTGC	282420	114616	TCACTTTGTCACCCAGGCTG
193247	25443	AGTAACAGAACTTGTGTCTA	237834	70030	AAGTGATCCTCCTGCCTCTG	282421	114617	CTCACTTTGTCACCCAGGCT
193248	25444	CAGTAACAGAACTTGTGTCT	237835	70031	CAAGTGATCCTCCTGCCTCT	282422	114618	TCTCACTTTGTCACCCAGGC
193249	25445	CCAGTAACAGAACTTGTGTC	237836	70032	TCAAGTGATCCTCCTGCCTC	282423	114619	GTCTCACTTTGTCACCCAGG
193250	25446	CCCAGTAACAGAACTTGTGT	237837	70033	CTCAAGTGATCCTCCTGCCT	282424	114620	GGTCTCACTTTGTCACCCAG
193251	25447	GCCCAGTAACAGAACTTGTG	237838	70034	GCTCAAGTGATCCTCCTGCC	282425	114621	GGGTCTCACTTTGTCACCCA
193252	25448	GGCCCAGTAACAGAACTTGT	237839	70035	GGCTCAAGTGATCCTCCTGC	282426	114622	AGGGTCTCACTTTGTCACCC
193253	25449	AGGCCCAGTAACAGAACTTG	237840	70036	GGGCTCAAGTGATCCTCCTG	282427	114623	TAGGGTCTCACTTTGTCACC
193254	25450	AAGGCCCAGTAACAGAACTT	237841	70037	TGGGCTCAAGTGATCCTCCT	282428	114624	ATAGGGTCTCACTTTGTCAC
193255	25451	AAAGGCCCAGTAACAGAACT	237842	70038	CTGGGCTCAAGTGATCCTCC	282429	114625	GATAGGGTCTCACTTTGTCA
193256	25452	CAAAGGCCCAGTAACAGAAC	237843	70039	CCTGGGCTCAAGTGATCCTC	282430	114626	AGATAGGGTCTCACTTTGTC
193257	25453	GCAAAGGCCCAGTAACAGAA	237844	70040	TCCTGGGCTCAAGTGATCCT	282431	114627	GAGATAGGGTCTCACTTTGT
193258	25454	TGCAAAGGCCCAGTAACAGA	237845	70041	CTCCTGGGCTCAAGTGATCC	282432	114628	TGAGATAGGGTCTCACTTTG
193259	25455	CTGCAAAGGCCCAGTAACAG	237846	70042	CCTCCTGGGCTCAAGTGATC	282433	114629	GTGAGATAGGGTCTCACTTT
193260	25456	CCTGCAAAGGCCCAGTAACA	237847	70043	GCCTCCTGGGCTCAAGTGAT	282434	114630	TGTGAGATAGGGTCTCACTT
193261	25457	GCCTGCAAAGGCCCAGTAAC	237848	70044	CGCCTCCTGGGCTCAAGTGA	282435	114631	TTGTGAGATAGGGTCTCACT
193262	25458	AGCCTGCAAAGGCCCAGTAA	237849	70045	CCGCCTCCTGGGCTCAAGTG	282436	114632	TTTGTGAGATAGGGTCTCAC
193263	25459	CAGCCTGCAAAGGCCCAGTA	237850	70046	TCCGCCTCCTGGGCTCAAGT	282437	114633	CTTTGTGAGATAGGGTCTCA
193264	25460	CCAGCCTGCAAAGGCCCAGT	237851	70047	CTCCGCCTCCTGGGCTCAAG	282438	114634	TCTTTGTGAGATAGGGTCTC
193265	25461	GCCAGCCTGCAAAGGCCCAG	237852	70048	CCTCCGCCTCCTGGGCTCAA	282439	114635	TTCTTTGTGAGATAGGGTCT
193266	25462	GGCCAGCCTGCAAAGGCCCA	237853	70049	ACCTCCGCCTCCTGGGCTCA	282440	114636	TTTCTTTGTGAGATAGGGTC
193267	25463	AGGCCAGCCTGCAAAGGCCC	237854	70050	AACCTCCGCCTCCTGGGCTC	282441	114637	TTTTCTTTGTGAGATAGGGT
193268	25464	CAGGCCAGCCTGCAAAGGCC	237855	70051	CAACCTCCGCCTCCTGGGCT	282442	114638	TTTTTCTTTGTGAGATAGGG
193269	25465	CCAGGCCAGCCTGCAAAGGC	237856	70052	GCAACCTCCGCCTCCTGGGC	282443	114639	TTTTTTCTTTGTGAGATAGG
193270	25466	CCCAGGCCAGCCTGCAAAGG	237857	70053	GGCAACCTCCGCCTCCTGGG	282444	114640	TTTTTTTCTTTGTGAGATAG
193271	25467	ACCCAGGCCAGCCTGCAAAG	237858	70054	CGGCAACCTCCGCCTCCTGG	282445	114641	TTTTTTTTCTTTGTGAGATA
193272	25468	TACCCAGGCCAGCCTGCAAA	237859	70055	ACGGCAACCTCCGCCTCCTG	282446	114642	GTTTTTTTCTTTGTGAGAT
193273	25469	GTACCCAGGCCAGCCTGCAA	237860	70056	CACGGCAACCTCCGCCTCCT	282447	114643	TGTTTTTTTTCTTTGTGAGA
193274	25470	GGTACCCAGGCCAGCCTGCA	237861	70057	TCACGGCAACCTCCGCCTCC	282448	114644	TTGTTTTTTTTCTTTGTGAG
193275	25471	AGGTACCCAGGCCAGCCTGC	237862	70058	CTCACGGCAACCTCCGCCTC	282449	114645	TTTGTTTTTTTTCTTTGTGA
193276	25472	CAGGTACCCAGGCCAGCCTG	237863	70059	GCTCACGGCAACCTCCGCCT	282450	114646	TTTTGTTTTTTTTCTTTGTG
193277	25473	CCAGGTACCCAGGCCAGCCT	237864	70060	GGCTCACGGCAACCTCCGCC	282451	114647	GTTTTGTTTTTTTTCTTTGT
193278	25474	GCCAGGTACCCAGGCCAGCC	237865	70061	TGGCTCACGGCAACCTCCGC	282452	114648	TGTTTTGTTTTTTTTCTTTG
193279	25475	AGCCAGGTACCCAGGCCAGC	237866	70062	TTGGCTCACGGCAACCTCCG	282453	114649	TTGTTTTGTTTTTTTTCTTT
193280	25476	CAGCCAGGTACCCAGGCCAG	237867	70063	CTTGGCTCACGGCAACCTCC	282454	114650	TTTGTTTTGTTTTTTTTCTT
193281	25477	GCAGCCAGGTACCCAGGCCA	237868	70064	TCTTGGCTCACGGCAACCTC	282455	114651	TTTTGTTTTGTTTTTTTTCT
193282	25478	GGCAGCCAGGTACCCAGGCC	237869	70065	ATCTTGGCTCACGGCAACCT	282456	114652	TTTTTGTTTTGTTTTTTTTC
193283	25479	TGGCAGCCAGGTACCCAGGC	237870	70066	GATCTTGGCTCACGGCAACC	282457	114653	TTTTTTGTTTTGTTTTTTTT
193284	25480	ATGGCAGCCAGGTACCCAGG	237871	70067	GGATCTTGGCTCACGGCAAC	282458	114654	GTTTTTTGTTTTGTTTTTTT
193285	25481	TATGGCAGCCAGGTACCCAG	237872	70068	GGGATCTTGGCTCACGGCAA	282459	114655	GGTTTTTTGTTTTGTTTTTT
193286	25482	CTATGGCAGCCAGGTACCCA	237873	70069	TGGGATCTTGGCTCACGGCA	282460	114656	GGGTTTTTTGTTTTGTTTTT
193287	25483	TCTATGGCAGCCAGGTACCC	237874	70070	GTGGGATCTTGGCTCACGGC	282461	114657	TGGGTTTTTTGTTTTGTTTT
193288	25484	GTCTATGGCAGCCAGGTACC	237875	70071	GGTGGGATCTTGGCTCACGG	282462	114658	TTGGGTTTTTTGTTTTGTTT
193289	25485	TGTCTATGGCAGCCAGGTAC	237876	70072	TGGTGGGATCTTGGCTCACG	282463	114659	TTTGGGTTTTTTGTTTTGTT
193290	25486	CTGTCTATGGCAGCCAGGTA	237877	70073	GTGGTGGGATCTTGGCTCAC	282464	114660	CTTTGGGTTTTTTGTTTTGT

193291	25487	CCTGTCTATGGCAGCCAGGT	237878	70074	AGTGGTGGGATCTTGGCTCA	282465	114661	GCTTTGGGTTTTTTGTTTTG
193292	25488	CCCTGTCTATGGCAGCCAGG	237879	70075	CAGTGGTGGGATCTTGGCTC	282466	114662	TGCTTTGGGTTTTTTGTTTT
193293	25489	TCCCTGTCTATGGCAGCCAG	237880	70076	GCAGTGGTGGGATCTTGGCT	282467	114663	GTGCTTTGGGTTTTTTGTTT
193294	25490	TTCCCTGTCTATGGCAGCCA	237881	70077	TGCAGTGGTGGGATCTTGGC	282468	114664	TGTGCTTTGGGTTTTTTGTT
193295	25491	GTTCCCTGTCTATGGCAGCC	237882	70078	GTGCAGTGGTGGGATCTTGG	282469	114665	GTGTGCTTTGGGTTTTTTGT
193296	25492	GGTTCCCTGTCTATGGCAGC	237883	70079	AGTGCAGTGGTGGGATCTTG	282470	114666	AGTGTGCTTTGGGTTTTTTG
193297	25493	AGGTTCCCTGTCTATGGCAG	237884	70080	GAGTGCAGTGGTGGGATCTT	282471	114667	CAGTGTGCTTTGGGTTTTTT
193298	25494	AAGGTTCCCTGTCTATGGCA	237885	70081	GGAGTGCAGTGGTGGGATCT	282472	114668	ACAGTGTGCTTTGGGTTTTT
193299	25495	GAAGGTTCCCTGTCTATGGC	237886	70082	TGGAGTGCAGTGGTGGGATC	282473	114669	AACAGTGTGCTTTGGGTTTT
193300	25496	GGAAGGTTCCCTGTCTATGG	237887	70083	CTGGAGTGCAGTGGTGGGAT	282474	114670	AAACAGTGTGCTTTGGGTTT
193301	25497	TGGAAGGTTCCCTGTCTATG	237888	70084	GCTGGAGTGCAGTGGTGGGA	282475	114671	GAAACAGTGTGCTTTGGGTT
193302	25498	CTGGAAGGTTCCCTGTCTAT	237889	70085	GGCTGGAGTGCAGTGGTGGG	282476	114672	GGAAACAGTGTGCTTTGGGT
193303	25499	TCTGGAAGGTTCCCTGTCTA	237890	70086	AGGCTGGAGTGCAGTGGTGG	282477	114673	TGGAAACAGTGTGCTTTGGG
193304	25500	ATCTGGAAGGTTCCCTGTCT	237891	70087	CAGGCTGGAGTGCAGTGGTG	282478	114674	GTGGAAACAGTGTGCTTTGG
193305	25501	CATCTGGAAGGTTCCCTGTC	237892	70088	CCAGGCTGGAGTGCAGTGGT	282479	114675	AGTGGAAACAGTGTGCTTTG
193306	25502	TCATCTGGAAGGTTCCCTGT	237893	70089	CCCAGGCTGGAGTGCAGTGG	282480	114676	CAGTGGAAACAGTGTGCTTT
193307	25503	CTCATCTGGAAGGTTCCCTG	237894	70090	GCCCAGGCTGGAGTGCAGTG	282481	114677	ACAGTGGAAACAGTGTGCTT
193308	25504	GCTCATCTGGAAGGTTCCCT	237895	70091	CGCCCAGGCTGGAGTGCAGT	282482	114678	AACAGTGGAAACAGTGTGCT
193309	25505	AGCTCATCTGGAAGGTTCCC	237896	70092	TCGCCCAGGCTGGAGTGCAG	282483	114679	AAACAGTGGAAACAGTGTGC
193310	25506	CAGCTCATCTGGAAGGTTCC	237897	70093	GTCGCCCAGGCTGGAGTGCA	282484	114680	GAAACAGTGGAAACAGTGTG
193311	25507	GCAGCTCATCTGGAAGGTTC	237898	70094	TGTCGCCCAGGCTGGAGTGC	282485	114681	GGAAACAGTGGAAACAGTGT
193312	25508	TGCAGCTCATCTGGAAGGTT	237899	70095	CTGTCGCCCAGGCTGGAGTG	282486	114682	TGGAAACAGTGGAAACAGTG
193313	25509	CTGCAGCTCATCTGGAAGGT	237900	70096	TCTGTCGCCCAGGCTGGAGT	282487	114683	CTGGAAACAGTGGAAACAGT
193314	25510	CCTGCAGCTCATCTGGAAGG	237901	70097	CTCTGTCGCCCAGGCTGGAG	282488	114684	TCTGGAAACAGTGGAAACAG
193315	25511	GCCTGCAGCTCATCTGGAAG	237902	70098	TCTCTGTCGCCCAGGCTGGA	282489	114685	CTCTGGAAACAGTGGAAACA
193316	25512	CGCCTGCAGCTCATCTGGAA	237903	70099	GTCTCTGTCGCCCAGGCTGG	282490	114686	ACTCTGGAAACAGTGGAAAC
193317	25513	ACGCCTGCAGCTCATCTGGA	237904	70100	GGTCTCTGTCGCCCAGGCTG	282491	114687	AACTCTGGAAACAGTGGAAA
193318	25514	CACGCCTGCAGCTCATCTGG	237905	70101	GGGTCTCTGTCGCCCAGGCT	282492	114688	GAACTCTGGAAACAGTGGAA
193319	25515	CCACGCCTGCAGCTCATCTG	237906	70102	GGGGTCTCTGTCGCCCAGGC	282493	114689	GGAACTCTGGAAACAGTGGA
193320	25516	TCCACGCCTGCAGCTCATCT	237907	70103	GGGGGTCTCTGTCGCCCAGG	282494	114690	AGGAACTCTGGAAACAGTGG
193321	25517	CTCCACGCCTGCAGCTCATC	237908	70104	TGGGGGTCTCTGTCGCCCAG	282495	114691	CAGGAACTCTGGAAACAGTG
193322	25518	GCTCCACGCCTGCAGCTCAT	237909	70105	ATGGGGGTCTCTGTCGCCCA	282496	114692	TCAGGAACTCTGGAAACAGT
193323	25519	TGCTCCACGCCTGCAGCTCA	237910	70106	CATGGGGGTCTCTGTCGCCC	282497	114693	CTCAGGAACTCTGGAAACAG
193324	25520	GTGCTCCACGCCTGCAGCTC	237911	70107	ACATGGGGGTCTCTGTCGCC	282498	114694	TCTCAGGAACTCTGGAAACA
193325	25521	TGTGCTCCACGCCTGCAGCT	237912	70108	GACATGGGGGTCTCTGTCGC	282499	114695	CTCTCAGGAACTCTGGAAAC
193326	25522	CTGTGCTCCACGCCTGCAGC	237913	70109	TGACATGGGGGTCTCTGTCG	282500	114696	CCTCTCAGGAACTCTGGAAA
193327	25523	CCTGTGCTCCACGCCTGCAG	237914	70110	TTGACATGGGGGTCTCTGTC	282501	114697	TCCTCTCAGGAACTCTGGAA
193328	25524	TCCTGTGCTCCACGCCTGCA	237915	70111	TTTGACATGGGGGTCTCTGT	282502	114698	TTCCTCTCAGGAACTCTGGA
193329	25525	CTCCTGTGCTCCACGCCTGC	237916	70112	ATTTGACATGGGGGTCTCTG	282503	114699	TTTCCTCTCAGGAACTCTGG
193330	25526	GCTCCTGTGCTCCACGCCTG	237917	70113	TATTTGACATGGGGGTCTCT	282504	114700	CTTTCCTCTCAGGAACTCTG
193331	25527	GGCTCCTGTGCTCCACGCCT	237918	70114	TTATTTGACATGGGGGTCTC	282505	114701	CCTTTCCTCTCAGGAACTCT
193332	25528	TGGCTCCTGTGCTCCACGCC	237919	70115	ATTATTTGACATGGGGGTCT	282506	114702	ACCTTTCCTCTCAGGAACTC
193333	25529	CTGGCTCCTGTGCTCCACGC	237920	70116	TATTATTTGACATGGGGGTC	282507	114703	GACCTTTCCTCTCAGGAACT
193334	25530	CCTGGCTCCTGTGCTCCACG	237921	70117	TTATTATTTGACATGGGGGT	282508	114704	TGACCTTTCCTCTCAGGAAC
193335	25531	CCCTGGCTCCTGTGCTCCAC	237922	70118	ATTATTATTTGACATGGGGG	282509	114705	GTGACCTTTCCTCTCAGGAA
193336	25532	ACCCTGGCTCCTGTGCTCCA	237923	70119	TATTATTATTTGACATGGGG	282510	114706	GGTGACCTTTCCTCTCAGGA
193337	25533	CACCCTGGCTCCTGTGCTCC	237924	70120	TTATTATTATTTGACATGGG	282511	114707	CGGTGACCTTTCCTCTCAGG
193338	25534	GCACCCTGGCTCCTGTGCTC	237925	70121	ATTATTATTATTTGACATGG	282512	114708	CCGGTGACCTTTCCTCTCAG
193339	25535	AGCACCCTGGCTCCTGTGCT	237926	70122	TATTATTATTATTTGACATG	282513	114709	CCCGGTGACCTTTCCTCTCA
193340	25536	GAGCACCCTGGCTCCTGTGC	237927	70123	TTATTATTATTATTTGACAT	282514	114710	ACCCGGTGACCTTTCCTCTC
193341	25537	AGAGCACCCTGGCTCCTGTG	237928	70124	ATTATTATTATTATTTGACA	282515	114711	CACCCGGTGACCTTTCCTCT
193342	25538	AAGAGCACCCTGGCTCCTGT	237929	70125	TATTATTATTATTATTTGAC	282516	114712	TCACCCGGTGACCTTTCCTC
193343	25539	GAAGAGCACCCTGGCTCCTG	237930	70126	TTATTATTATTATTATTTGA	282517	114713	CTCACCCGGTGACCTTTCCT
193344	25540	GGAAGAGCACCCTGGCTCCT	237931	70127	TTTATTATTATTATTATTTG	282518	114714	CCTCACCCGGTGACCTTTCC
193345	25541	AGGAAGAGCACCCTGGCTCC	237932	70128	ATTTATTATTATTATTATTT	282519	114715	TCCTCACCCGGTGACCTTTC
193346	25542	CAGGAAGAGCACCCTGGCTC	237933	70129	TATTTATTATTATTATTATT	282520	114716	TTCCTCACCCGGTGACCTTT
193347	25543	CCAGGAAGAGCACCCTGGCT	237934	70130	TTATTTATTATTATTATTAT	282521	114717	CTTCCTCACCCGGTGACCTT
193348	25544	CCCAGGAAGAGCACCCTGGC	237935	70131	TTTATTTATTATTATTATTA	282522	114718	TCTTCCTCACCCGGTGACCT
193349	25545	GCCCAGGAAGAGCACCCTGG	237936	70132	ATTTATTTATTATTATTATT	282523	114719	GTCTTCCTCACCCGGTGACC
193350	25546	AGCCCAGGAAGAGCACCCTG	237937	70133	GATTTATTTATTATTATTAT	282524	114720	CGTCTTCCTCACCCGGTGAC
193351	25547	GAGCCCAGGAAGAGCACCCT	237938	70134	GGATTTATTTATTATTATTA	282525	114721	ACGTCTTCCTCACCCGGTGA
193352	25548	AGAGCCCAGGAAGAGCACCC	237939	70135	AGGATTTATTTATTATTATT	282526	114722	AACGTCTTCCTCACCCGGTG
193353	25549	CAGAGCCCAGGAAGAGCACC	237940	70136	AAGGATTTATTTATTATTAT	282527	114723	GAACGTCTTCCTCACCCGGT
193354	25550	ACAGAGCCCAGGAAGAGCAC	237941	70137	GAAGGATTTATTTATTATTA	282528	114724	AGAACGTCTTCCTCACCCGG
193355	25551	GACAGAGCCCAGGAAGAGCA	237942	70138	AGAAGGATTTATTTATTATT	282529	114725	GAGAACGTCTTCCTCACCCG
193356	25552	GGACAGAGCCCAGGAAGAGC	237943	70139	GAGAAGGATTTATTTATTAT	282530	114726	TGAGAACGTCTTCCTCACCC
193357	25553	TGGACAGAGCCCAGGAAGAG	237944	70140	TGAGAAGGATTTATTTATTA	282531	114727	GTGAGAACGTCTTCCTCACC
193358	25554	GTGGACAGAGCCCAGGAAGA	237945	70141	CTGAGAAGGATTTATTTATT	282532	114728	AGTGAGAACGTCTTCCTCAC
193359	25555	TGTGGACAGAGCCCAGGAAG	237946	70142	ACTGAGAAGGATTTATTTAT	282533	114729	CAGTGAGAACGTCTTCCTCA
193360	25556	CTGTGGACAGAGCCCAGGAA	237947	70143	GACTGAGAAGGATTTATTTA	282534	114730	TCAGTGAGAACGTCTTCCTC
193361	25557	CCTGTGGACAGAGCCCAGGA	237948	70144	GGACTGAGAAGGATTTATTT	282535	114731	ATCAGTGAGAACGTCTTCCT
193362	25558	GCCTGTGGACAGAGCCCAGG	237949	70145	GGGACTGAGAAGGATTTATT	282536	114732	GATCAGTGAGAACGTCTTCC

193363	25559	TGCCTGTGGACAGAGCCCAG	237950	70146	AGGGACTGAGAAGGATTTAT	282537	114733	AGATCAGTGAGAACGTCTTC
193364	25560	CTGCCTGTGGACAGAGCCCA	237951	70147	AAGGGACTGAGAAGGATTTA	282538	114734	CAGATCAGTGAGAACGTCTT
193365	25561	TCTGCCTGTGGACAGAGCCC	237952	70148	GAAGGGACTGAGAAGGATTT	282539	114735	CCAGATCAGTGAGAACGTCT
193366	25562	TTCTGCCTGTGGACAGAGCC	237953	70149	GGAAGGGACTGAGAAGGATT	282540	114736	GCCAGATCAGTGAGAACGTC
193367	25563	GTTCTGCCTGTGGACAGAGC	237954	70150	AGGAAGGGACTGAGAAGGAT	282541	114737	TGCCAGATCAGTGAGAACGT
193368	25564	CGTTCTGCCTGTGGACAGAG	237955	70151	GAGGAAGGGACTGAGAAGGA	282542	114738	CTGCCAGATCAGTGAGAACG
193369	25565	ACGTTCTGCCTGTGGACAGA	237956	70152	TGAGGAAGGGACTGAGAAGG	282543	114739	TCTGCCAGATCAGTGAGAAC
193370	25566	TACGTTCTGCCTGTGGACAG	237957	70153	GTGAGGAAGGGACTGAGAAG	282544	114740	CTCTGCCAGATCAGTGAGAA
193371	25567	GTACGTTCTGCCTGTGGACA	237958	70154	AGTGAGGAAGGGACTGAGAA	282545	114741	TCTCTGCCAGATCAGTGAGA
193372	25568	TGTACGTTCTGCCTGTGGAC	237959	70155	CAGTGAGGAAGGGACTGAGA	282546	114742	TTCTCTGCCAGATCAGTGAG
193373	25569	GTGTACGTTCTGCCTGTGGA	237960	70156	ACAGTGAGGAAGGGACTGAG	282547	114743	TTTCTCTGCCAGATCAGTGA
193374	25570	TGTGTACGTTCTGCCTGTGG	237961	70157	CACAGTGAGGAAGGGACTGA	282548	114744	TTTTCTCTGCCAGATCAGTG
193375	25571	CTGTGTACGTTCTGCCTGTG	237962	70158	ACACAGTGAGGAAGGGACTG	282549	114745	ATTTTCTCTGCCAGATCAGT
193376	25572	ACTGTGTACGTTCTGCCTGT	237963	70159	GACACAGTGAGGAAGGGACT	282550	114746	CATTTTCTCTGCCAGATCAG
193377	25573	GACTGTGTACGTTCTGCCTG	237964	70160	GGACACAGTGAGGAAGGGAC	282551	114747	ACATTTTCTCTGCCAGATCA
193378	25574	AGACTGTGTACGTTCTGCCT	237965	70161	GGGACACAGTGAGGAAGGGA	282552	114748	GACATTTTCTCTGCCAGATC
193379	25575	AAGACTGTGTACGTTCTGCC	237966	70162	GGGGACACAGTGAGGAAGGG	282553	114749	GGACATTTTCTCTGCCAGAT
193380	25576	AAAGACTGTGTACGTTCTGC	237967	70163	GGGGGACACAGTGAGGAAGG	282554	114750	TGGACATTTTCTCTGCCAGA
193381	25577	CAAAGACTGTGTACGTTCTG	237968	70164	AGGGGGACACAGTGAGGAAG	282555	114751	CTGGACATTTTCTCTGCCAG
193382	25578	ACAAAGACTGTGTACGTTCT	237969	70165	GAGGGGGACACAGTGAGGAA	282556	114752	ACTGGACATTTTCTCTGCCA
193383	25579	TACAAAGACTGTGTACGTTC	237970	70166	GGAGGGGGACACAGTGAGGA	282557	114753	AACTGGACATTTTCTCTGCC
193384	25580	GTACAAAGACTGTGTACGTT	237971	70167	TGGAGGGGGACACAGTGAGG	282558	114754	AAACTGGACATTTTCTCTGC
193385	25581	TGTACAAAGACTGTGTACGT	237972	70168	GTGGAGGGGGACACAGTGAG	282559	114755	AAAACTGGACATTTTCTCTG
193386	25582	GTGTACAAAGACTGTGTACG	237973	70169	AGTGGAGGGGGACACAGTGA	282560	114756	AAAAACTGGACATTTTCTCT
193387	25583	CGTGTACAAAGACTGTGTAC	237974	70170	CAGTGGAGGGGGACACAGTG	282561	114757	GAAAAACTGGACATTTTCTC
193388	25584	ACGTGTACAAAGACTGTGTA	237975	70171	TCAGTGGAGGGGGACACAGT	282562	114758	GGAAAAACTGGACATTTTCT
193389	25585	GACGTGTACAAAGACTGTGT	237976	70172	TTCAGTGGAGGGGGACACAG	282563	114759	TGGAAAAACTGGACATTTTC
193390	25586	GGACGTGTACAAAGACTGTG	237977	70173	ATTCAGTGGAGGGGGACACA	282564	114760	TTGGAAAAACTGGACATTTT
193391	25587	CGGACGTGTACAAAGACTGT	237978	70174	AATTCAGTGGAGGGGGACAC	282565	114761	GTTGGAAAAACTGGACATTT
193392	25588	CCGGACGTGTACAAAGACTG	237979	70175	AAATTCAGTGGAGGGGGACA	282566	114762	AGTTGGAAAAACTGGACATT
193393	25589	GCCGGACGTGTACAAAGACT	237980	70176	AAAATTCAGTGGAGGGGGAC	282567	114763	GAGTTGGAAAAACTGGACAT
193394	25590	CGCCGGACGTGTACAAAGAC	237981	70177	AAAAATTCAGTGGAGGGGGA	282568	114764	GGAGTTGGAAAAACTGGACA
193395	25591	CCGCCGGACGTGTACAAAGA	237982	70178	GAAAAATTCAGTGGAGGGGG	282569	114765	GGGAGTTGGAAAAACTGGAC
193396	25592	GCCGCCGGACGTGTACAAAG	237983	70179	GGAAAAATTCAGTGGAGGGG	282570	114766	AGGGAGTTGGAAAAACTGGA
193397	25593	AGCCGCCGGACGTGTACAAA	237984	70180	TGGAAAAATTCAGTGGAGGG	282571	114767	TAGGGAGTTGGAAAAACTGG
193398	25594	GAGCCGCCGGACGTGTACAA	237985	70181	GTGGAAAAATTCAGTGGAGG	282572	114768	TTAGGGAGTTGGAAAAACTG
193399	25595	AGAGCCGCCGGACGTGTACA	237986	70182	GGTGGAAAAATTCAGTGGAG	282573	114769	TTTAGGGAGTTGGAAAAACT
193400	25596	CAGAGCCGCCGGACGTGTAC	237987	70183	AGGTGGAAAAATTCAGTGGA	282574	114770	GTTTAGGGAGTTGGAAAAAC
193401	25597	CCAGAGCCGCCGGACGTGTA	237988	70184	GAGGTGGAAAAATTCAGTGG	282575	114771	GGTTTAGGGAGTTGGAAAAA
193402	25598	ACCAGAGCCGCCGGACGTGT	237989	70185	GGAGGTGGAAAAATTCAGTG	282576	114772	TGGTTTAGGGAGTTGGAAAA
193403	25599	CACCAGAGCCGCCGGACGTG	237990	70186	AGGAGGTGGAAAAATTCAGT	282577	114773	ATGGTTTAGGGAGTTGGAAA
193404	25600	GCACCAGAGCCGCCGGACGT	237991	70187	GAGGAGGTGGAAAAATTCAG	282578	114774	CATGGTTTAGGGAGTTGGAA
193405	25601	GGCACCAGAGCCGCCGGACG	237992	70188	AGAGGAGGTGGAAAAATTCA	282579	114775	CCATGGTTTAGGGAGTTGGA
193406	25602	AGGCACCAGAGCCGCCGGAC	237993	70189	GAGAGGAGGTGGAAAAATTC	282580	114776	ACCATGGTTTAGGGAGTTGG
193407	25603	TAGGCACCAGAGCCGCCGGA	237994	70190	GGAGAGGAGGTGGAAAAATT	282581	114777	AACCATGGTTTAGGGAGTTG
193408	25604	ATAGGCACCAGAGCCGCCGG	237995	70191	GGGAGAGGAGGTGGAAAAAT	282582	114778	AAACCATGGTTTAGGGAGTT
193409	25605	AATAGGCACCAGAGCCGCCG	237996	70192	TGGGAGAGGAGGTGGAAAAA	282583	114779	AAAACCATGGTTTAGGGAGT
193410	25606	AAATAGGCACCAGAGCCGCC	237997	70193	GTGGGAGAGGAGGTGGAAAA	282584	114780	GAAAACCATGGTTTAGGGAG
193411	25607	AAAATAGGCACCAGAGCCGC	237998	70194	AGTGGGAGAGGAGGTGGAAA	282585	114781	AGAAAACCATGGTTTAGGGA
193412	25608	AAAAATAGGCACCAGAGCCG	237999	70195	AAGTGGGAGAGGAGGTGGAA	282586	114782	TAGAAAACCATGGTTTAGGG
193413	25609	CAAAAATAGGCACCAGAGCC	238000	70196	GAAGTGGGAGAGGAGGTGGA	282587	114783	ATAGAAAACCATGGTTTAGG
193414	25610	ACAAAAATAGGCACCAGAGC	238001	70197	GGAAGTGGGAGAGGAGGTGG	282588	114784	AATAGAAAACCATGGTTTAG
193415	25611	AACAAAAATAGGCACCAGAG	238002	70198	GGGAAGTGGGAGAGGAGGTG	282589	114785	AAATAGAAAACCATGGTTTA
193416	25612	AAACAAAAATAGGCACCAGA	238003	70199	GGGGAAGTGGGAGAGGAGGT	282590	114786	GAAATAGAAAACCATGGTTT
193417	25613	CAAACAAAAATAGGCACCAG	238004	70200	GGGGGAAGTGGGAGAGGAGG	282591	114787	TGAAATAGAAAACCATGGTT
193418	25614	ACAAACAAAAATAGGCACCA	238005	70201	TGGGGGAAGTGGGAGAGGAG	282592	114788	ATGAAATAGAAAACCATGGT
193419	25615	CACAAACAAAAATAGGCACC	238006	70202	GTGGGGGAAGTGGGAGAGGA	282593	114789	TATGAAATAGAAAACCATGG
193420	25616	ACACAAACAAAAATAGGCAC	238007	70203	AGTGGGGGAAGTGGGAGAGG	282594	114790	CTATGAAATAGAAAACCATG
193421	25617	AACACAAACAAAAATAGGCA	238008	70204	GAGTGGGGGAAGTGGGAGAG	282595	114791	ACTATGAAATAGAAAACCAT
193422	25618	AAACACAAACAAAAATAGGC	238009	70205	GGAGTGGGGGAAGTGGGAGA	282596	114792	AACTATGAAATAGAAAACCA
193423	25619	AAAACACAAACAAAAATAGG	238010	70206	GGGAGTGGGGGAAGTGGGAG	282597	114793	GAACTATGAAATAGAAAACC
193424	25620	AAAAACACAAACAAAAATAG	238011	70207	CGGGAGTGGGGGAAGTGGGA	282598	114794	AGAACTATGAAATAGAAAAC
193425	25621	GAAAAACACAAACAAAAATA	238012	70208	GCGGGAGTGGGGGAAGTGGG	282599	114795	AAGAACTATGAAATAGAAAA
193426	25622	AGAAAAACACAAACAAAAAT	238013	70209	AGCGGGAGTGGGGGAAGTGG	282600	114796	TAAGAACTATGAAATAGAAA
193427	25623	AAGAAAAACACAAACAAAAA	238014	70210	AAGCGGGAGTGGGGGAAGTG	282601	114797	CTAAGAACTATGAAATAGAA
193428	25624	AAAGAAAAACACAAACAAAA	238015	70211	AAAGCGGGAGTGGGGGAAGT	282602	114798	CCTAAGAACTATGAAATAGA
193429	25625	AAAAGAAAAACACAAACAAA	238016	70212	GAAAGCGGGAGTGGGGGAAG	282603	114799	GCCTAAGAACTATGAAATAG
193430	25626	CAAAAGAAAAACACAAACAA	238017	70213	GGAAAGCGGGAGTGGGGGAA	282604	114800	TGCCTAAGAACTATGAAATA
193431	25627	ACAAAAGAAAAACACAAACA	238018	70214	GGGAAAGCGGGAGTGGGGGA	282605	114801	TTGCCTAAGAACTATGAAAT
193432	25628	AACAAAAGAAAAACACAAAC	238019	70215	AGGGAAAGCGGGAGTGGGGG	282606	114802	TTTGCCTAAGAACTATGAAA
193433	25629	AAACAAAAGAAAAACACAAA	238020	70216	GAGGGAAAGCGGGAGTGGGG	282607	114803	ATTTGCCTAAGAACTATGAA
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193435	25631	CCAAACAAAAGAAAAACACA	238022	70218	GAGAGGGAAAGCGGGAGTGG	282609	114805	CAATTTGCCTAAGAACTATG
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193437	25633	CCCCAAACAAAAGAAAAACA	238024	70220	AGGAGAGGGAAAGCGGGAGT	282611	114807	ACCAATTTGCCTAAGAACTA
193438	25634	CCCCCAAACAAAAGAAAAAC	238025	70221	AAGGAGAGGGAAAGCGGGAG	282612	114808	TACCAATTTGCCTAAGAACT
193439	25635	CCCCCCAAACAAAAGAAAAA	238026	70222	GAAGGAGAGGGAAAGCGGGA	282613	114809	TTACCAATTTGCCTAAGAAC
193440	25636	TCCCCCCAAACAAAAGAAAA	238027	70223	AGAAGGAGAGGGAAAGCGGG	282614	114810	TTTACCAATTTGCCTAAGAA
193441	25637	ATCCCCCCAAACAAAAGAAA	238028	70224	GAGAAGGAGAGGGAAAGCGG	282615	114811	TTTTACCAATTTGCCTAAGA
193442	25638	CATCCCCCCAAACAAAAGAA	238029	70225	AGAGAAGGAGAGGGAAAGCG	282616	114812	TTTTTACCAATTTGCCTAAG
193443	25639	CCATCCCCCCAAACAAAAGA	238030	70226	GAGAGAAGGAGAGGGAAAGC	282617	114813	ATTTTTACCAATTTGCCTAA
193444	25640	TCCATCCCCCCAAACAAAAG	238031	70227	GGAGAGAAGGAGAGGGAAAG	282618	114814	GATTTTTACCAATTTGCCTA
193445	25641	ATCCATCCCCCCAAACAAAA	238032	70228	GGGAGAGAAGGAGAGGGAAA	282619	114815	TGATTTTTACCAATTTGCCT
193446	25642	AATCCATCCCCCCAAACAAA	238033	70229	GGGGAGAGAAGGAGAGGGAA	282620	114816	ATGATTTTTACCAATTTGCC
193447	25643	AAATCCATCCCCCCAAACAA	238034	70230	TGGGGAGAGAAGGAGAGGGA	282621	114817	AATGATTTTTACCAATTTGC
193448	25644	CAAATCCATCCCCCCAAACA	238035	70231	GTGGGGAGAGAAGGAGAGGG	282622	114818	AAATGATTTTTACCAATTTG
193449	25645	CCAAATCCATCCCCCCAAAC	238036	70232	AGTGGGGAGAGAAGGAGAGG	282623	114819	GAAATGATTTTTACCAATTT
193450	25646	ACCAAATCCATCCCCCCAAA	238037	70233	GAGTGGGGAGAGAAGGAGAG	282624	114820	AGAAATGATTTTTACCAATT
193451	25647	AACCAAATCCATCCCCCCAA	238038	70234	GGAGTGGGGAGAGAAGGAGA	282625	114821	GAGAAATGATTTTTACCAAT
193452	25648	AAACCAAATCCATCCCCCCA	238039	70235	TGGAGTGGGGAGAGAAGGAG	282626	114822	TGAGAAATGATTTTTACCAA
193453	25649	GAAACCAAATCCATCCCCCC	238040	70236	ATGGAGTGGGGAGAGAAGGA	282627	114823	ATGAGAAATGATTTTTACCA
193454	25650	GGAAACCAAATCCATCCCCC	238041	70237	GATGGAGTGGGGAGAGAAGG	282628	114824	GATGAGAAATGATTTTTACC
193455	25651	GGGAAACCAAATCCATCCCC	238042	70238	AGATGGAGTGGGGAGAGAAG	282629	114825	TGATGAGAAATGATTTTTAC
193456	25652	GGGGAAACCAAATCCATCCC	238043	70239	AAGATGGAGTGGGGAGAGAA	282630	114826	TTGATGAGAAATGATTTTTA
193457	25653	GGGGGAAACCAAATCCATCC	238044	70240	AAAGATGGAGTGGGGAGAGA	282631	114827	TTTGATGAGAAATGATTTTT
193458	25654	CGGGGGAAACCAAATCCATC	238045	70241	AAAAGATGGAGTGGGGAGAG	282632	114828	TTTTGATGAGAAATGATTTT
193459	25655	TCGGGGGAAACCAAATCCAT	238046	70242	AAAAAGATGGAGTGGGGAGA	282633	114829	GTTTTGATGAGAAATGATTT
193460	25656	CTCGGGGGAAACCAAATCCA	238047	70243	GAAAAAGATGGAGTGGGGAG	282634	114830	CGTTTTGATGAGAAATGATT
193461	25657	GCTCGGGGGAAACCAAATCC	238048	70244	AGAAAAAGATGGAGTGGGGA	282635	114831	GCGTTTTGATGAGAAATGAT
193462	25658	GGCTCGGGGGAAACCAAATC	238049	70245	AAGAAAAAGATGGAGTGGGG	282636	114832	AGCGTTTTGATGAGAAATGA
193463	25659	GGGCTCGGGGGAAACCAAAT	238050	70246	AAAGAAAAAGATGGAGTGGG	282637	114833	CAGCGTTTTGATGAGAAATG
193464	25660	AGGGCTCGGGGGAAACCAAA	238051	70247	GAAAGAAAAAGATGGAGTGG	282638	114834	TCAGCGTTTTGATGAGAAAT
193465	25661	GAGGGCTCGGGGGAAACCAA	238052	70248	AGAAAGAAAAAGATGGAGTG	282639	114835	ATCAGCGTTTTGATGAGAAA
193466	25662	AGAGGGCTCGGGGGAAACCA	238053	70249	GAGAAAGAAAAAGATGGAGT	282640	114836	TATCAGCGTTTTGATGAGAA
193467	25663	CAGAGGGCTCGGGGGAAACC	238054	70250	AGAGAAAGAAAAAGATGGAG	282641	114837	ATATCAGCGTTTTGATGAGA
193468	25664	ACAGAGGGCTCGGGGGAAAC	238055	70251	CAGAGAAAGAAAAAGATGGA	282642	114838	AATATCAGCGTTTTGATGAG
193469	25665	GACAGAGGGCTCGGGGGAAA	238056	70252	GCAGAGAAAGAAAAAGATGG	282643	114839	AAATATCAGCGTTTTGATGA
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193471	25667	AGGACAGAGGGCTCGGGGGA	238058	70254	CAGCAGAGAAAGAAAAAGAT	282645	114841	GAAAATATCAGCGTTTTGAT
193472	25668	GAGGACAGAGGGCTCGGGGG	238059	70255	ACAGCAGAGAAAGAAAAAGA	282646	114842	TGAAAATATCAGCGTTTTGA
193473	25669	GGAGGACAGAGGGCTCGGGG	238060	70256	AACAGCAGAGAAAGAAAAAG	282647	114843	GTGAAAATATCAGCGTTTTG
193474	25670	AGGAGGACAGAGGGCTCGGG	238061	70257	AAACAGCAGAGAAAGAAAAA	282648	114844	TGTGAAAATATCAGCGTTTT
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193477	25673	GACAGGAGGACAGAGGGCTC	238064	70260	GAGAAACAGCAGAGAAAGAA	282651	114847	AGGTGTGAAAATATCAGCGT
193478	25674	TGACAGGAGGACAGAGGGCT	238065	70261	CGAGAAACAGCAGAGAAAGA	282652	114848	GAGGTGTGAAAATATCAGCG
193479	25675	GTGACAGGAGGACAGAGGGC	238066	70262	ACGAGAAACAGCAGAGAAAG	282653	114849	GGAGGTGTGAAAATATCAGC
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193481	25677	AGGTGACAGGAGGACAGAGG	238068	70264	GGACGAGAAACAGCAGAGAA	282655	114851	AGGGAGGTGTGAAAATATCA
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193484	25680	GCCAGGTGACAGGAGGACAG	238071	70267	GAGGGACGAGAAACAGCAGA	282658	114854	ACCAGGGAGGTGTGAAAATA
193485	25681	AGCCAGGTGACAGGAGGACA	238072	70268	GGAGGGACGAGAAACAGCAG	282659	114855	CACCAGGGAGGTGTGAAAAT
193486	25682	CAGCCAGGTGACAGGAGGAC	238073	70269	GGGAGGGACGAGAAACAGCA	282660	114856	ACACCAGGGAGGTGTGAAAA
193487	25683	CCAGCCAGGTGACAGGAGGA	238074	70270	AGGGAGGGACGAGAAACAGC	282661	114857	GACACCAGGGAGGTGTGAAA
193488	25684	ACCAGCCAGGTGACAGGAGG	238075	70271	GAGGGAGGGACGAGAAACAG	282662	114858	AGACACCAGGGAGGTGTGAA
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193490	25686	GCACCAGCCAGGTGACAGGA	238077	70273	AGGAGGGAGGGACGAGAAAC	282664	114860	GCAGACACCAGGGAGGTGTG
193491	25687	AGCACCAGCCAGGTGACAGG	238078	70274	GAGGAGGGAGGGACGAGAAA	282665	114861	TGCAGACACCAGGGAGGTGT
193492	25688	GAGCACCAGCCAGGTGACAG	238079	70275	AGAGGAGGGAGGGACGAGAA	282666	114862	CTGCAGACACCAGGGAGGTG
193493	25689	CGAGCACCAGCCAGGTGACA	238080	70276	GAGAGGAGGGAGGGACGAGA	282667	114863	TCTGCAGACACCAGGGAGGT
193494	25690	CCGAGCACCAGCCAGGTGAC	238081	70277	GGAGAGGAGGGAGGGACGAG	282668	114864	TTCTGCAGACACCAGGGAGG
193495	25691	GCCGAGCACCAGCCAGGTGA	238082	70278	TGGAGAGGAGGGAGGGACGA	282669	114865	TTTCTGCAGACACCAGGGAG
193496	25692	TGCCGAGCACCAGCCAGGTG	238083	70279	ATGGAGAGGAGGGAGGGACG	282670	114866	CTTTCTGCAGACACCAGGGA
193497	25693	TTGCCGAGCACCAGCCAGGT	238084	70280	GATGGAGAGGAGGGAGGGAC	282671	114867	TCTTTCTGCAGACACCAGGG
193498	25694	ATTGCCGAGCACCAGCCAGG	238085	70281	GGATGGAGAGGAGGGAGGGA	282672	114868	TTCTTTCTGCAGACACCAGG
193499	25695	CATTGCCGAGCACCAGCCAG	238086	70282	GGGATGGAGAGGAGGGAGGG	282673	114869	GTTCTTTCTGCAGACACCAG
193500	25696	ACATTGCCGAGCACCAGCCA	238087	70283	TGGGATGGAGAGGAGGGAGG	282674	114870	GGTTCTTTCTGCAGACACCA
193501	25697	AACATTGCCGAGCACCAGCC	238088	70284	GTGGGATGGAGAGGAGGGAG	282675	114871	AGGTTCTTTCTGCAGACACC
193502	25698	CAACATTGCCGAGCACCAGC	238089	70285	TGTGGGATGGAGAGGAGGGA	282676	114872	AAGGTTCTTTCTGCAGACAC
193503	25699	TCAACATTGCCGAGCACCAG	238090	70286	TTGTGGGATGGAGAGGAGGG	282677	114873	GAAGGTTCTTTCTGCAGACA
193504	25700	GTCAACATTGCCGAGCACCA	238091	70287	GTTGTGGGATGGAGAGGAGG	282678	114874	GGAAGGTTCTTTCTGCAGAC
193505	25701	GGTCAACATTGCCGAGCACC	238092	70288	TGTTGTGGGATGGAGAGGAG	282679	114875	TGGAAGGTTCTTTCTGCAGA
193506	25702	TGGTCAACATTGCCGAGCAC	238093	70289	GTGTTGTGGGATGGAGAGGA	282680	114876	CTGGAAGGTTCTTTCTGCAG

193507	25703	CTGGTCAACATTGCCGAGCA	238094	70290	AGTGTTGTGGGATGGAGAGG	282681	114877	TCTGGAAGGTTCTTTCTGCA
193508	25704	GCTGGTCAACATTGCCGAGC	238095	70291	CAGTGTTGTGGGATGGAGAG	282682	114878	TTCTGGAAGGTTCTTTCTGC
193509	25705	AGCTGGTCAACATTGCCGAG	238096	70292	GCAGTGTTGTGGGATGGAGA	282683	114879	TTTCTGGAAGGTTCTTTCTG
193510	25706	CAGCTGGTCAACATTGCCGA	238097	70293	GGCAGTGTTGTGGGATGGAG	282684	114880	ATTTCTGGAAGGTTCTTTCT
193511	25707	GCAGCTGGTCAACATTGCCG	238098	70294	AGGCAGTGTTGTGGGATGGA	282685	114881	CATTTCTGGAAGGTTCTTTC
193512	25708	GGCAGCTGGTCAACATTGCC	238099	70295	TAGGCAGTGTTGTGGGATGG	282686	114882	GCATTTCTGGAAGGTTCTTT
193513	25709	AGGCAGCTGGTCAACATTGC	238100	70296	GTAGGCAGTGTTGTGGGATG	282687	114883	TGCATTTCTGGAAGGTTCTT
193514	25710	CAGGCAGCTGGTCAACATTG	238101	70297	GGTAGGCAGTGTTGTGGGAT	282688	114884	CTGCATTTCTGGAAGGTTCT
193515	25711	CCAGGCAGCTGGTCAACATT	238102	70298	GGGTAGGCAGTGTTGTGGGA	282689	114885	ACTGCATTTCTGGAAGGTTC
193516	25712	GCCAGGCAGCTGGTCAACAT	238103	70299	AGGGTAGGCAGTGTTGTGGG	282690	114886	GACTGCATTTCTGGAAGGTT
193517	25713	AGCCAGGCAGCTGGTCAACA	238104	70300	CAGGGTAGGCAGTGTTGTGG	282691	114887	CGACTGCATTTCTGGAAGGT
193518	25714	CAGCCAGGCAGCTGGTCAAC	238105	70301	ACAGGGTAGGCAGTGTTGTG	282692	114888	ACGACTGCATTTCTGGAAGG
193519	25715	CCAGCCAGGCAGCTGGTCAA	238106	70302	GACAGGGTAGGCAGTGTTGT	282693	114889	CACGACTGCATTTCTGGAAG
193520	25716	TCCAGCCAGGCAGCTGGTCA	238107	70303	GGACAGGGTAGGCAGTGTTG	282694	114890	CCACGACTGCATTTCTGGAA
193521	25717	CTCCAGCCAGGCAGCTGGTC	238108	70304	GGGACAGGGTAGGCAGTGTT	282695	114891	CCCACGACTGCATTTCTGGA
193522	25718	ACTCCAGCCAGGCAGCTGGT	238109	70305	AGGGACAGGGTAGGCAGTGT	282696	114892	TCCCACGACTGCATTTCTGG
193523	25719	AACTCCAGCCAGGCAGCTGG	238110	70306	CAGGGACAGGGTAGGCAGTG	282697	114893	CTCCCACGACTGCATTTCTG
193524	25720	CAACTCCAGCCAGGCAGCTG	238111	70307	GCAGGGACAGGGTAGGCAGT	282698	114894	TCTCCCACGACTGCATTTCT
193525	25721	CCAACTCCAGCCAGGCAGCT	238112	70308	GGCAGGGACAGGGTAGGCAG	282699	114895	GTCTCCCACGACTGCATTTC
193526	25722	GCCAACTCCAGCCAGGCAGC	238113	70309	GGGCAGGGACAGGGTAGGCA	282700	114896	GGTCTCCCACGACTGCATTT
193527	25723	TGCCAACTCCAGCCAGGCAG	238114	70310	GGGGCAGGGACAGGGTAGGC	282701	114897	GGGTCTCCCACGACTGCATT
193528	25724	CTGCCAACTCCAGCCAGGCA	238115	70311	TGGGGCAGGGACAGGGTAGG	282702	114898	TGGGTCTCCCACGACTGCAT
193529	25725	ACTGCCAACTCCAGCCAGGC	238116	70312	GTGGGGCAGGGACAGGGTAG	282703	114899	ATGGGTCTCCCACGACTGCA
193530	25726	CACTGCCAACTCCAGCCAGG	238117	70313	GGTGGGGCAGGGACAGGGTA	282704	114900	GATGGGTCTCCCACGACTGC
193531	25727	CCACTGCCAACTCCAGCCAG	238118	70314	GGGTGGGGCAGGGACAGGGT	282705	114901	GGATGGGTCTCCCACGACTG
193532	25728	GCCACTGCCAACTCCAGCCA	238119	70315	AGGGTGGGGCAGGGACAGGG	282706	114902	TGGATGGGTCTCCCACGACT
193533	25729	AGCCACTGCCAACTCCAGCC	238120	70316	CAGGGTGGGGCAGGGACAGG	282707	114903	CTGGATGGGTCTCCCACGAC
193534	25730	TAGCCACTGCCAACTCCAGC	238121	70317	CCAGGGTGGGGCAGGGACAG	282708	114904	CCTGGATGGGTCTCCCACGA
193535	25731	TTAGCCACTGCCAACTCCAG	238122	70318	ACCAGGGTGGGGCAGGGACA	282709	114905	GCCTGGATGGGTCTCCCACG
193536	25732	CTTAGCCACTGCCAACTCCA	238123	70319	CACCAGGGTGGGGCAGGGAC	282710	114906	GGCCTGGATGGGTCTCCCAC
193537	25733	CCTTAGCCACTGCCAACTCC	238124	70320	GCACCAGGGTGGGGCAGGGA	282711	114907	TGGCCTGGATGGGTCTCCCA
193538	25734	GCCTTAGCCACTGCCAACTC	238125	70321	AGCACCAGGGTGGGGCAGGG	282712	114908	GTGGCCTGGATGGGTCTCCC
193539	25735	AGCCTTAGCCACTGCCAACT	238126	70322	GAGCACCAGGGTGGGGCAGG	282713	114909	GGTGGCCTGGATGGGTCTCC
193540	25736	CAGCCTTAGCCACTGCCAAC	238127	70323	TGAGCACCAGGGTGGGGCAG	282714	114910	GGGTGGCCTGGATGGGTCTC
193541	25737	ACAGCCTTAGCCACTGCCAA	238128	70324	CTGAGCACCAGGGTGGGGCA	282715	114911	GGGGTGGCCTGGATGGGTCT
193542	25738	CACAGCCTTAGCCACTGCCA	238129	70325	CCTGAGCACCAGGGTGGGGC	282716	114912	AGGGGTGGCCTGGATGGGTC
193543	25739	TCACAGCCTTAGCCACTGCC	238130	70326	TCCTGAGCACCAGGGTGGGG	282717	114913	CAGGGGTGGCCTGGATGGGT
193544	25740	GTCACAGCCTTAGCCACTGC	238131	70327	ATCCTGAGCACCAGGGTGGG	282718	114914	GCAGGGGTGGCCTGGATGGG
193545	25741	TGTCACAGCCTTAGCCACTG	238132	70328	CATCCTGAGCACCAGGGTGG	282719	114915	AGCAGGGGTGGCCTGGATGG
193546	25742	CTGTCACAGCCTTAGCCACT	238133	70329	ACATCCTGAGCACCAGGGTG	282720	114916	AAGCAGGGGTGGCCTGGATG
193547	25743	GCTGTCACAGCCTTAGCCAC	238134	70330	CACATCCTGAGCACCAGGGT	282721	114917	TAAGCAGGGGTGGCCTGGAT
193548	25744	AGCTGTCACAGCCTTAGCCA	238135	70331	ACACATCCTGAGCACCAGGG	282722	114918	ATAAGCAGGGGTGGCCTGGA
193549	25745	TAGCTGTCACAGCCTTAGCC	238136	70332	CACACATCCTGAGCACCAGG	282723	114919	CATAAGCAGGGGTGGCCTGG
193550	25746	TTAGCTGTCACAGCCTTAGC	238137	70333	TCACACATCCTGAGCACCAG	282724	114920	CCATAAGCAGGGGTGGCCTG
193551	25747	GTTAGCTGTCACAGCCTTAG	238138	70334	TTCACACATCCTGAGCACCA	282725	114921	TCCATAAGCAGGGGTGGCCT
193552	25748	TGTTAGCTGTCACAGCCTTA	238139	70335	CTTCACACATCCTGAGCACC	282726	114922	TTCCATAAGCAGGGGTGGCC
193553	25749	ATGTTAGCTGTCACAGCCTT	238140	70336	ACTTCACACATCCTGAGCAC	282727	114923	CTTCCATAAGCAGGGGTGGC
193554	25750	CATGTTAGCTGTCACAGCCT	238141	70337	CACTTCACACATCCTGAGCA	282728	114924	TCTTCCATAAGCAGGGGTGG
193555	25751	ACATGTTAGCTGTCACAGCC	238142	70338	TCACTTCACACATCCTGAGC	282729	114925	CTCTTCCATAAGCAGGGGTG
193556	25752	AACATGTTAGCTGTCACAGC	238143	70339	CTCACTTCACACATCCTGAG	282730	114926	GCTCTTCCATAAGCAGGGGT
193557	25753	GAACATGTTAGCTGTCACAG	238144	70340	CCTCACTTCACACATCCTGA	282731	114927	AGCTCTTCCATAAGCAGGGG
193558	25754	GGAACATGTTAGCTGTCACA	238145	70341	CCCTCACTTCACACATCCTG	282732	114928	CAGCTCTTCCATAAGCAGGG
193559	25755	AGGAACATGTTAGCTGTCAC	238146	70342	CCCCTCACTTCACACATCCT	282733	114929	TCAGCTCTTCCATAAGCAGG
193560	25756	CAGGAACATGTTAGCTGTCA	238147	70343	ACCCCTCACTTCACACATCC	282734	114930	CTCAGCTCTTCCATAAGCAG
193561	25757	TCAGGAACATGTTAGCTGTC	238148	70344	CACCCCTCACTTCACACATC	282735	114931	TCTCAGCTCTTCCATAAGCA
193562	25758	CTCAGGAACATGTTAGCTGT	238149	70345	CCACCCCTCACTTCACACAT	282736	114932	TTCTCAGCTCTTCCATAAGC
193563	25759	ACTCAGGAACATGTTAGCTG	238150	70346	ACCACCCCTCACTTCACACA	282737	114933	TTTCTCAGCTCTTCCATAAG
193564	25760	GACTCAGGAACATGTTAGCT	238151	70347	TACCACCCCTCACTTCACAC	282738	114934	TTTTCTCAGCTCTTCCATAA
193565	25761	GGACTCAGGAACATGTTAGC	238152	70348	CTACCACCCCTCACTTCACA	282739	114935	TTTTTCTCAGCTCTTCCATA
193566	25762	AGGACTCAGGAACATGTTAG	238153	70349	GCTACCACCCCTCACTTCAC	282740	114936	CTTTTTCTCAGCTCTTCCAT
193567	25763	GAGGACTCAGGAACATGTTA	238154	70350	GGCTACCACCCCTCACTTCA	282741	114937	GCTTTTTCTCAGCTCTTCCA
193568	25764	AGAGGACTCAGGAACATGTT	238155	70351	GGGCTACCACCCCTCACTTC	282742	114938	GGCTTTTTCTCAGCTCTTCC
193569	25765	GAGAGGACTCAGGAACATGT	238156	70352	GGGGCTACCACCCCTCACTT	282743	114939	GGGCTTTTTCTCAGCTCTTC
193570	25766	TGAGAGGACTCAGGAACATG	238157	70353	GGGGGCTACCACCCCTCACT	282744	114940	GGGGCTTTTTCTCAGCTCTT
193571	25767	ATGAGAGGACTCAGGAACAT	238158	70354	TGGGGGCTACCACCCCTCAC	282745	114941	TGGGGCTTTTTCTCAGCTCT
193572	25768	AATGAGAGGACTCAGGAACA	238159	70355	TTGGGGGCTACCACCCCTCA	282746	114942	GTGGGGCTTTTTCTCAGCTC
193573	25769	AAATGAGAGGACTCAGGAAC	238160	70356	CTTGGGGGCTACCACCCCTC	282747	114943	CGTGGGGCTTTTTCTCAGCT
193574	25770	GAAATGAGAGGACTCAGGAA	238161	70357	TCTTGGGGGCTACCACCCCT	282748	114944	CCGTGGGGCTTTTTCTCAGC
193575	25771	AGAAATGAGAGGACTCAGGA	238162	70358	GTCTTGGGGGCTACCACCCC	282749	114945	CCCGTGGGGCTTTTTCTCAG
193576	25772	AAGAAATGAGAGGACTCAGG	238163	70359	GGTCTTGGGGGCTACCACCC	282750	114946	TCCCGTGGGGCTTTTTCTCA
193577	25773	GAAGAAATGAGAGGACTCAG	238164	70360	AGGTCTTGGGGGCTACCACC	282751	114947	CTCCCGTGGGGCTTTTTCTC
193578	25774	TGAAGAAATGAGAGGACTCA	238165	70361	GAGGTCTTGGGGGCTACCAC	282752	114948	GCTCCCGTGGGGCTTTTTCT

193579	25775	GTGAAGAAATGAGAGGACTC	238166	70362	TGAGGTCTTGGGGGCTACCA	282753	114949	TGCTCCCGTGGGGCTTTTTC
193580	25776	GGTGAAGAAATGAGAGGACT	238167	70363	TTGAGGTCTTGGGGGCTACC	282754	114950	ATGCTCCCGTGGGGCTTTTT
193581	25777	TGGTGAAGAAATGAGAGGAC	238168	70364	GTTGAGGTCTTGGGGGCTAC	282755	114951	AATGCTCCCGTGGGGCTTTT
193582	25778	ATGGTGAAGAAATGAGAGGA	238169	70365	GGTTGAGGTCTTGGGGGCTA	282756	114952	AAATGCTCCCGTGGGGCTTT
193583	25779	TATGGTGAAGAAATGAGAGG	238170	70366	GGGTTGAGGTCTTGGGGGCT	282757	114953	CAAATGCTCCCGTGGGGCTT
193584	25780	TTATGGTGAAGAAATGAGAG	238171	70367	GGGGTTGAGGTCTTGGGGGC	282758	114954	GCAAATGCTCCCGTGGGGCT
193585	25781	ATTATGGTGAAGAAATGAGA	238172	70368	CGGGGTTGAGGTCTTGGGGG	282759	114955	AGCAAATGCTCCCGTGGGGC
193586	25782	CATTATGGTGAAGAAATGAG	238173	70369	TCGGGGTTGAGGTCTTGGGG	282760	114956	GAGCAAATGCTCCCGTGGGG
193587	25783	GCATTATGGTGAAGAAATGA	238174	70370	TTCGGGGTTGAGGTCTTGGG	282761	114957	TGAGCAAATGCTCCCGTGGG
193588	25784	GGCATTATGGTGAAGAAATG	238175	70371	CTTCGGGGTTGAGGTCTTGG	282762	114958	CTGAGCAAATGCTCCCGTGG
193589	25785	GGGCATTATGGTGAAGAAAT	238176	70372	CCTTCGGGGTTGAGGTCTTG	282763	114959	GCTGAGCAAATGCTCCCGTG
193590	25786	AGGGCATTATGGTGAAGAAA	238177	70373	ACCTTCGGGGTTGAGGTCTT	282764	114960	AGCTGAGCAAATGCTCCCGT
193591	25787	CAGGGCATTATGGTGAAGAA	238178	70374	AACCTTCGGGGTTGAGGTCT	282765	114961	AAGCTGAGCAAATGCTCCCG
193592	25788	ACAGGGCATTATGGTGAAGA	238179	70375	TAACCTTCGGGGTTGAGGTC	282766	114962	GAAGCTGAGCAAATGCTCCC
193593	25789	AACAGGGCATTATGGTGAAG	238180	70376	CTAACCTTCGGGGTTGAGGT	282767	114963	GGAAGCTGAGCAAATGCTCC
193594	25790	CAACAGGGCATTATGGTGAA	238181	70377	GCTAACCTTCGGGGTTGAGG	282768	114964	CGGAAGCTGAGCAAATGCTC
193595	25791	TCAACAGGGCATTATGGTGA	238182	70378	GGCTAACCTTCGGGGTTGAG	282769	114965	ACGGAAGCTGAGCAAATGCT
193596	25792	CTCAACAGGGCATTATGGTG	238183	70379	AGGCTAACCTTCGGGGTTGA	282770	114966	AACGGAAGCTGAGCAAATGC
193597	25793	ACTCAACAGGGCATTATGGT	238184	70380	CAGGCTAACCTTCGGGGTTG	282771	114967	TAACGGAAGCTGAGCAAATG
193598	25794	AACTCAACAGGGCATTATGG	238185	70381	ACAGGCTAACCTTCGGGGTT	282772	114968	GTAACGGAAGCTGAGCAAAT
193599	25795	AAACTCAACAGGGCATTATG	238186	70382	AACAGGCTAACCTTCGGGGT	282773	114969	CGTAACGGAAGCTGAGCAAA
193600	25796	CAAACTCAACAGGGCATTAT	238187	70383	CAACAGGCTAACCTTCGGGG	282774	114970	GCGTAACGGAAGCTGAGCAA
193601	25797	GCAAACTCAACAGGGCATTA	238188	70384	TCAACAGGCTAACCTTCGGG	282775	114971	TGCGTAACGGAAGCTGAGCA
193602	25798	TGCAAACTCAACAGGGCATT	238189	70385	TTCAACAGGCTAACCTTCGG	282776	114972	GTGCGTAACGGAAGCTGAGC
193603	25799	CTGCAAACTCAACAGGGCAT	238190	70386	TTTCAACAGGCTAACCTTCG	282777	114973	GGTGCGTAACGGAAGCTGAG
193604	25800	TCTGCAAACTCAACAGGGCA	238191	70387	GTTTCAACAGGCTAACCTTC	282778	114974	AGGTGCGTAACGGAAGCTGA
193605	25801	ATCTGCAAACTCAACAGGGC	238192	70388	GGTTTCAACAGGCTAACCTT	282779	114975	TAGGTGCGTAACGGAAGCTG
193606	25802	TATCTGCAAACTCAACAGGG	238193	70389	TGGTTTCAACAGGCTAACCT	282780	114976	CTAGGTGCGTAACGGAAGCT
193607	25803	GTATCTGCAAACTCAACAGG	238194	70390	GTGGTTTCAACAGGCTAACC	282781	114977	ACTAGGTGCGTAACGGAAGC
193608	25804	AGTATCTGCAAACTCAACAG	238195	70391	AGTGGTTTCAACAGGCTAAC	282782	114978	CACTAGGTGCGTAACGGAAG
193609	25805	CAGTATCTGCAAACTCAACA	238196	70392	AAGTGGTTTCAACAGGCTAA	282783	114979	CCACTAGGTGCGTAACGGAA
193610	25806	ACAGTATCTGCAAACTCAAC	238197	70393	AAAGTGGTTTCAACAGGCTA	282784	114980	GCCACTAGGTGCGTAACGGA
193611	25807	GACAGTATCTGCAAACTCAA	238198	70394	GAAAGTGGTTTCAACAGGCT	282785	114981	TGCCACTAGGTGCGTAACGG
193612	25808	AGACAGTATCTGCAAACTCA	238199	70395	AGAAAGTGGTTTCAACAGGC	282786	114982	ATGCCACTAGGTGCGTAACG
193613	25809	GAGACAGTATCTGCAAACTC	238200	70396	GAGAAAGTGGTTTCAACAGG	282787	114983	AATGCCACTAGGTGCGTAAC
193614	25810	AGAGACAGTATCTGCAAACT	238201	70397	GGAGAAAGTGGTTTCAACAG	282788	114984	CAATGCCACTAGGTGCGTAA
193615	25811	CAGAGACAGTATCTGCAAAC	238202	70398	GGGAGAAAGTGGTTTCAACA	282789	114985	ACAATGCCACTAGGTGCGTA
193616	25812	ACAGAGACAGTATCTGCAAA	238203	70399	TGGGAGAAAGTGGTTTCAAC	282790	114986	CACAATGCCACTAGGTGCGT
193617	25813	AACAGAGACAGTATCTGCAA	238204	70400	CTGGGAGAAAGTGGTTTCAA	282791	114987	CCACAATGCCACTAGGTGCG
193618	25814	AAACAGAGACAGTATCTGCA	238205	70401	GCTGGGAGAAAGTGGTTTCA	282792	114988	CCCACAATGCCACTAGGTGC
193619	25815	AAAACAGAGACAGTATCTGC	238206	70402	AGCTGGGAGAAAGTGGTTTC	282793	114989	ACCCACAATGCCACTAGGTG
193620	25816	AAAAACAGAGACAGTATCTG	238207	70403	CAGCTGGGAGAAAGTGGTTT	282794	114990	CACCCACAATGCCACTAGGT
193621	25817	TAAAAACAGAGACAGTATCT	238208	70404	GCAGCTGGGAGAAAGTGGTT	282795	114991	CCACCCACAATGCCACTAGG
193622	25818	ATAAAAACAGAGACAGTATC	238209	70405	GGCAGCTGGGAGAAAGTGGT	282796	114992	CCCACCCACAATGCCACTAG
193623	25819	GATAAAAACAGAGACAGTAT	238210	70406	GGGCAGCTGGGAGAAAGTGG	282797	114993	TCCCACCCACAATGCCACTA
193624	25820	AGATAAAAACAGAGACAGTA	238211	70407	GGGGCAGCTGGGAGAAAGTG	282798	114994	CTCCCACCCACAATGCCACT
193625	25821	GAGATAAAAACAGAGACAGT	238212	70408	GGGGGCAGCTGGGAGAAAGT	282799	114995	TCTCCCACCCACAATGCCAC
193626	25822	GGAGATAAAAACAGAGACAG	238213	70409	GGGGGGCAGCTGGGAGAAAG	282800	114996	CTCTCCCACCCACAATGCCA
193627	25823	GGGAGATAAAAACAGAGACA	238214	70410	AGGGGGGCAGCTGGGAGAAA	282801	114997	CCTCTCCCACCCACAATGCC
193628	25824	CGGGAGATAAAAACAGAGAC	238215	70411	CAGGGGGGCAGCTGGGAGAA	282802	114998	CCCTCTCCCACCCACAATGC
193629	25825	CCGGGAGATAAAAACAGAGA	238216	70412	CCAGGGGGGCAGCTGGGAGA	282803	114999	GCCCTCTCCCACCCACAATG
193630	25826	CCCGGGAGATAAAAACAGAG	238217	70413	GCCAGGGGGGCAGCTGGGAG	282804	115000	AGCCCTCTCCCACCCACAAT
193631	25827	CCCCGGGAGATAAAAACAGA	238218	70414	TGCCAGGGGGGCAGCTGGGA	282805	115001	CAGCCCTCTCCCACCCACAA
193632	25828	TCCCCGGGAGATAAAAACAG	238219	70415	CTGCCAGGGGGGCAGCTGGG	282806	115002	CCAGCCCTCTCCCACCCACA
193633	25829	TTCCCCGGGAGATAAAAACA	238220	70416	ACTGCCAGGGGGGCAGCTGG	282807	115003	ACCAGCCCTCTCCCACCCAC
193634	25830	TTTCCCCGGGAGATAAAAAC	238221	70417	AACTGCCAGGGGGGCAGCTG	282808	115004	CACCAGCCCTCTCCCACCCA
193635	25831	GTTTCCCCGGGAGATAAAAA	238222	70418	CAACTGCCAGGGGGGCAGCT	282809	115005	CCACCAGCCCTCTCCCACCC
193636	25832	AGTTTCCCCGGGAGATAAAA	238223	70419	CCAACTGCCAGGGGGGCAGC	282810	115006	CCCACCAGCCCTCTCCCACC
193637	25833	CAGTTTCCCCGGGAGATAAA	238224	70420	ACCAACTGCCAGGGGGGCAG	282811	115007	ACCCACCAGCCCTCTCCCAC
193638	25834	TCAGTTTCCCCGGGAGATAA	238225	70421	CACCAACTGCCAGGGGGGCA	282812	115008	CACCCACCAGCCCTCTCCCA
193639	25835	CTCAGTTTCCCCGGGAGATA	238226	70422	GCACCAACTGCCAGGGGGGC	282813	115009	CCACCCACCAGCCCTCTCCC
193640	25836	CCTCAGTTTCCCCGGGAGAT	238227	70423	AGCACCAACTGCCAGGGGGG	282814	115010	TCCACCCACCAGCCCTCTCC
193641	25837	GCCTCAGTTTCCCCGGGAGA	238228	70424	CAGCACCAACTGCCAGGGGG	282815	115011	ATCCACCCACCAGCCCTCTC
193642	25838	AGCCTCAGTTTCCCCGGGAG	238229	70425	GCAGCACCAACTGCCAGGGG	282816	115012	CATCCACCCACCAGCCCTCT
193643	25839	GAGCCTCAGTTTCCCCGGGA	238230	70426	AGCAGCACCAACTGCCAGGG	282817	115013	CCATCCACCCACCAGCCCTC
193644	25840	TGAGCCTCAGTTTCCCCGGG	238231	70427	CAGCAGCACCAACTGCCAGG	282818	115014	TCCATCCACCCACCAGCCCT
193645	25841	CTGAGCCTCAGTTTCCCCGG	238232	70428	CCAGCAGCACCAACTGCCAG	282819	115015	TTCCATCCACCCACCAGCCC
193646	25842	TCTGAGCCTCAGTTTCCCCG	238233	70429	CCCAGCAGCACCAACTGCCA	282820	115016	CTTCCATCCACCCACCAGCC
193647	25843	CTCTGAGCCTCAGTTTCCCC	238234	70430	CCCCAGCAGCACCAACTGCC	282821	115017	CCTTCCATCCACCCACCAGC
193648	25844	ACTCTGAGCCTCAGTTTCCC	238235	70431	CCCCCAGCAGCACCAACTGC	282822	115018	TCCTTCCATCCACCCACCAG
193649	25845	CACTCTGAGCCTCAGTTTCC	238236	70432	TCCCCCAGCAGCACCAACTG	282823	115019	CTCCTTCCATCCACCCACCA
193650	25846	CCACTCTGAGCCTCAGTTTC	238237	70433	TTCCCCCAGCAGCACCAACT	282824	115020	TCTCCTTCCATCCACCCACC

193651	25847	GCCACTCTGAGCCTCAGTTT	238238	70434	TTTCCCCCAGCAGCACCAAC	282825	115021	TTCTCCTTCCATCCACCCAC
193652	25848	AGCCACTCTGAGCCTCAGTT	238239	70435	GTTTCCCCCAGCAGCACCAA	282826	115022	CTTCTCCTTCCATCCACCCA
193653	25849	TAGCCACTCTGAGCCTCAGT	238240	70436	AGTTTCCCCCAGCAGCACCA	282827	115023	CCTTCTCCTTCCATCCACCC
193654	25850	CTAGCCACTCTGAGCCTCAG	238241	70437	CAGTTTCCCCCAGCAGCACC	282828	115024	GCCTTCTCCTTCCATCCACC
193655	25851	CCTAGCCACTCTGAGCCTCA	238242	70438	CCAGTTTCCCCCAGCAGCAC	282829	115025	TGCCTTCTCCTTCCATCCAC
193656	25852	GCCTAGCCACTCTGAGCCTC	238243	70439	CCCAGTTTCCCCCAGCAGCA	282830	115026	GTGCCTTCTCCTTCCATCCA
193657	25853	GGCCTAGCCACTCTGAGCCT	238244	70440	TCCCAGTTTCCCCCAGCAGC	282831	115027	TGTGCCTTCTCCTTCCATCC
193658	25854	TGGCCTAGCCACTCTGAGCC	238245	70441	ATCCCAGTTTCCCCCAGCAG	282832	115028	CTGTGCCTTCTCCTTCCATC
193659	25855	GTGGCCTAGCCACTCTGAGC	238246	70442	AATCCCAGTTTCCCCCAGCA	282833	115029	GCTGTGCCTTCTCCTTCCAT
193660	25856	GGTGGCCTAGCCACTCTGAG	238247	70443	CAATCCCAGTTTCCCCCAGC	282834	115030	GGCTGTGCCTTCTCCTTCCA
193661	25857	AGGTGGCCTAGCCACTCTGA	238248	70444	CCAATCCCAGTTTCCCCCAG	282835	115031	GGGCTGTGCCTTCTCCTTCC
193662	25858	AAGGTGGCCTAGCCACTCTG	238249	70445	CCCAATCCCAGTTTCCCCCA	282836	115032	GGGGCTGTGCCTTCTCCTTC
193663	25859	GAAGGTGGCCTAGCCACTCT	238250	70446	CCCCAATCCCAGTTTCCCCC	282837	115033	GGGGGCTGTGCCTTCTCCTT
193664	25860	GGAAGGTGGCCTAGCCACTC	238251	70447	CCCCCAATCCCAGTTTCCCC	282838	115034	GGGGGGCTGTGCCTTCTCCT
193665	25861	GGGAAGGTGGCCTAGCCACT	238252	70448	GCCCCCAATCCCAGTTTCCC	282839	115035	GGGGGGGCTGTGCCTTCTCC
193666	25862	TGGGAAGGTGGCCTAGCCAC	238253	70449	GGCCCCCAATCCCAGTTTCC	282840	115036	AGGGGGGGCTGTGCCTTCTC
193667	25863	ATGGGAAGGTGGCCTAGCCA	238254	70450	TGGCCCCCAATCCCAGTTTC	282841	115037	AAGGGGGGGCTGTGCCTTCT
193668	25864	CATGGGAAGGTGGCCTAGCC	238255	70451	CTGGCCCCCAATCCCAGTTT	282842	115038	CAAGGGGGGGCTGTGCCTTC
193669	25865	CCATGGGAAGGTGGCCTAGC	238256	70452	TCTGGCCCCCAATCCCAGTT	282843	115039	GCAAGGGGGGGCTGTGCCTT
193670	25866	ACCATGGGAAGGTGGCCTAG	238257	70453	ATCTGGCCCCCAATCCCAGT	282844	115040	TGCAAGGGGGGGCTGTGCCT
193671	25867	GACCATGGGAAGGTGGCCTA	238258	70454	AATCTGGCCCCCAATCCCAG	282845	115041	CTGCAAGGGGGGGCTGTGCC
193672	25868	GGACCATGGGAAGGTGGCCT	238259	70455	AAATCTGGCCCCCAATCCCA	282846	115042	CCTGCAAGGGGGGGCTGTGC
193673	25869	GGGACCATGGGAAGGTGGCC	238260	70456	AAAATCTGGCCCCCAATCCC	282847	115043	CCCTGCAAGGGGGGGCTGTG
193674	25870	AGGGACCATGGGAAGGTGGC	238261	70457	CAAAATCTGGCCCCCAATCC	282848	115044	TCCCTGCAAGGGGGGGCTGT
193675	25871	GAGGGACCATGGGAAGGTGG	238262	70458	GCAAAATCTGGCCCCCAATC	282849	115045	GTCCCTGCAAGGGGGGGCTG
193676	25872	TGAGGGACCATGGGAAGGTG	238263	70459	GGCAAAATCTGGCCCCCAAT	282850	115046	TGTCCCTGCAAGGGGGGGCT
193677	25873	CTGAGGGACCATGGGAAGGT	238264	70460	AGGCAAAATCTGGCCCCCAA	282851	115047	CTGTCCCTGCAAGGGGGGGC
193678	25874	GCTGAGGGACCATGGGAAGG	238265	70461	GAGGCAAAATCTGGCCCCCA	282852	115048	TCTGTCCCTGCAAGGGGGGG
193679	25875	AGCTGAGGGACCATGGGAAG	238266	70462	AGAGGCAAAATCTGGCCCCC	282853	115049	CTCTGTCCCTGCAAGGGGGG
193680	25876	GAGCTGAGGGACCATGGGAA	238267	70463	AAGAGGCAAAATCTGGCCCC	282854	115050	GCTCTGTCCCTGCAAGGGGG
193681	25877	TGAGCTGAGGGACCATGGGA	238268	70464	AAAGAGGCAAAATCTGGCCC	282855	115051	GGCTCTGTCCCTGCAAGGGG
193682	25878	ATGAGCTGAGGGACCATGGG	238269	70465	AAAAGAGGCAAAATCTGGCC	282856	115052	GGGCTCTGTCCCTGCAAGGG
193683	25879	CATGAGCTGAGGGACCATGG	238270	70466	GAAAAGAGGCAAAATCTGGC	282857	115053	AGGGCTCTGTCCCTGCAAGG
193684	25880	TCATGAGCTGAGGGACCATG	238271	70467	GGAAAAGAGGCAAAATCTGG	282858	115054	GAGGGCTCTGTCCCTGCAAG
193685	25881	CTCATGAGCTGAGGGACCAT	238272	70468	AGGAAAAGAGGCAAAATCTG	282859	115055	CGAGGGCTCTGTCCCTGCAA
193686	25882	CCTCATGAGCTGAGGGACCA	238273	70469	CAGGAAAAGAGGCAAAATCT	282860	115056	ACGAGGGCTCTGTCCCTGCA
193687	25883	CCCTCATGAGCTGAGGGACC	238274	70470	TCAGGAAAAGAGGCAAAATC	282861	115057	TACGAGGGCTCTGTCCCTGC
193688	25884	GCCCTCATGAGCTGAGGGAC	238275	70471	GTCAGGAAAAGAGGCAAAAT	282862	115058	GTACGAGGGCTCTGTCCCTG
193689	25885	GGCCCTCATGAGCTGAGGGA	238276	70472	TGTCAGGAAAAGAGGCAAAA	282863	115059	TGTACGAGGGCTCTGTCCCT
193690	25886	TGGCCCTCATGAGCTGAGGG	238277	70473	TTGTCAGGAAAAGAGGCAAA	282864	115060	CTGTACGAGGGCTCTGTCCC
193691	25887	GTGGCCCTCATGAGCTGAGG	238278	70474	TTTGTCAGGAAAAGAGGCAA	282865	115061	TCTGTACGAGGGCTCTGTCC
193692	25888	TGTGGCCCTCATGAGCTGAG	238279	70475	CTTTGTCAGGAAAAGAGGCA	282866	115062	TTCTGTACGAGGGCTCTGTC
193693	25889	GTGTGGCCCTCATGAGCTGA	238280	70476	TCTTTGTCAGGAAAAGAGGC	282867	115063	CTTCTGTACGAGGGCTCTGT
193694	25890	TGTGTGGCCCTCATGAGCTG	238281	70477	CTCTTTGTCAGGAAAAGAGG	282868	115064	CCTTCTGTACGAGGGCTCTG
193695	25891	CTGTGTGGCCCTCATGAGCT	238282	70478	TCTCTTTGTCAGGAAAAGAG	282869	115065	CCCTTCTGTACGAGGGCTCT
193696	25892	CCTGTGTGGCCCTCATGAGC	238283	70479	CTCTCTTTGTCAGGAAAAGA	282870	115066	TCCCTTCTGTACGAGGGCTC
193697	25893	CCCTGTGTGGCCCTCATGAG	238284	70480	TCTCTCTTTGTCAGGAAAAG	282871	115067	GTCCCTTCTGTACGAGGGCT
193698	25894	GCCCTGTGTGGCCCTCATGA	238285	70481	ATCTCTCTTTGTCAGGAAAA	282872	115068	TGTCCCTTCTGTACGAGGGC
193699	25895	TGCCCTGTGTGGCCCTCATG	238286	70482	CATCTCTCTTTGTCAGGAAA	282873	115069	GTGTCCCTTCTGTACGAGGG
193700	25896	ATGCCCTGTGTGGCCCTCAT	238287	70483	TCATCTCTCTTTGTCAGGAA	282874	115070	GGTGTCCCTTCTGTACGAGG
193701	25897	AATGCCCTGTGTGGCCCTCA	238288	70484	TTCATCTCTCTTTGTCAGGA	282875	115071	GGGTGTCCCTTCTGTACGAG
193702	25898	CAATGCCCTGTGTGGCCCTC	238289	70485	CTTCATCTCTCTTTGTCAGG	282876	115072	GGGGTGTCCCTTCTGTACGA
193703	25899	GCAATGCCCTGTGTGGCCCT	238290	70486	TCTTCATCTCTCTTTGTCAG	282877	115073	TGGGGTGTCCCTTCTGTACG
193704	25900	CGCAATGCCCTGTGTGGCCC	238291	70487	CTCTTCATCTCTCTTTGTCA	282878	115074	GTGGGGTGTCCCTTCTGTAC
193705	25901	CCGCAATGCCCTGTGTGGCC	238292	70488	ACTCTTCATCTCTCTTTGTC	282879	115075	TGTGGGGTGTCCCTTCTGTA
193706	25902	ACCGCAATGCCCTGTGTGGC	238293	70489	AACTCTTCATCTCTCTTTGT	282880	115076	ATGTGGGGTGTCCCTTCTGT
193707	25903	CACCGCAATGCCCTGTGTGG	238294	70490	GAACTCTTCATCTCTCTTTG	282881	115077	AATGTGGGGTGTCCCTTCTG
193708	25904	CCACCGCAATGCCCTGTGTG	238295	70491	AGAACTCTTCATCTCTCTTT	282882	115078	AAATGTGGGGTGTCCCTTCT
193709	25905	GCCACCGCAATGCCCTGTGT	238296	70492	GAGAACTCTTCATCTCTCTT	282883	115079	CAAATGTGGGGTGTCCCTTC
193710	25906	GGCCACCGCAATGCCCTGTG	238297	70493	AGAGAACTCTTCATCTCTCT	282884	115080	ACAAATGTGGGGTGTCCCTT
193711	25907	AGGCCACCGCAATGCCCTGT	238298	70494	GAGAGAACTCTTCATCTCTC	282885	115081	GACAAATGTGGGGTGTCCCT
193712	25908	AAGGCCACCGCAATGCCCTG	238299	70495	TGAGAGAACTCTTCATCTCT	282886	115082	AGACAAATGTGGGGTGTCCC
193713	25909	GAAGGCCACCGCAATGCCCT	238300	70496	GTGAGAGAACTCTTCATCTC	282887	115083	AAGACAAATGTGGGGTGTCC
193714	25910	AGAAGGCCACCGCAATGCCC	238301	70497	GGTGAGAGAACTCTTCATCT	282888	115084	GAAGACAAATGTGGGGTGTC
193715	25911	GAGAAGGCCACCGCAATGCC	238302	70498	TGGTGAGAGAACTCTTCATC	282889	115085	GGAAGACAAATGTGGGGTGT
193716	25912	GGAGAAGGCCACCGCAATGC	238303	70499	CTGGTGAGAGAACTCTTCAT	282890	115086	GGGAAGACAAATGTGGGGTG
193717	25913	AGGAGAAGGCCACCGCAATG	238304	70500	CCTGGTGAGAGAACTCTTCA	282891	115087	GGGGAAGACAAATGTGGGGT
193718	25914	GAGGAGAAGGCCACCGCAAT	238305	70501	ACCTGGTGAGAGAACTCTTC	282892	115088	TGGGGAAGACAAATGTGGGG
193719	25915	TGAGGAGAAGGCCACCGCAA	238306	70502	CACCTGGTGAGAGAACTCTT	282893	115089	GTGGGGAAGACAAATGTGGG
193720	25916	CTGAGGAGAAGGCCACCGCA	238307	70503	GCACCTGGTGAGAGAACTCT	282894	115090	TGTGGGGAAGACAAATGTGG
193721	25917	GCTGAGGAGAAGGCCACCGC	238308	70504	GGCACCTGGTGAGAGAACTC	282895	115091	TTGTGGGGAAGACAAATGTG
193722	25918	GGCTGAGGAGAAGGCCACCG	238309	70505	AGGCACCTGGTGAGAGAACT	282896	115092	TTTGTGGGGAAGACAAATGT

193723	25919	AGGCTGAGGAGAAGGCCACC	238310	70506	CAGGCACCTGGTGAGAGAAC	282897	115093	CTTTGTGGGGAAGACAAATG
193724	25920	AAGGCTGAGGAGAAGGCCAC	238311	70507	CCAGGCACCTGGTGAGAGAA	282898	115094	GCTTTGTGGGGAAGACAAAT
193725	25921	CAAGGCTGAGGAGAAGGCCA	238312	70508	CCCAGGCACCTGGTGAGAGA	282899	115095	CGCTTTGTGGGGAAGACAAA
193726	25922	TCAAGGCTGAGGAGAAGGCC	238313	70509	TCCCAGGCACCTGGTGAGAG	282900	115096	CCGCTTTGTGGGGAAGACAA
193727	25923	GTCAAGGCTGAGGAGAAGGC	238314	70510	GTCCCAGGCACCTGGTGAGA	282901	115097	GCCGCTTTGTGGGGAAGACA
193728	25924	GGTCAAGGCTGAGGAGAAGG	238315	70511	AGTCCCAGGCACCTGGTGAG	282902	115098	GGCCGCTTTGTGGGGAAGAC
193729	25925	GGGTCAAGGCTGAGGAGAAG	238316	70512	CAGTCCCAGGCACCTGGTGA	282903	115099	AGGCCGCTTTGTGGGGAAGA
193730	25926	AGGGTCAAGGCTGAGGAGAA	238317	70513	CCAGTCCCAGGCACCTGGTG	282904	115100	CAGGCCGCTTTGTGGGGAAG
193731	25927	GAGGGTCAAGGCTGAGGAGA	238318	70514	CCCAGTCCCAGGCACCTGGT	282905	115101	ACAGGCCGCTTTGTGGGGAA
193732	25928	GGAGGGTCAAGGCTGAGGAG	238319	70515	CCCCAGTCCCAGGCACCTGG	282906	115102	CACAGGCCGCTTTGTGGGGA
193733	25929	CGGAGGGTCAAGGCTGAGGA	238320	70516	ACCCCAGTCCCAGGCACCTG	282907	115103	ACACAGGCCGCTTTGTGGGG
193734	25930	CCGGAGGGTCAAGGCTGAGG	238321	70517	CACCCCAGTCCCAGGCACCT	282908	115104	GACACAGGCCGCTTTGTGGG
193735	25931	GCCGGAGGGTCAAGGCTGAG	238322	70518	ACACCCCAGTCCCAGGCACC	282909	115105	GGACACAGGCCGCTTTGTGG
193736	25932	GGCCGGAGGGTCAAGGCTGA	238323	70519	CACACCCCAGTCCCAGGCAC	282910	115106	AGGACACAGGCCGCTTTGTG
193737	25933	GGGCCGGAGGGTCAAGGCTG	238324	70520	CCACACCCCAGTCCCAGGCA	282911	115107	CAGGACACAGGCCGCTTTGT
193738	25934	GGGGCCGGAGGGTCAAGGCT	238325	70521	CCCACACCCCAGTCCCAGGC	282912	115108	GCAGGACACAGGCCGCTTTG
193739	25935	TGGGGCCGGAGGGTCAAGGC	238326	70522	ACCCACACCCCAGTCCCAGG	282913	115109	GGCAGGACACAGGCCGCTTT
193740	25936	CTGGGGCCGGAGGGTCAAGG	238327	70523	CACCCACACCCCAGTCCCAG	282914	115110	AGGCAGGACACAGGCCGCTT
193741	25937	GCTGGGGCCGGAGGGTCAAG	238328	70524	ACACCCACACCCCAGTCCCA	282915	115111	TAGGCAGGACACAGGCCGCT
193742	25938	TGCTGGGGCCGGAGGGTCAA	238329	70525	GACACCCACACCCCAGTCCC	282916	115112	GTAGGCAGGACACAGGCCGC
193743	25939	ATGCTGGGGCCGGAGGGTCA	238330	70526	GGACACCCACACCCCAGTCC	282917	115113	CGTAGGCAGGACACAGGCCG
193744	25940	AATGCTGGGGCCGGAGGGTC	238331	70527	GGGACACCCACACCCCAGTC	282918	115114	CCGTAGGCAGGACACAGGCC
193745	25941	CAATGCTGGGGCCGGAGGGT	238332	70528	TGGGACACCCACACCCCAGT	282919	115115	CCCGTAGGCAGGACACAGGC
193746	25942	GCAATGCTGGGGCCGGAGGG	238333	70529	CTGGGACACCCACACCCCAG	282920	115116	CCCCGTAGGCAGGACACAGG
193747	25943	AGCAATGCTGGGGCCGGAGG	238334	70530	GCTGGGACACCCACACCCCA	282921	115117	ACCCCGTAGGCAGGACACAG
193748	25944	CAGCAATGCTGGGGCCGGAG	238335	70531	GGCTGGGACACCCACACCCC	282922	115118	GACCCCGTAGGCAGGACACA
193749	25945	GCAGCAATGCTGGGGCCGGA	238336	70532	AGGCTGGGACACCCACACCC	282923	115119	TGACCCCGTAGGCAGGACAC
193750	25946	GGCAGCAATGCTGGGGCCGG	238337	70533	TAGGCTGGGACACCCACACC	282924	115120	CTGACCCCGTAGGCAGGACA
193751	25947	AGGCAGCAATGCTGGGGCCG	238338	70534	ATAGGCTGGGACACCCACAC	282925	115121	CCTGACCCCGTAGGCAGGAC
193752	25948	GAGGCAGCAATGCTGGGGCC	238339	70535	GATAGGCTGGGACACCCACA	282926	115122	CCCTGACCCCGTAGGCAGGA
193753	25949	TGAGGCAGCAATGCTGGGGC	238340	70536	GGATAGGCTGGGACACCCAC	282927	115123	GCCCTGACCCCGTAGGCAGG
193754	25950	TTGAGGCAGCAATGCTGGGG	238341	70537	GGGATAGGCTGGGACACCCA	282928	115124	AGCCCTGACCCCGTAGGCAG
193755	25951	CTTGAGGCAGCAATGCTGGG	238342	70538	TGGGATAGGCTGGGACACCC	282929	115125	AAGCCCTGACCCCGTAGGCA
193756	25952	CCTTGAGGCAGCAATGCTGG	238343	70539	CTGGGATAGGCTGGGACACC	282930	115126	GAAGCCCTGACCCCGTAGGC
193757	25953	CCCTTGAGGCAGCAATGCTG	238344	70540	GCTGGGATAGGCTGGGACAC	282931	115127	AGAAGCCCTGACCCCGTAGG
193758	25954	CCCCTTGAGGCAGCAATGCT	238345	70541	CGCTGGGATAGGCTGGGACA	282932	115128	GAGAAGCCCTGACCCCGTAG
193759	25955	ACCCCTTGAGGCAGCAATGC	238346	70542	GCGCTGGGATAGGCTGGGAC	282933	115129	TGAGAAGCCCTGACCCCGTA
193760	25956	GACCCCTTGAGGCAGCAATG	238347	70543	TGCGCTGGGATAGGCTGGGA	282934	115130	TTGAGAAGCCCTGACCCCGT
193761	25957	AGACCCCTTGAGGCAGCAAT	238348	70544	ATGCGCTGGGATAGGCTGGG	282935	115131	TTTGAGAAGCCCTGACCCCG
193762	25958	GAGACCCCTTGAGGCAGCAA	238349	70545	GATGCGCTGGGATAGGCTGG	282936	115132	GTTTGAGAAGCCCTGACCCC
193763	25959	GGAGACCCCTTGAGGCAGCA	238350	70546	AGATGCGCTGGGATAGGCTG	282937	115133	GGTTTGAGAAGCCCTGACCC
193764	25960	AGGAGACCCCTTGAGGCAGC	238351	70547	CAGATGCGCTGGGATAGGCT	282938	115134	AGGTTTGAGAAGCCCTGACC
193765	25961	GAGGAGACCCCTTGAGGCAG	238352	70548	ACAGATGCGCTGGGATAGGC	282939	115135	CAGGTTTGAGAAGCCCTGAC
193766	25962	AGAGGAGACCCCTTGAGGCA	238353	70549	AACAGATGCGCTGGGATAGG	282940	115136	CCAGGTTTGAGAAGCCCTGA
193767	25963	CAGAGGAGACCCCTTGAGGC	238354	70550	GAACAGATGCGCTGGGATAG	282941	115137	GCCAGGTTTGAGAAGCCCTG
193768	25964	GCAGAGGAGACCCCTTGAGG	238355	70551	AGAACAGATGCGCTGGGATA	282942	115138	AGCCAGGTTTGAGAAGCCCT
193769	25965	AGCAGAGGAGACCCCTTGAG	238356	70552	CAGAACAGATGCGCTGGGAT	282943	115139	CAGCCAGGTTTGAGAAGCCC
193770	25966	CAGCAGAGGAGACCCCTTGA	238357	70553	GCAGAACAGATGCGCTGGGA	282944	115140	ACAGCCAGGTTTGAGAAGCC
193771	25967	TCAGCAGAGGAGACCCCTTG	238358	70554	TGCAGAACAGATGCGCTGGG	282945	115141	CACAGCCAGGTTTGAGAAGC
193772	25968	CTCAGCAGAGGAGACCCCTT	238359	70555	ATGCAGAACAGATGCGCTGG	282946	115142	ACACAGCCAGGTTTGAGAAG
193773	25969	GCTCAGCAGAGGAGACCCCT	238360	70556	GATGCAGAACAGATGCGCTG	282947	115143	CACACAGCCAGGTTTGAGAA
193774	25970	GGCTCAGCAGAGGAGACCCC	238361	70557	TGATGCAGAACAGATGCGCT	282948	115144	ACACACAGCCAGGTTTGAGA
193775	25971	CGGCTCAGCAGAGGAGACCC	238362	70558	ATGATGCAGAACAGATGCGC	282949	115145	GACACACAGCCAGGTTTGAG
193776	25972	ACGGCTCAGCAGAGGAGACC	238363	70559	CATGATGCAGAACAGATGCG	282950	115146	TGACACACAGCCAGGTTTGA
193777	25973	CACGGCTCAGCAGAGGAGAC	238364	70560	TCATGATGCAGAACAGATGC	282951	115147	CTGACACACAGCCAGGTTTG
193778	25974	GCACGGCTCAGCAGAGGAGA	238365	70561	ATCATGATGCAGAACAGATG	282952	115148	TCTGACACACAGCCAGGTTT
193779	25975	TGCACGGCTCAGCAGAGGAG	238366	70562	AATCATGATGCAGAACAGAT	282953	115149	TTCTGACACACAGCCAGGTT
193780	25976	GTGCACGGCTCAGCAGAGGA	238367	70563	TAATCATGATGCAGAACAGA	282954	115150	ATTCTGACACACAGCCAGGT
193781	25977	GGTGCACGGCTCAGCAGAGG	238368	70564	TTAATCATGATGCAGAACAG	282955	115151	GATTCTGACACACAGCCAGG
193782	25978	AGGTGCACGGCTCAGCAGAG	238369	70565	ATTAATCATGATGCAGAACA	282956	115152	TGATTCTGACACACAGCCAG
193783	25979	AAGGTGCACGGCTCAGCAGA	238370	70566	TATTAATCATGATGCAGAAC	282957	115153	GTGATTCTGACACACAGCCA
193784	25980	GAAGGTGCACGGCTCAGCAG	238371	70567	CTATTAATCATGATGCAGAA	282958	115154	GGTGATTCTGACACACAGCC
193785	25981	AGAAGGTGCACGGCTCAGCA	238372	70568	ACTATTAATCATGATGCAGA	282959	115155	TGGTGATTCTGACACACAGC
193786	25982	CAGAAGGTGCACGGCTCAGC	238373	70569	CACTATTAATCATGATGCAG	282960	115156	CTGGTGATTCTGACACACAG
193787	25983	GCAGAAGGTGCACGGCTCAG	238374	70570	GCACTATTAATCATGATGCA	282961	115157	CCTGGTGATTCTGACACACA
193788	25984	GGCAGAAGGTGCACGGCTCA	238375	70571	AGCACTATTAATCATGATGC	282962	115158	CCCTGGTGATTCTGACACAC
193789	25985	AGGCAGAAGGTGCACGGCTC	238376	70572	CAGCACTATTAATCATGATG	282963	115159	CCCCTGGTGATTCTGACACA
193790	25986	CAGGCAGAAGGTGCACGGCT	238377	70573	GCAGCACTATTAATCATGAT	282964	115160	TCCCCTGGTGATTCTGACAC
193791	25987	CCAGGCAGAAGGTGCACGGC	238378	70574	AGCAGCACTATTAATCATGA	282965	115161	TTCCCCTGGTGATTCTGACA
193792	25988	GCCAGGCAGAAGGTGCACGG	238379	70575	AAGCAGCACTATTAATCATG	282966	115162	GTTCCCCTGGTGATTCTGAC
193793	25989	TGCCAGGCAGAAGGTGCACG	238380	70576	AAAGCAGCACTATTAATCAT	282967	115163	AGTTCCCCTGGTGATTCTGA
193794	25990	CTGCCAGGCAGAAGGTGCAC	238381	70577	GAAAGCAGCACTATTAATCA	282968	115164	AAGTTCCCCTGGTGATTCTG

193795	25991	GCTGCCAGGCAGAAGGTGCA	238382	70578	TGAAAGCAGCACTATTAATC	282969	115165	AAAGTTCCCCTGGTGATTCT
193796	25992	AGCTGCCAGGCAGAAGGTGC	238383	70579	CTGAAAGCAGCACTATTAAT	282970	115166	AAAAGTTCCCCTGGTGATTC
193797	25993	GAGCTGCCAGGCAGAAGGTG	238384	70580	GCTGAAAGCAGCACTATTAA	282971	115167	GAAAAGTTCCCCTGGTGATT
193798	25994	GGAGCTGCCAGGCAGAAGGT	238385	70581	GGCTGAAAGCAGCACTATTA	282972	115168	TGAAAAGTTCCCCTGGTGAT
193799	25995	TGGAGCTGCCAGGCAGAAGG	238386	70582	CGGCTGAAAGCAGCACTATT	282973	115169	TTGAAAAGTTCCCCTGGTGA
193800	25996	TTGGAGCTGCCAGGCAGAAG	238387	70583	CCGGCTGAAAGCAGCACTAT	282974	115170	TTTGAAAAGTTCCCCTGGTG
193801	25997	GTTGGAGCTGCCAGGCAGAA	238388	70584	CCCGGCTGAAAGCAGCACTA	282975	115171	TTTTGAAAAGTTCCCCTGGT
193802	25998	AGTTGGAGCTGCCAGGCAGA	238389	70585	GCCCGGCTGAAAGCAGCACT	282976	115172	GTTTTGAAAAGTTCCCCTGG
193803	25999	GAGTTGGAGCTGCCAGGCAG	238390	70586	CGCCCGGCTGAAAGCAGCAC	282977	115173	AGTTTTGAAAAGTTCCCCTG
193804	26000	AGAGTTGGAGCTGCCAGGCA	238391	70587	GCGCCCGGCTGAAAGCAGCA	282978	115174	TAGTTTTGAAAAGTTCCCCT
193805	26001	CAGAGTTGGAGCTGCCAGGC	238392	70588	CGCGCCCGGCTGAAAGCAGC	282979	115175	CTAGTTTTGAAAAGTTCCCC
193806	26002	ACAGAGTTGGAGCTGCCAGG	238393	70589	CCGCGCCCGGCTGAAAGCAG	282980	115176	TCTAGTTTTGAAAAGTTCCC
193807	26003	CACAGAGTTGGAGCTGCCAG	238394	70590	ACCGCGCCCGGCTGAAAGCA	282981	115177	CTCTAGTTTTGAAAAGTTCC
193808	26004	CCACAGAGTTGGAGCTGCCA	238395	70591	CACCGCGCCCGGCTGAAAGC	282982	115178	TCTCTAGTTTTGAAAAGTTC
193809	26005	GCCACAGAGTTGGAGCTGCC	238396	70592	CCACCGCGCCCGGCTGAAAG	282983	115179	CTCTCTAGTTTTGAAAAGTT
193810	26006	AGCCACAGAGTTGGAGCTGC	238397	70593	GCCACCGCGCCCGGCTGAAA	282984	115180	TCTCTCTAGTTTTGAAAAGT
193811	26007	CAGCCACAGAGTTGGAGCTG	238398	70594	AGCCACCGCGCCCGGCTGAA	282985	115181	GTCTCTCTAGTTTTGAAAAG
193812	26008	ACAGCCACAGAGTTGGAGCT	238399	70595	GAGCCACCGCGCCCGGCTGA	282986	115182	AGTCTCTCTAGTTTTGAAAA
193813	26009	CACAGCCACAGAGTTGGAGC	238400	70596	TGAGCCACCGCGCCCGGCTG	282987	115183	CAGTCTCTCTAGTTTTGAAA
193814	26010	ACACAGCCACAGAGTTGGAG	238401	70597	GTGAGCCACCGCGCCCGGCT	282988	115184	TCAGTCTCTCTAGTTTTGAA
193815	26011	AACACAGCCACAGAGTTGGA	238402	70598	TGTGAGCCACCGCGCCCGGC	282989	115185	TTCAGTCTCTCTAGTTTTGA
193816	26012	GAACACAGCCACAGAGTTGG	238403	70599	GTGTGAGCCACCGCGCCCGG	282990	115186	CTTCAGTCTCTCTAGTTTTG
193817	26013	TGAACACAGCCACAGAGTTG	238404	70600	GGTGTGAGCCACCGCGCCCG	282991	115187	GCTTCAGTCTCTCTAGTTTT
193818	26014	CTGAACACAGCCACAGAGTT	238405	70601	AGGTGTGAGCCACCGCGCCC	282992	115188	GGCTTCAGTCTCTCTAGTTT
193819	26015	ACTGAACACAGCCACAGAGT	238406	70602	CAGGTGTGAGCCACCGCGCC	282993	115189	TGGCTTCAGTCTCTCTAGTT
193820	26016	CACTGAACACAGCCACAGAG	238407	70603	ACAGGTGTGAGCCACCGCGC	282994	115190	CTGGCTTCAGTCTCTCTAGT
193821	26017	CCACTGAACACAGCCACAGA	238408	70604	TACAGGTGTGAGCCACCGCG	282995	115191	TCTGGCTTCAGTCTCTCTAG
193822	26018	GCCACTGAACACAGCCACAG	238409	70605	TTACAGGTGTGAGCCACCGC	282996	115192	GTCTGGCTTCAGTCTCTCTA
193823	26019	AGCCACTGAACACAGCCACA	238410	70606	ATTACAGGTGTGAGCCACCG	282997	115193	AGTCTGGCTTCAGTCTCTCT
193824	26020	GAGCCACTGAACACAGCCAC	238411	70607	GATTACAGGTGTGAGCCACC	282998	115194	GAGTCTGGCTTCAGTCTCTC
193825	26021	TGAGCCACTGAACACAGCCA	238412	70608	GGATTACAGGTGTGAGCCAC	282999	115195	GGAGTCTGGCTTCAGTCTCT
193826	26022	CTGAGCCACTGAACACAGCC	238413	70609	GGGATTACAGGTGTGAGCCA	283000	115196	AGGAGTCTGGCTTCAGTCTC
193827	26023	GCTGAGCCACTGAACACAGC	238414	70610	TGGGATTACAGGTGTGAGCC	283001	115197	TAGGAGTCTGGCTTCAGTCT
193828	26024	TGCTGAGCCACTGAACACAG	238415	70611	CTGGGATTACAGGTGTGAGC	283002	115198	CTAGGAGTCTGGCTTCAGTC
193829	26025	GTGCTGAGCCACTGAACACA	238416	70612	GCTGGGATTACAGGTGTGAG	283003	115199	TCTAGGAGTCTGGCTTCAGT
193830	26026	AGTGCTGAGCCACTGAACAC	238417	70613	TGCTGGGATTACAGGTGTGA	283004	115200	ATCTAGGAGTCTGGCTTCAG
193831	26027	CAGTGCTGAGCCACTGAACA	238418	70614	GTGCTGGGATTACAGGTGTG	283005	115201	AATCTAGGAGTCTGGCTTCA
193832	26028	GCAGTGCTGAGCCACTGAAC	238419	70615	AGTGCTGGGATTACAGGTGT	283006	115202	GAATCTAGGAGTCTGGCTTC
193833	26029	GGCAGTGCTGAGCCACTGAA	238420	70616	AAGTGCTGGGATTACAGGTG	283007	115203	AGAATCTAGGAGTCTGGCTT
193834	26030	GGGCAGTGCTGAGCCACTGA	238421	70617	AAAGTGCTGGGATTACAGGT	283008	115204	TAGAATCTAGGAGTCTGGCT
193835	26031	GGGGCAGTGCTGAGCCACTG	238422	70618	CAAAGTGCTGGGATTACAGG	283009	115205	TTAGAATCTAGGAGTCTGGC
193836	26032	AGGGGCAGTGCTGAGCCACT	238423	70619	CCAAAGTGCTGGGATTACAG	283010	115206	ATTAGAATCTAGGAGTCTGG
193837	26033	AAGGGGCAGTGCTGAGCCAC	238424	70620	CCCAAAGTGCTGGGATTACA	283011	115207	AATTAGAATCTAGGAGTCTG
193838	26034	CAAGGGGCAGTGCTGAGCCA	238425	70621	TCCCAAAGTGCTGGGATTAC	283012	115208	GAATTAGAATCTAGGAGTCT
193839	26035	TCAAGGGGCAGTGCTGAGCC	238426	70622	CTCCCAAAGTGCTGGGATTA	283013	115209	AGAATTAGAATCTAGGAGTC
193840	26036	GTCAAGGGGCAGTGCTGAGC	238427	70623	CCTCCCAAAGTGCTGGGATT	283014	115210	TAGAATTAGAATCTAGGAGT
193841	26037	GGTCAAGGGGCAGTGCTGAG	238428	70624	GCCTCCCAAAGTGCTGGGAT	283015	115211	CTAGAATTAGAATCTAGGAG
193842	26038	GGGTCAAGGGGCAGTGCTGA	238429	70625	AGCCTCCCAAAGTGCTGGGA	283016	115212	CCTAGAATTAGAATCTAGGA
193843	26039	AGGGTCAAGGGGCAGTGCTG	238430	70626	TAGCCTCCCAAAGTGCTGGG	283017	115213	ACCTAGAATTAGAATCTAGG
193844	26040	GAGGGTCAAGGGGCAGTGCT	238431	70627	TTAGCCTCCCAAAGTGCTGG	283018	115214	GACCTAGAATTAGAATCTAG
193845	26041	GGAGGGTCAAGGGGCAGTGC	238432	70628	CTTAGCCTCCCAAAGTGCTG	283019	115215	TGACCTAGAATTAGAATCTA
193846	26042	GGGAGGGTCAAGGGGCAGTG	238433	70629	CCTTAGCCTCCCAAAGTGCT	283020	115216	CTGACCTAGAATTAGAATCT
193847	26043	AGGGAGGGTCAAGGGGCAGT	238434	70630	ACCTTAGCCTCCCAAAGTGC	283021	115217	CCTGACCTAGAATTAGAATC
193848	26044	CAGGGAGGGTCAAGGGGCAG	238435	70631	CACCTTAGCCTCCCAAAGTG	283022	115218	CCCTGACCTAGAATTAGAAT
193849	26045	CCAGGGAGGGTCAAGGGGCA	238436	70632	CCACCTTAGCCTCCCAAAGT	283023	115219	GCCCTGACCTAGAATTAGAA
193850	26046	GCCAGGGAGGGTCAAGGGGC	238437	70633	CCCACCTTAGCCTCCCAAAG	283024	115220	AGCCCTGACCTAGAATTAGA
193851	26047	GGCCAGGGAGGGTCAAGGGG	238438	70634	GCCCACCTTAGCCTCCCAAA	283025	115221	TAGCCCTGACCTAGAATTAG
193852	26048	AGGCCAGGGAGGGTCAAGGG	238439	70635	TGCCCACCTTAGCCTCCCAA	283026	115222	CTAGCCCTGACCTAGAATTA
193853	26049	AAGGCCAGGGAGGGTCAAGG	238440	70636	CTGCCCACCTTAGCCTCCCA	283027	115223	CCTAGCCCTGACCTAGAATT
193854	26050	GAAGGCCAGGGAGGGTCAAG	238441	70637	TCTGCCCACCTTAGCCTCCC	283028	115224	CCCTAGCCCTGACCTAGAAT
193855	26051	AGAAGGCCAGGGAGGGTCAA	238442	70638	ATCTGCCCACCTTAGCCTCC	283029	115225	CCCCTAGCCCTGACCTAGAA
193856	26052	CAGAAGGCCAGGGAGGGTCA	238443	70639	GATCTGCCCACCTTAGCCTC	283030	115226	GCCCCTAGCCCTGACCTAGA
193857	26053	GCAGAAGGCCAGGGAGGGTC	238444	70640	TGATCTGCCCACCTTAGCCT	283031	115227	AGCCCCTAGCCCTGACCTAG
193858	26054	CGCAGAAGGCCAGGGAGGGT	238445	70641	GTGATCTGCCCACCTTAGCC	283032	115228	CAGCCCCTAGCCCTGACCTA
193859	26055	CCGCAGAAGGCCAGGGAGGG	238446	70642	TGTGATCTGCCCACCTTAGC	283033	115229	TCAGCCCCTAGCCCTGACCT
193860	26056	TCCGCAGAAGGCCAGGGAGG	238447	70643	TTGTGATCTGCCCACCTTAG	283034	115230	CTCAGCCCCTAGCCCTGACC
193861	26057	ATCCGCAGAAGGCCAGGGAG	238448	70644	CTTGTGATCTGCCCACCTTA	283035	115231	TCTCAGCCCCTAGCCCTGAC
193862	26058	CATCCGCAGAAGGCCAGGGA	238449	70645	CCTTGTGATCTGCCCACCTT	283036	115232	ATCTCAGCCCCTAGCCCTGA
193863	26059	GCATCCGCAGAAGGCCAGGG	238450	70646	ACCTTGTGATCTGCCCACCT	283037	115233	AATCTCAGCCCCTAGCCCTG
193864	26060	GGCATCCGCAGAAGGCCAGG	238451	70647	GACCTTGTGATCTGCCCACC	283038	115234	CAATCTCAGCCCCTAGCCCT
193865	26061	TGGCATCCGCAGAAGGCCAG	238452	70648	TGACCTTGTGATCTGCCCAC	283039	115235	ACAATCTCAGCCCCTAGCCC
193866	26062	CTGGCATCCGCAGAAGGCCA	238453	70649	CTGACCTTGTGATCTGCCCA	283040	115236	TACAATCTCAGCCCCTAGCC

193867	26063	TCTGGCATCCGCAGAAGGCC	238454	70650	CCTGACCTTGTGATCTGCCC	283041	115237	TTACAATCTCAGCCCCTAGC
193868	26064	GTCTGGCATCCGCAGAAGGC	238455	70651	TCCTGACCTTGTGATCTGCC	283042	115238	TTTACAATCTCAGCCCCTAG
193869	26065	AGTCTGGCATCCGCAGAAGG	238456	70652	CTCCTGACCTTGTGATCTGC	283043	115239	TTTTACAATCTCAGCCCCTA
193870	26066	CAGTCTGGCATCCGCAGAAG	238457	70653	ACTCCTGACCTTGTGATCTG	283044	115240	TTTTTACAATCTCAGCCCCT
193871	26067	CCAGTCTGGCATCCGCAGAA	238458	70654	AACTCCTGACCTTGTGATCT	283045	115241	ATTTTTACAATCTCAGCCCC
193872	26068	TCCAGTCTGGCATCCGCAGA	238459	70655	GAACTCCTGACCTTGTGATC	283046	115242	GATTTTTACAATCTCAGCCC
193873	26069	CTCCAGTCTGGCATCCGCAG	238460	70656	CGAACTCCTGACCTTGTGAT	283047	115243	GGATTTTTACAATCTCAGCC
193874	26070	GCTCCAGTCTGGCATCCGCA	238461	70657	TCGAACTCCTGACCTTGTGA	283048	115244	TGGATTTTTACAATCTCAGC
193875	26071	TGCTCCAGTCTGGCATCCGC	238462	70658	CTCGAACTCCTGACCTTGTG	283049	115245	GTGGATTTTTACAATCTCAG
193876	26072	GTGCTCCAGTCTGGCATCCG	238463	70659	TCTCGAACTCCTGACCTTGT	283050	115246	TGTGGATTTTTACAATCTCA
193877	26073	AGTGCTCCAGTCTGGCATCC	238464	70660	GTCTCGAACTCCTGACCTTG	283051	115247	CTGTGGATTTTTACAATCTC
193878	26074	GAGTGCTCCAGTCTGGCATC	238465	70661	GGTCTCGAACTCCTGACCTT	283052	115248	CCTGTGGATTTTTACAATCT
193879	26075	AGAGTGCTCCAGTCTGGCAT	238466	70662	TGGTCTCGAACTCCTGACCT	283053	115249	ACCTGTGGATTTTTACAATC
193880	26076	CAGAGTGCTCCAGTCTGGCA	238467	70663	CTGGTCTCGAACTCCTGACC	283054	115250	CACCTGTGGATTTTTACAAT
193881	26077	TCAGAGTGCTCCAGTCTGGC	238468	70664	GCTGGTCTCGAACTCCTGAC	283055	115251	TCACCTGTGGATTTTTACAA
193882	26078	GTCAGAGTGCTCCAGTCTGG	238469	70665	GGCTGGTCTCGAACTCCTGA	283056	115252	ATCACCTGTGGATTTTTACA
193883	26079	TGTCAGAGTGCTCCAGTCTG	238470	70666	AGGCTGGTCTCGAACTCCTG	283057	115253	AATCACCTGTGGATTTTTAC
193884	26080	TTGTCAGAGTGCTCCAGTCT	238471	70667	CAGGCTGGTCTCGAACTCCT	283058	115254	GAATCACCTGTGGATTTTTA
193885	26081	CTTGTCAGAGTGCTCCAGTC	238472	70668	CCAGGCTGGTCTCGAACTCC	283059	115255	AGAATCACCTGTGGATTTTT
193886	26082	CCTTGTCAGAGTGCTCCAGT	238473	70669	GCCAGGCTGGTCTCGAACTC	283060	115256	CAGAATCACCTGTGGATTTT
193887	26083	ACCTTGTCAGAGTGCTCCAG	238474	70670	GGCCAGGCTGGTCTCGAACT	283061	115257	TCAGAATCACCTGTGGATTT
193888	26084	GACCTTGTCAGAGTGCTCCA	238475	70671	TGGCCAGGCTGGTCTCGAAC	283062	115258	ATCAGAATCACCTGTGGATT
193889	26085	AGACCTTGTCAGAGTGCTCC	238476	70672	TTGGCCAGGCTGGTCTCGAA	283063	115259	CATCAGAATCACCTGTGGAT
193890	26086	CAGACCTTGTCAGAGTGCTC	238477	70673	GTTGGCCAGGCTGGTCTCGA	283064	115260	GCATCAGAATCACCTGTGGA
193891	26087	CCAGACCTTGTCAGAGTGCT	238478	70674	TGTTGGCCAGGCTGGTCTCG	283065	115261	GGCATCAGAATCACCTGTGG
193892	26088	CCCAGACCTTGTCAGAGTGC	238479	70675	ATGTTGGCCAGGCTGGTCTC	283066	115262	GGGCATCAGAATCACCTGTG
193893	26089	CCCCAGACCTTGTCAGAGTG	238480	70676	CATGTTGGCCAGGCTGGTCT	283067	115263	CGGGCATCAGAATCACCTGT
193894	26090	ACCCCAGACCTTGTCAGAGT	238481	70677	CCATGTTGGCCAGGCTGGTC	283068	115264	CCGGGCATCAGAATCACCTG
193895	26091	CACCCCAGACCTTGTCAGAG	238482	70678	ACCATGTTGGCCAGGCTGGT	283069	115265	GCCGGGCATCAGAATCACCT
193896	26092	CCACCCCAGACCTTGTCAGA	238483	70679	CACCATGTTGGCCAGGCTGG	283070	115266	TGCCGGGCATCAGAATCACC
193897	26093	ACCACCCCAGACCTTGTCAG	238484	70680	TCACCATGTTGGCCAGGCTG	283071	115267	CTGCCGGGCATCAGAATCAC
193898	26094	AACCACCCCAGACCTTGTCA	238485	70681	TTCACCATGTTGGCCAGGCT	283072	115268	CCTGCCGGGCATCAGAATCA
193899	26095	CAACCACCCCAGACCTTGTC	238486	70682	TTTCACCATGTTGGCCAGGC	283073	115269	GCCTGCCGGGCATCAGAATC
193900	26096	ACAACCACCCCAGACCTTGT	238487	70683	GTTTCACCATGTTGGCCAGG	283074	115270	AGCCTGCCGGGCATCAGAAT
193901	26097	TACAACCACCCCAGACCTTG	238488	70684	GGTTTCACCATGTTGGCCAG	283075	115271	AAGCCTGCCGGGCATCAGAA
193902	26098	ATACAACCACCCCAGACCTT	238489	70685	AGGTTTCACCATGTTGGCCA	283076	115272	CAAGCCTGCCGGGCATCAGA
193903	26099	CATACAACCACCCCAGACCT	238490	70686	GAGGTTTCACCATGTTGGCC	283077	115273	TCAAGCCTGCCGGGCATCAG
193904	26100	CCATACAACCACCCCAGACC	238491	70687	CGAGGTTTCACCATGTTGGC	283078	115274	CTCAAGCCTGCCGGGCATCA
193905	26101	CCCATACAACCACCCCAGAC	238492	70688	ACGAGGTTTCACCATGTTGG	283079	115275	TCTCAAGCCTGCCGGGCATC
193906	26102	ACCCATACAACCACCCCAGA	238493	70689	GACGAGGTTTCACCATGTTG	283080	115276	TTCTCAAGCCTGCCGGGCAT
193907	26103	GACCCATACAACCACCCCAG	238494	70690	AGACGAGGTTTCACCATGTT	283081	115277	GTTCTCAAGCCTGCCGGGCA
193908	26104	GGACCCATACAACCACCCCA	238495	70691	GAGACGAGGTTTCACCATGT	283082	115278	TGTTCTCAAGCCTGCCGGGC
193909	26105	AGGACCCATACAACCACCCC	238496	70692	AGAGACGAGGTTTCACCATG	283083	115279	CTGTTCTCAAGCCTGCCGGG
193910	26106	CAGGACCCATACAACCACCC	238497	70693	TAGAGACGAGGTTTCACCAT	283084	115280	GCTGTTCTCAAGCCTGCCGG
193911	26107	ACAGGACCCATACAACCACC	238498	70694	GTAGAGACGAGGTTTCACCA	283085	115281	GGCTGTTCTCAAGCCTGCCG
193912	26108	CACAGGACCCATACAACCAC	238499	70695	AGTAGAGACGAGGTTTCACC	283086	115282	CGGCTGTTCTCAAGCCTGCC
193913	26109	TCACAGGACCCATACAACCA	238500	70696	TAGTAGAGACGAGGTTTCAC	283087	115283	GCGGCTGTTCTCAAGCCTGC
193914	26110	GTCACAGGACCCATACAACC	238501	70697	TTAGTAGAGACGAGGTTTCA	283088	115284	TGCGGCTGTTCTCAAGCCTG
193915	26111	GGTCACAGGACCCATACAAC	238502	70698	TTTAGTAGAGACGAGGTTTC	283089	115285	CTGCGGCTGTTCTCAAGCCT
193916	26112	AGGTCACAGGACCCATACAA	238503	70699	TTTTAGTAGAGACGAGGTTT	283090	115286	CCTGCGGCTGTTCTCAAGCC
193917	26113	GAGGTCACAGGACCCATACA	238504	70700	TTTTTAGTAGAGACGAGGTT	283091	115287	CCCTGCGGCTGTTCTCAAGC
193918	26114	AGAGGTCACAGGACCCATAC	238505	70701	ATTTTTAGTAGAGACGAGGT	283092	115288	TCCCTGCGGCTGTTCTCAAG
193919	26115	TAGAGGTCACAGGACCCATA	238506	70702	TATTTTTAGTAGAGACGAGG	283093	115289	CTCCCTGCGGCTGTTCTCAA
193920	26116	ATAGAGGTCACAGGACCCAT	238507	70703	GTATTTTTAGTAGAGACGAG	283094	115290	ACTCCCTGCGGCTGTTCTCA
193921	26117	TATAGAGGTCACAGGACCCA	238508	70704	TGTATTTTTAGTAGAGACGA	283095	115291	AACTCCCTGCGGCTGTTCTC
193922	26118	GTATAGAGGTCACAGGACCC	238509	70705	TTGTATTTTTAGTAGAGACG	283096	115292	GAACTCCCTGCGGCTGTTCT
193923	26119	TGTATAGAGGTCACAGGACC	238510	70706	TTTGTATTTTTAGTAGAGAC	283097	115293	AGAACTCCCTGCGGCTGTTC
193924	26120	GTGTATAGAGGTCACAGGAC	238511	70707	TTTTGTATTTTTAGTAGAGA	283098	115294	GAGAACTCCCTGCGGCTGTT
193925	26121	GGTGTATAGAGGTCACAGGA	238512	70708	TTTTTGTATTTTTAGTAGAG	283099	115295	AGAGAACTCCCTGCGGCTGT
193926	26122	AGGTGTATAGAGGTCACAGG	238513	70709	ATTTTTGTATTTTTAGTAGA	283100	115296	CAGAGAACTCCCTGCGGCTG
193927	26123	GAGGTGTATAGAGGTCACAG	238514	70710	AATTTTTGTATTTTTAGTAG	283101	115297	CCAGAGAACTCCCTGCGGCT
193928	26124	GGAGGTGTATAGAGGTCACA	238515	70711	TAATTTTTGTATTTTTAGTA	283102	115298	CCCAGAGAACTCCCTGCGGC
193929	26125	GGGAGGTGTATAGAGGTCAC	238516	70712	TTAATTTTTGTATTTTTAGT	283103	115299	TCCCAGAGAACTCCCTGCGG
193930	26126	TGGGAGGTGTATAGAGGTCA	238517	70713	GTTAATTTTTGTATTTTTAG	283104	115300	TTCCCAGAGAACTCCCTGCG
193931	26127	CTGGGAGGTGTATAGAGGTC	238518	70714	GGTTAATTTTTGTATTTTTA	283105	115301	ATTCCCAGAGAACTCCCTGC
193932	26128	ACTGGGAGGTGTATAGAGGT	238519	70715	TGGTTAATTTTTGTATTTTT	283106	115302	CATTCCCAGAGAACTCCCTG
193933	26129	CACTGGGAGGTGTATAGAGG	238520	70716	CTGGTTAATTTTTGTATTTT	283107	115303	ACATTCCCAGAGAACTCCCT
193934	26130	GCACTGGGAGGTGTATAGAG	238521	70717	CCTGGTTAATTTTTGTATTT	283108	115304	CACATTCCCAGAGAACTCCC
193935	26131	GGCACTGGGAGGTGTATAGA	238522	70718	ACCTGGTTAATTTTTGTATT	283109	115305	GCACATTCCCAGAGAACTCC
193936	26132	AGGCACTGGGAGGTGTATAG	238523	70719	CACCTGGTTAATTTTTGTAT	283110	115306	GGCACATTCCCAGAGAACTC
193937	26133	CAGGCACTGGGAGGTGTATA	238524	70720	ACACCTGGTTAATTTTTGTA	283111	115307	CGGCACATTCCCAGAGAACT
193938	26134	CCAGGCACTGGGAGGTGTAT	238525	70721	CACACCTGGTTAATTTTTGT	283112	115308	CCGGCACATTCCCAGAGAAC

193939	26135	CCCAGGCACTGGGAGGTGTA	238526	70722	CCACACCTGGTTAATTTTTG	283113	115309	ACCGGCACATTCCCAGAGAA
193940	26136	TCCCAGGCACTGGGAGGTGT	238527	70723	ACCACACCTGGTTAATTTTT	283114	115310	CACCGGCACATTCCCAGAGA
193941	26137	TTCCCAGGCACTGGGAGGTG	238528	70724	CACCACACCTGGTTAATTTT	283115	115311	CCACCGGCACATTCCCAGAG
193942	26138	ATTCCCAGGCACTGGGAGGT	238529	70725	CCACCACACCTGGTTAATTT	283116	115312	CCCACCGGCACATTCCCAGA
193943	26139	GATTCCCAGGCACTGGGAGG	238530	70726	ACCACCACACCTGGTTAATT	283117	115313	ACCCACCGGCACATTCCCAG
193944	26140	GGATTCCCAGGCACTGGGAG	238531	70727	CACCACCACACCTGGTTAAT	283118	115314	GACCCACCGGCACATTCCCA
193945	26141	AGGATTCCCAGGCACTGGGA	238532	70728	CCACCACCACACCTGGTTAA	283119	115315	AGACCCACCGGCACATTCCC
193946	26142	CAGGATTCCCAGGCACTGGG	238533	70729	CCCACCACCACACCTGGTTA	283120	115316	TAGACCCACCGGCACATTCC
193947	26143	GCAGGATTCCCAGGCACTGG	238534	70730	ACCCACCACCACACCTGGTT	283121	115317	CTAGACCCACCGGCACATTC
193948	26144	TGCAGGATTCCCAGGCACTG	238535	70731	CACCCACCACCACACCTGGT	283122	115318	GCTAGACCCACCGGCACATT
193949	26145	CTGCAGGATTCCCAGGCACT	238536	70732	GCACCCACCACCACACCTGG	283123	115319	GGCTAGACCCACCGGCACAT
193950	26146	TCTGCAGGATTCCCAGGCAC	238537	70733	GGCACCCACCACCACACCTG	283124	115320	TGGCTAGACCCACCGGCACA
193951	26147	ATCTGCAGGATTCCCAGGCA	238538	70734	AGGCACCCACCACCACACCT	283125	115321	CTGGCTAGACCCACCGGCAC
193952	26148	TATCTGCAGGATTCCCAGGC	238539	70735	CAGGCACCCACCACCACACC	283126	115322	CCTGGCTAGACCCACCGGCA
193953	26149	GTATCTGCAGGATTCCCAGG	238540	70736	ACAGGCACCCACCACCACAC	283127	115323	ACCTGGCTAGACCCACCGGC
193954	26150	TGTATCTGCAGGATTCCCAG	238541	70737	TACAGGCACCCACCACCACA	283128	115324	CACCTGGCTAGACCCACCGG
193955	26151	GTGTATCTGCAGGATTCCCA	238542	70738	CTACAGGCACCCACCACCAC	283129	115325	ACACCTGGCTAGACCCACCG
193956	26152	GGTGTATCTGCAGGATTCCC	238543	70739	ACTACAGGCACCCACCACCA	283130	115326	CACACCTGGCTAGACCCACC
193957	26153	GGGTGTATCTGCAGGATTCC	238544	70740	GACTACAGGCACCCACCACC	283131	115327	TCACACCTGGCTAGACCCAC
193958	26154	AGGGTGTATCTGCAGGATTC	238545	70741	GGACTACAGGCACCCACCAC	283132	115328	CTCACACCTGGCTAGACCCA
193959	26155	GAGGGTGTATCTGCAGGATT	238546	70742	GGGACTACAGGCACCCACCA	283133	115329	ACTCACACCTGGCTAGACCC
193960	26156	GGAGGGTGTATCTGCAGGAT	238547	70743	TGGGACTACAGGCACCCACC	283134	115330	CACTCACACCTGGCTAGACC
193961	26157	AGGAGGGTGTATCTGCAGGA	238548	70744	CTGGGACTACAGGCACCCAC	283135	115331	CCACTCACACCTGGCTAGAC
193962	26158	AAGGAGGGTGTATCTGCAGG	238549	70745	GCTGGGACTACAGGCACCCA	283136	115332	TCCACTCACACCTGGCTAGA
193963	26159	TAAGGAGGGTGTATCTGCAG	238550	70746	AGCTGGGACTACAGGCACCC	283137	115333	CTCCACTCACACCTGGCTAG
193964	26160	CTAAGGAGGGTGTATCTGCA	238551	70747	TAGCTGGGACTACAGGCACC	283138	115334	TCTCCACTCACACCTGGCTA
193965	26161	GCTAAGGAGGGTGTATCTGC	238552	70748	GTAGCTGGGACTACAGGCAC	283139	115335	ATCTCCACTCACACCTGGCT
193966	26162	GGCTAAGGAGGGTGTATCTG	238553	70749	AGTAGCTGGGACTACAGGCA	283140	115336	CATCTCCACTCACACCTGGC
193967	26163	CGGCTAAGGAGGGTGTATCT	238554	70750	AAGTAGCTGGGACTACAGGC	283141	115337	GCATCTCCACTCACACCTGG
193968	26164	ACGGCTAAGGAGGGTGTATC	238555	70751	CAAGTAGCTGGGACTACAGG	283142	115338	GGCATCTCCACTCACACCTG
193969	26165	GACGGCTAAGGAGGGTGTAT	238556	70752	CCAAGTAGCTGGGACTACAG	283143	115339	CGGCATCTCCACTCACACCT
193970	26166	GGACGGCTAAGGAGGGTGTA	238557	70753	CCCAAGTAGCTGGGACTACA	283144	115340	CCGGCATCTCCACTCACACC
193971	26167	GGGACGGCTAAGGAGGGTGT	238558	70754	TCCCAAGTAGCTGGGACTAC	283145	115341	CCCGGCATCTCCACTCACAC
193972	26168	AGGGACGGCTAAGGAGGGTG	238559	70755	CTCCCAAGTAGCTGGGACTA	283146	115342	CCCCGGCATCTCCACTCACA
193973	26169	TAGGGACGGCTAAGGAGGGT	238560	70756	CCTCCCAAGTAGCTGGGACT	283147	115343	TCCCCGGCATCTCCACTCAC
193974	26170	TTAGGGACGGCTAAGGAGGG	238561	70757	GCCTCCCAAGTAGCTGGGAC	283148	115344	TTCCCCGGCATCTCCACTCA
193975	26171	GTTAGGGACGGCTAAGGAGG	238562	70758	AGCCTCCCAAGTAGCTGGGA	283149	115345	GTTCCCCGGCATCTCCACTC
193976	26172	GGTTAGGGACGGCTAAGGAG	238563	70759	CAGCCTCCCAAGTAGCTGGG	283150	115346	AGTTCCCCGGCATCTCCACT
193977	26173	TGGTTAGGGACGGCTAAGGA	238564	70760	TCAGCCTCCCAAGTAGCTGG	283151	115347	AAGTTCCCCGGCATCTCCAC
193978	26174	ATGGTTAGGGACGGCTAAGG	238565	70761	CTCAGCCTCCCAAGTAGCTG	283152	115348	GAAGTTCCCCGGCATCTCCA
193979	26175	TATGGTTAGGGACGGCTAAG	238566	70762	CCTCAGCCTCCCAAGTAGCT	283153	115349	GGAAGTTCCCCGGCATCTCC
193980	26176	CTATGGTTAGGGACGGCTAA	238567	70763	GCCTCAGCCTCCCAAGTAGC	283154	115350	AGGAAGTTCCCCGGCATCTC
193981	26177	TCTATGGTTAGGGACGGCTA	238568	70764	TGCCTCAGCCTCCCAAGTAG	283155	115351	TAGGAAGTTCCCCGGCATCT
193982	26178	CTCTATGGTTAGGGACGGCT	238569	70765	CTGCCTCAGCCTCCCAAGTA	283156	115352	ATAGGAAGTTCCCCGGCATC
193983	26179	CCTCTATGGTTAGGGACGGC	238570	70766	CCTGCCTCAGCCTCCCAAGT	283157	115353	AATAGGAAGTTCCCCGGCAT
193984	26180	TCCTCTATGGTTAGGGACGG	238571	70767	TCCTGCCTCAGCCTCCCAAG	283158	115354	TAATAGGAAGTTCCCCGGCA
193985	26181	GTCCTCTATGGTTAGGGACG	238572	70768	CTCCTGCCTCAGCCTCCCAA	283159	115355	GTAATAGGAAGTTCCCCGGC
193986	26182	TGTCCTCTATGGTTAGGGAC	238573	70769	TCTCCTGCCTCAGCCTCCCA	283160	115356	AGTAATAGGAAGTTCCCCGG
193987	26183	ATGTCCTCTATGGTTAGGGA	238574	70770	TTCTCCTGCCTCAGCCTCCC	283161	115357	GAGTAATAGGAAGTTCCCCG
193988	26184	AATGTCCTCTATGGTTAGGG	238575	70771	ATTCTCCTGCCTCAGCCTCC	283162	115358	TGAGTAATAGGAAGTTCCCC
193989	26185	AAATGTCCTCTATGGTTAGG	238576	70772	GATTCTCCTGCCTCAGCCTC	283163	115359	GTGAGTAATAGGAAGTTCCC
193990	26186	GAAATGTCCTCTATGGTTAG	238577	70773	TGATTCTCCTGCCTCAGCCT	283164	115360	AGTGAGTAATAGGAAGTTCC
193991	26187	AGAAATGTCCTCTATGGTTA	238578	70774	GTGATTCTCCTGCCTCAGCC	283165	115361	GAGTGAGTAATAGGAAGTTC
193992	26188	CAGAAATGTCCTCTATGGTT	238579	70775	AGTGATTCTCCTGCCTCAGC	283166	115362	CGAGTGAGTAATAGGAAGTT
193993	26189	TCAGAAATGTCCTCTATGGT	238580	70776	AAGTGATTCTCCTGCCTCAG	283167	115363	ACGAGTGAGTAATAGGAAGT
193994	26190	CTCAGAAATGTCCTCTATGG	238581	70777	CAAGTGATTCTCCTGCCTCA	283168	115364	GACGAGTGAGTAATAGGAAG
193995	26191	CCTCAGAAATGTCCTCTATG	238582	70778	TCAAGTGATTCTCCTGCCTC	283169	115365	TGACGAGTGAGTAATAGGAA
193996	26192	ACCTCAGAAATGTCCTCTAT	238583	70779	TTCAAGTGATTCTCCTGCCT	283170	115366	CTGACGAGTGAGTAATAGGA
193997	26193	GACCTCAGAAATGTCCTCTA	238584	70780	ATTCAAGTGATTCTCCTGCC	283171	115367	ACTGACGAGTGAGTAATAGG
193998	26194	GGACCTCAGAAATGTCCTCT	238585	70781	GATTCAAGTGATTCTCCTGC	283172	115368	CACTGACGAGTGAGTAATAG
193999	26195	GGGACCTCAGAAATGTCCTC	238586	70782	AGATTCAAGTGATTCTCCTG	283173	115369	ACACTGACGAGTGAGTAATA
194000	26196	GGGGACCTCAGAAATGTCCT	238587	70783	CAGATTCAAGTGATTCTCCT	283174	115370	CACACTGACGAGTGAGTAAT
194001	26197	CGGGGACCTCAGAAATGTCC	238588	70784	CCAGATTCAAGTGATTCTCC	283175	115371	CCACACTGACGAGTGAGTAA
194002	26198	TCGGGGACCTCAGAAATGTC	238589	70785	CCCAGATTCAAGTGATTCTC	283176	115372	GCCACACTGACGAGTGAGTA
194003	26199	CTCGGGGACCTCAGAAATGT	238590	70786	TCCCAGATTCAAGTGATTCT	283177	115373	GGCCACACTGACGAGTGAGT
194004	26200	TCTCGGGGACCTCAGAAATG	238591	70787	TTCCCAGATTCAAGTGATTC	283178	115374	CGGCCACACTGACGAGTGAG
194005	26201	CTCTCGGGGACCTCAGAAAT	238592	70788	CTTCCCAGATTCAAGTGATT	283179	115375	TCGGCCACACTGACGAGTGA
194006	26202	TCTCTCGGGGACCTCAGAAA	238593	70789	GCTTCCCAGATTCAAGTGAT	283180	115376	TTCGGCCACACTGACGAGTG
194007	26203	CTCTCTCGGGGACCTCAGAA	238594	70790	TGCTTCCCAGATTCAAGTGA	283181	115377	GTTCGGCCACACTGACGAGT
194008	26204	ACTCTCTCGGGGACCTCAGA	238595	70791	CTGCTTCCCAGATTCAAGTG	283182	115378	TGTTCGGCCACACTGACGAG
194009	26205	CACTCTCTCGGGGACCTCAG	238596	70792	TCTGCTTCCCAGATTCAAGT	283183	115379	GTGTTCGGCCACACTGACGA
194010	26206	CCACTCTCTCGGGGACCTCA	238597	70793	CTCTGCTTCCCAGATTCAAG	283184	115380	TGTGTTCGGCCACACTGACG

194011	26207	CCCACTCTCTCGGGGACCTC	238598	70794	CCTCTGCTTCCCAGATTCAA	283185	115381	ATGTGTTCGGCCACACTGAC
194012	26208	CCCCACTCTCTCGGGGACCT	238599	70795	ACCTCTGCTTCCCAGATTCA	283186	115382	AATGTGTTCGGCCACACTGA
194013	26209	GCCCCACTCTCTCGGGGACC	238600	70796	AACCTCTGCTTCCCAGATTC	283187	115383	AAATGTGTTCGGCCACACTG
194014	26210	TGCCCCACTCTCTCGGGGAC	238601	70797	CAACCTCTGCTTCCCAGATT	283188	115384	AAAATGTGTTCGGCCACACT
194015	26211	GTGCCCCACTCTCTCGGGGA	238602	70798	GCAACCTCTGCTTCCCAGAT	283189	115385	AAAAATGTGTTCGGCCACAC
194016	26212	GGTGCCCCACTCTCTCGGGG	238603	70799	TGCAACCTCTGCTTCCCAGA	283190	115386	GAAAAATGTGTTCGGCCACA
194017	26213	GGGTGCCCCACTCTCTCGGG	238604	70800	CTGCAACCTCTGCTTCCCAG	283191	115387	TGAAAAATGTGTTCGGCCAC
194018	26214	GGGGTGCCCCACTCTCTCGG	238605	70801	ACTGCAACCTCTGCTTCCCA	283192	115388	GTGAAAAATGTGTTCGGCCA
194019	26215	AGGGGTGCCCCACTCTCTCG	238606	70802	CACTGCAACCTCTGCTTCCC	283193	115389	AGTGAAAAATGTGTTCGGCC
194020	26216	CAGGGGTGCCCCACTCTCTC	238607	70803	TCACTGCAACCTCTGCTTCC	283194	115390	AAGTGAAAAATGTGTTCGGC
194021	26217	GCAGGGGTGCCCCACTCTCT	238608	70804	CTCACTGCAACCTCTGCTTC	283195	115391	CAAGTGAAAAATGTGTTCGG
194022	26218	TGCAGGGGTGCCCCACTCTC	238609	70805	GCTCACTGCAACCTCTGCTT	283196	115392	TCAAGTGAAAAATGTGTTCG
194023	26219	CTGCAGGGGTGCCCCACTCT	238610	70806	GGCTCACTGCAACCTCTGCT	283197	115393	GTCAAGTGAAAAATGTGTTC
194024	26220	CCTGCAGGGGTGCCCCACTC	238611	70807	TGGCTCACTGCAACCTCTGC	283198	115394	GGTCAAGTGAAAAATGTGTT
194025	26221	TCCTGCAGGGGTGCCCCACT	238612	70808	TTGGCTCACTGCAACCTCTG	283199	115395	AGGTCAAGTGAAAAATGTGT
194026	26222	ATCCTGCAGGGGTGCCCCAC	238613	70809	CTTGGCTCACTGCAACCTCT	283200	115396	GAGGTCAAGTGAAAAATGTG
194027	26223	GATCCTGCAGGGGTGCCCCA	238614	70810	TCTTGGCTCACTGCAACCTC	283201	115397	TGAGGTCAAGTGAAAAATGT
194028	26224	GGATCCTGCAGGGGTGCCCC	238615	70811	ATCTTGGCTCACTGCAACCT	283202	115398	CTGAGGTCAAGTGAAAAATG
194029	26225	TGGATCCTGCAGGGGTGCCC	238616	70812	GATCTTGGCTCACTGCAACC	283203	115399	CCTGAGGTCAAGTGAAAAAT
194030	26226	TTGGATCCTGCAGGGGTGCC	238617	70813	CGATCTTGGCTCACTGCAAC	283204	115400	GCCTGAGGTCAAGTGAAAAA
194031	26227	GTTGGATCCTGCAGGGGTGC	238618	70814	ACGATCTTGGCTCACTGCAA	283205	115401	AGCCTGAGGTCAAGTGAAAA
194032	26228	AGTTGGATCCTGCAGGGGTG	238619	70815	CACGATCTTGGCTCACTGCA	283206	115402	CAGCCTGAGGTCAAGTGAAA
194033	26229	CAGTTGGATCCTGCAGGGGT	238620	70816	GCACGATCTTGGCTCACTGC	283207	115403	CCAGCCTGAGGTCAAGTGAA
194034	26230	GCAGTTGGATCCTGCAGGGG	238621	70817	GGCACGATCTTGGCTCACTG	283208	115404	ACCAGCCTGAGGTCAAGTGA
194035	26231	AGCAGTTGGATCCTGCAGGG	238622	70818	TGGCACGATCTTGGCTCACT	283209	115405	CACCAGCCTGAGGTCAAGTG
194036	26232	CAGCAGTTGGATCCTGCAGG	238623	70819	GTGGCACGATCTTGGCTCAC	283210	115406	TCACCAGCCTGAGGTCAAGT
194037	26233	CCAGCAGTTGGATCCTGCAG	238624	70820	AGTGGCACGATCTTGGCTCA	283211	115407	TTCACCAGCCTGAGGTCAAG
194038	26234	CCCAGCAGTTGGATCCTGCA	238625	70821	CAGTGGCACGATCTTGGCTC	283212	115408	GTTCACCAGCCTGAGGTCAA
194039	26235	GCCCAGCAGTTGGATCCTGC	238626	70822	GCAGTGGCACGATCTTGGCT	283213	115409	CGTTCACCAGCCTGAGGTCA
194040	26236	GGCCCAGCAGTTGGATCCTG	238627	70823	TGCAGTGGCACGATCTTGGC	283214	115410	GCGTTCACCAGCCTGAGGTC
194041	26237	GGGCCCAGCAGTTGGATCCT	238628	70824	GTGCAGTGGCACGATCTTGG	283215	115411	AGCGTTCACCAGCCTGAGGT
194042	26238	TGGGCCCAGCAGTTGGATCC	238629	70825	AGTGCAGTGGCACGATCTTG	283216	115412	GAGCGTTCACCAGCCTGAGG
194043	26239	CTGGGCCCAGCAGTTGGATC	238630	70826	GAGTGCAGTGGCACGATCTT	283217	115413	GGAGCGTTCACCAGCCTGAG
194044	26240	CCTGGGCCCAGCAGTTGGAT	238631	70827	GGAGTGCAGTGGCACGATCT	283218	115414	GGGAGCGTTCACCAGCCTGA
194045	26241	TCCTGGGCCCAGCAGTTGGA	238632	70828	TGGAGTGCAGTGGCACGATC	283219	115415	GGGGAGCGTTCACCAGCCTG
194046	26242	TTCCTGGGCCCAGCAGTTGG	238633	70829	CTGGAGTGCAGTGGCACGAT	283220	115416	AGGGGAGCGTTCACCAGCCT
194047	26243	CTTCCTGGGCCCAGCAGTTG	238634	70830	GCTGGAGTGCAGTGGCACGA	283221	115417	GAGGGGAGCGTTCACCAGCC
194048	26244	CCTTCCTGGGCCCAGCAGTT	238635	70831	GGCTGGAGTGCAGTGGCACG	283222	115418	AGAGGGGAGCGTTCACCAGC
194049	26245	TCCTTCCTGGGCCCAGCAGT	238636	70832	AGGCTGGAGTGCAGTGGCAC	283223	115419	CAGAGGGGAGCGTTCACCAG
194050	26246	ATCCTTCCTGGGCCCAGCAG	238637	70833	CAGGCTGGAGTGCAGTGGCA	283224	115420	CCAGAGGGGAGCGTTCACCA
194051	26247	TATCCTTCCTGGGCCCAGCA	238638	70834	CCAGGCTGGAGTGCAGTGGC	283225	115421	CCCAGAGGGGAGCGTTCACC
194052	26248	CTATCCTTCCTGGGCCCAGC	238639	70835	CCCAGGCTGGAGTGCAGTGG	283226	115422	CCCCAGAGGGGAGCGTTCAC
194053	26249	GCTATCCTTCCTGGGCCCAG	238640	70836	ACCCAGGCTGGAGTGCAGTG	283227	115423	ACCCCAGAGGGGAGCGTTCA
194054	26250	TGCTATCCTTCCTGGGCCCA	238641	70837	CACCCAGGCTGGAGTGCAGT	283228	115424	AACCCCAGAGGGGAGCGTTC
194055	26251	CTGCTATCCTTCCTGGGCCC	238642	70838	TCACCCAGGCTGGAGTGCAG	283229	115425	GAACCCCAGAGGGGAGCGTT
194056	26252	GCTGCTATCCTTCCTGGGCC	238643	70839	GTCACCCAGGCTGGAGTGCA	283230	115426	TGAACCCCAGAGGGGAGCGT
194057	26253	TGCTGCTATCCTTCCTGGGC	238644	70840	TGTCACCCAGGCTGGAGTGC	283231	115427	CTGAACCCCAGAGGGGAGCG
194058	26254	CTGCTGCTATCCTTCCTGGG	238645	70841	CTGTCACCCAGGCTGGAGTG	283232	115428	CCTGAACCCCAGAGGGGAGC
194059	26255	GCTGCTGCTATCCTTCCTGG	238646	70842	TCTGTCACCCAGGCTGGAGT	283233	115429	GCCTGAACCCCAGAGGGGAG
194060	26256	TGCTGCTGCTATCCTTCCTG	238647	70843	CTCTGTCACCCAGGCTGGAG	283234	115430	GGCCTGAACCCCAGAGGGGA
194061	26257	ATGCTGCTGCTATCCTTCCT	238648	70844	ACTCTGTCACCCAGGCTGGA	283235	115431	AGGCCTGAACCCCAGAGGGG
194062	26258	CATGCTGCTGCTATCCTTCC	238649	70845	CACTCTGTCACCCAGGCTGG	283236	115432	GAGGCCTGAACCCCAGAGGG
194063	26259	TCATGCTGCTGCTATCCTTC	238650	70846	TCACTCTGTCACCCAGGCTG	283237	115433	TGAGGCCTGAACCCCAGAGG
194064	26260	CTCATGCTGCTGCTATCCTT	238651	70847	CTCACTCTGTCACCCAGGCT	283238	115434	GTGAGGCCTGAACCCCAGAG
194065	26261	CCTCATGCTGCTGCTATCCT	238652	70848	TCTCACTCTGTCACCCAGGC	283239	115435	CGTGAGGCCTGAACCCCAGA
194066	26262	CCCTCATGCTGCTGCTATCC	238653	70849	GTCTCACTCTGTCACCCAGG	283240	115436	TCGTGAGGCCTGAACCCCAG
194067	26263	CCCCTCATGCTGCTGCTATC	238654	70850	AGTCTCACTCTGTCACCCAG	283241	115437	ATCGTGAGGCCTGAACCCCA
194068	26264	ACCCCTCATGCTGCTGCTAT	238655	70851	GAGTCTCACTCTGTCACCCA	283242	115438	CATCGTGAGGCCTGAACCCC
194069	26265	AACCCCTCATGCTGCTGCTA	238656	70852	GGAGTCTCACTCTGTCACCC	283243	115439	GCATCGTGAGGCCTGAACCC
194070	26266	GAACCCCTCATGCTGCTGCT	238657	70853	CGGAGTCTCACTCTGTCACC	283244	115440	GGCATCGTGAGGCCTGAACC
194071	26267	GGAACCCCTCATGCTGCTGC	238658	70854	ACGGAGTCTCACTCTGTCAC	283245	115441	TGGCATCGTGAGGCCTGAAC
194072	26268	TGGAACCCCTCATGCTGCTG	238659	70855	GACGGAGTCTCACTCTGTCA	283246	115442	ATGGCATCGTGAGGCCTGAA
194073	26269	ATGGAACCCCTCATGCTGCT	238660	70856	GGACGGAGTCTCACTCTGTC	283247	115443	GATGGCATCGTGAGGCCTGA
194074	26270	AATGGAACCCCTCATGCTGC	238661	70857	AGGACGGAGTCTCACTCTGT	283248	115444	GGATGGCATCGTGAGGCCTG
194075	26271	TAATGGAACCCCTCATGCTG	238662	70858	TAGGACGGAGTCTCACTCTG	283249	115445	AGGATGGCATCGTGAGGCCT
194076	26272	CTAATGGAACCCCTCATGCT	238663	70859	TTAGGACGGAGTCTCACTCT	283250	115446	AAGGATGGCATCGTGAGGCC
194077	26273	GCTAATGGAACCCCTCATGC	238664	70860	TTTAGGACGGAGTCTCACTC	283251	115447	AAAGGATGGCATCGTGAGGC
194078	26274	GGCTAATGGAACCCCTCATG	238665	70861	TTTTAGGACGGAGTCTCACT	283252	115448	AAAAGGATGGCATCGTGAGG
194079	26275	TGGCTAATGGAACCCCTCAT	238666	70862	TTTTTAGGACGGAGTCTCAC	283253	115449	CAAAAGGATGGCATCGTGAG
194080	26276	GTGGCTAATGGAACCCCTCA	238667	70863	TTTTTTAGGACGGAGTCTCA	283254	115450	ACAAAAGGATGGCATCGTGA
194081	26277	TGTGGCTAATGGAACCCCTC	238668	70864	TTTTTTTAGGACGGAGTCTC	283255	115451	CACAAAAGGATGGCATCGTG
194082	26278	TTGTGGCTAATGGAACCCCT	238669	70865	TTTTTTTTAGGACGGAGTCT	283256	115452	TCACAAAAGGATGGCATCGT

194083	26279	TTTGTGGCTAATGGAACCCC	238670	70866	TTTTTTTTTAGGACGGAGTC	283257	115453	TTCACAAAAGGATGGCATCG
194084	26280	GTTTGTGGCTAATGGAACCC	238671	70867	CTTTTTTTTTAGGACGGAGT	283258	115454	CTTCACAAAAGGATGGCATC
194085	26281	AGTTTGTGGCTAATGGAACC	238672	70868	CCTTTTTTTTTAGGACGGAG	283259	115455	ACTTCACAAAAGGATGGCAT
194086	26282	GAGTTTGTGGCTAATGGAAC	238673	70869	TCCTTTTTTTTTAGGACGGA	283260	115456	CACTTCACAAAAGGATGGCA
194087	26283	TGAGTTTGTGGCTAATGGAA	238674	70870	CTCCTTTTTTTTTAGGACGG	283261	115457	TCACTTCACAAAAGGATGGC
194088	26284	GTGAGTTTGTGGCTAATGGA	238675	70871	ACTCCTTTTTTTTTAGGACG	283262	115458	CTCACTTCACAAAAGGATGG
194089	26285	CGTGAGTTTGTGGCTAATGG	238676	70872	AACTCCTTTTTTTTTAGGAC	283263	115459	CCTCACTTCACAAAAGGATG
194090	26286	CCGTGAGTTTGTGGCTAATG	238677	70873	AAACTCCTTTTTTTTTAGGA	283264	115460	TCCTCACTTCACAAAAGGAT
194091	26287	GCCGTGAGTTTGTGGCTAAT	238678	70874	AAAACTCCTTTTTTTTTAGG	283265	115461	GTCCTCACTTCACAAAAGGA
194092	26288	TGCCGTGAGTTTGTGGCTAA	238679	70875	CAAAACTCCTTTTTTTTTAG	283266	115462	GGTCCTCACTTCACAAAAGG
194093	26289	ATGCCGTGAGTTTGTGGCTA	238680	70876	GCAAAACTCCTTTTTTTTTA	283267	115463	AGGTCCTCACTTCACAAAAG
194094	26290	CATGCCGTGAGTTTGTGGCT	238681	70877	AGCAAAACTCCTTTTTTTTT	283268	115464	CAGGTCCTCACTTCACAAAA
194095	26291	CCATGCCGTGAGTTTGTGGC	238682	70878	GAGCAAAACTCCTTTTTTTT	283269	115465	GCAGGTCCTCACTTCACAAA
194096	26292	TCCATGCCGTGAGTTTGTGG	238683	70879	AGAGCAAAACTCCTTTTTTT	283270	115466	TGCAGGTCCTCACTTCACAA
194097	26293	TTCCATGCCGTGAGTTTGTG	238684	70880	CAGAGCAAAACTCCTTTTTT	283271	115467	TTGCAGGTCCTCACTTCACA
194098	26294	GTTCCATGCCGTGAGTTTGT	238685	70881	ACAGAGCAAAACTCCTTTTT	283272	115468	ATTGCAGGTCCTCACTTCAC
194099	26295	GGTTCCATGCCGTGAGTTTG	238686	70882	GACAGAGCAAAACTCCTTTT	283273	115469	GATTGCAGGTCCTCACTTCA
194100	26296	AGGTTCCATGCCGTGAGTTT	238687	70883	CGACAGAGCAAAACTCCTTT	283274	115470	GGATTGCAGGTCCTCACTTC
194101	26297	AAGGTTCCATGCCGTGAGTT	238688	70884	GCGACAGAGCAAAACTCCTT	283275	115471	GGGATTGCAGGTCCTCACTT
194102	26298	GAAGGTTCCATGCCGTGAGT	238689	70885	GGCGACAGAGCAAAACTCCT	283276	115472	TGGGATTGCAGGTCCTCACT
194103	26299	TGAAGGTTCCATGCCGTGAG	238690	70886	GGGCGACAGAGCAAAACTCC	283277	115473	CTGGGATTGCAGGTCCTCAC
194104	26300	GTGAAGGTTCCATGCCGTGA	238691	70887	TGGGCGACAGAGCAAAACTC	283278	115474	GCTGGGATTGCAGGTCCTCA
194105	26301	GGTGAAGGTTCCATGCCGTG	238692	70888	CTGGGCGACAGAGCAAAACT	283279	115475	AGCTGGGATTGCAGGTCCTC
194106	26302	GGGTGAAGGTTCCATGCCGT	238693	70889	CCTGGGCGACAGAGCAAAAC	283280	115476	AAGCTGGGATTGCAGGTCCT
194107	26303	TGGGTGAAGGTTCCATGCCG	238694	70890	GCCTGGGCGACAGAGCAAAA	283281	115477	GAAGCTGGGATTGCAGGTCC
194108	26304	GTGGGTGAAGGTTCCATGCC	238695	70891	AGCCTGGGCGACAGAGCAAA	283282	115478	CGAAGCTGGGATTGCAGGTC
194109	26305	GGTGGGTGAAGGTTCCATGC	238696	70892	CAGCCTGGGCGACAGAGCAA	283283	115479	ACGAAGCTGGGATTGCAGGT
194110	26306	AGGTGGGTGAAGGTTCCATG	238697	70893	CCAGCCTGGGCGACAGAGCA	283284	115480	TACGAAGCTGGGATTGCAGG
194111	26307	GAGGTGGGTGAAGGTTCCAT	238698	70894	TCCAGCCTGGGCGACAGAGC	283285	115481	TTACGAAGCTGGGATTGCAG
194112	26308	CGAGGTGGGTGAAGGTTCCA	238699	70895	CTCCAGCCTGGGCGACAGAG	283286	115482	TTTACGAAGCTGGGATTGCA
194113	26309	GCGAGGTGGGTGAAGGTTCC	238700	70896	ACTCCAGCCTGGGCGACAGA	283287	115483	CTTTACGAAGCTGGGATTGC
194114	26310	GGCGAGGTGGGTGAAGGTTC	238701	70897	CACTCCAGCCTGGGCGACAG	283288	115484	GCTTTACGAAGCTGGGATTG
194115	26311	GGGCGAGGTGGGTGAAGGTT	238702	70898	ACACTCCAGCCTGGGCGACA	283289	115485	GGCTTTACGAAGCTGGGATT
194116	26312	GGGGCGAGGTGGGTGAAGGT	238703	70899	TACACTCCAGCCTGGGCGAC	283290	115486	GGGCTTTACGAAGCTGGGAT
194117	26313	AGGGGCGAGGTGGGTGAAGG	238704	70900	CTACACTCCAGCCTGGGCGA	283291	115487	CGGGCTTTACGAAGCTGGGA
194118	26314	GAGGGGCGAGGTGGGTGAAG	238705	70901	ACTACACTCCAGCCTGGGCG	283292	115488	GCGGGCTTTACGAAGCTGGG
194119	26315	TGAGGGGCGAGGTGGGTGAA	238706	70902	CACTACACTCCAGCCTGGGC	283293	115489	AGCGGGCTTTACGAAGCTGG
194120	26316	ATGAGGGGCGAGGTGGGTGA	238707	70903	CCACTACACTCCAGCCTGGG	283294	115490	CAGCGGGCTTTACGAAGCTG
194121	26317	GATGAGGGGCGAGGTGGGTG	238708	70904	GCCACTACACTCCAGCCTGG	283295	115491	CCAGCGGGCTTTACGAAGCT
194122	26318	AGATGAGGGGCGAGGTGGGT	238709	70905	CGCCACTACACTCCAGCCTG	283296	115492	TCCAGCGGGCTTTACGAAGC
194123	26319	CAGATGAGGGGCGAGGTGGG	238710	70906	GCGCCACTACACTCCAGCCT	283297	115493	TTCCAGCGGGCTTTACGAAG
194124	26320	GCAGATGAGGGGCGAGGTGG	238711	70907	GGCGCCACTACACTCCAGCC	283298	115494	TTTCCAGCGGGCTTTACGAA
194125	26321	AGCAGATGAGGGGCGAGGTG	238712	70908	TGGCGCCACTACACTCCAGC	283299	115495	ATTTCCAGCGGGCTTTACGA
194126	26322	CAGCAGATGAGGGGCGAGGT	238713	70909	ATGGCGCCACTACACTCCAG	283300	115496	GATTTCCAGCGGGCTTTACG
194127	26323	ACAGCAGATGAGGGGCGAGG	238714	70910	GATGGCGCCACTACACTCCA	283301	115497	TGATTTCCAGCGGGCTTTAC
194128	26324	AACAGCAGATGAGGGGCGAG	238715	70911	AGATGGCGCCACTACACTCC	283302	115498	GTGATTTCCAGCGGGCTTTA
194129	26325	AAACAGCAGATGAGGGGCGA	238716	70912	GAGATGGCGCCACTACACTC	283303	115499	AGTGATTTCCAGCGGGCTTT
194130	26326	TAAACAGCAGATGAGGGGCG	238717	70913	CGAGATGGCGCCACTACACT	283304	115500	GAGTGATTTCCAGCGGGCTT
194131	26327	CTAAACAGCAGATGAGGGGC	238718	70914	CCGAGATGGCGCCACTACAC	283305	115501	TGAGTGATTTCCAGCGGGCT
194132	26328	GCTAAACAGCAGATGAGGGG	238719	70915	GCCGAGATGGCGCCACTACA	283306	115502	GTGAGTGATTTCCAGCGGGC
194133	26329	TGCTAAACAGCAGATGAGGG	238720	70916	AGCCGAGATGGCGCCACTAC	283307	115503	TGTGAGTGATTTCCAGCGGG
194134	26330	GTGCTAAACAGCAGATGAGG	238721	70917	GAGCCGAGATGGCGCCACTA	283308	115504	GTGTGAGTGATTTCCAGCGG
194135	26331	GGTGCTAAACAGCAGATGAG	238722	70918	TGAGCCGAGATGGCGCCACT	283309	115505	AGTGTGAGTGATTTCCAGCG
194136	26332	AGGTGCTAAACAGCAGATGA	238723	70919	GTGAGCCGAGATGGCGCCAC	283310	115506	AAGTGTGAGTGATTTCCAGC
194137	26333	CAGGTGCTAAACAGCAGATG	238724	70920	GGTGAGCCGAGATGGCGCCA	283311	115507	GAAGTGTGAGTGATTTCCAG
194138	26334	CCAGGTGCTAAACAGCAGAT	238725	70921	CGGTGAGCCGAGATGGCGCC	283312	115508	AGAAGTGTGAGTGATTTCCA
194139	26335	GCCAGGTGCTAAACAGCAGA	238726	70922	GCGGTGAGCCGAGATGGCGC	283313	115509	CAGAAGTGTGAGTGATTTCC
194140	26336	TGCCAGGTGCTAAACAGCAG	238727	70923	TGCGGTGAGCCGAGATGGCG	283314	115510	CCAGAAGTGTGAGTGATTTC
194141	26337	GTGCCAGGTGCTAAACAGCA	238728	70924	TTGCGGTGAGCCGAGATGGC	283315	115511	CCCAGAAGTGTGAGTGATTT
194142	26338	CGTGCCAGGTGCTAAACAGC	238729	70925	GTTGCGGTGAGCCGAGATGG	283316	115512	TCCCAGAAGTGTGAGTGATT
194143	26339	GCGTGCCAGGTGCTAAACAG	238730	70926	GGTTGCGGTGAGCCGAGATG	283317	115513	ATCCCAGAAGTGTGAGTGAT
194144	26340	GGCGTGCCAGGTGCTAAACA	238731	70927	AGGTTGCGGTGAGCCGAGAT	283318	115514	CATCCCAGAAGTGTGAGTGA
194145	26341	CGGCGTGCCAGGTGCTAAAC	238732	70928	CAGGTTGCGGTGAGCCGAGA	283319	115515	GCATCCCAGAAGTGTGAGTG
194146	26342	ACGGCGTGCCAGGTGCTAAA	238733	70929	GCAGGTTGCGGTGAGCCGAG	283320	115516	GGCATCCCAGAAGTGTGAGT
194147	26343	CACGGCGTGCCAGGTGCTAA	238734	70930	CGCAGGTTGCGGTGAGCCGA	283321	115517	AGGCATCCCAGAAGTGTGAG
194148	26344	ACACGGCGTGCCAGGTGCTA	238735	70931	GCGCAGGTTGCGGTGAGCCG	283322	115518	AAGGCATCCCAGAAGTGTGA
194149	26345	TACACGGCGTGCCAGGTGCT	238736	70932	GGCGCAGGTTGCGGTGAGCC	283323	115519	GAAGGCATCCCAGAAGTGTG
194150	26346	ATACACGGCGTGCCAGGTGC	238737	70933	AGGCGCAGGTTGCGGTGAGC	283324	115520	TGAAGGCATCCCAGAAGTGT
194151	26347	TATACACGGCGTGCCAGGTG	238738	70934	GAGGCGCAGGTTGCGGTGAG	283325	115521	CTGAAGGCATCCCAGAAGTG
194152	26348	GTATACACGGCGTGCCAGGT	238739	70935	GGAGGCGCAGGTTGCGGTGA	283326	115522	TCTGAAGGCATCCCAGAAGT
194153	26349	AGTATACACGGCGTGCCAGG	238740	70936	GGGAGGCGCAGGTTGCGGTG	283327	115523	CTCTGAAGGCATCCCAGAAG
194154	26350	AAGTATACACGGCGTGCCAG	238741	70937	CGGGAGGCGCAGGTTGCGGT	283328	115524	GCTCTGAAGGCATCCCAGAA

194155	26351	TAAGTATACACGGCGTGCCA	238742	70938	CCGGGAGGCGCAGGTTGCGG	283329	115525	TGCTCTGAAGGCATCCCAGA
194156	26352	GTAAGTATACACGGCGTGCC	238743	70939	CCCGGGAGGCGCAGGTTGCG	283330	115526	CTGCTCTGAAGGCATCCCAG
194157	26353	AGTAAGTATACACGGCGTGC	238744	70940	ACCCGGGAGGCGCAGGTTGC	283331	115527	GCTGCTCTGAAGGCATCCCA
194158	26354	CAGTAAGTATACACGGCGTG	238745	70941	CACCCGGGAGGCGCAGGTTG	283332	115528	GGCTGCTCTGAAGGCATCCC
194159	26355	TCAGTAAGTATACACGGCGT	238746	70942	GCACCCGGGAGGCGCAGGTT	283333	115529	GGGCTGCTCTGAAGGCATCC
194160	26356	ATCAGTAAGTATACACGGCG	238747	70943	TGCACCCGGGAGGCGCAGGT	283334	115530	AGGGCTGCTCTGAAGGCATC
194161	26357	AATCAGTAAGTATACACGGC	238748	70944	TTGCACCCGGGAGGCGCAGG	283335	115531	GAGGGCTGCTCTGAAGGCAT
194162	26358	TAATCAGTAAGTATACACGG	238749	70945	CTTGCACCCGGGAGGCGCAG	283336	115532	AGAGGGCTGCTCTGAAGGCA
194163	26359	ATAATCAGTAAGTATACACG	238750	70946	GCTTGCACCCGGGAGGCGCA	283337	115533	TAGAGGGCTGCTCTGAAGGC
194164	26360	AATAATCAGTAAGTATACAC	238751	70947	CGCTTGCACCCGGGAGGCGC	283338	115534	ATAGAGGGCTGCTCTGAAGG
194165	26361	TAATAATCAGTAAGTATACA	238752	70948	TCGCTTGCACCCGGGAGGCG	283339	115535	GATAGAGGGCTGCTCTGAAG
194166	26362	GTAATAATCAGTAAGTATAC	238753	70949	ATCGCTTGCACCCGGGAGGC	283340	115536	GGATAGAGGGCTGCTCTGAA
194167	26363	TGTAATAATCAGTAAGTATA	238754	70950	AATCGCTTGCACCCGGGAGG	283341	115537	GGGATAGAGGGCTGCTCTGA
194168	26364	ATGTAATAATCAGTAAGTAT	238755	70951	GAATCGCTTGCACCCGGGAG	283342	115538	AGGGATAGAGGGCTGCTCTG
194169	26365	AATGTAATAATCAGTAAGTA	238756	70952	AGAATCGCTTGCACCCGGGA	283343	115539	AAGGGATAGAGGGCTGCTCT
194170	26366	AAATGTAATAATCAGTAAGT	238757	70953	GAGAATCGCTTGCACCCGGG	283344	115540	GAAGGGATAGAGGGCTGCTC
194171	26367	AAAATGTAATAATCAGTAAG	238758	70954	GGAGAATCGCTTGCACCCGG	283345	115541	TGAAGGGATAGAGGGCTGCT
194172	26368	TAAAATGTAATAATCAGTAA	238759	70955	AGGAGAATCGCTTGCACCCG	283346	115542	CTGAAGGGATAGAGGGCTGC
194173	26369	TTAAAATGTAATAATCAGTA	238760	70956	CAGGAGAATCGCTTGCACCC	283347	115543	GCTGAAGGGATAGAGGGCTG
194174	26370	ATTAAAATGTAATAATCAGT	238761	70957	GCAGGAGAATCGCTTGCACC	283348	115544	AGCTGAAGGGATAGAGGGCT
194175	26371	CATTAAAATGTAATAATCAG	238762	70958	GGCAGGAGAATCGCTTGCAC	283349	115545	GAGCTGAAGGGATAGAGGGC
194176	26372	CCATTAAAATGTAATAATCA	238763	70959	AGGCAGGAGAATCGCTTGCA	283350	115546	GGAGCTGAAGGGATAGAGGG
194177	26373	GCCATTAAAATGTAATAATC	238764	70960	GAGGCAGGAGAATCGCTTGC	283351	115547	GGGAGCTGAAGGGATAGAGG
194178	26374	TGCCATTAAAATGTAATAAT	238765	70961	TGAGGCAGGAGAATCGCTTG	283352	115548	GGGGAGCTGAAGGGATAGAG
194179	26375	TTGCCATTAAAATGTAATAA	238766	70962	CTGAGGCAGGAGAATCGCTT	283353	115549	AGGGGAGCTGAAGGGATAGA
194180	26376	TTTGCCATTAAAATGTAATA	238767	70963	GCTGAGGCAGGAGAATCGCT	283354	115550	CAGGGGAGCTGAAGGGATAG
194181	26377	ATTTGCCATTAAAATGTAAT	238768	70964	GGCTGAGGCAGGAGAATCGC	283355	115551	CCAGGGGAGCTGAAGGGATA
194182	26378	AATTTGCCATTAAAATGTAA	238769	70965	AGGCTGAGGCAGGAGAATCG	283356	115552	CCCAGGGGAGCTGAAGGGAT
194183	26379	TAATTTGCCATTAAAATGTA	238770	70966	GAGGCTGAGGCAGGAGAATC	283357	115553	TCCCAGGGGAGCTGAAGGGA
194184	26380	ATAATTTGCCATTAAAATGT	238771	70967	GGAGGCTGAGGCAGGAGAAT	283358	115554	ATCCCAGGGGAGCTGAAGGG
194185	26381	TATAATTTGCCATTAAAATG	238772	70968	GGGAGGCTGAGGCAGGAGAA	283359	115555	CATCCCAGGGGAGCTGAAGG
194186	26382	CTATAATTTGCCATTAAAAT	238773	70969	TGGGAGGCTGAGGCAGGAGA	283360	115556	ACATCCCAGGGGAGCTGAAG
194187	26383	ACTATAATTTGCCATTAAAA	238774	70970	TTGGGAGGCTGAGGCAGGAG	283361	115557	CACATCCCAGGGGAGCTGAA
194188	26384	CACTATAATTTGCCATTAAA	238775	70971	CTTGGGAGGCTGAGGCAGGA	283362	115558	TCACATCCCAGGGGAGCTGA
194189	26385	CCACTATAATTTGCCATTAA	238776	70972	ACTTGGGAGGCTGAGGCAGG	283363	115559	GTCACATCCCAGGGGAGCTG
194190	26386	GCCACTATAATTTGCCATTA	238777	70973	TACTTGGGAGGCTGAGGCAG	283364	115560	AGTCACATCCCAGGGGAGCT
194191	26387	TGCCACTATAATTTGCCATT	238778	70974	CTACTTGGGAGGCTGAGGCA	283365	115561	GAGTCACATCCCAGGGGAGC
194192	26388	TTGCCACTATAATTTGCCAT	238779	70975	GCTACTTGGGAGGCTGAGGC	283366	115562	TGAGTCACATCCCAGGGGAG
194193	26389	TTTGCCACTATAATTTGCCA	238780	70976	AGCTACTTGGGAGGCTGAGG	283367	115563	TTGAGTCACATCCCAGGGGA
194194	26390	GTTTGCCACTATAATTTGCC	238781	70977	TAGCTACTTGGGAGGCTGAG	283368	115564	GTTGAGTCACATCCCAGGGG
194195	26391	CGTTTGCCACTATAATTTGC	238782	70978	CTAGCTACTTGGGAGGCTGA	283369	115565	GGTTGAGTCACATCCCAGGG
194196	26392	ACGTTTGCCACTATAATTTG	238783	70979	CCTAGCTACTTGGGAGGCTG	283370	115566	AGGTTGAGTCACATCCCAGG
194197	26393	TACGTTTGCCACTATAATTT	238784	70980	TCCTAGCTACTTGGGAGGCT	283371	115567	GAGGTTGAGTCACATCCCAG
194198	26394	ATACGTTTGCCACTATAATT	238785	70981	ATCCTAGCTACTTGGGAGGC	283372	115568	GGAGGTTGAGTCACATCCCA
194199	26395	CATACGTTTGCCACTATAAT	238786	70982	AATCCTAGCTACTTGGGAGG	283373	115569	GGGAGGTTGAGTCACATCCC
194200	26396	GCATACGTTTGCCACTATAA	238787	70983	TAATCCTAGCTACTTGGGAG	283374	115570	CGGGAGGTTGAGTCACATCC
194201	26397	TGCATACGTTTGCCACTATA	238788	70984	GTAATCCTAGCTACTTGGGA	283375	115571	ACGGGAGGTTGAGTCACATC
194202	26398	ATGCATACGTTTGCCACTAT	238789	70985	TGTAATCCTAGCTACTTGGG	283376	115572	GACGGGAGGTTGAGTCACAT
194203	26399	GATGCATACGTTTGCCACTA	238790	70986	CTGTAATCCTAGCTACTTGG	283377	115573	TGACGGGAGGTTGAGTCACA
194204	26400	AGATGCATACGTTTGCCACT	238791	70987	CCTGTAATCCTAGCTACTTG	283378	115574	GTGACGGGAGGTTGAGTCAC
194205	26401	AAGATGCATACGTTTGCCAC	238792	70988	GCCTGTAATCCTAGCTACTT	283379	115575	AGTGACGGGAGGTTGAGTCA
194206	26402	AAAGATGCATACGTTTGCCA	238793	70989	CGCCTGTAATCCTAGCTACT	283380	115576	GAGTGACGGGAGGTTGAGTC
194207	26403	CAAAGATGCATACGTTTGCC	238794	70990	GCGCCTGTAATCCTAGCTAC	283381	115577	GGAGTGACGGGAGGTTGAGT
194208	26404	GCAAAGATGCATACGTTTGC	238795	70991	GGCGCCTGTAATCCTAGCTA	283382	115578	GGGAGTGACGGGAGGTTGAG
194209	26405	TGCAAAGATGCATACGTTTG	238796	70992	AGGCGCCTGTAATCCTAGCT	283383	115579	GGGGAGTGACGGGAGGTTGA
194210	26406	GTGCAAAGATGCATACGTTT	238797	70993	TAGGCGCCTGTAATCCTAGC	283384	115580	TGGGGAGTGACGGGAGGTTG
194211	26407	TGTGCAAAGATGCATACGTT	238798	70994	GTAGGCGCCTGTAATCCTAG	283385	115581	CTGGGGAGTGACGGGAGGTT
194212	26408	TTGTGCAAAGATGCATACGT	238799	70995	GGTAGGCGCCTGTAATCCTA	283386	115582	TCTGGGGAGTGACGGGAGGT
194213	26409	ATTGTGCAAAGATGCATACG	238800	70996	TGGTAGGCGCCTGTAATCCT	283387	115583	GTCTGGGGAGTGACGGGAGG
194214	26410	AATTGTGCAAAGATGCATAC	238801	70997	GTGGTAGGCGCCTGTAATCC	283388	115584	AGTCTGGGGAGTGACGGGAG
194215	26411	CAATTGTGCAAAGATGCATA	238802	70998	GGTGGTAGGCGCCTGTAATC	283389	115585	CAGTCTGGGGAGTGACGGGA
194216	26412	ACAATTGTGCAAAGATGCAT	238803	70999	TGGTGGTAGGCGCCTGTAAT	283390	115586	GCAGTCTGGGGAGTGACGGG
194217	26413	AACAATTGTGCAAAGATGCA	238804	71000	GTGGTGGTAGGCGCCTGTAA	283391	115587	GGCAGTCTGGGGAGTGACGG
194218	26414	CAACAATTGTGCAAAGATGC	238805	71001	CGTGGTGGTAGGCGCCTGTA	283392	115588	AGGCAGTCTGGGGAGTGACG
194219	26415	ACAACAATTGTGCAAAGATG	238806	71002	GCGTGGTGGTAGGCGCCTGT	283393	115589	GAGGCAGTCTGGGGAGTGAC
194220	26416	TACAACAATTGTGCAAAGAT	238807	71003	GGCGTGGTGGTAGGCGCCTG	283394	115590	AGAGGCAGTCTGGGGAGTGA
194221	26417	GTACAACAATTGTGCAAAGA	238808	71004	AGGCGTGGTGGTAGGCGCCT	283395	115591	CAGAGGCAGTCTGGGGAGTG
194222	26418	TGTACAACAATTGTGCAAAG	238809	71005	CAGGCGTGGTGGTAGGCGCC	283396	115592	GCAGAGGCAGTCTGGGGAGT
194223	26419	CTGTACAACAATTGTGCAAA	238810	71006	CCAGGCGTGGTGGTAGGCGC	283397	115593	GGCAGAGGCAGTCTGGGGAG
194224	26420	GCTGTACAACAATTGTGCAA	238811	71007	GCCAGGCGTGGTGGTAGGCG	283398	115594	TGGCAGAGGCAGTCTGGGGA
194225	26421	TGCTGTACAACAATTGTGCA	238812	71008	GGCCAGGCGTGGTGGTAGGC	283399	115595	TTGGCAGAGGCAGTCTGGGG
194226	26422	ATGCTGTACAACAATTGTGC	238813	71009	TGGCCAGGCGTGGTGGTAGG	283400	115596	CTTGGCAGAGGCAGTCTGGG

194227	26423	CATGCTGTACAACAATTGTG	238814	71010	CTGGCCAGGCGTGGTGGTAG	283401	115597	ACTTGGCAGAGGCAGTCTGG
194228	26424	TCATGCTGTACAACAATTGT	238815	71011	ACTGGCCAGGCGTGGTGGTA	283402	115598	GACTTGGCAGAGGCAGTCTG
194229	26425	ATCATGCTGTACAACAATTG	238816	71012	AACTGGCCAGGCGTGGTGGT	283403	115599	GGACTTGGCAGAGGCAGTCT
194230	26426	CATCATGCTGTACAACAATT	238817	71013	GAACTGGCCAGGCGTGGTGG	283404	115600	CGGACTTGGCAGAGGCAGTC
194231	26427	TCATCATGCTGTACAACAAT	238818	71014	AGAACTGGCCAGGCGTGGTG	283405	115601	TCGGACTTGGCAGAGGCAGT
194232	26428	TTCATCATGCTGTACAACAA	238819	71015	AAGAACTGGCCAGGCGTGGT	283406	115602	TTCGGACTTGGCAGAGGCAG
194233	26429	GTTCATCATGCTGTACAACA	238820	71016	CAAGAACTGGCCAGGCGTGG	283407	115603	TTTCGGACTTGGCAGAGGCA
194234	26430	TGTTCATCATGCTGTACAAC	238821	71017	ACAAGAACTGGCCAGGCGTG	283408	115604	CTTTCGGACTTGGCAGAGGC
194235	26431	TTGTTCATCATGCTGTACAA	238822	71018	TACAAGAACTGGCCAGGCGT	283409	115605	ACTTTCGGACTTGGCAGAGG
194236	26432	CTTGTTCATCATGCTGTACA	238823	71019	ATACAAGAACTGGCCAGGCG	283410	115606	CACTTTCGGACTTGGCAGAG
194237	26433	ACTTGTTCATCATGCTGTAC	238824	71020	AATACAAGAACTGGCCAGGC	283411	115607	CCACTTTCGGACTTGGCAGA
194238	26434	GACTTGTTCATCATGCTGTA	238825	71021	AAATACAAGAACTGGCCAGG	283412	115608	TCCACTTTCGGACTTGGCAG
194239	26435	TGACTTGTTCATCATGCTGT	238826	71022	AAAATACAAGAACTGGCCAG	283413	115609	CTCCACTTTCGGACTTGGCA
194240	26436	ATGACTTGTTCATCATGCTG	238827	71023	AAAAATACAAGAACTGGCCA	283414	115610	CCTCCACTTTCGGACTTGGC
194241	26437	AATGACTTGTTCATCATGCT	238828	71024	TAAAAATACAAGAACTGGCC	283415	115611	GCCTCCACTTTCGGACTTGG
194242	26438	TAATGACTTGTTCATCATGC	238829	71025	CTAAAAATACAAGAACTGGC	283416	115612	TGCCTCCACTTTCGGACTTG
194243	26439	TTAATGACTTGTTCATCATG	238830	71026	TCTAAAAATACAAGAACTGG	283417	115613	ATGCCTCCACTTTCGGACTT
194244	26440	ATTAATGACTTGTTCATCAT	238831	71027	TTCTAAAAATACAAGAACTG	283418	115614	GATGCCTCCACTTTCGGACT
194245	26441	TATTAATGACTTGTTCATCA	238832	71028	CTTCTAAAAATACAAGAACT	283419	115615	GGATGCCTCCACTTTCGGAC
194246	26442	CTATTAATGACTTGTTCATC	238833	71029	TCTTCTAAAAATACAAGAAC	283420	115616	AGGATGCCTCCACTTTCGGA
194247	26443	ACTATTAATGACTTGTTCAT	238834	71030	CTCTTCTAAAAATACAAGAA	283421	115617	AAGGATGCCTCCACTTTCGG
194248	26444	TACTATTAATGACTTGTTCA	238835	71031	TCTCTTCTAAAAATACAAGA	283422	115618	CAAGGATGCCTCCACTTTCG
194249	26445	TTACTATTAATGACTTGTTC	238836	71032	GTCTCTTCTAAAAATACAAG	283423	115619	GCAAGGATGCCTCCACTTTC
194250	26446	TTTACTATTAATGACTTGTT	238837	71033	CGTCTCTTCTAAAAATACAA	283424	115620	CGCAAGGATGCCTCCACTTT
194251	26447	CTTTACTATTAATGACTTGT	238838	71034	CCGTCTCTTCTAAAAATACA	283425	115621	TCGCAAGGATGCCTCCACTT
194252	26448	TCTTTACTATTAATGACTTG	238839	71035	CCCGTCTCTTCTAAAAATAC	283426	115622	CTCGCAAGGATGCCTCCACT
194253	26449	TTCTTTACTATTAATGACTT	238840	71036	CCCCGTCTCTTCTAAAAATA	283427	115623	GCTCGCAAGGATGCCTCCAC
194254	26450	ATTCTTTACTATTAATGACT	238841	71037	ACCCCGTCTCTTCTAAAAAT	283428	115624	TGCTCGCAAGGATGCCTCCA
194255	26451	TATTCTTTACTATTAATGAC	238842	71038	AACCCCGTCTCTTCTAAAAA	283429	115625	TTGCTCGCAAGGATGCCTCC
194256	26452	TTATTCTTTACTATTAATGA	238843	71039	AAACCCCGTCTCTTCTAAAA	283430	115626	CTTGCTCGCAAGGATGCCTC
194257	26453	TTTATTCTTTACTATTAATG	238844	71040	GAAACCCCGTCTCTTCTAAA	283431	115627	ACTTGCTCGCAAGGATGCCT
194258	26454	ATTTATTCTTTACTATTAAT	238845	71041	TGAAACCCCGTCTCTTCTAA	283432	115628	TACTTGCTCGCAAGGATGCC
194259	26455	CATTTATTCTTTACTATTAA	238846	71042	GTGAAACCCCGTCTCTTCTA	283433	115629	CTACTTGCTCGCAAGGATGC
194260	26456	ACATTTATTCTTTACTATTA	238847	71043	GGTGAAACCCCGTCTCTTCT	283434	115630	CCTACTTGCTCGCAAGGATG
194261	26457	CACATTTATTCTTTACTATT	238848	71044	GGGTGAAACCCCGTCTCTTC	283435	115631	GCCTACTTGCTCGCAAGGAT
194262	26458	TCACATTTATTCTTTACTAT	238849	71045	AGGGTGAAACCCCGTCTCTT	283436	115632	CGCCTACTTGCTCGCAAGGA
194263	26459	TTCACATTTATTCTTTACTA	238850	71046	CAGGGTGAAACCCCGTCTCT	283437	115633	CCGCCTACTTGCTCGCAAGG
194264	26460	TTTCACATTTATTCTTTACT	238851	71047	ACAGGGTGAAACCCCGTCTC	283438	115634	CCCGCCTACTTGCTCGCAAG
194265	26461	CTTTCACATTTATTCTTTAC	238852	71048	AACAGGGTGAAACCCCGTCT	283439	115635	ACCCGCCTACTTGCTCGCAA
194266	26462	ACTTTCACATTTATTCTTTA	238853	71049	CAACAGGGTGAAACCCCGTC	283440	115636	GACCCGCCTACTTGCTCGCA
194267	26463	CACTTTCACATTTATTCTTT	238854	71050	CCAACAGGGTGAAACCCCGT	283441	115637	GGACCCGCCTACTTGCTCGC
194268	26464	TCACTTTCACATTTATTCTT	238855	71051	GCCAACAGGGTGAAACCCCG	283442	115638	TGGACCCGCCTACTTGCTCG
194269	26465	CTCACTTTCACATTTATTCT	238856	71052	GGCCAACAGGGTGAAACCCC	283443	115639	CTGGACCCGCCTACTTGCTC
194270	26466	TCTCACTTTCACATTTATTC	238857	71053	TGGCCAACAGGGTGAAACCC	283444	115640	CCTGGACCCGCCTACTTGCT
194271	26467	TTCTCACTTTCACATTTATT	238858	71054	CTGGCCAACAGGGTGAAACC	283445	115641	CCCTGGACCCGCCTACTTGC
194272	26468	TTTCTCACTTTCACATTTAT	238859	71055	CCTGGCCAACAGGGTGAAAC	283446	115642	ACCCTGGACCCGCCTACTTG
194273	26469	TTTTCTCACTTTCACATTTA	238860	71056	GCCTGGCCAACAGGGTGAAA	283447	115643	CACCCTGGACCCGCCTACTT
194274	26470	TTTTTCTCACTTTCACATTT	238861	71057	AGCCTGGCCAACAGGGTGAA	283448	115644	CCACCCTGGACCCGCCTACT
194275	26471	ATTTTTCTCACTTTCACATT	238862	71058	GAGCCTGGCCAACAGGGTGA	283449	115645	GCCACCCTGGACCCGCCTAC
194276	26472	GATTTTTCTCACTTTCACAT	238863	71059	CGAGCCTGGCCAACAGGGTG	283450	115646	CGCCACCCTGGACCCGCCTA
194277	26473	AGATTTTTCTCACTTTCACA	238864	71060	ACGAGCCTGGCCAACAGGGT	283451	115647	GCGCCACCCTGGACCCGCCT
194278	26474	CAGATTTTTCTCACTTTCAC	238865	71061	GACGAGCCTGGCCAACAGGG	283452	115648	TGCGCCACCCTGGACCCGCC
194279	26475	TCAGATTTTTCTCACTTTCA	238866	71062	AGACGAGCCTGGCCAACAGG	283453	115649	ATGCGCCACCCTGGACCCGC
194280	26476	GTCAGATTTTTCTCACTTTC	238867	71063	CAGACGAGCCTGGCCAACAG	283454	115650	CATGCGCCACCCTGGACCCG
194281	26477	AGTCAGATTTTTCTCACTTT	238868	71064	CCAGACGAGCCTGGCCAACA	283455	115651	ACATGCGCCACCCTGGACCC
194282	26478	CAGTCAGATTTTTCTCACTT	238869	71065	CCCAGACGAGCCTGGCCAAC	283456	115652	GACATGCGCCACCCTGGACC
194283	26479	GCAGTCAGATTTTTCTCACT	238870	71066	TCCCAGACGAGCCTGGCCAA	283457	115653	TGACATGCGCCACCCTGGAC
194284	26480	GGCAGTCAGATTTTTCTCAC	238871	71067	GTCCCAGACGAGCCTGGCCA	283458	115654	GTGACATGCGCCACCCTGGA
194285	26481	TGGCAGTCAGATTTTTCTCA	238872	71068	AGTCCCAGACGAGCCTGGCC	283459	115655	AGTGACATGCGCCACCCTGG
194286	26482	TTGGCAGTCAGATTTTTCTC	238873	71069	GAGTCCCAGACGAGCCTGGC	283460	115656	GAGTGACATGCGCCACCCTG
194287	26483	TTTGGCAGTCAGATTTTTCT	238874	71070	GGAGTCCCAGACGAGCCTGG	283461	115657	TGAGTGACATGCGCCACCCT
194288	26484	CTTTGGCAGTCAGATTTTTC	238875	71071	AGGAGTCCCAGACGAGCCTG	283462	115658	ATGAGTGACATGCGCCACCC
194289	26485	ACTTTGGCAGTCAGATTTTT	238876	71072	CAGGAGTCCCAGACGAGCCT	283463	115659	GATGAGTGACATGCGCCACC
194290	26486	AACTTTGGCAGTCAGATTTT	238877	71073	TCAGGAGTCCCAGACGAGCC	283464	115660	CGATGAGTGACATGCGCCAC
194291	26487	AAACTTTGGCAGTCAGATTT	238878	71074	GTCAGGAGTCCCAGACGAGC	283465	115661	TCGATGAGTGACATGCGCCA
194292	26488	AAAACTTTGGCAGTCAGATT	238879	71075	GGTCAGGAGTCCCAGACGAG	283466	115662	TTCGATGAGTGACATGCGCC
194293	26489	AAAAACTTTGGCAGTCAGAT	238880	71076	AGGTCAGGAGTCCCAGACGA	283467	115663	TTTCGATGAGTGACATGCGC
194294	26490	TAAAAACTTTGGCAGTCAGA	238881	71077	GAGGTCAGGAGTCCCAGACG	283468	115664	CTTTCGATGAGTGACATGCG
194295	26491	GTAAAAACTTTGGCAGTCAG	238882	71078	TGAGGTCAGGAGTCCCAGAC	283469	115665	ACTTTCGATGAGTGACATGC
194296	26492	AGTAAAAACTTTGGCAGTCA	238883	71079	CTGAGGTCAGGAGTCCCAGA	283470	115666	CACTTTCGATGAGTGACATG
194297	26493	GAGTAAAAACTTTGGCAGTC	238884	71080	CCTGAGGTCAGGAGTCCCAG	283471	115667	CCACTTTCGATGAGTGACAT
194298	26494	GGAGTAAAAACTTTGGCAGT	238885	71081	ACCTGAGGTCAGGAGTCCCA	283472	115668	TCCACTTTCGATGAGTGACA

194299	26495	AGGAGTAAAAACTTTGGCAG	238886	71082	TACCTGAGGTCAGGAGTCCC	283473	115669	CTCCACTTTCGATGAGTGAC
194300	26496	AAGGAGTAAAAACTTTGGCA	238887	71083	TTACCTGAGGTCAGGAGTCC	283474	115670	CCTCCACTTTCGATGAGTGA
194301	26497	GAAGGAGTAAAAACTTTGGC	238888	71084	ATTACCTGAGGTCAGGAGTC	283475	115671	GCCTCCACTTTCGATGAGTG
194302	26498	GGAAGGAGTAAAAACTTTGG	238889	71085	GATTACCTGAGGTCAGGAGT	283476	115672	CGCCTCCACTTTCGATGAGT
194303	26499	AGGAAGGAGTAAAAACTTTG	238890	71086	GGATTACCTGAGGTCAGGAG	283477	115673	ACGCCTCCACTTTCGATGAG
194304	26500	AAGGAAGGAGTAAAAACTTT	238891	71087	CGGATTACCTGAGGTCAGGA	283478	115674	GACGCCTCCACTTTCGATGA
194305	26501	GAAGGAAGGAGTAAAAACTT	238892	71088	GCGGATTACCTGAGGTCAGG	283479	115675	GGACGCCTCCACTTTCGATG
194306	26502	GGAAGGAAGGAGTAAAAACT	238893	71089	GGCGGATTACCTGAGGTCAG	283480	115676	AGGACGCCTCCACTTTCGAT
194307	26503	GGGAAGGAAGGAGTAAAAAC	238894	71090	GGGCGGATTACCTGAGGTCA	283481	115677	AAGGACGCCTCCACTTTCGA
194308	26504	AGGGAAGGAAGGAGTAAAAA	238895	71091	TGGGCGGATTACCTGAGGTC	283482	115678	CAAGGACGCCTCCACTTTCG
194309	26505	GAGGGAAGGAAGGAGTAAAA	238896	71092	GTGGGCGGATTACCTGAGGT	283483	115679	GCAAGGACGCCTCCACTTTC
194310	26506	GGAGGGAAGGAAGGAGTAAA	238897	71093	GGTGGGCGGATTACCTGAGG	283484	115680	CGCAAGGACGCCTCCACTTT
194311	26507	GGGAGGGAAGGAAGGAGTAA	238898	71094	AGGTGGGCGGATTACCTGAG	283485	115681	TCGCAAGGACGCCTCCACTT
194312	26508	GGGGAGGGAAGGAAGGAGTA	238899	71095	GAGGTGGGCGGATTACCTGA	283486	115682	CTCGCAAGGACGCCTCCACT
194313	26509	TGGGGAGGGAAGGAAGGAGT	238900	71096	TGAGGTGGGCGGATTACCTG	283487	115683	GCTCGCAAGGACGCCTCCAC
194314	26510	CTGGGGAGGGAAGGAAGGAG	238901	71097	CTGAGGTGGGCGGATTACCT	283488	115684	TGCTCGCAAGGACGCCTCCA
194315	26511	TCTGGGGAGGGAAGGAAGGA	238902	71098	GCTGAGGTGGGCGGATTACC	283489	115685	TTGCTCGCAAGGACGCCTCC
194316	26512	GTCTGGGGAGGGAAGGAAGG	238903	71099	GGCTGAGGTGGGCGGATTAC	283490	115686	CTTGCTCGCAAGGACGCCTC
194317	26513	AGTCTGGGGAGGGAAGGAAG	238904	71100	AGGCTGAGGTGGGCGGATTA	283491	115687	GCTTGCTCGCAAGGACGCCT
194318	26514	AAGTCTGGGGAGGGAAGGAA	238905	71101	GAGGCTGAGGTGGGCGGATT	283492	115688	TGCTTGCTCGCAAGGACGCC
194319	26515	AAAGTCTGGGGAGGGAAGGA	238906	71102	GGAGGCTGAGGTGGGCGGAT	283493	115689	CTGCTTGCTCGCAAGGACGC
194320	26516	AAAAGTCTGGGGAGGGAAGG	238907	71103	GGGAGGCTGAGGTGGGCGGA	283494	115690	CCTGCTTGCTCGCAAGGACG
194321	26517	TAAAAGTCTGGGGAGGGAAG	238908	71104	TGGGAGGCTGAGGTGGGCGG	283495	115691	GCCTGCTTGCTCGCAAGGAC
194322	26518	TTAAAAGTCTGGGGAGGGAA	238909	71105	TTGGGAGGCTGAGGTGGGCG	283496	115692	CGCCTGCTTGCTCGCAAGGA
194323	26519	TTTAAAAGTCTGGGGAGGGA	238910	71106	TTTGGGAGGCTGAGGTGGGC	283497	115693	CCGCCTGCTTGCTCGCAAGG
194324	26520	ATTTAAAAGTCTGGGGAGGG	238911	71107	CTTTGGGAGGCTGAGGTGGG	283498	115694	CCCGCCTGCTTGCTCGCAAG
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194326	26522	TCATTTAAAAGTCTGGGGAG	238913	71109	CACTTTGGGAGGCTGAGGTG	283500	115696	GACCCGCCTGCTTGCTCGCA
194327	26523	TTCATTTAAAAGTCTGGGGA	238914	71110	GCACTTTGGGAGGCTGAGGT	283501	115697	GGACCCGCCTGCTTGCTCGC
194328	26524	TTTCATTTAAAAGTCTGGGG	238915	71111	AGCACTTTGGGAGGCTGAGG	283502	115698	TGGACCCGCCTGCTTGCTCG
194329	26525	CTTTCATTTAAAAGTCTGGG	238916	71112	CAGCACTTTGGGAGGCTGAG	283503	115699	CTGGACCCGCCTGCTTGCTC
194330	26526	ACTTTCATTTAAAAGTCTGG	238917	71113	CCAGCACTTTGGGAGGCTGA	283504	115700	CCTGGACCCGCCTGCTTGCT
194331	26527	AACTTTCATTTAAAAGTCTG	238918	71114	CCCAGCACTTTGGGAGGCTG	283505	115701	CCCTGGACCCGCCTGCTTGC
194332	26528	AAACTTTCATTTAAAAGTCT	238919	71115	TCCCAGCACTTTGGGAGGCT	283506	115702	ACCCTGGACCCGCCTGCTTG
194333	26529	TAAACTTTCATTTAAAAGTC	238920	71116	ATCCCAGCACTTTGGGAGGC	283507	115703	CACCCTGGACCCGCCTGCTT
194334	26530	CTAAACTTTCATTTAAAAGT	238921	71117	AATCCCAGCACTTTGGGAGG	283508	115704	CCACCCTGGACCCGCCTGCT
194335	26531	CCTAAACTTTCATTTAAAAG	238922	71118	CAATCCCAGCACTTTGGGAG	283509	115705	GCCACCCTGGACCCGCCTGC
194336	26532	CCCTAAACTTTCATTTAAAA	238923	71119	GCAATCCCAGCACTTTGGGA	283510	115706	CGCCACCCTGGACCCGCCTG
194337	26533	TCCCTAAACTTTCATTTAAA	238924	71120	TGCAATCCCAGCACTTTGGG	283511	115707	ACGCCACCCTGGACCCGCCT
194338	26534	ATCCCTAAACTTTCATTTAA	238925	71121	CTGCAATCCCAGCACTTTGG	283512	115708	CACGCCACCCTGGACCCGCC
194339	26535	TATCCCTAAACTTTCATTTA	238926	71122	CCTGCAATCCCAGCACTTTG	283513	115709	ACACGCCACCCTGGACCCGC
194340	26536	TTATCCCTAAACTTTCATTT	238927	71123	GCCTGCAATCCCAGCACTTT	283514	115710	GACACGCCACCCTGGACCCG
194341	26537	ATTATCCCTAAACTTTCATT	238928	71124	TGCCTGCAATCCCAGCACTT	283515	115711	TGACACGCCACCCTGGACCC
194342	26538	GATTATCCCTAAACTTTCAT	238929	71125	ATGCCTGCAATCCCAGCACT	283516	115712	GTGACACGCCACCCTGGACC
194343	26539	GGATTATCCCTAAACTTTCA	238930	71126	CATGCCTGCAATCCCAGCAC	283517	115713	AGTGACACGCCACCCTGGAC
194344	26540	GGGATTATCCCTAAACTTTC	238931	71127	TCATGCCTGCAATCCCAGCA	283518	115714	GAGTGACACGCCACCCTGGA
194345	26541	AGGGATTATCCCTAAACTTT	238932	71128	CTCATGCCTGCAATCCCAGC	283519	115715	TGAGTGACACGCCACCCTGG
194346	26542	AAGGGATTATCCCTAAACTT	238933	71129	GCTCATGCCTGCAATCCCAG	283520	115716	ATGAGTGACACGCCACCCTG
194347	26543	TAAGGGATTATCCCTAAACT	238934	71130	GGCTCATGCCTGCAATCCCA	283521	115717	GATGAGTGACACGCCACCCT
194348	26544	CTAAGGGATTATCCCTAAAC	238935	71131	TGGCTCATGCCTGCAATCCC	283522	115718	GGATGAGTGACACGCCACCC
194349	26545	ACTAAGGGATTATCCCTAAA	238936	71132	GTGGCTCATGCCTGCAATCC	283523	115719	AGGATGAGTGACACGCCACC
194350	26546	AACTAAGGGATTATCCCTAA	238937	71133	GGTGGCTCATGCCTGCAATC	283524	115720	AAGGATGAGTGACACGCCAC
194351	26547	CAACTAAGGGATTATCCCTA	238938	71134	CGGTGGCTCATGCCTGCAAT	283525	115721	AAAGGATGAGTGACACGCCA
194352	26548	ACAACTAAGGGATTATCCCT	238939	71135	ACGGTGGCTCATGCCTGCAA	283526	115722	AAAAGGATGAGTGACACGCC
194353	26549	GACAACTAAGGGATTATCCC	238940	71136	CACGGTGGCTCATGCCTGCA	283527	115723	AAAAAGGATGAGTGACACGC
194354	26550	GGACAACTAAGGGATTATCC	238941	71137	GCACGGTGGCTCATGCCTGC	283528	115724	AAAAAAGGATGAGTGACACG
194355	26551	AGGACAACTAAGGGATTATC	238942	71138	GGCACGGTGGCTCATGCCTG	283529	115725	GAAAAAAGGATGAGTGACAC
194356	26552	CAGGACAACTAAGGGATTAT	238943	71139	GGGCACGGTGGCTCATGCCT	283530	115726	AGAAAAAAGGATGAGTGACA
194357	26553	GCAGGACAACTAAGGGATTA	238944	71140	TGGGCACGGTGGCTCATGCC	283531	115727	CAGAAAAAAGGATGAGTGAC
194358	26554	AGCAGGACAACTAAGGGATT	238945	71141	CTGGGCACGGTGGCTCATGC	283532	115728	CCAGAAAAAAGGATGAGTGA
194359	26555	TAGCAGGACAACTAAGGGAT	238946	71142	ACTGGGCACGGTGGCTCATG	283533	115729	GCCAGAAAAAAGGATGAGTG
194360	26556	CTAGCAGGACAACTAAGGGA	238947	71143	GACTGGGCACGGTGGCTCAT	283534	115730	AGCCAGAAAAAAGGATGAGT
194361	26557	ACTAGCAGGACAACTAAGGG	238948	71144	TGACTGGGCACGGTGGCTCA	283535	115731	TAGCCAGAAAAAAGGATGAG
194362	26558	TACTAGCAGGACAACTAAGG	238949	71145	TTGACTGGGCACGGTGGCTC	283536	115732	GTAGCCAGAAAAAAGGATGA
194363	26559	CTACTAGCAGGACAACTAAG	238950	71146	GTTGACTGGGCACGGTGGCT	283537	115733	GGTAGCCAGAAAAAAGGATG
194364	26560	CCTACTAGCAGGACAACTAA	238951	71147	AGTTGACTGGGCACGGTGGC	283538	115734	TGGTAGCCAGAAAAAAGGAT
194365	26561	TCCTACTAGCAGGACAACTA	238952	71148	GAGTTGACTGGGCACGGTGG	283539	115735	TTGGTAGCCAGAAAAAAGGA
194366	26562	GTCCTACTAGCAGGACAACT	238953	71149	GGAGTTGACTGGGCACGGTG	283540	115736	TTTGGTAGCCAGAAAAAAGG
194367	26563	AGTCCTACTAGCAGGACAAC	238954	71150	AGGAGTTGACTGGGCACGGT	283541	115737	CTTTGGTAGCCAGAAAAAAG
194368	26564	AAGTCCTACTAGCAGGACAA	238955	71151	AAGGAGTTGACTGGGCACGG	283542	115738	CCTTTGGTAGCCAGAAAAAA
194369	26565	CAAGTCCTACTAGCAGGACA	238956	71152	GAAGGAGTTGACTGGGCACG	283543	115739	ACCTTTGGTAGCCAGAAAAA
194370	26566	GCAAGTCCTACTAGCAGGAC	238957	71153	AGAAGGAGTTGACTGGGCAC	283544	115740	CACCTTTGGTAGCCAGAAAA

194371	26567	TGCAAGTCCTACTAGCAGGA	238958	71154	GAGAAGGAGTTGACTGGGCA	283545	115741	GCACCTTTGGTAGCCAGAAA
194372	26568	TTGCAAGTCCTACTAGCAGG	238959	71155	TGAGAAGGAGTTGACTGGGC	283546	115742	TGCACCTTTGGTAGCCAGAA
194373	26569	ATTGCAAGTCCTACTAGCAG	238960	71156	TTGAGAAGGAGTTGACTGGG	283547	115743	CTGCACCTTTGGTAGCCAGA
194374	26570	AATTGCAAGTCCTACTAGCA	238961	71157	TTTGAGAAGGAGTTGACTGG	283548	115744	TCTGCACCTTTGGTAGCCAG
194375	26571	TAATTGCAAGTCCTACTAGC	238962	71158	TTTTGAGAAGGAGTTGACTG	283549	115745	ATCTGCACCTTTGGTAGCCA
194376	26572	TTAATTGCAAGTCCTACTAG	238963	71159	TTTTTGAGAAGGAGTTGACT	283550	115746	TATCTGCACCTTTGGTAGCC
194377	26573	TTTAATTGCAAGTCCTACTA	238964	71160	TTTTTTGAGAAGGAGTTGAC	283551	115747	TTATCTGCACCTTTGGTAGC
194378	26574	TTTTAATTGCAAGTCCTACT	238965	71161	TTTTTTTGAGAAGGAGTTGA	283552	115748	ATTATCTGCACCTTTGGTAG
194379	26575	CTTTTAATTGCAAGTCCTAC	238966	71162	TTTTTTTTGAGAAGGAGTTG	283553	115749	AATTATCTGCACCTTTGGTA
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194381	26577	TTCTTTTAATTGCAAGTCCT	238968	71164	TTTTTTTTTTGAGAAGGAGT	283555	115751	TTAATTATCTGCACCTTTGG
194382	26578	ATTCTTTTAATTGCAAGTCC	238969	71165	TTTTTTTTTTTGAGAAGGAG	283556	115752	ATTAATTATCTGCACCTTTG
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194384	26580	CAATTCTTTTAATTGCAAGT	238971	71167	TTTTTTTTTTTTTGAGAAGG	283558	115754	TTATTAATTATCTGCACCTT
194385	26581	CCAATTCTTTTAATTGCAAG	238972	71168	ATTTTTTTTTTTTTGAGAAG	283559	115755	CTTATTAATTATCTGCACCT
194386	26582	CCCAATTCTTTTAATTGCAA	238973	71169	TATTTTTTTTTTTTTGAGAA	283560	115756	TCTTATTAATTATCTGCACC
194387	26583	GCCCAATTCTTTTAATTGCA	238974	71170	CTATTTTTTTTTTTTTGAGA	283561	115757	TTCTTATTAATTATCTGCAC
194388	26584	GGCCCAATTCTTTTAATTGC	238975	71171	ACTATTTTTTTTTTTTTGAG	283562	115758	CTTCTTATTAATTATCTGCA
194389	26585	TGGCCCAATTCTTTTAATTG	238976	71172	CACTATTTTTTTTTTTTTGA	283563	115759	GCTTCTTATTAATTATCTGC
194390	26586	TTGGCCCAATTCTTTTAATT	238977	71173	GCACTATTTTTTTTTTTTTG	283564	115760	AGCTTCTTATTAATTATCTG
194391	26587	CTTGGCCCAATTCTTTTAAT	238978	71174	AGCACTATTTTTTTTTTTTT	283565	115761	CAGCTTCTTATTAATTATCT
194392	26588	TCTTGGCCCAATTCTTTTAA	238979	71175	CAGCACTATTTTTTTTTTTT	283566	115762	CCAGCTTCTTATTAATTATC
194393	26589	TTCTTGGCCCAATTCTTTTA	238980	71176	GCAGCACTATTTTTTTTTTT	283567	115763	TCCAGCTTCTTATTAATTAT
194394	26590	GTTCTTGGCCCAATTCTTTT	238981	71177	AGCAGCACTATTTTTTTTTT	283568	115764	ATCCAGCTTCTTATTAATTA
194395	26591	TGTTCTTGGCCCAATTCTTT	238982	71178	AAGCAGCACTATTTTTTTTT	283569	115765	GATCCAGCTTCTTATTAATT
194396	26592	GTGTTCTTGGCCCAATTCTT	238983	71179	AAAGCAGCACTATTTTTTTT	283570	115766	AGATCCAGCTTCTTATTAAT
194397	26593	AGTGTTCTTGGCCCAATTCT	238984	71180	GAAAGCAGCACTATTTTTTT	283571	115767	AAGATCCAGCTTCTTATTAA
194398	26594	AAGTGTTCTTGGCCCAATTC	238985	71181	AGAAAGCAGCACTATTTTTT	283572	115768	TAAGATCCAGCTTCTTATTA
194399	26595	GAAGTGTTCTTGGCCCAATT	238986	71182	GAGAAAGCAGCACTATTTTT	283573	115769	CTAAGATCCAGCTTCTTATT
194400	26596	AGAAGTGTTCTTGGCCCAAT	238987	71183	AGAGAAAGCAGCACTATTTT	283574	115770	GCTAAGATCCAGCTTCTTAT
194401	26597	TAGAAGTGTTCTTGGCCCAA	238988	71184	AAGAGAAAGCAGCACTATTT	283575	115771	TGCTAAGATCCAGCTTCTTA
194402	26598	GTAGAAGTGTTCTTGGCCCA	238989	71185	AAAGAGAAAGCAGCACTATT	283576	115772	TTGCTAAGATCCAGCTTCTT
194403	26599	CGTAGAAGTGTTCTTGGCCC	238990	71186	GAAAGAGAAAGCAGCACTAT	283577	115773	GTTGCTAAGATCCAGCTTCT
194404	26600	GCGTAGAAGTGTTCTTGGCC	238991	71187	TGAAAGAGAAAGCAGCACTA	283578	115774	CGTTGCTAAGATCCAGCTTC
194405	26601	AGCGTAGAAGTGTTCTTGGC	238992	71188	TTGAAAGAGAAAGCAGCACT	283579	115775	ACGTTGCTAAGATCCAGCTT
194406	26602	AAGCGTAGAAGTGTTCTTGG	238993	71189	CTTGAAAGAGAAAGCAGCAC	283580	115776	GACGTTGCTAAGATCCAGCT
194407	26603	GAAGCGTAGAAGTGTTCTTG	238994	71190	ACTTGAAAGAGAAAGCAGCA	283581	115777	GGACGTTGCTAAGATCCAGC
194408	26604	AGAAGCGTAGAAGTGTTCTT	238995	71191	CACTTGAAAGAGAAAGCAGC	283582	115778	TGGACGTTGCTAAGATCCAG
194409	26605	GAGAAGCGTAGAAGTGTTCT	238996	71192	ACACTTGAAAGAGAAAGCAG	283583	115779	CTGGACGTTGCTAAGATCCA
194410	26606	GGAGAAGCGTAGAAGTGTTC	238997	71193	GACACTTGAAAGAGAAAGCA	283584	115780	ACTGGACGTTGCTAAGATCC
194411	26607	AGGAGAAGCGTAGAAGTGTT	238998	71194	GGACACTTGAAAGAGAAAGC	283585	115781	GACTGGACGTTGCTAAGATC
194412	26608	AAGGAGAAGCGTAGAAGTGT	238999	71195	AGGACACTTGAAAGAGAAAG	283586	115782	GGACTGGACGTTGCTAAGAT
194413	26609	AAAGGAGAAGCGTAGAAGTG	239000	71196	CAGGACACTTGAAAGAGAAA	283587	115783	TGGACTGGACGTTGCTAAGA
194414	26610	AAAAGGAGAAGCGTAGAAGT	239001	71197	TCAGGACACTTGAAAGAGAA	283588	115784	TTGGACTGGACGTTGCTAAG
194415	26611	TAAAAGGAGAAGCGTAGAAG	239002	71198	ATCAGGACACTTGAAAGAGA	283589	115785	CTTGGACTGGACGTTGCTAA
194416	26612	CTAAAAGGAGAAGCGTAGAA	239003	71199	AATCAGGACACTTGAAAGAG	283590	115786	ACTTGGACTGGACGTTGCTA
194417	26613	CCTAAAAGGAGAAGCGTAGA	239004	71200	AAATCAGGACACTTGAAAGA	283591	115787	CACTTGGACTGGACGTTGCT
194418	26614	ACCTAAAAGGAGAAGCGTAG	239005	71201	CAAATCAGGACACTTGAAAG	283592	115788	ACACTTGGACTGGACGTTGC
194419	26615	AACCTAAAAGGAGAAGCGTA	239006	71202	CCAAATCAGGACACTTGAAA	283593	115789	CACACTTGGACTGGACGTTG
194420	26616	AAACCTAAAAGGAGAAGCGT	239007	71203	CCCAAATCAGGACACTTGAA	283594	115790	CCACACTTGGACTGGACGTT
194421	26617	CAAACCTAAAAGGAGAAGCG	239008	71204	ACCCAAATCAGGACACTTGA	283595	115791	GCCACACTTGGACTGGACGT
194422	26618	CCAAACCTAAAAGGAGAAGC	239009	71205	CACCCAAATCAGGACACTTG	283596	115792	AGCCACACTTGGACTGGACG
194423	26619	CCCAAACCTAAAAGGAGAAG	239010	71206	TCACCCAAATCAGGACACTT	283597	115793	GAGCCACACTTGGACTGGAC
194424	26620	ACCCAAACCTAAAAGGAGAA	239011	71207	ATCACCCAAATCAGGACACT	283598	115794	TGAGCCACACTTGGACTGGA
194425	26621	CACCCAAACCTAAAAGGAGA	239012	71208	TATCACCCAAATCAGGACAC	283599	115795	TTGAGCCACACTTGGACTGG
194426	26622	ACACCCAAACCTAAAAGGAG	239013	71209	CTATCACCCAAATCAGGACA	283600	115796	TTTGAGCCACACTTGGACTG
194427	26623	TACACCCAAACCTAAAAGGA	239014	71210	ACTATCACCCAAATCAGGAC	283601	115797	CTTTGAGCCACACTTGGACT
194428	26624	TTACACCCAAACCTAAAAGG	239015	71211	TACTATCACCCAAATCAGGA	283602	115798	CCTTTGAGCCACACTTGGAC
194429	26625	TTTACACCCAAACCTAAAAG	239016	71212	TTACTATCACCCAAATCAGG	283603	115799	TCCTTTGAGCCACACTTGGA
194430	26626	ATTTACACCCAAACCTAAAA	239017	71213	TTTACTATCACCCAAATCAG	283604	115800	ATCCTTTGAGCCACACTTGG
194431	26627	AATTTACACCCAAACCTAAA	239018	71214	ATTTACTATCACCCAAATCA	283605	115801	TATCCTTTGAGCCACACTTG
194432	26628	GAATTTACACCCAAACCTAA	239019	71215	CATTTACTATCACCCAAATC	283606	115802	TTATCCTTTGAGCCACACTT
194433	26629	CGAATTTACACCCAAACCTA	239020	71216	GCATTTACTATCACCCAAAT	283607	115803	ATTATCCTTTGAGCCACACT
194434	26630	CCGAATTTACACCCAAACCT	239021	71217	GGCATTTACTATCACCCAAA	283608	115804	TATTATCCTTTGAGCCACAC
194435	26631	CCCGAATTTACACCCAAACC	239022	71218	TGGCATTTACTATCACCCAA	283609	115805	ATATTATCCTTTGAGCCACA
194436	26632	CCCCGAATTTACACCCAAAC	239023	71219	GTGGCATTTACTATCACCCA	283610	115806	GATATTATCCTTTGAGCCAC
194437	26633	ACCCCGAATTTACACCCAAA	239024	71220	AGTGGCATTTACTATCACCC	283611	115807	TGATATTATCCTTTGAGCCA
194438	26634	TACCCCGAATTTACACCCAA	239025	71221	GAGTGGCATTTACTATCACC	283612	115808	TTGATATTATCCTTTGAGCC
194439	26635	ATACCCCGAATTTACACCCA	239026	71222	AGAGTGGCATTTACTATCAC	283613	115809	TTTGATATTATCCTTTGAGC
194440	26636	AATACCCCGAATTTACACCC	239027	71223	TAGAGTGGCATTTACTATCA	283614	115810	GTTTGATATTATCCTTTGAG
194441	26637	AAATACCCCGAATTTACACC	239028	71224	GTAGAGTGGCATTTACTATC	283615	115811	TGTTTGATATTATCCTTTGA
194442	26638	GAAATACCCCGAATTTACAC	239029	71225	AGTAGAGTGGCATTTACTAT	283616	115812	GTGTTTGATATTATCCTTTG

194443	26639	AGAAATACCCCGAATTTACA	239030	71226	AAGTAGAGTGGCATTTACTA	283617	115813	CGTGTTTGATATTATCCTTT
194444	26640	GAGAAATACCCCGAATTTAC	239031	71227	TAAGTAGAGTGGCATTTACT	283618	115814	ACGTGTTTGATATTATCCTT
194445	26641	TGAGAAATACCCCGAATTTA	239032	71228	ATAAGTAGAGTGGCATTTAC	283619	115815	GACGTGTTTGATATTATCCT
194446	26642	GTGAGAAATACCCCGAATTT	239033	71229	TATAAGTAGAGTGGCATTTA	283620	115816	GGACGTGTTTGATATTATCC
194447	26643	AGTGAGAAATACCCCGAATT	239034	71230	TTATAAGTAGAGTGGCATTT	283621	115817	GGGACGTGTTTGATATTATC
194448	26644	CAGTGAGAAATACCCCGAAT	239035	71231	CTTATAAGTAGAGTGGCATT	283622	115818	CGGGACGTGTTTGATATTAT
194449	26645	TCAGTGAGAAATACCCCGAA	239036	71232	CCTTATAAGTAGAGTGGCAT	283623	115819	CCGGGACGTGTTTGATATTA
194450	26646	ATCAGTGAGAAATACCCCGA	239037	71233	CCCTTATAAGTAGAGTGGCA	283624	115820	CCCGGGACGTGTTTGATATT
194451	26647	CATCAGTGAGAAATACCCCG	239038	71234	TCCCTTATAAGTAGAGTGGC	283625	115821	TCCCGGGACGTGTTTGATAT
194452	26648	TCATCAGTGAGAAATACCCC	239039	71235	ATCCCTTATAAGTAGAGTGG	283626	115822	CTCCCGGGACGTGTTTGATA
194453	26649	TTCATCAGTGAGAAATACCC	239040	71236	GATCCCTTATAAGTAGAGTG	283627	115823	CCTCCCGGGACGTGTTTGAT
194454	26650	TTTCATCAGTGAGAAATACC	239041	71237	AGATCCCTTATAAGTAGAGT	283628	115824	GCCTCCCGGGACGTGTTTGA
194455	26651	CTTTCATCAGTGAGAAATAC	239042	71238	TAGATCCCTTATAAGTAGAG	283629	115825	CGCCTCCCGGGACGTGTTTG
194456	26652	GCTTTCATCAGTGAGAAATA	239043	71239	GTAGATCCCTTATAAGTAGA	283630	115826	CCGCCTCCCGGGACGTGTTT
194457	26653	GGCTTTCATCAGTGAGAAAT	239044	71240	GGTAGATCCCTTATAAGTAG	283631	115827	GCCGCCTCCCGGGACGTGTT
194458	26654	AGGCTTTCATCAGTGAGAAA	239045	71241	AGGTAGATCCCTTATAAGTA	283632	115828	TGCCGCCTCCCGGGACGTGT
194459	26655	CAGGCTTTCATCAGTGAGAA	239046	71242	GAGGTAGATCCCTTATAAGT	283633	115829	CTGCCGCCTCCCGGGACGTG
194460	26656	CCAGGCTTTCATCAGTGAGA	239047	71243	TGAGGTAGATCCCTTATAAG	283634	115830	ACTGCCGCCTCCCGGGACGT
194461	26657	ACCAGGCTTTCATCAGTGAG	239048	71244	CTGAGGTAGATCCCTTATAA	283635	115831	CACTGCCGCCTCCCGGGACG
194462	26658	CACCAGGCTTTCATCAGTGA	239049	71245	TCTGAGGTAGATCCCTTATA	283636	115832	ACACTGCCGCCTCCCGGGAC
194463	26659	GCACCAGGCTTTCATCAGTG	239050	71246	TTCTGAGGTAGATCCCTTAT	283637	115833	CACACTGCCGCCTCCCGGGA
194464	26660	TGCACCAGGCTTTCATCAGT	239051	71247	ATTCTGAGGTAGATCCCTTA	283638	115834	TCACACTGCCGCCTCCCGGG
194465	26661	CTGCACCAGGCTTTCATCAG	239052	71248	CATTCTGAGGTAGATCCCTT	283639	115835	CTCACACTGCCGCCTCCCGG
194466	26662	CCTGCACCAGGCTTTCATCA	239053	71249	GCATTCTGAGGTAGATCCCT	283640	115836	ACTCACACTGCCGCCTCCCG
194467	26663	CCCTGCACCAGGCTTTCATC	239054	71250	AGCATTCTGAGGTAGATCCC	283641	115837	TACTCACACTGCCGCCTCCC
194468	26664	GCCCTGCACCAGGCTTTCAT	239055	71251	TAGCATTCTGAGGTAGATCC	283642	115838	GTACTCACACTGCCGCCTCC
194469	26665	TGCCCTGCACCAGGCTTTCA	239056	71252	TTAGCATTCTGAGGTAGATC	283643	115839	GGTACTCACACTGCCGCCTC
194470	26666	CTGCCCTGCACCAGGCTTTC	239057	71253	ATTAGCATTCTGAGGTAGAT	283644	115840	AGGTACTCACACTGCCGCCT
194471	26667	TCTGCCCTGCACCAGGCTTT	239058	71254	AATTAGCATTCTGAGGTAGA	283645	115841	AAGGTACTCACACTGCCGCC
194472	26668	GTCTGCCCTGCACCAGGCTT	239059	71255	CAATTAGCATTCTGAGGTAG	283646	115842	GAAGGTACTCACACTGCCGC
194473	26669	GGTCTGCCCTGCACCAGGCT	239060	71256	CCAATTAGCATTCTGAGGTA	283647	115843	TGAAGGTACTCACACTGCCG
194474	26670	CGGTCTGCCCTGCACCAGGC	239061	71257	CCCAATTAGCATTCTGAGGT	283648	115844	GTGAAGGTACTCACACTGCC
194475	26671	ACGGTCTGCCCTGCACCAGG	239062	71258	TCCCAATTAGCATTCTGAGG	283649	115845	TGTGAAGGTACTCACACTGC
194476	26672	CACGGTCTGCCCTGCACCAG	239063	71259	GTCCCAATTAGCATTCTGAG	283650	115846	GTGTGAAGGTACTCACACTG
194477	26673	CCACGGTCTGCCCTGCACCA	239064	71260	TGTCCCAATTAGCATTCTGA	283651	115847	CGTGTGAAGGTACTCACACT
194478	26674	CCCACGGTCTGCCCTGCACC	239065	71261	ATGTCCCAATTAGCATTCTG	283652	115848	ACGTGTGAAGGTACTCACAC
194479	26675	TCCCACGGTCTGCCCTGCAC	239066	71262	AATGTCCCAATTAGCATTCT	283653	115849	GACGTGTGAAGGTACTCACA
194480	26676	TTCCCACGGTCTGCCCTGCA	239067	71263	AAATGTCCCAATTAGCATTC	283654	115850	GGACGTGTGAAGGTACTCAC
194481	26677	CTTCCCACGGTCTGCCCTGC	239068	71264	AAAATGTCCCAATTAGCATT	283655	115851	GGGACGTGTGAAGGTACTCA
194482	26678	GCTTCCCACGGTCTGCCCTG	239069	71265	AAAAATGTCCCAATTAGCAT	283656	115852	TGGGACGTGTGAAGGTACTC
194483	26679	AGCTTCCCACGGTCTGCCCT	239070	71266	CAAAAATGTCCCAATTAGCA	283657	115853	ATGGGACGTGTGAAGGTACT
194484	26680	AAGCTTCCCACGGTCTGCCC	239071	71267	ACAAAAATGTCCCAATTAGC	283658	115854	CATGGGACGTGTGAAGGTAC
194485	26681	AAAGCTTCCCACGGTCTGCC	239072	71268	TACAAAAATGTCCCAATTAG	283659	115855	GCATGGGACGTGTGAAGGTA
194486	26682	GAAAGCTTCCCACGGTCTGC	239073	71269	CTACAAAAATGTCCCAATTA	283660	115856	CGCATGGGACGTGTGAAGGT
194487	26683	TGAAAGCTTCCCACGGTCTG	239074	71270	GCTACAAAAATGTCCCAATT	283661	115857	GCGCATGGGACGTGTGAAGG
194488	26684	ATGAAAGCTTCCCACGGTCT	239075	71271	TGCTACAAAAATGTCCCAAT	283662	115858	GGCGCATGGGACGTGTGAAG
194489	26685	AATGAAAGCTTCCCACGGTC	239076	71272	GTGCTACAAAAATGTCCCAA	283663	115859	CGGCGCATGGGACGTGTGAA
194490	26686	AAATGAAAGCTTCCCACGGT	239077	71273	AGTGCTACAAAAATGTCCCA	283664	115860	ACGGCGCATGGGACGTGTGA
194491	26687	GAAATGAAAGCTTCCCACGG	239078	71274	GAGTGCTACAAAAATGTCCC	283665	115861	CACGGCGCATGGGACGTGTG
194492	26688	GGAAATGAAAGCTTCCCACG	239079	71275	AGAGTGCTACAAAAATGTCC	283666	115862	GCACGGCGCATGGGACGTGT
194493	26689	CGGAAATGAAAGCTTCCCAC	239080	71276	TAGAGTGCTACAAAAATGTC	283667	115863	AGCACGGCGCATGGGACGTG
194494	26690	CCGGAAATGAAAGCTTCCCA	239081	71277	GTAGAGTGCTACAAAAATGT	283668	115864	CAGCACGGCGCATGGGACGT
194495	26691	TCCGGAAATGAAAGCTTCCC	239082	71278	AGTAGAGTGCTACAAAAATG	283669	115865	ACAGCACGGCGCATGGGACG
194496	26692	TTCCGGAAATGAAAGCTTCC	239083	71279	CAGTAGAGTGCTACAAAAAT	283670	115866	CACAGCACGGCGCATGGGAC
194497	26693	ATTCCGGAAATGAAAGCTTC	239084	71280	ACAGTAGAGTGCTACAAAAA	283671	115867	CCACAGCACGGCGCATGGGA
194498	26694	CATTCCGGAAATGAAAGCTT	239085	71281	AACAGTAGAGTGCTACAAAA	283672	115868	GCCACAGCACGGCGCATGGG
194499	26695	CCATTCCGGAAATGAAAGCT	239086	71282	CAACAGTAGAGTGCTACAAA	283673	115869	AGCCACAGCACGGCGCATGG
194500	26696	TCCATTCCGGAAATGAAAGC	239087	71283	CCAACAGTAGAGTGCTACAA	283674	115870	AAGCCACAGCACGGCGCATG
194501	26697	GTCCATTCCGGAAATGAAAG	239088	71284	GCCAACAGTAGAGTGCTACA	283675	115871	CAAGCCACAGCACGGCGCAT
194502	26698	GGTCCATTCCGGAAATGAAA	239089	71285	TGCCAACAGTAGAGTGCTAC	283676	115872	TCAAGCCACAGCACGGCGCA
194503	26699	TGGTCCATTCCGGAAATGAA	239090	71286	CTGCCAACAGTAGAGTGCTA	283677	115873	TTCAAGCCACAGCACGGCGC
194504	26700	ATGGTCCATTCCGGAAATGA	239091	71287	GCTGCCAACAGTAGAGTGCT	283678	115874	ATTCAAGCCACAGCACGGCG
194505	26701	GATGGTCCATTCCGGAAATG	239092	71288	TGCTGCCAACAGTAGAGTGC	283679	115875	AATTCAAGCCACAGCACGGC
194506	26702	TGATGGTCCATTCCGGAAAT	239093	71289	CTGCTGCCAACAGTAGAGTG	283680	115876	TAATTCAAGCCACAGCACGG
194507	26703	TTGATGGTCCATTCCGGAAA	239094	71290	CCTGCTGCCAACAGTAGAGT	283681	115877	ATAATTCAAGCCACAGCACG
194508	26704	GTTGATGGTCCATTCCGGAA	239095	71291	ACCTGCTGCCAACAGTAGAG	283682	115878	AATAATTCAAGCCACAGCAC
194509	26705	TGTTGATGGTCCATTCCGGA	239096	71292	CACCTGCTGCCAACAGTAGA	283683	115879	TAATAATTCAAGCCACAGCA
194510	26706	ATGTTGATGGTCCATTCCGG	239097	71293	TCACCTGCTGCCAACAGTAG	283684	115880	CTAATAATTCAAGCCACAGC
194511	26707	GATGTTGATGGTCCATTCCG	239098	71294	ATCACCTGCTGCCAACAGTA	283685	115881	CCTAATAATTCAAGCCACAG
194512	26708	GGATGTTGATGGTCCATTCC	239099	71295	CATCACCTGCTGCCAACAGT	283686	115882	TCCTAATAATTCAAGCCACA
194513	26709	GGGATGTTGATGGTCCATTC	239100	71296	GCATCACCTGCTGCCAACAG	283687	115883	TTCCTAATAATTCAAGCCAC
194514	26710	AGGGATGTTGATGGTCCATT	239101	71297	AGCATCACCTGCTGCCAACA	283688	115884	CTTCCTAATAATTCAAGCCA

194515	26711	AAGGGATGTTGATGGTCCAT	239102	71298	GAGCATCACCTGCTGCCAAC	283689	115885	ACTTCCTAATAATTCAAGCC
194516	26712	CAAGGGATGTTGATGGTCCA	239103	71299	TGAGCATCACCTGCTGCCAA	283690	115886	CACTTCCTAATAATTCAAGC
194517	26713	CCAAGGGATGTTGATGGTCC	239104	71300	GTGAGCATCACCTGCTGCCA	283691	115887	CCACTTCCTAATAATTCAAG
194518	26714	TCCAAGGGATGTTGATGGTC	239105	71301	TGTGAGCATCACCTGCTGCC	283692	115888	ACCACTTCCTAATAATTCAA
194519	26715	CTCCAAGGGATGTTGATGGT	239106	71302	TTGTGAGCATCACCTGCTGC	283693	115889	CACCACTTCCTAATAATTCA
194520	26716	TCTCCAAGGGATGTTGATGG	239107	71303	GTTGTGAGCATCACCTGCTG	283694	115890	ACACCACTTCCTAATAATTC
194521	26717	TTCTCCAAGGGATGTTGATG	239108	71304	TGTTGTGAGCATCACCTGCT	283695	115891	CACACCACTTCCTAATAATT
194522	26718	CTTCTCCAAGGGATGTTGAT	239109	71305	CTGTTGTGAGCATCACCTGC	283696	115892	TCACACCACTTCCTAATAAT
194523	26719	TCTTCTCCAAGGGATGTTGA	239110	71306	GCTGTTGTGAGCATCACCTG	283697	115893	CTCACACCACTTCCTAATAA
194524	26720	TTCTTCTCCAAGGGATGTTG	239111	71307	GGCTGTTGTGAGCATCACCT	283698	115894	ACTCACACCACTTCCTAATA
194525	26721	ATTCTTCTCCAAGGGATGTT	239112	71308	GGGCTGTTGTGAGCATCACC	283699	115895	CACTCACACCACTTCCTAAT
194526	26722	AATTCTTCTCCAAGGGATGT	239113	71309	CGGGCTGTTGTGAGCATCAC	283700	115896	GCACTCACACCACTTCCTAA
194527	26723	GAATTCTTCTCCAAGGGATG	239114	71310	ACGGGCTGTTGTGAGCATCA	283701	115897	CGCACTCACACCACTTCCTA
194528	26724	AGAATTCTTCTCCAAGGGAT	239115	71311	CACGGGCTGTTGTGAGCATC	283702	115898	ACGCACTCACACCACTTCCT
194529	26725	GAGAATTCTTCTCCAAGGGA	239116	71312	TCACGGGCTGTTGTGAGCAT	283703	115899	TACGCACTCACACCACTTCC
194530	26726	AGAGAATTCTTCTCCAAGGG	239117	71313	CTCACGGGCTGTTGTGAGCA	283704	115900	GTACGCACTCACACCACTTC
194531	26727	AAGAGAATTCTTCTCCAAGG	239118	71314	CCTCACGGGCTGTTGTGAGC	283705	115901	TGTACGCACTCACACCACTT
194532	26728	GAAGAGAATTCTTCTCCAAG	239119	71315	CCCTCACGGGCTGTTGTGAG	283706	115902	GTGTACGCACTCACACCACT
194533	26729	AGAAGAGAATTCTTCTCCAA	239120	71316	ACCCTCACGGGCTGTTGTGA	283707	115903	AGTGTACGCACTCACACCAC
194534	26730	GAGAAGAGAATTCTTCTCCA	239121	71317	CACCCTCACGGGCTGTTGTG	283708	115904	AAGTGTACGCACTCACACCA
194535	26731	GGAGAAGAGAATTCTTCTCC	239122	71318	CCACCCTCACGGGCTGTTGT	283709	115905	CAAGTGTACGCACTCACACC
194536	26732	TGGAGAAGAGAATTCTTCTC	239123	71319	TCCACCCTCACGGGCTGTTG	283710	115906	GCAAGTGTACGCACTCACAC
194537	26733	CTGGAGAAGAGAATTCTTCT	239124	71320	ATCCACCCTCACGGGCTGTT	283711	115907	CGCAAGTGTACGCACTCACA
194538	26734	TCTGGAGAAGAGAATTCTTC	239125	71321	CATCCACCCTCACGGGCTGT	283712	115908	TCGCAAGTGTACGCACTCAC
194539	26735	GTCTGGAGAAGAGAATTCTT	239126	71322	TCATCCACCCTCACGGGCTG	283713	115909	CTCGCAAGTGTACGCACTCA
194540	26736	GGTCTGGAGAAGAGAATTCT	239127	71323	GTCATCCACCCTCACGGGCT	283714	115910	TCTCGCAAGTGTACGCACTC
194541	26737	GGGTCTGGAGAAGAGAATTC	239128	71324	CGTCATCCACCCTCACGGGC	283715	115911	GTCTCGCAAGTGTACGCACT
194542	26738	TGGGTCTGGAGAAGAGAATT	239129	71325	ACGTCATCCACCCTCACGGG	283716	115912	TGTCTCGCAAGTGTACGCAC
194543	26739	CTGGGTCTGGAGAAGAGAAT	239130	71326	GACGTCATCCACCCTCACGG	283717	115913	GTGTCTCGCAAGTGTACGCA
194544	26740	TCTGGGTCTGGAGAAGAGAA	239131	71327	GGACGTCATCCACCCTCACG	283718	115914	AGTGTCTCGCAAGTGTACGC
194545	26741	GTCTGGGTCTGGAGAAGAGA	239132	71328	CGGACGTCATCCACCCTCAC	283719	115915	CAGTGTCTCGCAAGTGTACG
194546	26742	GGTCTGGGTCTGGAGAAGAG	239133	71329	GCGGACGTCATCCACCCTCA	283720	115916	GCAGTGTCTCGCAAGTGTAC
194547	26743	AGGTCTGGGTCTGGAGAAGA	239134	71330	AGCGGACGTCATCCACCCTC	283721	115917	TGCAGTGTCTCGCAAGTGTA
194548	26744	CAGGTCTGGGTCTGGAGAAG	239135	71331	AAGCGGACGTCATCCACCCT	283722	115918	ATGCAGTGTCTCGCAAGTGT
194549	26745	CCAGGTCTGGGTCTGGAGAA	239136	71332	GAAGCGGACGTCATCCACCC	283723	115919	TATGCAGTGTCTCGCAAGTG
194550	26746	ACCAGGTCTGGGTCTGGAGA	239137	71333	TGAAGCGGACGTCATCCACC	283724	115920	CTATGCAGTGTCTCGCAAGT
194551	26747	CACCAGGTCTGGGTCTGGAG	239138	71334	GTGAAGCGGACGTCATCCAC	283725	115921	TCTATGCAGTGTCTCGCAAG
194552	26748	ACACCAGGTCTGGGTCTGGA	239139	71335	TGTGAAGCGGACGTCATCCA	283726	115922	TTCTATGCAGTGTCTCGCAA
194553	26749	GACACCAGGTCTGGGTCTGG	239140	71336	CTGTGAAGCGGACGTCATCC	283727	115923	ATTCTATGCAGTGTCTCGCA
194554	26750	GGACACCAGGTCTGGGTCTG	239141	71337	TCTGTGAAGCGGACGTCATC	283728	115924	TATTCTATGCAGTGTCTCGC
194555	26751	AGGACACCAGGTCTGGGTCT	239142	71338	ATCTGTGAAGCGGACGTCAT	283729	115925	TTATTCTATGCAGTGTCTCG
194556	26752	CAGGACACCAGGTCTGGGTC	239143	71339	CATCTGTGAAGCGGACGTCA	283730	115926	TTTATTCTATGCAGTGTCTC
194557	26753	CCAGGACACCAGGTCTGGGT	239144	71340	TCATCTGTGAAGCGGACGTC	283731	115927	ATTTATTCTATGCAGTGTCT
194558	26754	GCCAGGACACCAGGTCTGGG	239145	71341	GTCATCTGTGAAGCGGACGT	283732	115928	GATTTATTCTATGCAGTGTC
194559	26755	TGCCAGGACACCAGGTCTGG	239146	71342	TGTCATCTGTGAAGCGGACG	283733	115929	GGATTTATTCTATGCAGTGT
194560	26756	GTGCCAGGACACCAGGTCTG	239147	71343	TTGTCATCTGTGAAGCGGAC	283734	115930	AGGATTTATTCTATGCAGTG
194561	26757	GGTGCCAGGACACCAGGTCT	239148	71344	TTTGTCATCTGTGAAGCGGA	283735	115931	AAGGATTTATTCTATGCAGT
194562	26758	GGGTGCCAGGACACCAGGTC	239149	71345	CTTTGTCATCTGTGAAGCGG	283736	115932	GAAGGATTTATTCTATGCAG
194563	26759	TGGGTGCCAGGACACCAGGT	239150	71346	CCTTTGTCATCTGTGAAGCG	283737	115933	AGAAGGATTTATTCTATGCA
194564	26760	ATGGGTGCCAGGACACCAGG	239151	71347	TCCTTTGTCATCTGTGAAGC	283738	115934	AAGAAGGATTTATTCTATGC
194565	26761	AATGGGTGCCAGGACACCAG	239152	71348	CTCCTTTGTCATCTGTGAAG	283739	115935	CAAGAAGGATTTATTCTATG
194566	26762	CAATGGGTGCCAGGACACCA	239153	71349	GCTCCTTTGTCATCTGTGAA	283740	115936	CCAAGAAGGATTTATTCTAT
194567	26763	CCAATGGGTGCCAGGACACC	239154	71350	GGCTCCTTTGTCATCTGTGA	283741	115937	CCCAAGAAGGATTTATTCTA
194568	26764	CCCAATGGGTGCCAGGACAC	239155	71351	AGGCTCCTTTGTCATCTGTG	283742	115938	GCCCAAGAAGGATTTATTCT
194569	26765	GCCCAATGGGTGCCAGGACA	239156	71352	GAGGCTCCTTTGTCATCTGT	283743	115939	AGCCCAAGAAGGATTTATTC
194570	26766	TGCCCAATGGGTGCCAGGAC	239157	71353	TGAGGCTCCTTTGTCATCTG	283744	115940	GAGCCCAAGAAGGATTTATT
194571	26767	TTGCCCAATGGGTGCCAGGA	239158	71354	ATGAGGCTCCTTTGTCATCT	283745	115941	AGAGCCCAAGAAGGATTTAT
194572	26768	CTTGCCCAATGGGTGCCAGG	239159	71355	CATGAGGCTCCTTTGTCATC	283746	115942	GAGAGCCCAAGAAGGATTTA
194573	26769	ACTTGCCCAATGGGTGCCAG	239160	71356	GCATGAGGCTCCTTTGTCAT	283747	115943	TGAGAGCCCAAGAAGGATTT
194574	26770	CACTTGCCCAATGGGTGCCA	239161	71357	AGCATGAGGCTCCTTTGTCA	283748	115944	CTGAGAGCCCAAGAAGGATT
194575	26771	CCACTTGCCCAATGGGTGCC	239162	71358	GAGCATGAGGCTCCTTTGTC	283749	115945	CCTGAGAGCCCAAGAAGGAT
194576	26772	CCCACTTGCCCAATGGGTGC	239163	71359	TGAGCATGAGGCTCCTTTGT	283750	115946	TCCTGAGAGCCCAAGAAGGA
194577	26773	ACCCACTTGCCCAATGGGTG	239164	71360	CTGAGCATGAGGCTCCTTTG	283751	115947	ATCCTGAGAGCCCAAGAAGG
194578	26774	GACCCACTTGCCCAATGGGT	239165	71361	TCTGAGCATGAGGCTCCTTT	283752	115948	GATCCTGAGAGCCCAAGAAG
194579	26775	GGACCCACTTGCCCAATGGG	239166	71362	GTCTGAGCATGAGGCTCCTT	283753	115949	AGATCCTGAGAGCCCAAGAA
194580	26776	AGGACCCACTTGCCCAATGG	239167	71363	GGTCTGAGCATGAGGCTCCT	283754	115950	CAGATCCTGAGAGCCCAAGA
194581	26777	TAGGACCCACTTGCCCAATG	239168	71364	CGGTCTGAGCATGAGGCTCC	283755	115951	CCAGATCCTGAGAGCCCAAG
194582	26778	CTAGGACCCACTTGCCCAAT	239169	71365	ACGGTCTGAGCATGAGGCTC	283756	115952	GCCAGATCCTGAGAGCCCAA
194583	26779	TCTAGGACCCACTTGCCCAA	239170	71366	CACGGTCTGAGCATGAGGCT	283757	115953	AGCCAGATCCTGAGAGCCCA
194584	26780	TTCTAGGACCCACTTGCCCA	239171	71367	CCACGGTCTGAGCATGAGGC	283758	115954	CAGCCAGATCCTGAGAGCCC
194585	26781	CTTCTAGGACCCACTTGCCC	239172	71368	CCCACGGTCTGAGCATGAGG	283759	115955	GCAGCCAGATCCTGAGAGCC
194586	26782	TCTTCTAGGACCCACTTGCC	239173	71369	GCCCACGGTCTGAGCATGAG	283760	115956	CGCAGCCAGATCCTGAGAGC

194587	26783	GTCTTCTAGGACCCACTTGC	239174	71370	AGCCCACGGTCTGAGCATGA	283761	115957	TCGCAGCCAGATCCTGAGAG
194588	26784	TGTCTTCTAGGACCCACTTG	239175	71371	CAGCCCACGGTCTGAGCATG	283762	115958	GTCGCAGCCAGATCCTGAGA
194589	26785	TTGTCTTCTAGGACCCACTT	239176	71372	GCAGCCCACGGTCTGAGCAT	283763	115959	GGTCGCAGCCAGATCCTGAG
194590	26786	TTTGTCTTCTAGGACCCACT	239177	71373	GGCAGCCCACGGTCTGAGCA	283764	115960	AGGTCGCAGCCAGATCCTGA
194591	26787	GTTTGTCTTCTAGGACCCAC	239178	71374	TGGCAGCCCACGGTCTGAGC	283765	115961	GAGGTCGCAGCCAGATCCTG
194592	26788	GGTTTGTCTTCTAGGACCCA	239179	71375	CTGGCAGCCCACGGTCTGAG	283766	115962	AGAGGTCGCAGCCAGATCCT
194593	26789	AGGTTTGTCTTCTAGGACCC	239180	71376	TCTGGCAGCCCACGGTCTGA	283767	115963	CAGAGGTCGCAGCCAGATCC
194594	26790	CAGGTTTGTCTTCTAGGACC	239181	71377	CTCTGGCAGCCCACGGTCTG	283768	115964	CCAGAGGTCGCAGCCAGATC
194595	26791	CCAGGTTTGTCTTCTAGGAC	239182	71378	GCTCTGGCAGCCCACGGTCT	283769	115965	CCCAGAGGTCGCAGCCAGAT
194596	26792	ACCAGGTTTGTCTTCTAGGA	239183	71379	TGCTCTGGCAGCCCACGGTC	283770	115966	ACCCAGAGGTCGCAGCCAGA
194597	26793	GACCAGGTTTGTCTTCTAGG	239184	71380	CTGCTCTGGCAGCCCACGGT	283771	115967	CACCCAGAGGTCGCAGCCAG
194598	26794	TGACCAGGTTTGTCTTCTAG	239185	71381	CCTGCTCTGGCAGCCCACGG	283772	115968	TCACCCAGAGGTCGCAGCCA
194599	26795	CTGACCAGGTTTGTCTTCTA	239186	71382	ACCTGCTCTGGCAGCCCACG	283773	115969	TTCACCCAGAGGTCGCAGCC
194600	26796	TCTGACCAGGTTTGTCTTCT	239187	71383	GACCTGCTCTGGCAGCCCAC	283774	115970	ATTCACCCAGAGGTCGCAGC
194601	26797	CTCTGACCAGGTTTGTCTTC	239188	71384	GGACCTGCTCTGGCAGCCCA	283775	115971	CATTCACCCAGAGGTCGCAG
194602	26798	GCTCTGACCAGGTTTGTCTT	239189	71385	TGGACCTGCTCTGGCAGCCC	283776	115972	ACATTCACCCAGAGGTCGCA
194603	26799	GGCTCTGACCAGGTTTGTCT	239190	71386	ATGGACCTGCTCTGGCAGCC	283777	115973	TACATTCACCCAGAGGTCGC
194604	26800	AGGCTCTGACCAGGTTTGTC	239191	71387	CATGGACCTGCTCTGGCAGC	283778	115974	CTACATTCACCCAGAGGTCG
194605	26801	CAGGCTCTGACCAGGTTTGT	239192	71388	CCATGGACCTGCTCTGGCAG	283779	115975	GCTACATTCACCCAGAGGTC
194606	26802	CCAGGCTCTGACCAGGTTTG	239193	71389	GCCATGGACCTGCTCTGGCA	283780	115976	GGCTACATTCACCCAGAGGT
194607	26803	TCCAGGCTCTGACCAGGTTT	239194	71390	AGCCATGGACCTGCTCTGGC	283781	115977	GGGCTACATTCACCCAGAGG
194608	26804	CTCCAGGCTCTGACCAGGTT	239195	71391	CAGCCATGGACCTGCTCTGG	283782	115978	CGGGCTACATTCACCCAGAG
194609	26805	CCTCCAGGCTCTGACCAGGT	239196	71392	GCAGCCATGGACCTGCTCTG	283783	115979	CCGGGCTACATTCACCCAGA
194610	26806	GCCTCCAGGCTCTGACCAGG	239197	71393	TGCAGCCATGGACCTGCTCT	283784	115980	GCCGGGCTACATTCACCCAG
194611	26807	AGCCTCCAGGCTCTGACCAG	239198	71394	CTGCAGCCATGGACCTGCTC	283785	115981	AGCCGGGCTACATTCACCCA
194612	26808	CAGCCTCCAGGCTCTGACCA	239199	71395	GCTGCAGCCATGGACCTGCT	283786	115982	GAGCCGGGCTACATTCACCC
194613	26809	GCAGCCTCCAGGCTCTGACC	239200	71396	GGCTGCAGCCATGGACCTGC	283787	115983	GGAGCCGGGCTACATTCACC
194614	26810	AGCAGCCTCCAGGCTCTGAC	239201	71397	GGGCTGCAGCCATGGACCTG	283788	115984	GGGAGCCGGGCTACATTCAC
194615	26811	AAGCAGCCTCCAGGCTCTGA	239202	71398	GGGGCTGCAGCCATGGACCT	283789	115985	GGGGAGCCGGGCTACATTCA
194616	26812	TAAGCAGCCTCCAGGCTCTG	239203	71399	TGGGGCTGCAGCCATGGACC	283790	115986	TGGGGAGCCGGGCTACATTC
194617	26813	CTAAGCAGCCTCCAGGCTCT	239204	71400	GTGGGGCTGCAGCCATGGAC	283791	115987	GTGGGGAGCCGGGCTACATT
194618	26814	GCTAAGCAGCCTCCAGGCTC	239205	71401	TGTGGGGCTGCAGCCATGGA	283792	115988	TGTGGGGAGCCGGGCTACAT
194619	26815	TGCTAAGCAGCCTCCAGGCT	239206	71402	ATGTGGGGCTGCAGCCATGG	283793	115989	ATGTGGGGAGCCGGGCTACA
194620	26816	ATGCTAAGCAGCCTCCAGGC	239207	71403	CATGTGGGGCTGCAGCCATG	283794	115990	AATGTGGGGAGCCGGGCTAC
194621	26817	AATGCTAAGCAGCCTCCAGG	239208	71404	CCATGTGGGGCTGCAGCCAT	283795	115991	GAATGTGGGGAGCCGGGCTA
194622	26818	GAATGCTAAGCAGCCTCCAG	239209	71405	TCCATGTGGGGCTGCAGCCA	283796	115992	GGAATGTGGGGAGCCGGGCT
194623	26819	GGAATGCTAAGCAGCCTCCA	239210	71406	GTCCATGTGGGGCTGCAGCC	283797	115993	GGGAATGTGGGGAGCCGGGC
194624	26820	GGGAATGCTAAGCAGCCTCC	239211	71407	GGTCCATGTGGGGCTGCAGC	283798	115994	GGGGAATGTGGGGAGCCGGG
194625	26821	GGGGAATGCTAAGCAGCCTC	239212	71408	TGGTCCATGTGGGGCTGCAG	283799	115995	GGGGGAATGTGGGGAGCCGG
194626	26822	TGGGGAATGCTAAGCAGCCT	239213	71409	ATGGTCCATGTGGGGCTGCA	283800	115996	TGGGGGAATGTGGGGAGCCG
194627	26823	GTGGGGAATGCTAAGCAGCC	239214	71410	TATGGTCCATGTGGGGCTGC	283801	115997	GTGGGGGAATGTGGGGAGCC
194628	26824	CGTGGGGAATGCTAAGCAGC	239215	71411	ATATGGTCCATGTGGGGCTG	283802	115998	TGTGGGGGAATGTGGGGAGC
194629	26825	GCGTGGGGAATGCTAAGCAG	239216	71412	AATATGGTCCATGTGGGGCT	283803	115999	GTGTGGGGGAATGTGGGGAG
194630	26826	TGCGTGGGGAATGCTAAGCA	239217	71413	AAATATGGTCCATGTGGGGC	283804	116000	CGTGTGGGGGAATGTGGGGA
194631	26827	GTGCGTGGGGAATGCTAAGC	239218	71414	GAAATATGGTCCATGTGGGG	283805	116001	CCGTGTGGGGGAATGTGGGG
194632	26828	TGTGCGTGGGGAATGCTAAG	239219	71415	GGAAATATGGTCCATGTGGG	283806	116002	ACCGTGTGGGGGAATGTGGG
194633	26829	ATGTGCGTGGGGAATGCTAA	239220	71416	GGGAAATATGGTCCATGTGG	283807	116003	GACCGTGTGGGGGAATGTGG
194634	26830	AATGTGCGTGGGGAATGCTA	239221	71417	GGGGAAATATGGTCCATGTG	283808	116004	GGACCGTGTGGGGGAATGTG
194635	26831	TAATGTGCGTGGGGAATGCT	239222	71418	GGGGGAAATATGGTCCATGT	283809	116005	TGGACCGTGTGGGGGAATGT
194636	26832	CTAATGTGCGTGGGGAATGC	239223	71419	AGGGGGAAATATGGTCCATG	283810	116006	GTGGACCGTGTGGGGGAATG
194637	26833	GCTAATGTGCGTGGGGAATG	239224	71420	AAGGGGGAAATATGGTCCAT	283811	116007	AGTGGACCGTGTGGGGGAAT
194638	26834	TGCTAATGTGCGTGGGGAAT	239225	71421	CAAGGGGGAAATATGGTCCA	283812	116008	CAGTGGACCGTGTGGGGGAA
194639	26835	CTGCTAATGTGCGTGGGGAA	239226	71422	ACAAGGGGGAAATATGGTCC	283813	116009	ACAGTGGACCGTGTGGGGGA
194640	26836	GCTGCTAATGTGCGTGGGGA	239227	71423	GACAAGGGGGAAATATGGTC	283814	116010	AACAGTGGACCGTGTGGGGG
194641	26837	AGCTGCTAATGTGCGTGGGG	239228	71424	TGACAAGGGGGAAATATGGT	283815	116011	GAACAGTGGACCGTGTGGGG
194642	26838	GAGCTGCTAATGTGCGTGGG	239229	71425	GTGACAAGGGGGAAATATGG	283816	116012	GGAACAGTGGACCGTGTGGG
194643	26839	CGAGCTGCTAATGTGCGTGG	239230	71426	AGTGACAAGGGGGAAATATG	283817	116013	GGGAACAGTGGACCGTGTGG
194644	26840	CCGAGCTGCTAATGTGCGTG	239231	71427	GAGTGACAAGGGGGAAATAT	283818	116014	TGGGAACAGTGGACCGTGTG
194645	26841	TCCGAGCTGCTAATGTGCGT	239232	71428	AGAGTGACAAGGGGGAAATA	283819	116015	CTGGGAACAGTGGACCGTGT
194646	26842	CTCCGAGCTGCTAATGTGCG	239233	71429	AAGAGTGACAAGGGGGAAAT	283820	116016	TCTGGGAACAGTGGACCGTG
194647	26843	TCTCCGAGCTGCTAATGTGC	239234	71430	AAAGAGTGACAAGGGGGAAA	283821	116017	TTCTGGGAACAGTGGACCGT
194648	26844	CTCTCCGAGCTGCTAATGTG	239235	71431	GAAAGAGTGACAAGGGGGAA	283822	116018	CTTCTGGGAACAGTGGACCG
194649	26845	GCTCTCCGAGCTGCTAATGT	239236	71432	GGAAAGAGTGACAAGGGGGA	283823	116019	GCTTCTGGGAACAGTGGACC
194650	26846	AGCTCTCCGAGCTGCTAATG	239237	71433	TGGAAAGAGTGACAAGGGGG	283824	116020	GGCTTCTGGGAACAGTGGAC
194651	26847	GAGCTCTCCGAGCTGCTAAT	239238	71434	GTGGAAAGAGTGACAAGGGG	283825	116021	GGGCTTCTGGGAACAGTGGA
194652	26848	TGAGCTCTCCGAGCTGCTAA	239239	71435	GGTGGAAAGAGTGACAAGGG	283826	116022	GGGGCTTCTGGGAACAGTGG
194653	26849	CTGAGCTCTCCGAGCTGCTA	239240	71436	TGGTGGAAAGAGTGACAAGG	283827	116023	AGGGGCTTCTGGGAACAGTG
194654	26850	CCTGAGCTCTCCGAGCTGCT	239241	71437	TTGGTGGAAAGAGTGACAAG	283828	116024	AAGGGGCTTCTGGGAACAGT
194655	26851	TCCTGAGCTCTCCGAGCTGC	239242	71438	CTTGGTGGAAAGAGTGACAA	283829	116025	GAAGGGGCTTCTGGGAACAG
194656	26852	TTCCTGAGCTCTCCGAGCTG	239243	71439	GCTTGGTGGAAAGAGTGACA	283830	116026	GGAAGGGGCTTCTGGGAACA
194657	26853	CTTCCTGAGCTCTCCGAGCT	239244	71440	AGCTTGGTGGAAAGAGTGAC	283831	116027	AGGAAGGGGCTTCTGGGAAC
194658	26854	GCTTCCTGAGCTCTCCGAGC	239245	71441	GAGCTTGGTGGAAAGAGTGA	283832	116028	GAGGAAGGGGCTTCTGGGAA

194659	26855	GGCTTCCTGAGCTCTCCGAG	239246	71442	GGAGCTTGGTGGAAAGAGTG	283833	116029	TGAGGAAGGGGCTTCTGGGA
194660	26856	CGGCTTCCTGAGCTCTCCGA	239247	71443	GGGAGCTTGGTGGAAAGAGT	283834	116030	ATGAGGAAGGGGCTTCTGGG
194661	26857	GCGGCTTCCTGAGCTCTCCG	239248	71444	AGGGAGCTTGGTGGAAAGAG	283835	116031	TATGAGGAAGGGGCTTCTGG
194662	26858	TGCGGCTTCCTGAGCTCTCC	239249	71445	AAGGGAGCTTGGTGGAAAGA	283836	116032	ATATGAGGAAGGGGCTTCTG
194663	26859	CTGCGGCTTCCTGAGCTCTC	239250	71446	CAAGGGAGCTTGGTGGAAAG	283837	116033	AATATGAGGAAGGGGCTTCT
194664	26860	GCTGCGGCTTCCTGAGCTCT	239251	71447	CCAAGGGAGCTTGGTGGAAA	283838	116034	GAATATGAGGAAGGGGCTTC
194665	26861	GGCTGCGGCTTCCTGAGCTC	239252	71448	TCCAAGGGAGCTTGGTGGAA	283839	116035	AGAATATGAGGAAGGGGCTT
194666	26862	GGGCTGCGGCTTCCTGAGCT	239253	71449	TTCCAAGGGAGCTTGGTGGA	283840	116036	TAGAATATGAGGAAGGGGCT
194667	26863	GGGGCTGCGGCTTCCTGAGC	239254	71450	GTTCCAAGGGAGCTTGGTGG	283841	116037	CTAGAATATGAGGAAGGGGC
194668	26864	AGGGGCTGCGGCTTCCTGAG	239255	71451	AGTTCCAAGGGAGCTTGGTG	283842	116038	CCTAGAATATGAGGAAGGGG
194669	26865	GAGGGGCTGCGGCTTCCTGA	239256	71452	AAGTTCCAAGGGAGCTTGGT	283843	116039	TCCTAGAATATGAGGAAGGG
194670	26866	GGAGGGGCTGCGGCTTCCTG	239257	71453	GAAGTTCCAAGGGAGCTTGG	283844	116040	CTCCTAGAATATGAGGAAGG
194671	26867	AGGAGGGGCTGCGGCTTCCT	239258	71454	TGAAGTTCCAAGGGAGCTTG	283845	116041	CCTCCTAGAATATGAGGAAG
194672	26868	AAGGAGGGGCTGCGGCTTCC	239259	71455	CTGAAGTTCCAAGGGAGCTT	283846	116042	CCCTCCTAGAATATGAGGAA
194673	26869	CAAGGAGGGGCTGCGGCTTC	239260	71456	ACTGAAGTTCCAAGGGAGCT	283847	116043	CCCCTCCTAGAATATGAGGA
194674	26870	GCAAGGAGGGGCTGCGGCTT	239261	71457	AACTGAAGTTCCAAGGGAGC	283848	116044	CCCCCTCCTAGAATATGAGG
194675	26871	GGCAAGGAGGGGCTGCGGCT	239262	71458	TAACTGAAGTTCCAAGGGAG	283849	116045	ACCCCCTCCTAGAATATGAG
194676	26872	AGGCAAGGAGGGGCTGCGGC	239263	71459	ATAACTGAAGTTCCAAGGGA	283850	116046	CACCCCCTCCTAGAATATGA
194677	26873	GAGGCAAGGAGGGGCTGCGG	239264	71460	AATAACTGAAGTTCCAAGGG	283851	116047	ACACCCCCTCCTAGAATATG
194678	26874	TGAGGCAAGGAGGGGCTGCG	239265	71461	TAATAACTGAAGTTCCAAGG	283852	116048	GACACCCCCTCCTAGAATAT
194679	26875	GTGAGGCAAGGAGGGGCTGC	239266	71462	TTAATAACTGAAGTTCCAAG	283853	116049	GGACACCCCCTCCTAGAATA
194680	26876	GGTGAGGCAAGGAGGGGCTG	239267	71463	CTTAATAACTGAAGTTCCAA	283854	116050	GGGACACCCCCTCCTAGAAT
194681	26877	TGGTGAGGCAAGGAGGGGCT	239268	71464	GCTTAATAACTGAAGTTCCA	283855	116051	TGGGACACCCCCTCCTAGAA
194682	26878	CTGGTGAGGCAAGGAGGGGC	239269	71465	AGCTTAATAACTGAAGTTCC	283856	116052	CTGGGACACCCCCTCCTAGA
194683	26879	GCTGGTGAGGCAAGGAGGGG	239270	71466	GAGCTTAATAACTGAAGTTC	283857	116053	GCTGGGACACCCCCTCCTAG
194684	26880	GGCTGGTGAGGCAAGGAGGG	239271	71467	AGAGCTTAATAACTGAAGTT	283858	116054	TGCTGGGACACCCCCTCCTA
194685	26881	AGGCTGGTGAGGCAAGGAGG	239272	71468	GAGAGCTTAATAACTGAAGT	283859	116055	ATGCTGGGACACCCCCTCCT
194686	26882	CAGGCTGGTGAGGCAAGGAG	239273	71469	AGAGAGCTTAATAACTGAAG	283860	116056	AATGCTGGGACACCCCCTCC
194687	26883	CCAGGCTGGTGAGGCAAGGA	239274	71470	AAGAGAGCTTAATAACTGAA	283861	116057	AAATGCTGGGACACCCCCTC
194688	26884	TCCAGGCTGGTGAGGCAAGG	239275	71471	CAAGAGAGCTTAATAACTGA	283862	116058	GAAATGCTGGGACACCCCCT
194689	26885	ATCCAGGCTGGTGAGGCAAG	239276	71472	CCAAGAGAGCTTAATAACTG	283863	116059	AGAAATGCTGGGACACCCCC
194690	26886	GATCCAGGCTGGTGAGGCAA	239277	71473	CCCAAGAGAGCTTAATAACT	283864	116060	CAGAAATGCTGGGACACCCC
194691	26887	TGATCCAGGCTGGTGAGGCA	239278	71474	ACCCAAGAGAGCTTAATAAC	283865	116061	CCAGAAATGCTGGGACACCC
194692	26888	CTGATCCAGGCTGGTGAGGC	239279	71475	CACCCAAGAGAGCTTAATAA	283866	116062	CCCAGAAATGCTGGGACACC
194693	26889	CCTGATCCAGGCTGGTGAGG	239280	71476	CCACCCAAGAGAGCTTAATA	283867	116063	ACCCAGAAATGCTGGGACAC
194694	26890	TCCTGATCCAGGCTGGTGAG	239281	71477	TCCACCCAAGAGAGCTTAAT	283868	116064	GACCCAGAAATGCTGGGACA
194695	26891	GTCCTGATCCAGGCTGGTGA	239282	71478	TTCCACCCAAGAGAGCTTAA	283869	116065	GGACCCAGAAATGCTGGGAC
194696	26892	TGTCCTGATCCAGGCTGGTG	239283	71479	ATTCCACCCAAGAGAGCTTA	283870	116066	GGGACCCAGAAATGCTGGGA
194697	26893	CTGTCCTGATCCAGGCTGGT	239284	71480	GATTCCACCCAAGAGAGCTT	283871	116067	GGGGACCCAGAAATGCTGGG
194698	26894	GCTGTCCTGATCCAGGCTGG	239285	71481	GGATTCCACCCAAGAGAGCT	283872	116068	GGGGGACCCAGAAATGCTGG
194699	26895	TGCTGTCCTGATCCAGGCTG	239286	71482	TGGATTCCACCCAAGAGAGC	283873	116069	TGGGGGACCCAGAAATGCTG
194700	26896	ATGCTGTCCTGATCCAGGCT	239287	71483	TTGGATTCCACCCAAGAGAG	283874	116070	CTGGGGGACCCAGAAATGCT
194701	26897	GATGCTGTCCTGATCCAGGC	239288	71484	CTTGGATTCCACCCAAGAGA	283875	116071	GCTGGGGGACCCAGAAATGC
194702	26898	GGATGCTGTCCTGATCCAGG	239289	71485	ACTTGGATTCCACCCAAGAG	283876	116072	GGCTGGGGGACCCAGAAATG
194703	26899	GGGATGCTGTCCTGATCCAG	239290	71486	AACTTGGATTCCACCCAAGA	283877	116073	AGGCTGGGGGACCCAGAAAT
194704	26900	GGGGATGCTGTCCTGATCCA	239291	71487	TAACTTGGATTCCACCCAAG	283878	116074	CAGGCTGGGGGACCCAGAAA
194705	26901	AGGGGATGCTGTCCTGATCC	239292	71488	CTAACTTGGATTCCACCCAA	283879	116075	GCAGGCTGGGGGACCCAGAA
194706	26902	CAGGGGATGCTGTCCTGATC	239293	71489	TCTAACTTGGATTCCACCCA	283880	116076	CGCAGGCTGGGGGACCCAGA
194707	26903	CCAGGGGATGCTGTCCTGAT	239294	71490	TTCTAACTTGGATTCCACCC	283881	116077	GCGCAGGCTGGGGGACCCAG
194708	26904	TCCAGGGGATGCTGTCCTGA	239295	71491	ATTCTAACTTGGATTCCACC	283882	116078	TGCGCAGGCTGGGGGACCCA
194709	26905	TTCCAGGGGATGCTGTCCTG	239296	71492	GATTCTAACTTGGATTCCAC	283883	116079	CTGCGCAGGCTGGGGGACCC
194710	26906	CTTCCAGGGGATGCTGTCCT	239297	71493	TGATTCTAACTTGGATTCCA	283884	116080	CCTGCGCAGGCTGGGGGACC
194711	26907	TCTTCCAGGGGATGCTGTCC	239298	71494	GTGATTCTAACTTGGATTCC	283885	116081	GCCTGCGCAGGCTGGGGGAC
194712	26908	GTCTTCCAGGGGATGCTGTC	239299	71495	TGTGATTCTAACTTGGATTC	283886	116082	AGCCTGCGCAGGCTGGGGGA
194713	26909	TGTCTTCCAGGGGATGCTGT	239300	71496	TTGTGATTCTAACTTGGATT	283887	116083	CAGCCTGCGCAGGCTGGGGG
194714	26910	GTGTCTTCCAGGGGATGCTG	239301	71497	GTTGTGATTCTAACTTGGAT	283888	116084	ACAGCCTGCGCAGGCTGGGG
194715	26911	TGTGTCTTCCAGGGGATGCT	239302	71498	TGTTGTGATTCTAACTTGGA	283889	116085	CACAGCCTGCGCAGGCTGGG
194716	26912	GTGTGTCTTCCAGGGGATGC	239303	71499	ATGTTGTGATTCTAACTTGG	283890	116086	ACACAGCCTGCGCAGGCTGG
194717	26913	TGTGTGTCTTCCAGGGGATG	239304	71500	CATGTTGTGATTCTAACTTG	283891	116087	CACACAGCCTGCGCAGGCTG
194718	26914	CTGTGTGTCTTCCAGGGGAT	239305	71501	ACATGTTGTGATTCTAACTT	283892	116088	CCACACAGCCTGCGCAGGCT
194719	26915	CCTGTGTGTCTTCCAGGGGA	239306	71502	CACATGTTGTGATTCTAACT	283893	116089	TCCACACAGCCTGCGCAGGC
194720	26916	CCCTGTGTGTCTTCCAGGGG	239307	71503	GCACATGTTGTGATTCTAAC	283894	116090	GTCCACACAGCCTGCGCAGG
194721	26917	GCCCTGTGTGTCTTCCAGGG	239308	71504	GGCACATGTTGTGATTCTAA	283895	116091	TGTCCACACAGCCTGCGCAG
194722	26918	GGCCCTGTGTGTCTTCCAGG	239309	71505	AGGCACATGTTGTGATTCTA	283896	116092	CTGTCCACACAGCCTGCGCA
194723	26919	AGGCCCTGTGTGTCTTCCAG	239310	71506	GAGGCACATGTTGTGATTCT	283897	116093	TCTGTCCACACAGCCTGCGC
194724	26920	CAGGCCCTGTGTGTCTTCCA	239311	71507	TGAGGCACATGTTGTGATTC	283898	116094	TTCTGTCCACACAGCCTGCG
194725	26921	CCAGGCCCTGTGTGTCTTCC	239312	71508	ATGAGGCACATGTTGTGATT	283899	116095	ATTCTGTCCACACAGCCTGC
194726	26922	GCCAGGCCCTGTGTGTCTTC	239313	71509	TATGAGGCACATGTTGTGAT	283900	116096	TATTCTGTCCACACAGCCTG
194727	26923	GGCCAGGCCCTGTGTGTCTT	239314	71510	ATATGAGGCACATGTTGTGA	283901	116097	CTATTCTGTCCACACAGCCT
194728	26924	AGGCCAGGCCCTGTGTGTCT	239315	71511	CATATGAGGCACATGTTGTG	283902	116098	CCTATTCTGTCCACACAGCC
194729	26925	GAGGCCAGGCCCTGTGTGTC	239316	71512	CCATATGAGGCACATGTTGT	283903	116099	CCCTATTCTGTCCACACAGC
194730	26926	AGAGGCCAGGCCCTGTGTGT	239317	71513	TCCATATGAGGCACATGTTG	283904	116100	GCCCTATTCTGTCCACACAG

194731	26927	CAGAGGCCAGGCCCTGTGTG	239318	71514	ATCCATATGAGGCACATGTT	283905	116101	TGCCCTATTCTGTCCACACA
194732	26928	TCAGAGGCCAGGCCCTGTGT	239319	71515	AATCCATATGAGGCACATGT	283906	116102	CTGCCCTATTCTGTCCACAC
194733	26929	ATCAGAGGCCAGGCCCTGTG	239320	71516	CAATCCATATGAGGCACATG	283907	116103	TCTGCCCTATTCTGTCCACA
194734	26930	AATCAGAGGCCAGGCCCTGT	239321	71517	ACAATCCATATGAGGCACAT	283908	116104	ATCTGCCCTATTCTGTCCAC
194735	26931	TAATCAGAGGCCAGGCCCTG	239322	71518	CACAATCCATATGAGGCACA	283909	116105	CATCTGCCCTATTCTGTCCA
194736	26932	GTAATCAGAGGCCAGGCCCT	239323	71519	GCACAATCCATATGAGGCAC	283910	116106	TCATCTGCCCTATTCTGTCC
194737	26933	GGTAATCAGAGGCCAGGCCC	239324	71520	GGCACAATCCATATGAGGCA	283911	116107	GTCATCTGCCCTATTCTGTC
194738	26934	GGGTAATCAGAGGCCAGGCC	239325	71521	TGGCACAATCCATATGAGGC	283912	116108	CGTCATCTGCCCTATTCTGT
194739	26935	TGGGTAATCAGAGGCCAGGC	239326	71522	CTGGCACAATCCATATGAGG	283913	116109	CCGTCATCTGCCCTATTCTG
194740	26936	CTGGGTAATCAGAGGCCAGG	239327	71523	ACTGGCACAATCCATATGAG	283914	116110	TCCGTCATCTGCCCTATTCT
194741	26937	GCTGGGTAATCAGAGGCCAG	239328	71524	CACTGGCACAATCCATATGA	283915	116111	GTCCGTCATCTGCCCTATTC
194742	26938	GGCTGGGTAATCAGAGGCCA	239329	71525	TCACTGGCACAATCCATATG	283916	116112	GGTCCGTCATCTGCCCTATT
194743	26939	AGGCTGGGTAATCAGAGGCC	239330	71526	TTCACTGGCACAATCCATAT	283917	116113	GGGTCCGTCATCTGCCCTAT
194744	26940	CAGGCTGGGTAATCAGAGGC	239331	71527	TTTCACTGGCACAATCCATA	283918	116114	AGGGTCCGTCATCTGCCCTA
194745	26941	CCAGGCTGGGTAATCAGAGG	239332	71528	TTTTCACTGGCACAATCCAT	283919	116115	GAGGGTCCGTCATCTGCCCT
194746	26942	TCCAGGCTGGGTAATCAGAG	239333	71529	TTTTTCACTGGCACAATCCA	283920	116116	AGAGGGTCCGTCATCTGCCC
194747	26943	CTCCAGGCTGGGTAATCAGA	239334	71530	ATTTTTCACTGGCACAATCC	283921	116117	GAGAGGGTCCGTCATCTGCC
194748	26944	CCTCCAGGCTGGGTAATCAG	239335	71531	CATTTTTCACTGGCACAATC	283922	116118	AGAGAGGGTCCGTCATCTGC
194749	26945	CCCTCCAGGCTGGGTAATCA	239336	71532	TCATTTTTCACTGGCACAAT	283923	116119	GAGAGAGGGTCCGTCATCTG
194750	26946	TCCCTCCAGGCTGGGTAATC	239337	71533	GTCATTTTTCACTGGCACAA	283924	116120	GGAGAGAGGGTCCGTCATCT
194751	26947	TTCCCTCCAGGCTGGGTAAT	239338	71534	TGTCATTTTTCACTGGCACA	283925	116121	CGGAGAGAGGGTCCGTCATC
194752	26948	TTTCCCTCCAGGCTGGGTAA	239339	71535	ATGTCATTTTTCACTGGCAC	283926	116122	CCGGAGAGAGGGTCCGTCAT
194753	26949	CTTTCCCTCCAGGCTGGGTA	239340	71536	AATGTCATTTTTCACTGGCA	283927	116123	TCCGGAGAGAGGGTCCGTCA
194754	26950	GCTTTCCCTCCAGGCTGGGT	239341	71537	GAATGTCATTTTTCACTGGC	283928	116124	GTCCGGAGAGAGGGTCCGTC
194755	26951	AGCTTTCCCTCCAGGCTGGG	239342	71538	AGAATGTCATTTTTCACTGG	283929	116125	GGTCCGGAGAGAGGGTCCGT
194756	26952	GAGCTTTCCCTCCAGGCTGG	239343	71539	TAGAATGTCATTTTTCACTG	283930	116126	GGGTCCGGAGAGAGGGTCCG
194757	26953	TGAGCTTTCCCTCCAGGCTG	239344	71540	ATAGAATGTCATTTTTCACT	283931	116127	AGGGTCCGGAGAGAGGGTCC
194758	26954	TTGAGCTTTCCCTCCAGGCT	239345	71541	AATAGAATGTCATTTTTCAC	283932	116128	CAGGGTCCGGAGAGAGGGTC
194759	26955	ATTGAGCTTTCCCTCCAGGC	239346	71542	AAATAGAATGTCATTTTTCA	283933	116129	GCAGGGTCCGGAGAGAGGGT
194760	26956	GATTGAGCTTTCCCTCCAGG	239347	71543	TAAATAGAATGTCATTTTTC	283934	116130	GGCAGGGTCCGGAGAGAGGG
194761	26957	CGATTGAGCTTTCCCTCCAG	239348	71544	CTAAATAGAATGTCATTTTT	283935	116131	AGGCAGGGTCCGGAGAGAGG
194762	26958	TCGATTGAGCTTTCCCTCCA	239349	71545	TCTAAATAGAATGTCATTTT	283936	116132	CAGGCAGGGTCCGGAGAGAG
194763	26959	CTCGATTGAGCTTTCCCTCC	239350	71546	CTCTAAATAGAATGTCATTT	283937	116133	CCAGGCAGGGTCCGGAGAGA
194764	26960	GCTCGATTGAGCTTTCCCTC	239351	71547	CCTCTAAATAGAATGTCATT	283938	116134	CCCAGGCAGGGTCCGGAGAG
194765	26961	TGCTCGATTGAGCTTTCCCT	239352	71548	GCCTCTAAATAGAATGTCAT	283939	116135	TCCCAGGCAGGGTCCGGAGA
194766	26962	ATGCTCGATTGAGCTTTCCC	239353	71549	TGCCTCTAAATAGAATGTCA	283940	116136	TTCCCAGGCAGGGTCCGGAG
194767	26963	GATGCTCGATTGAGCTTTCC	239354	71550	CTGCCTCTAAATAGAATGTC	283941	116137	CTTCCCAGGCAGGGTCCGGA
194768	26964	TGATGCTCGATTGAGCTTTC	239355	71551	CCTGCCTCTAAATAGAATGT	283942	116138	GCTTCCCAGGCAGGGTCCGG
194769	26965	ATGATGCTCGATTGAGCTTT	239356	71552	CCCTGCCTCTAAATAGAATG	283943	116139	AGCTTCCCAGGCAGGGTCCG
194770	26966	CATGATGCTCGATTGAGCTT	239357	71553	GCCCTGCCTCTAAATAGAAT	283944	116140	CAGCTTCCCAGGCAGGGTCC
194771	26967	ACATGATGCTCGATTGAGCT	239358	71554	TGCCCTGCCTCTAAATAGAA	283945	116141	TCAGCTTCCCAGGCAGGGTC
194772	26968	GACATGATGCTCGATTGAGC	239359	71555	CTGCCCTGCCTCTAAATAGA	283946	116142	CTCAGCTTCCCAGGCAGGGT
194773	26969	TGACATGATGCTCGATTGAG	239360	71556	GCTGCCCTGCCTCTAAATAG	283947	116143	TCTCAGCTTCCCAGGCAGGG
194774	26970	GTGACATGATGCTCGATTGA	239361	71557	GGCTGCCCTGCCTCTAAATA	283948	116144	TTCTCAGCTTCCCAGGCAGG
194775	26971	GGTGACATGATGCTCGATTG	239362	71558	AGGCTGCCCTGCCTCTAAAT	283949	116145	ATTCTCAGCTTCCCAGGCAG
194776	26972	GGGTGACATGATGCTCGATT	239363	71559	CAGGCTGCCCTGCCTCTAAA	283950	116146	TATTCTCAGCTTCCCAGGCA
194777	26973	CGGGTGACATGATGCTCGAT	239364	71560	CCAGGCTGCCCTGCCTCTAA	283951	116147	GTATTCTCAGCTTCCCAGGC
194778	26974	CCGGGTGACATGATGCTCGA	239365	71561	GCCAGGCTGCCCTGCCTCTA	283952	116148	GGTATTCTCAGCTTCCCAGG
194779	26975	ACCGGGTGACATGATGCTCG	239366	71562	AGCCAGGCTGCCCTGCCTCT	283953	116149	GGGTATTCTCAGCTTCCCAG
194780	26976	CACCGGGTGACATGATGCTC	239367	71563	AAGCCAGGCTGCCCTGCCTC	283954	116150	TGGGTATTCTCAGCTTCCCA
194781	26977	GCACCGGGTGACATGATGCT	239368	71564	TAAGCCAGGCTGCCCTGCCT	283955	116151	ATGGGTATTCTCAGCTTCCC
194782	26978	GGCACCGGGTGACATGATGC	239369	71565	CTAAGCCAGGCTGCCCTGCC	283956	116152	GATGGGTATTCTCAGCTTCC
194783	26979	GGGCACCGGGTGACATGATG	239370	71566	TCTAAGCCAGGCTGCCCTGC	283957	116153	TGATGGGTATTCTCAGCTTC
194784	26980	GGGGCACCGGGTGACATGAT	239371	71567	CTCTAAGCCAGGCTGCCCTG	283958	116154	TTGATGGGTATTCTCAGCTT
194785	26981	GGGGGCACCGGGTGACATGA	239372	71568	ACTCTAAGCCAGGCTGCCCT	283959	116155	TTTGATGGGTATTCTCAGCT
194786	26982	TGGGGGCACCGGGTGACATG	239373	71569	GACTCTAAGCCAGGCTGCCC	283960	116156	CTTTGATGGGTATTCTCAGC
194787	26983	ATGGGGGCACCGGGTGACAT	239374	71570	TGACTCTAAGCCAGGCTGCC	283961	116157	ACTTTGATGGGTATTCTCAG
194788	26984	CATGGGGGCACCGGGTGACA	239375	71571	CTGACTCTAAGCCAGGCTGC	283962	116158	GACTTTGATGGGTATTCTCA
194789	26985	GCATGGGGGCACCGGGTGAC	239376	71572	ACTGACTCTAAGCCAGGCTG	283963	116159	AGACTTTGATGGGTATTCTC
194790	26986	TGCATGGGGGCACCGGGTGA	239377	71573	AACTGACTCTAAGCCAGGCT	283964	116160	GAGACTTTGATGGGTATTCT
194791	26987	CTGCATGGGGGCACCGGGTG	239378	71574	AAACTGACTCTAAGCCAGGC	283965	116161	GGAGACTTTGATGGGTATTC
194792	26988	CCTGCATGGGGGCACCGGGT	239379	71575	TAAACTGACTCTAAGCCAGG	283966	116162	AGGAGACTTTGATGGGTATT
194793	26989	CCCTGCATGGGGGCACCGGG	239380	71576	TTAAACTGACTCTAAGCCAG	283967	116163	AAGGAGACTTTGATGGGTAT
194794	26990	ACCCTGCATGGGGGCACCGG	239381	71577	TTTAAACTGACTCTAAGCCA	283968	116164	GAAGGAGACTTTGATGGGTA
194795	26991	CACCCTGCATGGGGGCACCG	239382	71578	TTTTAAACTGACTCTAAGCC	283969	116165	GGAAGGAGACTTTGATGGGT
194796	26992	CCACCCTGCATGGGGGCACC	239383	71579	ATTTTAAACTGACTCTAAGC	283970	116166	TGGAAGGAGACTTTGATGGG
194797	26993	GCCACCCTGCATGGGGGCAC	239384	71580	TATTTTAAACTGACTCTAAG	283971	116167	GTGGAAGGAGACTTTGATGG
194798	26994	TGCCACCCTGCATGGGGGCA	239385	71581	ATATTTTAAACTGACTCTAA	283972	116168	AGTGGAAGGAGACTTTGATG
194799	26995	GTGCCACCCTGCATGGGGGC	239386	71582	CATATTTTAAACTGACTCTA	283973	116169	GAGTGGAAGGAGACTTTGAT
194800	26996	AGTGCCACCCTGCATGGGGG	239387	71583	ACATATTTTAAACTGACTCT	283974	116170	TGAGTGGAAGGAGACTTTGA
194801	26997	CAGTGCCACCCTGCATGGGG	239388	71584	TACATATTTTAAACTGACTC	283975	116171	ATGAGTGGAAGGAGACTTTG
194802	26998	CCAGTGCCACCCTGCATGGG	239389	71585	ATACATATTTTAAACTGACT	283976	116172	CATGAGTGGAAGGAGACTTT

194803	26999	ACCAGTGCCACCCTGCATGG	239390	71586	AATACATATTTTAAACTGAC	283977	116173	GCATGAGTGGAAGGAGACTT
194804	27000	CACCAGTGCCACCCTGCATG	239391	71587	TAATACATATTTTAAACTGA	283978	116174	GGCATGAGTGGAAGGAGACT
194805	27001	TCACCAGTGCCACCCTGCAT	239392	71588	ATAATACATATTTTAAACTG	283979	116175	GGGCATGAGTGGAAGGAGAC
194806	27002	CTCACCAGTGCCACCCTGCA	239393	71589	CATAATACATATTTTAAACT	283980	116176	TGGGCATGAGTGGAAGGAGA
194807	27003	TCTCACCAGTGCCACCCTGC	239394	71590	GCATAATACATATTTTAAAC	283981	116177	CTGGGCATGAGTGGAAGGAG
194808	27004	GTCTCACCAGTGCCACCCTG	239395	71591	AGCATAATACATATTTTAAA	283982	116178	GCTGGGCATGAGTGGAAGGA
194809	27005	GGTCTCACCAGTGCCACCCT	239396	71592	CAGCATAATACATATTTTAA	283983	116179	GGCTGGGCATGAGTGGAAGG
194810	27006	GGGTCTCACCAGTGCCACCC	239397	71593	GCAGCATAATACATATTTTA	283984	116180	GGGCTGGGCATGAGTGGAAG
194811	27007	GGGGTCTCACCAGTGCCACC	239398	71594	TGCAGCATAATACATATTTT	283985	116181	AGGGCTGGGCATGAGTGGAA
194812	27008	GGGGGTCTCACCAGTGCCAC	239399	71595	TTGCAGCATAATACATATTT	283986	116182	CAGGGCTGGGCATGAGTGGA
194813	27009	TGGGGGTCTCACCAGTGCCA	239400	71596	GTTGCAGCATAATACATATT	283987	116183	ACAGGGCTGGGCATGAGTGG
194814	27010	TTGGGGGTCTCACCAGTGCC	239401	71597	TGTTGCAGCATAATACATAT	283988	116184	GACAGGGCTGGGCATGAGTG
194815	27011	CTTGGGGGTCTCACCAGTGC	239402	71598	TTGTTGCAGCATAATACATA	283989	116185	GGACAGGGCTGGGCATGAGT
194816	27012	GCTTGGGGGTCTCACCAGTG	239403	71599	TTTGTTGCAGCATAATACAT	283990	116186	GGGACAGGGCTGGGCATGAG
194817	27013	GGCTTGGGGGTCTCACCAGT	239404	71600	ATTTGTTGCAGCATAATACA	283991	116187	GGGGACAGGGCTGGGCATGA
194818	27014	TGGCTTGGGGGTCTCACCAG	239405	71601	CATTTGTTGCAGCATAATAC	283992	116188	TGGGGACAGGGCTGGGCATG
194819	27015	TTGGCTTGGGGGTCTCACCA	239406	71602	ACATTTGTTGCAGCATAATA	283993	116189	CTGGGGACAGGGCTGGGCAT
194820	27016	ATTGGCTTGGGGGTCTCACC	239407	71603	TACATTTGTTGCAGCATAAT	283994	116190	CCTGGGGACAGGGCTGGGCA
194821	27017	CATTGGCTTGGGGGTCTCAC	239408	71604	GTACATTTGTTGCAGCATAA	283995	116191	TCCTGGGGACAGGGCTGGGC
194822	27018	TCATTGGCTTGGGGGTCTCA	239409	71605	GGTACATTTGTTGCAGCATA	283996	116192	CTCCTGGGGACAGGGCTGGG
194823	27019	ATCATTGGCTTGGGGGTCTC	239410	71606	TGGTACATTTGTTGCAGCAT	283997	116193	GCTCCTGGGGACAGGGCTGG
194824	27020	TATCATTGGCTTGGGGGTCT	239411	71607	ATGGTACATTTGTTGCAGCA	283998	116194	GGCTCCTGGGGACAGGGCTG
194825	27021	GTATCATTGGCTTGGGGGTC	239412	71608	CATGGTACATTTGTTGCAGC	283999	116195	GGGCTCCTGGGGACAGGGCT
194826	27022	GGTATCATTGGCTTGGGGGT	239413	71609	TCATGGTACATTTGTTGCAG	284000	116196	GGGGCTCCTGGGGACAGGGC
194827	27023	TGGTATCATTGGCTTGGGGG	239414	71610	ATCATGGTACATTTGTTGCA	284001	116197	TGGGGCTCCTGGGGACAGGG
194828	27024	GTGGTATCATTGGCTTGGGG	239415	71611	GATCATGGTACATTTGTTGC	284002	116198	ATGGGGCTCCTGGGGACAGG
194829	27025	GGTGGTATCATTGGCTTGGG	239416	71612	GGATCATGGTACATTTGTTG	284003	116199	TATGGGGCTCCTGGGGACAG
194830	27026	AGGTGGTATCATTGGCTTGG	239417	71613	AGGATCATGGTACATTTGTT	284004	116200	CTATGGGGCTCCTGGGGACA
194831	27027	GAGGTGGTATCATTGGCTTG	239418	71614	CAGGATCATGGTACATTTGT	284005	116201	GCTATGGGGCTCCTGGGGAC
194832	27028	TGAGGTGGTATCATTGGCTT	239419	71615	ACAGGATCATGGTACATTTG	284006	116202	GGCTATGGGGCTCCTGGGGA
194833	27029	GTGAGGTGGTATCATTGGCT	239420	71616	TACAGGATCATGGTACATTT	284007	116203	GGGCTATGGGGCTCCTGGGG
194834	27030	TGTGAGGTGGTATCATTGGC	239421	71617	TTACAGGATCATGGTACATT	284008	116204	TGGGCTATGGGGCTCCTGGG
194835	27031	CTGTGAGGTGGTATCATTGG	239422	71618	CTTACAGGATCATGGTACAT	284009	116205	ATGGGCTATGGGGCTCCTGG
194836	27032	CCTGTGAGGTGGTATCATTG	239423	71619	TCTTACAGGATCATGGTACA	284010	116206	AATGGGCTATGGGGCTCCTG
194837	27033	TCCTGTGAGGTGGTATCATT	239424	71620	ATCTTACAGGATCATGGTAC	284011	116207	CAATGGGCTATGGGGCTCCT
194838	27034	CTCCTGTGAGGTGGTATCAT	239425	71621	CATCTTACAGGATCATGGTA	284012	116208	CCAATGGGCTATGGGGCTCC
194839	27035	ACTCCTGTGAGGTGGTATCA	239426	71622	ACATCTTACAGGATCATGGT	284013	116209	TCCAATGGGCTATGGGGCTC
194840	27036	CACTCCTGTGAGGTGGTATC	239427	71623	AACATCTTACAGGATCATGG	284014	116210	TTCCAATGGGCTATGGGGCT
194841	27037	GCACTCCTGTGAGGTGGTAT	239428	71624	GAACATCTTACAGGATCATG	284015	116211	CTTCCAATGGGCTATGGGGC
194842	27038	TGCACTCCTGTGAGGTGGTA	239429	71625	TGAACATCTTACAGGATCAT	284016	116212	ACTTCCAATGGGCTATGGGG
194843	27039	CTGCACTCCTGTGAGGTGGT	239430	71626	GTGAACATCTTACAGGATCA	284017	116213	AACTTCCAATGGGCTATGGG
194844	27040	CCTGCACTCCTGTGAGGTGG	239431	71627	TGTGAACATCTTACAGGATC	284018	116214	CAACTTCCAATGGGCTATGG
194845	27041	GCCTGCACTCCTGTGAGGTG	239432	71628	TTGTGAACATCTTACAGGAT	284019	116215	CCAACTTCCAATGGGCTATG
194846	27042	GGCCTGCACTCCTGTGAGGT	239433	71629	GTTGTGAACATCTTACAGGA	284020	116216	CCCAACTTCCAATGGGCTAT
194847	27043	GGGCCTGCACTCCTGTGAGG	239434	71630	TGTTGTGAACATCTTACAGG	284021	116217	GCCCAACTTCCAATGGGCTA
194848	27044	TGGGCCTGCACTCCTGTGAG	239435	71631	TTGTTGTGAACATCTTACAG	284022	116218	AGCCCAACTTCCAATGGGCT
194849	27045	ATGGGCCTGCACTCCTGTGA	239436	71632	CTTGTTGTGAACATCTTACA	284023	116219	CAGCCCAACTTCCAATGGGC
194850	27046	AATGGGCCTGCACTCCTGTG	239437	71633	CCTTGTTGTGAACATCTTAC	284024	116220	TCAGCCCAACTTCCAATGGG
194851	27047	CAATGGGCCTGCACTCCTGT	239438	71634	CCCTTGTTGTGAACATCTTA	284025	116221	TTCAGCCCAACTTCCAATGG
194852	27048	ACAATGGGCCTGCACTCCTG	239439	71635	TCCCTTGTTGTGAACATCTT	284026	116222	CTTCAGCCCAACTTCCAATG
194853	27049	CACAATGGGCCTGCACTCCT	239440	71636	TTCCCTTGTTGTGAACATCT	284027	116223	CCTTCAGCCCAACTTCCAAT
194854	27050	CCACAATGGGCCTGCACTCC	239441	71637	GTTCCCTTGTTGTGAACATC	284028	116224	ACCTTCAGCCCAACTTCCAA
194855	27051	GCCACAATGGGCCTGCACTC	239442	71638	AGTTCCCTTGTTGTGAACAT	284029	116225	CACCTTCAGCCCAACTTCCA
194856	27052	GGCCACAATGGGCCTGCACT	239443	71639	CAGTTCCCTTGTTGTGAACA	284030	116226	CCACCTTCAGCCCAACTTCC
194857	27053	TGGCCACAATGGGCCTGCAC	239444	71640	CCAGTTCCCTTGTTGTGAAC	284031	116227	ACCACCTTCAGCCCAACTTC
194858	27054	CTGGCCACAATGGGCCTGCA	239445	71641	TCCAGTTCCCTTGTTGTGAA	284032	116228	CACCACCTTCAGCCCAACTT
194859	27055	TCTGGCCACAATGGGCCTGC	239446	71642	ATCCAGTTCCCTTGTTGTGA	284033	116229	CCACCACCTTCAGCCCAACT
194860	27056	ATCTGGCCACAATGGGCCTG	239447	71643	CATCCAGTTCCCTTGTTGTG	284034	116230	GCCACCACCTTCAGCCCAAC
194861	27057	GATCTGGCCACAATGGGCCT	239448	71644	ACATCCAGTTCCCTTGTTGT	284035	116231	TGCCACCACCTTCAGCCCAA
194862	27058	TGATCTGGCCACAATGGGCC	239449	71645	CACATCCAGTTCCCTTGTTG	284036	116232	GTGCCACCACCTTCAGCCCA
194863	27059	ATGATCTGGCCACAATGGGC	239450	71646	CCACATCCAGTTCCCTTGTT	284037	116233	GGTGCCACCACCTTCAGCCC
194864	27060	GATGATCTGGCCACAATGGG	239451	71647	CCCACATCCAGTTCCCTTGT	284038	116234	AGGTGCCACCACCTTCAGCC
194865	27061	AGATGATCTGGCCACAATGG	239452	71648	CCCCACATCCAGTTCCCTTG	284039	116235	CAGGTGCCACCACCTTCAGC
194866	27062	AAGATGATCTGGCCACAATG	239453	71649	ACCCCACATCCAGTTCCCTT	284040	116236	TCAGGTGCCACCACCTTCAG
194867	27063	CAAGATGATCTGGCCACAAT	239454	71650	TACCCCACATCCAGTTCCCT	284041	116237	CTCAGGTGCCACCACCTTCA
194868	27064	TCAAGATGATCTGGCCACAA	239455	71651	ATACCCCACATCCAGTTCCC	284042	116238	TCTCAGGTGCCACCACCTTC
194869	27065	GTCAAGATGATCTGGCCACA	239456	71652	TATACCCCACATCCAGTTCC	284043	116239	GTCTCAGGTGCCACCACCTT
194870	27066	AGTCAAGATGATCTGGCCAC	239457	71653	GTATACCCCACATCCAGTTC	284044	116240	AGTCTCAGGTGCCACCACCT
194871	27067	AAGTCAAGATGATCTGGCCA	239458	71654	AGTATACCCCACATCCAGTT	284045	116241	CAGTCTCAGGTGCCACCACC
194872	27068	AAAGTCAAGATGATCTGGCC	239459	71655	CAGTATACCCCACATCCAGT	284046	116242	CCAGTCTCAGGTGCCACCAC
194873	27069	AAAAGTCAAGATGATCTGGC	239460	71656	ACAGTATACCCCACATCCAG	284047	116243	CCCAGTCTCAGGTGCCACCA
194874	27070	GAAAAGTCAAGATGATCTGG	239461	71657	GACAGTATACCCCACATCCA	284048	116244	GCCCAGTCTCAGGTGCCACC

194875	27071	TGAAAAGTCAAGATGATCTG	239462	71658	AGACAGTATACCCCACATCC	284049	116245	AGCCCAGTCTCAGGTGCCAC
194876	27072	TTGAAAAGTCAAGATGATCT	239463	71659	CAGACAGTATACCCCACATC	284050	116246	CAGCCCAGTCTCAGGTGCCA
194877	27073	CTTGAAAAGTCAAGATGATC	239464	71660	ACAGACAGTATACCCCACAT	284051	116247	GCAGCCCAGTCTCAGGTGCC
194878	27074	TCTTGAAAAGTCAAGATGAT	239465	71661	TACAGACAGTATACCCCACA	284052	116248	GGCAGCCCAGTCTCAGGTGC
194879	27075	ATCTTGAAAAGTCAAGATGA	239466	71662	GTACAGACAGTATACCCCAC	284053	116249	CGGCAGCCCAGTCTCAGGTG
194880	27076	TATCTTGAAAAGTCAAGATG	239467	71663	AGTACAGACAGTATACCCCA	284054	116250	GCGGCAGCCCAGTCTCAGGT
194881	27077	TTATCTTGAAAAGTCAAGAT	239468	71664	TAGTACAGACAGTATACCCC	284055	116251	GGCGGCAGCCCAGTCTCAGG
194882	27078	TTTATCTTGAAAAGTCAAGA	239469	71665	TTAGTACAGACAGTATACCC	284056	116252	AGGCGGCAGCCCAGTCTCAG
194883	27079	ATTTATCTTGAAAAGTCAAG	239470	71666	GTTAGTACAGACAGTATACC	284057	116253	GAGGCGGCAGCCCAGTCTCA
194884	27080	GATTTATCTTGAAAAGTCAA	239471	71667	AGTTAGTACAGACAGTATAC	284058	116254	GGAGGCGGCAGCCCAGTCTC
194885	27081	TGATTTATCTTGAAAAGTCA	239472	71668	AAGTTAGTACAGACAGTATA	284059	116255	AGGAGGCGGCAGCCCAGTCT
194886	27082	CTGATTTATCTTGAAAAGTC	239473	71669	GAAGTTAGTACAGACAGTAT	284060	116256	GAGGAGGCGGCAGCCCAGTC
194887	27083	TCTGATTTATCTTGAAAAGT	239474	71670	TGAAGTTAGTACAGACAGTA	284061	116257	GGAGGAGGCGGCAGCCCAGT
194888	27084	TTCTGATTTATCTTGAAAAG	239475	71671	GTGAAGTTAGTACAGACAGT	284062	116258	GGGAGGAGGCGGCAGCCCAG
194889	27085	TTTCTGATTTATCTTGAAAA	239476	71672	TGTGAAGTTAGTACAGACAG	284063	116259	GGGGAGGAGGCGGCAGCCCA
194890	27086	ATTTCTGATTTATCTTGAAA	239477	71673	TTGTGAAGTTAGTACAGACA	284064	116260	GGGGGAGGAGGCGGCAGCCC
194891	27087	GATTTCTGATTTATCTTGAA	239478	71674	CTTGTGAAGTTAGTACAGAC	284065	116261	CGGGGGAGGAGGCGGCAGCC
194892	27088	CGATTTCTGATTTATCTTGA	239479	71675	ACTTGTGAAGTTAGTACAGA	284066	116262	TCGGGGGAGGAGGCGGCAGC
194893	27089	ACGATTTCTGATTTATCTTG	239480	71676	AACTTGTGAAGTTAGTACAG	284067	116263	GTCGGGGGAGGAGGCGGCAG
194894	27090	TACGATTTCTGATTTATCTT	239481	71677	AAACTTGTGAAGTTAGTACA	284068	116264	TGTCGGGGGAGGAGGCGGCA
194895	27091	ATACGATTTCTGATTTATCT	239482	71678	AAAACTTGTGAAGTTAGTAC	284069	116265	GTGTCGGGGGAGGAGGCGGC
194896	27092	AATACGATTTCTGATTTATC	239483	71679	GAAAACTTGTGAAGTTAGTA	284070	116266	GGTGTCGGGGGAGGAGGCGG
194897	27093	AAATACGATTTCTGATTTAT	239484	71680	AGAAAACTTGTGAAGTTAGT	284071	116267	AGGTGTCGGGGGAGGAGGCG
194898	27094	GAAATACGATTTCTGATTTA	239485	71681	CAGAAAACTTGTGAAGTTAG	284072	116268	CAGGTGTCGGGGGAGGAGGC
194899	27095	GGAAATACGATTTCTGATTT	239486	71682	ACAGAAAACTTGTGAAGTTA	284073	116269	CCAGGTGTCGGGGGAGGAGG
194900	27096	TGGAAATACGATTTCTGATT	239487	71683	TACAGAAAACTTGTGAAGTT	284074	116270	CCCAGGTGTCGGGGGAGGAG
194901	27097	ATGGAAATACGATTTCTGAT	239488	71684	TTACAGAAAACTTGTGAAGT	284075	116271	GCCCAGGTGTCGGGGGAGGA
194902	27098	CATGGAAATACGATTTCTGA	239489	71685	TTTACAGAAAACTTGTGAAG	284076	116272	TGCCCAGGTGTCGGGGGAGG
194903	27099	TCATGGAAATACGATTTCTG	239490	71686	ATTTACAGAAAACTTGTGAA	284077	116273	CTGCCCAGGTGTCGGGGGAG
194904	27100	CTCATGGAAATACGATTTCT	239491	71687	GATTTACAGAAAACTTGTGA	284078	116274	CCTGCCCAGGTGTCGGGGGA
194905	27101	TCTCATGGAAATACGATTTC	239492	71688	AGATTTACAGAAAACTTGTG	284079	116275	ACCTGCCCAGGTGTCGGGGG
194906	27102	ATCTCATGGAAATACGATTT	239493	71689	TAGATTTACAGAAAACTTGT	284080	116276	AACCTGCCCAGGTGTCGGGG
194907	27103	TATCTCATGGAAATACGATT	239494	71690	TTAGATTTACAGAAAACTTG	284081	116277	CAACCTGCCCAGGTGTCGGG
194908	27104	ATATCTCATGGAAATACGAT	239495	71691	TTTAGATTTACAGAAAACTT	284082	116278	TCAACCTGCCCAGGTGTCGG
194909	27105	GATATCTCATGGAAATACGA	239496	71692	TTTTAGATTTACAGAAAACT	284083	116279	GTCAACCTGCCCAGGTGTCG
194910	27106	GGATATCTCATGGAAATACG	239497	71693	GTTTTAGATTTACAGAAAAC	284084	116280	CGTCAACCTGCCCAGGTGTC
194911	27107	GGGATATCTCATGGAAATAC	239498	71694	AGTTTTAGATTTACAGAAAA	284085	116281	ACGTCAACCTGCCCAGGTGT
194912	27108	AGGGATATCTCATGGAAATA	239499	71695	CAGTTTTAGATTTACAGAAA	284086	116282	AACGTCAACCTGCCCAGGTG
194913	27109	TAGGGATATCTCATGGAAAT	239500	71696	ACAGTTTTAGATTTACAGAA	284087	116283	CAACGTCAACCTGCCCAGGT
194914	27110	ATAGGGATATCTCATGGAAA	239501	71697	AACAGTTTTAGATTTACAGA	284088	116284	TCAACGTCAACCTGCCCAGG
194915	27111	AATAGGGATATCTCATGGAA	239502	71698	GAACAGTTTTAGATTTACAG	284089	116285	CTCAACGTCAACCTGCCCAG
194916	27112	AAATAGGGATATCTCATGGA	239503	71699	GGAACAGTTTTAGATTTACA	284090	116286	ACTCAACGTCAACCTGCCCA
194917	27113	CAAATAGGGATATCTCATGG	239504	71700	TGGAACAGTTTTAGATTTAC	284091	116287	CACTCAACGTCAACCTGCCC
194918	27114	GCAAATAGGGATATCTCATG	239505	71701	TTGGAACAGTTTTAGATTTA	284092	116288	CCACTCAACGTCAACCTGCC
194919	27115	TGCAAATAGGGATATCTCAT	239506	71702	TTTGGAACAGTTTTAGATTT	284093	116289	GCCACTCAACGTCAACCTGC
194920	27116	TTGCAAATAGGGATATCTCA	239507	71703	TTTTGGAACAGTTTTAGATT	284094	116290	AGCCACTCAACGTCAACCTG
194921	27117	CTTGCAAATAGGGATATCTC	239508	71704	ATTTTGGAACAGTTTTAGAT	284095	116291	GAGCCACTCAACGTCAACCT
194922	27118	ACTTGCAAATAGGGATATCT	239509	71705	TATTTTGGAACAGTTTTAGA	284096	116292	GGAGCCACTCAACGTCAACC
194923	27119	CACTTGCAAATAGGGATATC	239510	71706	TTATTTTGGAACAGTTTTAG	284097	116293	TGGAGCCACTCAACGTCAAC
194924	27120	TCACTTGCAAATAGGGATAT	239511	71707	GTTATTTTGGAACAGTTTTA	284098	116294	GTGGAGCCACTCAACGTCAA
194925	27121	ATCACTTGCAAATAGGGATA	239512	71708	TGTTATTTTGGAACAGTTTT	284099	116295	AGTGGAGCCACTCAACGTCA
194926	27122	CATCACTTGCAAATAGGGAT	239513	71709	TTGTTATTTTGGAACAGTTT	284100	116296	CAGTGGAGCCACTCAACGTC
194927	27123	CCATCACTTGCAAATAGGGA	239514	71710	CTTGTTATTTTGGAACAGTT	284101	116297	ACAGTGGAGCCACTCAACGT
194928	27124	ACCATCACTTGCAAATAGGG	239515	71711	ACTTGTTATTTTGGAACAGT	284102	116298	CACAGTGGAGCCACTCAACG
194929	27125	CACCATCACTTGCAAATAGG	239516	71712	AACTTGTTATTTTGGAACAG	284103	116299	CCACAGTGGAGCCACTCAAC
194930	27126	TCACCATCACTTGCAAATAG	239517	71713	GAACTTGTTATTTTGGAACA	284104	116300	TCCACAGTGGAGCCACTCAA
194931	27127	GTCACCATCACTTGCAAATA	239518	71714	CGAACTTGTTATTTTGGAAC	284105	116301	GTCCACAGTGGAGCCACTCA
194932	27128	AGTCACCATCACTTGCAAAT	239519	71715	ACGAACTTGTTATTTTGGAA	284106	116302	TGTCCACAGTGGAGCCACTC
194933	27129	TAGTCACCATCACTTGCAAA	239520	71716	AACGAACTTGTTATTTTGGA	284107	116303	CTGTCCACAGTGGAGCCACT
194934	27130	TTAGTCACCATCACTTGCAA	239521	71717	AAACGAACTTGTTATTTTGG	284108	116304	CCTGTCCACAGTGGAGCCAC
194935	27131	TTTAGTCACCATCACTTGCA	239522	71718	TAAACGAACTTGTTATTTTG	284109	116305	ACCTGTCCACAGTGGAGCCA
194936	27132	ATTTAGTCACCATCACTTGC	239523	71719	TTAAACGAACTTGTTATTTT	284110	116306	CACCTGTCCACAGTGGAGCC
194937	27133	AATTTAGTCACCATCACTTG	239524	71720	TTTAAACGAACTTGTTATTT	284111	116307	TCACCTGTCCACAGTGGAGC
194938	27134	TAATTTAGTCACCATCACTT	239525	71721	TTTTAAACGAACTTGTTATT	284112	116308	GTCACCTGTCCACAGTGGAG
194939	27135	CTAATTTAGTCACCATCACT	239526	71722	ATTTTAAACGAACTTGTTAT	284113	116309	GGTCACCTGTCCACAGTGGA
194940	27136	TCTAATTTAGTCACCATCAC	239527	71723	AATTTTAAACGAACTTGTTA	284114	116310	GGGTCACCTGTCCACAGTGG
194941	27137	TTCTAATTTAGTCACCATCA	239528	71724	TAATTTTAAACGAACTTGTT	284115	116311	CGGGTCACCTGTCCACAGTG
194942	27138	CTTCTAATTTAGTCACCATC	239529	71725	TTAATTTTAAACGAACTTGT	284116	116312	ACGGGTCACCTGTCCACAGT
194943	27139	ACTTCTAATTTAGTCACCAT	239530	71726	GTTAATTTTAAACGAACTTG	284117	116313	AACGGGTCACCTGTCCACAG
194944	27140	AACTTCTAATTTAGTCACCA	239531	71727	AGTTAATTTTAAACGAACTT	284118	116314	AAACGGGTCACCTGTCCACA
194945	27141	AAACTTCTAATTTAGTCACC	239532	71728	GAGTTAATTTTAAACGAACT	284119	116315	CAAACGGGTCACCTGTCCAC
194946	27142	AAAACTTCTAATTTAGTCAC	239533	71729	GGAGTTAATTTTAAACGAAC	284120	116316	ACAAACGGGTCACCTGTCCA

194947	27143	AAAAACTTCTAATTTAGTCA	239534	71730	TGGAGTTAATTTTAAACGAA	284121	116317	AACAAACGGGTCACCTGTCC
194948	27144	CAAAAACTTCTAATTTAGTC	239535	71731	CTGGAGTTAATTTTAAACGA	284122	116318	GAACAAACGGGTCACCTGTC
194949	27145	TCAAAAACTTCTAATTTAGT	239536	71732	CCTGGAGTTAATTTTAAACG	284123	116319	AGAACAAACGGGTCACCTGT
194950	27146	TTCAAAAACTTCTAATTTAG	239537	71733	TCCTGGAGTTAATTTTAAAC	284124	116320	CAGAACAAACGGGTCACCTG
194951	27147	ATTCAAAAACTTCTAATTTA	239538	71734	CTCCTGGAGTTAATTTTAAA	284125	116321	TCAGAACAAACGGGTCACCT
194952	27148	TATTCAAAAACTTCTAATTT	239539	71735	TCTCCTGGAGTTAATTTTAA	284126	116322	ATCAGAACAAACGGGTCACC
194953	27149	ATATTCAAAAACTTCTAATT	239540	71736	GTCTCCTGGAGTTAATTTTA	284127	116323	CATCAGAACAAACGGGTCAC
194954	27150	AATATTCAAAAACTTCTAAT	239541	71737	GGTCTCCTGGAGTTAATTTT	284128	116324	TCATCAGAACAAACGGGTCA
194955	27151	CAATATTCAAAAACTTCTAA	239542	71738	TGGTCTCCTGGAGTTAATTT	284129	116325	CTCATCAGAACAAACGGGTC
194956	27152	ACAATATTCAAAAACTTCTA	239543	71739	CTGGTCTCCTGGAGTTAATT	284130	116326	GCTCATCAGAACAAACGGGT
194957	27153	TACAATATTCAAAAACTTCT	239544	71740	CCTGGTCTCCTGGAGTTAAT	284131	116327	CGCTCATCAGAACAAACGGG
194958	27154	TTACAATATTCAAAAACTTC	239545	71741	ACCTGGTCTCCTGGAGTTAA	284132	116328	CCGCTCATCAGAACAAACGG
194959	27155	GTTACAATATTCAAAAACTT	239546	71742	TACCTGGTCTCCTGGAGTTA	284133	116329	TCCGCTCATCAGAACAAACG
194960	27156	TGTTACAATATTCAAAAACT	239547	71743	GTACCTGGTCTCCTGGAGTT	284134	116330	GTCCGCTCATCAGAACAAAC
194961	27157	ATGTTACAATATTCAAAAAC	239548	71744	CGTACCTGGTCTCCTGGAGT	284135	116331	TGTCCGCTCATCAGAACAAA
194962	27158	CATGTTACAATATTCAAAAA	239549	71745	CCGTACCTGGTCTCCTGGAG	284136	116332	GTGTCCGCTCATCAGAACAA
194963	27159	ACATGTTACAATATTCAAAA	239550	71746	ACCGTACCTGGTCTCCTGGA	284137	116333	GGTGTCCGCTCATCAGAACA
194964	27160	AACATGTTACAATATTCAAA	239551	71747	TACCGTACCTGGTCTCCTGG	284138	116334	TGGTGTCCGCTCATCAGAAC
194965	27161	GAACATGTTACAATATTCAA	239552	71748	CTACCGTACCTGGTCTCCTG	284139	116335	TTGGTGTCCGCTCATCAGAA
194966	27162	CGAACATGTTACAATATTCA	239553	71749	GCTACCGTACCTGGTCTCCT	284140	116336	CTTGGTGTCCGCTCATCAGA
194967	27163	ACGAACATGTTACAATATTC	239554	71750	AGCTACCGTACCTGGTCTCC	284141	116337	CCTTGGTGTCCGCTCATCAG
194968	27164	TACGAACATGTTACAATATT	239555	71751	TAGCTACCGTACCTGGTCTC	284142	116338	ACCTTGGTGTCCGCTCATCA
194969	27165	CTACGAACATGTTACAATAT	239556	71752	TTAGCTACCGTACCTGGTCT	284143	116339	GACCTTGGTGTCCGCTCATC
194970	27166	CCTACGAACATGTTACAATA	239557	71753	ATTAGCTACCGTACCTGGTC	284144	116340	AGACCTTGGTGTCCGCTCAT
194971	27167	GCCTACGAACATGTTACAAT	239558	71754	CATTAGCTACCGTACCTGGT	284145	116341	AAGACCTTGGTGTCCGCTCA
194972	27168	AGCCTACGAACATGTTACAA	239559	71755	GCATTAGCTACCGTACCTGG	284146	116342	TAAGACCTTGGTGTCCGCTC
194973	27169	CAGCCTACGAACATGTTACA	239560	71756	GGCATTAGCTACCGTACCTG	284147	116343	GTAAGACCTTGGTGTCCGCT
194974	27170	ACAGCCTACGAACATGTTAC	239561	71757	AGGCATTAGCTACCGTACCT	284148	116344	AGTAAGACCTTGGTGTCCGC
194975	27171	AACAGCCTACGAACATGTTA	239562	71758	TAGGCATTAGCTACCGTACC	284149	116345	CAGTAAGACCTTGGTGTCCG
194976	27172	AAACAGCCTACGAACATGTT	239563	71759	ATAGGCATTAGCTACCGTAC	284150	116346	ACAGTAAGACCTTGGTGTCC
194977	27173	CAAACAGCCTACGAACATGT	239564	71760	TATAGGCATTAGCTACCGTA	284151	116347	GACAGTAAGACCTTGGTGTC
194978	27174	ACAAACAGCCTACGAACATG	239565	71761	TTATAGGCATTAGCTACCGT	284152	116348	GGACAGTAAGACCTTGGTGT
194979	27175	GACAAACAGCCTACGAACAT	239566	71762	ATTATAGGCATTAGCTACCG	284153	116349	AGGACAGTAAGACCTTGGTG
194980	27176	AGACAAACAGCCTACGAACA	239567	71763	GATTATAGGCATTAGCTACC	284154	116350	CAGGACAGTAAGACCTTGGT
194981	27177	CAGACAAACAGCCTACGAAC	239568	71764	GGATTATAGGCATTAGCTAC	284155	116351	GCAGGACAGTAAGACCTTGG
194982	27178	CCAGACAAACAGCCTACGAA	239569	71765	GGGATTATAGGCATTAGCTA	284156	116352	AGCAGGACAGTAAGACCTTG
194983	27179	ACCAGACAAACAGCCTACGA	239570	71766	TGGGATTATAGGCATTAGCT	284157	116353	GAGCAGGACAGTAAGACCTT
194984	27180	AACCAGACAAACAGCCTACG	239571	71767	CTGGGATTATAGGCATTAGC	284158	116354	TGAGCAGGACAGTAAGACCT
194985	27181	AAACCAGACAAACAGCCTAC	239572	71768	GCTGGGATTATAGGCATTAG	284159	116355	CTGAGCAGGACAGTAAGACC
194986	27182	TAAACCAGACAAACAGCCTA	239573	71769	TGCTGGGATTATAGGCATTA	284160	116356	GCTGAGCAGGACAGTAAGAC
194987	27183	TTAAACCAGACAAACAGCCT	239574	71770	GTGCTGGGATTATAGGCATT	284161	116357	AGCTGAGCAGGACAGTAAGA
194988	27184	TTTAAACCAGACAAACAGCC	239575	71771	AGTGCTGGGATTATAGGCAT	284162	116358	CAGCTGAGCAGGACAGTAAG
194989	27185	GTTTAAACCAGACAAACAGC	239576	71772	AAGTGCTGGGATTATAGGCA	284163	116359	GCAGCTGAGCAGGACAGTAA
194990	27186	AGTTTAAACCAGACAAACAG	239577	71773	GAAGTGCTGGGATTATAGGC	284164	116360	AGCAGCTGAGCAGGACAGTA
194991	27187	GAGTTTAAACCAGACAAACA	239578	71774	CGAAGTGCTGGGATTATAGG	284165	116361	CAGCAGCTGAGCAGGACAGT
194992	27188	AGAGTTTAAACCAGACAAAC	239579	71775	CCGAAGTGCTGGGATTATAG	284166	116362	GCAGCAGCTGAGCAGGACAG
194993	27189	TAGAGTTTAAACCAGACAAA	239580	71776	TCCGAAGTGCTGGGATTATA	284167	116363	AGCAGCAGCTGAGCAGGACA
194994	27190	ATAGAGTTTAAACCAGACAA	239581	71777	TTCCGAAGTGCTGGGATTAT	284168	116364	GAGCAGCAGCTGAGCAGGAC
194995	27191	GATAGAGTTTAAACCAGACA	239582	71778	CTTCCGAAGTGCTGGGATTA	284169	116365	GGAGCAGCAGCTGAGCAGGA
194996	27192	AGATAGAGTTTAAACCAGAC	239583	71779	CCTTCCGAAGTGCTGGGATT	284170	116366	AGGAGCAGCAGCTGAGCAGG
194997	27193	CAGATAGAGTTTAAACCAGA	239584	71780	GCCTTCCGAAGTGCTGGGAT	284171	116367	TAGGAGCAGCAGCTGAGCAG
194998	27194	CCAGATAGAGTTTAAACCAG	239585	71781	AGCCTTCCGAAGTGCTGGGA	284172	116368	GTAGGAGCAGCAGCTGAGCA
194999	27195	TCCAGATAGAGTTTAAACCA	239586	71782	CAGCCTTCCGAAGTGCTGGG	284173	116369	TGTAGGAGCAGCAGCTGAGC
195000	27196	CTCCAGATAGAGTTTAAACC	239587	71783	TCAGCCTTCCGAAGTGCTGG	284174	116370	GTGTAGGAGCAGCAGCTGAG
195001	27197	CCTCCAGATAGAGTTTAAAC	239588	71784	CTCAGCCTTCCGAAGTGCTG	284175	116371	CGTGTAGGAGCAGCAGCTGA
195002	27198	TCCTCCAGATAGAGTTTAAA	239589	71785	CCTCAGCCTTCCGAAGTGCT	284176	116372	ACGTGTAGGAGCAGCAGCTG
195003	27199	TTCCTCCAGATAGAGTTTAA	239590	71786	GCCTCAGCCTTCCGAAGTGC	284177	116373	AACGTGTAGGAGCAGCAGCT
195004	27200	ATTCCTCCAGATAGAGTTTA	239591	71787	TGCCTCAGCCTTCCGAAGTG	284178	116374	GAACGTGTAGGAGCAGCAGC
195005	27201	AATTCCTCCAGATAGAGTTT	239592	71788	CTGCCTCAGCCTTCCGAAGT	284179	116375	TGAACGTGTAGGAGCAGCAG
195006	27202	GAATTCCTCCAGATAGAGTT	239593	71789	CCTGCCTCAGCCTTCCGAAG	284180	116376	TTGAACGTGTAGGAGCAGCA
195007	27203	TGAATTCCTCCAGATAGAGT	239594	71790	ACCTGCCTCAGCCTTCCGAA	284181	116377	CTTGAACGTGTAGGAGCAGC
195008	27204	TTGAATTCCTCCAGATAGAG	239595	71791	CACCTGCCTCAGCCTTCCGA	284182	116378	CCTTGAACGTGTAGGAGCAG
195009	27205	CTTGAATTCCTCCAGATAGA	239596	71792	CCACCTGCCTCAGCCTTCCG	284183	116379	GCCTTGAACGTGTAGGAGCA
195010	27206	GCTTGAATTCCTCCAGATAG	239597	71793	TCCACCTGCCTCAGCCTTCC	284184	116380	TGCCTTGAACGTGTAGGAGC
195011	27207	AGCTTGAATTCCTCCAGATA	239598	71794	ATCCACCTGCCTCAGCCTTC	284185	116381	CTGCCTTGAACGTGTAGGAG
195012	27208	TAGCTTGAATTCCTCCAGAT	239599	71795	AATCCACCTGCCTCAGCCTT	284186	116382	CCTGCCTTGAACGTGTAGGA
195013	27209	CTAGCTTGAATTCCTCCAGA	239600	71796	CAATCCACCTGCCTCAGCCT	284187	116383	TCCTGCCTTGAACGTGTAGG
195014	27210	TCTAGCTTGAATTCCTCCAG	239601	71797	GCAATCCACCTGCCTCAGCC	284188	116384	CTCCTGCCTTGAACGTGTAG
195015	27211	GTCTAGCTTGAATTCCTCCA	239602	71798	AGCAATCCACCTGCCTCAGC	284189	116385	GCTCCTGCCTTGAACGTGTA
195016	27212	AGTCTAGCTTGAATTCCTCC	239603	71799	AAGCAATCCACCTGCCTCAG	284190	116386	GGCTCCTGCCTTGAACGTGT
195017	27213	AAGTCTAGCTTGAATTCCTC	239604	71800	CAAGCAATCCACCTGCCTCA	284191	116387	CGGCTCCTGCCTTGAACGTG
195018	27214	GAAGTCTAGCTTGAATTCCT	239605	71801	TCAAGCAATCCACCTGCCTC	284192	116388	TCGGCTCCTGCCTTGAACGT

195019	27215	TGAAGTCTAGCTTGAATTCC	239606	71802	CTCAAGCAATCCACCTGCCT	284193	116389	ATCGGCTCCTGCCTTGAACG
195020	27216	CTGAAGTCTAGCTTGAATTC	239607	71803	GCTCAAGCAATCCACCTGCC	284194	116390	AATCGGCTCCTGCCTTGAAC
195021	27217	CCTGAAGTCTAGCTTGAATT	239608	71804	GGCTCAAGCAATCCACCTGC	284195	116391	GAATCGGCTCCTGCCTTGAA
195022	27218	TCCTGAAGTCTAGCTTGAAT	239609	71805	GGGCTCAAGCAATCCACCTG	284196	116392	GGAATCGGCTCCTGCCTTGA
195023	27219	TTCCTGAAGTCTAGCTTGAA	239610	71806	TGGGCTCAAGCAATCCACCT	284197	116393	AGGAATCGGCTCCTGCCTTG
195024	27220	ATTCCTGAAGTCTAGCTTGA	239611	71807	CTGGGCTCAAGCAATCCACC	284198	116394	TAGGAATCGGCTCCTGCCTT
195025	27221	TATTCCTGAAGTCTAGCTTG	239612	71808	CCTGGGCTCAAGCAATCCAC	284199	116395	TTAGGAATCGGCTCCTGCCT
195026	27222	TTATTCCTGAAGTCTAGCTT	239613	71809	TCCTGGGCTCAAGCAATCCA	284200	116396	CTTAGGAATCGGCTCCTGCC
195027	27223	GTTATTCCTGAAGTCTAGCT	239614	71810	CTCCTGGGCTCAAGCAATCC	284201	116397	GCTTAGGAATCGGCTCCTGC
195028	27224	AGTTATTCCTGAAGTCTAGC	239615	71811	ACTCCTGGGCTCAAGCAATC	284202	116398	GGCTTAGGAATCGGCTCCTG
195029	27225	AAGTTATTCCTGAAGTCTAG	239616	71812	AACTCCTGGGCTCAAGCAAT	284203	116399	AGGCTTAGGAATCGGCTCCT
195030	27226	GAAGTTATTCCTGAAGTCTA	239617	71813	AAACTCCTGGGCTCAAGCAA	284204	116400	GAGGCTTAGGAATCGGCTCC
195031	27227	AGAAGTTATTCCTGAAGTCT	239618	71814	CAAACTCCTGGGCTCAAGCA	284205	116401	GGAGGCTTAGGAATCGGCTC
195032	27228	AAGAAGTTATTCCTGAAGTC	239619	71815	TCAAACTCCTGGGCTCAAGC	284206	116402	TGGAGGCTTAGGAATCGGCT
195033	27229	CAAGAAGTTATTCCTGAAGT	239620	71816	CTCAAACTCCTGGGCTCAAG	284207	116403	CTGGAGGCTTAGGAATCGGC
195034	27230	TCAAGAAGTTATTCCTGAAG	239621	71817	TCTCAAACTCCTGGGCTCAA	284208	116404	GCTGGAGGCTTAGGAATCGG
195035	27231	CTCAAGAAGTTATTCCTGAA	239622	71818	GTCTCAAACTCCTGGGCTCA	284209	116405	AGCTGGAGGCTTAGGAATCG
195036	27232	CCTCAAGAAGTTATTCCTGA	239623	71819	TGTCTCAAACTCCTGGGCTC	284210	116406	AAGCTGGAGGCTTAGGAATC
195037	27233	GCCTCAAGAAGTTATTCCTG	239624	71820	TTGTCTCAAACTCCTGGGCT	284211	116407	TAAGCTGGAGGCTTAGGAAT
195038	27234	TGCCTCAAGAAGTTATTCCT	239625	71821	CTTGTCTCAAACTCCTGGGC	284212	116408	ATAAGCTGGAGGCTTAGGAA
195039	27235	TTGCCTCAAGAAGTTATTCC	239626	71822	GCTTGTCTCAAACTCCTGGG	284213	116409	CATAAGCTGGAGGCTTAGGA
195040	27236	CTTGCCTCAAGAAGTTATTC	239627	71823	GGCTTGTCTCAAACTCCTGG	284214	116410	GCATAAGCTGGAGGCTTAGG
195041	27237	CCTTGCCTCAAGAAGTTATT	239628	71824	AGGCTTGTCTCAAACTCCTG	284215	116411	AGCATAAGCTGGAGGCTTAG
195042	27238	TCCTTGCCTCAAGAAGTTAT	239629	71825	CAGGCTTGTCTCAAACTCCT	284216	116412	AAGCATAAGCTGGAGGCTTA
195043	27239	ATCCTTGCCTCAAGAAGTTA	239630	71826	CCAGGCTTGTCTCAAACTCC	284217	116413	TAAGCATAAGCTGGAGGCTT
195044	27240	AATCCTTGCCTCAAGAAGTT	239631	71827	CCCAGGCTTGTCTCAAACTC	284218	116414	CTAAGCATAAGCTGGAGGCT
195045	27241	AAATCCTTGCCTCAAGAAGT	239632	71828	GCCCAGGCTTGTCTCAAACT	284219	116415	GCTAAGCATAAGCTGGAGGC
195046	27242	AAAATCCTTGCCTCAAGAAG	239633	71829	TGCCCAGGCTTGTCTCAAAC	284220	116416	GGCTAAGCATAAGCTGGAGG
195047	27243	CAAAATCCTTGCCTCAAGAA	239634	71830	TTGCCCAGGCTTGTCTCAAA	284221	116417	AGGCTAAGCATAAGCTGGAG
195048	27244	TCAAAATCCTTGCCTCAAGA	239635	71831	GTTGCCCAGGCTTGTCTCAA	284222	116418	CAGGCTAAGCATAAGCTGGA
195049	27245	CTCAAAATCCTTGCCTCAAG	239636	71832	TGTTGCCCAGGCTTGTCTCA	284223	116419	GCAGGCTAAGCATAAGCTGG
195050	27246	TCTCAAAATCCTTGCCTCAA	239637	71833	ATGTTGCCCAGGCTTGTCTC	284224	116420	CGCAGGCTAAGCATAAGCTG
195051	27247	GTCTCAAAATCCTTGCCTCA	239638	71834	CATGTTGCCCAGGCTTGTCT	284225	116421	GCGCAGGCTAAGCATAAGCT
195052	27248	GGTCTCAAAATCCTTGCCTC	239639	71835	CCATGTTGCCCAGGCTTGTC	284226	116422	GGCGCAGGCTAAGCATAAGC
195053	27249	AGGTCTCAAAATCCTTGCCT	239640	71836	ACCATGTTGCCCAGGCTTGT	284227	116423	TGGCGCAGGCTAAGCATAAG
195054	27250	AAGGTCTCAAAATCCTTGCC	239641	71837	CACCATGTTGCCCAGGCTTG	284228	116424	GTGGCGCAGGCTAAGCATAA
195055	27251	TAAGGTCTCAAAATCCTTGC	239642	71838	TCACCATGTTGCCCAGGCTT	284229	116425	GGTGGCGCAGGCTAAGCATA
195056	27252	CTAAGGTCTCAAAATCCTTG	239643	71839	TTCACCATGTTGCCCAGGCT	284230	116426	GGGTGGCGCAGGCTAAGCAT
195057	27253	CCTAAGGTCTCAAAATCCTT	239644	71840	TTTCACCATGTTGCCCAGGC	284231	116427	AGGGTGGCGCAGGCTAAGCA
195058	27254	CCCTAAGGTCTCAAAATCCT	239645	71841	ATTTCACCATGTTGCCCAGG	284232	116428	GAGGGTGGCGCAGGCTAAGC
195059	27255	TCCCTAAGGTCTCAAAATCC	239646	71842	GATTTCACCATGTTGCCCAG	284233	116429	AGAGGGTGGCGCAGGCTAAG
195060	27256	TTCCCTAAGGTCTCAAAATC	239647	71843	GGATTTCACCATGTTGCCCA	284234	116430	CAGAGGGTGGCGCAGGCTAA
195061	27257	TTTCCCTAAGGTCTCAAAAT	239648	71844	AGGATTTCACCATGTTGCCC	284235	116431	CCAGAGGGTGGCGCAGGCTA
195062	27258	CTTTCCCTAAGGTCTCAAAA	239649	71845	CAGGATTTCACCATGTTGCC	284236	116432	GCCAGAGGGTGGCGCAGGCT
195063	27259	TCTTTCCCTAAGGTCTCAAA	239650	71846	ACAGGATTTCACCATGTTGC	284237	116433	TGCCAGAGGGTGGCGCAGGC
195064	27260	TTCTTTCCCTAAGGTCTCAA	239651	71847	GACAGGATTTCACCATGTTG	284238	116434	CTGCCAGAGGGTGGCGCAGG
195065	27261	CTTCTTTCCCTAAGGTCTCA	239652	71848	AGACAGGATTTCACCATGTT	284239	116435	TCTGCCAGAGGGTGGCGCAG
195066	27262	CCTTCTTTCCCTAAGGTCTC	239653	71849	GAGACAGGATTTCACCATGT	284240	116436	CTCTGCCAGAGGGTGGCGCA
195067	27263	TCCTTCTTTCCCTAAGGTCT	239654	71850	AGAGACAGGATTTCACCATG	284241	116437	TCTCTGCCAGAGGGTGGCGC
195068	27264	GTCCTTCTTTCCCTAAGGTC	239655	71851	TAGAGACAGGATTTCACCAT	284242	116438	GTCTCTGCCAGAGGGTGGCG
195069	27265	CGTCCTTCTTTCCCTAAGGT	239656	71852	TTAGAGACAGGATTTCACCA	284243	116439	AGTCTCTGCCAGAGGGTGGC
195070	27266	ACGTCCTTCTTTCCCTAAGG	239657	71853	TTTAGAGACAGGATTTCACC	284244	116440	GAGTCTCTGCCAGAGGGTGG
195071	27267	GACGTCCTTCTTTCCCTAAG	239658	71854	TTTTAGAGACAGGATTTCAC	284245	116441	GGAGTCTCTGCCAGAGGGTG
195072	27268	AGACGTCCTTCTTTCCCTAA	239659	71855	TTTTTAGAGACAGGATTTCA	284246	116442	TGGAGTCTCTGCCAGAGGGT
195073	27269	AAGACGTCCTTCTTTCCCTA	239660	71856	TTTTTTAGAGACAGGATTTC	284247	116443	CTGGAGTCTCTGCCAGAGGG
195074	27270	CAAGACGTCCTTCTTTCCCT	239661	71857	TTTTTTTAGAGACAGGATTT	284248	116444	TCTGGAGTCTCTGCCAGAGG
195075	27271	CCAAGACGTCCTTCTTTCCC	239662	71858	TTTTTTTTAGAGACAGGATT	284249	116445	ATCTGGAGTCTCTGCCAGAG
195076	27272	CCCAAGACGTCCTTCTTTCC	239663	71859	ATTTTTTTTAGAGACAGGAT	284250	116446	CATCTGGAGTCTCTGCCAGA
195077	27273	CCCCAAGACGTCCTTCTTTC	239664	71860	GATTTTTTTTAGAGACAGGA	284251	116447	GCATCTGGAGTCTCTGCCAG
195078	27274	CCCCCAAGACGTCCTTCTTT	239665	71861	TGATTTTTTTTAGAGACAGG	284252	116448	TGCATCTGGAGTCTCTGCCA
195079	27275	ACCCCCAAGACGTCCTTCTT	239666	71862	GTGATTTTTTTTAGAGACAG	284253	116449	TTGCATCTGGAGTCTCTGCC
195080	27276	TACCCCCAAGACGTCCTTCT	239667	71863	TGTGATTTTTTTTAGAGACA	284254	116450	TTTGCATCTGGAGTCTCTGC
195081	27277	ATACCCCCAAGACGTCCTTC	239668	71864	TTGTGATTTTTTTTAGAGAC	284255	116451	CTTTGCATCTGGAGTCTCTG
195082	27278	AATACCCCCAAGACGTCCTT	239669	71865	TTTGTGATTTTTTTTAGAGA	284256	116452	TCTTTGCATCTGGAGTCTCT
195083	27279	GAATACCCCCAAGACGTCCT	239670	71866	TTTTGTGATTTTTTTTAGAG	284257	116453	CTCTTTGCATCTGGAGTCTC
195084	27280	AGAATACCCCCAAGACGTCC	239671	71867	TTTTTGTGATTTTTTTTAGA	284258	116454	GCTCTTTGCATCTGGAGTCT
195085	27281	CAGAATACCCCCAAGACGTC	239672	71868	ATTTTTGTGATTTTTTTTAG	284259	116455	GGCTCTTTGCATCTGGAGTC
195086	27282	TCAGAATACCCCCAAGACGT	239673	71869	AATTTTTGTGATTTTTTTTA	284260	116456	TGGCTCTTTGCATCTGGAGT
195087	27283	GTCAGAATACCCCCAAGACG	239674	71870	TAATTTTTGTGATTTTTTTT	284261	116457	TTGGCTCTTTGCATCTGGAG
195088	27284	AGTCAGAATACCCCCAAGAC	239675	71871	CTAATTTTTGTGATTTTTTT	284262	116458	TTTGGCTCTTTGCATCTGGA
195089	27285	CAGTCAGAATACCCCCAAGA	239676	71872	GCTAATTTTTGTGATTTTTT	284263	116459	GTTTGGCTCTTTGCATCTGG
195090	27286	ACAGTCAGAATACCCCCAAG	239677	71873	GGCTAATTTTTGTGATTTTT	284264	116460	GGTTTGGCTCTTTGCATCTG

195091	27287	AACAGTCAGAATACCCCCAA	239678	71874	TGGCTAATTTTTGTGATTTT	284265	116461	TGGTTTGGCTCTTTGCATCT
195092	27288	CAACAGTCAGAATACCCCCA	239679	71875	CTGGCTAATTTTTGTGATTT	284266	116462	TTGGTTTGGCTCTTTGCATC
195093	27289	ACAACAGTCAGAATACCCCC	239680	71876	CCTGGCTAATTTTTGTGATT	284267	116463	TTTGGTTTGGCTCTTTGCAT
195094	27290	GACAACAGTCAGAATACCCC	239681	71877	ACCTGGCTAATTTTTGTGAT	284268	116464	CTTTGGTTTGGCTCTTTGCA
195095	27291	GGACAACAGTCAGAATACCC	239682	71878	CACCTGGCTAATTTTTGTGA	284269	116465	ACTTTGGTTTGGCTCTTTGC
195096	27292	AGGACAACAGTCAGAATACC	239683	71879	ACACCTGGCTAATTTTTGTG	284270	116466	CACTTTGGTTTGGCTCTTTG
195097	27293	GAGGACAACAGTCAGAATAC	239684	71880	CACACCTGGCTAATTTTTGT	284271	116467	GCACTTTGGTTTGGCTCTTT
195098	27294	GGAGGACAACAGTCAGAATA	239685	71881	CCACACCTGGCTAATTTTTG	284272	116468	CGCACTTTGGTTTGGCTCTT
195099	27295	AGGAGGACAACAGTCAGAAT	239686	71882	ACCACACCTGGCTAATTTTT	284273	116469	TCGCACTTTGGTTTGGCTCT
195100	27296	CAGGAGGACAACAGTCAGAA	239687	71883	CACCACACCTGGCTAATTTT	284274	116470	GTCGCACTTTGGTTTGGCTC
195101	27297	CCAGGAGGACAACAGTCAGA	239688	71884	CCACCACACCTGGCTAATTT	284275	116471	TGTCGCACTTTGGTTTGGCT
195102	27298	TCCAGGAGGACAACAGTCAG	239689	71885	GCCACCACACCTGGCTAATT	284276	116472	CTGTCGCACTTTGGTTTGGC
195103	27299	TTCCAGGAGGACAACAGTCA	239690	71886	CGCCACCACACCTGGCTAAT	284277	116473	CCTGTCGCACTTTGGTTTGG
195104	27300	CTTCCAGGAGGACAACAGTC	239691	71887	GCGCCACCACACCTGGCTAA	284278	116474	ACCTGTCGCACTTTGGTTTG
195105	27301	CCTTCCAGGAGGACAACAGT	239692	71888	TGCGCCACCACACCTGGCTA	284279	116475	GACCTGTCGCACTTTGGTTT
195106	27302	CCCTTCCAGGAGGACAACAG	239693	71889	ATGCGCCACCACACCTGGCT	284280	116476	GGACCTGTCGCACTTTGGTT
195107	27303	TCCCTTCCAGGAGGACAACA	239694	71890	AATGCGCCACCACACCTGGC	284281	116477	GGGACCTGTCGCACTTTGGT
195108	27304	TTCCCTTCCAGGAGGACAAC	239695	71891	GAATGCGCCACCACACCTGG	284282	116478	AGGGACCTGTCGCACTTTGG
195109	27305	CTTCCCTTCCAGGAGGACAA	239696	71892	GGAATGCGCCACCACACCTG	284283	116479	GAGGGACCTGTCGCACTTTG
195110	27306	TCTTCCCTTCCAGGAGGACA	239697	71893	AGGAATGCGCCACCACACCT	284284	116480	AGAGGGACCTGTCGCACTTT
195111	27307	TTCTTCCCTTCCAGGAGGAC	239698	71894	CAGGAATGCGCCACCACACC	284285	116481	CAGAGGGACCTGTCGCACTT
195112	27308	GTTCTTCCCTTCCAGGAGGA	239699	71895	ACAGGAATGCGCCACCACAC	284286	116482	GCAGAGGGACCTGTCGCACT
195113	27309	TGTTCTTCCCTTCCAGGAGG	239700	71896	TACAGGAATGCGCCACCACA	284287	116483	GGCAGAGGGACCTGTCGCAC
195114	27310	CTGTTCTTCCCTTCCAGGAG	239701	71897	CTACAGGAATGCGCCACCAC	284288	116484	GGGCAGAGGGACCTGTCGCA
195115	27311	TCTGTTCTTCCCTTCCAGGA	239702	71898	ACTACAGGAATGCGCCACCA	284289	116485	TGGGCAGAGGGACCTGTCGC
195116	27312	CTCTGTTCTTCCCTTCCAGG	239703	71899	GACTACAGGAATGCGCCACC	284290	116486	CTGGGCAGAGGGACCTGTCG
195117	27313	TCTCTGTTCTTCCCTTCCAG	239704	71900	GGACTACAGGAATGCGCCAC	284291	116487	GCTGGGCAGAGGGACCTGTC
195118	27314	TTCTCTGTTCTTCCCTTCCA	239705	71901	GGGACTACAGGAATGCGCCA	284292	116488	CGCTGGGCAGAGGGACCTGT
195119	27315	GTTCTCTGTTCTTCCCTTCC	239706	71902	TGGGACTACAGGAATGCGCC	284293	116489	ACGCTGGGCAGAGGGACCTG
195120	27316	AGTTCTCTGTTCTTCCCTTC	239707	71903	CTGGGACTACAGGAATGCGC	284294	116490	AACGCTGGGCAGAGGGACCT
195121	27317	TAGTTCTCTGTTCTTCCCTT	239708	71904	GCTGGGACTACAGGAATGCG	284295	116491	CAACGCTGGGCAGAGGGACC
195122	27318	CTAGTTCTCTGTTCTTCCCT	239709	71905	AGCTGGGACTACAGGAATGC	284296	116492	TCAACGCTGGGCAGAGGGAC
195123	27319	TCTAGTTCTCTGTTCTTCCC	239710	71906	TAGCTGGGACTACAGGAATG	284297	116493	CTCAACGCTGGGCAGAGGGA
195124	27320	TTCTAGTTCTCTGTTCTTCC	239711	71907	GTAGCTGGGACTACAGGAAT	284298	116494	CCTCAACGCTGGGCAGAGGG
195125	27321	CTTCTAGTTCTCTGTTCTTC	239712	71908	AGTAGCTGGGACTACAGGAA	284299	116495	ACCTCAACGCTGGGCAGAGG
195126	27322	TCTTCTAGTTCTCTGTTCTT	239713	71909	AAGTAGCTGGGACTACAGGA	284300	116496	CACCTCAACGCTGGGCAGAG
195127	27323	GTCTTCTAGTTCTCTGTTCT	239714	71910	CAAGTAGCTGGGACTACAGG	284301	116497	ACACCTCAACGCTGGGCAGA
195128	27324	AGTCTTCTAGTTCTCTGTTC	239715	71911	GCAAGTAGCTGGGACTACAG	284302	116498	CACACCTCAACGCTGGGCAG
195129	27325	CAGTCTTCTAGTTCTCTGTT	239716	71912	CGCAAGTAGCTGGGACTACA	284303	116499	CCACACCTCAACGCTGGGCA
195130	27326	GCAGTCTTCTAGTTCTCTGT	239717	71913	CCGCAAGTAGCTGGGACTAC	284304	116500	GCCACACCTCAACGCTGGGC
195131	27327	GGCAGTCTTCTAGTTCTCTG	239718	71914	CCCGCAAGTAGCTGGGACTA	284305	116501	TGCCACACCTCAACGCTGGG
195132	27328	GGGCAGTCTTCTAGTTCTCT	239719	71915	CCCCGCAAGTAGCTGGGACT	284306	116502	CTGCCACACCTCAACGCTGG
195133	27329	AGGGCAGTCTTCTAGTTCTC	239720	71916	GCCCCGCAAGTAGCTGGGAC	284307	116503	TCTGCCACACCTCAACGCTG
195134	27330	AAGGGCAGTCTTCTAGTTCT	239721	71917	AGCCCCGCAAGTAGCTGGGA	284308	116504	CTCTGCCACACCTCAACGCT
195135	27331	TAAGGGCAGTCTTCTAGTTC	239722	71918	CAGCCCCGCAAGTAGCTGGG	284309	116505	TCTCTGCCACACCTCAACGC
195136	27332	CTAAGGGCAGTCTTCTAGTT	239723	71919	TCAGCCCCGCAAGTAGCTGG	284310	116506	TTCTCTGCCACACCTCAACG
195137	27333	GCTAAGGGCAGTCTTCTAGT	239724	71920	CTCAGCCCCGCAAGTAGCTG	284311	116507	TTTCTCTGCCACACCTCAAC
195138	27334	CGCTAAGGGCAGTCTTCTAG	239725	71921	CCTCAGCCCCGCAAGTAGCT	284312	116508	ATTTCTCTGCCACACCTCAA
195139	27335	TCGCTAAGGGCAGTCTTCTA	239726	71922	ACCTCAGCCCCGCAAGTAGC	284313	116509	CATTTCTCTGCCACACCTCA
195140	27336	TTCGCTAAGGGCAGTCTTCT	239727	71923	CACCTCAGCCCCGCAAGTAG	284314	116510	GCATTTCTCTGCCACACCTC
195141	27337	CTTCGCTAAGGGCAGTCTTC	239728	71924	CCACCTCAGCCCCGCAAGTA	284315	116511	AGCATTTCTCTGCCACACCT
195142	27338	ACTTCGCTAAGGGCAGTCTT	239729	71925	CCCACCTCAGCCCCGCAAGT	284316	116512	CAGCATTTCTCTGCCACACC
195143	27339	AACTTCGCTAAGGGCAGTCT	239730	71926	TCCCACCTCAGCCCCGCAAG	284317	116513	GCAGCATTTCTCTGCCACAC
195144	27340	GAACTTCGCTAAGGGCAGTC	239731	71927	CTCCCACCTCAGCCCCGCAA	284318	116514	AGCAGCATTTCTCTGCCACA
195145	27341	TGAACTTCGCTAAGGGCAGT	239732	71928	TCTCCCACCTCAGCCCCGCA	284319	116515	AAGCAGCATTTCTCTGCCAC
195146	27342	TTGAACTTCGCTAAGGGCAG	239733	71929	TTCTCCCACCTCAGCCCCGC	284320	116516	AAAGCAGCATTTCTCTGCCA
195147	27343	TTTGAACTTCGCTAAGGGCA	239734	71930	ATTCTCCCACCTCAGCCCCG	284321	116517	AAAAGCAGCATTTCTCTGCC
195148	27344	CTTTGAACTTCGCTAAGGGC	239735	71931	GATTCTCCCACCTCAGCCCC	284322	116518	CAAAAGCAGCATTTCTCTGC
195149	27345	GCTTTGAACTTCGCTAAGGG	239736	71932	TGATTCTCCCACCTCAGCCC	284323	116519	CCAAAAGCAGCATTTCTCTG
195150	27346	TGCTTTGAACTTCGCTAAGG	239737	71933	ATGATTCTCCCACCTCAGCC	284324	116520	GCCAAAAGCAGCATTTCTCT
195151	27347	GTGCTTTGAACTTCGCTAAG	239738	71934	GATGATTCTCCCACCTCAGC	284325	116521	GGCCAAAAGCAGCATTTCTC
195152	27348	GGTGCTTTGAACTTCGCTAA	239739	71935	AGATGATTCTCCCACCTCAG	284326	116522	GGGCCAAAAGCAGCATTTCT
195153	27349	AGGTGCTTTGAACTTCGCTA	239740	71936	CAGATGATTCTCCCACCTCA	284327	116523	AGGGCCAAAAGCAGCATTTC
195154	27350	TAGGTGCTTTGAACTTCGCT	239741	71937	TCAGATGATTCTCCCACCTC	284328	116524	AAGGGCCAAAAGCAGCATTT
195155	27351	TTAGGTGCTTTGAACTTCGC	239742	71938	CTCAGATGATTCTCCCACCT	284329	116525	AAAGGGCCAAAAGCAGCATT
195156	27352	CTTAGGTGCTTTGAACTTCG	239743	71939	GCTCAGATGATTCTCCCACC	284330	116526	AAAAGGGCCAAAAGCAGCAT
195157	27353	GCTTAGGTGCTTTGAACTTC	239744	71940	GGCTCAGATGATTCTCCCAC	284331	116527	TAAAAGGGCCAAAAGCAGCA
195158	27354	GGCTTAGGTGCTTTGAACTT	239745	71941	GGGCTCAGATGATTCTCCCA	284332	116528	CTAAAAGGGCCAAAAGCAGC
195159	27355	GGGCTTAGGTGCTTTGAACT	239746	71942	TGGGCTCAGATGATTCTCCC	284333	116529	TCTAAAAGGGCCAAAAGCAG
195160	27356	CGGGCTTAGGTGCTTTGAAC	239747	71943	CTGGGCTCAGATGATTCTCC	284334	116530	ATCTAAAAGGGCCAAAAGCA
195161	27357	CCGGGCTTAGGTGCTTTGAA	239748	71944	CCTGGGCTCAGATGATTCTC	284335	116531	AATCTAAAAGGGCCAAAAGC
195162	27358	CCCGGGCTTAGGTGCTTTGA	239749	71945	TCCTGGGCTCAGATGATTCT	284336	116532	AAATCTAAAAGGGCCAAAAG

195163	27359	TCCCGGGCTTAGGTGCTTTG	239750	71946	CTCCTGGGCTCAGATGATTC	284337	116533	CAAATCTAAAAGGGCCAAAA
195164	27360	GTCCCGGGCTTAGGTGCTTT	239751	71947	ACTCCTGGGCTCAGATGATT	284338	116534	CCAAATCTAAAAGGGCCAAA
195165	27361	GGTCCCGGGCTTAGGTGCTT	239752	71948	AACTCCTGGGCTCAGATGAT	284339	116535	GCCAAATCTAAAAGGGCCAA
195166	27362	GGGTCCCGGGCTTAGGTGCT	239753	71949	AAACTCCTGGGCTCAGATGA	284340	116536	AGCCAAATCTAAAAGGGCCA
195167	27363	AGGGTCCCGGGCTTAGGTGC	239754	71950	CAAACTCCTGGGCTCAGATG	284341	116537	CAGCCAAATCTAAAAGGGCC
195168	27364	GAGGGTCCCGGGCTTAGGTG	239755	71951	TCAAACTCCTGGGCTCAGAT	284342	116538	GCAGCCAAATCTAAAAGGGC
195169	27365	TGAGGGTCCCGGGCTTAGGT	239756	71952	CTCAAACTCCTGGGCTCAGA	284343	116539	GGCAGCCAAATCTAAAAGGG
195170	27366	CTGAGGGTCCCGGGCTTAGG	239757	71953	CCTCAAACTCCTGGGCTCAG	284344	116540	AGGCAGCCAAATCTAAAAGG
195171	27367	GCTGAGGGTCCCGGGCTTAG	239758	71954	GCCTCAAACTCCTGGGCTCA	284345	116541	GAGGCAGCCAAATCTAAAAG
195172	27368	TGCTGAGGGTCCCGGGCTTA	239759	71955	AGCCTCAAACTCCTGGGCTC	284346	116542	AGAGGCAGCCAAATCTAAAA
195173	27369	TTGCTGAGGGTCCCGGGCTT	239760	71956	CAGCCTCAAACTCCTGGGCT	284347	116543	AAGAGGCAGCCAAATCTAAA
195174	27370	CTTGCTGAGGGTCCCGGGCT	239761	71957	GCAGCCTCAAACTCCTGGGC	284348	116544	CAAGAGGCAGCCAAATCTAA
195175	27371	ACTTGCTGAGGGTCCCGGGC	239762	71958	TGCAGCCTCAAACTCCTGGG	284349	116545	GCAAGAGGCAGCCAAATCTA
195176	27372	CACTTGCTGAGGGTCCCGGG	239763	71959	CTGCAGCCTCAAACTCCTGG	284350	116546	GGCAAGAGGCAGCCAAATCT
195177	27373	ACACTTGCTGAGGGTCCCGG	239764	71960	ACTGCAGCCTCAAACTCCTG	284351	116547	TGGCAAGAGGCAGCCAAATC
195178	27374	AACACTTGCTGAGGGTCCCG	239765	71961	CACTGCAGCCTCAAACTCCT	284352	116548	CTGGCAAGAGGCAGCCAAAT
195179	27375	GAACACTTGCTGAGGGTCCC	239766	71962	TCACTGCAGCCTCAAACTCC	284353	116549	CCTGGCAAGAGGCAGCCAAA
195180	27376	AGAACACTTGCTGAGGGTCC	239767	71963	CTCACTGCAGCCTCAAACTC	284354	116550	TCCTGGCAAGAGGCAGCCAA
195181	27377	AAGAACACTTGCTGAGGGTC	239768	71964	GCTCACTGCAGCCTCAAACT	284355	116551	CTCCTGGCAAGAGGCAGCCA
195182	27378	CAAGAACACTTGCTGAGGGT	239769	71965	AGCTCACTGCAGCCTCAAAC	284356	116552	ACTCCTGGCAAGAGGCAGCC
195183	27379	TCAAGAACACTTGCTGAGGG	239770	71966	CAGCTCACTGCAGCCTCAAA	284357	116553	CACTCCTGGCAAGAGGCAGC
195184	27380	CTCAAGAACACTTGCTGAGG	239771	71967	ACAGCTCACTGCAGCCTCAA	284358	116554	CCACTCCTGGCAAGAGGCAG
195185	27381	ACTCAAGAACACTTGCTGAG	239772	71968	CACAGCTCACTGCAGCCTCA	284359	116555	ACCACTCCTGGCAAGAGGCA
195186	27382	GACTCAAGAACACTTGCTGA	239773	71969	TCACAGCTCACTGCAGCCTC	284360	116556	CACCACTCCTGGCAAGAGGC
195187	27383	TGACTCAAGAACACTTGCTG	239774	71970	ATCACAGCTCACTGCAGCCT	284361	116557	CCACCACTCCTGGCAAGAGG
195188	27384	GTGACTCAAGAACACTTGCT	239775	71971	AATCACAGCTCACTGCAGCC	284362	116558	GCCACCACTCCTGGCAAGAG
195189	27385	TGTGACTCAAGAACACTTGC	239776	71972	CAATCACAGCTCACTGCAGC	284363	116559	AGCCACCACTCCTGGCAAGA
195190	27386	CTGTGACTCAAGAACACTTG	239777	71973	ACAATCACAGCTCACTGCAG	284364	116560	GAGCCACCACTCCTGGCAAG
195191	27387	TCTGTGACTCAAGAACACTT	239778	71974	TACAATCACAGCTCACTGCA	284365	116561	CGAGCCACCACTCCTGGCAA
195192	27388	ATCTGTGACTCAAGAACACT	239779	71975	GTACAATCACAGCTCACTGC	284366	116562	ACGAGCCACCACTCCTGGCA
195193	27389	AATCTGTGACTCAAGAACAC	239780	71976	GGTACAATCACAGCTCACTG	284367	116563	CACGAGCCACCACTCCTGGC
195194	27390	GAATCTGTGACTCAAGAACA	239781	71977	TGGTACAATCACAGCTCACT	284368	116564	GCACGAGCCACCACTCCTGG
195195	27391	AGAATCTGTGACTCAAGAAC	239782	71978	GTGGTACAATCACAGCTCAC	284369	116565	GGCACGAGCCACCACTCCTG
195196	27392	GAGAATCTGTGACTCAAGAA	239783	71979	AGTGGTACAATCACAGCTCA	284370	116566	AGGCACGAGCCACCACTCCT
195197	27393	GGAGAATCTGTGACTCAAGA	239784	71980	CAGTGGTACAATCACAGCTC	284371	116567	CAGGCACGAGCCACCACTCC
195198	27394	GGGAGAATCTGTGACTCAAG	239785	71981	GCAGTGGTACAATCACAGCT	284372	116568	ACAGGCACGAGCCACCACTC
195199	27395	AGGGAGAATCTGTGACTCAA	239786	71982	TGCAGTGGTACAATCACAGC	284373	116569	TACAGGCACGAGCCACCACT
195200	27396	CAGGGAGAATCTGTGACTCA	239787	71983	GTGCAGTGGTACAATCACAG	284374	116570	TTACAGGCACGAGCCACCAC
195201	27397	TCAGGGAGAATCTGTGACTC	239788	71984	AGTGCAGTGGTACAATCACA	284375	116571	ATTACAGGCACGAGCCACCA
195202	27398	CTCAGGGAGAATCTGTGACT	239789	71985	GAGTGCAGTGGTACAATCAC	284376	116572	AATTACAGGCACGAGCCACC
195203	27399	CCTCAGGGAGAATCTGTGAC	239790	71986	GGAGTGCAGTGGTACAATCA	284377	116573	GAATTACAGGCACGAGCCAC
195204	27400	GCCTCAGGGAGAATCTGTGA	239791	71987	TGGAGTGCAGTGGTACAATC	284378	116574	GGAATTACAGGCACGAGCCA
195205	27401	CGCCTCAGGGAGAATCTGTG	239792	71988	TTGGAGTGCAGTGGTACAAT	284379	116575	TGGAATTACAGGCACGAGCC
195206	27402	GCGCCTCAGGGAGAATCTGT	239793	71989	GTTGGAGTGCAGTGGTACAA	284380	116576	CTGGAATTACAGGCACGAGC
195207	27403	GGCGCCTCAGGGAGAATCTG	239794	71990	GGTTGGAGTGCAGTGGTACA	284381	116577	GCTGGAATTACAGGCACGAG
195208	27404	AGGCGCCTCAGGGAGAATCT	239795	71991	AGGTTGGAGTGCAGTGGTAC	284382	116578	TGCTGGAATTACAGGCACGA
195209	27405	GAGGCGCCTCAGGGAGAATC	239796	71992	CAGGTTGGAGTGCAGTGGTA	284383	116579	GTGCTGGAATTACAGGCACG
195210	27406	AGAGGCGCCTCAGGGAGAAT	239797	71993	CCAGGTTGGAGTGCAGTGGT	284384	116580	AGTGCTGGAATTACAGGCAC
195211	27407	AAGAGGCGCCTCAGGGAGAA	239798	71994	CCCAGGTTGGAGTGCAGTGG	284385	116581	AAGTGCTGGAATTACAGGCA
195212	27408	AAAGAGGCGCCTCAGGGAGA	239799	71995	GCCCAGGTTGGAGTGCAGTG	284386	116582	AAAGTGCTGGAATTACAGGC
195213	27409	GAAAGAGGCGCCTCAGGGAG	239800	71996	TGCCCAGGTTGGAGTGCAGT	284387	116583	CAAAGTGCTGGAATTACAGG
195214	27410	AGAAAGAGGCGCCTCAGGGA	239801	71997	TTGCCCAGGTTGGAGTGCAG	284388	116584	CCAAAGTGCTGGAATTACAG
195215	27411	CAGAAAGAGGCGCCTCAGGG	239802	71998	GTTGCCCAGGTTGGAGTGCA	284389	116585	CCCAAAGTGCTGGAATTACA
195216	27412	CCAGAAAGAGGCGCCTCAGG	239803	71999	TGTTGCCCAGGTTGGAGTGC	284390	116586	TCCCAAAGTGCTGGAATTAC
195217	27413	GCCAGAAAGAGGCGCCTCAG	239804	72000	CTGTTGCCCAGGTTGGAGTG	284391	116587	CTCCCAAAGTGCTGGAATTA
195218	27414	AGCCAGAAAGAGGCGCCTCA	239805	72001	TCTGTTGCCCAGGTTGGAGT	284392	116588	TCTCCCAAAGTGCTGGAATT
195219	27415	GAGCCAGAAAGAGGCGCCTC	239806	72002	CTCTGTTGCCCAGGTTGGAG	284393	116589	GTCTCCCAAAGTGCTGGAAT
195220	27416	GGAGCCAGAAAGAGGCGCCT	239807	72003	GCTCTGTTGCCCAGGTTGGA	284394	116590	AGTCTCCCAAAGTGCTGGAA
195221	27417	TGGAGCCAGAAAGAGGCGCC	239808	72004	TGCTCTGTTGCCCAGGTTGG	284395	116591	TAGTCTCCCAAAGTGCTGGA
195222	27418	ATGGAGCCAGAAAGAGGCGC	239809	72005	TTGCTCTGTTGCCCAGGTTG	284396	116592	TTAGTCTCCCAAAGTGCTGG
195223	27419	TATGGAGCCAGAAAGAGGCG	239810	72006	CTTGCTCTGTTGCCCAGGTT	284397	116593	CTTAGTCTCCCAAAGTGCTG
195224	27420	CTATGGAGCCAGAAAGAGGC	239811	72007	TCTTGCTCTGTTGCCCAGGT	284398	116594	CCTTAGTCTCCCAAAGTGCT
195225	27421	TCTATGGAGCCAGAAAGAGG	239812	72008	GTCTTGCTCTGTTGCCCAGG	284399	116595	GCCTTAGTCTCCCAAAGTGC
195226	27422	TTCTATGGAGCCAGAAAGAG	239813	72009	GGTCTTGCTCTGTTGCCCAG	284400	116596	CGCCTTAGTCTCCCAAAGTG
195227	27423	ATTCTATGGAGCCAGAAAGA	239814	72010	GGGTCTTGCTCTGTTGCCCA	284401	116597	CCGCCTTAGTCTCCCAAAGT
195228	27424	CATTCTATGGAGCCAGAAAG	239815	72011	AGGGTCTTGCTCTGTTGCCC	284402	116598	CCCGCCTTAGTCTCCCAAAG
195229	27425	CCATTCTATGGAGCCAGAAA	239816	72012	CAGGGTCTTGCTCTGTTGCC	284403	116599	TCCCGCCTTAGTCTCCCAAA
195230	27426	GCCATTCTATGGAGCCAGAA	239817	72013	ACAGGGTCTTGCTCTGTTGC	284404	116600	CTCCCGCCTTAGTCTCCCAA
195231	27427	AGCCATTCTATGGAGCCAGA	239818	72014	GACAGGGTCTTGCTCTGTTG	284405	116601	CCTCCCGCCTTAGTCTCCCA
195232	27428	CAGCCATTCTATGGAGCCAG	239819	72015	AGACAGGGTCTTGCTCTGTT	284406	116602	ACCTCCCGCCTTAGTCTCCC
195233	27429	TCAGCCATTCTATGGAGCCA	239820	72016	GAGACAGGGTCTTGCTCTGT	284407	116603	AACCTCCCGCCTTAGTCTCC
195234	27430	ATCAGCCATTCTATGGAGCC	239821	72017	TGAGACAGGGTCTTGCTCTG	284408	116604	GAACCTCCCGCCTTAGTCTC

195235	27431	AATCAGCCATTCTATGGAGC	239822	72018	TTGAGACAGGGTCTTGCTCT	284409	116605	CGAACCTCCCGCCTTAGTCT
195236	27432	GAATCAGCCATTCTATGGAG	239823	72019	TTTGAGACAGGGTCTTGCTC	284410	116606	GCGAACCTCCCGCCTTAGTC
195237	27433	AGAATCAGCCATTCTATGGA	239824	72020	TTTTGAGACAGGGTCTTGCT	284411	116607	AGCGAACCTCCCGCCTTAGT
195238	27434	CAGAATCAGCCATTCTATGG	239825	72021	TTTTTGAGACAGGGTCTTGC	284412	116608	AAGCGAACCTCCCGCCTTAG
195239	27435	ACAGAATCAGCCATTCTATG	239826	72022	TTTTTTGAGACAGGGTCTTG	284413	116609	CAAGCGAACCTCCCGCCTTA
195240	27436	TACAGAATCAGCCATTCTAT	239827	72023	GTTTTTTGAGACAGGGTCTT	284414	116610	TCAAGCGAACCTCCCGCCTT
195241	27437	TTACAGAATCAGCCATTCTA	239828	72024	TGTTTTTTGAGACAGGGTCT	284415	116611	CTCAAGCGAACCTCCCGCCT
195242	27438	GTTACAGAATCAGCCATTCT	239829	72025	TTGTTTTTTGAGACAGGGTC	284416	116612	GCTCAAGCGAACCTCCCGCC
195243	27439	AGTTACAGAATCAGCCATTC	239830	72026	TTTGTTTTTTGAGACAGGGT	284417	116613	GGCTCAAGCGAACCTCCCGC
195244	27440	GAGTTACAGAATCAGCCATT	239831	72027	TTTTGTTTTTTGAGACAGGG	284418	116614	GGGCTCAAGCGAACCTCCCG
195245	27441	CGAGTTACAGAATCAGCCAT	239832	72028	TTTTTGTTTTTTGAGACAGG	284419	116615	TGGGCTCAAGCGAACCTCCC
195246	27442	CCGAGTTACAGAATCAGCCA	239833	72029	ATTTTTGTTTTTTGAGACAG	284420	116616	CTGGGCTCAAGCGAACCTCC
195247	27443	ACCGAGTTACAGAATCAGCC	239834	72030	CATTTTTGTTTTTTGAGACA	284421	116617	CCTGGGCTCAAGCGAACCTC
195248	27444	CACCGAGTTACAGAATCAGC	239835	72031	TCATTTTTGTTTTTTGAGAC	284422	116618	TCCTGGGCTCAAGCGAACCT
195249	27445	TCACCGAGTTACAGAATCAG	239836	72032	TTCATTTTTGTTTTTTGAGA	284423	116619	CTCCTGGGCTCAAGCGAACC
195250	27446	CTCACCGAGTTACAGAATCA	239837	72033	TTTCATTTTTGTTTTTTGAG	284424	116620	ACTCCTGGGCTCAAGCGAAC
195251	27447	ACTCACCGAGTTACAGAATC	239838	72034	ATTTCATTTTTGTTTTTTGA	284425	116621	AACTCCTGGGCTCAAGCGAA
195252	27448	AACTCACCGAGTTACAGAAT	239839	72035	TATTTCATTTTTGTTTTTTG	284426	116622	GAACTCCTGGGCTCAAGCGA
195253	27449	AAACTCACCGAGTTACAGAA	239840	72036	TTATTTCATTTTTGTTTTTT	284427	116623	TGAACTCCTGGGCTCAAGCG
195254	27450	CAAACTCACCGAGTTACAGA	239841	72037	TTTATTTCATTTTTGTTTTT	284428	116624	TTGAACTCCTGGGCTCAAGC
195255	27451	GCAAACTCACCGAGTTACAG	239842	72038	CTTTATTTCATTTTTGTTTT	284429	116625	CTTGAACTCCTGGGCTCAAG
195256	27452	AGCAAACTCACCGAGTTACA	239843	72039	ACTTTATTTCATTTTTGTTT	284430	116626	TCTTGAACTCCTGGGCTCAA
195257	27453	AAGCAAACTCACCGAGTTAC	239844	72040	GACTTTATTTCATTTTTGTT	284431	116627	GTCTTGAACTCCTGGGCTCA
195258	27454	AAAGCAAACTCACCGAGTTA	239845	72041	GGACTTTATTTCATTTTTGT	284432	116628	GGTCTTGAACTCCTGGGCTC
195259	27455	AAAAGCAAACTCACCGAGTT	239846	72042	TGGACTTTATTTCATTTTTG	284433	116629	TGGTCTTGAACTCCTGGGCT
195260	27456	AAAAAGCAAACTCACCGAGT	239847	72043	CTGGACTTTATTTCATTTTT	284434	116630	CTGGTCTTGAACTCCTGGGC
195261	27457	AAAAAAGCAAACTCACCGAG	239848	72044	CCTGGACTTTATTTCATTTT	284435	116631	GCTGGTCTTGAACTCCTGGG
195262	27458	AAAAAAAGCAAACTCACCGA	239849	72045	TCCTGGACTTTATTTCATTT	284436	116632	GGCTGGTCTTGAACTCCTGG
195263	27459	AAAAAAAAGCAAACTCACCG	239850	72046	TTCCTGGACTTTATTTCATT	284437	116633	AGGCTGGTCTTGAACTCCTG
195264	27460	AAAAAAAAAGCAAACTCACC	239851	72047	TTTCCTGGACTTTATTTCAT	284438	116634	CAGGCTGGTCTTGAACTCCT
195265	27461	AAAAAAAAAAGCAAACTCAC	239852	72048	CTTTCCTGGACTTTATTTCA	284439	116635	CCAGGCTGGTCTTGAACTCC
195266	27462	AAAAAAAAAAAGCAAACTCA	239853	72049	TCTTTCCTGGACTTTATTTC	284440	116636	CCCAGGCTGGTCTTGAACTC
195267	27463	GAAAAAAAAAAAGCAAACTC	239854	72050	TTCTTTCCTGGACTTTATTT	284441	116637	GCCCAGGCTGGTCTTGAACT
195268	27464	GGAAAAAAAAAAAGCAAACT	239855	72051	CTTCTTTCCTGGACTTTATT	284442	116638	TGCCCAGGCTGGTCTTGAAC
195269	27465	AGGAAAAAAAAAAAGCAAAC	239856	72052	ACTTCTTTCCTGGACTTTAT	284443	116639	TTGCCCAGGCTGGTCTTGAA
195270	27466	GAGGAAAAAAAAAAAGCAAA	239857	72053	TACTTCTTTCCTGGACTTTA	284444	116640	GTTGCCCAGGCTGGTCTTGA
195271	27467	GGAGGAAAAAAAAAAAAGCAA	239858	72054	CTACTTCTTTCCTGGACTTT	284445	116641	TGTTGCCCAGGCTGGTCTTG
195272	27468	TGGAGGAAAAAAAAAAAGCA	239859	72055	CCTACTTCTTTCCTGGACTT	284446	116642	TTGTTGCCCAGGCTGGTCTT
195273	27469	ATGGAGGAAAAAAAAAAAGC	239860	72056	ACCTACTTCTTTCCTGGACT	284447	116643	ATTGTTGCCCAGGCTGGTCT
195274	27470	GATGGAGGAAAAAAAAAAAG	239861	72057	AACCTACTTCTTTCCTGGAC	284448	116644	CATTGTTGCCCAGGCTGGTC
195275	27471	TGATGGAGGAAAAAAAAAAA	239862	72058	AAACCTACTTCTTTCCTGGA	284449	116645	TCATTGTTGCCCAGGCTGGT
195276	27472	GTGATGGAGGAAAAAAAAAA	239863	72059	AAAACCTACTTCTTTCCTGG	284450	116646	CTCATTGTTGCCCAGGCTGG
195277	27473	GGTGATGGAGGAAAAAAAAA	239864	72060	TAAAACCTACTTCTTTCCTG	284451	116647	TCTCATTGTTGCCCAGGCTG
195278	27474	GGGTGATGGAGGAAAAAAAA	239865	72061	GTAAAACCTACTTCTTTCCT	284452	116648	GTCTCATTGTTGCCCAGGCT
195279	27475	TGGGTGATGGAGGAAAAAAA	239866	72062	GGTAAAACCTACTTCTTTCC	284453	116649	GGTCTCATTGTTGCCCAGGC
195280	27476	CTGGGTGATGGAGGAAAAAA	239867	72063	TGGTAAAACCTACTTCTTTC	284454	116650	GGGTCTCATTGTTGCCCAGG
195281	27477	CCTGGGTGATGGAGGAAAAA	239868	72064	GTGGTAAAACCTACTTCTTT	284455	116651	GGGGTCTCATTGTTGCCCAG
195282	27478	GCCTGGGTGATGGAGGAAAA	239869	72065	AGTGGTAAAACCTACTTCTT	284456	116652	AGGGGTCTCATTGTTGCCCA
195283	27479	AGCCTGGGTGATGGAGGAAA	239870	72066	GAGTGGTAAAACCTACTTCT	284457	116653	CAGGGGTCTCATTGTTGCCC
195284	27480	CAGCCTGGGTGATGGAGGAA	239871	72067	AGAGTGGTAAAACCTACTTC	284458	116654	ACAGGGGTCTCATTGTTGCC
195285	27481	CCAGCCTGGGTGATGGAGGA	239872	72068	AAGAGTGGTAAAACCTACTT	284459	116655	CACAGGGGTCTCATTGTTGC
195286	27482	TCCAGCCTGGGTGATGGAGG	239873	72069	TAAGAGTGGTAAAACCTACT	284460	116656	ACACAGGGGTCTCATTGTTG
195287	27483	CTCCAGCCTGGGTGATGGAG	239874	72070	ATAAGAGTGGTAAAACCTAC	284461	116657	GACACAGGGGTCTCATTGTT
195288	27484	ACTCCAGCCTGGGTGATGGA	239875	72071	AATAAGAGTGGTAAAACCTA	284462	116658	AGACACAGGGGTCTCATTGT
195289	27485	CACTCCAGCCTGGGTGATGG	239876	72072	AAATAAGAGTGGTAAAACCT	284463	116659	TAGACACAGGGGTCTCATTG
195290	27486	GCACTCCAGCCTGGGTGATG	239877	72073	AAAATAAGAGTGGTAAAACC	284464	116660	GTAGACACAGGGGTCTCATT
195291	27487	TGCACTCCAGCCTGGGTGAT	239878	72074	GAAAATAAGAGTGGTAAAAC	284465	116661	TGTAGACACAGGGGTCTCAT
195292	27488	CTGCACTCCAGCCTGGGTGA	239879	72075	AGAAAATAAGAGTGGTAAAA	284466	116662	TTGTAGACACAGGGGTCTCA
195293	27489	ACTGCACTCCAGCCTGGGTG	239880	72076	CAGAAAATAAGAGTGGTAAA	284467	116663	TTTGTAGACACAGGGGTCTC
195294	27490	CACTGCACTCCAGCCTGGGT	239881	72077	TCAGAAAATAAGAGTGGTAA	284468	116664	TTTTGTAGACACAGGGGTCT
195295	27491	TCACTGCACTCCAGCCTGGG	239882	72078	TTCAGAAAATAAGAGTGGTA	284469	116665	TTTTTGTAGACACAGGGGTC
195296	27492	TTCACTGCACTCCAGCCTGG	239883	72079	CTTCAGAAAATAAGAGTGGT	284470	116666	CTTTTTGTAGACACAGGGGT
195297	27493	CTTCACTGCACTCCAGCCTG	239884	72080	TCTTCAGAAAATAAGAGTGG	284471	116667	TCTTTTTGTAGACACAGGGG
195298	27494	GCTTCACTGCACTCCAGCCT	239885	72081	CTCTTCAGAAAATAAGAGTG	284472	116668	TTCTTTTTGTAGACACAGGG
195299	27495	AGCTTCACTGCACTCCAGCC	239886	72082	TCTCTTCAGAAAATAAGAGT	284473	116669	ATTCTTTTTGTAGACACAGG
195300	27496	CAGCTTCACTGCACTCCAGC	239887	72083	TTCTCTTCAGAAAATAAGAG	284474	116670	AATTCTTTTTGTAGACACAG
195301	27497	CCAGCTTCACTGCACTCCAG	239888	72084	TTTCTCTTCAGAAAATAAGA	284475	116671	TAATTCTTTTTGTAGACACA
195302	27498	TCCAGCTTCACTGCACTCCA	239889	72085	TTTTCTCTTCAGAAAATAAG	284476	116672	TTAATTCTTTTTGTAGACAC
195303	27499	CTCCAGCTTCACTGCACTCC	239890	72086	GTTTTCTCTTCAGAAAATAA	284477	116673	TTTAATTCTTTTTGTAGACA
195304	27500	ACTCCAGCTTCACTGCACTC	239891	72087	AGTTTTCTCTTCAGAAAATA	284478	116674	TTTTAATTCTTTTTGTAGAC
195305	27501	CACTCCAGCTTCACTGCACT	239892	72088	TAGTTTTCTCTTCAGAAAAT	284479	116675	ATTTTAATTCTTTTTGTAGA
195306	27502	GCACTCCAGCTTCACTGCAC	239893	72089	TTAGTTTTCTCTTCAGAAAA	284480	116676	AATTTTAATTCTTTTTGTAG

195307	27503	GGCACTCCAGCTTCACTGCA	239894	72090	TTTAGTTTTCTCTTCAGAAA	284481	116677	TAATTTTAATTCTTTTTGTA
195308	27504	CGGCACTCCAGCTTCACTGC	239895	72091	ATTTAGTTTTCTCTTCAGAA	284482	116678	CTAATTTTAATTCTTTTTGT
195309	27505	ACGGCACTCCAGCTTCACTG	239896	72092	AATTTAGTTTTCTCTTCAGA	284483	116679	GCTAATTTTAATTCTTTTTG
195310	27506	CACGGCACTCCAGCTTCACT	239897	72093	AAATTTAGTTTTCTCTTCAG	284484	116680	GGCTAATTTTAATTCTTTTT
195311	27507	CCACGGCACTCCAGCTTCAC	239898	72094	TAAATTTAGTTTTCTCTTCA	284485	116681	TGGCTAATTTTAATTCTTTT
195312	27508	TCCACGGCACTCCAGCTTCA	239899	72095	TTAAATTTAGTTTTCTCTTC	284486	116682	CTGGCTAATTTTAATTCTTT
195313	27509	CTCCACGGCACTCCAGCTTC	239900	72096	ATTAAATTTAGTTTTCTCTT	284487	116683	CCTGGCTAATTTTAATTCTT
195314	27510	GCTCCACGGCACTCCAGCTT	239901	72097	CATTAAATTTAGTTTTCTCT	284488	116684	ACCTGGCTAATTTTAATTCT
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195316	27512	TCGCTCCACGGCACTCCAGC	239903	72099	CACATTAAATTTAGTTTTCT	284490	116686	ACACCTGGCTAATTTTAATT
195317	27513	ATCGCTCCACGGCACTCCAG	239904	72100	ACACATTAAATTTAGTTTTC	284491	116687	CACACCTGGCTAATTTTAAT
195318	27514	GATCGCTCCACGGCACTCCA	239905	72101	TACACATTAAATTTAGTTTT	284492	116688	CCACACCTGGCTAATTTTAA
195319	27515	TGATCGCTCCACGGCACTCC	239906	72102	TTACACATTAAATTTAGTTT	284493	116689	ACCACACCTGGCTAATTTTA
195320	27516	GTGATCGCTCCACGGCACTC	239907	72103	TTTACACATTAAATTTAGTT	284494	116690	CACCACACCTGGCTAATTTT
195321	27517	AGTGATCGCTCCACGGCACT	239908	72104	CTTTACACATTAAATTTAGT	284495	116691	CCACCACACCTGGCTAATTT
195322	27518	CAGTGATCGCTCCACGGCAC	239909	72105	ACTTTACACATTAAATTTAG	284496	116692	GCCACCACACCTGGCTAATT
195323	27519	GCAGTGATCGCTCCACGGCA	239910	72106	CACTTTACACATTAAATTTA	284497	116693	TGCCACCACACCTGGCTAAT
195324	27520	TGCAGTGATCGCTCCACGGC	239911	72107	TCACTTTACACATTAAATTT	284498	116694	GTGCCACCACACCTGGCTAA
195325	27521	TTGCAGTGATCGCTCCACGG	239912	72108	CTCACTTTACACATTAAATT	284499	116695	CGTGCCACCACACCTGGCTA
195326	27522	GTTGCAGTGATCGCTCCACG	239913	72109	CCTCACTTTACACATTAAAT	284500	116696	GCGTGCCACCACACCTGGCT
195327	27523	GGTTGCAGTGATCGCTCCAC	239914	72110	TCCTCACTTTACACATTAAA	284501	116697	TGCGTGCCACCACACCTGGC
195328	27524	AGGTTGCAGTGATCGCTCCA	239915	72111	GTCCTCACTTTACACATTAA	284502	116698	GTGCGTGCCACCACACCTGG
195329	27525	GAGGTTGCAGTGATCGCTCC	239916	72112	TGTCCTCACTTTACACATTA	284503	116699	GGTGCGTGCCACCACACCTG
195330	27526	AGAGGTTGCAGTGATCGCTC	239917	72113	TTGTCCTCACTTTACACATT	284504	116700	AGGTGCGTGCCACCACACCT
195331	27527	CAGAGGTTGCAGTGATCGCT	239918	72114	CTTGTCCTCACTTTACACAT	284505	116701	CAGGTGCGTGCCACCACACC
195332	27528	ACAGAGGTTGCAGTGATCGC	239919	72115	ACTTGTCCTCACTTTACACA	284506	116702	ACAGGTGCGTGCCACCACAC
195333	27529	GACAGAGGTTGCAGTGATCG	239920	72116	AACTTGTCCTCACTTTACAC	284507	116703	TACAGGTGCGTGCCACCACA
195334	27530	AGACAGAGGTTGCAGTGATC	239921	72117	GAACTTGTCCTCACTTTACA	284508	116704	CTACAGGTGCGTGCCACCAC
195335	27531	GAGACAGAGGTTGCAGTGAT	239922	72118	TGAACTTGTCCTCACTTTAC	284509	116705	ACTACAGGTGCGTGCCACCA
195336	27532	GGAGACAGAGGTTGCAGTGA	239923	72119	GTGAACTTGTCCTCACTTTA	284510	116706	GACTACAGGTGCGTGCCACC
195337	27533	GGGAGACAGAGGTTGCAGTG	239924	72120	GGTGAACTTGTCCTCACTTT	284511	116707	GGACTACAGGTGCGTGCCAC
195338	27534	TGGGAGACAGAGGTTGCAGT	239925	72121	TGGTGAACTTGTCCTCACTT	284512	116708	GGGACTACAGGTGCGTGCCA
195339	27535	CTGGGAGACAGAGGTTGCAG	239926	72122	TTGGTGAACTTGTCCTCACT	284513	116709	TGGGACTACAGGTGCGTGCC
195340	27536	CCTGGGAGACAGAGGTTGCA	239927	72123	CTTGGTGAACTTGTCCTCAC	284514	116710	CTGGGACTACAGGTGCGTGC
195341	27537	ACCTGGGAGACAGAGGTTGC	239928	72124	ACTTGGTGAACTTGTCCTCA	284515	116711	GCTGGGACTACAGGTGCGTG
195342	27538	AACCTGGGAGACAGAGGTTG	239929	72125	AACTTGGTGAACTTGTCCTC	284516	116712	AGCTGGGACTACAGGTGCGT
195343	27539	GAACCTGGGAGACAGAGGTT	239930	72126	TAACTTGGTGAACTTGTCCT	284517	116713	TAGCTGGGACTACAGGTGCG
195344	27540	TGAACCTGGGAGACAGAGGT	239931	72127	CTAACTTGGTGAACTTGTCC	284518	116714	GTAGCTGGGACTACAGGTGC
195345	27541	TTGAACCTGGGAGACAGAGG	239932	72128	ACTAACTTGGTGAACTTGTC	284519	116715	AGTAGCTGGGACTACAGGTG
195346	27542	CTTGAACCTGGGAGACAGAG	239933	72129	CACTAACTTGGTGAACTTGT	284520	116716	AAGTAGCTGGGACTACAGGT
195347	27543	GCTTGAACCTGGGAGACAGA	239934	72130	ACACTAACTTGGTGAACTTG	284521	116717	CAAGTAGCTGGGACTACAGG
195348	27544	TGCTTGAACCTGGGAGACAG	239935	72131	AACACTAACTTGGTGAACTT	284522	116718	CCAAGTAGCTGGGACTACAG
195349	27545	TTGCTTGAACCTGGGAGACA	239936	72132	AAACACTAACTTGGTGAACT	284523	116719	CCCAAGTAGCTGGGACTACA
195350	27546	ATTGCTTGAACCTGGGAGAC	239937	72133	CAAACACTAACTTGGTGAAC	284524	116720	TCCCAAGTAGCTGGGACTAC
195351	27547	AATTGCTTGAACCTGGGAGA	239938	72134	TCAAACACTAACTTGGTGAA	284525	116721	CTCCCAAGTAGCTGGGACTA
195352	27548	GAATTGCTTGAACCTGGGAG	239939	72135	CTCAAACACTAACTTGGTGA	284526	116722	CCTCCCAAGTAGCTGGGACT
195353	27549	AGAATTGCTTGAACCTGGGA	239940	72136	ACTCAAACACTAACTTGGTG	284527	116723	GCCTCCCAAGTAGCTGGGAC
195354	27550	GAGAATTGCTTGAACCTGGG	239941	72137	AACTCAAACACTAACTTGGT	284528	116724	AGCCTCCCAAGTAGCTGGGA
195355	27551	GGAGAATTGCTTGAACCTGG	239942	72138	CAACTCAAACACTAACTTGG	284529	116725	CAGCCTCCCAAGTAGCTGGG
195356	27552	AGGAGAATTGCTTGAACCTG	239943	72139	GCAACTCAAACACTAACTTG	284530	116726	TCAGCCTCCCAAGTAGCTGG
195357	27553	AAGGAGAATTGCTTGAACCT	239944	72140	GGCAACTCAAACACTAACTT	284531	116727	CTCAGCCTCCCAAGTAGCTG
195358	27554	GAAGGAGAATTGCTTGAACC	239945	72141	AGGCAACTCAAACACTAACT	284532	116728	CCTCAGCCTCCCAAGTAGCT
195359	27555	GGAAGGAGAATTGCTTGAAC	239946	72142	TAGGCAACTCAAACACTAAC	284533	116729	ACCTCAGCCTCCCAAGTAGC
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195361	27557	GAGGAAGGAGAATTGCTTGA	239948	72144	TTTAGGCAACTCAAACACTA	284535	116731	CCACCTCAGCCTCCCAAGTA
195362	27558	TGAGGAAGGAGAATTGCTTG	239949	72145	TTTTAGGCAACTCAAACACT	284536	116732	CCCACCTCAGCCTCCCAAGT
195363	27559	CTGAGGAAGGAGAATTGCTT	239950	72146	ATTTTAGGCAACTCAAACAC	284537	116733	TCCCACCTCAGCCTCCCAAG
195364	27560	GCTGAGGAAGGAGAATTGCT	239951	72147	TATTTTAGGCAACTCAAACA	284538	116734	CTCCCACCTCAGCCTCCCAA
195365	27561	GGCTGAGGAAGGAGAATTGC	239952	72148	ATATTTTAGGCAACTCAAAC	284539	116735	CCTCCCACCTCAGCCTCCCA
195366	27562	AGGCTGAGGAAGGAGAATTG	239953	72149	CATATTTTAGGCAACTCAAA	284540	116736	TCCTCCCACCTCAGCCTCCC
195367	27563	GAGGCTGAGGAAGGAGAATT	239954	72150	ACATATTTTAGGCAACTCAA	284541	116737	ATCCTCCCACCTCAGCCTCC
195368	27564	GGAGGCTGAGGAAGGAGAAT	239955	72151	AACATATTTTAGGCAACTCA	284542	116738	AATCCTCCCACCTCAGCCTC
195369	27565	GGGAGGCTGAGGAAGGAGAA	239956	72152	AAACATATTTTAGGCAACTC	284543	116739	CAATCCTCCCACCTCAGCCT
195370	27566	TGGGAGGCTGAGGAAGGAGA	239957	72153	CAAACATATTTTAGGCAACT	284544	116740	GCAATCCTCCCACCTCAGCC
195371	27567	TTGGGAGGCTGAGGAAGGAG	239958	72154	GCAAACATATTTTAGGCAAC	284545	116741	GGCAATCCTCCCACCTCAGC
195372	27568	CTTGGGAGGCTGAGGAAGGA	239959	72155	AGCAAACATATTTTAGGCAA	284546	116742	AGGCAATCCTCCCACCTCAG
195373	27569	ACTTGGGAGGCTGAGGAAGG	239960	72156	TAGCAAACATATTTTAGGCA	284547	116743	CAGGCAATCCTCCCACCTCA
195374	27570	TACTTGGGAGGCTGAGGAAG	239961	72157	TTAGCAAACATATTTTAGGC	284548	116744	TCAGGCAATCCTCCCACCTC
195375	27571	CTACTTGGGAGGCTGAGGAA	239962	72158	TTTAGCAAACATATTTTAGG	284549	116745	CTCAGGCAATCCTCCCACCT
195376	27572	GCTACTTGGGAGGCTGAGGA	239963	72159	TTTTAGCAAACATATTTTAG	284550	116746	ACTCAGGCAATCCTCCCACC
195377	27573	AGCTACTTGGGAGGCTGAGG	239964	72160	GTTTTAGCAAACATATTTTA	284551	116747	GACTCAGGCAATCCTCCCAC
195378	27574	CAGCTACTTGGGAGGCTGAG	239965	72161	AGTTTTAGCAAACATATTTT	284552	116748	GGACTCAGGCAATCCTCCCA

195379	27575	CCAGCTACTTGGGAGGCTGA	239966	72162	TAGTTTTAGCAAACATATTT	284553	116749	CGGACTCAGGCAATCCTCCC
195380	27576	CCCAGCTACTTGGGAGGCTG	239967	72163	ATAGTTTTAGCAAACATATT	284554	116750	CCGGACTCAGGCAATCCTCC
195381	27577	TCCCAGCTACTTGGGAGGCT	239968	72164	AATAGTTTTAGCAAACATAT	284555	116751	CCCGGACTCAGGCAATCCTC
195382	27578	ATCCCAGCTACTTGGGAGGC	239969	72165	GAATAGTTTTAGCAAACATA	284556	116752	TCCCGGACTCAGGCAATCCT
195383	27579	AATCCCAGCTACTTGGGAGG	239970	72166	TGAATAGTTTTAGCAAACAT	284557	116753	CTCCCGGACTCAGGCAATCC
195384	27580	TAATCCCAGCTACTTGGGAG	239971	72167	TTGAATAGTTTTAGCAAACA	284558	116754	CCTCCCGGACTCAGGCAATC
195385	27581	GTAATCCCAGCTACTTGGGA	239972	72168	TTTGAATAGTTTTAGCAAAC	284559	116755	GCCTCCCGGACTCAGGCAAT
195386	27582	TGTAATCCCAGCTACTTGGG	239973	72169	CTTTGAATAGTTTTAGCAAA	284560	116756	CGCCTCCCGGACTCAGGCAA
195387	27583	TTGTAATCCCAGCTACTTGG	239974	72170	GCTTTGAATAGTTTTAGCAA	284561	116757	CCGCCTCCCGGACTCAGGCA
195388	27584	CTTGTAATCCCAGCTACTTG	239975	72171	AGCTTTGAATAGTTTTAGCA	284562	116758	TCCGCCTCCCGGACTCAGGC
195389	27585	GCTTGTAATCCCAGCTACTT	239976	72172	AAGCTTTGAATAGTTTTAGC	284563	116759	TTCCGCCTCCCGGACTCAGG
195390	27586	TGCTTGTAATCCCAGCTACT	239977	72173	AAAGCTTTGAATAGTTTTAG	284564	116760	CTTCCGCCTCCCGGACTCAG
195391	27587	ATGCTTGTAATCCCAGCTAC	239978	72174	GAAAGCTTTGAATAGTTTTA	284565	116761	ACTTCCGCCTCCCGGACTCA
195392	27588	CATGCTTGTAATCCCAGCTA	239979	72175	TGAAAGCTTTGAATAGTTTT	284566	116762	AACTTCCGCCTCCCGGACTC
195393	27589	GCATGCTTGTAATCCCAGCT	239980	72176	GTGAAAGCTTTGAATAGTTT	284567	116763	CAACTTCCGCCTCCCGGACT
195394	27590	TGCATGCTTGTAATCCCAGC	239981	72177	TGTGAAAGCTTTGAATAGTT	284568	116764	GCAACTTCCGCCTCCCGGAC
195395	27591	CTGCATGCTTGTAATCCCAG	239982	72178	ATGTGAAAGCTTTGAATAGT	284569	116765	TGCAACTTCCGCCTCCCGGA
195396	27592	GCTGCATGCTTGTAATCCCA	239983	72179	TATGTGAAAGCTTTGAATAG	284570	116766	TTGCAACTTCCGCCTCCCGG
195397	27593	TGCTGCATGCTTGTAATCCC	239984	72180	TTATGTGAAAGCTTTGAATA	284571	116767	CTTGCAACTTCCGCCTCCCG
195398	27594	GTGCTGCATGCTTGTAATCC	239985	72181	TTTATGTGAAAGCTTTGAAT	284572	116768	CCTTGCAACTTCCGCCTCCC
195399	27595	GGTGCTGCATGCTTGTAATC	239986	72182	TTTTATGTGAAAGCTTTGAA	284573	116769	TCCTTGCAACTTCCGCCTCC
195400	27596	TGGTGCTGCATGCTTGTAAT	239987	72183	GTTTTATGTGAAAGCTTTGA	284574	116770	CTCCTTGCAACTTCCGCCTC
195401	27597	GTGGTGCTGCATGCTTGTAA	239988	72184	TGTTTTATGTGAAAGCTTTG	284575	116771	GCTCCTTGCAACTTCCGCCT
195402	27598	TGTGGTGCTGCATGCTTGTA	239989	72185	ATGTTTTATGTGAAAGCTTT	284576	116772	GGCTCCTTGCAACTTCCGCC
195403	27599	GTGTGGTGCTGCATGCTTGT	239990	72186	CATGTTTTATGTGAAAGCTT	284577	116773	TGGCTCCTTGCAACTTCCGC
195404	27600	GGTGTGGTGCTGCATGCTTG	239991	72187	TCATGTTTTATGTGAAAGCT	284578	116774	ATGGCTCCTTGCAACTTCCG
195405	27601	AGGTGTGGTGCTGCATGCTT	239992	72188	ATCATGTTTTATGTGAAAGC	284579	116775	CATGGCTCCTTGCAACTTCC
195406	27602	CAGGTGTGGTGCTGCATGCT	239993	72189	GATCATGTTTTATGTGAAAG	284580	116776	TCATGGCTCCTTGCAACTTC
195407	27603	CCAGGTGTGGTGCTGCATGC	239994	72190	TGATCATGTTTTATGTGAAA	284581	116777	ATCATGGCTCCTTGCAACTT
195408	27604	GCCAGGTGTGGTGCTGCATG	239995	72191	CTGATCATGTTTTATGTGAA	284582	116778	GATCATGGCTCCTTGCAACT
195409	27605	AGCCAGGTGTGGTGCTGCAT	239996	72192	TCTGATCATGTTTTATGTGA	284583	116779	CGATCATGGCTCCTTGCAAC
195410	27606	TAGCCAGGTGTGGTGCTGCA	239997	72193	TTCTGATCATGTTTTATGTG	284584	116780	GCGATCATGGCTCCTTGCAA
195411	27607	TTAGCCAGGTGTGGTGCTGC	239998	72194	CTTCTGATCATGTTTTATGT	284585	116781	CGCGATCATGGCTCCTTGCA
195412	27608	ATTAGCCAGGTGTGGTGCTG	239999	72195	ACTTCTGATCATGTTTTATG	284586	116782	GCGCGATCATGGCTCCTTGC
195413	27609	AATTAGCCAGGTGTGGTGCT	240000	72196	AACTTCTGATCATGTTTTAT	284587	116783	GGCGCGATCATGGCTCCTTG
195414	27610	AAATTAGCCAGGTGTGGTGC	240001	72197	GAACTTCTGATCATGTTTTA	284588	116784	TGGCGCGATCATGGCTCCTT
195415	27611	AAAATTAGCCAGGTGTGGTG	240002	72198	AGAACTTCTGATCATGTTTT	284589	116785	GTGGCGCGATCATGGCTCCT
195416	27612	AAAAATTAGCCAGGTGTGGT	240003	72199	TAGAACTTCTGATCATGTTT	284590	116786	AGTGGCGCGATCATGGCTCC
195417	27613	CAAAAATTAGCCAGGTGTGG	240004	72200	ATAGAACTTCTGATCATGTT	284591	116787	CAGTGGCGCGATCATGGCTC
195418	27614	ACAAAAATTAGCCAGGTGTG	240005	72201	CATAGAACTTCTGATCATGT	284592	116788	GCAGTGGCGCGATCATGGCT
195419	27615	CACAAAAATTAGCCAGGTGT	240006	72202	GCATAGAACTTCTGATCATG	284593	116789	TGCAGTGGCGCGATCATGGC
195420	27616	ACACAAAAATTAGCCAGGTG	240007	72203	GGCATAGAACTTCTGATCAT	284594	116790	GTGCAGTGGCGCGATCATGG
195421	27617	AACACAAAAATTAGCCAGGT	240008	72204	TGGCATAGAACTTCTGATCA	284595	116791	AGTGCAGTGGCGCGATCATG
195422	27618	AAACACAAAAATTAGCCAGG	240009	72205	TTGGCATAGAACTTCTGATC	284596	116792	AAGTGCAGTGGCGCGATCAT
195423	27619	AAAACACAAAAATTAGCCAG	240010	72206	TTTGGCATAGAACTTCTGAT	284597	116793	GAAGTGCAGTGGCGCGATCA
195424	27620	AAAAACACAAAAATTAGCCA	240011	72207	TTTTGGCATAGAACTTCTGA	284598	116794	TGAAGTGCAGTGGCGCGATC
195425	27621	TAAAAACACAAAAATTAGCC	240012	72208	GTTTTGGCATAGAACTTCTG	284599	116795	TTGAAGTGCAGTGGCGCGAT
195426	27622	TTAAAAACACAAAAATTAGC	240013	72209	TGTTTTGGCATAGAACTTCT	284600	116796	GTTGAAGTGCAGTGGCGCGA
195427	27623	ATTAAAAACACAAAAATTAG	240014	72210	ATGTTTTGGCATAGAACTTC	284601	116797	GGTTGAAGTGCAGTGGCGCG
195428	27624	TATTAAAAACACAAAAATTA	240015	72211	TATGTTTTGGCATAGAACTT	284602	116798	AGGTTGAAGTGCAGTGGCGC
195429	27625	CTATTAAAAACACAAAAATT	240016	72212	ATATGTTTTGGCATAGAACT	284603	116799	TAGGTTGAAGTGCAGTGGCG
195430	27626	TCTATTAAAAACACAAAAAT	240017	72213	CATATGTTTTGGCATAGAAC	284604	116800	CTAGGTTGAAGTGCAGTGGC
195431	27627	CTCTATTAAAAACACAAAAA	240018	72214	ACATATGTTTTGGCATAGAA	284605	116801	CCTAGGTTGAAGTGCAGTGG
195432	27628	TCTCTATTAAAAACACAAAA	240019	72215	CACATATGTTTTGGCATAGA	284606	116802	GCCTAGGTTGAAGTGCAGTG
195433	27629	GTCTCTATTAAAAACACAAA	240020	72216	ACACATATGTTTTGGCATAG	284607	116803	TGCCTAGGTTGAAGTGCAGT
195434	27630	CGTCTCTATTAAAAACACAA	240021	72217	CACACATATGTTTTGGCATA	284608	116804	TTGCCTAGGTTGAAGTGCAG
195435	27631	CCGTCTCTATTAAAAACACA	240022	72218	ACACACATATGTTTTGGCAT	284609	116805	GTTGCCTAGGTTGAAGTGCA
195436	27632	GCCGTCTCTATTAAAAACAC	240023	72219	CACACACATATGTTTTGGCA	284610	116806	TGTTGCCTAGGTTGAAGTGC
195437	27633	GGCCGTCTCTATTAAAAACA	240024	72220	ACACACACATATGTTTTGGC	284611	116807	CTGTTGCCTAGGTTGAAGTG
195438	27634	GGGCCGTCTCTATTAAAAAC	240025	72221	TACACACACATATGTTTTGG	284612	116808	TCTGTTGCCTAGGTTGAAGT
195439	27635	CGGGCCGTCTCTATTAAAAA	240026	72222	ATACACACACATATGTTTTG	284613	116809	CTCTGTTGCCTAGGTTGAAG
195440	27636	TCGGGCCGTCTCTATTAAAA	240027	72223	TATACACACACATATGTTTT	284614	116810	ACTCTGTTGCCTAGGTTGAA
195441	27637	TTCGGGCCGTCTCTATTAAA	240028	72224	ATATACACACACATATGTTT	284615	116811	CACTCTGTTGCCTAGGTTGA
195442	27638	CTTCGGGCCGTCTCTATTAA	240029	72225	TATATACACACACATATGTT	284616	116812	TCACTCTGTTGCCTAGGTTG
195443	27639	ACTTCGGGCCGTCTCTATTA	240030	72226	ATATATACACACACATATGT	284617	116813	CTCACTCTGTTGCCTAGGTT
195444	27640	CACTTCGGGCCGTCTCTATT	240031	72227	TATATATACACACACATATG	284618	116814	TCTCACTCTGTTGCCTAGGT
195445	27641	GCACTTCGGGCCGTCTCTAT	240032	72228	ATATATATACACACACATAT	284619	116815	GTCTCACTCTGTTGCCTAGG
195446	27642	AGCACTTCGGGCCGTCTCTA	240033	72229	TATATATATACACACACATA	284620	116816	AGTCTCACTCTGTTGCCTAG
195447	27643	TAGCACTTCGGGCCGTCTCT	240034	72230	ATATATATATACACACACAT	284621	116817	AAGTCTCACTCTGTTGCCTA
195448	27644	CTAGCACTTCGGGCCGTCTC	240035	72231	CATATATATATACACACACA	284622	116818	AAAGTCTCACTCTGTTGCCT
195449	27645	CCTAGCACTTCGGGCCGTCT	240036	72232	GCATATATATATACACACAC	284623	116819	CAAAGTCTCACTCTGTTGCC
195450	27646	TCCTAGCACTTCGGGCCGTC	240037	72233	TGCATATATATATACACACA	284624	116820	ACAAAGTCTCACTCTGTTGC

195451	27647	ATCCTAGCACTTCGGGCCGT	240038	72234	GTGCATATATATATACACAC	284625	116821	GACAAAGTCTCACTCTGTTG
195452	27648	AATCCTAGCACTTCGGGCCG	240039	72235	AGTGCATATATATATACACA	284626	116822	AGACAAAGTCTCACTCTGTT
195453	27649	TAATCCTAGCACTTCGGGCC	240040	72236	TAGTGCATATATATATACAC	284627	116823	GAGACAAAGTCTCACTCTGT
195454	27650	GTAATCCTAGCACTTCGGGC	240041	72237	ATAGTGCATATATATATACA	284628	116824	TGAGACAAAGTCTCACTCTG
195455	27651	TGTAATCCTAGCACTTCGGG	240042	72238	TATAGTGCATATATATATAC	284629	116825	TTGAGACAAAGTCTCACTCT
195456	27652	CTGTAATCCTAGCACTTCGG	240043	72239	ATATAGTGCATATATATATA	284630	116826	TTTGAGACAAAGTCTCACTC
195457	27653	CCTGTAATCCTAGCACTTCG	240044	72240	TATATAGTGCATATATATAT	284631	116827	TTTTGAGACAAAGTCTCACT
195458	27654	GCCTGTAATCCTAGCACTTC	240045	72241	ATATATAGTGCATATATATA	284632	116828	TTTTTGAGACAAAGTCTCAC
195459	27655	TGCCTGTAATCCTAGCACTT	240046	72242	TATATATAGTGCATATATAT	284633	116829	TTTTTTGAGACAAAGTCTCA
195460	27656	ATGCCTGTAATCCTAGCACT	240047	72243	GTATATATAGTGCATATATA	284634	116830	GTTTTTTGAGACAAAGTCTC
195461	27657	CATGCCTGTAATCCTAGCAC	240048	72244	AGTATATATAGTGCATATAT	284635	116831	TGTTTTTTGAGACAAAGTCT
195462	27658	TCATGCCTGTAATCCTAGCA	240049	72245	CAGTATATATAGTGCATATA	284636	116832	TTGTTTTTTGAGACAAAGTC
195463	27659	CTCATGCCTGTAATCCTAGC	240050	72246	ACAGTATATATAGTGCATAT	284637	116833	ATTGTTTTTTGAGACAAAGT
195464	27660	GCTCATGCCTGTAATCCTAG	240051	72247	TACAGTATATATAGTGCATA	284638	116834	GATTGTTTTTTGAGACAAAG
195465	27661	GGCTCATGCCTGTAATCCTA	240052	72248	ATACAGTATATATAGTGCAT	284639	116835	TGATTGTTTTTTGAGACAAA
195466	27662	TGGCTCATGCCTGTAATCCT	240053	72249	TATACAGTATATATAGTGCA	284640	116836	ATGATTGTTTTTTGAGACAA
195467	27663	GTGGCTCATGCCTGTAATCC	240054	72250	ATATACAGTATATATAGTGC	284641	116837	TATGATTGTTTTTTGAGACA
195468	27664	GGTGGCTCATGCCTGTAATC	240055	72251	TATATACAGTATATATAGTG	284642	116838	ATATGATTGTTTTTTGAGAC
195469	27665	CGGTGGCTCATGCCTGTAAT	240056	72252	TTATATACAGTATATATAGT	284643	116839	TATATGATTGTTTTTTGAGA
195470	27666	GCGGTGGCTCATGCCTGTAA	240057	72253	TTTATATACAGTATATATAG	284644	116840	TTATATGATTGTTTTTTGAG
195471	27667	CGCGGTGGCTCATGCCTGTA	240058	72254	TTTTATATACAGTATATATA	284645	116841	ATTATATGATTGTTTTTTGA
195472	27668	CCGCGGTGGCTCATGCCTGT	240059	72255	TTTTTATATACAGTATATAT	284646	116842	TATTATATGATTGTTTTTTG
195473	27669	GCCGCGGTGGCTCATGCCTG	240060	72256	ATTTTTATATACAGTATATA	284647	116843	TTATTATATGATTGTTTTTT
195474	27670	GGCCGCGGTGGCTCATGCCT	240061	72257	CATTTTTATATACAGTATAT	284648	116844	ATTATTATATGATTGTTTTT
195475	27671	TGGCCGCGGTGGCTCATGCC	240062	72258	GCATTTTTATATACAGTATA	284649	116845	AATTATTATATGATTGTTTT
195476	27672	CTGGCCGCGGTGGCTCATGC	240063	72259	TGCATTTTTATATACAGTAT	284650	116846	AAATTATTATATGATTGTTT
195477	27673	GCTGGCCGCGGTGGCTCATG	240064	72260	TTGCATTTTTATATACAGTA	284651	116847	AAAATTATTATATGATTGTT
195478	27674	GGCTGGCCGCGGTGGCTCAT	240065	72261	TTTGCATTTTTATATACAGT	284652	116848	TAAAATTATTATATGATTGT
195479	27675	TGGCTGGCCGCGGTGGCTCA	240066	72262	TTTTGCATTTTTATATACAG	284653	116849	TTAAAATTATTATATGATTG
195480	27676	ATGGCTGGCCGCGGTGGCTC	240067	72263	ATTTTGCATTTTTATATACA	284654	116850	TTTAAAATTATTATATGATT
195481	27677	TATGGCTGGCCGCGGTGGCT	240068	72264	GATTTTGCATTTTTATATAC	284655	116851	TTTTAAAATTATTATATGAT
195482	27678	TTATGGCTGGCCGCGGTGGC	240069	72265	AGATTTTGCATTTTTATATA	284656	116852	ATTTTAAAATTATTATATGA
195483	27679	GTTATGGCTGGCCGCGGTGG	240070	72266	TAGATTTTGCATTTTTATAT	284657	116853	TATTTTAAAATTATTATATG
195484	27680	AGTTATGGCTGGCCGCGGTG	240071	72267	TTAGATTTTGCATTTTTATA	284658	116854	TTATTTTAAAATTATTATAT
195485	27681	GAGTTATGGCTGGCCGCGGT	240072	72268	TTTAGATTTTGCATTTTTAT	284659	116855	TTTATTTTAAAATTATTATA
195486	27682	AGAGTTATGGCTGGCCGCGG	240073	72269	ATTTAGATTTTGCATTTTTA	284660	116856	ATTTATTTTAAAATTATTAT
195487	27683	CAGAGTTATGGCTGGCCGCG	240074	72270	AATTTAGATTTTGCATTTTT	284661	116857	TATTTATTTTAAAATTATTA
195488	27684	ACAGAGTTATGGCTGGCCGC	240075	72271	CAATTTAGATTTTGCATTTT	284662	116858	CTATTTATTTTAAAATTATT
195489	27685	CACAGAGTTATGGCTGGCCG	240076	72272	GCAATTTAGATTTTGCATTT	284663	116859	TCTATTTATTTTAAAATTAT
195490	27686	TCACAGAGTTATGGCTGGCC	240077	72273	GGCAATTTAGATTTTGCATT	284664	116860	ATCTATTTATTTTAAAATTA
195491	27687	GTCACAGAGTTATGGCTGGC	240078	72274	TGGCAATTTAGATTTTGCAT	284665	116861	AATCTATTTATTTTAAAATT
195492	27688	AGTCACAGAGTTATGGCTGG	240079	72275	TTGGCAATTTAGATTTTGCA	284666	116862	AAATCTATTTATTTTAAAAT
195493	27689	GAGTCACAGAGTTATGGCTG	240080	72276	GTTGGCAATTTAGATTTTGC	284667	116863	CAAATCTATTTATTTTAAAA
195494	27690	AGAGTCACAGAGTTATGGCT	240081	72277	GGTTGGCAATTTAGATTTTG	284668	116864	CCAAATCTATTTATTTTAAA
195495	27691	AAGAGTCACAGAGTTATGGC	240082	72278	AGGTTGGCAATTTAGATTTT	284669	116865	GCCAAATCTATTTATTTTAA
195496	27692	CAAGAGTCACAGAGTTATGG	240083	72279	AAGGTTGGCAATTTAGATTT	284670	116866	AGCCAAATCTATTTATTTTA
195497	27693	ACAAGAGTCACAGAGTTATG	240084	72280	AAAGGTTGGCAATTTAGATT	284671	116867	AAGCCAAATCTATTTATTTT
195498	27694	AACAAGAGTCACAGAGTTAT	240085	72281	AAAAGGTTGGCAATTTAGAT	284672	116868	GAAGCCAAATCTATTTATTT
195499	27695	TAACAAGAGTCACAGAGTTA	240086	72282	TAAAAGGTTGGCAATTTAGA	284673	116869	GGAAGCCAAATCTATTTATT
195500	27696	GTAACAAGAGTCACAGAGTT	240087	72283	CTAAAAGGTTGGCAATTTAG	284674	116870	AGGAAGCCAAATCTATTTAT
195501	27697	TGTAACAAGAGTCACAGAGT	240088	72284	TCTAAAAGGTTGGCAATTTA	284675	116871	GAGGAAGCCAAATCTATTTA
195502	27698	TTGTAACAAGAGTCACAGAG	240089	72285	TTCTAAAAGGTTGGCAATTT	284676	116872	AGAGGAAGCCAAATCTATTT
195503	27699	TTTGTAACAAGAGTCACAGA	240090	72286	TTTCTAAAAGGTTGGCAATT	284677	116873	TAGAGGAAGCCAAATCTATT
195504	27700	CTTTGTAACAAGAGTCACAG	240091	72287	ATTTCTAAAAGGTTGGCAAT	284678	116874	TTAGAGGAAGCCAAATCTAT
195505	27701	CCTTTGTAACAAGAGTCACA	240092	72288	AATTTCTAAAAGGTTGGCAA	284679	116875	TTTAGAGGAAGCCAAATCTA
195506	27702	GCCTTTGTAACAAGAGTCAC	240093	72289	CAATTTCTAAAAGGTTGGCA	284680	116876	ATTTAGAGGAAGCCAAATCT
195507	27703	GGCCTTTGTAACAAGAGTCA	240094	72290	GCAATTTCTAAAAGGTTGGC	284681	116877	CATTTAGAGGAAGCCAAATC
195508	27704	AGGCCTTTGTAACAAGAGTC	240095	72291	AGCAATTTCTAAAAGGTTGG	284682	116878	ACATTTAGAGGAAGCCAAAT
195509	27705	AAGGCCTTTGTAACAAGAGT	240096	72292	GAGCAATTTCTAAAAGGTTG	284683	116879	GACATTTAGAGGAAGCCAAA
195510	27706	TAAGGCCTTTGTAACAAGAG	240097	72293	AGAGCAATTTCTAAAAGGTT	284684	116880	GGACATTTAGAGGAAGCCAA
195511	27707	ATAAGGCCTTTGTAACAAGA	240098	72294	CAGAGCAATTTCTAAAAGGT	284685	116881	GGGACATTTAGAGGAAGCCA
195512	27708	TATAAGGCCTTTGTAACAAG	240099	72295	TCAGAGCAATTTCTAAAAGG	284686	116882	GGGGACATTTAGAGGAAGCC
195513	27709	ATATAAGGCCTTTGTAACAA	240100	72296	TTCAGAGCAATTTCTAAAAG	284687	116883	CGGGGACATTTAGAGGAAGC
195514	27710	AATATAAGGCCTTTGTAACA	240101	72297	TTTCAGAGCAATTTCTAAAA	284688	116884	CCGGGGACATTTAGAGGAAG
195515	27711	AAATATAAGGCCTTTGTAAC	240102	72298	CTTTCAGAGCAATTTCTAAA	284689	116885	CCCGGGGACATTTAGAGGAA
195516	27712	AAAATATAAGGCCTTTGTAA	240103	72299	CCTTTCAGAGCAATTTCTAA	284690	116886	CCCCGGGGACATTTAGAGGA
195517	27713	CAAAATATAAGGCCTTTGTA	240104	72300	TCCTTTCAGAGCAATTTCTA	284691	116887	TCCCCGGGGACATTTAGAGG
195518	27714	GCAAAATATAAGGCCTTTGT	240105	72301	TTCCTTTCAGAGCAATTTCT	284692	116888	GTCCCCGGGGACATTTAGAG
195519	27715	AGCAAAATATAAGGCCTTTG	240106	72302	TTTCCTTTCAGAGCAATTTC	284693	116889	AGTCCCCGGGGACATTTAGA
195520	27716	GAGCAAAATATAAGGCCTTT	240107	72303	CTTTCCTTTCAGAGCAATTT	284694	116890	GAGTCCCCGGGGACATTTAG
195521	27717	AGAGCAAAATATAAGGCCTT	240108	72304	GCTTTCCTTTCAGAGCAATT	284695	116891	GGAGTCCCCGGGGACATTTA
195522	27718	AAGAGCAAAATATAAGGCCT	240109	72305	TGCTTTCCTTTCAGAGCAAT	284696	116892	CGGAGTCCCCGGGGACATTT

195523	27719	AAAGAGCAAAATATAAGGCC	240110	72306	ATGCTTTCCTTTCAGAGCAA	284697	116893	ACGGAGTCCCCGGGGACATT
195524	27720	CAAAGAGCAAAATATAAGGC	240111	72307	AATGCTTTCCTTTCAGAGCA	284698	116894	CACGGAGTCCCCGGGGACAT
195525	27721	TCAAAGAGCAAAATATAAGG	240112	72308	AAATGCTTTCCTTTCAGAGC	284699	116895	GCACGGAGTCCCCGGGGACA
195526	27722	CTCAAAGAGCAAAATATAAG	240113	72309	GAAATGCTTTCCTTTCAGAG	284700	116896	TGCACGGAGTCCCCGGGGAC
195527	27723	CCTCAAAGAGCAAAATATAA	240114	72310	TGAAATGCTTTCCTTTCAGA	284701	116897	ATGCACGGAGTCCCCGGGGA
195528	27724	CCCTCAAAGAGCAAAATATA	240115	72311	TTGAAATGCTTTCCTTTCAG	284702	116898	GATGCACGGAGTCCCCGGGG
195529	27725	ACCCTCAAAGAGCAAAATAT	240116	72312	CTTGAAATGCTTTCCTTTCA	284703	116899	AGATGCACGGAGTCCCCGGG
195530	27726	CACCCTCAAAGAGCAAAATA	240117	72313	TCTTGAAATGCTTTCCTTTC	284704	116900	AAGATGCACGGAGTCCCCGG
195531	27727	CCACCCTCAAAGAGCAAAAT	240118	72314	ATCTTGAAATGCTTTCCTTT	284705	116901	GAAGATGCACGGAGTCCCCG
195532	27728	ACCACCCTCAAAGAGCAAAA	240119	72315	TATCTTGAAATGCTTTCCTT	284706	116902	AGAAGATGCACGGAGTCCCC
195533	27729	AACCACCCTCAAAGAGCAAA	240120	72316	TTATCTTGAAATGCTTTCCT	284707	116903	CAGAAGATGCACGGAGTCCC
195534	27730	AAACCACCCTCAAAGAGCAA	240121	72317	ATTATCTTGAAATGCTTTCC	284708	116904	ACAGAAGATGCACGGAGTCC
195535	27731	AAAACCACCCTCAAAGAGCA	240122	72318	AATTATCTTGAAATGCTTTC	284709	116905	CACAGAAGATGCACGGAGTC
195536	27732	CAAAACCACCCTCAAAGAGC	240123	72319	AAATTATCTTGAAATGCTTT	284710	116906	CCACAGAAGATGCACGGAGT
195537	27733	CCAAAACCACCCTCAAAGAG	240124	72320	CAAATTATCTTGAAATGCTT	284711	116907	TCCACAGAAGATGCACGGAG
195538	27734	ACCAAAACCACCCTCAAAGA	240125	72321	GCAAATTATCTTGAAATGCT	284712	116908	CTCCACAGAAGATGCACGGA
195539	27735	AACCAAAACCACCCTCAAAG	240126	72322	AGCAAATTATCTTGAAATGC	284713	116909	ACTCCACAGAAGATGCACGG
195540	27736	AAACCAAAACCACCCTCAAA	240127	72323	AAGCAAATTATCTTGAAATG	284714	116910	CACTCCACAGAAGATGCACG
195541	27737	CAAACCAAAACCACCCTCAA	240128	72324	TAAGCAAATTATCTTGAAAT	284715	116911	ACACTCCACAGAAGATGCAC
195542	27738	TCAAACCAAAACCACCCTCA	240129	72325	GTAAGCAAATTATCTTGAAA	284716	116912	GACACTCCACAGAAGATGCA
195543	27739	ATCAAACCAAAACCACCCTC	240130	72326	GGTAAGCAAATTATCTTGAA	284717	116913	AGACACTCCACAGAAGATGC
195544	27740	CATCAAACCAAAACCACCCT	240131	72327	GGGTAAGCAAATTATCTTGA	284718	116914	GAGACACTCCACAGAAGATG
195545	27741	GCATCAAACCAAAACCACCC	240132	72328	TGGGTAAGCAAATTATCTTG	284719	116915	GGAGACACTCCACAGAAGAT
195546	27742	GGCATCAAACCAAAACCACC	240133	72329	TTGGGTAAGCAAATTATCTT	284720	116916	CGGAGACACTCCACAGAAGA
195547	27743	AGGCATCAAACCAAAACCAC	240134	72330	TTTGGGTAAGCAAATTATCT	284721	116917	ACGGAGACACTCCACAGAAG
195548	27744	CAGGCATCAAACCAAAACCA	240135	72331	CTTTGGGTAAGCAAATTATC	284722	116918	CACGGAGACACTCCACAGAA
195549	27745	ACAGGCATCAAACCAAAACC	240136	72332	TCTTTGGGTAAGCAAATTAT	284723	116919	TCACGGAGACACTCCACAGA
195550	27746	AACAGGCATCAAACCAAAAC	240137	72333	TTCTTTGGGTAAGCAAATTA	284724	116920	CTCACGGAGACACTCCACAG
195551	27747	CAACAGGCATCAAACCAAAA	240138	72334	ATTCTTTGGGTAAGCAAATT	284725	116921	TCTCACGGAGACACTCCACA
195552	27748	CCAACAGGCATCAAACCAAA	240139	72335	TATTCTTTGGGTAAGCAAAT	284726	116922	ATCTCACGGAGACACTCCAC
195553	27749	ACCAACAGGCATCAAACCAA	240140	72336	ATATTCTTTGGGTAAGCAAA	284727	116923	AATCTCACGGAGACACTCCA
195554	27750	AACCAACAGGCATCAAACCA	240141	72337	TATATTCTTTGGGTAAGCAA	284728	116924	GAATCTCACGGAGACACTCC
195555	27751	CAACCAACAGGCATCAAACC	240142	72338	GTATATTCTTTGGGTAAGCA	284729	116925	CGAATCTCACGGAGACACTC
195556	27752	GCAACCAACAGGCATCAAAC	240143	72339	AGTATATTCTTTGGGTAAGC	284730	116926	CCGAATCTCACGGAGACACT
195557	27753	GGCAACCAACAGGCATCAAA	240144	72340	AAGTATATTCTTTGGGTAAG	284731	116927	CCCGAATCTCACGGAGACAC
195558	27754	TGGCAACCAACAGGCATCAA	240145	72341	AAAGTATATTCTTTGGGTAA	284732	116928	TCCCGAATCTCACGGAGACA
195559	27755	ATGGCAACCAACAGGCATCA	240146	72342	GAAAGTATATTCTTTGGGTA	284733	116929	GTCCCGAATCTCACGGAGAC
195560	27756	GATGGCAACCAACAGGCATC	240147	72343	GGAAAGTATATTCTTTGGGT	284734	116930	AGTCCCGAATCTCACGGAGA
195561	27757	AGATGGCAACCAACAGGCAT	240148	72344	TGGAAAGTATATTCTTTGGG	284735	116931	GAGTCCCGAATCTCACGGAG
195562	27758	AAGATGGCAACCAACAGGCA	240149	72345	TTGGAAAGTATATTCTTTGG	284736	116932	TGAGTCCCGAATCTCACGGA
195563	27759	AAAGATGGCAACCAACAGGC	240150	72346	CTTGGAAAGTATATTCTTTG	284737	116933	CTGAGTCCCGAATCTCACGG
195564	27760	AAAAGATGGCAACCAACAGG	240151	72347	TCTTGGAAAGTATATTCTTT	284738	116934	TCTGAGTCCCGAATCTCACG
195565	27761	TAAAAGATGGCAACCAACAG	240152	72348	TTCTTGGAAAGTATATTCTT	284739	116935	ATCTGAGTCCCGAATCTCAC
195566	27762	TTAAAAGATGGCAACCAACA	240153	72349	TTTCTTGGAAAGTATATTCT	284740	116936	GATCTGAGTCCCGAATCTCA
195567	27763	GTTAAAAGATGGCAACCAAC	240154	72350	CTTTCTTGGAAAGTATATTC	284741	116937	GGATCTGAGTCCCGAATCTC
195568	27764	AGTTAAAAGATGGCAACCAA	240155	72351	GCTTTCTTGGAAAGTATATT	284742	116938	AGGATCTGAGTCCCGAATCT
195569	27765	TAGTTAAAAGATGGCAACCA	240156	72352	TGCTTTCTTGGAAAGTATAT	284743	116939	GAGGATCTGAGTCCCGAATC
195570	27766	CTAGTTAAAAGATGGCAACC	240157	72353	TTGCTTTCTTGGAAAGTATA	284744	116940	TGAGGATCTGAGTCCCGAAT
195571	27767	CCTAGTTAAAAGATGGCAAC	240158	72354	CTTGCTTTCTTGGAAAGTAT	284745	116941	TTGAGGATCTGAGTCCCGAA
195572	27768	CCCTAGTTAAAAGATGGCAA	240159	72355	ACTTGCTTTCTTGGAAAGTA	284746	116942	CTTGAGGATCTGAGTCCCGA
195573	27769	TCCCTAGTTAAAAGATGGCA	240160	72356	TACTTGCTTTCTTGGAAAGT	284747	116943	ACTTGAGGATCTGAGTCCCG
195574	27770	ATCCCTAGTTAAAAGATGGC	240161	72357	TTACTTGCTTTCTTGGAAAG	284748	116944	CACTTGAGGATCTGAGTCCC
195575	27771	CATCCCTAGTTAAAAGATGG	240162	72358	ATTACTTGCTTTCTTGGAAA	284749	116945	GCACTTGAGGATCTGAGTCC
195576	27772	ACATCCCTAGTTAAAAGATG	240163	72359	TATTACTTGCTTTCTTGGAA	284750	116946	TGCACTTGAGGATCTGAGTC
195577	27773	AACATCCCTAGTTAAAAGAT	240164	72360	GTATTACTTGCTTTCTTGGA	284751	116947	TTGCACTTGAGGATCTGAGT
195578	27774	AAACATCCCTAGTTAAAAGA	240165	72361	AGTATTACTTGCTTTCTTGG	284752	116948	GTTGCACTTGAGGATCTGAG
195579	27775	AAAACATCCCTAGTTAAAAG	240166	72362	AAGTATTACTTGCTTTCTTG	284753	116949	AGTTGCACTTGAGGATCTGA
195580	27776	TAAAACATCCCTAGTTAAAA	240167	72363	TAAGTATTACTTGCTTTCTT	284754	116950	CAGTTGCACTTGAGGATCTG
195581	27777	ATAAAACATCCCTAGTTAAA	240168	72364	TTAAGTATTACTTGCTTTCT	284755	116951	TCAGTTGCACTTGAGGATCT
195582	27778	GATAAAACATCCCTAGTTAA	240169	72365	CTTAAGTATTACTTGCTTTC	284756	116952	GTCAGTTGCACTTGAGGATC
195583	27779	TGATAAAACATCCCTAGTTA	240170	72366	CCTTAAGTATTACTTGCTTT	284757	116953	GGTCAGTTGCACTTGAGGAT
195584	27780	TTGATAAAACATCCCTAGTT	240171	72367	ACCTTAAGTATTACTTGCTT	284758	116954	GGGTCAGTTGCACTTGAGGA
195585	27781	TTTGATAAAACATCCCTAGT	240172	72368	CACCTTAAGTATTACTTGCT	284759	116955	TGGGTCAGTTGCACTTGAGG
195586	27782	TTTTGATAAAACATCCCTAG	240173	72369	ACACCTTAAGTATTACTTGC	284760	116956	GTGGGTCAGTTGCACTTGAG
195587	27783	ATTTTGATAAAACATCCCTA	240174	72370	AACACCTTAAGTATTACTTG	284761	116957	GGTGGGTCAGTTGCACTTGA
195588	27784	CATTTTGATAAAACATCCCT	240175	72371	GAACACCTTAAGTATTACTT	284762	116958	GGGTGGGTCAGTTGCACTTG
195589	27785	GCATTTTGATAAAACATCCC	240176	72372	TGAACACCTTAAGTATTACT	284763	116959	CGGGTGGGTCAGTTGCACTT
195590	27786	GGCATTTTGATAAAACATCC	240177	72373	ATGAACACCTTAAGTATTAC	284764	116960	TCGGGTGGGTCAGTTGCACT
195591	27787	GGGCATTTTGATAAAACATC	240178	72374	TATGAACACCTTAAGTATTA	284765	116961	ATCGGGTGGGTCAGTTGCAC
195592	27788	TGGGCATTTTGATAAAACAT	240179	72375	TTATGAACACCTTAAGTATT	284766	116962	TATCGGGTGGGTCAGTTGCA
195593	27789	CTGGGCATTTTGATAAAACA	240180	72376	ATTATGAACACCTTAAGTAT	284767	116963	TTATCGGGTGGGTCAGTTGC
195594	27790	GCTGGGCATTTTGATAAAAC	240181	72377	GATTATGAACACCTTAAGTA	284768	116964	CTTATCGGGTGGGTCAGTTG

195595	27791	GGCTGGGCATTTTGATAAAA	240182	72378	GGATTATGAACACCTTAAGT	284769	116965	GCTTATCGGGTGGGTCAGTT
195596	27792	TGGCTGGGCATTTTGATAAA	240183	72379	AGGATTATGAACACCTTAAG	284770	116966	AGCTTATCGGGTGGGTCAGT
195597	27793	TTGGCTGGGCATTTTGATAA	240184	72380	GAGGATTATGAACACCTTAA	284771	116967	CAGCTTATCGGGTGGGTCAG
195598	27794	TTTGGCTGGGCATTTTGATA	240185	72381	TGAGGATTATGAACACCTTA	284772	116968	TCAGCTTATCGGGTGGGTCA
195599	27795	CTTTGGCTGGGCATTTTGAT	240186	72382	ATGAGGATTATGAACACCTT	284773	116969	CTCAGCTTATCGGGTGGGTC
195600	27796	ACTTTGGCTGGGCATTTTGA	240187	72383	GATGAGGATTATGAACACCT	284774	116970	CCTCAGCTTATCGGGTGGGT
195601	27797	CACTTTGGCTGGGCATTTTG	240188	72384	TGATGAGGATTATGAACACC	284775	116971	GCCTCAGCTTATCGGGTGGG
195602	27798	ACACTTTGGCTGGGCATTTT	240189	72385	TTGATGAGGATTATGAACAC	284776	116972	AGCCTCAGCTTATCGGGTGG
195603	27799	GACACTTTGGCTGGGCATTT	240190	72386	TTTGATGAGGATTATGAACA	284777	116973	AAGCCTCAGCTTATCGGGTG
195604	27800	GGACACTTTGGCTGGGCATT	240191	72387	ATTTGATGAGGATTATGAAC	284778	116974	GAAGCCTCAGCTTATCGGGT
195605	27801	TGGACACTTTGGCTGGGCAT	240192	72388	AATTTGATGAGGATTATGAA	284779	116975	TGAAGCCTCAGCTTATCGGG
195606	27802	TTGGACACTTTGGCTGGGCA	240193	72389	TAATTTGATGAGGATTATGA	284780	116976	ATGAAGCCTCAGCTTATCGG
195607	27803	TTTGGACACTTTGGCTGGGC	240194	72390	TTAATTTGATGAGGATTATG	284781	116977	GATGAAGCCTCAGCTTATCG
195608	27804	GTTTGGACACTTTGGCTGGG	240195	72391	ATTAATTTGATGAGGATTAT	284782	116978	TGATGAAGCCTCAGCTTATC
195609	27805	TGTTTGGACACTTTGGCTGG	240196	72392	AATTAATTTGATGAGGATTA	284783	116979	ATGATGAAGCCTCAGCTTAT
195610	27806	TTGTTTGGACACTTTGGCTG	240197	72393	GAATTAATTTGATGAGGATT	284784	116980	GATGATGAAGCCTCAGCTTA
195611	27807	TTTGTTTGGACACTTTGGCT	240198	72394	AGAATTAATTTGATGAGGAT	284785	116981	GGATGATGAAGCCTCAGCTT
195612	27808	ATTTGTTTGGACACTTTGGC	240199	72395	AAGAATTAATTTGATGAGGA	284786	116982	GGGATGATGAAGCCTCAGCT
195613	27809	AATTTGTTTGGACACTTTGG	240200	72396	CAAGAATTAATTTGATGAGG	284787	116983	GGGGATGATGAAGCCTCAGC
195614	27810	TAATTTGTTTGGACACTTTG	240201	72397	GCAAGAATTAATTTGATGAG	284788	116984	AGGGGATGATGAAGCCTCAG
195615	27811	ATAATTTGTTTGGACACTTT	240202	72398	AGCAAGAATTAATTTGATGA	284789	116985	CAGGGGATGATGAAGCCTCA
195616	27812	TATAATTTGTTTGGACACTT	240203	72399	TAGCAAGAATTAATTTGATG	284790	116986	CCAGGGGATGATGAAGCCTC
195617	27813	GTATAATTTGTTTGGACACT	240204	72400	GTAGCAAGAATTAATTTGAT	284791	116987	GCCAGGGGATGATGAAGCCT
195618	27814	GGTATAATTTGTTTGGACAC	240205	72401	AGTAGCAAGAATTAATTTGA	284792	116988	GGCCAGGGGATGATGAAGCC
195619	27815	AGGTATAATTTGTTTGGACA	240206	72402	CAGTAGCAAGAATTAATTTG	284793	116989	CGGCCAGGGGATGATGAAGC
195620	27816	AAGGTATAATTTGTTTGGAC	240207	72403	TCAGTAGCAAGAATTAATTT	284794	116990	CCGGCCAGGGGATGATGAAG
195621	27817	TAAGGTATAATTTGTTTGGA	240208	72404	TTCAGTAGCAAGAATTAATT	284795	116991	ACCGGCCAGGGGATGATGAA
195622	27818	TTAAGGTATAATTTGTTTGG	240209	72405	TTTCAGTAGCAAGAATTAAT	284796	116992	GACCGGCCAGGGGATGATGA
195623	27819	TTTAAGGTATAATTTGTTTG	240210	72406	CTTTCAGTAGCAAGAATTAA	284797	116993	AGACCGGCCAGGGGATGATG
195624	27820	CTTTAAGGTATAATTTGTTT	240211	72407	GCTTTCAGTAGCAAGAATTA	284798	116994	TAGACCGGCCAGGGGATGAT
195625	27821	ACTTTAAGGTATAATTTGTT	240212	72408	AGCTTTCAGTAGCAAGAATT	284799	116995	ATAGACCGGCCAGGGGATGA
195626	27822	AACTTTAAGGTATAATTTGT	240213	72409	AAGCTTTCAGTAGCAAGAAT	284800	116996	CATAGACCGGCCAGGGGATG
195627	27823	AAACTTTAAGGTATAATTTG	240214	72410	TAAGCTTTCAGTAGCAAGAA	284801	116997	ACATAGACCGGCCAGGGGAT
195628	27824	CAAACTTTAAGGTATAATTT	240215	72411	GTAAGCTTTCAGTAGCAAGA	284802	116998	GACATAGACCGGCCAGGGGA
195629	27825	TCAAACTTTAAGGTATAATT	240216	72412	TGTAAGCTTTCAGTAGCAAG	284803	116999	CGACATAGACCGGCCAGGGG
195630	27826	TTCAAACTTTAAGGTATAAT	240217	72413	TTGTAAGCTTTCAGTAGCAA	284804	117000	TCGACATAGACCGGCCAGGG
195631	27827	TTTCAAACTTTAAGGTATAA	240218	72414	CTTGTAAGCTTTCAGTAGCA	284805	117001	GTCGACATAGACCGGCCAGG
195632	27828	TTTTCAAACTTTAAGGTATA	240219	72415	CCTTGTAAGCTTTCAGTAGC	284806	117002	AGTCGACATAGACCGGCCAG
195633	27829	ATTTTCAAACTTTAAGGTAT	240220	72416	TCCTTGTAAGCTTTCAGTAG	284807	117003	CAGTCGACATAGACCGGCCA
195634	27830	CATTTTCAAACTTTAAGGTA	240221	72417	CTCCTTGTAAGCTTTCAGTA	284808	117004	CCAGTCGACATAGACCGGCC
195635	27831	ACATTTTCAAACTTTAAGGT	240222	72418	GCTCCTTGTAAGCTTTCAGT	284809	117005	CCCAGTCGACATAGACCGGC
195636	27832	GACATTTTCAAACTTTAAGG	240223	72419	AGCTCCTTGTAAGCTTTCAG	284810	117006	GCCCAGTCGACATAGACCGG
195637	27833	AGACATTTTCAAACTTTAAG	240224	72420	CAGCTCCTTGTAAGCTTTCA	284811	117007	TGCCCAGTCGACATAGACCG
195638	27834	CAGACATTTTCAAACTTTAA	240225	72421	ACAGCTCCTTGTAAGCTTTC	284812	117008	GTGCCCAGTCGACATAGACC
195639	27835	CCAGACATTTTCAAACTTTA	240226	72422	AACAGCTCCTTGTAAGCTTT	284813	117009	GGTGCCCAGTCGACATAGAC
195640	27836	GCCAGACATTTTCAAACTTT	240227	72423	AAACAGCTCCTTGTAAGCTT	284814	117010	GGGTGCCCAGTCGACATAGA
195641	27837	TGCCAGACATTTTCAAACTT	240228	72424	AAAACAGCTCCTTGTAAGCT	284815	117011	CGGGTGCCCAGTCGACATAG
195642	27838	GTGCCAGACATTTTCAAACT	240229	72425	CAAAACAGCTCCTTGTAAGC	284816	117012	TCGGGTGCCCAGTCGACATA
195643	27839	AGTGCCAGACATTTTCAAAC	240230	72426	TCAAAACAGCTCCTTGTAAG	284817	117013	CTCGGGTGCCCAGTCGACAT
195644	27840	AAGTGCCAGACATTTTCAAA	240231	72427	ATCAAAACAGCTCCTTGTAA	284818	117014	CCTCGGGTGCCCAGTCGACA
195645	27841	GAAGTGCCAGACATTTTCAA	240232	72428	CATCAAAACAGCTCCTTGTA	284819	117015	GCCTCGGGTGCCCAGTCGAC
195646	27842	AGAAGTGCCAGACATTTTCA	240233	72429	ACATCAAAACAGCTCCTTGT	284820	117016	AGCCTCGGGTGCCCAGTCGA
195647	27843	TAGAAGTGCCAGACATTTTC	240234	72430	GACATCAAAACAGCTCCTTG	284821	117017	GAGCCTCGGGTGCCCAGTCG
195648	27844	TTAGAAGTGCCAGACATTTT	240235	72431	CGACATCAAAACAGCTCCTT	284822	117018	GGAGCCTCGGGTGCCCAGTC
195649	27845	ATTAGAAGTGCCAGACATTT	240236	72432	CCGACATCAAAACAGCTCCT	284823	117019	AGGAGCCTCGGGTGCCCAGT
195650	27846	AATTAGAAGTGCCAGACATT	240237	72433	CCCGACATCAAAACAGCTCC	284824	117020	GAGGAGCCTCGGGTGCCCAG
195651	27847	GAATTAGAAGTGCCAGACAT	240238	72434	ACCCGACATCAAAACAGCTC	284825	117021	AGAGGAGCCTCGGGTGCCCA
195652	27848	TGAATTAGAAGTGCCAGACA	240239	72435	CACCCGACATCAAAACAGCT	284826	117022	GAGAGGAGCCTCGGGTGCCC
195653	27849	TTGAATTAGAAGTGCCAGAC	240240	72436	ACACCCGACATCAAAACAGC	284827	117023	GGAGAGGAGCCTCGGGTGCC
195654	27850	ATTGAATTAGAAGTGCCAGA	240241	72437	CACACCCGACATCAAAACAG	284828	117024	GGGAGAGGAGCCTCGGGTGC
195655	27851	CATTGAATTAGAAGTGCCAG	240242	72438	TCACACCCGACATCAAAACA	284829	117025	TGGGAGAGGAGCCTCGGGTG
195656	27852	GCATTGAATTAGAAGTGCCA	240243	72439	GTCACACCCGACATCAAAAC	284830	117026	GTGGGAGAGGAGCCTCGGGT
195657	27853	GGCATTGAATTAGAAGTGCC	240244	72440	TGTCACACCCGACATCAAAA	284831	117027	GGTGGGAGAGGAGCCTCGGG
195658	27854	AGGCATTGAATTAGAAGTGC	240245	72441	CTGTCACACCCGACATCAAA	284832	117028	TGGTGGGAGAGGAGCCTCGG
195659	27855	CAGGCATTGAATTAGAAGTG	240246	72442	CCTGTCACACCCGACATCAA	284833	117029	CTGGTGGGAGAGGAGCCTCG
195660	27856	ACAGGCATTGAATTAGAAGT	240247	72443	ACCTGTCACACCCGACATCA	284834	117030	GCTGGTGGGAGAGGAGCCTC
195661	27857	AACAGGCATTGAATTAGAAG	240248	72444	AACCTGTCACACCCGACATC	284835	117031	AGCTGGTGGGAGAGGAGCCT
195662	27858	CAACAGGCATTGAATTAGAA	240249	72445	AAACCTGTCACACCCGACAT	284836	117032	GAGCTGGTGGGAGAGGAGCC
195663	27859	ACAACAGGCATTGAATTAGA	240250	72446	CAAACCTGTCACACCCGACA	284837	117033	AGAGCTGGTGGGAGAGGAGC
195664	27860	CACAACAGGCATTGAATTAG	240251	72447	TCAAACCTGTCACACCCGAC	284838	117034	GAGAGCTGGTGGGAGAGGAG
195665	27861	GCACAACAGGCATTGAATTA	240252	72448	GTCAAACCTGTCACACCCGA	284839	117035	AGAGAGCTGGTGGGAGAGGA
195666	27862	GGCACAACAGGCATTGAATT	240253	72449	AGTCAAACCTGTCACACCCG	284840	117036	AAGAGAGCTGGTGGGAGAGG

195667	27863	TGGCACAACAGGCATTGAAT	240254	72450	AAGTCAAACCTGTCACACCC	284841	117037	CAAGAGAGCTGGTGGGAGAG
195668	27864	CTGGCACAACAGGCATTGAA	240255	72451	CAAGTCAAACCTGTCACACC	284842	117038	CCAAGAGAGCTGGTGGGAGA
195669	27865	CCTGGCACAACAGGCATTGA	240256	72452	CCAAGTCAAACCTGTCACAC	284843	117039	ACCAAGAGAGCTGGTGGGAG
195670	27866	GCCTGGCACAACAGGCATTG	240257	72453	GCCAAGTCAAACCTGTCACA	284844	117040	GACCAAGAGAGCTGGTGGGA
195671	27867	TGCCTGGCACAACAGGCATT	240258	72454	TGCCAAGTCAAACCTGTCAC	284845	117041	TGACCAAGAGAGCTGGTGGG
195672	27868	GTGCCTGGCACAACAGGCAT	240259	72455	CTGCCAAGTCAAACCTGTCA	284846	117042	CTGACCAAGAGAGCTGGTGG
195673	27869	AGTGCCTGGCACAACAGGCA	240260	72456	TCTGCCAAGTCAAACCTGTC	284847	117043	GCTGACCAAGAGAGCTGGTG
195674	27870	CAGTGCCTGGCACAACAGGC	240261	72457	TTCTGCCAAGTCAAACCTGT	284848	117044	AGCTGACCAAGAGAGCTGGT
195675	27871	CCAGTGCCTGGCACAACAGG	240262	72458	CTTCTGCCAAGTCAAACCTG	284849	117045	CAGCTGACCAAGAGAGCTGG
195676	27872	CCCAGTGCCTGGCACAACAG	240263	72459	CCTTCTGCCAAGTCAAACCT	284850	117046	TCAGCTGACCAAGAGAGCTG
195677	27873	GCCCAGTGCCTGGCACAACA	240264	72460	ACCTTCTGCCAAGTCAAACC	284851	117047	TTCAGCTGACCAAGAGAGCT
195678	27874	AGCCCAGTGCCTGGCACAAC	240265	72461	CACCTTCTGCCAAGTCAAAC	284852	117048	TTTCAGCTGACCAAGAGAGC
195679	27875	CAGCCCAGTGCCTGGCACAA	240266	72462	ACACCTTCTGCCAAGTCAAA	284853	117049	CTTTCAGCTGACCAAGAGAG
195680	27876	GCAGCCCAGTGCCTGGCACA	240267	72463	GACACCTTCTGCCAAGTCAA	284854	117050	GCTTTCAGCTGACCAAGAGA
195681	27877	AGCAGCCCAGTGCCTGGCAC	240268	72464	TGACACCTTCTGCCAAGTCA	284855	117051	TGCTTTCAGCTGACCAAGAG
195682	27878	CAGCAGCCCAGTGCCTGGCA	240269	72465	GTGACACCTTCTGCCAAGTC	284856	117052	TTGCTTTCAGCTGACCAAGA
195683	27879	TCAGCAGCCCAGTGCCTGGC	240270	72466	AGTGACACCTTCTGCCAAGT	284857	117053	TTTGCTTTCAGCTGACCAAG
195684	27880	CTCAGCAGCCCAGTGCCTGG	240271	72467	AAGTGACACCTTCTGCCAAG	284858	117054	GTTTGCTTTCAGCTGACCAA
195685	27881	CCTCAGCAGCCCAGTGCCTG	240272	72468	AAAGTGACACCTTCTGCCAA	284859	117055	AGTTTGCTTTCAGCTGACCA
195686	27882	TCCTCAGCAGCCCAGTGCCT	240273	72469	TAAAGTGACACCTTCTGCCA	284860	117056	CAGTTTGCTTTCAGCTGACC
195687	27883	TTCCTCAGCAGCCCAGTGCC	240274	72470	GTAAAGTGACACCTTCTGCC	284861	117057	ACAGTTTGCTTTCAGCTGAC
195688	27884	GTTCCTCAGCAGCCCAGTGC	240275	72471	AGTAAAGTGACACCTTCTGC	284862	117058	AACAGTTTGCTTTCAGCTGA
195689	27885	AGTTCCTCAGCAGCCCAGTG	240276	72472	TAGTAAAGTGACACCTTCTG	284863	117059	TAACAGTTTGCTTTCAGCTG
195690	27886	CAGTTCCTCAGCAGCCCAGT	240277	72473	TTAGTAAAGTGACACCTTCT	284864	117060	TTAACAGTTTGCTTTCAGCT
195691	27887	TCAGTTCCTCAGCAGCCCAG	240278	72474	GTTAGTAAAGTGACACCTTC	284865	117061	GTTAACAGTTTGCTTTCAGC
195692	27888	CTCAGTTCCTCAGCAGCCCA	240279	72475	TGTTAGTAAAGTGACACCTT	284866	117062	TGTTAACAGTTTGCTTTCAG
195693	27889	ACTCAGTTCCTCAGCAGCCC	240280	72476	TTGTTAGTAAAGTGACACCT	284867	117063	GTGTTAACAGTTTGCTTTCA
195694	27890	GACTCAGTTCCTCAGCAGCC	240281	72477	GTTGTTAGTAAAGTGACACC	284868	117064	GGTGTTAACAGTTTGCTTTC
195695	27891	GGACTCAGTTCCTCAGCAGC	240282	72478	TGTTGTTAGTAAAGTGACAC	284869	117065	GGGTGTTAACAGTTTGCTTT
195696	27892	GGGACTCAGTTCCTCAGCAG	240283	72479	ATGTTGTTAGTAAAGTGACA	284870	117066	AGGGTGTTAACAGTTTGCTT
195697	27893	CGGGACTCAGTTCCTCAGCA	240284	72480	AATGTTGTTAGTAAAGTGAC	284871	117067	CAGGGTGTTAACAGTTTGCT
195698	27894	ACGGGACTCAGTTCCTCAGC	240285	72481	AAATGTTGTTAGTAAAGTGA	284872	117068	CCAGGGTGTTAACAGTTTGC
195699	27895	GACGGGACTCAGTTCCTCAG	240286	72482	AAAATGTTGTTAGTAAAGTG	284873	117069	CCCAGGGTGTTAACAGTTTG
195700	27896	GGACGGGACTCAGTTCCTCA	240287	72483	TAAAATGTTGTTAGTAAAGT	284874	117070	CCCCAGGGTGTTAACAGTTT
195701	27897	GGGACGGGACTCAGTTCCTC	240288	72484	TTAAAATGTTGTTAGTAAAG	284875	117071	TCCCCAGGGTGTTAACAGTT
195702	27898	AGGGACGGGACTCAGTTCCT	240289	72485	TTTAAAATGTTGTTAGTAAA	284876	117072	CTCCCCAGGGTGTTAACAGT
195703	27899	CAGGGACGGGACTCAGTTCC	240290	72486	ATTTAAAATGTTGTTAGTAA	284877	117073	GCTCCCCAGGGTGTTAACAG
195704	27900	GCAGGGACGGGACTCAGTTC	240291	72487	TATTTAAAATGTTGTTAGTA	284878	117074	AGCTCCCCAGGGTGTTAACA
195705	27901	TGCAGGGACGGGACTCAGTT	240292	72488	TTATTTAAAATGTTGTTAGT	284879	117075	CAGCTCCCCAGGGTGTTAAC
195706	27902	CTGCAGGGACGGGACTCAGT	240293	72489	CTTATTTAAAATGTTGTTAG	284880	117076	CCAGCTCCCCAGGGTGTTAA
195707	27903	CCTGCAGGGACGGGACTCAG	240294	72490	ACTTATTTAAAATGTTGTTA	284881	117077	TCCAGCTCCCCAGGGTGTTA
195708	27904	GCCTGCAGGGACGGGACTCA	240295	72491	CACTTATTTAAAATGTTGTT	284882	117078	GTCCAGCTCCCCAGGGTGTT
195709	27905	AGCCTGCAGGGACGGGACTC	240296	72492	TCACTTATTTAAAATGTTGT	284883	117079	CGTCCAGCTCCCCAGGGTGT
195710	27906	TAGCCTGCAGGGACGGGACT	240297	72493	GTCACTTATTTAAAATGTTG	284884	117080	ACGTCCAGCTCCCCAGGGTG
195711	27907	CTAGCCTGCAGGGACGGGAC	240298	72494	TGTCACTTATTTAAAATGTT	284885	117081	TACGTCCAGCTCCCCAGGGT
195712	27908	GCTAGCCTGCAGGGACGGGA	240299	72495	CTGTCACTTATTTAAAATGT	284886	117082	ATACGTCCAGCTCCCCAGGG
195713	27909	AGCTAGCCTGCAGGGACGGG	240300	72496	TCTGTCACTTATTTAAAATG	284887	117083	CATACGTCCAGCTCCCCAGG
195714	27910	TAGCTAGCCTGCAGGGACGG	240301	72497	TTCTGTCACTTATTTAAAAT	284888	117084	TCATACGTCCAGCTCCCCAG
195715	27911	CTAGCTAGCCTGCAGGGACG	240302	72498	CTTCTGTCACTTATTTAAAA	284889	117085	CTCATACGTCCAGCTCCCCA
195716	27912	TCTAGCTAGCCTGCAGGGAC	240303	72499	TCTTCTGTCACTTATTTAAA	284890	117086	TCTCATACGTCCAGCTCCCC
195717	27913	CTCTAGCTAGCCTGCAGGGA	240304	72500	GTCTTCTGTCACTTATTTAA	284891	117087	GTCTCATACGTCCAGCTCCC
195718	27914	TCTCTAGCTAGCCTGCAGGG	240305	72501	TGTCTTCTGTCACTTATTTA	284892	117088	GGTCTCATACGTCCAGCTCC
195719	27915	TTCTCTAGCTAGCCTGCAGG	240306	72502	TTGTCTTCTGTCACTTATTT	284893	117089	GGGTCTCATACGTCCAGCTC
195720	27916	GTTCTCTAGCTAGCCTGCAG	240307	72503	CTTGTCTTCTGTCACTTATT	284894	117090	AGGGTCTCATACGTCCAGCT
195721	27917	TGTTCTCTAGCTAGCCTGCA	240308	72504	TCTTGTCTTCTGTCACTTAT	284895	117091	AAGGGTCTCATACGTCCAGC
195722	27918	GTGTTCTCTAGCTAGCCTGC	240309	72505	TTCTTGTCTTCTGTCACTTA	284896	117092	CAAGGGTCTCATACGTCCAG
195723	27919	TGTGTTCTCTAGCTAGCCTG	240310	72506	TTTCTTGTCTTCTGTCACTT	284897	117093	CCAAGGGTCTCATACGTCCA
195724	27920	GTGTGTTCTCTAGCTAGCCT	240311	72507	GTTTCTTGTCTTCTGTCACT	284898	117094	CCCAAGGGTCTCATACGTCC
195725	27921	TGTGTGTTCTCTAGCTAGCC	240312	72508	AGTTTCTTGTCTTCTGTCAC	284899	117095	CCCCAAGGGTCTCATACGTC
195726	27922	GTGTGTGTTCTCTAGCTAGC	240313	72509	TAGTTTCTTGTCTTCTGTCA	284900	117096	ACCCCAAGGGTCTCATACGT
195727	27923	TGTGTGTGTTCTCTAGCTAG	240314	72510	GTAGTTTCTTGTCTTCTGTC	284901	117097	CACCCCAAGGGTCTCATACG
195728	27924	GTGTGTGTGTTCTCTAGCTA	240315	72511	TGTAGTTTCTTGTCTTCTGT	284902	117098	CCACCCCAAGGGTCTCATAC
195729	27925	TGTGTGTGTGTTCTCTAGCT	240316	72512	GTGTAGTTTCTTGTCTTCTG	284903	117099	CCCACCCCAAGGGTCTCATA
195730	27926	GTGTGTGTGTGTTCTCTAGC	240317	72513	CGTGTAGTTTCTTGTCTTCT	284904	117100	TCCCACCCCAAGGGTCTCAT
195731	27927	TGTGTGTGTGTGTTCTCTAG	240318	72514	ACGTGTAGTTTCTTGTCTTC	284905	117101	CTCCCACCCCAAGGGTCTCA
195732	27928	GTGTGTGTGTGTGTTCTCTA	240319	72515	AACGTGTAGTTTCTTGTCTT	284906	117102	CCTCCCACCCCAAGGGTCTC
195733	27929	TGTGTGTGTGTGTGTTCTCT	240320	72516	TAACGTGTAGTTTCTTGTCT	284907	117103	GCCTCCCACCCCAAGGGTCT
195734	27930	GTGTGTGTGTGTGTGTTCTC	240321	72517	TTAACGTGTAGTTTCTTGTC	284908	117104	CGCCTCCCACCCCAAGGGTC
195735	27931	TGTGTGTGTGTGTGTGTTCT	240322	72518	TTTAACGTGTAGTTTCTTGT	284909	117105	ACGCCTCCCACCCCAAGGGT
195736	27932	GTGTGTGTGTGTGTGTGTTC	240323	72519	ATTTAACGTGTAGTTTCTTG	284910	117106	AACGCCTCCCACCCCAAGGG
195737	27933	TGTGTGTGTGTGTGTGTGTT	240324	72520	CATTTAACGTGTAGTTTCTT	284911	117107	CAACGCCTCCCACCCCAAGG
195738	27934	GTGTGTGTGTGTGTGTGTGT	240325	72521	GCATTTAACGTGTAGTTTCT	284912	117108	TCAACGCCTCCCACCCCAAG

195739	27935	TGTGTGTGTGTGTGTGTGTG	240326	72522	GGCATTTAACGTGTAGTTTC	284913	117109	ATCAACGCCTCCCACCCCAA
195740	27936	GTGTGTGTGTGTGTGTGTGT	240327	72523	TGGCATTTAACGTGTAGTTT	284914	117110	AATCAACGCCTCCCACCCCA
195741	27937	TGTGTGTGTGTGTGTGTGTG	240328	72524	CTGGCATTTAACGTGTAGTT	284915	117111	AAATCAACGCCTCCCACCCC
195742	27938	GTGTGTGTGTGTGTGTGTGT	240329	72525	TCTGGCATTTAACGTGTAGT	284916	117112	AAAATCAACGCCTCCCACCC
195743	27939	TGTGTGTGTGTGTGTGTGTG	240330	72526	TTCTGGCATTTAACGTGTAG	284917	117113	AAAAATCAACGCCTCCCACC
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195745	27941	TGTGTGTGTGTGTGTGTGTG	240332	72528	TGTTCTGGCATTTAACGTGT	284919	117115	TCAAAAATCAACGCCTCCCA
195746	27942	GTGTGTGTGTGTGTGTGTGT	240333	72529	TTGTTCTGGCATTTAACGTG	284920	117116	CTCAAAAATCAACGCCTCCC
195747	27943	TGTGTGTGTGTGTGTGTGTG	240334	72530	TTTGTTCTGGCATTTAACGT	284921	117117	TCTCAAAAATCAACGCCTCC
195748	27944	GTGTGTGTGTGTGTGTGTGT	240335	72531	CTTTGTTCTGGCATTTAACG	284922	117118	CTCTCAAAAATCAACGCCTC
195749	27945	TGTGTGTGTGTGTGTGTGTG	240336	72532	TCTTTGTTCTGGCATTTAAC	284923	117119	GCTCTCAAAAATCAACGCCT
195750	27946	GTGTGTGTGTGTGTGTGTGT	240337	72533	CTCTTTGTTCTGGCATTTAA	284924	117120	TGCTCTCAAAAATCAACGCC
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195752	27948	CTGTGTGTGTGTGTGTGTGT	240339	72535	CACTCTTTGTTCTGGCATTT	284926	117122	ATTGCTCTCAAAAATCAACG
195753	27949	TCTGTGTGTGTGTGTGTGTG	240340	72536	ACACTCTTTGTTCTGGCATT	284927	117123	GATTGCTCTCAAAAATCAAC
195754	27950	CTCTGTGTGTGTGTGTGTGT	240341	72537	GACACTCTTTGTTCTGGCAT	284928	117124	TGATTGCTCTCAAAAATCAA
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195760	27956	AGACCACTCTGTGTGTGTGT	240347	72543	CACTTAGACACTCTTTGTTC	284934	117130	GCCAGGTGATTGCTCTCAAA
195761	27957	AAGACCACTCTGTGTGTGTG	240348	72544	CCACTTAGACACTCTTTGTT	284935	117131	GGCCAGGTGATTGCTCTCAA
195762	27958	TAAGACCACTCTGTGTGTGT	240349	72545	TCCACTTAGACACTCTTTGT	284936	117132	GGGCCAGGTGATTGCTCTCA
195763	27959	GTAAGACCACTCTGTGTGTG	240350	72546	ATCCACTTAGACACTCTTTG	284937	117133	AGGGCCAGGTGATTGCTCTC
195764	27960	TGTAAGACCACTCTGTGTGT	240351	72547	CATCCACTTAGACACTCTTT	284938	117134	CAGGGCCAGGTGATTGCTCT
195765	27961	TTGTAAGACCACTCTGTGTG	240352	72548	GCATCCACTTAGACACTCTT	284939	117135	CCAGGGCCAGGTGATTGCTC
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195806	28002	AATAATACCTTTATTGCATA	240393	72589	CAGCTCTCTTGGGCAGGTAT	284980	117176	CAGCCCACCCCGGAGCCACA
195807	28003	TAATAATACCTTTATTGCAT	240394	72590	TCAGCTCTCTTGGGCAGGTA	284981	117177	ACAGCCCACCCCGGAGCCAC
195808	28004	ATAATAATACCTTTATTGCA	240395	72591	TTCAGCTCTCTTGGGCAGGT	284982	117178	GACAGCCCACCCCGGAGCCA
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195815	28011	CCTCAACATAATAATACCTT	240402	72598	TCTACTTTTCAGCTCTCTTG	284989	117185	TTCTGGAGACAGCCCACCCC
195816	28012	ACCTCAACATAATAATACCT	240403	72599	ATCTACTTTTCAGCTCTCTT	284990	117186	TTTCTGGAGACAGCCCACCC
195817	28013	CACCTCAACATAATAATACC	240404	72600	CATCTACTTTTCAGCTCTCT	284991	117187	TTTTCTGGAGACAGCCCACC
195818	28014	GCACCTCAACATAATAATAC	240405	72601	TCATCTACTTTTCAGCTCTC	284992	117188	ATTTTCTGGAGACAGCCCAC
195819	28015	GGCACCTCAACATAATAATA	240406	72602	TTCATCTACTTTTCAGCTCT	284993	117189	CATTTTCTGGAGACAGCCCA
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195851	28047	ATCCTCTCCTTTAAGAAAAA	240438	72634	ATTAGGGTGCACTAGTTTAT	285025	117221	GGGCTGGATGCGGGTGGCTG
195852	28048	CATCCTCTCCTTTAAGAAAA	240439	72635	CATTAGGGTGCACTAGTTTA	285026	117222	TGGGCTGGATGCGGGTGGCT
195853	28049	GCATCCTCTCCTTTAAGAAA	240440	72636	TCATTAGGGTGCACTAGTTT	285027	117223	CTGGGCTGGATGCGGGTGGC
195854	28050	GGCATCCTCTCCTTTAAGAA	240441	72637	TTCATTAGGGTGCACTAGTT	285028	117224	TCTGGGCTGGATGCGGGTGG
195855	28051	AGGCATCCTCTCCTTTAAGA	240442	72638	ATTCATTAGGGTGCACTAGT	285029	117225	CTCTGGGCTGGATGCGGGTG
195856	28052	TAGGCATCCTCTCCTTTAAG	240443	72639	AATTCATTAGGGTGCACTAG	285030	117226	CCTCTGGGCTGGATGCGGGT
195857	28053	TTAGGCATCCTCTCCTTTAA	240444	72640	TAATTCATTAGGGTGCACTA	285031	117227	CCCTCTGGGCTGGATGCGGG
195858	28054	TTTAGGCATCCTCTCCTTTA	240445	72641	TTAATTCATTAGGGTGCACT	285032	117228	ACCCTCTGGGCTGGATGCGG
195859	28055	TTTTAGGCATCCTCTCCTTT	240446	72642	TTTAATTCATTAGGGTGCAC	285033	117229	AACCCTCTGGGCTGGATGCG
195860	28056	GTTTTAGGCATCCTCTCCTT	240447	72643	TTTTAATTCATTAGGGTGCA	285034	117230	AAACCCTCTGGGCTGGATGC
195861	28057	TGTTTTAGGCATCCTCTCCT	240448	72644	CTTTTAATTCATTAGGGTGC	285035	117231	TAAACCCTCTGGGCTGGATG
195862	28058	CTGTTTTAGGCATCCTCTCC	240449	72645	CCTTTTAATTCATTAGGGTG	285036	117232	ATAAACCCTCTGGGCTGGAT
195863	28059	CCTGTTTTAGGCATCCTCTC	240450	72646	ACCTTTTAATTCATTAGGGT	285037	117233	AATAAACCCTCTGGGCTGGA
195864	28060	GCCTGTTTTAGGCATCCTCT	240451	72647	CACCTTTTAATTCATTAGGG	285038	117234	GAATAAACCCTCTGGGCTGG
195865	28061	TGCCTGTTTTAGGCATCCTC	240452	72648	ACACCTTTTAATTCATTAGG	285039	117235	AGAATAAACCCTCTGGGCTG
195866	28062	ATGCCTGTTTTAGGCATCCT	240453	72649	AACACCTTTTAATTCATTAG	285040	117236	AAGAATAAACCCTCTGGGCT
195867	28063	AATGCCTGTTTTAGGCATCC	240454	72650	CAACACCTTTTAATTCATTA	285041	117237	CAAGAATAAACCCTCTGGGC
195868	28064	TAATGCCTGTTTTAGGCATC	240455	72651	TCAACACCTTTTAATTCATT	285042	117238	GCAAGAATAAACCCTCTGGG
195869	28065	GTAATGCCTGTTTTAGGCAT	240456	72652	ATCAACACCTTTTAATTCAT	285043	117239	TGCAAGAATAAACCCTCTGG
195870	28066	GGTAATGCCTGTTTTAGGCA	240457	72653	CATCAACACCTTTTAATTCA	285044	117240	TTGCAAGAATAAACCCTCTG
195871	28067	AGGTAATGCCTGTTTTAGGC	240458	72654	TCATCAACACCTTTTAATTC	285045	117241	ATTGCAAGAATAAACCCTCT
195872	28068	CAGGTAATGCCTGTTTTAGG	240459	72655	CTCATCAACACCTTTTAATT	285046	117242	CATTGCAAGAATAAACCCTC
195873	28069	TCAGGTAATGCCTGTTTTAG	240460	72656	ACTCATCAACACCTTTTAAT	285047	117243	ACATTGCAAGAATAAACCCT
195874	28070	TTCAGGTAATGCCTGTTTTA	240461	72657	AACTCATCAACACCTTTTAA	285048	117244	CACATTGCAAGAATAAACCC
195875	28071	TTTCAGGTAATGCCTGTTTT	240462	72658	TAACTCATCAACACCTTTTA	285049	117245	GCACATTGCAAGAATAAACC
195876	28072	GTTTCAGGTAATGCCTGTTT	240463	72659	TTAACTCATCAACACCTTTT	285050	117246	AGCACATTGCAAGAATAAAC
195877	28073	GGTTTCAGGTAATGCCTGTT	240464	72660	GTTAACTCATCAACACCTTT	285051	117247	CAGCACATTGCAAGAATAAA
195878	28074	AGGTTTCAGGTAATGCCTGT	240465	72661	AGTTAACTCATCAACACCTT	285052	117248	GCAGCACATTGCAAGAATAA
195879	28075	GAGGTTTCAGGTAATGCCTG	240466	72662	AAGTTAACTCATCAACACCT	285053	117249	AGCAGCACATTGCAAGAATA
195880	28076	GGAGGTTTCAGGTAATGCCT	240467	72663	CAAGTTAACTCATCAACACC	285054	117250	CAGCAGCACATTGCAAGAAT
195881	28077	AGGAGGTTTCAGGTAATGCC	240468	72664	ACAAGTTAACTCATCAACAC	285055	117251	GCAGCAGCACATTGCAAGAA
195882	28078	GAGGAGGTTTCAGGTAATGC	240469	72665	AACAAGTTAACTCATCAACA	285056	117252	AGCAGCAGCACATTGCAAGA

195883	28079	AGAGGAGGTTTCAGGTAATG	240470	72666	TAACAAGTTAACTCATCAAC	285057	117253	AAGCAGCAGCACATTGCAAG
195884	28080	GAGAGGAGGTTTCAGGTAAT	240471	72667	ATAACAAGTTAACTCATCAA	285058	117254	GAAGCAGCAGCACATTGCAA
195885	28081	AGAGAGGAGGTTTCAGGTAA	240472	72668	CATAACAAGTTAACTCATCA	285059	117255	GGAAGCAGCAGCACATTGCA
195886	28082	GAGAGAGGAGGTTTCAGGTA	240473	72669	GCATAACAAGTTAACTCATC	285060	117256	AGGAAGCAGCAGCACATTGC
195887	28083	GGAGAGAGGAGGTTTCAGGT	240474	72670	GGCATAACAAGTTAACTCAT	285061	117257	CAGGAAGCAGCAGCACATTG
195888	28084	TGGAGAGAGGAGGTTTCAGG	240475	72671	AGGCATAACAAGTTAACTCA	285062	117258	GCAGGAAGCAGCAGCACATT
195889	28085	CTGGAGAGAGGAGGTTTCAG	240476	72672	AAGGCATAACAAGTTAACTC	285063	117259	GGCAGGAAGCAGCAGCACAT
195890	28086	GCTGGAGAGAGGAGGTTTCA	240477	72673	GAAGGCATAACAAGTTAACT	285064	117260	GGGCAGGAAGCAGCAGCACA
195891	28087	TGCTGGAGAGAGGAGGTTTC	240478	72674	GGAAGGCATAACAAGTTAAC	285065	117261	AGGGCAGGAAGCAGCAGCAC
195892	28088	ATGCTGGAGAGAGGAGGTTT	240479	72675	TGGAAGGCATAACAAGTTAA	285066	117262	CAGGGCAGGAAGCAGCAGCA
195893	28089	AATGCTGGAGAGAGGAGGTT	240480	72676	CTGGAAGGCATAACAAGTTA	285067	117263	TCAGGGCAGGAAGCAGCAGC
195894	28090	CAATGCTGGAGAGAGGAGGT	240481	72677	TCTGGAAGGCATAACAAGTT	285068	117264	CTCAGGGCAGGAAGCAGCAG
195895	28091	CCAATGCTGGAGAGAGGAGG	240482	72678	ATCTGGAAGGCATAACAAGT	285069	117265	GCTCAGGGCAGGAAGCAGCA
195896	28092	ACCAATGCTGGAGAGAGGAG	240483	72679	TATCTGGAAGGCATAACAAG	285070	117266	TGCTCAGGGCAGGAAGCAGC
195897	28093	AACCAATGCTGGAGAGAGGA	240484	72680	TTATCTGGAAGGCATAACAA	285071	117267	GTGCTCAGGGCAGGAAGCAG
195898	28094	CAACCAATGCTGGAGAGAGG	240485	72681	CTTATCTGGAAGGCATAACA	285072	117268	GGTGCTCAGGGCAGGAAGCA
195899	28095	ACAACCAATGCTGGAGAGAG	240486	72682	TCTTATCTGGAAGGCATAAC	285073	117269	AGGTGCTCAGGGCAGGAAGC
195900	28096	GACAACCAATGCTGGAGAGA	240487	72683	GTCTTATCTGGAAGGCATAA	285074	117270	CAGGTGCTCAGGGCAGGAAG
195901	28097	AGACAACCAATGCTGGAGAG	240488	72684	TGTCTTATCTGGAAGGCATA	285075	117271	CCAGGTGCTCAGGGCAGGAA
195902	28098	AAGACAACCAATGCTGGAGA	240489	72685	ATGTCTTATCTGGAAGGCAT	285076	117272	TCCAGGTGCTCAGGGCAGGA
195903	28099	GAAGACAACCAATGCTGGAG	240490	72686	CATGTCTTATCTGGAAGGCA	285077	117273	ATCCAGGTGCTCAGGGCAGG
195904	28100	AGAAGACAACCAATGCTGGA	240491	72687	GCATGTCTTATCTGGAAGGC	285078	117274	GATCCAGGTGCTCAGGGCAG
195905	28101	CAGAAGACAACCAATGCTGG	240492	72688	TGCATGTCTTATCTGGAAGG	285079	117275	GGATCCAGGTGCTCAGGGCA
195906	28102	ACAGAAGACAACCAATGCTG	240493	72689	TTGCATGTCTTATCTGGAAG	285080	117276	GGGATCCAGGTGCTCAGGGC
195907	28103	GACAGAAGACAACCAATGCT	240494	72690	TTTGCATGTCTTATCTGGAA	285081	117277	CGGGATCCAGGTGCTCAGGG
195908	28104	TGACAGAAGACAACCAATGC	240495	72691	ATTTGCATGTCTTATCTGGA	285082	117278	CCGGGATCCAGGTGCTCAGG
195909	28105	ATGACAGAAGACAACCAATG	240496	72692	CATTTGCATGTCTTATCTGG	285083	117279	GCCGGGATCCAGGTGCTCAG
195910	28106	CATGACAGAAGACAACCAAT	240497	72693	CCATTTGCATGTCTTATCTG	285084	117280	AGCCGGGATCCAGGTGCTCA
195911	28107	TCATGACAGAAGACAACCAA	240498	72694	CCCATTTGCATGTCTTATCT	285085	117281	AAGCCGGGATCCAGGTGCTC
195912	28108	GTCATGACAGAAGACAACCA	240499	72695	CCCCATTTGCATGTCTTATC	285086	117282	GAAGCCGGGATCCAGGTGCT
195913	28109	AGTCATGACAGAAGACAACC	240500	72696	GCCCCATTTGCATGTCTTAT	285087	117283	AGAAGCCGGGATCCAGGTGC
195914	28110	GAGTCATGACAGAAGACAAC	240501	72697	AGCCCCATTTGCATGTCTTA	285088	117284	CAGAAGCCGGGATCCAGGTG
195915	28111	TGAGTCATGACAGAAGACAA	240502	72698	AAGCCCCATTTGCATGTCTT	285089	117285	GCAGAAGCCGGGATCCAGGT
195916	28112	CTGAGTCATGACAGAAGACA	240503	72699	GAAGCCCCATTTGCATGTCT	285090	117286	GGCAGAAGCCGGGATCCAGG
195917	28113	CCTGAGTCATGACAGAAGAC	240504	72700	AGAAGCCCCATTTGCATGTC	285091	117287	GGGCAGAAGCCGGGATCCAG
195918	28114	CCCTGAGTCATGACAGAAGA	240505	72701	AAGAAGCCCCATTTGCATGT	285092	117288	AGGGCAGAAGCCGGGATCCA
195919	28115	ACCCTGAGTCATGACAGAAG	240506	72702	GAAGAAGCCCCATTTGCATG	285093	117289	CAGGGCAGAAGCCGGGATCC
195920	28116	AACCCTGAGTCATGACAGAA	240507	72703	GGAAGAAGCCCCATTTGCAT	285094	117290	TCAGGGCAGAAGCCGGGATC
195921	28117	AAACCCTGAGTCATGACAGA	240508	72704	AGGAAGAAGCCCCATTTGCA	285095	117291	CTCAGGGCAGAAGCCGGGAT
195922	28118	AAAACCCTGAGTCATGACAG	240509	72705	GAGGAAGAAGCCCCATTTGC	285096	117292	CCTCAGGGCAGAAGCCGGGA
195923	28119	GAAAACCCTGAGTCATGACA	240510	72706	GGAGGAAGAAGCCCCATTTG	285097	117293	GCCTCAGGGCAGAAGCCGGG
195924	28120	TGAAAACCCTGAGTCATGAC	240511	72707	AGGAGGAAGAAGCCCCATTT	285098	117294	GGCCTCAGGGCAGAAGCCGG
195925	28121	GTGAAAACCCTGAGTCATGA	240512	72708	AAGGAGGAAGAAGCCCCATT	285099	117295	GGGCCTCAGGGCAGAAGCCG
195926	28122	AGTGAAAACCCTGAGTCATG	240513	72709	GAAGGAGGAAGAAGCCCCAT	285100	117296	GGGGCCTCAGGGCAGAAGCC
195927	28123	CAGTGAAAACCCTGAGTCAT	240514	72710	TGAAGGAGGAAGAAGCCCCA	285101	117297	AGGGGCCTCAGGGCAGAAGC
195928	28124	TCAGTGAAAACCCTGAGTCA	240515	72711	GTGAAGGAGGAAGAAGCCCC	285102	117298	AAGGGGCCTCAGGGCAGAAG
195929	28125	CTCAGTGAAAACCCTGAGTC	240516	72712	AGTGAAGGAGGAAGAAGCCC	285103	117299	CAAGGGGCCTCAGGGCAGAA
195930	28126	TCTCAGTGAAAACCCTGAGT	240517	72713	TAGTGAAGGAGGAAGAAGCC	285104	117300	TCAAGGGGCCTCAGGGCAGA
195931	28127	TTCTCAGTGAAAACCCTGAG	240518	72714	GTAGTGAAGGAGGAAGAAGC	285105	117301	CTCAAGGGGCCTCAGGGCAG
195932	28128	ATTCTCAGTGAAAACCCTGA	240519	72715	AGTAGTGAAGGAGGAAGAAG	285106	117302	ACTCAAGGGGCCTCAGGGCA
195933	28129	CATTCTCAGTGAAAACCCTG	240520	72716	AAGTAGTGAAGGAGGAAGAA	285107	117303	GACTCAAGGGGCCTCAGGGC
195934	28130	CCATTCTCAGTGAAAACCCT	240521	72717	GAAGTAGTGAAGGAGGAAGA	285108	117304	GGACTCAAGGGGCCTCAGGG
195935	28131	CCCATTCTCAGTGAAAACCC	240522	72718	GGAAGTAGTGAAGGAGGAAG	285109	117305	GGGACTCAAGGGGCCTCAGG
195936	28132	TCCCATTCTCAGTGAAAACC	240523	72719	TGGAAGTAGTGAAGGAGGAA	285110	117306	TGGGACTCAAGGGGCCTCAG
195937	28133	ATCCCATTCTCAGTGAAAAC	240524	72720	TTGGAAGTAGTGAAGGAGGA	285111	117307	GTGGGACTCAAGGGGCCTCA
195938	28134	CATCCCATTCTCAGTGAAAA	240525	72721	CTTGGAAGTAGTGAAGGAGG	285112	117308	TGTGGGACTCAAGGGGCCTC
195939	28135	CCATCCCATTCTCAGTGAAA	240526	72722	CCTTGGAAGTAGTGAAGGAG	285113	117309	CTGTGGGACTCAAGGGGCCT
195940	28136	TCCATCCCATTCTCAGTGAA	240527	72723	CCCTTGGAAGTAGTGAAGGA	285114	117310	CCTGTGGGACTCAAGGGGCC
195941	28137	TTCCATCCCATTCTCAGTGA	240528	72724	TCCCTTGGAAGTAGTGAAGG	285115	117311	ACCTGTGGGACTCAAGGGGC
195942	28138	TTTCCATCCCATTCTCAGTG	240529	72725	ATCCCTTGGAAGTAGTGAAG	285116	117312	TACCTGTGGGACTCAAGGGG
195943	28139	ATTTCCATCCCATTCTCAGT	240530	72726	AATCCCTTGGAAGTAGTGAA	285117	117313	CTACCTGTGGGACTCAAGGG
195944	28140	CATTTCCATCCCATTCTCAG	240531	72727	AAATCCCTTGGAAGTAGTGA	285118	117314	GCTACCTGTGGGACTCAAGG
195945	28141	ACATTTCCATCCCATTCTCA	240532	72728	TAAATCCCTTGGAAGTAGTG	285119	117315	TGCTACCTGTGGGACTCAAG
195946	28142	CACATTTCCATCCCATTCTC	240533	72729	TTAAATCCCTTGGAAGTAGT	285120	117316	TTGCTACCTGTGGGACTCAA
195947	28143	CCACATTTCCATCCCATTCT	240534	72730	GTTAAATCCCTTGGAAGTAG	285121	117317	CTTGCTACCTGTGGGACTCA
195948	28144	ACCACATTTCCATCCCATTC	240535	72731	TGTTAAATCCCTTGGAAGTA	285122	117318	GCTTGCTACCTGTGGGACTC
195949	28145	GACCACATTTCCATCCCATT	240536	72732	TTGTTAAATCCCTTGGAAGT	285123	117319	CGCTTGCTACCTGTGGGACT
195950	28146	AGACCACATTTCCATCCCAT	240537	72733	CTTGTTAAATCCCTTGGAAG	285124	117320	GCGCTTGCTACCTGTGGGAC
195951	28147	TAGACCACATTTCCATCCCA	240538	72734	CCTTGTTAAATCCCTTGGAA	285125	117321	AGCGCTTGCTACCTGTGGGA
195952	28148	TTAGACCACATTTCCATCCC	240539	72735	TCCTTGTTAAATCCCTTGGA	285126	117322	AAGCGCTTGCTACCTGTGGG
195953	28149	TTTAGACCACATTTCCATCC	240540	72736	CTCCTTGTTAAATCCCTTGG	285127	117323	CAAGCGCTTGCTACCTGTGG
195954	28150	CTTTAGACCACATTTCCATC	240541	72737	TCTCCTTGTTAAATCCCTTG	285128	117324	GCAAGCGCTTGCTACCTGTG

195955	28151	TCTTTAGACCACATTTCCAT	240542	72738	GTCTCCTTGTTAAATCCCTT	285129	117325	GGCAAGCGCTTGCTACCTGT
195956	28152	ATCTTTAGACCACATTTCCA	240543	72739	GGTCTCCTTGTTAAATCCCT	285130	117326	GGGCAAGCGCTTGCTACCTG
195957	28153	TATCTTTAGACCACATTTCC	240544	72740	TGGTCTCCTTGTTAAATCCC	285131	117327	AGGGCAAGCGCTTGCTACCT
195958	28154	CTATCTTTAGACCACATTTC	240545	72741	TTGGTCTCCTTGTTAAATCC	285132	117328	CAGGGCAAGCGCTTGCTACC
195959	28155	CCTATCTTTAGACCACATTT	240546	72742	ATTGGTCTCCTTGTTAAATC	285133	117329	GCAGGGCAAGCGCTTGCTAC
195960	28156	CCCTATCTTTAGACCACATT	240547	72743	CATTGGTCTCCTTGTTAAAT	285134	117330	CGCAGGGCAAGCGCTTGCTA
195961	28157	GCCCTATCTTTAGACCACAT	240548	72744	GCATTGGTCTCCTTGTTAAA	285135	117331	CCGCAGGGCAAGCGCTTGCT
195962	28158	GGCCCTATCTTTAGACCACA	240549	72745	TGCATTGGTCTCCTTGTTAA	285136	117332	GCCGCAGGGCAAGCGCTTGC
195963	28159	TGGCCCTATCTTTAGACCAC	240550	72746	TTGCATTGGTCTCCTTGTTA	285137	117333	AGCCGCAGGGCAAGCGCTTG
195964	28160	TTGGCCCTATCTTTAGACCA	240551	72747	TTTGCATTGGTCTCCTTGTT	285138	117334	CAGCCGCAGGGCAAGCGCTT
195965	28161	ATTGGCCCTATCTTTAGACC	240552	72748	ATTTGCATTGGTCTCCTTGT	285139	117335	GCAGCCGCAGGGCAAGCGCT
195966	28162	CATTGGCCCTATCTTTAGAC	240553	72749	CATTTGCATTGGTCTCCTTG	285140	117336	AGCAGCCGCAGGGCAAGCGC
195967	28163	ACATTGGCCCTATCTTTAGA	240554	72750	TCATTTGCATTGGTCTCCTT	285141	117337	CAGCAGCCGCAGGGCAAGCG
195968	28164	AACATTGGCCCTATCTTTAG	240555	72751	ATCATTTGCATTGGTCTCCT	285142	117338	GCAGCAGCCGCAGGGCAAGC
195969	28165	CAACATTGGCCCTATCTTTA	240556	72752	TATCATTTGCATTGGTCTCC	285143	117339	TGCAGCAGCCGCAGGGCAAG
195970	28166	CCAACATTGGCCCTATCTTT	240557	72753	TTATCATTTGCATTGGTCTC	285144	117340	ATGCAGCAGCCGCAGGGCAA
195971	28167	CCCAACATTGGCCCTATCTT	240558	72754	CTTATCATTTGCATTGGTCT	285145	117341	CATGCAGCAGCCGCAGGGCA
195972	28168	TCCCAACATTGGCCCTATCT	240559	72755	CCTTATCATTTGCATTGGTC	285146	117342	CCATGCAGCAGCCGCAGGGC
195973	28169	GTCCCAACATTGGCCCTATC	240560	72756	TCCTTATCATTTGCATTGGT	285147	117343	CCCATGCAGCAGCCGCAGGG
195974	28170	AGTCCCAACATTGGCCCTAT	240561	72757	GTCCTTATCATTTGCATTGG	285148	117344	CCCCATGCAGCAGCCGCAGG
195975	28171	CAGTCCCAACATTGGCCCTA	240562	72758	AGTCCTTATCATTTGCATTG	285149	117345	GCCCCATGCAGCAGCCGCAG
195976	28172	CCAGTCCCAACATTGGCCCT	240563	72759	CAGTCCTTATCATTTGCATT	285150	117346	AGCCCCATGCAGCAGCCGCA
195977	28173	TCCAGTCCCAACATTGGCCC	240564	72760	ACAGTCCTTATCATTTGCAT	285151	117347	TAGCCCCATGCAGCAGCCGC
195978	28174	ATCCAGTCCCAACATTGGCC	240565	72761	TACAGTCCTTATCATTTGCA	285152	117348	TTAGCCCCATGCAGCAGCCG
195979	28175	GATCCAGTCCCAACATTGGC	240566	72762	CTACAGTCCTTATCATTTGC	285153	117349	GTTAGCCCCATGCAGCAGCC
195980	28176	GGATCCAGTCCCAACATTGG	240567	72763	CCTACAGTCCTTATCATTTG	285154	117350	AGTTAGCCCCATGCAGCAGC
195981	28177	GGGATCCAGTCCCAACATTG	240568	72764	CCCTACAGTCCTTATCATTT	285155	117351	TAGTTAGCCCCATGCAGCAG
195982	28178	GGGGATCCAGTCCCAACATT	240569	72765	GCCCTACAGTCCTTATCATT	285156	117352	TTAGTTAGCCCCATGCAGCA
195983	28179	AGGGGATCCAGTCCCAACAT	240570	72766	AGCCCTACAGTCCTTATCAT	285157	117353	GTTAGTTAGCCCCATGCAGC
195984	28180	GAGGGGATCCAGTCCCAACA	240571	72767	GAGCCCTACAGTCCTTATCA	285158	117354	CGTTAGTTAGCCCCATGCAG
195985	28181	AGAGGGGATCCAGTCCCAAC	240572	72768	TGAGCCCTACAGTCCTTATC	285159	117355	GCGTTAGTTAGCCCCATGCA
195986	28182	CAGAGGGGATCCAGTCCCAA	240573	72769	TTGAGCCCTACAGTCCTTAT	285160	117356	AGCGTTAGTTAGCCCCATGC
195987	28183	CCAGAGGGGATCCAGTCCCA	240574	72770	CTTGAGCCCTACAGTCCTTA	285161	117357	AAGCGTTAGTTAGCCCCATG
195988	28184	CCCAGAGGGGATCCAGTCCC	240575	72771	GCTTGAGCCCTACAGTCCTT	285162	117358	GAAGCGTTAGTTAGCCCCAT
195989	28185	TCCCAGAGGGGATCCAGTCC	240576	72772	AGCTTGAGCCCTACAGTCCT	285163	117359	GGAAGCGTTAGTTAGCCCCA
195990	28186	TTCCCAGAGGGGATCCAGTC	240577	72773	CAGCTTGAGCCCTACAGTCC	285164	117360	AGGAAGCGTTAGTTAGCCCC
195991	28187	CTTCCCAGAGGGGATCCAGT	240578	72774	CCAGCTTGAGCCCTACAGTC	285165	117361	GAGGAAGCGTTAGTTAGCCC
195992	28188	ACTTCCCAGAGGGGATCCAG	240579	72775	CCCAGCTTGAGCCCTACAGT	285166	117362	TGAGGAAGCGTTAGTTAGCC
195993	28189	GACTTCCCAGAGGGGATCCA	240580	72776	CCCCAGCTTGAGCCCTACAG	285167	117363	GTGAGGAAGCGTTAGTTAGC
195994	28190	TGACTTCCCAGAGGGGATCC	240581	72777	TCCCCAGCTTGAGCCCTACA	285168	117364	GGTGAGGAAGCGTTAGTTAG
195995	28191	CTGACTTCCCAGAGGGGATC	240582	72778	GTCCCCAGCTTGAGCCCTAC	285169	117365	TGGTGAGGAAGCGTTAGTTA
195996	28192	TCTGACTTCCCAGAGGGGAT	240583	72779	TGTCCCCAGCTTGAGCCCTA	285170	117366	CTGGTGAGGAAGCGTTAGTT
195997	28193	GTCTGACTTCCCAGAGGGGA	240584	72780	CTGTCCCCAGCTTGAGCCCT	285171	117367	ACTGGTGAGGAAGCGTTAGT
195998	28194	GGTCTGACTTCCCAGAGGGG	240585	72781	TCTGTCCCCAGCTTGAGCCC	285172	117368	CACTGGTGAGGAAGCGTTAG
195999	28195	TGGTCTGACTTCCCAGAGGG	240586	72782	ATCTGTCCCCAGCTTGAGCC	285173	117369	ACACTGGTGAGGAAGCGTTA
196000	28196	CTGGTCTGACTTCCCAGAGG	240587	72783	AATCTGTCCCCAGCTTGAGC	285174	117370	GACACTGGTGAGGAAGCGTT
196001	28197	CCTGGTCTGACTTCCCAGAG	240588	72784	CAATCTGTCCCCAGCTTGAG	285175	117371	AGACACTGGTGAGGAAGCGT
196002	28198	GCCTGGTCTGACTTCCCAGA	240589	72785	CCAATCTGTCCCCAGCTTGA	285176	117372	CAGACACTGGTGAGGAAGCG
196003	28199	AGCCTGGTCTGACTTCCCAG	240590	72786	CCCAATCTGTCCCCAGCTTG	285177	117373	GCAGACACTGGTGAGGAAGC
196004	28200	TAGCCTGGTCTGACTTCCCA	240591	72787	CCCCAATCTGTCCCCAGCTT	285178	117374	AGCAGACACTGGTGAGGAAG
196005	28201	CTAGCCTGGTCTGACTTCCC	240592	72788	TCCCCAATCTGTCCCCAGCT	285179	117375	TAGCAGACACTGGTGAGGAA
196006	28202	CCTAGCCTGGTCTGACTTCC	240593	72789	TTCCCCAATCTGTCCCCAGC	285180	117376	TTAGCAGACACTGGTGAGGA
196007	28203	CCCTAGCCTGGTCTGACTTC	240594	72790	TTTCCCCAATCTGTCCCCAG	285181	117377	CTTAGCAGACACTGGTGAGG
196008	28204	GCCCTAGCCTGGTCTGACTT	240595	72791	CTTTCCCCAATCTGTCCCCA	285182	117378	ACTTAGCAGACACTGGTGAG
196009	28205	TGCCCTAGCCTGGTCTGACT	240596	72792	CCTTTCCCCAATCTGTCCCC	285183	117379	CACTTAGCAGACACTGGTGA
196010	28206	CTGCCCTAGCCTGGTCTGAC	240597	72793	CCCTTTCCCCAATCTGTCCC	285184	117380	ACACTTAGCAGACACTGGTG
196011	28207	CCTGCCCTAGCCTGGTCTGA	240598	72794	CCCCTTTCCCCAATCTGTCC	285185	117381	GACACTTAGCAGACACTGGT
196012	28208	ACCTGCCCTAGCCTGGTCTG	240599	72795	CCCCCTTTCCCCAATCTGTC	285186	117382	AGACACTTAGCAGACACTGG
196013	28209	GACCTGCCCTAGCCTGGTCT	240600	72796	TCCCCCTTTCCCCAATCTGT	285187	117383	GAGACACTTAGCAGACACTG
196014	28210	GGACCTGCCCTAGCCTGGTC	240601	72797	GTCCCCCTTTCCCCAATCTG	285188	117384	GGAGACACTTAGCAGACACT
196015	28211	AGGACCTGCCCTAGCCTGGT	240602	72798	GGTCCCCCTTTCCCCAATCT	285189	117385	AGGAGACACTTAGCAGACAC
196016	28212	AAGGACCTGCCCTAGCCTGG	240603	72799	TGGTCCCCCTTTCCCCAATC	285190	117386	GAGGAGACACTTAGCAGACA
196017	28213	CAAGGACCTGCCCTAGCCTG	240604	72800	ATGGTCCCCCTTTCCCCAAT	285191	117387	AGAGGAGACACTTAGCAGAC
196018	28214	TCAAGGACCTGCCCTAGCCT	240605	72801	GATGGTCCCCCTTTCCCCAA	285192	117388	CAGAGGAGACACTTAGCAGA
196019	28215	TTCAAGGACCTGCCCTAGCC	240606	72802	TGATGGTCCCCCTTTCCCCA	285193	117389	ACAGAGGAGACACTTAGCAG
196020	28216	CTTCAAGGACCTGCCCTAGC	240607	72803	ATGATGGTCCCCCTTTCCCC	285194	117390	GACAGAGGAGACACTTAGCA
196021	28217	GCTTCAAGGACCTGCCCTAG	240608	72804	CATGATGGTCCCCCTTTCCC	285195	117391	AGACAGAGGAGACACTTAGC
196022	28218	GGCTTCAAGGACCTGCCCTA	240609	72805	GCATGATGGTCCCCCTTTCC	285196	117392	GAGACAGAGGAGACACTTAG
196023	28219	TGGCTTCAAGGACCTGCCCT	240610	72806	GGCATGATGGTCCCCCTTTC	285197	117393	GGAGACAGAGGAGACACTTA
196024	28220	ATGGCTTCAAGGACCTGCCC	240611	72807	GGGCATGATGGTCCCCCTTT	285198	117394	GGGAGACAGAGGAGACACTT
196025	28221	GATGGCTTCAAGGACCTGCC	240612	72808	TGGGCATGATGGTCCCCCTT	285199	117395	TGGGAGACAGAGGAGACACT
196026	28222	TGATGGCTTCAAGGACCTGC	240613	72809	ATGGGCATGATGGTCCCCCT	285200	117396	GTGGGAGACAGAGGAGACAC

196027	28223	CTGATGGCTTCAAGGACCTG	240614	72810	TATGGGCATGATGGTCCCCC	285201	117397	CGTGGGAGACAGAGGAGACA
196028	28224	CCTGATGGCTTCAAGGACCT	240615	72811	ATATGGGCATGATGGTCCCC	285202	117398	GCGTGGGAGACAGAGGAGAC
196029	28225	TCCTGATGGCTTCAAGGACC	240616	72812	TATATGGGCATGATGGTCCC	285203	117399	GGCGTGGGAGACAGAGGAGA
196030	28226	TTCCTGATGGCTTCAAGGAC	240617	72813	CTATATGGGCATGATGGTCC	285204	117400	GGGCGTGGGAGACAGAGGAG
196031	28227	TTTCCTGATGGCTTCAAGGA	240618	72814	TCTATATGGGCATGATGGTC	285205	117401	AGGGCGTGGGAGACAGAGGA
196032	28228	TTTTCCTGATGGCTTCAAGG	240619	72815	ATCTATATGGGCATGATGGT	285206	117402	CAGGGCGTGGGAGACAGAGG
196033	28229	CTTTTCCTGATGGCTTCAAG	240620	72816	CATCTATATGGGCATGATGG	285207	117403	GCAGGGCGTGGGAGACAGAG
196034	28230	GCTTTTCCTGATGGCTTCAA	240621	72817	ACATCTATATGGGCATGATG	285208	117404	AGCAGGGCGTGGGAGACAGA
196035	28231	GGCTTTTCCTGATGGCTTCA	240622	72818	GACATCTATATGGGCATGAT	285209	117405	GAGCAGGGCGTGGGAGACAG
196036	28232	AGGCTTTTCCTGATGGCTTC	240623	72819	GGACATCTATATGGGCATGA	285210	117406	AGAGCAGGGCGTGGGAGACA
196037	28233	GAGGCTTTTCCTGATGGCTT	240624	72820	GGGACATCTATATGGGCATG	285211	117407	GAGAGCAGGGCGTGGGAGAC
196038	28234	AGAGGCTTTTCCTGATGGCT	240625	72821	AGGGACATCTATATGGGCAT	285212	117408	GGAGAGCAGGGCGTGGGAGA
196039	28235	CAGAGGCTTTTCCTGATGGC	240626	72822	CAGGGACATCTATATGGGCA	285213	117409	AGGAGAGCAGGGCGTGGGAG
196040	28236	CCAGAGGCTTTTCCTGATGG	240627	72823	ACAGGGACATCTATATGGGC	285214	117410	CAGGAGAGCAGGGCGTGGGA
196041	28237	TCCAGAGGCTTTTCCTGATG	240628	72824	CACAGGGACATCTATATGGG	285215	117411	ACAGGAGAGCAGGGCGTGGG
196042	28238	CTCCAGAGGCTTTTCCTGAT	240629	72825	GCACAGGGACATCTATATGG	285216	117412	GACAGGAGAGCAGGGCGTGG
196043	28239	GCTCCAGAGGCTTTTCCTGA	240630	72826	GGCACAGGGACATCTATATG	285217	117413	GGACAGGAGAGCAGGGCGTG
196044	28240	GGCTCCAGAGGCTTTTCCTG	240631	72827	GGGCACAGGGACATCTATAT	285218	117414	GGGACAGGAGAGCAGGGCGT
196045	28241	TGGCTCCAGAGGCTTTTCCT	240632	72828	AGGGCACAGGGACATCTATA	285219	117415	GGGGACAGGAGAGCAGGGCG
196046	28242	CTGGCTCCAGAGGCTTTTCC	240633	72829	CAGGGCACAGGGACATCTAT	285220	117416	GGGGGACAGGAGAGCAGGGC
196047	28243	TCTGGCTCCAGAGGCTTTTC	240634	72830	CCAGGGCACAGGGACATCTA	285221	117417	GGGGGGACAGGAGAGCAGGG
196048	28244	TTCTGGCTCCAGAGGCTTTT	240635	72831	GCCAGGGCACAGGGACATCT	285222	117418	TGGGGGGACAGGAGAGCAGG
196049	28245	TTTCTGGCTCCAGAGGCTTT	240636	72832	TGCCAGGGCACAGGGACATC	285223	117419	CTGGGGGGACAGGAGAGCAG
196050	28246	GTTTCTGGCTCCAGAGGCTT	240637	72833	CTGCCAGGGCACAGGGACAT	285224	117420	ACTGGGGGGACAGGAGAGCA
196051	28247	TGTTTCTGGCTCCAGAGGCT	240638	72834	ACTGCCAGGGCACAGGGACA	285225	117421	AACTGGGGGGACAGGAGAGC
196052	28248	TTGTTTCTGGCTCCAGAGGC	240639	72835	GACTGCCAGGGCACAGGGAC	285226	117422	AAACTGGGGGGACAGGAGAG
196053	28249	TTTGTTTCTGGCTCCAGAGG	240640	72836	TGACTGCCAGGGCACAGGGA	285227	117423	CAAACTGGGGGGACAGGAGA
196054	28250	TTTTGTTTCTGGCTCCAGAG	240641	72837	TTGACTGCCAGGGCACAGGG	285228	117424	ACAAACTGGGGGGACAGGAG
196055	28251	GTTTTGTTTCTGGCTCCAGA	240642	72838	CTTGACTGCCAGGGCACAGG	285229	117425	GACAAACTGGGGGGACAGGA
196056	28252	TGTTTTGTTTCTGGCTCCAG	240643	72839	CCTTGACTGCCAGGGCACAG	285230	117426	AGACAAACTGGGGGGACAGG
196057	28253	TTGTTTTGTTTCTGGCTCCA	240644	72840	GCCTTGACTGCCAGGGCACA	285231	117427	CAGACAAACTGGGGGGACAG
196058	28254	TTTGTTTTGTTTCTGGCTCC	240645	72841	AGCCTTGACTGCCAGGGCAC	285232	117428	GCAGACAAACTGGGGGGACA
196059	28255	TTTTGTTTTGTTTCTGGCTC	240646	72842	CAGCCTTGACTGCCAGGGCA	285233	117429	AGCAGACAAACTGGGGGGAC
196060	28256	TTTTTGTTTTGTTTCTGGCT	240647	72843	GCAGCCTTGACTGCCAGGGC	285234	117430	CAGCAGACAAACTGGGGGGA
196061	28257	TTTTTTGTTTTGTTTCTGGC	240648	72844	AGCAGCCTTGACTGCCAGGG	285235	117431	ACAGCAGACAAACTGGGGGG
196062	28258	TTTTTTTGTTTTGTTTCTGG	240649	72845	CAGCAGCCTTGACTGCCAGG	285236	117432	CACAGCAGACAAACTGGGGG
196063	28259	TTTTTTTTGTTTTGTTTCTG	240650	72846	TCAGCAGCCTTGACTGCCAG	285237	117433	TCACAGCAGACAAACTGGGG
196064	28260	TTTTTTTTTGTTTTGTTTCT	240651	72847	TTCAGCAGCCTTGACTGCCA	285238	117434	CTCACAGCAGACAAACTGGG
196065	28261	TTTTTTTTTTGTTTTGTTTC	240652	72848	TTTCAGCAGCCTTGACTGCC	285239	117435	CCTCACAGCAGACAAACTGG
196066	28262	ATTTTTTTTTTGTTTTGTTT	240653	72849	TTTTCAGCAGCCTTGACTGC	285240	117436	CCCTCACAGCAGACAAACTG
196067	28263	CATTTTTTTTTTGTTTTGTT	240654	72850	TTTTTCAGCAGCCTTGACTG	285241	117437	CCCCTCACAGCAGACAAACT
196068	28264	CCATTTTTTTTTTGTTTTGT	240655	72851	ATTTTTCAGCAGCCTTGACT	285242	117438	TCCCCTCACAGCAGACAAAC
196069	28265	ACCATTTTTTTTTTGTTTTG	240656	72852	TATTTTTCAGCAGCCTTGAC	285243	117439	GTCCCCTCACAGCAGACAAA
196070	28266	CACCATTTTTTTTTTGTTTT	240657	72853	TTATTTTTCAGCAGCCTTGA	285244	117440	TGTCCCCTCACAGCAGACAA
196071	28267	ACACCATTTTTTTTTTGTTT	240658	72854	GTTATTTTTCAGCAGCCTTG	285245	117441	CTGTCCCCTCACAGCAGACA
196072	28268	AACACCATTTTTTTTTTGTT	240659	72855	TGTTATTTTTCAGCAGCCTT	285246	117442	TCTGTCCCCTCACAGCAGAC
196073	28269	TAACACCATTTTTTTTTTGT	240660	72856	TTGTTATTTTTCAGCAGCCT	285247	117443	TTCTGTCCCCTCACAGCAGA
196074	28270	TTAACACCATTTTTTTTTTG	240661	72857	TTTGTTATTTTTCAGCAGCC	285248	117444	CTTCTGTCCCCTCACAGCAG
196075	28271	GTTAACACCATTTTTTTTTT	240662	72858	TTTTGTTATTTTTCAGCAGC	285249	117445	TCTTCTGTCCCCTCACAGCA
196076	28272	AGTTAACACCATTTTTTTTT	240663	72859	GTTTTGTTATTTTTCAGCAG	285250	117446	CTCTTCTGTCCCCTCACAGC
196077	28273	TAGTTAACACCATTTTTTTT	240664	72860	GGTTTTGTTATTTTTCAGCA	285251	117447	CCTCTTCTGTCCCCTCACAG
196078	28274	TTAGTTAACACCATTTTTTT	240665	72861	GGGTTTTGTTATTTTTCAGC	285252	117448	ACCTCTTCTGTCCCCTCACA
196079	28275	TTTAGTTAACACCATTTTTT	240666	72862	TGGGTTTTGTTATTTTTCAG	285253	117449	CACCTCTTCTGTCCCCTCAC
196080	28276	GTTTAGTTAACACCATTTTT	240667	72863	CTGGGTTTTGTTATTTTTCA	285254	117450	ACACCTCTTCTGTCCCCTCA
196081	28277	AGTTTAGTTAACACCATTTT	240668	72864	TCTGGGTTTTGTTATTTTTC	285255	117451	CACACCTCTTCTGTCCCCTC
196082	28278	GAGTTTAGTTAACACCATTT	240669	72865	TTCTGGGTTTTGTTATTTTT	285256	117452	ACACACCTCTTCTGTCCCCT
196083	28279	TGAGTTTAGTTAACACCATT	240670	72866	CTTCTGGGTTTTGTTATTTT	285257	117453	CACACACCTCTTCTGTCCCC
196084	28280	CTGAGTTTAGTTAACACCAT	240671	72867	ACTTCTGGGTTTTGTTATTT	285258	117454	GCACACACCTCTTCTGTCCC
196085	28281	ACTGAGTTTAGTTAACACCA	240672	72868	GACTTCTGGGTTTTGTTATT	285259	117455	GGCACACACCTCTTCTGTCC
196086	28282	GACTGAGTTTAGTTAACACC	240673	72869	AGACTTCTGGGTTTTGTTAT	285260	117456	CGGCACACACCTCTTCTGTC
196087	28283	AGACTGAGTTTAGTTAACAC	240674	72870	CAGACTTCTGGGTTTTGTTA	285261	117457	GCGGCACACACCTCTTCTGT
196088	28284	GAGACTGAGTTTAGTTAACA	240675	72871	GCAGACTTCTGGGTTTTGTT	285262	117458	GGCGGCACACACCTCTTCTG
196089	28285	TGAGACTGAGTTTAGTTAAC	240676	72872	CGCAGACTTCTGGGTTTTGT	285263	117459	GGGCGGCACACACCTCTTCT
196090	28286	TTGAGACTGAGTTTAGTTAA	240677	72873	ACGCAGACTTCTGGGTTTTG	285264	117460	GGGGCGGCACACACCTCTTC
196091	28287	TTTGAGACTGAGTTTAGTTA	240678	72874	CACGCAGACTTCTGGGTTTT	285265	117461	GGGGGCGGCACACACCTCTT
196092	28288	ATTTGAGACTGAGTTTAGTT	240679	72875	TCACGCAGACTTCTGGGTTT	285266	117462	TGGGGGCGGCACACACCTCT
196093	28289	GATTTGAGACTGAGTTTAGT	240680	72876	ATCACGCAGACTTCTGGGTT	285267	117463	GTGGGGGCGGCACACACCTC
196094	28290	GGATTTGAGACTGAGTTTAG	240681	72877	CATCACGCAGACTTCTGGGT	285268	117464	GGTGGGGGCGGCACACACCT
196095	28291	AGGATTTGAGACTGAGTTTA	240682	72878	GCATCACGCAGACTTCTGGG	285269	117465	GGGTGGGGGCGGCACACACC
196096	28292	CAGGATTTGAGACTGAGTTT	240683	72879	AGCATCACGCAGACTTCTGG	285270	117466	GGGGTGGGGGCGGCACACAC
196097	28293	TCAGGATTTGAGACTGAGTT	240684	72880	CAGCATCACGCAGACTTCTG	285271	117467	AGGGGTGGGGGCGGCACACA
196098	28294	TTCAGGATTTGAGACTGAGT	240685	72881	GCAGCATCACGCAGACTTCT	285272	117468	CAGGGGTGGGGGCGGCACAC

196099	28295	ATTCAGGATTTGAGACTGAG	240686	72882	GGCAGCATCACGCAGACTTC	285273	117469	GCAGGGGTGGGGGCGGCACA
196100	28296	TATTCAGGATTTGAGACTGA	240687	72883	AGGCAGCATCACGCAGACTT	285274	117470	GGCAGGGGTGGGGGCGGCAC
196101	28297	CTATTCAGGATTTGAGACTG	240688	72884	GAGGCAGCATCACGCAGACT	285275	117471	GGGCAGGGGTGGGGGCGGCA
196102	28298	CCTATTCAGGATTTGAGACT	240689	72885	AGAGGCAGCATCACGCAGAC	285276	117472	CGGGCAGGGGTGGGGGCGGC
196103	28299	TCCTATTCAGGATTTGAGAC	240690	72886	GAGAGGCAGCATCACGCAGA	285277	117473	CCGGGCAGGGGTGGGGGCGG
196104	28300	GTCCTATTCAGGATTTGAGA	240691	72887	GGAGAGGCAGCATCACGCAG	285278	117474	CCCGGGCAGGGGTGGGGGCG
196105	28301	AGTCCTATTCAGGATTTGAG	240692	72888	TGGAGAGGCAGCATCACGCA	285279	117475	GCCCGGGCAGGGGTGGGGGC
196106	28302	GAGTCCTATTCAGGATTTGA	240693	72889	ATGGAGAGGCAGCATCACGC	285280	117476	GGCCCGGGCAGGGGTGGGGG
196107	28303	TGAGTCCTATTCAGGATTTG	240694	72890	AATGGAGAGGCAGCATCACG	285281	117477	GGGCCCGGGCAGGGGTGGGG
196108	28304	TTGAGTCCTATTCAGGATTT	240695	72891	AAATGGAGAGGCAGCATCAC	285282	117478	AGGGCCCGGGCAGGGGTGGG
196109	28305	CTTGAGTCCTATTCAGGATT	240696	72892	CAAATGGAGAGGCAGCATCA	285283	117479	AAGGGCCCGGGCAGGGGTGG
196110	28306	ACTTGAGTCCTATTCAGGAT	240697	72893	ACAAATGGAGAGGCAGCATC	285284	117480	CAAGGGCCCGGGCAGGGGTG
196111	28307	GACTTGAGTCCTATTCAGGA	240698	72894	GACAAATGGAGAGGCAGCAT	285285	117481	ACAAGGGCCCGGGCAGGGGT
196112	28308	TGACTTGAGTCCTATTCAGG	240699	72895	GGACAAATGGAGAGGCAGCA	285286	117482	AACAAGGGCCCGGGCAGGGG
196113	28309	TTGACTTGAGTCCTATTCAG	240700	72896	TGGACAAATGGAGAGGCAGC	285287	117483	GAACAAGGGCCCGGGCAGGG
196114	28310	CTTGACTTGAGTCCTATTCA	240701	72897	TTGGACAAATGGAGAGGCAG	285288	117484	GGAACAAGGGCCCGGGCAGG
196115	28311	GCTTGACTTGAGTCCTATTC	240702	72898	TTTGGACAAATGGAGAGGCA	285289	117485	AGGAACAAGGGCCCGGGCAG
196116	28312	TGCTTGACTTGAGTCCTATT	240703	72899	CTTTGGACAAATGGAGAGGC	285290	117486	CAGGAACAAGGGCCCGGGCA
196117	28313	TTGCTTGACTTGAGTCCTAT	240704	72900	GCTTTGGACAAATGGAGAGG	285291	117487	CCAGGAACAAGGGCCCGGGC
196118	28314	TTTGCTTGACTTGAGTCCTA	240705	72901	GGCTTTGGACAAATGGAGAG	285292	117488	CCCAGGAACAAGGGCCCGGG
196119	28315	TTTTGCTTGACTTGAGTCCT	240706	72902	AGGCTTTGGACAAATGGAGA	285293	117489	TCCCAGGAACAAGGGCCCGG
196120	28316	ATTTTGCTTGACTTGAGTCC	240707	72903	AAGGCTTTGGACAAATGGAG	285294	117490	ATCCCAGGAACAAGGGCCCG
196121	28317	TATTTTGCTTGACTTGAGTC	240708	72904	GAAGGCTTTGGACAAATGGA	285295	117491	AATCCCAGGAACAAGGGCCC
196122	28318	TTATTTTGCTTGACTTGAGT	240709	72905	AGAAGGCTTTGGACAAATGG	285296	117492	CAATCCCAGGAACAAGGGCC
196123	28319	ATTATTTTGCTTGACTTGAG	240710	72906	AAGAAGGCTTTGGACAAATG	285297	117493	GCAATCCCAGGAACAAGGGC
196124	28320	AATTATTTTGCTTGACTTGA	240711	72907	CAAGAAGGCTTTGGACAAAT	285298	117494	AGCAATCCCAGGAACAAGGG
196125	28321	TAATTATTTTGCTTGACTTG	240712	72908	GCAAGAAGGCTTTGGACAAA	285299	117495	CAGCAATCCCAGGAACAAGG
196126	28322	TTAATTATTTTGCTTGACTT	240713	72909	CGCAAGAAGGCTTTGGACAA	285300	117496	ACAGCAATCCCAGGAACAAG
196127	28323	TTTAATTATTTTGCTTGACT	240714	72910	CCGCAAGAAGGCTTTGGACA	285301	117497	AACAGCAATCCCAGGAACAA
196128	28324	CTTTAATTATTTTGCTTGAC	240715	72911	GCCGCAAGAAGGCTTTGGAC	285302	117498	AAACAGCAATCCCAGGAACA
196129	28325	CCTTTAATTATTTTGCTTGA	240716	72912	TGCCGCAAGAAGGCTTTGGA	285303	117499	AAAACAGCAATCCCAGGAAC
196130	28326	TCCTTTAATTATTTTGCTTG	240717	72913	CTGCCGCAAGAAGGCTTTGG	285304	117500	GAAAACAGCAATCCCAGGAA
196131	28327	CTCCTTTAATTATTTTGCTT	240718	72914	ACTGCCGCAAGAAGGCTTTG	285305	117501	TGAAAACAGCAATCCCAGGA
196132	28328	ACTCCTTTAATTATTTTGCT	240719	72915	AACTGCCGCAAGAAGGCTTT	285306	117502	CTGAAAACAGCAATCCCAGG
196133	28329	AACTCCTTTAATTATTTTGC	240720	72916	AAACTGCCGCAAGAAGGCTT	285307	117503	GCTGAAAACAGCAATCCCAG
196134	28330	TAACTCCTTTAATTATTTTG	240721	72917	CAAACTGCCGCAAGAAGGCT	285308	117504	AGCTGAAAACAGCAATCCCA
196135	28331	CTAACTCCTTTAATTATTTT	240722	72918	GCAAACTGCCGCAAGAAGGC	285309	117505	CAGCTGAAAACAGCAATCCC
196136	28332	GCTAACTCCTTTAATTATTT	240723	72919	TGCAAACTGCCGCAAGAAGG	285310	117506	ACAGCTGAAAACAGCAATCC
196137	28333	TGCTAACTCCTTTAATTATT	240724	72920	CTGCAAACTGCCGCAAGAAG	285311	117507	AACAGCTGAAAACAGCAATC
196138	28334	TTGCTAACTCCTTTAATTAT	240725	72921	CCTGCAAACTGCCGCAAGAA	285312	117508	AAACAGCTGAAAACAGCAAT
196139	28335	TTTGCTAACTCCTTTAATTA	240726	72922	GCCTGCAAACTGCCGCAAGA	285313	117509	CAAACAGCTGAAAACAGCAA
196140	28336	CTTTGCTAACTCCTTTAATT	240727	72923	AGCCTGCAAACTGCCGCAAG	285314	117510	TCAAACAGCTGAAAACAGCA
196141	28337	CCTTTGCTAACTCCTTTAAT	240728	72924	AAGCCTGCAAACTGCCGCAA	285315	117511	CTCAAACAGCTGAAAACAGC
196142	28338	CCCTTTGCTAACTCCTTTAA	240729	72925	AAAGCCTGCAAACTGCCGCA	285316	117512	GCTCAAACAGCTGAAAACAG
196143	28339	GCCCTTTGCTAACTCCTTTA	240730	72926	AAAAGCCTGCAAACTGCCGC	285317	117513	AGCTCAAACAGCTGAAAACA
196144	28340	TGCCCTTTGCTAACTCCTTT	240731	72927	CAAAAGCCTGCAAACTGCCG	285318	117514	AAGCTCAAACAGCTGAAAAC
196145	28341	TTGCCCTTTGCTAACTCCTT	240732	72928	GCAAAAGCCTGCAAACTGCC	285319	117515	AAAGCTCAAACAGCTGAAAA
196146	28342	CTTGCCCTTTGCTAACTCCT	240733	72929	TGCAAAAGCCTGCAAACTGC	285320	117516	CAAAGCTCAAACAGCTGAAA
196147	28343	ACTTGCCCTTTGCTAACTCC	240734	72930	TTGCAAAAGCCTGCAAACTG	285321	117517	TCAAAGCTCAAACAGCTGAA
196148	28344	GACTTGCCCTTTGCTAACTC	240735	72931	TTTGCAAAAGCCTGCAAACT	285322	117518	ATCAAAGCTCAAACAGCTGA
196149	28345	TGACTTGCCCTTTGCTAACT	240736	72932	TTTTGCAAAAGCCTGCAAAC	285323	117519	GATCAAAGCTCAAACAGCTG
196150	28346	CTGACTTGCCCTTTGCTAAC	240737	72933	CTTTTGCAAAAGCCTGCAAA	285324	117520	GGATCAAAGCTCAAACAGCT
196151	28347	TCTGACTTGCCCTTTGCTAA	240738	72934	GCTTTTGCAAAAGCCTGCAA	285325	117521	AGGATCAAAGCTCAAACAGC
196152	28348	CTCTGACTTGCCCTTTGCTA	240739	72935	AGCTTTTGCAAAAGCCTGCA	285326	117522	CAGGATCAAAGCTCAAACAG
196153	28349	TCTCTGACTTGCCCTTTGCT	240740	72936	GAGCTTTTGCAAAAGCCTGC	285327	117523	CCAGGATCAAAGCTCAAACA
196154	28350	CTCTCTGACTTGCCCTTTGC	240741	72937	GGAGCTTTTGCAAAAGCCTG	285328	117524	ACCAGGATCAAAGCTCAAAC
196155	28351	TCTCTCTGACTTGCCCTTTG	240742	72938	TGGAGCTTTTGCAAAAGCCT	285329	117525	AACCAGGATCAAAGCTCAAA
196156	28352	GTCTCTCTGACTTGCCCTTT	240743	72939	CTGGAGCTTTTGCAAAAGCC	285330	117526	GAACCAGGATCAAAGCTCAA
196157	28353	GGTCTCTCTGACTTGCCCTT	240744	72940	CCTGGAGCTTTTGCAAAAGC	285331	117527	AGAACCAGGATCAAAGCTCA
196158	28354	CGGTCTCTCTGACTTGCCCT	240745	72941	TCCTGGAGCTTTTGCAAAAG	285332	117528	GAGAACCAGGATCAAAGCTC
196159	28355	TCGGTCTCTCTGACTTGCCC	240746	72942	GTCCTGGAGCTTTTGCAAAA	285333	117529	AGAGAACCAGGATCAAAGCT
196160	28356	CTCGGTCTCTCTGACTTGCC	240747	72943	GGTCCTGGAGCTTTTGCAAA	285334	117530	CAGAGAACCAGGATCAAAGC
196161	28357	GCTCGGTCTCTCTGACTTGC	240748	72944	TGGTCCTGGAGCTTTTGCAA	285335	117531	CCAGAGAACCAGGATCAAAG
196162	28358	TGCTCGGTCTCTCTGACTTG	240749	72945	TTGGTCCTGGAGCTTTTGCA	285336	117532	GCCAGAGAACCAGGATCAAA
196163	28359	TTGCTCGGTCTCTCTGACTT	240750	72946	CTTGGTCCTGGAGCTTTTGC	285337	117533	AGCCAGAGAACCAGGATCAA
196164	28360	GTTGCTCGGTCTCTCTGACT	240751	72947	CCTTGGTCCTGGAGCTTTTG	285338	117534	AAGCCAGAGAACCAGGATCA
196165	28361	TGTTGCTCGGTCTCTCTGAC	240752	72948	TCCTTGGTCCTGGAGCTTTT	285339	117535	GAAGCCAGAGAACCAGGATC
196166	28362	GTGTTGCTCGGTCTCTCTGA	240753	72949	CTCCTTGGTCCTGGAGCTTT	285340	117536	GGAAGCCAGAGAACCAGGAT
196167	28363	GGTGTTGCTCGGTCTCTCTG	240754	72950	GCTCCTTGGTCCTGGAGCTT	285341	117537	AGGAAGCCAGAGAACCAGGA
196168	28364	TGGTGTTGCTCGGTCTCTCT	240755	72951	AGCTCCTTGGTCCTGGAGCT	285342	117538	GAGGAAGCCAGAGAACCAGG
196169	28365	TTGGTGTTGCTCGGTCTCTC	240756	72952	TAGCTCCTTGGTCCTGGAGC	285343	117539	TGAGGAAGCCAGAGAACCAG
196170	28366	ATTGGTGTTGCTCGGTCTCT	240757	72953	ATAGCTCCTTGGTCCTGGAG	285344	117540	TTGAGGAAGCCAGAGAACCA

196171	28367	CATTGGTGTTGCTCGGTCTC	240758	72954	CATAGCTCCTTGGTCCTGGA	285345	117541	TTTGAGGAAGCCAGAGAACC
196172	28368	ACATTGGTGTTGCTCGGTCT	240759	72955	ACATAGCTCCTTGGTCCTGG	285346	117542	CTTTGAGGAAGCCAGAGAAC
196173	28369	GACATTGGTGTTGCTCGGTC	240760	72956	AACATAGCTCCTTGGTCCTG	285347	117543	ACTTTGAGGAAGCCAGAGAA
196174	28370	AGACATTGGTGTTGCTCGGT	240761	72957	GAACATAGCTCCTTGGTCCT	285348	117544	CACTTTGAGGAAGCCAGAAG
196175	28371	AAGACATTGGTGTTGCTCGG	240762	72958	TGAACATAGCTCCTTGGTCC	285349	117545	TCACTTTGAGGAAGCCAGAG
196176	28372	GAAGACATTGGTGTTGCTCG	240763	72959	ATGAACATAGCTCCTTGGTC	285350	117546	CTCACTTTGAGGAAGCCAGA
196177	28373	GGAAGACATTGGTGTTGCTC	240764	72960	CATGAACATAGCTCCTTGGT	285351	117547	GCTCACTTTGAGGAAGCCAG
196178	28374	CGGAAGACATTGGTGTTGCT	240765	72961	GCATGAACATAGCTCCTTGG	285352	117548	AGCTCACTTTGAGGAAGCCA
196179	28375	CCGGAAGACATTGGTGTTGC	240766	72962	AGCATGAACATAGCTCCTTG	285353	117549	GAGCTCACTTTGAGGAAGCC
196180	28376	CCCGGAAGACATTGGTGTTG	240767	72963	CAGCATGAACATAGCTCCTT	285354	117550	CGAGCTCACTTTGAGGAAGC
196181	28377	TCCCGGAAGACATTGGTGTT	240768	72964	CCAGCATGAACATAGCTCCT	285355	117551	CCGAGCTCACTTTGAGGAAG
196182	28378	CTCCCGGAAGACATTGGTGT	240769	72965	TCCAGCATGAACATAGCTCC	285356	117552	GCCGAGCTCACTTTGAGGAA
196183	28379	GCTCCCGGAAGACATTGGTG	240770	72966	TTCCAGCATGAACATAGCTC	285357	117553	GGCCGAGCTCACTTTGAGGA
196184	28380	GGCTCCCGGAAGACATTGGT	240771	72967	CTTCCAGCATGAACATAGCT	285358	117554	TGGCCGAGCTCACTTTGAGG
196185	28381	GGGCTCCCGGAAGACATTGG	240772	72968	GCTTCCAGCATGAACATAGC	285359	117555	CTGGCCGAGCTCACTTTGAG
196186	28382	AGGGCTCCCGGAAGACATTG	240773	72969	AGCTTCCAGCATGAACATAG	285360	117556	TCTGGCCGAGCTCACTTTGA
196187	28383	CAGGGCTCCCGGAAGACATT	240774	72970	AAGCTTCCAGCATGAACATA	285361	117557	CTCTGGCCGAGCTCACTTTG
196188	28384	ACAGGGCTCCCGGAAGACAT	240775	72971	CAAGCTTCCAGCATGAACAT	285362	117558	CCTCTGGCCGAGCTCACTTT
196189	28385	CACAGGGCTCCCGGAAGACA	240776	72972	ACAAGCTTCCAGCATGAACA	285363	117559	TCCTCTGGCCGAGCTCACTT
196190	28386	CCACAGGGCTCCCGGAAGAC	240777	72973	AACAAGCTTCCAGCATGAAC	285364	117560	CTCCTCTGGCCGAGCTCACT
196191	28387	GCCACAGGGCTCCCGGAAGA	240778	72974	GAACAAGCTTCCAGCATGAA	285365	117561	CCTCCTCTGGCCGAGCTCAC
196192	28388	CGCCACAGGGCTCCCGGAAG	240779	72975	TGAACAAGCTTCCAGCATGA	285366	117562	TCCTCCTCTGGCCGAGCTCA
196193	28389	TCGCCACAGGGCTCCCGGAA	240780	72976	CTGAACAAGCTTCCAGCATG	285367	117563	TTCCTCCTCTGGCCGAGCTC
196194	28390	CTCGCCACAGGGCTCCCGGA	240781	72977	CCTGAACAAGCTTCCAGCAT	285368	117564	CTTCCTCCTCTGGCCGAGCT
196195	28391	ACTCGCCACAGGGCTCCCGG	240782	72978	TCCTGAACAAGCTTCCAGCA	285369	117565	CCTTCCTCCTCTGGCCGAGC
196196	28392	CACTCGCCACAGGGCTCCCG	240783	72979	ATCCTGAACAAGCTTCCAGC	285370	117566	GCCTTCCTCCTCTGGCCGAG
196197	28393	TCACTCGCCACAGGGCTCCC	240784	72980	AATCCTGAACAAGCTTCCAG	285371	117567	GGCCTTCCTCCTCTGGCCGA
196198	28394	GTCACTCGCCACAGGGCTCC	240785	72981	TAATCCTGAACAAGCTTCCA	285372	117568	TGGCCTTCCTCCTCTGGCCG
196199	28395	TGTCACTCGCCACAGGGCTC	240786	72982	CTAATCCTGAACAAGCTTCC	285373	117569	ATGGCCTTCCTCCTCTGGCC
196200	28396	CTGTCACTCGCCACAGGGCT	240787	72983	GCTAATCCTGAACAAGCTTC	285374	117570	CATGGCCTTCCTCCTCTGGC
196201	28397	TCTGTCACTCGCCACAGGGC	240788	72984	AGCTAATCCTGAACAAGCTT	285375	117571	ACATGGCCTTCCTCCTCTGG
196202	28398	CTCTGTCACTCGCCACAGGG	240789	72985	CAGCTAATCCTGAACAAGCT	285376	117572	CACATGGCCTTCCTCCTCTG
196203	28399	GCTCTGTCACTCGCCACAGG	240790	72986	ACAGCTAATCCTGAACAAGC	285377	117573	GCACATGGCCTTCCTCCTCT
196204	28400	GGCTCTGTCACTCGCCACAG	240791	72987	AACAGCTAATCCTGAACAAG	285378	117574	AGCACATGGCCTTCCTCCTC
196205	28401	AGGCTCTGTCACTCGCCACA	240792	72988	GAACAGCTAATCCTGAACAA	285379	117575	AAGCACATGGCCTTCCTCCT
196206	28402	CAGGCTCTGTCACTCGCCAC	240793	72989	AGAACAGCTAATCCTGAACA	285380	117576	AAAGCACATGGCCTTCCTCC
196207	28403	CCAGGCTCTGTCACTCGCCA	240794	72990	AAGAACAGCTAATCCTGAAC	285381	117577	GAAAGCACATGGCCTTCCTC
196208	28404	TCCAGGCTCTGTCACTCGCC	240795	72991	AAAGAACAGCTAATCCTGAA	285382	117578	AGAAAGCACATGGCCTTCCT
196209	28405	GTCCAGGCTCTGTCACTCGC	240796	72992	CAAAGAACAGCTAATCCTGA	285383	117579	CAGAAAGCACATGGCCTTCC
196210	28406	AGTCCAGGCTCTGTCACTCG	240797	72993	ACAAAGAACAGCTAATCCTG	285384	117580	CCAGAAAGCACATGGCCTTC
196211	28407	GAGTCCAGGCTCTGTCACTC	240798	72994	CACAAAGAACAGCTAATCCT	285385	117581	ACCAGAAAGCACATGGCCTT
196212	28408	AGAGTCCAGGCTCTGTCACT	240799	72995	CCACAAAGAACAGCTAATCC	285386	117582	AACCAGAAAGCACATGGCCT
196213	28409	CAGAGTCCAGGCTCTGTCAC	240800	72996	CCCACAAAGAACAGCTAATC	285387	117583	CAACCAGAAAGCACATGGCC
196214	28410	CCAGAGTCCAGGCTCTGTCA	240801	72997	TCCCACAAAGAACAGCTAAT	285388	117584	TCAACCAGAAAGCACATGGC
196215	28411	TCCAGAGTCCAGGCTCTGTC	240802	72998	ATCCCACAAAGAACAGCTAA	285389	117585	TTCAACCAGAAAGCACATGG
196216	28412	CTCCAGAGTCCAGGCTCTGT	240803	72999	CATCCCACAAAGAACAGCTA	285390	117586	CTTCAACCAGAAAGCACATG
196217	28413	ACTCCAGAGTCCAGGCTCTG	240804	73000	CCATCCCACAAAGAACAGCT	285391	117587	ACTTCAACCAGAAAGCACAT
196218	28414	TACTCCAGAGTCCAGGCTCT	240805	73001	CCCATCCCACAAAGAACAGC	285392	117588	GACTTCAACCAGAAAGCACA
196219	28415	CTACTCCAGAGTCCAGGCTC	240806	73002	ACCCATCCCACAAAGAACAG	285393	117589	TGACTTCAACCAGAAAGCAC
196220	28416	TCTACTCCAGAGTCCAGGCT	240807	73003	CACCCATCCCACAAAGAACA	285394	117590	TTGACTTCAACCAGAAAGCA
196221	28417	TTCTACTCCAGAGTCCAGGC	240808	73004	GCACCCATCCCACAAAGAAC	285395	117591	CTTGACTTCAACCAGAAAGC
196222	28418	GTTCTACTCCAGAGTCCAGG	240809	73005	TGCACCCATCCCACAAAGAA	285396	117592	ACTTGACTTCAACCAGAAAG
196223	28419	AGTTCTACTCCAGAGTCCAG	240810	73006	CTGCACCCATCCCACAAAGA	285397	117593	GACTTGACTTCAACCAGAAA
196224	28420	GAGTTCTACTCCAGAGTCCA	240811	73007	GCTGCACCCATCCCACAAAG	285398	117594	AGACTTGACTTCAACCAGAA
196225	28421	TGAGTTCTACTCCAGAGTCC	240812	73008	GGCTGCACCCATCCCACAAA	285399	117595	CAGACTTGACTTCAACCAGA
196226	28422	ATGAGTTCTACTCCAGAGTC	240813	73009	TGGCTGCACCCATCCCACAA	285400	117596	CCAGACTTGACTTCAACCAG
196227	28423	GATGAGTTCTACTCCAGAGT	240814	73010	CTGGCTGCACCCATCCCACA	285401	117597	ACCAGACTTGACTTCAACCA
196228	28424	AGATGAGTTCTACTCCAGAG	240815	73011	CCTGGCTGCACCCATCCCAC	285402	117598	CACCAGACTTGACTTCAACC
196229	28425	AAGATGAGTTCTACTCCAGA	240816	73012	CCCTGGCTGCACCCATCCCA	285403	117599	GCACCAGACTTGACTTCAAC
196230	28426	CAAGATGAGTTCTACTCCAG	240817	73013	GCCCTGGCTGCACCCATCCC	285404	117600	GGCACCAGACTTGACTTCAA
196231	28427	ACAAGATGAGTTCTACTCCA	240818	73014	GGCCCTGGCTGCACCCATCC	285405	117601	GGGCACCAGACTTGACTTCA
196232	28428	CACAAGATGAGTTCTACTCC	240819	73015	TGGCCCTGGCTGCACCCATC	285406	117602	AGGGCACCAGACTTGACTTC
196233	28429	ACACAAGATGAGTTCTACTC	240820	73016	CTGGCCCTGGCTGCACCCAT	285407	117603	CAGGGCACCAGACTTGACTT
196234	28430	GACACAAGATGAGTTCTACT	240821	73017	CCTGGCCCTGGCTGCACCCA	285408	117604	CCAGGGCACCAGACTTGACT
196235	28431	AGACACAAGATGAGTTCTAC	240822	73018	ACCTGGCCCTGGCTGCACCC	285409	117605	ACCAGGGCACCAGACTTGAC
196236	28432	AAGACACAAGATGAGTTCTA	240823	73019	CACCTGGCCCTGGCTGCACC	285410	117606	CACCAGGGCACCAGACTTGA
196237	28433	GAAGACACAAGATGAGTTCT	240824	73020	ACACCTGGCCCTGGCTGCAC	285411	117607	CCACCAGGGCACCAGACTTG
196238	28434	AGAAGACACAAGATGAGTTC	240825	73021	GACACCTGGCCCTGGCTGCA	285412	117608	TCCACCAGGGCACCAGACTT
196239	28435	AAGAAGACACAAGATGAGTT	240826	73022	GGACACCTGGCCCTGGCTGC	285413	117609	CTCCACCAGGGCACCAGACT
196240	28436	GAAGAAGACACAAGATGAGT	240827	73023	TGGACACCTGGCCCTGGCTG	285414	117610	CCTCCACCAGGGCACCAGAC
196241	28437	AGAAGAAGACACAAGATGAG	240828	73024	CTGGACACCTGGCCCTGGCT	285415	117611	GCCTCCACCAGGGCACCAGA
196242	28438	CAGAAGAAGACACAAGATGA	240829	73025	CCTGGACACCTGGCCCTGGC	285416	117612	AGCCTCCACCAGGGCACCAG

196243	28439	GCAGAAGAAGACACAAGATG	240830	73026	CCCTGGACACCTGGCCCTGG	285417	117613	CAGCCTCCACCAGGGCACCA
196244	28440	GGCAGAAGAAGACACAAGAT	240831	73027	TCCCTGGACACCTGGCCCTG	285418	117614	ACAGCCTCCACCAGGGCACC
196245	28441	TGGCAGAAGAAGACACAAGA	240832	73028	GTCCCTGGACACCTGGCCCT	285419	117615	CACAGCCTCCACCAGGGCAC
196246	28442	GTGGCAGAAGAAGACACAAG	240833	73029	TGTCCCTGGACACCTGGCCC	285420	117616	GCACAGCCTCCACCAGGGCA
196247	28443	AGTGGCAGAAGAAGACACAA	240834	73030	CTGTCCCTGGACACCTGGCC	285421	117617	AGCACAGCCTCCACCAGGGC
196248	28444	GAGTGGCAGAAGAAGACACA	240835	73031	ACTGTCCCTGGACACCTGGC	285422	117618	CAGCACAGCCTCCACCAGGG
196249	28445	CGAGTGGCAGAAGAAGACAC	240836	73032	CACTGTCCCTGGACACCTGG	285423	117619	GCAGCACAGCCTCCACCAGG
196250	28446	ACGAGTGGCAGAAGAAGACA	240837	73033	ACACTGTCCCTGGACACCTG	285424	117620	AGCAGCACAGCCTCCACCAG
196251	28447	AACGAGTGGCAGAAGAAGAC	240838	73034	AACACTGTCCCTGGACACCT	285425	117621	CAGCAGCACAGCCTCCACCA
196252	28448	TAACGAGTGGCAGAAGAAGA	240839	73035	AAACACTGTCCCTGGACACC	285426	117622	TCAGCAGCACAGCCTCCACC
196253	28449	CTAACGAGTGGCAGAAGAAG	240840	73036	AAAACACTGTCCCTGGACAC	285427	117623	CTCAGCAGCACAGCCTCCAC
196254	28450	GCTAACGAGTGGCAGAAGAA	240841	73037	TAAAACACTGTCCCTGGACA	285428	117624	CCTCAGCAGCACAGCCTCCA
196255	28451	AGCTAACGAGTGGCAGAAGA	240842	73038	TTAAAACACTGTCCCTGGAC	285429	117625	GCCTCAGCAGCACAGCCTCC
196256	28452	CAGCTAACGAGTGGCAGAAG	240843	73039	GTTAAAACACTGTCCCTGGA	285430	117626	CGCCTCAGCAGCACAGCCTC
196257	28453	CCAGCTAACGAGTGGCAGAA	240844	73040	TGTTAAAACACTGTCCCTGG	285431	117627	CCGCCTCAGCAGCACAGCCT
196258	28454	CCCAGCTAACGAGTGGCAGA	240845	73041	TTGTTAAAACACTGTCCCTG	285432	117628	TCCGCCTCAGCAGCACAGCC
196259	28455	ACCCAGCTAACGAGTGGCAG	240846	73042	TTTGTTAAAACACTGTCCCT	285433	117629	CTCCGCCTCAGCAGCACAGC
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196261	28457	TCACCCAGCTAACGAGTGGC	240848	73044	CCTTTGTTAAAACACTGTCC	285435	117631	AGCTCCGCCTCAGCAGCACA
196262	28458	GTCACCCAGCTAACGAGTGG	240849	73045	CCCTTTGTTAAAACACTGTC	285436	117632	CAGCTCCGCCTCAGCAGCAC
196263	28459	GGTCACCCAGCTAACGAGTG	240850	73046	GCCCTTTGTTAAAACACTGT	285437	117633	CCAGCTCCGCCTCAGCAGCA
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196267	28463	TCAAGGTCACCCAGCTAACG	240854	73050	TCATGCCCTTTGTTAAAACA	285441	117637	CTCCCCAGCTCCGCCTCAGC
196268	28464	CTCAAGGTCACCCAGCTAAC	240855	73051	CTCATGCCCTTTGTTAAAAC	285442	117638	TCTCCCCAGCTCCGCCTCAG
196269	28465	GCTCAAGGTCACCCAGCTAA	240856	73052	CCTCATGCCCTTTGTTAAAA	285443	117639	CTCTCCCCAGCTCCGCCTCA
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196271	28467	TGGCTCAAGGTCACCCAGCT	240858	73054	CACCTCATGCCCTTTGTTAA	285445	117641	CTCTCTCCCCAGCTCCGCCT
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196273	28469	CTTGGCTCAAGGTCACCCAG	240860	73056	GACACCTCATGCCCTTTGTT	285447	117643	CACTCTCTCCCCAGCTCCGC
196274	28470	GCTTGGCTCAAGGTCACCCA	240861	73057	AGACACCTCATGCCCTTTGT	285448	117644	GCACTCTCTCCCCAGCTCCG
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196276	28472	GGGCTTGGCTCAAGGTCACC	240863	73059	TCAGACACCTCATGCCCTTT	285450	117646	GTGCACTCTCTCCCCAGCTC
196277	28473	GGGGCTTGGCTCAAGGTCAC	240864	73060	ATCAGACACCTCATGCCCTT	285451	117647	TGTGCACTCTCTCCCCAGCT
196278	28474	AGGGGCTTGGCTCAAGGTCA	240865	73061	GATCAGACACCTCATGCCCT	285452	117648	GTGTGCACTCTCTCCCCAGC
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196280	28476	TAAGGGGCTTGGCTCAAGGT	240867	73063	GAGATCAGACACCTCATGCC	285454	117650	CCGTGTGCACTCTCTCCCCA
196281	28477	TTAAGGGGCTTGGCTCAAGG	240868	73064	TGAGATCAGACACCTCATGC	285455	117651	CCCGTGTGCACTCTCTCCCC
196282	28478	GTTAAGGGGCTTGGCTCAAG	240869	73065	GTGAGATCAGACACCTCATG	285456	117652	GCCCGTGTGCACTCTCTCCC
196283	28479	GGTTAAGGGGCTTGGCTCAA	240870	73066	TGTGAGATCAGACACCTCAT	285457	117653	AGCCCGTGTGCACTCTCTCC
196284	28480	AGGTTAAGGGGCTTGGCTCA	240871	73067	CTGTGAGATCAGACACCTCA	285458	117654	CAGCCCGTGTGCACTCTCTC
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196291	28487	GTCCAAGAGGTTAAGGGGCT	240878	73074	AGTTCCACTGTGAGATCAGA	285465	117661	GGCCACGCAGCCCGTGTGCA
196292	28488	GGTCCAAGAGGTTAAGGGGC	240879	73075	GAGTTCCACTGTGAGATCAG	285466	117662	TGGCCACGCAGCCCGTGTGC
196293	28489	GGGTCCAAGAGGTTAAGGGG	240880	73076	GGAGTTCCACTGTGAGATCA	285467	117663	TTGGCCACGCAGCCCGTGTG
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196295	28491	TAGGGTCCAAGAGGTTAAGG	240882	73078	GTGGAGTTCCACTGTGAGAT	285469	117665	GGTTGGCCACGCAGCCCGTG
196296	28492	ATAGGGTCCAAGAGGTTAAG	240883	73079	AGTGGAGTTCCACTGTGAGA	285470	117666	GGGTTGGCCACGCAGCCCGT
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196305	28501	GATAAGAACATAGGGTCCAA	240892	73088	AAAAAGGCAAGTGGAGTTCC	285479	117675	TACCCAGAGGGGTTGGCCAC
196306	28502	AGATAAGAACATAGGGTCCA	240893	73089	AAAAAAGGCAAGTGGAGTTC	285480	117676	CTACCCAGAGGGGTTGGCCA
196307	28503	GAGATAAGAACATAGGGTCC	240894	73090	AAAAAAAGGCAAGTGGAGTT	285481	117677	GCTACCCAGAGGGGTTGGCC
196308	28504	AGAGATAAGAACATAGGGTC	240895	73091	GAAAAAAAGGCAAGTGGAGT	285482	117678	AGCTACCCAGAGGGGTTGGC
196309	28505	TAGAGATAAGAACATAGGGT	240896	73092	TGAAAAAAAGGCAAGTGGAG	285483	117679	CAGCTACCCAGAGGGGTTGG
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196312	28508	ACTTAGAGATAAGAACATAG	240899	73095	AGATGAAAAAAAGGCAAGTG	285486	117682	CATCAGCTACCCAGAGGGGT
196313	28509	TACTTAGAGATAAGAACATA	240900	73096	AAGATGAAAAAAAGGCAAGT	285487	117683	GCATCAGCTACCCAGAGGGG
196314	28510	CTACTTAGAGATAAGAACAT	240901	73097	GAAGATGAAAAAAAGGCAAG	285488	117684	GGCATCAGCTACCCAGAGGG

196315	28511	CCTACTTAGAGATAAGAACA	240902	73098	AGAAGATGAAAAAAAGGCAA	285489	117685	GGGCATCAGCTACCCAGAGG
196316	28512	CCCTACTTAGAGATAAGAAC	240903	73099	GAGAAGATGAAAAAAAGGCA	285490	117686	TGGGCATCAGCTACCCAGAG
196317	28513	CCCCTACTTAGAGATAAGAA	240904	73100	TGAGAAGATGAAAAAAAGGC	285491	117687	TTGGGCATCAGCTACCCAGA
196318	28514	GCCCCTACTTAGAGATAAGA	240905	73101	ATGAGAAGATGAAAAAAAGG	285492	117688	TTTGGGCATCAGCTACCCAG
196319	28515	AGCCCCTACTTAGAGATAAG	240906	73102	AATGAGAAGATGAAAAAAAG	285493	117689	CTTTGGGCATCAGCTACCCA
196320	28516	CAGCCCCTACTTAGAGATAA	240907	73103	GAATGAGAAGATGAAAAAAA	285494	117690	TCTTTGGGCATCAGCTACCC
196321	28517	CCAGCCCCTACTTAGAGATA	240908	73104	AGAATGAGAAGATGAAAAAA	285495	117691	GTCTTTGGGCATCAGCTACC
196322	28518	ACCAGCCCCTACTTAGAGAT	240909	73105	CAGAATGAGAAGATGAAAAA	285496	117692	CGTCTTTGGGCATCAGCTAC
196323	28519	TACCAGCCCCTACTTAGAGA	240910	73106	GCAGAATGAGAAGATGAAAA	285497	117693	GCGTCTTTGGGCATCAGCTA
196324	28520	TTACCAGCCCCTACTTAGAG	240911	73107	AGCAGAATGAGAAGATGAAA	285498	117694	AGCGTCTTTGGGCATCAGCT
196325	28521	ATTACCAGCCCCTACTTAGA	240912	73108	AAGCAGAATGAGAAGATGAA	285499	117695	CAGCGTCTTTGGGCATCAGC
196326	28522	TATTACCAGCCCCTACTTAG	240913	73109	GAAGCAGAATGAGAAGATGA	285500	117696	GCAGCGTCTTTGGGCATCAG
196327	28523	ATATTACCAGCCCCTACTTA	240914	73110	TGAAGCAGAATGAGAAGATG	285501	117697	TGCAGCGTCTTTGGGCATCA
196328	28524	GATATTACCAGCCCCTACTT	240915	73111	ATGAAGCAGAATGAGAAGAT	285502	117698	CTGCAGCGTCTTTGGGCATC
196329	28525	AGATATTACCAGCCCCTACT	240916	73112	CATGAAGCAGAATGAGAAGA	285503	117699	ACTGCAGCGTCTTTGGGCAT
196330	28526	AAGATATTACCAGCCCCTAC	240917	73113	GCATGAAGCAGAATGAGAAG	285504	117700	CACTGCAGCGTCTTTGGGCA
196331	28527	GAAGATATTACCAGCCCCTA	240918	73114	TGCATGAAGCAGAATGAGAA	285505	117701	GCACTGCAGCGTCTTTGGGC
196332	28528	GGAAGATATTACCAGCCCCT	240919	73115	GTGCATGAAGCAGAATGAGA	285506	117702	GGCACTGCAGCGTCTTTGGG
196333	28529	GGGAAGATATTACCAGCCCC	240920	73116	TGTGCATGAAGCAGAATGAG	285507	117703	GGGCACTGCAGCGTCTTTGG
196334	28530	GGGGAAGATATTACCAGCCC	240921	73117	CTGTGCATGAAGCAGAATGA	285508	117704	TGGGCACTGCAGCGTCTTTG
196335	28531	AGGGGAAGATATTACCAGCC	240922	73118	TCTGTGCATGAAGCAGAATG	285509	117705	CTGGGCACTGCAGCGTCTTT
196336	28532	AAGGGGAAGATATTACCAGC	240923	73119	TTCTGTGCATGAAGCAGAAT	285510	117706	CCTGGGCACTGCAGCGTCTT
196337	28533	AAAGGGGAAGATATTACCAG	240924	73120	GTTCTGTGCATGAAGCAGAA	285511	117707	TCCTGGGCACTGCAGCGTCT
196338	28534	CAAAGGGGAAGATATTACCA	240925	73121	GGTTCTGTGCATGAAGCAGA	285512	117708	GTCCTGGGCACTGCAGCGTC
196339	28535	TCAAAGGGGAAGATATTACC	240926	73122	TGGTTCTGTGCATGAAGCAG	285513	117709	TGTCCTGGGCACTGCAGCGT
196340	28536	CTCAAAGGGGAAGATATTAC	240927	73123	CTGGTTCTGTGCATGAAGCA	285514	117710	ATGTCCTGGGCACTGCAGCG
196341	28537	CCTCAAAGGGGAAGATATTA	240928	73124	GCTGGTTCTGTGCATGAAGC	285515	117711	GATGTCCTGGGCACTGCAGC
196342	28538	TCCTCAAAGGGGAAGATATT	240929	73125	GGCTGGTTCTGTGCATGAAG	285516	117712	AGATGTCCTGGGCACTGCAG
196343	28539	TTCCTCAAAGGGGAAGATAT	240930	73126	GGGCTGGTTCTGTGCATGAA	285517	117713	CAGATGTCCTGGGCACTGCA
196344	28540	ATTCCTCAAAGGGGAAGATA	240931	73127	GGGGCTGGTTCTGTGCATGA	285518	117714	CCAGATGTCCTGGGCACTGC
196345	28541	CATTCCTCAAAGGGGAAGAT	240932	73128	TGGGGCTGGTTCTGTGCATG	285519	117715	CCCAGATGTCCTGGGCACTG
196346	28542	GCATTCCTCAAAGGGGAAGA	240933	73129	ATGGGGCTGGTTCTGTGCAT	285520	117716	TCCCAGATGTCCTGGGCACT
196347	28543	GGCATTCCTCAAAGGGGAAG	240934	73130	GATGGGGCTGGTTCTGTGCA	285521	117717	GTCCCAGATGTCCTGGGCAC
196348	28544	GGGCATTCCTCAAAGGGGAA	240935	73131	GGATGGGGCTGGTTCTGTGC	285522	117718	GGTCCCAGATGTCCTGGGCA
196349	28545	AGGGCATTCCTCAAAGGGGA	240936	73132	AGGATGGGGCTGGTTCTGTG	285523	117719	AGGTCCCAGATGTCCTGGGC
196350	28546	GAGGGCATTCCTCAAAGGGG	240937	73133	CAGGATGGGGCTGGTTCTGT	285524	117720	GAGGTCCCAGATGTCCTGGG
196351	28547	AGAGGGCATTCCTCAAAGGG	240938	73134	TCAGGATGGGGCTGGTTCTG	285525	117721	GGAGGTCCCAGATGTCCTGG
196352	28548	TAGAGGGCATTCCTCAAAGG	240939	73135	TTCAGGATGGGGCTGGTTCT	285526	117722	GGGAGGTCCCAGATGTCCTG
196353	28549	TTAGAGGGCATTCCTCAAAG	240940	73136	TTTCAGGATGGGGCTGGTTC	285527	117723	AGGGAGGTCCCAGATGTCCT
196354	28550	CTTAGAGGGCATTCCTCAAA	240941	73137	GTTTCAGGATGGGGCTGGTT	285528	117724	CAGGGAGGTCCCAGATGTCC
196355	28551	CCTTAGAGGGCATTCCTCAA	240942	73138	AGTTTCAGGATGGGGCTGGT	285529	117725	CCAGGGAGGTCCCAGATGTC
196356	28552	CCCTTAGAGGGCATTCCTCA	240943	73139	CAGTTTCAGGATGGGGCTGG	285530	117726	CCCAGGGAGGTCCCAGATGT
196357	28553	CCCCTTAGAGGGCATTCCTC	240944	73140	TCAGTTTCAGGATGGGGCTG	285531	117727	CCCCAGGGAGGTCCCAGATG
196358	28554	ACCCCTTAGAGGGCATTCCT	240945	73141	GTCAGTTTCAGGATGGGGCT	285532	117728	GCCCCAGGGAGGTCCCAGAT
196359	28555	CACCCCTTAGAGGGCATTCC	240946	73142	AGTCAGTTTCAGGATGGGGC	285533	117729	GGCCCCAGGGAGGTCCCAGA
196360	28556	ACACCCCTTAGAGGGCATTC	240947	73143	GAGTCAGTTTCAGGATGGGG	285534	117730	GGGCCCCAGGGAGGTCCCAG
196361	28557	AACACCCCTTAGAGGGCATT	240948	73144	AGAGTCAGTTTCAGGATGGG	285535	117731	CGGGCCCCAGGGAGGTCCCA
196362	28558	CAACACCCCTTAGAGGGCAT	240949	73145	TAGAGTCAGTTTCAGGATGG	285536	117732	GCGGGCCCCAGGGAGGTCCC
196363	28559	ACAACACCCCTTAGAGGGCA	240950	73146	TTAGAGTCAGTTTCAGGATG	285537	117733	GGCGGGCCCCAGGGAGGTCC
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196366	28562	TTCACAACACCCCTTAGAGG	240953	73149	AATTTAGAGTCAGTTTCAGG	285540	117736	ACGGGCGGGCCCCAGGGAGG
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196368	28564	TCTTCACAACACCCCTTAGA	240955	73151	GTAATTTAGAGTCAGTTTCA	285542	117738	ACACGGGCGGGCCCCAGGGA
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196370	28566	AATCTTCACAACACCCCTTA	240957	73153	GAGTAATTTAGAGTCAGTTT	285544	117740	ACACACGGGCGGGCCCCAGG
196371	28567	GAATCTTCACAACACCCCTT	240958	73154	GGAGTAATTTAGAGTCAGTT	285545	117741	GACACACGGGCGGGCCCCAG
196372	28568	CGAATCTTCACAACACCCCT	240959	73155	GGGAGTAATTTAGAGTCAGT	285546	117742	GGACACACGGGCGGGCCCCA
196373	28569	CCGAATCTTCACAACACCCC	240960	73156	CGGGAGTAATTTAGAGTCAG	285547	117743	GGGACACACGGGCGGGCCCC
196374	28570	ACCGAATCTTCACAACACCC	240961	73157	GCGGGAGTAATTTAGAGTCA	285548	117744	CGGGACACACGGGCGGGCCC
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196377	28573	CTTACCGAATCTTCACAACA	240964	73160	GGGGCGGGAGTAATTTAGAG	285551	117747	GCGCGGGACACACGGGCGGG
196378	28574	CCTTACCGAATCTTCACAAC	240965	73161	TGGGGCGGGAGTAATTTAGA	285552	117748	AGCGCGGGACACACGGGCGG
196379	28575	ACCTTACCGAATCTTCACAA	240966	73162	CTGGGGCGGGAGTAATTTAG	285553	117749	CAGCGCGGGACACACGGGCG
196380	28576	CACCTTACCGAATCTTCACA	240967	73163	CCTGGGGCGGGAGTAATTTA	285554	117750	ACAGCGCGGGACACACGGGC
196381	28577	CCACCTTACCGAATCTTCAC	240968	73164	ACCTGGGGCGGGAGTAATTT	285555	117751	CACAGCGCGGGACACACGGG
196382	28578	GCCACCTTACCGAATCTTCA	240969	73165	CACCTGGGGCGGGAGTAATT	285556	117752	ACACAGCGCGGGACACACGG
196383	28579	TGCCACCTTACCGAATCTTC	240970	73166	CCACCTGGGGCGGGAGTAAT	285557	117753	AACACAGCGCGGGACACACG
196384	28580	CTGCCACCTTACCGAATCTT	240971	73167	TCCACCTGGGGCGGGAGTAA	285558	117754	GAACACAGCGCGGGACACAC
196385	28581	CCTGCCACCTTACCGAATCT	240972	73168	CTCCACCTGGGGCGGGAGTA	285559	117755	TGAACACAGCGCGGGACACA
196386	28582	CCCTGCCACCTTACCGAATC	240973	73169	ACTCCACCTGGGGCGGGAGT	285560	117756	ATGAACACAGCGCGGGACAC

196387	28583	CCCCTGCCACCTTACCGAAT	240974	73170	CACTCCACCTGGGGCGGGAG	285561	117757	GATGAACACAGCGCGGGACA
196388	28584	ACCCCTGCCACCTTACCGAA	240975	73171	GCACTCCACCTGGGGCGGGA	285562	117758	AGATGAACACAGCGCGGGAC
196389	28585	TACCCCTGCCACCTTACCGA	240976	73172	GGCACTCCACCTGGGGCGGG	285563	117759	CAGATGAACACAGCGCGGGA
196390	28586	CTACCCCTGCCACCTTACCG	240977	73173	AGGCACTCCACCTGGGGCGG	285564	117760	GCAGATGAACACAGCGCGGG
196391	28587	CCTACCCCTGCCACCTTACC	240978	73174	AAGGCACTCCACCTGGGGCG	285565	117761	CGCAGATGAACACAGCGCGG
196392	28588	TCCTACCCCTGCCACCTTAC	240979	73175	AAAGGCACTCCACCTGGGGC	285566	117762	CCGCAGATGAACACAGCGCG
196393	28589	GTCCTACCCCTGCCACCTTA	240980	73176	GAAAGGCACTCCACCTGGGG	285567	117763	CCCGCAGATGAACACAGCGC
196394	28590	AGTCCTACCCCTGCCACCTT	240981	73177	AGAAAGGCACTCCACCTGGG	285568	117764	GCCCGCAGATGAACACAGCG
196395	28591	GAGTCCTACCCCTGCCACCT	240982	73178	GAGAAAGGCACTCCACCTGG	285569	117765	AGCCCGCAGATGAACACAGC
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196397	28593	AGGAGTCCTACCCCTGCCAC	240984	73180	CCGAGAAAGGCACTCCACCT	285571	117767	CTAGCCCGCAGATGAACACA
196398	28594	CAGGAGTCCTACCCCTGCCA	240985	73181	TCCGAGAAAGGCACTCCACC	285572	117768	GCTAGCCCGCAGATGAACAC
196399	28595	CCAGGAGTCCTACCCCTGCC	240986	73182	CTCCGAGAAAGGCACTCCAC	285573	117769	GGCTAGCCCGCAGATGAACA
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196401	28597	GGCCAGGAGTCCTACCCCTG	240988	73184	AACTCCGAGAAAGGCACTCC	285575	117771	CAGGCTAGCCCGCAGATGAA
196402	28598	TGGCCAGGAGTCCTACCCCT	240989	73185	GAACTCCGAGAAAGGCACTC	285576	117772	ACAGGCTAGCCCGCAGATGA
196403	28599	CTGGCCAGGAGTCCTACCCC	240990	73186	TGAACTCCGAGAAAGGCACT	285577	117773	CACAGGCTAGCCCGCAGATG
196404	28600	TCTGGCCAGGAGTCCTACCC	240991	73187	TTGAACTCCGAGAAAGGCAC	285578	117774	TCACAGGCTAGCCCGCAGAT
196405	28601	TTCTGGCCAGGAGTCCTACC	240992	73188	GTTGAACTCCGAGAAAGGCA	285579	117775	GTCACAGGCTAGCCCGCAGA
196406	28602	TTTCTGGCCAGGAGTCCTAC	240993	73189	TGTTGAACTCCGAGAAAGGC	285580	117776	GGTCACAGGCTAGCCCGCAG
196407	28603	GTTTCTGGCCAGGAGTCCTA	240994	73190	CTGTTGAACTCCGAGAAAGG	285581	117777	GGGTCACAGGCTAGCCCGCA
196408	28604	TGTTTCTGGCCAGGAGTCCT	240995	73191	TCTGTTGAACTCCGAGAAAG	285582	117778	CGGGTCACAGGCTAGCCCGC
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196412	28608	TGCCTGTTTCTGGCCAGGAG	240999	73195	AGGCTCTGTTGAACTCCGAG	285586	117782	AGCGCGGGTCACAGGCTAGC
196413	28609	GTGCCTGTTTCTGGCCAGGA	241000	73196	AAGGCTCTGTTGAACTCCGA	285587	117783	CAGCGCGGGTCACAGGCTAG
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196415	28611	ATGTGCCTGTTTCTGGCCAG	241002	73198	GGAAGGCTCTGTTGAACTCC	285589	117785	CACAGCGCGGGTCACAGGCT
196416	28612	TATGTGCCTGTTTCTGGCCA	241003	73199	AGGAAGGCTCTGTTGAACTC	285590	117786	GCACAGCGCGGGTCACAGGC
196417	28613	TTATGTGCCTGTTTCTGGCC	241004	73200	CAGGAAGGCTCTGTTGAACT	285591	117787	AGCACAGCGCGGGTCACAGG
196418	28614	ATTATGTGCCTGTTTCTGGC	241005	73201	ACAGGAAGGCTCTGTTGAAC	285592	117788	GAGCACAGCGCGGGTCACAG
196419	28615	TATTATGTGCCTGTTTCTGG	241006	73202	GACAGGAAGGCTCTGTTGAA	285593	117789	CGAGCACAGCGCGGGTCACA
196420	28616	TTATTATGTGCCTGTTTCTG	241007	73203	CGACAGGAAGGCTCTGTTGA	285594	117790	ACGAGCACAGCGCGGGTCAC
196421	28617	TTTATTATGTGCCTGTTTCT	241008	73204	GCGACAGGAAGGCTCTGTTG	285595	117791	GACGAGCACAGCGCGGGTCA
196422	28618	ATTTATTATGTGCCTGTTTC	241009	73205	GGCGACAGGAAGGCTCTGTT	285596	117792	AGACGAGCACAGCGCGGGTC
196423	28619	CATTTATTATGTGCCTGTTT	241010	73206	GGGCGACAGGAAGGCTCTGT	285597	117793	CAGACGAGCACAGCGCGGGT
196424	28620	GCATTTATTATGTGCCTGTT	241011	73207	TGGGCGACAGGAAGGCTCTG	285598	117794	GCAGACGAGCACAGCGCGGG
196425	28621	AGCATTTATTATGTGCCTGT	241012	73208	TTGGGCGACAGGAAGGCTCT	285599	117795	CGCAGACGAGCACAGCGCGG
196426	28622	TAGCATTTATTATGTGCCTG	241013	73209	CTTGGGCGACAGGAAGGCTC	285600	117796	CCGCAGACGAGCACAGCGCG
196427	28623	TTAGCATTTATTATGTGCCT	241014	73210	CCTTGGGCGACAGGAAGGCT	285601	117797	CCCGCAGACGAGCACAGCGC
196428	28624	CTTAGCATTTATTATGTGCC	241015	73211	CCCTTGGGCGACAGGAAGGC	285602	117798	GCCCGCAGACGAGCACAGCG
196429	28625	ACTTAGCATTTATTATGTGC	241016	73212	TCCCTTGGGCGACAGGAAGG	285603	117799	AGCCCGCAGACGAGCACAGC
196430	28626	GACTTAGCATTTATTATGTG	241017	73213	GTCCCTTGGGCGACAGGAAG	285604	117800	TAGCCCGCAGACGAGCACAG
196431	28627	AGACTTAGCATTTATTATGT	241018	73214	TGTCCCTTGGGCGACAGGAA	285605	117801	CTAGCCCGCAGACGAGCACA
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196433	28629	AGAGACTTAGCATTTATTAT	241020	73216	GTTGTCCCTTGGGCGACAGG	285607	117803	GGCTAGCCCGCAGACGAGCA
196434	28630	GAGAGACTTAGCATTTATTA	241021	73217	AGTTGTCCCTTGGGCGACAG	285608	117804	AGGCTAGCCCGCAGACGAGC
196435	28631	GGAGAGACTTAGCATTTATT	241022	73218	GAGTTGTCCCTTGGGCGACA	285609	117805	CAGGCTAGCCCGCAGACGAG
196436	28632	AGGAGAGACTTAGCATTTAT	241023	73219	GGAGTTGTCCCTTGGGCGAC	285610	117806	ACAGGCTAGCCCGCAGACGA
196437	28633	AAGGAGAGACTTAGCATTTA	241024	73220	TGGAGTTGTCCCTTGGGCGA	285611	117807	CACAGGCTAGCCCGCAGACG
196438	28634	GAAGGAGAGACTTAGCATTT	241025	73221	GTGGAGTTGTCCCTTGGGCG	285612	117808	ACACAGGCTAGCCCGCAGAC
196439	28635	AGAAGGAGAGACTTAGCATT	241026	73222	AGTGGAGTTGTCCCTTGGGC	285613	117809	GACACAGGCTAGCCCGCAGA
196440	28636	GAGAAGGAGAGACTTAGCAT	241027	73223	CAGTGGAGTTGTCCCTTGGG	285614	117810	GGACACAGGCTAGCCCGCAG
196441	28637	AGAGAAGGAGAGACTTAGCA	241028	73224	TCAGTGGAGTTGTCCCTTGG	285615	117811	GGGACACAGGCTAGCCCGCA
196442	28638	GAGAGAAGGAGAGACTTAGC	241029	73225	TTCAGTGGAGTTGTCCCTTG	285616	117812	CGGGACACAGGCTAGCCCGC
196443	28639	GGAGAGAAGGAGAGACTTAG	241030	73226	ATTCAGTGGAGTTGTCCCTT	285617	117813	GCGGGACACAGGCTAGCCCG
196444	28640	TGGAGAGAAGGAGAGACTTA	241031	73227	CATTCAGTGGAGTTGTCCCT	285618	117814	CGCGGGACACAGGCTAGCCC
196445	28641	GTGGAGAGAAGGAGAGACTT	241032	73228	GCATTCAGTGGAGTTGTCCC	285619	117815	GCGCGGGACACAGGCTAGCC
196446	28642	GGTGGAGAGAAGGAGAGACT	241033	73229	GGCATTCAGTGGAGTTGTCC	285620	117816	AGCGCGGGACACAGGCTAGC
196447	28643	AGGTGGAGAGAAGGAGAGAC	241034	73230	GGGCATTCAGTGGAGTTGTC	285621	117817	GAGCGCGGGACACAGGCTAG
196448	28644	CAGGTGGAGAGAAGGAGAGA	241035	73231	TGGGCATTCAGTGGAGTTGT	285622	117818	AGAGCGCGGGACACAGGCTA
196449	28645	GCAGGTGGAGAGAAGGAGAG	241036	73232	TTGGGCATTCAGTGGAGTTG	285623	117819	CAGAGCGCGGGACACAGGCT
196450	28646	AGCAGGTGGAGAGAAGGAGA	241037	73233	CTTGGGCATTCAGTGGAGTT	285624	117820	GCAGAGCGCGGGACACAGGC
196451	28647	CAGCAGGTGGAGAGAAGGAG	241038	73234	GCTTGGGCATTCAGTGGAGT	285625	117821	AGCAGAGCGCGGGACACAGG
196452	28648	CCAGCAGGTGGAGAGAAGGA	241039	73235	GGCTTGGGCATTCAGTGGAG	285626	117822	AAGCAGAGCGCGGGACACAG
196453	28649	TCCAGCAGGTGGAGAGAAGG	241040	73236	TGGCTTGGGCATTCAGTGGA	285627	117823	CAAGCAGAGCGCGGGACACA
196454	28650	ATCCAGCAGGTGGAGAGAAG	241041	73237	GTGGCTTGGGCATTCAGTGG	285628	117824	ACAAGCAGAGCGCGGGACAC
196455	28651	CATCCAGCAGGTGGAGAGAA	241042	73238	TGTGGCTTGGGCATTCAGTG	285629	117825	GACAAGCAGAGCGCGGGACA
196456	28652	GCATCCAGCAGGTGGAGAGA	241043	73239	GTGTGGCTTGGGCATTCAGT	285630	117826	AGACAAGCAGAGCGCGGGAC
196457	28653	AGCATCCAGCAGGTGGAGAG	241044	73240	GGTGTGGCTTGGGCATTCAG	285631	117827	CAGACAAGCAGAGCGCGGGA
196458	28654	CAGCATCCAGCAGGTGGAGA	241045	73241	GGGTGTGGCTTGGGCATTCA	285632	117828	GCAGACAAGCAGAGCGCGGG

196459	28655	ACAGCATCCAGCAGGTGGAG	241046	73242	TGGGTGTGGCTTGGGCATTC	285633	117829	CGCAGACAAGCAGAGCGCGG
196460	28656	TACAGCATCCAGCAGGTGGA	241047	73243	TTGGGTGTGGCTTGGGCATT	285634	117830	CCGCAGACAAGCAGAGCGCG
196461	28657	CTACAGCATCCAGCAGGTGG	241048	73244	TTTGGGTGTGGCTTGGGCAT	285635	117831	ACCGCAGACAAGCAGAGCGC
196462	28658	TCTACAGCATCCAGCAGGTG	241049	73245	TTTTGGGTGTGGCTTGGGCA	285636	117832	GACCGCAGACAAGCAGAGCG
196463	28659	ATCTACAGCATCCAGCAGGT	241050	73246	GTTTTGGGTGTGGCTTGGGC	285637	117833	AGACCGCAGACAAGCAGAGC
196464	28660	TATCTACAGCATCCAGCAGG	241051	73247	GGTTTTGGGTGTGGCTTGGG	285638	117834	TAGACCGCAGACAAGCAGAG
196465	28661	GTATCTACAGCATCCAGCAG	241052	73248	AGGTTTTGGGTGTGGCTTGG	285639	117835	CTAGACCGCAGACAAGCAGA
196466	28662	AGTATCTACAGCATCCAGCA	241053	73249	TAGGTTTTGGGTGTGGCTTG	285640	117836	GCTAGACCGCAGACAAGCAG
196467	28663	TAGTATCTACAGCATCCAGC	241054	73250	TTAGGTTTTGGGTGTGGCTT	285641	117837	GGCTAGACCGCAGACAAGCA
196468	28664	TTAGTATCTACAGCATCCAG	241055	73251	GTTAGGTTTTGGGTGTGGCT	285642	117838	AGGCTAGACCGCAGACAAGC
196469	28665	CTTAGTATCTACAGCATCCA	241056	73252	TGTTAGGTTTTGGGTGTGGC	285643	117839	CAGGCTAGACCGCAGACAAG
196470	28666	CCTTAGTATCTACAGCATCC	241057	73253	TTGTTAGGTTTTGGGTGTGG	285644	117840	ACAGGCTAGACCGCAGACAA
196471	28667	TCCTTAGTATCTACAGCATC	241058	73254	CTTGTTAGGTTTTGGGTGTG	285645	117841	CACAGGCTAGACCGCAGACA
196472	28668	ATCCTTAGTATCTACAGCAT	241059	73255	ACTTGTTAGGTTTTGGGTGT	285646	117842	TCACAGGCTAGACCGCAGAC
196473	28669	AATCCTTAGTATCTACAGCA	241060	73256	TACTTGTTAGGTTTTGGGTG	285647	117843	GTCACAGGCTAGACCGCAGA
196474	28670	AAATCCTTAGTATCTACAGC	241061	73257	TTACTTGTTAGGTTTTGGGT	285648	117844	GGTCACAGGCTAGACCGCAG
196475	28671	GAAATCCTTAGTATCTACAG	241062	73258	TTTACTTGTTAGGTTTTGGG	285649	117845	AGGTCACAGGCTAGACCGCA
196476	28672	CGAAATCCTTAGTATCTACA	241063	73259	TTTTACTTGTTAGGTTTTGG	285650	117846	CAGGTCACAGGCTAGACCGC
196477	28673	TCGAAATCCTTAGTATCTAC	241064	73260	TTTTTACTTGTTAGGTTTTG	285651	117847	CCAGGTCACAGGCTAGACCG
196478	28674	ATCGAAATCCTTAGTATCTA	241065	73261	GTTTTTACTTGTTAGGTTTT	285652	117848	GCCAGGTCACAGGCTAGACC
196479	28675	CATCGAAATCCTTAGTATCT	241066	73262	GGTTTTTACTTGTTAGGTTT	285653	117849	TGCCAGGTCACAGGCTAGAC
196480	28676	ACATCGAAATCCTTAGTATC	241067	73263	TGGTTTTTACTTGTTAGGTT	285654	117850	CTGCCAGGTCACAGGCTAGA
196481	28677	CACATCGAAATCCTTAGTAT	241068	73264	TTGGTTTTTACTTGTTAGGT	285655	117851	TCTGCCAGGTCACAGGCTAG
196482	28678	TCACATCGAAATCCTTAGTA	241069	73265	TTTGGTTTTTACTTGTTAGG	285656	117852	CTCTGCCAGGTCACAGGCTA
196483	28679	TTCACATCGAAATCCTTAGT	241070	73266	ATTTGGTTTTTACTTGTTAG	285657	117853	TCTCTGCCAGGTCACAGGCT
196484	28680	ATTCACATCGAAATCCTTAG	241071	73267	AATTTGGTTTTTACTTGTTA	285658	117854	CTCTCTGCCAGGTCACAGGC
196485	28681	CATTCACATCGAAATCCTTA	241072	73268	GAATTTGGTTTTTACTTGTT	285659	117855	GCTCTCTGCCAGGTCACAGG
196486	28682	TCATTCACATCGAAATCCTT	241073	73269	AGAATTTGGTTTTTACTTGT	285660	117856	GGCTCTCTGCCAGGTCACAG
196487	28683	CTCATTCACATCGAAATCCT	241074	73270	CAGAATTTGGTTTTTACTTG	285661	117857	TGGCTCTCTGCCAGGTCACA
196488	28684	TCTCATTCACATCGAAATCC	241075	73271	ACAGAATTTGGTTTTTACTT	285662	117858	GTGGCTCTCTGCCAGGTCAC
196489	28685	GTCTCATTCACATCGAAATC	241076	73272	CACAGAATTTGGTTTTTACT	285663	117859	GGTGGCTCTCTGCCAGGTCA
196490	28686	TGTCTCATTCACATCGAAAT	241077	73273	GCACAGAATTTGGTTTTTAC	285664	117860	TGGTGGCTCTCTGCCAGGTC
196491	28687	TTGTCTCATTCACATCGAAA	241078	73274	AGCACAGAATTTGGTTTTTA	285665	117861	CTGGTGGCTCTCTGCCAGGT
196492	28688	TTTGTCTCATTCACATCGAA	241079	73275	GAGCACAGAATTTGGTTTTT	285666	117862	TCTGGTGGCTCTCTGCCAGG
196493	28689	TTTTGTCTCATTCACATCGA	241080	73276	GGAGCACAGAATTTGGTTTT	285667	117863	ATCTGGTGGCTCTCTGCCAG
196494	28690	GTTTTGTCTCATTCACATCG	241081	73277	GGGAGCACAGAATTTGGTTT	285668	117864	CATCTGGTGGCTCTCTGCCA
196495	28691	GGTTTTGTCTCATTCACATC	241082	73278	GGGGAGCACAGAATTTGGTT	285669	117865	ACATCTGGTGGCTCTCTGCC
196496	28692	GGGTTTTGTCTCATTCACAT	241083	73279	GGGGGAGCACAGAATTTGGT	285670	117866	GACATCTGGTGGCTCTCTGC
196497	28693	GGGGTTTTGTCTCATTCACA	241084	73280	TGGGGGAGCACAGAATTTGG	285671	117867	GGACATCTGGTGGCTCTCTG
196498	28694	AGGGGTTTTGTCTCATTCAC	241085	73281	ATGGGGGAGCACAGAATTTG	285672	117868	GGGACATCTGGTGGCTCTCT
196499	28695	CAGGGGTTTTGTCTCATTCA	241086	73282	GATGGGGGAGCACAGAATTT	285673	117869	CGGGACATCTGGTGGCTCTC
196500	28696	GCAGGGGTTTTGTCTCATTC	241087	73283	GGATGGGGGAGCACAGAATT	285674	117870	CCGGGACATCTGGTGGCTCT
196501	28697	GGCAGGGGTTTTGTCTCATT	241088	73284	AGGATGGGGGAGCACAGAAT	285675	117871	CCCGGGACATCTGGTGGCTC
196502	28698	AGGCAGGGGTTTTGTCTCAT	241089	73285	CAGGATGGGGGAGCACAGAA	285676	117872	GCCCGGGACATCTGGTGGCT
196503	28699	AAGGCAGGGGTTTTGTCTCA	241090	73286	CCAGGATGGGGGAGCACAGA	285677	117873	AGCCCGGGACATCTGGTGGC
196504	28700	GAAGGCAGGGGTTTTGTCTC	241091	73287	CCCAGGATGGGGGAGCACAG	285678	117874	CAGCCCGGGACATCTGGTGG
196505	28701	GGAAGGCAGGGGTTTTGTCT	241092	73288	GCCCAGGATGGGGGAGCACA	285679	117875	TCAGCCCGGGACATCTGGTG
196506	28702	TGGAAGGCAGGGGTTTTGTC	241093	73289	GGCCCAGGATGGGGGAGCAC	285680	117876	CTCAGCCCGGGACATCTGGT
196507	28703	CTGGAAGGCAGGGGTTTTGT	241094	73290	TGGCCCAGGATGGGGGAGCA	285681	117877	GCTCAGCCCGGGACATCTGG
196508	28704	CCTGGAAGGCAGGGGTTTTG	241095	73291	ATGGCCCAGGATGGGGGAGC	285682	117878	TGCTCAGCCCGGGACATCTG
196509	28705	TCCTGGAAGGCAGGGGTTTT	241096	73292	AATGGCCCAGGATGGGGGAG	285683	117879	GTGCTCAGCCCGGGACATCT
196510	28706	CTCCTGGAAGGCAGGGGTTT	241097	73293	GAATGGCCCAGGATGGGGGA	285684	117880	AGTGCTCAGCCCGGGACATC
196511	28707	GCTCCTGGAAGGCAGGGGTT	241098	73294	GGAATGGCCCAGGATGGGGG	285685	117881	CAGTGCTCAGCCCGGGACAT
196512	28708	GGCTCCTGGAAGGCAGGGGT	241099	73295	AGGAATGGCCCAGGATGGGG	285686	117882	GCAGTGCTCAGCCCGGGACA
196513	28709	AGGCTCCTGGAAGGCAGGGG	241100	73296	CAGGAATGGCCCAGGATGGG	285687	117883	GGCAGTGCTCAGCCCGGGAC
196514	28710	AAGGCTCCTGGAAGGCAGGG	241101	73297	CCAGGAATGGCCCAGGATGG	285688	117884	GGGCAGTGCTCAGCCCGGGA
196515	28711	AAAGGCTCCTGGAAGGCAGG	241102	73298	ACCAGGAATGGCCCAGGATG	285689	117885	AGGGCAGTGCTCAGCCCGGG
196516	28712	CAAAGGCTCCTGGAAGGCAG	241103	73299	AACCAGGAATGGCCCAGGAT	285690	117886	GAGGGCAGTGCTCAGCCCGG
196517	28713	TCAAAGGCTCCTGGAAGGCA	241104	73300	AAACCAGGAATGGCCCAGGA	285691	117887	AGAGGGCAGTGCTCAGCCCG
196518	28714	CTCAAAGGCTCCTGGAAGGC	241105	73301	GAAACCAGGAATGGCCCAGG	285692	117888	CAGAGGGCAGTGCTCAGCCC
196519	28715	TCTCAAAGGCTCCTGGAAGG	241106	73302	AGAAACCAGGAATGGCCCAG	285693	117889	TCAGAGGGCAGTGCTCAGCC
196520	28716	TTCTCAAAGGCTCCTGGAAG	241107	73303	GAGAAACCAGGAATGGCCCA	285694	117890	CTCAGAGGGCAGTGCTCAGC
196521	28717	ATTCTCAAAGGCTCCTGGAA	241108	73304	AGAGAAACCAGGAATGGCCC	285695	117891	GCTCAGAGGGCAGTGCTCAG
196522	28718	GATTCTCAAAGGCTCCTGGA	241109	73305	TAGAGAAACCAGGAATGGCC	285696	117892	TGCTCAGAGGGCAGTGCTCA
196523	28719	TGATTCTCAAAGGCTCCTGG	241110	73306	GTAGAGAAACCAGGAATGGC	285697	117893	GTGCTCAGAGGGCAGTGCTC
196524	28720	CTGATTCTCAAAGGCTCCTG	241111	73307	AGTAGAGAAACCAGGAATGG	285698	117894	GGTGCTCAGAGGGCAGTGCT
196525	28721	TCTGATTCTCAAAGGCTCCT	241112	73308	CAGTAGAGAAACCAGGAATG	285699	117895	AGGTGCTCAGAGGGCAGTGC
196526	28722	CTCTGATTCTCAAAGGCTCC	241113	73309	GCAGTAGAGAAACCAGGAAT	285700	117896	AAGGTGCTCAGAGGGCAGTG
196527	28723	TCTCTGATTCTCAAAGGCTC	241114	73310	AGCAGTAGAGAAACCAGGAA	285701	117897	GAAGGTGCTCAGAGGGCAGT
196528	28724	TTCTCTGATTCTCAAAGGCT	241115	73311	CAGCAGTAGAGAAACCAGGA	285702	117898	TGAAGGTGCTCAGAGGGCAG
196529	28725	GTTCTCTGATTCTCAAAGGC	241116	73312	ACAGCAGTAGAGAAACCAGG	285703	117899	GTGAAGGTGCTCAGAGGGCA
196530	28726	AGTTCTCTGATTCTCAAAGG	241117	73313	AACAGCAGTAGAGAAACCAG	285704	117900	TGTGAAGGTGCTCAGAGGGC

196531	28727	TAGTTCTCTGATTCTCAAAG	241118	73314	CAACAGCAGTAGAGAAACCA	285705	117901	CTGTGAAGGTGCTCAGAGGG
196532	28728	CTAGTTCTCTGATTCTCAAA	241119	73315	CCAACAGCAGTAGAGAAACC	285706	117902	CCTGTGAAGGTGCTCAGAGG
196533	28729	TCTAGTTCTCTGATTCTCAA	241120	73316	ACCAACAGCAGTAGAGAAAC	285707	117903	TCCTGTGAAGGTGCTCAGAG
196534	28730	GTCTAGTTCTCTGATTCTCA	241121	73317	CACCAACAGCAGTAGAGAAA	285708	117904	TTCCTGTGAAGGTGCTCAGA
196535	28731	GGTCTAGTTCTCTGATTCTC	241122	73318	TCACCAACAGCAGTAGAGAA	285709	117905	CTTCCTGTGAAGGTGCTCAG
196536	28732	GGGTCTAGTTCTCTGATTCT	241123	73319	ATCACCAACAGCAGTAGAGA	285710	117906	GCTTCCTGTGAAGGTGCTCA
196537	28733	TGGGTCTAGTTCTCTGATTC	241124	73320	TATCACCAACAGCAGTAGAG	285711	117907	GGCTTCCTGTGAAGGTGCTC
196538	28734	ATGGGTCTAGTTCTCTGATT	241125	73321	GTATCACCAACAGCAGTAGA	285712	117908	GGGCTTCCTGTGAAGGTGCT
196539	28735	AATGGGTCTAGTTCTCTGAT	241126	73322	GGTATCACCAACAGCAGTAG	285713	117909	AGGGCTTCCTGTGAAGGTGC
196540	28736	AAATGGGTCTAGTTCTCTGA	241127	73323	TGGTATCACCAACAGCAGTA	285714	117910	AAGGGCTTCCTGTGAAGGTG
196541	28737	GAAATGGGTCTAGTTCTCTG	241128	73324	GTGGTATCACCAACAGCAGT	285715	117911	GAAGGGCTTCCTGTGAAGGT
196542	28738	GGAAATGGGTCTAGTTCTCT	241129	73325	GGTGGTATCACCAACAGCAG	285716	117912	AGAAGGGCTTCCTGTGAAGG
196543	28739	TGGAAATGGGTCTAGTTCTC	241130	73326	TGGTGGTATCACCAACAGCA	285717	117913	GAGAAGGGCTTCCTGTGAAG
196544	28740	CTGGAAATGGGTCTAGTTCT	241131	73327	ATGGTGGTATCACCAACAGC	285718	117914	GGAGAAGGGCTTCCTGTGAA
196545	28741	TCTGGAAATGGGTCTAGTTC	241132	73328	GATGGTGGTATCACCAACAG	285719	117915	AGGAGAAGGGCTTCCTGTGA
196546	28742	TTCTGGAAATGGGTCTAGTT	241133	73329	TGATGGTGGTATCACCAACA	285720	117916	CAGGAGAAGGGCTTCCTGTG
196547	28743	GTTCTGGAAATGGGTCTAGT	241134	73330	CTGATGGTGGTATCACCAAC	285721	117917	CCAGGAGAAGGGCTTCCTGT
196548	28744	TGTTCTGGAAATGGGTCTAG	241135	73331	GCTGATGGTGGTATCACCAA	285722	117918	ACCAGGAGAAGGGCTTCCTG
196549	28745	TTGTTCTGGAAATGGGTCTA	241136	73332	AGCTGATGGTGGTATCACCA	285723	117919	CACCAGGAGAAGGGCTTCCT
196550	28746	CTTGTTCTGGAAATGGGTCT	241137	73333	AAGCTGATGGTGGTATCACC	285724	117920	TCACCAGGAGAAGGGCTTCC
196551	28747	CCTTGTTCTGGAAATGGGTC	241138	73334	CAAGCTGATGGTGGTATCAC	285725	117921	CTCACCAGGAGAAGGGCTTC
196552	28748	CCCTTGTTCTGGAAATGGGT	241139	73335	ACAAGCTGATGGTGGTATCA	285726	117922	TCTCACCAGGAGAAGGGCTT
196553	28749	CCCCTTGTTCTGGAAATGGG	241140	73336	GACAAGCTGATGGTGGTATC	285727	117923	TTCTCACCAGGAGAAGGGCT
196554	28750	TCCCCTTGTTCTGGAAATGG	241141	73337	GGACAAGCTGATGGTGGTAT	285728	117924	CTTCTCACCAGGAGAAGGGC
196555	28751	ATCCCCTTGTTCTGGAAATG	241142	73338	TGGACAAGCTGATGGTGGTA	285729	117925	TCTTCTCACCAGGAGAAGGG
196556	28752	CATCCCCTTGTTCTGGAAAT	241143	73339	ATGGACAAGCTGATGGTGGT	285730	117926	CTCTTCTCACCAGGAGAAGG
196557	28753	GCATCCCCTTGTTCTGGAAA	241144	73340	GATGGACAAGCTGATGGTGG	285731	117927	TCTCTTCTCACCAGGAGAAG
196558	28754	TGCATCCCCTTGTTCTGGAA	241145	73341	TGATGGACAAGCTGATGGTG	285732	117928	ATCTCTTCTCACCAGGAGAA
196559	28755	CTGCATCCCCTTGTTCTGGA	241146	73342	ATGATGGACAAGCTGATGGT	285733	117929	CATCTCTTCTCACCAGGAGA
196560	28756	CCTGCATCCCCTTGTTCTGG	241147	73343	CATGATGGACAAGCTGATGG	285734	117930	GCATCTCTTCTCACCAGGAG
196561	28757	CCCTGCATCCCCTTGTTCTG	241148	73344	TCATGATGGACAAGCTGATG	285735	117931	GGCATCTCTTCTCACCAGGA
196562	28758	ACCCTGCATCCCCTTGTTCT	241149	73345	GTCATGATGGACAAGCTGAT	285736	117932	TGGCATCTCTTCTCACCAGG
196563	28759	GACCCTGCATCCCCTTGTTC	241150	73346	GGTCATGATGGACAAGCTGA	285737	117933	CTGGCATCTCTTCTCACCAG
196564	28760	AGACCCTGCATCCCCTTGTT	241151	73347	GGGTCATGATGGACAAGCTG	285738	117934	GCTGGCATCTCTTCTCACCA
196565	28761	CAGACCCTGCATCCCCTTGT	241152	73348	AGGGTCATGATGGACAAGCT	285739	117935	GGCTGGCATCTCTTCTCACC
196566	28762	CCAGACCCTGCATCCCCTTG	241153	73349	CAGGGTCATGATGGACAAGC	285740	117936	GGGCTGGCATCTCTTCTCAC
196567	28763	TCCAGACCCTGCATCCCCTT	241154	73350	CCAGGGTCATGATGGACAAG	285741	117937	GGGGCTGGCATCTCTTCTCA
196568	28764	ATCCAGACCCTGCATCCCCT	241155	73351	GCCAGGGTCATGATGGACAA	285742	117938	AGGGGCTGGCATCTCTTCTC
196569	28765	TATCCAGACCCTGCATCCCC	241156	73352	GGCCAGGGTCATGATGGACA	285743	117939	CAGGGGCTGGCATCTCTTCT
196570	28766	TTATCCAGACCCTGCATCCC	241157	73353	TGGCCAGGGTCATGATGGAC	285744	117940	CCAGGGGCTGGCATCTCTTC
196571	28767	TTTATCCAGACCCTGCATCC	241158	73354	CTGGCCAGGGTCATGATGGA	285745	117941	GCCAGGGGCTGGCATCTCTT
196572	28768	CTTTATCCAGACCCTGCATC	241159	73355	ACTGGCCAGGGTCATGATGG	285746	117942	TGCCAGGGGCTGGCATCTCT
196573	28769	ACTTTATCCAGACCCTGCAT	241160	73356	AACTGGCCAGGGTCATGATG	285747	117943	ATGCCAGGGGCTGGCATCTC
196574	28770	AACTTTATCCAGACCCTGCA	241161	73357	GAACTGGCCAGGGTCATGAT	285748	117944	GATGCCAGGGGCTGGCATCT
196575	28771	AAACTTTATCCAGACCCTGC	241162	73358	GGAACTGGCCAGGGTCATGA	285749	117945	AGATGCCAGGGGCTGGCATC
196576	28772	AAAACTTTATCCAGACCCTG	241163	73359	AGGAACTGGCCAGGGTCATG	285750	117946	CAGATGCCAGGGGCTGGCAT
196577	28773	CAAAACTTTATCCAGACCCT	241164	73360	GAGGAACTGGCCAGGGTCAT	285751	117947	CCAGATGCCAGGGGCTGGCA
196578	28774	CCAAAACTTTATCCAGACCC	241165	73361	GGAGGAACTGGCCAGGGTCA	285752	117948	CCCAGATGCCAGGGGCTGGC
196579	28775	CCCAAAACTTTATCCAGACC	241166	73362	GGGAGGAACTGGCCAGGGTC	285753	117949	CCCCAGATGCCAGGGGCTGG
196580	28776	CCCCAAAACTTTATCCAGAC	241167	73363	TGGGAGGAACTGGCCAGGGT	285754	117950	CCCCCAGATGCCAGGGGCTG
196581	28777	TCCCCAAAACTTTATCCAGA	241168	73364	GTGGGAGGAACTGGCCAGGG	285755	117951	GCCCCCAGATGCCAGGGGCT
196582	28778	ATCCCCAAAACTTTATCCAG	241169	73365	TGTGGGAGGAACTGGCCAGG	285756	117952	TGCCCCCAGATGCCAGGGGC
196583	28779	GATCCCCAAAACTTTATCCA	241170	73366	TTGTGGGAGGAACTGGCCAG	285757	117953	GTGCCCCCAGATGCCAGGGG
196584	28780	TGATCCCCAAAACTTTATCC	241171	73367	GTTGTGGGAGGAACTGGCCA	285758	117954	AGTGCCCCCAGATGCCAGGG
196585	28781	TTGATCCCCAAAACTTTATC	241172	73368	GGTTGTGGGAGGAACTGGCC	285759	117955	CAGTGCCCCCAGATGCCAGG
196586	28782	ATTGATCCCCAAAACTTTAT	241173	73369	GGGTTGTGGGAGGAACTGGC	285760	117956	CCAGTGCCCCCAGATGCCAG
196587	28783	TATTGATCCCCAAAACTTTA	241174	73370	AGGGTTGTGGGAGGAACTGG	285761	117957	TCCAGTGCCCCCAGATGCCA
196588	28784	CTATTGATCCCCAAAACTTT	241175	73371	GAGGGTTGTGGGAGGAACTG	285762	117958	ATCCAGTGCCCCCAGATGCC
196589	28785	TCTATTGATCCCCAAAACTT	241176	73372	GGAGGGTTGTGGGAGGAACT	285763	117959	GATCCAGTGCCCCCAGATGC
196590	28786	CTCTATTGATCCCCAAAACT	241177	73373	TGGAGGGTTGTGGGAGGAAC	285764	117960	GGATCCAGTGCCCCCAGATG
196591	28787	GCTCTATTGATCCCCAAAAC	241178	73374	GTGGAGGGTTGTGGGAGGAA	285765	117961	GGGATCCAGTGCCCCCAGAT
196592	28788	TGCTCTATTGATCCCCAAAA	241179	73375	TGTGGAGGGTTGTGGGAGGA	285766	117962	AGGGATCCAGTGCCCCCAGA
196593	28789	CTGCTCTATTGATCCCCAAA	241180	73376	CTGTGGAGGGTTGTGGGAGG	285767	117963	CAGGGATCCAGTGCCCCCAG
196594	28790	TCTGCTCTATTGATCCCCAA	241181	73377	GCTGTGGAGGGTTGTGGGAG	285768	117964	CCAGGGATCCAGTGCCCCCA
196595	28791	CTCTGCTCTATTGATCCCCA	241182	73378	TGCTGTGGAGGGTTGTGGGA	285769	117965	GCCAGGGATCCAGTGCCCCC
196596	28792	CCTCTGCTCTATTGATCCCC	241183	73379	GTGCTGTGGAGGGTTGTGGG	285770	117966	GGCCAGGGATCCAGTGCCCC
196597	28793	CCCTCTGCTCTATTGATCCC	241184	73380	GGTGCTGTGGAGGGTTGTGG	285771	117967	AGGCCAGGGATCCAGTGCCC
196598	28794	GCCCTCTGCTCTATTGATCC	241185	73381	GGGTGCTGTGGAGGGTTGTG	285772	117968	CAGGCCAGGGATCCAGTGCC
196599	28795	AGCCCTCTGCTCTATTGATC	241186	73382	TGGGTGCTGTGGAGGGTTGT	285773	117969	TCAGGCCAGGGATCCAGTGC
196600	28796	GAGCCCTCTGCTCTATTGAT	241187	73383	CTGGGTGCTGTGGAGGGTTG	285774	117970	CTCAGGCCAGGGATCCAGTG
196601	28797	GGAGCCCTCTGCTCTATTGA	241188	73384	CCTGGGTGCTGTGGAGGGTT	285775	117971	GCTCAGGCCAGGGATCCAGT
196602	28798	GGGAGCCCTCTGCTCTATTG	241189	73385	CCCTGGGTGCTGTGGAGGGT	285776	117972	GGCTCAGGCCAGGGATCCAG

196603	28799	TGGGAGCCCTCTGCTCTATT	241190	73386	TCCCTGGGTGCTGTGGAGGG	285777	117973	GGGCTCAGGCCAGGGATCCA
196604	28800	CTGGGAGCCCTCTGCTCTAT	241191	73387	GTCCCTGGGTGCTGTGGAGG	285778	117974	AGGGCTCAGGCCAGGGATCC
196605	28801	TCTGGGAGCCCTCTGCTCTA	241192	73388	GGTCCCTGGGTGCTGTGGAG	285779	117975	TAGGGCTCAGGCCAGGGATC
196606	28802	CTCTGGGAGCCCTCTGCTCT	241193	73389	AGGTCCCTGGGTGCTGTGGA	285780	117976	CTAGGGCTCAGGCCAGGGAT
196607	28803	CCTCTGGGAGCCCTCTGCTC	241194	73390	GAGGTCCCTGGGTGCTGTGG	285781	117977	GCTAGGGCTCAGGCCAGGGA
196608	28804	TCCTCTGGGAGCCCTCTGCT	241195	73391	TGAGGTCCCTGGGTGCTGTG	285782	117978	GGCTAGGGCTCAGGCCAGGG
196609	28805	ATCCTCTGGGAGCCCTCTGC	241196	73392	GTGAGGTCCCTGGGTGCTGT	285783	117979	AGGCTAGGGCTCAGGCCAGG
196610	28806	GATCCTCTGGGAGCCCTCTG	241197	73393	GGTGAGGTCCCTGGGTGCTG	285784	117980	GAGGCTAGGGCTCAGGCCAG
196611	28807	GGATCCTCTGGGAGCCCTCT	241198	73394	AGGTGAGGTCCCTGGGTGCT	285785	117981	AGAGGCTAGGGCTCAGGCCA
196612	28808	GGGATCCTCTGGGAGCCCTC	241199	73395	GAGGTGAGGTCCCTGGGTGC	285786	117982	GAGAGGCTAGGGCTCAGGCC
196613	28809	TGGGATCCTCTGGGAGCCCT	241200	73396	GGAGGTGAGGTCCCTGGGTG	285787	117983	GGAGAGGCTAGGGCTCAGGC
196614	28810	ATGGGATCCTCTGGGAGCCC	241201	73397	TGGAGGTGAGGTCCCTGGGT	285788	117984	GGGAGAGGCTAGGGCTCAGG
196615	28811	TATGGGATCCTCTGGGAGCC	241202	73398	ATGGAGGTGAGGTCCCTGGG	285789	117985	GGGGAGAGGCTAGGGCTCAG
196616	28812	CTATGGGATCCTCTGGGAGC	241203	73399	AATGGAGGTGAGGTCCCTGG	285790	117986	TGGGGAGAGGCTAGGGCTCA
196617	28813	CCTATGGGATCCTCTGGGAG	241204	73400	GAATGGAGGTGAGGTCCCTG	285791	117987	CTGGGGAGAGGCTAGGGCTC
196618	28814	CCCTATGGGATCCTCTGGGA	241205	73401	GGAATGGAGGTGAGGTCCCT	285792	117988	GCTGGGGAGAGGCTAGGGCT
196619	28815	ACCCTATGGGATCCTCTGGG	241206	73402	TGGAATGGAGGTGAGGTCCC	285793	117989	GGCTGGGGAGAGGCTAGGGC
196620	28816	AACCCTATGGGATCCTCTGG	241207	73403	ATGGAATGGAGGTGAGGTCC	285794	117990	AGGCTGGGGAGAGGCTAGGG
196621	28817	CAACCCTATGGGATCCTCTG	241208	73404	GATGGAATGGAGGTGAGGTC	285795	117991	CAGGCTGGGGAGAGGCTAGG
196622	28818	TCAACCCTATGGGATCCTCT	241209	73405	GGATGGAATGGAGGTGAGGT	285796	117992	CCAGGCTGGGGAGAGGCTAG
196623	28819	GTCAACCCTATGGGATCCTC	241210	73406	CGGATGGAATGGAGGTGAGG	285797	117993	CCCAGGCTGGGGAGAGGCTA
196624	28820	AGTCAACCCTATGGGATCCT	241211	73407	TCGGATGGAATGGAGGTGAG	285798	117994	CCCCAGGCTGGGGAGAGGCT
196625	28821	GAGTCAACCCTATGGGATCC	241212	73408	GTCGGATGGAATGGAGGTGA	285799	117995	CCCCCAGGCTGGGGAGAGGC
196626	28822	GGAGTCAACCCTATGGGATC	241213	73409	TGTCGGATGGAATGGAGGTG	285800	117996	GCCCCCAGGCTGGGGAGAGG
196627	28823	AGGAGTCAACCCTATGGGAT	241214	73410	GTGTCGGATGGAATGGAGGT	285801	117997	GGCCCCCAGGCTGGGGAGAG
196628	28824	TAGGAGTCAACCCTATGGGA	241215	73411	TGTGTCGGATGGAATGGAGG	285802	117998	GGGCCCCCAGGCTGGGGAGA
196629	28825	TTAGGAGTCAACCCTATGGG	241216	73412	CTGTGTCGGATGGAATGGAG	285803	117999	GGGGCCCCCAGGCTGGGGAG
196630	28826	GTTAGGAGTCAACCCTATGG	241217	73413	TCTGTGTCGGATGGAATGGA	285804	118000	AGGGGCCCCCAGGCTGGGGA
196631	28827	AGTTAGGAGTCAACCCTATG	241218	73414	ATCTGTGTCGGATGGAATGG	285805	118001	AAGGGGCCCCCAGGCTGGGG
196632	28828	GAGTTAGGAGTCAACCCTAT	241219	73415	GATCTGTGTCGGATGGAATG	285806	118002	GAAGGGGCCCCCAGGCTGGG
196633	28829	TGAGTTAGGAGTCAACCCTA	241220	73416	AGATCTGTGTCGGATGGAAT	285807	118003	GGAAGGGGCCCCCAGGCTGG
196634	28830	TTGAGTTAGGAGTCAACCCT	241221	73417	GAGATCTGTGTCGGATGGAA	285808	118004	GGGAAGGGGCCCCCAGGCTG
196635	28831	CTTGAGTTAGGAGTCAACCC	241222	73418	GGAGATCTGTGTCGGATGGA	285809	118005	TGGGAAGGGGCCCCCAGGCT
196636	28832	CCTTGAGTTAGGAGTCAACC	241223	73419	AGGAGATCTGTGTCGGATGG	285810	118006	CTGGGAAGGGGCCCCCAGGC
196637	28833	CCCTTGAGTTAGGAGTCAAC	241224	73420	GAGGAGATCTGTGTCGGATG	285811	118007	GCTGGGAAGGGGCCCCCAGG
196638	28834	GCCCTTGAGTTAGGAGTCAA	241225	73421	TGAGGAGATCTGTGTCGGAT	285812	118008	TGCTGGGAAGGGGCCCCCAG
196639	28835	TGCCCTTGAGTTAGGAGTCA	241226	73422	GTGAGGAGATCTGTGTCGGA	285813	118009	CTGCTGGGAAGGGGCCCCCA
196640	28836	ATGCCCTTGAGTTAGGAGTC	241227	73423	GGTGAGGAGATCTGTGTCGG	285814	118010	CCTGCTGGGAAGGGGCCCCC
196641	28837	CATGCCCTTGAGTTAGGAGT	241228	73424	TGGTGAGGAGATCTGTGTCG	285815	118011	GCCTGCTGGGAAGGGGCCCC
196642	28838	TCATGCCCTTGAGTTAGGAG	241229	73425	GTGGTGAGGAGATCTGTGTC	285816	118012	AGCCTGCTGGGAAGGGGCCC
196643	28839	CTCATGCCCTTGAGTTAGGA	241230	73426	TGTGGTGAGGAGATCTGTGT	285817	118013	CAGCCTGCTGGGAAGGGGCC
196644	28840	TCTCATGCCCTTGAGTTAGG	241231	73427	TTGTGGTGAGGAGATCTGTG	285818	118014	CCAGCCTGCTGGGAAGGGGC
196645	28841	GTCTCATGCCCTTGAGTTAG	241232	73428	TTTGTGGTGAGGAGATCTGT	285819	118015	GCCAGCCTGCTGGGAAGGGG
196646	28842	TGTCTCATGCCCTTGAGTTA	241233	73429	GTTTGTGGTGAGGAGATCTG	285820	118016	GGCCAGCCTGCTGGGAAGGG
196647	28843	TTGTCTCATGCCCTTGAGTT	241234	73430	GGTTTGTGGTGAGGAGATCT	285821	118017	GGGCCAGCCTGCTGGGAAGG
196648	28844	GTTGTCTCATGCCCTTGAGT	241235	73431	AGGTTTGTGGTGAGGAGATC	285822	118018	AGGGCCAGCCTGCTGGGAAG
196649	28845	GGTTGTCTCATGCCCTTGAG	241236	73432	AAGGTTTGTGGTGAGGAGAT	285823	118019	CAGGGCCAGCCTGCTGGGAA
196650	28846	GGGTTGTCTCATGCCCTTGA	241237	73433	CAAGGTTTGTGGTGAGGAGA	285824	118020	GCAGGGCCAGCCTGCTGGGA
196651	28847	GGGGTTGTCTCATGCCCTTG	241238	73434	CCAAGGTTTGTGGTGAGGAG	285825	118021	AGCAGGGCCAGCCTGCTGGG
196652	28848	GGGGGTTGTCTCATGCCCTT	241239	73435	ACCAAGGTTTGTGGTGAGGA	285826	118022	GAGCAGGGCCAGCCTGCTGG
196653	28849	TGGGGGTTGTCTCATGCCCT	241240	73436	AACCAAGGTTTGTGGTGAGG	285827	118023	GGAGCAGGGCCAGCCTGCTG
196654	28850	CTGGGGGTTGTCTCATGCCC	241241	73437	AAACCAAGGTTTGTGGTGAG	285828	118024	AGGAGCAGGGCCAGCCTGCT
196655	28851	CCTGGGGGTTGTCTCATGCC	241242	73438	AAAACCAAGGTTTGTGGTGA	285829	118025	AAGGAGCAGGGCCAGCCTGC
196656	28852	TCCTGGGGGTTGTCTCATGC	241243	73439	CAAAACCAAGGTTTGTGGTG	285830	118026	GAAGGAGCAGGGCCAGCCTG
196657	28853	TTCCTGGGGGTTGTCTCATG	241244	73440	GCAAAACCAAGGTTTGTGGT	285831	118027	AGAAGGAGCAGGGCCAGCCT
196658	28854	CTTCCTGGGGGTTGTCTCAT	241245	73441	TGCAAAACCAAGGTTTGTGG	285832	118028	GAGAAGGAGCAGGGCCAGCC
196659	28855	CCTTCCTGGGGGTTGTCTCA	241246	73442	TTGCAAAACCAAGGTTTGTG	285833	118029	AGAGAAGGAGCAGGGCCAGC
196660	28856	CCCTTCCTGGGGGTTGTCTC	241247	73443	GTTGCAAAACCAAGGTTTGT	285834	118030	TAGAGAAGGAGCAGGGCCAG
196661	28857	GCCCTTCCTGGGGGTTGTCT	241248	73444	TGTTGCAAAACCAAGGTTTG	285835	118031	GTAGAGAAGGAGCAGGGCCA
196662	28858	TGCCCTTCCTGGGGGTTGTC	241249	73445	CTGTTGCAAAACCAAGGTTT	285836	118032	GGTAGAGAAGGAGCAGGGCC
196663	28859	GTGCCCTTCCTGGGGGTTGT	241250	73446	GCTGTTGCAAAACCAAGGTT	285837	118033	AGGTAGAGAAGGAGCAGGGC
196664	28860	GGTGCCCTTCCTGGGGGTTG	241251	73447	TGCTGTTGCAAAACCAAGGT	285838	118034	CAGGTAGAGAAGGAGCAGGG
196665	28861	GGGTGCCCTTCCTGGGGGTT	241252	73448	CTGCTGTTGCAAAACCAAGG	285839	118035	CCAGGTAGAGAAGGAGCAGG
196666	28862	AGGGTGCCCTTCCTGGGGGT	241253	73449	GCTGCTGTTGCAAAACCAAG	285840	118036	CCCAGGTAGAGAAGGAGCAG
196667	28863	CAGGGTGCCCTTCCTGGGGG	241254	73450	GGCTGCTGTTGCAAAACCAA	285841	118037	TCCCAGGTAGAGAAGGAGCA
196668	28864	CCAGGGTGCCCTTCCTGGGG	241255	73451	TGGCTGCTGTTGCAAAACCA	285842	118038	GTCCCAGGTAGAGAAGGAGC
196669	28865	TCCAGGGTGCCCTTCCTGGG	241256	73452	ATGGCTGCTGTTGCAAAACC	285843	118039	GGTCCCAGGTAGAGAAGGAG
196670	28866	TTCCAGGGTGCCCTTCCTGG	241257	73453	CATGGCTGCTGTTGCAAAAC	285844	118040	GGGTCCCAGGTAGAGAAGGA
196671	28867	CTTCCAGGGTGCCCTTCCTG	241258	73454	TCATGGCTGCTGTTGCAAAA	285845	118041	AGGGTCCCAGGTAGAGAAGG
196672	28868	CCTTCCAGGGTGCCCTTCCT	241259	73455	CTCATGGCTGCTGTTGCAAA	285846	118042	AAGGGTCCCAGGTAGAGAAG
196673	28869	CCCTTCCAGGGTGCCCTTCC	241260	73456	TCTCATGGCTGCTGTTGCAA	285847	118043	GAAGGGTCCCAGGTAGAGAA
196674	28870	CCCCTTCCAGGGTGCCCTTC	241261	73457	GTCTCATGGCTGCTGTTGCA	285848	118044	AGAAGGGTCCCAGGTAGAGA

196675	28871	ACCCCTTCCAGGGTGCCCTT	241262	73458	GGTCTCATGGCTGCTGTTGC	285849	118045	CAGAAGGGTCCCAGGTAGAG
196676	28872	GACCCCTTCCAGGGTGCCCT	241263	73459	AGGTCTCATGGCTGCTGTTG	285850	118046	GCAGAAGGGTCCCAGGTAGA
196677	28873	GGACCCCTTCCAGGGTGCCC	241264	73460	AAGGTCTCATGGCTGCTGTT	285851	118047	GGCAGAAGGGTCCCAGGTAG
196678	28874	CGGACCCCTTCCAGGGTGCC	241265	73461	AAAGGTCTCATGGCTGCTGT	285852	118048	AGGCAGAAGGGTCCCAGGTA
196679	28875	CCGGACCCCTTCCAGGGTGC	241266	73462	TAAAGGTCTCATGGCTGCTG	285853	118049	GAGGCAGAAGGGTCCCAGGT
196680	28876	GCCGGACCCCTTCCAGGGTG	241267	73463	GTAAAGGTCTCATGGCTGCT	285854	118050	GGAGGCAGAAGGGTCCCAGG
196681	28877	AGCCGGACCCCTTCCAGGGT	241268	73464	TGTAAAGGTCTCATGGCTGC	285855	118051	AGGAGGCAGAAGGGTCCCAG
196682	28878	CAGCCGGACCCCTTCCAGGG	241269	73465	GTGTAAAGGTCTCATGGCTG	285856	118052	CAGGAGGCAGAAGGGTCCCA
196683	28879	ACAGCCGGACCCCTTCCAGG	241270	73466	GGTGTAAAGGTCTCATGGCT	285857	118053	CCAGGAGGCAGAAGGGTCCC
196684	28880	GACAGCCGGACCCCTTCCAG	241271	73467	GGGTGTAAAGGTCTCATGGC	285858	118054	GCCAGGAGGCAGAAGGGTCC
196685	28881	GGACAGCCGGACCCCTTCCA	241272	73468	AGGGTGTAAAGGTCTCATGG	285859	118055	AGCCAGGAGGCAGAAGGGTC
196686	28882	GGGACAGCCGGACCCCTTCC	241273	73469	GAGGGTGTAAAGGTCTCATG	285860	118056	CAGCCAGGAGGCAGAAGGGT
196687	28883	AGGGACAGCCGGACCCCTTC	241274	73470	GGAGGGTGTAAAGGTCTCAT	285861	118057	CCAGCCAGGAGGCAGAAGGG
196688	28884	CAGGGACAGCCGGACCCCTT	241275	73471	CGGAGGGTGTAAAGGTCTCA	285862	118058	TCCAGCCAGGAGGCAGAAGG
196689	28885	TCAGGGACAGCCGGACCCCT	241276	73472	GCGGAGGGTGTAAAGGTCTC	285863	118059	GTCCAGCCAGGAGGCAGAAG
196690	28886	ATCAGGGACAGCCGGACCCC	241277	73473	GGCGGAGGGTGTAAAGGTCT	285864	118060	GGTCCAGCCAGGAGGCAGAA
196691	28887	AATCAGGGACAGCCGGACCC	241278	73474	GGGCGGAGGGTGTAAAGGTC	285865	118061	GGGTCCAGCCAGGAGGCAGA
196692	28888	AAATCAGGGACAGCCGGACC	241279	73475	AGGGCGGAGGGTGTAAAGGT	285866	118062	AGGGTCCAGCCAGGAGGCAG
196693	28889	TAAATCAGGGACAGCCGGAC	241280	73476	AAGGGCGGAGGGTGTAAAGG	285867	118063	CAGGGTCCAGCCAGGAGGCA
196694	28890	GTAAATCAGGGACAGCCGGA	241281	73477	GAAGGGCGGAGGGTGTAAAG	285868	118064	CCAGGGTCCAGCCAGGAGGC
196695	28891	AGTAAATCAGGGACAGCCGG	241282	73478	TGAAGGGCGGAGGGTGTAAA	285869	118065	TCCAGGGTCCAGCCAGGAGG
196696	28892	AAGTAAATCAGGGACAGCCG	241283	73479	ATGAAGGGCGGAGGGTGTAA	285870	118066	TTCCAGGGTCCAGCCAGGAG
196697	28893	CAAGTAAATCAGGGACAGCC	241284	73480	GATGAAGGGCGGAGGGTGTA	285871	118067	CTTCCAGGGTCCAGCCAGGA
196698	28894	ACAAGTAAATCAGGGACAGC	241285	73481	GGATGAAGGGCGGAGGGTGT	285872	118068	GCTTCCAGGGTCCAGCCAGG
196699	28895	CACAAGTAAATCAGGGACAG	241286	73482	AGGATGAAGGGCGGAGGGTG	285873	118069	AGCTTCCAGGGTCCAGCCAG
196700	28896	CCACAAGTAAATCAGGGACA	241287	73483	CAGGATGAAGGGCGGAGGGT	285874	118070	GAGCTTCCAGGGTCCAGCCA
196701	28897	CCCACAAGTAAATCAGGGAC	241288	73484	ACAGGATGAAGGGCGGAGGG	285875	118071	AGAGCTTCCAGGGTCCAGCC
196702	28898	GCCCACAAGTAAATCAGGGA	241289	73485	GACAGGATGAAGGGCGGAGG	285876	118072	CAGAGCTTCCAGGGTCCAGC
196703	28899	TGCCCACAAGTAAATCAGGG	241290	73486	GGACAGGATGAAGGGCGGAG	285877	118073	GCAGAGCTTCCAGGGTCCAG
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196706	28902	CAGTGCCCACAAGTAAATCA	241293	73489	GGGGGACAGGATGAAGGGCG	285880	118076	CCTGCAGAGCTTCCAGGGTC
196707	28903	CCAGTGCCCACAAGTAAATC	241294	73490	TGGGGGACAGGATGAAGGGC	285881	118077	CCCTGCAGAGCTTCCAGGGT
196708	28904	CCCAGTGCCCACAAGTAAAT	241295	73491	GTGGGGGACAGGATGAAGGG	285882	118078	GCCCTGCAGAGCTTCCAGGG
196709	28905	CCCCAGTGCCCACAAGTAAA	241296	73492	AGTGGGGGACAGGATGAAGG	285883	118079	GGCCCTGCAGAGCTTCCAGG
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196713	28909	ATTCCCCCAGTGCCCACAAG	241300	73496	CCTCAGTGGGGGACAGGATG	285887	118083	AGCAGGCCCTGCAGAGCTTC
196714	28910	CATTCCCCCAGTGCCCACAA	241301	73497	GCCTCAGTGGGGGACAGGAT	285888	118084	CAGCAGGCCCTGCAGAGCTT
196715	28911	GCATTCCCCCAGTGCCCACA	241302	73498	GGCCTCAGTGGGGGACAGGA	285889	118085	ACAGCAGGCCCTGCAGAGCT
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196717	28913	GGGCATTCCCCCAGTGCCCA	241304	73500	GGGGCCTCAGTGGGGGACAG	285891	118087	GGACAGCAGGCCCTGCAGAG
196718	28914	CGGGCATTCCCCCAGTGCCC	241305	73501	TGGGGCCTCAGTGGGGGACA	285892	118088	GGGACAGCAGGCCCTGCAGA
196719	28915	CCGGGCATTCCCCCAGTGCC	241306	73502	CTGGGGCCTCAGTGGGGGAC	285893	118089	GGGGACAGCAGGCCCTGCAG
196720	28916	TCCGGGCATTCCCCCAGTGC	241307	73503	TCTGGGGCCTCAGTGGGGGA	285894	118090	GGGGGACAGCAGGCCCTGCA
196721	28917	CTCCGGGCATTCCCCCAGTG	241308	73504	CTCTGGGGCCTCAGTGGGGG	285895	118091	AGGGGGACAGCAGGCCCTGC
196722	28918	GCTCCGGGCATTCCCCCAGT	241309	73505	GCTCTGGGGCCTCAGTGGGG	285896	118092	GAGGGGGACAGCAGGCCCTG
196723	28919	GGCTCCGGGCATTCCCCCAG	241310	73506	GGCTCTGGGGCCTCAGTGGG	285897	118093	GGAGGGGGACAGCAGGCCCT
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196725	28921	ATGGCTCCGGGCATTCCCCC	241312	73508	ATGGCTCTGGGGCCTCAGTG	285899	118095	AGGGAGGGGGACAGCAGGCC
196726	28922	GATGGCTCCGGGCATTCCCC	241313	73509	AATGGCTCTGGGGCCTCAGT	285900	118096	CAGGGAGGGGGACAGCAGGC
196727	28923	GGATGGCTCCGGGCATTCCC	241314	73510	GAATGGCTCTGGGGCCTCAG	285901	118097	GCAGGGAGGGGGACAGCAGG
196728	28924	TGGATGGCTCCGGGCATTCC	241315	73511	GGAATGGCTCTGGGGCCTCA	285902	118098	GGCAGGGAGGGGGACAGCAG
196729	28925	CTGGATGGCTCCGGGCATTC	241316	73512	AGGAATGGCTCTGGGGCCTC	285903	118099	GGGCAGGGAGGGGGACAGCA
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196731	28927	GGCTGGATGGCTCCGGGCAT	241318	73514	TAAGGAATGGCTCTGGGGCC	285905	118101	GAGGGCAGGGAGGGGGACAG
196732	28928	GGGCTGGATGGCTCCGGGCA	241319	73515	TTAAGGAATGGCTCTGGGGC	285906	118102	GGAGGGCAGGGAGGGGGACA
196733	28929	AGGGCTGGATGGCTCCGGGC	241320	73516	TTTAAGGAATGGCTCTGGGG	285907	118103	TGGAGGGCAGGGAGGGGGAC
196734	28930	GAGGGCTGGATGGCTCCGGG	241321	73517	CTTTAAGGAATGGCTCTGGG	285908	118104	CTGGAGGGCAGGGAGGGGGA
196735	28931	TGAGGGCTGGATGGCTCCGG	241322	73518	GCTTTAAGGAATGGCTCTGG	285909	118105	CCTGGAGGGCAGGGAGGGGG
196736	28932	CTGAGGGCTGGATGGCTCCG	241323	73519	TGCTTTAAGGAATGGCTCTG	285910	118106	ACCTGGAGGGCAGGGAGGGG
196737	28933	CCTGAGGGCTGGATGGCTCC	241324	73520	CTGCTTTAAGGAATGGCTCT	285911	118107	TACCTGGAGGGCAGGGAGGG
196738	28934	CCCTGAGGGCTGGATGGCTC	241325	73521	GCTGCTTTAAGGAATGGCTC	285912	118108	ATACCTGGAGGGCAGGGAGG
196739	28935	GCCCTGAGGGCTGGATGGCT	241326	73522	CGCTGCTTTAAGGAATGGCT	285913	118109	GATACCTGGAGGGCAGGGAG
196740	28936	AGCCCTGAGGGCTGGATGGC	241327	73523	GCGCTGCTTTAAGGAATGGC	285914	118110	GGATACCTGGAGGGCAGGGA
196741	28937	GAGCCCTGAGGGCTGGATGG	241328	73524	CGCGCTGCTTTAAGGAATGG	285915	118111	AGGATACCTGGAGGGCAGGG
196742	28938	AGAGCCCTGAGGGCTGGATG	241329	73525	GCGCGCTGCTTTAAGGAATG	285916	118112	CAGGATACCTGGAGGGCAGG
196743	28939	CAGAGCCCTGAGGGCTGGAT	241330	73526	GGCGCGCTGCTTTAAGGAAT	285917	118113	TCAGGATACCTGGAGGGCAG
196744	28940	ACAGAGCCCTGAGGGCTGGA	241331	73527	TGGCGCGCTGCTTTAAGGAA	285918	118114	GTCAGGATACCTGGAGGGCA
196745	28941	CACAGAGCCCTGAGGGCTGG	241332	73528	GTGGCGCGCTGCTTTAAGGA	285919	118115	GGTCAGGATACCTGGAGGGC
196746	28942	ACACAGAGCCCTGAGGGCTG	241333	73529	TGTGGCGCGCTGCTTTAAGG	285920	118116	TGGTCAGGATACCTGGAGGG

196747	28943	CACACAGAGCCCTGAGGGCT	241334	73530	TTGTGGCGCGCTGCTTTAAG	285921	118117	GTGGTCAGGATACCTGGAGG
196748	28944	TCACACAGAGCCCTGAGGGC	241335	73531	TTTGTGGCGCGCTGCTTTAA	285922	118118	GGTGGTCAGGATACCTGGAG
196749	28945	ATCACACAGAGCCCTGAGGG	241336	73532	GTTTGTGGCGCGCTGCTTTA	285923	118119	CGGTGGTCAGGATACCTGGA
196750	28946	AATCACACAGAGCCCTGAGG	241337	73533	AGTTTGTGGCGCGCTGCTTT	285924	118120	CCGGTGGTCAGGATACCTGG
196751	28947	GAATCACACAGAGCCCTGAG	241338	73534	TAGTTTGTGGCGCGCTGCTT	285925	118121	GCCGGTGGTCAGGATACCTG
196752	28948	AGAATCACACAGAGCCCTGA	241339	73535	ATAGTTTGTGGCGCGCTGCT	285926	118122	GGCCGGTGGTCAGGATACCT
196753	28949	CAGAATCACACAGAGCCCTG	241340	73536	TATAGTTTGTGGCGCGCTGC	285927	118123	GGGCCGGTGGTCAGGATACC
196754	28950	CCAGAATCACACAGAGCCCT	241341	73537	TTATAGTTTGTGGCGCGCTG	285928	118124	AGGGCCGGTGGTCAGGATAC
196755	28951	CCCAGAATCACACAGAGCCC	241342	73538	GTTATAGTTTGTGGCGCGCT	285929	118125	CAGGGCCGGTGGTCAGGATA
196756	28952	ACCCAGAATCACACAGAGCC	241343	73539	GGTTATAGTTTGTGGCGCGC	285930	118126	CCAGGGCCGGTGGTCAGGAT
196757	28953	AACCCAGAATCACACAGAGC	241344	73540	GGGTTATAGTTTGTGGCGCG	285931	118127	GCCAGGGCCGGTGGTCAGGA
196758	28954	GAACCCAGAATCACACAGAG	241345	73541	TGGGTTATAGTTTGTGGCGC	285932	118128	AGCCAGGGCCGGTGGTCAGG
196759	28955	GGAACCCAGAATCACACAGA	241346	73542	GTGGGTTATAGTTTGTGGCG	285933	118129	GAGCCAGGGCCGGTGGTCAG
196760	28956	AGGAACCCAGAATCACACAG	241347	73543	TGTGGGTTATAGTTTGTGGC	285934	118130	GGAGCCAGGGCCGGTGGTCA
196761	28957	GAGGAACCCAGAATCACACA	241348	73544	TTGTGGGTTATAGTTTGTGG	285935	118131	GGGAGCCAGGGCCGGTGGTC
196762	28958	GGAGGAACCCAGAATCACAC	241349	73545	CTTGTGGGTTATAGTTTGTG	285936	118132	TGGGAGCCAGGGCCGGTGGT
196763	28959	GGGAGGAACCCAGAATCACA	241350	73546	GCTTGTGGGTTATAGTTTGT	285937	118133	GTGGGAGCCAGGGCCGGTGG
196764	28960	TGGGAGGAACCCAGAATCAC	241351	73547	GGCTTGTGGGTTATAGTTTG	285938	118134	AGTGGGAGCCAGGGCCGGTG
196765	28961	ATGGGAGGAACCCAGAATCA	241352	73548	TGGCTTGTGGGTTATAGTTT	285939	118135	CAGTGGGAGCCAGGGCCGGT
196766	28962	TATGGGAGGAACCCAGAATC	241353	73549	TTGGCTTGTGGGTTATAGTT	285940	118136	GCAGTGGGAGCCAGGGCCGG
196767	28963	TTATGGGAGGAACCCAGAAT	241354	73550	ATTGGCTTGTGGGTTATAGT	285941	118137	GGCAGTGGGAGCCAGGGCCG
196768	28964	TTTATGGGAGGAACCCAGAA	241355	73551	AATTGGCTTGTGGGTTATAG	285942	118138	TGGCAGTGGGAGCCAGGGCC
196769	28965	TTTTATGGGAGGAACCCAGA	241356	73552	GAATTGGCTTGTGGGTTATA	285943	118139	ATGGCAGTGGGAGCCAGGGC
196770	28966	CTTTTATGGGAGGAACCCAG	241357	73553	AGAATTGGCTTGTGGGTTAT	285944	118140	GATGGCAGTGGGAGCCAGGG
196771	28967	TCTTTTATGGGAGGAACCCA	241358	73554	CAGAATTGGCTTGTGGGTTA	285945	118141	GGATGGCAGTGGGAGCCAGG
196772	28968	ATCTTTTATGGGAGGAACCC	241359	73555	CCAGAATTGGCTTGTGGGTT	285946	118142	TGGATGGCAGTGGGAGCCAG
196773	28969	TATCTTTTATGGGAGGAACC	241360	73556	ACCAGAATTGGCTTGTGGGT	285947	118143	GTGGATGGCAGTGGGAGCCA
196774	28970	TTATCTTTTATGGGAGGAAC	241361	73557	TACCAGAATTGGCTTGTGGG	285948	118144	AGTGGATGGCAGTGGGAGCC
196775	28971	ATTATCTTTTATGGGAGGAA	241362	73558	GTACCAGAATTGGCTTGTGG	285949	118145	GAGTGGATGGCAGTGGGAGC
196776	28972	GATTATCTTTTATGGGAGGA	241363	73559	GGTACCAGAATTGGCTTGTG	285950	118146	GGAGTGGATGGCAGTGGGAG
196777	28973	TGATTATCTTTTATGGGAGG	241364	73560	GGGTACCAGAATTGGCTTGT	285951	118147	AGGAGTGGATGGCAGTGGGA
196778	28974	CTGATTATCTTTTATGGGAG	241365	73561	TGGGTACCAGAATTGGCTTG	285952	118148	GAGGAGTGGATGGCAGTGGG
196779	28975	TCTGATTATCTTTTATGGGA	241366	73562	CTGGGTACCAGAATTGGCTT	285953	118149	AGAGGAGTGGATGGCAGTGG
196780	28976	ATCTGATTATCTTTTATGGG	241367	73563	GCTGGGTACCAGAATTGGCT	285954	118150	GAGAGGAGTGGATGGCAGTG
196781	28977	AATCTGATTATCTTTTATGG	241368	73564	GGCTGGGTACCAGAATTGGC	285955	118151	GGAGAGGAGTGGATGGCAGT
196782	28978	GAATCTGATTATCTTTTATG	241369	73565	AGGCTGGGTACCAGAATTGG	285956	118152	AGGAGAGGAGTGGATGGCAG
196783	28979	AGAATCTGATTATCTTTTAT	241370	73566	CAGGCTGGGTACCAGAATTG	285957	118153	AAGGAGAGGAGTGGATGGCA
196784	28980	AAGAATCTGATTATCTTTTA	241371	73567	ACAGGCTGGGTACCAGAATT	285958	118154	AAAGGAGAGGAGTGGATGGC
196785	28981	AAAGAATCTGATTATCTTTT	241372	73568	AACAGGCTGGGTACCAGAAT	285959	118155	GAAAGGAGAGGAGTGGATGG
196786	28982	GAAAGAATCTGATTATCTTT	241373	73569	AAACAGGCTGGGTACCAGAA	285960	118156	AGAAAGGAGAGGAGTGGATG
196787	28983	TGAAAGAATCTGATTATCTT	241374	73570	AAAACAGGCTGGGTACCAGA	285961	118157	CAGAAAGGAGAGGAGTGGAT
196788	28984	GTGAAAGAATCTGATTATCT	241375	73571	CAAAACAGGCTGGGTACCAG	285962	118158	CCAGAAAGGAGAGGAGTGGA
196789	28985	CGTGAAAGAATCTGATTATC	241376	73572	GCAAAACAGGCTGGGTACCA	285963	118159	GCCAGAAAGGAGAGGAGTGG
196790	28986	ACGTGAAAGAATCTGATTAT	241377	73573	TGCAAAACAGGCTGGGTACC	285964	118160	GGCCAGAAAGGAGAGGAGTG
196791	28987	AACGTGAAAGAATCTGATTA	241378	73574	GTGCAAAACAGGCTGGGTAC	285965	118161	CGGCCAGAAAGGAGAGGAGT
196792	28988	TAACGTGAAAGAATCTGATT	241379	73575	TGTGCAAAACAGGCTGGGTA	285966	118162	ACGGCCAGAAAGGAGAGGAG
196793	28989	TTAACGTGAAAGAATCTGAT	241380	73576	CTGTGCAAAACAGGCTGGGT	285967	118163	AACGGCCAGAAAGGAGAGGA
196794	28990	ATTAACGTGAAAGAATCTGA	241381	73577	GCTGTGCAAAACAGGCTGGG	285968	118164	GAACGGCCAGAAAGGAGAGG
196795	28991	CATTAACGTGAAAGAATCTG	241382	73578	GGCTGTGCAAAACAGGCTGG	285969	118165	GGAACGGCCAGAAAGGAGAG
196796	28992	ACATTAACGTGAAAGAATCT	241383	73579	TGGCTGTGCAAAACAGGCTG	285970	118166	GGGAACGGCCAGAAAGGAGA
196797	28993	GACATTAACGTGAAAGAATC	241384	73580	CTGGCTGTGCAAAACAGGCT	285971	118167	AGGGAACGGCCAGAAAGGAG
196798	28994	AGACATTAACGTGAAAGAAT	241385	73581	ACTGGCTGTGCAAAACAGGC	285972	118168	CAGGGAACGGCCAGAAAGGA
196799	28995	AAGACATTAACGTGAAAGAA	241386	73582	CACTGGCTGTGCAAAACAGG	285973	118169	CCAGGGAACGGCCAGAAAGG
196800	28996	AAAGACATTAACGTGAAAGA	241387	73583	TCACTGGCTGTGCAAAACAG	285974	118170	ACCAGGGAACGGCCAGAAAG
196801	28997	GAAAGACATTAACGTGAAAG	241388	73584	TTCACTGGCTGTGCAAAACA	285975	118171	GACCAGGGAACGGCCAGAAA
196802	28998	AGAAAGACATTAACGTGAAA	241389	73585	GTTCACTGGCTGTGCAAAAC	285976	118172	GGACCAGGGAACGGCCAGAA
196803	28999	GAGAAAGACATTAACGTGAA	241390	73586	AGTTCACTGGCTGTGCAAAA	285977	118173	GGGACCAGGGAACGGCCAGA
196804	29000	GGAGAAAGACATTAACGTGA	241391	73587	CAGTTCACTGGCTGTGCAAA	285978	118174	AGGGACCAGGGAACGGCCAG
196805	29001	TGGAGAAAGACATTAACGTG	241392	73588	TCAGTTCACTGGCTGTGCAA	285979	118175	CAGGGACCAGGGAACGGCCA
196806	29002	GTGGAGAAAGACATTAACGT	241393	73589	GTCAGTTCACTGGCTGTGCA	285980	118176	ACAGGGACCAGGGAACGGCC
196807	29003	GGTGGAGAAAGACATTAACG	241394	73590	TGTCAGTTCACTGGCTGTGC	285981	118177	GACAGGGACCAGGGAACGGC
196808	29004	AGGTGGAGAAAGACATTAAC	241395	73591	TTGTCAGTTCACTGGCTGTG	285982	118178	GGACAGGGACCAGGGAACGG
196809	29005	GAGGTGGAGAAAGACATTAA	241396	73592	ATTGTCAGTTCACTGGCTGT	285983	118179	GGGACAGGGACCAGGGAACG
196810	29006	TGAGGTGGAGAAAGACATTA	241397	73593	CATTGTCAGTTCACTGGCTG	285984	118180	TGGGACAGGGACCAGGGAAC
196811	29007	ATGAGGTGGAGAAAGACATT	241398	73594	TCATTGTCAGTTCACTGGCT	285985	118181	CTGGGACAGGGACCAGGGAA
196812	29008	AATGAGGTGGAGAAAGACAT	241399	73595	ATCATTGTCAGTTCACTGGC	285986	118182	GCTGGGACAGGGACCAGGGA
196813	29009	CAATGAGGTGGAGAAAGACA	241400	73596	GATCATTGTCAGTTCACTGG	285987	118183	GGCTGGGACAGGGACCAGGG
196814	29010	GCAATGAGGTGGAGAAAGAC	241401	73597	AGATCATTGTCAGTTCACTG	285988	118184	GGGCTGGGACAGGGACCAGG
196815	29011	TGCAATGAGGTGGAGAAAGA	241402	73598	AAGATCATTGTCAGTTCACT	285989	118185	GGGGCTGGGACAGGGACCAG
196816	29012	GTGCAATGAGGTGGAGAAAG	241403	73599	AAAGATCATTGTCAGTTCAC	285990	118186	GGGGGCTGGGACAGGGACCA
196817	29013	TGTGCAATGAGGTGGAGAAA	241404	73600	AAAAGATCATTGTCAGTTCA	285991	118187	GGGGGGCTGGGACAGGGACC
196818	29014	ATGTGCAATGAGGTGGAGAA	241405	73601	GAAAAGATCATTGTCAGTTC	285992	118188	AGGGGGGCTGGGACAGGGAC

196819	29015	GATGTGCAATGAGGTGGAGA	241406	73602	TGAAAAGATCATTGTCAGTT	285993	118189	GAGGGGGGCTGGGACAGGGA
196820	29016	TGATGTGCAATGAGGTGGAG	241407	73603	ATGAAAAGATCATTGTCAGT	285994	118190	GGAGGGGGGCTGGGACAGGG
196821	29017	ATGATGTGCAATGAGGTGGA	241408	73604	TATGAAAAGATCATTGTCAG	285995	118191	GGGAGGGGGGCTGGGACAGG
196822	29018	CATGATGTGCAATGAGGTGG	241409	73605	GTATGAAAAGATCATTGTCA	285996	118192	GGGGAGGGGGGCTGGGACAG
196823	29019	GCATGATGTGCAATGAGGTG	241410	73606	TGTATGAAAAGATCATTGTC	285997	118193	GGGGGAGGGGGGCTGGGACA
196824	29020	TGCATGATGTGCAATGAGGT	241411	73607	CTGTATGAAAAGATCATTGT	285998	118194	AGGGGGAGGGGGGCTGGGAC
196825	29021	CTGCATGATGTGCAATGAGG	241412	73608	GCTGTATGAAAAGATCATTG	285999	118195	GAGGGGGAGGGGGGCTGGGA
196826	29022	GCTGCATGATGTGCAATGAG	241413	73609	GGCTGTATGAAAAGATCATT	286000	118196	AGAGGGGGAGGGGGGCTGGG
196827	29023	AGCTGCATGATGTGCAATGA	241414	73610	TGGCTGTATGAAAAGATCAT	286001	118197	GAGAGGGGGAGGGGGGCTGG
196828	29024	TAGCTGCATGATGTGCAATG	241415	73611	CTGGCTGTATGAAAAGATCA	286002	118198	TGAGAGGGGGAGGGGGGCTG
196829	29025	ATAGCTGCATGATGTGCAAT	241416	73612	TCTGGCTGTATGAAAAGATC	286003	118199	GTGAGAGGGGGAGGGGGGCT
196830	29026	AATAGCTGCATGATGTGCAA	241417	73613	TTCTGGCTGTATGAAAAGAT	286004	118200	CGTGAGAGGGGGAGGGGGGC
196831	29027	GAATAGCTGCATGATGTGCA	241418	73614	TTTCTGGCTGTATGAAAAGA	286005	118201	TCGTGAGAGGGGGAGGGGGG
196832	29028	TGAATAGCTGCATGATGTGC	241419	73615	TTTTCTGGCTGTATGAAAAG	286006	118202	CTCGTGAGAGGGGGAGGGGG
196833	29029	ATGAATAGCTGCATGATGTG	241420	73616	TTTTTCTGGCTGTATGAAAA	286007	118203	ACTCGTGAGAGGGGGAGGGG
196834	29030	AATGAATAGCTGCATGATGT	241421	73617	GTTTTTCTGGCTGTATGAAA	286008	118204	AACTCGTGAGAGGGGGAGGG
196835	29031	CAATGAATAGCTGCATGATG	241422	73618	TGTTTTTCTGGCTGTATGAA	286009	118205	TAACTCGTGAGAGGGGGAGG
196836	29032	TCAATGAATAGCTGCATGAT	241423	73619	TTGTTTTTCTGGCTGTATGA	286010	118206	GTAACTCGTGAGAGGGGGAG
196837	29033	GTCAATGAATAGCTGCATGA	241424	73620	TTTGTTTTTCTGGCTGTATG	286011	118207	GGTAACTCGTGAGAGGGGGA
196838	29034	AGTCAATGAATAGCTGCATG	241425	73621	TTTTGTTTTTCTGGCTGTAT	286012	118208	AGGTAACTCGTGAGAGGGGG
196839	29035	GAGTCAATGAATAGCTGCAT	241426	73622	GTTTTGTTTTTCTGGCTGTA	286013	118209	GAGGTAACTCGTGAGAGGGG
196840	29036	TGAGTCAATGAATAGCTGCA	241427	73623	TGTTTTGTTTTTCTGGCTGT	286014	118210	TGAGGTAACTCGTGAGAGGG
196841	29037	CTGAGTCAATGAATAGCTGC	241428	73624	TTGTTTTGTTTTTCTGGCTG	286015	118211	GTGAGGTAACTCGTGAGAGG
196842	29038	GCTGAGTCAATGAATAGCTG	241429	73625	TTTGTTTTGTTTTTCTGGCT	286016	118212	GGTGAGGTAACTCGTGAGAG
196843	29039	TGCTGAGTCAATGAATAGCT	241430	73626	TTTTGTTTTGTTTTTCTGGC	286017	118213	GGGTGAGGTAACTCGTGAGA
196844	29040	TTGCTGAGTCAATGAATAGC	241431	73627	GTTTTGTTTTGTTTTTCTGG	286018	118214	TGGGTGAGGTAACTCGTGAG
196845	29041	CTTGCTGAGTCAATGAATAG	241432	73628	TGTTTTGTTTTGTTTTTCTG	286019	118215	CTGGGTGAGGTAACTCGTGA
196846	29042	ACTTGCTGAGTCAATGAATA	241433	73629	TTGTTTTGTTTTGTTTTTCT	286020	118216	CCTGGGTGAGGTAACTCGTG
196847	29043	TACTTGCTGAGTCAATGAAT	241434	73630	TTTGTTTTGTTTTGTTTTTC	286021	118217	GCCTGGGTGAGGTAACTCGT
196848	29044	ATACTTGCTGAGTCAATGAA	241435	73631	TTTTGTTTTGTTTTGTTTTT	286022	118218	GGCCTGGGTGAGGTAACTCG
196849	29045	GATACTTGCTGAGTCAATGA	241436	73632	TTTTTGTTTTGTTTTGTTTT	286023	118219	TGGCCTGGGTGAGGTAACTC
196850	29046	TGATACTTGCTGAGTCAATG	241437	73633	TTTTTTGTTTTGTTTTGTTT	286024	118220	CTGGCCTGGGTGAGGTAACT
196851	29047	CTGATACTTGCTGAGTCAAT	241438	73634	GTTTTTTGTTTTGTTTTGTT	286025	118221	TCTGGCCTGGGTGAGGTAAC
196852	29048	GCTGATACTTGCTGAGTCAA	241439	73635	TGTTTTTTGTTTTGTTTTGT	286026	118222	CTCTGGCCTGGGTGAGGTAA
196853	29049	AGCTGATACTTGCTGAGTCA	241440	73636	TTGTTTTTTGTTTTGTTTTG	286027	118223	CCTCTGGCCTGGGTGAGGTA
196854	29050	AAGCTGATACTTGCTGAGTC	241441	73637	GTTGTTTTTTGTTTTGTTTT	286028	118224	CCCTCTGGCCTGGGTGAGGT
196855	29051	AAAGCTGATACTTGCTGAGT	241442	73638	TGTTGTTTTTTGTTTTGTTT	286029	118225	TCCCTCTGGCCTGGGTGAGG
196856	29052	CAAAGCTGATACTTGCTGAG	241443	73639	TTGTTGTTTTTTGTTTTGTT	286030	118226	TTCCCTCTGGCCTGGGTGAG
196857	29053	GCAAAGCTGATACTTGCTGA	241444	73640	TTTGTTGTTTTTTGTTTTGT	286031	118227	CTTCCCTCTGGCCTGGGTGA
196858	29054	TGCAAAGCTGATACTTGCTG	241445	73641	TTTTGTTGTTTTTTGTTTTG	286032	118228	TCTTCCCTCTGGCCTGGGTG
196859	29055	ATGCAAAGCTGATACTTGCT	241446	73642	TTTTTGTTGTTTTTTGTTTT	286033	118229	CTCTTCCCTCTGGCCTGGGT
196860	29056	CATGCAAAGCTGATACTTGC	241447	73643	TTTTTTGTTGTTTTTTGTTT	286034	118230	CCTCTTCCCTCTGGCCTGGG
196861	29057	GCATGCAAAGCTGATACTTG	241448	73644	TTTTTTTGTTGTTTTTTGTT	286035	118231	CCCTCTTCCCTCTGGCCTGG
196862	29058	CGCATGCAAAGCTGATACTT	241449	73645	TTTTTTTTGTTGTTTTTTGT	286036	118232	TCCCTCTTCCCTCTGGCCTG
196863	29059	TCGCATGCAAAGCTGATACT	241450	73646	TTTTTTTTTGTTGTTTTTTG	286037	118233	TTCCCTCTTCCCTCTGGCCT
196864	29060	GTCGCATGCAAAGCTGATAC	241451	73647	GTTTTTTTTTGTTGTTTTTT	286038	118234	CTTCCCTCTTCCCTCTGGCC
196865	29061	GGTCGCATGCAAAGCTGATA	241452	73648	GGTTTTTTTTTGTTGTTTTT	286039	118235	CCTTCCCTCTTCCCTCTGGC
196866	29062	AGGTCGCATGCAAAGCTGAT	241453	73649	GGGTTTTTTTTTGTTGTTTT	286040	118236	TCCTTCCCTCTTCCCTCTGG
196867	29063	AAGGTCGCATGCAAAGCTGA	241454	73650	GGGGTTTTTTTTTGTTGTTT	286041	118237	CTCCTTCCCTCTTCCCTCTG
196868	29064	CAAGGTCGCATGCAAAGCTG	241455	73651	TGGGGTTTTTTTTTGTTGTT	286042	118238	CCTCCTTCCCTCTTCCCTCT
196869	29065	CCAAGGTCGCATGCAAAGCT	241456	73652	GTGGGGTTTTTTTTTGTTGT	286043	118239	GCCTCCTTCCCTCTTCCCTC
196870	29066	GCCAAGGTCGCATGCAAAGC	241457	73653	GGTGGGGTTTTTTTTTGTTG	286044	118240	GGCCTCCTTCCCTCTTCCCT
196871	29067	GGCCAAGGTCGCATGCAAAG	241458	73654	TGGTGGGGTTTTTTTTTGTT	286045	118241	GGGCCTCCTTCCCTCTTCCC
196872	29068	AGGCCAAGGTCGCATGCAAA	241459	73655	ATGGTGGGGTTTTTTTTTGT	286046	118242	AGGGCCTCCTTCCCTCTTCC
196873	29069	TAGGCCAAGGTCGCATGCAA	241460	73656	AATGGTGGGGTTTTTTTTTG	286047	118243	CAGGGCCTCCTTCCCTCTTC
196874	29070	GTAGGCCAAGGTCGCATGCA	241461	73657	GAATGGTGGGGTTTTTTTTT	286048	118244	CCAGGGCCTCCTTCCCTCTT
196875	29071	GGTAGGCCAAGGTCGCATGC	241462	73658	AGAATGGTGGGGTTTTTTTT	286049	118245	ACCAGGGCCTCCTTCCCTCT
196876	29072	GGGTAGGCCAAGGTCGCATG	241463	73659	CAGAATGGTGGGGTTTTTTT	286050	118246	GACCAGGGCCTCCTTCCCTC
196877	29073	TGGGTAGGCCAAGGTCGCAT	241464	73660	TCAGAATGGTGGGGTTTTTT	286051	118247	TGACCAGGGCCTCCTTCCCT
196878	29074	GTGGGTAGGCCAAGGTCGCA	241465	73661	CTCAGAATGGTGGGGTTTTT	286052	118248	ATGACCAGGGCCTCCTTCCC
196879	29075	AGTGGGTAGGCCAAGGTCGC	241466	73662	GCTCAGAATGGTGGGGTTTT	286053	118249	TATGACCAGGGCCTCCTTCC
196880	29076	AAGTGGGTAGGCCAAGGTCG	241467	73663	TGCTCAGAATGGTGGGGTTT	286054	118250	GTATGACCAGGGCCTCCTTC
196881	29077	AAAGTGGGTAGGCCAAGGTC	241468	73664	ATGCTCAGAATGGTGGGGTT	286055	118251	GGTATGACCAGGGCCTCCTT
196882	29078	TAAAGTGGGTAGGCCAAGGT	241469	73665	CATGCTCAGAATGGTGGGGT	286056	118252	TGGTATGACCAGGGCCTCCT
196883	29079	CTAAAGTGGGTAGGCCAAGG	241470	73666	ACATGCTCAGAATGGTGGGG	286057	118253	CTGGTATGACCAGGGCCTCC
196884	29080	GCTAAAGTGGGTAGGCCAAG	241471	73667	CACATGCTCAGAATGGTGGG	286058	118254	GCTGGTATGACCAGGGCCTC
196885	29081	AGCTAAAGTGGGTAGGCCAA	241472	73668	TCACATGCTCAGAATGGTGG	286059	118255	TGCTGGTATGACCAGGGCCT
196886	29082	AAGCTAAAGTGGGTAGGCCA	241473	73669	GTCACATGCTCAGAATGGTG	286060	118256	GTGCTGGTATGACCAGGGCC
196887	29083	AAAGCTAAAGTGGGTAGGCC	241474	73670	AGTCACATGCTCAGAATGGT	286061	118257	CGTGCTGGTATGACCAGGGC
196888	29084	AAAAGCTAAAGTGGGTAGGC	241475	73671	AAGTCACATGCTCAGAATGG	286062	118258	ACGTGCTGGTATGACCAGGG
196889	29085	TAAAAGCTAAAGTGGGTAGG	241476	73672	GAAGTCACATGCTCAGAATG	286063	118259	GACGTGCTGGTATGACCAGG
196890	29086	CTAAAAGCTAAAGTGGGTAG	241477	73673	GGAAGTCACATGCTCAGAAT	286064	118260	GGACGTGCTGGTATGACCAG

196891	29087	ACTAAAAGCTAAAGTGGGTA	241478	73674	TGGAAGTCACATGCTCAGAA	286065	118261	AGGACGTGCTGGTATGACCA
196892	29088	TACTAAAAGCTAAAGTGGGT	241479	73675	ATGGAAGTCACATGCTCAGA	286066	118262	GAGGACGTGCTGGTATGACC
196893	29089	TTACTAAAAGCTAAAGTGGG	241480	73676	CATGGAAGTCACATGCTCAG	286067	118263	GGAGGACGTGCTGGTATGAC
196894	29090	ATTACTAAAAGCTAAAGTGG	241481	73677	ACATGGAAGTCACATGCTCA	286068	118264	GGGAGGACGTGCTGGTATGA
196895	29091	TATTACTAAAAGCTAAAGTG	241482	73678	AACATGGAAGTCACATGCTC	286069	118265	TGGGAGGACGTGCTGGTATG
196896	29092	CTATTACTAAAAGCTAAAGT	241483	73679	GAACATGGAAGTCACATGCT	286070	118266	GTGGGAGGACGTGCTGGTAT
196897	29093	GCTATTACTAAAAGCTAAAG	241484	73680	TGAACATGGAAGTCACATGC	286071	118267	GGTGGGAGGACGTGCTGGTA
196898	29094	AGCTATTACTAAAAGCTAAA	241485	73681	TTGAACATGGAAGTCACATG	286072	118268	AGGTGGGAGGACGTGCTGGT
196899	29095	GAGCTATTACTAAAAGCTAA	241486	73682	CTTGAACATGGAAGTCACAT	286073	118269	GAGGTGGGAGGACGTGCTGG
196900	29096	GGAGCTATTACTAAAAGCTA	241487	73683	TCTTGAACATGGAAGTCACA	286074	118270	GGAGGTGGGAGGACGTGCTG
196901	29097	GGGAGCTATTACTAAAAGCT	241488	73684	ATCTTGAACATGGAAGTCAC	286075	118271	GGGAGGTGGGAGGACGTGCT
196902	29098	AGGGAGCTATTACTAAAAGC	241489	73685	CATCTTGAACATGGAAGTCA	286076	118272	AGGGAGGTGGGAGGACGTGC
196903	29099	AAGGGAGCTATTACTAAAAG	241490	73686	ACATCTTGAACATGGAAGTC	286077	118273	GAGGGAGGTGGGAGGACGTG
196904	29100	GAAGGGAGCTATTACTAAAA	241491	73687	GACATCTTGAACATGGAAGT	286078	118274	CGAGGGAGGTGGGAGGACGT
196905	29101	AGAAGGGAGCTATTACTAAA	241492	73688	AGACATCTTGAACATGGAAG	286079	118275	CCGAGGGAGGTGGGAGGACG
196906	29102	AAGAAGGGAGCTATTACTAA	241493	73689	GAGACATCTTGAACATGGAA	286080	118276	GCCGAGGGAGGTGGGAGGAC
196907	29103	CAAGAAGGGAGCTATTACTA	241494	73690	TGAGACATCTTGAACATGGA	286081	118277	GGCCGAGGGAGGTGGGAGGA
196908	29104	TCAAGAAGGGAGCTATTACT	241495	73691	ATGAGACATCTTGAACATGG	286082	118278	GGGCCGAGGGAGGTGGGAGG
196909	29105	TTCAAGAAGGGAGCTATTAC	241496	73692	CATGAGACATCTTGAACATG	286083	118279	AGGGCCGAGGGAGGTGGGAG
196910	29106	ATTCAAGAAGGGAGCTATTA	241497	73693	ACATGAGACATCTTGAACAT	286084	118280	CAGGGCCGAGGGAGGTGGGA
196911	29107	TATTCAAGAAGGGAGCTATT	241498	73694	AACATGAGACATCTTGAACA	286085	118281	CCAGGGCCGAGGGAGGTGGG
196912	29108	TTATTCAAGAAGGGAGCTAT	241499	73695	GAACATGAGACATCTTGAAC	286086	118282	ACCAGGGCCGAGGGAGGTGG
196913	29109	ATTATTCAAGAAGGGAGCTA	241500	73696	TGAACATGAGACATCTTGAA	286087	118283	GACCAGGGCCGAGGGAGGTG
196914	29110	TATTATTCAAGAAGGGAGCT	241501	73697	CTGAACATGAGACATCTTGA	286088	118284	GGACCAGGGCCGAGGGAGGT
196915	29111	GTATTATTCAAGAAGGGAGC	241502	73698	TCTGAACATGAGACATCTTG	286089	118285	TGGACCAGGGCCGAGGGAGG
196916	29112	TGTATTATTCAAGAAGGGAG	241503	73699	TTCTGAACATGAGACATCTT	286090	118286	GTGGACCAGGGCCGAGGGAG
196917	29113	TTGTATTATTCAAGAAGGGA	241504	73700	TTTCTGAACATGAGACATCT	286091	118287	GGTGGACCAGGGCCGAGGGA
196918	29114	GTTGTATTATTCAAGAAGGG	241505	73701	CTTTCTGAACATGAGACATC	286092	118288	GGGTGGACCAGGGCCGAGGG
196919	29115	GGTTGTATTATTCAAGAAGG	241506	73702	CCTTTCTGAACATGAGACAT	286093	118289	GGGGTGGACCAGGGCCGAGG
196920	29116	TGGTTGTATTATTCAAGAAG	241507	73703	GCCTTTCTGAACATGAGACA	286094	118290	GGGGGTGGACCAGGGCCGAG
196921	29117	CTGGTTGTATTATTCAAGAA	241508	73704	GGCCTTTCTGAACATGAGAC	286095	118291	AGGGGGTGGACCAGGGCCGA
196922	29118	ACTGGTTGTATTATTCAAGA	241509	73705	GGGCCTTTCTGAACATGAGA	286096	118292	GAGGGGGTGGACCAGGGCCG
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196925	29121	CCCACTGGTTGTATTATTCA	241512	73708	CAGGGGCCTTTCTGAACATG	286099	118295	ACTGAGGGGGTGGACCAGGG
196926	29122	CCCCACTGGTTGTATTATTC	241513	73709	CCAGGGGCCTTTCTGAACAT	286100	118296	CACTGAGGGGGTGGACCAGG
196927	29123	TCCCCACTGGTTGTATTATT	241514	73710	TCCAGGGGCCTTTCTGAACA	286101	118297	GCACTGAGGGGGTGGACCAG
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196929	29125	TTTCCCCACTGGTTGTATTA	241516	73712	TTTCCAGGGGCCTTTCTGAA	286103	118299	CAGCACTGAGGGGGTGGACC
196930	29126	GTTTCCCCACTGGTTGTATT	241517	73713	TTTTCCAGGGGCCTTTCTGA	286104	118300	CCAGCACTGAGGGGGTGGAC
196931	29127	TGTTTCCCCACTGGTTGTAT	241518	73714	CTTTTCCAGGGGCCTTTCTG	286105	118301	GCCAGCACTGAGGGGGTGGA
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196933	29129	TCTGTTTCCCCACTGGTTGT	241520	73716	TCCTTTTCCAGGGGCCTTTC	286107	118303	AGGCCAGCACTGAGGGGGTG
196934	29130	TTCTGTTTCCCCACTGGTTG	241521	73717	CTCCTTTTCCAGGGGCCTTT	286108	118304	GAGGCCAGCACTGAGGGGGT
196935	29131	GTTCTGTTTCCCCACTGGTT	241522	73718	CCTCCTTTTCCAGGGGCCTT	286109	118305	TGAGGCCAGCACTGAGGGGG
196936	29132	GGTTCTGTTTCCCCACTGGT	241523	73719	TCCTCCTTTTCCAGGGGCCT	286110	118306	CTGAGGCCAGCACTGAGGGG
196937	29133	AGGTTCTGTTTCCCCACTGG	241524	73720	TTCCTCCTTTTCCAGGGGCC	286111	118307	TCTGAGGCCAGCACTGAGGG
196938	29134	TAGGTTCTGTTTCCCCACTG	241525	73721	CTTCCTCCTTTTCCAGGGGC	286112	118308	CTCTGAGGCCAGCACTGAGG
196939	29135	TTAGGTTCTGTTTCCCCACT	241526	73722	CCTTCCTCCTTTTCCAGGGG	286113	118309	GCTCTGAGGCCAGCACTGAG
196940	29136	GTTAGGTTCTGTTTCCCCAC	241527	73723	CCCTTCCTCCTTTTCCAGGG	286114	118310	TGCTCTGAGGCCAGCACTGA
196941	29137	AGTTAGGTTCTGTTTCCCCA	241528	73724	CCCCTTCCTCCTTTTCCAGG	286115	118311	GTGCTCTGAGGCCAGCACTG
196942	29138	GAGTTAGGTTCTGTTTCCCC	241529	73725	TCCCCTTCCTCCTTTTCCAG	286116	118312	TGTGCTCTGAGGCCAGCACT
196943	29139	AGAGTTAGGTTCTGTTTCCC	241530	73726	CTCCCCTTCCTCCTTTTCCA	286117	118313	CTGTGCTCTGAGGCCAGCAC
196944	29140	AAGAGTTAGGTTCTGTTTCC	241531	73727	GCTCCCCTTCCTCCTTTTCC	286118	118314	GCTGTGCTCTGAGGCCAGCA
196945	29141	TAAGAGTTAGGTTCTGTTTC	241532	73728	AGCTCCCCTTCCTCCTTTTC	286119	118315	AGCTGTGCTCTGAGGCCAGC
196946	29142	GTAAGAGTTAGGTTCTGTTT	241533	73729	CAGCTCCCCTTCCTCCTTTT	286120	118316	GAGCTGTGCTCTGAGGCCAG
196947	29143	GGTAAGAGTTAGGTTCTGTT	241534	73730	CCAGCTCCCCTTCCTCCTTT	286121	118317	AGAGCTGTGCTCTGAGGCCA
196948	29144	AGGTAAGAGTTAGGTTCTGT	241535	73731	CCCAGCTCCCCTTCCTCCTT	286122	118318	GAGAGCTGTGCTCTGAGGCC
196949	29145	GAGGTAAGAGTTAGGTTCTG	241536	73732	GCCCAGCTCCCCTTCCTCCT	286123	118319	AGAGAGCTGTGCTCTGAGGC
196950	29146	AGAGGTAAGAGTTAGGTTCT	241537	73733	TGCCCAGCTCCCCTTCCTCC	286124	118320	GAGAGAGCTGTGCTCTGAGG
196951	29147	CAGAGGTAAGAGTTAGGTTC	241538	73734	GTGCCCAGCTCCCCTTCCTC	286125	118321	GGAGAGAGCTGTGCTCTGAG
196952	29148	CCAGAGGTAAGAGTTAGGTT	241539	73735	TGTGCCCAGCTCCCCTTCCT	286126	118322	TGGAGAGAGCTGTGCTCTGA
196953	29149	CCCAGAGGTAAGAGTTAGGT	241540	73736	TTGTGCCCAGCTCCCCTTCC	286127	118323	TTGGAGAGAGCTGTGCTCTG
196954	29150	TCCCAGAGGTAAGAGTTAGG	241541	73737	TTTGTGCCCAGCTCCCCTTC	286128	118324	CTTGGAGAGAGCTGTGCTCT
196955	29151	CTCCCAGAGGTAAGAGTTAG	241542	73738	CTTTGTGCCCAGCTCCCCTT	286129	118325	GCTTGGAGAGAGCTGTGCTC
196956	29152	CCTCCCAGAGGTAAGAGTTA	241543	73739	CCTTTGTGCCCAGCTCCCCT	286130	118326	GGCTTGGAGAGAGCTGTGCT
196957	29153	GCCTCCCAGAGGTAAGAGTT	241544	73740	CCCTTTGTGCCCAGCTCCCC	286131	118327	TGGCTTGGAGAGAGCTGTGC
196958	29154	AGCCTCCCAGAGGTAAGAGT	241545	73741	TCCCTTTGTGCCCAGCTCCC	286132	118328	CTGGCTTGGAGAGAGCTGTG
196959	29155	AAGCCTCCCAGAGGTAAGAG	241546	73742	CTCCCTTTGTGCCCAGCTCC	286133	118329	CCTGGCTTGGAGAGAGCTGT
196960	29156	TAAGCCTCCCAGAGGTAAGA	241547	73743	TCTCCCTTTGTGCCCAGCTC	286134	118330	GCCTGGCTTGGAGAGAGCTG
196961	29157	ATAAGCCTCCCAGAGGTAAG	241548	73744	GTCTCCCTTTGTGCCCAGCT	286135	118331	GGCCTGGCTTGGAGAGAGCT
196962	29158	AATAAGCCTCCCAGAGGTAA	241549	73745	GGTCTCCCTTTGTGCCCAGC	286136	118332	CGGCCTGGCTTGGAGAGAGC

196963	29159	AAATAAGCCTCCCAGAGGTA	241550	73746	GGGTCTCCCTTTGTGCCCAG	286137	118333	GCGGCCTGGCTTGGAGAGAG
196964	29160	CAAATAAGCCTCCCAGAGGT	241551	73747	AGGGTCTCCCTTTGTGCCCA	286138	118334	CGCGGCCTGGCTTGGAGAGA
196965	29161	GCAAATAAGCCTCCCAGAGG	241552	73748	GAGGGTCTCCCTTTGTGCCC	286139	118335	GCGCGGCCTGGCTTGGAGAG
196966	29162	AGCAAATAAGCCTCCCAGAG	241553	73749	AGAGGGTCTCCCTTTGTGCC	286140	118336	CGCGCGGCCTGGCTTGGAGA
196967	29163	AAGCAAATAAGCCTCCCAGA	241554	73750	GAGAGGGTCTCCCTTTGTGC	286141	118337	GCGCGCGGCCTGGCTTGGAG
196968	29164	AAAGCAAATAAGCCTCCCAG	241555	73751	TGAGAGGGTCTCCCTTTGTG	286142	118338	GGCGCGCGGCCTGGCTTGGA
196969	29165	CAAAGCAAATAAGCCTCCCA	241556	73752	CTGAGAGGGTCTCCCTTTGT	286143	118339	TGGCGCGCGGCCTGGCTTGG
196970	29166	TCAAAGCAAATAAGCCTCCC	241557	73753	GCTGAGAGGGTCTCCCTTTG	286144	118340	ATGGCGCGCGGCCTGGCTTG
196971	29167	CTCAAAGCAAATAAGCCTCC	241558	73754	AGCTGAGAGGGTCTCCCTTT	286145	118341	GATGGCGCGCGGCCTGGCTT
196972	29168	TCTCAAAGCAAATAAGCCTC	241559	73755	CAGCTGAGAGGGTCTCCCTT	286146	118342	GGATGGCGCGCGGCCTGGCT
196973	29169	TTCTCAAAGCAAATAAGCCT	241560	73756	TCAGCTGAGAGGGTCTCCCT	286147	118343	TGGATGGCGCGCGGCCTGGC
196974	29170	GTTCTCAAAGCAAATAAGCC	241561	73757	CTCAGCTGAGAGGGTCTCCC	286148	118344	ATGGATGGCGCGCGGCCTGG
196975	29171	TGTTCTCAAAGCAAATAAGC	241562	73758	GCTCAGCTGAGAGGGTCTCC	286149	118345	GATGGATGGCGCGCGGCCTG
196976	29172	ATGTTCTCAAAGCAAATAAG	241563	73759	AGCTCAGCTGAGAGGGTCTC	286150	118346	GGATGGATGGCGCGCGGCCT
196977	29173	TATGTTCTCAAAGCAAATAA	241564	73760	GAGCTCAGCTGAGAGGGTCT	286151	118347	AGGATGGATGGCGCGCGGCC
196978	29174	ATATGTTCTCAAAGCAAATA	241565	73761	GGAGCTCAGCTGAGAGGGTC	286152	118348	GAGGATGGATGGCGCGCGGC
196979	29175	CATATGTTCTCAAAGCAAAT	241566	73762	AGGAGCTCAGCTGAGAGGGT	286153	118349	GGAGGATGGATGGCGCGCGG
196980	29176	ACATATGTTCTCAAAGCAAA	241567	73763	GAGGAGCTCAGCTGAGAGGG	286154	118350	GGGAGGATGGATGGCGCGCG
196981	29177	GACATATGTTCTCAAAGCAA	241568	73764	GGAGGAGCTCAGCTGAGAGG	286155	118351	AGGGAGGATGGATGGCGCGC
196982	29178	GGACATATGTTCTCAAAGCA	241569	73765	GGGAGGAGCTCAGCTGAGAG	286156	118352	CAGGGAGGATGGATGGCGCG
196983	29179	AGGACATATGTTCTCAAAGC	241570	73766	TGGGAGGAGCTCAGCTGAGA	286157	118353	ACAGGGAGGATGGATGGCGC
196984	29180	CAGGACATATGTTCTCAAAG	241571	73767	ATGGGAGGAGCTCAGCTGAG	286158	118354	GACAGGGAGGATGGATGGCG
196985	29181	GCAGGACATATGTTCTCAAA	241572	73768	GATGGGAGGAGCTCAGCTGA	286159	118355	GGACAGGGAGGATGGATGGC
196986	29182	TGCAGGACATATGTTCTCAA	241573	73769	GGATGGGAGGAGCTCAGCTG	286160	118356	GGGACAGGGAGGATGGATGG
196987	29183	CTGCAGGACATATGTTCTCA	241574	73770	TGGATGGGAGGAGCTCAGCT	286161	118357	GGGGACAGGGAGGATGGATG
196988	29184	ACTGCAGGACATATGTTCTC	241575	73771	CTGGATGGGAGGAGCTCAGC	286162	118358	GGGGGACAGGGAGGATGGAT
196989	29185	AACTGCAGGACATATGTTCT	241576	73772	TCTGGATGGGAGGAGCTCAG	286163	118359	TGGGGGACAGGGAGGATGGA
196990	29186	AAACTGCAGGACATATGTTC	241577	73773	GTCTGGATGGGAGGAGCTCA	286164	118360	TTGGGGGACAGGGAGGATGG
196991	29187	AAAACTGCAGGACATATGTT	241578	73774	TGTCTGGATGGGAGGAGCTC	286165	118361	GTTGGGGGACAGGGAGGATG
196992	29188	CAAAACTGCAGGACATATGT	241579	73775	ATGTCTGGATGGGAGGAGCT	286166	118362	CGTTGGGGGACAGGGAGGAT
196993	29189	ACAAAACTGCAGGACATATG	241580	73776	AATGTCTGGATGGGAGGAGC	286167	118363	ACGTTGGGGGACAGGGAGGA
196994	29190	AACAAAACTGCAGGACATAT	241581	73777	AAATGTCTGGATGGGAGGAG	286168	118364	GACGTTGGGGGACAGGGAGG
196995	29191	GAACAAAACTGCAGGACATA	241582	73778	AAAATGTCTGGATGGGAGGA	286169	118365	GGACGTTGGGGGACAGGGAG
196996	29192	TGAACAAAACTGCAGGACAT	241583	73779	GAAAATGTCTGGATGGGAGG	286170	118366	AGGACGTTGGGGGACAGGGA
196997	29193	ATGAACAAAACTGCAGGACA	241584	73780	GGAAAATGTCTGGATGGGAG	286171	118367	AAGGACGTTGGGGGACAGGG
196998	29194	TATGAACAAAACTGCAGGAC	241585	73781	AGGAAAATGTCTGGATGGGA	286172	118368	CAAGGACGTTGGGGGACAGG
196999	29195	ATATGAACAAAACTGCAGGA	241586	73782	CAGGAAAATGTCTGGATGGG	286173	118369	GCAAGGACGTTGGGGGACAG
197000	29196	CATATGAACAAAACTGCAGG	241587	73783	CCAGGAAAATGTCTGGATGG	286174	118370	GGCAAGGACGTTGGGGGACA
197001	29197	CCATATGAACAAAACTGCAG	241588	73784	TCCAGGAAAATGTCTGGATG	286175	118371	TGGCAAGGACGTTGGGGGAC
197002	29198	GCCATATGAACAAAACTGCA	241589	73785	GTCCAGGAAAATGTCTGGAT	286176	118372	GTGGCAAGGACGTTGGGGGA
197003	29199	TGCCATATGAACAAAACTGC	241590	73786	AGTCCAGGAAAATGTCTGGA	286177	118373	TGTGGCAAGGACGTTGGGGG
197004	29200	CTGCCATATGAACAAAACTG	241591	73787	AAGTCCAGGAAAATGTCTGG	286178	118374	CTGTGGCAAGGACGTTGGGG
197005	29201	ACTGCCATATGAACAAAACT	241592	73788	GAAGTCCAGGAAAATGTCTG	286179	118375	TCTGTGGCAAGGACGTTGGG
197006	29202	CACTGCCATATGAACAAAAC	241593	73789	GGAAGTCCAGGAAAATGTCT	286180	118376	ATCTGTGGCAAGGACGTTGG
197007	29203	TCACTGCCATATGAACAAAA	241594	73790	AGGAAGTCCAGGAAAATGTC	286181	118377	GATCTGTGGCAAGGACGTTG
197008	29204	TTCACTGCCATATGAACAAA	241595	73791	TAGGAAGTCCAGGAAAATGT	286182	118378	TGATCTGTGGCAAGGACGTT
197009	29205	CTTCACTGCCATATGAACAA	241596	73792	ATAGGAAGTCCAGGAAAATG	286183	118379	ATGATCTGTGGCAAGGACGT
197010	29206	ACTTCACTGCCATATGAACA	241597	73793	GATAGGAAGTCCAGGAAAAT	286184	118380	CATGATCTGTGGCAAGGACG
197011	29207	AACTTCACTGCCATATGAAC	241598	73794	GGATAGGAAGTCCAGGAAAA	286185	118381	ACATGATCTGTGGCAAGGAC
197012	29208	AAACTTCACTGCCATATGAA	241599	73795	TGGATAGGAAGTCCAGGAAA	286186	118382	GACATGATCTGTGGCAAGGA
197013	29209	GAAACTTCACTGCCATATGA	241600	73796	TTGGATAGGAAGTCCAGGAA	286187	118383	GGACATGATCTGTGGCAAGG
197014	29210	CGAAACTTCACTGCCATATG	241601	73797	ATTGGATAGGAAGTCCAGGA	286188	118384	CGGACATGATCTGTGGCAAG
197015	29211	ACGAAACTTCACTGCCATAT	241602	73798	CATTGGATAGGAAGTCCAGG	286189	118385	GCGGACATGATCTGTGGCAA
197016	29212	CACGAAACTTCACTGCCATA	241603	73799	TCATTGGATAGGAAGTCCAG	286190	118386	GGCGGACATGATCTGTGGCA
197017	29213	GCACGAAACTTCACTGCCAT	241604	73800	GTCATTGGATAGGAAGTCCA	286191	118387	GGGCGGACATGATCTGTGGC
197018	29214	TGCACGAAACTTCACTGCCA	241605	73801	AGTCATTGGATAGGAAGTCC	286192	118388	AGGGCGGACATGATCTGTGG
197019	29215	GTGCACGAAACTTCACTGCC	241606	73802	AAGTCATTGGATAGGAAGTC	286193	118389	CAGGGCGGACATGATCTGTG
197020	29216	TGTGCACGAAACTTCACTGC	241607	73803	GAAGTCATTGGATAGGAAGT	286194	118390	TCAGGGCGGACATGATCTGT
197021	29217	GTGTGCACGAAACTTCACTG	241608	73804	GGAAGTCATTGGATAGGAAG	286195	118391	GTCAGGGCGGACATGATCTG
197022	29218	TGTGTGCACGAAACTTCACT	241609	73805	GGGAAGTCATTGGATAGGAA	286196	118392	TGTCAGGGCGGACATGATCT
197023	29219	GTGTGTGCACGAAACTTCAC	241610	73806	AGGGAAGTCATTGGATAGGA	286197	118393	GTGTCAGGGCGGACATGATC
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197025	29221	GAGTGTGTGCACGAAACTTC	241612	73808	TAAGGGAAGTCATTGGATAG	286199	118395	GTGTGTCAGGGCGGACATGA
197026	29222	AGAGTGTGTGCACGAAACTT	241613	73809	CTAAGGGAAGTCATTGGATA	286200	118396	TGTGTGTCAGGGCGGACATG
197027	29223	TAGAGTGTGTGCACGAAACT	241614	73810	GCTAAGGGAAGTCATTGGAT	286201	118397	ATGTGTGTCAGGGCGGACAT
197028	29224	CTAGAGTGTGTGCACGAAAC	241615	73811	AGCTAAGGGAAGTCATTGGA	286202	118398	CATGTGTGTCAGGGCGGACA
197029	29225	TCTAGAGTGTGTGCACGAAA	241616	73812	AAGCTAAGGGAAGTCATTGG	286203	118399	CCATGTGTGTCAGGGCGGAC
197030	29226	CTCTAGAGTGTGTGCACGAA	241617	73813	GAAGCTAAGGGAAGTCATTG	286204	118400	CCCATGTGTGTCAGGGCGGA
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197032	29228	GGCTCTAGAGTGTGTGCACG	241619	73815	AAGAAGCTAAGGGAAGTCAT	286206	118402	GACCCATGTGTGTCAGGGCG
197033	29229	TGGCTCTAGAGTGTGTGCAC	241620	73816	TAAGAAGCTAAGGGAAGTCA	286207	118403	AGACCCATGTGTGTCAGGGC
197034	29230	CTGGCTCTAGAGTGTGTGCA	241621	73817	ATAAGAAGCTAAGGGAAGTC	286208	118404	GAGACCCATGTGTGTCAGGG

197035	29231	CCTGGCTCTAGAGTGTGTGC	241622	73818	GATAAGAAGCTAAGGGAAGT	286209	118405	TGAGACCCATGTGTGTCAGG
197036	29232	GCCTGGCTCTAGAGTGTGTG	241623	73819	TGATAAGAAGCTAAGGGAAG	286210	118406	CTGAGACCCATGTGTGTCAG
197037	29233	TGCCTGGCTCTAGAGTGTGT	241624	73820	CTGATAAGAAGCTAAGGGAA	286211	118407	GCTGAGACCCATGTGTGTCA
197038	29234	CTGCCTGGCTCTAGAGTGTG	241625	73821	GCTGATAAGAAGCTAAGGGA	286212	118408	GGCTGAGACCCATGTGTGTC
197039	29235	GCTGCCTGGCTCTAGAGTGT	241626	73822	GGCTGATAAGAAGCTAAGGG	286213	118409	TGGCTGAGACCCATGTGTGT
197040	29236	GGCTGCCTGGCTCTAGAGTG	241627	73823	TGGCTGATAAGAAGCTAAGG	286214	118410	ATGGCTGAGACCCATGTGTG
197041	29237	AGGCTGCCTGGCTCTAGAGT	241628	73824	GTGGCTGATAAGAAGCTAAG	286215	118411	GATGGCTGAGACCCATGTGT
197042	29238	CAGGCTGCCTGGCTCTAGAG	241629	73825	GGTGGCTGATAAGAAGCTAA	286216	118412	AGATGGCTGAGACCCATGTG
197043	29239	CCAGGCTGCCTGGCTCTAGA	241630	73826	GGGTGGCTGATAAGAAGCTA	286217	118413	GAGATGGCTGAGACCCATGT
197044	29240	CCCAGGCTGCCTGGCTCTAG	241631	73827	GGGGTGGCTGATAAGAAGCT	286218	118414	AGAGATGGCTGAGACCCATG
197045	29241	ACCCAGGCTGCCTGGCTCTA	241632	73828	AGGGGTGGCTGATAAGAAGC	286219	118415	CAGAGATGGCTGAGACCCAT
197046	29242	AACCCAGGCTGCCTGGCTCT	241633	73829	CAGGGGTGGCTGATAAGAAG	286220	118416	GCAGAGATGGCTGAGACCCA
197047	29243	GAACCCAGGCTGCCTGGCTC	241634	73830	ACAGGGGTGGCTGATAAGAA	286221	118417	GGCAGAGATGGCTGAGACCC
197048	29244	TGAACCCAGGCTGCCTGGCT	241635	73831	GACAGGGGTGGCTGATAAGA	286222	118418	GGGCAGAGATGGCTGAGACC
197049	29245	TTGAACCCAGGCTGCCTGGC	241636	73832	AGACAGGGGTGGCTGATAAG	286223	118419	GGGGCAGAGATGGCTGAGAC
197050	29246	TTTGAACCCAGGCTGCCTGG	241637	73833	CAGACAGGGGTGGCTGATAA	286224	118420	TGGGGCAGAGATGGCTGAGA
197051	29247	CTTTGAACCCAGGCTGCCTG	241638	73834	GCAGACAGGGGTGGCTGATA	286225	118421	CTGGGGCAGAGATGGCTGAG
197052	29248	GCTTTGAACCCAGGCTGCCT	241639	73835	GGCAGACAGGGGTGGCTGAT	286226	118422	ACTGGGGCAGAGATGGCTGA
197053	29249	CGCTTTGAACCCAGGCTGCC	241640	73836	GGGCAGACAGGGGTGGCTGA	286227	118423	AACTGGGGCAGAGATGGCTG
197054	29250	GCGCTTTGAACCCAGGCTGC	241641	73837	TGGGCAGACAGGGGTGGCTG	286228	118424	TAACTGGGGCAGAGATGGCT
197055	29251	TGCGCTTTGAACCCAGGCTG	241642	73838	CTGGGCAGACAGGGGTGGCT	286229	118425	TTAACTGGGGCAGAGATGGC
197056	29252	CTGCGCTTTGAACCCAGGCT	241643	73839	CCTGGGCAGACAGGGGTGGC	286230	118426	GTTAACTGGGGCAGAGATGG
197057	29253	GCTGCGCTTTGAACCCAGGC	241644	73840	TCCTGGGCAGACAGGGGTGG	286231	118427	AGTTAACTGGGGCAGAGATG
197058	29254	AGCTGCGCTTTGAACCCAGG	241645	73841	CTCCTGGGCAGACAGGGGTG	286232	118428	GAGTTAACTGGGGCAGAGAT
197059	29255	GAGCTGCGCTTTGAACCCAG	241646	73842	CCTCCTGGGCAGACAGGGGT	286233	118429	GGAGTTAACTGGGGCAGAGA
197060	29256	AGAGCTGCGCTTTGAACCCA	241647	73843	GCCTCCTGGGCAGACAGGGG	286234	118430	GGGAGTTAACTGGGGCAGAG
197061	29257	CAGAGCTGCGCTTTGAACCC	241648	73844	AGCCTCCTGGGCAGACAGGG	286235	118431	GGGGAGTTAACTGGGGCAGA
197062	29258	GCAGAGCTGCGCTTTGAACC	241649	73845	CAGCCTCCTGGGCAGACAGG	286236	118432	TGGGGAGTTAACTGGGGCAG
197063	29259	GGCAGAGCTGCGCTTTGAAC	241650	73846	CCAGCCTCCTGGGCAGACAG	286237	118433	ATGGGGAGTTAACTGGGGCA
197064	29260	TGGCAGAGCTGCGCTTTGAA	241651	73847	TCCAGCCTCCTGGGCAGACA	286238	118434	GATGGGGAGTTAACTGGGGC
197065	29261	CTGGCAGAGCTGCGCTTTGA	241652	73848	TTCCAGCCTCCTGGGCAGAC	286239	118435	GGATGGGGAGTTAACTGGGG
197066	29262	CCTGGCAGAGCTGCGCTTTG	241653	73849	CTTCCAGCCTCCTGGGCAGA	286240	118436	TGGATGGGGAGTTAACTGGG
197067	29263	ACCTGGCAGAGCTGCGCTTT	241654	73850	TCTTCCAGCCTCCTGGGCAG	286241	118437	ATGGATGGGGAGTTAACTGG
197068	29264	GACCTGGCAGAGCTGCGCTT	241655	73851	ATCTTCCAGCCTCCTGGGCA	286242	118438	TATGGATGGGGAGTTAACTG
197069	29265	GGACCTGGCAGAGCTGCGCT	241656	73852	CATCTTCCAGCCTCCTGGGC	286243	118439	TTATGGATGGGGAGTTAACT
197070	29266	AGGACCTGGCAGAGCTGCGC	241657	73853	ACATCTTCCAGCCTCCTGGG	286244	118440	TTTATGGATGGGGAGTTAAC
197071	29267	TAGGACCTGGCAGAGCTGCG	241658	73854	CACATCTTCCAGCCTCCTGG	286245	118441	CTTTATGGATGGGGAGTTAA
197072	29268	TTAGGACCTGGCAGAGCTGC	241659	73855	CCACATCTTCCAGCCTCCTG	286246	118442	TCTTTATGGATGGGGAGTTA
197073	29269	GTTAGGACCTGGCAGAGCTG	241660	73856	GCCACATCTTCCAGCCTCCT	286247	118443	CTCTTTATGGATGGGGAGTT
197074	29270	AGTTAGGACCTGGCAGAGCT	241661	73857	GGCCACATCTTCCAGCCTCC	286248	118444	GCTCTTTATGGATGGGGAGT
197075	29271	CAGTTAGGACCTGGCAGAGC	241662	73858	AGGCCACATCTTCCAGCCTC	286249	118445	TGCTCTTTATGGATGGGGAG
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197078	29274	ATGCAGTTAGGACCTGGCAG	241665	73861	AAAAGGCCACATCTTCCAGC	286252	118448	ATGTGCTCTTTATGGATGGG
197079	29275	CATGCAGTTAGGACCTGGCA	241666	73862	TAAAAGGCCACATCTTCCAG	286253	118449	CATGTGCTCTTTATGGATGG
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197081	29277	TTCATGCAGTTAGGACCTGG	241668	73864	GTTAAAAGGCCACATCTTCC	286255	118451	GGCATGTGCTCTTTATGGAT
197082	29278	ATTCATGCAGTTAGGACCTG	241669	73865	AGTTAAAAGGCCACATCTTC	286256	118452	TGGCATGTGCTCTTTATGGA
197083	29279	AATTCATGCAGTTAGGACCT	241670	73866	CAGTTAAAAGGCCACATCTT	286257	118453	CTGGCATGTGCTCTTTATGG
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197085	29281	CAAATTCATGCAGTTAGGAC	241672	73868	CCCAGTTAAAAGGCCACATC	286259	118455	AGCTGGCATGTGCTCTTTAT
197086	29282	CCAAATTCATGCAGTTAGGA	241673	73869	GCCCAGTTAAAAGGCCACAT	286260	118456	CAGCTGGCATGTGCTCTTTA
197087	29283	CCCAAATTCATGCAGTTAGG	241674	73870	TGCCCAGTTAAAAGGCCACA	286261	118457	TCAGCTGGCATGTGCTCTTT
197088	29284	GCCCAAATTCATGCAGTTAG	241675	73871	GTGCCCAGTTAAAAGGCCAC	286262	118458	GTCAGCTGGCATGTGCTCTT
197089	29285	TGCCCAAATTCATGCAGTTA	241676	73872	TGTGCCCAGTTAAAAGGCCA	286263	118459	TGTCAGCTGGCATGTGCTCT
197090	29286	TTGCCCAAATTCATGCAGTT	241677	73873	CTGTGCCCAGTTAAAAGGCC	286264	118460	GTGTCAGCTGGCATGTGCTC
197091	29287	CTTGCCCAAATTCATGCAGT	241678	73874	GCTGTGCCCAGTTAAAAGGC	286265	118461	GGTGTCAGCTGGCATGTGCT
197092	29288	ACTTGCCCAAATTCATGCAG	241679	73875	AGCTGTGCCCAGTTAAAAGG	286266	118462	TGGTGTCAGCTGGCATGTGC
197093	29289	GACTTGCCCAAATTCATGCA	241680	73876	GAGCTGTGCCCAGTTAAAAG	286267	118463	TTGGTGTCAGCTGGCATGTG
197094	29290	CGACTTGCCCAAATTCATGC	241681	73877	AGAGCTGTGCCCAGTTAAAA	286268	118464	TTTGGTGTCAGCTGGCATGT
197095	29291	GCGACTTGCCCAAATTCATG	241682	73878	CAGAGCTGTGCCCAGTTAAA	286269	118465	TTTTGGTGTCAGCTGGCATG
197096	29292	AGCGACTTGCCCAAATTCAT	241683	73879	ACAGAGCTGTGCCCAGTTAA	286270	118466	ATTTTGGTGTCAGCTGGCAT
197097	29293	GAGCGACTTGCCCAAATTCA	241684	73880	GACAGAGCTGTGCCCAGTTA	286271	118467	TATTTTGGTGTCAGCTGGCA
197098	29294	TGAGCGACTTGCCCAAATTC	241685	73881	GGACAGAGCTGTGCCCAGTT	286272	118468	TTATTTTGGTGTCAGCTGGC
197099	29295	TTGAGCGACTTGCCCAAATT	241686	73882	AGGACAGAGCTGTGCCCAGT	286273	118469	ATTATTTTGGTGTCAGCTGG
197100	29296	GTTGAGCGACTTGCCCAAAT	241687	73883	GAGGACAGAGCTGTGCCCAG	286274	118470	AATTATTTTGGTGTCAGCTG
197101	29297	GGTTGAGCGACTTGCCCAAA	241688	73884	AGAGGACAGAGCTGTGCCCA	286275	118471	GAATTATTTTGGTGTCAGCT
197102	29298	AGGTTGAGCGACTTGCCCAA	241689	73885	TAGAGGACAGAGCTGTGCCC	286276	118472	CGAATTATTTTGGTGTCAGC
197103	29299	GAGGTTGAGCGACTTGCCCA	241690	73886	ATAGAGGACAGAGCTGTGCC	286277	118473	CCGAATTATTTTGGTGTCAG
197104	29300	AGAGGTTGAGCGACTTGCCC	241691	73887	GATAGAGGACAGAGCTGTGC	286278	118474	CCCGAATTATTTTGGTGTCA
197105	29301	GAGAGGTTGAGCGACTTGCC	241692	73888	TGATAGAGGACAGAGCTGTG	286279	118475	TCCCGAATTATTTTGGTGTC
197106	29302	GGAGAGGTTGAGCGACTTGC	241693	73889	ATGATAGAGGACAGAGCTGT	286280	118476	ATCCCGAATTATTTTGGTGT

197107	29303	TGGAGAGGTTGAGCGACTTG	241694	73890	TATGATAGAGGACAGAGCTG	286281	118477	CATCCCGAATTATTTTGGTG
197108	29304	ATGGAGAGGTTGAGCGACTT	241695	73891	ATATGATAGAGGACAGAGCT	286282	118478	CCATCCCGAATTATTTTGGT
197109	29305	CATGGAGAGGTTGAGCGACT	241696	73892	GATATGATAGAGGACAGAGC	286283	118479	ACCATCCCGAATTATTTTGG
197110	29306	GCATGGAGAGGTTGAGCGAC	241697	73893	TGATATGATAGAGGACAGAG	286284	118480	AACCATCCCGAATTATTTTG
197111	29307	GGCATGGAGAGGTTGAGCGA	241698	73894	CTGATATGATAGAGGACAGA	286285	118481	GAACCATCCCGAATTATTTT
197112	29308	AGGCATGGAGAGGTTGAGCG	241699	73895	CCTGATATGATAGAGGACAG	286286	118482	GGAACCATCCCGAATTATTT
197113	29309	CAGGCATGGAGAGGTTGAGC	241700	73896	CCCTGATATGATAGAGGACA	286287	118483	TGGAACCATCCCGAATTATT
197114	29310	TCAGGCATGGAGAGGTTGAG	241701	73897	GCCCTGATATGATAGAGGAC	286288	118484	CTGGAACCATCCCGAATTAT
197115	29311	CTCAGGCATGGAGAGGTTGA	241702	73898	AGCCCTGATATGATAGAGGA	286289	118485	ACTGGAACCATCCCGAATTA
197116	29312	ACTCAGGCATGGAGAGGTTG	241703	73899	GAGCCCTGATATGATAGAGG	286290	118486	AACTGGAACCATCCCGAATT
197117	29313	AACTCAGGCATGGAGAGGTT	241704	73900	AGAGCCCTGATATGATAGAG	286291	118487	AAACTGGAACCATCCCGAAT
197118	29314	AAACTCAGGCATGGAGAGGT	241705	73901	CAGAGCCCTGATATGATAGA	286292	118488	TAAACTGGAACCATCCCGAA
197119	29315	GAAACTCAGGCATGGAGAGG	241706	73902	ACAGAGCCCTGATATGATAG	286293	118489	CTAAACTGGAACCATCCCGA
197120	29316	GGAAACTCAGGCATGGAGAG	241707	73903	AACAGAGCCCTGATATGATA	286294	118490	TCTAAACTGGAACCATCCCG
197121	29317	AGGAAACTCAGGCATGGAGA	241708	73904	GAACAGAGCCCTGATATGAT	286295	118491	GTCTAAACTGGAACCATCCC
197122	29318	GAGGAAACTCAGGCATGGAG	241709	73905	GGAACAGAGCCCTGATATGA	286296	118492	GGTCTAAACTGGAACCATCC
197123	29319	TGAGGAAACTCAGGCATGGA	241710	73906	GGGAACAGAGCCCTGATATG	286297	118493	AGGTCTAAACTGGAACCATC
197124	29320	ATGAGGAAACTCAGGCATGG	241711	73907	TGGGAACAGAGCCCTGATAT	286298	118494	TAGGTCTAAACTGGAACCAT
197125	29321	GATGAGGAAACTCAGGCATG	241712	73908	TTGGGAACAGAGCCCTGATA	286299	118495	TTAGGTCTAAACTGGAACCA
197126	29322	AGATGAGGAAACTCAGGCAT	241713	73909	CTTGGGAACAGAGCCCTGAT	286300	118496	CTTAGGTCTAAACTGGAACC
197127	29323	CAGATGAGGAAACTCAGGCA	241714	73910	CCTTGGGAACAGAGCCCTGA	286301	118497	ACTTAGGTCTAAACTGGAAC
197128	29324	ACAGATGAGGAAACTCAGGC	241715	73911	TCCTTGGGAACAGAGCCCTG	286302	118498	CACTTAGGTCTAAACTGGAA
197129	29325	TACAGATGAGGAAACTCAGG	241716	73912	CTCCTTGGGAACAGAGCCCT	286303	118499	CCACTTAGGTCTAAACTGGA
197130	29326	TTACAGATGAGGAAACTCAG	241717	73913	CCTCCTTGGGAACAGAGCCC	286304	118500	TCCACTTAGGTCTAAACTGG
197131	29327	CTTACAGATGAGGAAACTCA	241718	73914	CCCTCCTTGGGAACAGAGCC	286305	118501	TTCCACTTAGGTCTAAACTG
197132	29328	TCTTACAGATGAGGAAACTC	241719	73915	ACCCTCCTTGGGAACAGAGC	286306	118502	CTTCCACTTAGGTCTAAACT
197133	29329	ATCTTACAGATGAGGAAACT	241720	73916	TACCCTCCTTGGGAACAGAG	286307	118503	CCTTCCACTTAGGTCTAAAC
197134	29330	AATCTTACAGATGAGGAAAC	241721	73917	CTACCCTCCTTGGGAACAGA	286308	118504	TCCTTCCACTTAGGTCTAAA
197135	29331	CAATCTTACAGATGAGGAAA	241722	73918	TCTACCCTCCTTGGGAACAG	286309	118505	CTCCTTCCACTTAGGTCTAA
197136	29332	CCAATCTTACAGATGAGGAA	241723	73919	CTCTACCCTCCTTGGGAACA	286310	118506	TCTCCTTCCACTTAGGTCTA
197137	29333	TCCAATCTTACAGATGAGGA	241724	73920	TCTCTACCCTCCTTGGGAAC	286311	118507	TTCTCCTTCCACTTAGGTCT
197138	29334	CTCCAATCTTACAGATGAGG	241725	73921	CTCTCTACCCTCCTTGGGAA	286312	118508	TTTCTCCTTCCACTTAGGTC
197139	29335	GCTCCAATCTTACAGATGAG	241726	73922	TCTCTCTACCCTCCTTGGGA	286313	118509	GTTTCTCCTTCCACTTAGGT
197140	29336	TGCTCCAATCTTACAGATGA	241727	73923	TTCTCTCTACCCTCCTTGGG	286314	118510	GGTTTCTCCTTCCACTTAGG
197141	29337	TTGCTCCAATCTTACAGATG	241728	73924	ATTCTCTCTACCCTCCTTGG	286315	118511	TGGTTTCTCCTTCCACTTAG
197142	29338	ATTGCTCCAATCTTACAGAT	241729	73925	CATTCTCTCTACCCTCCTTG	286316	118512	GTGGTTTCTCCTTCCACTTA
197143	29339	CATTGCTCCAATCTTACAGA	241730	73926	CCATTCTCTCTACCCTCCTT	286317	118513	GGTGGTTTCTCCTTCCACTT
197144	29340	CCATTGCTCCAATCTTACAG	241731	73927	TCCATTCTCTCTACCCTCCT	286318	118514	TGGTGGTTTCTCCTTCCACT
197145	29341	ACCATTGCTCCAATCTTACA	241732	73928	GTCCATTCTCTCTACCCTCC	286319	118515	GTGGTGGTTTCTCCTTCCAC
197146	29342	TACCATTGCTCCAATCTTAC	241733	73929	TGTCCATTCTCTCTACCCTC	286320	118516	GGTGGTGGTTTCTCCTTCCA
197147	29343	TTACCATTGCTCCAATCTTA	241734	73930	GTGTCCATTCTCTCTACCCT	286321	118517	AGGTGGTGGTTTCTCCTTCC
197148	29344	ATTACCATTGCTCCAATCTT	241735	73931	GGTGTCCATTCTCTCTACCC	286322	118518	CAGGTGGTGGTTTCTCCTTC
197149	29345	TATTACCATTGCTCCAATCT	241736	73932	TGGTGTCCATTCTCTCTACC	286323	118519	GCAGGTGGTGGTTTCTCCTT
197150	29346	GTATTACCATTGCTCCAATC	241737	73933	CTGGTGTCCATTCTCTCTAC	286324	118520	GGCAGGTGGTGGTTTCTCCT
197151	29347	GGTATTACCATTGCTCCAAT	241738	73934	CCTGGTGTCCATTCTCTCTA	286325	118521	GGGCAGGTGGTGGTTTCTCC
197152	29348	AGGTATTACCATTGCTCCAA	241739	73935	ACCTGGTGTCCATTCTCTCT	286326	118522	AGGGCAGGTGGTGGTTTCTC
197153	29349	CAGGTATTACCATTGCTCCA	241740	73936	CACCTGGTGTCCATTCTCTC	286327	118523	CAGGGCAGGTGGTGGTTTCT
197154	29350	GCAGGTATTACCATTGCTCC	241741	73937	CCACCTGGTGTCCATTCTCT	286328	118524	GCAGGGCAGGTGGTGGTTTC
197155	29351	AGCAGGTATTACCATTGCTC	241742	73938	TCCACCTGGTGTCCATTCTC	286329	118525	TGCAGGGCAGGTGGTGGTTT
197156	29352	AAGCAGGTATTACCATTGCT	241743	73939	GTCCACCTGGTGTCCATTCT	286330	118526	GTGCAGGGCAGGTGGTGGTT
197157	29353	AAAGCAGGTATTACCATTGC	241744	73940	GGTCCACCTGGTGTCCATTC	286331	118527	GGTGCAGGGCAGGTGGTGGT
197158	29354	AAAAGCAGGTATTACCATTG	241745	73941	GGGTCCACCTGGTGTCCATT	286332	118528	AGGTGCAGGGCAGGTGGTGG
197159	29355	AAAAAGCAGGTATTACCATT	241746	73942	AGGGTCCACCTGGTGTCCAT	286333	118529	AAGGTGCAGGGCAGGTGGTG
197160	29356	TAAAAAGCAGGTATTACCAT	241747	73943	GAGGGTCCACCTGGTGTCCA	286334	118530	CAAGGTGCAGGGCAGGTGGT
197161	29357	CTAAAAAGCAGGTATTACCA	241748	73944	TGAGGGTCCACCTGGTGTCC	286335	118531	ACAAGGTGCAGGGCAGGTGG
197162	29358	CCTAAAAAGCAGGTATTACC	241749	73945	CTGAGGGTCCACCTGGTGTC	286336	118532	AACAAGGTGCAGGGCAGGTG
197163	29359	CCCTAAAAAGCAGGTATTAC	241750	73946	GCTGAGGGTCCACCTGGTGT	286337	118533	AAACAAGGTGCAGGGCAGGT
197164	29360	ACCCTAAAAAGCAGGTATTA	241751	73947	TGCTGAGGGTCCACCTGGTG	286338	118534	AAAACAAGGTGCAGGGCAGG
197165	29361	AACCCTAAAAAGCAGGTATT	241752	73948	CTGCTGAGGGTCCACCTGGT	286339	118535	AAAAACAAGGTGCAGGGCAG
197166	29362	CAACCCTAAAAAGCAGGTAT	241753	73949	ACTGCTGAGGGTCCACCTGG	286340	118536	AAAAAACAAGGTGCAGGGCA
197167	29363	TCAACCCTAAAAAGCAGGTA	241754	73950	GACTGCTGAGGGTCCACCTG	286341	118537	CAAAAAACAAGGTGCAGGGC
197168	29364	CTCAACCCTAAAAAGCAGGT	241755	73951	AGACTGCTGAGGGTCCACCT	286342	118538	CCAAAAAACAAGGTGCAGGG
197169	29365	TCTCAACCCTAAAAAGCAGG	241756	73952	CAGACTGCTGAGGGTCCACC	286343	118539	ACCAAAAAACAAGGTGCAGG
197170	29366	TTCTCAACCCTAAAAAGCAG	241757	73953	ACAGACTGCTGAGGGTCCAC	286344	118540	CACCAAAAAACAAGGTGCAG
197171	29367	CTTCTCAACCCTAAAAAGCA	241758	73954	CACAGACTGCTGAGGGTCCA	286345	118541	TCACCAAAAAACAAGGTGCA
197172	29368	TCTTCTCAACCCTAAAAAGC	241759	73955	GCACAGACTGCTGAGGGTCC	286346	118542	GTCACCAAAAAACAAGGTGC
197173	29369	CTCTTCTCAACCCTAAAAAG	241760	73956	GGCACAGACTGCTGAGGGTC	286347	118543	GGTCACCAAAAAACAAGGTG
197174	29370	TCTCTTCTCAACCCTAAAAA	241761	73957	TGGCACAGACTGCTGAGGGT	286348	118544	AGGTCACCAAAAAACAAGGT
197175	29371	TTCTCTTCTCAACCCTAAAA	241762	73958	GTGGCACAGACTGCTGAGGG	286349	118545	AAGGTCACCAAAAAACAAGG
197176	29372	ATTCTCTTCTCAACCCTAAA	241763	73959	TGTGGCACAGACTGCTGAGG	286350	118546	CAAGGTCACCAAAAAACAAG
197177	29373	AATTCTCTTCTCAACCCTAA	241764	73960	CTGTGGCACAGACTGCTGAG	286351	118547	TCAAGGTCACCAAAAAACAA
197178	29374	TAATTCTCTTCTCAACCCTA	241765	73961	TCTGTGGCACAGACTGCTGA	286352	118548	ATCAAGGTCACCAAAAAACA

197179	29375	TTAATTCTCTTCTCAACCCT	241766	73962	CTCTGTGGCACAGACTGCTG	286353	118549	TATCAAGGTCACCAAAAAAC
197180	29376	TTTAATTCTCTTCTCAACCC	241767	73963	CCTCTGTGGCACAGACTGCT	286354	118550	TTATCAAGGTCACCAAAAAA
197181	29377	ATTTAATTCTCTTCTCAACC	241768	73964	CCCTCTGTGGCACAGACTGC	286355	118551	TTTATCAAGGTCACCAAAAA
197182	29378	CATTTAATTCTCTTCTCAAC	241769	73965	TCCCTCTGTGGCACAGACTG	286356	118552	GTTTATCAAGGTCACCAAAA
197183	29379	TCATTTAATTCTCTTCTCAA	241770	73966	CTCCCTCTGTGGCACAGACT	286357	118553	GGTTTATCAAGGTCACCAAA
197184	29380	TTCATTTAATTCTCTTCTCA	241771	73967	ACTCCCTCTGTGGCACAGAC	286358	118554	TGGTTTATCAAGGTCACCAA
197185	29381	ATTCATTTAATTCTCTTCTC	241772	73968	CACTCCCTCTGTGGCACAGA	286359	118555	ATGGTTTATCAAGGTCACCA
197186	29382	AATTCATTTAATTCTCTTCT	241773	73969	ACACTCCCTCTGTGGCACAG	286360	118556	GATGGTTTATCAAGGTCACC
197187	29383	TAATTCATTTAATTCTCTTC	241774	73970	AACACTCCCTCTGTGGCACA	286361	118557	AGATGGTTTATCAAGGTCAC
197188	29384	TTAATTCATTTAATTCTCTT	241775	73971	AAACACTCCCTCTGTGGCAC	286362	118558	AAGATGGTTTATCAAGGTCA
197189	29385	CTTAATTCATTTAATTCTCT	241776	73972	CAAACACTCCCTCTGTGGCA	286363	118559	GAAGATGGTTTATCAAGGTC
197190	29386	TCTTAATTCATTTAATTCTC	241777	73973	GCAAACACTCCCTCTGTGGC	286364	118560	TGAAGATGGTTTATCAAGGT
197191	29387	ATCTTAATTCATTTAATTCT	241778	73974	TGCAAACACTCCCTCTGTGG	286365	118561	CTGAAGATGGTTTATCAAGG
197192	29388	CATCTTAATTCATTTAATTC	241779	73975	TTGCAAACACTCCCTCTGTG	286366	118562	GCTGAAGATGGTTTATCAAG
197193	29389	CCATCTTAATTCATTTAATT	241780	73976	ATTGCAAACACTCCCTCTGT	286367	118563	GGCTGAAGATGGTTTATCAA
197194	29390	CCCATCTTAATTCATTTAAT	241781	73977	AATTGCAAACACTCCCTCTG	286368	118564	TGGCTGAAGATGGTTTATCA
197195	29391	ACCCATCTTAATTCATTTAA	241782	73978	AAATTGCAAACACTCCCTCT	286369	118565	ATGGCTGAAGATGGTTTATC
197196	29392	TACCCATCTTAATTCATTTA	241783	73979	GAAATTGCAAACACTCCCTC	286370	118566	CATGGCTGAAGATGGTTTAT
197197	29393	TTACCCATCTTAATTCATTT	241784	73980	GGAAATTGCAAACACTCCCT	286371	118567	TCATGGCTGAAGATGGTTTA
197198	29394	TTTACCCATCTTAATTCATT	241785	73981	TGGAAATTGCAAACACTCCC	286372	118568	TTCATGGCTGAAGATGGTTT
197199	29395	CTTTACCCATCTTAATTCAT	241786	73982	CTGGAAATTGCAAACACTCC	286373	118569	CTTCATGGCTGAAGATGGTT
197200	29396	ACTTTACCCATCTTAATTCA	241787	73983	TCTGGAAATTGCAAACACTC	286374	118570	GCTTCATGGCTGAAGATGGT
197201	29397	CACTTTACCCATCTTAATTC	241788	73984	GTCTGGAAATTGCAAACACT	286375	118571	GGCTTCATGGCTGAAGATGG
197202	29398	GCACTTTACCCATCTTAATT	241789	73985	AGTCTGGAAATTGCAAACAC	286376	118572	TGGCTTCATGGCTGAAGATG
197203	29399	AGCACTTTACCCATCTTAAT	241790	73986	TAGTCTGGAAATTGCAAACA	286377	118573	CTGGCTTCATGGCTGAAGAT
197204	29400	AAGCACTTTACCCATCTTAA	241791	73987	TTAGTCTGGAAATTGCAAAC	286378	118574	GCTGGCTTCATGGCTGAAGA
197205	29401	TAAGCACTTTACCCATCTTA	241792	73988	TTTAGTCTGGAAATTGCAAA	286379	118575	AGCTGGCTTCATGGCTGAAG
197206	29402	CTAAGCACTTTACCCATCTT	241793	73989	TTTTAGTCTGGAAATTGCAA	286380	118576	CAGCTGGCTTCATGGCTGAA
197207	29403	TCTAAGCACTTTACCCATCT	241794	73990	CTTTTAGTCTGGAAATTGCA	286381	118577	ACAGCTGGCTTCATGGCTGA
197208	29404	CTCTAAGCACTTTACCCATC	241795	73991	ACTTTTAGTCTGGAAATTGC	286382	118578	GACAGCTGGCTTCATGGCTG
197209	29405	ACTCTAAGCACTTTACCCAT	241796	73992	GACTTTTAGTCTGGAAATTG	286383	118579	AGACAGCTGGCTTCATGGCT
197210	29406	CACTCTAAGCACTTTACCCA	241797	73993	GGACTTTTAGTCTGGAAATT	286384	118580	GAGACAGCTGGCTTCATGGC
197211	29407	CCACTCTAAGCACTTTACCC	241798	73994	GGGACTTTTAGTCTGGAAAT	286385	118581	GGAGACAGCTGGCTTCATGG
197212	29408	TCCACTCTAAGCACTTTACC	241799	73995	GGGGACTTTTAGTCTGGAAA	286386	118582	GGGAGACAGCTGGCTTCATG
197213	29409	CTCCACTCTAAGCACTTTAC	241800	73996	TGGGGACTTTTAGTCTGGAA	286387	118583	TGGGAGACAGCTGGCTTCAT
197214	29410	GCTCCACTCTAAGCACTTTA	241801	73997	ATGGGGACTTTTAGTCTGGA	286388	118584	CTGGGAGACAGCTGGCTTCA
197215	29411	AGCTCCACTCTAAGCACTTT	241802	73998	CATGGGGACTTTTAGTCTGG	286389	118585	CCTGGGAGACAGCTGGCTTC
197216	29412	AAGCTCCACTCTAAGCACTT	241803	73999	ACATGGGGACTTTTAGTCTG	286390	118586	TCCTGGGAGACAGCTGGCTT
197217	29413	AAAGCTCCACTCTAAGCACT	241804	74000	CACATGGGGACTTTTAGTCT	286391	118587	TTCCTGGGAGACAGCTGGCT
197218	29414	CAAAGCTCCACTCTAAGCAC	241805	74001	GCACATGGGGACTTTTAGTC	286392	118588	CTTCCTGGGAGACAGCTGGC
197219	29415	GCAAAGCTCCACTCTAAGCA	241806	74002	AGCACATGGGGACTTTTAGT	286393	118589	GCTTCCTGGGAGACAGCTGG
197220	29416	TGCAAAGCTCCACTCTAAGC	241807	74003	AAGCACATGGGGACTTTTAG	286394	118590	AGCTTCCTGGGAGACAGCTG
197221	29417	TTGCAAAGCTCCACTCTAAG	241808	74004	CAAGCACATGGGGACTTTTA	286395	118591	GAGCTTCCTGGGAGACAGCT
197222	29418	CTTGCAAAGCTCCACTCTAA	241809	74005	TCAAGCACATGGGGACTTTT	286396	118592	GGAGCTTCCTGGGAGACAGC
197223	29419	ACTTGCAAAGCTCCACTCTA	241810	74006	GTCAAGCACATGGGGACTTT	286397	118593	TGGAGCTTCCTGGGAGACAG
197224	29420	TACTTGCAAAGCTCCACTCT	241811	74007	CGTCAAGCACATGGGGACTT	286398	118594	CTGGAGCTTCCTGGGAGACA
197225	29421	CTACTTGCAAAGCTCCACTC	241812	74008	CCGTCAAGCACATGGGGACT	286399	118595	CCTGGAGCTTCCTGGGAGAC
197226	29422	ACTACTTGCAAAGCTCCACT	241813	74009	CCCGTCAAGCACATGGGGAC	286400	118596	CCCTGGAGCTTCCTGGGAGA
197227	29423	TACTACTTGCAAAGCTCCAC	241814	74010	CCCCGTCAAGCACATGGGGA	286401	118597	GCCCTGGAGCTTCCTGGGAG
197228	29424	TTACTACTTGCAAAGCTCCA	241815	74011	ACCCCGTCAAGCACATGGGG	286402	118598	CGCCCTGGAGCTTCCTGGGA
197229	29425	CTTACTACTTGCAAAGCTCC	241816	74012	TACCCCGTCAAGCACATGGG	286403	118599	CCGCCCTGGAGCTTCCTGGG
197230	29426	ACTTACTACTTGCAAAGCTC	241817	74013	ATACCCCGTCAAGCACATGG	286404	118600	ACCGCCCTGGAGCTTCCTGG
197231	29427	CACTTACTACTTGCAAAGCT	241818	74014	CATACCCCGTCAAGCACATG	286405	118601	CACCGCCCTGGAGCTTCCTG
197232	29428	GCACTTACTACTTGCAAAGC	241819	74015	ACATACCCCGTCAAGCACAT	286406	118602	GCACCGCCCTGGAGCTTCCT
197233	29429	AGCACTTACTACTTGCAAAG	241820	74016	CACATACCCCGTCAAGCACA	286407	118603	AGCACCGCCCTGGAGCTTCC
197234	29430	TAGCACTTACTACTTGCAAA	241821	74017	TCACATACCCCGTCAAGCAC	286408	118604	AAGCACCGCCCTGGAGCTTC
197235	29431	ATAGCACTTACTACTTGCAA	241822	74018	GTCACATACCCCGTCAAGCA	286409	118605	GAAGCACCGCCCTGGAGCTT
197236	29432	CATAGCACTTACTACTTGCA	241823	74019	AGTCACATACCCCGTCAAGC	286410	118606	GGAAGCACCGCCCTGGAGCT
197237	29433	ACATAGCACTTACTACTTGC	241824	74020	TAGTCACATACCCCGTCAAG	286411	118607	AGGAAGCACCGCCCTGGAGC
197238	29434	TACATAGCACTTACTACTTG	241825	74021	GTAGTCACATACCCCGTCAA	286412	118608	GAGGAAGCACCGCCCTGGAG
197239	29435	TTACATAGCACTTACTACTT	241826	74022	TGTAGTCACATACCCCGTCA	286413	118609	CGAGGAAGCACCGCCCTGGA
197240	29436	CTTACATAGCACTTACTACT	241827	74023	TTGTAGTCACATACCCCGTC	286414	118610	CCGAGGAAGCACCGCCCTGG
197241	29437	ACTTACATAGCACTTACTAC	241828	74024	GTTGTAGTCACATACCCCGT	286415	118611	CCCGAGGAAGCACCGCCCTG
197242	29438	CACTTACATAGCACTTACTA	241829	74025	CGTTGTAGTCACATACCCCG	286416	118612	TCCCGAGGAAGCACCGCCCT
197243	29439	ACACTTACATAGCACTTACT	241830	74026	ACGTTGTAGTCACATACCCC	286417	118613	CTCCCGAGGAAGCACCGCCC
197244	29440	AACACTTACATAGCACTTAC	241831	74027	CACGTTGTAGTCACATACCC	286418	118614	GCTCCCGAGGAAGCACCGCC
197245	29441	GAACACTTACATAGCACTTA	241832	74028	TCACGTTGTAGTCACATACC	286419	118615	AGCTCCCGAGGAAGCACCGC
197246	29442	CGAACACTTACATAGCACTT	241833	74029	ATCACGTTGTAGTCACATAC	286420	118616	CAGCTCCCGAGGAAGCACCG
197247	29443	TCGAACACTTACATAGCACT	241834	74030	CATCACGTTGTAGTCACATA	286421	118617	TCAGCTCCCGAGGAAGCACC
197248	29444	ATCGAACACTTACATAGCAC	241835	74031	GCATCACGTTGTAGTCACAT	286422	118618	GTCAGCTCCCGAGGAAGCAC
197249	29445	AATCGAACACTTACATAGCA	241836	74032	AGCATCACGTTGTAGTCACA	286423	118619	AGTCAGCTCCCGAGGAAGCA
197250	29446	AAATCGAACACTTACATAGC	241837	74033	AAGCATCACGTTGTAGTCAC	286424	118620	CAGTCAGCTCCCGAGGAAGC

197251	29447	TAAATCGAACACTTACATAG	241838	74034	CAAGCATCACGTTGTAGTCA	286425	118621	TCAGTCAGCTCCCGAGGAAG
197252	29448	TTAAATCGAACACTTACATA	241839	74035	TCAAGCATCACGTTGTAGTC	286426	118622	ATCAGTCAGCTCCCGAGGAA
197253	29449	TTTAAATCGAACACTTACAT	241840	74036	GTCAAGCATCACGTTGTAGT	286427	118623	TATCAGTCAGCTCCCGAGGA
197254	29450	TTTTAAATCGAACACTTACA	241841	74037	AGTCAAGCATCACGTTGTAG	286428	118624	CTATCAGTCAGCTCCCGAGG
197255	29451	ATTTTAAATCGAACACTTAC	241842	74038	AAGTCAAGCATCACGTTGTA	286429	118625	CCTATCAGTCAGCTCCCGAG
197256	29452	CATTTTAAATCGAACACTTA	241843	74039	AAAGTCAAGCATCACGTTGT	286430	118626	ACCTATCAGTCAGCTCCCGA
197257	29453	TCATTTTAAATCGAACACTT	241844	74040	AAAAGTCAAGCATCACGTTG	286431	118627	CACCTATCAGTCAGCTCCCG
197258	29454	TTCATTTTAAATCGAACACT	241845	74041	GAAAAGTCAAGCATCACGTT	286432	118628	CCACCTATCAGTCAGCTCCC
197259	29455	TTTCATTTTAAATCGAACAC	241846	74042	GGAAAAGTCAAGCATCACGT	286433	118629	CCCACCTATCAGTCAGCTCC
197260	29456	CTTTCATTTTAAATCGAACA	241847	74043	AGGAAAAGTCAAGCATCACG	286434	118630	TCCCACCTATCAGTCAGCTC
197261	29457	TCTTTCATTTTAAATCGAAC	241848	74044	GAGGAAAAGTCAAGCATCAC	286435	118631	CTCCCACCTATCAGTCAGCT
197262	29458	GTCTTTCATTTTAAATCGAA	241849	74045	TGAGGAAAAGTCAAGCATCA	286436	118632	CCTCCCACCTATCAGTCAGC
197263	29459	GGTCTTTCATTTTAAATCGA	241850	74046	ATGAGGAAAAGTCAAGCATC	286437	118633	ACCTCCCACCTATCAGTCAG
197264	29460	GGGTCTTTCATTTTAAATCG	241851	74047	TATGAGGAAAAGTCAAGCAT	286438	118634	CACCTCCCACCTATCAGTCA
197265	29461	AGGGTCTTTCATTTTAAATC	241852	74048	ATATGAGGAAAAGTCAAGCA	286439	118635	CCACCTCCCACCTATCAGTC
197266	29462	AAGGGTCTTTCATTTTAAAT	241853	74049	CATATGAGGAAAAGTCAAGC	286440	118636	GCCACCTCCCACCTATCAGT
197267	29463	TAAGGGTCTTTCATTTTAAA	241854	74050	TCATATGAGGAAAAGTCAAG	286441	118637	AGCCACCTCCCACCTATCAG
197268	29464	TTAAGGGTCTTTCATTTTAA	241855	74051	GTCATATGAGGAAAAGTCAA	286442	118638	CAGCCACCTCCCACCTATCA
197269	29465	TTTAAGGGTCTTTCATTTTA	241856	74052	GGTCATATGAGGAAAAGTCA	286443	118639	GCAGCCACCTCCCACCTATC
197270	29466	ATTTAAGGGTCTTTCATTTT	241857	74053	TGGTCATATGAGGAAAAGTC	286444	118640	GGCAGCCACCTCCCACCTAT
197271	29467	TATTTAAGGGTCTTTCATTT	241858	74054	CTGGTCATATGAGGAAAAGT	286445	118641	GGGCAGCCACCTCCCACCTA
197272	29468	GTATTTAAGGGTCTTTCATT	241859	74055	TCTGGTCATATGAGGAAAAG	286446	118642	GGGGCAGCCACCTCCCACCT
197273	29469	TGTATTTAAGGGTCTTTCAT	241860	74056	CTCTGGTCATATGAGGAAAA	286447	118643	GGGGGCAGCCACCTCCCACC
197274	29470	ATGTATTTAAGGGTCTTTCA	241861	74057	GCTCTGGTCATATGAGGAAA	286448	118644	AGGGGGCAGCCACCTCCCAC
197275	29471	AATGTATTTAAGGGTCTTTC	241862	74058	GGCTCTGGTCATATGAGGAA	286449	118645	AAGGGGGCAGCCACCTCCCA
197276	29472	GAATGTATTTAAGGGTCTTT	241863	74059	TGGCTCTGGTCATATGAGGA	286450	118646	CAAGGGGGCAGCCACCTCCC
197277	29473	AGAATGTATTTAAGGGTCTT	241864	74060	GTGGCTCTGGTCATATGAGG	286451	118647	GCAAGGGGGCAGCCACCTCC
197278	29474	AAGAATGTATTTAAGGGTCT	241865	74061	AGTGGCTCTGGTCATATGAG	286452	118648	TGCAAGGGGGCAGCCACCTC
197279	29475	AAAGAATGTATTTAAGGGTC	241866	74062	AAGTGGCTCTGGTCATATGA	286453	118649	GTGCAAGGGGGCAGCCACCT
197280	29476	CAAAGAATGTATTTAAGGGT	241867	74063	AAAGTGGCTCTGGTCATATG	286454	118650	GGTGCAAGGGGGCAGCCACC
197281	29477	ACAAAGAATGTATTTAAGGG	241868	74064	CAAAGTGGCTCTGGTCATAT	286455	118651	GGGTGCAAGGGGGCAGCCAC
197282	29478	AACAAAGAATGTATTTAAGG	241869	74065	ACAAAGTGGCTCTGGTCATA	286456	118652	AGGGTGCAAGGGGGCAGCCA
197283	29479	GAACAAAGAATGTATTTAAG	241870	74066	GACAAAGTGGCTCTGGTCAT	286457	118653	GAGGGTGCAAGGGGGCAGCC
197284	29480	TGAACAAAGAATGTATTTAA	241871	74067	GGACAAAGTGGCTCTGGTCA	286458	118654	TGAGGGTGCAAGGGGGCAGC
197285	29481	ATGAACAAAGAATGTATTTA	241872	74068	TGGACAAAGTGGCTCTGGTC	286459	118655	CTGAGGGTGCAAGGGGGCAG
197286	29482	AATGAACAAAGAATGTATTT	241873	74069	ATGGACAAAGTGGCTCTGGT	286460	118656	CCTGAGGGTGCAAGGGGGCA
197287	29483	AAATGAACAAAGAATGTATT	241874	74070	GATGGACAAAGTGGCTCTGG	286461	118657	ACCTGAGGGTGCAAGGGGGC
197288	29484	GAAATGAACAAAGAATGTAT	241875	74071	AGATGGACAAAGTGGCTCTG	286462	118658	CACCTGAGGGTGCAAGGGGG
197289	29485	TGAAATGAACAAAGAATGTA	241876	74072	CAGATGGACAAAGTGGCTCT	286463	118659	TCACCTGAGGGTGCAAGGGG
197290	29486	GTGAAATGAACAAAGAATGT	241877	74073	CCAGATGGACAAAGTGGCTC	286464	118660	GTCACCTGAGGGTGCAAGGG
197291	29487	TGTGAAATGAACAAAGAATG	241878	74074	ACCAGATGGACAAAGTGGCT	286465	118661	GGTCACCTGAGGGTGCAAGG
197292	29488	TTGTGAAATGAACAAAGAAT	241879	74075	TACCAGATGGACAAAGTGGC	286466	118662	GGGTCACCTGAGGGTGCAAG
197293	29489	CTTGTGAAATGAACAAAGAA	241880	74076	GTACCAGATGGACAAAGTGG	286467	118663	GGGGTCACCTGAGGGTGCAA
197294	29490	GCTTGTGAAATGAACAAAGA	241881	74077	TGTACCAGATGGACAAAGTG	286468	118664	TGGGGTCACCTGAGGGTGCA
197295	29491	GGCTTGTGAAATGAACAAAG	241882	74078	TTGTACCAGATGGACAAAGT	286469	118665	GTGGGGTCACCTGAGGGTGC
197296	29492	GGGCTTGTGAAATGAACAAA	241883	74079	ATTGTACCAGATGGACAAAG	286470	118666	TGTGGGGTCACCTGAGGGTG
197297	29493	AGGGCTTGTGAAATGAACAA	241884	74080	CATTGTACCAGATGGACAAA	286471	118667	GTGTGGGGTCACCTGAGGGT
197298	29494	AAGGGCTTGTGAAATGAACA	241885	74081	ACATTGTACCAGATGGACAA	286472	118668	TGTGTGGGGTCACCTGAGGG
197299	29495	GAAGGGCTTGTGAAATGAAC	241886	74082	GACATTGTACCAGATGGACA	286473	118669	TTGTGTGGGGTCACCTGAGG
197300	29496	TGAAGGGCTTGTGAAATGAA	241887	74083	TGACATTGTACCAGATGGAC	286474	118670	CTTGTGTGGGGTCACCTGAG
197301	29497	ATGAAGGGCTTGTGAAATGA	241888	74084	CTGACATTGTACCAGATGGA	286475	118671	CCTTGTGTGGGGTCACCTGA
197302	29498	AATGAAGGGCTTGTGAAATG	241889	74085	GCTGACATTGTACCAGATGG	286476	118672	GCCTTGTGTGGGGTCACCTG
197303	29499	AAATGAAGGGCTTGTGAAAT	241890	74086	AGCTGACATTGTACCAGATG	286477	118673	GGCCTTGTGTGGGGTCACCT
197304	29500	GAAATGAAGGGCTTGTGAAA	241891	74087	TAGCTGACATTGTACCAGAT	286478	118674	TGGCCTTGTGTGGGGTCACC
197305	29501	TGAAATGAAGGGCTTGTGAA	241892	74088	ATAGCTGACATTGTACCAGA	286479	118675	GTGGCCTTGTGTGGGGTCAC
197306	29502	GTGAAATGAAGGGCTTGTGA	241893	74089	GATAGCTGACATTGTACCAG	286480	118676	AGTGGCCTTGTGTGGGGTCA
197307	29503	TGTGAAATGAAGGGCTTGTG	241894	74090	AGATAGCTGACATTGTACCA	286481	118677	CAGTGGCCTTGTGTGGGGTC
197308	29504	TTGTGAAATGAAGGGCTTGT	241895	74091	CAGATAGCTGACATTGTACC	286482	118678	GCAGTGGCCTTGTGTGGGGT
197309	29505	GTTGTGAAATGAAGGGCTTG	241896	74092	GCAGATAGCTGACATTGTAC	286483	118679	AGCAGTGGCCTTGTGTGGGG
197310	29506	GGTTGTGAAATGAAGGGCTT	241897	74093	AGCAGATAGCTGACATTGTA	286484	118680	CAGCAGTGGCCTTGTGTGGG
197311	29507	AGGTTGTGAAATGAAGGGCT	241898	74094	TAGCAGATAGCTGACATTGT	286485	118681	CCAGCAGTGGCCTTGTGTGG
197312	29508	AAGGTTGTGAAATGAAGGGC	241899	74095	CTAGCAGATAGCTGACATTG	286486	118682	TCCAGCAGTGGCCTTGTGTG
197313	29509	TAAGGTTGTGAAATGAAGGG	241900	74096	CCTAGCAGATAGCTGACATT	286487	118683	CTCCAGCAGTGGCCTTGTGT
197314	29510	GTAAGGTTGTGAAATGAAGG	241901	74097	CCCTAGCAGATAGCTGACAT	286488	118684	CCTCCAGCAGTGGCCTTGTG
197315	29511	TGTAAGGTTGTGAAATGAAG	241902	74098	CCCCTAGCAGATAGCTGACA	286489	118685	GCCTCCAGCAGTGGCCTTGT
197316	29512	ATGTAAGGTTGTGAAATGAA	241903	74099	GCCCCTAGCAGATAGCTGAC	286490	118686	GGCCTCCAGCAGTGGCCTTG
197317	29513	AATGTAAGGTTGTGAAATGA	241904	74100	GGCCCCTAGCAGATAGCTGA	286491	118687	GGGCCTCCAGCAGTGGCCTT
197318	29514	AAATGTAAGGTTGTGAAATG	241905	74101	GGGCCCCTAGCAGATAGCTG	286492	118688	AGGGCCTCCAGCAGTGGCCT
197319	29515	GAAATGTAAGGTTGTGAAAT	241906	74102	AGGGCCCCTAGCAGATAGCT	286493	118689	CAGGGCCTCCAGCAGTGGCC
197320	29516	TGAAATGTAAGGTTGTGAAA	241907	74103	GAGGGCCCCTAGCAGATAGC	286494	118690	CCAGGGCCTCCAGCAGTGGC
197321	29517	GTGAAATGTAAGGTTGTGAA	241908	74104	GGAGGGCCCCTAGCAGATAG	286495	118691	CCCAGGGCCTCCAGCAGTGG
197322	29518	TGTGAAATGTAAGGTTGTGA	241909	74105	TGGAGGGCCCCTAGCAGATA	286496	118692	CCCCAGGGCCTCCAGCAGTG

197323	29519	TTGTGAAATGTAAGGTTGTG	241910	74106	CTGGAGGGCCCCTAGCAGAT	286497	118693	TCCCCAGGGCCTCCAGCAGT
197324	29520	GTTGTGAAATGTAAGGTTGT	241911	74107	CCTGGAGGGCCCCTAGCAGA	286498	118694	GTCCCCAGGGCCTCCAGCAG
197325	29521	GGTTGTGAAATGTAAGGTTG	241912	74108	TCCTGGAGGGCCCCTAGCAG	286499	118695	AGTCCCCAGGGCCTCCAGCA
197326	29522	TGGTTGTGAAATGTAAGGTT	241913	74109	ATCCTGGAGGGCCCCTAGCA	286500	118696	GAGTCCCCAGGGCCTCCAGC
197327	29523	TTGGTTGTGAAATGTAAGGT	241914	74110	AATCCTGGAGGGCCCCTAGC	286501	118697	GGAGTCCCCAGGGCCTCCAG
197328	29524	CTTGGTTGTGAAATGTAAGG	241915	74111	GAATCCTGGAGGGCCCCTAG	286502	118698	TGGAGTCCCCAGGGCCTCCA
197329	29525	GCTTGGTTGTGAAATGTAAG	241916	74112	GGAATCCTGGAGGGCCCCTA	286503	118699	CTGGAGTCCCCAGGGCCTCC
197330	29526	AGCTTGGTTGTGAAATGTAA	241917	74113	GGGAATCCTGGAGGGCCCCT	286504	118700	CCTGGAGTCCCCAGGGCCTC
197331	29527	GAGCTTGGTTGTGAAATGTA	241918	74114	TGGGAATCCTGGAGGGCCCC	286505	118701	TCCTGGAGTCCCCAGGGCCT
197332	29528	AGAGCTTGGTTGTGAAATGT	241919	74115	CTGGGAATCCTGGAGGGCCC	286506	118702	TTCCTGGAGTCCCCAGGGCC
197333	29529	CAGAGCTTGGTTGTGAAATG	241920	74116	ACTGGGAATCCTGGAGGGCC	286507	118703	ATTCCTGGAGTCCCCAGGGC
197334	29530	ACAGAGCTTGGTTGTGAAAT	241921	74117	GACTGGGAATCCTGGAGGGC	286508	118704	CATTCCTGGAGTCCCCAGGG
197335	29531	GACAGAGCTTGGTTGTGAAA	241922	74118	TGACTGGGAATCCTGGAGGG	286509	118705	ACATTCCTGGAGTCCCCAGG
197336	29532	AGACAGAGCTTGGTTGTGAA	241923	74119	TTGACTGGGAATCCTGGAGG	286510	118706	GACATTCCTGGAGTCCCCAG
197337	29533	GAGACAGAGCTTGGTTGTGA	241924	74120	ATTGACTGGGAATCCTGGAG	286511	118707	TGACATTCCTGGAGTCCCCA
197338	29534	GGAGACAGAGCTTGGTTGTG	241925	74121	AATTGACTGGGAATCCTGGA	286512	118708	TTGACATTCCTGGAGTCCCC
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197341	29537	AGGGGAGACAGAGCTTGGTT	241928	74124	TGGAATTGACTGGGAATCCT	286515	118711	TGATTGACATTCCTGGAGTC
197342	29538	CAGGGGAGACAGAGCTTGGT	241929	74125	ATGGAATTGACTGGGAATCC	286516	118712	CTGATTGACATTCCTGGAGT
197343	29539	CCAGGGGAGACAGAGCTTGG	241930	74126	TATGGAATTGACTGGGAATC	286517	118713	ACTGATTGACATTCCTGGAG
197344	29540	TCCAGGGGAGACAGAGCTTG	241931	74127	ATATGGAATTGACTGGGAAT	286518	118714	CACTGATTGACATTCCTGGA
197345	29541	TTCCAGGGGAGACAGAGCTT	241932	74128	GATATGGAATTGACTGGGAA	286519	118715	TCACTGATTGACATTCCTGG
197346	29542	ATTCCAGGGGAGACAGAGCT	241933	74129	AGATATGGAATTGACTGGGA	286520	118716	GTCACTGATTGACATTCCTG
197347	29543	GATTCCAGGGGAGACAGAGC	241934	74130	CAGATATGGAATTGACTGGG	286521	118717	GGTCACTGATTGACATTCCT
197348	29544	GGATTCCAGGGGAGACAGAG	241935	74131	GCAGATATGGAATTGACTGG	286522	118718	AGGTCACTGATTGACATTCC
197349	29545	TGGATTCCAGGGGAGACAGA	241936	74132	TGCAGATATGGAATTGACTG	286523	118719	CAGGTCACTGATTGACATTC
197350	29546	CTGGATTCCAGGGGAGACAG	241937	74133	ATGCAGATATGGAATTGACT	286524	118720	GCAGGTCACTGATTGACATT
197351	29547	GCTGGATTCCAGGGGAGACA	241938	74134	GATGCAGATATGGAATTGAC	286525	118721	GGCAGGTCACTGATTGACAT
197352	29548	GGCTGGATTCCAGGGGAGAC	241939	74135	TGATGCAGATATGGAATTGA	286526	118722	GGGCAGGTCACTGATTGACA
197353	29549	TGGCTGGATTCCAGGGGAGA	241940	74136	GTGATGCAGATATGGAATTG	286527	118723	GGGGCAGGTCACTGATTGAC
197354	29550	ATGGCTGGATTCCAGGGGAG	241941	74137	GGTGATGCAGATATGGAATT	286528	118724	GGGGGCAGGTCACTGATTGA
197355	29551	TATGGCTGGATTCCAGGGGA	241942	74138	TGGTGATGCAGATATGGAAT	286529	118725	GGGGGGCAGGTCACTGATTG
197356	29552	TTATGGCTGGATTCCAGGGG	241943	74139	GTGGTGATGCAGATATGGAA	286530	118726	TGGGGGGCAGGTCACTGATT
197357	29553	GTTATGGCTGGATTCCAGGG	241944	74140	GGTGGTGATGCAGATATGGA	286531	118727	CTGGGGGGCAGGTCACTGAT
197358	29554	AGTTATGGCTGGATTCCAGG	241945	74141	TGGTGGTGATGCAGATATGG	286532	118728	CCTGGGGGGCAGGTCACTGA
197359	29555	GAGTTATGGCTGGATTCCAG	241946	74142	ATGGTGGTGATGCAGATATG	286533	118729	GCCTGGGGGGCAGGTCACTG
197360	29556	AGAGTTATGGCTGGATTCCA	241947	74143	AATGGTGGTGATGCAGATAT	286534	118730	GGCCTGGGGGGCAGGTCACT
197361	29557	CAGAGTTATGGCTGGATTCC	241948	74144	CAATGGTGGTGATGCAGATA	286535	118731	GGGCCTGGGGGGCAGGTCAC
197362	29558	GCAGAGTTATGGCTGGATTC	241949	74145	CCAATGGTGGTGATGCAGAT	286536	118732	GGGGCCTGGGGGGCAGGTCA
197363	29559	AGCAGAGTTATGGCTGGATT	241950	74146	GCCAATGGTGGTGATGCAGA	286537	118733	TGGGGCCTGGGGGGCAGGTC
197364	29560	GAGCAGAGTTATGGCTGGAT	241951	74147	TGCCAATGGTGGTGATGCAG	286538	118734	GTGGGGCCTGGGGGGCAGGT
197365	29561	TGAGCAGAGTTATGGCTGGA	241952	74148	GTGCCAATGGTGGTGATGCA	286539	118735	TGTGGGGCCTGGGGGGCAGG
197366	29562	GTGAGCAGAGTTATGGCTGG	241953	74149	AGTGCCAATGGTGGTGATGC	286540	118736	GTGTGGGGCCTGGGGGGCAG
197367	29563	TGTGAGCAGAGTTATGGCTG	241954	74150	TAGTGCCAATGGTGGTGATG	286541	118737	TGTGTGGGGCCTGGGGGGCA
197368	29564	TTGTGAGCAGAGTTATGGCT	241955	74151	TTAGTGCCAATGGTGGTGAT	286542	118738	CTGTGTGGGGCCTGGGGGGC
197369	29565	CTTGTGAGCAGAGTTATGGC	241956	74152	TTTAGTGCCAATGGTGGTGA	286543	118739	GCTGTGTGGGGCCTGGGGGG
197370	29566	ACTTGTGAGCAGAGTTATGG	241957	74153	ATTTAGTGCCAATGGTGGTG	286544	118740	GGCTGTGTGGGGCCTGGGGG
197371	29567	CACTTGTGAGCAGAGTTATG	241958	74154	TATTTAGTGCCAATGGTGGT	286545	118741	TGGCTGTGTGGGGCCTGGGG
197372	29568	ACACTTGTGAGCAGAGTTAT	241959	74155	TTATTTAGTGCCAATGGTGG	286546	118742	ATGGCTGTGTGGGGCCTGGG
197373	29569	CACACTTGTGAGCAGAGTTA	241960	74156	TTTATTTAGTGCCAATGGTG	286547	118743	CATGGCTGTGTGGGGCCTGG
197374	29570	TCACACTTGTGAGCAGAGTT	241961	74157	TTTTATTTAGTGCCAATGGT	286548	118744	CCATGGCTGTGTGGGGCCTG
197375	29571	CTCACACTTGTGAGCAGAGT	241962	74158	ATTTTATTTAGTGCCAATGG	286549	118745	GCCATGGCTGTGTGGGGCCT
197376	29572	TCTCACACTTGTGAGCAGAG	241963	74159	TATTTTATTTAGTGCCAATG	286550	118746	AGCCATGGCTGTGTGGGGCC
197377	29573	GTCTCACACTTGTGAGCAGA	241964	74160	TTATTTTATTTAGTGCCAAT	286551	118747	CAGCCATGGCTGTGTGGGGC
197378	29574	TGTCTCACACTTGTGAGCAG	241965	74161	TTTATTTTATTTAGTGCCAA	286552	118748	GCAGCCATGGCTGTGTGGGG
197379	29575	CTGTCTCACACTTGTGAGCA	241966	74162	TTTTATTTTATTTAGTGCCA	286553	118749	TGCAGCCATGGCTGTGTGGG
197380	29576	CCTGTCTCACACTTGTGAGC	241967	74163	ATTTTATTTTATTTAGTGCC	286554	118750	ATGCAGCCATGGCTGTGTGG
197381	29577	GCCTGTCTCACACTTGTGAG	241968	74164	TATTTTATTTTATTTAGTGC	286555	118751	TATGCAGCCATGGCTGTGTG
197382	29578	GGCCTGTCTCACACTTGTGA	241969	74165	GTATTTTATTTTATTTAGTG	286556	118752	CTATGCAGCCATGGCTGTGT
197383	29579	GGGCCTGTCTCACACTTGTG	241970	74166	AGTATTTTATTTTATTTAGT	286557	118753	TCTATGCAGCCATGGCTGTG
197384	29580	GGGGCCTGTCTCACACTTGT	241971	74167	GAGTATTTTATTTTATTTAG	286558	118754	CTCTATGCAGCCATGGCTGT
197385	29581	TGGGGCCTGTCTCACACTTG	241972	74168	TGAGTATTTTATTTTATTTA	286559	118755	CCTCTATGCAGCCATGGCTG
197386	29582	CTGGGGCCTGTCTCACACTT	241973	74169	TTGAGTATTTTATTTTATTT	286560	118756	GCCTCTATGCAGCCATGGCT
197387	29583	GCTGGGGCCTGTCTCACACT	241974	74170	CTTGAGTATTTTATTTTATT	286561	118757	GGCCTCTATGCAGCCATGGC
197388	29584	TGCTGGGGCCTGTCTCACAC	241975	74171	ACTTGAGTATTTTATTTTAT	286562	118758	AGGCCTCTATGCAGCCATGG
197389	29585	CTGCTGGGGCCTGTCTCACA	241976	74172	AACTTGAGTATTTTATTTTA	286563	118759	CAGGCCTCTATGCAGCCATG
197390	29586	TCTGCTGGGGCCTGTCTCAC	241977	74173	GAACTTGAGTATTTTATTTT	286564	118760	GCAGGCCTCTATGCAGCCAT
197391	29587	CTCTGCTGGGGCCTGTCTCA	241978	74174	GGAACTTGAGTATTTTATTT	286565	118761	GGCAGGCCTCTATGCAGCCA
197392	29588	GCTCTGCTGGGGCCTGTCTC	241979	74175	AGGAACTTGAGTATTTTATT	286566	118762	AGGCAGGCCTCTATGCAGCC
197393	29589	AGCTCTGCTGGGGCCTGTCT	241980	74176	CAGGAACTTGAGTATTTTAT	286567	118763	GAGGCAGGCCTCTATGCAGC
197394	29590	CAGCTCTGCTGGGGCCTGTC	241981	74177	GCAGGAACTTGAGTATTTTA	286568	118764	GGAGGCAGGCCTCTATGCAG

197395	29591	GCAGCTCTGCTGGGGCCTGT	241982	74178	AGCAGGAACTTGAGTATTTT	286569	118765	TGGAGGCAGGCCTCTATGCA
197396	29592	TGCAGCTCTGCTGGGGCCTG	241983	74179	CAGCAGGAACTTGAGTATTT	286570	118766	TTGGAGGCAGGCCTCTATGC
197397	29593	GTGCAGCTCTGCTGGGGCCT	241984	74180	CCAGCAGGAACTTGAGTATT	286571	118767	CTTGGAGGCAGGCCTCTATG
197398	29594	CGTGCAGCTCTGCTGGGGCC	241985	74181	ACCAGCAGGAACTTGAGTAT	286572	118768	CCTTGGAGGCAGGCCTCTAT
197399	29595	TCGTGCAGCTCTGCTGGGGC	241986	74182	CACCAGCAGGAACTTGAGTA	286573	118769	CCCTTGGAGGCAGGCCTCTA
197400	29596	TTCGTGCAGCTCTGCTGGGG	241987	74183	TCACCAGCAGGAACTTGAGT	286574	118770	TCCCTTGGAGGCAGGCCTCT
197401	29597	CTTCGTGCAGCTCTGCTGGG	241988	74184	CTCACCAGCAGGAACTTGAG	286575	118771	GTCCCTTGGAGGCAGGCCTC
197402	29598	TCTTCGTGCAGCTCTGCTGG	241989	74185	GCTCACCAGCAGGAACTTGA	286576	118772	GGTCCCTTGGAGGCAGGCCT
197403	29599	CTCTTCGTGCAGCTCTGCTG	241990	74186	TGCTCACCAGCAGGAACTTG	286577	118773	AGGTCCCTTGGAGGCAGGCC
197404	29600	CCTCTTCGTGCAGCTCTGCT	241991	74187	ATGCTCACCAGCAGGAACTT	286578	118774	CAGGTCCCTTGGAGGCAGGC
197405	29601	TCCTCTTCGTGCAGCTCTGC	241992	74188	CATGCTCACCAGCAGGAACT	286579	118775	ACAGGTCCCTTGGAGGCAGG
197406	29602	CTCCTCTTCGTGCAGCTCTG	241993	74189	TCATGCTCACCAGCAGGAAC	286580	118776	GACAGGTCCCTTGGAGGCAG
197407	29603	TCTCCTCTTCGTGCAGCTCT	241994	74190	CTCATGCTCACCAGCAGGAA	286581	118777	AGACAGGTCCCTTGGAGGCA
197408	29604	CTCTCCTCTTCGTGCAGCTC	241995	74191	GCTCATGCTCACCAGCAGGA	286582	118778	CAGACAGGTCCCTTGGAGGC
197409	29605	TCTCTCCTCTTCGTGCAGCT	241996	74192	TGCTCATGCTCACCAGCAGG	286583	118779	ACAGACAGGTCCCTTGGAGG
197410	29606	TTCTCTCCTCTTCGTGCAGC	241997	74193	CTGCTCATGCTCACCAGCAG	286584	118780	GACAGACAGGTCCCTTGGAG
197411	29607	CTTCTCTCCTCTTCGTGCAG	241998	74194	ACTGCTCATGCTCACCAGCA	286585	118781	AGACAGACAGGTCCCTTGGA
197412	29608	CCTTCTCTCCTCTTCGTGCA	241999	74195	CACTGCTCATGCTCACCAGC	286586	118782	CAGACAGACAGGTCCCTTGG
197413	29609	GCCTTCTCTCCTCTTCGTGC	242000	74196	GCACTGCTCATGCTCACCAG	286587	118783	GCAGACAGACAGGTCCCTTG
197414	29610	TGCCTTCTCTCCTCTTCGTG	242001	74197	AGCACTGCTCATGCTCACCA	286588	118784	GGCAGACAGACAGGTCCCTT
197415	29611	CTGCCTTCTCTCCTCTTCGT	242002	74198	TAGCACTGCTCATGCTCACC	286589	118785	TGGCAGACAGACAGGTCCCT
197416	29612	GCTGCCTTCTCTCCTCTTCG	242003	74199	GTAGCACTGCTCATGCTCAC	286590	118786	GTGGCAGACAGACAGGTCCC
197417	29613	GGCTGCCTTCTCTCCTCTTC	242004	74200	TGTAGCACTGCTCATGCTCA	286591	118787	AGTGGCAGACAGACAGGTCC
197418	29614	GGGCTGCCTTCTCTCCTCTT	242005	74201	GTGTAGCACTGCTCATGCTC	286592	118788	CAGTGGCAGACAGACAGGTC
197419	29615	GGGGCTGCCTTCTCTCCTCT	242006	74202	AGTGTAGCACTGCTCATGCT	286593	118789	ACAGTGGCAGACAGACAGGT
197420	29616	GGGGGCTGCCTTCTCTCCTC	242007	74203	CAGTGTAGCACTGCTCATGC	286594	118790	CACAGTGGCAGACAGACAGG
197421	29617	GGGGGGCTGCCTTCTCTCCT	242008	74204	CCAGTGTAGCACTGCTCATG	286595	118791	CCACAGTGGCAGACAGACAG
197422	29618	TGGGGGGCTGCCTTCTCTCC	242009	74205	CCCAGTGTAGCACTGCTCAT	286596	118792	TCCACAGTGGCAGACAGACA
197423	29619	CTGGGGGGCTGCCTTCTCTC	242010	74206	GCCCAGTGTAGCACTGCTCA	286597	118793	CTCCACAGTGGCAGACAGAC
197424	29620	TCTGGGGGGCTGCCTTCTCT	242011	74207	GGCCCAGTGTAGCACTGCTC	286598	118794	ACTCCACAGTGGCAGACAGA
197425	29621	GTCTGGGGGGCTGCCTTCTC	242012	74208	GGGCCCAGTGTAGCACTGCT	286599	118795	GACTCCACAGTGGCAGACAG
197426	29622	AGTCTGGGGGGCTGCCTTCT	242013	74209	AGGGCCCAGTGTAGCACTGC	286600	118796	GGACTCCACAGTGGCAGACA
197427	29623	GAGTCTGGGGGGCTGCCTTC	242014	74210	AAGGGCCCAGTGTAGCACTG	286601	118797	GGGACTCCACAGTGGCAGAC
197428	29624	GGAGTCTGGGGGGCTGCCTT	242015	74211	GAAGGGCCCAGTGTAGCACT	286602	118798	AGGGACTCCACAGTGGCAGA
197429	29625	GGGAGTCTGGGGGGCTGCCT	242016	74212	TGAAGGGCCCAGTGTAGCAC	286603	118799	TAGGGACTCCACAGTGGCAG
197430	29626	TGGGAGTCTGGGGGGCTGCC	242017	74213	TTGAAGGGCCCAGTGTAGCA	286604	118800	GTAGGGACTCCACAGTGGCA
197431	29627	TTGGGAGTCTGGGGGGCTGC	242018	74214	GTTGAAGGGCCCAGTGTAGC	286605	118801	TGTAGGGACTCCACAGTGGC
197432	29628	GTTGGGAGTCTGGGGGGCTG	242019	74215	GGTTGAAGGGCCCAGTGTAG	286606	118802	CTGTAGGGACTCCACAGTGG
197433	29629	GGTTGGGAGTCTGGGGGGCT	242020	74216	TGGTTGAAGGGCCCAGTGTA	286607	118803	GCTGTAGGGACTCCACAGTG
197434	29630	GGGTTGGGAGTCTGGGGGGC	242021	74217	TTGGTTGAAGGGCCCAGTGT	286608	118804	CGCTGTAGGGACTCCACAGT
197435	29631	GGGGTTGGGAGTCTGGGGGG	242022	74218	CTTGGTTGAAGGGCCCAGTG	286609	118805	ACGCTGTAGGGACTCCACAG
197436	29632	GGGGGTTGGGAGTCTGGGGG	242023	74219	CCTTGGTTGAAGGGCCCAGT	286610	118806	CACGCTGTAGGGACTCCACA
197437	29633	AGGGGGTTGGGAGTCTGGGG	242024	74220	ACCTTGGTTGAAGGGCCCAG	286611	118807	GCACGCTGTAGGGACTCCAC
197438	29634	CAGGGGGTTGGGAGTCTGGG	242025	74221	CACCTTGGTTGAAGGGCCCA	286612	118808	GGCACGCTGTAGGGACTCCA
197439	29635	ACAGGGGGTTGGGAGTCTGG	242026	74222	TCACCTTGGTTGAAGGGCCC	286613	118809	GGGCACGCTGTAGGGACTCC
197440	29636	GACAGGGGGTTGGGAGTCTG	242027	74223	GTCACCTTGGTTGAAGGGCC	286614	118810	GGGGCACGCTGTAGGGACTC
197441	29637	GGACAGGGGGTTGGGAGTCT	242028	74224	TGTCACCTTGGTTGAAGGGC	286615	118811	GGGGGCACGCTGTAGGGACT
197442	29638	TGGACAGGGGGTTGGGAGTC	242029	74225	ATGTCACCTTGGTTGAAGGG	286616	118812	GGGGGGCACGCTGTAGGGAC
197443	29639	TTGGACAGGGGGTTGGGAGT	242030	74226	CATGTCACCTTGGTTGAAGG	286617	118813	TGGGGGGCACGCTGTAGGGA
197444	29640	CTTGGACAGGGGGTTGGGAG	242031	74227	TCATGTCACCTTGGTTGAAG	286618	118814	GTGGGGGGCACGCTGTAGGG
197445	29641	TCTTGGACAGGGGGTTGGGA	242032	74228	ATCATGTCACCTTGGTTGAA	286619	118815	TGTGGGGGGCACGCTGTAGG
197446	29642	ATCTTGGACAGGGGGTTGGG	242033	74229	TATCATGTCACCTTGGTTGA	286620	118816	CTGTGGGGGGCACGCTGTAG
197447	29643	CATCTTGGACAGGGGGTTGG	242034	74230	TTATCATGTCACCTTGGTTG	286621	118817	CCTGTGGGGGGCACGCTGTA
197448	29644	CCATCTTGGACAGGGGGTTG	242035	74231	ATTATCATGTCACCTTGGTT	286622	118818	CCCTGTGGGGGGCACGCTGT
197449	29645	GCCATCTTGGACAGGGGGTT	242036	74232	CATTATCATGTCACCTTGGT	286623	118819	CCCCTGTGGGGGGCACGCTG
197450	29646	TGCCATCTTGGACAGGGGGT	242037	74233	TCATTATCATGTCACCTTGG	286624	118820	TCCCCTGTGGGGGGCACGCT
197451	29647	TTGCCATCTTGGACAGGGGG	242038	74234	GTCATTATCATGTCACCTTG	286625	118821	CTCCCCTGTGGGGGGCACGC
197452	29648	TTTGCCATCTTGGACAGGGG	242039	74235	AGTCATTATCATGTCACCTT	286626	118822	GCTCCCCTGTGGGGGGCACG
197453	29649	TTTTGCCATCTTGGACAGGG	242040	74236	CAGTCATTATCATGTCACCT	286627	118823	AGCTCCCCTGTGGGGGGCAC
197454	29650	GTTTTGCCATCTTGGACAGG	242041	74237	TCAGTCATTATCATGTCACC	286628	118824	CAGCTCCCCTGTGGGGGGCA
197455	29651	GGTTTTGCCATCTTGGACAG	242042	74238	TTCAGTCATTATCATGTCAC	286629	118825	CCAGCTCCCCTGTGGGGGGC
197456	29652	TGGTTTTGCCATCTTGGACA	242043	74239	TTTCAGTCATTATCATGTCA	286630	118826	ACCAGCTCCCCTGTGGGGGG
197457	29653	CTGGTTTTGCCATCTTGGAC	242044	74240	TTTTCAGTCATTATCATGTC	286631	118827	AACCAGCTCCCCTGTGGGGG
197458	29654	TCTGGTTTTGCCATCTTGGA	242045	74241	ATTTTCAGTCATTATCATGT	286632	118828	GAACCAGCTCCCCTGTGGGG
197459	29655	TTCTGGTTTTGCCATCTTGG	242046	74242	TATTTTCAGTCATTATCATG	286633	118829	AGAACCAGCTCCCCTGTGGG
197460	29656	GTTCTGGTTTTGCCATCTTG	242047	74243	TTATTTTCAGTCATTATCAT	286634	118830	AAGAACCAGCTCCCCTGTGG
197461	29657	TGTTCTGGTTTTGCCATCTT	242048	74244	ATTATTTTCAGTCATTATCA	286635	118831	AAAGAACCAGCTCCCCTGTG
197462	29658	GTGTTCTGGTTTTGCCATCT	242049	74245	GATTATTTTCAGTCATTATC	286636	118832	CAAAGAACCAGCTCCCCTGT
197463	29659	TGTGTTCTGGTTTTGCCATC	242050	74246	TGATTATTTTCAGTCATTAT	286637	118833	TCAAAGAACCAGCTCCCCTG
197464	29660	CTGTGTTCTGGTTTTGCCAT	242051	74247	GTGATTATTTTCAGTCATTA	286638	118834	GTCAAAGAACCAGCTCCCCT
197465	29661	GCTGTGTTCTGGTTTTGCCA	242052	74248	AGTGATTATTTTCAGTCATT	286639	118835	AGTCAAAGAACCAGCTCCCC
197466	29662	GGCTGTGTTCTGGTTTTGCC	242053	74249	CAGTGATTATTTTCAGTCAT	286640	118836	CAGTCAAAGAACCAGCTCCC

197467	29663	AGGCTGTGTTCTGGTTTTGC	242054	74250	GCAGTGATTATTTTCAGTCA	286641	118837	TCAGTCAAAGAACCAGCTCC
197468	29664	GAGGCTGTGTTCTGGTTTTG	242055	74251	GGCAGTGATTATTTTCAGTC	286642	118838	CTCAGTCAAAGAACCAGCTC
197469	29665	AGAGGCTGTGTTCTGGTTTT	242056	74252	TGGCAGTGATTATTTTCAGT	286643	118839	TCTCAGTCAAAGAACCAGCT
197470	29666	CAGAGGCTGTGTTCTGGTTT	242057	74253	GTGGCAGTGATTATTTTCAG	286644	118840	ATCTCAGTCAAAGAACCAGC
197471	29667	ACAGAGGCTGTGTTCTGGTT	242058	74254	AGTGGCAGTGATTATTTTCA	286645	118841	GATCTCAGTCAAAGAACCAG
197472	29668	TACAGAGGCTGTGTTCTGGT	242059	74255	AAGTGGCAGTGATTATTTTC	286646	118842	TGATCTCAGTCAAAGAACCA
197473	29669	GTACAGAGGCTGTGTTCTGG	242060	74256	TAAGTGGCAGTGATTATTTT	286647	118843	CTGATCTCAGTCAAAGAACC
197474	29670	GGTACAGAGGCTGTGTTCTG	242061	74257	ATAAGTGGCAGTGATTATTT	286648	118844	GCTGATCTCAGTCAAAGAAC
197475	29671	TGGTACAGAGGCTGTGTTCT	242062	74258	AATAAGTGGCAGTGATTATT	286649	118845	AGCTGATCTCAGTCAAAGAA
197476	29672	GTGGTACAGAGGCTGTGTTC	242063	74259	CAATAAGTGGCAGTGATTAT	286650	118846	CAGCTGATCTCAGTCAAAGA
197477	29673	GGTGGTACAGAGGCTGTGTT	242064	74260	CCAATAAGTGGCAGTGATTA	286651	118847	CCAGCTGATCTCAGTCAAAG
197478	29674	GGGTGGTACAGAGGCTGTGT	242065	74261	CCCAATAAGTGGCAGTGATT	286652	118848	GCCAGCTGATCTCAGTCAAA
197479	29675	GGGGTGGTACAGAGGCTGTG	242066	74262	CCCCAATAAGTGGCAGTGAT	286653	118849	TGCCAGCTGATCTCAGTCAA
197480	29676	TGGGGTGGTACAGAGGCTGT	242067	74263	TCCCCAATAAGTGGCAGTGA	286654	118850	CTGCCAGCTGATCTCAGTCA
197481	29677	CTGGGGTGGTACAGAGGCTG	242068	74264	GTCCCCAATAAGTGGCAGTG	286655	118851	GCTGCCAGCTGATCTCAGTC
197482	29678	GCTGGGGTGGTACAGAGGCT	242069	74265	CGTCCCCAATAAGTGGCAGT	286656	118852	AGCTGCCAGCTGATCTCAGT
197483	29679	TGCTGGGGTGGTACAGAGGC	242070	74266	ACGTCCCCAATAAGTGGCAG	286657	118853	GAGCTGCCAGCTGATCTCAG
197484	29680	CTGCTGGGGTGGTACAGAGG	242071	74267	GACGTCCCCAATAAGTGGCA	286658	118854	TGAGCTGCCAGCTGATCTCA
197485	29681	CCTGCTGGGGTGGTACAGAG	242072	74268	AGACGTCCCCAATAAGTGGC	286659	118855	CTGAGCTGCCAGCTGATCTC
197486	29682	ACCTGCTGGGGTGGTACAGA	242073	74269	GAGACGTCCCCAATAAGTGG	286660	118856	CCTGAGCTGCCAGCTGATCT
197487	29683	TACCTGCTGGGGTGGTACAG	242074	74270	TGAGACGTCCCCAATAAGTG	286661	118857	CCCTGAGCTGCCAGCTGATC
197488	29684	ATACCTGCTGGGGTGGTACA	242075	74271	ATGAGACGTCCCCAATAAGT	286662	118858	ACCCTGAGCTGCCAGCTGAT
197489	29685	AATACCTGCTGGGGTGGTAC	242076	74272	GATGAGACGTCCCCAATAAG	286663	118859	GACCCTGAGCTGCCAGCTGA
197490	29686	GAATACCTGCTGGGGTGGTA	242077	74273	AGATGAGACGTCCCCAATAA	286664	118860	TGACCCTGAGCTGCCAGCTG
197491	29687	TGAATACCTGCTGGGGTGGT	242078	74274	CAGATGAGACGTCCCCAATA	286665	118861	ATGACCCTGAGCTGCCAGCT
197492	29688	CTGAATACCTGCTGGGGTGG	242079	74275	GCAGATGAGACGTCCCCAAT	286666	118862	GATGACCCTGAGCTGCCAGC
197493	29689	TCTGAATACCTGCTGGGGTG	242080	74276	GGCAGATGAGACGTCCCCAA	286667	118863	TGATGACCCTGAGCTGCCAG
197494	29690	TTCTGAATACCTGCTGGGGT	242081	74277	TGGCAGATGAGACGTCCCCA	286668	118864	ATGATGACCCTGAGCTGCCA
197495	29691	ATTCTGAATACCTGCTGGGG	242082	74278	CTGGCAGATGAGACGTCCCC	286669	118865	AATGATGACCCTGAGCTGCC
197496	29692	GATTCTGAATACCTGCTGGG	242083	74279	CCTGGCAGATGAGACGTCCC	286670	118866	GAATGATGACCCTGAGCTGC
197497	29693	AGATTCTGAATACCTGCTGG	242084	74280	GCCTGGCAGATGAGACGTCC	286671	118867	GGAATGATGACCCTGAGCTG
197498	29694	CAGATTCTGAATACCTGCTG	242085	74281	TGCCTGGCAGATGAGACGTC	286672	118868	GGGAATGATGACCCTGAGCT
197499	29695	GCAGATTCTGAATACCTGCT	242086	74282	ATGCCTGGCAGATGAGACGT	286673	118869	TGGGAATGATGACCCTGAGC
197500	29696	TGCAGATTCTGAATACCTGC	242087	74283	CATGCCTGGCAGATGAGACG	286674	118870	CTGGGAATGATGACCCTGAG
197501	29697	TTGCAGATTCTGAATACCTG	242088	74284	CCATGCCTGGCAGATGAGAC	286675	118871	TCTGGGAATGATGACCCTGA
197502	29698	ATTGCAGATTCTGAATACCT	242089	74285	ACCATGCCTGGCAGATGAGA	286676	118872	CTCTGGGAATGATGACCCTG
197503	29699	GATTGCAGATTCTGAATACC	242090	74286	TACCATGCCTGGCAGATGAG	286677	118873	CCTCTGGGAATGATGACCCT
197504	29700	AGATTGCAGATTCTGAATAC	242091	74287	GTACCATGCCTGGCAGATGA	286678	118874	CCCTCTGGGAATGATGACCC
197505	29701	GAGATTGCAGATTCTGAATA	242092	74288	TGTACCATGCCTGGCAGATG	286679	118875	TCCCTCTGGGAATGATGACC
197506	29702	GGAGATTGCAGATTCTGAAT	242093	74289	TTGTACCATGCCTGGCAGAT	286680	118876	CTCCCTCTGGGAATGATGAC
197507	29703	TGGAGATTGCAGATTCTGAA	242094	74290	TTTGTACCATGCCTGGCAGA	286681	118877	GCTCCCTCTGGGAATGATGA
197508	29704	TTGGAGATTGCAGATTCTGA	242095	74291	CTTTGTACCATGCCTGGCAG	286682	118878	CGCTCCCTCTGGGAATGATG
197509	29705	TTTGGAGATTGCAGATTCTG	242096	74292	ACTTTGTACCATGCCTGGCA	286683	118879	CCGCTCCCTCTGGGAATGAT
197510	29706	CTTTGGAGATTGCAGATTCT	242097	74293	CACTTTGTACCATGCCTGGC	286684	118880	ACCGCTCCCTCTGGGAATGA
197511	29707	GCTTTGGAGATTGCAGATTC	242098	74294	GCACTTTGTACCATGCCTGG	286685	118881	CACCGCTCCCTCTGGGAATG
197512	29708	GGCTTTGGAGATTGCAGATT	242099	74295	AGCACTTTGTACCATGCCTG	286686	118882	GCACCGCTCCCTCTGGGAAT
197513	29709	GGGCTTTGGAGATTGCAGAT	242100	74296	AAGCACTTTGTACCATGCCT	286687	118883	GGCACCGCTCCCTCTGGGAA
197514	29710	TGGGCTTTGGAGATTGCAGA	242101	74297	AAAGCACTTTGTACCATGCC	286688	118884	GGGCACCGCTCCCTCTGGGA
197515	29711	GTGGGCTTTGGAGATTGCAG	242102	74298	TAAAGCACTTTGTACCATGC	286689	118885	AGGGCACCGCTCCCTCTGGG
197516	29712	AGTGGGCTTTGGAGATTGCA	242103	74299	TTAAAGCACTTTGTACCATG	286690	118886	CAGGGCACCGCTCCCTCTGG
197517	29713	AAGTGGGCTTTGGAGATTGC	242104	74300	TTTAAAGCACTTTGTACCAT	286691	118887	CCAGGGCACCGCTCCCTCTG
197518	29714	GAAGTGGGCTTTGGAGATTG	242105	74301	ATTTAAAGCACTTTGTACCA	286692	118888	TCCAGGGCACCGCTCCCTCT
197519	29715	TGAAGTGGGCTTTGGAGATT	242106	74302	TATTTAAAGCACTTTGTACC	286693	118889	CTCCAGGGCACCGCTCCCTC
197520	29716	TTGAAGTGGGCTTTGGAGAT	242107	74303	TTATTTAAAGCACTTTGTAC	286694	118890	CCTCCAGGGCACCGCTCCCT
197521	29717	ATTGAAGTGGGCTTTGGAGA	242108	74304	CTTATTTAAAGCACTTTGTA	286695	118891	GCCTCCAGGGCACCGCTCCC
197522	29718	AATTGAAGTGGGCTTTGGAG	242109	74305	GCTTATTTAAAGCACTTTGT	286696	118892	GGCCTCCAGGGCACCGCTCC
197523	29719	CAATTGAAGTGGGCTTTGGA	242110	74306	TGCTTATTTAAAGCACTTTG	286697	118893	TGGCCTCCAGGGCACCGCTC
197524	29720	ACAATTGAAGTGGGCTTTGG	242111	74307	ATGCTTATTTAAAGCACTTT	286698	118894	GTGGCCTCCAGGGCACCGCT
197525	29721	TACAATTGAAGTGGGCTTTG	242112	74308	AATGCTTATTTAAAGCACTT	286699	118895	TGTGGCCTCCAGGGCACCGC
197526	29722	TTACAATTGAAGTGGGCTTT	242113	74309	GAATGCTTATTTAAAGCACT	286700	118896	CTGTGGCCTCCAGGGCACCG
197527	29723	TTTACAATTGAAGTGGGCTT	242114	74310	TGAATGCTTATTTAAAGCAC	286701	118897	CCTGTGGCCTCCAGGGCACC
197528	29724	ATTTACAATTGAAGTGGGCT	242115	74311	TTGAATGCTTATTTAAAGCA	286702	118898	GCCTGTGGCCTCCAGGGCAC
197529	29725	CATTTACAATTGAAGTGGGC	242116	74312	GTTGAATGCTTATTTAAAGC	286703	118899	GGCCTGTGGCCTCCAGGGCA
197530	29726	ACATTTACAATTGAAGTGGG	242117	74313	TGTTGAATGCTTATTTAAAG	286704	118900	AGGCCTGTGGCCTCCAGGGC
197531	29727	TACATTTACAATTGAAGTGG	242118	74314	TTGTTGAATGCTTATTTAAA	286705	118901	GAGGCCTGTGGCCTCCAGGG
197532	29728	CTACATTTACAATTGAAGTG	242119	74315	ATTGTTGAATGCTTATTTAA	286706	118902	GGAGGCCTGTGGCCTCCAGG
197533	29729	TCTACATTTACAATTGAAGT	242120	74316	AATTGTTGAATGCTTATTTA	286707	118903	AGGAGGCCTGTGGCCTCCAG
197534	29730	CTCTACATTTACAATTGAAG	242121	74317	AAATTGTTGAATGCTTATTT	286708	118904	GAGGAGGCCTGTGGCCTCCA
197535	29731	GCTCTACATTTACAATTGAA	242122	74318	GAAATTGTTGAATGCTTATT	286709	118905	TGAGGAGGCCTGTGGCCTCC
197536	29732	GGCTCTACATTTACAATTGA	242123	74319	TGAAATTGTTGAATGCTTAT	286710	118906	ATGAGGAGGCCTGTGGCCTC
197537	29733	TGGCTCTACATTTACAATTG	242124	74320	ATGAAATTGTTGAATGCTTA	286711	118907	CATGAGGAGGCCTGTGGCCT
197538	29734	GTGGCTCTACATTTACAATT	242125	74321	CATGAAATTGTTGAATGCTT	286712	118908	ACATGAGGAGGCCTGTGGCC

197539	29735	CGTGGCTCTACATTTACAAT	242126	74322	GCATGAAATTGTTGAATGCT	286713	118909	CACATGAGGAGGCCTGTGGC
197540	29736	ACGTGGCTCTACATTTACAA	242127	74323	AGCATGAAATTGTTGAATGC	286714	118910	ACACATGAGGAGGCCTGTGG
197541	29737	CACGTGGCTCTACATTTACA	242128	74324	CAGCATGAAATTGTTGAATG	286715	118911	CACACATGAGGAGGCCTGTG
197542	29738	GCACGTGGCTCTACATTTAC	242129	74325	TCAGCATGAAATTGTTGAAT	286716	118912	ACACACATGAGGAGGCCTGT
197543	29739	CGCACGTGGCTCTACATTTA	242130	74326	GTCAGCATGAAATTGTTGAA	286717	118913	GACACACATGAGGAGGCCTG
197544	29740	GCGCACGTGGCTCTACATTT	242131	74327	TGTCAGCATGAAATTGTTGA	286718	118914	AGACACACATGAGGAGGCCT
197545	29741	AGCGCACGTGGCTCTACATT	242132	74328	CTGTCAGCATGAAATTGTTG	286719	118915	CAGACACACATGAGGAGGCC
197546	29742	AAGCGCACGTGGCTCTACAT	242133	74329	TCTGTCAGCATGAAATTGTT	286720	118916	GCAGACACACATGAGGAGGC
197547	29743	AAAGCGCACGTGGCTCTACA	242134	74330	TTCTGTCAGCATGAAATTGT	286721	118917	CGCAGACACACATGAGGAGG
197548	29744	TAAAGCGCACGTGGCTCTAC	242135	74331	CTTCTGTCAGCATGAAATTG	286722	118918	ACGCAGACACACATGAGGAG
197549	29745	TTAAAGCGCACGTGGCTCTA	242136	74332	GCTTCTGTCAGCATGAAATT	286723	118919	GACGCAGACACACATGAGGA
197550	29746	CTTAAAGCGCACGTGGCTCT	242137	74333	GGCTTCTGTCAGCATGAAAT	286724	118920	GGACGCAGACACACATGAGG
197551	29747	ACTTAAAGCGCACGTGGCTC	242138	74334	GGGCTTCTGTCAGCATGAAA	286725	118921	CGGACGCAGACACACATGAG
197552	29748	GACTTAAAGCGCACGTGGCT	242139	74335	AGGGCTTCTGTCAGCATGAA	286726	118922	GCGGACGCAGACACACATGA
197553	29749	TGACTTAAAGCGCACGTGGC	242140	74336	CAGGGCTTCTGTCAGCATGA	286727	118923	AGCGGACGCAGACACACATG
197554	29750	GTGACTTAAAGCGCACGTGG	242141	74337	ACAGGGCTTCTGTCAGCATG	286728	118924	GAGCGGACGCAGACACACAT
197555	29751	GGTGACTTAAAGCGCACGTG	242142	74338	CACAGGGCTTCTGTCAGCAT	286729	118925	CGAGCGGACGCAGACACACA
197556	29752	AGGTGACTTAAAGCGCACGT	242143	74339	TCACAGGGCTTCTGTCAGCA	286730	118926	TCGAGCGGACGCAGACACAC
197557	29753	CAGGTGACTTAAAGCGCACG	242144	74340	CTCACAGGGCTTCTGTCAGC	286731	118927	CTCGAGCGGACGCAGACACA
197558	29754	ACAGGTGACTTAAAGCGCAC	242145	74341	GCTCACAGGGCTTCTGTCAG	286732	118928	GCTCGAGCGGACGCAGACAC
197559	29755	GACAGGTGACTTAAAGCGCA	242146	74342	GGCTCACAGGGCTTCTGTCA	286733	118929	AGCTCGAGCGGACGCAGACA
197560	29756	TGACAGGTGACTTAAAGCGC	242147	74343	TGGCTCACAGGGCTTCTGTC	286734	118930	AAGCTCGAGCGGACGCAGAC
197561	29757	GTGACAGGTGACTTAAAGCG	242148	74344	CTGGCTCACAGGGCTTCTGT	286735	118931	TAAGCTCGAGCGGACGCAGA
197562	29758	AGTGACAGGTGACTTAAAGC	242149	74345	ACTGGCTCACAGGGCTTCTG	286736	118932	GTAAGCTCGAGCGGACGCAG
197563	29759	GAGTGACAGGTGACTTAAAG	242150	74346	CACTGGCTCACAGGGCTTCT	286737	118933	AGTAAGCTCGAGCGGACGCA
197564	29760	AGAGTGACAGGTGACTTAAA	242151	74347	CCACTGGCTCACAGGGCTTC	286738	118934	CAGTAAGCTCGAGCGGACGC
197565	29761	CAGAGTGACAGGTGACTTAA	242152	74348	TCCACTGGCTCACAGGGCTT	286739	118935	TCAGTAAGCTCGAGCGGACG
197566	29762	CCAGAGTGACAGGTGACTTA	242153	74349	CTCCACTGGCTCACAGGGCT	286740	118936	CTCAGTAAGCTCGAGCGGAC
197567	29763	TCCAGAGTGACAGGTGACTT	242154	74350	GCTCCACTGGCTCACAGGGC	286741	118937	TCTCAGTAAGCTCGAGCGGA
197568	29764	CTCCAGAGTGACAGGTGACT	242155	74351	AGCTCCACTGGCTCACAGGG	286742	118938	GTCTCAGTAAGCTCGAGCGG
197569	29765	CCTCCAGAGTGACAGGTGAC	242156	74352	TAGCTCCACTGGCTCACAGG	286743	118939	TGTCTCAGTAAGCTCGAGCG
197570	29766	GCCTCCAGAGTGACAGGTGA	242157	74353	GTAGCTCCACTGGCTCACAG	286744	118940	GTGTCTCAGTAAGCTCGAGC
197571	29767	AGCCTCCAGAGTGACAGGTG	242158	74354	AGTAGCTCCACTGGCTCACA	286745	118941	AGTGTCTCAGTAAGCTCGAG
197572	29768	GAGCCTCCAGAGTGACAGGT	242159	74355	TAGTAGCTCCACTGGCTCAC	286746	118942	TAGTGTCTCAGTAAGCTCGA
197573	29769	AGAGCCTCCAGAGTGACAGG	242160	74356	GTAGTAGCTCCACTGGCTCA	286747	118943	TTAGTGTCTCAGTAAGCTCG
197574	29770	AAGAGCCTCCAGAGTGACAG	242161	74357	AGTAGTAGCTCCACTGGCTC	286748	118944	TTTAGTGTCTCAGTAAGCTC
197575	29771	AAAGAGCCTCCAGAGTGACA	242162	74358	TAGTAGTAGCTCCACTGGCT	286749	118945	ATTTAGTGTCTCAGTAAGCT
197576	29772	AAAAGAGCCTCCAGAGTGAC	242163	74359	ATAGTAGTAGCTCCACTGGC	286750	118946	GATTTAGTGTCTCAGTAAGC
197577	29773	CAAAAGAGCCTCCAGAGTGA	242164	74360	CATAGTAGTAGCTCCACTGG	286751	118947	AGATTTAGTGTCTCAGTAAG
197578	29774	GCAAAAGAGCCTCCAGAGTG	242165	74361	GCATAGTAGTAGCTCCACTG	286752	118948	CAGATTTAGTGTCTCAGTAA
197579	29775	AGCAAAAGAGCCTCCAGAGT	242166	74362	GGCATAGTAGTAGCTCCACT	286753	118949	ACAGATTTAGTGTCTCAGTA
197580	29776	GAGCAAAAGAGCCTCCAGAG	242167	74363	GGGCATAGTAGTAGCTCCAC	286754	118950	AACAGATTTAGTGTCTCAGT
197581	29777	TGAGCAAAAGAGCCTCCAGA	242168	74364	TGGGCATAGTAGTAGCTCCA	286755	118951	CAACAGATTTAGTGTCTCAG
197582	29778	CTGAGCAAAAGAGCCTCCAG	242169	74365	ATGGGCATAGTAGTAGCTCC	286756	118952	CCAACAGATTTAGTGTCTCA
197583	29779	ACTGAGCAAAAGAGCCTCCA	242170	74366	AATGGGCATAGTAGTAGCTC	286757	118953	ACCAACAGATTTAGTGTCTC
197584	29780	AACTGAGCAAAAGAGCCTCC	242171	74367	TAATGGGCATAGTAGTAGCT	286758	118954	AACCAACAGATTTAGTGTCT
197585	29781	GAACTGAGCAAAAGAGCCTC	242172	74368	ATAATGGGCATAGTAGTAGC	286759	118955	AAACCAACAGATTTAGTGTC
197586	29782	GGAACTGAGCAAAAGAGCCT	242173	74369	TATAATGGGCATAGTAGTAG	286760	118956	GAAACCAACAGATTTAGTGT
197587	29783	AGGAACTGAGCAAAAGAGCC	242174	74370	GTATAATGGGCATAGTAGTA	286761	118957	AGAAACCAACAGATTTAGTG
197588	29784	GAGGAACTGAGCAAAAGAGC	242175	74371	TGTATAATGGGCATAGTAGT	286762	118958	CAGAAACCAACAGATTTAGT
197589	29785	TGAGGAACTGAGCAAAAGAG	242176	74372	CTGTATAATGGGCATAGTAG	286763	118959	GCAGAAACCAACAGATTTAG
197590	29786	GTGAGGAACTGAGCAAAAGA	242177	74373	CCTGTATAATGGGCATAGTA	286764	118960	AGCAGAAACCAACAGATTTA
197591	29787	GGTGAGGAACTGAGCAAAAG	242178	74374	CCCTGTATAATGGGCATAGT	286765	118961	CAGCAGAAACCAACAGATTT
197592	29788	TGGTGAGGAACTGAGCAAAA	242179	74375	CCCCTGTATAATGGGCATAG	286766	118962	ACAGCAGAAACCAACAGATT
197593	29789	ATGGTGAGGAACTGAGCAAA	242180	74376	TCCCCTGTATAATGGGCATA	286767	118963	CACAGCAGAAACCAACAGAT
197594	29790	AATGGTGAGGAACTGAGCAA	242181	74377	CTCCCCTGTATAATGGGCAT	286768	118964	GCACAGCAGAAACCAACAGA
197595	29791	TAATGGTGAGGAACTGAGCA	242182	74378	TCTCCCCTGTATAATGGGCA	286769	118965	GGCACAGCAGAAACCAACAG
197596	29792	CTAATGGTGAGGAACTGAGC	242183	74379	TTCTCCCCTGTATAATGGGC	286770	118966	TGGCACAGCAGAAACCAACA
197597	29793	GCTAATGGTGAGGAACTGAG	242184	74380	TTTCTCCCCTGTATAATGGG	286771	118967	GTGGCACAGCAGAAACCAAC
197598	29794	TGCTAATGGTGAGGAACTGA	242185	74381	TTTTCTCCCCTGTATAATGG	286772	118968	GGTGGCACAGCAGAAACCAA
197599	29795	CTGCTAATGGTGAGGAACTG	242186	74382	GTTTTCTCCCCTGTATAATG	286773	118969	AGGTGGCACAGCAGAAACCA
197600	29796	CCTGCTAATGGTGAGGAACT	242187	74383	AGTTTTCTCCCCTGTATAAT	286774	118970	TAGGTGGCACAGCAGAAACC
197601	29797	CCCTGCTAATGGTGAGGAAC	242188	74384	CAGTTTTCTCCCCTGTATAA	286775	118971	GTAGGTGGCACAGCAGAAAC
197602	29798	TCCCTGCTAATGGTGAGGAA	242189	74385	TCAGTTTTCTCCCCTGTATA	286776	118972	GGTAGGTGGCACAGCAGAAA
197603	29799	ATCCCTGCTAATGGTGAGGA	242190	74386	CTCAGTTTTCTCCCCTGTAT	286777	118973	GGGTAGGTGGCACAGCAGAA
197604	29800	CATCCCTGCTAATGGTGAGG	242191	74387	CCTCAGTTTTCTCCCCTGTA	286778	118974	TGGGTAGGTGGCACAGCAGA
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197606	29802	GTCATCCCTGCTAATGGTGA	242193	74389	TGCCTCAGTTTTCTCCCCTG	286780	118976	GGTGGGTAGGTGGCACAGCA
197607	29803	TGTCATCCCTGCTAATGGTG	242194	74390	CTGCCTCAGTTTTCTCCCCT	286781	118977	GGGTGGGTAGGTGGCACAGC
197608	29804	CTGTCATCCCTGCTAATGGT	242195	74391	TCTGCCTCAGTTTTCTCCCC	286782	118978	AGGGTGGGTAGGTGGCACAG
197609	29805	CCTGTCATCCCTGCTAATGG	242196	74392	CTCTGCCTCAGTTTTCTCCC	286783	118979	CAGGGTGGGTAGGTGGCACA
197610	29806	CCCTGTCATCCCTGCTAATG	242197	74393	TCTCTGCCTCAGTTTTCTCC	286784	118980	ACAGGGTGGGTAGGTGGCAC

197611	29807	TCCCTGTCATCCCTGCTAAT	242198	74394	CTCTCTGCCTCAGTTTTCTC	286785	118981	AACAGGGTGGGTAGGTGGCA
197612	29808	CTCCCTGTCATCCCTGCTAA	242199	74395	TCTCTCTGCCTCAGTTTTCT	286786	118982	CAACAGGGTGGGTAGGTGGC
197613	29809	ACTCCCTGTCATCCCTGCTA	242200	74396	CTCTCTCTGCCTCAGTTTTC	286787	118983	CCAACAGGGTGGGTAGGTGG
197614	29810	CACTCCCTGTCATCCCTGCT	242201	74397	CCTCTCTCTGCCTCAGTTTT	286788	118984	ACCAACAGGGTGGGTAGGTG
197615	29811	GCACTCCCTGTCATCCCTGC	242202	74398	ACCTCTCTCTGCCTCAGTTT	286789	118985	CACCAACAGGGTGGGTAGGT
197616	29812	TGCACTCCCTGTCATCCCTG	242203	74399	AACCTCTCTCTGCCTCAGTT	286790	118986	ACACCAACAGGGTGGGTAGG
197617	29813	CTGCACTCCCTGTCATCCCT	242204	74400	TAACCTCTCTCTGCCTCAGT	286791	118987	AACACCAACAGGGTGGGTAG
197618	29814	CCTGCACTCCCTGTCATCCC	242205	74401	CTAACCTCTCTCTGCCTCAG	286792	118988	CAACACCAACAGGGTGGGTA
197619	29815	TCCTGCACTCCCTGTCATCC	242206	74402	CCTAACCTCTCTCTGCCTCA	286793	118989	GCAACACCAACAGGGTGGGT
197620	29816	CTCCTGCACTCCCTGTCATC	242207	74403	ACCTAACCTCTCTCTGCCTC	286794	118990	AGCAACACCAACAGGGTGGG
197621	29817	ACTCCTGCACTCCCTGTCAT	242208	74404	TACCTAACCTCTCTCTGCCT	286795	118991	AAGCAACACCAACAGGGTGG
197622	29818	CACTCCTGCACTCCCTGTCA	242209	74405	TTACCTAACCTCTCTCTGCC	286796	118992	AAAGCAACACCAACAGGGTG
197623	29819	GCACTCCTGCACTCCCTGTC	242210	74406	ATTACCTAACCTCTCTCTGC	286797	118993	CAAAGCAACACCAACAGGGT
197624	29820	CGCACTCCTGCACTCCCTGT	242211	74407	AATTACCTAACCTCTCTCTG	286798	118994	ACAAAGCAACACCAACAGGG
197625	29821	CCGCACTCCTGCACTCCCTG	242212	74408	GAATTACCTAACCTCTCTCT	286799	118995	AACAAAGCAACACCAACAGG
197626	29822	ACCGCACTCCTGCACTCCCT	242213	74409	CGAATTACCTAACCTCTCTC	286800	118996	GAACAAAGCAACACCAACAG
197627	29823	GACCGCACTCCTGCACTCCC	242214	74410	GCGAATTACCTAACCTCTCT	286801	118997	GGAACAAAGCAACACCAACA
197628	29824	CGACCGCACTCCTGCACTCC	242215	74411	AGCGAATTACCTAACCTCTC	286802	118998	AGGAACAAAGCAACACCAAC
197629	29825	TCGACCGCACTCCTGCACTC	242216	74412	GAGCGAATTACCTAACCTCT	286803	118999	TAGGAACAAAGCAACACCAA
197630	29826	GTCGACCGCACTCCTGCACT	242217	74413	TGAGCGAATTACCTAACCTC	286804	119000	ATAGGAACAAAGCAACACCA
197631	29827	AGTCGACCGCACTCCTGCAC	242218	74414	CTGAGCGAATTACCTAACCT	286805	119001	AATAGGAACAAAGCAACACC
197632	29828	GAGTCGACCGCACTCCTGCA	242219	74415	GCTGAGCGAATTACCTAACC	286806	119002	CAATAGGAACAAAGCAACAC
197633	29829	GGAGTCGACCGCACTCCTGC	242220	74416	GGCTGAGCGAATTACCTAAC	286807	119003	GCAATAGGAACAAAGCAACA
197634	29830	GGGAGTCGACCGCACTCCTG	242221	74417	AGGCTGAGCGAATTACCTAA	286808	119004	AGCAATAGGAACAAAGCAAC
197635	29831	TGGGAGTCGACCGCACTCCT	242222	74418	GAGGCTGAGCGAATTACCTA	286809	119005	TAGCAATAGGAACAAAGCAA
197636	29832	CTGGGAGTCGACCGCACTCC	242223	74419	TGAGGCTGAGCGAATTACCT	286810	119006	TTAGCAATAGGAACAAAGCA
197637	29833	TCTGGGAGTCGACCGCACTC	242224	74420	GTGAGGCTGAGCGAATTACC	286811	119007	TTTAGCAATAGGAACAAAGC
197638	29834	ATCTGGGAGTCGACCGCACT	242225	74421	TGTGAGGCTGAGCGAATTAC	286812	119008	CTTTAGCAATAGGAACAAAG
197639	29835	TATCTGGGAGTCGACCGCAC	242226	74422	GTGTGAGGCTGAGCGAATTA	286813	119009	TCTTTAGCAATAGGAACAAA
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197641	29837	AATATCTGGGAGTCGACCGC	242228	74424	TTGTGTGAGGCTGAGCGAAT	286815	119011	TGTCTTTAGCAATAGGAACA
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197643	29839	CCAATATCTGGGAGTCGACC	242230	74426	GGTTGTGTGAGGCTGAGCGA	286817	119013	CCTGTCTTTAGCAATAGGAA
197644	29840	TCCAATATCTGGGAGTCGAC	242231	74427	TGGTTGTGTGAGGCTGAGCG	286818	119014	TCCTGTCTTTAGCAATAGGA
197645	29841	CTCCAATATCTGGGAGTCGA	242232	74428	TTGGTTGTGTGAGGCTGAGC	286819	119015	TTCCTGTCTTTAGCAATAGG
197646	29842	TCTCCAATATCTGGGAGTCG	242233	74429	ATTGGTTGTGTGAGGCTGAG	286820	119016	ATTCCTGTCTTTAGCAATAG
197647	29843	CTCTCCAATATCTGGGAGTC	242234	74430	TATTGGTTGTGTGAGGCTGA	286821	119017	CATTCCTGTCTTTAGCAATA
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197652	29848	CAGCGCTCTCCAATATCTGG	242239	74435	CCACCTATTGGTTGTGTGAG	286826	119022	CTGGACATTCCTGTCTTTAG
197653	29849	CCAGCGCTCTCCAATATCTG	242240	74436	ACCACCTATTGGTTGTGTGA	286827	119023	CCTGGACATTCCTGTCTTTA
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197659	29855	GCTAGCCCAGCGCTCTCCAA	242246	74442	GGCTCCACCACCTATTGGTT	286833	119029	CAGTGTCCTGGACATTCCTG
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197661	29857	CAGCTAGCCCAGCGCTCTCC	242248	74444	CTGGCTCCACCACCTATTGG	286835	119031	CTCAGTGTCCTGGACATTCC
197662	29858	GCAGCTAGCCCAGCGCTCTC	242249	74445	CCTGGCTCCACCACCTATTG	286836	119032	ACTCAGTGTCCTGGACATTC
197663	29859	GGCAGCTAGCCCAGCGCTCT	242250	74446	TCCTGGCTCCACCACCTATT	286837	119033	CACTCAGTGTCCTGGACATT
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197667	29863	AATGGGCAGCTAGCCCAGCG	242254	74450	CAAATCCTGGCTCCACCACC	286841	119037	TGCACACTCAGTGTCCTGGA
197668	29864	GAATGGGCAGCTAGCCCAGC	242255	74451	CCAAATCCTGGCTCCACCAC	286842	119038	CTGCACACTCAGTGTCCTGG
197669	29865	AGAATGGGCAGCTAGCCCAG	242256	74452	CCCAAATCCTGGCTCCACCA	286843	119039	CCTGCACACTCAGTGTCCTG
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197677	29873	AGGCCGGGAGAATGGGCAGC	242264	74460	AGATGGGGCCCAAATCCTGG	286851	119047	AGCAGGCACCTGCACACTCA
197678	29874	GAGGCCGGGAGAATGGGCAG	242265	74461	CAGATGGGGCCCAAATCCTG	286852	119048	CAGCAGGCACCTGCACACTC
197679	29875	GGAGGCCGGGAGAATGGGCA	242266	74462	GCAGATGGGGCCCAAATCCT	286853	119049	CCAGCAGGCACCTGCACACT
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197681	29877	GTGGAGGCCGGGAGAATGGG	242268	74464	AGGCAGATGGGGCCCAAATC	286855	119051	AACCAGCAGGCACCTGCACA
197682	29878	AGTGGAGGCCGGGAGAATGG	242269	74465	CAGGCAGATGGGGCCCAAAT	286856	119052	GAACCAGCAGGCACCTGCAC

197683	29879	GAGTGGAGGCCGGGAGAATG	242270	74466	TCAGGCAGATGGGGCCCAAA	286857	119053	AGAACCAGCAGGCACCTGCA
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197689	29885	AAAGAGGAGTGGAGGCCGGG	242276	74472	AGAGAGTCAGGCAGATGGGG	286863	119059	GACGTGAGAACCAGCAGGCA
197690	29886	CAAAGAGGAGTGGAGGCCGG	242277	74473	TAGAGAGTCAGGCAGATGGG	286864	119060	GGACGTGAGAACCAGCAGGC
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197692	29888	AGCAAAGAGGAGTGGAGGCC	242279	74475	TCTAGAGAGTCAGGCAGATG	286866	119062	TCGGACGTGAGAACCAGCAG
197693	29889	CAGCAAAGAGGAGTGGAGGC	242280	74476	CTCTAGAGAGTCAGGCAGAT	286867	119063	CTCGGACGTGAGAACCAGCA
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197698	29894	CTGGACAGCAAAGAGGAGTG	242285	74481	AGAGCCTCTAGAGAGTCAGG	286872	119068	AGCAGCTCGGACGTGAGAAC
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197702	29898	ATGGCTGGACAGCAAAGAGG	242289	74485	AGATAGAGCCTCTAGAGAGT	286876	119072	GTTCAGCAGCTCGGACGTGA
197703	29899	GATGGCTGGACAGCAAAGAG	242290	74486	AAGATAGAGCCTCTAGAGAG	286877	119073	AGTTCAGCAGCTCGGACGTG
197704	29900	TGATGGCTGGACAGCAAAGA	242291	74487	GAAGATAGAGCCTCTAGAGA	286878	119074	GAGTTCAGCAGCTCGGACGT
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197706	29902	AGTGATGGCTGGACAGCAAA	242293	74489	TGGAAGATAGAGCCTCTAGA	286880	119076	CGGAGTTCAGCAGCTCGGAC
197707	29903	AAGTGATGGCTGGACAGCAA	242294	74490	CTGGAAGATAGAGCCTCTAG	286881	119077	GCGGAGTTCAGCAGCTCGGA
197708	29904	CAAGTGATGGCTGGACAGCA	242295	74491	ACTGGAAGATAGAGCCTCTA	286882	119078	AGCGGAGTTCAGCAGCTCGG
197709	29905	GCAAGTGATGGCTGGACAGC	242296	74492	GACTGGAAGATAGAGCCTCT	286883	119079	CAGCGGAGTTCAGCAGCTCG
197710	29906	AGCAAGTGATGGCTGGACAG	242297	74493	AGACTGGAAGATAGAGCCTC	286884	119080	CCAGCGGAGTTCAGCAGCTC
197711	29907	GAGCAAGTGATGGCTGGACA	242298	74494	AAGACTGGAAGATAGAGCCT	286885	119081	CCCAGCGGAGTTCAGCAGCT
197712	29908	AGAGCAAGTGATGGCTGGAC	242299	74495	GAAGACTGGAAGATAGAGCC	286886	119082	ACCCAGCGGAGTTCAGCAGC
197713	29909	AAGAGCAAGTGATGGCTGGA	242300	74496	GGAAGACTGGAAGATAGAGC	286887	119083	GACCCAGCGGAGTTCAGCAG
197714	29910	AAAGAGCAAGTGATGGCTGG	242301	74497	TGGAAGACTGGAAGATAGAG	286888	119084	GGACCCAGCGGAGTTCAGCA
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197716	29912	TCAAAGAGCAAGTGATGGCT	242303	74499	TCTGGAAGACTGGAAGATAG	286890	119086	CAGGACCCAGCGGAGTTCAG
197717	29913	TTCAAAGAGCAAGTGATGGC	242304	74500	CTCTGGAAGACTGGAAGATA	286891	119087	GCAGGACCCAGCGGAGTTCA
197718	29914	CTTCAAAGAGCAAGTGATGG	242305	74501	ACTCTGGAAGACTGGAAGAT	286892	119088	AGCAGGACCCAGCGGAGTTC
197719	29915	CCTTCAAAGAGCAAGTGATG	242306	74502	AACTCTGGAAGACTGGAAGA	286893	119089	AAGCAGGACCCAGCGGAGTT
197720	29916	GCCTTCAAAGAGCAAGTGAT	242307	74503	CAACTCTGGAAGACTGGAAG	286894	119090	TAAGCAGGACCCAGCGGAGT
197721	29917	TGCCTTCAAAGAGCAAGTGA	242308	74504	TCAACTCTGGAAGACTGGAA	286895	119091	GTAAGCAGGACCCAGCGGAG
197722	29918	TTGCCTTCAAAGAGCAAGTG	242309	74505	CTCAACTCTGGAAGACTGGA	286896	119092	AGTAAGCAGGACCCAGCGGA
197723	29919	TTTGCCTTCAAAGAGCAAGT	242310	74506	ACTCAACTCTGGAAGACTGG	286897	119093	CAGTAAGCAGGACCCAGCGG
197724	29920	GTTTGCCTTCAAAGAGCAAG	242311	74507	GACTCAACTCTGGAAGACTG	286898	119094	TCAGTAAGCAGGACCCAGCG
197725	29921	TGTTTGCCTTCAAAGAGCAA	242312	74508	AGACTCAACTCTGGAAGACT	286899	119095	ATCAGTAAGCAGGACCCAGC
197726	29922	TTGTTTGCCTTCAAAGAGCA	242313	74509	TAGACTCAACTCTGGAAGAC	286900	119096	CATCAGTAAGCAGGACCCAG
197727	29923	TTTGTTTGCCTTCAAAGAGC	242314	74510	TTAGACTCAACTCTGGAAGA	286901	119097	CCATCAGTAAGCAGGACCCA
197728	29924	TTTTGTTTGCCTTCAAAGAG	242315	74511	CTTAGACTCAACTCTGGAAG	286902	119098	ACCATCAGTAAGCAGGACCC
197729	29925	GTTTTGTTTGCCTTCAAAGA	242316	74512	GCTTAGACTCAACTCTGGAA	286903	119099	GACCATCAGTAAGCAGGACC
197730	29926	TGTTTTGTTTGCCTTCAAAG	242317	74513	GGCTTAGACTCAACTCTGGA	286904	119100	AGACCATCAGTAAGCAGGAC
197731	29927	CTGTTTTGTTTGCCTTCAAA	242318	74514	TGGCTTAGACTCAACTCTGG	286905	119101	AAGACCATCAGTAAGCAGGA
197732	29928	TCTGTTTTGTTTGCCTTCAA	242319	74515	ATGGCTTAGACTCAACTCTG	286906	119102	AAAGACCATCAGTAAGCAGG
197733	29929	TTCTGTTTTGTTTGCCTTCA	242320	74516	CATGGCTTAGACTCAACTCT	286907	119103	CAAAGACCATCAGTAAGCAG
197734	29930	TTTCTGTTTTGTTTGCCTTC	242321	74517	TCATGGCTTAGACTCAACTC	286908	119104	GCAAAGACCATCAGTAAGCA
197735	29931	TTTTCTGTTTTGTTTGCCTT	242322	74518	TTCATGGCTTAGACTCAACT	286909	119105	AGCAAAGACCATCAGTAAGC
197736	29932	GTTTTCTGTTTTGTTTGCCT	242323	74519	ATTCATGGCTTAGACTCAAC	286910	119106	GAGCAAAGACCATCAGTAAG
197737	29933	TGTTTTCTGTTTTGTTTGCC	242324	74520	TATTCATGGCTTAGACTCAA	286911	119107	AGAGCAAAGACCATCAGTAA
197738	29934	CTGTTTTCTGTTTTGTTTGC	242325	74521	CTATTCATGGCTTAGACTCA	286912	119108	TAGAGCAAAGACCATCAGTA
197739	29935	ACTGTTTTCTGTTTTGTTTG	242326	74522	CCTATTCATGGCTTAGACTC	286913	119109	CTAGAGCAAAGACCATCAGT
197740	29936	CACTGTTTTCTGTTTTGTTT	242327	74523	TCCTATTCATGGCTTAGACT	286914	119110	ACTAGAGCAAAGACCATCAG
197741	29937	GCACTGTTTTCTGTTTTGTT	242328	74524	GTCCTATTCATGGCTTAGAC	286915	119111	CACTAGAGCAAAGACCATCA
197742	29938	GGCACTGTTTTCTGTTTTGT	242329	74525	TGTCCTATTCATGGCTTAGA	286916	119112	GCACTAGAGCAAAGACCATC
197743	29939	TGGCACTGTTTTCTGTTTTG	242330	74526	TTGTCCTATTCATGGCTTAG	286917	119113	AGCACTAGAGCAAAGACCAT
197744	29940	TTGGCACTGTTTTCTGTTTT	242331	74527	ATTGTCCTATTCATGGCTTA	286918	119114	AAGCACTAGAGCAAAGACCA
197745	29941	TTTGGCACTGTTTTCTGTTT	242332	74528	AATTGTCCTATTCATGGCTT	286919	119115	AAAGCACTAGAGCAAAGACC
197746	29942	TTTTGGCACTGTTTTCTGTT	242333	74529	TAATTGTCCTATTCATGGCT	286920	119116	GAAAGCACTAGAGCAAAGAC
197747	29943	CTTTTGGCACTGTTTTCTGT	242334	74530	CTAATTGTCCTATTCATGGC	286921	119117	GGAAAGCACTAGAGCAAAGA
197748	29944	ACTTTTGGCACTGTTTTCTG	242335	74531	TCTAATTGTCCTATTCATGG	286922	119118	TGGAAAGCACTAGAGCAAAG
197749	29945	TACTTTTGGCACTGTTTTCT	242336	74532	GTCTAATTGTCCTATTCATG	286923	119119	CTGGAAAGCACTAGAGCAAA
197750	29946	ATACTTTTGGCACTGTTTTC	242337	74533	TGTCTAATTGTCCTATTCAT	286924	119120	CCTGGAAAGCACTAGAGCAA
197751	29947	CATACTTTTGGCACTGTTTT	242338	74534	CTGTCTAATTGTCCTATTCA	286925	119121	CCCTGGAAAGCACTAGAGCA
197752	29948	CCATACTTTTGGCACTGTTT	242339	74535	GCTGTCTAATTGTCCTATTC	286926	119122	ACCCTGGAAAGCACTAGAGC
197753	29949	CCCATACTTTTGGCACTGTT	242340	74536	TGCTGTCTAATTGTCCTATT	286927	119123	GACCCTGGAAAGCACTAGAG
197754	29950	TCCCATACTTTTGGCACTGT	242341	74537	CTGCTGTCTAATTGTCCTAT	286928	119124	GGACCCTGGAAAGCACTAGA

197755	29951	TTCCCATACTTTTGGCACTG	242342	74538	TCTGCTGTCTAATTGTCCTA	286929	119125	CGGACCCTGGAAAGCACTAG
197756	29952	CTTCCCATACTTTTGGCACT	242343	74539	CTCTGCTGTCTAATTGTCCT	286930	119126	ACGGACCCTGGAAAGCACTA
197757	29953	TCTTCCCATACTTTTGGCAC	242344	74540	CCTCTGCTGTCTAATTGTCC	286931	119127	CACGGACCCTGGAAAGCACT
197758	29954	TTCTTCCCATACTTTTGGCA	242345	74541	TCCTCTGCTGTCTAATTGTC	286932	119128	CCACGGACCCTGGAAAGCAC
197759	29955	TTTCTTCCCATACTTTTGGC	242346	74542	TTCCTCTGCTGTCTAATTGT	286933	119129	TCCACGGACCCTGGAAAGCA
197760	29956	CTTTCTTCCCATACTTTTGG	242347	74543	TTTCCTCTGCTGTCTAATTG	286934	119130	TTCCACGGACCCTGGAAAGC
197761	29957	GCTTTCTTCCCATACTTTTG	242348	74544	GTTTCCTCTGCTGTCTAATT	286935	119131	CTTCCACGGACCCTGGAAAG
197762	29958	GGCTTTCTTCCCATACTTTT	242349	74545	GGTTTCCTCTGCTGTCTAAT	286936	119132	GCTTCCACGGACCCTGGAAA
197763	29959	TGGCTTTCTTCCCATACTTT	242350	74546	GGGTTTCCTCTGCTGTCTAA	286937	119133	AGCTTCCACGGACCCTGGAA
197764	29960	CTGGCTTTCTTCCCATACTT	242351	74547	TGGGTTTCCTCTGCTGTCTA	286938	119134	AAGCTTCCACGGACCCTGGA
197765	29961	GCTGGCTTTCTTCCCATACT	242352	74548	ATGGGTTTCCTCTGCTGTCT	286939	119135	AAAGCTTCCACGGACCCTGG
197766	29962	AGCTGGCTTTCTTCCCATAC	242353	74549	AATGGGTTTCCTCTGCTGTC	286940	119136	AAAAGCTTCCACGGACCCTG
197767	29963	AAGCTGGCTTTCTTCCCATA	242354	74550	GAATGGGTTTCCTCTGCTGT	286941	119137	GAAAAGCTTCCACGGACCCT
197768	29964	GAAGCTGGCTTTCTTCCCAT	242355	74551	TGAATGGGTTTCCTCTGCTG	286942	119138	GGAAAAGCTTCCACGGACCC
197769	29965	AGAAGCTGGCTTTCTTCCCA	242356	74552	CTGAATGGGTTTCCTCTGCT	286943	119139	AGGAAAAGCTTCCACGGACC
197770	29966	GAGAAGCTGGCTTTCTTCCC	242357	74553	GCTGAATGGGTTTCCTCTGC	286944	119140	CAGGAAAAGCTTCCACGGAC
197771	29967	GGAGAAGCTGGCTTTCTTCC	242358	74554	GGCTGAATGGGTTTCCTCTG	286945	119141	CCAGGAAAAGCTTCCACGGA
197772	29968	GGGAGAAGCTGGCTTTCTTC	242359	74555	TGGCTGAATGGGTTTCCTCT	286946	119142	TCCAGGAAAAGCTTCCACGG
197773	29969	GGGGAGAAGCTGGCTTTCTT	242360	74556	GTGGCTGAATGGGTTTCCTC	286947	119143	TTCCAGGAAAAGCTTCCACG
197774	29970	AGGGGAGAAGCTGGCTTTCT	242361	74557	GGTGGCTGAATGGGTTTCCT	286948	119144	ATTCCAGGAAAAGCTTCCAC
197775	29971	CAGGGGAGAAGCTGGCTTTC	242362	74558	TGGTGGCTGAATGGGTTTCC	286949	119145	TATTCCAGGAAAAGCTTCCA
197776	29972	CCAGGGGAGAAGCTGGCTTT	242363	74559	ATGGTGGCTGAATGGGTTTC	286950	119146	TTATTCCAGGAAAAGCTTCC
197777	29973	CCCAGGGGAGAAGCTGGCTT	242364	74560	CATGGTGGCTGAATGGGTTT	286951	119147	TTTATTCCAGGAAAAGCTTC
197778	29974	CCCCAGGGGAGAAGCTGGCT	242365	74561	ACATGGTGGCTGAATGGGTT	286952	119148	CTTTATTCCAGGAAAAGCTT
197779	29975	ACCCCAGGGGAGAAGCTGGC	242366	74562	CACATGGTGGCTGAATGGGT	286953	119149	GCTTTATTCCAGGAAAAGCT
197780	29976	CACCCCAGGGGAGAAGCTGG	242367	74563	GCACATGGTGGCTGAATGGG	286954	119150	GGCTTTATTCCAGGAAAAGC
197781	29977	GCACCCCAGGGGAGAAGCTG	242368	74564	TGCACATGGTGGCTGAATGG	286955	119151	GGGCTTTATTCCAGGAAAAG
197782	29978	GGCACCCCAGGGGAGAAGCT	242369	74565	ATGCACATGGTGGCTGAATG	286956	119152	TGGGCTTTATTCCAGGAAAA
197783	29979	AGGCACCCCAGGGGAGAAGC	242370	74566	CATGCACATGGTGGCTGAAT	286957	119153	GTGGGCTTTATTCCAGGAAA
197784	29980	CAGGCACCCCAGGGGAGAAG	242371	74567	TCATGCACATGGTGGCTGAA	286958	119154	CGTGGGCTTTATTCCAGGAA
197785	29981	ACAGGCACCCCAGGGGAGAA	242372	74568	TTCATGCACATGGTGGCTGA	286959	119155	GCGTGGGCTTTATTCCAGGA
197786	29982	CACAGGCACCCCAGGGGAGA	242373	74569	CTTCATGCACATGGTGGCTG	286960	119156	TGCGTGGGCTTTATTCCAGG
197787	29983	TCACAGGCACCCCAGGGGAG	242374	74570	TCTTCATGCACATGGTGGCT	286961	119157	ATGCGTGGGCTTTATTCCAG
197788	29984	ATCACAGGCACCCCAGGGGA	242375	74571	CTCTTCATGCACATGGTGGC	286962	119158	GATGCGTGGGCTTTATTCCA
197789	29985	CATCACAGGCACCCCAGGGG	242376	74572	ACTCTTCATGCACATGGTGG	286963	119159	CGATGCGTGGGCTTTATTCC
197790	29986	GCATCACAGGCACCCCAGGG	242377	74573	TACTCTTCATGCACATGGTG	286964	119160	TCGATGCGTGGGCTTTATTC
197791	29987	GGCATCACAGGCACCCCAGG	242378	74574	TTACTCTTCATGCACATGGT	286965	119161	GTCGATGCGTGGGCTTTATT
197792	29988	TGGCATCACAGGCACCCCAG	242379	74575	CTTACTCTTCATGCACATGG	286966	119162	GGTCGATGCGTGGGCTTTAT
197793	29989	ATGGCATCACAGGCACCCCA	242380	74576	CCTTACTCTTCATGCACATG	286967	119163	GGGTCGATGCGTGGGCTTTA
197794	29990	CATGGCATCACAGGCACCCC	242381	74577	TCCTTACTCTTCATGCACAT	286968	119164	AGGGTCGATGCGTGGGCTTT
197795	29991	GCATGGCATCACAGGCACCC	242382	74578	TTCCTTACTCTTCATGCACA	286969	119165	GAGGGTCGATGCGTGGGCTT
197796	29992	GGCATGGCATCACAGGCACC	242383	74579	ATTCCTTACTCTTCATGCAC	286970	119166	TGAGGGTCGATGCGTGGGCT
197797	29993	GGGCATGGCATCACAGGCAC	242384	74580	AATTCCTTACTCTTCATGCA	286971	119167	GTGAGGGTCGATGCGTGGGC
197798	29994	TGGGCATGGCATCACAGGCA	242385	74581	AAATTCCTTACTCTTCATGC	286972	119168	TGTGAGGGTCGATGCGTGGG
197799	29995	GTGGGCATGGCATCACAGGC	242386	74582	GAAATTCCTTACTCTTCATG	286973	119169	CTGTGAGGGTCGATGCGTGG
197800	29996	GGTGGGCATGGCATCACAGG	242387	74583	AGAAATTCCTTACTCTTCAT	286974	119170	GCTGTGAGGGTCGATGCGTG
197801	29997	GGGTGGGCATGGCATCACAG	242388	74584	CAGAAATTCCTTACTCTTCA	286975	119171	CGCTGTGAGGGTCGATGCGT
197802	29998	AGGGTGGGCATGGCATCACA	242389	74585	ACAGAAATTCCTTACTCTTC	286976	119172	GCGCTGTGAGGGTCGATGCG
197803	29999	GAGGGTGGGCATGGCATCAC	242390	74586	GACAGAAATTCCTTACTCTT	286977	119173	GGCGCTGTGAGGGTCGATGC
197804	30000	GGAGGGTGGGCATGGCATCA	242391	74587	TGACAGAAATTCCTTACTCT	286978	119174	AGGCGCTGTGAGGGTCGATG
197805	30001	GGGAGGGTGGGCATGGCATC	242392	74588	ATGACAGAAATTCCTTACTC	286979	119175	GAGGCGCTGTGAGGGTCGAT
197806	30002	AGGGAGGGTGGGCATGGCAT	242393	74589	TATGACAGAAATTCCTTACT	286980	119176	GGAGGCGCTGTGAGGGTCGA
197807	30003	CAGGGAGGGTGGGCATGGCA	242394	74590	GTATGACAGAAATTCCTTAC	286981	119177	GGGAGGCGCTGTGAGGGTCG
197808	30004	TCAGGGAGGGTGGGCATGGC	242395	74591	TGTATGACAGAAATTCCTTA	286982	119178	GGGGAGGCGCTGTGAGGGTC
197809	30005	GTCAGGGAGGGTGGGCATGG	242396	74592	CTGTATGACAGAAATTCCTT	286983	119179	AGGGGAGGCGCTGTGAGGGT
197810	30006	GGTCAGGGAGGGTGGGCATG	242397	74593	TCTGTATGACAGAAATTCCT	286984	119180	GAGGGGAGGCGCTGTGAGGG
197811	30007	TGGTCAGGGAGGGTGGGCAT	242398	74594	CTCTGTATGACAGAAATTCC	286985	119181	AGAGGGGAGGCGCTGTGAGG
197812	30008	GTGGTCAGGGAGGGTGGGCA	242399	74595	CCTCTGTATGACAGAAATTC	286986	119182	AAGAGGGGAGGCGCTGTGAG
197813	30009	CGTGGTCAGGGAGGGTGGGC	242400	74596	CCCTCTGTATGACAGAAATT	286987	119183	AAAGAGGGGAGGCGCTGTGA
197814	30010	GCGTGGTCAGGGAGGGTGGG	242401	74597	CCCCTCTGTATGACAGAAAT	286988	119184	CAAAGAGGGGAGGCGCTGTG
197815	30011	TGCGTGGTCAGGGAGGGTGG	242402	74598	TCCCCTCTGTATGACAGAAA	286989	119185	TCAAAGAGGGGAGGCGCTGT
197816	30012	CTGCGTGGTCAGGGAGGGTG	242403	74599	CTCCCCTCTGTATGACAGAA	286990	119186	CTCAAAGAGGGGAGGCGCTG
197817	30013	GCTGCGTGGTCAGGGAGGGT	242404	74600	ACTCCCCTCTGTATGACAGA	286991	119187	CCTCAAAGAGGGGAGGCGCT
197818	30014	GGCTGCGTGGTCAGGGAGGG	242405	74601	CACTCCCCTCTGTATGACAG	286992	119188	GCCTCAAAGAGGGGAGGCGC
197819	30015	GGGCTGCGTGGTCAGGGAGG	242406	74602	TCACTCCCCTCTGTATGACA	286993	119189	GGCCTCAAAGAGGGGAGGCG
197820	30016	GGGGCTGCGTGGTCAGGGAG	242407	74603	TTCACTCCCCTCTGTATGAC	286994	119190	GGGCCTCAAAGAGGGGAGGC
197821	30017	AGGGGCTGCGTGGTCAGGGA	242408	74604	ATTCACTCCCCTCTGTATGA	286995	119191	TGGGCCTCAAAGAGGGGAGG
197822	30018	CAGGGGCTGCGTGGTCAGGG	242409	74605	AATTCACTCCCCTCTGTATG	286996	119192	CTGGGCCTCAAAGAGGGGAG
197823	30019	ACAGGGGCTGCGTGGTCAGG	242410	74606	GAATTCACTCCCCTCTGTAT	286997	119193	GCTGGGCCTCAAAGAGGGGA
197824	30020	CACAGGGGCTGCGTGGTCAG	242411	74607	TGAATTCACTCCCCTCTGTA	286998	119194	TGCTGGGCCTCAAAGAGGGG
197825	30021	CCACAGGGGCTGCGTGGTCA	242412	74608	GTGAATTCACTCCCCTCTGT	286999	119195	CTGCTGGGCCTCAAAGAGGG
197826	30022	TCCACAGGGGCTGCGTGGTC	242413	74609	AGTGAATTCACTCCCCTCTG	287000	119196	TCTGCTGGGCCTCAAAGAGG

197827	30023	GTCCACAGGGGCTGCGTGGT	242414	74610	CAGTGAATTCACTCCCCTCT	287001	119197	ATCTGCTGGGCCTCAAAGAG
197828	30024	GGTCCACAGGGGCTGCGTGG	242415	74611	TCAGTGAATTCACTCCCCTC	287002	119198	TATCTGCTGGGCCTCAAAGA
197829	30025	GGGTCCACAGGGGCTGCGTG	242416	74612	CTCAGTGAATTCACTCCCCT	287003	119199	GTATCTGCTGGGCCTCAAAG
197830	30026	AGGGTCCACAGGGGCTGCGT	242417	74613	GCTCAGTGAATTCACTCCCC	287004	119200	GGTATCTGCTGGGCCTCAAA
197831	30027	GAGGGTCCACAGGGGCTGCG	242418	74614	AGCTCAGTGAATTCACTCCC	287005	119201	GGGTATCTGCTGGGCCTCAA
197832	30028	TGAGGGTCCACAGGGGCTGC	242419	74615	CAGCTCAGTGAATTCACTCC	287006	119202	GGGGTATCTGCTGGGCCTCA
197833	30029	CTGAGGGTCCACAGGGGCTG	242420	74616	TCAGCTCAGTGAATTCACTC	287007	119203	TGGGGTATCTGCTGGGCCTC
197834	30030	CCTGAGGGTCCACAGGGGCT	242421	74617	CTCAGCTCAGTGAATTCACT	287008	119204	GTGGGGTATCTGCTGGGCCT
197835	30031	CCCTGAGGGTCCACAGGGGC	242422	74618	TCTCAGCTCAGTGAATTCAC	287009	119205	AGTGGGGTATCTGCTGGGCC
197836	30032	GCCCTGAGGGTCCACAGGGG	242423	74619	CTCTCAGCTCAGTGAATTCA	287010	119206	GAGTGGGGTATCTGCTGGGC
197837	30033	GGCCCTGAGGGTCCACAGGG	242424	74620	GCTCTCAGCTCAGTGAATTC	287011	119207	GGAGTGGGGTATCTGCTGGG
197838	30034	GGGCCCTGAGGGTCCACAGG	242425	74621	AGCTCTCAGCTCAGTGAATT	287012	119208	AGGAGTGGGGTATCTGCTGG
197839	30035	GGGGCCCTGAGGGTCCACAG	242426	74622	CAGCTCTCAGCTCAGTGAAT	287013	119209	CAGGAGTGGGGTATCTGCTG
197840	30036	TGGGGCCCTGAGGGTCCACA	242427	74623	TCAGCTCTCAGCTCAGTGAA	287014	119210	GCAGGAGTGGGGTATCTGCT
197841	30037	TTGGGGCCCTGAGGGTCCAC	242428	74624	CTCAGCTCTCAGCTCAGTGA	287015	119211	GGCAGGAGTGGGGTATCTGC
197842	30038	CTTGGGGCCCTGAGGGTCCA	242429	74625	CCTCAGCTCTCAGCTCAGTG	287016	119212	AGGCAGGAGTGGGGTATCTG
197843	30039	GCTTGGGGCCCTGAGGGTCC	242430	74626	TCCTCAGCTCTCAGCTCAGT	287017	119213	AAGGCAGGAGTGGGGTATCT
197844	30040	GGCTTGGGGCCCTGAGGGTC	242431	74627	TTCCTCAGCTCTCAGCTCAG	287018	119214	AAAGGCAGGAGTGGGGTATC
197845	30041	GGGCTTGGGGCCCTGAGGGT	242432	74628	GTTCCTCAGCTCTCAGCTCA	287019	119215	GAAAGGCAGGAGTGGGGTAT
197846	30042	GGGGCTTGGGGCCCTGAGGG	242433	74629	GGTTCCTCAGCTCTCAGCTC	287020	119216	GGAAAGGCAGGAGTGGGGTA
197847	30043	GGGGGCTTGGGGCCCTGAGG	242434	74630	TGGTTCCTCAGCTCTCAGCT	287021	119217	TGGAAAGGCAGGAGTGGGGT
197848	30044	TGGGGGCTTGGGGCCCTGAG	242435	74631	ATGGTTCCTCAGCTCTCAGC	287022	119218	CTGGAAAGGCAGGAGTGGGG
197849	30045	ATGGGGGCTTGGGGCCCTGA	242436	74632	AATGGTTCCTCAGCTCTCAG	287023	119219	GCTGGAAAGGCAGGAGTGGG
197850	30046	AATGGGGGCTTGGGGCCCTG	242437	74633	CAATGGTTCCTCAGCTCTCA	287024	119220	TGCTGGAAAGGCAGGAGTGG
197851	30047	AAATGGGGGCTTGGGGCCCT	242438	74634	TCAATGGTTCCTCAGCTCTC	287025	119221	TTGCTGGAAAGGCAGGAGTG
197852	30048	GAAATGGGGGCTTGGGGCCC	242439	74635	ATCAATGGTTCCTCAGCTCT	287026	119222	CTTGCTGGAAAGGCAGGAGT
197853	30049	GGAAATGGGGGCTTGGGGCC	242440	74636	GATCAATGGTTCCTCAGCTC	287027	119223	TCTTGCTGGAAAGGCAGGAG
197854	30050	TGGAAATGGGGGCTTGGGGC	242441	74637	AGATCAATGGTTCCTCAGCT	287028	119224	ATCTTGCTGGAAAGGCAGGA
197855	30051	ATGGAAATGGGGGCTTGGGG	242442	74638	CAGATCAATGGTTCCTCAGC	287029	119225	AATCTTGCTGGAAAGGCAGG
197856	30052	GATGGAAATGGGGGCTTGGG	242443	74639	TCAGATCAATGGTTCCTCAG	287030	119226	AAATCTTGCTGGAAAGGCAG
197857	30053	TGATGGAAATGGGGGCTTGG	242444	74640	ATCAGATCAATGGTTCCTCA	287031	119227	AAAATCTTGCTGGAAAGGCA
197858	30054	GTGATGGAAATGGGGGCTTG	242445	74641	CATCAGATCAATGGTTCCTC	287032	119228	AAAAATCTTGCTGGAAAGGC
197859	30055	TGTGATGGAAATGGGGGCTT	242446	74642	CCATCAGATCAATGGTTCCT	287033	119229	GAAAAATCTTGCTGGAAAGG
197860	30056	ATGTGATGGAAATGGGGGCT	242447	74643	GCCATCAGATCAATGGTTCC	287034	119230	TGAAAAATCTTGCTGGAAAG
197861	30057	CATGTGATGGAAATGGGGGC	242448	74644	AGCCATCAGATCAATGGTTC	287035	119231	CTGAAAAATCTTGCTGGAAA
197862	30058	GCATGTGATGGAAATGGGGG	242449	74645	CAGCCATCAGATCAATGGTT	287036	119232	TCTGAAAAATCTTGCTGGAA
197863	30059	CGCATGTGATGGAAATGGGG	242450	74646	TCAGCCATCAGATCAATGGT	287037	119233	ATCTGAAAAATCTTGCTGGA
197864	30060	ACGCATGTGATGGAAATGGG	242451	74647	CTCAGCCATCAGATCAATGG	287038	119234	CATCTGAAAAATCTTGCTGG
197865	30061	TACGCATGTGATGGAAATGG	242452	74648	TCTCAGCCATCAGATCAATG	287039	119235	GCATCTGAAAAATCTTGCTG
197866	30062	GTACGCATGTGATGGAAATG	242453	74649	GTCTCAGCCATCAGATCAAT	287040	119236	AGCATCTGAAAAATCTTGCT
197867	30063	TGTACGCATGTGATGGAAAT	242454	74650	TGTCTCAGCCATCAGATCAA	287041	119237	CAGCATCTGAAAAATCTTGC
197868	30064	GTGTACGCATGTGATGGAAA	242455	74651	GTGTCTCAGCCATCAGATCA	287042	119238	ACAGCATCTGAAAAATCTTG
197869	30065	GGTGTACGCATGTGATGGAA	242456	74652	GGTGTCTCAGCCATCAGATC	287043	119239	CACAGCATCTGAAAAATCTT
197870	30066	GGGTGTACGCATGTGATGGA	242457	74653	TGGTGTCTCAGCCATCAGAT	287044	119240	GCACAGCATCTGAAAAATCT
197871	30067	TGGGTGTACGCATGTGATGG	242458	74654	GTGGTGTCTCAGCCATCAGA	287045	119241	TGCACAGCATCTGAAAAATC
197872	30068	ATGGGTGTACGCATGTGATG	242459	74655	AGTGGTGTCTCAGCCATCAG	287046	119242	ATGCACAGCATCTGAAAAAT
197873	30069	CATGGGTGTACGCATGTGAT	242460	74656	CAGTGGTGTCTCAGCCATCA	287047	119243	TATGCACAGCATCTGAAAAA
197874	30070	ACATGGGTGTACGCATGTGA	242461	74657	CCAGTGGTGTCTCAGCCATC	287048	119244	GTATGCACAGCATCTGAAAA
197875	30071	CACATGGGTGTACGCATGTG	242462	74658	CCCAGTGGTGTCTCAGCCAT	287049	119245	AGTATGCACAGCATCTGAAA
197876	30072	ACACATGGGTGTACGCATGT	242463	74659	TCCCAGTGGTGTCTCAGCCA	287050	119246	GAGTATGCACAGCATCTGAA
197877	30073	CACACATGGGTGTACGCATG	242464	74660	TTCCCAGTGGTGTCTCAGCC	287051	119247	TGAGTATGCACAGCATCTGA
197878	30074	ACACACATGGGTGTACGCAT	242465	74661	CTTCCCAGTGGTGTCTCAGC	287052	119248	ATGAGTATGCACAGCATCTG
197879	30075	GACACACATGGGTGTACGCA	242466	74662	TCTTCCCAGTGGTGTCTCAG	287053	119249	GATGAGTATGCACAGCATCT
197880	30076	GGACACACATGGGTGTACGC	242467	74663	GTCTTCCCAGTGGTGTCTCA	287054	119250	TGATGAGTATGCACAGCATC
197881	30077	TGGACACACATGGGTGTACG	242468	74664	AGTCTTCCCAGTGGTGTCTC	287055	119251	ATGATGAGTATGCACAGCAT
197882	30078	ATGGACACACATGGGTGTAC	242469	74665	CAGTCTTCCCAGTGGTGTCT	287056	119252	TATGATGAGTATGCACAGCA
197883	30079	TATGGACACACATGGGTGTA	242470	74666	CCAGTCTTCCCAGTGGTGTC	287057	119253	ATATGATGAGTATGCACAGC
197884	30080	CTATGGACACACATGGGTGT	242471	74667	TCCAGTCTTCCCAGTGGTGT	287058	119254	AATATGATGAGTATGCACAG
197885	30081	GCTATGGACACACATGGGTG	242472	74668	CTCCAGTCTTCCCAGTGGTG	287059	119255	CAATATGATGAGTATGCACA
197886	30082	GGCTATGGACACACATGGGT	242473	74669	TCTCCAGTCTTCCCAGTGGT	287060	119256	TCAATATGATGAGTATGCAC
197887	30083	CGGCTATGGACACACATGGG	242474	74670	CTCTCCAGTCTTCCCAGTGG	287061	119257	ATCAATATGATGAGTATGCA
197888	30084	GCGGCTATGGACACACATGG	242475	74671	CCTCTCCAGTCTTCCCAGTG	287062	119258	GATCAATATGATGAGTATGC
197889	30085	GGCGGCTATGGACACACATG	242476	74672	GCCTCTCCAGTCTTCCCAGT	287063	119259	TGATCAATATGATGAGTATG
197890	30086	GGGCGGCTATGGACACACAT	242477	74673	AGCCTCTCCAGTCTTCCCAG	287064	119260	GTGATCAATATGATGAGTAT
197891	30087	TGGGCGGCTATGGACACACA	242478	74674	AAGCCTCTCCAGTCTTCCCA	287065	119261	AGTGATCAATATGATGAGTA
197892	30088	ATGGGCGGCTATGGACACAC	242479	74675	AAAGCCTCTCCAGTCTTCCC	287066	119262	AAGTGATCAATATGATGAGT
197893	30089	GATGGGCGGCTATGGACACA	242480	74676	AAAAGCCTCTCCAGTCTTCC	287067	119263	AAAGTGATCAATATGATGAG
197894	30090	AGATGGGCGGCTATGGACAC	242481	74677	GAAAAGCCTCTCCAGTCTTC	287068	119264	AAAAGTGATCAATATGATGA
197895	30091	GAGATGGGCGGCTATGGACA	242482	74678	AGAAAAGCCTCTCCAGTCTT	287069	119265	AAAAAGTGATCAATATGATG
197896	30092	TGAGATGGGCGGCTATGGAC	242483	74679	CAGAAAAGCCTCTCCAGTCT	287070	119266	AAAAAAGTGATCAATATGAT
197897	30093	CTGAGATGGGCGGCTATGGA	242484	74680	CCAGAAAAGCCTCTCCAGTC	287071	119267	GAAAAAAGTGATCAATATGA
197898	30094	ACTGAGATGGGCGGCTATGG	242485	74681	CCCAGAAAAGCCTCTCCAGT	287072	119268	AGAAAAAAGTGATCAATATG

197899	30095	GACTGAGATGGGCGGCTATG	242486	74682	GCCCAGAAAAGCCTCTCCAG	287073	119269	AAGAAAAAAGTGATCAATAT
197900	30096	TGACTGAGATGGGCGGCTAT	242487	74683	TGCCCAGAAAAGCCTCTCCA	287074	119270	GAAGAAAAAAGTGATCAATA
197901	30097	TTGACTGAGATGGGCGGCTA	242488	74684	ATGCCCAGAAAAGCCTCTCC	287075	119271	TGAAGAAAAAAGTGATCAAT
197902	30098	ATTGACTGAGATGGGCGGCT	242489	74685	CATGCCCAGAAAAGCCTCTC	287076	119272	ATGAAGAAAAAAGTGATCAA
197903	30099	TATTGACTGAGATGGGCGGC	242490	74686	GCATGCCCAGAAAAGCCTCT	287077	119273	CATGAAGAAAAAAGTGATCA
197904	30100	TTATTGACTGAGATGGGCGG	242491	74687	TGCATGCCCAGAAAAGCCTC	287078	119274	GCATGAAGAAAAAAGTGATC
197905	30101	CTTATTGACTGAGATGGGCG	242492	74688	CTGCATGCCCAGAAAAGCCT	287079	119275	GGCATGAAGAAAAAAGTGAT
197906	30102	CCTTATTGACTGAGATGGGC	242493	74689	ACTGCATGCCCAGAAAAGCC	287080	119276	AGGCATGAAGAAAAAAGTGA
197907	30103	GCCTTATTGACTGAGATGGG	242494	74690	CACTGCATGCCCAGAAAAGC	287081	119277	CAGGCATGAAGAAAAAAGTG
197908	30104	AGCCTTATTGACTGAGATGG	242495	74691	GCACTGCATGCCCAGAAAAG	287082	119278	TCAGGCATGAAGAAAAAAGT
197909	30105	CAGCCTTATTGACTGAGATG	242496	74692	GGCACTGCATGCCCAGAAAA	287083	119279	ATCAGGCATGAAGAAAAAAG
197910	30106	GCAGCCTTATTGACTGAGAT	242497	74693	TGGCACTGCATGCCCAGAAA	287084	119280	AATCAGGCATGAAGAAAAAA
197911	30107	AGCAGCCTTATTGACTGAGA	242498	74694	CTGGCACTGCATGCCCAGAA	287085	119281	CAATCAGGCATGAAGAAAAA
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197913	30109	GGAGCAGCCTTATTGACTGA	242500	74696	GCCTGGCACTGCATGCCCAG	287087	119283	CACAATCAGGCATGAAGAAA
197914	30110	AGGAGCAGCCTTATTGACTG	242501	74697	TGCCTGGCACTGCATGCCCA	287088	119284	TCACAATCAGGCATGAAGAA
197915	30111	CAGGAGCAGCCTTATTGACT	242502	74698	GTGCCTGGCACTGCATGCCC	287089	119285	ATCACAATCAGGCATGAAGA
197916	30112	GCAGGAGCAGCCTTATTGAC	242503	74699	TGTGCCTGGCACTGCATGCC	287090	119286	GATCACAATCAGGCATGAAG
197917	30113	GGCAGGAGCAGCCTTATTGA	242504	74700	CTGTGCCTGGCACTGCATGC	287091	119287	AGATCACAATCAGGCATGAA
197918	30114	GGGCAGGAGCAGCCTTATTG	242505	74701	CCTGTGCCTGGCACTGCATG	287092	119288	CAGATCACAATCAGGCATGA
197919	30115	TGGGCAGGAGCAGCCTTATT	242506	74702	TCCTGTGCCTGGCACTGCAT	287093	119289	ACAGATCACAATCAGGCATG
197920	30116	GTGGGCAGGAGCAGCCTTAT	242507	74703	CTCCTGTGCCTGGCACTGCA	287094	119290	GACAGATCACAATCAGGCAT
197921	30117	AGTGGGCAGGAGCAGCCTTA	242508	74704	CCTCCTGTGCCTGGCACTGC	287095	119291	TGACAGATCACAATCAGGCA
197922	30118	AAGTGGGCAGGAGCAGCCTT	242509	74705	TCCTCCTGTGCCTGGCACTG	287096	119292	TTGACAGATCACAATCAGGC
197923	30119	CAAGTGGGCAGGAGCAGCCT	242510	74706	CTCCTCCTGTGCCTGGCACT	287097	119293	ATTGACAGATCACAATCAGG
197924	30120	CCAAGTGGGCAGGAGCAGCC	242511	74707	GCTCCTCCTGTGCCTGGCAC	287098	119294	AATTGACAGATCACAATCAG
197925	30121	TCCAAGTGGGCAGGAGCAGC	242512	74708	AGCTCCTCCTGTGCCTGGCA	287099	119295	AAATTGACAGATCACAATCA
197926	30122	TTCCAAGTGGGCAGGAGCAG	242513	74709	CAGCTCCTCCTGTGCCTGGC	287100	119296	GAAATTGACAGATCACAATC
197927	30123	ATTCCAAGTGGGCAGGAGCA	242514	74710	TCAGCTCCTCCTGTGCCTGG	287101	119297	TGAAATTGACAGATCACAAT
197928	30124	TATTCCAAGTGGGCAGGAGC	242515	74711	CTCAGCTCCTCCTGTGCCTG	287102	119298	ATGAAATTGACAGATCACAA
197929	30125	CTATTCCAAGTGGGCAGGAG	242516	74712	CCTCAGCTCCTCCTGTGCCT	287103	119299	CATGAAATTGACAGATCACA
197930	30126	ACTATTCCAAGTGGGCAGGA	242517	74713	CCCTCAGCTCCTCCTGTGCC	287104	119300	ACATGAAATTGACAGATCAC
197931	30127	CACTATTCCAAGTGGGCAGG	242518	74714	TCCCTCAGCTCCTCCTGTGC	287105	119301	GACATGAAATTGACAGATCA
197932	30128	CCACTATTCCAAGTGGGCAG	242519	74715	TTCCCTCAGCTCCTCCTGTG	287106	119302	TGACATGAAATTGACAGATC
197933	30129	ACCACTATTCCAAGTGGGCA	242520	74716	CTTCCCTCAGCTCCTCCTGT	287107	119303	CTGACATGAAATTGACAGAT
197934	30130	CACCACTATTCCAAGTGGGC	242521	74717	TCTTCCCTCAGCTCCTCCTG	287108	119304	CCTGACATGAAATTGACAGA
197935	30131	TCACCACTATTCCAAGTGGG	242522	74718	ATCTTCCCTCAGCTCCTCCT	287109	119305	TCCTGACATGAAATTGACAG
197936	30132	GTCACCACTATTCCAAGTGG	242523	74719	CATCTTCCCTCAGCTCCTCC	287110	119306	TTCCTGACATGAAATTGACA
197937	30133	TGTCACCACTATTCCAAGTG	242524	74720	TCATCTTCCCTCAGCTCCTC	287111	119307	TTTCCTGACATGAAATTGAC
197938	30134	TTGTCACCACTATTCCAAGT	242525	74721	GTCATCTTCCCTCAGCTCCT	287112	119308	CTTTCCTGACATGAAATTGA
197939	30135	GTTGTCACCACTATTCCAAG	242526	74722	AGTCATCTTCCCTCAGCTCC	287113	119309	CCTTTCCTGACATGAAATTG
197940	30136	GGTTGTCACCACTATTCCAA	242527	74723	TAGTCATCTTCCCTCAGCTC	287114	119310	CCCTTTCCTGACATGAAATT
197941	30137	TGGTTGTCACCACTATTCCA	242528	74724	TTAGTCATCTTCCCTCAGCT	287115	119311	TCCCTTTCCTGACATGAAAT
197942	30138	CTGGTTGTCACCACTATTCC	242529	74725	CTTAGTCATCTTCCCTCAGC	287116	119312	CTCCCTTTCCTGACATGAAA
197943	30139	CCTGGTTGTCACCACTATTC	242530	74726	TCTTAGTCATCTTCCCTCAG	287117	119313	ACTCCCTTTCCTGACATGAA
197944	30140	TCCTGGTTGTCACCACTATT	242531	74727	CTCTTAGTCATCTTCCCTCA	287118	119314	CACTCCCTTTCCTGACATGA
197945	30141	CTCCTGGTTGTCACCACTAT	242532	74728	CCTCTTAGTCATCTTCCCTC	287119	119315	TCACTCCCTTTCCTGACATG
197946	30142	ACTCCTGGTTGTCACCACTA	242533	74729	ACCTCTTAGTCATCTTCCCT	287120	119316	GTCACTCCCTTTCCTGACAT
197947	30143	CACTCCTGGTTGTCACCACT	242534	74730	TACCTCTTAGTCATCTTCCC	287121	119317	TGTCACTCCCTTTCCTGACA
197948	30144	CCACTCCTGGTTGTCACCAC	242535	74731	GTACCTCTTAGTCATCTTCC	287122	119318	ATGTCACTCCCTTTCCTGAC
197949	30145	GCCACTCCTGGTTGTCACCA	242536	74732	AGTACCTCTTAGTCATCTTC	287123	119319	AATGTCACTCCCTTTCCTGA
197950	30146	AGCCACTCCTGGTTGTCACC	242537	74733	CAGTACCTCTTAGTCATCTT	287124	119320	AAATGTCACTCCCTTTCCTG
197951	30147	AAGCCACTCCTGGTTGTCAC	242538	74734	CCAGTACCTCTTAGTCATCT	287125	119321	AAAATGTCACTCCCTTTCCT
197952	30148	TAAGCCACTCCTGGTTGTCA	242539	74735	GCCAGTACCTCTTAGTCATC	287126	119322	AAAAATGTCACTCCCTTTCC
197953	30149	ATAAGCCACTCCTGGTTGTC	242540	74736	TGCCAGTACCTCTTAGTCAT	287127	119323	TAAAAATGTCACTCCCTTTC
197954	30150	CATAAGCCACTCCTGGTTGT	242541	74737	TTGCCAGTACCTCTTAGTCA	287128	119324	GTAAAAATGTCACTCCCTTT
197955	30151	CCATAAGCCACTCCTGGTTG	242542	74738	TTTGCCAGTACCTCTTAGTC	287129	119325	TGTAAAAATGTCACTCCCTT
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197957	30153	TCCCATAAGCCACTCCTGGT	242544	74740	TCTTTGCCAGTACCTCTTAG	287131	119327	AGTGTAAAAATGTCACTCCC
197958	30154	TTCCCATAAGCCACTCCTGG	242545	74741	TTCTTTGCCAGTACCTCTTA	287132	119328	AAGTGTAAAAATGTCACTCC
197959	30155	GTTCCCATAAGCCACTCCTG	242546	74742	ATTCTTTGCCAGTACCTCTT	287133	119329	TAAGTGTAAAAATGTCACTC
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197962	30158	ATAGTTCCCATAAGCCACTC	242549	74745	TGAATTCTTTGCCAGTACCT	287136	119332	GCTTAAGTGTAAAAATGTCA
197963	30159	GATAGTTCCCATAAGCCACT	242550	74746	CTGAATTCTTTGCCAGTACC	287137	119333	CGCTTAAGTGTAAAAATGTC
197964	30160	GGATAGTTCCCATAAGCCAC	242551	74747	TCTGAATTCTTTGCCAGTAC	287138	119334	ACGCTTAAGTGTAAAAATGT
197965	30161	GGGATAGTTCCCATAAGCCA	242552	74748	TTCTGAATTCTTTGCCAGTA	287139	119335	AACGCTTAAGTGTAAAAATG
197966	30162	TGGGATAGTTCCCATAAGCC	242553	74749	TTTCTGAATTCTTTGCCAGT	287140	119336	AAACGCTTAAGTGTAAAAAT
197967	30163	TTGGGATAGTTCCCATAAGC	242554	74750	ATTTCTGAATTCTTTGCCAG	287141	119337	CAAACGCTTAAGTGTAAAAA
197968	30164	ATTGGGATAGTTCCCATAAG	242555	74751	AATTTCTGAATTCTTTGCCA	287142	119338	GCAAACGCTTAAGTGTAAAA
197969	30165	CATTGGGATAGTTCCCATAA	242556	74752	GAATTTCTGAATTCTTTGCC	287143	119339	AGCAAACGCTTAAGTGTAAA
197970	30166	CCATTGGGATAGTTCCCATA	242557	74753	AGAATTTCTGAATTCTTTGC	287144	119340	CAGCAAACGCTTAAGTGTAA

197971	30167	GCCATTGGGATAGTTCCCAT	242558	74754	CAGAATTTCTGAATTCTTTG	287145	119341	TCAGCAAACGCTTAAGTGTA
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197973	30169	AGGCCATTGGGATAGTTCCC	242560	74756	ATCAGAATTTCTGAATTCTT	287147	119343	GCTCAGCAAACGCTTAAGTG
197974	30170	CAGGCCATTGGGATAGTTCC	242561	74757	CATCAGAATTTCTGAATTCT	287148	119344	TGCTCAGCAAACGCTTAAGT
197975	30171	TCAGGCCATTGGGATAGTTC	242562	74758	CCATCAGAATTTCTGAATTC	287149	119345	TTGCTCAGCAAACGCTTAAG
197976	30172	GTCAGGCCATTGGGATAGTT	242563	74759	TCCATCAGAATTTCTGAATT	287150	119346	TTTGCTCAGCAAACGCTTAA
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197978	30174	CTGTCAGGCCATTGGGATAG	242565	74761	CTTCCATCAGAATTTCTGAA	287152	119348	CATTTGCTCAGCAAACGCTT
197979	30175	GCTGTCAGGCCATTGGGATA	242566	74762	GCTTCCATCAGAATTTCTGA	287153	119349	ACATTTGCTCAGCAAACGCT
197980	30176	TGCTGTCAGGCCATTGGGAT	242567	74763	AGCTTCCATCAGAATTTCTG	287154	119350	GACATTTGCTCAGCAAACGC
197981	30177	ATGCTGTCAGGCCATTGGGA	242568	74764	AAGCTTCCATCAGAATTTCT	287155	119351	AGACATTTGCTCAGCAAACG
197982	30178	CATGCTGTCAGGCCATTGGG	242569	74765	AAAGCTTCCATCAGAATTTC	287156	119352	CAGACATTTGCTCAGCAAAC
197983	30179	ACATGCTGTCAGGCCATTGG	242570	74766	TAAAGCTTCCATCAGAATTT	287157	119353	CCAGACATTTGCTCAGCAAA
197984	30180	GACATGCTGTCAGGCCATTG	242571	74767	GTAAAGCTTCCATCAGAATT	287158	119354	CCCAGACATTTGCTCAGCAA
197985	30181	GGACATGCTGTCAGGCCATT	242572	74768	TGTAAAGCTTCCATCAGAAT	287159	119355	ACCCAGACATTTGCTCAGCA
197986	30182	CGGACATGCTGTCAGGCCAT	242573	74769	ATGTAAAGCTTCCATCAGAA	287160	119356	GACCCAGACATTTGCTCAGC
197987	30183	GCGGACATGCTGTCAGGCCA	242574	74770	CATGTAAAGCTTCCATCAGA	287161	119357	AGACCCAGACATTTGCTCAG
197988	30184	AGCGGACATGCTGTCAGGCC	242575	74771	ACATGTAAAGCTTCCATCAG	287162	119358	AAGACCCAGACATTTGCTCA
197989	30185	CAGCGGACATGCTGTCAGGC	242576	74772	AACATGTAAAGCTTCCATCA	287163	119359	CAAGACCCAGACATTTGCTC
197990	30186	GCAGCGGACATGCTGTCAGG	242577	74773	TAACATGTAAAGCTTCCATC	287164	119360	GCAAGACCCAGACATTTGCT
197991	30187	TGCAGCGGACATGCTGTCAG	242578	74774	GTAACATGTAAAGCTTCCAT	287165	119361	TGCAAGACCCAGACATTTGC
197992	30188	TTGCAGCGGACATGCTGTCA	242579	74775	GGTAACATGTAAAGCTTCCA	287166	119362	GTGCAAGACCCAGACATTTG
197993	30189	TTTGCAGCGGACATGCTGTC	242580	74776	TGGTAACATGTAAAGCTTCC	287167	119363	TGTGCAAGACCCAGACATTT
197994	30190	GTTTGCAGCGGACATGCTGT	242581	74777	ATGGTAACATGTAAAGCTTC	287168	119364	TTGTGCAAGACCCAGACATT
197995	30191	GGTTTGCAGCGGACATGCTG	242582	74778	GATGGTAACATGTAAAGCTT	287169	119365	ATTGTGCAAGACCCAGACAT
197996	30192	CGGTTTGCAGCGGACATGCT	242583	74779	TGATGGTAACATGTAAAGCT	287170	119366	CATTGTGCAAGACCCAGACA
197997	30193	GCGGTTTGCAGCGGACATGC	242584	74780	GTGATGGTAACATGTAAAGC	287171	119367	TCATTGTGCAAGACCCAGAC
197998	30194	AGCGGTTTGCAGCGGACATG	242585	74781	TGTGATGGTAACATGTAAAG	287172	119368	GTCATTGTGCAAGACCCAGA
197999	30195	CAGCGGTTTGCAGCGGACAT	242586	74782	ATGTGATGGTAACATGTAAA	287173	119369	TGTCATTGTGCAAGACCCAG
198000	30196	TCAGCGGTTTGCAGCGGACA	242587	74783	GATGTGATGGTAACATGTAA	287174	119370	TTGTCATTGTGCAAGACCCA
198001	30197	CTCAGCGGTTTGCAGCGGAC	242588	74784	GGATGTGATGGTAACATGTA	287175	119371	ATTGTCATTGTGCAAGACCC
198002	30198	CCTCAGCGGTTTGCAGCGGA	242589	74785	TGGATGTGATGGTAACATGT	287176	119372	CATTGTCATTGTGCAAGACC
198003	30199	ACCTCAGCGGTTTGCAGCGG	242590	74786	ATGGATGTGATGGTAACATG	287177	119373	CCATTGTCATTGTGCAAGAC
198004	30200	TACCTCAGCGGTTTGCAGCG	242591	74787	GATGGATGTGATGGTAACAT	287178	119374	CCCATTGTCATTGTGCAAGA
198005	30201	CTACCTCAGCGGTTTGCAGC	242592	74788	GGATGGATGTGATGGTAACA	287179	119375	ACCCATTGTCATTGTGCAAG
198006	30202	CCTACCTCAGCGGTTTGCAG	242593	74789	TGGATGGATGTGATGGTAAC	287180	119376	GACCCATTGTCATTGTGCAA
198007	30203	TCCTACCTCAGCGGTTTGCA	242594	74790	ATGGATGGATGTGATGGTAA	287181	119377	GGACCCATTGTCATTGTGCA
198008	30204	GTCCTACCTCAGCGGTTTGC	242595	74791	GATGGATGGATGTGATGGTA	287182	119378	GGGACCCATTGTCATTGTGC
198009	30205	TGTCCTACCTCAGCGGTTTG	242596	74792	AGATGGATGGATGTGATGGT	287183	119379	AGGGACCCATTGTCATTGTG
198010	30206	GTGTCCTACCTCAGCGGTTT	242597	74793	TAGATGGATGGATGTGATGG	287184	119380	CAGGGACCCATTGTCATTGT
198011	30207	AGTGTCCTACCTCAGCGGTT	242598	74794	ATAGATGGATGGATGTGATG	287185	119381	ACAGGGACCCATTGTCATTG
198012	30208	CAGTGTCCTACCTCAGCGGT	242599	74795	GATAGATGGATGGATGTGAT	287186	119382	AACAGGGACCCATTGTCATT
198013	30209	GCAGTGTCCTACCTCAGCGG	242600	74796	GGATAGATGGATGGATGTGA	287187	119383	AAACAGGGACCCATTGTCAT
198014	30210	GGCAGTGTCCTACCTCAGCG	242601	74797	TGGATAGATGGATGGATGTG	287188	119384	AAAACAGGGACCCATTGTCA
198015	30211	GGGCAGTGTCCTACCTCAGC	242602	74798	GTGGATAGATGGATGGATGT	287189	119385	AAAAACAGGGACCCATTGTC
198016	30212	AGGGCAGTGTCCTACCTCAG	242603	74799	GGTGGATAGATGGATGGATG	287190	119386	GAAAAACAGGGACCCATTGT
198017	30213	GAGGGCAGTGTCCTACCTCA	242604	74800	GGGTGGATAGATGGATGGAT	287191	119387	GGAAAAACAGGGACCCATTG
198018	30214	TGAGGGCAGTGTCCTACCTC	242605	74801	TGGGTGGATAGATGGATGGA	287192	119388	GGGAAAAACAGGGACCCATT
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198020	30216	CATGAGGGCAGTGTCCTACC	242607	74803	GATGGGTGGATAGATGGATG	287194	119390	CTGGGAAAAACAGGGACCCA
198021	30217	ACATGAGGGCAGTGTCCTAC	242608	74804	GGATGGGTGGATAGATGGAT	287195	119391	TCTGGGAAAAACAGGGACCC
198022	30218	GACATGAGGGCAGTGTCCTA	242609	74805	TGGATGGGTGGATAGATGGA	287196	119392	CTCTGGGAAAAACAGGGACC
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198024	30220	TAGACATGAGGGCAGTGTCC	242611	74807	GATGGATGGGTGGATAGATG	287198	119394	GCCTCTGGGAAAAACAGGGA
198025	30221	CTAGACATGAGGGCAGTGTC	242612	74808	GGATGGATGGGTGGATAGAT	287199	119395	AGCCTCTGGGAAAAACAGGG
198026	30222	GCTAGACATGAGGGCAGTGT	242613	74809	TGGATGGATGGGTGGATAGA	287200	119396	GAGCCTCTGGGAAAAACAGG
198027	30223	AGCTAGACATGAGGGCAGTG	242614	74810	GTGGATGGATGGGTGGATAG	287201	119397	AGAGCCTCTGGGAAAAACAG
198028	30224	CAGCTAGACATGAGGGCAGT	242615	74811	GGTGGATGGATGGGTGGATA	287202	119398	AAGAGCCTCTGGGAAAAACA
198029	30225	TCAGCTAGACATGAGGGCAG	242616	74812	GGGTGGATGGATGGGTGGAT	287203	119399	AAAGAGCCTCTGGGAAAAAC
198030	30226	ATCAGCTAGACATGAGGGCA	242617	74813	TGGGTGGATGGATGGGTGGA	287204	119400	AAAAGAGCCTCTGGGAAAAA
198031	30227	GATCAGCTAGACATGAGGGC	242618	74814	ATGGGTGGATGGATGGGTGG	287205	119401	CAAAAGAGCCTCTGGGAAAA
198032	30228	TGATCAGCTAGACATGAGGG	242619	74815	TATGGGTGGATGGATGGGTG	287206	119402	ACAAAAGAGCCTCTGGGAAA
198033	30229	CTGATCAGCTAGACATGAGG	242620	74816	ATATGGGTGGATGGATGGGT	287207	119403	AACAAAAGAGCCTCTGGGAA
198034	30230	GCTGATCAGCTAGACATGAG	242621	74817	GATATGGGTGGATGGATGGG	287208	119404	GAACAAAAGAGCCTCTGGGA
198035	30231	TGCTGATCAGCTAGACATGA	242622	74818	AGATATGGGTGGATGGATGG	287209	119405	AGAACAAAAGAGCCTCTGGG
198036	30232	TTGCTGATCAGCTAGACATG	242623	74819	AAGATATGGGTGGATGGATG	287210	119406	CAGAACAAAAGAGCCTCTGG
198037	30233	CTTGCTGATCAGCTAGACAT	242624	74820	GAAGATATGGGTGGATGGAT	287211	119407	GCAGAACAAAAGAGCCTCTG
198038	30234	TCTTGCTGATCAGCTAGACA	242625	74821	GGAAGATATGGGTGGATGGA	287212	119408	TGCAGAACAAAAGAGCCTCT
198039	30235	CTCTTGCTGATCAGCTAGAC	242626	74822	AGGAAGATATGGGTGGATGG	287213	119409	CTGCAGAACAAAAGAGCCTC
198040	30236	CCTCTTGCTGATCAGCTAGA	242627	74823	GAGGAAGATATGGGTGGATG	287214	119410	CCTGCAGAACAAAAGAGCCT
198041	30237	GCCTCTTGCTGATCAGCTAG	242628	74824	GGAGGAAGATATGGGTGGAT	287215	119411	CCCTGCAGAACAAAAGAGCC
198042	30238	CGCCTCTTGCTGATCAGCTA	242629	74825	GGGAGGAAGATATGGGTGGA	287216	119412	TCCCTGCAGAACAAAAGAGC

198043	30239	GCGCCTCTTGCTGATCAGCT	242630	74826	AGGGAGGAAGATATGGGTGG	287217	119413	ATCCCTGCAGAACAAAAGAG
198044	30240	TGCGCCTCTTGCTGATCAGC	242631	74827	GAGGGAGGAAGATATGGGTG	287218	119414	AATCCCTGCAGAACAAAAGA
198045	30241	CTGCGCCTCTTGCTGATCAG	242632	74828	GGAGGGAGGAAGATATGGGT	287219	119415	CAATCCCTGCAGAACAAAAG
198046	30242	ACTGCGCCTCTTGCTGATCA	242633	74829	TGGAGGGAGGAAGATATGGG	287220	119416	TCAATCCCTGCAGAACAAAA
198047	30243	AACTGCGCCTCTTGCTGATC	242634	74830	GTGGAGGGAGGAAGATATGG	287221	119417	TTCAATCCCTGCAGAACAAA
198048	30244	CAACTGCGCCTCTTGCTGAT	242635	74831	GGTGGAGGGAGGAAGATATG	287222	119418	CTTCAATCCCTGCAGAACAA
198049	30245	GCAACTGCGCCTCTTGCTGA	242636	74832	GGGTGGAGGGAGGAAGATAT	287223	119419	TCTTCAATCCCTGCAGAACA
198050	30246	AGCAACTGCGCCTCTTGCTG	242637	74833	TGGGTGGAGGGAGGAAGATA	287224	119420	GTCTTCAATCCCTGCAGAAC
198051	30247	AAGCAACTGCGCCTCTTGCT	242638	74834	TTGGGTGGAGGGAGGAAGAT	287225	119421	TGTCTTCAATCCCTGCAGAA
198052	30248	AAAGCAACTGCGCCTCTTGC	242639	74835	ATTGGGTGGAGGGAGGAAGA	287226	119422	GTGTCTTCAATCCCTGCAGA
198053	30249	GAAAGCAACTGCGCCTCTTG	242640	74836	GATTGGGTGGAGGGAGGAAG	287227	119423	AGTGTCTTCAATCCCTGCAG
198054	30250	AGAAAGCAACTGCGCCTCTT	242641	74837	TGATTGGGTGGAGGGAGGAA	287228	119424	GAGTGTCTTCAATCCCTGCA
198055	30251	AAGAAAGCAACTGCGCCTCT	242642	74838	ATGATTGGGTGGAGGGAGGA	287229	119425	GGAGTGTCTTCAATCCCTGC
198056	30252	TAAGAAAGCAACTGCGCCTC	242643	74839	CATGATTGGGTGGAGGGAGG	287230	119426	TGGAGTGTCTTCAATCCCTG
198057	30253	CTAAGAAAGCAACTGCGCCT	242644	74840	GCATGATTGGGTGGAGGGAG	287231	119427	CTGGAGTGTCTTCAATCCCT
198058	30254	CCTAAGAAAGCAACTGCGCC	242645	74841	TGCATGATTGGGTGGAGGGA	287232	119428	ACTGGAGTGTCTTCAATCCC
198059	30255	ACCTAAGAAAGCAACTGCGC	242646	74842	ATGCATGATTGGGTGGAGGG	287233	119429	GACTGGAGTGTCTTCAATCC
198060	30256	TACCTAAGAAAGCAACTGCG	242647	74843	TATGCATGATTGGGTGGAGG	287234	119430	GGACTGGAGTGTCTTCAATC
198061	30257	TTACCTAAGAAAGCAACTGC	242648	74844	GTATGCATGATTGGGTGGAG	287235	119431	GGGACTGGAGTGTCTTCAAT
198062	30258	GTTACCTAAGAAAGCAACTG	242649	74845	TGTATGCATGATTGGGTGGA	287236	119432	TGGGACTGGAGTGTCTTCAA
198063	30259	TGTTACCTAAGAAAGCAACT	242650	74846	ATGTATGCATGATTGGGTGG	287237	119433	GTGGGACTGGAGTGTCTTCA
198064	30260	ATGTTACCTAAGAAAGCAAC	242651	74847	GATGTATGCATGATTGGGTG	287238	119434	TGTGGGACTGGAGTGTCTTC
198065	30261	AATGTTACCTAAGAAAGCAA	242652	74848	GGATGTATGCATGATTGGGT	287239	119435	CTGTGGGACTGGAGTGTCTT
198066	30262	CAATGTTACCTAAGAAAGCA	242653	74849	TGGATGTATGCATGATTGGG	287240	119436	ACTGTGGGACTGGAGTGTCT
198067	30263	GCAATGTTACCTAAGAAAGC	242654	74850	CTGGATGTATGCATGATTGG	287241	119437	GACTGTGGGACTGGAGTGTC
198068	30264	AGCAATGTTACCTAAGAAAG	242655	74851	ACTGGATGTATGCATGATTG	287242	119438	GGACTGTGGGACTGGAGTGT
198069	30265	CAGCAATGTTACCTAAGAAA	242656	74852	GACTGGATGTATGCATGATT	287243	119439	GGGACTGTGGGACTGGAGTG
198070	30266	GCAGCAATGTTACCTAAGAA	242657	74853	TGACTGGATGTATGCATGAT	287244	119440	GGGGACTGTGGGACTGGAGT
198071	30267	AGCAGCAATGTTACCTAAGA	242658	74854	ATGACTGGATGTATGCATGA	287245	119441	TGGGGACTGTGGGACTGGAG
198072	30268	CAGCAGCAATGTTACCTAAG	242659	74855	GATGACTGGATGTATGCATG	287246	119442	CTGGGGACTGTGGGACTGGA
198073	30269	ACAGCAGCAATGTTACCTAA	242660	74856	AGATGACTGGATGTATGCAT	287247	119443	GCTGGGGACTGTGGGACTGG
198074	30270	CACAGCAGCAATGTTACCTA	242661	74857	TAGATGACTGGATGTATGCA	287248	119444	AGCTGGGGACTGTGGGACTG
198075	30271	ACACAGCAGCAATGTTACCT	242662	74858	ATAGATGACTGGATGTATGC	287249	119445	GAGCTGGGGACTGTGGGACT
198076	30272	GACACAGCAGCAATGTTACC	242663	74859	TATAGATGACTGGATGTATG	287250	119446	GGAGCTGGGGACTGTGGGAC
198077	30273	GGACACAGCAGCAATGTTAC	242664	74860	GTATAGATGACTGGATGTAT	287251	119447	GGGAGCTGGGGACTGTGGGA
198078	30274	AGGACACAGCAGCAATGTTA	242665	74861	TGTATAGATGACTGGATGTA	287252	119448	GGGGAGCTGGGGACTGTGGG
198079	30275	CAGGACACAGCAGCAATGTT	242666	74862	GTGTATAGATGACTGGATGT	287253	119449	AGGGGAGCTGGGGACTGTGG
198080	30276	CCAGGACACAGCAGCAATGT	242667	74863	GGTGTATAGATGACTGGATG	287254	119450	CAGGGGAGCTGGGGACTGTG
198081	30277	GCCAGGACACAGCAGCAATG	242668	74864	TGGTGTATAGATGACTGGAT	287255	119451	CCAGGGGAGCTGGGGACTGT
198082	30278	GGCCAGGACACAGCAGCAAT	242669	74865	GTGGTGTATAGATGACTGGA	287256	119452	CCCAGGGGAGCTGGGGACTG
198083	30279	TGGCCAGGACACAGCAGCAA	242670	74866	GGTGGTGTATAGATGACTGG	287257	119453	CCCCAGGGGAGCTGGGGACT
198084	30280	ATGGCCAGGACACAGCAGCA	242671	74867	GGGTGGTGTATAGATGACTG	287258	119454	GCCCCAGGGGAGCTGGGGAC
198085	30281	AATGGCCAGGACACAGCAGC	242672	74868	TGGGTGGTGTATAGATGACT	287259	119455	TGCCCCAGGGGAGCTGGGGA
198086	30282	CAATGGCCAGGACACAGCAG	242673	74869	GTGGGTGGTGTATAGATGAC	287260	119456	CTGCCCCAGGGGAGCTGGGG
198087	30283	GCAATGGCCAGGACACAGCA	242674	74870	GGTGGGTGGTGTATAGATGA	287261	119457	CCTGCCCCAGGGGAGCTGGG
198088	30284	AGCAATGGCCAGGACACAGC	242675	74871	GGGTGGGTGGTGTATAGATG	287262	119458	CCCTGCCCCAGGGGAGCTGG
198089	30285	CAGCAATGGCCAGGACACAG	242676	74872	TGGGTGGGTGGTGTATAGAT	287263	119459	ACCCTGCCCCAGGGGAGCTG
198090	30286	CCAGCAATGGCCAGGACACA	242677	74873	GTGGGTGGGTGGTGTATAGA	287264	119460	AACCCTGCCCCAGGGGAGCT
198091	30287	CCCAGCAATGGCCAGGACAC	242678	74874	GGTGGGTGGGTGGTGTATAG	287265	119461	CAACCCTGCCCCAGGGGAGC
198092	30288	CCCCAGCAATGGCCAGGACA	242679	74875	GGGTGGGTGGGTGGTGTATA	287266	119462	CCAACCCTGCCCCAGGGGAG
198093	30289	CCCCCAGCAATGGCCAGGAC	242680	74876	TGGGTGGGTGGGTGGTGTAT	287267	119463	GCCAACCCTGCCCCAGGGGA
198094	30290	CCCCCCAGCAATGGCCAGGA	242681	74877	ATGGGTGGGTGGGTGGTGTA	287268	119464	TGCCAACCCTGCCCCAGGGG
198095	30291	ACCCCCCAGCAATGGCCAGG	242682	74878	GATGGGTGGGTGGGTGGTGT	287269	119465	CTGCCAACCCTGCCCCAGGG
198096	30292	CACCCCCCAGCAATGGCCAG	242683	74879	GGATGGGTGGGTGGGTGGTG	287270	119466	TCTGCCAACCCTGCCCCAGG
198097	30293	CCACCCCCCAGCAATGGCCA	242684	74880	TGGATGGGTGGGTGGGTGGT	287271	119467	TTCTGCCAACCCTGCCCCAG
198098	30294	GCCACCCCCCAGCAATGGCC	242685	74881	ATGGATGGGTGGGTGGGTGG	287272	119468	ATTCTGCCAACCCTGCCCCA
198099	30295	TGCCACCCCCCAGCAATGGC	242686	74882	GATGGATGGGTGGGTGGGTG	287273	119469	AATTCTGCCAACCCTGCCCC
198100	30296	GTGCCACCCCCCAGCAATGG	242687	74883	GGATGGATGGGTGGGTGGGT	287274	119470	AAATTCTGCCAACCCTGCCC
198101	30297	AGTGCCACCCCCCAGCAATG	242688	74884	TGGATGGATGGGTGGGTGGG	287275	119471	GAAATTCTGCCAACCCTGCC
198102	30298	AAGTGCCACCCCCCAGCAAT	242689	74885	ATGGATGGATGGGTGGGTGG	287276	119472	CGAAATTCTGCCAACCCTGC
198103	30299	TAAGTGCCACCCCCCAGCAA	242690	74886	GATGGATGGATGGGTGGGTG	287277	119473	TCGAAATTCTGCCAACCCTG
198104	30300	TTAAGTGCCACCCCCCAGCA	242691	74887	GGATGGATGGATGGGTGGGT	287278	119474	GTCGAAATTCTGCCAACCCT
198105	30301	ATTAAGTGCCACCCCCCAGC	242692	74888	TGGATGGATGGATGGGTGGG	287279	119475	TGTCGAAATTCTGCCAACCC
198106	30302	GATTAAGTGCCACCCCCCAG	242693	74889	ATGGATGGATGGATGGGTGG	287280	119476	TTGTCGAAATTCTGCCAACC
198107	30303	AGATTAAGTGCCACCCCCCA	242694	74890	GATGGATGGATGGATGGGTG	287281	119477	GTTGTCGAAATTCTGCCAAC
198108	30304	TAGATTAAGTGCCACCCCCC	242695	74891	GGATGGATGGATGGATGGGT	287282	119478	TGTTGTCGAAATTCTGCCAA
198109	30305	GTAGATTAAGTGCCACCCCC	242696	74892	TGGATGGATGGATGGATGGG	287283	119479	GTGTTGTCGAAATTCTGCCA
198110	30306	TGTAGATTAAGTGCCACCCC	242697	74893	ATGGATGGATGGATGGATGG	287284	119480	TGTGTTGTCGAAATTCTGCC
198111	30307	GTGTAGATTAAGTGCCACCC	242698	74894	GATGGATGGATGGATGGATG	287285	119481	ATGTGTTGTCGAAATTCTGC
198112	30308	GGTGTAGATTAAGTGCCACC	242699	74895	GGATGGATGGATGGATGGAT	287286	119482	AATGTGTTGTCGAAATTCTG
198113	30309	TGGTGTAGATTAAGTGCCAC	242700	74896	GGGATGGATGGATGGATGGA	287287	119483	AAATGTGTTGTCGAAATTCT
198114	30310	CTGGTGTAGATTAAGTGCCA	242701	74897	AGGGATGGATGGATGGATGG	287288	119484	AAAATGTGTTGTCGAAATTC

198115	30311	TCTGGTGTAGATTAAGTGCC	242702	74898	AAGGGATGGATGGATGGATG	287289	119485	AAAAATGTGTTGTCGAAATT
198116	30312	TTCTGGTGTAGATTAAGTGC	242703	74899	GAAGGGATGGATGGATGGAT	287290	119486	GAAAAATGTGTTGTCGAAAT
198117	30313	ATTCTGGTGTAGATTAAGTG	242704	74900	TGAAGGGATGGATGGATGGA	287291	119487	GGAAAAATGTGTTGTCGAAA
198118	30314	AATTCTGGTGTAGATTAAGT	242705	74901	ATGAAGGGATGGATGGATGG	287292	119488	TGGAAAAATGTGTTGTCGAA
198119	30315	AAATTCTGGTGTAGATTAAG	242706	74902	GATGAAGGGATGGATGGATG	287293	119489	GTGGAAAAATGTGTTGTCGA
198120	30316	AAAATTCTGGTGTAGATTAA	242707	74903	GGATGAAGGGATGGATGGAT	287294	119490	GGTGGAAAAATGTGTTGTCG
198121	30317	GAAAATTCTGGTGTAGATTA	242708	74904	TGGATGAAGGGATGGATGGA	287295	119491	GGGTGGAAAAATGTGTTGTC
198122	30318	GGAAAATTCTGGTGTAGATT	242709	74905	ATGGATGAAGGGATGGATGG	287296	119492	AGGGTGGAAAAATGTGTTGT
198123	30319	GGGAAAATTCTGGTGTAGAT	242710	74906	GATGGATGAAGGGATGGATG	287297	119493	CAGGGTGGAAAAATGTGTTG
198124	30320	AGGGAAAATTCTGGTGTAGA	242711	74907	GGATGGATGAAGGGATGGAT	287298	119494	TCAGGGTGGAAAAATGTGTT
198125	30321	GAGGGAAAATTCTGGTGTAG	242712	74908	GGGATGGATGAAGGGATGGA	287299	119495	GTCAGGGTGGAAAAATGTGT
198126	30322	GGAGGGAAAATTCTGGTGTA	242713	74909	TGGGATGGATGAAGGGATGG	287300	119496	AGTCAGGGTGGAAAAATGTG
198127	30323	AGGAGGGAAAATTCTGGTGT	242714	74910	ATGGGATGGATGAAGGGATG	287301	119497	TAGTCAGGGTGGAAAAATGT
198128	30324	CAGGAGGGAAAATTCTGGTG	242715	74911	GATGGGATGGATGAAGGGAT	287302	119498	CTAGTCAGGGTGGAAAAATG
198129	30325	ACAGGAGGGAAAATTCTGGT	242716	74912	TGATGGGATGGATGAAGGGA	287303	119499	CCTAGTCAGGGTGGAAAAAT
198130	30326	TACAGGAGGGAAAATTCTGG	242717	74913	ATGATGGGATGGATGAAGGG	287304	119500	TCCTAGTCAGGGTGGAAAAA
198131	30327	ATACAGGAGGGAAAATTCTG	242718	74914	GATGATGGGATGGATGAAGG	287305	119501	ATCCTAGTCAGGGTGGAAAA
198132	30328	GATACAGGAGGGAAAATTCT	242719	74915	GGATGATGGGATGGATGAAG	287306	119502	CATCCTAGTCAGGGTGGAAA
198133	30329	AGATACAGGAGGGAAAATTC	242720	74916	TGGATGATGGGATGGATGAA	287307	119503	ACATCCTAGTCAGGGTGGAA
198134	30330	AAGATACAGGAGGGAAAATT	242721	74917	ATGGATGATGGGATGGATGA	287308	119504	CACATCCTAGTCAGGGTGGA
198135	30331	GAAGATACAGGAGGGAAAAT	242722	74918	GATGGATGATGGGATGGATG	287309	119505	GCACATCCTAGTCAGGGTGG
198136	30332	GGAAGATACAGGAGGGAAAA	242723	74919	GGATGGATGATGGGATGGAT	287310	119506	AGCACATCCTAGTCAGGGTG
198137	30333	TGGAAGATACAGGAGGGAAA	242724	74920	TGGATGGATGATGGGATGGA	287311	119507	GAGCACATCCTAGTCAGGGT
198138	30334	TTGGAAGATACAGGAGGGAA	242725	74921	TTGGATGGATGATGGGATGG	287312	119508	GGAGCACATCCTAGTCAGGG
198139	30335	CTTGGAAGATACAGGAGGGA	242726	74922	ATTGGATGGATGATGGGATG	287313	119509	AGGAGCACATCCTAGTCAGG
198140	30336	GCTTGGAAGATACAGGAGGG	242727	74923	AATTGGATGGATGATGGGAT	287314	119510	GAGGAGCACATCCTAGTCAG
198141	30337	AGCTTGGAAGATACAGGAGG	242728	74924	TAATTGGATGGATGATGGGA	287315	119511	TGAGGAGCACATCCTAGTCA
198142	30338	CAGCTTGGAAGATACAGGAG	242729	74925	ATAATTGGATGGATGATGGG	287316	119512	ATGAGGAGCACATCCTAGTC
198143	30339	GCAGCTTGGAAGATACAGGA	242730	74926	TATAATTGGATGGATGATGG	287317	119513	CATGAGGAGCACATCCTAGT
198144	30340	AGCAGCTTGGAAGATACAGG	242731	74927	GTATAATTGGATGGATGATG	287318	119514	CCATGAGGAGCACATCCTAG
198145	30341	AAGCAGCTTGGAAGATACAG	242732	74928	TGTATAATTGGATGGATGAT	287319	119515	GCCATGAGGAGCACATCCTA
198146	30342	CAAGCAGCTTGGAAGATACA	242733	74929	ATGTATAATTGGATGGATGA	287320	119516	TGCCATGAGGAGCACATCCT
198147	30343	CCAAGCAGCTTGGAAGATAC	242734	74930	TATGTATAATTGGATGGATG	287321	119517	CTGCCATGAGGAGCACATCC
198148	30344	TCCAAGCAGCTTGGAAGATA	242735	74931	GTATGTATAATTGGATGGAT	287322	119518	GCTGCCATGAGGAGCACATC
198149	30345	ATCCAAGCAGCTTGGAAGAT	242736	74932	TGTATGTATAATTGGATGGA	287323	119519	AGCTGCCATGAGGAGCACAT
198150	30346	GATCCAAGCAGCTTGGAAGA	242737	74933	ATGTATGTATAATTGGATGG	287324	119520	CAGCTGCCATGAGGAGCACA
198151	30347	AGATCCAAGCAGCTTGGAAG	242738	74934	GATGTATGTATAATTGGATG	287325	119521	CCAGCTGCCATGAGGAGCAC
198152	30348	AAGATCCAAGCAGCTTGGAA	242739	74935	GGATGTATGTATAATTGGAT	287326	119522	CCCAGCTGCCATGAGGAGCA
198153	30349	CAAGATCCAAGCAGCTTGGA	242740	74936	TGGATGTATGTATAATTGGA	287327	119523	TCCCAGCTGCCATGAGGAGC
198154	30350	CCAAGATCCAAGCAGCTTGG	242741	74937	TTGGATGTATGTATAATTGG	287328	119524	TTCCCAGCTGCCATGAGGAG
198155	30351	ACCAAGATCCAAGCAGCTTG	242742	74938	ATTGGATGTATGTATAATTG	287329	119525	GTTCCCAGCTGCCATGAGGA
198156	30352	CACCAAGATCCAAGCAGCTT	242743	74939	GATTGGATGTATGTATAATT	287330	119526	GGTTCCCAGCTGCCATGAGG
198157	30353	GCACCAAGATCCAAGCAGCT	242744	74940	TGATTGGATGTATGTATAAT	287331	119527	TGGTTCCCAGCTGCCATGAG
198158	30354	AGCACCAAGATCCAAGCAGC	242745	74941	ATGATTGGATGTATGTATAA	287332	119528	GTGGTTCCCAGCTGCCATGA
198159	30355	CAGCACCAAGATCCAAGCAG	242746	74942	TATGATTGGATGTATGTATA	287333	119529	AGTGGTTCCCAGCTGCCATG
198160	30356	TCAGCACCAAGATCCAAGCA	242747	74943	ATATGATTGGATGTATGTAT	287334	119530	CAGTGGTTCCCAGCTGCCAT
198161	30357	TTCAGCACCAAGATCCAAGC	242748	74944	TATATGATTGGATGTATGTA	287335	119531	ACAGTGGTTCCCAGCTGCCA
198162	30358	ATTCAGCACCAAGATCCAAG	242749	74945	ATATATGATTGGATGTATGT	287336	119532	GACAGTGGTTCCCAGCTGCC
198163	30359	AATTCAGCACCAAGATCCAA	242750	74946	GATATATGATTGGATGTATG	287337	119533	GGACAGTGGTTCCCAGCTGC
198164	30360	TAATTCAGCACCAAGATCCA	242751	74947	AGATATATGATTGGATGTAT	287338	119534	TGGACAGTGGTTCCCAGCTG
198165	30361	CTAATTCAGCACCAAGATCC	242752	74948	CAGATATATGATTGGATGTA	287339	119535	TTGGACAGTGGTTCCCAGCT
198166	30362	CCTAATTCAGCACCAAGATC	242753	74949	ACAGATATATGATTGGATGT	287340	119536	ATTGGACAGTGGTTCCCAGC
198167	30363	ACCTAATTCAGCACCAAGAT	242754	74950	TACAGATATATGATTGGATG	287341	119537	TATTGGACAGTGGTTCCCAG
198168	30364	AACCTAATTCAGCACCAAGA	242755	74951	GTACAGATATATGATTGGAT	287342	119538	TTATTGGACAGTGGTTCCCA
198169	30365	CAACCTAATTCAGCACCAAG	242756	74952	TGTACAGATATATGATTGGA	287343	119539	CTTATTGGACAGTGGTTCCC
198170	30366	CCAACCTAATTCAGCACCAA	242757	74953	ATGTACAGATATATGATTGG	287344	119540	CCTTATTGGACAGTGGTTCC
198171	30367	TCCAACCTAATTCAGCACCA	242758	74954	TATGTACAGATATATGATTG	287345	119541	CCCTTATTGGACAGTGGTTC
198172	30368	GTCCAACCTAATTCAGCACC	242759	74955	TTATGTACAGATATATGATT	287346	119542	GCCCTTATTGGACAGTGGTT
198173	30369	AGTCCAACCTAATTCAGCAC	242760	74956	ATTATGTACAGATATATGAT	287347	119543	GGCCCTTATTGGACAGTGGT
198174	30370	AAGTCCAACCTAATTCAGCA	242761	74957	GATTATGTACAGATATATGA	287348	119544	AGGCCCTTATTGGACAGTGG
198175	30371	AAAGTCCAACCTAATTCAGC	242762	74958	GGATTATGTACAGATATATG	287349	119545	CAGGCCCTTATTGGACAGTG
198176	30372	CAAAGTCCAACCTAATTCAG	242763	74959	TGGATTATGTACAGATATAT	287350	119546	CCAGGCCCTTATTGGACAGT
198177	30373	ACAAAGTCCAACCTAATTCA	242764	74960	ATGGATTATGTACAGATATA	287351	119547	CCCAGGCCCTTATTGGACAG
198178	30374	GACAAAGTCCAACCTAATTC	242765	74961	AATGGATTATGTACAGATAT	287352	119548	GCCCAGGCCCTTATTGGACA
198179	30375	AGACAAAGTCCAACCTAATT	242766	74962	GAATGGATTATGTACAGATA	287353	119549	AGCCCAGGCCCTTATTGGAC
198180	30376	AAGACAAAGTCCAACCTAAT	242767	74963	AGAATGGATTATGTACAGAT	287354	119550	AAGCCCAGGCCCTTATTGGA
198181	30377	CAAGACAAAGTCCAACCTAA	242768	74964	AAGAATGGATTATGTACAGA	287355	119551	TAAGCCCAGGCCCTTATTGG
198182	30378	ACAAGACAAAGTCCAACCTA	242769	74965	GAAGAATGGATTATGTACAG	287356	119552	GTAAGCCCAGGCCCTTATTG
198183	30379	CACAAGACAAAGTCCAACCT	242770	74966	GGAAGAATGGATTATGTACA	287357	119553	TGTAAGCCCAGGCCCTTATT
198184	30380	CCACAAGACAAAGTCCAACC	242771	74967	GGGAAGAATGGATTATGTAC	287358	119554	GTGTAAGCCCAGGCCCTTAT
198185	30381	CCCACAAGACAAAGTCCAAC	242772	74968	AGGGAAGAATGGATTATGTA	287359	119555	TGTGTAAGCCCAGGCCCTTA
198186	30382	CCCCACAAGACAAAGTCCAA	242773	74969	GAGGGAAGAATGGATTATGT	287360	119556	CTGTGTAAGCCCAGGCCCTT

198187	30383	TCCCCACAAGACAAAGTCCA	242774	74970	CGAGGGAAGAATGGATTATG	287361	119557	GCTGTGTAAGCCCAGGCCCT
198188	30384	TTCCCCACAAGACAAAGTCC	242775	74971	CCGAGGGAAGAATGGATTAT	287362	119558	AGCTGTGTAAGCCCAGGCCC
198189	30385	CTTCCCCACAAGACAAAGTC	242776	74972	ACCGAGGGAAGAATGGATTA	287363	119559	CAGCTGTGTAAGCCCAGGCC
198190	30386	CCTTCCCCACAAGACAAAGT	242777	74973	AACCGAGGGAAGAATGGATT	287364	119560	GCAGCTGTGTAAGCCCAGGC
198191	30387	CCCTTCCCCACAAGACAAAG	242778	74974	GAACCGAGGGAAGAATGGAT	287365	119561	AGCAGCTGTGTAAGCCCAGG
198192	30388	TCCCTTCCCCACAAGACAAA	242779	74975	TGAACCGAGGGAAGAATGGA	287366	119562	AAGCAGCTGTGTAAGCCCAG
198193	30389	CTCCCTTCCCCACAAGACAA	242780	74976	ATGAACCGAGGGAAGAATGG	287367	119563	GAAGCAGCTGTGTAAGCCCA
198194	30390	CCTCCCTTCCCCACAAGACA	242781	74977	GATGAACCGAGGGAAGAATG	287368	119564	AGAAGCAGCTGTGTAAGCCC
198195	30391	TCCTCCCTTCCCCACAAGAC	242782	74978	GGATGAACCGAGGGAAGAAT	287369	119565	GAGAAGCAGCTGTGTAAGCC
198196	30392	GTCCTCCCTTCCCCACAAGA	242783	74979	TGGATGAACCGAGGGAAGAA	287370	119566	TGAGAAGCAGCTGTGTAAGC
198197	30393	AGTCCTCCCTTCCCCACAAG	242784	74980	ATGGATGAACCGAGGGAAGA	287371	119567	ATGAGAAGCAGCTGTGTAAG
198198	30394	TAGTCCTCCCTTCCCCACAA	242785	74981	GATGGATGAACCGAGGGAAG	287372	119568	AATGAGAAGCAGCTGTGTAA
198199	30395	ATAGTCCTCCCTTCCCCACA	242786	74982	GGATGGATGAACCGAGGGAA	287373	119569	CAATGAGAAGCAGCTGTGTA
198200	30396	TATAGTCCTCCCTTCCCCAC	242787	74983	TGGATGGATGAACCGAGGGA	287374	119570	TCAATGAGAAGCAGCTGTGT
198201	30397	CTATAGTCCTCCCTTCCCCA	242788	74984	ATGGATGGATGAACCGAGGG	287375	119571	CTCAATGAGAAGCAGCTGTG
198202	30398	TCTATAGTCCTCCCTTCCCC	242789	74985	GATGGATGGATGAACCGAGG	287376	119572	ACTCAATGAGAAGCAGCTGT
198203	30399	GTCTATAGTCCTCCCTTCCC	242790	74986	GGATGGATGGATGAACCGAG	287377	119573	AACTCAATGAGAAGCAGCTG
198204	30400	GGTCTATAGTCCTCCCTTCC	242791	74987	TGGATGGATGGATGAACCGA	287378	119574	TAACTCAATGAGAAGCAGCT
198205	30401	GGGTCTATAGTCCTCCCTTC	242792	74988	ATGGATGGATGGATGAACCG	287379	119575	GTAACTCAATGAGAAGCAGC
198206	30402	AGGGTCTATAGTCCTCCCTT	242793	74989	AATGGATGGATGGATGAACC	287380	119576	TGTAACTCAATGAGAAGCAG
198207	30403	GAGGGTCTATAGTCCTCCCT	242794	74990	GAATGGATGGATGGATGAAC	287381	119577	GTGTAACTCAATGAGAAGCA
198208	30404	TGAGGGTCTATAGTCCTCCC	242795	74991	TGAATGGATGGATGGATGAA	287382	119578	GGTGTAACTCAATGAGAAGC
198209	30405	TTGAGGGTCTATAGTCCTCC	242796	74992	ATGAATGGATGGATGGATGA	287383	119579	GGGTGTAACTCAATGAGAAG
198210	30406	GTTGAGGGTCTATAGTCCTC	242797	74993	GATGAATGGATGGATGGATG	287384	119580	AGGGTGTAACTCAATGAGAA
198211	30407	CGTTGAGGGTCTATAGTCCT	242798	74994	GGATGAATGGATGGATGGAT	287385	119581	AAGGGTGTAACTCAATGAGA
198212	30408	ACGTTGAGGGTCTATAGTCC	242799	74995	TGGATGAATGGATGGATGGA	287386	119582	TAAGGGTGTAACTCAATGAG
198213	30409	TACGTTGAGGGTCTATAGTC	242800	74996	ATGGATGAATGGATGGATGG	287387	119583	TTAAGGGTGTAACTCAATGA
198214	30410	TTACGTTGAGGGTCTATAGT	242801	74997	GATGGATGAATGGATGGATG	287388	119584	ATTAAGGGTGTAACTCAATG
198215	30411	CTTACGTTGAGGGTCTATAG	242802	74998	GGATGGATGAATGGATGGAT	287389	119585	TATTAAGGGTGTAACTCAAT
198216	30412	GCTTACGTTGAGGGTCTATA	242803	74999	TGGATGGATGAATGGATGGA	287390	119586	TTATTAAGGGTGTAACTCAA
198217	30413	TGCTTACGTTGAGGGTCTAT	242804	75000	ATGGATGGATGAATGGATGG	287391	119587	TTTATTAAGGGTGTAACTCA
198218	30414	TTGCTTACGTTGAGGGTCTA	242805	75001	GATGGATGGATGAATGGATG	287392	119588	TTTTATTAAGGGTGTAACTC
198219	30415	ATTGCTTACGTTGAGGGTCT	242806	75002	GGATGGATGGATGAATGGAT	287393	119589	ATTTTATTAAGGGTGTAACT
198220	30416	CATTGCTTACGTTGAGGGTC	242807	75003	TGGATGGATGGATGAATGGA	287394	119590	TATTTTATTAAGGGTGTAAC
198221	30417	CCATTGCTTACGTTGAGGGT	242808	75004	GTGGATGGATGGATGAATGG	287395	119591	TTATTTTATTAAGGGTGTAA
198222	30418	ACCATTGCTTACGTTGAGGG	242809	75005	GGTGGATGGATGGATGAATG	287396	119592	ATTATTTTATTAAGGGTGTA
198223	30419	GACCATTGCTTACGTTGAGG	242810	75006	GGGTGGATGGATGGATGAAT	287397	119593	GATTATTTTATTAAGGGTGT
198224	30420	TGACCATTGCTTACGTTGAG	242811	75007	TGGGTGGATGGATGGATGAA	287398	119594	GGATTATTTTATTAAGGGTG
198225	30421	CTGACCATTGCTTACGTTGA	242812	75008	ATGGGTGGATGGATGGATGA	287399	119595	GGGATTATTTTATTAAGGGT
198226	30422	TCTGACCATTGCTTACGTTG	242813	75009	GATGGGTGGATGGATGGATG	287400	119596	TGGGATTATTTTATTAAGGG
198227	30423	GTCTGACCATTGCTTACGTT	242814	75010	GGATGGGTGGATGGATGGAT	287401	119597	ATGGGATTATTTTATTAAGG
198228	30424	AGTCTGACCATTGCTTACGT	242815	75011	GGGATGGGTGGATGGATGGA	287402	119598	AATGGGATTATTTTATTAAG
198229	30425	TAGTCTGACCATTGCTTACG	242816	75012	AGGGATGGGTGGATGGATGG	287403	119599	AAATGGGATTATTTTATTAA
198230	30426	ATAGTCTGACCATTGCTTAC	242817	75013	AAGGGATGGGTGGATGGATG	287404	119600	AAAATGGGATTATTTTATTA
198231	30427	AATAGTCTGACCATTGCTTA	242818	75014	GAAGGGATGGGTGGATGGAT	287405	119601	TAAAATGGGATTATTTTATT
198232	30428	GAATAGTCTGACCATTGCTT	242819	75015	GGAAGGGATGGGTGGATGGA	287406	119602	ATAAAATGGGATTATTTTAT
198233	30429	AGAATAGTCTGACCATTGCT	242820	75016	AGGAAGGGATGGGTGGATGG	287407	119603	GATAAAATGGGATTATTTTA
198234	30430	TAGAATAGTCTGACCATTGC	242821	75017	AAGGAAGGGATGGGTGGATG	287408	119604	GGATAAAATGGGATTATTTT
198235	30431	TTAGAATAGTCTGACCATTG	242822	75018	GAAGGAAGGGATGGGTGGAT	287409	119605	AGGATAAAATGGGATTATTT
198236	30432	CTTAGAATAGTCTGACCATT	242823	75019	TGAAGGAAGGGATGGGTGGA	287410	119606	AAGGATAAAATGGGATTATT
198237	30433	TCTTAGAATAGTCTGACCAT	242824	75020	ATGAAGGAAGGGATGGGTGG	287411	119607	AAAGGATAAAATGGGATTAT
198238	30434	TTCTTAGAATAGTCTGACCA	242825	75021	GATGAAGGAAGGGATGGGTG	287412	119608	AAAAGGATAAAATGGGATTA
198239	30435	TTTCTTAGAATAGTCTGACC	242826	75022	GGATGAAGGAAGGGATGGGT	287413	119609	AAAAAGGATAAAATGGGATT
198240	30436	TTTTCTTAGAATAGTCTGAC	242827	75023	AGGATGAAGGAAGGGATGGG	287414	119610	CAAAAAGGATAAAATGGGAT
198241	30437	GTTTTCTTAGAATAGTCTGA	242828	75024	AAGGATGAAGGAAGGGATGG	287415	119611	ACAAAAAGGATAAAATGGGA
198242	30438	AGTTTTCTTAGAATAGTCTG	242829	75025	GAAGGATGAAGGAAGGGATG	287416	119612	GACAAAAAGGATAAAATGGG
198243	30439	GAGTTTTCTTAGAATAGTCT	242830	75026	GGAAGGATGAAGGAAGGGAT	287417	119613	AGACAAAAAGGATAAAATGG
198244	30440	CGAGTTTTCTTAGAATAGTC	242831	75027	AGGAAGGATGAAGGAAGGGA	287418	119614	GAGACAAAAAGGATAAAATG
198245	30441	GCGAGTTTTCTTAGAATAGT	242832	75028	TAGGAAGGATGAAGGAAGGG	287419	119615	AGAGACAAAAAGGATAAAAT
198246	30442	GGCGAGTTTTCTTAGAATAG	242833	75029	ATAGGAAGGATGAAGGAAGG	287420	119616	GAGAGACAAAAAGGATAAAA
198247	30443	CGGCGAGTTTTCTTAGAATA	242834	75030	GATAGGAAGGATGAAGGAAG	287421	119617	AGAGAGACAAAAAGGATAAA
198248	30444	TCGGCGAGTTTTCTTAGAAT	242835	75031	TGATAGGAAGGATGAAGGAA	287422	119618	CAGAGAGACAAAAAGGATAA
198249	30445	TTCGGCGAGTTTTCTTAGAA	242836	75032	ATGATAGGAAGGATGAAGGA	287423	119619	ACAGAGAGACAAAAAGGATA
198250	30446	ATTCGGCGAGTTTTCTTAGA	242837	75033	GATGATAGGAAGGATGAAGG	287424	119620	GACAGAGAGACAAAAAGGAT
198251	30447	AATTCGGCGAGTTTTCTTAG	242838	75034	GGATGATAGGAAGGATGAAG	287425	119621	AGACAGAGAGACAAAAAGGA
198252	30448	TAATTCGGCGAGTTTTCTTA	242839	75035	TGGATGATAGGAAGGATGAA	287426	119622	AAGACAGAGAGACAAAAAGG
198253	30449	TTAATTCGGCGAGTTTTCTT	242840	75036	ATGGATGATAGGAAGGATGA	287427	119623	GAAGACAGAGAGACAAAAAG
198254	30450	TTTAATTCGGCGAGTTTTCT	242841	75037	GATGGATGATAGGAAGGATG	287428	119624	GGAAGACAGAGAGACAAAAA
198255	30451	CTTTAATTCGGCGAGTTTTC	242842	75038	GGATGGATGATAGGAAGGAT	287429	119625	AGGAAGACAGAGAGACAAAA
198256	30452	GCTTTAATTCGGCGAGTTTT	242843	75039	TGGATGGATGATAGGAAGGA	287430	119626	GAGGAAGACAGAGAGACAAA
198257	30453	TGCTTTAATTCGGCGAGTTT	242844	75040	TTGGATGGATGATAGGAAGG	287431	119627	AGAGGAAGACAGAGAGACAA
198258	30454	ATGCTTTAATTCGGCGAGTT	242845	75041	ATTGGATGGATGATAGGAAG	287432	119628	GAGAGGAAGACAGAGAGACA

198259	30455	CATGCTTTAATTCGGCGAGT	242846	75042	GATTGGATGGATGATAGGAA	287433	119629	AGAGAGGAAGACAGAGAGAC
198260	30456	TCATGCTTTAATTCGGCGAG	242847	75043	TGATTGGATGGATGATAGGA	287434	119630	GAGAGAGGAAGACAGAGAGA
198261	30457	CTCATGCTTTAATTCGGCGA	242848	75044	ATGATTGGATGGATGATAGG	287435	119631	AGAGAGAGGAAGACAGAGAG
198262	30458	CCTCATGCTTTAATTCGGCG	242849	75045	TATGATTGGATGGATGATAG	287436	119632	GAGAGAGAGGAAGACAGAGA
198263	30459	ACCTCATGCTTTAATTCGGC	242850	75046	ATATGATTGGATGGATGATA	287437	119633	AGAGAGAGAGGAAGACAGAG
198264	30460	TACCTCATGCTTTAATTCGG	242851	75047	TATATGATTGGATGGATGAT	287438	119634	CAGAGAGAGAGGAAGACAGA
198265	30461	TTACCTCATGCTTTAATTCG	242852	75048	ATATATGATTGGATGGATGA	287439	119635	GCAGAGAGAGAGGAAGACAG
198266	30462	TTTACCTCATGCTTTAATTC	242853	75049	GATATATGATTGGATGGATG	287440	119636	GGCAGAGAGAGAGGAAGACA
198267	30463	ATTTACCTCATGCTTTAATT	242854	75050	AGATATATGATTGGATGGAT	287441	119637	AGGCAGAGAGAGAGGAAGAC
198268	30464	AATTTACCTCATGCTTTAAT	242855	75051	CAGATATATGATTGGATGGA	287442	119638	AAGGCAGAGAGAGAGGAAGA
198269	30465	AAATTTACCTCATGCTTTAA	242856	75052	ACAGATATATGATTGGATGG	287443	119639	AAAGGCAGAGAGAGAGGAAG
198270	30466	TAAATTTACCTCATGCTTTA	242857	75053	TACAGATATATGATTGGATG	287444	119640	GAAAGGCAGAGAGAGAGGAA
198271	30467	CTAAATTTACCTCATGCTTT	242858	75054	GTACAGATATATGATTGGAT	287445	119641	GGAAAGGCAGAGAGAGAGGA
198272	30468	ACTAAATTTACCTCATGCTT	242859	75055	TGTACAGATATATGATTGGA	287446	119642	AGGAAAGGCAGAGAGAGAGG
198273	30469	AACTAAATTTACCTCATGCT	242860	75056	ATGTACAGATATATGATTGG	287447	119643	GAGGAAAGGCAGAGAGAGAG
198274	30470	GAACTAAATTTACCTCATGC	242861	75057	TATGTACAGATATATGATTG	287448	119644	AGAGGAAAGGCAGAGAGAGA
198275	30471	AGAACTAAATTTACCTCATG	242862	75058	TTATGTACAGATATATGATT	287449	119645	AAGAGGAAAGGCAGAGAGAG
198276	30472	CAGAACTAAATTTACCTCAT	242863	75059	ATTATGTACAGATATATGAT	287450	119646	GAAGAGGAAAGGCAGAGAGA
198277	30473	TCAGAACTAAATTTACCTCA	242864	75060	GATTATGTACAGATATATGA	287451	119647	AGAAGAGGAAAGGCAGAGAG
198278	30474	GTCAGAACTAAATTTACCTC	242865	75061	GGATTATGTACAGATATATG	287452	119648	GAGAAGAGGAAAGGCAGAGA
198279	30475	AGTCAGAACTAAATTTACCT	242866	75062	TGGATTATGTACAGATATAT	287453	119649	AGAGAAGAGGAAAGGCAGAG
198280	30476	AAGTCAGAACTAAATTTACC	242867	75063	ATGGATTATGTACAGATATA	287454	119650	GAGAGAAGAGGAAAGGCAGA
198281	30477	GAAGTCAGAACTAAATTTAC	242868	75064	AATGGATTATGTACAGATAT	287455	119651	AGAGAGAAGAGGAAAGGCAG
198282	30478	AGAAGTCAGAACTAAATTTA	242869	75065	GAATGGATTATGTACAGATA	287456	119652	GAGAGAGAAGAGGAAAGGCA
198283	30479	CAGAAGTCAGAACTAAATTT	242870	75066	AGAATGGATTATGTACAGAT	287457	119653	GGAGAGAGAAGAGGAAAGGC
198284	30480	ACAGAAGTCAGAACTAAATT	242871	75067	AAGAATGGATTATGTACAGA	287458	119654	AGGAGAGAGAAGAGGAAAGG
198285	30481	GACAGAAGTCAGAACTAAAT	242872	75068	GAAGAATGGATTATGTACAG	287459	119655	GAGGAGAGAGAAGAGGAAAG
198286	30482	GGACAGAAGTCAGAACTAAA	242873	75069	GGAAGAATGGATTATGTACA	287460	119656	GGAGGAGAGAGAAGAGGAAA
198287	30483	TGGACAGAAGTCAGAACTAA	242874	75070	GGGAAGAATGGATTATGTAC	287461	119657	AGGAGGAGAGAGAAGAGGAA
198288	30484	GTGGACAGAAGTCAGAACTA	242875	75071	AGGGAAGAATGGATTATGTA	287462	119658	GAGGAGGAGAGAGAAGAGGA
198289	30485	GGTGGACAGAAGTCAGAACT	242876	75072	GAGGGAAGAATGGATTATGT	287463	119659	AGAGGAGGAGAGAGAAGAGG
198290	30486	GGGTGGACAGAAGTCAGAAC	242877	75073	CGAGGGAAGAATGGATTATG	287464	119660	GAGAGGAGGAGAGAGAAGAG
198291	30487	GGGGTGGACAGAAGTCAGAA	242878	75074	CCGAGGGAAGAATGGATTAT	287465	119661	AGAGAGGAGGAGAGAGAAGA
198292	30488	TGGGGTGGACAGAAGTCAGA	242879	75075	ACCGAGGGAAGAATGGATTA	287466	119662	GAGAGAGGAGGAGAGAGAAG
198293	30489	GTGGGGTGGACAGAAGTCAG	242880	75076	AACCGAGGGAAGAATGGATT	287467	119663	TGAGAGAGGAGGAGAGAGAA
198294	30490	AGTGGGGTGGACAGAAGTCA	242881	75077	GAACCGAGGGAAGAATGGAT	287468	119664	ATGAGAGAGGAGGAGAGAGA
198295	30491	CAGTGGGGTGGACAGAAGTC	242882	75078	TGAACCGAGGGAAGAATGGA	287469	119665	GATGAGAGAGGAGGAGAGAG
198296	30492	GCAGTGGGGTGGACAGAAGT	242883	75079	ATGAACCGAGGGAAGAATGG	287470	119666	AGATGAGAGAGGAGGAGAGA
198297	30493	GGCAGTGGGGTGGACAGAAG	242884	75080	GATGAACCGAGGGAAGAATG	287471	119667	GAGATGAGAGAGGAGGAGAG
198298	30494	TGGCAGTGGGGTGGACAGAA	242885	75081	GGATGAACCGAGGGAAGAAT	287472	119668	GGAGATGAGAGAGGAGGAGA
198299	30495	GTGGCAGTGGGGTGGACAGA	242886	75082	TGGATGAACCGAGGGAAGAA	287473	119669	TGGAGATGAGAGAGGAGGAG
198300	30496	AGTGGCAGTGGGGTGGACAG	242887	75083	ATGGATGAACCGAGGGAAGA	287474	119670	CTGGAGATGAGAGAGGAGGA
198301	30497	CAGTGGCAGTGGGGTGGACA	242888	75084	GATGGATGAACCGAGGGAAG	287475	119671	CCTGGAGATGAGAGAGGAGG
198302	30498	ACAGTGGCAGTGGGGTGGAC	242889	75085	GGATGGATGAACCGAGGGAA	287476	119672	ACCTGGAGATGAGAGAGGAG
198303	30499	GACAGTGGCAGTGGGGTGGA	242890	75086	TGGATGGATGAACCGAGGGA	287477	119673	CACCTGGAGATGAGAGAGGA
198304	30500	GGACAGTGGCAGTGGGGTGG	242891	75087	ATGGATGGATGAACCGAGGG	287478	119674	GCACCTGGAGATGAGAGAGG
198305	30501	GGGACAGTGGCAGTGGGGTG	242892	75088	GATGGATGGATGAACCGAGG	287479	119675	TGCACCTGGAGATGAGAGAG
198306	30502	GGGGACAGTGGCAGTGGGGT	242893	75089	GGATGGATGGATGAACCGAG	287480	119676	TTGCACCTGGAGATGAGAGA
198307	30503	AGGGGACAGTGGCAGTGGGG	242894	75090	TGGATGGATGGATGAACCGA	287481	119677	TTTGCACCTGGAGATGAGAG
198308	30504	AAGGGGACAGTGGCAGTGGG	242895	75091	ATGGATGGATGGATGAACCG	287482	119678	ATTTGCACCTGGAGATGAGA
198309	30505	AAAGGGGACAGTGGCAGTGG	242896	75092	AATGGATGGATGGATGAACC	287483	119679	TATTTGCACCTGGAGATGAG
198310	30506	AAAAGGGGACAGTGGCAGTG	242897	75093	GAATGGATGGATGGATGAAC	287484	119680	CTATTTGCACCTGGAGATGA
198311	30507	TAAAAGGGGACAGTGGCAGT	242898	75094	TGAATGGATGGATGGATGAA	287485	119681	ACTATTTGCACCTGGAGATG
198312	30508	ATAAAAGGGGACAGTGGCAG	242899	75095	ATGAATGGATGGATGGATGA	287486	119682	GACTATTTGCACCTGGAGAT
198313	30509	GATAAAAGGGGACAGTGGCA	242900	75096	GATGAATGGATGGATGGATG	287487	119683	AGACTATTTGCACCTGGAGA
198314	30510	GGATAAAAGGGGACAGTGGC	242901	75097	GGATGAATGGATGGATGGAT	287488	119684	TAGACTATTTGCACCTGGAG
198315	30511	GGGATAAAAGGGGACAGTGG	242902	75098	TGGATGAATGGATGGATGGA	287489	119685	GTAGACTATTTGCACCTGGA
198316	30512	TGGGATAAAAGGGGACAGTG	242903	75099	ATGGATGAATGGATGGATGG	287490	119686	TGTAGACTATTTGCACCTGG
198317	30513	ATGGGATAAAAGGGGACAGT	242904	75100	GATGGATGAATGGATGGATG	287491	119687	TTGTAGACTATTTGCACCTG
198318	30514	CATGGGATAAAAGGGGACAG	242905	75101	GGATGGATGAATGGATGGAT	287492	119688	TTTGTAGACTATTTGCACCT
198319	30515	TCATGGGATAAAAGGGGACA	242906	75102	TGGATGGATGAATGGATGGA	287493	119689	GTTTGTAGACTATTTGCACC
198320	30516	ATCATGGGATAAAAGGGGAC	242907	75103	ATGGATGGATGAATGGATGG	287494	119690	GGTTTGTAGACTATTTGCAC
198321	30517	GATCATGGGATAAAAGGGGA	242908	75104	GATGGATGGATGAATGGATG	287495	119691	TGGTTTGTAGACTATTTGCA
198322	30518	GGATCATGGGATAAAAGGGG	242909	75105	GGATGGATGGATGAATGGAT	287496	119692	CTGGTTTGTAGACTATTTGC
198323	30519	GGGATCATGGGATAAAAGGG	242910	75106	TGGATGGATGGATGAATGGA	287497	119693	ACTGGTTTGTAGACTATTTG
198324	30520	AGGGATCATGGGATAAAAGG	242911	75107	GTGGATGGATGGATGAATGG	287498	119694	AACTGGTTTGTAGACTATTT
198325	30521	AAGGGATCATGGGATAAAAG	242912	75108	GGTGGATGGATGGATGAATG	287499	119695	CAACTGGTTTGTAGACTATT
198326	30522	CAAGGGATCATGGGATAAAA	242913	75109	GGGTGGATGGATGGATGAAT	287500	119696	TCAACTGGTTTGTAGACTAT
198327	30523	GCAAGGGATCATGGGATAAA	242914	75110	TGGGTGGATGGATGGATGAA	287501	119697	GTCAACTGGTTTGTAGACTA
198328	30524	AGCAAGGGATCATGGGATAA	242915	75111	ATGGGTGGATGGATGGATGA	287502	119698	GGTCAACTGGTTTGTAGACT
198329	30525	AAGCAAGGGATCATGGGATA	242916	75112	GATGGGTGGATGGATGGATG	287503	119699	AGGTCAACTGGTTTGTAGAC
198330	30526	AAAGCAAGGGATCATGGGAT	242917	75113	GGATGGGTGGATGGATGGAT	287504	119700	CAGGTCAACTGGTTTGTAGA

198331	30527	AAAAGCAAGGGATCATGGGA	242918	75114	GGGATGGGTGGATGGATGGA	287505	119701	TCAGGTCAACTGGTTTGTAG
198332	30528	GAAAAGCAAGGGATCATGGG	242919	75115	AGGGATGGGTGGATGGATGG	287506	119702	CTCAGGTCAACTGGTTTGTA
198333	30529	AGAAAAGCAAGGGATCATGG	242920	75116	AAGGGATGGGTGGATGGATG	287507	119703	GCTCAGGTCAACTGGTTTGT
198334	30530	AAGAAAAGCAAGGGATCATG	242921	75117	GAAGGGATGGGTGGATGGAT	287508	119704	TGCTCAGGTCAACTGGTTTG
198335	30531	AAAGAAAAGCAAGGGATCAT	242922	75118	GGAAGGGATGGGTGGATGGA	287509	119705	TTGCTCAGGTCAACTGGTTT
198336	30532	AAAAGAAAAGCAAGGGATCA	242923	75119	AGGAAGGGATGGGTGGATGG	287510	119706	CTTGCTCAGGTCAACTGGTT
198337	30533	GAAAAGAAAAGCAAGGGATC	242924	75120	AAGGAAGGGATGGGTGGATG	287511	119707	CCTTGCTCAGGTCAACTGGT
198338	30534	GGAAAAGAAAAGCAAGGGAT	242925	75121	GAAGGAAGGGATGGGTGGAT	287512	119708	ACCTTGCTCAGGTCAACTGG
198339	30535	AGGAAAAGAAAAGCAAGGGA	242926	75122	TGAAGGAAGGGATGGGTGGA	287513	119709	CACCTTGCTCAGGTCAACTG
198340	30536	GAGGAAAAGAAAAGCAAGGG	242927	75123	ATGAAGGAAGGGATGGGTGG	287514	119710	TCACCTTGCTCAGGTCAACT
198341	30537	GGAGGAAAAGAAAAGCAAGG	242928	75124	GATGAAGGAAGGGATGGGTG	287515	119711	GTCACCTTGCTCAGGTCAAC
198342	30538	AGGAGGAAAAGAAAAGCAAG	242929	75125	GGATGAAGGAAGGGATGGGT	287516	119712	GGTCACCTTGCTCAGGTCAA
198343	30539	GAGGAGGAAAAGAAAAGCAA	242930	75126	AGGATGAAGGAAGGGATGGG	287517	119713	AGGTCACCTTGCTCAGGTCA
198344	30540	AGAGGAGGAAAAGAAAAGCA	242931	75127	AAGGATGAAGGAAGGGATGG	287518	119714	GAGGTCACCTTGCTCAGGTC
198345	30541	GAGAGGAGGAAAAGAAAAGC	242932	75128	GAAGGATGAAGGAAGGGATG	287519	119715	GGAGGTCACCTTGCTCAGGT
198346	30542	AGAGAGGAGGAAAAGAAAAG	242933	75129	GGAAGGATGAAGGAAGGGAT	287520	119716	TGGAGGTCACCTTGCTCAGG
198347	30543	GAGAGAGGAGGAAAAGAAAA	242934	75130	AGGAAGGATGAAGGAAGGGA	287521	119717	TTGGAGGTCACCTTGCTCAG
198348	30544	GGAGAGAGGAGGAAAAGAAA	242935	75131	TAGGAAGGATGAAGGAAGGG	287522	119718	CTTGGAGGTCACCTTGCTCA
198349	30545	GGGAGAGAGGAGGAAAAGAA	242936	75132	ATAGGAAGGATGAAGGAAGG	287523	119719	ACTTGGAGGTCACCTTGCTC
198350	30546	AGGGAGAGAGGAGGAAAAGA	242937	75133	GATAGGAAGGATGAAGGAAG	287524	119720	CACTTGGAGGTCACCTTGCT
198351	30547	TAGGGAGAGAGGAGGAAAAG	242938	75134	TGATAGGAAGGATGAAGGAA	287525	119721	ACACTTGGAGGTCACCTTGC
198352	30548	ATAGGGAGAGAGGAGGAAAA	242939	75135	ATGATAGGAAGGATGAAGGA	287526	119722	CACACTTGGAGGTCACCTTG
198353	30549	GATAGGGAGAGAGGAGGAAA	242940	75136	GATGATAGGAAGGATGAAGG	287527	119723	CCACACTTGGAGGTCACCTT
198354	30550	AGATAGGGAGAGAGGAGGAA	242941	75137	GGATGATAGGAAGGATGAAG	287528	119724	GCCACACTTGGAGGTCACCT
198355	30551	GAGATAGGGAGAGAGGAGGA	242942	75138	TGGATGATAGGAAGGATGAA	287529	119725	AGCCACACTTGGAGGTCACC
198356	30552	AGAGATAGGGAGAGAGGAGG	242943	75139	ATGGATGATAGGAAGGATGA	287530	119726	GAGCCACACTTGGAGGTCAC
198357	30553	AAGAGATAGGGAGAGAGGAG	242944	75140	GATGGATGATAGGAAGGATG	287531	119727	TGAGCCACACTTGGAGGTCA
198358	30554	CAAGAGATAGGGAGAGAGGA	242945	75141	GGATGGATGATAGGAAGGAT	287532	119728	ATGAGCCACACTTGGAGGTC
198359	30555	ACAAGAGATAGGGAGAGAGG	242946	75142	TGGATGGATGATAGGAAGGA	287533	119729	AATGAGCCACACTTGGAGGT
198360	30556	CACAAGAGATAGGGAGAGAG	242947	75143	TTGGATGGATGATAGGAAGG	287534	119730	TAATGAGCCACACTTGGAGG
198361	30557	ACACAAGAGATAGGGAGAGA	242948	75144	ATTGGATGGATGATAGGAAG	287535	119731	CTAATGAGCCACACTTGGAG
198362	30558	AACACAAGAGATAGGGAGAG	242949	75145	GATTGGATGGATGATAGGAA	287536	119732	CCTAATGAGCCACACTTGGA
198363	30559	AAACACAAGAGATAGGGAGA	242950	75146	TGATTGGATGGATGATAGGA	287537	119733	GCCTAATGAGCCACACTTGG
198364	30560	CAAACACAAGAGATAGGGAG	242951	75147	ATGATTGGATGGATGATAGG	287538	119734	TGCCTAATGAGCCACACTTG
198365	30561	TCAAACACAAGAGATAGGGA	242952	75148	TATGATTGGATGGATGATAG	287539	119735	TTGCCTAATGAGCCACACTT
198366	30562	GTCAAACACAAGAGATAGGG	242953	75149	GTATGATTGGATGGATGATA	287540	119736	GTTGCCTAATGAGCCACACT
198367	30563	CGTCAAACACAAGAGATAGG	242954	75150	TGTATGATTGGATGGATGAT	287541	119737	TGTTGCCTAATGAGCCACAC
198368	30564	GCGTCAAACACAAGAGATAG	242955	75151	ATGTATGATTGGATGGATGA	287542	119738	ATGTTGCCTAATGAGCCACA
198369	30565	TGCGTCAAACACAAGAGATA	242956	75152	TATGTATGATTGGATGGATG	287543	119739	GATGTTGCCTAATGAGCCAC
198370	30566	ATGCGTCAAACACAAGAGAT	242957	75153	ATATGTATGATTGGATGGAT	287544	119740	GGATGTTGCCTAATGAGCCA
198371	30567	CATGCGTCAAACACAAGAGA	242958	75154	TATATGTATGATTGGATGGA	287545	119741	TGGATGTTGCCTAATGAGCC
198372	30568	TCATGCGTCAAACACAAGAG	242959	75155	ATATATGTATGATTGGATGG	287546	119742	ATGGATGTTGCCTAATGAGC
198373	30569	ATCATGCGTCAAACACAAGA	242960	75156	GATATATGTATGATTGGATG	287547	119743	GATGGATGTTGCCTAATGAG
198374	30570	TATCATGCGTCAAACACAAG	242961	75157	GGATATATGTATGATTGGAT	287548	119744	TGATGGATGTTGCCTAATGA
198375	30571	CTATCATGCGTCAAACACAA	242962	75158	TGGATATATGTATGATTGGA	287549	119745	ATGATGGATGTTGCCTAATG
198376	30572	CCTATCATGCGTCAAACACA	242963	75159	TTGGATATATGTATGATTGG	287550	119746	TATGATGGATGTTGCCTAAT
198377	30573	TCCTATCATGCGTCAAACAC	242964	75160	ATTGGATATATGTATGATTG	287551	119747	TTATGATGGATGTTGCCTAA
198378	30574	TTCCTATCATGCGTCAAACA	242965	75161	GATTGGATATATGTATGATT	287552	119748	TTTATGATGGATGTTGCCTA
198379	30575	ATTCCTATCATGCGTCAAAC	242966	75162	TGATTGGATATATGTATGAT	287553	119749	GTTTATGATGGATGTTGCCT
198380	30576	AATTCCTATCATGCGTCAAA	242967	75163	ATGATTGGATATATGTATGA	287554	119750	GGTTTATGATGGATGTTGCC
198381	30577	GAATTCCTATCATGCGTCAA	242968	75164	TATGATTGGATATATGTATG	287555	119751	TGGTTTATGATGGATGTTGC
198382	30578	TGAATTCCTATCATGCGTCA	242969	75165	GTATGATTGGATATATGTAT	287556	119752	CTGGTTTATGATGGATGTTG
198383	30579	CTGAATTCCTATCATGCGTC	242970	75166	TGTATGATTGGATATATGTA	287557	119753	CCTGGTTTATGATGGATGTT
198384	30580	TCTGAATTCCTATCATGCGT	242971	75167	ATGTATGATTGGATATATGT	287558	119754	ACCTGGTTTATGATGGATGT
198385	30581	TTCTGAATTCCTATCATGCG	242972	75168	GATGTATGATTGGATATATG	287559	119755	TACCTGGTTTATGATGGATG
198386	30582	TTTCTGAATTCCTATCATGC	242973	75169	AGATGTATGATTGGATATAT	287560	119756	CTACCTGGTTTATGATGGAT
198387	30583	ATTTCTGAATTCCTATCATG	242974	75170	CAGATGTATGATTGGATATA	287561	119757	GCTACCTGGTTTATGATGGA
198388	30584	TATTTCTGAATTCCTATCAT	242975	75171	GCAGATGTATGATTGGATAT	287562	119758	GGCTACCTGGTTTATGATGG
198389	30585	ATATTTCTGAATTCCTATCA	242976	75172	TGCAGATGTATGATTGGATA	287563	119759	GGGCTACCTGGTTTATGATG
198390	30586	TATATTTCTGAATTCCTATC	242977	75173	GTGCAGATGTATGATTGGAT	287564	119760	AGGGCTACCTGGTTTATGAT
198391	30587	ATATATTTCTGAATTCCTAT	242978	75174	TGTGCAGATGTATGATTGGA	287565	119761	CAGGGCTACCTGGTTTATGA
198392	30588	CATATATTTCTGAATTCCTA	242979	75175	ATGTGCAGATGTATGATTGG	287566	119762	ACAGGGCTACCTGGTTTATG
198393	30589	ACATATATTTCTGAATTCCT	242980	75176	GATGTGCAGATGTATGATTG	287567	119763	CACAGGGCTACCTGGTTTAT
198394	30590	AACATATATTTCTGAATTCC	242981	75177	TGATGTGCAGATGTATGATT	287568	119764	CCACAGGGCTACCTGGTTTA
198395	30591	AAACATATATTTCTGAATTC	242982	75178	GTGATGTGCAGATGTATGAT	287569	119765	TCCACAGGGCTACCTGGTTT
198396	30592	CAAACATATATTTCTGAATT	242983	75179	GGTGATGTGCAGATGTATGA	287570	119766	TTCCACAGGGCTACCTGGTT
198397	30593	ACAAACATATATTTCTGAAT	242984	75180	TGGTGATGTGCAGATGTATG	287571	119767	CTTCCACAGGGCTACCTGGT
198398	30594	CACAAACATATATTTCTGAA	242985	75181	CTGGTGATGTGCAGATGTAT	287572	119768	CCTTCCACAGGGCTACCTGG
198399	30595	CCACAAACATATATTTCTGA	242986	75182	GCTGGTGATGTGCAGATGTA	287573	119769	ACCTTCCACAGGGCTACCTG
198400	30596	TCCACAAACATATATTTCTG	242987	75183	AGCTGGTGATGTGCAGATGT	287574	119770	CACCTTCCACAGGGCTACCT
198401	30597	ATCCACAAACATATATTTCT	242988	75184	GAGCTGGTGATGTGCAGATG	287575	119771	TCACCTTCCACAGGGCTACC
198402	30598	AATCCACAAACATATATTTC	242989	75185	TGAGCTGGTGATGTGCAGAT	287576	119772	CTCACCTTCCACAGGGCTAC

198403	30599	AAATCCACAAACATATATTT	242990	75186	ATGAGCTGGTGATGTGCAGA	287577	119773	CCTCACCTTCCACAGGGCTA
198404	30600	CAAATCCACAAACATATATT	242991	75187	GATGAGCTGGTGATGTGCAG	287578	119774	CCCTCACCTTCCACAGGGCT
198405	30601	ACAAATCCACAAACATATAT	242992	75188	GGATGAGCTGGTGATGTGCA	287579	119775	ACCCTCACCTTCCACAGGGC
198406	30602	AACAAATCCACAAACATATA	242993	75189	TGGATGAGCTGGTGATGTGC	287580	119776	AACCCTCACCTTCCACAGGG
198407	30603	AAACAAATCCACAAACATAT	242994	75190	ATGGATGAGCTGGTGATGTG	287581	119777	CAACCCTCACCTTCCACAGG
198408	30604	TAAACAAATCCACAAACATA	242995	75191	GATGGATGAGCTGGTGATGT	287582	119778	CCAACCCTCACCTTCCACAG
198409	30605	ATAAACAAATCCACAAACAT	242996	75192	AGATGGATGAGCTGGTGATG	287583	119779	CCCAACCCTCACCTTCCACA
198410	30606	AATAAACAAATCCACAAACA	242997	75193	TAGATGGATGAGCTGGTGAT	287584	119780	TCCCAACCCTCACCTTCCAC
198411	30607	GAATAAACAAATCCACAAAC	242998	75194	ATAGATGGATGAGCTGGTGA	287585	119781	GTCCCAACCCTCACCTTCCA
198412	30608	TGAATAAACAAATCCACAAA	242999	75195	GATAGATGGATGAGCTGGTG	287586	119782	CGTCCCAACCCTCACCTTCC
198413	30609	GTGAATAAACAAATCCACAA	243000	75196	GGATAGATGGATGAGCTGGT	287587	119783	CCGTCCCAACCCTCACCTTC
198414	30610	CGTGAATAAACAAATCCACA	243001	75197	TGGATAGATGGATGAGCTGG	287588	119784	CCCGTCCCAACCCTCACCTT
198415	30611	ACGTGAATAAACAAATCCAC	243002	75198	ATGGATAGATGGATGAGCTG	287589	119785	TCCCGTCCCAACCCTCACCT
198416	30612	TACGTGAATAAACAAATCCA	243003	75199	AATGGATAGATGGATGAGCT	287590	119786	CTCCCGTCCCAACCCTCACC
198417	30613	CTACGTGAATAAACAAATCC	243004	75200	AAATGGATAGATGGATGAGC	287591	119787	CCTCCCGTCCCAACCCTCAC
198418	30614	GCTACGTGAATAAACAAATC	243005	75201	TAAATGGATAGATGGATGAG	287592	119788	CCCTCCCGTCCCAACCCTCA
198419	30615	TGCTACGTGAATAAACAAAT	243006	75202	ATAAATGGATAGATGGATGA	287593	119789	ACCCTCCCGTCCCAACCCTC
198420	30616	TTGCTACGTGAATAAACAAA	243007	75203	GATAAATGGATAGATGGATG	287594	119790	CACCCTCCCGTCCCAACCCT
198421	30617	TTTGCTACGTGAATAAACAA	243008	75204	GGATAAATGGATAGATGGAT	287595	119791	GCACCCTCCCGTCCCAACCC
198422	30618	GTTTGCTACGTGAATAAACA	243009	75205	TGGATAAATGGATAGATGGA	287596	119792	TGCACCCTCCCGTCCCAACC
198423	30619	GGTTTGCTACGTGAATAAAC	243010	75206	ATGGATAAATGGATAGATGG	287597	119793	CTGCACCCTCCCGTCCCAAC
198424	30620	TGGTTTGCTACGTGAATAAA	243011	75207	GATGGATAAATGGATAGATG	287598	119794	CCTGCACCCTCCCGTCCCAA
198425	30621	ATGGTTTGCTACGTGAATAA	243012	75208	GGATGGATAAATGGATAGAT	287599	119795	CCCTGCACCCTCCCGTCCCA
198426	30622	AATGGTTTGCTACGTGAATA	243013	75209	TGGATGGATAAATGGATAGA	287600	119796	CCCCTGCACCCTCCCGTCCC
198427	30623	AAATGGTTTGCTACGTGAAT	243014	75210	ATGGATGGATAAATGGATAG	287601	119797	CCCCCTGCACCCTCCCGTCC
198428	30624	GAAATGGTTTGCTACGTGAA	243015	75211	GATGGATGGATAAATGGATA	287602	119798	ACCCCCTGCACCCTCCCGTC
198429	30625	AGAAATGGTTTGCTACGTGA	243016	75212	GGATGGATGGATAAATGGAT	287603	119799	CACCCCCTGCACCCTCCCGT
198430	30626	AAGAAATGGTTTGCTACGTG	243017	75213	AGGATGGATGGATAAATGGA	287604	119800	CCACCCCCTGCACCCTCCCG
198431	30627	CAAGAAATGGTTTGCTACGT	243018	75214	AAGGATGGATGGATAAATGG	287605	119801	TCCACCCCCTGCACCCTCCC
198432	30628	TCAAGAAATGGTTTGCTACG	243019	75215	GAAGGATGGATGGATAAATG	287606	119802	CTCCACCCCCTGCACCCTCC
198433	30629	CTCAAGAAATGGTTTGCTAC	243020	75216	GGAAGGATGGATGGATAAAT	287607	119803	CCTCCACCCCCTGCACCCTC
198434	30630	ACTCAAGAAATGGTTTGCTA	243021	75217	AGGAAGGATGGATGGATAAA	287608	119804	TCCTCCACCCCCTGCACCCT
198435	30631	CACTCAAGAAATGGTTTGCT	243022	75218	AAGGAAGGATGGATGGATAA	287609	119805	CTCCTCCACCCCCTGCACCC
198436	30632	GCACTCAAGAAATGGTTTGC	243023	75219	GAAGGAAGGATGGATGGATA	287610	119806	ACTCCTCCACCCCCTGCACC
198437	30633	GGCACTCAAGAAATGGTTTG	243024	75220	GGAAGGAAGGATGGATGGAT	287611	119807	GACTCCTCCACCCCCTGCAC
198438	30634	AGGCACTCAAGAAATGGTTT	243025	75221	TGGAAGGAAGGATGGATGGA	287612	119808	GGACTCCTCCACCCCCTGCA
198439	30635	TAGGCACTCAAGAAATGGTT	243026	75222	ATGGAAGGAAGGATGGATGG	287613	119809	AGGACTCCTCCACCCCCTGC
198440	30636	GTAGGCACTCAAGAAATGGT	243027	75223	GATGGAAGGAAGGATGGATG	287614	119810	CAGGACTCCTCCACCCCCTG
198441	30637	GGTAGGCACTCAAGAAATGG	243028	75224	GGATGGAAGGAAGGATGGAT	287615	119811	CCAGGACTCCTCCACCCCCT
198442	30638	TGGTAGGCACTCAAGAAATG	243029	75225	TGGATGGAAGGAAGGATGGA	287616	119812	ACCAGGACTCCTCCACCCCC
198443	30639	ATGGTAGGCACTCAAGAAAT	243030	75226	ATGGATGGAAGGAAGGATGG	287617	119813	CACCAGGACTCCTCCACCCC
198444	30640	CATGGTAGGCACTCAAGAAA	243031	75227	GATGGATGGAAGGAAGGATG	287618	119814	TCACCAGGACTCCTCCACCC
198445	30641	CCATGGTAGGCACTCAAGAA	243032	75228	TGATGGATGGAAGGAAGGAT	287619	119815	CTCACCAGGACTCCTCCACC
198446	30642	CCCATGGTAGGCACTCAAGA	243033	75229	ATGATGGATGGAAGGAAGGA	287620	119816	CCTCACCAGGACTCCTCCAC
198447	30643	GCCCATGGTAGGCACTCAAG	243034	75230	AATGATGGATGGAAGGAAGG	287621	119817	GCCTCACCAGGACTCCTCCA
198448	30644	GGCCCATGGTAGGCACTCAA	243035	75231	GAATGATGGATGGAAGGAAG	287622	119818	AGCCTCACCAGGACTCCTCC
198449	30645	TGGCCCATGGTAGGCACTCA	243036	75232	TGAATGATGGATGGAAGGAA	287623	119819	CAGCCTCACCAGGACTCCTC
198450	30646	CTGGCCCATGGTAGGCACTC	243037	75233	ATGAATGATGGATGGAAGGA	287624	119820	CCAGCCTCACCAGGACTCCT
198451	30647	CCTGGCCCATGGTAGGCACT	243038	75234	GATGAATGATGGATGGAAGG	287625	119821	TCCAGCCTCACCAGGACTCC
198452	30648	ACCTGGCCCATGGTAGGCAC	243039	75235	GGATGAATGATGGATGGAAG	287626	119822	TTCCAGCCTCACCAGGACTC
198453	30649	TACCTGGCCCATGGTAGGCA	243040	75236	TGGATGAATGATGGATGGAA	287627	119823	GTTCCAGCCTCACCAGGACT
198454	30650	CTACCTGGCCCATGGTAGGC	243041	75237	ATGGATGAATGATGGATGGA	287628	119824	AGTTCCAGCCTCACCAGGAC
198455	30651	TCTACCTGGCCCATGGTAGG	243042	75238	GATGGATGAATGATGGATGG	287629	119825	CAGTTCCAGCCTCACCAGGA
198456	30652	TTCTACCTGGCCCATGGTAG	243043	75239	TGATGGATGAATGATGGATG	287630	119826	GCAGTTCCAGCCTCACCAGG
198457	30653	ATTCTACCTGGCCCATGGTA	243044	75240	ATGATGGATGAATGATGGAT	287631	119827	AGCAGTTCCAGCCTCACCAG
198458	30654	CATTCTACCTGGCCCATGGT	243045	75241	TATGATGGATGAATGATGGA	287632	119828	GAGCAGTTCCAGCCTCACCA
198459	30655	CCATTCTACCTGGCCCATGG	243046	75242	GTATGATGGATGAATGATGG	287633	119829	GGAGCAGTTCCAGCCTCACC
198460	30656	CCCATTCTACCTGGCCCATG	243047	75243	TGTATGATGGATGAATGATG	287634	119830	TGGAGCAGTTCCAGCCTCAC
198461	30657	GCCCATTCTACCTGGCCCAT	243048	75244	ATGTATGATGGATGAATGAT	287635	119831	CTGGAGCAGTTCCAGCCTCA
198462	30658	CGCCCATTCTACCTGGCCCA	243049	75245	TATGTATGATGGATGAATGA	287636	119832	TCTGGAGCAGTTCCAGCCTC
198463	30659	CCGCCCATTCTACCTGGCCC	243050	75246	GTATGTATGATGGATGAATG	287637	119833	GTCTGGAGCAGTTCCAGCCT
198464	30660	GCCGCCCATTCTACCTGGCC	243051	75247	TGTATGTATGATGGATGAAT	287638	119834	AGTCTGGAGCAGTTCCAGCC
198465	30661	GGCCGCCCATTCTACCTGGC	243052	75248	ATGTATGTATGATGGATGAA	287639	119835	AAGTCTGGAGCAGTTCCAGC
198466	30662	GGGCCGCCCATTCTACCTGG	243053	75249	GATGTATGTATGATGGATGA	287640	119836	GAAGTCTGGAGCAGTTCCAG
198467	30663	GGGGCCGCCCATTCTACCTG	243054	75250	AGATGTATGTATGATGGATG	287641	119837	TGAAGTCTGGAGCAGTTCCA
198468	30664	CGGGGCCGCCCATTCTACCT	243055	75251	TAGATGTATGTATGATGGAT	287642	119838	CTGAAGTCTGGAGCAGTTCC
198469	30665	CCGGGGCCGCCCATTCTACC	243056	75252	TTAGATGTATGTATGATGGA	287643	119839	TCTGAAGTCTGGAGCAGTTC
198470	30666	CCCGGGGCCGCCCATTCTAC	243057	75253	GTTAGATGTATGTATGATGG	287644	119840	TTCTGAAGTCTGGAGCAGTT
198471	30667	GCCCGGGGCCGCCCATTCTA	243058	75254	GGTTAGATGTATGTATGATG	287645	119841	CTTCTGAAGTCTGGAGCAGT
198472	30668	AGCCCGGGGCCGCCCATTCT	243059	75255	TGGTTAGATGTATGTATGAT	287646	119842	CCTTCTGAAGTCTGGAGCAG
198473	30669	CAGCCCGGGGCCGCCCATTC	243060	75256	ATGGTTAGATGTATGTATGA	287647	119843	CCCTTCTGAAGTCTGGAGCA
198474	30670	GCAGCCCGGGGCCGCCCATT	243061	75257	TATGGTTAGATGTATGTATG	287648	119844	CCCCTTCTGAAGTCTGGAGC

198475	30671	TGCAGCCCGGGGCCGCCCAT	243062	75258	GTATGGTTAGATGTATGTAT	287649	119845	GCCCCTTCTGAAGTCTGGAG
198476	30672	CTGCAGCCCGGGGCCGCCCA	243063	75259	TGTATGGTTAGATGTATGTA	287650	119846	AGCCCCTTCTGAAGTCTGGA
198477	30673	ACTGCAGCCCGGGGCCGCCC	243064	75260	ATGTATGGTTAGATGTATGT	287651	119847	CAGCCCCTTCTGAAGTCTGG
198478	30674	CACTGCAGCCCGGGGCCGCC	243065	75261	GATGTATGGTTAGATGTATG	287652	119848	CCAGCCCCTTCTGAAGTCTG
198479	30675	CCACTGCAGCCCGGGGCCGC	243066	75262	AGATGTATGGTTAGATGTAT	287653	119849	TCCAGCCCCTTCTGAAGTCT
198480	30676	ACCACTGCAGCCCGGGGCCG	243067	75263	GAGATGTATGGTTAGATGTA	287654	119850	TTCCAGCCCCTTCTGAAGTC
198481	30677	AACCACTGCAGCCCGGGGCC	243068	75264	AGAGATGTATGGTTAGATGT	287655	119851	TTTCCAGCCCCTTCTGAAGT
198482	30678	AAACCACTGCAGCCCGGGGC	243069	75265	TAGAGATGTATGGTTAGATG	287656	119852	CTTTCCAGCCCCTTCTGAAG
198483	30679	GAAACCACTGCAGCCCGGGG	243070	75266	GTAGAGATGTATGGTTAGAT	287657	119853	CCTTTCCAGCCCCTTCTGAA
198484	30680	AGAAACCACTGCAGCCCGGG	243071	75267	TGTAGAGATGTATGGTTAGA	287658	119854	TCCTTTCCAGCCCCTTCTGA
198485	30681	AAGAAACCACTGCAGCCCGG	243072	75268	ATGTAGAGATGTATGGTTAG	287659	119855	ATCCTTTCCAGCCCCTTCTG
198486	30682	GAAGAAACCACTGCAGCCCG	243073	75269	GATGTAGAGATGTATGGTTA	287660	119856	TATCCTTTCCAGCCCCTTCT
198487	30683	TGAAGAAACCACTGCAGCCC	243074	75270	TGATGTAGAGATGTATGGTT	287661	119857	ATATCCTTTCCAGCCCCTTC
198488	30684	CTGAAGAAACCACTGCAGCC	243075	75271	ATGATGTAGAGATGTATGGT	287662	119858	AATATCCTTTCCAGCCCCTT
198489	30685	GCTGAAGAAACCACTGCAGC	243076	75272	AATGATGTAGAGATGTATGG	287663	119859	AAATATCCTTTCCAGCCCCT
198490	30686	GGCTGAAGAAACCACTGCAG	243077	75273	GAATGATGTAGAGATGTATG	287664	119860	AAAATATCCTTTCCAGCCCC
198491	30687	GGGCTGAAGAAACCACTGCA	243078	75274	TGAATGATGTAGAGATGTAT	287665	119861	TAAAATATCCTTTCCAGCCC
198492	30688	GGGGCTGAAGAAACCACTGC	243079	75275	ATGAATGATGTAGAGATGTA	287666	119862	CTAAAATATCCTTTCCAGCC
198493	30689	AGGGGCTGAAGAAACCACTG	243080	75276	AATGAATGATGTAGAGATGT	287667	119863	CCTAAAATATCCTTTCCAGC
198494	30690	GAGGGGCTGAAGAAACCACT	243081	75277	GAATGAATGATGTAGAGATG	287668	119864	ACCTAAAATATCCTTTCCAG
198495	30691	AGAGGGGCTGAAGAAACCAC	243082	75278	AGAATGAATGATGTAGAGAT	287669	119865	TACCTAAAATATCCTTTCCA
198496	30692	GAGAGGGGCTGAAGAAACCA	243083	75279	AAGAATGAATGATGTAGAGA	287670	119866	CTACCTAAAATATCCTTTCC
198497	30693	GGAGAGGGGCTGAAGAAACC	243084	75280	GAAGAATGAATGATGTAGAG	287671	119867	TCTACCTAAAATATCCTTTC
198498	30694	TGGAGAGGGGCTGAAGAAAC	243085	75281	GGAAGAATGAATGATGTAGA	287672	119868	GTCTACCTAAAATATCCTTT
198499	30695	CTGGAGAGGGGCTGAAGAAA	243086	75282	TGGAAGAATGAATGATGTAG	287673	119869	GGTCTACCTAAAATATCCTT
198500	30696	CCTGGAGAGGGGCTGAAGAA	243087	75283	ATGGAAGAATGAATGATGTA	287674	119870	AGGTCTACCTAAAATATCCT
198501	30697	CCCTGGAGAGGGGCTGAAGA	243088	75284	GATGGAAGAATGAATGATGT	287675	119871	TAGGTCTACCTAAAATATCC
198502	30698	ACCCTGGAGAGGGGCTGAAG	243089	75285	CGATGGAAGAATGAATGATG	287676	119872	GTAGGTCTACCTAAAATATC
198503	30699	AACCCTGGAGAGGGGCTGAA	243090	75286	TCGATGGAAGAATGAATGAT	287677	119873	TGTAGGTCTACCTAAAATAT
198504	30700	AAACCCTGGAGAGGGGCTGA	243091	75287	ATCGATGGAAGAATGAATGA	287678	119874	ATGTAGGTCTACCTAAAATA
198505	30701	TAAACCCTGGAGAGGGGCTG	243092	75288	AATCGATGGAAGAATGAATG	287679	119875	GATGTAGGTCTACCTAAAAT
198506	30702	GTAAACCCTGGAGAGGGGCT	243093	75289	GAATCGATGGAAGAATGAAT	287680	119876	TGATGTAGGTCTACCTAAAA
198507	30703	TGTAAACCCTGGAGAGGGGC	243094	75290	TGAATCGATGGAAGAATGAA	287681	119877	TTGATGTAGGTCTACCTAAA
198508	30704	GTGTAAACCCTGGAGAGGGG	243095	75291	ATGAATCGATGGAAGAATGA	287682	119878	CTTGATGTAGGTCTACCTAA
198509	30705	AGTGTAAACCCTGGAGAGGG	243096	75292	GATGAATCGATGGAAGAATG	287683	119879	CCTTGATGTAGGTCTACCTA
198510	30706	CAGTGTAAACCCTGGAGAGG	243097	75293	GGATGAATCGATGGAAGAAT	287684	119880	TCCTTGATGTAGGTCTACCT
198511	30707	ACAGTGTAAACCCTGGAGAG	243098	75294	TGGATGAATCGATGGAAGAA	287685	119881	TTCCTTGATGTAGGTCTACC
198512	30708	CACAGTGTAAACCCTGGAGA	243099	75295	TTGGATGAATCGATGGAAGA	287686	119882	TTTCCTTGATGTAGGTCTAC
198513	30709	GCACAGTGTAAACCCTGGAG	243100	75296	ATTGGATGAATCGATGGAAG	287687	119883	CTTTCCTTGATGTAGGTCTA
198514	30710	TGCACAGTGTAAACCCTGGA	243101	75297	AATTGGATGAATCGATGGAA	287688	119884	ACTTTCCTTGATGTAGGTCT
198515	30711	TTGCACAGTGTAAACCCTGG	243102	75298	TAATTGGATGAATCGATGGA	287689	119885	CACTTTCCTTGATGTAGGTC
198516	30712	CTTGCACAGTGTAAACCCTG	243103	75299	ATAATTGGATGAATCGATGG	287690	119886	ACACTTTCCTTGATGTAGGT
198517	30713	TCTTGCACAGTGTAAACCCT	243104	75300	GATAATTGGATGAATCGATG	287691	119887	AACACTTTCCTTGATGTAGG
198518	30714	GTCTTGCACAGTGTAAACCC	243105	75301	GGATAATTGGATGAATCGAT	287692	119888	CAACACTTTCCTTGATGTAG
198519	30715	CGTCTTGCACAGTGTAAACC	243106	75302	TGGATAATTGGATGAATCGA	287693	119889	TCAACACTTTCCTTGATGTA
198520	30716	CCGTCTTGCACAGTGTAAAC	243107	75303	ATGGATAATTGGATGAATCG	287694	119890	CTCAACACTTTCCTTGATGT
198521	30717	ACCGTCTTGCACAGTGTAAA	243108	75304	GATGGATAATTGGATGAATC	287695	119891	ACTCAACACTTTCCTTGATG
198522	30718	AACCGTCTTGCACAGTGTAA	243109	75305	TGATGGATAATTGGATGAAT	287696	119892	CACTCAACACTTTCCTTGAT
198523	30719	AAACCGTCTTGCACAGTGTA	243110	75306	ATGATGGATAATTGGATGAA	287697	119893	ACACTCAACACTTTCCTTGA
198524	30720	CAAACCGTCTTGCACAGTGT	243111	75307	AATGATGGATAATTGGATGA	287698	119894	CACACTCAACACTTTCCTTG
198525	30721	ACAAACCGTCTTGCACAGTG	243112	75308	GAATGATGGATAATTGGATG	287699	119895	TCACACTCAACACTTTCCTT
198526	30722	CACAAACCGTCTTGCACAGT	243113	75309	GGAATGATGGATAATTGGAT	287700	119896	TTCACACTCAACACTTTCCT
198527	30723	TCACAAACCGTCTTGCACAG	243114	75310	AGGAATGATGGATAATTGGA	287701	119897	TTTCACACTCAACACTTTCC
198528	30724	ATCACAAACCGTCTTGCACA	243115	75311	AAGGAATGATGGATAATTGG	287702	119898	GTTTCACACTCAACACTTTC
198529	30725	CATCACAAACCGTCTTGCAC	243116	75312	GAAGGAATGATGGATAATTG	287703	119899	AGTTTCACACTCAACACTTT
198530	30726	CCATCACAAACCGTCTTGCA	243117	75313	GGAAGGAATGATGGATAATT	287704	119900	AAGTTTCACACTCAACACTT
198531	30727	CCCATCACAAACCGTCTTGC	243118	75314	AGGAAGGAATGATGGATAAT	287705	119901	CAAGTTTCACACTCAACACT
198532	30728	ACCCATCACAAACCGTCTTG	243119	75315	GAGGAAGGAATGATGGATAA	287706	119902	GCAAGTTTCACACTCAACAC
198533	30729	GACCCATCACAAACCGTCTT	243120	75316	GGAGGAAGGAATGATGGATA	287707	119903	CGCAAGTTTCACACTCAACA
198534	30730	GGACCCATCACAAACCGTCT	243121	75317	TGGAGGAAGGAATGATGGAT	287708	119904	CCGCAAGTTTCACACTCAAC
198535	30731	AGGACCCATCACAAACCGTC	243122	75318	ATGGAGGAAGGAATGATGGA	287709	119905	CCCGCAAGTTTCACACTCAA
198536	30732	GAGGACCCATCACAAACCGT	243123	75319	GATGGAGGAAGGAATGATGG	287710	119906	TCCCGCAAGTTTCACACTCA
198537	30733	GGAGGACCCATCACAAACCG	243124	75320	GGATGGAGGAAGGAATGATG	287711	119907	CTCCCGCAAGTTTCACACTC
198538	30734	GGGAGGACCCATCACAAACC	243125	75321	TGGATGGAGGAAGGAATGAT	287712	119908	GCTCCCGCAAGTTTCACACT
198539	30735	TGGGAGGACCCATCACAAAC	243126	75322	ATGGATGGAGGAAGGAATGA	287713	119909	GGCTCCCGCAAGTTTCACAC
198540	30736	ATGGGAGGACCCATCACAAA	243127	75323	GATGGATGGAGGAAGGAATG	287714	119910	GGGCTCCCGCAAGTTTCACA
198541	30737	GATGGGAGGACCCATCACAA	243128	75324	GGATGGATGGAGGAAGGAAT	287715	119911	TGGGCTCCCGCAAGTTTCAC
198542	30738	CGATGGGAGGACCCATCACA	243129	75325	GGGATGGATGGAGGAAGGAA	287716	119912	CTGGGCTCCCGCAAGTTTCA
198543	30739	TCGATGGGAGGACCCATCAC	243130	75326	TGGGATGGATGGAGGAAGGA	287717	119913	CCTGGGCTCCCGCAAGTTTC
198544	30740	CTCGATGGGAGGACCCATCA	243131	75327	ATGGGATGGATGGAGGAAGG	287718	119914	TCCTGGGCTCCCGCAAGTTT
198545	30741	CCTCGATGGGAGGACCCATC	243132	75328	AATGGGATGGATGGAGGAAG	287719	119915	CTCCTGGGCTCCCGCAAGTT
198546	30742	TCCTCGATGGGAGGACCCAT	243133	75329	TAATGGGATGGATGGAGGAA	287720	119916	CCTCCTGGGCTCCCGCAAGT

198547	30743	GTCCTCGATGGGAGGACCCA	243134	75330	ATAATGGGATGGATGGAGGA	287721	119917	GCCTCCTGGGCTCCCGCAAG
198548	30744	GGTCCTCGATGGGAGGACCC	243135	75331	GATAATGGGATGGATGGAGG	287722	119918	CGCCTCCTGGGCTCCCGCAA
198549	30745	TGGTCCTCGATGGGAGGACC	243136	75332	GGATAATGGGATGGATGGAG	287723	119919	ACGCCTCCTGGGCTCCCGCA
198550	30746	GTGGTCCTCGATGGGAGGAC	243137	75333	TGGATAATGGGATGGATGGA	287724	119920	CACGCCTCCTGGGCTCCCGC
198551	30747	TGTGGTCCTCGATGGGAGGA	243138	75334	ATGGATAATGGGATGGATGG	287725	119921	CCACGCCTCCTGGGCTCCCG
198552	30748	GTGTGGTCCTCGATGGGAGG	243139	75335	AATGGATAATGGGATGGATG	287726	119922	ACCACGCCTCCTGGGCTCCC
198553	30749	AGTGTGGTCCTCGATGGGAG	243140	75336	AAATGGATAATGGGATGGAT	287727	119923	CACCACGCCTCCTGGGCTCC
198554	30750	GAGTGTGGTCCTCGATGGGA	243141	75337	CAAATGGATAATGGGATGGA	287728	119924	CCACCACGCCTCCTGGGCTC
198555	30751	AGAGTGTGGTCCTCGATGGG	243142	75338	TCAAATGGATAATGGGATGG	287729	119925	GCCACCACGCCTCCTGGGCT
198556	30752	AAGAGTGTGGTCCTCGATGG	243143	75339	ATCAAATGGATAATGGGATG	287730	119926	AGCCACCACGCCTCCTGGGC
198557	30753	GAAGAGTGTGGTCCTCGATG	243144	75340	GATCAAATGGATAATGGGAT	287731	119927	GAGCCACCACGCCTCCTGGG
198558	30754	AGAAGAGTGTGGTCCTCGAT	243145	75341	TGATCAAATGGATAATGGGA	287732	119928	GGAGCCACCACGCCTCCTGG
198559	30755	AAGAAGAGTGTGGTCCTCGA	243146	75342	ATGATCAAATGGATAATGGG	287733	119929	TGGAGCCACCACGCCTCCTG
198560	30756	AAAGAAGAGTGTGGTCCTCG	243147	75343	TATGATCAAATGGATAATGG	287734	119930	CTGGAGCCACCACGCCTCCT
198561	30757	GAAAGAAGAGTGTGGTCCTC	243148	75344	GTATGATCAAATGGATAATG	287735	119931	GCTGGAGCCACCACGCCTCC
198562	30758	AGAAAGAAGAGTGTGGTCCT	243149	75345	TGTATGATCAAATGGATAAT	287736	119932	AGCTGGAGCCACCACGCCTC
198563	30759	GAGAAAGAAGAGTGTGGTCC	243150	75346	ATGTATGATCAAATGGATAA	287737	119933	GAGCTGGAGCCACCACGCCT
198564	30760	AGAGAAAGAAGAGTGTGGTC	243151	75347	TATGTATGATCAAATGGATA	287738	119934	CGAGCTGGAGCCACCACGCC
198565	30761	CAGAGAAAGAAGAGTGTGGT	243152	75348	ATATGTATGATCAAATGGAT	287739	119935	GCGAGCTGGAGCCACCACGC
198566	30762	ACAGAGAAAGAAGAGTGTGG	243153	75349	TATATGTATGATCAAATGGA	287740	119936	AGCGAGCTGGAGCCACCACG
198567	30763	CACAGAGAAAGAAGAGTGTG	243154	75350	ATATATGTATGATCAAATGG	287741	119937	GAGCGAGCTGGAGCCACCAC
198568	30764	GCACAGAGAAAGAAGAGTGT	243155	75351	GATATATGTATGATCAAATG	287742	119938	GGAGCGAGCTGGAGCCACCA
198569	30765	GGCACAGAGAAAGAAGAGTG	243156	75352	TGATATATGTATGATCAAAT	287743	119939	AGGAGCGAGCTGGAGCCACC
198570	30766	GGGCACAGAGAAAGAAGAGT	243157	75353	ATGATATATGTATGATCAAA	287744	119940	CAGGAGCGAGCTGGAGCCAC
198571	30767	GGGGCACAGAGAAAGAAGAG	243158	75354	GATGATATATGTATGATCAA	287745	119941	GCAGGAGCGAGCTGGAGCCA
198572	30768	AGGGGCACAGAGAAAGAAGA	243159	75355	AGATGATATATGTATGATCA	287746	119942	GGCAGGAGCGAGCTGGAGCC
198573	30769	AAGGGGCACAGAGAAAGAAG	243160	75356	TAGATGATATATGTATGATC	287747	119943	GGGCAGGAGCGAGCTGGAGC
198574	30770	CAAGGGGCACAGAGAAAGAA	243161	75357	ATAGATGATATATGTATGAT	287748	119944	TGGGCAGGAGCGAGCTGGAG
198575	30771	CCAAGGGGCACAGAGAAAGA	243162	75358	TATAGATGATATATGTATGA	287749	119945	CTGGGCAGGAGCGAGCTGGA
198576	30772	ACCAAGGGGCACAGAGAAAG	243163	75359	GTATAGATGATATATGTATG	287750	119946	CCTGGGCAGGAGCGAGCTGG
198577	30773	GACCAAGGGGCACAGAGAAA	243164	75360	TGTATAGATGATATATGTAT	287751	119947	GCCTGGGCAGGAGCGAGCTG
198578	30774	GGACCAAGGGGCACAGAGAA	243165	75361	ATGTATAGATGATATATGTA	287752	119948	GGCCTGGGCAGGAGCGAGCT
198579	30775	AGGACCAAGGGGCACAGAGA	243166	75362	GATGTATAGATGATATATGT	287753	119949	TGGCCTGGGCAGGAGCGAGC
198580	30776	GAGGACCAAGGGGCACAGAG	243167	75363	TGATGTATAGATGATATATG	287754	119950	ATGGCCTGGGCAGGAGCGAG
198581	30777	TGAGGACCAAGGGGCACAGA	243168	75364	ATGATGTATAGATGATATAT	287755	119951	CATGGCCTGGGCAGGAGCGA
198582	30778	CTGAGGACCAAGGGGCACAG	243169	75365	GATGATGTATAGATGATATA	287756	119952	GCATGGCCTGGGCAGGAGCG
198583	30779	ACTGAGGACCAAGGGGCACA	243170	75366	GGATGATGTATAGATGATAT	287757	119953	AGCATGGCCTGGGCAGGAGC
198584	30780	GACTGAGGACCAAGGGGCAC	243171	75367	TGGATGATGTATAGATGATA	287758	119954	CAGCATGGCCTGGGCAGGAG
198585	30781	AGACTGAGGACCAAGGGGCA	243172	75368	ATGGATGATGTATAGATGAT	287759	119955	GCAGCATGGCCTGGGCAGGA
198586	30782	GAGACTGAGGACCAAGGGGC	243173	75369	AATGGATGATGTATAGATGA	287760	119956	GGCAGCATGGCCTGGGCAGG
198587	30783	AGAGACTGAGGACCAAGGGG	243174	75370	GAATGGATGATGTATAGATG	287761	119957	GGGCAGCATGGCCTGGGCAG
198588	30784	CAGAGACTGAGGACCAAGGG	243175	75371	TGAATGGATGATGTATAGAT	287762	119958	TGGGCAGCATGGCCTGGGCA
198589	30785	TCAGAGACTGAGGACCAAGG	243176	75372	ATGAATGGATGATGTATAGA	287763	119959	TTGGGCAGCATGGCCTGGGC
198590	30786	GTCAGAGACTGAGGACCAAG	243177	75373	GATGAATGGATGATGTATAG	287764	119960	CTTGGGCAGCATGGCCTGGG
198591	30787	GGTCAGAGACTGAGGACCAA	243178	75374	GGATGAATGGATGATGTATA	287765	119961	TCTTGGGCAGCATGGCCTGG
198592	30788	GGGTCAGAGACTGAGGACCA	243179	75375	TGGATGAATGGATGATGTAT	287766	119962	GTCTTGGGCAGCATGGCCTG
198593	30789	GGGGTCAGAGACTGAGGACC	243180	75376	ATGGATGAATGGATGATGTA	287767	119963	TGTCTTGGGCAGCATGGCCT
198594	30790	TGGGGTCAGAGACTGAGGAC	243181	75377	GATGGATGAATGGATGATGT	287768	119964	TTGTCTTGGGCAGCATGGCC
198595	30791	GTGGGGTCAGAGACTGAGGA	243182	75378	GGATGGATGAATGGATGATG	287769	119965	CTTGTCTTGGGCAGCATGGC
198596	30792	AGTGGGGTCAGAGACTGAGG	243183	75379	TGGATGGATGAATGGATGAT	287770	119966	CCTTGTCTTGGGCAGCATGG
198597	30793	AAGTGGGGTCAGAGACTGAG	243184	75380	ATGGATGGATGAATGGATGA	287771	119967	ACCTTGTCTTGGGCAGCATG
198598	30794	GAAGTGGGGTCAGAGACTGA	243185	75381	GATGGATGGATGAATGGATG	287772	119968	CACCTTGTCTTGGGCAGCAT
198599	30795	TGAAGTGGGGTCAGAGACTG	243186	75382	GGATGGATGGATGAATGGAT	287773	119969	TCACCTTGTCTTGGGCAGCA
198600	30796	TTGAAGTGGGGTCAGAGACT	243187	75383	TGGATGGATGGATGAATGGA	287774	119970	CTCACCTTGTCTTGGGCAGC
198601	30797	TTTGAAGTGGGGTCAGAGAC	243188	75384	ATGGATGGATGGATGAATGG	287775	119971	CCTCACCTTGTCTTGGGCAG
198602	30798	CTTTGAAGTGGGGTCAGAGA	243189	75385	GATGGATGGATGGATGAATG	287776	119972	GCCTCACCTTGTCTTGGGCA
198603	30799	CCTTTGAAGTGGGGTCAGAG	243190	75386	GGATGGATGGATGGATGAAT	287777	119973	CGCCTCACCTTGTCTTGGGC
198604	30800	GCCTTTGAAGTGGGGTCAGA	243191	75387	TGGATGGATGGATGGATGAA	287778	119974	CCGCCTCACCTTGTCTTGGG
198605	30801	TGCCTTTGAAGTGGGGTCAG	243192	75388	ATGGATGGATGGATGGATGA	287779	119975	CCCGCCTCACCTTGTCTTGG
198606	30802	CTGCCTTTGAAGTGGGGTCA	243193	75389	GATGGATGGATGGATGGATG	287780	119976	TCCCGCCTCACCTTGTCTTG
198607	30803	GCTGCCTTTGAAGTGGGGTC	243194	75390	GGATGGATGGATGGATGGAT	287781	119977	CTCCCGCCTCACCTTGTCTT
198608	30804	TGCTGCCTTTGAAGTGGGGT	243195	75391	TGGATGGATGGATGGATGGA	287782	119978	ACTCCCGCCTCACCTTGTCT
198609	30805	ATGCTGCCTTTGAAGTGGGG	243196	75392	GTGGATGGATGGATGGATGG	287783	119979	CACTCCCGCCTCACCTTGTC
198610	30806	AATGCTGCCTTTGAAGTGGG	243197	75393	GGTGGATGGATGGATGGATG	287784	119980	TCACTCCCGCCTCACCTTGT
198611	30807	GAATGCTGCCTTTGAAGTGG	243198	75394	GGGTGGATGGATGGATGGAT	287785	119981	TTCACTCCCGCCTCACCTTG
198612	30808	TGAATGCTGCCTTTGAAGTG	243199	75395	TGGGTGGATGGATGGATGGA	287786	119982	CTTCACTCCCGCCTCACCTT
198613	30809	GTGAATGCTGCCTTTGAAGT	243200	75396	ATGGGTGGATGGATGGATGG	287787	119983	ACTTCACTCCCGCCTCACCT
198614	30810	AGTGAATGCTGCCTTTGAAG	243201	75397	TATGGGTGGATGGATGGATG	287788	119984	CACTTCACTCCCGCCTCACC
198615	30811	GAGTGAATGCTGCCTTTGAA	243202	75398	ATATGGGTGGATGGATGGAT	287789	119985	TCACTTCACTCCCGCCTCAC
198616	30812	TGAGTGAATGCTGCCTTTGA	243203	75399	GATATGGGTGGATGGATGGA	287790	119986	TTCACTTCACTCCCGCCTCA
198617	30813	CTGAGTGAATGCTGCCTTTG	243204	75400	AGATATGGGTGGATGGATGG	287791	119987	TTTCACTTCACTCCCGCCTC
198618	30814	CCTGAGTGAATGCTGCCTTT	243205	75401	AAGATATGGGTGGATGGATG	287792	119988	ATTTCACTTCACTCCCGCCT

198619	30815	CCCTGAGTGAATGCTGCCTT	243206	75402	GAAGATATGGGTGGATGGAT	287793	119989	TATTTCACTTCACTCCCGCC
198620	30816	TCCCTGAGTGAATGCTGCCT	243207	75403	TGAAGATATGGGTGGATGGA	287794	119990	TTATTTCACTTCACTCCCGC
198621	30817	TTCCCTGAGTGAATGCTGCC	243208	75404	ATGAAGATATGGGTGGATGG	287795	119991	CTTATTTCACTTCACTCCCG
198622	30818	CTTCCCTGAGTGAATGCTGC	243209	75405	GATGAAGATATGGGTGGATG	287796	119992	CCTTATTTCACTTCACTCCC
198623	30819	GCTTCCCTGAGTGAATGCTG	243210	75406	GGATGAAGATATGGGTGGAT	287797	119993	GCCTTATTTCACTTCACTCC
198624	30820	AGCTTCCCTGAGTGAATGCT	243211	75407	TGGATGAAGATATGGGTGGA	287798	119994	TGCCTTATTTCACTTCACTC
198625	30821	GAGCTTCCCTGAGTGAATGC	243212	75408	TTGGATGAAGATATGGGTGG	287799	119995	CTGCCTTATTTCACTTCACT
198626	30822	GGAGCTTCCCTGAGTGAATG	243213	75409	ATTGGATGAAGATATGGGTG	287800	119996	CCTGCCTTATTTCACTTCAC
198627	30823	GGGAGCTTCCCTGAGTGAAT	243214	75410	GATTGGATGAAGATATGGGT	287801	119997	GCCTGCCTTATTTCACTTCA
198628	30824	TGGGAGCTTCCCTGAGTGAA	243215	75411	TGATTGGATGAAGATATGGG	287802	119998	TGCCTGCCTTATTTCACTTC
198629	30825	ATGGGAGCTTCCCTGAGTGA	243216	75412	TTGATTGGATGAAGATATGG	287803	119999	GTGCCTGCCTTATTTCACTT
198630	30826	TATGGGAGCTTCCCTGAGTG	243217	75413	ATTGATTGGATGAAGATATG	287804	120000	TGTGCCTGCCTTATTTCACT
198631	30827	GTATGGGAGCTTCCCTGAGT	243218	75414	GATTGATTGGATGAAGATAT	287805	120001	CTGTGCCTGCCTTATTTCAC
198632	30828	TGTATGGGAGCTTCCCTGAG	243219	75415	TGATTGATTGGATGAAGATA	287806	120002	TCTGTGCCTGCCTTATTTCA
198633	30829	TTGTATGGGAGCTTCCCTGA	243220	75416	ATGATTGATTGGATGAAGAT	287807	120003	TTCTGTGCCTGCCTTATTTC
198634	30830	ATTGTATGGGAGCTTCCCTG	243221	75417	TATGATTGATTGGATGAAGA	287808	120004	TTTCTGTGCCTGCCTTATTT
198635	30831	CATTGTATGGGAGCTTCCCT	243222	75418	GTATGATTGATTGGATGAAG	287809	120005	CTTTCTGTGCCTGCCTTATT
198636	30832	GCATTGTATGGGAGCTTCCC	243223	75419	TGTATGATTGATTGGATGAA	287810	120006	TCTTTCTGTGCCTGCCTTAT
198637	30833	AGCATTGTATGGGAGCTTCC	243224	75420	ATGTATGATTGATTGGATGA	287811	120007	TTCTTTCTGTGCCTGCCTTA
198638	30834	TAGCATTGTATGGGAGCTTC	243225	75421	TATGTATGATTGATTGGATG	287812	120008	TTTCTTTCTGTGCCTGCCTT
198639	30835	CTAGCATTGTATGGGAGCTT	243226	75422	GTATGTATGATTGATTGGAT	287813	120009	CTTTCTTTCTGTGCCTGCCT
198640	30836	ACTAGCATTGTATGGGAGCT	243227	75423	TGTATGTATGATTGATTGGA	287814	120010	GCTTTCTTTCTGTGCCTGCC
198641	30837	GACTAGCATTGTATGGGAGC	243228	75424	ATGTATGTATGATTGATTGG	287815	120011	TGCTTTCTTTCTGTGCCTGC
198642	30838	TGACTAGCATTGTATGGGAG	243229	75425	GATGTATGTATGATTGATTG	287816	120012	GTGCTTTCTTTCTGTGCCTG
198643	30839	CTGACTAGCATTGTATGGGA	243230	75426	CGATGTATGTATGATTGATT	287817	120013	TGTGCTTTCTTTCTGTGCCT
198644	30840	TCTGACTAGCATTGTATGGG	243231	75427	TCGATGTATGTATGATTGAT	287818	120014	ATGTGCTTTCTTTCTGTGCC
198645	30841	CTCTGACTAGCATTGTATGG	243232	75428	TTCGATGTATGTATGATTGA	287819	120015	TATGTGCTTTCTTTCTGTGC
198646	30842	ACTCTGACTAGCATTGTATG	243233	75429	ATTCGATGTATGTATGATTG	287820	120016	ATATGTGCTTTCTTTCTGTG
198647	30843	TACTCTGACTAGCATTGTAT	243234	75430	GATTCGATGTATGTATGATT	287821	120017	AATATGTGCTTTCTTTCTGT
198648	30844	TTACTCTGACTAGCATTGTA	243235	75431	TGATTCGATGTATGTATGAT	287822	120018	GAATATGTGCTTTCTTTCTG
198649	30845	TTTACTCTGACTAGCATTGT	243236	75432	ATGATTCGATGTATGTATGA	287823	120019	AGAATATGTGCTTTCTTTCT
198650	30846	TTTTACTCTGACTAGCATTG	243237	75433	GATGATTCGATGTATGTATG	287824	120020	GAGAATATGTGCTTTCTTTC
198651	30847	CTTTTACTCTGACTAGCATT	243238	75434	AGATGATTCGATGTATGTAT	287825	120021	CGAGAATATGTGCTTTCTTT
198652	30848	ACTTTTACTCTGACTAGCAT	243239	75435	TAGATGATTCGATGTATGTA	287826	120022	CCGAGAATATGTGCTTTCTT
198653	30849	AACTTTTACTCTGACTAGCA	243240	75436	GTAGATGATTCGATGTATGT	287827	120023	GCCGAGAATATGTGCTTTCT
198654	30850	AAACTTTTACTCTGACTAGC	243241	75437	TGTAGATGATTCGATGTATG	287828	120024	GGCCGAGAATATGTGCTTTC
198655	30851	CAAACTTTTACTCTGACTAG	243242	75438	GTGTAGATGATTCGATGTAT	287829	120025	CGGCCGAGAATATGTGCTTT
198656	30852	CCAAACTTTTACTCTGACTA	243243	75439	TGTGTAGATGATTCGATGTA	287830	120026	CCGGCCGAGAATATGTGCTT
198657	30853	TCCAAACTTTTACTCTGACT	243244	75440	ATGTGTAGATGATTCGATGT	287831	120027	CCCGGCCGAGAATATGTGCT
198658	30854	GTCCAAACTTTTACTCTGAC	243245	75441	GATGTGTAGATGATTCGATG	287832	120028	GCCCGGCCGAGAATATGTGC
198659	30855	TGTCCAAACTTTTACTCTGA	243246	75442	TGATGTGTAGATGATTCGAT	287833	120029	CGCCCGGCCGAGAATATGTG
198660	30856	TTGTCCAAACTTTTACTCTG	243247	75443	GTGATGTGTAGATGATTCGA	287834	120030	GCGCCCGGCCGAGAATATGT
198661	30857	TTTGTCCAAACTTTTACTCT	243248	75444	GGTGATGTGTAGATGATTCG	287835	120031	AGCGCCCGGCCGAGAATATG
198662	30858	ATTTGTCCAAACTTTTACTC	243249	75445	GGGTGATGTGTAGATGATTC	287836	120032	CAGCGCCCGGCCGAGAATAT
198663	30859	AATTTGTCCAAACTTTTACT	243250	75446	TGGGTGATGTGTAGATGATT	287837	120033	ACAGCGCCCGGCCGAGAATA
198664	30860	CAATTTGTCCAAACTTTTAC	243251	75447	ATGGGTGATGTGTAGATGAT	287838	120034	CACAGCGCCCGGCCGAGAAT
198665	30861	GCAATTTGTCCAAACTTTTA	243252	75448	GATGGGTGATGTGTAGATGA	287839	120035	CCACAGCGCCCGGCCGAGAA
198666	30862	GGCAATTTGTCCAAACTTTT	243253	75449	GGATGGGTGATGTGTAGATG	287840	120036	GCCACAGCGCCCGGCCGAGA
198667	30863	TGGCAATTTGTCCAAACTTT	243254	75450	TGGATGGGTGATGTGTAGAT	287841	120037	AGCCACAGCGCCCGGCCGAG
198668	30864	CTGGCAATTTGTCCAAACTT	243255	75451	ATGGATGGGTGATGTGTAGA	287842	120038	GAGCCACAGCGCCCGGCCGA
198669	30865	CCTGGCAATTTGTCCAAACT	243256	75452	GATGGATGGGTGATGTGTAG	287843	120039	TGAGCCACAGCGCCCGGCCG
198670	30866	TCCTGGCAATTTGTCCAAAC	243257	75453	GGATGGATGGGTGATGTGTA	287844	120040	GTGAGCCACAGCGCCCGGCC
198671	30867	TTCCTGGCAATTTGTCCAAA	243258	75454	TGGATGGATGGGTGATGTGT	287845	120041	CGTGAGCCACAGCGCCCGGC
198672	30868	CTTCCTGGCAATTTGTCCAA	243259	75455	ATGGATGGATGGGTGATGTG	287846	120042	GCGTGAGCCACAGCGCCCGG
198673	30869	GCTTCCTGGCAATTTGTCCA	243260	75456	GATGGATGGATGGGTGATGT	287847	120043	GGCGTGAGCCACAGCGCCCG
198674	30870	TGCTTCCTGGCAATTTGTCC	243261	75457	GGATGGATGGATGGGTGATG	287848	120044	AGGCGTGAGCCACAGCGCCC
198675	30871	CTGCTTCCTGGCAATTTGTC	243262	75458	TGGATGGATGGATGGGTGAT	287849	120045	CAGGCGTGAGCCACAGCGCC
198676	30872	GCTGCTTCCTGGCAATTTGT	243263	75459	ATGGATGGATGGATGGGTGA	287850	120046	ACAGGCGTGAGCCACAGCGC
198677	30873	AGCTGCTTCCTGGCAATTTG	243264	75460	GATGGATGGATGGATGGGTG	287851	120047	TACAGGCGTGAGCCACAGCG
198678	30874	AAGCTGCTTCCTGGCAATTT	243265	75461	GGATGGATGGATGGATGGGT	287852	120048	TTACAGGCGTGAGCCACAGC
198679	30875	CAAGCTGCTTCCTGGCAATT	243266	75462	TGGATGGATGGATGGATGGG	287853	120049	ATTACAGGCGTGAGCCACAG
198680	30876	ACAAGCTGCTTCCTGGCAAT	243267	75463	ATGGATGGATGGATGGATGG	287854	120050	AATTACAGGCGTGAGCCACA
198681	30877	GACAAGCTGCTTCCTGGCAA	243268	75464	AATGGATGGATGGATGGATG	287855	120051	GAATTACAGGCGTGAGCCAC
198682	30878	TGACAAGCTGCTTCCTGGCA	243269	75465	GAATGGATGGATGGATGGAT	287856	120052	GGAATTACAGGCGTGAGCCA
198683	30879	CTGACAAGCTGCTTCCTGGC	243270	75466	TGAATGGATGGATGGATGGA	287857	120053	TGGAATTACAGGCGTGAGCC
198684	30880	ACTGACAAGCTGCTTCCTGG	243271	75467	ATGAATGGATGGATGGATGG	287858	120054	CTGGAATTACAGGCGTGAGC
198685	30881	TACTGACAAGCTGCTTCCTG	243272	75468	GATGAATGGATGGATGGATG	287859	120055	GCTGGAATTACAGGCGTGAG
198686	30882	ATACTGACAAGCTGCTTCCT	243273	75469	AGATGAATGGATGGATGGAT	287860	120056	TGCTGGAATTACAGGCGTGA
198687	30883	CATACTGACAAGCTGCTTCC	243274	75470	TAGATGAATGGATGGATGGA	287861	120057	GTGCTGGAATTACAGGCGTG
198688	30884	GCATACTGACAAGCTGCTTC	243275	75471	ATAGATGAATGGATGGATGG	287862	120058	AGTGCTGGAATTACAGGCGT
198689	30885	TGCATACTGACAAGCTGCTT	243276	75472	GATAGATGAATGGATGGATG	287863	120059	AAGTGCTGGAATTACAGGCG
198690	30886	ATGCATACTGACAAGCTGCT	243277	75473	GGATAGATGAATGGATGGAT	287864	120060	AAAGTGCTGGAATTACAGGC

198691	30887	TATGCATACTGACAAGCTGC	243278	75474	TGGATAGATGAATGGATGGA	287865	120061	CAAAGTGCTGGAATTACAGG
198692	30888	TTATGCATACTGACAAGCTG	243279	75475	GTGGATAGATGAATGGATGG	287866	120062	CCAAAGTGCTGGAATTACAG
198693	30889	TTTATGCATACTGACAAGCT	243280	75476	GGTGGATAGATGAATGGATG	287867	120063	CCCAAAGTGCTGGAATTACA
198694	30890	GTTTATGCATACTGACAAGC	243281	75477	GGGTGGATAGATGAATGGAT	287868	120064	TCCCAAAGTGCTGGAATTAC
198695	30891	TGTTTATGCATACTGACAAG	243282	75478	TGGGTGGATAGATGAATGGA	287869	120065	CTCCCAAAGTGCTGGAATTA
198696	30892	CTGTTTATGCATACTGACAA	243283	75479	ATGGGTGGATAGATGAATGG	287870	120066	CCTCCCAAAGTGCTGGAATT
198697	30893	GCTGTTTATGCATACTGACA	243284	75480	GATGGGTGGATAGATGAATG	287871	120067	GCCTCCCAAAGTGCTGGAAT
198698	30894	GGCTGTTTATGCATACTGAC	243285	75481	GGATGGGTGGATAGATGAAT	287872	120068	GGCCTCCCAAAGTGCTGGAA
198699	30895	AGGCTGTTTATGCATACTGA	243286	75482	TGGATGGGTGGATAGATGAA	287873	120069	TGGCCTCCCAAAGTGCTGGA
198700	30896	AAGGCTGTTTATGCATACTG	243287	75483	ATGGATGGGTGGATAGATGA	287874	120070	TTGGCCTCCCAAAGTGCTGG
198701	30897	AAAGGCTGTTTATGCATACT	243288	75484	GATGGATGGGTGGATAGATG	287875	120071	CTTGGCCTCCCAAAGTGCTG
198702	30898	TAAAGGCTGTTTATGCATAC	243289	75485	GGATGGATGGGTGGATAGAT	287876	120072	CCTTGGCCTCCCAAAGTGCT
198703	30899	TTAAAGGCTGTTTATGCATA	243290	75486	TGGATGGATGGGTGGATAGA	287877	120073	ACCTTGGCCTCCCAAAGTGC
198704	30900	TTTAAAGGCTGTTTATGCAT	243291	75487	ATGGATGGATGGGTGGATAG	287878	120074	CACCTTGGCCTCCCAAAGTG
198705	30901	TTTTAAAGGCTGTTTATGCA	243292	75488	GATGGATGGATGGGTGGATA	287879	120075	CCACCTTGGCCTCCCAAAGT
198706	30902	ATTTTAAAGGCTGTTTATGC	243293	75489	GGATGGATGGATGGGTGGAT	287880	120076	CCCACCTTGGCCTCCCAAAG
198707	30903	TATTTTAAAGGCTGTTTATG	243294	75490	TGGATGGATGGATGGGTGGA	287881	120077	ACCCACCTTGGCCTCCCAAA
198708	30904	ATATTTTAAAGGCTGTTTAT	243295	75491	ATGGATGGATGGATGGGTGG	287882	120078	CACCCACCTTGGCCTCCCAA
198709	30905	AATATTTTAAAGGCTGTTTA	243296	75492	GATGGATGGATGGATGGGTG	287883	120079	CCACCCACCTTGGCCTCCCA
198710	30906	TAATATTTTAAAGGCTGTTT	243297	75493	GGATGGATGGATGGATGGGT	287884	120080	TCCACCCACCTTGGCCTCCC
198711	30907	GTAATATTTTAAAGGCTGTT	243298	75494	TGGATGGATGGATGGATGGG	287885	120081	ATCCACCCACCTTGGCCTCC
198712	30908	AGTAATATTTTAAAGGCTGT	243299	75495	ATGGATGGATGGATGGATGG	287886	120082	GATCCACCCACCTTGGCCTC
198713	30909	TAGTAATATTTTAAAGGCTG	243300	75496	GATGGATGGATGGATGGATG	287887	120083	TGATCCACCCACCTTGGCCT
198714	30910	GTAGTAATATTTTAAAGGCT	243301	75497	GGATGGATGGATGGATGGAT	287888	120084	ATGATCCACCCACCTTGGCC
198715	30911	AGTAGTAATATTTTAAAGGC	243302	75498	TGGATGGATGGATGGATGGA	287889	120085	CATGATCCACCCACCTTGGC
198716	30912	GAGTAGTAATATTTTAAAGG	243303	75499	ATGGATGGATGGATGGATGG	287890	120086	TCATGATCCACCCACCTTGG
198717	30913	AGAGTAGTAATATTTTAAAG	243304	75500	AATGGATGGATGGATGGATG	287891	120087	CTCATGATCCACCCACCTTG
198718	30914	AAGAGTAGTAATATTTTAAA	243305	75501	GAATGGATGGATGGATGGAT	287892	120088	CCTCATGATCCACCCACCTT
198719	30915	AAAGAGTAGTAATATTTTAA	243306	75502	TGAATGGATGGATGGATGGA	287893	120089	ACCTCATGATCCACCCACCT
198720	30916	CAAAGAGTAGTAATATTTTA	243307	75503	ATGAATGGATGGATGGATGG	287894	120090	GACCTCATGATCCACCCACC
198721	30917	TCAAAGAGTAGTAATATTTT	243308	75504	GATGAATGGATGGATGGATG	287895	120091	TGACCTCATGATCCACCCAC
198722	30918	GTCAAAGAGTAGTAATATTT	243309	75505	AGATGAATGGATGGATGGAT	287896	120092	CTGACCTCATGATCCACCCA
198723	30919	GGTCAAAGAGTAGTAATATT	243310	75506	TAGATGAATGGATGGATGGA	287897	120093	CCTGACCTCATGATCCACCC
198724	30920	GGGTCAAAGAGTAGTAATAT	243311	75507	ATAGATGAATGGATGGATGG	287898	120094	TCCTGACCTCATGATCCACC
198725	30921	TGGGTCAAAGAGTAGTAATA	243312	75508	GATAGATGAATGGATGGATG	287899	120095	CTCCTGACCTCATGATCCAC
198726	30922	CTGGGTCAAAGAGTAGTAAT	243313	75509	GGATAGATGAATGGATGGAT	287900	120096	TCTCCTGACCTCATGATCCA
198727	30923	TCTGGGTCAAAGAGTAGTAA	243314	75510	TGGATAGATGAATGGATGGA	287901	120097	ATCTCCTGACCTCATGATCC
198728	30924	TTCTGGGTCAAAGAGTAGTA	243315	75511	GTGGATAGATGAATGGATGG	287902	120098	AATCTCCTGACCTCATGATC
198729	30925	ATTCTGGGTCAAAGAGTAGT	243316	75512	GGTGGATAGATGAATGGATG	287903	120099	CAATCTCCTGACCTCATGAT
198730	30926	AATTCTGGGTCAAAGAGTAG	243317	75513	GGGTGGATAGATGAATGGAT	287904	120100	TCAATCTCCTGACCTCATGA
198731	30927	AAATTCTGGGTCAAAGAGTA	243318	75514	TGGGTGGATAGATGAATGGA	287905	120101	CTCAATCTCCTGACCTCATG
198732	30928	GAAATTCTGGGTCAAAGAGT	243319	75515	ATGGGTGGATAGATGAATGG	287906	120102	TCTCAATCTCCTGACCTCAT
198733	30929	TGAAATTCTGGGTCAAAGAG	243320	75516	GATGGGTGGATAGATGAATG	287907	120103	GTCTCAATCTCCTGACCTCA
198734	30930	GTGAAATTCTGGGTCAAAGA	243321	75517	GGATGGGTGGATAGATGAAT	287908	120104	GGTCTCAATCTCCTGACCTC
198735	30931	AGTGAAATTCTGGGTCAAAG	243322	75518	TGGATGGGTGGATAGATGAA	287909	120105	TGGTCTCAATCTCCTGACCT
198736	30932	AAGTGAAATTCTGGGTCAAA	243323	75519	ATGGATGGGTGGATAGATGA	287910	120106	ATGGTCTCAATCTCCTGACC
198737	30933	GAAGTGAAATTCTGGGTCAA	243324	75520	GATGGATGGGTGGATAGATG	287911	120107	GATGGTCTCAATCTCCTGAC
198738	30934	AGAAGTGAAATTCTGGGTCA	243325	75521	GGATGGATGGGTGGATAGAT	287912	120108	GGATGGTCTCAATCTCCTGA
198739	30935	TAGAAGTGAAATTCTGGGTC	243326	75522	TGGATGGATGGGTGGATAGA	287913	120109	AGGATGGTCTCAATCTCCTG
198740	30936	CTAGAAGTGAAATTCTGGGT	243327	75523	ATGGATGGATGGGTGGATAG	287914	120110	CAGGATGGTCTCAATCTCCT
198741	30937	CCTAGAAGTGAAATTCTGGG	243328	75524	GATGGATGGATGGGTGGATA	287915	120111	CCAGGATGGTCTCAATCTCC
198742	30938	TCCTAGAAGTGAAATTCTGG	243329	75525	GGATGGATGGATGGGTGGAT	287916	120112	GCCAGGATGGTCTCAATCTC
198743	30939	TTCCTAGAAGTGAAATTCTG	243330	75526	TGGATGGATGGATGGGTGGA	287917	120113	AGCCAGGATGGTCTCAATCT
198744	30940	ATTCCTAGAAGTGAAATTCT	243331	75527	ATGGATGGATGGATGGGTGG	287918	120114	TAGCCAGGATGGTCTCAATC
198745	30941	GATTCCTAGAAGTGAAATTC	243332	75528	GATGGATGGATGGATGGGTG	287919	120115	TTAGCCAGGATGGTCTCAAT
198746	30942	AGATTCCTAGAAGTGAAATT	243333	75529	GGATGGATGGATGGATGGGT	287920	120116	GTTAGCCAGGATGGTCTCAA
198747	30943	CAGATTCCTAGAAGTGAAAT	243334	75530	TGGATGGATGGATGGATGGG	287921	120117	TGTTAGCCAGGATGGTCTCA
198748	30944	ACAGATTCCTAGAAGTGAAA	243335	75531	ATGGATGGATGGATGGATGG	287922	120118	GTGTTAGCCAGGATGGTCTC
198749	30945	GACAGATTCCTAGAAGTGAA	243336	75532	GATGGATGGATGGATGGATG	287923	120119	TGTGTTAGCCAGGATGGTCT
198750	30946	GGACAGATTCCTAGAAGTGA	243337	75533	GGATGGATGGATGGATGGAT	287924	120120	CTGTGTTAGCCAGGATGGTC
198751	30947	AGGACAGATTCCTAGAAGTG	243338	75534	TGGATGGATGGATGGATGGA	287925	120121	ACTGTGTTAGCCAGGATGGT
198752	30948	TAGGACAGATTCCTAGAAGT	243339	75535	ATGGATGGATGGATGGATGG	287926	120122	CACTGTGTTAGCCAGGATGG
198753	30949	TTAGGACAGATTCCTAGAAG	243340	75536	GATGGATGGATGGATGGATG	287927	120123	TCACTGTGTTAGCCAGGATG
198754	30950	CTTAGGACAGATTCCTAGAA	243341	75537	GGATGGATGGATGGATGGAT	287928	120124	TTCACTGTGTTAGCCAGGAT
198755	30951	CCTTAGGACAGATTCCTAGA	243342	75538	TGGATGGATGGATGGATGGA	287929	120125	TTTCACTGTGTTAGCCAGGA
198756	30952	TCCTTAGGACAGATTCCTAG	243343	75539	ATGGATGGATGGATGGATGG	287930	120126	GTTTCACTGTGTTAGCCAGG
198757	30953	TTCCTTAGGACAGATTCCTA	243344	75540	GATGGATGGATGGATGGATG	287931	120127	GGTTTCACTGTGTTAGCCAG
198758	30954	CTTCCTTAGGACAGATTCCT	243345	75541	GGATGGATGGATGGATGGAT	287932	120128	GGGTTTCACTGTGTTAGCCA
198759	30955	ACTTCCTTAGGACAGATTCC	243346	75542	TGGATGGATGGATGGATGGA	287933	120129	GGGGTTTCACTGTGTTAGCC
198760	30956	TACTTCCTTAGGACAGATTC	243347	75543	ATGGATGGATGGATGGATGG	287934	120130	CGGGGTTTCACTGTGTTAGC
198761	30957	CTACTTCCTTAGGACAGATT	243348	75544	CATGGATGGATGGATGGATG	287935	120131	ACGGGGTTTCACTGTGTTAG
198762	30958	ACTACTTCCTTAGGACAGAT	243349	75545	ACATGGATGGATGGATGGAT	287936	120132	GACGGGGTTTCACTGTGTTA

198763	30959	GACTACTTCCTTAGGACAGA	243350	75546	TACATGGATGGATGGATGGA	287937	120133	AGACGGGGTTTCACTGTGTT
198764	30960	TGACTACTTCCTTAGGACAG	243351	75547	TTACATGGATGGATGGATGG	287938	120134	GAGACGGGGTTTCACTGTGT
198765	30961	GTGACTACTTCCTTAGGACA	243352	75548	GTTACATGGATGGATGGATG	287939	120135	AGAGACGGGGTTTCACTGTG
198766	30962	TGTGACTACTTCCTTAGGAC	243353	75549	GGTTACATGGATGGATGGAT	287940	120136	TAGAGACGGGGTTTCACTGT
198767	30963	ATGTGACTACTTCCTTAGGA	243354	75550	TGGTTACATGGATGGATGGA	287941	120137	GTAGAGACGGGGTTTCACTG
198768	30964	CATGTGACTACTTCCTTAGG	243355	75551	ATGGTTACATGGATGGATGG	287942	120138	AGTAGAGACGGGGTTTCACT
198769	30965	GCATGTGACTACTTCCTTAG	243356	75552	GATGGTTACATGGATGGATG	287943	120139	TAGTAGAGACGGGGTTTCAC
198770	30966	TGCATGTGACTACTTCCTTA	243357	75553	GGATGGTTACATGGATGGAT	287944	120140	TTAGTAGAGACGGGGTTTCA
198771	30967	TTGCATGTGACTACTTCCTT	243358	75554	TGGATGGTTACATGGATGGA	287945	120141	TTTAGTAGAGACGGGGTTTC
198772	30968	TTTGCATGTGACTACTTCCT	243359	75555	CTGGATGGTTACATGGATGG	287946	120142	TTTTAGTAGAGACGGGGTTT
198773	30969	TTTTGCATGTGACTACTTCC	243360	75556	ACTGGATGGTTACATGGATG	287947	120143	TTTTTAGTAGAGACGGGGTT
198774	30970	CTTTTGCATGTGACTACTTC	243361	75557	GACTGGATGGTTACATGGAT	287948	120144	ATTTTTAGTAGAGACGGGGT
198775	30971	TCTTTTGCATGTGACTACTT	243362	75558	TGACTGGATGGTTACATGGA	287949	120145	TATTTTTAGTAGAGACGGGG
198776	30972	ATCTTTTGCATGTGACTACT	243363	75559	ATGACTGGATGGTTACATGG	287950	120146	GTATTTTTAGTAGAGACGGG
198777	30973	AATCTTTTGCATGTGACTAC	243364	75560	TATGACTGGATGGTTACATG	287951	120147	TGTATTTTTAGTAGAGACGG
198778	30974	AAATCTTTTGCATGTGACTA	243365	75561	ATATGACTGGATGGTTACAT	287952	120148	TTGTATTTTTAGTAGAGACG
198779	30975	TAAATCTTTTGCATGTGACT	243366	75562	TATATGACTGGATGGTTACA	287953	120149	TTTGTATTTTTAGTAGAGAC
198780	30976	ATAAATCTTTTGCATGTGAC	243367	75563	ATATATGACTGGATGGTTAC	287954	120150	TTTTGTATTTTTAGTAGAGA
198781	30977	CATAAATCTTTTGCATGTGA	243368	75564	GATATATGACTGGATGGTTA	287955	120151	TTTTTGTATTTTTAGTAGAG
198782	30978	ACATAAATCTTTTGCATGTG	243369	75565	GGATATATGACTGGATGGTT	287956	120152	TTTTTTGTATTTTTAGTAGA
198783	30979	TACATAAATCTTTTGCATGT	243370	75566	TGGATATATGACTGGATGGT	287957	120153	ATTTTTTGTATTTTTAGTAG
198784	30980	GTACATAAATCTTTTGCATG	243371	75567	TTGGATATATGACTGGATGG	287958	120154	AATTTTTTGTATTTTTAGTA
198785	30981	GGTACATAAATCTTTTGCAT	243372	75568	ATTGGATATATGACTGGATG	287959	120155	TAATTTTTTGTATTTTTAGT
198786	30982	TGGTACATAAATCTTTTGCA	243373	75569	AATTGGATATATGACTGGAT	287960	120156	CTAATTTTTTGTATTTTTAG
198787	30983	TTGGTACATAAATCTTTTGC	243374	75570	TAATTGGATATATGACTGGA	287961	120157	GCTAATTTTTTGTATTTTTA
198788	30984	CTTGGTACATAAATCTTTTG	243375	75571	GTAATTGGATATATGACTGG	287962	120158	GGCTAATTTTTTGTATTTTT
198789	30985	TCTTGGTACATAAATCTTTT	243376	75572	TGTAATTGGATATATGACTG	287963	120159	CGGCTAATTTTTTGTATTTT
198790	30986	ATCTTGGTACATAAATCTTT	243377	75573	GTGTAATTGGATATATGACT	287964	120160	CCGGCTAATTTTTTGTATTT
198791	30987	CATCTTGGTACATAAATCTT	243378	75574	TGTGTAATTGGATATATGAC	287965	120161	CCCGGCTAATTTTTTGTATT
198792	30988	ACATCTTGGTACATAAATCT	243379	75575	ATGTGTAATTGGATATATGA	287966	120162	GCCCGGCTAATTTTTTGTAT
198793	30989	AACATCTTGGTACATAAATC	243380	75576	GATGTGTAATTGGATATATG	287967	120163	CGCCCGGCTAATTTTTTGTA
198794	30990	GAACATCTTGGTACATAAAT	243381	75577	GGATGTGTAATTGGATATAT	287968	120164	ACGCCCGGCTAATTTTTTGT
198795	30991	TGAACATCTTGGTACATAAA	243382	75578	TGGATGTGTAATTGGATATA	287969	120165	CACGCCCGGCTAATTTTTTG
198796	30992	ATGAACATCTTGGTACATAA	243383	75579	ATGGATGTGTAATTGGATAT	287970	120166	CCACGCCCGGCTAATTTTTT
198797	30993	GATGAACATCTTGGTACATA	243384	75580	GATGGATGTGTAATTGGATA	287971	120167	ACCACGCCCGGCTAATTTTT
198798	30994	TGATGAACATCTTGGTACAT	243385	75581	GGATGGATGTGTAATTGGAT	287972	120168	CACCACGCCCGGCTAATTTT
198799	30995	TTGATGAACATCTTGGTACA	243386	75582	TGGATGGATGTGTAATTGGA	287973	120169	CCACCACGCCCGGCTAATTT
198800	30996	TTTGATGAACATCTTGGTAC	243387	75583	CTGGATGGATGTGTAATTGG	287974	120170	ACCACCACGCCCGGCTAATT
198801	30997	CTTTGATGAACATCTTGGTA	243388	75584	ACTGGATGGATGTGTAATTG	287975	120171	CACCACCACGCCCGGCTAAT
198802	30998	ACTTTGATGAACATCTTGGT	243389	75585	AACTGGATGGATGTGTAATT	287976	120172	CCACCACCACGCCCGGCTAA
198803	30999	CACTTTGATGAACATCTTGG	243390	75586	TAACTGGATGGATGTGTAAT	287977	120173	CCCACCACCACGCCCGGCTA
198804	31000	ACACTTTGATGAACATCTTG	243391	75587	ATAACTGGATGGATGTGTAA	287978	120174	GCCCACCACCACGCCCGGCT
198805	31001	AACACTTTGATGAACATCTT	243392	75588	TATAACTGGATGGATGTGTA	287979	120175	CGCCCACCACCACGCCCGGC
198806	31002	CAACACTTTGATGAACATCT	243393	75589	GTATAACTGGATGGATGTGT	287980	120176	GCGCCCACCACCACGCCCGG
198807	31003	ACAACACTTTGATGAACATC	243394	75590	TGTATAACTGGATGGATGTG	287981	120177	GGCGCCCACCACCACGCCCG
198808	31004	AACAACACTTTGATGAACAT	243395	75591	ATGTATAACTGGATGGATGT	287982	120178	AGGCGCCCACCACCACGCCC
198809	31005	AAACAACACTTTGATGAACA	243396	75592	AATGTATAACTGGATGGATG	287983	120179	CAGGCGCCCACCACCACGCC
198810	31006	AAAACAACACTTTGATGAAC	243397	75593	GAATGTATAACTGGATGGAT	287984	120180	ACAGGCGCCCACCACCACGC
198811	31007	TAAAACAACACTTTGATGAA	243398	75594	TGAATGTATAACTGGATGGA	287985	120181	TACAGGCGCCCACCACCACG
198812	31008	ATAAAACAACACTTTGATGA	243399	75595	ATGAATGTATAACTGGATGG	287986	120182	CTACAGGCGCCCACCACCAC
198813	31009	TATAAAACAACACTTTGATG	243400	75596	TATGAATGTATAACTGGATG	287987	120183	ACTACAGGCGCCCACCACCA
198814	31010	TTATAAAACAACACTTTGAT	243401	75597	GTATGAATGTATAACTGGAT	287988	120184	GACTACAGGCGCCCACCACC
198815	31011	GTTATAAAACAACACTTTGA	243402	75598	TGTATGAATGTATAACTGGA	287989	120185	GGACTACAGGCGCCCACCAC
198816	31012	TGTTATAAAACAACACTTTG	243403	75599	ATGTATGAATGTATAACTGG	287990	120186	GGGACTACAGGCGCCCACCA
198817	31013	CTGTTATAAAACAACACTTT	243404	75600	CATGTATGAATGTATAACTG	287991	120187	TGGGACTACAGGCGCCCACC
198818	31014	CCTGTTATAAAACAACACTT	243405	75601	GCATGTATGAATGTATAACT	287992	120188	CTGGGACTACAGGCGCCCAC
198819	31015	TCCTGTTATAAAACAACACT	243406	75602	TGCATGTATGAATGTATAAC	287993	120189	GCTGGGACTACAGGCGCCCA
198820	31016	TTCCTGTTATAAAACAACAC	243407	75603	ATGCATGTATGAATGTATAA	287994	120190	AGCTGGGACTACAGGCGCCC
198821	31017	CTTCCTGTTATAAAACAACA	243408	75604	GATGCATGTATGAATGTATA	287995	120191	TAGCTGGGACTACAGGCGCC
198822	31018	ACTTCCTGTTATAAAACAAC	243409	75605	AGATGCATGTATGAATGTAT	287996	120192	GTAGCTGGGACTACAGGCGC
198823	31019	GACTTCCTGTTATAAAACAA	243410	75606	TAGATGCATGTATGAATGTA	287997	120193	AGTAGCTGGGACTACAGGCG
198824	31020	AGACTTCCTGTTATAAAACA	243411	75607	TTAGATGCATGTATGAATGT	287998	120194	GAGTAGCTGGGACTACAGGC
198825	31021	GAGACTTCCTGTTATAAAAC	243412	75608	ATTAGATGCATGTATGAATG	287999	120195	GGAGTAGCTGGGACTACAGG
198826	31022	TGAGACTTCCTGTTATAAAA	243413	75609	GATTAGATGCATGTATGAAT	288000	120196	CGGAGTAGCTGGGACTACAG
198827	31023	CTGAGACTTCCTGTTATAAA	243414	75610	TGATTAGATGCATGTATGAA	288001	120197	CCGGAGTAGCTGGGACTACA
198828	31024	TCTGAGACTTCCTGTTATAA	243415	75611	ATGATTAGATGCATGTATGA	288002	120198	TCCGGAGTAGCTGGGACTAC
198829	31025	TTCTGAGACTTCCTGTTATA	243416	75612	AATGATTAGATGCATGTATG	288003	120199	CTCCGGAGTAGCTGGGACTA
198830	31026	CTTCTGAGACTTCCTGTTAT	243417	75613	GAATGATTAGATGCATGTAT	288004	120200	CCTCCGGAGTAGCTGGGACT
198831	31027	GCTTCTGAGACTTCCTGTTA	243418	75614	TGAATGATTAGATGCATGTA	288005	120201	GCCTCCGGAGTAGCTGGGAC
198832	31028	AGCTTCTGAGACTTCCTGTT	243419	75615	TTGAATGATTAGATGCATGT	288006	120202	AGCCTCCGGAGTAGCTGGGA
198833	31029	CAGCTTCTGAGACTTCCTGT	243420	75616	ATTGAATGATTAGATGCATG	288007	120203	CAGCCTCCGGAGTAGCTGGG
198834	31030	CCAGCTTCTGAGACTTCCTG	243421	75617	AATTGAATGATTAGATGCAT	288008	120204	TCAGCCTCCGGAGTAGCTGG

198835	31031	TCCAGCTTCTGAGACTTCCT	243422	75618	TAATTGAATGATTAGATGCA	288009	120205	CTCAGCCTCCGGAGTAGCTG
198836	31032	ATCCAGCTTCTGAGACTTCC	243423	75619	ATAATTGAATGATTAGATGC	288010	120206	CCTCAGCCTCCGGAGTAGCT
198837	31033	TATCCAGCTTCTGAGACTTC	243424	75620	TATAATTGAATGATTAGATG	288011	120207	GCCTCAGCCTCCGGAGTAGC
198838	31034	TTATCCAGCTTCTGAGACTT	243425	75621	GTATAATTGAATGATTAGAT	288012	120208	TGCCTCAGCCTCCGGAGTAG
198839	31035	TTTATCCAGCTTCTGAGACT	243426	75622	TGTATAATTGAATGATTAGA	288013	120209	CTGCCTCAGCCTCCGGAGTA
198840	31036	ATTTATCCAGCTTCTGAGAC	243427	75623	ATGTATAATTGAATGATTAG	288014	120210	CCTGCCTCAGCCTCCGGAGT
198841	31037	TATTTATCCAGCTTCTGAGA	243428	75624	TATGTATAATTGAATGATTA	288015	120211	TCCTGCCTCAGCCTCCGGAG
198842	31038	ATATTTATCCAGCTTCTGAG	243429	75625	GTATGTATAATTGAATGATT	288016	120212	TTCCTGCCTCAGCCTCCGGA
198843	31039	GATATTTATCCAGCTTCTGA	243430	75626	TGTATGTATAATTGAATGAT	288017	120213	TTTCCTGCCTCAGCCTCCGG
198844	31040	GGATATTTATCCAGCTTCTG	243431	75627	GTGTATGTATAATTGAATGA	288018	120214	TTTTCCTGCCTCAGCCTCCG
198845	31041	TGGATATTTATCCAGCTTCT	243432	75628	TGTGTATGTATAATTGAATG	288019	120215	ATTTTCCTGCCTCAGCCTCC
198846	31042	TTGGATATTTATCCAGCTTC	243433	75629	GTGTGTATGTATAATTGAAT	288020	120216	CATTTTCCTGCCTCAGCCTC
198847	31043	GTTGGATATTTATCCAGCTT	243434	75630	TGTGTGTATGTATAATTGAA	288021	120217	CCATTTTCCTGCCTCAGCCT
198848	31044	GGTTGGATATTTATCCAGCT	243435	75631	ATGTGTGTATGTATAATTGA	288022	120218	GCCATTTTCCTGCCTCAGCC
198849	31045	AGGTTGGATATTTATCCAGC	243436	75632	GATGTGTGTATGTATAATTG	288023	120219	CGCCATTTTCCTGCCTCAGC
198850	31046	GAGGTTGGATATTTATCCAG	243437	75633	GGATGTGTGTATGTATAATT	288024	120220	ACGCCATTTTCCTGCCTCAG
198851	31047	AGAGGTTGGATATTTATCCA	243438	75634	TGGATGTGTGTATGTATAAT	288025	120221	CACGCCATTTTCCTGCCTCA
198852	31048	CAGAGGTTGGATATTTATCC	243439	75635	ATGGATGTGTGTATGTATAA	288026	120222	TCACGCCATTTTCCTGCCTC
198853	31049	CCAGAGGTTGGATATTTATC	243440	75636	TATGGATGTGTGTATGTATA	288027	120223	TTCACGCCATTTTCCTGCCT
198854	31050	TCCAGAGGTTGGATATTTAT	243441	75637	ATATGGATGTGTGTATGTAT	288028	120224	GTTCACGCCATTTTCCTGCC
198855	31051	TTCCAGAGGTTGGATATTTA	243442	75638	TATATGGATGTGTGTATGTA	288029	120225	GGTTCACGCCATTTTCCTGC
198856	31052	TTTCCAGAGGTTGGATATTT	243443	75639	TTATATGGATGTGTGTATGT	288030	120226	GGGTTCACGCCATTTTCCTG
198857	31053	ATTTCCAGAGGTTGGATATT	243444	75640	ATTATATGGATGTGTGTATG	288031	120227	CGGGTTCACGCCATTTTCCT
198858	31054	CATTTCCAGAGGTTGGATAT	243445	75641	AATTATATGGATGTGTGTAT	288032	120228	CCGGGTTCACGCCATTTTCC
198859	31055	CCATTTCCAGAGGTTGGATA	243446	75642	GAATTATATGGATGTGTGTA	288033	120229	TCCGGGTTCACGCCATTTTC
198860	31056	ACCATTTCCAGAGGTTGGAT	243447	75643	AGAATTATATGGATGTGTGT	288034	120230	TTCCGGGTTCACGCCATTTT
198861	31057	AACCATTTCCAGAGGTTGGA	243448	75644	TAGAATTATATGGATGTGTG	288035	120231	CTTCCGGGTTCACGCCATTT
198862	31058	TAACCATTTCCAGAGGTTGG	243449	75645	GTAGAATTATATGGATGTGT	288036	120232	CCTTCCGGGTTCACGCCATT
198863	31059	CTAACCATTTCCAGAGGTTG	243450	75646	TGTAGAATTATATGGATGTG	288037	120233	GCCTTCCGGGTTCACGCCAT
198864	31060	TCTAACCATTTCCAGAGGTT	243451	75647	ATGTAGAATTATATGGATGT	288038	120234	CGCCTTCCGGGTTCACGCCA
198865	31061	ATCTAACCATTTCCAGAGGT	243452	75648	GATGTAGAATTATATGGATG	288039	120235	CCGCCTTCCGGGTTCACGCC
198866	31062	TATCTAACCATTTCCAGAGG	243453	75649	GGATGTAGAATTATATGGAT	288040	120236	TCCGCCTTCCGGGTTCACGC
198867	31063	CTATCTAACCATTTCCAGAG	243454	75650	TGGATGTAGAATTATATGGA	288041	120237	CTCCGCCTTCCGGGTTCACG
198868	31064	TCTATCTAACCATTTCCAGA	243455	75651	TTGGATGTAGAATTATATGG	288042	120238	GCTCCGCCTTCCGGGTTCAC
198869	31065	TTCTATCTAACCATTTCCAG	243456	75652	ATTGGATGTAGAATTATATG	288043	120239	AGCTCCGCCTTCCGGGTTCA
198870	31066	ATTCTATCTAACCATTTCCA	243457	75653	AATTGGATGTAGAATTATAT	288044	120240	AAGCTCCGCCTTCCGGGTTC
198871	31067	TATTCTATCTAACCATTTCC	243458	75654	TAATTGGATGTAGAATTATA	288045	120241	CAAGCTCCGCCTTCCGGGTT
198872	31068	CTATTCTATCTAACCATTTC	243459	75655	ATAATTGGATGTAGAATTAT	288046	120242	GCAAGCTCCGCCTTCCGGGT
198873	31069	ACTATTCTATCTAACCATTT	243460	75656	TATAATTGGATGTAGAATTA	288047	120243	TGCAAGCTCCGCCTTCCGGG
198874	31070	TACTATTCTATCTAACCATT	243461	75657	GTATAATTGGATGTAGAATT	288048	120244	CTGCAAGCTCCGCCTTCCGG
198875	31071	ATACTATTCTATCTAACCAT	243462	75658	GGTATAATTGGATGTAGAAT	288049	120245	ACTGCAAGCTCCGCCTTCCG
198876	31072	CATACTATTCTATCTAACCA	243463	75659	AGGTATAATTGGATGTAGAA	288050	120246	CACTGCAAGCTCCGCCTTCC
198877	31073	ACATACTATTCTATCTAACC	243464	75660	GAGGTATAATTGGATGTAGA	288051	120247	TCACTGCAAGCTCCGCCTTC
198878	31074	TACATACTATTCTATCTAAC	243465	75661	GGAGGTATAATTGGATGTAG	288052	120248	CTCACTGCAAGCTCCGCCTT
198879	31075	CTACATACTATTCTATCTAA	243466	75662	TGGAGGTATAATTGGATGTA	288053	120249	GCTCACTGCAAGCTCCGCCT
198880	31076	GCTACATACTATTCTATCTA	243467	75663	ATGGAGGTATAATTGGATGT	288054	120250	CGCTCACTGCAAGCTCCGCC
198881	31077	GGCTACATACTATTCTATCT	243468	75664	GATGGAGGTATAATTGGATG	288055	120251	CCGCTCACTGCAAGCTCCGC
198882	31078	TGGCTACATACTATTCTATC	243469	75665	GGATGGAGGTATAATTGGAT	288056	120252	TCCGCTCACTGCAAGCTCCG
198883	31079	ATGGCTACATACTATTCTAT	243470	75666	TGGATGGAGGTATAATTGGA	288057	120253	CTCCGCTCACTGCAAGCTCC
198884	31080	AATGGCTACATACTATTCTA	243471	75667	TTGGATGGAGGTATAATTGG	288058	120254	ACTCCGCTCACTGCAAGCTC
198885	31081	TAATGGCTACATACTATTCT	243472	75668	ATTGGATGGAGGTATAATTG	288059	120255	CACTCCGCTCACTGCAAGCT
198886	31082	CTAATGGCTACATACTATTC	243473	75669	AATTGGATGGAGGTATAATT	288060	120256	TCACTCCGCTCACTGCAAGC
198887	31083	TCTAATGGCTACATACTATT	243474	75670	TAATTGGATGGAGGTATAAT	288061	120257	CTCACTCCGCTCACTGCAAG
198888	31084	TTCTAATGGCTACATACTAT	243475	75671	GTAATTGGATGGAGGTATAA	288062	120258	GCTCACTCCGCTCACTGCAA
198889	31085	TTTCTAATGGCTACATACTA	243476	75672	TGTAATTGGATGGAGGTATA	288063	120259	TGCTCACTCCGCTCACTGCA
198890	31086	TTTTCTAATGGCTACATACT	243477	75673	GTGTAATTGGATGGAGGTAT	288064	120260	CTGCTCACTCCGCTCACTGC
198891	31087	ATTTTCTAATGGCTACATAC	243478	75674	TGTGTAATTGGATGGAGGTA	288065	120261	TCTGCTCACTCCGCTCACTG
198892	31088	AATTTTCTAATGGCTACATA	243479	75675	ATGTGTAATTGGATGGAGGT	288066	120262	CTCTGCTCACTCCGCTCACT
198893	31089	TAATTTTCTAATGGCTACAT	243480	75676	AATGTGTAATTGGATGGAGG	288067	120263	TCTCTGCTCACTCCGCTCAC
198894	31090	ATAATTTTCTAATGGCTACA	243481	75677	GAATGTGTAATTGGATGGAG	288068	120264	ATCTCTGCTCACTCCGCTCA
198895	31091	CATAATTTTCTAATGGCTAC	243482	75678	TGAATGTGTAATTGGATGGA	288069	120265	GATCTCTGCTCACTCCGCTC
198896	31092	ACATAATTTTCTAATGGCTA	243483	75679	ATGAATGTGTAATTGGATGG	288070	120266	CGATCTCTGCTCACTCCGCT
198897	31093	GACATAATTTTCTAATGGCT	243484	75680	TATGAATGTGTAATTGGATG	288071	120267	GCGATCTCTGCTCACTCCGC
198898	31094	AGACATAATTTTCTAATGGC	243485	75681	GTATGAATGTGTAATTGGAT	288072	120268	CGCGATCTCTGCTCACTCCG
198899	31095	TAGACATAATTTTCTAATGG	243486	75682	TGTATGAATGTGTAATTGGA	288073	120269	GCGCGATCTCTGCTCACTCC
198900	31096	ATAGACATAATTTTCTAATG	243487	75683	GTGTATGAATGTGTAATTGG	288074	120270	GGCGCGATCTCTGCTCACTC
198901	31097	CATAGACATAATTTTCTAAT	243488	75684	GGTGTATGAATGTGTAATTG	288075	120271	TGGCGCGATCTCTGCTCACT
198902	31098	CCATAGACATAATTTTCTAA	243489	75685	GGGTGTATGAATGTGTAATT	288076	120272	GTGGCGCGATCTCTGCTCAC
198903	31099	CCCATAGACATAATTTTCTA	243490	75686	TGGGTGTATGAATGTGTAAT	288077	120273	AGTGGCGCGATCTCTGCTCA
198904	31100	CCCCATAGACATAATTTTCT	243491	75687	GTGGGTGTATGAATGTGTAA	288078	120274	CAGTGGCGCGATCTCTGCTC
198905	31101	ACCCCATAGACATAATTTTC	243492	75688	GGTGGGTGTATGAATGTGTA	288079	120275	GCAGTGGCGCGATCTCTGCT
198906	31102	AACCCCATAGACATAATTTT	243493	75689	AGGTGGGTGTATGAATGTGT	288080	120276	TGCAGTGGCGCGATCTCTGC

198907	31103	AAACCCCATAGACATAATTT	243494	75690	TAGGTGGGTGTATGAATGTG	288081	120277	GTGCAGTGGCGCGATCTCTG
198908	31104	TAAACCCCATAGACATAATT	243495	75691	TTAGGTGGGTGTATGAATGT	288082	120278	AGTGCAGTGGCGCGATCTCT
198909	31105	TTAAACCCCATAGACATAAT	243496	75692	ATTAGGTGGGTGTATGAATG	288083	120279	GAGTGCAGTGGCGCGATCTC
198910	31106	TTTAAACCCCATAGACATAA	243497	75693	TATTAGGTGGGTGTATGAAT	288084	120280	GGAGTGCAGTGGCGCGATCT
198911	31107	TTTTAAACCCCATAGACATA	243498	75694	TTATTAGGTGGGTGTATGAA	288085	120281	TGGAGTGCAGTGGCGCGATC
198912	31108	ATTTTAAACCCCATAGACAT	243499	75695	TTTATTAGGTGGGTGTATGA	288086	120282	CTGGAGTGCAGTGGCGCGAT
198913	31109	CATTTTAAACCCCATAGACA	243500	75696	ATTTATTAGGTGGGTGTATG	288087	120283	GCTGGAGTGCAGTGGCGCGA
198914	31110	ACATTTTAAACCCCATAGAC	243501	75697	AATTTATTAGGTGGGTGTAT	288088	120284	GGCTGGAGTGCAGTGGCGCG
198915	31111	GACATTTTAAACCCCATAGA	243502	75698	TAATTTATTAGGTGGGTGTA	288089	120285	AGGCTGGAGTGCAGTGGCGC
198916	31112	TGACATTTTAAACCCCATAG	243503	75699	ATAATTTATTAGGTGGGTGT	288090	120286	CAGGCTGGAGTGCAGTGGCG
198917	31113	ATGACATTTTAAACCCCATA	243504	75700	AATAATTTATTAGGTGGGTG	288091	120287	CCAGGCTGGAGTGCAGTGGC
198918	31114	CATGACATTTTAAACCCCAT	243505	75701	TAATAATTTATTAGGTGGGT	288092	120288	CCCAGGCTGGAGTGCAGTGG
198919	31115	CCATGACATTTTAAACCCCA	243506	75702	TTAATAATTTATTAGGTGGG	288093	120289	GCCCAGGCTGGAGTGCAGTG
198920	31116	CCCATGACATTTTAAACCCC	243507	75703	ATTAATAATTTATTAGGTGG	288094	120290	CGCCCAGGCTGGAGTGCAGT
198921	31117	TCCCATGACATTTTAAACCC	243508	75704	AATTAATAATTTATTAGGTG	288095	120291	TCGCCCAGGCTGGAGTGCAG
198922	31118	TTCCCATGACATTTTAAACC	243509	75705	GAATTAATAATTTATTAGGT	288096	120292	GTCGCCCAGGCTGGAGTGCA
198923	31119	TTTCCCATGACATTTTAAAC	243510	75706	TGAATTAATAATTTATTAGG	288097	120293	TGTCGCCCAGGCTGGAGTGC
198924	31120	TTTTCCCATGACATTTTAAA	243511	75707	ATGAATTAATAATTTATTAG	288098	120294	CTGTCGCCCAGGCTGGAGTG
198925	31121	GTTTTCCCATGACATTTTAA	243512	75708	TATGAATTAATAATTTATTA	288099	120295	TCTGTCGCCCAGGCTGGAGT
198926	31122	TGTTTTCCCATGACATTTTA	243513	75709	ATATGAATTAATAATTTATT	288100	120296	CTCTGTCGCCCAGGCTGGAG
198927	31123	GTGTTTTCCCATGACATTTT	243514	75710	TATATGAATTAATAATTTAT	288101	120297	GCTCTGTCGCCCAGGCTGGA
198928	31124	AGTGTTTTCCCATGACATTT	243515	75711	ATATATGAATTAATAATTTA	288102	120298	CGCTCTGTCGCCCAGGCTGG
198929	31125	AAGTGTTTTCCCATGACATT	243516	75712	GATATATGAATTAATAATTT	288103	120299	TCGCTCTGTCGCCCAGGCTG
198930	31126	GAAGTGTTTTCCCATGACAT	243517	75713	GGATATATGAATTAATAATT	288104	120300	CTCGCTCTGTCGCCCAGGCT
198931	31127	AGAAGTGTTTTCCCATGACA	243518	75714	TGGATATATGAATTAATAAT	288105	120301	TCTCGCTCTGTCGCCCAGGC
198932	31128	CAGAAGTGTTTTCCCATGAC	243519	75715	ATGGATATATGAATTAATAA	288106	120302	GTCTCGCTCTGTCGCCCAGG
198933	31129	TCAGAAGTGTTTTCCCATGA	243520	75716	GATGGATATATGAATTAATA	288107	120303	AGTCTCGCTCTGTCGCCCAG
198934	31130	GTCAGAAGTGTTTTCCCATG	243521	75717	GGATGGATATATGAATTAAT	288108	120304	GAGTCTCGCTCTGTCGCCCA
198935	31131	TGTCAGAAGTGTTTTCCCAT	243522	75718	TGGATGGATATATGAATTAA	288109	120305	GGAGTCTCGCTCTGTCGCCC
198936	31132	ATGTCAGAAGTGTTTTCCCA	243523	75719	ATGGATGGATATATGAATTA	288110	120306	CGGAGTCTCGCTCTGTCGCC
198937	31133	TATGTCAGAAGTGTTTTCCC	243524	75720	TATGGATGGATATATGAATT	288111	120307	ACGGAGTCTCGCTCTGTCGC
198938	31134	TTATGTCAGAAGTGTTTTCC	243525	75721	ATATGGATGGATATATGAAT	288112	120308	GACGGAGTCTCGCTCTGTCG
198939	31135	TTTATGTCAGAAGTGTTTTC	243526	75722	TATATGGATGGATATATGAA	288113	120309	AGACGGAGTCTCGCTCTGTC
198940	31136	TTTTATGTCAGAAGTGTTTT	243527	75723	TTATATGGATGGATATATGA	288114	120310	GAGACGGAGTCTCGCTCTGT
198941	31137	CTTTTATGTCAGAAGTGTTT	243528	75724	ATTATATGGATGGATATATG	288115	120311	TGAGACGGAGTCTCGCTCTG
198942	31138	TCTTTTATGTCAGAAGTGTT	243529	75725	AATTATATGGATGGATATAT	288116	120312	TTGAGACGGAGTCTCGCTCT
198943	31139	CTCTTTTATGTCAGAAGTGT	243530	75726	TAATTATATGGATGGATATA	288117	120313	TTTGAGACGGAGTCTCGCTC
198944	31140	GCTCTTTTATGTCAGAAGTG	243531	75727	ATAATTATATGGATGGATAT	288118	120314	TTTTGAGACGGAGTCTCGCT
198945	31141	TGCTCTTTTATGTCAGAAGT	243532	75728	TATAATTATATGGATGGATA	288119	120315	TTTTTGAGACGGAGTCTCGC
198946	31142	ATGCTCTTTTATGTCAGAAG	243533	75729	GTATAATTATATGGATGGAT	288120	120316	TTTTTTGAGACGGAGTCTCG
198947	31143	CATGCTCTTTTATGTCAGAA	243534	75730	TGTATAATTATATGGATGGA	288121	120317	TTTTTTTGAGACGGAGTCTC
198948	31144	TCATGCTCTTTTATGTCAGA	243535	75731	ATGTATAATTATATGGATGG	288122	120318	TTTTTTTTGAGACGGAGTCT
198949	31145	CTCATGCTCTTTTATGTCAG	243536	75732	GATGTATAATTATATGGATG	288123	120319	TTTTTTTTGAGACGGAGTC
198950	31146	TCTCATGCTCTTTTATGTCA	243537	75733	TGATGTATAATTATATGGAT	288124	120320	TTTTTTTTTGAGACGGAGT
198951	31147	TTCTCATGCTCTTTTATGTC	243538	75734	TTGATGTATAATTATATGGA	288125	120321	TTTTTTTTTTGAGACGGAG
198952	31148	GTTCTCATGCTCTTTTATGT	243539	75735	ATTGATGTATAATTATATGG	288126	120322	CTTTTTTTTTTGAGACGGA
198953	31149	AGTTCTCATGCTCTTTTATG	243540	75736	AATTGATGTATAATTATATG	288127	120323	GCTTTTTTTTTTTGAGACGG
198954	31150	CAGTTCTCATGCTCTTTTAT	243541	75737	TAATTGATGTATAATTATAT	288128	120324	TGCTTTTTTTTTTTGAGACG
198955	31151	ACAGTTCTCATGCTCTTTTA	243542	75738	ATAATTGATGTATAATTATA	288129	120325	GTGCTTTTTTTTTTTGAGAC
198956	31152	TACAGTTCTCATGCTCTTTT	243543	75739	TATAATTGATGTATAATTAT	288130	120326	TGTGCTTTTTTTTTTTGAGA
198957	31153	ATACAGTTCTCATGCTCTTT	243544	75740	GTATAATTGATGTATAATTA	288131	120327	ATGTGCTTTTTTTTTTTGAG
198958	31154	TATACAGTTCTCATGCTCTT	243545	75741	TGTATAATTGATGTATAATT	288132	120328	CATGTGCTTTTTTTTTTTGA
198959	31155	ATATACAGTTCTCATGCTCT	243546	75742	ATGTATAATTGATGTATAAT	288133	120329	ACATGTGCTTTTTTTTTTTG
198960	31156	AATATACAGTTCTCATGCTC	243547	75743	GATGTATAATTGATGTATAA	288134	120330	AACATGTGCTTTTTTTTTTT
198961	31157	AAATATACAGTTCTCATGCT	243548	75744	GGATGTATAATTGATGTATA	288135	120331	GAACATGTGCTTTTTTTTTT
198962	31158	TAAATATACAGTTCTCATGC	243549	75745	TGGATGTATAATTGATGTAT	288136	120332	AGAACATGTGCTTTTTTTTT
198963	31159	CTAAATATACAGTTCTCATG	243550	75746	ATGGATGTATAATTGATGTA	288137	120333	GAGAACATGTGCTTTTTTTT
198964	31160	GCTAAATATACAGTTCTCAT	243551	75747	GATGGATGTATAATTGATGT	288138	120334	CGAGAACATGTGCTTTTTTT
198965	31161	TGCTAAATATACAGTTCTCA	243552	75748	AGATGGATGTATAATTGATG	288139	120335	GCGAGAACATGTGCTTTTTT
198966	31162	ATGCTAAATATACAGTTCTC	243553	75749	TAGATGGATGTATAATTGAT	288140	120336	AGCGAGAACATGTGCTTTTT
198967	31163	TATGCTAAATATACAGTTCT	243554	75750	TTAGATGGATGTATAATTGA	288141	120337	AAGCGAGAACATGTGCTTTT
198968	31164	TTATGCTAAATATACAGTTC	243555	75751	ATTAGATGGATGTATAATTG	288142	120338	GAAGCGAGAACATGTGCTTT
198969	31165	ATTATGCTAAATATACAGTT	243556	75752	GATTAGATGGATGTATAATT	288143	120339	AGAAGCGAGAACATGTGCTT
198970	31166	GATTATGCTAAATATACAGT	243557	75753	TGATTAGATGGATGTATAAT	288144	120340	AAGAAGCGAGAACATGTGCT
198971	31167	AGATTATGCTAAATATACAG	243558	75754	ATGATTAGATGGATGTATAA	288145	120341	AAAGAAGCGAGAACATGTGC
198972	31168	AAGATTATGCTAAATATACA	243559	75755	AATGATTAGATGGATGTATA	288146	120342	CAAAGAAGCGAGAACATGTG
198973	31169	TAAGATTATGCTAAATATAC	243560	75756	GAATGATTAGATGGATGTAT	288147	120343	ACAAAGAAGCGAGAACATGT
198974	31170	TTAAGATTATGCTAAATATA	243561	75757	TGAATGATTAGATGGATGTA	288148	120344	CACAAAGAAGCGAGAACATG
198975	31171	GTTAAGATTATGCTAAATAT	243562	75758	CTGAATGATTAGATGGATGT	288149	120345	CCACAAAGAAGCGAGAACAT
198976	31172	AGTTAAGATTATGCTAAATA	243563	75759	ACTGAATGATTAGATGGATG	288150	120346	CCCACAAAGAAGCGAGAACA
198977	31173	TAGTTAAGATTATGCTAAAT	243564	75760	TACTGAATGATTAGATGGAT	288151	120347	TCCCACAAAGAAGCGAGAAC
198978	31174	ATAGTTAAGATTATGCTAAA	243565	75761	TTACTGAATGATTAGATGGA	288152	120348	ATCCCACAAAGAAGCGAGAA

198979	31175	CATAGTTAAGATTATGCTAA	243566	75762	ATTACTGAATGATTAGATGG	288153	120349	GATCCCACAAAGAAGCGAGA
198980	31176	ACATAGTTAAGATTATGCTA	243567	75763	AATTACTGAATGATTAGATG	288154	120350	GGATCCCACAAAGAAGCGAG
198981	31177	AACATAGTTAAGATTATGCT	243568	75764	GAATTACTGAATGATTAGAT	288155	120351	TGGATCCCACAAAGAAGCGA
198982	31178	AAACATAGTTAAGATTATGC	243569	75765	TGAATTACTGAATGATTAGA	288156	120352	CTGGATCCCACAAAGAAGCG
198983	31179	AAAACATAGTTAAGATTATG	243570	75766	GTGAATTACTGAATGATTAG	288157	120353	CCTGGATCCCACAAAGAAGC
198984	31180	TAAAACATAGTTAAGATTAT	243571	75767	GGTGAATTACTGAATGATTA	288158	120354	TCCTGGATCCCACAAAGAAG
198985	31181	CTAAAACATAGTTAAGATTA	243572	75768	GGGTGAATTACTGAATGATT	288159	120355	CTCCTGGATCCCACAAAGAA
198986	31182	TCTAAAACATAGTTAAGATT	243573	75769	TGGGTGAATTACTGAATGAT	288160	120356	TCTCCTGGATCCCACAAAGA
198987	31183	TTCTAAAACATAGTTAAGAT	243574	75770	GTGGGTGAATTACTGAATGA	288161	120357	ATCTCCTGGATCCCACAAAG
198988	31184	ATTCTAAAACATAGTTAAGA	243575	75771	GGTGGGTGAATTACTGAATG	288162	120358	TATCTCCTGGATCCCACAAA
198989	31185	CATTCTAAAACATAGTTAAG	243576	75772	TGGTGGGTGAATTACTGAAT	288163	120359	CTATCTCCTGGATCCCACAA
198990	31186	GCATTCTAAAACATAGTTAA	243577	75773	ATGGTGGGTGAATTACTGAA	288164	120360	TCTATCTCCTGGATCCCACA
198991	31187	TGCATTCTAAAACATAGTTA	243578	75774	GATGGTGGGTGAATTACTGA	288165	120361	CTCTATCTCCTGGATCCCAC
198992	31188	GTGCATTCTAAAACATAGTT	243579	75775	GGATGGTGGGTGAATTACTG	288166	120362	TCTCTATCTCCTGGATCCCA
198993	31189	TGTGCATTCTAAAACATAGT	243580	75776	TGGATGGTGGGTGAATTACT	288167	120363	TTCTCTATCTCCTGGATCCC
198994	31190	CTGTGCATTCTAAAACATAG	243581	75777	CTGGATGGTGGGTGAATTAC	288168	120364	ATTCTCTATCTCCTGGATCC
198995	31191	CCTGTGCATTCTAAAACATA	243582	75778	ACTGGATGGTGGGTGAATTA	288169	120365	TATTCTCTATCTCCTGGATC
198996	31192	TCCTGTGCATTCTAAAACAT	243583	75779	GACTGGATGGTGGGTGAATT	288170	120366	CTATTCTCTATCTCCTGGAT
198997	31193	TTCCTGTGCATTCTAAAACA	243584	75780	TGACTGGATGGTGGGTGAAT	288171	120367	TCTATTCTCTATCTCCTGGA
198998	31194	TTTCCTGTGCATTCTAAAAC	243585	75781	ATGACTGGATGGTGGGTGAA	288172	120368	TTCTATTCTCTATCTCCTGG
198999	31195	TTTTCCTGTGCATTCTAAAA	243586	75782	GATGACTGGATGGTGGGTGA	288173	120369	CTTCTATTCTCTATCTCCTG
199000	31196	TTTTTCCTGTGCATTCTAAA	243587	75783	AGATGACTGGATGGTGGGTG	288174	120370	CCTTCTATTCTCTATCTCCT
199001	31197	TTTTTTCCTGTGCATTCTAA	243588	75784	TAGATGACTGGATGGTGGGT	288175	120371	TCCTTCTATTCTCTATCTCC
199002	31198	TTTTTTTCCTGTGCATTCTA	243589	75785	ATAGATGACTGGATGGTGGG	288176	120372	ATCCTTCTATTCTCTATCTC
199003	31199	ATTTTTTTCCTGTGCATTCT	243590	75786	GATAGATGACTGGATGGTGG	288177	120373	CATCCTTCTATTCTCTATCT
199004	31200	CATTTTTTTCCTGTGCATTC	243591	75787	GGATAGATGACTGGATGGTG	288178	120374	CCATCCTTCTATTCTCTATC
199005	31201	ACATTTTTTTCCTGTGCATT	243592	75788	TGGATAGATGACTGGATGGT	288179	120375	ACCATCCTTCTATTCTCTAT
199006	31202	TACATTTTTTTCCTGTGCAT	243593	75789	TTGGATAGATGACTGGATGG	288180	120376	AACCATCCTTCTATTCTCTA
199007	31203	GTACATTTTTTTCCTGTGCA	243594	75790	ATTGGATAGATGACTGGATG	288181	120377	TAACCATCCTTCTATTCTCT
199008	31204	TGTACATTTTTTTCCTGTGC	243595	75791	TATTGGATAGATGACTGGAT	288182	120378	GTAACCATCCTTCTATTCTC
199009	31205	TTGTACATTTTTTTCCTGTG	243596	75792	TTATTGGATAGATGACTGGA	288183	120379	GGTAACCATCCTTCTATTCT
199010	31206	TTTGTACATTTTTTTCCTGT	243597	75793	ATTATTGGATAGATGACTGG	288184	120380	TGGTAACCATCCTTCTATTC
199011	31207	GTTTGTACATTTTTTTCCTG	243598	75794	TATTATTGGATAGATGACTG	288185	120381	CTGGTAACCATCCTTCTATT
199012	31208	TGTTTGTACATTTTTTTCCT	243599	75795	GTATTATTGGATAGATGACT	288186	120382	TCTGGTAACCATCCTTCTAT
199013	31209	ATGTTTGTACATTTTTTTCC	243600	75796	TGTATTATTGGATAGATGAC	288187	120383	CTCTGGTAACCATCCTTCTA
199014	31210	TATGTTTGTACATTTTTTTC	243601	75797	ATGTATTATTGGATAGATGA	288188	120384	CCTCTGGTAACCATCCTTCT
199015	31211	ATATGTTTGTACATTTTTTT	243602	75798	AATGTATTATTGGATAGATG	288189	120385	GCCTCTGGTAACCATCCTTC
199016	31212	AATATGTTTGTACATTTTTT	243603	75799	GAATGTATTATTGGATAGAT	288190	120386	AGCCTCTGGTAACCATCCTT
199017	31213	GAATATGTTTGTACATTTTT	243604	75800	TGAATGTATTATTGGATAGA	288191	120387	CAGCCTCTGGTAACCATCCT
199018	31214	TGAATATGTTTGTACATTTT	243605	75801	ATGAATGTATTATTGGATAG	288192	120388	CCAGCCTCTGGTAACCATCC
199019	31215	ATGAATATGTTTGTACATTT	243606	75802	GATGAATGTATTATTGGATA	288193	120389	CCCAGCCTCTGGTAACCATC
199020	31216	TATGAATATGTTTGTACATT	243607	75803	GGATGAATGTATTATTGGAT	288194	120390	TCCCAGCCTCTGGTAACCAT
199021	31217	CTATGAATATGTTTGTACAT	243608	75804	TGGATGAATGTATTATTGGA	288195	120391	TTCCCAGCCTCTGGTAACCA
199022	31218	ACTATGAATATGTTTGTACA	243609	75805	TTGGATGAATGTATTATTGG	288196	120392	CTTCCCAGCCTCTGGTAACC
199023	31219	CACTATGAATATGTTTGTAC	243610	75806	ATTGGATGAATGTATTATTG	288197	120393	CCTTCCCAGCCTCTGGTAAC
199024	31220	TCACTATGAATATGTTTGTA	243611	75807	GATTGGATGAATGTATTATT	288198	120394	CCCTTCCCAGCCTCTGGTAA
199025	31221	ATCACTATGAATATGTTTGT	243612	75808	TGATTGGATGAATGTATTAT	288199	120395	ACCCTTCCCAGCCTCTGGTA
199026	31222	CATCACTATGAATATGTTTG	243613	75809	ATGATTGGATGAATGTATTA	288200	120396	TACCCTTCCCAGCCTCTGGT
199027	31223	ACATCACTATGAATATGTTT	243614	75810	GATGATTGGATGAATGTATT	288201	120397	CTACCCTTCCCAGCCTCTGG
199028	31224	GACATCACTATGAATATGTT	243615	75811	GGATGATTGGATGAATGTAT	288202	120398	ACTACCCTTCCCAGCCTCTG
199029	31225	AGACATCACTATGAATATGT	243616	75812	TGGATGATTGGATGAATGTA	288203	120399	CACTACCCTTCCCAGCCTCT
199030	31226	GAGACATCACTATGAATATG	243617	75813	ATGGATGATTGGATGAATGT	288204	120400	TCACTACCCTTCCCAGCCTC
199031	31227	AGAGACATCACTATGAATAT	243618	75814	GATGGATGATTGGATGAATG	288205	120401	CTCACTACCCTTCCCAGCCT
199032	31228	CAGAGACATCACTATGAATA	243619	75815	GGATGGATGATTGGATGAAT	288206	120402	CCTCACTACCCTTCCCAGCC
199033	31229	CCAGAGACATCACTATGAAT	243620	75816	TGGATGGATGATTGGATGAA	288207	120403	CCCTCACTACCCTTCCCAGC
199034	31230	ACCAGAGACATCACTATGAA	243621	75817	ATGGATGGATGATTGGATGA	288208	120404	CCCCTCACTACCCTTCCCAG
199035	31231	CACCAGAGACATCACTATGA	243622	75818	GATGGATGGATGATTGGATG	288209	120405	TCCCCTCACTACCCTTCCCA
199036	31232	CCACCAGAGACATCACTATG	243623	75819	GGATGGATGGATGATTGGAT	288210	120406	ATCCCCTCACTACCCTTCCC
199037	31233	ACCACCAGAGACATCACTAT	243624	75820	TGGATGGATGGATGATTGGA	288211	120407	CATCCCCTCACTACCCTTCC
199038	31234	TACCACCAGAGACATCACTA	243625	75821	ATGGATGGATGGATGATTGG	288212	120408	CCATCCCCTCACTACCCTTC
199039	31235	CTACCACCAGAGACATCACT	243626	75822	GATGGATGGATGGATGATTG	288213	120409	ACCATCCCCTCACTACCCTT
199040	31236	CCTACCACCAGAGACATCAC	243627	75823	GGATGGATGGATGGATGATT	288214	120410	CACCATCCCCTCACTACCCT
199041	31237	TCCTACCACCAGAGACATCA	243628	75824	TGGATGGATGGATGGATGAT	288215	120411	CCACCATCCCCTCACTACCC
199042	31238	ATCCTACCACCAGAGACATC	243629	75825	GTGGATGGATGGATGGATGA	288216	120412	CCCACCATCCCCTCACTACC
199043	31239	AATCCTACCACCAGAGACAT	243630	75826	GGTGGATGGATGGATGGATG	288217	120413	CCCCACCATCCCCTCACTAC
199044	31240	TAATCCTACCACCAGAGACA	243631	75827	GGGTGGATGGATGGATGGAT	288218	120414	CCCCCACCATCCCCTCACTA
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199050	31246	TGATCATAATCCTACCACCA	243637	75833	ATGAATGGGTGGATGGATGG	288224	120420	ACCATCCCCCCACCATCCCC

199051	31247	CTGATCATAATCCTACCACC	243638	75834	GATGAATGGGTGGATGGATG	288225	120421	GACCATCCCCCCACCATCCC
199052	31248	ACTGATCATAATCCTACCAC	243639	75835	GGATGAATGGGTGGATGGAT	288226	120422	TGACCATCCCCCCACCATCC
199053	31249	TACTGATCATAATCCTACCA	243640	75836	TGGATGAATGGGTGGATGGA	288227	120423	TTGACCATCCCCCCACCATC
199054	31250	TTACTGATCATAATCCTACC	243641	75837	ATGGATGAATGGGTGGATGG	288228	120424	ATTGACCATCCCCCCACCAT
199055	31251	CTTACTGATCATAATCCTAC	243642	75838	GATGGATGAATGGGTGGATG	288229	120425	CATTGACCATCCCCCCACCA
199056	31252	ACTTACTGATCATAATCCTA	243643	75839	GGATGGATGAATGGGTGGAT	288230	120426	CCATTGACCATCCCCCCACC
199057	31253	TACTTACTGATCATAATCCT	243644	75840	TGGATGGATGAATGGGTGGA	288231	120427	CCCATTGACCATCCCCCCAC
199058	31254	GTACTTACTGATCATAATCC	243645	75841	ATGGATGGATGAATGGGTGG	288232	120428	ACCCATTGACCATCCCCCCA
199059	31255	AGTACTTACTGATCATAATC	243646	75842	GATGGATGGATGAATGGGTG	288233	120429	TACCCATTGACCATCCCCCC
199060	31256	AAGTACTTACTGATCATAAT	243647	75843	GGATGGATGGATGAATGGGT	288234	120430	GTACCCATTGACCATCCCCC
199061	31257	GAAGTACTTACTGATCATAA	243648	75844	CGGATGGATGGATGAATGGG	288235	120431	TGTACCCATTGACCATCCCC
199062	31258	AGAAGTACTTACTGATCATA	243649	75845	ACGGATGGATGGATGAATGG	288236	120432	TTGTACCCATTGACCATCCC
199063	31259	CAGAAGTACTTACTGATCAT	243650	75846	GACGGATGGATGGATGAATG	288237	120433	TTTGTACCCATTGACCATCC
199064	31260	ACAGAAGTACTTACTGATCA	243651	75847	GGACGGATGGATGGATGAAT	288238	120434	TTTTGTACCCATTGACCATC
199065	31261	GACAGAAGTACTTACTGATC	243652	75848	CGGACGGATGGATGGATGAA	288239	120435	TTTTTGTACCCATTGACCAT
199066	31262	AGACAGAAGTACTTACTGAT	243653	75849	ACGGACGGATGGATGGATGA	288240	120436	TTTTTTGTACCCATTGACCA
199067	31263	GAGACAGAAGTACTTACTGA	243654	75850	GACGGACGGATGGATGGATG	288241	120437	TTTTTTTGTACCCATTGACC
199068	31264	AGAGACAGAAGTACTTACTG	243655	75851	GGACGGACGGATGGATGGAT	288242	120438	TTTTTTTTGTACCCATTGAC
199069	31265	AAGAGACAGAAGTACTTACT	243656	75852	TGGACGGACGGATGGATGGA	288243	120439	ATTTTTTTTGTACCCATTGA
199070	31266	GAAGAGACAGAAGTACTTAC	243657	75853	GTGGACGGACGGATGGATGG	288244	120440	TATTTTTTTTGTACCCATTG
199071	31267	TGAAGAGACAGAAGTACTTA	243658	75854	GGTGGACGGACGGATGGATG	288245	120441	CTATTTTTTTTGTACCCATT
199072	31268	ATGAAGAGACAGAAGTACTT	243659	75855	GGGTGGACGGACGGATGGAT	288246	120442	TCTATTTTTTTTGTACCCAT
199073	31269	TATGAAGAGACAGAAGTACT	243660	75856	TGGGTGGACGGACGGATGGA	288247	120443	TTCTATTTTTTTTGTACCCA
199074	31270	ATATGAAGAGACAGAAGTAC	243661	75857	ATGGGTGGACGGACGGATGG	288248	120444	ATTCTATTTTTTTTGTACCC
199075	31271	AATATGAAGAGACAGAAGTA	243662	75858	GATGGGTGGACGGACGGATG	288249	120445	TATTCTATTTTTTTTGTACC
199076	31272	AAATATGAAGAGACAGAAGT	243663	75859	TGATGGGTGGACGGACGGAT	288250	120446	TTATTCTATTTTTTTTGTAC
199077	31273	AAAATATGAAGAGACAGAAG	243664	75860	ATGATGGGTGGACGGACGGA	288251	120447	CTTATTCTATTTTTTTTGTA
199078	31274	GAAAATATGAAGAGACAGAA	243665	75861	CATGATGGGTGGACGGACGG	288252	120448	TCTTATTCTATTTTTTTTGT
199079	31275	GGAAAATATGAAGAGACAGA	243666	75862	CCATGATGGGTGGACGGACG	288253	120449	GTCTTATTCTATTTTTTTTG
199080	31276	AGGAAAATATGAAGAGACAG	243667	75863	ACCATGATGGGTGGACGGAC	288254	120450	GGTCTTATTCTATTTTTTTT
199081	31277	CAGGAAAATATGAAGAGACA	243668	75864	TACCATGATGGGTGGACGGA	288255	120451	AGGTCTTATTCTATTTTTTT
199082	31278	ACAGGAAAATATGAAGAGAC	243669	75865	ATACCATGATGGGTGGACGG	288256	120452	TAGGTCTTATTCTATTTTTT
199083	31279	TACAGGAAAATATGAAGAGA	243670	75866	CATACCATGATGGGTGGACG	288257	120453	CTAGGTCTTATTCTATTTTT
199084	31280	ATACAGGAAAATATGAAGAG	243671	75867	TCATACCATGATGGGTGGAC	288258	120454	ACTAGGTCTTATTCTATTTT
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199086	31282	AAATACAGGAAAATATGAAG	243673	75869	GCTCATACCATGATGGGTGG	288260	120456	ATACTAGGTCTTATTCTATT
199087	31283	CAAATACAGGAAAATATGAA	243674	75870	GGCTCATACCATGATGGGTG	288261	120457	AATACTAGGTCTTATTCTAT
199088	31284	TCAAATACAGGAAAATATGA	243675	75871	TGGCTCATACCATGATGGGT	288262	120458	AAATACTAGGTCTTATTCTA
199089	31285	ATCAAATACAGGAAAATATG	243676	75872	ATGGCTCATACCATGATGGG	288263	120459	CAAATACTAGGTCTTATTCT
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199091	31287	TTATCAAATACAGGAAAATA	243678	75874	TCATGGCTCATACCATGATG	288265	120461	ATCAAATACTAGGTCTTATT
199092	31288	ATTATCAAATACAGGAAAAT	243679	75875	ATCATGGCTCATACCATGAT	288266	120462	TATCAAATACTAGGTCTTAT
199093	31289	TATTATCAAATACAGGAAAA	243680	75876	AATCATGGCTCATACCATGA	288267	120463	CTATCAAATACTAGGTCTTA
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199096	31292	ATGTATTATCAAATACAGGA	243683	75879	GTAAATCATGGCTCATACCA	288270	120466	GCACTATCAAATACTAGGTC
199097	31293	CATGTATTATCAAATACAGG	243684	75880	GGTAAATCATGGCTCATACC	288271	120467	TGCACTATCAAATACTAGGT
199098	31294	GCATGTATTATCAAATACAG	243685	75881	TGGTAAATCATGGCTCATAC	288272	120468	TTGCACTATCAAATACTAGG
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199100	31296	ATGCATGTATTATCAAATAC	243687	75883	CGTGGTAAATCATGGCTCAT	288274	120470	TGTTGCACTATCAAATACTA
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199102	31298	ATATGCATGTATTATCAAAT	243689	75885	ATCGTGGTAAATCATGGCTC	288276	120472	CCTGTTGCACTATCAAATAC
199103	31299	CATATGCATGTATTATCAAA	243690	75886	CATCGTGGTAAATCATGGCT	288277	120473	CCCTGTTGCACTATCAAATA
199104	31300	ACATATGCATGTATTATCAA	243691	75887	CCATCGTGGTAAATCATGGC	288278	120474	ACCCTGTTGCACTATCAAAT
199105	31301	AACATATGCATGTATTATCA	243692	75888	ACCATCGTGGTAAATCATGG	288279	120475	CACCCTGTTGCACTATCAAA
199106	31302	CAACATATGCATGTATTATC	243693	75889	GACCATCGTGGTAAATCATG	288280	120476	TCACCCTGTTGCACTATCAA
199107	31303	ACAACATATGCATGTATTAT	243694	75890	GGACCATCGTGGTAAATCAT	288281	120477	GTCACCCTGTTGCACTATCA
199108	31304	AACAACATATGCATGTATTA	243695	75891	GGGACCATCGTGGTAAATCA	288282	120478	AGTCACCCTGTTGCACTATC
199109	31305	AAACAACATATGCATGTATT	243696	75892	GGGGACCATCGTGGTAAATC	288283	120479	TAGTCACCCTGTTGCACTAT
199110	31306	AAAACAACATATGCATGTAT	243697	75893	AGGGGACCATCGTGGTAAAT	288284	120480	ATAGTCACCCTGTTGCACTA
199111	31307	AAAAACAACATATGCATGTA	243698	75894	CAGGGGACCATCGTGGTAAA	288285	120481	TATAGTCACCCTGTTGCACT
199112	31308	TAAAAACAACATATGCATGT	243699	75895	ACAGGGGACCATCGTGGTAA	288286	120482	CTATAGTCACCCTGTTGCAC
199113	31309	TTAAAAACAACATATGCATG	243700	75896	CACAGGGGACCATCGTGGTA	288287	120483	ACTATAGTCACCCTGTTGCA
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199116	31312	ATTTTAAAAACAACATATGC	243703	75899	GTCCACAGGGGACCATCGTG	288290	120486	TTGACTATAGTCACCCTGTT
199117	31313	TATTTTAAAAACAACATATG	243704	75900	TGTCCACAGGGGACCATCGT	288291	120487	ATTGACTATAGTCACCCTGT
199118	31314	TTATTTTAAAAACAACATAT	243705	75901	CTGTCCACAGGGGACCATCG	288292	120488	TATTGACTATAGTCACCCTG
199119	31315	CTTATTTTAAAAACAACATA	243706	75902	GCTGTCCACAGGGGACCATC	288293	120489	TTATTGACTATAGTCACCCT
199120	31316	TCTTATTTTAAAAACAACAT	243707	75903	GGCTGTCCACAGGGGACCAT	288294	120490	ATTATTGACTATAGTCACCC
199121	31317	TTCTTATTTTAAAAACAACA	243708	75904	GGGCTGTCCACAGGGGACCA	288295	120491	TATTATTGACTATAGTCACC
199122	31318	TTTCTTATTTTAAAAACAAC	243709	75905	TGGGCTGTCCACAGGGGACC	288296	120492	TTATTATTGACTATAGTCAC

199123	31319	TTTTCTTATTTTAAAAACAA	243710	75906	CTGGGCTGTCCACAGGGGAC	288297	120493	ATTATTATTGACTATAGTCA
199124	31320	TTTTTCTTATTTTAAAAACA	243711	75907	CCTGGGCTGTCCACAGGGGA	288298	120494	AATTATTATTGACTATAGTC
199125	31321	ATTTTTCTTATTTTAAAAAC	243712	75908	ACCTGGGCTGTCCACAGGGG	288299	120495	AAATTATTATTGACTATAGT
199126	31322	AATTTTTCTTATTTTAAAAA	243713	75909	CACCTGGGCTGTCCACAGGG	288300	120496	TAAATTATTATTGACTATAG
199127	31323	AAATTTTTCTTATTTTAAAA	243714	75910	CCACCTGGGCTGTCCACAGG	288301	120497	TTAAATTATTATTGACTATA
199128	31324	AAAATTTTTCTTATTTTAAA	243715	75911	CCCACCTGGGCTGTCCACAG	288302	120498	ATTAAATTATTATTGACTAT
199129	31325	TAAAATTTTTCTTATTTTAA	243716	75912	CCCCACCTGGGCTGTCCACA	288303	120499	AATTAAATTATTATTGACTA
199130	31326	TTAAAATTTTTCTTATTTTA	243717	75913	GCCCCACCTGGGCTGTCCAC	288304	120500	CAATTAAATTATTATTGACT
199131	31327	CTTAAAATTTTTCTTATTTT	243718	75914	TGCCCCACCTGGGCTGTCCA	288305	120501	ACAATTAAATTATTATTGAC
199132	31328	ACTTAAAATTTTTCTTATTT	243719	75915	CTGCCCCACCTGGGCTGTCC	288306	120502	TACAATTAAATTATTATTGA
199133	31329	AACTTAAAATTTTTCTTATT	243720	75916	TCTGCCCCACCTGGGCTGTC	288307	120503	GTACAATTAAATTATTATTG
199134	31330	AAACTTAAAATTTTTCTTAT	243721	75917	TTCTGCCCCACCTGGGCTGT	288308	120504	TGTACAATTAAATTATTATT
199135	31331	TAAACTTAAAATTTTTCTTA	243722	75918	GTTCTGCCCCACCTGGGCTG	288309	120505	ATGTACAATTAAATTATTAT
199136	31332	TTAAACTTAAAATTTTTCTT	243723	75919	AGTTCTGCCCCACCTGGGCT	288310	120506	AATGTACAATTAAATTATTA
199137	31333	TTTAAACTTAAAATTTTTCT	243724	75920	CAGTTCTGCCCCACCTGGGC	288311	120507	AAATGTACAATTAAATTATT
199138	31334	TTTTAAACTTAAAATTTTTC	243725	75921	TCAGTTCTGCCCCACCTGGG	288312	120508	TAAATGTACAATTAAATTAT
199139	31335	ATTTTAAACTTAAAATTTTT	243726	75922	TTCAGTTCTGCCCCACCTGG	288313	120509	TTAAATGTACAATTAAATTA
199140	31336	AATTTTAAACTTAAAATTTT	243727	75923	CTTCAGTTCTGCCCCACCTG	288314	120510	TTTAAATGTACAATTAAATT
199141	31337	CAATTTTAAACTTAAAATTT	243728	75924	CCTTCAGTTCTGCCCCACCT	288315	120511	TTTTAAATGTACAATTAAAT
199142	31338	CCAATTTTAAACTTAAAATT	243729	75925	CCCTTCAGTTCTGCCCCACC	288316	120512	TTTTTAAATGTACAATTAAA
199143	31339	TCCAATTTTAAACTTAAAAT	243730	75926	TCCCTTCAGTTCTGCCCCAC	288317	120513	ATTTTTAAATGTACAATTAA
199144	31340	CTCCAATTTTAAACTTAAAA	243731	75927	TTCCCTTCAGTTCTGCCCCA	288318	120514	TATTTTTAAATGTACAATTA
199145	31341	GCTCCAATTTTAAACTTAAA	243732	75928	CTTCCCTTCAGTTCTGCCCC	288319	120515	TTATTTTTAAATGTACAATT
199146	31342	AGCTCCAATTTTAAACTTAA	243733	75929	GCTTCCCTTCAGTTCTGCCC	288320	120516	GTTATTTTTAAATGTACAAT
199147	31343	CAGCTCCAATTTTAAACTTA	243734	75930	GGCTTCCCTTCAGTTCTGCC	288321	120517	AGTTATTTTTAAATGTACAA
199148	31344	TCAGCTCCAATTTTAAACTT	243735	75931	GGGCTTCCCTTCAGTTCTGC	288322	120518	TAGTTATTTTTAAATGTACA
199149	31345	TTCAGCTCCAATTTTAAACT	243736	75932	TGGGCTTCCCTTCAGTTCTG	288323	120519	TTAGTTATTTTTAAATGTAC
199150	31346	TTTCAGCTCCAATTTTAAAC	243737	75933	CTGGGCTTCCCTTCAGTTCT	288324	120520	TTTAGTTATTTTTAAATGTA
199151	31347	TTTTCAGCTCCAATTTTAAA	243738	75934	CCTGGGCTTCCCTTCAGTTC	288325	120521	TTTTAGTTATTTTTAAATGT
199152	31348	CTTTTCAGCTCCAATTTTAA	243739	75935	CCCTGGGCTTCCCTTCAGTT	288326	120522	CTTTTAGTTATTTTTAAATG
199153	31349	ACTTTTCAGCTCCAATTTTA	243740	75936	GCCCTGGGCTTCCCTTCAGT	288327	120523	TCTTTTAGTTATTTTTAAAT
199154	31350	CACTTTTCAGCTCCAATTTT	243741	75937	AGCCCTGGGCTTCCCTTCAG	288328	120524	ATCTTTTAGTTATTTTTAAA
199155	31351	ACACTTTTCAGCTCCAATTT	243742	75938	CAGCCCTGGGCTTCCCTTCA	288329	120525	TATCTTTTAGTTATTTTTAA
199156	31352	AACACTTTTCAGCTCCAATT	243743	75939	GCAGCCCTGGGCTTCCCTTC	288330	120526	CTATCTTTTAGTTATTTTTA
199157	31353	AAACACTTTTCAGCTCCAAT	243744	75940	GGCAGCCCTGGGCTTCCCTT	288331	120527	GCTATCTTTTAGTTATTTTT
199158	31354	AAAACACTTTTCAGCTCCAA	243745	75941	GGGCAGCCCTGGGCTTCCCT	288332	120528	GGCTATCTTTTAGTTATTTT
199159	31355	AAAAACACTTTTCAGCTCCA	243746	75942	GGGGCAGCCCTGGGCTTCCC	288333	120529	CGGCTATCTTTTAGTTATTT
199160	31356	TAAAAACACTTTTCAGCTCC	243747	75943	GGGGGCAGCCCTGGGCTTCC	288334	120530	CCGGCTATCTTTTAGTTATT
199161	31357	CTAAAAACACTTTTCAGCTC	243748	75944	TGGGGGCAGCCCTGGGCTTC	288335	120531	CCCGGCTATCTTTTAGTTAT
199162	31358	CCTAAAAACACTTTTCAGCT	243749	75945	ATGGGGGCAGCCCTGGGCTT	288336	120532	ACCCGGCTATCTTTTAGTTA
199163	31359	ACCTAAAAACACTTTTCAGC	243750	75946	TATGGGGGCAGCCCTGGGCT	288337	120533	CACCCGGCTATCTTTTAGTT
199164	31360	GACCTAAAAACACTTTTCAG	243751	75947	TTATGGGGGCAGCCCTGGGC	288338	120534	GCACCCGGCTATCTTTTAGT
199165	31361	TGACCTAAAAACACTTTTCA	243752	75948	TTTATGGGGGCAGCCCTGGG	288339	120535	TGCACCCGGCTATCTTTTAG
199166	31362	CTGACCTAAAAACACTTTTC	243753	75949	GTTTATGGGGGCAGCCCTGG	288340	120536	CTGCACCCGGCTATCTTTTA
199167	31363	CCTGACCTAAAAACACTTTT	243754	75950	TGTTTATGGGGGCAGCCCTG	288341	120537	ACTGCACCCGGCTATCTTTT
199168	31364	GCCTGACCTAAAAACACTTT	243755	75951	ATGTTTATGGGGGCAGCCCT	288342	120538	CACTGCACCCGGCTATCTTT
199169	31365	CGCCTGACCTAAAAACACTT	243756	75952	AATGTTTATGGGGGCAGCCC	288343	120539	CCACTGCACCCGGCTATCTT
199170	31366	TCGCCTGACCTAAAAACACT	243757	75953	AAATGTTTATGGGGGCAGCC	288344	120540	GCCACTGCACCCGGCTATCT
199171	31367	CTCGCCTGACCTAAAAACAC	243758	75954	CAAATGTTTATGGGGGCAGC	288345	120541	AGCCACTGCACCCGGCTATC
199172	31368	CCTCGCCTGACCTAAAAACA	243759	75955	GCAAATGTTTATGGGGGCAG	288346	120542	AAGCCACTGCACCCGGCTAT
199173	31369	ACCTCGCCTGACCTAAAAAC	243760	75956	GGCAAATGTTTATGGGGGCA	288347	120543	TAAGCCACTGCACCCGGCTA
199174	31370	CACCTCGCCTGACCTAAAAA	243761	75957	AGGCAAATGTTTATGGGGGC	288348	120544	GTAAGCCACTGCACCCGGCT
199175	31371	CCACCTCGCCTGACCTAAAA	243762	75958	GAGGCAAATGTTTATGGGGG	288349	120545	CGTAAGCCACTGCACCCGGC
199176	31372	GCCACCTCGCCTGACCTAAA	243763	75959	GGAGGCAAATGTTTATGGGG	288350	120546	ACGTAAGCCACTGCACCCGG
199177	31373	AGCCACCTCGCCTGACCTAA	243764	75960	AGGAGGCAAATGTTTATGGG	288351	120547	GACGTAAGCCACTGCACCCG
199178	31374	GAGCCACCTCGCCTGACCTA	243765	75961	AAGGAGGCAAATGTTTATGG	288352	120548	AGACGTAAGCCACTGCACCC
199179	31375	TGAGCCACCTCGCCTGACCT	243766	75962	AAAGGAGGCAAATGTTTATG	288353	120549	CAGACGTAAGCCACTGCACC
199180	31376	GTGAGCCACCTCGCCTGACC	243767	75963	TAAAGGAGGCAAATGTTTAT	288354	120550	ACAGACGTAAGCCACTGCAC
199181	31377	TGTGAGCCACCTCGCCTGAC	243768	75964	GTAAAGGAGGCAAATGTTTA	288355	120551	TACAGACGTAAGCCACTGCA
199182	31378	GTGTGAGCCACCTCGCCTGA	243769	75965	TGTAAAGGAGGCAAATGTTT	288356	120552	TTACAGACGTAAGCCACTGC
199183	31379	GGTGTGAGCCACCTCGCCTG	243770	75966	ATGTAAAGGAGGCAAATGTT	288357	120553	ATTACAGACGTAAGCCACTG
199184	31380	AGGTGTGAGCCACCTCGCCT	243771	75967	CATGTAAAGGAGGCAAATGT	288358	120554	GATTACAGACGTAAGCCACT
199185	31381	CAGGTGTGAGCCACCTCGCC	243772	75968	CCATGTAAAGGAGGCAAATG	288359	120555	GGATTACAGACGTAAGCCAC
199186	31382	ACAGGTGTGAGCCACCTCGC	243773	75969	TCCATGTAAAGGAGGCAAAT	288360	120556	GGGATTACAGACGTAAGCCA
199187	31383	TACAGGTGTGAGCCACCTCG	243774	75970	ATCCATGTAAAGGAGGCAAA	288361	120557	TGGGATTACAGACGTAAGCC
199188	31384	TTACAGGTGTGAGCCACCTC	243775	75971	CATCCATGTAAAGGAGGCAA	288362	120558	CTGGGATTACAGACGTAAGC
199189	31385	ATTACAGGTGTGAGCCACCT	243776	75972	TCATCCATGTAAAGGAGGCA	288363	120559	ACTGGGATTACAGACGTAAG
199190	31386	TATTACAGGTGTGAGCCACC	243777	75973	CTCATCCATGTAAAGGAGGC	288364	120560	TACTGGGATTACAGACGTAA
199191	31387	CTATTACAGGTGTGAGCCAC	243778	75974	TCTCATCCATGTAAAGGAGG	288365	120561	GTACTGGGATTACAGACGTA
199192	31388	GCTATTACAGGTGTGAGCCA	243779	75975	TTCTCATCCATGTAAAGGAG	288366	120562	AGTACTGGGATTACAGACGT
199193	31389	TGCTATTACAGGTGTGAGCC	243780	75976	GTTCTCATCCATGTAAAGGA	288367	120563	AAGTACTGGGATTACAGACG
199194	31390	GTGCTATTACAGGTGTGAGC	243781	75977	AGTTCTCATCCATGTAAAGG	288368	120564	AAAGTACTGGGATTACAGAC

199195	31391	GGTGCTATTACAGGTGTGAG	243782	75978	TAGTTCTCATCCATGTAAAG	288369	120565	CAAAGTACTGGGATTACAGA
199196	31392	TGGTGCTATTACAGGTGTGA	243783	75979	CTAGTTCTCATCCATGTAAA	288370	120566	CCAAAGTACTGGGATTACAG
199197	31393	GTGGTGCTATTACAGGTGTG	243784	75980	TCTAGTTCTCATCCATGTAA	288371	120567	CCCAAAGTACTGGGATTACA
199198	31394	AGTGGTGCTATTACAGGTGT	243785	75981	ATCTAGTTCTCATCCATGTA	288372	120568	TCCCAAAGTACTGGGATTAC
199199	31395	AAGTGGTGCTATTACAGGTG	243786	75982	GATCTAGTTCTCATCCATGT	288373	120569	CTCCCAAAGTACTGGGATTA
199200	31396	AAAGTGGTGCTATTACAGGT	243787	75983	GGATCTAGTTCTCATCCATG	288374	120570	CCTCCCAAAGTACTGGGATT
199201	31397	CAAAGTGGTGCTATTACAGG	243788	75984	TGGATCTAGTTCTCATCCAT	288375	120571	GCCTCCCAAAGTACTGGGAT
199202	31398	CCAAAGTGGTGCTATTACAG	243789	75985	GTGGATCTAGTTCTCATCCA	288376	120572	AGCCTCCCAAAGTACTGGGA
199203	31399	CCCAAAGTGGTGCTATTACA	243790	75986	TGTGGATCTAGTTCTCATCC	288377	120573	CAGCCTCCCAAAGTACTGGG
199204	31400	TCCCAAAGTGGTGCTATTAC	243791	75987	ATGTGGATCTAGTTCTCATC	288378	120574	TCAGCCTCCCAAAGTACTGG
199205	31401	CTCCCAAAGTGGTGCTATTA	243792	75988	CATGTGGATCTAGTTCTCAT	288379	120575	CTCAGCCTCCCAAAGTACTG
199206	31402	CCTCCCAAAGTGGTGCTATT	243793	75989	ACATGTGGATCTAGTTCTCA	288380	120576	CCTCAGCCTCCCAAAGTACT
199207	31403	GCCTCCCAAAGTGGTGCTAT	243794	75990	TACATGTGGATCTAGTTCTC	288381	120577	ACCTCAGCCTCCCAAAGTAC
199208	31404	AGCCTCCCAAAGTGGTGCTA	243795	75991	ATACATGTGGATCTAGTTCT	288382	120578	CACCTCAGCCTCCCAAAGTA
199209	31405	CAGCCTCCCAAAGTGGTGCT	243796	75992	TATACATGTGGATCTAGTTC	288383	120579	CCACCTCAGCCTCCCAAAGT
199210	31406	TCAGCCTCCCAAAGTGGTGC	243797	75993	TTATACATGTGGATCTAGTT	288384	120580	CCCACCTCAGCCTCCCAAAG
199211	31407	CTCAGCCTCCCAAAGTGGTG	243798	75994	TTTATACATGTGGATCTAGT	288385	120581	GCCCACCTCAGCCTCCCAAA
199212	31408	CCTCAGCCTCCCAAAGTGGT	243799	75995	ATTTATACATGTGGATCTAG	288386	120582	CGCCCACCTCAGCCTCCCAA
199213	31409	GCCTCAGCCTCCCAAAGTGG	243800	75996	GATTTATACATGTGGATCTA	288387	120583	ACGCCCACCTCAGCCTCCCA
199214	31410	TGCCTCAGCCTCCCAAAGTG	243801	75997	GGATTTATACATGTGGATCT	288388	120584	AACGCCCACCTCAGCCTCCC
199215	31411	CTGCCTCAGCCTCCCAAAGT	243802	75998	AGGATTTATACATGTGGATC	288389	120585	AAACGCCCACCTCAGCCTCC
199216	31412	ACTGCCTCAGCCTCCCAAAG	243803	75999	GAGGATTTATACATGTGGAT	288390	120586	CAAACGCCCACCTCAGCCTC
199217	31413	GACTGCCTCAGCCTCCCAAA	243804	76000	TGAGGATTTATACATGTGGA	288391	120587	TCAAACGCCCACCTCAGCCT
199218	31414	TGACTGCCTCAGCCTCCCAA	243805	76001	ATGAGGATTTATACATGTGG	288392	120588	CTCAAACGCCCACCTCAGCC
199219	31415	CTGACTGCCTCAGCCTCCCA	243806	76002	CATGAGGATTTATACATGTG	288393	120589	TCTCAAACGCCCACCTCAGC
199220	31416	TCTGACTGCCTCAGCCTCCC	243807	76003	TCATGAGGATTTATACATGT	288394	120590	GTCTCAAACGCCCACCTCAG
199221	31417	ATCTGACTGCCTCAGCCTCC	243808	76004	ATCATGAGGATTTATACATG	288395	120591	GGTCTCAAACGCCCACCTCA
199222	31418	GATCTGACTGCCTCAGCCTC	243809	76005	AATCATGAGGATTTATACAT	288396	120592	TGGTCTCAAACGCCCACCTC
199223	31419	TGATCTGACTGCCTCAGCCT	243810	76006	AAATCATGAGGATTTATACA	288397	120593	CTGGTCTCAAACGCCCACCT
199224	31420	GTGATCTGACTGCCTCAGCC	243811	76007	CAAATCATGAGGATTTATAC	288398	120594	GCTGGTCTCAAACGCCCACC
199225	31421	AGTGATCTGACTGCCTCAGC	243812	76008	TCAAATCATGAGGATTTATA	288399	120595	GGCTGGTCTCAAACGCCCAC
199226	31422	AAGTGATCTGACTGCCTCAG	243813	76009	TTCAAATCATGAGGATTTAT	288400	120596	AGGCTGGTCTCAAACGCCCA
199227	31423	CAAGTGATCTGACTGCCTCA	243814	76010	CTTCAAATCATGAGGATTTA	288401	120597	CAGGCTGGTCTCAAACGCCC
199228	31424	TCAAGTGATCTGACTGCCTC	243815	76011	CCTTCAAATCATGAGGATTT	288402	120598	CCAGGCTGGTCTCAAACGCC
199229	31425	CTCAAGTGATCTGACTGCCT	243816	76012	ACCTTCAAATCATGAGGATT	288403	120599	GCCAGGCTGGTCTCAAACGC
199230	31426	GCTCAAGTGATCTGACTGCC	243817	76013	CACCTTCAAATCATGAGGAT	288404	120600	GGCCAGGCTGGTCTCAAACG
199231	31427	GGCTCAAGTGATCTGACTGC	243818	76014	GCACCTTCAAATCATGAGGA	288405	120601	TGGCCAGGCTGGTCTCAAAC
199232	31428	GGGCTCAAGTGATCTGACTG	243819	76015	AGCACCTTCAAATCATGAGG	288406	120602	TTGGCCAGGCTGGTCTCAAA
199233	31429	TGGGCTCAAGTGATCTGACT	243820	76016	AAGCACCTTCAAATCATGAG	288407	120603	GTTGGCCAGGCTGGTCTCAA
199234	31430	CTGGGCTCAAGTGATCTGAC	243821	76017	AAAGCACCTTCAAATCATGA	288408	120604	TGTTGGCCAGGCTGGTCTCA
199235	31431	CCTGGGCTCAAGTGATCTGA	243822	76018	AAAAGCACCTTCAAATCATG	288409	120605	ATGTTGGCCAGGCTGGTCTC
199236	31432	TCCTGGGCTCAAGTGATCTG	243823	76019	TAAAAGCACCTTCAAATCAT	288410	120606	CATGTTGGCCAGGCTGGTCT
199237	31433	CTCCTGGGCTCAAGTGATCT	243824	76020	GTAAAAGCACCTTCAAATCA	288411	120607	CCATGTTGGCCAGGCTGGTC
199238	31434	ACTCCTGGGCTCAAGTGATC	243825	76021	GGTAAAAGCACCTTCAAATC	288412	120608	ACCATGTTGGCCAGGCTGGT
199239	31435	AACTCCTGGGCTCAAGTGAT	243826	76022	TGGTAAAAGCACCTTCAAAT	288413	120609	CACCATGTTGGCCAGGCTGG
199240	31436	GAACTCCTGGGCTCAAGTGA	243827	76023	TTGGTAAAAGCACCTTCAAA	288414	120610	TCACCATGTTGGCCAGGCTG
199241	31437	CGAACTCCTGGGCTCAAGTG	243828	76024	GTTGGTAAAAGCACCTTCAA	288415	120611	TTCACCATGTTGGCCAGGCT
199242	31438	TCGAACTCCTGGGCTCAAGT	243829	76025	TGTTGGTAAAAGCACCTTCA	288416	120612	TTTCACCATGTTGGCCAGGC
199243	31439	CTCGAACTCCTGGGCTCAAG	243830	76026	ATGTTGGTAAAAGCACCTTC	288417	120613	GTTTCACCATGTTGGCCAGG
199244	31440	TCTCGAACTCCTGGGCTCAA	243831	76027	AATGTTGGTAAAAGCACCTT	288418	120614	GGTTTCACCATGTTGGCCAG
199245	31441	GTCTCGAACTCCTGGGCTCA	243832	76028	GAATGTTGGTAAAAGCACCT	288419	120615	GGGTTTCACCATGTTGGCCA
199246	31442	GGTCTCGAACTCCTGGGCTC	243833	76029	TGAATGTTGGTAAAAGCACC	288420	120616	GGGGTTTCACCATGTTGGCC
199247	31443	TGGTCTCGAACTCCTGGGCT	243834	76030	GTGAATGTTGGTAAAAGCAC	288421	120617	TGGGGTTTCACCATGTTGGC
199248	31444	CTGGTCTCGAACTCCTGGGC	243835	76031	AGTGAATGTTGGTAAAAGCA	288422	120618	ATGGGGTTTCACCATGTTGG
199249	31445	GCTGGTCTCGAACTCCTGGG	243836	76032	GAGTGAATGTTGGTAAAAGC	288423	120619	GATGGGGTTTCACCATGTTG
199250	31446	GGCTGGTCTCGAACTCCTGG	243837	76033	TGAGTGAATGTTGGTAAAAG	288424	120620	AGATGGGGTTTCACCATGTT
199251	31447	AGGCTGGTCTCGAACTCCTG	243838	76034	ATGAGTGAATGTTGGTAAAA	288425	120621	GAGATGGGGTTTCACCATGT
199252	31448	CAGGCTGGTCTCGAACTCCT	243839	76035	CATGAGTGAATGTTGGTAAA	288426	120622	AGAGATGGGGTTTCACCATG
199253	31449	CCAGGCTGGTCTCGAACTCC	243840	76036	CCATGAGTGAATGTTGGTAA	288427	120623	TAGAGATGGGGTTTCACCAT
199254	31450	GCCAGGCTGGTCTCGAACTC	243841	76037	CCCATGAGTGAATGTTGGTA	288428	120624	GTAGAGATGGGGTTTCACCA
199255	31451	GGCCAGGCTGGTCTCGAACT	243842	76038	TCCCATGAGTGAATGTTGGT	288429	120625	AGTAGAGATGGGGTTTCACC
199256	31452	TGGCCAGGCTGGTCTCGAAC	243843	76039	ATCCCATGAGTGAATGTTGG	288430	120626	TAGTAGAGATGGGGTTTCAC
199257	31453	TTGGCCAGGCTGGTCTCGAA	243844	76040	AATCCCATGAGTGAATGTTG	288431	120627	TTAGTAGAGATGGGGTTTCA
199258	31454	GTTGGCCAGGCTGGTCTCGA	243845	76041	GAATCCCATGAGTGAATGTT	288432	120628	TTTAGTAGAGATGGGGTTTC
199259	31455	TGTTGGCCAGGCTGGTCTCG	243846	76042	AGAATCCCATGAGTGAATGT	288433	120629	TTTTAGTAGAGATGGGGTTT
199260	31456	ATGTTGGCCAGGCTGGTCTC	243847	76043	GAGAATCCCATGAGTGAATG	288434	120630	TTTTTAGTAGAGATGGGGTT
199261	31457	CATGTTGGCCAGGCTGGTCT	243848	76044	GGAGAATCCCATGAGTGAAT	288435	120631	ATTTTTAGTAGAGATGGGGT
199262	31458	CCATGTTGGCCAGGCTGGTC	243849	76045	GGGAGAATCCCATGAGTGAA	288436	120632	TATTTTTAGTAGAGATGGGG
199263	31459	ACCATGTTGGCCAGGCTGGT	243850	76046	TGGGAGAATCCCATGAGTGA	288437	120633	GTATTTTTAGTAGAGATGGG
199264	31460	CACCATGTTGGCCAGGCTGG	243851	76047	CTGGGAGAATCCCATGAGTG	288438	120634	TGTATTTTTAGTAGAGATGG
199265	31461	TCACCATGTTGGCCAGGCTG	243852	76048	CCTGGGAGAATCCCATGAGT	288439	120635	TTGTATTTTTAGTAGAGATG
199266	31462	TTCACCATGTTGGCCAGGCT	243853	76049	TCCTGGGAGAATCCCATGAG	288440	120636	TTTGTATTTTTAGTAGAGAT

199267	31463	TTTCACCATGTTGGCCAGGC	243854	76050	CTCCTGGGAGAATCCCATGA	288441	120637	TTTTGTATTTTTAGTAGAGA
199268	31464	GTTTCACCATGTTGGCCAGG	243855	76051	GCTCCTGGGAGAATCCCATG	288442	120638	TTTTTGTATTTTTAGTAGAG
199269	31465	GGTTTCACCATGTTGGCCAG	243856	76052	AGCTCCTGGGAGAATCCCAT	288443	120639	ATTTTTGTATTTTTAGTAGA
199270	31466	GGGTTTCACCATGTTGGCCA	243857	76053	GAGCTCCTGGGAGAATCCCA	288444	120640	AATTTTTGTATTTTTAGTAG
199271	31467	GGGGTTTCACCATGTTGGCC	243858	76054	AGAGCTCCTGGGAGAATCCC	288445	120641	TAATTTTTGTATTTTTAGTA
199272	31468	TGGGGTTTCACCATGTTGGC	243859	76055	TAGAGCTCCTGGGAGAATCC	288446	120642	CTAATTTTTGTATTTTTAGT
199273	31469	ATGGGGTTTCACCATGTTGG	243860	76056	CTAGAGCTCCTGGGAGAATC	288447	120643	GCTAATTTTTGTATTTTTAG
199274	31470	GATGGGGTTTCACCATGTTG	243861	76057	CCTAGAGCTCCTGGGAGAAT	288448	120644	GGCTAATTTTTGTATTTTTA
199275	31471	AGATGGGGTTTCACCATGTT	243862	76058	TCCTAGAGCTCCTGGGAGAA	288449	120645	TGGCTAATTTTTGTATTTTT
199276	31472	GAGATGGGGTTTCACCATGT	243863	76059	CTCCTAGAGCTCCTGGGAGA	288450	120646	CTGGCTAATTTTTGTATTTT
199277	31473	AGAGATGGGGTTTCACCATG	243864	76060	CCTCCTAGAGCTCCTGGGAG	288451	120647	CCTGGCTAATTTTTGTATTT
199278	31474	TAGAGATGGGGTTTCACCAT	243865	76061	TCCTCCTAGAGCTCCTGGGA	288452	120648	GCCTGGCTAATTTTTGTATT
199279	31475	GTAGAGATGGGGTTTCACCA	243866	76062	CTCCTCCTAGAGCTCCTGGG	288453	120649	TGCCTGGCTAATTTTTGTAT
199280	31476	AGTAGAGATGGGGTTTCACC	243867	76063	CCTCCTCCTAGAGCTCCTGG	288454	120650	ATGCCTGGCTAATTTTTGTA
199281	31477	TAGTAGAGATGGGGTTTCAC	243868	76064	GCCTCCTCCTAGAGCTCCTG	288455	120651	CATGCCTGGCTAATTTTTGT
199282	31478	TTAGTAGAGATGGGGTTTCA	243869	76065	TGCCTCCTCCTAGAGCTCCT	288456	120652	CCATGCCTGGCTAATTTTTG
199283	31479	TTTAGTAGAGATGGGGTTTC	243870	76066	CTGCCTCCTCCTAGAGCTCC	288457	120653	ACCATGCCTGGCTAATTTTT
199284	31480	TTTTAGTAGAGATGGGGTTT	243871	76067	CCTGCCTCCTCCTAGAGCTC	288458	120654	CACCATGCCTGGCTAATTTT
199285	31481	TTTTTAGTAGAGATGGGGTT	243872	76068	ACCTGCCTCCTCCTAGAGCT	288459	120655	CCACCATGCCTGGCTAATTT
199286	31482	ATTTTTAGTAGAGATGGGGT	243873	76069	TACCTGCCTCCTCCTAGAGC	288460	120656	GCCACCATGCCTGGCTAATT
199287	31483	TATTTTTAGTAGAGATGGGG	243874	76070	CTACCTGCCTCCTCCTAGAG	288461	120657	CGCCACCATGCCTGGCTAAT
199288	31484	TTATTTTTAGTAGAGATGGG	243875	76071	TCTACCTGCCTCCTCCTAGA	288462	120658	CCGCCACCATGCCTGGCTAA
199289	31485	TTTATTTTTAGTAGAGATGG	243876	76072	CTCTACCTGCCTCCTCCTAG	288463	120659	CCCGCCACCATGCCTGGCTA
199290	31486	TTTTATTTTTAGTAGAGATG	243877	76073	ACTCTACCTGCCTCCTCCTA	288464	120660	GCCCGCCACCATGCCTGGCT
199291	31487	TTTTTATTTTTAGTAGAGAT	243878	76074	AACTCTACCTGCCTCCTCCT	288465	120661	CGCCCGCCACCATGCCTGGC
199292	31488	TTTTTTATTTTTAGTAGAGA	243879	76075	CAACTCTACCTGCCTCCTCC	288466	120662	GCGCCCGCCACCATGCCTGG
199293	31489	TTTTTTTATTTTTAGTAGAG	243880	76076	TCAACTCTACCTGCCTCCTC	288467	120663	GGCGCCCGCCACCATGCCTG
199294	31490	ATTTTTTTATTTTTAGTAGA	243881	76077	CTCAACTCTACCTGCCTCCT	288468	120664	AGGCGCCCGCCACCATGCCT
199295	31491	AATTTTTTTATTTTTAGTAG	243882	76078	CCTCAACTCTACCTGCCTCC	288469	120665	CAGGCGCCCGCCACCATGCC
199296	31492	TAATTTTTTTATTTTTAGTA	243883	76079	ACCTCAACTCTACCTGCCTC	288470	120666	ACAGGCGCCCGCCACCATGC
199297	31493	CTAATTTTTTTATTTTTAGT	243884	76080	GACCTCAACTCTACCTGCCT	288471	120667	TACAGGCGCCCGCCACCATG
199298	31494	GCTAATTTTTTTATTTTTAG	243885	76081	TGACCTCAACTCTACCTGCC	288472	120668	TTACAGGCGCCCGCCACCAT
199299	31495	GGCTAATTTTTTTATTTTTA	243886	76082	ATGACCTCAACTCTACCTGC	288473	120669	ATTACAGGCGCCCGCCACCA
199300	31496	TGGCTAATTTTTTTATTTTT	243887	76083	GATGACCTCAACTCTACCTG	288474	120670	GATTACAGGCGCCCGCCACC
199301	31497	ATGGCTAATTTTTTTATTTT	243888	76084	AGATGACCTCAACTCTACCT	288475	120671	GGATTACAGGCGCCCGCCAC
199302	31498	CATGGCTAATTTTTTTATTT	243889	76085	GAGATGACCTCAACTCTACC	288476	120672	GGGATTACAGGCGCCCGCCA
199303	31499	ACATGGCTAATTTTTTTATT	243890	76086	TGAGATGACCTCAACTCTAC	288477	120673	TGGGATTACAGGCGCCCGCC
199304	31500	CACATGGCTAATTTTTTTAT	243891	76087	GTGAGATGACCTCAACTCTA	288478	120674	CTGGGATTACAGGCGCCCGC
199305	31501	ACACATGGCTAATTTTTTTA	243892	76088	CGTGAGATGACCTCAACTCT	288479	120675	GCTGGGATTACAGGCGCCCG
199306	31502	CACACATGGCTAATTTTTTT	243893	76089	GCGTGAGATGACCTCAACTC	288480	120676	AGCTGGGATTACAGGCGCCC
199307	31503	CCACACATGGCTAATTTTTT	243894	76090	TGCGTGAGATGACCTCAACT	288481	120677	TAGCTGGGATTACAGGCGCC
199308	31504	ACCACACATGGCTAATTTTT	243895	76091	ATGCGTGAGATGACCTCAAC	288482	120678	GTAGCTGGGATTACAGGCGC
199309	31505	CACCACACATGGCTAATTTT	243896	76092	AATGCGTGAGATGACCTCAA	288483	120679	AGTAGCTGGGATTACAGGCG
199310	31506	CCACCACACATGGCTAATTT	243897	76093	AAATGCGTGAGATGACCTCA	288484	120680	GAGTAGCTGGGATTACAGGC
199311	31507	GCCACCACACATGGCTAATT	243898	76094	AAAATGCGTGAGATGACCTC	288485	120681	CGAGTAGCTGGGATTACAGG
199312	31508	TGCCACCACACATGGCTAAT	243899	76095	TAAAATGCGTGAGATGACCT	288486	120682	CCGAGTAGCTGGGATTACAG
199313	31509	GTGCCACCACACATGGCTAA	243900	76096	GTAAAATGCGTGAGATGACC	288487	120683	CCCGAGTAGCTGGGATTACA
199314	31510	TGTGCCACCACACATGGCTA	243901	76097	TGTAAAATGCGTGAGATGAC	288488	120684	TCCCGAGTAGCTGGGATTAC
199315	31511	GTGTGCCACCACACATGGCT	243902	76098	CTGTAAAATGCGTGAGATGA	288489	120685	CTCCCGAGTAGCTGGGATTA
199316	31512	TGTGTGCCACCACACATGGC	243903	76099	TCTGTAAAATGCGTGAGATG	288490	120686	CCTCCCGAGTAGCTGGGATT
199317	31513	ATGTGTGCCACCACACATGG	243904	76100	ATCTGTAAAATGCGTGAGAT	288491	120687	GCCTCCCGAGTAGCTGGGAT
199318	31514	GATGTGTGCCACCACACATG	243905	76101	CATCTGTAAAATGCGTGAGA	288492	120688	AGCCTCCCGAGTAGCTGGGA
199319	31515	AGATGTGTGCCACCACACAT	243906	76102	TCATCTGTAAAATGCGTGAG	288493	120689	CAGCCTCCCGAGTAGCTGGG
199320	31516	CAGATGTGTGCCACCACACA	243907	76103	CTCATCTGTAAAATGCGTGA	288494	120690	TCAGCCTCCCGAGTAGCTGG
199321	31517	ACAGATGTGTGCCACCACAC	243908	76104	CCTCATCTGTAAAATGCGTG	288495	120691	CTCAGCCTCCCGAGTAGCTG
199322	31518	TACAGATGTGTGCCACCACA	243909	76105	TCCTCATCTGTAAAATGCGT	288496	120692	CCTCAGCCTCCCGAGTAGCT
199323	31519	TTACAGATGTGTGCCACCAC	243910	76106	TTCCTCATCTGTAAAATGCG	288497	120693	GCCTCAGCCTCCCGAGTAGC
199324	31520	ATTACAGATGTGTGCCACCA	243911	76107	TTTCCTCATCTGTAAAATGC	288498	120694	TGCCTCAGCCTCCCGAGTAG
199325	31521	GATTACAGATGTGTGCCACC	243912	76108	GTTTCCTCATCTGTAAAATG	288499	120695	CTGCCTCAGCCTCCCGAGTA
199326	31522	GGATTACAGATGTGTGCCAC	243913	76109	CGTTTCCTCATCTGTAAAAT	288500	120696	CCTGCCTCAGCCTCCCGAGT
199327	31523	GGGATTACAGATGTGTGCCA	243914	76110	CCGTTTCCTCATCTGTAAAA	288501	120697	TCCTGCCTCAGCCTCCCGAG
199328	31524	TGGGATTACAGATGTGTGCC	243915	76111	TCCGTTTCCTCATCTGTAAA	288502	120698	CTCCTGCCTCAGCCTCCCGA
199329	31525	CTGGGATTACAGATGTGTGC	243916	76112	CTCCGTTTCCTCATCTGTAA	288503	120699	TCTCCTGCCTCAGCCTCCCG
199330	31526	GCTGGGATTACAGATGTGTG	243917	76113	CCTCCGTTTCCTCATCTGTA	288504	120700	TTCTCCTGCCTCAGCCTCCC
199331	31527	AGCTGGGATTACAGATGTGT	243918	76114	GCCTCCGTTTCCTCATCTGT	288505	120701	ATTCTCCTGCCTCAGCCTCC
199332	31528	TAGCTGGGATTACAGATGTG	243919	76115	GGCCTCCGTTTCCTCATCTG	288506	120702	GATTCTCCTGCCTCAGCCTC
199333	31529	GTAGCTGGGATTACAGATGT	243920	76116	GGGCCTCCGTTTCCTCATCT	288507	120703	TGATTCTCCTGCCTCAGCCT
199334	31530	AGTAGCTGGGATTACAGATG	243921	76117	AGGGCCTCCGTTTCCTCATC	288508	120704	GTGATTCTCCTGCCTCAGCC
199335	31531	AAGTAGCTGGGATTACAGAT	243922	76118	CAGGGCCTCCGTTTCCTCAT	288509	120705	AGTGATTCTCCTGCCTCAGC
199336	31532	CAAGTAGCTGGGATTACAGA	243923	76119	TCAGGGCCTCCGTTTCCTCA	288510	120706	AAGTGATTCTCCTGCCTCAG
199337	31533	CCAAGTAGCTGGGATTACAG	243924	76120	CTCAGGGCCTCCGTTTCCTC	288511	120707	CAAGTGATTCTCCTGCCTCA
199338	31534	CCCAAGTAGCTGGGATTACA	243925	76121	TCTCAGGGCCTCCGTTTCCT	288512	120708	TCAAGTGATTCTCCTGCCTC

199339	31535	TCCCAAGTAGCTGGGATTAC	243926	76122	CTCTCAGGGCCTCCGTTTCC	288513	120709	TTCAAGTGATTCTCCTGCCT
199340	31536	CTCCCAAGTAGCTGGGATTA	243927	76123	CCTCTCAGGGCCTCCGTTTC	288514	120710	GTTCAAGTGATTCTCCTGCC
199341	31537	CCTCCCAAGTAGCTGGGATT	243928	76124	GCCTCTCAGGGCCTCCGTTT	288515	120711	GGTTCAAGTGATTCTCCTGC
199342	31538	GCCTCCCAAGTAGCTGGGAT	243929	76125	TGCCTCTCAGGGCCTCCGTT	288516	120712	AGGTTCAAGTGATTCTCCTG
199343	31539	AGCCTCCCAAGTAGCTGGGA	243930	76126	CTGCCTCTCAGGGCCTCCGT	288517	120713	CAGGTTCAAGTGATTCTCCT
199344	31540	CAGCCTCCCAAGTAGCTGGG	243931	76127	CCTGCCTCTCAGGGCCTCCG	288518	120714	CCAGGTTCAAGTGATTCTCC
199345	31541	TCAGCCTCCCAAGTAGCTGG	243932	76128	ACCTGCCTCTCAGGGCCTCC	288519	120715	CCCAGGTTCAAGTGATTCTC
199346	31542	CTCAGCCTCCCAAGTAGCTG	243933	76129	GACCTGCCTCTCAGGGCCTC	288520	120716	TCCCAGGTTCAAGTGATTCT
199347	31543	CCTCAGCCTCCCAAGTAGCT	243934	76130	GGACCTGCCTCTCAGGGCCT	288521	120717	CTCCCAGGTTCAAGTGATTC
199348	31544	GCCTCAGCCTCCCAAGTAGC	243935	76131	TGGACCTGCCTCTCAGGGCC	288522	120718	CCTCCCAGGTTCAAGTGATT
199349	31545	TGCCTCAGCCTCCCAAGTAG	243936	76132	TTGGACCTGCCTCTCAGGGC	288523	120719	GCCTCCCAGGTTCAAGTGAT
199350	31546	ATGCCTCAGCCTCCCAAGTA	243937	76133	CTTGGACCTGCCTCTCAGGG	288524	120720	TGCCTCCCAGGTTCAAGTGA
199351	31547	CATGCCTCAGCCTCCCAAGT	243938	76134	CCTTGGACCTGCCTCTCAGG	288525	120721	CTGCCTCCCAGGTTCAAGTG
199352	31548	TCATGCCTCAGCCTCCCAAG	243939	76135	GCCTTGGACCTGCCTCTCAG	288526	120722	TCTGCCTCCCAGGTTCAAGT
199353	31549	CTCATGCCTCAGCCTCCCAA	243940	76136	GGCCTTGGACCTGCCTCTCA	288527	120723	CTCTGCCTCCCAGGTTCAAG
199354	31550	TCTCATGCCTCAGCCTCCCA	243941	76137	TGGCCTTGGACCTGCCTCTC	288528	120724	CCTCTGCCTCCCAGGTTCAA
199355	31551	TTCTCATGCCTCAGCCTCCC	243942	76138	GTGGCCTTGGACCTGCCTCT	288529	120725	ACCTCTGCCTCCCAGGTTCA
199356	31552	ATTCTCATGCCTCAGCCTCC	243943	76139	GGTGGCCTTGGACCTGCCTC	288530	120726	AACCTCTGCCTCCCAGGTTC
199357	31553	AATTCTCATGCCTCAGCCTC	243944	76140	AGGTGGCCTTGGACCTGCCT	288531	120727	CAACCTCTGCCTCCCAGGTT
199358	31554	CAATTCTCATGCCTCAGCCT	243945	76141	CAGGTGGCCTTGGACCTGCC	288532	120728	GCAACCTCTGCCTCCCAGGT
199359	31555	GCAATTCTCATGCCTCAGCC	243946	76142	TCAGGTGGCCTTGGACCTGC	288533	120729	TGCAACCTCTGCCTCCCAGG
199360	31556	AGCAATTCTCATGCCTCAGC	243947	76143	GTCAGGTGGCCTTGGACCTG	288534	120730	CTGCAACCTCTGCCTCCCAG
199361	31557	AAGCAATTCTCATGCCTCAG	243948	76144	GGTCAGGTGGCCTTGGACCT	288535	120731	ACTGCAACCTCTGCCTCCCA
199362	31558	CAAGCAATTCTCATGCCTCA	243949	76145	TGGTCAGGTGGCCTTGGACC	288536	120732	CACTGCAACCTCTGCCTCCC
199363	31559	TCAAGCAATTCTCATGCCTC	243950	76146	CTGGTCAGGTGGCCTTGGAC	288537	120733	TCACTGCAACCTCTGCCTCC
199364	31560	TTCAAGCAATTCTCATGCCT	243951	76147	TCTGGTCAGGTGGCCTTGGA	288538	120734	CTCACTGCAACCTCTGCCTC
199365	31561	GTTCAAGCAATTCTCATGCC	243952	76148	TTCTGGTCAGGTGGCCTTGG	288539	120735	GCTCACTGCAACCTCTGCCT
199366	31562	GGTTCAAGCAATTCTCATGC	243953	76149	TTTCTGGTCAGGTGGCCTTG	288540	120736	GGCTCACTGCAACCTCTGCC
199367	31563	GGGTTCAAGCAATTCTCATG	243954	76150	CTTTCTGGTCAGGTGGCCTT	288541	120737	CGGCTCACTGCAACCTCTGC
199368	31564	TGGGTTCAAGCAATTCTCAT	243955	76151	TCTTTCTGGTCAGGTGGCCT	288542	120738	TCGGCTCACTGCAACCTCTG
199369	31565	CTGGGTTCAAGCAATTCTCA	243956	76152	TTCTTTCTGGTCAGGTGGCC	288543	120739	CTCGGCTCACTGCAACCTCT
199370	31566	CCTGGGTTCAAGCAATTCTC	243957	76153	CTTCTTTCTGGTCAGGTGGC	288544	120740	TCTCGGCTCACTGCAACCTC
199371	31567	TCCTGGGTTCAAGCAATTCT	243958	76154	ACTTCTTTCTGGTCAGGTGG	288545	120741	ATCTCGGCTCACTGCAACCT
199372	31568	CTCCTGGGTTCAAGCAATTC	243959	76155	CACTTCTTTCTGGTCAGGTG	288546	120742	GATCTCGGCTCACTGCAACC
199373	31569	CCTCCTGGGTTCAAGCAATT	243960	76156	CCACTTCTTTCTGGTCAGGT	288547	120743	AGATCTCGGCTCACTGCAAC
199374	31570	ACCTCCTGGGTTCAAGCAAT	243961	76157	TCCACTTCTTTCTGGTCAGG	288548	120744	AAGATCTCGGCTCACTGCAA
199375	31571	CACCTCCTGGGTTCAAGCAA	243962	76158	TTCCACTTCTTTCTGGTCAG	288549	120745	CAAGATCTCGGCTCACTGCA
199376	31572	CCACCTCCTGGGTTCAAGCA	243963	76159	GTTCCACTTCTTTCTGGTCA	288550	120746	GCAAGATCTCGGCTCACTGC
199377	31573	TCCACCTCCTGGGTTCAAGC	243964	76160	AGTTCCACTTCTTTCTGGTC	288551	120747	GGCAAGATCTCGGCTCACTG
199378	31574	CTCCACCTCCTGGGTTCAAG	243965	76161	CAGTTCCACTTCTTTCTGGT	288552	120748	TGGCAAGATCTCGGCTCACT
199379	31575	CCTCCACCTCCTGGGTTCAA	243966	76162	CCAGTTCCACTTCTTTCTGG	288553	120749	GTGGCAAGATCTCGGCTCAC
199380	31576	ACCTCCACCTCCTGGGTTCA	243967	76163	CCCAGTTCCACTTCTTTCTG	288554	120750	AGTGGCAAGATCTCGGCTCA
199381	31577	AACCTCCACCTCCTGGGTTC	243968	76164	TCCCAGTTCCACTTCTTTCT	288555	120751	CAGTGGCAAGATCTCGGCTC
199382	31578	CAACCTCCACCTCCTGGGTT	243969	76165	GTCCCAGTTCCACTTCTTTC	288556	120752	GCAGTGGCAAGATCTCGGCT
199383	31579	GCAACCTCCACCTCCTGGGT	243970	76166	AGTCCCAGTTCCACTTCTTT	288557	120753	TGCAGTGGCAAGATCTCGGC
199384	31580	TGCAACCTCCACCTCCTGGG	243971	76167	AAGTCCCAGTTCCACTTCTT	288558	120754	GTGCAGTGGCAAGATCTCGG
199385	31581	CTGCAACCTCCACCTCCTGG	243972	76168	CAAGTCCCAGTTCCACTTCT	288559	120755	AGTGCAGTGGCAAGATCTCG
199386	31582	ACTGCAACCTCCACCTCCTG	243973	76169	TCAAGTCCCAGTTCCACTTC	288560	120756	GAGTGCAGTGGCAAGATCTC
199387	31583	CACTGCAACCTCCACCTCCT	243974	76170	TTCAAGTCCCAGTTCCACTT	288561	120757	GGAGTGCAGTGGCAAGATCT
199388	31584	TCACTGCAACCTCCACCTCC	243975	76171	GTTCAAGTCCCAGTTCCACT	288562	120758	TGGAGTGCAGTGGCAAGATC
199389	31585	CTCACTGCAACCTCCACCTC	243976	76172	GGTTCAAGTCCCAGTTCCAC	288563	120759	CTGGAGTGCAGTGGCAAGAT
199390	31586	GCTCACTGCAACCTCCACCT	243977	76173	GGGTTCAAGTCCCAGTTCCA	288564	120760	GCTGGAGTGCAGTGGCAAGA
199391	31587	GGCTCACTGCAACCTCCACC	243978	76174	TGGGTTCAAGTCCCAGTTCC	288565	120761	GGCTGGAGTGCAGTGGCAAG
199392	31588	TGGCTCACTGCAACCTCCAC	243979	76175	CTGGGTTCAAGTCCCAGTTC	288566	120762	AGGCTGGAGTGCAGTGGCAA
199393	31589	TTGGCTCACTGCAACCTCCA	243980	76176	GCTGGGTTCAAGTCCCAGTT	288567	120763	CAGGCTGGAGTGCAGTGGCA
199394	31590	CTTGGCTCACTGCAACCTCC	243981	76177	GGCTGGGTTCAAGTCCCAGT	288568	120764	CCAGGCTGGAGTGCAGTGGC
199395	31591	TCTTGGCTCACTGCAACCTC	243982	76178	TGGCTGGGTTCAAGTCCCAG	288569	120765	CCCAGGCTGGAGTGCAGTGG
199396	31592	ATCTTGGCTCACTGCAACCT	243983	76179	ATGGCTGGGTTCAAGTCCCA	288570	120766	ACCCAGGCTGGAGTGCAGTG
199397	31593	GATCTTGGCTCACTGCAACC	243984	76180	GATGGCTGGGTTCAAGTCCC	288571	120767	CACCCAGGCTGGAGTGCAGT
199398	31594	CGATCTTGGCTCACTGCAAC	243985	76181	AGATGGCTGGGTTCAAGTCC	288572	120768	TCACCCAGGCTGGAGTGCAG
199399	31595	ACGATCTTGGCTCACTGCAA	243986	76182	AAGATGGCTGGGTTCAAGTC	288573	120769	GTCACCCAGGCTGGAGTGCA
199400	31596	CACGATCTTGGCTCACTGCA	243987	76183	CAAGATGGCTGGGTTCAAGT	288574	120770	TGTCACCCAGGCTGGAGTGC
199401	31597	GCACGATCTTGGCTCACTGC	243988	76184	GCAAGATGGCTGGGTTCAAG	288575	120771	CTGTCACCCAGGCTGGAGTG
199402	31598	GGCACGATCTTGGCTCACTG	243989	76185	GGCAAGATGGCTGGGTTCAA	288576	120772	ACTGTCACCCAGGCTGGAGT
199403	31599	TGGCACGATCTTGGCTCACT	243990	76186	GGGCAAGATGGCTGGGTTCA	288577	120773	CACTGTCACCCAGGCTGGAG
199404	31600	GTGGCACGATCTTGGCTCAC	243991	76187	GGGGCAAGATGGCTGGGTTC	288578	120774	TCACTGTCACCCAGGCTGGA
199405	31601	AGTGGCACGATCTTGGCTCA	243992	76188	AGGGGCAAGATGGCTGGGTT	288579	120775	TTCACTGTCACCCAGGCTGG
199406	31602	CAGTGGCACGATCTTGGCTC	243993	76189	AAGGGGCAAGATGGCTGGGT	288580	120776	TTTCACTGTCACCCAGGCTG
199407	31603	GCAGTGGCACGATCTTGGCT	243994	76190	CAAGGGGCAAGATGGCTGGG	288581	120777	GTTTCACTGTCACCCAGGCT
199408	31604	TGCAGTGGCACGATCTTGGC	243995	76191	CCAAGGGGCAAGATGGCTGG	288582	120778	AGTTTCACTGTCACCCAGGC
199409	31605	GTGCAGTGGCACGATCTTGG	243996	76192	ACCAAGGGGCAAGATGGCTG	288583	120779	GAGTTTCACTGTCACCCAGG
199410	31606	AGTGCAGTGGCACGATCTTG	243997	76193	GACCAAGGGGCAAGATGGCT	288584	120780	GGAGTTTCACTGTCACCCAG

199411	31607	GAGTGCAGTGGCACGATCTT	243998	76194	GGACCAAGGGGCAAGATGGC	288585	120781	CGGAGTTTCACTGTCACCCA
199412	31608	AGAGTGCAGTGGCACGATCT	243999	76195	GGGACCAAGGGGCAAGATGG	288586	120782	ACGGAGTTTCACTGTCACCC
199413	31609	TAGAGTGCAGTGGCACGATC	244000	76196	TGGGACCAAGGGGCAAGATG	288587	120783	GACGGAGTTTCACTGTCACC
199414	31610	CTAGAGTGCAGTGGCACGAT	244001	76197	ATGGGACCAAGGGGCAAGAT	288588	120784	AGACGGAGTTTCACTGTCAC
199415	31611	ACTAGAGTGCAGTGGCACGA	244002	76198	CATGGGACCAAGGGGCAAGA	288589	120785	GAGACGGAGTTTCACTGTCA
199416	31612	GACTAGAGTGCAGTGGCACG	244003	76199	GCATGGGACCAAGGGGCAAG	288590	120786	TGAGACGGAGTTTCACTGTC
199417	31613	AGACTAGAGTGCAGTGGCAC	244004	76200	AGCATGGGACCAAGGGGCAA	288591	120787	TTGAGACGGAGTTTCACTGT
199418	31614	CAGACTAGAGTGCAGTGGCA	244005	76201	GAGCATGGGACCAAGGGGCA	288592	120788	TTTGAGACGGAGTTTCACTG
199419	31615	CCAGACTAGAGTGCAGTGGC	244006	76202	AGAGCATGGGACCAAGGGGC	288593	120789	TTTTGAGACGGAGTTTCACT
199420	31616	CCCAGACTAGAGTGCAGTGG	244007	76203	GAGAGCATGGGACCAAGGGG	288594	120790	TTTTTGAGACGGAGTTTCAC
199421	31617	GCCCAGACTAGAGTGCAGTG	244008	76204	AGAGAGCATGGGACCAAGGG	288595	120791	ATTTTTGAGACGGAGTTTCA
199422	31618	TGCCCAGACTAGAGTGCAGT	244009	76205	TAGAGAGCATGGGACCAAGG	288596	120792	TATTTTTGAGACGGAGTTTC
199423	31619	TTGCCCAGACTAGAGTGCAG	244010	76206	CTAGAGAGCATGGGACCAAG	288597	120793	TTATTTTTGAGACGGAGTTT
199424	31620	GTTGCCCAGACTAGAGTGCA	244011	76207	GCTAGAGAGCATGGGACCAA	288598	120794	TTTATTTTTGAGACGGAGTT
199425	31621	TGTTGCCCAGACTAGAGTGC	244012	76208	GGCTAGAGAGCATGGGACCA	288599	120795	TTTTATTTTTGAGACGGAGT
199426	31622	CTGTTGCCCAGACTAGAGTG	244013	76209	AGGCTAGAGAGCATGGGACC	288600	120796	TTTTTATTTTTGAGACGGAG
199427	31623	TCTGTTGCCCAGACTAGAGT	244014	76210	CAGGCTAGAGAGCATGGGAC	288601	120797	ATTTTTATTTTTGAGACGGA
199428	31624	CTCTGTTGCCCAGACTAGAG	244015	76211	ACAGGCTAGAGAGCATGGGA	288602	120798	TATTTTTATTTTTGAGACGG
199429	31625	ACTCTGTTGCCCAGACTAGA	244016	76212	TACAGGCTAGAGAGCATGGG	288603	120799	TTATTTTTATTTTTGAGACG
199430	31626	TACTCTGTTGCCCAGACTAG	244017	76213	TTACAGGCTAGAGAGCATGG	288604	120800	TTTATTTTTATTTTTGAGAC
199431	31627	TTACTCTGTTGCCCAGACTA	244018	76214	GTTACAGGCTAGAGAGCATG	288605	120801	TTTTATTTTTATTTTTGAGA
199432	31628	CTTACTCTGTTGCCCAGACT	244019	76215	AGTTACAGGCTAGAGAGCAT	288606	120802	TTTTTATTTTTATTTTTGAG
199433	31629	TCTTACTCTGTTGCCCAGAC	244020	76216	GAGTTACAGGCTAGAGAGCA	288607	120803	ATTTTTATTTTTATTTTTGA
199434	31630	GTCTTACTCTGTTGCCCAGA	244021	76217	GGAGTTACAGGCTAGAGAGC	288608	120804	TATTTTTATTTTTATTTTTG
199435	31631	AGTCTTACTCTGTTGCCCAG	244022	76218	AGGAGTTACAGGCTAGAGAG	288609	120805	GTATTTTTATTTTTATTTTT
199436	31632	GAGTCTTACTCTGTTGCCCA	244023	76219	CAGGAGTTACAGGCTAGAGA	288610	120806	TGTATTTTTATTTTTATTTT
199437	31633	AGAGTCTTACTCTGTTGCCC	244024	76220	GCAGGAGTTACAGGCTAGAG	288611	120807	CTGTATTTTTATTTTTATTT
199438	31634	TAGAGTCTTACTCTGTTGCC	244025	76221	AGCAGGAGTTACAGGCTAGA	288612	120808	GCTGTATTTTTATTTTTATT
199439	31635	ATAGAGTCTTACTCTGTTGC	244026	76222	AAGCAGGAGTTACAGGCTAG	288613	120809	AGCTGTATTTTTATTTTTAT
199440	31636	CATAGAGTCTTACTCTGTTG	244027	76223	GAAGCAGGAGTTACAGGCTA	288614	120810	CAGCTGTATTTTTATTTTTA
199441	31637	ACATAGAGTCTTACTCTGTT	244028	76224	GGAAGCAGGAGTTACAGGCT	288615	120811	CCAGCTGTATTTTTATTTTT
199442	31638	GACATAGAGTCTTACTCTGT	244029	76225	AGGAAGCAGGAGTTACAGGC	288616	120812	CCCAGCTGTATTTTTATTTT
199443	31639	TGACATAGAGTCTTACTCTG	244030	76226	CAGGAAGCAGGAGTTACAGG	288617	120813	GCCCAGCTGTATTTTTATTT
199444	31640	TTGACATAGAGTCTTACTCT	244031	76227	CCAGGAAGCAGGAGTTACAG	288618	120814	TGCCCAGCTGTATTTTTATT
199445	31641	TTTGACATAGAGTCTTACTC	244032	76228	ACCAGGAAGCAGGAGTTACA	288619	120815	GTGCCCAGCTGTATTTTTAT
199446	31642	CTTTGACATAGAGTCTTACT	244033	76229	CACCAGGAAGCAGGAGTTAC	288620	120816	CGTGCCCAGCTGTATTTTTA
199447	31643	TCTTTGACATAGAGTCTTAC	244034	76230	CCACCAGGAAGCAGGAGTTA	288621	120817	CCGTGCCCAGCTGTATTTTT
199448	31644	TTCTTTGACATAGAGTCTTA	244035	76231	CCCACCAGGAAGCAGGAGTT	288622	120818	ACCGTGCCCAGCTGTATTTT
199449	31645	TTTCTTTGACATAGAGTCTT	244036	76232	CCCCACCAGGAAGCAGGAGT	288623	120819	CACCGTGCCCAGCTGTATTT
199450	31646	TTTTCTTTGACATAGAGTCT	244037	76233	GCCCCACCAGGAAGCAGGAG	288624	120820	CCACCGTGCCCAGCTGTATT
199451	31647	TTTTTCTTTGACATAGAGTC	244038	76234	TGCCCCACCAGGAAGCAGGA	288625	120821	GCCACCGTGCCCAGCTGTAT
199452	31648	TTTTTTCTTTGACATAGAGT	244039	76235	ATGCCCCACCAGGAAGCAGG	288626	120822	AGCCACCGTGCCCAGCTGTA
199453	31649	TTTTTTTCTTTGACATAGAG	244040	76236	GATGCCCCACCAGGAAGCAG	288627	120823	GAGCCACCGTGCCCAGCTGT
199454	31650	TTTTTTTTCTTTGACATAGA	244041	76237	AGATGCCCCACCAGGAAGCA	288628	120824	TGAGCCACCGTGCCCAGCTG
199455	31651	TTTTTTTTTCTTTGACATAG	244042	76238	GAGATGCCCCACCAGGAAGC	288629	120825	GTGAGCCACCGTGCCCAGCT
199456	31652	TTTTTTTTTTCTTTGACATA	244043	76239	GGAGATGCCCCACCAGGAAG	288630	120826	CGTGAGCCACCGTGCCCAGC
199457	31653	TTTTTTTTTTTCTTTGACAT	244044	76240	TGGAGATGCCCCACCAGGAA	288631	120827	GCGTGAGCCACCGTGCCCAG
199458	31654	TTTTTTTTTTTTCTTTGACA	244045	76241	CTGGAGATGCCCCACCAGGA	288632	120828	GGCGTGAGCCACCGTGCCCA
199459	31655	CTTTTTTTTTTTTCTTTGAC	244046	76242	CCTGGAGATGCCCCACCAGG	288633	120829	AGGCGTGAGCCACCGTGCCC
199460	31656	TCTTTTTTTTTTTTCTTTGA	244047	76243	TCCTGGAGATGCCCCACCAG	288634	120830	CAGGCGTGAGCCACCGTGCC
199461	31657	TTCTTTTTTTTTTTTCTTTG	244048	76244	CTCCTGGAGATGCCCCACCA	288635	120831	ACAGGCGTGAGCCACCGTGC
199462	31658	TTTCTTTTTTTTTTTTCTTT	244049	76245	CCTCCTGGAGATGCCCCACC	288636	120832	TACAGGCGTGAGCCACCGTG
199463	31659	TTTTCTTTTTTTTTTTTCTT	244050	76246	TCCTCCTGGAGATGCCCCAC	288637	120833	TTACAGGCGTGAGCCACCGT
199464	31660	CTTTTCTTTTTTTTTTTTCT	244051	76247	GTCCTCCTGGAGATGCCCCA	288638	120834	ATTACAGGCGTGAGCCACCG
199465	31661	GCTTTTCTTTTTTTTTTTTC	244052	76248	GGTCCTCCTGGAGATGCCCC	288639	120835	GATTACAGGCGTGAGCCACC
199466	31662	GGCTTTTCTTTTTTTTTTTT	244053	76249	GGGTCCTCCTGGAGATGCCC	288640	120836	GGATTACAGGCGTGAGCCAC
199467	31663	AGGCTTTTCTTTTTTTTTTT	244054	76250	AGGGTCCTCCTGGAGATGCC	288641	120837	GGGATTACAGGCGTGAGCCA
199468	31664	AAGGCTTTTCTTTTTTTTTT	244055	76251	TAGGGTCCTCCTGGAGATGC	288642	120838	TGGGATTACAGGCGTGAGCC
199469	31665	AAAGGCTTTTCTTTTTTTTT	244056	76252	ATAGGGTCCTCCTGGAGATG	288643	120839	CTGGGATTACAGGCGTGAGC
199470	31666	AAAAGGCTTTTCTTTTTTTT	244057	76253	GATAGGGTCCTCCTGGAGAT	288644	120840	GCTGGGATTACAGGCGTGAG
199471	31667	AAAAAGGCTTTTCTTTTTTT	244058	76254	CGATAGGGTCCTCCTGGAGA	288645	120841	TGCTGGGATTACAGGCGTGA
199472	31668	TAAAAAGGCTTTTCTTTTTT	244059	76255	CCGATAGGGTCCTCCTGGAG	288646	120842	GTGCTGGGATTACAGGCGTG
199473	31669	TTAAAAAGGCTTTTCTTTTT	244060	76256	GCCGATAGGGTCCTCCTGGA	288647	120843	AGTGCTGGGATTACAGGCGT
199474	31670	TTTAAAAAGGCTTTTCTTTT	244061	76257	AGCCGATAGGGTCCTCCTGG	288648	120844	AAGTGCTGGGATTACAGGCG
199475	31671	GTTTAAAAAGGCTTTTCTTT	244062	76258	CAGCCGATAGGGTCCTCCTG	288649	120845	AAAGTGCTGGGATTACAGGC
199476	31672	TGTTTAAAAAGGCTTTTCTT	244063	76259	CCAGCCGATAGGGTCCTCCT	288650	120846	CAAAGTGCTGGGATTACAGG
199477	31673	CTGTTTAAAAAGGCTTTTCT	244064	76260	GCCAGCCGATAGGGTCCTCC	288651	120847	CCAAAGTGCTGGGATTACAG
199478	31674	ACTGTTTAAAAAGGCTTTTC	244065	76261	GGCCAGCCGATAGGGTCCTC	288652	120848	CCCAAAGTGCTGGGATTACA
199479	31675	TACTGTTTAAAAAGGCTTTT	244066	76262	TGGCCAGCCGATAGGGTCCT	288653	120849	TCCCAAAGTGCTGGGATTAC
199480	31676	CTACTGTTTAAAAAGGCTTT	244067	76263	ATGGCCAGCCGATAGGGTCC	288654	120850	CTCCCAAAGTGCTGGGATTA
199481	31677	GCTACTGTTTAAAAAGGCTT	244068	76264	CATGGCCAGCCGATAGGGTC	288655	120851	CCTCCCAAAGTGCTGGGATT
199482	31678	TGCTACTGTTTAAAAAGGCT	244069	76265	CCATGGCCAGCCGATAGGGT	288656	120852	GCCTCCCAAAGTGCTGGGAT

199483	31679	CTGCTACTGTTTAAAAAGGC	244070	76266	CCCATGGCCAGCCGATAGGG	288657	120853	GGCCTCCCAAAGTGCTGGGA
199484	31680	TCTGCTACTGTTTAAAAAGG	244071	76267	GCCCATGGCCAGCCGATAGG	288658	120854	CGGCCTCCCAAAGTGCTGGG
199485	31681	GTCTGCTACTGTTTAAAAAG	244072	76268	GGCCCATGGCCAGCCGATAG	288659	120855	TCGGCCTCCCAAAGTGCTGG
199486	31682	TGTCTGCTACTGTTTAAAAA	244073	76269	AGGCCCATGGCCAGCCGATA	288660	120856	CTCGGCCTCCCAAAGTGCTG
199487	31683	ATGTCTGCTACTGTTTAAAA	244074	76270	CAGGCCCATGGCCAGCCGAT	288661	120857	CCTCGGCCTCCCAAAGTGCT
199488	31684	TATGTCTGCTACTGTTTAAA	244075	76271	GCAGGCCCATGGCCAGCCGA	288662	120858	GCCTCGGCCTCCCAAAGTGC
199489	31685	TTATGTCTGCTACTGTTTAA	244076	76272	GGCAGGCCCATGGCCAGCCG	288663	120859	CGCCTCGGCCTCCCAAAGTG
199490	31686	GTTATGTCTGCTACTGTTTA	244077	76273	GGGCAGGCCCATGGCCAGCC	288664	120860	TCGCCTCGGCCTCCCAAAGT
199491	31687	AGTTATGTCTGCTACTGTTT	244078	76274	AGGGCAGGCCCATGGCCAGC	288665	120861	CTCGCCTCGGCCTCCCAAAG
199492	31688	TAGTTATGTCTGCTACTGTT	244079	76275	CAGGGCAGGCCCATGGCCAG	288666	120862	GCTCGCCTCGGCCTCCCAAA
199493	31689	ATAGTTATGTCTGCTACTGT	244080	76276	CCAGGGCAGGCCCATGGCCA	288667	120863	CGCTCGCCTCGGCCTCCCAA
199494	31690	TATAGTTATGTCTGCTACTG	244081	76277	TCCAGGGCAGGCCCATGGCC	288668	120864	CCGCTCGCCTCGGCCTCCCA
199495	31691	ATATAGTTATGTCTGCTACT	244082	76278	CTCCAGGGCAGGCCCATGGC	288669	120865	TCCGCTCGCCTCGGCCTCCC
199496	31692	TATATAGTTATGTCTGCTAC	244083	76279	ACTCCAGGGCAGGCCCATGG	288670	120866	ATCCGCTCGCCTCGGCCTCC
199497	31693	TTATATAGTTATGTCTGCTA	244084	76280	GACTCCAGGGCAGGCCCATG	288671	120867	GATCCGCTCGCCTCGGCCTC
199498	31694	ATTATATAGTTATGTCTGCT	244085	76281	AGACTCCAGGGCAGGCCCAT	288672	120868	TGATCCGCTCGCCTCGGCCT
199499	31695	GATTATATAGTTATGTCTGC	244086	76282	AAGACTCCAGGGCAGGCCCA	288673	120869	GTGATCCGCTCGCCTCGGCC
199500	31696	GGATTATATAGTTATGTCTG	244087	76283	AAAGACTCCAGGGCAGGCCC	288674	120870	TGTGATCCGCTCGCCTCGGC
199501	31697	AGGATTATATAGTTATGTCT	244088	76284	AAAAGACTCCAGGGCAGGCC	288675	120871	TTGTGATCCGCTCGCCTCGG
199502	31698	AAGGATTATATAGTTATGTC	244089	76285	CAAAAGACTCCAGGGCAGGC	288676	120872	CTTGTGATCCGCTCGCCTCG
199503	31699	TAAGGATTATATAGTTATGT	244090	76286	GCAAAAGACTCCAGGGCAGG	288677	120873	CCTTGTGATCCGCTCGCCTC
199504	31700	GTAAGGATTATATAGTTATG	244091	76287	AGCAAAAGACTCCAGGGCAG	288678	120874	ACCTTGTGATCCGCTCGCCT
199505	31701	AGTAAGGATTATATAGTTAT	244092	76288	GAGCAAAAGACTCCAGGGCA	288679	120875	GACCTTGTGATCCGCTCGCC
199506	31702	TAGTAAGGATTATATAGTTA	244093	76289	AGAGCAAAAGACTCCAGGGC	288680	120876	TGACCTTGTGATCCGCTCGC
199507	31703	TTAGTAAGGATTATATAGTT	244094	76290	CAGAGCAAAAGACTCCAGGG	288681	120877	CTGACCTTGTGATCCGCTCG
199508	31704	CTTAGTAAGGATTATATAGT	244095	76291	ACAGAGCAAAAGACTCCAGG	288682	120878	CCTGACCTTGTGATCCGCTC
199509	31705	GCTTAGTAAGGATTATATAG	244096	76292	CACAGAGCAAAAGACTCCAG	288683	120879	TCCTGACCTTGTGATCCGCT
199510	31706	AGCTTAGTAAGGATTATATA	244097	76293	ACACAGAGCAAAAGACTCCA	288684	120880	CTCCTGACCTTGTGATCCGC
199511	31707	CAGCTTAGTAAGGATTATAT	244098	76294	CACACAGAGCAAAAGACTCC	288685	120881	TCTCCTGACCTTGTGATCCG
199512	31708	ACAGCTTAGTAAGGATTATA	244099	76295	CCACACAGAGCAAAAGACTC	288686	120882	ATCTCCTGACCTTGTGATCC
199513	31709	GACAGCTTAGTAAGGATTAT	244100	76296	GCCACACAGAGCAAAAGACT	288687	120883	TATCTCCTGACCTTGTGATC
199514	31710	CGACAGCTTAGTAAGGATTA	244101	76297	GGCCACACAGAGCAAAAGAC	288688	120884	ATATCTCCTGACCTTGTGAT
199515	31711	CCGACAGCTTAGTAAGGATT	244102	76298	TGGCCACACAGAGCAAAAGA	288689	120885	TATATCTCCTGACCTTGTGA
199516	31712	ACCGACAGCTTAGTAAGGAT	244103	76299	ATGGCCACACAGAGCAAAAG	288690	120886	CTATATCTCCTGACCTTGTG
199517	31713	GACCGACAGCTTAGTAAGGA	244104	76300	GATGGCCACACAGAGCAAAA	288691	120887	TCTATATCTCCTGACCTTGT
199518	31714	TGACCGACAGCTTAGTAAGG	244105	76301	GGATGGCCACACAGAGCAAA	288692	120888	GTCTATATCTCCTGACCTTG
199519	31715	TTGACCGACAGCTTAGTAAG	244106	76302	AGGATGGCCACACAGAGCAA	288693	120889	GGTCTATATCTCCTGACCTT
199520	31716	TTTGACCGACAGCTTAGTAA	244107	76303	AAGGATGGCCACACAGAGCA	288694	120890	TGGTCTATATCTCCTGACCT
199521	31717	ATTTGACCGACAGCTTAGTA	244108	76304	GAAGGATGGCCACACAGAGC	288695	120891	ATGGTCTATATCTCCTGACC
199522	31718	AATTTGACCGACAGCTTAGT	244109	76305	GGAAGGATGGCCACACAGAG	288696	120892	GATGGTCTATATCTCCTGAC
199523	31719	AAATTTGACCGACAGCTTAG	244110	76306	AGGAAGGATGGCCACACAGA	288697	120893	GGATGGTCTATATCTCCTGA
199524	31720	AAAATTTGACCGACAGCTTA	244111	76307	GAGGAAGGATGGCCACACAG	288698	120894	AGGATGGTCTATATCTCCTG
199525	31721	AAAAATTTGACCGACAGCTT	244112	76308	GGAGGAAGGATGGCCACACA	288699	120895	CAGGATGGTCTATATCTCCT
199526	31722	TAAAAATTTGACCGACAGCT	244113	76309	GGGAGGAAGGATGGCCACAC	288700	120896	CCAGGATGGTCTATATCTCC
199527	31723	ATAAAAATTTGACCGACAGC	244114	76310	AGGGAGGAAGGATGGCCACA	288701	120897	GCCAGGATGGTCTATATCTC
199528	31724	AATAAAAATTTGACCGACAG	244115	76311	GAGGGAGGAAGGATGGCCAC	288702	120898	AGCCAGGATGGTCTATATCT
199529	31725	AAATAAAAATTTGACCGACA	244116	76312	TGAGGGAGGAAGGATGGCCA	288703	120899	TAGCCAGGATGGTCTATATC
199530	31726	TAAATAAAAATTTGACCGAC	244117	76313	CTGAGGGAGGAAGGATGGCC	288704	120900	TTAGCCAGGATGGTCTATAT
199531	31727	ATAAATAAAAATTTGACCGA	244118	76314	CCTGAGGGAGGAAGGATGGC	288705	120901	GTTAGCCAGGATGGTCTATA
199532	31728	TATAAATAAAAATTTGACCG	244119	76315	TCCTGAGGGAGGAAGGATGG	288706	120902	TGTTAGCCAGGATGGTCTAT
199533	31729	ATATAAATAAAAATTTGACC	244120	76316	CTCCTGAGGGAGGAAGGATG	288707	120903	GTGTTAGCCAGGATGGTCTA
199534	31730	TATATAAATAAAAATTTGAC	244121	76317	TCTCCTGAGGGAGGAAGGAT	288708	120904	CGTGTTAGCCAGGATGGTCT
199535	31731	ATATATAAATAAAAATTTGA	244122	76318	CTCTCCTGAGGGAGGAAGGA	288709	120905	CCGTGTTAGCCAGGATGGTC
199536	31732	AATATATAAATAAAAATTTG	244123	76319	ACTCTCCTGAGGGAGGAAGG	288710	120906	ACCGTGTTAGCCAGGATGGT
199537	31733	AAATATATAAATAAAAATTT	244124	76320	CACTCTCCTGAGGGAGGAAG	288711	120907	CACCGTGTTAGCCAGGATGG
199538	31734	TAAATATATAAATAAAAATT	244125	76321	ACACTCTCCTGAGGGAGGAA	288712	120908	TCACCGTGTTAGCCAGGATG
199539	31735	ATAAATATATAAATAAAAAT	244126	76322	CACACTCTCCTGAGGGAGGA	288713	120909	TTCACCGTGTTAGCCAGGAT
199540	31736	AATAAATATATAAATAAAAA	244127	76323	ACACACTCTCCTGAGGGAGG	288714	120910	TTTCACCGTGTTAGCCAGGA
199541	31737	AAATAAATATATAAATAAAA	244128	76324	CACACACTCTCCTGAGGGAG	288715	120911	GTTTCACCGTGTTAGCCAGG
199542	31738	AAAATAAATATATAAATAAA	244129	76325	GCACACACTCTCCTGAGGGA	288716	120912	GGTTTCACCGTGTTAGCCAG
199543	31739	TAAAATAAATATATAAATAA	244130	76326	AGCACACACTCTCCTGAGGG	288717	120913	GGGTTTCACCGTGTTAGCCA
199544	31740	ATAAAATAAATATATAAATA	244131	76327	GAGCACACACTCTCCTGAGG	288718	120914	CGGGTTTCACCGTGTTAGCC
199545	31741	AATAAAATAAATATATAAAT	244132	76328	GGAGCACACACTCTCCTGAG	288719	120915	CCGGGTTTCACCGTGTTAGC
199546	31742	GAATAAAATAAATATATAAA	244133	76329	GGGAGCACACACTCTCCTGA	288720	120916	ACCGGGTTTCACCGTGTTAG
199547	31743	TGAATAAAATAAATATATAA	244134	76330	TGGGAGCACACACTCTCCTG	288721	120917	GACCGGGTTTCACCGTGTTA
199548	31744	ATGAATAAAATAAATATATA	244135	76331	CTGGGAGCACACACTCTCCT	288722	120918	AGACCGGGTTTCACCGTGTT
199549	31745	AATGAATAAAATAAATATAT	244136	76332	TCTGGGAGCACACACTCTCC	288723	120919	GAGACCGGGTTTCACCGTGT
199550	31746	AAATGAATAAAATAAATATA	244137	76333	CTCTGGGAGCACACACTCTC	288724	120920	AGAGACCGGGTTTCACCGTG
199551	31747	TAAATGAATAAAATAAATAT	244138	76334	GCTCTGGGAGCACACACTCT	288725	120921	TAGAGACCGGGTTTCACCGT
199552	31748	ATAAATGAATAAAATAAATA	244139	76335	TGCTCTGGGAGCACACACTC	288726	120922	GTAGAGACCGGGTTTCACCG
199553	31749	AATAAATGAATAAAATAAAT	244140	76336	GTGCTCTGGGAGCACACACT	288727	120923	AGTAGAGACCGGGTTTCACC
199554	31750	TAATAAATGAATAAAATAAA	244141	76337	TGTGCTCTGGGAGCACACAC	288728	120924	TAGTAGAGACCGGGTTTCAC

199555	31751	ATAATAAATGAATAAAATAA	244142	76338	CTGTGCTCTGGGAGCACACA	288729	120925	TTAGTAGAGACCGGGTTTCA
199556	31752	AATAATAAATGAATAAAATA	244143	76339	CCTGTGCTCTGGGAGCACAC	288730	120926	TTTAGTAGAGACCGGGTTTC
199557	31753	AAATAATAAATGAATAAAAT	244144	76340	GCCTGTGCTCTGGGAGCACA	288731	120927	TTTTAGTAGAGACCGGGTTT
199558	31754	AAAATAATAAATGAATAAAA	244145	76341	AGCCTGTGCTCTGGGAGCAC	288732	120928	TTTTTAGTAGAGACCGGGTT
199559	31755	AAAAATAATAAATGAATAAA	244146	76342	CAGCCTGTGCTCTGGGAGCA	288733	120929	ATTTTTAGTAGAGACCGGGT
199560	31756	TAAAAATAATAAATGAATAA	244147	76343	ACAGCCTGTGCTCTGGGAGC	288734	120930	TATTTTTAGTAGAGACCGGG
199561	31757	CTAAAAATAATAAATGAATA	244148	76344	TACAGCCTGTGCTCTGGGAG	288735	120931	GTATTTTTAGTAGAGACCGG
199562	31758	TCTAAAAATAATAAATGAAT	244149	76345	ATACAGCCTGTGCTCTGGGA	288736	120932	TGTATTTTTAGTAGAGACCG
199563	31759	GTCTAAAAATAATAAATGAA	244150	76346	GATACAGCCTGTGCTCTGGG	288737	120933	TTGTATTTTTAGTAGAGACC
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199566	31762	CCTGTCTAAAAATAATAAAT	244153	76349	GAAGATACAGCCTGTGCTCT	288740	120936	TTTTTGTATTTTTAGTAGAG
199567	31763	CCCTGTCTAAAAATAATAAA	244154	76350	AGAAGATACAGCCTGTGCTC	288741	120937	TTTTTTGTATTTTTAGTAGA
199568	31764	ACCCTGTCTAAAAATAATAA	244155	76351	CAGAAGATACAGCCTGTGCT	288742	120938	ATTTTTTGTATTTTTAGTAG
199569	31765	GACCCTGTCTAAAAATAATA	244156	76352	TCAGAAGATACAGCCTGTGC	288743	120939	AATTTTTTGTATTTTTAGTA
199570	31766	AGACCCTGTCTAAAAATAAT	244157	76353	CTCAGAAGATACAGCCTGTG	288744	120940	TAATTTTTTGTATTTTTAGT
199571	31767	GAGACCCTGTCTAAAAATAA	244158	76354	GCTCAGAAGATACAGCCTGT	288745	120941	CTAATTTTTTGTATTTTTAG
199572	31768	TGAGACCCTGTCTAAAAATA	244159	76355	TGCTCAGAAGATACAGCCTG	288746	120942	GCTAATTTTTTGTATTTTTA
199573	31769	GTGAGACCCTGTCTAAAAAT	244160	76356	ATGCTCAGAAGATACAGCCT	288747	120943	GGCTAATTTTTTGTATTTTT
199574	31770	AGTGAGACCCTGTCTAAAAA	244161	76357	AATGCTCAGAAGATACAGCC	288748	120944	TGGCTAATTTTTTGTATTTT
199575	31771	GAGTGAGACCCTGTCTAAAA	244162	76358	AAATGCTCAGAAGATACAGC	288749	120945	CTGGCTAATTTTTTGTATTT
199576	31772	AGAGTGAGACCCTGTCTAAA	244163	76359	AAAATGCTCAGAAGATACAG	288750	120946	CCTGGCTAATTTTTTGTATT
199577	31773	CAGAGTGAGACCCTGTCTAA	244164	76360	CAAAATGCTCAGAAGATACA	288751	120947	GCCTGGCTAATTTTTTGTAT
199578	31774	ACAGAGTGAGACCCTGTCTA	244165	76361	ACAAAATGCTCAGAAGATAC	288752	120948	CGCCTGGCTAATTTTTTGTA
199579	31775	AACAGAGTGAGACCCTGTCT	244166	76362	GACAAAATGCTCAGAAGATA	288753	120949	ACGCCTGGCTAATTTTTTGT
199580	31776	CAACAGAGTGAGACCCTGTC	244167	76363	GGACAAAATGCTCAGAAGAT	288754	120950	CACGCCTGGCTAATTTTTTG
199581	31777	GCAACAGAGTGAGACCCTGT	244168	76364	GGGACAAAATGCTCAGAAGA	288755	120951	CCACGCCTGGCTAATTTTTT
199582	31778	GGCAACAGAGTGAGACCCTG	244169	76365	AGGGACAAAATGCTCAGAAG	288756	120952	ACCACGCCTGGCTAATTTTT
199583	31779	GGGCAACAGAGTGAGACCCT	244170	76366	AAGGGACAAAATGCTCAGAA	288757	120953	CACCACGCCTGGCTAATTTT
199584	31780	TGGGCAACAGAGTGAGACCC	244171	76367	GAAGGGACAAAATGCTCAGA	288758	120954	CCACCACGCCTGGCTAATTT
199585	31781	CTGGGCAACAGAGTGAGACC	244172	76368	GGAAGGGACAAAATGCTCAG	288759	120955	GCCACCACGCCTGGCTAATT
199586	31782	CCTGGGCAACAGAGTGAGAC	244173	76369	GGGAAGGGACAAAATGCTCA	288760	120956	TGCCACCACGCCTGGCTAAT
199587	31783	GCCTGGGCAACAGAGTGAGA	244174	76370	TGGGAAGGGACAAAATGCTC	288761	120957	CTGCCACCACGCCTGGCTAA
199588	31784	AGCCTGGGCAACAGAGTGAG	244175	76371	CTGGGAAGGGACAAAATGCT	288762	120958	CCTGCCACCACGCCTGGCTA
199589	31785	CAGCCTGGGCAACAGAGTGA	244176	76372	ACTGGGAAGGGACAAAATGC	288763	120959	ACCTGCCACCACGCCTGGCT
199590	31786	CCAGCCTGGGCAACAGAGTG	244177	76373	TACTGGGAAGGGACAAAATG	288764	120960	CACCTGCCACCACGCCTGGC
199591	31787	TCCAGCCTGGGCAACAGAGT	244178	76374	GTACTGGGAAGGGACAAAAT	288765	120961	GCACCTGCCACCACGCCTGG
199592	31788	CTCCAGCCTGGGCAACAGAG	244179	76375	GGTACTGGGAAGGGACAAAA	288766	120962	GGCACCTGCCACCACGCCTG
199593	31789	ACTCCAGCCTGGGCAACAGA	244180	76376	AGGTACTGGGAAGGGACAAA	288767	120963	AGGCACCTGCCACCACGCCT
199594	31790	TACTCCAGCCTGGGCAACAG	244181	76377	TAGGTACTGGGAAGGGACAA	288768	120964	TAGGCACCTGCCACCACGCC
199595	31791	GTACTCCAGCCTGGGCAACA	244182	76378	CTAGGTACTGGGAAGGGACA	288769	120965	ATAGGCACCTGCCACCACGC
199596	31792	TGTACTCCAGCCTGGGCAAC	244183	76379	GCTAGGTACTGGGAAGGGAC	288770	120966	TATAGGCACCTGCCACCACG
199597	31793	CTGTACTCCAGCCTGGGCAA	244184	76380	TGCTAGGTACTGGGAAGGGA	288771	120967	CTATAGGCACCTGCCACCAC
199598	31794	ACTGTACTCCAGCCTGGGCA	244185	76381	GTGCTAGGTACTGGGAAGGG	288772	120968	ACTATAGGCACCTGCCACCA
199599	31795	CACTGTACTCCAGCCTGGGC	244186	76382	AGTGCTAGGTACTGGGAAGG	288773	120969	GACTATAGGCACCTGCCACC
199600	31796	CCACTGTACTCCAGCCTGGG	244187	76383	GAGTGCTAGGTACTGGGAAG	288774	120970	GGACTATAGGCACCTGCCAC
199601	31797	GCCACTGTACTCCAGCCTGG	244188	76384	TGAGTGCTAGGTACTGGGAA	288775	120971	GGGACTATAGGCACCTGCCA
199602	31798	CGCCACTGTACTCCAGCCTG	244189	76385	CTGAGTGCTAGGTACTGGGA	288776	120972	TGGGACTATAGGCACCTGCC
199603	31799	ACGCCACTGTACTCCAGCCT	244190	76386	GCTGAGTGCTAGGTACTGGG	288777	120973	CTGGGACTATAGGCACCTGC
199604	31800	CACGCCACTGTACTCCAGCC	244191	76387	AGCTGAGTGCTAGGTACTGG	288778	120974	GCTGGGACTATAGGCACCTG
199605	31801	TCACGCCACTGTACTCCAGC	244192	76388	GAGCTGAGTGCTAGGTACTG	288779	120975	AGCTGGGACTATAGGCACCT
199606	31802	ATCACGCCACTGTACTCCAG	244193	76389	AGAGCTGAGTGCTAGGTACT	288780	120976	TAGCTGGGACTATAGGCACC
199607	31803	GATCACGCCACTGTACTCCA	244194	76390	CAGAGCTGAGTGCTAGGTAC	288781	120977	GTAGCTGGGACTATAGGCAC
199608	31804	TGATCACGCCACTGTACTCC	244195	76391	ACAGAGCTGAGTGCTAGGTA	288782	120978	AGTAGCTGGGACTATAGGCA
199609	31805	ATGATCACGCCACTGTACTC	244196	76392	TACAGAGCTGAGTGCTAGGT	288783	120979	GAGTAGCTGGGACTATAGGC
199610	31806	CATGATCACGCCACTGTACT	244197	76393	ATACAGAGCTGAGTGCTAGG	288784	120980	TGAGTAGCTGGGACTATAGG
199611	31807	CCATGATCACGCCACTGTAC	244198	76394	TATACAGAGCTGAGTGCTAG	288785	120981	GTGAGTAGCTGGGACTATAG
199612	31808	GCCATGATCACGCCACTGTA	244199	76395	GTATACAGAGCTGAGTGCTA	288786	120982	TGTGAGTAGCTGGGACTATA
199613	31809	AGCCATGATCACGCCACTGT	244200	76396	TGTATACAGAGCTGAGTGCT	288787	120983	TTGTGAGTAGCTGGGACTAT
199614	31810	GAGCCATGATCACGCCACTG	244201	76397	ATGTATACAGAGCTGAGTGC	288788	120984	CTTGTGAGTAGCTGGGACTA
199615	31811	AGAGCCATGATCACGCCACT	244202	76398	AATGTATACAGAGCTGAGTG	288789	120985	CCTTGTGAGTAGCTGGGACT
199616	31812	GAGAGCCATGATCACGCCAC	244203	76399	CAATGTATACAGAGCTGAGT	288790	120986	GCCTTGTGAGTAGCTGGGAC
199617	31813	AGAGAGCCATGATCACGCCA	244204	76400	CCAATGTATACAGAGCTGAG	288791	120987	AGCCTTGTGAGTAGCTGGGA
199618	31814	AAGAGAGCCATGATCACGCC	244205	76401	CCCAATGTATACAGAGCTGA	288792	120988	CAGCCTTGTGAGTAGCTGGG
199619	31815	GAAGAGAGCCATGATCACGC	244206	76402	GCCCAATGTATACAGAGCTG	288793	120989	TCAGCCTTGTGAGTAGCTGG
199620	31816	TGAAGAGAGCCATGATCACG	244207	76403	AGCCCAATGTATACAGAGCT	288794	120990	CTCAGCCTTGTGAGTAGCTG
199621	31817	TTGAAGAGAGCCATGATCAC	244208	76404	GAGCCCAATGTATACAGAGC	288795	120991	CCTCAGCCTTGTGAGTAGCT
199622	31818	TTTGAAGAGAGCCATGATCA	244209	76405	AGAGCCCAATGTATACAGAG	288796	120992	GCCTCAGCCTTGTGAGTAGC
199623	31819	GTTTGAAGAGAGCCATGATC	244210	76406	GAGAGCCCAATGTATACAGA	288797	120993	TGCCTCAGCCTTGTGAGTAG
199624	31820	AGTTTGAAGAGAGCCATGAT	244211	76407	TGAGAGCCCAATGTATACAG	288798	120994	CTGCCTCAGCCTTGTGAGTA
199625	31821	AAGTTTGAAGAGAGCCATGA	244212	76408	TTGAGAGCCCAATGTATACA	288799	120995	CCTGCCTCAGCCTTGTGAGT
199626	31822	CAAGTTTGAAGAGAGCCATG	244213	76409	CTTGAGAGCCCAATGTATAC	288800	120996	TCCTGCCTCAGCCTTGTGAG

199627	31823	TCAAGTTTGAAGAGAGCCAT	244214	76410	TCTTGAGAGCCCAATGTATA	288801	120997	CTCCTGCCTCAGCCTTGTGA
199628	31824	GTCAAGTTTGAAGAGAGCCA	244215	76411	TTCTTGAGAGCCCAATGTAT	288802	120998	TCTCCTGCCTCAGCCTTGTG
199629	31825	GGTCAAGTTTGAAGAGAGCC	244216	76412	ATTCTTGAGAGCCCAATGTA	288803	120999	TTCTCCTGCCTCAGCCTTGT
199630	31826	AGGTCAAGTTTGAAGAGAGC	244217	76413	AATTCTTGAGAGCCCAATGT	288804	121000	ATTCTCCTGCCTCAGCCTTG
199631	31827	GAGGTCAAGTTTGAAGAGAG	244218	76414	GAATTCTTGAGAGCCCAATG	288805	121001	CATTCTCCTGCCTCAGCCTT
199632	31828	GGAGGTCAAGTTTGAAGAGA	244219	76415	AGAATTCTTGAGAGCCCAAT	288806	121002	CCATTCTCCTGCCTCAGCCT
199633	31829	GGGAGGTCAAGTTTGAAGAG	244220	76416	GAGAATTCTTGAGAGCCCAA	288807	121003	GCCATTCTCCTGCCTCAGCC
199634	31830	CGGGAGGTCAAGTTTGAAGA	244221	76417	TGAGAATTCTTGAGAGCCCA	288808	121004	TGCCATTCTCCTGCCTCAGC
199635	31831	CCGGGAGGTCAAGTTTGAAG	244222	76418	TTGAGAATTCTTGAGAGCCC	288809	121005	ATGCCATTCTCCTGCCTCAG
199636	31832	CCCGGGAGGTCAAGTTTGAA	244223	76419	GTTGAGAATTCTTGAGAGCC	288810	121006	CATGCCATTCTCCTGCCTCA
199637	31833	GCCCGGGAGGTCAAGTTTGA	244224	76420	GGTTGAGAATTCTTGAGAGC	288811	121007	TCATGCCATTCTCCTGCCTC
199638	31834	AGCCCGGGAGGTCAAGTTTG	244225	76421	AGGTTGAGAATTCTTGAGAG	288812	121008	TTCATGCCATTCTCCTGCCT
199639	31835	GAGCCCGGGAGGTCAAGTTT	244226	76422	AAGGTTGAGAATTCTTGAGA	288813	121009	GTTCATGCCATTCTCCTGCC
199640	31836	TGAGCCCGGGAGGTCAAGTT	244227	76423	GAAGGTTGAGAATTCTTGAG	288814	121010	GGTTCATGCCATTCTCCTGC
199641	31837	TTGAGCCCGGGAGGTCAAGT	244228	76424	GGAAGGTTGAGAATTCTTGA	288815	121011	AGGTTCATGCCATTCTCCTG
199642	31838	CTTGAGCCCGGGAGGTCAAG	244229	76425	TGGAAGGTTGAGAATTCTTG	288816	121012	CAGGTTCATGCCATTCTCCT
199643	31839	ACTTGAGCCCGGGAGGTCAA	244230	76426	CTGGAAGGTTGAGAATTCTT	288817	121013	CCAGGTTCATGCCATTCTCC
199644	31840	CACTTGAGCCCGGGAGGTCA	244231	76427	TCTGGAAGGTTGAGAATTCT	288818	121014	CCCAGGTTCATGCCATTCTC
199645	31841	TCACTTGAGCCCGGGAGGTC	244232	76428	CTCTGGAAGGTTGAGAATTC	288819	121015	TCCCAGGTTCATGCCATTCT
199646	31842	ATCACTTGAGCCCGGGAGGT	244233	76429	ACTCTGGAAGGTTGAGAATT	288820	121016	CTCCCAGGTTCATGCCATTC
199647	31843	GATCACTTGAGCCCGGGAGG	244234	76430	CACTCTGGAAGGTTGAGAAT	288821	121017	CCTCCCAGGTTCATGCCATT
199648	31844	GGATCACTTGAGCCCGGGAG	244235	76431	ACACTCTGGAAGGTTGAGAA	288822	121018	GCCTCCCAGGTTCATGCCAT
199649	31845	AGGATCACTTGAGCCCGGGA	244236	76432	TACACTCTGGAAGGTTGAGA	288823	121019	CGCCTCCCAGGTTCATGCCA
199650	31846	GAGGATCACTTGAGCCCGGG	244237	76433	TTACACTCTGGAAGGTTGAG	288824	121020	CCGCCTCCCAGGTTCATGCC
199651	31847	GGAGGATCACTTGAGCCCGG	244238	76434	CTTACACTCTGGAAGGTTGA	288825	121021	TCCGCCTCCCAGGTTCATGC
199652	31848	GGGAGGATCACTTGAGCCCG	244239	76435	CCTTACACTCTGGAAGGTTG	288826	121022	CTCCGCCTCCCAGGTTCATG
199653	31849	TGGGAGGATCACTTGAGCCC	244240	76436	GCCTTACACTCTGGAAGGTT	288827	121023	GCTCCGCCTCCCAGGTTCAT
199654	31850	ATGGGAGGATCACTTGAGCC	244241	76437	GGCCTTACACTCTGGAAGGT	288828	121024	AGCTCCGCCTCCCAGGTTCA
199655	31851	GATGGGAGGATCACTTGAGC	244242	76438	AGGCCTTACACTCTGGAAGG	288829	121025	AAGCTCCGCCTCCCAGGTTC
199656	31852	AGATGGGAGGATCACTTGAG	244243	76439	AAGGCCTTACACTCTGGAAG	288830	121026	CAAGCTCCGCCTCCCAGGTT
199657	31853	AAGATGGGAGGATCACTTGA	244244	76440	CAAGGCCTTACACTCTGGAA	288831	121027	GCAAGCTCCGCCTCCCAGGT
199658	31854	TAAGATGGGAGGATCACTTG	244245	76441	TCAAGGCCTTACACTCTGGA	288832	121028	TGCAAGCTCCGCCTCCCAGG
199659	31855	CTAAGATGGGAGGATCACTT	244246	76442	GTCAAGGCCTTACACTCTGG	288833	121029	CTGCAAGCTCCGCCTCCCAG
199660	31856	GCTAAGATGGGAGGATCACT	244247	76443	GGTCAAGGCCTTACACTCTG	288834	121030	ACTGCAAGCTCCGCCTCCCA
199661	31857	GGCTAAGATGGGAGGATCAC	244248	76444	AGGTCAAGGCCTTACACTCT	288835	121031	CACTGCAAGCTCCGCCTCCC
199662	31858	AGGCTAAGATGGGAGGATCA	244249	76445	CAGGTCAAGGCCTTACACTC	288836	121032	TCACTGCAAGCTCCGCCTCC
199663	31859	GAGGCTAAGATGGGAGGATC	244250	76446	GCAGGTCAAGGCCTTACACT	288837	121033	CTCACTGCAAGCTCCGCCTC
199664	31860	GGAGGCTAAGATGGGAGGAT	244251	76447	AGCAGGTCAAGGCCTTACAC	288838	121034	GCTCACTGCAAGCTCCGCCT
199665	31861	GGGAGGCTAAGATGGGAGGA	244252	76448	GAGCAGGTCAAGGCCTTACA	288839	121035	GGCTCACTGCAAGCTCCGCC
199666	31862	TGGGAGGCTAAGATGGGAGG	244253	76449	TGAGCAGGTCAAGGCCTTAC	288840	121036	CGGCTCACTGCAAGCTCCGC
199667	31863	TTGGGAGGCTAAGATGGGAG	244254	76450	CTGAGCAGGTCAAGGCCTTA	288841	121037	TCGGCTCACTGCAAGCTCCG
199668	31864	CTTGGGAGGCTAAGATGGGA	244255	76451	GCTGAGCAGGTCAAGGCCTT	288842	121038	CTCGGCTCACTGCAAGCTCC
199669	31865	ACTTGGGAGGCTAAGATGGG	244256	76452	GGCTGAGCAGGTCAAGGCCT	288843	121039	TCTCGGCTCACTGCAAGCTC
199670	31866	TACTTGGGAGGCTAAGATGG	244257	76453	GGGCTGAGCAGGTCAAGGCC	288844	121040	ATCTCGGCTCACTGCAAGCT
199671	31867	CTACTTGGGAGGCTAAGATG	244258	76454	AGGGCTGAGCAGGTCAAGGC	288845	121041	AATCTCGGCTCACTGCAAGC
199672	31868	TCTACTTGGGAGGCTAAGAT	244259	76455	CAGGGCTGAGCAGGTCAAGG	288846	121042	CAATCTCGGCTCACTGCAAG
199673	31869	ATCTACTTGGGAGGCTAAGA	244260	76456	CCAGGGCTGAGCAGGTCAAG	288847	121043	ACAATCTCGGCTCACTGCAA
199674	31870	CATCTACTTGGGAGGCTAAG	244261	76457	TCCAGGGCTGAGCAGGTCAA	288848	121044	CACAATCTCGGCTCACTGCA
199675	31871	CCATCTACTTGGGAGGCTAA	244262	76458	ATCCAGGGCTGAGCAGGTCA	288849	121045	GCACAATCTCGGCTCACTGC
199676	31872	CCCATCTACTTGGGAGGCTA	244263	76459	TATCCAGGGCTGAGCAGGTC	288850	121046	GGCACAATCTCGGCTCACTG
199677	31873	TCCCATCTACTTGGGAGGCT	244264	76460	GTATCCAGGGCTGAGCAGGT	288851	121047	TGGCACAATCTCGGCTCACT
199678	31874	GTCCCATCTACTTGGGAGGC	244265	76461	AGTATCCAGGGCTGAGCAGG	288852	121048	GTGGCACAATCTCGGCTCAC
199679	31875	GGTCCCATCTACTTGGGAGG	244266	76462	CAGTATCCAGGGCTGAGCAG	288853	121049	AGTGGCACAATCTCGGCTCA
199680	31876	TGGTCCCATCTACTTGGGAG	244267	76463	GCAGTATCCAGGGCTGAGCA	288854	121050	CAGTGGCACAATCTCGGCTC
199681	31877	GTGGTCCCATCTACTTGGGA	244268	76464	TGCAGTATCCAGGGCTGAGC	288855	121051	GCAGTGGCACAATCTCGGCT
199682	31878	TGTGGTCCCATCTACTTGGG	244269	76465	ATGCAGTATCCAGGGCTGAG	288856	121052	TGCAGTGGCACAATCTCGGC
199683	31879	CTGTGGTCCCATCTACTTGG	244270	76466	CATGCAGTATCCAGGGCTGA	288857	121053	GTGCAGTGGCACAATCTCGG
199684	31880	CCTGTGGTCCCATCTACTTG	244271	76467	TCATGCAGTATCCAGGGCTG	288858	121054	AGTGCAGTGGCACAATCTCG
199685	31881	ACCTGTGGTCCCATCTACTT	244272	76468	ATCATGCAGTATCCAGGGCT	288859	121055	GAGTGCAGTGGCACAATCTC
199686	31882	CACCTGTGGTCCCATCTACT	244273	76469	CATCATGCAGTATCCAGGGC	288860	121056	GGAGTGCAGTGGCACAATCT
199687	31883	GCACCTGTGGTCCCATCTAC	244274	76470	GCATCATGCAGTATCCAGGG	288861	121057	TGGAGTGCAGTGGCACAATC
199688	31884	TGCACCTGTGGTCCCATCTA	244275	76471	TGCATCATGCAGTATCCAGG	288862	121058	CTGGAGTGCAGTGGCACAAT
199689	31885	ATGCACCTGTGGTCCCATCT	244276	76472	ATGCATCATGCAGTATCCAG	288863	121059	GCTGGAGTGCAGTGGCACAA
199690	31886	TATGCACCTGTGGTCCCATC	244277	76473	AATGCATCATGCAGTATCCA	288864	121060	GGCTGGAGTGCAGTGGCACA
199691	31887	GTATGCACCTGTGGTCCCAT	244278	76474	CAATGCATCATGCAGTATCC	288865	121061	AGGCTGGAGTGCAGTGGCAC
199692	31888	GGTATGCACCTGTGGTCCCA	244279	76475	TCAATGCATCATGCAGTATC	288866	121062	CAGGCTGGAGTGCAGTGGCA
199693	31889	TGGTATGCACCTGTGGTCCC	244280	76476	ATCAATGCATCATGCAGTAT	288867	121063	CCAGGCTGGAGTGCAGTGGC
199694	31890	GTGGTATGCACCTGTGGTCC	244281	76477	TATCAATGCATCATGCAGTA	288868	121064	CCCAGGCTGGAGTGCAGTGG
199695	31891	GGTGGTATGCACCTGTGGTC	244282	76478	TTATCAATGCATCATGCAGT	288869	121065	GCCCAGGCTGGAGTGCAGTG
199696	31892	TGGTGGTATGCACCTGTGGT	244283	76479	CTTATCAATGCATCATGCAG	288870	121066	CGCCCAGGCTGGAGTGCAGT
199697	31893	GTGGTGGTATGCACCTGTGG	244284	76480	GCTTATCAATGCATCATGCA	288871	121067	TCGCCCAGGCTGGAGTGCAG
199698	31894	TGTGGTGGTATGCACCTGTG	244285	76481	GGCTTATCAATGCATCATGC	288872	121068	CTCGCCCAGGCTGGAGTGCA

199699	31895	GTGTGGTGGTATGCACCTGT	244286	76482	GGGCTTATCAATGCATCATG	288873	121069	TCTCGCCCAGGCTGGAGTGC
199700	31896	GGTGTGGTGGTATGCACCTG	244287	76483	TGGGCTTATCAATGCATCAT	288874	121070	CTCTCGCCCAGGCTGGAGTG
199701	31897	AGGTGTGGTGGTATGCACCT	244288	76484	ATGGGCTTATCAATGCATCA	288875	121071	TCTCTCGCCCAGGCTGGAGT
199702	31898	CAGGTGTGGTGGTATGCACC	244289	76485	TATGGGCTTATCAATGCATC	288876	121072	CTCTCTCGCCCAGGCTGGAG
199703	31899	CCAGGTGTGGTGGTATGCAC	244290	76486	TTATGGGCTTATCAATGCAT	288877	121073	ACTCTCTCGCCCAGGCTGGA
199704	31900	GCCAGGTGTGGTGGTATGCA	244291	76487	TTTATGGGCTTATCAATGCA	288878	121074	CACTCTCTCGCCCAGGCTGG
199705	31901	AGCCAGGTGTGGTGGTATGC	244292	76488	TTTTATGGGCTTATCAATGC	288879	121075	TCACTCTCTCGCCCAGGCTG
199706	31902	TAGCCAGGTGTGGTGGTATG	244293	76489	ATTTTATGGGCTTATCAATG	288880	121076	CTCACTCTCTCGCCCAGGCT
199707	31903	TTAGCCAGGTGTGGTGGTAT	244294	76490	TATTTTATGGGCTTATCAAT	288881	121077	TCTCACTCTCTCGCCCAGGC
199708	31904	ATTAGCCAGGTGTGGTGGTA	244295	76491	TTATTTTATGGGCTTATCAA	288882	121078	GTCTCACTCTCTCGCCCAGG
199709	31905	AATTAGCCAGGTGTGGTGGT	244296	76492	GTTATTTTATGGGCTTATCA	288883	121079	AGTCTCACTCTCTCGCCCAG
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199716	31912	TAAAAAAAATTAGCCAGGTG	244303	76499	TGCCCTGGTTATTTTATGGG	288890	121086	GAGACGGAGTCTCACTCTCT
199717	31913	ATAAAAAAAATTAGCCAGGT	244304	76500	CTGCCCTGGTTATTTTATGG	288891	121087	TGAGACGGAGTCTCACTCTC
199718	31914	AATAAAAAAAATTAGCCAGG	244305	76501	TCTGCCCTGGTTATTTTATG	288892	121088	TTGAGACGGAGTCTCACTCT
199719	31915	AAATAAAAAAAATTAGCCAG	244306	76502	ATCTGCCCTGGTTATTTTAT	288893	121089	TTTGAGACGGAGTCTCACTC
199720	31916	AAAATAAAAAAAATTAGCCA	244307	76503	AATCTGCCCTGGTTATTTTA	288894	121090	TTTTGAGACGGAGTCTCACT
199721	31917	AAAAATAAAAAAAATTAGCC	244308	76504	CAATCTGCCCTGGTTATTTT	288895	121091	GTTTTGAGACGGAGTCTCAC
199722	31918	AAAAAATAAAAAAAATTAGC	244309	76505	TCAATCTGCCCTGGTTATTT	288896	121092	TGTTTTGAGACGGAGTCTCA
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199726	31922	AAATAAAAAATAAAAAAAAT	244313	76509	GGAGTCAATCTGCCCTGGTT	288900	121096	TTTTTGTTTTGAGACGGAGT
199727	31923	AAAATAAAAAATAAAAAAAA	244314	76510	GGGAGTCAATCTGCCCTGGT	288901	121097	GTTTTTGTTTTGAGACGGAG
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199729	31925	TAAAAATAAAAAATAAAAAA	244316	76512	CTGGGAGTCAATCTGCCCTG	288903	121099	TTGTTTTTGTTTTGAGACGG
199730	31926	CTAAAAATAAAAAATAAAAA	244317	76513	ACTGGGAGTCAATCTGCCCT	288904	121100	TTTGTTTTTGTTTTGAGACG
199731	31927	TCTAAAAATAAAAAATAAAA	244318	76514	CACTGGGAGTCAATCTGCCC	288905	121101	TTTTGTTTTTGTTTTGAGAC
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199733	31929	TCTCTAAAAATAAAAAATAA	244320	76516	GCCACTGGGAGTCAATCTGC	288907	121103	GTTTTTGTTTTTGTTTTGAG
199734	31930	ATCTCTAAAAATAAAAAATA	244321	76517	GGCCACTGGGAGTCAATCTG	288908	121104	TGTTTTTGTTTTTGTTTTGA
199735	31931	CATCTCTAAAAATAAAAAAT	244322	76518	TGGCCACTGGGAGTCAATCT	288909	121105	TTGTTTTTGTTTTTGTTTTG
199736	31932	CCATCTCTAAAAATAAAAAA	244323	76519	TTGGCCACTGGGAGTCAATC	288910	121106	TTTGTTTTTGTTTTTGTTTT
199737	31933	ACCATCTCTAAAAATAAAAA	244324	76520	TTTGGCCACTGGGAGTCAAT	288911	121107	TTTTGTTTTTGTTTTTGTTT
199738	31934	CACCATCTCTAAAAATAAAA	244325	76521	CTTTGGCCACTGGGAGTCAA	288912	121108	TTTTTGTTTTTGTTTTTGTT
199739	31935	ACACCATCTCTAAAAATAAA	244326	76522	ACTTTGGCCACTGGGAGTCA	288913	121109	GTTTTTGTTTTTGTTTTTGT
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199741	31937	AAACACCATCTCTAAAAATA	244328	76524	GCACTTTGGCCACTGGGAGT	288915	121111	TTGTTTTTGTTTTTGTTTTT
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199743	31939	GTAAACACCATCTCTAAAAA	244330	76526	TGGCACTTTGGCCACTGGGA	288917	121113	TTTTGTTTTTGTTTTTGTTT
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199745	31941	TAGTAAACACCATCTCTAAA	244332	76528	TGTGGCACTTTGGCCACTGG	288919	121115	GTTTTTGTTTTTGTTTTTGT
199746	31942	ATAGTAAACACCATCTCTAA	244333	76529	CTGTGGCACTTTGGCCACTG	288920	121116	TGTTTTTGTTTTTGTTTTTG
199747	31943	CATAGTAAACACCATCTCTA	244334	76530	CCTGTGGCACTTTGGCCACT	288921	121117	TTGTTTTTGTTTTTGTTTTT
199748	31944	ACATAGTAAACACCATCTCT	244335	76531	CCCTGTGGCACTTTGGCCAC	288922	121118	TTTGTTTTTGTTTTTGTTTT
199749	31945	AACATAGTAAACACCATCTC	244336	76532	TCCCTGTGGCACTTTGGCCA	288923	121119	GTTTGTTTTTGTTTTTGTTT
199750	31946	CAACATAGTAAACACCATCT	244337	76533	TTCCCTGTGGCACTTTGGCC	288924	121120	TGTTTGTTTTTGTTTTTGTT
199751	31947	GCAACATAGTAAACACCATC	244338	76534	CTTCCCTGTGGCACTTTGGC	288925	121121	GTGTTTGTTTTTGTTTTTGT
199752	31948	GGCAACATAGTAAACACCAT	244339	76535	CCTTCCCTGTGGCACTTTGG	288926	121122	TGTGTTTGTTTTTGTTTTTG
199753	31949	GGGCAACATAGTAAACACCA	244340	76536	CCCTTCCCTGTGGCACTTTG	288927	121123	GTGTGTTTGTTTTTGTTTTT
199754	31950	TGGGCAACATAGTAAACACC	244341	76537	TCCCTTCCCTGTGGCACTTT	288928	121124	TGTGTGTTTGTTTTTGTTTT
199755	31951	CTGGGCAACATAGTAAACAC	244342	76538	GTCCCTTCCCTGTGGCACTT	288929	121125	TTGTGTGTTTGTTTTTGTTT
199756	31952	CCTGGGCAACATAGTAAACA	244343	76539	TGTCCCTTCCCTGTGGCACT	288930	121126	GTTGTGTGTTTGTTTTTGTT
199757	31953	GCCTGGGCAACATAGTAAAC	244344	76540	TTGTCCCTTCCCTGTGGCAC	288931	121127	TGTTGTGTGTTTGTTTTTGT
199758	31954	AGCCTGGGCAACATAGTAAA	244345	76541	ATTGTCCCTTCCCTGTGGCA	288932	121128	TTGTTGTGTGTTTGTTTTTG
199759	31955	TAGCCTGGGCAACATAGTAA	244346	76542	AATTGTCCCTTCCCTGTGGC	288933	121129	TTTGTTGTGTGTTTGTTTTT
199760	31956	CTAGCCTGGGCAACATAGTA	244347	76543	GAATTGTCCCTTCCCTGTGG	288934	121130	TTTTGTTGTGTGTTTGTTTT
199761	31957	ACTAGCCTGGGCAACATAGT	244348	76544	TGAATTGTCCCTTCCCTGTG	288935	121131	TTTTTGTTGTGTGTTTGTTT
199762	31958	GACTAGCCTGGGCAACATAG	244349	76545	CTGAATTGTCCCTTCCCTGT	288936	121132	GTTTTTGTTGTGTGTTTGTT
199763	31959	AGACTAGCCTGGGCAACATA	244350	76546	GCTGAATTGTCCCTTCCCTG	288937	121133	GGTTTTTGTTGTGTGTTTGT
199764	31960	GAGACTAGCCTGGGCAACAT	244351	76547	GGCTGAATTGTCCCTTCCCT	288938	121134	AGGTTTTTGTTGTGTGTTTG
199765	31961	TGAGACTAGCCTGGGCAACA	244352	76548	GGGCTGAATTGTCCCTTCCC	288939	121135	TAGGTTTTTGTTGTGTGTTT
199766	31962	TTGAGACTAGCCTGGGCAAC	244353	76549	AGGGCTGAATTGTCCCTTCC	288940	121136	TTAGGTTTTTGTTGTGTGTT
199767	31963	TTTGAGACTAGCCTGGGCAA	244354	76550	AAGGGCTGAATTGTCCCTTC	288941	121137	TTTAGGTTTTTGTTGTGTGT
199768	31964	GTTTGAGACTAGCCTGGGCA	244355	76551	GAAGGGCTGAATTGTCCCTT	288942	121138	TTTTAGGTTTTTGTTGTGTG
199769	31965	AGTTTGAGACTAGCCTGGGC	244356	76552	AGAAGGGCTGAATTGTCCCT	288943	121139	CTTTTAGGTTTTTGTTGTGT
199770	31966	GAGTTTGAGACTAGCCTGGG	244357	76553	TAGAAGGGCTGAATTGTCCC	288944	121140	TCTTTTAGGTTTTTGTTGTG

199771	31967	GGAGTTTGAGACTAGCCTGG	244358	76554	CTAGAAGGGCTGAATTGTCC	288945	121141	TTCTTTTAGGTTTTTGTTGT
199772	31968	AGGAGTTTGAGACTAGCCTG	244359	76555	CCTAGAAGGGCTGAATTGTC	288946	121142	ATTCTTTTAGGTTTTTGTTG
199773	31969	CAGGAGTTTGAGACTAGCCT	244360	76556	TCCTAGAAGGGCTGAATTGT	288947	121143	TATTCTTTTAGGTTTTTGTT
199774	31970	CCAGGAGTTTGAGACTAGCC	244361	76557	CTCCTAGAAGGGCTGAATTG	288948	121144	ATATTCTTTTAGGTTTTTGT
199775	31971	CCCAGGAGTTTGAGACTAGC	244362	76558	CCTCCTAGAAGGGCTGAATT	288949	121145	TATATTCTTTTAGGTTTTTG
199776	31972	GCCCAGGAGTTTGAGACTAG	244363	76559	TCCTCCTAGAAGGGCTGAAT	288950	121146	TTATATTCTTTTAGGTTTTT
199777	31973	AGCCCAGGAGTTTGAGACTA	244364	76560	CTCCTCCTAGAAGGGCTGAA	288951	121147	TTTATATTCTTTTAGGTTTT
199778	31974	GAGCCCAGGAGTTTGAGACT	244365	76561	CCTCCTCCTAGAAGGGCTGA	288952	121148	ATTTATATTCTTTTAGGTTT
199779	31975	TGAGCCCAGGAGTTTGAGAC	244366	76562	TCCTCCTCCTAGAAGGGCTG	288953	121149	CATTTATATTCTTTTAGGTT
199780	31976	TTGAGCCCAGGAGTTTGAGA	244367	76563	CTCCTCCTCCTAGAAGGGCT	288954	121150	CCATTTATATTCTTTTAGGT
199781	31977	CTTGAGCCCAGGAGTTTGAG	244368	76564	CCTCCTCCTCCTAGAAGGGC	288955	121151	TCCATTTATATTCTTTTAGG
199782	31978	GCTTGAGCCCAGGAGTTTGA	244369	76565	TCCTCCTCCTCCTAGAAGGG	288956	121152	ATCCATTTATATTCTTTTAG
199783	31979	AGCTTGAGCCCAGGAGTTTG	244370	76566	CTCCTCCTCCTCCTAGAAGG	288957	121153	AATCCATTTATATTCTTTTA
199784	31980	TAGCTTGAGCCCAGGAGTTT	244371	76567	CCTCCTCCTCCTCCTAGAAG	288958	121154	CAATCCATTTATATTCTTTT
199785	31981	ATAGCTTGAGCCCAGGAGTT	244372	76568	ACCTCCTCCTCCTCCTAGAA	288959	121155	ACAATCCATTTATATTCTTT
199786	31982	GATAGCTTGAGCCCAGGAGT	244373	76569	TACCTCCTCCTCCTCCTAGA	288960	121156	AACAATCCATTTATATTCTT
199787	31983	GGATAGCTTGAGCCCAGGAG	244374	76570	CTACCTCCTCCTCCTCCTAG	288961	121157	AAACAATCCATTTATATTCT
199788	31984	AGGATAGCTTGAGCCCAGGA	244375	76571	ACTACCTCCTCCTCCTCCTA	288962	121158	CAAACAATCCATTTATATTC
199789	31985	GAGGATAGCTTGAGCCCAGG	244376	76572	AACTACCTCCTCCTCCTCCT	288963	121159	ACAAACAATCCATTTATATT
199790	31986	GGAGGATAGCTTGAGCCCAG	244377	76573	AAACTACCTCCTCCTCCTCC	288964	121160	TACAAACAATCCATTTATAT
199791	31987	GGGAGGATAGCTTGAGCCCA	244378	76574	AAAACTACCTCCTCCTCCTC	288965	121161	TTACAAACAATCCATTTATA
199792	31988	TGGGAGGATAGCTTGAGCCC	244379	76575	GAAAACTACCTCCTCCTCCT	288966	121162	GTTACAAACAATCCATTTAT
199793	31989	GTGGGAGGATAGCTTGAGCC	244380	76576	AGAAAACTACCTCCTCCTCC	288967	121163	TGTTACAAACAATCCATTTA
199794	31990	GGTGGGAGGATAGCTTGAGC	244381	76577	GAGAAAACTACCTCCTCCTC	288968	121164	GTGTTACAAACAATCCATTT
199795	31991	AGGTGGGAGGATAGCTTGAG	244382	76578	TGAGAAAACTACCTCCTCCT	288969	121165	TGTGTTACAAACAATCCATT
199796	31992	GAGGTGGGAGGATAGCTTGA	244383	76579	ATGAGAAAACTACCTCCTCC	288970	121166	TTGTGTTACAAACAATCCAT
199797	31993	CGAGGTGGGAGGATAGCTTG	244384	76580	AATGAGAAAACTACCTCCTC	288971	121167	TTTGTGTTACAAACAATCCA
199798	31994	CCGAGGTGGGAGGATAGCTT	244385	76581	AAATGAGAAAACTACCTCCT	288972	121168	CTTTGTGTTACAAACAATCC
199799	31995	GCCGAGGTGGGAGGATAGCT	244386	76582	GAAATGAGAAAACTACCTCC	288973	121169	CCTTTGTGTTACAAACAATC
199800	31996	GGCCGAGGTGGGAGGATAGC	244387	76583	AGAAATGAGAAAACTACCTC	288974	121170	TCCTTTGTGTTACAAACAAT
199801	31997	AGGCCGAGGTGGGAGGATAG	244388	76584	TAGAAATGAGAAAACTACCT	288975	121171	GTCCTTTGTGTTACAAACAA
199802	31998	GAGGCCGAGGTGGGAGGATA	244389	76585	ATAGAAATGAGAAAACTACC	288976	121172	TGTCCTTTGTGTTACAAACA
199803	31999	GGAGGCCGAGGTGGGAGGAT	244390	76586	AATAGAAATGAGAAAACTAC	288977	121173	TTGTCCTTTGTGTTACAAAC
199804	32000	GGGAGGCCGAGGTGGGAGGA	244391	76587	TAATAGAAATGAGAAAACTA	288978	121174	TTTGTCCTTTGTGTTACAAA
199805	32001	CGGGAGGCCGAGGTGGGAGG	244392	76588	TTAATAGAAATGAGAAAACT	288979	121175	ATTTGTCCTTTGTGTTACAA
199806	32002	TCGGGAGGCCGAGGTGGGAG	244393	76589	CTTAATAGAAATGAGAAAAC	288980	121176	CATTTGTCCTTTGTGTTACA
199807	32003	TTCGGGAGGCCGAGGTGGGA	244394	76590	CCTTAATAGAAATGAGAAAA	288981	121177	ACATTTGTCCTTTGTGTTAC
199808	32004	CTTCGGGAGGCCGAGGTGGG	244395	76591	GCCTTAATAGAAATGAGAAA	288982	121178	AACATTTGTCCTTTGTGTTA
199809	32005	ACTTCGGGAGGCCGAGGTGG	244396	76592	TGCCTTAATAGAAATGAGAA	288983	121179	AAACATTTGTCCTTTGTGTT
199810	32006	CACTTCGGGAGGCCGAGGTG	244397	76593	TTGCCTTAATAGAAATGAGA	288984	121180	CAAACATTTGTCCTTTGTGT
199811	32007	GCACTTCGGGAGGCCGAGGT	244398	76594	GTTGCCTTAATAGAAATGAG	288985	121181	TCAAACATTTGTCCTTTGTG
199812	32008	AGCACTTCGGGAGGCCGAGG	244399	76595	TGTTGCCTTAATAGAAATGA	288986	121182	CTCAAACATTTGTCCTTTGT
199813	32009	CAGCACTTCGGGAGGCCGAG	244400	76596	TTGTTGCCTTAATAGAAATG	288987	121183	CCTCAAACATTTGTCCTTTG
199814	32010	CCAGCACTTCGGGAGGCCGA	244401	76597	TTTGTTGCCTTAATAGAAAT	288988	121184	CCCTCAAACATTTGTCCTTT
199815	32011	CCCAGCACTTCGGGAGGCCG	244402	76598	TTTTGTTGCCTTAATAGAAA	288989	121185	CCCCTCAAACATTTGTCCTT
199816	32012	CCCCAGCACTTCGGGAGGCC	244403	76599	CTTTTGTTGCCTTAATAGAA	288990	121186	TCCCCTCAAACATTTGTCCT
199817	32013	ACCCCAGCACTTCGGGAGGC	244404	76600	GCTTTTGTTGCCTTAATAGA	288991	121187	ATCCCCTCAAACATTTGTCC
199818	32014	AACCCCAGCACTTCGGGAGG	244405	76601	AGCTTTTGTTGCCTTAATAG	288992	121188	CATCCCCTCAAACATTTGTC
199819	32015	TAACCCCAGCACTTCGGGAG	244406	76602	CAGCTTTTGTTGCCTTAATA	288993	121189	CCATCCCCTCAAACATTTGT
199820	32016	GTAACCCCAGCACTTCGGGA	244407	76603	GCAGCTTTTGTTGCCTTAAT	288994	121190	TCCATCCCCTCAAACATTTG
199821	32017	GGTAACCCCAGCACTTCGGG	244408	76604	GGCAGCTTTTGTTGCCTTAA	288995	121191	ATCCATCCCCTCAAACATTT
199822	32018	TGGTAACCCCAGCACTTCGG	244409	76605	AGGCAGCTTTTGTTGCCTTA	288996	121192	TATCCATCCCCTCAAACATT
199823	32019	CTGGTAACCCCAGCACTTCG	244410	76606	AAGGCAGCTTTTGTTGCCTT	288997	121193	GTATCCATCCCCTCAAACAT
199824	32020	GCTGGTAACCCCAGCACTTC	244411	76607	TAAGGCAGCTTTTGTTGCCT	288998	121194	GGTATCCATCCCCTCAAACA
199825	32021	TGCTGGTAACCCCAGCACTT	244412	76608	GTAAGGCAGCTTTTGTTGCC	288999	121195	GGGTATCCATCCCCTCAAAC
199826	32022	ATGCTGGTAACCCCAGCACT	244413	76609	AGTAAGGCAGCTTTTGTTGC	289000	121196	GGGGTATCCATCCCCTCAAA
199827	32023	CATGCTGGTAACCCCAGCAC	244414	76610	TAGTAAGGCAGCTTTTGTTG	289001	121197	TGGGGTATCCATCCCCTCAA
199828	32024	TCATGCTGGTAACCCCAGCA	244415	76611	TTAGTAAGGCAGCTTTTGTT	289002	121198	ATGGGGTATCCATCCCCTCA
199829	32025	CTCATGCTGGTAACCCCAGC	244416	76612	CTTAGTAAGGCAGCTTTTGT	289003	121199	AATGGGGTATCCATCCCCTC
199830	32026	GCTCATGCTGGTAACCCCAG	244417	76613	CCTTAGTAAGGCAGCTTTTG	289004	121200	AAATGGGGTATCCATCCCCT
199831	32027	GGCTCATGCTGGTAACCCCA	244418	76614	TCCTTAGTAAGGCAGCTTTT	289005	121201	AAAATGGGGTATCCATCCCC
199832	32028	TGGCTCATGCTGGTAACCCC	244419	76615	GTCCTTAGTAAGGCAGCTTT	289006	121202	GAAAATGGGGTATCCATCCC
199833	32029	GTGGCTCATGCTGGTAACCC	244420	76616	TGTCCTTAGTAAGGCAGCTT	289007	121203	GGAAAATGGGGTATCCATCC
199834	32030	AGTGGCTCATGCTGGTAACC	244421	76617	ATGTCCTTAGTAAGGCAGCT	289008	121204	TGGAAAATGGGGTATCCATC
199835	32031	CAGTGGCTCATGCTGGTAAC	244422	76618	AATGTCCTTAGTAAGGCAGC	289009	121205	ATGGAAAATGGGGTATCCAT
199836	32032	ACAGTGGCTCATGCTGGTAA	244423	76619	GAATGTCCTTAGTAAGGCAG	289010	121206	CATGGAAAATGGGGTATCCA
199837	32033	TACAGTGGCTCATGCTGGTA	244424	76620	AGAATGTCCTTAGTAAGGCA	289011	121207	TCATGGAAAATGGGGTATCC
199838	32034	GTACAGTGGCTCATGCTGGT	244425	76621	AAGAATGTCCTTAGTAAGGC	289012	121208	ATCATGGAAAATGGGGTATC
199839	32035	GGTACAGTGGCTCATGCTGG	244426	76622	CAAGAATGTCCTTAGTAAGG	289013	121209	CATCATGGAAAATGGGGTAT
199840	32036	GGGTACAGTGGCTCATGCTG	244427	76623	CCAAGAATGTCCTTAGTAAG	289014	121210	ACATCATGGAAAATGGGGTA
199841	32037	TGGGTACAGTGGCTCATGCT	244428	76624	ACCAAGAATGTCCTTAGTAA	289015	121211	CACATCATGGAAAATGGGGT
199842	32038	CTGGGTACAGTGGCTCATGC	244429	76625	CACCAAGAATGTCCTTAGTA	289016	121212	TCACATCATGGAAAATGGGG

199843	32039	GCTGGGTACAGTGGCTCATG	244430	76626	CCACCAAGAATGTCCTTAGT	289017	121213	ATCACATCATGGAAAATGGG
199844	32040	GGCTGGGTACAGTGGCTCAT	244431	76627	TCCACCAAGAATGTCCTTAG	289018	121214	AATCACATCATGGAAAATGG
199845	32041	GGGCTGGGTACAGTGGCTCA	244432	76628	CTCCACCAAGAATGTCCTTA	289019	121215	TAATCACATCATGGAAAATG
199846	32042	AGGGCTGGGTACAGTGGCTC	244433	76629	CCTCCACCAAGAATGTCCTT	289020	121216	ATAATCACATCATGGAAAAT
199847	32043	GAGGGCTGGGTACAGTGGCT	244434	76630	CCCTCCACCAAGAATGTCCT	289021	121217	AATAATCACATCATGGAAAA
199848	32044	TGAGGGCTGGGTACAGTGGC	244435	76631	GCCCTCCACCAAGAATGTCC	289022	121218	TAATAATCACATCATGGAAA
199849	32045	TTGAGGGCTGGGTACAGTGG	244436	76632	CGCCCTCCACCAAGAATGTC	289023	121219	ATAATAATCACATCATGGAA
199850	32046	TTTGAGGGCTGGGTACAGTG	244437	76633	ACGCCCTCCACCAAGAATGT	289024	121220	TATAATAATCACATCATGGA
199851	32047	ATTTGAGGGCTGGGTACAGT	244438	76634	CACGCCCTCCACCAAGAATG	289025	121221	GTATAATAATCACATCATGG
199852	32048	AATTTGAGGGCTGGGTACAG	244439	76635	TCACGCCCTCCACCAAGAAT	289026	121222	TGTATAATAATCACATCATG
199853	32049	AAATTTGAGGGCTGGGTACA	244440	76636	GTCACGCCCTCCACCAAGAA	289027	121223	ATGTATAATAATCACATCAT
199854	32050	AAAATTTGAGGGCTGGGTAC	244441	76637	AGTCACGCCCTCCACCAAGA	289028	121224	AATGTATAATAATCACATCA
199855	32051	AAAAATTTGAGGGCTGGGTA	244442	76638	CAGTCACGCCCTCCACCAAG	289029	121225	CAATGTATAATAATCACATC
199856	32052	TAAAAATTTGAGGGCTGGGT	244443	76639	ACAGTCACGCCCTCCACCAA	289030	121226	ACAATGTATAATAATCACAT
199857	32053	TTAAAAATTTGAGGGCTGGG	244444	76640	GACAGTCACGCCCTCCACCA	289031	121227	CACAATGTATAATAATCACA
199858	32054	TTTAAAAATTTGAGGGCTGG	244445	76641	TGACAGTCACGCCCTCCACC	289032	121228	ACACAATGTATAATAATCAC
199859	32055	TTTTAAAAATTTGAGGGCTG	244446	76642	TTGACAGTCACGCCCTCCAC	289033	121229	CACACAATGTATAATAATCA
199860	32056	TTTTTAAAAATTTGAGGGCT	244447	76643	GTTGACAGTCACGCCCTCCA	289034	121230	ACACACAATGTATAATAATC
199861	32057	ATTTTTAAAAATTTGAGGGC	244448	76644	GGTTGACAGTCACGCCCTCC	289035	121231	GACACACAATGTATAATAAT
199862	32058	GATTTTTAAAAATTTGAGGG	244449	76645	TGGTTGACAGTCACGCCCTC	289036	121232	AGACACACAATGTATAATAA
199863	32059	AGATTTTTAAAAATTTGAGG	244450	76646	GTGGTTGACAGTCACGCCCT	289037	121233	CAGACACACAATGTATAATA
199864	32060	TAGATTTTTAAAAATTTGAG	244451	76647	AGTGGTTGACAGTCACGCCC	289038	121234	ACAGACACACAATGTATAAT
199865	32061	ATAGATTTTTAAAAATTTGA	244452	76648	CAGTGGTTGACAGTCACGCC	289039	121235	TACAGACACACAATGTATAA
199866	32062	TATAGATTTTTAAAAATTTG	244453	76649	ACAGTGGTTGACAGTCACGC	289040	121236	ATACAGACACACAATGTATA
199867	32063	TTATAGATTTTTAAAAATTT	244454	76650	CACAGTGGTTGACAGTCACG	289041	121237	GATACAGACACACAATGTAT
199868	32064	CTTATAGATTTTTAAAAATT	244455	76651	TCACAGTGGTTGACAGTCAC	289042	121238	TGATACAGACACACAATGTA
199869	32065	TCTTATAGATTTTTAAAAAT	244456	76652	ATCACAGTGGTTGACAGTCA	289043	121239	TTGATACAGACACACAATGT
199870	32066	CTCTTATAGATTTTTAAAAA	244457	76653	GATCACAGTGGTTGACAGTC	289044	121240	TTTGATACAGACACACAATG
199871	32067	TCTCTTATAGATTTTTAAAA	244458	76654	TGATCACAGTGGTTGACAGT	289045	121241	TTTTGATACAGACACACAAT
199872	32068	GTCTCTTATAGATTTTTAAA	244459	76655	ATGATCACAGTGGTTGACAG	289046	121242	GTTTTGATACAGACACACAA
199873	32069	TGTCTCTTATAGATTTTTAA	244460	76656	AATGATCACAGTGGTTGACA	289047	121243	TGTTTTGATACAGACACACA
199874	32070	ATGTCTCTTATAGATTTTTA	244461	76657	AAATGATCACAGTGGTTGAC	289048	121244	ATGTTTTGATACAGACACAC
199875	32071	AATGTCTCTTATAGATTTTT	244462	76658	CAAATGATCACAGTGGTTGA	289049	121245	GATGTTTTGATACAGACACA
199876	32072	TAATGTCTCTTATAGATTTT	244463	76659	CCAAATGATCACAGTGGTTG	289050	121246	AGATGTTTTGATACAGACAC
199877	32073	ATAATGTCTCTTATAGATTT	244464	76660	CCCAAATGATCACAGTGGTT	289051	121247	GAGATGTTTTGATACAGACA
199878	32074	AATAATGTCTCTTATAGATT	244465	76661	GCCCAAATGATCACAGTGGT	289052	121248	TGAGATGTTTTGATACAGAC
199879	32075	CAATAATGTCTCTTATAGAT	244466	76662	GGCCCAAATGATCACAGTGG	289053	121249	ATGAGATGTTTTGATACAGA
199880	32076	CCAATAATGTCTCTTATAGA	244467	76663	AGGCCCAAATGATCACAGTG	289054	121250	CATGAGATGTTTTGATACAG
199881	32077	TCCAATAATGTCTCTTATAG	244468	76664	GAGGCCCAAATGATCACAGT	289055	121251	TCATGAGATGTTTTGATACA
199882	32078	GTCCAATAATGTCTCTTATA	244469	76665	AGAGGCCCAAATGATCACAG	289056	121252	CTCATGAGATGTTTTGATAC
199883	32079	TGTCCAATAATGTCTCTTAT	244470	76666	GAGAGGCCCAAATGATCACA	289057	121253	GCTCATGAGATGTTTTGATA
199884	32080	TTGTCCAATAATGTCTCTTA	244471	76667	AGAGAGGCCCAAATGATCAC	289058	121254	GGCTCATGAGATGTTTTGAT
199885	32081	ATTGTCCAATAATGTCTCTT	244472	76668	AAGAGAGGCCCAAATGATCA	289059	121255	GGGCTCATGAGATGTTTTGA
199886	32082	AATTGTCCAATAATGTCTCT	244473	76669	CAAGAGAGGCCCAAATGATC	289060	121256	GGGGCTCATGAGATGTTTTG
199887	32083	TAATTGTCCAATAATGTCTC	244474	76670	GCAAGAGAGGCCCAAATGAT	289061	121257	TGGGGCTCATGAGATGTTTT
199888	32084	CTAATTGTCCAATAATGTCT	244475	76671	GGCAAGAGAGGCCCAAATGA	289062	121258	ATGGGGCTCATGAGATGTTT
199889	32085	TCTAATTGTCCAATAATGTC	244476	76672	GGGCAAGAGAGGCCCAAATG	289063	121259	TATGGGGCTCATGAGATGTT
199890	32086	CTCTAATTGTCCAATAATGT	244477	76673	TGGGCAAGAGAGGCCCAAAT	289064	121260	TTATGGGGCTCATGAGATGT
199891	32087	TCTCTAATTGTCCAATAATG	244478	76674	CTGGGCAAGAGAGGCCCAAA	289065	121261	TTTATGGGGCTCATGAGATG
199892	32088	TTCTCTAATTGTCCAATAAT	244479	76675	CCTGGGCAAGAGAGGCCCAA	289066	121262	ATTTATGGGGCTCATGAGAT
199893	32089	TTTCTCTAATTGTCCAATAA	244480	76676	GCCTGGGCAAGAGAGGCCCA	289067	121263	TATTTATGGGGCTCATGAGA
199894	32090	ATTTCTCTAATTGTCCAATA	244481	76677	AGCCTGGGCAAGAGAGGCCC	289068	121264	ATATTTATGGGGCTCATGAG
199895	32091	AATTTCTCTAATTGTCCAAT	244482	76678	AAGCCTGGGCAAGAGAGGCC	289069	121265	TATATTTATGGGGCTCATGA
199896	32092	GAATTTCTCTAATTGTCCAA	244483	76679	GAAGCCTGGGCAAGAGAGGC	289070	121266	ATATATTTATGGGGCTCATG
199897	32093	TGAATTTCTCTAATTGTCCA	244484	76680	GGAAGCCTGGGCAAGAGAGG	289071	121267	TATATATTTATGGGGCTCAT
199898	32094	GTGAATTTCTCTAATTGTCC	244485	76681	GGGAAGCCTGGGCAAGAGAG	289072	121268	GTATATATTTATGGGGCTCA
199899	32095	TGTGAATTTCTCTAATTGTC	244486	76682	TGGGAAGCCTGGGCAAGAGA	289073	121269	TGTATATATTTATGGGGCTC
199900	32096	ATGTGAATTTCTCTAATTGT	244487	76683	ATGGGAAGCCTGGGCAAGAG	289074	121270	GTGTATATATTTATGGGGCT
199901	32097	TATGTGAATTTCTCTAATTG	244488	76684	AATGGGAAGCCTGGGCAAGA	289075	121271	GGTGTATATATTTATGGGGC
199902	32098	ATATGTGAATTTCTCTAATT	244489	76685	GAATGGGAAGCCTGGGCAAG	289076	121272	AGGTGTATATATTTATGGGG
199903	32099	CATATGTGAATTTCTCTAAT	244490	76686	AGAATGGGAAGCCTGGGCAA	289077	121273	TAGGTGTATATATTTATGGG
199904	32100	CCATATGTGAATTTCTCTAA	244491	76687	CAGAATGGGAAGCCTGGGCA	289078	121274	TTAGGTGTATATATTTATGG
199905	32101	TCCATATGTGAATTTCTCTA	244492	76688	TCAGAATGGGAAGCCTGGGC	289079	121275	GTTAGGTGTATATATTTATG
199906	32102	GTCCATATGTGAATTTCTCT	244493	76689	TTCAGAATGGGAAGCCTGGG	289080	121276	AGTTAGGTGTATATATTTAT
199907	32103	AGTCCATATGTGAATTTCTC	244494	76690	TTTCAGAATGGGAAGCCTGG	289081	121277	TAGTTAGGTGTATATATTTA
199908	32104	AAGTCCATATGTGAATTTCT	244495	76691	CTTTCAGAATGGGAAGCCTG	289082	121278	ATAGTTAGGTGTATATATTT
199909	32105	TAAGTCCATATGTGAATTTC	244496	76692	CCTTTCAGAATGGGAAGCCT	289083	121279	CATAGTTAGGTGTATATATT
199910	32106	ATAAGTCCATATGTGAATTT	244497	76693	TCCTTTCAGAATGGGAAGCC	289084	121280	ACATAGTTAGGTGTATATAT
199911	32107	TATAAGTCCATATGTGAATT	244498	76694	GTCCTTTCAGAATGGGAAGC	289085	121281	TACATAGTTAGGTGTATATA
199912	32108	TTATAAGTCCATATGTGAAT	244499	76695	TGTCCTTTCAGAATGGGAAG	289086	121282	GTACATAGTTAGGTGTATAT
199913	32109	ATTATAAGTCCATATGTGAA	244500	76696	CTGTCCTTTCAGAATGGGAA	289087	121283	GGTACATAGTTAGGTGTATA
199914	32110	TATTATAAGTCCATATGTGA	244501	76697	ACTGTCCTTTCAGAATGGGA	289088	121284	GGGTACATAGTTAGGTGTAT

199915	32111	CTATTATAAGTCCATATGTG	244502	76698	AACTGTCCTTTCAGAATGGG	289089	121285	TGGGTACATAGTTAGGTGTA
199916	32112	ACTATTATAAGTCCATATGT	244503	76699	AAACTGTCCTTTCAGAATGG	289090	121286	GTGGGTACATAGTTAGGTGT
199917	32113	TACTATTATAAGTCCATATG	244504	76700	AAAACTGTCCTTTCAGAATG	289091	121287	TGTGGGTACATAGTTAGGTG
199918	32114	ATACTATTATAAGTCCATAT	244505	76701	TAAAACTGTCCTTTCAGAAT	289092	121288	TTGTGGGTACATAGTTAGGT
199919	32115	GATACTATTATAAGTCCATA	244506	76702	ATAAAACTGTCCTTTCAGAA	289093	121289	TTTGTGGGTACATAGTTAGG
199920	32116	TGATACTATTATAAGTCCAT	244507	76703	AATAAAACTGTCCTTTCAGA	289094	121290	TTTTGTGGGTACATAGTTAG
199921	32117	CTGATACTATTATAAGTCCA	244508	76704	CAATAAAACTGTCCTTTCAG	289095	121291	TTTTTGTGGGTACATAGTTA
199922	32118	TCTGATACTATTATAAGTCC	244509	76705	ACAATAAAACTGTCCTTTCA	289096	121292	ATTTTTGTGGGTACATAGTT
199923	32119	CTCTGATACTATTATAAGTC	244510	76706	TACAATAAAACTGTCCTTTC	289097	121293	AATTTTTGTGGGTACATAGT
199924	32120	ACTCTGATACTATTATAAGT	244511	76707	CTACAATAAAACTGTCCTTT	289098	121294	TAATTTTTGTGGGTACATAG
199925	32121	CACTCTGATACTATTATAAG	244512	76708	CCTACAATAAAACTGTCCTT	289099	121295	TTAATTTTTGTGGGTACATA
199926	32122	ACACTCTGATACTATTATAA	244513	76709	ACCTACAATAAAACTGTCCT	289100	121296	TTTAATTTTTGTGGGTACAT
199927	32123	CACACTCTGATACTATTATA	244514	76710	TACCTACAATAAAACTGTCC	289101	121297	TTTTAATTTTTGTGGGTACA
199928	32124	ACACACTCTGATACTATTAT	244515	76711	GTACCTACAATAAAACTGTC	289102	121298	TTTTTAATTTTTGTGGGTAC
199929	32125	CACACACTCTGATACTATTA	244516	76712	TGTACCTACAATAAAACTGT	289103	121299	TTTTTTAATTTTTGTGGGTA
199930	32126	CCACACACTCTGATACTATT	244517	76713	GTGTACCTACAATAAAACTG	289104	121300	TTTTTTTAATTTTTGTGGGT
199931	32127	ACCACACACTCTGATACTAT	244518	76714	TGTGTACCTACAATAAAACT	289105	121301	ATTTTTTTAATTTTTGTGGG
199932	32128	CACCACACACTCTGATACTA	244519	76715	ATGTGTACCTACAATAAAAC	289106	121302	TATTTTTTTAATTTTTGTGG
199933	32129	ACACCACACACTCTGATACT	244520	76716	CATGTGTACCTACAATAAAA	289107	121303	ATATTTTTTTAATTTTTGTG
199934	32130	CACACCACACACTCTGATAC	244521	76717	CCATGTGTACCTACAATAAA	289108	121304	TATATTTTTTTAATTTTTGT
199935	32131	TCACACCACACACTCTGATA	244522	76718	GCCATGTGTACCTACAATAA	289109	121305	ATATATTTTTTTAATTTTTG
199936	32132	ATCACACCACACACTCTGAT	244523	76719	AGCCATGTGTACCTACAATA	289110	121306	AATATATTTTTTTAATTTTT
199937	32133	CATCACACCACACACTCTGA	244524	76720	CAGCCATGTGTACCTACAAT	289111	121307	AAATATATTTTTTTAATTTT
199938	32134	CCATCACACCACACACTCTG	244525	76721	GCAGCCATGTGTACCTACAA	289112	121308	AAAATATATTTTTTTAATTT
199939	32135	ACCATCACACCACACACTCT	244526	76722	GGCAGCCATGTGTACCTACA	289113	121309	AAAAATATATTTTTTTAATT
199940	32136	AACCATCACACCACACACTC	244527	76723	TGGCAGCCATGTGTACCTAC	289114	121310	AAAAAATATATTTTTTTAAT
199941	32137	GAACCATCACACCACACACT	244528	76724	ATGGCAGCCATGTGTACCTA	289115	121311	TAAAAAATATATTTTTTTAA
199942	32138	AGAACCATCACACCACACAC	244529	76725	AATGGCAGCCATGTGTACCT	289116	121312	TTAAAAAATATATTTTTTTA
199943	32139	CAGAACCATCACACCACACA	244530	76726	AAATGGCAGCCATGTGTACC	289117	121313	CTTAAAAAATATATTTTTTT
199944	32140	CCAGAACCATCACACCACAC	244531	76727	GAAATGGCAGCCATGTGTAC	289118	121314	CCTTAAAAAATATATTTTTT
199945	32141	TCCAGAACCATCACACCACA	244532	76728	TGAAATGGCAGCCATGTGTA	289119	121315	ACCTTAAAAAATATATTTTT
199946	32142	CTCCAGAACCATCACACCAC	244533	76729	TTGAAATGGCAGCCATGTGT	289120	121316	CACCTTAAAAAATATATTTT
199947	32143	CCTCCAGAACCATCACACCA	244534	76730	TTTGAAATGGCAGCCATGTG	289121	121317	TCACCTTAAAAAATATATTT
199948	32144	CCCTCCAGAACCATCACACC	244535	76731	ATTTGAAATGGCAGCCATGT	289122	121318	TTCACCTTAAAAAATATATT
199949	32145	TCCCTCCAGAACCATCACAC	244536	76732	CATTTGAAATGGCAGCCATG	289123	121319	CTTCACCTTAAAAAATATAT
199950	32146	TTCCCTCCAGAACCATCACA	244537	76733	ACATTTGAAATGGCAGCCAT	289124	121320	TCTTCACCTTAAAAAATATA
199951	32147	ATTCCCTCCAGAACCATCAC	244538	76734	TACATTTGAAATGGCAGCCA	289125	121321	CTCTTCACCTTAAAAAATAT
199952	32148	CATTCCCTCCAGAACCATCA	244539	76735	TTACATTTGAAATGGCAGCC	289126	121322	CCTCTTCACCTTAAAAAATA
199953	32149	CCATTCCCTCCAGAACCATC	244540	76736	GTTACATTTGAAATGGCAGC	289127	121323	CCCTCTTCACCTTAAAAAAT
199954	32150	TCCATTCCCTCCAGAACCAT	244541	76737	AGTTACATTTGAAATGGCAG	289128	121324	TCCCTCTTCACCTTAAAAAA
199955	32151	GTCCATTCCCTCCAGAACCA	244542	76738	GAGTTACATTTGAAATGGCA	289129	121325	CTCCCTCTTCACCTTAAAAA
199956	32152	AGTCCATTCCCTCCAGAACC	244543	76739	TGAGTTACATTTGAAATGGC	289130	121326	CCTCCCTCTTCACCTTAAAA
199957	32153	AAGTCCATTCCCTCCAGAAC	244544	76740	GTGAGTTACATTTGAAATGG	289131	121327	GCCTCCCTCTTCACCTTAAA
199958	32154	AAAGTCCATTCCCTCCAGAA	244545	76741	TGTGAGTTACATTTGAAATG	289132	121328	CGCCTCCCTCTTCACCTTAA
199959	32155	AAAAGTCCATTCCCTCCAGA	244546	76742	CTGTGAGTTACATTTGAAAT	289133	121329	TCGCCTCCCTCTTCACCTTA
199960	32156	AAAAAGTCCATTCCCTCCAG	244547	76743	GCTGTGAGTTACATTTGAAA	289134	121330	CTCGCCTCCCTCTTCACCTT
199961	32157	GAAAAAGTCCATTCCCTCCA	244548	76744	AGCTGTGAGTTACATTTGAA	289135	121331	TCTCGCCTCCCTCTTCACCT
199962	32158	AGAAAAAGTCCATTCCCTCC	244549	76745	AAGCTGTGAGTTACATTTGA	289136	121332	ATCTCGCCTCCCTCTTCACC
199963	32159	AAGAAAAAGTCCATTCCCTC	244550	76746	CAAGCTGTGAGTTACATTTG	289137	121333	CATCTCGCCTCCCTCTTCAC
199964	32160	AAAGAAAAAGTCCATTCCCT	244551	76747	ACAAGCTGTGAGTTACATTT	289138	121334	GCATCTCGCCTCCCTCTTCA
199965	32161	CAAAGAAAAAGTCCATTCCC	244552	76748	GACAAGCTGTGAGTTACATT	289139	121335	AGCATCTCGCCTCCCTCTTC
199966	32162	CCAAAGAAAAAGTCCATTCC	244553	76749	GGACAAGCTGTGAGTTACAT	289140	121336	CAGCATCTCGCCTCCCTCTT
199967	32163	TCCAAAGAAAAAGTCCATTC	244554	76750	TGGACAAGCTGTGAGTTACA	289141	121337	CCAGCATCTCGCCTCCCTCT
199968	32164	CTCCAAAGAAAAAGTCCATT	244555	76751	ATGGACAAGCTGTGAGTTAC	289142	121338	GCCAGCATCTCGCCTCCCTC
199969	32165	TCTCCAAAGAAAAAGTCCAT	244556	76752	GATGGACAAGCTGTGAGTTA	289143	121339	GGCCAGCATCTCGCCTCCCT
199970	32166	GTCTCCAAAGAAAAAGTCCA	244557	76753	TGATGGACAAGCTGTGAGTT	289144	121340	AGGCCAGCATCTCGCCTCCC
199971	32167	TGTCTCCAAAGAAAAAGTCC	244558	76754	CTGATGGACAAGCTGTGAGT	289145	121341	AAGGCCAGCATCTCGCCTCC
199972	32168	CTGTCTCCAAAGAAAAAGTC	244559	76755	ACTGATGGACAAGCTGTGAG	289146	121342	TAAGGCCAGCATCTCGCCTC
199973	32169	CCTGTCTCCAAAGAAAAAGT	244560	76756	GACTGATGGACAAGCTGTGA	289147	121343	TTAAGGCCAGCATCTCGCCT
199974	32170	GCCTGTCTCCAAAGAAAAAG	244561	76757	GGACTGATGGACAAGCTGTG	289148	121344	GTTAAGGCCAGCATCTCGCC
199975	32171	AGCCTGTCTCCAAAGAAAAA	244562	76758	AGGACTGATGGACAAGCTGT	289149	121345	GGTTAAGGCCAGCATCTCGC
199976	32172	AAGCCTGTCTCCAAAGAAAA	244563	76759	AAGGACTGATGGACAAGCTG	289150	121346	GGGTTAAGGCCAGCATCTCG
199977	32173	AAAGCCTGTCTCCAAAGAAA	244564	76760	CAAGGACTGATGGACAAGCT	289151	121347	GGGGTTAAGGCCAGCATCTC
199978	32174	AAAAGCCTGTCTCCAAAGAA	244565	76761	CCAAGGACTGATGGACAAGC	289152	121348	AGGGGTTAAGGCCAGCATCT
199979	32175	GAAAAGCCTGTCTCCAAAGA	244566	76762	TCCAAGGACTGATGGACAAG	289153	121349	TAGGGGTTAAGGCCAGCATC
199980	32176	AGAAAAGCCTGTCTCCAAAG	244567	76763	CTCCAAGGACTGATGGACAA	289154	121350	TTAGGGGTTAAGGCCAGCAT
199981	32177	TAGAAAAGCCTGTCTCCAAA	244568	76764	CCTCCAAGGACTGATGGACA	289155	121351	GTTAGGGGTTAAGGCCAGCA
199982	32178	ATAGAAAAGCCTGTCTCCAA	244569	76765	ACCTCCAAGGACTGATGGAC	289156	121352	GGTTAGGGGTTAAGGCCAGC
199983	32179	CATAGAAAAGCCTGTCTCCA	244570	76766	GACCTCCAAGGACTGATGGA	289157	121353	GGGTTAGGGGTTAAGGCCAG
199984	32180	GCATAGAAAAGCCTGTCTCC	244571	76767	AGACCTCCAAGGACTGATGG	289158	121354	CGGGTTAGGGGTTAAGGCCA
199985	32181	GGCATAGAAAAGCCTGTCTC	244572	76768	AAGACCTCCAAGGACTGATG	289159	121355	ACGGGTTAGGGGTTAAGGCC
199986	32182	GGGCATAGAAAAGCCTGTCT	244573	76769	AAAGACCTCCAAGGACTGAT	289160	121356	AACGGGTTAGGGGTTAAGGC

199987	32183	TGGGCATAGAAAAGCCTGTC	244574	76770	GAAAGACCTCCAAGGACTGA	289161	121357	CAACGGGTTAGGGGTTAAGG
199988	32184	GTGGGCATAGAAAAGCCTGT	244575	76771	AGAAAGACCTCCAAGGACTG	289162	121358	ACAACGGGTTAGGGGTTAAG
199989	32185	GGTGGGCATAGAAAAGCCTG	244576	76772	TAGAAAGACCTCCAAGGACT	289163	121359	AACAACGGGTTAGGGGTTAA
199990	32186	GGGTGGGCATAGAAAAGCCT	244577	76773	ATAGAAAGACCTCCAAGGAC	289164	121360	GAACAACGGGTTAGGGGTTA
199991	32187	AGGGTGGGCATAGAAAAGCC	244578	76774	CATAGAAAGACCTCCAAGGA	289165	121361	AGAACAACGGGTTAGGGGTT
199992	32188	AAGGGTGGGCATAGAAAAGC	244579	76775	TCATAGAAAGACCTCCAAGG	289166	121362	GAGAACAACGGGTTAGGGGT
199993	32189	AAAGGGTGGGCATAGAAAAG	244580	76776	TTCATAGAAAGACCTCCAAG	289167	121363	GGAGAACAACGGGTTAGGGG
199994	32190	AAAAGGGTGGGCATAGAAAA	244581	76777	TTTCATAGAAAGACCTCCAA	289168	121364	GGGAGAACAACGGGTTAGGG
199995	32191	TAAAAGGGTGGGCATAGAAA	244582	76778	CTTTCATAGAAAGACCTCCA	289169	121365	AGGGAGAACAACGGGTTAGG
199996	32192	ATAAAAGGGTGGGCATAGAA	244583	76779	CCTTTCATAGAAAGACCTCC	289170	121366	CAGGGAGAACAACGGGTTAG
199997	32193	GATAAAAGGGTGGGCATAGA	244584	76780	TCCTTTCATAGAAAGACCTC	289171	121367	GCAGGGAGAACAACGGGTTA
199998	32194	AGATAAAAGGGTGGGCATAG	244585	76781	CTCCTTTCATAGAAAGACCT	289172	121368	TGCAGGGAGAACAACGGGTT
199999	32195	AAGATAAAAGGGTGGGCATA	244586	76782	GCTCCTTTCATAGAAAGACC	289173	121369	TTGCAGGGAGAACAACGGGT
200000	32196	CAAGATAAAAGGGTGGGCAT	244587	76783	AGCTCCTTTCATAGAAAGAC	289174	121370	CTTGCAGGGAGAACAACGGG
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200002	32198	AGCAAGATAAAAGGGTGGGC	244589	76785	CAAGCTCCTTTCATAGAAAG	289176	121372	AGCTTGCAGGGAGAACAACG
200003	32199	TAGCAAGATAAAAGGGTGGG	244590	76786	CCAAGCTCCTTTCATAGAAA	289177	121373	CAGCTTGCAGGGAGAACAAC
200004	32200	TTAGCAAGATAAAAGGGTGG	244591	76787	ACCAAGCTCCTTTCATAGAA	289178	121374	ACAGCTTGCAGGGAGAACAA
200005	32201	GTTAGCAAGATAAAAGGGTG	244592	76788	CACCAAGCTCCTTTCATAGA	289179	121375	GACAGCTTGCAGGGAGAACA
200006	32202	AGTTAGCAAGATAAAAGGGT	244593	76789	CCACCAAGCTCCTTTCATAG	289180	121376	GGACAGCTTGCAGGGAGAAC
200007	32203	AAGTTAGCAAGATAAAAGGG	244594	76790	GCCACCAAGCTCCTTTCATA	289181	121377	TGGACAGCTTGCAGGGAGAA
200008	32204	TAAGTTAGCAAGATAAAAGG	244595	76791	CGCCACCAAGCTCCTTTCAT	289182	121378	GTGGACAGCTTGCAGGGAGA
200009	32205	ATAAGTTAGCAAGATAAAAG	244596	76792	ACGCCACCAAGCTCCTTTCA	289183	121379	TGTGGACAGCTTGCAGGGAG
200010	32206	GATAAGTTAGCAAGATAAAA	244597	76793	GACGCCACCAAGCTCCTTTC	289184	121380	CTGTGGACAGCTTGCAGGGA
200011	32207	TGATAAGTTAGCAAGATAAA	244598	76794	GGACGCCACCAAGCTCCTTT	289185	121381	CCTGTGGACAGCTTGCAGGG
200012	32208	ATGATAAGTTAGCAAGATAA	244599	76795	TGGACGCCACCAAGCTCCTT	289186	121382	CCCTGTGGACAGCTTGCAGG
200013	32209	GATGATAAGTTAGCAAGATA	244600	76796	TTGGACGCCACCAAGCTCCT	289187	121383	GCCCTGTGGACAGCTTGCAG
200014	32210	TGATGATAAGTTAGCAAGAT	244601	76797	TTTGGACGCCACCAAGCTCC	289188	121384	GGCCCTGTGGACAGCTTGCA
200015	32211	ATGATGATAAGTTAGCAAGA	244602	76798	GTTTGGACGCCACCAAGCTC	289189	121385	AGGCCCTGTGGACAGCTTGC
200016	32212	GATGATGATAAGTTAGCAAG	244603	76799	TGTTTGGACGCCACCAAGCT	289190	121386	GAGGCCCTGTGGACAGCTTG
200017	32213	GGATGATGATAAGTTAGCAA	244604	76800	GTGTTTGGACGCCACCAAGC	289191	121387	AGAGGCCCTGTGGACAGCTT
200018	32214	TGGATGATGATAAGTTAGCA	244605	76801	GGTGTTTGGACGCCACCAAG	289192	121388	GAGAGGCCCTGTGGACAGCT
200019	32215	CTGGATGATGATAAGTTAGC	244606	76802	TGGTGTTTGGACGCCACCAA	289193	121389	TGAGAGGCCCTGTGGACAGC
200020	32216	CCTGGATGATGATAAGTTAG	244607	76803	GTGGTGTTTGGACGCCACCA	289194	121390	CTGAGAGGCCCTGTGGACAG
200021	32217	ACCTGGATGATGATAAGTTA	244608	76804	GGTGGTGTTTGGACGCCACC	289195	121391	TCTGAGAGGCCCTGTGGACA
200022	32218	AACCTGGATGATGATAAGTT	244609	76805	GGGTGGTGTTTGGACGCCAC	289196	121392	GTCTGAGAGGCCCTGTGGAC
200023	32219	GAACCTGGATGATGATAAGT	244610	76806	TGGGTGGTGTTTGGACGCCA	289197	121393	AGTCTGAGAGGCCCTGTGGA
200024	32220	GGAACCTGGATGATGATAAG	244611	76807	TTGGGTGGTGTTTGGACGCC	289198	121394	GAGTCTGAGAGGCCCTGTGG
200025	32221	TGGAACCTGGATGATGATAA	244612	76808	ATTGGGTGGTGTTTGGACGC	289199	121395	CGAGTCTGAGAGGCCCTGTG
200026	32222	CTGGAACCTGGATGATGATA	244613	76809	CATTGGGTGGTGTTTGGACG	289200	121396	TCGAGTCTGAGAGGCCCTGT
200027	32223	GCTGGAACCTGGATGATGAT	244614	76810	ACATTGGGTGGTGTTTGGAC	289201	121397	CTCGAGTCTGAGAGGCCCTG
200028	32224	TGCTGGAACCTGGATGATGA	244615	76811	GACATTGGGTGGTGTTTGGA	289202	121398	CCTCGAGTCTGAGAGGCCCT
200029	32225	CTGCTGGAACCTGGATGATG	244616	76812	GGACATTGGGTGGTGTTTGG	289203	121399	ACCTCGAGTCTGAGAGGCCC
200030	32226	TCTGCTGGAACCTGGATGAT	244617	76813	TGGACATTGGGTGGTGTTTG	289204	121400	AACCTCGAGTCTGAGAGGCC
200031	32227	TTCTGCTGGAACCTGGATGA	244618	76814	GTGGACATTGGGTGGTGTTT	289205	121401	GAACCTCGAGTCTGAGAGGC
200032	32228	TTTCTGCTGGAACCTGGATG	244619	76815	AGTGGACATTGGGTGGTGTT	289206	121402	TGAACCTCGAGTCTGAGAGG
200033	32229	GTTTCTGCTGGAACCTGGAT	244620	76816	AAGTGGACATTGGGTGGTGT	289207	121403	CTGAACCTCGAGTCTGAGAG
200034	32230	TGTTTCTGCTGGAACCTGGA	244621	76817	TAAGTGGACATTGGGTGGTG	289208	121404	GCTGAACCTCGAGTCTGAGA
200035	32231	ATGTTTCTGCTGGAACCTGG	244622	76818	CTAAGTGGACATTGGGTGGT	289209	121405	AGCTGAACCTCGAGTCTGAG
200036	32232	AATGTTTCTGCTGGAACCTG	244623	76819	TCTAAGTGGACATTGGGTGG	289210	121406	TAGCTGAACCTCGAGTCTGA
200037	32233	TAATGTTTCTGCTGGAACCT	244624	76820	TTCTAAGTGGACATTGGGTG	289211	121407	ATAGCTGAACCTCGAGTCTG
200038	32234	GTAATGTTTCTGCTGGAACC	244625	76821	CTTCTAAGTGGACATTGGGT	289212	121408	TATAGCTGAACCTCGAGTCT
200039	32235	AGTAATGTTTCTGCTGGAAC	244626	76822	ACTTCTAAGTGGACATTGGG	289213	121409	ATATAGCTGAACCTCGAGTC
200040	32236	AAGTAATGTTTCTGCTGGAA	244627	76823	TACTTCTAAGTGGACATTGG	289214	121410	CATATAGCTGAACCTCGAGT
200041	32237	GAAGTAATGTTTCTGCTGGA	244628	76824	TTACTTCTAAGTGGACATTG	289215	121411	CCATATAGCTGAACCTCGAG
200042	32238	GGAAGTAATGTTTCTGCTGG	244629	76825	CTTACTTCTAAGTGGACATT	289216	121412	TCCATATAGCTGAACCTCGA
200043	32239	GGGAAGTAATGTTTCTGCTG	244630	76826	GCTTACTTCTAAGTGGACAT	289217	121413	ATCCATATAGCTGAACCTCG
200044	32240	GGGGAAGTAATGTTTCTGCT	244631	76827	TGCTTACTTCTAAGTGGACA	289218	121414	CATCCATATAGCTGAACCTC
200045	32241	GGGGGAAGTAATGTTTCTGC	244632	76828	GTGCTTACTTCTAAGTGGAC	289219	121415	GCATCCATATAGCTGAACCT
200046	32242	TGGGGGAAGTAATGTTTCTG	244633	76829	GGTGCTTACTTCTAAGTGGA	289220	121416	TGCATCCATATAGCTGAACC
200047	32243	CTGGGGGAAGTAATGTTTCT	244634	76830	CGGTGCTTACTTCTAAGTGG	289221	121417	ATGCATCCATATAGCTGAAC
200048	32244	CCTGGGGGAAGTAATGTTTC	244635	76831	ACGGTGCTTACTTCTAAGTG	289222	121418	CATGCATCCATATAGCTGAA
200049	32245	TCCTGGGGGAAGTAATGTTT	244636	76832	CACGGTGCTTACTTCTAAGT	289223	121419	TCATGCATCCATATAGCTGA
200050	32246	TTCCTGGGGGAAGTAATGTT	244637	76833	ACACGGTGCTTACTTCTAAG	289224	121420	CTCATGCATCCATATAGCTG
200051	32247	TTTCCTGGGGGAAGTAATGT	244638	76834	GACACGGTGCTTACTTCTAA	289225	121421	GCTCATGCATCCATATAGCT
200052	32248	ATTTCCTGGGGGAAGTAATG	244639	76835	AGACACGGTGCTTACTTCTA	289226	121422	AGCTCATGCATCCATATAGC
200053	32249	AATTTCCTGGGGGAAGTAAT	244640	76836	CAGACACGGTGCTTACTTCT	289227	121423	AAGCTCATGCATCCATATAG
200054	32250	AAATTTCCTGGGGGAAGTAA	244641	76837	GCAGACACGGTGCTTACTTC	289228	121424	CAAGCTCATGCATCCATATA
200055	32251	GAAATTTCCTGGGGGAAGTA	244642	76838	GGCAGACACGGTGCTTACTT	289229	121425	CCAAGCTCATGCATCCATAT
200056	32252	AGAAATTTCCTGGGGGAAGT	244643	76839	GGGCAGACACGGTGCTTACT	289230	121426	ACCAAGCTCATGCATCCATA
200057	32253	AAGAAATTTCCTGGGGGAAG	244644	76840	AGGGCAGACACGGTGCTTAC	289231	121427	GACCAAGCTCATGCATCCAT
200058	32254	TAAGAAATTTCCTGGGGGAA	244645	76841	CAGGGCAGACACGGTGCTTA	289232	121428	GGACCAAGCTCATGCATCCA

200059	32255	TTAAGAAATTTCCTGGGGGA	244646	76842	TCAGGGCAGACACGGTGCTT	289233	121429	GGGACCAAGCTCATGCATCC
200060	32256	CTTAAGAAATTTCCTGGGGG	244647	76843	CTCAGGGCAGACACGGTGCT	289234	121430	GGGGACCAAGCTCATGCATC
200061	32257	CCTTAAGAAATTTCCTGGGG	244648	76844	GCTCAGGGCAGACACGGTGC	289235	121431	TGGGGACCAAGCTCATGCAT
200062	32258	CCCTTAAGAAATTTCCTGGG	244649	76845	AGCTCAGGGCAGACACGGTG	289236	121432	CTGGGGACCAAGCTCATGCA
200063	32259	ACCCTTAAGAAATTTCCTGG	244650	76846	CAGCTCAGGGCAGACACGGT	289237	121433	GCTGGGGACCAAGCTCATGC
200064	32260	CACCCTTAAGAAATTTCCTG	244651	76847	TCAGCTCAGGGCAGACACGG	289238	121434	GGCTGGGGACCAAGCTCATG
200065	32261	GCACCCTTAAGAAATTTCCT	244652	76848	GTCAGCTCAGGGCAGACACG	289239	121435	TGGCTGGGGACCAAGCTCAT
200066	32262	TGCACCCTTAAGAAATTTCC	244653	76849	AGTCAGCTCAGGGCAGACAC	289240	121436	TTGGCTGGGGACCAAGCTCA
200067	32263	CTGCACCCTTAAGAAATTTC	244654	76850	GAGTCAGCTCAGGGCAGACA	289241	121437	GTTGGCTGGGGACCAAGCTC
200068	32264	ACTGCACCCTTAAGAAATTT	244655	76851	GGAGTCAGCTCAGGGCAGAC	289242	121438	TGTTGGCTGGGGACCAAGCT
200069	32265	TACTGCACCCTTAAGAAATT	244656	76852	AGGAGTCAGCTCAGGGCAGA	289243	121439	ATGTTGGCTGGGGACCAAGC
200070	32266	ATACTGCACCCTTAAGAAAT	244657	76853	AAGGAGTCAGCTCAGGGCAG	289244	121440	CATGTTGGCTGGGGACCAAG
200071	32267	GATACTGCACCCTTAAGAAA	244658	76854	AAAGGAGTCAGCTCAGGGCA	289245	121441	CCATGTTGGCTGGGGACCAA
200072	32268	TGATACTGCACCCTTAAGAA	244659	76855	AAAAGGAGTCAGCTCAGGGC	289246	121442	CCCATGTTGGCTGGGGACCA
200073	32269	ATGATACTGCACCCTTAAGA	244660	76856	GAAAAGGAGTCAGCTCAGGG	289247	121443	TCCCATGTTGGCTGGGGACC
200074	32270	CATGATACTGCACCCTTAAG	244661	76857	GGAAAAGGAGTCAGCTCAGG	289248	121444	CTCCCATGTTGGCTGGGGAC
200075	32271	TCATGATACTGCACCCTTAA	244662	76858	TGGAAAAGGAGTCAGCTCAG	289249	121445	TCTCCCATGTTGGCTGGGGA
200076	32272	ATCATGATACTGCACCCTTA	244663	76859	TTGGAAAAGGAGTCAGCTCA	289250	121446	GTCTCCCATGTTGGCTGGGG
200077	32273	CATCATGATACTGCACCCTT	244664	76860	CTTGGAAAAGGAGTCAGCTC	289251	121447	TGTCTCCCATGTTGGCTGGG
200078	32274	ACATCATGATACTGCACCCT	244665	76861	CCTTGGAAAAGGAGTCAGCT	289252	121448	GTGTCTCCCATGTTGGCTGG
200079	32275	GACATCATGATACTGCACCC	244666	76862	TCCTTGGAAAAGGAGTCAGC	289253	121449	AGTGTCTCCCATGTTGGCTG
200080	32276	AGACATCATGATACTGCACC	244667	76863	TTCCTTGGAAAAGGAGTCAG	289254	121450	AAGTGTCTCCCATGTTGGCT
200081	32277	CAGACATCATGATACTGCAC	244668	76864	CTTCCTTGGAAAAGGAGTCA	289255	121451	GAAGTGTCTCCCATGTTGGC
200082	32278	GCAGACATCATGATACTGCA	244669	76865	CCTTCCTTGGAAAAGGAGTC	289256	121452	TGAAGTGTCTCCCATGTTGG
200083	32279	TGCAGACATCATGATACTGC	244670	76866	CCCTTCCTTGGAAAAGGAGT	289257	121453	GTGAAGTGTCTCCCATGTTG
200084	32280	CTGCAGACATCATGATACTG	244671	76867	CCCCTTCCTTGGAAAAGGAG	289258	121454	GGTGAAGTGTCTCCCATGTT
200085	32281	GCTGCAGACATCATGATACT	244672	76868	ACCCCTTCCTTGGAAAAGGA	289259	121455	TGGTGAAGTGTCTCCCATGT
200086	32282	TGCTGCAGACATCATGATAC	244673	76869	AACCCCTTCCTTGGAAAAGG	289260	121456	ATGGTGAAGTGTCTCCCATG
200087	32283	TTGCTGCAGACATCATGATA	244674	76870	CAACCCCTTCCTTGGAAAAG	289261	121457	GATGGTGAAGTGTCTCCCAT
200088	32284	TTTGCTGCAGACATCATGAT	244675	76871	CCAACCCCTTCCTTGGAAAA	289262	121458	CGATGGTGAAGTGTCTCCCA
200089	32285	ATTTGCTGCAGACATCATGA	244676	76872	TCCAACCCCTTCCTTGGAAA	289263	121459	CCGATGGTGAAGTGTCTCCC
200090	32286	AATTTGCTGCAGACATCATG	244677	76873	ATCCAACCCCTTCCTTGGAA	289264	121460	GCCGATGGTGAAGTGTCTCC
200091	32287	GAATTTGCTGCAGACATCAT	244678	76874	GATCCAACCCCTTCCTTGGA	289265	121461	TGCCGATGGTGAAGTGTCTC
200092	32288	AGAATTTGCTGCAGACATCA	244679	76875	CGATCCAACCCCTTCCTTGG	289266	121462	CTGCCGATGGTGAAGTGTCT
200093	32289	GAGAATTTGCTGCAGACATC	244680	76876	GCGATCCAACCCCTTCCTTG	289267	121463	GCTGCCGATGGTGAAGTGTC
200094	32290	TGAGAATTTGCTGCAGACAT	244681	76877	AGCGATCCAACCCCTTCCTT	289268	121464	TGCTGCCGATGGTGAAGTGT
200095	32291	TTGAGAATTTGCTGCAGACA	244682	76878	CAGCGATCCAACCCCTTCCT	289269	121465	CTGCTGCCGATGGTGAAGTG
200096	32292	TTTGAGAATTTGCTGCAGAC	244683	76879	TCAGCGATCCAACCCCTTCC	289270	121466	GCTGCTGCCGATGGTGAAGT
200097	32293	ATTTGAGAATTTGCTGCAGA	244684	76880	CTCAGCGATCCAACCCCTTC	289271	121467	AGCTGCTGCCGATGGTGAAG
200098	32294	TATTTGAGAATTTGCTGCAG	244685	76881	ACTCAGCGATCCAACCCCTT	289272	121468	TAGCTGCTGCCGATGGTGAA
200099	32295	CTATTTGAGAATTTGCTGCA	244686	76882	CACTCAGCGATCCAACCCCT	289273	121469	GTAGCTGCTGCCGATGGTGA
200100	32296	GCTATTTGAGAATTTGCTGC	244687	76883	ACACTCAGCGATCCAACCCC	289274	121470	TGTAGCTGCTGCCGATGGTG
200101	32297	AGCTATTTGAGAATTTGCTG	244688	76884	AACACTCAGCGATCCAACCC	289275	121471	CTGTAGCTGCTGCCGATGGT
200102	32298	GAGCTATTTGAGAATTTGCT	244689	76885	AAACACTCAGCGATCCAACC	289276	121472	GCTGTAGCTGCTGCCGATGG
200103	32299	TGAGCTATTTGAGAATTTGC	244690	76886	AAAACACTCAGCGATCCAAC	289277	121473	TGCTGTAGCTGCTGCCGATG
200104	32300	CTGAGCTATTTGAGAATTTG	244691	76887	AAAAACACTCAGCGATCCAA	289278	121474	GTGCTGTAGCTGCTGCCGAT
200105	32301	CCTGAGCTATTTGAGAATTT	244692	76888	GAAAAACACTCAGCGATCCA	289279	121475	TGTGCTGTAGCTGCTGCCGA
200106	32302	TCCTGAGCTATTTGAGAATT	244693	76889	GGAAAAACACTCAGCGATCC	289280	121476	CTGTGCTGTAGCTGCTGCCG
200107	32303	TTCCTGAGCTATTTGAGAAT	244694	76890	TGGAAAAACACTCAGCGATC	289281	121477	CCTGTGCTGTAGCTGCTGCC
200108	32304	TTTCCTGAGCTATTTGAGAA	244695	76891	CTGGAAAAACACTCAGCGAT	289282	121478	TCCTGTGCTGTAGCTGCTGC
200109	32305	TTTTCCTGAGCTATTTGAGA	244696	76892	CCTGGAAAAACACTCAGCGA	289283	121479	TTCCTGTGCTGTAGCTGCTG
200110	32306	TTTTTCCTGAGCTATTTGAG	244697	76893	ACCTGGAAAAACACTCAGCG	289284	121480	GTTCCTGTGCTGTAGCTGCT
200111	32307	TTTTTTCCTGAGCTATTTGA	244698	76894	CACCTGGAAAAACACTCAGC	289285	121481	GGTTCCTGTGCTGTAGCTGC
200112	32308	CTTTTTTCCTGAGCTATTTG	244699	76895	ACACCTGGAAAAACACTCAG	289286	121482	GGGTTCCTGTGCTGTAGCTG
200113	32309	ACTTTTTTCCTGAGCTATTT	244700	76896	GACACCTGGAAAAACACTCA	289287	121483	AGGGTTCCTGTGCTGTAGCT
200114	32310	TACTTTTTTCCTGAGCTATT	244701	76897	AGACACCTGGAAAAACACTC	289288	121484	CAGGGTTCCTGTGCTGTAGC
200115	32311	GTACTTTTTTCCTGAGCTAT	244702	76898	TAGACACCTGGAAAAACACT	289289	121485	CCAGGGTTCCTGTGCTGTAG
200116	32312	CGTACTTTTTTCCTGAGCTA	244703	76899	GTAGACACCTGGAAAAACAC	289290	121486	CCCAGGGTTCCTGTGCTGTA
200117	32313	ACGTACTTTTTTCCTGAGCT	244704	76900	AGTAGACACCTGGAAAAACA	289291	121487	ACCCAGGGTTCCTGTGCTGT
200118	32314	CACGTACTTTTTTCCTGAGC	244705	76901	AAGTAGACACCTGGAAAAAC	289292	121488	GACCCAGGGTTCCTGTGCTG
200119	32315	ACACGTACTTTTTTCCTGAG	244706	76902	CAAGTAGACACCTGGAAAAA	289293	121489	TGACCCAGGGTTCCTGTGCT
200120	32316	CACACGTACTTTTTTCCTGA	244707	76903	ACAAGTAGACACCTGGAAAA	289294	121490	GTGACCCAGGGTTCCTGTGC
200121	32317	ACACACGTACTTTTTTCCTG	244708	76904	AACAAGTAGACACCTGGAAA	289295	121491	AGTGACCCAGGGTTCCTGTG
200122	32318	CACACACGTACTTTTTTCCT	244709	76905	CAACAAGTAGACACCTGGAA	289296	121492	CAGTGACCCAGGGTTCCTGT
200123	32319	CCACACACGTACTTTTTTCC	244710	76906	ACAACAAGTAGACACCTGGA	289297	121493	GCAGTGACCCAGGGTTCCTG
200124	32320	ACCACACACGTACTTTTTTC	244711	76907	AACAACAAGTAGACACCTGG	289298	121494	GGCAGTGACCCAGGGTTCCT
200125	32321	TACCACACACGTACTTTTTT	244712	76908	TAACAACAAGTAGACACCTG	289299	121495	TGGCAGTGACCCAGGGTTCC
200126	32322	ATACCACACACGTACTTTTT	244713	76909	TTAACAACAAGTAGACACCT	289300	121496	ATGGCAGTGACCCAGGGTTC
200127	32323	CATACCACACACGTACTTTT	244714	76910	ATTAACAACAAGTAGACACC	289301	121497	CATGGCAGTGACCCAGGGTT
200128	32324	TCATACCACACACGTACTTT	244715	76911	AATTAACAACAAGTAGACAC	289302	121498	ACATGGCAGTGACCCAGGGT
200129	32325	CTCATACCACACACGTACTT	244716	76912	TAATTAACAACAAGTAGACA	289303	121499	GACATGGCAGTGACCCAGGG
200130	32326	ACTCATACCACACACGTACT	244717	76913	TTAATTAACAACAAGTAGAC	289304	121500	GGACATGGCAGTGACCCAGG

200131	32327	CACTCATACCACACACGTAC	244718	76914	ATTAATTAACAACAAGTAGA	289305	121501	GGGACATGGCAGTGACCCAG
200132	32328	ACACTCATACCACACACGTA	244719	76915	TATTAATTAACAACAAGTAG	289306	121502	GGGGACATGGCAGTGACCCA
200133	32329	CACACTCATACCACACACGT	244720	76916	CTATTAATTAACAACAAGTA	289307	121503	AGGGGACATGGCAGTGACCC
200134	32330	ACACACTCATACCACACACG	244721	76917	GCTATTAATTAACAACAAGT	289308	121504	GAGGGGACATGGCAGTGACC
200135	32331	CACACACTCATACCACACAC	244722	76918	TGCTATTAATTAACAACAAG	289309	121505	AGAGGGGACATGGCAGTGAC
200136	32332	ACACACACTCATACCACACA	244723	76919	TTGCTATTAATTAACAACAA	289310	121506	CAGAGGGGACATGGCAGTGA
200137	32333	TACACACACTCATACCACAC	244724	76920	ATTGCTATTAATTAACAACA	289311	121507	ACAGAGGGGACATGGCAGTG
200138	32334	ATACACACACTCATACCACA	244725	76921	CATTGCTATTAATTAACAAC	289312	121508	CACAGAGGGGACATGGCAGT
200139	32335	CATACACACACTCATACCAC	244726	76922	TCATTGCTATTAATTAACAA	289313	121509	TCACAGAGGGGACATGGCAG
200140	32336	ACATACACACACTCATACCA	244727	76923	GTCATTGCTATTAATTAACA	289314	121510	GTCACAGAGGGGACATGGCA
200141	32337	TACATACACACACTCATACC	244728	76924	TGTCATTGCTATTAATTAAC	289315	121511	AGTCACAGAGGGGACATGGC
200142	32338	ATACATACACACACTCATAC	244729	76925	TTGTCATTGCTATTAATTAA	289316	121512	AAGTCACAGAGGGGACATGG
200143	32339	CATACATACACACACTCATA	244730	76926	TTTGTCATTGCTATTAATTA	289317	121513	AAAGTCACAGAGGGGACATG
200144	32340	ACATACATACACACACTCAT	244731	76927	CTTTGTCATTGCTATTAATT	289318	121514	CAAAGTCACAGAGGGGACAT
200145	32341	CACATACATACACACACTCA	244732	76928	GCTTTGTCATTGCTATTAAT	289319	121515	ACAAAGTCACAGAGGGGACA
200146	32342	ACACATACATACACACACTC	244733	76929	TGCTTTGTCATTGCTATTAA	289320	121516	AACAAAGTCACAGAGGGGAC
200147	32343	CACACATACATACACACACT	244734	76930	CTGCTTTGTCATTGCTATTA	289321	121517	AAACAAAGTCACAGAGGGGA
200148	32344	ACACACATACATACACACAC	244735	76931	TCTGCTTTGTCATTGCTATT	289322	121518	TAAACAAAGTCACAGAGGGG
200149	32345	TACACACATACATACACACA	244736	76932	TTCTGCTTTGTCATTGCTAT	289323	121519	TTAAACAAAGTCACAGAGGG
200150	32346	ATACACACATACATACACAC	244737	76933	CTTCTGCTTTGTCATTGCTA	289324	121520	TTTAAACAAAGTCACAGAGG
200151	32347	TATACACACATACATACACA	244738	76934	CCTTCTGCTTTGTCATTGCT	289325	121521	GTTTAAACAAAGTCACAGAG
200152	32348	ATATACACACATACATACAC	244739	76935	ACCTTCTGCTTTGTCATTGC	289326	121522	TGTTTAAACAAAGTCACAGA
200153	32349	TATATACACACATACATACA	244740	76936	AACCTTCTGCTTTGTCATTG	289327	121523	CTGTTTAAACAAAGTCACAG
200154	32350	ATATATACACACATACATAC	244741	76937	GAACCTTCTGCTTTGTCATT	289328	121524	TCTGTTTAAACAAAGTCACA
200155	32351	TATATATACACACATACATA	244742	76938	TGAACCTTCTGCTTTGTCAT	289329	121525	TTCTGTTTAAACAAAGTCAC
200156	32352	ATATATATACACACATACAT	244743	76939	ATGAACCTTCTGCTTTGTCA	289330	121526	TTTCTGTTTAAACAAAGTCA
200157	32353	TATATATATACACACATACA	244744	76940	CATGAACCTTCTGCTTTGTC	289331	121527	TTTTCTGTTTAAACAAAGTC
200158	32354	GTATATATATACACACATAC	244745	76941	GCATGAACCTTCTGCTTTGT	289332	121528	ATTTTCTGTTTAAACAAAGT
200159	32355	TGTATATATATACACACATA	244746	76942	CGCATGAACCTTCTGCTTTG	289333	121529	CATTTTCTGTTTAAACAAAG
200160	32356	GTGTATATATATACACACAT	244747	76943	ACGCATGAACCTTCTGCTTT	289334	121530	TCATTTTCTGTTTAAACAAA
200161	32357	TGTGTATATATATACACACA	244748	76944	TACGCATGAACCTTCTGCTT	289335	121531	ATCATTTTCTGTTTAAACAA
200162	32358	ATGTGTATATATATACACAC	244749	76945	CTACGCATGAACCTTCTGCT	289336	121532	CATCATTTTCTGTTTAAACA
200163	32359	TATGTGTATATATATACACA	244750	76946	GCTACGCATGAACCTTCTGC	289337	121533	GCATCATTTTCTGTTTAAAC
200164	32360	ATATGTGTATATATATACAC	244751	76947	AGCTACGCATGAACCTTCTG	289338	121534	AGCATCATTTTCTGTTTAAA
200165	32361	TATATGTGTATATATATACA	244752	76948	GAGCTACGCATGAACCTTCT	289339	121535	GAGCATCATTTTCTGTTTAA
200166	32362	ATATATGTGTATATATATAC	244753	76949	CGAGCTACGCATGAACCTTC	289340	121536	AGAGCATCATTTTCTGTTTA
200167	32363	TATATATGTGTATATATATA	244754	76950	CCGAGCTACGCATGAACCTT	289341	121537	CAGAGCATCATTTTCTGTTT
200168	32364	GTATATATGTGTATATATAT	244755	76951	GCCGAGCTACGCATGAACCT	289342	121538	CCAGAGCATCATTTTCTGTT
200169	32365	TGTATATATGTGTATATATA	244756	76952	AGCCGAGCTACGCATGAACC	289343	121539	CCCAGAGCATCATTTTCTGT
200170	32366	GTGTATATATGTGTATATAT	244757	76953	AAGCCGAGCTACGCATGAAC	289344	121540	GCCCAGAGCATCATTTTCTG
200171	32367	TGTGTATATATGTGTATATA	244758	76954	AAAGCCGAGCTACGCATGAA	289345	121541	GGCCCAGAGCATCATTTTCT
200172	32368	ATGTGTATATATGTGTATAT	244759	76955	GAAAGCCGAGCTACGCATGA	289346	121542	CGGCCCAGAGCATCATTTTC
200173	32369	TATGTGTATATATGTGTATA	244760	76956	AGAAAGCCGAGCTACGCATG	289347	121543	CCGGCCCAGAGCATCATTTT
200174	32370	ATATGTGTATATATGTGTAT	244761	76957	CAGAAAGCCGAGCTACGCAT	289348	121544	GCCGGCCCAGAGCATCATTT
200175	32371	TATATGTGTATATATGTGTA	244762	76958	CCAGAAAGCCGAGCTACGCA	289349	121545	AGCCGGCCCAGAGCATCATT
200176	32372	ATATATGTGTATATATGTGT	244763	76959	ACCAGAAAGCCGAGCTACGC	289350	121546	CAGCCGGCCCAGAGCATCAT
200177	32373	TATATATGTGTATATATGTG	244764	76960	TACCAGAAAGCCGAGCTACG	289351	121547	ACAGCCGGCCCAGAGCATCA
200178	32374	ATATATATGTGTATATATGT	244765	76961	ATACCAGAAAGCCGAGCTAC	289352	121548	CACAGCCGGCCCAGAGCATC
200179	32375	TATATATATGTGTATATATG	244766	76962	AATACCAGAAAGCCGAGCTA	289353	121549	CCACAGCCGGCCCAGAGCAT
200180	32376	GTATATATATGTGTATATAT	244767	76963	AAATACCAGAAAGCCGAGCT	289354	121550	ACCACAGCCGGCCCAGAGCA
200181	32377	TGTATATATATGTGTATATA	244768	76964	CAAATACCAGAAAGCCGAGC	289355	121551	CACCACAGCCGGCCCAGAGC
200182	32378	ATGTATATATATGTGTATAT	244769	76965	GCAAATACCAGAAAGCCGAG	289356	121552	CCACCACAGCCGGCCCAGAG
200183	32379	TATGTATATATATGTGTATA	244770	76966	AGCAAATACCAGAAAGCCGA	289357	121553	GCCACCACAGCCGGCCCAGA
200184	32380	ATATGTATATATATGTGTAT	244771	76967	CAGCAAATACCAGAAAGCCG	289358	121554	GGCCACCACAGCCGGCCCAG
200185	32381	TATATGTATATATATGTGTA	244772	76968	GCAGCAAATACCAGAAAGCC	289359	121555	GGGCCACCACAGCCGGCCCA
200186	32382	ATATATGTATATATATGTGT	244773	76969	GGCAGCAAATACCAGAAAGC	289360	121556	TGGGCCACCACAGCCGGCCC
200187	32383	CATATATGTATATATATGTG	244774	76970	GGGCAGCAAATACCAGAAAG	289361	121557	GTGGGCCACCACAGCCGGCC
200188	32384	ACATATATGTATATATATGT	244775	76971	CGGGCAGCAAATACCAGAAA	289362	121558	TGTGGGCCACCACAGCCGGC
200189	32385	CACATATATGTATATATATG	244776	76972	ACGGGCAGCAAATACCAGAA	289363	121559	GTGTGGGCCACCACAGCCGG
200190	32386	ACACATATATGTATATATAT	244777	76973	AACGGGCAGCAAATACCAGA	289364	121560	GGTGTGGGCCACCACAGCCG
200191	32387	TACACATATATGTATATATA	244778	76974	CAACGGGCAGCAAATACCAG	289365	121561	AGGTGTGGGCCACCACAGCC
200192	32388	ATACACATATATGTATATAT	244779	76975	TCAACGGGCAGCAAATACCA	289366	121562	TAGGTGTGGGCCACCACAGC
200193	32389	TATACACATATATGTATATA	244780	76976	GTCAACGGGCAGCAAATACC	289367	121563	ATAGGTGTGGGCCACCACAG
200194	32390	ATATACACATATATGTATAT	244781	76977	GGTCAACGGGCAGCAAATAC	289368	121564	TATAGGTGTGGGCCACCACA
200195	32391	TATATACACATATATGTATA	244782	76978	TGGTCAACGGGCAGCAAATA	289369	121565	TTATAGGTGTGGGCCACCAC
200196	32392	ATATATACACATATATGTAT	244783	76979	TTGGTCAACGGGCAGCAAAT	289370	121566	ATTATAGGTGTGGGCCACCA
200197	32393	TATATATACACATATATGTA	244784	76980	ATTGGTCAACGGGCAGCAAA	289371	121567	GATTATAGGTGTGGGCCACC
200198	32394	ATATATATACACATATATGT	244785	76981	CATTGGTCAACGGGCAGCAA	289372	121568	GGATTATAGGTGTGGGCCAC
200199	32395	TATATATATACACATATATG	244786	76982	CCATTGGTCAACGGGCAGCA	289373	121569	GGGATTATAGGTGTGGGCCA
200200	32396	GTATATATATACACATATAT	244787	76983	TCCATTGGTCAACGGGCAGC	289374	121570	TGGGATTATAGGTGTGGGCC
200201	32397	TGTATATATATACACATATA	244788	76984	TTCCATTGGTCAACGGGCAG	289375	121571	CTGGGATTATAGGTGTGGGC
200202	32398	ATGTATATATATACACATAT	244789	76985	CTTCCATTGGTCAACGGGCA	289376	121572	GCTGGGATTATAGGTGTGGG

200203	32399	TATGTATATATATACACATA	244790	76986	TCTTCCATTGGTCAACGGGC	289377	121573	TGCTGGGATTATAGGTGTGG
200204	32400	ATATGTATATATATACACAT	244791	76987	ATCTTCCATTGGTCAACGGG	289378	121574	GTGCTGGGATTATAGGTGTG
200205	32401	TATATGTATATATATACACA	244792	76988	TATCTTCCATTGGTCAACGG	289379	121575	GGTGCTGGGATTATAGGTGT
200206	32402	ATATATGTATATATATACAC	244793	76989	TTATCTTCCATTGGTCAACG	289380	121576	AGGTGCTGGGATTATAGGTG
200207	32403	CATATATGTATATATATACA	244794	76990	TTTATCTTCCATTGGTCAAC	289381	121577	AAGGTGCTGGGATTATAGGT
200208	32404	ACATATATGTATATATATAC	244795	76991	GTTTATCTTCCATTGGTCAA	289382	121578	CAAGGTGCTGGGATTATAGG
200209	32405	CACATATATGTATATATATA	244796	76992	GGTTTATCTTCCATTGGTCA	289383	121579	CCAAGGTGCTGGGATTATAG
200210	32406	ACACATATATGTATATATAT	244797	76993	AGGTTTATCTTCCATTGGTC	289384	121580	CCCAAGGTGCTGGGATTATA
200211	32407	TACACATATATGTATATATA	244798	76994	AAGGTTTATCTTCCATTGGT	289385	121581	TCCCAAGGTGCTGGGATTAT
200212	32408	ATACACATATATGTATATAT	244799	76995	AAAGGTTTATCTTCCATTGG	289386	121582	CTCCCAAGGTGCTGGGATTA
200213	32409	TATACACATATATGTATATA	244800	76996	CAAAGGTTTATCTTCCATTG	289387	121583	CCTCCCAAGGTGCTGGGATT
200214	32410	ATATACACATATATGTATAT	244801	76997	GCAAAGGTTTATCTTCCATT	289388	121584	GCCTCCCAAGGTGCTGGGAT
200215	32411	TATATACACATATATGTATA	244802	76998	GGCAAAGGTTTATCTTCCAT	289389	121585	CGCCTCCCAAGGTGCTGGGA
200216	32412	ATATATACACATATATGTAT	244803	76999	AGGCAAAGGTTTATCTTCCA	289390	121586	CCGCCTCCCAAGGTGCTGGG
200217	32413	TATATATACACATATATGTA	244804	77000	GAGGCAAAGGTTTATCTTCC	289391	121587	CCCGCCTCCCAAGGTGCTGG
200218	32414	ATATATATACACATATATGT	244805	77001	TGAGGCAAAGGTTTATCTTC	289392	121588	CCCCGCCTCCCAAGGTGCTG
200219	32415	TATATATATACACATATATG	244806	77002	CTGAGGCAAAGGTTTATCTT	289393	121589	CCCCCGCCTCCCAAGGTGCT
200220	32416	GTATATATATACACATATAT	244807	77003	CCTGAGGCAAAGGTTTATCT	289394	121590	ACCCCCGCCTCCCAAGGTGC
200221	32417	TGTATATATATACACATATA	244808	77004	ACCTGAGGCAAAGGTTTATC	289395	121591	CACCCCCGCCTCCCAAGGTG
200222	32418	GTGTATATATATACACATAT	244809	77005	CACCTGAGGCAAAGGTTTAT	289396	121592	CCACCCCCGCCTCCCAAGGT
200223	32419	TGTGTATATATATACACATA	244810	77006	CCACCTGAGGCAAAGGTTTA	289397	121593	CCCACCCCCGCCTCCCAAGG
200224	32420	GTGTGTATATATATACACAT	244811	77007	GCCACCTGAGGCAAAGGTTT	289398	121594	GCCCACCCCCGCCTCCCAAG
200225	32421	TGTGTGTATATATATACACA	244812	77008	TGCCACCTGAGGCAAAGGTT	289399	121595	TGCCCACCCCCGCCTCCCAA
200226	32422	GTGTGTGTATATATATACAC	244813	77009	GTGCCACCTGAGGCAAAGGT	289400	121596	CTGCCCACCCCCGCCTCCCA
200227	32423	TGTGTGTGTATATATATACA	244814	77010	GGTGCCACCTGAGGCAAAGG	289401	121597	TCTGCCCACCCCCGCCTCCC
200228	32424	ATGTGTGTGTATATATATAC	244815	77011	TGGTGCCACCTGAGGCAAAG	289402	121598	ATCTGCCCACCCCCGCCTCC
200229	32425	TATGTGTGTGTATATATATA	244816	77012	GTGGTGCCACCTGAGGCAAA	289403	121599	AATCTGCCCACCCCCGCCTC
200230	32426	GTATGTGTGTGTATATATAT	244817	77013	AGTGGTGCCACCTGAGGCAA	289404	121600	CAATCTGCCCACCCCCGCCT
200231	32427	TGTATGTGTGTGTATATATA	244818	77014	TAGTGGTGCCACCTGAGGCA	289405	121601	GCAATCTGCCCACCCCCGCC
200232	32428	GTGTATGTGTGTGTATATAT	244819	77015	CTAGTGGTGCCACCTGAGGC	289406	121602	GGCAATCTGCCCACCCCCGC
200233	32429	TGTGTATGTGTGTGTATATA	244820	77016	GCTAGTGGTGCCACCTGAGG	289407	121603	AGGCAATCTGCCCACCCCCG
200234	32430	ATGTGTATGTGTGTGTATAT	244821	77017	AGCTAGTGGTGCCACCTGAG	289408	121604	CAGGCAATCTGCCCACCCCC
200235	32431	TATGTGTATGTGTGTGTATA	244822	77018	CAGCTAGTGGTGCCACCTGA	289409	121605	TCAGGCAATCTGCCCACCCC
200236	32432	ATATGTGTATGTGTGTGTAT	244823	77019	CCAGCTAGTGGTGCCACCTG	289410	121606	CTCAGGCAATCTGCCCACCC
200237	32433	TATATGTGTATGTGTGTGTA	244824	77020	ACCAGCTAGTGGTGCCACCT	289411	121607	CCTCAGGCAATCTGCCCACC
200238	32434	ATATATGTGTATGTGTGTGT	244825	77021	AACCAGCTAGTGGTGCCACC	289412	121608	ACCTCAGGCAATCTGCCCAC
200239	32435	TATATATGTGTATGTGTGTG	244826	77022	TAACCAGCTAGTGGTGCCAC	289413	121609	GACCTCAGGCAATCTGCCCA
200240	32436	ATATATATGTGTATGTGTGT	244827	77023	TTAACCAGCTAGTGGTGCCA	289414	121610	TGACCTCAGGCAATCTGCCC
200241	32437	TATATATATGTGTATGTGTG	244828	77024	CTTAACCAGCTAGTGGTGCC	289415	121611	CTGACCTCAGGCAATCTGCC
200242	32438	GTATATATATGTGTATGTGT	244829	77025	TCTTAACCAGCTAGTGGTGC	289416	121612	CCTGACCTCAGGCAATCTGC
200243	32439	TGTATATATATGTGTATGTG	244830	77026	CTCTTAACCAGCTAGTGGTG	289417	121613	TCCTGACCTCAGGCAATCTG
200244	32440	GTGTATATATATGTGTATGT	244831	77027	CCTCTTAACCAGCTAGTGGT	289418	121614	CTCCTGACCTCAGGCAATCT
200245	32441	TGTGTATATATATGTGTATG	244832	77028	GCCTCTTAACCAGCTAGTGG	289419	121615	ACTCCTGACCTCAGGCAATC
200246	32442	GTGTGTATATATATGTGTAT	244833	77029	TGCCTCTTAACCAGCTAGTG	289420	121616	AACTCCTGACCTCAGGCAAT
200247	32443	TGTGTGTATATATATGTGTA	244834	77030	GTGCCTCTTAACCAGCTAGT	289421	121617	CAACTCCTGACCTCAGGCAA
200248	32444	GTGTGTGTATATATATGTGT	244835	77031	AGTGCCTCTTAACCAGCTAG	289422	121618	CCAACTCCTGACCTCAGGCA
200249	32445	TGTGTGTGTATATATATGTG	244836	77032	AAGTGCCTCTTAACCAGCTA	289423	121619	TCCAACTCCTGACCTCAGGC
200250	32446	GTGTGTGTGTATATATATGT	244837	77033	AAAGTGCCTCTTAACCAGCT	289424	121620	CTCCAACTCCTGACCTCAGG
200251	32447	TGTGTGTGTGTATATATATG	244838	77034	CAAAGTGCCTCTTAACCAGC	289425	121621	TCTCCAACTCCTGACCTCAG
200252	32448	ATGTGTGTGTGTATATATAT	244839	77035	ACAAAGTGCCTCTTAACCAG	289426	121622	ATCTCCAACTCCTGACCTCA
200253	32449	TATGTGTGTGTGTATATATA	244840	77036	GACAAAGTGCCTCTTAACCA	289427	121623	GATCTCCAACTCCTGACCTC
200254	32450	GTATGTGTGTGTGTATATAT	244841	77037	GGACAAAGTGCCTCTTAACC	289428	121624	TGATCTCCAACTCCTGACCT
200255	32451	TGTATGTGTGTGTGTATATA	244842	77038	AGGACAAAGTGCCTCTTAAC	289429	121625	CTGATCTCCAACTCCTGACC
200256	32452	ATGTATGTGTGTGTGTATAT	244843	77039	AAGGACAAAGTGCCTCTTAA	289430	121626	GCTGATCTCCAACTCCTGAC
200257	32453	TATGTATGTGTGTGTGTATA	244844	77040	AAAGGACAAAGTGCCTCTTA	289431	121627	GGCTGATCTCCAACTCCTGA
200258	32454	GTATGTATGTGTGTGTGTAT	244845	77041	GAAAGGACAAAGTGCCTCTT	289432	121628	AGGCTGATCTCCAACTCCTG
200259	32455	TGTATGTATGTGTGTGTGTA	244846	77042	TGAAAGGACAAAGTGCCTCT	289433	121629	CAGGCTGATCTCCAACTCCT
200260	32456	ATGTATGTATGTGTGTGTGT	244847	77043	GTGAAAGGACAAAGTGCCTC	289434	121630	CCAGGCTGATCTCCAACTCC
200261	32457	CATGTATGTATGTGTGTGTG	244848	77044	GGTGAAAGGACAAAGTGCCT	289435	121631	GCCAGGCTGATCTCCAACTC
200262	32458	ACATGTATGTATGTGTGTGT	244849	77045	GGGTGAAAGGACAAAGTGCC	289436	121632	GGCCAGGCTGATCTCCAACT
200263	32459	TACATGTATGTATGTGTGTG	244850	77046	TGGGTGAAAGGACAAAGTGC	289437	121633	CGGCCAGGCTGATCTCCAAC
200264	32460	ATACATGTATGTATGTGTGT	244851	77047	CTGGGTGAAAGGACAAAGTG	289438	121634	TCGGCCAGGCTGATCTCCAA
200265	32461	AATACATGTATGTATGTGTG	244852	77048	CCTGGGTGAAAGGACAAAGT	289439	121635	GTCGGCCAGGCTGATCTCCA
200266	32462	AAATACATGTATGTATGTGT	244853	77049	TCCTGGGTGAAAGGACAAAG	289440	121636	TGTCGGCCAGGCTGATCTCC
200267	32463	AAAATACATGTATGTATGTG	244854	77050	CTCCTGGGTGAAAGGACAAA	289441	121637	ATGTCGGCCAGGCTGATCTC
200268	32464	AAAAATACATGTATGTATGT	244855	77051	GCTCCTGGGTGAAAGGACAA	289442	121638	CATGTCGGCCAGGCTGATCT
200269	32465	TAAAAATACATGTATGTATG	244856	77052	TGCTCCTGGGTGAAAGGACA	289443	121639	CCATGTCGGCCAGGCTGATC
200270	32466	ATAAAAATACATGTATGTAT	244857	77053	TTGCTCCTGGGTGAAAGGAC	289444	121640	GCCATGTCGGCCAGGCTGAT
200271	32467	TATAAAAATACATGTATGTA	244858	77054	TTTGCTCCTGGGTGAAAGGA	289445	121641	CGCCATGTCGGCCAGGCTGA
200272	32468	ATATAAAAATACATGTATGT	244859	77055	GTTTGCTCCTGGGTGAAAGG	289446	121642	TCGCCATGTCGGCCAGGCTG
200273	32469	TATATAAAAATACATGTATG	244860	77056	CGTTTGCTCCTGGGTGAAAG	289447	121643	TTCGCCATGTCGGCCAGGCT
200274	32470	TTATATAAAAATACATGTAT	244861	77057	GCGTTTGCTCCTGGGTGAAA	289448	121644	TTTCGCCATGTCGGCCAGGC

200275	32471	ATTATATAAAAATACATGTA	244862	77058	TGCGTTTGCTCCTGGGTGAA	289449	121645	GTTTCGCCATGTCGGCCAGG
200276	32472	AATTATATAAAAATACATGT	244863	77059	GTGCGTTTGCTCCTGGGTGA	289450	121646	GGTTTCGCCATGTCGGCCAG
200277	32473	TAATTATATAAAAATACATG	244864	77060	TGTGCGTTTGCTCCTGGGTG	289451	121647	GGGTTTCGCCATGTCGGCCA
200278	32474	ATAATTATATAAAAATACAT	244865	77061	ATGTGCGTTTGCTCCTGGGT	289452	121648	GGGGTTTCGCCATGTCGGCC
200279	32475	TATAATTATATAAAAATACA	244866	77062	GATGTGCGTTTGCTCCTGGG	289453	121649	TGGGGTTTCGCCATGTCGGC
200280	32476	ATATAATTATATAAAAATAC	244867	77063	TGATGTGCGTTTGCTCCTGG	289454	121650	ATGGGGTTTCGCCATGTCGG
200281	32477	TATATAATTATATAAAAATA	244868	77064	GTGATGTGCGTTTGCTCCTG	289455	121651	CATGGGGTTTCGCCATGTCG
200282	32478	ATATATAATTATATAAAAAT	244869	77065	GGTGATGTGCGTTTGCTCCT	289456	121652	ACATGGGGTTTCGCCATGTC
200283	32479	CATATATAATTATATAAAAA	244870	77066	AGGTGATGTGCGTTTGCTCC	289457	121653	GACATGGGGTTTCGCCATGT
200284	32480	GCATATATAATTATATAAAA	244871	77067	CAGGTGATGTGCGTTTGCTC	289458	121654	AGACATGGGGTTTCGCCATG
200285	32481	TGCATATATAATTATATAAA	244872	77068	ACAGGTGATGTGCGTTTGCT	289459	121655	TAGACATGGGGTTTCGCCAT
200286	32482	CTGCATATATAATTATATAA	244873	77069	CACAGGTGATGTGCGTTTGC	289460	121656	GTAGACATGGGGTTTCGCCA
200287	32483	TCTGCATATATAATTATATA	244874	77070	ACACAGGTGATGTGCGTTTG	289461	121657	AGTAGACATGGGGTTTCGCC
200288	32484	CTCTGCATATATAATTATAT	244875	77071	GACACAGGTGATGTGCGTTT	289462	121658	TAGTAGACATGGGGTTTCGC
200289	32485	TCTCTGCATATATAATTATA	244876	77072	GGACACAGGTGATGTGCGTT	289463	121659	TTAGTAGACATGGGGTTTCG
200290	32486	CTCTCTGCATATATAATTAT	244877	77073	AGGACACAGGTGATGTGCGT	289464	121660	TTTAGTAGACATGGGGTTTC
200291	32487	ACTCTCTGCATATATAATTA	244878	77074	GAGGACACAGGTGATGTGCG	289465	121661	TTTTAGTAGACATGGGGTTT
200292	32488	CACTCTCTGCATATATAATT	244879	77075	TGAGGACACAGGTGATGTGC	289466	121662	TTTTTAGTAGACATGGGGTT
200293	32489	GCACTCTCTGCATATATAAT	244880	77076	ATGAGGACACAGGTGATGTG	289467	121663	ATTTTTAGTAGACATGGGGT
200294	32490	TGCACTCTCTGCATATATAA	244881	77077	GATGAGGACACAGGTGATGT	289468	121664	TATTTTTAGTAGACATGGGG
200295	32491	TTGCACTCTCTGCATATATA	244882	77078	AGATGAGGACACAGGTGATG	289469	121665	GTATTTTTAGTAGACATGGG
200296	32492	TTTGCACTCTCTGCATATAT	244883	77079	CAGATGAGGACACAGGTGAT	289470	121666	TGTATTTTTAGTAGACATGG
200297	32493	ATTTGCACTCTCTGCATATA	244884	77080	TCAGATGAGGACACAGGTGA	289471	121667	TTGTATTTTTAGTAGACATG
200298	32494	CATTTGCACTCTCTGCATAT	244885	77081	ATCAGATGAGGACACAGGTG	289472	121668	TTTGTATTTTTAGTAGACAT
200299	32495	ACATTTGCACTCTCTGCATA	244886	77082	CATCAGATGAGGACACAGGT	289473	121669	TTTTGTATTTTTAGTAGACA
200300	32496	AACATTTGCACTCTCTGCAT	244887	77083	CCATCAGATGAGGACACAGG	289474	121670	TTTTTGTATTTTTAGTAGAC
200301	32497	CAACATTTGCACTCTCTGCA	244888	77084	GCCATCAGATGAGGACACAG	289475	121671	GTTTTTGTATTTTTAGTAGA
200302	32498	GCAACATTTGCACTCTCTGC	244889	77085	GGCCATCAGATGAGGACACA	289476	121672	AGTTTTTGTATTTTTAGTAG
200303	32499	GGCAACATTTGCACTCTCTG	244890	77086	GGGCCATCAGATGAGGACAC	289477	121673	TAGTTTTTGTATTTTTAGTA
200304	32500	TGGCAACATTTGCACTCTCT	244891	77087	AGGGCCATCAGATGAGGACA	289478	121674	CTAGTTTTTGTATTTTTAGT
200305	32501	TTGGCAACATTTGCACTCTC	244892	77088	CAGGGCCATCAGATGAGGAC	289479	121675	GCTAGTTTTTGTATTTTTAG
200306	32502	CTTGGCAACATTTGCACTCT	244893	77089	CCAGGGCCATCAGATGAGGA	289480	121676	GGCTAGTTTTTGTATTTTTA
200307	32503	ACTTGGCAACATTTGCACTC	244894	77090	ACCAGGGCCATCAGATGAGG	289481	121677	TGGCTAGTTTTTGTATTTTT
200308	32504	AACTTGGCAACATTTGCACT	244895	77091	CACCAGGGCCATCAGATGAG	289482	121678	CTGGCTAGTTTTTGTATTTT
200309	32505	TAACTTGGCAACATTTGCAC	244896	77092	ACACCAGGGCCATCAGATGA	289483	121679	CCTGGCTAGTTTTTGTATTT
200310	32506	TTAACTTGGCAACATTTGCA	244897	77093	CACACCAGGGCCATCAGATG	289484	121680	GCCTGGCTAGTTTTTGTATT
200311	32507	TTTAACTTGGCAACATTTGC	244898	77094	CCACACCAGGGCCATCAGAT	289485	121681	TGCCTGGCTAGTTTTTGTAT
200312	32508	CTTTAACTTGGCAACATTTG	244899	77095	CCCACACCAGGGCCATCAGA	289486	121682	ATGCCTGGCTAGTTTTTGTA
200313	32509	TCTTTAACTTGGCAACATTT	244900	77096	CCCCACACCAGGGCCATCAG	289487	121683	CATGCCTGGCTAGTTTTTGT
200314	32510	ATCTTTAACTTGGCAACATT	244901	77097	GCCCCACACCAGGGCCATCA	289488	121684	CCATGCCTGGCTAGTTTTTG
200315	32511	AATCTTTAACTTGGCAACAT	244902	77098	TGCCCCACACCAGGGCCATC	289489	121685	ACCATGCCTGGCTAGTTTTT
200316	32512	CAATCTTTAACTTGGCAACA	244903	77099	GTGCCCCACACCAGGGCCAT	289490	121686	CACCATGCCTGGCTAGTTTT
200317	32513	CCAATCTTTAACTTGGCAAC	244904	77100	TGTGCCCCACACCAGGGCCA	289491	121687	CCACCATGCCTGGCTAGTTT
200318	32514	ACCAATCTTTAACTTGGCAA	244905	77101	CTGTGCCCCACACCAGGGCC	289492	121688	GCCACCATGCCTGGCTAGTT
200319	32515	CACCAATCTTTAACTTGGCA	244906	77102	ACTGTGCCCCACACCAGGGC	289493	121689	TGCCACCATGCCTGGCTAGT
200320	32516	TCACCAATCTTTAACTTGGC	244907	77103	GACTGTGCCCCACACCAGGG	289494	121690	GTGCCACCATGCCTGGCTAG
200321	32517	CTCACCAATCTTTAACTTGG	244908	77104	CGACTGTGCCCCACACCAGG	289495	121691	TGTGCCACCATGCCTGGCTA
200322	32518	ACTCACCAATCTTTAACTTG	244909	77105	ACGACTGTGCCCCACACCAG	289496	121692	ATGTGCCACCATGCCTGGCT
200323	32519	GACTCACCAATCTTTAACTT	244910	77106	CACGACTGTGCCCCACACCA	289497	121693	CATGTGCCACCATGCCTGGC
200324	32520	AGACTCACCAATCTTTAACT	244911	77107	ACACGACTGTGCCCCACACC	289498	121694	GCATGTGCCACCATGCCTGG
200325	32521	TAGACTCACCAATCTTTAAC	244912	77108	AACACGACTGTGCCCCACAC	289499	121695	GGCATGTGCCACCATGCCTG
200326	32522	CTAGACTCACCAATCTTTAA	244913	77109	CAACACGACTGTGCCCCACA	289500	121696	AGGCATGTGCCACCATGCCT
200327	32523	CCTAGACTCACCAATCTTTA	244914	77110	CCAACACGACTGTGCCCCAC	289501	121697	CAGGCATGTGCCACCATGCC
200328	32524	ACCTAGACTCACCAATCTTT	244915	77111	GCCAACACGACTGTGCCCCA	289502	121698	ACAGGCATGTGCCACCATGC
200329	32525	CACCTAGACTCACCAATCTT	244916	77112	TGCCAACACGACTGTGCCCC	289503	121699	TACAGGCATGTGCCACCATG
200330	32526	TCACCTAGACTCACCAATCT	244917	77113	CTGCCAACACGACTGTGCCC	289504	121700	TTACAGGCATGTGCCACCAT
200331	32527	TTCACCTAGACTCACCAATC	244918	77114	CCTGCCAACACGACTGTGCC	289505	121701	ATTACAGGCATGTGCCACCA
200332	32528	CTTCACCTAGACTCACCAAT	244919	77115	CCCTGCCAACACGACTGTGC	289506	121702	GATTACAGGCATGTGCCACC
200333	32529	CCTTCACCTAGACTCACCAA	244920	77116	TCCCTGCCAACACGACTGTG	289507	121703	GGATTACAGGCATGTGCCAC
200334	32530	CCCTTCACCTAGACTCACCA	244921	77117	CTCCCTGCCAACACGACTGT	289508	121704	GGGATTACAGGCATGTGCCA
200335	32531	TCCCTTCACCTAGACTCACC	244922	77118	CCTCCCTGCCAACACGACTG	289509	121705	TGGGATTACAGGCATGTGCC
200336	32532	TTCCCTTCACCTAGACTCAC	244923	77119	CCCTCCCTGCCAACACGACT	289510	121706	CTGGGATTACAGGCATGTGC
200337	32533	ATTCCCTTCACCTAGACTCA	244924	77120	TCCCTCCCTGCCAACACGAC	289511	121707	GCTGGGATTACAGGCATGTG
200338	32534	TATTCCCTTCACCTAGACTC	244925	77121	CTCCCTCCCTGCCAACACGA	289512	121708	AGCTGGGATTACAGGCATGT
200339	32535	ATATTCCCTTCACCTAGACT	244926	77122	CCTCCCTCCCTGCCAACACG	289513	121709	TAGCTGGGATTACAGGCATG
200340	32536	CATATTCCCTTCACCTAGAC	244927	77123	ACCTCCCTCCCTGCCAACAC	289514	121710	GTAGCTGGGATTACAGGCAT
200341	32537	CCATATTCCCTTCACCTAGA	244928	77124	CACCTCCCTCCCTGCCAACA	289515	121711	AGTAGCTGGGATTACAGGCA
200342	32538	ACCATATTCCCTTCACCTAG	244929	77125	CCACCTCCCTCCCTGCCAAC	289516	121712	AAGTAGCTGGGATTACAGGC
200343	32539	TACCATATTCCCTTCACCTA	244930	77126	CCCACCTCCCTCCCTGCCAA	289517	121713	CAAGTAGCTGGGATTACAGG
200344	32540	ATACCATATTCCCTTCACCT	244931	77127	CCCCACCTCCCTCCCTGCCA	289518	121714	CCAAGTAGCTGGGATTACAG
200345	32541	AATACCATATTCCCTTCACC	244932	77128	ACCCCACCTCCCTCCCTGCC	289519	121715	CCCAAGTAGCTGGGATTACA
200346	32542	AAATACCATATTCCCTTCAC	244933	77129	AACCCCACCTCCCTCCCTGC	289520	121716	TCCCAAGTAGCTGGGATTAC

200347	32543	TAAATACCATATTCCCTTCA	244934	77130	CAACCCCACCTCCCTCCCTG	289521	121717	CTCCCAAGTAGCTGGGATTA
200348	32544	ATAAATACCATATTCCCTTC	244935	77131	CCAACCCCACCTCCCTCCCT	289522	121718	CCTCCCAAGTAGCTGGGATT
200349	32545	AATAAATACCATATTCCCTT	244936	77132	ACCAACCCCACCTCCCTCCC	289523	121719	GCCTCCCAAGTAGCTGGGAT
200350	32546	CAATAAATACCATATTCCCT	244937	77133	GACCAACCCCACCTCCCTCC	289524	121720	AGCCTCCCAAGTAGCTGGGA
200351	32547	ACAATAAATACCATATTCCC	244938	77134	GGACCAACCCCACCTCCCTC	289525	121721	CAGCCTCCCAAGTAGCTGGG
200352	32548	TACAATAAATACCATATTCC	244939	77135	GGGACCAACCCCACCTCCCT	289526	121722	TCAGCCTCCCAAGTAGCTGG
200353	32549	ATACAATAAATACCATATTC	244940	77136	GGGGACCAACCCCACCTCCC	289527	121723	TTCAGCCTCCCAAGTAGCTG
200354	32550	AATACAATAAATACCATATT	244941	77137	AGGGGACCAACCCCACCTCC	289528	121724	CTTCAGCCTCCCAAGTAGCT
200355	32551	TAATACAATAAATACCATAT	244942	77138	AAGGGGACCAACCCCACCTC	289529	121725	GCTTCAGCCTCCCAAGTAGC
200356	32552	ATAATACAATAAATACCATA	244943	77139	AAAGGGGACCAACCCCACCT	289530	121726	TGCTTCAGCCTCCCAAGTAG
200357	32553	AATAATACAATAAATACCAT	244944	77140	CAAAGGGGACCAACCCCACC	289531	121727	CTGCTTCAGCCTCCCAAGTA
200358	32554	AAATAATACAATAAATACCA	244945	77141	ACAAAGGGGACCAACCCCAC	289532	121728	CCTGCTTCAGCCTCCCAAGT
200359	32555	CAAATAATACAATAAATACC	244946	77142	CACAAAGGGGACCAACCCCA	289533	121729	TCCTGCTTCAGCCTCCCAAG
200360	32556	ACAAATAATACAATAAATAC	244947	77143	CCACAAAGGGGACCAACCCC	289534	121730	CTCCTGCTTCAGCCTCCCAA
200361	32557	CACAAATAATACAATAAATA	244948	77144	CCCACAAAGGGGACCAACCC	289535	121731	TCTCCTGCTTCAGCCTCCCA
200362	32558	GCACAAATAATACAATAAAT	244949	77145	ACCCACAAAGGGGACCAACC	289536	121732	TTCTCCTGCTTCAGCCTCCC
200363	32559	TGCACAAATAATACAATAAA	244950	77146	AACCCACAAAGGGGACCAAC	289537	121733	ATTCTCCTGCTTCAGCCTCC
200364	32560	TTGCACAAATAATACAATAA	244951	77147	AAACCCACAAAGGGGACCAA	289538	121734	GATTCTCCTGCTTCAGCCTC
200365	32561	GTTGCACAAATAATACAATA	244952	77148	CAAACCCACAAAGGGGACCA	289539	121735	TGATTCTCCTGCTTCAGCCT
200366	32562	AGTTGCACAAATAATACAAT	244953	77149	ACAAACCCACAAAGGGGACC	289540	121736	GTGATTCTCCTGCTTCAGCC
200367	32563	AAGTTGCACAAATAATACAA	244954	77150	AACAAACCCACAAAGGGGAC	289541	121737	AGTGATTCTCCTGCTTCAGC
200368	32564	AAAGTTGCACAAATAATACA	244955	77151	CAACAAACCCACAAAGGGGA	289542	121738	AAGTGATTCTCCTGCTTCAG
200369	32565	AAAAGTTGCACAAATAATAC	244956	77152	GCAACAAACCCACAAAGGGG	289543	121739	CAAGTGATTCTCCTGCTTCA
200370	32566	GAAAAGTTGCACAAATAATA	244957	77153	CGCAACAAACCCACAAAGGG	289544	121740	TCAAGTGATTCTCCTGCTTC
200371	32567	AGAAAAGTTGCACAAATAAT	244958	77154	TCGCAACAAACCCACAAAGG	289545	121741	TTCAAGTGATTCTCCTGCTT
200372	32568	AAGAAAAGTTGCACAAATAA	244959	77155	CTCGCAACAAACCCACAAAG	289546	121742	GTTCAAGTGATTCTCCTGCT
200373	32569	TAAGAAAAGTTGCACAAATA	244960	77156	CCTCGCAACAAACCCACAAA	289547	121743	GGTTCAAGTGATTCTCCTGC
200374	32570	TTAAGAAAAGTTGCACAAAT	244961	77157	GCCTCGCAACAAACCCACAA	289548	121744	GGGTTCAAGTGATTCTCCTG
200375	32571	CTTAAGAAAAGTTGCACAAA	244962	77158	GGCCTCGCAACAAACCCACA	289549	121745	TGGGTTCAAGTGATTCTCCT
200376	32572	ACTTAAGAAAAGTTGCACAA	244963	77159	CGGCCTCGCAACAAACCCAC	289550	121746	CTGGGTTCAAGTGATTCTCC
200377	32573	AACTTAAGAAAAGTTGCACA	244964	77160	ACGGCCTCGCAACAAACCCA	289551	121747	CCTGGGTTCAAGTGATTCTC
200378	32574	AAACTTAAGAAAAGTTGCAC	244965	77161	CACGGCCTCGCAACAAACCC	289552	121748	TCCTGGGTTCAAGTGATTCT
200379	32575	CAAACTTAAGAAAAGTTGCA	244966	77162	ACACGGCCTCGCAACAAACC	289553	121749	CTCCTGGGTTCAAGTGATTC
200380	32576	TCAAACTTAAGAAAAGTTGC	244967	77163	AACACGGCCTCGCAACAAAC	289554	121750	CCTCCTGGGTTCAAGTGATT
200381	32577	TTCAAACTTAAGAAAAGTTG	244968	77164	GAACACGGCCTCGCAACAAA	289555	121751	GCCTCCTGGGTTCAAGTGAT
200382	32578	TTTCAAACTTAAGAAAAGTT	244969	77165	GGAACACGGCCTCGCAACAA	289556	121752	TGCCTCCTGGGTTCAAGTGA
200383	32579	TTTTCAAACTTAAGAAAAGT	244970	77166	TGGAACACGGCCTCGCAACA	289557	121753	CTGCCTCCTGGGTTCAAGTG
200384	32580	ATTTTCAAACTTAAGAAAAG	244971	77167	CTGGAACACGGCCTCGCAAC	289558	121754	TCTGCCTCCTGGGTTCAAGT
200385	32581	AATTTTCAAACTTAAGAAAA	244972	77168	GCTGGAACACGGCCTCGCAA	289559	121755	CTCTGCCTCCTGGGTTCAAG
200386	32582	AAATTTTCAAACTTAAGAAA	244973	77169	AGCTGGAACACGGCCTCGCA	289560	121756	CCTCTGCCTCCTGGGTTCAA
200387	32583	AAAATTTTCAAACTTAAGAA	244974	77170	CAGCTGGAACACGGCCTCGC	289561	121757	GCCTCTGCCTCCTGGGTTCA
200388	32584	GAAAATTTTCAAACTTAAGA	244975	77171	ACAGCTGGAACACGGCCTCG	289562	121758	AGCCTCTGCCTCCTGGGTTC
200389	32585	TGAAAATTTTCAAACTTAAG	244976	77172	AACAGCTGGAACACGGCCTC	289563	121759	CAGCCTCTGCCTCCTGGGTT
200390	32586	TTGAAAATTTTCAAACTTAA	244977	77173	AAACAGCTGGAACACGGCCT	289564	121760	TCAGCCTCTGCCTCCTGGGT
200391	32587	TTTGAAAATTTTCAAACTTA	244978	77174	GAAACAGCTGGAACACGGCC	289565	121761	CTCAGCCTCTGCCTCCTGGG
200392	32588	TTTTGAAAATTTTCAAACTT	244979	77175	GGAAACAGCTGGAACACGGC	289566	121762	ACTCAGCCTCTGCCTCCTGG
200393	32589	GTTTTGAAAATTTTCAAACT	244980	77176	TGGAAACAGCTGGAACACGG	289567	121763	CACTCAGCCTCTGCCTCCTG
200394	32590	TGTTTTGAAAATTTTCAAAC	244981	77177	GTGGAAACAGCTGGAACACG	289568	121764	TCACTCAGCCTCTGCCTCCT
200395	32591	TTGTTTTGAAAATTTTCAAA	244982	77178	TGTGGAAACAGCTGGAACAC	289569	121765	CTCACTCAGCCTCTGCCTCC
200396	32592	TTTGTTTTGAAAATTTTCAA	244983	77179	CTGTGGAAACAGCTGGAACA	289570	121766	GCTCACTCAGCCTCTGCCTC
200397	32593	TTTTGTTTTGAAAATTTTCA	244984	77180	CCTGTGGAAACAGCTGGAAC	289571	121767	GGCTCACTCAGCCTCTGCCT
200398	32594	TTTTTGTTTTGAAAATTTTC	244985	77181	CCCTGTGGAAACAGCTGGAA	289572	121768	TGGCTCACTCAGCCTCTGCC
200399	32595	TTTTTTGTTTTGAAAATTTT	244986	77182	TCCCTGTGGAAACAGCTGGA	289573	121769	TTGGCTCACTCAGCCTCTGC
200400	32596	ATTTTTTGTTTTGAAAATTT	244987	77183	CTCCCTGTGGAAACAGCTGG	289574	121770	CTTGGCTCACTCAGCCTCTG
200401	32597	AATTTTTTGTTTTGAAAATT	244988	77184	GCTCCCTGTGGAAACAGCTG	289575	121771	TCTTGGCTCACTCAGCCTCT
200402	32598	CAATTTTTTGTTTTGAAAAT	244989	77185	CGCTCCCTGTGGAAACAGCT	289576	121772	ATCTTGGCTCACTCAGCCTC
200403	32599	CCAATTTTTTGTTTTGAAAA	244990	77186	TCGCTCCCTGTGGAAACAGC	289577	121773	GATCTTGGCTCACTCAGCCT
200404	32600	TCCAATTTTTTGTTTTGAAA	244991	77187	ATCGCTCCCTGTGGAAACAG	289578	121774	CGATCTTGGCTCACTCAGCC
200405	32601	CTCCAATTTTTTGTTTTGAA	244992	77188	AATCGCTCCCTGTGGAAACA	289579	121775	ACGATCTTGGCTCACTCAGC
200406	32602	CCTCCAATTTTTTGTTTTGA	244993	77189	AAATCGCTCCCTGTGGAAAC	289580	121776	CACGATCTTGGCTCACTCAG
200407	32603	TCCTCCAATTTTTTGTTTTG	244994	77190	AAAATCGCTCCCTGTGGAAA	289581	121777	GCACGATCTTGGCTCACTCA
200408	32604	TTCCTCCAATTTTTTGTTTT	244995	77191	GAAAATCGCTCCCTGTGGAA	289582	121778	GGCACGATCTTGGCTCACTC
200409	32605	CTTCCTCCAATTTTTTGTTT	244996	77192	TGAAAATCGCTCCCTGTGGA	289583	121779	TGGCACGATCTTGGCTCACT
200410	32606	TCTTCCTCCAATTTTTTGTT	244997	77193	CTGAAAATCGCTCCCTGTGG	289584	121780	TTGGCACGATCTTGGCTCAC
200411	32607	TTCTTCCTCCAATTTTTTGT	244998	77194	GCTGAAAATCGCTCCCTGTG	289585	121781	ATTGGCACGATCTTGGCTCA
200412	32608	CTTCTTCCTCCAATTTTTTG	244999	77195	AGCTGAAAATCGCTCCCTGT	289586	121782	CATTGGCACGATCTTGGCTC
200413	32609	CCTTCTTCCTCCAATTTTTT	245000	77196	GAGCTGAAAATCGCTCCCTG	289587	121783	GCATTGGCACGATCTTGGCT
200414	32610	GCCTTCTTCCTCCAATTTTT	245001	77197	GGAGCTGAAAATCGCTCCCT	289588	121784	TGCATTGGCACGATCTTGGC
200415	32611	TGCCTTCTTCCTCCAATTTT	245002	77198	TGGAGCTGAAAATCGCTCCC	289589	121785	GTGCATTGGCACGATCTTGG
200416	32612	ATGCCTTCTTCCTCCAATTT	245003	77199	GTGGAGCTGAAAATCGCTCC	289590	121786	AGTGCATTGGCACGATCTTG
200417	32613	CATGCCTTCTTCCTCCAATT	245004	77200	TGTGGAGCTGAAAATCGCTC	289591	121787	GAGTGCATTGGCACGATCTT
200418	32614	GCATGCCTTCTTCCTCCAAT	245005	77201	CTGTGGAGCTGAAAATCGCT	289592	121788	GGAGTGCATTGGCACGATCT

200419	32615	GGCATGCCTTCTTCCTCCAA	245006	77202	CCTGTGGAGCTGAAAATCGC	289593	121789	TGGAGTGCATTGGCACGATC
200420	32616	TGGCATGCCTTCTTCCTCCA	245007	77203	TCCTGTGGAGCTGAAAATCG	289594	121790	CTGGAGTGCATTGGCACGAT
200421	32617	CTGGCATGCCTTCTTCCTCC	245008	77204	GTCCTGTGGAGCTGAAAATC	289595	121791	GCTGGAGTGCATTGGCACGA
200422	32618	ACTGGCATGCCTTCTTCCTC	245009	77205	TGTCCTGTGGAGCTGAAAAT	289596	121792	AGCTGGAGTGCATTGGCACG
200423	32619	GACTGGCATGCCTTCTTCCT	245010	77206	GTGTCCTGTGGAGCTGAAAA	289597	121793	AAGCTGGAGTGCATTGGCAC
200424	32620	AGACTGGCATGCCTTCTTCC	245011	77207	AGTGTCCTGTGGAGCTGAAA	289598	121794	CAAGCTGGAGTGCATTGGCA
200425	32621	TAGACTGGCATGCCTTCTTC	245012	77208	CAGTGTCCTGTGGAGCTGAA	289599	121795	CCAAGCTGGAGTGCATTGGC
200426	32622	GTAGACTGGCATGCCTTCTT	245013	77209	GCAGTGTCCTGTGGAGCTGA	289600	121796	CCCAAGCTGGAGTGCATTGG
200427	32623	GGTAGACTGGCATGCCTTCT	245014	77210	AGCAGTGTCCTGTGGAGCTG	289601	121797	ACCCAAGCTGGAGTGCATTG
200428	32624	GGGTAGACTGGCATGCCTTC	245015	77211	GAGCAGTGTCCTGTGGAGCT	289602	121798	CACCCAAGCTGGAGTGCATT
200429	32625	GGGGTAGACTGGCATGCCTT	245016	77212	GGAGCAGTGTCCTGTGGAGC	289603	121799	TCACCCAAGCTGGAGTGCAT
200430	32626	TGGGGTAGACTGGCATGCCT	245017	77213	GGGAGCAGTGTCCTGTGGAG	289604	121800	CTCACCCAAGCTGGAGTGCA
200431	32627	TTGGGGTAGACTGGCATGCC	245018	77214	GGGGAGCAGTGTCCTGTGGA	289605	121801	CCTCACCCAAGCTGGAGTGC
200432	32628	CTTGGGGTAGACTGGCATGC	245019	77215	TGGGGAGCAGTGTCCTGTGG	289606	121802	CCCTCACCCAAGCTGGAGTG
200433	32629	GCTTGGGGTAGACTGGCATG	245020	77216	CTGGGGAGCAGTGTCCTGTG	289607	121803	TCCCTCACCCAAGCTGGAGT
200434	32630	GGCTTGGGGTAGACTGGCAT	245021	77217	ACTGGGGAGCAGTGTCCTGT	289608	121804	CTCCCTCACCCAAGCTGGAG
200435	32631	GGGCTTGGGGTAGACTGGCA	245022	77218	AACTGGGGAGCAGTGTCCTG	289609	121805	ACTCCCTCACCCAAGCTGGA
200436	32632	AGGGCTTGGGGTAGACTGGC	245023	77219	GAACTGGGGAGCAGTGTCCT	289610	121806	CACTCCCTCACCCAAGCTGG
200437	32633	GAGGGCTTGGGGTAGACTGG	245024	77220	GGAACTGGGGAGCAGTGTCC	289611	121807	TCACTCCCTCACCCAAGCTG
200438	32634	GGAGGGCTTGGGGTAGACTG	245025	77221	AGGAACTGGGGAGCAGTGTC	289612	121808	CTCACTCCCTCACCCAAGCT
200439	32635	TGGAGGGCTTGGGGTAGACT	245026	77222	GAGGAACTGGGGAGCAGTGT	289613	121809	TCTCACTCCCTCACCCAAGC
200440	32636	ATGGAGGGCTTGGGGTAGAC	245027	77223	GGAGGAACTGGGGAGCAGTG	289614	121810	GTCTCACTCCCTCACCCAAG
200441	32637	AATGGAGGGCTTGGGGTAGA	245028	77224	AGGAGGAACTGGGGAGCAGT	289615	121811	AGTCTCACTCCCTCACCCAA
200442	32638	CAATGGAGGGCTTGGGGTAG	245029	77225	CAGGAGGAACTGGGGAGCAG	289616	121812	GAGTCTCACTCCCTCACCCA
200443	32639	CCAATGGAGGGCTTGGGGTA	245030	77226	TCAGGAGGAACTGGGGAGCA	289617	121813	GGAGTCTCACTCCCTCACCC
200444	32640	TCCAATGGAGGGCTTGGGGT	245031	77227	CTCAGGAGGAACTGGGGAGC	289618	121814	CGGAGTCTCACTCCCTCACC
200445	32641	TTCCAATGGAGGGCTTGGGG	245032	77228	TCTCAGGAGGAACTGGGGAG	289619	121815	ACGGAGTCTCACTCCCTCAC
200446	32642	ATTCCAATGGAGGGCTTGGG	245033	77229	TTCTCAGGAGGAACTGGGGA	289620	121816	GACGGAGTCTCACTCCCTCA
200447	32643	CATTCCAATGGAGGGCTTGG	245034	77230	GTTCTCAGGAGGAACTGGGG	289621	121817	AGACGGAGTCTCACTCCCTC
200448	32644	GCATTCCAATGGAGGGCTTG	245035	77231	TGTTCTCAGGAGGAACTGGG	289622	121818	GAGACGGAGTCTCACTCCCT
200449	32645	AGCATTCCAATGGAGGGCTT	245036	77232	TTGTTCTCAGGAGGAACTGG	289623	121819	TGAGACGGAGTCTCACTCCC
200450	32646	CAGCATTCCAATGGAGGGCT	245037	77233	TTTGTTCTCAGGAGGAACTG	289624	121820	TTGAGACGGAGTCTCACTCC
200451	32647	TCAGCATTCCAATGGAGGGC	245038	77234	TTTTGTTCTCAGGAGGAACT	289625	121821	TTTGAGACGGAGTCTCACTC
200452	32648	TTCAGCATTCCAATGGAGGG	245039	77235	CTTTTGTTCTCAGGAGGAAC	289626	121822	TTTTGAGACGGAGTCTCACT
200453	32649	TTTCAGCATTCCAATGGAGG	245040	77236	CCTTTTGTTCTCAGGAGGAA	289627	121823	TTTTTGAGACGGAGTCTCAC
200454	32650	TTTTCAGCATTCCAATGGAG	245041	77237	CCCTTTTGTTCTCAGGAGGA	289628	121824	TTTTTTGAGACGGAGTCTCA
200455	32651	ATTTTCAGCATTCCAATGGA	245042	77238	CCCCTTTTGTTCTCAGGAGG	289629	121825	TTTTTTTGAGACGGAGTCTC
200456	32652	GATTTTCAGCATTCCAATGG	245043	77239	CCCCCTTTTGTTCTCAGGAG	289630	121826	TTTTTTTTGAGACGGAGTCT
200457	32653	AGATTTTCAGCATTCCAATG	245044	77240	GCCCCCTTTTGTTCTCAGGA	289631	121827	TTTTTTTTTGAGACGGAGTC
200458	32654	TAGATTTTCAGCATTCCAAT	245045	77241	CGCCCCCTTTTGTTCTCAGG	289632	121828	TTTTTTTTTTGAGACGGAGT
200459	32655	TTAGATTTTCAGCATTCCAA	245046	77242	GCGCCCCCTTTTGTTCTCAG	289633	121829	TTTTTTTTTTTGAGACGGAG
200460	32656	TTTAGATTTTCAGCATTCCA	245047	77243	AGCGCCCCCTTTTGTTCTCA	289634	121830	TTTTTTTTTTTTGAGACGGA
200461	32657	GTTTAGATTTTCAGCATTCC	245048	77244	CAGCGCCCCCTTTTGTTCTC	289635	121831	TTTTTTTTTTTTTGAGACGG
200462	32658	TGTTTAGATTTTCAGCATTC	245049	77245	CCAGCGCCCCCTTTTGTTCT	289636	121832	TTTTTTTTTTTTTTGAGACG
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200464	32660	ATTGTTTAGATTTTCAGCAT	245051	77247	CCCCAGCGCCCCCTTTTGTT	289638	121834	CTTTTTTTTTTTTTTTGAGA
200465	32661	CATTGTTTAGATTTTCAGCA	245052	77248	TCCCCAGCGCCCCCTTTTGT	289639	121835	TCTTTTTTTTTTTTTTTGAG
200466	32662	ACATTGTTTAGATTTTCAGC	245053	77249	CTCCCCAGCGCCCCCTTTTG	289640	121836	TTCTTTTTTTTTTTTTTTGA
200467	32663	CACATTGTTTAGATTTTCAG	245054	77250	TCTCCCCAGCGCCCCCTTTT	289641	121837	TTTCTTTTTTTTTTTTTTTG
200468	32664	TCACATTGTTTAGATTTTCA	245055	77251	CTCTCCCCAGCGCCCCCTTT	289642	121838	CTTTCTTTTTTTTTTTTTTT
200469	32665	ATCACATTGTTTAGATTTTC	245056	77252	CCTCTCCCCAGCGCCCCCTT	289643	121839	TCTTTCTTTTTTTTTTTTTT
200470	32666	AATCACATTGTTTAGATTTT	245057	77253	GCCTCTCCCCAGCGCCCCCT	289644	121840	TTCTTTCTTTTTTTTTTTTT
200471	32667	AAATCACATTGTTTAGATTT	245058	77254	GGCCTCTCCCCAGCGCCCCC	289645	121841	TTTCTTTCTTTTTTTTTTTT
200472	32668	CAAATCACATTGTTTAGATT	245059	77255	TGGCCTCTCCCCAGCGCCCC	289646	121842	TTTTCTTTCTTTTTTTTTTT
200473	32669	CCAAATCACATTGTTTAGAT	245060	77256	GTGGCCTCTCCCCAGCGCCC	289647	121843	TTTTTCTTTCTTTTTTTTTT
200474	32670	GCCAAATCACATTGTTTAGA	245061	77257	GGTGGCCTCTCCCCAGCGCC	289648	121844	CTTTTTCTTTCTTTTTTTTT
200475	32671	TGCCAAATCACATTGTTTAG	245062	77258	CGGTGGCCTCTCCCCAGCGC	289649	121845	TCTTTTTCTTTCTTTTTTTT
200476	32672	TTGCCAAATCACATTGTTTA	245063	77259	ACGGTGGCCTCTCCCCAGCG	289650	121846	TTCTTTTTCTTTCTTTTTTT
200477	32673	ATTGCCAAATCACATTGTTT	245064	77260	AACGGTGGCCTCTCCCCAGC	289651	121847	TTTCTTTTTCTTTCTTTTTT
200478	32674	AATTGCCAAATCACATTGTT	245065	77261	GAACGGTGGCCTCTCCCCAG	289652	121848	TTTTCTTTTTCTTTCTTTTT
200479	32675	AAATTGCCAAATCACATTGT	245066	77262	AGAACGGTGGCCTCTCCCCA	289653	121849	CTTTTCTTTTTCTTTCTTTT
200480	32676	GAAATTGCCAAATCACATTG	245067	77263	CAGAACGGTGGCCTCTCCCC	289654	121850	TCTTTTCTTTTTCTTTCTTT
200481	32677	TGAAATTGCCAAATCACATT	245068	77264	TCAGAACGGTGGCCTCTCCC	289655	121851	TTCTTTTCTTTTTCTTTCTT
200482	32678	ATGAAATTGCCAAATCACAT	245069	77265	CTCAGAACGGTGGCCTCTCC	289656	121852	TTTCTTTTCTTTTTCTTTCT
200483	32679	AATGAAATTGCCAAATCACA	245070	77266	CCTCAGAACGGTGGCCTCTC	289657	121853	CTTTCTTTTCTTTTTCTTTC
200484	32680	AAATGAAATTGCCAAATCAC	245071	77267	CCCTCAGAACGGTGGCCTCT	289658	121854	ACTTTCTTTTCTTTTTCTTT
200485	32681	GAAATGAAATTGCCAAATCA	245072	77268	GCCCTCAGAACGGTGGCCTC	289659	121855	CACTTTCTTTTCTTTTTCTT
200486	32682	AGAAATGAAATTGCCAAATC	245073	77269	AGCCCTCAGAACGGTGGCCT	289660	121856	TCACTTTCTTTTCTTTTTCT
200487	32683	AAGAAATGAAATTGCCAAAT	245074	77270	GAGCCCTCAGAACGGTGGCC	289661	121857	ATCACTTTCTTTTCTTTTTC
200488	32684	AAAGAAATGAAATTGCCAAA	245075	77271	TGAGCCCTCAGAACGGTGGC	289662	121858	GATCACTTTCTTTTCTTTTT
200489	32685	AAAAGAAATGAAATTGCCAA	245076	77272	GTGAGCCCTCAGAACGGTGG	289663	121859	GGATCACTTTCTTTTCTTTT
200490	32686	GAAAAGAAATGAAATTGCCA	245077	77273	AGTGAGCCCTCAGAACGGTG	289664	121860	AGGATCACTTTCTTTTCTTT

200491	32687	AGAAAAGAAATGAAATTGCC	245078	77274	CAGTGAGCCCTCAGAACGGT	289665	121861	TAGGATCACTTTCTTTTCTT
200492	32688	CAGAAAAGAAATGAAATTGC	245079	77275	ACAGTGAGCCCTCAGAACGG	289666	121862	GTAGGATCACTTTCTTTTCT
200493	32689	ACAGAAAAGAAATGAAATTG	245080	77276	TACAGTGAGCCCTCAGAACG	289667	121863	AGTAGGATCACTTTCTTTTC
200494	32690	AACAGAAAAGAAATGAAATT	245081	77277	ATACAGTGAGCCCTCAGAAC	289668	121864	CAGTAGGATCACTTTCTTTT
200495	32691	CAACAGAAAAGAAATGAAAT	245082	77278	CATACAGTGAGCCCTCAGAA	289669	121865	CCAGTAGGATCACTTTCTTT
200496	32692	ACAACAGAAAAGAAATGAAA	245083	77279	ACATACAGTGAGCCCTCAGA	289670	121866	TCCAGTAGGATCACTTTCTT
200497	32693	CACAACAGAAAAGAAATGAA	245084	77280	CACATACAGTGAGCCCTCAG	289671	121867	TTCCAGTAGGATCACTTTCT
200498	32694	CCACAACAGAAAAGAAATGA	245085	77281	ACACATACAGTGAGCCCTCA	289672	121868	GTTCCAGTAGGATCACTTTC
200499	32695	CCCACAACAGAAAAGAAATG	245086	77282	AACACATACAGTGAGCCCTC	289673	121869	GGTTCCAGTAGGATCACTTT
200500	32696	GCCCACAACAGAAAAGAAAT	245087	77283	GAACACATACAGTGAGCCCT	289674	121870	TGGTTCCAGTAGGATCACTT
200501	32697	GGCCCACAACAGAAAAGAAA	245088	77284	GGAACACATACAGTGAGCCC	289675	121871	ATGGTTCCAGTAGGATCACT
200502	32698	TGGCCCACAACAGAAAAGAA	245089	77285	TGGAACACATACAGTGAGCC	289676	121872	CATGGTTCCAGTAGGATCAC
200503	32699	CTGGCCCACAACAGAAAAGA	245090	77286	CTGGAACACATACAGTGAGC	289677	121873	GCATGGTTCCAGTAGGATCA
200504	32700	ACTGGCCCACAACAGAAAAG	245091	77287	TCTGGAACACATACAGTGAG	289678	121874	AGCATGGTTCCAGTAGGATC
200505	32701	TACTGGCCCACAACAGAAAA	245092	77288	TTCTGGAACACATACAGTGA	289679	121875	AAGCATGGTTCCAGTAGGAT
200506	32702	CTACTGGCCCACAACAGAAA	245093	77289	ATTCTGGAACACATACAGTG	289680	121876	TAAGCATGGTTCCAGTAGGA
200507	32703	ACTACTGGCCCACAACAGAA	245094	77290	GATTCTGGAACACATACAGT	289681	121877	GTAAGCATGGTTCCAGTAGG
200508	32704	GACTACTGGCCCACAACAGA	245095	77291	AGATTCTGGAACACATACAG	289682	121878	AGTAAGCATGGTTCCAGTAG
200509	32705	GGACTACTGGCCCACAACAG	245096	77292	GAGATTCTGGAACACATACA	289683	121879	GAGTAAGCATGGTTCCAGTA
200510	32706	AGGACTACTGGCCCACAACA	245097	77293	GGAGATTCTGGAACACATAC	289684	121880	GGAGTAAGCATGGTTCCAGT
200511	32707	AAGGACTACTGGCCCACAAC	245098	77294	GGGAGATTCTGGAACACATA	289685	121881	GGGAGTAAGCATGGTTCCAG
200512	32708	TAAGGACTACTGGCCCACAA	245099	77295	GGGGAGATTCTGGAACACAT	289686	121882	GGGGAGTAAGCATGGTTCCA
200513	32709	CTAAGGACTACTGGCCCACA	245100	77296	AGGGGAGATTCTGGAACACA	289687	121883	AGGGGAGTAAGCATGGTTCC
200514	32710	TCTAAGGACTACTGGCCCAC	245101	77297	CAGGGGAGATTCTGGAACAC	289688	121884	GAGGGGAGTAAGCATGGTTC
200515	32711	ATCTAAGGACTACTGGCCCA	245102	77298	GCAGGGGAGATTCTGGAACA	289689	121885	GGAGGGGAGTAAGCATGGTT
200516	32712	CATCTAAGGACTACTGGCCC	245103	77299	TGCAGGGGAGATTCTGGAAC	289690	121886	GGGAGGGGAGTAAGCATGGT
200517	32713	ACATCTAAGGACTACTGGCC	245104	77300	CTGCAGGGGAGATTCTGGAA	289691	121887	GGGGAGGGGAGTAAGCATGG
200518	32714	AACATCTAAGGACTACTGGC	245105	77301	TCTGCAGGGGAGATTCTGGA	289692	121888	TGGGGAGGGGAGTAAGCATG
200519	32715	CAACATCTAAGGACTACTGG	245106	77302	GTCTGCAGGGGAGATTCTGG	289693	121889	GTGGGGAGGGGAGTAAGCAT
200520	32716	CCAACATCTAAGGACTACTG	245107	77303	GGTCTGCAGGGGAGATTCTG	289694	121890	GGTGGGGAGGGGAGTAAGCA
200521	32717	CCCAACATCTAAGGACTACT	245108	77304	GGGTCTGCAGGGGAGATTCT	289695	121891	AGGTGGGGAGGGGAGTAAGC
200522	32718	CCCCAACATCTAAGGACTAC	245109	77305	GGGGTCTGCAGGGGAGATTC	289696	121892	GAGGTGGGGAGGGGAGTAAG
200523	32719	TCCCCAACATCTAAGGACTA	245110	77306	GGGGGTCTGCAGGGGAGATT	289697	121893	TGAGGTGGGGAGGGGAGTAA
200524	32720	TTCCCCAACATCTAAGGACT	245111	77307	TGGGGGTCTGCAGGGGAGAT	289698	121894	GTGAGGTGGGGAGGGGAGTA
200525	32721	CTTCCCCAACATCTAAGGAC	245112	77308	GTGGGGGTCTGCAGGGGAGA	289699	121895	TGTGAGGTGGGGAGGGGAGT
200526	32722	CCTTCCCCAACATCTAAGGA	245113	77309	AGTGGGGGTCTGCAGGGGAG	289700	121896	GTGTGAGGTGGGGAGGGGAG
200527	32723	CCCTTCCCCAACATCTAAGG	245114	77310	CAGTGGGGGTCTGCAGGGGA	289701	121897	AGTGTGAGGTGGGGAGGGGA
200528	32724	CCCCTTCCCCAACATCTAAG	245115	77311	TCAGTGGGGGTCTGCAGGGG	289702	121898	CAGTGTGAGGTGGGGAGGGG
200529	32725	CCCCCTTCCCCAACATCTAA	245116	77312	CTCAGTGGGGGTCTGCAGGG	289703	121899	ACAGTGTGAGGTGGGGAGGG
200530	32726	ACCCCCTTCCCCAACATCTA	245117	77313	CCTCAGTGGGGGTCTGCAGG	289704	121900	CACAGTGTGAGGTGGGGAGG
200531	32727	TACCCCCTTCCCCAACATCT	245118	77314	TCCTCAGTGGGGGTCTGCAG	289705	121901	ACACAGTGTGAGGTGGGGAG
200532	32728	CTACCCCCTTCCCCAACATC	245119	77315	GTCCTCAGTGGGGGTCTGCA	289706	121902	TACACAGTGTGAGGTGGGGA
200533	32729	ACTACCCCCTTCCCCAACAT	245120	77316	CGTCCTCAGTGGGGGTCTGC	289707	121903	CTACACAGTGTGAGGTGGGG
200534	32730	GACTACCCCCTTCCCCAACA	245121	77317	CCGTCCTCAGTGGGGGTCTG	289708	121904	TCTACACAGTGTGAGGTGGG
200535	32731	CGACTACCCCCTTCCCCAAC	245122	77318	TCCGTCCTCAGTGGGGGTCT	289709	121905	TTCTACACAGTGTGAGGTGG
200536	32732	GCGACTACCCCCTTCCCCAA	245123	77319	ATCCGTCCTCAGTGGGGGTC	289710	121906	TTTCTACACAGTGTGAGGTG
200537	32733	AGCGACTACCCCCTTCCCCA	245124	77320	GATCCGTCCTCAGTGGGGGT	289711	121907	ATTTCTACACAGTGTGAGGT
200538	32734	CAGCGACTACCCCCTTCCCC	245125	77321	AGATCCGTCCTCAGTGGGGG	289712	121908	AATTTCTACACAGTGTGAGG
200539	32735	TCAGCGACTACCCCCTTCCC	245126	77322	CAGATCCGTCCTCAGTGGGG	289713	121909	TAATTTCTACACAGTGTGAG
200540	32736	CTCAGCGACTACCCCCTTCC	245127	77323	TCAGATCCGTCCTCAGTGGG	289714	121910	CTAATTTCTACACAGTGTGA
200541	32737	CCTCAGCGACTACCCCCTTC	245128	77324	CTCAGATCCGTCCTCAGTGG	289715	121911	ACTAATTTCTACACAGTGTG
200542	32738	ACCTCAGCGACTACCCCCTT	245129	77325	CCTCAGATCCGTCCTCAGTG	289716	121912	CACTAATTTCTACACAGTGT
200543	32739	CACCTCAGCGACTACCCCCT	245130	77326	TCCTCAGATCCGTCCTCAGT	289717	121913	GCACTAATTTCTACACAGTG
200544	32740	ACACCTCAGCGACTACCCCC	245131	77327	TTCCTCAGATCCGTCCTCAG	289718	121914	AGCACTAATTTCTACACAGT
200545	32741	CACACCTCAGCGACTACCCC	245132	77328	GTTCCTCAGATCCGTCCTCA	289719	121915	CAGCACTAATTTCTACACAG
200546	32742	CCACACCTCAGCGACTACCC	245133	77329	GGTTCCTCAGATCCGTCCTC	289720	121916	ACAGCACTAATTTCTACACA
200547	32743	ACCACACCTCAGCGACTACC	245134	77330	CGGTTCCTCAGATCCGTCCT	289721	121917	GACAGCACTAATTTCTACAC
200548	32744	AACCACACCTCAGCGACTAC	245135	77331	CCGGTTCCTCAGATCCGTCC	289722	121918	CGACAGCACTAATTTCTACA
200549	32745	CAACCACACCTCAGCGACTA	245136	77332	CCCGGTTCCTCAGATCCGTC	289723	121919	CCGACAGCACTAATTTCTAC
200550	32746	TCAACCACACCTCAGCGACT	245137	77333	GCCCGGTTCCTCAGATCCGT	289724	121920	GCCGACAGCACTAATTTCTA
200551	32747	GTCAACCACACCTCAGCGAC	245138	77334	AGCCCGGTTCCTCAGATCCG	289725	121921	GGCCGACAGCACTAATTTCT
200552	32748	AGTCAACCACACCTCAGCGA	245139	77335	GAGCCCGGTTCCTCAGATCC	289726	121922	TGGCCGACAGCACTAATTTC
200553	32749	AAGTCAACCACACCTCAGCG	245140	77336	AGAGCCCGGTTCCTCAGATC	289727	121923	CTGGCCGACAGCACTAATTT
200554	32750	TAAGTCAACCACACCTCAGC	245141	77337	CAGAGCCCGGTTCCTCAGAT	289728	121924	CCTGGCCGACAGCACTAATT
200555	32751	CTAAGTCAACCACACCTCAG	245142	77338	TCAGAGCCCGGTTCCTCAGA	289729	121925	GCCTGGCCGACAGCACTAAT
200556	32752	CCTAAGTCAACCACACCTCA	245143	77339	TTCAGAGCCCGGTTCCTCAG	289730	121926	CGCCTGGCCGACAGCACTAA
200557	32753	TCCTAAGTCAACCACACCTC	245144	77340	TTTCAGAGCCCGGTTCCTCA	289731	121927	GCGCCTGGCCGACAGCACTA
200558	32754	ATCCTAAGTCAACCACACCT	245145	77341	GTTTCAGAGCCCGGTTCCTC	289732	121928	CGCGCCTGGCCGACAGCACT
200559	32755	CATCCTAAGTCAACCACACC	245146	77342	GGTTTCAGAGCCCGGTTCCT	289733	121929	CCGCGCCTGGCCGACAGCAC
200560	32756	CCATCCTAAGTCAACCACAC	245147	77343	AGGTTTCAGAGCCCGGTTCC	289734	121930	ACCGCGCCTGGCCGACAGCA
200561	32757	TCCATCCTAAGTCAACCACA	245148	77344	GAGGTTTCAGAGCCCGGTTC	289735	121931	CACCGCGCCTGGCCGACAGC
200562	32758	TTCCATCCTAAGTCAACCAC	245149	77345	AGAGGTTTCAGAGCCCGGTT	289736	121932	CCACCGCGCCTGGCCGACAG

200563	32759	CTTCCATCCTAAGTCAACCA	245150	77346	CAGAGGTTTCAGAGCCCGGT	289737	121933	GCCACCGCGCCTGGCCGACA
200564	32760	TCTTCCATCCTAAGTCAACC	245151	77347	TCAGAGGTTTCAGAGCCCGG	289738	121934	AGCCACCGCGCCTGGCCGAC
200565	32761	TTCTTCCATCCTAAGTCAAC	245152	77348	ATCAGAGGTTTCAGAGCCCG	289739	121935	GAGCCACCGCGCCTGGCCGA
200566	32762	CTTCTTCCATCCTAAGTCAA	245153	77349	CATCAGAGGTTTCAGAGCCC	289740	121936	TGAGCCACCGCGCCTGGCCG
200567	32763	GCTTCTTCCATCCTAAGTCA	245154	77350	GCATCAGAGGTTTCAGAGCC	289741	121937	ATGAGCCACCGCGCCTGGCC
200568	32764	TGCTTCTTCCATCCTAAGTC	245155	77351	AGCATCAGAGGTTTCAGAGC	289742	121938	CATGAGCCACCGCGCCTGGC
200569	32765	CTGCTTCTTCCATCCTAAGT	245156	77352	TAGCATCAGAGGTTTCAGAG	289743	121939	GCATGAGCCACCGCGCCTGG
200570	32766	TCTGCTTCTTCCATCCTAAG	245157	77353	TTAGCATCAGAGGTTTCAGA	289744	121940	GGCATGAGCCACCGCGCCTG
200571	32767	TTCTGCTTCTTCCATCCTAA	245158	77354	CTTAGCATCAGAGGTTTCAG	289745	121941	AGGCATGAGCCACCGCGCCT
200572	32768	CTTCTGCTTCTTCCATCCTA	245159	77355	TCTTAGCATCAGAGGTTTCA	289746	121942	CAGGCATGAGCCACCGCGCC
200573	32769	ACTTCTGCTTCTTCCATCCT	245160	77356	CTCTTAGCATCAGAGGTTTC	289747	121943	ACAGGCATGAGCCACCGCGC
200574	32770	GACTTCTGCTTCTTCCATCC	245161	77357	GCTCTTAGCATCAGAGGTTT	289748	121944	TACAGGCATGAGCCACCGCG
200575	32771	TGACTTCTGCTTCTTCCATC	245162	77358	TGCTCTTAGCATCAGAGGTT	289749	121945	TTACAGGCATGAGCCACCGC
200576	32772	TTGACTTCTGCTTCTTCCAT	245163	77359	GTGCTCTTAGCATCAGAGGT	289750	121946	ATTACAGGCATGAGCCACCG
200577	32773	CTTGACTTCTGCTTCTTCCA	245164	77360	AGTGCTCTTAGCATCAGAGG	289751	121947	GATTACAGGCATGAGCCACC
200578	32774	TCTTGACTTCTGCTTCTTCC	245165	77361	GAGTGCTCTTAGCATCAGAG	289752	121948	CGATTACAGGCATGAGCCAC
200579	32775	GTCTTGACTTCTGCTTCTTC	245166	77362	GGAGTGCTCTTAGCATCAGA	289753	121949	GCGATTACAGGCATGAGCCA
200580	32776	AGTCTTGACTTCTGCTTCTT	245167	77363	TGGAGTGCTCTTAGCATCAG	289754	121950	TGCGATTACAGGCATGAGCC
200581	32777	GAGTCTTGACTTCTGCTTCT	245168	77364	TTGGAGTGCTCTTAGCATCA	289755	121951	CTGCGATTACAGGCATGAGC
200582	32778	GGAGTCTTGACTTCTGCTTC	245169	77365	GTTGGAGTGCTCTTAGCATC	289756	121952	GCTGCGATTACAGGCATGAG
200583	32779	GGGAGTCTTGACTTCTGCTT	245170	77366	TGTTGGAGTGCTCTTAGCAT	289757	121953	TGCTGCGATTACAGGCATGA
200584	32780	TGGGAGTCTTGACTTCTGCT	245171	77367	CTGTTGGAGTGCTCTTAGCA	289758	121954	GTGCTGCGATTACAGGCATG
200585	32781	CTGGGAGTCTTGACTTCTGC	245172	77368	GCTGTTGGAGTGCTCTTAGC	289759	121955	AGTGCTGCGATTACAGGCAT
200586	32782	CCTGGGAGTCTTGACTTCTG	245173	77369	CGCTGTTGGAGTGCTCTTAG	289760	121956	AAGTGCTGCGATTACAGGCA
200587	32783	CCCTGGGAGTCTTGACTTCT	245174	77370	CCGCTGTTGGAGTGCTCTTA	289761	121957	AAAGTGCTGCGATTACAGGC
200588	32784	ACCCTGGGAGTCTTGACTTC	245175	77371	TCCGCTGTTGGAGTGCTCTT	289762	121958	CAAAGTGCTGCGATTACAGG
200589	32785	GACCCTGGGAGTCTTGACTT	245176	77372	TTCCGCTGTTGGAGTGCTCT	289763	121959	CCAAAGTGCTGCGATTACAG
200590	32786	TGACCCTGGGAGTCTTGACT	245177	77373	CTTCCGCTGTTGGAGTGCTC	289764	121960	CCCAAAGTGCTGCGATTACA
200591	32787	TTGACCCTGGGAGTCTTGAC	245178	77374	CCTTCCGCTGTTGGAGTGCT	289765	121961	TCCCAAAGTGCTGCGATTAC
200592	32788	TTTGACCCTGGGAGTCTTGA	245179	77375	ACCTTCCGCTGTTGGAGTGC	289766	121962	CTCCCAAAGTGCTGCGATTA
200593	32789	CTTTGACCCTGGGAGTCTTG	245180	77376	CACCTTCCGCTGTTGGAGTG	289767	121963	CCTCCCAAAGTGCTGCGATT
200594	32790	ACTTTGACCCTGGGAGTCTT	245181	77377	CCACCTTCCGCTGTTGGAGT	289768	121964	GCCTCCCAAAGTGCTGCGAT
200595	32791	CACTTTGACCCTGGGAGTCT	245182	77378	CCCACCTTCCGCTGTTGGAG	289769	121965	GGCCTCCCAAAGTGCTGCGA
200596	32792	CCACTTTGACCCTGGGAGTC	245183	77379	GCCCACCTTCCGCTGTTGGA	289770	121966	TGGCCTCCCAAAGTGCTGCG
200597	32793	ACCACTTTGACCCTGGGAGT	245184	77380	GGCCCACCTTCCGCTGTTGG	289771	121967	TTGGCCTCCCAAAGTGCTGC
200598	32794	AACCACTTTGACCCTGGGAG	245185	77381	GGGCCCACCTTCCGCTGTTG	289772	121968	CTTGGCCTCCCAAAGTGCTG
200599	32795	AAACCACTTTGACCCTGGGA	245186	77382	GGGGCCCACCTTCCGCTGTT	289773	121969	CCTTGGCCTCCCAAAGTGCT
200600	32796	CAAACCACTTTGACCCTGGG	245187	77383	GGGGGCCCACCTTCCGCTGT	289774	121970	GCCTTGGCCTCCCAAAGTGC
200601	32797	GCAAACCACTTTGACCCTGG	245188	77384	GGGGGGCCCACCTTCCGCTG	289775	121971	TGCCTTGGCCTCCCAAAGTG
200602	32798	AGCAAACCACTTTGACCCTG	245189	77385	AGGGGGGCCCACCTTCCGCT	289776	121972	CTGCCTTGGCCTCCCAAAGT
200603	32799	GAGCAAACCACTTTGACCCT	245190	77386	AAGGGGGGCCCACCTTCCGC	289777	121973	CCTGCCTTGGCCTCCCAAAG
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200605	32801	CAGAGCAAACCACTTTGACC	245192	77388	TGAAGGGGGGCCCACCTTCC	289779	121975	CGCCTGCCTTGGCCTCCCAA
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200607	32803	AGCAGAGCAAACCACTTTGA	245194	77390	TCTGAAGGGGGGCCCACCTT	289781	121977	TCCGCCTGCCTTGGCCTCCC
200608	32804	CAGCAGAGCAAACCACTTTG	245195	77391	GTCTGAAGGGGGGCCCACCT	289782	121978	ATCCGCCTGCCTTGGCCTCC
200609	32805	TCAGCAGAGCAAACCACTTT	245196	77392	CGTCTGAAGGGGGGCCCACC	289783	121979	GATCCGCCTGCCTTGGCCTC
200610	32806	GTCAGCAGAGCAAACCACTT	245197	77393	GCGTCTGAAGGGGGGCCCAC	289784	121980	TGATCCGCCTGCCTTGGCCT
200611	32807	GGTCAGCAGAGCAAACCACT	245198	77394	GGCGTCTGAAGGGGGGCCCA	289785	121981	GTGATCCGCCTGCCTTGGCC
200612	32808	GGGTCAGCAGAGCAAACCAC	245199	77395	GGGCGTCTGAAGGGGGGCCC	289786	121982	CGTGATCCGCCTGCCTTGGC
200613	32809	TGGGTCAGCAGAGCAAACCA	245200	77396	GGGGCGTCTGAAGGGGGGCC	289787	121983	TCGTGATCCGCCTGCCTTGG
200614	32810	TTGGGTCAGCAGAGCAAACC	245201	77397	GGGGGCGTCTGAAGGGGGGC	289788	121984	CTCGTGATCCGCCTGCCTTG
200615	32811	CTTGGGTCAGCAGAGCAAAC	245202	77398	AGGGGGCGTCTGAAGGGGGG	289789	121985	CCTCGTGATCCGCCTGCCTT
200616	32812	ACTTGGGTCAGCAGAGCAAA	245203	77399	GAGGGGGCGTCTGAAGGGGG	289790	121986	ACCTCGTGATCCGCCTGCCT
200617	32813	CACTTGGGTCAGCAGAGCAA	245204	77400	GGAGGGGGCGTCTGAAGGGG	289791	121987	GACCTCGTGATCCGCCTGCC
200618	32814	ACACTTGGGTCAGCAGAGCA	245205	77401	TGGAGGGGGCGTCTGAAGGG	289792	121988	TGACCTCGTGATCCGCCTGC
200619	32815	CACACTTGGGTCAGCAGAGC	245206	77402	ATGGAGGGGGCGTCTGAAGG	289793	121989	CTGACCTCGTGATCCGCCTG
200620	32816	CCACACTTGGGTCAGCAGAG	245207	77403	CATGGAGGGGGCGTCTGAAG	289794	121990	CCTGACCTCGTGATCCGCCT
200621	32817	CCCACACTTGGGTCAGCAGA	245208	77404	GCATGGAGGGGGCGTCTGAA	289795	121991	TCCTGACCTCGTGATCCGCC
200622	32818	TCCCACACTTGGGTCAGCAG	245209	77405	GGCATGGAGGGGGCGTCTGA	289796	121992	CTCCTGACCTCGTGATCCGC
200623	32819	CTCCCACACTTGGGTCAGCA	245210	77406	AGGCATGGAGGGGGCGTCTG	289797	121993	TCTCCTGACCTCGTGATCCG
200624	32820	CCTCCCACACTTGGGTCAGC	245211	77407	GAGGCATGGAGGGGGCGTCT	289798	121994	ATCTCCTGACCTCGTGATCC
200625	32821	GCCTCCCACACTTGGGTCAG	245212	77408	GGAGGCATGGAGGGGGCGTC	289799	121995	GATCTCCTGACCTCGTGATC
200626	32822	GGCCTCCCACACTTGGGTCA	245213	77409	TGGAGGCATGGAGGGGGCGT	289800	121996	TGATCTCCTGACCTCGTGAT
200627	32823	GGGCCTCCCACACTTGGGTC	245214	77410	CTGGAGGCATGGAGGGGGCG	289801	121997	TTGATCTCCTGACCTCGTGA
200628	32824	TGGGCCTCCCACACTTGGGT	245215	77411	GCTGGAGGCATGGAGGGGGC	289802	121998	CTTGATCTCCTGACCTCGTG
200629	32825	CTGGGCCTCCCACACTTGGG	245216	77412	GGCTGGAGGCATGGAGGGGG	289803	121999	TCTTGATCTCCTGACCTCGT
200630	32826	TCTGGGCCTCCCACACTTGG	245217	77413	AGGCTGGAGGCATGGAGGGG	289804	122000	GTCTTGATCTCCTGACCTCG
200631	32827	CTCTGGGCCTCCCACACTTG	245218	77414	CAGGCTGGAGGCATGGAGGG	289805	122001	GGTCTTGATCTCCTGACCTC
200632	32828	ACTCTGGGCCTCCCACACTT	245219	77415	ACAGGCTGGAGGCATGGAGG	289806	122002	TGGTCTTGATCTCCTGACCT
200633	32829	GACTCTGGGCCTCCCACACT	245220	77416	CACAGGCTGGAGGCATGGAG	289807	122003	ATGGTCTTGATCTCCTGACC
200634	32830	TGACTCTGGGCCTCCCACAC	245221	77417	GCACAGGCTGGAGGCATGGA	289808	122004	GATGGTCTTGATCTCCTGAC

200635	32831	CTGACTCTGGGCCTCCCACA	245222	77418	AGCACAGGCTGGAGGCATGG	289809	122005	GGATGGTCTTGATCTCCTGA
200636	32832	GCTGACTCTGGGCCTCCCAC	245223	77419	AAGCACAGGCTGGAGGCATG	289810	122006	AGGATGGTCTTGATCTCCTG
200637	32833	CGCTGACTCTGGGCCTCCCA	245224	77420	TAAGCACAGGCTGGAGGCAT	289811	122007	CAGGATGGTCTTGATCTCCT
200638	32834	ACGCTGACTCTGGGCCTCCC	245225	77421	CTAAGCACAGGCTGGAGGCA	289812	122008	CCAGGATGGTCTTGATCTCC
200639	32835	AACGCTGACTCTGGGCCTCC	245226	77422	GCTAAGCACAGGCTGGAGGC	289813	122009	GCCAGGATGGTCTTGATCTC
200640	32836	AAACGCTGACTCTGGGCCTC	245227	77423	GGCTAAGCACAGGCTGGAGG	289814	122010	AGCCAGGATGGTCTTGATCT
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200643	32839	CTGAAACGCTGACTCTGGGC	245230	77426	CACGGCTAAGCACAGGCTGG	289817	122013	GTTAGCCAGGATGGTCTTGA
200644	32840	CCTGAAACGCTGACTCTGGG	245231	77427	GCACGGCTAAGCACAGGCTG	289818	122014	TGTTAGCCAGGATGGTCTTG
200645	32841	ACCTGAAACGCTGACTCTGG	245232	77428	AGCACGGCTAAGCACAGGCT	289819	122015	GTGTTAGCCAGGATGGTCTT
200646	32842	CACCTGAAACGCTGACTCTG	245233	77429	AAGCACGGCTAAGCACAGGC	289820	122016	TGTGTTAGCCAGGATGGTCT
200647	32843	ACACCTGAAACGCTGACTCT	245234	77430	AAAGCACGGCTAAGCACAGG	289821	122017	CTGTGTTAGCCAGGATGGTC
200648	32844	CACACCTGAAACGCTGACTC	245235	77431	CAAAGCACGGCTAAGCACAG	289822	122018	ACTGTGTTAGCCAGGATGGT
200649	32845	GCACACCTGAAACGCTGACT	245236	77432	TCAAAGCACGGCTAAGCACA	289823	122019	CACTGTGTTAGCCAGGATGG
200650	32846	AGCACACCTGAAACGCTGAC	245237	77433	CTCAAAGCACGGCTAAGCAC	289824	122020	TCACTGTGTTAGCCAGGATG
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200652	32848	TTAGCACACCTGAAACGCTG	245239	77435	GGCTCAAAGCACGGCTAAGC	289826	122022	TTTCACTGTGTTAGCCAGGA
200653	32849	ATTAGCACACCTGAAACGCT	245240	77436	AGGCTCAAAGCACGGCTAAG	289827	122023	GTTTCACTGTGTTAGCCAGG
200654	32850	AATTAGCACACCTGAAACGC	245241	77437	GAGGCTCAAAGCACGGCTAA	289828	122024	GGTTTCACTGTGTTAGCCAG
200655	32851	GAATTAGCACACCTGAAACG	245242	77438	GGAGGCTCAAAGCACGGCTA	289829	122025	GGGTTTCACTGTGTTAGCCA
200656	32852	TGAATTAGCACACCTGAAAC	245243	77439	GGGAGGCTCAAAGCACGGCT	289830	122026	AGGGTTTCACTGTGTTAGCC
200657	32853	CTGAATTAGCACACCTGAAA	245244	77440	AGGGAGGCTCAAAGCACGGC	289831	122027	CAGGGTTTCACTGTGTTAGC
200658	32854	GCTGAATTAGCACACCTGAA	245245	77441	GAGGGAGGCTCAAAGCACGG	289832	122028	ACAGGGTTTCACTGTGTTAG
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200660	32856	ATGCTGAATTAGCACACCTG	245247	77443	AGGAGGGAGGCTCAAAGCAC	289834	122030	AGACAGGGTTTCACTGTGTT
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200662	32858	CCATGCTGAATTAGCACACC	245249	77445	CCAGGAGGGAGGCTCAAAGC	289836	122032	AGAGACAGGGTTTCACTGTG
200663	32859	ACCATGCTGAATTAGCACAC	245250	77446	GCCAGGAGGGAGGCTCAAAG	289837	122033	TAGAGACAGGGTTTCACTGT
200664	32860	AACCATGCTGAATTAGCACA	245251	77447	AGCCAGGAGGGAGGCTCAAA	289838	122034	GTAGAGACAGGGTTTCACTG
200665	32861	GAACCATGCTGAATTAGCAC	245252	77448	CAGCCAGGAGGGAGGCTCAA	289839	122035	AGTAGAGACAGGGTTTCACT
200666	32862	AGAACCATGCTGAATTAGCA	245253	77449	GCAGCCAGGAGGGAGGCTCA	289840	122036	TAGTAGAGACAGGGTTTCAC
200667	32863	TAGAACCATGCTGAATTAGC	245254	77450	TGCAGCCAGGAGGGAGGCTC	289841	122037	TTAGTAGAGACAGGGTTTCA
200668	32864	ATAGAACCATGCTGAATTAG	245255	77451	ATGCAGCCAGGAGGGAGGCT	289842	122038	TTTAGTAGAGACAGGGTTTC
200669	32865	AATAGAACCATGCTGAATTA	245256	77452	GATGCAGCCAGGAGGGAGGC	289843	122039	TTTTAGTAGAGACAGGGTTT
200670	32866	GAATAGAACCATGCTGAATT	245257	77453	AGATGCAGCCAGGAGGGAGG	289844	122040	TTTTTAGTAGAGACAGGGTT
200671	32867	TGAATAGAACCATGCTGAAT	245258	77454	CAGATGCAGCCAGGAGGGAG	289845	122041	ATTTTTAGTAGAGACAGGGT
200672	32868	GTGAATAGAACCATGCTGAA	245259	77455	GCAGATGCAGCCAGGAGGGA	289846	122042	TATTTTTAGTAGAGACAGGG
200673	32869	CGTGAATAGAACCATGCTGA	245260	77456	AGCAGATGCAGCCAGGAGGG	289847	122043	GTATTTTTAGTAGAGACAGG
200674	32870	CCGTGAATAGAACCATGCTG	245261	77457	CAGCAGATGCAGCCAGGAGG	289848	122044	TGTATTTTTAGTAGAGACAG
200675	32871	GCCGTGAATAGAACCATGCT	245262	77458	GCAGCAGATGCAGCCAGGAG	289849	122045	TTGTATTTTTAGTAGAGACA
200676	32872	GGCCGTGAATAGAACCATGC	245263	77459	AGCAGCAGATGCAGCCAGGA	289850	122046	TTTGTATTTTTAGTAGAGAC
200677	32873	TGGCCGTGAATAGAACCATG	245264	77460	GAGCAGCAGATGCAGCCAGG	289851	122047	TTTTGTATTTTTAGTAGAGA
200678	32874	TTGGCCGTGAATAGAACCAT	245265	77461	GGAGCAGCAGATGCAGCCAG	289852	122048	TTTTTGTATTTTTAGTAGAG
200679	32875	TTTGGCCGTGAATAGAACCA	245266	77462	GGGAGCAGCAGATGCAGCCA	289853	122049	TTTTTTGTATTTTTAGTAGA
200680	32876	CTTTGGCCGTGAATAGAACC	245267	77463	GGGGAGCAGCAGATGCAGCC	289854	122050	ATTTTTTGTATTTTTAGTAG
200681	32877	ACTTTGGCCGTGAATAGAAC	245268	77464	GGGGGAGCAGCAGATGCAGC	289855	122051	AATTTTTTGTATTTTTAGTA
200682	32878	GACTTTGGCCGTGAATAGAA	245269	77465	AGGGGGAGCAGCAGATGCAG	289856	122052	TAATTTTTTGTATTTTTAGT
200683	32879	GGACTTTGGCCGTGAATAGA	245270	77466	CAGGGGGAGCAGCAGATGCA	289857	122053	CTAATTTTTTGTATTTTTAG
200684	32880	TGGACTTTGGCCGTGAATAG	245271	77467	CCAGGGGGAGCAGCAGATGC	289858	122054	GCTAATTTTTTGTATTTTTA
200685	32881	GTGGACTTTGGCCGTGAATA	245272	77468	GCCAGGGGGAGCAGCAGATG	289859	122055	GGCTAATTTTTTGTATTTTT
200686	32882	GGTGGACTTTGGCCGTGAAT	245273	77469	AGCCAGGGGGAGCAGCAGAT	289860	122056	CGGCTAATTTTTTGTATTTT
200687	32883	GGGTGGACTTTGGCCGTGAA	245274	77470	CAGCCAGGGGGAGCAGCAGA	289861	122057	CCGGCTAATTTTTTGTATTT
200688	32884	AGGGTGGACTTTGGCCGTGA	245275	77471	TCAGCCAGGGGGAGCAGCAG	289862	122058	CCCGGCTAATTTTTTGTATT
200689	32885	CAGGGTGGACTTTGGCCGTG	245276	77472	CTCAGCCAGGGGGAGCAGCA	289863	122059	GCCCGGCTAATTTTTTGTAT
200690	32886	CCAGGGTGGACTTTGGCCGT	245277	77473	TCTCAGCCAGGGGGAGCAGC	289864	122060	TGCCCGGCTAATTTTTTGTA
200691	32887	CCCAGGGTGGACTTTGGCCG	245278	77474	CTCTCAGCCAGGGGGAGCAG	289865	122061	ATGCCCGGCTAATTTTTTGT
200692	32888	GCCCAGGGTGGACTTTGGCC	245279	77475	TCTCTCAGCCAGGGGGAGCA	289866	122062	CATGCCCGGCTAATTTTTTG
200693	32889	TGCCCAGGGTGGACTTTGGC	245280	77476	ATCTCTCAGCCAGGGGGAGC	289867	122063	CCATGCCCGGCTAATTTTTT
200694	32890	GTGCCCAGGGTGGACTTTGG	245281	77477	CATCTCTCAGCCAGGGGGAG	289868	122064	ACCATGCCCGGCTAATTTTT
200695	32891	GGTGCCCAGGGTGGACTTTG	245282	77478	ACATCTCTCAGCCAGGGGGA	289869	122065	CACCATGCCCGGCTAATTTT
200696	32892	AGGTGCCCAGGGTGGACTTT	245283	77479	CACATCTCTCAGCCAGGGGG	289870	122066	CCACCATGCCCGGCTAATTT
200697	32893	GAGGTGCCCAGGGTGGACTT	245284	77480	GCACATCTCTCAGCCAGGGG	289871	122067	GCCACCATGCCCGGCTAATT
200698	32894	AGAGGTGCCCAGGGTGGACT	245285	77481	AGCACATCTCTCAGCCAGGG	289872	122068	TGCCACCATGCCCGGCTAAT
200699	32895	GAGAGGTGCCCAGGGTGGAC	245286	77482	GAGCACATCTCTCAGCCAGG	289873	122069	CTGCCACCATGCCCGGCTAA
200700	32896	AGAGAGGTGCCCAGGGTGGA	245287	77483	TGAGCACATCTCTCAGCCAG	289874	122070	CCTGCCACCATGCCCGGCTA
200701	32897	CAGAGAGGTGCCCAGGGTGG	245288	77484	GTGAGCACATCTCTCAGCCA	289875	122071	GCCTGCCACCATGCCCGGCT
200702	32898	CCAGAGAGGTGCCCAGGGTG	245289	77485	AGTGAGCACATCTCTCAGCC	289876	122072	TGCCTGCCACCATGCCCGGC
200703	32899	GCCAGAGAGGTGCCCAGGGT	245290	77486	GAGTGAGCACATCTCTCAGC	289877	122073	GTGCCTGCCACCATGCCCGG
200704	32900	TGCCAGAGAGGTGCCCAGGG	245291	77487	GGAGTGAGCACATCTCTCAG	289878	122074	GGTGCCTGCCACCATGCCCG
200705	32901	CTGCCAGAGAGGTGCCCAGG	245292	77488	AGGAGTGAGCACATCTCTCA	289879	122075	AGGTGCCTGCCACCATGCCC
200706	32902	GCTGCCAGAGAGGTGCCCAG	245293	77489	AAGGAGTGAGCACATCTCTC	289880	122076	CAGGTGCCTGCCACCATGCC

200707	32903	TGCTGCCAGAGAGGTGCCCA	245294	77490	GAAGGAGTGAGCACATCTCT	289881	122077	ACAGGTGCCTGCCACCATGC
200708	32904	TTGCTGCCAGAGAGGTGCCC	245295	77491	CGAAGGAGTGAGCACATCTC	289882	122078	TACAGGTGCCTGCCACCATG
200709	32905	ATTGCTGCCAGAGAGGTGCC	245296	77492	CCGAAGGAGTGAGCACATCT	289883	122079	CTACAGGTGCCTGCCACCAT
200710	32906	GATTGCTGCCAGAGAGGTGC	245297	77493	ACCGAAGGAGTGAGCACATC	289884	122080	ACTACAGGTGCCTGCCACCA
200711	32907	AGATTGCTGCCAGAGAGGTG	245298	77494	CACCGAAGGAGTGAGCACAT	289885	122081	GACTACAGGTGCCTGCCACC
200712	32908	AAGATTGCTGCCAGAGAGGT	245299	77495	GCACCGAAGGAGTGAGCACA	289886	122082	GGACTACAGGTGCCTGCCAC
200713	32909	CAAGATTGCTGCCAGAGAGG	245300	77496	AGCACCGAAGGAGTGAGCAC	289887	122083	GGGACTACAGGTGCCTGCCA
200714	32910	CCAAGATTGCTGCCAGAGAG	245301	77497	AAGCACCGAAGGAGTGAGCA	289888	122084	TGGGACTACAGGTGCCTGCC
200715	32911	CCCAAGATTGCTGCCAGAGA	245302	77498	AAAGCACCGAAGGAGTGAGC	289889	122085	TTGGGACTACAGGTGCCTGC
200716	32912	ACCCAAGATTGCTGCCAGAG	245303	77499	CAAAGCACCGAAGGAGTGAG	289890	122086	GTTGGGACTACAGGTGCCTG
200717	32913	CACCCAAGATTGCTGCCAGA	245304	77500	GCAAAGCACCGAAGGAGTGA	289891	122087	AGTTGGGACTACAGGTGCCT
200718	32914	TCACCCAAGATTGCTGCCAG	245305	77501	TGCAAAGCACCGAAGGAGTG	289892	122088	TAGTTGGGACTACAGGTGCC
200719	32915	GTCACCCAAGATTGCTGCCA	245306	77502	CTGCAAAGCACCGAAGGAGT	289893	122089	GTAGTTGGGACTACAGGTGC
200720	32916	AGTCACCCAAGATTGCTGCC	245307	77503	CCTGCAAAGCACCGAAGGAG	289894	122090	AGTAGTTGGGACTACAGGTG
200721	32917	GAGTCACCCAAGATTGCTGC	245308	77504	TCCTGCAAAGCACCGAAGGA	289895	122091	AAGTAGTTGGGACTACAGGT
200722	32918	AGAGTCACCCAAGATTGCTG	245309	77505	GTCCTGCAAAGCACCGAAGG	289896	122092	CAAGTAGTTGGGACTACAGG
200723	32919	TAGAGTCACCCAAGATTGCT	245310	77506	TGTCCTGCAAAGCACCGAAG	289897	122093	CCAAGTAGTTGGGACTACAG
200724	32920	GTAGAGTCACCCAAGATTGC	245311	77507	CTGTCCTGCAAAGCACCGAA	289898	122094	CCCAAGTAGTTGGGACTACA
200725	32921	AGTAGAGTCACCCAAGATTG	245312	77508	GCTGTCCTGCAAAGCACCGA	289899	122095	TCCCAAGTAGTTGGGACTAC
200726	32922	TAGTAGAGTCACCCAAGATT	245313	77509	CGCTGTCCTGCAAAGCACCG	289900	122096	CTCCCAAGTAGTTGGGACTA
200727	32923	TTAGTAGAGTCACCCAAGAT	245314	77510	ACGCTGTCCTGCAAAGCACC	289901	122097	CCTCCCAAGTAGTTGGGACT
200728	32924	CTTAGTAGAGTCACCCAAGA	245315	77511	CACGCTGTCCTGCAAAGCAC	289902	122098	GCCTCCCAAGTAGTTGGGAC
200729	32925	CCTTAGTAGAGTCACCCAAG	245316	77512	CCACGCTGTCCTGCAAAGCA	289903	122099	AGCCTCCCAAGTAGTTGGGA
200730	32926	GCCTTAGTAGAGTCACCCAA	245317	77513	ACCACGCTGTCCTGCAAAGC	289904	122100	CAGCCTCCCAAGTAGTTGGG
200731	32927	GGCCTTAGTAGAGTCACCCA	245318	77514	CACCACGCTGTCCTGCAAAG	289905	122101	TCAGCCTCCCAAGTAGTTGG
200732	32928	TGGCCTTAGTAGAGTCACCC	245319	77515	CCACCACGCTGTCCTGCAAA	289906	122102	CTCAGCCTCCCAAGTAGTTG
200733	32929	CTGGCCTTAGTAGAGTCACC	245320	77516	CCCACCACGCTGTCCTGCAA	289907	122103	CCTCAGCCTCCCAAGTAGTT
200734	32930	CCTGGCCTTAGTAGAGTCAC	245321	77517	TCCCACCACGCTGTCCTGCA	289908	122104	GCCTCAGCCTCCCAAGTAGT
200735	32931	GCCTGGCCTTAGTAGAGTCA	245322	77518	CTCCCACCACGCTGTCCTGC	289909	122105	TGCCTCAGCCTCCCAAGTAG
200736	32932	GGCCTGGCCTTAGTAGAGTC	245323	77519	GCTCCCACCACGCTGTCCTG	289910	122106	CTGCCTCAGCCTCCCAAGTA
200737	32933	AGGCCTGGCCTTAGTAGAGT	245324	77520	AGCTCCCACCACGCTGTCCT	289911	122107	CCTGCCTCAGCCTCCCAAGT
200738	32934	GAGGCCTGGCCTTAGTAGAG	245325	77521	CAGCTCCCACCACGCTGTCC	289912	122108	TCCTGCCTCAGCCTCCCAAG
200739	32935	GGAGGCCTGGCCTTAGTAGA	245326	77522	TCAGCTCCCACCACGCTGTC	289913	122109	CTCCTGCCTCAGCCTCCCAA
200740	32936	TGGAGGCCTGGCCTTAGTAG	245327	77523	CTCAGCTCCCACCACGCTGT	289914	122110	TCTCCTGCCTCAGCCTCCCA
200741	32937	ATGGAGGCCTGGCCTTAGTA	245328	77524	GCTCAGCTCCCACCACGCTG	289915	122111	TTCTCCTGCCTCAGCCTCCC
200742	32938	CATGGAGGCCTGGCCTTAGT	245329	77525	GGCTCAGCTCCCACCACGCT	289916	122112	ATTCTCCTGCCTCAGCCTCC
200743	32939	TCATGGAGGCCTGGCCTTAG	245330	77526	AGGCTCAGCTCCCACCACGC	289917	122113	CATTCTCCTGCCTCAGCCTC
200744	32940	GTCATGGAGGCCTGGCCTTA	245331	77527	AAGGCTCAGCTCCCACCACG	289918	122114	CCATTCTCCTGCCTCAGCCT
200745	32941	GGTCATGGAGGCCTGGCCTT	245332	77528	CAAGGCTCAGCTCCCACCAC	289919	122115	GCCATTCTCCTGCCTCAGCC
200746	32942	GGGTCATGGAGGCCTGGCCT	245333	77529	GCAAGGCTCAGCTCCCACCA	289920	122116	TGCCATTCTCCTGCCTCAGC
200747	32943	AGGGTCATGGAGGCCTGGCC	245334	77530	CGCAAGGCTCAGCTCCCACC	289921	122117	ATGCCATTCTCCTGCCTCAG
200748	32944	TAGGGTCATGGAGGCCTGGC	245335	77531	ACGCAAGGCTCAGCTCCCAC	289922	122118	CATGCCATTCTCCTGCCTCA
200749	32945	ATAGGGTCATGGAGGCCTGG	245336	77532	GACGCAAGGCTCAGCTCCCA	289923	122119	TCATGCCATTCTCCTGCCTC
200750	32946	CATAGGGTCATGGAGGCCTG	245337	77533	CGACGCAAGGCTCAGCTCCC	289924	122120	TTCATGCCATTCTCCTGCCT
200751	32947	ACATAGGGTCATGGAGGCCT	245338	77534	TCGACGCAAGGCTCAGCTCC	289925	122121	GTTCATGCCATTCTCCTGCC
200752	32948	GACATAGGGTCATGGAGGCC	245339	77535	ATCGACGCAAGGCTCAGCTC	289926	122122	GGTTCATGCCATTCTCCTGC
200753	32949	AGACATAGGGTCATGGAGGC	245340	77536	CATCGACGCAAGGCTCAGCT	289927	122123	AGGTTCATGCCATTCTCCTG
200754	32950	CAGACATAGGGTCATGGAGG	245341	77537	GCATCGACGCAAGGCTCAGC	289928	122124	CAGGTTCATGCCATTCTCCT
200755	32951	CCAGACATAGGGTCATGGAG	245342	77538	GGCATCGACGCAAGGCTCAG	289929	122125	CCAGGTTCATGCCATTCTCC
200756	32952	TCCAGACATAGGGTCATGGA	245343	77539	AGGCATCGACGCAAGGCTCA	289930	122126	CCCAGGTTCATGCCATTCTC
200757	32953	ATCCAGACATAGGGTCATGG	245344	77540	AAGGCATCGACGCAAGGCTC	289931	122127	TCCCAGGTTCATGCCATTCT
200758	32954	GATCCAGACATAGGGTCATG	245345	77541	CAAGGCATCGACGCAAGGCT	289932	122128	CTCCCAGGTTCATGCCATTC
200759	32955	GGATCCAGACATAGGGTCAT	245346	77542	GCAAGGCATCGACGCAAGGC	289933	122129	CCTCCCAGGTTCATGCCATT
200760	32956	GGGATCCAGACATAGGGTCA	245347	77543	AGCAAGGCATCGACGCAAGG	289934	122130	GCCTCCCAGGTTCATGCCAT
200761	32957	TGGGATCCAGACATAGGGTC	245348	77544	AAGCAAGGCATCGACGCAAG	289935	122131	CGCCTCCCAGGTTCATGCCA
200762	32958	ATGGGATCCAGACATAGGGT	245349	77545	CAAGCAAGGCATCGACGCAA	289936	122132	CCGCCTCCCAGGTTCATGCC
200763	32959	TATGGGATCCAGACATAGGG	245350	77546	GCAAGCAAGGCATCGACGCA	289937	122133	TCCGCCTCCCAGGTTCATGC
200764	32960	ATATGGGATCCAGACATAGG	245351	77547	AGCAAGCAAGGCATCGACGC	289938	122134	CTCCGCCTCCCAGGTTCATG
200765	32961	GATATGGGATCCAGACATAG	245352	77548	CAGCAAGCAAGGCATCGACG	289939	122135	GCTCCGCCTCCCAGGTTCAT
200766	32962	AGATATGGGATCCAGACATA	245353	77549	CCAGCAAGCAAGGCATCGAC	289940	122136	AGCTCCGCCTCCCAGGTTCA
200767	32963	GAGATATGGGATCCAGACAT	245354	77550	ACCAGCAAGCAAGGCATCGA	289941	122137	AAGCTCCGCCTCCCAGGTTC
200768	32964	GGAGATATGGGATCCAGACA	245355	77551	CACCAGCAAGCAAGGCATCG	289942	122138	CAAGCTCCGCCTCCCAGGTT
200769	32965	TGGAGATATGGGATCCAGAC	245356	77552	GCACCAGCAAGCAAGGCATC	289943	122139	GCAAGCTCCGCCTCCCAGGT
200770	32966	GTGGAGATATGGGATCCAGA	245357	77553	AGCACCAGCAAGCAAGGCAT	289944	122140	TGCAAGCTCCGCCTCCCAGG
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200772	32968	AGGTGGAGATATGGGATCCA	245359	77555	TCAGCACCAGCAAGCAAGGC	289946	122142	ACTGCAAGCTCCGCCTCCCA
200773	32969	GAGGTGGAGATATGGGATCC	245360	77556	CTCAGCACCAGCAAGCAAGG	289947	122143	CACTGCAAGCTCCGCCTCCC
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200775	32971	GAGAGGTGGAGATATGGGAT	245362	77558	CACTCAGCACCAGCAAGCAA	289949	122145	CTCACTGCAAGCTCCGCCTC
200776	32972	GGAGAGGTGGAGATATGGGA	245363	77559	ACACTCAGCACCAGCAAGCA	289950	122146	GCTCACTGCAAGCTCCGCCT
200777	32973	GGGAGAGGTGGAGATATGGG	245364	77560	CACACTCAGCACCAGCAAGC	289951	122147	GGCTCACTGCAAGCTCCGCC
200778	32974	TGGGAGAGGTGGAGATATGG	245365	77561	CCACACTCAGCACCAGCAAG	289952	122148	TGGCTCACTGCAAGCTCCGC

200779	32975	GTGGGAGAGGTGGAGATATG	245366	77562	CCCACACTCAGCACCAGCAA	289953	122149	TTGGCTCACTGCAAGCTCCG
200780	32976	AGTGGGAGAGGTGGAGATAT	245367	77563	GCCCACACTCAGCACCAGCA	289954	122150	CTTGGCTCACTGCAAGCTCC
200781	32977	CAGTGGGAGAGGTGGAGATA	245368	77564	TGCCCACACTCAGCACCAGC	289955	122151	TCTTGGCTCACTGCAAGCTC
200782	32978	ACAGTGGGAGAGGTGGAGAT	245369	77565	GTGCCCACACTCAGCACCAG	289956	122152	ATCTTGGCTCACTGCAAGCT
200783	32979	GACAGTGGGAGAGGTGGAGA	245370	77566	GGTGCCCACACTCAGCACCA	289957	122153	GATCTTGGCTCACTGCAAGC
200784	32980	AGACAGTGGGAGAGGTGGAG	245371	77567	AGGTGCCCACACTCAGCACC	289958	122154	CGATCTTGGCTCACTGCAAG
200785	32981	GAGACAGTGGGAGAGGTGGA	245372	77568	AAGGTGCCCACACTCAGCAC	289959	122155	GCGATCTTGGCTCACTGCAA
200786	32982	TGAGACAGTGGGAGAGGTGG	245373	77569	GAAGGTGCCCACACTCAGCA	289960	122156	CGCGATCTTGGCTCACTGCA
200787	32983	CTGAGACAGTGGGAGAGGTG	245374	77570	TGAAGGTGCCCACACTCAGC	289961	122157	GCGCGATCTTGGCTCACTGC
200788	32984	CCTGAGACAGTGGGAGAGGT	245375	77571	ATGAAGGTGCCCACACTCAG	289962	122158	GGCGCGATCTTGGCTCACTG
200789	32985	TCCTGAGACAGTGGGAGAGG	245376	77572	GATGAAGGTGCCCACACTCA	289963	122159	TGGCGCGATCTTGGCTCACT
200790	32986	TTCCTGAGACAGTGGGAGAG	245377	77573	GGATGAAGGTGCCCACACTC	289964	122160	GTGGCGCGATCTTGGCTCAC
200791	32987	GTTCCTGAGACAGTGGGAGA	245378	77574	GGGATGAAGGTGCCCACACT	289965	122161	AGTGGCGCGATCTTGGCTCA
200792	32988	CGTTCCTGAGACAGTGGGAG	245379	77575	CGGGATGAAGGTGCCCACAC	289966	122162	CAGTGGCGCGATCTTGGCTC
200793	32989	CCGTTCCTGAGACAGTGGGA	245380	77576	ACGGGATGAAGGTGCCCACA	289967	122163	GCAGTGGCGCGATCTTGGCT
200794	32990	ACCGTTCCTGAGACAGTGGG	245381	77577	CACGGGATGAAGGTGCCCAC	289968	122164	TGCAGTGGCGCGATCTTGGC
200795	32991	CACCGTTCCTGAGACAGTGG	245382	77578	ACACGGGATGAAGGTGCCCA	289969	122165	ATGCAGTGGCGCGATCTTGG
200796	32992	GCACCGTTCCTGAGACAGTG	245383	77579	CACACGGGATGAAGGTGCCC	289970	122166	TATGCAGTGGCGCGATCTTG
200797	32993	AGCACCGTTCCTGAGACAGT	245384	77580	ACACACGGGATGAAGGTGCC	289971	122167	GTATGCAGTGGCGCGATCTT
200798	32994	AAGCACCGTTCCTGAGACAG	245385	77581	CACACACGGGATGAAGGTGC	289972	122168	GGTATGCAGTGGCGCGATCT
200799	32995	TAAGCACCGTTCCTGAGACA	245386	77582	GCACACACGGGATGAAGGTG	289973	122169	TGGTATGCAGTGGCGCGATC
200800	32996	CTAAGCACCGTTCCTGAGAC	245387	77583	AGCACACACGGGATGAAGGT	289974	122170	CTGGTATGCAGTGGCGCGAT
200801	32997	GCTAAGCACCGTTCCTGAGA	245388	77584	GAGCACACACGGGATGAAGG	289975	122171	GCTGGTATGCAGTGGCGCGA
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200803	32999	AAGCTAAGCACCGTTCCTGA	245390	77586	CAGAGCACACACGGGATGAA	289977	122173	AGGCTGGTATGCAGTGGCGC
200804	33000	AAAGCTAAGCACCGTTCCTG	245391	77587	CCAGAGCACACACGGGATGA	289978	122174	TAGGCTGGTATGCAGTGGCG
200805	33001	AAAAGCTAAGCACCGTTCCT	245392	77588	TCCAGAGCACACACGGGATG	289979	122175	CTAGGCTGGTATGCAGTGGC
200806	33002	AAAAAGCTAAGCACCGTTCC	245393	77589	CTCCAGAGCACACACGGGAT	289980	122176	CCTAGGCTGGTATGCAGTGG
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200808	33004	AGAAAAAGCTAAGCACCGTT	245395	77591	GCCTCCAGAGCACACACGGG	289982	122178	CACCTAGGCTGGTATGCAGT
200809	33005	AAGAAAAAGCTAAGCACCGT	245396	77592	TGCCTCCAGAGCACACACGG	289983	122179	TCACCTAGGCTGGTATGCAG
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200811	33007	AAAAGAAAAAGCTAAGCACC	245398	77594	GCTGCCTCCAGAGCACACAC	289985	122181	TGTCACCTAGGCTGGTATGC
200812	33008	GAAAAGAAAAAGCTAAGCAC	245399	77595	GGCTGCCTCCAGAGCACACA	289986	122182	CTGTCACCTAGGCTGGTATG
200813	33009	GGAAAAGAAAAAGCTAAGCA	245400	77596	TGGCTGCCTCCAGAGCACAC	289987	122183	TCTGTCACCTAGGCTGGTAT
200814	33010	GGGAAAAGAAAAAGCTAAGC	245401	77597	GTGGCTGCCTCCAGAGCACA	289988	122184	CTCTGTCACCTAGGCTGGTA
200815	33011	AGGGAAAAGAAAAAGCTAAG	245402	77598	GGTGGCTGCCTCCAGAGCAC	289989	122185	ACTCTGTCACCTAGGCTGGT
200816	33012	GAGGGAAAAGAAAAAGCTAA	245403	77599	GGGTGGCTGCCTCCAGAGCA	289990	122186	CACTCTGTCACCTAGGCTGG
200817	33013	AGAGGGAAAAGAAAAAGCTA	245404	77600	AGGGTGGCTGCCTCCAGAGC	289991	122187	TCACTCTGTCACCTAGGCTG
200818	33014	GAGAGGGAAAAGAAAAAGCT	245405	77601	AAGGGTGGCTGCCTCCAGAG	289992	122188	CTCACTCTGTCACCTAGGCT
200819	33015	GGAGAGGGAAAAGAAAAAGC	245406	77602	CAAGGGTGGCTGCCTCCAGA	289993	122189	TCTCACTCTGTCACCTAGGC
200820	33016	AGGAGAGGGAAAAGAAAAAG	245407	77603	CCAAGGGTGGCTGCCTCCAG	289994	122190	GTCTCACTCTGTCACCTAGG
200821	33017	CAGGAGAGGGAAAAGAAAAA	245408	77604	TCCAAGGGTGGCTGCCTCCA	289995	122191	AGTCTCACTCTGTCACCTAG
200822	33018	ACAGGAGAGGGAAAAGAAAA	245409	77605	GTCCAAGGGTGGCTGCCTCC	289996	122192	GAGTCTCACTCTGTCACCTA
200823	33019	GACAGGAGAGGGAAAAGAAA	245410	77606	TGTCCAAGGGTGGCTGCCTC	289997	122193	TGAGTCTCACTCTGTCACCT
200824	33020	AGACAGGAGAGGGAAAAGAA	245411	77607	CTGTCCAAGGGTGGCTGCCT	289998	122194	CTGAGTCTCACTCTGTCACC
200825	33021	AAGACAGGAGAGGGAAAAGA	245412	77608	ACTGTCCAAGGGTGGCTGCC	289999	122195	GCTGAGTCTCACTCTGTCAC
200826	33022	GAAGACAGGAGAGGGAAAAG	245413	77609	GACTGTCCAAGGGTGGCTGC	290000	122196	TGCTGAGTCTCACTCTGTCA
200827	33023	AGAAGACAGGAGAGGGAAAA	245414	77610	GGACTGTCCAAGGGTGGCTG	290001	122197	TTGCTGAGTCTCACTCTGTC
200828	33024	AAGAAGACAGGAGAGGGAAA	245415	77611	GGGACTGTCCAAGGGTGGCT	290002	122198	TTTGCTGAGTCTCACTCTGT
200829	33025	AAAGAAGACAGGAGAGGGAA	245416	77612	CGGGACTGTCCAAGGGTGGC	290003	122199	TTTTGCTGAGTCTCACTCTG
200830	33026	CAAAGAAGACAGGAGAGGGA	245417	77613	GCGGGACTGTCCAAGGGTGG	290004	122200	TTTTTGCTGAGTCTCACTCT
200831	33027	GCAAAGAAGACAGGAGAGGG	245418	77614	CGCGGGACTGTCCAAGGGTG	290005	122201	TTTTTTGCTGAGTCTCACTC
200832	33028	GGCAAAGAAGACAGGAGAGG	245419	77615	GCGCGGGACTGTCCAAGGGT	290006	122202	TTTTTTGCTGAGTCTCACT
200833	33029	TGGCAAAGAAGACAGGAGAG	245420	77616	TGCGCGGGACTGTCCAAGGG	290007	122203	CTTTTTTTGCTGAGTCTCAC
200834	33030	CTGGCAAAGAAGACAGGAGA	245421	77617	GTGCGCGGGACTGTCCAAGG	290008	122204	TCTTTTTTTGCTGAGTCTCA
200835	33031	GCTGGCAAAGAAGACAGGAG	245422	77618	TGTGCGCGGGACTGTCCAAG	290009	122205	TTCTTTTTTTGCTGAGTCTC
200836	33032	TGCTGGCAAAGAAGACAGGA	245423	77619	CTGTGCGCGGGACTGTCCAA	290010	122206	TTTCTTTTTTTGCTGAGTCT
200837	33033	ATGCTGGCAAAGAAGACAGG	245424	77620	GCTGTGCGCGGGACTGTCCA	290011	122207	CTTTCTTTTTTTGCTGAGTC
200838	33034	CATGCTGGCAAAGAAGACAG	245425	77621	AGCTGTGCGCGGGACTGTCC	290012	122208	TCTTTCTTTTTTTGCTGAGT
200839	33035	ACATGCTGGCAAAGAAGACA	245426	77622	GAGCTGTGCGCGGGACTGTC	290013	122209	TTCTTTCTTTTTTTGCTGAG
200840	33036	TACATGCTGGCAAAGAAGAC	245427	77623	GGAGCTGTGCGCGGGACTGT	290014	122210	TTTCTTTCTTTTTTTGCTGA
200841	33037	CTACATGCTGGCAAAGAAGA	245428	77624	TGGAGCTGTGCGCGGGACTG	290015	122211	CTTTCTTTCTTTTTTTGCTG
200842	33038	TCTACATGCTGGCAAAGAAG	245429	77625	GTGGAGCTGTGCGCGGGACT	290016	122212	TCTTTCTTTCTTTTTTTGCT
200843	33039	TTCTACATGCTGGCAAAGAA	245430	77626	TGTGGAGCTGTGCGCGGGAC	290017	122213	TTCTTTCTTTCTTTTTTTGC
200844	33040	TTTCTACATGCTGGCAAAGA	245431	77627	TTGTGGAGCTGTGCGCGGGA	290018	122214	TTTCTTTCTTTCTTTTTTTG
200845	33041	CTTTCTACATGCTGGCAAAG	245432	77628	TTTGTGGAGCTGTGCGCGGG	290019	122215	CTTTCTTTCTTTCTTTTTTT
200846	33042	ACTTTCTACATGCTGGCAAA	245433	77629	CTTTGTGGAGCTGTGCGCGG	290020	122216	TCTTTCTTTCTTTCTTTTTT
200847	33043	AACTTTCTACATGCTGGCAA	245434	77630	GCTTTGTGGAGCTGTGCGCG	290021	122217	TTCTTTCTTTCTTTCTTTTT
200848	33044	AAACTTTCTACATGCTGGCA	245435	77631	GGCTTTGTGGAGCTGTGCGC	290022	122218	TTTCTTTCTTTCTTTCTTTT
200849	33045	TAAACTTTCTACATGCTGGC	245436	77632	GGGCTTTGTGGAGCTGTGCG	290023	122219	CTTTCTTTCTTTCTTTCTTT
200850	33046	TTAAACTTTCTACATGCTGG	245437	77633	GGGGCTTTGTGGAGCTGTGC	290024	122220	TCTTTCTTTCTTTCTTTCTT

200851	33047	TTTAAACTTTCTACATGCTG	245438	77634	CGGGGCTTTGTGGAGCTGTG	290025	122221	TTCTTTCTTTCTTTCTTTCT
200852	33048	ATTTAAACTTTCTACATGCT	245439	77635	GCGGGGCTTTGTGGAGCTGT	290026	122222	TTTCTTTCTTTCTTTCTTTC
200853	33049	TATTTAAACTTTCTACATGC	245440	77636	AGCGGGGCTTTGTGGAGCTG	290027	122223	ATTTCTTTCTTTCTTTCTTT
200854	33050	TTATTTAAACTTTCTACATG	245441	77637	GAGCGGGGCTTTGTGGAGCT	290028	122224	GATTTCTTTCTTTCTTTCTT
200855	33051	ATTATTTAAACTTTCTACAT	245442	77638	GGAGCGGGGCTTTGTGGAGC	290029	122225	TGATTTCTTTCTTTCTTTCT
200856	33052	AATTATTTAAACTTTCTACA	245443	77639	TGGAGCGGGGCTTTGTGGAG	290030	122226	CTGATTTCTTTCTTTCTTTC
200857	33053	GAATTATTTAAACTTTCTAC	245444	77640	ATGGAGCGGGGCTTTGTGGA	290031	122227	ACTGATTTCTTTCTTTCTTT
200858	33054	GGAATTATTTAAACTTTCTA	245445	77641	TATGGAGCGGGGCTTTGTGG	290032	122228	CACTGATTTCTTTCTTTCTT
200859	33055	GGGAATTATTTAAACTTTCT	245446	77642	GTATGGAGCGGGGCTTTGTG	290033	122229	GCACTGATTTCTTTCTTTCT
200860	33056	GGGGAATTATTTAAACTTTC	245447	77643	CGTATGGAGCGGGGCTTTGT	290034	122230	AGCACTGATTTCTTTCTTTC
200861	33057	AGGGGAATTATTTAAACTTT	245448	77644	TCGTATGGAGCGGGGCTTTG	290035	122231	CAGCACTGATTTCTTTCTTT
200862	33058	GAGGGGAATTATTTAAACTT	245449	77645	ATCGTATGGAGCGGGGCTTT	290036	122232	ACAGCACTGATTTCTTTCTT
200863	33059	AGAGGGGAATTATTTAAACT	245450	77646	AATCGTATGGAGCGGGGCTT	290037	122233	GACAGCACTGATTTCTTTCT
200864	33060	AAGAGGGGAATTATTTAAAC	245451	77647	CAATCGTATGGAGCGGGGCT	290038	122234	AGACAGCACTGATTTCTTTC
200865	33061	AAAGAGGGGAATTATTTAAA	245452	77648	ACAATCGTATGGAGCGGGGC	290039	122235	TAGACAGCACTGATTTCTTT
200866	33062	TAAAGAGGGGAATTATTTAA	245453	77649	GACAATCGTATGGAGCGGGG	290040	122236	ATAGACAGCACTGATTTCTT
200867	33063	GTAAAGAGGGGAATTATTTA	245454	77650	GGACAATCGTATGGAGCGGG	290041	122237	TATAGACAGCACTGATTTCT
200868	33064	TGTAAAGAGGGGAATTATTT	245455	77651	AGGACAATCGTATGGAGCGG	290042	122238	GTATAGACAGCACTGATTTC
200869	33065	TTGTAAAGAGGGGAATTATT	245456	77652	GAGGACAATCGTATGGAGCG	290043	122239	AGTATAGACAGCACTGATTT
200870	33066	GTTGTAAAGAGGGGAATTAT	245457	77653	GGAGGACAATCGTATGGAGC	290044	122240	AAGTATAGACAGCACTGATT
200871	33067	TGTTGTAAAGAGGGGAATTA	245458	77654	GGGAGGACAATCGTATGGAG	290045	122241	GAAGTATAGACAGCACTGAT
200872	33068	TTGTTGTAAAGAGGGGAATT	245459	77655	TGGGAGGACAATCGTATGGA	290046	122242	AGAAGTATAGACAGCACTGA
200873	33069	TTTGTTGTAAAGAGGGGAAT	245460	77656	GTGGGAGGACAATCGTATGG	290047	122243	AAGAAGTATAGACAGCACTG
200874	33070	TTTTGTTGTAAAGAGGGGAA	245461	77657	TGTGGGAGGACAATCGTATG	290048	122244	AAAGAAGTATAGACAGCACT
200875	33071	GTTTTGTTGTAAAGAGGGGA	245462	77658	GTGTGGGAGGACAATCGTAT	290049	122245	GAAAGAAGTATAGACAGCAC
200876	33072	TGTTTTGTTGTAAAGAGGGG	245463	77659	GGTGTGGGAGGACAATCGTA	290050	122246	AGAAAGAAGTATAGACAGCA
200877	33073	TTGTTTTGTTGTAAAGAGGG	245464	77660	GGGTGTGGGAGGACAATCGT	290051	122247	CAGAAAGAAGTATAGACAGC
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200879	33075	TTTTGTTTTGTTGTAAAGAG	245466	77662	GGGGGTGTGGGAGGACAATC	290053	122249	TGCAGAAAGAAGTATAGACA
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200881	33077	TGTTTTGTTTTGTTGTAAAG	245468	77664	AAGGGGGTGTGGGAGGACAA	290055	122251	ACTGCAGAAAGAAGTATAGA
200882	33078	ATGTTTTGTTTTGTTGTAAA	245469	77665	GAAGGGGGTGTGGGAGGACA	290056	122252	CACTGCAGAAAGAAGTATAG
200883	33079	TATGTTTTGTTTTGTTGTAA	245470	77666	TGAAGGGGGTGTGGGAGGAC	290057	122253	TCACTGCAGAAAGAAGTATA
200884	33080	GTATGTTTTGTTTTGTTGTA	245471	77667	TTGAAGGGGGTGTGGGAGGA	290058	122254	ATCACTGCAGAAAGAAGTAT
200885	33081	GGTATGTTTTGTTTTGTTGT	245472	77668	TTTGAAGGGGGTGTGGGAGG	290059	122255	CATCACTGCAGAAAGAAGTA
200886	33082	GGGTATGTTTTGTTTTGTTG	245473	77669	TTTTGAAGGGGGTGTGGGAG	290060	122256	CCATCACTGCAGAAAGAAGT
200887	33083	GGGGTATGTTTTGTTTTGTT	245474	77670	CTTTTGAAGGGGGTGTGGGA	290061	122257	TCCATCACTGCAGAAAGAAG
200888	33084	GGGGGTATGTTTTGTTTTGT	245475	77671	GCTTTTGAAGGGGGTGTGGG	290062	122258	TTCCATCACTGCAGAAAGAA
200889	33085	AGGGGGTATGTTTTGTTTTG	245476	77672	GGCTTTTGAAGGGGGTGTGG	290063	122259	TTTCCATCACTGCAGAAAGA
200890	33086	AAGGGGGTATGTTTTGTTTT	245477	77673	GGGCTTTTGAAGGGGGTGTG	290064	122260	ATTTCCATCACTGCAGAAAG
200891	33087	GAAGGGGGTATGTTTTGTTT	245478	77674	GGGGCTTTTGAAGGGGGTGT	290065	122261	TATTTCCATCACTGCAGAAA
200892	33088	TGAAGGGGGTATGTTTTGTT	245479	77675	GGGGGCTTTTGAAGGGGGTG	290066	122262	ATATTTCCATCACTGCAGAA
200893	33089	CTGAAGGGGGTATGTTTTGT	245480	77676	AGGGGGCTTTTGAAGGGGGT	290067	122263	AATATTTCCATCACTGCAGA
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200898	33094	GTTGACTGAAGGGGGTATGT	245485	77681	AGAGGAGGGGGCTTTTGAAG	290072	122268	TACAGAATATTTCCATCACT
200899	33095	GGTTGACTGAAGGGGGTATG	245486	77682	GAGAGGAGGGGGCTTTTGAA	290073	122269	ATACAGAATATTTCCATCAC
200900	33096	TGGTTGACTGAAGGGGGTAT	245487	77683	AGAGAGGAGGGGGCTTTTGA	290074	122270	GATACAGAATATTTCCATCA
200901	33097	GTGGTTGACTGAAGGGGGTA	245488	77684	GAGAGAGGAGGGGGCTTTTG	290075	122271	AGATACAGAATATTTCCATC
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200903	33099	GGGTGGTTGACTGAAGGGGG	245490	77686	AAGAGAGAGGAGGGGGCTTT	290077	122273	ACAGATACAGAATATTTCCA
200904	33100	AGGGTGGTTGACTGAAGGGG	245491	77687	AAAGAGAGAGGAGGGGGCTT	290078	122274	CACAGATACAGAATATTTCC
200905	33101	TAGGGTGGTTGACTGAAGGG	245492	77688	GAAAGAGAGAGGAGGGGGCT	290079	122275	GCACAGATACAGAATATTTC
200906	33102	CTAGGGTGGTTGACTGAAGG	245493	77689	AGAAAGAGAGAGGAGGGGGC	290080	122276	AGCACAGATACAGAATATTT
200907	33103	GCTAGGGTGGTTGACTGAAG	245494	77690	AAGAAAGAGAGAGGAGGGGG	290081	122277	CAGCACAGATACAGAATATT
200908	33104	AGCTAGGGTGGTTGACTGAA	245495	77691	GAAGAAAGAGAGAGGAGGGG	290082	122278	ACAGCACAGATACAGAATAT
200909	33105	GAGCTAGGGTGGTTGACTGA	245496	77692	TGAAGAAAGAGAGAGGAGGG	290083	122279	GACAGCACAGATACAGAATA
200910	33106	AGAGCTAGGGTGGTTGACTG	245497	77693	CTGAAGAAAGAGAGAGGAGG	290084	122280	GGACAGCACAGATACAGAAT
200911	33107	GAGAGCTAGGGTGGTTGACT	245498	77694	CCTGAAGAAAGAGAGAGGAG	290085	122281	TGGACAGCACAGATACAGAA
200912	33108	AGAGAGCTAGGGTGGTTGAC	245499	77695	CCCTGAAGAAAGAGAGAGGA	290086	122282	CTGGACAGCACAGATACAGA
200913	33109	AAGAGAGCTAGGGTGGTTGA	245500	77696	CCCCTGAAGAAAGAGAGAGG	290087	122283	ACTGGACAGCACAGATACAG
200914	33110	GAAGAGAGCTAGGGTGGTTG	245501	77697	GCCCCTGAAGAAAGAGAGAG	290088	122284	TACTGGACAGCACAGATACA
200915	33111	AGAAGAGAGCTAGGGTGGTT	245502	77698	GGCCCCTGAAGAAAGAGAGA	290089	122285	ATACTGGACAGCACAGATAC
200916	33112	GAGAAGAGAGCTAGGGTGGT	245503	77699	TGGCCCCTGAAGAAAGAGAG	290090	122286	TATACTGGACAGCACAGATA
200917	33113	GGAGAAGAGAGCTAGGGTGG	245504	77700	CTGGCCCCTGAAGAAAGAGA	290091	122287	CTATACTGGACAGCACAGAT
200918	33114	AGGAGAAGAGAGCTAGGGTG	245505	77701	ACTGGCCCCTGAAGAAAGAG	290092	122288	ACTATACTGGACAGCACAGA
200919	33115	AAGGAGAAGAGAGCTAGGGT	245506	77702	TACTGGCCCCTGAAGAAAGA	290093	122289	TACTATACTGGACAGCACAG
200920	33116	AAAGGAGAAGAGAGCTAGGG	245507	77703	CTACTGGCCCCTGAAGAAAG	290094	122290	CTACTATACTGGACAGCACA
200921	33117	AAAAGGAGAAGAGAGCTAGG	245508	77704	CCTACTGGCCCCTGAAGAAA	290095	122291	GCTACTATACTGGACAGCAC
200922	33118	GAAAAGGAGAAGAGAGCTAG	245509	77705	ACCTACTGGCCCCTGAAGAA	290096	122292	GGCTACTATACTGGACAGCA

200923	33119	GGAAAAGGAGAAGAGAGCTA	245510	77706	GACCTACTGGCCCCTGAAGA	290097	122293	TGGCTACTATACTGGACAGC
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200925	33121	TGGGAAAAGGAGAAGAGAGC	245512	77708	GGGACCTACTGGCCCCTGAA	290099	122295	AGTGGCTACTATACTGGACA
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200929	33125	TGGCTGGGAAAAGGAGAAGA	245516	77712	CTCTGGGACCTACTGGCCCC	290103	122299	AGCTAGTGGCTACTATACTG
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200931	33127	TCTGGCTGGGAAAAGGAGAA	245518	77714	TGCTCTGGGACCTACTGGCC	290105	122301	GTAGCTAGTGGCTACTATAC
200932	33128	ATCTGGCTGGGAAAAGGAGA	245519	77715	CTGCTCTGGGACCTACTGGC	290106	122302	TGTAGCTAGTGGCTACTATA
200933	33129	AATCTGGCTGGGAAAAGGAG	245520	77716	GCTGCTCTGGGACCTACTGG	290107	122303	ATGTAGCTAGTGGCTACTAT
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200935	33131	AAAATCTGGCTGGGAAAAGG	245522	77718	TGGCTGCTCTGGGACCTACT	290109	122305	ACATGTAGCTAGTGGCTACT
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200948	33144	GGATGCTTTTAAAAAAATCT	245535	77731	TCCCTCAGCCAAATGGCTGC	290122	122318	TGTTTCAAGTGCCACATGTA
200949	33145	AGGATGCTTTTAAAAAAATC	245536	77732	TTCCCTCAGCCAAATGGCTG	290123	122319	ATGTTTCAAGTGCCACATGT
200950	33146	TAGGATGCTTTTAAAAAAAT	245537	77733	CTTCCCTCAGCCAAATGGCT	290124	122320	CATGTTTCAAGTGCCACATG
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200955	33151	TGGCCTAGGATGCTTTTAAA	245542	77738	TGCCCCTTCCCTCAGCCAAA	290129	122325	CCAGCCATGTTTCAAGTGCC
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200963	33159	ACCGCGCCTGGCCTAGGATG	245550	77746	CACTGACCTGCCCCTTCCCT	290137	122333	CAACTGTACCAGCCATGTTT
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200965	33161	TCACCGCGCCTGGCCTAGGA	245552	77748	TCCACTGACCTGCCCCTTCC	290139	122335	CTCAACTGTACCAGCCATGT
200966	33162	GTCACCGCGCCTGGCCTAGG	245553	77749	GTCCACTGACCTGCCCCTTC	290140	122336	CCTCAACTGTACCAGCCATG
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200973	33169	GGCGTGAGTCACCGCGCCTG	245560	77756	ATCAGATGTCCACTGACCTG	290147	122343	CACTCTTCCTCAACTGTACC
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200975	33171	CAGGCGTGAGTCACCGCGCC	245562	77758	AGATCAGATGTCCACTGACC	290149	122345	GCCACTCTTCCTCAACTGTA
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200977	33173	TACAGGCGTGAGTCACCGCG	245564	77760	CAAGATCAGATGTCCACTGA	290151	122347	CAGCCACTCTTCCTCAACTG
200978	33174	TTACAGGCGTGAGTCACCGC	245565	77761	CCAAGATCAGATGTCCACTG	290152	122348	GCAGCCACTCTTCCTCAACT
200979	33175	ATTACAGGCGTGAGTCACCG	245566	77762	ACCAAGATCAGATGTCCACT	290153	122349	GGCAGCCACTCTTCCTCAAC
200980	33176	AATTACAGGCGTGAGTCACC	245567	77763	AACCAAGATCAGATGTCCAC	290154	122350	TGGCAGCCACTCTTCCTCAA
200981	33177	GAATTACAGGCGTGAGTCAC	245568	77764	AAACCAAGATCAGATGTCCA	290155	122351	ATGGCAGCCACTCTTCCTCA
200982	33178	GGAATTACAGGCGTGAGTCA	245569	77765	TAAACCAAGATCAGATGTCC	290156	122352	TATGGCAGCCACTCTTCCTC
200983	33179	TGGAATTACAGGCGTGAGTC	245570	77766	CTAAACCAAGATCAGATGTC	290157	122353	ATATGGCAGCCACTCTTCCT
200984	33180	CTGGAATTACAGGCGTGAGT	245571	77767	ACTAAACCAAGATCAGATGT	290158	122354	GATATGGCAGCCACTCTTCC
200985	33181	GCTGGAATTACAGGCGTGAG	245572	77768	TACTAAACCAAGATCAGATG	290159	122355	CGATATGGCAGCCACTCTTC
200986	33182	TGCTGGAATTACAGGCGTGA	245573	77769	ATACTAAACCAAGATCAGAT	290160	122356	CCGATATGGCAGCCACTCTT
200987	33183	GTGCTGGAATTACAGGCGTG	245574	77770	GATACTAAACCAAGATCAGA	290161	122357	TCCGATATGGCAGCCACTCT
200988	33184	AGTGCTGGAATTACAGGCGT	245575	77771	GGATACTAAACCAAGATCAG	290162	122358	GTCCGATATGGCAGCCACTC
200989	33185	AAGTGCTGGAATTACAGGCG	245576	77772	AGGATACTAAACCAAGATCA	290163	122359	CGTCCGATATGGCAGCCACT
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200991	33187	CAAAGTGCTGGAATTACAGG	245578	77774	GAAGGATACTAAACCAAGAT	290165	122361	GTCGTCCGATATGGCAGCCA
200992	33188	CCAAAGTGCTGGAATTACAG	245579	77775	TGAAGGATACTAAACCAAGA	290166	122362	TGTCGTCCGATATGGCAGCC
200993	33189	CCCAAAGTGCTGGAATTACA	245580	77776	ATGAAGGATACTAAACCAAG	290167	122363	GTGTCGTCCGATATGGCAGC
200994	33190	TCCCAAAGTGCTGGAATTAC	245581	77777	AATGAAGGATACTAAACCAA	290168	122364	TGTGTCGTCCGATATGGCAG

200995	33191	CTCCCAAAGTGCTGGAATTA	245582	77778	AAATGAAGGATACTAAACCA	290169	122365	CTGTGTCGTCCGATATGGCA
200996	33192	CCTCCCAAAGTGCTGGAATT	245583	77779	AAAATGAAGGATACTAAACC	290170	122366	GCTGTGTCGTCCGATATGGC
200997	33193	GCCTCCCAAAGTGCTGGAAT	245584	77780	CAAAATGAAGGATACTAAAC	290171	122367	AGCTGTGTCGTCCGATATGG
200998	33194	GGCCTCCCAAAGTGCTGGAA	245585	77781	CCAAAATGAAGGATACTAAA	290172	122368	TAGCTGTGTCGTCCGATATG
200999	33195	TGGCCTCCCAAAGTGCTGGA	245586	77782	CCCAAAATGAAGGATACTAA	290173	122369	ATAGCTGTGTCGTCCGATAT
201000	33196	TTGGCCTCCCAAAGTGCTGG	245587	77783	CCCCAAAATGAAGGATACTA	290174	122370	TATAGCTGTGTCGTCCGATA
201001	33197	CTTGGCCTCCCAAAGTGCTG	245588	77784	CCCCCAAAATGAAGGATACT	290175	122371	CTATAGCTGTGTCGTCCGAT
201002	33198	CCTTGGCCTCCCAAAGTGCT	245589	77785	GCCCCCAAAATGAAGGATAC	290176	122372	TCTATAGCTGTGTCGTCCGA
201003	33199	ACCTTGGCCTCCCAAAGTGC	245590	77786	AGCCCCCAAAATGAAGGATA	290177	122373	ATCTATAGCTGTGTCGTCCG
201004	33200	CACCTTGGCCTCCCAAAGTG	245591	77787	GAGCCCCCAAAATGAAGGAT	290178	122374	AATCTATAGCTGTGTCGTCC
201005	33201	CCACCTTGGCCTCCCAAAGT	245592	77788	AGAGCCCCCAAAATGAAGGA	290179	122375	GAATCTATAGCTGTGTCGTC
201006	33202	CCCACCTTGGCCTCCCAAAG	245593	77789	CAGAGCCCCCAAAATGAAGG	290180	122376	AGAATCTATAGCTGTGTCGT
201007	33203	ACCCACCTTGGCCTCCCAAA	245594	77790	CCAGAGCCCCCAAAATGAAG	290181	122377	CAGAATCTATAGCTGTGTCG
201008	33204	CACCCACCTTGGCCTCCCAA	245595	77791	CCCAGAGCCCCCAAAATGAA	290182	122378	ACAGAATCTATAGCTGTGTC
201009	33205	CCACCCACCTTGGCCTCCCA	245596	77792	ACCCAGAGCCCCCAAAATGA	290183	122379	GACAGAATCTATAGCTGTGT
201010	33206	TCCACCCACCTTGGCCTCCC	245597	77793	CACCCAGAGCCCCCAAAATG	290184	122380	TGACAGAATCTATAGCTGTG
201011	33207	ATCCACCCACCTTGGCCTCC	245598	77794	ACACCCAGAGCCCCCAAAAT	290185	122381	GTGACAGAATCTATAGCTGT
201012	33208	GATCCACCCACCTTGGCCTC	245599	77795	CACACCCAGAGCCCCCAAAA	290186	122382	GGTGACAGAATCTATAGCTG
201013	33209	TGATCCACCCACCTTGGCCT	245600	77796	CCACACCCAGAGCCCCCAAA	290187	122383	GGGTGACAGAATCTATAGCT
201014	33210	GTGATCCACCCACCTTGGCC	245601	77797	GCCACACCCAGAGCCCCCAA	290188	122384	GGGGTGACAGAATCTATAGC
201015	33211	TGTGATCCACCCACCTTGGC	245602	77798	GGCCACACCCAGAGCCCCCA	290189	122385	TGGGGTGACAGAATCTATAG
201016	33212	TTGTGATCCACCCACCTTGG	245603	77799	AGGCCACACCCAGAGCCCCC	290190	122386	GTGGGGTGACAGAATCTATA
201017	33213	CTTGTGATCCACCCACCTTG	245604	77800	CAGGCCACACCCAGAGCCCC	290191	122387	GGTGGGGTGACAGAATCTAT
201018	33214	CCTTGTGATCCACCCACCTT	245605	77801	CCAGGCCACACCCAGAGCCC	290192	122388	GGGTGGGGTGACAGAATCTA
201019	33215	ACCTTGTGATCCACCCACCT	245606	77802	CCCAGGCCACACCCAGAGCC	290193	122389	GGGGTGGGGTGACAGAATCT
201020	33216	GACCTTGTGATCCACCCACC	245607	77803	GCCCAGGCCACACCCAGAGC	290194	122390	CGGGGTGGGGTGACAGAATC
201021	33217	TGACCTTGTGATCCACCCAC	245608	77804	GGCCCAGGCCACACCCAGAG	290195	122391	TCGGGGTGGGGTGACAGAAT
201022	33218	CTGACCTTGTGATCCACCCA	245609	77805	AGGCCCAGGCCACACCCAGA	290196	122392	CTCGGGGTGGGGTGACAGAA
201023	33219	CCTGACCTTGTGATCCACCC	245610	77806	GAGGCCCAGGCCACACCCAG	290197	122393	TCTCGGGGTGGGGTGACAGA
201024	33220	TCCTGACCTTGTGATCCACC	245611	77807	AGAGGCCCAGGCCACACCCA	290198	122394	CTCTCGGGGTGGGGTGACAG
201025	33221	CTCCTGACCTTGTGATCCAC	245612	77808	CAGAGGCCCAGGCCACACCC	290199	122395	ACTCTCGGGGTGGGGTGACA
201026	33222	TCTCCTGACCTTGTGATCCA	245613	77809	CCAGAGGCCCAGGCCACACC	290200	122396	GACTCTCGGGGTGGGGTGAC
201027	33223	ATCTCCTGACCTTGTGATCC	245614	77810	TCCAGAGGCCCAGGCCACAC	290201	122397	GGACTCTCGGGGTGGGGTGA
201028	33224	GATCTCCTGACCTTGTGATC	245615	77811	GTCCAGAGGCCCAGGCCACA	290202	122398	TGGACTCTCGGGGTGGGGTG
201029	33225	CGATCTCCTGACCTTGTGAT	245616	77812	AGTCCAGAGGCCCAGGCCAC	290203	122399	CTGGACTCTCGGGGTGGGGT
201030	33226	TCGATCTCCTGACCTTGTGA	245617	77813	AAGTCCAGAGGCCCAGGCCA	290204	122400	TCTGGACTCTCGGGGTGGGG
201031	33227	CTCGATCTCCTGACCTTGTG	245618	77814	AAAGTCCAGAGGCCCAGGCC	290205	122401	CTCTGGACTCTCGGGGTGGG
201032	33228	TCTCGATCTCCTGACCTTGT	245619	77815	CAAAGTCCAGAGGCCCAGGC	290206	122402	GCTCTGGACTCTCGGGGTGG
201033	33229	GTCTCGATCTCCTGACCTTG	245620	77816	CCAAAGTCCAGAGGCCCAGG	290207	122403	CGCTCTGGACTCTCGGGGTG
201034	33230	GGTCTCGATCTCCTGACCTT	245621	77817	GCCAAAGTCCAGAGGCCCAG	290208	122404	CCGCTCTGGACTCTCGGGGT
201035	33231	TGGTCTCGATCTCCTGACCT	245622	77818	GGCCAAAGTCCAGAGGCCCA	290209	122405	CCCGCTCTGGACTCTCGGGG
201036	33232	ATGGTCTCGATCTCCTGACC	245623	77819	TGGCCAAAGTCCAGAGGCCC	290210	122406	CCCCGCTCTGGACTCTCGGG
201037	33233	GATGGTCTCGATCTCCTGAC	245624	77820	GTGGCCAAAGTCCAGAGGCC	290211	122407	TCCCCGCTCTGGACTCTCGG
201038	33234	GGATGGTCTCGATCTCCTGA	245625	77821	CGTGGCCAAAGTCCAGAGGC	290212	122408	GTCCCCGCTCTGGACTCTCG
201039	33235	AGGATGGTCTCGATCTCCTG	245626	77822	CCGTGGCCAAAGTCCAGAGG	290213	122409	AGTCCCCGCTCTGGACTCTC
201040	33236	CAGGATGGTCTCGATCTCCT	245627	77823	ACCGTGGCCAAAGTCCAGAG	290214	122410	AAGTCCCCGCTCTGGACTCT
201041	33237	CCAGGATGGTCTCGATCTCC	245628	77824	CACCGTGGCCAAAGTCCAGA	290215	122411	GAAGTCCCCGCTCTGGACTC
201042	33238	GCCAGGATGGTCTCGATCTC	245629	77825	ACACCGTGGCCAAAGTCCAG	290216	122412	AGAAGTCCCCGCTCTGGACT
201043	33239	AGCCAGGATGGTCTCGATCT	245630	77826	AACACCGTGGCCAAAGTCCA	290217	122413	CAGAAGTCCCCGCTCTGGAC
201044	33240	TAGCCAGGATGGTCTCGATC	245631	77827	AAACACCGTGGCCAAAGTCC	290218	122414	GCAGAAGTCCCCGCTCTGGA
201045	33241	TTAGCCAGGATGGTCTCGAT	245632	77828	CAAACACCGTGGCCAAAGTC	290219	122415	GGCAGAAGTCCCCGCTCTGG
201046	33242	GTTAGCCAGGATGGTCTCGA	245633	77829	ACAAACACCGTGGCCAAAGT	290220	122416	AGGCAGAAGTCCCCGCTCTG
201047	33243	TGTTAGCCAGGATGGTCTCG	245634	77830	AACAAACACCGTGGCCAAAG	290221	122417	AAGGCAGAAGTCCCCGCTCT
201048	33244	ATGTTAGCCAGGATGGTCTC	245635	77831	GAACAAACACCGTGGCCAAA	290222	122418	TAAGGCAGAAGTCCCCGCTC
201049	33245	CATGTTAGCCAGGATGGTCT	245636	77832	GGAACAAACACCGTGGCCAA	290223	122419	CTAAGGCAGAAGTCCCCGCT
201050	33246	CCATGTTAGCCAGGATGGTC	245637	77833	TGGAACAAACACCGTGGCCA	290224	122420	CCTAAGGCAGAAGTCCCCGC
201051	33247	ACCATGTTAGCCAGGATGGT	245638	77834	CTGGAACAAACACCGTGGCC	290225	122421	GCCTAAGGCAGAAGTCCCCG
201052	33248	CACCATGTTAGCCAGGATGG	245639	77835	GCTGGAACAAACACCGTGGC	290226	122422	GGCCTAAGGCAGAAGTCCCC
201053	33249	TCACCATGTTAGCCAGGATG	245640	77836	GGCTGGAACAAACACCGTGG	290227	122423	GGGCCTAAGGCAGAAGTCCC
201054	33250	TTCACCATGTTAGCCAGGAT	245641	77837	GGGCTGGAACAAACACCGTG	290228	122424	AGGGCCTAAGGCAGAAGTCC
201055	33251	TTTCACCATGTTAGCCAGGA	245642	77838	AGGGCTGGAACAAACACCGT	290229	122425	TAGGGCCTAAGGCAGAAGTC
201056	33252	GTTTCACCATGTTAGCCAGG	245643	77839	AAGGGCTGGAACAAACACCG	290230	122426	ATAGGGCCTAAGGCAGAAGT
201057	33253	GGTTTCACCATGTTAGCCAG	245644	77840	GAAGGGCTGGAACAAACACC	290231	122427	AATAGGGCCTAAGGCAGAAG
201058	33254	GGGTTTCACCATGTTAGCCA	245645	77841	AGAAGGGCTGGAACAAACAC	290232	122428	GAATAGGGCCTAAGGCAGAA
201059	33255	GGGGTTTCACCATGTTAGCC	245646	77842	GAGAAGGGCTGGAACAAACA	290233	122429	TGAATAGGGCCTAAGGCAGA
201060	33256	TGGGGTTTCACCATGTTAGC	245647	77843	GGAGAAGGGCTGGAACAAAC	290234	122430	CTGAATAGGGCCTAAGGCAG
201061	33257	ATGGGGTTTCACCATGTTAG	245648	77844	AGGAGAAGGGCTGGAACAAA	290235	122431	CCTGAATAGGGCCTAAGGCA
201062	33258	GATGGGGTTTCACCATGTTA	245649	77845	TAGGAGAAGGGCTGGAACAA	290236	122432	CCCTGAATAGGGCCTAAGGC
201063	33259	AGATGGGGTTTCACCATGTT	245650	77846	TTAGGAGAAGGGCTGGAACA	290237	122433	GCCCTGAATAGGGCCTAAGG
201064	33260	GAGATGGGGTTTCACCATGT	245651	77847	GTTAGGAGAAGGGCTGGAAC	290238	122434	AGCCCTGAATAGGGCCTAAG
201065	33261	AGAGATGGGGTTTCACCATG	245652	77848	GGTTAGGAGAAGGGCTGGAA	290239	122435	CAGCCCTGAATAGGGCCTAA
201066	33262	TAGAGATGGGGTTTCACCAT	245653	77849	AGGTTAGGAGAAGGGCTGGA	290240	122436	TCAGCCCTGAATAGGGCCTA

201067	33263	GTAGAGATGGGGTTTCACCA	245654	77850	CAGGTTAGGAGAAGGGCTGG	290241	122437	ATCAGCCCTGAATAGGGCCT
201068	33264	AGTAGAGATGGGGTTTCACC	245655	77851	ACAGGTTAGGAGAAGGGCTG	290242	122438	AATCAGCCCTGAATAGGGCC
201069	33265	TAGTAGAGATGGGGTTTCAC	245656	77852	GACAGGTTAGGAGAAGGGCT	290243	122439	AAATCAGCCCTGAATAGGGC
201070	33266	TTAGTAGAGATGGGGTTTCA	245657	77853	GGACAGGTTAGGAGAAGGGC	290244	122440	AAAATCAGCCCTGAATAGGG
201071	33267	TTTAGTAGAGATGGGGTTTC	245658	77854	AGGACAGGTTAGGAGAAGGG	290245	122441	AAAAATCAGCCCTGAATAGG
201072	33268	TTTTAGTAGAGATGGGGTTT	245659	77855	AAGGACAGGTTAGGAGAAGG	290246	122442	TAAAAATCAGCCCTGAATAG
201073	33269	TTTTTAGTAGAGATGGGGTT	245660	77856	AAAGGACAGGTTAGGAGAAG	290247	122443	GTAAAAATCAGCCCTGAATA
201074	33270	ATTTTTAGTAGAGATGGGGT	245661	77857	GAAAGGACAGGTTAGGAGAA	290248	122444	AGTAAAAATCAGCCCTGAAT
201075	33271	TATTTTTAGTAGAGATGGGG	245662	77858	GGAAAGGACAGGTTAGGAGA	290249	122445	AAGTAAAAATCAGCCCTGAA
201076	33272	GTATTTTTAGTAGAGATGGG	245663	77859	TGGAAAGGACAGGTTAGGAG	290250	122446	CAAGTAAAAATCAGCCCTGA
201077	33273	TGTATTTTTAGTAGAGATGG	245664	77860	CTGGAAAGGACAGGTTAGGA	290251	122447	TCAAGTAAAAATCAGCCCTG
201078	33274	TTGTATTTTTAGTAGAGATG	245665	77861	TCTGGAAAGGACAGGTTAGG	290252	122448	TTCAAGTAAAAATCAGCCCT
201079	33275	TTTGTATTTTTAGTAGAGAT	245666	77862	GTCTGGAAAGGACAGGTTAG	290253	122449	GTTCAAGTAAAAATCAGCCC
201080	33276	TTTTGTATTTTTAGTAGAGA	245667	77863	TGTCTGGAAAGGACAGGTTA	290254	122450	GGTTCAAGTAAAAATCAGCC
201081	33277	TTTTTGTATTTTTAGTAGAG	245668	77864	GTGTCTGGAAAGGACAGGTT	290255	122451	GGGTTCAAGTAAAAATCAGC
201082	33278	TTTTTTGTATTTTTAGTAGA	245669	77865	AGTGTCTGGAAAGGACAGGT	290256	122452	AGGGTTCAAGTAAAAATCAG
201083	33279	CTTTTTTGTATTTTTAGTAG	245670	77866	GAGTGTCTGGAAAGGACAGG	290257	122453	AAGGGTTCAAGTAAAAATCA
201084	33280	ACTTTTTTGTATTTTTAGTA	245671	77867	CGAGTGTCTGGAAAGGACAG	290258	122454	TAAGGGTTCAAGTAAAAATC
201085	33281	TACTTTTTTGTATTTTTAGT	245672	77868	CCGAGTGTCTGGAAAGGACA	290259	122455	GTAAGGGTTCAAGTAAAAAT
201086	33282	CTACTTTTTTGTATTTTTAG	245673	77869	GCCGAGTGTCTGGAAAGGAC	290260	122456	AGTAAGGGTTCAAGTAAAAA
201087	33283	GCTACTTTTTTGTATTTTTA	245674	77870	TGCCGAGTGTCTGGAAAGGA	290261	122457	CAGTAAGGGTTCAAGTAAAA
201088	33284	GGCTACTTTTTTGTATTTTT	245675	77871	ATGCCGAGTGTCTGGAAAGG	290262	122458	ACAGTAAGGGTTCAAGTAAA
201089	33285	CGGCTACTTTTTTGTATTTT	245676	77872	GATGCCGAGTGTCTGGAAAG	290263	122459	CACAGTAAGGGTTCAAGTAA
201090	33286	CCGGCTACTTTTTTGTATTT	245677	77873	AGATGCCGAGTGTCTGGAAA	290264	122460	CCACAGTAAGGGTTCAAGTA
201091	33287	CCCGGCTACTTTTTTGTATT	245678	77874	TAGATGCCGAGTGTCTGGAA	290265	122461	CCCACAGTAAGGGTTCAAGT
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201093	33289	CTCCCGGCTACTTTTTTGTA	245680	77876	CCTAGATGCCGAGTGTCTGG	290267	122463	TTCCCACAGTAAGGGTTCAA
201094	33290	ACTCCCGGCTACTTTTTTGT	245681	77877	ACCTAGATGCCGAGTGTCTG	290268	122464	CTTCCCACAGTAAGGGTTCA
201095	33291	CACTCCCGGCTACTTTTTTG	245682	77878	AACCTAGATGCCGAGTGTCT	290269	122465	TCTTCCCACAGTAAGGGTTC
201096	33292	CCACTCCCGGCTACTTTTTT	245683	77879	TAACCTAGATGCCGAGTGTC	290270	122466	CTCTTCCCACAGTAAGGGTT
201097	33293	ACCACTCCCGGCTACTTTTT	245684	77880	ATAACCTAGATGCCGAGTGT	290271	122467	TCTCTTCCCACAGTAAGGGT
201098	33294	CACCACTCCCGGCTACTTTT	245685	77881	AATAACCTAGATGCCGAGTG	290272	122468	TTCTCTTCCCACAGTAAGGG
201099	33295	CCACCACTCCCGGCTACTTT	245686	77882	TAATAACCTAGATGCCGAGT	290273	122469	CTTCTCTTCCCACAGTAAGG
201100	33296	GCCACCACTCCCGGCTACTT	245687	77883	CTAATAACCTAGATGCCGAG	290274	122470	CCTTCTCTTCCCACAGTAAG
201101	33297	TGCCACCACTCCCGGCTACT	245688	77884	GCTAATAACCTAGATGCCGA	290275	122471	GCCTTCTCTTCCCACAGTAA
201102	33298	CTGCCACCACTCCCGGCTAC	245689	77885	TGCTAATAACCTAGATGCCG	290276	122472	GGCCTTCTCTTCCCACAGTA
201103	33299	CCTGCCACCACTCCCGGCTA	245690	77886	GTGCTAATAACCTAGATGCC	290277	122473	TGGCCTTCTCTTCCCACAGT
201104	33300	ACCTGCCACCACTCCCGGCT	245691	77887	GGTGCTAATAACCTAGATGC	290278	122474	ATGGCCTTCTCTTCCCACAG
201105	33301	CACCTGCCACCACTCCCGGC	245692	77888	AGGTGCTAATAACCTAGATG	290279	122475	CATGGCCTTCTCTTCCCACA
201106	33302	GCACCTGCCACCACTCCCGG	245693	77889	GAGGTGCTAATAACCTAGAT	290280	122476	TCATGGCCTTCTCTTCCCAC
201107	33303	GGCACCTGCCACCACTCCCG	245694	77890	CGAGGTGCTAATAACCTAGA	290281	122477	CTCATGGCCTTCTCTTCCCA
201108	33304	AGGCACCTGCCACCACTCCC	245695	77891	GCGAGGTGCTAATAACCTAG	290282	122478	TCTCATGGCCTTCTCTTCCC
201109	33305	CAGGCACCTGCCACCACTCC	245696	77892	TGCGAGGTGCTAATAACCTA	290283	122479	TTCTCATGGCCTTCTCTTCC
201110	33306	ACAGGCACCTGCCACCACTC	245697	77893	ATGCGAGGTGCTAATAACCT	290284	122480	CTTCTCATGGCCTTCTCTTC
201111	33307	TACAGGCACCTGCCACCACT	245698	77894	TATGCGAGGTGCTAATAACC	290285	122481	ACTTCTCATGGCCTTCTCTT
201112	33308	CTACAGGCACCTGCCACCAC	245699	77895	GTATGCGAGGTGCTAATAAC	290286	122482	AACTTCTCATGGCCTTCTCT
201113	33309	ACTACAGGCACCTGCCACCA	245700	77896	AGTATGCGAGGTGCTAATAA	290287	122483	GAACTTCTCATGGCCTTCTC
201114	33310	GACTACAGGCACCTGCCACC	245701	77897	AAGTATGCGAGGTGCTAATA	290288	122484	TGAACTTCTCATGGCCTTCT
201115	33311	GGACTACAGGCACCTGCCAC	245702	77898	AAAGTATGCGAGGTGCTAAT	290289	122485	CTGAACTTCTCATGGCCTTC
201116	33312	GGGACTACAGGCACCTGCCA	245703	77899	GAAAGTATGCGAGGTGCTAA	290290	122486	ACTGAACTTCTCATGGCCTT
201117	33313	TGGGACTACAGGCACCTGCC	245704	77900	AGAAAGTATGCGAGGTGCTA	290291	122487	GACTGAACTTCTCATGGCCT
201118	33314	CTGGGACTACAGGCACCTGC	245705	77901	CAGAAAGTATGCGAGGTGCT	290292	122488	AGACTGAACTTCTCATGGCC
201119	33315	GCTGGGACTACAGGCACCTG	245706	77902	TCAGAAAGTATGCGAGGTGC	290293	122489	TAGACTGAACTTCTCATGGC
201120	33316	AGCTGGGACTACAGGCACCT	245707	77903	GTCAGAAAGTATGCGAGGTG	290294	122490	CTAGACTGAACTTCTCATGG
201121	33317	TAGCTGGGACTACAGGCACC	245708	77904	TGTCAGAAAGTATGCGAGGT	290295	122491	TCTAGACTGAACTTCTCATG
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201123	33319	AGTAGCTGGGACTACAGGCA	245710	77906	CATGTCAGAAAGTATGCGAG	290297	122493	ATTCTAGACTGAACTTCTCA
201124	33320	GAGTAGCTGGGACTACAGGC	245711	77907	GCATGTCAGAAAGTATGCGA	290298	122494	CATTCTAGACTGAACTTCTC
201125	33321	CGAGTAGCTGGGACTACAGG	245712	77908	AGCATGTCAGAAAGTATGCG	290299	122495	ACATTCTAGACTGAACTTCT
201126	33322	CCGAGTAGCTGGGACTACAG	245713	77909	GAGCATGTCAGAAAGTATGC	290300	122496	CACATTCTAGACTGAACTTC
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201128	33324	TCCCGAGTAGCTGGGACTAC	245715	77911	AGGAGCATGTCAGAAAGTAT	290302	122498	GTCACATTCTAGACTGAACT
201129	33325	CTCCCGAGTAGCTGGGACTA	245716	77912	GAGGAGCATGTCAGAAAGTA	290303	122499	AGTCACATTCTAGACTGAAC
201130	33326	CCTCCCGAGTAGCTGGGACT	245717	77913	TGAGGAGCATGTCAGAAAGT	290304	122500	GAGTCACATTCTAGACTGAA
201131	33327	GCCTCCCGAGTAGCTGGGAC	245718	77914	CTGAGGAGCATGTCAGAAAG	290305	122501	GGAGTCACATTCTAGACTGA
201132	33328	AGCCTCCCGAGTAGCTGGGA	245719	77915	ACTGAGGAGCATGTCAGAAA	290306	122502	AGGAGTCACATTCTAGACTG
201133	33329	CAGCCTCCCGAGTAGCTGGG	245720	77916	GACTGAGGAGCATGTCAGAA	290307	122503	AAGGAGTCACATTCTAGACT
201134	33330	TCAGCCTCCCGAGTAGCTGG	245721	77917	GGACTGAGGAGCATGTCAGA	290308	122504	TAAGGAGTCACATTCTAGAC
201135	33331	CTCAGCCTCCCGAGTAGCTG	245722	77918	AGGACTGAGGAGCATGTCAG	290309	122505	ATAAGGAGTCACATTCTAGA
201136	33332	CCTCAGCCTCCCGAGTAGCT	245723	77919	CAGGACTGAGGAGCATGTCA	290310	122506	AATAAGGAGTCACATTCTAG
201137	33333	GCCTCAGCCTCCCGAGTAGC	245724	77920	TCAGGACTGAGGAGCATGTC	290311	122507	AAATAAGGAGTCACATTCTA
201138	33334	TGCCTCAGCCTCCCGAGTAG	245725	77921	ATCAGGACTGAGGAGCATGT	290312	122508	AAAATAAGGAGTCACATTCT

201139	33335	CTGCCTCAGCCTCCCGAGTA	245726	77922	AATCAGGACTGAGGAGCATG	290313	122509	GAAAATAAGGAGTCACATTC
201140	33336	CCTGCCTCAGCCTCCCGAGT	245727	77923	AAATCAGGACTGAGGAGCAT	290314	122510	AGAAAATAAGGAGTCACATT
201141	33337	TCCTGCCTCAGCCTCCCGAG	245728	77924	AAAATCAGGACTGAGGAGCA	290315	122511	CAGAAAATAAGGAGTCACAT
201142	33338	CTCCTGCCTCAGCCTCCCGA	245729	77925	CAAAATCAGGACTGAGGAGC	290316	122512	CCAGAAAATAAGGAGTCACA
201143	33339	TCTCCTGCCTCAGCCTCCCG	245730	77926	TCAAAATCAGGACTGAGGAG	290317	122513	GCCAGAAAATAAGGAGTCAC
201144	33340	TTCTCCTGCCTCAGCCTCCC	245731	77927	GTCAAAATCAGGACTGAGGA	290318	122514	AGCCAGAAAATAAGGAGTCA
201145	33341	ATTCTCCTGCCTCAGCCTCC	245732	77928	GGTCAAAATCAGGACTGAGG	290319	122515	GAGCCAGAAAATAAGGAGTC
201146	33342	CATTCTCCTGCCTCAGCCTC	245733	77929	TGGTCAAAATCAGGACTGAG	290320	122516	GGAGCCAGAAAATAAGGAGT
201147	33343	CCATTCTCCTGCCTCAGCCT	245734	77930	ATGGTCAAAATCAGGACTGA	290321	122517	GGGAGCCAGAAAATAAGGAG
201148	33344	GCCATTCTCCTGCCTCAGCC	245735	77931	GATGGTCAAAATCAGGACTG	290322	122518	AGGGAGCCAGAAAATAAGGA
201149	33345	CGCCATTCTCCTGCCTCAGC	245736	77932	AGATGGTCAAAATCAGGACT	290323	122519	AAGGGAGCCAGAAAATAAGG
201150	33346	ACGCCATTCTCCTGCCTCAG	245737	77933	AAGATGGTCAAAATCAGGAC	290324	122520	CAAGGGAGCCAGAAAATAAG
201151	33347	CACGCCATTCTCCTGCCTCA	245738	77934	GAAGATGGTCAAAATCAGGA	290325	122521	CCAAGGGAGCCAGAAAATAA
201152	33348	TCACGCCATTCTCCTGCCTC	245739	77935	AGAAGATGGTCAAAATCAGG	290326	122522	TCCAAGGGAGCCAGAAAATA
201153	33349	TTCACGCCATTCTCCTGCCT	245740	77936	GAGAAGATGGTCAAAATCAG	290327	122523	GTCCAAGGGAGCCAGAAAAT
201154	33350	GTTCACGCCATTCTCCTGCC	245741	77937	AGAGAAGATGGTCAAAATCA	290328	122524	TGTCCAAGGGAGCCAGAAAA
201155	33351	GGTTCACGCCATTCTCCTGC	245742	77938	AAGAGAAGATGGTCAAAATC	290329	122525	GTGTCCAAGGGAGCCAGAAA
201156	33352	AGGTTCACGCCATTCTCCTG	245743	77939	CAAGAGAAGATGGTCAAAAT	290330	122526	AGTGTCCAAGGGAGCCAGAA
201157	33353	CAGGTTCACGCCATTCTCCT	245744	77940	GCAAGAGAAGATGGTCAAAA	290331	122527	AAGTGTCCAAGGGAGCCAGA
201158	33354	CCAGGTTCACGCCATTCTCC	245745	77941	AGCAAGAGAAGATGGTCAAA	290332	122528	AAAGTGTCCAAGGGAGCCAG
201159	33355	ACCAGGTTCACGCCATTCTC	245746	77942	AAGCAAGAGAAGATGGTCAA	290333	122529	CAAAGTGTCCAAGGGAGCCA
201160	33356	TACCAGGTTCACGCCATTCT	245747	77943	GAAGCAAGAGAAGATGGTCA	290334	122530	ACAAAGTGTCCAAGGGAGCC
201161	33357	CTACCAGGTTCACGCCATTC	245748	77944	GGAAGCAAGAGAAGATGGTC	290335	122531	CACAAAGTGTCCAAGGGAGC
201162	33358	CCTACCAGGTTCACGCCATT	245749	77945	GGGAAGCAAGAGAAGATGGT	290336	122532	CCACAAAGTGTCCAAGGGAG
201163	33359	GCCTACCAGGTTCACGCCAT	245750	77946	TGGGAAGCAAGAGAAGATGG	290337	122533	CCCACAAAGTGTCCAAGGGA
201164	33360	CGCCTACCAGGTTCACGCCA	245751	77947	ATGGGAAGCAAGAGAAGATG	290338	122534	TCCCACAAAGTGTCCAAGGG
201165	33361	CCGCCTACCAGGTTCACGCC	245752	77948	GATGGGAAGCAAGAGAAGAT	290339	122535	ATCCCACAAAGTGTCCAAGG
201166	33362	TCCGCCTACCAGGTTCACGC	245753	77949	AGATGGGAAGCAAGAGAAGA	290340	122536	AATCCCACAAAGTGTCCAAG
201167	33363	CTCCGCCTACCAGGTTCACG	245754	77950	CAGATGGGAAGCAAGAGAAG	290341	122537	AAATCCCACAAAGTGTCCAA
201168	33364	CCTCCGCCTACCAGGTTCAC	245755	77951	ACAGATGGGAAGCAAGAGAA	290342	122538	TAAATCCCACAAAGTGTCCA
201169	33365	ACCTCCGCCTACCAGGTTCA	245756	77952	CACAGATGGGAAGCAAGAGA	290343	122539	CTAAATCCCACAAAGTGTCC
201170	33366	AACCTCCGCCTACCAGGTTC	245757	77953	ACACAGATGGGAAGCAAGAG	290344	122540	ACTAAATCCCACAAAGTGTC
201171	33367	CAACCTCCGCCTACCAGGTT	245758	77954	GACACAGATGGGAAGCAAGA	290345	122541	GACTAAATCCCACAAAGTGT
201172	33368	GCAACCTCCGCCTACCAGGT	245759	77955	TGACACAGATGGGAAGCAAG	290346	122542	AGACTAAATCCCACAAAGTG
201173	33369	TGCAACCTCCGCCTACCAGG	245760	77956	CTGACACAGATGGGAAGCAA	290347	122543	GAGACTAAATCCCACAAAGT
201174	33370	CTGCAACCTCCGCCTACCAG	245761	77957	ACTGACACAGATGGGAAGCA	290348	122544	GGAGACTAAATCCCACAAAG
201175	33371	ACTGCAACCTCCGCCTACCA	245762	77958	GACTGACACAGATGGGAAGC	290349	122545	GGGAGACTAAATCCCACAAA
201176	33372	CACTGCAACCTCCGCCTACC	245763	77959	TGACTGACACAGATGGGAAG	290350	122546	AGGGAGACTAAATCCCACAA
201177	33373	TCACTGCAACCTCCGCCTAC	245764	77960	TTGACTGACACAGATGGGAA	290351	122547	CAGGGAGACTAAATCCCACA
201178	33374	CTCACTGCAACCTCCGCCTA	245765	77961	CTTGACTGACACAGATGGGA	290352	122548	ACAGGGAGACTAAATCCCAC
201179	33375	GCTCACTGCAACCTCCGCCT	245766	77962	TCTTGACTGACACAGATGGG	290353	122549	CACAGGGAGACTAAATCCCA
201180	33376	GGCTCACTGCAACCTCCGCC	245767	77963	GTCTTGACTGACACAGATGG	290354	122550	CCACAGGGAGACTAAATCCC
201181	33377	CGGCTCACTGCAACCTCCGC	245768	77964	AGTCTTGACTGACACAGATG	290355	122551	TCCACAGGGAGACTAAATCC
201182	33378	TCGGCTCACTGCAACCTCCG	245769	77965	CAGTCTTGACTGACACAGAT	290356	122552	TTCCACAGGGAGACTAAATC
201183	33379	CTCGGCTCACTGCAACCTCC	245770	77966	GCAGTCTTGACTGACACAGA	290357	122553	TTTCCACAGGGAGACTAAAT
201184	33380	TCTCGGCTCACTGCAACCTC	245771	77967	TGCAGTCTTGACTGACACAG	290358	122554	CTTTCCACAGGGAGACTAAA
201185	33381	ATCTCGGCTCACTGCAACCT	245772	77968	ATGCAGTCTTGACTGACACA	290359	122555	ACTTTCCACAGGGAGACTAA
201186	33382	CATCTCGGCTCACTGCAACC	245773	77969	AATGCAGTCTTGACTGACAC	290360	122556	TACTTTCCACAGGGAGACTA
201187	33383	CCATCTCGGCTCACTGCAAC	245774	77970	AAATGCAGTCTTGACTGACA	290361	122557	ATACTTTCCACAGGGAGACT
201188	33384	GCCATCTCGGCTCACTGCAA	245775	77971	CAAATGCAGTCTTGACTGAC	290362	122558	AATACTTTCCACAGGGAGAC
201189	33385	CGCCATCTCGGCTCACTGCA	245776	77972	CCAAATGCAGTCTTGACTGA	290363	122559	GAATACTTTCCACAGGGAGA
201190	33386	GCGCCATCTCGGCTCACTGC	245777	77973	GCCAAATGCAGTCTTGACTG	290364	122560	GGAATACTTTCCACAGGGAG
201191	33387	GGCGCCATCTCGGCTCACTG	245778	77974	AGCCAAATGCAGTCTTGACT	290365	122561	TGGAATACTTTCCACAGGGA
201192	33388	TGGCGCCATCTCGGCTCACT	245779	77975	CAGCCAAATGCAGTCTTGAC	290366	122562	GTGGAATACTTTCCACAGGG
201193	33389	GTGGCGCCATCTCGGCTCAC	245780	77976	ACAGCCAAATGCAGTCTTGA	290367	122563	TGTGGAATACTTTCCACAGG
201194	33390	AGTGGCGCCATCTCGGCTCA	245781	77977	TACAGCCAAATGCAGTCTTG	290368	122564	TTGTGGAATACTTTCCACAG
201195	33391	CAGTGGCGCCATCTCGGCTC	245782	77978	TTACAGCCAAATGCAGTCTT	290369	122565	CTTGTGGAATACTTTCCACA
201196	33392	GCAGTGGCGCCATCTCGGCT	245783	77979	CTTACAGCCAAATGCAGTCT	290370	122566	ACTTGTGGAATACTTTCCAC
201197	33393	TGCAGTGGCGCCATCTCGGC	245784	77980	TCTTACAGCCAAATGCAGTC	290371	122567	CACTTGTGGAATACTTTCCA
201198	33394	GTGCAGTGGCGCCATCTCGG	245785	77981	TTCTTACAGCCAAATGCAGT	290372	122568	CCACTTGTGGAATACTTTCC
201199	33395	AGTGCAGTGGCGCCATCTCG	245786	77982	TTTCTTACAGCCAAATGCAG	290373	122569	ACCACTTGTGGAATACTTTC
201200	33396	GAGTGCAGTGGCGCCATCTC	245787	77983	GTTTCTTACAGCCAAATGCA	290374	122570	CACCACTTGTGGAATACTTT
201201	33397	GGAGTGCAGTGGCGCCATCT	245788	77984	TGTTTCTTACAGCCAAATGC	290375	122571	GCACCACTTGTGGAATACTT
201202	33398	TGGAGTGCAGTGGCGCCATC	245789	77985	CTGTTTCTTACAGCCAAATG	290376	122572	GGCACCACTTGTGGAATACT
201203	33399	CTGGAGTGCAGTGGCGCCAT	245790	77986	TCTGTTTCTTACAGCCAAAT	290377	122573	TGGCACCACTTGTGGAATAC
201204	33400	GCTGGAGTGCAGTGGCGCCA	245791	77987	TTCTGTTTCTTACAGCCAAA	290378	122574	GTGGCACCACTTGTGGAATA
201205	33401	GGCTGGAGTGCAGTGGCGCC	245792	77988	TTTCTGTTTCTTACAGCCAA	290379	122575	GGTGGCACCACTTGTGGAAT
201206	33402	AGGCTGGAGTGCAGTGGCGC	245793	77989	GTTTCTGTTTCTTACAGCCA	290380	122576	TGGTGGCACCACTTGTGGAA
201207	33403	CAGGCTGGAGTGCAGTGGCG	245794	77990	GGTTTCTGTTTCTTACAGCC	290381	122577	GTGGTGGCACCACTTGTGGA
201208	33404	CCAGGCTGGAGTGCAGTGGC	245795	77991	GGGTTTCTGTTTCTTACAGC	290382	122578	GGTGGTGGCACCACTTGTGG
201209	33405	CCCAGGCTGGAGTGCAGTGG	245796	77992	GGGGTTTCTGTTTCTTACAG	290383	122579	GGGTGGTGGCACCACTTGTG
201210	33406	ACCCAGGCTGGAGTGCAGTG	245797	77993	TGGGGTTTCTGTTTCTTACA	290384	122580	GGGGTGGTGGCACCACTTGT

201211	33407	CACCCAGGCTGGAGTGCAGT	245798	77994	TTGGGGTTTCTGTTTCTTAC	290385	122581	TGGGGTGGTGGCACCACTTG
201212	33408	TCACCCAGGCTGGAGTGCAG	245799	77995	GTTGGGGTTTCTGTTTCTTA	290386	122582	CTGGGGTGGTGGCACCACTT
201213	33409	GTCACCCAGGCTGGAGTGCA	245800	77996	AGTTGGGGTTTCTGTTTCTT	290387	122583	GCTGGGGTGGTGGCACCACT
201214	33410	TGTCACCCAGGCTGGAGTGC	245801	77997	TAGTTGGGGTTTCTGTTTCT	290388	122584	AGCTGGGGTGGTGGCACCAC
201215	33411	CTGTCACCCAGGCTGGAGTG	245802	77998	TTAGTTGGGGTTTCTGTTTC	290389	122585	CAGCTGGGGTGGTGGCACCA
201216	33412	TCTGTCACCCAGGCTGGAGT	245803	77999	GTTAGTTGGGGTTTCTGTTT	290390	122586	ACAGCTGGGGTGGTGGCACC
201217	33413	CTCTGTCACCCAGGCTGGAG	245804	78000	AGTTAGTTGGGGTTTCTGTT	290391	122587	CACAGCTGGGGTGGTGGCAC
201218	33414	ACTCTGTCACCCAGGCTGGA	245805	78001	CAGTTAGTTGGGGTTTCTGT	290392	122588	TCACAGCTGGGGTGGTGGCA
201219	33415	CACTCTGTCACCCAGGCTGG	245806	78002	ACAGTTAGTTGGGGTTTCTG	290393	122589	CTCACAGCTGGGGTGGTGGC
201220	33416	TCACTCTGTCACCCAGGCTG	245807	78003	CACAGTTAGTTGGGGTTTCT	290394	122590	TCTCACAGCTGGGGTGGTGG
201221	33417	CTCACTCTGTCACCCAGGCT	245808	78004	CCACAGTTAGTTGGGGTTTC	290395	122591	CTCTCACAGCTGGGGTGGTG
201222	33418	TCTCACTCTGTCACCCAGGC	245809	78005	GCCACAGTTAGTTGGGGTTT	290396	122592	GCTCTCACAGCTGGGGTGGT
201223	33419	GTCTCACTCTGTCACCCAGG	245810	78006	TGCCACAGTTAGTTGGGGTT	290397	122593	TGCTCTCACAGCTGGGGTGG
201224	33420	AGTCTCACTCTGTCACCCAG	245811	78007	ATGCCACAGTTAGTTGGGGT	290398	122594	CTGCTCTCACAGCTGGGGTG
201225	33421	GAGTCTCACTCTGTCACCCA	245812	78008	AATGCCACAGTTAGTTGGGG	290399	122595	GCTGCTCTCACAGCTGGGGT
201226	33422	GGAGTCTCACTCTGTCACCC	245813	78009	AAATGCCACAGTTAGTTGGG	290400	122596	AGCTGCTCTCACAGCTGGGG
201227	33423	CGGAGTCTCACTCTGTCACC	245814	78010	TAAATGCCACAGTTAGTTGG	290401	122597	CAGCTGCTCTCACAGCTGGG
201228	33424	ACGGAGTCTCACTCTGTCAC	245815	78011	GTAAATGCCACAGTTAGTTG	290402	122598	CCAGCTGCTCTCACAGCTGG
201229	33425	GACGGAGTCTCACTCTGTCA	245816	78012	TGTAAATGCCACAGTTAGTT	290403	122599	CCCAGCTGCTCTCACAGCTG
201230	33426	AGACGGAGTCTCACTCTGTC	245817	78013	ATGTAAATGCCACAGTTAGT	290404	122600	TCCCAGCTGCTCTCACAGCT
201231	33427	GAGACGGAGTCTCACTCTGT	245818	78014	CATGTAAATGCCACAGTTAG	290405	122601	CTCCCAGCTGCTCTCACAGC
201232	33428	TGAGACGGAGTCTCACTCTG	245819	78015	TCATGTAAATGCCACAGTTA	290406	122602	GCTCCCAGCTGCTCTCACAG
201233	33429	CTGAGACGGAGTCTCACTCT	245820	78016	TTCATGTAAATGCCACAGTT	290407	122603	AGCTCCCAGCTGCTCTCACA
201234	33430	CCTGAGACGGAGTCTCACTC	245821	78017	CTTCATGTAAATGCCACAGT	290408	122604	CAGCTCCCAGCTGCTCTCAC
201235	33431	TCCTGAGACGGAGTCTCACT	245822	78018	TCTTCATGTAAATGCCACAG	290409	122605	GCAGCTCCCAGCTGCTCTCA
201236	33432	TTCCTGAGACGGAGTCTCAC	245823	78019	CTCTTCATGTAAATGCCACA	290410	122606	AGCAGCTCCCAGCTGCTCTC
201237	33433	TTTCCTGAGACGGAGTCTCA	245824	78020	CCTCTTCATGTAAATGCCAC	290411	122607	AAGCAGCTCCCAGCTGCTCT
201238	33434	TTTTCCTGAGACGGAGTCTC	245825	78021	ACCTCTTCATGTAAATGCCA	290412	122608	AAAGCAGCTCCCAGCTGCTC
201239	33435	TTTTTCCTGAGACGGAGTCT	245826	78022	AACCTCTTCATGTAAATGCC	290413	122609	AAAAGCAGCTCCCAGCTGCT
201240	33436	TTTTTTCCTGAGACGGAGTC	245827	78023	AAACCTCTTCATGTAAATGC	290414	122610	CAAAAGCAGCTCCCAGCTGC
201241	33437	TTTTTTTCCTGAGACGGAGT	245828	78024	TAAACCTCTTCATGTAAATG	290415	122611	ACAAAAGCAGCTCCCAGCTG
201242	33438	TTTTTTTTCCTGAGACGGAG	245829	78025	GTAAACCTCTTCATGTAAAT	290416	122612	GACAAAAGCAGCTCCCAGCT
201243	33439	TTTTTTTTTCCTGAGACGGA	245830	78026	AGTAAACCTCTTCATGTAAA	290417	122613	TGACAAAAGCAGCTCCCAGC
201244	33440	TTTTTTTTTTCCTGAGACGG	245831	78027	AAGTAAACCTCTTCATGTAA	290418	122614	ATGACAAAAGCAGCTCCCAG
201245	33441	TTTTTTTTTTTCCTGAGACG	245832	78028	AAAGTAAACCTCTTCATGTA	290419	122615	GATGACAAAAGCAGCTCCCA
201246	33442	TTTTTTTTTTTTCCTGAGAC	245833	78029	AAAAGTAAACCTCTTCATGT	290420	122616	AGATGACAAAAGCAGCTCCC
201247	33443	TTTTTTTTTTTTTCCTGAGA	245834	78030	GAAAAGTAAACCTCTTCATG	290421	122617	AAGATGACAAAAGCAGCTCC
201248	33444	TTTTTTTTTTTTTTCCTGAG	245835	78031	AGAAAAGTAAACCTCTTCAT	290422	122618	AAAGATGACAAAAGCAGCTC
201249	33445	TTTTTTTTTTTTTTTCCTGA	245836	78032	GAGAAAAGTAAACCTCTTCA	290423	122619	GAAAGATGACAAAAGCAGCT
201250	33446	TTTTTTTTTTTTTTTTCCTG	245837	78033	TGAGAAAAGTAAACCTCTTC	290424	122620	GGAAAGATGACAAAAGCAGC
201251	33447	TTTTTTTTTTTTTTTTTCCT	245838	78034	GTGAGAAAAGTAAACCTCTT	290425	122621	GGGAAAGATGACAAAAGCAG
201252	33448	TTTTTTTTTTTTTTTTTTCC	245839	78035	TGTGAGAAAAGTAAACCTCT	290426	122622	AGGGAAAGATGACAAAAGCA
201253	33449	TTTTTTTTTTTTTTTTTTTC	245840	78036	ATGTGAGAAAAGTAAACCTC	290427	122623	CAGGGAAAGATGACAAAAGC
201254	33450	TTTTTTTTTTTTTTTTTTT	245841	78037	TATGTGAGAAAAGTAAACCT	290428	122624	CCAGGGAAAGATGACAAAAG
201255	33451	TTTTTTTTTTTTTTTTTTT	245842	78038	TTATGTGAGAAAAGTAAACC	290429	122625	TCCAGGGAAAGATGACAAAA
201256	33452	TTTTTTTTTTTTTTTTTTT	245843	78039	ATTATGTGAGAAAAGTAAAC	290430	122626	TTCCAGGGAAAGATGACAAA
201257	33453	TTTTTTTTTTTTTTTTTTT	245844	78040	GATTATGTGAGAAAAGTAAA	290431	122627	TTTCCAGGGAAAGATGACAA
201258	33454	TTTTTTTTTTTTTTTTTTT	245845	78041	TGATTATGTGAGAAAAGTAA	290432	122628	CTTTCCAGGGAAAGATGACA
201259	33455	TTTTTTTTTTTTTTTTTTT	245846	78042	CTGATTATGTGAGAAAAGTA	290433	122629	ACTTTCCAGGGAAAGATGAC
201260	33456	CTTTTTTTTTTTTTTTTTT	245847	78043	TCTGATTATGTGAGAAAAGT	290434	122630	GACTTTCCAGGGAAAGATGA
201261	33457	GCTTTTTTTTTTTTTTTTT	245848	78044	ATCTGATTATGTGAGAAAAG	290435	122631	GGACTTTCCAGGGAAAGATG
201262	33458	TGCTTTTTTTTTTTTTTTT	245849	78045	CATCTGATTATGTGAGAAAA	290436	122632	AGGACTTTCCAGGGAAAGAT
201263	33459	ATGCTTTTTTTTTTTTTTT	245850	78046	ACATCTGATTATGTGAGAAA	290437	122633	CAGGACTTTCCAGGGAAAGA
201264	33460	GATGCTTTTTTTTTTTTTT	245851	78047	GACATCTGATTATGTGAGAA	290438	122634	ACAGGACTTTCCAGGGAAAG
201265	33461	GGATGCTTTTTTTTTTTTT	245852	78048	AGACATCTGATTATGTGAGA	290439	122635	CACAGGACTTTCCAGGGAAA
201266	33462	AGGATGCTTTTTTTTTTTT	245853	78049	TAGACATCTGATTATGTGAG	290440	122636	CCACAGGACTTTCCAGGGAA
201267	33463	GAGGATGCTTTTTTTTTTT	245854	78050	CTAGACATCTGATTATGTGA	290441	122637	CCCACAGGACTTTCCAGGGA
201268	33464	TGAGGATGCTTTTTTTTTT	245855	78051	TCTAGACATCTGATTATGTG	290442	122638	GCCCACAGGACTTTCCAGGG
201269	33465	CTGAGGATGCTTTTTTTTT	245856	78052	GTCTAGACATCTGATTATGT	290443	122639	AGCCCACAGGACTTTCCAGG
201270	33466	GCTGAGGATGCTTTTTTTT	245857	78053	AGTCTAGACATCTGATTATG	290444	122640	CAGCCCACAGGACTTTCCAG
201271	33467	TGCTGAGGATGCTTTTTTT	245858	78054	AAGTCTAGACATCTGATTAT	290445	122641	ACAGCCCACAGGACTTTCCA
201272	33468	GTGCTGAGGATGCTTTTTT	245859	78055	CAAGTCTAGACATCTGATTA	290446	122642	GACAGCCCACAGGACTTTCC
201273	33469	AGTGCTGAGGATGCTTTTT	245860	78056	CCAAGTCTAGACATCTGATT	290447	122643	AGACAGCCCACAGGACTTTC
201274	33470	AAGTGCTGAGGATGCTTTT	245861	78057	GCCAAGTCTAGACATCTGAT	290448	122644	GAGACAGCCCACAGGACTTT
201275	33471	AAAGTGCTGAGGATGCTTT	245862	78058	GGCCAAGTCTAGACATCTGA	290449	122645	AGAGACAGCCCACAGGACTT
201276	33472	CAAAGTGCTGAGGATGCTT	245863	78059	TGGCCAAGTCTAGACATCTG	290450	122646	AAGAGACAGCCCACAGGACT
201277	33473	CCAAAGTGCTGAGGATGCT	245864	78060	CTGGCCAAGTCTAGACATCT	290451	122647	GAAGAGACAGCCCACAGGAC
201278	33474	GCCAAAGTGCTGAGGATGC	245865	78061	GCTGGCCAAGTCTAGACATC	290452	122648	GGAAGAGACAGCCCACAGGA
201279	33475	TGCCAAAGTGCTGAGGATGC	245866	78062	TGCTGGCCAAGTCTAGACAT	290453	122649	AGGAAGAGACAGCCCACAGG
201280	33476	TTGCCAAAGTGCTGAGGATG	245867	78063	GTGCTGGCCAAGTCTAGACA	290454	122650	GAGGAAGAGACAGCCCACAG
201281	33477	GTTGCCAAAGTGCTGAGGAT	245868	78064	GGTGCTGGCCAAGTCTAGAC	290455	122651	TGAGGAAGAGACAGCCCACA
201282	33478	AGTTGCCAAAGTGCTGAGGA	245869	78065	AGGTGCTGGCCAAGTCTAGA	290456	122652	ATGAGGAAGAGACAGCCCAC

201283	33479	GAGTTGCCAAAGTGCTGAGG	245870	78066	GAGGTGCTGGCCAAGTCTAG	290457	122653	CATGAGGAAGAGACAGCCCA
201284	33480	GGAGTTGCCAAAGTGCTGAG	245871	78067	TGAGGTGCTGGCCAAGTCTA	290458	122654	GCATGAGGAAGAGACAGCCC
201285	33481	TGGAGTTGCCAAAGTGCTGA	245872	78068	TTGAGGTGCTGGCCAAGTCT	290459	122655	GGCATGAGGAAGAGACAGCC
201286	33482	ATGGAGTTGCCAAAGTGCTG	245873	78069	CTTGAGGTGCTGGCCAAGTC	290460	122656	AGGCATGAGGAAGAGACAGC
201287	33483	GATGGAGTTGCCAAAGTGCT	245874	78070	CCTTGAGGTGCTGGCCAAGT	290461	122657	AAGGCATGAGGAAGAGACAG
201288	33484	AGATGGAGTTGCCAAAGTGC	245875	78071	CCCTTGAGGTGCTGGCCAAG	290462	122658	CAAGGCATGAGGAAGAGACA
201289	33485	GAGATGGAGTTGCCAAAGTG	245876	78072	ACCCTTGAGGTGCTGGCCAA	290463	122659	ACAAGGCATGAGGAAGAGAC
201290	33486	GGAGATGGAGTTGCCAAAGT	245877	78073	GACCCTTGAGGTGCTGGCCA	290464	122660	GACAAGGCATGAGGAAGAGA
201291	33487	AGGAGATGGAGTTGCCAAAG	245878	78074	TGACCCTTGAGGTGCTGGCC	290465	122661	GGACAAGGCATGAGGAAGAG
201292	33488	GAGGAGATGGAGTTGCCAAA	245879	78075	ATGACCCTTGAGGTGCTGGC	290466	122662	GGGACAAGGCATGAGGAAGA
201293	33489	GGAGGAGATGGAGTTGCCAA	245880	78076	AATGACCCTTGAGGTGCTGG	290467	122663	TGGGACAAGGCATGAGGAAG
201294	33490	GGGAGGAGATGGAGTTGCCA	245881	78077	CAATGACCCTTGAGGTGCTG	290468	122664	ATGGGACAAGGCATGAGGAA
201295	33491	TGGGAGGAGATGGAGTTGCC	245882	78078	TCAATGACCCTTGAGGTGCT	290469	122665	CATGGGACAAGGCATGAGGA
201296	33492	TTGGGAGGAGATGGAGTTGC	245883	78079	ATCAATGACCCTTGAGGTGC	290470	122666	GCATGGGACAAGGCATGAGG
201297	33493	GTTGGGAGGAGATGGAGTTG	245884	78080	CATCAATGACCCTTGAGGTG	290471	122667	AGCATGGGACAAGGCATGAG
201298	33494	TGTTGGGAGGAGATGGAGTT	245885	78081	GCATCAATGACCCTTGAGGT	290472	122668	AAGCATGGGACAAGGCATGA
201299	33495	ATGTTGGGAGGAGATGGAGT	245886	78082	AGCATCAATGACCCTTGAGG	290473	122669	CAAGCATGGGACAAGGCATG
201300	33496	CATGTTGGGAGGAGATGGAG	245887	78083	GAGCATCAATGACCCTTGAG	290474	122670	CCAAGCATGGGACAAGGCAT
201301	33497	ACATGTTGGGAGGAGATGGA	245888	78084	AGAGCATCAATGACCCTTGA	290475	122671	CCCAAGCATGGGACAAGGCA
201302	33498	GACATGTTGGGAGGAGATGG	245889	78085	GAGAGCATCAATGACCCTTG	290476	122672	GCCCAAGCATGGGACAAGGC
201303	33499	GGACATGTTGGGAGGAGATG	245890	78086	GGAGAGCATCAATGACCCTT	290477	122673	TGCCCAAGCATGGGACAAGG
201304	33500	GGGACATGTTGGGAGGAGAT	245891	78087	AGGAGAGCATCAATGACCCT	290478	122674	ATGCCCAAGCATGGGACAAG
201305	33501	AGGGACATGTTGGGAGGAGA	245892	78088	CAGGAGAGCATCAATGACCC	290479	122675	CATGCCCAAGCATGGGACAA
201306	33502	CAGGGACATGTTGGGAGGAG	245893	78089	ACAGGAGAGCATCAATGACC	290480	122676	CCATGCCCAAGCATGGGACA
201307	33503	ACAGGGACATGTTGGGAGGA	245894	78090	GACAGGAGAGCATCAATGAC	290481	122677	ACCATGCCCAAGCATGGGAC
201308	33504	AACAGGGACATGTTGGGAGG	245895	78091	AGACAGGAGAGCATCAATGA	290482	122678	CACCATGCCCAAGCATGGGA
201309	33505	TAACAGGGACATGTTGGGAG	245896	78092	AAGACAGGAGAGCATCAATG	290483	122679	ACACCATGCCCAAGCATGGG
201310	33506	GTAACAGGGACATGTTGGGA	245897	78093	AAAGACAGGAGAGCATCAAT	290484	122680	GACACCATGCCCAAGCATGG
201311	33507	AGTAACAGGGACATGTTGGG	245898	78094	TAAAGACAGGAGAGCATCAA	290485	122681	TGACACCATGCCCAAGCATG
201312	33508	CAGTAACAGGGACATGTTGG	245899	78095	ATAAAGACAGGAGAGCATCA	290486	122682	TTGACACCATGCCCAAGCAT
201313	33509	CCAGTAACAGGGACATGTTG	245900	78096	AATAAAGACAGGAGAGCATC	290487	122683	CTTGACACCATGCCCAAGCA
201314	33510	TCCAGTAACAGGGACATGTT	245901	78097	AAATAAAGACAGGAGAGCAT	290488	122684	GCTTGACACCATGCCCAAGC
201315	33511	TTCCAGTAACAGGGACATGT	245902	78098	AAAATAAAGACAGGAGAGCA	290489	122685	CGCTTGACACCATGCCCAAG
201316	33512	ATTCCAGTAACAGGGACATG	245903	78099	GAAAATAAAGACAGGAGAGC	290490	122686	ACGCTTGACACCATGCCCAA
201317	33513	GATTCCAGTAACAGGGACAT	245904	78100	AGAAAATAAAGACAGGAGAG	290491	122687	GACGCTTGACACCATGCCCA
201318	33514	GGATTCCAGTAACAGGGACA	245905	78101	CAGAAAATAAAGACAGGAGA	290492	122688	TGACGCTTGACACCATGCCC
201319	33515	TGGATTCCAGTAACAGGGAC	245906	78102	ACAGAAAATAAAGACAGGAG	290493	122689	CTGACGCTTGACACCATGCC
201320	33516	CTGGATTCCAGTAACAGGGA	245907	78103	GACAGAAAATAAAGACAGGA	290494	122690	CCTGACGCTTGACACCATGC
201321	33517	GCTGGATTCCAGTAACAGGG	245908	78104	TGACAGAAAATAAAGACAGG	290495	122691	TCCTGACGCTTGACACCATG
201322	33518	GGCTGGATTCCAGTAACAGG	245909	78105	ATGACAGAAAATAAAGACAG	290496	122692	CTCCTGACGCTTGACACCAT
201323	33519	TGGCTGGATTCCAGTAACAG	245910	78106	GATGACAGAAAATAAAGACA	290497	122693	CCTCCTGACGCTTGACACCA
201324	33520	CTGGCTGGATTCCAGTAACA	245911	78107	AGATGACAGAAAATAAAGAC	290498	122694	CCCTCCTGACGCTTGACACC
201325	33521	CCTGGCTGGATTCCAGTAAC	245912	78108	AAGATGACAGAAAATAAAGA	290499	122695	TCCCTCCTGACGCTTGACAC
201326	33522	TCCTGGCTGGATTCCAGTAA	245913	78109	AAAGATGACAGAAAATAAAG	290500	122696	CTCCCTCCTGACGCTTGACA
201327	33523	GTCCTGGCTGGATTCCAGTA	245914	78110	TAAAGATGACAGAAAATAAA	290501	122697	TCTCCCTCCTGACGCTTGAC
201328	33524	AGTCCTGGCTGGATTCCAGT	245915	78111	CTAAAGATGACAGAAAATAA	290502	122698	TTCTCCCTCCTGACGCTTGA
201329	33525	GAGTCCTGGCTGGATTCCAG	245916	78112	ACTAAAGATGACAGAAAATA	290503	122699	TTTCTCCCTCCTGACGCTTG
201330	33526	TGAGTCCTGGCTGGATTCCA	245917	78113	CACTAAAGATGACAGAAAAT	290504	122700	CTTTCTCCCTCCTGACGCTT
201331	33527	CTGAGTCCTGGCTGGATTCC	245918	78114	CCACTAAAGATGACAGAAAA	290505	122701	CCTTTCTCCCTCCTGACGCT
201332	33528	GCTGAGTCCTGGCTGGATTC	245919	78115	ACCACTAAAGATGACAGAAA	290506	122702	CCCTTTCTCCCTCCTGACGC
201333	33529	GGCTGAGTCCTGGCTGGATT	245920	78116	AACCACTAAAGATGACAGAA	290507	122703	ACCCTTTCTCCCTCCTGACG
201334	33530	GGGCTGAGTCCTGGCTGGAT	245921	78117	CAACCACTAAAGATGACAGA	290508	122704	GACCCTTTCTCCCTCCTGAC
201335	33531	GGGGCTGAGTCCTGGCTGGA	245922	78118	CCAACCACTAAAGATGACAG	290509	122705	GGACCCTTTCTCCCTCCTGA
201336	33532	CGGGGCTGAGTCCTGGCTGG	245923	78119	TCCAACCACTAAAGATGACA	290510	122706	AGGACCCTTTCTCCCTCCTG
201337	33533	TCGGGGCTGAGTCCTGGCTG	245924	78120	ATCCAACCACTAAAGATGAC	290511	122707	AAGGACCCTTTCTCCCTCCT
201338	33534	ATCGGGGCTGAGTCCTGGCT	245925	78121	AATCCAACCACTAAAGATGA	290512	122708	TAAGGACCCTTTCTCCCTCC
201339	33535	GATCGGGGCTGAGTCCTGGC	245926	78122	CAATCCAACCACTAAAGATG	290513	122709	ATAAGGACCCTTTCTCCCTC
201340	33536	AGATCGGGGCTGAGTCCTGG	245927	78123	ACAATCCAACCACTAAAGAT	290514	122710	AATAAGGACCCTTTCTCCCT
201341	33537	AAGATCGGGGCTGAGTCCTG	245928	78124	AACAATCCAACCACTAAAGA	290515	122711	AAATAAGGACCCTTTCTCCC
201342	33538	AAAGATCGGGGCTGAGTCCT	245929	78125	CAACAATCCAACCACTAAAG	290516	122712	TAAATAAGGACCCTTTCTCC
201343	33539	GAAAGATCGGGGCTGAGTCC	245930	78126	GCAACAATCCAACCACTAAA	290517	122713	ATAAATAAGGACCCTTTCTC
201344	33540	AGAAAGATCGGGGCTGAGTC	245931	78127	GGCAACAATCCAACCACTAA	290518	122714	AATAAATAAGGACCCTTTCT
201345	33541	TAGAAAGATCGGGGCTGAGT	245932	78128	AGGCAACAATCCAACCACTA	290519	122715	AAATAAATAAGGACCCTTTC
201346	33542	GTAGAAAGATCGGGGCTGAG	245933	78129	GAGGCAACAATCCAACCACT	290520	122716	TAAATAAATAAGGACCCTTT
201347	33543	AGTAGAAAGATCGGGGCTGA	245934	78130	TGAGGCAACAATCCAACCAC	290521	122717	ATAAATAAATAAGGACCCTT
201348	33544	GAGTAGAAAGATCGGGGCTG	245935	78131	ATGAGGCAACAATCCAACCA	290522	122718	AATAAATAAATAAGGACCCT
201349	33545	AGAGTAGAAAGATCGGGGCT	245936	78132	CATGAGGCAACAATCCAACC	290523	122719	AAATAAATAAATAAGGACCC
201350	33546	TAGAGTAGAAAGATCGGGGC	245937	78133	CCATGAGGCAACAATCCAAC	290524	122720	TAAATAAATAAATAAGGACC
201351	33547	TTAGAGTAGAAAGATCGGGG	245938	78134	ACCATGAGGCAACAATCCAA	290525	122721	CTAAATAAATAAATAAGGAC
201352	33548	GTTAGAGTAGAAAGATCGGG	245939	78135	AACCATGAGGCAACAATCCA	290526	122722	TCTAAATAAATAAATAAGGA
201353	33549	GGTTAGAGTAGAAAGATCGG	245940	78136	TAACCATGAGGCAACAATCC	290527	122723	CTCTAAATAAATAAATAAGG
201354	33550	TGGTTAGAGTAGAAAGATCG	245941	78137	GTAACCATGAGGCAACAATC	290528	122724	TCTCTAAATAAATAAATAAG

201355	33551	CTGGTTAGAGTAGAAAGATC	245942	78138	TGTAACCATGAGGCAACAAT	290529	122725	CTCTCTAAATAAATAAATAA
201356	33552	ACTGGTTAGAGTAGAAAGAT	245943	78139	TTGTAACCATGAGGCAACAA	290530	122726	CCTCTCTAAATAAATAAATA
201357	33553	AACTGGTTAGAGTAGAAAGA	245944	78140	TTTGTAACCATGAGGCAACA	290531	122727	CCCTCTCTAAATAAATAAAT
201358	33554	CAACTGGTTAGAGTAGAAAG	245945	78141	CTTTGTAACCATGAGGCAAC	290532	122728	TCCCTCTCTAAATAAATAAA
201359	33555	ACAACTGGTTAGAGTAGAAA	245946	78142	ACTTTGTAACCATGAGGCAA	290533	122729	GTCCCTCTCTAAATAAATAA
201360	33556	GACAACTGGTTAGAGTAGAA	245947	78143	CACTTTGTAACCATGAGGCA	290534	122730	GGTCCCTCTCTAAATAAATA
201361	33557	AGACAACTGGTTAGAGTAGA	245948	78144	CCACTTTGTAACCATGAGGC	290535	122731	GGGTCCCTCTCTAAATAAAT
201362	33558	GAGACAACTGGTTAGAGTAG	245949	78145	GCCACTTTGTAACCATGAGG	290536	122732	AGGGTCCCTCTCTAAATAAA
201363	33559	TGAGACAACTGGTTAGAGTA	245950	78146	AGCCACTTTGTAACCATGAG	290537	122733	AAGGGTCCCTCTCTAAATAA
201364	33560	CTGAGACAACTGGTTAGAGT	245951	78147	CAGCCACTTTGTAACCATGA	290538	122734	GAAGGGTCCCTCTCTAAATA
201365	33561	ACTGAGACAACTGGTTAGAG	245952	78148	GCAGCCACTTTGTAACCATG	290539	122735	AGAAGGGTCCCTCTCTAAAT
201366	33562	AACTGAGACAACTGGTTAGA	245953	78149	AGCAGCCACTTTGTAACCAT	290540	122736	AAGAAGGGTCCCTCTCTAAA
201367	33563	TAACTGAGACAACTGGTTAG	245954	78150	CAGCAGCCACTTTGTAACCA	290541	122737	GAAGAAGGGTCCCTCTCTAA
201368	33564	TTAACTGAGACAACTGGTTA	245955	78151	GCAGCAGCCACTTTGTAACC	290542	122738	AGAAGAAGGGTCCCTCTCTA
201369	33565	GTTAACTGAGACAACTGGTT	245956	78152	TGCAGCAGCCACTTTGTAAC	290543	122739	CAGAAGAAGGGTCCCTCTCT
201370	33566	TGTTAACTGAGACAACTGGT	245957	78153	GTGCAGCAGCCACTTTGTAA	290544	122740	ACAGAAGAAGGGTCCCTCTC
201371	33567	TTGTTAACTGAGACAACTGG	245958	78154	AGTGCAGCAGCCACTTTGTA	290545	122741	AACAGAAGAAGGGTCCCTCT
201372	33568	CTTGTTAACTGAGACAACTG	245959	78155	AAGTGCAGCAGCCACTTTGT	290546	122742	GAACAGAAGAAGGGTCCCTC
201373	33569	CCTTGTTAACTGAGACAACT	245960	78156	GAAGTGCAGCAGCCACTTTG	290547	122743	GGAACAGAAGAAGGGTCCCT
201374	33570	TCCTTGTTAACTGAGACAAC	245961	78157	GGAAGTGCAGCAGCCACTTT	290548	122744	GGGAACAGAAGAAGGGTCCC
201375	33571	GTCCTTGTTAACTGAGACAA	245962	78158	TGGAAGTGCAGCAGCCACTT	290549	122745	TGGGAACAGAAGAAGGGTCC
201376	33572	TGTCCTTGTTAACTGAGACA	245963	78159	CTGGAAGTGCAGCAGCCACT	290550	122746	CTGGGAACAGAAGAAGGGTC
201377	33573	CTGTCCTTGTTAACTGAGAC	245964	78160	CCTGGAAGTGCAGCAGCCAC	290551	122747	CCTGGGAACAGAAGAAGGGT
201378	33574	CCTGTCCTTGTTAACTGAGA	245965	78161	GCCTGGAAGTGCAGCAGCCA	290552	122748	GCCTGGGAACAGAAGAAGGG
201379	33575	ACCTGTCCTTGTTAACTGAG	245966	78162	TGCCTGGAAGTGCAGCAGCC	290553	122749	AGCCTGGGAACAGAAGAAGG
201380	33576	AACCTGTCCTTGTTAACTGA	245967	78163	ATGCCTGGAAGTGCAGCAGC	290554	122750	CAGCCTGGGAACAGAAGAAG
201381	33577	AAACCTGTCCTTGTTAACTG	245968	78164	GATGCCTGGAAGTGCAGCAG	290555	122751	CCAGCCTGGGAACAGAAGAA
201382	33578	TAAACCTGTCCTTGTTAACT	245969	78165	TGATGCCTGGAAGTGCAGCA	290556	122752	TCCAGCCTGGGAACAGAAGA
201383	33579	ATAAACCTGTCCTTGTTAAC	245970	78166	GTGATGCCTGGAAGTGCAGC	290557	122753	CTCCAGCCTGGGAACAGAAG
201384	33580	CATAAACCTGTCCTTGTTAA	245971	78167	TGTGATGCCTGGAAGTGCAG	290558	122754	ACTCCAGCCTGGGAACAGAA
201385	33581	GCATAAACCTGTCCTTGTTA	245972	78168	ATGTGATGCCTGGAAGTGCA	290559	122755	CACTCCAGCCTGGGAACAGA
201386	33582	AGCATAAACCTGTCCTTGTT	245973	78169	GATGTGATGCCTGGAAGTGC	290560	122756	GCACTCCAGCCTGGGAACAG
201387	33583	CAGCATAAACCTGTCCTTGT	245974	78170	AGATGTGATGCCTGGAAGTG	290561	122757	TGCACTCCAGCCTGGGAACA
201388	33584	GCAGCATAAACCTGTCCTTG	245975	78171	CAGATGTGATGCCTGGAAGT	290562	122758	CTGCACTCCAGCCTGGGAAC
201389	33585	TGCAGCATAAACCTGTCCTT	245976	78172	GCAGATGTGATGCCTGGAAG	290563	122759	ACTGCACTCCAGCCTGGGAA
201390	33586	CTGCAGCATAAACCTGTCCT	245977	78173	GGCAGATGTGATGCCTGGAA	290564	122760	CACTGCACTCCAGCCTGGGA
201391	33587	ACTGCAGCATAAACCTGTCC	245978	78174	AGGCAGATGTGATGCCTGGA	290565	122761	CCACTGCACTCCAGCCTGGG
201392	33588	CACTGCAGCATAAACCTGTC	245979	78175	AAGGCAGATGTGATGCCTGG	290566	122762	ACCACTGCACTCCAGCCTGG
201393	33589	TCACTGCAGCATAAACCTGT	245980	78176	AAAGGCAGATGTGATGCCTG	290567	122763	CACCACTGCACTCCAGCCTG
201394	33590	GTCACTGCAGCATAAACCTG	245981	78177	CAAAGGCAGATGTGATGCCT	290568	122764	GCACCACTGCACTCCAGCCT
201395	33591	TGTCACTGCAGCATAAACCT	245982	78178	TCAAAGGCAGATGTGATGCC	290569	122765	CGCACCACTGCACTCCAGCC
201396	33592	TTGTCACTGCAGCATAAACC	245983	78179	TTCAAAGGCAGATGTGATGC	290570	122766	TCGCACCACTGCACTCCAGC
201397	33593	TTTGTCACTGCAGCATAAAC	245984	78180	CTTCAAAGGCAGATGTGATG	290571	122767	ATCGCACCACTGCACTCCAG
201398	33594	GTTTGTCACTGCAGCATAAA	245985	78181	GCTTCAAAGGCAGATGTGAT	290572	122768	GATCGCACCACTGCACTCCA
201399	33595	TGTTTGTCACTGCAGCATAA	245986	78182	TGCTTCAAAGGCAGATGTGA	290573	122769	AGATCGCACCACTGCACTCC
201400	33596	TTGTTTGTCACTGCAGCATA	245987	78183	CTGCTTCAAAGGCAGATGTG	290574	122770	GAGATCGCACCACTGCACTC
201401	33597	CTTGTTTGTCACTGCAGCAT	245988	78184	CCTGCTTCAAAGGCAGATGT	290575	122771	CGAGATCGCACCACTGCACT
201402	33598	TCTTGTTTGTCACTGCAGCA	245989	78185	TCCTGCTTCAAAGGCAGATG	290576	122772	CCGAGATCGCACCACTGCAC
201403	33599	ATCTTGTTTGTCACTGCAGC	245990	78186	TTCCTGCTTCAAAGGCAGAT	290577	122773	GCCGAGATCGCACCACTGCA
201404	33600	GATCTTGTTTGTCACTGCAG	245991	78187	GTTCCTGCTTCAAAGGCAGA	290578	122774	AGCCGAGATCGCACCACTGC
201405	33601	GGATCTTGTTTGTCACTGCA	245992	78188	TGTTCCTGCTTCAAAGGCAG	290579	122775	GAGCCGAGATCGCACCACTG
201406	33602	GGGATCTTGTTTGTCACTGC	245993	78189	TTGTTCCTGCTTCAAAGGCA	290580	122776	TGAGCCGAGATCGCACCACT
201407	33603	TGGGATCTTGTTTGTCACTG	245994	78190	CTTGTTCCTGCTTCAAAGGC	290581	122777	GTGAGCCGAGATCGCACCAC
201408	33604	TTGGGATCTTGTTTGTCACT	245995	78191	ACTTGTTCCTGCTTCAAAGG	290582	122778	AGTGAGCCGAGATCGCACCA
201409	33605	TTTGGGATCTTGTTTGTCAC	245996	78192	AACTTGTTCCTGCTTCAAAG	290583	122779	CAGTGAGCCGAGATCGCACC
201410	33606	ATTTGGGATCTTGTTTGTCA	245997	78193	CAACTTGTTCCTGCTTCAAA	290584	122780	GCAGTGAGCCGAGATCGCAC
201411	33607	AATTTGGGATCTTGTTTGTC	245998	78194	GCAACTTGTTCCTGCTTCAA	290585	122781	TGCAGTGAGCCGAGATCGCA
201412	33608	GAATTTGGGATCTTGTTTGT	245999	78195	TGCAACTTGTTCCTGCTTCA	290586	122782	TTGCAGTGAGCCGAGATCGC
201413	33609	AGAATTTGGGATCTTGTTTG	246000	78196	TTGCAACTTGTTCCTGCTTC	290587	122783	GTTGCAGTGAGCCGAGATCG
201414	33610	AAGAATTTGGGATCTTGTTT	246001	78197	TTTGCAACTTGTTCCTGCTT	290588	122784	GGTTGCAGTGAGCCGAGATC
201415	33611	CAAGAATTTGGGATCTTGTT	246002	78198	CTTTGCAACTTGTTCCTGCT	290589	122785	AGGTTGCAGTGAGCCGAGAT
201416	33612	ACAAGAATTTGGGATCTTGT	246003	78199	ACTTTGCAACTTGTTCCTGC	290590	122786	GAGGTTGCAGTGAGCCGAGA
201417	33613	CACAAGAATTTGGGATCTTG	246004	78200	TACTTTGCAACTTGTTCCTG	290591	122787	GGAGGTTGCAGTGAGCCGAG
201418	33614	CCACAAGAATTTGGGATCTT	246005	78201	TTACTTTGCAACTTGTTCCT	290592	122788	CGGAGGTTGCAGTGAGCCGA
201419	33615	GCCACAAGAATTTGGGATCT	246006	78202	TTTACTTTGCAACTTGTTCC	290593	122789	GCGGAGGTTGCAGTGAGCCG
201420	33616	AGCCACAAGAATTTGGGATC	246007	78203	CTTTACTTTGCAACTTGTTC	290594	122790	GGCGGAGGTTGCAGTGAGCC
201421	33617	AAGCCACAAGAATTTGGGAT	246008	78204	ACTTTACTTTGCAACTTGTT	290595	122791	AGGCGGAGGTTGCAGTGAGC
201422	33618	GAAGCCACAAGAATTTGGGA	246009	78205	CACTTTACTTTGCAACTTGT	290596	122792	GAGGCGGAGGTTGCAGTGAG
201423	33619	TGAAGCCACAAGAATTTGGG	246010	78206	CCACTTTACTTTGCAACTTG	290597	122793	GGAGGCGGAGGTTGCAGTGA
201424	33620	GTGAAGCCACAAGAATTTGG	246011	78207	GCCACTTTACTTTGCAACTT	290598	122794	AGGAGGCGGAGGTTGCAGTG
201425	33621	TGTGAAGCCACAAGAATTTG	246012	78208	GGCCACTTTACTTTGCAACT	290599	122795	CAGGAGGCGGAGGTTGCAGT
201426	33622	GTGTGAAGCCACAAGAATTT	246013	78209	TGGCCACTTTACTTTGCAAC	290600	122796	CCAGGAGGCGGAGGTTGCAG

201427	33623	TGTGTGAAGCCACAAGAATT	246014	78210	TTGGCCACTTTACTTTGCAA	290601	122797	CCCAGGAGGCGGAGGTTGCA
201428	33624	ATGTGTGAAGCCACAAGAAT	246015	78211	TTTGGCCACTTTACTTTGCA	290602	122798	ACCCAGGAGGCGGAGGTTGC
201429	33625	GATGTGTGAAGCCACAAGAA	246016	78212	TTTTGGCCACTTTACTTTGC	290603	122799	AACCCAGGAGGCGGAGGTTG
201430	33626	AGATGTGTGAAGCCACAAGA	246017	78213	CTTTTGGCCACTTTACTTTG	290604	122800	GAACCCAGGAGGCGGAGGTT
201431	33627	CAGATGTGTGAAGCCACAAG	246018	78214	CCTTTTGGCCACTTTACTTT	290605	122801	TGAACCCAGGAGGCGGAGGT
201432	33628	CCAGATGTGTGAAGCCACAA	246019	78215	CCCTTTTGGCCACTTTACTT	290606	122802	TTGAACCCAGGAGGCGGAGG
201433	33629	GCCAGATGTGTGAAGCCACA	246020	78216	GCCCTTTTGGCCACTTTACT	290607	122803	CTTGAACCCAGGAGGCGGAG
201434	33630	TGCCAGATGTGTGAAGCCAC	246021	78217	GGCCCTTTTGGCCACTTTAC	290608	122804	ACTTGAACCCAGGAGGCGGA
201435	33631	GTGCCAGATGTGTGAAGCCA	246022	78218	GGGCCCTTTTGGCCACTTTA	290609	122805	CACTTGAACCCAGGAGGCGG
201436	33632	GGTGCCAGATGTGTGAAGCC	246023	78219	AGGGCCCTTTTGGCCACTTT	290610	122806	TCACTTGAACCCAGGAGGCG
201437	33633	TGGTGCCAGATGTGTGAAGC	246024	78220	CAGGGCCCTTTTGGCCACTT	290611	122807	ATCACTTGAACCCAGGAGGC
201438	33634	GTGGTGCCAGATGTGTGAAG	246025	78221	TCAGGGCCCTTTTGGCCACT	290612	122808	AATCACTTGAACCCAGGAGG
201439	33635	GGTGGTGCCAGATGTGTGAA	246026	78222	TTCAGGGCCCTTTTGGCCAC	290613	122809	GAATCACTTGAACCCAGGAG
201440	33636	AGGTGGTGCCAGATGTGTGA	246027	78223	TTTCAGGGCCCTTTTGGCCA	290614	122810	AGAATCACTTGAACCCAGGA
201441	33637	GAGGTGGTGCCAGATGTGTG	246028	78224	GTTTCAGGGCCCTTTTGGCC	290615	122811	GAGAATCACTTGAACCCAGG
201442	33638	TGAGGTGGTGCCAGATGTGT	246029	78225	AGTTTCAGGGCCCTTTTGGC	290616	122812	GGAGAATCACTTGAACCCAG
201443	33639	ATGAGGTGGTGCCAGATGTG	246030	78226	TAGTTTCAGGGCCCTTTTGG	290617	122813	AGGAGAATCACTTGAACCCA
201444	33640	GATGAGGTGGTGCCAGATGT	246031	78227	TTAGTTTCAGGGCCCTTTTG	290618	122814	CAGGAGAATCACTTGAACCC
201445	33641	AGATGAGGTGGTGCCAGATG	246032	78228	TTTAGTTTCAGGGCCCTTTT	290619	122815	GCAGGAGAATCACTTGAACC
201446	33642	AAGATGAGGTGGTGCCAGAT	246033	78229	ATTTAGTTTCAGGGCCCTTT	290620	122816	GGCAGGAGAATCACTTGAAC
201447	33643	GAAGATGAGGTGGTGCCAGA	246034	78230	CATTTAGTTTCAGGGCCCTT	290621	122817	AGGCAGGAGAATCACTTGAA
201448	33644	GGAAGATGAGGTGGTGCCAG	246035	78231	ACATTTAGTTTCAGGGCCCT	290622	122818	GAGGCAGGAGAATCACTTGA
201449	33645	TGGAAGATGAGGTGGTGCCA	246036	78232	CACATTTAGTTTCAGGGCCC	290623	122819	TGAGGCAGGAGAATCACTTG
201450	33646	CTGGAAGATGAGGTGGTGCC	246037	78233	ACACATTTAGTTTCAGGGCC	290624	122820	CTGAGGCAGGAGAATCACTT
201451	33647	GCTGGAAGATGAGGTGGTGC	246038	78234	GACACATTTAGTTTCAGGGC	290625	122821	GCTGAGGCAGGAGAATCACT
201452	33648	GGCTGGAAGATGAGGTGGTG	246039	78235	GGACACATTTAGTTTCAGGG	290626	122822	GGCTGAGGCAGGAGAATCAC
201453	33649	AGGCTGGAAGATGAGGTGGT	246040	78236	GGGACACATTTAGTTTCAGG	290627	122823	AGGCTGAGGCAGGAGAATCA
201454	33650	AAGGCTGGAAGATGAGGTGG	246041	78237	GGGGACACATTTAGTTTCAG	290628	122824	GAGGCTGAGGCAGGAGAATC
201455	33651	TAAGGCTGGAAGATGAGGTG	246042	78238	AGGGGACACATTTAGTTTCA	290629	122825	GGAGGCTGAGGCAGGAGAAT
201456	33652	CTAAGGCTGGAAGATGAGGT	246043	78239	AAGGGGACACATTTAGTTTC	290630	122826	AGGAGGCTGAGGCAGGAGAA
201457	33653	CCTAAGGCTGGAAGATGAGG	246044	78240	TAAGGGGACACATTTAGTTT	290631	122827	CAGGAGGCTGAGGCAGGAGA
201458	33654	TCCTAAGGCTGGAAGATGAG	246045	78241	CTAAGGGGACACATTTAGTT	290632	122828	TCAGGAGGCTGAGGCAGGAG
201459	33655	CTCCTAAGGCTGGAAGATGA	246046	78242	CCTAAGGGGACACATTTAGT	290633	122829	CTCAGGAGGCTGAGGCAGGA
201460	33656	ACTCCTAAGGCTGGAAGATG	246047	78243	TCCTAAGGGGACACATTTAG	290634	122830	ACTCAGGAGGCTGAGGCAGG
201461	33657	GACTCCTAAGGCTGGAAGAT	246048	78244	TTCCTAAGGGGACACATTTA	290635	122831	TACTCAGGAGGCTGAGGCAG
201462	33658	TGACTCCTAAGGCTGGAAGA	246049	78245	TTTCCTAAGGGGACACATTT	290636	122832	CTACTCAGGAGGCTGAGGCA
201463	33659	ATGACTCCTAAGGCTGGAAG	246050	78246	CTTTCCTAAGGGGACACATT	290637	122833	GCTACTCAGGAGGCTGAGGC
201464	33660	GATGACTCCTAAGGCTGGAA	246051	78247	GCTTTCCTAAGGGGACACAT	290638	122834	AGCTACTCAGGAGGCTGAGG
201465	33661	AGATGACTCCTAAGGCTGGA	246052	78248	TGCTTTCCTAAGGGGACACA	290639	122835	CAGCTACTCAGGAGGCTGAG
201466	33662	AAGATGACTCCTAAGGCTGG	246053	78249	CTGCTTTCCTAAGGGGACAC	290640	122836	TCAGCTACTCAGGAGGCTGA
201467	33663	AAAGATGACTCCTAAGGCTG	246054	78250	CCTGCTTTCCTAAGGGGACA	290641	122837	CTCAGCTACTCAGGAGGCTG
201468	33664	AAAAGATGACTCCTAAGGCT	246055	78251	TCCTGCTTTCCTAAGGGGAC	290642	122838	TCTCAGCTACTCAGGAGGCT
201469	33665	TAAAAGATGACTCCTAAGGC	246056	78252	CTCCTGCTTTCCTAAGGGGA	290643	122839	ATCTCAGCTACTCAGGAGGC
201470	33666	CTAAAAGATGACTCCTAAGG	246057	78253	ACTCCTGCTTTCCTAAGGGG	290644	122840	AATCTCAGCTACTCAGGAGG
201471	33667	ACTAAAAGATGACTCCTAAG	246058	78254	AACTCCTGCTTTCCTAAGGG	290645	122841	TAATCTCAGCTACTCAGGAG
201472	33668	AACTAAAAGATGACTCCTAA	246059	78255	AAACTCCTGCTTTCCTAAGG	290646	122842	GTAATCTCAGCTACTCAGGA
201473	33669	GAACTAAAAGATGACTCCTA	246060	78256	AAAACTCCTGCTTTCCTAAG	290647	122843	TGTAATCTCAGCTACTCAGG
201474	33670	GGAACTAAAAGATGACTCCT	246061	78257	GAAAACTCCTGCTTTCCTAA	290648	122844	CTGTAATCTCAGCTACTCAG
201475	33671	AGGAACTAAAAGATGACTCC	246062	78258	AGAAAACTCCTGCTTTCCTA	290649	122845	CCTGTAATCTCAGCTACTCA
201476	33672	AAGGAACTAAAAGATGACTC	246063	78259	AAGAAAACTCCTGCTTTCCT	290650	122846	GCCTGTAATCTCAGCTACTC
201477	33673	CAAGGAACTAAAAGATGACT	246064	78260	CAAGAAAACTCCTGCTTTCC	290651	122847	TGCCTGTAATCTCAGCTACT
201478	33674	TCAAGGAACTAAAAGATGAC	246065	78261	GCAAGAAAACTCCTGCTTTC	290652	122848	GTGCCTGTAATCTCAGCTAC
201479	33675	TTCAAGGAACTAAAAGATGA	246066	78262	TGCAAGAAAACTCCTGCTTT	290653	122849	TGTGCCTGTAATCTCAGCTA
201480	33676	TTTCAAGGAACTAAAAGATG	246067	78263	TTGCAAGAAAACTCCTGCTT	290654	122850	ATGTGCCTGTAATCTCAGCT
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201482	33678	GTTTTCAAGGAACTAAAAGA	246069	78265	ACTTGCAAGAAAACTCCTGC	290656	122852	GCATGTGCCTGTAATCTCAG
201483	33679	AGTTTTCAAGGAACTAAAAG	246070	78266	CACTTGCAAGAAAACTCCTG	290657	122853	GGCATGTGCCTGTAATCTCA
201484	33680	GAGTTTTCAAGGAACTAAAA	246071	78267	CCACTTGCAAGAAAACTCCT	290658	122854	TGGCATGTGCCTGTAATCTC
201485	33681	AGAGTTTTCAAGGAACTAAA	246072	78268	GCCACTTGCAAGAAAACTCC	290659	122855	TTGGCATGTGCCTGTAATCT
201486	33682	AAGAGTTTTCAAGGAACTAA	246073	78269	TGCCACTTGCAAGAAAACTC	290660	122856	GTTGGCATGTGCCTGTAATC
201487	33683	AAAGAGTTTTCAAGGAACTA	246074	78270	TTGCCACTTGCAAGAAAACT	290661	122857	TGTTGGCATGTGCCTGTAAT
201488	33684	TAAAGAGTTTTCAAGGAACT	246075	78271	ATTGCCACTTGCAAGAAAAC	290662	122858	ATGTTGGCATGTGCCTGTAA
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201497	33693	AGAAAACTGTAAAGAGTTTT	246084	78280	AAGCAGAAGATTGCCACTTG	290671	122867	TAGCCAGGCATGTTGGCATG
201498	33694	CAGAAAACTGTAAAGAGTTT	246085	78281	TAAGCAGAAGATTGCCACTT	290672	122868	TTAGCCAGGCATGTTGGCAT

201499	33695	ACAGAAAACTGTAAAGAGTT	246086	78282	ATAAGCAGAAGATTGCCACT	290673	122869	ATTAGCCAGGCATGTTGGCA
201500	33696	AACAGAAAACTGTAAAGAGT	246087	78283	CATAAGCAGAAGATTGCCAC	290674	122870	AATTAGCCAGGCATGTTGGC
201501	33697	CAACAGAAAACTGTAAAGAG	246088	78284	ACATAAGCAGAAGATTGCCA	290675	122871	AAATTAGCCAGGCATGTTGG
201502	33698	CCAACAGAAAACTGTAAAGA	246089	78285	GACATAAGCAGAAGATTGCC	290676	122872	AAAATTAGCCAGGCATGTTG
201503	33699	CCCAACAGAAAACTGTAAAG	246090	78286	AGACATAAGCAGAAGATTGC	290677	122873	AAAAATTAGCCAGGCATGTT
201504	33700	CCCCAACAGAAAACTGTAAA	246091	78287	GAGACATAAGCAGAAGATTG	290678	122874	AAAAAATTAGCCAGGCATGT
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201509	33705	CAAGGCCCCAACAGAAAACT	246096	78292	CCAATGAGACATAAGCAGAA	290683	122879	AAAAAAAAAAATTAGCCAGG
201510	33706	ACAAGGCCCCAACAGAAAAC	246097	78293	GCCAATGAGACATAAGCAGA	290684	122880	AAAAAAAAAAAATTAGCCAG
201511	33707	GACAAGGCCCCAACAGAAAA	246098	78294	GGCCAATGAGACATAAGCAG	290685	122881	AAAAAAAAAAAAATTAGCCA
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201513	33709	ATGACAAGGCCCCAACAGAA	246100	78296	CTGGCCAATGAGACATAAGC	290687	122883	AAAAAAAAAAAAAAATTAGC
201514	33710	TATGACAAGGCCCCAACAGA	246101	78297	TCTGGCCAATGAGACATAAG	290688	122884	AAAAAAAAAAAAAAAATTAG
201515	33711	ATATGACAAGGCCCCAACAG	246102	78298	CTCTGGCCAATGAGACATAA	290689	122885	AAAAAAAAAAAAAAAAATTA
201516	33712	TATATGACAAGGCCCCAACA	246103	78299	GCTCTGGCCAATGAGACATA	290690	122886	AAAAAAAAAAAAAAAAAATT
201517	33713	GTATATGACAAGGCCCCAAC	246104	78300	AGCTCTGGCCAATGAGACAT	290691	122887	AAAAAAAAAAAAAAAAAAAT
201518	33714	AGTATATGACAAGGCCCCAA	246105	78301	CAGCTCTGGCCAATGAGACA	290692	122888	AAAAAAAAAAAAAAAAAAAA
201519	33715	TAGTATATGACAAGGCCCCA	246106	78302	CCAGCTCTGGCCAATGAGAC	290693	122889	AAAAAAAAAAAAAAAAAAAA
201520	33716	ATAGTATATGACAAGGCCCC	246107	78303	CCCAGCTCTGGCCAATGAGA	290694	122890	AAAAAAAAAAAAAAAAAAAA
201521	33717	AATAGTATATGACAAGGCCC	246108	78304	ACCCAGCTCTGGCCAATGAG	290695	122891	AAAAAAAAAAAAAAAAAAAA
201522	33718	GAATAGTATATGACAAGGCC	246109	78305	GACCCAGCTCTGGCCAATGA	290696	122892	AAAAAAAAAAAAAAAAAAAA
201523	33719	GGAATAGTATATGACAAGGC	246110	78306	AGACCCAGCTCTGGCCAATG	290697	122893	AAAAAAAAAAAAAAAAAAAA
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201530	33726	TTCCAGGGGAATAGTATATG	246117	78313	GGCCGTAAGACCCAGCTCTG	290704	122900	TCAAAAAAAAAAAAAAAAAA
201531	33727	ATTCCAGGGGAATAGTATAT	246118	78314	TGGCCGTAAGACCCAGCTCT	290705	122901	CTCAAAAAAAAAAAAAAAAA
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201533	33729	ACATTCCAGGGGAATAGTAT	246120	78316	GGTGGCCGTAAGACCCAGCT	290707	122903	ATCTCAAAAAAAAAAAAAAA
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201535	33731	GAACATTCCAGGGGAATAGT	246122	78318	GGGGTGGCCGTAAGACCCAG	290709	122905	CCATCTCAAAAAAAAAAAAA
201536	33732	AGAACATTCCAGGGGAATAG	246123	78319	AGGGGTGGCCGTAAGACCCA	290710	122906	TCCATCTCAAAAAAAAAAAA
201537	33733	AAGAACATTCCAGGGGAATA	246124	78320	AAGGGGTGGCCGTAAGACCC	290711	122907	CTCCATCTCAAAAAAAAAAA
201538	33734	AAAGAACATTCCAGGGGAAT	246125	78321	CAAGGGGTGGCCGTAAGACC	290712	122908	ACTCCATCTCAAAAAAAAAA
201539	33735	GAAAGAACATTCCAGGGGAA	246126	78322	GCAAGGGGTGGCCGTAAGAC	290713	122909	AACTCCATCTCAAAAAAAAA
201540	33736	GGAAAGAACATTCCAGGGGA	246127	78323	AGCAAGGGGTGGCCGTAAGA	290714	122910	CAACTCCATCTCAAAAAAAA
201541	33737	AGGAAAGAACATTCCAGGGG	246128	78324	CAGCAAGGGGTGGCCGTAAG	290715	122911	ACAACTCCATCTCAAAAAAA
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201546	33742	GGGATAGGAAAGAACATTCC	246133	78329	GCTCGCAGCAAGGGGTGGCC	290720	122916	AGAGTACAACTCCATCTCAA
201547	33743	GGGGATAGGAAAGAACATTC	246134	78330	TGCTCGCAGCAAGGGGTGGC	290721	122917	GAGAGTACAACTCCATCTCA
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201549	33745	GAGGGGATAGGAAAGAACAT	246136	78332	CTTGCTCGCAGCAAGGGGTG	290723	122919	ATGAGAGTACAACTCCATCT
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201555	33751	GAAAGGGAGGGGATAGGAAA	246142	78338	CCCAGCCTTGCTCGCAGCAA	290729	122925	TGGGCAATGAGAGTACAACT
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201568	33764	AAGTTAGCAAGGTGAAAGGG	246155	78351	AAATGCTCAATGTCCCAGCC	290742	122938	TTACATTCCAGCCTGGGCAA
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201579	33775	AGGATGGGCACAAGTTAGCA	246166	78362	GTTGGACGGCAAAATGCTCA	290753	122949	AGATTGTGCCATTACATTCC
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201600	33796	GATGTTTCTGCTGAGACCTG	246187	78383	TTGGTTTATTCTGCTAAAGA	290774	122970	GGTGGAGGTTGCAGTGAGCC
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201604	33800	AAGTGATGTTTCTGCTGAGA	246191	78387	CCCCTTGGTTTATTCTGCTA	290778	122974	AGGAGGTGGAGGTTGCAGTG
201605	33801	GAAGTGATGTTTCTGCTGAG	246192	78388	CCCCCTTGGTTTATTCTGCT	290779	122975	CAGGAGGTGGAGGTTGCAGT
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201607	33803	AGGAAGTGATGTTTCTGCTG	246194	78390	TTCCCCCTTGGTTTATTCTG	290781	122977	TCCAGGAGGTGGAGGTTGCA
201608	33804	AAGGAAGTGATGTTTCTGCT	246195	78391	CTTCCCCCTTGGTTTATTCT	290782	122978	ATCCAGGAGGTGGAGGTTGC
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201611	33807	CCCAAGGAAGTGATGTTTCT	246198	78394	GTTCTTCCCCCTTGGTTTAT	290785	122981	TGAATCCAGGAGGTGGAGGT
201612	33808	CCCCAAGGAAGTGATGTTTC	246199	78395	CGTTCTTCCCCCTTGGTTTA	290786	122982	TTGAATCCAGGAGGTGGAGG
201613	33809	TCCCCAAGGAAGTGATGTTT	246200	78396	ACGTTCTTCCCCCTTGGTTT	290787	122983	CTTGAATCCAGGAGGTGGAG
201614	33810	TTCCCCAAGGAAGTGATGTT	246201	78397	AACGTTCTTCCCCCTTGGTT	290788	122984	GCTTGAATCCAGGAGGTGGA
201615	33811	CTTCCCCAAGGAAGTGATGT	246202	78398	TAACGTTCTTCCCCCTTGGT	290789	122985	TGCTTGAATCCAGGAGGTGG
201616	33812	ACTTCCCCAAGGAAGTGATG	246203	78399	TTAACGTTCTTCCCCCTTGG	290790	122986	TTGCTTGAATCCAGGAGGTG
201617	33813	AACTTCCCCAAGGAAGTGAT	246204	78400	ATTAACGTTCTTCCCCCTTG	290791	122987	ATTGCTTGAATCCAGGAGGT
201618	33814	AAACTTCCCCAAGGAAGTGA	246205	78401	TATTAACGTTCTTCCCCCTT	290792	122988	AATTGCTTGAATCCAGGAGG
201619	33815	AAAACTTCCCCAAGGAAGTG	246206	78402	CTATTAACGTTCTTCCCCCT	290793	122989	GAATTGCTTGAATCCAGGAG
201620	33816	GAAAACTTCCCCAAGGAAGT	246207	78403	ACTATTAACGTTCTTCCCCC	290794	122990	AGAATTGCTTGAATCCAGGA
201621	33817	AGAAAACTTCCCCAAGGAAG	246208	78404	CACTATTAACGTTCTTCCCC	290795	122991	GAGAATTGCTTGAATCCAGG
201622	33818	GAGAAAACTTCCCCAAGGAA	246209	78405	CCACTATTAACGTTCTTCCC	290796	122992	GGAGAATTGCTTGAATCCAG
201623	33819	GGAGAAAACTTCCCCAAGGA	246210	78406	GCCACTATTAACGTTCTTCC	290797	122993	AGGAGAATTGCTTGAATCCA
201624	33820	TGGAGAAAACTTCCCCAAGG	246211	78407	AGCCACTATTAACGTTCTTC	290798	122994	CAGGAGAATTGCTTGAATCC
201625	33821	TTGGAGAAAACTTCCCCAAG	246212	78408	AAGCCACTATTAACGTTCTT	290799	122995	ACAGGAGAATTGCTTGAATC
201626	33822	GTTGGAGAAAACTTCCCCAA	246213	78409	AAAGCCACTATTAACGTTCT	290800	122996	GACAGGAGAATTGCTTGAAT
201627	33823	TGTTGGAGAAAACTTCCCCA	246214	78410	AAAAGCCACTATTAACGTTC	290801	122997	AGACAGGAGAATTGCTTGAA
201628	33824	GTGTTGGAGAAAACTTCCCC	246215	78411	CAAAAGCCACTATTAACGTT	290802	122998	GAGACAGGAGAATTGCTTGA
201629	33825	GGTGTTGGAGAAAACTTCCC	246216	78412	TCAAAAGCCACTATTAACGT	290803	122999	TGAGACAGGAGAATTGCTTG
201630	33826	GGGTGTTGGAGAAAACTTCC	246217	78413	CTCAAAAGCCACTATTAACG	290804	123000	CTGAGACAGGAGAATTGCTT
201631	33827	TGGGTGTTGGAGAAAACTTC	246218	78414	ACTCAAAAGCCACTATTAAC	290805	123001	GCTGAGACAGGAGAATTGCT
201632	33828	GTGGGTGTTGGAGAAAACTT	246219	78415	GACTCAAAAGCCACTATTAA	290806	123002	AGCTGAGACAGGAGAATTGC
201633	33829	TGTGGGTGTTGGAGAAAACT	246220	78416	TGACTCAAAAGCCACTATTA	290807	123003	AAGCTGAGACAGGAGAATTG
201634	33830	GTGTGGGTGTTGGAGAAAAC	246221	78417	GTGACTCAAAAGCCACTATT	290808	123004	GAAGCTGAGACAGGAGAATT
201635	33831	AGTGTGGGTGTTGGAGAAAA	246222	78418	AGTGACTCAAAAGCCACTAT	290809	123005	GGAAGCTGAGACAGGAGAAT
201636	33832	TAGTGTGGGTGTTGGAGAAA	246223	78419	TAGTGACTCAAAAGCCACTA	290810	123006	GGGAAGCTGAGACAGGAGAA
201637	33833	GTAGTGTGGGTGTTGGAGAA	246224	78420	CTAGTGACTCAAAAGCCACT	290811	123007	TGGGAAGCTGAGACAGGAGA
201638	33834	TGTAGTGTGGGTGTTGGAGA	246225	78421	ACTAGTGACTCAAAAGCCAC	290812	123008	TTGGGAAGCTGAGACAGGAG
201639	33835	GTGTAGTGTGGGTGTTGGAG	246226	78422	AACTAGTGACTCAAAAGCCA	290813	123009	CTTGGGAAGCTGAGACAGGA
201640	33836	TGTGTAGTGTGGGTGTTGGA	246227	78423	CAACTAGTGACTCAAAAGCC	290814	123010	ACTTGGGAAGCTGAGACAGG
201641	33837	CTGTGTAGTGTGGGTGTTGG	246228	78424	CCAACTAGTGACTCAAAAGC	290815	123011	TACTTGGGAAGCTGAGACAG
201642	33838	CCTGTGTAGTGTGGGTGTTG	246229	78425	GCCAACTAGTGACTCAAAAG	290816	123012	CTACTTGGGAAGCTGAGACA

201643	33839	ACCTGTGTAGTGTGGGTGTT	246230	78426	TGCCAACTAGTGACTCAAAA	290817	123013	GCTACTTGGGAAGCTGAGAC
201644	33840	CACCTGTGTAGTGTGGGTGT	246231	78427	CTGCCAACTAGTGACTCAAA	290818	123014	AGCTACTTGGGAAGCTGAGA
201645	33841	ACACCTGTGTAGTGTGGGTG	246232	78428	ACTGCCAACTAGTGACTCAA	290819	123015	CAGCTACTTGGGAAGCTGAG
201646	33842	GACACCTGTGTAGTGTGGGT	246233	78429	TACTGCCAACTAGTGACTCA	290820	123016	CCAGCTACTTGGGAAGCTGA
201647	33843	GGACACCTGTGTAGTGTGGG	246234	78430	ATACTGCCAACTAGTGACTC	290821	123017	CCCAGCTACTTGGGAAGCTG
201648	33844	GGGACACCTGTGTAGTGTGG	246235	78431	GATACTGCCAACTAGTGACT	290822	123018	TCCCAGCTACTTGGGAAGCT
201649	33845	TGGGACACCTGTGTAGTGTG	246236	78432	AGATACTGCCAACTAGTGAC	290823	123019	ATCCCAGCTACTTGGGAAGC
201650	33846	ATGGGACACCTGTGTAGTGT	246237	78433	CAGATACTGCCAACTAGTGA	290824	123020	AATCCCAGCTACTTGGGAAG
201651	33847	GATGGGACACCTGTGTAGTG	246238	78434	GCAGATACTGCCAACTAGTG	290825	123021	TAATCCCAGCTACTTGGGAA
201652	33848	AGATGGGACACCTGTGTAGT	246239	78435	GGCAGATACTGCCAACTAGT	290826	123022	GTAATCCCAGCTACTTGGGA
201653	33849	TAGATGGGACACCTGTGTAG	246240	78436	GGGCAGATACTGCCAACTAG	290827	123023	TGTAATCCCAGCTACTTGGG
201654	33850	GTAGATGGGACACCTGTGTA	246241	78437	GGGGCAGATACTGCCAACTA	290828	123024	CTGTAATCCCAGCTACTTGG
201655	33851	TGTAGATGGGACACCTGTGT	246242	78438	AGGGGCAGATACTGCCAACT	290829	123025	CCTGTAATCCCAGCTACTTG
201656	33852	GTGTAGATGGGACACCTGTG	246243	78439	GAGGGGCAGATACTGCCAAC	290830	123026	ACCTGTAATCCCAGCTACTT
201657	33853	AGTGTAGATGGGACACCTGT	246244	78440	AGAGGGGCAGATACTGCCAA	290831	123027	CACCTGTAATCCCAGCTACT
201658	33854	GAGTGTAGATGGGACACCTG	246245	78441	TAGAGGGGCAGATACTGCCA	290832	123028	GCACCTGTAATCCCAGCTAC
201659	33855	GGAGTGTAGATGGGACACCT	246246	78442	ATAGAGGGGCAGATACTGCC	290833	123029	GGCACCTGTAATCCCAGCTA
201660	33856	AGGAGTGTAGATGGGACACC	246247	78443	GATAGAGGGGCAGATACTGC	290834	123030	GGGCACCTGTAATCCCAGCT
201661	33857	TAGGAGTGTAGATGGGACAC	246248	78444	AGATAGAGGGGCAGATACTG	290835	123031	CGGGCACCTGTAATCCCAGC
201662	33858	ATAGGAGTGTAGATGGGACA	246249	78445	AAGATAGAGGGGCAGATACT	290836	123032	GCGGGCACCTGTAATCCCAG
201663	33859	CATAGGAGTGTAGATGGGAC	246250	78446	AAAGATAGAGGGGCAGATAC	290837	123033	GGCGGGCACCTGTAATCCCA
201664	33860	TCATAGGAGTGTAGATGGGA	246251	78447	GAAAGATAGAGGGGCAGATA	290838	123034	TGGCGGGCACCTGTAATCCC
201665	33861	GTCATAGGAGTGTAGATGGG	246252	78448	GGAAAGATAGAGGGGCAGAT	290839	123035	GTGGCGGGCACCTGTAATCC
201666	33862	AGTCATAGGAGTGTAGATGG	246253	78449	TGGAAAGATAGAGGGGCAGA	290840	123036	GGTGGCGGGCACCTGTAATC
201667	33863	AAGTCATAGGAGTGTAGATG	246254	78450	ATGGAAAGATAGAGGGGCAG	290841	123037	TGGTGGCGGGCACCTGTAAT
201668	33864	AAAGTCATAGGAGTGTAGAT	246255	78451	GATGGAAAGATAGAGGGGCA	290842	123038	ATGGTGGCGGGCACCTGTAA
201669	33865	CAAAGTCATAGGAGTGTAGA	246256	78452	GGATGGAAAGATAGAGGGGC	290843	123039	CATGGTGGCGGGCACCTGTA
201670	33866	ACAAAGTCATAGGAGTGTAG	246257	78453	AGGATGGAAAGATAGAGGGG	290844	123040	GCATGGTGGCGGGCACCTGT
201671	33867	CACAAAGTCATAGGAGTGTA	246258	78454	GAGGATGGAAAGATAGAGGG	290845	123041	AGCATGGTGGCGGGCACCTG
201672	33868	CCACAAAGTCATAGGAGTGT	246259	78455	GGAGGATGGAAAGATAGAGG	290846	123042	GAGCATGGTGGCGGGCACCT
201673	33869	ACCACAAAGTCATAGGAGTG	246260	78456	GGGAGGATGGAAAGATAGAG	290847	123043	TGAGCATGGTGGCGGGCACC
201674	33870	TACCACAAAGTCATAGGAGT	246261	78457	GGGGAGGATGGAAAGATAGA	290848	123044	TTGAGCATGGTGGCGGGCAC
201675	33871	GTACCACAAAGTCATAGGAG	246262	78458	TGGGGAGGATGGAAAGATAG	290849	123045	GTTGAGCATGGTGGCGGGCA
201676	33872	AGTACCACAAAGTCATAGGA	246263	78459	ATGGGGAGGATGGAAAGATA	290850	123046	AGTTGAGCATGGTGGCGGGC
201677	33873	AAGTACCACAAAGTCATAGG	246264	78460	CATGGGGAGGATGGAAAGAT	290851	123047	TAGTTGAGCATGGTGGCGGG
201678	33874	CAAGTACCACAAAGTCATAG	246265	78461	CCATGGGGAGGATGGAAAGA	290852	123048	TTAGTTGAGCATGGTGGCGG
201679	33875	ACAAGTACCACAAAGTCATA	246266	78462	TCCATGGGGAGGATGGAAAG	290853	123049	ATTAGTTGAGCATGGTGGCG
201680	33876	GACAAGTACCACAAAGTCAT	246267	78463	CTCCATGGGGAGGATGGAAA	290854	123050	AATTAGTTGAGCATGGTGGC
201681	33877	AGACAAGTACCACAAAGTCA	246268	78464	ACTCCATGGGGAGGATGGAA	290855	123051	AAATTAGTTGAGCATGGTGG
201682	33878	GAGACAAGTACCACAAAGTC	246269	78465	AACTCCATGGGGAGGATGGA	290856	123052	AAAATTAGTTGAGCATGGTG
201683	33879	TGAGACAAGTACCACAAAGT	246270	78466	AAACTCCATGGGGAGGATGG	290857	123053	AAAAATTAGTTGAGCATGGT
201684	33880	GTGAGACAAGTACCACAAAG	246271	78467	GAAACTCCATGGGGAGGATG	290858	123054	CAAAAATTAGTTGAGCATGG
201685	33881	AGTGAGACAAGTACCACAAA	246272	78468	TGAAACTCCATGGGGAGGAT	290859	123055	ACAAAAATTAGTTGAGCATG
201686	33882	AAGTGAGACAAGTACCACAA	246273	78469	TTGAAACTCCATGGGGAGGA	290860	123056	TACAAAAATTAGTTGAGCAT
201687	33883	GAAGTGAGACAAGTACCACA	246274	78470	CTTGAAACTCCATGGGGAGG	290861	123057	ATACAAAAATTAGTTGAGCA
201688	33884	TGAAGTGAGACAAGTACCAC	246275	78471	CCTTGAAACTCCATGGGGAG	290862	123058	AATACAAAAATTAGTTGAGC
201689	33885	ATGAAGTGAGACAAGTACCA	246276	78472	ACCTTGAAACTCCATGGGGA	290863	123059	AAATACAAAAATTAGTTGAG
201690	33886	AATGAAGTGAGACAAGTACC	246277	78473	AACCTTGAAACTCCATGGGG	290864	123060	AAAATACAAAAATTAGTTGA
201691	33887	AAATGAAGTGAGACAAGTAC	246278	78474	GAACCTTGAAACTCCATGGG	290865	123061	AAAAATACAAAAATTAGTTG
201692	33888	AAAATGAAGTGAGACAAGTA	246279	78475	GGAACCTTGAAACTCCATGG	290866	123062	AAAAAATACAAAAATTAGTT
201693	33889	GAAAATGAAGTGAGACAAGT	246280	78476	AGGAACCTTGAAACTCCATG	290867	123063	AAAAAAATACAAAAATTAGT
201694	33890	GGAAAATGAAGTGAGACAAG	246281	78477	AAGGAACCTTGAAACTCCAT	290868	123064	AAAAAAAATACAAAAATTAG
201695	33891	TGGAAAATGAAGTGAGACAA	246282	78478	AAAGGAACCTTGAAACTCCA	290869	123065	AAAAAAAAATACAAAAATTA
201696	33892	GTGGAAAATGAAGTGAGACA	246283	78479	GAAAGGAACCTTGAAACTCC	290870	123066	AAAAAAAAAATACAAAAATT
201697	33893	AGTGGAAAATGAAGTGAGAC	246284	78480	AGAAAGGAACCTTGAAACTC	290871	123067	TAAAAAAAAAATACAAAAAT
201698	33894	CAGTGGAAAATGAAGTGAGA	246285	78481	GAGAAAGGAACCTTGAAACT	290872	123068	CTAAAAAAAAAATACAAAAA
201699	33895	GCAGTGGAAAATGAAGTGAG	246286	78482	TGAGAAAGGAACCTTGAAAC	290873	123069	ACTAAAAAAAAAATACAAAA
201700	33896	GGCAGTGGAAAATGAAGTGA	246287	78483	CTGAGAAAGGAACCTTGAAA	290874	123070	TACTAAAAAAAAAATACAAA
201701	33897	AGGCAGTGGAAAATGAAGTG	246288	78484	ACTGAGAAAGGAACCTTGAA	290875	123071	CTACTAAAAAAAAAATACAA
201702	33898	AAGGCAGTGGAAAATGAAGT	246289	78485	TACTGAGAAAGGAACCTTGA	290876	123072	TCTACTAAAAAAAAAATACA
201703	33899	GAAGGCAGTGGAAAATGAAG	246290	78486	GTACTGAGAAAGGAACCTTG	290877	123073	CTCTACTAAAAAAAAAATAC
201704	33900	GGAAGGCAGTGGAAAATGAA	246291	78487	AGTACTGAGAAAGGAACCTT	290878	123074	TCTCTACTAAAAAAAAAATA
201705	33901	GGGAAGGCAGTGGAAAATGA	246292	78488	AAGTACTGAGAAAGGAACCT	290879	123075	GTCTCTACTAAAAAAAAAAT
201706	33902	GGGGAAGGCAGTGGAAAATG	246293	78489	GAAGTACTGAGAAAGGAACC	290880	123076	CGTCTCTACTAAAAAAAAAA
201707	33903	TGGGGAAGGCAGTGGAAAAT	246294	78490	AGAAGTACTGAGAAAGGAAC	290881	123077	TCGTCTCTACTAAAAAAAAA
201708	33904	GTGGGGAAGGCAGTGGAAAA	246295	78491	AAGAAGTACTGAGAAAGGAA	290882	123078	CTCGTCTCTACTAAAAAAAA
201709	33905	TGTGGGGAAGGCAGTGGAAA	246296	78492	GAAGAAGTACTGAGAAAGGA	290883	123079	CCTCGTCTCTACTAAAAAAA
201710	33906	TTGTGGGGAAGGCAGTGGAA	246297	78493	TGAAGAAGTACTGAGAAAGG	290884	123080	ACCTCGTCTCTACTAAAAAA
201711	33907	CTTGTGGGGAAGGCAGTGGA	246298	78494	CTGAAGAAGTACTGAGAAAG	290885	123081	AACCTCGTCTCTACTAAAAA
201712	33908	CCTTGTGGGGAAGGCAGTGG	246299	78495	CCTGAAGAAGTACTGAGAAA	290886	123082	AAACCTCGTCTCTACTAAAA
201713	33909	GCCTTGTGGGGAAGGCAGTG	246300	78496	GCCTGAAGAAGTACTGAGAA	290887	123083	GAAACCTCGTCTCTACTAAA
201714	33910	TGCCTTGTGGGGAAGGCAGT	246301	78497	AGCCTGAAGAAGTACTGAGA	290888	123084	TGAAACCTCGTCTCTACTAA

201715	33911	GTGCCTTGTGGGGAAGGCAG	246302	78498	GAGCCTGAAGAAGTACTGAG	290889	123085	GTGAAACCTCGTCTCTACTA
201716	33912	GGTGCCTTGTGGGGAAGGCA	246303	78499	AGAGCCTGAAGAAGTACTGA	290890	123086	GGTGAAACCTCGTCTCTACT
201717	33913	AGGTGCCTTGTGGGGAAGGC	246304	78500	CAGAGCCTGAAGAAGTACTG	290891	123087	TGGTGAAACCTCGTCTCTAC
201718	33914	CAGGTGCCTTGTGGGGAAGG	246305	78501	GCAGAGCCTGAAGAAGTACT	290892	123088	ATGGTGAAACCTCGTCTCTA
201719	33915	GCAGGTGCCTTGTGGGGAAG	246306	78502	TGCAGAGCCTGAAGAAGTAC	290893	123089	CATGGTGAAACCTCGTCTCT
201720	33916	TGCAGGTGCCTTGTGGGGAA	246307	78503	GTGCAGAGCCTGAAGAAGTA	290894	123090	ACATGGTGAAACCTCGTCTC
201721	33917	GTGCAGGTGCCTTGTGGGGA	246308	78504	CGTGCAGAGCCTGAAGAAGT	290895	123091	AACATGGTGAAACCTCGTCT
201722	33918	TGTGCAGGTGCCTTGTGGGG	246309	78505	ACGTGCAGAGCCTGAAGAAG	290896	123092	CAACATGGTGAAACCTCGTC
201723	33919	TTGTGCAGGTGCCTTGTGGG	246310	78506	AACGTGCAGAGCCTGAAGAA	290897	123093	CCAACATGGTGAAACCTCGT
201724	33920	CTTGTGCAGGTGCCTTGTGG	246311	78507	GAACGTGCAGAGCCTGAAGA	290898	123094	ACCAACATGGTGAAACCTCG
201725	33921	CCTTGTGCAGGTGCCTTGTG	246312	78508	TGAACGTGCAGAGCCTGAAG	290899	123095	GACCAACATGGTGAAACCTC
201726	33922	CCCTTGTGCAGGTGCCTTGT	246313	78509	ATGAACGTGCAGAGCCTGAA	290900	123096	TGACCAACATGGTGAAACCT
201727	33923	GCCCTTGTGCAGGTGCCTTG	246314	78510	AATGAACGTGCAGAGCCTGA	290901	123097	CTGACCAACATGGTGAAACC
201728	33924	TGCCCTTGTGCAGGTGCCTT	246315	78511	AAATGAACGTGCAGAGCCTG	290902	123098	TCTGACCAACATGGTGAAAC
201729	33925	TTGCCCTTGTGCAGGTGCCT	246316	78512	CAAATGAACGTGCAGAGCCT	290903	123099	GTCTGACCAACATGGTGAAA
201730	33926	CTTGCCCTTGTGCAGGTGCC	246317	78513	CCAAATGAACGTGCAGAGCC	290904	123100	AGTCTGACCAACATGGTGAA
201731	33927	CCTTGCCCTTGTGCAGGTGC	246318	78514	TCCAAATGAACGTGCAGAGC	290905	123101	CAGTCTGACCAACATGGTGA
201732	33928	TCCTTGCCCTTGTGCAGGTG	246319	78515	ATCCAAATGAACGTGCAGAG	290906	123102	CCAGTCTGACCAACATGGTG
201733	33929	GTCCTTGCCCTTGTGCAGGT	246320	78516	GATCCAAATGAACGTGCAGA	290907	123103	ACCAGTCTGACCAACATGGT
201734	33930	GGTCCTTGCCCTTGTGCAGG	246321	78517	AGATCCAAATGAACGTGCAG	290908	123104	GACCAGTCTGACCAACATGG
201735	33931	CGGTCCTTGCCCTTGTGCAG	246322	78518	AAGATCCAAATGAACGTGCA	290909	123105	AGACCAGTCTGACCAACATG
201736	33932	ACGGTCCTTGCCCTTGTGCA	246323	78519	CAAGATCCAAATGAACGTGC	290910	123106	GAGACCAGTCTGACCAACAT
201737	33933	TACGGTCCTTGCCCTTGTGC	246324	78520	ACAAGATCCAAATGAACGTG	290911	123107	TGAGACCAGTCTGACCAACA
201738	33934	GTACGGTCCTTGCCCTTGTG	246325	78521	CACAAGATCCAAATGAACGT	290912	123108	TTGAGACCAGTCTGACCAAC
201739	33935	GGTACGGTCCTTGCCCTTGT	246326	78522	ACACAAGATCCAAATGAACG	290913	123109	TTTGAGACCAGTCTGACCAA
201740	33936	TGGTACGGTCCTTGCCCTTG	246327	78523	GACACAAGATCCAAATGAAC	290914	123110	GTTTGAGACCAGTCTGACCA
201741	33937	GTGGTACGGTCCTTGCCCTT	246328	78524	AGACACAAGATCCAAATGAA	290915	123111	AGTTTGAGACCAGTCTGACC
201742	33938	AGTGGTACGGTCCTTGCCCT	246329	78525	AAGACACAAGATCCAAATGA	290916	123112	GAGTTTGAGACCAGTCTGAC
201743	33939	CAGTGGTACGGTCCTTGCCC	246330	78526	CAAGACACAAGATCCAAATG	290917	123113	GGAGTTTGAGACCAGTCTGA
201744	33940	ACAGTGGTACGGTCCTTGCC	246331	78527	CCAAGACACAAGATCCAAAT	290918	123114	AGGAGTTTGAGACCAGTCTG
201745	33941	TACAGTGGTACGGTCCTTGC	246332	78528	CCCAAGACACAAGATCCAAA	290919	123115	CAGGAGTTTGAGACCAGTCT
201746	33942	GTACAGTGGTACGGTCCTTG	246333	78529	CCCCAAGACACAAGATCCAA	290920	123116	TCAGGAGTTTGAGACCAGTC
201747	33943	GGTACAGTGGTACGGTCCTT	246334	78530	ACCCCAAGACACAAGATCCA	290921	123117	GTCAGGAGTTTGAGACCAGT
201748	33944	AGGTACAGTGGTACGGTCCT	246335	78531	CACCCCAAGACACAAGATCC	290922	123118	GGTCAGGAGTTTGAGACCAG
201749	33945	TAGGTACAGTGGTACGGTCC	246336	78532	TCACCCCAAGACACAAGATC	290923	123119	AGGTCAGGAGTTTGAGACCA
201750	33946	ATAGGTACAGTGGTACGGTC	246337	78533	TTCACCCCAAGACACAAGAT	290924	123120	GAGGTCAGGAGTTTGAGACC
201751	33947	CATAGGTACAGTGGTACGGT	246338	78534	TTTCACCCCAAGACACAAGA	290925	123121	TGAGGTCAGGAGTTTGAGAC
201752	33948	ACATAGGTACAGTGGTACGG	246339	78535	TTTTCACCCCAAGACACAAG	290926	123122	CTGAGGTCAGGAGTTTGAGA
201753	33949	GACATAGGTACAGTGGTACG	246340	78536	TTTTTCACCCCAAGACACAA	290927	123123	CCTGAGGTCAGGAGTTTGAG
201754	33950	TGACATAGGTACAGTGGTAC	246341	78537	GTTTTTCACCCCAAGACACA	290928	123124	ACCTGAGGTCAGGAGTTTGA
201755	33951	GTGACATAGGTACAGTGGTA	246342	78538	AGTTTTTCACCCCAAGACAC	290929	123125	CACCTGAGGTCAGGAGTTTG
201756	33952	AGTGACATAGGTACAGTGGT	246343	78539	CAGTTTTTCACCCCAAGACA	290930	123126	TCACCTGAGGTCAGGAGTTT
201757	33953	GAGTGACATAGGTACAGTGG	246344	78540	CCAGTTTTTCACCCCAAGAC	290931	123127	ATCACCTGAGGTCAGGAGTT
201758	33954	TGAGTGACATAGGTACAGTG	246345	78541	GCCAGTTTTTCACCCCAAGA	290932	123128	GATCACCTGAGGTCAGGAGT
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201760	33956	AATGAGTGACATAGGTACAG	246347	78543	GGGCCAGTTTTTCACCCCAA	290934	123130	TGGATCACCTGAGGTCAGGA
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201762	33958	GCAATGAGTGACATAGGTAC	246349	78545	TTGGGCCAGTTTTTCACCCC	290936	123132	GGTGGATCACCTGAGGTCAG
201763	33959	AGCAATGAGTGACATAGGTA	246350	78546	CTTGGGCCAGTTTTTCACCC	290937	123133	AGGTGGATCACCTGAGGTCA
201764	33960	CAGCAATGAGTGACATAGGT	246351	78547	ACTTGGGCCAGTTTTTCACC	290938	123134	CAGGTGGATCACCTGAGGTC
201765	33961	ACAGCAATGAGTGACATAGG	246352	78548	CACTTGGGCCAGTTTTTCAC	290939	123135	GCAGGTGGATCACCTGAGGT
201766	33962	CACAGCAATGAGTGACATAG	246353	78549	ACACTTGGGCCAGTTTTTCA	290940	123136	GGCAGGTGGATCACCTGAGG
201767	33963	CCACAGCAATGAGTGACATA	246354	78550	GACACTTGGGCCAGTTTTTC	290941	123137	AGGCAGGTGGATCACCTGAG
201768	33964	ACCACAGCAATGAGTGACAT	246355	78551	AGACACTTGGGCCAGTTTTT	290942	123138	GAGGCAGGTGGATCACCTGA
201769	33965	GACCACAGCAATGAGTGACA	246356	78552	GAGACACTTGGGCCAGTTTT	290943	123139	CGAGGCAGGTGGATCACCTG
201770	33966	TGACCACAGCAATGAGTGAC	246357	78553	GGAGACACTTGGGCCAGTTT	290944	123140	CCGAGGCAGGTGGATCACCT
201771	33967	GTGACCACAGCAATGAGTGA	246358	78554	GGGAGACACTTGGGCCAGTT	290945	123141	GCCGAGGCAGGTGGATCACC
201772	33968	GGTGACCACAGCAATGAGTG	246359	78555	GGGGAGACACTTGGGCCAGT	290946	123142	GGCCGAGGCAGGTGGATCAC
201773	33969	AGGTGACCACAGCAATGAGT	246360	78556	TGGGGAGACACTTGGGCCAG	290947	123143	AGGCCGAGGCAGGTGGATCA
201774	33970	CAGGTGACCACAGCAATGAG	246361	78557	TTGGGGAGACACTTGGGCCA	290948	123144	GAGGCCGAGGCAGGTGGATC
201775	33971	GCAGGTGACCACAGCAATGA	246362	78558	CTTGGGGAGACACTTGGGCC	290949	123145	GGAGGCCGAGGCAGGTGGAT
201776	33972	TGCAGGTGACCACAGCAATG	246363	78559	GCTTGGGGAGACACTTGGGC	290950	123146	GGGAGGCCGAGGCAGGTGGA
201777	33973	GTGCAGGTGACCACAGCAAT	246364	78560	TGCTTGGGGAGACACTTGGG	290951	123147	TGGGAGGCCGAGGCAGGTGG
201778	33974	AGTGCAGGTGACCACAGCAA	246365	78561	ATGCTTGGGGAGACACTTGG	290952	123148	TTGGGAGGCCGAGGCAGGTG
201779	33975	GAGTGCAGGTGACCACAGCA	246366	78562	GATGCTTGGGGAGACACTTG	290953	123149	TTTGGGAGGCCGAGGCAGGT
201780	33976	AGAGTGCAGGTGACCACAGC	246367	78563	GGATGCTTGGGGAGACACTT	290954	123150	CTTTGGGAGGCCGAGGCAGG
201781	33977	CAGAGTGCAGGTGACCACAG	246368	78564	TGGATGCTTGGGGAGACACT	290955	123151	ACTTTGGGAGGCCGAGGCAG
201782	33978	CCAGAGTGCAGGTGACCACA	246369	78565	GTGGATGCTTGGGGAGACAC	290956	123152	CACTTTGGGAGGCCGAGGCA
201783	33979	GCCAGAGTGCAGGTGACCAC	246370	78566	GGTGGATGCTTGGGGAGACA	290957	123153	GCACTTTGGGAGGCCGAGGC
201784	33980	AGCCAGAGTGCAGGTGACCA	246371	78567	AGGTGGATGCTTGGGGAGAC	290958	123154	AGCACTTTGGGAGGCCGAGG
201785	33981	CAGCCAGAGTGCAGGTGACC	246372	78568	AAGGTGGATGCTTGGGGAGA	290959	123155	TAGCACTTTGGGAGGCCGAG
201786	33982	GCAGCCAGAGTGCAGGTGAC	246373	78569	AAAGGTGGATGCTTGGGGAG	290960	123156	CTAGCACTTTGGGAGGCCGA

201787	33983	GGCAGCCAGAGTGCAGGTGA	246374	78570	CAAAGGTGGATGCTTGGGGA	290961	123157	CCTAGCACTTTGGGAGGCCG
201788	33984	AGGCAGCCAGAGTGCAGGTG	246375	78571	CCAAAGGTGGATGCTTGGGG	290962	123158	TCCTAGCACTTTGGGAGGCC
201789	33985	TAGGCAGCCAGAGTGCAGGT	246376	78572	TCCAAAGGTGGATGCTTGGG	290963	123159	ATCCTAGCACTTTGGGAGGC
201790	33986	GTAGGCAGCCAGAGTGCAGG	246377	78573	ATCCAAAGGTGGATGCTTGG	290964	123160	AATCCTAGCACTTTGGGAGG
201791	33987	GGTAGGCAGCCAGAGTGCAG	246378	78574	AATCCAAAGGTGGATGCTTG	290965	123161	TAATCCTAGCACTTTGGGAG
201792	33988	AGGTAGGCAGCCAGAGTGCA	246379	78575	TAATCCAAAGGTGGATGCTT	290966	123162	GTAATCCTAGCACTTTGGGA
201793	33989	AAGGTAGGCAGCCAGAGTGC	246380	78576	TTAATCCAAAGGTGGATGCT	290967	123163	TGTAATCCTAGCACTTTGGG
201794	33990	TAAGGTAGGCAGCCAGAGTG	246381	78577	ATTAATCCAAAGGTGGATGC	290968	123164	CTGTAATCCTAGCACTTTGG
201795	33991	TTAAGGTAGGCAGCCAGAGT	246382	78578	AATTAATCCAAAGGTGGATG	290969	123165	CCTGTAATCCTAGCACTTTG
201796	33992	GTTAAGGTAGGCAGCCAGAG	246383	78579	AAATTAATCCAAAGGTGGAT	290970	123166	GCCTGTAATCCTAGCACTTT
201797	33993	AGTTAAGGTAGGCAGCCAGA	246384	78580	CAAATTAATCCAAAGGTGGA	290971	123167	TGCCTGTAATCCTAGCACTT
201798	33994	TAGTTAAGGTAGGCAGCCAG	246385	78581	CCAAATTAATCCAAAGGTGG	290972	123168	ATGCCTGTAATCCTAGCACT
201799	33995	GTAGTTAAGGTAGGCAGCCA	246386	78582	TCCAAATTAATCCAAAGGTG	290973	123169	CATGCCTGTAATCCTAGCAC
201800	33996	TGTAGTTAAGGTAGGCAGCC	246387	78583	TTCCAAATTAATCCAAAGGT	290974	123170	TCATGCCTGTAATCCTAGCA
201801	33997	GTGTAGTTAAGGTAGGCAGC	246388	78584	TTTCCAAATTAATCCAAAGG	290975	123171	CTCATGCCTGTAATCCTAGC
201802	33998	TGTGTAGTTAAGGTAGGCAG	246389	78585	TTTTCCAAATTAATCCAAAG	290976	123172	GCTCATGCCTGTAATCCTAG
201803	33999	ATGTGTAGTTAAGGTAGGCA	246390	78586	ATTTTCCAAATTAATCCAAA	290977	123173	GGCTCATGCCTGTAATCCTA
201804	34000	AATGTGTAGTTAAGGTAGGC	246391	78587	CATTTTCCAAATTAATCCAA	290978	123174	TGGCTCATGCCTGTAATCCT
201805	34001	TAATGTGTAGTTAAGGTAGG	246392	78588	CCATTTTCCAAATTAATCCA	290979	123175	GTGGCTCATGCCTGTAATCC
201806	34002	CTAATGTGTAGTTAAGGTAG	246393	78589	GCCATTTTCCAAATTAATCC	290980	123176	GGTGGCTCATGCCTGTAATC
201807	34003	TCTAATGTGTAGTTAAGGTA	246394	78590	AGCCATTTTCCAAATTAATC	290981	123177	TGGTGGCTCATGCCTGTAAT
201808	34004	TTCTAATGTGTAGTTAAGGT	246395	78591	CAGCCATTTTCCAAATTAAT	290982	123178	GTGGTGGCTCATGCCTGTAA
201809	34005	ATTCTAATGTGTAGTTAAGG	246396	78592	ACAGCCATTTTCCAAATTAA	290983	123179	CGTGGTGGCTCATGCCTGTA
201810	34006	GATTCTAATGTGTAGTTAAG	246397	78593	GACAGCCATTTTCCAAATTA	290984	123180	GCGTGGTGGCTCATGCCTGT
201811	34007	TGATTCTAATGTGTAGTTAA	246398	78594	TGACAGCCATTTTCCAAATT	290985	123181	GGCGTGGTGGCTCATGCCTG
201812	34008	GTGATTCTAATGTGTAGTTA	246399	78595	TTGACAGCCATTTTCCAAAT	290986	123182	GGGCGTGGTGGCTCATGCCT
201813	34009	GGTGATTCTAATGTGTAGTT	246400	78596	CTTGACAGCCATTTTCCAAA	290987	123183	CGGGCGTGGTGGCTCATGCC
201814	34010	AGGTGATTCTAATGTGTAGT	246401	78597	ACTTGACAGCCATTTTCCAA	290988	123184	CCGGGCGTGGTGGCTCATGC
201815	34011	CAGGTGATTCTAATGTGTAG	246402	78598	CACTTGACAGCCATTTTCCA	290989	123185	GCCGGGCGTGGTGGCTCATG
201816	34012	TCAGGTGATTCTAATGTGTA	246403	78599	GCACTTGACAGCCATTTTCC	290990	123186	GGCCGGGCGTGGTGGCTCAT
201817	34013	CTCAGGTGATTCTAATGTGT	246404	78600	GGCACTTGACAGCCATTTTC	290991	123187	AGGCCGGGCGTGGTGGCTCA
201818	34014	CCTCAGGTGATTCTAATGTG	246405	78601	GGGCACTTGACAGCCATTTT	290992	123188	CAGGCCGGGCGTGGTGGCTC
201819	34015	TCCTCAGGTGATTCTAATGT	246406	78602	CGGGCACTTGACAGCCATTT	290993	123189	TCAGGCCGGGCGTGGTGGCT
201820	34016	CTCCTCAGGTGATTCTAATG	246407	78603	GCGGGCACTTGACAGCCATT	290994	123190	TTCAGGCCGGGCGTGGTGGC
201821	34017	GCTCCTCAGGTGATTCTAAT	246408	78604	GGCGGGCACTTGACAGCCAT	290995	123191	TTTCAGGCCGGGCGTGGTGG
201822	34018	AGCTCCTCAGGTGATTCTAA	246409	78605	AGGCGGGCACTTGACAGCCA	290996	123192	CTTTCAGGCCGGGCGTGGTG
201823	34019	AAGCTCCTCAGGTGATTCTA	246410	78606	GAGGCGGGCACTTGACAGCC	290997	123193	CCTTTCAGGCCGGGCGTGGT
201824	34020	AAAGCTCCTCAGGTGATTCT	246411	78607	AGAGGCGGGCACTTGACAGC	290998	123194	CCCTTTCAGGCCGGGCGTGG
201825	34021	AAAAGCTCCTCAGGTGATTC	246412	78608	AAGAGGCGGGCACTTGACAG	290999	123195	ACCCTTTCAGGCCGGGCGTG
201826	34022	TAAAAGCTCCTCAGGTGATT	246413	78609	CAAGAGGCGGGCACTTGACA	291000	123196	AACCCTTTCAGGCCGGGCGT
201827	34023	TTAAAAGCTCCTCAGGTGAT	246414	78610	GCAAGAGGCGGGCACTTGAC	291001	123197	GAACCCTTTCAGGCCGGGCG
201828	34024	TTTAAAAGCTCCTCAGGTGA	246415	78611	AGCAAGAGGCGGGCACTTGA	291002	123198	AGAACCCTTTCAGGCCGGGC
201829	34025	CTTTAAAAGCTCCTCAGGTG	246416	78612	AAGCAAGAGGCGGGCACTTG	291003	123199	AAGAACCCTTTCAGGCCGGG
201830	34026	GCTTTAAAAGCTCCTCAGGT	246417	78613	CAAGCAAGAGGCGGGCACTT	291004	123200	TAAGAACCCTTTCAGGCCGG
201831	34027	GGCTTTAAAAGCTCCTCAGG	246418	78614	CCAAGCAAGAGGCGGGCACT	291005	123201	ATAAGAACCCTTTCAGGCCG
201832	34028	TGGCTTTAAAAGCTCCTCAG	246419	78615	ACCAAGCAAGAGGCGGGCAC	291006	123202	AATAAGAACCCTTTCAGGCC
201833	34029	GTGGCTTTAAAAGCTCCTCA	246420	78616	TACCAAGCAAGAGGCGGGCA	291007	123203	AAATAAGAACCCTTTCAGGC
201834	34030	TGTGGCTTTAAAAGCTCCTC	246421	78617	ATACCAAGCAAGAGGCGGGC	291008	123204	TAAATAAGAACCCTTTCAGG
201835	34031	TTGTGGCTTTAAAAGCTCCT	246422	78618	TATACCAAGCAAGAGGCGGG	291009	123205	CTAAATAAGAACCCTTTCAG
201836	34032	ATTGTGGCTTTAAAAGCTCC	246423	78619	TTATACCAAGCAAGAGGCGG	291010	123206	ACTAAATAAGAACCCTTTCA
201837	34033	CATTGTGGCTTTAAAAGCTC	246424	78620	ATTATACCAAGCAAGAGGCG	291011	123207	CACTAAATAAGAACCCTTTC
201838	34034	GCATTGTGGCTTTAAAAGCT	246425	78621	CATTATACCAAGCAAGAGGC	291012	123208	ACACTAAATAAGAACCCTTT
201839	34035	TGCATTGTGGCTTTAAAAGC	246426	78622	GCATTATACCAAGCAAGAGG	291013	123209	CACACTAAATAAGAACCCTT
201840	34036	TTGCATTGTGGCTTTAAAAG	246427	78623	AGCATTATACCAAGCAAGAG	291014	123210	GCACACTAAATAAGAACCCT
201841	34037	CTTGCATTGTGGCTTTAAAA	246428	78624	TAGCATTATACCAAGCAAGA	291015	123211	TGCACACTAAATAAGAACCC
201842	34038	TCTTGCATTGTGGCTTTAAA	246429	78625	GTAGCATTATACCAAGCAAG	291016	123212	ATGCACACTAAATAAGAACC
201843	34039	GTCTTGCATTGTGGCTTTAA	246430	78626	TGTAGCATTATACCAAGCAA	291017	123213	AATGCACACTAAATAAGAAC
201844	34040	AGTCTTGCATTGTGGCTTTA	246431	78627	CTGTAGCATTATACCAAGCA	291018	123214	AAATGCACACTAAATAAGAA
201845	34041	GAGTCTTGCATTGTGGCTTT	246432	78628	GCTGTAGCATTATACCAAGC	291019	123215	AAAATGCACACTAAATAAGA
201846	34042	GGAGTCTTGCATTGTGGCTT	246433	78629	AGCTGTAGCATTATACCAAG	291020	123216	CAAAATGCACACTAAATAAG
201847	34043	TGGAGTCTTGCATTGTGGCT	246434	78630	AAGCTGTAGCATTATACCAA	291021	123217	TCAAAATGCACACTAAATAA
201848	34044	GTGGAGTCTTGCATTGTGGC	246435	78631	AAAGCTGTAGCATTATACCA	291022	123218	GTCAAAATGCACACTAAATA
201849	34045	GGTGGAGTCTTGCATTGTGG	246436	78632	TAAAGCTGTAGCATTATACC	291023	123219	TGTCAAAATGCACACTAAAT
201850	34046	GGGTGGAGTCTTGCATTGTG	246437	78633	CTAAAGCTGTAGCATTATAC	291024	123220	ATGTCAAAATGCACACTAAA
201851	34047	AGGGTGGAGTCTTGCATTGT	246438	78634	TCTAAAGCTGTAGCATTATA	291025	123221	AATGTCAAAATGCACACTAA
201852	34048	TAGGGTGGAGTCTTGCATTG	246439	78635	CTCTAAAGCTGTAGCATTAT	291026	123222	GAATGTCAAAATGCACACTA
201853	34049	CTAGGGTGGAGTCTTGCATT	246440	78636	CCTCTAAAGCTGTAGCATTA	291027	123223	TGAATGTCAAAATGCACACT
201854	34050	CCTAGGGTGGAGTCTTGCAT	246441	78637	TCCTCTAAAGCTGTAGCATT	291028	123224	TTGAATGTCAAAATGCACAC
201855	34051	GCCTAGGGTGGAGTCTTGCA	246442	78638	GTCCTCTAAAGCTGTAGCAT	291029	123225	ATTGAATGTCAAAATGCACA
201856	34052	GGCCTAGGGTGGAGTCTTGC	246443	78639	CGTCCTCTAAAGCTGTAGCA	291030	123226	AATTGAATGTCAAAATGCAC
201857	34053	TGGCCTAGGGTGGAGTCTTG	246444	78640	GCGTCCTCTAAAGCTGTAGC	291031	123227	AAATTGAATGTCAAAATGCA
201858	34054	TTGGCCTAGGGTGGAGTCTT	246445	78641	TGCGTCCTCTAAAGCTGTAG	291032	123228	TAAATTGAATGTCAAAATGC

201859	34055	ATTGGCCTAGGGTGGAGTCT	246446	78642	CTGCGTCCTCTAAAGCTGTA	291033	123229	TTAAATTGAATGTCAAAATG
201860	34056	AATTGGCCTAGGGTGGAGTC	246447	78643	GCTGCGTCCTCTAAAGCTGT	291034	123230	ATTAAATTGAATGTCAAAAT
201861	34057	CAATTGGCCTAGGGTGGAGT	246448	78644	TGCTGCGTCCTCTAAAGCTG	291035	123231	AATTAAATTGAATGTCAAAA
201862	34058	CCAATTGGCCTAGGGTGGAG	246449	78645	CTGCTGCGTCCTCTAAAGCT	291036	123232	GAATTAAATTGAATGTCAAA
201863	34059	TCCAATTGGCCTAGGGTGGA	246450	78646	CCTGCTGCGTCCTCTAAAGC	291037	123233	GGAATTAAATTGAATGTCAA
201864	34060	ATCCAATTGGCCTAGGGTGG	246451	78647	GCCTGCTGCGTCCTCTAAAG	291038	123234	TGGAATTAAATTGAATGTCA
201865	34061	GATCCAATTGGCCTAGGGTG	246452	78648	TGCCTGCTGCGTCCTCTAAA	291039	123235	TTGGAATTAAATTGAATGTC
201866	34062	GGATCCAATTGGCCTAGGGT	246453	78649	ATGCCTGCTGCGTCCTCTAA	291040	123236	CTTGGAATTAAATTGAATGT
201867	34063	TGGATCCAATTGGCCTAGGG	246454	78650	CATGCCTGCTGCGTCCTCTA	291041	123237	CCTTGGAATTAAATTGAATG
201868	34064	TTGGATCCAATTGGCCTAGG	246455	78651	CCATGCCTGCTGCGTCCTCT	291042	123238	ACCTTGGAATTAAATTGAAT
201869	34065	TTTGGATCCAATTGGCCTAG	246456	78652	CCCATGCCTGCTGCGTCCTC	291043	123239	GACCTTGGAATTAAATTGAA
201870	34066	ATTTGGATCCAATTGGCCTA	246457	78653	GCCCATGCCTGCTGCGTCCT	291044	123240	AGACCTTGGAATTAAATTGA
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201872	34068	GGATTTGGATCCAATTGGCC	246459	78655	AGGCCCATGCCTGCTGCGTC	291046	123242	CAAGACCTTGGAATTAAATT
201873	34069	GGGATTTGGATCCAATTGGC	246460	78656	AAGGCCCATGCCTGCTGCGT	291047	123243	ACAAGACCTTGGAATTAAAT
201874	34070	AGGGATTTGGATCCAATTGG	246461	78657	CAAGGCCCATGCCTGCTGCG	291048	123244	CACAAGACCTTGGAATTAAA
201875	34071	CAGGGATTTGGATCCAATTG	246462	78658	GCAAGGCCCATGCCTGCTGC	291049	123245	CCACAAGACCTTGGAATTAA
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201877	34073	CCCAGGGATTTGGATCCAAT	246464	78660	CGGCAAGGCCCATGCCTGCT	291051	123247	CCCCACAAGACCTTGGAATT
201878	34074	CCCCAGGGATTTGGATCCAA	246465	78661	GCGGCAAGGCCCATGCCTGC	291052	123248	ACCCCACAAGACCTTGGAAT
201879	34075	ACCCCAGGGATTTGGATCCA	246466	78662	AGCGGCAAGGCCCATGCCTG	291053	123249	GACCCCACAAGACCTTGGAA
201880	34076	TACCCCAGGGATTTGGATCC	246467	78663	CAGCGGCAAGGCCCATGCCT	291054	123250	TGACCCCACAAGACCTTGGA
201881	34077	CTACCCCAGGGATTTGGATC	246468	78664	TCAGCGGCAAGGCCCATGCC	291055	123251	ATGACCCCACAAGACCTTGG
201882	34078	CCTACCCCAGGGATTTGGAT	246469	78665	CTCAGCGGCAAGGCCCATGC	291056	123252	CATGACCCCACAAGACCTTG
201883	34079	CCCTACCCCAGGGATTTGGA	246470	78666	CCTCAGCGGCAAGGCCCATG	291057	123253	CCATGACCCCACAAGACCTT
201884	34080	GCCCTACCCCAGGGATTTGG	246471	78667	ACCTCAGCGGCAAGGCCCAT	291058	123254	ACCATGACCCCACAAGACCT
201885	34081	GGCCCTACCCCAGGGATTTG	246472	78668	AACCTCAGCGGCAAGGCCCA	291059	123255	AACCATGACCCCACAAGACC
201886	34082	TGGCCCTACCCCAGGGATTT	246473	78669	GAACCTCAGCGGCAAGGCCC	291060	123256	AAACCATGACCCCACAAGAC
201887	34083	CTGGCCCTACCCCAGGGATT	246474	78670	AGAACCTCAGCGGCAAGGCC	291061	123257	TAAACCATGACCCCACAAGA
201888	34084	TCTGGCCCTACCCCAGGGAT	246475	78671	AAGAACCTCAGCGGCAAGGC	291062	123258	GTAAACCATGACCCCACAAG
201889	34085	GTCTGGCCCTACCCCAGGGA	246476	78672	TAAGAACCTCAGCGGCAAGG	291063	123259	TGTAAACCATGACCCCACAA
201890	34086	TGTCTGGCCCTACCCCAGGG	246477	78673	CTAAGAACCTCAGCGGCAAG	291064	123260	CTGTAAACCATGACCCCACA
201891	34087	ATGTCTGGCCCTACCCCAGG	246478	78674	GCTAAGAACCTCAGCGGCAA	291065	123261	CCTGTAAACCATGACCCCAC
201892	34088	GATGTCTGGCCCTACCCCAG	246479	78675	GGCTAAGAACCTCAGCGGCA	291066	123262	TCCTGTAAACCATGACCCCA
201893	34089	TGATGTCTGGCCCTACCCCA	246480	78676	AGGCTAAGAACCTCAGCGGC	291067	123263	ATCCTGTAAACCATGACCCC
201894	34090	CTGATGTCTGGCCCTACCCC	246481	78677	GAGGCTAAGAACCTCAGCGG	291068	123264	CATCCTGTAAACCATGACCC
201895	34091	ACTGATGTCTGGCCCTACCC	246482	78678	TGAGGCTAAGAACCTCAGCG	291069	123265	ACATCCTGTAAACCATGACC
201896	34092	CACTGATGTCTGGCCCTACC	246483	78679	ATGAGGCTAAGAACCTCAGC	291070	123266	AACATCCTGTAAACCATGAC
201897	34093	CCACTGATGTCTGGCCCTAC	246484	78680	CATGAGGCTAAGAACCTCAG	291071	123267	CAACATCCTGTAAACCATGA
201898	34094	TCCACTGATGTCTGGCCCTA	246485	78681	TCATGAGGCTAAGAACCTCA	291072	123268	TCAACATCCTGTAAACCATG
201899	34095	CTCCACTGATGTCTGGCCCT	246486	78682	CTCATGAGGCTAAGAACCTC	291073	123269	ATCAACATCCTGTAAACCAT
201900	34096	ACTCCACTGATGTCTGGCCC	246487	78683	TCTCATGAGGCTAAGAACCT	291074	123270	TATCAACATCCTGTAAACCA
201901	34097	AACTCCACTGATGTCTGGCC	246488	78684	TTCTCATGAGGCTAAGAACC	291075	123271	ATATCAACATCCTGTAAACC
201902	34098	TAACTCCACTGATGTCTGGC	246489	78685	ATTCTCATGAGGCTAAGAAC	291076	123272	TATATCAACATCCTGTAAAC
201903	34099	ATAACTCCACTGATGTCTGG	246490	78686	TATTCTCATGAGGCTAAGAA	291077	123273	CTATATCAACATCCTGTAAA
201904	34100	TATAACTCCACTGATGTCTG	246491	78687	ATATTCTCATGAGGCTAAGA	291078	123274	TCTATATCAACATCCTGTAA
201905	34101	ATATAACTCCACTGATGTCT	246492	78688	GATATTCTCATGAGGCTAAG	291079	123275	TTCTATATCAACATCCTGTA
201906	34102	TATATAACTCCACTGATGTC	246493	78689	GGATATTCTCATGAGGCTAA	291080	123276	TTTCTATATCAACATCCTGT
201907	34103	ATATATAACTCCACTGATGT	246494	78690	TGGATATTCTCATGAGGCTA	291081	123277	TTTTCTATATCAACATCCTG
201908	34104	TATATATAACTCCACTGATG	246495	78691	CTGGATATTCTCATGAGGCT	291082	123278	CTTTTCTATATCAACATCCT
201909	34105	GTATATATAACTCCACTGAT	246496	78692	TCTGGATATTCTCATGAGGC	291083	123279	TCTTTTCTATATCAACATCC
201910	34106	TGTATATATAACTCCACTGA	246497	78693	ATCTGGATATTCTCATGAGG	291084	123280	GTCTTTTCTATATCAACATC
201911	34107	ATGTATATATAACTCCACTG	246498	78694	GATCTGGATATTCTCATGAG	291085	123281	AGTCTTTTCTATATCAACAT
201912	34108	TATGTATATATAACTCCACT	246499	78695	TGATCTGGATATTCTCATGA	291086	123282	AAGTCTTTTCTATATCAACA
201913	34109	ATATGTATATATAACTCCAC	246500	78696	CTGATCTGGATATTCTCATG	291087	123283	GAAGTCTTTTCTATATCAAC
201914	34110	TATATGTATATATAACTCCA	246501	78697	TCTGATCTGGATATTCTCAT	291088	123284	TGAAGTCTTTTCTATATCAA
201915	34111	ATATATGTATATATAACTCC	246502	78698	ATCTGATCTGGATATTCTCA	291089	123285	GTGAAGTCTTTTCTATATCA
201916	34112	TATATATGTATATATAACTC	246503	78699	AATCTGATCTGGATATTCTC	291090	123286	AGTGAAGTCTTTTCTATATC
201917	34113	ATATATATGTATATATAACT	246504	78700	GAATCTGATCTGGATATTCT	291091	123287	AAGTGAAGTCTTTTCTATAT
201918	34114	TATATATATGTATATATAAC	246505	78701	AGAATCTGATCTGGATATTC	291092	123288	TAAGTGAAGTCTTTTCTATA
201919	34115	ATATATATATGTATATATAA	246506	78702	GAGAATCTGATCTGGATATT	291093	123289	TTAAGTGAAGTCTTTTCTAT
201920	34116	AATATATATATGTATATATA	246507	78703	AGAGAATCTGATCTGGATAT	291094	123290	ATTAAGTGAAGTCTTTTCTA
201921	34117	AAATATATATATGTATATAT	246508	78704	AAGAGAATCTGATCTGGATA	291095	123291	CATTAAGTGAAGTCTTTTCT
201922	34118	AAAATATATATATGTATATA	246509	78705	CAAGAGAATCTGATCTGGAT	291096	123292	CCATTAAGTGAAGTCTTTTC
201923	34119	CAAAATATATATATGTATAT	246510	78706	CCAAGAGAATCTGATCTGGA	291097	123293	CCCATTAAGTGAAGTCTTTT
201924	34120	ACAAAATATATATATGTATA	246511	78707	GCCAAGAGAATCTGATCTGG	291098	123294	GCCCATTAAGTGAAGTCTTT
201925	34121	AACAAAATATATATATGTAT	246512	78708	AGCCAAGAGAATCTGATCTG	291099	123295	GGCCCATTAAGTGAAGTCTT
201926	34122	AAACAAAATATATATATGTA	246513	78709	GAGCCAAGAGAATCTGATCT	291100	123296	CGGCCCATTAAGTGAAGTCT
201927	34123	CAAACAAAATATATATATGT	246514	78710	GGAGCCAAGAGAATCTGATC	291101	123297	CCGGCCCATTAAGTGAAGTC
201928	34124	ACAAACAAAATATATATATG	246515	78711	AGGAGCCAAGAGAATCTGAT	291102	123298	CCCGGCCCATTAAGTGAAGT
201929	34125	AACAAACAAAATATATATAT	246516	78712	AAGGAGCCAAGAGAATCTGA	291103	123299	GCCCGGCCCATTAAGTGAAG
201930	34126	AAACAAACAAAATATATATA	246517	78713	GAAGGAGCCAAGAGAATCTG	291104	123300	CGCCCGGCCCATTAAGTGAA

201931	34127	CAAACAAACAAAATATATAT	246518	78714	AGAAGGAGCCAAGAGAATCT	291105	123301	GCGCCCGGCCCATTAAGTGA
201932	34128	ACAAACAAACAAAATATATA	246519	78715	AAGAAGGAGCCAAGAGAATC	291106	123302	TGCGCCCGGCCCATTAAGTG
201933	34129	AACAAACAAACAAAATATAT	246520	78716	TAAGAAGGAGCCAAGAGAAT	291107	123303	CTGCGCCCGGCCCATTAAGT
201934	34130	AAACAAACAAACAAAATATA	246521	78717	CTAAGAAGGAGCCAAGAGAA	291108	123304	ACTGCGCCCGGCCCATTAAG
201935	34131	CAAACAAACAAACAAAATAT	246522	78718	TCTAAGAAGGAGCCAAGAGA	291109	123305	CACTGCGCCCGGCCCATTAA
201936	34132	ACAAACAAACAAACAAAATA	246523	78719	CTCTAAGAAGGAGCCAAGAG	291110	123306	CCACTGCGCCCGGCCCATTA
201937	34133	AACAAACAAACAAACAAAAT	246524	78720	GCTCTAAGAAGGAGCCAAGA	291111	123307	GCCACTGCGCCCGGCCCATT
201938	34134	AAACAAACAAACAAACAAAA	246525	78721	GGCTCTAAGAAGGAGCCAAG	291112	123308	AGCCACTGCGCCCGGCCCAT
201939	34135	CAAACAAACAAACAAACAAA	246526	78722	TGGCTCTAAGAAGGAGCCAA	291113	123309	GAGCCACTGCGCCCGGCCCA
201940	34136	ACAAACAAACAAACAAACAA	246527	78723	CTGGCTCTAAGAAGGAGCCA	291114	123310	TGAGCCACTGCGCCCGGCCC
201941	34137	AACAAACAAACAAACAAACA	246528	78724	ACTGGCTCTAAGAAGGAGCC	291115	123311	ATGAGCCACTGCGCCCGGCC
201942	34138	AAACAAACAAACAAACAAAC	246529	78725	CACTGGCTCTAAGAAGGAGC	291116	123312	CATGAGCCACTGCGCCCGGC
201943	34139	AAAACAAACAAACAAACAAA	246530	78726	TCACTGGCTCTAAGAAGGAG	291117	123313	GCATGAGCCACTGCGCCCGG
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201945	34141	AAAAAACAAACAAACAAACA	246532	78728	CATCACTGGCTCTAAGAAGG	291119	123315	AGGCATGAGCCACTGCGCCC
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201973	34169	CCTGGGTGACAGAGCAAAAC	246560	78756	CCCGACAAGATGAGCAGGAA	291147	123343	CCTCGGCCTCCCAAAGTGCT
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201984	34180	CTGCACTCCAGCCTGGGTGA	246571	78767	TGTAAAACCGTCCCGACAAG	291158	123354	TGATCTGCCTGCCTCGGCCT
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202016	34212	GGCGGAGCTTGCAGTGAGCC	246603	78799	TTTTGTAGACTTTCTCAGGA	291190	123386	TTAGCCAGGATGGTCTCAAT
202017	34213	AGGCGGAGCTTGCAGTGAGC	246604	78800	GTTTTGTAGACTTTCTCAGG	291191	123387	GTTAGCCAGGATGGTCTCAA
202018	34214	GAGGCGGAGCTTGCAGTGAG	246605	78801	CGTTTTGTAGACTTTCTCAG	291192	123388	TGTTAGCCAGGATGGTCTCA
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202020	34216	GAGAGGCGGAGCTTGCAGTG	246607	78803	ATCGTTTTGTAGACTTTCTC	291194	123390	TGTGTTAGCCAGGATGGTCT
202021	34217	CGAGAGGCGGAGCTTGCAGT	246608	78804	CATCGTTTTGTAGACTTTCT	291195	123391	CTGTGTTAGCCAGGATGGTC
202022	34218	CCGAGAGGCGGAGCTTGCAG	246609	78805	GCATCGTTTTGTAGACTTTC	291196	123392	ACTGTGTTAGCCAGGATGGT
202023	34219	CCCGAGAGGCGGAGCTTGCA	246610	78806	GGCATCGTTTTGTAGACTTT	291197	123393	CACTGTGTTAGCCAGGATGG
202024	34220	ACCCGAGAGGCGGAGCTTGC	246611	78807	TGGCATCGTTTTGTAGACTT	291198	123394	TCACTGTGTTAGCCAGGATG
202025	34221	AACCCGAGAGGCGGAGCTTG	246612	78808	CTGGCATCGTTTTGTAGACT	291199	123395	TTCACTGTGTTAGCCAGGAT
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202027	34223	TGAACCCGAGAGGCGGAGCT	246614	78810	GTCTGGCATCGTTTTGTAGA	291201	123397	GTTTCACTGTGTTAGCCAGG
202028	34224	GTGAACCCGAGAGGCGGAGC	246615	78811	GGTCTGGCATCGTTTTGTAG	291202	123398	GGTTTCACTGTGTTAGCCAG
202029	34225	TGTGAACCCGAGAGGCGGAG	246616	78812	AGGTCTGGCATCGTTTTGTA	291203	123399	GGGTTTCACTGTGTTAGCCA
202030	34226	GTGTGAACCCGAGAGGCGGA	246617	78813	GAGGTCTGGCATCGTTTTGT	291204	123400	GGGGTTTCACTGTGTTAGCC
202031	34227	GGTGTGAACCCGAGAGGCGG	246618	78814	TGAGGTCTGGCATCGTTTTG	291205	123401	TGGGGTTTCACTGTGTTAGC
202032	34228	TGGTGTGAACCCGAGAGGCG	246619	78815	ATGAGGTCTGGCATCGTTTT	291206	123402	ATGGGGTTTCACTGTGTTAG
202033	34229	ATGGTGTGAACCCGAGAGGC	246620	78816	CATGAGGTCTGGCATCGTTT	291207	123403	GATGGGGTTTCACTGTGTTA
202034	34230	AATGGTGTGAACCCGAGAGG	246621	78817	GCATGAGGTCTGGCATCGTT	291208	123404	AGATGGGGTTTCACTGTGTT
202035	34231	GAATGGTGTGAACCCGAGAG	246622	78818	GGCATGAGGTCTGGCATCGT	291209	123405	GAGATGGGGTTTCACTGTGT
202036	34232	AGAATGGTGTGAACCCGAGA	246623	78819	TGGCATGAGGTCTGGCATCG	291210	123406	AGAGATGGGGTTTCACTGTG
202037	34233	GAGAATGGTGTGAACCCGAG	246624	78820	CTGGCATGAGGTCTGGCATC	291211	123407	TAGAGATGGGGTTTCACTGT
202038	34234	GGAGAATGGTGTGAACCCGA	246625	78821	GCTGGCATGAGGTCTGGCAT	291212	123408	GTAGAGATGGGGTTTCACTG
202039	34235	AGGAGAATGGTGTGAACCCG	246626	78822	AGCTGGCATGAGGTCTGGCA	291213	123409	AGTAGAGATGGGGTTTCACT
202040	34236	CAGGAGAATGGTGTGAACCC	246627	78823	AAGCTGGCATGAGGTCTGGC	291214	123410	CAGTAGAGATGGGGTTTCAC
202041	34237	GCAGGAGAATGGTGTGAACC	246628	78824	GAAGCTGGCATGAGGTCTGG	291215	123411	TCAGTAGAGATGGGGTTTCA
202042	34238	GGCAGGAGAATGGTGTGAAC	246629	78825	GGAAGCTGGCATGAGGTCTG	291216	123412	TTCAGTAGAGATGGGGTTTC
202043	34239	AGGCAGGAGAATGGTGTGAA	246630	78826	GGGAAGCTGGCATGAGGTCT	291217	123413	TTTCAGTAGAGATGGGGTTT
202044	34240	GAGGCAGGAGAATGGTGTGA	246631	78827	TGGGAAGCTGGCATGAGGTC	291218	123414	TTTTCAGTAGAGATGGGGTT
202045	34241	TGAGGCAGGAGAATGGTGTG	246632	78828	TTGGGAAGCTGGCATGAGGT	291219	123415	ATTTTCAGTAGAGATGGGGT
202046	34242	CTGAGGCAGGAGAATGGTGT	246633	78829	CTTGGGAAGCTGGCATGAGG	291220	123416	TATTTTCAGTAGAGATGGGG
202047	34243	GCTGAGGCAGGAGAATGGTG	246634	78830	GCTTGGGAAGCTGGCATGAG	291221	123417	GTATTTTCAGTAGAGATGGG
202048	34244	GGCTGAGGCAGGAGAATGGT	246635	78831	GGCTTGGGAAGCTGGCATGA	291222	123418	TGTATTTTCAGTAGAGATGG
202049	34245	AGGCTGAGGCAGGAGAATGG	246636	78832	AGGCTTGGGAAGCTGGCATG	291223	123419	TTGTATTTTCAGTAGAGATG
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202051	34247	GGAGGCTGAGGCAGGAGAAT	246638	78834	CAAGGCTTGGGAAGCTGGCA	291225	123421	TTTTGTATTTTCAGTAGAGA
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202053	34249	CAGGAGGCTGAGGCAGGAGA	246640	78836	GTCAAGGCTTGGGAAGCTGG	291227	123423	TTTTTTGTATTTTCAGTAGA
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202062	34258	CCAGCCACTCAGGAGGCTGA	246649	78845	GCACTGAGAGTCAAGGCTTG	291236	123432	CCCAGCTAATTTTTTGTATT
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202071	34267	CTTGTAGTTCCAGCCACTCA	246658	78854	GTTGAGGGAGCACTGAGAGT	291245	123441	GCCACCACGCCCAGCTAATT
202072	34268	ACTTGTAGTTCCAGCCACTC	246659	78855	TGTTGAGGGAGCACTGAGAG	291246	123442	TGCCACCACGCCCAGCTAAT
202073	34269	CACTTGTAGTTCCAGCCACT	246660	78856	CTGTTGAGGGAGCACTGAGA	291247	123443	CTGCCACCACGCCCAGCTAA
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202077	34273	CGAGCACTTGTAGTTCCAGC	246664	78860	AATCCTGTTGAGGGAGCACT	291251	123447	GTGCCTGCCACCACGCCCAG
202078	34274	GCGAGCACTTGTAGTTCCAG	246665	78861	GAATCCTGTTGAGGGAGCAC	291252	123448	GGTGCCTGCCACCACGCCCA
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202082	34278	GGTGGCGAGCACTTGTAGTT	246669	78865	TCCAGAATCCTGTTGAGGGA	291256	123452	TACAGGTGCCTGCCACCACG
202083	34279	TGGTGGCGAGCACTTGTAGT	246670	78866	TTCCAGAATCCTGTTGAGGG	291257	123453	CTACAGGTGCCTGCCACCAC
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202086	34282	GCGTGGTGGCGAGCACTTGT	246673	78869	TTCTTCCAGAATCCTGTTGA	291260	123456	GGACTACAGGTGCCTGCCAC
202087	34283	GGCGTGGTGGCGAGCACTTG	246674	78870	ATTCTTCCAGAATCCTGTTG	291261	123457	GGGACTACAGGTGCCTGCCA
202088	34284	GGGCGTGGTGGCGAGCACTT	246675	78871	GATTCTTCCAGAATCCTGTT	291262	123458	TGGGACTACAGGTGCCTGCC
202089	34285	TGGGCGTGGTGGCGAGCACT	246676	78872	AGATTCTTCCAGAATCCTGT	291263	123459	CTGGGACTACAGGTGCCTGC
202090	34286	CTGGGCGTGGTGGCGAGCAC	246677	78873	GAGATTCTTCCAGAATCCTG	291264	123460	GCTGGGACTACAGGTGCCTG
202091	34287	GCTGGGCGTGGTGGCGAGCA	246678	78874	GGAGATTCTTCCAGAATCCT	291265	123461	GGCTGGGACTACAGGTGCCT
202092	34288	AGCTGGGCGTGGTGGCGAGC	246679	78875	GGGAGATTCTTCCAGAATCC	291266	123462	TGGCTGGGACTACAGGTGCC
202093	34289	TAGCTGGGCGTGGTGGCGAG	246680	78876	TGGGAGATTCTTCCAGAATC	291267	123463	GTGGCTGGGACTACAGGTGC
202094	34290	TTAGCTGGGCGTGGTGGCGA	246681	78877	TTGGGAGATTCTTCCAGAAT	291268	123464	AGTGGCTGGGACTACAGGTG
202095	34291	ATTAGCTGGGCGTGGTGGCG	246682	78878	TTTGGGAGATTCTTCCAGAA	291269	123465	GAGTGGCTGGGACTACAGGT
202096	34292	AATTAGCTGGGCGTGGTGGC	246683	78879	GTTTGGGAGATTCTTCCAGA	291270	123466	CGAGTGGCTGGGACTACAGG
202097	34293	AAATTAGCTGGGCGTGGTGG	246684	78880	TGTTTGGGAGATTCTTCCAG	291271	123467	CCGAGTGGCTGGGACTACAG
202098	34294	AAAATTAGCTGGGCGTGGTG	246685	78881	TTGTTTGGGAGATTCTTCCA	291272	123468	ACCGAGTGGCTGGGACTACA
202099	34295	AAAAATTAGCTGGGCGTGGT	246686	78882	CTTGTTTGGGAGATTCTTCC	291273	123469	AACCGAGTGGCTGGGACTAC
202100	34296	AAAAAATTAGCTGGGCGTGG	246687	78883	ACTTGTTTGGGAGATTCTTC	291274	123470	CAACCGAGTGGCTGGGACTA
202101	34297	AAAAAAATTAGCTGGGCGTG	246688	78884	GACTTGTTTGGGAGATTCTT	291275	123471	CCAACCGAGTGGCTGGGACT
202102	34298	CAAAAAAATTAGCTGGGCGT	246689	78885	CGACTTGTTTGGGAGATTCT	291276	123472	GCCAACCGAGTGGCTGGGAC
202103	34299	ACAAAAAAATTAGCTGGGCG	246690	78886	GCGACTTGTTTGGGAGATTC	291277	123473	AGCCAACCGAGTGGCTGGGA
202104	34300	CACAAAAAAATTAGCTGGGC	246691	78887	TGCGACTTGTTTGGGAGATT	291278	123474	CAGCCAACCGAGTGGCTGGG
202105	34301	ACACAAAAAAATTAGCTGGG	246692	78888	TTGCGACTTGTTTGGGAGAT	291279	123475	TCAGCCAACCGAGTGGCTGG
202106	34302	AACACAAAAAAATTAGCTGG	246693	78889	ATTGCGACTTGTTTGGGAGA	291280	123476	CTCAGCCAACCGAGTGGCTG
202107	34303	AAACACAAAAAAATTAGCTG	246694	78890	CATTGCGACTTGTTTGGGAG	291281	123477	CCTCAGCCAACCGAGTGGCT
202108	34304	AAAACACAAAAAAATTAGCT	246695	78891	GCATTGCGACTTGTTTGGGA	291282	123478	GCCTCAGCCAACCGAGTGGC
202109	34305	AAAAACACAAAAAAATTAGC	246696	78892	GGCATTGCGACTTGTTTGGG	291283	123479	TGCCTCAGCCAACCGAGTGG
202110	34306	TAAAAACACAAAAAAATTAG	246697	78893	GGGCATTGCGACTTGTTTGG	291284	123480	CTGCCTCAGCCAACCGAGTG
202111	34307	CTAAAAACACAAAAAAATTA	246698	78894	AGGGCATTGCGACTTGTTTG	291285	123481	CCTGCCTCAGCCAACCGAGT
202112	34308	ACTAAAAACACAAAAAAATT	246699	78895	GAGGGCATTGCGACTTGTTT	291286	123482	TCCTGCCTCAGCCAACCGAG
202113	34309	TACTAAAAACACAAAAAAAT	246700	78896	AGAGGGCATTGCGACTTGTT	291287	123483	CTCCTGCCTCAGCCAACCGA
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202115	34311	TCTACTAAAAACACAAAAAA	246702	78898	CCAGAGGGCATTGCGACTTG	291289	123485	TTCTCCTGCCTCAGCCAACC
202116	34312	CTCTACTAAAAACACAAAAA	246703	78899	TCCAGAGGGCATTGCGACTT	291290	123486	ATTCTCCTGCCTCAGCCAAC
202117	34313	TCTCTACTAAAAACACAAAA	246704	78900	GTCCAGAGGGCATTGCGACT	291291	123487	CATTCTCCTGCCTCAGCCAA
202118	34314	ATCTCTACTAAAAACACAAA	246705	78901	GGTCCAGAGGGCATTGCGAC	291292	123488	CCATTCTCCTGCCTCAGCCA
202119	34315	CATCTCTACTAAAAACACAA	246706	78902	GGGTCCAGAGGGCATTGCGA	291293	123489	GCCATTCTCCTGCCTCAGCC
202120	34316	CCATCTCTACTAAAAACACA	246707	78903	AGGGTCCAGAGGGCATTGCG	291294	123490	TGCCATTCTCCTGCCTCAGC
202121	34317	CCCATCTCTACTAAAAACAC	246708	78904	CAGGGTCCAGAGGGCATTGC	291295	123491	ATGCCATTCTCCTGCCTCAG
202122	34318	CCCCATCTCTACTAAAAACA	246709	78905	ACAGGGTCCAGAGGGCATTG	291296	123492	CATGCCATTCTCCTGCCTCA
202123	34319	ACCCCATCTCTACTAAAAAC	246710	78906	CACAGGGTCCAGAGGGCATT	291297	123493	TCATGCCATTCTCCTGCCTC
202124	34320	AACCCCATCTCTACTAAAAA	246711	78907	GCACAGGGTCCAGAGGGCAT	291298	123494	TTCATGCCATTCTCCTGCCT
202125	34321	AAACCCCATCTCTACTAAAA	246712	78908	TGCACAGGGTCCAGAGGGCA	291299	123495	GTTCATGCCATTCTCCTGCC
202126	34322	GAAACCCCATCTCTACTAAA	246713	78909	CTGCACAGGGTCCAGAGGGC	291300	123496	GGTTCATGCCATTCTCCTGC
202127	34323	TGAAACCCCATCTCTACTAA	246714	78910	CCTGCACAGGGTCCAGAGGG	291301	123497	GGGTTCATGCCATTCTCCTG
202128	34324	GTGAAACCCCATCTCTACTA	246715	78911	GCCTGCACAGGGTCCAGAGG	291302	123498	CGGGTTCATGCCATTCTCCT
202129	34325	GGTGAAACCCCATCTCTACT	246716	78912	TGCCTGCACAGGGTCCAGAG	291303	123499	CCGGGTTCATGCCATTCTCC
202130	34326	CGGTGAAACCCCATCTCTAC	246717	78913	ATGCCTGCACAGGGTCCAGA	291304	123500	CCCGGGTTCATGCCATTCTC
202131	34327	ACGGTGAAACCCCATCTCTA	246718	78914	CATGCCTGCACAGGGTCCAG	291305	123501	TCCCGGGTTCATGCCATTCT
202132	34328	CACGGTGAAACCCCATCTCT	246719	78915	TCATGCCTGCACAGGGTCCA	291306	123502	CTCCCGGGTTCATGCCATTC
202133	34329	ACACGGTGAAACCCCATCTC	246720	78916	CTCATGCCTGCACAGGGTCC	291307	123503	CCTCCCGGGTTCATGCCATT
202134	34330	AACACGGTGAAACCCCATCT	246721	78917	TCTCATGCCTGCACAGGGTC	291308	123504	GCCTCCCGGGTTCATGCCAT
202135	34331	TAACACGGTGAAACCCCATC	246722	78918	GTCTCATGCCTGCACAGGGT	291309	123505	CGCCTCCCGGGTTCATGCCA
202136	34332	CTAACACGGTGAAACCCCAT	246723	78919	AGTCTCATGCCTGCACAGGG	291310	123506	CCGCCTCCCGGGTTCATGCC
202137	34333	GCTAACACGGTGAAACCCCA	246724	78920	GAGTCTCATGCCTGCACAGG	291311	123507	TCCGCCTCCCGGGTTCATGC
202138	34334	GGCTAACACGGTGAAACCCC	246725	78921	TGAGTCTCATGCCTGCACAG	291312	123508	CTCCGCCTCCCGGGTTCATG
202139	34335	TGGCTAACACGGTGAAACCC	246726	78922	TTGAGTCTCATGCCTGCACA	291313	123509	GCTCCGCCTCCCGGGTTCAT
202140	34336	CTGGCTAACACGGTGAAACC	246727	78923	CTTGAGTCTCATGCCTGCAC	291314	123510	AGCTCCGCCTCCCGGGTTCA
202141	34337	CCTGGCTAACACGGTGAAAC	246728	78924	TCTTGAGTCTCATGCCTGCA	291315	123511	AAGCTCCGCCTCCCGGGTTC
202142	34338	TCCTGGCTAACACGGTGAAA	246729	78925	CTCTTGAGTCTCATGCCTGC	291316	123512	CAAGCTCCGCCTCCCGGGTT
202143	34339	ATCCTGGCTAACACGGTGAA	246730	78926	GCTCTTGAGTCTCATGCCTG	291317	123513	GCAAGCTCCGCCTCCCGGGT
202144	34340	CATCCTGGCTAACACGGTGA	246731	78927	TGCTCTTGAGTCTCATGCCT	291318	123514	TGCAAGCTCCGCCTCCCGGG
202145	34341	CCATCCTGGCTAACACGGTG	246732	78928	ATGCTCTTGAGTCTCATGCC	291319	123515	CTGCAAGCTCCGCCTCCCGG
202146	34342	ACCATCCTGGCTAACACGGT	246733	78929	AATGCTCTTGAGTCTCATGC	291320	123516	ACTGCAAGCTCCGCCTCCCG

202147	34343	GACCATCCTGGCTAACACGG	246734	78930	CAATGCTCTTGAGTCTCATG	291321	123517	CACTGCAAGCTCCGCCTCCC
202148	34344	AGACCATCCTGGCTAACACG	246735	78931	CCAATGCTCTTGAGTCTCAT	291322	123518	TCACTGCAAGCTCCGCCTCC
202149	34345	GAGACCATCCTGGCTAACAC	246736	78932	GCCAATGCTCTTGAGTCTCA	291323	123519	CTCACTGCAAGCTCCGCCTC
202150	34346	CGAGACCATCCTGGCTAACA	246737	78933	AGCCAATGCTCTTGAGTCTC	291324	123520	GCTCACTGCAAGCTCCGCCT
202151	34347	TCGAGACCATCCTGGCTAAC	246738	78934	GAGCCAATGCTCTTGAGTCT	291325	123521	TGCTCACTGCAAGCTCCGCC
202152	34348	ATCGAGACCATCCTGGCTAA	246739	78935	GGAGCCAATGCTCTTGAGTC	291326	123522	CTGCTCACTGCAAGCTCCGC
202153	34349	GATCGAGACCATCCTGGCTA	246740	78936	GGGAGCCAATGCTCTTGAGT	291327	123523	TCTGCTCACTGCAAGCTCCG
202154	34350	AGATCGAGACCATCCTGGCT	246741	78937	TGGGAGCCAATGCTCTTGAG	291328	123524	CTCTGCTCACTGCAAGCTCC
202155	34351	GAGATCGAGACCATCCTGGC	246742	78938	GTGGGAGCCAATGCTCTTGA	291329	123525	TCTCTGCTCACTGCAAGCTC
202156	34352	GGAGATCGAGACCATCCTGG	246743	78939	GGTGGGAGCCAATGCTCTTG	291330	123526	GTCTCTGCTCACTGCAAGCT
202157	34353	AGGAGATCGAGACCATCCTG	246744	78940	GGGTGGGAGCCAATGCTCTT	291331	123527	GGTCTCTGCTCACTGCAAGC
202158	34354	CAGGAGATCGAGACCATCCT	246745	78941	GGGGTGGGAGCCAATGCTCT	291332	123528	TGGTCTCTGCTCACTGCAAG
202159	34355	TCAGGAGATCGAGACCATCC	246746	78942	AGGGGTGGGAGCCAATGCTC	291333	123529	ATGGTCTCTGCTCACTGCAA
202160	34356	GTCAGGAGATCGAGACCATC	246747	78943	CAGGGGTGGGAGCCAATGCT	291334	123530	CATGGTCTCTGCTCACTGCA
202161	34357	GGTCAGGAGATCGAGACCAT	246748	78944	CCAGGGGTGGGAGCCAATGC	291335	123531	GCATGGTCTCTGCTCACTGC
202162	34358	AGGTCAGGAGATCGAGACCA	246749	78945	ACCAGGGGTGGGAGCCAATG	291336	123532	GGCATGGTCTCTGCTCACTG
202163	34359	GAGGTCAGGAGATCGAGACC	246750	78946	CACCAGGGGTGGGAGCCAAT	291337	123533	TGGCATGGTCTCTGCTCACT
202164	34360	TGAGGTCAGGAGATCGAGAC	246751	78947	CCACCAGGGGTGGGAGCCAA	291338	123534	GTGGCATGGTCTCTGCTCAC
202165	34361	ATGAGGTCAGGAGATCGAGA	246752	78948	TCCACCAGGGGTGGGAGCCA	291339	123535	AGTGGCATGGTCTCTGCTCA
202166	34362	CATGAGGTCAGGAGATCGAG	246753	78949	CTCCACCAGGGGTGGGAGCC	291340	123536	CAGTGGCATGGTCTCTGCTC
202167	34363	TCATGAGGTCAGGAGATCGA	246754	78950	CCTCCACCAGGGGTGGGAGC	291341	123537	GCAGTGGCATGGTCTCTGCT
202168	34364	ATCATGAGGTCAGGAGATCG	246755	78951	CCCTCCACCAGGGGTGGGAG	291342	123538	TGCAGTGGCATGGTCTCTGC
202169	34365	GATCATGAGGTCAGGAGATC	246756	78952	TCCCTCCACCAGGGGTGGGA	291343	123539	GTGCAGTGGCATGGTCTCTG
202170	34366	AGATCATGAGGTCAGGAGAT	246757	78953	TTCCCTCCACCAGGGGTGGG	291344	123540	AGTGCAGTGGCATGGTCTCT
202171	34367	CAGATCATGAGGTCAGGAGA	246758	78954	GTTCCCTCCACCAGGGGTGG	291345	123541	GAGTGCAGTGGCATGGTCTC
202172	34368	GCAGATCATGAGGTCAGGAG	246759	78955	TGTTCCCTCCACCAGGGGTG	291346	123542	GGAGTGCAGTGGCATGGTCT
202173	34369	GGCAGATCATGAGGTCAGGA	246760	78956	GTGTTCCCTCCACCAGGGGT	291347	123543	TGGAGTGCAGTGGCATGGTC
202174	34370	AGGCAGATCATGAGGTCAGG	246761	78957	AGTGTTCCCTCCACCAGGGG	291348	123544	CTGGAGTGCAGTGGCATGGT
202175	34371	CAGGCAGATCATGAGGTCAG	246762	78958	CAGTGTTCCCTCCACCAGGG	291349	123545	GCTGGAGTGCAGTGGCATGG
202176	34372	GCAGGCAGATCATGAGGTCA	246763	78959	GCAGTGTTCCCTCCACCAGG	291350	123546	GGCTGGAGTGCAGTGGCATG
202177	34373	GGCAGGCAGATCATGAGGTC	246764	78960	AGCAGTGTTCCCTCCACCAG	291351	123547	AGGCTGGAGTGCAGTGGCAT
202178	34374	AGGCAGGCAGATCATGAGGT	246765	78961	CAGCAGTGTTCCCTCCACCA	291352	123548	CAGGCTGGAGTGCAGTGGCA
202179	34375	GAGGCAGGCAGATCATGAGG	246766	78962	CCAGCAGTGTTCCCTCCACC	291353	123549	CCAGGCTGGAGTGCAGTGGC
202180	34376	TGAGGCAGGCAGATCATGAG	246767	78963	CCCAGCAGTGTTCCCTCCAC	291354	123550	CCCAGGCTGGAGTGCAGTGG
202181	34377	ATGAGGCAGGCAGATCATGA	246768	78964	CCCCAGCAGTGTTCCCTCCA	291355	123551	GCCCAGGCTGGAGTGCAGTG
202182	34378	GATGAGGCAGGCAGATCATG	246769	78965	GCCCCAGCAGTGTTCCCTCC	291356	123552	CGCCCAGGCTGGAGTGCAGT
202183	34379	TGATGAGGCAGGCAGATCAT	246770	78966	AGCCCCAGCAGTGTTCCCTC	291357	123553	TCGCCCAGGCTGGAGTGCAG
202184	34380	CTGATGAGGCAGGCAGATCA	246771	78967	CAGCCCCAGCAGTGTTCCCT	291358	123554	GTCGCCCAGGCTGGAGTGCA
202185	34381	GCTGATGAGGCAGGCAGATC	246772	78968	CCAGCCCCAGCAGTGTTCCC	291359	123555	TGTCGCCCAGGCTGGAGTGC
202186	34382	GGCTGATGAGGCAGGCAGAT	246773	78969	CCCAGCCCCAGCAGTGTTCC	291360	123556	CTGTCGCCCAGGCTGGAGTG
202187	34383	AGGCTGATGAGGCAGGCAGA	246774	78970	TCCCAGCCCCAGCAGTGTTC	291361	123557	TCTGTCGCCCAGGCTGGAGT
202188	34384	GAGGCTGATGAGGCAGGCAG	246775	78971	ATCCCAGCCCCAGCAGTGTT	291362	123558	CTCTGTCGCCCAGGCTGGAG
202189	34385	GGAGGCTGATGAGGCAGGCA	246776	78972	GATCCCAGCCCCAGCAGTGT	291363	123559	GCTCTGTCGCCCAGGCTGGA
202190	34386	GGGAGGCTGATGAGGCAGGC	246777	78973	AGATCCCAGCCCCAGCAGTG	291364	123560	TGCTCTGTCGCCCAGGCTGG
202191	34387	TGGGAGGCTGATGAGGCAGG	246778	78974	AAGATCCCAGCCCCAGCAGT	291365	123561	TTGCTCTGTCGCCCAGGCTG
202192	34388	CTGGGAGGCTGATGAGGCAG	246779	78975	CAAGATCCCAGCCCCAGCAG	291366	123562	CTTGCTCTGTCGCCCAGGCT
202193	34389	TCTGGGAGGCTGATGAGGCA	246780	78976	GCAAGATCCCAGCCCCAGCA	291367	123563	TCTTGCTCTGTCGCCCAGGC
202194	34390	CTCTGGGAGGCTGATGAGGC	246781	78977	GGCAAGATCCCAGCCCCAGC	291368	123564	GTCTTGCTCTGTCGCCCAGG
202195	34391	ACTCTGGGAGGCTGATGAGG	246782	78978	AGGCAAGATCCCAGCCCCAG	291369	123565	AGTCTTGCTCTGTCGCCCAG
202196	34392	CACTCTGGGAGGCTGATGAG	246783	78979	CAGGCAAGATCCCAGCCCCA	291370	123566	GAGTCTTGCTCTGTCGCCCA
202197	34393	GCACTCTGGGAGGCTGATGA	246784	78980	CCAGGCAAGATCCCAGCCCC	291371	123567	AGAGTCTTGCTCTGTCGCCC
202198	34394	AGCACTCTGGGAGGCTGATG	246785	78981	ACCAGGCAAGATCCCAGCCC	291372	123568	CAGAGTCTTGCTCTGTCGCC
202199	34395	CAGCACTCTGGGAGGCTGAT	246786	78982	AACCAGGCAAGATCCCAGCC	291373	123569	ACAGAGTCTTGCTCTGTCGC
202200	34396	CCAGCACTCTGGGAGGCTGA	246787	78983	CAACCAGGCAAGATCCCAGC	291374	123570	GACAGAGTCTTGCTCTGTCG
202201	34397	CCCAGCACTCTGGGAGGCTG	246788	78984	GCAACCAGGCAAGATCCCAG	291375	123571	AGACAGAGTCTTGCTCTGTC
202202	34398	TCCCAGCACTCTGGGAGGCT	246789	78985	AGCAACCAGGCAAGATCCCA	291376	123572	GAGACAGAGTCTTGCTCTGT
202203	34399	ATCCCAGCACTCTGGGAGGC	246790	78986	GAGCAACCAGGCAAGATCCC	291377	123573	TGAGACAGAGTCTTGCTCTG
202204	34400	AATCCCAGCACTCTGGGAGG	246791	78987	GGAGCAACCAGGCAAGATCC	291378	123574	TTGAGACAGAGTCTTGCTCT
202205	34401	TAATCCCAGCACTCTGGGAG	246792	78988	CGGAGCAACCAGGCAAGATC	291379	123575	CTTGAGACAGAGTCTTGCTC
202206	34402	GTAATCCCAGCACTCTGGGA	246793	78989	GCGGAGCAACCAGGCAAGAT	291380	123576	TCTTGAGACAGAGTCTTGCT
202207	34403	TGTAATCCCAGCACTCTGGG	246794	78990	GGCGGAGCAACCAGGCAAGA	291381	123577	TTCTTGAGACAGAGTCTTGC
202208	34404	CTGTAATCCCAGCACTCTGG	246795	78991	AGGCGGAGCAACCAGGCAAG	291382	123578	TTTCTTGAGACAGAGTCTTG
202209	34405	CCTGTAATCCCAGCACTCTG	246796	78992	CAGGCGGAGCAACCAGGCAA	291383	123579	TTTTCTTGAGACAGAGTCTT
202210	34406	GCCTGTAATCCCAGCACTCT	246797	78993	GCAGGCGGAGCAACCAGGCA	291384	123580	TTTTTCTTGAGACAGAGTCT
202211	34407	TGCCTGTAATCCCAGCACTC	246798	78994	TGCAGGCGGAGCAACCAGGC	291385	123581	TTTTTTCTTGAGACAGAGTC
202212	34408	ATGCCTGTAATCCCAGCACT	246799	78995	GTGCAGGCGGAGCAACCAGG	291386	123582	TTTTTTTCTTGAGACAGAGT
202213	34409	CATGCCTGTAATCCCAGCAC	246800	78996	GGTGCAGGCGGAGCAACCAG	291387	123583	TTTTTTTTCTTGAGACAGAG
202214	34410	TCATGCCTGTAATCCCAGCA	246801	78997	GGGTGCAGGCGGAGCAACCA	291388	123584	TTTTTTTTTCTTGAGACAGA
202215	34411	CTCATGCCTGTAATCCCAGC	246802	78998	TGGGTGCAGGCGGAGCAACC	291389	123585	TTTTTTTTTTCTTGAGACAG
202216	34412	GCTCATGCCTGTAATCCCAG	246803	78999	TTGGGTGCAGGCGGAGCAAC	291390	123586	TTTTTTTTTTTCTTGAGACA
202217	34413	GGCTCATGCCTGTAATCCCA	246804	79000	CTTGGGTGCAGGCGGAGCAA	291391	123587	TTTTTTTTTTTTCTTGAGAC
202218	34414	TGGCTCATGCCTGTAATCCC	246805	79001	TCTTGGGTGCAGGCGGAGCA	291392	123588	TTTTTTTTTTTTTCTTGAGA

202219	34415	GTGGCTCATGCCTGTAATCC	246806	79002	GTCTTGGGTGCAGGCGGAGC	291393	123589	TTTTTTTTTTTTTCTTGAG
202220	34416	AGTGGCTCATGCCTGTAATC	246807	79003	TGTCTTGGGTGCAGGCGGAG	291394	123590	TTTTTTTTTTTTTCTTGA
202221	34417	CAGTGGCTCATGCCTGTAAT	246808	79004	TTGTCTTGGGTGCAGGCGGA	291395	123591	TTTTTTTTTTTTTTCTTG
202222	34418	GCAGTGGCTCATGCCTGTAA	246809	79005	GTTGTCTTGGGTGCAGGCGG	291396	123592	GTTTTTTTTTTTTTTCTT
202223	34419	TGCAGTGGCTCATGCCTGTA	246810	79006	GGTTGTCTTGGGTGCAGGCG	291397	123593	TGTTTTTTTTTTTTTTCT
202224	34420	GTGCAGTGGCTCATGCCTGT	246811	79007	TGGTTGTCTTGGGTGCAGGC	291398	123594	CTGTTTTTTTTTTTTTTTC
202225	34421	GGTGCAGTGGCTCATGCCTG	246812	79008	ATGGTTGTCTTGGGTGCAGG	291399	123595	TCTGTTTTTTTTTTTTTTT
202226	34422	GGGTGCAGTGGCTCATGCCT	246813	79009	TATGGTTGTCTTGGGTGCAG	291400	123596	GTCTGTTTTTTTTTTTTTT
202227	34423	CGGGTGCAGTGGCTCATGCC	246814	79010	TTATGGTTGTCTTGGGTGCA	291401	123597	AGTCTGTTTTTTTTTTTTT
202228	34424	CCGGGTGCAGTGGCTCATGC	246815	79011	ATTATGGTTGTCTTGGGTGC	291402	123598	AAGTCTGTTTTTTTTTTTT
202229	34425	GCCGGGTGCAGTGGCTCATG	246816	79012	AATTATGGTTGTCTTGGGTG	291403	123599	AAAGTCTGTTTTTTTTTTT
202230	34426	GGCCGGGTGCAGTGGCTCAT	246817	79013	TAATTATGGTTGTCTTGGGT	291404	123600	TAAAGTCTGTTTTTTTTTT
202231	34427	TGGCCGGGTGCAGTGGCTCA	246818	79014	TTAATTATGGTTGTCTTGGG	291405	123601	GTAAAGTCTGTTTTTTTTT
202232	34428	ATGGCCGGGTGCAGTGGCTC	246819	79015	TTTAATTATGGTTGTCTTGG	291406	123602	AGTAAAGTCTGTTTTTTTT
202233	34429	GATGGCCGGGTGCAGTGGCT	246820	79016	TTTTAATTATGGTTGTCTTG	291407	123603	AAGTAAAGTCTGTTTTTTT
202234	34430	TGATGGCCGGGTGCAGTGGC	246821	79017	ATTTTAATTATGGTTGTCTT	291408	123604	TAAGTAAAGTCTGTTTTTT
202235	34431	CTGATGGCCGGGTGCAGTGG	246822	79018	CATTTTAATTATGGTTGTCT	291409	123605	GTAAGTAAAGTCTGTTTTT
202236	34432	ACTGATGGCCGGGTGCAGTG	246823	79019	ACATTTTAATTATGGTTGTC	291410	123606	AGTAAGTAAAGTCTGTTTT
202237	34433	CACTGATGGCCGGGTGCAGT	246824	79020	GACATTTTAATTATGGTTGT	291411	123607	CAGTAAGTAAAGTCTGTTT
202238	34434	CCACTGATGGCCGGGTGCAG	246825	79021	GGACATTTTAATTATGGTTG	291412	123608	CCAGTAAGTAAAGTCTGTT
202239	34435	TCCACTGATGGCCGGGTGCA	246826	79022	AGGACATTTTAATTATGGTT	291413	123609	TCCAGTAAGTAAAGTCTGT
202240	34436	ATCCACTGATGGCCGGGTGC	246827	79023	AAGGACATTTTAATTATGGT	291414	123610	TTCCAGTAAGTAAAGTCTGT
202241	34437	TATCCACTGATGGCCGGGTG	246828	79024	GAAGGACATTTTAATTATGG	291415	123611	CTTCCAGTAAGTAAAGTCTG
202242	34438	ATATCCACTGATGGCCGGGT	246829	79025	TGAAGGACATTTTAATTATG	291416	123612	GCTTCCAGTAAGTAAAGTCT
202243	34439	TATATCCACTGATGGCCGGG	246830	79026	ATGAAGGACATTTTAATTAT	291417	123613	GGCTTCCAGTAAGTAAAGTC
202244	34440	ATATATCCACTGATGGCCGG	246831	79027	AATGAAGGACATTTTAATTA	291418	123614	TGGCTTCCAGTAAGTAAAGT
202245	34441	AATATATCCACTGATGGCCG	246832	79028	CAATGAAGGACATTTTAATT	291419	123615	TTGGCTTCCAGTAAGTAAAG
202246	34442	AAATATATCCACTGATGGCC	246833	79029	TCAATGAAGGACATTTTAAT	291420	123616	GTTGGCTTCCAGTAAGTAAA
202247	34443	AAAATATATCCACTGATGGC	246834	79030	TTCAATGAAGGACATTTTAA	291421	123617	GGTTGGCTTCCAGTAAGTAA
202248	34444	AAAAATATATCCACTGATGG	246835	79031	GTTCAATGAAGGACATTTTA	291422	123618	TGGTTGGCTTCCAGTAAGTA
202249	34445	TAAAAATATATCCACTGATG	246836	79032	AGTTCAATGAAGGACATTTT	291423	123619	TTGGTTGGCTTCCAGTAAGT
202250	34446	TTAAAAATATATCCACTGAT	246837	79033	AAGTTCAATGAAGGACATTT	291424	123620	ATTGGTTGGCTTCCAGTAAG
202251	34447	TTTAAAAATATATCCACTGA	246838	79034	CAAGTTCAATGAAGGACATT	291425	123621	CATTGGTTGGCTTCCAGTAA
202252	34448	CTTTAAAAATATATCCACTG	246839	79035	CCAAGTTCAATGAAGGACAT	291426	123622	ACATTGGTTGGCTTCCAGTA
202253	34449	GCTTTAAAAATATATCCACT	246840	79036	TCCAAGTTCAATGAAGGACA	291427	123623	TACATTGGTTGGCTTCCAGT
202254	34450	TGCTTTAAAAATATATCCAC	246841	79037	TTCCAAGTTCAATGAAGGAC	291428	123624	ATACATTGGTTGGCTTCCAG
202255	34451	GTGCTTTAAAAATATATCCA	246842	79038	TTTCCAAGTTCAATGAAGGA	291429	123625	TATACATTGGTTGGCTTCCA
202256	34452	AGTGCTTTAAAAATATATCC	246843	79039	CTTTCCAAGTTCAATGAAGG	291430	123626	ATATACATTGGTTGGCTTCC
202257	34453	CAGTGCTTTAAAAATATATC	246844	79040	GCTTTCCAAGTTCAATGAAG	291431	123627	AATATACATTGGTTGGCTTC
202258	34454	GCAGTGCTTTAAAAATATAT	246845	79041	GGCTTTCCAAGTTCAATGAA	291432	123628	AAATATACATTGGTTGGCTT
202259	34455	TGCAGTGCTTTAAAAATATA	246846	79042	AGGCTTTCCAAGTTCAATGA	291433	123629	TAAATATACATTGGTTGGCT
202260	34456	CTGCAGTGCTTTAAAAATAT	246847	79043	AAGGCTTTCCAAGTTCAATG	291434	123630	CTAAATATACATTGGTTGGC
202261	34457	TCTGCAGTGCTTTAAAAATA	246848	79044	GAAGGCTTTCCAAGTTCAAT	291435	123631	TCTAAATATACATTGGTTGG
202262	34458	CTCTGCAGTGCTTTAAAAAT	246849	79045	TGAAGGCTTTCCAAGTTCAA	291436	123632	CTCTAAATATACATTGGTTG
202263	34459	TCTCTGCAGTGCTTTAAAAA	246850	79046	TTGAAGGCTTTCCAAGTTCA	291437	123633	ACTCTAAATATACATTGGTT
202264	34460	TTCTCTGCAGTGCTTTAAAA	246851	79047	TTTGAAGGCTTTCCAAGTTC	291438	123634	TACTCTAAATATACATTGGT
202265	34461	ATTCTCTGCAGTGCTTTAAA	246852	79048	CTTTGAAGGCTTTCCAAGTT	291439	123635	TTACTCTAAATATACATTGG
202266	34462	AATTCTCTGCAGTGCTTTAA	246853	79049	GCTTTGAAGGCTTTCCAAGT	291440	123636	ATTACTCTAAATATACATTG
202267	34463	GAATTCTCTGCAGTGCTTTA	246854	79050	AGCTTTGAAGGCTTTCCAAG	291441	123637	AATTACTCTAAATATACATT
202268	34464	AGAATTCTCTGCAGTGCTTT	246855	79051	CAGCTTTGAAGGCTTTCCAA	291442	123638	AAATTACTCTAAATATACAT
202269	34465	CAGAATTCTCTGCAGTGCTT	246856	79052	TCAGCTTTGAAGGCTTTCCA	291443	123639	AAAATTACTCTAAATATACA
202270	34466	ACAGAATTCTCTGCAGTGCT	246857	79053	GTCAGCTTTGAAGGCTTTCC	291444	123640	AAAAATTACTCTAAATATAC
202271	34467	AACAGAATTCTCTGCAGTGC	246858	79054	TGTCAGCTTTGAAGGCTTTC	291445	123641	GAAAAATTACTCTAAATATA
202272	34468	CAACAGAATTCTCTGCAGTG	246859	79055	TTGTCAGCTTTGAAGGCTTT	291446	123642	GGAAAAATTACTCTAAATAT
202273	34469	GCAACAGAATTCTCTGCAGT	246860	79056	GTTGTCAGCTTTGAAGGCTT	291447	123643	AGGAAAAATTACTCTAAATA
202274	34470	TGCAACAGAATTCTCTGCAG	246861	79057	AGTTGTCAGCTTTGAAGGCT	291448	123644	CAGGAAAAATTACTCTAAAT
202275	34471	ATGCAACAGAATTCTCTGCA	246862	79058	GAGTTGTCAGCTTTGAAGGC	291449	123645	CCAGGAAAAATTACTCTAAA
202276	34472	GATGCAACAGAATTCTCTGC	246863	79059	GGAGTTGTCAGCTTTGAAGG	291450	123646	CCCAGGAAAAATTACTCTAA
202277	34473	TGATGCAACAGAATTCTCTG	246864	79060	AGGAGTTGTCAGCTTTGAAG	291451	123647	GCCCAGGAAAAATTACTCTA
202278	34474	CTGATGCAACAGAATTCTCT	246865	79061	AAGGAGTTGTCAGCTTTGAA	291452	123648	AGCCCAGGAAAAATTACTCT
202279	34475	GCTGATGCAACAGAATTCTC	246866	79062	TAAGGAGTTGTCAGCTTTGA	291453	123649	CAGCCCAGGAAAAATTACTC
202280	34476	AGCTGATGCAACAGAATTCT	246867	79063	ATAAGGAGTTGTCAGCTTTG	291454	123650	TCAGCCCAGGAAAAATTACT
202281	34477	AAGCTGATGCAACAGAATTC	246868	79064	CATAAGGAGTTGTCAGCTTT	291455	123651	CTCAGCCCAGGAAAAATTAC
202282	34478	CAAGCTGATGCAACAGAATT	246869	79065	ACATAAGGAGTTGTCAGCTT	291456	123652	GCTCAGCCCAGGAAAAATTA
202283	34479	TCAAGCTGATGCAACAGAAT	246870	79066	CACATAAGGAGTTGTCAGCT	291457	123653	AGCTCAGCCCAGGAAAAATT
202284	34480	CTCAAGCTGATGCAACAGAA	246871	79067	ACACATAAGGAGTTGTCAGC	291458	123654	CAGCTCAGCCCAGGAAAAAT
202285	34481	TCTCAAGCTGATGCAACAGA	246872	79068	TACACATAAGGAGTTGTCAG	291459	123655	ACAGCTCAGCCCAGGAAAAA
202286	34482	TTCTCAAGCTGATGCAACAG	246873	79069	GTACACATAAGGAGTTGTCA	291460	123656	GACAGCTCAGCCCAGGAAAA
202287	34483	GTTCTCAAGCTGATGCAACA	246874	79070	GGTACACATAAGGAGTTGTC	291461	123657	TGACAGCTCAGCCCAGGAAA
202288	34484	GGTTCTCAAGCTGATGCAAC	246875	79071	GGGTACACATAAGGAGTTGT	291462	123658	ATGACAGCTCAGCCCAGGAA
202289	34485	TGGTTCTCAAGCTGATGCAA	246876	79072	CGGGTACACATAAGGAGTTG	291463	123659	AATGACAGCTCAGCCCAGGA
202290	34486	GTGGTTCTCAAGCTGATGCA	246877	79073	CCGGGTACACATAAGGAGTT	291464	123660	AAATGACAGCTCAGCCCAGG

202291	34487	AGTGGTTCTCAAGCTGATGC	246878	79074	TCCGGGTACACATAAGGAGT	291465	123661	TAAATGACAGCTCAGCCCAG
202292	34488	CAGTGGTTCTCAAGCTGATG	246879	79075	TTCCGGGTACACATAAGGAG	291466	123662	GTAAATGACAGCTCAGCCCA
202293	34489	TCAGTGGTTCTCAAGCTGAT	246880	79076	TTTCCGGGTACACATAAGGA	291467	123663	AGTAAATGACAGCTCAGCCC
202294	34490	ATCAGTGGTTCTCAAGCTGA	246881	79077	CTTTCCGGGTACACATAAGG	291468	123664	AAGTAAATGACAGCTCAGCC
202295	34491	GATCAGTGGTTCTCAAGCTG	246882	79078	CCTTTCCGGGTACACATAAG	291469	123665	AAAGTAAATGACAGCTCAGC
202296	34492	AGATCAGTGGTTCTCAAGCT	246883	79079	GCCTTTCCGGGTACACATAA	291470	123666	AAAAGTAAATGACAGCTCAG
202297	34493	CAGATCAGTGGTTCTCAAGC	246884	79080	GGCCTTTCCGGGTACACATA	291471	123667	CAAAAGTAAATGACAGCTCA
202298	34494	GCAGATCAGTGGTTCTCAAG	246885	79081	AGGCCTTTCCGGGTACACAT	291472	123668	GCAAAAGTAAATGACAGCTC
202299	34495	GGCAGATCAGTGGTTCTCAA	246886	79082	CAGGCCTTTCCGGGTACACA	291473	123669	TGCAAAAGTAAATGACAGCT
202300	34496	AGGCAGATCAGTGGTTCTCA	246887	79083	CCAGGCCTTTCCGGGTACAC	291474	123670	CTGCAAAAGTAAATGACAGC
202301	34497	AAGGCAGATCAGTGGTTCTC	246888	79084	CCCAGGCCTTTCCGGGTACA	291475	123671	ACTGCAAAAGTAAATGACAG
202302	34498	CAAGGCAGATCAGTGGTTCT	246889	79085	TCCCAGGCCTTTCCGGGTAC	291476	123672	TACTGCAAAAGTAAATGACA
202303	34499	ACAAGGCAGATCAGTGGTTC	246890	79086	CTCCCAGGCCTTTCCGGGTA	291477	123673	ATACTGCAAAAGTAAATGAC
202304	34500	CACAAGGCAGATCAGTGGTT	246891	79087	ACTCCCAGGCCTTTCCGGGT	291478	123674	GATACTGCAAAAGTAAATGA
202305	34501	GCACAAGGCAGATCAGTGGT	246892	79088	CACTCCCAGGCCTTTCCGGG	291479	123675	AGATACTGCAAAAGTAAATG
202306	34502	AGCACAAGGCAGATCAGTGG	246893	79089	ACACTCCCAGGCCTTTCCGG	291480	123676	GAGATACTGCAAAAGTAAAT
202307	34503	AAGCACAAGGCAGATCAGTG	246894	79090	CACACTCCCAGGCCTTTCCG	291481	123677	TGAGATACTGCAAAAGTAAA
202308	34504	GAAGCACAAGGCAGATCAGT	246895	79091	GCACACTCCCAGGCCTTTCC	291482	123678	TTGAGATACTGCAAAAGTAA
202309	34505	TGAAGCACAAGGCAGATCAG	246896	79092	GGCACACTCCCAGGCCTTTC	291483	123679	CTTGAGATACTGCAAAAGTA
202310	34506	GTGAAGCACAAGGCAGATCA	246897	79093	TGGCACACTCCCAGGCCTTT	291484	123680	TCTTGAGATACTGCAAAAGT
202311	34507	TGTGAAGCACAAGGCAGATC	246898	79094	CTGGCACACTCCCAGGCCTT	291485	123681	TTCTTGAGATACTGCAAAAG
202312	34508	ATGTGAAGCACAAGGCAGAT	246899	79095	CCTGGCACACTCCCAGGCCT	291486	123682	CTTCTTGAGATACTGCAAAA
202313	34509	AATGTGAAGCACAAGGCAGA	246900	79096	CCCTGGCACACTCCCAGGCC	291487	123683	TCTTCTTGAGATACTGCAAA
202314	34510	AAATGTGAAGCACAAGGCAG	246901	79097	GCCCTGGCACACTCCCAGGC	291488	123684	TTCTTCTTGAGATACTGCAA
202315	34511	TAAATGTGAAGCACAAGGCA	246902	79098	TGCCCTGGCACACTCCCAGG	291489	123685	CTTCTTCTTGAGATACTGCA
202316	34512	TTAAATGTGAAGCACAAGGC	246903	79099	ATGCCCTGGCACACTCCCAG	291490	123686	TCTTCTTCTTGAGATACTGC
202317	34513	TTTAAATGTGAAGCACAAGG	246904	79100	AATGCCCTGGCACACTCCCA	291491	123687	CTCTTCTTCTTGAGATACTG
202318	34514	TTTTAAATGTGAAGCACAAG	246905	79101	CAATGCCCTGGCACACTCCC	291492	123688	ACTCTTCTTCTTGAGATACT
202319	34515	GTTTTAAATGTGAAGCACAA	246906	79102	GCAATGCCCTGGCACACTCC	291493	123689	AACTCTTCTTCTTGAGATAC
202320	34516	AGTTTTAAATGTGAAGCACA	246907	79103	AGCAATGCCCTGGCACACTC	291494	123690	AAACTCTTCTTCTTGAGATA
202321	34517	AAGTTTTAAATGTGAAGCAC	246908	79104	GAGCAATGCCCTGGCACACT	291495	123691	TAAACTCTTCTTCTTGAGAT
202322	34518	AAAGTTTTAAATGTGAAGCA	246909	79105	CGAGCAATGCCCTGGCACAC	291496	123692	GTAAACTCTTCTTCTTGAGA
202323	34519	AAAAGTTTTAAATGTGAAGC	246910	79106	CCGAGCAATGCCCTGGCACA	291497	123693	TGTAAACTCTTCTTCTTGAG
202324	34520	AAAAAGTTTTAAATGTGAAG	246911	79107	CCCGAGCAATGCCCTGGCAC	291498	123694	CTGTAAACTCTTCTTCTTGA
202325	34521	AAAAAAGTTTTAAATGTGAA	246912	79108	TCCCGAGCAATGCCCTGGCA	291499	123695	ACTGTAAACTCTTCTTCTTG
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202327	34523	AAAAAAAAGTTTTAAATGTG	246914	79110	CCTCCCGAGCAATGCCCTGG	291501	123697	ACACTGTAAACTCTTCTTCT
202328	34524	TAAAAAAAAGTTTTAAATGT	246915	79111	CCCTCCCGAGCAATGCCCTG	291502	123698	TACACTGTAAACTCTTCTTC
202329	34525	TTAAAAAAAAGTTTTAAATG	246916	79112	TCCCTCCCGAGCAATGCCCT	291503	123699	TTACACTGTAAACTCTTCTT
202330	34526	ATTAAAAAAAAGTTTTAAAT	246917	79113	GTCCCTCCCGAGCAATGCCC	291504	123700	TTTACACTGTAAACTCTTCT
202331	34527	CATTAAAAAAAAGTTTTAAA	246918	79114	CGTCCCTCCCGAGCAATGCC	291505	123701	ATTTACACTGTAAACTCTTC
202332	34528	TCATTAAAAAAAAGTTTTAA	246919	79115	GCGTCCCTCCCGAGCAATGC	291506	123702	TATTTACACTGTAAACTCTT
202333	34529	TTCATTAAAAAAAAGTTTTA	246920	79116	AGCGTCCCTCCCGAGCAATG	291507	123703	ATATTTACACTGTAAACTCT
202334	34530	ATTCATTAAAAAAAAGTTTT	246921	79117	CAGCGTCCCTCCCGAGCAAT	291508	123704	AATATTTACACTGTAAACTC
202335	34531	TATTCATTAAAAAAAAGTTT	246922	79118	TCAGCGTCCCTCCCGAGCAA	291509	123705	AAATATTTACACTGTAAACT
202336	34532	TTATTCATTAAAAAAAAGTT	246923	79119	ATCAGCGTCCCTCCCGAGCA	291510	123706	CAAATATTTACACTGTAAAC
202337	34533	TTTATTCATTAAAAAAAAGT	246924	79120	AATCAGCGTCCCTCCCGAGC	291511	123707	TCAAATATTTACACTGTAAA
202338	34534	ATTTATTCATTAAAAAAAAG	246925	79121	AAATCAGCGTCCCTCCCGAG	291512	123708	ATCAAATATTTACACTGTAA
202339	34535	TATTTATTCATTAAAAAAAA	246926	79122	CAAATCAGCGTCCCTCCCGA	291513	123709	CATCAAATATTTACACTGTA
202340	34536	TTATTTATTCATTAAAAAAA	246927	79123	CCAAATCAGCGTCCCTCCCG	291514	123710	GCATCAAATATTTACACTGT
202341	34537	TTTATTTATTCATTAAAAAA	246928	79124	TCCAAATCAGCGTCCCTCCC	291515	123711	TGCATCAAATATTTACACTG
202342	34538	GTTTATTTATTCATTAAAAA	246929	79125	TTCCAAATCAGCGTCCCTCC	291516	123712	GTGCATCAAATATTTACACT
202343	34539	GGTTTATTTATTCATTAAAA	246930	79126	CTTCCAAATCAGCGTCCCTC	291517	123713	TGTGCATCAAATATTTACAC
202344	34540	GGGTTTATTTATTCATTAAA	246931	79127	GCTTCCAAATCAGCGTCCCT	291518	123714	GTGTGCATCAAATATTTACA
202345	34541	GGGGTTTATTTATTCATTAA	246932	79128	TGCTTCCAAATCAGCGTCCC	291519	123715	AGTGTGCATCAAATATTTAC
202346	34542	TGGGGTTTATTTATTCATTA	246933	79129	ATGCTTCCAAATCAGCGTCC	291520	123716	AAGTGTGCATCAAATATTTA
202347	34543	TTGGGGTTTATTTATTCATT	246934	79130	AATGCTTCCAAATCAGCGTC	291521	123717	AAAGTGTGCATCAAATATTT
202348	34544	TTTGGGGTTTATTTATTCAT	246935	79131	AAATGCTTCCAAATCAGCGT	291522	123718	CAAAGTGTGCATCAAATATT
202349	34545	TTTTGGGGTTTATTTATTCA	246936	79132	TAAATGCTTCCAAATCAGCG	291523	123719	TCAAAGTGTGCATCAAATAT
202350	34546	TTTTTGGGGTTTATTTATTC	246937	79133	GTAAATGCTTCCAAATCAGC	291524	123720	ATCAAAGTGTGCATCAAATA
202351	34547	TTTTTTGGGGTTTATTTATT	246938	79134	GGTAAATGCTTCCAAATCAG	291525	123721	AATCAAAGTGTGCATCAAAT
202352	34548	ATTTTTTGGGGTTTATTTAT	246939	79135	AGGTAAATGCTTCCAAATCA	291526	123722	TAATCAAAGTGTGCATCAAA
202353	34549	AATTTTTTGGGGTTTATTTA	246940	79136	CAGGTAAATGCTTCCAAATC	291527	123723	ATAATCAAAGTGTGCATCAA
202354	34550	TAATTTTTTGGGGTTTATTT	246941	79137	TCAGGTAAATGCTTCCAAAT	291528	123724	TATAATCAAAGTGTGCATCA
202355	34551	TTAATTTTTTGGGGTTTATT	246942	79138	ATCAGGTAAATGCTTCCAAA	291529	123725	ATATAATCAAAGTGTGCATC
202356	34552	ATTAATTTTTTGGGGTTTAT	246943	79139	CATCAGGTAAATGCTTCCAA	291530	123726	TATATAATCAAAGTGTGCAT
202357	34553	GATTAATTTTTTGGGGTTTA	246944	79140	TCATCAGGTAAATGCTTCCA	291531	123727	CTATATAATCAAAGTGTGCA
202358	34554	AGATTAATTTTTTGGGGTTT	246945	79141	CTCATCAGGTAAATGCTTCC	291532	123728	TCTATATAATCAAAGTGTGC
202359	34555	GAGATTAATTTTTTGGGGTT	246946	79142	TCTCATCAGGTAAATGCTTC	291533	123729	ATCTATATAATCAAAGTGTG
202360	34556	GGAGATTAATTTTTTGGGGT	246947	79143	CTCTCATCAGGTAAATGCTT	291534	123730	CATCTATATAATCAAAGTGT
202361	34557	GGGAGATTAATTTTTTGGGG	246948	79144	TCTCTCATCAGGTAAATGCT	291535	123731	TCATCTATATAATCAAAGTG
202362	34558	AGGGAGATTAATTTTTTGGG	246949	79145	GTCTCTCATCAGGTAAATGC	291536	123732	TTCATCTATATAATCAAAGT

202363	34559	TAGGGAGATTAATTTTTTGG	246950	79146	AGTCTCTCATCAGGTAAATG	291537	123733	CTTCATCTATATAATCAAAG
202364	34560	TTAGGGAGATTAATTTTTTG	246951	79147	CAGTCTCTCATCAGGTAAAT	291538	123734	GCTTCATCTATATAATCAAA
202365	34561	CTTAGGGAGATTAATTTTTT	246952	79148	TCAGTCTCTCATCAGGTAAA	291539	123735	TGCTTCATCTATATAATCAA
202366	34562	GCTTAGGGAGATTAATTTTT	246953	79149	GTCAGTCTCTCATCAGGTAA	291540	123736	TTGCTTCATCTATATAATCA
202367	34563	GGCTTAGGGAGATTAATTTT	246954	79150	TGTCAGTCTCTCATCAGGTA	291541	123737	TTTGCTTCATCTATATAATC
202368	34564	AGGCTTAGGGAGATTAATTT	246955	79151	CTGTCAGTCTCTCATCAGGT	291542	123738	GTTTGCTTCATCTATATAAT
202369	34565	GAGGCTTAGGGAGATTAATT	246956	79152	GCTGTCAGTCTCTCATCAGG	291543	123739	AGTTTGCTTCATCTATATAA
202370	34566	GGAGGCTTAGGGAGATTAAT	246957	79153	TGCTGTCAGTCTCTCATCAG	291544	123740	TAGTTTGCTTCATCTATATA
202371	34567	GGGAGGCTTAGGGAGATTAA	246958	79154	CTGCTGTCAGTCTCTCATCA	291545	123741	ATAGTTTGCTTCATCTATAT
202372	34568	AGGGAGGCTTAGGGAGATTA	246959	79155	GCTGCTGTCAGTCTCTCATC	291546	123742	AATAGTTTGCTTCATCTATA
202373	34569	TAGGGAGGCTTAGGGAGATT	246960	79156	AGCTGCTGTCAGTCTCTCAT	291547	123743	AAATAGTTTGCTTCATCTAT
202374	34570	CTAGGGAGGCTTAGGGAGAT	246961	79157	GAGCTGCTGTCAGTCTCTCA	291548	123744	AAAATAGTTTGCTTCATCTA
202375	34571	TCTAGGGAGGCTTAGGGAGA	246962	79158	GGAGCTGCTGTCAGTCTCTC	291549	123745	GAAAATAGTTTGCTTCATCT
202376	34572	TTCTAGGGAGGCTTAGGGAG	246963	79159	AGGAGCTGCTGTCAGTCTCT	291550	123746	TGAAAATAGTTTGCTTCATC
202377	34573	CTTCTAGGGAGGCTTAGGGA	246964	79160	CAGGAGCTGCTGTCAGTCTC	291551	123747	TTGAAAATAGTTTGCTTCAT
202378	34574	TCTTCTAGGGAGGCTTAGGG	246965	79161	CCAGGAGCTGCTGTCAGTCT	291552	123748	CTTGAAAATAGTTTGCTTCA
202379	34575	ATCTTCTAGGGAGGCTTAGG	246966	79162	ACCAGGAGCTGCTGTCAGTC	291553	123749	TCTTGAAAATAGTTTGCTTC
202380	34576	TATCTTCTAGGGAGGCTTAG	246967	79163	TACCAGGAGCTGCTGTCAGT	291554	123750	CTCTTGAAAATAGTTTGCTT
202381	34577	CTATCTTCTAGGGAGGCTTA	246968	79164	CTACCAGGAGCTGCTGTCAG	291555	123751	GCTCTTGAAAATAGTTTGCT
202382	34578	CCTATCTTCTAGGGAGGCTT	246969	79165	GCTACCAGGAGCTGCTGTCA	291556	123752	AGCTCTTGAAAATAGTTTGC
202383	34579	TCCTATCTTCTAGGGAGGCT	246970	79166	GGCTACCAGGAGCTGCTGTC	291557	123753	AAGCTCTTGAAAATAGTTTG
202384	34580	ATCCTATCTTCTAGGGAGGC	246971	79167	CGGCTACCAGGAGCTGCTGT	291558	123754	AAAGCTCTTGAAAATAGTTT
202385	34581	CATCCTATCTTCTAGGGAGG	246972	79168	TCGGCTACCAGGAGCTGCTG	291559	123755	CAAAGCTCTTGAAAATAGTT
202386	34582	CCATCCTATCTTCTAGGGAG	246973	79169	CTCGGCTACCAGGAGCTGCT	291560	123756	GCAAAGCTCTTGAAAATAGT
202387	34583	ACCATCCTATCTTCTAGGGA	246974	79170	GCTCGGCTACCAGGAGCTGC	291561	123757	TGCAAAGCTCTTGAAAATAG
202388	34584	TACCATCCTATCTTCTAGGG	246975	79171	AGCTCGGCTACCAGGAGCTG	291562	123758	TTGCAAAGCTCTTGAAAATA
202389	34585	TTACCATCCTATCTTCTAGG	246976	79172	AAGCTCGGCTACCAGGAGCT	291563	123759	CTTGCAAAGCTCTTGAAAAT
202390	34586	CTTACCATCCTATCTTCTAG	246977	79173	AAAGCTCGGCTACCAGGAGC	291564	123760	CCTTGCAAAGCTCTTGAAAA
202391	34587	CCTTACCATCCTATCTTCTA	246978	79174	GAAAGCTCGGCTACCAGGAG	291565	123761	TCCTTGCAAAGCTCTTGAAA
202392	34588	TCCTTACCATCCTATCTTCT	246979	79175	GGAAAGCTCGGCTACCAGGA	291566	123762	GTCCTTGCAAAGCTCTTGAA
202393	34589	ATCCTTACCATCCTATCTTC	246980	79176	GGGAAAGCTCGGCTACCAGG	291567	123763	AGTCCTTGCAAAGCTCTTGA
202394	34590	TATCCTTACCATCCTATCTT	246981	79177	AGGGAAAGCTCGGCTACCAG	291568	123764	AAGTCCTTGCAAAGCTCTTG
202395	34591	ATATCCTTACCATCCTATCT	246982	79178	GAGGGAAAGCTCGGCTACCA	291569	123765	TAAGTCCTTGCAAAGCTCTT
202396	34592	AATATCCTTACCATCCTATC	246983	79179	GGAGGGAAAGCTCGGCTACC	291570	123766	GTAAGTCCTTGCAAAGCTCT
202397	34593	AAATATCCTTACCATCCTAT	246984	79180	AGGAGGGAAAGCTCGGCTAC	291571	123767	AGTAAGTCCTTGCAAAGCTC
202398	34594	AAAATATCCTTACCATCCTA	246985	79181	CAGGAGGGAAAGCTCGGCTA	291572	123768	AAGTAAGTCCTTGCAAAGCT
202399	34595	GAAAATATCCTTACCATCCT	246986	79182	GCAGGAGGGAAAGCTCGGCT	291573	123769	CAAGTAAGTCCTTGCAAAGC
202400	34596	GGAAAATATCCTTACCATCC	246987	79183	GGCAGGAGGGAAAGCTCGGC	291574	123770	ACAAGTAAGTCCTTGCAAAG
202401	34597	AGGAAAATATCCTTACCATC	246988	79184	AGGCAGGAGGGAAAGCTCGG	291575	123771	TACAAGTAAGTCCTTGCAAA
202402	34598	TAGGAAAATATCCTTACCAT	246989	79185	GAGGCAGGAGGGAAAGCTCG	291576	123772	ATACAAGTAAGTCCTTGCAA
202403	34599	CTAGGAAAATATCCTTACCA	246990	79186	AGAGGCAGGAGGGAAAGCTC	291577	123773	GATACAAGTAAGTCCTTGCA
202404	34600	CCTAGGAAAATATCCTTACC	246991	79187	CAGAGGCAGGAGGGAAAGCT	291578	123774	GGATACAAGTAAGTCCTTGC
202405	34601	ACCTAGGAAAATATCCTTAC	246992	79188	GCAGAGGCAGGAGGGAAAGC	291579	123775	TGGATACAAGTAAGTCCTTG
202406	34602	TACCTAGGAAAATATCCTTA	246993	79189	AGCAGAGGCAGGAGGGAAAG	291580	123776	TTGGATACAAGTAAGTCCTT
202407	34603	TTACCTAGGAAAATATCCTT	246994	79190	CAGCAGAGGCAGGAGGGAAA	291581	123777	TTTGGATACAAGTAAGTCCT
202408	34604	TTTACCTAGGAAAATATCCT	246995	79191	ACAGCAGAGGCAGGAGGGAA	291582	123778	GTTTGGATACAAGTAAGTCC
202409	34605	TTTTACCTAGGAAAATATCC	246996	79192	CACAGCAGAGGCAGGAGGGA	291583	123779	TGTTTGGATACAAGTAAGTC
202410	34606	TTTTTACCTAGGAAAATATC	246997	79193	TCACAGCAGAGGCAGGAGGG	291584	123780	GTGTTTGGATACAAGTAAGT
202411	34607	ATTTTTACCTAGGAAAATAT	246998	79194	TTCACAGCAGAGGCAGGAGG	291585	123781	GGTGTTTGGATACAAGTAAG
202412	34608	TATTTTTACCTAGGAAAATA	246999	79195	CTTCACAGCAGAGGCAGGAG	291586	123782	TGGTGTTTGGATACAAGTAA
202413	34609	ATATTTTTACCTAGGAAAAT	247000	79196	CCTTCACAGCAGAGGCAGGA	291587	123783	ATGGTGTTTGGATACAAGTA
202414	34610	CATATTTTTACCTAGGAAAA	247001	79197	ACCTTCACAGCAGAGGCAGG	291588	123784	AATGGTGTTTGGATACAAGT
202415	34611	ACATATTTTTACCTAGGAAA	247002	79198	CACCTTCACAGCAGAGGCAG	291589	123785	GAATGGTGTTTGGATACAAG
202416	34612	AACATATTTTTACCTAGGAA	247003	79199	CCACCTTCACAGCAGAGGCA	291590	123786	AGAATGGTGTTTGGATACAA
202417	34613	TAACATATTTTTACCTAGGA	247004	79200	TCCACCTTCACAGCAGAGGC	291591	123787	TAGAATGGTGTTTGGATACA
202418	34614	TTAACATATTTTTACCTAGG	247005	79201	GTCCACCTTCACAGCAGAGG	291592	123788	TTAGAATGGTGTTTGGATAC
202419	34615	ATTAACATATTTTTACCTAG	247006	79202	GGTCCACCTTCACAGCAGAG	291593	123789	TTTAGAATGGTGTTTGGATA
202420	34616	AATTAACATATTTTTACCTA	247007	79203	GGGTCCACCTTCACAGCAGA	291594	123790	CTTTAGAATGGTGTTTGGAT
202421	34617	AAATTAACATATTTTTACCT	247008	79204	TGGGTCCACCTTCACAGCAG	291595	123791	CCTTTAGAATGGTGTTTGGA
202422	34618	GAAATTAACATATTTTTACC	247009	79205	ATGGGTCCACCTTCACAGCA	291596	123792	TCCTTTAGAATGGTGTTTGG
202423	34619	TGAAATTAACATATTTTTAC	247010	79206	GATGGGTCCACCTTCACAGC	291597	123793	CTCCTTTAGAATGGTGTTTG
202424	34620	ATGAAATTAACATATTTTTA	247011	79207	GGATGGGTCCACCTTCACAG	291598	123794	ACTCCTTTAGAATGGTGTTT
202425	34621	TATGAAATTAACATATTTTT	247012	79208	TGGATGGGTCCACCTTCACA	291599	123795	GACTCCTTTAGAATGGTGTT
202426	34622	ATATGAAATTAACATATTTT	247013	79209	TTGGATGGGTCCACCTTCAC	291600	123796	AGACTCCTTTAGAATGGTGT
202427	34623	AATATGAAATTAACATATTT	247014	79210	GTTGGATGGGTCCACCTTCA	291601	123797	AAGACTCCTTTAGAATGGTG
202428	34624	AAATATGAAATTAACATATT	247015	79211	TGTTGGATGGGTCCACCTTC	291602	123798	TAAGACTCCTTTAGAATGGT
202429	34625	GAAATATGAAATTAACATAT	247016	79212	CTGTTGGATGGGTCCACCTT	291603	123799	GTAAGACTCCTTTAGAATGG
202430	34626	TGAAATATGAAATTAACATA	247017	79213	ACTGTTGGATGGGTCCACCT	291604	123800	GGTAAGACTCCTTTAGAATG
202431	34627	ATGAAATATGAAATTAACAT	247018	79214	GACTGTTGGATGGGTCCACC	291605	123801	AGGTAAGACTCCTTTAGAAT
202432	34628	CATGAAATATGAAATTAACA	247019	79215	TGACTGTTGGATGGGTCCAC	291606	123802	TAGGTAAGACTCCTTTAGAA
202433	34629	TCATGAAATATGAAATTAAC	247020	79216	TTGACTGTTGGATGGGTCCA	291607	123803	GTAGGTAAGACTCCTTTAGA
202434	34630	TTCATGAAATATGAAATTAA	247021	79217	TTTGACTGTTGGATGGGTCC	291608	123804	AGTAGGTAAGACTCCTTTAG

202435	34631	TTTCATGAAATATGAAATTA	247022	79218	ATTTGACTGTTGGATGGGTC	291609	123805	AAGTAGGTAAGACTCCTTTA
202436	34632	ATTTCATGAAATATGAAATT	247023	79219	CATTTGACTGTTGGATGGGT	291610	123806	GAAGTAGGTAAGACTCCTTT
202437	34633	AATTTCATGAAATATGAAAT	247024	79220	GCATTTGACTGTTGGATGGG	291611	123807	AGAAGTAGGTAAGACTCCTT
202438	34634	AAATTTCATGAAATATGAAA	247025	79221	GGCATTTGACTGTTGGATGG	291612	123808	TAGAAGTAGGTAAGACTCCT
202439	34635	GAAATTTCATGAAATATGAA	247026	79222	AGGCATTTGACTGTTGGATG	291613	123809	TTAGAAGTAGGTAAGACTCC
202440	34636	TGAAATTTCATGAAATATGA	247027	79223	CAGGCATTTGACTGTTGGAT	291614	123810	TTTAGAAGTAGGTAAGACTC
202441	34637	ATGAAATTTCATGAAATATG	247028	79224	TCAGGCATTTGACTGTTGGA	291615	123811	CTTTAGAAGTAGGTAAGACT
202442	34638	CATGAAATTTCATGAAATAT	247029	79225	GTCAGGCATTTGACTGTTGG	291616	123812	CCTTTAGAAGTAGGTAAGAC
202443	34639	ACATGAAATTTCATGAAATA	247030	79226	AGTCAGGCATTTGACTGTTG	291617	123813	GCCTTTAGAAGTAGGTAAGA
202444	34640	AACATGAAATTTCATGAAAT	247031	79227	GAGTCAGGCATTTGACTGTT	291618	123814	AGCCTTTAGAAGTAGGTAAG
202445	34641	AAACATGAAATTTCATGAAA	247032	79228	AGAGTCAGGCATTTGACTGT	291619	123815	CAGCCTTTAGAAGTAGGTAA
202446	34642	GAAACATGAAATTTCATGAA	247033	79229	CAGAGTCAGGCATTTGACTG	291620	123816	CCAGCCTTTAGAAGTAGGTA
202447	34643	TGAAACATGAAATTTCATGA	247034	79230	CCAGAGTCAGGCATTTGACT	291621	123817	ACCAGCCTTTAGAAGTAGGT
202448	34644	ATGAAACATGAAATTTCATG	247035	79231	TCCAGAGTCAGGCATTTGAC	291622	123818	GACCAGCCTTTAGAAGTAGG
202449	34645	AATGAAACATGAAATTTCAT	247036	79232	GTCCAGAGTCAGGCATTTGA	291623	123819	AGACCAGCCTTTAGAAGTAG
202450	34646	AAATGAAACATGAAATTTCA	247037	79233	TGTCCAGAGTCAGGCATTTG	291624	123820	GAGACCAGCCTTTAGAAGTA
202451	34647	GAAATGAAACATGAAATTTC	247038	79234	CTGTCCAGAGTCAGGCATTT	291625	123821	AGAGACCAGCCTTTAGAAGT
202452	34648	TGAAATGAAACATGAAATTT	247039	79235	CCTGTCCAGAGTCAGGCATT	291626	123822	TAGAGACCAGCCTTTAGAAG
202453	34649	TTGAAATGAAACATGAAATT	247040	79236	TCCTGTCCAGAGTCAGGCAT	291627	123823	GTAGAGACCAGCCTTTAGAA
202454	34650	ATTGAAATGAAACATGAAAT	247041	79237	CTCCTGTCCAGAGTCAGGCA	291628	123824	AGTAGAGACCAGCCTTTAGA
202455	34651	GATTGAAATGAAACATGAAA	247042	79238	GCTCCTGTCCAGAGTCAGGC	291629	123825	AAGTAGAGACCAGCCTTTAG
202456	34652	TGATTGAAATGAAACATGAA	247043	79239	CGCTCCTGTCCAGAGTCAGG	291630	123826	CAAGTAGAGACCAGCCTTTA
202457	34653	TTGATTGAAATGAAACATGA	247044	79240	CCGCTCCTGTCCAGAGTCAG	291631	123827	CCAAGTAGAGACCAGCCTTT
202458	34654	CTTGATTGAAATGAAACATG	247045	79241	TCCGCTCCTGTCCAGAGTCA	291632	123828	TCCAAGTAGAGACCAGCCTT
202459	34655	GCTTGATTGAAATGAAACAT	247046	79242	GTCCGCTCCTGTCCAGAGTC	291633	123829	TTCCAAGTAGAGACCAGCCT
202460	34656	AGCTTGATTGAAATGAAACA	247047	79243	GGTCCGCTCCTGTCCAGAGT	291634	123830	GTTCCAAGTAGAGACCAGCC
202461	34657	GAGCTTGATTGAAATGAAAC	247048	79244	AGGTCCGCTCCTGTCCAGAG	291635	123831	GGTTCCAAGTAGAGACCAGC
202462	34658	AGAGCTTGATTGAAATGAAA	247049	79245	TAGGTCCGCTCCTGTCCAGA	291636	123832	TGGTTCCAAGTAGAGACCAG
202463	34659	CAGAGCTTGATTGAAATGAA	247050	79246	ATAGGTCCGCTCCTGTCCAG	291637	123833	GTGGTTCCAAGTAGAGACCA
202464	34660	ACAGAGCTTGATTGAAATGA	247051	79247	AATAGGTCCGCTCCTGTCCA	291638	123834	AGTGGTTCCAAGTAGAGACC
202465	34661	GACAGAGCTTGATTGAAATG	247052	79248	AAATAGGTCCGCTCCTGTCC	291639	123835	AAGTGGTTCCAAGTAGAGAC
202466	34662	TGACAGAGCTTGATTGAAAT	247053	79249	TAAATAGGTCCGCTCCTGTC	291640	123836	CAAGTGGTTCCAAGTAGAGA
202467	34663	ATGACAGAGCTTGATTGAAA	247054	79250	ATAAATAGGTCCGCTCCTGT	291641	123837	GCAAGTGGTTCCAAGTAGAG
202468	34664	TATGACAGAGCTTGATTGAA	247055	79251	AATAAATAGGTCCGCTCCTG	291642	123838	AGCAAGTGGTTCCAAGTAGA
202469	34665	GTATGACAGAGCTTGATTGA	247056	79252	CAATAAATAGGTCCGCTCCT	291643	123839	AAGCAAGTGGTTCCAAGTAG
202470	34666	TGTATGACAGAGCTTGATTG	247057	79253	GCAATAAATAGGTCCGCTCC	291644	123840	CAAGCAAGTGGTTCCAAGTA
202471	34667	GTGTATGACAGAGCTTGATT	247058	79254	GGCAATAAATAGGTCCGCTC	291645	123841	CCAAGCAAGTGGTTCCAAGT
202472	34668	GGTGTATGACAGAGCTTGAT	247059	79255	TGGCAATAAATAGGTCCGCT	291646	123842	GCCAAGCAAGTGGTTCCAAG
202473	34669	AGGTGTATGACAGAGCTTGA	247060	79256	ATGGCAATAAATAGGTCCGC	291647	123843	GGCCAAGCAAGTGGTTCCAA
202474	34670	AAGGTGTATGACAGAGCTTG	247061	79257	CATGGCAATAAATAGGTCCG	291648	123844	GGGCCAAGCAAGTGGTTCCA
202475	34671	TAAGGTGTATGACAGAGCTT	247062	79258	GCATGGCAATAAATAGGTCC	291649	123845	AGGGCCAAGCAAGTGGTTCC
202476	34672	GTAAGGTGTATGACAGAGCT	247063	79259	TGCATGGCAATAAATAGGTC	291650	123846	CAGGGCCAAGCAAGTGGTTC
202477	34673	TGTAAGGTGTATGACAGAGC	247064	79260	TTGCATGGCAATAAATAGGT	291651	123847	CCAGGGCCAAGCAAGTGGTT
202478	34674	ATGTAAGGTGTATGACAGAG	247065	79261	CTTGCATGGCAATAAATAGG	291652	123848	ACCAGGGCCAAGCAAGTGGT
202479	34675	CATGTAAGGTGTATGACAGA	247066	79262	CCTTGCATGGCAATAAATAG	291653	123849	AACCAGGGCCAAGCAAGTGG
202480	34676	CCATGTAAGGTGTATGACAG	247067	79263	CCCTTGCATGGCAATAAATA	291654	123850	GAACCAGGGCCAAGCAAGTG
202481	34677	CCCATGTAAGGTGTATGACA	247068	79264	TCCCTTGCATGGCAATAAAT	291655	123851	TGAACCAGGGCCAAGCAAGT
202482	34678	CCCCATGTAAGGTGTATGAC	247069	79265	GTCCCTTGCATGGCAATAAA	291656	123852	TTGAACCAGGGCCAAGCAAG
202483	34679	GCCCCATGTAAGGTGTATGA	247070	79266	AGTCCCTTGCATGGCAATAA	291657	123853	CTTGAACCAGGGCCAAGCAA
202484	34680	TGCCCCATGTAAGGTGTATG	247071	79267	GAGTCCCTTGCATGGCAATA	291658	123854	ACTTGAACCAGGGCCAAGCA
202485	34681	TTGCCCCATGTAAGGTGTAT	247072	79268	AGAGTCCCTTGCATGGCAAT	291659	123855	GACTTGAACCAGGGCCAAGC
202486	34682	CTTGCCCCATGTAAGGTGTA	247073	79269	CAGAGTCCCTTGCATGGCAA	291660	123856	GGACTTGAACCAGGGCCAAG
202487	34683	GCTTGCCCCATGTAAGGTGT	247074	79270	GCAGAGTCCCTTGCATGGCA	291661	123857	AGGACTTGAACCAGGGCCAA
202488	34684	GGCTTGCCCCATGTAAGGTG	247075	79271	TGCAGAGTCCCTTGCATGGC	291662	123858	CAGGACTTGAACCAGGGCCA
202489	34685	GGGCTTGCCCCATGTAAGGT	247076	79272	GTGCAGAGTCCCTTGCATGG	291663	123859	GCAGGACTTGAACCAGGGCC
202490	34686	TGGGCTTGCCCCATGTAAGG	247077	79273	AGTGCAGAGTCCCTTGCATG	291664	123860	AGCAGGACTTGAACCAGGGC
202491	34687	CTGGGCTTGCCCCATGTAAG	247078	79274	AAGTGCAGAGTCCCTTGCAT	291665	123861	CAGCAGGACTTGAACCAGGG
202492	34688	ACTGGGCTTGCCCCATGTAA	247079	79275	AAAGTGCAGAGTCCCTTGCA	291666	123862	GCAGCAGGACTTGAACCAGG
202493	34689	CACTGGGCTTGCCCCATGTA	247080	79276	AAAAGTGCAGAGTCCCTTGC	291667	123863	TGCAGCAGGACTTGAACCAG
202494	34690	GCACTGGGCTTGCCCCATGT	247081	79277	CAAAAGTGCAGAGTCCCTTG	291668	123864	TTGCAGCAGGACTTGAACCA
202495	34691	GGCACTGGGCTTGCCCCATG	247082	79278	TCAAAAGTGCAGAGTCCCTT	291669	123865	TTTGCAGCAGGACTTGAACC
202496	34692	AGGCACTGGGCTTGCCCCAT	247083	79279	TTCAAAAGTGCAGAGTCCCT	291670	123866	GTTTGCAGCAGGACTTGAAC
202497	34693	CAGGCACTGGGCTTGCCCCA	247084	79280	ATTCAAAAGTGCAGAGTCCC	291671	123867	GGTTTGCAGCAGGACTTGAA
202498	34694	CCAGGCACTGGGCTTGCCCC	247085	79281	AATTCAAAAGTGCAGAGTCC	291672	123868	AGGTTTGCAGCAGGACTTGA
202499	34695	CCCAGGCACTGGGCTTGCCC	247086	79282	CAATTCAAAAGTGCAGAGTC	291673	123869	CAGGTTTGCAGCAGGACTTG
202500	34696	GCCCAGGCACTGGGCTTGCC	247087	79283	ACAATTCAAAAGTGCAGAGT	291674	123870	CCAGGTTTGCAGCAGGACTT
202501	34697	TGCCCAGGCACTGGGCTTGC	247088	79284	CACAATTCAAAAGTGCAGAG	291675	123871	TCCAGGTTTGCAGCAGGACT
202502	34698	CTGCCCAGGCACTGGGCTTG	247089	79285	CCACAATTCAAAAGTGCAGA	291676	123872	TTCCAGGTTTGCAGCAGGAC
202503	34699	CCTGCCCAGGCACTGGGCTT	247090	79286	CCCACAATTCAAAAGTGCAG	291677	123873	CTTCCAGGTTTGCAGCAGGA
202504	34700	CCCTGCCCAGGCACTGGGCT	247091	79287	ACCCACAATTCAAAAGTGCA	291678	123874	ACTTCCAGGTTTGCAGCAGG
202505	34701	ACCCTGCCCAGGCACTGGGC	247092	79288	GACCCACAATTCAAAAGTGC	291679	123875	GACTTCCAGGTTTGCAGCAG
202506	34702	CACCCTGCCCAGGCACTGGG	247093	79289	TGACCCACAATTCAAAAGTG	291680	123876	GGACTTCCAGGTTTGCAGCA

202507	34703	ACACCCTGCCCAGGCACTGG	247094	79290	ATGACCCACAATTCAAAAGT	291681	123877	AGGACTTCCAGGTTTGCAGC
202508	34704	TACACCCTGCCCAGGCACTG	247095	79291	CATGACCCACAATTCAAAAG	291682	123878	CAGGACTTCCAGGTTTGCAG
202509	34705	TTACACCCTGCCCAGGCACT	247096	79292	CCATGACCCACAATTCAAAA	291683	123879	ACAGGACTTCCAGGTTTGCA
202510	34706	ATTACACCCTGCCCAGGCAC	247097	79293	CCCATGACCCACAATTCAAA	291684	123880	GACAGGACTTCCAGGTTTGC
202511	34707	AATTACACCCTGCCCAGGCA	247098	79294	GCCCATGACCCACAATTCAA	291685	123881	TGACAGGACTTCCAGGTTTG
202512	34708	TAATTACACCCTGCCCAGGC	247099	79295	AGCCCATGACCCACAATTCA	291686	123882	ATGACAGGACTTCCAGGTTT
202513	34709	ATAATTACACCCTGCCCAGG	247100	79296	AAGCCCATGACCCACAATTC	291687	123883	AATGACAGGACTTCCAGGTT
202514	34710	TATAATTACACCCTGCCCAG	247101	79297	CAAGCCCATGACCCACAATT	291688	123884	CAATGACAGGACTTCCAGGT
202515	34711	GTATAATTACACCCTGCCCA	247102	79298	CCAAGCCCATGACCCACAAT	291689	123885	ACAATGACAGGACTTCCAGG
202516	34712	AGTATAATTACACCCTGCCC	247103	79299	TCCAAGCCCATGACCCACAA	291690	123886	GACAATGACAGGACTTCCAG
202517	34713	GAGTATAATTACACCCTGCC	247104	79300	ATCCAAGCCCATGACCCACA	291691	123887	AGACAATGACAGGACTTCCA
202518	34714	TGAGTATAATTACACCCTGC	247105	79301	AATCCAAGCCCATGACCCAC	291692	123888	AAGACAATGACAGGACTTCC
202519	34715	ATGAGTATAATTACACCCTG	247106	79302	AAATCCAAGCCCATGACCCA	291693	123889	GAAGACAATGACAGGACTTC
202520	34716	AATGAGTATAATTACACCCT	247107	79303	TAAATCCAAGCCCATGACCC	291694	123890	AGAAGACAATGACAGGACTT
202521	34717	TAATGAGTATAATTACACCC	247108	79304	CTAAATCCAAGCCCATGACC	291695	123891	AAGAAGACAATGACAGGACT
202522	34718	GTAATGAGTATAATTACACC	247109	79305	CCTAAATCCAAGCCCATGAC	291696	123892	GAAGAAGACAATGACAGGAC
202523	34719	TGTAATGAGTATAATTACAC	247110	79306	CCCTAAATCCAAGCCCATGA	291697	123893	GGAAGAAGACAATGACAGGA
202524	34720	GTGTAATGAGTATAATTACA	247111	79307	CCCCTAAATCCAAGCCCATG	291698	123894	GGGAAGAAGACAATGACAGG
202525	34721	TGTGTAATGAGTATAATTAC	247112	79308	ACCCCTAAATCCAAGCCCAT	291699	123895	AGGGAAGAAGACAATGACAG
202526	34722	CTGTGTAATGAGTATAATTA	247113	79309	AACCCCTAAATCCAAGCCCA	291700	123896	GAGGGAAGAAGACAATGACA
202527	34723	CCTGTGTAATGAGTATAATT	247114	79310	TAACCCCTAAATCCAAGCCC	291701	123897	GGAGGGAAGAAGACAATGAC
202528	34724	GCCTGTGTAATGAGTATAAT	247115	79311	CTAACCCCTAAATCCAAGCC	291702	123898	TGGAGGGAAGAAGACAATGA
202529	34725	TGCCTGTGTAATGAGTATAA	247116	79312	TCTAACCCCTAAATCCAAGC	291703	123899	CTGGAGGGAAGAAGACAATG
202530	34726	TTGCCTGTGTAATGAGTATA	247117	79313	CTCTAACCCCTAAATCCAAG	291704	123900	TCTGGAGGGAAGAAGACAAT
202531	34727	CTTGCCTGTGTAATGAGTAT	247118	79314	GCTCTAACCCCTAAATCCAA	291705	123901	CTCTGGAGGGAAGAAGACAA
202532	34728	CCTTGCCTGTGTAATGAGTA	247119	79315	AGCTCTAACCCCTAAATCCA	291706	123902	GCTCTGGAGGGAAGAAGACA
202533	34729	TCCTTGCCTGTGTAATGAGT	247120	79316	CAGCTCTAACCCCTAAATCC	291707	123903	TGCTCTGGAGGGAAGAAGAC
202534	34730	TTCCTTGCCTGTGTAATGAG	247121	79317	CCAGCTCTAACCCCTAAATC	291708	123904	CTGCTCTGGAGGGAAGAAGA
202535	34731	TTTCCTTGCCTGTGTAATGA	247122	79318	CCCAGCTCTAACCCCTAAAT	291709	123905	ACTGCTCTGGAGGGAAGAAG
202536	34732	TTTTCCTTGCCTGTGTAATG	247123	79319	TCCCAGCTCTAACCCCTAAA	291710	123906	CACTGCTCTGGAGGGAAGAA
202537	34733	CTTTTCCTTGCCTGTGTAAT	247124	79320	CTCCCAGCTCTAACCCCTAA	291711	123907	CCACTGCTCTGGAGGGAAGA
202538	34734	ACTTTTCCTTGCCTGTGTAA	247125	79321	TCTCCCAGCTCTAACCCCTA	291712	123908	GCCACTGCTCTGGAGGGAAG
202539	34735	GACTTTTCCTTGCCTGTGTA	247126	79322	TTCTCCCAGCTCTAACCCCT	291713	123909	TGCCACTGCTCTGGAGGGAA
202540	34736	TGACTTTTCCTTGCCTGTGT	247127	79323	CTTCTCCCAGCTCTAACCCC	291714	123910	GTGCCACTGCTCTGGAGGGA
202541	34737	GTGACTTTTCCTTGCCTGTG	247128	79324	ACTTCTCCCAGCTCTAACCC	291715	123911	GGTGCCACTGCTCTGGAGGG
202542	34738	TGTGACTTTTCCTTGCCTGT	247129	79325	GACTTCTCCCAGCTCTAACC	291716	123912	GGGTGCCACTGCTCTGGAGG
202543	34739	ATGTGACTTTTCCTTGCCTG	247130	79326	AGACTTCTCCCAGCTCTAAC	291717	123913	TGGGTGCCACTGCTCTGGAG
202544	34740	AATGTGACTTTTCCTTGCCT	247131	79327	AAGACTTCTCCCAGCTCTAA	291718	123914	TTGGGTGCCACTGCTCTGGA
202545	34741	TAATGTGACTTTTCCTTGCC	247132	79328	CAAGACTTCTCCCAGCTCTA	291719	123915	ATTGGGTGCCACTGCTCTGG
202546	34742	CTAATGTGACTTTTCCTTGC	247133	79329	CCAAGACTTCTCCCAGCTCT	291720	123916	GATTGGGTGCCACTGCTCTG
202547	34743	CCTAATGTGACTTTTCCTTG	247134	79330	TCCAAGACTTCTCCCAGCTC	291721	123917	AGATTGGGTGCCACTGCTCT
202548	34744	ACCTAATGTGACTTTTCCTT	247135	79331	TTCCAAGACTTCTCCCAGCT	291722	123918	TAGATTGGGTGCCACTGCTC
202549	34745	CACCTAATGTGACTTTTCCT	247136	79332	CTTCCAAGACTTCTCCCAGC	291723	123919	TTAGATTGGGTGCCACTGCT
202550	34746	TCACCTAATGTGACTTTTCC	247137	79333	ACTTCCAAGACTTCTCCCAG	291724	123920	ATTAGATTGGGTGCCACTGC
202551	34747	ATCACCTAATGTGACTTTTC	247138	79334	GACTTCCAAGACTTCTCCCA	291725	123921	AATTAGATTGGGTGCCACTG
202552	34748	CATCACCTAATGTGACTTTT	247139	79335	TGACTTCCAAGACTTCTCCC	291726	123922	AAATTAGATTGGGTGCCACT
202553	34749	CCATCACCTAATGTGACTTT	247140	79336	GTGACTTCCAAGACTTCTCC	291727	123923	AAAATTAGATTGGGTGCCAC
202554	34750	TCCATCACCTAATGTGACTT	247141	79337	GGTGACTTCCAAGACTTCTC	291728	123924	AAAAATTAGATTGGGTGCCA
202555	34751	CTCCATCACCTAATGTGACT	247142	79338	AGGTGACTTCCAAGACTTCT	291729	123925	CAAAAATTAGATTGGGTGCC
202556	34752	GCTCCATCACCTAATGTGAC	247143	79339	TAGGTGACTTCCAAGACTTC	291730	123926	GCAAAAATTAGATTGGGTGC
202557	34753	TGCTCCATCACCTAATGTGA	247144	79340	CTAGGTGACTTCCAAGACTT	291731	123927	AGCAAAAATTAGATTGGGTG
202558	34754	GTGCTCCATCACCTAATGTG	247145	79341	TCTAGGTGACTTCCAAGACT	291732	123928	CAGCAAAAATTAGATTGGGT
202559	34755	TGTGCTCCATCACCTAATGT	247146	79342	CTCTAGGTGACTTCCAAGAC	291733	123929	ACAGCAAAAATTAGATTGGG
202560	34756	TTGTGCTCCATCACCTAATG	247147	79343	TCTCTAGGTGACTTCCAAGA	291734	123930	CACAGCAAAAATTAGATTGG
202561	34757	TTTGTGCTCCATCACCTAAT	247148	79344	ATCTCTAGGTGACTTCCAAG	291735	123931	GCACAGCAAAAATTAGATTG
202562	34758	ATTTGTGCTCCATCACCTAA	247149	79345	CATCTCTAGGTGACTTCCAA	291736	123932	GGCACAGCAAAAATTAGATT
202563	34759	TATTTGTGCTCCATCACCTA	247150	79346	TCATCTCTAGGTGACTTCCA	291737	123933	GGGCACAGCAAAAATTAGAT
202564	34760	CTATTTGTGCTCCATCACCT	247151	79347	GTCATCTCTAGGTGACTTCC	291738	123934	GGGGCACAGCAAAAATTAGA
202565	34761	CCTATTTGTGCTCCATCACC	247152	79348	TGTCATCTCTAGGTGACTTC	291739	123935	TGGGGCACAGCAAAAATTAG
202566	34762	GCCTATTTGTGCTCCATCAC	247153	79349	GTGTCATCTCTAGGTGACTT	291740	123936	CTGGGGCACAGCAAAAATTA
202567	34763	TGCCTATTTGTGCTCCATCA	247154	79350	AGTGTCATCTCTAGGTGACT	291741	123937	GCTGGGGCACAGCAAAAATT
202568	34764	CTGCCTATTTGTGCTCCATC	247155	79351	CAGTGTCATCTCTAGGTGAC	291742	123938	TGCTGGGGCACAGCAAAAAT
202569	34765	ACTGCCTATTTGTGCTCCAT	247156	79352	GCAGTGTCATCTCTAGGTGA	291743	123939	CTGCTGGGGCACAGCAAAAA
202570	34766	AACTGCCTATTTGTGCTCCA	247157	79353	GGCAGTGTCATCTCTAGGTG	291744	123940	GCTGCTGGGGCACAGCAAAA
202571	34767	TAACTGCCTATTTGTGCTCC	247158	79354	TGGCAGTGTCATCTCTAGGT	291745	123941	GGCTGCTGGGGCACAGCAAA
202572	34768	TTAACTGCCTATTTGTGCTC	247159	79355	ATGGCAGTGTCATCTCTAGG	291746	123942	GGGCTGCTGGGGCACAGCAA
202573	34769	ATTAACTGCCTATTTGTGCT	247160	79356	AATGGCAGTGTCATCTCTAG	291747	123943	GGGGCTGCTGGGGCACAGCA
202574	34770	CATTAACTGCCTATTTGTGC	247161	79357	AAATGGCAGTGTCATCTCTA	291748	123944	AGGGGCTGCTGGGGCACAGC
202575	34771	CCATTAACTGCCTATTTGTG	247162	79358	AAAATGGCAGTGTCATCTCT	291749	123945	CAGGGGCTGCTGGGGCACAG
202576	34772	ACCATTAACTGCCTATTTGT	247163	79359	CAAAATGGCAGTGTCATCTC	291750	123946	CCAGGGGCTGCTGGGGCACA
202577	34773	AACCATTAACTGCCTATTTG	247164	79360	GCAAAATGGCAGTGTCATCT	291751	123947	GCCAGGGGCTGCTGGGGCAC
202578	34774	AAACCATTAACTGCCTATTT	247165	79361	TGCAAAATGGCAGTGTCATC	291752	123948	TGCCAGGGGCTGCTGGGGCA

202579	34775	GAAACCATTAACTGCCTATT	247166	79362	CTGCAAAATGGCAGTGTCAT	291753	123949	GTGCCAGGGGCTGCTGGGGC
202580	34776	TGAAACCATTAACTGCCTAT	247167	79363	TCTGCAAAATGGCAGTGTCA	291754	123950	AGTGCCAGGGGCTGCTGGGG
202581	34777	CTGAAACCATTAACTGCCTA	247168	79364	ATCTGCAAAATGGCAGTGTC	291755	123951	AAGTGCCAGGGGCTGCTGGG
202582	34778	CCTGAAACCATTAACTGCCT	247169	79365	CATCTGCAAAATGGCAGTGT	291756	123952	AAAGTGCCAGGGGCTGCTGG
202583	34779	CCCTGAAACCATTAACTGCC	247170	79366	TCATCTGCAAAATGGCAGTG	291757	123953	CAAAGTGCCAGGGGCTGCTG
202584	34780	GCCCTGAAACCATTAACTGC	247171	79367	CTCATCTGCAAAATGGCAGT	291758	123954	GCAAAGTGCCAGGGGCTGCT
202585	34781	AGCCCTGAAACCATTAACTG	247172	79368	CCTCATCTGCAAAATGGCAG	291759	123955	GGCAAAGTGCCAGGGGCTGC
202586	34782	TAGCCCTGAAACCATTAACT	247173	79369	TCCTCATCTGCAAAATGGCA	291760	123956	GGGCAAAGTGCCAGGGGCTG
202587	34783	CTAGCCCTGAAACCATTAAC	247174	79370	TTCCTCATCTGCAAAATGGC	291761	123957	AGGGCAAAGTGCCAGGGGCT
202588	34784	ACTAGCCCTGAAACCATTAA	247175	79371	TTTCCTCATCTGCAAAATGG	291762	123958	CAGGGCAAAGTGCCAGGGGC
202589	34785	AACTAGCCCTGAAACCATTA	247176	79372	GTTTCCTCATCTGCAAAATG	291763	123959	ACAGGGCAAAGTGCCAGGGG
202590	34786	TAACTAGCCCTGAAACCATT	247177	79373	GGTTTCCTCATCTGCAAAAT	291764	123960	TACAGGGCAAAGTGCCAGGG
202591	34787	CTAACTAGCCCTGAAACCAT	247178	79374	CGGTTTCCTCATCTGCAAAA	291765	123961	CTACAGGGCAAAGTGCCAGG
202592	34788	CCTAACTAGCCCTGAAACCA	247179	79375	ACGGTTTCCTCATCTGCAAA	291766	123962	TCTACAGGGCAAAGTGCCAG
202593	34789	TCCTAACTAGCCCTGAAACC	247180	79376	GACGGTTTCCTCATCTGCAA	291767	123963	GTCTACAGGGCAAAGTGCCA
202594	34790	ATCCTAACTAGCCCTGAAAC	247181	79377	GGACGGTTTCCTCATCTGCA	291768	123964	AGTCTACAGGGCAAAGTGCC
202595	34791	TATCCTAACTAGCCCTGAAA	247182	79378	TGGACGGTTTCCTCATCTGC	291769	123965	CAGTCTACAGGGCAAAGTGC
202596	34792	ATATCCTAACTAGCCCTGAA	247183	79379	TTGGACGGTTTCCTCATCTG	291770	123966	GCAGTCTACAGGGCAAAGTG
202597	34793	CATATCCTAACTAGCCCTGA	247184	79380	ATTGGACGGTTTCCTCATCT	291771	123967	TGCAGTCTACAGGGCAAAGT
202598	34794	ACATATCCTAACTAGCCCTG	247185	79381	GATTGGACGGTTTCCTCATC	291772	123968	CTGCAGTCTACAGGGCAAAG
202599	34795	AACATATCCTAACTAGCCCT	247186	79382	TGATTGGACGGTTTCCTCAT	291773	123969	TCTGCAGTCTACAGGGCAAA
202600	34796	AAACATATCCTAACTAGCCC	247187	79383	TTGATTGGACGGTTTCCTCA	291774	123970	GTCTGCAGTCTACAGGGCAA
202601	34797	CAAACATATCCTAACTAGCC	247188	79384	TTTGATTGGACGGTTTCCTC	291775	123971	GGTCTGCAGTCTACAGGGCA
202602	34798	ACAAACATATCCTAACTAGC	247189	79385	TTTTGATTGGACGGTTTCCT	291776	123972	AGGTCTGCAGTCTACAGGGC
202603	34799	GACAAACATATCCTAACTAG	247190	79386	ATTTTGATTGGACGGTTTCC	291777	123973	GAGGTCTGCAGTCTACAGGG
202604	34800	AGACAAACATATCCTAACTA	247191	79387	CATTTTGATTGGACGGTTTC	291778	123974	TGAGGTCTGCAGTCTACAGG
202605	34801	AAGACAAACATATCCTAACT	247192	79388	CCATTTTGATTGGACGGTTT	291779	123975	ATGAGGTCTGCAGTCTACAG
202606	34802	AAAGACAAACATATCCTAAC	247193	79389	TCCATTTTGATTGGACGGTT	291780	123976	CATGAGGTCTGCAGTCTACA
202607	34803	GAAAGACAAACATATCCTAA	247194	79390	GTCCATTTTGATTGGACGGT	291781	123977	ACATGAGGTCTGCAGTCTAC
202608	34804	TGAAAGACAAACATATCCTA	247195	79391	GGTCCATTTTGATTGGACGG	291782	123978	TACATGAGGTCTGCAGTCTA
202609	34805	TTGAAAGACAAACATATCCT	247196	79392	TGGTCCATTTTGATTGGACG	291783	123979	TTACATGAGGTCTGCAGTCT
202610	34806	ATTGAAAGACAAACATATCC	247197	79393	TTGGTCCATTTTGATTGGAC	291784	123980	ATTACATGAGGTCTGCAGTC
202611	34807	AATTGAAAGACAAACATATC	247198	79394	CTTGGTCCATTTTGATTGGA	291785	123981	CATTACATGAGGTCTGCAGT
202612	34808	CAATTGAAAGACAAACATAT	247199	79395	CCTTGGTCCATTTTGATTGG	291786	123982	ACATTACATGAGGTCTGCAG
202613	34809	GCAATTGAAAGACAAACATA	247200	79396	TCCTTGGTCCATTTTGATTG	291787	123983	TACATTACATGAGGTCTGCA
202614	34810	TGCAATTGAAAGACAAACAT	247201	79397	GTCCTTGGTCCATTTTGATT	291788	123984	ATACATTACATGAGGTCTGC
202615	34811	TTGCAATTGAAAGACAAACA	247202	79398	AGTCCTTGGTCCATTTTGAT	291789	123985	CATACATTACATGAGGTCTG
202616	34812	CTTGCAATTGAAAGACAAAC	247203	79399	AAGTCCTTGGTCCATTTTGA	291790	123986	ACATACATTACATGAGGTCT
202617	34813	ACTTGCAATTGAAAGACAAA	247204	79400	CAAGTCCTTGGTCCATTTTG	291791	123987	AACATACATTACATGAGGTC
202618	34814	TACTTGCAATTGAAAGACAA	247205	79401	GCAAGTCCTTGGTCCATTTT	291792	123988	TAACATACATTACATGAGGT
202619	34815	TTACTTGCAATTGAAAGACA	247206	79402	GGCAAGTCCTTGGTCCATTT	291793	123989	TTAACATACATTACATGAGG
202620	34816	ATTACTTGCAATTGAAAGAC	247207	79403	GGGCAAGTCCTTGGTCCATT	291794	123990	CTTAACATACATTACATGAG
202621	34817	TATTACTTGCAATTGAAAGA	247208	79404	TGGGCAAGTCCTTGGTCCAT	291795	123991	ACTTAACATACATTACATGA
202622	34818	CTATTACTTGCAATTGAAAG	247209	79405	TTGGGCAAGTCCTTGGTCCA	291796	123992	GACTTAACATACATTACATG
202623	34819	TCTATTACTTGCAATTGAAA	247210	79406	TTTGGGCAAGTCCTTGGTCC	291797	123993	GGACTTAACATACATTACAT
202624	34820	TTCTATTACTTGCAATTGAA	247211	79407	CTTTGGGCAAGTCCTTGGTC	291798	123994	TGGACTTAACATACATTACA
202625	34821	CTTCTATTACTTGCAATTGA	247212	79408	GCTTTGGGCAAGTCCTTGGT	291799	123995	GTGGACTTAACATACATTAC
202626	34822	GCTTCTATTACTTGCAATTG	247213	79409	GGCTTTGGGCAAGTCCTTGG	291800	123996	TGTGGACTTAACATACATTA
202627	34823	GGCTTCTATTACTTGCAATT	247214	79410	AGGCTTTGGGCAAGTCCTTG	291801	123997	CTGTGGACTTAACATACATT
202628	34824	GGGCTTCTATTACTTGCAAT	247215	79411	GAGGCTTTGGGCAAGTCCTT	291802	123998	TCTGTGGACTTAACATACAT
202629	34825	TGGGCTTCTATTACTTGCAA	247216	79412	TGAGGCTTTGGGCAAGTCCT	291803	123999	TTCTGTGGACTTAACATACA
202630	34826	TTGGGCTTCTATTACTTGCA	247217	79413	GTGAGGCTTTGGGCAAGTCC	291804	124000	GTTCTGTGGACTTAACATAC
202631	34827	TTTGGGCTTCTATTACTTGC	247218	79414	TGTGAGGCTTTGGGCAAGTC	291805	124001	GGTTCTGTGGACTTAACATA
202632	34828	CTTTGGGCTTCTATTACTTG	247219	79415	CTGTGAGGCTTTGGGCAAGT	291806	124002	TGGTTCTGTGGACTTAACAT
202633	34829	TCTTTGGGCTTCTATTACTT	247220	79416	GCTGTGAGGCTTTGGGCAAG	291807	124003	GTGGTTCTGTGGACTTAACA
202634	34830	TTCTTTGGGCTTCTATTACT	247221	79417	TGCTGTGAGGCTTTGGGCAA	291808	124004	TGTGGTTCTGTGGACTTAAC
202635	34831	TTTCTTTGGGCTTCTATTAC	247222	79418	TTGCTGTGAGGCTTTGGGCA	291809	124005	CTGTGGTTCTGTGGACTTAA
202636	34832	ATTTCTTTGGGCTTCTATTA	247223	79419	TTTGCTGTGAGGCTTTGGGC	291810	124006	TCTGTGGTTCTGTGGACTTA
202637	34833	AATTTCTTTGGGCTTCTATT	247224	79420	TTTTGCTGTGAGGCTTTGGG	291811	124007	TTCTGTGGTTCTGTGGACTT
202638	34834	CAATTTCTTTGGGCTTCTAT	247225	79421	GTTTTGCTGTGAGGCTTTGG	291812	124008	CTTCTGTGGTTCTGTGGACT
202639	34835	CCAATTTCTTTGGGCTTCTA	247226	79422	GGTTTTGCTGTGAGGCTTTG	291813	124009	TCTTCTGTGGTTCTGTGGAC
202640	34836	ACCAATTTCTTTGGGCTTCT	247227	79423	TGGTTTTGCTGTGAGGCTTT	291814	124010	ATCTTCTGTGGTTCTGTGGA
202641	34837	AACCAATTTCTTTGGGCTTC	247228	79424	ATGGTTTTGCTGTGAGGCTT	291815	124011	CATCTTCTGTGGTTCTGTGG
202642	34838	TAACCAATTTCTTTGGGCTT	247229	79425	TATGGTTTTGCTGTGAGGCT	291816	124012	TCATCTTCTGTGGTTCTGTG
202643	34839	ATAACCAATTTCTTTGGGCT	247230	79426	CTATGGTTTTGCTGTGAGGC	291817	124013	ATCATCTTCTGTGGTTCTGT
202644	34840	AATAACCAATTTCTTTGGGC	247231	79427	CCTATGGTTTTGCTGTGAGG	291818	124014	CATCATCTTCTGTGGTTCTG
202645	34841	AAATAACCAATTTCTTTGGG	247232	79428	GCCTATGGTTTTGCTGTGAG	291819	124015	CCATCATCTTCTGTGGTTCT
202646	34842	TAAATAACCAATTTCTTTGG	247233	79429	GGCCTATGGTTTTGCTGTGA	291820	124016	GCCATCATCTTCTGTGGTTC
202647	34843	ATAAATAACCAATTTCTTTG	247234	79430	GGGCCTATGGTTTTGCTGTG	291821	124017	TGCCATCATCTTCTGTGGTT
202648	34844	TATAAATAACCAATTTCTTT	247235	79431	GGGGCCTATGGTTTTGCTGT	291822	124018	TTGCCATCATCTTCTGTGGT
202649	34845	ATATAAATAACCAATTTCTT	247236	79432	GGGGGCCTATGGTTTTGCTG	291823	124019	CTTGCCATCATCTTCTGTGG
202650	34846	TATATAAATAACCAATTTCT	247237	79433	CGGGGGCCTATGGTTTTGCT	291824	124020	TCTTGCCATCATCTTCTGTG

202651	34847	TTATATAAATAACCAATTTC	247238	79434	GCGGGGGCCTATGGTTTTGC	291825	124021	ATCTTGCCATCATCTTCTGT
202652	34848	ATTATATAAATAACCAATTT	247239	79435	TGCGGGGGCCTATGGTTTTG	291826	124022	CATCTTGCCATCATCTTCTG
202653	34849	TATTATATAAATAACCAATT	247240	79436	GTGCGGGGGCCTATGGTTTT	291827	124023	GCATCTTGCCATCATCTTCT
202654	34850	ATATTATATAAATAACCAAT	247241	79437	AGTGCGGGGGCCTATGGTTT	291828	124024	AGCATCTTGCCATCATCTTC
202655	34851	TATATTATATAAATAACCAA	247242	79438	TAGTGCGGGGGCCTATGGTT	291829	124025	GAGCATCTTGCCATCATCTT
202656	34852	TTATATTATATAAATAACCA	247243	79439	TTAGTGCGGGGGCCTATGGT	291830	124026	AGAGCATCTTGCCATCATCT
202657	34853	ATTATATTATATAAATAACC	247244	79440	GTTAGTGCGGGGGCCTATGG	291831	124027	AAGAGCATCTTGCCATCATC
202658	34854	AATTATATTATATAAATAAC	247245	79441	GGTTAGTGCGGGGGCCTATG	291832	124028	CAAGAGCATCTTGCCATCAT
202659	34855	CAATTATATTATATAAATAA	247246	79442	GGGTTAGTGCGGGGGCCTAT	291833	124029	ACAAGAGCATCTTGCCATCA
202660	34856	TCAATTATATTATATAAATA	247247	79443	GGGGTTAGTGCGGGGGCCTA	291834	124030	CACAAGAGCATCTTGCCATC
202661	34857	ATCAATTATATTATATAAAT	247248	79444	TGGGGTTAGTGCGGGGGCCT	291835	124031	ACACAAGAGCATCTTGCCAT
202662	34858	AATCAATTATATTATATAAA	247249	79445	CTGGGGTTAGTGCGGGGGCC	291836	124032	CACACAAGAGCATCTTGCCA
202663	34859	CAATCAATTATATTATATAA	247250	79446	TCTGGGGTTAGTGCGGGGGC	291837	124033	ACACACAAGAGCATCTTGCC
202664	34860	CCAATCAATTATATTATATA	247251	79447	CTCTGGGGTTAGTGCGGGGG	291838	124034	CACACACAAGAGCATCTTGC
202665	34861	ACCAATCAATTATATTATAT	247252	79448	ACTCTGGGGTTAGTGCGGGG	291839	124035	ACACACACAAGAGCATCTTG
202666	34862	AACCAATCAATTATATTATA	247253	79449	GACTCTGGGGTTAGTGCGGG	291840	124036	AACACACACAAGAGCATCTT
202667	34863	GAACCAATCAATTATATTAT	247254	79450	GGACTCTGGGGTTAGTGCGG	291841	124037	CAACACACACAAGAGCATCT
202668	34864	GGAACCAATCAATTATATTA	247255	79451	GGGACTCTGGGGTTAGTGCG	291842	124038	ACAACACACACAAGAGCATC
202669	34865	GGGAACCAATCAATTATATT	247256	79452	AGGGACTCTGGGGTTAGTGC	291843	124039	CACAACACACACAAGAGCAT
202670	34866	TGGGAACCAATCAATTATAT	247257	79453	CAGGGACTCTGGGGTTAGTG	291844	124040	ACACAACACACACAAGAGCA
202671	34867	TTGGGAACCAATCAATTATA	247258	79454	ACAGGGACTCTGGGGTTAGT	291845	124041	AACACAACACACACAAGAGC
202672	34868	TTTGGGAACCAATCAATTAT	247259	79455	CACAGGGACTCTGGGGTTAG	291846	124042	GAACACAACACACACAAGAG
202673	34869	ATTTGGGAACCAATCAATTA	247260	79456	GCACAGGGACTCTGGGGTTA	291847	124043	AGAACACAACACACACAAGA
202674	34870	AATTTGGGAACCAATCAATT	247261	79457	AGCACAGGGACTCTGGGGTT	291848	124044	TAGAACACAACACACACAAG
202675	34871	AAATTTGGGAACCAATCAAT	247262	79458	CAGCACAGGGACTCTGGGGT	291849	124045	CTAGAACACAACACACACAA
202676	34872	CAAATTTGGGAACCAATCAA	247263	79459	ACAGCACAGGGACTCTGGGG	291850	124046	CCTAGAACACAACACACACA
202677	34873	TCAAATTTGGGAACCAATCA	247264	79460	GACAGCACAGGGACTCTGGG	291851	124047	TCCTAGAACACAACACACAC
202678	34874	TTCAAATTTGGGAACCAATC	247265	79461	AGACAGCACAGGGACTCTGG	291852	124048	CTCCTAGAACACAACACACA
202679	34875	TTTCAAATTTGGGAACCAAT	247266	79462	AAGACAGCACAGGGACTCTG	291853	124049	CCTCCTAGAACACAACACAC
202680	34876	TTTTCAAATTTGGGAACCAA	247267	79463	TAAGACAGCACAGGGACTCT	291854	124050	ACCTCCTAGAACACAACACA
202681	34877	TTTTTCAAATTTGGGAACCA	247268	79464	TTAAGACAGCACAGGGACTC	291855	124051	CACCTCCTAGAACACAACAC
202682	34878	ATTTTTCAAATTTGGGAACC	247269	79465	CTTAAGACAGCACAGGGACT	291856	124052	CCACCTCCTAGAACACAACA
202683	34879	AATTTTTCAAATTTGGGAAC	247270	79466	CCTTAAGACAGCACAGGGAC	291857	124053	GCCACCTCCTAGAACACAAC
202684	34880	GAATTTTTCAAATTTGGGAA	247271	79467	TCCTTAAGACAGCACAGGGA	291858	124054	GGCCACCTCCTAGAACACAA
202685	34881	TGAATTTTTCAAATTTGGGA	247272	79468	ATCCTTAAGACAGCACAGGG	291859	124055	TGGCCACCTCCTAGAACACA
202686	34882	CTGAATTTTTCAAATTTGGG	247273	79469	GATCCTTAAGACAGCACAGG	291860	124056	CTGGCCACCTCCTAGAACAC
202687	34883	CCTGAATTTTTCAAATTTGG	247274	79470	TGATCCTTAAGACAGCACAG	291861	124057	CCTGGCCACCTCCTAGAACA
202688	34884	TCCTGAATTTTTCAAATTTG	247275	79471	ATGATCCTTAAGACAGCACA	291862	124058	ACCTGGCCACCTCCTAGAAC
202689	34885	TTCCTGAATTTTTCAAATTT	247276	79472	TATGATCCTTAAGACAGCAC	291863	124059	CACCTGGCCACCTCCTAGAA
202690	34886	ATTCCTGAATTTTTCAAATT	247277	79473	ATATGATCCTTAAGACAGCA	291864	124060	CCACCTGGCCACCTCCTAGA
202691	34887	TATTCCTGAATTTTTCAAAT	247278	79474	TATATGATCCTTAAGACAGC	291865	124061	TCCACCTGGCCACCTCCTAG
202692	34888	CTATTCCTGAATTTTTCAAA	247279	79475	CTATATGATCCTTAAGACAG	291866	124062	TTCCACCTGGCCACCTCCTA
202693	34889	TCTATTCCTGAATTTTTCAA	247280	79476	ACTATATGATCCTTAAGACA	291867	124063	CTTCCACCTGGCCACCTCCT
202694	34890	GTCTATTCCTGAATTTTTCA	247281	79477	AACTATATGATCCTTAAGAC	291868	124064	ACTTCCACCTGGCCACCTCC
202695	34891	GGTCTATTCCTGAATTTTTC	247282	79478	CAACTATATGATCCTTAAGA	291869	124065	TACTTCCACCTGGCCACCTC
202696	34892	GGGTCTATTCCTGAATTTTT	247283	79479	ACAACTATATGATCCTTAAG	291870	124066	TTACTTCCACCTGGCCACCT
202697	34893	TGGGTCTATTCCTGAATTTT	247284	79480	TACAACTATATGATCCTTAA	291871	124067	TTTACTTCCACCTGGCCACC
202698	34894	CTGGGTCTATTCCTGAATTT	247285	79481	TTACAACTATATGATCCTTA	291872	124068	TTTTACTTCCACCTGGCCAC
202699	34895	GCTGGGTCTATTCCTGAATT	247286	79482	CTTACAACTATATGATCCTT	291873	124069	ATTTTACTTCCACCTGGCCA
202700	34896	AGCTGGGTCTATTCCTGAAT	247287	79483	GCTTACAACTATATGATCCT	291874	124070	GATTTTACTTCCACCTGGCC
202701	34897	AAGCTGGGTCTATTCCTGAA	247288	79484	TGCTTACAACTATATGATCC	291875	124071	AGATTTTACTTCCACCTGGC
202702	34898	TAAGCTGGGTCTATTCCTGA	247289	79485	TTGCTTACAACTATATGATC	291876	124072	CAGATTTTACTTCCACCTGG
202703	34899	CTAAGCTGGGTCTATTCCTG	247290	79486	ATTGCTTACAACTATATGAT	291877	124073	TCAGATTTTACTTCCACCTG
202704	34900	CCTAAGCTGGGTCTATTCCT	247291	79487	GATTGCTTACAACTATATGA	291878	124074	CTCAGATTTTACTTCCACCT
202705	34901	ACCTAAGCTGGGTCTATTCC	247292	79488	TGATTGCTTACAACTATATG	291879	124075	TCTCAGATTTTACTTCCACC
202706	34902	TACCTAAGCTGGGTCTATTC	247293	79489	ATGATTGCTTACAACTATAT	291880	124076	TTCTCAGATTTTACTTCCAC
202707	34903	GTACCTAAGCTGGGTCTATT	247294	79490	GATGATTGCTTACAACTATA	291881	124077	CTTCTCAGATTTTACTTCCA
202708	34904	TGTACCTAAGCTGGGTCTAT	247295	79491	AGATGATTGCTTACAACTAT	291882	124078	GCTTCTCAGATTTTACTTCC
202709	34905	CTGTACCTAAGCTGGGTCTA	247296	79492	CAGATGATTGCTTACAACTA	291883	124079	AGCTTCTCAGATTTTACTTC
202710	34906	GCTGTACCTAAGCTGGGTCT	247297	79493	CCAGATGATTGCTTACAACT	291884	124080	AAGCTTCTCAGATTTTACTT
202711	34907	AGCTGTACCTAAGCTGGGTC	247298	79494	ACCAGATGATTGCTTACAAC	291885	124081	CAAGCTTCTCAGATTTTACT
202712	34908	CAGCTGTACCTAAGCTGGGT	247299	79495	AACCAGATGATTGCTTACAA	291886	124082	TCAAGCTTCTCAGATTTTAC
202713	34909	CCAGCTGTACCTAAGCTGGG	247300	79496	AAACCAGATGATTGCTTACA	291887	124083	GTCAAGCTTCTCAGATTTTA
202714	34910	TCCAGCTGTACCTAAGCTGG	247301	79497	AAAACCAGATGATTGCTTAC	291888	124084	AGTCAAGCTTCTCAGATTTT
202715	34911	ATCCAGCTGTACCTAAGCTG	247302	79498	GAAAACCAGATGATTGCTTA	291889	124085	AAGTCAAGCTTCTCAGATTT
202716	34912	GATCCAGCTGTACCTAAGCT	247303	79499	TGAAAACCAGATGATTGCTT	291890	124086	GAAGTCAAGCTTCTCAGATT
202717	34913	GGATCCAGCTGTACCTAAGC	247304	79500	CTGAAAACCAGATGATTGCT	291891	124087	TGAAGTCAAGCTTCTCAGAT
202718	34914	TGGATCCAGCTGTACCTAAG	247305	79501	ACTGAAAACCAGATGATTGC	291892	124088	TTGAAGTCAAGCTTCTCAGA
202719	34915	CTGGATCCAGCTGTACCTAA	247306	79502	TACTGAAAACCAGATGATTG	291893	124089	CTTGAAGTCAAGCTTCTCAG
202720	34916	ACTGGATCCAGCTGTACCTA	247307	79503	ATACTGAAAACCAGATGATT	291894	124090	CCTTGAAGTCAAGCTTCTCA
202721	34917	GACTGGATCCAGCTGTACCT	247308	79504	AATACTGAAAACCAGATGAT	291895	124091	TCCTTGAAGTCAAGCTTCTC
202722	34918	TGACTGGATCCAGCTGTACC	247309	79505	AAATACTGAAAACCAGATGA	291896	124092	GTCCTTGAAGTCAAGCTTCT

202723	34919	GTGACTGGATCCAGCTGTAC	247310	79506	GAAATACTGAAAACCAGATG	291897	124093	TGTCCTTGAAGTCAAGCTTC
202724	34920	AGTGACTGGATCCAGCTGTA	247311	79507	AGAAATACTGAAAACCAGAT	291898	124094	CTGTCCTTGAAGTCAAGCTT
202725	34921	GAGTGACTGGATCCAGCTGT	247312	79508	AAGAAATACTGAAAACCAGA	291899	124095	TCTGTCCTTGAAGTCAAGCT
202726	34922	TGAGTGACTGGATCCAGCTG	247313	79509	GAAGAAATACTGAAAACCAG	291900	124096	CTCTGTCCTTGAAGTCAAGC
202727	34923	TTGAGTGACTGGATCCAGCT	247314	79510	AGAAGAAATACTGAAAACCA	291901	124097	ACTCTGTCCTTGAAGTCAAG
202728	34924	TTTGAGTGACTGGATCCAGC	247315	79511	AAGAAGAAATACTGAAAACC	291902	124098	GACTCTGTCCTTGAAGTCAA
202729	34925	GTTTGAGTGACTGGATCCAG	247316	79512	AAAGAAGAAATACTGAAAAC	291903	124099	GGACTCTGTCCTTGAAGTCA
202730	34926	TGTTTGAGTGACTGGATCCA	247317	79513	AAAAGAAGAAATACTGAAAA	291904	124100	TGGACTCTGTCCTTGAAGTC
202731	34927	TTGTTTGAGTGACTGGATCC	247318	79514	TAAAAGAAGAAATACTGAAA	291905	124101	CTGGACTCTGTCCTTGAAGT
202732	34928	ATTGTTTGAGTGACTGGATC	247319	79515	TTAAAAGAAGAAATACTGAA	291906	124102	ACTGGACTCTGTCCTTGAAG
202733	34929	CATTGTTTGAGTGACTGGAT	247320	79516	TTTAAAAGAAGAAATACTGA	291907	124103	GACTGGACTCTGTCCTTGAA
202734	34930	ACATTGTTTGAGTGACTGGA	247321	79517	TTTTAAAAGAAGAAATACTG	291908	124104	CGACTGGACTCTGTCCTTGA
202735	34931	GACATTGTTTGAGTGACTGG	247322	79518	ATTTTAAAAGAAGAAATACT	291909	124105	TCGACTGGACTCTGTCCTTG
202736	34932	TGACATTGTTTGAGTGACTG	247323	79519	CATTTTAAAAGAAGAAATAC	291910	124106	TTCGACTGGACTCTGTCCTT
202737	34933	GTGACATTGTTTGAGTGACT	247324	79520	GCATTTTAAAAGAAGAAATA	291911	124107	CTTCGACTGGACTCTGTCCT
202738	34934	TGTGACATTGTTTGAGTGAC	247325	79521	GGCATTTTAAAAGAAGAAAT	291912	124108	TCTTCGACTGGACTCTGTCC
202739	34935	TTGTGACATTGTTTGAGTGA	247326	79522	AGGCATTTTAAAAGAAGAAA	291913	124109	ATCTTCGACTGGACTCTGTC
202740	34936	TTTGTGACATTGTTTGAGTG	247327	79523	CAGGCATTTTAAAAGAAGAA	291914	124110	AATCTTCGACTGGACTCTGT
202741	34937	CTTTGTGACATTGTTTGAGT	247328	79524	CCAGGCATTTTAAAAGAAGA	291915	124111	CAATCTTCGACTGGACTCTG
202742	34938	TCTTTGTGACATTGTTTGAG	247329	79525	CCCAGGCATTTTAAAAGAAG	291916	124112	CCAATCTTCGACTGGACTCT
202743	34939	TTCTTTGTGACATTGTTTGA	247330	79526	CCCCAGGCATTTTAAAAGAA	291917	124113	CCCAATCTTCGACTGGACTC
202744	34940	GTTCTTTGTGACATTGTTTG	247331	79527	GCCCCAGGCATTTTAAAAGA	291918	124114	ACCCAATCTTCGACTGGACT
202745	34941	GGTTCTTTGTGACATTGTTT	247332	79528	GGCCCCAGGCATTTTAAAAG	291919	124115	GACCCAATCTTCGACTGGAC
202746	34942	GGGTTCTTTGTGACATTGTT	247333	79529	TGGCCCCAGGCATTTTAAAA	291920	124116	GGACCCAATCTTCGACTGGA
202747	34943	AGGGTTCTTTGTGACATTGT	247334	79530	ATGGCCCCAGGCATTTTAAA	291921	124117	GGGACCCAATCTTCGACTGG
202748	34944	AAGGGTTCTTTGTGACATTG	247335	79531	CATGGCCCCAGGCATTTTAA	291922	124118	AGGGACCCAATCTTCGACTG
202749	34945	AAAGGGTTCTTTGTGACATT	247336	79532	GCATGGCCCCAGGCATTTTA	291923	124119	CAGGGACCCAATCTTCGACT
202750	34946	CAAAGGGTTCTTTGTGACAT	247337	79533	GGCATGGCCCCAGGCATTTT	291924	124120	CCAGGGACCCAATCTTCGAC
202751	34947	TCAAAGGGTTCTTTGTGACA	247338	79534	GGGCATGGCCCCAGGCATTT	291925	124121	TCCAGGGACCCAATCTTCGA
202752	34948	GTCAAAGGGTTCTTTGTGAC	247339	79535	TGGGCATGGCCCCAGGCATT	291926	124122	GTCCAGGGACCCAATCTTCG
202753	34949	TGTCAAAGGGTTCTTTGTGA	247340	79536	CTGGGCATGGCCCCAGGCAT	291927	124123	TGTCCAGGGACCCAATCTTC
202754	34950	CTGTCAAAGGGTTCTTTGTG	247341	79537	GCTGGGCATGGCCCCAGGCA	291928	124124	TTGTCCAGGGACCCAATCTT
202755	34951	CCTGTCAAAGGGTTCTTTGT	247342	79538	TGCTGGGCATGGCCCCAGGC	291929	124125	ATTGTCCAGGGACCCAATCT
202756	34952	TCCTGTCAAAGGGTTCTTTG	247343	79539	CTGCTGGGCATGGCCCCAGG	291930	124126	TATTGTCCAGGGACCCAATC
202757	34953	TTCCTGTCAAAGGGTTCTTT	247344	79540	ACTGCTGGGCATGGCCCCAG	291931	124127	ATATTGTCCAGGGACCCAAT
202758	34954	ATTCCTGTCAAAGGGTTCTT	247345	79541	GACTGCTGGGCATGGCCCCA	291932	124128	GATATTGTCCAGGGACCCAA
202759	34955	CATTCCTGTCAAAGGGTTCT	247346	79542	AGACTGCTGGGCATGGCCCC	291933	124129	TGATATTGTCCAGGGACCCA
202760	34956	ACATTCCTGTCAAAGGGTTC	247347	79543	CAGACTGCTGGGCATGGCCC	291934	124130	GTGATATTGTCCAGGGACCC
202761	34957	TACATTCCTGTCAAAGGGTT	247348	79544	ACAGACTGCTGGGCATGGCC	291935	124131	GGTGATATTGTCCAGGGACC
202762	34958	ATACATTCCTGTCAAAGGGT	247349	79545	AACAGACTGCTGGGCATGGC	291936	124132	GGGTGATATTGTCCAGGGAC
202763	34959	GATACATTCCTGTCAAAGGG	247350	79546	AAACAGACTGCTGGGCATGG	291937	124133	TGGGTGATATTGTCCAGGGA
202764	34960	GGATACATTCCTGTCAAAGG	247351	79547	GAAACAGACTGCTGGGCATG	291938	124134	GTGGGTGATATTGTCCAGGG
202765	34961	AGGATACATTCCTGTCAAAG	247352	79548	TGAAACAGACTGCTGGGCAT	291939	124135	CGTGGGTGATATTGTCCAGG
202766	34962	CAGGATACATTCCTGTCAAA	247353	79549	GTGAAACAGACTGCTGGGCA	291940	124136	ACGTGGGTGATATTGTCCAG
202767	34963	ACAGGATACATTCCTGTCAA	247354	79550	AGTGAAACAGACTGCTGGGC	291941	124137	GACGTGGGTGATATTGTCCA
202768	34964	CACAGGATACATTCCTGTCA	247355	79551	CAGTGAAACAGACTGCTGGG	291942	124138	GGACGTGGGTGATATTGTCC
202769	34965	ACACAGGATACATTCCTGTC	247356	79552	GCAGTGAAACAGACTGCTGG	291943	124139	GGGACGTGGGTGATATTGTC
202770	34966	AACACAGGATACATTCCTGT	247357	79553	TGCAGTGAAACAGACTGCTG	291944	124140	AGGGACGTGGGTGATATTGT
202771	34967	CAACACAGGATACATTCCTG	247358	79554	CTGCAGTGAAACAGACTGCT	291945	124141	CAGGGACGTGGGTGATATTG
202772	34968	TCAACACAGGATACATTCCT	247359	79555	GCTGCAGTGAAACAGACTGC	291946	124142	CCAGGGACGTGGGTGATATT
202773	34969	GTCAACACAGGATACATTCC	247360	79556	CGCTGCAGTGAAACAGACTG	291947	124143	GCCAGGGACGTGGGTGATAT
202774	34970	AGTCAACACAGGATACATTC	247361	79557	ACGCTGCAGTGAAACAGACT	291948	124144	CGCCAGGGACGTGGGTGATA
202775	34971	GAGTCAACACAGGATACATT	247362	79558	AACGCTGCAGTGAAACAGAC	291949	124145	CCGCCAGGGACGTGGGTGAT
202776	34972	AGAGTCAACACAGGATACAT	247363	79559	AAACGCTGCAGTGAAACAGA	291950	124146	TCCGCCAGGGACGTGGGTGA
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202779	34975	AGTAGAGTCAACACAGGATA	247366	79562	TGTAAACGCTGCAGTGAAAC	291953	124149	TCCTCCGCCAGGGACGTGGG
202780	34976	AAGTAGAGTCAACACAGGAT	247367	79563	GTGTAAACGCTGCAGTGAAA	291954	124150	TTCCTCCGCCAGGGACGTGG
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202783	34979	GCAAAGTAGAGTCAACACAG	247370	79566	CCTGTGTAAACGCTGCAGTG	291957	124153	TATTTCCTCCGCCAGGGACG
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202785	34981	GAGCAAAGTAGAGTCAACAC	247372	79568	GCCCTGTGTAAACGCTGCAG	291959	124155	TTTATTTCCTCCGCCAGGGA
202786	34982	AGAGCAAAGTAGAGTCAACA	247373	79569	AGCCCTGTGTAAACGCTGCA	291960	124156	TTTTATTTCCTCCGCCAGGG
202787	34983	CAGAGCAAAGTAGAGTCAAC	247374	79570	CAGCCCTGTGTAAACGCTGC	291961	124157	TTTTTATTTCCTCCGCCAGG
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202789	34985	CTCAGAGCAAAGTAGAGTCA	247376	79572	GGCAGCCCTGTGTAAACGCT	291963	124159	CCTTTTTATTTCCTCCGCCA
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202791	34987	TACTCAGAGCAAAGTAGAGT	247378	79574	CCGGCAGCCCTGTGTAAACG	291965	124161	TACCTTTTTATTTCCTCCGC
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202795	34991	AGACTACTCAGAGCAAAGTA	247382	79578	AAGCCCGGCAGCCCTGTGTA	291969	124165	CCTTTACCTTTTTATTTCCT
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202800	34996	GGGAAAGACTACTCAGAGCA	247387	79583	CAGGAAAGCCCGGCAGCCCT	291974	124170	TACCCCCTTTACCTTTTTAT
202801	34997	GGGGAAAGACTACTCAGAGC	247388	79584	CCAGGAAAGCCCGGCAGCCC	291975	124171	CTACCCCCTTTACCTTTTTA
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202805	35001	ACCTGGGGAAAGACTACTCA	247392	79588	TCCACCAGGAAAGCCCGGCA	291979	124175	CACCCTACCCCCTTTACCTT
202806	35002	CACCTGGGGAAAGACTACTC	247393	79589	ATCCACCAGGAAAGCCCGGC	291980	124176	CCACCCTACCCCCTTTACCT
202807	35003	TCACCTGGGGAAAGACTACT	247394	79590	CATCCACCAGGAAAGCCCGG	291981	124177	CCCACCCTACCCCCTTTACC
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202809	35005	CATCACCTGGGGAAAGACTA	247396	79592	CTCATCCACCAGGAAAGCCC	291983	124179	AACCCACCCTACCCCCTTTA
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202811	35007	ATCATCACCTGGGGAAAGAC	247398	79594	AGCTCATCCACCAGGAAAGC	291985	124181	CCAACCCACCCTACCCCCTT
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202814	35010	TTTATCATCACCTGGGGAAA	247401	79597	CCCAGCTCATCCACCAGGAA	291988	124184	CATCCAACCCACCCTACCCC
202815	35011	TTTTATCATCACCTGGGGAA	247402	79598	GCCCAGCTCATCCACCAGGA	291989	124185	GCATCCAACCCACCCTACCC
202816	35012	TTTTTATCATCACCTGGGGA	247403	79599	CGCCCAGCTCATCCACCAGG	291990	124186	AGCATCCAACCCACCCTACC
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202827	35023	GATGATGACCATTTTTATCA	247414	79610	GGCTCATGAACCGCCCAGCT	292001	124197	TACCCAAGGGCAGCATCCAA
202828	35024	CGATGATGACCATTTTTATC	247415	79611	TGGCTCATGAACCGCCCAGC	292002	124198	ATACCCAAGGGCAGCATCCA
202829	35025	GCGATGATGACCATTTTTAT	247416	79612	CTGGCTCATGAACCGCCCAG	292003	124199	TATACCCAAGGGCAGCATCC
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202832	35028	CTGGCGATGATGACCATTTT	247419	79615	GTTCTGGCTCATGAACCGCC	292006	124202	CCATATACCCAAGGGCAGCA
202833	35029	CCTGGCGATGATGACCATTT	247420	79616	GGTTCTGGCTCATGAACCGC	292007	124203	CCCATATACCCAAGGGCAGC
202834	35030	GCCTGGCGATGATGACCATT	247421	79617	TGGTTCTGGCTCATGAACCG	292008	124204	GCCCATATACCCAAGGGCAG
202835	35031	AGCCTGGCGATGATGACCAT	247422	79618	GTGGTTCTGGCTCATGAACC	292009	124205	TGCCCATATACCCAAGGGCA
202836	35032	AAGCCTGGCGATGATGACCA	247423	79619	AGTGGTTCTGGCTCATGAAC	292010	124206	ATGCCCATATACCCAAGGGC
202837	35033	CAAGCCTGGCGATGATGACC	247424	79620	GAGTGGTTCTGGCTCATGAA	292011	124207	AATGCCCATATACCCAAGGG
202838	35034	ACAAGCCTGGCGATGATGAC	247425	79621	TGAGTGGTTCTGGCTCATGA	292012	124208	TAATGCCCATATACCCAAGG
202839	35035	CACAAGCCTGGCGATGATGA	247426	79622	CTGAGTGGTTCTGGCTCATG	292013	124209	TTAATGCCCATATACCCAAG
202840	35036	ACACAAGCCTGGCGATGATG	247427	79623	GCTGAGTGGTTCTGGCTCAT	292014	124210	ATTAATGCCCATATACCCAA
202841	35037	GACACAAGCCTGGCGATGAT	247428	79624	TGCTGAGTGGTTCTGGCTCA	292015	124211	GATTAATGCCCATATACCCA
202842	35038	GGACACAAGCCTGGCGATGA	247429	79625	CTGCTGAGTGGTTCTGGCTC	292016	124212	TGATTAATGCCCATATACCC
202843	35039	AGGACACAAGCCTGGCGATG	247430	79626	GCTGCTGAGTGGTTCTGGCT	292017	124213	TTGATTAATGCCCATATACC
202844	35040	CAGGACACAAGCCTGGCGAT	247431	79627	TGCTGCTGAGTGGTTCTGGC	292018	124214	CTTGATTAATGCCCATATAC
202845	35041	ACAGGACACAAGCCTGGCGA	247432	79628	ATGCTGCTGAGTGGTTCTGG	292019	124215	ACTTGATTAATGCCCATATA
202846	35042	AACAGGACACAAGCCTGGCG	247433	79629	CATGCTGCTGAGTGGTTCTG	292020	124216	AACTTGATTAATGCCCATAT
202847	35043	AAACAGGACACAAGCCTGGC	247434	79630	ACATGCTGCTGAGTGGTTCT	292021	124217	CAACTTGATTAATGCCCATA
202848	35044	TAAACAGGACACAAGCCTGG	247435	79631	GACATGCTGCTGAGTGGTTC	292022	124218	TCAACTTGATTAATGCCCAT
202849	35045	CTAAACAGGACACAAGCCTG	247436	79632	TGACATGCTGCTGAGTGGTT	292023	124219	CTCAACTTGATTAATGCCCA
202850	35046	ACTAAACAGGACACAAGCCT	247437	79633	CTGACATGCTGCTGAGTGGT	292024	124220	ACTCAACTTGATTAATGCCC
202851	35047	TACTAAACAGGACACAAGCC	247438	79634	ACTGACATGCTGCTGAGTGG	292025	124221	CACTCAACTTGATTAATGCC
202852	35048	CTACTAAACAGGACACAAGC	247439	79635	CACTGACATGCTGCTGAGTG	292026	124222	CCACTCAACTTGATTAATGC
202853	35049	CCTACTAAACAGGACACAAG	247440	79636	ACACTGACATGCTGCTGAGT	292027	124223	TCCACTCAACTTGATTAATG
202854	35050	TCCTACTAAACAGGACACAA	247441	79637	CACACTGACATGCTGCTGAG	292028	124224	GTCCACTCAACTTGATTAAT
202855	35051	TTCCTACTAAACAGGACACA	247442	79638	GCACACTGACATGCTGCTGA	292029	124225	TGTCCACTCAACTTGATTAA
202856	35052	ATTCCTACTAAACAGGACAC	247443	79639	AGCACACTGACATGCTGCTG	292030	124226	TTGTCCACTCAACTTGATTA
202857	35053	TATTCCTACTAAACAGGACA	247444	79640	AAGCACACTGACATGCTGCT	292031	124227	TTTGTCCACTCAACTTGATT
202858	35054	ATATTCCTACTAAACAGGAC	247445	79641	GAAGCACACTGACATGCTGC	292032	124228	CTTTGTCCACTCAACTTGAT
202859	35055	TATATTCCTACTAAACAGGA	247446	79642	GGAAGCACACTGACATGCTG	292033	124229	CCTTTGTCCACTCAACTTGA
202860	35056	GTATATTCCTACTAAACAGG	247447	79643	AGGAAGCACACTGACATGCT	292034	124230	GCCTTTGTCCACTCAACTTG
202861	35057	TGTATATTCCTACTAAACAG	247448	79644	CAGGAAGCACACTGACATGC	292035	124231	AGCCTTTGTCCACTCAACTT
202862	35058	TTGTATATTCCTACTAAACA	247449	79645	CCAGGAAGCACACTGACATG	292036	124232	CAGCCTTTGTCCACTCAACT
202863	35059	CTTGTATATTCCTACTAAAC	247450	79646	CCCAGGAAGCACACTGACAT	292037	124233	CCAGCCTTTGTCCACTCAAC
202864	35060	TCTTGTATATTCCTACTAAA	247451	79647	CCCCAGGAAGCACACTGACA	292038	124234	ACCAGCCTTTGTCCACTCAA
202865	35061	TTCTTGTATATTCCTACTAA	247452	79648	TCCCCAGGAAGCACACTGAC	292039	124235	GACCAGCCTTTGTCCACTCA
202866	35062	CTTCTTGTATATTCCTACTA	247453	79649	CTCCCCAGGAAGCACACTGA	292040	124236	GGACCAGCCTTTGTCCACTC

202867	35063	TCTTCTTGTATATTCCTACT	247454	79650	GCTCCCCAGGAAGCACACTG	292041	124237	TGGACCAGCCTTTGTCCACT
202868	35064	CTCTTCTTGTATATTCCTAC	247455	79651	AGCTCCCCAGGAAGCACACT	292042	124238	CTGGACCAGCCTTTGTCCAC
202869	35065	GCTCTTCTTGTATATTCCTA	247456	79652	CAGCTCCCCAGGAAGCACAC	292043	124239	ACTGGACCAGCCTTTGTCCA
202870	35066	AGCTCTTCTTGTATATTCCT	247457	79653	CCAGCTCCCCAGGAAGCACA	292044	124240	AACTGGACCAGCCTTTGTCC
202871	35067	GAGCTCTTCTTGTATATTCC	247458	79654	ACCAGCTCCCCAGGAAGCAC	292045	124241	GAACTGGACCAGCCTTTGTC
202872	35068	TGAGCTCTTCTTGTATATTC	247459	79655	TACCAGCTCCCCAGGAAGCA	292046	124242	GGAACTGGACCAGCCTTTGT
202873	35069	CTGAGCTCTTCTTGTATATT	247460	79656	CTACCAGCTCCCCAGGAAGC	292047	124243	GGGAACTGGACCAGCCTTTG
202874	35070	ACTGAGCTCTTCTTGTATAT	247461	79657	GCTACCAGCTCCCCAGGAAG	292048	124244	TGGGAACTGGACCAGCCTTT
202875	35071	TACTGAGCTCTTCTTGTATA	247462	79658	TGCTACCAGCTCCCCAGGAA	292049	124245	CTGGGAACTGGACCAGCCTT
202876	35072	TTACTGAGCTCTTCTTGTAT	247463	79659	CTGCTACCAGCTCCCCAGGA	292050	124246	TCTGGGAACTGGACCAGCCT
202877	35073	TTTACTGAGCTCTTCTTGTA	247464	79660	CCTGCTACCAGCTCCCCAGG	292051	124247	CTCTGGGAACTGGACCAGCC
202878	35074	ATTTACTGAGCTCTTCTTGT	247465	79661	CCCTGCTACCAGCTCCCCAG	292052	124248	CCTCTGGGAACTGGACCAGC
202879	35075	CATTTACTGAGCTCTTCTTG	247466	79662	CCCCTGCTACCAGCTCCCCA	292053	124249	TCCTCTGGGAACTGGACCAG
202880	35076	GCATTTACTGAGCTCTTCTT	247467	79663	GCCCCTGCTACCAGCTCCCC	292054	124250	CTCCTCTGGGAACTGGACCA
202881	35077	AGCATTTACTGAGCTCTTCT	247468	79664	AGCCCCTGCTACCAGCTCCC	292055	124251	CCTCCTCTGGGAACTGGACC
202882	35078	CAGCATTTACTGAGCTCTTC	247469	79665	GAGCCCCTGCTACCAGCTCC	292056	124252	TCCTCCTCTGGGAACTGGAC
202883	35079	CCAGCATTTACTGAGCTCTT	247470	79666	GGAGCCCCTGCTACCAGCTC	292057	124253	TTCCTCCTCTGGGAACTGGA
202884	35080	GCCAGCATTTACTGAGCTCT	247471	79667	CGGAGCCCCTGCTACCAGCT	292058	124254	TTTCCTCCTCTGGGAACTGG
202885	35081	GGCCAGCATTTACTGAGCTC	247472	79668	CCGGAGCCCCTGCTACCAGC	292059	124255	TTTTCCTCCTCTGGGAACTG
202886	35082	GGGCCAGCATTTACTGAGCT	247473	79669	CCCGGAGCCCCTGCTACCAG	292060	124256	GTTTTCCTCCTCTGGGAACT
202887	35083	GGGGCCAGCATTTACTGAGC	247474	79670	GCCCGGAGCCCCTGCTACCA	292061	124257	TGTTTTCCTCCTCTGGGAAC
202888	35084	TGGGGCCAGCATTTACTGAG	247475	79671	GGCCCGGAGCCCCTGCTACC	292062	124258	CTGTTTTCCTCCTCTGGGAA
202889	35085	GTGGGGCCAGCATTTACTGA	247476	79672	GGGCCCGGAGCCCCTGCTAC	292063	124259	TCTGTTTTCCTCCTCTGGGA
202890	35086	GGTGGGGCCAGCATTTACTG	247477	79673	AGGGCCCGGAGCCCCTGCTA	292064	124260	CTCTGTTTTCCTCCTCTGGG
202891	35087	TGGTGGGGCCAGCATTTACT	247478	79674	TAGGGCCCGGAGCCCCTGCT	292065	124261	CCTCTGTTTTCCTCCTCTGG
202892	35088	GTGGTGGGGCCAGCATTTAC	247479	79675	GTAGGGCCCGGAGCCCCTGC	292066	124262	GCCTCTGTTTTCCTCCTCTG
202893	35089	AGTGGTGGGGCCAGCATTTA	247480	79676	AGTAGGGCCCGGAGCCCCTG	292067	124263	AGCCTCTGTTTTCCTCCTCT
202894	35090	TAGTGGTGGGGCCAGCATTT	247481	79677	AAGTAGGGCCCGGAGCCCCT	292068	124264	AAGCCTCTGTTTTCCTCCTC
202895	35091	TTAGTGGTGGGGCCAGCATT	247482	79678	GAAGTAGGGCCCGGAGCCCC	292069	124265	GAAGCCTCTGTTTTCCTCCT
202896	35092	CTTAGTGGTGGGGCCAGCAT	247483	79679	TGAAGTAGGGCCCGGAGCCC	292070	124266	AGAAGCCTCTGTTTTCCTCC
202897	35093	GCTTAGTGGTGGGGCCAGCA	247484	79680	CTGAAGTAGGGCCCGGAGCC	292071	124267	CAGAAGCCTCTGTTTTCCTC
202898	35094	TGCTTAGTGGTGGGGCCAGC	247485	79681	CCTGAAGTAGGGCCCGGAGC	292072	124268	ACAGAAGCCTCTGTTTTCCT
202899	35095	TTGCTTAGTGGTGGGGCCAG	247486	79682	CCCTGAAGTAGGGCCCGGAG	292073	124269	CACAGAAGCCTCTGTTTTCC
202900	35096	TTTGCTTAGTGGTGGGGCCA	247487	79683	GCCCTGAAGTAGGGCCCGGA	292074	124270	ACACAGAAGCCTCTGTTTTC
202901	35097	TTTTGCTTAGTGGTGGGGCC	247488	79684	AGCCCTGAAGTAGGGCCCGG	292075	124271	AACACAGAAGCCTCTGTTTT
202902	35098	TTTTTGCTTAGTGGTGGGGC	247489	79685	CAGCCCTGAAGTAGGGCCCG	292076	124272	CAACACAGAAGCCTCTGTTT
202903	35099	GTTTTTGCTTAGTGGTGGGG	247490	79686	GCAGCCCTGAAGTAGGGCCC	292077	124273	TCAACACAGAAGCCTCTGTT
202904	35100	TGTTTTTGCTTAGTGGTGGG	247491	79687	AGCAGCCCTGAAGTAGGGCC	292078	124274	GTCAACACAGAAGCCTCTGT
202905	35101	TTGTTTTTGCTTAGTGGTGG	247492	79688	AAGCAGCCCTGAAGTAGGGC	292079	124275	AGTCAACACAGAAGCCTCTG
202906	35102	TTTGTTTTTGCTTAGTGGTG	247493	79689	AAAGCAGCCCTGAAGTAGGG	292080	124276	CAGTCAACACAGAAGCCTCT
202907	35103	TTTTGTTTTTGCTTAGTGGT	247494	79690	GAAAGCAGCCCTGAAGTAGG	292081	124277	CCAGTCAACACAGAAGCCTC
202908	35104	GTTTTGTTTTTGCTTAGTGG	247495	79691	AGAAAGCAGCCCTGAAGTAG	292082	124278	GCCAGTCAACACAGAAGCCT
202909	35105	AGTTTTGTTTTTGCTTAGTG	247496	79692	CAGAAAGCAGCCCTGAAGTA	292083	124279	AGCCAGTCAACACAGAAGCC
202910	35106	AAGTTTTGTTTTTGCTTAGT	247497	79693	CCAGAAAGCAGCCCTGAAGT	292084	124280	CAGCCAGTCAACACAGAAGC
202911	35107	AAAGTTTTGTTTTTGCTTAG	247498	79694	GCCAGAAAGCAGCCCTGAAG	292085	124281	CCAGCCAGTCAACACAGAAG
202912	35108	AAAAGTTTTGTTTTTGCTTA	247499	79695	TGCCAGAAAGCAGCCCTGAA	292086	124282	TCCAGCCAGTCAACACAGAA
202913	35109	CAAAAGTTTTGTTTTTGCTT	247500	79696	ATGCCAGAAAGCAGCCCTGA	292087	124283	ATCCAGCCAGTCAACACAGA
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202915	35111	AACAAAAGTTTTGTTTTTGC	247502	79698	ATATGCCAGAAAGCAGCCCT	292089	124285	ACATCCAGCCAGTCAACACA
202916	35112	CAACAAAAGTTTTGTTTTTG	247503	79699	CATATGCCAGAAAGCAGCCC	292090	124286	CACATCCAGCCAGTCAACAC
202917	35113	ACAACAAAAGTTTTGTTTTT	247504	79700	CCATATGCCAGAAAGCAGCC	292091	124287	CCACATCCAGCCAGTCAACA
202918	35114	AACAACAAAAGTTTTGTTTT	247505	79701	GCCATATGCCAGAAAGCAGC	292092	124288	CCCACATCCAGCCAGTCAAC
202919	35115	CAACAACAAAAGTTTTGTTT	247506	79702	AGCCATATGCCAGAAAGCAG	292093	124289	GCCCACATCCAGCCAGTCAA
202920	35116	ACAACAACAAAAGTTTTGTT	247507	79703	CAGCCATATGCCAGAAAGCA	292094	124290	GGCCCACATCCAGCCAGTCA
202921	35117	AACAACAACAAAAGTTTTGT	247508	79704	TCAGCCATATGCCAGAAAGC	292095	124291	GGGCCCACATCCAGCCAGTC
202922	35118	TAACAACAACAAAAGTTTTG	247509	79705	ATCAGCCATATGCCAGAAAG	292096	124292	AGGGCCCACATCCAGCCAGT
202923	35119	ATAACAACAACAAAAGTTTT	247510	79706	GATCAGCCATATGCCAGAAA	292097	124293	GAGGGCCCACATCCAGCCAG
202924	35120	AATAACAACAACAAAAGTTT	247511	79707	GGATCAGCCATATGCCAGAA	292098	124294	TGAGGGCCCACATCCAGCCA
202925	35121	CAATAACAACAACAAAAGTT	247512	79708	GGGATCAGCCATATGCCAGA	292099	124295	CTGAGGGCCCACATCCAGCC
202926	35122	ACAATAACAACAACAAAAGT	247513	79709	GGGGATCAGCCATATGCCAG	292100	124296	GCTGAGGGCCCACATCCAGC
202927	35123	AACAATAACAACAACAAAAG	247514	79710	AGGGGATCAGCCATATGCCA	292101	124297	TGCTGAGGGCCCACATCCAG
202928	35124	CAACAATAACAACAACAAAA	247515	79711	GAGGGGATCAGCCATATGCC	292102	124298	CTGCTGAGGGCCCACATCCA
202929	35125	ACAACAATAACAACAACAAA	247516	79712	GGAGGGGATCAGCCATATGC	292103	124299	GCTGCTGAGGGCCCACATCC
202930	35126	AACAACAATAACAACAACAA	247517	79713	AGGAGGGGATCAGCCATATG	292104	124300	TGCTGCTGAGGGCCCACATC
202931	35127	AAACAACAATAACAACAACA	247518	79714	GAGGAGGGGATCAGCCATAT	292105	124301	ATGCTGCTGAGGGCCCACAT
202932	35128	AAAACAACAATAACAACAAC	247519	79715	TGAGGAGGGGATCAGCCATA	292106	124302	GATGCTGCTGAGGGCCCACA
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202934	35130	TTAAAACAACAATAACAACA	247521	79717	AGTGAGGAGGGGATCAGCCA	292108	124304	TGGATGCTGCTGAGGGCCCA
202935	35131	TTTAAAACAACAATAACAAC	247522	79718	GAGTGAGGAGGGGATCAGCC	292109	124305	CTGGATGCTGCTGAGGGCCC
202936	35132	ATTTAAAACAACAATAACAA	247523	79719	GGAGTGAGGAGGGGATCAGC	292110	124306	ACTGGATGCTGCTGAGGGCC
202937	35133	TATTTAAAACAACAATAACA	247524	79720	AGGAGTGAGGAGGGGATCAG	292111	124307	CACTGGATGCTGCTGAGGGC
202938	35134	TTATTTAAAACAACAATAAC	247525	79721	GAGGAGTGAGGAGGGGATCA	292112	124308	CCACTGGATGCTGCTGAGGG

202939	35135	GTTATTTAAAACAACAATAA	247526	79722	GGAGGAGTGAGGAGGGGATC	292113	124309	CCCACTGGATGCTGCTGAGG
202940	35136	TGTTATTTAAAACAACAATA	247527	79723	AGGAGGAGTGAGGAGGGGAT	292114	124310	ACCCACTGGATGCTGCTGAG
202941	35137	CTGTTATTTAAAACAACAAT	247528	79724	GAGGAGGAGTGAGGAGGGGA	292115	124311	GACCCACTGGATGCTGCTGA
202942	35138	GCTGTTATTTAAAACAACAA	247529	79725	GGAGGAGGAGTGAGGAGGGG	292116	124312	AGACCCACTGGATGCTGCTG
202943	35139	AGCTGTTATTTAAAACAACA	247530	79726	GGGAGGAGGAGTGAGGAGGG	292117	124313	GAGACCCACTGGATGCTGCT
202944	35140	AAGCTGTTATTTAAAACAAC	247531	79727	AGGGAGGAGGAGTGAGGAGG	292118	124314	GGAGACCCACTGGATGCTGC
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202953	35149	GAAAGGTCTAAGCTGTTATT	247540	79736	GAGCAATGCAGGGAGGAGGA	292127	124323	ACAGGCAGTGGAGACCCACT
202954	35150	AGAAAGGTCTAAGCTGTTAT	247541	79737	GGAGCAATGCAGGGAGGAGG	292128	124324	GACAGGCAGTGGAGACCCAC
202955	35151	AAGAAAGGTCTAAGCTGTTA	247542	79738	AGGAGCAATGCAGGGAGGAG	292129	124325	AGACAGGCAGTGGAGACCCA
202956	35152	GAAGAAAGGTCTAAGCTGTT	247543	79739	CAGGAGCAATGCAGGGAGGA	292130	124326	GAGACAGGCAGTGGAGACCC
202957	35153	AGAAGAAAGGTCTAAGCTGT	247544	79740	GCAGGAGCAATGCAGGGAGG	292131	124327	TGAGACAGGCAGTGGAGACC
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202959	35155	AAAGAAGAAAGGTCTAAGCT	247546	79742	GCGCAGGAGCAATGCAGGGA	292133	124329	ATTGAGACAGGCAGTGGAGA
202960	35156	GAAAGAAGAAAGGTCTAAGC	247547	79743	TGCGCAGGAGCAATGCAGGG	292134	124330	GATTGAGACAGGCAGTGGAG
202961	35157	GGAAAGAAGAAAGGTCTAAG	247548	79744	TTGCGCAGGAGCAATGCAGG	292135	124331	TGATTGAGACAGGCAGTGGA
202962	35158	AGGAAAGAAGAAAGGTCTAA	247549	79745	CTTGCGCAGGAGCAATGCAG	292136	124332	GTGATTGAGACAGGCAGTGG
202963	35159	AAGGAAAGAAGAAAGGTCTA	247550	79746	TCTTGCGCAGGAGCAATGCA	292137	124333	GGTGATTGAGACAGGCAGTG
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202965	35161	ACAAGGAAAGAAGAAAGGTC	247552	79748	CTTCTTGCGCAGGAGCAATG	292139	124335	CAGGTGATTGAGACAGGCAG
202966	35162	AACAAGGAAAGAAGAAAGGT	247553	79749	GCTTCTTGCGCAGGAGCAAT	292140	124336	CCAGGTGATTGAGACAGGCA
202967	35163	TAACAAGGAAAGAAGAAAGG	247554	79750	TGCTTCTTGCGCAGGAGCAA	292141	124337	TCCAGGTGATTGAGACAGGC
202968	35164	ATAACAAGGAAAGAAGAAAG	247555	79751	TTGCTTCTTGCGCAGGAGCA	292142	124338	CTCCAGGTGATTGAGACAGG
202969	35165	AATAACAAGGAAAGAAGAAA	247556	79752	TTTGCTTCTTGCGCAGGAGC	292143	124339	GCTCCAGGTGATTGAGACAG
202970	35166	GAATAACAAGGAAAGAAGAA	247557	79753	CTTTGCTTCTTGCGCAGGAG	292144	124340	AGCTCCAGGTGATTGAGACA
202971	35167	AGAATAACAAGGAAAGAAGA	247558	79754	CCTTTGCTTCTTGCGCAGGA	292145	124341	AAGCTCCAGGTGATTGAGAC
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202973	35169	AGAGAATAACAAGGAAAGAA	247560	79756	CACCTTTGCTTCTTGCGCAG	292147	124343	TAAAGCTCCAGGTGATTGAG
202974	35170	AAGAGAATAACAAGGAAAGA	247561	79757	TCACCTTTGCTTCTTGCGCA	292148	124344	CTAAAGCTCCAGGTGATTGA
202975	35171	AAAGAGAATAACAAGGAAAG	247562	79758	CTCACCTTTGCTTCTTGCGC	292149	124345	GCTAAAGCTCCAGGTGATTG
202976	35172	GAAAGAGAATAACAAGGAAA	247563	79759	CCTCACCTTTGCTTCTTGCG	292150	124346	TGCTAAAGCTCCAGGTGATT
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202981	35177	CAGATGAAAGAGAATAACAA	247568	79764	CAGCCCCTCACCTTTGCTTC	292155	124351	AAACGTGCTAAAGCTCCAGG
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202985	35181	ATTACAGATGAAAGAGAATA	247572	79768	TACCCAGCCCCTCACCTTTG	292159	124355	TGTGAAACGTGCTAAAGCTC
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202987	35183	GGATTACAGATGAAAGAGAA	247574	79770	CATACCCAGCCCCTCACCTT	292161	124357	GGTGTGAAACGTGCTAAAGC
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202990	35186	ACTGGATTACAGATGAAAGA	247577	79773	AGCCATACCCAGCCCCTCAC	292164	124360	CCAGGTGTGAAACGTGCTAA
202991	35187	AACTGGATTACAGATGAAAG	247578	79774	GAGCCATACCCAGCCCCTCA	292165	124361	CCCAGGTGTGAAACGTGCTA
202992	35188	AAACTGGATTACAGATGAAA	247579	79775	CGAGCCATACCCAGCCCCTC	292166	124362	GCCCAGGTGTGAAACGTGCT
202993	35189	AAAACTGGATTACAGATGAA	247580	79776	ACGAGCCATACCCAGCCCCT	292167	124363	GGCCCAGGTGTGAAACGTGC
202994	35190	GAAAACTGGATTACAGATGA	247581	79777	GACGAGCCATACCCAGCCCC	292168	124364	GGGCCCAGGTGTGAAACGTG
202995	35191	AGAAAACTGGATTACAGATG	247582	79778	GGACGAGCCATACCCAGCCC	292169	124365	GGGGCCCAGGTGTGAAACGT
202996	35192	TAGAAAACTGGATTACAGAT	247583	79779	AGGACGAGCCATACCCAGCC	292170	124366	TGGGGCCCAGGTGTGAAACG
202997	35193	GTAGAAAACTGGATTACAGA	247584	79780	CAGGACGAGCCATACCCAGC	292171	124367	TTGGGGCCCAGGTGTGAAAC
202998	35194	AGTAGAAAACTGGATTACAG	247585	79781	CCAGGACGAGCCATACCCAG	292172	124368	GTTGGGGCCCAGGTGTGAAA
202999	35195	AAGTAGAAAACTGGATTACA	247586	79782	GCCAGGACGAGCCATACCCA	292173	124369	GGTTGGGGCCCAGGTGTGAA
203000	35196	GAAGTAGAAAACTGGATTAC	247587	79783	GGCCAGGACGAGCCATACCC	292174	124370	AGGTTGGGGCCCAGGTGTGA
203001	35197	AGAAGTAGAAAACTGGATTA	247588	79784	GGGCCAGGACGAGCCATACC	292175	124371	CAGGTTGGGGCCCAGGTGTG
203002	35198	CAGAAGTAGAAAACTGGATT	247589	79785	GGGGCCAGGACGAGCCATAC	292176	124372	CCAGGTTGGGGCCCAGGTGT
203003	35199	TCAGAAGTAGAAAACTGGAT	247590	79786	AGGGGCCAGGACGAGCCATA	292177	124373	TCCAGGTTGGGGCCCAGGTG
203004	35200	TTCAGAAGTAGAAAACTGGA	247591	79787	GAGGGGCCAGGACGAGCCAT	292178	124374	CTCCAGGTTGGGGCCCAGGT
203005	35201	CTTCAGAAGTAGAAAACTGG	247592	79788	AGAGGGGCCAGGACGAGCCA	292179	124375	TCTCCAGGTTGGGGCCCAGG
203006	35202	ACTTCAGAAGTAGAAAACTG	247593	79789	TAGAGGGGCCAGGACGAGCC	292180	124376	CTCTCCAGGTTGGGGCCCAG
203007	35203	TACTTCAGAAGTAGAAAACT	247594	79790	TTAGAGGGGCCAGGACGAGC	292181	124377	CCTCTCCAGGTTGGGGCCCA
203008	35204	ATACTTCAGAAGTAGAAAAC	247595	79791	CTTAGAGGGGCCAGGACGAG	292182	124378	GCCTCTCCAGGTTGGGGCCC
203009	35205	TATACTTCAGAAGTAGAAAA	247596	79792	CCTTAGAGGGGCCAGGACGA	292183	124379	AGCCTCTCCAGGTTGGGGCC
203010	35206	CTATACTTCAGAAGTAGAAA	247597	79793	ACCTTAGAGGGGCCAGGACG	292184	124380	CAGCCTCTCCAGGTTGGGGC

203011	35207	TCTATACTTCAGAAGTAGAA	247598	79794	CACCTTAGAGGGGCCAGGAC	292185	124381	TCAGCCTCTCCAGGTTGGGG
203012	35208	TTCTATACTTCAGAAGTAGA	247599	79795	CCACCTTAGAGGGGCCAGGA	292186	124382	GTCAGCCTCTCCAGGTTGGG
203013	35209	ATTCTATACTTCAGAAGTAG	247600	79796	TCCACCTTAGAGGGGCCAGG	292187	124383	GGTCAGCCTCTCCAGGTTGG
203014	35210	CATTCTATACTTCAGAAGTA	247601	79797	ATCCACCTTAGAGGGGCCAG	292188	124384	TGGTCAGCCTCTCCAGGTTG
203015	35211	ACATTCTATACTTCAGAAGT	247602	79798	GATCCACCTTAGAGGGGCCA	292189	124385	TTGGTCAGCCTCTCCAGGTT
203016	35212	AACATTCTATACTTCAGAAG	247603	79799	AGATCCACCTTAGAGGGGCC	292190	124386	ATTGGTCAGCCTCTCCAGGT
203017	35213	GAACATTCTATACTTCAGAA	247604	79800	GAGATCCACCTTAGAGGGGC	292191	124387	CATTGGTCAGCCTCTCCAGG
203018	35214	AGAACATTCTATACTTCAGA	247605	79801	CGAGATCCACCTTAGAGGGG	292192	124388	CCATTGGTCAGCCTCTCCAG
203019	35215	CAGAACATTCTATACTTCAG	247606	79802	CCGAGATCCACCTTAGAGGG	292193	124389	CCCATTGGTCAGCCTCTCCA
203020	35216	TCAGAACATTCTATACTTCA	247607	79803	ACCGAGATCCACCTTAGAGG	292194	124390	ACCCATTGGTCAGCCTCTCC
203021	35217	ATCAGAACATTCTATACTTC	247608	79804	CACCGAGATCCACCTTAGAG	292195	124391	GACCCATTGGTCAGCCTCTC
203022	35218	CATCAGAACATTCTATACTT	247609	79805	CCACCGAGATCCACCTTAGA	292196	124392	AGACCCATTGGTCAGCCTCT
203023	35219	TCATCAGAACATTCTATACT	247610	79806	ACCACCGAGATCCACCTTAG	292197	124393	GAGACCCATTGGTCAGCCTC
203024	35220	ATCATCAGAACATTCTATAC	247611	79807	AACCACCGAGATCCACCTTA	292198	124394	TGAGACCCATTGGTCAGCCT
203025	35221	AATCATCAGAACATTCTATA	247612	79808	AAACCACCGAGATCCACCTT	292199	124395	CTGAGACCCATTGGTCAGCC
203026	35222	AAATCATCAGAACATTCTAT	247613	79809	GAAACCACCGAGATCCACCT	292200	124396	CCTGAGACCCATTGGTCAGC
203027	35223	TAAATCATCAGAACATTCTA	247614	79810	AGAAACCACCGAGATCCACC	292201	124397	CCCTGAGACCCATTGGTCAG
203028	35224	ATAAATCATCAGAACATTCT	247615	79811	TAGAAACCACCGAGATCCAC	292202	124398	CCCCTGAGACCCATTGGTCA
203029	35225	AATAAATCATCAGAACATTC	247616	79812	CTAGAAACCACCGAGATCCA	292203	124399	GCCCCTGAGACCCATTGGTC
203030	35226	GAATAAATCATCAGAACATT	247617	79813	TCTAGAAACCACCGAGATCC	292204	124400	TGCCCCTGAGACCCATTGGT
203031	35227	AGAATAAATCATCAGAACAT	247618	79814	ATCTAGAAACCACCGAGATC	292205	124401	CTGCCCCTGAGACCCATTGG
203032	35228	AAGAATAAATCATCAGAACA	247619	79815	CATCTAGAAACCACCGAGAT	292206	124402	GCTGCCCCTGAGACCCATTG
203033	35229	GAAGAATAAATCATCAGAAC	247620	79816	ACATCTAGAAACCACCGAGA	292207	124403	AGCTGCCCCTGAGACCCATT
203034	35230	TGAAGAATAAATCATCAGAA	247621	79817	CACATCTAGAAACCACCGAG	292208	124404	GAGCTGCCCCTGAGACCCAT
203035	35231	ATGAAGAATAAATCATCAGA	247622	79818	TCACATCTAGAAACCACCGA	292209	124405	CGAGCTGCCCCTGAGACCCA
203036	35232	AATGAAGAATAAATCATCAG	247623	79819	GTCACATCTAGAAACCACCG	292210	124406	CCGAGCTGCCCCTGAGACCC
203037	35233	TAATGAAGAATAAATCATCA	247624	79820	TGTCACATCTAGAAACCACC	292211	124407	ACCGAGCTGCCCCTGAGACC
203038	35234	GTAATGAAGAATAAATCATC	247625	79821	CTGTCACATCTAGAAACCAC	292212	124408	AACCGAGCTGCCCCTGAGAC
203039	35235	GGTAATGAAGAATAAATCAT	247626	79822	GCTGTCACATCTAGAAACCA	292213	124409	CAACCGAGCTGCCCCTGAGA
203040	35236	GGGTAATGAAGAATAAATCA	247627	79823	TGCTGTCACATCTAGAAACC	292214	124410	GCAACCGAGCTGCCCCTGAG
203041	35237	TGGGTAATGAAGAATAAATC	247628	79824	GTGCTGTCACATCTAGAAAC	292215	124411	AGCAACCGAGCTGCCCCTGA
203042	35238	GTGGGTAATGAAGAATAAAT	247629	79825	GGTGCTGTCACATCTAGAAA	292216	124412	CAGCAACCGAGCTGCCCCTG
203043	35239	TGTGGGTAATGAAGAATAAA	247630	79826	GGGTGCTGTCACATCTAGAA	292217	124413	CCAGCAACCGAGCTGCCCCT
203044	35240	TTGTGGGTAATGAAGAATAA	247631	79827	AGGGTGCTGTCACATCTAGA	292218	124414	TCCAGCAACCGAGCTGCCCC
203045	35241	GTTGTGGGTAATGAAGAATA	247632	79828	AAGGGTGCTGTCACATCTAG	292219	124415	CTCCAGCAACCGAGCTGCCC
203046	35242	AGTTGTGGGTAATGAAGAAT	247633	79829	TAAGGGTGCTGTCACATCTA	292220	124416	ACTCCAGCAACCGAGCTGCC
203047	35243	AAGTTGTGGGTAATGAAGAA	247634	79830	CTAAGGGTGCTGTCACATCT	292221	124417	AACTCCAGCAACCGAGCTGC
203048	35244	CAAGTTGTGGGTAATGAAGA	247635	79831	ACTAAGGGTGCTGTCACATC	292222	124418	AAACTCCAGCAACCGAGCTG
203049	35245	GCAAGTTGTGGGTAATGAAG	247636	79832	CACTAAGGGTGCTGTCACAT	292223	124419	AAAACTCCAGCAACCGAGCT
203050	35246	TGCAAGTTGTGGGTAATGAA	247637	79833	CCACTAAGGGTGCTGTCACA	292224	124420	AAAAACTCCAGCAACCGAGC
203051	35247	GTGCAAGTTGTGGGTAATGA	247638	79834	TCCACTAAGGGTGCTGTCAC	292225	124421	CAAAAACTCCAGCAACCGAG
203052	35248	TGTGCAAGTTGTGGGTAATG	247639	79835	ATCCACTAAGGGTGCTGTCA	292226	124422	ACAAAAACTCCAGCAACCGA
203053	35249	ATGTGCAAGTTGTGGGTAAT	247640	79836	CATCCACTAAGGGTGCTGTC	292227	124423	AACAAAAACTCCAGCAACCG
203054	35250	CATGTGCAAGTTGTGGGTAA	247641	79837	TCATCCACTAAGGGTGCTGT	292228	124424	AAACAAAAACTCCAGCAACC
203055	35251	ACATGTGCAAGTTGTGGGTA	247642	79838	CTCATCCACTAAGGGTGCTG	292229	124425	AAAACAAAAACTCCAGCAAC
203056	35252	AACATGTGCAAGTTGTGGGT	247643	79839	CCTCATCCACTAAGGGTGCT	292230	124426	AAAAACAAAAACTCCAGCAA
203057	35253	AAACATGTGCAAGTTGTGGG	247644	79840	CCCTCATCCACTAAGGGTGC	292231	124427	TAAAAACAAAAACTCCAGCA
203058	35254	TAAACATGTGCAAGTTGTGG	247645	79841	TCCCTCATCCACTAAGGGTG	292232	124428	ATAAAAACAAAAACTCCAGC
203059	35255	ATAAACATGTGCAAGTTGTG	247646	79842	CTCCCTCATCCACTAAGGGT	292233	124429	AATAAAAACAAAAACTCCAG
203060	35256	AATAAACATGTGCAAGTTGT	247647	79843	GCTCCCTCATCCACTAAGGG	292234	124430	AAATAAAAACAAAAACTCCA
203061	35257	AAATAAACATGTGCAAGTTG	247648	79844	AGCTCCCTCATCCACTAAGG	292235	124431	TAAATAAAAACAAAAACTCC
203062	35258	TAAATAAACATGTGCAAGTT	247649	79845	GAGCTCCCTCATCCACTAAG	292236	124432	ATAAATAAAAACAAAAACTC
203063	35259	TTAAATAAACATGTGCAAGT	247650	79846	GGAGCTCCCTCATCCACTAA	292237	124433	AATAAATAAAAACAAAAACT
203064	35260	TTTAAATAAACATGTGCAAG	247651	79847	GGGAGCTCCCTCATCCACTA	292238	124434	AAATAAATAAAAACAAAAAC
203065	35261	TTTTAAATAAACATGTGCAA	247652	79848	CGGGAGCTCCCTCATCCACT	292239	124435	AAAATAAATAAAAACAAAAA
203066	35262	TTTTTAAATAAACATGTGCA	247653	79849	CCGGGAGCTCCCTCATCCAC	292240	124436	AAAAATAAATAAAAACAAAA
203067	35263	ATTTTTAAATAAACATGTGC	247654	79850	GCCGGGAGCTCCCTCATCCA	292241	124437	TAAAAATAAATAAAAACAAA
203068	35264	CATTTTTAAATAAACATGTG	247655	79851	TGCCGGGAGCTCCCTCATCC	292242	124438	ATAAAAATAAATAAAAACAA
203069	35265	GCATTTTTAAATAAACATGT	247656	79852	TTGCCGGGAGCTCCCTCATC	292243	124439	CATAAAAATAAATAAAAACA
203070	35266	GGCATTTTTAAATAAACATG	247657	79853	CTTGCCGGGAGCTCCCTCAT	292244	124440	ACATAAAAATAAATAAAAAC
203071	35267	TGGCATTTTTAAATAAACAT	247658	79854	GCTTGCCGGGAGCTCCCTCA	292245	124441	TACATAAAAATAAATAAAAA
203072	35268	CTGGCATTTTTAAATAAACA	247659	79855	TGCTTGCCGGGAGCTCCCTC	292246	124442	ATACATAAAAATAAATAAAA
203073	35269	CCTGGCATTTTTAAATAAAC	247660	79856	CTGCTTGCCGGGAGCTCCCT	292247	124443	AATACATAAAAATAAATAAA
203074	35270	TCCTGGCATTTTTAAATAAA	247661	79857	CCTGCTTGCCGGGAGCTCCC	292248	124444	AAATACATAAAAATAAATAA
203075	35271	ATCCTGGCATTTTTAAATAA	247662	79858	GCCTGCTTGCCGGGAGCTCC	292249	124445	TAAATACATAAAAATAAATA
203076	35272	AATCCTGGCATTTTTAAATA	247663	79859	AGCCTGCTTGCCGGGAGCTC	292250	124446	TTAAATACATAAAAATAAAT
203077	35273	CAATCCTGGCATTTTTAAAT	247664	79860	CAGCCTGCTTGCCGGGAGCT	292251	124447	CTTAAATACATAAAAATAAA
203078	35274	GCAATCCTGGCATTTTTAAA	247665	79861	GCAGCCTGCTTGCCGGGAGC	292252	124448	CCTTAAATACATAAAAATAA
203079	35275	GGCAATCCTGGCATTTTTAA	247666	79862	GGCAGCCTGCTTGCCGGGAG	292253	124449	GCCTTAAATACATAAAAATA
203080	35276	AGGCAATCCTGGCATTTTTA	247667	79863	CGGCAGCCTGCTTGCCGGGA	292254	124450	TGCCTTAAATACATAAAAAT
203081	35277	CAGGCAATCCTGGCATTTTT	247668	79864	GCGGCAGCCTGCTTGCCGGG	292255	124451	CTGCCTTAAATACATAAAAA
203082	35278	CCAGGCAATCCTGGCATTTT	247669	79865	CGCGGCAGCCTGCTTGCCGG	292256	124452	CCTGCCTTAAATACATAAAA

203083	35279	GCCAGGCAATCCTGGCATTT	247670	79866	GCGCGGCAGCCTGCTTGCCG	292257	124453	CCCTGCCTTAAATACATAAA
203084	35280	GGCCAGGCAATCCTGGCATT	247671	79867	TGCGCGGCAGCCTGCTTGCC	292258	124454	ACCCTGCCTTAAATACATAA
203085	35281	CGGCCAGGCAATCCTGGCAT	247672	79868	CTGCGCGGCAGCCTGCTTGC	292259	124455	GACCCTGCCTTAAATACATA
203086	35282	ACGGCCAGGCAATCCTGGCA	247673	79869	GCTGCGCGGCAGCCTGCTTG	292260	124456	AGACCCTGCCTTAAATACAT
203087	35283	AACGGCCAGGCAATCCTGGC	247674	79870	GGCTGCGCGGCAGCCTGCTT	292261	124457	GAGACCCTGCCTTAAATACA
203088	35284	CAACGGCCAGGCAATCCTGG	247675	79871	GGGCTGCGCGGCAGCCTGCT	292262	124458	AGAGACCCTGCCTTAAATAC
203089	35285	ACAACGGCCAGGCAATCCTG	247676	79872	GGGGCTGCGCGGCAGCCTGC	292263	124459	CAGAGACCCTGCCTTAAATA
203090	35286	CACAACGGCCAGGCAATCCT	247677	79873	TGGGGCTGCGCGGCAGCCTG	292264	124460	ACAGAGACCCTGCCTTAAAT
203091	35287	ACACAACGGCCAGGCAATCC	247678	79874	GTGGGGCTGCGCGGCAGCCT	292265	124461	TACAGAGACCCTGCCTTAAA
203092	35288	CACACAACGGCCAGGCAATC	247679	79875	TGTGGGGCTGCGCGGCAGCC	292266	124462	ATACAGAGACCCTGCCTTAA
203093	35289	GCACACAACGGCCAGGCAAT	247680	79876	GTGTGGGGCTGCGCGGCAGC	292267	124463	AATACAGAGACCCTGCCTTA
203094	35290	AGCACACAACGGCCAGGCAA	247681	79877	CGTGTGGGGCTGCGCGGCAG	292268	124464	TAATACAGAGACCCTGCCTT
203095	35291	CAGCACACAACGGCCAGGCA	247682	79878	CCGTGTGGGGCTGCGCGGCA	292269	124465	CTAATACAGAGACCCTGCCT
203096	35292	ACAGCACACAACGGCCAGGC	247683	79879	TCCGTGTGGGGCTGCGCGGC	292270	124466	ACTAATACAGAGACCCTGCC
203097	35293	AACAGCACACAACGGCCAGG	247684	79880	CTCCGTGTGGGGCTGCGCGG	292271	124467	GACTAATACAGAGACCCTGC
203098	35294	TAACAGCACACAACGGCCAG	247685	79881	TCTCCGTGTGGGGCTGCGCG	292272	124468	GGACTAATACAGAGACCCTG
203099	35295	TTAACAGCACACAACGGCCA	247686	79882	ATCTCCGTGTGGGGCTGCGC	292273	124469	TGGACTAATACAGAGACCCT
203100	35296	GTTAACAGCACACAACGGCC	247687	79883	GATCTCCGTGTGGGGCTGCG	292274	124470	ATGGACTAATACAGAGACCC
203101	35297	GGTTAACAGCACACAACGGC	247688	79884	GGATCTCCGTGTGGGGCTGC	292275	124471	AATGGACTAATACAGAGACC
203102	35298	AGGTTAACAGCACACAACGG	247689	79885	GGGATCTCCGTGTGGGGCTG	292276	124472	GAATGGACTAATACAGAGAC
203103	35299	AAGGTTAACAGCACACAACG	247690	79886	TGGGATCTCCGTGTGGGGCT	292277	124473	AGAATGGACTAATACAGAGA
203104	35300	AAAGGTTAACAGCACACAAC	247691	79887	CTGGGATCTCCGTGTGGGGC	292278	124474	GAGAATGGACTAATACAGAG
203105	35301	CAAAGGTTAACAGCACACAA	247692	79888	TCTGGGATCTCCGTGTGGGG	292279	124475	TGAGAATGGACTAATACAGA
203106	35302	ACAAAGGTTAACAGCACACA	247693	79889	TTCTGGGATCTCCGTGTGGG	292280	124476	GTGAGAATGGACTAATACAG
203107	35303	AACAAAGGTTAACAGCACAC	247694	79890	CTTCTGGGATCTCCGTGTGG	292281	124477	TGTGAGAATGGACTAATACA
203108	35304	AAACAAAGGTTAACAGCACA	247695	79891	CCTTCTGGGATCTCCGTGTG	292282	124478	GTGTGAGAATGGACTAATAC
203109	35305	CAAACAAAGGTTAACAGCAC	247696	79892	TCCTTCTGGGATCTCCGTGT	292283	124479	AGTGTGAGAATGGACTAATA
203110	35306	GCAAACAAAGGTTAACAGCA	247697	79893	TTCCTTCTGGGATCTCCGTG	292284	124480	CAGTGTGAGAATGGACTAAT
203111	35307	AGCAAACAAAGGTTAACAGC	247698	79894	GTTCCTTCTGGGATCTCCGT	292285	124481	GCAGTGTGAGAATGGACTAA
203112	35308	CAGCAAACAAAGGTTAACAG	247699	79895	GGTTCCTTCTGGGATCTCCG	292286	124482	AGCAGTGTGAGAATGGACTA
203113	35309	ACAGCAAACAAAGGTTAACA	247700	79896	TGGTTCCTTCTGGGATCTCC	292287	124483	TAGCAGTGTGAGAATGGACT
203114	35310	AACAGCAAACAAAGGTTAAC	247701	79897	GTGGTTCCTTCTGGGATCTC	292288	124484	TTAGCAGTGTGAGAATGGAC
203115	35311	TAACAGCAAACAAAGGTTAA	247702	79898	TGTGGTTCCTTCTGGGATCT	292289	124485	ATTAGCAGTGTGAGAATGGA
203116	35312	CTAACAGCAAACAAAGGTTA	247703	79899	CTGTGGTTCCTTCTGGGATC	292290	124486	TATTAGCAGTGTGAGAATGG
203117	35313	ACTAACAGCAAACAAAGGTT	247704	79900	CCTGTGGTTCCTTCTGGGAT	292291	124487	TTATTAGCAGTGTGAGAATG
203118	35314	CACTAACAGCAAACAAAGGT	247705	79901	ACCTGTGGTTCCTTCTGGGA	292292	124488	TTTATTAGCAGTGTGAGAAT
203119	35315	CCACTAACAGCAAACAAAGG	247706	79902	CACCTGTGGTTCCTTCTGGG	292293	124489	CTTTATTAGCAGTGTGAGAA
203120	35316	TCCACTAACAGCAAACAAAG	247707	79903	TCACCTGTGGTTCCTTCTGG	292294	124490	TCTTTATTAGCAGTGTGAGA
203121	35317	ATCCACTAACAGCAAACAAA	247708	79904	CTCACCTGTGGTTCCTTCTG	292295	124491	GTCTTTATTAGCAGTGTGAG
203122	35318	GATCCACTAACAGCAAACAA	247709	79905	CCTCACCTGTGGTTCCTTCT	292296	124492	TGTCTTTATTAGCAGTGTGA
203123	35319	GGATCCACTAACAGCAAACA	247710	79906	CCCTCACCTGTGGTTCCTTC	292297	124493	ATGTCTTTATTAGCAGTGTG
203124	35320	GGGATCCACTAACAGCAAAC	247711	79907	ACCCTCACCTGTGGTTCCTT	292298	124494	TATGTCTTTATTAGCAGTGT
203125	35321	AGGGATCCACTAACAGCAAA	247712	79908	TACCCTCACCTGTGGTTCCT	292299	124495	GTATGTCTTTATTAGCAGTG
203126	35322	CAGGGATCCACTAACAGCAA	247713	79909	TTACCCTCACCTGTGGTTCC	292300	124496	GGTATGTCTTTATTAGCAGT
203127	35323	TCAGGGATCCACTAACAGCA	247714	79910	CTTACCCTCACCTGTGGTTC	292301	124497	GGGTATGTCTTTATTAGCAG
203128	35324	TTCAGGGATCCACTAACAGC	247715	79911	GCTTACCCTCACCTGTGGTT	292302	124498	TGGGTATGTCTTTATTAGCA
203129	35325	CTTCAGGGATCCACTAACAG	247716	79912	GGCTTACCCTCACCTGTGGT	292303	124499	TTGGGTATGTCTTTATTAGC
203130	35326	ACTTCAGGGATCCACTAACA	247717	79913	GGGCTTACCCTCACCTGTGG	292304	124500	CTTGGGTATGTCTTTATTAG
203131	35327	AACTTCAGGGATCCACTAAC	247718	79914	GGGGCTTACCCTCACCTGTG	292305	124501	TCTTGGGTATGTCTTTATTA
203132	35328	GAACTTCAGGGATCCACTAA	247719	79915	TGGGGCTTACCCTCACCTGT	292306	124502	GTCTTGGGTATGTCTTTATT
203133	35329	TGAACTTCAGGGATCCACTA	247720	79916	CTGGGGCTTACCCTCACCTG	292307	124503	AGTCTTGGGTATGTCTTTAT
203134	35330	CTGAACTTCAGGGATCCACT	247721	79917	TCTGGGGCTTACCCTCACCT	292308	124504	CAGTCTTGGGTATGTCTTTA
203135	35331	CCTGAACTTCAGGGATCCAC	247722	79918	CTCTGGGGCTTACCCTCACC	292309	124505	CCAGTCTTGGGTATGTCTTT
203136	35332	GCCTGAACTTCAGGGATCCA	247723	79919	TCTCTGGGGCTTACCCTCAC	292310	124506	CCCAGTCTTGGGTATGTCTT
203137	35333	AGCCTGAACTTCAGGGATCC	247724	79920	GTCTCTGGGGCTTACCCTCA	292311	124507	ACCCAGTCTTGGGTATGTCT
203138	35334	GAGCCTGAACTTCAGGGATC	247725	79921	GGTCTCTGGGGCTTACCCTC	292312	124508	TACCCAGTCTTGGGTATGTC
203139	35335	GGAGCCTGAACTTCAGGGAT	247726	79922	GGGTCTCTGGGGCTTACCCT	292313	124509	TTACCCAGTCTTGGGTATGT
203140	35336	GGGAGCCTGAACTTCAGGGA	247727	79923	GGGGTCTCTGGGGCTTACCC	292314	124510	ATTACCCAGTCTTGGGTATG
203141	35337	TGGGAGCCTGAACTTCAGGG	247728	79924	GGGGGTCTCTGGGGCTTACC	292315	124511	AATTACCCAGTCTTGGGTAT
203142	35338	CTGGGAGCCTGAACTTCAGG	247729	79925	TGGGGGTCTCTGGGGCTTAC	292316	124512	AAATTACCCAGTCTTGGGTA
203143	35339	CCTGGGAGCCTGAACTTCAG	247730	79926	CTGGGGGTCTCTGGGGCTTA	292317	124513	TAAATTACCCAGTCTTGGGT
203144	35340	CCCTGGGAGCCTGAACTTCA	247731	79927	CCTGGGGGTCTCTGGGGCTT	292318	124514	ATAAATTACCCAGTCTTGGG
203145	35341	CCCCTGGGAGCCTGAACTTC	247732	79928	GCCTGGGGGTCTCTGGGGCT	292319	124515	TATAAATTACCCAGTCTTGG
203146	35342	TCCCCTGGGAGCCTGAACTT	247733	79929	TGCCTGGGGGTCTCTGGGGC	292320	124516	TTATAAATTACCCAGTCTTG
203147	35343	CTCCCCTGGGAGCCTGAACT	247734	79930	CTGCCTGGGGGTCTCTGGGG	292321	124517	TTTATAAATTACCCAGTCTT
203148	35344	GCTCCCCTGGGAGCCTGAAC	247735	79931	ACTGCCTGGGGGTCTCTGGG	292322	124518	CTTTATAAATTACCCAGTCT
203149	35345	TGCTCCCCTGGGAGCCTGAA	247736	79932	GACTGCCTGGGGGTCTCTGG	292323	124519	CCTTTATAAATTACCCAGTC
203150	35346	CTGCTCCCCTGGGAGCCTGA	247737	79933	TGACTGCCTGGGGGTCTCTG	292324	124520	TCCTTTATAAATTACCCAGT
203151	35347	TCTGCTCCCCTGGGAGCCTG	247738	79934	TTGACTGCCTGGGGGTCTCT	292325	124521	TTCCTTTATAAATTACCCAG
203152	35348	ATCTGCTCCCCTGGGAGCCT	247739	79935	CTTGACTGCCTGGGGGTCTC	292326	124522	TTTCCTTTATAAATTACCCA
203153	35349	TATCTGCTCCCCTGGGAGCC	247740	79936	CCTTGACTGCCTGGGGGTCT	292327	124523	CTTTCCTTTATAAATTACCC
203154	35350	TTATCTGCTCCCCTGGGAGC	247741	79937	GCCTTGACTGCCTGGGGGTC	292328	124524	TCTTTCCTTTATAAATTACC

203155	35351	ATTATCTGCTCCCCTGGGAG	247742	79938	GGCCTTGACTGCCTGGGGGT	292329	124525	CTCTTTCCTTTATAAATTAC
203156	35352	CATTATCTGCTCCCCTGGGA	247743	79939	GGGCCTTGACTGCCTGGGGG	292330	124526	CCTCTTTCCTTTATAAATTA
203157	35353	CCATTATCTGCTCCCCTGGG	247744	79940	AGGGCCTTGACTGCCTGGGG	292331	124527	ACCTCTTTCCTTTATAAATT
203158	35354	CCCATTATCTGCTCCCCTGG	247745	79941	CAGGGCCTTGACTGCCTGGG	292332	124528	AACCTCTTTCCTTTATAAAT
203159	35355	ACCCATTATCTGCTCCCCTG	247746	79942	GCAGGGCCTTGACTGCCTGG	292333	124529	AAACCTCTTTCCTTTATAAA
203160	35356	TACCCATTATCTGCTCCCCT	247747	79943	AGCAGGGCCTTGACTGCCTG	292334	124530	TAAACCTCTTTCCTTTATAA
203161	35357	ATACCCATTATCTGCTCCCC	247748	79944	CAGCAGGGCCTTGACTGCCT	292335	124531	TTAAACCTCTTTCCTTTATA
203162	35358	GATACCCATTATCTGCTCCC	247749	79945	CCAGCAGGGCCTTGACTGCC	292336	124532	ATTAAACCTCTTTCCTTTAT
203163	35359	GGATACCCATTATCTGCTCC	247750	79946	CCCAGCAGGGCCTTGACTGC	292337	124533	CATTAAACCTCTTTCCTTTA
203164	35360	TGGATACCCATTATCTGCTC	247751	79947	ACCCAGCAGGGCCTTGACTG	292338	124534	CCATTAAACCTCTTTCCTTT
203165	35361	CTGGATACCCATTATCTGCT	247752	79948	CACCCAGCAGGGCCTTGACT	292339	124535	TCCATTAAACCTCTTTCCTT
203166	35362	ACTGGATACCCATTATCTGC	247753	79949	GCACCCAGCAGGGCCTTGAC	292340	124536	GTCCATTAAACCTCTTTCCT
203167	35363	AACTGGATACCCATTATCTG	247754	79950	GGCACCCAGCAGGGCCTTGA	292341	124537	AGTCCATTAAACCTCTTTCC
203168	35364	GAACTGGATACCCATTATCT	247755	79951	GGGCACCCAGCAGGGCCTTG	292342	124538	GAGTCCATTAAACCTCTTTC
203169	35365	GGAACTGGATACCCATTATC	247756	79952	GGGGCACCCAGCAGGGCCTT	292343	124539	TGAGTCCATTAAACCTCTTT
203170	35366	AGGAACTGGATACCCATTAT	247757	79953	TGGGGCACCCAGCAGGGCCT	292344	124540	GTGAGTCCATTAAACCTCTT
203171	35367	CAGGAACTGGATACCCATTA	247758	79954	CTGGGGCACCCAGCAGGGCC	292345	124541	TGTGAGTCCATTAAACCTCT
203172	35368	GCAGGAACTGGATACCCATT	247759	79955	GCTGGGGCACCCAGCAGGGC	292346	124542	CTGTGAGTCCATTAAACCTC
203173	35369	TGCAGGAACTGGATACCCAT	247760	79956	AGCTGGGGCACCCAGCAGGG	292347	124543	ACTGTGAGTCCATTAAACCT
203174	35370	TTGCAGGAACTGGATACCCA	247761	79957	CAGCTGGGGCACCCAGCAGG	292348	124544	AACTGTGAGTCCATTAAACC
203175	35371	ATTGCAGGAACTGGATACCC	247762	79958	TCAGCTGGGGCACCCAGCAG	292349	124545	GAACTGTGAGTCCATTAAAC
203176	35372	TATTGCAGGAACTGGATACC	247763	79959	GTCAGCTGGGGCACCCAGCA	292350	124546	GGAACTGTGAGTCCATTAAA
203177	35373	ATATTGCAGGAACTGGATAC	247764	79960	GGTCAGCTGGGGCACCCAGC	292351	124547	TGGAACTGTGAGTCCATTAA
203178	35374	GATATTGCAGGAACTGGATA	247765	79961	AGGTCAGCTGGGGCACCCAG	292352	124548	GTGGAACTGTGAGTCCATTA
203179	35375	GGATATTGCAGGAACTGGAT	247766	79962	CAGGTCAGCTGGGGCACCCA	292353	124549	TGTGGAACTGTGAGTCCATT
203180	35376	TGGATATTGCAGGAACTGGA	247767	79963	ACAGGTCAGCTGGGGCACCC	292354	124550	ATGTGGAACTGTGAGTCCAT
203181	35377	GTGGATATTGCAGGAACTGG	247768	79964	CACAGGTCAGCTGGGGCACC	292355	124551	CATGTGGAACTGTGAGTCCA
203182	35378	GGTGGATATTGCAGGAACTG	247769	79965	TCACAGGTCAGCTGGGGCAC	292356	124552	CCATGTGGAACTGTGAGTCC
203183	35379	GGGTGGATATTGCAGGAACT	247770	79966	GTCACAGGTCAGCTGGGGCA	292357	124553	GCCATGTGGAACTGTGAGTC
203184	35380	AGGGTGGATATTGCAGGAAC	247771	79967	TGTCACAGGTCAGCTGGGGC	292358	124554	AGCCATGTGGAACTGTGAGT
203185	35381	GAGGGTGGATATTGCAGGAA	247772	79968	CTGTCACAGGTCAGCTGGGG	292359	124555	CAGCCATGTGGAACTGTGAG
203186	35382	AGAGGGTGGATATTGCAGGA	247773	79969	TCTGTCACAGGTCAGCTGGG	292360	124556	CCAGCCATGTGGAACTGTGA
203187	35383	CAGAGGGTGGATATTGCAGG	247774	79970	TTCTGTCACAGGTCAGCTGG	292361	124557	CCCAGCCATGTGGAACTGTG
203188	35384	CCAGAGGGTGGATATTGCAG	247775	79971	CTTCTGTCACAGGTCAGCTG	292362	124558	CCCCAGCCATGTGGAACTGT
203189	35385	GCCAGAGGGTGGATATTGCA	247776	79972	ACTTCTGTCACAGGTCAGCT	292363	124559	TCCCCAGCCATGTGGAACTG
203190	35386	TGCCAGAGGGTGGATATTGC	247777	79973	CACTTCTGTCACAGGTCAGC	292364	124560	CTCCCCAGCCATGTGGAACT
203191	35387	TTGCCAGAGGGTGGATATTG	247778	79974	TCACTTCTGTCACAGGTCAG	292365	124561	CCTCCCCAGCCATGTGGAAC
203192	35388	CTTGCCAGAGGGTGGATATT	247779	79975	CTCACTTCTGTCACAGGTCA	292366	124562	GCCTCCCCAGCCATGTGGAA
203193	35389	GCTTGCCAGAGGGTGGATAT	247780	79976	CCTCACTTCTGTCACAGGTC	292367	124563	GGCCTCCCCAGCCATGTGGA
203194	35390	GGCTTGCCAGAGGGTGGATA	247781	79977	CCCTCACTTCTGTCACAGGT	292368	124564	AGGCCTCCCCAGCCATGTGG
203195	35391	TGGCTTGCCAGAGGGTGGAT	247782	79978	TCCCTCACTTCTGTCACAGG	292369	124565	GAGGCCTCCCCAGCCATGTG
203196	35392	TTGGCTTGCCAGAGGGTGGA	247783	79979	CTCCCTCACTTCTGTCACAG	292370	124566	TGAGGCCTCCCCAGCCATGT
203197	35393	CTTGGCTTGCCAGAGGGTGG	247784	79980	GCTCCCTCACTTCTGTCACA	292371	124567	TTGAGGCCTCCCCAGCCATG
203198	35394	ACTTGGCTTGCCAGAGGGTG	247785	79981	AGCTCCCTCACTTCTGTCAC	292372	124568	TTTGAGGCCTCCCCAGCCAT
203199	35395	AACTTGGCTTGCCAGAGGGT	247786	79982	AAGCTCCCTCACTTCTGTCA	292373	124569	TTTTGAGGCCTCCCCAGCCA
203200	35396	GAACTTGGCTTGCCAGAGGG	247787	79983	AAAGCTCCCTCACTTCTGTC	292374	124570	ATTTTGAGGCCTCCCCAGCC
203201	35397	GGAACTTGGCTTGCCAGAGG	247788	79984	CAAAGCTCCCTCACTTCTGT	292375	124571	GATTTTGAGGCCTCCCCAGC
203202	35398	AGGAACTTGGCTTGCCAGAG	247789	79985	GCAAAGCTCCCTCACTTCTG	292376	124572	TGATTTTGAGGCCTCCCCAG
203203	35399	AAGGAACTTGGCTTGCCAGA	247790	79986	CGCAAAGCTCCCTCACTTCT	292377	124573	ATGATTTTGAGGCCTCCCCA
203204	35400	GAAGGAACTTGGCTTGCCAG	247791	79987	ACGCAAAGCTCCCTCACTTC	292378	124574	CATGATTTTGAGGCCTCCCC
203205	35401	GGAAGGAACTTGGCTTGCCA	247792	79988	CACGCAAAGCTCCCTCACTT	292379	124575	CCATGATTTTGAGGCCTCCC
203206	35402	AGGAAGGAACTTGGCTTGCC	247793	79989	ACACGCAAAGCTCCCTCACT	292380	124576	GCCATGATTTTGAGGCCTCC
203207	35403	CAGGAAGGAACTTGGCTTGC	247794	79990	AACACGCAAAGCTCCCTCAC	292381	124577	CGCCATGATTTTGAGGCCTC
203208	35404	CCAGGAAGGAACTTGGCTTG	247795	79991	AAACACGCAAAGCTCCCTCA	292382	124578	CCGCCATGATTTTGAGGCCT
203209	35405	CCCAGGAAGGAACTTGGCTT	247796	79992	TAAACACGCAAAGCTCCCTC	292383	124579	TCCGCCATGATTTTGAGGCC
203210	35406	ACCCAGGAAGGAACTTGGCT	247797	79993	ATAAACACGCAAAGCTCCCT	292384	124580	TTCCGCCATGATTTTGAGGC
203211	35407	TACCCAGGAAGGAACTTGGC	247798	79994	GATAAACACGCAAAGCTCCC	292385	124581	CTTCCGCCATGATTTTGAGG
203212	35408	TTACCCAGGAAGGAACTTGG	247799	79995	GGATAAACACGCAAAGCTCC	292386	124582	CCTTCCGCCATGATTTTGAG
203213	35409	CTTACCCAGGAAGGAACTTG	247800	79996	AGGATAAACACGCAAAGCTC	292387	124583	GCCTTCCGCCATGATTTTGA
203214	35410	CCTTACCCAGGAAGGAACTT	247801	79997	GAGGATAAACACGCAAAGCT	292388	124584	TGCCTTCCGCCATGATTTTG
203215	35411	ACCTTACCCAGGAAGGAACT	247802	79998	GGAGGATAAACACGCAAAGC	292389	124585	TTGCCTTCCGCCATGATTTT
203216	35412	AACCTTACCCAGGAAGGAAC	247803	79999	AGGAGGATAAACACGCAAAG	292390	124586	TTTGCCTTCCGCCATGATTT
203217	35413	AAACCTTACCCAGGAAGGAA	247804	80000	CAGGAGGATAAACACGCAAA	292391	124587	CTTTGCCTTCCGCCATGATT
203218	35414	AAAACCTTACCCAGGAAGGA	247805	80001	ACAGGAGGATAAACACGCAA	292392	124588	CCTTTGCCTTCCGCCATGAT
203219	35415	CAAAACCTTACCCAGGAAGG	247806	80002	CACAGGAGGATAAACACGCA	292393	124589	TCCTTTGCCTTCCGCCATGA
203220	35416	GCAAAACCTTACCCAGGAAG	247807	80003	CCACAGGAGGATAAACACGC	292394	124590	CTCCTTTGCCTTCCGCCATG
203221	35417	GGCAAAACCTTACCCAGGAA	247808	80004	CCCACAGGAGGATAAACACG	292395	124591	TCTCCTTTGCCTTCCGCCAT
203222	35418	AGGCAAAACCTTACCCAGGA	247809	80005	CCCCACAGGAGGATAAACAC	292396	124592	TTCTCCTTTGCCTTCCGCCA
203223	35419	TAGGCAAAACCTTACCCAGG	247810	80006	GCCCCACAGGAGGATAAACA	292397	124593	CTTCTCCTTTGCCTTCCGCC
203224	35420	GTAGGCAAAACCTTACCCAG	247811	80007	TGCCCCACAGGAGGATAAAC	292398	124594	GCTTCTCCTTTGCCTTCCGC
203225	35421	GGTAGGCAAAACCTTACCCA	247812	80008	CTGCCCCACAGGAGGATAAA	292399	124595	TGCTTCTCCTTTGCCTTCCG
203226	35422	AGGTAGGCAAAACCTTACCC	247813	80009	CCTGCCCCACAGGAGGATAA	292400	124596	TTGCTTCTCCTTTGCCTTCC

203227	35423	CAGGTAGGCAAAACCTTACC	247814	80010	TCCTGCCCCACAGGAGGATA	292401	124597	TTTGCTTCTCCTTTGCCTTC
203228	35424	GCAGGTAGGCAAAACCTTAC	247815	80011	TTCCTGCCCCACAGGAGGAT	292402	124598	CTTTGCTTCTCCTTTGCCTT
203229	35425	TGCAGGTAGGCAAAACCTTA	247816	80012	GTTCCTGCCCCACAGGAGGA	292403	124599	CCTTTGCTTCTCCTTTGCCT
203230	35426	ATGCAGGTAGGCAAAACCTT	247817	80013	TGTTCCTGCCCCACAGGAGG	292404	124600	GCCTTTGCTTCTCCTTTGCC
203231	35427	AATGCAGGTAGGCAAAACCT	247818	80014	ATGTTCCTGCCCCACAGGAG	292405	124601	TGCCTTTGCTTCTCCTTTGC
203232	35428	GAATGCAGGTAGGCAAAACC	247819	80015	CATGTTCCTGCCCCACAGGA	292406	124602	ATGCCTTTGCTTCTCCTTTG
203233	35429	GGAATGCAGGTAGGCAAAAC	247820	80016	CCATGTTCCTGCCCCACAGG	292407	124603	AATGCCTTTGCTTCTCCTTT
203234	35430	AGGAATGCAGGTAGGCAAAA	247821	80017	CCCATGTTCCTGCCCCACAG	292408	124604	AAATGCCTTTGCTTCTCCTT
203235	35431	TAGGAATGCAGGTAGGCAAA	247822	80018	ACCCATGTTCCTGCCCCACA	292409	124605	GAAATGCCTTTGCTTCTCCT
203236	35432	CTAGGAATGCAGGTAGGCAA	247823	80019	CACCCATGTTCCTGCCCCAC	292410	124606	AGAAATGCCTTTGCTTCTCC
203237	35433	CCTAGGAATGCAGGTAGGCA	247824	80020	CCACCCATGTTCCTGCCCCA	292411	124607	AAGAAATGCCTTTGCTTCTC
203238	35434	CCCTAGGAATGCAGGTAGGC	247825	80021	TCCACCCATGTTCCTGCCCC	292412	124608	TAAGAAATGCCTTTGCTTCT
203239	35435	TCCCTAGGAATGCAGGTAGG	247826	80022	ATCCACCCATGTTCCTGCCC	292413	124609	GTAAGAAATGCCTTTGCTTC
203240	35436	TTCCCTAGGAATGCAGGTAG	247827	80023	AATCCACCCATGTTCCTGCC	292414	124610	TGTAAGAAATGCCTTTGCTT
203241	35437	CTTCCCTAGGAATGCAGGTA	247828	80024	GAATCCACCCATGTTCCTGC	292415	124611	ATGTAAGAAATGCCTTTGCT
203242	35438	ACTTCCCTAGGAATGCAGGT	247829	80025	AGAATCCACCCATGTTCCTG	292416	124612	CATGTAAGAAATGCCTTTGC
203243	35439	AACTTCCCTAGGAATGCAGG	247830	80026	CAGAATCCACCCATGTTCCT	292417	124613	CCATGTAAGAAATGCCTTTG
203244	35440	AAACTTCCCTAGGAATGCAG	247831	80027	CCAGAATCCACCCATGTTCC	292418	124614	GCCATGTAAGAAATGCCTTT
203245	35441	GAAACTTCCCTAGGAATGCA	247832	80028	GCCAGAATCCACCCATGTTC	292419	124615	CGCCATGTAAGAAATGCCTT
203246	35442	AGAAACTTCCCTAGGAATGC	247833	80029	AGCCAGAATCCACCCATGTT	292420	124616	TCGCCATGTAAGAAATGCCT
203247	35443	CAGAAACTTCCCTAGGAATG	247834	80030	GAGCCAGAATCCACCCATGT	292421	124617	GTCGCCATGTAAGAAATGCC
203248	35444	CCAGAAACTTCCCTAGGAAT	247835	80031	GGAGCCAGAATCCACCCATG	292422	124618	TGTCGCCATGTAAGAAATGC
203249	35445	CCCAGAAACTTCCCTAGGAA	247836	80032	AGGAGCCAGAATCCACCCAT	292423	124619	CTGTCGCCATGTAAGAAATG
203250	35446	GCCCAGAAACTTCCCTAGGA	247837	80033	CAGGAGCCAGAATCCACCCA	292424	124620	CCTGTCGCCATGTAAGAAAT
203251	35447	GGCCCAGAAACTTCCCTAGG	247838	80034	CCAGGAGCCAGAATCCACCC	292425	124621	GCCTGTCGCCATGTAAGAAA
203252	35448	AGGCCCAGAAACTTCCCTAG	247839	80035	CCCAGGAGCCAGAATCCACC	292426	124622	TGCCTGTCGCCATGTAAGAA
203253	35449	CAGGCCCAGAAACTTCCCTA	247840	80036	TCCCAGGAGCCAGAATCCAC	292427	124623	TTGCCTGTCGCCATGTAAGA
203254	35450	TCAGGCCCAGAAACTTCCCT	247841	80037	TTCCCAGGAGCCAGAATCCA	292428	124624	CTTGCCTGTCGCCATGTAAG
203255	35451	GTCAGGCCCAGAAACTTCCC	247842	80038	ATTCCCAGGAGCCAGAATCC	292429	124625	TCTTGCCTGTCGCCATGTAA
203256	35452	GGTCAGGCCCAGAAACTTCC	247843	80039	GATTCCCAGGAGCCAGAATC	292430	124626	CTCTTGCCTGTCGCCATGTA
203257	35453	TGGTCAGGCCCAGAAACTTC	247844	80040	AGATTCCCAGGAGCCAGAAT	292431	124627	TCTCTTGCCTGTCGCCATGT
203258	35454	GTGGTCAGGCCCAGAAACTT	247845	80041	AAGATTCCCAGGAGCCAGAA	292432	124628	CTCTCTTGCCTGTCGCCATG
203259	35455	GGTGGTCAGGCCCAGAAACT	247846	80042	CAAGATTCCCAGGAGCCAGA	292433	124629	GCTCTCTTGCCTGTCGCCAT
203260	35456	TGGTGGTCAGGCCCAGAAAC	247847	80043	CCAAGATTCCCAGGAGCCAG	292434	124630	CGCTCTCTTGCCTGTCGCCA
203261	35457	TTGGTGGTCAGGCCCAGAAA	247848	80044	CCCAAGATTCCCAGGAGCCA	292435	124631	ACGCTCTCTTGCCTGTCGCC
203262	35458	CTTGGTGGTCAGGCCCAGAA	247849	80045	ACCCAAGATTCCCAGGAGCC	292436	124632	CACGCTCTCTTGCCTGTCGC
203263	35459	GCTTGGTGGTCAGGCCCAGA	247850	80046	AACCCAAGATTCCCAGGAGC	292437	124633	ACACGCTCTCTTGCCTGTCG
203264	35460	GGCTTGGTGGTCAGGCCCAG	247851	80047	CAACCCAAGATTCCCAGGAG	292438	124634	CACACGCTCTCTTGCCTGTC
203265	35461	TGGCTTGGTGGTCAGGCCCA	247852	80048	ACAACCCAAGATTCCCAGGA	292439	124635	GCACACGCTCTCTTGCCTGT
203266	35462	CTGGCTTGGTGGTCAGGCCC	247853	80049	CACAACCCAAGATTCCCAGG	292440	124636	TGCACACGCTCTCTTGCCTG
203267	35463	GCTGGCTTGGTGGTCAGGCC	247854	80050	TCACAACCCAAGATTCCCAG	292441	124637	CTGCACACGCTCTCTTGCCT
203268	35464	AGCTGGCTTGGTGGTCAGGC	247855	80051	CTCACAACCCAAGATTCCCA	292442	124638	CCTGCACACGCTCTCTTGCC
203269	35465	GAGCTGGCTTGGTGGTCAGG	247856	80052	ACTCACAACCCAAGATTCCC	292443	124639	CCCTGCACACGCTCTCTTGC
203270	35466	AGAGCTGGCTTGGTGGTCAG	247857	80053	TACTCACAACCCAAGATTCC	292444	124640	CCCCTGCACACGCTCTCTTG
203271	35467	CAGAGCTGGCTTGGTGGTCA	247858	80054	CTACTCACAACCCAAGATTC	292445	124641	TCCCCTGCACACGCTCTCTT
203272	35468	TCAGAGCTGGCTTGGTGGTC	247859	80055	GCTACTCACAACCCAAGATT	292446	124642	TTCCCCTGCACACGCTCTCT
203273	35469	CTCAGAGCTGGCTTGGTGGT	247860	80056	AGCTACTCACAACCCAAGAT	292447	124643	GTTCCCCTGCACACGCTCTC
203274	35470	TCTCAGAGCTGGCTTGGTGG	247861	80057	GAGCTACTCACAACCCAAGA	292448	124644	AGTTCCCCTGCACACGCTCT
203275	35471	TTCTCAGAGCTGGCTTGGTG	247862	80058	CGAGCTACTCACAACCCAAG	292449	124645	GAGTTCCCCTGCACACGCTC
203276	35472	CTTCTCAGAGCTGGCTTGGT	247863	80059	TCGAGCTACTCACAACCCAA	292450	124646	GGAGTTCCCCTGCACACGCT
203277	35473	CCTTCTCAGAGCTGGCTTGG	247864	80060	ATCGAGCTACTCACAACCCA	292451	124647	GGGAGTTCCCCTGCACACGC
203278	35474	CCCTTCTCAGAGCTGGCTTG	247865	80061	CATCGAGCTACTCACAACCC	292452	124648	TGGGAGTTCCCCTGCACACG
203279	35475	CCCCTTCTCAGAGCTGGCTT	247866	80062	GCATCGAGCTACTCACAACC	292453	124649	ATGGGAGTTCCCCTGCACAC
203280	35476	ACCCCTTCTCAGAGCTGGCT	247867	80063	GGCATCGAGCTACTCACAAC	292454	124650	AATGGGAGTTCCCCTGCACA
203281	35477	CACCCCTTCTCAGAGCTGGC	247868	80064	AGGCATCGAGCTACTCACAA	292455	124651	AAATGGGAGTTCCCCTGCAC
203282	35478	GCACCCCTTCTCAGAGCTGG	247869	80065	AAGGCATCGAGCTACTCACA	292456	124652	TAAATGGGAGTTCCCCTGCA
203283	35479	TGCACCCCTTCTCAGAGCTG	247870	80066	CAAGGCATCGAGCTACTCAC	292457	124653	ATAAATGGGAGTTCCCCTGC
203284	35480	ATGCACCCCTTCTCAGAGCT	247871	80067	CCAAGGCATCGAGCTACTCA	292458	124654	TATAAATGGGAGTTCCCCTG
203285	35481	TATGCACCCCTTCTCAGAGC	247872	80068	ACCAAGGCATCGAGCTACTC	292459	124655	TTATAAATGGGAGTTCCCCT
203286	35482	TTATGCACCCCTTCTCAGAG	247873	80069	CACCAAGGCATCGAGCTACT	292460	124656	TTTATAAATGGGAGTTCCCC
203287	35483	CTTATGCACCCCTTCTCAGA	247874	80070	GCACCAAGGCATCGAGCTAC	292461	124657	TTTTATAAATGGGAGTTCCC
203288	35484	GCTTATGCACCCCTTCTCAG	247875	80071	AGCACCAAGGCATCGAGCTA	292462	124658	GTTTTATAAATGGGAGTTCC
203289	35485	GGCTTATGCACCCCTTCTCA	247876	80072	GAGCACCAAGGCATCGAGCT	292463	124659	GGTTTTATAAATGGGAGTTC
203290	35486	GGGCTTATGCACCCCTTCTC	247877	80073	TGAGCACCAAGGCATCGAGC	292464	124660	TGGTTTTATAAATGGGAGTT
203291	35487	GGGGCTTATGCACCCCTTCT	247878	80074	CTGAGCACCAAGGCATCGAG	292465	124661	ATGGTTTTATAAATGGGAGT
203292	35488	TGGGGCTTATGCACCCCTTC	247879	80075	ACTGAGCACCAAGGCATCGA	292466	124662	GATGGTTTTATAAATGGGAG
203293	35489	GTGGGGCTTATGCACCCCTT	247880	80076	AACTGAGCACCAAGGCATCG	292467	124663	TGATGGTTTTATAAATGGGA
203294	35490	GGTGGGGCTTATGCACCCCT	247881	80077	TAACTGAGCACCAAGGCATC	292468	124664	CTGATGGTTTTATAAATGGG
203295	35491	TGGTGGGGCTTATGCACCCC	247882	80078	GTAACTGAGCACCAAGGCAT	292469	124665	TCTGATGGTTTTATAAATGG
203296	35492	ATGGTGGGGCTTATGCACCC	247883	80079	GGTAACTGAGCACCAAGGCA	292470	124666	GTCTGATGGTTTTATAAATG
203297	35493	CATGGTGGGGCTTATGCACC	247884	80080	AGGTAACTGAGCACCAAGGC	292471	124667	GGTCTGATGGTTTTATAAAT
203298	35494	GCATGGTGGGGCTTATGCAC	247885	80081	GAGGTAACTGAGCACCAAGG	292472	124668	AGGTCTGATGGTTTTATAAA

203299	35495	AGCATGGTGGGGCTTATGCA	247886	80082	GGAGGTAACTGAGCACCAAG	292473	124669	GAGGTCTGATGGTTTTATAA
203300	35496	AAGCATGGTGGGGCTTATGC	247887	80083	GGGAGGTAACTGAGCACCAA	292474	124670	TGAGGTCTGATGGTTTTATA
203301	35497	AAAGCATGGTGGGGCTTATG	247888	80084	AGGGAGGTAACTGAGCACCA	292475	124671	ATGAGGTCTGATGGTTTTAT
203302	35498	CAAAGCATGGTGGGGCTTAT	247889	80085	CAGGGAGGTAACTGAGCACC	292476	124672	CATGAGGTCTGATGGTTTTA
203303	35499	CCAAAGCATGGTGGGGCTTA	247890	80086	CCAGGGAGGTAACTGAGCAC	292477	124673	TCATGAGGTCTGATGGTTTT
203304	35500	GCCAAAGCATGGTGGGGCTT	247891	80087	GCCAGGGAGGTAACTGAGCA	292478	124674	CTCATGAGGTCTGATGGTTT
203305	35501	AGCCAAAGCATGGTGGGGCT	247892	80088	AGCCAGGGAGGTAACTGAGC	292479	124675	TCTCATGAGGTCTGATGGTT
203306	35502	GAGCCAAAGCATGGTGGGGC	247893	80089	CAGCCAGGGAGGTAACTGAG	292480	124676	ATCTCATGAGGTCTGATGGT
203307	35503	AGAGCCAAAGCATGGTGGGG	247894	80090	GCAGCCAGGGAGGTAACTGA	292481	124677	AATCTCATGAGGTCTGATGG
203308	35504	CAGAGCCAAAGCATGGTGGG	247895	80091	GGCAGCCAGGGAGGTAACTG	292482	124678	AAATCTCATGAGGTCTGATG
203309	35505	ACAGAGCCAAAGCATGGTGG	247896	80092	AGGCAGCCAGGGAGGTAACT	292483	124679	TAAATCTCATGAGGTCTGAT
203310	35506	GACAGAGCCAAAGCATGGTG	247897	80093	CAGGCAGCCAGGGAGGTAAC	292484	124680	ATAAATCTCATGAGGTCTGA
203311	35507	GGACAGAGCCAAAGCATGGT	247898	80094	GCAGGCAGCCAGGGAGGTAA	292485	124681	AATAAATCTCATGAGGTCTG
203312	35508	GGGACAGAGCCAAAGCATGG	247899	80095	GGCAGGCAGCCAGGGAGGTA	292486	124682	GAATAAATCTCATGAGGTCT
203313	35509	AGGGACAGAGCCAAAGCATG	247900	80096	TGGCAGGCAGCCAGGGAGGT	292487	124683	TGAATAAATCTCATGAGGTC
203314	35510	TAGGGACAGAGCCAAAGCAT	247901	80097	CTGGCAGGCAGCCAGGGAGG	292488	124684	GTGAATAAATCTCATGAGGT
203315	35511	ATAGGGACAGAGCCAAAGCA	247902	80098	GCTGGCAGGCAGCCAGGGAG	292489	124685	AGTGAATAAATCTCATGAGG
203316	35512	TATAGGGACAGAGCCAAAGC	247903	80099	GGCTGGCAGGCAGCCAGGGA	292490	124686	TAGTGAATAAATCTCATGAG
203317	35513	CTATAGGGACAGAGCCAAAG	247904	80100	AGGCTGGCAGGCAGCCAGGG	292491	124687	ATAGTGAATAAATCTCATGA
203318	35514	TCTATAGGGACAGAGCCAAA	247905	80101	GAGGCTGGCAGGCAGCCAGG	292492	124688	GATAGTGAATAAATCTCATG
203319	35515	TTCTATAGGGACAGAGCCAA	247906	80102	AGAGGCTGGCAGGCAGCCAG	292493	124689	TGATAGTGAATAAATCTCAT
203320	35516	ATTCTATAGGGACAGAGCCA	247907	80103	GAGAGGCTGGCAGGCAGCCA	292494	124690	ATGATAGTGAATAAATCTCA
203321	35517	TATTCTATAGGGACAGAGCC	247908	80104	TGAGAGGCTGGCAGGCAGCC	292495	124691	CATGATAGTGAATAAATCTC
203322	35518	ATATTCTATAGGGACAGAGC	247909	80105	CTGAGAGGCTGGCAGGCAGC	292496	124692	TCATGATAGTGAATAAATCT
203323	35519	AATATTCTATAGGGACAGAG	247910	80106	TCTGAGAGGCTGGCAGGCAG	292497	124693	CTCATGATAGTGAATAAATC
203324	35520	AAATATTCTATAGGGACAGA	247911	80107	CTCTGAGAGGCTGGCAGGCA	292498	124694	TCTCATGATAGTGAATAAAT
203325	35521	AAAATATTCTATAGGGACAG	247912	80108	GCTCTGAGAGGCTGGCAGGC	292499	124695	TTCTCATGATAGTGAATAAA
203326	35522	TAAAATATTCTATAGGGACA	247913	80109	TGCTCTGAGAGGCTGGCAGG	292500	124696	GTTCTCATGATAGTGAATAA
203327	35523	ATAAAATATTCTATAGGGAC	247914	80110	ATGCTCTGAGAGGCTGGCAG	292501	124697	TGTTCTCATGATAGTGAATA
203328	35524	CATAAAATATTCTATAGGGA	247915	80111	AATGCTCTGAGAGGCTGGCA	292502	124698	CTGTTCTCATGATAGTGAAT
203329	35525	ACATAAAATATTCTATAGGG	247916	80112	AAATGCTCTGAGAGGCTGGC	292503	124699	GCTGTTCTCATGATAGTGAA
203330	35526	AACATAAAATATTCTATAGG	247917	80113	TAAATGCTCTGAGAGGCTGG	292504	124700	TGCTGTTCTCATGATAGTGA
203331	35527	CAACATAAAATATTCTATAG	247918	80114	CTAAATGCTCTGAGAGGCTG	292505	124701	ATGCTGTTCTCATGATAGTG
203332	35528	ACAACATAAAATATTCTATA	247919	80115	CCTAAATGCTCTGAGAGGCT	292506	124702	CATGCTGTTCTCATGATAGT
203333	35529	AACAACATAAAATATTCTAT	247920	80116	CCCTAAATGCTCTGAGAGGC	292507	124703	CCATGCTGTTCTCATGATAG
203334	35530	TAACAACATAAAATATTCTA	247921	80117	GCCCTAAATGCTCTGAGAGG	292508	124704	CCCATGCTGTTCTCATGATA
203335	35531	GTAACAACATAAAATATTCT	247922	80118	GGCCCTAAATGCTCTGAGAG	292509	124705	TCCCATGCTGTTCTCATGAT
203336	35532	AGTAACAACATAAAATATTC	247923	80119	AGGCCCTAAATGCTCTGAGA	292510	124706	TTCCCATGCTGTTCTCATGA
203337	35533	CAGTAACAACATAAAATATT	247924	80120	AAGGCCCTAAATGCTCTGAG	292511	124707	TTTCCCATGCTGTTCTCATG
203338	35534	TCAGTAACAACATAAAATAT	247925	80121	GAAGGCCCTAAATGCTCTGA	292512	124708	CTTTCCCATGCTGTTCTCAT
203339	35535	TTCAGTAACAACATAAAATA	247926	80122	AGAAGGCCCTAAATGCTCTG	292513	124709	TCTTTCCCATGCTGTTCTCA
203340	35536	TTTCAGTAACAACATAAAAT	247927	80123	CAGAAGGCCCTAAATGCTCT	292514	124710	GTCTTTCCCATGCTGTTCTC
203341	35537	TTTTCAGTAACAACATAAAA	247928	80124	CCAGAAGGCCCTAAATGCTC	292515	124711	GGTCTTTCCCATGCTGTTCT
203342	35538	GTTTTCAGTAACAACATAAA	247929	80125	TCCAGAAGGCCCTAAATGCT	292516	124712	GGGTCTTTCCCATGCTGTTC
203343	35539	AGTTTTCAGTAACAACATAA	247930	80126	GTCCAGAAGGCCCTAAATGC	292517	124713	CGGGTCTTTCCCATGCTGTT
203344	35540	TAGTTTTCAGTAACAACATA	247931	80127	AGTCCAGAAGGCCCTAAATG	292518	124714	GCGGGTCTTTCCCATGCTGT
203345	35541	TTAGTTTTCAGTAACAACAT	247932	80128	AAGTCCAGAAGGCCCTAAAT	292519	124715	GGCGGGTCTTTCCCATGCTG
203346	35542	TTTAGTTTTCAGTAACAACA	247933	80129	GAAGTCCAGAAGGCCCTAAA	292520	124716	GGGCGGGTCTTTCCCATGCT
203347	35543	CTTTAGTTTTCAGTAACAAC	247934	80130	AGAAGTCCAGAAGGCCCTAA	292521	124717	GGGGCGGGTCTTTCCCATGC
203348	35544	CCTTTAGTTTTCAGTAACAA	247935	80131	TAGAAGTCCAGAAGGCCCTA	292522	124718	GGGGGCGGGTCTTTCCCATG
203349	35545	TCCTTTAGTTTTCAGTAACA	247936	80132	CTAGAAGTCCAGAAGGCCCT	292523	124719	TGGGGGCGGGTCTTTCCCAT
203350	35546	TTCCTTTAGTTTTCAGTAAC	247937	80133	TCTAGAAGTCCAGAAGGCCC	292524	124720	ATGGGGGCGGGTCTTTCCCA
203351	35547	CTTCCTTTAGTTTTCAGTAA	247938	80134	ATCTAGAAGTCCAGAAGGCC	292525	124721	CATGGGGGCGGGTCTTTCCC
203352	35548	TCTTCCTTTAGTTTTCAGTA	247939	80135	CATCTAGAAGTCCAGAAGGC	292526	124722	TCATGGGGGCGGGTCTTTCC
203353	35549	ATCTTCCTTTAGTTTTCAGT	247940	80136	GCATCTAGAAGTCCAGAAGG	292527	124723	ATCATGGGGGCGGGTCTTTC
203354	35550	CATCTTCCTTTAGTTTTCAG	247941	80137	AGCATCTAGAAGTCCAGAAG	292528	124724	AATCATGGGGGCGGGTCTTT
203355	35551	CCATCTTCCTTTAGTTTTCA	247942	80138	GAGCATCTAGAAGTCCAGAA	292529	124725	GAATCATGGGGGCGGGTCTT
203356	35552	CCCATCTTCCTTTAGTTTTC	247943	80139	GGAGCATCTAGAAGTCCAGA	292530	124726	TGAATCATGGGGGCGGGTCT
203357	35553	ACCCATCTTCCTTTAGTTTT	247944	80140	AGGAGCATCTAGAAGTCCAG	292531	124727	CTGAATCATGGGGGCGGGTC
203358	35554	CACCCATCTTCCTTTAGTTT	247945	80141	GAGGAGCATCTAGAAGTCCA	292532	124728	ACTGAATCATGGGGGCGGGT
203359	35555	GCACCCATCTTCCTTTAGTT	247946	80142	TGAGGAGCATCTAGAAGTCC	292533	124729	AACTGAATCATGGGGGCGGG
203360	35556	CGCACCCATCTTCCTTTAGT	247947	80143	ATGAGGAGCATCTAGAAGTC	292534	124730	TAACTGAATCATGGGGGCGG
203361	35557	CCGCACCCATCTTCCTTTAG	247948	80144	GATGAGGAGCATCTAGAAGT	292535	124731	GTAACTGAATCATGGGGGCG
203362	35558	ACCGCACCCATCTTCCTTTA	247949	80145	AGATGAGGAGCATCTAGAAG	292536	124732	GGTAACTGAATCATGGGGGC
203363	35559	CACCGCACCCATCTTCCTTT	247950	80146	AAGATGAGGAGCATCTAGAA	292537	124733	AGGTAACTGAATCATGGGGG
203364	35560	CCACCGCACCCATCTTCCTT	247951	80147	CAAGATGAGGAGCATCTAGA	292538	124734	GAGGTAACTGAATCATGGGG
203365	35561	GCCACCGCACCCATCTTCCT	247952	80148	GCAAGATGAGGAGCATCTAG	292539	124735	GGAGGTAACTGAATCATGGG
203366	35562	AGCCACCGCACCCATCTTCC	247953	80149	GGCAAGATGAGGAGCATCTA	292540	124736	GGGAGGTAACTGAATCATGG
203367	35563	GAGCCACCGCACCCATCTTC	247954	80150	AGGCAAGATGAGGAGCATCT	292541	124737	TGGGAGGTAACTGAATCATG
203368	35564	TGAGCCACCGCACCCATCTT	247955	80151	GAGGCAAGATGAGGAGCATC	292542	124738	GTGGGAGGTAACTGAATCAT
203369	35565	ATGAGCCACCGCACCCATCT	247956	80152	TGAGGCAAGATGAGGAGCAT	292543	124739	AGTGGGAGGTAACTGAATCA
203370	35566	CATGAGCCACCGCACCCATC	247957	80153	CTGAGGCAAGATGAGGAGCA	292544	124740	CAGTGGGAGGTAACTGAATC

203371	35567	GCATGAGCCACCGCACCCAT	247958	80154	ACTGAGGCAAGATGAGGAGC	292545	124741	CCAGTGGGAGGTAACTGAAT
203372	35568	GGCATGAGCCACCGCACCCA	247959	80155	GACTGAGGCAAGATGAGGAG	292546	124742	CCCAGTGGGAGGTAACTGAA
203373	35569	AGGCATGAGCCACCGCACCC	247960	80156	TGACTGAGGCAAGATGAGGA	292547	124743	ACCCAGTGGGAGGTAACTGA
203374	35570	CAGGCATGAGCCACCGCACC	247961	80157	CTGACTGAGGCAAGATGAGG	292548	124744	GACCCAGTGGGAGGTAACTG
203375	35571	ACAGGCATGAGCCACCGCAC	247962	80158	GCTGACTGAGGCAAGATGAG	292549	124745	GGACCCAGTGGGAGGTAACT
203376	35572	TACAGGCATGAGCCACCGCA	247963	80159	CGCTGACTGAGGCAAGATGA	292550	124746	GGGACCCAGTGGGAGGTAAC
203377	35573	TTACAGGCATGAGCCACCGC	247964	80160	GCGCTGACTGAGGCAAGATG	292551	124747	AGGGACCCAGTGGGAGGTAA
203378	35574	ATTACAGGCATGAGCCACCG	247965	80161	CGCGCTGACTGAGGCAAGAT	292552	124748	GAGGGACCCAGTGGGAGGTA
203379	35575	GATTACAGGCATGAGCCACC	247966	80162	ACGCGCTGACTGAGGCAAGA	292553	124749	GGAGGGACCCAGTGGGAGGT
203380	35576	GGATTACAGGCATGAGCCAC	247967	80163	GACGCGCTGACTGAGGCAAG	292554	124750	GGGAGGGACCCAGTGGGAGG
203381	35577	GGGATTACAGGCATGAGCCA	247968	80164	TGACGCGCTGACTGAGGCAA	292555	124751	TGGGAGGGACCCAGTGGGAG
203382	35578	TGGGATTACAGGCATGAGCC	247969	80165	CTGACGCGCTGACTGAGGCA	292556	124752	ATGGGAGGGACCCAGTGGGA
203383	35579	CTGGGATTACAGGCATGAGC	247970	80166	ACTGACGCGCTGACTGAGGC	292557	124753	CATGGGAGGGACCCAGTGGG
203384	35580	GCTGGGATTACAGGCATGAG	247971	80167	AACTGACGCGCTGACTGAGG	292558	124754	TCATGGGAGGGACCCAGTGG
203385	35581	TGCTGGGATTACAGGCATGA	247972	80168	GAACTGACGCGCTGACTGAG	292559	124755	GTCATGGGAGGGACCCAGTG
203386	35582	GTGCTGGGATTACAGGCATG	247973	80169	GGAACTGACGCGCTGACTGA	292560	124756	TGTCATGGGAGGGACCCAGT
203387	35583	AGTGCTGGGATTACAGGCAT	247974	80170	TGGAACTGACGCGCTGACTG	292561	124757	GTGTCATGGGAGGGACCCAG
203388	35584	AAGTGCTGGGATTACAGGCA	247975	80171	CTGGAACTGACGCGCTGACT	292562	124758	TGTGTCATGGGAGGGACCCA
203389	35585	AAAGTGCTGGGATTACAGGC	247976	80172	TCTGGAACTGACGCGCTGAC	292563	124759	ATGTGTCATGGGAGGGACCC
203390	35586	CAAAGTGCTGGGATTACAGG	247977	80173	CTCTGGAACTGACGCGCTGA	292564	124760	CATGTGTCATGGGAGGGACC
203391	35587	CCAAAGTGCTGGGATTACAG	247978	80174	TCTCTGGAACTGACGCGCTG	292565	124761	CCATGTGTCATGGGAGGGAC
203392	35588	CCCAAAGTGCTGGGATTACA	247979	80175	GTCTCTGGAACTGACGCGCT	292566	124762	TCCATGTGTCATGGGAGGGA
203393	35589	TCCCAAAGTGCTGGGATTAC	247980	80176	AGTCTCTGGAACTGACGCGC	292567	124763	TTCCATGTGTCATGGGAGGG
203394	35590	CTCCCAAAGTGCTGGGATTA	247981	80177	AAGTCTCTGGAACTGACGCG	292568	124764	ATTCCATGTGTCATGGGAGG
203395	35591	CCTCCCAAAGTGCTGGGATT	247982	80178	GAAGTCTCTGGAACTGACGC	292569	124765	AATTCCATGTGTCATGGGAG
203396	35592	GCCTCCCAAAGTGCTGGGAT	247983	80179	AGAAGTCTCTGGAACTGACG	292570	124766	TAATTCCATGTGTCATGGGA
203397	35593	GGCCTCCCAAAGTGCTGGGA	247984	80180	GAGAAGTCTCTGGAACTGAC	292571	124767	ATAATTCCATGTGTCATGGG
203398	35594	TGGCCTCCCAAAGTGCTGGG	247985	80181	AGAGAAGTCTCTGGAACTGA	292572	124768	CATAATTCCATGTGTCATGG
203399	35595	TTGGCCTCCCAAAGTGCTGG	247986	80182	CAGAGAAGTCTCTGGAACTG	292573	124769	CCATAATTCCATGTGTCATG
203400	35596	CTTGGCCTCCCAAAGTGCTG	247987	80183	GCAGAGAAGTCTCTGGAACT	292574	124770	CCCATAATTCCATGTGTCAT
203401	35597	TCTTGGCCTCCCAAAGTGCT	247988	80184	TGCAGAGAAGTCTCTGGAAC	292575	124771	TCCCATAATTCCATGTGTCA
203402	35598	GTCTTGGCCTCCCAAAGTGC	247989	80185	CTGCAGAGAAGTCTCTGGAA	292576	124772	CTCCCATAATTCCATGTGTC
203403	35599	TGTCTTGGCCTCCCAAAGTG	247990	80186	CCTGCAGAGAAGTCTCTGGA	292577	124773	GCTCCCATAATTCCATGTGT
203404	35600	CTGTCTTGGCCTCCCAAAGT	247991	80187	CCCTGCAGAGAAGTCTCTGG	292578	124774	AGCTCCCATAATTCCATGTG
203405	35601	TCTGTCTTGGCCTCCCAAAG	247992	80188	ACCCTGCAGAGAAGTCTCTG	292579	124775	TAGCTCCCATAATTCCATGT
203406	35602	ATCTGTCTTGGCCTCCCAAA	247993	80189	AACCCTGCAGAGAAGTCTCT	292580	124776	GTAGCTCCCATAATTCCATG
203407	35603	AATCTGTCTTGGCCTCCCAA	247994	80190	AAACCCTGCAGAGAAGTCTC	292581	124777	TGTAGCTCCCATAATTCCAT
203408	35604	CAATCTGTCTTGGCCTCCCA	247995	80191	AAAACCCTGCAGAGAAGTCT	292582	124778	TTGTAGCTCCCATAATTCCA
203409	35605	TCAATCTGTCTTGGCCTCCC	247996	80192	GAAAACCCTGCAGAGAAGTC	292583	124779	ATTGTAGCTCCCATAATTCC
203410	35606	ATCAATCTGTCTTGGCCTCC	247997	80193	AGAAAACCCTGCAGAGAAGT	292584	124780	AATTGTAGCTCCCATAATTC
203411	35607	GATCAATCTGTCTTGGCCTC	247998	80194	CAGAAAACCCTGCAGAGAAG	292585	124781	GAATTGTAGCTCCCATAATT
203412	35608	TGATCAATCTGTCTTGGCCT	247999	80195	CCAGAAAACCCTGCAGAGAA	292586	124782	TGAATTGTAGCTCCCATAAT
203413	35609	GTGATCAATCTGTCTTGGCC	248000	80196	CCCAGAAAACCCTGCAGAGA	292587	124783	TTGAATTGTAGCTCCCATAA
203414	35610	AGTGATCAATCTGTCTTGGC	248001	80197	CCCCAGAAAACCCTGCAGAG	292588	124784	CTTGAATTGTAGCTCCCATA
203415	35611	GAGTGATCAATCTGTCTTGG	248002	80198	GCCCCAGAAAACCCTGCAGA	292589	124785	TCTTGAATTGTAGCTCCCAT
203416	35612	CGAGTGATCAATCTGTCTTG	248003	80199	TGCCCCAGAAAACCCTGCAG	292590	124786	ATCTTGAATTGTAGCTCCCA
203417	35613	TCGAGTGATCAATCTGTCTT	248004	80200	CTGCCCCAGAAAACCCTGCA	292591	124787	CATCTTGAATTGTAGCTCCC
203418	35614	ATCGAGTGATCAATCTGTCT	248005	80201	CCTGCCCCAGAAAACCCTGC	292592	124788	TCATCTTGAATTGTAGCTCC
203419	35615	CATCGAGTGATCAATCTGTC	248006	80202	ACCTGCCCCAGAAAACCCTG	292593	124789	CTCATCTTGAATTGTAGCTC
203420	35616	GCATCGAGTGATCAATCTGT	248007	80203	CACCTGCCCCAGAAAACCCT	292594	124790	TCTCATCTTGAATTGTAGCT
203421	35617	GGCATCGAGTGATCAATCTG	248008	80204	CCACCTGCCCCAGAAAACCC	292595	124791	ATCTCATCTTGAATTGTAGC
203422	35618	TGGCATCGAGTGATCAATCT	248009	80205	ACCACCTGCCCCAGAAAACC	292596	124792	AATCTCATCTTGAATTGTAG
203423	35619	CTGGCATCGAGTGATCAATC	248010	80206	CACCACCTGCCCCAGAAAAC	292597	124793	AAATCTCATCTTGAATTGTA
203424	35620	CCTGGCATCGAGTGATCAAT	248011	80207	CCACCACCTGCCCCAGAAAA	292598	124794	CAAATCTCATCTTGAATTGT
203425	35621	TCCTGGCATCGAGTGATCAA	248012	80208	GCCACCACCTGCCCCAGAAA	292599	124795	CCAAATCTCATCTTGAATTG
203426	35622	CTCCTGGCATCGAGTGATCA	248013	80209	TGCCACCACCTGCCCCAGAA	292600	124796	CCCAAATCTCATCTTGAATT
203427	35623	ACTCCTGGCATCGAGTGATC	248014	80210	CTGCCACCACCTGCCCCAGA	292601	124797	ACCCAAATCTCATCTTGAAT
203428	35624	AACTCCTGGCATCGAGTGAT	248015	80211	TCTGCCACCACCTGCCCCAG	292602	124798	CACCCAAATCTCATCTTGAA
203429	35625	GAACTCCTGGCATCGAGTGA	248016	80212	GTCTGCCACCACCTGCCCCA	292603	124799	CCACCCAAATCTCATCTTGA
203430	35626	TGAACTCCTGGCATCGAGTG	248017	80213	GGTCTGCCACCACCTGCCCC	292604	124800	CCCACCCAAATCTCATCTTG
203431	35627	TTGAACTCCTGGCATCGAGT	248018	80214	GGGTCTGCCACCACCTGCCC	292605	124801	CCCCACCCAAATCTCATCTT
203432	35628	CTTGAACTCCTGGCATCGAG	248019	80215	CGGGTCTGCCACCACCTGCC	292606	124802	TCCCCACCCAAATCTCATCT
203433	35629	TCTTGAACTCCTGGCATCGA	248020	80216	ACGGGTCTGCCACCACCTGC	292607	124803	GTCCCCACCCAAATCTCATC
203434	35630	GTCTTGAACTCCTGGCATCG	248021	80217	CACGGGTCTGCCACCACCTG	292608	124804	TGTCCCCACCCAAATCTCAT
203435	35631	GGTCTTGAACTCCTGGCATC	248022	80218	GCACGGGTCTGCCACCACCT	292609	124805	GTGTCCCCACCCAAATCTCA
203436	35632	TGGTCTTGAACTCCTGGCAT	248023	80219	GGCACGGGTCTGCCACCACC	292610	124806	TGTGTCCCCACCCAAATCTC
203437	35633	CTGGTCTTGAACTCCTGGCA	248024	80220	AGGCACGGGTCTGCCACCAC	292611	124807	CTGTGTCCCCACCCAAATCT
203438	35634	GCTGGTCTTGAACTCCTGGC	248025	80221	AAGGCACGGGTCTGCCACCA	292612	124808	GCTGTGTCCCCACCCAAATC
203439	35635	GGCTGGTCTTGAACTCCTGG	248026	80222	GAAGGCACGGGTCTGCCACC	292613	124809	GGCTGTGTCCCCACCCAAAT
203440	35636	AGGCTGGTCTTGAACTCCTG	248027	80223	AGAAGGCACGGGTCTGCCAC	292614	124810	TGGCTGTGTCCCCACCCAAA
203441	35637	CAGGCTGGTCTTGAACTCCT	248028	80224	AAGAAGGCACGGGTCTGCCA	292615	124811	TTGGCTGTGTCCCCACCCAA
203442	35638	CCAGGCTGGTCTTGAACTCC	248029	80225	CAAGAAGGCACGGGTCTGCC	292616	124812	TTTGGCTGTGTCCCCACCCA

203443	35639	GCCAGGCTGGTCTTGAACTC	248030	80226	TCAAGAAGGCACGGGTCTGC	292617	124813	GTTTGGCTGTGTCCCCACCC
203444	35640	GGCCAGGCTGGTCTTGAACT	248031	80227	GTCAAGAAGGCACGGGTCTG	292618	124814	GGTTTGGCTGTGTCCCCACC
203445	35641	TGGCCAGGCTGGTCTTGAAC	248032	80228	TGTCAAGAAGGCACGGGTCT	292619	124815	TGGTTTGGCTGTGTCCCCAC
203446	35642	TTGGCCAGGCTGGTCTTGAA	248033	80229	GTGTCAAGAAGGCACGGGTC	292620	124816	ATGGTTTGGCTGTGTCCCCA
203447	35643	GTTGGCCAGGCTGGTCTTGA	248034	80230	GGTGTCAAGAAGGCACGGGT	292621	124817	TATGGTTTGGCTGTGTCCCC
203448	35644	TGTTGGCCAGGCTGGTCTTG	248035	80231	AGGTGTCAAGAAGGCACGGG	292622	124818	ATATGGTTTGGCTGTGTCCC
203449	35645	ATGTTGGCCAGGCTGGTCTT	248036	80232	CAGGTGTCAAGAAGGCACGG	292623	124819	GATATGGTTTGGCTGTGTCC
203450	35646	CATGTTGGCCAGGCTGGTCT	248037	80233	TCAGGTGTCAAGAAGGCACG	292624	124820	TGATATGGTTTGGCTGTGTC
203451	35647	CCATGTTGGCCAGGCTGGTC	248038	80234	CTCAGGTGTCAAGAAGGCAC	292625	124821	CTGATATGGTTTGGCTGTGT
203452	35648	ACCATGTTGGCCAGGCTGGT	248039	80235	CCTCAGGTGTCAAGAAGGCA	292626	124822	ACTGATATGGTTTGGCTGTG
203453	35649	CACCATGTTGGCCAGGCTGG	248040	80236	ACCTCAGGTGTCAAGAAGGC	292627	124823	GACTGATATGGTTTGGCTGT
203454	35650	TCACCATGTTGGCCAGGCTG	248041	80237	GACCTCAGGTGTCAAGAAGG	292628	124824	AGACTGATATGGTTTGGCTG
203455	35651	TTCACCATGTTGGCCAGGCT	248042	80238	TGACCTCAGGTGTCAAGAAG	292629	124825	GAGACTGATATGGTTTGGCT
203456	35652	TTTCACCATGTTGGCCAGGC	248043	80239	CTGACCTCAGGTGTCAAGAA	292630	124826	GGAGACTGATATGGTTTGGC
203457	35653	GTTTCACCATGTTGGCCAGG	248044	80240	ACTGACCTCAGGTGTCAAGA	292631	124827	GGGAGACTGATATGGTTTGG
203458	35654	GGTTTCACCATGTTGGCCAG	248045	80241	GACTGACCTCAGGTGTCAAG	292632	124828	AGGGAGACTGATATGGTTTG
203459	35655	AGGTTTCACCATGTTGGCCA	248046	80242	GGACTGACCTCAGGTGTCAA	292633	124829	GAGGGAGACTGATATGGTTT
203460	35656	AAGGTTTCACCATGTTGGCC	248047	80243	TGGACTGACCTCAGGTGTCA	292634	124830	AGAGGGAGACTGATATGGTT
203461	35657	CAAGGTTTCACCATGTTGGC	248048	80244	GTGGACTGACCTCAGGTGTC	292635	124831	CAGAGGGAGACTGATATGGT
203462	35658	ACAAGGTTTCACCATGTTGG	248049	80245	GGTGGACTGACCTCAGGTGT	292636	124832	ACAGAGGGAGACTGATATGG
203463	35659	GACAAGGTTTCACCATGTTG	248050	80246	GGGTGGACTGACCTCAGGTG	292637	124833	GACAGAGGGAGACTGATATG
203464	35660	AGACAAGGTTTCACCATGTT	248051	80247	AGGGTGGACTGACCTCAGGT	292638	124834	TGACAGAGGGAGACTGATAT
203465	35661	GAGACAAGGTTTCACCATGT	248052	80248	GAGGGTGGACTGACCTCAGG	292639	124835	ATGACAGAGGGAGACTGATA
203466	35662	AGAGACAAGGTTTCACCATG	248053	80249	GGAGGGTGGACTGACCTCAG	292640	124836	GATGACAGAGGGAGACTGAT
203467	35663	TAGAGACAAGGTTTCACCAT	248054	80250	AGGAGGGTGGACTGACCTCA	292641	124837	GGATGACAGAGGGAGACTGA
203468	35664	GTAGAGACAAGGTTTCACCA	248055	80251	CAGGAGGGTGGACTGACCTC	292642	124838	TGGATGACAGAGGGAGACTG
203469	35665	TGTAGAGACAAGGTTTCACC	248056	80252	GCAGGAGGGTGGACTGACCT	292643	124839	CTGGATGACAGAGGGAGACT
203470	35666	TTGTAGAGACAAGGTTTCAC	248057	80253	AGCAGGAGGGTGGACTGACC	292644	124840	CCTGGATGACAGAGGGAGAC
203471	35667	TTTGTAGAGACAAGGTTTCA	248058	80254	GAGCAGGAGGGTGGACTGAC	292645	124841	GCCTGGATGACAGAGGGAGA
203472	35668	TTTTGTAGAGACAAGGTTTC	248059	80255	TGAGCAGGAGGGTGGACTGA	292646	124842	AGCCTGGATGACAGAGGGAG
203473	35669	TTTTTGTAGAGACAAGGTTT	248060	80256	CTGAGCAGGAGGGTGGACTG	292647	124843	CAGCCTGGATGACAGAGGGA
203474	35670	GTTTTTGTAGAGACAAGGTT	248061	80257	TCTGAGCAGGAGGGTGGACT	292648	124844	CCAGCCTGGATGACAGAGGG
203475	35671	TGTTTTTGTAGAGACAAGGT	248062	80258	GTCTGAGCAGGAGGGTGGAC	292649	124845	TCCAGCCTGGATGACAGAGG
203476	35672	TTGTTTTTGTAGAGACAAGG	248063	80259	AGTCTGAGCAGGAGGGTGGA	292650	124846	CTCCAGCCTGGATGACAGAG
203477	35673	TTTGTTTTTGTAGAGACAAG	248064	80260	CAGTCTGAGCAGGAGGGTGG	292651	124847	ACTCCAGCCTGGATGACAGA
203478	35674	TTTTGTTTTTGTAGAGACAA	248065	80261	GCAGTCTGAGCAGGAGGGTG	292652	124848	CACTCCAGCCTGGATGACAG
203479	35675	GTTTTGTTTTTGTAGAGACA	248066	80262	GGCAGTCTGAGCAGGAGGGT	292653	124849	GCACTCCAGCCTGGATGACA
203480	35676	TGTTTTGTTTTTGTAGAGAC	248067	80263	GGGCAGTCTGAGCAGGAGGG	292654	124850	TGCACTCCAGCCTGGATGAC
203481	35677	TTGTTTTGTTTTTGTAGAGA	248068	80264	TGGGCAGTCTGAGCAGGAGG	292655	124851	GTGCACTCCAGCCTGGATGA
203482	35678	TTTGTTTTGTTTTTGTAGAG	248069	80265	CTGGGCAGTCTGAGCAGGAG	292656	124852	AGTGCACTCCAGCCTGGATG
203483	35679	TTTTGTTTTGTTTTTGTAGA	248070	80266	GCTGGGCAGTCTGAGCAGGA	292657	124853	CAGTGCACTCCAGCCTGGAT
203484	35680	GTTTTGTTTTGTTTTTGTAG	248071	80267	TGCTGGGCAGTCTGAGCAGG	292658	124854	CCAGTGCACTCCAGCCTGGA
203485	35681	TGTTTTGTTTTGTTTTTGTA	248072	80268	GTGCTGGGCAGTCTGAGCAG	292659	124855	GCCAGTGCACTCCAGCCTGG
203486	35682	TTGTTTTGTTTTGTTTTTGT	248073	80269	TGTGCTGGGCAGTCTGAGCA	292660	124856	TGCCAGTGCACTCCAGCCTG
203487	35683	TTTGTTTTGTTTTGTTTTTG	248074	80270	CTGTGCTGGGCAGTCTGAGC	292661	124857	ATGCCAGTGCACTCCAGCCT
203488	35684	TTTTGTTTTGTTTTGTTTTT	248075	80271	CCTGTGCTGGGCAGTCTGAG	292662	124858	CATGCCAGTGCACTCCAGCC
203489	35685	TTTTTGTTTTGTTTTGTTTT	248076	80272	CCCTGTGCTGGGCAGTCTGA	292663	124859	TCATGCCAGTGCACTCCAGC
203490	35686	ATTTTTGTTTTGTTTTGTTT	248077	80273	ACCCTGTGCTGGGCAGTCTG	292664	124860	ATCATGCCAGTGCACTCCAG
203491	35687	AATTTTTGTTTTGTTTTGTT	248078	80274	GACCCTGTGCTGGGCAGTCT	292665	124861	GATCATGCCAGTGCACTCCA
203492	35688	TAATTTTTGTTTTGTTTTGT	248079	80275	TGACCCTGTGCTGGGCAGTC	292666	124862	AGATCATGCCAGTGCACTCC
203493	35689	CTAATTTTTGTTTTGTTTTG	248080	80276	GTGACCCTGTGCTGGGCAGT	292667	124863	GAGATCATGCCAGTGCACTC
203494	35690	GCTAATTTTTGTTTTGTTTT	248081	80277	GGTGACCCTGTGCTGGGCAG	292668	124864	CGAGATCATGCCAGTGCACT
203495	35691	GGCTAATTTTTGTTTTGTTT	248082	80278	AGGTGACCCTGTGCTGGGCA	292669	124865	CCGAGATCATGCCAGTGCAC
203496	35692	CGGCTAATTTTTGTTTTGTT	248083	80279	GAGGTGACCCTGTGCTGGGC	292670	124866	GCCGAGATCATGCCAGTGCA
203497	35693	CCGGCTAATTTTTGTTTTGT	248084	80280	GGAGGTGACCCTGTGCTGGG	292671	124867	AGCCGAGATCATGCCAGTGC
203498	35694	CCCGGCTAATTTTTGTTTTG	248085	80281	GGGAGGTGACCCTGTGCTGG	292672	124868	GAGCCGAGATCATGCCAGTG
203499	35695	ACCCGGCTAATTTTTGTTTT	248086	80282	TGGGAGGTGACCCTGTGCTG	292673	124869	TGAGCCGAGATCATGCCAGT
203500	35696	TACCCGGCTAATTTTTGTTT	248087	80283	TTGGGAGGTGACCCTGTGCT	292674	124870	GTGAGCCGAGATCATGCCAG
203501	35697	ATACCCGGCTAATTTTTGTT	248088	80284	CTTGGGAGGTGACCCTGTGC	292675	124871	AGTGAGCCGAGATCATGCCA
203502	35698	CATACCCGGCTAATTTTTGT	248089	80285	CCTTGGGAGGTGACCCTGTG	292676	124872	CAGTGAGCCGAGATCATGCC
203503	35699	CCATACCCGGCTAATTTTTG	248090	80286	CCCTTGGGAGGTGACCCTGT	292677	124873	GCAGTGAGCCGAGATCATGC
203504	35700	ACCATACCCGGCTAATTTTT	248091	80287	CCCCTTGGGAGGTGACCCTG	292678	124874	TGCAGTGAGCCGAGATCATG
203505	35701	CACCATACCCGGCTAATTTT	248092	80288	ACCCCTTGGGAGGTGACCCT	292679	124875	CTGCAGTGAGCCGAGATCAT
203506	35702	CCACCATACCCGGCTAATTT	248093	80289	CACCCCTTGGGAGGTGACCC	292680	124876	GCTGCAGTGAGCCGAGATCA
203507	35703	GCCACCATACCCGGCTAATT	248094	80290	CCACCCCTTGGGAGGTGACC	292681	124877	GGCTGCAGTGAGCCGAGATC
203508	35704	TGCCACCATACCCGGCTAAT	248095	80291	TCCACCCCTTGGGAGGTGAC	292682	124878	AGGCTGCAGTGAGCCGAGAT
203509	35705	ATGCCACCATACCCGGCTAA	248096	80292	GTCCACCCCTTGGGAGGTGA	292683	124879	GAGGCTGCAGTGAGCCGAGA
203510	35706	CATGCCACCATACCCGGCTA	248097	80293	GGTCCACCCCTTGGGAGGTG	292684	124880	AGAGGCTGCAGTGAGCCGAG
203511	35707	GCATGCCACCATACCCGGCT	248098	80294	GGGTCCACCCCTTGGGAGGT	292685	124881	TAGAGGCTGCAGTGAGCCGA
203512	35708	TGCATGCCACCATACCCGGC	248099	80295	GGGGTCCACCCCTTGGGAGG	292686	124882	GTAGAGGCTGCAGTGAGCCG
203513	35709	GTGCATGCCACCATACCCGG	248100	80296	TGGGGTCCACCCCTTGGGAG	292687	124883	GGTAGAGGCTGCAGTGAGCC
203514	35710	GGTGCATGCCACCATACCCG	248101	80297	TTGGGGTCCACCCCTTGGGA	292688	124884	AGGTAGAGGCTGCAGTGAGC

203515	35711	AGGTGCATGCCACCATACCC	248102	80298	CTTGGGGTCCACCCCTTGGG	292689	124885	GAGGTAGAGGCTGCAGTGAG
203516	35712	CAGGTGCATGCCACCATACC	248103	80299	TCTTGGGGTCCACCCCTTGG	292690	124886	GGAGGTAGAGGCTGCAGTGA
203517	35713	ACAGGTGCATGCCACCATAC	248104	80300	ATCTTGGGGTCCACCCCTTG	292691	124887	GGGAGGTAGAGGCTGCAGTG
203518	35714	CACAGGTGCATGCCACCATA	248105	80301	GATCTTGGGGTCCACCCCTT	292692	124888	AGGGAGGTAGAGGCTGCAGT
203519	35715	CCACAGGTGCATGCCACCAT	248106	80302	TGATCTTGGGGTCCACCCCT	292693	124889	CAGGGAGGTAGAGGCTGCAG
203520	35716	ACCACAGGTGCATGCCACCA	248107	80303	GTGATCTTGGGGTCCACCCC	292694	124890	CCAGGGAGGTAGAGGCTGCA
203521	35717	TACCACAGGTGCATGCCACC	248108	80304	GGTGATCTTGGGGTCCACCC	292695	124891	CCCAGGGAGGTAGAGGCTGC
203522	35718	GTACCACAGGTGCATGCCAC	248109	80305	AGGTGATCTTGGGGTCCACC	292696	124892	ACCCAGGGAGGTAGAGGCTG
203523	35719	GGTACCACAGGTGCATGCCA	248110	80306	CAGGTGATCTTGGGGTCCAC	292697	124893	GACCCAGGGAGGTAGAGGCT
203524	35720	TGGTACCACAGGTGCATGCC	248111	80307	TCAGGTGATCTTGGGGTCCA	292698	124894	TGACCCAGGGAGGTAGAGGC
203525	35721	CTGGTACCACAGGTGCATGC	248112	80308	CTCAGGTGATCTTGGGGTCC	292699	124895	CTGACCCAGGGAGGTAGAGG
203526	35722	GCTGGTACCACAGGTGCATG	248113	80309	GCTCAGGTGATCTTGGGGTC	292700	124896	CCTGACCCAGGGAGGTAGAG
203527	35723	AGCTGGTACCACAGGTGCAT	248114	80310	CGCTCAGGTGATCTTGGGGT	292701	124897	ACCTGACCCAGGGAGGTAGA
203528	35724	TAGCTGGTACCACAGGTGCA	248115	80311	GCGCTCAGGTGATCTTGGGG	292702	124898	CACCTGACCCAGGGAGGTAG
203529	35725	GTAGCTGGTACCACAGGTGC	248116	80312	TGCGCTCAGGTGATCTTGGG	292703	124899	TCACCTGACCCAGGGAGGTA
203530	35726	AGTAGCTGGTACCACAGGTG	248117	80313	GTGCGCTCAGGTGATCTTGG	292704	124900	ATCACCTGACCCAGGGAGGT
203531	35727	GAGTAGCTGGTACCACAGGT	248118	80314	TGTGCGCTCAGGTGATCTTG	292705	124901	GATCACCTGACCCAGGGAGG
203532	35728	TGAGTAGCTGGTACCACAGG	248119	80315	CTGTGCGCTCAGGTGATCTT	292706	124902	AGATCACCTGACCCAGGGAG
203533	35729	TTGAGTAGCTGGTACCACAG	248120	80316	TCTGTGCGCTCAGGTGATCT	292707	124903	AAGATCACCTGACCCAGGGA
203534	35730	CTTGAGTAGCTGGTACCACA	248121	80317	CTCTGTGCGCTCAGGTGATC	292708	124904	GAAGATCACCTGACCCAGGG
203535	35731	TCTTGAGTAGCTGGTACCAC	248122	80318	CCTCTGTGCGCTCAGGTGAT	292709	124905	GGAAGATCACCTGACCCAGG
203536	35732	CTCTTGAGTAGCTGGTACCA	248123	80319	CCCTCTGTGCGCTCAGGTGA	292710	124906	GGGAAGATCACCTGACCCAG
203537	35733	CCTCTTGAGTAGCTGGTACC	248124	80320	ACCCTCTGTGCGCTCAGGTG	292711	124907	TGGGAAGATCACCTGACCCA
203538	35734	GCCTCTTGAGTAGCTGGTAC	248125	80321	CACCCTCTGTGCGCTCAGGT	292712	124908	GTGGGAAGATCACCTGACCC
203539	35735	AGCCTCTTGAGTAGCTGGTA	248126	80322	GCACCCTCTGTGCGCTCAGG	292713	124909	GGTGGGAAGATCACCTGACC
203540	35736	CAGCCTCTTGAGTAGCTGGT	248127	80323	TGCACCCTCTGTGCGCTCAG	292714	124910	AGGTGGGAAGATCACCTGAC
203541	35737	TCAGCCTCTTGAGTAGCTGG	248128	80324	CTGCACCCTCTGTGCGCTCA	292715	124911	GAGGTGGGAAGATCACCTGA
203542	35738	CTCAGCCTCTTGAGTAGCTG	248129	80325	TCTGCACCCTCTGTGCGCTC	292716	124912	TGAGGTGGGAAGATCACCTG
203543	35739	CCTCAGCCTCTTGAGTAGCT	248130	80326	ATCTGCACCCTCTGTGCGCT	292717	124913	CTGAGGTGGGAAGATCACCT
203544	35740	GCCTCAGCCTCTTGAGTAGC	248131	80327	CATCTGCACCCTCTGTGCGC	292718	124914	GCTGAGGTGGGAAGATCACC
203545	35741	TGCCTCAGCCTCTTGAGTAG	248132	80328	TCATCTGCACCCTCTGTGCG	292719	124915	GGCTGAGGTGGGAAGATCAC
203546	35742	GTGCCTCAGCCTCTTGAGTA	248133	80329	GTCATCTGCACCCTCTGTGC	292720	124916	AGGCTGAGGTGGGAAGATCA
203547	35743	TGTGCCTCAGCCTCTTGAGT	248134	80330	AGTCATCTGCACCCTCTGTG	292721	124917	GAGGCTGAGGTGGGAAGATC
203548	35744	TTGTGCCTCAGCCTCTTGAG	248135	80331	CAGTCATCTGCACCCTCTGT	292722	124918	GGAGGCTGAGGTGGGAAGAT
203549	35745	CTTGTGCCTCAGCCTCTTGA	248136	80332	CCAGTCATCTGCACCCTCTG	292723	124919	GGGAGGCTGAGGTGGGAAGA
203550	35746	TCTTGTGCCTCAGCCTCTTG	248137	80333	TCCAGTCATCTGCACCCTCT	292724	124920	TGGGAGGCTGAGGTGGGAAG
203551	35747	TTCTTGTGCCTCAGCCTCTT	248138	80334	GTCCAGTCATCTGCACCCTC	292725	124921	CTGGGAGGCTGAGGTGGGAA
203552	35748	ATTCTTGTGCCTCAGCCTCT	248139	80335	GGTCCAGTCATCTGCACCCT	292726	124922	CCTGGGAGGCTGAGGTGGGA
203553	35749	GATTCTTGTGCCTCAGCCTC	248140	80336	TGGTCCAGTCATCTGCACCC	292727	124923	ACCTGGGAGGCTGAGGTGGG
203554	35750	AGATTCTTGTGCCTCAGCCT	248141	80337	GTGGTCCAGTCATCTGCACC	292728	124924	TACCTGGGAGGCTGAGGTGG
203555	35751	GAGATTCTTGTGCCTCAGCC	248142	80338	TGTGGTCCAGTCATCTGCAC	292729	124925	CTACCTGGGAGGCTGAGGTG
203556	35752	AGAGATTCTTGTGCCTCAGC	248143	80339	GTGTGGTCCAGTCATCTGCA	292730	124926	GCTACCTGGGAGGCTGAGGT
203557	35753	AAGAGATTCTTGTGCCTCAG	248144	80340	GGTGTGGTCCAGTCATCTGC	292731	124927	AGCTACCTGGGAGGCTGAGG
203558	35754	CAAGAGATTCTTGTGCCTCA	248145	80341	AGGTGTGGTCCAGTCATCTG	292732	124928	CAGCTACCTGGGAGGCTGAG
203559	35755	TCAAGAGATTCTTGTGCCTC	248146	80342	AAGGTGTGGTCCAGTCATCT	292733	124929	CCAGCTACCTGGGAGGCTGA
203560	35756	TTCAAGAGATTCTTGTGCCT	248147	80343	AAAGGTGTGGTCCAGTCATC	292734	124930	TCCAGCTACCTGGGAGGCTG
203561	35757	GTTCAAGAGATTCTTGTGCC	248148	80344	AAAAGGTGTGGTCCAGTCAT	292735	124931	TTCCAGCTACCTGGGAGGCT
203562	35758	GGTTCAAGAGATTCTTGTGC	248149	80345	CAAAAGGTGTGGTCCAGTCA	292736	124932	GTTCCAGCTACCTGGGAGGC
203563	35759	AGGTTCAAGAGATTCTTGTG	248150	80346	CCAAAAGGTGTGGTCCAGTC	292737	124933	AGTTCCAGCTACCTGGGAGG
203564	35760	CAGGTTCAAGAGATTCTTGT	248151	80347	ACCAAAAGGTGTGGTCCAGT	292738	124934	TAGTTCCAGCTACCTGGGAG
203565	35761	CCAGGTTCAAGAGATTCTTG	248152	80348	CACCAAAAGGTGTGGTCCAG	292739	124935	GTAGTTCCAGCTACCTGGGA
203566	35762	CCCAGGTTCAAGAGATTCTT	248153	80349	TCACCAAAAGGTGTGGTCCA	292740	124936	TGTAGTTCCAGCTACCTGGG
203567	35763	TCCCAGGTTCAAGAGATTCT	248154	80350	ATCACCAAAAGGTGTGGTCC	292741	124937	CTGTAGTTCCAGCTACCTGG
203568	35764	CTCCCAGGTTCAAGAGATTC	248155	80351	GATCACCAAAAGGTGTGGTC	292742	124938	CCTGTAGTTCCAGCTACCTG
203569	35765	CCTCCCAGGTTCAAGAGATT	248156	80352	AGATCACCAAAAGGTGTGGT	292743	124939	ACCTGTAGTTCCAGCTACCT
203570	35766	ACCTCCCAGGTTCAAGAGAT	248157	80353	AAGATCACCAAAAGGTGTGG	292744	124940	TACCTGTAGTTCCAGCTACC
203571	35767	TACCTCCCAGGTTCAAGAGA	248158	80354	TAAGATCACCAAAAGGTGTG	292745	124941	GTACCTGTAGTTCCAGCTAC
203572	35768	CTACCTCCCAGGTTCAAGAG	248159	80355	TTAAGATCACCAAAAGGTGT	292746	124942	GGTACCTGTAGTTCCAGCTA
203573	35769	TCTACCTCCCAGGTTCAAGA	248160	80356	ATTAAGATCACCAAAAGGTG	292747	124943	AGGTACCTGTAGTTCCAGCT
203574	35770	CTCTACCTCCCAGGTTCAAG	248161	80357	CATTAAGATCACCAAAAGGT	292748	124944	CAGGTACCTGTAGTTCCAGC
203575	35771	CCTCTACCTCCCAGGTTCAA	248162	80358	TCATTAAGATCACCAAAAGG	292749	124945	GCAGGTACCTGTAGTTCCAG
203576	35772	ACCTCTACCTCCCAGGTTCA	248163	80359	CTCATTAAGATCACCAAAAG	292750	124946	GGCAGGTACCTGTAGTTCCA
203577	35773	AACCTCTACCTCCCAGGTTC	248164	80360	CCTCATTAAGATCACCAAAA	292751	124947	TGGCAGGTACCTGTAGTTCC
203578	35774	CAACCTCTACCTCCCAGGTT	248165	80361	ACCTCATTAAGATCACCAAA	292752	124948	GTGGCAGGTACCTGTAGTTC
203579	35775	GCAACCTCTACCTCCCAGGT	248166	80362	CACCTCATTAAGATCACCAA	292753	124949	AGTGGCAGGTACCTGTAGTT
203580	35776	TGCAACCTCTACCTCCCAGG	248167	80363	CCACCTCATTAAGATCACCA	292754	124950	TAGTGGCAGGTACCTGTAGT
203581	35777	CTGCAACCTCTACCTCCCAG	248168	80364	ACCACCTCATTAAGATCACC	292755	124951	ATAGTGGCAGGTACCTGTAG
203582	35778	ACTGCAACCTCTACCTCCCA	248169	80365	GACCACCTCATTAAGATCAC	292756	124952	CATAGTGGCAGGTACCTGTA
203583	35779	CACTGCAACCTCTACCTCCC	248170	80366	GGACCACCTCATTAAGATCA	292757	124953	GCATAGTGGCAGGTACCTGT
203584	35780	TCACTGCAACCTCTACCTCC	248171	80367	GGGACCACCTCATTAAGATC	292758	124954	GGCATAGTGGCAGGTACCTG
203585	35781	CTCACTGCAACCTCTACCTC	248172	80368	TGGGACCACCTCATTAAGAT	292759	124955	AGGCATAGTGGCAGGTACCT
203586	35782	GCTCACTGCAACCTCTACCT	248173	80369	CTGGGACCACCTCATTAAGA	292760	124956	CAGGCATAGTGGCAGGTACC

203587	35783	GGCTCACTGCAACCTCTACC	248174	80370	TCTGGGACCACCTCATTAAG	292761	124957	CCAGGCATAGTGGCAGGTAC
203588	35784	CGGCTCACTGCAACCTCTAC	248175	80371	CTCTGGGACCACCTCATTAA	292762	124958	GCCAGGCATAGTGGCAGGTA
203589	35785	TCGGCTCACTGCAACCTCTA	248176	80372	CCTCTGGGACCACCTCATTA	292763	124959	AGCCAGGCATAGTGGCAGGT
203590	35786	CTCGGCTCACTGCAACCTCT	248177	80373	TCCTCTGGGACCACCTCATT	292764	124960	TAGCCAGGCATAGTGGCAGG
203591	35787	TCTCGGCTCACTGCAACCTC	248178	80374	CTCCTCTGGGACCACCTCAT	292765	124961	TTAGCCAGGCATAGTGGCAG
203592	35788	ATCTCGGCTCACTGCAACCT	248179	80375	GCTCCTCTGGGACCACCTCA	292766	124962	TTTAGCCAGGCATAGTGGCA
203593	35789	GATCTCGGCTCACTGCAACC	248180	80376	AGCTCCTCTGGGACCACCTC	292767	124963	ATTTAGCCAGGCATAGTGGC
203594	35790	CGATCTCGGCTCACTGCAAC	248181	80377	GAGCTCCTCTGGGACCACCT	292768	124964	TATTTAGCCAGGCATAGTGG
203595	35791	GCGATCTCGGCTCACTGCAA	248182	80378	TGAGCTCCTCTGGGACCACC	292769	124965	ATATTTAGCCAGGCATAGTG
203596	35792	TGCGATCTCGGCTCACTGCA	248183	80379	CTGAGCTCCTCTGGGACCAC	292770	124966	AATATTTAGCCAGGCATAGT
203597	35793	GTGCGATCTCGGCTCACTGC	248184	80380	TCTGAGCTCCTCTGGGACCA	292771	124967	AAATATTTAGCCAGGCATAG
203598	35794	AGTGCGATCTCGGCTCACTG	248185	80381	GTCTGAGCTCCTCTGGGACC	292772	124968	AAAATATTTAGCCAGGCATA
203599	35795	TAGTGCGATCTCGGCTCACT	248186	80382	TGTCTGAGCTCCTCTGGGAC	292773	124969	CAAAATATTTAGCCAGGCAT
203600	35796	GTAGTGCGATCTCGGCTCAC	248187	80383	ATGTCTGAGCTCCTCTGGGA	292774	124970	ACAAAATATTTAGCCAGGCA
203601	35797	AGTAGTGCGATCTCGGCTCA	248188	80384	CATGTCTGAGCTCCTCTGGG	292775	124971	TACAAAATATTTAGCCAGGC
203602	35798	CAGTAGTGCGATCTCGGCTC	248189	80385	GCATGTCTGAGCTCCTCTGG	292776	124972	ATACAAAATATTTAGCCAGG
203603	35799	GCAGTAGTGCGATCTCGGCT	248190	80386	TGCATGTCTGAGCTCCTCTG	292777	124973	AATACAAAATATTTAGCCAG
203604	35800	TGCAGTAGTGCGATCTCGGC	248191	80387	TTGCATGTCTGAGCTCCTCT	292778	124974	AAATACAAAATATTTAGCCA
203605	35801	ATGCAGTAGTGCGATCTCGG	248192	80388	ATTGCATGTCTGAGCTCCTC	292779	124975	GAAATACAAAATATTTAGCC
203606	35802	AATGCAGTAGTGCGATCTCG	248193	80389	GATTGCATGTCTGAGCTCCT	292780	124976	GGAAATACAAAATATTTAGC
203607	35803	GAATGCAGTAGTGCGATCTC	248194	80390	AGATTGCATGTCTGAGCTCC	292781	124977	AGGAAATACAAAATATTTAG
203608	35804	GGAATGCAGTAGTGCGATCT	248195	80391	TAGATTGCATGTCTGAGCTC	292782	124978	CAGGAAATACAAAATATTTA
203609	35805	TGGAATGCAGTAGTGCGATC	248196	80392	CTAGATTGCATGTCTGAGCT	292783	124979	ACAGGAAATACAAAATATTT
203610	35806	CTGGAATGCAGTAGTGCGAT	248197	80393	GCTAGATTGCATGTCTGAGC	292784	124980	CACAGGAAATACAAAATATT
203611	35807	GCTGGAATGCAGTAGTGCGA	248198	80394	TGCTAGATTGCATGTCTGAG	292785	124981	CCACAGGAAATACAAAATAT
203612	35808	GGCTGGAATGCAGTAGTGCG	248199	80395	ATGCTAGATTGCATGTCTGA	292786	124982	TCCACAGGAAATACAAAATA
203613	35809	AGGCTGGAATGCAGTAGTGC	248200	80396	GATGCTAGATTGCATGTCTG	292787	124983	CTCCACAGGAAATACAAAAT
203614	35810	CAGGCTGGAATGCAGTAGTG	248201	80397	GGATGCTAGATTGCATGTCT	292788	124984	TCTCCACAGGAAATACAAAA
203615	35811	CCAGGCTGGAATGCAGTAGT	248202	80398	TGGATGCTAGATTGCATGTC	292789	124985	GTCTCCACAGGAAATACAAA
203616	35812	CCCAGGCTGGAATGCAGTAG	248203	80399	CTGGATGCTAGATTGCATGT	292790	124986	CGTCTCCACAGGAAATACAA
203617	35813	ACCCAGGCTGGAATGCAGTA	248204	80400	ACTGGATGCTAGATTGCATG	292791	124987	TCGTCTCCACAGGAAATACA
203618	35814	CACCCAGGCTGGAATGCAGT	248205	80401	AACTGGATGCTAGATTGCAT	292792	124988	CTCGTCTCCACAGGAAATAC
203619	35815	TCACCCAGGCTGGAATGCAG	248206	80402	GAACTGGATGCTAGATTGCA	292793	124989	CCTCGTCTCCACAGGAAATA
203620	35816	GTCACCCAGGCTGGAATGCA	248207	80403	AGAACTGGATGCTAGATTGC	292794	124990	ACCTCGTCTCCACAGGAAAT
203621	35817	TGTCACCCAGGCTGGAATGC	248208	80404	CAGAACTGGATGCTAGATTG	292795	124991	AACCTCGTCTCCACAGGAAA
203622	35818	CTGTCACCCAGGCTGGAATG	248209	80405	CCAGAACTGGATGCTAGATT	292796	124992	AAACCTCGTCTCCACAGGAA
203623	35819	TCTGTCACCCAGGCTGGAAT	248210	80406	CCCAGAACTGGATGCTAGAT	292797	124993	AAAACCTCGTCTCCACAGGA
203624	35820	CTCTGTCACCCAGGCTGGAA	248211	80407	TCCCAGAACTGGATGCTAGA	292798	124994	CAAAACCTCGTCTCCACAGG
203625	35821	GCTCTGTCACCCAGGCTGGA	248212	80408	GTCCCAGAACTGGATGCTAG	292799	124995	GCAAAACCTCGTCTCCACAG
203626	35822	TGCTCTGTCACCCAGGCTGG	248213	80409	AGTCCCAGAACTGGATGCTA	292800	124996	GGCAAAACCTCGTCTCCACA
203627	35823	TTGCTCTGTCACCCAGGCTG	248214	80410	GAGTCCCAGAACTGGATGCT	292801	124997	TGGCAAAACCTCGTCTCCAC
203628	35824	CTTGCTCTGTCACCCAGGCT	248215	80411	AGAGTCCCAGAACTGGATGC	292802	124998	GTGGCAAAACCTCGTCTCCA
203629	35825	TCTTGCTCTGTCACCCAGGC	248216	80412	CAGAGTCCCAGAACTGGATG	292803	124999	CGTGGCAAAACCTCGTCTCC
203630	35826	ATCTTGCTCTGTCACCCAGG	248217	80413	ACAGAGTCCCAGAACTGGAT	292804	125000	ACGTGGCAAAACCTCGTCTC
203631	35827	AATCTTGCTCTGTCACCCAG	248218	80414	GACAGAGTCCCAGAACTGGA	292805	125001	AACGTGGCAAAACCTCGTCT
203632	35828	GAATCTTGCTCTGTCACCCA	248219	80415	AGACAGAGTCCCAGAACTGG	292806	125002	CAACGTGGCAAAACCTCGTC
203633	35829	AGAATCTTGCTCTGTCACCC	248220	80416	GAGACAGAGTCCCAGAACTG	292807	125003	GCAACGTGGCAAAACCTCGT
203634	35830	CAGAATCTTGCTCTGTCACC	248221	80417	GGAGACAGAGTCCCAGAACT	292808	125004	GGCAACGTGGCAAAACCTCG
203635	35831	ACAGAATCTTGCTCTGTCAC	248222	80418	AGGAGACAGAGTCCCAGAAC	292809	125005	GGGCAACGTGGCAAAACCTC
203636	35832	GACAGAATCTTGCTCTGTCA	248223	80419	AAGGAGACAGAGTCCCAGAA	292810	125006	TGGGCAACGTGGCAAAACCT
203637	35833	AGACAGAATCTTGCTCTGTC	248224	80420	AAAGGAGACAGAGTCCCAGA	292811	125007	CTGGGCAACGTGGCAAAACC
203638	35834	GAGACAGAATCTTGCTCTGT	248225	80421	AAAAGGAGACAGAGTCCCAG	292812	125008	CCTGGGCAACGTGGCAAAAC
203639	35835	GGAGACAGAATCTTGCTCTG	248226	80422	GAAAAGGAGACAGAGTCCCA	292813	125009	GCCTGGGCAACGTGGCAAAA
203640	35836	TGGAGACAGAATCTTGCTCT	248227	80423	TGAAAAGGAGACAGAGTCCC	292814	125010	AGCCTGGGCAACGTGGCAAA
203641	35837	TTGGAGACAGAATCTTGCTC	248228	80424	TTGAAAAGGAGACAGAGTCC	292815	125011	CAGCCTGGGCAACGTGGCAA
203642	35838	TTTGGAGACAGAATCTTGCT	248229	80425	TTTGAAAAGGAGACAGAGTC	292816	125012	CCAGCCTGGGCAACGTGGCA
203643	35839	TTTTGGAGACAGAATCTTGC	248230	80426	GTTTGAAAAGGAGACAGAGT	292817	125013	ACCAGCCTGGGCAACGTGGC
203644	35840	TTTTTGGAGACAGAATCTTG	248231	80427	CGTTTGAAAAGGAGACAGAG	292818	125014	GACCAGCCTGGGCAACGTGG
203645	35841	TTTTTTGGAGACAGAATCTT	248232	80428	ACGTTTGAAAAGGAGACAGA	292819	125015	AGACCAGCCTGGGCAACGTG
203646	35842	TTTTTTTGGAGACAGAATCT	248233	80429	TACGTTTGAAAAGGAGACAG	292820	125016	AAGACCAGCCTGGGCAACGT
203647	35843	TTTTTTTTGGAGACAGAATC	248234	80430	ATACGTTTGAAAAGGAGACA	292821	125017	CAAGACCAGCCTGGGCAACG
203648	35844	TTTTTTTTTGGAGACAGAAT	248235	80431	AATACGTTTGAAAAGGAGAC	292822	125018	TCAAGACCAGCCTGGGCAAC
203649	35845	TTTTTTTTTTGGAGACAGAA	248236	80432	GAATACGTTTGAAAAGGAGA	292823	125019	TTCAAGACCAGCCTGGGCAA
203650	35846	TTTTTTTTTTTGGAGACAGA	248237	80433	TGAATACGTTTGAAAAGGAG	292824	125020	GTTCAAGACCAGCCTGGGCA
203651	35847	TTTTTTTTTTTTGGAGACAG	248238	80434	ATGAATACGTTTGAAAAGGA	292825	125021	AGTTCAAGACCAGCCTGGGC
203652	35848	TTTTTTTTTTTTTGGAGACA	248239	80435	CATGAATACGTTTGAAAAGG	292826	125022	GAGTTCAAGACCAGCCTGGG
203653	35849	TTTTTTTTTTTTTTGGAGAC	248240	80436	ACATGAATACGTTTGAAAAG	292827	125023	GGAGTTCAAGACCAGCCTGG
203654	35850	TTTTTTTTTTTTTTTGGAGA	248241	80437	TACATGAATACGTTTGAAAA	292828	125024	AGGAGTTCAAGACCAGCCTG
203655	35851	TTTTTTTTTTTTTTTTGGAG	248242	80438	CTACATGAATACGTTTGAAA	292829	125025	CAGGAGTTCAAGACCAGCCT
203656	35852	TTTTTTTTTTTTTTTTTGGA	248243	80439	TCTACATGAATACGTTTGAA	292830	125026	TCAGGAGTTCAAGACCAGCC
203657	35853	CTTTTTTTTTTTTTTTTGG	248244	80440	TTCTACATGAATACGTTTGA	292831	125027	CTCAGGAGTTCAAGACCAGC
203658	35854	TCTTTTTTTTTTTTTTTTG	248245	80441	GTTCTACATGAATACGTTTG	292832	125028	CCTCAGGAGTTCAAGACCAG

203659	35855	TTCTTTTTTTTTTTTTTTT	248246	80442	TGTTCTACATGAATACGTTT	292833	125029	ACCTCAGGAGTTCAAGACCA
203660	35856	TTTCTTTTTTTTTTTTTTT	248247	80443	CTGTTCTACATGAATACGTT	292834	125030	GACCTCAGGAGTTCAAGACC
203661	35857	TTTTCTTTTTTTTTTTTTT	248248	80444	CCTGTTCTACATGAATACGT	292835	125031	TGACCTCAGGAGTTCAAGAC
203662	35858	CTTTTCTTTTTTTTTTTTT	248249	80445	GCCTGTTCTACATGAATACG	292836	125032	TTGACCTCAGGAGTTCAAGA
203663	35859	CCTTTTCTTTTTTTTTTTT	248250	80446	TGCCTGTTCTACATGAATAC	292837	125033	CTTGACCTCAGGAGTTCAAG
203664	35860	TCCTTTTCTTTTTTTTTTT	248251	80447	ATGCCTGTTCTACATGAATA	292838	125034	GCTTGACCTCAGGAGTTCAA
203665	35861	TTCCTTTTCTTTTTTTTTT	248252	80448	CATGCCTGTTCTACATGAAT	292839	125035	TGCTTGACCTCAGGAGTTCA
203666	35862	TTTCCTTTTCTTTTTTTTT	248253	80449	TCATGCCTGTTCTACATGAA	292840	125036	TTGCTTGACCTCAGGAGTTC
203667	35863	CTTTCCTTTTCTTTTTTTT	248254	80450	GTCATGCCTGTTCTACATGA	292841	125037	ATTGCTTGACCTCAGGAGTT
203668	35864	GCTTTCCTTTTCTTTTTTT	248255	80451	CGTCATGCCTGTTCTACATG	292842	125038	TATTGCTTGACCTCAGGAGT
203669	35865	AGCTTTCCTTTTCTTTTTT	248256	80452	TCGTCATGCCTGTTCTACAT	292843	125039	ATATTGCTTGACCTCAGGAG
203670	35866	TAGCTTTCCTTTTCTTTTT	248257	80453	CTCGTCATGCCTGTTCTACA	292844	125040	CATATTGCTTGACCTCAGGA
203671	35867	TTAGCTTTCCTTTTCTTTT	248258	80454	TCTCGTCATGCCTGTTCTAC	292845	125041	GCATATTGCTTGACCTCAGG
203672	35868	TTTAGCTTTCCTTTTCTTT	248259	80455	TTCTCGTCATGCCTGTTCTA	292846	125042	GGCATATTGCTTGACCTCAG
203673	35869	CTTTAGCTTTCCTTTTCTT	248260	80456	ATTCTCGTCATGCCTGTTCT	292847	125043	GGGCATATTGCTTGACCTCA
203674	35870	CCTTTAGCTTTCCTTTTCT	248261	80457	CATTCTCGTCATGCCTGTTC	292848	125044	TGGGCATATTGCTTGACCTC
203675	35871	TCCTTTAGCTTTCCTTTTC	248262	80458	GCATTCTCGTCATGCCTGTT	292849	125045	GTGGGCATATTGCTTGACCT
203676	35872	CTCCTTTAGCTTTCCTTTC	248263	80459	GGCATTCTCGTCATGCCTGT	292850	125046	GGTGGGCATATTGCTTGACC
203677	35873	TCTCCTTTAGCTTTCCTTT	248264	80460	AGGCATTCTCGTCATGCCTG	292851	125047	AGGTGGGCATATTGCTTGAC
203678	35874	CTCTCCTTTAGCTTTCCTT	248265	80461	AAGGCATTCTCGTCATGCCT	292852	125048	GAGGTGGGCATATTGCTTGA
203679	35875	TCTCTCCTTTAGCTTTCCT	248266	80462	CAAGGCATTCTCGTCATGCC	292853	125049	CGAGGTGGGCATATTGCTTG
203680	35876	CTCTCTCCTTTAGCTTTCC	248267	80463	ACAAGGCATTCTCGTCATGC	292854	125050	CCGAGGTGGGCATATTGCTT
203681	35877	TCTCTCTCCTTTAGCTTTC	248268	80464	GACAAGGCATTCTCGTCATG	292855	125051	GCCGAGGTGGGCATATTGCT
203682	35878	GTCTCTCTCCTTTAGCTTT	248269	80465	TGACAAGGCATTCTCGTCAT	292856	125052	GGCCGAGGTGGGCATATTGC
203683	35879	AGTCTCTCTCCTTTAGCTT	248270	80466	TTGACAAGGCATTCTCGTCA	292857	125053	AGGCCGAGGTGGGCATATTG
203684	35880	TAGTCTCTCTCCTTTAGCT	248271	80467	GTTGACAAGGCATTCTCGTC	292858	125054	GAGGCCGAGGTGGGCATATT
203685	35881	TTAGTCTCTCTCCTTTAGC	248272	80468	TGTTGACAAGGCATTCTCGT	292859	125055	GGAGGCCGAGGTGGGCATAT
203686	35882	TTTAGTCTCTCTCCTTTAG	248273	80469	ATGTTGACAAGGCATTCTCG	292860	125056	GGGAGGCCGAGGTGGGCATA
203687	35883	TTTTAGTCTCTCTCCTTTA	248274	80470	CATGTTGACAAGGCATTCTC	292861	125057	TGGGAGGCCGAGGTGGGCAT
203688	35884	ATTTTAGTCTCTCTCCTTTA	248275	80471	CCATGTTGACAAGGCATTCT	292862	125058	TTGGGAGGCCGAGGTGGGCA
203689	35885	CATTTTAGTCTCTCTCCTTT	248276	80472	CCCATGTTGACAAGGCATTC	292863	125059	CTTGGGAGGCCGAGGTGGGC
203690	35886	TCATTTTAGTCTCTCTCCTT	248277	80473	ACCCATGTTGACAAGGCATT	292864	125060	CCTTGGGAGGCCGAGGTGGG
203691	35887	ATCATTTTAGTCTCTCTCCT	248278	80474	CACCCATGTTGACAAGGCAT	292865	125061	ACCTTGGGAGGCCGAGGTGG
203692	35888	TATCATTTTAGTCTCTCTCC	248279	80475	TCACCCATGTTGACAAGGCA	292866	125062	CACCTTGGGAGGCCGAGGTG
203693	35889	ATATCATTTTAGTCTCTCTC	248280	80476	ATCACCCATGTTGACAAGGC	292867	125063	GCACCTTGGGAGGCCGAGGT
203694	35890	GATATCATTTTAGTCTCTCT	248281	80477	CATCACCCATGTTGACAAGG	292868	125064	AGCACCTTGGGAGGCCGAGG
203695	35891	TGATATCATTTTAGTCTCTC	248282	80478	CCATCACCCATGTTGACAAG	292869	125065	CAGCACCTTGGGAGGCCGAG
203696	35892	CTGATATCATTTTAGTCTCT	248283	80479	CCCATCACCCATGTTGACAA	292870	125066	CCAGCACCTTGGGAGGCCGA
203697	35893	CCTGATATCATTTTAGTCTC	248284	80480	CCCCATCACCCATGTTGACA	292871	125067	CCCAGCACCTTGGGAGGCCG
203698	35894	ACCTGATATCATTTTAGTCT	248285	80481	TCCCCATCACCCATGTTGAC	292872	125068	TCCCAGCACCTTGGGAGGCC
203699	35895	AACCTGATATCATTTTAGTC	248286	80482	TTCCCCATCACCCATGTTGA	292873	125069	ATCCCAGCACCTTGGGAGGC
203700	35896	GAACCTGATATCATTTTAGT	248287	80483	ATTCCCCATCACCCATGTTG	292874	125070	AATCCCAGCACCTTGGGAGG
203701	35897	GGAACCTGATATCATTTTAG	248288	80484	GATTCCCCATCACCCATGTT	292875	125071	TAATCCCAGCACCTTGGGAG
203702	35898	AGGAACCTGATATCATTTTA	248289	80485	TGATTCCCCATCACCCATGT	292876	125072	GTAATCCCAGCACCTTGGGA
203703	35899	CAGGAACCTGATATCATTTT	248290	80486	TTGATTCCCCATCACCCATG	292877	125073	TGTAATCCCAGCACCTTGGG
203704	35900	CCAGGAACCTGATATCATTT	248291	80487	ATTGATTCCCCATCACCCAT	292878	125074	CTGTAATCCCAGCACCTTGG
203705	35901	TCCAGGAACCTGATATCATT	248292	80488	GATTGATTCCCCATCACCCA	292879	125075	CCTGTAATCCCAGCACCTTG
203706	35902	CTCCAGGAACCTGATATCAT	248293	80489	TGATTGATTCCCCATCACCC	292880	125076	ACCTGTAATCCCAGCACCTT
203707	35903	TCTCCAGGAACCTGATATCA	248294	80490	CTGATTGATTCCCCATCACC	292881	125077	CACCTGTAATCCCAGCACCT
203708	35904	TTCTCCAGGAACCTGATATC	248295	80491	TCTGATTGATTCCCCATCAC	292882	125078	ACACCTGTAATCCCAGCACC
203709	35905	GTTCTCCAGGAACCTGATAT	248296	80492	GTCTGATTGATTCCCCATCA	292883	125079	CACACCTGTAATCCCAGCAC
203710	35906	TGTTCTCCAGGAACCTGATA	248297	80493	TGTCTGATTGATTCCCCATC	292884	125080	TCACACCTGTAATCCCAGCA
203711	35907	TTGTTCTCCAGGAACCTGAT	248298	80494	CTGTCTGATTGATTCCCCAT	292885	125081	CTCACACCTGTAATCCCAGC
203712	35908	TTTGTTCTCCAGGAACCTGA	248299	80495	CCTGTCTGATTGATTCCCCA	292886	125082	GCTCACACCTGTAATCCCAG
203713	35909	GTTTGTTCTCCAGGAACCTG	248300	80496	CCCTGTCTGATTGATTCCCC	292887	125083	GGCTCACACCTGTAATCCCA
203714	35910	TGTTTGTTCTCCAGGAACCT	248301	80497	GCCCTGTCTGATTGATTCCC	292888	125084	TGGCTCACACCTGTAATCCC
203715	35911	CTGTTTGTTCTCCAGGAACC	248302	80498	CGCCCTGTCTGATTGATTCC	292889	125085	GTGGCTCACACCTGTAATCC
203716	35912	TCTGTTTGTTCTCCAGGAAC	248303	80499	GCGCCCTGTCTGATTGATTC	292890	125086	TGTGGCTCACACCTGTAATC
203717	35913	GTCTGTTTGTTCTCCAGGAA	248304	80500	GGCGCCCTGTCTGATTGATT	292891	125087	CTGTGGCTCACACCTGTAAT
203718	35914	TGTCTGTTTGTTCTCCAGGA	248305	80501	CGGCGCCCTGTCTGATTGAT	292892	125088	ACTGTGGCTCACACCTGTAA
203719	35915	ATGTCTGTTTGTTCTCCAGG	248306	80502	CCGGCGCCCTGTCTGATTGA	292893	125089	CACTGTGGCTCACACCTGTA
203720	35916	CATGTCTGTTTGTTCTCCAG	248307	80503	CCCGGCGCCCTGTCTGATTG	292894	125090	GCACTGTGGCTCACACCTGT
203721	35917	TCATGTCTGTTTGTTCTCCA	248308	80504	GCCCGGCGCCCTGTCTGATT	292895	125091	AGCACTGTGGCTCACACCTG
203722	35918	ATCATGTCTGTTTGTTCTCC	248309	80505	AGCCCGGCGCCCTGTCTGAT	292896	125092	GAGCACTGTGGCTCACACCT
203723	35919	AATCATGTCTGTTTGTTCTC	248310	80506	GAGCCCGGCGCCCTGTCTGA	292897	125093	CGAGCACTGTGGCTCACACC
203724	35920	AAATCATGTCTGTTTGTTCT	248311	80507	TGAGCCCGGCGCCCTGTCTG	292898	125094	CCGAGCACTGTGGCTCACAC
203725	35921	AAAATCATGTCTGTTTGTTC	248312	80508	TTGAGCCCGGCGCCCTGTCT	292899	125095	GCCGAGCACTGTGGCTCACA
203726	35922	CAAAATCATGTCTGTTTGTT	248313	80509	CTTGAGCCCGGCGCCCTGTC	292900	125096	GGCCGAGCACTGTGGCTCAC
203727	35923	GCAAAATCATGTCTGTTTGT	248314	80510	CCTTGAGCCCGGCGCCCTGT	292901	125097	AGGCCGAGCACTGTGGCTCA
203728	35924	AGCAAAATCATGTCTGTTTG	248315	80511	GCCTTGAGCCCGGCGCCCTG	292902	125098	TAGGCCGAGCACTGTGGCTC
203729	35925	AAGCAAAATCATGTCTGTTT	248316	80512	AGCCTTGAGCCCGGCGCCCT	292903	125099	TTAGGCCGAGCACTGTGGCT
203730	35926	GAAGCAAAATCATGTCTGTT	248317	80513	CAGCCTTGAGCCCGGCGCCC	292904	125100	CTTAGGCCGAGCACTGTGGC

203731	35927	TGAAGCAAAATCATGTCTGT	248318	80514	GCAGCCTTGAGCCCGGCGCC	292905	125101	ACTTAGGCCGAGCACTGTGG
203732	35928	ATGAAGCAAAATCATGTCTG	248319	80515	TGCAGCCTTGAGCCCGGCGC	292906	125102	GACTTAGGCCGAGCACTGTG
203733	35929	CATGAAGCAAAATCATGTCT	248320	80516	CTGCAGCCTTGAGCCCGGCG	292907	125103	TGACTTAGGCCGAGCACTGT
203734	35930	CCATGAAGCAAAATCATGTC	248321	80517	ACTGCAGCCTTGAGCCCGGC	292908	125104	GTGACTTAGGCCGAGCACTG
203735	35931	GCCATGAAGCAAAATCATGT	248322	80518	GACTGCAGCCTTGAGCCCGG	292909	125105	AGTGACTTAGGCCGAGCACT
203736	35932	TGCCATGAAGCAAAATCATG	248323	80519	TGACTGCAGCCTTGAGCCCG	292910	125106	CAGTGACTTAGGCCGAGCAC
203737	35933	CTGCCATGAAGCAAAATCAT	248324	80520	GTGACTGCAGCCTTGAGCCC	292911	125107	GCAGTGACTTAGGCCGAGCA
203738	35934	CCTGCCATGAAGCAAAATCA	248325	80521	GGTGACTGCAGCCTTGAGCC	292912	125108	TGCAGTGACTTAGGCCGAGC
203739	35935	TCCTGCCATGAAGCAAAATC	248326	80522	GGGTGACTGCAGCCTTGAGC	292913	125109	CTGCAGTGACTTAGGCCGAG
203740	35936	GTCCTGCCATGAAGCAAAAT	248327	80523	TGGGTGACTGCAGCCTTGAG	292914	125110	ACTGCAGTGACTTAGGCCGA
203741	35937	TGTCCTGCCATGAAGCAAAA	248328	80524	TTGGGTGACTGCAGCCTTGA	292915	125111	AACTGCAGTGACTTAGGCCG
203742	35938	CTGTCCTGCCATGAAGCAAA	248329	80525	CTTGGGTGACTGCAGCCTTG	292916	125112	AAACTGCAGTGACTTAGGCC
203743	35939	GCTGTCCTGCCATGAAGCAA	248330	80526	TCTTGGGTGACTGCAGCCTT	292917	125113	AAAACTGCAGTGACTTAGGC
203744	35940	GGCTGTCCTGCCATGAAGCA	248331	80527	CTCTTGGGTGACTGCAGCCT	292918	125114	AAAAACTGCAGTGACTTAGG
203745	35941	CGGCTGTCCTGCCATGAAGC	248332	80528	ACTCTTGGGTGACTGCAGCC	292919	125115	TAAAAACTGCAGTGACTTAG
203746	35942	CCGGCTGTCCTGCCATGAAG	248333	80529	CACTCTTGGGTGACTGCAGC	292920	125116	TTAAAAACTGCAGTGACTTA
203747	35943	TCCGGCTGTCCTGCCATGAA	248334	80530	CCACTCTTGGGTGACTGCAG	292921	125117	TTTAAAAACTGCAGTGACTT
203748	35944	TTCCGGCTGTCCTGCCATGA	248335	80531	GCCACTCTTGGGTGACTGCA	292922	125118	CTTTAAAAACTGCAGTGACT
203749	35945	CTTCCGGCTGTCCTGCCATG	248336	80532	AGCCACTCTTGGGTGACTGC	292923	125119	GCTTTAAAAACTGCAGTGAC
203750	35946	TCTTCCGGCTGTCCTGCCAT	248337	80533	GAGCCACTCTTGGGTGACTG	292924	125120	AGCTTTAAAAACTGCAGTGA
203751	35947	TTCTTCCGGCTGTCCTGCCA	248338	80534	TGAGCCACTCTTGGGTGACT	292925	125121	GAGCTTTAAAAACTGCAGTG
203752	35948	CTTCTTCCGGCTGTCCTGCC	248339	80535	CTGAGCCACTCTTGGGTGAC	292926	125122	GGAGCTTTAAAAACTGCAGT
203753	35949	ACTTCTTCCGGCTGTCCTGC	248340	80536	GCTGAGCCACTCTTGGGTGA	292927	125123	GGGAGCTTTAAAAACTGCAG
203754	35950	CACTTCTTCCGGCTGTCCTG	248341	80537	GGCTGAGCCACTCTTGGGTG	292928	125124	TGGGAGCTTTAAAAACTGCA
203755	35951	CCACTTCTTCCGGCTGTCCT	248342	80538	GGGCTGAGCCACTCTTGGGT	292929	125125	CTGGGAGCTTTAAAAACTGC
203756	35952	CCCACTTCTTCCGGCTGTCC	248343	80539	TGGGCTGAGCCACTCTTGGG	292930	125126	CCTGGGAGCTTTAAAAACTG
203757	35953	TCCCACTTCTTCCGGCTGTC	248344	80540	GTGGGCTGAGCCACTCTTGG	292931	125127	ACCTGGGAGCTTTAAAAACT
203758	35954	ATCCCACTTCTTCCGGCTGT	248345	80541	GGTGGGCTGAGCCACTCTTG	292932	125128	CACCTGGGAGCTTTAAAAAC
203759	35955	AATCCCACTTCTTCCGGCTG	248346	80542	TGGTGGGCTGAGCCACTCTT	292933	125129	TCACCTGGGAGCTTTAAAAA
203760	35956	TAATCCCACTTCTTCCGGCT	248347	80543	CTGGTGGGCTGAGCCACTCT	292934	125130	ATCACCTGGGAGCTTTAAAA
203761	35957	ATAATCCCACTTCTTCCGGC	248348	80544	CCTGGTGGGCTGAGCCACTC	292935	125131	AATCACCTGGGAGCTTTAAA
203762	35958	TATAATCCCACTTCTTCCGG	248349	80545	GCCTGGTGGGCTGAGCCACT	292936	125132	GAATCACCTGGGAGCTTTAA
203763	35959	ATATAATCCCACTTCTTCCG	248350	80546	GGCCTGGTGGGCTGAGCCAC	292937	125133	AGAATCACCTGGGAGCTTTA
203764	35960	GATATAATCCCACTTCTTCC	248351	80547	GGGCCTGGTGGGCTGAGCCA	292938	125134	AAGAATCACCTGGGAGCTTT
203765	35961	GGATATAATCCCACTTCTTC	248352	80548	AGGGCCTGGTGGGCTGAGCC	292939	125135	GAAGAATCACCTGGGAGCTT
203766	35962	AGGATATAATCCCACTTCTT	248353	80549	TAGGGCCTGGTGGGCTGAGC	292940	125136	TGAAGAATCACCTGGGAGCT
203767	35963	GAGGATATAATCCCACTTCT	248354	80550	CTAGGGCCTGGTGGGCTGAG	292941	125137	CTGAAGAATCACCTGGGAGC
203768	35964	TGAGGATATAATCCCACTTC	248355	80551	CCTAGGGCCTGGTGGGCTGA	292942	125138	ACTGAAGAATCACCTGGGAG
203769	35965	GTGAGGATATAATCCCACTT	248356	80552	TCCTAGGGCCTGGTGGGCTG	292943	125139	CACTGAAGAATCACCTGGGA
203770	35966	TGTGAGGATATAATCCCACT	248357	80553	TTCCTAGGGCCTGGTGGGCT	292944	125140	GCACTGAAGAATCACCTGGG
203771	35967	ATGTGAGGATATAATCCCAC	248358	80554	TTTCCTAGGGCCTGGTGGGC	292945	125141	TGCACTGAAGAATCACCTGG
203772	35968	AATGTGAGGATATAATCCCA	248359	80555	GTTTCCTAGGGCCTGGTGGG	292946	125142	CTGCACTGAAGAATCACCTG
203773	35969	TAATGTGAGGATATAATCCC	248360	80556	CGTTTCCTAGGGCCTGGTGG	292947	125143	ACTGCACTGAAGAATCACCT
203774	35970	GTAATGTGAGGATATAATCC	248361	80557	GCGTTTCCTAGGGCCTGGTG	292948	125144	GACTGCACTGAAGAATCACC
203775	35971	TGTAATGTGAGGATATAATC	248362	80558	GGCGTTTCCTAGGGCCTGGT	292949	125145	TGACTGCACTGAAGAATCAC
203776	35972	TTGTAATGTGAGGATATAAT	248363	80559	AGGCGTTTCCTAGGGCCTGG	292950	125146	TTGACTGCACTGAAGAATCA
203777	35973	TTTGTAATGTGAGGATATAA	248364	80560	CAGGCGTTTCCTAGGGCCTG	292951	125147	TTTGACTGCACTGAAGAATC
203778	35974	ATTTGTAATGTGAGGATATA	248365	80561	GCAGGCGTTTCCTAGGGCCT	292952	125148	TTTTGACTGCACTGAAGAAT
203779	35975	TATTTGTAATGTGAGGATAT	248366	80562	TGCAGGCGTTTCCTAGGGCC	292953	125149	CTTTTGACTGCACTGAAGAA
203780	35976	TTATTTGTAATGTGAGGATA	248367	80563	GTGCAGGCGTTTCCTAGGGC	292954	125150	ACTTTTGACTGCACTGAAGA
203781	35977	CTTATTTGTAATGTGAGGAT	248368	80564	TGTGCAGGCGTTTCCTAGGG	292955	125151	CACTTTTGACTGCACTGAAG
203782	35978	TCTTATTTGTAATGTGAGGA	248369	80565	CTGTGCAGGCGTTTCCTAGG	292956	125152	TCACTTTTGACTGCACTGAA
203783	35979	TTCTTATTTGTAATGTGAGG	248370	80566	GCTGTGCAGGCGTTTCCTAG	292957	125153	CTCACTTTTGACTGCACTGA
203784	35980	TTTCTTATTTGTAATGTGAG	248371	80567	GGCTGTGCAGGCGTTTCCTA	292958	125154	TCTCACTTTTGACTGCACTG
203785	35981	TTTTCTTATTTGTAATGTGA	248372	80568	AGGCTGTGCAGGCGTTTCCT	292959	125155	TTCTCACTTTTGACTGCACT
203786	35982	GTTTTCTTATTTGTAATGTG	248373	80569	CAGGCTGTGCAGGCGTTTCC	292960	125156	GTTCTCACTTTTGACTGCAC
203787	35983	AGTTTTCTTATTTGTAATGT	248374	80570	CCAGGCTGTGCAGGCGTTTC	292961	125157	AGTTCTCACTTTTGACTGCA
203788	35984	CAGTTTTCTTATTTGTAATG	248375	80571	TCCAGGCTGTGCAGGCGTTT	292962	125158	CAGTTCTCACTTTTGACTGC
203789	35985	TCAGTTTTCTTATTTGTAAT	248376	80572	CTCCAGGCTGTGCAGGCGTT	292963	125159	CCAGTTCTCACTTTTGACTG
203790	35986	CTCAGTTTTCTTATTTGTAA	248377	80573	GCTCCAGGCTGTGCAGGCGT	292964	125160	GCCAGTTCTCACTTTTGACT
203791	35987	TCTCAGTTTTCTTATTTGTA	248378	80574	AGCTCCAGGCTGTGCAGGCG	292965	125161	AGCCAGTTCTCACTTTTGAC
203792	35988	GTCTCAGTTTTCTTATTTGT	248379	80575	GAGCTCCAGGCTGTGCAGGC	292966	125162	CAGCCAGTTCTCACTTTTGA
203793	35989	AGTCTCAGTTTTCTTATTTG	248380	80576	GGAGCTCCAGGCTGTGCAGG	292967	125163	CCAGCCAGTTCTCACTTTTG
203794	35990	GAGTCTCAGTTTTCTTATTT	248381	80577	AGGAGCTCCAGGCTGTGCAG	292968	125164	CCCAGCCAGTTCTCACTTTT
203795	35991	TGAGTCTCAGTTTTCTTATT	248382	80578	CAGGAGCTCCAGGCTGTGCA	292969	125165	ACCCAGCCAGTTCTCACTTT
203796	35992	CTGAGTCTCAGTTTTCTTAT	248383	80579	CCAGGAGCTCCAGGCTGTGC	292970	125166	CACCCAGCCAGTTCTCACTT
203797	35993	TCTGAGTCTCAGTTTTCTTA	248384	80580	TCCAGGAGCTCCAGGCTGTG	292971	125167	GCACCCAGCCAGTTCTCACT
203798	35994	TTCTGAGTCTCAGTTTTCTT	248385	80581	CTCCAGGAGCTCCAGGCTGT	292972	125168	CGCACCCAGCCAGTTCTCAC
203799	35995	ATTCTGAGTCTCAGTTTTCT	248386	80582	ACTCCAGGAGCTCCAGGCTG	292973	125169	CCGCACCCAGCCAGTTCTCA
203800	35996	CATTCTGAGTCTCAGTTTTC	248387	80583	GACTCCAGGAGCTCCAGGCT	292974	125170	ACCGCACCCAGCCAGTTCTC
203801	35997	CCATTCTGAGTCTCAGTTTT	248388	80584	TGACTCCAGGAGCTCCAGGC	292975	125171	CACCGCACCCAGCCAGTTCT
203802	35998	ACCATTCTGAGTCTCAGTTT	248389	80585	ATGACTCCAGGAGCTCCAGG	292976	125172	CCACCGCACCCAGCCAGTTC

203803	35999	AACCATTCTGAGTCTCAGTT	248390	80586	AATGACTCCAGGAGCTCCAG	292977	125173	GCCACCGCACCCAGCCAGTT
203804	36000	TAACCATTCTGAGTCTCAGT	248391	80587	AAATGACTCCAGGAGCTCCA	292978	125174	AGCCACCGCACCCAGCCAGT
203805	36001	TTAACCATTCTGAGTCTCAG	248392	80588	GAAATGACTCCAGGAGCTCC	292979	125175	GAGCCACCGCACCCAGCCAG
203806	36002	CTTAACCATTCTGAGTCTCA	248393	80589	GGAAATGACTCCAGGAGCTC	292980	125176	TGAGCCACCGCACCCAGCCA
203807	36003	ACTTAACCATTCTGAGTCTC	248394	80590	AGGAAATGACTCCAGGAGCT	292981	125177	ATGAGCCACCGCACCCAGCC
203808	36004	GACTTAACCATTCTGAGTCT	248395	80591	AAGGAAATGACTCCAGGAGC	292982	125178	CATGAGCCACCGCACCCAGC
203809	36005	TGACTTAACCATTCTGAGTC	248396	80592	GAAGGAAATGACTCCAGGAG	292983	125179	GCATGAGCCACCGCACCCAG
203810	36006	GTGACTTAACCATTCTGAGT	248397	80593	TGAAGGAAATGACTCCAGGA	292984	125180	GGCATGAGCCACCGCACCCA
203811	36007	AGTGACTTAACCATTCTGAG	248398	80594	ATGAAGGAAATGACTCCAGG	292985	125181	AGGCATGAGCCACCGCACCC
203812	36008	AAGTGACTTAACCATTCTGA	248399	80595	CATGAAGGAAATGACTCCAG	292986	125182	CAGGCATGAGCCACCGCACC
203813	36009	CAAGTGACTTAACCATTCTG	248400	80596	ACATGAAGGAAATGACTCCA	292987	125183	ACAGGCATGAGCCACCGCAC
203814	36010	ACAAGTGACTTAACCATTCT	248401	80597	GACATGAAGGAAATGACTCC	292988	125184	TACAGGCATGAGCCACCGCA
203815	36011	GACAAGTGACTTAACCATTC	248402	80598	AGACATGAAGGAAATGACTC	292989	125185	TTACAGGCATGAGCCACCGC
203816	36012	GGACAAGTGACTTAACCATT	248403	80599	AAGACATGAAGGAAATGACT	292990	125186	ATTACAGGCATGAGCCACCG
203817	36013	GGGACAAGTGACTTAACCAT	248404	80600	GAAGACATGAAGGAAATGAC	292991	125187	GATTACAGGCATGAGCCACC
203818	36014	TGGGACAAGTGACTTAACCA	248405	80601	AGAAGACATGAAGGAAATGA	292992	125188	GGATTACAGGCATGAGCCAC
203819	36015	CTGGGACAAGTGACTTAACC	248406	80602	AAGAAGACATGAAGGAAATG	292993	125189	GGGATTACAGGCATGAGCCA
203820	36016	CCTGGGACAAGTGACTTAAC	248407	80603	GAAGAAGACATGAAGGAAAT	292994	125190	TGGGATTACAGGCATGAGCC
203821	36017	GCCTGGGACAAGTGACTTAA	248408	80604	TGAAGAAGACATGAAGGAAA	292995	125191	CTGGGATTACAGGCATGAGC
203822	36018	GGCCTGGGACAAGTGACTTA	248409	80605	GTGAAGAAGACATGAAGGAA	292996	125192	GCTGGGATTACAGGCATGAG
203823	36019	TGGCCTGGGACAAGTGACTT	248410	80606	AGTGAAGAAGACATGAAGGA	292997	125193	TGCTGGGATTACAGGCATGA
203824	36020	GTGGCCTGGGACAAGTGACT	248411	80607	CAGTGAAGAAGACATGAAGG	292998	125194	GTGCTGGGATTACAGGCATG
203825	36021	TGTGGCCTGGGACAAGTGAC	248412	80608	GCAGTGAAGAAGACATGAAG	292999	125195	GGTGCTGGGATTACAGGCAT
203826	36022	GTGTGGCCTGGGACAAGTGA	248413	80609	TGCAGTGAAGAAGACATGAA	293000	125196	AGGTGCTGGGATTACAGGCA
203827	36023	TGTGTGGCCTGGGACAAGTG	248414	80610	GTGCAGTGAAGAAGACATGA	293001	125197	AAGGTGCTGGGATTACAGGC
203828	36024	CTGTGTGGCCTGGGACAAGT	248415	80611	AGTGCAGTGAAGAAGACATG	293002	125198	CAAGGTGCTGGGATTACAGG
203829	36025	GCTGTGTGGCCTGGGACAAG	248416	80612	AAGTGCAGTGAAGAAGACAT	293003	125199	CCAAGGTGCTGGGATTACAG
203830	36026	GGCTGTGTGGCCTGGGACAA	248417	80613	TAAGTGCAGTGAAGAAGACA	293004	125200	CCCAAGGTGCTGGGATTACA
203831	36027	TGGCTGTGTGGCCTGGGACA	248418	80614	GTAAGTGCAGTGAAGAAGAC	293005	125201	TCCCAAGGTGCTGGGATTAC
203832	36028	CTGGCTGTGTGGCCTGGGAC	248419	80615	CGTAAGTGCAGTGAAGAAGA	293006	125202	CTCCCAAGGTGCTGGGATTA
203833	36029	ACTGGCTGTGTGGCCTGGGA	248420	80616	ACGTAAGTGCAGTGAAGAAG	293007	125203	CCTCCCAAGGTGCTGGGATT
203834	36030	TACTGGCTGTGTGGCCTGGG	248421	80617	TACGTAAGTGCAGTGAAGAA	293008	125204	GCCTCCCAAGGTGCTGGGAT
203835	36031	TTACTGGCTGTGTGGCCTGG	248422	80618	TTACGTAAGTGCAGTGAAGA	293009	125205	CGCCTCCCAAGGTGCTGGGA
203836	36032	TTTACTGGCTGTGTGGCCTG	248423	80619	TTTACGTAAGTGCAGTGAAG	293010	125206	TCGCCTCCCAAGGTGCTGGG
203837	36033	ATTTACTGGCTGTGTGGCCT	248424	80620	CTTTACGTAAGTGCAGTGAA	293011	125207	TTCGCCTCCCAAGGTGCTGG
203838	36034	AATTTACTGGCTGTGTGGCC	248425	80621	TCTTTACGTAAGTGCAGTGA	293012	125208	CTTCGCCTCCCAAGGTGCTG
203839	36035	TAATTTACTGGCTGTGTGGC	248426	80622	ATCTTTACGTAAGTGCAGTG	293013	125209	CCTTCGCCTCCCAAGGTGCT
203840	36036	GTAATTTACTGGCTGTGTGG	248427	80623	CATCTTTACGTAAGTGCAGT	293014	125210	ACCTTCGCCTCCCAAGGTGC
203841	36037	TGTAATTTACTGGCTGTGTG	248428	80624	GCATCTTTACGTAAGTGCAG	293015	125211	CACCTTCGCCTCCCAAGGTG
203842	36038	CTGTAATTTACTGGCTGTGT	248429	80625	GGCATCTTTACGTAAGTGCA	293016	125212	CCACCTTCGCCTCCCAAGGT
203843	36039	TCTGTAATTTACTGGCTGTG	248430	80626	TGGCATCTTTACGTAAGTGC	293017	125213	CCCACCTTCGCCTCCCAAGG
203844	36040	TTCTGTAATTTACTGGCTGT	248431	80627	CTGGCATCTTTACGTAAGTG	293018	125214	GCCCACCTTCGCCTCCCAAG
203845	36041	TTTCTGTAATTTACTGGCTG	248432	80628	GCTGGCATCTTTACGTAAGT	293019	125215	TGCCCACCTTCGCCTCCCAA
203846	36042	GTTTCTGTAATTTACTGGCT	248433	80629	GGCTGGCATCTTTACGTAAG	293020	125216	CTGCCCACCTTCGCCTCCCA
203847	36043	TGTTTCTGTAATTTACTGGC	248434	80630	TGGCTGGCATCTTTACGTAA	293021	125217	TCTGCCCACCTTCGCCTCCC
203848	36044	CTGTTTCTGTAATTTACTGG	248435	80631	ATGGCTGGCATCTTTACGTA	293022	125218	ATCTGCCCACCTTCGCCTCC
203849	36045	TCTGTTTCTGTAATTTACTG	248436	80632	AATGGCTGGCATCTTTACGT	293023	125219	CATCTGCCCACCTTCGCCTC
203850	36046	TTCTGTTTCTGTAATTTACT	248437	80633	CAATGGCTGGCATCTTTACG	293024	125220	CCATCTGCCCACCTTCGCCT
203851	36047	ATTCTGTTTCTGTAATTTAC	248438	80634	CCAATGGCTGGCATCTTTAC	293025	125221	GCCATCTGCCCACCTTCGCC
203852	36048	AATTCTGTTTCTGTAATTTA	248439	80635	ACCAATGGCTGGCATCTTTA	293026	125222	AGCCATCTGCCCACCTTCGC
203853	36049	AAATTCTGTTTCTGTAATTT	248440	80636	AACCAATGGCTGGCATCTTT	293027	125223	AAGCCATCTGCCCACCTTCG
203854	36050	CAAATTCTGTTTCTGTAATT	248441	80637	AAACCAATGGCTGGCATCTT	293028	125224	CAAGCCATCTGCCCACCTTC
203855	36051	TCAAATTCTGTTTCTGTAAT	248442	80638	CAAACCAATGGCTGGCATCT	293029	125225	TCAAGCCATCTGCCCACCTT
203856	36052	TTCAAATTCTGTTTCTGTAA	248443	80639	CCAAACCAATGGCTGGCATC	293030	125226	CTCAAGCCATCTGCCCACCT
203857	36053	GTTCAAATTCTGTTTCTGTA	248444	80640	ACCAAACCAATGGCTGGCAT	293031	125227	CCTCAAGCCATCTGCCCACC
203858	36054	GGTTCAAATTCTGTTTCTGT	248445	80641	CACCAAACCAATGGCTGGCA	293032	125228	ACCTCAAGCCATCTGCCCAC
203859	36055	GGGTTCAAATTCTGTTTCTG	248446	80642	TCACCAAACCAATGGCTGGC	293033	125229	GACCTCAAGCCATCTGCCCA
203860	36056	TGGGTTCAAATTCTGTTTCT	248447	80643	ATCACCAAACCAATGGCTGG	293034	125230	TGACCTCAAGCCATCTGCCC
203861	36057	TTGGGTTCAAATTCTGTTTC	248448	80644	AATCACCAAACCAATGGCTG	293035	125231	CTGACCTCAAGCCATCTGCC
203862	36058	TTTGGGTTCAAATTCTGTTT	248449	80645	AAATCACCAAACCAATGGCT	293036	125232	CCTGACCTCAAGCCATCTGC
203863	36059	ATTTGGGTTCAAATTCTGTT	248450	80646	CAAATCACCAAACCAATGGC	293037	125233	TCCTGACCTCAAGCCATCTG
203864	36060	GATTTGGGTTCAAATTCTGT	248451	80647	CCAAATCACCAAACCAATGG	293038	125234	CTCCTGACCTCAAGCCATCT
203865	36061	AGATTTGGGTTCAAATTCTG	248452	80648	TCCAAATCACCAAACCAATG	293039	125235	ACTCCTGACCTCAAGCCATC
203866	36062	AAGATTTGGGTTCAAATTCT	248453	80649	CTCCAAATCACCAAACCAAT	293040	125236	AACTCCTGACCTCAAGCCAT
203867	36063	GAAGATTTGGGTTCAAATTC	248454	80650	CCTCCAAATCACCAAACCAA	293041	125237	GAACTCCTGACCTCAAGCCA
203868	36064	GGAAGATTTGGGTTCAAATT	248455	80651	CCCTCCAAATCACCAAACCA	293042	125238	TGAACTCCTGACCTCAAGCC
203869	36065	TGGAAGATTTGGGTTCAAAT	248456	80652	ACCCTCCAAATCACCAAACC	293043	125239	TTGAACTCCTGACCTCAAGC
203870	36066	CTGGAAGATTTGGGTTCAAA	248457	80653	CACCCTCCAAATCACCAAAC	293044	125240	CTTGAACTCCTGACCTCAAG
203871	36067	GCTGGAAGATTTGGGTTCAA	248458	80654	GCACCCTCCAAATCACCAAA	293045	125241	TCTTGAACTCCTGACCTCAA
203872	36068	AGCTGGAAGATTTGGGTTCA	248459	80655	GGCACCCTCCAAATCACCAA	293046	125242	GTCTTGAACTCCTGACCTCA
203873	36069	GAGCTGGAAGATTTGGGTTC	248460	80656	GGGCACCCTCCAAATCACCA	293047	125243	GGTCTTGAACTCCTGACCTC
203874	36070	GGAGCTGGAAGATTTGGGTT	248461	80657	TGGGCACCCTCCAAATCACC	293048	125244	TGGTCTTGAACTCCTGACCT

203875	36071	TGGAGCTGGAAGATTTGGGT	248462	80658	CTGGGCACCCTCCAAATCAC	293049	125245	CTGGTCTTGAACTCCTGACC
203876	36072	TTGGAGCTGGAAGATTTGGG	248463	80659	ACTGGGCACCCTCCAAATCA	293050	125246	GCTGGTCTTGAACTCCTGAC
203877	36073	TTTGGAGCTGGAAGATTTGG	248464	80660	AACTGGGCACCCTCCAAATC	293051	125247	GGCTGGTCTTGAACTCCTGA
203878	36074	CTTTGGAGCTGGAAGATTTG	248465	80661	CAACTGGGCACCCTCCAAAT	293052	125248	AGGCTGGTCTTGAACTCCTG
203879	36075	GCTTTGGAGCTGGAAGATTT	248466	80662	GCAACTGGGCACCCTCCAAA	293053	125249	CAGGCTGGTCTTGAACTCCT
203880	36076	AGCTTTGGAGCTGGAAGATT	248467	80663	GGCAACTGGGCACCCTCCAA	293054	125250	CCAGGCTGGTCTTGAACTCC
203881	36077	AAGCTTTGGAGCTGGAAGAT	248468	80664	GGGCAACTGGGCACCCTCCA	293055	125251	GCCAGGCTGGTCTTGAACTC
203882	36078	CAAGCTTTGGAGCTGGAAGA	248469	80665	TGGGCAACTGGGCACCCTCC	293056	125252	GGCCAGGCTGGTCTTGAACT
203883	36079	ACAAGCTTTGGAGCTGGAAG	248470	80666	TTGGGCAACTGGGCACCCTC	293057	125253	TGGCCAGGCTGGTCTTGAAC
203884	36080	CACAAGCTTTGGAGCTGGAA	248471	80667	GTTGGGCAACTGGGCACCCT	293058	125254	TTGGCCAGGCTGGTCTTGAA
203885	36081	ACACAAGCTTTGGAGCTGGA	248472	80668	TGTTGGGCAACTGGGCACCC	293059	125255	GTTGGCCAGGCTGGTCTTGA
203886	36082	AACACAAGCTTTGGAGCTGG	248473	80669	TTGTTGGGCAACTGGGCACC	293060	125256	TGTTGGCCAGGCTGGTCTTG
203887	36083	GAACACAAGCTTTGGAGCTG	248474	80670	CTTGTTGGGCAACTGGGCAC	293061	125257	ATGTTGGCCAGGCTGGTCTT
203888	36084	AGAACACAAGCTTTGGAGCT	248475	80671	TCTTGTTGGGCAACTGGGCA	293062	125258	CATGTTGGCCAGGCTGGTCT
203889	36085	AAGAACACAAGCTTTGGAGC	248476	80672	TTCTTGTTGGGCAACTGGGC	293063	125259	CCATGTTGGCCAGGCTGGTC
203890	36086	AAAGAACACAAGCTTTGGAG	248477	80673	TTTCTTGTTGGGCAACTGGG	293064	125260	ACCATGTTGGCCAGGCTGGT
203891	36087	AAAAGAACACAAGCTTTGGA	248478	80674	ATTTCTTGTTGGGCAACTGG	293065	125261	TACCATGTTGGCCAGGCTGG
203892	36088	GAAAAGAACACAAGCTTTGG	248479	80675	CATTTCTTGTTGGGCAACTG	293066	125262	TTACCATGTTGGCCAGGCTG
203893	36089	TGAAAAGAACACAAGCTTTG	248480	80676	GCATTTCTTGTTGGGCAACT	293067	125263	TTTACCATGTTGGCCAGGCT
203894	36090	GTGAAAAGAACACAAGCTTT	248481	80677	TGCATTTCTTGTTGGGCAAC	293068	125264	TTTTACCATGTTGGCCAGGC
203895	36091	AGTGAAAAGAACACAAGCTT	248482	80678	CTGCATTTCTTGTTGGGCAA	293069	125265	GTTTTACCATGTTGGCCAGG
203896	36092	TAGTGAAAAGAACACAAGCT	248483	80679	TCTGCATTTCTTGTTGGGCA	293070	125266	GGTTTTACCATGTTGGCCAG
203897	36093	GTAGTGAAAAGAACACAAGC	248484	80680	TTCTGCATTTCTTGTTGGGC	293071	125267	GGGTTTTACCATGTTGGCCA
203898	36094	GGTAGTGAAAAGAACACAAG	248485	80681	CTTCTGCATTTCTTGTTGGG	293072	125268	GGGGTTTTACCATGTTGGCC
203899	36095	AGGTAGTGAAAAGAACACAA	248486	80682	TCTTCTGCATTTCTTGTTGG	293073	125269	TGGGGTTTTACCATGTTGGC
203900	36096	GAGGTAGTGAAAAGAACACA	248487	80683	CTCTTCTGCATTTCTTGTTG	293074	125270	ATGGGGTTTTACCATGTTGG
203901	36097	GGAGGTAGTGAAAAGAACAC	248488	80684	CCTCTTCTGCATTTCTTGTT	293075	125271	GATGGGGTTTTACCATGTTG
203902	36098	AGGAGGTAGTGAAAAGAACA	248489	80685	GCCTCTTCTGCATTTCTTGT	293076	125272	AGATGGGGTTTTACCATGTT
203903	36099	CAGGAGGTAGTGAAAAGAAC	248490	80686	GGCCTCTTCTGCATTTCTTG	293077	125273	GAGATGGGGTTTTACCATGT
203904	36100	GCAGGAGGTAGTGAAAAGAA	248491	80687	AGGCCTCTTCTGCATTTCTT	293078	125274	AGAGATGGGGTTTTACCATG
203905	36101	AGCAGGAGGTAGTGAAAAGA	248492	80688	TAGGCCTCTTCTGCATTTCT	293079	125275	TAGAGATGGGGTTTTACCAT
203906	36102	AAGCAGGAGGTAGTGAAAAG	248493	80689	CTAGGCCTCTTCTGCATTTC	293080	125276	GTAGAGATGGGGTTTTACCA
203907	36103	TAAGCAGGAGGTAGTGAAAA	248494	80690	GCTAGGCCTCTTCTGCATTT	293081	125277	AGTAGAGATGGGGTTTTACC
203908	36104	TTAAGCAGGAGGTAGTGAAA	248495	80691	GGCTAGGCCTCTTCTGCATT	293082	125278	TAGTAGAGATGGGGTTTTAC
203909	36105	ATTAAGCAGGAGGTAGTGAA	248496	80692	TGGCTAGGCCTCTTCTGCAT	293083	125279	TTAGTAGAGATGGGGTTTTA
203910	36106	AATTAAGCAGGAGGTAGTGA	248497	80693	CTGGCTAGGCCTCTTCTGCA	293084	125280	TTTAGTAGAGATGGGGTTTT
203911	36107	AAATTAAGCAGGAGGTAGTG	248498	80694	CCTGGCTAGGCCTCTTCTGC	293085	125281	TTTTAGTAGAGATGGGGTTT
203912	36108	AAAATTAAGCAGGAGGTAGT	248499	80695	TCCTGGCTAGGCCTCTTCTG	293086	125282	TTTTTAGTAGAGATGGGGTT
203913	36109	AAAAATTAAGCAGGAGGTAG	248500	80696	ATCCTGGCTAGGCCTCTTCT	293087	125283	ATTTTTAGTAGAGATGGGGT
203914	36110	AAAAAATTAAGCAGGAGGTA	248501	80697	AATCCTGGCTAGGCCTCTTC	293088	125284	TATTTTTAGTAGAGATGGGG
203915	36111	TAAAAAATTAAGCAGGAGGT	248502	80698	AAATCCTGGCTAGGCCTCTT	293089	125285	GTATTTTTAGTAGAGATGGG
203916	36112	TTAAAAAATTAAGCAGGAGG	248503	80699	GAAATCCTGGCTAGGCCTCT	293090	125286	TGTATTTTTAGTAGAGATGG
203917	36113	ATTAAAAAATTAAGCAGGAG	248504	80700	TGAAATCCTGGCTAGGCCTC	293091	125287	TTGTATTTTTAGTAGAGATG
203918	36114	AATTAAAAAATTAAGCAGGA	248505	80701	GTGAAATCCTGGCTAGGCCT	293092	125288	TTTGTATTTTTAGTAGAGAT
203919	36115	AAATTAAAAAATTAAGCAGG	248506	80702	GGTGAAATCCTGGCTAGGCC	293093	125289	TTTTGTATTTTTAGTAGAGA
203920	36116	GAAATTAAAAAATTAAGCAG	248507	80703	TGGTGAAATCCTGGCTAGGC	293094	125290	CTTTTGTATTTTTAGTAGAG
203921	36117	AGAAATTAAAAAATTAAGCA	248508	80704	CTGGTGAAATCCTGGCTAGG	293095	125291	ACTTTTGTATTTTTAGTAGA
203922	36118	TAGAAATTAAAAAATTAAGC	248509	80705	GCTGGTGAAATCCTGGCTAG	293096	125292	AACTTTTGTATTTTTAGTAG
203923	36119	TTAGAAATTAAAAAATTAAG	248510	80706	TGCTGGTGAAATCCTGGCTA	293097	125293	TAACTTTTGTATTTTTAGTA
203924	36120	CTTAGAAATTAAAAAATTAA	248511	80707	CTGCTGGTGAAATCCTGGCT	293098	125294	CTAACTTTTGTATTTTTAGT
203925	36121	TCTTAGAAATTAAAAAATTA	248512	80708	ACTGCTGGTGAAATCCTGGC	293099	125295	GCTAACTTTTGTATTTTTAG
203926	36122	ATCTTAGAAATTAAAAAATT	248513	80709	CACTGCTGGTGAAATCCTGG	293100	125296	AGCTAACTTTTGTATTTTTA
203927	36123	AATCTTAGAAATTAAAAAAT	248514	80710	CCACTGCTGGTGAAATCCTG	293101	125297	CAGCTAACTTTTGTATTTTT
203928	36124	TAATCTTAGAAATTAAAAAA	248515	80711	TCCACTGCTGGTGAAATCCT	293102	125298	CCAGCTAACTTTTGTATTTT
203929	36125	CTAATCTTAGAAATTAAAAA	248516	80712	CTCCACTGCTGGTGAAATCC	293103	125299	CCCAGCTAACTTTTGTATTT
203930	36126	TCTAATCTTAGAAATTAAAA	248517	80713	TCTCCACTGCTGGTGAAATC	293104	125300	ACCCAGCTAACTTTTGTATT
203931	36127	GTCTAATCTTAGAAATTAAA	248518	80714	CTCTCCACTGCTGGTGAAAT	293105	125301	CACCCAGCTAACTTTTGTAT
203932	36128	GGTCTAATCTTAGAAATTAA	248519	80715	ACTCTCCACTGCTGGTGAAA	293106	125302	ACACCCAGCTAACTTTTGTA
203933	36129	GGGTCTAATCTTAGAAATTA	248520	80716	TACTCTCCACTGCTGGTGAA	293107	125303	CACACCCAGCTAACTTTTGT
203934	36130	AGGGTCTAATCTTAGAAATT	248521	80717	CTACTCTCCACTGCTGGTGA	293108	125304	CCACACCCAGCTAACTTTTG
203935	36131	AAGGGTCTAATCTTAGAAAT	248522	80718	TCTACTCTCCACTGCTGGTG	293109	125305	ACCACACCCAGCTAACTTTT
203936	36132	GAAGGGTCTAATCTTAGAAA	248523	80719	CTCTACTCTCCACTGCTGGT	293110	125306	CACCACACCCAGCTAACTTT
203937	36133	TGAAGGGTCTAATCTTAGAA	248524	80720	TCTCTACTCTCCACTGCTGG	293111	125307	CCACCACACCCAGCTAACTT
203938	36134	ATGAAGGGTCTAATCTTAGA	248525	80721	TTCTCTACTCTCCACTGCTG	293112	125308	ACCACCACACCCAGCTAACT
203939	36135	GATGAAGGGTCTAATCTTAG	248526	80722	CTTCTCTACTCTCCACTGCT	293113	125309	CACCACCACACCCAGCTAAC
203940	36136	AGATGAAGGGTCTAATCTTA	248527	80723	TCTTCTCTACTCTCCACTGC	293114	125310	GCACCACCACACCCAGCTAA
203941	36137	TAGATGAAGGGTCTAATCTT	248528	80724	ATCTTCTCTACTCTCCACTG	293115	125311	CGCACCACCACACCCAGCTA
203942	36138	ATAGATGAAGGGTCTAATCT	248529	80725	CATCTTCTCTACTCTCCACT	293116	125312	ACGCACCACCACACCCAGCT
203943	36139	GATAGATGAAGGGTCTAATC	248530	80726	ACATCTTCTCTACTCTCCAC	293117	125313	CACGCACCACCACACCCAGC
203944	36140	GGATAGATGAAGGGTCTAAT	248531	80727	CACATCTTCTCTACTCTCCA	293118	125314	GCACGCACCACCACACCCAG
203945	36141	TGGATAGATGAAGGGTCTAA	248532	80728	CCACATCTTCTCTACTCTCC	293119	125315	GGCACGCACCACCACACCCA
203946	36142	ATGGATAGATGAAGGGTCTA	248533	80729	GCCACATCTTCTCTACTCTC	293120	125316	AGGCACGCACCACCACACCC

203947	36143	CATGGATAGATGAAGGGTCT	248534	80730	GGCCACATCTTCTCTACTCT	293121	125317	CAGGCACGCACCACCACACC
203948	36144	TCATGGATAGATGAAGGGTC	248535	80731	TGGCCACATCTTCTCTACTC	293122	125318	ACAGGCACGCACCACCACAC
203949	36145	GTCATGGATAGATGAAGGGT	248536	80732	CTGGCCACATCTTCTCTACT	293123	125319	TACAGGCACGCACCACCACA
203950	36146	TGTCATGGATAGATGAAGGG	248537	80733	TCTGGCCACATCTTCTCTAC	293124	125320	TTACAGGCACGCACCACCAC
203951	36147	GTGTCATGGATAGATGAAGG	248538	80734	TTCTGGCCACATCTTCTCTA	293125	125321	ATTACAGGCACGCACCACCA
203952	36148	GGTGTCATGGATAGATGAAG	248539	80735	TTTCTGGCCACATCTTCTCT	293126	125322	GATTACAGGCACGCACCACC
203953	36149	AGGTGTCATGGATAGATGAA	248540	80736	TTTTCTGGCCACATCTTCTC	293127	125323	GGATTACAGGCACGCACCAC
203954	36150	CAGGTGTCATGGATAGATGA	248541	80737	CTTTTCTGGCCACATCTTCT	293128	125324	GGGATTACAGGCACGCACCA
203955	36151	GCAGGTGTCATGGATAGATG	248542	80738	TCTTTTCTGGCCACATCTTC	293129	125325	TGGGATTACAGGCACGCACC
203956	36152	GGCAGGTGTCATGGATAGAT	248543	80739	CTCTTTTCTGGCCACATCTT	293130	125326	CTGGGATTACAGGCACGCAC
203957	36153	AGGCAGGTGTCATGGATAGA	248544	80740	ACTCTTTTCTGGCCACATCT	293131	125327	GCTGGGATTACAGGCACGCA
203958	36154	CAGGCAGGTGTCATGGATAG	248545	80741	AACTCTTTTCTGGCCACATC	293132	125328	AGCTGGGATTACAGGCACGC
203959	36155	ACAGGCAGGTGTCATGGATA	248546	80742	AAACTCTTTTCTGGCCACAT	293133	125329	TAGCTGGGATTACAGGCACG
203960	36156	GACAGGCAGGTGTCATGGAT	248547	80743	GAAACTCTTTTCTGGCCACA	293134	125330	GTAGCTGGGATTACAGGCAC
203961	36157	TGACAGGCAGGTGTCATGGA	248548	80744	GGAAACTCTTTTCTGGCCAC	293135	125331	AGTAGCTGGGATTACAGGCA
203962	36158	ATGACAGGCAGGTGTCATGG	248549	80745	AGGAAACTCTTTTCTGGCCA	293136	125332	AAGTAGCTGGGATTACAGGC
203963	36159	GATGACAGGCAGGTGTCATG	248550	80746	AAGGAAACTCTTTTCTGGCC	293137	125333	CAAGTAGCTGGGATTACAGG
203964	36160	GGATGACAGGCAGGTGTCAT	248551	80747	AAAGGAAACTCTTTTCTGGC	293138	125334	CCAAGTAGCTGGGATTACAG
203965	36161	GGGATGACAGGCAGGTGTCA	248552	80748	GAAAGGAAACTCTTTTCTGG	293139	125335	CCCAAGTAGCTGGGATTACA
203966	36162	GGGGATGACAGGCAGGTGTC	248553	80749	GGAAAGGAAACTCTTTTCTG	293140	125336	TCCCAAGTAGCTGGGATTAC
203967	36163	AGGGGATGACAGGCAGGTGT	248554	80750	GGGAAAGGAAACTCTTTTCT	293141	125337	CTCCCAAGTAGCTGGGATTA
203968	36164	CAGGGGATGACAGGCAGGTG	248555	80751	AGGGAAAGGAAACTCTTTTC	293142	125338	CCTCCCAAGTAGCTGGGATT
203969	36165	TCAGGGGATGACAGGCAGGT	248556	80752	GAGGGAAAGGAAACTCTTTT	293143	125339	GCCTCCCAAGTAGCTGGGAT
203970	36166	TTCAGGGGATGACAGGCAGG	248557	80753	GGAGGGAAAGGAAACTCTTT	293144	125340	AGCCTCCCAAGTAGCTGGGA
203971	36167	TTTCAGGGGATGACAGGCAG	248558	80754	AGGAGGGAAAGGAAACTCTT	293145	125341	CAGCCTCCCAAGTAGCTGGG
203972	36168	TTTTCAGGGGATGACAGGCA	248559	80755	TAGGAGGGAAAGGAAACTCT	293146	125342	TCAGCCTCCCAAGTAGCTGG
203973	36169	TTTTTCAGGGGATGACAGGC	248560	80756	TTAGGAGGGAAAGGAAACTC	293147	125343	CTCAGCCTCCCAAGTAGCTG
203974	36170	TTTTTTCAGGGGATGACAGG	248561	80757	TTTAGGAGGGAAAGGAAACT	293148	125344	CCTCAGCCTCCCAAGTAGCT
203975	36171	CTTTTTTCAGGGGATGACAG	248562	80758	CTTTAGGAGGGAAAGGAAAC	293149	125345	GCCTCAGCCTCCCAAGTAGC
203976	36172	CCTTTTTTCAGGGGATGACA	248563	80759	TCTTTAGGAGGGAAAGGAAA	293150	125346	TGCCTCAGCCTCCCAAGTAG
203977	36173	ACCTTTTTTCAGGGGATGAC	248564	80760	ATCTTTAGGAGGGAAAGGAA	293151	125347	ATGCCTCAGCCTCCCAAGTA
203978	36174	CACCTTTTTTCAGGGGATGA	248565	80761	CATCTTTAGGAGGGAAAGGA	293152	125348	CATGCCTCAGCCTCCCAAGT
203979	36175	TCACCTTTTTTCAGGGGATG	248566	80762	CCATCTTTAGGAGGGAAAGG	293153	125349	TCATGCCTCAGCCTCCCAAG
203980	36176	TTCACCTTTTTTCAGGGGAT	248567	80763	ACCATCTTTAGGAGGGAAAG	293154	125350	CTCATGCCTCAGCCTCCCAA
203981	36177	GTTCACCTTTTTTCAGGGGA	248568	80764	TACCATCTTTAGGAGGGAAA	293155	125351	TCTCATGCCTCAGCCTCCCA
203982	36178	CGTTCACCTTTTTTCAGGGG	248569	80765	GTACCATCTTTAGGAGGGAA	293156	125352	TTCTCATGCCTCAGCCTCCC
203983	36179	GCGTTCACCTTTTTTCAGGG	248570	80766	AGTACCATCTTTAGGAGGGA	293157	125353	ATTCTCATGCCTCAGCCTCC
203984	36180	GGCGTTCACCTTTTTTCAGG	248571	80767	GAGTACCATCTTTAGGAGGG	293158	125354	AATTCTCATGCCTCAGCCTC
203985	36181	CGGCGTTCACCTTTTTTCAG	248572	80768	GGAGTACCATCTTTAGGAGG	293159	125355	CAATTCTCATGCCTCAGCCT
203986	36182	ACGGCGTTCACCTTTTTTCA	248573	80769	GGGAGTACCATCTTTAGGAG	293160	125356	GCAATTCTCATGCCTCAGCC
203987	36183	AACGGCGTTCACCTTTTTTC	248574	80770	AGGGAGTACCATCTTTAGGA	293161	125357	AGCAATTCTCATGCCTCAGC
203988	36184	GAACGGCGTTCACCTTTTTT	248575	80771	CAGGGAGTACCATCTTTAGG	293162	125358	AAGCAATTCTCATGCCTCAG
203989	36185	TGAACGGCGTTCACCTTTTT	248576	80772	GCAGGGAGTACCATCTTTAG	293163	125359	CAAGCAATTCTCATGCCTCA
203990	36186	CTGAACGGCGTTCACCTTTT	248577	80773	TGCAGGGAGTACCATCTTTA	293164	125360	TCAAGCAATTCTCATGCCTC
203991	36187	TCTGAACGGCGTTCACCTTT	248578	80774	CTGCAGGGAGTACCATCTTT	293165	125361	TTCAAGCAATTCTCATGCCT
203992	36188	TTCTGAACGGCGTTCACCTT	248579	80775	GCTGCAGGGAGTACCATCTT	293166	125362	GTTCAAGCAATTCTCATGCC
203993	36189	TTTCTGAACGGCGTTCACCT	248580	80776	AGCTGCAGGGAGTACCATCT	293167	125363	GGTTCAAGCAATTCTCATGC
203994	36190	ATTTCTGAACGGCGTTCACC	248581	80777	TAGCTGCAGGGAGTACCATC	293168	125364	GGGTTCAAGCAATTCTCATG
203995	36191	AATTTCTGAACGGCGTTCAC	248582	80778	GTAGCTGCAGGGAGTACCAT	293169	125365	TGGGTTCAAGCAATTCTCAT
203996	36192	AAATTTCTGAACGGCGTTCA	248583	80779	AGTAGCTGCAGGGAGTACCA	293170	125366	CTGGGTTCAAGCAATTCTCA
203997	36193	AAAATTTCTGAACGGCGTTC	248584	80780	CAGTAGCTGCAGGGAGTACC	293171	125367	CCTGGGTTCAAGCAATTCTC
203998	36194	AAAAATTTCTGAACGGCGTT	248585	80781	CCAGTAGCTGCAGGGAGTAC	293172	125368	CCCTGGGTTCAAGCAATTCT
203999	36195	GAAAAATTTCTGAACGGCGT	248586	80782	CCCAGTAGCTGCAGGGAGTA	293173	125369	CCCCTGGGTTCAAGCAATTC
204000	36196	AGAAAAATTTCTGAACGGCG	248587	80783	CCCCAGTAGCTGCAGGGAGT	293174	125370	TCCCCTGGGTTCAAGCAATT
204001	36197	TAGAAAAATTTCTGAACGGC	248588	80784	TCCCCAGTAGCTGCAGGGAG	293175	125371	GTCCCCTGGGTTCAAGCAAT
204002	36198	CTAGAAAAATTTCTGAACGG	248589	80785	TTCCCCAGTAGCTGCAGGGA	293176	125372	TGTCCCCTGGGTTCAAGCAA
204003	36199	GCTAGAAAAATTTCTGAACG	248590	80786	CTTCCCCAGTAGCTGCAGGG	293177	125373	CTGTCCCCTGGGTTCAAGCA
204004	36200	GGCTAGAAAAATTTCTGAAC	248591	80787	GCTTCCCCAGTAGCTGCAGG	293178	125374	TCTGTCCCCTGGGTTCAAGC
204005	36201	AGGCTAGAAAAATTTCTGAA	248592	80788	GGCTTCCCCAGTAGCTGCAG	293179	125375	CTCTGTCCCCTGGGTTCAAG
204006	36202	CAGGCTAGAAAAATTTCTGA	248593	80789	AGGCTTCCCCAGTAGCTGCA	293180	125376	CCTCTGTCCCCTGGGTTCAA
204007	36203	TCAGGCTAGAAAAATTTCTG	248594	80790	CAGGCTTCCCCAGTAGCTGC	293181	125377	ACCTCTGTCCCCTGGGTTCA
204008	36204	CTCAGGCTAGAAAAATTTCT	248595	80791	GCAGGCTTCCCCAGTAGCTG	293182	125378	AACCTCTGTCCCCTGGGTTC
204009	36205	GCTCAGGCTAGAAAAATTTC	248596	80792	TGCAGGCTTCCCCAGTAGCT	293183	125379	CAACCTCTGTCCCCTGGGTT
204010	36206	AGCTCAGGCTAGAAAAATTT	248597	80793	CTGCAGGCTTCCCCAGTAGC	293184	125380	ACAACCTCTGTCCCCTGGGT
204011	36207	GAGCTCAGGCTAGAAAAATT	248598	80794	GCTGCAGGCTTCCCCAGTAG	293185	125381	TACAACCTCTGTCCCCTGGG
204012	36208	TGAGCTCAGGCTAGAAAAAT	248599	80795	TGCTGCAGGCTTCCCCAGTA	293186	125382	CTACAACCTCTGTCCCCTGG
204013	36209	GTGAGCTCAGGCTAGAAAAA	248600	80796	ATGCTGCAGGCTTCCCCAGT	293187	125383	ACTACAACCTCTGTCCCCTG
204014	36210	AGTGAGCTCAGGCTAGAAAA	248601	80797	AATGCTGCAGGCTTCCCCAG	293188	125384	CACTACAACCTCTGTCCCCT
204015	36211	GAGTGAGCTCAGGCTAGAAA	248602	80798	GAATGCTGCAGGCTTCCCCA	293189	125385	TCACTACAACCTCTGTCCCC
204016	36212	GGAGTGAGCTCAGGCTAGAA	248603	80799	AGAATGCTGCAGGCTTCCCC	293190	125386	CTCACTACAACCTCTGTCCC
204017	36213	GGGAGTGAGCTCAGGCTAGA	248604	80800	GAGAATGCTGCAGGCTTCCC	293191	125387	GCTCACTACAACCTCTGTCC
204018	36214	TGGGAGTGAGCTCAGGCTAG	248605	80801	AGAGAATGCTGCAGGCTTCC	293192	125388	GGCTCACTACAACCTCTGTC

204019	36215	CTGGGAGTGAGCTCAGGCTA	248606	80802	TAGAGAATGCTGCAGGCTTC	293193	125389	CGGCTCACTACAACCTCTGT
204020	36216	ACTGGGAGTGAGCTCAGGCT	248607	80803	CTAGAGAATGCTGCAGGCTT	293194	125390	TCGGCTCACTACAACCTCTG
204021	36217	AACTGGGAGTGAGCTCAGGC	248608	80804	CCTAGAGAATGCTGCAGGCT	293195	125391	CTCGGCTCACTACAACCTCT
204022	36218	GAACTGGGAGTGAGCTCAGG	248609	80805	CCCTAGAGAATGCTGCAGGC	293196	125392	TCTCGGCTCACTACAACCTC
204023	36219	TGAACTGGGAGTGAGCTCAG	248610	80806	GCCCTAGAGAATGCTGCAGG	293197	125393	ATCTCGGCTCACTACAACCT
204024	36220	GTGAACTGGGAGTGAGCTCA	248611	80807	AGCCCTAGAGAATGCTGCAG	293198	125394	GATCTCGGCTCACTACAACC
204025	36221	AGTGAACTGGGAGTGAGCTC	248612	80808	GAGCCCTAGAGAATGCTGCA	293199	125395	CGATCTCGGCTCACTACAAC
204026	36222	AAGTGAACTGGGAGTGAGCT	248613	80809	AGAGCCCTAGAGAATGCTGC	293200	125396	ACGATCTCGGCTCACTACAA
204027	36223	TAAGTGAACTGGGAGTGAGC	248614	80810	CAGAGCCCTAGAGAATGCTG	293201	125397	CACGATCTCGGCTCACTACA
204028	36224	ATAAGTGAACTGGGAGTGAG	248615	80811	ACAGAGCCCTAGAGAATGCT	293202	125398	GCACGATCTCGGCTCACTAC
204029	36225	AATAAGTGAACTGGGAGTGA	248616	80812	CACAGAGCCCTAGAGAATGC	293203	125399	GGCACGATCTCGGCTCACTA
204030	36226	AAATAAGTGAACTGGGAGTG	248617	80813	ACACAGAGCCCTAGAGAATG	293204	125400	TGGCACGATCTCGGCTCACT
204031	36227	AAAATAAGTGAACTGGGAGT	248618	80814	CACACAGAGCCCTAGAGAAT	293205	125401	GTGGCACGATCTCGGCTCAC
204032	36228	AAAAATAAGTGAACTGGGAG	248619	80815	ACACACAGAGCCCTAGAGAA	293206	125402	AGTGGCACGATCTCGGCTCA
204033	36229	CAAAAATAAGTGAACTGGGA	248620	80816	AACACACAGAGCCCTAGAGA	293207	125403	CAGTGGCACGATCTCGGCTC
204034	36230	GCAAAAATAAGTGAACTGGG	248621	80817	CAACACACAGAGCCCTAGAG	293208	125404	GCAGTGGCACGATCTCGGCT
204035	36231	AGCAAAAATAAGTGAACTGG	248622	80818	TCAACACACAGAGCCCTAGA	293209	125405	TGCAGTGGCACGATCTCGGC
204036	36232	AAGCAAAAATAAGTGAACTG	248623	80819	CTCAACACACAGAGCCCTAG	293210	125406	GTGCAGTGGCACGATCTCGG
204037	36233	AAAGCAAAAATAAGTGAACT	248624	80820	TCTCAACACACAGAGCCCTA	293211	125407	AGTGCAGTGGCACGATCTCG
204038	36234	CAAAGCAAAAATAAGTGAAC	248625	80821	CTCTCAACACACAGAGCCCT	293212	125408	GAGTGCAGTGGCACGATCTC
204039	36235	ACAAAGCAAAAATAAGTGAA	248626	80822	GCTCTCAACACACAGAGCCC	293213	125409	GGAGTGCAGTGGCACGATCT
204040	36236	GACAAAGCAAAAATAAGTGA	248627	80823	TGCTCTCAACACACAGAGCC	293214	125410	TGGAGTGCAGTGGCACGATC
204041	36237	TGACAAAGCAAAAATAAGTG	248628	80824	CTGCTCTCAACACACAGAGC	293215	125411	CTGGAGTGCAGTGGCACGAT
204042	36238	ATGACAAAGCAAAAATAAGT	248629	80825	GCTGCTCTCAACACACAGAG	293216	125412	GCTGGAGTGCAGTGGCACGA
204043	36239	CATGACAAAGCAAAAATAAG	248630	80826	GGCTGCTCTCAACACACAGA	293217	125413	GGCTGGAGTGCAGTGGCACG
204044	36240	CCATGACAAAGCAAAAATAA	248631	80827	GGGCTGCTCTCAACACACAG	293218	125414	AGGCTGGAGTGCAGTGGCAC
204045	36241	GCCATGACAAAGCAAAAATA	248632	80828	GGGGCTGCTCTCAACACACA	293219	125415	CAGGCTGGAGTGCAGTGGCA
204046	36242	AGCCATGACAAAGCAAAAAT	248633	80829	TGGGGCTGCTCTCAACACAC	293220	125416	CCAGGCTGGAGTGCAGTGGC
204047	36243	CAGCCATGACAAAGCAAAAA	248634	80830	GTGGGGCTGCTCTCAACACA	293221	125417	CCCAGGCTGGAGTGCAGTGG
204048	36244	GCAGCCATGACAAAGCAAAA	248635	80831	GGTGGGGCTGCTCTCAACAC	293222	125418	GCCCAGGCTGGAGTGCAGTG
204049	36245	GGCAGCCATGACAAAGCAAA	248636	80832	GGGTGGGGCTGCTCTCAACA	293223	125419	TGCCCAGGCTGGAGTGCAGT
204050	36246	GGGCAGCCATGACAAAGCAA	248637	80833	AGGGTGGGGCTGCTCTCAAC	293224	125420	TTGCCCAGGCTGGAGTGCAG
204051	36247	TGGGCAGCCATGACAAAGCA	248638	80834	CAGGGTGGGGCTGCTCTCAA	293225	125421	GTTGCCCAGGCTGGAGTGCA
204052	36248	CTGGGCAGCCATGACAAAGC	248639	80835	CCAGGGTGGGGCTGCTCTCA	293226	125422	TGTTGCCCAGGCTGGAGTGC
204053	36249	ACTGGGCAGCCATGACAAAG	248640	80836	GCCAGGGTGGGGCTGCTCTC	293227	125423	CTGTTGCCCAGGCTGGAGTG
204054	36250	GACTGGGCAGCCATGACAAA	248641	80837	GGCCAGGGTGGGGCTGCTCT	293228	125424	TCTGTTGCCCAGGCTGGAGT
204055	36251	GGACTGGGCAGCCATGACAA	248642	80838	GGGCCAGGGTGGGGCTGCTC	293229	125425	CTCTGTTGCCCAGGCTGGAG
204056	36252	GGGACTGGGCAGCCATGACA	248643	80839	GGGGCCAGGGTGGGGCTGCT	293230	125426	ACTCTGTTGCCCAGGCTGGA
204057	36253	GGGGACTGGGCAGCCATGAC	248644	80840	AGGGGCCAGGGTGGGGCTGC	293231	125427	CACTCTGTTGCCCAGGCTGG
204058	36254	TGGGGACTGGGCAGCCATGA	248645	80841	AAGGGGCCAGGGTGGGGCTG	293232	125428	TCACTCTGTTGCCCAGGCTG
204059	36255	GTGGGGACTGGGCAGCCATG	248646	80842	GAAGGGGCCAGGGTGGGGCT	293233	125429	CTCACTCTGTTGCCCAGGCT
204060	36256	AGTGGGGACTGGGCAGCCAT	248647	80843	AGAAGGGGCCAGGGTGGGGC	293234	125430	TCTCACTCTGTTGCCCAGGC
204061	36257	AAGTGGGGACTGGGCAGCCA	248648	80844	CAGAAGGGGCCAGGGTGGGG	293235	125431	ATCTCACTCTGTTGCCCAGG
204062	36258	CAAGTGGGGACTGGGCAGCC	248649	80845	TCAGAAGGGGCCAGGGTGGG	293236	125432	AATCTCACTCTGTTGCCCAG
204063	36259	ACAAGTGGGGACTGGGCAGC	248650	80846	CTCAGAAGGGGCCAGGGTGG	293237	125433	GAATCTCACTCTGTTGCCCA
204064	36260	TACAAGTGGGGACTGGGCAG	248651	80847	ACTCAGAAGGGGCCAGGGTG	293238	125434	GGAATCTCACTCTGTTGCCC
204065	36261	CTACAAGTGGGGACTGGGCA	248652	80848	CACTCAGAAGGGGCCAGGGT	293239	125435	TGGAATCTCACTCTGTTGCC
204066	36262	TCTACAAGTGGGGACTGGGC	248653	80849	GCACTCAGAAGGGGCCAGGG	293240	125436	ATGGAATCTCACTCTGTTGC
204067	36263	GTCTACAAGTGGGGACTGGG	248654	80850	TGCACTCAGAAGGGGCCAGG	293241	125437	GATGGAATCTCACTCTGTTG
204068	36264	GGTCTACAAGTGGGGACTGG	248655	80851	ATGCACTCAGAAGGGGCCAG	293242	125438	AGATGGAATCTCACTCTGTT
204069	36265	TGGTCTACAAGTGGGGACTG	248656	80852	AATGCACTCAGAAGGGGCCA	293243	125439	GAGATGGAATCTCACTCTGT
204070	36266	CTGGTCTACAAGTGGGGACT	248657	80853	AAATGCACTCAGAAGGGGCC	293244	125440	TGAGATGGAATCTCACTCTG
204071	36267	CCTGGTCTACAAGTGGGGAC	248658	80854	GAAATGCACTCAGAAGGGGC	293245	125441	GTGAGATGGAATCTCACTCT
204072	36268	TCCTGGTCTACAAGTGGGGA	248659	80855	AGAAATGCACTCAGAAGGGG	293246	125442	TGTGAGATGGAATCTCACTC
204073	36269	TTCCTGGTCTACAAGTGGGG	248660	80856	CAGAAATGCACTCAGAAGGG	293247	125443	TTGTGAGATGGAATCTCACT
204074	36270	ATTCCTGGTCTACAAGTGGG	248661	80857	GCAGAAATGCACTCAGAAGG	293248	125444	TTTGTGAGATGGAATCTCAC
204075	36271	TATTCCTGGTCTACAAGTGG	248662	80858	AGCAGAAATGCACTCAGAAG	293249	125445	TTTTGTGAGATGGAATCTCA
204076	36272	CTATTCCTGGTCTACAAGTG	248663	80859	AAGCAGAAATGCACTCAGAA	293250	125446	TTTTTGTGAGATGGAATCTC
204077	36273	CCTATTCCTGGTCTACAAGT	248664	80860	AAAGCAGAAATGCACTCAGA	293251	125447	TTTTTTGTGAGATGGAATCT
204078	36274	ACCTATTCCTGGTCTACAAG	248665	80861	CAAAGCAGAAATGCACTCAG	293252	125448	TTTTTTTGTGAGATGGAATC
204079	36275	GACCTATTCCTGGTCTACAA	248666	80862	ACAAAGCAGAAATGCACTCA	293253	125449	TTTTTTTTGTGAGATGGAAT
204080	36276	TGACCTATTCCTGGTCTACA	248667	80863	CACAAAGCAGAAATGCACTC	293254	125450	TTTTTTTTTGTGAGATGGAA
204081	36277	ATGACCTATTCCTGGTCTAC	248668	80864	TCACAAAGCAGAAATGCACT	293255	125451	TTTTTTTTTTGTGAGATGGA
204082	36278	CATGACCTATTCCTGGTCTA	248669	80865	GTCACAAAGCAGAAATGCAC	293256	125452	TTTTTTTTTTTGTGAGATGG
204083	36279	CCATGACCTATTCCTGGTCT	248670	80866	AGTCACAAAGCAGAAATGCA	293257	125453	TTTTTTTTTTTTGTGAGATG
204084	36280	GCCATGACCTATTCCTGGTC	248671	80867	AAGTCACAAAGCAGAAATGC	293258	125454	TTTTTTTTTTTTTGTGAGAT
204085	36281	AGCCATGACCTATTCCTGGT	248672	80868	CAAGTCACAAAGCAGAAATG	293259	125455	TTTTTTTTTTTTTTGTGAGA
204086	36282	CAGCCATGACCTATTCCTGG	248673	80869	TCAAGTCACAAAGCAGAAAT	293260	125456	TTTTTTTTTTTTTTTGTGAG
204087	36283	GCAGCCATGACCTATTCCTG	248674	80870	ATCAAGTCACAAAGCAGAAA	293261	125457	TTTTTTTTTTTTTTTGTGA
204088	36284	CGCAGCCATGACCTATTCCT	248675	80871	GATCAAGTCACAAAGCAGAA	293262	125458	CTTTTTTTTTTTTTTTGTG
204089	36285	CCGCAGCCATGACCTATTCC	248676	80872	GGATCAAGTCACAAAGCAGA	293263	125459	GCTTTTTTTTTTTTTTTGT
204090	36286	CCCGCAGCCATGACCTATTC	248677	80873	CGGATCAAGTCACAAAGCAG	293264	125460	CGCTTTTTTTTTTTTTTTG

204091	36287	CCCCGCAGCCATGACCTATT	248678	80874	ACGGATCAAGTCACAAAGCA	293265	125461	TCGCTTTTTTTTTTTTTTT
204092	36288	TCCCCGCAGCCATGACCTAT	248679	80875	CACGGATCAAGTCACAAAGC	293266	125462	CTCGCTTTTTTTTTTTTTT
204093	36289	GTCCCCGCAGCCATGACCTA	248680	80876	TCACGGATCAAGTCACAAAG	293267	125463	TCTCGCTTTTTTTTTTTTT
204094	36290	AGTCCCCGCAGCCATGACCT	248681	80877	TTCACGGATCAAGTCACAAA	293268	125464	TTCTCGCTTTTTTTTTTTT
204095	36291	TAGTCCCCGCAGCCATGACC	248682	80878	CTTCACGGATCAAGTCACAA	293269	125465	GTTCTCGCTTTTTTTTTTT
204096	36292	GTAGTCCCCGCAGCCATGAC	248683	80879	ACTTCACGGATCAAGTCACA	293270	125466	GGTTCTCGCTTTTTTTTTT
204097	36293	TGTAGTCCCCGCAGCCATGA	248684	80880	GACTTCACGGATCAAGTCAC	293271	125467	TGGTTCTCGCTTTTTTTTT
204098	36294	GTGTAGTCCCCGCAGCCATG	248685	80881	GGACTTCACGGATCAAGTCA	293272	125468	GTGGTTCTCGCTTTTTTTT
204099	36295	CGTGTAGTCCCCGCAGCCAT	248686	80882	GGGACTTCACGGATCAAGTC	293273	125469	AGTGGTTCTCGCTTTTTTT
204100	36296	GCGTGTAGTCCCCGCAGCCA	248687	80883	GGGGACTTCACGGATCAAGT	293274	125470	CAGTGGTTCTCGCTTTTTT
204101	36297	AGCGTGTAGTCCCCGCAGCC	248688	80884	AGGGGACTTCACGGATCAAG	293275	125471	ACAGTGGTTCTCGCTTTTT
204102	36298	CAGCGTGTAGTCCCCGCAGC	248689	80885	CAGGGGACTTCACGGATCAA	293276	125472	GACAGTGGTTCTCGCTTTT
204103	36299	ACAGCGTGTAGTCCCCGCAG	248690	80886	TCAGGGGACTTCACGGATCA	293277	125473	GGACAGTGGTTCTCGCTTT
204104	36300	GACAGCGTGTAGTCCCCGCA	248691	80887	CTCAGGGGACTTCACGGATC	293278	125474	AGGACAGTGGTTCTCGCTT
204105	36301	CGACAGCGTGTAGTCCCCGC	248692	80888	TCTCAGGGGACTTCACGGAT	293279	125475	TAGGACAGTGGTTCTCGCTT
204106	36302	GCGACAGCGTGTAGTCCCCG	248693	80889	ATCTCAGGGGACTTCACGGA	293280	125476	CTAGGACAGTGGTTCTCGCT
204107	36303	AGCGACAGCGTGTAGTCCCC	248694	80890	CATCTCAGGGGACTTCACGG	293281	125477	CCTAGGACAGTGGTTCTCGC
204108	36304	CAGCGACAGCGTGTAGTCCC	248695	80891	CCATCTCAGGGGACTTCACG	293282	125478	GCCTAGGACAGTGGTTCTCG
204109	36305	GCAGCGACAGCGTGTAGTCC	248696	80892	CCCATCTCAGGGGACTTCAC	293283	125479	GGCCTAGGACAGTGGTTCTC
204110	36306	AGCAGCGACAGCGTGTAGTC	248697	80893	GCCCATCTCAGGGGACTTCA	293284	125480	GGGCCTAGGACAGTGGTTCT
204111	36307	CAGCAGCGACAGCGTGTAGT	248698	80894	TGCCCATCTCAGGGGACTTC	293285	125481	AGGGCCTAGGACAGTGGTTC
204112	36308	GCAGCAGCGACAGCGTGTAG	248699	80895	CTGCCCATCTCAGGGGACTT	293286	125482	CAGGGCCTAGGACAGTGGTT
204113	36309	TGCAGCAGCGACAGCGTGTA	248700	80896	TCTGCCCATCTCAGGGGACT	293287	125483	TCAGGGCCTAGGACAGTGGT
204114	36310	TTGCAGCAGCGACAGCGTGT	248701	80897	CTCTGCCCATCTCAGGGGAC	293288	125484	ATCAGGGCCTAGGACAGTGG
204115	36311	CTTGCAGCAGCGACAGCGTG	248702	80898	CCTCTGCCCATCTCAGGGGA	293289	125485	CATCAGGGCCTAGGACAGTG
204116	36312	CCTTGCAGCAGCGACAGCGT	248703	80899	CCCTCTGCCCATCTCAGGGG	293290	125486	ACATCAGGGCCTAGGACAGT
204117	36313	CCCTTGCAGCAGCGACAGCG	248704	80900	CCCCTCTGCCCATCTCAGGG	293291	125487	AACATCAGGGCCTAGGACAG
204118	36314	GCCCTTGCAGCAGCGACAGC	248705	80901	TCCCCTCTGCCCATCTCAGG	293292	125488	AAACATCAGGGCCTAGGACA
204119	36315	GGCCCTTGCAGCAGCGACAG	248706	80902	ATCCCCTCTGCCCATCTCAG	293293	125489	CAAACATCAGGGCCTAGGAC
204120	36316	CGGCCCTTGCAGCAGCGACA	248707	80903	CATCCCCTCTGCCCATCTCA	293294	125490	GCAAACATCAGGGCCTAGGA
204121	36317	CCGGCCCTTGCAGCAGCGAC	248708	80904	ACATCCCCTCTGCCCATCTC	293295	125491	TGCAAACATCAGGGCCTAGG
204122	36318	GCCGGCCCTTGCAGCAGCGA	248709	80905	GACATCCCCTCTGCCCATCT	293296	125492	CTGCAAACATCAGGGCCTAG
204123	36319	GGCCGGCCCTTGCAGCAGCG	248710	80906	GGACATCCCCTCTGCCCATC	293297	125493	CCTGCAAACATCAGGGCCTA
204124	36320	AGGCCGGCCCTTGCAGCAGC	248711	80907	AGGACATCCCCTCTGCCCAT	293298	125494	GCCTGCAAACATCAGGGCCT
204125	36321	GAGGCCGGCCCTTGCAGCAG	248712	80908	GAGGACATCCCCTCTGCCCA	293299	125495	TGCCTGCAAACATCAGGGCC
204126	36322	AGAGGCCGGCCCTTGCAGCA	248713	80909	CGAGGACATCCCCTCTGCCC	293300	125496	TTGCCTGCAAACATCAGGGC
204127	36323	CAGAGGCCGGCCCTTGCAGC	248714	80910	TCGAGGACATCCCCTCTGCC	293301	125497	GTTGCCTGCAAACATCAGGG
204128	36324	ACAGAGGCCGGCCCTTGCAG	248715	80911	TTCGAGGACATCCCCTCTGC	293302	125498	AGTTGCCTGCAAACATCAGG
204129	36325	AACAGAGGCCGGCCCTTGCA	248716	80912	CTTCGAGGACATCCCCTCTG	293303	125499	TAGTTGCCTGCAAACATCAG
204130	36326	AAACAGAGGCCGGCCCTTGC	248717	80913	GCTTCGAGGACATCCCCTCT	293304	125500	TTAGTTGCCTGCAAACATCA
204131	36327	GAAACAGAGGCCGGCCCTTG	248718	80914	AGCTTCGAGGACATCCCCTC	293305	125501	TTTAGTTGCCTGCAAACATC
204132	36328	GGAAACAGAGGCCGGCCCTT	248719	80915	CAGCTTCGAGGACATCCCCT	293306	125502	TTTTAGTTGCCTGCAAACAT
204133	36329	CGGAAACAGAGGCCGGCCCT	248720	80916	CCAGCTTCGAGGACATCCCC	293307	125503	TTTTTAGTTGCCTGCAAACA
204134	36330	CCGGAAACAGAGGCCGGCCC	248721	80917	CCCAGCTTCGAGGACATCCC	293308	125504	TTTTTTAGTTGCCTGCAAAC
204135	36331	CCCGGAAACAGAGGCCGGCC	248722	80918	CCCCAGCTTCGAGGACATCC	293309	125505	CTTTTTTAGTTGCCTGCAAA
204136	36332	CCCCGGAAACAGAGGCCGGC	248723	80919	GCCCCAGCTTCGAGGACATC	293310	125506	CCTTTTTTAGTTGCCTGCAA
204137	36333	GCCCCGGAAACAGAGGCCGG	248724	80920	TGCCCCAGCTTCGAGGACAT	293311	125507	TCCTTTTTTAGTTGCCTGCA
204138	36334	AGCCCCGGAAACAGAGGCCG	248725	80921	CTGCCCCAGCTTCGAGGACA	293312	125508	TTCCTTTTTTAGTTGCCTGC
204139	36335	CAGCCCCGGAAACAGAGGCC	248726	80922	TCTGCCCCAGCTTCGAGGAC	293313	125509	CTTCCTTTTTTAGTTGCCTG
204140	36336	TCAGCCCCGGAAACAGAGGC	248727	80923	CTCTGCCCCAGCTTCGAGGA	293314	125510	ACTTCCTTTTTTAGTTGCCT
204141	36337	CTCAGCCCCGGAAACAGAGG	248728	80924	GCTCTGCCCCAGCTTCGAGG	293315	125511	CACTTCCTTTTTTAGTTGCC
204142	36338	ACTCAGCCCCGGAAACAGAG	248729	80925	GGCTCTGCCCCAGCTTCGAG	293316	125512	CCACTTCCTTTTTTAGTTGC
204143	36339	CACTCAGCCCCGGAAACAGA	248730	80926	AGGCTCTGCCCCAGCTTCGA	293317	125513	TCCACTTCCTTTTTTAGTTG
204144	36340	CCACTCAGCCCCGGAAACAG	248731	80927	GAGGCTCTGCCCCAGCTTCG	293318	125514	GTCCACTTCCTTTTTTAGTT
204145	36341	CCCACTCAGCCCCGGAAACA	248732	80928	TGAGGCTCTGCCCCAGCTTC	293319	125515	TGTCCACTTCCTTTTTTAGT
204146	36342	CCCCACTCAGCCCCGGAAAC	248733	80929	ATGAGGCTCTGCCCCAGCTT	293320	125516	ATGTCCACTTCCTTTTTTAG
204147	36343	CCCCCACTCAGCCCCGGAAA	248734	80930	GATGAGGCTCTGCCCCAGCT	293321	125517	GATGTCCACTTCCTTTTTTA
204148	36344	GCCCCCACTCAGCCCCGGAA	248735	80931	GGATGAGGCTCTGCCCCAGC	293322	125518	GGATGTCCACTTCCTTTTTT
204149	36345	GGCCCCCACTCAGCCCCGGA	248736	80932	AGGATGAGGCTCTGCCCCAG	293323	125519	GGGATGTCCACTTCCTTTTT
204150	36346	TGGCCCCCACTCAGCCCCGG	248737	80933	AAGGATGAGGCTCTGCCCCA	293324	125520	GGGGATGTCCACTTCCTTTT
204151	36347	CTGGCCCCCACTCAGCCCCG	248738	80934	CAAGGATGAGGCTCTGCCCC	293325	125521	TGGGGATGTCCACTTCCTTT
204152	36348	TCTGGCCCCCACTCAGCCCC	248739	80935	TCAAGGATGAGGCTCTGCCC	293326	125522	CTGGGGATGTCCACTTCCTT
204153	36349	GTCTGGCCCCCACTCAGCCC	248740	80936	TTCAAGGATGAGGCTCTGCC	293327	125523	ACTGGGGATGTCCACTTCCT
204154	36350	GGTCTGGCCCCCACTCAGCC	248741	80937	GTTCAAGGATGAGGCTCTGC	293328	125524	GACTGGGGATGTCCACTTCC
204155	36351	AGGTCTGGCCCCCACTCAGC	248742	80938	CGTTCAAGGATGAGGCTCTG	293329	125525	TGACTGGGGATGTCCACTTC
204156	36352	CAGGTCTGGCCCCCACTCAG	248743	80939	ACGTTCAAGGATGAGGCTCT	293330	125526	CTGACTGGGGATGTCCACTT
204157	36353	GCAGGTCTGGCCCCCACTCA	248744	80940	CACGTTCAAGGATGAGGCTC	293331	125527	GCTGACTGGGGATGTCCACT
204158	36354	GGCAGGTCTGGCCCCCACTC	248745	80941	TCACGTTCAAGGATGAGGCT	293332	125528	AGCTGACTGGGGATGTCCAC
204159	36355	TGGCAGGTCTGGCCCCCACT	248746	80942	TTCACGTTCAAGGATGAGGC	293333	125529	CAGCTGACTGGGGATGTCCA
204160	36356	CTGGCAGGTCTGGCCCCCAC	248747	80943	CTTCACGTTCAAGGATGAGG	293334	125530	ACAGCTGACTGGGGATGTCC
204161	36357	CCTGGCAGGTCTGGCCCCCA	248748	80944	CCTTCACGTTCAAGGATGAG	293335	125531	CACAGCTGACTGGGGATGTC
204162	36358	TCCTGGCAGGTCTGGCCCCC	248749	80945	TCCTTCACGTTCAAGGATGA	293336	125532	CCACAGCTGACTGGGGATGT

204163	36359	CTCCTGGCAGGTCTGGCCCC	248750	80946	GTCCTTCACGTTCAAGGATG	293337	125533	GCCACAGCTGACTGGGGATG
204164	36360	GCTCCTGGCAGGTCTGGCCC	248751	80947	CGTCCTTCACGTTCAAGGAT	293338	125534	CGCCACAGCTGACTGGGGAT
204165	36361	TGCTCCTGGCAGGTCTGGCC	248752	80948	ACGTCCTTCACGTTCAAGGA	293339	125535	GCGCCACAGCTGACTGGGGA
204166	36362	GTGCTCCTGGCAGGTCTGGC	248753	80949	AACGTCCTTCACGTTCAAGG	293340	125536	TGCGCCACAGCTGACTGGGG
204167	36363	GGTGCTCCTGGCAGGTCTGG	248754	80950	AAACGTCCTTCACGTTCAAG	293341	125537	GTGCGCCACAGCTGACTGGG
204168	36364	TGGTGCTCCTGGCAGGTCTG	248755	80951	CAAACGTCCTTCACGTTCAA	293342	125538	GGTGCGCCACAGCTGACTGG
204169	36365	ATGGTGCTCCTGGCAGGTCT	248756	80952	TCAAACGTCCTTCACGTTCA	293343	125539	TGGTGCGCCACAGCTGACTG
204170	36366	GATGGTGCTCCTGGCAGGTC	248757	80953	TTCAAACGTCCTTCACGTTC	293344	125540	TTGGTGCGCCACAGCTGACT
204171	36367	AGATGGTGCTCCTGGCAGGT	248758	80954	CTTCAAACGTCCTTCACGTT	293345	125541	CTTGGTGCGCCACAGCTGAC
204172	36368	AAGATGGTGCTCCTGGCAGG	248759	80955	TCTTCAAACGTCCTTCACGT	293346	125542	TCTTGGTGCGCCACAGCTGA
204173	36369	GAAGATGGTGCTCCTGGCAG	248760	80956	GTCTTCAAACGTCCTTCACG	293347	125543	TTCTTGGTGCGCCACAGCTG
204174	36370	AGAAGATGGTGCTCCTGGCA	248761	80957	AGTCTTCAAACGTCCTTCAC	293348	125544	GTTCTTGGTGCGCCACAGCT
204175	36371	CAGAAGATGGTGCTCCTGGC	248762	80958	CAGTCTTCAAACGTCCTTCA	293349	125545	TGTTCTTGGTGCGCCACAGC
204176	36372	ACAGAAGATGGTGCTCCTGG	248763	80959	ACAGTCTTCAAACGTCCTTC	293350	125546	TTGTTCTTGGTGCGCCACAG
204177	36373	CACAGAAGATGGTGCTCCTG	248764	80960	CACAGTCTTCAAACGTCCTT	293351	125547	CTTGTTCTTGGTGCGCCACA
204178	36374	CCACAGAAGATGGTGCTCCT	248765	80961	CCACAGTCTTCAAACGTCCT	293352	125548	ACTTGTTCTTGGTGCGCCAC
204179	36375	CCCACAGAAGATGGTGCTCC	248766	80962	GCCACAGTCTTCAAACGTCC	293353	125549	GACTTGTTCTTGGTGCGCCA
204180	36376	ACCCACAGAAGATGGTGCTC	248767	80963	TGCCACAGTCTTCAAACGTC	293354	125550	TGACTTGTTCTTGGTGCGCC
204181	36377	GACCCACAGAAGATGGTGCT	248768	80964	ATGCCACAGTCTTCAAACGT	293355	125551	ATGACTTGTTCTTGGTGCGC
204182	36378	GGACCCACAGAAGATGGTGC	248769	80965	CATGCCACAGTCTTCAAACG	293356	125552	CATGACTTGTTCTTGGTGCG
204183	36379	AGGACCCACAGAAGATGGTG	248770	80966	TCATGCCACAGTCTTCAAAC	293357	125553	CCATGACTTGTTCTTGGTGC
204184	36380	CAGGACCCACAGAAGATGGT	248771	80967	ATCATGCCACAGTCTTCAAA	293358	125554	CCCATGACTTGTTCTTGGTG
204185	36381	GCAGGACCCACAGAAGATGG	248772	80968	GATCATGCCACAGTCTTCAA	293359	125555	TCCCATGACTTGTTCTTGGT
204186	36382	GGCAGGACCCACAGAAGATG	248773	80969	TGATCATGCCACAGTCTTCA	293360	125556	TTCCCATGACTTGTTCTTGG
204187	36383	AGGCAGGACCCACAGAAGAT	248774	80970	GTGATCATGCCACAGTCTTC	293361	125557	GTTCCCATGACTTGTTCTTG
204188	36384	CAGGCAGGACCCACAGAAGA	248775	80971	TGTGATCATGCCACAGTCTT	293362	125558	TGTTCCCATGACTTGTTCTT
204189	36385	CCAGGCAGGACCCACAGAAG	248776	80972	CTGTGATCATGCCACAGTCT	293363	125559	ATGTTCCCATGACTTGTTCT
204190	36386	TCCAGGCAGGACCCACAGAA	248777	80973	CCTGTGATCATGCCACAGTC	293364	125560	TATGTTCCCATGACTTGTTC
204191	36387	ATCCAGGCAGGACCCACAGA	248778	80974	TCCTGTGATCATGCCACAGT	293365	125561	TTATGTTCCCATGACTTGTT
204192	36388	CATCCAGGCAGGACCCACAG	248779	80975	ATCCTGTGATCATGCCACAG	293366	125562	GTTATGTTCCCATGACTTGT
204193	36389	ACATCCAGGCAGGACCCACA	248780	80976	CATCCTGTGATCATGCCACA	293367	125563	GGTTATGTTCCCATGACTTG
204194	36390	GACATCCAGGCAGGACCCAC	248781	80977	TCATCCTGTGATCATGCCAC	293368	125564	AGGTTATGTTCCCATGACTT
204195	36391	TGACATCCAGGCAGGACCCA	248782	80978	CTCATCCTGTGATCATGCCA	293369	125565	TAGGTTATGTTCCCATGACT
204196	36392	GTGACATCCAGGCAGGACCC	248783	80979	TCTCATCCTGTGATCATGCC	293370	125566	TTAGGTTATGTTCCCATGAC
204197	36393	TGTGACATCCAGGCAGGACC	248784	80980	ATCTCATCCTGTGATCATGC	293371	125567	ATTAGGTTATGTTCCCATGA
204198	36394	ATGTGACATCCAGGCAGGAC	248785	80981	GATCTCATCCTGTGATCATG	293372	125568	AATTAGGTTATGTTCCCATG
204199	36395	GATGTGACATCCAGGCAGGA	248786	80982	TGATCTCATCCTGTGATCAT	293373	125569	AAATTAGGTTATGTTCCCAT
204200	36396	GGATGTGACATCCAGGCAGG	248787	80983	GTGATCTCATCCTGTGATCA	293374	125570	AAAATTAGGTTATGTTCCCA
204201	36397	GGGATGTGACATCCAGGCAG	248788	80984	TGTGATCTCATCCTGTGATC	293375	125571	GAAAATTAGGTTATGTTCCC
204202	36398	CGGGATGTGACATCCAGGCA	248789	80985	CTGTGATCTCATCCTGTGAT	293376	125572	AGAAAATTAGGTTATGTTCC
204203	36399	CCGGGATGTGACATCCAGGC	248790	80986	CCTGTGATCTCATCCTGTGA	293377	125573	TAGAAAATTAGGTTATGTTC
204204	36400	GCCGGGATGTGACATCCAGG	248791	80987	CCCTGTGATCTCATCCTGTG	293378	125574	TTAGAAAATTAGGTTATGTT
204205	36401	GGCCGGGATGTGACATCCAG	248792	80988	TCCCTGTGATCTCATCCTGT	293379	125575	TTTAGAAAATTAGGTTATGT
204206	36402	GGGCCGGGATGTGACATCCA	248793	80989	TTCCCTGTGATCTCATCCTG	293380	125576	ATTTAGAAAATTAGGTTATG
204207	36403	GGGGCCGGGATGTGACATCC	248794	80990	GTTCCCTGTGATCTCATCCT	293381	125577	CATTTAGAAAATTAGGTTAT
204208	36404	TGGGGCCGGGATGTGACATC	248795	80991	AGTTCCCTGTGATCTCATCC	293382	125578	CCATTTAGAAAATTAGGTTA
204209	36405	TTGGGGCCGGGATGTGACAT	248796	80992	AAGTTCCCTGTGATCTCATC	293383	125579	CCCATTTAGAAAATTAGGTT
204210	36406	CTTGGGGCCGGGATGTGACA	248797	80993	CAAGTTCCCTGTGATCTCAT	293384	125580	ACCCATTTAGAAAATTAGGT
204211	36407	TCTTGGGGCCGGGATGTGAC	248798	80994	TCAAGTTCCCTGTGATCTCA	293385	125581	AACCCATTTAGAAAATTAGG
204212	36408	TTCTTGGGGCCGGGATGTGA	248799	80995	CTCAAGTTCCCTGTGATCTC	293386	125582	TAACCCATTTAGAAAATTAG
204213	36409	CTTCTTGGGGCCGGGATGTG	248800	80996	ACTCAAGTTCCCTGTGATCT	293387	125583	GTAACCCATTTAGAAAATTA
204214	36410	ACTTCTTGGGGCCGGGATGT	248801	80997	AACTCAAGTTCCCTGTGATC	293388	125584	AGTAACCCATTTAGAAAATT
204215	36411	GACTTCTTGGGGCCGGGATG	248802	80998	AAACTCAAGTTCCCTGTGAT	293389	125585	TAGTAACCCATTTAGAAAAT
204216	36412	TGACTTCTTGGGGCCGGGAT	248803	80999	GAAACTCAAGTTCCCTGTGA	293390	125586	CTAGTAACCCATTTAGAAAA
204217	36413	GTGACTTCTTGGGGCCGGGA	248804	81000	AGAAACTCAAGTTCCCTGTG	293391	125587	CCTAGTAACCCATTTAGAAA
204218	36414	AGTGACTTCTTGGGGCCGGG	248805	81001	GAGAAACTCAAGTTCCCTGT	293392	125588	GCCTAGTAACCCATTTAGAA
204219	36415	CAGTGACTTCTTGGGGCCGG	248806	81002	AGAGAAACTCAAGTTCCCTG	293393	125589	TGCCTAGTAACCCATTTAGA
204220	36416	GCAGTGACTTCTTGGGGCCG	248807	81003	GAGAGAAACTCAAGTTCCCT	293394	125590	GTGCCTAGTAACCCATTTAG
204221	36417	TGCAGTGACTTCTTGGGGCC	248808	81004	GGAGAGAAACTCAAGTTCCC	293395	125591	AGTGCCTAGTAACCCATTTA
204222	36418	TTGCAGTGACTTCTTGGGGC	248809	81005	AGGAGAGAAACTCAAGTTCC	293396	125592	AAGTGCCTAGTAACCCATTT
204223	36419	TTTGCAGTGACTTCTTGGGG	248810	81006	GAGGAGAGAAACTCAAGTTC	293397	125593	TAAGTGCCTAGTAACCCATT
204224	36420	GTTTGCAGTGACTTCTTGGG	248811	81007	GGAGGAGAGAAACTCAAGTT	293398	125594	CTAAGTGCCTAGTAACCCAT
204225	36421	GGTTTGCAGTGACTTCTTGG	248812	81008	AGGAGGAGAGAAACTCAAGT	293399	125595	TCTAAGTGCCTAGTAACCCA
204226	36422	AGGTTTGCAGTGACTTCTTG	248813	81009	GAGGAGGAGAGAAACTCAAG	293400	125596	CTCTAAGTGCCTAGTAACCC
204227	36423	AAGGTTTGCAGTGACTTCTT	248814	81010	AGAGGAGGAGAGAAACTCAA	293401	125597	GCTCTAAGTGCCTAGTAACC
204228	36424	GAAGGTTTGCAGTGACTTCT	248815	81011	GAGAGGAGGAGAGAAACTCA	293402	125598	TGCTCTAAGTGCCTAGTAAC
204229	36425	CGAAGGTTTGCAGTGACTTC	248816	81012	GGAGAGGAGGAGAGAAACTC	293403	125599	TTGCTCTAAGTGCCTAGTAA
204230	36426	ACGAAGGTTTGCAGTGACTT	248817	81013	GGGAGAGGAGGAGAGAAACT	293404	125600	TTTGCTCTAAGTGCCTAGTA
204231	36427	TACGAAGGTTTGCAGTGACT	248818	81014	AGGGAGAGGAGGAGAGAAAC	293405	125601	TTTTGCTCTAAGTGCCTAGT
204232	36428	ATACGAAGGTTTGCAGTGAC	248819	81015	AAGGGAGAGGAGGAGAGAAA	293406	125602	GTTTTGCTCTAAGTGCCTAG
204233	36429	AATACGAAGGTTTGCAGTGA	248820	81016	GAAGGGAGAGGAGGAGAGAA	293407	125603	TGTTTTGCTCTAAGTGCCTA
204234	36430	TAATACGAAGGTTTGCAGTG	248821	81017	TGAAGGGAGAGGAGGAGAGA	293408	125604	TTGTTTTGCTCTAAGTGCCT

204235	36431	ATAATACGAAGGTTTGCAGT	248822	81018	GTGAAGGGAGAGGAGGAGAG	293409	125605	ATTGTTTTGCTCTAAGTGCC
204236	36432	AATAATACGAAGGTTTGCAG	248823	81019	TGTGAAGGGAGAGGAGGAGA	293410	125606	CATTGTTTTGCTCTAAGTGC
204237	36433	CAATAATACGAAGGTTTGCA	248824	81020	CTGTGAAGGGAGAGGAGGAG	293411	125607	TCATTGTTTTGCTCTAAGTG
204238	36434	TCAATAATACGAAGGTTTGC	248825	81021	ACTGTGAAGGGAGAGGAGGA	293412	125608	ATCATTGTTTTGCTCTAAGT
204239	36435	CTCAATAATACGAAGGTTTG	248826	81022	AACTGTGAAGGGAGAGGAGG	293413	125609	CATCATTGTTTTGCTCTAAG
204240	36436	GCTCAATAATACGAAGGTTT	248827	81023	TAACTGTGAAGGGAGAGGAG	293414	125610	GCATCATTGTTTTGCTCTAA
204241	36437	AGCTCAATAATACGAAGGTT	248828	81024	ATAACTGTGAAGGGAGAGGA	293415	125611	GGCATCATTGTTTTGCTCTA
204242	36438	AAGCTCAATAATACGAAGGT	248829	81025	AATAACTGTGAAGGGAGAGG	293416	125612	CGGCATCATTGTTTTGCTCT
204243	36439	GAAGCTCAATAATACGAAGG	248830	81026	AAATAACTGTGAAGGGAGAG	293417	125613	TCGGCATCATTGTTTTGCTC
204244	36440	TGAAGCTCAATAATACGAAG	248831	81027	GAAATAACTGTGAAGGGAGA	293418	125614	TTCGGCATCATTGTTTTGCT
204245	36441	GTGAAGCTCAATAATACGAA	248832	81028	TGAAATAACTGTGAAGGGAG	293419	125615	TTTCGGCATCATTGTTTTGC
204246	36442	TGTGAAGCTCAATAATACGA	248833	81029	GTGAAATAACTGTGAAGGGA	293420	125616	ATTTCGGCATCATTGTTTTG
204247	36443	ATGTGAAGCTCAATAATACG	248834	81030	AGTGAAATAACTGTGAAGGG	293421	125617	GATTTCGGCATCATTGTTTT
204248	36444	GATGTGAAGCTCAATAATAC	248835	81031	CAGTGAAATAACTGTGAAGG	293422	125618	GGATTTCGGCATCATTGTTT
204249	36445	GGATGTGAAGCTCAATAATA	248836	81032	TCAGTGAAATAACTGTGAAG	293423	125619	AGGATTTCGGCATCATTGTT
204250	36446	AGGATGTGAAGCTCAATAAT	248837	81033	CTCAGTGAAATAACTGTGAA	293424	125620	CAGGATTTCGGCATCATTGT
204251	36447	TAGGATGTGAAGCTCAATAA	248838	81034	CCTCAGTGAAATAACTGTGA	293425	125621	TCAGGATTTCGGCATCATTG
204252	36448	CTAGGATGTGAAGCTCAATA	248839	81035	CCCTCAGTGAAATAACTGTG	293426	125622	ATCAGGATTTCGGCATCATT
204253	36449	TCTAGGATGTGAAGCTCAAT	248840	81036	TCCCTCAGTGAAATAACTGT	293427	125623	AATCAGGATTTCGGCATCAT
204254	36450	TTCTAGGATGTGAAGCTCAA	248841	81037	TTCCCTCAGTGAAATAACTG	293428	125624	AAATCAGGATTTCGGCATCA
204255	36451	ATTCTAGGATGTGAAGCTCA	248842	81038	TTTCCCTCAGTGAAATAACT	293429	125625	GAAATCAGGATTTCGGCATC
204256	36452	AATTCTAGGATGTGAAGCTC	248843	81039	ATTTCCCTCAGTGAAATAAC	293430	125626	TGAAATCAGGATTTCGGCAT
204257	36453	AAATTCTAGGATGTGAAGCT	248844	81040	GATTTCCCTCAGTGAAATAA	293431	125627	CTGAAATCAGGATTTCGGCA
204258	36454	CAAATTCTAGGATGTGAAGC	248845	81041	GGATTTCCCTCAGTGAAATA	293432	125628	GCTGAAATCAGGATTTCGGC
204259	36455	GCAAATTCTAGGATGTGAAG	248846	81042	GGGATTTCCCTCAGTGAAAT	293433	125629	TGCTGAAATCAGGATTTCGG
204260	36456	AGCAAATTCTAGGATGTGAA	248847	81043	AGGGATTTCCCTCAGTGAAA	293434	125630	TTGCTGAAATCAGGATTTCG
204261	36457	CAGCAAATTCTAGGATGTGA	248848	81044	GAGGGATTTCCCTCAGTGAA	293435	125631	TTTGCTGAAATCAGGATTTC
204262	36458	ACAGCAAATTCTAGGATGTG	248849	81045	GGAGGGATTTCCCTCAGTGA	293436	125632	CTTTGCTGAAATCAGGATTT
204263	36459	GACAGCAAATTCTAGGATGT	248850	81046	GGGAGGGATTTCCCTCAGTG	293437	125633	GCTTTGCTGAAATCAGGATT
204264	36460	TGACAGCAAATTCTAGGATG	248851	81047	GGGGAGGGATTTCCCTCAGT	293438	125634	GGCTTTGCTGAAATCAGGAT
204265	36461	GTGACAGCAAATTCTAGGAT	248852	81048	AGGGGAGGGATTTCCCTCAG	293439	125635	AGGCTTTGCTGAAATCAGGA
204266	36462	AGTGACAGCAAATTCTAGGA	248853	81049	CAGGGGAGGGATTTCCCTCA	293440	125636	GAGGCTTTGCTGAAATCAGG
204267	36463	CAGTGACAGCAAATTCTAGG	248854	81050	GCAGGGGAGGGATTTCCCTC	293441	125637	AGAGGCTTTGCTGAAATCAG
204268	36464	ACAGTGACAGCAAATTCTAG	248855	81051	GGCAGGGGAGGGATTTCCCT	293442	125638	CAGAGGCTTTGCTGAAATCA
204269	36465	CACAGTGACAGCAAATTCTA	248856	81052	GGGCAGGGGAGGGATTTCCC	293443	125639	GCAGAGGCTTTGCTGAAATC
204270	36466	CCACAGTGACAGCAAATTCT	248857	81053	TGGGCAGGGGAGGGATTTCC	293444	125640	GGCAGAGGCTTTGCTGAAAT
204271	36467	GCCACAGTGACAGCAAATTC	248858	81054	CTGGGCAGGGGAGGGATTTC	293445	125641	AGGCAGAGGCTTTGCTGAAA
204272	36468	AGCCACAGTGACAGCAAATT	248859	81055	TCTGGGCAGGGGAGGGATTT	293446	125642	CAGGCAGAGGCTTTGCTGAA
204273	36469	CAGCCACAGTGACAGCAAAT	248860	81056	TTCTGGGCAGGGGAGGGATT	293447	125643	GCAGGCAGAGGCTTTGCTGA
204274	36470	GCAGCCACAGTGACAGCAAA	248861	81057	ATTCTGGGCAGGGGAGGGAT	293448	125644	GGCAGGCAGAGGCTTTGCTG
204275	36471	AGCAGCCACAGTGACAGCAA	248862	81058	CATTCTGGGCAGGGGAGGGA	293449	125645	AGGCAGGCAGAGGCTTTGCT
204276	36472	CAGCAGCCACAGTGACAGCA	248863	81059	TCATTCTGGGCAGGGGAGGG	293450	125646	CAGGCAGGCAGAGGCTTTGC
204277	36473	GCAGCAGCCACAGTGACAGC	248864	81060	TTCATTCTGGGCAGGGGAGG	293451	125647	ACAGGCAGGCAGAGGCTTTG
204278	36474	TGCAGCAGCCACAGTGACAG	248865	81061	TTTCATTCTGGGCAGGGGAG	293452	125648	GACAGGCAGGCAGAGGCTTT
204279	36475	ATGCAGCAGCCACAGTGACA	248866	81062	TTTTCATTCTGGGCAGGGGA	293453	125649	AGACAGGCAGGCAGAGGCTT
204280	36476	CATGCAGCAGCCACAGTGAC	248867	81063	GTTTTCATTCTGGGCAGGGG	293454	125650	AAGACAGGCAGGCAGAGGCT
204281	36477	TCATGCAGCAGCCACAGTGA	248868	81064	AGTTTTCATTCTGGGCAGGG	293455	125651	CAAGACAGGCAGGCAGAGGC
204282	36478	TTCATGCAGCAGCCACAGTG	248869	81065	GAGTTTTCATTCTGGGCAGG	293456	125652	CCAAGACAGGCAGGCAGAGG
204283	36479	CTTCATGCAGCAGCCACAGT	248870	81066	AGAGTTTTCATTCTGGGCAG	293457	125653	TCCAAGACAGGCAGGCAGAG
204284	36480	ACTTCATGCAGCAGCCACAG	248871	81067	TAGAGTTTTCATTCTGGGCA	293458	125654	TTCCAAGACAGGCAGGCAGA
204285	36481	AACTTCATGCAGCAGCCACA	248872	81068	CTAGAGTTTTCATTCTGGGC	293459	125655	CTTCCAAGACAGGCAGGCAG
204286	36482	CAACTTCATGCAGCAGCCAC	248873	81069	GCTAGAGTTTTCATTCTGGG	293460	125656	ACTTCCAAGACAGGCAGGCA
204287	36483	ACAACTTCATGCAGCAGCCA	248874	81070	GGCTAGAGTTTTCATTCTGG	293461	125657	TACTTCCAAGACAGGCAGGC
204288	36484	GACAACTTCATGCAGCAGCC	248875	81071	TGGCTAGAGTTTTCATTCTG	293462	125658	ATACTTCCAAGACAGGCAGG
204289	36485	GGACAACTTCATGCAGCAGC	248876	81072	TTGGCTAGAGTTTTCATTCT	293463	125659	GATACTTCCAAGACAGGCAG
204290	36486	AGGACAACTTCATGCAGCAG	248877	81073	GTTGGCTAGAGTTTTCATTC	293464	125660	GGATACTTCCAAGACAGGCA
204291	36487	CAGGACAACTTCATGCAGCA	248878	81074	AGTTGGCTAGAGTTTTCATT	293465	125661	TGGATACTTCCAAGACAGGC
204292	36488	TCAGGACAACTTCATGCAGC	248879	81075	GAGTTGGCTAGAGTTTTCAT	293466	125662	GTGGATACTTCCAAGACAGG
204293	36489	CTCAGGACAACTTCATGCAG	248880	81076	AGAGTTGGCTAGAGTTTTCA	293467	125663	TGTGGATACTTCCAAGACAG
204294	36490	TCTCAGGACAACTTCATGCA	248881	81077	AAGAGTTGGCTAGAGTTTTC	293468	125664	ATGTGGATACTTCCAAGACA
204295	36491	CTCTCAGGACAACTTCATGC	248882	81078	CAAGAGTTGGCTAGAGTTTT	293469	125665	CATGTGGATACTTCCAAGAC
204296	36492	TCTCTCAGGACAACTTCATG	248883	81079	TCAAGAGTTGGCTAGAGTTT	293470	125666	TCATGTGGATACTTCCAAGA
204297	36493	TTCTCTCAGGACAACTTCAT	248884	81080	GTCAAGAGTTGGCTAGAGTT	293471	125667	CTCATGTGGATACTTCCAAG
204298	36494	TTTCTCTCAGGACAACTTCA	248885	81081	AGTCAAGAGTTGGCTAGAGT	293472	125668	CCTCATGTGGATACTTCCAA
204299	36495	GTTTCTCTCAGGACAACTTC	248886	81082	AAGTCAAGAGTTGGCTAGAG	293473	125669	GCCTCATGTGGATACTTCCA
204300	36496	CGTTTCTCTCAGGACAACTT	248887	81083	AAAGTCAAGAGTTGGCTAGA	293474	125670	AGCCTCATGTGGATACTTCC
204301	36497	CCGTTTCTCTCAGGACAACT	248888	81084	AAAAGTCAAGAGTTGGCTAG	293475	125671	CAGCCTCATGTGGATACTTC
204302	36498	CCCGTTTCTCTCAGGACAAC	248889	81085	GAAAAGTCAAGAGTTGGCTA	293476	125672	GCAGCCTCATGTGGATACTT
204303	36499	GCCCGTTTCTCTCAGGACAA	248890	81086	GGAAAAGTCAAGAGTTGGCT	293477	125673	AGCAGCCTCATGTGGATACT
204304	36500	TGCCCGTTTCTCTCAGGACA	248891	81087	TGGAAAAGTCAAGAGTTGGC	293478	125674	CAGCAGCCTCATGTGGATAC
204305	36501	ATGCCCGTTTCTCTCAGGAC	248892	81088	ATGGAAAAGTCAAGAGTTGG	293479	125675	CCAGCAGCCTCATGTGGATA
204306	36502	AATGCCCGTTTCTCTCAGGA	248893	81089	GATGGAAAAGTCAAGAGTTG	293480	125676	CCCAGCAGCCTCATGTGGAT

204307	36503	CAATGCCCGTTTCTCTCAGG	248894	81090	TGATGGAAAAGTCAAGAGTT	293481	125677	CCCCAGCAGCCTCATGTGGA
204308	36504	ACAATGCCCGTTTCTCTCAG	248895	81091	GTGATGGAAAAGTCAAGAGT	293482	125678	GCCCCAGCAGCCTCATGTGG
204309	36505	GACAATGCCCGTTTCTCTCA	248896	81092	AGTGATGGAAAAGTCAAGAG	293483	125679	GGCCCCAGCAGCCTCATGTG
204310	36506	TGACAATGCCCGTTTCTCTC	248897	81093	GAGTGATGGAAAAGTCAAGA	293484	125680	AGGCCCCAGCAGCCTCATGT
204311	36507	ATGACAATGCCCGTTTCTCT	248898	81094	GGAGTGATGGAAAAGTCAAG	293485	125681	AAGGCCCCAGCAGCCTCATG
204312	36508	AATGACAATGCCCGTTTCTC	248899	81095	TGGAGTGATGGAAAAGTCAA	293486	125682	CAAGGCCCCAGCAGCCTCAT
204313	36509	TAATGACAATGCCCGTTTCT	248900	81096	TTGGAGTGATGGAAAAGTCA	293487	125683	CCAAGGCCCCAGCAGCCTCA
204314	36510	TTAATGACAATGCCCGTTTC	248901	81097	TTTGGAGTGATGGAAAAGTC	293488	125684	ACCAAGGCCCCAGCAGCCTC
204315	36511	GTTAATGACAATGCCCGTTT	248902	81098	CTTTGGAGTGATGGAAAAGT	293489	125685	CACCAAGGCCCCAGCAGCCT
204316	36512	TGTTAATGACAATGCCCGTT	248903	81099	ACTTTGGAGTGATGGAAAAG	293490	125686	ACACCAAGGCCCCAGCAGCC
204317	36513	CTGTTAATGACAATGCCCGT	248904	81100	TACTTTGGAGTGATGGAAAA	293491	125687	GACACCAAGGCCCCAGCAGC
204318	36514	CCTGTTAATGACAATGCCCG	248905	81101	CTACTTTGGAGTGATGGAAA	293492	125688	GGACACCAAGGCCCCAGCAG
204319	36515	CCCTGTTAATGACAATGCCC	248906	81102	ACTACTTTGGAGTGATGGAA	293493	125689	GGGACACCAAGGCCCCAGCA
204320	36516	TCCCTGTTAATGACAATGCC	248907	81103	AACTACTTTGGAGTGATGGA	293494	125690	GGGGACACCAAGGCCCCAGC
204321	36517	TTCCCTGTTAATGACAATGC	248908	81104	CAACTACTTTGGAGTGATGG	293495	125691	TGGGGACACCAAGGCCCCAG
204322	36518	TTTCCCTGTTAATGACAATG	248909	81105	TCAACTACTTTGGAGTGATG	293496	125692	CTGGGGACACCAAGGCCCCA
204323	36519	ATTTCCCTGTTAATGACAAT	248910	81106	TTCAACTACTTTGGAGTGAT	293497	125693	GCTGGGGACACCAAGGCCCC
204324	36520	AATTTCCCTGTTAATGACAA	248911	81107	TTTCAACTACTTTGGAGTGA	293498	125694	TGCTGGGGACACCAAGGCCC
204325	36521	CAATTTCCCTGTTAATGACA	248912	81108	CTTTCAACTACTTTGGAGTG	293499	125695	CTGCTGGGGACACCAAGGCC
204326	36522	TCAATTTCCCTGTTAATGAC	248913	81109	ACTTTCAACTACTTTGGAGT	293500	125696	ACTGCTGGGGACACCAAGGC
204327	36523	ATCAATTTCCCTGTTAATGA	248914	81110	TACTTTCAACTACTTTGGAG	293501	125697	AACTGCTGGGGACACCAAGG
204328	36524	CATCAATTTCCCTGTTAATG	248915	81111	GTACTTTCAACTACTTTGGA	293502	125698	AAACTGCTGGGGACACCAAG
204329	36525	CCATCAATTTCCCTGTTAAT	248916	81112	TGTACTTTCAACTACTTTGG	293503	125699	GAAACTGCTGGGGACACCAA
204330	36526	ACCATCAATTTCCCTGTTAA	248917	81113	ATGTACTTTCAACTACTTTG	293504	125700	AGAAACTGCTGGGGACACCA
204331	36527	GACCATCAATTTCCCTGTTA	248918	81114	AATGTACTTTCAACTACTTT	293505	125701	TAGAAACTGCTGGGGACACC
204332	36528	AGACCATCAATTTCCCTGTT	248919	81115	TAATGTACTTTCAACTACTT	293506	125702	CTAGAAACTGCTGGGGACAC
204333	36529	CAGACCATCAATTTCCCTGT	248920	81116	CTAATGTACTTTCAACTACT	293507	125703	ACTAGAAACTGCTGGGGACA
204334	36530	CCAGACCATCAATTTCCCTG	248921	81117	ACTAATGTACTTTCAACTAC	293508	125704	GACTAGAAACTGCTGGGGAC
204335	36531	CCCAGACCATCAATTTCCCT	248922	81118	GACTAATGTACTTTCAACTA	293509	125705	AGACTAGAAACTGCTGGGGA
204336	36532	CCCCAGACCATCAATTTCCC	248923	81119	AGACTAATGTACTTTCAACT	293510	125706	GAGACTAGAAACTGCTGGGG
204337	36533	CCCCCAGACCATCAATTTCC	248924	81120	GAGACTAATGTACTTTCAAC	293511	125707	AGAGACTAGAAACTGCTGGG
204338	36534	TCCCCCAGACCATCAATTTC	248925	81121	GGAGACTAATGTACTTTCAA	293512	125708	TAGAGACTAGAAACTGCTGG
204339	36535	TTCCCCCAGACCATCAATTT	248926	81122	TGGAGACTAATGTACTTTCA	293513	125709	CTAGAGACTAGAAACTGCTG
204340	36536	TTTCCCCCAGACCATCAATT	248927	81123	GTGGAGACTAATGTACTTTC	293514	125710	CCTAGAGACTAGAAACTGCT
204341	36537	TTTTCCCCCAGACCATCAAT	248928	81124	TGTGGAGACTAATGTACTTT	293515	125711	ACCTAGAGACTAGAAACTGC
204342	36538	CTTTTCCCCCAGACCATCAA	248929	81125	CTGTGGAGACTAATGTACTT	293516	125712	GACCTAGAGACTAGAAACTG
204343	36539	ACTTTTCCCCCAGACCATCA	248930	81126	ACTGTGGAGACTAATGTACT	293517	125713	AGACCTAGAGACTAGAAACT
204344	36540	GACTTTTCCCCCAGACCATC	248931	81127	CACTGTGGAGACTAATGTAC	293518	125714	AAGACCTAGAGACTAGAAAC
204345	36541	TGACTTTTCCCCCAGACCAT	248932	81128	CCACTGTGGAGACTAATGTA	293519	125715	CAAGACCTAGAGACTAGAAA
204346	36542	ATGACTTTTCCCCCAGACCA	248933	81129	GCCACTGTGGAGACTAATGT	293520	125716	GCAAGACCTAGAGACTAGAA
204347	36543	GATGACTTTTCCCCCAGACC	248934	81130	TGCCACTGTGGAGACTAATG	293521	125717	AGCAAGACCTAGAGACTAGA
204348	36544	GGATGACTTTTCCCCCAGAC	248935	81131	TTGCCACTGTGGAGACTAAT	293522	125718	CAGCAAGACCTAGAGACTAG
204349	36545	AGGATGACTTTTCCCCCAGA	248936	81132	TTTGCCACTGTGGAGACTAA	293523	125719	ACAGCAAGACCTAGAGACTA
204350	36546	GAGGATGACTTTTCCCCCAG	248937	81133	TTTTGCCACTGTGGAGACTA	293524	125720	CACAGCAAGACCTAGAGACT
204351	36547	TGAGGATGACTTTTCCCCCA	248938	81134	GTTTTGCCACTGTGGAGACT	293525	125721	CCACAGCAAGACCTAGAGAC
204352	36548	ATGAGGATGACTTTTCCCCC	248939	81135	TGTTTTGCCACTGTGGAGAC	293526	125722	CCCACAGCAAGACCTAGAGA
204353	36549	AATGAGGATGACTTTTCCCC	248940	81136	CTGTTTTGCCACTGTGGAGA	293527	125723	ACCCACAGCAAGACCTAGAG
204354	36550	GAATGAGGATGACTTTTCCC	248941	81137	ACTGTTTTGCCACTGTGGAG	293528	125724	CACCCACAGCAAGACCTAGA
204355	36551	AGAATGAGGATGACTTTTCC	248942	81138	CACTGTTTTGCCACTGTGGA	293529	125725	ACACCCACAGCAAGACCTAG
204356	36552	GAGAATGAGGATGACTTTTC	248943	81139	ACACTGTTTTGCCACTGTGG	293530	125726	GACACCCACAGCAAGACCTA
204357	36553	AGAGAATGAGGATGACTTTT	248944	81140	CACACTGTTTTGCCACTGTG	293531	125727	AGACACCCACAGCAAGACCT
204358	36554	AAGAGAATGAGGATGACTTT	248945	81141	GCACACTGTTTTGCCACTGT	293532	125728	CAGACACCCACAGCAAGACC
204359	36555	CAAGAGAATGAGGATGACTT	248946	81142	TGCACACTGTTTTGCCACTG	293533	125729	ACAGACACCCACAGCAAGAC
204360	36556	GCAAGAGAATGAGGATGACT	248947	81143	TTGCACACTGTTTTGCCACT	293534	125730	CACAGACACCCACAGCAAGA
204361	36557	TGCAAGAGAATGAGGATGAC	248948	81144	TTTGCACACTGTTTTGCCAC	293535	125731	GCACAGACACCCACAGCAAG
204362	36558	CTGCAAGAGAATGAGGATGA	248949	81145	TTTTGCACACTGTTTTGCCA	293536	125732	TGCACAGACACCCACAGCAA
204363	36559	TCTGCAAGAGAATGAGGATG	248950	81146	CTTTTGCACACTGTTTTGCC	293537	125733	CTGCACAGACACCCACAGCA
204364	36560	ATCTGCAAGAGAATGAGGAT	248951	81147	GCTTTTGCACACTGTTTTGC	293538	125734	ACTGCACAGACACCCACAGC
204365	36561	GATCTGCAAGAGAATGAGGA	248952	81148	AGCTTTTGCACACTGTTTTG	293539	125735	CACTGCACAGACACCCACAG
204366	36562	AGATCTGCAAGAGAATGAGG	248953	81149	TAGCTTTTGCACACTGTTTT	293540	125736	TCACTGCACAGACACCCACA
204367	36563	TAGATCTGCAAGAGAATGAG	248954	81150	TTAGCTTTTGCACACTGTTT	293541	125737	CTCACTGCACAGACACCCAC
204368	36564	ATAGATCTGCAAGAGAATGA	248955	81151	TTTAGCTTTTGCACACTGTT	293542	125738	CCTCACTGCACAGACACCCA
204369	36565	CATAGATCTGCAAGAGAATG	248956	81152	ATTTAGCTTTTGCACACTGT	293543	125739	CCCTCACTGCACAGACACCC
204370	36566	CCATAGATCTGCAAGAGAAT	248957	81153	TATTTAGCTTTTGCACACTG	293544	125740	ACCCTCACTGCACAGACACC
204371	36567	CCCATAGATCTGCAAGAGAA	248958	81154	TTATTTAGCTTTTGCACACT	293545	125741	CACCCTCACTGCACAGACAC
204372	36568	ACCCATAGATCTGCAAGAGA	248959	81155	ATTATTTAGCTTTTGCACAC	293546	125742	ACACCCTCACTGCACAGACA
204373	36569	CACCCATAGATCTGCAAGAG	248960	81156	AATTATTTAGCTTTTGCACA	293547	125743	CACACCCTCACTGCACAGAC
204374	36570	TCACCCATAGATCTGCAAGA	248961	81157	TAATTATTTAGCTTTTGCAC	293548	125744	ACACACCCTCACTGCACAGA
204375	36571	ATCACCCATAGATCTGCAAG	248962	81158	CTAATTATTTAGCTTTTGCA	293549	125745	CACACACCCTCACTGCACAG
204376	36572	AATCACCCATAGATCTGCAA	248963	81159	TCTAATTATTTAGCTTTTGC	293550	125746	ACACACACCCTCACTGCACA
204377	36573	CAATCACCCATAGATCTGCA	248964	81160	TTCTAATTATTTAGCTTTTG	293551	125747	CACACACACCCTCACTGCAC
204378	36574	TCAATCACCCATAGATCTGC	248965	81161	GTTCTAATTATTTAGCTTTT	293552	125748	CCACACACACCCTCACTGCA

204379	36575	CTCAATCACCCATAGATCTG	248966	81162	TGTTCTAATTATTTAGCTTT	293553	125749	GCCACACACACCCTCACTGC
204380	36576	TCTCAATCACCCATAGATCT	248967	81163	CTGTTCTAATTATTTAGCTT	293554	125750	CGCCACACACACCCTCACTG
204381	36577	GTCTCAATCACCCATAGATC	248968	81164	GCTGTTCTAATTATTTAGCT	293555	125751	GCGCCACACACACCCTCACT
204382	36578	AGTCTCAATCACCCATAGAT	248969	81165	GGCTGTTCTAATTATTTAGC	293556	125752	AGCGCCACACACACCCTCAC
204383	36579	CAGTCTCAATCACCCATAGA	248970	81166	TGGCTGTTCTAATTATTTAG	293557	125753	CAGCGCCACACACACCCTCA
204384	36580	CCAGTCTCAATCACCCATAG	248971	81167	CTGGCTGTTCTAATTATTTA	293558	125754	CCAGCGCCACACACACCCTC
204385	36581	GCCAGTCTCAATCACCCATA	248972	81168	ACTGGCTGTTCTAATTATTT	293559	125755	CCCAGCGCCACACACACCCT
204386	36582	AGCCAGTCTCAATCACCCAT	248973	81169	GACTGGCTGTTCTAATTATT	293560	125756	ACCCAGCGCCACACACACCC
204387	36583	CAGCCAGTCTCAATCACCCA	248974	81170	GGACTGGCTGTTCTAATTAT	293561	125757	CACCCAGCGCCACACACACC
204388	36584	TCAGCCAGTCTCAATCACCC	248975	81171	GGGACTGGCTGTTCTAATTA	293562	125758	TCACCCAGCGCCACACACAC
204389	36585	ATCAGCCAGTCTCAATCACC	248976	81172	TGGGACTGGCTGTTCTAATT	293563	125759	CTCACCCAGCGCCACACACA
204390	36586	CATCAGCCAGTCTCAATCAC	248977	81173	ATGGGACTGGCTGTTCTAAT	293564	125760	GCTCACCCAGCGCCACACAC
204391	36587	ACATCAGCCAGTCTCAATCA	248978	81174	CATGGGACTGGCTGTTCTAA	293565	125761	AGCTCACCCAGCGCCACACA
204392	36588	AACATCAGCCAGTCTCAATC	248979	81175	ACATGGGACTGGCTGTTCTA	293566	125762	GAGCTCACCCAGCGCCACAC
204393	36589	CAACATCAGCCAGTCTCAAT	248980	81176	CACATGGGACTGGCTGTTCT	293567	125763	AGAGCTCACCCAGCGCCACA
204394	36590	TCAACATCAGCCAGTCTCAA	248981	81177	TCACATGGGACTGGCTGTTC	293568	125764	CAGAGCTCACCCAGCGCCAC
204395	36591	TTCAACATCAGCCAGTCTCA	248982	81178	GTCACATGGGACTGGCTGTT	293569	125765	ACAGAGCTCACCCAGCGCCA
204396	36592	CTTCAACATCAGCCAGTCTC	248983	81179	TGTCACATGGGACTGGCTGT	293570	125766	GACAGAGCTCACCCAGCGCC
204397	36593	CCTTCAACATCAGCCAGTCT	248984	81180	CTGTCACATGGGACTGGCTG	293571	125767	AGACAGAGCTCACCCAGCGC
204398	36594	CCCTTCAACATCAGCCAGTC	248985	81181	ACTGTCACATGGGACTGGCT	293572	125768	TAGACAGAGCTCACCCAGCG
204399	36595	CCCCTTCAACATCAGCCAGT	248986	81182	GACTGTCACATGGGACTGGC	293573	125769	CTAGACAGAGCTCACCCAGC
204400	36596	ACCCCTTCAACATCAGCCAG	248987	81183	TGACTGTCACATGGGACTGG	293574	125770	CCTAGACAGAGCTCACCCAG
204401	36597	AACCCCTTCAACATCAGCCA	248988	81184	TTGACTGTCACATGGGACTG	293575	125771	GCCTAGACAGAGCTCACCCA
204402	36598	AAACCCCTTCAACATCAGCC	248989	81185	TTTGACTGTCACATGGGACT	293576	125772	GGCCTAGACAGAGCTCACCC
204403	36599	GAAACCCCTTCAACATCAGC	248990	81186	CTTTGACTGTCACATGGGAC	293577	125773	AGGCCTAGACAGAGCTCACC
204404	36600	AGAAACCCCTTCAACATCAG	248991	81187	GCTTTGACTGTCACATGGGA	293578	125774	CAGGCCTAGACAGAGCTCAC
204405	36601	GAGAAACCCCTTCAACATCA	248992	81188	AGCTTTGACTGTCACATGGG	293579	125775	CCAGGCCTAGACAGAGCTCA
204406	36602	TGAGAAACCCCTTCAACATC	248993	81189	AAGCTTTGACTGTCACATGG	293580	125776	GCCAGGCCTAGACAGAGCTC
204407	36603	CTGAGAAACCCCTTCAACAT	248994	81190	GAAGCTTTGACTGTCACATG	293581	125777	TGCCAGGCCTAGACAGAGCT
204408	36604	GCTGAGAAACCCCTTCAACA	248995	81191	AGAAGCTTTGACTGTCACAT	293582	125778	GTGCCAGGCCTAGACAGAGC
204409	36605	GGCTGAGAAACCCCTTCAAC	248996	81192	TAGAAGCTTTGACTGTCACA	293583	125779	TGTGCCAGGCCTAGACAGAG
204410	36606	TGGCTGAGAAACCCCTTCAA	248997	81193	TTAGAAGCTTTGACTGTCAC	293584	125780	CTGTGCCAGGCCTAGACAGA
204411	36607	ATGGCTGAGAAACCCCTTCA	248998	81194	GTTAGAAGCTTTGACTGTCA	293585	125781	CCTGTGCCAGGCCTAGACAG
204412	36608	GATGGCTGAGAAACCCCTTC	248999	81195	AGTTAGAAGCTTTGACTGTC	293586	125782	TCCTGTGCCAGGCCTAGACA
204413	36609	CGATGGCTGAGAAACCCCTT	249000	81196	GAGTTAGAAGCTTTGACTGT	293587	125783	ATCCTGTGCCAGGCCTAGAC
204414	36610	ACGATGGCTGAGAAACCCCT	249001	81197	GGAGTTAGAAGCTTTGACTG	293588	125784	CATCCTGTGCCAGGCCTAGA
204415	36611	CACGATGGCTGAGAAACCCC	249002	81198	TGGAGTTAGAAGCTTTGACT	293589	125785	GCATCCTGTGCCAGGCCTAG
204416	36612	ACACGATGGCTGAGAAACCC	249003	81199	ATGGAGTTAGAAGCTTTGAC	293590	125786	CGCATCCTGTGCCAGGCCTA
204417	36613	CACACGATGGCTGAGAAACC	249004	81200	AATGGAGTTAGAAGCTTTGA	293591	125787	CCGCATCCTGTGCCAGGCCT
204418	36614	GCACACGATGGCTGAGAAAC	249005	81201	GAATGGAGTTAGAAGCTTTG	293592	125788	ACCGCATCCTGTGCCAGGCC
204419	36615	GGCACACGATGGCTGAGAAA	249006	81202	TGAATGGAGTTAGAAGCTTT	293593	125789	GACCGCATCCTGTGCCAGGC
204420	36616	TGGCACACGATGGCTGAGAA	249007	81203	TTGAATGGAGTTAGAAGCTT	293594	125790	AGACCGCATCCTGTGCCAGG
204421	36617	ATGGCACACGATGGCTGAGA	249008	81204	TTTGAATGGAGTTAGAAGCT	293595	125791	CAGACCGCATCCTGTGCCAG
204422	36618	CATGGCACACGATGGCTGAG	249009	81205	CTTTGAATGGAGTTAGAAGC	293596	125792	CCAGACCGCATCCTGTGCCA
204423	36619	ACATGGCACACGATGGCTGA	249010	81206	ACTTTGAATGGAGTTAGAAG	293597	125793	ACCAGACCGCATCCTGTGCC
204424	36620	AACATGGCACACGATGGCTG	249011	81207	AACTTTGAATGGAGTTAGAA	293598	125794	TACCAGACCGCATCCTGTGC
204425	36621	TAACATGGCACACGATGGCT	249012	81208	CAACTTTGAATGGAGTTAGA	293599	125795	CTACCAGACCGCATCCTGTG
204426	36622	ATAACATGGCACACGATGGC	249013	81209	GCAACTTTGAATGGAGTTAG	293600	125796	GCTACCAGACCGCATCCTGT
204427	36623	CATAACATGGCACACGATGG	249014	81210	TGCAACTTTGAATGGAGTTA	293601	125797	AGCTACCAGACCGCATCCTG
204428	36624	CCATAACATGGCACACGATG	249015	81211	CTGCAACTTTGAATGGAGTT	293602	125798	CAGCTACCAGACCGCATCCT
204429	36625	TCCATAACATGGCACACGAT	249016	81212	GCTGCAACTTTGAATGGAGT	293603	125799	GCAGCTACCAGACCGCATCC
204430	36626	TTCCATAACATGGCACACGA	249017	81213	GGCTGCAACTTTGAATGGAG	293604	125800	AGCAGCTACCAGACCGCATC
204431	36627	GTTCCATAACATGGCACACG	249018	81214	TGGCTGCAACTTTGAATGGA	293605	125801	CAGCAGCTACCAGACCGCAT
204432	36628	TGTTCCATAACATGGCACAC	249019	81215	ATGGCTGCAACTTTGAATGG	293606	125802	GCAGCAGCTACCAGACCGCA
204433	36629	CTGTTCCATAACATGGCACA	249020	81216	AATGGCTGCAACTTTGAATG	293607	125803	AGCAGCAGCTACCAGACCGC
204434	36630	ACTGTTCCATAACATGGCAC	249021	81217	GAATGGCTGCAACTTTGAAT	293608	125804	AAGCAGCAGCTACCAGACCG
204435	36631	CACTGTTCCATAACATGGCA	249022	81218	GGAATGGCTGCAACTTTGAA	293609	125805	GAAGCAGCAGCTACCAGACC
204436	36632	CCACTGTTCCATAACATGGC	249023	81219	GGGAATGGCTGCAACTTTGA	293610	125806	AGAAGCAGCAGCTACCAGAC
204437	36633	ACCACTGTTCCATAACATGG	249024	81220	GGGGAATGGCTGCAACTTTG	293611	125807	GAGAAGCAGCAGCTACCAGA
204438	36634	CACCACTGTTCCATAACATG	249025	81221	AGGGGAATGGCTGCAACTTT	293612	125808	AGAGAAGCAGCAGCTACCAG
204439	36635	ACACCACTGTTCCATAACAT	249026	81222	GAGGGGAATGGCTGCAACTT	293613	125809	AAGAGAAGCAGCAGCTACCA
204440	36636	TACACCACTGTTCCATAACA	249027	81223	CGAGGGGAATGGCTGCAACT	293614	125810	GAAGAGAAGCAGCAGCTACC
204441	36637	CTACACCACTGTTCCATAAC	249028	81224	TCGAGGGGAATGGCTGCAAC	293615	125811	AGAAGAGAAGCAGCAGCTAC
204442	36638	GCTACACCACTGTTCCATAA	249029	81225	CTCGAGGGGAATGGCTGCAA	293616	125812	CAGAAGAGAAGCAGCAGCTA
204443	36639	GGCTACACCACTGTTCCATA	249030	81226	CCTCGAGGGGAATGGCTGCA	293617	125813	GCAGAAGAGAAGCAGCAGCT
204444	36640	TGGCTACACCACTGTTCCAT	249031	81227	CCCTCGAGGGGAATGGCTGC	293618	125814	TGCAGAAGAGAAGCAGCAGC
204445	36641	CTGGCTACACCACTGTTCCA	249032	81228	GCCCTCGAGGGGAATGGCTG	293619	125815	CTGCAGAAGAGAAGCAGCAG
204446	36642	GCTGGCTACACCACTGTTCC	249033	81229	AGCCCTCGAGGGGAATGGCT	293620	125816	TCTGCAGAAGAGAAGCAGCA
204447	36643	GGCTGGCTACACCACTGTTC	249034	81230	CAGCCCTCGAGGGGAATGGC	293621	125817	TTCTGCAGAAGAGAAGCAGC
204448	36644	TGGCTGGCTACACCACTGTT	249035	81231	CCAGCCCTCGAGGGGAATGG	293622	125818	CTTCTGCAGAAGAGAAGCAG
204449	36645	ATGGCTGGCTACACCACTGT	249036	81232	GCCAGCCCTCGAGGGGAATG	293623	125819	GCTTCTGCAGAAGAGAAGCA
204450	36646	AATGGCTGGCTACACCACTG	249037	81233	TGCCAGCCCTCGAGGGGAAT	293624	125820	CGCTTCTGCAGAAGAGAAGC

204451	36647	AAATGGCTGGCTACACCACT	249038	81234	CTGCCAGCCCTCGAGGGGAA	293625	125821	GCGCTTCTGCAGAAGAGAAG
204452	36648	CAAATGGCTGGCTACACCAC	249039	81235	CCTGCCAGCCCTCGAGGGGA	293626	125822	TGCGCTTCTGCAGAAGAGAA
204453	36649	TCAAATGGCTGGCTACACCA	249040	81236	CCCTGCCAGCCCTCGAGGGG	293627	125823	CTGCGCTTCTGCAGAAGAGA
204454	36650	GTCAAATGGCTGGCTACACC	249041	81237	TCCCTGCCAGCCCTCGAGGG	293628	125824	GCTGCGCTTCTGCAGAAGAG
204455	36651	TGTCAAATGGCTGGCTACAC	249042	81238	CTCCCTGCCAGCCCTCGAGG	293629	125825	GGCTGCGCTTCTGCAGAAGA
204456	36652	GTGTCAAATGGCTGGCTACA	249043	81239	CCTCCCTGCCAGCCCTCGAG	293630	125826	TGGCTGCGCTTCTGCAGAAG
204457	36653	GGTGTCAAATGGCTGGCTAC	249044	81240	CCCTCCCTGCCAGCCCTCGA	293631	125827	TTGGCTGCGCTTCTGCAGAA
204458	36654	GGGTGTCAAATGGCTGGCTA	249045	81241	CCCCTCCCTGCCAGCCCTCG	293632	125828	CTTGGCTGCGCTTCTGCAGA
204459	36655	TGGGTGTCAAATGGCTGGCT	249046	81242	TCCCCTCCCTGCCAGCCCTC	293633	125829	GCTTGGCTGCGCTTCTGCAG
204460	36656	CTGGGTGTCAAATGGCTGGC	249047	81243	CTCCCCTCCCTGCCAGCCCT	293634	125830	TGCTTGGCTGCGCTTCTGCA
204461	36657	GCTGGGTGTCAAATGGCTGG	249048	81244	CCTCCCCTCCCTGCCAGCCC	293635	125831	GTGCTTGGCTGCGCTTCTGC
204462	36658	CGCTGGGTGTCAAATGGCTG	249049	81245	CCCTCCCCTCCCTGCCAGCC	293636	125832	GGTGCTTGGCTGCGCTTCTG
204463	36659	GCGCTGGGTGTCAAATGGCT	249050	81246	CCCCTCCCCTCCCTGCCAGC	293637	125833	GGGTGCTTGGCTGCGCTTCT
204464	36660	AGCGCTGGGTGTCAAATGGC	249051	81247	ACCCCTCCCCTCCCTGCCAG	293638	125834	AGGGTGCTTGGCTGCGCTTC
204465	36661	CAGCGCTGGGTGTCAAATGG	249052	81248	TACCCCTCCCCTCCCTGCCA	293639	125835	GAGGGTGCTTGGCTGCGCTT
204466	36662	TCAGCGCTGGGTGTCAAATG	249053	81249	TTACCCCTCCCCTCCCTGCC	293640	125836	AGAGGGTGCTTGGCTGCGCT
204467	36663	GTCAGCGCTGGGTGTCAAAT	249054	81250	CTTACCCCTCCCCTCCCTGC	293641	125837	CAGAGGGTGCTTGGCTGCGC
204468	36664	GGTCAGCGCTGGGTGTCAAA	249055	81251	TCTTACCCCTCCCCTCCCTG	293642	125838	CCAGAGGGTGCTTGGCTGCG
204469	36665	AGGTCAGCGCTGGGTGTCAA	249056	81252	CTCTTACCCCTCCCCTCCCT	293643	125839	CCCAGAGGGTGCTTGGCTGC
204470	36666	AAGGTCAGCGCTGGGTGTCA	249057	81253	TCTCTTACCCCTCCCCTCCC	293644	125840	CCCCAGAGGGTGCTTGGCTG
204471	36667	AAAGGTCAGCGCTGGGTGTC	249058	81254	TTCTCTTACCCCTCCCCTCC	293645	125841	ACCCCAGAGGGTGCTTGGCT
204472	36668	CAAAGGTCAGCGCTGGGTGT	249059	81255	TTTCTCTTACCCCTCCCCTC	293646	125842	AACCCCAGAGGGTGCTTGGC
204473	36669	ACAAAGGTCAGCGCTGGGTG	249060	81256	GTTTCTCTTACCCCTCCCCT	293647	125843	AAACCCCAGAGGGTGCTTGG
204474	36670	AACAAAGGTCAGCGCTGGGT	249061	81257	TGTTTCTCTTACCCCTCCCC	293648	125844	GAAACCCCAGAGGGTGCTTG
204475	36671	AAACAAAGGTCAGCGCTGGG	249062	81258	CTGTTTCTCTTACCCCTCCC	293649	125845	TGAAACCCCAGAGGGTGCTT
204476	36672	TAAACAAAGGTCAGCGCTGG	249063	81259	CCTGTTTCTCTTACCCCTCC	293650	125846	CTGAAACCCCAGAGGGTGCT
204477	36673	TTAAACAAAGGTCAGCGCTG	249064	81260	TCCTGTTTCTCTTACCCCTC	293651	125847	CCTGAAACCCCAGAGGGTGC
204478	36674	GTTAAACAAAGGTCAGCGCT	249065	81261	TTCCTGTTTCTCTTACCCCT	293652	125848	GCCTGAAACCCCAGAGGGTG
204479	36675	TGTTAAACAAAGGTCAGCGC	249066	81262	CTTCCTGTTTCTCTTACCCC	293653	125849	GGCCTGAAACCCCAGAGGGT
204480	36676	TTGTTAAACAAAGGTCAGCG	249067	81263	CCTTCCTGTTTCTCTTACCC	293654	125850	GGGCCTGAAACCCCAGAGGG
204481	36677	GTTGTTAAACAAAGGTCAGC	249068	81264	ACCTTCCTGTTTCTCTTACC	293655	125851	TGGGCCTGAAACCCCAGAGG
204482	36678	GGTTGTTAAACAAAGGTCAG	249069	81265	AACCTTCCTGTTTCTCTTAC	293656	125852	GTGGGCCTGAAACCCCAGAG
204483	36679	AGGTTGTTAAACAAAGGTCA	249070	81266	GAACCTTCCTGTTTCTCTTA	293657	125853	TGTGGGCCTGAAACCCCAGA
204484	36680	GAGGTTGTTAAACAAAGGTC	249071	81267	AGAACCTTCCTGTTTCTCTT	293658	125854	GTGTGGGCCTGAAACCCCAG
204485	36681	TGAGGTTGTTAAACAAAGGT	249072	81268	AAGAACCTTCCTGTTTCTCT	293659	125855	GGTGTGGGCCTGAAACCCCA
204486	36682	GTGAGGTTGTTAAACAAAGG	249073	81269	TAAGAACCTTCCTGTTTCTC	293660	125856	GGGTGTGGGCCTGAAACCCC
204487	36683	GGTGAGGTTGTTAAACAAAG	249074	81270	GTAAGAACCTTCCTGTTTCT	293661	125857	TGGGTGTGGGCCTGAAACCC
204488	36684	AGGTGAGGTTGTTAAACAAA	249075	81271	AGTAAGAACCTTCCTGTTTC	293662	125858	CTGGGTGTGGGCCTGAAACC
204489	36685	TAGGTGAGGTTGTTAAACAA	249076	81272	CAGTAAGAACCTTCCTGTTT	293663	125859	GCTGGGTGTGGGCCTGAAAC
204490	36686	ATAGGTGAGGTTGTTAAACA	249077	81273	TCAGTAAGAACCTTCCTGTT	293664	125860	GGCTGGGTGTGGGCCTGAAA
204491	36687	TATAGGTGAGGTTGTTAAAC	249078	81274	CTCAGTAAGAACCTTCCTGT	293665	125861	AGGCTGGGTGTGGGCCTGAA
204492	36688	ATATAGGTGAGGTTGTTAAA	249079	81275	ACTCAGTAAGAACCTTCCTG	293666	125862	CAGGCTGGGTGTGGGCCTGA
204493	36689	TATATAGGTGAGGTTGTTAA	249080	81276	AACTCAGTAAGAACCTTCCT	293667	125863	TCAGGCTGGGTGTGGGCCTG
204494	36690	ATATATAGGTGAGGTTGTTA	249081	81277	CAACTCAGTAAGAACCTTCC	293668	125864	TTCAGGCTGGGTGTGGGCCT
204495	36691	CATATATAGGTGAGGTTGTT	249082	81278	CCAACTCAGTAAGAACCTTC	293669	125865	CTTCAGGCTGGGTGTGGGCC
204496	36692	TCATATATAGGTGAGGTTGT	249083	81279	ACCAACTCAGTAAGAACCTT	293670	125866	ACTTCAGGCTGGGTGTGGGC
204497	36693	GTCATATATAGGTGAGGTTG	249084	81280	GACCAACTCAGTAAGAACCT	293671	125867	AACTTCAGGCTGGGTGTGGG
204498	36694	TGTCATATATAGGTGAGGTT	249085	81281	GGACCAACTCAGTAAGAACC	293672	125868	GAACTTCAGGCTGGGTGTGG
204499	36695	TTGTCATATATAGGTGAGGT	249086	81282	AGGACCAACTCAGTAAGAAC	293673	125869	AGAACTTCAGGCTGGGTGTG
204500	36696	TTTGTCATATATAGGTGAGG	249087	81283	CAGGACCAACTCAGTAAGAA	293674	125870	CAGAACTTCAGGCTGGGTGT
204501	36697	TTTTGTCATATATAGGTGAG	249088	81284	CCAGGACCAACTCAGTAAGA	293675	125871	CCAGAACTTCAGGCTGGGTG
204502	36698	ATTTTGTCATATATAGGTGA	249089	81285	ACCAGGACCAACTCAGTAAG	293676	125872	CCCAGAACTTCAGGCTGGGT
204503	36699	CATTTTGTCATATATAGGTG	249090	81286	CACCAGGACCAACTCAGTAA	293677	125873	TCCCAGAACTTCAGGCTGGG
204504	36700	TCATTTTGTCATATATAGGT	249091	81287	ACACCAGGACCAACTCAGTA	293678	125874	CTCCCAGAACTTCAGGCTGG
204505	36701	ATCATTTTGTCATATATAGG	249092	81288	CACACCAGGACCAACTCAGT	293679	125875	ACTCCCAGAACTTCAGGCTG
204506	36702	AATCATTTTGTCATATATAG	249093	81289	TCACACCAGGACCAACTCAG	293680	125876	CACTCCCAGAACTTCAGGCT
204507	36703	CAATCATTTTGTCATATATA	249094	81290	CTCACACCAGGACCAACTCA	293681	125877	CCACTCCCAGAACTTCAGGC
204508	36704	ACAATCATTTTGTCATATAT	249095	81291	GCTCACACCAGGACCAACTC	293682	125878	GCCACTCCCAGAACTTCAGG
204509	36705	GACAATCATTTTGTCATATA	249096	81292	AGCTCACACCAGGACCAACT	293683	125879	AGCCACTCCCAGAACTTCAG
204510	36706	TGACAATCATTTTGTCATAT	249097	81293	CAGCTCACACCAGGACCAAC	293684	125880	GAGCCACTCCCAGAACTTCA
204511	36707	CTGACAATCATTTTGTCATA	249098	81294	GCAGCTCACACCAGGACCAA	293685	125881	TGAGCCACTCCCAGAACTTC
204512	36708	TCTGACAATCATTTTGTCAT	249099	81295	CGCAGCTCACACCAGGACCA	293686	125882	GTGAGCCACTCCCAGAACTT
204513	36709	TTCTGACAATCATTTTGTCA	249100	81296	ACGCAGCTCACACCAGGACC	293687	125883	AGTGAGCCACTCCCAGAACT
204514	36710	TTTCTGACAATCATTTTGTC	249101	81297	GACGCAGCTCACACCAGGAC	293688	125884	AAGTGAGCCACTCCCAGAAC
204515	36711	ATTTCTGACAATCATTTTGT	249102	81298	TGACGCAGCTCACACCAGGA	293689	125885	AAAGTGAGCCACTCCCAGAA
204516	36712	TATTTCTGACAATCATTTTG	249103	81299	GTGACGCAGCTCACACCAGG	293690	125886	GAAAGTGAGCCACTCCCAGA
204517	36713	TTATTTCTGACAATCATTTT	249104	81300	TGTGACGCAGCTCACACCAG	293691	125887	GGAAAGTGAGCCACTCCCAG
204518	36714	ATTATTTCTGACAATCATTT	249105	81301	GTGTGACGCAGCTCACACCA	293692	125888	TGGAAAGTGAGCCACTCCCA
204519	36715	GATTATTTCTGACAATCATT	249106	81302	AGTGTGACGCAGCTCACACC	293693	125889	TTGGAAAGTGAGCCACTCCC
204520	36716	CGATTATTTCTGACAATCAT	249107	81303	GAGTGTGACGCAGCTCACAC	293694	125890	GTTGGAAAGTGAGCCACTCC
204521	36717	ACGATTATTTCTGACAATCA	249108	81304	GGAGTGTGACGCAGCTCACA	293695	125891	GGTTGGAAAGTGAGCCACTC
204522	36718	CACGATTATTTCTGACAATC	249109	81305	GGGAGTGTGACGCAGCTCAC	293696	125892	AGGTTGGAAAGTGAGCCACT

204523	36719	ACACGATTATTTCTGACAAT	249110	81306	AGGGAGTGTGACGCAGCTCA	293697	125893	AAGGTTGGAAAGTGAGCCAC
204524	36720	TACACGATTATTTCTGACAA	249111	81307	CAGGGAGTGTGACGCAGCTC	293698	125894	GAAGGTTGGAAAGTGAGCCA
204525	36721	TTACACGATTATTTCTGACA	249112	81308	GCAGGGAGTGTGACGCAGCT	293699	125895	TGAAGGTTGGAAAGTGAGCC
204526	36722	ATTACACGATTATTTCTGAC	249113	81309	TGCAGGGAGTGTGACGCAGC	293700	125896	CTGAAGGTTGGAAAGTGAGC
204527	36723	CATTACACGATTATTTCTGA	249114	81310	CTGCAGGGAGTGTGACGCAG	293701	125897	CCTGAAGGTTGGAAAGTGAG
204528	36724	TCATTACACGATTATTTCTG	249115	81311	TCTGCAGGGAGTGTGACGCA	293702	125898	CCCTGAAGGTTGGAAAGTGA
204529	36725	TTCATTACACGATTATTTCT	249116	81312	CTCTGCAGGGAGTGTGACGC	293703	125899	ACCCTGAAGGTTGGAAAGTG
204530	36726	TTTCATTACACGATTATTTC	249117	81313	CCTCTGCAGGGAGTGTGACG	293704	125900	GACCCTGAAGGTTGGAAAGT
204531	36727	ATTTCATTACACGATTATTT	249118	81314	ACCTCTGCAGGGAGTGTGAC	293705	125901	AGACCCTGAAGGTTGGAAAG
204532	36728	CATTTCATTACACGATTATT	249119	81315	AACCTCTGCAGGGAGTGTGA	293706	125902	GAGACCCTGAAGGTTGGAAA
204533	36729	TCATTTCATTACACGATTAT	249120	81316	AAACCTCTGCAGGGAGTGTG	293707	125903	GGAGACCCTGAAGGTTGGAA
204534	36730	GTCATTTCATTACACGATTA	249121	81317	GAAACCTCTGCAGGGAGTGT	293708	125904	GGGAGACCCTGAAGGTTGGA
204535	36731	AGTCATTTCATTACACGATT	249122	81318	TGAAACCTCTGCAGGGAGTG	293709	125905	TGGGAGACCCTGAAGGTTGG
204536	36732	CAGTCATTTCATTACACGAT	249123	81319	TTGAAACCTCTGCAGGGAGT	293710	125906	CTGGGAGACCCTGAAGGTTG
204537	36733	ACAGTCATTTCATTACACGA	249124	81320	CTTGAAACCTCTGCAGGGAG	293711	125907	GCTGGGAGACCCTGAAGGTT
204538	36734	TACAGTCATTTCATTACACG	249125	81321	CCTTGAAACCTCTGCAGGGA	293712	125908	TGCTGGGAGACCCTGAAGGT
204539	36735	TTACAGTCATTTCATTACAC	249126	81322	TCCTTGAAACCTCTGCAGGG	293713	125909	CTGCTGGGAGACCCTGAAGG
204540	36736	ATTACAGTCATTTCATTACA	249127	81323	CTCCTTGAAACCTCTGCAGG	293714	125910	GCTGCTGGGAGACCCTGAAG
204541	36737	TATTACAGTCATTTCATTAC	249128	81324	TCTCCTTGAAACCTCTGCAG	293715	125911	AGCTGCTGGGAGACCCTGAA
204542	36738	TTATTACAGTCATTTCATTA	249129	81325	GTCTCCTTGAAACCTCTGCA	293716	125912	CAGCTGCTGGGAGACCCTGA
204543	36739	ATTATTACAGTCATTTCATT	249130	81326	AGTCTCCTTGAAACCTCTGC	293717	125913	TCAGCTGCTGGGAGACCCTG
204544	36740	CATTATTACAGTCATTTCAT	249131	81327	GAGTCTCCTTGAAACCTCTG	293718	125914	GTCAGCTGCTGGGAGACCCT
204545	36741	CCATTATTACAGTCATTTCA	249132	81328	AGAGTCTCCTTGAAACCTCT	293719	125915	AGTCAGCTGCTGGGAGACCC
204546	36742	GCCATTATTACAGTCATTTC	249133	81329	GAGAGTCTCCTTGAAACCTC	293720	125916	CAGTCAGCTGCTGGGAGACC
204547	36743	GGCCATTATTACAGTCATTT	249134	81330	AGAGAGTCTCCTTGAAACCT	293721	125917	CCAGTCAGCTGCTGGGAGAC
204548	36744	TGGCCATTATTACAGTCATT	249135	81331	GAGAGAGTCTCCTTGAAACC	293722	125918	CCCAGTCAGCTGCTGGGAGA
204549	36745	CTGGCCATTATTACAGTCAT	249136	81332	AGAGAGAGTCTCCTTGAAAC	293723	125919	CCCCAGTCAGCTGCTGGGAG
204550	36746	TCTGGCCATTATTACAGTCA	249137	81333	GAGAGAGAGTCTCCTTGAAA	293724	125920	TCCCCAGTCAGCTGCTGGGA
204551	36747	TTCTGGCCATTATTACAGTC	249138	81334	AGAGAGAGAGTCTCCTTGAA	293725	125921	CTCCCCAGTCAGCTGCTGGG
204552	36748	TTTCTGGCCATTATTACAGT	249139	81335	GAGAGAGAGAGTCTCCTTGA	293726	125922	ACTCCCCAGTCAGCTGCTGG
204553	36749	TTTTCTGGCCATTATTACAG	249140	81336	AGAGAGAGAGAGTCTCCTTG	293727	125923	CACTCCCCAGTCAGCTGCTG
204554	36750	CTTTTCTGGCCATTATTACA	249141	81337	GAGAGAGAGAGAGTCTCCTT	293728	125924	CCACTCCCCAGTCAGCTGCT
204555	36751	TCTTTTCTGGCCATTATTAC	249142	81338	AGAGAGAGAGAGAGTCTCCT	293729	125925	ACCACTCCCCAGTCAGCTGC
204556	36752	TTCTTTTCTGGCCATTATTA	249143	81339	CAGAGAGAGAGAGAGTCTCC	293730	125926	CACCACTCCCCAGTCAGCTG
204557	36753	TTTCTTTTCTGGCCATTATT	249144	81340	ACAGAGAGAGAGAGAGTCTC	293731	125927	CCACCACTCCCCAGTCAGCT
204558	36754	GTTTCTTTTCTGGCCATTAT	249145	81341	GACAGAGAGAGAGAGAGTCT	293732	125928	TCCACCACTCCCCAGTCAGC
204559	36755	CGTTTCTTTTCTGGCCATTA	249146	81342	AGACAGAGAGAGAGAGAGTC	293733	125929	CTCCACCACTCCCCAGTCAG
204560	36756	GCGTTTCTTTTCTGGCCATT	249147	81343	GAGACAGAGAGAGAGAGAGT	293734	125930	CCTCCACCACTCCCCAGTCA
204561	36757	TGCGTTTCTTTTCTGGCCAT	249148	81344	GGAGACAGAGAGAGAGAGAG	293735	125931	CCCTCCACCACTCCCCAGTC
204562	36758	CTGCGTTTCTTTTCTGGCCA	249149	81345	TGGAGACAGAGAGAGAGAGA	293736	125932	TCCCTCCACCACTCCCCAGT
204563	36759	TCTGCGTTTCTTTTCTGGCC	249150	81346	ATGGAGACAGAGAGAGAGAG	293737	125933	TTCCCTCCACCACTCCCCAG
204564	36760	ATCTGCGTTTCTTTTCTGGC	249151	81347	CATGGAGACAGAGAGAGAGA	293738	125934	TTTCCCTCCACCACTCCCCA
204565	36761	TATCTGCGTTTCTTTTCTGG	249152	81348	CCATGGAGACAGAGAGAGAG	293739	125935	TTTTCCCTCCACCACTCCCC
204566	36762	CTATCTGCGTTTCTTTTCTG	249153	81349	CCCATGGAGACAGAGAGAGA	293740	125936	CTTTTCCCTCCACCACTCCC
204567	36763	ACTATCTGCGTTTCTTTTCT	249154	81350	CCCCATGGAGACAGAGAGAG	293741	125937	CCTTTTCCCTCCACCACTCC
204568	36764	TACTATCTGCGTTTCTTTTC	249155	81351	TCCCCATGGAGACAGAGAGA	293742	125938	CCCTTTTCCCTCCACCACTC
204569	36765	TTACTATCTGCGTTTCTTTT	249156	81352	GTCCCCATGGAGACAGAGAG	293743	125939	TCCCTTTTCCCTCCACCACT
204570	36766	TTTACTATCTGCGTTTCTTT	249157	81353	GGTCCCCATGGAGACAGAGA	293744	125940	ATCCCTTTTCCCTCCACCAC
204571	36767	TTTTACTATCTGCGTTTCTT	249158	81354	AGGTCCCCATGGAGACAGAG	293745	125941	AATCCCTTTTCCCTCCACCA
204572	36768	ATTTTACTATCTGCGTTTCT	249159	81355	AAGGTCCCCATGGAGACAGA	293746	125942	CAATCCCTTTTCCCTCCACC
204573	36769	CATTTTACTATCTGCGTTTC	249160	81356	TAAGGTCCCCATGGAGACAG	293747	125943	ACAATCCCTTTTCCCTCCAC
204574	36770	ACATTTTACTATCTGCGTTT	249161	81357	ATAAGGTCCCCATGGAGACA	293748	125944	TACAATCCCTTTTCCCTCCA
204575	36771	AACATTTTACTATCTGCGTT	249162	81358	AATAAGGTCCCCATGGAGAC	293749	125945	ATACAATCCCTTTTCCCTCC
204576	36772	AAACATTTTACTATCTGCGT	249163	81359	AAATAAGGTCCCCATGGAGA	293750	125946	AATACAATCCCTTTTCCCTC
204577	36773	GAAACATTTTACTATCTGCG	249164	81360	CAAATAAGGTCCCCATGGAG	293751	125947	TAATACAATCCCTTTTCCCT
204578	36774	AGAAACATTTTACTATCTGC	249165	81361	TCAAATAAGGTCCCCATGGA	293752	125948	CTAATACAATCCCTTTTCCC
204579	36775	GAGAAACATTTTACTATCTG	249166	81362	TTCAAATAAGGTCCCCATGG	293753	125949	ACTAATACAATCCCTTTTCC
204580	36776	AGAGAAACATTTTACTATCT	249167	81363	ATTCAAATAAGGTCCCCATG	293754	125950	GACTAATACAATCCCTTTTC
204581	36777	AAGAGAAACATTTTACTATC	249168	81364	AATTCAAATAAGGTCCCCAT	293755	125951	GGACTAATACAATCCCTTTT
204582	36778	CAAGAGAAACATTTTACTAT	249169	81365	GAATTCAAATAAGGTCCCCA	293756	125952	CGGACTAATACAATCCCTTT
204583	36779	ACAAGAGAAACATTTTACTA	249170	81366	AGAATTCAAATAAGGTCCCC	293757	125953	ACGGACTAATACAATCCCTT
204584	36780	AACAAGAGAAACATTTTACT	249171	81367	AAGAATTCAAATAAGGTCCC	293758	125954	AACGGACTAATACAATCCCT
204585	36781	CAACAAGAGAAACATTTTAC	249172	81368	GAAGAATTCAAATAAGGTCC	293759	125955	AAACGGACTAATACAATCCC
204586	36782	TCAACAAGAGAAACATTTTA	249173	81369	AGAAGAATTCAAATAAGGTC	293760	125956	AAAACGGACTAATACAATCC
204587	36783	TTCAACAAGAGAAACATTTT	249174	81370	TAGAAGAATTCAAATAAGGT	293761	125957	GAAAACGGACTAATACAATC
204588	36784	GTTCAACAAGAGAAACATTT	249175	81371	GTAGAAGAATTCAAATAAGG	293762	125958	TGAAAACGGACTAATACAAT
204589	36785	AGTTCAACAAGAGAAACATT	249176	81372	AGTAGAAGAATTCAAATAAG	293763	125959	GTGAAAACGGACTAATACAA
204590	36786	GAGTTCAACAAGAGAAACAT	249177	81373	GAGTAGAAGAATTCAAATAA	293764	125960	CGTGAAAACGGACTAATACA
204591	36787	AGAGTTCAACAAGAGAAACA	249178	81374	AGAGTAGAAGAATTCAAATA	293765	125961	GCGTGAAAACGGACTAATAC
204592	36788	CAGAGTTCAACAAGAGAAAC	249179	81375	AAGAGTAGAAGAATTCAAAT	293766	125962	GGCGTGAAAACGGACTAATA
204593	36789	ACAGAGTTCAACAAGAGAAA	249180	81376	TAAGAGTAGAAGAATTCAAA	293767	125963	CGGCGTGAAAACGGACTAAT
204594	36790	TACAGAGTTCAACAAGAGAA	249181	81377	GTAAGAGTAGAAGAATTCAA	293768	125964	GCGGCGTGAAAACGGACTAA

204595	36791	GTACAGAGTTCAACAAGAGA	249182	81378	GGTAAGAGTAGAAGAATTCA	293769	125965	AGCGGCGTGAAAACGGACTA
204596	36792	TGTACAGAGTTCAACAAGAG	249183	81379	GGGTAAGAGTAGAAGAATTC	293770	125966	CAGCGGCGTGAAAACGGACT
204597	36793	ATGTACAGAGTTCAACAAGA	249184	81380	GGGGTAAGAGTAGAAGAATT	293771	125967	TCAGCGGCGTGAAAACGGAC
204598	36794	TATGTACAGAGTTCAACAAG	249185	81381	TGGGGTAAGAGTAGAAGAAT	293772	125968	ATCAGCGGCGTGAAAACGGA
204599	36795	ATATGTACAGAGTTCAACAA	249186	81382	CTGGGGTAAGAGTAGAAGAA	293773	125969	CATCAGCGGCGTGAAAACGG
204600	36796	TATATGTACAGAGTTCAACA	249187	81383	GCTGGGGTAAGAGTAGAAGA	293774	125970	TCATCAGCGGCGTGAAAACG
204601	36797	TTATATGTACAGAGTTCAAC	249188	81384	GGCTGGGGTAAGAGTAGAAG	293775	125971	TTCATCAGCGGCGTGAAAAC
204602	36798	ATTATATGTACAGAGTTCAA	249189	81385	AGGCTGGGGTAAGAGTAGAA	293776	125972	CTTCATCAGCGGCGTGAAAA
204603	36799	AATTATATGTACAGAGTTCA	249190	81386	CAGGCTGGGGTAAGAGTAGA	293777	125973	TCTTCATCAGCGGCGTGAAA
204604	36800	CAATTATATGTACAGAGTTC	249191	81387	GCAGGCTGGGGTAAGAGTAG	293778	125974	GTCTTCATCAGCGGCGTGAA
204605	36801	GCAATTATATGTACAGAGTT	249192	81388	GGCAGGCTGGGGTAAGAGTA	293779	125975	TGTCTTCATCAGCGGCGTGA
204606	36802	TGCAATTATATGTACAGAGT	249193	81389	TGGCAGGCTGGGGTAAGAGT	293780	125976	ATGTCTTCATCAGCGGCGTG
204607	36803	GTGCAATTATATGTACAGAG	249194	81390	ATGGCAGGCTGGGGTAAGAG	293781	125977	TATGTCTTCATCAGCGGCGT
204608	36804	GGTGCAATTATATGTACAGA	249195	81391	GATGGCAGGCTGGGGTAAGA	293782	125978	GTATGTCTTCATCAGCGGCG
204609	36805	TGGTGCAATTATATGTACAG	249196	81392	AGATGGCAGGCTGGGGTAAG	293783	125979	GGTATGTCTTCATCAGCGGC
204610	36806	CTGGTGCAATTATATGTACA	249197	81393	GAGATGGCAGGCTGGGGTAA	293784	125980	GGGTATGTCTTCATCAGCGG
204611	36807	CCTGGTGCAATTATATGTAC	249198	81394	GGAGATGGCAGGCTGGGGTA	293785	125981	CGGGTATGTCTTCATCAGCG
204612	36808	TCCTGGTGCAATTATATGTA	249199	81395	TGGAGATGGCAGGCTGGGGT	293786	125982	TCGGGTATGTCTTCATCAGC
204613	36809	ATCCTGGTGCAATTATATGT	249200	81396	CTGGAGATGGCAGGCTGGGG	293787	125983	ATCGGGTATGTCTTCATCAG
204614	36810	AATCCTGGTGCAATTATATG	249201	81397	GCTGGAGATGGCAGGCTGGG	293788	125984	TATCGGGTATGTCTTCATCA
204615	36811	AAATCCTGGTGCAATTATAT	249202	81398	AGCTGGAGATGGCAGGCTGG	293789	125985	GTATCGGGTATGTCTTCATC
204616	36812	AAAATCCTGGTGCAATTATA	249203	81399	TAGCTGGAGATGGCAGGCTG	293790	125986	AGTATCGGGTATGTCTTCAT
204617	36813	AAAAATCCTGGTGCAATTAT	249204	81400	ATAGCTGGAGATGGCAGGCT	293791	125987	CAGTATCGGGTATGTCTTCA
204618	36814	AAAAAATCCTGGTGCAATTA	249205	81401	GATAGCTGGAGATGGCAGGC	293792	125988	CCAGTATCGGGTATGTCTTC
204619	36815	AAAAAAATCCTGGTGCAATT	249206	81402	GGATAGCTGGAGATGGCAGG	293793	125989	CCCAGTATCGGGTATGTCTT
204620	36816	GAAAAAAATCCTGGTGCAAT	249207	81403	AGGATAGCTGGAGATGGCAG	293794	125990	GCCCAGTATCGGGTATGTCT
204621	36817	TGAAAAAAATCCTGGTGCAA	249208	81404	GAGGATAGCTGGAGATGGCA	293795	125991	TGCCCAGTATCGGGTATGTC
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204623	36819	TTTGAAAAAAATCCTGGTGC	249210	81406	GGGAGGATAGCTGGAGATGG	293797	125993	ACTGCCCAGTATCGGGTATG
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204635	36831	ATTTACTTTTTATTTGAAAA	249222	81418	AGGGCTCTTCAGGGGAGGAT	293809	126005	TCTATCTTTTAGACTGCCCA
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204637	36833	ATATTTACTTTTTATTTGAA	249224	81420	GAAGGGCTCTTCAGGGGAGG	293811	126007	CCTCTATCTTTTAGACTGCC
204638	36834	AATATTTACTTTTTATTTGA	249225	81421	AGAAGGGCTCTTCAGGGGAG	293812	126008	ACCTCTATCTTTTAGACTGC
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204641	36837	TATAATATTTACTTTTTATT	249228	81424	AGCAGAAGGGCTCTTCAGGG	293815	126011	CAGACCTCTATCTTTTAGAC
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204643	36839	AGTATAATATTTACTTTTTA	249230	81426	GCAGCAGAAGGGCTCTTCAG	293817	126013	ATCAGACCTCTATCTTTTAG
204644	36840	TAGTATAATATTTACTTTTT	249231	81427	CGCAGCAGAAGGGCTCTTCA	293818	126014	CATCAGACCTCTATCTTTTA
204645	36841	GTAGTATAATATTTACTTTT	249232	81428	GCGCAGCAGAAGGGCTCTTC	293819	126015	CCATCAGACCTCTATCTTTT
204646	36842	TGTAGTATAATATTTACTTT	249233	81429	AGCGCAGCAGAAGGGCTCTT	293820	126016	TCCATCAGACCTCTATCTTT
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204650	36846	TTTTTGTAGTATAATATTTA	249237	81433	ATCCAGCGCAGCAGAAGGGC	293824	126020	TGAGTCCATCAGACCTCTAT
204651	36847	TTTTTTGTAGTATAATATTT	249238	81434	AATCCAGCGCAGCAGAAGGG	293825	126021	GTGAGTCCATCAGACCTCTA
204652	36848	CTTTTTTGTAGTATAATATT	249239	81435	GAATCCAGCGCAGCAGAAGG	293826	126022	TGTGAGTCCATCAGACCTCT
204653	36849	CCTTTTTTGTAGTATAATAT	249240	81436	AGAATCCAGCGCAGCAGAAG	293827	126023	CTGTGAGTCCATCAGACCTC
204654	36850	CCCTTTTTTGTAGTATAATA	249241	81437	CAGAATCCAGCGCAGCAGAA	293828	126024	ACTGTGAGTCCATCAGACCT
204655	36851	TCCCTTTTTTGTAGTATAAT	249242	81438	CCAGAATCCAGCGCAGCAGA	293829	126025	AACTGTGAGTCCATCAGACC
204656	36852	TTCCCTTTTTTGTAGTATAA	249243	81439	ACCAGAATCCAGCGCAGCAG	293830	126026	GAACTGTGAGTCCATCAGAC
204657	36853	TTTCCCTTTTTTGTAGTATA	249244	81440	CACCAGAATCCAGCGCAGCA	293831	126027	GGAACTGTGAGTCCATCAGA
204658	36854	TTTTCCCTTTTTTGTAGTAT	249245	81441	CCACCAGAATCCAGCGCAGC	293832	126028	TGGAACTGTGAGTCCATCAG
204659	36855	TTTTTCCCTTTTTTGTAGTA	249246	81442	GCCACCAGAATCCAGCGCAG	293833	126029	GTGGAACTGTGAGTCCATCA
204660	36856	CTTTTTCCCTTTTTTGTAGT	249247	81443	GGCCACCAGAATCCAGCGCA	293834	126030	CGTGGAACTGTGAGTCCATC
204661	36857	GCTTTTTCCCTTTTTTGTAG	249248	81444	TGGCCACCAGAATCCAGCGC	293835	126031	ACGTGGAACTGTGAGTCCAT
204662	36858	TGCTTTTTCCCTTTTTTGTA	249249	81445	ATGGCCACCAGAATCCAGCG	293836	126032	CACGTGGAACTGTGAGTCCA
204663	36859	GTGCTTTTTCCCTTTTTTGT	249250	81446	CATGGCCACCAGAATCCAGC	293837	126033	TCACGTGGAACTGTGAGTCC
204664	36860	TGTGCTTTTTCCCTTTTTTG	249251	81447	ACATGGCCACCAGAATCCAG	293838	126034	GTCACGTGGAACTGTGAGTC
204665	36861	TTGTGCTTTTTCCCTTTTTT	249252	81448	GACATGGCCACCAGAATCCA	293839	126035	AGTCACGTGGAACTGTGAGT
204666	36862	CTTGTGCTTTTTCCCTTTTT	249253	81449	TGACATGGCCACCAGAATCC	293840	126036	CAGTCACGTGGAACTGTGAG

204667	36863	GCTTGTGCTTTTTCCCTTTT	249254	81450	ATGACATGGCCACCAGAATC	293841	126037	CCAGTCACGTGGAACTGTGA
204668	36864	TGCTTGTGCTTTTTCCCTTT	249255	81451	GATGACATGGCCACCAGAAT	293842	126038	CCCAGTCACGTGGAACTGTG
204669	36865	ATGCTTGTGCTTTTTCCCTT	249256	81452	AGATGACATGGCCACCAGAA	293843	126039	CCCCAGTCACGTGGAACTGT
204670	36866	AATGCTTGTGCTTTTTCCCT	249257	81453	GAGATGACATGGCCACCAGA	293844	126040	TCCCCAGTCACGTGGAACTG
204671	36867	AAATGCTTGTGCTTTTTCCC	249258	81454	GGAGATGACATGGCCACCAG	293845	126041	CTCCCCAGTCACGTGGAACT
204672	36868	TAAATGCTTGTGCTTTTTCC	249259	81455	AGGAGATGACATGGCCACCA	293846	126042	CCTCCCCAGTCACGTGGAAC
204673	36869	ATAAATGCTTGTGCTTTTTC	249260	81456	GAGGAGATGACATGGCCACC	293847	126043	GCCTCCCCAGTCACGTGGAA
204674	36870	AATAAATGCTTGTGCTTTTT	249261	81457	CGAGGAGATGACATGGCCAC	293848	126044	GGCCTCCCCAGTCACGTGGA
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204676	36872	TTAATAAATGCTTGTGCTTT	249263	81459	GCCGAGGAGATGACATGGCC	293850	126046	CAGGCCTCCCCAGTCACGTG
204677	36873	TTTAATAAATGCTTGTGCTT	249264	81460	GGCCGAGGAGATGACATGGC	293851	126047	TCAGGCCTCCCCAGTCACGT
204678	36874	ATTTAATAAATGCTTGTGCT	249265	81461	GGGCCGAGGAGATGACATGG	293852	126048	GTCAGGCCTCCCCAGTCACG
204679	36875	TATTTAATAAATGCTTGTGC	249266	81462	GGGGCCGAGGAGATGACATG	293853	126049	TGTCAGGCCTCCCCAGTCAC
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204681	36877	GCTATTTAATAAATGCTTGT	249268	81464	ACGGGGCCGAGGAGATGACA	293855	126051	ATTGTCAGGCCTCCCCAGTC
204682	36878	AGCTATTTAATAAATGCTTG	249269	81465	CACGGGGCCGAGGAGATGAC	293856	126052	GATTGTCAGGCCTCCCCAGT
204683	36879	AAGCTATTTAATAAATGCTT	249270	81466	CCACGGGGCCGAGGAGATGA	293857	126053	TGATTGTCAGGCCTCCCCAG
204684	36880	AAAGCTATTTAATAAATGCT	249271	81467	CCCACGGGGCCGAGGAGATG	293858	126054	ATGATTGTCAGGCCTCCCCA
204685	36881	GAAAGCTATTTAATAAATGC	249272	81468	TCCCACGGGGCCGAGGAGAT	293859	126055	CATGATTGTCAGGCCTCCCC
204686	36882	AGAAAGCTATTTAATAAATG	249273	81469	CTCCCACGGGGCCGAGGAGA	293860	126056	CCATGATTGTCAGGCCTCCC
204687	36883	TAGAAAGCTATTTAATAAAT	249274	81470	ACTCCCACGGGGCCGAGGAG	293861	126057	ACCATGATTGTCAGGCCTCC
204688	36884	ATAGAAAGCTATTTAATAAA	249275	81471	GACTCCCACGGGGCCGAGGA	293862	126058	CACCATGATTGTCAGGCCTC
204689	36885	TATAGAAAGCTATTTAATAA	249276	81472	AGACTCCCACGGGGCCGAGG	293863	126059	CCACCATGATTGTCAGGCCT
204690	36886	ATATAGAAAGCTATTTAATA	249277	81473	CAGACTCCCACGGGGCCGAG	293864	126060	TCCACCATGATTGTCAGGCC
204691	36887	GATATAGAAAGCTATTTAAT	249278	81474	TCAGACTCCCACGGGGCCGA	293865	126061	TTCCACCATGATTGTCAGGC
204692	36888	AGATATAGAAAGCTATTTAA	249279	81475	TTCAGACTCCCACGGGGCCG	293866	126062	CTTCCACCATGATTGTCAGG
204693	36889	AAGATATAGAAAGCTATTTA	249280	81476	CTTCAGACTCCCACGGGGCC	293867	126063	CCTTCCACCATGATTGTCAG
204694	36890	AAAGATATAGAAAGCTATTT	249281	81477	TCTTCAGACTCCCACGGGGC	293868	126064	ACCTTCCACCATGATTGTCA
204695	36891	GAAAGATATAGAAAGCTATT	249282	81478	ATCTTCAGACTCCCACGGGG	293869	126065	CACCTTCCACCATGATTGTC
204696	36892	AGAAAGATATAGAAAGCTAT	249283	81479	GATCTTCAGACTCCCACGGG	293870	126066	TCACCTTCCACCATGATTGT
204697	36893	CAGAAAGATATAGAAAGCTA	249284	81480	AGATCTTCAGACTCCCACGG	293871	126067	TTCACCTTCCACCATGATTG
204698	36894	TCAGAAAGATATAGAAAGCT	249285	81481	CAGATCTTCAGACTCCCACG	293872	126068	TTTCACCTTCCACCATGATT
204699	36895	CTCAGAAAGATATAGAAAGC	249286	81482	CCAGATCTTCAGACTCCCAC	293873	126069	CTTTCACCTTCCACCATGAT
204700	36896	ACTCAGAAAGATATAGAAAG	249287	81483	GCCAGATCTTCAGACTCCCA	293874	126070	CCTTTCACCTTCCACCATGA
204701	36897	AACTCAGAAAGATATAGAAA	249288	81484	AGCCAGATCTTCAGACTCCC	293875	126071	GCCTTTCACCTTCCACCATG
204702	36898	AAACTCAGAAAGATATAGAA	249289	81485	CAGCCAGATCTTCAGACTCC	293876	126072	AGCCTTTCACCTTCCACCAT
204703	36899	AAAACTCAGAAAGATATAGA	249290	81486	GCAGCCAGATCTTCAGACTC	293877	126073	AAGCCTTTCACCTTCCACCA
204704	36900	CAAAACTCAGAAAGATATAG	249291	81487	TGCAGCCAGATCTTCAGACT	293878	126074	CAAGCCTTTCACCTTCCACC
204705	36901	TCAAAACTCAGAAAGATATA	249292	81488	CTGCAGCCAGATCTTCAGAC	293879	126075	ACAAGCCTTTCACCTTCCAC
204706	36902	ATCAAAACTCAGAAAGATAT	249293	81489	GCTGCAGCCAGATCTTCAGA	293880	126076	GACAAGCCTTTCACCTTCCA
204707	36903	GATCAAAACTCAGAAAGATA	249294	81490	GGCTGCAGCCAGATCTTCAG	293881	126077	AGACAAGCCTTTCACCTTCC
204708	36904	GGATCAAAACTCAGAAAGAT	249295	81491	AGGCTGCAGCCAGATCTTCA	293882	126078	GAGACAAGCCTTTCACCTTC
204709	36905	AGGATCAAAACTCAGAAAGA	249296	81492	GAGGCTGCAGCCAGATCTTC	293883	126079	TGAGACAAGCCTTTCACCTT
204710	36906	AAGGATCAAAACTCAGAAAG	249297	81493	TGAGGCTGCAGCCAGATCTT	293884	126080	GTGAGACAAGCCTTTCACCT
204711	36907	AAAGGATCAAAACTCAGAAA	249298	81494	GTGAGGCTGCAGCCAGATCT	293885	126081	TGTGAGACAAGCCTTTCACC
204712	36908	CAAAGGATCAAAACTCAGAA	249299	81495	GGTGAGGCTGCAGCCAGATC	293886	126082	GTGTGAGACAAGCCTTTCAC
204713	36909	TCAAAGGATCAAAACTCAGA	249300	81496	AGGTGAGGCTGCAGCCAGAT	293887	126083	CGTGTGAGACAAGCCTTTCA
204714	36910	ATCAAAGGATCAAAACTCAG	249301	81497	GAGGTGAGGCTGCAGCCAGA	293888	126084	CCGTGTGAGACAAGCCTTTC
204715	36911	AATCAAAGGATCAAAACTCA	249302	81498	AGAGGTGAGGCTGCAGCCAG	293889	126085	ACCGTGTGAGACAAGCCTTT
204716	36912	CAATCAAAGGATCAAAACTC	249303	81499	CAGAGGTGAGGCTGCAGCCA	293890	126086	CACCGTGTGAGACAAGCCTT
204717	36913	GCAATCAAAGGATCAAAACT	249304	81500	TCAGAGGTGAGGCTGCAGCC	293891	126087	CCACCGTGTGAGACAAGCCT
204718	36914	TGCAATCAAAGGATCAAAAC	249305	81501	CTCAGAGGTGAGGCTGCAGC	293892	126088	GCCACCGTGTGAGACAAGCC
204719	36915	CTGCAATCAAAGGATCAAAA	249306	81502	CCTCAGAGGTGAGGCTGCAG	293893	126089	TGCCACCGTGTGAGACAAGC
204720	36916	TCTGCAATCAAAGGATCAAA	249307	81503	ACCTCAGAGGTGAGGCTGCA	293894	126090	CTGCCACCGTGTGAGACAAG
204721	36917	GTCTGCAATCAAAGGATCAA	249308	81504	GACCTCAGAGGTGAGGCTGC	293895	126091	TCTGCCACCGTGTGAGACAA
204722	36918	AGTCTGCAATCAAAGGATCA	249309	81505	GGACCTCAGAGGTGAGGCTG	293896	126092	GTCTGCCACCGTGTGAGACA
204723	36919	CAGTCTGCAATCAAAGGATC	249310	81506	AGGACCTCAGAGGTGAGGCT	293897	126093	TGTCTGCCACCGTGTGAGAC
204724	36920	TCAGTCTGCAATCAAAGGAT	249311	81507	CAGGACCTCAGAGGTGAGGC	293898	126094	TTGTCTGCCACCGTGTGAGA
204725	36921	ATCAGTCTGCAATCAAAGGA	249312	81508	GCAGGACCTCAGAGGTGAGG	293899	126095	CTTGTCTGCCACCGTGTGAG
204726	36922	CATCAGTCTGCAATCAAAGG	249313	81509	AGCAGGACCTCAGAGGTGAG	293900	126096	TCTTGTCTGCCACCGTGTGA
204727	36923	ACATCAGTCTGCAATCAAAG	249314	81510	TAGCAGGACCTCAGAGGTGA	293901	126097	CTCTTGTCTGCCACCGTGTG
204728	36924	TACATCAGTCTGCAATCAAA	249315	81511	CTAGCAGGACCTCAGAGGTG	293902	126098	TCTCTTGTCTGCCACCGTGT
204729	36925	TTACATCAGTCTGCAATCAA	249316	81512	ACTAGCAGGACCTCAGAGGT	293903	126099	TTCTCTTGTCTGCCACCGTG
204730	36926	ATTACATCAGTCTGCAATCA	249317	81513	AACTAGCAGGACCTCAGAGG	293904	126100	TTTCTCTTGTCTGCCACCGT
204731	36927	TATTACATCAGTCTGCAATC	249318	81514	CAACTAGCAGGACCTCAGAG	293905	126101	TTTTCTCTTGTCTGCCACCG
204732	36928	ATATTACATCAGTCTGCAAT	249319	81515	GCAACTAGCAGGACCTCAGA	293906	126102	CTTTTCTCTTGTCTGCCACC
204733	36929	AATATTACATCAGTCTGCAA	249320	81516	GGCAACTAGCAGGACCTCAG	293907	126103	TCTTTTCTCTTGTCTGCCAC
204734	36930	AAATATTACATCAGTCTGCA	249321	81517	TGGCAACTAGCAGGACCTCA	293908	126104	CTCTTTTCTCTTGTCTGCCA
204735	36931	AAAATATTACATCAGTCTGC	249322	81518	GTGGCAACTAGCAGGACCTC	293909	126105	GCTCTTTTCTCTTGTCTGCC
204736	36932	TAAAATATTACATCAGTCTG	249323	81519	GGTGGCAACTAGCAGGACCT	293910	126106	AGCTCTTTTCTCTTGTCTGC
204737	36933	ATAAAATATTACATCAGTCT	249324	81520	AGGTGGCAACTAGCAGGACC	293911	126107	AAGCTCTTTTCTCTTGTCTG
204738	36934	CATAAAATATTACATCAGTC	249325	81521	GAGGTGGCAACTAGCAGGAC	293912	126108	CAAGCTCTTTTCTCTTGTCT

204739	36935	ACATAAAATATTACATCAGT	249326	81522	AGAGGTGGCAACTAGCAGGA	293913	126109	ACAAGCTCTTTTCTCTTGTC
204740	36936	TACATAAAATATTACATCAG	249327	81523	AAGAGGTGGCAACTAGCAGG	293914	126110	CACAAGCTCTTTTCTCTTGT
204741	36937	TTACATAAAATATTACATCA	249328	81524	TAAGAGGTGGCAACTAGCAG	293915	126111	GCACAAGCTCTTTTCTCTTG
204742	36938	TTTACATAAAATATTACATC	249329	81525	TTAAGAGGTGGCAACTAGCA	293916	126112	TGCACAAGCTCTTTTCTCTT
204743	36939	ATTTACATAAAATATTACAT	249330	81526	TTTAAGAGGTGGCAACTAGC	293917	126113	CTGCACAAGCTCTTTTCTCT
204744	36940	GATTTACATAAAATATTACA	249331	81527	GTTTAAGAGGTGGCAACTAG	293918	126114	CCTGCACAAGCTCTTTTCTC
204745	36941	TGATTTACATAAAATATTAC	249332	81528	TGTTTAAGAGGTGGCAACTA	293919	126115	CCCTGCACAAGCTCTTTTCT
204746	36942	ATGATTTACATAAAATATTA	249333	81529	ATGTTTAAGAGGTGGCAACT	293920	126116	CCCCTGCACAAGCTCTTTTC
204747	36943	AATGATTTACATAAAATATT	249334	81530	CATGTTTAAGAGGTGGCAAC	293921	126117	TCCCCTGCACAAGCTCTTTT
204748	36944	CAATGATTTACATAAAATAT	249335	81531	TCATGTTTAAGAGGTGGCAA	293922	126118	TTCCCCTGCACAAGCTCTTT
204749	36945	GCAATGATTTACATAAAATA	249336	81532	ATCATGTTTAAGAGGTGGCA	293923	126119	GTTCCCCTGCACAAGCTCTT
204750	36946	AGCAATGATTTACATAAAAT	249337	81533	GATCATGTTTAAGAGGTGGC	293924	126120	AGTTCCCCTGCACAAGCTCT
204751	36947	AAGCAATGATTTACATAAAA	249338	81534	AGATCATGTTTAAGAGGTGG	293925	126121	GAGTTCCCCTGCACAAGCTC
204752	36948	CAAGCAATGATTTACATAAA	249339	81535	CAGATCATGTTTAAGAGGTG	293926	126122	GGAGTTCCCCTGCACAAGCT
204753	36949	CCAAGCAATGATTTACATAA	249340	81536	TCAGATCATGTTTAAGAGGT	293927	126123	GGGAGTTCCCCTGCACAAGC
204754	36950	ACCAAGCAATGATTTACATA	249341	81537	CTCAGATCATGTTTAAGAGG	293928	126124	GGGGAGTTCCCCTGCACAAG
204755	36951	AACCAAGCAATGATTTACAT	249342	81538	CCTCAGATCATGTTTAAGAG	293929	126125	AGGGGAGTTCCCCTGCACAA
204756	36952	TAACCAAGCAATGATTTACA	249343	81539	GCCTCAGATCATGTTTAAGA	293930	126126	AAGGGGAGTTCCCCTGCACA
204757	36953	GTAACCAAGCAATGATTTAC	249344	81540	AGCCTCAGATCATGTTTAAG	293931	126127	AAAGGGGAGTTCCCCTGCAC
204758	36954	AGTAACCAAGCAATGATTTA	249345	81541	GAGCCTCAGATCATGTTTAA	293932	126128	TAAAGGGGAGTTCCCCTGCA
204759	36955	TAGTAACCAAGCAATGATTT	249346	81542	GGAGCCTCAGATCATGTTTA	293933	126129	ATAAAGGGGAGTTCCCCTGC
204760	36956	TTAGTAACCAAGCAATGATT	249347	81543	GGGAGCCTCAGATCATGTTT	293934	126130	TATAAAGGGGAGTTCCCCTG
204761	36957	CTTAGTAACCAAGCAATGAT	249348	81544	TGGGAGCCTCAGATCATGTT	293935	126131	TTATAAAGGGGAGTTCCCCT
204762	36958	ACTTAGTAACCAAGCAATGA	249349	81545	ATGGGAGCCTCAGATCATGT	293936	126132	TTTATAAAGGGGAGTTCCCC
204763	36959	CACTTAGTAACCAAGCAATG	249350	81546	CATGGGAGCCTCAGATCATG	293937	126133	TTTTATAAAGGGGAGTTCCC
204764	36960	TCACTTAGTAACCAAGCAAT	249351	81547	GCATGGGAGCCTCAGATCAT	293938	126134	GTTTTATAAAGGGGAGTTCC
204765	36961	TTCACTTAGTAACCAAGCAA	249352	81548	TGCATGGGAGCCTCAGATCA	293939	126135	GGTTTTATAAAGGGGAGTTC
204766	36962	GTTCACTTAGTAACCAAGCA	249353	81549	GTGCATGGGAGCCTCAGATC	293940	126136	TGGTTTTATAAAGGGGAGTT
204767	36963	AGTTCACTTAGTAACCAAGC	249354	81550	AGTGCATGGGAGCCTCAGAT	293941	126137	ATGGTTTTATAAAGGGGAGT
204768	36964	AAGTTCACTTAGTAACCAAG	249355	81551	GAGTGCATGGGAGCCTCAGA	293942	126138	GATGGTTTTATAAAGGGGAG
204769	36965	AAAGTTCACTTAGTAACCAA	249356	81552	AGAGTGCATGGGAGCCTCAG	293943	126139	TGATGGTTTTATAAAGGGGA
204770	36966	TAAAGTTCACTTAGTAACCA	249357	81553	CAGAGTGCATGGGAGCCTCA	293944	126140	CTGATGGTTTTATAAAGGGG
204771	36967	TTAAAGTTCACTTAGTAACC	249358	81554	TCAGAGTGCATGGGAGCCTC	293945	126141	TCTGATGGTTTTATAAAGGG
204772	36968	CTTAAAGTTCACTTAGTAAC	249359	81555	GTCAGAGTGCATGGGAGCCT	293946	126142	ATCTGATGGTTTTATAAAGG
204773	36969	TCTTAAAGTTCACTTAGTAA	249360	81556	GGTCAGAGTGCATGGGAGCC	293947	126143	GATCTGATGGTTTTATAAAG
204774	36970	TTCTTAAAGTTCACTTAGTA	249361	81557	AGGTCAGAGTGCATGGGAGC	293948	126144	AGATCTGATGGTTTTATAAA
204775	36971	TTTCTTAAAGTTCACTTAGT	249362	81558	CAGGTCAGAGTGCATGGGAG	293949	126145	GAGATCTGATGGTTTTATAA
204776	36972	TTTTCTTAAAGTTCACTTAG	249363	81559	ACAGGTCAGAGTGCATGGGA	293950	126146	CGAGATCTGATGGTTTTATA
204777	36973	CTTTTCTTAAAGTTCACTTA	249364	81560	CACAGGTCAGAGTGCATGGG	293951	126147	CCGAGATCTGATGGTTTTAT
204778	36974	ACTTTTCTTAAAGTTCACTT	249365	81561	GCACAGGTCAGAGTGCATGG	293952	126148	CCCGAGATCTGATGGTTTTA
204779	36975	CACTTTTCTTAAAGTTCACT	249366	81562	GGCACAGGTCAGAGTGCATG	293953	126149	TCCCGAGATCTGATGGTTTT
204780	36976	TCACTTTTCTTAAAGTTCAC	249367	81563	GGGCACAGGTCAGAGTGCAT	293954	126150	CTCCCGAGATCTGATGGTTT
204781	36977	CTCACTTTTCTTAAAGTTCA	249368	81564	TGGGCACAGGTCAGAGTGCA	293955	126151	TCTCCCGAGATCTGATGGTT
204782	36978	TCTCACTTTTCTTAAAGTTC	249369	81565	GTGGGCACAGGTCAGAGTGC	293956	126152	GTCTCCCGAGATCTGATGGT
204783	36979	GTCTCACTTTTCTTAAAGTT	249370	81566	TGTGGGCACAGGTCAGAGTG	293957	126153	AGTCTCCCGAGATCTGATGG
204784	36980	CGTCTCACTTTTCTTAAAGT	249371	81567	ATGTGGGCACAGGTCAGAGT	293958	126154	AAGTCTCCCGAGATCTGATG
204785	36981	ACGTCTCACTTTTCTTAAAG	249372	81568	CATGTGGGCACAGGTCAGAG	293959	126155	TAAGTCTCCCGAGATCTGAT
204786	36982	GACGTCTCACTTTTCTTAAA	249373	81569	CCATGTGGGCACAGGTCAGA	293960	126156	ATAAGTCTCCCGAGATCTGA
204787	36983	AGACGTCTCACTTTTCTTAA	249374	81570	CCCATGTGGGCACAGGTCAG	293961	126157	AATAAGTCTCCCGAGATCTG
204788	36984	CAGACGTCTCACTTTTCTTA	249375	81571	CCCCATGTGGGCACAGGTCA	293962	126158	GAATAAGTCTCCCGAGATCT
204789	36985	GCAGACGTCTCACTTTTCTT	249376	81572	GCCCCATGTGGGCACAGGTC	293963	126159	TGAATAAGTCTCCCGAGATC
204790	36986	TGCAGACGTCTCACTTTTCT	249377	81573	GGCCCCATGTGGGCACAGGT	293964	126160	GTGAATAAGTCTCCCGAGAT
204791	36987	CTGCAGACGTCTCACTTTTC	249378	81574	GGGCCCCATGTGGGCACAGG	293965	126161	AGTGAATAAGTCTCCCGAGA
204792	36988	TCTGCAGACGTCTCACTTTT	249379	81575	TGGGCCCCATGTGGGCACAG	293966	126162	TAGTGAATAAGTCTCCCGAG
204793	36989	TTCTGCAGACGTCTCACTTT	249380	81576	GTGGGCCCCATGTGGGCACA	293967	126163	ATAGTGAATAAGTCTCCCGA
204794	36990	CTTCTGCAGACGTCTCACTT	249381	81577	CGTGGGCCCCATGTGGGCAC	293968	126164	GATAGTGAATAAGTCTCCCG
204795	36991	ACTTCTGCAGACGTCTCACT	249382	81578	CCGTGGGCCCCATGTGGGCA	293969	126165	TGATAGTGAATAAGTCTCCC
204796	36992	AACTTCTGCAGACGTCTCAC	249383	81579	CCCGTGGGCCCCATGTGGGC	293970	126166	ATGATAGTGAATAAGTCTCC
204797	36993	CAACTTCTGCAGACGTCTCA	249384	81580	TCCCGTGGGCCCCATGTGGG	293971	126167	CATGATAGTGAATAAGTCTC
204798	36994	GCAACTTCTGCAGACGTCTC	249385	81581	TTCCCGTGGGCCCCATGTGG	293972	126168	TCATGATAGTGAATAAGTCT
204799	36995	GGCAACTTCTGCAGACGTCT	249386	81582	TTTCCCGTGGGCCCCATGTG	293973	126169	CTCATGATAGTGAATAAGTC
204800	36996	GGGCAACTTCTGCAGACGTC	249387	81583	GTTTCCCGTGGGCCCCATGT	293974	126170	TCTCATGATAGTGAATAAGT
204801	36997	TGGGCAACTTCTGCAGACGT	249388	81584	TGTTTCCCGTGGGCCCCATG	293975	126171	TTCTCATGATAGTGAATAAG
204802	36998	ATGGGCAACTTCTGCAGACG	249389	81585	GTGTTTCCCGTGGGCCCCAT	293976	126172	GTTCTCATGATAGTGAATAA
204803	36999	TATGGGCAACTTCTGCAGAC	249390	81586	CGTGTTTCCCGTGGGCCCCA	293977	126173	TGTTCTCATGATAGTGAATA
204804	37000	TTATGGGCAACTTCTGCAGA	249391	81587	GCGTGTTTCCCGTGGGCCCC	293978	126174	CTGTTCTCATGATAGTGAAT
204805	37001	ATTATGGGCAACTTCTGCAG	249392	81588	AGCGTGTTTCCCGTGGGCCC	293979	126175	GCTGTTCTCATGATAGTGAA
204806	37002	AATTATGGGCAACTTCTGCA	249393	81589	CAGCGTGTTTCCCGTGGGCC	293980	126176	TGCTGTTCTCATGATAGTGA
204807	37003	AAATTATGGGCAACTTCTGC	249394	81590	CCAGCGTGTTTCCCGTGGGC	293981	126177	GTGCTGTTCTCATGATAGTG
204808	37004	TAAATTATGGGCAACTTCTG	249395	81591	GCCAGCGTGTTTCCCGTGGG	293982	126178	CGTGCTGTTCTCATGATAGT
204809	37005	CTAAATTATGGGCAACTTCT	249396	81592	TGCCAGCGTGTTTCCCGTGG	293983	126179	CCGTGCTGTTCTCATGATAG
204810	37006	GCTAAATTATGGGCAACTTC	249397	81593	TTGCCAGCGTGTTTCCCGTG	293984	126180	CCCGTGCTGTTCTCATGATA

204811	37007	TGCTAAATTATGGGCAACTT	249398	81594	CTTGCCAGCGTGTTTCCCGT	293985	126181	TCCCGTGCTGTTCTCATGAT
204812	37008	CTGCTAAATTATGGGCAACT	249399	81595	GCTTGCCAGCGTGTTTCCCG	293986	126182	TTCCCGTGCTGTTCTCATGA
204813	37009	GCTGCTAAATTATGGGCAAC	249400	81596	TGCTTGCCAGCGTGTTTCCC	293987	126183	TTTCCCGTGCTGTTCTCATG
204814	37010	AGCTGCTAAATTATGGGCAA	249401	81597	TTGCTTGCCAGCGTGTTTCC	293988	126184	CTTTCCCGTGCTGTTCTCAT
204815	37011	TAGCTGCTAAATTATGGGCA	249402	81598	TTTGCTTGCCAGCGTGTTTC	293989	126185	TCTTTCCCGTGCTGTTCTCA
204816	37012	GTAGCTGCTAAATTATGGGC	249403	81599	GTTTGCTTGCCAGCGTGTTT	293990	126186	GTCTTTCCCGTGCTGTTCTC
204817	37013	AGTAGCTGCTAAATTATGGG	249404	81600	AGTTTGCTTGCCAGCGTGTT	293991	126187	GGTCTTTCCCGTGCTGTTCT
204818	37014	CAGTAGCTGCTAAATTATGG	249405	81601	CAGTTTGCTTGCCAGCGTGT	293992	126188	GGGTCTTTCCCGTGCTGTTC
204819	37015	ACAGTAGCTGCTAAATTATG	249406	81602	ACAGTTTGCTTGCCAGCGTG	293993	126189	AGGGTCTTTCCCGTGCTGTT
204820	37016	TACAGTAGCTGCTAAATTAT	249407	81603	CACAGTTTGCTTGCCAGCGT	293994	126190	GAGGGTCTTTCCCGTGCTGT
204821	37017	ATACAGTAGCTGCTAAATTA	249408	81604	CCACAGTTTGCTTGCCAGCG	293995	126191	GGAGGGTCTTTCCCGTGCTG
204822	37018	AATACAGTAGCTGCTAAATT	249409	81605	CCCACAGTTTGCTTGCCAGC	293996	126192	AGGAGGGTCTTTCCCGTGCT
204823	37019	CAATACAGTAGCTGCTAAAT	249410	81606	ACCCACAGTTTGCTTGCCAG	293997	126193	GAGGAGGGTCTTTCCCGTGC
204824	37020	ACAATACAGTAGCTGCTAAA	249411	81607	CACCCACAGTTTGCTTGCCA	293998	126194	AGAGGAGGGTCTTTCCCGTG
204825	37021	TACAATACAGTAGCTGCTAA	249412	81608	ACACCCACAGTTTGCTTGCC	293999	126195	TAGAGGAGGGTCTTTCCCGT
204826	37022	GTACAATACAGTAGCTGCTA	249413	81609	CACACCCACAGTTTGCTTGC	294000	126196	ATAGAGGAGGGTCTTTCCCG
204827	37023	GGTACAATACAGTAGCTGCT	249414	81610	GCACACCCACAGTTTGCTTG	294001	126197	CATAGAGGAGGGTCTTTCCC
204828	37024	TGGTACAATACAGTAGCTGC	249415	81611	TGCACACCCACAGTTTGCTT	294002	126198	TCATAGAGGAGGGTCTTTCC
204829	37025	ATGGTACAATACAGTAGCTG	249416	81612	CTGCACACCCACAGTTTGCT	294003	126199	ATCATAGAGGAGGGTCTTTC
204830	37026	AATGGTACAATACAGTAGCT	249417	81613	TCTGCACACCCACAGTTTGC	294004	126200	AATCATAGAGGAGGGTCTTT
204831	37027	CAATGGTACAATACAGTAGC	249418	81614	GTCTGCACACCCACAGTTTG	294005	126201	GAATCATAGAGGAGGGTCTT
204832	37028	TCAATGGTACAATACAGTAG	249419	81615	CGTCTGCACACCCACAGTTT	294006	126202	TGAATCATAGAGGAGGGTCT
204833	37029	ATCAATGGTACAATACAGTA	249420	81616	CCGTCTGCACACCCACAGTT	294007	126203	TTGAATCATAGAGGAGGGTC
204834	37030	CATCAATGGTACAATACAGT	249421	81617	ACCGTCTGCACACCCACAGT	294008	126204	ATTGAATCATAGAGGAGGGT
204835	37031	ACATCAATGGTACAATACAG	249422	81618	AACCGTCTGCACACCCACAG	294009	126205	AATTGAATCATAGAGGAGGG
204836	37032	TACATCAATGGTACAATACA	249423	81619	GAACCGTCTGCACACCCACA	294010	126206	TAATTGAATCATAGAGGAGG
204837	37033	GTACATCAATGGTACAATAC	249424	81620	AGAACCGTCTGCACACCCAC	294011	126207	GTAATTGAATCATAGAGGAG
204838	37034	CGTACATCAATGGTACAATA	249425	81621	GAGAACCGTCTGCACACCCA	294012	126208	GGTAATTGAATCATAGAGGA
204839	37035	CCGTACATCAATGGTACAAT	249426	81622	TGAGAACCGTCTGCACACCC	294013	126209	AGGTAATTGAATCATAGAGG
204840	37036	GCCGTACATCAATGGTACAA	249427	81623	CTGAGAACCGTCTGCACACC	294014	126210	GAGGTAATTGAATCATAGAG
204841	37037	AGCCGTACATCAATGGTACA	249428	81624	CCTGAGAACCGTCTGCACAC	294015	126211	GGAGGTAATTGAATCATAGA
204842	37038	AAGCCGTACATCAATGGTAC	249429	81625	CCCTGAGAACCGTCTGCACA	294016	126212	GGGAGGTAATTGAATCATAG
204843	37039	AAAGCCGTACATCAATGGTA	249430	81626	GCCCTGAGAACCGTCTGCAC	294017	126213	TGGGAGGTAATTGAATCATA
204844	37040	TAAAGCCGTACATCAATGGT	249431	81627	AGCCCTGAGAACCGTCTGCA	294018	126214	GTGGGAGGTAATTGAATCAT
204845	37041	ATAAAGCCGTACATCAATGG	249432	81628	CAGCCCTGAGAACCGTCTGC	294019	126215	GGTGGGAGGTAATTGAATCA
204846	37042	AATAAAGCCGTACATCAATG	249433	81629	GCAGCCCTGAGAACCGTCTG	294020	126216	TGGTGGGAGGTAATTGAATC
204847	37043	AAATAAAGCCGTACATCAAT	249434	81630	TGCAGCCCTGAGAACCGTCT	294021	126217	CTGGTGGGAGGTAATTGAAT
204848	37044	AAAATAAAGCCGTACATCAA	249435	81631	CTGCAGCCCTGAGAACCGTC	294022	126218	CCTGGTGGGAGGTAATTGAA
204849	37045	GAAAATAAAGCCGTACATCA	249436	81632	GCTGCAGCCCTGAGAACCGT	294023	126219	ACCTGGTGGGAGGTAATTGA
204850	37046	AGAAAATAAAGCCGTACATC	249437	81633	TGCTGCAGCCCTGAGAACCG	294024	126220	GACCTGGTGGGAGGTAATTG
204851	37047	AAGAAAATAAAGCCGTACAT	249438	81634	GTGCTGCAGCCCTGAGAACC	294025	126221	GGACCTGGTGGGAGGTAATT
204852	37048	CAAGAAAATAAAGCCGTACA	249439	81635	GGTGCTGCAGCCCTGAGAAC	294026	126222	GGGACCTGGTGGGAGGTAAT
204853	37049	TCAAGAAAATAAAGCCGTAC	249440	81636	AGGTGCTGCAGCCCTGAGAA	294027	126223	AGGGACCTGGTGGGAGGTAA
204854	37050	ATCAAGAAAATAAAGCCGTA	249441	81637	CAGGTGCTGCAGCCCTGAGA	294028	126224	GAGGGACCTGGTGGGAGGTA
204855	37051	AATCAAGAAAATAAAGCCGT	249442	81638	ACAGGTGCTGCAGCCCTGAG	294029	126225	GGAGGGACCTGGTGGGAGGT
204856	37052	TAATCAAGAAAATAAAGCCG	249443	81639	GACAGGTGCTGCAGCCCTGA	294030	126226	GGGAGGGACCTGGTGGGAGG
204857	37053	TTAATCAAGAAAATAAAGCC	249444	81640	GGACAGGTGCTGCAGCCCTG	294031	126227	TGGGAGGGACCTGGTGGGAG
204858	37054	ATTAATCAAGAAAATAAAGC	249445	81641	AGGACAGGTGCTGCAGCCCT	294032	126228	GTGGGAGGGACCTGGTGGGA
204859	37055	AATTAATCAAGAAAATAAAG	249446	81642	AAGGACAGGTGCTGCAGCCC	294033	126229	TGTGGGAGGGACCTGGTGGG
204860	37056	TAATTAATCAAGAAAATAAA	249447	81643	AAAGGACAGGTGCTGCAGCC	294034	126230	TTGTGGGAGGGACCTGGTGG
204861	37057	ATAATTAATCAAGAAAATAA	249448	81644	CAAAGGACAGGTGCTGCAGC	294035	126231	GTTGTGGGAGGGACCTGGTG
204862	37058	AATAATTAATCAAGAAAATA	249449	81645	GCAAAGGACAGGTGCTGCAG	294036	126232	TGTTGTGGGAGGGACCTGGT
204863	37059	AAATAATTAATCAAGAAAAT	249450	81646	AGCAAAGGACAGGTGCTGCA	294037	126233	ATGTTGTGGGAGGGACCTGG
204864	37060	TAAATAATTAATCAAGAAAA	249451	81647	GAGCAAAGGACAGGTGCTGC	294038	126234	CATGTTGTGGGAGGGACCTG
204865	37061	TTAAATAATTAATCAAGAAA	249452	81648	AGAGCAAAGGACAGGTGCTG	294039	126235	ACATGTTGTGGGAGGGACCT
204866	37062	TTTAAATAATTAATCAAGAA	249453	81649	CAGAGCAAAGGACAGGTGCT	294040	126236	TACATGTTGTGGGAGGGACC
204867	37063	GTTTAAATAATTAATCAAGA	249454	81650	GCAGAGCAAAGGACAGGTGC	294041	126237	CTACATGTTGTGGGAGGGAC
204868	37064	TGTTTAAATAATTAATCAAG	249455	81651	GGCAGAGCAAAGGACAGGTG	294042	126238	CCTACATGTTGTGGGAGGGA
204869	37065	TTGTTTAAATAATTAATCAA	249456	81652	GGGCAGAGCAAAGGACAGGT	294043	126239	TCCTACATGTTGTGGGAGGG
204870	37066	ATTGTTTAAATAATTAATCA	249457	81653	GGGGCAGAGCAAAGGACAGG	294044	126240	TTCCTACATGTTGTGGGAGG
204871	37067	TATTGTTTAAATAATTAATC	249458	81654	GGGGGCAGAGCAAAGGACAG	294045	126241	ATTCCTACATGTTGTGGGAG
204872	37068	ATATTGTTTAAATAATTAAT	249459	81655	TGGGGGCAGAGCAAAGGACA	294046	126242	AATTCCTACATGTTGTGGGA
204873	37069	TATATTGTTTAAATAATTAA	249460	81656	TTGGGGGCAGAGCAAAGGAC	294047	126243	CAATTCCTACATGTTGTGGG
204874	37070	TTATATTGTTTAAATAATTA	249461	81657	TTTGGGGGCAGAGCAAAGGA	294048	126244	ACAATTCCTACATGTTGTGG
204875	37071	ATTATATTGTTTAAATAATT	249462	81658	CTTTGGGGGCAGAGCAAAGG	294049	126245	CACAATTCCTACATGTTGTG
204876	37072	AATTATATTGTTTAAATAAT	249463	81659	GCTTTGGGGGCAGAGCAAAG	294050	126246	CCACAATTCCTACATGTTGT
204877	37073	GAATTATATTGTTTAAATAA	249464	81660	TGCTTTGGGGGCAGAGCAAA	294051	126247	CCCACAATTCCTACATGTTG
204878	37074	TGAATTATATTGTTTAAATA	249465	81661	TTGCTTTGGGGGCAGAGCAA	294052	126248	TCCCACAATTCCTACATGTT
204879	37075	GTGAATTATATTGTTTAAAT	249466	81662	CTTGCTTTGGGGGCAGAGCA	294053	126249	TTCCCACAATTCCTACATGT
204880	37076	TGTGAATTATATTGTTTAAA	249467	81663	CCTTGCTTTGGGGGCAGAGC	294054	126250	GTTCCCACAATTCCTACATG
204881	37077	TTGTGAATTATATTGTTTAA	249468	81664	GCCTTGCTTTGGGGGCAGAG	294055	126251	AGTTCCCACAATTCCTACAT
204882	37078	ATTGTGAATTATATTGTTTA	249469	81665	GGCCTTGCTTTGGGGGCAGA	294056	126252	TAGTTCCCACAATTCCTACA

204883	37079	AATTGTGAATTATATTGTTT	249470	81666	TGGCCTTGCTTTGGGGGCAG	294057	126253	GTAGTTCCCACAATTCCTAC
204884	37080	AAATTGTGAATTATATTGTT	249471	81667	CTGGCCTTGCTTTGGGGGCA	294058	126254	TGTAGTTCCCACAATTCCTA
204885	37081	AAAATTGTGAATTATATTGT	249472	81668	GCTGGCCTTGCTTTGGGGGC	294059	126255	TTGTAGTTCCCACAATTCCT
204886	37082	TAAAATTGTGAATTATATTG	249473	81669	GGCTGGCCTTGCTTTGGGGG	294060	126256	ATTGTAGTTCCCACAATTCC
204887	37083	TTAAAATTGTGAATTATATT	249474	81670	GGGCTGGCCTTGCTTTGGGG	294061	126257	AATTGTAGTTCCCACAATTC
204888	37084	TTTAAAATTGTGAATTATAT	249475	81671	TGGGCTGGCCTTGCTTTGGG	294062	126258	GAATTGTAGTTCCCACAATT
204889	37085	TTTTAAAATTGTGAATTATA	249476	81672	ATGGGCTGGCCTTGCTTTGG	294063	126259	TGAATTGTAGTTCCCACAAT
204890	37086	ATTTTAAAATTGTGAATTAT	249477	81673	GATGGGCTGGCCTTGCTTTG	294064	126260	TTGAATTGTAGTTCCCACAA
204891	37087	TATTTTAAAATTGTGAATTA	249478	81674	AGATGGGCTGGCCTTGCTTT	294065	126261	CTTGAATTGTAGTTCCCACA
204892	37088	TTATTTTAAAATTGTGAATT	249479	81675	AAGATGGGCTGGCCTTGCTT	294066	126262	TCTTGAATTGTAGTTCCCAC
204893	37089	ATTATTTTAAAATTGTGAAT	249480	81676	GAAGATGGGCTGGCCTTGCT	294067	126263	ATCTTGAATTGTAGTTCCCA
204894	37090	TATTATTTTAAAATTGTGAA	249481	81677	GGAAGATGGGCTGGCCTTGC	294068	126264	CATCTTGAATTGTAGTTCCC
204895	37091	TTATTATTTTAAAATTGTGA	249482	81678	TGGAAGATGGGCTGGCCTTG	294069	126265	TCATCTTGAATTGTAGTTCC
204896	37092	TTTATTATTTTAAAATTGTG	249483	81679	ATGGAAGATGGGCTGGCCTT	294070	126266	GTCATCTTGAATTGTAGTTC
204897	37093	ATTTATTATTTTAAAATTGT	249484	81680	GATGGAAGATGGGCTGGCCT	294071	126267	TGTCATCTTGAATTGTAGTT
204898	37094	AATTTATTATTTTAAAATTG	249485	81681	GGATGGAAGATGGGCTGGCC	294072	126268	ATGTCATCTTGAATTGTAGT
204899	37095	AAATTTATTATTTTAAAATT	249486	81682	AGGATGGAAGATGGGCTGGC	294073	126269	AATGTCATCTTGAATTGTAG
204900	37096	GAAATTTATTATTTTAAAAT	249487	81683	GAGGATGGAAGATGGGCTGG	294074	126270	AAATGTCATCTTGAATTGTA
204901	37097	GGAAATTTATTATTTTAAAA	249488	81684	AGAGGATGGAAGATGGGCTG	294075	126271	CAAATGTCATCTTGAATTGT
204902	37098	TGGAAATTTATTATTTTAAA	249489	81685	TAGAGGATGGAAGATGGGCT	294076	126272	CCAAATGTCATCTTGAATTG
204903	37099	GTGGAAATTTATTATTTTAA	249490	81686	CTAGAGGATGGAAGATGGGC	294077	126273	CCCAAATGTCATCTTGAATT
204904	37100	AGTGGAAATTTATTATTTTA	249491	81687	ACTAGAGGATGGAAGATGGG	294078	126274	ACCCAAATGTCATCTTGAAT
204905	37101	AAGTGGAAATTTATTATTTT	249492	81688	CACTAGAGGATGGAAGATGG	294079	126275	CACCCAAATGTCATCTTGAA
204906	37102	TAAGTGGAAATTTATTATTT	249493	81689	ACACTAGAGGATGGAAGATG	294080	126276	CCACCCAAATGTCATCTTGA
204907	37103	TTAAGTGGAAATTTATTATT	249494	81690	AACACTAGAGGATGGAAGAT	294081	126277	CCCACCCAAATGTCATCTTG
204908	37104	TTTAAGTGGAAATTTATTAT	249495	81691	GAACACTAGAGGATGGAAGA	294082	126278	CCCCACCCAAATGTCATCTT
204909	37105	TTTTAAGTGGAAATTTATTA	249496	81692	GGAACACTAGAGGATGGAAG	294083	126279	TCCCCACCCAAATGTCATCT
204910	37106	ATTTTAAGTGGAAATTTATT	249497	81693	AGGAACACTAGAGGATGGAA	294084	126280	GTCCCCACCCAAATGTCATC
204911	37107	CATTTTAAGTGGAAATTTAT	249498	81694	AAGGAACACTAGAGGATGGA	294085	126281	TGTCCCCACCCAAATGTCAT
204912	37108	CCATTTTAAGTGGAAATTTA	249499	81695	CAAGGAACACTAGAGGATGG	294086	126282	GTGTCCCCACCCAAATGTCA
204913	37109	ACCATTTTAAGTGGAAATTT	249500	81696	CCAAGGAACACTAGAGGATG	294087	126283	TGTGTCCCCACCCAAATGTC
204914	37110	TACCATTTTAAGTGGAAATT	249501	81697	ACCAAGGAACACTAGAGGAT	294088	126284	CTGTGTCCCCACCCAAATGT
204915	37111	ATACCATTTTAAGTGGAAAT	249502	81698	CACCAAGGAACACTAGAGGA	294089	126285	GCTGTGTCCCCACCCAAATG
204916	37112	AATACCATTTTAAGTGGAAA	249503	81699	CCACCAAGGAACACTAGAGG	294090	126286	GGCTGTGTCCCCACCCAAAT
204917	37113	AAATACCATTTTAAGTGGAA	249504	81700	CCCACCAAGGAACACTAGAG	294091	126287	TGGCTGTGTCCCCACCCAAA
204918	37114	TAAATACCATTTTAAGTGGA	249505	81701	CCCCACCAAGGAACACTAGA	294092	126288	TTGGCTGTGTCCCCACCCAA
204919	37115	TTAAATACCATTTTAAGTGG	249506	81702	GCCCCACCAAGGAACACTAG	294093	126289	TTTGGCTGTGTCCCCACCCA
204920	37116	TTTAAATACCATTTTAAGTG	249507	81703	GGCCCCACCAAGGAACACTA	294094	126290	GTTTGGCTGTGTCCCCACCC
204921	37117	GTTTAAATACCATTTTAAGT	249508	81704	GGGCCCCACCAAGGAACACT	294095	126291	GGTTTGGCTGTGTCCCCACC
204922	37118	AGTTTAAATACCATTTTAAG	249509	81705	AGGGCCCCACCAAGGAACAC	294096	126292	TGGTTTGGCTGTGTCCCCAC
204923	37119	GAGTTTAAATACCATTTTAA	249510	81706	CAGGGCCCCACCAAGGAACA	294097	126293	ATGGTTTGGCTGTGTCCCCA
204924	37120	TGAGTTTAAATACCATTTTA	249511	81707	TCAGGGCCCCACCAAGGAAC	294098	126294	TATGGTTTGGCTGTGTCCCC
204925	37121	CTGAGTTTAAATACCATTTT	249512	81708	GTCAGGGCCCCACCAAGGAA	294099	126295	ATATGGTTTGGCTGTGTCCC
204926	37122	GCTGAGTTTAAATACCATTT	249513	81709	GGTCAGGGCCCCACCAAGGA	294100	126296	GATATGGTTTGGCTGTGTCC
204927	37123	TGCTGAGTTTAAATACCATT	249514	81710	TGGTCAGGGCCCCACCAAGG	294101	126297	TGATATGGTTTGGCTGTGTC
204928	37124	TTGCTGAGTTTAAATACCAT	249515	81711	GTGGTCAGGGCCCCACCAAG	294102	126298	CTGATATGGTTTGGCTGTGT
204929	37125	TTTGCTGAGTTTAAATACCA	249516	81712	TGTGGTCAGGGCCCCACCAA	294103	126299	CCTGATATGGTTTGGCTGTG
204930	37126	TTTTGCTGAGTTTAAATACC	249517	81713	CTGTGGTCAGGGCCCCACCA	294104	126300	CCCTGATATGGTTTGGCTGT
204931	37127	ATTTTGCTGAGTTTAAATAC	249518	81714	ACTGTGGTCAGGGCCCCACC	294105	126301	GCCCTGATATGGTTTGGCTG
204932	37128	TATTTTGCTGAGTTTAAATA	249519	81715	GACTGTGGTCAGGGCCCCAC	294106	126302	CGCCCTGATATGGTTTGGCT
204933	37129	ATATTTTGCTGAGTTTAAAT	249520	81716	GGACTGTGGTCAGGGCCCCA	294107	126303	ACGCCCTGATATGGTTTGGC
204934	37130	TATATTTTGCTGAGTTTAAA	249521	81717	TGGACTGTGGTCAGGGCCCC	294108	126304	GACGCCCTGATATGGTTTGG
204935	37131	ATATATTTTGCTGAGTTTAA	249522	81718	GTGGACTGTGGTCAGGGCCC	294109	126305	GGACGCCCTGATATGGTTTG
204936	37132	GATATATTTTGCTGAGTTTA	249523	81719	GGTGGACTGTGGTCAGGGCC	294110	126306	GGGACGCCCTGATATGGTTT
204937	37133	TGATATATTTTGCTGAGTTT	249524	81720	TGGTGGACTGTGGTCAGGGC	294111	126307	TGGGACGCCCTGATATGGTT
204938	37134	ATGATATATTTTGCTGAGTT	249525	81721	CTGGTGGACTGTGGTCAGGG	294112	126308	CTGGGACGCCCTGATATGGT
204939	37135	GATGATATATTTTGCTGAGT	249526	81722	CCTGGTGGACTGTGGTCAGG	294113	126309	TCTGGGACGCCCTGATATGG
204940	37136	AGATGATATATTTTGCTGAG	249527	81723	ACCTGGTGGACTGTGGTCAG	294114	126310	TTCTGGGACGCCCTGATATG
204941	37137	TAGATGATATATTTTGCTGA	249528	81724	GACCTGGTGGACTGTGGTCA	294115	126311	TTTCTGGGACGCCCTGATAT
204942	37138	ATAGATGATATATTTTGCTG	249529	81725	GGACCTGGTGGACTGTGGTC	294116	126312	CTTTCTGGGACGCCCTGATA
204943	37139	CATAGATGATATATTTTGCT	249530	81726	GGGACCTGGTGGACTGTGGT	294117	126313	CCTTTCTGGGACGCCCTGAT
204944	37140	TCATAGATGATATATTTTGC	249531	81727	AGGGACCTGGTGGACTGTGG	294118	126314	CCCTTTCTGGGACGCCCTGA
204945	37141	CTCATAGATGATATATTTTG	249532	81728	TAGGGACCTGGTGGACTGTG	294119	126315	ACCCTTTCTGGGACGCCCTG
204946	37142	ACTCATAGATGATATATTTT	249533	81729	TTAGGGACCTGGTGGACTGT	294120	126316	TACCCTTTCTGGGACGCCCT
204947	37143	TACTCATAGATGATATATTT	249534	81730	GTTAGGGACCTGGTGGACTG	294121	126317	ATACCCTTTCTGGGACGCCC
204948	37144	TTACTCATAGATGATATATT	249535	81731	GGTTAGGGACCTGGTGGACT	294122	126318	TATACCCTTTCTGGGACGCC
204949	37145	TTTACTCATAGATGATATAT	249536	81732	TGGTTAGGGACCTGGTGGAC	294123	126319	CTATACCCTTTCTGGGACGC
204950	37146	TTTTACTCATAGATGATATA	249537	81733	CTGGTTAGGGACCTGGTGGA	294124	126320	CCTATACCCTTTCTGGGACG
204951	37147	ATTTTACTCATAGATGATAT	249538	81734	TCTGGTTAGGGACCTGGTGG	294125	126321	CCCTATACCCTTTCTGGGAC
204952	37148	AATTTTACTCATAGATGATA	249539	81735	CTCTGGTTAGGGACCTGGTG	294126	126322	ACCCTATACCCTTTCTGGGA
204953	37149	AAATTTTACTCATAGATGAT	249540	81736	CCTCTGGTTAGGGACCTGGT	294127	126323	GACCCTATACCCTTTCTGGG
204954	37150	CAAATTTTACTCATAGATGA	249541	81737	CCCTCTGGTTAGGGACCTGG	294128	126324	AGACCCTATACCCTTTCTGG

204955	37151	ACAAATTTTACTCATAGATG	249542	81738	CCCCTCTGGTTAGGGACCTG	294129	126325	CAGACCCTATACCCTTTCTG
204956	37152	TACAAATTTTACTCATAGAT	249543	81739	TCCCCTCTGGTTAGGGACCT	294130	126326	TCAGACCCTATACCCTTTCT
204957	37153	ATACAAATTTTACTCATAGA	249544	81740	GTCCCCTCTGGTTAGGGACC	294131	126327	CTCAGACCCTATACCCTTTC
204958	37154	AATACAAATTTTACTCATAG	249545	81741	TGTCCCCTCTGGTTAGGGAC	294132	126328	TCTCAGACCCTATACCCTTT
204959	37155	AAATACAAATTTTACTCATA	249546	81742	GTGTCCCCTCTGGTTAGGGA	294133	126329	GTCTCAGACCCTATACCCTT
204960	37156	TAAATACAAATTTTACTCAT	249547	81743	TGTGTCCCCTCTGGTTAGGG	294134	126330	GGTCTCAGACCCTATACCCT
204961	37157	GTAAATACAAATTTTACTCA	249548	81744	GTGTGTCCCCTCTGGTTAGG	294135	126331	GGGTCTCAGACCCTATACCC
204962	37158	GGTAAATACAAATTTTACTC	249549	81745	TGTGTGTCCCCTCTGGTTAG	294136	126332	TGGGTCTCAGACCCTATACC
204963	37159	TGGTAAATACAAATTTTACT	249550	81746	GTGTGTGTCCCCTCTGGTTA	294137	126333	TTGGGTCTCAGACCCTATAC
204964	37160	TTGGTAAATACAAATTTTAC	249551	81747	GGTGTGTGTCCCCTCTGGTT	294138	126334	CTTGGGTCTCAGACCCTATA
204965	37161	CTTGGTAAATACAAATTTTA	249552	81748	TGGTGTGTGTCCCCTCTGGT	294139	126335	ACTTGGGTCTCAGACCCTAT
204966	37162	GCTTGGTAAATACAAATTTT	249553	81749	CTGGTGTGTGTCCCCTCTGG	294140	126336	GACTTGGGTCTCAGACCCTA
204967	37163	TGCTTGGTAAATACAAATTT	249554	81750	CCTGGTGTGTGTCCCCTCTG	294141	126337	TGACTTGGGTCTCAGACCCT
204968	37164	TTGCTTGGTAAATACAAATT	249555	81751	ACCTGGTGTGTGTCCCCTCT	294142	126338	CTGACTTGGGTCTCAGACCC
204969	37165	TTTGCTTGGTAAATACAAAT	249556	81752	CACCTGGTGTGTGTCCCCTC	294143	126339	GCTGACTTGGGTCTCAGACC
204970	37166	TTTTGCTTGGTAAATACAAA	249557	81753	ACACCTGGTGTGTGTCCCCT	294144	126340	TGCTGACTTGGGTCTCAGAC
204971	37167	TTTTTGCTTGGTAAATACAA	249558	81754	GACACCTGGTGTGTGTCCCC	294145	126341	ATGCTGACTTGGGTCTCAGA
204972	37168	ATTTTTGCTTGGTAAATACA	249559	81755	GGACACCTGGTGTGTGTCCC	294146	126342	CATGCTGACTTGGGTCTCAG
204973	37169	TATTTTTGCTTGGTAAATAC	249560	81756	AGGACACCTGGTGTGTGTCC	294147	126343	TCATGCTGACTTGGGTCTCA
204974	37170	ATATTTTTGCTTGGTAAATA	249561	81757	GAGGACACCTGGTGTGTGTC	294148	126344	CTCATGCTGACTTGGGTCTC
204975	37171	AATATTTTTGCTTGGTAAAT	249562	81758	TGAGGACACCTGGTGTGTGT	294149	126345	TCTCATGCTGACTTGGGTCT
204976	37172	TAATATTTTTGCTTGGTAAA	249563	81759	TTGAGGACACCTGGTGTGTG	294150	126346	TTCTCATGCTGACTTGGGTC
204977	37173	GTAATATTTTTGCTTGGTAA	249564	81760	ATTGAGGACACCTGGTGTGT	294151	126347	TTTCTCATGCTGACTTGGGT
204978	37174	TGTAATATTTTTGCTTGGTA	249565	81761	CATTGAGGACACCTGGTGTG	294152	126348	CTTTCTCATGCTGACTTGGG
204979	37175	CTGTAATATTTTTGCTTGGT	249566	81762	ACATTGAGGACACCTGGTGT	294153	126349	ACTTTCTCATGCTGACTTGG
204980	37176	ACTGTAATATTTTTGCTTGG	249567	81763	TACATTGAGGACACCTGGTG	294154	126350	TACTTTCTCATGCTGACTTG
204981	37177	AACTGTAATATTTTTGCTTG	249568	81764	ATACATTGAGGACACCTGGT	294155	126351	ATACTTTCTCATGCTGACTT
204982	37178	AAACTGTAATATTTTTGCTT	249569	81765	AATACATTGAGGACACCTGG	294156	126352	CATACTTTCTCATGCTGACT
204983	37179	CAAACTGTAATATTTTTGCT	249570	81766	CAATACATTGAGGACACCTG	294157	126353	GCATACTTTCTCATGCTGAC
204984	37180	ACAAACTGTAATATTTTTGC	249571	81767	GCAATACATTGAGGACACCT	294158	126354	AGCATACTTTCTCATGCTGA
204985	37181	CACAAACTGTAATATTTTTG	249572	81768	GGCAATACATTGAGGACACC	294159	126355	AAGCATACTTTCTCATGCTG
204986	37182	CCACAAACTGTAATATTTTT	249573	81769	AGGCAATACATTGAGGACAC	294160	126356	GAAGCATACTTTCTCATGCT
204987	37183	ACCACAAACTGTAATATTTT	249574	81770	AAGGCAATACATTGAGGACA	294161	126357	AGAAGCATACTTTCTCATGC
204988	37184	AACCACAAACTGTAATATTT	249575	81771	CAAGGCAATACATTGAGGAC	294162	126358	GAGAAGCATACTTTCTCATG
204989	37185	GAACCACAAACTGTAATATT	249576	81772	TCAAGGCAATACATTGAGGA	294163	126359	TGAGAAGCATACTTTCTCAT
204990	37186	TGAACCACAAACTGTAATAT	249577	81773	TTCAAGGCAATACATTGAGG	294164	126360	ATGAGAAGCATACTTTCTCA
204991	37187	GTGAACCACAAACTGTAATA	249578	81774	TTTCAAGGCAATACATTGAG	294165	126361	CATGAGAAGCATACTTTCTC
204992	37188	TGTGAACCACAAACTGTAAT	249579	81775	GTTTCAAGGCAATACATTGA	294166	126362	CCATGAGAAGCATACTTTCT
204993	37189	ATGTGAACCACAAACTGTAA	249580	81776	TGTTTCAAGGCAATACATTG	294167	126363	ACCATGAGAAGCATACTTTC
204994	37190	CATGTGAACCACAAACTGTA	249581	81777	CTGTTTCAAGGCAATACATT	294168	126364	CACCATGAGAAGCATACTTT
204995	37191	GCATGTGAACCACAAACTGT	249582	81778	ACTGTTTCAAGGCAATACAT	294169	126365	CCACCATGAGAAGCATACTT
204996	37192	AGCATGTGAACCACAAACTG	249583	81779	AACTGTTTCAAGGCAATACA	294170	126366	GCCACCATGAGAAGCATACT
204997	37193	CAGCATGTGAACCACAAACT	249584	81780	CAACTGTTTCAAGGCAATAC	294171	126367	GGCCACCATGAGAAGCATAC
204998	37194	ACAGCATGTGAACCACAAAC	249585	81781	ACAACTGTTTCAAGGCAATA	294172	126368	GGGCCACCATGAGAAGCATA
204999	37195	GACAGCATGTGAACCACAAA	249586	81782	CACAACTGTTTCAAGGCAAT	294173	126369	TGGGCCACCATGAGAAGCAT
205000	37196	AGACAGCATGTGAACCACAA	249587	81783	GCACAACTGTTTCAAGGCAA	294174	126370	CTGGGCCACCATGAGAAGCA
205001	37197	GAGACAGCATGTGAACCACA	249588	81784	AGCACAACTGTTTCAAGGCA	294175	126371	ACTGGGCCACCATGAGAAGC
205002	37198	TGAGACAGCATGTGAACCAC	249589	81785	CAGCACAACTGTTTCAAGGC	294176	126372	AACTGGGCCACCATGAGAAG
205003	37199	GTGAGACAGCATGTGAACCA	249590	81786	CCAGCACAACTGTTTCAAGG	294177	126373	CAACTGGGCCACCATGAGAA
205004	37200	AGTGAGACAGCATGTGAACC	249591	81787	CCCAGCACAACTGTTTCAAG	294178	126374	CCAACTGGGCCACCATGAGA
205005	37201	CAGTGAGACAGCATGTGAAC	249592	81788	TCCCAGCACAACTGTTTCAA	294179	126375	CCCAACTGGGCCACCATGAG
205006	37202	ACAGTGAGACAGCATGTGAA	249593	81789	GTCCCAGCACAACTGTTTCA	294180	126376	ACCCAACTGGGCCACCATGA
205007	37203	AACAGTGAGACAGCATGTGA	249594	81790	AGTCCCAGCACAACTGTTTC	294181	126377	CACCCAACTGGGCCACCATG
205008	37204	AAACAGTGAGACAGCATGTG	249595	81791	CAGTCCCAGCACAACTGTTT	294182	126378	CCACCCAACTGGGCCACCAT
205009	37205	AAAACAGTGAGACAGCATGT	249596	81792	ACAGTCCCAGCACAACTGTT	294183	126379	TCCACCCAACTGGGCCACCA
205010	37206	TAAAACAGTGAGACAGCATG	249597	81793	CACAGTCCCAGCACAACTGT	294184	126380	TTCCACCCAACTGGGCCACC
205011	37207	TTAAAACAGTGAGACAGCAT	249598	81794	TCACAGTCCCAGCACAACTG	294185	126381	CTTCCACCCAACTGGGCCAC
205012	37208	TTTAAAACAGTGAGACAGCA	249599	81795	ATCACAGTCCCAGCACAACT	294186	126382	ACTTCCACCCAACTGGGCCA
205013	37209	ATTTAAAACAGTGAGACAGC	249600	81796	CATCACAGTCCCAGCACAAC	294187	126383	CACTTCCACCCAACTGGGCC
205014	37210	AATTTAAAACAGTGAGACAG	249601	81797	CCATCACAGTCCCAGCACAA	294188	126384	CCACTTCCACCCAACTGGGC
205015	37211	AAATTTAAAACAGTGAGACA	249602	81798	CCCATCACAGTCCCAGCACA	294189	126385	GCCACTTCCACCCAACTGGG
205016	37212	AAAATTTAAAACAGTGAGAC	249603	81799	CCCCATCACAGTCCCAGCAC	294190	126386	TGCCACTTCCACCCAACTGG
205017	37213	TAAAATTTAAAACAGTGAGA	249604	81800	CCCCCATCACAGTCCCAGCA	294191	126387	CTGCCACTTCCACCCAACTG
205018	37214	TTAAAATTTAAAACAGTGAG	249605	81801	CCCCCCATCACAGTCCCAGC	294192	126388	GCTGCCACTTCCACCCAACT
205019	37215	TTTAAAATTTAAAACAGTGA	249606	81802	ACCCCCCATCACAGTCCCAG	294193	126389	GGCTGCCACTTCCACCCAAC
205020	37216	ATTTAAAATTTAAAACAGTG	249607	81803	CACCCCCCATCACAGTCCCA	294194	126390	CGGCTGCCACTTCCACCCAA
205021	37217	TATTTAAAATTTAAAACAGT	249608	81804	CCACCCCCCATCACAGTCCC	294195	126391	CCGGCTGCCACTTCCACCCA
205022	37218	GTATTTAAAATTTAAAACAG	249609	81805	GCCACCCCCCATCACAGTCC	294196	126392	CCCGGCTGCCACTTCCACCC
205023	37219	TGTATTTAAAATTTAAAACA	249610	81806	GGCCACCCCCCATCACAGTC	294197	126393	GCCCGGCTGCCACTTCCACC
205024	37220	TTGTATTTAAAATTTAAAAC	249611	81807	TGGCCACCCCCCATCACAGT	294198	126394	GGCCCGGCTGCCACTTCCAC
205025	37221	TTTGTATTTAAAATTTAAAA	249612	81808	ATGGCCACCCCCCATCACAG	294199	126395	CGGCCCGGCTGCCACTTCCA
205026	37222	TTTTGTATTTAAAATTTAAA	249613	81809	CATGGCCACCCCCCATCACA	294200	126396	ACGGCCCGGCTGCCACTTCC

205027	37223	TTTTTGTATTTAAAATTTAA	249614	81810	ACATGGCCACCCCCCATCAC	294201	126397	GACGGCCCGGCTGCCACTTC
205028	37224	GTTTTTGTATTTAAAATTTA	249615	81811	TACATGGCCACCCCCCATCA	294202	126398	AGACGGCCCGGCTGCCACTT
205029	37225	AGTTTTTGTATTTAAAATTT	249616	81812	CTACATGGCCACCCCCCATC	294203	126399	AAGACGGCCCGGCTGCCACT
205030	37226	GAGTTTTTGTATTTAAAATT	249617	81813	GCTACATGGCCACCCCCCAT	294204	126400	AAAGACGGCCCGGCTGCCAC
205031	37227	GGAGTTTTTGTATTTAAAAT	249618	81814	GGCTACATGGCCACCCCCCA	294205	126401	GAAAGACGGCCCGGCTGCCA
205032	37228	TGGAGTTTTTGTATTTAAAA	249619	81815	TGGCTACATGGCCACCCCCC	294206	126402	GGAAAGACGGCCCGGCTGCC
205033	37229	TTGGAGTTTTTGTATTTAAA	249620	81816	GTGGCTACATGGCCACCCCC	294207	126403	TGGAAAGACGGCCCGGCTGC
205034	37230	CTTGGAGTTTTTGTATTTAA	249621	81817	GGTGGCTACATGGCCACCCC	294208	126404	GTGGAAAGACGGCCCGGCTG
205035	37231	ACTTGGAGTTTTTGTATTTA	249622	81818	GGGTGGCTACATGGCCACCC	294209	126405	GGTGGAAAGACGGCCCGGCT
205036	37232	TACTTGGAGTTTTTGTATTT	249623	81819	GGGGTGGCTACATGGCCACC	294210	126406	TGGTGGAAAGACGGCCCGGC
205037	37233	CTACTTGGAGTTTTTGTATT	249624	81820	GGGGGTGGCTACATGGCCAC	294211	126407	CTGGTGGAAAGACGGCCCGG
205038	37234	CCTACTTGGAGTTTTTGTAT	249625	81821	TGGGGGTGGCTACATGGCCA	294212	126408	CCTGGTGGAAAGACGGCCCG
205039	37235	GCCTACTTGGAGTTTTTGTA	249626	81822	GTGGGGGTGGCTACATGGCC	294213	126409	GCCTGGTGGAAAGACGGCCC
205040	37236	AGCCTACTTGGAGTTTTTGT	249627	81823	GGTGGGGGTGGCTACATGGC	294214	126410	GGCCTGGTGGAAAGACGGCC
205041	37237	CAGCCTACTTGGAGTTTTTG	249628	81824	TGGTGGGGGTGGCTACATGG	294215	126411	TGGCCTGGTGGAAAGACGGC
205042	37238	CCAGCCTACTTGGAGTTTTT	249629	81825	GTGGTGGGGGTGGCTACATG	294216	126412	GTGGCCTGGTGGAAAGACGG
205043	37239	CCCAGCCTACTTGGAGTTTT	249630	81826	GGTGGTGGGGGTGGCTACAT	294217	126413	AGTGGCCTGGTGGAAAGACG
205044	37240	ACCCAGCCTACTTGGAGTTT	249631	81827	GGGTGGTGGGGGTGGCTACA	294218	126414	GAGTGGCCTGGTGGAAAGAC
205045	37241	CACCCAGCCTACTTGGAGTT	249632	81828	GGGGTGGTGGGGGTGGCTAC	294219	126415	TGAGTGGCCTGGTGGAAAGA
205046	37242	ACACCCAGCCTACTTGGAGT	249633	81829	GGGGGTGGTGGGGGTGGCTA	294220	126416	TTGAGTGGCCTGGTGGAAAG
205047	37243	CACACCCAGCCTACTTGGAG	249634	81830	TGGGGGTGGTGGGGGTGGCT	294221	126417	CTTGAGTGGCCTGGTGGAAA
205048	37244	CCACACCCAGCCTACTTGGA	249635	81831	TTGGGGGTGGTGGGGGTGGC	294222	126418	ACTTGAGTGGCCTGGTGGAA
205049	37245	ACCACACCCAGCCTACTTGG	249636	81832	CTTGGGGGTGGTGGGGGTGG	294223	126419	TACTTGAGTGGCCTGGTGGA
205050	37246	CACCACACCCAGCCTACTTG	249637	81833	GCTTGGGGGTGGTGGGGGTG	294224	126420	CTACTTGAGTGGCCTGGTGG
205051	37247	CCACCACACCCAGCCTACTT	249638	81834	GGCTTGGGGGTGGTGGGGGT	294225	126421	GCTACTTGAGTGGCCTGGTG
205052	37248	GCCACCACACCCAGCCTACT	249639	81835	TGGCTTGGGGGTGGTGGGGG	294226	126422	TGCTACTTGAGTGGCCTGGT
205053	37249	AGCCACCACACCCAGCCTAC	249640	81836	GTGGCTTGGGGGTGGTGGGG	294227	126423	CTGCTACTTGAGTGGCCTGG
205054	37250	GAGCCACCACACCCAGCCTA	249641	81837	AGTGGCTTGGGGGTGGTGGG	294228	126424	GCTGCTACTTGAGTGGCCTG
205055	37251	TGAGCCACCACACCCAGCCT	249642	81838	GAGTGGCTTGGGGGTGGTGG	294229	126425	AGCTGCTACTTGAGTGGCCT
205056	37252	GTGAGCCACCACACCCAGCC	249643	81839	AGAGTGGCTTGGGGGTGGTG	294230	126426	CAGCTGCTACTTGAGTGGCC
205057	37253	TGTGAGCCACCACACCCAGC	249644	81840	GAGAGTGGCTTGGGGGTGGT	294231	126427	TCAGCTGCTACTTGAGTGGC
205058	37254	GTGTGAGCCACCACACCCAG	249645	81841	AGAGAGTGGCTTGGGGGTGG	294232	126428	CTCAGCTGCTACTTGAGTGG
205059	37255	GGTGTGAGCCACCACACCCA	249646	81842	GAGAGAGTGGCTTGGGGGTG	294233	126429	TCTCAGCTGCTACTTGAGTG
205060	37256	AGGTGTGAGCCACCACACCC	249647	81843	GGAGAGAGTGGCTTGGGGGT	294234	126430	CTCTCAGCTGCTACTTGAGT
205061	37257	CAGGTGTGAGCCACCACACC	249648	81844	TGGAGAGAGTGGCTTGGGGG	294235	126431	TCTCTCAGCTGCTACTTGAG
205062	37258	ACAGGTGTGAGCCACCACAC	249649	81845	TTGGAGAGAGTGGCTTGGGG	294236	126432	GTCTCTCAGCTGCTACTTGA
205063	37259	TACAGGTGTGAGCCACCACA	249650	81846	CTTGGAGAGAGTGGCTTGGG	294237	126433	GGTCTCTCAGCTGCTACTTG
205064	37260	TTACAGGTGTGAGCCACCAC	249651	81847	CCTTGGAGAGAGTGGCTTGG	294238	126434	GGGTCTCTCAGCTGCTACTT
205065	37261	ATTACAGGTGTGAGCCACCA	249652	81848	TCCTTGGAGAGAGTGGCTTG	294239	126435	GGGGTCTCTCAGCTGCTACT
205066	37262	GATTACAGGTGTGAGCCACC	249653	81849	TTCCTTGGAGAGAGTGGCTT	294240	126436	AGGGGTCTCTCAGCTGCTAC
205067	37263	GGATTACAGGTGTGAGCCAC	249654	81850	TTTCCTTGGAGAGAGTGGCT	294241	126437	CAGGGGTCTCTCAGCTGCTA
205068	37264	GGGATTACAGGTGTGAGCCA	249655	81851	ATTTCCTTGGAGAGAGTGGC	294242	126438	GCAGGGGTCTCTCAGCTGCT
205069	37265	TGGGATTACAGGTGTGAGCC	249656	81852	GATTTCCTTGGAGAGAGTGG	294243	126439	GGCAGGGGTCTCTCAGCTGC
205070	37266	CTGGGATTACAGGTGTGAGC	249657	81853	GGATTTCCTTGGAGAGAGTG	294244	126440	GGGCAGGGGTCTCTCAGCTG
205071	37267	ACTGGGATTACAGGTGTGAG	249658	81854	AGGATTTCCTTGGAGAGAGT	294245	126441	AGGGCAGGGGTCTCTCAGCT
205072	37268	TACTGGGATTACAGGTGTGA	249659	81855	GAGGATTTCCTTGGAGAGAG	294246	126442	CAGGGCAGGGGTCTCTCAGC
205073	37269	GTACTGGGATTACAGGTGTG	249660	81856	GGAGGATTTCCTTGGAGAGA	294247	126443	CCAGGGCAGGGGTCTCTCAG
205074	37270	AGTACTGGGATTACAGGTGT	249661	81857	AGGAGGATTTCCTTGGAGAG	294248	126444	GCCAGGGCAGGGGTCTCTCA
205075	37271	AAGTACTGGGATTACAGGTG	249662	81858	TAGGAGGATTTCCTTGGAGA	294249	126445	GGCCAGGGCAGGGGTCTCTC
205076	37272	AAAGTACTGGGATTACAGGT	249663	81859	TTAGGAGGATTTCCTTGGAG	294250	126446	TGGCCAGGGCAGGGGTCTCT
205077	37273	CAAAGTACTGGGATTACAGG	249664	81860	TTTAGGAGGATTTCCTTGGA	294251	126447	CTGGCCAGGGCAGGGGTCTC
205078	37274	CCAAAGTACTGGGATTACAG	249665	81861	CTTTAGGAGGATTTCCTTGG	294252	126448	ACTGGCCAGGGCAGGGGTCT
205079	37275	CCCAAAGTACTGGGATTACA	249666	81862	TCTTTAGGAGGATTTCCTTG	294253	126449	GACTGGCCAGGGCAGGGGTC
205080	37276	TCCCAAAGTACTGGGATTAC	249667	81863	ATCTTTAGGAGGATTTCCTT	294254	126450	GGACTGGCCAGGGCAGGGGT
205081	37277	CTCCCAAAGTACTGGGATTA	249668	81864	GATCTTTAGGAGGATTTCCT	294255	126451	GGGACTGGCCAGGGCAGGGG
205082	37278	CCTCCCAAAGTACTGGGATT	249669	81865	GGATCTTTAGGAGGATTTCC	294256	126452	GGGGACTGGCCAGGGCAGGG
205083	37279	GCCTCCCAAAGTACTGGGAT	249670	81866	GGGATCTTTAGGAGGATTTC	294257	126453	CGGGGACTGGCCAGGGCAGG
205084	37280	AGCCTCCCAAAGTACTGGGA	249671	81867	AGGGATCTTTAGGAGGATTT	294258	126454	GCGGGGACTGGCCAGGGCAG
205085	37281	CAGCCTCCCAAAGTACTGGG	249672	81868	AAGGGATCTTTAGGAGGATT	294259	126455	GGCGGGGACTGGCCAGGGCA
205086	37282	TCAGCCTCCCAAAGTACTGG	249673	81869	AAAGGGATCTTTAGGAGGAT	294260	126456	GGGCGGGGACTGGCCAGGGC
205087	37283	CTCAGCCTCCCAAAGTACTG	249674	81870	TAAAGGGATCTTTAGGAGGA	294261	126457	AGGGCGGGGACTGGCCAGGG
205088	37284	CCTCAGCCTCCCAAAGTACT	249675	81871	GTAAAGGGATCTTTAGGAGG	294262	126458	GAGGGCGGGGACTGGCCAGG
205089	37285	GCCTCAGCCTCCCAAAGTAC	249676	81872	TGTAAAGGGATCTTTAGGAG	294263	126459	GGAGGGCGGGGACTGGCCAG
205090	37286	TGCCTCAGCCTCCCAAAGTA	249677	81873	ATGTAAAGGGATCTTTAGGA	294264	126460	GGGAGGGCGGGGACTGGCCA
205091	37287	CTGCCTCAGCCTCCCAAAGT	249678	81874	GATGTAAAGGGATCTTTAGG	294265	126461	GGGGAGGGCGGGGACTGGCC
205092	37288	CCTGCCTCAGCCTCCCAAAG	249679	81875	GGATGTAAAGGGATCTTTAG	294266	126462	AGGGGAGGGCGGGGACTGGC
205093	37289	GCCTGCCTCAGCCTCCCAAA	249680	81876	AGGATGTAAAGGGATCTTTA	294267	126463	GAGGGGAGGGCGGGGACTGG
205094	37290	TGCCTGCCTCAGCCTCCCAA	249681	81877	GAGGATGTAAAGGGATCTTT	294268	126464	AGAGGGGAGGGCGGGGACTG
205095	37291	ATGCCTGCCTCAGCCTCCCA	249682	81878	GGAGGATGTAAAGGGATCTT	294269	126465	AAGAGGGGAGGGCGGGGACT
205096	37292	TATGCCTGCCTCAGCCTCCC	249683	81879	TGGAGGATGTAAAGGGATCT	294270	126466	CAAGAGGGGAGGGCGGGGAC
205097	37293	ATATGCCTGCCTCAGCCTCC	249684	81880	ATGGAGGATGTAAAGGGATC	294271	126467	GCAAGAGGGGAGGGCGGGGA
205098	37294	GATATGCCTGCCTCAGCCTC	249685	81881	CATGGAGGATGTAAAGGGAT	294272	126468	GGCAAGAGGGGAGGGCGGGG

205099	37295	CGATATGCCTGCCTCAGCCT	249686	81882	ACATGGAGGATGTAAAGGGA	294273	126469	TGGCAAGAGGGGAGGGCGGG
205100	37296	GCGATATGCCTGCCTCAGCC	249687	81883	CACATGGAGGATGTAAAGGG	294274	126470	GTGGCAAGAGGGGAGGGCGG
205101	37297	AGCGATATGCCTGCCTCAGC	249688	81884	CCACATGGAGGATGTAAAGG	294275	126471	AGTGGCAAGAGGGGAGGGCG
205102	37298	AAGCGATATGCCTGCCTCAG	249689	81885	ACCACATGGAGGATGTAAAG	294276	126472	CAGTGGCAAGAGGGGAGGGC
205103	37299	CAAGCGATATGCCTGCCTCA	249690	81886	CACCACATGGAGGATGTAAA	294277	126473	GCAGTGGCAAGAGGGGAGGG
205104	37300	TCAAGCGATATGCCTGCCTC	249691	81887	CCACCACATGGAGGATGTAA	294278	126474	GGCAGTGGCAAGAGGGGAGG
205105	37301	CTCAAGCGATATGCCTGCCT	249692	81888	CCCACCACATGGAGGATGTA	294279	126475	AGGCAGTGGCAAGAGGGGAG
205106	37302	ACTCAAGCGATATGCCTGCC	249693	81889	CCCCACCACATGGAGGATGT	294280	126476	GAGGCAGTGGCAAGAGGGGA
205107	37303	AACTCAAGCGATATGCCTGC	249694	81890	TCCCCACCACATGGAGGATG	294281	126477	AGAGGCAGTGGCAAGAGGGG
205108	37304	GAACTCAAGCGATATGCCTG	249695	81891	CTCCCCACCACATGGAGGAT	294282	126478	CAGAGGCAGTGGCAAGAGGG
205109	37305	TGAACTCAAGCGATATGCCT	249696	81892	CCTCCCCACCACATGGAGGA	294283	126479	CCAGAGGCAGTGGCAAGAGG
205110	37306	CTGAACTCAAGCGATATGCC	249697	81893	ACCTCCCCACCACATGGAGG	294284	126480	ACCAGAGGCAGTGGCAAGAG
205111	37307	CCTGAACTCAAGCGATATGC	249698	81894	AACCTCCCCACCACATGGAG	294285	126481	AACCAGAGGCAGTGGCAAGA
205112	37308	TCCTGAACTCAAGCGATATG	249699	81895	GAACCTCCCCACCACATGGA	294286	126482	GAACCAGAGGCAGTGGCAAG
205113	37309	CTCCTGAACTCAAGCGATAT	249700	81896	AGAACCTCCCCACCACATGG	294287	126483	AGAACCAGAGGCAGTGGCAA
205114	37310	ACTCCTGAACTCAAGCGATA	249701	81897	TAGAACCTCCCCACCACATG	294288	126484	CAGAACCAGAGGCAGTGGCA
205115	37311	AACTCCTGAACTCAAGCGAT	249702	81898	CTAGAACCTCCCCACCACAT	294289	126485	TCAGAACCAGAGGCAGTGGC
205116	37312	GAACTCCTGAACTCAAGCGA	249703	81899	TCTAGAACCTCCCCACCACA	294290	126486	TTCAGAACCAGAGGCAGTGG
205117	37313	TGAACTCCTGAACTCAAGCG	249704	81900	CTCTAGAACCTCCCCACCAC	294291	126487	GTTCAGAACCAGAGGCAGTG
205118	37314	TTGAACTCCTGAACTCAAGC	249705	81901	ACTCTAGAACCTCCCCACCA	294292	126488	TGTTCAGAACCAGAGGCAGT
205119	37315	CTTGAACTCCTGAACTCAAG	249706	81902	AACTCTAGAACCTCCCCACC	294293	126489	CTGTTCAGAACCAGAGGCAG
205120	37316	TCTTGAACTCCTGAACTCAA	249707	81903	CAACTCTAGAACCTCCCCAC	294294	126490	TCTGTTCAGAACCAGAGGCA
205121	37317	ATCTTGAACTCCTGAACTCA	249708	81904	CCAACTCTAGAACCTCCCCA	294295	126491	ATCTGTTCAGAACCAGAGGC
205122	37318	AATCTTGAACTCCTGAACTC	249709	81905	CCCAACTCTAGAACCTCCCC	294296	126492	CATCTGTTCAGAACCAGAGG
205123	37319	AAATCTTGAACTCCTGAACT	249710	81906	ACCCAACTCTAGAACCTCCC	294297	126493	CCATCTGTTCAGAACCAGAG
205124	37320	CAAATCTTGAACTCCTGAAC	249711	81907	CACCCAACTCTAGAACCTCC	294298	126494	CCCATCTGTTCAGAACCAGA
205125	37321	GCAAATCTTGAACTCCTGAA	249712	81908	GCACCCAACTCTAGAACCTC	294299	126495	GCCCATCTGTTCAGAACCAG
205126	37322	GGCAAATCTTGAACTCCTGA	249713	81909	TGCACCCAACTCTAGAACCT	294300	126496	TGCCCATCTGTTCAGAACCA
205127	37323	AGGCAAATCTTGAACTCCTG	249714	81910	ATGCACCCAACTCTAGAACC	294301	126497	GTGCCCATCTGTTCAGAACC
205128	37324	CAGGCAAATCTTGAACTCCT	249715	81911	CATGCACCCAACTCTAGAAC	294302	126498	GGTGCCCATCTGTTCAGAAC
205129	37325	CCAGGCAAATCTTGAACTCC	249716	81912	ACATGCACCCAACTCTAGAA	294303	126499	GGGTGCCCATCTGTTCAGAA
205130	37326	CCCAGGCAAATCTTGAACTC	249717	81913	CACATGCACCCAACTCTAGA	294304	126500	AGGGTGCCCATCTGTTCAGA
205131	37327	GCCCAGGCAAATCTTGAACT	249718	81914	ACACATGCACCCAACTCTAG	294305	126501	GAGGGTGCCCATCTGTTCAG
205132	37328	TGCCCAGGCAAATCTTGAAC	249719	81915	GACACATGCACCCAACTCTA	294306	126502	TGAGGGTGCCCATCTGTTCA
205133	37329	TTGCCCAGGCAAATCTTGAA	249720	81916	AGACACATGCACCCAACTCT	294307	126503	ATGAGGGTGCCCATCTGTTC
205134	37330	GTTGCCCAGGCAAATCTTGA	249721	81917	AAGACACATGCACCCAACTC	294308	126504	GATGAGGGTGCCCATCTGTT
205135	37331	TGTTGCCCAGGCAAATCTTG	249722	81918	GAAGACACATGCACCCAACT	294309	126505	AGATGAGGGTGCCCATCTGT
205136	37332	ATGTTGCCCAGGCAAATCTT	249723	81919	TGAAGACACATGCACCCAAC	294310	126506	AAGATGAGGGTGCCCATCTG
205137	37333	TATGTTGCCCAGGCAAATCT	249724	81920	CTGAAGACACATGCACCCAA	294311	126507	CAAGATGAGGGTGCCCATCT
205138	37334	CTATGTTGCCCAGGCAAATC	249725	81921	GCTGAAGACACATGCACCCA	294312	126508	ACAAGATGAGGGTGCCCATC
205139	37335	ACTATGTTGCCCAGGCAAAT	249726	81922	AGCTGAAGACACATGCACCC	294313	126509	TACAAGATGAGGGTGCCCAT
205140	37336	CACTATGTTGCCCAGGCAAA	249727	81923	TAGCTGAAGACACATGCACC	294314	126510	ATACAAGATGAGGGTGCCCA
205141	37337	TCACTATGTTGCCCAGGCAA	249728	81924	GTAGCTGAAGACACATGCAC	294315	126511	AATACAAGATGAGGGTGCCC
205142	37338	CTCACTATGTTGCCCAGGCA	249729	81925	AGTAGCTGAAGACACATGCA	294316	126512	AAATACAAGATGAGGGTGCC
205143	37339	TCTCACTATGTTGCCCAGGC	249730	81926	CAGTAGCTGAAGACACATGC	294317	126513	CAAATACAAGATGAGGGTGC
205144	37340	ATCTCACTATGTTGCCCAGG	249731	81927	TCAGTAGCTGAAGACACATG	294318	126514	ACAAATACAAGATGAGGGTG
205145	37341	GATCTCACTATGTTGCCCAG	249732	81928	GTCAGTAGCTGAAGACACAT	294319	126515	CACAAATACAAGATGAGGGT
205146	37342	GGATCTCACTATGTTGCCCA	249733	81929	TGTCAGTAGCTGAAGACACA	294320	126516	TCACAAATACAAGATGAGGG
205147	37343	AGGATCTCACTATGTTGCCC	249734	81930	TTGTCAGTAGCTGAAGACAC	294321	126517	ATCACAAATACAAGATGAGG
205148	37344	CAGGATCTCACTATGTTGCC	249735	81931	ATTGTCAGTAGCTGAAGACA	294322	126518	AATCACAAATACAAGATGAG
205149	37345	ACAGGATCTCACTATGTTGC	249736	81932	CATTGTCAGTAGCTGAAGAC	294323	126519	TAATCACAAATACAAGATGA
205150	37346	GACAGGATCTCACTATGTTG	249737	81933	GCATTGTCAGTAGCTGAAGA	294324	126520	TTAATCACAAATACAAGATG
205151	37347	AGACAGGATCTCACTATGTT	249738	81934	TGCATTGTCAGTAGCTGAAG	294325	126521	ATTAATCACAAATACAAGAT
205152	37348	GAGACAGGATCTCACTATGT	249739	81935	CTGCATTGTCAGTAGCTGAA	294326	126522	CATTAATCACAAATACAAGA
205153	37349	AGAGACAGGATCTCACTATG	249740	81936	TCTGCATTGTCAGTAGCTGA	294327	126523	ACATTAATCACAAATACAAG
205154	37350	TAGAGACAGGATCTCACTAT	249741	81937	GTCTGCATTGTCAGTAGCTG	294328	126524	GACATTAATCACAAATACAA
205155	37351	GTAGAGACAGGATCTCACTA	249742	81938	GGTCTGCATTGTCAGTAGCT	294329	126525	AGACATTAATCACAAATACA
205156	37352	AGTAGAGACAGGATCTCACT	249743	81939	AGGTCTGCATTGTCAGTAGC	294330	126526	TAGACATTAATCACAAATAC
205157	37353	CAGTAGAGACAGGATCTCAC	249744	81940	AAGGTCTGCATTGTCAGTAG	294331	126527	TTAGACATTAATCACAAATA
205158	37354	TCAGTAGAGACAGGATCTCA	249745	81941	TAAGGTCTGCATTGTCAGTA	294332	126528	GTTAGACATTAATCACAAAT
205159	37355	TTCAGTAGAGACAGGATCTC	249746	81942	CTAAGGTCTGCATTGTCAGT	294333	126529	TGTTAGACATTAATCACAAA
205160	37356	TTTCAGTAGAGACAGGATCT	249747	81943	ACTAAGGTCTGCATTGTCAG	294334	126530	TTGTTAGACATTAATCACAA
205161	37357	TTTTCAGTAGAGACAGGATC	249748	81944	AACTAAGGTCTGCATTGTCA	294335	126531	ATTGTTAGACATTAATCACA
205162	37358	GTTTTCAGTAGAGACAGGAT	249749	81945	CAACTAAGGTCTGCATTGTC	294336	126532	CATTGTTAGACATTAATCAC
205163	37359	TGTTTTCAGTAGAGACAGGA	249750	81946	CCAACTAAGGTCTGCATTGT	294337	126533	ACATTGTTAGACATTAATCA
205164	37360	TTGTTTTCAGTAGAGACAGG	249751	81947	GCCAACTAAGGTCTGCATTG	294338	126534	TACATTGTTAGACATTAATC
205165	37361	ATTGTTTTCAGTAGAGACAG	249752	81948	TGCCAACTAAGGTCTGCATT	294339	126535	CTACATTGTTAGACATTAAT
205166	37362	AATTGTTTTCAGTAGAGACA	249753	81949	GTGCCAACTAAGGTCTGCAT	294340	126536	ACTACATTGTTAGACATTAA
205167	37363	TAATTGTTTTCAGTAGAGAC	249754	81950	GGTGCCAACTAAGGTCTGCA	294341	126537	AACTACATTGTTAGACATTA
205168	37364	CTAATTGTTTTCAGTAGAGA	249755	81951	AGGTGCCAACTAAGGTCTGC	294342	126538	AAACTACATTGTTAGACATT
205169	37365	GCTAATTGTTTTCAGTAGAG	249756	81952	GAGGTGCCAACTAAGGTCTG	294343	126539	AAAACTACATTGTTAGACAT
205170	37366	AGCTAATTGTTTTCAGTAGA	249757	81953	CGAGGTGCCAACTAAGGTCT	294344	126540	CAAAACTACATTGTTAGACA

205171	37367	CAGCTAATTGTTTTCAGTAG	249758	81954	GCGAGGTGCCAACTAAGGTC	294345	126541	ACAAAACTACATTGTTAGAC
205172	37368	CCAGCTAATTGTTTTCAGTA	249759	81955	AGCGAGGTGCCAACTAAGGT	294346	126542	CACAAAACTACATTGTTAGA
205173	37369	CCCAGCTAATTGTTTTCAGT	249760	81956	GAGCGAGGTGCCAACTAAGG	294347	126543	TCACAAAACTACATTGTTAG
205174	37370	ACCCAGCTAATTGTTTTCAG	249761	81957	AGAGCGAGGTGCCAACTAAG	294348	126544	CTCACAAAACTACATTGTTA
205175	37371	CACCCAGCTAATTGTTTTCA	249762	81958	CAGAGCGAGGTGCCAACTAA	294349	126545	TCTCACAAAACTACATTGTT
205176	37372	ACACCCAGCTAATTGTTTTC	249763	81959	CCAGAGCGAGGTGCCAACTA	294350	126546	TTCTCACAAAACTACATTGT
205177	37373	CACACCCAGCTAATTGTTTT	249764	81960	GCCAGAGCGAGGTGCCAACT	294351	126547	CTTCTCACAAAACTACATTG
205178	37374	CCACACCCAGCTAATTGTTT	249765	81961	GGCCAGAGCGAGGTGCCAAC	294352	126548	CCTTCTCACAAAACTACATT
205179	37375	ACCACACCCAGCTAATTGTT	249766	81962	AGGCCAGAGCGAGGTGCCAA	294353	126549	CCCTTCTCACAAAACTACAT
205180	37376	CACCACACCCAGCTAATTGT	249767	81963	TAGGCCAGAGCGAGGTGCCA	294354	126550	ACCCTTCTCACAAAACTACA
205181	37377	CCACCACACCCAGCTAATTG	249768	81964	ATAGGCCAGAGCGAGGTGCC	294355	126551	AACCCTTCTCACAAAACTAC
205182	37378	GCCACCACACCCAGCTAATT	249769	81965	GATAGGCCAGAGCGAGGTGC	294356	126552	AAACCCTTCTCACAAAACTA
205183	37379	TGCCACCACACCCAGCTAAT	249770	81966	GGATAGGCCAGAGCGAGGTG	294357	126553	CAAACCCTTCTCACAAAACT
205184	37380	GTGCCACCACACCCAGCTAA	249771	81967	AGGATAGGCCAGAGCGAGGT	294358	126554	GCAAACCCTTCTCACAAAAC
205185	37381	TGTGCCACCACACCCAGCTA	249772	81968	CAGGATAGGCCAGAGCGAGG	294359	126555	AGCAAACCCTTCTCACAAAA
205186	37382	ATGTGCCACCACACCCAGCT	249773	81969	ACAGGATAGGCCAGAGCGAG	294360	126556	CAGCAAACCCTTCTCACAAA
205187	37383	CATGTGCCACCACACCCAGC	249774	81970	AACAGGATAGGCCAGAGCGA	294361	126557	TCAGCAAACCCTTCTCACAA
205188	37384	GCATGTGCCACCACACCCAG	249775	81971	AAACAGGATAGGCCAGAGCG	294362	126558	ATCAGCAAACCCTTCTCACA
205189	37385	GGCATGTGCCACCACACCCA	249776	81972	CAAACAGGATAGGCCAGAGC	294363	126559	TATCAGCAAACCCTTCTCAC
205190	37386	AGGCATGTGCCACCACACCC	249777	81973	GCAAACAGGATAGGCCAGAG	294364	126560	GTATCAGCAAACCCTTCTCA
205191	37387	CAGGCATGTGCCACCACACC	249778	81974	AGCAAACAGGATAGGCCAGA	294365	126561	TGTATCAGCAAACCCTTCTC
205192	37388	GCAGGCATGTGCCACCACAC	249779	81975	CAGCAAACAGGATAGGCCAG	294366	126562	CTGTATCAGCAAACCCTTCT
205193	37389	CGCAGGCATGTGCCACCACA	249780	81976	ACAGCAAACAGGATAGGCCA	294367	126563	GCTGTATCAGCAAACCCTTC
205194	37390	CCGCAGGCATGTGCCACCAC	249781	81977	AACAGCAAACAGGATAGGCC	294368	126564	GGCTGTATCAGCAAACCCTT
205195	37391	ACCGCAGGCATGTGCCACCA	249782	81978	GAACAGCAAACAGGATAGGC	294369	126565	AGGCTGTATCAGCAAACCCT
205196	37392	GACCGCAGGCATGTGCCACC	249783	81979	AGAACAGCAAACAGGATAGG	294370	126566	AAGGCTGTATCAGCAAACCC
205197	37393	GGACCGCAGGCATGTGCCAC	249784	81980	AAGAACAGCAAACAGGATAG	294371	126567	CAAGGCTGTATCAGCAAACC
205198	37394	GGGACCGCAGGCATGTGCCA	249785	81981	CAAGAACAGCAAACAGGATA	294372	126568	GCAAGGCTGTATCAGCAAAC
205199	37395	TGGGACCGCAGGCATGTGCC	249786	81982	CCAAGAACAGCAAACAGGAT	294373	126569	AGCAAGGCTGTATCAGCAAA
205200	37396	CTGGGACCGCAGGCATGTGC	249787	81983	GCCAAGAACAGCAAACAGGA	294374	126570	CAGCAAGGCTGTATCAGCAA
205201	37397	GCTGGGACCGCAGGCATGTG	249788	81984	CGCCAAGAACAGCAAACAGG	294375	126571	GCAGCAAGGCTGTATCAGCA
205202	37398	AGCTGGGACCGCAGGCATGT	249789	81985	GCGCCAAGAACAGCAAACAG	294376	126572	TGCAGCAAGGCTGTATCAGC
205203	37399	TAGCTGGGACCGCAGGCATG	249790	81986	AGCGCCAAGAACAGCAAACA	294377	126573	CTGCAGCAAGGCTGTATCAG
205204	37400	GTAGCTGGGACCGCAGGCAT	249791	81987	GAGCGCCAAGAACAGCAAAC	294378	126574	TCTGCAGCAAGGCTGTATCA
205205	37401	AGTAGCTGGGACCGCAGGCA	249792	81988	GGAGCGCCAAGAACAGCAAA	294379	126575	ATCTGCAGCAAGGCTGTATC
205206	37402	GAGTAGCTGGGACCGCAGGC	249793	81989	TGGAGCGCCAAGAACAGCAA	294380	126576	CATCTGCAGCAAGGCTGTAT
205207	37403	TGAGTAGCTGGGACCGCAGG	249794	81990	CTGGAGCGCCAAGAACAGCA	294381	126577	GCATCTGCAGCAAGGCTGTA
205208	37404	CTGAGTAGCTGGGACCGCAG	249795	81991	ACTGGAGCGCCAAGAACAGC	294382	126578	AGCATCTGCAGCAAGGCTGT
205209	37405	CCTGAGTAGCTGGGACCGCA	249796	81992	CACTGGAGCGCCAAGAACAG	294383	126579	CAGCATCTGCAGCAAGGCTG
205210	37406	TCCTGAGTAGCTGGGACCGC	249797	81993	TCACTGGAGCGCCAAGAACA	294384	126580	GCAGCATCTGCAGCAAGGCT
205211	37407	CTCCTGAGTAGCTGGGACCG	249798	81994	TTCACTGGAGCGCCAAGAAC	294385	126581	CGCAGCATCTGCAGCAAGGC
205212	37408	CCTCCTGAGTAGCTGGGACC	249799	81995	TTTCACTGGAGCGCCAAGAA	294386	126582	TCGCAGCATCTGCAGCAAGG
205213	37409	GCCTCCTGAGTAGCTGGGAC	249800	81996	GTTTCACTGGAGCGCCAAGA	294387	126583	TTCGCAGCATCTGCAGCAAG
205214	37410	AGCCTCCTGAGTAGCTGGGA	249801	81997	AGTTTCACTGGAGCGCCAAG	294388	126584	GTTCGCAGCATCTGCAGCAA
205215	37411	CAGCCTCCTGAGTAGCTGGG	249802	81998	GAGTTTCACTGGAGCGCCAA	294389	126585	AGTTCGCAGCATCTGCAGCA
205216	37412	TCAGCCTCCTGAGTAGCTGG	249803	81999	GGAGTTTCACTGGAGCGCCA	294390	126586	CAGTTCGCAGCATCTGCAGC
205217	37413	CTCAGCCTCCTGAGTAGCTG	249804	82000	GGGAGTTTCACTGGAGCGCC	294391	126587	ACAGTTCGCAGCATCTGCAG
205218	37414	TCTCAGCCTCCTGAGTAGCT	249805	82001	GGGGAGTTTCACTGGAGCGC	294392	126588	CACAGTTCGCAGCATCTGCA
205219	37415	ATCTCAGCCTCCTGAGTAGC	249806	82002	TGGGGAGTTTCACTGGAGCG	294393	126589	CCACAGTTCGCAGCATCTGC
205220	37416	TATCTCAGCCTCCTGAGTAG	249807	82003	ATGGGGAGTTTCACTGGAGC	294394	126590	GCCACAGTTCGCAGCATCTG
205221	37417	CTATCTCAGCCTCCTGAGTA	249808	82004	CATGGGGAGTTTCACTGGAG	294395	126591	GGCCACAGTTCGCAGCATCT
205222	37418	CCTATCTCAGCCTCCTGAGT	249809	82005	CCATGGGGAGTTTCACTGGA	294396	126592	AGGCCACAGTTCGCAGCATC
205223	37419	TCCTATCTCAGCCTCCTGAG	249810	82006	CCCATGGGGAGTTTCACTGG	294397	126593	CAGGCCACAGTTCGCAGCAT
205224	37420	CTCCTATCTCAGCCTCCTGA	249811	82007	GCCCATGGGGAGTTTCACTG	294398	126594	CCAGGCCACAGTTCGCAGCA
205225	37421	CCTCCTATCTCAGCCTCCTG	249812	82008	GGCCCATGGGGAGTTTCACT	294399	126595	CCCAGGCCACAGTTCGCAGC
205226	37422	TCCTCCTATCTCAGCCTCCT	249813	82009	TGGCCCATGGGGAGTTTCAC	294400	126596	CCCCAGGCCACAGTTCGCAG
205227	37423	ATCCTCCTATCTCAGCCTCC	249814	82010	ATGGCCCATGGGGAGTTTCA	294401	126597	GCCCCAGGCCACAGTTCGCA
205228	37424	GATCCTCCTATCTCAGCCTC	249815	82011	GATGGCCCATGGGGAGTTTC	294402	126598	TGCCCCAGGCCACAGTTCGC
205229	37425	TGATCCTCCTATCTCAGCCT	249816	82012	GGATGGCCCATGGGGAGTTT	294403	126599	CTGCCCCAGGCCACAGTTCG
205230	37426	GTGATCCTCCTATCTCAGCC	249817	82013	TGGATGGCCCATGGGGAGTT	294404	126600	TCTGCCCCAGGCCACAGTTC
205231	37427	AGTGATCCTCCTATCTCAGC	249818	82014	CTGGATGGCCCATGGGGAGT	294405	126601	GTCTGCCCCAGGCCACAGTT
205232	37428	AAGTGATCCTCCTATCTCAG	249819	82015	ACTGGATGGCCCATGGGGAG	294406	126602	GGTCTGCCCCAGGCCACAGT
205233	37429	CAAGTGATCCTCCTATCTCA	249820	82016	AACTGGATGGCCCATGGGGA	294407	126603	AGGTCTGCCCCAGGCCACAG
205234	37430	TCAAGTGATCCTCCTATCTC	249821	82017	CAACTGGATGGCCCATGGGG	294408	126604	AAGGTCTGCCCCAGGCCACA
205235	37431	TTCAAGTGATCCTCCTATCT	249822	82018	CCAACTGGATGGCCCATGGG	294409	126605	TAAGGTCTGCCCCAGGCCAC
205236	37432	GTTCAAGTGATCCTCCTATC	249823	82019	CCCAACTGGATGGCCCATGG	294410	126606	GTAAGGTCTGCCCCAGGCCA
205237	37433	GGTTCAAGTGATCCTCCTAT	249824	82020	CCCCAACTGGATGGCCCATG	294411	126607	GGTAAGGTCTGCCCCAGGCC
205238	37434	GGGTTCAAGTGATCCTCCTA	249825	82021	ACCCCAACTGGATGGCCCAT	294412	126608	AGGTAAGGTCTGCCCCAGGC
205239	37435	AGGGTTCAAGTGATCCTCCT	249826	82022	CACCCCAACTGGATGGCCCA	294413	126609	GAGGTAAGGTCTGCCCCAGG
205240	37436	CAGGGTTCAAGTGATCCTCC	249827	82023	GCACCCCAACTGGATGGCCC	294414	126610	GGAGGTAAGGTCTGCCCCAG
205241	37437	CCAGGGTTCAAGTGATCCTC	249828	82024	TGCACCCCAACTGGATGGCC	294415	126611	TGGAGGTAAGGTCTGCCCCA
205242	37438	CCCAGGGTTCAAGTGATCCT	249829	82025	CTGCACCCCAACTGGATGGC	294416	126612	CTGGAGGTAAGGTCTGCCCC

205243	37439	CCCCAGGGTTCAAGTGATCC	249830	82026	ACTGCACCCCAACTGGATGG	294417	126613	TCTGGAGGTAAGGTCTGCCC
205244	37440	CCCCCAGGGTTCAAGTGATC	249831	82027	CACTGCACCCCAACTGGATG	294418	126614	GTCTGGAGGTAAGGTCTGCC
205245	37441	TCCCCCAGGGTTCAAGTGAT	249832	82028	ACACTGCACCCCAACTGGAT	294419	126615	TGTCTGGAGGTAAGGTCTGC
205246	37442	GTCCCCCAGGGTTCAAGTGA	249833	82029	CACACTGCACCCCAACTGGA	294420	126616	GTGTCTGGAGGTAAGGTCTG
205247	37443	TGTCCCCCAGGGTTCAAGTG	249834	82030	CCACACTGCACCCCAACTGG	294421	126617	CGTGTCTGGAGGTAAGGTCT
205248	37444	CTGTCCCCCAGGGTTCAAGT	249835	82031	GCCACACTGCACCCCAACTG	294422	126618	GCGTGTCTGGAGGTAAGGTC
205249	37445	TCTGTCCCCCAGGGTTCAAG	249836	82032	GGCCACACTGCACCCCAACT	294423	126619	GGCGTGTCTGGAGGTAAGGT
205250	37446	CTCTGTCCCCCAGGGTTCAA	249837	82033	TGGCCACACTGCACCCCAAC	294424	126620	GGGCGTGTCTGGAGGTAAGG
205251	37447	CCTCTGTCCCCCAGGGTTCA	249838	82034	GTGGCCACACTGCACCCCAA	294425	126621	AGGGCGTGTCTGGAGGTAAG
205252	37448	ACCTCTGTCCCCCAGGGTTC	249839	82035	GGTGGCCACACTGCACCCCA	294426	126622	CAGGGCGTGTCTGGAGGTAA
205253	37449	AACCTCTGTCCCCCAGGGTT	249840	82036	GGGTGGCCACACTGCACCCC	294427	126623	TCAGGGCGTGTCTGGAGGTA
205254	37450	CAACCTCTGTCCCCCAGGGT	249841	82037	GGGGTGGCCACACTGCACCC	294428	126624	CTCAGGGCGTGTCTGGAGGT
205255	37451	GCAACCTCTGTCCCCCAGGG	249842	82038	GGGGGTGGCCACACTGCACC	294429	126625	CCTCAGGGCGTGTCTGGAGG
205256	37452	TGCAACCTCTGTCCCCCAGG	249843	82039	AGGGGGTGGCCACACTGCAC	294430	126626	GCCTCAGGGCGTGTCTGGAG
205257	37453	CTGCAACCTCTGTCCCCCAG	249844	82040	AAGGGGGTGGCCACACTGCA	294431	126627	TGCCTCAGGGCGTGTCTGGA
205258	37454	ACTGCAACCTCTGTCCCCCA	249845	82041	CAAGGGGGTGGCCACACTGC	294432	126628	CTGCCTCAGGGCGTGTCTGG
205259	37455	CACTGCAACCTCTGTCCCCC	249846	82042	GCAAGGGGGTGGCCACACTG	294433	126629	CCTGCCTCAGGGCGTGTCTG
205260	37456	TCACTGCAACCTCTGTCCCC	249847	82043	TGCAAGGGGGTGGCCACACT	294434	126630	CCCTGCCTCAGGGCGTGTCT
205261	37457	CTCACTGCAACCTCTGTCCC	249848	82044	CTGCAAGGGGGTGGCCACAC	294435	126631	CCCCTGCCTCAGGGCGTGTC
205262	37458	CCTCACTGCAACCTCTGTCC	249849	82045	CCTGCAAGGGGGTGGCCACA	294436	126632	TCCCCTGCCTCAGGGCGTGT
205263	37459	GCCTCACTGCAACCTCTGTC	249850	82046	ACCTGCAAGGGGGTGGCCAC	294437	126633	CTCCCCTGCCTCAGGGCGTG
205264	37460	TGCCTCACTGCAACCTCTGT	249851	82047	AACCTGCAAGGGGGTGGCCA	294438	126634	CCTCCCCTGCCTCAGGGCGT
205265	37461	TTGCCTCACTGCAACCTCTG	249852	82048	GAACCTGCAAGGGGGTGGCC	294439	126635	CCCTCCCCTGCCTCAGGGCG
205266	37462	CTTGCCTCACTGCAACCTCT	249853	82049	GGAACCTGCAAGGGGGTGGC	294440	126636	GCCCTCCCCTGCCTCAGGGC
205267	37463	TCTTGCCTCACTGCAACCTC	249854	82050	AGGAACCTGCAAGGGGGTGG	294441	126637	TGCCCTCCCCTGCCTCAGGG
205268	37464	ATCTTGCCTCACTGCAACCT	249855	82051	CAGGAACCTGCAAGGGGGTG	294442	126638	GTGCCCTCCCCTGCCTCAGG
205269	37465	AATCTTGCCTCACTGCAACC	249856	82052	GCAGGAACCTGCAAGGGGGT	294443	126639	AGTGCCCTCCCCTGCCTCAG
205270	37466	CAATCTTGCCTCACTGCAAC	249857	82053	GGCAGGAACCTGCAAGGGGG	294444	126640	CAGTGCCCTCCCCTGCCTCA
205271	37467	GCAATCTTGCCTCACTGCAA	249858	82054	AGGCAGGAACCTGCAAGGGG	294445	126641	CCAGTGCCCTCCCCTGCCTC
205272	37468	TGCAATCTTGCCTCACTGCA	249859	82055	AAGGCAGGAACCTGCAAGGG	294446	126642	GCCAGTGCCCTCCCCTGCCT
205273	37469	GTGCAATCTTGCCTCACTGC	249860	82056	CAAGGCAGGAACCTGCAAGG	294447	126643	GGCCAGTGCCCTCCCCTGCC
205274	37470	GGTGCAATCTTGCCTCACTG	249861	82057	GCAAGGCAGGAACCTGCAAG	294448	126644	GGGCCAGTGCCCTCCCCTGC
205275	37471	TGGTGCAATCTTGCCTCACT	249862	82058	AGCAAGGCAGGAACCTGCAA	294449	126645	CGGGCCAGTGCCCTCCCCTG
205276	37472	GTGGTGCAATCTTGCCTCAC	249863	82059	CAGCAAGGCAGGAACCTGCA	294450	126646	ACGGGCCAGTGCCCTCCCCT
205277	37473	AGTGGTGCAATCTTGCCTCA	249864	82060	CCAGCAAGGCAGGAACCTGC	294451	126647	TACGGGCCAGTGCCCTCCCC
205278	37474	CAGTGGTGCAATCTTGCCTC	249865	82061	TCCAGCAAGGCAGGAACCTG	294452	126648	CTACGGGCCAGTGCCCTCCC
205279	37475	GCAGTGGTGCAATCTTGCCT	249866	82062	CTCCAGCAAGGCAGGAACCT	294453	126649	GCTACGGGCCAGTGCCCTCC
205280	37476	TGCAGTGGTGCAATCTTGCC	249867	82063	TCTCCAGCAAGGCAGGAACC	294454	126650	AGCTACGGGCCAGTGCCCTC
205281	37477	GTGCAGTGGTGCAATCTTGC	249868	82064	CTCTCCAGCAAGGCAGGAAC	294455	126651	CAGCTACGGGCCAGTGCCCT
205282	37478	AGTGCAGTGGTGCAATCTTG	249869	82065	GCTCTCCAGCAAGGCAGGAA	294456	126652	CCAGCTACGGGCCAGTGCCC
205283	37479	GAGTGCAGTGGTGCAATCTT	249870	82066	TGCTCTCCAGCAAGGCAGGA	294457	126653	GCCAGCTACGGGCCAGTGCC
205284	37480	GGAGTGCAGTGGTGCAATCT	249871	82067	GTGCTCTCCAGCAAGGCAGG	294458	126654	GGCCAGCTACGGGCCAGTGC
205285	37481	TGGAGTGCAGTGGTGCAATC	249872	82068	TGTGCTCTCCAGCAAGGCAG	294459	126655	CGGCCAGCTACGGGCCAGTG
205286	37482	CTGGAGTGCAGTGGTGCAAT	249873	82069	CTGTGCTCTCCAGCAAGGCA	294460	126656	TCGGCCAGCTACGGGCCAGT
205287	37483	GCTGGAGTGCAGTGGTGCAA	249874	82070	CCTGTGCTCTCCAGCAAGGC	294461	126657	CTCGGCCAGCTACGGGCCAG
205288	37484	GGCTGGAGTGCAGTGGTGCA	249875	82071	CCCTGTGCTCTCCAGCAAGG	294462	126658	TCTCGGCCAGCTACGGGCCA
205289	37485	AGGCTGGAGTGCAGTGGTGC	249876	82072	GCCCTGTGCTCTCCAGCAAG	294463	126659	CTCTCGGCCAGCTACGGGCC
205290	37486	CAGGCTGGAGTGCAGTGGTG	249877	82073	GGCCCTGTGCTCTCCAGCAA	294464	126660	GCTCTCGGCCAGCTACGGGC
205291	37487	CCAGGCTGGAGTGCAGTGGT	249878	82074	GGGCCCTGTGCTCTCCAGCA	294465	126661	AGCTCTCGGCCAGCTACGGG
205292	37488	CCCAGGCTGGAGTGCAGTGG	249879	82075	AGGGCCCTGTGCTCTCCAGC	294466	126662	GAGCTCTCGGCCAGCTACGG
205293	37489	ACCCAGGCTGGAGTGCAGTG	249880	82076	GAGGGCCCTGTGCTCTCCAG	294467	126663	AGAGCTCTCGGCCAGCTACG
205294	37490	CACCCAGGCTGGAGTGCAGT	249881	82077	GGAGGGCCCTGTGCTCTCCA	294468	126664	GAGAGCTCTCGGCCAGCTAC
205295	37491	TCACCCAGGCTGGAGTGCAG	249882	82078	AGGAGGGCCCTGTGCTCTCC	294469	126665	CGAGAGCTCTCGGCCAGCTA
205296	37492	GTCACCCAGGCTGGAGTGCA	249883	82079	CAGGAGGGCCCTGTGCTCTC	294470	126666	CCGAGAGCTCTCGGCCAGCT
205297	37493	TGTCACCCAGGCTGGAGTGC	249884	82080	CCAGGAGGGCCCTGTGCTCT	294471	126667	CCCGAGAGCTCTCGGCCAGC
205298	37494	CTGTCACCCAGGCTGGAGTG	249885	82081	GCCAGGAGGGCCCTGTGCTC	294472	126668	ACCCGAGAGCTCTCGGCCAG
205299	37495	TCTGTCACCCAGGCTGGAGT	249886	82082	AGCCAGGAGGGCCCTGTGCT	294473	126669	AACCCGAGAGCTCTCGGCCA
205300	37496	ATCTGTCACCCAGGCTGGAG	249887	82083	GAGCCAGGAGGGCCCTGTGC	294474	126670	CAACCCGAGAGCTCTCGGCC
205301	37497	AATCTGTCACCCAGGCTGGA	249888	82084	AGAGCCAGGAGGGCCCTGTG	294475	126671	GCAACCCGAGAGCTCTCGGC
205302	37498	CAATCTGTCACCCAGGCTGG	249889	82085	AAGAGCCAGGAGGGCCCTGT	294476	126672	CGCAACCCGAGAGCTCTCGG
205303	37499	TCAATCTGTCACCCAGGCTG	249890	82086	CAAGAGCCAGGAGGGCCCTG	294477	126673	GCGCAACCCGAGAGCTCTCG
205304	37500	CTCAATCTGTCACCCAGGCT	249891	82087	ACAAGAGCCAGGAGGGCCCT	294478	126674	CGCGCAACCCGAGAGCTCTC
205305	37501	TCTCAATCTGTCACCCAGGC	249892	82088	TACAAGAGCCAGGAGGGCCC	294479	126675	TCGCGCAACCCGAGAGCTCT
205306	37502	GTCTCAATCTGTCACCCAGG	249893	82089	TTACAAGAGCCAGGAGGGCC	294480	126676	GTCGCGCAACCCGAGAGCTC
205307	37503	GGTCTCAATCTGTCACCCAG	249894	82090	TTTACAAGAGCCAGGAGGGC	294481	126677	TGTCGCGCAACCCGAGAGCT
205308	37504	GGGTCTCAATCTGTCACCCA	249895	82091	TTTTACAAGAGCCAGGAGGG	294482	126678	CTGTCGCGCAACCCGAGAGC
205309	37505	AGGGTCTCAATCTGTCACCC	249896	82092	GTTTTACAAGAGCCAGGAGG	294483	126679	CCTGTCGCGCAACCCGAGAG
205310	37506	CAGGGTCTCAATCTGTCACC	249897	82093	TGTTTTACAAGAGCCAGGAG	294484	126680	CCCTGTCGCGCAACCCGAGA
205311	37507	ACAGGGTCTCAATCTGTCAC	249898	82094	GTGTTTTACAAGAGCCAGGA	294485	126681	TCCCTGTCGCGCAACCCGAG
205312	37508	GACAGGGTCTCAATCTGTCA	249899	82095	AGTGTTTTACAAGAGCCAGG	294486	126682	ATCCCTGTCGCGCAACCCGA
205313	37509	AGACAGGGTCTCAATCTGTC	249900	82096	GAGTGTTTTACAAGAGCCAG	294487	126683	TATCCCTGTCGCGCAACCCG
205314	37510	GAGACAGGGTCTCAATCTGT	249901	82097	GGAGTGTTTTACAAGAGCCA	294488	126684	GTATCCCTGTCGCGCAACCC

205315	37511	TGAGACAGGGTCTCAATCTG	249902	82098	GGGAGTGTTTTACAAGAGCC	294489	126685	AGTATCCCTGTCGCGCAACC
205316	37512	TTGAGACAGGGTCTCAATCT	249903	82099	GGGGAGTGTTTTACAAGAGC	294490	126686	AAGTATCCCTGTCGCGCAAC
205317	37513	TTTGAGACAGGGTCTCAATC	249904	82100	TGGGGAGTGTTTTACAAGAG	294491	126687	AAAGTATCCCTGTCGCGCAA
205318	37514	TTTTGAGACAGGGTCTCAAT	249905	82101	ATGGGGAGTGTTTTACAAGA	294492	126688	AAAAGTATCCCTGTCGCGCA
205319	37515	TTTTTGAGACAGGGTCTCAA	249906	82102	CATGGGGAGTGTTTTACAAG	294493	126689	GAAAAGTATCCCTGTCGCGC
205320	37516	TTTTTTGAGACAGGGTCTCA	249907	82103	CCATGGGGAGTGTTTTACAA	294494	126690	TGAAAAGTATCCCTGTCGCG
205321	37517	TTTTTTTGAGACAGGGTCTC	249908	82104	ACCATGGGGAGTGTTTTACA	294495	126691	CTGAAAAGTATCCCTGTCGC
205322	37518	CTTTTTTTGAGACAGGGTCT	249909	82105	TACCATGGGGAGTGTTTTAC	294496	126692	GCTGAAAAGTATCCCTGTCG
205323	37519	TCTTTTTTTGAGACAGGGTC	249910	82106	GTACCATGGGGAGTGTTTTA	294497	126693	CGCTGAAAAGTATCCCTGTC
205324	37520	TTCTTTTTTTGAGACAGGGT	249911	82107	TGTACCATGGGGAGTGTTTT	294498	126694	CCGCTGAAAAGTATCCCTGT
205325	37521	TTTCTTTTTTTGAGACAGGG	249912	82108	CTGTACCATGGGGAGTGTTT	294499	126695	GCCGCTGAAAAGTATCCCTG
205326	37522	TTTTCTTTTTTTGAGACAGG	249913	82109	TCTGTACCATGGGGAGTGTT	294500	126696	AGCCGCTGAAAAGTATCCCT
205327	37523	TTTTTCTTTTTTTGAGACAG	249914	82110	CTCTGTACCATGGGGAGTGT	294501	126697	CAGCCGCTGAAAAGTATCCC
205328	37524	TTTTTTCTTTTTTTGAGACA	249915	82111	TCTCTGTACCATGGGGAGTG	294502	126698	CCAGCCGCTGAAAAGTATCC
205329	37525	TTTTTTTCTTTTTTTGAGAC	249916	82112	CTCTCTGTACCATGGGGAGT	294503	126699	CCCAGCCGCTGAAAAGTATC
205330	37526	TTTTTTTTCTTTTTTTGAGA	249917	82113	CCTCTCTGTACCATGGGGAG	294504	126700	ACCCAGCCGCTGAAAAGTAT
205331	37527	TTTTTTTTTCTTTTTTTGAG	249918	82114	GCCTCTCTGTACCATGGGGA	294505	126701	GACCCAGCCGCTGAAAAGTA
205332	37528	TTTTTTTTTTCTTTTTTTGA	249919	82115	GGCCTCTCTGTACCATGGGG	294506	126702	CGACCCAGCCGCTGAAAAGT
205333	37529	TTTTTTTTTTTCTTTTTTTG	249920	82116	TGGCCTCTCTGTACCATGGG	294507	126703	GCGACCCAGCCGCTGAAAAG
205334	37530	TTTTTTTTTTTTCTTTTTTT	249921	82117	CTGGCCTCTCTGTACCATGG	294508	126704	AGCGACCCAGCCGCTGAAAA
205335	37531	CTTTTTTTTTTTTCTTTTTT	249922	82118	GCTGGCCTCTCTGTACCATG	294509	126705	TAGCGACCCAGCCGCTGAAA
205336	37532	TCTTTTTTTTTTTTCTTTTT	249923	82119	TGCTGGCCTCTCTGTACCAT	294510	126706	ATAGCGACCCAGCCGCTGAA
205337	37533	TTCTTTTTTTTTTTTCTTTT	249924	82120	CTGCTGGCCTCTCTGTACCA	294511	126707	GATAGCGACCCAGCCGCTGA
205338	37534	TTTCTTTTTTTTTTTTCTTT	249925	82121	ACTGCTGGCCTCTCTGTACC	294512	126708	GGATAGCGACCCAGCCGCTG
205339	37535	GTTTCTTTTTTTTTTTTCTT	249926	82122	CACTGCTGGCCTCTCTGTAC	294513	126709	TGGATAGCGACCCAGCCGCT
205340	37536	TGTTTCTTTTTTTTTTTTCT	249927	82123	TCACTGCTGGCCTCTCTGTA	294514	126710	TTGGATAGCGACCCAGCCGC
205341	37537	GTGTTTCTTTTTTTTTTTTC	249928	82124	ATCACTGCTGGCCTCTCTGT	294515	126711	TTTGGATAGCGACCCAGCCG
205342	37538	TGTGTTTCTTTTTTTTTTTT	249929	82125	CATCACTGCTGGCCTCTCTG	294516	126712	CTTTGGATAGCGACCCAGCC
205343	37539	TTGTGTTTCTTTTTTTTTTT	249930	82126	ACATCACTGCTGGCCTCTCT	294517	126713	ACTTTGGATAGCGACCCAGC
205344	37540	TTTGTGTTTCTTTTTTTTTT	249931	82127	CACATCACTGCTGGCCTCTC	294518	126714	CACTTTGGATAGCGACCCAG
205345	37541	TTTTGTGTTTCTTTTTTTTT	249932	82128	TCACATCACTGCTGGCCTCT	294519	126715	TCACTTTGGATAGCGACCCA
205346	37542	TTTTTGTGTTTCTTTTTTTT	249933	82129	CTCACATCACTGCTGGCCTC	294520	126716	CTCACTTTGGATAGCGACCC
205347	37543	GTTTTTGTGTTTCTTTTTTT	249934	82130	CCTCACATCACTGCTGGCCT	294521	126717	TCTCACTTTGGATAGCGACC
205348	37544	AGTTTTTGTGTTTCTTTTTT	249935	82131	GCCTCACATCACTGCTGGCC	294522	126718	TTCTCACTTTGGATAGCGAC
205349	37545	GAGTTTTTGTGTTTCTTTTT	249936	82132	GGCCTCACATCACTGCTGGC	294523	126719	TTTCTCACTTTGGATAGCGA
205350	37546	GGAGTTTTTGTGTTTCTTTT	249937	82133	GGGCCTCACATCACTGCTGG	294524	126720	TTTTCTCACTTTGGATAGCG
205351	37547	TGGAGTTTTTGTGTTTCTTT	249938	82134	TGGGCCTCACATCACTGCTG	294525	126721	GTTTTCTCACTTTGGATAGC
205352	37548	CTGGAGTTTTTGTGTTTCTT	249939	82135	TTGGGCCTCACATCACTGCT	294526	126722	CGTTTTCTCACTTTGGATAG
205353	37549	CCTGGAGTTTTTGTGTTTCT	249940	82136	GTTGGGCCTCACATCACTGC	294527	126723	TCGTTTTCTCACTTTGGATA
205354	37550	ACCTGGAGTTTTTGTGTTTC	249941	82137	GGTTGGGCCTCACATCACTG	294528	126724	CTCGTTTTCTCACTTTGGAT
205355	37551	CACCTGGAGTTTTTGTGTTT	249942	82138	AGGTTGGGCCTCACATCACT	294529	126725	CCTCGTTTTCTCACTTTGGA
205356	37552	CCACCTGGAGTTTTTGTGTT	249943	82139	GAGGTTGGGCCTCACATCAC	294530	126726	TCCTCGTTTTCTCACTTTGG
205357	37553	ACCACCTGGAGTTTTTGTGT	249944	82140	GGAGGTTGGGCCTCACATCA	294531	126727	CTCCTCGTTTTCTCACTTTG
205358	37554	GACCACCTGGAGTTTTTGTG	249945	82141	GGGAGGTTGGGCCTCACATC	294532	126728	CCTCCTCGTTTTCTCACTTT
205359	37555	CGACCACCTGGAGTTTTTGT	249946	82142	AGGGAGGTTGGGCCTCACAT	294533	126729	CCCTCCTCGTTTTCTCACTT
205360	37556	GCGACCACCTGGAGTTTTTG	249947	82143	GAGGGAGGTTGGGCCTCACA	294534	126730	TCCCTCCTCGTTTTCTCACT
205361	37557	TGCGACCACCTGGAGTTTTT	249948	82144	GGAGGGAGGTTGGGCCTCAC	294535	126731	GTCCCTCCTCGTTTTCTCAC
205362	37558	GTGCGACCACCTGGAGTTTT	249949	82145	TGGAGGGAGGTTGGGCCTCA	294536	126732	GGTCCCTCCTCGTTTTCTCA
205363	37559	TGTGCGACCACCTGGAGTTT	249950	82146	ATGGAGGGAGGTTGGGCCTC	294537	126733	TGGTCCCTCCTCGTTTTCTC
205364	37560	CTGTGCGACCACCTGGAGTT	249951	82147	CATGGAGGGAGGTTGGGCCT	294538	126734	CTGGTCCCTCCTCGTTTTCT
205365	37561	TCTGTGCGACCACCTGGAGT	249952	82148	CCATGGAGGGAGGTTGGGCC	294539	126735	CCTGGTCCCTCCTCGTTTTC
205366	37562	TTCTGTGCGACCACCTGGAG	249953	82149	ACCATGGAGGGAGGTTGGGC	294540	126736	TCCTGGTCCCTCCTCGTTTT
205367	37563	ATTCTGTGCGACCACCTGGA	249954	82150	CACCATGGAGGGAGGTTGGG	294541	126737	CTCCTGGTCCCTCCTCGTTT
205368	37564	CATTCTGTGCGACCACCTGG	249955	82151	ACACCATGGAGGGAGGTTGG	294542	126738	CCTCCTGGTCCCTCCTCGTT
205369	37565	TCATTCTGTGCGACCACCTG	249956	82152	AACACCATGGAGGGAGGTTG	294543	126739	GCCTCCTGGTCCCTCCTCGT
205370	37566	GTCATTCTGTGCGACCACCT	249957	82153	GAACACCATGGAGGGAGGTT	294544	126740	AGCCTCCTGGTCCCTCCTCG
205371	37567	TGTCATTCTGTGCGACCACC	249958	82154	GGAACACCATGGAGGGAGGT	294545	126741	CAGCCTCCTGGTCCCTCCTC
205372	37568	CTGTCATTCTGTGCGACCAC	249959	82155	GGGAACACCATGGAGGGAGG	294546	126742	ACAGCCTCCTGGTCCCTCCT
205373	37569	CCTGTCATTCTGTGCGACCA	249960	82156	TGGGAACACCATGGAGGGAG	294547	126743	GACAGCCTCCTGGTCCCTCC
205374	37570	TCCTGTCATTCTGTGCGACC	249961	82157	TTGGGAACACCATGGAGGGA	294548	126744	GGACAGCCTCCTGGTCCCTC
205375	37571	GTCCTGTCATTCTGTGCGAC	249962	82158	CTTGGGAACACCATGGAGGG	294549	126745	CGGACAGCCTCCTGGTCCCT
205376	37572	AGTCCTGTCATTCTGTGCGA	249963	82159	GCTTGGGAACACCATGGAGG	294550	126746	GCGGACAGCCTCCTGGTCCC
205377	37573	CAGTCCTGTCATTCTGTGCG	249964	82160	TGCTTGGGAACACCATGGAG	294551	126747	GGCGGACAGCCTCCTGGTCC
205378	37574	TCAGTCCTGTCATTCTGTGC	249965	82161	CTGCTTGGGAACACCATGGA	294552	126748	AGGCGGACAGCCTCCTGGTC
205379	37575	TTCAGTCCTGTCATTCTGTG	249966	82162	GCTGCTTGGGAACACCATGG	294553	126749	GAGGCGGACAGCCTCCTGGT
205380	37576	CTTCAGTCCTGTCATTCTGT	249967	82163	AGCTGCTTGGGAACACCATG	294554	126750	TGAGGCGGACAGCCTCCTGG
205381	37577	ACTTCAGTCCTGTCATTCTG	249968	82164	GAGCTGCTTGGGAACACCAT	294555	126751	TTGAGGCGGACAGCCTCCTG
205382	37578	TACTTCAGTCCTGTCATTCT	249969	82165	GGAGCTGCTTGGGAACACCA	294556	126752	CTTGAGGCGGACAGCCTCCT
205383	37579	TTACTTCAGTCCTGTCATTC	249970	82166	GGGAGCTGCTTGGGAACACC	294557	126753	TCTTGAGGCGGACAGCCTCC
205384	37580	GTTACTTCAGTCCTGTCATT	249971	82167	AGGGAGCTGCTTGGGAACAC	294558	126754	CTCTTGAGGCGGACAGCCTC
205385	37581	AGTTACTTCAGTCCTGTCAT	249972	82168	AAGGGAGCTGCTTGGGAACA	294559	126755	TCTCTTGAGGCGGACAGCCT
205386	37582	AAGTTACTTCAGTCCTGTCA	249973	82169	AAAGGGAGCTGCTTGGGAAC	294560	126756	ATCTCTTGAGGCGGACAGCC

205387	37583	TAAGTTACTTCAGTCCTGTC	249974	82170	GAAAGGGAGCTGCTTGGGAA	294561	126757	CATCTCTTGAGGCGGACAGC
205388	37584	CTAAGTTACTTCAGTCCTGT	249975	82171	AGAAAGGGAGCTGCTTGGGA	294562	126758	ACATCTCTTGAGGCGGACAG
205389	37585	GCTAAGTTACTTCAGTCCTG	249976	82172	CAGAAAGGGAGCTGCTTGGG	294563	126759	CACATCTCTTGAGGCGGACA
205390	37586	AGCTAAGTTACTTCAGTCCT	249977	82173	CCAGAAAGGGAGCTGCTTGG	294564	126760	CCACATCTCTTGAGGCGGAC
205391	37587	GAGCTAAGTTACTTCAGTCC	249978	82174	CCCAGAAAGGGAGCTGCTTG	294565	126761	CCCACATCTCTTGAGGCGGA
205392	37588	GGAGCTAAGTTACTTCAGTC	249979	82175	CCCCAGAAAGGGAGCTGCTT	294566	126762	CCCCACATCTCTTGAGGCGG
205393	37589	TGGAGCTAAGTTACTTCAGT	249980	82176	ACCCCAGAAAGGGAGCTGCT	294567	126763	CCCCCACATCTCTTGAGGCG
205394	37590	TTGGAGCTAAGTTACTTCAG	249981	82177	GACCCCAGAAAGGGAGCTGC	294568	126764	GCCCCCACATCTCTTGAGGC
205395	37591	ATTGGAGCTAAGTTACTTCA	249982	82178	TGACCCCAGAAAGGGAGCTG	294569	126765	GGCCCCCACATCTCTTGAGG
205396	37592	AATTGGAGCTAAGTTACTTC	249983	82179	TTGACCCCAGAAAGGGAGCT	294570	126766	TGGCCCCCACATCTCTTGAG
205397	37593	AAATTGGAGCTAAGTTACTT	249984	82180	CTTGACCCCAGAAAGGGAGC	294571	126767	CTGGCCCCCACATCTCTTGA
205398	37594	GAAATTGGAGCTAAGTTACT	249985	82181	CCTTGACCCCAGAAAGGGAG	294572	126768	CCTGGCCCCCACATCTCTTG
205399	37595	AGAAATTGGAGCTAAGTTAC	249986	82182	CCCTTGACCCCAGAAAGGGA	294573	126769	ACCTGGCCCCCACATCTCTT
205400	37596	CAGAAATTGGAGCTAAGTTA	249987	82183	CCCCTTGACCCCAGAAAGGG	294574	126770	GACCTGGCCCCCACATCTCT
205401	37597	ACAGAAATTGGAGCTAAGTT	249988	82184	ACCCCTTGACCCCAGAAAGG	294575	126771	GGACCTGGCCCCCACATCTC
205402	37598	GACAGAAATTGGAGCTAAGT	249989	82185	CACCCCTTGACCCCAGAAAG	294576	126772	TGGACCTGGCCCCCACATCT
205403	37599	AGACAGAAATTGGAGCTAAG	249990	82186	CCACCCCTTGACCCCAGAAA	294577	126773	CTGGACCTGGCCCCCACATC
205404	37600	AAGACAGAAATTGGAGCTAA	249991	82187	GCCACCCCTTGACCCCAGAA	294578	126774	ACTGGACCTGGCCCCCACAT
205405	37601	GAAGACAGAAATTGGAGCTA	249992	82188	TGCCACCCCTTGACCCCAGA	294579	126775	AACTGGACCTGGCCCCCACA
205406	37602	TGAAGACAGAAATTGGAGCT	249993	82189	TTGCCACCCCTTGACCCCAG	294580	126776	TAACTGGACCTGGCCCCCAC
205407	37603	ATGAAGACAGAAATTGGAGC	249994	82190	TTTGCCACCCCTTGACCCCA	294581	126777	ATAACTGGACCTGGCCCCCA
205408	37604	TATGAAGACAGAAATTGGAG	249995	82191	CTTTGCCACCCCTTGACCCC	294582	126778	GATAACTGGACCTGGCCCCC
205409	37605	TTATGAAGACAGAAATTGGA	249996	82192	TCTTTGCCACCCCTTGACCC	294583	126779	AGATAACTGGACCTGGCCCC
205410	37606	ATTATGAAGACAGAAATTGG	249997	82193	GTCTTTGCCACCCCTTGACC	294584	126780	CAGATAACTGGACCTGGCCC
205411	37607	GATTATGAAGACAGAAATTG	249998	82194	TGTCTTTGCCACCCCTTGAC	294585	126781	CCAGATAACTGGACCTGGCC
205412	37608	TGATTATGAAGACAGAAATT	249999	82195	CTGTCTTTGCCACCCCTTGA	294586	126782	CCCAGATAACTGGACCTGGC
205413	37609	GTGATTATGAAGACAGAAAT	250000	82196	ACTGTCTTTGCCACCCCTTG	294587	126783	CCCCAGATAACTGGACCTGG
205414	37610	AGTGATTATGAAGACAGAAA	250001	82197	CACTGTCTTTGCCACCCCTT	294588	126784	TCCCCAGATAACTGGACCTG
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205416	37612	ACAGTGATTATGAAGACAGA	250003	82199	TGCACTGTCTTTGCCACCCC	294590	126786	CTTCCCCAGATAACTGGACC
205417	37613	GACAGTGATTATGAAGACAG	250004	82200	CTGCACTGTCTTTGCCACCC	294591	126787	GCTTCCCCAGATAACTGGAC
205418	37614	GGACAGTGATTATGAAGACA	250005	82201	GCTGCACTGTCTTTGCCACC	294592	126788	TGCTTCCCCAGATAACTGGA
205419	37615	AGGACAGTGATTATGAAGAC	250006	82202	CGCTGCACTGTCTTTGCCAC	294593	126789	CTGCTTCCCCAGATAACTGG
205420	37616	TAGGACAGTGATTATGAAGA	250007	82203	ACGCTGCACTGTCTTTGCCA	294594	126790	ACTGCTTCCCCAGATAACTG
205421	37617	GTAGGACAGTGATTATGAAG	250008	82204	GACGCTGCACTGTCTTTGCC	294595	126791	TACTGCTTCCCCAGATAACT
205422	37618	GGTAGGACAGTGATTATGAA	250009	82205	GGACGCTGCACTGTCTTTGC	294596	126792	TTACTGCTTCCCCAGATAAC
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205424	37620	ATGGTAGGACAGTGATTATG	250011	82207	TTGGACGCTGCACTGTCTTT	294598	126794	GCTTACTGCTTCCCCAGATA
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205426	37622	CAATGGTAGGACAGTGATTA	250013	82209	AATTGGACGCTGCACTGTCT	294600	126796	AAGCTTACTGCTTCCCCAGA
205427	37623	ACAATGGTAGGACAGTGATT	250014	82210	AAATTGGACGCTGCACTGTC	294601	126797	GAAGCTTACTGCTTCCCCAG
205428	37624	GACAATGGTAGGACAGTGAT	250015	82211	GAAATTGGACGCTGCACTGT	294602	126798	AGAAGCTTACTGCTTCCCCA
205429	37625	AGACAATGGTAGGACAGTGA	250016	82212	AGAAATTGGACGCTGCACTG	294603	126799	GAGAAGCTTACTGCTTCCCC
205430	37626	CAGACAATGGTAGGACAGTG	250017	82213	CAGAAATTGGACGCTGCACT	294604	126800	AGAGAAGCTTACTGCTTCCC
205431	37627	ACAGACAATGGTAGGACAGT	250018	82214	TCAGAAATTGGACGCTGCAC	294605	126801	CAGAGAAGCTTACTGCTTCC
205432	37628	CACAGACAATGGTAGGACAG	250019	82215	GTCAGAAATTGGACGCTGCA	294606	126802	GCAGAGAAGCTTACTGCTTC
205433	37629	GCACAGACAATGGTAGGACA	250020	82216	AGTCAGAAATTGGACGCTGC	294607	126803	AGCAGAGAAGCTTACTGCTT
205434	37630	AGCACAGACAATGGTAGGAC	250021	82217	GAGTCAGAAATTGGACGCTG	294608	126804	CAGCAGAGAAGCTTACTGCT
205435	37631	AAGCACAGACAATGGTAGGA	250022	82218	TGAGTCAGAAATTGGACGCT	294609	126805	ACAGCAGAGAAGCTTACTGC
205436	37632	TAAGCACAGACAATGGTAGG	250023	82219	TTGAGTCAGAAATTGGACGC	294610	126806	AACAGCAGAGAAGCTTACTG
205437	37633	CTAAGCACAGACAATGGTAG	250024	82220	CTTGAGTCAGAAATTGGACG	294611	126807	AAACAGCAGAGAAGCTTACT
205438	37634	TCTAAGCACAGACAATGGTA	250025	82221	GCTTGAGTCAGAAATTGGAC	294612	126808	GAAACAGCAGAGAAGCTTAC
205439	37635	TTCTAAGCACAGACAATGGT	250026	82222	GGCTTGAGTCAGAAATTGGA	294613	126809	AGAAACAGCAGAGAAGCTTA
205440	37636	ATTCTAAGCACAGACAATGG	250027	82223	CGGCTTGAGTCAGAAATTGG	294614	126810	TAGAAACAGCAGAGAAGCTT
205441	37637	GATTCTAAGCACAGACAATG	250028	82224	CCGGCTTGAGTCAGAAATTG	294615	126811	TTAGAAACAGCAGAGAAGCT
205442	37638	AGATTCTAAGCACAGACAAT	250029	82225	CCCGGCTTGAGTCAGAAATT	294616	126812	GTTAGAAACAGCAGAGAAGC
205443	37639	TAGATTCTAAGCACAGACAA	250030	82226	GCCCGGCTTGAGTCAGAAAT	294617	126813	GGTTAGAAACAGCAGAGAAG
205444	37640	GTAGATTCTAAGCACAGACA	250031	82227	GGCCCGGCTTGAGTCAGAAA	294618	126814	GGGTTAGAAACAGCAGAGAA
205445	37641	AGTAGATTCTAAGCACAGAC	250032	82228	AGGCCCGGCTTGAGTCAGAA	294619	126815	GGGGTTAGAAACAGCAGAGA
205446	37642	AAGTAGATTCTAAGCACAGA	250033	82229	CAGGCCCGGCTTGAGTCAGA	294620	126816	TGGGGTTAGAAACAGCAGAG
205447	37643	CAAGTAGATTCTAAGCACAG	250034	82230	CCAGGCCCGGCTTGAGTCAG	294621	126817	CTGGGGTTAGAAACAGCAGA
205448	37644	GCAAGTAGATTCTAAGCACA	250035	82231	GCCAGGCCCGGCTTGAGTCA	294622	126818	CCTGGGGTTAGAAACAGCAG
205449	37645	AGCAAGTAGATTCTAAGCAC	250036	82232	AGCCAGGCCCGGCTTGAGTC	294623	126819	GCCTGGGGTTAGAAACAGCA
205450	37646	AAGCAAGTAGATTCTAAGCA	250037	82233	TAGCCAGGCCCGGCTTGAGT	294624	126820	GGCCTGGGGTTAGAAACAGC
205451	37647	TAAGCAAGTAGATTCTAAGC	250038	82234	ATAGCCAGGCCCGGCTTGAG	294625	126821	AGGCCTGGGGTTAGAAACAG
205452	37648	TTAAGCAAGTAGATTCTAAG	250039	82235	GATAGCCAGGCCCGGCTTGA	294626	126822	GAGGCCTGGGGTTAGAAACA
205453	37649	ATTAAGCAAGTAGATTCTAA	250040	82236	CGATAGCCAGGCCCGGCTTG	294627	126823	GGAGGCCTGGGGTTAGAAAC
205454	37650	CATTAAGCAAGTAGATTCTA	250041	82237	GCGATAGCCAGGCCCGGCTT	294628	126824	GGGAGGCCTGGGGTTAGAAA
205455	37651	GCATTAAGCAAGTAGATTCT	250042	82238	TGCGATAGCCAGGCCCGGCT	294629	126825	GGGGAGGCCTGGGGTTAGAA
205456	37652	TGCATTAAGCAAGTAGATTC	250043	82239	CTGCGATAGCCAGGCCCGGC	294630	126826	AGGGGAGGCCTGGGGTTAGA
205457	37653	CTGCATTAAGCAAGTAGATT	250044	82240	GCTGCGATAGCCAGGCCCGG	294631	126827	CAGGGGAGGCCTGGGGTTAG
205458	37654	CCTGCATTAAGCAAGTAGAT	250045	82241	AGCTGCGATAGCCAGGCCCG	294632	126828	CCAGGGGAGGCCTGGGGTTA

205459	37655	TCCTGCATTAAGCAAGTAGA	250046	82242	GAGCTGCGATAGCCAGGCCC	294633	126829	ACCAGGGGAGGCCTGGGGTT
205460	37656	TTCCTGCATTAAGCAAGTAG	250047	82243	AGAGCTGCGATAGCCAGGCC	294634	126830	GACCAGGGGAGGCCTGGGGT
205461	37657	GTTCCTGCATTAAGCAAGTA	250048	82244	CAGAGCTGCGATAGCCAGGC	294635	126831	AGACCAGGGGAGGCCTGGGG
205462	37658	TGTTCCTGCATTAAGCAAGT	250049	82245	GCAGAGCTGCGATAGCCAGG	294636	126832	TAGACCAGGGGAGGCCTGGG
205463	37659	ATGTTCCTGCATTAAGCAAG	250050	82246	TGCAGAGCTGCGATAGCCAG	294637	126833	TTAGACCAGGGGAGGCCTGG
205464	37660	CATGTTCCTGCATTAAGCAA	250051	82247	GTGCAGAGCTGCGATAGCCA	294638	126834	CTTAGACCAGGGGAGGCCTG
205465	37661	ACATGTTCCTGCATTAAGCA	250052	82248	AGTGCAGAGCTGCGATAGCC	294639	126835	CCTTAGACCAGGGGAGGCCT
205466	37662	CACATGTTCCTGCATTAAGC	250053	82249	CAGTGCAGAGCTGCGATAGC	294640	126836	GCCTTAGACCAGGGGAGGCC
205467	37663	ACACATGTTCCTGCATTAAG	250054	82250	ACAGTGCAGAGCTGCGATAG	294641	126837	TGCCTTAGACCAGGGGAGGC
205468	37664	AACACATGTTCCTGCATTAA	250055	82251	CACAGTGCAGAGCTGCGATA	294642	126838	CTGCCTTAGACCAGGGGAGG
205469	37665	GAACACATGTTCCTGCATTA	250056	82252	ACACAGTGCAGAGCTGCGAT	294643	126839	CCTGCCTTAGACCAGGGGAG
205470	37666	AGAACACATGTTCCTGCATT	250057	82253	CACACAGTGCAGAGCTGCGA	294644	126840	CCCTGCCTTAGACCAGGGGA
205471	37667	GAGAACACATGTTCCTGCAT	250058	82254	ACACACAGTGCAGAGCTGCG	294645	126841	GCCCTGCCTTAGACCAGGGG
205472	37668	TGAGAACACATGTTCCTGCA	250059	82255	CACACACAGTGCAGAGCTGC	294646	126842	GGCCCTGCCTTAGACCAGGG
205473	37669	GTGAGAACACATGTTCCTGC	250060	82256	TCACACACAGTGCAGAGCTG	294647	126843	AGGCCCTGCCTTAGACCAGG
205474	37670	TGTGAGAACACATGTTCCTG	250061	82257	GTCACACACAGTGCAGAGCT	294648	126844	GAGGCCCTGCCTTAGACCAG
205475	37671	CTGTGAGAACACATGTTCCT	250062	82258	TGTCACACACAGTGCAGAGC	294649	126845	GGAGGCCCTGCCTTAGACCA
205476	37672	TCTGTGAGAACACATGTTCC	250063	82259	CTGTCACACACAGTGCAGAG	294650	126846	GGGAGGCCCTGCCTTAGACC
205477	37673	CTCTGTGAGAACACATGTTC	250064	82260	GCTGTCACACACAGTGCAGA	294651	126847	TGGGAGGCCCTGCCTTAGAC
205478	37674	TCTCTGTGAGAACACATGTT	250065	82261	TGCTGTCACACACAGTGCAG	294652	126848	CTGGGAGGCCCTGCCTTAGA
205479	37675	ATCTCTGTGAGAACACATGT	250066	82262	TTGCTGTCACACACAGTGCA	294653	126849	GCTGGGAGGCCCTGCCTTAG
205480	37676	CATCTCTGTGAGAACACATG	250067	82263	CTTGCTGTCACACACAGTGC	294654	126850	GGCTGGGAGGCCCTGCCTTA
205481	37677	CCATCTCTGTGAGAACACAT	250068	82264	CCTTGCTGTCACACACAGTG	294655	126851	AGGCTGGGAGGCCCTGCCTT
205482	37678	TCCATCTCTGTGAGAACACA	250069	82265	GCCTTGCTGTCACACACAGT	294656	126852	GAGGCTGGGAGGCCCTGCCT
205483	37679	TTCCATCTCTGTGAGAACAC	250070	82266	TGCCTTGCTGTCACACACAG	294657	126853	CGAGGCTGGGAGGCCCTGCC
205484	37680	TTTCCATCTCTGTGAGAACA	250071	82267	TTGCCTTGCTGTCACACACA	294658	126854	CCGAGGCTGGGAGGCCCTGC
205485	37681	TTTTCCATCTCTGTGAGAAC	250072	82268	GTTGCCTTGCTGTCACACAC	294659	126855	CCCGAGGCTGGGAGGCCCTG
205486	37682	ATTTTCCATCTCTGTGAGAA	250073	82269	AGTTGCCTTGCTGTCACACA	294660	126856	CCCCGAGGCTGGGAGGCCCT
205487	37683	CATTTTCCATCTCTGTGAGA	250074	82270	GAGTTGCCTTGCTGTCACAC	294661	126857	GCCCCGAGGCTGGGAGGCCC
205488	37684	GCATTTTCCATCTCTGTGAG	250075	82271	TGAGTTGCCTTGCTGTCACA	294662	126858	TGCCCCGAGGCTGGGAGGCC
205489	37685	TGCATTTTCCATCTCTGTGA	250076	82272	GTGAGTTGCCTTGCTGTCAC	294663	126859	GTGCCCCGAGGCTGGGAGGC
205490	37686	TTGCATTTTCCATCTCTGTG	250077	82273	GGTGAGTTGCCTTGCTGTCA	294664	126860	AGTGCCCCGAGGCTGGGAGG
205491	37687	TTTGCATTTTCCATCTCTGT	250078	82274	GGGTGAGTTGCCTTGCTGTC	294665	126861	AAGTGCCCCGAGGCTGGGAG
205492	37688	ATTTGCATTTTCCATCTCTG	250079	82275	TGGGTGAGTTGCCTTGCTGT	294666	126862	AAAGTGCCCCGAGGCTGGGA
205493	37689	CATTTGCATTTTCCATCTCT	250080	82276	CTGGGTGAGTTGCCTTGCTG	294667	126863	TAAAGTGCCCCGAGGCTGGG
205494	37690	CCATTTGCATTTTCCATCTC	250081	82277	ACTGGGTGAGTTGCCTTGCT	294668	126864	TTAAAGTGCCCCGAGGCTGG
205495	37691	GCCATTTGCATTTTCCATCT	250082	82278	CACTGGGTGAGTTGCCTTGC	294669	126865	TTTAAAGTGCCCCGAGGCTG
205496	37692	CGCCATTTGCATTTTCCATC	250083	82279	GCACTGGGTGAGTTGCCTTG	294670	126866	CTTTAAAGTGCCCCGAGGCT
205497	37693	GCGCCATTTGCATTTTCCAT	250084	82280	GGCACTGGGTGAGTTGCCTT	294671	126867	TCTTTAAAGTGCCCCGAGGC
205498	37694	GGCGCCATTTGCATTTTCCA	250085	82281	CGGCACTGGGTGAGTTGCCT	294672	126868	ATCTTTAAAGTGCCCCGAGG
205499	37695	TGGCGCCATTTGCATTTTCC	250086	82282	ACGGCACTGGGTGAGTTGCC	294673	126869	TATCTTTAAAGTGCCCCGAG
205500	37696	CTGGCGCCATTTGCATTTTC	250087	82283	CACGGCACTGGGTGAGTTGC	294674	126870	ATATCTTTAAAGTGCCCCGA
205501	37697	TCTGGCGCCATTTGCATTTT	250088	82284	CCACGGCACTGGGTGAGTTG	294675	126871	GATATCTTTAAAGTGCCCCG
205502	37698	TTCTGGCGCCATTTGCATTT	250089	82285	GCCACGGCACTGGGTGAGTT	294676	126872	AGATATCTTTAAAGTGCCCC
205503	37699	CTTCTGGCGCCATTTGCATT	250090	82286	TGCCACGGCACTGGGTGAGT	294677	126873	CAGATATCTTTAAAGTGCCC
205504	37700	GCTTCTGGCGCCATTTGCAT	250091	82287	CTGCCACGGCACTGGGTGAG	294678	126874	CCAGATATCTTTAAAGTGCC
205505	37701	TGCTTCTGGCGCCATTTGCA	250092	82288	ACTGCCACGGCACTGGGTGA	294679	126875	CCCAGATATCTTTAAAGTGC
205506	37702	TTGCTTCTGGCGCCATTTGC	250093	82289	CACTGCCACGGCACTGGGTG	294680	126876	GCCCAGATATCTTTAAAGTG
205507	37703	CTTGCTTCTGGCGCCATTTG	250094	82290	TCACTGCCACGGCACTGGGT	294681	126877	GGCCCAGATATCTTTAAAGT
205508	37704	GCTTGCTTCTGGCGCCATTT	250095	82291	GTCACTGCCACGGCACTGGG	294682	126878	AGGCCCAGATATCTTTAAAG
205509	37705	AGCTTGCTTCTGGCGCCATT	250096	82292	GGTCACTGCCACGGCACTGG	294683	126879	CAGGCCCAGATATCTTTAAA
205510	37706	CAGCTTGCTTCTGGCGCCAT	250097	82293	CGGTCACTGCCACGGCACTG	294684	126880	CCAGGCCCAGATATCTTTAA
205511	37707	CCAGCTTGCTTCTGGCGCCA	250098	82294	ACGGTCACTGCCACGGCACT	294685	126881	GCCAGGCCCAGATATCTTTA
205512	37708	TCCAGCTTGCTTCTGGCGCC	250099	82295	CACGGTCACTGCCACGGCAC	294686	126882	GGCCAGGCCCAGATATCTTT
205513	37709	TTCCAGCTTGCTTCTGGCGC	250100	82296	ACACGGTCACTGCCACGGCA	294687	126883	GGGCCAGGCCCAGATATCTT
205514	37710	TTTCCAGCTTGCTTCTGGCG	250101	82297	GACACGGTCACTGCCACGGC	294688	126884	GGGGCCAGGCCCAGATATCT
205515	37711	ATTTCCAGCTTGCTTCTGGC	250102	82298	GGACACGGTCACTGCCACGG	294689	126885	TGGGGCCAGGCCCAGATATC
205516	37712	AATTTCCAGCTTGCTTCTGG	250103	82299	CGGACACGGTCACTGCCACG	294690	126886	ATGGGGCCAGGCCCAGATAT
205517	37713	GAATTTCCAGCTTGCTTCTG	250104	82300	TCGGACACGGTCACTGCCAC	294691	126887	GATGGGGCCAGGCCCAGATA
205518	37714	AGAATTTCCAGCTTGCTTCT	250105	82301	CTCGGACACGGTCACTGCCA	294692	126888	GGATGGGGCCAGGCCCAGAT
205519	37715	CAGAATTTCCAGCTTGCTTC	250106	82302	CCTCGGACACGGTCACTGCC	294693	126889	GGGATGGGGCCAGGCCCAGA
205520	37716	TCAGAATTTCCAGCTTGCTT	250107	82303	TCCTCGGACACGGTCACTGC	294694	126890	GGGGATGGGGCCAGGCCCAG
205521	37717	TTCAGAATTTCCAGCTTGCT	250108	82304	TTCCTCGGACACGGTCACTG	294695	126891	TGGGGATGGGGCCAGGCCCA
205522	37718	GTTCAGAATTTCCAGCTTGC	250109	82305	CTTCCTCGGACACGGTCACT	294696	126892	GTGGGGATGGGGCCAGGCCC
205523	37719	GGTTCAGAATTTCCAGCTTG	250110	82306	GCTTCCTCGGACACGGTCAC	294697	126893	TGTGGGGATGGGGCCAGGCC
205524	37720	TGGTTCAGAATTTCCAGCTT	250111	82307	GGCTTCCTCGGACACGGTCA	294698	126894	CTGTGGGGATGGGGCCAGGC
205525	37721	ATGGTTCAGAATTTCCAGCT	250112	82308	AGGCTTCCTCGGACACGGTC	294699	126895	ACTGTGGGGATGGGGCCAGG
205526	37722	AATGGTTCAGAATTTCCAGC	250113	82309	GAGGCTTCCTCGGACACGGT	294700	126896	GACTGTGGGGATGGGGCCAG
205527	37723	TAATGGTTCAGAATTTCCAG	250114	82310	GGAGGCTTCCTCGGACACGG	294701	126897	AGACTGTGGGGATGGGGCCA
205528	37724	TTAATGGTTCAGAATTTCCA	250115	82311	AGGAGGCTTCCTCGGACACG	294702	126898	CAGACTGTGGGGATGGGGCC
205529	37725	CTTAATGGTTCAGAATTTCC	250116	82312	GAGGAGGCTTCCTCGGACAC	294703	126899	TCAGACTGTGGGGATGGGGC
205530	37726	TCTTAATGGTTCAGAATTTC	250117	82313	TGAGGAGGCTTCCTCGGACA	294704	126900	GTCAGACTGTGGGGATGGGG

205531	37727	TTCTTAATGGTTCAGAATTT	250118	82314	GTGAGGAGGCTTCCTCGGAC	294705	126901	AGTCAGACTGTGGGGATGGG
205532	37728	ATTCTTAATGGTTCAGAATT	250119	82315	TGTGAGGAGGCTTCCTCGGA	294706	126902	CAGTCAGACTGTGGGGATGG
205533	37729	AATTCTTAATGGTTCAGAAT	250120	82316	GTGTGAGGAGGCTTCCTCGG	294707	126903	TCAGTCAGACTGTGGGGATG
205534	37730	AAATTCTTAATGGTTCAGAA	250121	82317	GGTGTGAGGAGGCTTCCTCG	294708	126904	CTCAGTCAGACTGTGGGGAT
205535	37731	TAAATTCTTAATGGTTCAGA	250122	82318	GGGTGTGAGGAGGCTTCCTC	294709	126905	ACTCAGTCAGACTGTGGGGA
205536	37732	GTAAATTCTTAATGGTTCAG	250123	82319	AGGGTGTGAGGAGGCTTCCT	294710	126906	CACTCAGTCAGACTGTGGGG
205537	37733	AGTAAATTCTTAATGGTTCA	250124	82320	GAGGGTGTGAGGAGGCTTCC	294711	126907	CCACTCAGTCAGACTGTGGG
205538	37734	GAGTAAATTCTTAATGGTTC	250125	82321	AGAGGGTGTGAGGAGGCTTC	294712	126908	CCCACTCAGTCAGACTGTGG
205539	37735	AGAGTAAATTCTTAATGGTT	250126	82322	CAGAGGGTGTGAGGAGGCTT	294713	126909	ACCCACTCAGTCAGACTGTG
205540	37736	GAGAGTAAATTCTTAATGGT	250127	82323	ACAGAGGGTGTGAGGAGGCT	294714	126910	GACCCACTCAGTCAGACTGT
205541	37737	AGAGAGTAAATTCTTAATGG	250128	82324	GACAGAGGGTGTGAGGAGGC	294715	126911	AGACCCACTCAGTCAGACTG
205542	37738	CAGAGAGTAAATTCTTAATG	250129	82325	AGACAGAGGGTGTGAGGAGG	294716	126912	CAGACCCACTCAGTCAGACT
205543	37739	GCAGAGAGTAAATTCTTAAT	250130	82326	GAGACAGAGGGTGTGAGGAG	294717	126913	CCAGACCCACTCAGTCAGAC
205544	37740	GGCAGAGAGTAAATTCTTAA	250131	82327	TGAGACAGAGGGTGTGAGGA	294718	126914	TCCAGACCCACTCAGTCAGA
205545	37741	TGGCAGAGAGTAAATTCTTA	250132	82328	TTGAGACAGAGGGTGTGAGG	294719	126915	ATCCAGACCCACTCAGTCAG
205546	37742	CTGGCAGAGAGTAAATTCTT	250133	82329	CTTGAGACAGAGGGTGTGAG	294720	126916	TATCCAGACCCACTCAGTCA
205547	37743	CCTGGCAGAGAGTAAATTCT	250134	82330	CCTTGAGACAGAGGGTGTGA	294721	126917	CTATCCAGACCCACTCAGTC
205548	37744	GCCTGGCAGAGAGTAAATTC	250135	82331	TCCTTGAGACAGAGGGTGTG	294722	126918	CCTATCCAGACCCACTCAGT
205549	37745	TGCCTGGCAGAGAGTAAATT	250136	82332	GTCCTTGAGACAGAGGGTGT	294723	126919	CCCTATCCAGACCCACTCAG
205550	37746	GTGCCTGGCAGAGAGTAAAT	250137	82333	AGTCCTTGAGACAGAGGGTG	294724	126920	GCCCTATCCAGACCCACTCA
205551	37747	CGTGCCTGGCAGAGAGTAAA	250138	82334	GAGTCCTTGAGACAGAGGGT	294725	126921	GGCCCTATCCAGACCCACTC
205552	37748	CCGTGCCTGGCAGAGAGTAA	250139	82335	AGAGTCCTTGAGACAGAGGG	294726	126922	AGGCCCTATCCAGACCCACT
205553	37749	ACCGTGCCTGGCAGAGAGTA	250140	82336	CAGAGTCCTTGAGACAGAGG	294727	126923	CAGGCCCTATCCAGACCCAC
205554	37750	CACCGTGCCTGGCAGAGAGT	250141	82337	CCAGAGTCCTTGAGACAGAG	294728	126924	TCAGGCCCTATCCAGACCCA
205555	37751	CCACCGTGCCTGGCAGAGAG	250142	82338	GCCAGAGTCCTTGAGACAGA	294729	126925	CTCAGGCCCTATCCAGACCC
205556	37752	GCCACCGTGCCTGGCAGAGA	250143	82339	TGCCAGAGTCCTTGAGACAG	294730	126926	GCTCAGGCCCTATCCAGACC
205557	37753	AGCCACCGTGCCTGGCAGAG	250144	82340	ATGCCAGAGTCCTTGAGACA	294731	126927	TGCTCAGGCCCTATCCAGAC
205558	37754	GAGCCACCGTGCCTGGCAGA	250145	82341	AATGCCAGAGTCCTTGAGAC	294732	126928	ATGCTCAGGCCCTATCCAGA
205559	37755	TGAGCCACCGTGCCTGGCAG	250146	82342	AAATGCCAGAGTCCTTGAGA	294733	126929	AATGCTCAGGCCCTATCCAG
205560	37756	GTGAGCCACCGTGCCTGGCA	250147	82343	TAAATGCCAGAGTCCTTGAG	294734	126930	CAATGCTCAGGCCCTATCCA
205561	37757	CGTGAGCCACCGTGCCTGGC	250148	82344	CTAAATGCCAGAGTCCTTGA	294735	126931	CCAATGCTCAGGCCCTATCC
205562	37758	GCGTGAGCCACCGTGCCTGG	250149	82345	GCTAAATGCCAGAGTCCTTG	294736	126932	ACCAATGCTCAGGCCCTATC
205563	37759	GGCGTGAGCCACCGTGCCTG	250150	82346	AGCTAAATGCCAGAGTCCTT	294737	126933	CACCAATGCTCAGGCCCTAT
205564	37760	AGGCGTGAGCCACCGTGCCT	250151	82347	CAGCTAAATGCCAGAGTCCT	294738	126934	TCACCAATGCTCAGGCCCTA
205565	37761	CAGGCGTGAGCCACCGTGCC	250152	82348	CCAGCTAAATGCCAGAGTCC	294739	126935	ATCACCAATGCTCAGGCCCT
205566	37762	ACAGGCGTGAGCCACCGTGC	250153	82349	TCCAGCTAAATGCCAGAGTC	294740	126936	AATCACCAATGCTCAGGCCC
205567	37763	TACAGGCGTGAGCCACCGTG	250154	82350	GTCCAGCTAAATGCCAGAGT	294741	126937	AAATCACCAATGCTCAGGCC
205568	37764	TTACAGGCGTGAGCCACCGT	250155	82351	AGTCCAGCTAAATGCCAGAG	294742	126938	GAAATCACCAATGCTCAGGC
205569	37765	ATTACAGGCGTGAGCCACCG	250156	82352	AAGTCCAGCTAAATGCCAGA	294743	126939	GGAAATCACCAATGCTCAGG
205570	37766	GATTACAGGCGTGAGCCACC	250157	82353	CAAGTCCAGCTAAATGCCAG	294744	126940	AGGAAATCACCAATGCTCAG
205571	37767	GGATTACAGGCGTGAGCCAC	250158	82354	GCAAGTCCAGCTAAATGCCA	294745	126941	CAGGAAATCACCAATGCTCA
205572	37768	GGGATTACAGGCGTGAGCCA	250159	82355	AGCAAGTCCAGCTAAATGCC	294746	126942	CCAGGAAATCACCAATGCTC
205573	37769	TGGGATTACAGGCGTGAGCC	250160	82356	CAGCAAGTCCAGCTAAATGC	294747	126943	CCCAGGAAATCACCAATGCT
205574	37770	CTGGGATTACAGGCGTGAGC	250161	82357	ACAGCAAGTCCAGCTAAATG	294748	126944	ACCCAGGAAATCACCAATGC
205575	37771	CCTGGGATTACAGGCGTGAG	250162	82358	TACAGCAAGTCCAGCTAAAT	294749	126945	CACCCAGGAAATCACCAATG
205576	37772	TCCTGGGATTACAGGCGTGA	250163	82359	CTACAGCAAGTCCAGCTAAA	294750	126946	TCACCCAGGAAATCACCAAT
205577	37773	GTCCTGGGATTACAGGCGTG	250164	82360	GCTACAGCAAGTCCAGCTAA	294751	126947	TTCACCCAGGAAATCACCAA
205578	37774	AGTCCTGGGATTACAGGCGT	250165	82361	AGCTACAGCAAGTCCAGCTA	294752	126948	TTTCACCCAGGAAATCACCA
205579	37775	AAGTCCTGGGATTACAGGCG	250166	82362	GAGCTACAGCAAGTCCAGCT	294753	126949	CTTTCACCCAGGAAATCACC
205580	37776	AAAGTCCTGGGATTACAGGC	250167	82363	AGAGCTACAGCAAGTCCAGC	294754	126950	CCTTTCACCCAGGAAATCAC
205581	37777	CAAAGTCCTGGGATTACAGG	250168	82364	CAGAGCTACAGCAAGTCCAG	294755	126951	TCCTTTCACCCAGGAAATCA
205582	37778	CCAAAGTCCTGGGATTACAG	250169	82365	TCAGAGCTACAGCAAGTCCA	294756	126952	CTCCTTTCACCCAGGAAATC
205583	37779	CCCAAAGTCCTGGGATTACA	250170	82366	CTCAGAGCTACAGCAAGTCC	294757	126953	CCTCCTTTCACCCAGGAAAT
205584	37780	TCCCAAAGTCCTGGGATTAC	250171	82367	GCTCAGAGCTACAGCAAGTC	294758	126954	GCCTCCTTTCACCCAGGAAA
205585	37781	CTCCCAAAGTCCTGGGATTA	250172	82368	GGCTCAGAGCTACAGCAAGT	294759	126955	GGCCTCCTTTCACCCAGGAA
205586	37782	CCTCCCAAAGTCCTGGGATT	250173	82369	AGGCTCAGAGCTACAGCAAG	294760	126956	GGGCCTCCTTTCACCCAGGA
205587	37783	GCCTCCCAAAGTCCTGGGAT	250174	82370	AAGGCTCAGAGCTACAGCAA	294761	126957	GGGGCCTCCTTTCACCCAGG
205588	37784	AGCCTCCCAAAGTCCTGGGA	250175	82371	AAAGGCTCAGAGCTACAGCA	294762	126958	AGGGGCCTCCTTTCACCCAG
205589	37785	CAGCCTCCCAAAGTCCTGGG	250176	82372	GAAAGGCTCAGAGCTACAGC	294763	126959	GAGGGGCCTCCTTTCACCCA
205590	37786	TCAGCCTCCCAAAGTCCTGG	250177	82373	AGAAAGGCTCAGAGCTACAG	294764	126960	TGAGGGGCCTCCTTTCACCC
205591	37787	CTCAGCCTCCCAAAGTCCTG	250178	82374	CAGAAAGGCTCAGAGCTACA	294765	126961	GTGAGGGGCCTCCTTTCACC
205592	37788	CCTCAGCCTCCCAAAGTCCT	250179	82375	GCAGAAAGGCTCAGAGCTAC	294766	126962	TGTGAGGGGCCTCCTTTCAC
205593	37789	GCCTCAGCCTCCCAAAGTCC	250180	82376	GGCAGAAAGGCTCAGAGCTA	294767	126963	CTGTGAGGGGCCTCCTTTCA
205594	37790	TGCCTCAGCCTCCCAAAGTC	250181	82377	TGGCAGAAAGGCTCAGAGCT	294768	126964	ACTGTGAGGGGCCTCCTTTC
205595	37791	CTGCCTCAGCCTCCCAAAGT	250182	82378	ATGGCAGAAAGGCTCAGAGC	294769	126965	GACTGTGAGGGGCCTCCTTT
205596	37792	CCTGCCTCAGCCTCCCAAAG	250183	82379	AATGGCAGAAAGGCTCAGAG	294770	126966	AGACTGTGAGGGGCCTCCTT
205597	37793	GCCTGCCTCAGCCTCCCAAA	250184	82380	CAATGGCAGAAAGGCTCAGA	294771	126967	GAGACTGTGAGGGGCCTCCT
205598	37794	TGCCTGCCTCAGCCTCCCAA	250185	82381	GCAATGGCAGAAAGGCTCAG	294772	126968	AGAGACTGTGAGGGGCCTCC
205599	37795	CTGCCTGCCTCAGCCTCCCA	250186	82382	GGCAATGGCAGAAAGGCTCA	294773	126969	CAGAGACTGTGAGGGGCCTC
205600	37796	TCTGCCTGCCTCAGCCTCCC	250187	82383	TGGCAATGGCAGAAAGGCTC	294774	126970	CCAGAGACTGTGAGGGGCCT
205601	37797	ATCTGCCTGCCTCAGCCTCC	250188	82384	ATGGCAATGGCAGAAAGGCT	294775	126971	TCCAGAGACTGTGAGGGGCC
205602	37798	GATCTGCCTGCCTCAGCCTC	250189	82385	GATGGCAATGGCAGAAAGGC	294776	126972	TTCCAGAGACTGTGAGGGGC

205603	37799	TGATCTGCCTGCCTCAGCCT	250190	82386	TGATGGCAATGGCAGAAAGG	294777	126973	CTTCCAGAGACTGTGAGGGG
205604	37800	ATGATCTGCCTGCCTCAGCC	250191	82387	GTGATGGCAATGGCAGAAAG	294778	126974	GCTTCCAGAGACTGTGAGGG
205605	37801	GATGATCTGCCTGCCTCAGC	250192	82388	GGTGATGGCAATGGCAGAAA	294779	126975	AGCTTCCAGAGACTGTGAGG
205606	37802	AGATGATCTGCCTGCCTCAG	250193	82389	AGGTGATGGCAATGGCAGAA	294780	126976	AAGCTTCCAGAGACTGTGAG
205607	37803	CAGATGATCTGCCTGCCTCA	250194	82390	AAGGTGATGGCAATGGCAGA	294781	126977	GAAGCTTCCAGAGACTGTGA
205608	37804	TCAGATGATCTGCCTGCCTC	250195	82391	CAAGGTGATGGCAATGGCAG	294782	126978	AGAAGCTTCCAGAGACTGTG
205609	37805	CTCAGATGATCTGCCTGCCT	250196	82392	ACAAGGTGATGGCAATGGCA	294783	126979	GAGAAGCTTCCAGAGACTGT
205610	37806	CCTCAGATGATCTGCCTGCC	250197	82393	GACAAGGTGATGGCAATGGC	294784	126980	AGAGAAGCTTCCAGAGACTG
205611	37807	ACCTCAGATGATCTGCCTGC	250198	82394	TGACAAGGTGATGGCAATGG	294785	126981	CAGAGAAGCTTCCAGAGACT
205612	37808	GACCTCAGATGATCTGCCTG	250199	82395	CTGACAAGGTGATGGCAATG	294786	126982	ACAGAGAAGCTTCCAGAGAC
205613	37809	TGACCTCAGATGATCTGCCT	250200	82396	TCTGACAAGGTGATGGCAAT	294787	126983	CACAGAGAAGCTTCCAGAGA
205614	37810	CTGACCTCAGATGATCTGCC	250201	82397	TTCTGACAAGGTGATGGCAA	294788	126984	ACACAGAGAAGCTTCCAGAG
205615	37811	CCTGACCTCAGATGATCTGC	250202	82398	TTTCTGACAAGGTGATGGCA	294789	126985	AACACAGAGAAGCTTCCAGA
205616	37812	TCCTGACCTCAGATGATCTG	250203	82399	GTTTCTGACAAGGTGATGGC	294790	126986	TAACACAGAGAAGCTTCCAG
205617	37813	CTCCTGACCTCAGATGATCT	250204	82400	AGTTTCTGACAAGGTGATGG	294791	126987	CTAACACAGAGAAGCTTCCA
205618	37814	ACTCCTGACCTCAGATGATC	250205	82401	GAGTTTCTGACAAGGTGATG	294792	126988	CCTAACACAGAGAAGCTTCC
205619	37815	AACTCCTGACCTCAGATGAT	250206	82402	TGAGTTTCTGACAAGGTGAT	294793	126989	TCCTAACACAGAGAAGCTTC
205620	37816	GAACTCCTGACCTCAGATGA	250207	82403	CTGAGTTTCTGACAAGGTGA	294794	126990	TTCCTAACACAGAGAAGCTT
205621	37817	TGAACTCCTGACCTCAGATG	250208	82404	CCTGAGTTTCTGACAAGGTG	294795	126991	TTTCCTAACACAGAGAAGCT
205622	37818	TTGAACTCCTGACCTCAGAT	250209	82405	GCCTGAGTTTCTGACAAGGT	294796	126992	TTTTCCTAACACAGAGAAGC
205623	37819	CTTGAACTCCTGACCTCAGA	250210	82406	GGCCTGAGTTTCTGACAAGG	294797	126993	CTTTTCCTAACACAGAGAAG
205624	37820	TCTTGAACTCCTGACCTCAG	250211	82407	CGGCCTGAGTTTCTGACAAG	294798	126994	GCTTTTCCTAACACAGAGAA
205625	37821	GTCTTGAACTCCTGACCTCA	250212	82408	TCGGCCTGAGTTTCTGACAA	294799	126995	AGCTTTTCCTAACACAGAGA
205626	37822	GGTCTTGAACTCCTGACCTC	250213	82409	TTCGGCCTGAGTTTCTGACA	294800	126996	GAGCTTTTCCTAACACAGAG
205627	37823	TGGTCTTGAACTCCTGACCT	250214	82410	ATTCGGCCTGAGTTTCTGAC	294801	126997	AGAGCTTTTCCTAACACAGA
205628	37824	CTGGTCTTGAACTCCTGACC	250215	82411	GATTCGGCCTGAGTTTCTGA	294802	126998	CAGAGCTTTTCCTAACACAG
205629	37825	GCTGGTCTTGAACTCCTGAC	250216	82412	AGATTCGGCCTGAGTTTCTG	294803	126999	CCAGAGCTTTTCCTAACACA
205630	37826	GGCTGGTCTTGAACTCCTGA	250217	82413	CAGATTCGGCCTGAGTTTCT	294804	127000	CCCAGAGCTTTTCCTAACAC
205631	37827	AGGCTGGTCTTGAACTCCTG	250218	82414	GCAGATTCGGCCTGAGTTTC	294805	127001	GCCCAGAGCTTTTCCTAACA
205632	37828	CAGGCTGGTCTTGAACTCCT	250219	82415	TGCAGATTCGGCCTGAGTTT	294806	127002	AGCCCAGAGCTTTTCCTAAC
205633	37829	CCAGGCTGGTCTTGAACTCC	250220	82416	GTGCAGATTCGGCCTGAGTT	294807	127003	AAGCCCAGAGCTTTTCCTAA
205634	37830	GCCAGGCTGGTCTTGAACTC	250221	82417	AGTGCAGATTCGGCCTGAGT	294808	127004	CAAGCCCAGAGCTTTTCCTA
205635	37831	GGCCAGGCTGGTCTTGAACT	250222	82418	GAGTGCAGATTCGGCCTGAG	294809	127005	TCAAGCCCAGAGCTTTTCCT
205636	37832	TGGCCAGGCTGGTCTTGAAC	250223	82419	TGAGTGCAGATTCGGCCTGA	294810	127006	GTCAAGCCCAGAGCTTTTCC
205637	37833	TTGGCCAGGCTGGTCTTGAA	250224	82420	CTGAGTGCAGATTCGGCCTG	294811	127007	AGTCAAGCCCAGAGCTTTTC
205638	37834	GTTGGCCAGGCTGGTCTTGA	250225	82421	TCTGAGTGCAGATTCGGCCT	294812	127008	GAGTCAAGCCCAGAGCTTTT
205639	37835	TGTTGGCCAGGCTGGTCTTG	250226	82422	CTCTGAGTGCAGATTCGGCC	294813	127009	AGAGTCAAGCCCAGAGCTTT
205640	37836	ATGTTGGCCAGGCTGGTCTT	250227	82423	ACTCTGAGTGCAGATTCGGC	294814	127010	CAGAGTCAAGCCCAGAGCTT
205641	37837	CATGTTGGCCAGGCTGGTCT	250228	82424	AACTCTGAGTGCAGATTCGG	294815	127011	GCAGAGTCAAGCCCAGAGCT
205642	37838	CCATGTTGGCCAGGCTGGTC	250229	82425	CAACTCTGAGTGCAGATTCG	294816	127012	AGCAGAGTCAAGCCCAGAGC
205643	37839	ACCATGTTGGCCAGGCTGGT	250230	82426	ACAACTCTGAGTGCAGATTC	294817	127013	AAGCAGAGTCAAGCCCAGAG
205644	37840	CACCATGTTGGCCAGGCTGG	250231	82427	CACAACTCTGAGTGCAGATT	294818	127014	AAAGCAGAGTCAAGCCCAGA
205645	37841	TCACCATGTTGGCCAGGCTG	250232	82428	GCACAACTCTGAGTGCAGAT	294819	127015	CAAAGCAGAGTCAAGCCCAG
205646	37842	TTCACCATGTTGGCCAGGCT	250233	82429	GGCACAACTCTGAGTGCAGA	294820	127016	TCAAAGCAGAGTCAAGCCCA
205647	37843	TTTCACCATGTTGGCCAGGC	250234	82430	GGGCACAACTCTGAGTGCAG	294821	127017	TTCAAAGCAGAGTCAAGCCC
205648	37844	GTTTCACCATGTTGGCCAGG	250235	82431	TGGGCACAACTCTGAGTGCA	294822	127018	TTTCAAAGCAGAGTCAAGCC
205649	37845	AGTTTCACCATGTTGGCCAG	250236	82432	CTGGGCACAACTCTGAGTGC	294823	127019	CTTTCAAAGCAGAGTCAAGC
205650	37846	AAGTTTCACCATGTTGGCCA	250237	82433	CCTGGGCACAACTCTGAGTG	294824	127020	ACTTTCAAAGCAGAGTCAAG
205651	37847	GAAGTTTCACCATGTTGGCC	250238	82434	GCCTGGGCACAACTCTGAGT	294825	127021	GACTTTCAAAGCAGAGTCAA
205652	37848	TGAAGTTTCACCATGTTGGC	250239	82435	TGCCTGGGCACAACTCTGAG	294826	127022	TGACTTTCAAAGCAGAGTCA
205653	37849	ATGAAGTTTCACCATGTTGG	250240	82436	CTGCCTGGGCACAACTCTGA	294827	127023	TTGACTTTCAAAGCAGAGTC
205654	37850	GATGAAGTTTCACCATGTTG	250241	82437	ACTGCCTGGGCACAACTCTG	294828	127024	CTTGACTTTCAAAGCAGAGT
205655	37851	AGATGAAGTTTCACCATGTT	250242	82438	AACTGCCTGGGCACAACTCT	294829	127025	TCTTGACTTTCAAAGCAGAG
205656	37852	GAGATGAAGTTTCACCATGT	250243	82439	CAACTGCCTGGGCACAACTC	294830	127026	ATCTTGACTTTCAAAGCAGA
205657	37853	AGAGATGAAGTTTCACCATG	250244	82440	TCAACTGCCTGGGCACAACT	294831	127027	GATCTTGACTTTCAAAGCAG
205658	37854	TAGAGATGAAGTTTCACCAT	250245	82441	CTCAACTGCCTGGGCACAAC	294832	127028	GGATCTTGACTTTCAAAGCA
205659	37855	GTAGAGATGAAGTTTCACCA	250246	82442	GCTCAACTGCCTGGGCACAA	294833	127029	CGGATCTTGACTTTCAAAGC
205660	37856	TGTAGAGATGAAGTTTCACC	250247	82443	GGCTCAACTGCCTGGGCACA	294834	127030	GCGGATCTTGACTTTCAAAG
205661	37857	TTGTAGAGATGAAGTTTCAC	250248	82444	TGGCTCAACTGCCTGGGCAC	294835	127031	TGCGGATCTTGACTTTCAAA
205662	37858	TTTGTAGAGATGAAGTTTCA	250249	82445	TTGGCTCAACTGCCTGGGCA	294836	127032	TTGCGGATCTTGACTTTCAA
205663	37859	TTTTGTAGAGATGAAGTTTC	250250	82446	GTTGGCTCAACTGCCTGGGC	294837	127033	TTTGCGGATCTTGACTTTCA
205664	37860	TTTTTGTAGAGATGAAGTTT	250251	82447	TGTTGGCTCAACTGCCTGGG	294838	127034	ATTTGCGGATCTTGACTTTC
205665	37861	ATTTTTGTAGAGATGAAGTT	250252	82448	GTGTTGGCTCAACTGCCTGG	294839	127035	GATTTGCGGATCTTGACTTT
205666	37862	TATTTTTGTAGAGATGAAGT	250253	82449	AGTGTTGGCTCAACTGCCTG	294840	127036	GGATTTGCGGATCTTGACTT
205667	37863	GTATTTTTGTAGAGATGAAG	250254	82450	AAGTGTTGGCTCAACTGCCT	294841	127037	AGGATTTGCGGATCTTGACT
205668	37864	TGTATTTTTGTAGAGATGAA	250255	82451	CAAGTGTTGGCTCAACTGCC	294842	127038	GAGGATTTGCGGATCTTGAC
205669	37865	TTGTATTTTTGTAGAGATGA	250256	82452	GCAAGTGTTGGCTCAACTGC	294843	127039	AGAGGATTTGCGGATCTTGA
205670	37866	TTTGTATTTTTGTAGAGATG	250257	82453	AGCAAGTGTTGGCTCAACTG	294844	127040	GAGAGGATTTGCGGATCTTG
205671	37867	TTTTGTATTTTTGTAGAGAT	250258	82454	GAGCAAGTGTTGGCTCAACT	294845	127041	TGAGAGGATTTGCGGATCTT
205672	37868	TTTTTGTATTTTTGTAGAGA	250259	82455	TGAGCAAGTGTTGGCTCAAC	294846	127042	CTGAGAGGATTTGCGGATCT
205673	37869	ATTTTTGTATTTTTGTAGAG	250260	82456	CTGAGCAAGTGTTGGCTCAA	294847	127043	GCTGAGAGGATTTGCGGATC
205674	37870	AATTTTTGTATTTTTGTAGA	250261	82457	GCTGAGCAAGTGTTGGCTCA	294848	127044	GGCTGAGAGGATTTGCGGAT

205675	37871	TAATTTTTGTATTTTTGTAG	250262	82458	CGCTGAGCAAGTGTTGGCTC	294849	127045	AGGCTGAGAGGATTTGCGGA
205676	37872	CTAATTTTTGTATTTTTGTA	250263	82459	TCGCTGAGCAAGTGTTGGCT	294850	127046	GAGGCTGAGAGGATTTGCGG
205677	37873	GCTAATTTTTGTATTTTTGT	250264	82460	ATCGCTGAGCAAGTGTTGGC	294851	127047	TGAGGCTGAGAGGATTTGCG
205678	37874	GGCTAATTTTTGTATTTTTG	250265	82461	TATCGCTGAGCAAGTGTTGG	294852	127048	CTGAGGCTGAGAGGATTTGC
205679	37875	TGGCTAATTTTTGTATTTTT	250266	82462	ATATCGCTGAGCAAGTGTTG	294853	127049	ACTGAGGCTGAGAGGATTTG
205680	37876	CTGGCTAATTTTTGTATTTT	250267	82463	AATATCGCTGAGCAAGTGTT	294854	127050	AACTGAGGCTGAGAGGATTT
205681	37877	CCTGGCTAATTTTTGTATTT	250268	82464	CAATATCGCTGAGCAAGTGT	294855	127051	AAACTGAGGCTGAGAGGATT
205682	37878	GCCTGGCTAATTTTTGTATT	250269	82465	ACAATATCGCTGAGCAAGTG	294856	127052	GAAACTGAGGCTGAGAGGAT
205683	37879	TGCCTGGCTAATTTTTGTAT	250270	82466	GACAATATCGCTGAGCAAGT	294857	127053	AGAAACTGAGGCTGAGAGGA
205684	37880	ATGCCTGGCTAATTTTTGTA	250271	82467	TGACAATATCGCTGAGCAAG	294858	127054	GAGAAACTGAGGCTGAGAGG
205685	37881	CATGCCTGGCTAATTTTTGT	250272	82468	GTGACAATATCGCTGAGCAA	294859	127055	GGAGAAACTGAGGCTGAGAG
205686	37882	TCATGCCTGGCTAATTTTTG	250273	82469	TGTGACAATATCGCTGAGCA	294860	127056	AGGAGAAACTGAGGCTGAGA
205687	37883	ATCATGCCTGGCTAATTTTT	250274	82470	ATGTGACAATATCGCTGAGC	294861	127057	AAGGAGAAACTGAGGCTGAG
205688	37884	CATCATGCCTGGCTAATTTT	250275	82471	CATGTGACAATATCGCTGAG	294862	127058	GAAGGAGAAACTGAGGCTGA
205689	37885	CCATCATGCCTGGCTAATTT	250276	82472	TCATGTGACAATATCGCTGA	294863	127059	TGAAGGAGAAACTGAGGCTG
205690	37886	ACCATCATGCCTGGCTAATT	250277	82473	GTCATGTGACAATATCGCTG	294864	127060	CTGAAGGAGAAACTGAGGCT
205691	37887	CACCATCATGCCTGGCTAAT	250278	82474	TGTCATGTGACAATATCGCT	294865	127061	GCTGAAGGAGAAACTGAGGC
205692	37888	CCACCATCATGCCTGGCTAA	250279	82475	TTGTCATGTGACAATATCGC	294866	127062	TGCTGAAGGAGAAACTGAGG
205693	37889	CCCACCATCATGCCTGGCTA	250280	82476	CTTGTCATGTGACAATATCG	294867	127063	TTGCTGAAGGAGAAACTGAG
205694	37890	ACCCACCATCATGCCTGGCT	250281	82477	CCTTGTCATGTGACAATATC	294868	127064	CTTGCTGAAGGAGAAACTGA
205695	37891	CACCCACCATCATGCCTGGC	250282	82478	GCCTTGTCATGTGACAATAT	294869	127065	TCTTGCTGAAGGAGAAACTG
205696	37892	GCACCCACCATCATGCCTGG	250283	82479	TGCCTTGTCATGTGACAATA	294870	127066	ATCTTGCTGAAGGAGAAACT
205697	37893	GGCACCCACCATCATGCCTG	250284	82480	GTGCCTTGTCATGTGACAAT	294871	127067	CATCTTGCTGAAGGAGAAAC
205698	37894	AGGCACCCACCATCATGCCT	250285	82481	AGTGCCTTGTCATGTGACAA	294872	127068	TCATCTTGCTGAAGGAGAAA
205699	37895	CAGGCACCCACCATCATGCC	250286	82482	CAGTGCCTTGTCATGTGACA	294873	127069	TTCATCTTGCTGAAGGAGAA
205700	37896	ACAGGCACCCACCATCATGC	250287	82483	ACAGTGCCTTGTCATGTGAC	294874	127070	TTTCATCTTGCTGAAGGAGA
205701	37897	TACAGGCACCCACCATCATG	250288	82484	GACAGTGCCTTGTCATGTGA	294875	127071	ATTTCATCTTGCTGAAGGAG
205702	37898	TTACAGGCACCCACCATCAT	250289	82485	TGACAGTGCCTTGTCATGTG	294876	127072	CATTTCATCTTGCTGAAGGA
205703	37899	ATTACAGGCACCCACCATCA	250290	82486	GTGACAGTGCCTTGTCATGT	294877	127073	CCATTTCATCTTGCTGAAGG
205704	37900	GATTACAGGCACCCACCATC	250291	82487	GGTGACAGTGCCTTGTCATG	294878	127074	TCCATTTCATCTTGCTGAAG
205705	37901	GGATTACAGGCACCCACCAT	250292	82488	TGGTGACAGTGCCTTGTCAT	294879	127075	TTCCATTTCATCTTGCTGAA
205706	37902	GGGATTACAGGCACCCACCA	250293	82489	GTGGTGACAGTGCCTTGTCA	294880	127076	TTTCCATTTCATCTTGCTGA
205707	37903	TGGGATTACAGGCACCCACC	250294	82490	AGTGGTGACAGTGCCTTGTC	294881	127077	ATTTCCATTTCATCTTGCTG
205708	37904	CTGGGATTACAGGCACCCAC	250295	82491	CAGTGGTGACAGTGCCTTGT	294882	127078	CATTTCCATTTCATCTTGCT
205709	37905	GCTGGGATTACAGGCACCCA	250296	82492	CCAGTGGTGACAGTGCCTTG	294883	127079	GCATTTCCATTTCATCTTGC
205710	37906	AGCTGGGATTACAGGCACCC	250297	82493	CCCAGTGGTGACAGTGCCTT	294884	127080	AGCATTTCCATTTCATCTTG
205711	37907	TAGCTGGGATTACAGGCACC	250298	82494	GCCCAGTGGTGACAGTGCCT	294885	127081	CAGCATTTCCATTTCATCTT
205712	37908	GTAGCTGGGATTACAGGCAC	250299	82495	TGCCCAGTGGTGACAGTGCC	294886	127082	ACAGCATTTCCATTTCATCT
205713	37909	AGTAGCTGGGATTACAGGCA	250300	82496	ATGCCCAGTGGTGACAGTGC	294887	127083	TACAGCATTTCCATTTCATC
205714	37910	GAGTAGCTGGGATTACAGGC	250301	82497	GATGCCCAGTGGTGACAGTG	294888	127084	GTACAGCATTTCCATTTCAT
205715	37911	CGAGTAGCTGGGATTACAGG	250302	82498	CGATGCCCAGTGGTGACAGT	294889	127085	GGTACAGCATTTCCATTTCA
205716	37912	CCGAGTAGCTGGGATTACAG	250303	82499	ACGATGCCCAGTGGTGACAG	294890	127086	AGGTACAGCATTTCCATTTC
205717	37913	CCCGAGTAGCTGGGATTACA	250304	82500	CACGATGCCCAGTGGTGACA	294891	127087	TAGGTACAGCATTTCCATTT
205718	37914	TCCCGAGTAGCTGGGATTAC	250305	82501	CCACGATGCCCAGTGGTGAC	294892	127088	GTAGGTACAGCATTTCCATT
205719	37915	CTCCCGAGTAGCTGGGATTA	250306	82502	CCCACGATGCCCAGTGGTGA	294893	127089	CGTAGGTACAGCATTTCCAT
205720	37916	CCTCCCGAGTAGCTGGGATT	250307	82503	ACCCACGATGCCCAGTGGTG	294894	127090	ACGTAGGTACAGCATTTCCA
205721	37917	GCCTCCCGAGTAGCTGGGAT	250308	82504	TACCCACGATGCCCAGTGGT	294895	127091	GACGTAGGTACAGCATTTCC
205722	37918	AGCCTCCCGAGTAGCTGGGA	250309	82505	CTACCCACGATGCCCAGTGG	294896	127092	GGACGTAGGTACAGCATTTC
205723	37919	CAGCCTCCCGAGTAGCTGGG	250310	82506	GCTACCCACGATGCCCAGTG	294897	127093	GGGACGTAGGTACAGCATTT
205724	37920	TCAGCCTCCCGAGTAGCTGG	250311	82507	CGCTACCCACGATGCCCAGT	294898	127094	CGGGACGTAGGTACAGCATT
205725	37921	CTCAGCCTCCCGAGTAGCTG	250312	82508	GCGCTACCCACGATGCCCAG	294899	127095	CCGGGACGTAGGTACAGCAT
205726	37922	CCTCAGCCTCCCGAGTAGCT	250313	82509	TGCGCTACCCACGATGCCCA	294900	127096	CCCGGGACGTAGGTACAGCA
205727	37923	GCCTCAGCCTCCCGAGTAGC	250314	82510	CTGCGCTACCCACGATGCCC	294901	127097	CCCCGGGACGTAGGTACAGC
205728	37924	TGCCTCAGCCTCCCGAGTAG	250315	82511	ACTGCGCTACCCACGATGCC	294902	127098	ACCCCGGGACGTAGGTACAG
205729	37925	CTGCCTCAGCCTCCCGAGTA	250316	82512	CACTGCGCTACCCACGATGC	294903	127099	CACCCCGGGACGTAGGTACA
205730	37926	CCTGCCTCAGCCTCCCGAGT	250317	82513	ACACTGCGCTACCCACGATG	294904	127100	CCACCCCGGGACGTAGGTAC
205731	37927	TCCTGCCTCAGCCTCCCGAG	250318	82514	GACACTGCGCTACCCACGAT	294905	127101	ACCACCCCGGGACGTAGGTA
205732	37928	CTCCTGCCTCAGCCTCCCGA	250319	82515	CGACACTGCGCTACCCACGA	294906	127102	AACCACCCCGGGACGTAGGT
205733	37929	TCTCCTGCCTCAGCCTCCCG	250320	82516	CCGACACTGCGCTACCCACG	294907	127103	CAACCACCCCGGGACGTAGG
205734	37930	TTCTCCTGCCTCAGCCTCCC	250321	82517	GCCGACACTGCGCTACCCAC	294908	127104	ACAACCACCCCGGGACGTAG
205735	37931	ATTCTCCTGCCTCAGCCTCC	250322	82518	AGCCGACACTGCGCTACCCA	294909	127105	CACAACCACCCCGGGACGTA
205736	37932	GATTCTCCTGCCTCAGCCTC	250323	82519	CAGCCGACACTGCGCTACCC	294910	127106	TCACAACCACCCCGGGACGT
205737	37933	CGATTCTCCTGCCTCAGCCT	250324	82520	CCAGCCGACACTGCGCTACC	294911	127107	CTCACAACCACCCCGGGACG
205738	37934	GCGATTCTCCTGCCTCAGCC	250325	82521	TCCAGCCGACACTGCGCTAC	294912	127108	TCTCACAACCACCCCGGGAC
205739	37935	AGCGATTCTCCTGCCTCAGC	250326	82522	ATCCAGCCGACACTGCGCTA	294913	127109	GTCTCACAACCACCCCGGGA
205740	37936	AAGCGATTCTCCTGCCTCAG	250327	82523	CATCCAGCCGACACTGCGCT	294914	127110	GGTCTCACAACCACCCCGGG
205741	37937	CAAGCGATTCTCCTGCCTCA	250328	82524	CCATCCAGCCGACACTGCGC	294915	127111	GGGTCTCACAACCACCCCGG
205742	37938	GCAAGCGATTCTCCTGCCTC	250329	82525	TCCATCCAGCCGACACTGCG	294916	127112	TGGGTCTCACAACCACCCCG
205743	37939	TGCAAGCGATTCTCCTGCCT	250330	82526	GTCCATCCAGCCGACACTGC	294917	127113	TTGGGTCTCACAACCACCCC
205744	37940	GTGCAAGCGATTCTCCTGCC	250331	82527	GGTCCATCCAGCCGACACTG	294918	127114	TTTGGGTCTCACAACCACCC
205745	37941	GGTGCAAGCGATTCTCCTGC	250332	82528	GGGTCCATCCAGCCGACACT	294919	127115	TTTTGGGTCTCACAACCACC
205746	37942	AGGTGCAAGCGATTCTCCTG	250333	82529	CGGGTCCATCCAGCCGACAC	294920	127116	TTTTTGGGTCTCACAACCAC

205747	37943	CAGGTGCAAGCGATTCTCCT	250334	82530	CCGGGTCCATCCAGCCGACA	294921	127117	TTTTTTGGGTCTCACAACCA
205748	37944	TCAGGTGCAAGCGATTCTCC	250335	82531	TCCGGGTCCATCCAGCCGAC	294922	127118	CTTTTTTGGGTCTCACAACC
205749	37945	CTCAGGTGCAAGCGATTCTC	250336	82532	CTCCGGGTCCATCCAGCCGA	294923	127119	TCTTTTTTGGGTCTCACAAC
205750	37946	TCTCAGGTGCAAGCGATTCT	250337	82533	CCTCCGGGTCCATCCAGCCG	294924	127120	GTCTTTTTTGGGTCTCACAA
205751	37947	CTCTCAGGTGCAAGCGATTC	250338	82534	CCCTCCGGGTCCATCCAGCC	294925	127121	TGTCTTTTTTGGGTCTCACA
205752	37948	CCTCTCAGGTGCAAGCGATT	250339	82535	ACCCTCCGGGTCCATCCAGC	294926	127122	TTGTCTTTTTTGGGTCTCAC
205753	37949	ACCTCTCAGGTGCAAGCGAT	250340	82536	CACCCTCCGGGTCCATCCAG	294927	127123	ATTGTCTTTTTTGGGTCTCA
205754	37950	CACCTCTCAGGTGCAAGCGA	250341	82537	ACACCCTCCGGGTCCATCCA	294928	127124	CATTGTCTTTTTTGGGTCTC
205755	37951	CCACCTCTCAGGTGCAAGCG	250342	82538	GACACCCTCCGGGTCCATCC	294929	127125	ACATTGTCTTTTTTGGGTCT
205756	37952	TCCACCTCTCAGGTGCAAGC	250343	82539	AGACACCCTCCGGGTCCATC	294930	127126	AACATTGTCTTTTTTGGGTC
205757	37953	CTCCACCTCTCAGGTGCAAG	250344	82540	CAGACACCCTCCGGGTCCAT	294931	127127	GAACATTGTCTTTTTTGGGT
205758	37954	CCTCCACCTCTCAGGTGCAA	250345	82541	ACAGACACCCTCCGGGTCCA	294932	127128	AGAACATTGTCTTTTTTGGG
205759	37955	ACCTCCACCTCTCAGGTGCA	250346	82542	CACAGACACCCTCCGGGTCC	294933	127129	CAGAACATTGTCTTTTTTGG
205760	37956	AACCTCCACCTCTCAGGTGC	250347	82543	ACACAGACACCCTCCGGGTC	294934	127130	CCAGAACATTGTCTTTTTTG
205761	37957	CAACCTCCACCTCTCAGGTG	250348	82544	GACACAGACACCCTCCGGGT	294935	127131	TCCAGAACATTGTCTTTTTT
205762	37958	GCAACCTCCACCTCTCAGGT	250349	82545	TGACACAGACACCCTCCGGG	294936	127132	TTCCAGAACATTGTCTTTTT
205763	37959	TGCAACCTCCACCTCTCAGG	250350	82546	ATGACACAGACACCCTCCGG	294937	127133	CTTCCAGAACATTGTCTTTT
205764	37960	CTGCAACCTCCACCTCTCAG	250351	82547	CATGACACAGACACCCTCCG	294938	127134	CCTTCCAGAACATTGTCTTT
205765	37961	ACTGCAACCTCCACCTCTCA	250352	82548	GCATGACACAGACACCCTCC	294939	127135	ACCTTCCAGAACATTGTCTT
205766	37962	CACTGCAACCTCCACCTCTC	250353	82549	AGCATGACACAGACACCCTC	294940	127136	AACCTTCCAGAACATTGTCT
205767	37963	TCACTGCAACCTCCACCTCT	250354	82550	TAGCATGACACAGACACCCT	294941	127137	GAACCTTCCAGAACATTGTC
205768	37964	CTCACTGCAACCTCCACCTC	250355	82551	CTAGCATGACACAGACACCC	294942	127138	GGAACCTTCCAGAACATTGT
205769	37965	GCTCACTGCAACCTCCACCT	250356	82552	ACTAGCATGACACAGACACC	294943	127139	AGGAACCTTCCAGAACATTG
205770	37966	GGCTCACTGCAACCTCCACC	250357	82553	CACTAGCATGACACAGACAC	294944	127140	CAGGAACCTTCCAGAACATT
205771	37967	CGGCTCACTGCAACCTCCAC	250358	82554	GCACTAGCATGACACAGACA	294945	127141	CCAGGAACCTTCCAGAACAT
205772	37968	TCGGCTCACTGCAACCTCCA	250359	82555	AGCACTAGCATGACACAGAC	294946	127142	ACCAGGAACCTTCCAGAACA
205773	37969	CTCGGCTCACTGCAACCTCC	250360	82556	TAGCACTAGCATGACACAGA	294947	127143	CACCAGGAACCTTCCAGAAC
205774	37970	TCTCGGCTCACTGCAACCTC	250361	82557	CTAGCACTAGCATGACACAG	294948	127144	GCACCAGGAACCTTCCAGAA
205775	37971	ATCTCGGCTCACTGCAACCT	250362	82558	ACTAGCACTAGCATGACACA	294949	127145	CGCACCAGGAACCTTCCAGA
205776	37972	GATCTCGGCTCACTGCAACC	250363	82559	CACTAGCACTAGCATGACAC	294950	127146	ACGCACCAGGAACCTTCCAG
205777	37973	AGATCTCGGCTCACTGCAAC	250364	82560	TCACTAGCACTAGCATGACA	294951	127147	AACGCACCAGGAACCTTCCA
205778	37974	TAGATCTCGGCTCACTGCAA	250365	82561	ATCACTAGCACTAGCATGAC	294952	127148	CAACGCACCAGGAACCTTCC
205779	37975	ATAGATCTCGGCTCACTGCA	250366	82562	CATCACTAGCACTAGCATGA	294953	127149	GCAACGCACCAGGAACCTTC
205780	37976	GATAGATCTCGGCTCACTGC	250367	82563	CCATCACTAGCACTAGCATG	294954	127150	TGCAACGCACCAGGAACCTT
205781	37977	AGATAGATCTCGGCTCACTG	250368	82564	CCCATCACTAGCACTAGCAT	294955	127151	CTGCAACGCACCAGGAACCT
205782	37978	CAGATAGATCTCGGCTCACT	250369	82565	TCCCATCACTAGCACTAGCA	294956	127152	ACTGCAACGCACCAGGAACC
205783	37979	GCAGATAGATCTCGGCTCAC	250370	82566	CTCCCATCACTAGCACTAGC	294957	127153	GACTGCAACGCACCAGGAAC
205784	37980	TGCAGATAGATCTCGGCTCA	250371	82567	GCTCCCATCACTAGCACTAG	294958	127154	GGACTGCAACGCACCAGGAA
205785	37981	GTGCAGATAGATCTCGGCTC	250372	82568	GGCTCCCATCACTAGCACTA	294959	127155	AGGACTGCAACGCACCAGGA
205786	37982	GGTGCAGATAGATCTCGGCT	250373	82569	GGGCTCCCATCACTAGCACT	294960	127156	GAGGACTGCAACGCACCAGG
205787	37983	TGGTGCAGATAGATCTCGGC	250374	82570	GGGGCTCCCATCACTAGCAC	294961	127157	AGAGGACTGCAACGCACCAG
205788	37984	ATGGTGCAGATAGATCTCGG	250375	82571	CGGGGCTCCCATCACTAGCA	294962	127158	TAGAGGACTGCAACGCACCA
205789	37985	AATGGTGCAGATAGATCTCG	250376	82572	ACGGGGCTCCCATCACTAGC	294963	127159	TTAGAGGACTGCAACGCACC
205790	37986	CAATGGTGCAGATAGATCTC	250377	82573	CACGGGGCTCCCATCACTAG	294964	127160	CTTAGAGGACTGCAACGCAC
205791	37987	GCAATGGTGCAGATAGATCT	250378	82574	TCACGGGGCTCCCATCACTA	294965	127161	TCTTAGAGGACTGCAACGCA
205792	37988	TGCAATGGTGCAGATAGATC	250379	82575	CTCACGGGGCTCCCATCACT	294966	127162	TTCTTAGAGGACTGCAACGC
205793	37989	GTGCAATGGTGCAGATAGAT	250380	82576	GCTCACGGGGCTCCCATCAC	294967	127163	GTTCTTAGAGGACTGCAACG
205794	37990	AGTGCAATGGTGCAGATAGA	250381	82577	GGCTCACGGGGCTCCCATCA	294968	127164	GGTTCTTAGAGGACTGCAAC
205795	37991	AAGTGCAATGGTGCAGATAG	250382	82578	GGGCTCACGGGGCTCCCATC	294969	127165	AGGTTCTTAGAGGACTGCAA
205796	37992	GAAGTGCAATGGTGCAGATA	250383	82579	TGGGCTCACGGGGCTCCCAT	294970	127166	CAGGTTCTTAGAGGACTGCA
205797	37993	TGAAGTGCAATGGTGCAGAT	250384	82580	ATGGGCTCACGGGGCTCCCA	294971	127167	TCAGGTTCTTAGAGGACTGC
205798	37994	CTGAAGTGCAATGGTGCAGA	250385	82581	AATGGGCTCACGGGGCTCCC	294972	127168	CTCAGGTTCTTAGAGGACTG
205799	37995	GCTGAAGTGCAATGGTGCAG	250386	82582	CAATGGGCTCACGGGGCTCC	294973	127169	ACTCAGGTTCTTAGAGGACT
205800	37996	GGCTGAAGTGCAATGGTGCA	250387	82583	GCAATGGGCTCACGGGGCTC	294974	127170	AACTCAGGTTCTTAGAGGAC
205801	37997	AGGCTGAAGTGCAATGGTGC	250388	82584	GGCAATGGGCTCACGGGGCT	294975	127171	TAACTCAGGTTCTTAGAGGA
205802	37998	CAGGCTGAAGTGCAATGGTG	250389	82585	GGGCAATGGGCTCACGGGGC	294976	127172	CTAACTCAGGTTCTTAGAGG
205803	37999	CCAGGCTGAAGTGCAATGGT	250390	82586	CGGGCAATGGGCTCACGGGG	294977	127173	TCTAACTCAGGTTCTTAGAG
205804	38000	CCCAGGCTGAAGTGCAATGG	250391	82587	GCGGGCAATGGGCTCACGGG	294978	127174	CTCTAACTCAGGTTCTTAGA
205805	38001	TCCCAGGCTGAAGTGCAATG	250392	82588	GGCGGGCAATGGGCTCACGG	294979	127175	GCTCTAACTCAGGTTCTTAG
205806	38002	CTCCCAGGCTGAAGTGCAAT	250393	82589	GGGCGGGCAATGGGCTCACG	294980	127176	GGCTCTAACTCAGGTTCTTA
205807	38003	TCTCCCAGGCTGAAGTGCAA	250394	82590	AGGGCGGGCAATGGGCTCAC	294981	127177	TGGCTCTAACTCAGGTTCTT
205808	38004	GTCTCCCAGGCTGAAGTGCA	250395	82591	GAGGGCGGGCAATGGGCTCA	294982	127178	GTGGCTCTAACTCAGGTTCT
205809	38005	TGTCTCCCAGGCTGAAGTGC	250396	82592	GGAGGGCGGGCAATGGGCTC	294983	127179	CGTGGCTCTAACTCAGGTTC
205810	38006	CTGTCTCCCAGGCTGAAGTG	250397	82593	GGGAGGGCGGGCAATGGGCT	294984	127180	GCGTGGCTCTAACTCAGGTT
205811	38007	TCTGTCTCCCAGGCTGAAGT	250398	82594	TGGGAGGGCGGGCAATGGGC	294985	127181	AGCGTGGCTCTAACTCAGGT
205812	38008	CTCTGTCTCCCAGGCTGAAG	250399	82595	ATGGGAGGGCGGGCAATGGG	294986	127182	CAGCGTGGCTCTAACTCAGG
205813	38009	ACTCTGTCTCCCAGGCTGAA	250400	82596	CATGGGAGGGCGGGCAATGG	294987	127183	TCAGCGTGGCTCTAACTCAG
205814	38010	TACTCTGTCTCCCAGGCTGA	250401	82597	GCATGGGAGGGCGGGCAATG	294988	127184	CTCAGCGTGGCTCTAACTCA
205815	38011	TTACTCTGTCTCCCAGGCTG	250402	82598	GGCATGGGAGGGCGGGCAAT	294989	127185	ACTCAGCGTGGCTCTAACTC
205816	38012	CTTACTCTGTCTCCCAGGCT	250403	82599	GGGCATGGGAGGGCGGGCAA	294990	127186	GACTCAGCGTGGCTCTAACT
205817	38013	TCTTACTCTGTCTCCCAGGC	250404	82600	AGGGCATGGGAGGGCGGGCA	294991	127187	AGACTCAGCGTGGCTCTAAC
205818	38014	GTCTTACTCTGTCTCCCAGG	250405	82601	GAGGGCATGGGAGGGCGGGC	294992	127188	GAGACTCAGCGTGGCTCTAA

205819	38015	AGTCTTACTCTGTCTCCCAG	250406	82602	TGAGGGCATGGGAGGGCGGG	294993	127189	TGAGACTCAGCGTGGCTCTA
205820	38016	GAGTCTTACTCTGTCTCCCA	250407	82603	CTGAGGGCATGGGAGGGCGG	294994	127190	CTGAGACTCAGCGTGGCTCT
205821	38017	GGAGTCTTACTCTGTCTCCC	250408	82604	GCTGAGGGCATGGGAGGGCG	294995	127191	GCTGAGACTCAGCGTGGCTC
205822	38018	TGGAGTCTTACTCTGTCTCC	250409	82605	TGCTGAGGGCATGGGAGGGC	294996	127192	AGCTGAGACTCAGCGTGGCT
205823	38019	ATGGAGTCTTACTCTGTCTC	250410	82606	CTGCTGAGGGCATGGGAGGG	294997	127193	AAGCTGAGACTCAGCGTGGC
205824	38020	GATGGAGTCTTACTCTGTCT	250411	82607	GCTGCTGAGGGCATGGGAGG	294998	127194	GAAGCTGAGACTCAGCGTGG
205825	38021	AGATGGAGTCTTACTCTGTC	250412	82608	AGCTGCTGAGGGCATGGGAG	294999	127195	AGAAGCTGAGACTCAGCGTG
205826	38022	GAGATGGAGTCTTACTCTGT	250413	82609	CAGCTGCTGAGGGCATGGGA	295000	127196	AAGAAGCTGAGACTCAGCGT
205827	38023	TGAGATGGAGTCTTACTCTG	250414	82610	GCAGCTGCTGAGGGCATGGG	295001	127197	CAAGAAGCTGAGACTCAGCG
205828	38024	TTGAGATGGAGTCTTACTCT	250415	82611	GGCAGCTGCTGAGGGCATGG	295002	127198	CCAAGAAGCTGAGACTCAGC
205829	38025	TTTGAGATGGAGTCTTACTC	250416	82612	AGGCAGCTGCTGAGGGCATG	295003	127199	GCCAAGAAGCTGAGACTCAG
205830	38026	TTTTGAGATGGAGTCTTACT	250417	82613	CAGGCAGCTGCTGAGGGCAT	295004	127200	AGCCAAGAAGCTGAGACTCA
205831	38027	TTTTTGAGATGGAGTCTTAC	250418	82614	CCAGGCAGCTGCTGAGGGCA	295005	127201	GAGCCAAGAAGCTGAGACTC
205832	38028	TTTTTTGAGATGGAGTCTTA	250419	82615	CCCAGGCAGCTGCTGAGGGC	295006	127202	GGAGCCAAGAAGCTGAGACT
205833	38029	TTTTTTTGAGATGGAGTCTT	250420	82616	CCCCAGGCAGCTGCTGAGGG	295007	127203	AGGAGCCAAGAAGCTGAGAC
205834	38030	TTTTTTTTGAGATGGAGTCT	250421	82617	TCCCCAGGCAGCTGCTGAGG	295008	127204	AAGGAGCCAAGAAGCTGAGA
205835	38031	TTTTTTTTTGAGATGGAGTC	250422	82618	GTCCCCAGGCAGCTGCTGAG	295009	127205	GAAGGAGCCAAGAAGCTGAG
205836	38032	TTTTTTTTTTGAGATGGAGT	250423	82619	TGTCCCCAGGCAGCTGCTGA	295010	127206	AGAAGGAGCCAAGAAGCTGA
205837	38033	TTTTTTTTTTTGAGATGGAG	250424	82620	CTGTCCCCAGGCAGCTGCTG	295011	127207	CAGAAGGAGCCAAGAAGCTG
205838	38034	TTTTTTTTTTTTGAGATGGA	250425	82621	GCTGTCCCCAGGCAGCTGCT	295012	127208	ACAGAAGGAGCCAAGAAGCT
205839	38035	TTTTTTTTTTTTTGAGATGG	250426	82622	GGCTGTCCCCAGGCAGCTGC	295013	127209	AACAGAAGGAGCCAAGAAGC
205840	38036	TTTTTTTTTTTTTTGAGATG	250427	82623	TGGCTGTCCCCAGGCAGCTG	295014	127210	AAACAGAAGGAGCCAAGAAG
205841	38037	TTTTTTTTTTTTTTTGAGAT	250428	82624	TTGGCTGTCCCCAGGCAGCT	295015	127211	GAAACAGAAGGAGCCAAGAA
205842	38038	TTTTTTTTTTTTTTTTGAGA	250429	82625	ATTGGCTGTCCCCAGGCAGC	295016	127212	TGAAACAGAAGGAGCCAAGA
205843	38039	TTTTTTTTTTTTTTTTTGAG	250430	82626	CATTGGCTGTCCCCAGGCAG	295017	127213	TTGAAACAGAAGGAGCCAAG
205844	38040	TTTTTTTTTTTTTTTTTTGA	250431	82627	CCATTGGCTGTCCCCAGGCA	295018	127214	TTTGAAACAGAAGGAGCCAA
205845	38041	TTTTTTTTTTTTTTTTTTTG	250432	82628	GCCATTGGCTGTCCCCAGGC	295019	127215	GTTTGAAACAGAAGGAGCCA
205846	38042	TTTTTTTTTTTTTTTTTTT	250433	82629	GGCCATTGGCTGTCCCCAGG	295020	127216	AGTTTGAAACAGAAGGAGCC
205847	38043	TTTTTTTTTTTTTTTTTTT	250434	82630	AGGCCATTGGCTGTCCCCAG	295021	127217	GAGTTTGAAACAGAAGGAGC
205848	38044	CTTTTTTTTTTTTTTTTTT	250435	82631	CAGGCCATTGGCTGTCCCCA	295022	127218	CGAGTTTGAAACAGAAGGAG
205849	38045	TCTTTTTTTTTTTTTTTTT	250436	82632	CCAGGCCATTGGCTGTCCCC	295023	127219	ACGAGTTTGAAACAGAAGGA
205850	38046	TTCTTTTTTTTTTTTTTTT	250437	82633	CCCAGGCCATTGGCTGTCCC	295024	127220	GACGAGTTTGAAACAGAAGG
205851	38047	GTTCTTTTTTTTTTTTTTT	250438	82634	ACCCAGGCCATTGGCTGTCC	295025	127221	GGACGAGTTTGAAACAGAAG
205852	38048	AGTTCTTTTTTTTTTTTTT	250439	82635	CACCCAGGCCATTGGCTGTC	295026	127222	TGGACGAGTTTGAAACAGAA
205853	38049	AAGTTCTTTTTTTTTTTTT	250440	82636	ACACCCAGGCCATTGGCTGT	295027	127223	ATGGACGAGTTTGAAACAGA
205854	38050	TAAGTTCTTTTTTTTTTTT	250441	82637	AACACCCAGGCCATTGGCTG	295028	127224	CATGGACGAGTTTGAAACAG
205855	38051	GTAAGTTCTTTTTTTTTTT	250442	82638	AAACACCCAGGCCATTGGCT	295029	127225	ACATGGACGAGTTTGAAACA
205856	38052	AGTAAGTTCTTTTTTTTTT	250443	82639	GAAACACCCAGGCCATTGGC	295030	127226	CACATGGACGAGTTTGAAAC
205857	38053	GAGTAAGTTCTTTTTTTTT	250444	82640	AGAAACACCCAGGCCATTGG	295031	127227	TCACATGGACGAGTTTGAAA
205858	38054	AGAGTAAGTTCTTTTTTTT	250445	82641	CAGAAACACCCAGGCCATTG	295032	127228	ATCACATGGACGAGTTTGAA
205859	38055	GAGAGTAAGTTCTTTTTTT	250446	82642	TCAGAAACACCCAGGCCATT	295033	127229	TATCACATGGACGAGTTTGA
205860	38056	TGAGAGTAAGTTCTTTTTTT	250447	82643	CTCAGAAACACCCAGGCCAT	295034	127230	CTATCACATGGACGAGTTTG
205861	38057	TTGAGAGTAAGTTCTTTTTT	250448	82644	CCTCAGAAACACCCAGGCCA	295035	127231	GCTATCACATGGACGAGTTT
205862	38058	TTTGAGAGTAAGTTCTTTTT	250449	82645	GCCTCAGAAACACCCAGGCC	295036	127232	AGCTATCACATGGACGAGTT
205863	38059	TTTTGAGAGTAAGTTCTTTT	250450	82646	AGCCTCAGAAACACCCAGGC	295037	127233	GAGCTATCACATGGACGAGT
205864	38060	ATTTTGAGAGTAAGTTCTTT	250451	82647	TAGCCTCAGAAACACCCAGG	295038	127234	TGAGCTATCACATGGACGAG
205865	38061	TATTTTGAGAGTAAGTTCTT	250452	82648	GTAGCCTCAGAAACACCCAG	295039	127235	CTGAGCTATCACATGGACGA
205866	38062	TTATTTTGAGAGTAAGTTCT	250453	82649	GGTAGCCTCAGAAACACCCA	295040	127236	CCTGAGCTATCACATGGACG
205867	38063	TTTATTTTGAGAGTAAGTTC	250454	82650	TGGTAGCCTCAGAAACACCC	295041	127237	TCCTGAGCTATCACATGGAC
205868	38064	ATTTATTTTGAGAGTAAGTT	250455	82651	GTGGTAGCCTCAGAAACACC	295042	127238	TTCCTGAGCTATCACATGGA
205869	38065	TATTTATTTTGAGAGTAAGT	250456	82652	TGTGGTAGCCTCAGAAACAC	295043	127239	CTTCCTGAGCTATCACATGG
205870	38066	GTATTTATTTTGAGAGTAAG	250457	82653	ATGTGGTAGCCTCAGAAACA	295044	127240	CCTTCCTGAGCTATCACATG
205871	38067	CGTATTTATTTTGAGAGTAA	250458	82654	CATGTGGTAGCCTCAGAAAC	295045	127241	CCCTTCCTGAGCTATCACAT
205872	38068	ACGTATTTATTTTGAGAGTA	250459	82655	CCATGTGGTAGCCTCAGAAA	295046	127242	ACCCTTCCTGAGCTATCACA
205873	38069	CACGTATTTATTTTGAGAGT	250460	82656	GCCATGTGGTAGCCTCAGAA	295047	127243	TACCCTTCCTGAGCTATCAC
205874	38070	ACACGTATTTATTTTGAGAG	250461	82657	AGCCATGTGGTAGCCTCAGA	295048	127244	CTACCCTTCCTGAGCTATCA
205875	38071	CACACGTATTTATTTTGAGA	250462	82658	AAGCCATGTGGTAGCCTCAG	295049	127245	CCTACCCTTCCTGAGCTATC
205876	38072	CCACACGTATTTATTTTGAG	250463	82659	GAAGCCATGTGGTAGCCTCA	295050	127246	GCCTACCCTTCCTGAGCTAT
205877	38073	GCCACACGTATTTATTTTGA	250464	82660	GGAAGCCATGTGGTAGCCTC	295051	127247	TGCCTACCCTTCCTGAGCTA
205878	38074	AGCCACACGTATTTATTTTG	250465	82661	TGGAAGCCATGTGGTAGCCT	295052	127248	CTGCCTACCCTTCCTGAGCT
205879	38075	CAGCCACACGTATTTATTTT	250466	82662	CTGGAAGCCATGTGGTAGCC	295053	127249	CCTGCCTACCCTTCCTGAGC
205880	38076	TCAGCCACACGTATTTATTT	250467	82663	CCTGGAAGCCATGTGGTAGC	295054	127250	CCCTGCCTACCCTTCCTGAG
205881	38077	GTCAGCCACACGTATTTATT	250468	82664	TCCTGGAAGCCATGTGGTAG	295055	127251	GCCCTGCCTACCCTTCCTGA
205882	38078	AGTCAGCCACACGTATTTAT	250469	82665	TTCCTGGAAGCCATGTGGTA	295056	127252	GGCCCTGCCTACCCTTCCTG
205883	38079	GAGTCAGCCACACGTATTTA	250470	82666	TTTCCTGGAAGCCATGTGGT	295057	127253	GGGCCCTGCCTACCCTTCCT
205884	38080	GGAGTCAGCCACACGTATTT	250471	82667	GTTTCCTGGAAGCCATGTGG	295058	127254	AGGGCCCTGCCTACCCTTCC
205885	38081	TGGAGTCAGCCACACGTATT	250472	82668	AGTTTCCTGGAAGCCATGTG	295059	127255	CAGGGCCCTGCCTACCCTTC
205886	38082	GTGGAGTCAGCCACACGTAT	250473	82669	GAGTTTCCTGGAAGCCATGT	295060	127256	GCAGGGCCCTGCCTACCCTT
205887	38083	TGTGGAGTCAGCCACACGTA	250474	82670	CGAGTTTCCTGGAAGCCATG	295061	127257	GGCAGGGCCCTGCCTACCCT
205888	38084	ATGTGGAGTCAGCCACACGT	250475	82671	TCGAGTTTCCTGGAAGCCAT	295062	127258	GGGCAGGGCCCTGCCTACCC
205889	38085	TATGTGGAGTCAGCCACACG	250476	82672	CTCGAGTTTCCTGGAAGCCA	295063	127259	GGGGCAGGGCCCTGCCTACC
205890	38086	ATATGTGGAGTCAGCCACAC	250477	82673	TCTCGAGTTTCCTGGAAGCC	295064	127260	GGGGGCAGGGCCCTGCCTAC

205891	38087	CATATGTGGAGTCAGCCACA	250478	82674	TTCTCGAGTTTCCTGGAAGC	295065	127261	AGGGGGCAGGGCCCTGCCTA
205892	38088	CCATATGTGGAGTCAGCCAC	250479	82675	GTTCTCGAGTTTCCTGGAAG	295066	127262	TAGGGGGCAGGGCCCTGCCT
205893	38089	ACCATATGTGGAGTCAGCCA	250480	82676	GGTTCTCGAGTTTCCTGGAA	295067	127263	GTAGGGGGCAGGGCCCTGCC
205894	38090	TACCATATGTGGAGTCAGCC	250481	82677	AGGTTCTCGAGTTTCCTGGA	295068	127264	AGTAGGGGGCAGGGCCCTGC
205895	38091	CTACCATATGTGGAGTCAGC	250482	82678	AAGGTTCTCGAGTTTCCTGG	295069	127265	GAGTAGGGGGCAGGGCCCTG
205896	38092	CCTACCATATGTGGAGTCAG	250483	82679	AAAGGTTCTCGAGTTTCCTG	295070	127266	TGAGTAGGGGGCAGGGCCCT
205897	38093	CCCTACCATATGTGGAGTCA	250484	82680	GAAAGGTTCTCGAGTTTCCT	295071	127267	CTGAGTAGGGGGCAGGGCCC
205898	38094	GCCCTACCATATGTGGAGTC	250485	82681	AGAAAGGTTCTCGAGTTTCC	295072	127268	TCTGAGTAGGGGGCAGGGCC
205899	38095	GGCCCTACCATATGTGGAGT	250486	82682	GAGAAAGGTTCTCGAGTTTC	295073	127269	TTCTGAGTAGGGGGCAGGGC
205900	38096	TGGCCCTACCATATGTGGAG	250487	82683	AGAGAAAGGTTCTCGAGTTT	295074	127270	TTTCTGAGTAGGGGGCAGGG
205901	38097	TTGGCCCTACCATATGTGGA	250488	82684	GAGAGAAAGGTTCTCGAGTT	295075	127271	TTTTCTGAGTAGGGGGCAGG
205902	38098	GTTGGCCCTACCATATGTGG	250489	82685	GGAGAGAAAGGTTCTCGAGT	295076	127272	GTTTTCTGAGTAGGGGGCAG
205903	38099	AGTTGGCCCTACCATATGTG	250490	82686	GGGAGAGAAAGGTTCTCGAG	295077	127273	TGTTTTCTGAGTAGGGGGCA
205904	38100	CAGTTGGCCCTACCATATGT	250491	82687	AGGGAGAGAAAGGTTCTCGA	295078	127274	GTGTTTTCTGAGTAGGGGGC
205905	38101	ACAGTTGGCCCTACCATATG	250492	82688	AAGGGAGAGAAAGGTTCTCG	295079	127275	GGTGTTTTCTGAGTAGGGGG
205906	38102	TACAGTTGGCCCTACCATAT	250493	82689	CAAGGGAGAGAAAGGTTCTC	295080	127276	TGGTGTTTTCTGAGTAGGGG
205907	38103	ATACAGTTGGCCCTACCATA	250494	82690	GCAAGGGAGAGAAAGGTTCT	295081	127277	ATGGTGTTTTCTGAGTAGGG
205908	38104	TATACAGTTGGCCCTACCAT	250495	82691	GGCAAGGGAGAGAAAGGTTC	295082	127278	GATGGTGTTTTCTGAGTAGG
205909	38105	TTATACAGTTGGCCCTACCA	250496	82692	AGGCAAGGGAGAGAAAGGTT	295083	127279	GGATGGTGTTTTCTGAGTAG
205910	38106	GTTATACAGTTGGCCCTACC	250497	82693	TAGGCAAGGGAGAGAAAGGT	295084	127280	AGGATGGTGTTTTCTGAGTA
205911	38107	AGTTATACAGTTGGCCCTAC	250498	82694	GTAGGCAAGGGAGAGAAAGG	295085	127281	CAGGATGGTGTTTTCTGAGT
205912	38108	TAGTTATACAGTTGGCCCTA	250499	82695	TGTAGGCAAGGGAGAGAAAG	295086	127282	CCAGGATGGTGTTTTCTGAG
205913	38109	CTAGTTATACAGTTGGCCCT	250500	82696	GTGTAGGCAAGGGAGAGAAA	295087	127283	ACCAGGATGGTGTTTTCTGA
205914	38110	TCTAGTTATACAGTTGGCCC	250501	82697	AGTGTAGGCAAGGGAGAGAA	295088	127284	GACCAGGATGGTGTTTTCTG
205915	38111	TTCTAGTTATACAGTTGGCC	250502	82698	GAGTGTAGGCAAGGGAGAGA	295089	127285	GGACCAGGATGGTGTTTTCT
205916	38112	CTTCTAGTTATACAGTTGGC	250503	82699	AGAGTGTAGGCAAGGGAGAG	295090	127286	AGGACCAGGATGGTGTTTTC
205917	38113	ACTTCTAGTTATACAGTTGG	250504	82700	AAGAGTGTAGGCAAGGGAGA	295091	127287	CAGGACCAGGATGGTGTTTT
205918	38114	AACTTCTAGTTATACAGTTG	250505	82701	GAAGAGTGTAGGCAAGGGAG	295092	127288	CCAGGACCAGGATGGTGTTT
205919	38115	GAACTTCTAGTTATACAGTT	250506	82702	TGAAGAGTGTAGGCAAGGGA	295093	127289	CCCAGGACCAGGATGGTGTT
205920	38116	AGAACTTCTAGTTATACAGT	250507	82703	GTGAAGAGTGTAGGCAAGGG	295094	127290	CCCCAGGACCAGGATGGTGT
205921	38117	GAGAACTTCTAGTTATACAG	250508	82704	TGTGAAGAGTGTAGGCAAGG	295095	127291	TCCCCAGGACCAGGATGGTG
205922	38118	GGAGAACTTCTAGTTATACA	250509	82705	GTGTGAAGAGTGTAGGCAAG	295096	127292	ATCCCCAGGACCAGGATGGT
205923	38119	TGGAGAACTTCTAGTTATAC	250510	82706	TGTGTGAAGAGTGTAGGCAA	295097	127293	GATCCCCAGGACCAGGATGG
205924	38120	TTGGAGAACTTCTAGTTATA	250511	82707	CTGTGTGAAGAGTGTAGGCA	295098	127294	GGATCCCCAGGACCAGGATG
205925	38121	TTTGGAGAACTTCTAGTTAT	250512	82708	CCTGTGTGAAGAGTGTAGGC	295099	127295	GGGATCCCCAGGACCAGGAT
205926	38122	ATTTGGAGAACTTCTAGTTA	250513	82709	GCCTGTGTGAAGAGTGTAGG	295100	127296	GGGGATCCCCAGGACCAGGA
205927	38123	TATTTGGAGAACTTCTAGTT	250514	82710	GGCCTGTGTGAAGAGTGTAG	295101	127297	CGGGGATCCCCAGGACCAGG
205928	38124	TTATTTGGAGAACTTCTAGT	250515	82711	AGGCCTGTGTGAAGAGTGTA	295102	127298	GCGGGGATCCCCAGGACCAG
205929	38125	GTTATTTGGAGAACTTCTAG	250516	82712	CAGGCCTGTGTGAAGAGTGT	295103	127299	TGCGGGGATCCCCAGGACCA
205930	38126	AGTTATTTGGAGAACTTCTA	250517	82713	ACAGGCCTGTGTGAAGAGTG	295104	127300	CTGCGGGGATCCCCAGGACC
205931	38127	AAGTTATTTGGAGAACTTCT	250518	82714	CACAGGCCTGTGTGAAGAGT	295105	127301	GCTGCGGGGATCCCCAGGAC
205932	38128	GAAGTTATTTGGAGAACTTC	250519	82715	GCACAGGCCTGTGTGAAGAG	295106	127302	TGCTGCGGGGATCCCCAGGA
205933	38129	AGAAGTTATTTGGAGAACTT	250520	82716	AGCACAGGCCTGTGTGAAGA	295107	127303	ATGCTGCGGGGATCCCCAGG
205934	38130	CAGAAGTTATTTGGAGAACT	250521	82717	CAGCACAGGCCTGTGTGAAG	295108	127304	AATGCTGCGGGGATCCCCAG
205935	38131	ACAGAAGTTATTTGGAGAAC	250522	82718	CCAGCACAGGCCTGTGTGAA	295109	127305	TAATGCTGCGGGGATCCCCA
205936	38132	CACAGAAGTTATTTGGAGAA	250523	82719	GCCAGCACAGGCCTGTGTGA	295110	127306	CTAATGCTGCGGGGATCCCC
205937	38133	CCACAGAAGTTATTTGGAGA	250524	82720	GGCCAGCACAGGCCTGTGTG	295111	127307	ACTAATGCTGCGGGGATCCC
205938	38134	TCCACAGAAGTTATTTGGAG	250525	82721	TGGCCAGCACAGGCCTGTGT	295112	127308	GACTAATGCTGCGGGGATCC
205939	38135	CTCCACAGAAGTTATTTGGA	250526	82722	CTGGCCAGCACAGGCCTGTG	295113	127309	GGACTAATGCTGCGGGGATC
205940	38136	TCTCCACAGAAGTTATTTGG	250527	82723	GCTGGCCAGCACAGGCCTGT	295114	127310	GGGACTAATGCTGCGGGGAT
205941	38137	TTCTCCACAGAAGTTATTTG	250528	82724	CGCTGGCCAGCACAGGCCTG	295115	127311	GGGGACTAATGCTGCGGGGA
205942	38138	TTTCTCCACAGAAGTTATTT	250529	82725	CCGCTGGCCAGCACAGGCCT	295116	127312	AGGGGACTAATGCTGCGGGG
205943	38139	TTTTCTCCACAGAAGTTATT	250530	82726	ACCGCTGGCCAGCACAGGCC	295117	127313	CAGGGGACTAATGCTGCGGG
205944	38140	TTTTTCTCCACAGAAGTTAT	250531	82727	CACCGCTGGCCAGCACAGGC	295118	127314	ACAGGGGACTAATGCTGCGG
205945	38141	TTTTTTCTCCACAGAAGTTA	250532	82728	CCACCGCTGGCCAGCACAGG	295119	127315	AACAGGGGACTAATGCTGCG
205946	38142	TTTTTTTCTCCACAGAAGTT	250533	82729	CCCACCGCTGGCCAGCACAG	295120	127316	AAACAGGGGACTAATGCTGC
205947	38143	TTTTTTTTCTCCACAGAAGT	250534	82730	CCCCACCGCTGGCCAGCACA	295121	127317	AAAACAGGGGACTAATGCTG
205948	38144	CTTTTTTTTCTCCACAGAAG	250535	82731	TCCCCACCGCTGGCCAGCAC	295122	127318	GAAAACAGGGGACTAATGCT
205949	38145	ACTTTTTTTTCTCCACAGAA	250536	82732	ATCCCCACCGCTGGCCAGCA	295123	127319	GGAAAACAGGGGACTAATGC
205950	38146	AACTTTTTTTTCTCCACAGA	250537	82733	GATCCCCACCGCTGGCCAGC	295124	127320	GGGAAAACAGGGGACTAATG
205951	38147	AAACTTTTTTTTCTCCACAG	250538	82734	GGATCCCCACCGCTGGCCAG	295125	127321	TGGGAAAACAGGGGACTAAT
205952	38148	TAAACTTTTTTTTCTCCACA	250539	82735	CGGATCCCCACCGCTGGCCA	295126	127322	CTGGGAAAACAGGGGACTAA
205953	38149	ATAAACTTTTTTTTCTCCAC	250540	82736	CCGGATCCCCACCGCTGGCC	295127	127323	ACTGGGAAAACAGGGGACTA
205954	38150	AATAAACTTTTTTTTCTCCA	250541	82737	GCCGGATCCCCACCGCTGGC	295128	127324	CACTGGGAAAACAGGGGACT
205955	38151	TAATAAACTTTTTTTTCTCC	250542	82738	TGCCGGATCCCCACCGCTGG	295129	127325	ACACTGGGAAAACAGGGGAC
205956	38152	TTAATAAACTTTTTTTTCTC	250543	82739	ATGCCGGATCCCCACCGCTG	295130	127326	TACACTGGGAAAACAGGGGA
205957	38153	TTTAATAAACTTTTTTTTCT	250544	82740	AATGCCGGATCCCCACCGCT	295131	127327	ATACACTGGGAAAACAGGGG
205958	38154	CTTTAATAAACTTTTTTTTC	250545	82741	GAATGCCGGATCCCCACCGC	295132	127328	AATACACTGGGAAAACAGGG
205959	38155	CCTTTAATAAACTTTTTTTT	250546	82742	GGAATGCCGGATCCCCACCG	295133	127329	CAATACACTGGGAAAACAGG
205960	38156	ACCTTTAATAAACTTTTTTT	250547	82743	AGGAATGCCGGATCCCCACC	295134	127330	TCAATACACTGGGAAAACAG
205961	38157	AACCTTTAATAAACTTTTTT	250548	82744	TAGGAATGCCGGATCCCCAC	295135	127331	CTCAATACACTGGGAAAACA
205962	38158	TAACCTTTAATAAACTTTTT	250549	82745	ATAGGAATGCCGGATCCCCA	295136	127332	TCTCAATACACTGGGAAAAC

205963	38159	TTAACCTTTAATAAACTTTT	250550	82746	GATAGGAATGCCGGATCCCC	295137	127333	TTCTCAATACACTGGGAAAA
205964	38160	GTTAACCTTTAATAAACTTT	250551	82747	AGATAGGAATGCCGGATCCC	295138	127334	TTTCTCAATACACTGGGAAA
205965	38161	AGTTAACCTTTAATAAACTT	250552	82748	AAGATAGGAATGCCGGATCC	295139	127335	TTTTCTCAATACACTGGGAA
205966	38162	AAGTTAACCTTTAATAAACT	250553	82749	TAAGATAGGAATGCCGGATC	295140	127336	TTTTTCTCAATACACTGGGA
205967	38163	AAAGTTAACCTTTAATAAAC	250554	82750	CTAAGATAGGAATGCCGGAT	295141	127337	ATTTTTCTCAATACACTGGG
205968	38164	AAAAGTTAACCTTTAATAAA	250555	82751	CCTAAGATAGGAATGCCGGA	295142	127338	AATTTTTCTCAATACACTGG
205969	38165	AAAAAGTTAACCTTTAATAA	250556	82752	ACCTAAGATAGGAATGCCGG	295143	127339	CAATTTTTCTCAATACACTG
205970	38166	AAAAAAGTTAACCTTTAATA	250557	82753	CACCTAAGATAGGAATGCCG	295144	127340	GCAATTTTTCTCAATACACT
205971	38167	TAAAAAAGTTAACCTTTAAT	250558	82754	GCACCTAAGATAGGAATGCC	295145	127341	AGCAATTTTTCTCAATACAC
205972	38168	TTAAAAAAGTTAACCTTTAA	250559	82755	TGCACCTAAGATAGGAATGC	295146	127342	TAGCAATTTTTCTCAATACA
205973	38169	TTTAAAAAAGTTAACCTTTA	250560	82756	CTGCACCTAAGATAGGAATG	295147	127343	TTAGCAATTTTTCTCAATAC
205974	38170	CTTTAAAAAAGTTAACCTTT	250561	82757	TCTGCACCTAAGATAGGAAT	295148	127344	GTTAGCAATTTTTCTCAATA
205975	38171	ACTTTAAAAAAGTTAACCTT	250562	82758	CTCTGCACCTAAGATAGGAA	295149	127345	TGTTAGCAATTTTTCTCAAT
205976	38172	CACTTTAAAAAAGTTAACCT	250563	82759	TCTCTGCACCTAAGATAGGA	295150	127346	TTGTTAGCAATTTTTCTCAA
205977	38173	GCACTTTAAAAAAGTTAACC	250564	82760	CTCTCTGCACCTAAGATAGG	295151	127347	CTTGTTAGCAATTTTTCTCA
205978	38174	AGCACTTTAAAAAAGTTAAC	250565	82761	ACTCTCTGCACCTAAGATAG	295152	127348	GCTTGTTAGCAATTTTTCTC
205979	38175	TAGCACTTTAAAAAAGTTAA	250566	82762	CACTCTCTGCACCTAAGATA	295153	127349	TGCTTGTTAGCAATTTTTCT
205980	38176	TTAGCACTTTAAAAAAGTTA	250567	82763	TCACTCTCTGCACCTAAGAT	295154	127350	CTGCTTGTTAGCAATTTTTC
205981	38177	GTTAGCACTTTAAAAAAGTT	250568	82764	GTCACTCTCTGCACCTAAGA	295155	127351	ACTGCTTGTTAGCAATTTTT
205982	38178	AGTTAGCACTTTAAAAAAGT	250569	82765	AGTCACTCTCTGCACCTAAG	295156	127352	CACTGCTTGTTAGCAATTTT
205983	38179	TAGTTAGCACTTTAAAAAAG	250570	82766	CAGTCACTCTCTGCACCTAA	295157	127353	CCACTGCTTGTTAGCAATTT
205984	38180	CTAGTTAGCACTTTAAAAAA	250571	82767	TCAGTCACTCTCTGCACCTA	295158	127354	CCCACTGCTTGTTAGCAATT
205985	38181	TCTAGTTAGCACTTTAAAAA	250572	82768	GTCAGTCACTCTCTGCACCT	295159	127355	CCCCACTGCTTGTTAGCAAT
205986	38182	TTCTAGTTAGCACTTTAAAA	250573	82769	AGTCAGTCACTCTCTGCACC	295160	127356	GCCCCACTGCTTGTTAGCAA
205987	38183	GTTCTAGTTAGCACTTTAAA	250574	82770	GAGTCAGTCACTCTCTGCAC	295161	127357	TGCCCCACTGCTTGTTAGCA
205988	38184	GGTTCTAGTTAGCACTTTAA	250575	82771	TGAGTCAGTCACTCTCTGCA	295162	127358	GTGCCCCACTGCTTGTTAGC
205989	38185	AGGTTCTAGTTAGCACTTTA	250576	82772	ATGAGTCAGTCACTCTCTGC	295163	127359	TGTGCCCCACTGCTTGTTAG
205990	38186	AAGGTTCTAGTTAGCACTTT	250577	82773	AATGAGTCAGTCACTCTCTG	295164	127360	GTGTGCCCCACTGCTTGTTA
205991	38187	TAAGGTTCTAGTTAGCACTT	250578	82774	CAATGAGTCAGTCACTCTCT	295165	127361	GGTGTGCCCCACTGCTTGTT
205992	38188	GTAAGGTTCTAGTTAGCACT	250579	82775	GCAATGAGTCAGTCACTCTC	295166	127362	TGGTGTGCCCCACTGCTTGT
205993	38189	AGTAAGGTTCTAGTTAGCAC	250580	82776	TGCAATGAGTCAGTCACTCT	295167	127363	GTGGTGTGCCCCACTGCTTG
205994	38190	TAGTAAGGTTCTAGTTAGCA	250581	82777	CTGCAATGAGTCAGTCACTC	295168	127364	GGTGGTGTGCCCCACTGCTT
205995	38191	TTAGTAAGGTTCTAGTTAGC	250582	82778	CCTGCAATGAGTCAGTCACT	295169	127365	TGGTGGTGTGCCCCACTGCT
205996	38192	GTTAGTAAGGTTCTAGTTAG	250583	82779	GCCTGCAATGAGTCAGTCAC	295170	127366	CTGGTGGTGTGCCCCACTGC
205997	38193	TGTTAGTAAGGTTCTAGTTA	250584	82780	GGCCTGCAATGAGTCAGTCA	295171	127367	GCTGGTGGTGTGCCCCACTG
205998	38194	GTGTTAGTAAGGTTCTAGTT	250585	82781	AGGCCTGCAATGAGTCAGTC	295172	127368	GGCTGGTGGTGTGCCCCACT
205999	38195	AGTGTTAGTAAGGTTCTAGT	250586	82782	CAGGCCTGCAATGAGTCAGT	295173	127369	AGGCTGGTGGTGTGCCCCAC
206000	38196	CAGTGTTAGTAAGGTTCTAG	250587	82783	CCAGGCCTGCAATGAGTCAG	295174	127370	GAGGCTGGTGGTGTGCCCCA
206001	38197	TCAGTGTTAGTAAGGTTCTA	250588	82784	CCCAGGCCTGCAATGAGTCA	295175	127371	GGAGGCTGGTGGTGTGCCCC
206002	38198	CTCAGTGTTAGTAAGGTTCT	250589	82785	TCCCAGGCCTGCAATGAGTC	295176	127372	AGGAGGCTGGTGGTGTGCCC
206003	38199	TCTCAGTGTTAGTAAGGTTC	250590	82786	CTCCCAGGCCTGCAATGAGT	295177	127373	CAGGAGGCTGGTGGTGTGCC
206004	38200	ATCTCAGTGTTAGTAAGGTT	250591	82787	TCTCCCAGGCCTGCAATGAG	295178	127374	CCAGGAGGCTGGTGGTGTGC
206005	38201	GATCTCAGTGTTAGTAAGGT	250592	82788	ATCTCCCAGGCCTGCAATGA	295179	127375	CCCAGGAGGCTGGTGGTGTG
206006	38202	CGATCTCAGTGTTAGTAAGG	250593	82789	TATCTCCCAGGCCTGCAATG	295180	127376	ACCCAGGAGGCTGGTGGTGT
206007	38203	GCGATCTCAGTGTTAGTAAG	250594	82790	TTATCTCCCAGGCCTGCAAT	295181	127377	AACCCAGGAGGCTGGTGGTG
206008	38204	TGCGATCTCAGTGTTAGTAA	250595	82791	CTTATCTCCCAGGCCTGCAA	295182	127378	GAACCCAGGAGGCTGGTGGT
206009	38205	GTGCGATCTCAGTGTTAGTA	250596	82792	TCTTATCTCCCAGGCCTGCA	295183	127379	GGAACCCAGGAGGCTGGTGG
206010	38206	GGTGCGATCTCAGTGTTAGT	250597	82793	GTCTTATCTCCCAGGCCTGC	295184	127380	AGGAACCCAGGAGGCTGGTG
206011	38207	TGGTGCGATCTCAGTGTTAG	250598	82794	AGTCTTATCTCCCAGGCCTG	295185	127381	AAGGAACCCAGGAGGCTGGT
206012	38208	TTGGTGCGATCTCAGTGTTA	250599	82795	CAGTCTTATCTCCCAGGCCT	295186	127382	AAAGGAACCCAGGAGGCTGG
206013	38209	ATTGGTGCGATCTCAGTGTT	250600	82796	TCAGTCTTATCTCCCAGGCC	295187	127383	GAAAGGAACCCAGGAGGCTG
206014	38210	AATTGGTGCGATCTCAGTGT	250601	82797	ATCAGTCTTATCTCCCAGGC	295188	127384	TGAAAGGAACCCAGGAGGCT
206015	38211	CAATTGGTGCGATCTCAGTG	250602	82798	CATCAGTCTTATCTCCCAGG	295189	127385	CTGAAAGGAACCCAGGAGGC
206016	38212	ACAATTGGTGCGATCTCAGT	250603	82799	CCATCAGTCTTATCTCCCAG	295190	127386	ACTGAAAGGAACCCAGGAGG
206017	38213	AACAATTGGTGCGATCTCAG	250604	82800	GCCATCAGTCTTATCTCCCA	295191	127387	AACTGAAAGGAACCCAGGAG
206018	38214	AAACAATTGGTGCGATCTCA	250605	82801	GGCCATCAGTCTTATCTCCC	295192	127388	AAACTGAAAGGAACCCAGGA
206019	38215	TAAACAATTGGTGCGATCTC	250606	82802	GGGCCATCAGTCTTATCTCC	295193	127389	CAAACTGAAAGGAACCCAGG
206020	38216	ATAAACAATTGGTGCGATCT	250607	82803	TGGGCCATCAGTCTTATCTC	295194	127390	CCAAACTGAAAGGAACCCAG
206021	38217	TATAAACAATTGGTGCGATC	250608	82804	CTGGGCCATCAGTCTTATCT	295195	127391	CCCAAACTGAAAGGAACCCA
206022	38218	TTATAAACAATTGGTGCGAT	250609	82805	GCTGGGCCATCAGTCTTATC	295196	127392	CCCCAAACTGAAAGGAACCC
206023	38219	GTTATAAACAATTGGTGCGA	250610	82806	GGCTGGGCCATCAGTCTTAT	295197	127393	TCCCCAAACTGAAAGGAACC
206024	38220	AGTTATAAACAATTGGTGCG	250611	82807	TGGCTGGGCCATCAGTCTTA	295198	127394	ATCCCCAAACTGAAAGGAAC
206025	38221	AAGTTATAAACAATTGGTGC	250612	82808	CTGGCTGGGCCATCAGTCTT	295199	127395	AATCCCCAAACTGAAAGGAA
206026	38222	TAAGTTATAAACAATTGGTG	250613	82809	GCTGGCTGGGCCATCAGTCT	295200	127396	AAATCCCCAAACTGAAAGGA
206027	38223	CTAAGTTATAAACAATTGGT	250614	82810	TGCTGGCTGGGCCATCAGTC	295201	127397	AAAATCCCCAAACTGAAAGG
206028	38224	TCTAAGTTATAAACAATTGG	250615	82811	TTGCTGGCTGGGCCATCAGT	295202	127398	AAAAATCCCCAAACTGAAAG
206029	38225	GTCTAAGTTATAAACAATTG	250616	82812	CTTGCTGGCTGGGCCATCAG	295203	127399	CAAAAATCCCCAAACTGAAA
206030	38226	TGTCTAAGTTATAAACAATT	250617	82813	TCTTGCTGGCTGGGCCATCA	295204	127400	CCAAAAATCCCCAAACTGAA
206031	38227	CTGTCTAAGTTATAAACAAT	250618	82814	ATCTTGCTGGCTGGGCCATC	295205	127401	TCCAAAAATCCCCAAACTGA
206032	38228	CCTGTCTAAGTTATAAACAA	250619	82815	CATCTTGCTGGCTGGGCCAT	295206	127402	GTCCAAAAATCCCCAAACTG
206033	38229	CCCTGTCTAAGTTATAAACA	250620	82816	ACATCTTGCTGGCTGGGCCA	295207	127403	TGTCCAAAAATCCCCAAACT
206034	38230	GCCCTGTCTAAGTTATAAAC	250621	82817	TACATCTTGCTGGCTGGGCC	295208	127404	ATGTCCAAAAATCCCCAAAC

206035	38231	GGCCCTGTCTAAGTTATAAA	250622	82818	ATACATCTTGCTGGCTGGGC	295209	127405	AATGTCCAAAAATCCCCAAA
206036	38232	CGGCCCTGTCTAAGTTATAA	250623	82819	CATACATCTTGCTGGCTGGG	295210	127406	GAATGTCCAAAAATCCCCAA
206037	38233	CCGGCCCTGTCTAAGTTATA	250624	82820	CCATACATCTTGCTGGCTGG	295211	127407	GGAATGTCCAAAAATCCCCA
206038	38234	CCCGGCCCTGTCTAAGTTAT	250625	82821	TCCATACATCTTGCTGGCTG	295212	127408	GGGAATGTCCAAAAATCCCC
206039	38235	ACCCGGCCCTGTCTAAGTTA	250626	82822	ATCCATACATCTTGCTGGCT	295213	127409	TGGGAATGTCCAAAAATCCC
206040	38236	CACCCGGCCCTGTCTAAGTT	250627	82823	AATCCATACATCTTGCTGGC	295214	127410	CTGGGAATGTCCAAAAATCC
206041	38237	GCACCCGGCCCTGTCTAAGT	250628	82824	AAATCCATACATCTTGCTGG	295215	127411	CCTGGGAATGTCCAAAAATC
206042	38238	TGCACCCGGCCCTGTCTAAG	250629	82825	GAAATCCATACATCTTGCTG	295216	127412	TCCTGGGAATGTCCAAAAAT
206043	38239	CTGCACCCGGCCCTGTCTAA	250630	82826	AGAAATCCATACATCTTGCT	295217	127413	TTCCTGGGAATGTCCAAAAA
206044	38240	ACTGCACCCGGCCCTGTCTA	250631	82827	GAGAAATCCATACATCTTGC	295218	127414	ATTCCTGGGAATGTCCAAAA
206045	38241	CACTGCACCCGGCCCTGTCT	250632	82828	TGAGAAATCCATACATCTTG	295219	127415	CATTCCTGGGAATGTCCAAA
206046	38242	CCACTGCACCCGGCCCTGTC	250633	82829	CTGAGAAATCCATACATCTT	295220	127416	ACATTCCTGGGAATGTCCAA
206047	38243	GCCACTGCACCCGGCCCTGT	250634	82830	TCTGAGAAATCCATACATCT	295221	127417	GACATTCCTGGGAATGTCCA
206048	38244	AGCCACTGCACCCGGCCCTG	250635	82831	CTCTGAGAAATCCATACATC	295222	127418	AGACATTCCTGGGAATGTCC
206049	38245	GAGCCACTGCACCCGGCCCT	250636	82832	CCTCTGAGAAATCCATACAT	295223	127419	AAGACATTCCTGGGAATGTC
206050	38246	TGAGCCACTGCACCCGGCCC	250637	82833	GCCTCTGAGAAATCCATACA	295224	127420	TAAGACATTCCTGGGAATGT
206051	38247	ATGAGCCACTGCACCCGGCC	250638	82834	TGCCTCTGAGAAATCCATAC	295225	127421	TTAAGACATTCCTGGGAATG
206052	38248	CATGAGCCACTGCACCCGGC	250639	82835	CTGCCTCTGAGAAATCCATA	295226	127422	TTTAAGACATTCCTGGGAAT
206053	38249	GCATGAGCCACTGCACCCGG	250640	82836	ACTGCCTCTGAGAAATCCAT	295227	127423	TTTTAAGACATTCCTGGGAA
206054	38250	GGCATGAGCCACTGCACCCG	250641	82837	CACTGCCTCTGAGAAATCCA	295228	127424	TTTTTAAGACATTCCTGGGA
206055	38251	AGGCATGAGCCACTGCACCC	250642	82838	CCACTGCCTCTGAGAAATCC	295229	127425	TTTTTTAAGACATTCCTGGG
206056	38252	TAGGCATGAGCCACTGCACC	250643	82839	GCCACTGCCTCTGAGAAATC	295230	127426	GTTTTTTAAGACATTCCTGG
206057	38253	ATAGGCATGAGCCACTGCAC	250644	82840	GGCCACTGCCTCTGAGAAAT	295231	127427	TGTTTTTTAAGACATTCCTG
206058	38254	TATAGGCATGAGCCACTGCA	250645	82841	AGGCCACTGCCTCTGAGAAA	295232	127428	GTGTTTTTTAAGACATTCCT
206059	38255	TTATAGGCATGAGCCACTGC	250646	82842	GAGGCCACTGCCTCTGAGAA	295233	127429	AGTGTTTTTTAAGACATTCC
206060	38256	ATTATAGGCATGAGCCACTG	250647	82843	AGAGGCCACTGCCTCTGAGA	295234	127430	AAGTGTTTTTTAAGACATTC
206061	38257	GATTATAGGCATGAGCCACT	250648	82844	CAGAGGCCACTGCCTCTGAG	295235	127431	GAAGTGTTTTTTAAGACATT
206062	38258	GGATTATAGGCATGAGCCAC	250649	82845	ACAGAGGCCACTGCCTCTGA	295236	127432	TGAAGTGTTTTTTAAGACAT
206063	38259	GGGATTATAGGCATGAGCCA	250650	82846	GACAGAGGCCACTGCCTCTG	295237	127433	TTGAAGTGTTTTTTAAGACA
206064	38260	TGGGATTATAGGCATGAGCC	250651	82847	TGACAGAGGCCACTGCCTCT	295238	127434	TTTGAAGTGTTTTTTAAGAC
206065	38261	TTGGGATTATAGGCATGAGC	250652	82848	ATGACAGAGGCCACTGCCTC	295239	127435	TTTTGAAGTGTTTTTTAAGA
206066	38262	GTTGGGATTATAGGCATGAG	250653	82849	AATGACAGAGGCCACTGCCT	295240	127436	TTTTTGAAGTGTTTTTTAAG
206067	38263	TGTTGGGATTATAGGCATGA	250654	82850	CAATGACAGAGGCCACTGCC	295241	127437	TTTTTTGAAGTGTTTTTTAA
206068	38264	GTGTTGGGATTATAGGCATG	250655	82851	ACAATGACAGAGGCCACTGC	295242	127438	GTTTTTTGAAGTGTTTTTTA
206069	38265	AGTGTTGGGATTATAGGCAT	250656	82852	GACAATGACAGAGGCCACTG	295243	127439	TGTTTTTTGAAGTGTTTTTT
206070	38266	AAGTGTTGGGATTATAGGCA	250657	82853	GGACAATGACAGAGGCCACT	295244	127440	ATGTTTTTTGAAGTGTTTTT
206071	38267	AAAGTGTTGGGATTATAGGC	250658	82854	AGGACAATGACAGAGGCCAC	295245	127441	AATGTTTTTTGAAGTGTTTT
206072	38268	CAAAGTGTTGGGATTATAGG	250659	82855	GAGGACAATGACAGAGGCCA	295246	127442	TAATGTTTTTTGAAGTGTTT
206073	38269	CCAAAGTGTTGGGATTATAG	250660	82856	TGAGGACAATGACAGAGGCC	295247	127443	TTAATGTTTTTTGAAGTGTT
206074	38270	CCCAAAGTGTTGGGATTATA	250661	82857	CTGAGGACAATGACAGAGGC	295248	127444	GTTAATGTTTTTTGAAGTGT
206075	38271	TCCCAAAGTGTTGGGATTAT	250662	82858	CCTGAGGACAATGACAGAGG	295249	127445	TGTTAATGTTTTTTGAAGTG
206076	38272	CTCCCAAAGTGTTGGGATTA	250663	82859	TCCTGAGGACAATGACAGAG	295250	127446	ATGTTAATGTTTTTTGAAGT
206077	38273	CCTCCCAAAGTGTTGGGATT	250664	82860	TTCCTGAGGACAATGACAGA	295251	127447	TATGTTAATGTTTTTTGAAG
206078	38274	GCCTCCCAAAGTGTTGGGAT	250665	82861	TTTCCTGAGGACAATGACAG	295252	127448	TTATGTTAATGTTTTTTGAA
206079	38275	GGCCTCCCAAAGTGTTGGGA	250666	82862	ATTTCCTGAGGACAATGACA	295253	127449	TTTATGTTAATGTTTTTTGA
206080	38276	CGGCCTCCCAAAGTGTTGGG	250667	82863	CATTTCCTGAGGACAATGAC	295254	127450	ATTTATGTTAATGTTTTTTG
206081	38277	TCGGCCTCCCAAAGTGTTGG	250668	82864	GCATTTCCTGAGGACAATGA	295255	127451	TATTTATGTTAATGTTTTTT
206082	38278	CTCGGCCTCCCAAAGTGTTG	250669	82865	AGCATTTCCTGAGGACAATG	295256	127452	ATATTTATGTTAATGTTTTT
206083	38279	CCTCGGCCTCCCAAAGTGTT	250670	82866	CAGCATTTCCTGAGGACAAT	295257	127453	AATATTTATGTTAATGTTTT
206084	38280	GCCTCGGCCTCCCAAAGTGT	250671	82867	CCAGCATTTCCTGAGGACAA	295258	127454	AAATATTTATGTTAATGTTT
206085	38281	TGCCTCGGCCTCCCAAAGTG	250672	82868	ACCAGCATTTCCTGAGGACA	295259	127455	AAAATATTTATGTTAATGTT
206086	38282	CTGCCTCGGCCTCCCAAAGT	250673	82869	CACCAGCATTTCCTGAGGAC	295260	127456	AAAAATATTTATGTTAATGT
206087	38283	CCTGCCTCGGCCTCCCAAAG	250674	82870	TCACCAGCATTTCCTGAGGA	295261	127457	TAAAAATATTTATGTTAATG
206088	38284	ACCTGCCTCGGCCTCCCAAA	250675	82871	ATCACCAGCATTTCCTGAGG	295262	127458	ATAAAAATATTTATGTTAAT
206089	38285	CACCTGCCTCGGCCTCCCAA	250676	82872	AATCACCAGCATTTCCTGAG	295263	127459	GATAAAAATATTTATGTTAA
206090	38286	CCACCTGCCTCGGCCTCCCA	250677	82873	GAATCACCAGCATTTCCTGA	295264	127460	TGATAAAAATATTTATGTTA
206091	38287	TCCACCTGCCTCGGCCTCCC	250678	82874	AGAATCACCAGCATTTCCTG	295265	127461	TTGATAAAAATATTTATGTT
206092	38288	ATCCACCTGCCTCGGCCTCC	250679	82875	CAGAATCACCAGCATTTCCT	295266	127462	TTTGATAAAAATATTTATGT
206093	38289	GATCCACCTGCCTCGGCCTC	250680	82876	CCAGAATCACCAGCATTTCC	295267	127463	CTTTGATAAAAATATTTATG
206094	38290	TGATCCACCTGCCTCGGCCT	250681	82877	ACCAGAATCACCAGCATTTC	295268	127464	GCTTTGATAAAAATATTTAT
206095	38291	GTGATCCACCTGCCTCGGCC	250682	82878	CACCAGAATCACCAGCATTT	295269	127465	GGCTTTGATAAAAATATTTA
206096	38292	AGTGATCCACCTGCCTCGGC	250683	82879	CCACCAGAATCACCAGCATT	295270	127466	AGGCTTTGATAAAAATATTT
206097	38293	AAGTGATCCACCTGCCTCGG	250684	82880	GCCACCAGAATCACCAGCAT	295271	127467	CAGGCTTTGATAAAAATATT
206098	38294	CAAGTGATCCACCTGCCTCG	250685	82881	GGCCACCAGAATCACCAGCA	295272	127468	ACAGGCTTTGATAAAAATAT
206099	38295	TCAAGTGATCCACCTGCCTC	250686	82882	AGGCCACCAGAATCACCAGC	295273	127469	TACAGGCTTTGATAAAAATA
206100	38296	ATCAAGTGATCCACCTGCCT	250687	82883	CAGGCCACCAGAATCACCAG	295274	127470	ATACAGGCTTTGATAAAAAT
206101	38297	CATCAAGTGATCCACCTGCC	250688	82884	TCAGGCCACCAGAATCACCA	295275	127471	AATACAGGCTTTGATAAAAA
206102	38298	ACATCAAGTGATCCACCTGC	250689	82885	CTCAGGCCACCAGAATCACC	295276	127472	TAATACAGGCTTTGATAAAA
206103	38299	GACATCAAGTGATCCACCTG	250690	82886	CCTCAGGCCACCAGAATCAC	295277	127473	TTAATACAGGCTTTGATAAA
206104	38300	TGACATCAAGTGATCCACCT	250691	82887	ACCTCAGGCCACCAGAATCA	295278	127474	TTTAATACAGGCTTTGATAA
206105	38301	CTGACATCAAGTGATCCACC	250692	82888	GACCTCAGGCCACCAGAATC	295279	127475	ATTTAATACAGGCTTTGATA
206106	38302	CCTGACATCAAGTGATCCAC	250693	82889	TGACCTCAGGCCACCAGAAT	295280	127476	CATTTAATACAGGCTTTGAT

206107	38303	TCCTGACATCAAGTGATCCA	250694	82890	TTGACCTCAGGCCACCAGAA	295281	127477	CCATTTAATACAGGCTTTGA
206108	38304	CTCCTGACATCAAGTGATCC	250695	82891	ATTGACCTCAGGCCACCAGA	295282	127478	ACCATTTAATACAGGCTTTG
206109	38305	ACTCCTGACATCAAGTGATC	250696	82892	CATTGACCTCAGGCCACCAG	295283	127479	GACCATTTAATACAGGCTTT
206110	38306	AACTCCTGACATCAAGTGAT	250697	82893	GCATTGACCTCAGGCCACCA	295284	127480	AGACCATTTAATACAGGCTT
206111	38307	GAACTCCTGACATCAAGTGA	250698	82894	TGCATTGACCTCAGGCCACC	295285	127481	AAGACCATTTAATACAGGCT
206112	38308	CGAACTCCTGACATCAAGTG	250699	82895	ATGCATTGACCTCAGGCCAC	295286	127482	AAAGACCATTTAATACAGGC
206113	38309	TCGAACTCCTGACATCAAGT	250700	82896	CATGCATTGACCTCAGGCCA	295287	127483	GAAAGACCATTTAATACAGG
206114	38310	CTCGAACTCCTGACATCAAG	250701	82897	ACATGCATTGACCTCAGGCC	295288	127484	TGAAAGACCATTTAATACAG
206115	38311	TCTCGAACTCCTGACATCAA	250702	82898	GACATGCATTGACCTCAGGC	295289	127485	TTGAAAGACCATTTAATACA
206116	38312	GTCTCGAACTCCTGACATCA	250703	82899	TGACATGCATTGACCTCAGG	295290	127486	CTTGAAAGACCATTTAATAC
206117	38313	GGTCTCGAACTCCTGACATC	250704	82900	TTGACATGCATTGACCTCAG	295291	127487	TCTTGAAAGACCATTTAATA
206118	38314	TGGTCTCGAACTCCTGACAT	250705	82901	GTTGACATGCATTGACCTCA	295292	127488	TTCTTGAAAGACCATTTAAT
206119	38315	CTGGTCTCGAACTCCTGACA	250706	82902	CGTTGACATGCATTGACCTC	295293	127489	TTTCTTGAAAGACCATTTAA
206120	38316	GCTGGTCTCGAACTCCTGAC	250707	82903	ACGTTGACATGCATTGACCT	295294	127490	TTTTCTTGAAAGACCATTTA
206121	38317	GGCTGGTCTCGAACTCCTGA	250708	82904	CACGTTGACATGCATTGACC	295295	127491	ATTTTCTTGAAAGACCATTT
206122	38318	AGGCTGGTCTCGAACTCCTG	250709	82905	CCACGTTGACATGCATTGAC	295296	127492	TATTTTCTTGAAAGACCATT
206123	38319	TAGGCTGGTCTCGAACTCCT	250710	82906	GCCACGTTGACATGCATTGA	295297	127493	GTATTTTCTTGAAAGACCAT
206124	38320	TTAGGCTGGTCTCGAACTCC	250711	82907	GGCCACGTTGACATGCATTG	295298	127494	TGTATTTTCTTGAAAGACCA
206125	38321	GTTAGGCTGGTCTCGAACTC	250712	82908	TGGCCACGTTGACATGCATT	295299	127495	CTGTATTTTCTTGAAAGACC
206126	38322	GGTTAGGCTGGTCTCGAACT	250713	82909	TTGGCCACGTTGACATGCAT	295300	127496	ACTGTATTTTCTTGAAAGAC
206127	38323	TGGTTAGGCTGGTCTCGAAC	250714	82910	GTTGGCCACGTTGACATGCA	295301	127497	TACTGTATTTTCTTGAAAGA
206128	38324	TTGGTTAGGCTGGTCTCGAA	250715	82911	AGTTGGCCACGTTGACATGC	295302	127498	TTACTGTATTTTCTTGAAAG
206129	38325	GTTGGTTAGGCTGGTCTCGA	250716	82912	AAGTTGGCCACGTTGACATG	295303	127499	GTTACTGTATTTTCTTGAAA
206130	38326	TGTTGGTTAGGCTGGTCTCG	250717	82913	CAAGTTGGCCACGTTGACAT	295304	127500	TGTTACTGTATTTTCTTGAA
206131	38327	ATGTTGGTTAGGCTGGTCTC	250718	82914	GCAAGTTGGCCACGTTGACA	295305	127501	CTGTTACTGTATTTTCTTGA
206132	38328	CATGTTGGTTAGGCTGGTCT	250719	82915	GGCAAGTTGGCCACGTTGAC	295306	127502	CCTGTTACTGTATTTTCTTG
206133	38329	TCATGTTGGTTAGGCTGGTC	250720	82916	AGGCAAGTTGGCCACGTTGA	295307	127503	ACCTGTTACTGTATTTTCTT
206134	38330	ATCATGTTGGTTAGGCTGGT	250721	82917	AAGGCAAGTTGGCCACGTTG	295308	127504	GACCTGTTACTGTATTTTCT
206135	38331	CATCATGTTGGTTAGGCTGG	250722	82918	TAAGGCAAGTTGGCCACGTT	295309	127505	TGACCTGTTACTGTATTTTC
206136	38332	TCATCATGTTGGTTAGGCTG	250723	82919	ATAAGGCAAGTTGGCCACGT	295310	127506	CTGACCTGTTACTGTATTTT
206137	38333	TTCATCATGTTGGTTAGGCT	250724	82920	TATAAGGCAAGTTGGCCACG	295311	127507	CCTGACCTGTTACTGTATTT
206138	38334	TTTCATCATGTTGGTTAGGC	250725	82921	TTATAAGGCAAGTTGGCCAC	295312	127508	GCCTGACCTGTTACTGTATT
206139	38335	GTTTCATCATGTTGGTTAGG	250726	82922	TTTATAAGGCAAGTTGGCCA	295313	127509	TGCCTGACCTGTTACTGTAT
206140	38336	GGTTTCATCATGTTGGTTAG	250727	82923	GTTTATAAGGCAAGTTGGCC	295314	127510	ATGCCTGACCTGTTACTGTA
206141	38337	GGGTTTCATCATGTTGGTTA	250728	82924	AGTTTATAAGGCAAGTTGGC	295315	127511	CATGCCTGACCTGTTACTGT
206142	38338	GGGGTTTCATCATGTTGGTT	250729	82925	AAGTTTATAAGGCAAGTTGG	295316	127512	CCATGCCTGACCTGTTACTG
206143	38339	TGGGGTTTCATCATGTTGGT	250730	82926	AAAGTTTATAAGGCAAGTTG	295317	127513	ACCATGCCTGACCTGTTACT
206144	38340	ATGGGGTTTCATCATGTTGG	250731	82927	AAAAGTTTATAAGGCAAGTT	295318	127514	CACCATGCCTGACCTGTTAC
206145	38341	GATGGGGTTTCATCATGTTG	250732	82928	AAAAAGTTTATAAGGCAAGT	295319	127515	CCACCATGCCTGACCTGTTA
206146	38342	AGATGGGGTTTCATCATGTT	250733	82929	AAAAAAGTTTATAAGGCAAG	295320	127516	GCCACCATGCCTGACCTGTT
206147	38343	GAGATGGGGTTTCATCATGT	250734	82930	AAAAAAAGTTTATAAGGCAA	295321	127517	AGCCACCATGCCTGACCTGT
206148	38344	AGAGATGGGGTTTCATCATG	250735	82931	GAAAAAAAGTTTATAAGGCA	295322	127518	GAGCCACCATGCCTGACCTG
206149	38345	TAGAGATGGGGTTTCATCAT	250736	82932	AGAAAAAAAGTTTATAAGGC	295323	127519	TGAGCCACCATGCCTGACCT
206150	38346	GTAGAGATGGGGTTTCATCA	250737	82933	CAGAAAAAAAGTTTATAAGG	295324	127520	ATGAGCCACCATGCCTGACC
206151	38347	AGTAGAGATGGGGTTTCATC	250738	82934	CCAGAAAAAAAGTTTATAAG	295325	127521	CATGAGCCACCATGCCTGAC
206152	38348	TAGTAGAGATGGGGTTTCAT	250739	82935	TCCAGAAAAAAAGTTTATAA	295326	127522	GCATGAGCCACCATGCCTGA
206153	38349	TTAGTAGAGATGGGGTTTCA	250740	82936	GTCCAGAAAAAAAGTTTATA	295327	127523	GGCATGAGCCACCATGCCTG
206154	38350	TTTAGTAGAGATGGGGTTTC	250741	82937	TGTCCAGAAAAAAAGTTTAT	295328	127524	AGGCATGAGCCACCATGCCT
206155	38351	TTTTAGTAGAGATGGGGTTT	250742	82938	TTGTCCAGAAAAAAAGTTTA	295329	127525	CAGGCATGAGCCACCATGCC
206156	38352	TTTTTAGTAGAGATGGGGTT	250743	82939	ATTGTCCAGAAAAAAAGTTT	295330	127526	ACAGGCATGAGCCACCATGC
206157	38353	ATTTTTAGTAGAGATGGGGT	250744	82940	AATTGTCCAGAAAAAAAGTT	295331	127527	TACAGGCATGAGCCACCATG
206158	38354	TATTTTTAGTAGAGATGGGG	250745	82941	CAATTGTCCAGAAAAAAAGT	295332	127528	TTACAGGCATGAGCCACCAT
206159	38355	GTATTTTTAGTAGAGATGGG	250746	82942	GCAATTGTCCAGAAAAAAAG	295333	127529	GTTACAGGCATGAGCCACCA
206160	38356	TGTATTTTTAGTAGAGATGG	250747	82943	CGCAATTGTCCAGAAAAAAA	295334	127530	GGTTACAGGCATGAGCCACC
206161	38357	TTGTATTTTTAGTAGAGATG	250748	82944	ACGCAATTGTCCAGAAAAAA	295335	127531	GGGTTACAGGCATGAGCCAC
206162	38358	TTTGTATTTTTAGTAGAGAT	250749	82945	CACGCAATTGTCCAGAAAAA	295336	127532	GGGGTTACAGGCATGAGCCA
206163	38359	TTTTGTATTTTTAGTAGAGA	250750	82946	GCACGCAATTGTCCAGAAAA	295337	127533	TGGGGTTACAGGCATGAGCC
206164	38360	TTTTTGTATTTTTAGTAGAG	250751	82947	TGCACGCAATTGTCCAGAAA	295338	127534	CTGGGGTTACAGGCATGAGC
206165	38361	ATTTTTGTATTTTTAGTAGA	250752	82948	GTGCACGCAATTGTCCAGAA	295339	127535	GCTGGGGTTACAGGCATGAG
206166	38362	AATTTTTGTATTTTTAGTAG	250753	82949	AGTGCACGCAATTGTCCAGA	295340	127536	TGCTGGGGTTACAGGCATGA
206167	38363	TAATTTTTGTATTTTTAGTA	250754	82950	CAGTGCACGCAATTGTCCAG	295341	127537	GTGCTGGGGTTACAGGCATG
206168	38364	CTAATTTTTGTATTTTTAGT	250755	82951	ACAGTGCACGCAATTGTCCA	295342	127538	AGTGCTGGGGTTACAGGCAT
206169	38365	GCTAATTTTTGTATTTTTAG	250756	82952	GACAGTGCACGCAATTGTCC	295343	127539	AAGTGCTGGGGTTACAGGCA
206170	38366	GGCTAATTTTTGTATTTTTA	250757	82953	GGACAGTGCACGCAATTGTC	295344	127540	AAAGTGCTGGGGTTACAGGC
206171	38367	TGGCTAATTTTTGTATTTTT	250758	82954	AGGACAGTGCACGCAATTGT	295345	127541	CAAAGTGCTGGGGTTACAGG
206172	38368	CTGGCTAATTTTTGTATTTT	250759	82955	CAGGACAGTGCACGCAATTG	295346	127542	CCAAAGTGCTGGGGTTACAG
206173	38369	CCTGGCTAATTTTTGTATTT	250760	82956	ACAGGACAGTGCACGCAATT	295347	127543	CCCAAAGTGCTGGGGTTACA
206174	38370	GCCTGGCTAATTTTTGTATT	250761	82957	TACAGGACAGTGCACGCAAT	295348	127544	TCCCAAAGTGCTGGGGTTAC
206175	38371	TGCCTGGCTAATTTTTGTAT	250762	82958	TTACAGGACAGTGCACGCAA	295349	127545	CTCCCAAAGTGCTGGGGTTA
206176	38372	GTGCCTGGCTAATTTTTGTA	250763	82959	GTTACAGGACAGTGCACGCA	295350	127546	CCTCCCAAAGTGCTGGGGTT
206177	38373	CGTGCCTGGCTAATTTTTGT	250764	82960	TGTTACAGGACAGTGCACGC	295351	127547	GCCTCCCAAAGTGCTGGGGT
206178	38374	CCGTGCCTGGCTAATTTTTG	250765	82961	CTGTTACAGGACAGTGCACG	295352	127548	GGCCTCCCAAAGTGCTGGGG

206179	38375	ACCGTGCCTGGCTAATTTTT	250766	82962	ACTGTTACAGGACAGTGCAC	295353	127549	TGGCCTCCCAAAGTGCTGGG
206180	38376	CACCGTGCCTGGCTAATTTT	250767	82963	CACTGTTACAGGACAGTGCA	295354	127550	TTGGCCTCCCAAAGTGCTGG
206181	38377	CCACCGTGCCTGGCTAATTT	250768	82964	ACACTGTTACAGGACAGTGC	295355	127551	CTTGGCCTCCCAAAGTGCTG
206182	38378	ACCACCGTGCCTGGCTAATT	250769	82965	GACACTGTTACAGGACAGTG	295356	127552	CCTTGGCCTCCCAAAGTGCT
206183	38379	TACCACCGTGCCTGGCTAAT	250770	82966	GGACACTGTTACAGGACAGT	295357	127553	GCCTTGGCCTCCCAAAGTGC
206184	38380	GTACCACCGTGCCTGGCTAA	250771	82967	AGGACACTGTTACAGGACAG	295358	127554	TGCCTTGGCCTCCCAAAGTG
206185	38381	TGTACCACCGTGCCTGGCTA	250772	82968	CAGGACACTGTTACAGGACA	295359	127555	CTGCCTTGGCCTCCCAAAGT
206186	38382	GTGTACCACCGTGCCTGGCT	250773	82969	ACAGGACACTGTTACAGGAC	295360	127556	CCTGCCTTGGCCTCCCAAAG
206187	38383	CGTGTACCACCGTGCCTGGC	250774	82970	AACAGGACACTGTTACAGGA	295361	127557	GCCTGCCTTGGCCTCCCAAA
206188	38384	GCGTGTACCACCGTGCCTGG	250775	82971	CAACAGGACACTGTTACAGG	295362	127558	TGCCTGCCTTGGCCTCCCAA
206189	38385	GGCGTGTACCACCGTGCCTG	250776	82972	ACAACAGGACACTGTTACAG	295363	127559	CTGCCTGCCTTGGCCTCCCA
206190	38386	AGGCGTGTACCACCGTGCCT	250777	82973	AACAACAGGACACTGTTACA	295364	127560	TCTGCCTGCCTTGGCCTCCC
206191	38387	CAGGCGTGTACCACCGTGCC	250778	82974	AAACAACAGGACACTGTTAC	295365	127561	ATCTGCCTGCCTTGGCCTCC
206192	38388	ACAGGCGTGTACCACCGTGC	250779	82975	TAAACAACAGGACACTGTTA	295366	127562	GATCTGCCTGCCTTGGCCTC
206193	38389	TACAGGCGTGTACCACCGTG	250780	82976	ATAAACAACAGGACACTGTT	295367	127563	TGATCTGCCTGCCTTGGCCT
206194	38390	TTACAGGCGTGTACCACCGT	250781	82977	CATAAACAACAGGACACTGT	295368	127564	GTGATCTGCCTGCCTTGGCC
206195	38391	ATTACAGGCGTGTACCACCG	250782	82978	TCATAAACAACAGGACACTG	295369	127565	GGTGATCTGCCTGCCTTGGC
206196	38392	GATTACAGGCGTGTACCACC	250783	82979	ATCATAAACAACAGGACACT	295370	127566	AGGTGATCTGCCTGCCTTGG
206197	38393	GGATTACAGGCGTGTACCAC	250784	82980	CATCATAAACAACAGGACAC	295371	127567	CAGGTGATCTGCCTGCCTTG
206198	38394	GGGATTACAGGCGTGTACCA	250785	82981	GCATCATAAACAACAGGACA	295372	127568	TCAGGTGATCTGCCTGCCTT
206199	38395	TGGGATTACAGGCGTGTACC	250786	82982	TGCATCATAAACAACAGGAC	295373	127569	TTCAGGTGATCTGCCTGCCT
206200	38396	CTGGGATTACAGGCGTGTAC	250787	82983	CTGCATCATAAACAACAGGA	295374	127570	TTTCAGGTGATCTGCCTGCC
206201	38397	GCTGGGATTACAGGCGTGTA	250788	82984	TCTGCATCATAAACAACAGG	295375	127571	ATTTCAGGTGATCTGCCTGC
206202	38398	AGCTGGGATTACAGGCGTGT	250789	82985	TTCTGCATCATAAACAACAG	295376	127572	GATTTCAGGTGATCTGCCTG
206203	38399	TAGCTGGGATTACAGGCGTG	250790	82986	TTTCTGCATCATAAACAACA	295377	127573	TGATTTCAGGTGATCTGCCT
206204	38400	GTAGCTGGGATTACAGGCGT	250791	82987	ATTTCTGCATCATAAACAAC	295378	127574	CTGATTTCAGGTGATCTGCC
206205	38401	AGTAGCTGGGATTACAGGCG	250792	82988	TATTTCTGCATCATAAACAA	295379	127575	CCTGATTTCAGGTGATCTGC
206206	38402	CAGTAGCTGGGATTACAGGC	250793	82989	CTATTTCTGCATCATAAACA	295380	127576	TCCTGATTTCAGGTGATCTG
206207	38403	CCAGTAGCTGGGATTACAGG	250794	82990	CCTATTTCTGCATCATAAAC	295381	127577	CTCCTGATTTCAGGTGATCT
206208	38404	CCCAGTAGCTGGGATTACAG	250795	82991	ACCTATTTCTGCATCATAAA	295382	127578	ACTCCTGATTTCAGGTGATC
206209	38405	CCCCAGTAGCTGGGATTACA	250796	82992	CACCTATTTCTGCATCATAA	295383	127579	AACTCCTGATTTCAGGTGAT
206210	38406	TCCCCAGTAGCTGGGATTAC	250797	82993	ACACCTATTTCTGCATCATA	295384	127580	GAACTCCTGATTTCAGGTGA
206211	38407	CTCCCCAGTAGCTGGGATTA	250798	82994	AACACCTATTTCTGCATCAT	295385	127581	TGAACTCCTGATTTCAGGTG
206212	38408	CCTCCCCAGTAGCTGGGATT	250799	82995	AAACACCTATTTCTGCATCA	295386	127582	TTGAACTCCTGATTTCAGGT
206213	38409	CCCTCCCCAGTAGCTGGGAT	250800	82996	AAAACACCTATTTCTGCATC	295387	127583	CTTGAACTCCTGATTTCAGG
206214	38410	ACCCTCCCCAGTAGCTGGGA	250801	82997	AAAAACACCTATTTCTGCAT	295388	127584	TCTTGAACTCCTGATTTCAG
206215	38411	CACCCTCCCCAGTAGCTGGG	250802	82998	TAAAAACACCTATTTCTGCA	295389	127585	GTCTTGAACTCCTGATTTCA
206216	38412	TCACCCTCCCCAGTAGCTGG	250803	82999	TTAAAAACACCTATTTCTGC	295390	127586	GGTCTTGAACTCCTGATTTC
206217	38413	CTCACCCTCCCCAGTAGCTG	250804	83000	TTTAAAAACACCTATTTCTG	295391	127587	TGGTCTTGAACTCCTGATTT
206218	38414	CCTCACCCTCCCCAGTAGCT	250805	83001	CTTTAAAAACACCTATTTCT	295392	127588	TTGGTCTTGAACTCCTGATT
206219	38415	GCCTCACCCTCCCCAGTAGC	250806	83002	GCTTTAAAAACACCTATTTC	295393	127589	GTTGGTCTTGAACTCCTGAT
206220	38416	TGCCTCACCCTCCCCAGTAG	250807	83003	GGCTTTAAAAACACCTATTT	295394	127590	GGTTGGTCTTGAACTCCTGA
206221	38417	CTGCCTCACCCTCCCCAGTA	250808	83004	AGGCTTTAAAAACACCTATT	295395	127591	AGGTTGGTCTTGAACTCCTG
206222	38418	CCTGCCTCACCCTCCCCAGT	250809	83005	TAGGCTTTAAAAACACCTAT	295396	127592	CAGGTTGGTCTTGAACTCCT
206223	38419	TCCTGCCTCACCCTCCCCAG	250810	83006	ATAGGCTTTAAAAACACCTA	295397	127593	CCAGGTTGGTCTTGAACTCC
206224	38420	CTCCTGCCTCACCCTCCCCA	250811	83007	AATAGGCTTTAAAAACACCT	295398	127594	GCCAGGTTGGTCTTGAACTC
206225	38421	TCTCCTGCCTCACCCTCCCC	250812	83008	CAATAGGCTTTAAAAACACC	295399	127595	GGCCAGGTTGGTCTTGAACT
206226	38422	TTCTCCTGCCTCACCCTCCC	250813	83009	TCAATAGGCTTTAAAAACAC	295400	127596	TGGCCAGGTTGGTCTTGAAC
206227	38423	ATTCTCCTGCCTCACCCTCC	250814	83010	ATCAATAGGCTTTAAAAACA	295401	127597	TTGGCCAGGTTGGTCTTGAA
206228	38424	GATTCTCCTGCCTCACCCTC	250815	83011	AATCAATAGGCTTTAAAAAC	295402	127598	GTTGGCCAGGTTGGTCTTGA
206229	38425	AGATTCTCCTGCCTCACCCT	250816	83012	AAATCAATAGGCTTTAAAAA	295403	127599	TGTTGGCCAGGTTGGTCTTG
206230	38426	GAGATTCTCCTGCCTCACCC	250817	83013	AAAATCAATAGGCTTTAAAA	295404	127600	GTGTTGGCCAGGTTGGTCTT
206231	38427	AGAGATTCTCCTGCCTCACC	250818	83014	CAAAATCAATAGGCTTTAAA	295405	127601	TGTGTTGGCCAGGTTGGTCT
206232	38428	AAGAGATTCTCCTGCCTCAC	250819	83015	CCAAAATCAATAGGCTTTAA	295406	127602	CTGTGTTGGCCAGGTTGGTC
206233	38429	CAAGAGATTCTCCTGCCTCA	250820	83016	ACCAAAATCAATAGGCTTTA	295407	127603	GCTGTGTTGGCCAGGTTGGT
206234	38430	TCAAGAGATTCTCCTGCCTC	250821	83017	TACCAAAATCAATAGGCTTT	295408	127604	GGCTGTGTTGGCCAGGTTGG
206235	38431	TTCAAGAGATTCTCCTGCCT	250822	83018	GTACCAAAATCAATAGGCTT	295409	127605	TGGCTGTGTTGGCCAGGTTG
206236	38432	GTTCAAGAGATTCTCCTGCC	250823	83019	AGTACCAAAATCAATAGGCT	295410	127606	TTGGCTGTGTTGGCCAGGTT
206237	38433	GGTTCAAGAGATTCTCCTGC	250824	83020	TAGTACCAAAATCAATAGGC	295411	127607	TTTGGCTGTGTTGGCCAGGT
206238	38434	GGGTTCAAGAGATTCTCCTG	250825	83021	ATAGTACCAAAATCAATAGG	295412	127608	ATTTGGCTGTGTTGGCCAGG
206239	38435	TGGGTTCAAGAGATTCTCCT	250826	83022	AATAGTACCAAAATCAATAG	295413	127609	GATTTGGCTGTGTTGGCCAG
206240	38436	CTGGGTTCAAGAGATTCTCC	250827	83023	TAATAGTACCAAAATCAATA	295414	127610	GGATTTGGCTGTGTTGGCCA
206241	38437	CCTGGGTTCAAGAGATTCTC	250828	83024	TTAATAGTACCAAAATCAAT	295415	127611	GGGATTTGGCTGTGTTGGCC
206242	38438	TCCTGGGTTCAAGAGATTCT	250829	83025	ATTAATAGTACCAAAATCAA	295416	127612	TGGGATTTGGCTGTGTTGGC
206243	38439	CTCCTGGGTTCAAGAGATTC	250830	83026	CATTAATAGTACCAAAATCA	295417	127613	ATGGGATTTGGCTGTGTTGG
206244	38440	CCTCCTGGGTTCAAGAGATT	250831	83027	ACATTAATAGTACCAAAATC	295418	127614	GATGGGATTTGGCTGTGTTG
206245	38441	GCCTCCTGGGTTCAAGAGAT	250832	83028	CACATTAATAGTACCAAAAT	295419	127615	AGATGGGATTTGGCTGTGTT
206246	38442	CGCCTCCTGGGTTCAAGAGA	250833	83029	CCACATTAATAGTACCAAAA	295420	127616	GAGATGGGATTTGGCTGTGT
206247	38443	CCGCCTCCTGGGTTCAAGAG	250834	83030	ACCACATTAATAGTACCAAA	295421	127617	AGAGATGGGATTTGGCTGTG
206248	38444	TCCGCCTCCTGGGTTCAAGA	250835	83031	GACCACATTAATAGTACCAA	295422	127618	TAGAGATGGGATTTGGCTGT
206249	38445	CTCCGCCTCCTGGGTTCAAG	250836	83032	TGACCACATTAATAGTACCA	295423	127619	GTAGAGATGGGATTTGGCTG
206250	38446	TCTCCGCCTCCTGGGTTCAA	250837	83033	CTGACCACATTAATAGTACC	295424	127620	TGTAGAGATGGGATTTGGCT

206251	38447	ATCTCCGCCTCCTGGGTTCA	250838	83034	CCTGACCACATTAATAGTAC	295425	127621	TTGTAGAGATGGGATTTGGC
206252	38448	AATCTCCGCCTCCTGGGTTC	250839	83035	TCCTGACCACATTAATAGTA	295426	127622	TTTGTAGAGATGGGATTTGG
206253	38449	CAATCTCCGCCTCCTGGGTT	250840	83036	TTCCTGACCACATTAATAGT	295427	127623	TTTTGTAGAGATGGGATTTG
206254	38450	GCAATCTCCGCCTCCTGGGT	250841	83037	GTTCCTGACCACATTAATAG	295428	127624	TTTTTGTAGAGATGGGATTT
206255	38451	TGCAATCTCCGCCTCCTGGG	250842	83038	AGTTCCTGACCACATTAATA	295429	127625	TTTTTTGTAGAGATGGGATT
206256	38452	CTGCAATCTCCGCCTCCTGG	250843	83039	AAGTTCCTGACCACATTAAT	295430	127626	ATTTTTTGTAGAGATGGGAT
206257	38453	ACTGCAATCTCCGCCTCCTG	250844	83040	AAAGTTCCTGACCACATTAA	295431	127627	TATTTTTTGTAGAGATGGGA
206258	38454	CACTGCAATCTCCGCCTCCT	250845	83041	GAAAGTTCCTGACCACATTA	295432	127628	GTATTTTTTGTAGAGATGGG
206259	38455	CCACTGCAATCTCCGCCTCC	250846	83042	AGAAAGTTCCTGACCACATT	295433	127629	TGTATTTTTTGTAGAGATGG
206260	38456	CCCACTGCAATCTCCGCCTC	250847	83043	GAGAAAGTTCCTGACCACAT	295434	127630	TTGTATTTTTTGTAGAGATG
206261	38457	GCCCACTGCAATCTCCGCCT	250848	83044	TGAGAAAGTTCCTGACCACA	295435	127631	TTTGTATTTTTTGTAGAGAT
206262	38458	GGCCCACTGCAATCTCCGCC	250849	83045	CTGAGAAAGTTCCTGACCAC	295436	127632	TTTTGTATTTTTTGTAGAGA
206263	38459	TGGCCCACTGCAATCTCCGC	250850	83046	ACTGAGAAAGTTCCTGACCA	295437	127633	TTTTTGTATTTTTTGTAGAG
206264	38460	TTGGCCCACTGCAATCTCCG	250851	83047	GACTGAGAAAGTTCCTGACC	295438	127634	ATTTTTGTATTTTTTGTAGA
206265	38461	CTTGGCCCACTGCAATCTCC	250852	83048	AGACTGAGAAAGTTCCTGAC	295439	127635	AATTTTTGTATTTTTTGTAG
206266	38462	TCTTGGCCCACTGCAATCTC	250853	83049	AAGACTGAGAAAGTTCCTGA	295440	127636	TAATTTTTGTATTTTTTGTA
206267	38463	ATCTTGGCCCACTGCAATCT	250854	83050	AAAGACTGAGAAAGTTCCTG	295441	127637	CTAATTTTTGTATTTTTTGT
206268	38464	GATCTTGGCCCACTGCAATC	250855	83051	GAAAGACTGAGAAAGTTCCT	295442	127638	GCTAATTTTTGTATTTTTTG
206269	38465	CGATCTTGGCCCACTGCAAT	250856	83052	AGAAAGACTGAGAAAGTTCC	295443	127639	AGCTAATTTTTGTATTTTTT
206270	38466	GCGATCTTGGCCCACTGCAA	250857	83053	AAGAAAGACTGAGAAAGTTC	295444	127640	CAGCTAATTTTTGTATTTTT
206271	38467	TGCGATCTTGGCCCACTGCA	250858	83054	CAAGAAAGACTGAGAAAGTT	295445	127641	CCAGCTAATTTTTGTATTTT
206272	38468	GTGCGATCTTGGCCCACTGC	250859	83055	ACAAGAAAGACTGAGAAAGT	295446	127642	CCCAGCTAATTTTTGTATTT
206273	38469	GGTGCGATCTTGGCCCACTG	250860	83056	AACAAGAAAGACTGAGAAAG	295447	127643	ACCCAGCTAATTTTTGTATT
206274	38470	TGGTGCGATCTTGGCCCACT	250861	83057	AAACAAGAAAGACTGAGAAA	295448	127644	CACCCAGCTAATTTTTGTAT
206275	38471	ATGGTGCGATCTTGGCCCAC	250862	83058	CAAACAAGAAAGACTGAGAA	295449	127645	ACACCCAGCTAATTTTTGTA
206276	38472	AATGGTGCGATCTTGGCCCA	250863	83059	CCAAACAAGAAAGACTGAGA	295450	127646	CACACCCAGCTAATTTTTGT
206277	38473	CAATGGTGCGATCTTGGCCC	250864	83060	CCCAAACAAGAAAGACTGAG	295451	127647	CCACACCCAGCTAATTTTTG
206278	38474	GCAATGGTGCGATCTTGGCC	250865	83061	CCCCAAACAAGAAAGACTGA	295452	127648	ACCACACCCAGCTAATTTTT
206279	38475	TGCAATGGTGCGATCTTGGC	250866	83062	ACCCCAAACAAGAAAGACTG	295453	127649	CACCACACCCAGCTAATTTT
206280	38476	GTGCAATGGTGCGATCTTGG	250867	83063	CACCCCAAACAAGAAAGACT	295454	127650	CCACCACACCCAGCTAATTT
206281	38477	AGTGCAATGGTGCGATCTTG	250868	83064	TCACCCCAAACAAGAAAGAC	295455	127651	GCCACCACACCCAGCTAATT
206282	38478	GAGTGCAATGGTGCGATCTT	250869	83065	CTCACCCCAAACAAGAAAGA	295456	127652	TGCCACCACACCCAGCTAAT
206283	38479	AGAGTGCAATGGTGCGATCT	250870	83066	GCTCACCCCAAACAAGAAAG	295457	127653	GTGCCACCACACCCAGCTAA
206284	38480	TAGAGTGCAATGGTGCGATC	250871	83067	AGCTCACCCCAAACAAGAAA	295458	127654	TGTGCCACCACACCCAGCTA
206285	38481	CTAGAGTGCAATGGTGCGAT	250872	83068	CAGCTCACCCCAAACAAGAA	295459	127655	GTGTGCCACCACACCCAGCT
206286	38482	GCTAGAGTGCAATGGTGCGA	250873	83069	ACAGCTCACCCCAAACAAGA	295460	127656	TGTGTGCCACCACACCCAGC
206287	38483	GGCTAGAGTGCAATGGTGCG	250874	83070	CACAGCTCACCCCAAACAAG	295461	127657	GTGTGTGCCACCACACCCAG
206288	38484	GGGCTAGAGTGCAATGGTGC	250875	83071	CCACAGCTCACCCCAAACAA	295462	127658	GGTGTGTGCCACCACACCCA
206289	38485	GGGGCTAGAGTGCAATGGTG	250876	83072	GCCACAGCTCACCCCAAACA	295463	127659	AGGTGTGTGCCACCACACCC
206290	38486	TGGGGCTAGAGTGCAATGGT	250877	83073	AGCCACAGCTCACCCCAAAC	295464	127660	CAGGTGTGTGCCACCACACC
206291	38487	CTGGGGCTAGAGTGCAATGG	250878	83074	AAGCCACAGCTCACCCCAAA	295465	127661	ACAGGTGTGTGCCACCACAC
206292	38488	GCTGGGGCTAGAGTGCAATG	250879	83075	GAAGCCACAGCTCACCCCAA	295466	127662	TACAGGTGTGTGCCACCACA
206293	38489	TGCTGGGGCTAGAGTGCAAT	250880	83076	GGAAGCCACAGCTCACCCCA	295467	127663	CTACAGGTGTGTGCCACCAC
206294	38490	TTGCTGGGGCTAGAGTGCAA	250881	83077	AGGAAGCCACAGCTCACCCC	295468	127664	ACTACAGGTGTGTGCCACCA
206295	38491	GTTGCTGGGGCTAGAGTGCA	250882	83078	TAGGAAGCCACAGCTCACCC	295469	127665	GACTACAGGTGTGTGCCACC
206296	38492	TGTTGCTGGGGCTAGAGTGC	250883	83079	TTAGGAAGCCACAGCTCACC	295470	127666	GGACTACAGGTGTGTGCCAC
206297	38493	TTGTTGCTGGGGCTAGAGTG	250884	83080	TTTAGGAAGCCACAGCTCAC	295471	127667	GGGACTACAGGTGTGTGCCA
206298	38494	CTTGTTGCTGGGGCTAGAGT	250885	83081	GTTTAGGAAGCCACAGCTCA	295472	127668	TGGGACTACAGGTGTGTGCC
206299	38495	TCTTGTTGCTGGGGCTAGAG	250886	83082	TGTTTAGGAAGCCACAGCTC	295473	127669	CTGGGACTACAGGTGTGTGC
206300	38496	CTCTTGTTGCTGGGGCTAGA	250887	83083	CTGTTTAGGAAGCCACAGCT	295474	127670	GCTGGGACTACAGGTGTGTG
206301	38497	ACTCTTGTTGCTGGGGCTAG	250888	83084	CCTGTTTAGGAAGCCACAGC	295475	127671	AGCTGGGACTACAGGTGTGT
206302	38498	CACTCTTGTTGCTGGGGCTA	250889	83085	TCCTGTTTAGGAAGCCACAG	295476	127672	TAGCTGGGACTACAGGTGTG
206303	38499	TCACTCTTGTTGCTGGGGCT	250890	83086	TTCCTGTTTAGGAAGCCACA	295477	127673	GTAGCTGGGACTACAGGTGT
206304	38500	TTCACTCTTGTTGCTGGGGC	250891	83087	GTTCCTGTTTAGGAAGCCAC	295478	127674	AGTAGCTGGGACTACAGGTG
206305	38501	TTTCACTCTTGTTGCTGGGG	250892	83088	GGTTCCTGTTTAGGAAGCCA	295479	127675	AAGTAGCTGGGACTACAGGT
206306	38502	GTTTCACTCTTGTTGCTGGG	250893	83089	GGGTTCCTGTTTAGGAAGCC	295480	127676	CAAGTAGCTGGGACTACAGG
206307	38503	AGTTTCACTCTTGTTGCTGG	250894	83090	TGGGTTCCTGTTTAGGAAGC	295481	127677	CCAAGTAGCTGGGACTACAG
206308	38504	GAGTTTCACTCTTGTTGCTG	250895	83091	TTGGGTTCCTGTTTAGGAAG	295482	127678	CCCAAGTAGCTGGGACTACA
206309	38505	AGAGTTTCACTCTTGTTGCT	250896	83092	CTTGGGTTCCTGTTTAGGAA	295483	127679	TCCCAAGTAGCTGGGACTAC
206310	38506	CAGAGTTTCACTCTTGTTGC	250897	83093	TCTTGGGTTCCTGTTTAGGA	295484	127680	CTCCCAAGTAGCTGGGACTA
206311	38507	ACAGAGTTTCACTCTTGTTG	250898	83094	GTCTTGGGTTCCTGTTTAGG	295485	127681	CCTCCCAAGTAGCTGGGACT
206312	38508	AACAGAGTTTCACTCTTGTT	250899	83095	TGTCTTGGGTTCCTGTTTAG	295486	127682	GCCTCCCAAGTAGCTGGGAC
206313	38509	AAACAGAGTTTCACTCTTGT	250900	83096	GTGTCTTGGGTTCCTGTTTA	295487	127683	GGCCTCCCAAGTAGCTGGGA
206314	38510	GAAACAGAGTTTCACTCTTG	250901	83097	GGTGTCTTGGGTTCCTGTTT	295488	127684	CGGCCTCCCAAGTAGCTGGG
206315	38511	TGAAACAGAGTTTCACTCTT	250902	83098	GGGTGTCTTGGGTTCCTGTT	295489	127685	TCGGCCTCCCAAGTAGCTGG
206316	38512	TTGAAACAGAGTTTCACTCT	250903	83099	GGGGTGTCTTGGGTTCCTGT	295490	127686	CTCGGCCTCCCAAGTAGCTG
206317	38513	TTTGAAACAGAGTTTCACTC	250904	83100	GGGGGTGTCTTGGGTTCCTG	295491	127687	CCTCGGCCTCCCAAGTAGCT
206318	38514	GTTTGAAACAGAGTTTCACT	250905	83101	TGGGGGTGTCTTGGGTTCCT	295492	127688	GCCTCGGCCTCCCAAGTAGC
206319	38515	TGTTTGAAACAGAGTTTCAC	250906	83102	TTGGGGGTGTCTTGGGTTCC	295493	127689	TGCCTCGGCCTCCCAAGTAG
206320	38516	TTGTTTGAAACAGAGTTTCA	250907	83103	TTTGGGGGTGTCTTGGGTTC	295494	127690	CTGCCTCGGCCTCCCAAGTA
206321	38517	TTTGTTTGAAACAGAGTTTC	250908	83104	TTTTGGGGGTGTCTTGGGTT	295495	127691	CCTGCCTCGGCCTCCCAAGT
206322	38518	GTTTGTTTGAAACAGAGTTT	250909	83105	CTTTTGGGGGTGTCTTGGGT	295496	127692	TCCTGCCTCGGCCTCCCAAG

206323	38519	TGTTTGTTTGAAACAGAGTT	250910	83106	GCTTTTGGGGGTGTCTTGGG	295497	127693	CTCCTGCCTCGGCCTCCCAA
206324	38520	TTGTTTGTTTGAAACAGAGT	250911	83107	AGCTTTTGGGGGTGTCTTGG	295498	127694	TCTCCTGCCTCGGCCTCCCA
206325	38521	TTTGTTTGTTTGAAACAGAG	250912	83108	CAGCTTTTGGGGGTGTCTTG	295499	127695	TTCTCCTGCCTCGGCCTCCC
206326	38522	GTTTGTTTGTTTGAAACAGA	250913	83109	GCAGCTTTTGGGGGTGTCTT	295500	127696	ATTCTCCTGCCTCGGCCTCC
206327	38523	TGTTTGTTTGTTTGAAACAG	250914	83110	AGCAGCTTTTGGGGGTGTCT	295501	127697	AATTCTCCTGCCTCGGCCTC
206328	38524	TTGTTTGTTTGTTTGAAACA	250915	83111	GAGCAGCTTTTGGGGGTGTC	295502	127698	CAATTCTCCTGCCTCGGCCT
206329	38525	TTTGTTTGTTTGTTTGAAAC	250916	83112	TGAGCAGCTTTTGGGGGTGT	295503	127699	GCAATTCTCCTGCCTCGGCC
206330	38526	TTTTGTTTGTTTGTTTGAAA	250917	83113	GTGAGCAGCTTTTGGGGGTG	295504	127700	AGCAATTCTCCTGCCTCGGC
206331	38527	TTTTTGTTTGTTTGTTTGAA	250918	83114	GGTGAGCAGCTTTTGGGGGT	295505	127701	AAGCAATTCTCCTGCCTCGG
206332	38528	TTTTTTGTTTGTTTGTTTGA	250919	83115	TGGTGAGCAGCTTTTGGGGG	295506	127702	CAAGCAATTCTCCTGCCTCG
206333	38529	TTTTTTTGTTTGTTTGTTTG	250920	83116	CTGGTGAGCAGCTTTTGGGG	295507	127703	TCAAGCAATTCTCCTGCCTC
206334	38530	TTTTTTTTGTTTGTTTGTTT	250921	83117	GCTGGTGAGCAGCTTTTGGG	295508	127704	ATCAAGCAATTCTCCTGCCT
206335	38531	TTTTTTTTTGTTTGTTTGTT	250922	83118	TGCTGGTGAGCAGCTTTTGG	295509	127705	GATCAAGCAATTCTCCTGCC
206336	38532	TTTTTTTTTTGTTTGTTTGT	250923	83119	GTGCTGGTGAGCAGCTTTTG	295510	127706	GGATCAAGCAATTCTCCTGC
206337	38533	TTTTTTTTTTTGTTTGTTTG	250924	83120	AGTGCTGGTGAGCAGCTTTT	295511	127707	GGGATCAAGCAATTCTCCTG
206338	38534	GTTTTTTTTTTTGTTTGTTT	250925	83121	CAGTGCTGGTGAGCAGCTTT	295512	127708	CGGGATCAAGCAATTCTCCT
206339	38535	GGTTTTTTTTTTTGTTTGTT	250926	83122	GCAGTGCTGGTGAGCAGCTT	295513	127709	CCGGGATCAAGCAATTCTCC
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206341	38537	GAGGTTTTTTTTTTTGTTTG	250928	83124	TGGCAGTGCTGGTGAGCAGC	295515	127711	CTCCGGGATCAAGCAATTCT
206342	38538	AGAGGTTTTTTTTTTTGTTT	250929	83125	CTGGCAGTGCTGGTGAGCAG	295516	127712	CCTCCGGGATCAAGCAATTC
206343	38539	AAGAGGTTTTTTTTTTTGTT	250930	83126	GCTGGCAGTGCTGGTGAGCA	295517	127713	GCCTCCGGGATCAAGCAATT
206344	38540	CAAGAGGTTTTTTTTTTTGT	250931	83127	GGCTGGCAGTGCTGGTGAGC	295518	127714	CGCCTCCGGGATCAAGCAAT
206345	38541	CCAAGAGGTTTTTTTTTTTG	250932	83128	AGGCTGGCAGTGCTGGTGAG	295519	127715	CCGCCTCCGGGATCAAGCAA
206346	38542	TCCAAGAGGTTTTTTTTTTT	250933	83129	GAGGCTGGCAGTGCTGGTGA	295520	127716	TCCGCCTCCGGGATCAAGCA
206347	38543	GTCCAAGAGGTTTTTTTTTT	250934	83130	GGAGGCTGGCAGTGCTGGTG	295521	127717	CTCCGCCTCCGGGATCAAGC
206348	38544	GGTCCAAGAGGTTTTTTTTT	250935	83131	GGGAGGCTGGCAGTGCTGGT	295522	127718	CCTCCGCCTCCGGGATCAAG
206349	38545	TGGTCCAAGAGGTTTTTTTT	250936	83132	AGGGAGGCTGGCAGTGCTGG	295523	127719	ACCTCCGCCTCCGGGATCAA
206350	38546	CTGGTCCAAGAGGTTTTTTT	250937	83133	GAGGGAGGCTGGCAGTGCTG	295524	127720	AACCTCCGCCTCCGGGATCA
206351	38547	CCTGGTCCAAGAGGTTTTTT	250938	83134	AGAGGGAGGCTGGCAGTGCT	295525	127721	CAACCTCCGCCTCCGGGATC
206352	38548	TCCTGGTCCAAGAGGTTTTT	250939	83135	AAGAGGGAGGCTGGCAGTGC	295526	127722	GCAACCTCCGCCTCCGGGAT
206353	38549	TTCCTGGTCCAAGAGGTTTT	250940	83136	TAAGAGGGAGGCTGGCAGTG	295527	127723	TGCAACCTCCGCCTCCGGGA
206354	38550	TTTCCTGGTCCAAGAGGTTT	250941	83137	GTAAGAGGGAGGCTGGCAGT	295528	127724	CTGCAACCTCCGCCTCCGGG
206355	38551	TTTTCCTGGTCCAAGAGGTT	250942	83138	GGTAAGAGGGAGGCTGGCAG	295529	127725	ACTGCAACCTCCGCCTCCGG
206356	38552	ATTTTCCTGGTCCAAGAGGT	250943	83139	TGGTAAGAGGGAGGCTGGCA	295530	127726	CACTGCAACCTCCGCCTCCG
206357	38553	TATTTTCCTGGTCCAAGAGG	250944	83140	TTGGTAAGAGGGAGGCTGGC	295531	127727	TCACTGCAACCTCCGCCTCC
206358	38554	ATATTTTCCTGGTCCAAGAG	250945	83141	CTTGGTAAGAGGGAGGCTGG	295532	127728	CTCACTGCAACCTCCGCCTC
206359	38555	AATATTTTCCTGGTCCAAGA	250946	83142	ACTTGGTAAGAGGGAGGCTG	295533	127729	GCTCACTGCAACCTCCGCCT
206360	38556	AAATATTTTCCTGGTCCAAG	250947	83143	TACTTGGTAAGAGGGAGGCT	295534	127730	AGCTCACTGCAACCTCCGCC
206361	38557	AAAATATTTTCCTGGTCCAA	250948	83144	CTACTTGGTAAGAGGGAGGC	295535	127731	CAGCTCACTGCAACCTCCGC
206362	38558	AAAAATATTTTCCTGGTCCA	250949	83145	GCTACTTGGTAAGAGGGAGG	295536	127732	TCAGCTCACTGCAACCTCCG
206363	38559	AAAAAATATTTTCCTGGTCC	250950	83146	TGCTACTTGGTAAGAGGGAG	295537	127733	CTCAGCTCACTGCAACCTCC
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206365	38561	TTAAAAAATATTTTCCTGGT	250952	83148	GGTGCTACTTGGTAAGAGGG	295539	127735	ATCTCAGCTCACTGCAACCT
206366	38562	CTTAAAAAATATTTTCCTGG	250953	83149	GGGTGCTACTTGGTAAGAGG	295540	127736	GATCTCAGCTCACTGCAACC
206367	38563	CCTTAAAAAATATTTTCCTG	250954	83150	CGGGTGCTACTTGGTAAGAG	295541	127737	CGATCTCAGCTCACTGCAAC
206368	38564	CCCTTAAAAAATATTTTCCT	250955	83151	ACGGGTGCTACTTGGTAAGA	295542	127738	ACGATCTCAGCTCACTGCAA
206369	38565	TCCCTTAAAAAATATTTTCC	250956	83152	AACGGGTGCTACTTGGTAAG	295543	127739	CACGATCTCAGCTCACTGCA
206370	38566	CTCCCTTAAAAAATATTTTC	250957	83153	GAACGGGTGCTACTTGGTAA	295544	127740	GCACGATCTCAGCTCACTGC
206371	38567	CCTCCCTTAAAAAATATTTT	250958	83154	TGAACGGGTGCTACTTGGTA	295545	127741	GGCACGATCTCAGCTCACTG
206372	38568	TCCTCCCTTAAAAAATATTT	250959	83155	CTGAACGGGTGCTACTTGGT	295546	127742	TGGCACGATCTCAGCTCACT
206373	38569	CTCCTCCCTTAAAAAATATT	250960	83156	CCTGAACGGGTGCTACTTGG	295547	127743	GTGGCACGATCTCAGCTCAC
206374	38570	ACTCCTCCCTTAAAAAATAT	250961	83157	TCCTGAACGGGTGCTACTTG	295548	127744	AGTGGCACGATCTCAGCTCA
206375	38571	TACTCCTCCCTTAAAAAATA	250962	83158	GTCCTGAACGGGTGCTACTT	295549	127745	CAGTGGCACGATCTCAGCTC
206376	38572	ATACTCCTCCCTTAAAAAAT	250963	83159	TGTCCTGAACGGGTGCTACT	295550	127746	GCAGTGGCACGATCTCAGCT
206377	38573	AATACTCCTCCCTTAAAAAA	250964	83160	ATGTCCTGAACGGGTGCTAC	295551	127747	TGCAGTGGCACGATCTCAGC
206378	38574	AAATACTCCTCCCTTAAAAA	250965	83161	AATGTCCTGAACGGGTGCTA	295552	127748	GTGCAGTGGCACGATCTCAG
206379	38575	AAAATACTCCTCCCTTAAAA	250966	83162	GAATGTCCTGAACGGGTGCT	295553	127749	AGTGCAGTGGCACGATCTCA
206380	38576	TAAAATACTCCTCCCTTAAA	250967	83163	AGAATGTCCTGAACGGGTGC	295554	127750	GAGTGCAGTGGCACGATCTC
206381	38577	ATAAAATACTCCTCCCTTAA	250968	83164	CAGAATGTCCTGAACGGGTG	295555	127751	GGAGTGCAGTGGCACGATCT
206382	38578	GATAAAATACTCCTCCCTTA	250969	83165	GCAGAATGTCCTGAACGGGT	295556	127752	TGGAGTGCAGTGGCACGATC
206383	38579	TGATAAAATACTCCTCCCTT	250970	83166	CGCAGAATGTCCTGAACGGG	295557	127753	CTGGAGTGCAGTGGCACGAT
206384	38580	GTGATAAAATACTCCTCCCT	250971	83167	TCGCAGAATGTCCTGAACGG	295558	127754	GCTGGAGTGCAGTGGCACGA
206385	38581	AGTGATAAAATACTCCTCCC	250972	83168	TTCGCAGAATGTCCTGAACG	295559	127755	CGCTGGAGTGCAGTGGCACG
206386	38582	CAGTGATAAAATACTCCTCC	250973	83169	TTTCGCAGAATGTCCTGAAC	295560	127756	ACGCTGGAGTGCAGTGGCAC
206387	38583	CCAGTGATAAAATACTCCTC	250974	83170	CTTTCGCAGAATGTCCTGAA	295561	127757	CACGCTGGAGTGCAGTGGCA
206388	38584	GCCAGTGATAAAATACTCCT	250975	83171	CCTTTCGCAGAATGTCCTGA	295562	127758	CCACGCTGGAGTGCAGTGGC
206389	38585	TGCCAGTGATAAAATACTCC	250976	83172	GCCTTTCGCAGAATGTCCTG	295563	127759	CCCACGCTGGAGTGCAGTGG
206390	38586	ATGCCAGTGATAAAATACTC	250977	83173	TGCCTTTCGCAGAATGTCCT	295564	127760	ACCCACGCTGGAGTGCAGTG
206391	38587	AATGCCAGTGATAAAATACT	250978	83174	ATGCCTTTCGCAGAATGTCC	295565	127761	CACCCACGCTGGAGTGCAGT
206392	38588	CAATGCCAGTGATAAAATAC	250979	83175	AATGCCTTTCGCAGAATGTC	295566	127762	TCACCCACGCTGGAGTGCAG
206393	38589	ACAATGCCAGTGATAAAATA	250980	83176	AAATGCCTTTCGCAGAATGT	295567	127763	GTCACCCACGCTGGAGTGCA
206394	38590	AACAATGCCAGTGATAAAAT	250981	83177	CAAATGCCTTTCGCAGAATG	295568	127764	TGTCACCCACGCTGGAGTGC

206395	38591	AAACAATGCCAGTGATAAAA	250982	83178	GCAAATGCCTTTCGCAGAAT	295569	127765	TTGTCACCCACGCTGGAGTG
206396	38592	TAAACAATGCCAGTGATAAA	250983	83179	GGCAAATGCCTTTCGCAGAA	295570	127766	CTTGTCACCCACGCTGGAGT
206397	38593	CTAAACAATGCCAGTGATAA	250984	83180	GGGCAAATGCCTTTCGCAGA	295571	127767	CCTTGTCACCCACGCTGGAG
206398	38594	CCTAAACAATGCCAGTGATA	250985	83181	TGGGCAAATGCCTTTCGCAG	295572	127768	ACCTTGTCACCCACGCTGGA
206399	38595	TCCTAAACAATGCCAGTGAT	250986	83182	CTGGGCAAATGCCTTTCGCA	295573	127769	CACCTTGTCACCCACGCTGG
206400	38596	ATCCTAAACAATGCCAGTGA	250987	83183	TCTGGGCAAATGCCTTTCGC	295574	127770	TCACCTTGTCACCCACGCTG
206401	38597	AATCCTAAACAATGCCAGTG	250988	83184	TTCTGGGCAAATGCCTTTCG	295575	127771	TTCACCTTGTCACCCACGCT
206402	38598	CAATCCTAAACAATGCCAGT	250989	83185	CTTCTGGGCAAATGCCTTTC	295576	127772	ATTCACCTTGTCACCCACGC
206403	38599	GCAATCCTAAACAATGCCAG	250990	83186	ACTTCTGGGCAAATGCCTTT	295577	127773	GATTCACCTTGTCACCCACG
206404	38600	TGCAATCCTAAACAATGCCA	250991	83187	AACTTCTGGGCAAATGCCTT	295578	127774	AGATTCACCTTGTCACCCAC
206405	38601	CTGCAATCCTAAACAATGCC	250992	83188	CAACTTCTGGGCAAATGCCT	295579	127775	AAGATTCACCTTGTCACCCA
206406	38602	CCTGCAATCCTAAACAATGC	250993	83189	CCAACTTCTGGGCAAATGCC	295580	127776	AAAGATTCACCTTGTCACCC
206407	38603	GCCTGCAATCCTAAACAATG	250994	83190	CCCAACTTCTGGGCAAATGC	295581	127777	CAAAGATTCACCTTGTCACC
206408	38604	TGCCTGCAATCCTAAACAAT	250995	83191	TCCCAACTTCTGGGCAAATG	295582	127778	ACAAAGATTCACCTTGTCAC
206409	38605	GTGCCTGCAATCCTAAACAA	250996	83192	CTCCCAACTTCTGGGCAAAT	295583	127779	GACAAAGATTCACCTTGTCA
206410	38606	TGTGCCTGCAATCCTAAACA	250997	83193	CCTCCCAACTTCTGGGCAAA	295584	127780	AGACAAAGATTCACCTTGTC
206411	38607	ATGTGCCTGCAATCCTAAAC	250998	83194	TCCTCCCAACTTCTGGGCAA	295585	127781	GAGACAAAGATTCACCTTGT
206412	38608	CATGTGCCTGCAATCCTAAA	250999	83195	TTCCTCCCAACTTCTGGGCA	295586	127782	TGAGACAAAGATTCACCTTG
206413	38609	TCATGTGCCTGCAATCCTAA	251000	83196	CTTCCTCCCAACTTCTGGGC	295587	127783	TTGAGACAAAGATTCACCTT
206414	38610	ATCATGTGCCTGCAATCCTA	251001	83197	CCTTCCTCCCAACTTCTGGG	295588	127784	TTTGAGACAAAGATTCACCT
206415	38611	CATCATGTGCCTGCAATCCT	251002	83198	TCCTTCCTCCCAACTTCTGG	295589	127785	TTTTGAGACAAAGATTCACC
206416	38612	GCATCATGTGCCTGCAATCC	251003	83199	TTCCTTCCTCCCAACTTCTG	295590	127786	TTTTTGAGACAAAGATTCAC
206417	38613	AGCATCATGTGCCTGCAATC	251004	83200	TTTCCTTCCTCCCAACTTCT	295591	127787	TTTTTTGAGACAAAGATTCA
206418	38614	TAGCATCATGTGCCTGCAAT	251005	83201	ATTTCCTTCCTCCCAACTTC	295592	127788	TTTTTTTGAGACAAAGATTC
206419	38615	TTAGCATCATGTGCCTGCAA	251006	83202	CATTTCCTTCCTCCCAACTT	295593	127789	TTTTTTTTGAGACAAAGATT
206420	38616	ATTAGCATCATGTGCCTGCA	251007	83203	ACATTTCCTTCCTCCCAACT	295594	127790	TTTTTTTTTGAGACAAAGAT
206421	38617	CATTAGCATCATGTGCCTGC	251008	83204	TACATTTCCTTCCTCCCAAC	295595	127791	TTTTTTTTTTGAGACAAAGA
206422	38618	TCATTAGCATCATGTGCCTG	251009	83205	TTACATTTCCTTCCTCCCAA	295596	127792	TTTTTTTTTTTGAGACAAAG
206423	38619	TTCATTAGCATCATGTGCCT	251010	83206	GTTACATTTCCTTCCTCCCA	295597	127793	TTTTTTTTTTTTGAGACAAA
206424	38620	TTTCATTAGCATCATGTGCC	251011	83207	TGTTACATTTCCTTCCTCCC	295598	127794	TTTTTTTTTTTTTGAGACAA
206425	38621	TTTTCATTAGCATCATGTGC	251012	83208	ATGTTACATTTCCTTCCTCC	295599	127795	TTTTTTTTTTTTTTGAGACA
206426	38622	CTTTTCATTAGCATCATGTG	251013	83209	AATGTTACATTTCCTTCCTC	295600	127796	TTTTTTTTTTTTTTTGAGAC
206427	38623	GCTTTTCATTAGCATCATGT	251014	83210	AAATGTTACATTTCCTTCCT	295601	127797	TTTTTTTTTTTTTTTTGAGA
206428	38624	TGCTTTTCATTAGCATCATG	251015	83211	AAAATGTTACATTTCCTTCC	295602	127798	TTTTTTTTTTTTTTTTTGAG
206429	38625	CTGCTTTTCATTAGCATCAT	251016	83212	CAAAATGTTACATTTCCTTC	295603	127799	TTTTTTTTTTTTTTTTTGA
206430	38626	TCTGCTTTTCATTAGCATCA	251017	83213	CCAAAATGTTACATTTCCTT	295604	127800	TTTTTTTTTTTTTTTTTTG
206431	38627	GTCTGCTTTTCATTAGCATC	251018	83214	CCCAAAATGTTACATTTCCT	295605	127801	TTTTTTTTTTTTTTTTTTT
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206433	38629	TAGTCTGCTTTTCATTAGCA	251020	83216	GCCCCAAAATGTTACATTTC	295607	127803	TCTTTTTTTTTTTTTTTTT
206434	38630	TTAGTCTGCTTTTCATTAGC	251021	83217	TGCCCCAAAATGTTACATTT	295608	127804	ATCTTTTTTTTTTTTTTTT
206435	38631	GTTAGTCTGCTTTTCATTAG	251022	83218	GTGCCCCAAAATGTTACATT	295609	127805	TATCTTTTTTTTTTTTTTT
206436	38632	AGTTAGTCTGCTTTTCATTA	251023	83219	GGTGCCCCAAAATGTTACAT	295610	127806	TTATCTTTTTTTTTTTTTT
206437	38633	TAGTTAGTCTGCTTTTCATT	251024	83220	AGGTGCCCCAAAATGTTACA	295611	127807	TTTATCTTTTTTTTTTTTT
206438	38634	ATAGTTAGTCTGCTTTTCAT	251025	83221	TAGGTGCCCCAAAATGTTAC	295612	127808	TTTTATCTTTTTTTTTTTT
206439	38635	AATAGTTAGTCTGCTTTTCA	251026	83222	GTAGGTGCCCCAAAATGTTA	295613	127809	ATTTTATCTTTTTTTTTTT
206440	38636	TAATAGTTAGTCTGCTTTTC	251027	83223	GGTAGGTGCCCCAAAATGTT	295614	127810	TATTTTATCTTTTTTTTTT
206441	38637	CTAATAGTTAGTCTGCTTTT	251028	83224	TGGTAGGTGCCCCAAAATGT	295615	127811	GTATTTTATCTTTTTTTTT
206442	38638	ACTAATAGTTAGTCTGCTTT	251029	83225	ATGGTAGGTGCCCCAAAATG	295616	127812	TGTATTTTATCTTTTTTTT
206443	38639	AACTAATAGTTAGTCTGCTT	251030	83226	TATGGTAGGTGCCCCAAAAT	295617	127813	CTGTATTTTATCTTTTTTT
206444	38640	CAACTAATAGTTAGTCTGCT	251031	83227	ATATGGTAGGTGCCCCAAAA	295618	127814	ACTGTATTTTATCTTTTTTT
206445	38641	CCAACTAATAGTTAGTCTGC	251032	83228	CATATGGTAGGTGCCCCAAA	295619	127815	TACTGTATTTTATCTTTTTT
206446	38642	ACCAACTAATAGTTAGTCTG	251033	83229	GCATATGGTAGGTGCCCCAA	295620	127816	ATACTGTATTTTATCTTTTT
206447	38643	AACCAACTAATAGTTAGTCT	251034	83230	GGCATATGGTAGGTGCCCCA	295621	127817	TATACTGTATTTTATCTTTT
206448	38644	AAACCAACTAATAGTTAGTC	251035	83231	TGGCATATGGTAGGTGCCCC	295622	127818	GTATACTGTATTTTATCTTT
206449	38645	AAAACCAACTAATAGTTAGT	251036	83232	CTGGCATATGGTAGGTGCCC	295623	127819	TGTATACTGTATTTTATCTT
206450	38646	TAAAACCAACTAATAGTTAG	251037	83233	CCTGGCATATGGTAGGTGCC	295624	127820	CTGTATACTGTATTTTATCT
206451	38647	ATAAAACCAACTAATAGTTA	251038	83234	GCCTGGCATATGGTAGGTGC	295625	127821	ACTGTATACTGTATTTTATC
206452	38648	AATAAAACCAACTAATAGTT	251039	83235	TGCCTGGCATATGGTAGGTG	295626	127822	TACTGTATACTGTATTTTAT
206453	38649	TAATAAAACCAACTAATAGT	251040	83236	GTGCCTGGCATATGGTAGGT	295627	127823	TTACTGTATACTGTATTTTA
206454	38650	GTAATAAAACCAACTAATAG	251041	83237	GGTGCCTGGCATATGGTAGG	295628	127824	ATTACTGTATACTGTATTTT
206455	38651	AGTAATAAAACCAACTAATA	251042	83238	TGGTGCCTGGCATATGGTAG	295629	127825	TATTACTGTATACTGTATTT
206456	38652	CAGTAATAAAACCAACTAAT	251043	83239	CTGGTGCCTGGCATATGGTA	295630	127826	CTATTACTGTATACTGTATT
206457	38653	ACAGTAATAAAACCAACTAA	251044	83240	CCTGGTGCCTGGCATATGGT	295631	127827	TCTATTACTGTATACTGTAT
206458	38654	AACAGTAATAAAACCAACTA	251045	83241	GCCTGGTGCCTGGCATATGG	295632	127828	CTCTATTACTGTATACTGTA
206459	38655	AAACAGTAATAAAACCAACT	251046	83242	AGCCTGGTGCCTGGCATATG	295633	127829	TCTCTATTACTGTATACTGT
206460	38656	AAAACAGTAATAAAACCAAC	251047	83243	TAGCCTGGTGCCTGGCATAT	295634	127830	TTCTCTATTACTGTATACTG
206461	38657	AAAAACAGTAATAAAACCAA	251048	83244	TTAGCCTGGTGCCTGGCATA	295635	127831	GTTCTCTATTACTGTATACT
206462	38658	CAAAAACAGTAATAAAACCA	251049	83245	TTTAGCCTGGTGCCTGGCAT	295636	127832	TGTTCTCTATTACTGTATAC
206463	38659	TCAAAAACAGTAATAAAACC	251050	83246	GTTTAGCCTGGTGCCTGGCA	295637	127833	TTGTTCTCTATTACTGTATA
206464	38660	TTCAAAAACAGTAATAAAAC	251051	83247	CGTTTAGCCTGGTGCCTGGC	295638	127834	ATTGTTCTCTATTACTGTAT
206465	38661	GTTCAAAAACAGTAATAAAA	251052	83248	ACGTTTAGCCTGGTGCCTGG	295639	127835	GATTGTTCTCTATTACTGTA
206466	38662	AGTTCAAAAACAGTAATAAA	251053	83249	CACGTTTAGCCTGGTGCCTG	295640	127836	GGATTGTTCTCTATTACTGT

206467	38663	GAGTTCAAAAACAGTAATAA	251054	83250	ACACGTTTAGCCTGGTGCCT	295641	127837	AGGATTGTTCTCTATTACTG
206468	38664	AGAGTTCAAAAACAGTAATA	251055	83251	AACACGTTTAGCCTGGTGCC	295642	127838	AAGGATTGTTCTCTATTACT
206469	38665	GAGAGTTCAAAAACAGTAAT	251056	83252	GAACACGTTTAGCCTGGTGC	295643	127839	AAAGGATTGTTCTCTATTAC
206470	38666	AGAGAGTTCAAAAACAGTAA	251057	83253	TGAACACGTTTAGCCTGGTG	295644	127840	AAAAGGATTGTTCTCTATTA
206471	38667	GAGAGAGTTCAAAAACAGTA	251058	83254	GTGAACACGTTTAGCCTGGT	295645	127841	AAAAAGGATTGTTCTCTATT
206472	38668	AGAGAGAGTTCAAAAACAGT	251059	83255	TGTGAACACGTTTAGCCTGG	295646	127842	AAAAAAGGATTGTTCTCTAT
206473	38669	GAGAGAGAGTTCAAAAACAG	251060	83256	GTGTGAACACGTTTAGCCTG	295647	127843	GAAAAAAGGATTGTTCTCTA
206474	38670	AGAGAGAGAGTTCAAAAACA	251061	83257	TGTGTGAACACGTTTAGCCT	295648	127844	TGAAAAAAGGATTGTTCTCT
206475	38671	GAGAGAGAGAGTTCAAAAAC	251062	83258	TTGTGTGAACACGTTTAGCC	295649	127845	TTGAAAAAAGGATTGTTCTC
206476	38672	GGAGAGAGAGAGTTCAAAAA	251063	83259	TTTGTGTGAACACGTTTAGC	295650	127846	TTTGAAAAAAGGATTGTTCT
206477	38673	GGGAGAGAGAGAGTTCAAAA	251064	83260	ATTTGTGTGAACACGTTTAG	295651	127847	CTTTGAAAAAAGGATTGTTC
206478	38674	AGGGAGAGAGAGAGTTCAAA	251065	83261	AATTTGTGTGAACACGTTTA	295652	127848	ACTTTGAAAAAAGGATTGTT
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206483	38679	AAAAAAGGGAGAGAGAGAGT	251070	83266	AAGAGAATTTGTGTGAACAC	295657	127853	TCACTACTTTGAAAAAAGGA
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206496	38692	GTCTCAAAAAAAAAAAAAAG	251083	83279	GGTGAGGGTTAGTAAGAGAA	295670	127866	TGTTCATTTGGGGTCACTAC
206497	38693	TGTCTCAAAAAAAAAAAAAA	251084	83280	TGGTGAGGGTTAGTAAGAGA	295671	127867	TTGTTCATTTGGGGTCACTA
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206500	38696	CTCTGTCTCAAAAAAAAAAA	251087	83283	GGATGGTGAGGGTTAGTAAG	295674	127870	ATTTTGTTCATTTGGGGTCA
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206502	38698	GACTCTGTCTCAAAAAAAAA	251089	83285	AAGGATGGTGAGGGTTAGTA	295676	127872	ATATTTTGTTCATTTGGGGT
206503	38699	AGACTCTGTCTCAAAAAAAA	251090	83286	GAAGGATGGTGAGGGTTAGT	295677	127873	CATATTTTGTTCATTTGGGG
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206506	38702	GAGAGACTCTGTCTCAAAAA	251093	83289	GTAGAAGGATGGTGAGGGTT	295680	127876	ATGCATATTTTGTTCATTTG
206507	38703	AGAGAGACTCTGTCTCAAAA	251094	83290	TGTAGAAGGATGGTGAGGGT	295681	127877	GATGCATATTTTGTTCATTT
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206509	38705	AGAGAGAGACTCTGTCTCAA	251096	83292	CTTGTAGAAGGATGGTGAGG	295683	127879	TAGATGCATATTTTGTTCAT
206510	38706	GAGAGAGAGACTCTGTCTCA	251097	83293	TCTTGTAGAAGGATGGTGAG	295684	127880	CTAGATGCATATTTTGTTCA
206511	38707	AGAGAGAGAGACTCTGTCTC	251098	83294	GTCTTGTAGAAGGATGGTGA	295685	127881	GCTAGATGCATATTTTGTTC
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206514	38710	GACAGAGAGAGAGACTCTGT	251101	83297	TTTGTCTTGTAGAAGGATGG	295688	127884	TAAGCTAGATGCATATTTTG
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206517	38713	GGTGACAGAGAGAGAGACTC	251104	83300	TAGTTTGTCTTGTAGAAGGA	295691	127887	ATTTAAGCTAGATGCATATT
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206523	38719	AGCCTGGGTGACAGAGAGAG	251110	83306	AGATACTAGTTTGTCTTGTA	295697	127893	GTTCGCATTTAAGCTAGATG
206524	38720	CAGCCTGGGTGACAGAGAGA	251111	83307	AAGATACTAGTTTGTCTTGT	295698	127894	GGTTCGCATTTAAGCTAGAT
206525	38721	CCAGCCTGGGTGACAGAGAG	251112	83308	GAAGATACTAGTTTGTCTTG	295699	127895	AGGTTCGCATTTAAGCTAGA
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206527	38723	TTCCAGCCTGGGTGACAGAG	251114	83310	ATGAAGATACTAGTTTGTCT	295701	127897	CCAGGTTCGCATTTAAGCTA
206528	38724	ATTCCAGCCTGGGTGACAGA	251115	83311	GATGAAGATACTAGTTTGTC	295702	127898	ACCAGGTTCGCATTTAAGCT
206529	38725	CATTCCAGCCTGGGTGACAG	251116	83312	AGATGAAGATACTAGTTTGT	295703	127899	AACCAGGTTCGCATTTAAGC
206530	38726	GCATTCCAGCCTGGGTGACA	251117	83313	AAGATGAAGATACTAGTTTG	295704	127900	AAACCAGGTTCGCATTTAAG
206531	38727	TGCATTCCAGCCTGGGTGAC	251118	83314	CAAGATGAAGATACTAGTTT	295705	127901	AAAACCAGGTTCGCATTTAA
206532	38728	CTGCATTCCAGCCTGGGTGA	251119	83315	CCAAGATGAAGATACTAGTT	295706	127902	GAAAACCAGGTTCGCATTTA
206533	38729	ACTGCATTCCAGCCTGGGTG	251120	83316	CCCAAGATGAAGATACTAGT	295707	127903	AGAAAACCAGGTTCGCATTT
206534	38730	CACTGCATTCCAGCCTGGGT	251121	83317	CCCCAAGATGAAGATACTAG	295708	127904	GAGAAAACCAGGTTCGCATT
206535	38731	TCACTGCATTCCAGCCTGGG	251122	83318	ACCCCAAGATGAAGATACTA	295709	127905	AGAGAAAACCAGGTTCGCAT
206536	38732	GTCACTGCATTCCAGCCTGG	251123	83319	AACCCCAAGATGAAGATACT	295710	127906	TAGAGAAAACCAGGTTCGCA
206537	38733	AGTCACTGCATTCCAGCCTG	251124	83320	GAACCCCAAGATGAAGATAC	295711	127907	GTAGAGAAAACCAGGTTCGC
206538	38734	CAGTCACTGCATTCCAGCCT	251125	83321	TGAACCCCAAGATGAAGATA	295712	127908	CGTAGAGAAAACCAGGTTCG

206539	38735	GCAGTCACTGCATTCCAGCC	251126	83322	TTGAACCCCAAGATGAAGAT	295713	127909	GCGTAGAGAAAACCAGGTTC
206540	38736	TGCAGTCACTGCATTCCAGC	251127	83323	CTTGAACCCCAAGATGAAGA	295714	127910	GGCGTAGAGAAAACCAGGTT
206541	38737	CTGCAGTCACTGCATTCCAG	251128	83324	TCTTGAACCCCAAGATGAAG	295715	127911	GGGCGTAGAGAAAACCAGGT
206542	38738	ACTGCAGTCACTGCATTCCA	251129	83325	ATCTTGAACCCCAAGATGAA	295716	127912	TGGGCGTAGAGAAAACCAGG
206543	38739	GACTGCAGTCACTGCATTCC	251130	83326	CATCTTGAACCCCAAGATGA	295717	127913	ATGGGCGTAGAGAAAACCAG
206544	38740	AGACTGCAGTCACTGCATTC	251131	83327	TCATCTTGAACCCCAAGATG	295718	127914	AATGGGCGTAGAGAAAACCA
206545	38741	GAGACTGCAGTCACTGCATT	251132	83328	CTCATCTTGAACCCCAAGAT	295719	127915	GAATGGGCGTAGAGAAAACC
206546	38742	TGAGACTGCAGTCACTGCAT	251133	83329	CCTCATCTTGAACCCCAAGA	295720	127916	TGAATGGGCGTAGAGAAAAC
206547	38743	CTGAGACTGCAGTCACTGCA	251134	83330	TCCTCATCTTGAACCCCAAG	295721	127917	TTGAATGGGCGTAGAGAAAA
206548	38744	GCTGAGACTGCAGTCACTGC	251135	83331	TTCCTCATCTTGAACCCCAA	295722	127918	CTTGAATGGGCGTAGAGAAA
206549	38745	AGCTGAGACTGCAGTCACTG	251136	83332	TTTCCTCATCTTGAACCCCA	295723	127919	GCTTGAATGGGCGTAGAGAA
206550	38746	GAGCTGAGACTGCAGTCACT	251137	83333	ATTTCCTCATCTTGAACCCC	295724	127920	GGCTTGAATGGGCGTAGAGA
206551	38747	TGAGCTGAGACTGCAGTCAC	251138	83334	CATTTCCTCATCTTGAACCC	295725	127921	GGGCTTGAATGGGCGTAGAG
206552	38748	GTGAGCTGAGACTGCAGTCA	251139	83335	CCATTTCCTCATCTTGAACC	295726	127922	GGGGCTTGAATGGGCGTAGA
206553	38749	AGTGAGCTGAGACTGCAGTC	251140	83336	TCCATTTCCTCATCTTGAAC	295727	127923	AGGGGCTTGAATGGGCGTAG
206554	38750	TAGTGAGCTGAGACTGCAGT	251141	83337	CTCCATTTCCTCATCTTGAA	295728	127924	CAGGGGCTTGAATGGGCGTA
206555	38751	GTAGTGAGCTGAGACTGCAG	251142	83338	CCTCCATTTCCTCATCTTGA	295729	127925	GCAGGGGCTTGAATGGGCGT
206556	38752	TGTAGTGAGCTGAGACTGCA	251143	83339	GCCTCCATTTCCTCATCTTG	295730	127926	TGCAGGGGCTTGAATGGGCG
206557	38753	ATGTAGTGAGCTGAGACTGC	251144	83340	AGCCTCCATTTCCTCATCTT	295731	127927	TTGCAGGGGCTTGAATGGGC
206558	38754	GATGTAGTGAGCTGAGACTG	251145	83341	GAGCCTCCATTTCCTCATCT	295732	127928	ATTGCAGGGGCTTGAATGGG
206559	38755	GGATGTAGTGAGCTGAGACT	251146	83342	TGAGCCTCCATTTCCTCATC	295733	127929	TATTGCAGGGGCTTGAATGG
206560	38756	AGGATGTAGTGAGCTGAGAC	251147	83343	CTGAGCCTCCATTTCCTCAT	295734	127930	CTATTGCAGGGGCTTGAATG
206561	38757	GAGGATGTAGTGAGCTGAGA	251148	83344	TCTGAGCCTCCATTTCCTCA	295735	127931	CCTATTGCAGGGGCTTGAAT
206562	38758	AGAGGATGTAGTGAGCTGAG	251149	83345	CTCTGAGCCTCCATTTCCTC	295736	127932	CCCTATTGCAGGGGCTTGAA
206563	38759	CAGAGGATGTAGTGAGCTGA	251150	83346	TCTCTGAGCCTCCATTTCCT	295737	127933	CCCCTATTGCAGGGGCTTGA
206564	38760	GCAGAGGATGTAGTGAGCTG	251151	83347	CTCTCTGAGCCTCCATTTCC	295738	127934	GCCCCTATTGCAGGGGCTTG
206565	38761	GGCAGAGGATGTAGTGAGCT	251152	83348	CCTCTCTGAGCCTCCATTTC	295739	127935	GGCCCCTATTGCAGGGGCTT
206566	38762	AGGCAGAGGATGTAGTGAGC	251153	83349	ACCTCTCTGAGCCTCCATTT	295740	127936	GGGCCCCTATTGCAGGGGCT
206567	38763	GAGGCAGAGGATGTAGTGAG	251154	83350	AACCTCTCTGAGCCTCCATT	295741	127937	AGGGCCCCTATTGCAGGGGC
206568	38764	GGAGGCAGAGGATGTAGTGA	251155	83351	CAACCTCTCTGAGCCTCCAT	295742	127938	AAGGGCCCCTATTGCAGGGG
206569	38765	AGGAGGCAGAGGATGTAGTG	251156	83352	TCAACCTCTCTGAGCCTCCA	295743	127939	GAAGGGCCCCTATTGCAGGG
206570	38766	GAGGAGGCAGAGGATGTAGT	251157	83353	TTCAACCTCTCTGAGCCTCC	295744	127940	TGAAGGGCCCCTATTGCAGG
206571	38767	TGAGGAGGCAGAGGATGTAG	251158	83354	ATTCAACCTCTCTGAGCCTC	295745	127941	GTGAAGGGCCCCTATTGCAG
206572	38768	CTGAGGAGGCAGAGGATGTA	251159	83355	CATTCAACCTCTCTGAGCCT	295746	127942	GGTGAAGGGCCCCTATTGCA
206573	38769	ACTGAGGAGGCAGAGGATGT	251160	83356	TCATTCAACCTCTCTGAGCC	295747	127943	GGGTGAAGGGCCCCTATTGC
206574	38770	AACTGAGGAGGCAGAGGATG	251161	83357	TTCATTCAACCTCTCTGAGC	295748	127944	GGGGTGAAGGGCCCCTATTG
206575	38771	GAACTGAGGAGGCAGAGGAT	251162	83358	ATTCATTCAACCTCTCTGAG	295749	127945	CGGGGTGAAGGGCCCCTATT
206576	38772	TGAACTGAGGAGGCAGAGGA	251163	83359	CATTCATTCAACCTCTCTGA	295750	127946	GCGGGGTGAAGGGCCCCTAT
206577	38773	TTGAACTGAGGAGGCAGAGG	251164	83360	GCATTCATTCAACCTCTCTG	295751	127947	TGCGGGGTGAAGGGCCCCTA
206578	38774	CTTGAACTGAGGAGGCAGAG	251165	83361	GGCATTCATTCAACCTCTCT	295752	127948	ATGCGGGGTGAAGGGCCCCT
206579	38775	ACTTGAACTGAGGAGGCAGA	251166	83362	CGGCATTCATTCAACCTCTC	295753	127949	GATGCGGGGTGAAGGGCCCC
206580	38776	CACTTGAACTGAGGAGGCAG	251167	83363	CCGGCATTCATTCAACCTCT	295754	127950	GGATGCGGGGTGAAGGGCCC
206581	38777	TCACTTGAACTGAGGAGGCA	251168	83364	ACCGGCATTCATTCAACCTC	295755	127951	TGGATGCGGGGTGAAGGGCC
206582	38778	ATCACTTGAACTGAGGAGGC	251169	83365	CACCGGCATTCATTCAACCT	295756	127952	ATGGATGCGGGGTGAAGGGC
206583	38779	AATCACTTGAACTGAGGAGG	251170	83366	GCACCGGCATTCATTCAACC	295757	127953	CATGGATGCGGGGTGAAGGG
206584	38780	GAATCACTTGAACTGAGGAG	251171	83367	GGCACCGGCATTCATTCAAC	295758	127954	CCATGGATGCGGGGTGAAGG
206585	38781	AGAATCACTTGAACTGAGGA	251172	83368	AGGCACCGGCATTCATTCAA	295759	127955	TCCATGGATGCGGGGTGAAG
206586	38782	GAGAATCACTTGAACTGAGG	251173	83369	CAGGCACCGGCATTCATTCA	295760	127956	GTCCATGGATGCGGGGTGAA
206587	38783	CGAGAATCACTTGAACTGAG	251174	83370	CCAGGCACCGGCATTCATTC	295761	127957	AGTCCATGGATGCGGGGTGA
206588	38784	ACGAGAATCACTTGAACTGA	251175	83371	TCCAGGCACCGGCATTCATT	295762	127958	GAGTCCATGGATGCGGGGTG
206589	38785	CACGAGAATCACTTGAACTG	251176	83372	ATCCAGGCACCGGCATTCAT	295763	127959	GGAGTCCATGGATGCGGGGT
206590	38786	GCACGAGAATCACTTGAACT	251177	83373	TATCCAGGCACCGGCATTCA	295764	127960	AGGAGTCCATGGATGCGGGG
206591	38787	GGCACGAGAATCACTTGAAC	251178	83374	ATATCCAGGCACCGGCATTC	295765	127961	TAGGAGTCCATGGATGCGGG
206592	38788	AGGCACGAGAATCACTTGAA	251179	83375	CATATCCAGGCACCGGCATT	295766	127962	TTAGGAGTCCATGGATGCGG
206593	38789	GAGGCACGAGAATCACTTGA	251180	83376	TCATATCCAGGCACCGGCAT	295767	127963	TTTAGGAGTCCATGGATGCG
206594	38790	TGAGGCACGAGAATCACTTG	251181	83377	TTCATATCCAGGCACCGGCA	295768	127964	TTTTAGGAGTCCATGGATGC
206595	38791	CTGAGGCACGAGAATCACTT	251182	83378	GTTCATATCCAGGCACCGGC	295769	127965	ATTTTAGGAGTCCATGGATG
206596	38792	GCTGAGGCACGAGAATCACT	251183	83379	GGTTCATATCCAGGCACCGG	295770	127966	AATTTTAGGAGTCCATGGAT
206597	38793	GGCTGAGGCACGAGAATCAC	251184	83380	GGGTTCATATCCAGGCACCG	295771	127967	TAATTTTAGGAGTCCATGGA
206598	38794	AGGCTGAGGCACGAGAATCA	251185	83381	GGGGTTCATATCCAGGCACC	295772	127968	ATAATTTTAGGAGTCCATGG
206599	38795	GAGGCTGAGGCACGAGAATC	251186	83382	TGGGGTTCATATCCAGGCAC	295773	127969	TATAATTTTAGGAGTCCATG
206600	38796	GGAGGCTGAGGCACGAGAAT	251187	83383	ATGGGGTTCATATCCAGGCA	295774	127970	ATATAATTTTAGGAGTCCAT
206601	38797	GGGAGGCTGAGGCACGAGAA	251188	83384	GATGGGGTTCATATCCAGGC	295775	127971	CATATAATTTTAGGAGTCCA
206602	38798	CGGGAGGCTGAGGCACGAGA	251189	83385	AGATGGGGTTCATATCCAGG	295776	127972	CCATATAATTTTAGGAGTCC
206603	38799	TCGGGAGGCTGAGGCACGAG	251190	83386	CAGATGGGGTTCATATCCAG	295777	127973	TCCATATAATTTTAGGAGTC
206604	38800	CTCGGGAGGCTGAGGCACGA	251191	83387	GCAGATGGGGTTCATATCCA	295778	127974	TTCCATATAATTTTAGGAGT
206605	38801	ACTCGGGAGGCTGAGGCACG	251192	83388	GGCAGATGGGGTTCATATCC	295779	127975	TTTCCATATAATTTTAGGAG
206606	38802	TACTCGGGAGGCTGAGGCAC	251193	83389	AGGCAGATGGGGTTCATATC	295780	127976	TTTTCCATATAATTTTAGGA
206607	38803	CTACTCGGGAGGCTGAGGCA	251194	83390	CAGGCAGATGGGGTTCATAT	295781	127977	ATTTTCCATATAATTTTAGG
206608	38804	GCTACTCGGGAGGCTGAGGC	251195	83391	TCAGGCAGATGGGGTTCATA	295782	127978	CATTTTCCATATAATTTTAG
206609	38805	AGCTACTCGGGAGGCTGAGG	251196	83392	GTCAGGCAGATGGGGTTCAT	295783	127979	CCATTTTCCATATAATTTTA
206610	38806	CAGCTACTCGGGAGGCTGAG	251197	83393	AGTCAGGCAGATGGGGTTCA	295784	127980	GCCATTTTCCATATAATTTT

206611	38807	CCAGCTACTCGGGAGGCTGA	251198	83394	GAGTCAGGCAGATGGGGTTC	295785	127981	AGCCATTTTCCATATAATTT
206612	38808	CCCAGCTACTCGGGAGGCTG	251199	83395	GGAGTCAGGCAGATGGGGTT	295786	127982	CAGCCATTTTCCATATAATT
206613	38809	TCCCAGCTACTCGGGAGGCT	251200	83396	CGGAGTCAGGCAGATGGGGT	295787	127983	ACAGCCATTTTCCATATAAT
206614	38810	ATCCCAGCTACTCGGGAGGC	251201	83397	GCGGAGTCAGGCAGATGGGG	295788	127984	CACAGCCATTTTCCATATAA
206615	38811	AATCCCAGCTACTCGGGAGG	251202	83398	TGCGGAGTCAGGCAGATGGG	295789	127985	ACACAGCCATTTTCCATATA
206616	38812	TAATCCCAGCTACTCGGGAG	251203	83399	TTGCGGAGTCAGGCAGATGG	295790	127986	CACACAGCCATTTTCCATAT
206617	38813	GTAATCCCAGCTACTCGGGA	251204	83400	GTTGCGGAGTCAGGCAGATG	295791	127987	ACACACAGCCATTTTCCATA
206618	38814	TGTAATCCCAGCTACTCGGG	251205	83401	GGTTGCGGAGTCAGGCAGAT	295792	127988	CACACACAGCCATTTTCCAT
206619	38815	CTGTAATCCCAGCTACTCGG	251206	83402	GGGTTGCGGAGTCAGGCAGA	295793	127989	TCACACACAGCCATTTTCCA
206620	38816	CCTGTAATCCCAGCTACTCG	251207	83403	TGGGTTGCGGAGTCAGGCAG	295794	127990	CTCACACACAGCCATTTTCC
206621	38817	CCCTGTAATCCCAGCTACTC	251208	83404	CTGGGTTGCGGAGTCAGGCA	295795	127991	ACTCACACACAGCCATTTTC
206622	38818	GCCCTGTAATCCCAGCTACT	251209	83405	CCTGGGTTGCGGAGTCAGGC	295796	127992	CACTCACACACAGCCATTTT
206623	38819	TGCCCTGTAATCCCAGCTAC	251210	83406	GCCTGGGTTGCGGAGTCAGG	295797	127993	ACACTCACACACAGCCATTT
206624	38820	GTGCCCTGTAATCCCAGCTA	251211	83407	TGCCTGGGTTGCGGAGTCAG	295798	127994	CACACTCACACACAGCCATT
206625	38821	GGTGCCCTGTAATCCCAGCT	251212	83408	TTGCCTGGGTTGCGGAGTCA	295799	127995	CCACACTCACACACAGCCAT
206626	38822	TGGTGCCCTGTAATCCCAGC	251213	83409	TTTGCCTGGGTTGCGGAGTC	295800	127996	TCCACACTCACACACAGCCA
206627	38823	GTGGTGCCCTGTAATCCCAG	251214	83410	CTTTGCCTGGGTTGCGGAGT	295801	127997	ATCCACACTCACACACAGCC
206628	38824	TGTGGTGCCCTGTAATCCCA	251215	83411	ACTTTGCCTGGGTTGCGGAG	295802	127998	CATCCACACTCACACACAGC
206629	38825	GTGTGGTGCCCTGTAATCCC	251216	83412	GACTTTGCCTGGGTTGCGGA	295803	127999	CCATCCACACTCACACACAG
206630	38826	GGTGTGGTGCCCTGTAATCC	251217	83413	AGACTTTGCCTGGGTTGCGG	295804	128000	TCCATCCACACTCACACACA
206631	38827	TGGTGTGGTGCCCTGTAATC	251218	83414	AAGACTTTGCCTGGGTTGCG	295805	128001	GTCCATCCACACTCACACAC
206632	38828	CTGGTGTGGTGCCCTGTAAT	251219	83415	AAAGACTTTGCCTGGGTTGC	295806	128002	TGTCCATCCACACTCACACA
206633	38829	CCTGGTGTGGTGCCCTGTAA	251220	83416	GAAAGACTTTGCCTGGGTTG	295807	128003	ATGTCCATCCACACTCACAC
206634	38830	GCCTGGTGTGGTGCCCTGTA	251221	83417	GGAAAGACTTTGCCTGGGTT	295808	128004	CATGTCCATCCACACTCACA
206635	38831	AGCCTGGTGTGGTGCCCTGT	251222	83418	AGGAAAGACTTTGCCTGGGT	295809	128005	ACATGTCCATCCACACTCAC
206636	38832	TAGCCTGGTGTGGTGCCCTG	251223	83419	AAGGAAAGACTTTGCCTGGG	295810	128006	CACATGTCCATCCACACTCA
206637	38833	TTAGCCTGGTGTGGTGCCCT	251224	83420	CAAGGAAAGACTTTGCCTGG	295811	128007	GCACATGTCCATCCACACTC
206638	38834	CTTAGCCTGGTGTGGTGCCC	251225	83421	TCAAGGAAAGACTTTGCCTG	295812	128008	TGCACATGTCCATCCACACT
206639	38835	ACTTAGCCTGGTGTGGTGCC	251226	83422	TTCAAGGAAAGACTTTGCCT	295813	128009	GTGCACATGTCCATCCACAC
206640	38836	AACTTAGCCTGGTGTGGTGC	251227	83423	GTTCAAGGAAAGACTTTGCC	295814	128010	TGTGCACATGTCCATCCACA
206641	38837	AAACTTAGCCTGGTGTGGTG	251228	83424	AGTTCAAGGAAAGACTTTGC	295815	128011	GTGTGCACATGTCCATCCAC
206642	38838	AAAACTTAGCCTGGTGTGGT	251229	83425	AAGTTCAAGGAAAGACTTTG	295816	128012	TGTGTGCACATGTCCATCCA
206643	38839	AAAAACTTAGCCTGGTGTGG	251230	83426	GAAGTTCAAGGAAAGACTTT	295817	128013	ATGTGTGCACATGTCCATCC
206644	38840	CAAAAACTTAGCCTGGTGTG	251231	83427	GGAAGTTCAAGGAAAGACTT	295818	128014	TATGTGTGCACATGTCCATC
206645	38841	ACAAAAACTTAGCCTGGTGT	251232	83428	GGGAAGTTCAAGGAAAGACT	295819	128015	ATATGTGTGCACATGTCCAT
206646	38842	TACAAAAACTTAGCCTGGTG	251233	83429	TGGGAAGTTCAAGGAAAGAC	295820	128016	AATATGTGTGCACATGTCCA
206647	38843	ATACAAAAACTTAGCCTGGT	251234	83430	CTGGGAAGTTCAAGGAAAGA	295821	128017	AAATATGTGTGCACATGTCC
206648	38844	AATACAAAAACTTAGCCTGG	251235	83431	GCTGGGAAGTTCAAGGAAAG	295822	128018	AAAATATGTGTGCACATGTC
206649	38845	AAATACAAAAACTTAGCCTG	251236	83432	TGCTGGGAAGTTCAAGGAAA	295823	128019	AAAAATATGTGTGCACATGT
206650	38846	AAAATACAAAAACTTAGCCT	251237	83433	CTGCTGGGAAGTTCAAGGAA	295824	128020	CAAAAATATGTGTGCACATG
206651	38847	AAAAATACAAAAACTTAGCC	251238	83434	GCTGCTGGGAAGTTCAAGGA	295825	128021	CCAAAAATATGTGTGCACAT
206652	38848	TAAAAATACAAAAACTTAGC	251239	83435	GGCTGCTGGGAAGTTCAAGG	295826	128022	GCCAAAAATATGTGTGCACA
206653	38849	CTAAAAATACAAAAACTTAG	251240	83436	TGGCTGCTGGGAAGTTCAAG	295827	128023	AGCCAAAAATATGTGTGCAC
206654	38850	ACTAAAAATACAAAAACTTA	251241	83437	GTGGCTGCTGGGAAGTTCAA	295828	128024	AAGCCAAAAATATGTGTGCA
206655	38851	TACTAAAAATACAAAAACTT	251242	83438	AGTGGCTGCTGGGAAGTTCA	295829	128025	AAAGCCAAAAATATGTGTGC
206656	38852	CTACTAAAAATACAAAAACT	251243	83439	CAGTGGCTGCTGGGAAGTTC	295830	128026	TAAAGCCAAAAATATGTGTG
206657	38853	TCTACTAAAAATACAAAAAC	251244	83440	GCAGTGGCTGCTGGGAAGTT	295831	128027	GTAAAGCCAAAAATATGTGT
206658	38854	CTCTACTAAAAATACAAAAA	251245	83441	AGCAGTGGCTGCTGGGAAGT	295832	128028	GGTAAAGCCAAAAATATGTG
206659	38855	CCTCTACTAAAAATACAAAA	251246	83442	AAGCAGTGGCTGCTGGGAAG	295833	128029	TGGTAAAGCCAAAAATATGT
206660	38856	GCCTCTACTAAAAATACAAA	251247	83443	TAAGCAGTGGCTGCTGGGAA	295834	128030	CTGGTAAAGCCAAAAATATG
206661	38857	TGCCTCTACTAAAAATACAA	251248	83444	CTAAGCAGTGGCTGCTGGGA	295835	128031	TCTGGTAAAGCCAAAAATAT
206662	38858	CTGCCTCTACTAAAAATACA	251249	83445	TCTAAGCAGTGGCTGCTGGG	295836	128032	ATCTGGTAAAGCCAAAAATA
206663	38859	CCTGCCTCTACTAAAAATAC	251250	83446	GTCTAAGCAGTGGCTGCTGG	295837	128033	CATCTGGTAAAGCCAAAAAT
206664	38860	CCCTGCCTCTACTAAAAATA	251251	83447	TGTCTAAGCAGTGGCTGCTG	295838	128034	GCATCTGGTAAAGCCAAAAA
206665	38861	ACCCTGCCTCTACTAAAAAT	251252	83448	GTGTCTAAGCAGTGGCTGCT	295839	128035	AGCATCTGGTAAAGCCAAAA
206666	38862	AACCCTGCCTCTACTAAAAA	251253	83449	TGTGTCTAAGCAGTGGCTGC	295840	128036	GAGCATCTGGTAAAGCCAAA
206667	38863	AAACCCTGCCTCTACTAAAA	251254	83450	CTGTGTCTAAGCAGTGGCTG	295841	128037	TGAGCATCTGGTAAAGCCAA
206668	38864	GAAACCCTGCCTCTACTAAA	251255	83451	GCTGTGTCTAAGCAGTGGCT	295842	128038	TTGAGCATCTGGTAAAGCCA
206669	38865	TGAAACCCTGCCTCTACTAA	251256	83452	GGCTGTGTCTAAGCAGTGGC	295843	128039	TTTGAGCATCTGGTAAAGCC
206670	38866	GTGAAACCCTGCCTCTACTA	251257	83453	AGGCTGTGTCTAAGCAGTGG	295844	128040	CTTTGAGCATCTGGTAAAGC
206671	38867	GGTGAAACCCTGCCTCTACT	251258	83454	GAGGCTGTGTCTAAGCAGTG	295845	128041	TCTTTGAGCATCTGGTAAAG
206672	38868	TGGTGAAACCCTGCCTCTAC	251259	83455	GGAGGCTGTGTCTAAGCAGT	295846	128042	CTCTTTGAGCATCTGGTAAA
206673	38869	ATGGTGAAACCCTGCCTCTA	251260	83456	TGGAGGCTGTGTCTAAGCAG	295847	128043	GCTCTTTGAGCATCTGGTAA
206674	38870	CATGGTGAAACCCTGCCTCT	251261	83457	GTGGAGGCTGTGTCTAAGCA	295848	128044	GGCTCTTTGAGCATCTGGTA
206675	38871	ACATGGTGAAACCCTGCCTC	251262	83458	TGTGGAGGCTGTGTCTAAGC	295849	128045	AGGCTCTTTGAGCATCTGGT
206676	38872	AACATGGTGAAACCCTGCCT	251263	83459	TTGTGGAGGCTGTGTCTAAG	295850	128046	TAGGCTCTTTGAGCATCTGG
206677	38873	CAACATGGTGAAACCCTGCC	251264	83460	GTTGTGGAGGCTGTGTCTAA	295851	128047	CTAGGCTCTTTGAGCATCTG
206678	38874	GCAACATGGTGAAACCCTGC	251265	83461	GGTTGTGGAGGCTGTGTCTA	295852	128048	CCTAGGCTCTTTGAGCATCT
206679	38875	GGCAACATGGTGAAACCCTG	251266	83462	TGGTTGTGGAGGCTGTGTCT	295853	128049	TCCTAGGCTCTTTGAGCATC
206680	38876	GGGCAACATGGTGAAACCCT	251267	83463	ATGGTTGTGGAGGCTGTGTC	295854	128050	GTCCTAGGCTCTTTGAGCAT
206681	38877	TGGGCAACATGGTGAAACCC	251268	83464	CATGGTTGTGGAGGCTGTGT	295855	128051	GGTCCTAGGCTCTTTGAGCA
206682	38878	CTGGGCAACATGGTGAAACC	251269	83465	CCATGGTTGTGGAGGCTGTG	295856	128052	GGGTCCTAGGCTCTTTGAGC

206683	38879	CCTGGGCAACATGGTGAAAC	251270	83466	GCCATGGTTGTGGAGGCTGT	295857	128053	TGGGTCCTAGGCTCTTTGAG
206684	38880	GCCTGGGCAACATGGTGAAA	251271	83467	AGCCATGGTTGTGGAGGCTG	295858	128054	TTGGGTCCTAGGCTCTTTGA
206685	38881	AGCCTGGGCAACATGGTGAA	251272	83468	GAGCCATGGTTGTGGAGGCT	295859	128055	TTTGGGTCCTAGGCTCTTTG
206686	38882	CAGCCTGGGCAACATGGTGA	251273	83469	TGAGCCATGGTTGTGGAGGC	295860	128056	TTTTGGGTCCTAGGCTCTTT
206687	38883	CCAGCCTGGGCAACATGGTG	251274	83470	CTGAGCCATGGTTGTGGAGG	295861	128057	TTTTTGGGTCCTAGGCTCTT
206688	38884	ACCAGCCTGGGCAACATGGT	251275	83471	GCTGAGCCATGGTTGTGGAG	295862	128058	CTTTTTGGGTCCTAGGCTCT
206689	38885	GACCAGCCTGGGCAACATGG	251276	83472	TGCTGAGCCATGGTTGTGGA	295863	128059	CCTTTTTGGGTCCTAGGCTC
206690	38886	AGACCAGCCTGGGCAACATG	251277	83473	CTGCTGAGCCATGGTTGTGG	295864	128060	CCCTTTTTGGGTCCTAGGCT
206691	38887	GAGACCAGCCTGGGCAACAT	251278	83474	GCTGCTGAGCCATGGTTGTG	295865	128061	GCCCTTTTTGGGTCCTAGGC
206692	38888	TGAGACCAGCCTGGGCAACA	251279	83475	TGCTGCTGAGCCATGGTTGT	295866	128062	AGCCCTTTTTGGGTCCTAGG
206693	38889	TTGAGACCAGCCTGGGCAAC	251280	83476	TTGCTGCTGAGCCATGGTTG	295867	128063	CAGCCCTTTTTGGGTCCTAG
206694	38890	TTTGAGACCAGCCTGGGCAA	251281	83477	TTTGCTGCTGAGCCATGGTT	295868	128064	TCAGCCCTTTTTGGGTCCTA
206695	38891	GTTTGAGACCAGCCTGGGCA	251282	83478	ATTTGCTGCTGAGCCATGGT	295869	128065	CTCAGCCCTTTTTGGGTCCT
206696	38892	AGTTTGAGACCAGCCTGGGC	251283	83479	AATTTGCTGCTGAGCCATGG	295870	128066	TCTCAGCCCTTTTTGGGTCC
206697	38893	GAGTTTGAGACCAGCCTGGG	251284	83480	CAATTTGCTGCTGAGCCATG	295871	128067	TTCTCAGCCCTTTTTGGGTC
206698	38894	GGAGTTTGAGACCAGCCTGG	251285	83481	GCAATTTGCTGCTGAGCCAT	295872	128068	ATTCTCAGCCCTTTTTGGGT
206699	38895	AGGAGTTTGAGACCAGCCTG	251286	83482	AGCAATTTGCTGCTGAGCCA	295873	128069	CATTCTCAGCCCTTTTTGGG
206700	38896	CAGGAGTTTGAGACCAGCCT	251287	83483	AAGCAATTTGCTGCTGAGCC	295874	128070	TCATTCTCAGCCCTTTTTGG
206701	38897	CCAGGAGTTTGAGACCAGCC	251288	83484	GAAGCAATTTGCTGCTGAGC	295875	128071	GTCATTCTCAGCCCTTTTTG
206702	38898	GCCAGGAGTTTGAGACCAGC	251289	83485	AGAAGCAATTTGCTGCTGAG	295876	128072	GGTCATTCTCAGCCCTTTTT
206703	38899	GGCCAGGAGTTTGAGACCAG	251290	83486	GAGAAGCAATTTGCTGCTGA	295877	128073	CGGTCATTCTCAGCCCTTTT
206704	38900	AGGCCAGGAGTTTGAGACCA	251291	83487	AGAGAAGCAATTTGCTGCTG	295878	128074	ACGGTCATTCTCAGCCCTTT
206705	38901	GAGGCCAGGAGTTTGAGACC	251292	83488	CAGAGAAGCAATTTGCTGCT	295879	128075	CACGGTCATTCTCAGCCCTT
206706	38902	TGAGGCCAGGAGTTTGAGAC	251293	83489	TCAGAGAAGCAATTTGCTGC	295880	128076	ACACGGTCATTCTCAGCCCT
206707	38903	TTGAGGCCAGGAGTTTGAGA	251294	83490	GTCAGAGAAGCAATTTGCTG	295881	128077	GACACGGTCATTCTCAGCCC
206708	38904	CTTGAGGCCAGGAGTTTGAG	251295	83491	GGTCAGAGAAGCAATTTGCT	295882	128078	CGACACGGTCATTCTCAGCC
206709	38905	GCTTGAGGCCAGGAGTTTGA	251296	83492	AGGTCAGAGAAGCAATTTGC	295883	128079	CCGACACGGTCATTCTCAGC
206710	38906	CGCTTGAGGCCAGGAGTTTG	251297	83493	GAGGTCAGAGAAGCAATTTG	295884	128080	GCCGACACGGTCATTCTCAG
206711	38907	TCGCTTGAGGCCAGGAGTTT	251298	83494	TGAGGTCAGAGAAGCAATTT	295885	128081	GGCCGACACGGTCATTCTCA
206712	38908	ATCGCTTGAGGCCAGGAGTT	251299	83495	GTGAGGTCAGAGAAGCAATT	295886	128082	TGGCCGACACGGTCATTCTC
206713	38909	GATCGCTTGAGGCCAGGAGT	251300	83496	AGTGAGGTCAGAGAAGCAAT	295887	128083	GTGGCCGACACGGTCATTCT
206714	38910	AGATCGCTTGAGGCCAGGAG	251301	83497	GAGTGAGGTCAGAGAAGCAA	295888	128084	AGTGGCCGACACGGTCATTC
206715	38911	CAGATCGCTTGAGGCCAGGA	251302	83498	TGAGTGAGGTCAGAGAAGCA	295889	128085	AAGTGGCCGACACGGTCATT
206716	38912	GCAGATCGCTTGAGGCCAGG	251303	83499	CTGAGTGAGGTCAGAGAAGC	295890	128086	GAAGTGGCCGACACGGTCAT
206717	38913	GGCAGATCGCTTGAGGCCAG	251304	83500	GCTGAGTGAGGTCAGAGAAG	295891	128087	TGAAGTGGCCGACACGGTCA
206718	38914	GGGCAGATCGCTTGAGGCCA	251305	83501	GGCTGAGTGAGGTCAGAGAA	295892	128088	CTGAAGTGGCCGACACGGTC
206719	38915	TGGGCAGATCGCTTGAGGCC	251306	83502	AGGCTGAGTGAGGTCAGAGA	295893	128089	CCTGAAGTGGCCGACACGGT
206720	38916	ATGGGCAGATCGCTTGAGGC	251307	83503	CAGGCTGAGTGAGGTCAGAG	295894	128090	CCCTGAAGTGGCCGACACGG
206721	38917	GATGGGCAGATCGCTTGAGG	251308	83504	ACAGGCTGAGTGAGGTCAGA	295895	128091	ACCCTGAAGTGGCCGACACG
206722	38918	AGATGGGCAGATCGCTTGAG	251309	83505	CACAGGCTGAGTGAGGTCAG	295896	128092	GACCCTGAAGTGGCCGACAC
206723	38919	AAGATGGGCAGATCGCTTGA	251310	83506	ACACAGGCTGAGTGAGGTCA	295897	128093	TGACCCTGAAGTGGCCGACA
206724	38920	CAAGATGGGCAGATCGCTTG	251311	83507	CACACAGGCTGAGTGAGGTC	295898	128094	ATGACCCTGAAGTGGCCGAC
206725	38921	TCAAGATGGGCAGATCGCTT	251312	83508	ACACACAGGCTGAGTGAGGT	295899	128095	GATGACCCTGAAGTGGCCGA
206726	38922	GTCAAGATGGGCAGATCGCT	251313	83509	GACACACAGGCTGAGTGAGG	295900	128096	TGATGACCCTGAAGTGGCCG
206727	38923	GGTCAAGATGGGCAGATCGC	251314	83510	GGACACACAGGCTGAGTGAG	295901	128097	CTGATGACCCTGAAGTGGCC
206728	38924	AGGTCAAGATGGGCAGATCG	251315	83511	AGGACACACAGGCTGAGTGA	295902	128098	CCTGATGACCCTGAAGTGGC
206729	38925	GAGGTCAAGATGGGCAGATC	251316	83512	AAGGACACACAGGCTGAGTG	295903	128099	TCCTGATGACCCTGAAGTGG
206730	38926	GGAGGTCAAGATGGGCAGAT	251317	83513	CAAGGACACACAGGCTGAGT	295904	128100	TTCCTGATGACCCTGAAGTG
206731	38927	GGGAGGTCAAGATGGGCAGA	251318	83514	ACAAGGACACACAGGCTGAG	295905	128101	ATTCCTGATGACCCTGAAGT
206732	38928	TGGGAGGTCAAGATGGGCAG	251319	83515	AACAAGGACACACAGGCTGA	295906	128102	AATTCCTGATGACCCTGAAG
206733	38929	TTGGGAGGTCAAGATGGGCA	251320	83516	CAACAAGGACACACAGGCTG	295907	128103	CAATTCCTGATGACCCTGAA
206734	38930	TTTGGGAGGTCAAGATGGGC	251321	83517	TCAACAAGGACACACAGGCT	295908	128104	GCAATTCCTGATGACCCTGA
206735	38931	CTTTGGGAGGTCAAGATGGG	251322	83518	CTCAACAAGGACACACAGGC	295909	128105	AGCAATTCCTGATGACCCTG
206736	38932	ACTTTGGGAGGTCAAGATGG	251323	83519	ACTCAACAAGGACACACAGG	295910	128106	CAGCAATTCCTGATGACCCT
206737	38933	CACTTTGGGAGGTCAAGATG	251324	83520	CACTCAACAAGGACACACAG	295911	128107	ACAGCAATTCCTGATGACCC
206738	38934	ACACTTTGGGAGGTCAAGAT	251325	83521	TCACTCAACAAGGACACACA	295912	128108	CACAGCAATTCCTGATGACC
206739	38935	AACACTTTGGGAGGTCAAGA	251326	83522	CTCACTCAACAAGGACACAC	295913	128109	GCACAGCAATTCCTGATGAC
206740	38936	CAACACTTTGGGAGGTCAAG	251327	83523	CCTCACTCAACAAGGACACA	295914	128110	TGCACAGCAATTCCTGATGA
206741	38937	CCAACACTTTGGGAGGTCAA	251328	83524	GCCTCACTCAACAAGGACAC	295915	128111	GTGCACAGCAATTCCTGATG
206742	38938	CCCAACACTTTGGGAGGTCA	251329	83525	TGCCTCACTCAACAAGGACA	295916	128112	AGTGCACAGCAATTCCTGAT
206743	38939	TCCCAACACTTTGGGAGGTC	251330	83526	ATGCCTCACTCAACAAGGAC	295917	128113	CAGTGCACAGCAATTCCTGA
206744	38940	ATCCCAACACTTTGGGAGGT	251331	83527	AATGCCTCACTCAACAAGGA	295918	128114	GCAGTGCACAGCAATTCCTG
206745	38941	AATCCCAACACTTTGGGAGG	251332	83528	GAATGCCTCACTCAACAAGG	295919	128115	AGCAGTGCACAGCAATTCCT
206746	38942	TAATCCCAACACTTTGGGAG	251333	83529	TGAATGCCTCACTCAACAAG	295920	128116	GAGCAGTGCACAGCAATTCC
206747	38943	GTAATCCCAACACTTTGGGA	251334	83530	CTGAATGCCTCACTCAACAA	295921	128117	TGAGCAGTGCACAGCAATTC
206748	38944	TGTAATCCCAACACTTTGGG	251335	83531	CCTGAATGCCTCACTCAACA	295922	128118	GTGAGCAGTGCACAGCAATT
206749	38945	CTGTAATCCCAACACTTTGG	251336	83532	TCCTGAATGCCTCACTCAAC	295923	128119	AGTGAGCAGTGCACAGCAAT
206750	38946	CCTGTAATCCCAACACTTTG	251337	83533	GTCCTGAATGCCTCACTCAA	295924	128120	AAGTGAGCAGTGCACAGCAA
206751	38947	GCCTGTAATCCCAACACTTT	251338	83534	GGTCCTGAATGCCTCACTCA	295925	128121	GAAGTGAGCAGTGCACAGCA
206752	38948	CGCCTGTAATCCCAACACTT	251339	83535	GGGTCCTGAATGCCTCACTC	295926	128122	AGAAGTGAGCAGTGCACAGC
206753	38949	ACGCCTGTAATCCCAACACT	251340	83536	AGGGTCCTGAATGCCTCACT	295927	128123	GAGAAGTGAGCAGTGCACAG
206754	38950	CACGCCTGTAATCCCAACAC	251341	83537	CAGGGTCCTGAATGCCTCAC	295928	128124	GGAGAAGTGAGCAGTGCACA

206755	38951	TCACGCCTGTAATCCCAACA	251342	83538	CCAGGGTCCTGAATGCCTCA	295929	128125	TGGAGAAGTGAGCAGTGCAC
206756	38952	CTCACGCCTGTAATCCCAAC	251343	83539	ACCAGGGTCCTGAATGCCTC	295930	128126	CTGGAGAAGTGAGCAGTGCA
206757	38953	GCTCACGCCTGTAATCCCAA	251344	83540	GACCAGGGTCCTGAATGCCT	295931	128127	ACTGGAGAAGTGAGCAGTGC
206758	38954	GGCTCACGCCTGTAATCCCA	251345	83541	GGACCAGGGTCCTGAATGCC	295932	128128	CACTGGAGAAGTGAGCAGTG
206759	38955	TGGCTCACGCCTGTAATCCC	251346	83542	GGGACCAGGGTCCTGAATGC	295933	128129	TCACTGGAGAAGTGAGCAGT
206760	38956	GTGGCTCACGCCTGTAATCC	251347	83543	TGGGACCAGGGTCCTGAATG	295934	128130	TTCACTGGAGAAGTGAGCAG
206761	38957	GGTGGCTCACGCCTGTAATC	251348	83544	TTGGGACCAGGGTCCTGAAT	295935	128131	GTTCACTGGAGAAGTGAGCA
206762	38958	CGGTGGCTCACGCCTGTAAT	251349	83545	TTTGGGACCAGGGTCCTGAA	295936	128132	TGTTCACTGGAGAAGTGAGC
206763	38959	ACGGTGGCTCACGCCTGTAA	251350	83546	CTTTGGGACCAGGGTCCTGA	295937	128133	GTGTTCACTGGAGAAGTGAG
206764	38960	CACGGTGGCTCACGCCTGTA	251351	83547	ACTTTGGGACCAGGGTCCTG	295938	128134	AGTGTTCACTGGAGAAGTGA
206765	38961	GCACGGTGGCTCACGCCTGT	251352	83548	CACTTTGGGACCAGGGTCCT	295939	128135	AAGTGTTCACTGGAGAAGTG
206766	38962	GGCACGGTGGCTCACGCCTG	251353	83549	CCACTTTGGGACCAGGGTCC	295940	128136	AAAGTGTTCACTGGAGAAGT
206767	38963	AGGCACGGTGGCTCACGCCT	251354	83550	TCCACTTTGGGACCAGGGTC	295941	128137	GAAAGTGTTCACTGGAGAAG
206768	38964	TAGGCACGGTGGCTCACGCC	251355	83551	CTCCACTTTGGGACCAGGGT	295942	128138	AGAAAGTGTTCACTGGAGAA
206769	38965	CTAGGCACGGTGGCTCACGC	251356	83552	TCTCCACTTTGGGACCAGGG	295943	128139	CAGAAAGTGTTCACTGGAGA
206770	38966	GCTAGGCACGGTGGCTCACG	251357	83553	TTCTCCACTTTGGGACCAGG	295944	128140	GCAGAAAGTGTTCACTGGAG
206771	38967	GGCTAGGCACGGTGGCTCAC	251358	83554	TTTCTCCACTTTGGGACCAG	295945	128141	AGCAGAAAGTGTTCACTGGA
206772	38968	GGGCTAGGCACGGTGGCTCA	251359	83555	CTTTCTCCACTTTGGGACCA	295946	128142	AAGCAGAAAGTGTTCACTGG
206773	38969	AGGGCTAGGCACGGTGGCTC	251360	83556	ACTTTCTCCACTTTGGGACC	295947	128143	GAAGCAGAAAGTGTTCACTG
206774	38970	CAGGGCTAGGCACGGTGGCT	251361	83557	GACTTTCTCCACTTTGGGAC	295948	128144	AGAAGCAGAAAGTGTTCACT
206775	38971	ACAGGGCTAGGCACGGTGGC	251362	83558	AGACTTTCTCCACTTTGGGA	295949	128145	CAGAAGCAGAAAGTGTTCAC
206776	38972	AACAGGGCTAGGCACGGTGG	251363	83559	AAGACTTTCTCCACTTTGGG	295950	128146	ACAGAAGCAGAAAGTGTTCA
206777	38973	AAACAGGGCTAGGCACGGTG	251364	83560	AAAGACTTTCTCCACTTTGG	295951	128147	CACAGAAGCAGAAAGTGTTC
206778	38974	AAAACAGGGCTAGGCACGGT	251365	83561	GAAAGACTTTCTCCACTTTG	295952	128148	ACACAGAAGCAGAAAGTGTT
206779	38975	AAAAACAGGGCTAGGCACGG	251366	83562	GGAAAGACTTTCTCCACTTT	295953	128149	AACACAGAAGCAGAAAGTGT
206780	38976	CAAAAACAGGGCTAGGCACG	251367	83563	AGGAAAGACTTTCTCCACTT	295954	128150	AAACACAGAAGCAGAAAGTG
206781	38977	TCAAAAACAGGGCTAGGCAC	251368	83564	TAGGAAAGACTTTCTCCACT	295955	128151	GAAACACAGAAGCAGAAAGT
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206783	38979	GTTCAAAAACAGGGCTAGGC	251370	83566	AGTAGGAAAGACTTTCTCCA	295957	128153	AGGAAACACAGAAGCAGAAA
206784	38980	AGTTCAAAAACAGGGCTAGG	251371	83567	TAGTAGGAAAGACTTTCTCC	295958	128154	CAGGAAACACAGAAGCAGAA
206785	38981	GAGTTCAAAAACAGGGCTAG	251372	83568	CTAGTAGGAAAGACTTTCTC	295959	128155	CCAGGAAACACAGAAGCAGA
206786	38982	AGAGTTCAAAAACAGGGCTA	251373	83569	CCTAGTAGGAAAGACTTTCT	295960	128156	ACCAGGAAACACAGAAGCAG
206787	38983	GAGAGTTCAAAAACAGGGCT	251374	83570	ACCTAGTAGGAAAGACTTTC	295961	128157	TACCAGGAAACACAGAAGCA
206788	38984	AGAGAGTTCAAAAACAGGGC	251375	83571	GACCTAGTAGGAAAGACTTT	295962	128158	ATACCAGGAAACACAGAAGC
206789	38985	TAGAGAGTTCAAAAACAGGG	251376	83572	TGACCTAGTAGGAAAGACTT	295963	128159	GATACCAGGAAACACAGAAG
206790	38986	CTAGAGAGTTCAAAAACAGG	251377	83573	ATGACCTAGTAGGAAAGACT	295964	128160	GGATACCAGGAAACACAGAA
206791	38987	TCTAGAGAGTTCAAAAACAG	251378	83574	TATGACCTAGTAGGAAAGAC	295965	128161	AGGATACCAGGAAACACAGA
206792	38988	CTCTAGAGAGTTCAAAAACA	251379	83575	CTATGACCTAGTAGGAAAGA	295966	128162	AAGGATACCAGGAAACACAG
206793	38989	TCTCTAGAGAGTTCAAAAAC	251380	83576	GCTATGACCTAGTAGGAAAG	295967	128163	AAAGGATACCAGGAAACACA
206794	38990	GTCTCTAGAGAGTTCAAAAA	251381	83577	AGCTATGACCTAGTAGGAAA	295968	128164	CAAAGGATACCAGGAAACAC
206795	38991	TGTCTCTAGAGAGTTCAAAA	251382	83578	TAGCTATGACCTAGTAGGAA	295969	128165	CCAAAGGATACCAGGAAACA
206796	38992	CTGTCTCTAGAGAGTTCAAA	251383	83579	GTAGCTATGACCTAGTAGGA	295970	128166	CCCAAAGGATACCAGGAAAC
206797	38993	ACTGTCTCTAGAGAGTTCAA	251384	83580	TGTAGCTATGACCTAGTAGG	295971	128167	TCCCAAAGGATACCAGGAAA
206798	38994	GACTGTCTCTAGAGAGTTCA	251385	83581	GTGTAGCTATGACCTAGTAG	295972	128168	GTCCCAAAGGATACCAGGAA
206799	38995	GGACTGTCTCTAGAGAGTTC	251386	83582	GGTGTAGCTATGACCTAGTA	295973	128169	AGTCCCAAAGGATACCAGGA
206800	38996	TGGACTGTCTCTAGAGAGTT	251387	83583	AGGTGTAGCTATGACCTAGT	295974	128170	GAGTCCCAAAGGATACCAGG
206801	38997	CTGGACTGTCTCTAGAGAGT	251388	83584	CAGGTGTAGCTATGACCTAG	295975	128171	GGAGTCCCAAAGGATACCAG
206802	38998	GCTGGACTGTCTCTAGAGAG	251389	83585	GCAGGTGTAGCTATGACCTA	295976	128172	AGGAGTCCCAAAGGATACCA
206803	38999	GGCTGGACTGTCTCTAGAGA	251390	83586	TGCAGGTGTAGCTATGACCT	295977	128173	CAGGAGTCCCAAAGGATACC
206804	39000	GGGCTGGACTGTCTCTAGAG	251391	83587	ATGCAGGTGTAGCTATGACC	295978	128174	CCAGGAGTCCCAAAGGATAC
206805	39001	GGGGCTGGACTGTCTCTAGA	251392	83588	CATGCAGGTGTAGCTATGAC	295979	128175	GCCAGGAGTCCCAAAGGATA
206806	39002	AGGGGCTGGACTGTCTCTAG	251393	83589	ACATGCAGGTGTAGCTATGA	295980	128176	AGCCAGGAGTCCCAAAGGAT
206807	39003	AAGGGGCTGGACTGTCTCTA	251394	83590	CACATGCAGGTGTAGCTATG	295981	128177	TAGCCAGGAGTCCCAAAGGA
206808	39004	TAAGGGGCTGGACTGTCTCT	251395	83591	CCACATGCAGGTGTAGCTAT	295982	128178	CTAGCCAGGAGTCCCAAAGG
206809	39005	ATAAGGGGCTGGACTGTCTC	251396	83592	CCCACATGCAGGTGTAGCTA	295983	128179	CCTAGCCAGGAGTCCCAAAG
206810	39006	AATAAGGGGCTGGACTGTCT	251397	83593	ACCCACATGCAGGTGTAGCT	295984	128180	ACCTAGCCAGGAGTCCCAAA
206811	39007	TAATAAGGGGCTGGACTGTC	251398	83594	CACCCACATGCAGGTGTAGC	295985	128181	GACCTAGCCAGGAGTCCCAA
206812	39008	GTAATAAGGGGCTGGACTGT	251399	83595	GCACCCACATGCAGGTGTAG	295986	128182	TGACCTAGCCAGGAGTCCCA
206813	39009	AGTAATAAGGGGCTGGACTG	251400	83596	AGCACCCACATGCAGGTGTA	295987	128183	ATGACCTAGCCAGGAGTCCC
206814	39010	AAGTAATAAGGGGCTGGACT	251401	83597	CAGCACCCACATGCAGGTGT	295988	128184	CATGACCTAGCCAGGAGTCC
206815	39011	CAAGTAATAAGGGGCTGGAC	251402	83598	ACAGCACCCACATGCAGGTG	295989	128185	ACATGACCTAGCCAGGAGTC
206816	39012	ACAAGTAATAAGGGGCTGGA	251403	83599	CACAGCACCCACATGCAGGT	295990	128186	CACATGACCTAGCCAGGAGT
206817	39013	GACAAGTAATAAGGGGCTGG	251404	83600	GCACAGCACCCACATGCAGG	295991	128187	ACACATGACCTAGCCAGGAG
206818	39014	GGACAAGTAATAAGGGGCTG	251405	83601	GGCACAGCACCCACATGCAG	295992	128188	AACACATGACCTAGCCAGGA
206819	39015	AGGACAAGTAATAAGGGGCT	251406	83602	AGGCACAGCACCCACATGCA	295993	128189	AAACACATGACCTAGCCAGG
206820	39016	CAGGACAAGTAATAAGGGGC	251407	83603	AAGGCACAGCACCCACATGC	295994	128190	GAAACACATGACCTAGCCAG
206821	39017	TCAGGACAAGTAATAAGGGG	251408	83604	AAAGGCACAGCACCCACATG	295995	128191	AGAAACACATGACCTAGCCA
206822	39018	CTCAGGACAAGTAATAAGGG	251409	83605	AAAAGGCACAGCACCCACAT	295996	128192	GAGAAACACATGACCTAGCC
206823	39019	CCTCAGGACAAGTAATAAGG	251410	83606	CAAAAGGCACAGCACCCACA	295997	128193	AGAGAAACACATGACCTAGC
206824	39020	GCCTCAGGACAAGTAATAAG	251411	83607	ACAAAAGGCACAGCACCCAC	295998	128194	TAGAGAAACACATGACCTAG
206825	39021	TGCCTCAGGACAAGTAATAA	251412	83608	AACAAAAGGCACAGCACCCA	295999	128195	GTAGAGAAACACATGACCTA
206826	39022	CTGCCTCAGGACAAGTAATA	251413	83609	AAACAAAAGGCACAGCACCC	296000	128196	AGTAGAGAAACACATGACCT

206827	39023	GCTGCCTCAGGACAAGTAAT	251414	83610	TAAACAAAAGGCACAGCACC	296001	128197	AAGTAGAGAAACACATGACC
206828	39024	AGCTGCCTCAGGACAAGTAA	251415	83611	CTAAACAAAAGGCACAGCAC	296002	128198	AAAGTAGAGAAACACATGAC
206829	39025	CAGCTGCCTCAGGACAAGTA	251416	83612	ACTAAACAAAAGGCACAGCA	296003	128199	GAAAGTAGAGAAACACATGA
206830	39026	GCAGCTGCCTCAGGACAAGT	251417	83613	CACTAAACAAAAGGCACAGC	296004	128200	TGAAAGTAGAGAAACACATG
206831	39027	AGCAGCTGCCTCAGGACAAG	251418	83614	TCACTAAACAAAAGGCACAG	296005	128201	TTGAAAGTAGAGAAACACAT
206832	39028	GAGCAGCTGCCTCAGGACAA	251419	83615	TTCACTAAACAAAAGGCACA	296006	128202	TTTGAAAGTAGAGAAACACA
206833	39029	GGAGCAGCTGCCTCAGGACA	251420	83616	GTTCACTAAACAAAAGGCAC	296007	128203	TTTTGAAAGTAGAGAAACAC
206834	39030	GGGAGCAGCTGCCTCAGGAC	251421	83617	AGTTCACTAAACAAAAGGCA	296008	128204	CTTTTGAAAGTAGAGAAACA
206835	39031	AGGGAGCAGCTGCCTCAGGA	251422	83618	AAGTTCACTAAACAAAAGGC	296009	128205	CCTTTTGAAAGTAGAGAAAC
206836	39032	AAGGGAGCAGCTGCCTCAGG	251423	83619	AAAGTTCACTAAACAAAAGG	296010	128206	CCCTTTTGAAAGTAGAGAAA
206837	39033	GAAGGGAGCAGCTGCCTCAG	251424	83620	AAAAGTTCACTAAACAAAAG	296011	128207	GCCCTTTTGAAAGTAGAGAA
206838	39034	TGAAGGGAGCAGCTGCCTCA	251425	83621	TAAAAGTTCACTAAACAAAA	296012	128208	AGCCCTTTTGAAAGTAGAGA
206839	39035	GTGAAGGGAGCAGCTGCCTC	251426	83622	ATAAAAGTTCACTAAACAAA	296013	128209	AAGCCCTTTTGAAAGTAGAG
206840	39036	GGTGAAGGGAGCAGCTGCCT	251427	83623	GATAAAAGTTCACTAAACAA	296014	128210	GAAGCCCTTTTGAAAGTAGA
206841	39037	AGGTGAAGGGAGCAGCTGCC	251428	83624	TGATAAAAGTTCACTAAACA	296015	128211	TGAAGCCCTTTTGAAAGTAG
206842	39038	CAGGTGAAGGGAGCAGCTGC	251429	83625	GTGATAAAAGTTCACTAAAC	296016	128212	CTGAAGCCCTTTTGAAAGTA
206843	39039	CCAGGTGAAGGGAGCAGCTG	251430	83626	GGTGATAAAAGTTCACTAAA	296017	128213	GCTGAAGCCCTTTTGAAAGT
206844	39040	GCCAGGTGAAGGGAGCAGCT	251431	83627	TGGTGATAAAAGTTCACTAA	296018	128214	GGCTGAAGCCCTTTTGAAAG
206845	39041	GGCCAGGTGAAGGGAGCAGC	251432	83628	CTGGTGATAAAAGTTCACTA	296019	128215	TGGCTGAAGCCCTTTTGAAA
206846	39042	GGGCCAGGTGAAGGGAGCAG	251433	83629	GCTGGTGATAAAAGTTCACT	296020	128216	CTGGCTGAAGCCCTTTTGAA
206847	39043	GGGGCCAGGTGAAGGGAGCA	251434	83630	TGCTGGTGATAAAAGTTCAC	296021	128217	CCTGGCTGAAGCCCTTTTGA
206848	39044	GGGGGCCAGGTGAAGGGAGC	251435	83631	ATGCTGGTGATAAAAGTTCA	296022	128218	GCCTGGCTGAAGCCCTTTTG
206849	39045	GGGGGGCCAGGTGAAGGGAG	251436	83632	GATGCTGGTGATAAAAGTTC	296023	128219	TGCCTGGCTGAAGCCCTTTT
206850	39046	CGGGGGGCCAGGTGAAGGGA	251437	83633	GGATGCTGGTGATAAAAGTT	296024	128220	GTGCCTGGCTGAAGCCCTTT
206851	39047	GCGGGGGGCCAGGTGAAGGG	251438	83634	AGGATGCTGGTGATAAAAGT	296025	128221	CGTGCCTGGCTGAAGCCCTT
206852	39048	TGCGGGGGGCCAGGTGAAGG	251439	83635	GAGGATGCTGGTGATAAAAG	296026	128222	TCGTGCCTGGCTGAAGCCCT
206853	39049	ATGCGGGGGGCCAGGTGAAG	251440	83636	TGAGGATGCTGGTGATAAAA	296027	128223	ATCGTGCCTGGCTGAAGCCC
206854	39050	AATGCGGGGGGCCAGGTGAA	251441	83637	CTGAGGATGCTGGTGATAAA	296028	128224	CATCGTGCCTGGCTGAAGCC
206855	39051	CAATGCGGGGGGCCAGGTGA	251442	83638	GCTGAGGATGCTGGTGATAA	296029	128225	CCATCGTGCCTGGCTGAAGC
206856	39052	ACAATGCGGGGGGCCAGGTG	251443	83639	TGCTGAGGATGCTGGTGATA	296030	128226	GCCATCGTGCCTGGCTGAAG
206857	39053	CACAATGCGGGGGGCCAGGT	251444	83640	TTGCTGAGGATGCTGGTGAT	296031	128227	TGCCATCGTGCCTGGCTGAA
206858	39054	ACACAATGCGGGGGGCCAGG	251445	83641	ATTGCTGAGGATGCTGGTGA	296032	128228	ATGCCATCGTGCCTGGCTGA
206859	39055	AACACAATGCGGGGGGCCAG	251446	83642	CATTGCTGAGGATGCTGGTG	296033	128229	CATGCCATCGTGCCTGGCTG
206860	39056	GAACACAATGCGGGGGGCCA	251447	83643	TCATTGCTGAGGATGCTGGT	296034	128230	TCATGCCATCGTGCCTGGCT
206861	39057	GGAACACAATGCGGGGGGCC	251448	83644	GTCATTGCTGAGGATGCTGG	296035	128231	CTCATGCCATCGTGCCTGGC
206862	39058	CGGAACACAATGCGGGGGGC	251449	83645	TGTCATTGCTGAGGATGCTG	296036	128232	GCTCATGCCATCGTGCCTGG
206863	39059	CCGGAACACAATGCGGGGGG	251450	83646	ATGTCATTGCTGAGGATGCT	296037	128233	GGCTCATGCCATCGTGCCTG
206864	39060	TCCGGAACACAATGCGGGGG	251451	83647	AATGTCATTGCTGAGGATGC	296038	128234	AGGCTCATGCCATCGTGCCT
206865	39061	GTCCGGAACACAATGCGGGG	251452	83648	AAATGTCATTGCTGAGGATG	296039	128235	CAGGCTCATGCCATCGTGCC
206866	39062	GGTCCGGAACACAATGCGGG	251453	83649	CAAATGTCATTGCTGAGGAT	296040	128236	ACAGGCTCATGCCATCGTGC
206867	39063	GGGTCCGGAACACAATGCGG	251454	83650	GCAAATGTCATTGCTGAGGA	296041	128237	TACAGGCTCATGCCATCGTG
206868	39064	AGGGTCCGGAACACAATGCG	251455	83651	TGCAAATGTCATTGCTGAGG	296042	128238	CTACAGGCTCATGCCATCGT
206869	39065	AAGGGTCCGGAACACAATGC	251456	83652	CTGCAAATGTCATTGCTGAG	296043	128239	ACTACAGGCTCATGCCATCG
206870	39066	CAAGGGTCCGGAACACAATG	251457	83653	TCTGCAAATGTCATTGCTGA	296044	128240	GACTACAGGCTCATGCCATC
206871	39067	ACAAGGGTCCGGAACACAAT	251458	83654	CTCTGCAAATGTCATTGCTG	296045	128241	GGACTACAGGCTCATGCCAT
206872	39068	GACAAGGGTCCGGAACACAA	251459	83655	TCTCTGCAAATGTCATTGCT	296046	128242	GGGACTACAGGCTCATGCCA
206873	39069	GGACAAGGGTCCGGAACACA	251460	83656	TTCTCTGCAAATGTCATTGC	296047	128243	TGGGACTACAGGCTCATGCC
206874	39070	AGGACAAGGGTCCGGAACAC	251461	83657	CTTCTCTGCAAATGTCATTG	296048	128244	CTGGGACTACAGGCTCATGC
206875	39071	CAGGACAAGGGTCCGGAACA	251462	83658	GCTTCTCTGCAAATGTCATT	296049	128245	ACTGGGACTACAGGCTCATG
206876	39072	CCAGGACAAGGGTCCGGAAC	251463	83659	GGCTTCTCTGCAAATGTCAT	296050	128246	AACTGGGACTACAGGCTCAT
206877	39073	ACCAGGACAAGGGTCCGGAA	251464	83660	TGGCTTCTCTGCAAATGTCA	296051	128247	CAACTGGGACTACAGGCTCA
206878	39074	CACCAGGACAAGGGTCCGGA	251465	83661	CTGGCTTCTCTGCAAATGTC	296052	128248	GCAACTGGGACTACAGGCTC
206879	39075	CCACCAGGACAAGGGTCCGG	251466	83662	TCTGGCTTCTCTGCAAATGT	296053	128249	AGCAACTGGGACTACAGGCT
206880	39076	ACCACCAGGACAAGGGTCCG	251467	83663	CTCTGGCTTCTCTGCAAATG	296054	128250	GAGCAACTGGGACTACAGGC
206881	39077	CACCACCAGGACAAGGGTCC	251468	83664	GCTCTGGCTTCTCTGCAAAT	296055	128251	AGAGCAACTGGGACTACAGG
206882	39078	GCACCACCAGGACAAGGGTC	251469	83665	AGCTCTGGCTTCTCTGCAAA	296056	128252	CAGAGCAACTGGGACTACAG
206883	39079	AGCACCACCAGGACAAGGGT	251470	83666	CAGCTCTGGCTTCTCTGCAA	296057	128253	CCAGAGCAACTGGGACTACA
206884	39080	TAGCACCACCAGGACAAGGG	251471	83667	TCAGCTCTGGCTTCTCTGCA	296058	128254	TCCAGAGCAACTGGGACTAC
206885	39081	TTAGCACCACCAGGACAAGG	251472	83668	CTCAGCTCTGGCTTCTCTGC	296059	128255	CTCCAGAGCAACTGGGACTA
206886	39082	TTTAGCACCACCAGGACAAG	251473	83669	CCTCAGCTCTGGCTTCTCTG	296060	128256	CCTCCAGAGCAACTGGGACT
206887	39083	CTTTAGCACCACCAGGACAA	251474	83670	GCCTCAGCTCTGGCTTCTCT	296061	128257	ACCTCCAGAGCAACTGGGAC
206888	39084	TCTTTAGCACCACCAGGACA	251475	83671	TGCCTCAGCTCTGGCTTCTC	296062	128258	AACCTCCAGAGCAACTGGGA
206889	39085	TTCTTTAGCACCACCAGGAC	251476	83672	GTGCCTCAGCTCTGGCTTCT	296063	128259	TAACCTCCAGAGCAACTGGG
206890	39086	ATTCTTTAGCACCACCAGGA	251477	83673	GGTGCCTCAGCTCTGGCTTC	296064	128260	TTAACCTCCAGAGCAACTGG
206891	39087	TATTCTTTAGCACCACCAGG	251478	83674	AGGTGCCTCAGCTCTGGCTT	296065	128261	CTTAACCTCCAGAGCAACTG
206892	39088	ATATTCTTTAGCACCACCAG	251479	83675	AAGGTGCCTCAGCTCTGGCT	296066	128262	CCTTAACCTCCAGAGCAACT
206893	39089	GATATTCTTTAGCACCACCA	251480	83676	CAAGGTGCCTCAGCTCTGGC	296067	128263	ACCTTAACCTCCAGAGCAAC
206894	39090	AGATATTCTTTAGCACCACC	251481	83677	CCAAGGTGCCTCAGCTCTGG	296068	128264	CACCTTAACCTCCAGAGCAA
206895	39091	GAGATATTCTTTAGCACCAC	251482	83678	ACCAAGGTGCCTCAGCTCTG	296069	128265	CCACCTTAACCTCCAGAGCA
206896	39092	AGAGATATTCTTTAGCACCA	251483	83679	TACCAAGGTGCCTCAGCTCT	296070	128266	CCCACCTTAACCTCCAGAGC
206897	39093	CAGAGATATTCTTTAGCACC	251484	83680	ATACCAAGGTGCCTCAGCTC	296071	128267	TCCCACCTTAACCTCCAGAG
206898	39094	ACAGAGATATTCTTTAGCAC	251485	83681	AATACCAAGGTGCCTCAGCT	296072	128268	TTCCCACCTTAACCTCCAGA

206899	39095	GACAGAGATATTCTTTAGCA	251486	83682	GAATACCAAGGTGCCTCAGC	296073	128269	CTTCCCACCTTAACCTCCAG
206900	39096	CGACAGAGATATTCTTTAGC	251487	83683	AGAATACCAAGGTGCCTCAG	296074	128270	TCTTCCCACCTTAACCTCCA
206901	39097	TCGACAGAGATATTCTTTAG	251488	83684	AAGAATACCAAGGTGCCTCA	296075	128271	ATCTTCCCACCTTAACCTCC
206902	39098	ATCGACAGAGATATTCTTTA	251489	83685	CAAGAATACCAAGGTGCCTC	296076	128272	AATCTTCCCACCTTAACCTC
206903	39099	GATCGACAGAGATATTCTTT	251490	83686	CCAAGAATACCAAGGTGCCT	296077	128273	CAATCTTCCCACCTTAACCT
206904	39100	GGATCGACAGAGATATTCTT	251491	83687	CCCAAGAATACCAAGGTGCC	296078	128274	GCAATCTTCCCACCTTAACC
206905	39101	AGGATCGACAGAGATATTCT	251492	83688	TCCCAAGAATACCAAGGTGC	296079	128275	AGCAATCTTCCCACCTTAAC
206906	39102	AAGGATCGACAGAGATATTC	251493	83689	ATCCCAAGAATACCAAGGTG	296080	128276	AAGCAATCTTCCCACCTTAA
206907	39103	AAAGGATCGACAGAGATATT	251494	83690	CATCCCAAGAATACCAAGGT	296081	128277	CAAGCAATCTTCCCACCTTA
206908	39104	CAAAGGATCGACAGAGATAT	251495	83691	ACATCCCAAGAATACCAAGG	296082	128278	TCAAGCAATCTTCCCACCTT
206909	39105	CCAAAGGATCGACAGAGATA	251496	83692	CACATCCCAAGAATACCAAG	296083	128279	CTCAAGCAATCTTCCCACCT
206910	39106	CCCAAAGGATCGACAGAGAT	251497	83693	TCACATCCCAAGAATACCAA	296084	128280	GCTCAAGCAATCTTCCCACC
206911	39107	CCCCAAAGGATCGACAGAGA	251498	83694	GTCACATCCCAAGAATACCA	296085	128281	GGCTCAAGCAATCTTCCCAC
206912	39108	TCCCCAAAGGATCGACAGAG	251499	83695	AGTCACATCCCAAGAATACC	296086	128282	GGGCTCAAGCAATCTTCCCA
206913	39109	GTCCCCAAAGGATCGACAGA	251500	83696	AAGTCACATCCCAAGAATAC	296087	128283	TGGGCTCAAGCAATCTTCCC
206914	39110	AGTCCCCAAAGGATCGACAG	251501	83697	AAAGTCACATCCCAAGAATA	296088	128284	CTGGGCTCAAGCAATCTTCC
206915	39111	CAGTCCCCAAAGGATCGACA	251502	83698	GAAAGTCACATCCCAAGAAT	296089	128285	CCTGGGCTCAAGCAATCTTC
206916	39112	CCAGTCCCCAAAGGATCGAC	251503	83699	GGAAAGTCACATCCCAAGAA	296090	128286	TCCTGGGCTCAAGCAATCTT
206917	39113	CCCAGTCCCCAAAGGATCGA	251504	83700	AGGAAAGTCACATCCCAAGA	296091	128287	TTCCTGGGCTCAAGCAATCT
206918	39114	CCCCAGTCCCCAAAGGATCG	251505	83701	CAGGAAAGTCACATCCCAAG	296092	128288	ATTCCTGGGCTCAAGCAATC
206919	39115	TCCCCAGTCCCCAAAGGATC	251506	83702	TCAGGAAAGTCACATCCCAA	296093	128289	AATTCCTGGGCTCAAGCAAT
206920	39116	TTCCCCAGTCCCCAAAGGAT	251507	83703	TTCAGGAAAGTCACATCCCA	296094	128290	AAATTCCTGGGCTCAAGCAA
206921	39117	TTTCCCCAGTCCCCAAAGGA	251508	83704	ATTCAGGAAAGTCACATCCC	296095	128291	CAAATTCCTGGGCTCAAGCA
206922	39118	GTTTCCCCAGTCCCCAAAGG	251509	83705	CATTCAGGAAAGTCACATCC	296096	128292	TCAAATTCCTGGGCTCAAGC
206923	39119	AGTTTCCCCAGTCCCCAAAG	251510	83706	ACATTCAGGAAAGTCACATC	296097	128293	CTCAAATTCCTGGGCTCAAG
206924	39120	CAGTTTCCCCAGTCCCCAAA	251511	83707	AACATTCAGGAAAGTCACAT	296098	128294	CCTCAAATTCCTGGGCTCAA
206925	39121	TCAGTTTCCCCAGTCCCCAA	251512	83708	AAACATTCAGGAAAGTCACA	296099	128295	GCCTCAAATTCCTGGGCTCA
206926	39122	CTCAGTTTCCCCAGTCCCCA	251513	83709	TAAACATTCAGGAAAGTCAC	296100	128296	GGCCTCAAATTCCTGGGCTC
206927	39123	CCTCAGTTTCCCCAGTCCCC	251514	83710	TTAAACATTCAGGAAAGTCA	296101	128297	TGGCCTCAAATTCCTGGGCT
206928	39124	GCCTCAGTTTCCCCAGTCCC	251515	83711	CTTAAACATTCAGGAAAGTC	296102	128298	CTGGCCTCAAATTCCTGGGC
206929	39125	GGCCTCAGTTTCCCCAGTCC	251516	83712	CCTTAAACATTCAGGAAAGT	296103	128299	GCTGGCCTCAAATTCCTGGG
206930	39126	GGGCCTCAGTTTCCCCAGTC	251517	83713	CCCTTAAACATTCAGGAAAG	296104	128300	GGCTGGCCTCAAATTCCTGG
206931	39127	TGGGCCTCAGTTTCCCCAGT	251518	83714	TCCCTTAAACATTCAGGAAA	296105	128301	AGGCTGGCCTCAAATTCCTG
206932	39128	CTGGGCCTCAGTTTCCCCAG	251519	83715	TTCCCTTAAACATTCAGGAA	296106	128302	CAGGCTGGCCTCAAATTCCT
206933	39129	ACTGGGCCTCAGTTTCCCCA	251520	83716	TTTCCCTTAAACATTCAGGA	296107	128303	CCAGGCTGGCCTCAAATTCC
206934	39130	CACTGGGCCTCAGTTTCCCC	251521	83717	TTTTCCCTTAAACATTCAGG	296108	128304	CCCAGGCTGGCCTCAAATTC
206935	39131	GCACTGGGCCTCAGTTTCCC	251522	83718	ATTTTCCCTTAAACATTCAG	296109	128305	GCCCAGGCTGGCCTCAAATT
206936	39132	GGCACTGGGCCTCAGTTTCC	251523	83719	CATTTTCCCTTAAACATTCA	296110	128306	TGCCCAGGCTGGCCTCAAAT
206937	39133	TGGCACTGGGCCTCAGTTTC	251524	83720	GCATTTTCCCTTAAACATTC	296111	128307	TTGCCCAGGCTGGCCTCAAA
206938	39134	GTGGCACTGGGCCTCAGTTT	251525	83721	GGCATTTTCCCTTAAACATT	296112	128308	CTTGCCCAGGCTGGCCTCAA
206939	39135	CGTGGCACTGGGCCTCAGTT	251526	83722	GGGCATTTTCCCTTAAACAT	296113	128309	ACTTGCCCAGGCTGGCCTCA
206940	39136	GCGTGGCACTGGGCCTCAGT	251527	83723	CGGGCATTTTCCCTTAAACA	296114	128310	TACTTGCCCAGGCTGGCCTC
206941	39137	CGCGTGGCACTGGGCCTCAG	251528	83724	TCGGGCATTTTCCCTTAAAC	296115	128311	CTACTTGCCCAGGCTGGCCT
206942	39138	TCGCGTGGCACTGGGCCTCA	251529	83725	TTCGGGCATTTTCCCTTAAA	296116	128312	TCTACTTGCCCAGGCTGGCC
206943	39139	ATCGCGTGGCACTGGGCCTC	251530	83726	CTTCGGGCATTTTCCCTTAA	296117	128313	ATCTACTTGCCCAGGCTGGC
206944	39140	CATCGCGTGGCACTGGGCCT	251531	83727	CCTTCGGGCATTTTCCCTTA	296118	128314	TATCTACTTGCCCAGGCTGG
206945	39141	GCATCGCGTGGCACTGGGCC	251532	83728	ACCTTCGGGCATTTTCCCTT	296119	128315	CTATCTACTTGCCCAGGCTG
206946	39142	GGCATCGCGTGGCACTGGGC	251533	83729	TACCTTCGGGCATTTTCCCT	296120	128316	CCTATCTACTTGCCCAGGCT
206947	39143	TGGCATCGCGTGGCACTGGG	251534	83730	GTACCTTCGGGCATTTTCCC	296121	128317	ACCTATCTACTTGCCCAGGC
206948	39144	ATGGCATCGCGTGGCACTGG	251535	83731	TGTACCTTCGGGCATTTTCC	296122	128318	TACCTATCTACTTGCCCAGG
206949	39145	AATGGCATCGCGTGGCACTG	251536	83732	CTGTACCTTCGGGCATTTTC	296123	128319	CTACCTATCTACTTGCCCAG
206950	39146	AAATGGCATCGCGTGGCACT	251537	83733	TCTGTACCTTCGGGCATTTT	296124	128320	TCTACCTATCTACTTGCCCA
206951	39147	CAAATGGCATCGCGTGGCAC	251538	83734	CTCTGTACCTTCGGGCATTT	296125	128321	ATCTACCTATCTACTTGCCC
206952	39148	ACAAATGGCATCGCGTGGCA	251539	83735	TCTCTGTACCTTCGGGCATT	296126	128322	CATCTACCTATCTACTTGCC
206953	39149	AACAAATGGCATCGCGTGGC	251540	83736	CTCTCTGTACCTTCGGGCAT	296127	128323	TCATCTACCTATCTACTTGC
206954	39150	GAACAAATGGCATCGCGTGG	251541	83737	GCTCTCTGTACCTTCGGGCA	296128	128324	ATCATCTACCTATCTACTTG
206955	39151	TGAACAAATGGCATCGCGTG	251542	83738	AGCTCTCTGTACCTTCGGGC	296129	128325	AATCATCTACCTATCTACTT
206956	39152	CTGAACAAATGGCATCGCGT	251543	83739	AAGCTCTCTGTACCTTCGGG	296130	128326	CAATCATCTACCTATCTACT
206957	39153	CCTGAACAAATGGCATCGCG	251544	83740	CAAGCTCTCTGTACCTTCGG	296131	128327	TCAATCATCTACCTATCTAC
206958	39154	CCCTGAACAAATGGCATCGC	251545	83741	CCAAGCTCTCTGTACCTTCG	296132	128328	ATCAATCATCTACCTATCTA
206959	39155	TCCCTGAACAAATGGCATCG	251546	83742	ACCAAGCTCTCTGTACCTTC	296133	128329	TATCAATCATCTACCTATCT
206960	39156	TTCCCTGAACAAATGGCATC	251547	83743	AACCAAGCTCTCTGTACCTT	296134	128330	CTATCAATCATCTACCTATC
206961	39157	CTTCCCTGAACAAATGGCAT	251548	83744	AAACCAAGCTCTCTGTACCT	296135	128331	TCTATCAATCATCTACCTAT
206962	39158	TCTTCCCTGAACAAATGGCA	251549	83745	GAAACCAAGCTCTCTGTACC	296136	128332	ATCTATCAATCATCTACCTA
206963	39159	ATCTTCCCTGAACAAATGGC	251550	83746	AGAAACCAAGCTCTCTGTAC	296137	128333	TATCTATCAATCATCTACCT
206964	39160	AATCTTCCCTGAACAAATGG	251551	83747	TAGAAACCAAGCTCTCTGTA	296138	128334	CTATCTATCAATCATCTACC
206965	39161	TAATCTTCCCTGAACAAATG	251552	83748	CTAGAAACCAAGCTCTCTGT	296139	128335	TCTATCTATCAATCATCTAC
206966	39162	CTAATCTTCCCTGAACAAAT	251553	83749	ACTAGAAACCAAGCTCTCTG	296140	128336	ATCTATCTATCAATCATCTA
206967	39163	CCTAATCTTCCCTGAACAAA	251554	83750	TACTAGAAACCAAGCTCTCT	296141	128337	TATCTATCTATCAATCATCT
206968	39164	ACCTAATCTTCCCTGAACAA	251555	83751	TTACTAGAAACCAAGCTCTC	296142	128338	CTATCTATCTATCAATCATC
206969	39165	GACCTAATCTTCCCTGAACA	251556	83752	TTTACTAGAAACCAAGCTCT	296143	128339	TCTATCTATCTATCAATCAT
206970	39166	TGACCTAATCTTCCCTGAAC	251557	83753	GTTTACTAGAAACCAAGCTC	296144	128340	ATCTATCTATCTATCAATCA

206971	39167	ATGACCTAATCTTCCCTGAA	251558	83754	TGTTTACTAGAAACCAAGCT	296145	128341	TATCTATCTATCTATCAATC
206972	39168	GATGACCTAATCTTCCCTGA	251559	83755	TTGTTTACTAGAAACCAAGC	296146	128342	CTATCTATCTATCTATCAAT
206973	39169	AGATGACCTAATCTTCCCTG	251560	83756	ATTGTTTACTAGAAACCAAG	296147	128343	TCTATCTATCTATCTATCAA
206974	39170	CAGATGACCTAATCTTCCCT	251561	83757	TATTGTTTACTAGAAACCAA	296148	128344	ATCTATCTATCTATCTATCA
206975	39171	GCAGATGACCTAATCTTCCC	251562	83758	TTATTGTTTACTAGAAACCA	296149	128345	TATCTATCTATCTATCTATC
206976	39172	AGCAGATGACCTAATCTTCC	251563	83759	GTTATTGTTTACTAGAAACC	296150	128346	TTATCTATCTATCTATCTAT
206977	39173	TAGCAGATGACCTAATCTTC	251564	83760	AGTTATTGTTTACTAGAAAC	296151	128347	TTTATCTATCTATCTATCTA
206978	39174	CTAGCAGATGACCTAATCTT	251565	83761	CAGTTATTGTTTACTAGAAA	296152	128348	ATTTATCTATCTATCTATCT
206979	39175	CCTAGCAGATGACCTAATCT	251566	83762	ACAGTTATTGTTTACTAGAA	296153	128349	TATTTATCTATCTATCTATC
206980	39176	ACCTAGCAGATGACCTAATC	251567	83763	GACAGTTATTGTTTACTAGA	296154	128350	CTATTTATCTATCTATCTAT
206981	39177	GACCTAGCAGATGACCTAAT	251568	83764	AGACAGTTATTGTTTACTAG	296155	128351	TCTATTTATCTATCTATCTA
206982	39178	GGACCTAGCAGATGACCTAA	251569	83765	AAGACAGTTATTGTTTACTA	296156	128352	ATCTATTTATCTATCTATCT
206983	39179	GGGACCTAGCAGATGACCTA	251570	83766	CAAGACAGTTATTGTTTACT	296157	128353	CATCTATTTATCTATCTATC
206984	39180	GGGGACCTAGCAGATGACCT	251571	83767	GCAAGACAGTTATTGTTTAC	296158	128354	CCATCTATTTATCTATCTAT
206985	39181	TGGGGACCTAGCAGATGACC	251572	83768	AGCAAGACAGTTATTGTTTA	296159	128355	TCCATCTATTTATCTATCTA
206986	39182	CTGGGGACCTAGCAGATGAC	251573	83769	AAGCAAGACAGTTATTGTTT	296160	128356	ATCCATCTATTTATCTATCT
206987	39183	ACTGGGGACCTAGCAGATGA	251574	83770	AAAGCAAGACAGTTATTGTT	296161	128357	TATCCATCTATTTATCTATC
206988	39184	GACTGGGGACCTAGCAGATG	251575	83771	AAAAGCAAGACAGTTATTGT	296162	128358	CTATCCATCTATTTATCTAT
206989	39185	TGACTGGGGACCTAGCAGAT	251576	83772	TAAAAGCAAGACAGTTATTG	296163	128359	TCTATCCATCTATTTATCTA
206990	39186	GTGACTGGGGACCTAGCAGA	251577	83773	GTAAAAGCAAGACAGTTATT	296164	128360	ATCTATCCATCTATTTATCT
206991	39187	AGTGACTGGGGACCTAGCAG	251578	83774	GGTAAAAGCAAGACAGTTAT	296165	128361	TATCTATCCATCTATTTATC
206992	39188	AAGTGACTGGGGACCTAGCA	251579	83775	GGGTAAAAGCAAGACAGTTA	296166	128362	TTATCTATCCATCTATTTAT
206993	39189	CAAGTGACTGGGGACCTAGC	251580	83776	GGGGTAAAAGCAAGACAGTT	296167	128363	CTTATCTATCCATCTATTTA
206994	39190	TCAAGTGACTGGGGACCTAG	251581	83777	GGGGGTAAAAGCAAGACAGT	296168	128364	ACTTATCTATCCATCTATTT
206995	39191	GTCAAGTGACTGGGGACCTA	251582	83778	GGGGGGTAAAAGCAAGACAG	296169	128365	GACTTATCTATCCATCTATT
206996	39192	GGTCAAGTGACTGGGGACCT	251583	83779	AGGGGGGTAAAAGCAAGACA	296170	128366	CGACTTATCTATCCATCTAT
206997	39193	AGGTCAAGTGACTGGGGACC	251584	83780	AAGGGGGGTAAAAGCAAGAC	296171	128367	GCGACTTATCTATCCATCTA
206998	39194	AAGGTCAAGTGACTGGGGAC	251585	83781	GAAGGGGGGTAAAAGCAAGA	296172	128368	AGCGACTTATCTATCCATCT
206999	39195	GAAGGTCAAGTGACTGGGGA	251586	83782	TGAAGGGGGGTAAAAGCAAG	296173	128369	TAGCGACTTATCTATCCATC
207000	39196	AGAAGGTCAAGTGACTGGGG	251587	83783	ATGAAGGGGGGTAAAAGCAA	296174	128370	CTAGCGACTTATCTATCCAT
207001	39197	AAGAAGGTCAAGTGACTGGG	251588	83784	AATGAAGGGGGGTAAAAGCA	296175	128371	TCTAGCGACTTATCTATCCA
207002	39198	GAAGAAGGTCAAGTGACTGG	251589	83785	AAATGAAGGGGGGTAAAAGC	296176	128372	GTCTAGCGACTTATCTATCC
207003	39199	GGAAGAAGGTCAAGTGACTG	251590	83786	CAAATGAAGGGGGGTAAAAG	296177	128373	TGTCTAGCGACTTATCTATC
207004	39200	GGGAAGAAGGTCAAGTGACT	251591	83787	GCAAATGAAGGGGGGTAAAA	296178	128374	CTGTCTAGCGACTTATCTAT
207005	39201	TGGGAAGAAGGTCAAGTGAC	251592	83788	AGCAAATGAAGGGGGGTAAA	296179	128375	ACTGTCTAGCGACTTATCTA
207006	39202	CTGGGAAGAAGGTCAAGTGA	251593	83789	CAGCAAATGAAGGGGGGTAA	296180	128376	GACTGTCTAGCGACTTATCT
207007	39203	TCTGGGAAGAAGGTCAAGTG	251594	83790	TCAGCAAATGAAGGGGGGTA	296181	128377	TGACTGTCTAGCGACTTATC
207008	39204	GTCTGGGAAGAAGGTCAAGT	251595	83791	GTCAGCAAATGAAGGGGGGT	296182	128378	ATGACTGTCTAGCGACTTAT
207009	39205	TGTCTGGGAAGAAGGTCAAG	251596	83792	TGTCAGCAAATGAAGGGGGG	296183	128379	GATGACTGTCTAGCGACTTA
207010	39206	CTGTCTGGGAAGAAGGTCAA	251597	83793	GTGTCAGCAAATGAAGGGGG	296184	128380	GGATGACTGTCTAGCGACTT
207011	39207	CCTGTCTGGGAAGAAGGTCA	251598	83794	TGTGTCAGCAAATGAAGGGG	296185	128381	TGGATGACTGTCTAGCGACT
207012	39208	TCCTGTCTGGGAAGAAGGTC	251599	83795	ATGTGTCAGCAAATGAAGGG	296186	128382	ATGGATGACTGTCTAGCGAC
207013	39209	TTCCTGTCTGGGAAGAAGGT	251600	83796	TATGTGTCAGCAAATGAAGG	296187	128383	GATGGATGACTGTCTAGCGA
207014	39210	CTTCCTGTCTGGGAAGAAGG	251601	83797	GTATGTGTCAGCAAATGAAG	296188	128384	GGATGGATGACTGTCTAGCG
207015	39211	TCTTCCTGTCTGGGAAGAAG	251602	83798	TGTATGTGTCAGCAAATGAA	296189	128385	TGGATGGATGACTGTCTAGC
207016	39212	TTCTTCCTGTCTGGGAAGAA	251603	83799	GTGTATGTGTCAGCAAATGA	296190	128386	GTGGATGGATGACTGTCTAG
207017	39213	CTTCTTCCTGTCTGGGAAGA	251604	83800	GGTGTATGTGTCAGCAAATG	296191	128387	GGTGGATGGATGACTGTCTA
207018	39214	GCTTCTTCCTGTCTGGGAAG	251605	83801	TGGTGTATGTGTCAGCAAAT	296192	128388	GGGTGGATGGATGACTGTCT
207019	39215	AGCTTCTTCCTGTCTGGGAA	251606	83802	CTGGTGTATGTGTCAGCAAA	296193	128389	TGGGTGGATGGATGACTGTC
207020	39216	CAGCTTCTTCCTGTCTGGGA	251607	83803	GCTGGTGTATGTGTCAGCAA	296194	128390	ATGGGTGGATGGATGACTGT
207021	39217	GCAGCTTCTTCCTGTCTGGG	251608	83804	AGCTGGTGTATGTGTCAGCA	296195	128391	GATGGGTGGATGGATGACTG
207022	39218	AGCAGCTTCTTCCTGTCTGG	251609	83805	CAGCTGGTGTATGTGTCAGC	296196	128392	GGATGGGTGGATGGATGACT
207023	39219	GAGCAGCTTCTTCCTGTCTG	251610	83806	TCAGCTGGTGTATGTGTCAG	296197	128393	TGGATGGGTGGATGGATGAC
207024	39220	AGAGCAGCTTCTTCCTGTCT	251611	83807	TTCAGCTGGTGTATGTGTCA	296198	128394	GTGGATGGGTGGATGGATGA
207025	39221	CAGAGCAGCTTCTTCCTGTC	251612	83808	CTTCAGCTGGTGTATGTGTC	296199	128395	TGTGGATGGGTGGATGGATG
207026	39222	CCAGAGCAGCTTCTTCCTGT	251613	83809	TCTTCAGCTGGTGTATGTGT	296200	128396	GTGTGGATGGGTGGATGGAT
207027	39223	CCCAGAGCAGCTTCTTCCTG	251614	83810	TTCTTCAGCTGGTGTATGTG	296201	128397	TGTGTGGATGGGTGGATGGA
207028	39224	ACCCAGAGCAGCTTCTTCCT	251615	83811	CTTCTTCAGCTGGTGTATGT	296202	128398	ATGTGTGGATGGGTGGATGG
207029	39225	GACCCAGAGCAGCTTCTTCC	251616	83812	GCTTCTTCAGCTGGTGTATG	296203	128399	TATGTGTGGATGGGTGGATG
207030	39226	AGACCCAGAGCAGCTTCTTC	251617	83813	TGCTTCTTCAGCTGGTGTAT	296204	128400	TTATGTGTGGATGGGTGGAT
207031	39227	GAGACCCAGAGCAGCTTCTT	251618	83814	CTGCTTCTTCAGCTGGTGTA	296205	128401	TTTATGTGTGGATGGGTGGA
207032	39228	AGAGACCCAGAGCAGCTTCT	251619	83815	CCTGCTTCTTCAGCTGGTGT	296206	128402	TTTTATGTGTGGATGGGTGG
207033	39229	GAGAGACCCAGAGCAGCTTC	251620	83816	GCCTGCTTCTTCAGCTGGTG	296207	128403	TTTTTATGTGTGGATGGGTG
207034	39230	TGAGAGACCCAGAGCAGCTT	251621	83817	TGCCTGCTTCTTCAGCTGGT	296208	128404	CTTTTTATGTGTGGATGGGT
207035	39231	CTGAGAGACCCAGAGCAGCT	251622	83818	ATGCCTGCTTCTTCAGCTGG	296209	128405	CCTTTTTATGTGTGGATGGG
207036	39232	ACTGAGAGACCCAGAGCAGC	251623	83819	AATGCCTGCTTCTTCAGCTG	296210	128406	GCCTTTTTATGTGTGGATGG
207037	39233	CACTGAGAGACCCAGAGCAG	251624	83820	CAATGCCTGCTTCTTCAGCT	296211	128407	GGCCTTTTTATGTGTGGATG
207038	39234	GCACTGAGAGACCCAGAGCA	251625	83821	CCAATGCCTGCTTCTTCAGC	296212	128408	AGGCCTTTTTATGTGTGGAT
207039	39235	AGCACTGAGAGACCCAGAGC	251626	83822	TCCAATGCCTGCTTCTTCAG	296213	128409	AAGGCCTTTTTATGTGTGGA
207040	39236	GAGCACTGAGAGACCCAGAG	251627	83823	CTCCAATGCCTGCTTCTTCA	296214	128410	AAAGGCCTTTTTATGTGTGG
207041	39237	GGAGCACTGAGAGACCCAGA	251628	83824	TCTCCAATGCCTGCTTCTTC	296215	128411	CAAAGGCCTTTTTATGTGTG
207042	39238	TGGAGCACTGAGAGACCCAG	251629	83825	GTCTCCAATGCCTGCTTCTT	296216	128412	ACAAAGGCCTTTTTATGTGT

207043	39239	GTGGAGCACTGAGAGACCCA	251630	83826	TGTCTCCAATGCCTGCTTCT	296217	128413	GACAAAGGCCTTTTTATGTG
207044	39240	CGTGGAGCACTGAGAGACCC	251631	83827	GTGTCTCCAATGCCTGCTTC	296218	128414	TGACAAAGGCCTTTTTATGT
207045	39241	ACGTGGAGCACTGAGAGACC	251632	83828	GGTGTCTCCAATGCCTGCTT	296219	128415	ATGACAAAGGCCTTTTTATG
207046	39242	CACGTGGAGCACTGAGAGAC	251633	83829	GGGTGTCTCCAATGCCTGCT	296220	128416	CATGACAAAGGCCTTTTTAT
207047	39243	ACACGTGGAGCACTGAGAGA	251634	83830	GGGGTGTCTCCAATGCCTGC	296221	128417	ACATGACAAAGGCCTTTTTA
207048	39244	GACACGTGGAGCACTGAGAG	251635	83831	GGGGGTGTCTCCAATGCCTG	296222	128418	GACATGACAAAGGCCTTTTT
207049	39245	AGACACGTGGAGCACTGAGA	251636	83832	TGGGGGTGTCTCCAATGCCT	296223	128419	TGACATGACAAAGGCCTTTT
207050	39246	AAGACACGTGGAGCACTGAG	251637	83833	CTGGGGGTGTCTCCAATGCC	296224	128420	ATGACATGACAAAGGCCTTT
207051	39247	AAAGACACGTGGAGCACTGA	251638	83834	GCTGGGGGTGTCTCCAATGC	296225	128421	CATGACATGACAAAGGCCTT
207052	39248	CAAAGACACGTGGAGCACTG	251639	83835	GGCTGGGGGTGTCTCCAATG	296226	128422	ACATGACATGACAAAGGCCT
207053	39249	GCAAAGACACGTGGAGCACT	251640	83836	AGGCTGGGGGTGTCTCCAAT	296227	128423	AACATGACATGACAAAGGCC
207054	39250	TGCAAAGACACGTGGAGCAC	251641	83837	CAGGCTGGGGGTGTCTCCAA	296228	128424	AAACATGACATGACAAAGGC
207055	39251	GTGCAAAGACACGTGGAGCA	251642	83838	CCAGGCTGGGGGTGTCTCCA	296229	128425	AAAACATGACATGACAAAGG
207056	39252	TGTGCAAAGACACGTGGAGC	251643	83839	TCCAGGCTGGGGGTGTCTCC	296230	128426	CAAAACATGACATGACAAAG
207057	39253	ATGTGCAAAGACACGTGGAG	251644	83840	TTCCAGGCTGGGGGTGTCTC	296231	128427	ACAAAACATGACATGACAAA
207058	39254	AATGTGCAAAGACACGTGGA	251645	83841	CTTCCAGGCTGGGGGTGTCT	296232	128428	CACAAAACATGACATGACAA
207059	39255	CAATGTGCAAAGACACGTGG	251646	83842	TCTTCCAGGCTGGGGGTGTC	296233	128429	CCACAAAACATGACATGACA
207060	39256	TCAATGTGCAAAGACACGTG	251647	83843	GTCTTCCAGGCTGGGGGTGT	296234	128430	GCCACAAAACATGACATGAC
207061	39257	TTCAATGTGCAAAGACACGT	251648	83844	CGTCTTCCAGGCTGGGGGTG	296235	128431	GGCCACAAAACATGACATGA
207062	39258	TTTCAATGTGCAAAGACACG	251649	83845	TCGTCTTCCAGGCTGGGGGT	296236	128432	GGGCCACAAAACATGACATG
207063	39259	ATTTCAATGTGCAAAGACAC	251650	83846	TTCGTCTTCCAGGCTGGGGG	296237	128433	TGGGCCACAAAACATGACAT
207064	39260	CATTTCAATGTGCAAAGACA	251651	83847	CTTCGTCTTCCAGGCTGGGG	296238	128434	GTGGGCCACAAAACATGACA
207065	39261	ACATTTCAATGTGCAAAGAC	251652	83848	GCTTCGTCTTCCAGGCTGGG	296239	128435	GGTGGGCCACAAAACATGAC
207066	39262	AACATTTCAATGTGCAAAGA	251653	83849	AGCTTCGTCTTCCAGGCTGG	296240	128436	AGGTGGGCCACAAAACATGA
207067	39263	AAACATTTCAATGTGCAAAG	251654	83850	CAGCTTCGTCTTCCAGGCTG	296241	128437	CAGGTGGGCCACAAAACATG
207068	39264	AAAACATTTCAATGTGCAAA	251655	83851	GCAGCTTCGTCTTCCAGGCT	296242	128438	GCAGGTGGGCCACAAAACAT
207069	39265	GAAAACATTTCAATGTGCAA	251656	83852	AGCAGCTTCGTCTTCCAGGC	296243	128439	GGCAGGTGGGCCACAAAACA
207070	39266	AGAAAACATTTCAATGTGCA	251657	83853	CAGCAGCTTCGTCTTCCAGG	296244	128440	TGGCAGGTGGGCCACAAAAC
207071	39267	CAGAAAACATTTCAATGTGC	251658	83854	CCAGCAGCTTCGTCTTCCAG	296245	128441	CTGGCAGGTGGGCCACAAAA
207072	39268	TCAGAAAACATTTCAATGTG	251659	83855	ACCAGCAGCTTCGTCTTCCA	296246	128442	ACTGGCAGGTGGGCCACAAA
207073	39269	ATCAGAAAACATTTCAATGT	251660	83856	GACCAGCAGCTTCGTCTTCC	296247	128443	CACTGGCAGGTGGGCCACAA
207074	39270	AATCAGAAAACATTTCAATG	251661	83857	TGACCAGCAGCTTCGTCTTC	296248	128444	ACACTGGCAGGTGGGCCACA
207075	39271	AAATCAGAAAACATTTCAAT	251662	83858	GTGACCAGCAGCTTCGTCTT	296249	128445	AACACTGGCAGGTGGGCCAC
207076	39272	AAAATCAGAAAACATTTCAA	251663	83859	CGTGACCAGCAGCTTCGTCT	296250	128446	CAACACTGGCAGGTGGGCCA
207077	39273	AAAAATCAGAAAACATTTCA	251664	83860	ACGTGACCAGCAGCTTCGTC	296251	128447	GCAACACTGGCAGGTGGGCC
207078	39274	AAAAAATCAGAAAACATTTC	251665	83861	CACGTGACCAGCAGCTTCGT	296252	128448	GGCAACACTGGCAGGTGGGC
207079	39275	AAAAAAATCAGAAAACATTT	251666	83862	TCACGTGACCAGCAGCTTCG	296253	128449	GGGCAACACTGGCAGGTGGG
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207081	39277	AAAAAAAAATCAGAAAACAT	251668	83864	GGTCACGTGACCAGCAGCTT	296255	128451	GTGGGCAACACTGGCAGGTG
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207083	39279	AAAAAAAAAAATCAGAAAAC	251670	83866	TGGGTCACGTGACCAGCAGC	296257	128453	CTGTGGGCAACACTGGCAGG
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207085	39281	AAAAAAAAAAAAATCAGAAA	251672	83868	CTTGGGTCACGTGACCAGCA	296259	128455	AACTGTGGGCAACACTGGCA
207086	39282	AAAAAAAAAAAAAATCAGAA	251673	83869	CCTTGGGTCACGTGACCAGC	296260	128456	CAACTGTGGGCAACACTGGC
207087	39283	AAAAAAAAAAAAAAATCAGA	251674	83870	ACCTTGGGTCACGTGACCAG	296261	128457	GCAACTGTGGGCAACACTGG
207088	39284	AAAAAAAAAAAAAAAATCAG	251675	83871	GACCTTGGGTCACGTGACCA	296262	128458	AGCAACTGTGGGCAACACTG
207089	39285	AAAAAAAAAAAAAAAAATCA	251676	83872	TGACCTTGGGTCACGTGACC	296263	128459	CAGCAACTGTGGGCAACACT
207090	39286	AAAAAAAAAAAAAAAAAATC	251677	83873	CTGACCTTGGGTCACGTGAC	296264	128460	GCAGCAACTGTGGGCAACAC
207091	39287	CAAAAAAAAAAAAAAAAAAT	251678	83874	ACTGACCTTGGGTCACGTGA	296265	128461	GGCAGCAACTGTGGGCAACA
207092	39288	GCAAAAAAAAAAAAAAAAAA	251679	83875	CACTGACCTTGGGTCACGTG	296266	128462	GGGCAGCAACTGTGGGCAAC
207093	39289	AGCAAAAAAAAAAAAAAAAA	251680	83876	TCACTGACCTTGGGTCACGT	296267	128463	GGGGCAGCAACTGTGGGCAA
207094	39290	CAGCAAAAAAAAAAAAAAAA	251681	83877	TTCACTGACCTTGGGTCACG	296268	128464	AGGGGCAGCAACTGTGGGCA
207095	39291	ACAGCAAAAAAAAAAAAAAA	251682	83878	GTTCACTGACCTTGGGTCAC	296269	128465	GAGGGGCAGCAACTGTGGGC
207096	39292	AACAGCAAAAAAAAAAAAAA	251683	83879	AGTTCACTGACCTTGGGTCA	296270	128466	GGAGGGGCAGCAACTGTGGG
207097	39293	TAACAGCAAAAAAAAAAAAA	251684	83880	CAGTTCACTGACCTTGGGTC	296271	128467	TGGAGGGGCAGCAACTGTGG
207098	39294	GTAACAGCAAAAAAAAAAAA	251685	83881	CCAGTTCACTGACCTTGGGT	296272	128468	TTGGAGGGGCAGCAACTGTG
207099	39295	TGTAACAGCAAAAAAAAAAA	251686	83882	TCCAGTTCACTGACCTTGGG	296273	128469	TTTGGAGGGGCAGCAACTGT
207100	39296	ATGTAACAGCAAAAAAAAAA	251687	83883	TTCCAGTTCACTGACCTTGG	296274	128470	GTTTGGAGGGGCAGCAACTG
207101	39297	AATGTAACAGCAAAAAAAAA	251688	83884	ATTCCAGTTCACTGACCTTG	296275	128471	AGTTTGGAGGGGCAGCAACT
207102	39298	AAATGTAACAGCAAAAAAAA	251689	83885	AATTCCAGTTCACTGACCTT	296276	128472	GAGTTTGGAGGGGCAGCAAC
207103	39299	TAAATGTAACAGCAAAAAAA	251690	83886	CAATTCCAGTTCACTGACCT	296277	128473	TGAGTTTGGAGGGGCAGCAA
207104	39300	GTAAATGTAACAGCAAAAAA	251691	83887	GCAATTCCAGTTCACTGACC	296278	128474	ATGAGTTTGGAGGGGCAGCA
207105	39301	AGTAAATGTAACAGCAAAAA	251692	83888	GGCAATTCCAGTTCACTGAC	296279	128475	GATGAGTTTGGAGGGGCAGC
207106	39302	AAGTAAATGTAACAGCAAAA	251693	83889	AGGCAATTCCAGTTCACTGA	296280	128476	TGATGAGTTTGGAGGGGCAG
207107	39303	AAAGTAAATGTAACAGCAAA	251694	83890	CAGGCAATTCCAGTTCACTG	296281	128477	CTGATGAGTTTGGAGGGGCA
207108	39304	AAAAGTAAATGTAACAGCAA	251695	83891	GCAGGCAATTCCAGTTCACT	296282	128478	ACTGATGAGTTTGGAGGGGC
207109	39305	TAAAAGTAAATGTAACAGCA	251696	83892	GGCAGGCAATTCCAGTTCAC	296283	128479	GACTGATGAGTTTGGAGGGG
207110	39306	TTAAAAGTAAATGTAACAGC	251697	83893	TGGCAGGCAATTCCAGTTCA	296284	128480	TGACTGATGAGTTTGGAGGG
207111	39307	TTTAAAAGTAAATGTAACAG	251698	83894	ATGGCAGGCAATTCCAGTTC	296285	128481	GTGACTGATGAGTTTGGAGG
207112	39308	TTTTAAAAGTAAATGTAACA	251699	83895	CATGGCAGGCAATTCCAGTT	296286	128482	AGTGACTGATGAGTTTGGAG
207113	39309	TTTTTAAAAGTAAATGTAAC	251700	83896	TCATGGCAGGCAATTCCAGT	296287	128483	CAGTGACTGATGAGTTTGGA
207114	39310	TTTTTTAAAAGTAAATGTAA	251701	83897	GTCATGGCAGGCAATTCCAG	296288	128484	CCAGTGACTGATGAGTTTGG

207115	39311	ATTTTTTAAAAGTAAATGTA	251702	83898	AGTCATGGCAGGCAATTCCA	296289	128485	GCCAGTGACTGATGAGTTTG
207116	39312	TATTTTTTAAAAGTAAATGT	251703	83899	AAGTCATGGCAGGCAATTCC	296290	128486	TGCCAGTGACTGATGAGTTT
207117	39313	TTATTTTTTAAAAGTAAATG	251704	83900	CAAGTCATGGCAGGCAATTC	296291	128487	TTGCCAGTGACTGATGAGTT
207118	39314	GTTATTTTTTAAAAGTAAAT	251705	83901	CCAAGTCATGGCAGGCAATT	296292	128488	TTTGCCAGTGACTGATGAGT
207119	39315	TGTTATTTTTTAAAAGTAAA	251706	83902	CCCAAGTCATGGCAGGCAAT	296293	128489	GTTTGCCAGTGACTGATGAG
207120	39316	TTGTTATTTTTTAAAAGTAA	251707	83903	CCCCAAGTCATGGCAGGCAA	296294	128490	TGTTTGCCAGTGACTGATGA
207121	39317	CTTGTTATTTTTTAAAAGTA	251708	83904	CCCCCAAGTCATGGCAGGCA	296295	128491	CTGTTTGCCAGTGACTGATG
207122	39318	GCTTGTTATTTTTTAAAAGT	251709	83905	ACCCCCAAGTCATGGCAGGC	296296	128492	CCTGTTTGCCAGTGACTGAT
207123	39319	TGCTTGTTATTTTTTAAAAG	251710	83906	AACCCCCAAGTCATGGCAGG	296297	128493	TCCTGTTTGCCAGTGACTGA
207124	39320	TTGCTTGTTATTTTTTAAAA	251711	83907	CAACCCCCAAGTCATGGCAG	296298	128494	CTCCTGTTTGCCAGTGACTG
207125	39321	ATTGCTTGTTATTTTTTAAA	251712	83908	CCAACCCCCAAGTCATGGCA	296299	128495	CCTCCTGTTTGCCAGTGACT
207126	39322	TATTGCTTGTTATTTTTTAA	251713	83909	CCCAACCCCCAAGTCATGGC	296300	128496	TCCTCCTGTTTGCCAGTGAC
207127	39323	TTATTGCTTGTTATTTTTTA	251714	83910	CCCCAACCCCCAAGTCATGG	296301	128497	TTCCTCCTGTTTGCCAGTGA
207128	39324	TTTATTGCTTGTTATTTTTT	251715	83911	CCCCCAACCCCCAAGTCATG	296302	128498	ATTCCTCCTGTTTGCCAGTG
207129	39325	TTTTATTGCTTGTTATTTTT	251716	83912	CCCCCCAACCCCCAAGTCAT	296303	128499	CATTCCTCCTGTTTGCCAGT
207130	39326	ATTTTATTGCTTGTTATTTT	251717	83913	TCCCCCCAACCCCCAAGTCA	296304	128500	ACATTCCTCCTGTTTGCCAG
207131	39327	CATTTTATTGCTTGTTATTT	251718	83914	CTCCCCCCAACCCCCAAGTC	296305	128501	CACATTCCTCCTGTTTGCCA
207132	39328	ACATTTTATTGCTTGTTATT	251719	83915	CCTCCCCCCAACCCCCAAGT	296306	128502	ACACATTCCTCCTGTTTGCC
207133	39329	AACATTTTATTGCTTGTTAT	251720	83916	CCCTCCCCCCAACCCCCAAG	296307	128503	CACACATTCCTCCTGTTTGC
207134	39330	TAACATTTTATTGCTTGTTA	251721	83917	TCCCTCCCCCCAACCCCCAA	296308	128504	CCACACATTCCTCCTGTTTG
207135	39331	GTAACATTTTATTGCTTGTT	251722	83918	GTCCCTCCCCCCAACCCCCA	296309	128505	GCCACACATTCCTCCTGTTT
207136	39332	TGTAACATTTTATTGCTTGT	251723	83919	TGTCCCTCCCCCCAACCCCC	296310	128506	AGCCACACATTCCTCCTGTT
207137	39333	ATGTAACATTTTATTGCTTG	251724	83920	ATGTCCCTCCCCCCAACCCC	296311	128507	GAGCCACACATTCCTCCTGT
207138	39334	AATGTAACATTTTATTGCTT	251725	83921	CATGTCCCTCCCCCCAACCC	296312	128508	TGAGCCACACATTCCTCCTG
207139	39335	AAATGTAACATTTTATTGCT	251726	83922	CCATGTCCCTCCCCCCAACC	296313	128509	ATGAGCCACACATTCCTCCT
207140	39336	CAAATGTAACATTTTATTGC	251727	83923	CCCATGTCCCTCCCCCCAAC	296314	128510	CATGAGCCACACATTCCTCC
207141	39337	TCAAATGTAACATTTTATTG	251728	83924	CCCCATGTCCCTCCCCCCAA	296315	128511	ACATGAGCCACACATTCCTC
207142	39338	CTCAAATGTAACATTTTATT	251729	83925	ACCCCATGTCCCTCCCCCCA	296316	128512	GACATGAGCCACACATTCCT
207143	39339	TCTCAAATGTAACATTTTAT	251730	83926	CACCCCATGTCCCTCCCCCC	296317	128513	AGACATGAGCCACACATTCC
207144	39340	TTCTCAAATGTAACATTTTA	251731	83927	CCACCCCATGTCCCTCCCCC	296318	128514	CAGACATGAGCCACACATTC
207145	39341	CTTCTCAAATGTAACATTTT	251732	83928	CCCACCCCATGTCCCTCCCC	296319	128515	CCAGACATGAGCCACACATT
207146	39342	CCTTCTCAAATGTAACATTT	251733	83929	GCCCACCCCATGTCCCTCCC	296320	128516	CCCAGACATGAGCCACACAT
207147	39343	ACCTTCTCAAATGTAACATT	251734	83930	AGCCCACCCCATGTCCCTCC	296321	128517	GCCCAGACATGAGCCACACA
207148	39344	AACCTTCTCAAATGTAACAT	251735	83931	GAGCCCACCCCATGTCCCTC	296322	128518	TGCCCAGACATGAGCCACAC
207149	39345	CAACCTTCTCAAATGTAACA	251736	83932	AGAGCCCACCCCATGTCCCT	296323	128519	ATGCCCAGACATGAGCCACA
207150	39346	TCAACCTTCTCAAATGTAAC	251737	83933	CAGAGCCCACCCCATGTCCC	296324	128520	GATGCCCAGACATGAGCCAC
207151	39347	TTCAACCTTCTCAAATGTAA	251738	83934	GCAGAGCCCACCCCATGTCC	296325	128521	TGATGCCCAGACATGAGCCA
207152	39348	TTTCAACCTTCTCAAATGTA	251739	83935	GGCAGAGCCCACCCCATGTC	296326	128522	CTGATGCCCAGACATGAGCC
207153	39349	ATTTCAACCTTCTCAAATGT	251740	83936	GGGCAGAGCCCACCCCATGT	296327	128523	ACTGATGCCCAGACATGAGC
207154	39350	CATTTCAACCTTCTCAAATG	251741	83937	AGGGCAGAGCCCACCCCATG	296328	128524	CACTGATGCCCAGACATGAG
207155	39351	TCATTTCAACCTTCTCAAAT	251742	83938	CAGGGCAGAGCCCACCCCAT	296329	128525	CCACTGATGCCCAGACATGA
207156	39352	CTCATTTCAACCTTCTCAAA	251743	83939	TCAGGGCAGAGCCCACCCCA	296330	128526	GCCACTGATGCCCAGACATG
207157	39353	TCTCATTTCAACCTTCTCAA	251744	83940	TTCAGGGCAGAGCCCACCCC	296331	128527	AGCCACTGATGCCCAGACAT
207158	39354	TTCTCATTTCAACCTTCTCA	251745	83941	TTTCAGGGCAGAGCCCACCC	296332	128528	CAGCCACTGATGCCCAGACA
207159	39355	ATTCTCATTTCAACCTTCTC	251746	83942	TTTTCAGGGCAGAGCCCACC	296333	128529	ACAGCCACTGATGCCCAGAC
207160	39356	AATTCTCATTTCAACCTTCT	251747	83943	CTTTTCAGGGCAGAGCCCAC	296334	128530	CACAGCCACTGATGCCCAGA
207161	39357	CAATTCTCATTTCAACCTTC	251748	83944	TCTTTTCAGGGCAGAGCCCA	296335	128531	CCACAGCCACTGATGCCCAG
207162	39358	TCAATTCTCATTTCAACCTT	251749	83945	ATCTTTTCAGGGCAGAGCCC	296336	128532	CCCACAGCCACTGATGCCCA
207163	39359	ATCAATTCTCATTTCAACCT	251750	83946	GATCTTTTCAGGGCAGAGCC	296337	128533	TCCCACAGCCACTGATGCCC
207164	39360	AATCAATTCTCATTTCAACC	251751	83947	TGATCTTTTCAGGGCAGAGC	296338	128534	CTCCCACAGCCACTGATGCC
207165	39361	AAATCAATTCTCATTTCAAC	251752	83948	ATGATCTTTTCAGGGCAGAG	296339	128535	TCTCCCACAGCCACTGATGC
207166	39362	CAAATCAATTCTCATTTCAA	251753	83949	AATGATCTTTTCAGGGCAGA	296340	128536	GTCTCCCACAGCCACTGATG
207167	39363	TCAAATCAATTCTCATTTCA	251754	83950	AAATGATCTTTTCAGGGCAG	296341	128537	TGTCTCCCACAGCCACTGAT
207168	39364	CTCAAATCAATTCTCATTTC	251755	83951	CAAATGATCTTTTCAGGGCA	296342	128538	ATGTCTCCCACAGCCACTGA
207169	39365	ACTCAAATCAATTCTCATTT	251756	83952	CCAAATGATCTTTTCAGGGC	296343	128539	GATGTCTCCCACAGCCACTG
207170	39366	AACTCAAATCAATTCTCATT	251757	83953	TCCAAATGATCTTTTCAGGG	296344	128540	GGATGTCTCCCACAGCCACT
207171	39367	TAACTCAAATCAATTCTCAT	251758	83954	GTCCAAATGATCTTTTCAGG	296345	128541	AGGATGTCTCCCACAGCCAC
207172	39368	TTAACTCAAATCAATTCTCA	251759	83955	GGTCCAAATGATCTTTTCAG	296346	128542	AAGGATGTCTCCCACAGCCA
207173	39369	TTTAACTCAAATCAATTCTC	251760	83956	AGGTCCAAATGATCTTTTCA	296347	128543	CAAGGATGTCTCCCACAGCC
207174	39370	ATTTAACTCAAATCAATTCT	251761	83957	CAGGTCCAAATGATCTTTTC	296348	128544	TCAAGGATGTCTCCCACAGC
207175	39371	AATTTAACTCAAATCAATTC	251762	83958	TCAGGTCCAAATGATCTTTT	296349	128545	ATCAAGGATGTCTCCCACAG
207176	39372	GAATTTAACTCAAATCAATT	251763	83959	CTCAGGTCCAAATGATCTTT	296350	128546	GATCAAGGATGTCTCCCACA
207177	39373	AGAATTTAACTCAAATCAAT	251764	83960	GCTCAGGTCCAAATGATCTT	296351	128547	AGATCAAGGATGTCTCCCAC
207178	39374	TAGAATTTAACTCAAATCAA	251765	83961	AGCTCAGGTCCAAATGATCT	296352	128548	AAGATCAAGGATGTCTCCCA
207179	39375	CTAGAATTTAACTCAAATCA	251766	83962	GAGCTCAGGTCCAAATGATC	296353	128549	GAAGATCAAGGATGTCTCCC
207180	39376	GCTAGAATTTAACTCAAATC	251767	83963	AGAGCTCAGGTCCAAATGAT	296354	128550	AGAAGATCAAGGATGTCTCC
207181	39377	TGCTAGAATTTAACTCAAAT	251768	83964	TAGAGCTCAGGTCCAAATGA	296355	128551	GAGAAGATCAAGGATGTCTC
207182	39378	CTGCTAGAATTTAACTCAAA	251769	83965	TTAGAGCTCAGGTCCAAATG	296356	128552	GGAGAAGATCAAGGATGTCT
207183	39379	TCTGCTAGAATTTAACTCAA	251770	83966	ATTAGAGCTCAGGTCCAAAT	296357	128553	TGGAGAAGATCAAGGATGTC
207184	39380	ATCTGCTAGAATTTAACTCA	251771	83967	AATTAGAGCTCAGGTCCAAA	296358	128554	CTGGAGAAGATCAAGGATGT
207185	39381	AATCTGCTAGAATTTAACTC	251772	83968	GAATTAGAGCTCAGGTCCAA	296359	128555	GCTGGAGAAGATCAAGGATG
207186	39382	AAATCTGCTAGAATTTAACT	251773	83969	TGAATTAGAGCTCAGGTCCA	296360	128556	AGCTGGAGAAGATCAAGGAT

207187	39383	AAAATCTGCTAGAATTTAAC	251774	83970	GTGAATTAGAGCTCAGGTCC	296361	128557	AAGCTGGAGAAGATCAAGGA
207188	39384	AAAAATCTGCTAGAATTTAA	251775	83971	TGTGAATTAGAGCTCAGGTC	296362	128558	GAAGCTGGAGAAGATCAAGG
207189	39385	GAAAAATCTGCTAGAATTTA	251776	83972	TTGTGAATTAGAGCTCAGGT	296363	128559	AGAAGCTGGAGAAGATCAAG
207190	39386	AGAAAAATCTGCTAGAATTT	251777	83973	CTTGTGAATTAGAGCTCAGG	296364	128560	GAGAAGCTGGAGAAGATCAA
207191	39387	AAGAAAAATCTGCTAGAATT	251778	83974	ACTTGTGAATTAGAGCTCAG	296365	128561	GGAGAAGCTGGAGAAGATCA
207192	39388	TAAGAAAAATCTGCTAGAAT	251779	83975	GACTTGTGAATTAGAGCTCA	296366	128562	AGGAGAAGCTGGAGAAGATC
207193	39389	CTAAGAAAAATCTGCTAGAA	251780	83976	GGACTTGTGAATTAGAGCTC	296367	128563	AAGGAGAAGCTGGAGAAGAT
207194	39390	TCTAAGAAAAATCTGCTAGA	251781	83977	TGGACTTGTGAATTAGAGCT	296368	128564	GAAGGAGAAGCTGGAGAAGA
207195	39391	TTCTAAGAAAAATCTGCTAG	251782	83978	CTGGACTTGTGAATTAGAGC	296369	128565	GGAAGGAGAAGCTGGAGAAG
207196	39392	CTTCTAAGAAAAATCTGCTA	251783	83979	CCTGGACTTGTGAATTAGAG	296370	128566	TGGAAGGAGAAGCTGGAGAA
207197	39393	TCTTCTAAGAAAAATCTGCT	251784	83980	TCCTGGACTTGTGAATTAGA	296371	128567	GTGGAAGGAGAAGCTGGAGA
207198	39394	TTCTTCTAAGAAAAATCTGC	251785	83981	CTCCTGGACTTGTGAATTAG	296372	128568	TGTGGAAGGAGAAGCTGGAG
207199	39395	ATTCTTCTAAGAAAAATCTG	251786	83982	TCTCCTGGACTTGTGAATTA	296373	128569	ATGTGGAAGGAGAAGCTGGA
207200	39396	CATTCTTCTAAGAAAAATCT	251787	83983	ATCTCCTGGACTTGTGAATT	296374	128570	AATGTGGAAGGAGAAGCTGG
207201	39397	TCATTCTTCTAAGAAAAATC	251788	83984	AATCTCCTGGACTTGTGAAT	296375	128571	AAATGTGGAAGGAGAAGCTG
207202	39398	ATCATTCTTCTAAGAAAAAT	251789	83985	AAATCTCCTGGACTTGTGAA	296376	128572	AAAATGTGGAAGGAGAAGCT
207203	39399	TATCATTCTTCTAAGAAAAA	251790	83986	AAAATCTCCTGGACTTGTGA	296377	128573	GAAAATGTGGAAGGAGAAGC
207204	39400	ATATCATTCTTCTAAGAAAA	251791	83987	TAAAATCTCCTGGACTTGTG	296378	128574	GGAAAATGTGGAAGGAGAAG
207205	39401	GATATCATTCTTCTAAGAAA	251792	83988	CTAAAATCTCCTGGACTTGT	296379	128575	AGGAAAATGTGGAAGGAGAA
207206	39402	TGATATCATTCTTCTAAGAA	251793	83989	CCTAAAATCTCCTGGACTTG	296380	128576	AAGGAAAATGTGGAAGGAGA
207207	39403	ATGATATCATTCTTCTAAGA	251794	83990	CCCTAAAATCTCCTGGACTT	296381	128577	AAAGGAAAATGTGGAAGGAG
207208	39404	GATGATATCATTCTTCTAAG	251795	83991	TCCCTAAAATCTCCTGGACT	296382	128578	CAAAGGAAAATGTGGAAGGA
207209	39405	TGATGATATCATTCTTCTAA	251796	83992	CTCCCTAAAATCTCCTGGAC	296383	128579	GCAAAGGAAAATGTGGAAGG
207210	39406	ATGATGATATCATTCTTCTA	251797	83993	ACTCCCTAAAATCTCCTGGA	296384	128580	TGCAAAGGAAAATGTGGAAG
207211	39407	GATGATGATATCATTCTTCT	251798	83994	AACTCCCTAAAATCTCCTGG	296385	128581	TTGCAAAGGAAAATGTGGAA
207212	39408	AGATGATGATATCATTCTTC	251799	83995	CAACTCCCTAAAATCTCCTG	296386	128582	ATTGCAAAGGAAAATGTGGA
207213	39409	GAGATGATGATATCATTCTT	251800	83996	CCAACTCCCTAAAATCTCCT	296387	128583	GATTGCAAAGGAAAATGTGG
207214	39410	GGAGATGATGATATCATTCT	251801	83997	ACCAACTCCCTAAAATCTCC	296388	128584	AGATTGCAAAGGAAAATGTG
207215	39411	TGGAGATGATGATATCATTC	251802	83998	AACCAACTCCCTAAAATCTC	296389	128585	CAGATTGCAAAGGAAAATGT
207216	39412	CTGGAGATGATGATATCATT	251803	83999	GAACCAACTCCCTAAAATCT	296390	128586	CCAGATTGCAAAGGAAAATG
207217	39413	GCTGGAGATGATGATATCAT	251804	84000	AGAACCAACTCCCTAAAATC	296391	128587	GCCAGATTGCAAAGGAAAAT
207218	39414	AGCTGGAGATGATGATATCA	251805	84001	AAGAACCAACTCCCTAAAAT	296392	128588	TGCCAGATTGCAAAGGAAAA
207219	39415	TAGCTGGAGATGATGATATC	251806	84002	TAAGAACCAACTCCCTAAAA	296393	128589	TTGCCAGATTGCAAAGGAAA
207220	39416	GTAGCTGGAGATGATGATAT	251807	84003	ATAAGAACCAACTCCCTAAA	296394	128590	ATTGCCAGATTGCAAAGGAA
207221	39417	GGTAGCTGGAGATGATGATA	251808	84004	GATAAGAACCAACTCCCTAA	296395	128591	TATTGCCAGATTGCAAAGGA
207222	39418	AGGTAGCTGGAGATGATGAT	251809	84005	TGATAAGAACCAACTCCCTA	296396	128592	ATATTGCCAGATTGCAAAGG
207223	39419	CAGGTAGCTGGAGATGATGA	251810	84006	TTGATAAGAACCAACTCCCT	296397	128593	GATATTGCCAGATTGCAAAG
207224	39420	GCAGGTAGCTGGAGATGATG	251811	84007	TTTGATAAGAACCAACTCCC	296398	128594	AGATATTGCCAGATTGCAAA
207225	39421	TGCAGGTAGCTGGAGATGAT	251812	84008	CTTTGATAAGAACCAACTCC	296399	128595	TAGATATTGCCAGATTGCAA
207226	39422	TTGCAGGTAGCTGGAGATGA	251813	84009	CCTTTGATAAGAACCAACTC	296400	128596	ATAGATATTGCCAGATTGCA
207227	39423	ATTGCAGGTAGCTGGAGATG	251814	84010	ACCTTTGATAAGAACCAACT	296401	128597	AATAGATATTGCCAGATTGC
207228	39424	AATTGCAGGTAGCTGGAGAT	251815	84011	AACCTTTGATAAGAACCAAC	296402	128598	TAATAGATATTGCCAGATTG
207229	39425	CAATTGCAGGTAGCTGGAGA	251816	84012	CAACCTTTGATAAGAACCAA	296403	128599	TTAATAGATATTGCCAGATT
207230	39426	TCAATTGCAGGTAGCTGGAG	251817	84013	CCAACCTTTGATAAGAACCA	296404	128600	TTTAATAGATATTGCCAGAT
207231	39427	ATCAATTGCAGGTAGCTGGA	251818	84014	GCCAACCTTTGATAAGAACC	296405	128601	TTTTAATAGATATTGCCAGA
207232	39428	GATCAATTGCAGGTAGCTGG	251819	84015	AGCCAACCTTTGATAAGAAC	296406	128602	ATTTTAATAGATATTGCCAG
207233	39429	AGATCAATTGCAGGTAGCTG	251820	84016	TAGCCAACCTTTGATAAGAA	296407	128603	TATTTTAATAGATATTGCCA
207234	39430	TAGATCAATTGCAGGTAGCT	251821	84017	GTAGCCAACCTTTGATAAGA	296408	128604	TTATTTTAATAGATATTGCC
207235	39431	GTAGATCAATTGCAGGTAGC	251822	84018	AGTAGCCAACCTTTGATAAG	296409	128605	TTTATTTTAATAGATATTGC
207236	39432	AGTAGATCAATTGCAGGTAG	251823	84019	GAGTAGCCAACCTTTGATAA	296410	128606	TTTTATTTTAATAGATATTG
207237	39433	GAGTAGATCAATTGCAGGTA	251824	84020	TGAGTAGCCAACCTTTGATA	296411	128607	ATTTTATTTTAATAGATATT
207238	39434	AGAGTAGATCAATTGCAGGT	251825	84021	CTGAGTAGCCAACCTTTGAT	296412	128608	CATTTTATTTTAATAGATAT
207239	39435	CAGAGTAGATCAATTGCAGG	251826	84022	TCTGAGTAGCCAACCTTTGA	296413	128609	ACATTTTATTTTAATAGATA
207240	39436	TCAGAGTAGATCAATTGCAG	251827	84023	ATCTGAGTAGCCAACCTTTG	296414	128610	CACATTTTATTTTAATAGAT
207241	39437	TTCAGAGTAGATCAATTGCA	251828	84024	TATCTGAGTAGCCAACCTTT	296415	128611	GCACATTTTATTTTAATAGA
207242	39438	ATTCAGAGTAGATCAATTGC	251829	84025	ATATCTGAGTAGCCAACCTT	296416	128612	TGCACATTTTATTTTAATAG
207243	39439	AATTCAGAGTAGATCAATTG	251830	84026	TATATCTGAGTAGCCAACCT	296417	128613	ATGCACATTTTATTTTAATA
207244	39440	TAATTCAGAGTAGATCAATT	251831	84027	CTATATCTGAGTAGCCAACC	296418	128614	CATGCACATTTTATTTTAAT
207245	39441	TTAATTCAGAGTAGATCAAT	251832	84028	TCTATATCTGAGTAGCCAAC	296419	128615	GCATGCACATTTTATTTTAA
207246	39442	CTTAATTCAGAGTAGATCAA	251833	84029	TTCTATATCTGAGTAGCCAA	296420	128616	GGCATGCACATTTTATTTTA
207247	39443	TCTTAATTCAGAGTAGATCA	251834	84030	TTTCTATATCTGAGTAGCCA	296421	128617	AGGCATGCACATTTTATTTT
207248	39444	TTCTTAATTCAGAGTAGATC	251835	84031	CTTTCTATATCTGAGTAGCC	296422	128618	AAGGCATGCACATTTTATTT
207249	39445	TTTCTTAATTCAGAGTAGAT	251836	84032	TCTTTCTATATCTGAGTAGC	296423	128619	AAAGGCATGCACATTTTATT
207250	39446	CTTTCTTAATTCAGAGTAGA	251837	84033	CTCTTTCTATATCTGAGTAG	296424	128620	AAAAGGCATGCACATTTTAT
207251	39447	TCTTTCTTAATTCAGAGTAG	251838	84034	GCTCTTTCTATATCTGAGTA	296425	128621	CAAAAGGCATGCACATTTTA
207252	39448	CTCTTTCTTAATTCAGAGTA	251839	84035	GGCTCTTTCTATATCTGAGT	296426	128622	TCAAAAGGCATGCACATTTT
207253	39449	TCTCTTTCTTAATTCAGAGT	251840	84036	GGGCTCTTTCTATATCTGAG	296427	128623	GTCAAAAGGCATGCACATTT
207254	39450	GTCTCTTTCTTAATTCAGAG	251841	84037	AGGGCTCTTTCTATATCTGA	296428	128624	GGTCAAAAGGCATGCACATT
207255	39451	AGTCTCTTTCTTAATTCAGA	251842	84038	TAGGGCTCTTTCTATATCTG	296429	128625	AGGTCAAAAGGCATGCACAT
207256	39452	AAGTCTCTTTCTTAATTCAG	251843	84039	CTAGGGCTCTTTCTATATCT	296430	128626	TAGGTCAAAAGGCATGCACA
207257	39453	GAAGTCTCTTTCTTAATTCA	251844	84040	ACTAGGGCTCTTTCTATATC	296431	128627	TTAGGTCAAAAGGCATGCAC
207258	39454	GGAAGTCTCTTTCTTAATTC	251845	84041	CACTAGGGCTCTTTCTATAT	296432	128628	CTTAGGTCAAAAGGCATGCA

207259	39455	TGGAAGTCTCTTTCTTAATT	251846	84042	CCACTAGGGCTCTTTCTATA	296433	128629	TCTTAGGTCAAAAGGCATGC
207260	39456	ATGGAAGTCTCTTTCTTAAT	251847	84043	ACCACTAGGGCTCTTTCTAT	296434	128630	CTCTTAGGTCAAAAGGCATG
207261	39457	AATGGAAGTCTCTTTCTTAA	251848	84044	AACCACTAGGGCTCTTTCTA	296435	128631	GCTCTTAGGTCAAAAGGCAT
207262	39458	AAATGGAAGTCTCTTTCTTA	251849	84045	AAACCACTAGGGCTCTTTCT	296436	128632	AGCTCTTAGGTCAAAAGGCA
207263	39459	CAAATGGAAGTCTCTTTCTT	251850	84046	AAAACCACTAGGGCTCTTTC	296437	128633	AAGCTCTTAGGTCAAAAGGC
207264	39460	ACAAATGGAAGTCTCTTTCT	251851	84047	AAAAACCACTAGGGCTCTTT	296438	128634	GAAGCTCTTAGGTCAAAAGG
207265	39461	AACAAATGGAAGTCTCTTTC	251852	84048	AAAAAACCACTAGGGCTCTT	296439	128635	TGAAGCTCTTAGGTCAAAAG
207266	39462	CAACAAATGGAAGTCTCTTT	251853	84049	AAAAAAACCACTAGGGCTCT	296440	128636	GTGAAGCTCTTAGGTCAAAA
207267	39463	ACAACAAATGGAAGTCTCTT	251854	84050	GAAAAAAACCACTAGGGCTC	296441	128637	AGTGAAGCTCTTAGGTCAAA
207268	39464	AACAACAAATGGAAGTCTCT	251855	84051	AGAAAAAAACCACTAGGGCT	296442	128638	AAGTGAAGCTCTTAGGTCAA
207269	39465	AAACAACAAATGGAAGTCTC	251856	84052	TAGAAAAAAACCACTAGGGC	296443	128639	GAAGTGAAGCTCTTAGGTCA
207270	39466	TAAACAACAAATGGAAGTCT	251857	84053	TTAGAAAAAAACCACTAGGG	296444	128640	AGAAGTGAAGCTCTTAGGTC
207271	39467	ATAAACAACAAATGGAAGTC	251858	84054	ATTAGAAAAAAACCACTAGG	296445	128641	TAGAAGTGAAGCTCTTAGGT
207272	39468	TATAAACAACAAATGGAAGT	251859	84055	TATTAGAAAAAAACCACTAG	296446	128642	CTAGAAGTGAAGCTCTTAGG
207273	39469	ATATAAACAACAAATGGAAG	251860	84056	GTATTAGAAAAAAACCACTA	296447	128643	CCTAGAAGTGAAGCTCTTAG
207274	39470	AATATAAACAACAAATGGAA	251861	84057	GGTATTAGAAAAAAACCACT	296448	128644	TCCTAGAAGTGAAGCTCTTA
207275	39471	AAATATAAACAACAAATGGA	251862	84058	TGGTATTAGAAAAAAACCAC	296449	128645	GTCCTAGAAGTGAAGCTCTT
207276	39472	AAAATATAAACAACAAATGG	251863	84059	ATGGTATTAGAAAAAAACCA	296450	128646	GGTCCTAGAAGTGAAGCTCT
207277	39473	CAAAATATAAACAACAAATG	251864	84060	AATGGTATTAGAAAAAAACC	296451	128647	GGGTCCTAGAAGTGAAGCTC
207278	39474	GCAAAATATAAACAACAAAT	251865	84061	AAATGGTATTAGAAAAAAAC	296452	128648	TGGGTCCTAGAAGTGAAGCT
207279	39475	TGCAAAATATAAACAACAAA	251866	84062	GAAATGGTATTAGAAAAAAA	296453	128649	GTGGGTCCTAGAAGTGAAGC
207280	39476	GTGCAAAATATAAACAACAA	251867	84063	AGAAATGGTATTAGAAAAAA	296454	128650	AGTGGGTCCTAGAAGTGAAG
207281	39477	AGTGCAAAATATAAACAACA	251868	84064	CAGAAATGGTATTAGAAAAA	296455	128651	AAGTGGGTCCTAGAAGTGAA
207282	39478	GAGTGCAAAATATAAACAAC	251869	84065	CCAGAAATGGTATTAGAAAA	296456	128652	TAAGTGGGTCCTAGAAGTGA
207283	39479	AGAGTGCAAAATATAAACAA	251870	84066	CCCAGAAATGGTATTAGAAA	296457	128653	GTAAGTGGGTCCTAGAAGTG
207284	39480	AAGAGTGCAAAATATAAACA	251871	84067	ACCCAGAAATGGTATTAGAA	296458	128654	TGTAAGTGGGTCCTAGAAGT
207285	39481	CAAGAGTGCAAAATATAAAC	251872	84068	TACCCAGAAATGGTATTAGA	296459	128655	GTGTAAGTGGGTCCTAGAAG
207286	39482	TCAAGAGTGCAAAATATAAA	251873	84069	TTACCCAGAAATGGTATTAG	296460	128656	CGTGTAAGTGGGTCCTAGAA
207287	39483	ATCAAGAGTGCAAAATATAA	251874	84070	ATTACCCAGAAATGGTATTA	296461	128657	ACGTGTAAGTGGGTCCTAGA
207288	39484	CATCAAGAGTGCAAAATATA	251875	84071	AATTACCCAGAAATGGTATT	296462	128658	CACGTGTAAGTGGGTCCTAG
207289	39485	ACATCAAGAGTGCAAAATAT	251876	84072	GAATTACCCAGAAATGGTAT	296463	128659	ACACGTGTAAGTGGGTCCTA
207290	39486	CACATCAAGAGTGCAAAATA	251877	84073	GGAATTACCCAGAAATGGTA	296464	128660	CACACGTGTAAGTGGGTCCT
207291	39487	ACACATCAAGAGTGCAAAAT	251878	84074	AGGAATTACCCAGAAATGGT	296465	128661	ACACACGTGTAAGTGGGTCC
207292	39488	AACACATCAAGAGTGCAAAA	251879	84075	TAGGAATTACCCAGAAATGG	296466	128662	CACACACGTGTAAGTGGGTC
207293	39489	AAACACATCAAGAGTGCAAA	251880	84076	TTAGGAATTACCCAGAAATG	296467	128663	TCACACACGTGTAAGTGGGT
207294	39490	GAAACACATCAAGAGTGCAA	251881	84077	CTTAGGAATTACCCAGAAAT	296468	128664	GTCACACACGTGTAAGTGGG
207295	39491	AGAAACACATCAAGAGTGCA	251882	84078	CCTTAGGAATTACCCAGAAA	296469	128665	TGTCACACACGTGTAAGTGG
207296	39492	AAGAAACACATCAAGAGTGC	251883	84079	GCCTTAGGAATTACCCAGAA	296470	128666	ATGTCACACACGTGTAAGTG
207297	39493	AAAGAAACACATCAAGAGTG	251884	84080	TGCCTTAGGAATTACCCAGA	296471	128667	CATGTCACACACGTGTAAGT
207298	39494	TAAAGAAACACATCAAGAGT	251885	84081	ATGCCTTAGGAATTACCCAG	296472	128668	TCATGTCACACACGTGTAAG
207299	39495	TTAAAGAAACACATCAAGAG	251886	84082	AATGCCTTAGGAATTACCCA	296473	128669	ATCATGTCACACACGTGTAA
207300	39496	TTTAAAGAAACACATCAAGA	251887	84083	AAATGCCTTAGGAATTACCC	296474	128670	CATCATGTCACACACGTGTA
207301	39497	ATTTAAAGAAACACATCAAG	251888	84084	TAAATGCCTTAGGAATTACC	296475	128671	ACATCATGTCACACACGTGT
207302	39498	AATTTAAAGAAACACATCAA	251889	84085	CTAAATGCCTTAGGAATTAC	296476	128672	AACATCATGTCACACACGTG
207303	39499	TAATTTAAAGAAACACATCA	251890	84086	ACTAAATGCCTTAGGAATTA	296477	128673	GAACATCATGTCACACACGT
207304	39500	ATAATTTAAAGAAACACATC	251891	84087	CACTAAATGCCTTAGGAATT	296478	128674	TGAACATCATGTCACACACG
207305	39501	CATAATTTAAAGAAACACAT	251892	84088	ACACTAAATGCCTTAGGAAT	296479	128675	ATGAACATCATGTCACACAC
207306	39502	CCATAATTTAAAGAAACACA	251893	84089	AACACTAAATGCCTTAGGAA	296480	128676	TATGAACATCATGTCACACA
207307	39503	ACCATAATTTAAAGAAACAC	251894	84090	GAACACTAAATGCCTTAGGA	296481	128677	GTATGAACATCATGTCACAC
207308	39504	GACCATAATTTAAAGAAACA	251895	84091	AGAACACTAAATGCCTTAGG	296482	128678	CGTATGAACATCATGTCACA
207309	39505	TGACCATAATTTAAAGAAAC	251896	84092	CAGAACACTAAATGCCTTAG	296483	128679	CCGTATGAACATCATGTCAC
207310	39506	ATGACCATAATTTAAAGAAA	251897	84093	TCAGAACACTAAATGCCTTA	296484	128680	CCCGTATGAACATCATGTCA
207311	39507	CATGACCATAATTTAAAGAA	251898	84094	TTCAGAACACTAAATGCCTT	296485	128681	ACCCGTATGAACATCATGTC
207312	39508	CCATGACCATAATTTAAAGA	251899	84095	TTTCAGAACACTAAATGCCT	296486	128682	AACCCGTATGAACATCATGT
207313	39509	CCCATGACCATAATTTAAAG	251900	84096	CTTTCAGAACACTAAATGCC	296487	128683	AAACCCGTATGAACATCATG
207314	39510	GCCCATGACCATAATTTAAA	251901	84097	TCTTTCAGAACACTAAATGC	296488	128684	TAAACCCGTATGAACATCAT
207315	39511	GGCCCATGACCATAATTTAA	251902	84098	ATCTTTCAGAACACTAAATG	296489	128685	ATAAACCCGTATGAACATCA
207316	39512	TGGCCCATGACCATAATTTA	251903	84099	CATCTTTCAGAACACTAAAT	296490	128686	AATAAACCCGTATGAACATC
207317	39513	CTGGCCCATGACCATAATTT	251904	84100	GCATCTTTCAGAACACTAAA	296491	128687	AAATAAACCCGTATGAACAT
207318	39514	CCTGGCCCATGACCATAATT	251905	84101	AGCATCTTTCAGAACACTAA	296492	128688	TAAATAAACCCGTATGAACA
207319	39515	ACCTGGCCCATGACCATAAT	251906	84102	TAGCATCTTTCAGAACACTA	296493	128689	ATAAATAAACCCGTATGAAC
207320	39516	CACCTGGCCCATGACCATAA	251907	84103	CTAGCATCTTTCAGAACACT	296494	128690	GATAAATAAACCCGTATGAA
207321	39517	ACACCTGGCCCATGACCATA	251908	84104	GCTAGCATCTTTCAGAACAC	296495	128691	AGATAAATAAACCCGTATGA
207322	39518	TACACCTGGCCCATGACCAT	251909	84105	GGCTAGCATCTTTCAGAACA	296496	128692	CAGATAAATAAACCCGTATG
207323	39519	CTACACCTGGCCCATGACCA	251910	84106	AGGCTAGCATCTTTCAGAAC	296497	128693	TCAGATAAATAAACCCGTAT
207324	39520	CCTACACCTGGCCCATGACC	251911	84107	AAGGCTAGCATCTTTCAGAA	296498	128694	CTCAGATAAATAAACCCGTA
207325	39521	TCCTACACCTGGCCCATGAC	251912	84108	CAAGGCTAGCATCTTTCAGA	296499	128695	CCTCAGATAAATAAACCCGT
207326	39522	CTCCTACACCTGGCCCATGA	251913	84109	ACAAGGCTAGCATCTTTCAG	296500	128696	ACCTCAGATAAATAAACCCG
207327	39523	GCTCCTACACCTGGCCCATG	251914	84110	GACAAGGCTAGCATCTTTCA	296501	128697	AACCTCAGATAAATAAACCC
207328	39524	AGCTCCTACACCTGGCCCAT	251915	84111	GGACAAGGCTAGCATCTTTC	296502	128698	CAACCTCAGATAAATAAACC
207329	39525	GAGCTCCTACACCTGGCCCA	251916	84112	TGGACAAGGCTAGCATCTTT	296503	128699	ACAACCTCAGATAAATAAAC
207330	39526	TGAGCTCCTACACCTGGCCC	251917	84113	CTGGACAAGGCTAGCATCTT	296504	128700	AACAACCTCAGATAAATAAA

207331	39527	GTGAGCTCCTACACCTGGCC	251918	84114	GCTGGACAAGGCTAGCATCT	296505	128701	GAACAACCTCAGATAAATAA
207332	39528	TGTGAGCTCCTACACCTGGC	251919	84115	GGCTGGACAAGGCTAGCATC	296506	128702	TGAACAACCTCAGATAAATA
207333	39529	GTGTGAGCTCCTACACCTGG	251920	84116	AGGCTGGACAAGGCTAGCAT	296507	128703	ATGAACAACCTCAGATAAAT
207334	39530	GGTGTGAGCTCCTACACCTG	251921	84117	CAGGCTGGACAAGGCTAGCA	296508	128704	TATGAACAACCTCAGATAAA
207335	39531	AGGTGTGAGCTCCTACACCT	251922	84118	CCAGGCTGGACAAGGCTAGC	296509	128705	GTATGAACAACCTCAGATAA
207336	39532	CAGGTGTGAGCTCCTACACC	251923	84119	CCCAGGCTGGACAAGGCTAG	296510	128706	TGTATGAACAACCTCAGATA
207337	39533	ACAGGTGTGAGCTCCTACAC	251924	84120	TCCCAGGCTGGACAAGGCTA	296511	128707	GTGTATGAACAACCTCAGAT
207338	39534	TACAGGTGTGAGCTCCTACA	251925	84121	CTCCCAGGCTGGACAAGGCT	296512	128708	TGTGTATGAACAACCTCAGA
207339	39535	TTACAGGTGTGAGCTCCTAC	251926	84122	ACTCCCAGGCTGGACAAGGC	296513	128709	GTGTGTATGAACAACCTCAG
207340	39536	ATTACAGGTGTGAGCTCCTA	251927	84123	AACTCCCAGGCTGGACAAGG	296514	128710	GGTGTGTATGAACAACCTCA
207341	39537	GATTACAGGTGTGAGCTCCT	251928	84124	CAACTCCCAGGCTGGACAAG	296515	128711	TGGTGTGTATGAACAACCTC
207342	39538	GGATTACAGGTGTGAGCTCC	251929	84125	TCAACTCCCAGGCTGGACAA	296516	128712	ATGGTGTGTATGAACAACCT
207343	39539	GGGATTACAGGTGTGAGCTC	251930	84126	CTCAACTCCCAGGCTGGACA	296517	128713	AATGGTGTGTATGAACAACC
207344	39540	TGGGATTACAGGTGTGAGCT	251931	84127	TCTCAACTCCCAGGCTGGAC	296518	128714	CAATGGTGTGTATGAACAAC
207345	39541	CTGGGATTACAGGTGTGAGC	251932	84128	TTCTCAACTCCCAGGCTGGA	296519	128715	GCAATGGTGTGTATGAACAA
207346	39542	GCTGGGATTACAGGTGTGAG	251933	84129	ATTCTCAACTCCCAGGCTGG	296520	128716	GGCAATGGTGTGTATGAACA
207347	39543	TGCTGGGATTACAGGTGTGA	251934	84130	CATTCTCAACTCCCAGGCTG	296521	128717	AGGCAATGGTGTGTATGAAC
207348	39544	GTGCTGGGATTACAGGTGTG	251935	84131	TCATTCTCAACTCCCAGGCT	296522	128718	CAGGCAATGGTGTGTATGAA
207349	39545	GGTGCTGGGATTACAGGTGT	251936	84132	TTCATTCTCAACTCCCAGGC	296523	128719	ACAGGCAATGGTGTGTATGA
207350	39546	AGGTGCTGGGATTACAGGTG	251937	84133	ATTCATTCTCAACTCCCAGG	296524	128720	TACAGGCAATGGTGTGTATG
207351	39547	AAGGTGCTGGGATTACAGGT	251938	84134	CATTCATTCTCAACTCCCAG	296525	128721	TTACAGGCAATGGTGTGTAT
207352	39548	CAAGGTGCTGGGATTACAGG	251939	84135	ACATTCATTCTCAACTCCCA	296526	128722	ATTACAGGCAATGGTGTGTA
207353	39549	CCAAGGTGCTGGGATTACAG	251940	84136	GACATTCATTCTCAACTCCC	296527	128723	GATTACAGGCAATGGTGTGT
207354	39550	CCCAAGGTGCTGGGATTACA	251941	84137	AGACATTCATTCTCAACTCC	296528	128724	TGATTACAGGCAATGGTGTG
207355	39551	TCCCAAGGTGCTGGGATTAC	251942	84138	TAGACATTCATTCTCAACTC	296529	128725	GTGATTACAGGCAATGGTGT
207356	39552	GTCCCAAGGTGCTGGGATTA	251943	84139	TTAGACATTCATTCTCAACT	296530	128726	AGTGATTACAGGCAATGGTG
207357	39553	AGTCCCAAGGTGCTGGGATT	251944	84140	GTTAGACATTCATTCTCAAC	296531	128727	TAGTGATTACAGGCAATGGT
207358	39554	GAGTCCCAAGGTGCTGGGAT	251945	84141	TGTTAGACATTCATTCTCAA	296532	128728	TTAGTGATTACAGGCAATGG
207359	39555	AGAGTCCCAAGGTGCTGGGA	251946	84142	CTGTTAGACATTCATTCTCA	296533	128729	TTTAGTGATTACAGGCAATG
207360	39556	CAGAGTCCCAAGGTGCTGGG	251947	84143	TCTGTTAGACATTCATTCTC	296534	128730	CTTTAGTGATTACAGGCAAT
207361	39557	TCAGAGTCCCAAGGTGCTGG	251948	84144	TTCTGTTAGACATTCATTCT	296535	128731	CCTTTAGTGATTACAGGCAA
207362	39558	CTCAGAGTCCCAAGGTGCTG	251949	84145	TTTCTGTTAGACATTCATTC	296536	128732	GCCTTTAGTGATTACAGGCA
207363	39559	CCTCAGAGTCCCAAGGTGCT	251950	84146	GTTTCTGTTAGACATTCATT	296537	128733	CGCCTTTAGTGATTACAGGC
207364	39560	TCCTCAGAGTCCCAAGGTGC	251951	84147	AGTTTCTGTTAGACATTCAT	296538	128734	CCGCCTTTAGTGATTACAGG
207365	39561	CTCCTCAGAGTCCCAAGGTG	251952	84148	GAGTTTCTGTTAGACATTCA	296539	128735	CCCGCCTTTAGTGATTACAG
207366	39562	CCTCCTCAGAGTCCCAAGGT	251953	84149	AGAGTTTCTGTTAGACATTC	296540	128736	TCCCGCCTTTAGTGATTACA
207367	39563	CCCTCCTCAGAGTCCCAAGG	251954	84150	TAGAGTTTCTGTTAGACATT	296541	128737	CTCCCGCCTTTAGTGATTAC
207368	39564	TCCCTCCTCAGAGTCCCAAG	251955	84151	CTAGAGTTTCTGTTAGACAT	296542	128738	GCTCCCGCCTTTAGTGATTA
207369	39565	CTCCCTCCTCAGAGTCCCAA	251956	84152	CCTAGAGTTTCTGTTAGACA	296543	128739	TGCTCCCGCCTTTAGTGATT
207370	39566	CCTCCCTCCTCAGAGTCCCA	251957	84153	GCCTAGAGTTTCTGTTAGAC	296544	128740	CTGCTCCCGCCTTTAGTGAT
207371	39567	TCCTCCCTCCTCAGAGTCCC	251958	84154	GGCCTAGAGTTTCTGTTAGA	296545	128741	GCTGCTCCCGCCTTTAGTGA
207372	39568	ATCCTCCCTCCTCAGAGTCC	251959	84155	CGGCCTAGAGTTTCTGTTAG	296546	128742	GGCTGCTCCCGCCTTTAGTG
207373	39569	GATCCTCCCTCCTCAGAGTC	251960	84156	CCGGCCTAGAGTTTCTGTTA	296547	128743	AGGCTGCTCCCGCCTTTAGT
207374	39570	TGATCCTCCCTCCTCAGAGT	251961	84157	CCCGGCCTAGAGTTTCTGTT	296548	128744	TAGGCTGCTCCCGCCTTTAG
207375	39571	GTGATCCTCCCTCCTCAGAG	251962	84158	GCCCGGCCTAGAGTTTCTGT	296549	128745	GTAGGCTGCTCCCGCCTTTA
207376	39572	AGTGATCCTCCCTCCTCAGA	251963	84159	GGCCCGGCCTAGAGTTTCTG	296550	128746	TGTAGGCTGCTCCCGCCTTT
207377	39573	CAGTGATCCTCCCTCCTCAG	251964	84160	AGGCCCGGCCTAGAGTTTCT	296551	128747	GTGTAGGCTGCTCCCGCCTT
207378	39574	CCAGTGATCCTCCCTCCTCA	251965	84161	CAGGCCCGGCCTAGAGTTTC	296552	128748	TGTGTAGGCTGCTCCCGCCT
207379	39575	TCCAGTGATCCTCCCTCCTC	251966	84162	CCAGGCCCGGCCTAGAGTTT	296553	128749	ATGTGTAGGCTGCTCCCGCC
207380	39576	CTCCAGTGATCCTCCCTCCT	251967	84163	ACCAGGCCCGGCCTAGAGTT	296554	128750	GATGTGTAGGCTGCTCCCGC
207381	39577	CCTCCAGTGATCCTCCCTCC	251968	84164	CACCAGGCCCGGCCTAGAGT	296555	128751	GGATGTGTAGGCTGCTCCCG
207382	39578	GCCTCCAGTGATCCTCCCTC	251969	84165	CCACCAGGCCCGGCCTAGAG	296556	128752	TGGATGTGTAGGCTGCTCCC
207383	39579	GGCCTCCAGTGATCCTCCCT	251970	84166	GCCACCAGGCCCGGCCTAGA	296557	128753	ATGGATGTGTAGGCTGCTCC
207384	39580	TGGCCTCCAGTGATCCTCCC	251971	84167	AGCCACCAGGCCCGGCCTAG	296558	128754	GATGGATGTGTAGGCTGCTC
207385	39581	CTGGCCTCCAGTGATCCTCC	251972	84168	GAGCCACCAGGCCCGGCCTA	296559	128755	GGATGGATGTGTAGGCTGCT
207386	39582	CCTGGCCTCCAGTGATCCTC	251973	84169	TGAGCCACCAGGCCCGGCCT	296560	128756	TGGATGGATGTGTAGGCTGC
207387	39583	TCCTGGCCTCCAGTGATCCT	251974	84170	GTGAGCCACCAGGCCCGGCC	296561	128757	GTGGATGGATGTGTAGGCTG
207388	39584	CTCCTGGCCTCCAGTGATCC	251975	84171	CGTGAGCCACCAGGCCCGGC	296562	128758	TGTGGATGGATGTGTAGGCT
207389	39585	ACTCCTGGCCTCCAGTGATC	251976	84172	GCGTGAGCCACCAGGCCCGG	296563	128759	CTGTGGATGGATGTGTAGGC
207390	39586	AACTCCTGGCCTCCAGTGAT	251977	84173	GGCGTGAGCCACCAGGCCCG	296564	128760	TCTGTGGATGGATGTGTAGG
207391	39587	GAACTCCTGGCCTCCAGTGA	251978	84174	AGGCGTGAGCCACCAGGCCC	296565	128761	CTCTGTGGATGGATGTGTAG
207392	39588	TGAACTCCTGGCCTCCAGTG	251979	84175	GAGGCGTGAGCCACCAGGCC	296566	128762	CCTCTGTGGATGGATGTGTA
207393	39589	TTGAACTCCTGGCCTCCAGT	251980	84176	AGAGGCGTGAGCCACCAGGC	296567	128763	TCCTCTGTGGATGGATGTGT
207394	39590	CTTGAACTCCTGGCCTCCAG	251981	84177	TAGAGGCGTGAGCCACCAGG	296568	128764	CTCCTCTGTGGATGGATGTG
207395	39591	TCTTGAACTCCTGGCCTCCA	251982	84178	TTAGAGGCGTGAGCCACCAG	296569	128765	ACTCCTCTGTGGATGGATGT
207396	39592	GTCTTGAACTCCTGGCCTCC	251983	84179	ATTAGAGGCGTGAGCCACCA	296570	128766	TACTCCTCTGTGGATGGATG
207397	39593	GGTCTTGAACTCCTGGCCTC	251984	84180	GATTAGAGGCGTGAGCCACC	296571	128767	CTACTCCTCTGTGGATGGAT
207398	39594	AGGTCTTGAACTCCTGGCCT	251985	84181	GGATTAGAGGCGTGAGCCAC	296572	128768	TCTACTCCTCTGTGGATGGA
207399	39595	GAGGTCTTGAACTCCTGGCC	251986	84182	GGGATTAGAGGCGTGAGCCA	296573	128769	ATCTACTCCTCTGTGGATGG
207400	39596	CGAGGTCTTGAACTCCTGGC	251987	84183	TGGGATTAGAGGCGTGAGCC	296574	128770	CATCTACTCCTCTGTGGATG
207401	39597	ACGAGGTCTTGAACTCCTGG	251988	84184	CTGGGATTAGAGGCGTGAGC	296575	128771	GCATCTACTCCTCTGTGGAT
207402	39598	GACGAGGTCTTGAACTCCTG	251989	84185	GCTGGGATTAGAGGCGTGAG	296576	128772	GGCATCTACTCCTCTGTGGA

207403	39599	AGACGAGGTCTTGAACTCCT	251990	84186	TGCTGGGATTAGAGGCGTGA	296577	128773	AGGCATCTACTCCTCTGTGG
207404	39600	CAGACGAGGTCTTGAACTCC	251991	84187	GTGCTGGGATTAGAGGCGTG	296578	128774	AAGGCATCTACTCCTCTGTG
207405	39601	ACAGACGAGGTCTTGAACTC	251992	84188	AGTGCTGGGATTAGAGGCGT	296579	128775	AAAGGCATCTACTCCTCTGT
207406	39602	TACAGACGAGGTCTTGAACT	251993	84189	TAGTGCTGGGATTAGAGGCG	296580	128776	AAAAGGCATCTACTCCTCTG
207407	39603	GTACAGACGAGGTCTTGAAC	251994	84190	ATAGTGCTGGGATTAGAGGC	296581	128777	CAAAAGGCATCTACTCCTCT
207408	39604	TGTACAGACGAGGTCTTGAA	251995	84191	CATAGTGCTGGGATTAGAGG	296582	128778	CCAAAAGGCATCTACTCCTC
207409	39605	CTGTACAGACGAGGTCTTGA	251996	84192	CCATAGTGCTGGGATTAGAG	296583	128779	ACCAAAAGGCATCTACTCCT
207410	39606	ACTGTACAGACGAGGTCTTG	251997	84193	CCCATAGTGCTGGGATTAGA	296584	128780	TACCAAAAGGCATCTACTCC
207411	39607	TACTGTACAGACGAGGTCTT	251998	84194	TCCCATAGTGCTGGGATTAG	296585	128781	GTACCAAAAGGCATCTACTC
207412	39608	TTACTGTACAGACGAGGTCT	251999	84195	CTCCCATAGTGCTGGGATTA	296586	128782	TGTACCAAAAGGCATCTACT
207413	39609	TTTACTGTACAGACGAGGTC	252000	84196	TCTCCCATAGTGCTGGGATT	296587	128783	ATGTACCAAAAGGCATCTAC
207414	39610	ATTTACTGTACAGACGAGGT	252001	84197	GTCTCCCATAGTGCTGGGAT	296588	128784	GATGTACCAAAAGGCATCTA
207415	39611	AATTTACTGTACAGACGAGG	252002	84198	GGTCTCCCATAGTGCTGGGA	296589	128785	GGATGTACCAAAAGGCATCT
207416	39612	AAATTTACTGTACAGACGAG	252003	84199	GGGTCTCCCATAGTGCTGGG	296590	128786	CGGATGTACCAAAAGGCATC
207417	39613	AAAATTTACTGTACAGACGA	252004	84200	TGGGTCTCCCATAGTGCTGG	296591	128787	ACGGATGTACCAAAAGGCAT
207418	39614	TAAAATTTACTGTACAGACG	252005	84201	CTGGGTCTCCCATAGTGCTG	296592	128788	CACGGATGTACCAAAAGGCA
207419	39615	TTAAAATTTACTGTACAGAC	252006	84202	CCTGGGTCTCCCATAGTGCT	296593	128789	CCACGGATGTACCAAAAGGC
207420	39616	TTTAAAATTTACTGTACAGA	252007	84203	ACCTGGGTCTCCCATAGTGC	296594	128790	GCCACGGATGTACCAAAAGG
207421	39617	TTTTAAAATTTACTGTACAG	252008	84204	CACCTGGGTCTCCCATAGTG	296595	128791	CGCCACGGATGTACCAAAAG
207422	39618	TTTTTAAAATTTACTGTACA	252009	84205	CCACCTGGGTCTCCCATAGT	296596	128792	TCGCCACGGATGTACCAAAA
207423	39619	ATTTTTAAAATTTACTGTAC	252010	84206	CCCACCTGGGTCTCCCATAG	296597	128793	GTCGCCACGGATGTACCAAA
207424	39620	AATTTTTAAAATTTACTGTA	252011	84207	GCCCACCTGGGTCTCCCATA	296598	128794	CGTCGCCACGGATGTACCAA
207425	39621	TAATTTTTAAAATTTACTGT	252012	84208	TGCCCACCTGGGTCTCCCAT	296599	128795	CCGTCGCCACGGATGTACCA
207426	39622	CTAATTTTTAAAATTTACTG	252013	84209	CTGCCCACCTGGGTCTCCCA	296600	128796	TCCGTCGCCACGGATGTACC
207427	39623	GCTAATTTTTAAAATTTACT	252014	84210	TCTGCCCACCTGGGTCTCCC	296601	128797	TTCCGTCGCCACGGATGTAC
207428	39624	GGCTAATTTTTAAAATTTAC	252015	84211	ATCTGCCCACCTGGGTCTCC	296602	128798	ATTCCGTCGCCACGGATGTA
207429	39625	TGGCTAATTTTTAAAATTTA	252016	84212	GATCTGCCCACCTGGGTCTC	296603	128799	TATTCCGTCGCCACGGATGT
207430	39626	CTGGCTAATTTTTAAAATTT	252017	84213	TGATCTGCCCACCTGGGTCT	296604	128800	GTATTCCGTCGCCACGGATG
207431	39627	CCTGGCTAATTTTTAAAATT	252018	84214	GTGATCTGCCCACCTGGGTC	296605	128801	AGTATTCCGTCGCCACGGAT
207432	39628	GCCTGGCTAATTTTTAAAAT	252019	84215	GGTGATCTGCCCACCTGGGT	296606	128802	TAGTATTCCGTCGCCACGGA
207433	39629	TGCCTGGCTAATTTTTAAAA	252020	84216	AGGTGATCTGCCCACCTGGG	296607	128803	TTAGTATTCCGTCGCCACGG
207434	39630	ATGCCTGGCTAATTTTTAAA	252021	84217	CAGGTGATCTGCCCACCTGG	296608	128804	CTTAGTATTCCGTCGCCACG
207435	39631	CATGCCTGGCTAATTTTTAA	252022	84218	TCAGGTGATCTGCCCACCTG	296609	128805	GCTTAGTATTCCGTCGCCAC
207436	39632	CCATGCCTGGCTAATTTTTA	252023	84219	CTCAGGTGATCTGCCCACCT	296610	128806	TGCTTAGTATTCCGTCGCCA
207437	39633	ACCATGCCTGGCTAATTTTT	252024	84220	CCTCAGGTGATCTGCCCACC	296611	128807	CTGCTTAGTATTCCGTCGCC
207438	39634	TACCATGCCTGGCTAATTTT	252025	84221	ACCTCAGGTGATCTGCCCAC	296612	128808	GCTGCTTAGTATTCCGTCGC
207439	39635	CTACCATGCCTGGCTAATTT	252026	84222	GACCTCAGGTGATCTGCCCA	296613	128809	GGCTGCTTAGTATTCCGTCG
207440	39636	GCTACCATGCCTGGCTAATT	252027	84223	TGACCTCAGGTGATCTGCCC	296614	128810	AGGCTGCTTAGTATTCCGTC
207441	39637	TGCTACCATGCCTGGCTAAT	252028	84224	CTGACCTCAGGTGATCTGCC	296615	128811	CAGGCTGCTTAGTATTCCGT
207442	39638	ATGCTACCATGCCTGGCTAA	252029	84225	CCTGACCTCAGGTGATCTGC	296616	128812	ACAGGCTGCTTAGTATTCCG
207443	39639	AATGCTACCATGCCTGGCTA	252030	84226	TCCTGACCTCAGGTGATCTG	296617	128813	CACAGGCTGCTTAGTATTCC
207444	39640	GAATGCTACCATGCCTGGCT	252031	84227	CTCCTGACCTCAGGTGATCT	296618	128814	ACACAGGCTGCTTAGTATTC
207445	39641	TGAATGCTACCATGCCTGGC	252032	84228	ACTCCTGACCTCAGGTGATC	296619	128815	TACACAGGCTGCTTAGTATT
207446	39642	GTGAATGCTACCATGCCTGG	252033	84229	AACTCCTGACCTCAGGTGAT	296620	128816	ATACACAGGCTGCTTAGTAT
207447	39643	GGTGAATGCTACCATGCCTG	252034	84230	AAACTCCTGACCTCAGGTGA	296621	128817	GATACACAGGCTGCTTAGTA
207448	39644	AGGTGAATGCTACCATGCCT	252035	84231	CAAACTCCTGACCTCAGGTG	296622	128818	AGATACACAGGCTGCTTAGT
207449	39645	CAGGTGAATGCTACCATGCC	252036	84232	TCAAACTCCTGACCTCAGGT	296623	128819	TAGATACACAGGCTGCTTAG
207450	39646	ACAGGTGAATGCTACCATGC	252037	84233	CTCAAACTCCTGACCTCAGG	296624	128820	ATAGATACACAGGCTGCTTA
207451	39647	TACAGGTGAATGCTACCATG	252038	84234	TCTCAAACTCCTGACCTCAG	296625	128821	TATAGATACACAGGCTGCTT
207452	39648	CTACAGGTGAATGCTACCAT	252039	84235	GTCTCAAACTCCTGACCTCA	296626	128822	GTATAGATACACAGGCTGCT
207453	39649	ACTACAGGTGAATGCTACCA	252040	84236	GGTCTCAAACTCCTGACCTC	296627	128823	TGTATAGATACACAGGCTGC
207454	39650	GACTACAGGTGAATGCTACC	252041	84237	TGGTCTCAAACTCCTGACCT	296628	128824	GTGTATAGATACACAGGCTG
207455	39651	AGACTACAGGTGAATGCTAC	252042	84238	CTGGTCTCAAACTCCTGACC	296629	128825	AGTGTATAGATACACAGGCT
207456	39652	AAGACTACAGGTGAATGCTA	252043	84239	GCTGGTCTCAAACTCCTGAC	296630	128826	GAGTGTATAGATACACAGGC
207457	39653	TAAGACTACAGGTGAATGCT	252044	84240	GGCTGGTCTCAAACTCCTGA	296631	128827	TGAGTGTATAGATACACAGG
207458	39654	CTAAGACTACAGGTGAATGC	252045	84241	AGGCTGGTCTCAAACTCCTG	296632	128828	GTGAGTGTATAGATACACAG
207459	39655	GCTAAGACTACAGGTGAATG	252046	84242	CAGGCTGGTCTCAAACTCCT	296633	128829	TGTGAGTGTATAGATACACA
207460	39656	AGCTAAGACTACAGGTGAAT	252047	84243	CCAGGCTGGTCTCAAACTCC	296634	128830	GTGTGAGTGTATAGATACAC
207461	39657	TAGCTAAGACTACAGGTGAA	252048	84244	GCCAGGCTGGTCTCAAACTC	296635	128831	CGTGTGAGTGTATAGATACA
207462	39658	GTAGCTAAGACTACAGGTGA	252049	84245	GGCCAGGCTGGTCTCAAACT	296636	128832	ACGTGTGAGTGTATAGATAC
207463	39659	AGTAGCTAAGACTACAGGTG	252050	84246	TGGCCAGGCTGGTCTCAAAC	296637	128833	CACGTGTGAGTGTATAGATA
207464	39660	AAGTAGCTAAGACTACAGGT	252051	84247	TTGGCCAGGCTGGTCTCAAA	296638	128834	ACACGTGTGAGTGTATAGAT
207465	39661	CAAGTAGCTAAGACTACAGG	252052	84248	GTTGGCCAGGCTGGTCTCAA	296639	128835	AACACGTGTGAGTGTATAGA
207466	39662	CCAAGTAGCTAAGACTACAG	252053	84249	TGTTGGCCAGGCTGGTCTCA	296640	128836	AAACACGTGTGAGTGTATAG
207467	39663	CCCAAGTAGCTAAGACTACA	252054	84250	ATGTTGGCCAGGCTGGTCTC	296641	128837	CAAACACGTGTGAGTGTATA
207468	39664	TCCCAAGTAGCTAAGACTAC	252055	84251	CATGTTGGCCAGGCTGGTCT	296642	128838	ACAAACACGTGTGAGTGTAT
207469	39665	CTCCCAAGTAGCTAAGACTA	252056	84252	ACATGTTGGCCAGGCTGGTC	296643	128839	AACAAACACGTGTGAGTGTA
207470	39666	CCTCCCAAGTAGCTAAGACT	252057	84253	CACATGTTGGCCAGGCTGGT	296644	128840	AAACAAACACGTGTGAGTGT
207471	39667	GCCTCCCAAGTAGCTAAGAC	252058	84254	TCACATGTTGGCCAGGCTGG	296645	128841	TAAACAAACACGTGTGAGTG
207472	39668	AGCCTCCCAAGTAGCTAAGA	252059	84255	TTCACATGTTGGCCAGGCTG	296646	128842	ATAAACAAACACGTGTGAGT
207473	39669	CAGCCTCCCAAGTAGCTAAG	252060	84256	TTTCACATGTTGGCCAGGCT	296647	128843	CATAAACAAACACGTGTGAG
207474	39670	TCAGCCTCCCAAGTAGCTAA	252061	84257	ATTTCACATGTTGGCCAGGC	296648	128844	ACATAAACAAACACGTGTGA

207475	39671	CTCAGCCTCCCAAGTAGCTA	252062	84258	GATTTCACATGTTGGCCAGG	296649	128845	CACATAAACAAACACGTGTG
207476	39672	TCTCAGCCTCCCAAGTAGCT	252063	84259	GGATTTCACATGTTGGCCAG	296650	128846	ACACATAAACAAACACGTGT
207477	39673	ATCTCAGCCTCCCAAGTAGC	252064	84260	AGGATTTCACATGTTGGCCA	296651	128847	CACACATAAACAAACACGTG
207478	39674	CATCTCAGCCTCCCAAGTAG	252065	84261	CAGGATTTCACATGTTGGCC	296652	128848	CCACACATAAACAAACACGT
207479	39675	CCATCTCAGCCTCCCAAGTA	252066	84262	ACAGGATTTCACATGTTGGC	296653	128849	TCCACACATAAACAAACACG
207480	39676	CCCATCTCAGCCTCCCAAGT	252067	84263	GACAGGATTTCACATGTTGG	296654	128850	TTCCACACATAAACAAACAC
207481	39677	TCCCATCTCAGCCTCCCAAG	252068	84264	AGACAGGATTTCACATGTTG	296655	128851	ATTCCACACATAAACAAACA
207482	39678	CTCCCATCTCAGCCTCCCAA	252069	84265	GAGACAGGATTTCACATGTT	296656	128852	TATTCCACACATAAACAAAC
207483	39679	CCTCCCATCTCAGCCTCCCA	252070	84266	TGAGACAGGATTTCACATGT	296657	128853	ATATTCCACACATAAACAAA
207484	39680	TCCTCCCATCTCAGCCTCCC	252071	84267	GTGAGACAGGATTTCACATG	296658	128854	GATATTCCACACATAAACAA
207485	39681	ATCCTCCCATCTCAGCCTCC	252072	84268	AGTGAGACAGGATTTCACAT	296659	128855	AGATATTCCACACATAAACA
207486	39682	AATCCTCCCATCTCAGCCTC	252073	84269	TAGTGAGACAGGATTTCACA	296660	128856	GAGATATTCCACACATAAAC
207487	39683	CAATCCTCCCATCTCAGCCT	252074	84270	GTAGTGAGACAGGATTTCAC	296661	128857	AGAGATATTCCACACATAAA
207488	39684	GCAATCCTCCCATCTCAGCC	252075	84271	TGTAGTGAGACAGGATTTCA	296662	128858	CAGAGATATTCCACACATAA
207489	39685	AGCAATCCTCCCATCTCAGC	252076	84272	TTGTAGTGAGACAGGATTTC	296663	128859	CCAGAGATATTCCACACATA
207490	39686	AAGCAATCCTCCCATCTCAG	252077	84273	TTTGTAGTGAGACAGGATTT	296664	128860	TCCAGAGATATTCCACACAT
207491	39687	CAAGCAATCCTCCCATCTCA	252078	84274	ATTTGTAGTGAGACAGGATT	296665	128861	CTCCAGAGATATTCCACACA
207492	39688	TCAAGCAATCCTCCCATCTC	252079	84275	TATTTGTAGTGAGACAGGAT	296666	128862	CCTCCAGAGATATTCCACAC
207493	39689	CTCAAGCAATCCTCCCATCT	252080	84276	TTATTTGTAGTGAGACAGGA	296667	128863	CCCTCCAGAGATATTCCACA
207494	39690	GCTCAAGCAATCCTCCCATC	252081	84277	TTTATTTGTAGTGAGACAGG	296668	128864	ACCCTCCAGAGATATTCCAC
207495	39691	GGCTCAAGCAATCCTCCCAT	252082	84278	TTTTATTTGTAGTGAGACAG	296669	128865	TACCCTCCAGAGATATTCCA
207496	39692	TGGCTCAAGCAATCCTCCCA	252083	84279	TTTTTATTTGTAGTGAGACA	296670	128866	GTACCCTCCAGAGATATTCC
207497	39693	CTGGCTCAAGCAATCCTCCC	252084	84280	TTTTTTATTTGTAGTGAGAC	296671	128867	TGTACCCTCCAGAGATATTC
207498	39694	TCTGGCTCAAGCAATCCTCC	252085	84281	TTTTTTTATTTGTAGTGAGA	296672	128868	GTGTACCCTCCAGAGATATT
207499	39695	TTCTGGCTCAAGCAATCCTC	252086	84282	ATTTTTTTATTTGTAGTGAG	296673	128869	TGTGTACCCTCCAGAGATAT
207500	39696	GTTCTGGCTCAAGCAATCCT	252087	84283	AATTTTTTTATTTGTAGTGA	296674	128870	TTGTGTACCCTCCAGAGATA
207501	39697	AGTTCTGGCTCAAGCAATCC	252088	84284	TAATTTTTTTATTTGTAGTG	296675	128871	CTTGTGTACCCTCCAGAGAT
207502	39698	AAGTTCTGGCTCAAGCAATC	252089	84285	CTAATTTTTTTATTTGTAGT	296676	128872	TCTTGTGTACCCTCCAGAGA
207503	39699	AAAGTTCTGGCTCAAGCAAT	252090	84286	GCTAATTTTTTTATTTGTAG	296677	128873	TTCTTGTGTACCCTCCAGAG
207504	39700	CAAAGTTCTGGCTCAAGCAA	252091	84287	GGCTAATTTTTTTATTTGTA	296678	128874	TTTCTTGTGTACCCTCCAGA
207505	39701	TCAAAGTTCTGGCTCAAGCA	252092	84288	CGGCTAATTTTTTTATTTGT	296679	128875	GTTTCTTGTGTACCCTCCAG
207506	39702	CTCAAAGTTCTGGCTCAAGC	252093	84289	CCGGCTAATTTTTTTATTTG	296680	128876	AGTTTCTTGTGTACCCTCCA
207507	39703	CCTCAAAGTTCTGGCTCAAG	252094	84290	CCCGGCTAATTTTTTTATTT	296681	128877	AAGTTTCTTGTGTACCCTCC
207508	39704	GCCTCAAAGTTCTGGCTCAA	252095	84291	ACCCGGCTAATTTTTTTATT	296682	128878	TAAGTTTCTTGTGTACCCTC
207509	39705	AGCCTCAAAGTTCTGGCTCA	252096	84292	CACCCGGCTAATTTTTTTAT	296683	128879	TTAAGTTTCTTGTGTACCCT
207510	39706	TAGCCTCAAAGTTCTGGCTC	252097	84293	ACACCCGGCTAATTTTTTTA	296684	128880	TTTAAGTTTCTTGTGTACCC
207511	39707	GTAGCCTCAAAGTTCTGGCT	252098	84294	CACACCCGGCTAATTTTTTT	296685	128881	TTTTAAGTTTCTTGTGTACC
207512	39708	TGTAGCCTCAAAGTTCTGGC	252099	84295	CCACACCCGGCTAATTTTTT	296686	128882	ATTTTAAGTTTCTTGTGTAC
207513	39709	CTGTAGCCTCAAAGTTCTGG	252100	84296	ACCACACCCGGCTAATTTTT	296687	128883	CATTTTAAGTTTCTTGTGTA
207514	39710	ACTGTAGCCTCAAAGTTCTG	252101	84297	CACCACACCCGGCTAATTTT	296688	128884	TCATTTTAAGTTTCTTGTGT
207515	39711	CACTGTAGCCTCAAAGTTCT	252102	84298	CCACCACACCCGGCTAATTT	296689	128885	ATCATTTTAAGTTTCTTGTG
207516	39712	TCACTGTAGCCTCAAAGTTC	252103	84299	ACCACCACACCCGGCTAATT	296690	128886	GATCATTTTAAGTTTCTTGT
207517	39713	CTCACTGTAGCCTCAAAGTT	252104	84300	TACCACCACACCCGGCTAAT	296691	128887	TGATCATTTTAAGTTTCTTG
207518	39714	ACTCACTGTAGCCTCAAAGT	252105	84301	CTACCACCACACCCGGCTAA	296692	128888	GTGATCATTTTAAGTTTCTT
207519	39715	AACTCACTGTAGCCTCAAAG	252106	84302	CCTACCACCACACCCGGCTA	296693	128889	AGTGATCATTTTAAGTTTCT
207520	39716	TAACTCACTGTAGCCTCAAA	252107	84303	ACCTACCACCACACCCGGCT	296694	128890	CAGTGATCATTTTAAGTTTC
207521	39717	ATAACTCACTGTAGCCTCAA	252108	84304	CACCTACCACCACACCCGGC	296695	128891	ACAGTGATCATTTTAAGTTT
207522	39718	AATAACTCACTGTAGCCTCA	252109	84305	GCACCTACCACCACACCCGG	296696	128892	GACAGTGATCATTTTAAGTT
207523	39719	AAATAACTCACTGTAGCCTC	252110	84306	GGCACCTACCACCACACCCG	296697	128893	AGACAGTGATCATTTTAAGT
207524	39720	AAAATAACTCACTGTAGCCT	252111	84307	AGGCACCTACCACCACACCC	296698	128894	GAGACAGTGATCATTTTAAG
207525	39721	GAAAATAACTCACTGTAGCC	252112	84308	TAGGCACCTACCACCACACC	296699	128895	AGAGACAGTGATCATTTTAA
207526	39722	TGAAAATAACTCACTGTAGC	252113	84309	ATAGGCACCTACCACCACAC	296700	128896	CAGAGACAGTGATCATTTTA
207527	39723	GTGAAAATAACTCACTGTAG	252114	84310	TATAGGCACCTACCACCACA	296701	128897	CCAGAGACAGTGATCATTTT
207528	39724	CGTGAAAATAACTCACTGTA	252115	84311	TTATAGGCACCTACCACCAC	296702	128898	CCCAGAGACAGTGATCATTT
207529	39725	GCGTGAAAATAACTCACTGT	252116	84312	ATTATAGGCACCTACCACCA	296703	128899	CCCCAGAGACAGTGATCATT
207530	39726	GGCGTGAAAATAACTCACTG	252117	84313	GATTATAGGCACCTACCACC	296704	128900	TCCCCAGAGACAGTGATCAT
207531	39727	TGGCGTGAAAATAACTCACT	252118	84314	GGATTATAGGCACCTACCAC	296705	128901	CTCCCCAGAGACAGTGATCA
207532	39728	GTGGCGTGAAAATAACTCAC	252119	84315	GGGATTATAGGCACCTACCA	296706	128902	CCTCCCCAGAGACAGTGATC
207533	39729	AGTGGCGTGAAAATAACTCA	252120	84316	TGGGATTATAGGCACCTACC	296707	128903	CCCTCCCCAGAGACAGTGAT
207534	39730	CAGTGGCGTGAAAATAACTC	252121	84317	CTGGGATTATAGGCACCTAC	296708	128904	ACCCTCCCCAGAGACAGTGA
207535	39731	GCAGTGGCGTGAAAATAACT	252122	84318	GCTGGGATTATAGGCACCTA	296709	128905	TACCCTCCCCAGAGACAGTG
207536	39732	GGCAGTGGCGTGAAAATAAC	252123	84319	AGCTGGGATTATAGGCACCT	296710	128906	GTACCCTCCCCAGAGACAGT
207537	39733	GGGCAGTGGCGTGAAAATAA	252124	84320	TAGCTGGGATTATAGGCACC	296711	128907	GGTACCCTCCCCAGAGACAG
207538	39734	AGGGCAGTGGCGTGAAAATA	252125	84321	GTAGCTGGGATTATAGGCAC	296712	128908	AGGTACCCTCCCCAGAGACA
207539	39735	GAGGGCAGTGGCGTGAAAAT	252126	84322	AGTAGCTGGGATTATAGGCA	296713	128909	CAGGTACCCTCCCCAGAGAC
207540	39736	AGAGGGCAGTGGCGTGAAAA	252127	84323	GAGTAGCTGGGATTATAGGC	296714	128910	CCAGGTACCCTCCCCAGAGA
207541	39737	TAGAGGGCAGTGGCGTGAAA	252128	84324	TGAGTAGCTGGGATTATAGG	296715	128911	CCCAGGTACCCTCCCCAGAG
207542	39738	CTAGAGGGCAGTGGCGTGAA	252129	84325	CTGAGTAGCTGGGATTATAG	296716	128912	ACCCAGGTACCCTCCCCAGA
207543	39739	GCTAGAGGGCAGTGGCGTGA	252130	84326	CCTGAGTAGCTGGGATTATA	296717	128913	CACCCAGGTACCCTCCCCAG
207544	39740	GGCTAGAGGGCAGTGGCGTG	252131	84327	TCCTGAGTAGCTGGGATTAT	296718	128914	GCACCCAGGTACCCTCCCCA
207545	39741	AGGCTAGAGGGCAGTGGCGT	252132	84328	CTCCTGAGTAGCTGGGATTA	296719	128915	GGCACCCAGGTACCCTCCCC
207546	39742	CAGGCTAGAGGGCAGTGGCG	252133	84329	CCTCCTGAGTAGCTGGGATT	296720	128916	AGGCACCCAGGTACCCTCCC

207547	39743	CCAGGCTAGAGGGCAGTGGC	252134	84330	GCCTCCTGAGTAGCTGGGAT	296721	128917	CAGGCACCCAGGTACCCTCC
207548	39744	GCCAGGCTAGAGGGCAGTGG	252135	84331	AGCCTCCTGAGTAGCTGGGA	296722	128918	CCAGGCACCCAGGTACCCTC
207549	39745	AGCCAGGCTAGAGGGCAGTG	252136	84332	CAGCCTCCTGAGTAGCTGGG	296723	128919	CCCAGGCACCCAGGTACCCT
207550	39746	CAGCCAGGCTAGAGGGCAGT	252137	84333	TCAGCCTCCTGAGTAGCTGG	296724	128920	TCCCAGGCACCCAGGTACCC
207551	39747	TCAGCCAGGCTAGAGGGCAG	252138	84334	CTCAGCCTCCTGAGTAGCTG	296725	128921	CTCCCAGGCACCCAGGTACC
207552	39748	GTCAGCCAGGCTAGAGGGCA	252139	84335	CCTCAGCCTCCTGAGTAGCT	296726	128922	CCTCCCAGGCACCCAGGTAC
207553	39749	TGTCAGCCAGGCTAGAGGGC	252140	84336	GCCTCAGCCTCCTGAGTAGC	296727	128923	GCCTCCCAGGCACCCAGGTA
207554	39750	CTGTCAGCCAGGCTAGAGGG	252141	84337	TGCCTCAGCCTCCTGAGTAG	296728	128924	TGCCTCCCAGGCACCCAGGT
207555	39751	TCTGTCAGCCAGGCTAGAGG	252142	84338	CTGCCTCAGCCTCCTGAGTA	296729	128925	CTGCCTCCCAGGCACCCAGG
207556	39752	CTCTGTCAGCCAGGCTAGAG	252143	84339	CCTGCCTCAGCCTCCTGAGT	296730	128926	CCTGCCTCCCAGGCACCCAG
207557	39753	GCTCTGTCAGCCAGGCTAGA	252144	84340	TCCTGCCTCAGCCTCCTGAG	296731	128927	ACCTGCCTCCCAGGCACCCA
207558	39754	TGCTCTGTCAGCCAGGCTAG	252145	84341	GTCCTGCCTCAGCCTCCTGA	296732	128928	GACCTGCCTCCCAGGCACCC
207559	39755	TTGCTCTGTCAGCCAGGCTA	252146	84342	TGTCCTGCCTCAGCCTCCTG	296733	128929	TGACCTGCCTCCCAGGCACC
207560	39756	CTTGCTCTGTCAGCCAGGCT	252147	84343	TTGTCCTGCCTCAGCCTCCT	296734	128930	CTGACCTGCCTCCCAGGCAC
207561	39757	TCTTGCTCTGTCAGCCAGGC	252148	84344	ATTGTCCTGCCTCAGCCTCC	296735	128931	CCTGACCTGCCTCCCAGGCA
207562	39758	GTCTTGCTCTGTCAGCCAGG	252149	84345	GATTGTCCTGCCTCAGCCTC	296736	128932	CCCTGACCTGCCTCCCAGGC
207563	39759	GGTCTTGCTCTGTCAGCCAG	252150	84346	CGATTGTCCTGCCTCAGCCT	296737	128933	TCCCTGACCTGCCTCCCAGG
207564	39760	AGGTCTTGCTCTGTCAGCCA	252151	84347	GCGATTGTCCTGCCTCAGCC	296738	128934	TTCCCTGACCTGCCTCCCAG
207565	39761	CAGGTCTTGCTCTGTCAGCC	252152	84348	AGCGATTGTCCTGCCTCAGC	296739	128935	CTTCCCTGACCTGCCTCCCA
207566	39762	GCAGGTCTTGCTCTGTCAGC	252153	84349	GAGCGATTGTCCTGCCTCAG	296740	128936	CCTTCCCTGACCTGCCTCCC
207567	39763	GGCAGGTCTTGCTCTGTCAG	252154	84350	CGAGCGATTGTCCTGCCTCA	296741	128937	TCCTTCCCTGACCTGCCTCC
207568	39764	AGGCAGGTCTTGCTCTGTCA	252155	84351	TCGAGCGATTGTCCTGCCTC	296742	128938	CTCCTTCCCTGACCTGCCTC
207569	39765	GAGGCAGGTCTTGCTCTGTC	252156	84352	TTCGAGCGATTGTCCTGCCT	296743	128939	ACTCCTTCCCTGACCTGCCT
207570	39766	TGAGGCAGGTCTTGCTCTGT	252157	84353	GTTCGAGCGATTGTCCTGCC	296744	128940	CACTCCTTCCCTGACCTGCC
207571	39767	TTGAGGCAGGTCTTGCTCTG	252158	84354	GGTTCGAGCGATTGTCCTGC	296745	128941	CCACTCCTTCCCTGACCTGC
207572	39768	TTTGAGGCAGGTCTTGCTCT	252159	84355	GGGTTCGAGCGATTGTCCTG	296746	128942	CCCACTCCTTCCCTGACCTG
207573	39769	TTTTGAGGCAGGTCTTGCTC	252160	84356	TGGGTTCGAGCGATTGTCCT	296747	128943	GCCCACTCCTTCCCTGACCT
207574	39770	TTTTTGAGGCAGGTCTTGCT	252161	84357	CTGGGTTCGAGCGATTGTCC	296748	128944	TGCCCACTCCTTCCCTGACC
207575	39771	TTTTTTGAGGCAGGTCTTGC	252162	84358	CCTGGGTTCGAGCGATTGTC	296749	128945	GTGCCCACTCCTTCCCTGAC
207576	39772	TTTTTTTGAGGCAGGTCTTG	252163	84359	TCCTGGGTTCGAGCGATTGT	296750	128946	TGTGCCCACTCCTTCCCTGA
207577	39773	ATTTTTTTGAGGCAGGTCTT	252164	84360	CTCCTGGGTTCGAGCGATTG	296751	128947	CTGTGCCCACTCCTTCCCTG
207578	39774	TATTTTTTTGAGGCAGGTCT	252165	84361	CCTCCTGGGTTCGAGCGATT	296752	128948	CCTGTGCCCACTCCTTCCCT
207579	39775	TTATTTTTTTGAGGCAGGTC	252166	84362	ACCTCCTGGGTTCGAGCGAT	296753	128949	ACCTGTGCCCACTCCTTCCC
207580	39776	CTTATTTTTTTGAGGCAGGT	252167	84363	CACCTCCTGGGTTCGAGCGA	296754	128950	TACCTGTGCCCACTCCTTCC
207581	39777	ACTTATTTTTTTGAGGCAGG	252168	84364	CCACCTCCTGGGTTCGAGCG	296755	128951	ATACCTGTGCCCACTCCTTC
207582	39778	TACTTATTTTTTTGAGGCAG	252169	84365	TCCACCTCCTGGGTTCGAGC	296756	128952	AATACCTGTGCCCACTCCTT
207583	39779	TTACTTATTTTTTTGAGGCA	252170	84366	GTCCACCTCCTGGGTTCGAG	296757	128953	TAATACCTGTGCCCACTCCT
207584	39780	TTTACTTATTTTTTTGAGGC	252171	84367	CGTCCACCTCCTGGGTTCGA	296758	128954	GTAATACCTGTGCCCACTCC
207585	39781	TTTTACTTATTTTTTTGAGG	252172	84368	ACGTCCACCTCCTGGGTTCG	296759	128955	GGTAATACCTGTGCCCACTC
207586	39782	TTTTTACTTATTTTTTTGAG	252173	84369	AACGTCCACCTCCTGGGTTC	296760	128956	TGGTAATACCTGTGCCCACT
207587	39783	TTTTTTACTTATTTTTTTGA	252174	84370	CAACGTCCACCTCCTGGGTT	296761	128957	TTGGTAATACCTGTGCCCAC
207588	39784	ATTTTTTACTTATTTTTTTG	252175	84371	GCAACGTCCACCTCCTGGGT	296762	128958	ATTGGTAATACCTGTGCCCA
207589	39785	TATTTTTTACTTATTTTTTT	252176	84372	TGCAACGTCCACCTCCTGGG	296763	128959	AATTGGTAATACCTGTGCCC
207590	39786	TTATTTTTTACTTATTTTTT	252177	84373	CTGCAACGTCCACCTCCTGG	296764	128960	CAATTGGTAATACCTGTGCC
207591	39787	TTTATTTTTTACTTATTTTT	252178	84374	ACTGCAACGTCCACCTCCTG	296765	128961	CCAATTGGTAATACCTGTGC
207592	39788	ATTTATTTTTTACTTATTTT	252179	84375	CACTGCAACGTCCACCTCCT	296766	128962	TCCAATTGGTAATACCTGTG
207593	39789	AATTTATTTTTTACTTATTT	252180	84376	TCACTGCAACGTCCACCTCC	296767	128963	TTCCAATTGGTAATACCTGT
207594	39790	TAATTTATTTTTTACTTATT	252181	84377	CTCACTGCAACGTCCACCTC	296768	128964	CTTCCAATTGGTAATACCTG
207595	39791	TTAATTTATTTTTTACTTAT	252182	84378	GCTCACTGCAACGTCCACCT	296769	128965	TCTTCCAATTGGTAATACCT
207596	39792	TTTAATTTATTTTTTACTTA	252183	84379	GGCTCACTGCAACGTCCACC	296770	128966	GTCTTCCAATTGGTAATACC
207597	39793	ATTTAATTTATTTTTTACTT	252184	84380	CGGCTCACTGCAACGTCCAC	296771	128967	TGTCTTCCAATTGGTAATAC
207598	39794	AATTTAATTTATTTTTTACT	252185	84381	TCGGCTCACTGCAACGTCCA	296772	128968	TTGTCTTCCAATTGGTAATA
207599	39795	AAATTTAATTTATTTTTTAC	252186	84382	CTCGGCTCACTGCAACGTCC	296773	128969	ATTGTCTTCCAATTGGTAAT
207600	39796	GAAATTTAATTTATTTTTTA	252187	84383	TCTCGGCTCACTGCAACGTC	296774	128970	TATTGTCTTCCAATTGGTAA
207601	39797	TGAAATTTAATTTATTTTTT	252188	84384	ATCTCGGCTCACTGCAACGT	296775	128971	TTATTGTCTTCCAATTGGTA
207602	39798	TTGAAATTTAATTTATTTTT	252189	84385	GATCTCGGCTCACTGCAACG	296776	128972	TTTATTGTCTTCCAATTGGT
207603	39799	ATTGAAATTTAATTTATTTT	252190	84386	CGATCTCGGCTCACTGCAAC	296777	128973	TTTTATTGTCTTCCAATTGG
207604	39800	GATTGAAATTTAATTTATTT	252191	84387	GCGATCTCGGCTCACTGCAA	296778	128974	TTTTTATTGTCTTCCAATTG
207605	39801	TGATTGAAATTTAATTTATT	252192	84388	TGCGATCTCGGCTCACTGCA	296779	128975	GTTTTTATTGTCTTCCAATT
207606	39802	ATGATTGAAATTTAATTTAT	252193	84389	ATGCGATCTCGGCTCACTGC	296780	128976	TGTTTTTATTGTCTTCCAAT
207607	39803	AATGATTGAAATTTAATTTA	252194	84390	GATGCGATCTCGGCTCACTG	296781	128977	TTGTTTTTATTGTCTTCCAA
207608	39804	TAATGATTGAAATTTAATTT	252195	84391	TGATGCGATCTCGGCTCACT	296782	128978	GTTGTTTTTATTGTCTTCCA
207609	39805	CTAATGATTGAAATTTAATT	252196	84392	ATGATGCGATCTCGGCTCAC	296783	128979	TGTTGTTTTTATTGTCTTCC
207610	39806	GCTAATGATTGAAATTTAAT	252197	84393	AATGATGCGATCTCGGCTCA	296784	128980	CTGTTGTTTTTATTGTCTTC
207611	39807	TGCTAATGATTGAAATTTAA	252198	84394	CAATGATGCGATCTCGGCTC	296785	128981	GCTGTTGTTTTTATTGTCTT
207612	39808	CTGCTAATGATTGAAATTTA	252199	84395	GCAATGATGCGATCTCGGCT	296786	128982	AGCTGTTGTTTTTATTGTCT
207613	39809	ACTGCTAATGATTGAAATTT	252200	84396	TGCAATGATGCGATCTCGGC	296787	128983	GAGCTGTTGTTTTTATTGTC
207614	39810	GACTGCTAATGATTGAAATT	252201	84397	GTGCAATGATGCGATCTCGG	296788	128984	GGAGCTGTTGTTTTTATTGT
207615	39811	TGACTGCTAATGATTGAAAT	252202	84398	AGTGCAATGATGCGATCTCG	296789	128985	AGGAGCTGTTGTTTTTATTG
207616	39812	ATGACTGCTAATGATTGAAA	252203	84399	GAGTGCAATGATGCGATCTC	296790	128986	CAGGAGCTGTTGTTTTTATT
207617	39813	AATGACTGCTAATGATTGAA	252204	84400	GGAGTGCAATGATGCGATCT	296791	128987	CCAGGAGCTGTTGTTTTTAT
207618	39814	TAATGACTGCTAATGATTGA	252205	84401	TGGAGTGCAATGATGCGATC	296792	128988	GCCAGGAGCTGTTGTTTTTA

207619	39815	CTAATGACTGCTAATGATTG	252206	84402	CTGGAGTGCAATGATGCGAT	296793	128989	GGCCAGGAGCTGTTGTTTTT
207620	39816	CCTAATGACTGCTAATGATT	252207	84403	GCTGGAGTGCAATGATGCGA	296794	128990	TGGCCAGGAGCTGTTGTTTT
207621	39817	TCCTAATGACTGCTAATGAT	252208	84404	GGCTGGAGTGCAATGATGCG	296795	128991	CTGGCCAGGAGCTGTTGTTT
207622	39818	ATCCTAATGACTGCTAATGA	252209	84405	AGGCTGGAGTGCAATGATGC	296796	128992	CCTGGCCAGGAGCTGTTGTT
207623	39819	TATCCTAATGACTGCTAATG	252210	84406	CAGGCTGGAGTGCAATGATG	296797	128993	GCCTGGCCAGGAGCTGTTGT
207624	39820	ATATCCTAATGACTGCTAAT	252211	84407	CCAGGCTGGAGTGCAATGAT	296798	128994	CGCCTGGCCAGGAGCTGTTG
207625	39821	AATATCCTAATGACTGCTAA	252212	84408	CCCAGGCTGGAGTGCAATGA	296799	128995	GCGCCTGGCCAGGAGCTGTT
207626	39822	AAATATCCTAATGACTGCTA	252213	84409	GCCCAGGCTGGAGTGCAATG	296800	128996	TGCGCCTGGCCAGGAGCTGT
207627	39823	TAAATATCCTAATGACTGCT	252214	84410	TGCCCAGGCTGGAGTGCAAT	296801	128997	CTGCGCCTGGCCAGGAGCTG
207628	39824	TTAAATATCCTAATGACTGC	252215	84411	TTGCCCAGGCTGGAGTGCAA	296802	128998	ACTGCGCCTGGCCAGGAGCT
207629	39825	TTTAAATATCCTAATGACTG	252216	84412	GTTGCCCAGGCTGGAGTGCA	296803	128999	CACTGCGCCTGGCCAGGAGC
207630	39826	ATTTAAATATCCTAATGACT	252217	84413	TGTTGCCCAGGCTGGAGTGC	296804	129000	CCACTGCGCCTGGCCAGGAG
207631	39827	TATTTAAATATCCTAATGAC	252218	84414	TTGTTGCCCAGGCTGGAGTG	296805	129001	GCCACTGCGCCTGGCCAGGA
207632	39828	GTATTTAAATATCCTAATGA	252219	84415	TTTGTTGCCCAGGCTGGAGT	296806	129002	AGCCACTGCGCCTGGCCAGG
207633	39829	TGTATTTAAATATCCTAATG	252220	84416	TTTTGTTGCCCAGGCTGGAG	296807	129003	GAGCCACTGCGCCTGGCCAG
207634	39830	CTGTATTTAAATATCCTAAT	252221	84417	CTTTTGTTGCCCAGGCTGGA	296808	129004	TGAGCCACTGCGCCTGGCCA
207635	39831	ACTGTATTTAAATATCCTAA	252222	84418	GCTTTTGTTGCCCAGGCTGG	296809	129005	GTGAGCCACTGCGCCTGGCC
207636	39832	TACTGTATTTAAATATCCTA	252223	84419	TGCTTTTGTTGCCCAGGCTG	296810	129006	CGTGAGCCACTGCGCCTGGC
207637	39833	ATACTGTATTTAAATATCCT	252224	84420	TTGCTTTTGTTGCCCAGGCT	296811	129007	GCGTGAGCCACTGCGCCTGG
207638	39834	CATACTGTATTTAAATATCC	252225	84421	TTTGCTTTTGTTGCCCAGGC	296812	129008	GGCGTGAGCCACTGCGCCTG
207639	39835	ACATACTGTATTTAAATATC	252226	84422	TTTTGCTTTTGTTGCCCAGG	296813	129009	AGGCGTGAGCCACTGCGCCT
207640	39836	AACATACTGTATTTAAATAT	252227	84423	GTTTTGCTTTTGTTGCCCAG	296814	129010	CAGGCGTGAGCCACTGCGCC
207641	39837	CAACATACTGTATTTAAATA	252228	84424	AGTTTTGCTTTTGTTGCCCA	296815	129011	ACAGGCGTGAGCCACTGCGC
207642	39838	TCAACATACTGTATTTAAAT	252229	84425	GAGTTTTGCTTTTGTTGCCC	296816	129012	TACAGGCGTGAGCCACTGCG
207643	39839	TTCAACATACTGTATTTAAA	252230	84426	GGAGTTTTGCTTTTGTTGCC	296817	129013	TTACAGGCGTGAGCCACTGC
207644	39840	ATTCAACATACTGTATTTAA	252231	84427	CGGAGTTTTGCTTTTGTTGC	296818	129014	ATTACAGGCGTGAGCCACTG
207645	39841	GATTCAACATACTGTATTTA	252232	84428	ACGGAGTTTTGCTTTTGTTG	296819	129015	CATTACAGGCGTGAGCCACT
207646	39842	TGATTCAACATACTGTATTT	252233	84429	GACGGAGTTTTGCTTTTGTT	296820	129016	CCATTACAGGCGTGAGCCAC
207647	39843	TTGATTCAACATACTGTATT	252234	84430	AGACGGAGTTTTGCTTTTGT	296821	129017	GCCATTACAGGCGTGAGCCA
207648	39844	TTTGATTCAACATACTGTAT	252235	84431	GAGACGGAGTTTTGCTTTTG	296822	129018	TGCCATTACAGGCGTGAGCC
207649	39845	CTTTGATTCAACATACTGTA	252236	84432	TGAGACGGAGTTTTGCTTTT	296823	129019	CTGCCATTACAGGCGTGAGC
207650	39846	ACTTTGATTCAACATACTGT	252237	84433	TTGAGACGGAGTTTTGCTTT	296824	129020	GCTGCCATTACAGGCGTGAG
207651	39847	AACTTTGATTCAACATACTG	252238	84434	TTTGAGACGGAGTTTTGCTT	296825	129021	TGCTGCCATTACAGGCGTGA
207652	39848	TAACTTTGATTCAACATACT	252239	84435	TTTTGAGACGGAGTTTTGCT	296826	129022	GTGCTGCCATTACAGGCGTG
207653	39849	GTAACTTTGATTCAACATAC	252240	84436	TTTTTGAGACGGAGTTTTGC	296827	129023	AGTGCTGCCATTACAGGCGT
207654	39850	CGTAACTTTGATTCAACATA	252241	84437	TTTTTTGAGACGGAGTTTTG	296828	129024	GAGTGCTGCCATTACAGGCG
207655	39851	GCGTAACTTTGATTCAACAT	252242	84438	TTTTTTTGAGACGGAGTTTT	296829	129025	AGAGTGCTGCCATTACAGGC
207656	39852	TGCGTAACTTTGATTCAACA	252243	84439	TTTTTTTTGAGACGGAGTTT	296830	129026	CAGAGTGCTGCCATTACAGG
207657	39853	ATGCGTAACTTTGATTCAAC	252244	84440	TTTTTTTTTGAGACGGAGTT	296831	129027	TCAGAGTGCTGCCATTACAG
207658	39854	CATGCGTAACTTTGATTCAA	252245	84441	TTTTTTTTTTGAGACGGAGT	296832	129028	CTCAGAGTGCTGCCATTACA
207659	39855	ACATGCGTAACTTTGATTCA	252246	84442	TTTTTTTTTTTGAGACGGAG	296833	129029	TCTCAGAGTGCTGCCATTAC
207660	39856	CACATGCGTAACTTTGATTC	252247	84443	TTTTTTTTTTTTGAGACGGA	296834	129030	CTCTCAGAGTGCTGCCATTA
207661	39857	ACACATGCGTAACTTTGATT	252248	84444	CTTTTTTTTTTTGAGACGG	296835	129031	CCTCTCAGAGTGCTGCCATT
207662	39858	CACACATGCGTAACTTTGAT	252249	84445	TCTTTTTTTTTTTTGAGACG	296836	129032	GCCTCTCAGAGTGCTGCCAT
207663	39859	ACACACATGCGTAACTTTGA	252250	84446	TTCTTTTTTTTTTTTGAGAC	296837	129033	AGCCTCTCAGAGTGCTGCCA
207664	39860	TACACACATGCGTAACTTTG	252251	84447	TTTCTTTTTTTTTTTTGAGA	296838	129034	CAGCCTCTCAGAGTGCTGCC
207665	39861	ATACACACATGCGTAACTTT	252252	84448	GTTTCTTTTTTTTTTTTGAG	296839	129035	TCAGCCTCTCAGAGTGCTGC
207666	39862	AATACACACATGCGTAACTT	252253	84449	AGTTTCTTTTTTTTTTTTGA	296840	129036	CTCAGCCTCTCAGAGTGCTG
207667	39863	AAATACACACATGCGTAACT	252254	84450	GAGTTTCTTTTTTTTTTTTG	296841	129037	CCTCAGCCTCTCAGAGTGCT
207668	39864	AAAATACACACATGCGTAAC	252255	84451	TGAGTTTCTTTTTTTTTTTT	296842	129038	GCCTCAGCCTCTCAGAGTGC
207669	39865	AAAAATACACACATGCGTAA	252256	84452	TTGAGTTTCTTTTTTTTTTT	296843	129039	CGCCTCAGCCTCTCAGAGTG
207670	39866	AAAAAATACACACATGCGTA	252257	84453	TTTGAGTTTCTTTTTTTTTT	296844	129040	CCGCCTCAGCCTCTCAGAGT
207671	39867	AAAAAAATACACACATGCGT	252258	84454	ATTTGAGTTTCTTTTTTTTT	296845	129041	CCCGCCTCAGCCTCTCAGAG
207672	39868	AAAAAAAATACACACATGCG	252259	84455	TATTTGAGTTTCTTTTTTTT	296846	129042	GCCCGCCTCAGCCTCTCAGA
207673	39869	AAAAAAAAATACACACATGC	252260	84456	ATATTTGAGTTTCTTTTTTT	296847	129043	TGCCCGCCTCAGCCTCTCAG
207674	39870	GAAAAAAAAATACACACATG	252261	84457	CATATTTGAGTTTCTTTTTT	296848	129044	CTGCCCGCCTCAGCCTCTCA
207675	39871	GGAAAAAAAAATACACACAT	252262	84458	ACATATTTGAGTTTCTTTTT	296849	129045	TCTGCCCGCCTCAGCCTCTC
207676	39872	TGGAAAAAAAAATACACACA	252263	84459	CACATATTTGAGTTTCTTTT	296850	129046	ATCTGCCCGCCTCAGCCTCT
207677	39873	CTGGAAAAAAAAATACACAC	252264	84460	ACACATATTTGAGTTTCTTT	296851	129047	AATCTGCCCGCCTCAGCCTC
207678	39874	TCTGGAAAAAAAAATACACA	252265	84461	CACACATATTTGAGTTTCTT	296852	129048	CAATCTGCCCGCCTCAGCCT
207679	39875	CTCTGGAAAAAAAAATACAC	252266	84462	TCACACATATTTGAGTTTCT	296853	129049	GCAATCTGCCCGCCTCAGCC
207680	39876	TCTCTGGAAAAAAAAATACA	252267	84463	GTCACACATATTTGAGTTTC	296854	129050	AGCAATCTGCCCGCCTCAGC
207681	39877	CTCTCTGGAAAAAAAAATAC	252268	84464	TGTCACACATATTTGAGTTT	296855	129051	AAGCAATCTGCCCGCCTCAG
207682	39878	ACTCTCTGGAAAAAAAAATA	252269	84465	CTGTCACACATATTTGAGTT	296856	129052	CAAGCAATCTGCCCGCCTCA
207683	39879	AACTCTCTGGAAAAAAAAAT	252270	84466	CCTGTCACACATATTTGAGT	296857	129053	GCAAGCAATCTGCCCGCCTC
207684	39880	CAACTCTCTGGAAAAAAAAA	252271	84467	GCCTGTCACACATATTTGAG	296858	129054	CGCAAGCAATCTGCCCGCCT
207685	39881	ACAACTCTCTGGAAAAAAAA	252272	84468	CGCCTGTCACACATATTTGA	296859	129055	ACGCAAGCAATCTGCCCGCC
207686	39882	AACAACTCTCTGGAAAAAAA	252273	84469	TCGCCTGTCACACATATTTG	296860	129056	GACGCAAGCAATCTGCCCGC
207687	39883	AAACAACTCTCTGGAAAAAA	252274	84470	ATCGCCTGTCACACATATTT	296861	129057	GGACGCAAGCAATCTGCCCG
207688	39884	TAAACAACTCTCTGGAAAAA	252275	84471	AATCGCCTGTCACACATATT	296862	129058	TGGACGCAAGCAATCTGCCC
207689	39885	ATAAACAACTCTCTGGAAAA	252276	84472	GAATCGCCTGTCACACATAT	296863	129059	CTGGACGCAAGCAATCTGCC
207690	39886	GATAAACAACTCTCTGGAAA	252277	84473	AGAATCGCCTGTCACACATA	296864	129060	CCTGGACGCAAGCAATCTGC

207691	39887	TGATAAACAACTCTCTGGAA	252278	84474	GAGAATCGCCTGTCACACAT	296865	129061	TCCTGGACGCAAGCAATCTG
207692	39888	ATGATAAACAACTCTCTGGA	252279	84475	TGAGAATCGCCTGTCACACA	296866	129062	CTCCTGGACGCAAGCAATCT
207693	39889	CATGATAAACAACTCTCTGG	252280	84476	GTGAGAATCGCCTGTCACAC	296867	129063	ACTCCTGGACGCAAGCAATC
207694	39890	ACATGATAAACAACTCTCTG	252281	84477	AGTGAGAATCGCCTGTCACA	296868	129064	AACTCCTGGACGCAAGCAAT
207695	39891	CACATGATAAACAACTCTCT	252282	84478	CAGTGAGAATCGCCTGTCAC	296869	129065	GAACTCCTGGACGCAAGCAA
207696	39892	CCACATGATAAACAACTCTC	252283	84479	GCAGTGAGAATCGCCTGTCA	296870	129066	TGAACTCCTGGACGCAAGCA
207697	39893	CCCACATGATAAACAACTCT	252284	84480	TGCAGTGAGAATCGCCTGTC	296871	129067	TTGAACTCCTGGACGCAAGC
207698	39894	ACCCACATGATAAACAACTC	252285	84481	CTGCAGTGAGAATCGCCTGT	296872	129068	CTTGAACTCCTGGACGCAAG
207699	39895	AACCCACATGATAAACAACT	252286	84482	CCTGCAGTGAGAATCGCCTG	296873	129069	TCTTGAACTCCTGGACGCAA
207700	39896	AAACCCACATGATAAACAAC	252287	84483	GCCTGCAGTGAGAATCGCCT	296874	129070	GTCTTGAACTCCTGGACGCA
207701	39897	AAAACCCACATGATAAACAA	252288	84484	AGCCTGCAGTGAGAATCGCC	296875	129071	GGTCTTGAACTCCTGGACGC
207702	39898	TAAAACCCACATGATAAACA	252289	84485	CAGCCTGCAGTGAGAATCGC	296876	129072	TGGTCTTGAACTCCTGGACG
207703	39899	TTAAAACCCACATGATAAAC	252290	84486	GCAGCCTGCAGTGAGAATCG	296877	129073	CTGGTCTTGAACTCCTGGAC
207704	39900	ATTAAAACCCACATGATAAA	252291	84487	GGCAGCCTGCAGTGAGAATC	296878	129074	GCTGGTCTTGAACTCCTGGA
207705	39901	AATTAAAACCCACATGATAA	252292	84488	GGGCAGCCTGCAGTGAGAAT	296879	129075	GGCTGGTCTTGAACTCCTGG
207706	39902	AAATTAAAACCCACATGATA	252293	84489	AGGGCAGCCTGCAGTGAGAA	296880	129076	AGGCTGGTCTTGAACTCCTG
207707	39903	TAAATTAAAACCCACATGAT	252294	84490	CAGGGCAGCCTGCAGTGAGA	296881	129077	CAGGCTGGTCTTGAACTCCT
207708	39904	TTAAATTAAAACCCACATGA	252295	84491	ACAGGGCAGCCTGCAGTGAG	296882	129078	CCAGGCTGGTCTTGAACTCC
207709	39905	GTTAAATTAAAACCCACATG	252296	84492	CACAGGGCAGCCTGCAGTGA	296883	129079	CCCAGGCTGGTCTTGAACTC
207710	39906	AGTTAAATTAAAACCCACAT	252297	84493	CCACAGGGCAGCCTGCAGTG	296884	129080	GCCCAGGCTGGTCTTGAACT
207711	39907	AAGTTAAATTAAAACCCACA	252298	84494	GCCACAGGGCAGCCTGCAGT	296885	129081	TGCCCAGGCTGGTCTTGAAC
207712	39908	AAAGTTAAATTAAAACCCAC	252299	84495	AGCCACAGGGCAGCCTGCAG	296886	129082	TTGCCCAGGCTGGTCTTGAA
207713	39909	TAAAGTTAAATTAAAACCCA	252300	84496	CAGCCACAGGGCAGCCTGCA	296887	129083	GTTGCCCAGGCTGGTCTTGA
207714	39910	TTAAAGTTAAATTAAAACCC	252301	84497	TCAGCCACAGGGCAGCCTGC	296888	129084	TGTTGCCCAGGCTGGTCTTG
207715	39911	TTTAAAGTTAAATTAAAACC	252302	84498	ATCAGCCACAGGGCAGCCTG	296889	129085	ATGTTGCCCAGGCTGGTCTT
207716	39912	TTTTAAAGTTAAATTAAAAC	252303	84499	GATCAGCCACAGGGCAGCCT	296890	129086	TATGTTGCCCAGGCTGGTCT
207717	39913	TTTTTAAAGTTAAATTAAAA	252304	84500	GGATCAGCCACAGGGCAGCC	296891	129087	CTATGTTGCCCAGGCTGGTC
207718	39914	TTTTTTAAAGTTAAATTAAA	252305	84501	TGGATCAGCCACAGGGCAGC	296892	129088	GCTATGTTGCCCAGGCTGGT
207719	39915	TTTTTTTAAAGTTAAATTAA	252306	84502	CTGGATCAGCCACAGGGCAG	296893	129089	TGCTATGTTGCCCAGGCTGG
207720	39916	ATTTTTTTAAAGTTAAATTA	252307	84503	CCTGGATCAGCCACAGGGCA	296894	129090	TTGCTATGTTGCCCAGGCTG
207721	39917	CATTTTTTTAAAGTTAAATT	252308	84504	TCCTGGATCAGCCACAGGGC	296895	129091	TTTGCTATGTTGCCCAGGCT
207722	39918	ACATTTTTTTAAAGTTAAAT	252309	84505	CTCCTGGATCAGCCACAGGG	296896	129092	TTTTGCTATGTTGCCCAGGC
207723	39919	AACATTTTTTTAAAGTTAAA	252310	84506	GCTCCTGGATCAGCCACAGG	296897	129093	GTTTTGCTATGTTGCCCAGG
207724	39920	CAACATTTTTTTAAAGTTAA	252311	84507	TGCTCCTGGATCAGCCACAG	296898	129094	GGTTTTGCTATGTTGCCCAG
207725	39921	CCAACATTTTTTTAAAGTTA	252312	84508	TTGCTCCTGGATCAGCCACA	296899	129095	GGGTTTTGCTATGTTGCCCA
207726	39922	GCCAACATTTTTTTAAAGTT	252313	84509	CTTGCTCCTGGATCAGCCAC	296900	129096	GGGGTTTTGCTATGTTGCCC
207727	39923	AGCCAACATTTTTTTAAAGT	252314	84510	CCTTGCTCCTGGATCAGCCA	296901	129097	CGGGGTTTTGCTATGTTGCC
207728	39924	CAGCCAACATTTTTTTAAAG	252315	84511	GCCTTGCTCCTGGATCAGCC	296902	129098	ACGGGGTTTTGCTATGTTGC
207729	39925	CCAGCCAACATTTTTTTAAA	252316	84512	GGCCTTGCTCCTGGATCAGC	296903	129099	AACGGGGTTTTGCTATGTTG
207730	39926	TCCAGCCAACATTTTTTTAA	252317	84513	AGGCCTTGCTCCTGGATCAG	296904	129100	AAACGGGGTTTTGCTATGTT
207731	39927	GTCCAGCCAACATTTTTTTA	252318	84514	AAGGCCTTGCTCCTGGATCA	296905	129101	GAAACGGGGTTTTGCTATGT
207732	39928	TGTCCAGCCAACATTTTTTT	252319	84515	TAAGGCCTTGCTCCTGGATC	296906	129102	AGAAACGGGGTTTTGCTATG
207733	39929	CTGTCCAGCCAACATTTTTT	252320	84516	TTAAGGCCTTGCTCCTGGAT	296907	129103	TAGAAACGGGGTTTTGCTAT
207734	39930	ACTGTCCAGCCAACATTTTT	252321	84517	GTTAAGGCCTTGCTCCTGGA	296908	129104	ATAGAAACGGGGTTTTGCTA
207735	39931	AACTGTCCAGCCAACATTTT	252322	84518	GGTTAAGGCCTTGCTCCTGG	296909	129105	AATAGAAACGGGGTTTTGCT
207736	39932	CAACTGTCCAGCCAACATTT	252323	84519	TGGTTAAGGCCTTGCTCCTG	296910	129106	TAATAGAAACGGGGTTTTGC
207737	39933	GCAACTGTCCAGCCAACATT	252324	84520	ATGGTTAAGGCCTTGCTCCT	296911	129107	TTAATAGAAACGGGGTTTTG
207738	39934	GGCAACTGTCCAGCCAACAT	252325	84521	CATGGTTAAGGCCTTGCTCC	296912	129108	TTTAATAGAAACGGGGTTTT
207739	39935	GGGCAACTGTCCAGCCAACA	252326	84522	ACATGGTTAAGGCCTTGCTC	296913	129109	TTTTAATAGAAACGGGGTTT
207740	39936	TGGGCAACTGTCCAGCCAAC	252327	84523	GACATGGTTAAGGCCTTGCT	296914	129110	TTTTTAATAGAAACGGGGTT
207741	39937	TTGGGCAACTGTCCAGCCAA	252328	84524	TGACATGGTTAAGGCCTTGC	296915	129111	ATTTTTAATAGAAACGGGGT
207742	39938	TTTGGGCAACTGTCCAGCCA	252329	84525	ATGACATGGTTAAGGCCTTG	296916	129112	TATTTTTAATAGAAACGGGG
207743	39939	ATTTGGGCAACTGTCCAGCC	252330	84526	GATGACATGGTTAAGGCCTT	296917	129113	GTATTTTTAATAGAAACGGG
207744	39940	CATTTGGGCAACTGTCCAGC	252331	84527	GGATGACATGGTTAAGGCCT	296918	129114	TGTATTTTTAATAGAAACGG
207745	39941	CCATTTGGGCAACTGTCCAG	252332	84528	GGGATGACATGGTTAAGGCC	296919	129115	TTGTATTTTTAATAGAAACG
207746	39942	ACCATTTGGGCAACTGTCCA	252333	84529	GGGGATGACATGGTTAAGGC	296920	129116	TTTGTATTTTTAATAGAAAC
207747	39943	TACCATTTGGGCAACTGTCC	252334	84530	TGGGGATGACATGGTTAAGG	296921	129117	TTTTGTATTTTTAATAGAAA
207748	39944	ATACCATTTGGGCAACTGTC	252335	84531	TTGGGGATGACATGGTTAAG	296922	129118	TTTTTGTATTTTTAATAGAA
207749	39945	GATACCATTTGGGCAACTGT	252336	84532	CTTGGGGATGACATGGTTAA	296923	129119	TTTTTTGTATTTTTAATAGA
207750	39946	TGATACCATTTGGGCAACTG	252337	84533	GCTTGGGGATGACATGGTTA	296924	129120	ATTTTTTGTATTTTTAATAG
207751	39947	ATGATACCATTTGGGCAACT	252338	84534	CGCTTGGGGATGACATGGTT	296925	129121	AATTTTTTGTATTTTTAATA
207752	39948	GATGATACCATTTGGGCAAC	252339	84535	TCGCTTGGGGATGACATGGT	296926	129122	TAATTTTTTGTATTTTTAAT
207753	39949	TGATGATACCATTTGGGCAA	252340	84536	ATCGCTTGGGGATGACATGG	296927	129123	CTAATTTTTTGTATTTTTAA
207754	39950	CTGATGATACCATTTGGGCA	252341	84537	AATCGCTTGGGGATGACATG	296928	129124	GCTAATTTTTTGTATTTTTA
207755	39951	GCTGATGATACCATTTGGGC	252342	84538	CAATCGCTTGGGGATGACAT	296929	129125	GGCTAATTTTTTGTATTTTT
207756	39952	GGCTGATGATACCATTTGGG	252343	84539	GCAATCGCTTGGGGATGACA	296930	129126	TGGCTAATTTTTTGTATTTT
207757	39953	TGGCTGATGATACCATTTGG	252344	84540	AGCAATCGCTTGGGGATGAC	296931	129127	CTGGCTAATTTTTTGTATTT
207758	39954	ATGGCTGATGATACCATTTG	252345	84541	AAGCAATCGCTTGGGGATGA	296932	129128	CCTGGCTAATTTTTTGTATT
207759	39955	AATGGCTGATGATACCATTT	252346	84542	CAAGCAATCGCTTGGGGATG	296933	129129	ACCTGGCTAATTTTTTGTAT
207760	39956	AAATGGCTGATGATACCATT	252347	84543	ACAAGCAATCGCTTGGGGAT	296934	129130	CACCTGGCTAATTTTTTGTA
207761	39957	CAAATGGCTGATGATACCAT	252348	84544	TACAAGCAATCGCTTGGGGA	296935	129131	ACACCTGGCTAATTTTTTGT
207762	39958	CCAAATGGCTGATGATACCA	252349	84545	TTACAAGCAATCGCTTGGGG	296936	129132	CACACCTGGCTAATTTTTTG

207763	39959	ACCAAATGGCTGATGATACC	252350	84546	TTTACAAGCAATCGCTTGGG	296937	129133	CCACACCTGGCTAATTTTTT
207764	39960	AACCAAATGGCTGATGATAC	252351	84547	GTTTACAAGCAATCGCTTGG	296938	129134	ACCACACCTGGCTAATTTTT
207765	39961	CAACCAAATGGCTGATGATA	252352	84548	AGTTTACAAGCAATCGCTTG	296939	129135	CACCACACCTGGCTAATTTT
207766	39962	TCAACCAAATGGCTGATGAT	252353	84549	AAGTTTACAAGCAATCGCTT	296940	129136	CCACCACACCTGGCTAATTT
207767	39963	CTCAACCAAATGGCTGATGA	252354	84550	AAAGTTTACAAGCAATCGCT	296941	129137	GCCACCACACCTGGCTAATT
207768	39964	TCTCAACCAAATGGCTGATG	252355	84551	GAAAGTTTACAAGCAATCGC	296942	129138	TGCCACCACACCTGGCTAAT
207769	39965	TTCTCAACCAAATGGCTGAT	252356	84552	AGAAAGTTTACAAGCAATCG	296943	129139	ATGCCACCACACCTGGCTAA
207770	39966	GTTCTCAACCAAATGGCTGA	252357	84553	AAGAAAGTTTACAAGCAATC	296944	129140	CATGCCACCACACCTGGCTA
207771	39967	CGTTCTCAACCAAATGGCTG	252358	84554	GAAGAAAGTTTACAAGCAAT	296945	129141	GCATGCCACCACACCTGGCT
207772	39968	ACGTTCTCAACCAAATGGCT	252359	84555	AGAAGAAAGTTTACAAGCAA	296946	129142	TGCATGCCACCACACCTGGC
207773	39969	TACGTTCTCAACCAAATGGC	252360	84556	CAGAAGAAAGTTTACAAGCA	296947	129143	GTGCATGCCACCACACCTGG
207774	39970	ATACGTTCTCAACCAAATGG	252361	84557	ACAGAAGAAAGTTTACAAGC	296948	129144	GGTGCATGCCACCACACCTG
207775	39971	CATACGTTCTCAACCAAATG	252362	84558	CACAGAAGAAAGTTTACAAG	296949	129145	AGGTGCATGCCACCACACCT
207776	39972	ACATACGTTCTCAACCAAAT	252363	84559	GCACAGAAGAAAGTTTACAA	296950	129146	CAGGTGCATGCCACCACACC
207777	39973	GACATACGTTCTCAACCAAA	252364	84560	TGCACAGAAGAAAGTTTACA	296951	129147	ACAGGTGCATGCCACCACAC
207778	39974	GGACATACGTTCTCAACCAA	252365	84561	CTGCACAGAAGAAAGTTTAC	296952	129148	TACAGGTGCATGCCACCACA
207779	39975	AGGACATACGTTCTCAACCA	252366	84562	GCTGCACAGAAGAAAGTTTA	296953	129149	TTACAGGTGCATGCCACCAC
207780	39976	CAGGACATACGTTCTCAACC	252367	84563	GGCTGCACAGAAGAAAGTTT	296954	129150	ATTACAGGTGCATGCCACCA
207781	39977	GCAGGACATACGTTCTCAAC	252368	84564	AGGCTGCACAGAAGAAAGTT	296955	129151	GATTACAGGTGCATGCCACC
207782	39978	CGCAGGACATACGTTCTCAA	252369	84565	AAGGCTGCACAGAAGAAAGT	296956	129152	GGATTACAGGTGCATGCCAC
207783	39979	CCGCAGGACATACGTTCTCA	252370	84566	GAAGGCTGCACAGAAGAAAG	296957	129153	GGGATTACAGGTGCATGCCA
207784	39980	CCCGCAGGACATACGTTCTC	252371	84567	TGAAGGCTGCACAGAAGAAA	296958	129154	TGGGATTACAGGTGCATGCC
207785	39981	GCCCGCAGGACATACGTTCT	252372	84568	TTGAAGGCTGCACAGAAGAA	296959	129155	CTGGGATTACAGGTGCATGC
207786	39982	AGCCCGCAGGACATACGTTC	252373	84569	GTTGAAGGCTGCACAGAAGA	296960	129156	GCTGGGATTACAGGTGCATG
207787	39983	GAGCCCGCAGGACATACGTT	252374	84570	GGTTGAAGGCTGCACAGAAG	296961	129157	AGCTGGGATTACAGGTGCAT
207788	39984	GGAGCCCGCAGGACATACGT	252375	84571	GGGTTGAAGGCTGCACAGAA	296962	129158	TAGCTGGGATTACAGGTGCA
207789	39985	AGGAGCCCGCAGGACATACG	252376	84572	AGGGTTGAAGGCTGCACAGA	296963	129159	GTAGCTGGGATTACAGGTGC
207790	39986	GAGGAGCCCGCAGGACATAC	252377	84573	AAGGGTTGAAGGCTGCACAG	296964	129160	AGTAGCTGGGATTACAGGTG
207791	39987	AGAGGAGCCCGCAGGACATA	252378	84574	TAAGGGTTGAAGGCTGCACA	296965	129161	GAGTAGCTGGGATTACAGGT
207792	39988	CAGAGGAGCCCGCAGGACAT	252379	84575	ATAAGGGTTGAAGGCTGCAC	296966	129162	CGAGTAGCTGGGATTACAGG
207793	39989	ACAGAGGAGCCCGCAGGACA	252380	84576	AATAAGGGTTGAAGGCTGCA	296967	129163	CCGAGTAGCTGGGATTACAG
207794	39990	GACAGAGGAGCCCGCAGGAC	252381	84577	TAATAAGGGTTGAAGGCTGC	296968	129164	CCCGAGTAGCTGGGATTACA
207795	39991	TGACAGAGGAGCCCGCAGGA	252382	84578	ATAATAAGGGTTGAAGGCTG	296969	129165	TCCCGAGTAGCTGGGATTAC
207796	39992	GTGACAGAGGAGCCCGCAGG	252383	84579	CATAATAAGGGTTGAAGGCT	296970	129166	CTCCCGAGTAGCTGGGATTA
207797	39993	AGTGACAGAGGAGCCCGCAG	252384	84580	TCATAATAAGGGTTGAAGGC	296971	129167	CCTCCCGAGTAGCTGGGATT
207798	39994	CAGTGACAGAGGAGCCCGCA	252385	84581	ATCATAATAAGGGTTGAAGG	296972	129168	GCCTCCCGAGTAGCTGGGAT
207799	39995	CCAGTGACAGAGGAGCCCGC	252386	84582	AATCATAATAAGGGTTGAAG	296973	129169	AGCCTCCCGAGTAGCTGGGA
207800	39996	TCCAGTGACAGAGGAGCCCG	252387	84583	AAATCATAATAAGGGTTGAA	296974	129170	CAGCCTCCCGAGTAGCTGGG
207801	39997	CTCCAGTGACAGAGGAGCCC	252388	84584	AAAATCATAATAAGGGTTGA	296975	129171	TCAGCCTCCCGAGTAGCTGG
207802	39998	ACTCCAGTGACAGAGGAGCC	252389	84585	GAAAATCATAATAAGGGTTG	296976	129172	CTCAGCCTCCCGAGTAGCTG
207803	39999	AACTCCAGTGACAGAGGAGC	252390	84586	AGAAAATCATAATAAGGGTT	296977	129173	CCTCAGCCTCCCGAGTAGCT
207804	40000	AAACTCCAGTGACAGAGGAG	252391	84587	AAGAAAATCATAATAAGGGT	296978	129174	ACCTCAGCCTCCCGAGTAGC
207805	40001	AAAACTCCAGTGACAGAGGA	252392	84588	GAAGAAAATCATAATAAGGG	296979	129175	CACCTCAGCCTCCCGAGTAG
207806	40002	CAAAACTCCAGTGACAGAGG	252393	84589	AGAAGAAAATCATAATAAGG	296980	129176	CCACCTCAGCCTCCCGAGTA
207807	40003	GCAAAACTCCAGTGACAGAG	252394	84590	GAGAAGAAAATCATAATAAG	296981	129177	CCCACCTCAGCCTCCCGAGT
207808	40004	AGCAAAACTCCAGTGACAGA	252395	84591	TGAGAAGAAAATCATAATAA	296982	129178	TCCCACCTCAGCCTCCCGAG
207809	40005	TAGCAAAACTCCAGTGACAG	252396	84592	CTGAGAAGAAAATCATAATA	296983	129179	CTCCCACCTCAGCCTCCCGA
207810	40006	CTAGCAAAACTCCAGTGACA	252397	84593	CCTGAGAAGAAAATCATAAT	296984	129180	TCTCCCACCTCAGCCTCCCG
207811	40007	GCTAGCAAAACTCCAGTGAC	252398	84594	TCCTGAGAAGAAAATCATAA	296985	129181	TTCTCCCACCTCAGCCTCCC
207812	40008	AGCTAGCAAAACTCCAGTGA	252399	84595	TTCCTGAGAAGAAAATCATA	296986	129182	ATTCTCCCACCTCAGCCTCC
207813	40009	CAGCTAGCAAAACTCCAGTG	252400	84596	GTTCCTGAGAAGAAAATCAT	296987	129183	GATTCTCCCACCTCAGCCTC
207814	40010	TCAGCTAGCAAAACTCCAGT	252401	84597	GGTTCCTGAGAAGAAAATCA	296988	129184	TGATTCTCCCACCTCAGCCT
207815	40011	GTCAGCTAGCAAAACTCCAG	252402	84598	TGGTTCCTGAGAAGAAAATC	296989	129185	GTGATTCTCCCACCTCAGCC
207816	40012	TGTCAGCTAGCAAAACTCCA	252403	84599	TTGGTTCCTGAGAAGAAAAT	296990	129186	GGTGATTCTCCCACCTCAGC
207817	40013	CTGTCAGCTAGCAAAACTCC	252404	84600	TTTGGTTCCTGAGAAGAAAA	296991	129187	AGGTGATTCTCCCACCTCAG
207818	40014	GCTGTCAGCTAGCAAAACTC	252405	84601	GTTTGGTTCCTGAGAAGAAA	296992	129188	CAGGTGATTCTCCCACCTCA
207819	40015	GGCTGTCAGCTAGCAAAACT	252406	84602	AGTTTGGTTCCTGAGAAGAA	296993	129189	TCAGGTGATTCTCCCACCTC
207820	40016	TGGCTGTCAGCTAGCAAAAC	252407	84603	CAGTTTGGTTCCTGAGAAGA	296994	129190	CTCAGGTGATTCTCCCACCT
207821	40017	GTGGCTGTCAGCTAGCAAAA	252408	84604	GCAGTTTGGTTCCTGAGAAG	296995	129191	GCTCAGGTGATTCTCCCACC
207822	40018	AGTGGCTGTCAGCTAGCAAA	252409	84605	AGCAGTTTGGTTCCTGAGAA	296996	129192	GGCTCAGGTGATTCTCCCAC
207823	40019	CAGTGGCTGTCAGCTAGCAA	252410	84606	CAGCAGTTTGGTTCCTGAGA	296997	129193	AGGCTCAGGTGATTCTCCCA
207824	40020	CCAGTGGCTGTCAGCTAGCA	252411	84607	ACAGCAGTTTGGTTCCTGAG	296998	129194	CAGGCTCAGGTGATTCTCCC
207825	40021	GCCAGTGGCTGTCAGCTAGC	252412	84608	TACAGCAGTTTGGTTCCTGA	296999	129195	CCAGGCTCAGGTGATTCTCC
207826	40022	AGCCAGTGGCTGTCAGCTAG	252413	84609	ATACAGCAGTTTGGTTCCTG	297000	129196	CCCAGGCTCAGGTGATTCTC
207827	40023	TAGCCAGTGGCTGTCAGCTA	252414	84610	AATACAGCAGTTTGGTTCCT	297001	129197	TCCCAGGCTCAGGTGATTCT
207828	40024	CTAGCCAGTGGCTGTCAGCT	252415	84611	GAATACAGCAGTTTGGTTCC	297002	129198	CTCCCAGGCTCAGGTGATTC
207829	40025	ACTAGCCAGTGGCTGTCAGC	252416	84612	TGAATACAGCAGTTTGGTTC	297003	129199	CCTCCCAGGCTCAGGTGATT
207830	40026	AACTAGCCAGTGGCTGTCAG	252417	84613	TTGAATACAGCAGTTTGGTT	297004	129200	ACCTCCCAGGCTCAGGTGAT
207831	40027	TAACTAGCCAGTGGCTGTCA	252418	84614	CTTGAATACAGCAGTTTGGT	297005	129201	GACCTCCCAGGCTCAGGTGA
207832	40028	CTAACTAGCCAGTGGCTGTC	252419	84615	TCTTGAATACAGCAGTTTGG	297006	129202	TGACCTCCCAGGCTCAGGTG
207833	40029	TCTAACTAGCCAGTGGCTGT	252420	84616	TTCTTGAATACAGCAGTTTG	297007	129203	TTGACCTCCCAGGCTCAGGT
207834	40030	CTCTAACTAGCCAGTGGCTG	252421	84617	TTTCTTGAATACAGCAGTTT	297008	129204	CTTGACCTCCCAGGCTCAGG

207835	40031	TCTCTAACTAGCCAGTGGCT	252422	84618	CTTTCTTGAATACAGCAGTT	297009	129205	CCTTGACCTCCCAGGCTCAG
207836	40032	GTCTCTAACTAGCCAGTGGC	252423	84619	CCTTTCTTGAATACAGCAGT	297010	129206	GCCTTGACCTCCCAGGCTCA
207837	40033	AGTCTCTAACTAGCCAGTGG	252424	84620	GCCTTTCTTGAATACAGCAG	297011	129207	AGCCTTGACCTCCCAGGCTC
207838	40034	CAGTCTCTAACTAGCCAGTG	252425	84621	TGCCTTTCTTGAATACAGCA	297012	129208	CAGCCTTGACCTCCCAGGCT
207839	40035	GCAGTCTCTAACTAGCCAGT	252426	84622	CTGCCTTTCTTGAATACAGC	297013	129209	GCAGCCTTGACCTCCCAGGC
207840	40036	TGCAGTCTCTAACTAGCCAG	252427	84623	GCTGCCTTTCTTGAATACAG	297014	129210	TGCAGCCTTGACCTCCCAGG
207841	40037	CTGCAGTCTCTAACTAGCCA	252428	84624	AGCTGCCTTTCTTGAATACA	297015	129211	CTGCAGCCTTGACCTCCCAG
207842	40038	ACTGCAGTCTCTAACTAGCC	252429	84625	AAGCTGCCTTTCTTGAATAC	297016	129212	ACTGCAGCCTTGACCTCCCA
207843	40039	GACTGCAGTCTCTAACTAGC	252430	84626	AAAGCTGCCTTTCTTGAATA	297017	129213	CACTGCAGCCTTGACCTCCC
207844	40040	TGACTGCAGTCTCTAACTAG	252431	84627	CAAAGCTGCCTTTCTTGAAT	297018	129214	TCACTGCAGCCTTGACCTCC
207845	40041	CTGACTGCAGTCTCTAACTA	252432	84628	ACAAAGCTGCCTTTCTTGAA	297019	129215	CTCACTGCAGCCTTGACCTC
207846	40042	GCTGACTGCAGTCTCTAACT	252433	84629	CACAAAGCTGCCTTTCTTGA	297020	129216	CCTCACTGCAGCCTTGACCT
207847	40043	TGCTGACTGCAGTCTCTAAC	252434	84630	ACACAAAGCTGCCTTTCTTG	297021	129217	ACCTCACTGCAGCCTTGACC
207848	40044	GTGCTGACTGCAGTCTCTAA	252435	84631	TACACAAAGCTGCCTTTCTT	297022	129218	CACCTCACTGCAGCCTTGAC
207849	40045	TGTGCTGACTGCAGTCTCTA	252436	84632	TTACACAAAGCTGCCTTTCT	297023	129219	TCACCTCACTGCAGCCTTGA
207850	40046	CTGTGCTGACTGCAGTCTCT	252437	84633	ATTACACAAAGCTGCCTTTC	297024	129220	CTCACCTCACTGCAGCCTTG
207851	40047	TCTGTGCTGACTGCAGTCTC	252438	84634	GATTACACAAAGCTGCCTTT	297025	129221	TCTCACCTCACTGCAGCCTT
207852	40048	ATCTGTGCTGACTGCAGTCT	252439	84635	TGATTACACAAAGCTGCCTT	297026	129222	ATCTCACCTCACTGCAGCCT
207853	40049	CATCTGTGCTGACTGCAGTC	252440	84636	ATGATTACACAAAGCTGCCT	297027	129223	AATCTCACCTCACTGCAGCC
207854	40050	GCATCTGTGCTGACTGCAGT	252441	84637	AATGATTACACAAAGCTGCC	297028	129224	CAATCTCACCTCACTGCAGC
207855	40051	TGCATCTGTGCTGACTGCAG	252442	84638	AAATGATTACACAAAGCTGC	297029	129225	ACAATCTCACCTCACTGCAG
207856	40052	CTGCATCTGTGCTGACTGCA	252443	84639	TAAATGATTACACAAAGCTG	297030	129226	CACAATCTCACCTCACTGCA
207857	40053	CCTGCATCTGTGCTGACTGC	252444	84640	ATAAATGATTACACAAAGCT	297031	129227	GCACAATCTCACCTCACTGC
207858	40054	GCCTGCATCTGTGCTGACTG	252445	84641	GATAAATGATTACACAAAGC	297032	129228	GGCACAATCTCACCTCACTG
207859	40055	CGCCTGCATCTGTGCTGACT	252446	84642	TGATAAATGATTACACAAAG	297033	129229	TGGCACAATCTCACCTCACT
207860	40056	ACGCCTGCATCTGTGCTGAC	252447	84643	ATGATAAATGATTACACAAA	297034	129230	GTGGCACAATCTCACCTCAC
207861	40057	CACGCCTGCATCTGTGCTGA	252448	84644	TATGATAAATGATTACACAA	297035	129231	GGTGGCACAATCTCACCTCA
207862	40058	CCACGCCTGCATCTGTGCTG	252449	84645	TTATGATAAATGATTACACA	297036	129232	CGGTGGCACAATCTCACCTC
207863	40059	TCCACGCCTGCATCTGTGCT	252450	84646	TTTATGATAAATGATTACAC	297037	129233	GCGGTGGCACAATCTCACCT
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207865	40061	AGTCCACGCCTGCATCTGTG	252452	84648	TATTTATGATAAATGATTAC	297039	129235	GTGCGGTGGCACAATCTCAC
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207867	40063	CAAGTCCACGCCTGCATCTG	252454	84650	GATATTTATGATAAATGATT	297041	129237	GAGTGCGGTGGCACAATCTC
207868	40064	GCAAGTCCACGCCTGCATCT	252455	84651	AGATATTTATGATAAATGAT	297042	129238	AGAGTGCGGTGGCACAATCT
207869	40065	CGCAAGTCCACGCCTGCATC	252456	84652	AAGATATTTATGATAAATGA	297043	129239	TAGAGTGCGGTGGCACAATC
207870	40066	GCGCAAGTCCACGCCTGCAT	252457	84653	TAAGATATTTATGATAAATG	297044	129240	CTAGAGTGCGGTGGCACAAT
207871	40067	TGCGCAAGTCCACGCCTGCA	252458	84654	TTAAGATATTTATGATAAAT	297045	129241	GCTAGAGTGCGGTGGCACAA
207872	40068	GTGCGCAAGTCCACGCCTGC	252459	84655	CTTAAGATATTTATGATAAA	297046	129242	GGCTAGAGTGCGGTGGCACA
207873	40069	CGTGCGCAAGTCCACGCCTG	252460	84656	TCTTAAGATATTTATGATAA	297047	129243	AGGCTAGAGTGCGGTGGCAC
207874	40070	ACGTGCGCAAGTCCACGCCT	252461	84657	TTCTTAAGATATTTATGATA	297048	129244	CAGGCTAGAGTGCGGTGGCA
207875	40071	TACGTGCGCAAGTCCACGCC	252462	84658	TTTCTTAAGATATTTATGAT	297049	129245	CCAGGCTAGAGTGCGGTGGC
207876	40072	TTACGTGCGCAAGTCCACGC	252463	84659	TTTTCTTAAGATATTTATGA	297050	129246	CCCAGGCTAGAGTGCGGTGG
207877	40073	GTTACGTGCGCAAGTCCACG	252464	84660	TTTTTCTTAAGATATTTATG	297051	129247	GCCCAGGCTAGAGTGCGGTG
207878	40074	GGTTACGTGCGCAAGTCCAC	252465	84661	ATTTTTCTTAAGATATTTAT	297052	129248	CGCCCAGGCTAGAGTGCGGT
207879	40075	TGGTTACGTGCGCAAGTCCA	252466	84662	GATTTTTCTTAAGATATTTA	297053	129249	TCGCCCAGGCTAGAGTGCGG
207880	40076	ATGGTTACGTGCGCAAGTCC	252467	84663	GGATTTTTCTTAAGATATTT	297054	129250	ATCGCCCAGGCTAGAGTGCG
207881	40077	CATGGTTACGTGCGCAAGTC	252468	84664	AGGATTTTTCTTAAGATATT	297055	129251	TATCGCCCAGGCTAGAGTGC
207882	40078	ACATGGTTACGTGCGCAAGT	252469	84665	TAGGATTTTTCTTAAGATAT	297056	129252	CTATCGCCCAGGCTAGAGTG
207883	40079	GACATGGTTACGTGCGCAAG	252470	84666	CTAGGATTTTTCTTAAGATA	297057	129253	TCTATCGCCCAGGCTAGAGT
207884	40080	TGACATGGTTACGTGCGCAA	252471	84667	TCTAGGATTTTTCTTAAGAT	297058	129254	CTCTATCGCCCAGGCTAGAG
207885	40081	TTGACATGGTTACGTGCGCA	252472	84668	CTCTAGGATTTTTCTTAAGA	297059	129255	GCTCTATCGCCCAGGCTAGA
207886	40082	ATTGACATGGTTACGTGCGC	252473	84669	TCTCTAGGATTTTTCTTAAG	297060	129256	TGCTCTATCGCCCAGGCTAG
207887	40083	CATTGACATGGTTACGTGCG	252474	84670	ATCTCTAGGATTTTTCTTAA	297061	129257	TTGCTCTATCGCCCAGGCTA
207888	40084	GCATTGACATGGTTACGTGC	252475	84671	AATCTCTAGGATTTTTCTTA	297062	129258	CTTGCTCTATCGCCCAGGCT
207889	40085	TGCATTGACATGGTTACGTG	252476	84672	GAATCTCTAGGATTTTTCTT	297063	129259	TCTTGCTCTATCGCCCAGGC
207890	40086	TTGCATTGACATGGTTACGT	252477	84673	GGAATCTCTAGGATTTTTCT	297064	129260	GTCTTGCTCTATCGCCCAGG
207891	40087	TTTGCATTGACATGGTTACG	252478	84674	AGGAATCTCTAGGATTTTTC	297065	129261	GGTCTTGCTCTATCGCCCAG
207892	40088	CTTTGCATTGACATGGTTAC	252479	84675	TAGGAATCTCTAGGATTTTT	297066	129262	GGGTCTTGCTCTATCGCCCA
207893	40089	GCTTTGCATTGACATGGTTA	252480	84676	TTAGGAATCTCTAGGATTTT	297067	129263	AGGGTCTTGCTCTATCGCCC
207894	40090	GGCTTTGCATTGACATGGTT	252481	84677	ATTAGGAATCTCTAGGATTT	297068	129264	CAGGGTCTTGCTCTATCGCC
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207896	40092	ATGGCTTTGCATTGACATGG	252483	84679	AAATTAGGAATCTCTAGGAT	297070	129266	GACAGGGTCTTGCTCTATCG
207897	40093	GATGGCTTTGCATTGACATG	252484	84680	AAAATTAGGAATCTCTAGGA	297071	129267	AGACAGGGTCTTGCTCTATC
207898	40094	TGATGGCTTTGCATTGACAT	252485	84681	TAAAATTAGGAATCTCTAGG	297072	129268	GAGACAGGGTCTTGCTCTAT
207899	40095	GTGATGGCTTTGCATTGACA	252486	84682	CTAAAATTAGGAATCTCTAG	297073	129269	TGAGACAGGGTCTTGCTCTA
207900	40096	AGTGATGGCTTTGCATTGAC	252487	84683	CCTAAAATTAGGAATCTCTA	297074	129270	TTGAGACAGGGTCTTGCTCT
207901	40097	AAGTGATGGCTTTGCATTGA	252488	84684	TCCTAAAATTAGGAATCTCT	297075	129271	TTTGAGACAGGGTCTTGCTC
207902	40098	GAAGTGATGGCTTTGCATTG	252489	84685	TTCCTAAAATTAGGAATCTC	297076	129272	TTTTGAGACAGGGTCTTGCT
207903	40099	AGAAGTGATGGCTTTGCATT	252490	84686	TTTCCTAAAATTAGGAATCT	297077	129273	TTTTTGAGACAGGGTCTTGC
207904	40100	AAGAAGTGATGGCTTTGCAT	252491	84687	ATTTCCTAAAATTAGGAATC	297078	129274	GTTTTTGAGACAGGGTCTTG
207905	40101	TAAGAAGTGATGGCTTTGCA	252492	84688	CATTTCCTAAAATTAGGAAT	297079	129275	TGTTTTTGAGACAGGGTCTT
207906	40102	TTAAGAAGTGATGGCTTTGC	252493	84689	CCATTTCCTAAAATTAGGAA	297080	129276	TTGTTTTTGAGACAGGGTCT

207907	40103	TTTAAGAAGTGATGGCTTTG	252494	84690	CCCATTTCCTAAAATTAGGA	297081	129277	TTTGTTTTTGAGACAGGGTC
207908	40104	TTTTAAGAAGTGATGGCTTT	252495	84691	TCCCATTTCCTAAAATTAGG	297082	129278	GTTTGTTTTTGAGACAGGGT
207909	40105	TTTTTAAGAAGTGATGGCTT	252496	84692	CTCCCATTTCCTAAAATTAG	297083	129279	TGTTTGTTTTTGAGACAGGG
207910	40106	ATTTTTAAGAAGTGATGGCT	252497	84693	TCTCCCATTTCCTAAAATTA	297084	129280	TTGTTTGTTTTTGAGACAGG
207911	40107	AATTTTTAAGAAGTGATGGC	252498	84694	GTCTCCCATTTCCTAAAATT	297085	129281	TTTGTTTGTTTTTGAGACAG
207912	40108	GAATTTTTAAGAAGTGATGG	252499	84695	GGTCTCCCATTTCCTAAAAT	297086	129282	TTTTGTTTGTTTTTGAGACA
207913	40109	AGAATTTTTAAGAAGTGATG	252500	84696	AGGTCTCCCATTTCCTAAAA	297087	129283	TTTTTGTTTGTTTTTGAGAC
207914	40110	CAGAATTTTTAAGAAGTGAT	252501	84697	TAGGTCTCCCATTTCCTAAA	297088	129284	TTTTTTGTTTGTTTTTGAGA
207915	40111	TCAGAATTTTTAAGAAGTGA	252502	84698	ATAGGTCTCCCATTTCCTAA	297089	129285	GTTTTTTGTTTGTTTTTGAG
207916	40112	TTCAGAATTTTTAAGAAGTG	252503	84699	CATAGGTCTCCCATTTCCTA	297090	129286	TGTTTTTTGTTTGTTTTTGA
207917	40113	GTTCAGAATTTTTAAGAAGT	252504	84700	CCATAGGTCTCCCATTTCCT	297091	129287	CTGTTTTTTGTTTGTTTTTG
207918	40114	GGTTCAGAATTTTTAAGAAG	252505	84701	ACCATAGGTCTCCCATTTCC	297092	129288	ACTGTTTTTTGTTTGTTTTT
207919	40115	GGGTTCAGAATTTTTAAGAA	252506	84702	TACCATAGGTCTCCCATTTC	297093	129289	GACTGTTTTTTGTTTGTTTT
207920	40116	AGGGTTCAGAATTTTTAAGA	252507	84703	GTACCATAGGTCTCCCATTT	297094	129290	GGACTGTTTTTTGTTTGTTT
207921	40117	CAGGGTTCAGAATTTTTAAG	252508	84704	AGTACCATAGGTCTCCCATT	297095	129291	GGGACTGTTTTTTGTTTGTT
207922	40118	GCAGGGTTCAGAATTTTTAA	252509	84705	CAGTACCATAGGTCTCCCAT	297096	129292	AGGGACTGTTTTTTGTTTGT
207923	40119	AGCAGGGTTCAGAATTTTTA	252510	84706	TCAGTACCATAGGTCTCCCA	297097	129293	CAGGGACTGTTTTTTGTTTG
207924	40120	CAGCAGGGTTCAGAATTTTT	252511	84707	ATCAGTACCATAGGTCTCCC	297098	129294	CCAGGGACTGTTTTTTGTTT
207925	40121	ACAGCAGGGTTCAGAATTTT	252512	84708	TATCAGTACCATAGGTCTCC	297099	129295	GCCAGGGACTGTTTTTTGTT
207926	40122	GACAGCAGGGTTCAGAATTT	252513	84709	ATATCAGTACCATAGGTCTC	297100	129296	TGCCAGGGACTGTTTTTTGT
207927	40123	AGACAGCAGGGTTCAGAATT	252514	84710	TATATCAGTACCATAGGTCT	297101	129297	GTGCCAGGGACTGTTTTTTG
207928	40124	CAGACAGCAGGGTTCAGAAT	252515	84711	TTATATCAGTACCATAGGTC	297102	129298	AGTGCCAGGGACTGTTTTTT
207929	40125	TCAGACAGCAGGGTTCAGAA	252516	84712	ATTATATCAGTACCATAGGT	297103	129299	GAGTGCCAGGGACTGTTTTT
207930	40126	CTCAGACAGCAGGGTTCAGA	252517	84713	CATTATATCAGTACCATAGG	297104	129300	AGAGTGCCAGGGACTGTTTT
207931	40127	TCTCAGACAGCAGGGTTCAG	252518	84714	ACATTATATCAGTACCATAG	297105	129301	CAGAGTGCCAGGGACTGTTT
207932	40128	ATCTCAGACAGCAGGGTTCA	252519	84715	CACATTATATCAGTACCATA	297106	129302	CCAGAGTGCCAGGGACTGTT
207933	40129	CATCTCAGACAGCAGGGTTC	252520	84716	CCACATTATATCAGTACCAT	297107	129303	CCCAGAGTGCCAGGGACTGT
207934	40130	CCATCTCAGACAGCAGGGTT	252521	84717	CCCACATTATATCAGTACCA	297108	129304	GCCCAGAGTGCCAGGGACTG
207935	40131	ACCATCTCAGACAGCAGGGT	252522	84718	GCCCACATTATATCAGTACC	297109	129305	GGCCCAGAGTGCCAGGGACT
207936	40132	CACCATCTCAGACAGCAGGG	252523	84719	AGCCCACATTATATCAGTAC	297110	129306	TGGCCCAGAGTGCCAGGGAC
207937	40133	CCACCATCTCAGACAGCAGG	252524	84720	CAGCCCACATTATATCAGTA	297111	129307	CTGGCCCAGAGTGCCAGGGA
207938	40134	ACCACCATCTCAGACAGCAG	252525	84721	CCAGCCCACATTATATCAGT	297112	129308	CCTGGCCCAGAGTGCCAGGG
207939	40135	CACCACCATCTCAGACAGCA	252526	84722	CCCAGCCCACATTATATCAG	297113	129309	GCCTGGCCCAGAGTGCCAGG
207940	40136	GCACCACCATCTCAGACAGC	252527	84723	GCCCAGCCCACATTATATCA	297114	129310	GGCCTGGCCCAGAGTGCCAG
207941	40137	TGCACCACCATCTCAGACAG	252528	84724	AGCCCAGCCCACATTATATC	297115	129311	AGGCCTGGCCCAGAGTGCCA
207942	40138	CTGCACCACCATCTCAGACA	252529	84725	AAGCCCAGCCCACATTATAT	297116	129312	CAGGCCTGGCCCAGAGTGCC
207943	40139	GCTGCACCACCATCTCAGAC	252530	84726	CAAGCCCAGCCCACATTATA	297117	129313	CCAGGCCTGGCCCAGAGTGC
207944	40140	CGCTGCACCACCATCTCAGA	252531	84727	ACAAGCCCAGCCCACATTAT	297118	129314	GCCAGGCCTGGCCCAGAGTG
207945	40141	CCGCTGCACCACCATCTCAG	252532	84728	AACAAGCCCAGCCCACATTA	297119	129315	TGCCAGGCCTGGCCCAGAGT
207946	40142	TCCGCTGCACCACCATCTCA	252533	84729	AAACAAGCCCAGCCCACATT	297120	129316	CTGCCAGGCCTGGCCCAGAG
207947	40143	ATCCGCTGCACCACCATCTC	252534	84730	AAAACAAGCCCAGCCCACAT	297121	129317	CCTGCCAGGCCTGGCCCAGA
207948	40144	TATCCGCTGCACCACCATCT	252535	84731	GAAAACAAGCCCAGCCCACA	297122	129318	CCCTGCCAGGCCTGGCCCAG
207949	40145	CTATCCGCTGCACCACCATC	252536	84732	AGAAAACAAGCCCAGCCCAC	297123	129319	GCCCTGCCAGGCCTGGCCCA
207950	40146	TCTATCCGCTGCACCACCAT	252537	84733	CAGAAAACAAGCCCAGCCCA	297124	129320	TGCCCTGCCAGGCCTGGCCC
207951	40147	TTCTATCCGCTGCACCACCA	252538	84734	ACAGAAAACAAGCCCAGCCC	297125	129321	CTGCCCTGCCAGGCCTGGCC
207952	40148	GTTCTATCCGCTGCACCACC	252539	84735	GACAGAAAACAAGCCCAGCC	297126	129322	ACTGCCCTGCCAGGCCTGGC
207953	40149	AGTTCTATCCGCTGCACCAC	252540	84736	TGACAGAAAACAAGCCCAGC	297127	129323	AACTGCCCTGCCAGGCCTGG
207954	40150	GAGTTCTATCCGCTGCACCA	252541	84737	ATGACAGAAAACAAGCCCAG	297128	129324	CAACTGCCCTGCCAGGCCTG
207955	40151	AGAGTTCTATCCGCTGCACC	252542	84738	AATGACAGAAAACAAGCCCA	297129	129325	CCAACTGCCCTGCCAGGCCT
207956	40152	CAGAGTTCTATCCGCTGCAC	252543	84739	AAATGACAGAAAACAAGCCC	297130	129326	GCCAACTGCCCTGCCAGGCC
207957	40153	GCAGAGTTCTATCCGCTGCA	252544	84740	CAAATGACAGAAAACAAGCC	297131	129327	TGCCAACTGCCCTGCCAGGC
207958	40154	AGCAGAGTTCTATCCGCTGC	252545	84741	GCAAATGACAGAAAACAAGC	297132	129328	CTGCCAACTGCCCTGCCAGG
207959	40155	GAGCAGAGTTCTATCCGCTG	252546	84742	AGCAAATGACAGAAAACAAG	297133	129329	CCTGCCAACTGCCCTGCCAG
207960	40156	AGAGCAGAGTTCTATCCGCT	252547	84743	TAGCAAATGACAGAAAACAA	297134	129330	CCCTGCCAACTGCCCTGCCA
207961	40157	TAGAGCAGAGTTCTATCCGC	252548	84744	CTAGCAAATGACAGAAAACA	297135	129331	GCCCTGCCAACTGCCCTGCC
207962	40158	TTAGAGCAGAGTTCTATCCG	252549	84745	TCTAGCAAATGACAGAAAAC	297136	129332	AGCCCTGCCAACTGCCCTGC
207963	40159	CTTAGAGCAGAGTTCTATCC	252550	84746	ATCTAGCAAATGACAGAAAA	297137	129333	CAGCCCTGCCAACTGCCCTG
207964	40160	TCTTAGAGCAGAGTTCTATC	252551	84747	TATCTAGCAAATGACAGAAA	297138	129334	CCAGCCCTGCCAACTGCCCT
207965	40161	CTCTTAGAGCAGAGTTCTAT	252552	84748	TTATCTAGCAAATGACAGAA	297139	129335	ACCAGCCCTGCCAACTGCCC
207966	40162	CCTCTTAGAGCAGAGTTCTA	252553	84749	TTTATCTAGCAAATGACAGA	297140	129336	GACCAGCCCTGCCAACTGCC
207967	40163	GCCTCTTAGAGCAGAGTTCT	252554	84750	ATTTATCTAGCAAATGACAG	297141	129337	AGACCAGCCCTGCCAACTGC
207968	40164	TGCCTCTTAGAGCAGAGTTC	252555	84751	CATTTATCTAGCAAATGACA	297142	129338	AAGACCAGCCCTGCCAACTG
207969	40165	CTGCCTCTTAGAGCAGAGTT	252556	84752	TCATTTATCTAGCAAATGAC	297143	129339	AAAGACCAGCCCTGCCAACT
207970	40166	ACTGCCTCTTAGAGCAGAGT	252557	84753	TTCATTTATCTAGCAAATGA	297144	129340	GAAAGACCAGCCCTGCCAAC
207971	40167	TACTGCCTCTTAGAGCAGAG	252558	84754	GTTCATTTATCTAGCAAATG	297145	129341	AGAAAGACCAGCCCTGCCAA
207972	40168	CTACTGCCTCTTAGAGCAGA	252559	84755	AGTTCATTTATCTAGCAAAT	297146	129342	GAGAAAGACCAGCCCTGCCA
207973	40169	GCTACTGCCTCTTAGAGCAG	252560	84756	AAGTTCATTTATCTAGCAAA	297147	129343	AGAGAAAGACCAGCCCTGCC
207974	40170	AGCTACTGCCTCTTAGAGCA	252561	84757	CAAGTTCATTTATCTAGCAA	297148	129344	CAGAGAAAGACCAGCCCTGC
207975	40171	TAGCTACTGCCTCTTAGAGC	252562	84758	TCAAGTTCATTTATCTAGCA	297149	129345	CCAGAGAAAGACCAGCCCTG
207976	40172	TTAGCTACTGCCTCTTAGAG	252563	84759	CTCAAGTTCATTTATCTAGC	297150	129346	GCCAGAGAAAGACCAGCCCT
207977	40173	ATTAGCTACTGCCTCTTAGA	252564	84760	TCTCAAGTTCATTTATCTAG	297151	129347	TGCCAGAGAAAGACCAGCCC
207978	40174	AATTAGCTACTGCCTCTTAG	252565	84761	CTCTCAAGTTCATTTATCTA	297152	129348	GTGCCAGAGAAAGACCAGCC

207979	40175	GAATTAGCTACTGCCTCTTA	252566	84762	GCTCTCAAGTTCATTTATCT	297153	129349	AGTGCCAGAGAAAGACCAGC
207980	40176	GGAATTAGCTACTGCCTCTT	252567	84763	GGCTCTCAAGTTCATTTATC	297154	129350	AAGTGCCAGAGAAAGACCAG
207981	40177	TGGAATTAGCTACTGCCTCT	252568	84764	AGGCTCTCAAGTTCATTTAT	297155	129351	GAAGTGCCAGAGAAAGACCA
207982	40178	ATGGAATTAGCTACTGCCTC	252569	84765	TAGGCTCTCAAGTTCATTTA	297156	129352	TGAAGTGCCAGAGAAAGACC
207983	40179	CATGGAATTAGCTACTGCCT	252570	84766	GTAGGCTCTCAAGTTCATTT	297157	129353	ATGAAGTGCCAGAGAAAGAC
207984	40180	ACATGGAATTAGCTACTGCC	252571	84767	AGTAGGCTCTCAAGTTCATT	297158	129354	GATGAAGTGCCAGAGAAAGA
207985	40181	GACATGGAATTAGCTACTGC	252572	84768	CAGTAGGCTCTCAAGTTCAT	297159	129355	AGATGAAGTGCCAGAGAAAG
207986	40182	AGACATGGAATTAGCTACTG	252573	84769	ACAGTAGGCTCTCAAGTTCA	297160	129356	GAGATGAAGTGCCAGAGAAA
207987	40183	AAGACATGGAATTAGCTACT	252574	84770	TACAGTAGGCTCTCAAGTTC	297161	129357	TGAGATGAAGTGCCAGAGAA
207988	40184	GAAGACATGGAATTAGCTAC	252575	84771	TTACAGTAGGCTCTCAAGTT	297162	129358	GTGAGATGAAGTGCCAGAGA
207989	40185	AGAAGACATGGAATTAGCTA	252576	84772	TTTACAGTAGGCTCTCAAGT	297163	129359	GGTGAGATGAAGTGCCAGAG
207990	40186	AAGAAGACATGGAATTAGCT	252577	84773	TTTTACAGTAGGCTCTCAAG	297164	129360	GGGTGAGATGAAGTGCCAGA
207991	40187	AAAGAAGACATGGAATTAGC	252578	84774	ATTTTACAGTAGGCTCTCAA	297165	129361	AGGGTGAGATGAAGTGCCAG
207992	40188	CAAAGAAGACATGGAATTAG	252579	84775	CATTTTACAGTAGGCTCTCA	297166	129362	GAGGGTGAGATGAAGTGCCA
207993	40189	GCAAAGAAGACATGGAATTA	252580	84776	ACATTTTACAGTAGGCTCTC	297167	129363	GGAGGGTGAGATGAAGTGCC
207994	40190	GGCAAAGAAGACATGGAATT	252581	84777	CACATTTTACAGTAGGCTCT	297168	129364	GGGAGGGTGAGATGAAGTGC
207995	40191	GGGCAAAGAAGACATGGAAT	252582	84778	CCACATTTTACAGTAGGCTC	297169	129365	AGGGAGGGTGAGATGAAGTG
207996	40192	AGGGCAAAGAAGACATGGAA	252583	84779	TCCACATTTTACAGTAGGCT	297170	129366	GAGGGAGGGTGAGATGAAGT
207997	40193	AAGGGCAAAGAAGACATGGA	252584	84780	TTCCACATTTTACAGTAGGC	297171	129367	GGAGGGAGGGTGAGATGAAG
207998	40194	CAAGGGCAAAGAAGACATGG	252585	84781	CTTCCACATTTTACAGTAGG	297172	129368	GGGAGGGAGGGTGAGATGAA
207999	40195	TCAAGGGCAAAGAAGACATG	252586	84782	GCTTCCACATTTTACAGTAG	297173	129369	AGGGAGGGAGGGTGAGATGA
208000	40196	GTCAAGGGCAAAGAAGACAT	252587	84783	AGCTTCCACATTTTACAGTA	297174	129370	AAGGGAGGGAGGGTGAGATG
208001	40197	AGTCAAGGGCAAAGAAGACA	252588	84784	AAGCTTCCACATTTTACAGT	297175	129371	GAAGGGAGGGAGGGTGAGAT
208002	40198	TAGTCAAGGGCAAAGAAGAC	252589	84785	GAAGCTTCCACATTTTACAG	297176	129372	GGAAGGGAGGGAGGGTGAGA
208003	40199	CTAGTCAAGGGCAAAGAAGA	252590	84786	AGAAGCTTCCACATTTTACA	297177	129373	AGGAAGGGAGGGAGGGTGAG
208004	40200	GCTAGTCAAGGGCAAAGAAG	252591	84787	TAGAAGCTTCCACATTTTAC	297178	129374	GAGGAAGGGAGGGAGGGTGA
208005	40201	AGCTAGTCAAGGGCAAAGAA	252592	84788	CTAGAAGCTTCCACATTTTA	297179	129375	AGAGGAAGGGAGGGAGGGTG
208006	40202	CAGCTAGTCAAGGGCAAAGA	252593	84789	TCTAGAAGCTTCCACATTTT	297180	129376	AAGAGGAAGGGAGGGAGGGT
208007	40203	TCAGCTAGTCAAGGGCAAAG	252594	84790	ATCTAGAAGCTTCCACATTT	297181	129377	GAAGAGGAAGGGAGGGAGGG
208008	40204	CTCAGCTAGTCAAGGGCAAA	252595	84791	AATCTAGAAGCTTCCACATT	297182	129378	AGAAGAGGAAGGGAGGGAGG
208009	40205	ACTCAGCTAGTCAAGGGCAA	252596	84792	CAATCTAGAAGCTTCCACAT	297183	129379	AAGAAGAGGAAGGGAGGGAG
208010	40206	CACTCAGCTAGTCAAGGGCA	252597	84793	GCAATCTAGAAGCTTCCACA	297184	129380	CAAGAAGAGGAAGGGAGGGA
208011	40207	TCACTCAGCTAGTCAAGGGC	252598	84794	TGCAATCTAGAAGCTTCCAC	297185	129381	GCAAGAAGAGGAAGGGAGGG
208012	40208	GTCACTCAGCTAGTCAAGGG	252599	84795	CTGCAATCTAGAAGCTTCCA	297186	129382	TGCAAGAAGAGGAAGGGAGG
208013	40209	AGTCACTCAGCTAGTCAAGG	252600	84796	TCTGCAATCTAGAAGCTTCC	297187	129383	CTGCAAGAAGAGGAAGGGAG
208014	40210	AAGTCACTCAGCTAGTCAAG	252601	84797	TTCTGCAATCTAGAAGCTTC	297188	129384	TCTGCAAGAAGAGGAAGGGA
208015	40211	AAAGTCACTCAGCTAGTCAA	252602	84798	CTTCTGCAATCTAGAAGCTT	297189	129385	ATCTGCAAGAAGAGGAAGGG
208016	40212	CAAAGTCACTCAGCTAGTCA	252603	84799	CCTTCTGCAATCTAGAAGCT	297190	129386	AATCTGCAAGAAGAGGAAGG
208017	40213	GCAAAGTCACTCAGCTAGTC	252604	84800	CCCTTCTGCAATCTAGAAGC	297191	129387	CAATCTGCAAGAAGAGGAAG
208018	40214	TGCAAAGTCACTCAGCTAGT	252605	84801	GCCCTTCTGCAATCTAGAAG	297192	129388	TCAATCTGCAAGAAGAGGAA
208019	40215	GTGCAAAGTCACTCAGCTAG	252606	84802	AGCCCTTCTGCAATCTAGAA	297193	129389	TTCAATCTGCAAGAAGAGGA
208020	40216	TGTGCAAAGTCACTCAGCTA	252607	84803	CAGCCCTTCTGCAATCTAGA	297194	129390	TTTCAATCTGCAAGAAGAGG
208021	40217	ATGTGCAAAGTCACTCAGCT	252608	84804	CCAGCCCTTCTGCAATCTAG	297195	129391	GTTTCAATCTGCAAGAAGAG
208022	40218	CATGTGCAAAGTCACTCAGC	252609	84805	TCCAGCCCTTCTGCAATCTA	297196	129392	GGTTTCAATCTGCAAGAAGA
208023	40219	CCATGTGCAAAGTCACTCAG	252610	84806	TTCCAGCCCTTCTGCAATCT	297197	129393	GGGTTTCAATCTGCAAGAAG
208024	40220	CCCATGTGCAAAGTCACTCA	252611	84807	TTTCCAGCCCTTCTGCAATC	297198	129394	TGGGTTTCAATCTGCAAGAA
208025	40221	CCCCATGTGCAAAGTCACTC	252612	84808	CTTTCCAGCCCTTCTGCAAT	297199	129395	GTGGGTTTCAATCTGCAAGA
208026	40222	GCCCCATGTGCAAAGTCACT	252613	84809	TCTTTCCAGCCCTTCTGCAA	297200	129396	TGTGGGTTTCAATCTGCAAG
208027	40223	AGCCCCATGTGCAAAGTCAC	252614	84810	GTCTTTCCAGCCCTTCTGCA	297201	129397	TTGTGGGTTTCAATCTGCAA
208028	40224	AAGCCCCATGTGCAAAGTCA	252615	84811	TGTCTTTCCAGCCCTTCTGC	297202	129398	CTTGTGGGTTTCAATCTGCA
208029	40225	CAAGCCCCATGTGCAAAGTC	252616	84812	GTGTCTTTCCAGCCCTTCTG	297203	129399	GCTTGTGGGTTTCAATCTGC
208030	40226	GCAAGCCCCATGTGCAAAGT	252617	84813	AGTGTCTTTCCAGCCCTTCT	297204	129400	AGCTTGTGGGTTTCAATCTG
208031	40227	GGCAAGCCCCATGTGCAAAG	252618	84814	CAGTGTCTTTCCAGCCCTTC	297205	129401	CAGCTTGTGGGTTTCAATCT
208032	40228	AGGCAAGCCCCATGTGCAAA	252619	84815	ACAGTGTCTTTCCAGCCCTT	297206	129402	TCAGCTTGTGGGTTTCAATC
208033	40229	GAGGCAAGCCCCATGTGCAA	252620	84816	AACAGTGTCTTTCCAGCCCT	297207	129403	GTCAGCTTGTGGGTTTCAAT
208034	40230	AGAGGCAAGCCCCATGTGCA	252621	84817	GAACAGTGTCTTTCCAGCCC	297208	129404	GGTCAGCTTGTGGGTTTCAA
208035	40231	GAGAGGCAAGCCCCATGTGC	252622	84818	AGAACAGTGTCTTTCCAGCC	297209	129405	AGGTCAGCTTGTGGGTTTCA
208036	40232	AGAGAGGCAAGCCCCATGTG	252623	84819	AAGAACAGTGTCTTTCCAGC	297210	129406	AAGGTCAGCTTGTGGGTTTC
208037	40233	CAGAGAGGCAAGCCCCATGT	252624	84820	AAAGAACAGTGTCTTTCCAG	297211	129407	GAAGGTCAGCTTGTGGGTTT
208038	40234	ACAGAGAGGCAAGCCCCATG	252625	84821	AAAAGAACAGTGTCTTTCCA	297212	129408	GGAAGGTCAGCTTGTGGGTT
208039	40235	AACAGAGAGGCAAGCCCCAT	252626	84822	GAAAAGAACAGTGTCTTTCC	297213	129409	CGGAAGGTCAGCTTGTGGGT
208040	40236	CAACAGAGAGGCAAGCCCCA	252627	84823	AGAAAAGAACAGTGTCTTTC	297214	129410	GCGGAAGGTCAGCTTGTGGG
208041	40237	GCAACAGAGAGGCAAGCCCC	252628	84824	GAGAAAAGAACAGTGTCTTT	297215	129411	CGCGGAAGGTCAGCTTGTGG
208042	40238	GGCAACAGAGAGGCAAGCCC	252629	84825	GGAGAAAAGAACAGTGTCTT	297216	129412	TCGCGGAAGGTCAGCTTGTG
208043	40239	AGGCAACAGAGAGGCAAGCC	252630	84826	GGGAGAAAAGAACAGTGTCT	297217	129413	CTCGCGGAAGGTCAGCTTGT
208044	40240	AAGGCAACAGAGAGGCAAGC	252631	84827	CGGGAGAAAAGAACAGTGTC	297218	129414	TCTCGCGGAAGGTCAGCTTG
208045	40241	CAAGGCAACAGAGAGGCAAG	252632	84828	TCGGGAGAAAAGAACAGTGT	297219	129415	TTCTCGCGGAAGGTCAGCTT
208046	40242	ACAAGGCAACAGAGAGGCAA	252633	84829	CTCGGGAGAAAAGAACAGTG	297220	129416	GTTCTCGCGGAAGGTCAGCT
208047	40243	GACAAGGCAACAGAGAGGCA	252634	84830	ACTCGGGAGAAAAGAACAGT	297221	129417	CGTTCTCGCGGAAGGTCAGC
208048	40244	AGACAAGGCAACAGAGAGGC	252635	84831	CACTCGGGAGAAAAGAACAG	297222	129418	GCGTTCTCGCGGAAGGTCAG
208049	40245	CAGACAAGGCAACAGAGAGG	252636	84832	TCACTCGGGAGAAAAGAACA	297223	129419	GGCGTTCTCGCGGAAGGTCA
208050	40246	GCAGACAAGGCAACAGAGAG	252637	84833	ATCACTCGGGAGAAAAGAAC	297224	129420	TGGCGTTCTCGCGGAAGGTC

208051	40247	TGCAGACAAGGCAACAGAGA	252638	84834	CATCACTCGGGAGAAAAGAA	297225	129421	TTGGCGTTCTCGCGGAAGGT
208052	40248	TTGCAGACAAGGCAACAGAG	252639	84835	CCATCACTCGGGAGAAAAGA	297226	129422	TTTGGCGTTCTCGCGGAAGG
208053	40249	TTTGCAGACAAGGCAACAGA	252640	84836	CCCATCACTCGGGAGAAAAG	297227	129423	CTTTGGCGTTCTCGCGGAAG
208054	40250	CTTTGCAGACAAGGCAACAG	252641	84837	TCCCATCACTCGGGAGAAAA	297228	129424	GCTTTGGCGTTCTCGCGGAA
208055	40251	ACTTTGCAGACAAGGCAACA	252642	84838	ATCCCATCACTCGGGAGAAA	297229	129425	GGCTTTGGCGTTCTCGCGGA
208056	40252	CACTTTGCAGACAAGGCAAC	252643	84839	GATCCCATCACTCGGGAGAA	297230	129426	TGGCTTTGGCGTTCTCGCGG
208057	40253	CCACTTTGCAGACAAGGCAA	252644	84840	AGATCCCATCACTCGGGAGA	297231	129427	TTGGCTTTGGCGTTCTCGCG
208058	40254	TCCACTTTGCAGACAAGGCA	252645	84841	CAGATCCCATCACTCGGGAG	297232	129428	CTTGGCTTTGGCGTTCTCGC
208059	40255	TTCCACTTTGCAGACAAGGC	252646	84842	ACAGATCCCATCACTCGGGA	297233	129429	TCTTGGCTTTGGCGTTCTCG
208060	40256	ATTCCACTTTGCAGACAAGG	252647	84843	GACAGATCCCATCACTCGGG	297234	129430	GTCTTGGCTTTGGCGTTCTC
208061	40257	GATTCCACTTTGCAGACAAG	252648	84844	GGACAGATCCCATCACTCGG	297235	129431	TGTCTTGGCTTTGGCGTTCT
208062	40258	TGATTCCACTTTGCAGACAA	252649	84845	TGGACAGATCCCATCACTCG	297236	129432	CTGTCTTGGCTTTGGCGTTC
208063	40259	ATGATTCCACTTTGCAGACA	252650	84846	CTGGACAGATCCCATCACTC	297237	129433	TCTGTCTTGGCTTTGGCGTT
208064	40260	GATGATTCCACTTTGCAGAC	252651	84847	ACTGGACAGATCCCATCACT	297238	129434	GTCTGTCTTGGCTTTGGCGT
208065	40261	AGATGATTCCACTTTGCAGA	252652	84848	TACTGGACAGATCCCATCAC	297239	129435	GGTCTGTCTTGGCTTTGGCG
208066	40262	AAGATGATTCCACTTTGCAG	252653	84849	ATACTGGACAGATCCCATCA	297240	129436	TGGTCTGTCTTGGCTTTGGC
208067	40263	AAAGATGATTCCACTTTGCA	252654	84850	AATACTGGACAGATCCCATC	297241	129437	GTGGTCTGTCTTGGCTTTGG
208068	40264	AAAAGATGATTCCACTTTGC	252655	84851	AAATACTGGACAGATCCCAT	297242	129438	CGTGGTCTGTCTTGGCTTTG
208069	40265	GAAAAGATGATTCCACTTTG	252656	84852	TAAATACTGGACAGATCCCA	297243	129439	CCGTGGTCTGTCTTGGCTTT
208070	40266	GGAAAAGATGATTCCACTTT	252657	84853	CTAAATACTGGACAGATCCC	297244	129440	CCCGTGGTCTGTCTTGGCTT
208071	40267	AGGAAAAGATGATTCCACTT	252658	84854	TCTAAATACTGGACAGATCC	297245	129441	CCCCGTGGTCTGTCTTGGCT
208072	40268	AAGGAAAAGATGATTCCACT	252659	84855	CTCTAAATACTGGACAGATC	297246	129442	GCCCCGTGGTCTGTCTTGGC
208073	40269	CAAGGAAAAGATGATTCCAC	252660	84856	GCTCTAAATACTGGACAGAT	297247	129443	CGCCCCGTGGTCTGTCTTGG
208074	40270	GCAAGGAAAAGATGATTCCA	252661	84857	AGCTCTAAATACTGGACAGA	297248	129444	CCGCCCCGTGGTCTGTCTTG
208075	40271	AGCAAGGAAAAGATGATTCC	252662	84858	CAGCTCTAAATACTGGACAG	297249	129445	TCCGCCCCGTGGTCTGTCTT
208076	40272	TAGCAAGGAAAAGATGATTC	252663	84859	GCAGCTCTAAATACTGGACA	297250	129446	CTCCGCCCCGTGGTCTGTCT
208077	40273	CTAGCAAGGAAAAGATGATT	252664	84860	GGCAGCTCTAAATACTGGAC	297251	129447	TCTCCGCCCCGTGGTCTGTC
208078	40274	TCTAGCAAGGAAAAGATGAT	252665	84861	AGGCAGCTCTAAATACTGGA	297252	129448	ATCTCCGCCCCGTGGTCTGT
208079	40275	GTCTAGCAAGGAAAAGATGA	252666	84862	GAGGCAGCTCTAAATACTGG	297253	129449	GATCTCCGCCCCGTGGTCTG
208080	40276	TGTCTAGCAAGGAAAAGATG	252667	84863	AGAGGCAGCTCTAAATACTG	297254	129450	CGATCTCCGCCCCGTGGTCT
208081	40277	CTGTCTAGCAAGGAAAAGAT	252668	84864	CAGAGGCAGCTCTAAATACT	297255	129451	ACGATCTCCGCCCCGTGGTC
208082	40278	TCTGTCTAGCAAGGAAAAGA	252669	84865	TCAGAGGCAGCTCTAAATAC	297256	129452	CACGATCTCCGCCCCGTGGT
208083	40279	TTCTGTCTAGCAAGGAAAAG	252670	84866	CTCAGAGGCAGCTCTAAATA	297257	129453	ACACGATCTCCGCCCCGTGG
208084	40280	CTTCTGTCTAGCAAGGAAAA	252671	84867	CCTCAGAGGCAGCTCTAAAT	297258	129454	TACACGATCTCCGCCCCGTG
208085	40281	CCTTCTGTCTAGCAAGGAAA	252672	84868	GCCTCAGAGGCAGCTCTAAA	297259	129455	GTACACGATCTCCGCCCCGT
208086	40282	ACCTTCTGTCTAGCAAGGAA	252673	84869	GGCCTCAGAGGCAGCTCTAA	297260	129456	TGTACACGATCTCCGCCCCG
208087	40283	CACCTTCTGTCTAGCAAGGA	252674	84870	TGGCCTCAGAGGCAGCTCTA	297261	129457	TTGTACACGATCTCCGCCCC
208088	40284	CCACCTTCTGTCTAGCAAGG	252675	84871	ATGGCCTCAGAGGCAGCTCT	297262	129458	CTTGTACACGATCTCCGCCC
208089	40285	TCCACCTTCTGTCTAGCAAG	252676	84872	GATGGCCTCAGAGGCAGCTC	297263	129459	ACTTGTACACGATCTCCGCC
208090	40286	GTCCACCTTCTGTCTAGCAA	252677	84873	AGATGGCCTCAGAGGCAGCT	297264	129460	GACTTGTACACGATCTCCGC
208091	40287	GGTCCACCTTCTGTCTAGCA	252678	84874	CAGATGGCCTCAGAGGCAGC	297265	129461	CGACTTGTACACGATCTCCG
208092	40288	GGGTCCACCTTCTGTCTAGC	252679	84875	TCAGATGGCCTCAGAGGCAG	297266	129462	GCGACTTGTACACGATCTCC
208093	40289	AGGGTCCACCTTCTGTCTAG	252680	84876	ATCAGATGGCCTCAGAGGCA	297267	129463	GGCGACTTGTACACGATCTC
208094	40290	CAGGGTCCACCTTCTGTCTA	252681	84877	AATCAGATGGCCTCAGAGGC	297268	129464	TGGCGACTTGTACACGATCT
208095	40291	CCAGGGTCCACCTTCTGTCT	252682	84878	GAATCAGATGGCCTCAGAGG	297269	129465	CTGGCGACTTGTACACGATC
208096	40292	TCCAGGGTCCACCTTCTGTC	252683	84879	AGAATCAGATGGCCTCAGAG	297270	129466	ACTGGCGACTTGTACACGAT
208097	40293	GTCCAGGGTCCACCTTCTGT	252684	84880	TAGAATCAGATGGCCTCAGA	297271	129467	CACTGGCGACTTGTACACGA
208098	40294	GGTCCAGGGTCCACCTTCTG	252685	84881	CTAGAATCAGATGGCCTCAG	297272	129468	CCACTGGCGACTTGTACACG
208099	40295	AGGTCCAGGGTCCACCTTCT	252686	84882	CCTAGAATCAGATGGCCTCA	297273	129469	ACCACTGGCGACTTGTACAC
208100	40296	TAGGTCCAGGGTCCACCTTC	252687	84883	TCCTAGAATCAGATGGCCTC	297274	129470	CACCACTGGCGACTTGTACA
208101	40297	ATAGGTCCAGGGTCCACCTT	252688	84884	CTCCTAGAATCAGATGGCCT	297275	129471	ACACCACTGGCGACTTGTAC
208102	40298	CATAGGTCCAGGGTCCACCT	252689	84885	TCTCCTAGAATCAGATGGCC	297276	129472	GACACCACTGGCGACTTGTA
208103	40299	CCATAGGTCCAGGGTCCACC	252690	84886	GTCTCCTAGAATCAGATGGC	297277	129473	AGACACCACTGGCGACTTGT
208104	40300	GCCATAGGTCCAGGGTCCAC	252691	84887	AGTCTCCTAGAATCAGATGG	297278	129474	CAGACACCACTGGCGACTTG
208105	40301	GGCCATAGGTCCAGGGTCCA	252692	84888	GAGTCTCCTAGAATCAGATG	297279	129475	CCAGACACCACTGGCGACTT
208106	40302	AGGCCATAGGTCCAGGGTCC	252693	84889	AGAGTCTCCTAGAATCAGAT	297280	129476	CCCAGACACCACTGGCGACT
208107	40303	AAGGCCATAGGTCCAGGGTC	252694	84890	CAGAGTCTCCTAGAATCAGA	297281	129477	CCCCAGACACCACTGGCGAC
208108	40304	AAAGGCCATAGGTCCAGGGT	252695	84891	GCAGAGTCTCCTAGAATCAG	297282	129478	TCCCCAGACACCACTGGCGA
208109	40305	AAAAGGCCATAGGTCCAGGG	252696	84892	GGCAGAGTCTCCTAGAATCA	297283	129479	GTCCCCAGACACCACTGGCG
208110	40306	AAAAAGGCCATAGGTCCAGG	252697	84893	AGGCAGAGTCTCCTAGAATC	297284	129480	TGTCCCCAGACACCACTGGC
208111	40307	CAAAAAGGCCATAGGTCCAG	252698	84894	GAGGCAGAGTCTCCTAGAAT	297285	129481	GTGTCCCCAGACACCACTGG
208112	40308	TCAAAAAGGCCATAGGTCCA	252699	84895	CGAGGCAGAGTCTCCTAGAA	297286	129482	CGTGTCCCCAGACACCACTG
208113	40309	CTCAAAAAGGCCATAGGTCC	252700	84896	ACGAGGCAGAGTCTCCTAGA	297287	129483	ACGTGTCCCCAGACACCACT
208114	40310	ACTCAAAAAGGCCATAGGTC	252701	84897	AACGAGGCAGAGTCTCCTAG	297288	129484	GACGTGTCCCCAGACACCAC
208115	40311	AACTCAAAAAGGCCATAGGT	252702	84898	CAACGAGGCAGAGTCTCCTA	297289	129485	AGACGTGTCCCCAGACACCA
208116	40312	AAACTCAAAAAGGCCATAGG	252703	84899	TCAACGAGGCAGAGTCTCCT	297290	129486	GAGACGTGTCCCCAGACACC
208117	40313	GAAACTCAAAAAGGCCATAG	252704	84900	CTCAACGAGGCAGAGTCTCC	297291	129487	GGAGACGTGTCCCCAGACAC
208118	40314	GGAAACTCAAAAAGGCCATA	252705	84901	CCTCAACGAGGCAGAGTCTC	297292	129488	TGGAGACGTGTCCCCAGACA
208119	40315	GGGAAACTCAAAAAGGCCAT	252706	84902	TCCTCAACGAGGCAGAGTCT	297293	129489	GTGGAGACGTGTCCCCAGAC
208120	40316	GGGGAAACTCAAAAAGGCCA	252707	84903	ATCCTCAACGAGGCAGAGTC	297294	129490	CGTGGAGACGTGTCCCCAGA
208121	40317	GGGGGAAACTCAAAAAGGCC	252708	84904	TATCCTCAACGAGGCAGAGT	297295	129491	CCGTGGAGACGTGTCCCCAG
208122	40318	GGGGGGAAACTCAAAAAGGC	252709	84905	ATATCCTCAACGAGGCAGAG	297296	129492	GCCGTGGAGACGTGTCCCCA

208123	40319	GGGGGGGAAACTCAAAAAGG	252710	84906	AATATCCTCAACGAGGCAGA	297297	129493	TGCCGTGGAGACGTGTCCCC
208124	40320	CGGGGGGGAAACTCAAAAAG	252711	84907	AAATATCCTCAACGAGGCAG	297298	129494	ATGCCGTGGAGACGTGTCCC
208125	40321	GCGGGGGGGAAACTCAAAAA	252712	84908	AAAATATCCTCAACGAGGCA	297299	129495	GATGCCGTGGAGACGTGTCC
208126	40322	AGCGGGGGGGAAACTCAAAA	252713	84909	CAAAATATCCTCAACGAGGC	297300	129496	AGATGCCGTGGAGACGTGTC
208127	40323	AAGCGGGGGGGAAACTCAAA	252714	84910	TCAAAATATCCTCAACGAGG	297301	129497	GAGATGCCGTGGAGACGTGT
208128	40324	GAAGCGGGGGGGAAACTCAA	252715	84911	CTCAAAATATCCTCAACGAG	297302	129498	TGAGATGCCGTGGAGACGTG
208129	40325	AGAAGCGGGGGGGAAACTCA	252716	84912	CCTCAAAATATCCTCAACGA	297303	129499	CTGAGATGCCGTGGAGACGT
208130	40326	AAGAAGCGGGGGGGAAACTC	252717	84913	GCCTCAAAATATCCTCAACG	297304	129500	GCTGAGATGCCGTGGAGACG
208131	40327	TAAGAAGCGGGGGGGAAACT	252718	84914	GGCCTCAAAATATCCTCAAC	297305	129501	TGCTGAGATGCCGTGGAGAC
208132	40328	CTAAGAAGCGGGGGGGAAAC	252719	84915	AGGCCTCAAAATATCCTCAA	297306	129502	TTGCTGAGATGCCGTGGAGA
208133	40329	TCTAAGAAGCGGGGGGGAAA	252720	84916	TAGGCCTCAAAATATCCTCA	297307	129503	ATTGCTGAGATGCCGTGGAG
208134	40330	TTCTAAGAAGCGGGGGGGAA	252721	84917	TTAGGCCTCAAAATATCCTC	297308	129504	CATTGCTGAGATGCCGTGGA
208135	40331	CTTCTAAGAAGCGGGGGGGA	252722	84918	GTTAGGCCTCAAAATATCCT	297309	129505	ACATTGCTGAGATGCCGTGG
208136	40332	CCTTCTAAGAAGCGGGGGGG	252723	84919	AGTTAGGCCTCAAAATATCC	297310	129506	GACATTGCTGAGATGCCGTG
208137	40333	TCCTTCTAAGAAGCGGGGGG	252724	84920	TAGTTAGGCCTCAAAATATC	297311	129507	AGACATTGCTGAGATGCCGT
208138	40334	GTCCTTCTAAGAAGCGGGGG	252725	84921	GTAGTTAGGCCTCAAAATAT	297312	129508	GAGACATTGCTGAGATGCCG
208139	40335	GGTCCTTCTAAGAAGCGGGG	252726	84922	TGTAGTTAGGCCTCAAAATA	297313	129509	GGAGACATTGCTGAGATGCC
208140	40336	AGGTCCTTCTAAGAAGCGGG	252727	84923	GTGTAGTTAGGCCTCAAAAT	297314	129510	AGGAGACATTGCTGAGATGC
208141	40337	GAGGTCCTTCTAAGAAGCGG	252728	84924	TGTGTAGTTAGGCCTCAAAA	297315	129511	GAGGAGACATTGCTGAGATG
208142	40338	AGAGGTCCTTCTAAGAAGCG	252729	84925	ATGTGTAGTTAGGCCTCAAA	297316	129512	GGAGGAGACATTGCTGAGAT
208143	40339	CAGAGGTCCTTCTAAGAAGC	252730	84926	AATGTGTAGTTAGGCCTCAA	297317	129513	TGGAGGAGACATTGCTGAGA
208144	40340	TCAGAGGTCCTTCTAAGAAG	252731	84927	GAATGTGTAGTTAGGCCTCA	297318	129514	GTGGAGGAGACATTGCTGAG
208145	40341	ATCAGAGGTCCTTCTAAGAA	252732	84928	GGAATGTGTAGTTAGGCCTC	297319	129515	GGTGGAGGAGACATTGCTGA
208146	40342	GATCAGAGGTCCTTCTAAGA	252733	84929	AGGAATGTGTAGTTAGGCCT	297320	129516	CGGTGGAGGAGACATTGCTG
208147	40343	GGATCAGAGGTCCTTCTAAG	252734	84930	CAGGAATGTGTAGTTAGGCC	297321	129517	CCGGTGGAGGAGACATTGCT
208148	40344	AGGATCAGAGGTCCTTCTAA	252735	84931	GCAGGAATGTGTAGTTAGGC	297322	129518	GCCGGTGGAGGAGACATTGC
208149	40345	TAGGATCAGAGGTCCTTCTA	252736	84932	GGCAGGAATGTGTAGTTAGG	297323	129519	TGCCGGTGGAGGAGACATTG
208150	40346	GTAGGATCAGAGGTCCTTCT	252737	84933	GGGCAGGAATGTGTAGTTAG	297324	129520	CTGCCGGTGGAGGAGACATT
208151	40347	AGTAGGATCAGAGGTCCTTC	252738	84934	GGGGCAGGAATGTGTAGTTA	297325	129521	GCTGCCGGTGGAGGAGACAT
208152	40348	CAGTAGGATCAGAGGTCCTT	252739	84935	GGGGGCAGGAATGTGTAGTT	297326	129522	TGCTGCCGGTGGAGGAGACA
208153	40349	TCAGTAGGATCAGAGGTCCT	252740	84936	TGGGGGCAGGAATGTGTAGT	297327	129523	ATGCTGCCGGTGGAGGAGAC
208154	40350	CTCAGTAGGATCAGAGGTCC	252741	84937	CTGGGGGCAGGAATGTGTAG	297328	129524	GATGCTGCCGGTGGAGGAGA
208155	40351	ACTCAGTAGGATCAGAGGTC	252742	84938	TCTGGGGGCAGGAATGTGTA	297329	129525	CGATGCTGCCGGTGGAGGAG
208156	40352	AACTCAGTAGGATCAGAGGT	252743	84939	CTCTGGGGGCAGGAATGTGT	297330	129526	TCGATGCTGCCGGTGGAGGA
208157	40353	AAACTCAGTAGGATCAGAGG	252744	84940	TCTCTGGGGGCAGGAATGTG	297331	129527	GTCGATGCTGCCGGTGGAGG
208158	40354	TAAACTCAGTAGGATCAGAG	252745	84941	CTCTCTGGGGGCAGGAATGT	297332	129528	TGTCGATGCTGCCGGTGGAG
208159	40355	TTAAACTCAGTAGGATCAGA	252746	84942	CCTCTCTGGGGGCAGGAATG	297333	129529	ATGTCGATGCTGCCGGTGGA
208160	40356	ATTAAACTCAGTAGGATCAG	252747	84943	ACCTCTCTGGGGGCAGGAAT	297334	129530	CATGTCGATGCTGCCGGTGG
208161	40357	TATTAAACTCAGTAGGATCA	252748	84944	GACCTCTCTGGGGGCAGGAA	297335	129531	CCATGTCGATGCTGCCGGTG
208162	40358	GTATTAAACTCAGTAGGATC	252749	84945	TGACCTCTCTGGGGGCAGGA	297336	129532	ACCATGTCGATGCTGCCGGT
208163	40359	GGTATTAAACTCAGTAGGAT	252750	84946	GTGACCTCTCTGGGGGCAGG	297337	129533	TACCATGTCGATGCTGCCGG
208164	40360	GGGTATTAAACTCAGTAGGA	252751	84947	TGTGACCTCTCTGGGGGCAG	297338	129534	CTACCATGTCGATGCTGCCG
208165	40361	TGGGTATTAAACTCAGTAGG	252752	84948	CTGTGACCTCTCTGGGGGCA	297339	129535	TCTACCATGTCGATGCTGCC
208166	40362	GTGGGTATTAAACTCAGTAG	252753	84949	GCTGTGACCTCTCTGGGGGC	297340	129536	GTCTACCATGTCGATGCTGC
208167	40363	CGTGGGTATTAAACTCAGTA	252754	84950	GGCTGTGACCTCTCTGGGGG	297341	129537	AGTCTACCATGTCGATGCTG
208168	40364	CCGTGGGTATTAAACTCAGT	252755	84951	AGGCTGTGACCTCTCTGGGG	297342	129538	GAGTCTACCATGTCGATGCT
208169	40365	CCCGTGGGTATTAAACTCAG	252756	84952	TAGGCTGTGACCTCTCTGGG	297343	129539	CGAGTCTACCATGTCGATGC
208170	40366	ACCCGTGGGTATTAAACTCA	252757	84953	ATAGGCTGTGACCTCTCTGG	297344	129540	GCGAGTCTACCATGTCGATG
208171	40367	AACCCGTGGGTATTAAACTC	252758	84954	TATAGGCTGTGACCTCTCTG	297345	129541	GGCGAGTCTACCATGTCGAT
208172	40368	TAACCCGTGGGTATTAAACT	252759	84955	CTATAGGCTGTGACCTCTCT	297346	129542	GGGCGAGTCTACCATGTCGA
208173	40369	TTAACCCGTGGGTATTAAAC	252760	84956	GCTATAGGCTGTGACCTCTC	297347	129543	GGGGCGAGTCTACCATGTCG
208174	40370	ATTAACCCGTGGGTATTAAA	252761	84957	TGCTATAGGCTGTGACCTCT	297348	129544	TGGGGCGAGTCTACCATGTC
208175	40371	TATTAACCCGTGGGTATTAA	252762	84958	CTGCTATAGGCTGTGACCTC	297349	129545	CTGGGGCGAGTCTACCATGT
208176	40372	TTATTAACCCGTGGGTATTA	252763	84959	CCTGCTATAGGCTGTGACCT	297350	129546	GCTGGGGCGAGTCTACCATG
208177	40373	ATTATTAACCCGTGGGTATT	252764	84960	GCCTGCTATAGGCTGTGACC	297351	129547	AGCTGGGGCGAGTCTACCAT
208178	40374	AATTATTAACCCGTGGGTAT	252765	84961	AGCCTGCTATAGGCTGTGAC	297352	129548	GAGCTGGGGCGAGTCTACCA
208179	40375	CAATTATTAACCCGTGGGTA	252766	84962	CAGCCTGCTATAGGCTGTGA	297353	129549	CGAGCTGGGGCGAGTCTACC
208180	40376	CCAATTATTAACCCGTGGGT	252767	84963	TCAGCCTGCTATAGGCTGTG	297354	129550	GCGAGCTGGGGCGAGTCTAC
208181	40377	CCCAATTATTAACCCGTGGG	252768	84964	ATCAGCCTGCTATAGGCTGT	297355	129551	GGCGAGCTGGGGCGAGTCTA
208182	40378	TCCCAATTATTAACCCGTGG	252769	84965	CATCAGCCTGCTATAGGCTG	297356	129552	TGGCGAGCTGGGGCGAGTCT
208183	40379	TTCCCAATTATTAACCCGTG	252770	84966	ACATCAGCCTGCTATAGGCT	297357	129553	GTGGCGAGCTGGGGCGAGTC
208184	40380	TTTCCCAATTATTAACCCGT	252771	84967	AACATCAGCCTGCTATAGGC	297358	129554	CGTGGCGAGCTGGGGCGAGT
208185	40381	TTTTCCCAATTATTAACCCG	252772	84968	AAACATCAGCCTGCTATAGG	297359	129555	GCGTGGCGAGCTGGGGCGAG
208186	40382	CTTTTCCCAATTATTAACCC	252773	84969	GAAACATCAGCCTGCTATAG	297360	129556	AGCGTGGCGAGCTGGGGCGA
208187	40383	GCTTTTCCCAATTATTAACC	252774	84970	AGAAACATCAGCCTGCTATA	297361	129557	TAGCGTGGCGAGCTGGGGCG
208188	40384	TGCTTTTCCCAATTATTAAC	252775	84971	GAGAAACATCAGCCTGCTAT	297362	129558	CTAGCGTGGCGAGCTGGGGC
208189	40385	TTGCTTTTCCCAATTATTAA	252776	84972	TGAGAAACATCAGCCTGCTA	297363	129559	GCTAGCGTGGCGAGCTGGGG
208190	40386	TTTGCTTTTCCCAATTATTA	252777	84973	ATGAGAAACATCAGCCTGCT	297364	129560	AGCTAGCGTGGCGAGCTGGG
208191	40387	CTTTGCTTTTCCCAATTATT	252778	84974	CATGAGAAACATCAGCCTGC	297365	129561	CAGCTAGCGTGGCGAGCTGG
208192	40388	CCTTTGCTTTTCCCAATTAT	252779	84975	ACATGAGAAACATCAGCCTG	297366	129562	TCAGCTAGCGTGGCGAGCTG
208193	40389	TCCTTTGCTTTTCCCAATTA	252780	84976	GACATGAGAAACATCAGCCT	297367	129563	GTCAGCTAGCGTGGCGAGCT
208194	40390	TTCCTTTGCTTTTCCCAATT	252781	84977	TGACATGAGAAACATCAGCC	297368	129564	CGTCAGCTAGCGTGGCGAGC

208195	40391	CTTCCTTTGCTTTTCCCAAT	252782	84978	GTGACATGAGAAACATCAGC	297369	129565	TCGTCAGCTAGCGTGGCGAG
208196	40392	GCTTCCTTTGCTTTTCCCAA	252783	84979	TGTGACATGAGAAACATCAG	297370	129566	CTCGTCAGCTAGCGTGGCGA
208197	40393	CGCTTCCTTTGCTTTTCCCA	252784	84980	ATGTGACATGAGAAACATCA	297371	129567	CCTCGTCAGCTAGCGTGGCG
208198	40394	GCGCTTCCTTTGCTTTTCCC	252785	84981	CATGTGACATGAGAAACATC	297372	129568	ACCTCGTCAGCTAGCGTGGC
208199	40395	AGCGCTTCCTTTGCTTTTCC	252786	84982	CCATGTGACATGAGAAACAT	297373	129569	CACCTCGTCAGCTAGCGTGG
208200	40396	AAGCGCTTCCTTTGCTTTTC	252787	84983	GCCATGTGACATGAGAAACA	297374	129570	ACACCTCGTCAGCTAGCGTG
208201	40397	GAAGCGCTTCCTTTGCTTTT	252788	84984	TGCCATGTGACATGAGAAAC	297375	129571	GACACCTCGTCAGCTAGCGT
208202	40398	AGAAGCGCTTCCTTTGCTTT	252789	84985	GTGCCATGTGACATGAGAAA	297376	129572	AGACACCTCGTCAGCTAGCG
208203	40399	CAGAAGCGCTTCCTTTGCTT	252790	84986	TGTGCCATGTGACATGAGAA	297377	129573	CAGACACCTCGTCAGCTAGC
208204	40400	ACAGAAGCGCTTCCTTTGCT	252791	84987	CTGTGCCATGTGACATGAGA	297378	129574	GCAGACACCTCGTCAGCTAG
208205	40401	AACAGAAGCGCTTCCTTTGC	252792	84988	TCTGTGCCATGTGACATGAG	297379	129575	GGCAGACACCTCGTCAGCTA
208206	40402	AAACAGAAGCGCTTCCTTTG	252793	84989	TTCTGTGCCATGTGACATGA	297380	129576	AGGCAGACACCTCGTCAGCT
208207	40403	TAAACAGAAGCGCTTCCTTT	252794	84990	TTTCTGTGCCATGTGACATG	297381	129577	GAGGCAGACACCTCGTCAGC
208208	40404	CTAAACAGAAGCGCTTCCTT	252795	84991	CTTTCTGTGCCATGTGACAT	297382	129578	GGAGGCAGACACCTCGTCAG
208209	40405	CCTAAACAGAAGCGCTTCCT	252796	84992	CCTTTCTGTGCCATGTGACA	297383	129579	GGGAGGCAGACACCTCGTCA
208210	40406	ACCTAAACAGAAGCGCTTCC	252797	84993	GCCTTTCTGTGCCATGTGAC	297384	129580	AGGGAGGCAGACACCTCGTC
208211	40407	TACCTAAACAGAAGCGCTTC	252798	84994	TGCCTTTCTGTGCCATGTGA	297385	129581	CAGGGAGGCAGACACCTCGT
208212	40408	TTACCTAAACAGAAGCGCTT	252799	84995	GTGCCTTTCTGTGCCATGTG	297386	129582	CCAGGGAGGCAGACACCTCG
208213	40409	ATTACCTAAACAGAAGCGCT	252800	84996	TGTGCCTTTCTGTGCCATGT	297387	129583	GCCAGGGAGGCAGACACCTC
208214	40410	AATTACCTAAACAGAAGCGC	252801	84997	ATGTGCCTTTCTGTGCCATG	297388	129584	GGCCAGGGAGGCAGACACCT
208215	40411	TAATTACCTAAACAGAAGCG	252802	84998	AATGTGCCTTTCTGTGCCAT	297389	129585	TGGCCAGGGAGGCAGACACC
208216	40412	ATAATTACCTAAACAGAAGC	252803	84999	AAATGTGCCTTTCTGTGCCA	297390	129586	TTGGCCAGGGAGGCAGACAC
208217	40413	TATAATTACCTAAACAGAAG	252804	85000	AAAATGTGCCTTTCTGTGCC	297391	129587	CTTGGCCAGGGAGGCAGACA
208218	40414	ATATAATTACCTAAACAGAA	252805	85001	GAAAATGTGCCTTTCTGTGC	297392	129588	GCTTGGCCAGGGAGGCAGAC
208219	40415	CATATAATTACCTAAACAGA	252806	85002	CGAAAATGTGCCTTTCTGTG	297393	129589	TGCTTGGCCAGGGAGGCAGA
208220	40416	GCATATAATTACCTAAACAG	252807	85003	ACGAAAATGTGCCTTTCTGT	297394	129590	CTGCTTGGCCAGGGAGGCAG
208221	40417	TGCATATAATTACCTAAACA	252808	85004	AACGAAAATGTGCCTTTCTG	297395	129591	CCTGCTTGGCCAGGGAGGCA
208222	40418	ATGCATATAATTACCTAAAC	252809	85005	GAACGAAAATGTGCCTTTCT	297396	129592	CCCTGCTTGGCCAGGGAGGC
208223	40419	CATGCATATAATTACCTAAA	252810	85006	AGAACGAAAATGTGCCTTTC	297397	129593	ACCCTGCTTGGCCAGGGAGG
208224	40420	ACATGCATATAATTACCTAA	252811	85007	GAGAACGAAAATGTGCCTTT	297398	129594	AACCCTGCTTGGCCAGGGAG
208225	40421	AACATGCATATAATTACCTA	252812	85008	TGAGAACGAAAATGTGCCTT	297399	129595	AAACCCTGCTTGGCCAGGGA
208226	40422	AAACATGCATATAATTACCT	252813	85009	CTGAGAACGAAAATGTGCCT	297400	129596	CAAACCCTGCTTGGCCAGGG
208227	40423	AAAACATGCATATAATTACC	252814	85010	CCTGAGAACGAAAATGTGCC	297401	129597	ACAAACCCTGCTTGGCCAGG
208228	40424	AAAAACATGCATATAATTAC	252815	85011	GCCTGAGAACGAAAATGTGC	297402	129598	CACAAACCCTGCTTGGCCAG
208229	40425	CAAAAACATGCATATAATTA	252816	85012	AGCCTGAGAACGAAAATGTG	297403	129599	TCACAAACCCTGCTTGGCCA
208230	40426	ACAAAAACATGCATATAATT	252817	85013	TAGCCTGAGAACGAAAATGT	297404	129600	ATCACAAACCCTGCTTGGCC
208231	40427	GACAAAAACATGCATATAAT	252818	85014	TTAGCCTGAGAACGAAAATG	297405	129601	GATCACAAACCCTGCTTGGC
208232	40428	AGACAAAAACATGCATATAA	252819	85015	GTTAGCCTGAGAACGAAAAT	297406	129602	TGATCACAAACCCTGCTTGG
208233	40429	AAGACAAAAACATGCATATA	252820	85016	TGTTAGCCTGAGAACGAAAA	297407	129603	CTGATCACAAACCCTGCTTG
208234	40430	AAAGACAAAAACATGCATAT	252821	85017	TTGTTAGCCTGAGAACGAAA	297408	129604	CCTGATCACAAACCCTGCTT
208235	40431	AAAAGACAAAAACATGCATA	252822	85018	TTTGTTAGCCTGAGAACGAA	297409	129605	GCCTGATCACAAACCCTGCT
208236	40432	AAAAAGACAAAAACATGCAT	252823	85019	CTTTGTTAGCCTGAGAACGA	297410	129606	GGCCTGATCACAAACCCTGC
208237	40433	GAAAAAGACAAAAACATGCA	252824	85020	TCTTTGTTAGCCTGAGAACG	297411	129607	GGGCCTGATCACAAACCCTG
208238	40434	AGAAAAAGACAAAAACATGC	252825	85021	CTCTTTGTTAGCCTGAGAAC	297412	129608	GGGGCCTGATCACAAACCCT
208239	40435	CAGAAAAAGACAAAAACATG	252826	85022	GCTCTTTGTTAGCCTGAGAA	297413	129609	AGGGGCCTGATCACAAACCC
208240	40436	CCAGAAAAAGACAAAAACAT	252827	85023	AGCTCTTTGTTAGCCTGAGA	297414	129610	CAGGGGCCTGATCACAAACC
208241	40437	GCCAGAAAAAGACAAAAACA	252828	85024	AAGCTCTTTGTTAGCCTGAG	297415	129611	CCAGGGGCCTGATCACAAAC
208242	40438	AGCCAGAAAAAGACAAAAAC	252829	85025	GAAGCTCTTTGTTAGCCTGA	297416	129612	CCCAGGGGCCTGATCACAAA
208243	40439	CAGCCAGAAAAAGACAAAAA	252830	85026	TGAAGCTCTTTGTTAGCCTG	297417	129613	CCCCAGGGGCCTGATCACAA
208244	40440	CCAGCCAGAAAAAGACAAAA	252831	85027	TTGAAGCTCTTTGTTAGCCT	297418	129614	GCCCCAGGGGCCTGATCACA
208245	40441	TCCAGCCAGAAAAAGACAAA	252832	85028	TTTGAAGCTCTTTGTTAGCC	297419	129615	CGCCCCAGGGGCCTGATCAC
208246	40442	TTCCAGCCAGAAAAAGACAA	252833	85029	TTTTGAAGCTCTTTGTTAGC	297420	129616	CCGCCCCAGGGGCCTGATCA
208247	40443	TTTCCAGCCAGAAAAAGACA	252834	85030	TTTTTGAAGCTCTTTGTTAG	297421	129617	ACCGCCCCAGGGGCCTGATC
208248	40444	CTTTCCAGCCAGAAAAAGAC	252835	85031	GTTTTTGAAGCTCTTTGTTA	297422	129618	GACCGCCCCAGGGGCCTGAT
208249	40445	TCTTTCCAGCCAGAAAAAGA	252836	85032	AGTTTTTGAAGCTCTTTGTT	297423	129619	TGACCGCCCCAGGGGCCTGA
208250	40446	ATCTTTCCAGCCAGAAAAAG	252837	85033	TAGTTTTTGAAGCTCTTTGT	297424	129620	TTGACCGCCCCAGGGGCCTG
208251	40447	TATCTTTCCAGCCAGAAAAA	252838	85034	ATAGTTTTTGAAGCTCTTTG	297425	129621	ATTGACCGCCCCAGGGGCCT
208252	40448	ATATCTTTCCAGCCAGAAAA	252839	85035	AATAGTTTTTGAAGCTCTTT	297426	129622	TATTGACCGCCCCAGGGGCC
208253	40449	GATATCTTTCCAGCCAGAAA	252840	85036	TAATAGTTTTTGAAGCTCTT	297427	129623	TTATTGACCGCCCCAGGGGC
208254	40450	GGATATCTTTCCAGCCAGAA	252841	85037	CTAATAGTTTTTGAAGCTCT	297428	129624	ATTATTGACCGCCCCAGGGG
208255	40451	TGGATATCTTTCCAGCCAGA	252842	85038	TCTAATAGTTTTTGAAGCTC	297429	129625	AATTATTGACCGCCCCAGGG
208256	40452	TTGGATATCTTTCCAGCCAG	252843	85039	TTCTAATAGTTTTTGAAGCT	297430	129626	CAATTATTGACCGCCCCAGG
208257	40453	CTTGGATATCTTTCCAGCCA	252844	85040	CTTCTAATAGTTTTTGAAGC	297431	129627	ACAATTATTGACCGCCCCAG
208258	40454	GCTTGGATATCTTTCCAGCC	252845	85041	CCTTCTAATAGTTTTTGAAG	297432	129628	CACAATTATTGACCGCCCCA
208259	40455	GGCTTGGATATCTTTCCAGC	252846	85042	CCCTTCTAATAGTTTTTGAA	297433	129629	CCACAATTATTGACCGCCCC
208260	40456	TGGCTTGGATATCTTTCCAG	252847	85043	TCCCTTCTAATAGTTTTTGA	297434	129630	TCCACAATTATTGACCGCCC
208261	40457	GTGGCTTGGATATCTTTCCA	252848	85044	GTCCCTTCTAATAGTTTTTG	297435	129631	CTCCACAATTATTGACCGCC
208262	40458	AGTGGCTTGGATATCTTTCC	252849	85045	TGTCCCTTCTAATAGTTTTT	297436	129632	TCTCCACAATTATTGACCGC
208263	40459	CAGTGGCTTGGATATCTTTC	252850	85046	CTGTCCCTTCTAATAGTTTT	297437	129633	CTCTCCACAATTATTGACCG
208264	40460	CCAGTGGCTTGGATATCTTT	252851	85047	ACTGTCCCTTCTAATAGTTT	297438	129634	CCTCTCCACAATTATTGACC
208265	40461	CCCAGTGGCTTGGATATCTT	252852	85048	CACTGTCCCTTCTAATAGTT	297439	129635	TCCTCTCCACAATTATTGAC
208266	40462	TCCCAGTGGCTTGGATATCT	252853	85049	CCACTGTCCCTTCTAATAGT	297440	129636	CTCCTCTCCACAATTATTGA

208267	40463	TTCCCAGTGGCTTGGATATC	252854	85050	GCCACTGTCCCTTCTAATAG	297441	129637	TCTCCTCTCCACAATTATTG
208268	40464	CTTCCCAGTGGCTTGGATAT	252855	85051	AGCCACTGTCCCTTCTAATA	297442	129638	CTCTCCTCTCCACAATTATT
208269	40465	CCTTCCCAGTGGCTTGGATA	252856	85052	TAGCCACTGTCCCTTCTAAT	297443	129639	TCTCTCCTCTCCACAATTAT
208270	40466	ACCTTCCCAGTGGCTTGGAT	252857	85053	ATAGCCACTGTCCCTTCTAA	297444	129640	TTCTCTCCTCTCCACAATTA
208271	40467	GACCTTCCCAGTGGCTTGGA	252858	85054	TATAGCCACTGTCCCTTCTA	297445	129641	ATTCTCTCCTCTCCACAATT
208272	40468	GGACCTTCCCAGTGGCTTGG	252859	85055	TTATAGCCACTGTCCCTTCT	297446	129642	CATTCTCTCCTCTCCACAAT
208273	40469	CGGACCTTCCCAGTGGCTTG	252860	85056	CTTATAGCCACTGTCCCTTC	297447	129643	TCATTCTCTCCTCTCCACAA
208274	40470	ACGGACCTTCCCAGTGGCTT	252861	85057	TCTTATAGCCACTGTCCCTT	297448	129644	CTCATTCTCTCCTCTCCACA
208275	40471	CACGGACCTTCCCAGTGGCT	252862	85058	CTCTTATAGCCACTGTCCCT	297449	129645	TCTCATTCTCTCCTCTCCAC
208276	40472	CCACGGACCTTCCCAGTGGC	252863	85059	TCTCTTATAGCCACTGTCCC	297450	129646	CTCTCATTCTCTCCTCTCCA
208277	40473	GCCACGGACCTTCCCAGTGG	252864	85060	TTCTCTTATAGCCACTGTCC	297451	129647	TCTCTCATTCTCTCCTCTCC
208278	40474	AGCCACGGACCTTCCCAGTG	252865	85061	CTTCTCTTATAGCCACTGTC	297452	129648	CTCTCTCATTCTCTCCTCTC
208279	40475	TAGCCACGGACCTTCCCAGT	252866	85062	TCTTCTCTTATAGCCACTGT	297453	129649	ACTCTCTCATTCTCTCCTCT
208280	40476	GTAGCCACGGACCTTCCCAG	252867	85063	TTCTTCTCTTATAGCCACTG	297454	129650	CACTCTCTCATTCTCTCCTC
208281	40477	GGTAGCCACGGACCTTCCCA	252868	85064	GTTCTTCTCTTATAGCCACT	297455	129651	ACACTCTCTCATTCTCTCCT
208282	40478	GGGTAGCCACGGACCTTCCC	252869	85065	GGTTCTTCTCTTATAGCCAC	297456	129652	CACACTCTCTCATTCTCTCC
208283	40479	TGGGTAGCCACGGACCTTCC	252870	85066	AGGTTCTTCTCTTATAGCCA	297457	129653	CCACACTCTCTCATTCTCTC
208284	40480	CTGGGTAGCCACGGACCTTC	252871	85067	GAGGTTCTTCTCTTATAGCC	297458	129654	TCCACACTCTCTCATTCTCT
208285	40481	CCTGGGTAGCCACGGACCTT	252872	85068	TGAGGTTCTTCTCTTATAGC	297459	129655	TTCCACACTCTCTCATTCTC
208286	40482	CCCTGGGTAGCCACGGACCT	252873	85069	CTGAGGTTCTTCTCTTATAG	297460	129656	TTTCCACACTCTCTCATTCT
208287	40483	ACCCTGGGTAGCCACGGACC	252874	85070	ACTGAGGTTCTTCTCTTATA	297461	129657	TTTTCCACACTCTCTCATTC
208288	40484	TACCCTGGGTAGCCACGGAC	252875	85071	GACTGAGGTTCTTCTCTTAT	297462	129658	TTTTTCCACACTCTCTCATT
208289	40485	CTACCCTGGGTAGCCACGGA	252876	85072	TGACTGAGGTTCTTCTCTTA	297463	129659	TTTTTTCCACACTCTCTCAT
208290	40486	GCTACCCTGGGTAGCCACGG	252877	85073	TTGACTGAGGTTCTTCTCTT	297464	129660	TTTTTTTCCACACTCTCTCA
208291	40487	GGCTACCCTGGGTAGCCACG	252878	85074	ATTGACTGAGGTTCTTCTCT	297465	129661	TTTTTTTTCCACACTCTCTC
208292	40488	GGGCTACCCTGGGTAGCCAC	252879	85075	CATTGACTGAGGTTCTTCTC	297466	129662	TTTTTTTTTCCACACTCTCT
208293	40489	AGGGCTACCCTGGGTAGCCA	252880	85076	ACATTGACTGAGGTTCTTCT	297467	129663	CTTTTTTTTTCCACACTCTC
208294	40490	GAGGGCTACCCTGGGTAGCC	252881	85077	CACATTGACTGAGGTTCTTC	297468	129664	TCTTTTTTTTTCCACACTCT
208295	40491	AGAGGGCTACCCTGGGTAGC	252882	85078	ACACATTGACTGAGGTTCTT	297469	129665	TTCTTTTTTTTTCCACACTC
208296	40492	GAGAGGGCTACCCTGGGTAG	252883	85079	CACACATTGACTGAGGTTCT	297470	129666	ATTCTTTTTTTTTCCACACT
208297	40493	AGAGAGGGCTACCCTGGGTA	252884	85080	TCACACATTGACTGAGGTTC	297471	129667	TATTCTTTTTTTTTCCACAC
208298	40494	CAGAGAGGGCTACCCTGGGT	252885	85081	TTCACACATTGACTGAGGTT	297472	129668	TTATTCTTTTTTTTTCCACA
208299	40495	CCAGAGAGGGCTACCCTGGG	252886	85082	TTTCACACATTGACTGAGGT	297473	129669	ATTATTCTTTTTTTTTCCAC
208300	40496	CCCAGAGAGGGCTACCCTGG	252887	85083	ATTTCACACATTGACTGAGG	297474	129670	CATTATTCTTTTTTTTTCCA
208301	40497	CCCCAGAGAGGGCTACCCTG	252888	85084	AATTTCACACATTGACTGAG	297475	129671	TCATTATTCTTTTTTTTTCC
208302	40498	TCCCCAGAGAGGGCTACCCT	252889	85085	TAATTTCACACATTGACTGA	297476	129672	GTCATTATTCTTTTTTTTTC
208303	40499	CTCCCCAGAGAGGGCTACCC	252890	85086	TTAATTTCACACATTGACTG	297477	129673	GGTCATTATTCTTTTTTTTT
208304	40500	CCTCCCCAGAGAGGGCTACC	252891	85087	GTTAATTTCACACATTGACT	297478	129674	GGGTCATTATTCTTTTTTTT
208305	40501	CCCTCCCCAGAGAGGGCTAC	252892	85088	AGTTAATTTCACACATTGAC	297479	129675	CGGGTCATTATTCTTTTTTT
208306	40502	GCCCTCCCCAGAGAGGGCTA	252893	85089	TAGTTAATTTCACACATTGA	297480	129676	CCGGGTCATTATTCTTTTTT
208307	40503	AGCCCTCCCCAGAGAGGGCT	252894	85090	CTAGTTAATTTCACACATTG	297481	129677	GCCGGGTCATTATTCTTTTT
208308	40504	CAGCCCTCCCCAGAGAGGGC	252895	85091	CCTAGTTAATTTCACACATT	297482	129678	GGCCGGGTCATTATTCTTTT
208309	40505	GCAGCCCTCCCCAGAGAGGG	252896	85092	TCCTAGTTAATTTCACACAT	297483	129679	GGGCCGGGTCATTATTCTTT
208310	40506	AGCAGCCCTCCCCAGAGAGG	252897	85093	TTCCTAGTTAATTTCACACA	297484	129680	GGGGCCGGGTCATTATTCTT
208311	40507	TAGCAGCCCTCCCCAGAGAG	252898	85094	GTTCCTAGTTAATTTCACAC	297485	129681	GGGGGCCGGGTCATTATTCT
208312	40508	ATAGCAGCCCTCCCCAGAGA	252899	85095	GGTTCCTAGTTAATTTCACA	297486	129682	CGGGGGCCGGGTCATTATTC
208313	40509	TATAGCAGCCCTCCCCAGAG	252900	85096	AGGTTCCTAGTTAATTTCAC	297487	129683	GCGGGGGCCGGGTCATTATT
208314	40510	ATATAGCAGCCCTCCCCAGA	252901	85097	CAGGTTCCTAGTTAATTTCA	297488	129684	GGCGGGGGCCGGGTCATTAT
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208316	40512	GGATATAGCAGCCCTCCCCA	252903	85099	GCCAGGTTCCTAGTTAATTT	297490	129686	AGGGCGGGGGCCGGGTCATT
208317	40513	TGGATATAGCAGCCCTCCCC	252904	85100	AGCCAGGTTCCTAGTTAATT	297491	129687	GAGGGCGGGGGCCGGGTCAT
208318	40514	TTGGATATAGCAGCCCTCCC	252905	85101	GAGCCAGGTTCCTAGTTAAT	297492	129688	AGAGGGCGGGGGCCGGGTCA
208319	40515	CTTGGATATAGCAGCCCTCC	252906	85102	GGAGCCAGGTTCCTAGTTAA	297493	129689	CAGAGGGCGGGGGCCGGGTC
208320	40516	TCTTGGATATAGCAGCCCTC	252907	85103	AGGAGCCAGGTTCCTAGTTA	297494	129690	GCAGAGGGCGGGGGCCGGGT
208321	40517	CTCTTGGATATAGCAGCCCT	252908	85104	CAGGAGCCAGGTTCCTAGTT	297495	129691	GGCAGAGGGCGGGGGCCGGG
208322	40518	GCTCTTGGATATAGCAGCCC	252909	85105	ACAGGAGCCAGGTTCCTAGT	297496	129692	GGGCAGAGGGCGGGGGCCGG
208323	40519	GGCTCTTGGATATAGCAGCC	252910	85106	AACAGGAGCCAGGTTCCTAG	297497	129693	GGGGCAGAGGGCGGGGGCCG
208324	40520	GGGCTCTTGGATATAGCAGC	252911	85107	AAACAGGAGCCAGGTTCCTA	297498	129694	GGGGGCAGAGGGCGGGGGCC
208325	40521	GGGGCTCTTGGATATAGCAG	252912	85108	GAAACAGGAGCCAGGTTCCT	297499	129695	TGGGGGCAGAGGGCGGGGGC
208326	40522	AGGGGCTCTTGGATATAGCA	252913	85109	AGAAACAGGAGCCAGGTTCC	297500	129696	CTGGGGGCAGAGGGCGGGGG
208327	40523	GAGGGGCTCTTGGATATAGC	252914	85110	AAGAAACAGGAGCCAGGTTC	297501	129697	GCTGGGGGCAGAGGGCGGGG
208328	40524	TGAGGGGCTCTTGGATATAG	252915	85111	AAAGAAACAGGAGCCAGGTT	297502	129698	AGCTGGGGGCAGAGGGCGGG
208329	40525	ATGAGGGGCTCTTGGATATA	252916	85112	AAAAGAAACAGGAGCCAGGT	297503	129699	CAGCTGGGGGCAGAGGGCGG
208330	40526	CATGAGGGGCTCTTGGATAT	252917	85113	TAAAAGAAACAGGAGCCAGG	297504	129700	GCAGCTGGGGGCAGAGGGCG
208331	40527	TCATGAGGGGCTCTTGGATA	252918	85114	CTAAAAGAAACAGGAGCCAG	297505	129701	AGCAGCTGGGGGCAGAGGGC
208332	40528	CTCATGAGGGGCTCTTGGAT	252919	85115	CCTAAAAGAAACAGGAGCCA	297506	129702	GAGCAGCTGGGGGCAGAGGG
208333	40529	TCTCATGAGGGGCTCTTGGA	252920	85116	ACCTAAAAGAAACAGGAGCC	297507	129703	GGAGCAGCTGGGGGCAGAGG
208334	40530	TTCTCATGAGGGGCTCTTGG	252921	85117	GACCTAAAAGAAACAGGAGC	297508	129704	AGGAGCAGCTGGGGGCAGAG
208335	40531	ATTCTCATGAGGGGCTCTTG	252922	85118	TGACCTAAAAGAAACAGGAG	297509	129705	GAGGAGCAGCTGGGGGCAGA
208336	40532	AATTCTCATGAGGGGCTCTT	252923	85119	ATGACCTAAAAGAAACAGGA	297510	129706	CGAGGAGCAGCTGGGGGCAG
208337	40533	AAATTCTCATGAGGGGCTCT	252924	85120	CATGACCTAAAAGAAACAGG	297511	129707	GCGAGGAGCAGCTGGGGGCA
208338	40534	CAAATTCTCATGAGGGGCTC	252925	85121	ACATGACCTAAAAGAAACAG	297512	129708	TGCGAGGAGCAGCTGGGGGC

208339	40535	TCAAATTCTCATGAGGGGCT	252926	85122	AACATGACCTAAAAGAAACA	297513	129709	CTGCGAGGAGCAGCTGGGGG
208340	40536	TTCAAATTCTCATGAGGGGC	252927	85123	AAACATGACCTAAAAGAAAC	297514	129710	ACTGCGAGGAGCAGCTGGGG
208341	40537	TTTCAAATTCTCATGAGGGG	252928	85124	AAAACATGACCTAAAAGAAA	297515	129711	AACTGCGAGGAGCAGCTGGG
208342	40538	TTTTCAAATTCTCATGAGGG	252929	85125	AAAAACATGACCTAAAAGAA	297516	129712	GAACTGCGAGGAGCAGCTGG
208343	40539	ATTTTCAAATTCTCATGAGG	252930	85126	GAAAAACATGACCTAAAAGA	297517	129713	CGAACTGCGAGGAGCAGCTG
208344	40540	GATTTTCAAATTCTCATGAG	252931	85127	TGAAAAACATGACCTAAAAG	297518	129714	CCGAACTGCGAGGAGCAGCT
208345	40541	CGATTTTCAAATTCTCATGA	252932	85128	CTGAAAAACATGACCTAAAA	297519	129715	ACCGAACTGCGAGGAGCAGC
208346	40542	TCGATTTTCAAATTCTCATG	252933	85129	GCTGAAAAACATGACCTAAA	297520	129716	AACCGAACTGCGAGGAGCAG
208347	40543	GTCGATTTTCAAATTCTCAT	252934	85130	AGCTGAAAAACATGACCTAA	297521	129717	TAACCGAACTGCGAGGAGCA
208348	40544	GGTCGATTTTCAAATTCTCA	252935	85131	AAGCTGAAAAACATGACCTA	297522	129718	TTAACCGAACTGCGAGGAGC
208349	40545	TGGTCGATTTTCAAATTCTC	252936	85132	TAAGCTGAAAAACATGACCT	297523	129719	ATTAACCGAACTGCGAGGAG
208350	40546	ATGGTCGATTTTCAAATTCT	252937	85133	CTAAGCTGAAAAACATGACC	297524	129720	AATTAACCGAACTGCGAGGA
208351	40547	CATGGTCGATTTTCAAATTC	252938	85134	CCTAAGCTGAAAAACATGAC	297525	129721	CAATTAACCGAACTGCGAGG
208352	40548	CCATGGTCGATTTTCAAATT	252939	85135	ACCTAAGCTGAAAAACATGA	297526	129722	CCAATTAACCGAACTGCGAG
208353	40549	ACCATGGTCGATTTTCAAAT	252940	85136	TACCTAAGCTGAAAAACATG	297527	129723	ACCAATTAACCGAACTGCGA
208354	40550	TACCATGGTCGATTTTCAAA	252941	85137	TTACCTAAGCTGAAAAACAT	297528	129724	AACCAATTAACCGAACTGCG
208355	40551	CTACCATGGTCGATTTTCAA	252942	85138	TTTACCTAAGCTGAAAAACA	297529	129725	TAACCAATTAACCGAACTGC
208356	40552	CCTACCATGGTCGATTTTCA	252943	85139	TTTTACCTAAGCTGAAAAAC	297530	129726	TTAACCAATTAACCGAACTG
208357	40553	CCCTACCATGGTCGATTTTC	252944	85140	GTTTTACCTAAGCTGAAAAA	297531	129727	ATTAACCAATTAACCGAACT
208358	40554	GCCCTACCATGGTCGATTTT	252945	85141	AGTTTTACCTAAGCTGAAAA	297532	129728	GATTAACCAATTAACCGAAC
208359	40555	GGCCCTACCATGGTCGATTT	252946	85142	TAGTTTTACCTAAGCTGAAA	297533	129729	TGATTAACCAATTAACCGAA
208360	40556	AGGCCCTACCATGGTCGATT	252947	85143	CTAGTTTTACCTAAGCTGAA	297534	129730	GTGATTAACCAATTAACCGA
208361	40557	CAGGCCCTACCATGGTCGAT	252948	85144	TCTAGTTTTACCTAAGCTGA	297535	129731	AGTGATTAACCAATTAACCG
208362	40558	GCAGGCCCTACCATGGTCGA	252949	85145	CTCTAGTTTTACCTAAGCTG	297536	129732	AAGTGATTAACCAATTAACC
208363	40559	AGCAGGCCCTACCATGGTCG	252950	85146	CCTCTAGTTTTACCTAAGCT	297537	129733	TAAGTGATTAACCAATTAAC
208364	40560	CAGCAGGCCCTACCATGGTC	252951	85147	GCCTCTAGTTTTACCTAAGC	297538	129734	TTAAGTGATTAACCAATTAA
208365	40561	TCAGCAGGCCCTACCATGGT	252952	85148	AGCCTCTAGTTTTACCTAAG	297539	129735	GTTAAGTGATTAACCAATTA
208366	40562	GTCAGCAGGCCCTACCATGG	252953	85149	AAGCCTCTAGTTTTACCTAA	297540	129736	GGTTAAGTGATTAACCAATT
208367	40563	AGTCAGCAGGCCCTACCATG	252954	85150	AAAGCCTCTAGTTTTACCTA	297541	129737	AGGTTAAGTGATTAACCAAT
208368	40564	AAGTCAGCAGGCCCTACCAT	252955	85151	CAAAGCCTCTAGTTTTACCT	297542	129738	CAGGTTAAGTGATTAACCAA
208369	40565	AAAGTCAGCAGGCCCTACCA	252956	85152	TCAAAGCCTCTAGTTTTACC	297543	129739	GCAGGTTAAGTGATTAACCA
208370	40566	AAAAGTCAGCAGGCCCTACC	252957	85153	ATCAAAGCCTCTAGTTTTAC	297544	129740	AGCAGGTTAAGTGATTAACC
208371	40567	CAAAAGTCAGCAGGCCCTAC	252958	85154	TATCAAAGCCTCTAGTTTTA	297545	129741	AAGCAGGTTAAGTGATTAAC
208372	40568	TCAAAAGTCAGCAGGCCCTA	252959	85155	TTATCAAAGCCTCTAGTTTT	297546	129742	AAAGCAGGTTAAGTGATTAA
208373	40569	GTCAAAAGTCAGCAGGCCCT	252960	85156	TTTATCAAAGCCTCTAGTTT	297547	129743	AAAAGCAGGTTAAGTGATTA
208374	40570	TGTCAAAAGTCAGCAGGCCC	252961	85157	CTTTATCAAAGCCTCTAGTT	297548	129744	CAAAAGCAGGTTAAGTGATT
208375	40571	CTGTCAAAAGTCAGCAGGCC	252962	85158	GCTTTATCAAAGCCTCTAGT	297549	129745	ACAAAAGCAGGTTAAGTGAT
208376	40572	GCTGTCAAAAGTCAGCAGGC	252963	85159	TGCTTTATCAAAGCCTCTAG	297550	129746	GACAAAAGCAGGTTAAGTGA
208377	40573	AGCTGTCAAAAGTCAGCAGG	252964	85160	ATGCTTTATCAAAGCCTCTA	297551	129747	TGACAAAAGCAGGTTAAGTG
208378	40574	TAGCTGTCAAAAGTCAGCAG	252965	85161	CATGCTTTATCAAAGCCTCT	297552	129748	GTGACAAAAGCAGGTTAAGT
208379	40575	TTAGCTGTCAAAAGTCAGCA	252966	85162	TCATGCTTTATCAAAGCCTC	297553	129749	AGTGACAAAAGCAGGTTAAG
208380	40576	ATTAGCTGTCAAAAGTCAGC	252967	85163	GTCATGCTTTATCAAAGCCT	297554	129750	GAGTGACAAAAGCAGGTTAA
208381	40577	CATTAGCTGTCAAAAGTCAG	252968	85164	GGTCATGCTTTATCAAAGCC	297555	129751	CGAGTGACAAAAGCAGGTTA
208382	40578	CCATTAGCTGTCAAAAGTCA	252969	85165	AGGTCATGCTTTATCAAAGC	297556	129752	CCGAGTGACAAAAGCAGGTT
208383	40579	ACCATTAGCTGTCAAAAGTC	252970	85166	GAGGTCATGCTTTATCAAAG	297557	129753	GCCGAGTGACAAAAGCAGGT
208384	40580	CACCATTAGCTGTCAAAAGT	252971	85167	AGAGGTCATGCTTTATCAAA	297558	129754	AGCCGAGTGACAAAAGCAGG
208385	40581	ACACCATTAGCTGTCAAAAG	252972	85168	TAGAGGTCATGCTTTATCAA	297559	129755	AAGCCGAGTGACAAAAGCAG
208386	40582	CACACCATTAGCTGTCAAAA	252973	85169	CTAGAGGTCATGCTTTATCA	297560	129756	AAAGCCGAGTGACAAAAGCA
208387	40583	GCACACCATTAGCTGTCAAA	252974	85170	TCTAGAGGTCATGCTTTATC	297561	129757	CAAAGCCGAGTGACAAAAGC
208388	40584	AGCACACCATTAGCTGTCAA	252975	85171	TTCTAGAGGTCATGCTTTAT	297562	129758	CCAAAGCCGAGTGACAAAAG
208389	40585	CAGCACACCATTAGCTGTCA	252976	85172	TTTCTAGAGGTCATGCTTTA	297563	129759	GCCAAAGCCGAGTGACAAAA
208390	40586	TCAGCACACCATTAGCTGTC	252977	85173	ATTTCTAGAGGTCATGCTTT	297564	129760	AGCCAAAGCCGAGTGACAAA
208391	40587	CTCAGCACACCATTAGCTGT	252978	85174	GATTTCTAGAGGTCATGCTT	297565	129761	GAGCCAAAGCCGAGTGACAA
208392	40588	TCTCAGCACACCATTAGCTG	252979	85175	TGATTTCTAGAGGTCATGCT	297566	129762	CGAGCCAAAGCCGAGTGACA
208393	40589	TTCTCAGCACACCATTAGCT	252980	85176	ATGATTTCTAGAGGTCATGC	297567	129763	CCGAGCCAAAGCCGAGTGAC
208394	40590	ATTCTCAGCACACCATTAGC	252981	85177	AATGATTTCTAGAGGTCATG	297568	129764	CCCGAGCCAAAGCCGAGTGA
208395	40591	AATTCTCAGCACACCATTAG	252982	85178	CAATGATTTCTAGAGGTCAT	297569	129765	TCCCGAGCCAAAGCCGAGTG
208396	40592	CAATTCTCAGCACACCATTA	252983	85179	GCAATGATTTCTAGAGGTCA	297570	129766	GTCCCGAGCCAAAGCCGAGT
208397	40593	ACAATTCTCAGCACACCATT	252984	85180	AGCAATGATTTCTAGAGGTC	297571	129767	AGTCCCGAGCCAAAGCCGAG
208398	40594	GACAATTCTCAGCACACCAT	252985	85181	AAGCAATGATTTCTAGAGGT	297572	129768	AAGTCCCGAGCCAAAGCCGA
208399	40595	GGACAATTCTCAGCACACCA	252986	85182	AAAGCAATGATTTCTAGAGG	297573	129769	GAAGTCCCGAGCCAAAGCCG
208400	40596	GGGACAATTCTCAGCACACC	252987	85183	AAAAGCAATGATTTCTAGAG	297574	129770	TGAAGTCCCGAGCCAAAGCC
208401	40597	AGGGACAATTCTCAGCACAC	252988	85184	GAAAAGCAATGATTTCTAGA	297575	129771	TTGAAGTCCCGAGCCAAAGC
208402	40598	GAGGGACAATTCTCAGCACA	252989	85185	TGAAAAGCAATGATTTCTAG	297576	129772	TTTGAAGTCCCGAGCCAAAG
208403	40599	GGAGGGACAATTCTCAGCAC	252990	85186	ATGAAAAGCAATGATTTCTA	297577	129773	TTTTGAAGTCCCGAGCCAAA
208404	40600	TGGAGGGACAATTCTCAGCA	252991	85187	TATGAAAAGCAATGATTTCT	297578	129774	ATTTTGAAGTCCCGAGCCAA
208405	40601	TTGGAGGGACAATTCTCAGC	252992	85188	TTATGAAAAGCAATGATTTC	297579	129775	GATTTTGAAGTCCCGAGCCA
208406	40602	TTTGGAGGGACAATTCTCAG	252993	85189	TTTATGAAAAGCAATGATTT	297580	129776	TGATTTTGAAGTCCCGAGCC
208407	40603	CTTTGGAGGGACAATTCTCA	252994	85190	ATTTATGAAAAGCAATGATT	297581	129777	CTGATTTTGAAGTCCCGAGC
208408	40604	TCTTTGGAGGGACAATTCTC	252995	85191	CATTTATGAAAAGCAATGAT	297582	129778	ACTGATTTTGAAGTCCCGAG
208409	40605	ATCTTTGGAGGGACAATTCT	252996	85192	CCATTTATGAAAAGCAATGA	297583	129779	CACTGATTTTGAAGTCCCGA
208410	40606	CATCTTTGGAGGGACAATTC	252997	85193	TCCATTTATGAAAAGCAATG	297584	129780	TCACTGATTTTGAAGTCCCG

208411	40607	GCATCTTTGGAGGGACAATT	252998	85194	TTCCATTTATGAAAAGCAAT	297585	129781	ATCACTGATTTTGAAGTCCC
208412	40608	GGCATCTTTGGAGGGACAAT	252999	85195	CTTCCATTTATGAAAAGCAA	297586	129782	CATCACTGATTTTGAAGTCC
208413	40609	AGGCATCTTTGGAGGGACAA	253000	85196	ACTTCCATTTATGAAAAGCA	297587	129783	CCATCACTGATTTTGAAGTC
208414	40610	AAGGCATCTTTGGAGGGACA	253001	85197	CACTTCCATTTATGAAAAGC	297588	129784	CCCATCACTGATTTTGAAGT
208415	40611	AAAGGCATCTTTGGAGGGAC	253002	85198	CCACTTCCATTTATGAAAAG	297589	129785	TCCCATCACTGATTTTGAAG
208416	40612	GAAAGGCATCTTTGGAGGGA	253003	85199	CCCACTTCCATTTATGAAAA	297590	129786	CTCCCATCACTGATTTTGAA
208417	40613	GGAAAGGCATCTTTGGAGGG	253004	85200	ACCCACTTCCATTTATGAAA	297591	129787	ACTCCCATCACTGATTTTGA
208418	40614	TGGAAAGGCATCTTTGGAGG	253005	85201	AACCCACTTCCATTTATGAA	297592	129788	TACTCCCATCACTGATTTTG
208419	40615	ATGGAAAGGCATCTTTGGAG	253006	85202	AAACCCACTTCCATTTATGA	297593	129789	TTACTCCCATCACTGATTTT
208420	40616	AATGGAAAGGCATCTTTGGA	253007	85203	CAAACCCACTTCCATTTATG	297594	129790	CTTACTCCCATCACTGATTT
208421	40617	GAATGGAAAGGCATCTTTGG	253008	85204	TCAAACCCACTTCCATTTAT	297595	129791	TCTTACTCCCATCACTGATT
208422	40618	GGAATGGAAAGGCATCTTTG	253009	85205	CTCAAACCCACTTCCATTTA	297596	129792	CTCTTACTCCCATCACTGAT
208423	40619	GGGAATGGAAAGGCATCTTT	253010	85206	ACTCAAACCCACTTCCATTT	297597	129793	GCTCTTACTCCCATCACTGA
208424	40620	AGGGAATGGAAAGGCATCTT	253011	85207	AACTCAAACCCACTTCCATT	297598	129794	TGCTCTTACTCCCATCACTG
208425	40621	GAGGGAATGGAAAGGCATCT	253012	85208	AAACTCAAACCCACTTCCAT	297599	129795	TTGCTCTTACTCCCATCACT
208426	40622	CGAGGGAATGGAAAGGCATC	253013	85209	AAAACTCAAACCCACTTCCA	297600	129796	TTTGCTCTTACTCCCATCAC
208427	40623	CCGAGGGAATGGAAAGGCAT	253014	85210	AAAAACTCAAACCCACTTCC	297601	129797	ATTTGCTCTTACTCCCATCA
208428	40624	CCCGAGGGAATGGAAAGGCA	253015	85211	AAAAAACTCAAACCCACTTC	297602	129798	AATTTGCTCTTACTCCCATC
208429	40625	TCCCGAGGGAATGGAAAGGC	253016	85212	GAAAAAACTCAAACCCACTT	297603	129799	AAATTTGCTCTTACTCCCAT
208430	40626	CTCCCGAGGGAATGGAAAGG	253017	85213	AGAAAAAACTCAAACCCACT	297604	129800	GAAATTTGCTCTTACTCCCA
208431	40627	TCTCCCGAGGGAATGGAAAG	253018	85214	TAGAAAAAACTCAAACCCAC	297605	129801	TGAAATTTGCTCTTACTCCC
208432	40628	CTCTCCCGAGGGAATGGAAA	253019	85215	GTAGAAAAAACTCAAACCCA	297606	129802	ATGAAATTTGCTCTTACTCC
208433	40629	ACTCTCCCGAGGGAATGGAA	253020	85216	AGTAGAAAAAACTCAAACCC	297607	129803	GATGAAATTTGCTCTTACTC
208434	40630	GACTCTCCCGAGGGAATGGA	253021	85217	CAGTAGAAAAAACTCAAACC	297608	129804	AGATGAAATTTGCTCTTACT
208435	40631	AGACTCTCCCGAGGGAATGG	253022	85218	TCAGTAGAAAAAACTCAAAC	297609	129805	AAGATGAAATTTGCTCTTAC
208436	40632	CAGACTCTCCCGAGGGAATG	253023	85219	ATCAGTAGAAAAAACTCAAA	297610	129806	AAAGATGAAATTTGCTCTTA
208437	40633	CCAGACTCTCCCGAGGGAAT	253024	85220	AATCAGTAGAAAAAACTCAA	297611	129807	GAAAGATGAAATTTGCTCTT
208438	40634	CCCAGACTCTCCCGAGGGAA	253025	85221	CAATCAGTAGAAAAAACTCA	297612	129808	GGAAAGATGAAATTTGCTCT
208439	40635	GCCCAGACTCTCCCGAGGGA	253026	85222	ACAATCAGTAGAAAAAACTC	297613	129809	TGGAAAGATGAAATTTGCTC
208440	40636	TGCCCAGACTCTCCCGAGGG	253027	85223	AACAATCAGTAGAAAAAACT	297614	129810	TTGGAAAGATGAAATTTGCT
208441	40637	CTGCCCAGACTCTCCCGAGG	253028	85224	TAACAATCAGTAGAAAAAAC	297615	129811	TTTGGAAAGATGAAATTTGC
208442	40638	GCTGCCCAGACTCTCCCGAG	253029	85225	CTAACAATCAGTAGAAAAAA	297616	129812	ATTTGGAAAGATGAAATTTG
208443	40639	GGCTGCCCAGACTCTCCCGA	253030	85226	ACTAACAATCAGTAGAAAAA	297617	129813	AATTTGGAAAGATGAAATTT
208444	40640	GGGCTGCCCAGACTCTCCCG	253031	85227	CACTAACAATCAGTAGAAAA	297618	129814	CAATTTGGAAAGATGAAATT
208445	40641	GGGGCTGCCCAGACTCTCCC	253032	85228	GCACTAACAATCAGTAGAAA	297619	129815	TCAATTTGGAAAGATGAAAT
208446	40642	AGGGGCTGCCCAGACTCTCC	253033	85229	TGCACTAACAATCAGTAGAA	297620	129816	ATCAATTTGGAAAGATGAAA
208447	40643	TAGGGGCTGCCCAGACTCTC	253034	85230	CTGCACTAACAATCAGTAGA	297621	129817	CATCAATTTGGAAAGATGAA
208448	40644	GTAGGGGCTGCCCAGACTCT	253035	85231	CCTGCACTAACAATCAGTAG	297622	129818	CCATCAATTTGGAAAGATGA
208449	40645	AGTAGGGGCTGCCCAGACTC	253036	85232	ACCTGCACTAACAATCAGTA	297623	129819	CCCATCAATTTGGAAAGATG
208450	40646	CAGTAGGGGCTGCCCAGACT	253037	85233	CACCTGCACTAACAATCAGT	297624	129820	ACCCATCAATTTGGAAAGAT
208451	40647	CCAGTAGGGGCTGCCCAGAC	253038	85234	TCACCTGCACTAACAATCAG	297625	129821	CACCCATCAATTTGGAAAGA
208452	40648	CCCAGTAGGGGCTGCCCAGA	253039	85235	ATCACCTGCACTAACAATCA	297626	129822	CCACCCATCAATTTGGAAAG
208453	40649	CCCCAGTAGGGGCTGCCCAG	253040	85236	CATCACCTGCACTAACAATC	297627	129823	CCCACCCATCAATTTGGAAA
208454	40650	CCCCCAGTAGGGGCTGCCCA	253041	85237	ACATCACCTGCACTAACAAT	297628	129824	GCCCACCCATCAATTTGGAA
208455	40651	GCCCCCAGTAGGGGCTGCCC	253042	85238	GACATCACCTGCACTAACAA	297629	129825	AGCCCACCCATCAATTTGGA
208456	40652	AGCCCCCAGTAGGGGCTGCC	253043	85239	AGACATCACCTGCACTAACA	297630	129826	TAGCCCACCCATCAATTTGG
208457	40653	CAGCCCCCAGTAGGGGCTGC	253044	85240	TAGACATCACCTGCACTAAC	297631	129827	CTAGCCCACCCATCAATTTG
208458	40654	CCAGCCCCCAGTAGGGGCTG	253045	85241	GTAGACATCACCTGCACTAA	297632	129828	ACTAGCCCACCCATCAATTT
208459	40655	CCCAGCCCCCAGTAGGGGCT	253046	85242	TGTAGACATCACCTGCACTA	297633	129829	TACTAGCCCACCCATCAATT
208460	40656	TCCCAGCCCCCAGTAGGGGC	253047	85243	ATGTAGACATCACCTGCACT	297634	129830	TTACTAGCCCACCCATCAAT
208461	40657	ATCCCAGCCCCCAGTAGGGG	253048	85244	CATGTAGACATCACCTGCAC	297635	129831	ATTACTAGCCCACCCATCAA
208462	40658	CATCCCAGCCCCCAGTAGGG	253049	85245	GCATGTAGACATCACCTGCA	297636	129832	TATTACTAGCCCACCCATCA
208463	40659	GCATCCCAGCCCCCAGTAGG	253050	85246	GGCATGTAGACATCACCTGC	297637	129833	TTATTACTAGCCCACCCATC
208464	40660	AGCATCCCAGCCCCCAGTAG	253051	85247	GGGCATGTAGACATCACCTG	297638	129834	TTTATTACTAGCCCACCCAT
208465	40661	CAGCATCCCAGCCCCCAGTA	253052	85248	GGGGCATGTAGACATCACCT	297639	129835	TTTTATTACTAGCCCACCCA
208466	40662	CCAGCATCCCAGCCCCCAGT	253053	85249	GGGGGCATGTAGACATCACC	297640	129836	ATTTTATTACTAGCCCACCC
208467	40663	GCCAGCATCCCAGCCCCCAG	253054	85250	TGGGGGCATGTAGACATCAC	297641	129837	TATTTTATTACTAGCCCACC
208468	40664	AGCCAGCATCCCAGCCCCCA	253055	85251	CTGGGGGCATGTAGACATCA	297642	129838	ATATTTTATTACTAGCCCAC
208469	40665	GAGCCAGCATCCCAGCCCCC	253056	85252	TCTGGGGGCATGTAGACATC	297643	129839	AATATTTTATTACTAGCCCA
208470	40666	AGAGCCAGCATCCCAGCCCC	253057	85253	TTCTGGGGGCATGTAGACAT	297644	129840	AAATATTTTATTACTAGCCC
208471	40667	AAGAGCCAGCATCCCAGCCC	253058	85254	GTTCTGGGGGCATGTAGACA	297645	129841	TAAATATTTTATTACTAGCC
208472	40668	GAAGAGCCAGCATCCCAGCC	253059	85255	TGTTCTGGGGGCATGTAGAC	297646	129842	TTAAATATTTTATTACTAGC
208473	40669	GGAAGAGCCAGCATCCCAGC	253060	85256	ATGTTCTGGGGGCATGTAGA	297647	129843	TTTAAATATTTTATTACTAG
208474	40670	GGGAAGAGCCAGCATCCCAG	253061	85257	TATGTTCTGGGGGCATGTAG	297648	129844	TTTTAAATATTTTATTACTA
208475	40671	AGGGAAGAGCCAGCATCCCA	253062	85258	ATATGTTCTGGGGGCATGTA	297649	129845	TTTTTAAATATTTTATTACT
208476	40672	GAGGGAAGAGCCAGCATCCC	253063	85259	AATATGTTCTGGGGGCATGT	297650	129846	TTTTTTAAATATTTTATTAC
208477	40673	TGAGGGAAGAGCCAGCATCC	253064	85260	GAATATGTTCTGGGGGCATG	297651	129847	TTTTTTTAAATATTTTATTA
208478	40674	CTGAGGGAAGAGCCAGCATC	253065	85261	GGAATATGTTCTGGGGGCAT	297652	129848	TTTTTTTTAAATATTTTATT
208479	40675	GCTGAGGGAAGAGCCAGCAT	253066	85262	TGGAATATGTTCTGGGGGCA	297653	129849	TTTTTTTTTAAATATTTTAT
208480	40676	GGCTGAGGGAAGAGCCAGCA	253067	85263	ATGGAATATGTTCTGGGGGC	297654	129850	GTTTTTTTTTAAATATTTTA
208481	40677	AGGCTGAGGGAAGAGCCAGC	253068	85264	CATGGAATATGTTCTGGGGG	297655	129851	TGTTTTTTTTTAAATATTTT
208482	40678	GAGGCTGAGGGAAGAGCCAG	253069	85265	GCATGGAATATGTTCTGGGG	297656	129852	ATGTTTTTTTTTAAATATTT

208483	40679	GGAGGCTGAGGGAAGAGCCA	253070	85266	TGCATGGAATATGTTCTGGG	297657	129853	AATGTTTTTTTTTAAATATT
208484	40680	TGGAGGCTGAGGGAAGAGCC	253071	85267	TTGCATGGAATATGTTCTGG	297658	129854	GAATGTTTTTTTTAAATAT
208485	40681	GTGGAGGCTGAGGGAAGAGC	253072	85268	GTTGCATGGAATATGTTCTG	297659	129855	TGAATGTTTTTTTTTAAATA
208486	40682	GGTGGAGGCTGAGGGAAGAG	253073	85269	TGTTGCATGGAATATGTTCT	297660	129856	TTGAATGTTTTTTTTAAAT
208487	40683	GGGTGGAGGCTGAGGGAAGA	253074	85270	TTGTTGCATGGAATATGTTC	297661	129857	TTTGAATGTTTTTTTTAAA
208488	40684	GGGGTGGAGGCTGAGGGAAG	253075	85271	TTTGTTGCATGGAATATGTT	297662	129858	TTTTGAATGTTTTTTTTAA
208489	40685	TGGGGTGGAGGCTGAGGGAA	253076	85272	TTTTGTTGCATGGAATATGT	297663	129859	TTTTTGAATGTTTTTTTTA
208490	40686	TTGGGGTGGAGGCTGAGGGA	253077	85273	TTTTTGTTGCATGGAATATG	297664	129860	GTTTTTGAATGTTTTTTTTT
208491	40687	GTTGGGGTGGAGGCTGAGGG	253078	85274	TTTTTTGTTGCATGGAATAT	297665	129861	TGTTTTTGAATGTTTTTTTT
208492	40688	AGTTGGGGTGGAGGCTGAGG	253079	85275	TTTTTTTGTTGCATGGAATA	297666	129862	ATGTTTTTGAATGTTTTTTT
208493	40689	CAGTTGGGGTGGAGGCTGAG	253080	85276	CTTTTTTTGTTGCATGGAAT	297667	129863	CATGTTTTTGAATGTTTTTT
208494	40690	GCAGTTGGGGTGGAGGCTGA	253081	85277	GCTTTTTTTGTTGCATGGAA	297668	129864	CCATGTTTTTGAATGTTTTT
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208496	40692	GAGCAGTTGGGGTGGAGGCT	253083	85279	GGGCTTTTTTTGTTGCATGG	297670	129866	GGCCATGTTTTTGAATGTTT
208497	40693	AGAGCAGTTGGGGTGGAGGC	253084	85280	TGGGCTTTTTTTGTTGCATG	297671	129867	TGGCCATGTTTTTGAATGTT
208498	40694	GAGAGCAGTTGGGGTGGAGG	253085	85281	CTGGGCTTTTTTTGTTGCAT	297672	129868	GTGGCCATGTTTTTGAATGT
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208500	40696	AAGAGAGCAGTTGGGGTGGA	253087	85283	ACCTGGGCTTTTTTTGTTGC	297674	129870	ATGTGGCCATGTTTTTGAAT
208501	40697	GAAGAGAGCAGTTGGGGTGG	253088	85284	GACCTGGGCTTTTTTTGTTG	297675	129871	GATGTGGCCATGTTTTTGAA
208502	40698	GGAAGAGAGCAGTTGGGGTG	253089	85285	TGACCTGGGCTTTTTTTGTT	297676	129872	GGATGTGGCCATGTTTTTGA
208503	40699	GGGAAGAGAGCAGTTGGGGT	253090	85286	GTGACCTGGGCTTTTTTTGT	297677	129873	TGGATGTGGCCATGTTTTTG
208504	40700	AGGGAAGAGAGCAGTTGGGG	253091	85287	GGTGACCTGGGCTTTTTTTG	297678	129874	TTGGATGTGGCCATGTTTTT
208505	40701	GAGGGAAGAGAGCAGTTGGG	253092	85288	CGGTGACCTGGGCTTTTTTT	297679	129875	GTTGGATGTGGCCATGTTTT
208506	40702	GGAGGGAAGAGAGCAGTTGG	253093	85289	ACGGTGACCTGGGCTTTTTT	297680	129876	TGTTGGATGTGGCCATGTTT
208507	40703	AGGAGGGAAGAGAGCAGTTG	253094	85290	GACGGTGACCTGGGCTTTTT	297681	129877	ATGTTGGATGTGGCCATGTT
208508	40704	GAGGAGGGAAGAGAGCAGTT	253095	85291	AGACGGTGACCTGGGCTTTT	297682	129878	AATGTTGGATGTGGCCATGT
208509	40705	GGAGGAGGGAAGAGAGCAGT	253096	85292	AAGACGGTGACCTGGGCTTT	297683	129879	AAATGTTGGATGTGGCCATG
208510	40706	GGGAGGAGGGAAGAGAGCAG	253097	85293	AAAGACGGTGACCTGGGCTT	297684	129880	GAAATGTTGGATGTGGCCAT
208511	40707	GGGGAGGAGGGAAGAGAGCA	253098	85294	CAAAGACGGTGACCTGGGCT	297685	129881	GGAAATGTTGGATGTGGCCA
208512	40708	AGGGGAGGAGGGAAGAGAGC	253099	85295	GCAAAGACGGTGACCTGGGC	297686	129882	AGGAAATGTTGGATGTGGCC
208513	40709	GAGGGGAGGAGGGAAGAGAG	253100	85296	AGCAAAGACGGTGACCTGGG	297687	129883	GAGGAAATGTTGGATGTGGC
208514	40710	GGAGGGGAGGAGGGAAGAGA	253101	85297	CAGCAAAGACGGTGACCTGG	297688	129884	TGAGGAAATGTTGGATGTGG
208515	40711	GGGAGGGGAGGAGGGAAGAG	253102	85298	CCAGCAAAGACGGTGACCTG	297689	129885	CTGAGGAAATGTTGGATGTG
208516	40712	GGGGAGGGGAGGAGGGAAGA	253103	85299	CCCAGCAAAGACGGTGACCT	297690	129886	CCTGAGGAAATGTTGGATGT
208517	40713	TGGGGAGGGGAGGAGGGAAG	253104	85300	TCCCAGCAAAGACGGTGACC	297691	129887	GCCTGAGGAAATGTTGGATG
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208519	40715	GCTGGGGAGGGGAGGAGGGA	253106	85302	GTTCCCAGCAAAGACGGTGA	297693	129889	TTGCCTGAGGAAATGTTGGA
208520	40716	GGCTGGGGAGGGGAGGAGGG	253107	85303	AGTTCCCAGCAAAGACGGTG	297694	129890	ATTGCCTGAGGAAATGTTGG
208521	40717	GGGCTGGGGAGGGGAGGAGG	253108	85304	AAGTTCCCAGCAAAGACGGT	297695	129891	AATTGCCTGAGGAAATGTTG
208522	40718	GGGGCTGGGGAGGGGAGGAG	253109	85305	CAAGTTCCCAGCAAAGACGG	297696	129892	GAATTGCCTGAGGAAATGTT
208523	40719	GGGGGCTGGGGAGGGGAGGA	253110	85306	TCAAGTTCCCAGCAAAGACG	297697	129893	GGAATTGCCTGAGGAAATGT
208524	40720	AGGGGGCTGGGGAGGGGAGG	253111	85307	GTCAAGTTCCCAGCAAAGAC	297698	129894	AGGAATTGCCTGAGGAAATG
208525	40721	TAGGGGGCTGGGGAGGGGAG	253112	85308	AGTCAAGTTCCCAGCAAAGA	297699	129895	AAGGAATTGCCTGAGGAAAT
208526	40722	TTAGGGGGCTGGGGAGGGGA	253113	85309	AAGTCAAGTTCCCAGCAAAG	297700	129896	AAAGGAATTGCCTGAGGAAA
208527	40723	ATTAGGGGGCTGGGGAGGGG	253114	85310	AAAGTCAAGTTCCCAGCAAA	297701	129897	AAAAGGAATTGCCTGAGGAA
208528	40724	AATTAGGGGGCTGGGGAGGG	253115	85311	AAAAGTCAAGTTCCCAGCAA	297702	129898	CAAAAGGAATTGCCTGAGGA
208529	40725	AAATTAGGGGGCTGGGGAGG	253116	85312	CAAAAGTCAAGTTCCCAGCA	297703	129899	TCAAAAGGAATTGCCTGAGG
208530	40726	GAAATTAGGGGGCTGGGGAG	253117	85313	ACAAAAGTCAAGTTCCCAGC	297704	129900	ATCAAAAGGAATTGCCTGAG
208531	40727	AGAAATTAGGGGGCTGGGGA	253118	85314	CACAAAAGTCAAGTTCCCAG	297705	129901	AATCAAAAGGAATTGCCTGA
208532	40728	GAGAAATTAGGGGGCTGGGG	253119	85315	GCACAAAAGTCAAGTTCCCA	297706	129902	GAATCAAAAGGAATTGCCTG
208533	40729	AGAGAAATTAGGGGGCTGGG	253120	85316	AGCACAAAAGTCAAGTTCCC	297707	129903	AGAATCAAAAGGAATTGCCT
208534	40730	GAGAGAAATTAGGGGGCTGG	253121	85317	GAGCACAAAAGTCAAGTTCC	297708	129904	AAGAATCAAAAGGAATTGCC
208535	40731	TGAGAGAAATTAGGGGGCTG	253122	85318	TGAGCACAAAAGTCAAGTTC	297709	129905	AAAGAATCAAAAGGAATTGC
208536	40732	GTGAGAGAAATTAGGGGGCT	253123	85319	GTGAGCACAAAAGTCAAGTT	297710	129906	AAAAGAATCAAAAGGAATTG
208537	40733	TGTGAGAGAAATTAGGGGGC	253124	85320	AGTGAGCACAAAAGTCAAGT	297711	129907	AAAAAGAATCAAAAGGAATT
208538	40734	TTGTGAGAGAAATTAGGGGG	253125	85321	CAGTGAGCACAAAAGTCAAG	297712	129908	AAAAAAGAATCAAAAGGAAT
208539	40735	CTTGTGAGAGAAATTAGGGG	253126	85322	TCAGTGAGCACAAAAGTCAA	297713	129909	GAAAAAAGAATCAAAAGGAA
208540	40736	CCTTGTGAGAGAAATTAGGG	253127	85323	TTCAGTGAGCACAAAAGTCA	297714	129910	AGAAAAAAGAATCAAAAGGA
208541	40737	GCCTTGTGAGAGAAATTAGG	253128	85324	ATTCAGTGAGCACAAAAGTC	297715	129911	AAGAAAAAAGAATCAAAAGG
208542	40738	AGCCTTGTGAGAGAAATTAG	253129	85325	AATTCAGTGAGCACAAAAGT	297716	129912	GAAGAAAAAAGAATCAAAAG
208543	40739	AAGCCTTGTGAGAGAAATTA	253130	85326	AAATTCAGTGAGCACAAAAG	297717	129913	GGAAGAAAAAAGAATCAAAA
208544	40740	AAAGCCTTGTGAGAGAAATT	253131	85327	AAAATTCAGTGAGCACAAAA	297718	129914	GGGAAGAAAAAAGAATCAAA
208545	40741	CAAAGCCTTGTGAGAGAAAT	253132	85328	TAAAATTCAGTGAGCACAAA	297719	129915	GGGGAAGAAAAAAGAATCAA
208546	40742	ACAAAGCCTTGTGAGAGAAA	253133	85329	TTAAAATTCAGTGAGCACAA	297720	129916	GGGGGAAGAAAAAAGAATCA
208547	40743	AACAAAGCCTTGTGAGAGAA	253134	85330	CTTAAAATTCAGTGAGCACA	297721	129917	AGGGGGAAGAAAAAAGAATC
208548	40744	GAACAAAGCCTTGTGAGAGA	253135	85331	GCTTAAAATTCAGTGAGCAC	297722	129918	GAGGGGGAAGAAAAAAGAAT
208549	40745	AGAACAAAGCCTTGTGAGAG	253136	85332	AGCTTAAAATTCAGTGAGCA	297723	129919	GGAGGGGGAAGAAAAAAGAA
208550	40746	CAGAACAAAGCCTTGTGAGA	253137	85333	AAGCTTAAAATTCAGTGAGC	297724	129920	TGGAGGGGGAAGAAAAAAGA
208551	40747	GCAGAACAAAGCCTTGTGAG	253138	85334	AAAGCTTAAAATTCAGTGAG	297725	129921	ATGGAGGGGGAAGAAAAAAG
208552	40748	TGCAGAACAAAGCCTTGTGA	253139	85335	GAAAGCTTAAAATTCAGTGA	297726	129922	CATGGAGGGGGAAGAAAAAA
208553	40749	CTGCAGAACAAAGCCTTGTG	253140	85336	AGAAAGCTTAAAATTCAGTG	297727	129923	ACATGGAGGGGGAAGAAAAA
208554	40750	GCTGCAGAACAAAGCCTTGT	253141	85337	CAGAAAGCTTAAAATTCAGT	297728	129924	TACATGGAGGGGGAAGAAAA

208555	40751	TGCTGCAGAACAAAGCCTTG	253142	85338	TCAGAAAGCTTAAAATTCAG	297729	129925	CTACATGGAGGGGGAAGAAA
208556	40752	TTGCTGCAGAACAAAGCCTT	253143	85339	GTCAGAAAGCTTAAAATTCA	297730	129926	TCTACATGGAGGGGGAAGAA
208557	40753	GTTGCTGCAGAACAAAGCCT	253144	85340	TGTCAGAAAGCTTAAAATTC	297731	129927	TTCTACATGGAGGGGGAAGA
208558	40754	GGTTGCTGCAGAACAAAGCC	253145	85341	CTGTCAGAAAGCTTAAAATT	297732	129928	CTTCTACATGGAGGGGGAAG
208559	40755	AGGTTGCTGCAGAACAAAGC	253146	85342	GCTGTCAGAAAGCTTAAAAT	297733	129929	TCTTCTACATGGAGGGGGAA
208560	40756	AAGGTTGCTGCAGAACAAAG	253147	85343	TGCTGTCAGAAAGCTTAAAA	297734	129930	CTCTTCTACATGGAGGGGGA
208561	40757	AAAGGTTGCTGCAGAACAAA	253148	85344	CTGCTGTCAGAAAGCTTAAA	297735	129931	CCTCTTCTACATGGAGGGGG
208562	40758	GAAAGGTTGCTGCAGAACAA	253149	85345	GCTGCTGTCAGAAAGCTTAA	297736	129932	CCCTCTTCTACATGGAGGGG
208563	40759	GGAAAGGTTGCTGCAGAACA	253150	85346	GGCTGCTGTCAGAAAGCTTA	297737	129933	TCCCTCTTCTACATGGAGGG
208564	40760	AGGAAAGGTTGCTGCAGAAC	253151	85347	AGGCTGCTGTCAGAAAGCTT	297738	129934	CTCCCTCTTCTACATGGAGG
208565	40761	TAGGAAAGGTTGCTGCAGAA	253152	85348	CAGGCTGCTGTCAGAAAGCT	297739	129935	TCTCCCTCTTCTACATGGAG
208566	40762	TTAGGAAAGGTTGCTGCAGA	253153	85349	CCAGGCTGCTGTCAGAAAGC	297740	129936	TTCTCCCTCTTCTACATGGA
208567	40763	ATTAGGAAAGGTTGCTGCAG	253154	85350	TCCAGGCTGCTGTCAGAAAG	297741	129937	CTTCTCCCTCTTCTACATGG
208568	40764	CATTAGGAAAGGTTGCTGCA	253155	85351	TTCCAGGCTGCTGTCAGAAA	297742	129938	CCTTCTCCCTCTTCTACATG
208569	40765	GCATTAGGAAAGGTTGCTGC	253156	85352	ATTCCAGGCTGCTGTCAGAA	297743	129939	TCCTTCTCCCTCTTCTACAT
208570	40766	TGCATTAGGAAAGGTTGCTG	253157	85353	GATTCCAGGCTGCTGTCAGA	297744	129940	CTCCTTCTCCCTCTTCTACA
208571	40767	CTGCATTAGGAAAGGTTGCT	253158	85354	TGATTCCAGGCTGCTGTCAG	297745	129941	TCTCCTTCTCCCTCTTCTAC
208572	40768	ACTGCATTAGGAAAGGTTGC	253159	85355	ATGATTCCAGGCTGCTGTCA	297746	129942	CTCTCCTTCTCCCTCTTCTA
208573	40769	GACTGCATTAGGAAAGGTTG	253160	85356	CATGATTCCAGGCTGCTGTC	297747	129943	CCTCTCCTTCTCCCTCTTCT
208574	40770	GGACTGCATTAGGAAAGGTT	253161	85357	CCATGATTCCAGGCTGCTGT	297748	129944	GCCTCTCCTTCTCCCTCTTC
208575	40771	AGGACTGCATTAGGAAAGGT	253162	85358	TCCATGATTCCAGGCTGCTG	297749	129945	AGCCTCTCCTTCTCCCTCTT
208576	40772	CAGGACTGCATTAGGAAAGG	253163	85359	CTCCATGATTCCAGGCTGCT	297750	129946	GAGCCTCTCCTTCTCCCTCT
208577	40773	CCAGGACTGCATTAGGAAAG	253164	85360	CCTCCATGATTCCAGGCTGC	297751	129947	AGAGCCTCTCCTTCTCCCTC
208578	40774	GCCAGGACTGCATTAGGAAA	253165	85361	CCCTCCATGATTCCAGGCTG	297752	129948	CAGAGCCTCTCCTTCTCCCT
208579	40775	GGCCAGGACTGCATTAGGAA	253166	85362	TCCCTCCATGATTCCAGGCT	297753	129949	TCAGAGCCTCTCCTTCTCCC
208580	40776	AGGCCAGGACTGCATTAGGA	253167	85363	ATCCCTCCATGATTCCAGGC	297754	129950	TTCAGAGCCTCTCCTTCTCC
208581	40777	GAGGCCAGGACTGCATTAGG	253168	85364	TATCCCTCCATGATTCCAGG	297755	129951	TTTCAGAGCCTCTCCTTCTC
208582	40778	AGAGGCCAGGACTGCATTAG	253169	85365	TTATCCCTCCATGATTCCAG	297756	129952	CTTTCAGAGCCTCTCCTTCT
208583	40779	AAGAGGCCAGGACTGCATTA	253170	85366	TTTATCCCTCCATGATTCCA	297757	129953	GCTTTCAGAGCCTCTCCTTC
208584	40780	GAAGAGGCCAGGACTGCATT	253171	85367	CTTTATCCCTCCATGATTCC	297758	129954	AGCTTTCAGAGCCTCTCCTT
208585	40781	CGAAGAGGCCAGGACTGCAT	253172	85368	ACTTTATCCCTCCATGATTC	297759	129955	CAGCTTTCAGAGCCTCTCCT
208586	40782	GCGAAGAGGCCAGGACTGCA	253173	85369	TACTTTATCCCTCCATGATT	297760	129956	GCAGCTTTCAGAGCCTCTCC
208587	40783	TGCGAAGAGGCCAGGACTGC	253174	85370	GTACTTTATCCCTCCATGAT	297761	129957	AGCAGCTTTCAGAGCCTCTC
208588	40784	CTGCGAAGAGGCCAGGACTG	253175	85371	GGTACTTTATCCCTCCATGA	297762	129958	AAGCAGCTTTCAGAGCCTCT
208589	40785	GCTGCGAAGAGGCCAGGACT	253176	85372	AGGTACTTTATCCCTCCATG	297763	129959	GAAGCAGCTTTCAGAGCCTC
208590	40786	AGCTGCGAAGAGGCCAGGAC	253177	85373	TAGGTACTTTATCCCTCCAT	297764	129960	AGAAGCAGCTTTCAGAGCCT
208591	40787	AAGCTGCGAAGAGGCCAGGA	253178	85374	ATAGGTACTTTATCCCTCCA	297765	129961	CAGAAGCAGCTTTCAGAGCC
208592	40788	GAAGCTGCGAAGAGGCCAGG	253179	85375	AATAGGTACTTTATCCCTCC	297766	129962	CCAGAAGCAGCTTTCAGAGC
208593	40789	TGAAGCTGCGAAGAGGCCAG	253180	85376	TAATAGGTACTTTATCCCTC	297767	129963	CCCAGAAGCAGCTTTCAGAG
208594	40790	ATGAAGCTGCGAAGAGGCCA	253181	85377	CTAATAGGTACTTTATCCCT	297768	129964	CCCCAGAAGCAGCTTTCAGA
208595	40791	AATGAAGCTGCGAAGAGGCC	253182	85378	ACTAATAGGTACTTTATCCC	297769	129965	CCCCCAGAAGCAGCTTTCAG
208596	40792	TAATGAAGCTGCGAAGAGGC	253183	85379	TACTAATAGGTACTTTATCC	297770	129966	TCCCCCAGAAGCAGCTTTCA
208597	40793	GTAATGAAGCTGCGAAGAGG	253184	85380	TTACTAATAGGTACTTTATC	297771	129967	ATCCCCCAGAAGCAGCTTTC
208598	40794	TGTAATGAAGCTGCGAAGAG	253185	85381	CTTACTAATAGGTACTTTAT	297772	129968	AATCCCCCAGAAGCAGCTTT
208599	40795	ATGTAATGAAGCTGCGAAGA	253186	85382	TCTTACTAATAGGTACTTTA	297773	129969	AAATCCCCCAGAAGCAGCTT
208600	40796	TATGTAATGAAGCTGCGAAG	253187	85383	ATCTTACTAATAGGTACTTT	297774	129970	GAAATCCCCCAGAAGCAGCT
208601	40797	TTATGTAATGAAGCTGCGAA	253188	85384	CATCTTACTAATAGGTACTT	297775	129971	TGAAATCCCCCAGAAGCAGC
208602	40798	GTTATGTAATGAAGCTGCGA	253189	85385	CCATCTTACTAATAGGTACT	297776	129972	TTGAAATCCCCCAGAAGCAG
208603	40799	GGTTATGTAATGAAGCTGCG	253190	85386	TCCATCTTACTAATAGGTAC	297777	129973	CTTGAAATCCCCCAGAAGCA
208604	40800	AGGTTATGTAATGAAGCTGC	253191	85387	TTCCATCTTACTAATAGGTA	297778	129974	CCTTGAAATCCCCCAGAAGC
208605	40801	AAGGTTATGTAATGAAGCTG	253192	85388	TTTCCATCTTACTAATAGGT	297779	129975	CCCTTGAAATCCCCCAGAAG
208606	40802	GAAGGTTATGTAATGAAGCT	253193	85389	TTTTCCATCTTACTAATAGG	297780	129976	TCCCTTGAAATCCCCCAGAA
208607	40803	GGAAGGTTATGTAATGAAGC	253194	85390	TTTTTCCATCTTACTAATAG	297781	129977	GTCCCTTGAAATCCCCCAGA
208608	40804	CGGAAGGTTATGTAATGAAG	253195	85391	CTTTTTCCATCTTACTAATA	297782	129978	AGTCCCTTGAAATCCCCCAG
208609	40805	ACGGAAGGTTATGTAATGAA	253196	85392	CCTTTTTCCATCTTACTAAT	297783	129979	CAGTCCCTTGAAATCCCCCA
208610	40806	CACGGAAGGTTATGTAATGA	253197	85393	ACCTTTTTCCATCTTACTAA	297784	129980	CCAGTCCCTTGAAATCCCCC
208611	40807	CCACGGAAGGTTATGTAATG	253198	85394	CACCTTTTTCCATCTTACTA	297785	129981	CCCAGTCCCTTGAAATCCCC
208612	40808	TCCACGGAAGGTTATGTAAT	253199	85395	ACACCTTTTTCCATCTTACT	297786	129982	CCCCAGTCCCTTGAAATCCC
208613	40809	GTCCACGGAAGGTTATGTAA	253200	85396	AACACCTTTTTCCATCTTAC	297787	129983	CCCCCAGTCCCTTGAAATCC
208614	40810	AGTCCACGGAAGGTTATGTA	253201	85397	AAACACCTTTTTCCATCTTA	297788	129984	ACCCCCAGTCCCTTGAAATC
208615	40811	GAGTCCACGGAAGGTTATGT	253202	85398	GAAACACCTTTTTCCATCTT	297789	129985	CACCCCCAGTCCCTTGAAAT
208616	40812	GGAGTCCACGGAAGGTTATG	253203	85399	TGAAACACCTTTTTCCATCT	297790	129986	GCACCCCCAGTCCCTTGAAA
208617	40813	AGGAGTCCACGGAAGGTTAT	253204	85400	CTGAAACACCTTTTTCCATC	297791	129987	GGCACCCCCAGTCCCTTGAA
208618	40814	CAGGAGTCCACGGAAGGTTA	253205	85401	CCTGAAACACCTTTTTCCAT	297792	129988	TGGCACCCCCAGTCCCTTGA
208619	40815	CCAGGAGTCCACGGAAGGTT	253206	85402	ACCTGAAACACCTTTTTCCA	297793	129989	TTGGCACCCCCAGTCCCTTG
208620	40816	ACCAGGAGTCCACGGAAGGT	253207	85403	AACCTGAAACACCTTTTTCC	297794	129990	GTTGGCACCCCCAGTCCCTT
208621	40817	GACCAGGAGTCCACGGAAGG	253208	85404	CAACCTGAAACACCTTTTTC	297795	129991	GGTTGGCACCCCCAGTCCCT
208622	40818	GGACCAGGAGTCCACGGAAG	253209	85405	CCAACCTGAAACACCTTTTT	297796	129992	TGGTTGGCACCCCCAGTCCC
208623	40819	TGGACCAGGAGTCCACGGAA	253210	85406	TCCAACCTGAAACACCTTTT	297797	129993	GTGGTTGGCACCCCCAGTCC
208624	40820	TTGGACCAGGAGTCCACGGA	253211	85407	CTCCAACCTGAAACACCTTT	297798	129994	GGTGGTTGGCACCCCCAGTC
208625	40821	CTTGGACCAGGAGTCCACGG	253212	85408	GCTCCAACCTGAAACACCTT	297799	129995	AGGTGGTTGGCACCCCCAGT
208626	40822	CCTTGGACCAGGAGTCCACG	253213	85409	AGCTCCAACCTGAAACACCT	297800	129996	GAGGTGGTTGGCACCCCCAG

208627	40823	TCCTTGGACCAGGAGTCCAC	253214	85410	CAGCTCCAACCTGAAACACC	297801	129997	AGAGGTGGTTGGCACCCCCA
208628	40824	ATCCTTGGACCAGGAGTCCA	253215	85411	GCAGCTCCAACCTGAAACAC	297802	129998	CAGAGGTGGTTGGCACCCCC
208629	40825	GATCCTTGGACCAGGAGTCC	253216	85412	TGCAGCTCCAACCTGAAACA	297803	129999	CCAGAGGTGGTTGGCACCCC
208630	40826	TGATCCTTGGACCAGGAGTC	253217	85413	CTGCAGCTCCAACCTGAAAC	297804	130000	GCCAGAGGTGGTTGGCACCC
208631	40827	GTGATCCTTGGACCAGGAGT	253218	85414	ACTGCAGCTCCAACCTGAAA	297805	130001	GGCCAGAGGTGGTTGGCACC
208632	40828	GGTGATCCTTGGACCAGGAG	253219	85415	GACTGCAGCTCCAACCTGAA	297806	130002	GGGCCAGAGGTGGTTGGCAC
208633	40829	GGGTGATCCTTGGACCAGGA	253220	85416	AGACTGCAGCTCCAACCTGA	297807	130003	AGGGCCAGAGGTGGTTGGCA
208634	40830	GGGGTGATCCTTGGACCAGG	253221	85417	CAGACTGCAGCTCCAACCTG	297808	130004	CAGGGCCAGAGGTGGTTGGC
208635	40831	TGGGGTGATCCTTGGACCAG	253222	85418	ACAGACTGCAGCTCCAACCT	297809	130005	ACAGGGCCAGAGGTGGTTGG
208636	40832	CTGGGGTGATCCTTGGACCA	253223	85419	AACAGACTGCAGCTCCAACC	297810	130006	AACAGGGCCAGAGGTGGTTG
208637	40833	TCTGGGGTGATCCTTGGACC	253224	85420	CAACAGACTGCAGCTCCAAC	297811	130007	CAACAGGGCCAGAGGTGGTT
208638	40834	TTCTGGGGTGATCCTTGGAC	253225	85421	TCAACAGACTGCAGCTCCAA	297812	130008	ACAACAGGGCCAGAGGTGGT
208639	40835	TTTCTGGGGTGATCCTTGGA	253226	85422	CTCAACAGACTGCAGCTCCA	297813	130009	CACAACAGGGCCAGAGGTGG
208640	40836	CTTTCTGGGGTGATCCTTGG	253227	85423	TCTCAACAGACTGCAGCTCC	297814	130010	CCACAACAGGGCCAGAGGTG
208641	40837	GCTTTCTGGGGTGATCCTTG	253228	85424	CTCTCAACAGACTGCAGCTC	297815	130011	CCCACAACAGGGCCAGAGGT
208642	40838	GGCTTTCTGGGGTGATCCTT	253229	85425	ACTCTCAACAGACTGCAGCT	297816	130012	CCCCACAACAGGGCCAGAGG
208643	40839	TGGCTTTCTGGGGTGATCCT	253230	85426	TACTCTCAACAGACTGCAGC	297817	130013	CCCCCACAACAGGGCCAGAG
208644	40840	CTGGCTTTCTGGGGTGATCC	253231	85427	TTACTCTCAACAGACTGCAG	297818	130014	ACCCCCACAACAGGGCCAGA
208645	40841	ACTGGCTTTCTGGGGTGATC	253232	85428	CTTACTCTCAACAGACTGCA	297819	130015	CACCCCCACAACAGGGCCAG
208646	40842	GACTGGCTTTCTGGGGTGAT	253233	85429	GCTTACTCTCAACAGACTGC	297820	130016	ACACCCCCACAACAGGGCCA
208647	40843	TGACTGGCTTTCTGGGGTGA	253234	85430	AGCTTACTCTCAACAGACTG	297821	130017	GACACCCCCACAACAGGGCC
208648	40844	CTGACTGGCTTTCTGGGGTG	253235	85431	TAGCTTACTCTCAACAGACT	297822	130018	TGACACCCCCACAACAGGGC
208649	40845	TCTGACTGGCTTTCTGGGGT	253236	85432	ATAGCTTACTCTCAACAGAC	297823	130019	GTGACACCCCCACAACAGGG
208650	40846	CTCTGACTGGCTTTCTGGGG	253237	85433	CATAGCTTACTCTCAACAGA	297824	130020	TGTGACACCCCCACAACAGG
208651	40847	CCTCTGACTGGCTTTCTGGG	253238	85434	CCATAGCTTACTCTCAACAG	297825	130021	CTGTGACACCCCCACAACAG
208652	40848	ACCTCTGACTGGCTTTCTGG	253239	85435	CCCATAGCTTACTCTCAACA	297826	130022	TCTGTGACACCCCCACAACA
208653	40849	TACCTCTGACTGGCTTTCTG	253240	85436	TCCCATAGCTTACTCTCAAC	297827	130023	CTCTGTGACACCCCCACAAC
208654	40850	CTACCTCTGACTGGCTTTCT	253241	85437	TTCCCATAGCTTACTCTCAA	297828	130024	CCTCTGTGACACCCCCACAA
208655	40851	CCTACCTCTGACTGGCTTTC	253242	85438	CTTCCCATAGCTTACTCTCA	297829	130025	GCCTCTGTGACACCCCCACA
208656	40852	GCCTACCTCTGACTGGCTTT	253243	85439	CCTTCCCATAGCTTACTCTC	297830	130026	TGCCTCTGTGACACCCCCAC
208657	40853	TGCCTACCTCTGACTGGCTT	253244	85440	GCCTTCCCATAGCTTACTCT	297831	130027	CTGCCTCTGTGACACCCCCA
208658	40854	GTGCCTACCTCTGACTGGCT	253245	85441	GGCCTTCCCATAGCTTACTC	297832	130028	ACTGCCTCTGTGACACCCCC
208659	40855	CGTGCCTACCTCTGACTGGC	253246	85442	AGGCCTTCCCATAGCTTACT	297833	130029	CACTGCCTCTGTGACACCCC
208660	40856	GCGTGCCTACCTCTGACTGG	253247	85443	CAGGCCTTCCCATAGCTTAC	297834	130030	CCACTGCCTCTGTGACACCC
208661	40857	TGCGTGCCTACCTCTGACTG	253248	85444	ACAGGCCTTCCCATAGCTTA	297835	130031	GCCACTGCCTCTGTGACACC
208662	40858	CTGCGTGCCTACCTCTGACT	253249	85445	TACAGGCCTTCCCATAGCTT	297836	130032	TGCCACTGCCTCTGTGACAC
208663	40859	GCTGCGTGCCTACCTCTGAC	253250	85446	ATACAGGCCTTCCCATAGCT	297837	130033	CTGCCACTGCCTCTGTGACA
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208665	40861	CAGCTGCGTGCCTACCTCTG	253252	85448	GTATACAGGCCTTCCCATAG	297839	130035	TGCTGCCACTGCCTCTGTGA
208666	40862	CCAGCTGCGTGCCTACCTCT	253253	85449	CGTATACAGGCCTTCCCATA	297840	130036	TTGCTGCCACTGCCTCTGTG
208667	40863	CCCAGCTGCGTGCCTACCTC	253254	85450	TCGTATACAGGCCTTCCCAT	297841	130037	GTTGCTGCCACTGCCTCTGT
208668	40864	CCCCAGCTGCGTGCCTACCT	253255	85451	CTCGTATACAGGCCTTCCCA	297842	130038	TGTTGCTGCCACTGCCTCTG
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208670	40866	GACCCCAGCTGCGTGCCTAC	253257	85453	CCCTCGTATACAGGCCTTCC	297844	130040	TTTGTTGCTGCCACTGCCTC
208671	40867	GGACCCCAGCTGCGTGCCTA	253258	85454	CCCCTCGTATACAGGCCTTC	297845	130041	CTTTGTTGCTGCCACTGCCT
208672	40868	TGGACCCCAGCTGCGTGCCT	253259	85455	ACCCCTCGTATACAGGCCTT	297846	130042	CCTTTGTTGCTGCCACTGCC
208673	40869	ATGGACCCCAGCTGCGTGCC	253260	85456	CACCCCTCGTATACAGGCCT	297847	130043	TCCTTTGTTGCTGCCACTGC
208674	40870	AATGGACCCCAGCTGCGTGC	253261	85457	CCACCCCTCGTATACAGGCC	297848	130044	ATCCTTTGTTGCTGCCACTG
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208676	40872	TAAATGGACCCCAGCTGCGT	253263	85459	GTCCACCCCTCGTATACAGG	297850	130046	AAATCCTTTGTTGCTGCCAC
208677	40873	GTAAATGGACCCCAGCTGCG	253264	85460	AGTCCACCCCTCGTATACAG	297851	130047	CAAATCCTTTGTTGCTGCCA
208678	40874	AGTAAATGGACCCCAGCTGC	253265	85461	AAGTCCACCCCTCGTATACA	297852	130048	TCAAATCCTTTGTTGCTGCC
208679	40875	AAGTAAATGGACCCCAGCTG	253266	85462	AAAGTCCACCCCTCGTATAC	297853	130049	TTCAAATCCTTTGTTGCTGC
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208681	40877	GTAAGTAAATGGACCCCAGC	253268	85464	GAAAAGTCCACCCCTCGTAT	297855	130051	GTTTCAAATCCTTTGTTGCT
208682	40878	GGTAAGTAAATGGACCCCAG	253269	85465	AGAAAAGTCCACCCCTCGTA	297856	130052	AGTTTCAAATCCTTTGTTGC
208683	40879	AGGTAAGTAAATGGACCCCA	253270	85466	AAGAAAAGTCCACCCCTCGT	297857	130053	AAGTTTCAAATCCTTTGTTG
208684	40880	AAGGTAAGTAAATGGACCCC	253271	85467	GAAGAAAAGTCCACCCCTCG	297858	130054	CAAGTTTCAAATCCTTTGTT
208685	40881	GAAGGTAAGTAAATGGACCC	253272	85468	AGAAGAAAAGTCCACCCCTC	297859	130055	CCAAGTTTCAAATCCTTTGT
208686	40882	GGAAGGTAAGTAAATGGACC	253273	85469	CAGAAGAAAAGTCCACCCCT	297860	130056	ACCAAGTTTCAAATCCTTTG
208687	40883	GGGAAGGTAAGTAAATGGAC	253274	85470	ACAGAAGAAAAGTCCACCCC	297861	130057	CACCAAGTTTCAAATCCTTT
208688	40884	GGGGAAGGTAAGTAAATGGA	253275	85471	TACAGAAGAAAAGTCCACCC	297862	130058	ACACCAAGTTTCAAATCCTT
208689	40885	TGGGGAAGGTAAGTAAATGG	253276	85472	TTACAGAAGAAAAGTCCACC	297863	130059	CACACCAAGTTTCAAATCCT
208690	40886	GTGGGGAAGGTAAGTAAATG	253277	85473	CTTACAGAAGAAAAGTCCAC	297864	130060	ACACACCAAGTTTCAAATCC
208691	40887	GGTGGGGAAGGTAAGTAAAT	253278	85474	ACTTACAGAAGAAAAGTCCA	297865	130061	AACACACCAAGTTTCAAATC
208692	40888	GGGTGGGGAAGGTAAGTAAA	253279	85475	CACTTACAGAAGAAAAGTCC	297866	130062	GAACACACCAAGTTTCAAAT
208693	40889	GGGGTGGGGAAGGTAAGTAA	253280	85476	ACACTTACAGAAGAAAAGTC	297867	130063	CGAACACACCAAGTTTCAAA
208694	40890	GGGGGTGGGGAAGGTAAGTA	253281	85477	GACACTTACAGAAGAAAAGT	297868	130064	ACGAACACACCAAGTTTCAA
208695	40891	AGGGGGTGGGGAAGGTAAGT	253282	85478	GGACACTTACAGAAGAAAAG	297869	130065	CACGAACACACCAAGTTTCA
208696	40892	GAGGGGGTGGGGAAGGTAAG	253283	85479	TGGACACTTACAGAAGAAAA	297870	130066	CCACGAACACACCAAGTTTC
208697	40893	CGAGGGGGTGGGGAAGGTAA	253284	85480	CTGGACACTTACAGAAGAAA	297871	130067	TCCACGAACACACCAAGTTT
208698	40894	CCGAGGGGGTGGGGAAGGTA	253285	85481	TCTGGACACTTACAGAAGAA	297872	130068	CTCCACGAACACACCAAGTT

208699	40895	TCCGAGGGGGTGGGGAAGGT	253286	85482	CTCTGGACACTTACAGAAGA	297873	130069	GCTCCACGAACACACCAAGT
208700	40896	TTCCGAGGGGGTGGGGAAGG	253287	85483	TCTCTGGACACTTACAGAAG	297874	130070	GGCTCCACGAACACACCAAG
208701	40897	GTTCCGAGGGGGTGGGGAAG	253288	85484	GTCTCTGGACACTTACAGAA	297875	130071	TGGCTCCACGAACACACCAA
208702	40898	AGTTCCGAGGGGGTGGGGAA	253289	85485	GGTCTCTGGACACTTACAGA	297876	130072	GTGGCTCCACGAACACACCA
208703	40899	GAGTTCCGAGGGGGTGGGGA	253290	85486	TGGTCTCTGGACACTTACAG	297877	130073	TGTGGCTCCACGAACACACC
208704	40900	TGAGTTCCGAGGGGGTGGGG	253291	85487	CTGGTCTCTGGACACTTACA	297878	130074	CTGTGGCTCCACGAACACAC
208705	40901	CTGAGTTCCGAGGGGGTGGG	253292	85488	CCTGGTCTCTGGACACTTAC	297879	130075	CCTGTGGCTCCACGAACACA
208706	40902	TCTGAGTTCCGAGGGGGTGG	253293	85489	GCCTGGTCTCTGGACACTTA	297880	130076	GCCTGTGGCTCCACGAACAC
208707	40903	CTCTGAGTTCCGAGGGGGTG	253294	85490	GGCCTGGTCTCTGGACACTT	297881	130077	TGCCTGTGGCTCCACGAACA
208708	40904	CCTCTGAGTTCCGAGGGGGT	253295	85491	AGGCCTGGTCTCTGGACACT	297882	130078	CTGCCTGTGGCTCCACGAAC
208709	40905	ACCTCTGAGTTCCGAGGGGG	253296	85492	GAGGCCTGGTCTCTGGACAC	297883	130079	TCTGCCTGTGGCTCCACGAA
208710	40906	CACCTCTGAGTTCCGAGGGG	253297	85493	GGAGGCCTGGTCTCTGGACA	297884	130080	GTCTGCCTGTGGCTCCACGA
208711	40907	CCACCTCTGAGTTCCGAGGG	253298	85494	AGGAGGCCTGGTCTCTGGAC	297885	130081	CGTCTGCCTGTGGCTCCACG
208712	40908	ACCACCTCTGAGTTCCGAGG	253299	85495	CAGGAGGCCTGGTCTCTGGA	297886	130082	TCGTCTGCCTGTGGCTCCAC
208713	40909	CACCACCTCTGAGTTCCGAG	253300	85496	TCAGGAGGCCTGGTCTCTGG	297887	130083	ATCGTCTGCCTGTGGCTCCA
208714	40910	GCACCACCTCTGAGTTCCGA	253301	85497	TTCAGGAGGCCTGGTCTCTG	297888	130084	CATCGTCTGCCTGTGGCTCC
208715	40911	TGCACCACCTCTGAGTTCCG	253302	85498	CTTCAGGAGGCCTGGTCTCT	297889	130085	ACATCGTCTGCCTGTGGCTC
208716	40912	CTGCACCACCTCTGAGTTCC	253303	85499	TCTTCAGGAGGCCTGGTCTC	297890	130086	GACATCGTCTGCCTGTGGCT
208717	40913	CCTGCACCACCTCTGAGTTC	253304	85500	CTCTTCAGGAGGCCTGGTCT	297891	130087	TGACATCGTCTGCCTGTGGC
208718	40914	TCCTGCACCACCTCTGAGTT	253305	85501	CCTCTTCAGGAGGCCTGGTC	297892	130088	TTGACATCGTCTGCCTGTGG
208719	40915	TTCCTGCACCACCTCTGAGT	253306	85502	CCCTCTTCAGGAGGCCTGGT	297893	130089	GTTGACATCGTCTGCCTGTG
208720	40916	ATTCCTGCACCACCTCTGAG	253307	85503	GCCCTCTTCAGGAGGCCTGG	297894	130090	GGTTGACATCGTCTGCCTGT
208721	40917	AATTCCTGCACCACCTCTGA	253308	85504	TGCCCTCTTCAGGAGGCCTG	297895	130091	AGGTTGACATCGTCTGCCTG
208722	40918	AAATTCCTGCACCACCTCTG	253309	85505	ATGCCCTCTTCAGGAGGCCT	297896	130092	AAGGTTGACATCGTCTGCCT
208723	40919	CAAATTCCTGCACCACCTCT	253310	85506	CATGCCCTCTTCAGGAGGCC	297897	130093	CAAGGTTGACATCGTCTGCC
208724	40920	CCAAATTCCTGCACCACCTC	253311	85507	CCATGCCCTCTTCAGGAGGC	297898	130094	ACAAGGTTGACATCGTCTGC
208725	40921	TCCAAATTCCTGCACCACCT	253312	85508	CCCATGCCCTCTTCAGGAGG	297899	130095	CACAAGGTTGACATCGTCTG
208726	40922	GTCCAAATTCCTGCACCACC	253313	85509	CCCCATGCCCTCTTCAGGAG	297900	130096	ACACAAGGTTGACATCGTCT
208727	40923	AGTCCAAATTCCTGCACCAC	253314	85510	CCCCCATGCCCTCTTCAGGA	297901	130097	CACACAAGGTTGACATCGTC
208728	40924	GAGTCCAAATTCCTGCACCA	253315	85511	GCCCCCATGCCCTCTTCAGG	297902	130098	TCACACAAGGTTGACATCGT
208729	40925	GGAGTCCAAATTCCTGCACC	253316	85512	AGCCCCCATGCCCTCTTCAG	297903	130099	CTCACACAAGGTTGACATCG
208730	40926	TGGAGTCCAAATTCCTGCAC	253317	85513	AAGCCCCCATGCCCTCTTCA	297904	130100	ACTCACACAAGGTTGACATC
208731	40927	TTGGAGTCCAAATTCCTGCA	253318	85514	TAAGCCCCCATGCCCTCTTC	297905	130101	CACTCACACAAGGTTGACAT
208732	40928	CTTGGAGTCCAAATTCCTGC	253319	85515	TTAAGCCCCCATGCCCTCTT	297906	130102	ACACTCACACAAGGTTGACA
208733	40929	TCTTGGAGTCCAAATTCCTG	253320	85516	GTTAAGCCCCCATGCCCTCT	297907	130103	CACACTCACACAAGGTTGAC
208734	40930	TTCTTGGAGTCCAAATTCCT	253321	85517	AGTTAAGCCCCCATGCCCTC	297908	130104	TCACACTCACACAAGGTTGA
208735	40931	ATTCTTGGAGTCCAAATTCC	253322	85518	AAGTTAAGCCCCCATGCCCT	297909	130105	GTCACACTCACACAAGGTTG
208736	40932	AATTCTTGGAGTCCAAATTC	253323	85519	TAAGTTAAGCCCCCATGCCC	297910	130106	CGTCACACTCACACAAGGTT
208737	40933	TAATTCTTGGAGTCCAAATT	253324	85520	GTAAGTTAAGCCCCCATGCC	297911	130107	CCGTCACACTCACACAAGGT
208738	40934	TTAATTCTTGGAGTCCAAAT	253325	85521	GGTAAGTTAAGCCCCCATGC	297912	130108	CCCGTCACACTCACACAAGG
208739	40935	GTTAATTCTTGGAGTCCAAA	253326	85522	AGGTAAGTTAAGCCCCCATG	297913	130109	CCCCGTCACACTCACACAAG
208740	40936	TGTTAATTCTTGGAGTCCAA	253327	85523	CAGGTAAGTTAAGCCCCCAT	297914	130110	CCCCCGTCACACTCACACAA
208741	40937	CTGTTAATTCTTGGAGTCCA	253328	85524	CCAGGTAAGTTAAGCCCCCA	297915	130111	ACCCCCGTCACACTCACACA
208742	40938	GCTGTTAATTCTTGGAGTCC	253329	85525	TCCAGGTAAGTTAAGCCCCC	297916	130112	AACCCCCGTCACACTCACAC
208743	40939	AGCTGTTAATTCTTGGAGTC	253330	85526	GTCCAGGTAAGTTAAGCCCC	297917	130113	CAACCCCCGTCACACTCACA
208744	40940	GAGCTGTTAATTCTTGGAGT	253331	85527	AGTCCAGGTAAGTTAAGCCC	297918	130114	CCAACCCCCGTCACACTCAC
208745	40941	GGAGCTGTTAATTCTTGGAG	253332	85528	TAGTCCAGGTAAGTTAAGCC	297919	130115	CCCAACCCCCGTCACACTCA
208746	40942	TGGAGCTGTTAATTCTTGGA	253333	85529	GTAGTCCAGGTAAGTTAAGC	297920	130116	CCCCAACCCCCGTCACACTC
208747	40943	GTGGAGCTGTTAATTCTTGG	253334	85530	AGTAGTCCAGGTAAGTTAAG	297921	130117	ACCCCAACCCCCGTCACACT
208748	40944	GGTGGAGCTGTTAATTCTTG	253335	85531	CAGTAGTCCAGGTAAGTTAA	297922	130118	CACCCCAACCCCCGTCACAC
208749	40945	TGGTGGAGCTGTTAATTCTT	253336	85532	ACAGTAGTCCAGGTAAGTTA	297923	130119	CCACCCCAACCCCCGTCACA
208750	40946	GTGGTGGAGCTGTTAATTCT	253337	85533	CACAGTAGTCCAGGTAAGTT	297924	130120	CCCACCCCAACCCCCGTCAC
208751	40947	GGTGGTGGAGCTGTTAATTC	253338	85534	ACACAGTAGTCCAGGTAAGT	297925	130121	CCCCACCCCAACCCCCGTCA
208752	40948	TGGTGGTGGAGCTGTTAATT	253339	85535	AACACAGTAGTCCAGGTAAG	297926	130122	GCCCCACCCCAACCCCCGTC
208753	40949	ATGGTGGTGGAGCTGTTAAT	253340	85536	AAACACAGTAGTCCAGGTAA	297927	130123	CGCCCCACCCCAACCCCCGT
208754	40950	GATGGTGGTGGAGCTGTTAA	253341	85537	TAAACACAGTAGTCCAGGTA	297928	130124	CCGCCCCACCCCAACCCCCG
208755	40951	TGATGGTGGTGGAGCTGTTA	253342	85538	GTAAACACAGTAGTCCAGGT	297929	130125	CCCGCCCCACCCCAACCCCC
208756	40952	GTGATGGTGGTGGAGCTGTT	253343	85539	TGTAAACACAGTAGTCCAGG	297930	130126	TCCCGCCCCACCCCAACCCC
208757	40953	GGTGATGGTGGTGGAGCTGT	253344	85540	TTGTAAACACAGTAGTCCAG	297931	130127	CTCCCGCCCCACCCCAACCC
208758	40954	TGGTGATGGTGGTGGAGCTG	253345	85541	ATTGTAAACACAGTAGTCCA	297932	130128	CCTCCCGCCCCACCCCAACC
208759	40955	CTGGTGATGGTGGTGGAGCT	253346	85542	TATTGTAAACACAGTAGTCC	297933	130129	GCCTCCCGCCCCACCCCAAC
208760	40956	TCTGGTGATGGTGGTGGAGC	253347	85543	GTATTGTAAACACAGTAGTC	297934	130130	GGCCTCCCGCCCCACCCCAA
208761	40957	CTCTGGTGATGGTGGTGGAG	253348	85544	AGTATTGTAAACACAGTAGT	297935	130131	TGGCCTCCCGCCCCACCCCA
208762	40958	GCTCTGGTGATGGTGGTGGA	253349	85545	GAGTATTGTAAACACAGTAG	297936	130132	GTGGCCTCCCGCCCCACCCC
208763	40959	GGCTCTGGTGATGGTGGTGG	253350	85546	TGAGTATTGTAAACACAGTA	297937	130133	CGTGGCCTCCCGCCCCACCC
208764	40960	TGGCTCTGGTGATGGTGGTG	253351	85547	ATGAGTATTGTAAACACAGT	297938	130134	CCGTGGCCTCCCGCCCCACC
208765	40961	TTGGCTCTGGTGATGGTGGT	253352	85548	AATGAGTATTGTAAACACAG	297939	130135	CCCGTGGCCTCCCGCCCCAC
208766	40962	TTTGGCTCTGGTGATGGTGG	253353	85549	AAATGAGTATTGTAAACACA	297940	130136	CCCCGTGGCCTCCCGCCCCA
208767	40963	TTTTGGCTCTGGTGATGGTG	253354	85550	TAAATGAGTATTGTAAACAC	297941	130137	CCCCCGTGGCCTCCCGCCCC
208768	40964	GTTTTGGCTCTGGTGATGGT	253355	85551	ATAAATGAGTATTGTAAACA	297942	130138	TCCCCCGTGGCCTCCCGCCC
208769	40965	AGTTTTGGCTCTGGTGATGG	253356	85552	GATAAATGAGTATTGTAAAC	297943	130139	CTCCCCCGTGGCCTCCCGCC
208770	40966	GAGTTTTGGCTCTGGTGATG	253357	85553	AGATAAATGAGTATTGTAAA	297944	130140	CCTCCCCCGTGGCCTCCCGC

208771	40967	TGAGTTTTGGCTCTGGTGAT	253358	85554	AAGATAAATGAGTATTGTAA	297945	130141	GCCTCCCCCGTGGCCTCCCG
208772	40968	CTGAGTTTTGGCTCTGGTGA	253359	85555	CAAGATAAATGAGTATTGTA	297946	130142	GGCCTCCCCCGTGGCCTCCC
208773	40969	CCTGAGTTTTGGCTCTGGTG	253360	85556	TCAAGATAAATGAGTATTGT	297947	130143	CGGCCTCCCCCGTGGCCTCC
208774	40970	TCCTGAGTTTTGGCTCTGGT	253361	85557	TTCAAGATAAATGAGTATTG	297948	130144	TCGGCCTCCCCCGTGGCCTC
208775	40971	ATCCTGAGTTTTGGCTCTGG	253362	85558	GTTCAAGATAAATGAGTATT	297949	130145	CTCGGCCTCCCCCGTGGCCT
208776	40972	CATCCTGAGTTTTGGCTCTG	253363	85559	AGTTCAAGATAAATGAGTAT	297950	130146	CCTCGGCCTCCCCCGTGGCC
208777	40973	GCATCCTGAGTTTTGGCTCT	253364	85560	GAGTTCAAGATAAATGAGTA	297951	130147	GCCTCGGCCTCCCCCGTGGC
208778	40974	TGCATCCTGAGTTTTGGCTC	253365	85561	GGAGTTCAAGATAAATGAGT	297952	130148	TGCCTCGGCCTCCCCCGTGG
208779	40975	ATGCATCCTGAGTTTTGGCT	253366	85562	AGGAGTTCAAGATAAATGAG	297953	130149	CTGCCTCGGCCTCCCCCGTG
208780	40976	CATGCATCCTGAGTTTTGGC	253367	85563	GAGGAGTTCAAGATAAATGA	297954	130150	CCTGCCTCGGCCTCCCCCGT
208781	40977	ACATGCATCCTGAGTTTTGG	253368	85564	GGAGGAGTTCAAGATAAATG	297955	130151	CCCTGCCTCGGCCTCCCCCG
208782	40978	CACATGCATCCTGAGTTTTG	253369	85565	AGGAGGAGTTCAAGATAAAT	297956	130152	CCCCTGCCTCGGCCTCCCCC
208783	40979	GCACATGCATCCTGAGTTTT	253370	85566	TAGGAGGAGTTCAAGATAAA	297957	130153	GCCCCTGCCTCGGCCTCCCC
208784	40980	AGCACATGCATCCTGAGTTT	253371	85567	TTAGGAGGAGTTCAAGATAA	297958	130154	AGCCCCTGCCTCGGCCTCCC
208785	40981	AAGCACATGCATCCTGAGTT	253372	85568	GTTAGGAGGAGTTCAAGATA	297959	130155	CAGCCCCTGCCTCGGCCTCC
208786	40982	GAAGCACATGCATCCTGAGT	253373	85569	GGTTAGGAGGAGTTCAAGAT	297960	130156	CCAGCCCCTGCCTCGGCCTC
208787	40983	TGAAGCACATGCATCCTGAG	253374	85570	GGGTTAGGAGGAGTTCAAGA	297961	130157	CCCAGCCCCTGCCTCGGCCT
208788	40984	ATGAAGCACATGCATCCTGA	253375	85571	GGGGTTAGGAGGAGTTCAAG	297962	130158	GCCCAGCCCCTGCCTCGGCC
208789	40985	GATGAAGCACATGCATCCTG	253376	85572	AGGGGTTAGGAGGAGTTCAA	297963	130159	TGCCCAGCCCCTGCCTCGGC
208790	40986	AGATGAAGCACATGCATCCT	253377	85573	CAGGGGTTAGGAGGAGTTCA	297964	130160	CTGCCCAGCCCCTGCCTCGG
208791	40987	CAGATGAAGCACATGCATCC	253378	85574	TCAGGGGTTAGGAGGAGTTC	297965	130161	TCTGCCCAGCCCCTGCCTCG
208792	40988	GCAGATGAAGCACATGCATC	253379	85575	CTCAGGGGTTAGGAGGAGTT	297966	130162	CTCTGCCCAGCCCCTGCCTC
208793	40989	AGCAGATGAAGCACATGCAT	253380	85576	TCTCAGGGGTTAGGAGGAGT	297967	130163	CCTCTGCCCAGCCCCTGCCT
208794	40990	CAGCAGATGAAGCACATGCA	253381	85577	TTCTCAGGGGTTAGGAGGAG	297968	130164	CCCTCTGCCCAGCCCCTGCC
208795	40991	GCAGCAGATGAAGCACATGC	253382	85578	ATTCTCAGGGGTTAGGAGGA	297969	130165	CCCCTCTGCCCAGCCCCTGC
208796	40992	AGCAGCAGATGAAGCACATG	253383	85579	AATTCTCAGGGGTTAGGAGG	297970	130166	TCCCCTCTGCCCAGCCCCTG
208797	40993	AAGCAGCAGATGAAGCACAT	253384	85580	CAATTCTCAGGGGTTAGGAG	297971	130167	CTCCCCTCTGCCCAGCCCCT
208798	40994	TAAGCAGCAGATGAAGCACA	253385	85581	GCAATTCTCAGGGGTTAGGA	297972	130168	TCTCCCCTCTGCCCAGCCCC
208799	40995	ATAAGCAGCAGATGAAGCAC	253386	85582	AGCAATTCTCAGGGGTTAGG	297973	130169	CTCTCCCCTCTGCCCAGCCC
208800	40996	AATAAGCAGCAGATGAAGCA	253387	85583	TAGCAATTCTCAGGGGTTAG	297974	130170	CCTCTCCCCTCTGCCCAGCC
208801	40997	AAATAAGCAGCAGATGAAGC	253388	85584	GTAGCAATTCTCAGGGGTTA	297975	130171	TCCTCTCCCCTCTGCCCAGC
208802	40998	GAAATAAGCAGCAGATGAAG	253389	85585	TGTAGCAATTCTCAGGGGTT	297976	130172	TTCCTCTCCCCTCTGCCCAG
208803	40999	GGAAATAAGCAGCAGATGAA	253390	85586	ATGTAGCAATTCTCAGGGGT	297977	130173	CTTCCTCTCCCCTCTGCCCA
208804	41000	TGGAAATAAGCAGCAGATGA	253391	85587	AATGTAGCAATTCTCAGGGG	297978	130174	GCTTCCTCTCCCCTCTGCCC
208805	41001	CTGGAAATAAGCAGCAGATG	253392	85588	AAATGTAGCAATTCTCAGGG	297979	130175	TGCTTCCTCTCCCCTCTGCC
208806	41002	GCTGGAAATAAGCAGCAGAT	253393	85589	TAAATGTAGCAATTCTCAGG	297980	130176	GTGCTTCCTCTCCCCTCTGC
208807	41003	AGCTGGAAATAAGCAGCAGA	253394	85590	CTAAATGTAGCAATTCTCAG	297981	130177	TGTGCTTCCTCTCCCCTCTG
208808	41004	CAGCTGGAAATAAGCAGCAG	253395	85591	ACTAAATGTAGCAATTCTCA	297982	130178	TTGTGCTTCCTCTCCCCTCT
208809	41005	TCAGCTGGAAATAAGCAGCA	253396	85592	TACTAAATGTAGCAATTCTC	297983	130179	CTTGTGCTTCCTCTCCCCTC
208810	41006	CTCAGCTGGAAATAAGCAGC	253397	85593	ATACTAAATGTAGCAATTCT	297984	130180	TCTTGTGCTTCCTCTCCCCT
208811	41007	TCTCAGCTGGAAATAAGCAG	253398	85594	AATACTAAATGTAGCAATTC	297985	130181	TTCTTGTGCTTCCTCTCCCC
208812	41008	CTCTCAGCTGGAAATAAGCA	253399	85595	AAATACTAAATGTAGCAATT	297986	130182	CTTCTTGTGCTTCCTCTCCC
208813	41009	GCTCTCAGCTGGAAATAAGC	253400	85596	CAAATACTAAATGTAGCAAT	297987	130183	ACTTCTTGTGCTTCCTCTCC
208814	41010	GGCTCTCAGCTGGAAATAAG	253401	85597	GCAAATACTAAATGTAGCAA	297988	130184	CACTTCTTGTGCTTCCTCTC
208815	41011	TGGCTCTCAGCTGGAAATAA	253402	85598	AGCAAATACTAAATGTAGCA	297989	130185	CCACTTCTTGTGCTTCCTCT
208816	41012	CTGGCTCTCAGCTGGAAATA	253403	85599	CAGCAAATACTAAATGTAGC	297990	130186	CCCACTTCTTGTGCTTCCTC
208817	41013	ACTGGCTCTCAGCTGGAAAT	253404	85600	TCAGCAAATACTAAATGTAG	297991	130187	TCCCACTTCTTGTGCTTCCT
208818	41014	CACTGGCTCTCAGCTGGAAA	253405	85601	CTCAGCAAATACTAAATGTA	297992	130188	CTCCCACTTCTTGTGCTTCC
208819	41015	CCACTGGCTCTCAGCTGGAA	253406	85602	ACTCAGCAAATACTAAATGT	297993	130189	ACTCCCACTTCTTGTGCTTC
208820	41016	ACCACTGGCTCTCAGCTGGA	253407	85603	TACTCAGCAAATACTAAATG	297994	130190	CACTCCCACTTCTTGTGCTT
208821	41017	CACCACTGGCTCTCAGCTGG	253408	85604	GTACTCAGCAAATACTAAAT	297995	130191	CCACTCCCACTTCTTGTGCT
208822	41018	GCACCACTGGCTCTCAGCTG	253409	85605	AGTACTCAGCAAATACTAAA	297996	130192	CCCACTCCCACTTCTTGTGC
208823	41019	GGCACCACTGGCTCTCAGCT	253410	85606	AAGTACTCAGCAAATACTAA	297997	130193	TCCCACTCCCACTTCTTGTG
208824	41020	TGGCACCACTGGCTCTCAGC	253411	85607	GAAGTACTCAGCAAATACTA	297998	130194	CTCCCACTCCCACTTCTTGT
208825	41021	ATGGCACCACTGGCTCTCAG	253412	85608	GGAAGTACTCAGCAAATACT	297999	130195	TCTCCCACTCCCACTTCTTG
208826	41022	CATGGCACCACTGGCTCTCA	253413	85609	AGGAAGTACTCAGCAAATAC	298000	130196	CTCTCCCACTCCCACTTCTT
208827	41023	CCATGGCACCACTGGCTCTC	253414	85610	TAGGAAGTACTCAGCAAATA	298001	130197	CCTCTCCCACTCCCACTTCT
208828	41024	ACCATGGCACCACTGGCTCT	253415	85611	CTAGGAAGTACTCAGCAAAT	298002	130198	TCCTCTCCCACTCCCACTTC
208829	41025	AACCATGGCACCACTGGCTC	253416	85612	GCTAGGAAGTACTCAGCAAA	298003	130199	TTCCTCTCCCACTCCCACTT
208830	41026	GAACCATGGCACCACTGGCT	253417	85613	TGCTAGGAAGTACTCAGCAA	298004	130200	CTTCCTCTCCCACTCCCACT
208831	41027	GGAACCATGGCACCACTGGC	253418	85614	ATGCTAGGAAGTACTCAGCA	298005	130201	GCTTCCTCTCCCACTCCCAC
208832	41028	AGGAACCATGGCACCACTGG	253419	85615	GATGCTAGGAAGTACTCAGC	298006	130202	GGCTTCCTCTCCCACTCCCA
208833	41029	AAGGAACCATGGCACCACTG	253420	85616	GGATGCTAGGAAGTACTCAG	298007	130203	TGGCTTCCTCTCCCACTCCC
208834	41030	TAAGGAACCATGGCACCACT	253421	85617	AGGATGCTAGGAAGTACTCA	298008	130204	GTGGCTTCCTCTCCCACTCC
208835	41031	CTAAGGAACCATGGCACCAC	253422	85618	TAGGATGCTAGGAAGTACTC	298009	130205	CGTGGCTTCCTCTCCCACTC
208836	41032	CCTAAGGAACCATGGCACCA	253423	85619	CTAGGATGCTAGGAAGTACT	298010	130206	ACGTGGCTTCCTCTCCCACT
208837	41033	CCCTAAGGAACCATGGCACC	253424	85620	CCTAGGATGCTAGGAAGTAC	298011	130207	CACGTGGCTTCCTCTCCCAC
208838	41034	TCCCTAAGGAACCATGGCAC	253425	85621	CCCTAGGATGCTAGGAAGTA	298012	130208	GCACGTGGCTTCCTCTCCCA
208839	41035	CTCCCTAAGGAACCATGGCA	253426	85622	TCCCTAGGATGCTAGGAAGT	298013	130209	AGCACGTGGCTTCCTCTCCC
208840	41036	GCTCCCTAAGGAACCATGGC	253427	85623	TTCCCTAGGATGCTAGGAAG	298014	130210	CAGCACGTGGCTTCCTCTCC
208841	41037	GGCTCCCTAAGGAACCATGG	253428	85624	ATTCCCTAGGATGCTAGGAA	298015	130211	CCAGCACGTGGCTTCCTCTC
208842	41038	CGGCTCCCTAAGGAACCATG	253429	85625	GATTCCCTAGGATGCTAGGA	298016	130212	TCCAGCACGTGGCTTCCTCT

208843	41039	CCGGCTCCCTAAGGAACCAT	253430	85626	TGATTCCCTAGGATGCTAGG	298017	130213	CTCCAGCACGTGGCTTCCTC
208844	41040	ACCGGCTCCCTAAGGAACCA	253431	85627	TTGATTCCCTAGGATGCTAG	298018	130214	TCTCCAGCACGTGGCTTCCT
208845	41041	GACCGGCTCCCTAAGGAACC	253432	85628	ATTGATTCCCTAGGATGCTA	298019	130215	CTCTCCAGCACGTGGCTTCC
208846	41042	GGACCGGCTCCCTAAGGAAC	253433	85629	TATTGATTCCCTAGGATGCT	298020	130216	ACTCTCCAGCACGTGGCTTC
208847	41043	GGGACCGGCTCCCTAAGGAA	253434	85630	CTATTGATTCCCTAGGATGC	298021	130217	TACTCTCCAGCACGTGGCTT
208848	41044	GGGGACCGGCTCCCTAAGGA	253435	85631	TCTATTGATTCCCTAGGATG	298022	130218	CTACTCTCCAGCACGTGGCT
208849	41045	AGGGGACCGGCTCCCTAAGG	253436	85632	TTCTATTGATTCCCTAGGAT	298023	130219	TCTACTCTCCAGCACGTGGC
208850	41046	CAGGGGACCGGCTCCCTAAG	253437	85633	GTTCTATTGATTCCCTAGGA	298024	130220	GTCTACTCTCCAGCACGTGG
208851	41047	TCAGGGGACCGGCTCCCTAA	253438	85634	TGTTCTATTGATTCCCTAGG	298025	130221	TGTCTACTCTCCAGCACGTG
208852	41048	ATCAGGGGACCGGCTCCCTA	253439	85635	ATGTTCTATTGATTCCCTAG	298026	130222	ATGTCTACTCTCCAGCACGT
208853	41049	CATCAGGGGACCGGCTCCCT	253440	85636	AATGTTCTATTGATTCCCTA	298027	130223	GATGTCTACTCTCCAGCACG
208854	41050	GCATCAGGGGACCGGCTCCC	253441	85637	GAATGTTCTATTGATTCCCT	298028	130224	GGATGTCTACTCTCCAGCAC
208855	41051	GGCATCAGGGGACCGGCTCC	253442	85638	AGAATGTTCTATTGATTCCC	298029	130225	GGGATGTCTACTCTCCAGCA
208856	41052	CGGCATCAGGGGACCGGCTC	253443	85639	GAGAATGTTCTATTGATTCC	298030	130226	GGGGATGTCTACTCTCCAGC
208857	41053	CCGGCATCAGGGGACCGGCT	253444	85640	GGAGAATGTTCTATTGATTC	298031	130227	GGGGGATGTCTACTCTCCAG
208858	41054	GCCGGCATCAGGGGACCGGC	253445	85641	GGGAGAATGTTCTATTGATT	298032	130228	AGGGGGATGTCTACTCTCCA
208859	41055	AGCCGGCATCAGGGGACCGG	253446	85642	TGGGAGAATGTTCTATTGAT	298033	130229	GAGGGGGATGTCTACTCTCC
208860	41056	GAGCCGGCATCAGGGGACCG	253447	85643	TTGGGAGAATGTTCTATTGA	298034	130230	GGAGGGGGATGTCTACTCTC
208861	41057	GGAGCCGGCATCAGGGGACC	253448	85644	GTTGGGAGAATGTTCTATTG	298035	130231	AGGAGGGGGATGTCTACTCT
208862	41058	AGGAGCCGGCATCAGGGGAC	253449	85645	GGTTGGGAGAATGTTCTATT	298036	130232	AAGGAGGGGGATGTCTACTC
208863	41059	CAGGAGCCGGCATCAGGGGA	253450	85646	TGGTTGGGAGAATGTTCTAT	298037	130233	CAAGGAGGGGGATGTCTACT
208864	41060	CCAGGAGCCGGCATCAGGGG	253451	85647	CTGGTTGGGAGAATGTTCTA	298038	130234	GCAAGGAGGGGGATGTCTAC
208865	41061	GCCAGGAGCCGGCATCAGGG	253452	85648	CCTGGTTGGGAGAATGTTCT	298039	130235	GGCAAGGAGGGGGATGTCTA
208866	41062	GGCCAGGAGCCGGCATCAGG	253453	85649	GCCTGGTTGGGAGAATGTTC	298040	130236	CGGCAAGGAGGGGGATGTCT
208867	41063	GGGCCAGGAGCCGGCATCAG	253454	85650	AGCCTGGTTGGGAGAATGTT	298041	130237	GCGGCAAGGAGGGGGATGTC
208868	41064	GGGGCCAGGAGCCGGCATCA	253455	85651	CAGCCTGGTTGGGAGAATGT	298042	130238	AGCGGCAAGGAGGGGGATGT
208869	41065	TGGGGCCAGGAGCCGGCATC	253456	85652	CCAGCCTGGTTGGGAGAATG	298043	130239	CAGCGGCAAGGAGGGGGATG
208870	41066	TTGGGGCCAGGAGCCGGCAT	253457	85653	CCCAGCCTGGTTGGGAGAAT	298044	130240	CCAGCGGCAAGGAGGGGGAT
208871	41067	TTTGGGGCCAGGAGCCGGCA	253458	85654	ACCCAGCCTGGTTGGGAGAA	298045	130241	CCCAGCGGCAAGGAGGGGGA
208872	41068	ATTTGGGGCCAGGAGCCGGC	253459	85655	CACCCAGCCTGGTTGGGAGA	298046	130242	TCCCAGCGGCAAGGAGGGGG
208873	41069	GATTTGGGGCCAGGAGCCGG	253460	85656	GCACCCAGCCTGGTTGGGAG	298047	130243	CTCCCAGCGGCAAGGAGGGG
208874	41070	AGATTTGGGGCCAGGAGCCG	253461	85657	CGCACCCAGCCTGGTTGGGA	298048	130244	TCTCCCAGCGGCAAGGAGGG
208875	41071	GAGATTTGGGGCCAGGAGCC	253462	85658	CCGCACCCAGCCTGGTTGGG	298049	130245	CTCTCCCAGCGGCAAGGAGG
208876	41072	AGAGATTTGGGGCCAGGAGC	253463	85659	ACCGCACCCAGCCTGGTTGG	298050	130246	GCTCTCCCAGCGGCAAGGAG
208877	41073	GAGAGATTTGGGGCCAGGAG	253464	85660	CACCGCACCCAGCCTGGTTG	298051	130247	GGCTCTCCCAGCGGCAAGGA
208878	41074	AGAGAGATTTGGGGCCAGGA	253465	85661	CCACCGCACCCAGCCTGGTT	298052	130248	TGGCTCTCCCAGCGGCAAGG
208879	41075	CAGAGAGATTTGGGGCCAGG	253466	85662	GCCACCGCACCCAGCCTGGT	298053	130249	TTGGCTCTCCCAGCGGCAAG
208880	41076	TCAGAGAGATTTGGGGCCAG	253467	85663	AGCCACCGCACCCAGCCTGG	298054	130250	CTTGGCTCTCCCAGCGGCAA
208881	41077	ATCAGAGAGATTTGGGGCCA	253468	85664	GAGCCACCGCACCCAGCCTG	298055	130251	CCTTGGCTCTCCCAGCGGCA
208882	41078	GATCAGAGAGATTTGGGGCC	253469	85665	TGAGCCACCGCACCCAGCCT	298056	130252	GCCTTGGCTCTCCCAGCGGC
208883	41079	GGATCAGAGAGATTTGGGGC	253470	85666	ATGAGCCACCGCACCCAGCC	298057	130253	GGCCTTGGCTCTCCCAGCGG
208884	41080	CGGATCAGAGAGATTTGGGG	253471	85667	CATGAGCCACCGCACCCAGC	298058	130254	AGGCCTTGGCTCTCCCAGCG
208885	41081	CCGGATCAGAGAGATTTGGG	253472	85668	ACATGAGCCACCGCACCCAG	298059	130255	TAGGCCTTGGCTCTCCCAGC
208886	41082	CCCGGATCAGAGAGATTTGG	253473	85669	GACATGAGCCACCGCACCCA	298060	130256	ATAGGCCTTGGCTCTCCCAG
208887	41083	GCCCGGATCAGAGAGATTTG	253474	85670	AGACATGAGCCACCGCACCC	298061	130257	CATAGGCCTTGGCTCTCCCA
208888	41084	AGCCCGGATCAGAGAGATTT	253475	85671	CAGACATGAGCCACCGCACC	298062	130258	GCATAGGCCTTGGCTCTCCC
208889	41085	GAGCCCGGATCAGAGAGATT	253476	85672	ACAGACATGAGCCACCGCAC	298063	130259	GGCATAGGCCTTGGCTCTCC
208890	41086	AGAGCCCGGATCAGAGAGAT	253477	85673	TACAGACATGAGCCACCGCA	298064	130260	TGGCATAGGCCTTGGCTCTC
208891	41087	AAGAGCCCGGATCAGAGAGA	253478	85674	TTACAGACATGAGCCACCGC	298065	130261	GTGGCATAGGCCTTGGCTCT
208892	41088	GAAGAGCCCGGATCAGAGAG	253479	85675	ATTACAGACATGAGCCACCG	298066	130262	GGTGGCATAGGCCTTGGCTC
208893	41089	GGAAGAGCCCGGATCAGAGA	253480	85676	GATTACAGACATGAGCCACC	298067	130263	AGGTGGCATAGGCCTTGGCT
208894	41090	TGGAAGAGCCCGGATCAGAG	253481	85677	GGATTACAGACATGAGCCAC	298068	130264	CAGGTGGCATAGGCCTTGGC
208895	41091	CTGGAAGAGCCCGGATCAGA	253482	85678	GGGATTACAGACATGAGCCA	298069	130265	GCAGGTGGCATAGGCCTTGG
208896	41092	TCTGGAAGAGCCCGGATCAG	253483	85679	TGGGATTACAGACATGAGCC	298070	130266	TGCAGGTGGCATAGGCCTTG
208897	41093	TTCTGGAAGAGCCCGGATCA	253484	85680	CTGGGATTACAGACATGAGC	298071	130267	CTGCAGGTGGCATAGGCCTT
208898	41094	ATTCTGGAAGAGCCCGGATC	253485	85681	GCTGGGATTACAGACATGAG	298072	130268	GCTGCAGGTGGCATAGGCCT
208899	41095	CATTCTGGAAGAGCCCGGAT	253486	85682	TGCTGGGATTACAGACATGA	298073	130269	CGCTGCAGGTGGCATAGGCC
208900	41096	ACATTCTGGAAGAGCCCGGA	253487	85683	GTGCTGGGATTACAGACATG	298074	130270	ACGCTGCAGGTGGCATAGGC
208901	41097	GACATTCTGGAAGAGCCCGG	253488	85684	AGTGCTGGGATTACAGACAT	298075	130271	GACGCTGCAGGTGGCATAGG
208902	41098	AGACATTCTGGAAGAGCCCG	253489	85685	AAGTGCTGGGATTACAGACA	298076	130272	AGACGCTGCAGGTGGCATAG
208903	41099	AAGACATTCTGGAAGAGCCC	253490	85686	AAAGTGCTGGGATTACAGAC	298077	130273	CAGACGCTGCAGGTGGCATA
208904	41100	CAAGACATTCTGGAAGAGCC	253491	85687	CAAAGTGCTGGGATTACAGA	298078	130274	TCAGACGCTGCAGGTGGCAT
208905	41101	ACAAGACATTCTGGAAGAGC	253492	85688	CCAAAGTGCTGGGATTACAG	298079	130275	CTCAGACGCTGCAGGTGGCA
208906	41102	GACAAGACATTCTGGAAGAG	253493	85689	CCCAAAGTGCTGGGATTACA	298080	130276	GCTCAGACGCTGCAGGTGGC
208907	41103	AGACAAGACATTCTGGAAGA	253494	85690	TCCCAAAGTGCTGGGATTAC	298081	130277	CGCTCAGACGCTGCAGGTGG
208908	41104	GAGACAAGACATTCTGGAAG	253495	85691	CTCCCAAAGTGCTGGGATTA	298082	130278	CCGCTCAGACGCTGCAGGTG
208909	41105	GGAGACAAGACATTCTGGAA	253496	85692	CCTCCCAAAGTGCTGGGATT	298083	130279	GCCGCTCAGACGCTGCAGGT
208910	41106	TGGAGACAAGACATTCTGGA	253497	85693	GCCTCCCAAAGTGCTGGGAT	298084	130280	GGCCGCTCAGACGCTGCAGG
208911	41107	GTGGAGACAAGACATTCTGG	253498	85694	GGCCTCCCAAAGTGCTGGGA	298085	130281	CGGCCGCTCAGACGCTGCAG
208912	41108	GGTGGAGACAAGACATTCTG	253499	85695	TGGCCTCCCAAAGTGCTGGG	298086	130282	GCGGCCGCTCAGACGCTGCA
208913	41109	TGGTGGAGACAAGACATTCT	253500	85696	TTGGCCTCCCAAAGTGCTGG	298087	130283	GGCGGCCGCTCAGACGCTGC
208914	41110	ATGGTGGAGACAAGACATTC	253501	85697	CTTGGCCTCCCAAAGTGCTG	298088	130284	AGGCGGCCGCTCAGACGCTG

208915	41111	GATGGTGGAGACAAGACATT	253502	85698	CCTTGGCCTCCCAAAGTGCT	298089	130285	CAGGCGGCCGCTCAGACGCT
208916	41112	CGATGGTGGAGACAAGACAT	253503	85699	ACCTTGGCCTCCCAAAGTGC	298090	130286	ACAGGCGGCCGCTCAGACGC
208917	41113	GCGATGGTGGAGACAAGACA	253504	85700	TACCTTGGCCTCCCAAAGTG	298091	130287	GACAGGCGGCCGCTCAGACG
208918	41114	GGCGATGGTGGAGACAAGAC	253505	85701	CTACCTTGGCCTCCCAAAGT	298092	130288	GGACAGGCGGCCGCTCAGAC
208919	41115	AGGCGATGGTGGAGACAAGA	253506	85702	CCTACCTTGGCCTCCCAAAG	298093	130289	AGGACAGGCGGCCGCTCAGA
208920	41116	AAGGCGATGGTGGAGACAAG	253507	85703	GCCTACCTTGGCCTCCCAAA	298094	130290	AAGGACAGGCGGCCGCTCAG
208921	41117	AAAGGCGATGGTGGAGACAA	253508	85704	TGCCTACCTTGGCCTCCCAA	298095	130291	CAAGGACAGGCGGCCGCTCA
208922	41118	CAAAGGCGATGGTGGAGACA	253509	85705	CTGCCTACCTTGGCCTCCCA	298096	130292	CCAAGGACAGGCGGCCGCTC
208923	41119	TCAAAGGCGATGGTGGAGAC	253510	85706	TCTGCCTACCTTGGCCTCCC	298097	130293	ACCAAGGACAGGCGGCCGCT
208924	41120	GTCAAAGGCGATGGTGGAGA	253511	85707	ATCTGCCTACCTTGGCCTCC	298098	130294	CACCAAGGACAGGCGGCCGC
208925	41121	GGTCAAAGGCGATGGTGGAG	253512	85708	GATCTGCCTACCTTGGCCTC	298099	130295	CCACCAAGGACAGGCGGCCG
208926	41122	TGGTCAAAGGCGATGGTGGA	253513	85709	GGATCTGCCTACCTTGGCCT	298100	130296	GCCACCAAGGACAGGCGGCC
208927	41123	TTGGTCAAAGGCGATGGTGG	253514	85710	GGGATCTGCCTACCTTGGCC	298101	130297	GGCCACCAAGGACAGGCGGC
208928	41124	ATTGGTCAAAGGCGATGGTG	253515	85711	AGGGATCTGCCTACCTTGGC	298102	130298	CGGCCACCAAGGACAGGCGG
208929	41125	CATTGGTCAAAGGCGATGGT	253516	85712	AAGGGATCTGCCTACCTTGG	298103	130299	CCGGCCACCAAGGACAGGCG
208930	41126	CCATTGGTCAAAGGCGATGG	253517	85713	CAAGGGATCTGCCTACCTTG	298104	130300	CCCGGCCACCAAGGACAGGC
208931	41127	ACCATTGGTCAAAGGCGATG	253518	85714	TCAAGGGATCTGCCTACCTT	298105	130301	CCCCGGCCACCAAGGACAGG
208932	41128	CACCATTGGTCAAAGGCGAT	253519	85715	CTCAAGGGATCTGCCTACCT	298106	130302	CCCCCGGCCACCAAGGACAG
208933	41129	ACACCATTGGTCAAAGGCGA	253520	85716	CCTCAAGGGATCTGCCTACC	298107	130303	ACCCCCGGCCACCAAGGACA
208934	41130	GACACCATTGGTCAAAGGCG	253521	85717	GCCTCAAGGGATCTGCCTAC	298108	130304	CACCCCCGGCCACCAAGGAC
208935	41131	GGACACCATTGGTCAAAGGC	253522	85718	GGCCTCAAGGGATCTGCCTA	298109	130305	CCACCCCCGGCCACCAAGGA
208936	41132	GGGACACCATTGGTCAAAGG	253523	85719	TGGCCTCAAGGGATCTGCCT	298110	130306	CCCACCCCCGGCCACCAAGG
208937	41133	AGGGACACCATTGGTCAAAG	253524	85720	CTGGCCTCAAGGGATCTGCC	298111	130307	CCCCACCCCCGGCCACCAAG
208938	41134	AAGGGACACCATTGGTCAAA	253525	85721	CCTGGCCTCAAGGGATCTGC	298112	130308	CCCCCACCCCCGGCCACCAA
208939	41135	AAAGGGACACCATTGGTCAA	253526	85722	TCCTGGCCTCAAGGGATCTG	298113	130309	GCCCCCACCCCCGGCCACCA
208940	41136	CAAAGGGACACCATTGGTCA	253527	85723	CTCCTGGCCTCAAGGGATCT	298114	130310	GGCCCCCACCCCCGGCCACC
208941	41137	GCAAAGGGACACCATTGGTC	253528	85724	ACTCCTGGCCTCAAGGGATC	298115	130311	AGGCCCCCACCCCCGGCCAC
208942	41138	GGCAAAGGGACACCATTGGT	253529	85725	CACTCCTGGCCTCAAGGGAT	298116	130312	CAGGCCCCCACCCCCGGCCA
208943	41139	AGGCAAAGGGACACCATTGG	253530	85726	GCACTCCTGGCCTCAAGGGA	298117	130313	GCAGGCCCCCACCCCCGGCC
208944	41140	CAGGCAAAGGGACACCATTG	253531	85727	TGCACTCCTGGCCTCAAGGG	298118	130314	AGCAGGCCCCCACCCCCGGC
208945	41141	CCAGGCAAAGGGACACCATT	253532	85728	TTGCACTCCTGGCCTCAAGG	298119	130315	CAGCAGGCCCCCACCCCCGG
208946	41142	ACCAGGCAAAGGGACACCAT	253533	85729	CTTGCACTCCTGGCCTCAAG	298120	130316	ACAGCAGGCCCCCACCCCCG
208947	41143	TACCAGGCAAAGGGACACCA	253534	85730	TCTTGCACTCCTGGCCTCAA	298121	130317	CACAGCAGGCCCCCACCCCC
208948	41144	TTACCAGGCAAAGGGACACC	253535	85731	GTCTTGCACTCCTGGCCTCA	298122	130318	CCACAGCAGGCCCCCACCCC
208949	41145	ATTACCAGGCAAAGGGACAC	253536	85732	AGTCTTGCACTCCTGGCCTC	298123	130319	CCCACAGCAGGCCCCCACCC
208950	41146	CATTACCAGGCAAAGGGACA	253537	85733	TAGTCTTGCACTCCTGGCCT	298124	130320	ACCCACAGCAGGCCCCCACC
208951	41147	ACATTACCAGGCAAAGGGAC	253538	85734	CTAGTCTTGCACTCCTGGCC	298125	130321	GACCCACAGCAGGCCCCCAC
208952	41148	GACATTACCAGGCAAAGGGA	253539	85735	GCTAGTCTTGCACTCCTGGC	298126	130322	TGACCCACAGCAGGCCCCCA
208953	41149	GGACATTACCAGGCAAAGGG	253540	85736	GGCTAGTCTTGCACTCCTGG	298127	130323	CTGACCCACAGCAGGCCCCC
208954	41150	GGGACATTACCAGGCAAAGG	253541	85737	AGGCTAGTCTTGCACTCCTG	298128	130324	ACTGACCCACAGCAGGCCCC
208955	41151	GGGGACATTACCAGGCAAAG	253542	85738	CAGGCTAGTCTTGCACTCCT	298129	130325	CACTGACCCACAGCAGGCCC
208956	41152	AGGGGACATTACCAGGCAAA	253543	85739	CCAGGCTAGTCTTGCACTCC	298130	130326	ACACTGACCCACAGCAGGCC
208957	41153	AAGGGGACATTACCAGGCAA	253544	85740	GCCAGGCTAGTCTTGCACTC	298131	130327	CACACTGACCCACAGCAGGC
208958	41154	AAAGGGGACATTACCAGGCA	253545	85741	AGCCAGGCTAGTCTTGCACT	298132	130328	GCACACTGACCCACAGCAGG
208959	41155	CAAAGGGGACATTACCAGGC	253546	85742	CAGCCAGGCTAGTCTTGCAC	298133	130329	GGCACACTGACCCACAGCAG
208960	41156	GCAAAGGGGACATTACCAGG	253547	85743	TCAGCCAGGCTAGTCTTGCA	298134	130330	TGGCACACTGACCCACAGCA
208961	41157	GGCAAAGGGGACATTACCAG	253548	85744	GTCAGCCAGGCTAGTCTTGC	298135	130331	GTGGCACACTGACCCACAGC
208962	41158	AGGCAAAGGGGACATTACCA	253549	85745	TGTCAGCCAGGCTAGTCTTG	298136	130332	GGTGGCACACTGACCCACAG
208963	41159	CAGGCAAAGGGGACATTACC	253550	85746	ATGTCAGCCAGGCTAGTCTT	298137	130333	GGGTGGCACACTGACCCACA
208964	41160	TCAGGCAAAGGGGACATTAC	253551	85747	CATGTCAGCCAGGCTAGTCT	298138	130334	AGGGTGGCACACTGACCCAC
208965	41161	ATCAGGCAAAGGGGACATTA	253552	85748	CCATGTCAGCCAGGCTAGTC	298139	130335	GAGGGTGGCACACTGACCCA
208966	41162	CATCAGGCAAAGGGGACATT	253553	85749	ACCATGTCAGCCAGGCTAGT	298140	130336	AGAGGGTGGCACACTGACCC
208967	41163	TCATCAGGCAAAGGGGACAT	253554	85750	CACCATGTCAGCCAGGCTAG	298141	130337	CAGAGGGTGGCACACTGACC
208968	41164	ATCATCAGGCAAAGGGGACA	253555	85751	TCACCATGTCAGCCAGGCTA	298142	130338	GCAGAGGGTGGCACACTGAC
208969	41165	CATCATCAGGCAAAGGGGAC	253556	85752	TTCACCATGTCAGCCAGGCT	298143	130339	TGCAGAGGGTGGCACACTGA
208970	41166	CCATCATCAGGCAAAGGGGA	253557	85753	TTTCACCATGTCAGCCAGGC	298144	130340	CTGCAGAGGGTGGCACACTG
208971	41167	GCCATCATCAGGCAAAGGGG	253558	85754	GTTTCACCATGTCAGCCAGG	298145	130341	CCTGCAGAGGGTGGCACACT
208972	41168	GGCCATCATCAGGCAAAGGG	253559	85755	GGTTTCACCATGTCAGCCAG	298146	130342	CCCTGCAGAGGGTGGCACAC
208973	41169	GGGCCATCATCAGGCAAAGG	253560	85756	GGGTTTCACCATGTCAGCCA	298147	130343	GCCCTGCAGAGGGTGGCACA
208974	41170	AGGGCCATCATCAGGCAAAG	253561	85757	GGGGTTTCACCATGTCAGCC	298148	130344	TGCCCTGCAGAGGGTGGCAC
208975	41171	CAGGGCCATCATCAGGCAAA	253562	85758	CGGGGTTTCACCATGTCAGC	298149	130345	CTGCCCTGCAGAGGGTGGCA
208976	41172	ACAGGGCCATCATCAGGCAA	253563	85759	ACGGGGTTTCACCATGTCAG	298150	130346	GCTGCCCTGCAGAGGGTGGC
208977	41173	GACAGGGCCATCATCAGGCA	253564	85760	GACGGGGTTTCACCATGTCA	298151	130347	GGCTGCCCTGCAGAGGGTGG
208978	41174	TGACAGGGCCATCATCAGGC	253565	85761	AGACGGGGTTTCACCATGTC	298152	130348	AGGCTGCCCTGCAGAGGGTG
208979	41175	GTGACAGGGCCATCATCAGG	253566	85762	AAGACGGGGTTTCACCATGT	298153	130349	CAGGCTGCCCTGCAGAGGGT
208980	41176	AGTGACAGGGCCATCATCAG	253567	85763	AAAGACGGGGTTTCACCATG	298154	130350	ACAGGCTGCCCTGCAGAGGG
208981	41177	GAGTGACAGGGCCATCATCA	253568	85764	TAAAGACGGGGTTTCACCAT	298155	130351	CACAGGCTGCCCTGCAGAGG
208982	41178	GGAGTGACAGGGCCATCATC	253569	85765	GTAAAGACGGGGTTTCACCA	298156	130352	CCACAGGCTGCCCTGCAGAG
208983	41179	AGGAGTGACAGGGCCATCAT	253570	85766	AGTAAAGACGGGGTTTCACC	298157	130353	CCCACAGGCTGCCCTGCAGA
208984	41180	GAGGAGTGACAGGGCCATCA	253571	85767	TAGTAAAGACGGGGTTTCAC	298158	130354	TCCCACAGGCTGCCCTGCAG
208985	41181	AGAGGAGTGACAGGGCCATC	253572	85768	TTAGTAAAGACGGGGTTTCA	298159	130355	CTCCCACAGGCTGCCCTGCA
208986	41182	GAGAGGAGTGACAGGGCCAT	253573	85769	TTTAGTAAAGACGGGGTTTC	298160	130356	TCTCCCACAGGCTGCCCTGC

208987	41183	AGAGAGGAGTGACAGGGCCA	253574	85770	TTTTAGTAAAGACGGGGTTT	298161	130357	TTCTCCCACAGGCTGCCCTG
208988	41184	AAGAGAGGAGTGACAGGGCC	253575	85771	TTTTTAGTAAAGACGGGGTT	298162	130358	CTTCTCCCACAGGCTGCCCT
208989	41185	AAAGAGAGGAGTGACAGGGC	253576	85772	ATTTTTAGTAAAGACGGGGT	298163	130359	CCTTCTCCCACAGGCTGCCC
208990	41186	TAAAGAGAGGAGTGACAGGG	253577	85773	TATTTTTAGTAAAGACGGGG	298164	130360	CCCTTCTCCCACAGGCTGCC
208991	41187	CTAAAGAGAGGAGTGACAGG	253578	85774	GTATTTTTAGTAAAGACGGG	298165	130361	TCCCTTCTCCCACAGGCTGC
208992	41188	GCTAAAGAGAGGAGTGACAG	253579	85775	TGTATTTTTAGTAAAGACGG	298166	130362	GTCCCTTCTCCCACAGGCTG
208993	41189	TGCTAAAGAGAGGAGTGACA	253580	85776	TTGTATTTTTAGTAAAGACG	298167	130363	TGTCCCTTCTCCCACAGGCT
208994	41190	GTGCTAAAGAGAGGAGTGAC	253581	85777	TTTGTATTTTTAGTAAAGAC	298168	130364	CTGTCCCTTCTCCCACAGGC
208995	41191	TGTGCTAAAGAGAGGAGTGA	253582	85778	TTTTGTATTTTTAGTAAAGA	298169	130365	GCTGTCCCTTCTCCCACAGG
208996	41192	CTGTGCTAAAGAGAGGAGTG	253583	85779	CTTTTGTATTTTTAGTAAAG	298170	130366	CGCTGTCCCTTCTCCCACAG
208997	41193	TCTGTGCTAAAGAGAGGAGT	253584	85780	ACTTTTGTATTTTTAGTAAA	298171	130367	CCGCTGTCCCTTCTCCCACA
208998	41194	CTCTGTGCTAAAGAGAGGAG	253585	85781	AACTTTTGTATTTTTAGTAA	298172	130368	CCCGCTGTCCCTTCTCCCAC
208999	41195	CCTCTGTGCTAAAGAGAGGA	253586	85782	TAACTTTTGTATTTTTAGTA	298173	130369	ACCCGCTGTCCCTTCTCCCA
209000	41196	TCCTCTGTGCTAAAGAGAGG	253587	85783	CTAACTTTTGTATTTTTAGT	298174	130370	TACCCGCTGTCCCTTCTCCC
209001	41197	CTCCTCTGTGCTAAAGAGAG	253588	85784	GCTAACTTTTGTATTTTTAG	298175	130371	TTACCCGCTGTCCCTTCTCC
209002	41198	CCTCCTCTGTGCTAAAGAGA	253589	85785	GGCTAACTTTTGTATTTTTA	298176	130372	TTTACCCGCTGTCCCTTCTC
209003	41199	GCCTCCTCTGTGCTAAAGAG	253590	85786	TGGCTAACTTTTGTATTTTT	298177	130373	TTTTACCCGCTGTCCCTTCT
209004	41200	AGCCTCCTCTGTGCTAAAGA	253591	85787	CTGGCTAACTTTTGTATTTT	298178	130374	TTTTTACCCGCTGTCCCTTC
209005	41201	CAGCCTCCTCTGTGCTAAAG	253592	85788	CCTGGCTAACTTTTGTATTT	298179	130375	CTTTTTACCCGCTGTCCCTT
209006	41202	ACAGCCTCCTCTGTGCTAAA	253593	85789	GCCTGGCTAACTTTTGTATT	298180	130376	TCTTTTTACCCGCTGTCCCT
209007	41203	AACAGCCTCCTCTGTGCTAA	253594	85790	TGCCTGGCTAACTTTTGTAT	298181	130377	CTCTTTTTACCCGCTGTCCC
209008	41204	AAACAGCCTCCTCTGTGCTA	253595	85791	ATGCCTGGCTAACTTTTGTA	298182	130378	TCTCTTTTTACCCGCTGTCC
209009	41205	GAAACAGCCTCCTCTGTGCT	253596	85792	CATGCCTGGCTAACTTTTGT	298183	130379	TTCTCTTTTTACCCGCTGTC
209010	41206	TGAAACAGCCTCCTCTGTGC	253597	85793	CCATGCCTGGCTAACTTTTG	298184	130380	CTTCTCTTTTTACCCGCTGT
209011	41207	ATGAAACAGCCTCCTCTGTG	253598	85794	ACCATGCCTGGCTAACTTTT	298185	130381	CCTTCTCTTTTTACCCGCTG
209012	41208	GATGAAACAGCCTCCTCTGT	253599	85795	CACCATGCCTGGCTAACTTT	298186	130382	GCCTTCTCTTTTTACCCGCT
209013	41209	GGATGAAACAGCCTCCTCTG	253600	85796	CCACCATGCCTGGCTAACTT	298187	130383	TGCCTTCTCTTTTTACCCGC
209014	41210	GGGATGAAACAGCCTCCTCT	253601	85797	ACCACCATGCCTGGCTAACT	298188	130384	TTGCCTTCTCTTTTTACCCG
209015	41211	AGGGATGAAACAGCCTCCTC	253602	85798	TACCACCATGCCTGGCTAAC	298189	130385	CTTGCCTTCTCTTTTTACCC
209016	41212	AAGGGATGAAACAGCCTCCT	253603	85799	GTACCACCATGCCTGGCTAA	298190	130386	GCTTGCCTTCTCTTTTTACC
209017	41213	GAAGGGATGAAACAGCCTCC	253604	85800	TGTACCACCATGCCTGGCTA	298191	130387	AGCTTGCCTTCTCTTTTTAC
209018	41214	TGAAGGGATGAAACAGCCTC	253605	85801	GTGTACCACCATGCCTGGCT	298192	130388	CAGCTTGCCTTCTCTTTTTA
209019	41215	TTGAAGGGATGAAACAGCCT	253606	85802	TGTGTACCACCATGCCTGGC	298193	130389	CCAGCTTGCCTTCTCTTTTT
209020	41216	CTTGAAGGGATGAAACAGCC	253607	85803	GTGTGTACCACCATGCCTGG	298194	130390	GCCAGCTTGCCTTCTCTTTT
209021	41217	GCTTGAAGGGATGAAACAGC	253608	85804	GGTGTGTACCACCATGCCTG	298195	130391	TGCCAGCTTGCCTTCTCTTT
209022	41218	GGCTTGAAGGGATGAAACAG	253609	85805	AGGTGTGTACCACCATGCCT	298196	130392	CTGCCAGCTTGCCTTCTCTT
209023	41219	AGGCTTGAAGGGATGAAACA	253610	85806	CAGGTGTGTACCACCATGCC	298197	130393	CCTGCCAGCTTGCCTTCTCT
209024	41220	CAGGCTTGAAGGGATGAAAC	253611	85807	ACAGGTGTGTACCACCATGC	298198	130394	TCCTGCCAGCTTGCCTTCTC
209025	41221	GCAGGCTTGAAGGGATGAAA	253612	85808	TACAGGTGTGTACCACCATG	298199	130395	CTCCTGCCAGCTTGCCTTCT
209026	41222	GGCAGGCTTGAAGGGATGAA	253613	85809	TTACAGGTGTGTACCACCAT	298200	130396	CCTCCTGCCAGCTTGCCTTC
209027	41223	GGGCAGGCTTGAAGGGATGA	253614	85810	ATTACAGGTGTGTACCACCA	298201	130397	CCCTCCTGCCAGCTTGCCTT
209028	41224	AGGGCAGGCTTGAAGGGATG	253615	85811	GATTACAGGTGTGTACCACC	298202	130398	ACCCTCCTGCCAGCTTGCCT
209029	41225	GAGGGCAGGCTTGAAGGGAT	253616	85812	GGATTACAGGTGTGTACCAC	298203	130399	CACCCTCCTGCCAGCTTGCC
209030	41226	GGAGGGCAGGCTTGAAGGGA	253617	85813	GGGATTACAGGTGTGTACCA	298204	130400	CCACCCTCCTGCCAGCTTGC
209031	41227	GGGAGGGCAGGCTTGAAGGG	253618	85814	TGGGATTACAGGTGTGTACC	298205	130401	GCCACCCTCCTGCCAGCTTG
209032	41228	AGGGAGGGCAGGCTTGAAGG	253619	85815	CTGGGATTACAGGTGTGTAC	298206	130402	TGCCACCCTCCTGCCAGCTT
209033	41229	AAGGGAGGGCAGGCTTGAAG	253620	85816	GCTGGGATTACAGGTGTGTA	298207	130403	GTGCCACCCTCCTGCCAGCT
209034	41230	GAAGGGAGGGCAGGCTTGAA	253621	85817	AGCTGGGATTACAGGTGTGT	298208	130404	AGTGCCACCCTCCTGCCAGC
209035	41231	TGAAGGGAGGGCAGGCTTGA	253622	85818	TAGCTGGGATTACAGGTGTG	298209	130405	AAGTGCCACCCTCCTGCCAG
209036	41232	TTGAAGGGAGGGCAGGCTTG	253623	85819	GTAGCTGGGATTACAGGTGT	298210	130406	GAAGTGCCACCCTCCTGCCA
209037	41233	CTTGAAGGGAGGGCAGGCTT	253624	85820	TGTAGCTGGGATTACAGGTG	298211	130407	CGAAGTGCCACCCTCCTGCC
209038	41234	ACTTGAAGGGAGGGCAGGCT	253625	85821	ATGTAGCTGGGATTACAGGT	298212	130408	ACGAAGTGCCACCCTCCTGC
209039	41235	GACTTGAAGGGAGGGCAGGC	253626	85822	CATGTAGCTGGGATTACAGG	298213	130409	CACGAAGTGCCACCCTCCTG
209040	41236	AGACTTGAAGGGAGGGCAGG	253627	85823	CCATGTAGCTGGGATTACAG	298214	130410	CCACGAAGTGCCACCCTCCT
209041	41237	AAGACTTGAAGGGAGGGCAG	253628	85824	CCCATGTAGCTGGGATTACA	298215	130411	TCCACGAAGTGCCACCCTCC
209042	41238	TAAGACTTGAAGGGAGGGCA	253629	85825	TCCCATGTAGCTGGGATTAC	298216	130412	ATCCACGAAGTGCCACCCTC
209043	41239	CTAAGACTTGAAGGGAGGGC	253630	85826	CTCCCATGTAGCTGGGATTA	298217	130413	CATCCACGAAGTGCCACCCT
209044	41240	GCTAAGACTTGAAGGGAGGG	253631	85827	CCTCCCATGTAGCTGGGATT	298218	130414	TCATCCACGAAGTGCCACCC
209045	41241	AGCTAAGACTTGAAGGGAGG	253632	85828	TCCTCCCATGTAGCTGGGAT	298219	130415	GTCATCCACGAAGTGCCACC
209046	41242	GAGCTAAGACTTGAAGGGAG	253633	85829	CTCCTCCCATGTAGCTGGGA	298220	130416	GGTCATCCACGAAGTGCCAC
209047	41243	TGAGCTAAGACTTGAAGGGA	253634	85830	ACTCCTCCCATGTAGCTGGG	298221	130417	AGGTCATCCACGAAGTGCCA
209048	41244	TTGAGCTAAGACTTGAAGGG	253635	85831	TACTCCTCCCATGTAGCTGG	298222	130418	GAGGTCATCCACGAAGTGCC
209049	41245	CTTGAGCTAAGACTTGAAGG	253636	85832	CTACTCCTCCCATGTAGCTG	298223	130419	GGAGGTCATCCACGAAGTGC
209050	41246	ACTTGAGCTAAGACTTGAAG	253637	85833	CCTACTCCTCCCATGTAGCT	298224	130420	AGGAGGTCATCCACGAAGTG
209051	41247	AACTTGAGCTAAGACTTGAA	253638	85834	TCCTACTCCTCCCATGTAGC	298225	130421	AAGGAGGTCATCCACGAAGT
209052	41248	GAACTTGAGCTAAGACTTGA	253639	85835	CTCCTACTCCTCCCATGTAG	298226	130422	TAAGGAGGTCATCCACGAAG
209053	41249	TGAACTTGAGCTAAGACTTG	253640	85836	CCTCCTACTCCTCCCATGTA	298227	130423	CTAAGGAGGTCATCCACGAA
209054	41250	GTGAACTTGAGCTAAGACTT	253641	85837	GCCTCCTACTCCTCCCATGT	298228	130424	TCTAAGGAGGTCATCCACGA
209055	41251	GGTGAACTTGAGCTAAGACT	253642	85838	TGCCTCCTACTCCTCCCATG	298229	130425	TTCTAAGGAGGTCATCCACG
209056	41252	AGGTGAACTTGAGCTAAGAC	253643	85839	CTGCCTCCTACTCCTCCCAT	298230	130426	TTTCTAAGGAGGTCATCCAC
209057	41253	AAGGTGAACTTGAGCTAAGA	253644	85840	CCTGCCTCCTACTCCTCCCA	298231	130427	TTTTCTAAGGAGGTCATCCA
209058	41254	GAAGGTGAACTTGAGCTAAG	253645	85841	TCCTGCCTCCTACTCCTCCC	298232	130428	CTTTTCTAAGGAGGTCATCC

209059	41255	AGAAGGTGAACTTGAGCTAA	253646	85842	CTCCTGCCTCCTACTCCTCC	298233	130429	TCTTTTCTAAGGAGGTCATC
209060	41256	GAGAAGGTGAACTTGAGCTA	253647	85843	TCTCCTGCCTCCTACTCCTC	298234	130430	GTCTTTTCTAAGGAGGTCAT
209061	41257	GGAGAAGGTGAACTTGAGCT	253648	85844	TTCTCCTGCCTCCTACTCCT	298235	130431	AGTCTTTTCTAAGGAGGTCA
209062	41258	CGGAGAAGGTGAACTTGAGC	253649	85845	ATTCTCCTGCCTCCTACTCC	298236	130432	CAGTCTTTTCTAAGGAGGTC
209063	41259	GCGGAGAAGGTGAACTTGAG	253650	85846	AATTCTCCTGCCTCCTACTC	298237	130433	TCAGTCTTTTCTAAGGAGGT
209064	41260	TGCGGAGAAGGTGAACTTGA	253651	85847	CAATTCTCCTGCCTCCTACT	298238	130434	GTCAGTCTTTTCTAAGGAGG
209065	41261	CTGCGGAGAAGGTGAACTTG	253652	85848	GCAATTCTCCTGCCTCCTAC	298239	130435	GGTCAGTCTTTTCTAAGGAG
209066	41262	TCTGCGGAGAAGGTGAACTT	253653	85849	AGCAATTCTCCTGCCTCCTA	298240	130436	AGGTCAGTCTTTTCTAAGGA
209067	41263	CTCTGCGGAGAAGGTGAACT	253654	85850	AAGCAATTCTCCTGCCTCCT	298241	130437	AAGGTCAGTCTTTTCTAAGG
209068	41264	GCTCTGCGGAGAAGGTGAAC	253655	85851	CAAGCAATTCTCCTGCCTCC	298242	130438	CAAGGTCAGTCTTTTCTAAG
209069	41265	GGCTCTGCGGAGAAGGTGAA	253656	85852	TCAAGCAATTCTCCTGCCTC	298243	130439	TCAAGGTCAGTCTTTTCTAA
209070	41266	AGGCTCTGCGGAGAAGGTGA	253657	85853	TTCAAGCAATTCTCCTGCCT	298244	130440	ATCAAGGTCAGTCTTTTCTA
209071	41267	AAGGCTCTGCGGAGAAGGTG	253658	85854	GTTCAAGCAATTCTCCTGCC	298245	130441	CATCAAGGTCAGTCTTTTCT
209072	41268	GAAGGCTCTGCGGAGAAGGT	253659	85855	GGTTCAAGCAATTCTCCTGC	298246	130442	ACATCAAGGTCAGTCTTTTC
209073	41269	AGAAGGCTCTGCGGAGAAGG	253660	85856	AGGTTCAAGCAATTCTCCTG	298247	130443	GACATCAAGGTCAGTCTTTT
209074	41270	GAGAAGGCTCTGCGGAGAAG	253661	85857	CAGGTTCAAGCAATTCTCCT	298248	130444	AGACATCAAGGTCAGTCTTT
209075	41271	GGAGAAGGCTCTGCGGAGAA	253662	85858	CCAGGTTCAAGCAATTCTCC	298249	130445	AAGACATCAAGGTCAGTCTT
209076	41272	TGGAGAAGGCTCTGCGGAGA	253663	85859	CCCAGGTTCAAGCAATTCTC	298250	130446	CAAGACATCAAGGTCAGTCT
209077	41273	TTGGAGAAGGCTCTGCGGAG	253664	85860	TCCCAGGTTCAAGCAATTCT	298251	130447	TCAAGACATCAAGGTCAGTC
209078	41274	ATTGGAGAAGGCTCTGCGGA	253665	85861	CTCCCAGGTTCAAGCAATTC	298252	130448	CTCAAGACATCAAGGTCAGT
209079	41275	GATTGGAGAAGGCTCTGCGG	253666	85862	CCTCCCAGGTTCAAGCAATT	298253	130449	TCTCAAGACATCAAGGTCAG
209080	41276	AGATTGGAGAAGGCTCTGCG	253667	85863	ACCTCCCAGGTTCAAGCAAT	298254	130450	CTCTCAAGACATCAAGGTCA
209081	41277	AAGATTGGAGAAGGCTCTGC	253668	85864	CACCTCCCAGGTTCAAGCAA	298255	130451	GCTCTCAAGACATCAAGGTC
209082	41278	GAAGATTGGAGAAGGCTCTG	253669	85865	CCACCTCCCAGGTTCAAGCA	298256	130452	CGCTCTCAAGACATCAAGGT
209083	41279	AGAAGATTGGAGAAGGCTCT	253670	85866	TCCACCTCCCAGGTTCAAGC	298257	130453	GCGCTCTCAAGACATCAAGG
209084	41280	AAGAAGATTGGAGAAGGCTC	253671	85867	CTCCACCTCCCAGGTTCAAG	298258	130454	AGCGCTCTCAAGACATCAAG
209085	41281	CAAGAAGATTGGAGAAGGCT	253672	85868	CCTCCACCTCCCAGGTTCAA	298259	130455	CAGCGCTCTCAAGACATCAA
209086	41282	TCAAGAAGATTGGAGAAGGC	253673	85869	ACCTCCACCTCCCAGGTTCA	298260	130456	CCAGCGCTCTCAAGACATCA
209087	41283	GTCAAGAAGATTGGAGAAGG	253674	85870	AACCTCCACCTCCCAGGTTC	298261	130457	GCCAGCGCTCTCAAGACATC
209088	41284	AGTCAAGAAGATTGGAGAAG	253675	85871	CAACCTCCACCTCCCAGGTT	298262	130458	GGCCAGCGCTCTCAAGACAT
209089	41285	TAGTCAAGAAGATTGGAGAA	253676	85872	GCAACCTCCACCTCCCAGGT	298263	130459	AGGCCAGCGCTCTCAAGACA
209090	41286	GTAGTCAAGAAGATTGGAGA	253677	85873	AGCAACCTCCACCTCCCAGG	298264	130460	GAGGCCAGCGCTCTCAAGAC
209091	41287	CGTAGTCAAGAAGATTGGAG	253678	85874	CAGCAACCTCCACCTCCCAG	298265	130461	AGAGGCCAGCGCTCTCAAGA
209092	41288	ACGTAGTCAAGAAGATTGGA	253679	85875	ACAGCAACCTCCACCTCCCA	298266	130462	AAGAGGCCAGCGCTCTCAAG
209093	41289	GACGTAGTCAAGAAGATTGG	253680	85876	CACAGCAACCTCCACCTCCC	298267	130463	GAAGAGGCCAGCGCTCTCAA
209094	41290	AGACGTAGTCAAGAAGATTG	253681	85877	TCACAGCAACCTCCACCTCC	298268	130464	GGAAGAGGCCAGCGCTCTCA
209095	41291	GAGACGTAGTCAAGAAGATT	253682	85878	CTCACAGCAACCTCCACCTC	298269	130465	AGGAAGAGGCCAGCGCTCTC
209096	41292	GGAGACGTAGTCAAGAAGAT	253683	85879	GCTCACAGCAACCTCCACCT	298270	130466	GAGGAAGAGGCCAGCGCTCT
209097	41293	AGGAGACGTAGTCAAGAAGA	253684	85880	GGCTCACAGCAACCTCCACC	298271	130467	GGAGGAAGAGGCCAGCGCTC
209098	41294	GAGGAGACGTAGTCAAGAAG	253685	85881	CGGCTCACAGCAACCTCCAC	298272	130468	GGGAGGAAGAGGCCAGCGCT
209099	41295	AGAGGAGACGTAGTCAAGAA	253686	85882	TCGGCTCACAGCAACCTCCA	298273	130469	AGGGAGGAAGAGGCCAGCGC
209100	41296	GAGAGGAGACGTAGTCAAGA	253687	85883	CTCGGCTCACAGCAACCTCC	298274	130470	GAGGGAGGAAGAGGCCAGCG
209101	41297	TGAGAGGAGACGTAGTCAAG	253688	85884	TCTCGGCTCACAGCAACCTC	298275	130471	GGAGGGAGGAAGAGGCCAGC
209102	41298	CTGAGAGGAGACGTAGTCAA	253689	85885	ATCTCGGCTCACAGCAACCT	298276	130472	GGGAGGGAGGAAGAGGCCAG
209103	41299	GCTGAGAGGAGACGTAGTCA	253690	85886	GATCTCGGCTCACAGCAACC	298277	130473	AGGGAGGGAGGAAGAGGCCA
209104	41300	AGCTGAGAGGAGACGTAGTC	253691	85887	TGATCTCGGCTCACAGCAAC	298278	130474	CAGGGAGGGAGGAAGAGGCC
209105	41301	GAGCTGAGAGGAGACGTAGT	253692	85888	ATGATCTCGGCTCACAGCAA	298279	130475	GCAGGGAGGGAGGAAGAGGC
209106	41302	GGAGCTGAGAGGAGACGTAG	253693	85889	CATGATCTCGGCTCACAGCA	298280	130476	TGCAGGGAGGGAGGAAGAGG
209107	41303	TGGAGCTGAGAGGAGACGTA	253694	85890	GCATGATCTCGGCTCACAGC	298281	130477	CTGCAGGGAGGGAGGAAGAG
209108	41304	CTGGAGCTGAGAGGAGACGT	253695	85891	GGCATGATCTCGGCTCACAG	298282	130478	CCTGCAGGGAGGGAGGAAGA
209109	41305	GCTGGAGCTGAGAGGAGACG	253696	85892	TGGCATGATCTCGGCTCACA	298283	130479	CCCTGCAGGGAGGGAGGAAG
209110	41306	TGCTGGAGCTGAGAGGAGAC	253697	85893	GTGGCATGATCTCGGCTCAC	298284	130480	ACCCTGCAGGGAGGGAGGAA
209111	41307	TTGCTGGAGCTGAGAGGAGA	253698	85894	AGTGGCATGATCTCGGCTCA	298285	130481	TACCCTGCAGGGAGGGAGGA
209112	41308	GTTGCTGGAGCTGAGAGGAG	253699	85895	CAGTGGCATGATCTCGGCTC	298286	130482	CTACCCTGCAGGGAGGGAGG
209113	41309	GGTTGCTGGAGCTGAGAGGA	253700	85896	GCAGTGGCATGATCTCGGCT	298287	130483	CCTACCCTGCAGGGAGGGAG
209114	41310	AGGTTGCTGGAGCTGAGAGG	253701	85897	TGCAGTGGCATGATCTCGGC	298288	130484	CCCTACCCTGCAGGGAGGGA
209115	41311	GAGGTTGCTGGAGCTGAGAG	253702	85898	GTGCAGTGGCATGATCTCGG	298289	130485	CCCCTACCCTGCAGGGAGGG
209116	41312	AGAGGTTGCTGGAGCTGAGA	253703	85899	AGTGCAGTGGCATGATCTCG	298290	130486	CCCCCTACCCTGCAGGGAGG
209117	41313	CAGAGGTTGCTGGAGCTGAG	253704	85900	GAGTGCAGTGGCATGATCTC	298291	130487	GCCCCCTACCCTGCAGGGAG
209118	41314	ACAGAGGTTGCTGGAGCTGA	253705	85901	GGAGTGCAGTGGCATGATCT	298292	130488	GGCCCCCTACCCTGCAGGGA
209119	41315	GACAGAGGTTGCTGGAGCTG	253706	85902	TGGAGTGCAGTGGCATGATC	298293	130489	AGGCCCCCTACCCTGCAGGG
209120	41316	AGACAGAGGTTGCTGGAGCT	253707	85903	CTGGAGTGCAGTGGCATGAT	298294	130490	CAGGCCCCCTACCCTGCAGG
209121	41317	GAGACAGAGGTTGCTGGAGC	253708	85904	GCTGGAGTGCAGTGGCATGA	298295	130491	TCAGGCCCCCTACCCTGCAG
209122	41318	AGAGACAGAGGTTGCTGGAG	253709	85905	GGCTGGAGTGCAGTGGCATG	298296	130492	CTCAGGCCCCCTACCCTGCA
209123	41319	CAGAGACAGAGGTTGCTGGA	253710	85906	AGGCTGGAGTGCAGTGGCAT	298297	130493	ACTCAGGCCCCCTACCCTGC
209124	41320	CCAGAGACAGAGGTTGCTGG	253711	85907	CAGGCTGGAGTGCAGTGGCA	298298	130494	AACTCAGGCCCCCTACCCTG
209125	41321	GCCAGAGACAGAGGTTGCTG	253712	85908	CCAGGCTGGAGTGCAGTGGC	298299	130495	CAACTCAGGCCCCCTACCCT
209126	41322	TGCCAGAGACAGAGGTTGCT	253713	85909	CCCAGGCTGGAGTGCAGTGG	298300	130496	TCAACTCAGGCCCCCTACCC
209127	41323	GTGCCAGAGACAGAGGTTGC	253714	85910	GCCCAGGCTGGAGTGCAGTG	298301	130497	CTCAACTCAGGCCCCCTACC
209128	41324	AGTGCCAGAGACAGAGGTTG	253715	85911	CGCCCAGGCTGGAGTGCAGT	298302	130498	CCTCAACTCAGGCCCCCTAC
209129	41325	CAGTGCCAGAGACAGAGGTT	253716	85912	TCGCCCAGGCTGGAGTGCAG	298303	130499	CCCTCAACTCAGGCCCCCTA
209130	41326	TCAGTGCCAGAGACAGAGGT	253717	85913	GTCGCCCAGGCTGGAGTGCA	298304	130500	CCCCTCAACTCAGGCCCCCT

209131	41327	ATCAGTGCCAGAGACAGAGG	253718	85914	TGTCGCCCAGGCTGGAGTGC	298305	130501	GCCCCTCAACTCAGGCCCCC
209132	41328	AATCAGTGCCAGAGACAGAG	253719	85915	CTGTCGCCCAGGCTGGAGTG	298306	130502	AGCCCCTCAACTCAGGCCCC
209133	41329	GAATCAGTGCCAGAGACAGA	253720	85916	TCTGTCGCCCAGGCTGGAGT	298307	130503	AAGCCCCTCAACTCAGGCCC
209134	41330	GGAATCAGTGCCAGAGACAG	253721	85917	CTCTGTCGCCCAGGCTGGAG	298308	130504	GAAGCCCCTCAACTCAGGCC
209135	41331	AGGAATCAGTGCCAGAGACA	253722	85918	ACTCTGTCGCCCAGGCTGGA	298309	130505	GGAAGCCCCTCAACTCAGGC
209136	41332	AAGGAATCAGTGCCAGAGAC	253723	85919	CACTCTGTCGCCCAGGCTGG	298310	130506	GGGAAGCCCCTCAACTCAGG
209137	41333	TAAGGAATCAGTGCCAGAGA	253724	85920	TCACTCTGTCGCCCAGGCTG	298311	130507	AGGGAAGCCCCTCAACTCAG
209138	41334	GTAAGGAATCAGTGCCAGAG	253725	85921	CTCACTCTGTCGCCCAGGCT	298312	130508	GAGGGAAGCCCCTCAACTCA
209139	41335	AGTAAGGAATCAGTGCCAGA	253726	85922	ACTCACTCTGTCGCCCAGGC	298313	130509	AGAGGGAAGCCCCTCAACTC
209140	41336	AAGTAAGGAATCAGTGCCAG	253727	85923	CACTCACTCTGTCGCCCAGG	298314	130510	CAGAGGGAAGCCCCTCAACT
209141	41337	TAAGTAAGGAATCAGTGCCA	253728	85924	TCACTCACTCTGTCGCCCAG	298315	130511	GCAGAGGGAAGCCCCTCAAC
209142	41338	CTAAGTAAGGAATCAGTGCC	253729	85925	CTCACTCACTCTGTCGCCCA	298316	130512	AGCAGAGGGAAGCCCCTCAA
209143	41339	GCTAAGTAAGGAATCAGTGC	253730	85926	TCTCACTCACTCTGTCGCCC	298317	130513	GAGCAGAGGGAAGCCCCTCA
209144	41340	AGCTAAGTAAGGAATCAGTG	253731	85927	GTCTCACTCACTCTGTCGCC	298318	130514	GGAGCAGAGGGAAGCCCCTC
209145	41341	TAGCTAAGTAAGGAATCAGT	253732	85928	AGTCTCACTCACTCTGTCGC	298319	130515	TGGAGCAGAGGGAAGCCCCT
209146	41342	TTAGCTAAGTAAGGAATCAG	253733	85929	GAGTCTCACTCACTCTGTCG	298320	130516	GTGGAGCAGAGGGAAGCCCC
209147	41343	CTTAGCTAAGTAAGGAATCA	253734	85930	AGAGTCTCACTCACTCTGTC	298321	130517	TGTGGAGCAGAGGGAAGCCC
209148	41344	TCTTAGCTAAGTAAGGAATC	253735	85931	CAGAGTCTCACTCACTCTGT	298322	130518	CTGTGGAGCAGAGGGAAGCC
209149	41345	CTCTTAGCTAAGTAAGGAAT	253736	85932	ACAGAGTCTCACTCACTCTG	298323	130519	TCTGTGGAGCAGAGGGAAGC
209150	41346	TCTCTTAGCTAAGTAAGGAA	253737	85933	AACAGAGTCTCACTCACTCT	298324	130520	TTCTGTGGAGCAGAGGGAAG
209151	41347	TTCTCTTAGCTAAGTAAGGA	253738	85934	AAACAGAGTCTCACTCACTC	298325	130521	TTTCTGTGGAGCAGAGGGAA
209152	41348	ATTCTCTTAGCTAAGTAAGG	253739	85935	TAAACAGAGTCTCACTCACT	298326	130522	GTTTCTGTGGAGCAGAGGGA
209153	41349	GATTCTCTTAGCTAAGTAAG	253740	85936	TTAAACAGAGTCTCACTCAC	298327	130523	GGTTTCTGTGGAGCAGAGGG
209154	41350	TGATTCTCTTAGCTAAGTAA	253741	85937	TTTAAACAGAGTCTCACTCA	298328	130524	GGGTTTCTGTGGAGCAGAGG
209155	41351	GTGATTCTCTTAGCTAAGTA	253742	85938	TTTTAAACAGAGTCTCACTC	298329	130525	AGGGTTTCTGTGGAGCAGAG
209156	41352	TGTGATTCTCTTAGCTAAGT	253743	85939	TTTTTAAACAGAGTCTCACT	298330	130526	CAGGGTTTCTGTGGAGCAGA
209157	41353	CTGTGATTCTCTTAGCTAAG	253744	85940	TTTTTTAAACAGAGTCTCAC	298331	130527	ACAGGGTTTCTGTGGAGCAG
209158	41354	TCTGTGATTCTCTTAGCTAA	253745	85941	TTTTTTTAAACAGAGTCTCA	298332	130528	AACAGGGTTTCTGTGGAGCA
209159	41355	GTCTGTGATTCTCTTAGCTA	253746	85942	TTTTTTTTAAACAGAGTCTC	298333	130529	AAACAGGGTTTCTGTGGAGC
209160	41356	TGTCTGTGATTCTCTTAGCT	253747	85943	TTTTTTTTTAAACAGAGTCT	298334	130530	AAAACAGGGTTTCTGTGGAG
209161	41357	GTGTCTGTGATTCTCTTAGC	253748	85944	TTTTTTTTTTAAACAGAGTC	298335	130531	TAAAACAGGGTTTCTGTGGA
209162	41358	AGTGTCTGTGATTCTCTTAG	253749	85945	TTTTTTTTTTTAAACAGAGT	298336	130532	ATAAAACAGGGTTTCTGTGG
209163	41359	AAGTGTCTGTGATTCTCTTA	253750	85946	TTTTTTTTTTTTAAACAGAG	298337	130533	AATAAAACAGGGTTTCTGTG
209164	41360	CAAGTGTCTGTGATTCTCTT	253751	85947	TTTTTTTTTTTTTAAACAGA	298338	130534	CAATAAAACAGGGTTTCTGT
209165	41361	CCAAGTGTCTGTGATTCTCT	253752	85948	TTTTTTTTTTTTTTAAACAG	298339	130535	TCAATAAAACAGGGTTTCTG
209166	41362	CCCAAGTGTCTGTGATTCTC	253753	85949	TTTTTTTTTTTTTTTAAACA	298340	130536	CTCAATAAAACAGGGTTTCT
209167	41363	CCCCAAGTGTCTGTGATTCT	253754	85950	TTTTTTTTTTTTTTTTAAAC	298341	130537	ACTCAATAAAACAGGGTTTC
209168	41364	GCCCCAAGTGTCTGTGATTC	253755	85951	TTTTTTTTTTTTTTTTTAAA	298342	130538	AACTCAATAAAACAGGGTTT
209169	41365	AGCCCCAAGTGTCTGTGATT	253756	85952	CTTTTTTTTTTTTTTTTTAA	298343	130539	GAACTCAATAAAACAGGGTT
209170	41366	GAGCCCCAAGTGTCTGTGAT	253757	85953	TCTTTTTTTTTTTTTTTTTA	298344	130540	AGAACTCAATAAAACAGGGT
209171	41367	TGAGCCCCAAGTGTCTGTGA	253758	85954	TTCTTTTTTTTTTTTTTTTT	298345	130541	CAGAACTCAATAAAACAGGG
209172	41368	CTGAGCCCCAAGTGTCTGTG	253759	85955	GTTCTTTTTTTTTTTTTTTT	298346	130542	TCAGAACTCAATAAAACAGG
209173	41369	CCTGAGCCCCAAGTGTCTGT	253760	85956	TGTTCTTTTTTTTTTTTTTT	298347	130543	TTCAGAACTCAATAAAACAG
209174	41370	TCCTGAGCCCCAAGTGTCTG	253761	85957	ATGTTCTTTTTTTTTTTTTT	298348	130544	CTTCAGAACTCAATAAAACA
209175	41371	GTCCTGAGCCCCAAGTGTCT	253762	85958	AATGTTCTTTTTTTTTTTTT	298349	130545	CCTTCAGAACTCAATAAAAC
209176	41372	TGTCCTGAGCCCCAAGTGTC	253763	85959	GAATGTTCTTTTTTTTTTTT	298350	130546	ACCTTCAGAACTCAATAAAA
209177	41373	TTGTCCTGAGCCCCAAGTGT	253764	85960	AGAATGTTCTTTTTTTTTTT	298351	130547	AACCTTCAGAACTCAATAAA
209178	41374	ATTGTCCTGAGCCCCAAGTG	253765	85961	GAGAATGTTCTTTTTTTTTT	298352	130548	CAACCTTCAGAACTCAATAA
209179	41375	GATTGTCCTGAGCCCCAAGT	253766	85962	GGAGAATGTTCTTTTTTTTT	298353	130549	CCAACCTTCAGAACTCAATA
209180	41376	AGATTGTCCTGAGCCCCAAG	253767	85963	AGGAGAATGTTCTTTTTTTT	298354	130550	TCCAACCTTCAGAACTCAAT
209181	41377	CAGATTGTCCTGAGCCCCAA	253768	85964	TAGGAGAATGTTCTTTTTTT	298355	130551	TTCCAACCTTCAGAACTCAA
209182	41378	GCAGATTGTCCTGAGCCCCA	253769	85965	TTAGGAGAATGTTCTTTTTT	298356	130552	GTTCCAACCTTCAGAACTCA
209183	41379	AGCAGATTGTCCTGAGCCCC	253770	85966	GTTAGGAGAATGTTCTTTTT	298357	130553	AGTTCCAACCTTCAGAACTC
209184	41380	AAGCAGATTGTCCTGAGCCC	253771	85967	GGTTAGGAGAATGTTCTTTT	298358	130554	CAGTTCCAACCTTCAGAACT
209185	41381	AAAGCAGATTGTCCTGAGCC	253772	85968	AGGTTAGGAGAATGTTCTTT	298359	130555	GCAGTTCCAACCTTCAGAAC
209186	41382	GAAAGCAGATTGTCCTGAGC	253773	85969	CAGGTTAGGAGAATGTTCTT	298360	130556	AGCAGTTCCAACCTTCAGAA
209187	41383	AGAAAGCAGATTGTCCTGAG	253774	85970	CCAGGTTAGGAGAATGTTCT	298361	130557	CAGCAGTTCCAACCTTCAGA
209188	41384	GAGAAAGCAGATTGTCCTGA	253775	85971	GCCAGGTTAGGAGAATGTTC	298362	130558	GCAGCAGTTCCAACCTTCAG
209189	41385	AGAGAAAGCAGATTGTCCTG	253776	85972	AGCCAGGTTAGGAGAATGTT	298363	130559	GGCAGCAGTTCCAACCTTCA
209190	41386	GAGAGAAAGCAGATTGTCCT	253777	85973	AAGCCAGGTTAGGAGAATGT	298364	130560	TGGCAGCAGTTCCAACCTTC
209191	41387	AGAGAGAAAGCAGATTGTCC	253778	85974	GAAGCCAGGTTAGGAGAATG	298365	130561	ATGGCAGCAGTTCCAACCTT
209192	41388	AAGAGAGAAAGCAGATTGTC	253779	85975	AGAAGCCAGGTTAGGAGAAT	298366	130562	CATGGCAGCAGTTCCAACCT
209193	41389	GAAGAGAGAAAGCAGATTGT	253780	85976	AAGAAGCCAGGTTAGGAGAA	298367	130563	TCATGGCAGCAGTTCCAACC
209194	41390	AGAAGAGAGAAAGCAGATTG	253781	85977	GAAGAAGCCAGGTTAGGAGA	298368	130564	ATCATGGCAGCAGTTCCAAC
209195	41391	AAGAAGAGAGAAAGCAGATT	253782	85978	GGAAGAAGCCAGGTTAGGAG	298369	130565	AATCATGGCAGCAGTTCCAA
209196	41392	TAAGAAGAGAGAAAGCAGAT	253783	85979	AGGAAGAAGCCAGGTTAGGA	298370	130566	AAATCATGGCAGCAGTTCCA
209197	41393	GTAAGAAGAGAGAAAGCAGA	253784	85980	GAGGAAGAAGCCAGGTTAGG	298371	130567	AAAATCATGGCAGCAGTTCC
209198	41394	GGTAAGAAGAGAGAAAGCAG	253785	85981	GGAGGAAGAAGCCAGGTTAG	298372	130568	CAAAATCATGGCAGCAGTTC
209199	41395	GGGTAAGAAGAGAGAAAGCA	253786	85982	TGGAGGAAGAAGCCAGGTTA	298373	130569	CCAAAATCATGGCAGCAGTT
209200	41396	TGGGTAAGAAGAGAGAAAGC	253787	85983	CTGGAGGAAGAAGCCAGGTT	298374	130570	GCCAAAATCATGGCAGCAGT
209201	41397	ATGGGTAAGAAGAGAGAAAG	253788	85984	CCTGGAGGAAGAAGCCAGGT	298375	130571	GGCCAAAATCATGGCAGCAG
209202	41398	CATGGGTAAGAAGAGAGAAA	253789	85985	CCCTGGAGGAAGAAGCCAGG	298376	130572	TGGCCAAAATCATGGCAGCA

209203	41399	CCATGGGTAAGAAGAGAGAA	253790	85986	CCCCTGGAGGAAGAAGCCAG	298377	130573	GTGGCCAAAATCATGGCAGC
209204	41400	GCCATGGGTAAGAAGAGAGA	253791	85987	ACCCCTGGAGGAAGAAGCCA	298378	130574	AGTGGCCAAAATCATGGCAG
209205	41401	GGCCATGGGTAAGAAGAGAG	253792	85988	CACCCCTGGAGGAAGAAGCC	298379	130575	AAGTGGCCAAAATCATGGCA
209206	41402	AGGCCATGGGTAAGAAGAGA	253793	85989	ACACCCCTGGAGGAAGAAGC	298380	130576	AAAGTGGCCAAAATCATGGC
209207	41403	AAGGCCATGGGTAAGAAGAG	253794	85990	TACACCCCTGGAGGAAGAAG	298381	130577	CAAAGTGGCCAAAATCATGG
209208	41404	CAAGGCCATGGGTAAGAAGA	253795	85991	TTACACCCCTGGAGGAAGAA	298382	130578	GCAAAGTGGCCAAAATCATG
209209	41405	CCAAGGCCATGGGTAAGAAG	253796	85992	ATTACACCCCTGGAGGAAGA	298383	130579	TGCAAAGTGGCCAAAATCAT
209210	41406	TCCAAGGCCATGGGTAAGAA	253797	85993	AATTACACCCCTGGAGGAAG	298384	130580	CTGCAAAGTGGCCAAAATCA
209211	41407	GTCCAAGGCCATGGGTAAGA	253798	85994	TAATTACACCCCTGGAGGAA	298385	130581	TCTGCAAAGTGGCCAAAATC
209212	41408	AGTCCAAGGCCATGGGTAAG	253799	85995	TTAATTACACCCCTGGAGGA	298386	130582	GTCTGCAAAGTGGCCAAAAT
209213	41409	CAGTCCAAGGCCATGGGTAA	253800	85996	ATTAATTACACCCCTGGAGG	298387	130583	GGTCTGCAAAGTGGCCAAAA
209214	41410	ACAGTCCAAGGCCATGGGTA	253801	85997	GATTAATTACACCCCTGGAG	298388	130584	AGGTCTGCAAAGTGGCCAAA
209215	41411	CACAGTCCAAGGCCATGGGT	253802	85998	TGATTAATTACACCCCTGGA	298389	130585	CAGGTCTGCAAAGTGGCCAA
209216	41412	ACACAGTCCAAGGCCATGGG	253803	85999	ATGATTAATTACACCCCTGG	298390	130586	CCAGGTCTGCAAAGTGGCCA
209217	41413	CACACAGTCCAAGGCCATGG	253804	86000	CATGATTAATTACACCCCTG	298391	130587	CCCAGGTCTGCAAAGTGGCC
209218	41414	ACACACAGTCCAAGGCCATG	253805	86001	ACATGATTAATTACACCCCT	298392	130588	TCCCAGGTCTGCAAAGTGGC
209219	41415	TACACACAGTCCAAGGCCAT	253806	86002	GACATGATTAATTACACCCC	298393	130589	GTCCCAGGTCTGCAAAGTGG
209220	41416	GTACACACAGTCCAAGGCCA	253807	86003	TGACATGATTAATTACACCC	298394	130590	AGTCCCAGGTCTGCAAAGTG
209221	41417	GGTACACACAGTCCAAGGCC	253808	86004	CTGACATGATTAATTACACC	298395	130591	AAGTCCCAGGTCTGCAAAGT
209222	41418	AGGTACACACAGTCCAAGGC	253809	86005	ACTGACATGATTAATTACAC	298396	130592	AAAGTCCCAGGTCTGCAAAG
209223	41419	GAGGTACACACAGTCCAAGG	253810	86006	AACTGACATGATTAATTACA	298397	130593	TAAAGTCCCAGGTCTGCAAA
209224	41420	AGAGGTACACACAGTCCAAG	253811	86007	AAACTGACATGATTAATTAC	298398	130594	CTAAAGTCCCAGGTCTGCAA
209225	41421	AAGAGGTACACACAGTCCAA	253812	86008	GAAACTGACATGATTAATTA	298399	130595	CCTAAAGTCCCAGGTCTGCA
209226	41422	AAAGAGGTACACACAGTCCA	253813	86009	GGAAACTGACATGATTAATT	298400	130596	CCCTAAAGTCCCAGGTCTGC
209227	41423	CAAAGAGGTACACACAGTCC	253814	86010	AGGAAACTGACATGATTAAT	298401	130597	GCCCTAAAGTCCCAGGTCTG
209228	41424	ACAAAGAGGTACACACAGTC	253815	86011	GAGGAAACTGACATGATTAA	298402	130598	AGCCCTAAAGTCCCAGGTCT
209229	41425	GACAAAGAGGTACACACAGT	253816	86012	TGAGGAAACTGACATGATTA	298403	130599	TAGCCCTAAAGTCCCAGGTC
209230	41426	AGACAAAGAGGTACACACAG	253817	86013	ATGAGGAAACTGACATGATT	298404	130600	TTAGCCCTAAAGTCCCAGGT
209231	41427	GAGACAAAGAGGTACACACA	253818	86014	AATGAGGAAACTGACATGAT	298405	130601	GTTAGCCCTAAAGTCCCAGG
209232	41428	GGAGACAAAGAGGTACACAC	253819	86015	CAATGAGGAAACTGACATGA	298406	130602	GGTTAGCCCTAAAGTCCCAG
209233	41429	TGGAGACAAAGAGGTACACA	253820	86016	TCAATGAGGAAACTGACATG	298407	130603	TGGTTAGCCCTAAAGTCCCA
209234	41430	GTGGAGACAAAGAGGTACAC	253821	86017	ATCAATGAGGAAACTGACAT	298408	130604	CTGGTTAGCCCTAAAGTCCC
209235	41431	AGTGGAGACAAAGAGGTACA	253822	86018	TATCAATGAGGAAACTGACA	298409	130605	ACTGGTTAGCCCTAAAGTCC
209236	41432	GAGTGGAGACAAAGAGGTAC	253823	86019	GTATCAATGAGGAAACTGAC	298410	130606	AACTGGTTAGCCCTAAAGTC
209237	41433	GGAGTGGAGACAAAGAGGTA	253824	86020	TGTATCAATGAGGAAACTGA	298411	130607	GAACTGGTTAGCCCTAAAGT
209238	41434	GGGAGTGGAGACAAAGAGGT	253825	86021	GTGTATCAATGAGGAAACTG	298412	130608	AGAACTGGTTAGCCCTAAAG
209239	41435	TGGGAGTGGAGACAAAGAGG	253826	86022	TGTGTATCAATGAGGAAACT	298413	130609	GAGAACTGGTTAGCCCTAAA
209240	41436	TTGGGAGTGGAGACAAAGAG	253827	86023	GTGTGTATCAATGAGGAAAC	298414	130610	AGAGAACTGGTTAGCCCTAA
209241	41437	TTTGGGAGTGGAGACAAAGA	253828	86024	TGTGTGTATCAATGAGGAAA	298415	130611	AAGAGAACTGGTTAGCCCTA
209242	41438	GTTTGGGAGTGGAGACAAAG	253829	86025	GTGTGTGTATCAATGAGGAA	298416	130612	AAAGAGAACTGGTTAGCCCT
209243	41439	GGTTTGGGAGTGGAGACAAA	253830	86026	TGTGTGTGTATCAATGAGGA	298417	130613	CAAAGAGAACTGGTTAGCCC
209244	41440	GGGTTTGGGAGTGGAGACAA	253831	86027	GTGTGTGTGTATCAATGAGG	298418	130614	ACAAAGAGAACTGGTTAGCC
209245	41441	TGGGTTTGGGAGTGGAGACA	253832	86028	TGTGTGTGTGTATCAATGAG	298419	130615	TACAAAGAGAACTGGTTAGC
209246	41442	TTGGGTTTGGGAGTGGAGAC	253833	86029	GTGTGTGTGTGTATCAATGA	298420	130616	TTACAAAGAGAACTGGTTAG
209247	41443	GTTGGGTTTGGGAGTGGAGA	253834	86030	TGTGTGTGTGTGTATCAATG	298421	130617	CTTACAAAGAGAACTGGTTA
209248	41444	GGTTGGGTTTGGGAGTGGAG	253835	86031	GTGTGTGTGTGTGTATCAAT	298422	130618	CCTTACAAAGAGAACTGGTT
209249	41445	GGGTTGGGTTTGGGAGTGGA	253836	86032	TGTGTGTGTGTGTGTATCAA	298423	130619	TCCTTACAAAGAGAACTGGT
209250	41446	GGGGTTGGGTTTGGGAGTGG	253837	86033	GTGTGTGTGTGTGTGTATCA	298424	130620	GTCCTTACAAAGAGAACTGG
209251	41447	GGGGGTTGGGTTTGGGAGTG	253838	86034	AGTGTGTGTGTGTGTGTATC	298425	130621	AGTCCTTACAAAGAGAACTG
209252	41448	TGGGGGTTGGGTTTGGGAGT	253839	86035	TAGTGTGTGTGTGTGTGTAT	298426	130622	AAGTCCTTACAAAGAGAACT
209253	41449	CTGGGGGTTGGGTTTGGGAG	253840	86036	GTAGTGTGTGTGTGTGTGTA	298427	130623	CAAGTCCTTACAAAGAGAAC
209254	41450	TCTGGGGGTTGGGTTTGGGA	253841	86037	TGTAGTGTGTGTGTGTGTGT	298428	130624	ACAAGTCCTTACAAAGAGAA
209255	41451	CTCTGGGGGTTGGGTTTGGG	253842	86038	TTGTAGTGTGTGTGTGTGTG	298429	130625	CACAAGTCCTTACAAAGAGA
209256	41452	CCTCTGGGGGTTGGGTTTGG	253843	86039	ATTGTAGTGTGTGTGTGTGT	298430	130626	GCACAAGTCCTTACAAAGAG
209257	41453	CCCTCTGGGGGTTGGGTTTG	253844	86040	GATTGTAGTGTGTGTGTGTG	298431	130627	GGCACAAGTCCTTACAAAGA
209258	41454	GCCCTCTGGGGGTTGGGTTT	253845	86041	GGATTGTAGTGTGTGTGTGT	298432	130628	AGGCACAAGTCCTTACAAAG
209259	41455	TGCCCTCTGGGGGTTGGGTT	253846	86042	AGGATTGTAGTGTGTGTGTG	298433	130629	GAGGCACAAGTCCTTACAAA
209260	41456	CTGCCCTCTGGGGGTTGGGT	253847	86043	CAGGATTGTAGTGTGTGTGT	298434	130630	AGAGGCACAAGTCCTTACAA
209261	41457	TCTGCCCTCTGGGGGTTGGG	253848	86044	ACAGGATTGTAGTGTGTGTG	298435	130631	AAGAGGCACAAGTCCTTACA
209262	41458	CTCTGCCCTCTGGGGGTTGG	253849	86045	TACAGGATTGTAGTGTGTGT	298436	130632	CAAGAGGCACAAGTCCTTAC
209263	41459	TCTCTGCCCTCTGGGGGTTG	253850	86046	ATACAGGATTGTAGTGTGTG	298437	130633	CCAAGAGGCACAAGTCCTTA
209264	41460	CTCTCTGCCCTCTGGGGGTT	253851	86047	GATACAGGATTGTAGTGTGT	298438	130634	CCCAAGAGGCACAAGTCCTT
209265	41461	GCTCTCTGCCCTCTGGGGGT	253852	86048	GGATACAGGATTGTAGTGTG	298439	130635	TCCCAAGAGGCACAAGTCCT
209266	41462	TGCTCTCTGCCCTCTGGGGG	253853	86049	TGGATACAGGATTGTAGTGT	298440	130636	CTCCCAAGAGGCACAAGTCC
209267	41463	ATGCTCTCTGCCCTCTGGGG	253854	86050	ATGGATACAGGATTGTAGTG	298441	130637	TCTCCCAAGAGGCACAAGTC
209268	41464	CATGCTCTCTGCCCTCTGGG	253855	86051	AATGGATACAGGATTGTAGT	298442	130638	GTCTCCCAAGAGGCACAAGT
209269	41465	ACATGCTCTCTGCCCTCTGG	253856	86052	TAATGGATACAGGATTGTAG	298443	130639	CGTCTCCCAAGAGGCACAAG
209270	41466	AACATGCTCTCTGCCCTCTG	253857	86053	GTAATGGATACAGGATTGTA	298444	130640	ACGTCTCCCAAGAGGCACAA
209271	41467	CAACATGCTCTCTGCCCTCT	253858	86054	AGTAATGGATACAGGATTGT	298445	130641	GACGTCTCCCAAGAGGCACA
209272	41468	ACAACATGCTCTCTGCCCTC	253859	86055	AAGTAATGGATACAGGATTG	298446	130642	GGACGTCTCCCAAGAGGCAC
209273	41469	GACAACATGCTCTCTGCCCT	253860	86056	AAAGTAATGGATACAGGATT	298447	130643	TGGACGTCTCCCAAGAGGCA
209274	41470	AGACAACATGCTCTCTGCCC	253861	86057	AAAAGTAATGGATACAGGAT	298448	130644	GTGGACGTCTCCCAAGAGGC

209275	41471	CAGACAACATGCTCTCTGCC	253862	86058	GAAAAGTAATGGATACAGGA	298449	130645	GGTGGACGTCTCCCAAGAGG
209276	41472	ACAGACAACATGCTCTCTGC	253863	86059	TGAAAAGTAATGGATACAGG	298450	130646	GGGTGGACGTCTCCCAAGAG
209277	41473	GACAGACAACATGCTCTCTG	253864	86060	TTGAAAAGTAATGGATACAG	298451	130647	CGGGTGGACGTCTCCCAAGA
209278	41474	GGACAGACAACATGCTCTCT	253865	86061	CTTGAAAAGTAATGGATACA	298452	130648	ACGGGTGGACGTCTCCCAAG
209279	41475	GGGACAGACAACATGCTCTC	253866	86062	CCTTGAAAAGTAATGGATAC	298453	130649	AACGGGTGGACGTCTCCCAA
209280	41476	AGGGACAGACAACATGCTCT	253867	86063	ACCTTGAAAAGTAATGGATA	298454	130650	AAACGGGTGGACGTCTCCCA
209281	41477	AAGGGACAGACAACATGCTC	253868	86064	TACCTTGAAAAGTAATGGAT	298455	130651	GAAACGGGTGGACGTCTCCC
209282	41478	AAAGGGACAGACAACATGCT	253869	86065	GTACCTTGAAAAGTAATGGA	298456	130652	GGAAACGGGTGGACGTCTCC
209283	41479	CAAAGGGACAGACAACATGC	253870	86066	TGTACCTTGAAAAGTAATGG	298457	130653	TGGAAACGGGTGGACGTCTC
209284	41480	GCAAAGGGACAGACAACATG	253871	86067	ATGTACCTTGAAAAGTAATG	298458	130654	TTGGAAACGGGTGGACGTCT
209285	41481	AGCAAAGGGACAGACAACAT	253872	86068	AATGTACCTTGAAAAGTAAT	298459	130655	CTTGGAAACGGGTGGACGTC
209286	41482	GAGCAAAGGGACAGACAACA	253873	86069	AAATGTACCTTGAAAAGTAA	298460	130656	GCTTGGAAACGGGTGGACGT
209287	41483	TGAGCAAAGGGACAGACAAC	253874	86070	TAAATGTACCTTGAAAAGTA	298461	130657	GGCTTGGAAACGGGTGGACG
209288	41484	CTGAGCAAAGGGACAGACAA	253875	86071	GTAAATGTACCTTGAAAAGT	298462	130658	AGGCTTGGAAACGGGTGGAC
209289	41485	GCTGAGCAAAGGGACAGACA	253876	86072	AGTAAATGTACCTTGAAAAG	298463	130659	CAGGCTTGGAAACGGGTGGA
209290	41486	TGCTGAGCAAAGGGACAGAC	253877	86073	TAGTAAATGTACCTTGAAAA	298464	130660	CCAGGCTTGGAAACGGGTGG
209291	41487	ATGCTGAGCAAAGGGACAGA	253878	86074	ATAGTAAATGTACCTTGAAA	298465	130661	CCCAGGCTTGGAAACGGGTG
209292	41488	CATGCTGAGCAAAGGGACAG	253879	86075	AATAGTAAATGTACCTTGAA	298466	130662	GCCCAGGCTTGGAAACGGGT
209293	41489	TCATGCTGAGCAAAGGGACA	253880	86076	AAATAGTAAATGTACCTTGA	298467	130663	GGCCCAGGCTTGGAAACGGG
209294	41490	TTCATGCTGAGCAAAGGGAC	253881	86077	TAAATAGTAAATGTACCTTG	298468	130664	TGGCCCAGGCTTGGAAACGG
209295	41491	CTTCATGCTGAGCAAAGGGA	253882	86078	GTAAATAGTAAATGTACCTT	298469	130665	GTGGCCCAGGCTTGGAAACG
209296	41492	GCTTCATGCTGAGCAAAGGG	253883	86079	CGTAAATAGTAAATGTACCT	298470	130666	AGTGGCCCAGGCTTGGAAAC
209297	41493	GGCTTCATGCTGAGCAAAGG	253884	86080	ACGTAAATAGTAAATGTACC	298471	130667	CAGTGGCCCAGGCTTGGAAA
209298	41494	TGGCTTCATGCTGAGCAAAG	253885	86081	AACGTAAATAGTAAATGTAC	298472	130668	CCAGTGGCCCAGGCTTGGAA
209299	41495	ATGGCTTCATGCTGAGCAAA	253886	86082	AAACGTAAATAGTAAATGTA	298473	130669	GCCAGTGGCCCAGGCTTGGA
209300	41496	CATGGCTTCATGCTGAGCAA	253887	86083	CAAACGTAAATAGTAAATGT	298474	130670	TGCCAGTGGCCCAGGCTTGG
209301	41497	GCATGGCTTCATGCTGAGCA	253888	86084	CCAAACGTAAATAGTAAATG	298475	130671	ATGCCAGTGGCCCAGGCTTG
209302	41498	CGCATGGCTTCATGCTGAGC	253889	86085	CCCAAACGTAAATAGTAAAT	298476	130672	GATGCCAGTGGCCCAGGCTT
209303	41499	ACGCATGGCTTCATGCTGAG	253890	86086	CCCCAAACGTAAATAGTAAA	298477	130673	AGATGCCAGTGGCCCAGGCT
209304	41500	CACGCATGGCTTCATGCTGA	253891	86087	ACCCCAAACGTAAATAGTAA	298478	130674	GAGATGCCAGTGGCCCAGGC
209305	41501	ACACGCATGGCTTCATGCTG	253892	86088	GACCCCAAACGTAAATAGTA	298479	130675	AGAGATGCCAGTGGCCCAGG
209306	41502	CACACGCATGGCTTCATGCT	253893	86089	GGACCCCAAACGTAAATAGT	298480	130676	CAGAGATGCCAGTGGCCCAG
209307	41503	CCACACGCATGGCTTCATGC	253894	86090	AGGACCCCAAACGTAAATAG	298481	130677	CCAGAGATGCCAGTGGCCCA
209308	41504	ACCACACGCATGGCTTCATG	253895	86091	AAGGACCCCAAACGTAAATA	298482	130678	TCCAGAGATGCCAGTGGCCC
209309	41505	TACCACACGCATGGCTTCAT	253896	86092	CAAGGACCCCAAACGTAAAT	298483	130679	CTCCAGAGATGCCAGTGGCC
209310	41506	CTACCACACGCATGGCTTCA	253897	86093	ACAAGGACCCCAAACGTAAA	298484	130680	ACTCCAGAGATGCCAGTGGC
209311	41507	TCTACCACACGCATGGCTTC	253898	86094	GACAAGGACCCCAAACGTAA	298485	130681	CACTCCAGAGATGCCAGTGG
209312	41508	ATCTACCACACGCATGGCTT	253899	86095	AGACAAGGACCCCAAACGTA	298486	130682	ACACTCCAGAGATGCCAGTG
209313	41509	GATCTACCACACGCATGGCT	253900	86096	GAGACAAGGACCCCAAACGT	298487	130683	CACACTCCAGAGATGCCAGT
209314	41510	CGATCTACCACACGCATGGC	253901	86097	AGAGACAAGGACCCCAAACG	298488	130684	ACACACTCCAGAGATGCCAG
209315	41511	CCGATCTACCACACGCATGG	253902	86098	AAGAGACAAGGACCCCAAAC	298489	130685	CACACACTCCAGAGATGCCA
209316	41512	GCCGATCTACCACACGCATG	253903	86099	AAAGAGACAAGGACCCCAAA	298490	130686	CCACACACTCCAGAGATGCC
209317	41513	TGCCGATCTACCACACGCAT	253904	86100	AAAAGAGACAAGGACCCCAA	298491	130687	CCCACACACTCCAGAGATGC
209318	41514	CTGCCGATCTACCACACGCA	253905	86101	AAAAAGAGACAAGGACCCCA	298492	130688	CCCCACACACTCCAGAGATG
209319	41515	TCTGCCGATCTACCACACGC	253906	86102	AAAAAAGAGACAAGGACCCC	298493	130689	CCCCCACACACTCCAGAGAT
209320	41516	CTCTGCCGATCTACCACACG	253907	86103	TAAAAAAGAGACAAGGACCC	298494	130690	ACCCCCACACACTCCAGAGA
209321	41517	ACTCTGCCGATCTACCACAC	253908	86104	TTAAAAAAGAGACAAGGACC	298495	130691	GACCCCCACACACTCCAGAG
209322	41518	AACTCTGCCGATCTACCACA	253909	86105	ATTAAAAAAGAGACAAGGAC	298496	130692	AGACCCCCACACACTCCAGA
209323	41519	GAACTCTGCCGATCTACCAC	253910	86106	TATTAAAAAAGAGACAAGGA	298497	130693	CAGACCCCCACACACTCCAG
209324	41520	GGAACTCTGCCGATCTACCA	253911	86107	CTATTAAAAAAGAGACAAGG	298498	130694	CCAGACCCCCACACACTCCA
209325	41521	TGGAACTCTGCCGATCTACC	253912	86108	ACTATTAAAAAAGAGACAAG	298499	130695	CCCAGACCCCCACACACTCC
209326	41522	ATGGAACTCTGCCGATCTAC	253913	86109	CACTATTAAAAAAGAGACAA	298500	130696	TCCCAGACCCCCACACACTC
209327	41523	TATGGAACTCTGCCGATCTA	253914	86110	ACACTATTAAAAAAGAGACA	298501	130697	CTCCCAGACCCCCACACACT
209328	41524	TTATGGAACTCTGCCGATCT	253915	86111	AACACTATTAAAAAAGAGAC	298502	130698	CCTCCCAGACCCCCACACAC
209329	41525	GTTATGGAACTCTGCCGATC	253916	86112	AAACACTATTAAAAAAGAGA	298503	130699	GCCTCCCAGACCCCCACACA
209330	41526	AGTTATGGAACTCTGCCGAT	253917	86113	GAAACACTATTAAAAAAGAG	298504	130700	TGCCTCCCAGACCCCCACAC
209331	41527	AAGTTATGGAACTCTGCCGA	253918	86114	AGAAACACTATTAAAAAAGA	298505	130701	CTGCCTCCCAGACCCCCACA
209332	41528	CAAGTTATGGAACTCTGCCG	253919	86115	AAGAAACACTATTAAAAAAG	298506	130702	CCTGCCTCCCAGACCCCCAC
209333	41529	ACAAGTTATGGAACTCTGCC	253920	86116	TAAGAAACACTATTAAAAAA	298507	130703	ACCTGCCTCCCAGACCCCCA
209334	41530	CACAAGTTATGGAACTCTGC	253921	86117	TTAAGAAACACTATTAAAAA	298508	130704	GACCTGCCTCCCAGACCCCC
209335	41531	ACACAAGTTATGGAACTCTG	253922	86118	TTTAAGAAACACTATTAAAA	298509	130705	GGACCTGCCTCCCAGACCCC
209336	41532	AACACAAGTTATGGAACTCT	253923	86119	CTTTAAGAAACACTATTAAA	298510	130706	GGGACCTGCCTCCCAGACCC
209337	41533	CAACACAAGTTATGGAACTC	253924	86120	ACTTTAAGAAACACTATTAA	298511	130707	CGGGACCTGCCTCCCAGACC
209338	41534	TCAACACAAGTTATGGAACT	253925	86121	GACTTTAAGAAACACTATTA	298512	130708	TCGGGACCTGCCTCCCAGAC
209339	41535	GTCAACACAAGTTATGGAAC	253926	86122	AGACTTTAAGAAACACTATT	298513	130709	CTCGGGACCTGCCTCCCAGA
209340	41536	GGTCAACACAAGTTATGGAA	253927	86123	AAGACTTTAAGAAACACTAT	298514	130710	GCTCGGGACCTGCCTCCCAG
209341	41537	CGGTCAACACAAGTTATGGA	253928	86124	CAAGACTTTAAGAAACACTA	298515	130711	GGCTCGGGACCTGCCTCCCA
209342	41538	TCGGTCAACACAAGTTATGG	253929	86125	ACAAGACTTTAAGAAACACT	298516	130712	GGGCTCGGGACCTGCCTCCC
209343	41539	CTCGGTCAACACAAGTTATG	253930	86126	TACAAGACTTTAAGAAACAC	298517	130713	GGGGCTCGGGACCTGCCTCC
209344	41540	CCTCGGTCAACACAAGTTAT	253931	86127	ATACAAGACTTTAAGAAACA	298518	130714	GGGGGCTCGGGACCTGCCTC
209345	41541	CCCTCGGTCAACACAAGTTA	253932	86128	AATACAAGACTTTAAGAAAC	298519	130715	AGGGGGCTCGGGACCTGCCT
209346	41542	CCCCTCGGTCAACACAAGTT	253933	86129	TAATACAAGACTTTAAGAAA	298520	130716	CAGGGGGCTCGGGACCTGCC

209347	41543	ACCCCTCGGTCAACACAAGT	253934	86130	ATAATACAAGACTTTAAGAA	298521	130717	ACAGGGGGCTCGGGACCTGC
209348	41544	GACCCCTCGGTCAACACAAG	253935	86131	TATAATACAAGACTTTAAGA	298522	130718	GACAGGGGGCTCGGGACCTG
209349	41545	TGACCCCTCGGTCAACACAA	253936	86132	ATATAATACAAGACTTTAAG	298523	130719	GGACAGGGGGCTCGGGACCT
209350	41546	GTGACCCCTCGGTCAACACA	253937	86133	GATATAATACAAGACTTTAA	298524	130720	AGGACAGGGGGCTCGGGACC
209351	41547	AGTGACCCCTCGGTCAACAC	253938	86134	TGATATAATACAAGACTTTA	298525	130721	AAGGACAGGGGGCTCGGGAC
209352	41548	AAGTGACCCCTCGGTCAACA	253939	86135	CTGATATAATACAAGACTTT	298526	130722	GAAGGACAGGGGGCTCGGGA
209353	41549	AAAGTGACCCCTCGGTCAAC	253940	86136	TCTGATATAATACAAGACTT	298527	130723	GGAAGGACAGGGGGCTCGGG
209354	41550	CAAAGTGACCCCTCGGTCAA	253941	86137	CTCTGATATAATACAAGACT	298528	130724	GGGAAGGACAGGGGGCTCGG
209355	41551	GCAAAGTGACCCCTCGGTCA	253942	86138	ACTCTGATATAATACAAGAC	298529	130725	TGGGAAGGACAGGGGGCTCG
209356	41552	AGCAAAGTGACCCCTCGGTC	253943	86139	TACTCTGATATAATACAAGA	298530	130726	GTGGGAAGGACAGGGGGCTC
209357	41553	GAGCAAAGTGACCCCTCGGT	253944	86140	GTACTCTGATATAATACAAG	298531	130727	CGTGGGAAGGACAGGGGGCT
209358	41554	AGAGCAAAGTGACCCCTCGG	253945	86141	TGTACTCTGATATAATACAA	298532	130728	CCGTGGGAAGGACAGGGGGC
209359	41555	CAGAGCAAAGTGACCCCTCG	253946	86142	CTGTACTCTGATATAATACA	298533	130729	GCCGTGGGAAGGACAGGGGG
209360	41556	TCAGAGCAAAGTGACCCCTC	253947	86143	ACTGTACTCTGATATAATAC	298534	130730	GGCCGTGGGAAGGACAGGGG
209361	41557	TTCAGAGCAAAGTGACCCCT	253948	86144	TACTGTACTCTGATATAATA	298535	130731	TGGCCGTGGGAAGGACAGGG
209362	41558	TTTCAGAGCAAAGTGACCCC	253949	86145	TTACTGTACTCTGATATAAT	298536	130732	GTGGCCGTGGGAAGGACAGG
209363	41559	ATTTCAGAGCAAAGTGACCC	253950	86146	GTTACTGTACTCTGATATAA	298537	130733	AGTGGCCGTGGGAAGGACAG
209364	41560	AATTTCAGAGCAAAGTGACC	253951	86147	TGTTACTGTACTCTGATATA	298538	130734	CAGTGGCCGTGGGAAGGACA
209365	41561	TAATTTCAGAGCAAAGTGAC	253952	86148	ATGTTACTGTACTCTGATAT	298539	130735	GCAGTGGCCGTGGGAAGGAC
209366	41562	GTAATTTCAGAGCAAAGTGA	253953	86149	GATGTTACTGTACTCTGATA	298540	130736	TGCAGTGGCCGTGGGAAGGA
209367	41563	GGTAATTTCAGAGCAAAGTG	253954	86150	GGATGTTACTGTACTCTGAT	298541	130737	CTGCAGTGGCCGTGGGAAGG
209368	41564	GGGTAATTTCAGAGCAAAGT	253955	86151	GGGATGTTACTGTACTCTGA	298542	130738	ACTGCAGTGGCCGTGGGAAG
209369	41565	GGGGTAATTTCAGAGCAAAG	253956	86152	TGGGATGTTACTGTACTCTG	298543	130739	GACTGCAGTGGCCGTGGGAA
209370	41566	AGGGGTAATTTCAGAGCAAA	253957	86153	CTGGGATGTTACTGTACTCT	298544	130740	TGACTGCAGTGGCCGTGGGA
209371	41567	CAGGGGTAATTTCAGAGCAA	253958	86154	ACTGGGATGTTACTGTACTC	298545	130741	GTGACTGCAGTGGCCGTGGG
209372	41568	ACAGGGGTAATTTCAGAGCA	253959	86155	GACTGGGATGTTACTGTACT	298546	130742	GGTGACTGCAGTGGCCGTGG
209373	41569	CACAGGGGTAATTTCAGAGC	253960	86156	TGACTGGGATGTTACTGTAC	298547	130743	GGGTGACTGCAGTGGCCGTG
209374	41570	ACACAGGGGTAATTTCAGAG	253961	86157	TTGACTGGGATGTTACTGTA	298548	130744	GGGGTGACTGCAGTGGCCGT
209375	41571	GACACAGGGGTAATTTCAGA	253962	86158	CTTGACTGGGATGTTACTGT	298549	130745	CGGGGTGACTGCAGTGGCCG
209376	41572	GGACACAGGGGTAATTTCAG	253963	86159	TCTTGACTGGGATGTTACTG	298550	130746	ACGGGGTGACTGCAGTGGCC
209377	41573	AGGACACAGGGGTAATTTCA	253964	86160	CTCTTGACTGGGATGTTACT	298551	130747	GACGGGGTGACTGCAGTGGC
209378	41574	AAGGACACAGGGGTAATTTC	253965	86161	GCTCTTGACTGGGATGTTAC	298552	130748	AGACGGGGTGACTGCAGTGG
209379	41575	GAAGGACACAGGGGTAATTT	253966	86162	TGCTCTTGACTGGGATGTTA	298553	130749	CAGACGGGGTGACTGCAGTG
209380	41576	TGAAGGACACAGGGGTAATT	253967	86163	GTGCTCTTGACTGGGATGTT	298554	130750	GCAGACGGGGTGACTGCAGT
209381	41577	CTGAAGGACACAGGGGTAAT	253968	86164	AGTGCTCTTGACTGGGATGT	298555	130751	CGCAGACGGGGTGACTGCAG
209382	41578	ACTGAAGGACACAGGGGTAA	253969	86165	GAGTGCTCTTGACTGGGATG	298556	130752	GCGCAGACGGGGTGACTGCA
209383	41579	TACTGAAGGACACAGGGGTA	253970	86166	AGAGTGCTCTTGACTGGGAT	298557	130753	GGCGCAGACGGGGTGACTGC
209384	41580	ATACTGAAGGACACAGGGGT	253971	86167	TAGAGTGCTCTTGACTGGGA	298558	130754	CGGCGCAGACGGGGTGACTG
209385	41581	AATACTGAAGGACACAGGGG	253972	86168	CTAGAGTGCTCTTGACTGGG	298559	130755	GCGGCGCAGACGGGGTGACT
209386	41582	AAATACTGAAGGACACAGGG	253973	86169	ACTAGAGTGCTCTTGACTGG	298560	130756	AGCGGCGCAGACGGGGTGAC
209387	41583	CAAATACTGAAGGACACAGG	253974	86170	TACTAGAGTGCTCTTGACTG	298561	130757	CAGCGGCGCAGACGGGGTGA
209388	41584	GCAAATACTGAAGGACACAG	253975	86171	TTACTAGAGTGCTCTTGACT	298562	130758	ACAGCGGCGCAGACGGGGTG
209389	41585	TGCAAATACTGAAGGACACA	253976	86172	CTTACTAGAGTGCTCTTGAC	298563	130759	CACAGCGGCGCAGACGGGGT
209390	41586	GTGCAAATACTGAAGGACAC	253977	86173	GCTTACTAGAGTGCTCTTGA	298564	130760	GCACAGCGGCGCAGACGGGG
209391	41587	TGTGCAAATACTGAAGGACA	253978	86174	AGCTTACTAGAGTGCTCTTG	298565	130761	AGCACAGCGGCGCAGACGGG
209392	41588	CTGTGCAAATACTGAAGGAC	253979	86175	GAGCTTACTAGAGTGCTCTT	298566	130762	CAGCACAGCGGCGCAGACGG
209393	41589	TCTGTGCAAATACTGAAGGA	253980	86176	AGAGCTTACTAGAGTGCTCT	298567	130763	ACAGCACAGCGGCGCAGACG
209394	41590	ATCTGTGCAAATACTGAAGG	253981	86177	TAGAGCTTACTAGAGTGCTC	298568	130764	AACAGCACAGCGGCGCAGAC
209395	41591	TATCTGTGCAAATACTGAAG	253982	86178	CTAGAGCTTACTAGAGTGCT	298569	130765	CAACAGCACAGCGGCGCAGA
209396	41592	CTATCTGTGCAAATACTGAA	253983	86179	CCTAGAGCTTACTAGAGTGC	298570	130766	ACAACAGCACAGCGGCGCAG
209397	41593	GCTATCTGTGCAAATACTGA	253984	86180	TCCTAGAGCTTACTAGAGTG	298571	130767	GACAACAGCACAGCGGCGCA
209398	41594	AGCTATCTGTGCAAATACTG	253985	86181	CTCCTAGAGCTTACTAGAGT	298572	130768	AGACAACAGCACAGCGGCGC
209399	41595	AAGCTATCTGTGCAAATACT	253986	86182	CCTCCTAGAGCTTACTAGAG	298573	130769	CAGACAACAGCACAGCGGCG
209400	41596	GAAGCTATCTGTGCAAATAC	253987	86183	TCCTCCTAGAGCTTACTAGA	298574	130770	GCAGACAACAGCACAGCGGC
209401	41597	GGAAGCTATCTGTGCAAATA	253988	86184	TTCCTCCTAGAGCTTACTAG	298575	130771	GGCAGACAACAGCACAGCGG
209402	41598	AGGAAGCTATCTGTGCAAAT	253989	86185	TTTCCTCCTAGAGCTTACTA	298576	130772	CGGCAGACAACAGCACAGCG
209403	41599	CAGGAAGCTATCTGTGCAAA	253990	86186	CTTTCCTCCTAGAGCTTACT	298577	130773	ACGGCAGACAACAGCACAGC
209404	41600	CCAGGAAGCTATCTGTGCAA	253991	86187	GCTTTCCTCCTAGAGCTTAC	298578	130774	CACGGCAGACAACAGCACAG
209405	41601	GCCAGGAAGCTATCTGTGCA	253992	86188	CGCTTTCCTCCTAGAGCTTA	298579	130775	TCACGGCAGACAACAGCACA
209406	41602	GGCCAGGAAGCTATCTGTGC	253993	86189	TCGCTTTCCTCCTAGAGCTT	298580	130776	CTCACGGCAGACAACAGCAC
209407	41603	TGGCCAGGAAGCTATCTGTG	253994	86190	GTCGCTTTCCTCCTAGAGCT	298581	130777	TCTCACGGCAGACAACAGCA
209408	41604	CTGGCCAGGAAGCTATCTGT	253995	86191	AGTCGCTTTCCTCCTAGAGC	298582	130778	CTCTCACGGCAGACAACAGC
209409	41605	TCTGGCCAGGAAGCTATCTG	253996	86192	AAGTCGCTTTCCTCCTAGAG	298583	130779	GCTCTCACGGCAGACAACAG
209410	41606	GTCTGGCCAGGAAGCTATCT	253997	86193	GAAGTCGCTTTCCTCCTAGA	298584	130780	GGCTCTCACGGCAGACAACA
209411	41607	GGTCTGGCCAGGAAGCTATC	253998	86194	GGAAGTCGCTTTCCTCCTAG	298585	130781	GGGCTCTCACGGCAGACAAC
209412	41608	CGGTCTGGCCAGGAAGCTAT	253999	86195	CGGAAGTCGCTTTCCTCCTA	298586	130782	TGGGCTCTCACGGCAGACAA
209413	41609	TCGGTCTGGCCAGGAAGCTA	254000	86196	CCGGAAGTCGCTTTCCTCCT	298587	130783	TTGGGCTCTCACGGCAGACA
209414	41610	TTCGGTCTGGCCAGGAAGCT	254001	86197	TCCGGAAGTCGCTTTCCTCC	298588	130784	ATTGGGCTCTCACGGCAGAC
209415	41611	ATTCGGTCTGGCCAGGAAGC	254002	86198	TTCCGGAAGTCGCTTTCCTC	298589	130785	GATTGGGCTCTCACGGCAGA
209416	41612	TATTCGGTCTGGCCAGGAAG	254003	86199	CTTCCGGAAGTCGCTTTCCT	298590	130786	TGATTGGGCTCTCACGGCAG
209417	41613	ATATTCGGTCTGGCCAGGAA	254004	86200	CCTTCCGGAAGTCGCTTTCC	298591	130787	GTGATTGGGCTCTCACGGCA
209418	41614	TATATTCGGTCTGGCCAGGA	254005	86201	GCCTTCCGGAAGTCGCTTTC	298592	130788	AGTGATTGGGCTCTCACGGC

209419	41615	ATATATTCGGTCTGGCCAGG	254006	86202	TGCCTTCCGGAAGTCGCTTT	298593	130789	CAGTGATTGGGCTCTCACGG
209420	41616	GATATATTCGGTCTGGCCAG	254007	86203	CTGCCTTCCGGAAGTCGCTT	298594	130790	GCAGTGATTGGGCTCTCACG
209421	41617	GGATATATTCGGTCTGGCCA	254008	86204	ACTGCCTTCCGGAAGTCGCT	298595	130791	GGCAGTGATTGGGCTCTCAC
209422	41618	TGGATATATTCGGTCTGGCC	254009	86205	CACTGCCTTCCGGAAGTCGC	298596	130792	AGGCAGTGATTGGGCTCTCA
209423	41619	TTGGATATATTCGGTCTGGC	254010	86206	CCACTGCCTTCCGGAAGTCG	298597	130793	TAGGCAGTGATTGGGCTCTC
209424	41620	CTTGGATATATTCGGTCTGG	254011	86207	TCCACTGCCTTCCGGAAGTC	298598	130794	ATAGGCAGTGATTGGGCTCT
209425	41621	CCTTGGATATATTCGGTCTG	254012	86208	CTCCACTGCCTTCCGGAAGT	298599	130795	TATAGGCAGTGATTGGGCTC
209426	41622	CCCTTGGATATATTCGGTCT	254013	86209	TCTCCACTGCCTTCCGGAAG	298600	130796	GTATAGGCAGTGATTGGGCT
209427	41623	GCCCTTGGATATATTCGGTC	254014	86210	GTCTCCACTGCCTTCCGGAA	298601	130797	GGTATAGGCAGTGATTGGGC
209428	41624	TGCCCTTGGATATATTCGGT	254015	86211	GGTCTCCACTGCCTTCCGGA	298602	130798	GGGTATAGGCAGTGATTGGG
209429	41625	ATGCCCTTGGATATATTCGG	254016	86212	AGGTCTCCACTGCCTTCCGG	298603	130799	GGGGTATAGGCAGTGATTGG
209430	41626	CATGCCCTTGGATATATTCG	254017	86213	CAGGTCTCCACTGCCTTCCG	298604	130800	AGGGGTATAGGCAGTGATTG
209431	41627	CCATGCCCTTGGATATATTC	254018	86214	ACAGGTCTCCACTGCCTTCC	298605	130801	GAGGGGTATAGGCAGTGATT
209432	41628	GCCATGCCCTTGGATATATT	254019	86215	GACAGGTCTCCACTGCCTTC	298606	130802	TGAGGGGTATAGGCAGTGAT
209433	41629	GGCCATGCCCTTGGATATAT	254020	86216	GGACAGGTCTCCACTGCCTT	298607	130803	ATGAGGGGTATAGGCAGTGA
209434	41630	GGGCCATGCCCTTGGATATA	254021	86217	AGGACAGGTCTCCACTGCCT	298608	130804	GATGAGGGGTATAGGCAGTG
209435	41631	TGGGCCATGCCCTTGGATAT	254022	86218	CAGGACAGGTCTCCACTGCC	298609	130805	TGATGAGGGGTATAGGCAGT
209436	41632	GTGGGCCATGCCCTTGGATA	254023	86219	ACAGGACAGGTCTCCACTGC	298610	130806	GTGATGAGGGGTATAGGCAG
209437	41633	GGTGGGCCATGCCCTTGGAT	254024	86220	AACAGGACAGGTCTCCACTG	298611	130807	TGTGATGAGGGGTATAGGCA
209438	41634	AGGTGGGCCATGCCCTTGGA	254025	86221	CAACAGGACAGGTCTCCACT	298612	130808	GTGTGATGAGGGGTATAGGC
209439	41635	GAGGTGGGCCATGCCCTTGG	254026	86222	CCAACAGGACAGGTCTCCAC	298613	130809	CGTGTGATGAGGGGTATAGG
209440	41636	AGAGGTGGGCCATGCCCTTG	254027	86223	CCCAACAGGACAGGTCTCCA	298614	130810	ACGTGTGATGAGGGGTATAG
209441	41637	CAGAGGTGGGCCATGCCCTT	254028	86224	CCCCAACAGGACAGGTCTCC	298615	130811	GACGTGTGATGAGGGGTATA
209442	41638	GCAGAGGTGGGCCATGCCCT	254029	86225	GCCCCAACAGGACAGGTCTC	298616	130812	TGACGTGTGATGAGGGGTAT
209443	41639	AGCAGAGGTGGGCCATGCCC	254030	86226	TGCCCCAACAGGACAGGTCT	298617	130813	GTGACGTGTGATGAGGGGTA
209444	41640	GAGCAGAGGTGGGCCATGCC	254031	86227	CTGCCCCAACAGGACAGGTC	298618	130814	TGTGACGTGTGATGAGGGGT
209445	41641	GGAGCAGAGGTGGGCCATGC	254032	86228	GCTGCCCCAACAGGACAGGT	298619	130815	TTGTGACGTGTGATGAGGGG
209446	41642	AGGAGCAGAGGTGGGCCATG	254033	86229	TGCTGCCCCAACAGGACAGG	298620	130816	ATTGTGACGTGTGATGAGGG
209447	41643	CAGGAGCAGAGGTGGGCCAT	254034	86230	ATGCTGCCCCAACAGGACAG	298621	130817	CATTGTGACGTGTGATGAGG
209448	41644	ACAGGAGCAGAGGTGGGCCA	254035	86231	TATGCTGCCCCAACAGGACA	298622	130818	ACATTGTGACGTGTGATGAG
209449	41645	AACAGGAGCAGAGGTGGGCC	254036	86232	CTATGCTGCCCCAACAGGAC	298623	130819	GACATTGTGACGTGTGATGA
209450	41646	AAACAGGAGCAGAGGTGGGC	254037	86233	CCTATGCTGCCCCAACAGGA	298624	130820	GGACATTGTGACGTGTGATG
209451	41647	GAAACAGGAGCAGAGGTGGG	254038	86234	CCCTATGCTGCCCCAACAGG	298625	130821	GGGACATTGTGACGTGTGAT
209452	41648	GGAAACAGGAGCAGAGGTGG	254039	86235	CCCCTATGCTGCCCCAACAG	298626	130822	CGGGACATTGTGACGTGTGA
209453	41649	TGGAAACAGGAGCAGAGGTG	254040	86236	GCCCCTATGCTGCCCCAACA	298627	130823	TCGGGACATTGTGACGTGTG
209454	41650	CTGGAAACAGGAGCAGAGGT	254041	86237	TGCCCCTATGCTGCCCCAAC	298628	130824	TTCGGGACATTGTGACGTGT
209455	41651	CCTGGAAACAGGAGCAGAGG	254042	86238	CTGCCCCTATGCTGCCCCAA	298629	130825	ATTCGGGACATTGTGACGTG
209456	41652	ACCTGGAAACAGGAGCAGAG	254043	86239	GCTGCCCCTATGCTGCCCCA	298630	130826	AATTCGGGACATTGTGACGT
209457	41653	GACCTGGAAACAGGAGCAGA	254044	86240	GGCTGCCCCTATGCTGCCCC	298631	130827	GAATTCGGGACATTGTGACG
209458	41654	GGACCTGGAAACAGGAGCAG	254045	86241	GGGCTGCCCCTATGCTGCCC	298632	130828	GGAATTCGGGACATTGTGAC
209459	41655	GGGACCTGGAAACAGGAGCA	254046	86242	GGGGCTGCCCCTATGCTGCC	298633	130829	GGGAATTCGGGACATTGTGA
209460	41656	AGGGACCTGGAAACAGGAGC	254047	86243	AGGGGCTGCCCCTATGCTGC	298634	130830	TGGGAATTCGGGACATTGTG
209461	41657	CAGGGACCTGGAAACAGGAG	254048	86244	CAGGGGCTGCCCCTATGCTG	298635	130831	CTGGGAATTCGGGACATTGT
209462	41658	CCAGGGACCTGGAAACAGGA	254049	86245	GCAGGGGCTGCCCCTATGCT	298636	130832	GCTGGGAATTCGGGACATTG
209463	41659	ACCAGGGACCTGGAAACAGG	254050	86246	GGCAGGGGCTGCCCCTATGC	298637	130833	GGCTGGGAATTCGGGACATT
209464	41660	CACCAGGGACCTGGAAACAG	254051	86247	AGGCAGGGGCTGCCCCTATG	298638	130834	AGGCTGGGAATTCGGGACAT
209465	41661	CCACCAGGGACCTGGAAACA	254052	86248	GAGGCAGGGGCTGCCCCTAT	298639	130835	GAGGCTGGGAATTCGGGACA
209466	41662	CCCACCAGGGACCTGGAAAC	254053	86249	AGAGGCAGGGGCTGCCCCTA	298640	130836	TGAGGCTGGGAATTCGGGAC
209467	41663	CCCCACCAGGGACCTGGAAA	254054	86250	CAGAGGCAGGGGCTGCCCCT	298641	130837	GTGAGGCTGGGAATTCGGGA
209468	41664	CCCCCACCAGGGACCTGGAA	254055	86251	CCAGAGGCAGGGGCTGCCCC	298642	130838	GGTGAGGCTGGGAATTCGGG
209469	41665	ACCCCCACCAGGGACCTGGA	254056	86252	ACCAGAGGCAGGGGCTGCCC	298643	130839	TGGTGAGGCTGGGAATTCGG
209470	41666	AACCCCCACCAGGGACCTGG	254057	86253	GACCAGAGGCAGGGGCTGCC	298644	130840	GTGGTGAGGCTGGGAATTCG
209471	41667	TAACCCCCACCAGGGACCTG	254058	86254	TGACCAGAGGCAGGGGCTGC	298645	130841	GGTGGTGAGGCTGGGAATTC
209472	41668	CTAACCCCCACCAGGGACCT	254059	86255	CTGACCAGAGGCAGGGGCTG	298646	130842	GGGTGGTGAGGCTGGGAATT
209473	41669	ACTAACCCCCACCAGGGACC	254060	86256	ACTGACCAGAGGCAGGGGCT	298647	130843	GGGGTGGTGAGGCTGGGAAT
209474	41670	AACTAACCCCCACCAGGGAC	254061	86257	AACTGACCAGAGGCAGGGGC	298648	130844	AGGGGTGGTGAGGCTGGGAA
209475	41671	GAACTAACCCCCACCAGGGA	254062	86258	GAACTGACCAGAGGCAGGGG	298649	130845	AAGGGGTGGTGAGGCTGGGA
209476	41672	TGAACTAACCCCCACCAGGG	254063	86259	AGAACTGACCAGAGGCAGGG	298650	130846	GAAGGGGTGGTGAGGCTGGG
209477	41673	ATGAACTAACCCCCACCAGG	254064	86260	CAGAACTGACCAGAGGCAGG	298651	130847	AGAAGGGGTGGTGAGGCTGG
209478	41674	CATGAACTAACCCCCACCAG	254065	86261	CCAGAACTGACCAGAGGCAG	298652	130848	GAGAAGGGGTGGTGAGGCTG
209479	41675	GCATGAACTAACCCCCACCA	254066	86262	GCCAGAACTGACCAGAGGCA	298653	130849	TGAGAAGGGGTGGTGAGGCT
209480	41676	GGCATGAACTAACCCCCACC	254067	86263	CGCCAGAACTGACCAGAGGC	298654	130850	CTGAGAAGGGGTGGTGAGGC
209481	41677	AGGCATGAACTAACCCCCAC	254068	86264	GCGCCAGAACTGACCAGAGG	298655	130851	ACTGAGAAGGGGTGGTGAGG
209482	41678	AAGGCATGAACTAACCCCCA	254069	86265	AGCGCCAGAACTGACCAGAG	298656	130852	TACTGAGAAGGGGTGGTGAG
209483	41679	GAAGGCATGAACTAACCCCC	254070	86266	GAGCGCCAGAACTGACCAGA	298657	130853	TTACTGAGAAGGGGTGGTGA
209484	41680	GGAAGGCATGAACTAACCCC	254071	86267	TGAGCGCCAGAACTGACCAG	298658	130854	ATTACTGAGAAGGGGTGGTG
209485	41681	AGGAAGGCATGAACTAACCC	254072	86268	CTGAGCGCCAGAACTGACCA	298659	130855	CATTACTGAGAAGGGGTGGT
209486	41682	GAGGAAGGCATGAACTAACC	254073	86269	CCTGAGCGCCAGAACTGACC	298660	130856	TCATTACTGAGAAGGGGTGG
209487	41683	TGAGGAAGGCATGAACTAAC	254074	86270	GCCTGAGCGCCAGAACTGAC	298661	130857	GTCATTACTGAGAAGGGGTG
209488	41684	ATGAGGAAGGCATGAACTAA	254075	86271	AGCCTGAGCGCCAGAACTGA	298662	130858	GGTCATTACTGAGAAGGGGT
209489	41685	TATGAGGAAGGCATGAACTA	254076	86272	GAGCCTGAGCGCCAGAACTG	298663	130859	GGGTCATTACTGAGAAGGGG
209490	41686	TTATGAGGAAGGCATGAACT	254077	86273	TGAGCCTGAGCGCCAGAACT	298664	130860	AGGGTCATTACTGAGAAGGG

209491	41687	ATTATGAGGAAGGCATGAAC	254078	86274	CTGAGCCTGAGCGCCAGAAC	298665	130861	CAGGGTCATTACTGAGAAGG
209492	41688	GATTATGAGGAAGGCATGAA	254079	86275	CCTGAGCCTGAGCGCCAGAA	298666	130862	CCAGGGTCATTACTGAGAAG
209493	41689	AGATTATGAGGAAGGCATGA	254080	86276	CCCTGAGCCTGAGCGCCAGA	298667	130863	ACCAGGGTCATTACTGAGAA
209494	41690	CAGATTATGAGGAAGGCATG	254081	86277	ACCCTGAGCCTGAGCGCCAG	298668	130864	AACCAGGGTCATTACTGAGA
209495	41691	GCAGATTATGAGGAAGGCAT	254082	86278	AACCCTGAGCCTGAGCGCCA	298669	130865	CAACCAGGGTCATTACTGAG
209496	41692	GGCAGATTATGAGGAAGGCA	254083	86279	CAACCCTGAGCCTGAGCGCC	298670	130866	CCAACCAGGGTCATTACTGA
209497	41693	GGGCAGATTATGAGGAAGGC	254084	86280	GCAACCCTGAGCCTGAGCGC	298671	130867	ACCAACCAGGGTCATTACTG
209498	41694	TGGGCAGATTATGAGGAAGG	254085	86281	GGCAACCCTGAGCCTGAGCG	298672	130868	AACCAACCAGGGTCATTACT
209499	41695	GTGGGCAGATTATGAGGAAG	254086	86282	AGGCAACCCTGAGCCTGAGC	298673	130869	CAACCAACCAGGGTCATTAC
209500	41696	AGTGGGCAGATTATGAGGAA	254087	86283	GAGGCAACCCTGAGCCTGAG	298674	130870	GCAACCAACCAGGGTCATTA
209501	41697	CAGTGGGCAGATTATGAGGA	254088	86284	AGAGGCAACCCTGAGCCTGA	298675	130871	TGCAACCAACCAGGGTCATT
209502	41698	CCAGTGGGCAGATTATGAGG	254089	86285	CAGAGGCAACCCTGAGCCTG	298676	130872	CTGCAACCAACCAGGGTCAT
209503	41699	GCCAGTGGGCAGATTATGAG	254090	86286	CCAGAGGCAACCCTGAGCCT	298677	130873	CCTGCAACCAACCAGGGTCA
209504	41700	GGCCAGTGGGCAGATTATGA	254091	86287	CCCAGAGGCAACCCTGAGCC	298678	130874	TCCTGCAACCAACCAGGGTC
209505	41701	AGGCCAGTGGGCAGATTATG	254092	86288	GCCCAGAGGCAACCCTGAGC	298679	130875	CTCCTGCAACCAACCAGGGT
209506	41702	CAGGCCAGTGGGCAGATTAT	254093	86289	AGCCCAGAGGCAACCCTGAG	298680	130876	CCTCCTGCAACCAACCAGGG
209507	41703	CCAGGCCAGTGGGCAGATTA	254094	86290	CAGCCCAGAGGCAACCCTGA	298681	130877	ACCTCCTGCAACCAACCAGG
209508	41704	ACCAGGCCAGTGGGCAGATT	254095	86291	ACAGCCCAGAGGCAACCCTG	298682	130878	TACCTCCTGCAACCAACCAG
209509	41705	GACCAGGCCAGTGGGCAGAT	254096	86292	AACAGCCCAGAGGCAACCCT	298683	130879	GTACCTCCTGCAACCAACCA
209510	41706	GGACCAGGCCAGTGGGCAGA	254097	86293	GAACAGCCCAGAGGCAACCC	298684	130880	GGTACCTCCTGCAACCAACC
209511	41707	AGGACCAGGCCAGTGGGCAG	254098	86294	AGAACAGCCCAGAGGCAACC	298685	130881	AGGTACCTCCTGCAACCAAC
209512	41708	GAGGACCAGGCCAGTGGGCA	254099	86295	AAGAACAGCCCAGAGGCAAC	298686	130882	TAGGTACCTCCTGCAACCAA
209513	41709	TGAGGACCAGGCCAGTGGGC	254100	86296	GAAGAACAGCCCAGAGGCAA	298687	130883	GTAGGTACCTCCTGCAACCA
209514	41710	TTGAGGACCAGGCCAGTGGG	254101	86297	GGAAGAACAGCCCAGAGGCA	298688	130884	AGTAGGTACCTCCTGCAACC
209515	41711	CTTGAGGACCAGGCCAGTGG	254102	86298	GGGAAGAACAGCCCAGAGGC	298689	130885	GAGTAGGTACCTCCTGCAAC
209516	41712	CCTTGAGGACCAGGCCAGTG	254103	86299	TGGGAAGAACAGCCCAGAGG	298690	130886	GGAGTAGGTACCTCCTGCAA
209517	41713	ACCTTGAGGACCAGGCCAGT	254104	86300	CTGGGAAGAACAGCCCAGAG	298691	130887	TGGAGTAGGTACCTCCTGCA
209518	41714	GACCTTGAGGACCAGGCCAG	254105	86301	TCTGGGAAGAACAGCCCAGA	298692	130888	ATGGAGTAGGTACCTCCTGC
209519	41715	AGACCTTGAGGACCAGGCCA	254106	86302	CTCTGGGAAGAACAGCCCAG	298693	130889	TATGGAGTAGGTACCTCCTG
209520	41716	AAGACCTTGAGGACCAGGCC	254107	86303	TCTCTGGGAAGAACAGCCCA	298694	130890	GTATGGAGTAGGTACCTCCT
209521	41717	GAAGACCTTGAGGACCAGGC	254108	86304	GTCTCTGGGAAGAACAGCCC	298695	130891	AGTATGGAGTAGGTACCTCC
209522	41718	GGAAGACCTTGAGGACCAGG	254109	86305	AGTCTCTGGGAAGAACAGCC	298696	130892	CAGTATGGAGTAGGTACCTC
209523	41719	GGGAAGACCTTGAGGACCAG	254110	86306	CAGTCTCTGGGAAGAACAGC	298697	130893	TCAGTATGGAGTAGGTACCT
209524	41720	TGGGAAGACCTTGAGGACCA	254111	86307	TCAGTCTCTGGGAAGAACAG	298698	130894	CTCAGTATGGAGTAGGTACC
209525	41721	TTGGGAAGACCTTGAGGACC	254112	86308	GTCAGTCTCTGGGAAGAACA	298699	130895	CCTCAGTATGGAGTAGGTAC
209526	41722	GTTGGGAAGACCTTGAGGAC	254113	86309	TGTCAGTCTCTGGGAAGAAC	298700	130896	CCCTCAGTATGGAGTAGGTA
209527	41723	AGTTGGGAAGACCTTGAGGA	254114	86310	TTGTCAGTCTCTGGGAAGAA	298701	130897	ACCCTCAGTATGGAGTAGGT
209528	41724	CAGTTGGGAAGACCTTGAGG	254115	86311	TTTGTCAGTCTCTGGGAAGA	298702	130898	CACCCTCAGTATGGAGTAGG
209529	41725	GCAGTTGGGAAGACCTTGAG	254116	86312	CTTTGTCAGTCTCTGGGAAG	298703	130899	TCACCCTCAGTATGGAGTAG
209530	41726	AGCAGTTGGGAAGACCTTGA	254117	86313	CCTTTGTCAGTCTCTGGGAA	298704	130900	TTCACCCTCAGTATGGAGTA
209531	41727	GAGCAGTTGGGAAGACCTTG	254118	86314	CCCTTTGTCAGTCTCTGGGA	298705	130901	TTTCACCCTCAGTATGGAGT
209532	41728	TGAGCAGTTGGGAAGACCTT	254119	86315	GCCCTTTGTCAGTCTCTGGG	298706	130902	ATTTCACCCTCAGTATGGAG
209533	41729	CTGAGCAGTTGGGAAGACCT	254120	86316	AGCCCTTTGTCAGTCTCTGG	298707	130903	AATTTCACCCTCAGTATGGA
209534	41730	GCTGAGCAGTTGGGAAGACC	254121	86317	GAGCCCTTTGTCAGTCTCTG	298708	130904	TAATTTCACCCTCAGTATGG
209535	41731	GGCTGAGCAGTTGGGAAGAC	254122	86318	GGAGCCCTTTGTCAGTCTCT	298709	130905	TTAATTTCACCCTCAGTATG
209536	41732	TGGCTGAGCAGTTGGGAAGA	254123	86319	GGGAGCCCTTTGTCAGTCTC	298710	130906	CTTAATTTCACCCTCAGTAT
209537	41733	CTGGCTGAGCAGTTGGGAAG	254124	86320	TGGGAGCCCTTTGTCAGTCT	298711	130907	CCTTAATTTCACCCTCAGTA
209538	41734	TCTGGCTGAGCAGTTGGGAA	254125	86321	ATGGGAGCCCTTTGTCAGTC	298712	130908	CCCTTAATTTCACCCTCAGT
209539	41735	CTCTGGCTGAGCAGTTGGGA	254126	86322	TATGGGAGCCCTTTGTCAGT	298713	130909	TCCCTTAATTTCACCCTCAG
209540	41736	ACTCTGGCTGAGCAGTTGGG	254127	86323	TTATGGGAGCCCTTTGTCAG	298714	130910	TTCCCTTAATTTCACCCTCA
209541	41737	AACTCTGGCTGAGCAGTTGG	254128	86324	CTTATGGGAGCCCTTTGTCA	298715	130911	CTTCCCTTAATTTCACCCTC
209542	41738	CAACTCTGGCTGAGCAGTTG	254129	86325	CCTTATGGGAGCCCTTTGTC	298716	130912	CCTTCCCTTAATTTCACCCT
209543	41739	TCAACTCTGGCTGAGCAGTT	254130	86326	GCCTTATGGGAGCCCTTTGT	298717	130913	GCCTTCCCTTAATTTCACCC
209544	41740	CTCAACTCTGGCTGAGCAGT	254131	86327	TGCCTTATGGGAGCCCTTTG	298718	130914	TGCCTTCCCTTAATTTCACC
209545	41741	TCTCAACTCTGGCTGAGCAG	254132	86328	GTGCCTTATGGGAGCCCTTT	298719	130915	TTGCCTTCCCTTAATTTCAC
209546	41742	TTCTCAACTCTGGCTGAGCA	254133	86329	GGTGCCTTATGGGAGCCCTT	298720	130916	TTTGCCTTCCCTTAATTTCA
209547	41743	TTTCTCAACTCTGGCTGAGC	254134	86330	AGGTGCCTTATGGGAGCCCT	298721	130917	CTTTGCCTTCCCTTAATTTC
209548	41744	TTTTCTCAACTCTGGCTGAG	254135	86331	CAGGTGCCTTATGGGAGCCC	298722	130918	ACTTTGCCTTCCCTTAATTT
209549	41745	ATTTTCTCAACTCTGGCTGA	254136	86332	GCAGGTGCCTTATGGGAGCC	298723	130919	GACTTTGCCTTCCCTTAATT
209550	41746	CATTTTCTCAACTCTGGCTG	254137	86333	TGCAGGTGCCTTATGGGAGC	298724	130920	GGACTTTGCCTTCCCTTAAT
209551	41747	CCATTTTCTCAACTCTGGCT	254138	86334	CTGCAGGTGCCTTATGGGAG	298725	130921	TGGACTTTGCCTTCCCTTAA
209552	41748	CCCATTTTCTCAACTCTGGC	254139	86335	TCTGCAGGTGCCTTATGGGA	298726	130922	CTGGACTTTGCCTTCCCTTA
209553	41749	ACCCATTTTCTCAACTCTGG	254140	86336	CTCTGCAGGTGCCTTATGGG	298727	130923	CCTGGACTTTGCCTTCCCTT
209554	41750	GACCCATTTTCTCAACTCTG	254141	86337	GCTCTGCAGGTGCCTTATGG	298728	130924	GCCTGGACTTTGCCTTCCCT
209555	41751	CGACCCATTTTCTCAACTCT	254142	86338	GGCTCTGCAGGTGCCTTATG	298729	130925	TGCCTGGACTTTGCCTTCCC
209556	41752	GCGACCCATTTTCTCAACTC	254143	86339	AGGCTCTGCAGGTGCCTTAT	298730	130926	GTGCCTGGACTTTGCCTTCC
209557	41753	AGCGACCCATTTTCTCAACT	254144	86340	CAGGCTCTGCAGGTGCCTTA	298731	130927	TGTGCCTGGACTTTGCCTTC
209558	41754	GAGCGACCCATTTTCTCAAC	254145	86341	ACAGGCTCTGCAGGTGCCTT	298732	130928	TTGTGCCTGGACTTTGCCTT
209559	41755	GGAGCGACCCATTTTCTCAA	254146	86342	CACAGGCTCTGCAGGTGCCT	298733	130929	CTTGTGCCTGGACTTTGCCT
209560	41756	TGGAGCGACCCATTTTCTCA	254147	86343	TCACAGGCTCTGCAGGTGCC	298734	130930	TCTTGTGCCTGGACTTTGCC
209561	41757	ATGGAGCGACCCATTTTCTC	254148	86344	CTCACAGGCTCTGCAGGTGC	298735	130931	CTCTTGTGCCTGGACTTTGC
209562	41758	GATGGAGCGACCCATTTTCT	254149	86345	TCTCACAGGCTCTGCAGGTG	298736	130932	ACTCTTGTGCCTGGACTTTG

209563	41759	GGATGGAGCGACCCATTTTC	254150	86346	TTCTCACAGGCTCTGCAGGT	298737	130933	CACTCTTGTGCCTGGACTTT
209564	41760	AGGATGGAGCGACCCATTTT	254151	86347	CTTCTCACAGGCTCTGCAGG	298738	130934	CCACTCTTGTGCCTGGACTT
209565	41761	CAGGATGGAGCGACCCATTT	254152	86348	GCTTCTCACAGGCTCTGCAG	298739	130935	CCCACTCTTGTGCCTGGACT
209566	41762	ACAGGATGGAGCGACCCATT	254153	86349	AGCTTCTCACAGGCTCTGCA	298740	130936	TCCCACTCTTGTGCCTGGAC
209567	41763	AACAGGATGGAGCGACCCAT	254154	86350	CAGCTTCTCACAGGCTCTGC	298741	130937	GTCCCACTCTTGTGCCTGGA
209568	41764	AAACAGGATGGAGCGACCCA	254155	86351	TCAGCTTCTCACAGGCTCTG	298742	130938	GGTCCCACTCTTGTGCCTGG
209569	41765	CAAACAGGATGGAGCGACCC	254156	86352	TTCAGCTTCTCACAGGCTCT	298743	130939	GGGTCCCACTCTTGTGCCTG
209570	41766	ACAAACAGGATGGAGCGACC	254157	86353	CTTCAGCTTCTCACAGGCTC	298744	130940	GGGGTCCCACTCTTGTGCCT
209571	41767	CACAAACAGGATGGAGCGAC	254158	86354	ACTTCAGCTTCTCACAGGCT	298745	130941	TGGGGTCCCACTCTTGTGCC
209572	41768	ACACAAACAGGATGGAGCGA	254159	86355	GACTTCAGCTTCTCACAGGC	298746	130942	CTGGGGTCCCACTCTTGTGC
209573	41769	GACACAAACAGGATGGAGCG	254160	86356	TGACTTCAGCTTCTCACAGG	298747	130943	GCTGGGGTCCCACTCTTGTG
209574	41770	CGACACAAACAGGATGGAGC	254161	86357	TTGACTTCAGCTTCTCACAG	298748	130944	GGCTGGGGTCCCACTCTTGT
209575	41771	ACGACACAAACAGGATGGAG	254162	86358	ATTGACTTCAGCTTCTCACA	298749	130945	AGGCTGGGGTCCCACTCTTG
209576	41772	AACGACACAAACAGGATGGA	254163	86359	CATTGACTTCAGCTTCTCAC	298750	130946	GAGGCTGGGGTCCCACTCTT
209577	41773	GAACGACACAAACAGGATGG	254164	86360	ACATTGACTTCAGCTTCTCA	298751	130947	AGAGGCTGGGGTCCCACTCT
209578	41774	AGAACGACACAAACAGGATG	254165	86361	AACATTGACTTCAGCTTCTC	298752	130948	GAGAGGCTGGGGTCCCACTC
209579	41775	GAGAACGACACAAACAGGAT	254166	86362	AAACATTGACTTCAGCTTCT	298753	130949	TGAGAGGCTGGGGTCCCACT
209580	41776	AGAGAACGACACAAACAGGA	254167	86363	AAAACATTGACTTCAGCTTC	298754	130950	GTGAGAGGCTGGGGTCCCAC
209581	41777	GAGAGAACGACACAAACAGG	254168	86364	GAAAACATTGACTTCAGCTT	298755	130951	AGTGAGAGGCTGGGGTCCCA
209582	41778	GGAGAGAACGACACAAACAG	254169	86365	GGAAAACATTGACTTCAGCT	298756	130952	GAGTGAGAGGCTGGGGTCCC
209583	41779	AGGAGAGAACGACACAAACA	254170	86366	AGGAAAACATTGACTTCAGC	298757	130953	AGAGTGAGAGGCTGGGGTCC
209584	41780	AAGGAGAGAACGACACAAAC	254171	86367	CAGGAAAACATTGACTTCAG	298758	130954	GAGAGTGAGAGGCTGGGGTC
209585	41781	GAAGGAGAGAACGACACAAA	254172	86368	TCAGGAAAACATTGACTTCA	298759	130955	TGAGAGTGAGAGGCTGGGGT
209586	41782	GGAAGGAGAGAACGACACAA	254173	86369	GTCAGGAAAACATTGACTTC	298760	130956	CTGAGAGTGAGAGGCTGGGG
209587	41783	AGGAAGGAGAGAACGACACA	254174	86370	TGTCAGGAAAACATTGACTT	298761	130957	ACTGAGAGTGAGAGGCTGGG
209588	41784	CAGGAAGGAGAGAACGACAC	254175	86371	GTGTCAGGAAAACATTGACT	298762	130958	AACTGAGAGTGAGAGGCTGG
209589	41785	CCAGGAAGGAGAGAACGACA	254176	86372	GGTGTCAGGAAAACATTGAC	298763	130959	GAACTGAGAGTGAGAGGCTG
209590	41786	GCCAGGAAGGAGAGAACGAC	254177	86373	TGGTGTCAGGAAAACATTGA	298764	130960	GGAACTGAGAGTGAGAGGCT
209591	41787	GGCCAGGAAGGAGAGAACGA	254178	86374	CTGGTGTCAGGAAAACATTG	298765	130961	TGGAACTGAGAGTGAGAGGC
209592	41788	GGGCCAGGAAGGAGAGAACG	254179	86375	ACTGGTGTCAGGAAAACATT	298766	130962	GTGGAACTGAGAGTGAGAGG
209593	41789	TGGGCCAGGAAGGAGAGAAC	254180	86376	AACTGGTGTCAGGAAAACAT	298767	130963	AGTGGAACTGAGAGTGAGAG
209594	41790	GTGGGCCAGGAAGGAGAGAA	254181	86377	CAACTGGTGTCAGGAAAACA	298768	130964	GAGTGGAACTGAGAGTGAGA
209595	41791	AGTGGGCCAGGAAGGAGAGA	254182	86378	TCAACTGGTGTCAGGAAAAC	298769	130965	TGAGTGGAACTGAGAGTGAG
209596	41792	GAGTGGGCCAGGAAGGAGAG	254183	86379	ATCAACTGGTGTCAGGAAAA	298770	130966	ATGAGTGGAACTGAGAGTGA
209597	41793	AGAGTGGGCCAGGAAGGAGA	254184	86380	GATCAACTGGTGTCAGGAAA	298771	130967	GATGAGTGGAACTGAGAGTG
209598	41794	GAGAGTGGGCCAGGAAGGAG	254185	86381	AGATCAACTGGTGTCAGGAA	298772	130968	GGATGAGTGGAACTGAGAGT
209599	41795	GGAGAGTGGGCCAGGAAGGA	254186	86382	CAGATCAACTGGTGTCAGGA	298773	130969	TGGATGAGTGGAACTGAGAG
209600	41796	AGGAGAGTGGGCCAGGAAGG	254187	86383	ACAGATCAACTGGTGTCAGG	298774	130970	TTGGATGAGTGGAACTGAGA
209601	41797	CAGGAGAGTGGGCCAGGAAG	254188	86384	CACAGATCAACTGGTGTCAG	298775	130971	GTTGGATGAGTGGAACTGAG
209602	41798	GCAGGAGAGTGGGCCAGGAA	254189	86385	GCACAGATCAACTGGTGTCA	298776	130972	AGTTGGATGAGTGGAACTGA
209603	41799	GGCAGGAGAGTGGGCCAGGA	254190	86386	TGCACAGATCAACTGGTGTC	298777	130973	CAGTTGGATGAGTGGAACTG
209604	41800	GGGCAGGAGAGTGGGCCAGG	254191	86387	CTGCACAGATCAACTGGTGT	298778	130974	CCAGTTGGATGAGTGGAACT
209605	41801	TGGGCAGGAGAGTGGGCCAG	254192	86388	CCTGCACAGATCAACTGGTG	298779	130975	CCCAGTTGGATGAGTGGAAC
209606	41802	GTGGGCAGGAGAGTGGGCCA	254193	86389	TCCTGCACAGATCAACTGGT	298780	130976	TCCCAGTTGGATGAGTGGAA
209607	41803	TGTGGGCAGGAGAGTGGGCC	254194	86390	ATCCTGCACAGATCAACTGG	298781	130977	GTCCCAGTTGGATGAGTGGA
209608	41804	CTGTGGGCAGGAGAGTGGGC	254195	86391	GATCCTGCACAGATCAACTG	298782	130978	GGTCCCAGTTGGATGAGTGG
209609	41805	CCTGTGGGCAGGAGAGTGGG	254196	86392	GGATCCTGCACAGATCAACT	298783	130979	GGGTCCCAGTTGGATGAGTG
209610	41806	ACCTGTGGGCAGGAGAGTGG	254197	86393	TGGATCCTGCACAGATCAAC	298784	130980	AGGGTCCCAGTTGGATGAGT
209611	41807	TACCTGTGGGCAGGAGAGTG	254198	86394	ATGGATCCTGCACAGATCAA	298785	130981	GAGGGTCCCAGTTGGATGAG
209612	41808	ATACCTGTGGGCAGGAGAGT	254199	86395	AATGGATCCTGCACAGATCA	298786	130982	TGAGGGTCCCAGTTGGATGA
209613	41809	GATACCTGTGGGCAGGAGAG	254200	86396	CAATGGATCCTGCACAGATC	298787	130983	GTGAGGGTCCCAGTTGGATG
209614	41810	GGATACCTGTGGGCAGGAGA	254201	86397	TCAATGGATCCTGCACAGAT	298788	130984	GGTGAGGGTCCCAGTTGGAT
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209616	41812	CTGGATACCTGTGGGCAGGA	254203	86399	AATCAATGGATCCTGCACAG	298790	130986	GTGGTGAGGGTCCCAGTTGG
209617	41813	CCTGGATACCTGTGGGCAGG	254204	86400	AAATCAATGGATCCTGCACA	298791	130987	CGTGGTGAGGGTCCCAGTTG
209618	41814	CCCTGGATACCTGTGGGCAG	254205	86401	TAAATCAATGGATCCTGCAC	298792	130988	TCGTGGTGAGGGTCCCAGTT
209619	41815	CCCCTGGATACCTGTGGGCA	254206	86402	TTAAATCAATGGATCCTGCA	298793	130989	TTCGTGGTGAGGGTCCCAGT
209620	41816	GCCCCTGGATACCTGTGGGC	254207	86403	GTTAAATCAATGGATCCTGC	298794	130990	ATTCGTGGTGAGGGTCCCAG
209621	41817	AGCCCCTGGATACCTGTGGG	254208	86404	GGTTAAATCAATGGATCCTG	298795	130991	GATTCGTGGTGAGGGTCCCA
209622	41818	CAGCCCCTGGATACCTGTGG	254209	86405	TGGTTAAATCAATGGATCCT	298796	130992	AGATTCGTGGTGAGGGTCCC
209623	41819	GCAGCCCCTGGATACCTGTG	254210	86406	GTGGTTAAATCAATGGATCC	298797	130993	GAGATTCGTGGTGAGGGTCC
209624	41820	GGCAGCCCCTGGATACCTGT	254211	86407	GGTGGTTAAATCAATGGATC	298798	130994	TGAGATTCGTGGTGAGGGTC
209625	41821	AGGCAGCCCCTGGATACCTG	254212	86408	AGGTGGTTAAATCAATGGAT	298799	130995	ATGAGATTCGTGGTGAGGGT
209626	41822	CAGGCAGCCCCTGGATACCT	254213	86409	CAGGTGGTTAAATCAATGGA	298800	130996	CATGAGATTCGTGGTGAGGG
209627	41823	ACAGGCAGCCCCTGGATACC	254214	86410	GCAGGTGGTTAAATCAATGG	298801	130997	TCATGAGATTCGTGGTGAGG
209628	41824	TACAGGCAGCCCCTGGATAC	254215	86411	AGCAGGTGGTTAAATCAATG	298802	130998	ATCATGAGATTCGTGGTGAG
209629	41825	CTACAGGCAGCCCCTGGATA	254216	86412	CAGCAGGTGGTTAAATCAAT	298803	130999	GATCATGAGATTCGTGGTGA
209630	41826	GCTACAGGCAGCCCCTGGAT	254217	86413	ACAGCAGGTGGTTAAATCAA	298804	131000	AGATCATGAGATTCGTGGTG
209631	41827	TGCTACAGGCAGCCCCTGGA	254218	86414	CACAGCAGGTGGTTAAATCA	298805	131001	CAGATCATGAGATTCGTGGT
209632	41828	ATGCTACAGGCAGCCCCTGG	254219	86415	ACACAGCAGGTGGTTAAATC	298806	131002	TCAGATCATGAGATTCGTGG
209633	41829	AATGCTACAGGCAGCCCCTG	254220	86416	CACACAGCAGGTGGTTAAAT	298807	131003	ATCAGATCATGAGATTCGTG
209634	41830	TAATGCTACAGGCAGCCCCT	254221	86417	CCACACAGCAGGTGGTTAAA	298808	131004	AATCAGATCATGAGATTCGT

209635	41831	CTAATGCTACAGGCAGCCCC	254222	86418	GCCACACAGCAGGTGGTTAA	298809	131005	GAATCAGATCATGAGATTCG
209636	41832	TCTAATGCTACAGGCAGCCC	254223	86419	TGCCACACAGCAGGTGGTTA	298810	131006	CGAATCAGATCATGAGATTC
209637	41833	CTCTAATGCTACAGGCAGCC	254224	86420	ATGCCACACAGCAGGTGGTT	298811	131007	CCGAATCAGATCATGAGATT
209638	41834	CCTCTAATGCTACAGGCAGC	254225	86421	CATGCCACACAGCAGGTGGT	298812	131008	ACCGAATCAGATCATGAGAT
209639	41835	TCCTCTAATGCTACAGGCAG	254226	86422	GCATGCCACACAGCAGGTGG	298813	131009	AACCGAATCAGATCATGAGA
209640	41836	GTCCTCTAATGCTACAGGCA	254227	86423	TGCATGCCACACAGCAGGTG	298814	131010	GAACCGAATCAGATCATGAG
209641	41837	TGTCCTCTAATGCTACAGGC	254228	86424	GTGCATGCCACACAGCAGGT	298815	131011	GGAACCGAATCAGATCATGA
209642	41838	ATGTCCTCTAATGCTACAGG	254229	86425	AGTGCATGCCACACAGCAGG	298816	131012	GGGAACCGAATCAGATCATG
209643	41839	TATGTCCTCTAATGCTACAG	254230	86426	CAGTGCATGCCACACAGCAG	298817	131013	AGGGAACCGAATCAGATCAT
209644	41840	GTATGTCCTCTAATGCTACA	254231	86427	ACAGTGCATGCCACACAGCA	298818	131014	CAGGGAACCGAATCAGATCA
209645	41841	TGTATGTCCTCTAATGCTAC	254232	86428	CACAGTGCATGCCACACAGC	298819	131015	ACAGGGAACCGAATCAGATC
209646	41842	ATGTATGTCCTCTAATGCTA	254233	86429	CCACAGTGCATGCCACACAG	298820	131016	GACAGGGAACCGAATCAGAT
209647	41843	CATGTATGTCCTCTAATGCT	254234	86430	ACCACAGTGCATGCCACACA	298821	131017	AGACAGGGAACCGAATCAGA
209648	41844	GCATGTATGTCCTCTAATGC	254235	86431	GACCACAGTGCATGCCACAC	298822	131018	GAGACAGGGAACCGAATCAG
209649	41845	TGCATGTATGTCCTCTAATG	254236	86432	CGACCACAGTGCATGCCACA	298823	131019	GGAGACAGGGAACCGAATCA
209650	41846	GTGCATGTATGTCCTCTAAT	254237	86433	TCGACCACAGTGCATGCCAC	298824	131020	AGGAGACAGGGAACCGAATC
209651	41847	TGTGCATGTATGTCCTCTAA	254238	86434	ATCGACCACAGTGCATGCCA	298825	131021	GAGGAGACAGGGAACCGAAT
209652	41848	ATGTGCATGTATGTCCTCTA	254239	86435	CATCGACCACAGTGCATGCC	298826	131022	GGAGGAGACAGGGAACCGAA
209653	41849	CATGTGCATGTATGTCCTCT	254240	86436	GCATCGACCACAGTGCATGC	298827	131023	AGGAGGAGACAGGGAACCGA
209654	41850	GCATGTGCATGTATGTCCTC	254241	86437	GGCATCGACCACAGTGCATG	298828	131024	GAGGAGGAGACAGGGAACCG
209655	41851	CGCATGTGCATGTATGTCCT	254242	86438	TGGCATCGACCACAGTGCAT	298829	131025	GGAGGAGGAGACAGGGAACC
209656	41852	ACGCATGTGCATGTATGTCC	254243	86439	CTGGCATCGACCACAGTGCA	298830	131026	GGGAGGAGGAGACAGGGAAC
209657	41853	CACGCATGTGCATGTATGTC	254244	86440	CCTGGCATCGACCACAGTGC	298831	131027	CGGGAGGAGGAGACAGGGAA
209658	41854	CCACGCATGTGCATGTATGT	254245	86441	TCCTGGCATCGACCACAGTG	298832	131028	ACGGGAGGAGGAGACAGGGA
209659	41855	CCCACGCATGTGCATGTATG	254246	86442	TTCCTGGCATCGACCACAGT	298833	131029	GACGGGAGGAGGAGACAGGG
209660	41856	GCCCACGCATGTGCATGTAT	254247	86443	GTTCCTGGCATCGACCACAG	298834	131030	TGACGGGAGGAGGAGACAGG
209661	41857	TGCCCACGCATGTGCATGTA	254248	86444	TGTTCCTGGCATCGACCACA	298835	131031	GTGACGGGAGGAGGAGACAG
209662	41858	ATGCCCACGCATGTGCATGT	254249	86445	CTGTTCCTGGCATCGACCAC	298836	131032	TGTGACGGGAGGAGGAGACA
209663	41859	CATGCCCACGCATGTGCATG	254250	86446	CCTGTTCCTGGCATCGACCA	298837	131033	CTGTGACGGGAGGAGGAGAC
209664	41860	CCATGCCCACGCATGTGCAT	254251	86447	TCCTGTTCCTGGCATCGACC	298838	131034	TCTGTGACGGGAGGAGGAGA
209665	41861	CCCATGCCCACGCATGTGCA	254252	86448	TTCCTGTTCCTGGCATCGAC	298839	131035	ATCTGTGACGGGAGGAGGAG
209666	41862	TCCCATGCCCACGCATGTGC	254253	86449	ATTCCTGTTCCTGGCATCGA	298840	131036	CATCTGTGACGGGAGGAGGA
209667	41863	GTCCCATGCCCACGCATGTG	254254	86450	AATTCCTGTTCCTGGCATCG	298841	131037	ACATCTGTGACGGGAGGAGG
209668	41864	TGTCCCATGCCCACGCATGT	254255	86451	CAATTCCTGTTCCTGGCATC	298842	131038	CACATCTGTGACGGGAGGAG
209669	41865	GTGTCCCATGCCCACGCATG	254256	86452	CCAATTCCTGTTCCTGGCAT	298843	131039	TCACATCTGTGACGGGAGGA
209670	41866	AGTGTCCCATGCCCACGCAT	254257	86453	TCCAATTCCTGTTCCTGGCA	298844	131040	CTCACATCTGTGACGGGAGG
209671	41867	GAGTGTCCCATGCCCACGCA	254258	86454	CTCCAATTCCTGTTCCTGGC	298845	131041	GCTCACATCTGTGACGGGAG
209672	41868	TGAGTGTCCCATGCCCACGC	254259	86455	CCTCCAATTCCTGTTCCTGG	298846	131042	GGCTCACATCTGTGACGGGA
209673	41869	GTGAGTGTCCCATGCCCACG	254260	86456	CCCTCCAATTCCTGTTCCTG	298847	131043	TGGCTCACATCTGTGACGGG
209674	41870	CGTGAGTGTCCCATGCCCAC	254261	86457	CCCCTCCAATTCCTGTTCCT	298848	131044	CTGGCTCACATCTGTGACGG
209675	41871	ACGTGAGTGTCCCATGCCCA	254262	86458	GCCCCTCCAATTCCTGTTCC	298849	131045	CCTGGCTCACATCTGTGACG
209676	41872	TACGTGAGTGTCCCATGCCC	254263	86459	GGCCCCTCCAATTCCTGTTC	298850	131046	CCCTGGCTCACATCTGTGAC
209677	41873	CTACGTGAGTGTCCCATGCC	254264	86460	GGGCCCCTCCAATTCCTGTT	298851	131047	GCCCTGGCTCACATCTGTGA
209678	41874	GCTACGTGAGTGTCCCATGC	254265	86461	TGGGCCCCTCCAATTCCTGT	298852	131048	TGCCCTGGCTCACATCTGTG
209679	41875	GGCTACGTGAGTGTCCCATG	254266	86462	ATGGGCCCCTCCAATTCCTG	298853	131049	GTGCCCTGGCTCACATCTGT
209680	41876	AGGCTACGTGAGTGTCCCAT	254267	86463	CATGGGCCCCTCCAATTCCT	298854	131050	AGTGCCCTGGCTCACATCTG
209681	41877	GAGGCTACGTGAGTGTCCCA	254268	86464	TCATGGGCCCCTCCAATTCC	298855	131051	CAGTGCCCTGGCTCACATCT
209682	41878	GGAGGCTACGTGAGTGTCCC	254269	86465	CTCATGGGCCCCTCCAATTC	298856	131052	GCAGTGCCCTGGCTCACATC
209683	41879	TGGAGGCTACGTGAGTGTCC	254270	86466	GCTCATGGGCCCCTCCAATT	298857	131053	AGCAGTGCCCTGGCTCACAT
209684	41880	TTGGAGGCTACGTGAGTGTC	254271	86467	TGCTCATGGGCCCCTCCAAT	298858	131054	GAGCAGTGCCCTGGCTCACA
209685	41881	CTTGGAGGCTACGTGAGTGT	254272	86468	ATGCTCATGGGCCCCTCCAA	298859	131055	TGAGCAGTGCCCTGGCTCAC
209686	41882	GCTTGGAGGCTACGTGAGTG	254273	86469	CATGCTCATGGGCCCCTCCA	298860	131056	CTGAGCAGTGCCCTGGCTCA
209687	41883	TGCTTGGAGGCTACGTGAGT	254274	86470	CCATGCTCATGGGCCCCTCC	298861	131057	GCTGAGCAGTGCCCTGGCTC
209688	41884	GTGCTTGGAGGCTACGTGAG	254275	86471	GCCATGCTCATGGGCCCCTC	298862	131058	AGCTGAGCAGTGCCCTGGCT
209689	41885	TGTGCTTGGAGGCTACGTGA	254276	86472	GGCCATGCTCATGGGCCCCT	298863	131059	CAGCTGAGCAGTGCCCTGGC
209690	41886	CTGTGCTTGGAGGCTACGTG	254277	86473	TGGCCATGCTCATGGGCCCC	298864	131060	ACAGCTGAGCAGTGCCCTGG
209691	41887	GCTGTGCTTGGAGGCTACGT	254278	86474	CTGGCCATGCTCATGGGCCC	298865	131061	CACAGCTGAGCAGTGCCCTG
209692	41888	TGCTGTGCTTGGAGGCTACG	254279	86475	ACTGGCCATGCTCATGGGCC	298866	131062	TCACAGCTGAGCAGTGCCCT
209693	41889	ATGCTGTGCTTGGAGGCTAC	254280	86476	TACTGGCCATGCTCATGGGC	298867	131063	GTCACAGCTGAGCAGTGCCC
209694	41890	GATGCTGTGCTTGGAGGCTA	254281	86477	ATACTGGCCATGCTCATGGG	298868	131064	GGTCACAGCTGAGCAGTGCC
209695	41891	TGATGCTGTGCTTGGAGGCT	254282	86478	GATACTGGCCATGCTCATGG	298869	131065	GGGTCACAGCTGAGCAGTGC
209696	41892	TTGATGCTGTGCTTGGAGGC	254283	86479	TGATACTGGCCATGCTCATG	298870	131066	AGGGTCACAGCTGAGCAGTG
209697	41893	ATTGATGCTGTGCTTGGAGG	254284	86480	GTGATACTGGCCATGCTCAT	298871	131067	TAGGGTCACAGCTGAGCAGT
209698	41894	TATTGATGCTGTGCTTGGAG	254285	86481	TGTGATACTGGCCATGCTCA	298872	131068	CTAGGGTCACAGCTGAGCAG
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209700	41896	ATTATTGATGCTGTGCTTGG	254287	86483	CCTGTGATACTGGCCATGCT	298874	131070	ACCTAGGGTCACAGCTGAGC
209701	41897	CATTATTGATGCTGTGCTTG	254288	86484	GCCTGTGATACTGGCCATGC	298875	131071	CACCTAGGGTCACAGCTGAG
209702	41898	GCATTATTGATGCTGTGCTT	254289	86485	AGCCTGTGATACTGGCCATG	298876	131072	ACACCTAGGGTCACAGCTGA
209703	41899	TGCATTATTGATGCTGTGCT	254290	86486	CAGCCTGTGATACTGGCCAT	298877	131073	AACACCTAGGGTCACAGCTG
209704	41900	ATGCATTATTGATGCTGTGC	254291	86487	CCAGCCTGTGATACTGGCCA	298878	131074	AAACACCTAGGGTCACAGCT
209705	41901	AATGCATTATTGATGCTGTG	254292	86488	TCCAGCCTGTGATACTGGCC	298879	131075	GAAACACCTAGGGTCACAGC
209706	41902	GAATGCATTATTGATGCTGT	254293	86489	CTCCAGCCTGTGATACTGGC	298880	131076	AGAAACACCTAGGGTCACAG

209707	41903	AGAATGCATTATTGATGCTG	254294	86490	CCTCCAGCCTGTGATACTGG	298881	131077	CAGAAACACCTAGGGTCACA
209708	41904	CAGAATGCATTATTGATGCT	254295	86491	ACCTCCAGCCTGTGATACTG	298882	131078	GCAGAAACACCTAGGGTCAC
209709	41905	ACAGAATGCATTATTGATGC	254296	86492	CACCTCCAGCCTGTGATACT	298883	131079	GGCAGAAACACCTAGGGTCA
209710	41906	CACAGAATGCATTATTGATG	254297	86493	GCACCTCCAGCCTGTGATAC	298884	131080	AGGCAGAAACACCTAGGGTC
209711	41907	GCACAGAATGCATTATTGAT	254298	86494	AGCACCTCCAGCCTGTGATA	298885	131081	AAGGCAGAAACACCTAGGGT
209712	41908	AGCACAGAATGCATTATTGA	254299	86495	CAGCACCTCCAGCCTGTGAT	298886	131082	CAAGGCAGAAACACCTAGGG
209713	41909	AAGCACAGAATGCATTATTG	254300	86496	GCAGCACCTCCAGCCTGTGA	298887	131083	ACAAGGCAGAAACACCTAGG
209714	41910	AAAGCACAGAATGCATTATT	254301	86497	AGCAGCACCTCCAGCCTGTG	298888	131084	AACAAGGCAGAAACACCTAG
209715	41911	TAAAGCACAGAATGCATTAT	254302	86498	CAGCAGCACCTCCAGCCTGT	298889	131085	CAACAAGGCAGAAACACCTA
209716	41912	ATAAAGCACAGAATGCATTA	254303	86499	GCAGCAGCACCTCCAGCCTG	298890	131086	TCAACAAGGCAGAAACACCT
209717	41913	TATAAAGCACAGAATGCATT	254304	86500	CGCAGCAGCACCTCCAGCCT	298891	131087	GTCAACAAGGCAGAAACACC
209718	41914	CTATAAAGCACAGAATGCAT	254305	86501	GCGCAGCAGCACCTCCAGCC	298892	131088	TGTCAACAAGGCAGAAACAC
209719	41915	GCTATAAAGCACAGAATGCA	254306	86502	AGCGCAGCAGCACCTCCAGC	298893	131089	ATGTCAACAAGGCAGAAACA
209720	41916	TGCTATAAAGCACAGAATGC	254307	86503	GAGCGCAGCAGCACCTCCAG	298894	131090	CATGTCAACAAGGCAGAAAC
209721	41917	ATGCTATAAAGCACAGAATG	254308	86504	AGAGCGCAGCAGCACCTCCA	298895	131091	CCATGTCAACAAGGCAGAAA
209722	41918	CATGCTATAAAGCACAGAAT	254309	86505	CAGAGCGCAGCAGCACCTCC	298896	131092	TCCATGTCAACAAGGCAGAA
209723	41919	CCATGCTATAAAGCACAGAA	254310	86506	TCAGAGCGCAGCAGCACCTC	298897	131093	CTCCATGTCAACAAGGCAGA
209724	41920	TCCATGCTATAAAGCACAGA	254311	86507	GTCAGAGCGCAGCAGCACCT	298898	131094	TCTCCATGTCAACAAGGCAG
209725	41921	TTCCATGCTATAAAGCACAG	254312	86508	GGTCAGAGCGCAGCAGCACC	298899	131095	CTCTCCATGTCAACAAGGCA
209726	41922	TTTCCATGCTATAAAGCACA	254313	86509	CGGTCAGAGCGCAGCAGCAC	298900	131096	TCTCTCCATGTCAACAAGGC
209727	41923	CTTTCCATGCTATAAAGCAC	254314	86510	CCGGTCAGAGCGCAGCAGCA	298901	131097	CTCTCTCCATGTCAACAAGG
209728	41924	GCTTTCCATGCTATAAAGCA	254315	86511	CCCGGTCAGAGCGCAGCAGC	298902	131098	GCTCTCTCCATGTCAACAAG
209729	41925	AGCTTTCCATGCTATAAAGC	254316	86512	GCCCGGTCAGAGCGCAGCAG	298903	131099	GGCTCTCTCCATGTCAACAA
209730	41926	CAGCTTTCCATGCTATAAAG	254317	86513	GGCCCGGTCAGAGCGCAGCA	298904	131100	GGGCTCTCTCCATGTCAACA
209731	41927	GCAGCTTTCCATGCTATAAA	254318	86514	AGGCCCGGTCAGAGCGCAGC	298905	131101	AGGGCTCTCTCCATGTCAAC
209732	41928	AGCAGCTTTCCATGCTATAA	254319	86515	GAGGCCCGGTCAGAGCGCAG	298906	131102	AAGGGCTCTCTCCATGTCAA
209733	41929	GAGCAGCTTTCCATGCTATA	254320	86516	AGAGGCCCGGTCAGAGCGCA	298907	131103	AAAGGGCTCTCTCCATGTCA
209734	41930	AGAGCAGCTTTCCATGCTAT	254321	86517	AAGAGGCCCGGTCAGAGCGC	298908	131104	GAAAGGGCTCTCTCCATGTC
209735	41931	TAGAGCAGCTTTCCATGCTA	254322	86518	CAAGAGGCCCGGTCAGAGCG	298909	131105	GGAAAGGGCTCTCTCCATGT
209736	41932	TTAGAGCAGCTTTCCATGCT	254323	86519	CCAAGAGGCCCGGTCAGAGC	298910	131106	GGGAAAGGGCTCTCTCCATG
209737	41933	TTTAGAGCAGCTTTCCATGC	254324	86520	CCCAAGAGGCCCGGTCAGAG	298911	131107	GGGGAAAGGGCTCTCTCCAT
209738	41934	GTTTAGAGCAGCTTTCCATG	254325	86521	CCCCAAGAGGCCCGGTCAGA	298912	131108	AGGGGAAAGGGCTCTCTCCA
209739	41935	AGTTTAGAGCAGCTTTCCAT	254326	86522	TCCCCAAGAGGCCCGGTCAG	298913	131109	CAGGGGAAAGGGCTCTCTCC
209740	41936	AAGTTTAGAGCAGCTTTCCA	254327	86523	ATCCCCAAGAGGCCCGGTCA	298914	131110	TCAGGGGAAAGGGCTCTCTC
209741	41937	AAAGTTTAGAGCAGCTTTCC	254328	86524	CATCCCCAAGAGGCCCGGTC	298915	131111	CTCAGGGGAAAGGGCTCTCT
209742	41938	TAAAGTTTAGAGCAGCTTTC	254329	86525	TCATCCCCAAGAGGCCCGGT	298916	131112	TCTCAGGGGAAAGGGCTCTC
209743	41939	ATAAAGTTTAGAGCAGCTTT	254330	86526	CTCATCCCCAAGAGGCCCGG	298917	131113	TTCTCAGGGGAAAGGGCTCT
209744	41940	AATAAAGTTTAGAGCAGCTT	254331	86527	GCTCATCCCCAAGAGGCCCG	298918	131114	CTTCTCAGGGGAAAGGGCTC
209745	41941	TAATAAAGTTTAGAGCAGCT	254332	86528	GGCTCATCCCCAAGAGGCCC	298919	131115	CCTTCTCAGGGGAAAGGGCT
209746	41942	GTAATAAAGTTTAGAGCAGC	254333	86529	GGGCTCATCCCCAAGAGGCC	298920	131116	GCCTTCTCAGGGGAAAGGGC
209747	41943	TGTAATAAAGTTTAGAGCAG	254334	86530	TGGGCTCATCCCCAAGAGGC	298921	131117	GGCCTTCTCAGGGGAAAGGG
209748	41944	GTGTAATAAAGTTTAGAGCA	254335	86531	ATGGGCTCATCCCCAAGAGG	298922	131118	AGGCCTTCTCAGGGGAAAGG
209749	41945	TGTGTAATAAAGTTTAGAGC	254336	86532	CATGGGCTCATCCCCAAGAG	298923	131119	CAGGCCTTCTCAGGGGAAAG
209750	41946	CTGTGTAATAAAGTTTAGAG	254337	86533	ACATGGGCTCATCCCCAAGA	298924	131120	CCAGGCCTTCTCAGGGGAAA
209751	41947	ACTGTGTAATAAAGTTTAGA	254338	86534	GACATGGGCTCATCCCCAAG	298925	131121	GCCAGGCCTTCTCAGGGGAA
209752	41948	CACTGTGTAATAAAGTTTAG	254339	86535	TGACATGGGCTCATCCCCAA	298926	131122	GGCCAGGCCTTCTCAGGGGA
209753	41949	CCACTGTGTAATAAAGTTTA	254340	86536	TTGACATGGGCTCATCCCCA	298927	131123	GGGCCAGGCCTTCTCAGGGG
209754	41950	TCCACTGTGTAATAAAGTTT	254341	86537	GTTGACATGGGCTCATCCCC	298928	131124	GGGGCCAGGCCTTCTCAGGG
209755	41951	GTCCACTGTGTAATAAAGTT	254342	86538	GGTTGACATGGGCTCATCCC	298929	131125	AGGGGCCAGGCCTTCTCAGG
209756	41952	TGTCCACTGTGTAATAAAGT	254343	86539	TGGTTGACATGGGCTCATCC	298930	131126	AAGGGGCCAGGCCTTCTCAG
209757	41953	ATGTCCACTGTGTAATAAAG	254344	86540	GTGGTTGACATGGGCTCATC	298931	131127	GAAGGGGCCAGGCCTTCTCA
209758	41954	CATGTCCACTGTGTAATAAA	254345	86541	GGTGGTTGACATGGGCTCAT	298932	131128	GGAAGGGGCCAGGCCTTCTC
209759	41955	ACATGTCCACTGTGTAATAA	254346	86542	AGGTGGTTGACATGGGCTCA	298933	131129	AGGAAGGGGCCAGGCCTTCT
209760	41956	GACATGTCCACTGTGTAATA	254347	86543	AAGGTGGTTGACATGGGCTC	298934	131130	CAGGAAGGGGCCAGGCCTTC
209761	41957	AGACATGTCCACTGTGTAAT	254348	86544	CAAGGTGGTTGACATGGGCT	298935	131131	ACAGGAAGGGGCCAGGCCTT
209762	41958	CAGACATGTCCACTGTGTAA	254349	86545	GCAAGGTGGTTGACATGGGC	298936	131132	CACAGGAAGGGGCCAGGCCT
209763	41959	TCAGACATGTCCACTGTGTA	254350	86546	GGCAAGGTGGTTGACATGGG	298937	131133	GCACAGGAAGGGGCCAGGCC
209764	41960	TTCAGACATGTCCACTGTGT	254351	86547	AGGCAAGGTGGTTGACATGG	298938	131134	AGCACAGGAAGGGGCCAGGC
209765	41961	CTTCAGACATGTCCACTGTG	254352	86548	GAGGCAAGGTGGTTGACATG	298939	131135	CAGCACAGGAAGGGGCCAGG
209766	41962	GCTTCAGACATGTCCACTGT	254353	86549	GGAGGCAAGGTGGTTGACAT	298940	131136	TCAGCACAGGAAGGGGCCAG
209767	41963	TGCTTCAGACATGTCCACTG	254354	86550	CGGAGGCAAGGTGGTTGACA	298941	131137	CTCAGCACAGGAAGGGGCCA
209768	41964	CTGCTTCAGACATGTCCACT	254355	86551	TCGGAGGCAAGGTGGTTGAC	298942	131138	GCTCAGCACAGGAAGGGGCC
209769	41965	GCTGCTTCAGACATGTCCAC	254356	86552	ATCGGAGGCAAGGTGGTTGA	298943	131139	GGCTCAGCACAGGAAGGGGC
209770	41966	AGCTGCTTCAGACATGTCCA	254357	86553	CATCGGAGGCAAGGTGGTTG	298944	131140	GGGCTCAGCACAGGAAGGGG
209771	41967	GAGCTGCTTCAGACATGTCC	254358	86554	CCATCGGAGGCAAGGTGGTT	298945	131141	TGGGCTCAGCACAGGAAGGG
209772	41968	GGAGCTGCTTCAGACATGTC	254359	86555	CCCATCGGAGGCAAGGTGGT	298946	131142	GTGGGCTCAGCACAGGAAGG
209773	41969	GGGAGCTGCTTCAGACATGT	254360	86556	CCCCATCGGAGGCAAGGTGG	298947	131143	TGTGGGCTCAGCACAGGAAG
209774	41970	TGGGAGCTGCTTCAGACATG	254361	86557	ACCCCATCGGAGGCAAGGTG	298948	131144	CTGTGGGCTCAGCACAGGAA
209775	41971	TTGGGAGCTGCTTCAGACAT	254362	86558	GACCCCATCGGAGGCAAGGT	298949	131145	GCTGTGGGCTCAGCACAGGA
209776	41972	TTTGGGAGCTGCTTCAGACA	254363	86559	CGACCCCATCGGAGGCAAGG	298950	131146	TGCTGTGGGCTCAGCACAGG
209777	41973	ATTTGGGAGCTGCTTCAGAC	254364	86560	CCGACCCCATCGGAGGCAAG	298951	131147	CTGCTGTGGGCTCAGCACAG
209778	41974	GATTTGGGAGCTGCTTCAGA	254365	86561	CCCGACCCCATCGGAGGCAA	298952	131148	GCTGCTGTGGGCTCAGCACA

209779	41975	GGATTTGGGAGCTGCTTCAG	254366	86562	GCCCGACCCCATCGGAGGCA	298953	131149	TGCTGCTGTGGGCTCAGCAC
209780	41976	TGGATTTGGGAGCTGCTTCA	254367	86563	GGCCCGACCCCATCGGAGGC	298954	131150	CTGCTGCTGTGGGCTCAGCA
209781	41977	GTGGATTTGGGAGCTGCTTC	254368	86564	GGGCCCGACCCCATCGGAGG	298955	131151	CCTGCTGCTGTGGGCTCAGC
209782	41978	GGTGGATTTGGGAGCTGCTT	254369	86565	TGGGCCCGACCCCATCGGAG	298956	131152	GCCTGCTGCTGTGGGCTCAG
209783	41979	GGGTGGATTTGGGAGCTGCT	254370	86566	GTGGGCCCGACCCCATCGGA	298957	131153	AGCCTGCTGCTGTGGGCTCA
209784	41980	GGGGTGGATTTGGGAGCTGC	254371	86567	TGTGGGCCCGACCCCATCGG	298958	131154	CAGCCTGCTGCTGTGGGCTC
209785	41981	AGGGGTGGATTTGGGAGCTG	254372	86568	CTGTGGGCCCGACCCCATCG	298959	131155	CCAGCCTGCTGCTGTGGGCT
209786	41982	CAGGGGTGGATTTGGGAGCT	254373	86569	CCTGTGGGCCCGACCCCATC	298960	131156	CCCAGCCTGCTGCTGTGGGC
209787	41983	TCAGGGGTGGATTTGGGAGC	254374	86570	ACCTGTGGGCCCGACCCCAT	298961	131157	ACCCAGCCTGCTGCTGTGGG
209788	41984	CTCAGGGGTGGATTTGGGAG	254375	86571	AACCTGTGGGCCCGACCCCA	298962	131158	CACCCAGCCTGCTGCTGTGG
209789	41985	ACTCAGGGGTGGATTTGGGA	254376	86572	TAACCTGTGGGCCCGACCCC	298963	131159	ACACCCAGCCTGCTGCTGTG
209790	41986	CACTCAGGGGTGGATTTGGG	254377	86573	GTAACCTGTGGGCCCGACCC	298964	131160	GACACCCAGCCTGCTGCTGT
209791	41987	ACACTCAGGGGTGGATTTGG	254378	86574	GGTAACCTGTGGGCCCGACC	298965	131161	AGACACCCAGCCTGCTGCTG
209792	41988	CACACTCAGGGGTGGATTTG	254379	86575	AGGTAACCTGTGGGCCCGAC	298966	131162	AAGACACCCAGCCTGCTGCT
209793	41989	ACACACTCAGGGGTGGATTT	254380	86576	AAGGTAACCTGTGGGCCCGA	298967	131163	CAAGACACCCAGCCTGCTGC
209794	41990	AACACACTCAGGGGTGGATT	254381	86577	AAAGGTAACCTGTGGGCCCG	298968	131164	CCAAGACACCCAGCCTGCTG
209795	41991	CAACACACTCAGGGGTGGAT	254382	86578	CAAAGGTAACCTGTGGGCCC	298969	131165	ACCAAGACACCCAGCCTGCT
209796	41992	CCAACACACTCAGGGGTGGA	254383	86579	ACAAAGGTAACCTGTGGGCC	298970	131166	AACCAAGACACCCAGCCTGC
209797	41993	TCCAACACACTCAGGGGTGG	254384	86580	CACAAAGGTAACCTGTGGGC	298971	131167	CAACCAAGACACCCAGCCTG
209798	41994	TTCCAACACACTCAGGGGTG	254385	86581	ACACAAAGGTAACCTGTGGG	298972	131168	ACAACCAAGACACCCAGCCT
209799	41995	ATTCCAACACACTCAGGGGT	254386	86582	CACACAAAGGTAACCTGTGG	298973	131169	GACAACCAAGACACCCAGCC
209800	41996	AATTCCAACACACTCAGGGG	254387	86583	ACACACAAAGGTAACCTGTG	298974	131170	TGACAACCAAGACACCCAGC
209801	41997	CAATTCCAACACACTCAGGG	254388	86584	GACACACAAAGGTAACCTGT	298975	131171	CTGACAACCAAGACACCCAG
209802	41998	CCAATTCCAACACACTCAGG	254389	86585	GGACACACAAAGGTAACCTG	298976	131172	ACTGACAACCAAGACACCCA
209803	41999	GCCAATTCCAACACACTCAG	254390	86586	TGGACACACAAAGGTAACCT	298977	131173	CACTGACAACCAAGACACCC
209804	42000	TGCCAATTCCAACACACTCA	254391	86587	ATGGACACACAAAGGTAACC	298978	131174	CCACTGACAACCAAGACACC
209805	42001	TTGCCAATTCCAACACACTC	254392	86588	CATGGACACACAAAGGTAAC	298979	131175	ACCACTGACAACCAAGACAC
209806	42002	CTTGCCAATTCCAACACACT	254393	86589	TCATGGACACACAAAGGTAA	298980	131176	CACCACTGACAACCAAGACA
209807	42003	GCTTGCCAATTCCAACACAC	254394	86590	GTCATGGACACACAAAGGTA	298981	131177	CCACCACTGACAACCAAGAC
209808	42004	GGCTTGCCAATTCCAACACA	254395	86591	GGTCATGGACACACAAAGGT	298982	131178	GCCACCACTGACAACCAAGA
209809	42005	AGGCTTGCCAATTCCAACAC	254396	86592	TGGTCATGGACACACAAAGG	298983	131179	TGCCACCACTGACAACCAAG
209810	42006	TAGGCTTGCCAATTCCAACA	254397	86593	GTGGTCATGGACACACAAAG	298984	131180	GTGCCACCACTGACAACCAA
209811	42007	ATAGGCTTGCCAATTCCAAC	254398	86594	TGTGGTCATGGACACACAAA	298985	131181	GGTGCCACCACTGACAACCA
209812	42008	GATAGGCTTGCCAATTCCAA	254399	86595	GTGTGGTCATGGACACACAA	298986	131182	TGGTGCCACCACTGACAACC
209813	42009	TGATAGGCTTGCCAATTCCA	254400	86596	GGTGTGGTCATGGACACACA	298987	131183	CTGGTGCCACCACTGACAAC
209814	42010	GTGATAGGCTTGCCAATTCC	254401	86597	AGGTGTGGTCATGGACACAC	298988	131184	CCTGGTGCCACCACTGACAA
209815	42011	AGTGATAGGCTTGCCAATTC	254402	86598	AAGGTGTGGTCATGGACACA	298989	131185	TCCTGGTGCCACCACTGACA
209816	42012	AAGTGATAGGCTTGCCAATT	254403	86599	GAAGGTGTGGTCATGGACAC	298990	131186	ATCCTGGTGCCACCACTGAC
209817	42013	CAAGTGATAGGCTTGCCAAT	254404	86600	GGAAGGTGTGGTCATGGACA	298991	131187	CATCCTGGTGCCACCACTGA
209818	42014	CCAAGTGATAGGCTTGCCAA	254405	86601	AGGAAGGTGTGGTCATGGAC	298992	131188	CCATCCTGGTGCCACCACTG
209819	42015	CCCAAGTGATAGGCTTGCCA	254406	86602	GAGGAAGGTGTGGTCATGGA	298993	131189	TCCATCCTGGTGCCACCACT
209820	42016	TCCCAAGTGATAGGCTTGCC	254407	86603	GGAGGAAGGTGTGGTCATGG	298994	131190	TTCCATCCTGGTGCCACCAC
209821	42017	CTCCCAAGTGATAGGCTTGC	254408	86604	GGGAGGAAGGTGTGGTCATG	298995	131191	CTTCCATCCTGGTGCCACCA
209822	42018	ACTCCCAAGTGATAGGCTTG	254409	86605	GGGGAGGAAGGTGTGGTCAT	298996	131192	CCTTCCATCCTGGTGCCACC
209823	42019	GACTCCCAAGTGATAGGCTT	254410	86606	CGGGGAGGAAGGTGTGGTCA	298997	131193	CCCTTCCATCCTGGTGCCAC
209824	42020	AGACTCCCAAGTGATAGGCT	254411	86607	TCGGGGAGGAAGGTGTGGTC	298998	131194	GCCCTTCCATCCTGGTGCCA
209825	42021	TAGACTCCCAAGTGATAGGC	254412	86608	GTCGGGGAGGAAGGTGTGGT	298999	131195	TGCCCTTCCATCCTGGTGCC
209826	42022	CTAGACTCCCAAGTGATAGG	254413	86609	GGTCGGGGAGGAAGGTGTGG	299000	131196	TTGCCCTTCCATCCTGGTGC
209827	42023	ACTAGACTCCCAAGTGATAG	254414	86610	AGGTCGGGGAGGAAGGTGTG	299001	131197	CTTGCCCTTCCATCCTGGTG
209828	42024	AACTAGACTCCCAAGTGATA	254415	86611	GAGGTCGGGGAGGAAGGTGT	299002	131198	CCTTGCCCTTCCATCCTGGT
209829	42025	AAACTAGACTCCCAAGTGAT	254416	86612	TGAGGTCGGGGAGGAAGGTG	299003	131199	GCCTTGCCCTTCCATCCTGG
209830	42026	AAAACTAGACTCCCAAGTGA	254417	86613	ATGAGGTCGGGGAGGAAGGT	299004	131200	TGCCTTGCCCTTCCATCCTG
209831	42027	AAAAACTAGACTCCCAAGTG	254418	86614	GATGAGGTCGGGGAGGAAGG	299005	131201	GTGCCTTGCCCTTCCATCCT
209832	42028	AAAAAACTAGACTCCCAAGT	254419	86615	GGATGAGGTCGGGGAGGAAG	299006	131202	GGTGCCTTGCCCTTCCATCC
209833	42029	AAAAAAACTAGACTCCCAAG	254420	86616	TGGATGAGGTCGGGGAGGAA	299007	131203	GGGTGCCTTGCCCTTCCATC
209834	42030	CAAAAAAACTAGACTCCCAA	254421	86617	TTGGATGAGGTCGGGGAGGA	299008	131204	TGGGTGCCTTGCCCTTCCAT
209835	42031	ACAAAAAAACTAGACTCCCA	254422	86618	TTTGGATGAGGTCGGGGAGG	299009	131205	CTGGGTGCCTTGCCCTTCCA
209836	42032	AACAAAAAAACTAGACTCCC	254423	86619	ATTTGGATGAGGTCGGGGAG	299010	131206	CCTGGGTGCCTTGCCCTTCC
209837	42033	GAACAAAAAAACTAGACTCC	254424	86620	GATTTGGATGAGGTCGGGGA	299011	131207	CCCTGGGTGCCTTGCCCTTC
209838	42034	CGAACAAAAAAACTAGACTC	254425	86621	AGATTTGGATGAGGTCGGGG	299012	131208	GCCCTGGGTGCCTTGCCCTT
209839	42035	ACGAACAAAAAAACTAGACT	254426	86622	GAGATTTGGATGAGGTCGGG	299013	131209	TGCCCTGGGTGCCTTGCCCT
209840	42036	AACGAACAAAAAAACTAGAC	254427	86623	AGAGATTTGGATGAGGTCGG	299014	131210	CTGCCCTGGGTGCCTTGCCC
209841	42037	TAACGAACAAAAAAACTAGA	254428	86624	AAGAGATTTGGATGAGGTCG	299015	131211	CCTGCCCTGGGTGCCTTGCC
209842	42038	TTAACGAACAAAAAAACTAG	254429	86625	AAAGAGATTTGGATGAGGTC	299016	131212	GCCTGCCCTGGGTGCCTTGC
209843	42039	ATTAACGAACAAAAAAACTA	254430	86626	GAAAGAGATTTGGATGAGGT	299017	131213	GGCCTGCCCTGGGTGCCTTG
209844	42040	TATTAACGAACAAAAAAACT	254431	86627	AGAAAGAGATTTGGATGAGG	299018	131214	GGGCCTGCCCTGGGTGCCTT
209845	42041	TTATTAACGAACAAAAAAAC	254432	86628	AAGAAAGAGATTTGGATGAG	299019	131215	TGGGCCTGCCCTGGGTGCCT
209846	42042	ATTATTAACGAACAAAAAAA	254433	86629	AAAGAAAGAGATTTGGATGA	299020	131216	GTGGGCCTGCCCTGGGTGCC
209847	42043	TATTATTAACGAACAAAAAA	254434	86630	AAAAGAAAGAGATTTGGATG	299021	131217	TGTGGGCCTGCCCTGGGTGC
209848	42044	CTATTATTAACGAACAAAAA	254435	86631	GAAAAGAAAGAGATTTGGAT	299022	131218	CTGTGGGCCTGCCCTGGGTG
209849	42045	TCTATTATTAACGAACAAAA	254436	86632	GGAAAAGAAAGAGATTTGGA	299023	131219	ACTGTGGGCCTGCCCTGGGT
209850	42046	ATCTATTATTAACGAACAAA	254437	86633	TGGAAAAGAAAGAGATTTGG	299024	131220	GACTGTGGGCCTGCCCTGGG

209851	42047	CATCTATTATTAACGAACAA	254438	86634	TTGGAAAAGAAAGAGATTTG	299025	131221	GGACTGTGGGCCTGCCCTGG
209852	42048	GCATCTATTATTAACGAACA	254439	86635	CTTGGAAAAGAAAGAGATTT	299026	131222	GGGACTGTGGGCCTGCCCTG
209853	42049	AGCATCTATTATTAACGAAC	254440	86636	GCTTGGAAAAGAAAGAGATT	299027	131223	CGGGACTGTGGGCCTGCCCT
209854	42050	AAGCATCTATTATTAACGAA	254441	86637	GGCTTGGAAAAGAAAGAGAT	299028	131224	GCGGGACTGTGGGCCTGCCC
209855	42051	GAAGCATCTATTATTAACGA	254442	86638	GGGCTTGGAAAAGAAAGAGA	299029	131225	AGCGGGACTGTGGGCCTGCC
209856	42052	GGAAGCATCTATTATTAACG	254443	86639	GGGGCTTGGAAAAGAAAGAG	299030	131226	CAGCGGGACTGTGGGCCTGC
209857	42053	AGGAAGCATCTATTATTAAC	254444	86640	AGGGGCTTGGAAAAGAAAGA	299031	131227	ACAGCGGGACTGTGGGCCTG
209858	42054	CAGGAAGCATCTATTATTAA	254445	86641	CAGGGGCTTGGAAAAGAAAG	299032	131228	GACAGCGGGACTGTGGGCCT
209859	42055	ACAGGAAGCATCTATTATTA	254446	86642	TCAGGGGCTTGGAAAAGAAA	299033	131229	GGACAGCGGGACTGTGGGCC
209860	42056	CACAGGAAGCATCTATTATT	254447	86643	TTCAGGGGCTTGGAAAAGAA	299034	131230	GGGACAGCGGGACTGTGGGC
209861	42057	CCACAGGAAGCATCTATTAT	254448	86644	ATTCAGGGGCTTGGAAAAGA	299035	131231	GGGGACAGCGGGACTGTGGG
209862	42058	GCCACAGGAAGCATCTATTA	254449	86645	GATTCAGGGGCTTGGAAAAG	299036	131232	GGGGGACAGCGGGACTGTGG
209863	42059	GGCCACAGGAAGCATCTATT	254450	86646	GGATTCAGGGGCTTGGAAAA	299037	131233	TGGGGGACAGCGGGACTGTG
209864	42060	GGGCCACAGGAAGCATCTAT	254451	86647	AGGATTCAGGGGCTTGGAAA	299038	131234	GTGGGGGACAGCGGGACTGT
209865	42061	GGGGCCACAGGAAGCATCTA	254452	86648	AAGGATTCAGGGGCTTGGAA	299039	131235	AGTGGGGGACAGCGGGACTG
209866	42062	TGGGGCCACAGGAAGCATCT	254453	86649	GAAGGATTCAGGGGCTTGGA	299040	131236	AAGTGGGGGACAGCGGGACT
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209868	42064	GCTGGGGCCACAGGAAGCAT	254455	86651	CTGAAGGATTCAGGGGCTTG	299042	131238	GCAAGTGGGGGACAGCGGGA
209869	42065	AGCTGGGGCCACAGGAAGCA	254456	86652	CCTGAAGGATTCAGGGGCTT	299043	131239	TGCAAGTGGGGGACAGCGGG
209870	42066	AAGCTGGGGCCACAGGAAGC	254457	86653	CCCTGAAGGATTCAGGGGCT	299044	131240	GTGCAAGTGGGGGACAGCGG
209871	42067	CAAGCTGGGGCCACAGGAAG	254458	86654	GCCCTGAAGGATTCAGGGGC	299045	131241	GGTGCAAGTGGGGGACAGCG
209872	42068	CCAAGCTGGGGCCACAGGAA	254459	86655	AGCCCTGAAGGATTCAGGGG	299046	131242	GGGTGCAAGTGGGGGACAGC
209873	42069	GCCAAGCTGGGGCCACAGGA	254460	86656	CAGCCCTGAAGGATTCAGGG	299047	131243	AGGGTGCAAGTGGGGGACAG
209874	42070	TGCCAAGCTGGGGCCACAGG	254461	86657	GCAGCCCTGAAGGATTCAGG	299048	131244	TAGGGTGCAAGTGGGGGACA
209875	42071	TTGCCAAGCTGGGGCCACAG	254462	86658	TGCAGCCCTGAAGGATTCAG	299049	131245	CTAGGGTGCAAGTGGGGGAC
209876	42072	ATTGCCAAGCTGGGGCCACA	254463	86659	CTGCAGCCCTGAAGGATTCA	299050	131246	GCTAGGGTGCAAGTGGGGGA
209877	42073	AATTGCCAAGCTGGGGCCAC	254464	86660	CCTGCAGCCCTGAAGGATTC	299051	131247	AGCTAGGGTGCAAGTGGGGG
209878	42074	AAATTGCCAAGCTGGGGCCA	254465	86661	ACCTGCAGCCCTGAAGGATT	299052	131248	AAGCTAGGGTGCAAGTGGGG
209879	42075	AAAATTGCCAAGCTGGGGCC	254466	86662	AACCTGCAGCCCTGAAGGAT	299053	131249	CAAGCTAGGGTGCAAGTGGG
209880	42076	CAAAATTGCCAAGCTGGGGC	254467	86663	AAACCTGCAGCCCTGAAGGA	299054	131250	ACAAGCTAGGGTGCAAGTGG
209881	42077	TCAAAATTGCCAAGCTGGGG	254468	86664	AAAACCTGCAGCCCTGAAGG	299055	131251	TACAAGCTAGGGTGCAAGTG
209882	42078	ATCAAAATTGCCAAGCTGGG	254469	86665	CAAAACCTGCAGCCCTGAAG	299056	131252	CTACAAGCTAGGGTGCAAGT
209883	42079	AATCAAAATTGCCAAGCTGG	254470	86666	ACAAAACCTGCAGCCCTGAA	299057	131253	GCTACAAGCTAGGGTGCAAG
209884	42080	AAATCAAAATTGCCAAGCTG	254471	86667	AACAAAACCTGCAGCCCTGA	299058	131254	AGCTACAAGCTAGGGTGCAA
209885	42081	TAAATCAAAATTGCCAAGCT	254472	86668	AAACAAAACCTGCAGCCCTG	299059	131255	CAGCTACAAGCTAGGGTGCA
209886	42082	TTAAATCAAAATTGCCAAGC	254473	86669	TAAACAAAACCTGCAGCCCT	299060	131256	GCAGCTACAAGCTAGGGTGC
209887	42083	TTTAAATCAAAATTGCCAAG	254474	86670	TTAAACAAAACCTGCAGCCC	299061	131257	GGCAGCTACAAGCTAGGGTG
209888	42084	CTTTAAATCAAAATTGCCAA	254475	86671	TTTAAACAAAACCTGCAGCC	299062	131258	TGGCAGCTACAAGCTAGGGT
209889	42085	ACTTTAAATCAAAATTGCCA	254476	86672	CTTTAAACAAAACCTGCAGC	299063	131259	TTGGCAGCTACAAGCTAGGG
209890	42086	CACTTTAAATCAAAATTGCC	254477	86673	GCTTTAAACAAAACCTGCAG	299064	131260	GTTGGCAGCTACAAGCTAGG
209891	42087	TCACTTTAAATCAAAATTGC	254478	86674	TGCTTTAAACAAAACCTGCA	299065	131261	GGTTGGCAGCTACAAGCTAG
209892	42088	ATCACTTTAAATCAAAATTG	254479	86675	CTGCTTTAAACAAAACCTGC	299066	131262	AGGTTGGCAGCTACAAGCTA
209893	42089	GATCACTTTAAATCAAAATT	254480	86676	TCTGCTTTAAACAAAACCTG	299067	131263	GAGGTTGGCAGCTACAAGCT
209894	42090	AGATCACTTTAAATCAAAAT	254481	86677	CTCTGCTTTAAACAAAACCT	299068	131264	GGAGGTTGGCAGCTACAAGC
209895	42091	AAGATCACTTTAAATCAAAA	254482	86678	GCTCTGCTTTAAACAAAACC	299069	131265	GGGAGGTTGGCAGCTACAAG
209896	42092	TAAGATCACTTTAAATCAAA	254483	86679	AGCTCTGCTTTAAACAAAAC	299070	131266	TGGGAGGTTGGCAGCTACAA
209897	42093	TTAAGATCACTTTAAATCAA	254484	86680	CAGCTCTGCTTTAAACAAAA	299071	131267	CTGGGAGGTTGGCAGCTACA
209898	42094	GTTAAGATCACTTTAAATCA	254485	86681	CCAGCTCTGCTTTAAACAAA	299072	131268	TCTGGGAGGTTGGCAGCTAC
209899	42095	AGTTAAGATCACTTTAAATC	254486	86682	ACCAGCTCTGCTTTAAACAA	299073	131269	GTCTGGGAGGTTGGCAGCTA
209900	42096	CAGTTAAGATCACTTTAAAT	254487	86683	CACCAGCTCTGCTTTAAACA	299074	131270	TGTCTGGGAGGTTGGCAGCT
209901	42097	TCAGTTAAGATCACTTTAAA	254488	86684	TCACCAGCTCTGCTTTAAAC	299075	131271	CTGTCTGGGAGGTTGGCAGC
209902	42098	TTCAGTTAAGATCACTTTAA	254489	86685	CTCACCAGCTCTGCTTTAAA	299076	131272	GCTGTCTGGGAGGTTGGCAG
209903	42099	CTTCAGTTAAGATCACTTTA	254490	86686	ACTCACCAGCTCTGCTTTAA	299077	131273	GGCTGTCTGGGAGGTTGGCA
209904	42100	TCTTCAGTTAAGATCACTTT	254491	86687	AACTCACCAGCTCTGCTTTA	299078	131274	GGGCTGTCTGGGAGGTTGGC
209905	42101	CTCTTCAGTTAAGATCACTT	254492	86688	CAACTCACCAGCTCTGCTTT	299079	131275	TGGGCTGTCTGGGAGGTTGG
209906	42102	TCTCTTCAGTTAAGATCACT	254493	86689	GCAACTCACCAGCTCTGCTT	299080	131276	CTGGGCTGTCTGGGAGGTTG
209907	42103	GTCTCTTCAGTTAAGATCAC	254494	86690	TGCAACTCACCAGCTCTGCT	299081	131277	GCTGGGCTGTCTGGGAGGTT
209908	42104	AGTCTCTTCAGTTAAGATCA	254495	86691	ATGCAACTCACCAGCTCTGC	299082	131278	GGCTGGGCTGTCTGGGAGGT
209909	42105	TAGTCTCTTCAGTTAAGATC	254496	86692	TATGCAACTCACCAGCTCTG	299083	131279	GGGCTGGGCTGTCTGGGAGG
209910	42106	TTAGTCTCTTCAGTTAAGAT	254497	86693	CTATGCAACTCACCAGCTCT	299084	131280	CGGGCTGGGCTGTCTGGGAG
209911	42107	ATTAGTCTCTTCAGTTAAGA	254498	86694	CCTATGCAACTCACCAGCTC	299085	131281	GCGGGCTGGGCTGTCTGGGA
209912	42108	CATTAGTCTCTTCAGTTAAG	254499	86695	ACCTATGCAACTCACCAGCT	299086	131282	AGCGGGCTGGGCTGTCTGGG
209913	42109	CCATTAGTCTCTTCAGTTAA	254500	86696	AACCTATGCAACTCACCAGC	299087	131283	CAGCGGGCTGGGCTGTCTGG
209914	42110	TCCATTAGTCTCTTCAGTTA	254501	86697	CAACCTATGCAACTCACCAG	299088	131284	GCAGCGGGCTGGGCTGTCTG
209915	42111	GTCCATTAGTCTCTTCAGTT	254502	86698	ACAACCTATGCAACTCACCA	299089	131285	AGCAGCGGGCTGGGCTGTCT
209916	42112	CGTCCATTAGTCTCTTCAGT	254503	86699	AACAACCTATGCAACTCACC	299090	131286	GAGCAGCGGGCTGGGCTGTC
209917	42113	CCGTCCATTAGTCTCTTCAG	254504	86700	CAACAACCTATGCAACTCAC	299091	131287	TGAGCAGCGGGCTGGGCTGT
209918	42114	CCCGTCCATTAGTCTCTTCA	254505	86701	GCAACAACCTATGCAACTCA	299092	131288	CTGAGCAGCGGGCTGGGCTG
209919	42115	ACCCGTCCATTAGTCTCTTC	254506	86702	TGCAACAACCTATGCAACTC	299093	131289	GCTGAGCAGCGGGCTGGGCT
209920	42116	GACCCGTCCATTAGTCTCTT	254507	86703	ATGCAACAACCTATGCAACT	299094	131290	AGCTGAGCAGCGGGCTGGGC
209921	42117	AGACCCGTCCATTAGTCTCT	254508	86704	AATGCAACAACCTATGCAAC	299095	131291	GAGCTGAGCAGCGGGCTGGG
209922	42118	CAGACCCGTCCATTAGTCTC	254509	86705	CAATGCAACAACCTATGCAA	299096	131292	GGAGCTGAGCAGCGGGCTGG

209923	42119	TCAGACCCGTCCATTAGTCT	254510	86706	CCAATGCAACAACCTATGCA	299097	131293	TGGAGCTGAGCAGCGGGCTG
209924	42120	TTCAGACCCGTCCATTAGTC	254511	86707	CCCAATGCAACAACCTATGC	299098	131294	GTGGAGCTGAGCAGCGGGCT
209925	42121	ATTCAGACCCGTCCATTAGT	254512	86708	TCCCAATGCAACAACCTATG	299099	131295	TGTGGAGCTGAGCAGCGGGC
209926	42122	AATTCAGACCCGTCCATTAG	254513	86709	GTCCCAATGCAACAACCTAT	299100	131296	ATGTGGAGCTGAGCAGCGGG
209927	42123	AAATTCAGACCCGTCCATTA	254514	86710	AGTCCCAATGCAACAACCTA	299101	131297	CATGTGGAGCTGAGCAGCGG
209928	42124	CAAATTCAGACCCGTCCATT	254515	86711	TAGTCCCAATGCAACAACCT	299102	131298	GCATGTGGAGCTGAGCAGCG
209929	42125	ACAAATTCAGACCCGTCCAT	254516	86712	CTAGTCCCAATGCAACAACC	299103	131299	TGCATGTGGAGCTGAGCAGC
209930	42126	CACAAATTCAGACCCGTCCA	254517	86713	TCTAGTCCCAATGCAACAAC	299104	131300	ATGCATGTGGAGCTGAGCAG
209931	42127	GCACAAATTCAGACCCGTCC	254518	86714	ATCTAGTCCCAATGCAACAA	299105	131301	TATGCATGTGGAGCTGAGCA
209932	42128	GGCACAAATTCAGACCCGTC	254519	86715	CATCTAGTCCCAATGCAACA	299106	131302	CTATGCATGTGGAGCTGAGC
209933	42129	AGGCACAAATTCAGACCCGT	254520	86716	CCATCTAGTCCCAATGCAAC	299107	131303	ACTATGCATGTGGAGCTGAG
209934	42130	AAGGCACAAATTCAGACCCG	254521	86717	CCCATCTAGTCCCAATGCAA	299108	131304	TACTATGCATGTGGAGCTGA
209935	42131	AAAGGCACAAATTCAGACCC	254522	86718	CCCCATCTAGTCCCAATGCA	299109	131305	ATACTATGCATGTGGAGCTG
209936	42132	AAAAGGCACAAATTCAGACC	254523	86719	ACCCCATCTAGTCCCAATGC	299110	131306	GATACTATGCATGTGGAGCT
209937	42133	TAAAAGGCACAAATTCAGAC	254524	86720	CACCCCATCTAGTCCCAATG	299111	131307	TGATACTATGCATGTGGAGC
209938	42134	TTAAAAGGCACAAATTCAGA	254525	86721	ACACCCCATCTAGTCCCAAT	299112	131308	CTGATACTATGCATGTGGAG
209939	42135	CTTAAAAGGCACAAATTCAG	254526	86722	AACACCCCATCTAGTCCCAA	299113	131309	GCTGATACTATGCATGTGGA
209940	42136	GCTTAAAAGGCACAAATTCA	254527	86723	GAACACCCCATCTAGTCCCA	299114	131310	GGCTGATACTATGCATGTGG
209941	42137	TGCTTAAAAGGCACAAATTC	254528	86724	TGAACACCCCATCTAGTCCC	299115	131311	GGGCTGATACTATGCATGTG
209942	42138	GTGCTTAAAAGGCACAAATT	254529	86725	TTGAACACCCCATCTAGTCC	299116	131312	AGGGCTGATACTATGCATGT
209943	42139	TGTGCTTAAAAGGCACAAAT	254530	86726	TTTGAACACCCCATCTAGTC	299117	131313	GAGGGCTGATACTATGCATG
209944	42140	TTGTGCTTAAAAGGCACAAA	254531	86727	CTTTGAACACCCCATCTAGT	299118	131314	GGAGGGCTGATACTATGCAT
209945	42141	TTTGTGCTTAAAAGGCACAA	254532	86728	TCTTTGAACACCCCATCTAG	299119	131315	TGGAGGGCTGATACTATGCA
209946	42142	CTTTGTGCTTAAAAGGCACA	254533	86729	CTCTTTGAACACCCCATCTA	299120	131316	GTGGAGGGCTGATACTATGC
209947	42143	ACTTTGTGCTTAAAAGGCAC	254534	86730	ACTCTTTGAACACCCCATCT	299121	131317	TGTGGAGGGCTGATACTATG
209948	42144	TACTTTGTGCTTAAAAGGCA	254535	86731	AACTCTTTGAACACCCCATC	299122	131318	GTGTGGAGGGCTGATACTAT
209949	42145	ATACTTTGTGCTTAAAAGGC	254536	86732	CAACTCTTTGAACACCCCAT	299123	131319	GGTGTGGAGGGCTGATACTA
209950	42146	AATACTTTGTGCTTAAAAGG	254537	86733	CCAACTCTTTGAACACCCCA	299124	131320	GGGTGTGGAGGGCTGATACT
209951	42147	CAATACTTTGTGCTTAAAAG	254538	86734	CCCAACTCTTTGAACACCCC	299125	131321	CGGGTGTGGAGGGCTGATAC
209952	42148	GCAATACTTTGTGCTTAAAA	254539	86735	TCCCAACTCTTTGAACACCC	299126	131322	TCGGGTGTGGAGGGCTGATA
209953	42149	AGCAATACTTTGTGCTTAAA	254540	86736	CTCCCAACTCTTTGAACACC	299127	131323	GTCGGGTGTGGAGGGCTGAT
209954	42150	GAGCAATACTTTGTGCTTAA	254541	86737	ACTCCCAACTCTTTGAACAC	299128	131324	TGTCGGGTGTGGAGGGCTGA
209955	42151	AGAGCAATACTTTGTGCTTA	254542	86738	AACTCCCAACTCTTTGAACA	299129	131325	TTGTCGGGTGTGGAGGGCTG
209956	42152	AAGAGCAATACTTTGTGCTT	254543	86739	TAACTCCCAACTCTTTGAAC	299130	131326	TTTGTCGGGTGTGGAGGGCT
209957	42153	TAAGAGCAATACTTTGTGCT	254544	86740	TTAACTCCCAACTCTTTGAA	299131	131327	CTTTGTCGGGTGTGGAGGGC
209958	42154	TTAAGAGCAATACTTTGTGC	254545	86741	TTTAACTCCCAACTCTTTGA	299132	131328	CCTTTGTCGGGTGTGGAGGG
209959	42155	ATTAAGAGCAATACTTTGTG	254546	86742	TTTTAACTCCCAACTCTTTG	299133	131329	CCCTTTGTCGGGTGTGGAGG
209960	42156	AATTAAGAGCAATACTTTGT	254547	86743	TTTTTAACTCCCAACTCTTT	299134	131330	CCCCTTTGTCGGGTGTGGAG
209961	42157	TAATTAAGAGCAATACTTTG	254548	86744	TTTTTTAACTCCCAACTCTT	299135	131331	TCCCCTTTGTCGGGTGTGGA
209962	42158	TTAATTAAGAGCAATACTTT	254549	86745	GTTTTTTAACTCCCAACTCT	299136	131332	TTCCCCTTTGTCGGGTGTGG
209963	42159	GTTAATTAAGAGCAATACTT	254550	86746	TGTTTTTTAACTCCCAACTC	299137	131333	GTTCCCCTTTGTCGGGTGTG
209964	42160	AGTTAATTAAGAGCAATACT	254551	86747	ATGTTTTTTAACTCCCAACT	299138	131334	TGTTCCCCTTTGTCGGGTGT
209965	42161	CAGTTAATTAAGAGCAATAC	254552	86748	TATGTTTTTTAACTCCCAAC	299139	131335	GTGTTCCCCTTTGTCGGGTG
209966	42162	CCAGTTAATTAAGAGCAATA	254553	86749	TTATGTTTTTTAACTCCCAA	299140	131336	TGTGTTCCCCTTTGTCGGGT
209967	42163	TCCAGTTAATTAAGAGCAAT	254554	86750	TTTATGTTTTTTAACTCCCA	299141	131337	GTGTGTTCCCCTTTGTCGGG
209968	42164	ATCCAGTTAATTAAGAGCAA	254555	86751	CTTTATGTTTTTTAACTCCC	299142	131338	GGTGTGTTCCCCTTTGTCGG
209969	42165	AATCCAGTTAATTAAGAGCA	254556	86752	CCTTTATGTTTTTTAACTCC	299143	131339	GGGTGTGTTCCCCTTTGTCG
209970	42166	GAATCCAGTTAATTAAGAGC	254557	86753	CCCTTTATGTTTTTTAACTC	299144	131340	GGGGTGTGTTCCCCTTTGTC
209971	42167	AGAATCCAGTTAATTAAGAG	254558	86754	ACCCTTTATGTTTTTTAACT	299145	131341	GGGGGGTGTGTTCCCCTTTGT
209972	42168	TAGAATCCAGTTAATTAAGA	254559	86755	TACCCTTTATGTTTTTTAAC	299146	131342	AGGGGGTGTGTTCCCCTTTG
209973	42169	ATAGAATCCAGTTAATTAAG	254560	86756	ATACCCTTTATGTTTTTTAA	299147	131343	AAGGGGGTGTGTTCCCCTTT
209974	42170	GATAGAATCCAGTTAATTAA	254561	86757	AATACCCTTTATGTTTTTTA	299148	131344	CAAGGGGGTGTGTTCCCCTT
209975	42171	GGATAGAATCCAGTTAATTA	254562	86758	AAATACCCTTTATGTTTTTT	299149	131345	CCAAGGGGGTGTGTTCCCCT
209976	42172	AGGATAGAATCCAGTTAATT	254563	86759	TAAATACCCTTTATGTTTTT	299150	131346	TCCAAGGGGGTGTGTTCCCC
209977	42173	AAGGATAGAATCCAGTTAAT	254564	86760	ATAAATACCCTTTATGTTTT	299151	131347	TTCCAAGGGGGTGTGTTCCC
209978	42174	AAAGGATAGAATCCAGTTAA	254565	86761	AATAAATACCCTTTATGTTT	299152	131348	TTTCCAAGGGGGTGTGTTCC
209979	42175	CAAAGGATAGAATCCAGTTA	254566	86762	TAATAAATACCCTTTATGTT	299153	131349	ATTTCCAAGGGGGTGTGTTC
209980	42176	TCAAAGGATAGAATCCAGTT	254567	86763	CTAATAAATACCCTTTATGT	299154	131350	CATTTCCAAGGGGGTGTGTT
209981	42177	CTCAAAGGATAGAATCCAGT	254568	86764	CCTAATAAATACCCTTTATG	299155	131351	CCATTTCCAAGGGGGTGTGT
209982	42178	GCTCAAAGGATAGAATCCAG	254569	86765	TCCTAATAAATACCCTTTAT	299156	131352	ACCATTTCCAAGGGGGTGTG
209983	42179	TGCTCAAAGGATAGAATCCA	254570	86766	CTCCTAATAAATACCCTTTA	299157	131353	AACCATTTCCAAGGGGGTGT
209984	42180	CTGCTCAAAGGATAGAATCC	254571	86767	TCTCCTAATAAATACCCTTT	299158	131354	GAACCATTTCCAAGGGGGTG
209985	42181	CCTGCTCAAAGGATAGAATC	254572	86768	TTCTCCTAATAAATACCCTT	299159	131355	AGAACCATTTCCAAGGGGGT
209986	42182	GCCTGCTCAAAGGATAGAAT	254573	86769	GTTCTCCTAATAAATACCCT	299160	131356	AAGAACCATTTCCAAGGGGG
209987	42183	TGCCTGCTCAAAGGATAGAA	254574	86770	GGTTCTCCTAATAAATACCC	299161	131357	AAAGAACCATTTCCAAGGGG
209988	42184	CTGCCTGCTCAAAGGATAGA	254575	86771	TGGTTCTCCTAATAAATACC	299162	131358	AAAAGAACCATTTCCAAGGG
209989	42185	TCTGCCTGCTCAAAGGATAG	254576	86772	TTGGTTCTCCTAATAAATAC	299163	131359	GAAAAGAACCATTTCCAAGG
209990	42186	CTCTGCCTGCTCAAAGGATA	254577	86773	CTTGGTTCTCCTAATAAATA	299164	131360	GGAAAAGAACCATTTCCAAG
209991	42187	CCTCTGCCTGCTCAAAGGAT	254578	86774	CCTTGGTTCTCCTAATAAAT	299165	131361	GGGAAAAGAACCATTTCCAA
209992	42188	GCCTCTGCCTGCTCAAAGGA	254579	86775	TCCTTGGTTCTCCTAATAAA	299166	131362	GGGGAAAAGAACCATTTCCA
209993	42189	GGCCTCTGCCTGCTCAAAGG	254580	86776	CTCCTTGGTTCTCCTAATAA	299167	131363	GGGGGAAAAGAACCATTTCC
209994	42190	AGGCCTCTGCCTGCTCAAAG	254581	86777	ACTCCTTGGTTCTCCTAATA	299168	131364	TGGGGGAAAAGAACCATTTC

209995	42191	AAGGCCTCTGCCTGCTCAAA	254582	86778	CACTCCTTGGTTCTCCTAAT	299169	131365	CTGGGGGAAAAGAACCATTT
209996	42192	GAAGGCCTCTGCCTGCTCAA	254583	86779	ACACTCCTTGGTTCTCCTAA	299170	131366	ACTGGGGGAAAAGAACCATT
209997	42193	GGAAGGCCTCTGCCTGCTCA	254584	86780	TACACTCCTTGGTTCTCCTA	299171	131367	GACTGGGGGAAAAGAACCAT
209998	42194	GGGAAGGCCTCTGCCTGCTC	254585	86781	TTACACTCCTTGGTTCTCCT	299172	131368	GGACTGGGGGAAAAGAACCA
209999	42195	GGGGAAGGCCTCTGCCTGCT	254586	86782	ATTACACTCCTTGGTTCTCC	299173	131369	GGGACTGGGGGAAAAGAACC
210000	42196	GGGGGAAGGCCTCTGCCTGC	254587	86783	AATTACACTCCTTGGTTCTC	299174	131370	TGGGACTGGGGGAAAAGAAC
210001	42197	TGGGGGAAGGCCTCTGCCTG	254588	86784	GAATTACACTCCTTGGTTCT	299175	131371	CTGGGACTGGGGGAAAAGAA
210002	42198	TTGGGGGAAGGCCTCTGCCT	254589	86785	AGAATTACACTCCTTGGTTC	299176	131372	GCTGGGACTGGGGGAAAAGA
210003	42199	CTTGGGGGAAGGCCTCTGCC	254590	86786	GAGAATTACACTCCTTGGTT	299177	131373	AGCTGGGACTGGGGGAAAAG
210004	42200	CCTTGGGGGAAGGCCTCTGC	254591	86787	GGAGAATTACACTCCTTGGT	299178	131374	CAGCTGGGACTGGGGGAAAA
210005	42201	CCCTTGGGGGAAGGCCTCTG	254592	86788	AGGAGAATTACACTCCTTGG	299179	131375	CCAGCTGGGACTGGGGGAAA
210006	42202	GCCCTTGGGGGAAGGCCTCT	254593	86789	CAGGAGAATTACACTCCTTG	299180	131376	TCCAGCTGGGACTGGGGGAA
210007	42203	CGCCCTTGGGGGAAGGCCTC	254594	86790	ACAGGAGAATTACACTCCTT	299181	131377	TTCCAGCTGGGACTGGGGGA
210008	42204	ACGCCCTTGGGGGAAGGCCT	254595	86791	AACAGGAGAATTACACTCCT	299182	131378	CTTCCAGCTGGGACTGGGGG
210009	42205	GACGCCCTTGGGGGAAGGCC	254596	86792	GAACAGGAGAATTACACTCC	299183	131379	GCTTCCAGCTGGGACTGGGG
210010	42206	TGACGCCCTTGGGGGAAGGC	254597	86793	AGAACAGGAGAATTACACTC	299184	131380	GGCTTCCAGCTGGGACTGGG
210011	42207	ATGACGCCCTTGGGGGAAGG	254598	86794	AAGAACAGGAGAATTACACT	299185	131381	TGGCTTCCAGCTGGGACTGG
210012	42208	AATGACGCCCTTGGGGGAAG	254599	86795	TAAGAACAGGAGAATTACAC	299186	131382	ATGGCTTCCAGCTGGGACTG
210013	42209	TAATGACGCCCTTGGGGGAA	254600	86796	TTAAGAACAGGAGAATTACA	299187	131383	CATGGCTTCCAGCTGGGACT
210014	42210	TTAATGACGCCCTTGGGGGA	254601	86797	ATTAAGAACAGGAGAATTAC	299188	131384	GCATGGCTTCCAGCTGGGAC
210015	42211	GTTAATGACGCCCTTGGGGG	254602	86798	TATTAAGAACAGGAGAATTA	299189	131385	AGCATGGCTTCCAGCTGGGA
210016	42212	CGTTAATGACGCCCTTGGGG	254603	86799	ATATTAAGAACAGGAGAATT	299190	131386	CAGCATGGCTTCCAGCTGGG
210017	42213	TCGTTAATGACGCCCTTGGG	254604	86800	CATATTAAGAACAGGAGAAT	299191	131387	ACAGCATGGCTTCCAGCTGG
210018	42214	ATCGTTAATGACGCCCTTGG	254605	86801	GCATATTAAGAACAGGAGAA	299192	131388	GACAGCATGGCTTCCAGCTG
210019	42215	GATCGTTAATGACGCCCTTG	254606	86802	CGCATATTAAGAACAGGAGA	299193	131389	AGACAGCATGGCTTCCAGCT
210020	42216	GGATCGTTAATGACGCCCTT	254607	86803	CCGCATATTAAGAACAGGAG	299194	131390	CAGACAGCATGGCTTCCAGC
210021	42217	TGGATCGTTAATGACGCCCT	254608	86804	GCCGCATATTAAGAACAGGA	299195	131391	ACAGACAGCATGGCTTCCAG
210022	42218	GTGGATCGTTAATGACGCCC	254609	86805	GGCCGCATATTAAGAACAGG	299196	131392	AACAGACAGCATGGCTTCCA
210023	42219	TGTGGATCGTTAATGACGCC	254610	86806	TGGCCGCATATTAAGAACAG	299197	131393	GAACAGACAGCATGGCTTCC
210024	42220	ATGTGGATCGTTAATGACGC	254611	86807	CTGGCCGCATATTAAGAACA	299198	131394	AGAACAGACAGCATGGCTTC
210025	42221	GATGTGGATCGTTAATGACG	254612	86808	CCTGGCCGCATATTAAGAAC	299199	131395	CAGAACAGACAGCATGGCTT
210026	42222	AGATGTGGATCGTTAATGAC	254613	86809	ACCTGGCCGCATATTAAGAA	299200	131396	GCAGAACAGACAGCATGGCT
210027	42223	CAGATGTGGATCGTTAATGA	254614	86810	AACCTGGCCGCATATTAAGA	299201	131397	AGCAGAACAGACAGCATGGC
210028	42224	CCAGATGTGGATCGTTAATG	254615	86811	TAACCTGGCCGCATATTAAG	299202	131398	CAGCAGAACAGACAGCATGG
210029	42225	TCCAGATGTGGATCGTTAAT	254616	86812	TTAACCTGGCCGCATATTAA	299203	131399	CCAGCAGAACAGACAGCATG
210030	42226	GTCCAGATGTGGATCGTTAA	254617	86813	ATTAACCTGGCCGCATATTA	299204	131400	TCCAGCAGAACAGACAGCAT
210031	42227	TGTCCAGATGTGGATCGTTA	254618	86814	CATTAACCTGGCCGCATATT	299205	131401	CTCCAGCAGAACAGACAGCA
210032	42228	ATGTCCAGATGTGGATCGTT	254619	86815	TCATTAACCTGGCCGCATAT	299206	131402	GCTCCAGCAGAACAGACAGC
210033	42229	GATGTCCAGATGTGGATCGT	254620	86816	TTCATTAACCTGGCCGCATA	299207	131403	TGCTCCAGCAGAACAGACAG
210034	42230	AGATGTCCAGATGTGGATCG	254621	86817	ATTCATTAACCTGGCCGCAT	299208	131404	CTGCTCCAGCAGAACAGACA
210035	42231	AAGATGTCCAGATGTGGATC	254622	86818	CATTCATTAACCTGGCCGCA	299209	131405	GCTGCTCCAGCAGAACAGAC
210036	42232	GAAGATGTCCAGATGTGGAT	254623	86819	ACATTCATTAACCTGGCCGC	299210	131406	AGCTGCTCCAGCAGAACAGA
210037	42233	GGAAGATGTCCAGATGTGGA	254624	86820	GACATTCATTAACCTGGCCG	299211	131407	CAGCTGCTCCAGCAGAACAG
210038	42234	TGGAAGATGTCCAGATGTGG	254625	86821	TGACATTCATTAACCTGGCC	299212	131408	TCAGCTGCTCCAGCAGAACA
210039	42235	TTGGAAGATGTCCAGATGTG	254626	86822	GTGACATTCATTAACCTGGC	299213	131409	TTCAGCTGCTCCAGCAGAAC
210040	42236	TTTGGAAGATGTCCAGATGT	254627	86823	CGTGACATTCATTAACCTGG	299214	131410	GTTCAGCTGCTCCAGCAGAA
210041	42237	CTTTGGAAGATGTCCAGATG	254628	86824	ACGTGACATTCATTAACCTG	299215	131411	TGTTCAGCTGCTCCAGCAGA
210042	42238	GCTTTGGAAGATGTCCAGAT	254629	86825	CACGTGACATTCATTAACCT	299216	131412	ATGTTCAGCTGCTCCAGCAG
210043	42239	GGCTTTGGAAGATGTCCAGA	254630	86826	TCACGTGACATTCATTAACC	299217	131413	TATGTTCAGCTGCTCCAGCA
210044	42240	AGGCTTTGGAAGATGTCCAG	254631	86827	TTCACGTGACATTCATTAAC	299218	131414	ATATGTTCAGCTGCTCCAGC
210045	42241	AAGGCTTTGGAAGATGTCCA	254632	86828	ATTCACGTGACATTCATTAA	299219	131415	TATATGTTCAGCTGCTCCAG
210046	42242	GAAGGCTTTGGAAGATGTCC	254633	86829	CATTCACGTGACATTCATTA	299220	131416	GTATATGTTCAGCTGCTCCA
210047	42243	AGAAGGCTTTGGAAGATGTC	254634	86830	TCATTCACGTGACATTCATT	299221	131417	TGTATATGTTCAGCTGCTCC
210048	42244	AAGAAGGCTTTGGAAGATGT	254635	86831	TTCATTCACGTGACATTCAT	299222	131418	ATGTATATGTTCAGCTGCTC
210049	42245	GAAGAAGGCTTTGGAAGATG	254636	86832	GTTCATTCACGTGACATTCA	299223	131419	TATGTATATGTTCAGCTGCT
210050	42246	AGAAGAAGGCTTTGGAAGAT	254637	86833	GGTTCATTCACGTGACATTC	299224	131420	CTATGTATATGTTCAGCTGC
210051	42247	CAGAAGAAGGCTTTGGAAGA	254638	86834	TGGTTCATTCACGTGACATT	299225	131421	TCTATGTATATGTTCAGCTG
210052	42248	ACAGAAGAAGGCTTTGGAAG	254639	86835	CTGGTTCATTCACGTGACAT	299226	131422	ATCTATGTATATGTTCAGCT
210053	42249	AACAGAAGAAGGCTTTGGAA	254640	86836	TCTGGTTCATTCACGTGACA	299227	131423	CATCTATGTATATGTTCAGC
210054	42250	AAACAGAAGAAGGCTTTGGA	254641	86837	TTCTGGTTCATTCACGTGAC	299228	131424	ACATCTATGTATATGTTCAG
210055	42251	GAAACAGAAGAAGGCTTTGG	254642	86838	TTTCTGGTTCATTCACGTGA	299229	131425	AACATCTATGTATATGTTCA
210056	42252	TGAAACAGAAGAAGGCTTTG	254643	86839	TTTTCTGGTTCATTCACGTG	299230	131426	CAACATCTATGTATATGTTC
210057	42253	CTGAAACAGAAGAAGGCTTT	254644	86840	TTTTTCTGGTTCATTCACGT	299231	131427	GCAACATCTATGTATATGTT
210058	42254	CCTGAAACAGAAGAAGGCTT	254645	86841	TTTTTTCTGGTTCATTCACG	299232	131428	GGCAACATCTATGTATATGT
210059	42255	GCCTGAAACAGAAGAAGGCT	254646	86842	TTTTTTTCTGGTTCATTCAC	299233	131429	GGGCAACATCTATGTATATG
210060	42256	GGCCTGAAACAGAAGAAGGC	254647	86843	ATTTTTTTCTGGTTCATTCA	299234	131430	AGGGCAACATCTATGTATAT
210061	42257	TGGCCTGAAACAGAAGAAGG	254648	86844	CATTTTTTTCTGGTTCATTC	299235	131431	CAGGGCAACATCTATGTATA
210062	42258	TTGGCCTGAAACAGAAGAAG	254649	86845	TCATTTTTTTCTGGTTCATT	299236	131432	GCAGGGCAACATCTATGTAT
210063	42259	GTTGGCCTGAAACAGAAGAA	254650	86846	TTCATTTTTTTCTGGTTCAT	299237	131433	GGCAGGGCAACATCTATGTA
210064	42260	GGTTGGCCTGAAACAGAAGA	254651	86847	CTTCATTTTTTTCTGGTTCA	299238	131434	GGGCAGGGCAACATCTATGT
210065	42261	CGGTTGGCCTGAAACAGAAG	254652	86848	ACTTCATTTTTTTCTGGTTC	299239	131435	AGGGCAGGGCAACATCTATG
210066	42262	GCGGTTGGCCTGAAACAGAA	254653	86849	CACTTCATTTTTTTCTGGTT	299240	131436	GAGGGCAGGGCAACATCTAT

210067	42263	TGCGGTTGGCCTGAAACAGA	254654	86850	ACACTTCATTTTTTTCTGGT	299241	131437	GGAGGGCAGGGCAACATCTA
210068	42264	CTGCGGTTGGCCTGAAACAG	254655	86851	CACACTTCATTTTTTTCTGG	299242	131438	GGGAGGGCAGGGCAACATCT
210069	42265	CCTGCGGTTGGCCTGAAACA	254656	86852	GCACACTTCATTTTTTTCTG	299243	131439	GGGGAGGGCAGGGCAACATC
210070	42266	ACCTGCGGTTGGCCTGAAAC	254657	86853	GGCACACTTCATTTTTTTCT	299244	131440	TGGGGAGGGCAGGGCAACAT
210071	42267	CACCTGCGGTTGGCCTGAAA	254658	86854	GGGCACACTTCATTTTTTTC	299245	131441	ATGGGGAGGGCAGGGCAACA
210072	42268	ACACCTGCGGTTGGCCTGAA	254659	86855	AGGGCACACTTCATTTTTTT	299246	131442	GATGGGGAGGGCAGGGCAAC
210073	42269	CACACCTGCGGTTGGCCTGA	254660	86856	AAGGGCACACTTCATTTTTT	299247	131443	AGATGGGGAGGGCAGGGCAA
210074	42270	ACACACCTGCGGTTGGCCTG	254661	86857	CAAGGGCACACTTCATTTTT	299248	131444	CAGATGGGGAGGGCAGGGCA
210075	42271	AACACACCTGCGGTTGGCCT	254662	86858	TCAAGGGCACACTTCATTTT	299249	131445	GCAGATGGGGAGGGCAGGGC
210076	42272	GAACACACCTGCGGTTGGCC	254663	86859	ATCAAGGGCACACTTCATTT	299250	131446	TGCAGATGGGGAGGGCAGGG
210077	42273	GGAACACACCTGCGGTTGGC	254664	86860	GATCAAGGGCACACTTCATT	299251	131447	GTGCAGATGGGGAGGGCAGG
210078	42274	AGGAACACACCTGCGGTTGG	254665	86861	TGATCAAGGGCACACTTCAT	299252	131448	GGTGCAGATGGGGAGGGCAG
210079	42275	CAGGAACACACCTGCGGTTG	254666	86862	CTGATCAAGGGCACACTTCA	299253	131449	GGGTGCAGATGGGGAGGGCA
210080	42276	TCAGGAACACACCTGCGGTT	254667	86863	GCTGATCAAGGGCACACTTC	299254	131450	AGGGTGCAGATGGGGAGGGC
210081	42277	TTCAGGAACACACCTGCGGT	254668	86864	AGCTGATCAAGGGCACACTT	299255	131451	CAGGGTGCAGATGGGGAGGG
210082	42278	GTTCAGGAACACACCTGCGG	254669	86865	CAGCTGATCAAGGGCACACT	299256	131452	ACAGGGTGCAGATGGGGAGG
210083	42279	TGTTCAGGAACACACCTGCG	254670	86866	CCAGCTGATCAAGGGCACAC	299257	131453	AACAGGGTGCAGATGGGGAG
210084	42280	GTGTTCAGGAACACACCTGC	254671	86867	CCCAGCTGATCAAGGGCACA	299258	131454	CAACAGGGTGCAGATGGGGA
210085	42281	GGTGTTCAGGAACACACCTG	254672	86868	ACCCAGCTGATCAAGGGCAC	299259	131455	TCAACAGGGTGCAGATGGGG
210086	42282	GGGTGTTCAGGAACACACCT	254673	86869	AACCCAGCTGATCAAGGGCA	299260	131456	CTCAACAGGGTGCAGATGGG
210087	42283	TGGGTGTTCAGGAACACACC	254674	86870	CAACCCAGCTGATCAAGGGC	299261	131457	ACTCAACAGGGTGCAGATGG
210088	42284	CTGGGTGTTCAGGAACACAC	254675	86871	CCAACCCAGCTGATCAAGGG	299262	131458	AACTCAACAGGGTGCAGATG
210089	42285	CCTGGGTGTTCAGGAACACA	254676	86872	ACCAACCCAGCTGATCAAGG	299263	131459	CAACTCAACAGGGTGCAGAT
210090	42286	TCCTGGGTGTTCAGGAACAC	254677	86873	CACCAACCCAGCTGATCAAG	299264	131460	ACAACTCAACAGGGTGCAGA
210091	42287	CTCCTGGGTGTTCAGGAACA	254678	86874	ACACCAACCCAGCTGATCAA	299265	131461	TACAACTCAACAGGGTGCAG
210092	42288	CCTCCTGGGTGTTCAGGAAC	254679	86875	CACACCAACCCAGCTGATCA	299266	131462	CTACAACTCAACAGGGTGCA
210093	42289	GCCTCCTGGGTGTTCAGGAA	254680	86876	GCACACCAACCCAGCTGATC	299267	131463	ACTACAACTCAACAGGGTGC
210094	42290	AGCCTCCTGGGTGTTCAGGA	254681	86877	TGCACACCAACCCAGCTGAT	299268	131464	AACTACAACTCAACAGGGTG
210095	42291	TAGCCTCCTGGGTGTTCAGG	254682	86878	CTGCACACCAACCCAGCTGA	299269	131465	CAACTACAACTCAACAGGGT
210096	42292	ATAGCCTCCTGGGTGTTCAG	254683	86879	GCTGCACACCAACCCAGCTG	299270	131466	CCAACTACAACTCAACAGGG
210097	42293	CATAGCCTCCTGGGTGTTCA	254684	86880	TGCTGCACACCAACCCAGCT	299271	131467	TCCAACTACAACTCAACAGG
210098	42294	TCATAGCCTCCTGGGTGTTC	254685	86881	TTGCTGCACACCAACCCAGC	299272	131468	ATCCAACTACAACTCAACAG
210099	42295	CTCATAGCCTCCTGGGTGTT	254686	86882	CTTGCTGCACACCAACCCAG	299273	131469	AATCCAACTACAACTCAACA
210100	42296	TCTCATAGCCTCCTGGGTGT	254687	86883	GCTTGCTGCACACCAACCCA	299274	131470	AAATCCAACTACAACTCAAC
210101	42297	CTCTCATAGCCTCCTGGGTG	254688	86884	AGCTTGCTGCACACCAACCC	299275	131471	CAAATCCAACTACAACTCAA
210102	42298	GCTCTCATAGCCTCCTGGGT	254689	86885	CAGCTTGCTGCACACCAACC	299276	131472	ACAAATCCAACTACAACTCA
210103	42299	GGCTCTCATAGCCTCCTGGG	254690	86886	ACAGCTTGCTGCACACCAAC	299277	131473	GACAAATCCAACTACAACTC
210104	42300	TGGCTCTCATAGCCTCCTGG	254691	86887	CACAGCTTGCTGCACACCAA	299278	131474	AGACAAATCCAACTACAACT
210105	42301	GTGGCTCTCATAGCCTCCTG	254692	86888	ACACAGCTTGCTGCACACCA	299279	131475	CAGACAAATCCAACTACAAC
210106	42302	TGTGGCTCTCATAGCCTCCT	254693	86889	CACACAGCTTGCTGCACACC	299280	131476	ACAGACAAATCCAACTACAA
210107	42303	ATGTGGCTCTCATAGCCTCC	254694	86890	TCACACAGCTTGCTGCACAC	299281	131477	AACAGACAAATCCAACTACA
210108	42304	TATGTGGCTCTCATAGCCTC	254695	86891	GTCACACAGCTTGCTGCACA	299282	131478	AAACAGACAAATCCAACTAC
210109	42305	ATATGTGGCTCTCATAGCCT	254696	86892	GGTCACACAGCTTGCTGCAC	299283	131479	TAAACAGACAAATCCAACTA
210110	42306	CATATGTGGCTCTCATAGCC	254697	86893	TGGTCACACAGCTTGCTGCA	299284	131480	ATAAACAGACAAATCCAACT
210111	42307	GCATATGTGGCTCTCATAGC	254698	86894	CTGGTCACACAGCTTGCTGC	299285	131481	CATAAACAGACAAATCCAAC
210112	42308	GGCATATGTGGCTCTCATAG	254699	86895	CCTGGTCACACAGCTTGCTG	299286	131482	GCATAAACAGACAAATCCAA
210113	42309	AGGCATATGTGGCTCTCATA	254700	86896	CCCTGGTCACACAGCTTGCT	299287	131483	AGCATAAACAGACAAATCCA
210114	42310	GAGGCATATGTGGCTCTCAT	254701	86897	CCCCTGGTCACACAGCTTGC	299288	131484	AAGCATAAACAGACAAATCC
210115	42311	GGAGGCATATGTGGCTCTCA	254702	86898	TCCCCTGGTCACACAGCTTG	299289	131485	CAAGCATAAACAGACAAATC
210116	42312	GGGAGGCATATGTGGCTCTC	254703	86899	GTCCCCTGGTCACACAGCTT	299290	131486	CCAAGCATAAACAGACAAAT
210117	42313	TGGGAGGCATATGTGGCTCT	254704	86900	TGTCCCCTGGTCACACAGCT	299291	131487	TCCAAGCATAAACAGACAAA
210118	42314	TTGGGAGGCATATGTGGCTC	254705	86901	CTGTCCCCTGGTCACACAGC	299292	131488	ATCCAAGCATAAACAGACAA
210119	42315	TTTGGGAGGCATATGTGGCT	254706	86902	GCTGTCCCCTGGTCACACAG	299293	131489	AATCCAAGCATAAACAGACA
210120	42316	ATTTGGGAGGCATATGTGGC	254707	86903	TGCTGTCCCCTGGTCACACA	299294	131490	GAATCCAAGCATAAACAGAC
210121	42317	TATTTGGGAGGCATATGTGG	254708	86904	CTGCTGTCCCCTGGTCACAC	299295	131491	TGAATCCAAGCATAAACAGA
210122	42318	GTATTTGGGAGGCATATGTG	254709	86905	ACTGCTGTCCCCTGGTCACA	299296	131492	GTGAATCCAAGCATAAACAG
210123	42319	TGTATTTGGGAGGCATATGT	254710	86906	CACTGCTGTCCCCTGGTCAC	299297	131493	GGTGAATCCAAGCATAAACA
210124	42320	GTGTATTTGGGAGGCATATG	254711	86907	CCACTGCTGTCCCCTGGTCA	299298	131494	TGGTGAATCCAAGCATAAAC
210125	42321	TGTGTATTTGGGAGGCATAT	254712	86908	ACCACTGCTGTCCCCTGGTC	299299	131495	CTGGTGAATCCAAGCATAAA
210126	42322	GTGTGTATTTGGGAGGCATA	254713	86909	GACCACTGCTGTCCCCTGGT	299300	131496	TCTGGTGAATCCAAGCATAA
210127	42323	TGTGTGTATTTGGGAGGCAT	254714	86910	GGACCACTGCTGTCCCCTGG	299301	131497	CTCTGGTGAATCCAAGCATA
210128	42324	CTGTGTGTATTTGGGAGGCA	254715	86911	AGGACCACTGCTGTCCCCTG	299302	131498	ACTCTGGTGAATCCAAGCAT
210129	42325	ACTGTGTGTATTTGGGAGGC	254716	86912	CAGGACCACTGCTGTCCCCT	299303	131499	CACTCTGGTGAATCCAAGCA
210130	42326	CACTGTGTGTATTTGGGAGG	254717	86913	TCAGGACCACTGCTGTCCCC	299304	131500	TCACTCTGGTGAATCCAAGC
210131	42327	ACACTGTGTGTATTTGGGAG	254718	86914	CTCAGGACCACTGCTGTCCC	299305	131501	GTCACTCTGGTGAATCCAAG
210132	42328	CACACTGTGTGTATTTGGGA	254719	86915	CCTCAGGACCACTGCTGTCC	299306	131502	AGTCACTCTGGTGAATCCAA
210133	42329	GCACACTGTGTGTATTTGGG	254720	86916	CCCTCAGGACCACTGCTGTC	299307	131503	TAGTCACTCTGGTGAATCCA
210134	42330	TGCACACTGTGTGTATTTGG	254721	86917	GCCCTCAGGACCACTGCTGT	299308	131504	ATAGTCACTCTGGTGAATCC
210135	42331	ATGCACACTGTGTGTATTTG	254722	86918	GGCCCTCAGGACCACTGCTG	299309	131505	CATAGTCACTCTGGTGAATC
210136	42332	CATGCACACTGTGTGTATTT	254723	86919	CGGCCCTCAGGACCACTGCT	299310	131506	TCATAGTCACTCTGGTGAAT
210137	42333	GCATGCACACTGTGTGTATT	254724	86920	ACGGCCCTCAGGACCACTGC	299311	131507	ATCATAGTCACTCTGGTGAA
210138	42334	GGCATGCACACTGTGTGTAT	254725	86921	GACGGCCCTCAGGACCACTG	299312	131508	TATCATAGTCACTCTGGTGA

210139	42335	GGGCATGCACACTGTGTGTA	254726	86922	TGACGGCCCTCAGGACCACT	299313	131509	CTATCATAGTCACTCTGGTG
210140	42336	TGGGCATGCACACTGTGTGT	254727	86923	GTGACGGCCCTCAGGACCAC	299314	131510	ACTATCATAGTCACTCTGGT
210141	42337	CTGGGCATGCACACTGTGTG	254728	86924	AGTGACGGCCCTCAGGACCA	299315	131511	CACTATCATAGTCACTCTGG
210142	42338	CCTGGGCATGCACACTGTGT	254729	86925	CAGTGACGGCCCTCAGGACC	299316	131512	TCACTATCATAGTCACTCTG
210143	42339	CCCTGGGCATGCACACTGTG	254730	86926	ACAGTGACGGCCCTCAGGAC	299317	131513	TTCACTATCATAGTCACTCT
210144	42340	TCCCTGGGCATGCACACTGT	254731	86927	GACAGTGACGGCCCTCAGGA	299318	131514	TTTCACTATCATAGTCACTC
210145	42341	GTCCCTGGGCATGCACACTG	254732	86928	AGACAGTGACGGCCCTCAGG	299319	131515	TTTTCACTATCATAGTCACT
210146	42342	TGTCCCTGGGCATGCACACT	254733	86929	CAGACAGTGACGGCCCTCAG	299320	131516	CTTTTCACTATCATAGTCAC
210147	42343	ATGTCCCTGGGCATGCACAC	254734	86930	GCAGACAGTGACGGCCCTCA	299321	131517	TCTTTTCACTATCATAGTCA
210148	42344	TATGTCCCTGGGCATGCACA	254735	86931	GGCAGACAGTGACGGCCCTC	299322	131518	TTCTTTTCACTATCATAGTC
210149	42345	CTATGTCCCTGGGCATGCAC	254736	86932	CGGCAGACAGTGACGGCCCT	299323	131519	TTTCTTTTCACTATCATAGT
210150	42346	TCTATGTCCCTGGGCATGCA	254737	86933	ACGGCAGACAGTGACGGCCC	299324	131520	TTTTCTTTTCACTATCATAG
210151	42347	CTCTATGTCCCTGGGCATGC	254738	86934	CACGGCAGACAGTGACGGCC	299325	131521	TTTTTCTTTTCACTATCATA
210152	42348	GCTCTATGTCCCTGGGCATG	254739	86935	GCACGGCAGACAGTGACGGC	299326	131522	TTTTTTCTTTTCACTATCAT
210153	42349	TGCTCTATGTCCCTGGGCAT	254740	86936	TGCACGGCAGACAGTGACGG	299327	131523	TTTTTTTCTTTTCACTATCA
210154	42350	CTGCTCTATGTCCCTGGGCA	254741	86937	CTGCACGGCAGACAGTGACG	299328	131524	TTTTTTTTCTTTTCACTATC
210155	42351	ACTGCTCTATGTCCCTGGGC	254742	86938	TCTGCACGGCAGACAGTGAC	299329	131525	TTTTTTTTTCTTTTCACTAT
210156	42352	CACTGCTCTATGTCCCTGGG	254743	86939	CTCTGCACGGCAGACAGTGA	299330	131526	TTTTTTTTTTCTTTTCACTA
210157	42353	ACACTGCTCTATGTCCCTGG	254744	86940	GCTCTGCACGGCAGACAGTG	299331	131527	TTTTTTTTTTTCTTTTCACT
210158	42354	CACACTGCTCTATGTCCCTG	254745	86941	GGCTCTGCACGGCAGACAGT	299332	131528	TTTTTTTTTTTTCTTTTCAC
210159	42355	GCACACTGCTCTATGTCCCT	254746	86942	GGGCTCTGCACGGCAGACAG	299333	131529	TTTTTTTTTTTTTCTTTTCA
210160	42356	TGCACACTGCTCTATGTCCC	254747	86943	AGGGCTCTGCACGGCAGACA	299334	131530	TTTTTTTTTTTTTTCTTTTC
210161	42357	TTGCACACTGCTCTATGTCC	254748	86944	AAGGGCTCTGCACGGCAGAC	299335	131531	TTTTTTTTTTTTTTTCTTTT
210162	42358	TTTGCACACTGCTCTATGTC	254749	86945	GAAGGGCTCTGCACGGCAGA	299336	131532	TTTTTTTTTTTTTTTTCTTT
210163	42359	CTTTGCACACTGCTCTATGT	254750	86946	GGAAGGGCTCTGCACGGCAG	299337	131533	TTTTTTTTTTTTTTTTTCTT
210164	42360	ACTTTGCACACTGCTCTATG	254751	86947	AGGAAGGGCTCTGCACGGCA	299338	131534	TTTTTTTTTTTTTTTTTCT
210165	42361	GACTTTGCACACTGCTCTAT	254752	86948	GAGGAAGGGCTCTGCACGGC	299339	131535	CTTTTTTTTTTTTTTTTTC
210166	42362	GGACTTTGCACACTGCTCTA	254753	86949	GGAGGAAGGGCTCTGCACGG	299340	131536	CCTTTTTTTTTTTTTTTTT
210167	42363	GGGACTTTGCACACTGCTCT	254754	86950	GGGAGGAAGGGCTCTGCACG	299341	131537	TCCTTTTTTTTTTTTTTTT
210168	42364	TGGGACTTTGCACACTGCTC	254755	86951	TGGGAGGAAGGGCTCTGCAC	299342	131538	GTCCTTTTTTTTTTTTTTT
210169	42365	ATGGGACTTTGCACACTGCT	254756	86952	GTGGGAGGAAGGGCTCTGCA	299343	131539	CGTCCTTTTTTTTTTTTTT
210170	42366	AATGGGACTTTGCACACTGC	254757	86953	CGTGGGAGGAAGGGCTCTGC	299344	131540	GCGTCCTTTTTTTTTTTTT
210171	42367	GAATGGGACTTTGCACACTG	254758	86954	CCGTGGGAGGAAGGGCTCTG	299345	131541	TGCGTCCTTTTTTTTTTTT
210172	42368	GGAATGGGACTTTGCACACT	254759	86955	CCCGTGGGAGGAAGGGCTCT	299346	131542	ATGCGTCCTTTTTTTTTTT
210173	42369	TGGAATGGGACTTTGCACAC	254760	86956	CCCCGTGGGAGGAAGGGCTC	299347	131543	CATGCGTCCTTTTTTTTTT
210174	42370	ATGGAATGGGACTTTGCACA	254761	86957	CCCCCGTGGGAGGAAGGGCT	299348	131544	ACATGCGTCCTTTTTTTTT
210175	42371	GATGGAATGGGACTTTGCAC	254762	86958	GCCCCCGTGGGAGGAAGGGC	299349	131545	TACATGCGTCCTTTTTTTT
210176	42372	AGATGGAATGGGACTTTGCA	254763	86959	GGCCCCCGTGGGAGGAAGGG	299350	131546	ATACATGCGTCCTTTTTTT
210177	42373	GAGATGGAATGGGACTTTGC	254764	86960	AGGCCCCCGTGGGAGGAAGG	299351	131547	GATACATGCGTCCTTTTTTT
210178	42374	AGAGATGGAATGGGACTTTG	254765	86961	TAGGCCCCCGTGGGAGGAAG	299352	131548	AGATACATGCGTCCTTTTTT
210179	42375	GAGAGATGGAATGGGACTTT	254766	86962	GTAGGCCCCCGTGGGAGGAA	299353	131549	AAGATACATGCGTCCTTTTT
210180	42376	AGAGAGATGGAATGGGACTT	254767	86963	GGTAGGCCCCCGTGGGAGGA	299354	131550	CAAGATACATGCGTCCTTTT
210181	42377	GAGAGAGATGGAATGGGACT	254768	86964	AGGTAGGCCCCCGTGGGAGG	299355	131551	TCAAGATACATGCGTCCTTT
210182	42378	GGAGAGAGATGGAATGGGAC	254769	86965	GAGGTAGGCCCCCGTGGGAG	299356	131552	TTCAAGATACATGCGTCCTT
210183	42379	TGGAGAGAGATGGAATGGGA	254770	86966	TGAGGTAGGCCCCCGTGGGA	299357	131553	TTTCAAGATACATGCGTCCT
210184	42380	GTGGAGAGAGATGGAATGGG	254771	86967	GTGAGGTAGGCCCCCGTGGG	299358	131554	ATTTCAAGATACATGCGTCC
210185	42381	GGTGGAGAGAGATGGAATGG	254772	86968	GGTGAGGTAGGCCCCCGTGG	299359	131555	CATTTCAAGATACATGCGTC
210186	42382	AGGTGGAGAGAGATGGAATG	254773	86969	AGGTGAGGTAGGCCCCCGTG	299360	131556	GCATTTCAAGATACATGCGT
210187	42383	CAGGTGGAGAGAGATGGAAT	254774	86970	CAGGTGAGGTAGGCCCCCGT	299361	131557	AGCATTTCAAGATACATGCG
210188	42384	CCAGGTGGAGAGAGATGGAA	254775	86971	ACAGGTGAGGTAGGCCCCCG	299362	131558	AAGCATTTCAAGATACATGC
210189	42385	CCCAGGTGGAGAGAGATGGA	254776	86972	CACAGGTGAGGTAGGCCCCC	299363	131559	CAAGCATTTCAAGATACATG
210190	42386	TCCCAGGTGGAGAGAGATGG	254777	86973	GCACAGGTGAGGTAGGCCCC	299364	131560	ACAAGCATTTCAAGATACAT
210191	42387	CTCCCAGGTGGAGAGAGATG	254778	86974	GGCACAGGTGAGGTAGGCCC	299365	131561	TACAAGCATTTCAAGATACA
210192	42388	TCTCCCAGGTGGAGAGAGAT	254779	86975	TGGCACAGGTGAGGTAGGCC	299366	131562	TTACAAGCATTTCAAGATAC
210193	42389	CTCTCCCAGGTGGAGAGAGA	254780	86976	TTGGCACAGGTGAGGTAGGC	299367	131563	TTTACAAGCATTTCAAGATA
210194	42390	CCTCTCCCAGGTGGAGAGAG	254781	86977	CTTGGCACAGGTGAGGTAGG	299368	131564	CTTTACAAGCATTTCAAGAT
210195	42391	TCCTCTCCCAGGTGGAGAGA	254782	86978	CCTTGGCACAGGTGAGGTAG	299369	131565	TCTTTACAAGCATTTCAAGA
210196	42392	ATCCTCTCCCAGGTGGAGAG	254783	86979	CCCTTGGCACAGGTGAGGTA	299370	131566	CTCTTTACAAGCATTTCAAG
210197	42393	CATCCTCTCCCAGGTGGAGA	254784	86980	GCCCTTGGCACAGGTGAGGT	299371	131567	CCTCTTTACAAGCATTTCAA
210198	42394	CCATCCTCTCCCAGGTGGAG	254785	86981	AGCCCTTGGCACAGGTGAGG	299372	131568	ACCTCTTTACAAGCATTTCA
210199	42395	GCCATCCTCTCCCAGGTGGA	254786	86982	AAGCCCTTGGCACAGGTGAG	299373	131569	AACCTCTTTACAAGCATTTC
210200	42396	AGCCATCCTCTCCCAGGTGG	254787	86983	CAAGCCCTTGGCACAGGTGA	299374	131570	AAACCTCTTTACAAGCATTT
210201	42397	GAGCCATCCTCTCCCAGGTG	254788	86984	ACAAGCCCTTGGCACAGGTG	299375	131571	GAAACCTCTTTACAAGCATT
210202	42398	AGAGCCATCCTCTCCCAGGT	254789	86985	GACAAGCCCTTGGCACAGGT	299376	131572	AGAAACCTCTTTACAAGCAT
210203	42399	AAGAGCCATCCTCTCCCAGG	254790	86986	AGACAAGCCCTTGGCACAGG	299377	131573	TAGAAACCTCTTTACAAGCA
210204	42400	GAAGAGCCATCCTCTCCCAG	254791	86987	CAGACAAGCCCTTGGCACAG	299378	131574	TTAGAAACCTCTTTACAAGC
210205	42401	AGAAGAGCCATCCTCTCCCA	254792	86988	ACAGACAAGCCCTTGGCACA	299379	131575	GTTAGAAACCTCTTTACAAG
210206	42402	CAGAAGAGCCATCCTCTCCC	254793	86989	CACAGACAAGCCCTTGGCAC	299380	131576	GGTTAGAAACCTCTTTACAA
210207	42403	ACAGAAGAGCCATCCTCTCC	254794	86990	CCACAGACAAGCCCTTGGCA	299381	131577	GGGTTAGAAACCTCTTTACA
210208	42404	GACAGAAGAGCCATCCTCTC	254795	86991	ACCACAGACAAGCCCTTGGC	299382	131578	TGGGTTAGAAACCTCTTTAC
210209	42405	AGACAGAAGAGCCATCCTCT	254796	86992	GACCACAGACAAGCCCTTGG	299383	131579	GTGGGTTAGAAACCTCTTTA
210210	42406	CAGACAGAAGAGCCATCCTC	254797	86993	TGACCACAGACAAGCCCTTG	299384	131580	GGTGGGTTAGAAACCTCTTT

210211	42407	TCAGACAGAAGAGCCATCCT	254798	86994	CTGACCACAGACAAGCCCTT	299385	131581	GGGTGGGTTAGAAACCTCTT
210212	42408	ATCAGACAGAAGAGCCATCC	254799	86995	ACTGACCACAGACAAGCCCT	299386	131582	AGGGTGGGTTAGAAACCTCT
210213	42409	AATCAGACAGAAGAGCCATC	254800	86996	CACTGACCACAGACAAGCCC	299387	131583	GAGGGTGGGTTAGAAACCTC
210214	42410	GAATCAGACAGAAGAGCCAT	254801	86997	TCACTGACCACAGACAAGCC	299388	131584	TGAGGGTGGGTTAGAAACCT
210215	42411	TGAATCAGACAGAAGAGCCA	254802	86998	GTCACTGACCACAGACAAGC	299389	131585	GTGAGGGTGGGTTAGAAACC
210216	42412	ATGAATCAGACAGAAGAGCC	254803	86999	GGTCACTGACCACAGACAAG	299390	131586	CGTGAGGGTGGGTTAGAAAC
210217	42413	CATGAATCAGACAGAAGAGC	254804	87000	AGGTCACTGACCACAGACAA	299391	131587	TCGTGAGGGTGGGTTAGAAA
210218	42414	CCATGAATCAGACAGAAGAG	254805	87001	CAGGTCACTGACCACAGACA	299392	131588	CTCGTGAGGGTGGGTTAGAA
210219	42415	GCCATGAATCAGACAGAAGA	254806	87002	CCAGGTCACTGACCACAGAC	299393	131589	CCTCGTGAGGGTGGGTTAGA
210220	42416	AGCCATGAATCAGACAGAAG	254807	87003	TCCAGGTCACTGACCACAGA	299394	131590	ACCTCGTGAGGGTGGGTTAG
210221	42417	GAGCCATGAATCAGACAGAA	254808	87004	ATCCAGGTCACTGACCACAG	299395	131591	CACCTCGTGAGGGTGGGTTA
210222	42418	TGAGCCATGAATCAGACAGA	254809	87005	TATCCAGGTCACTGACCACA	299396	131592	ACACCTCGTGAGGGTGGGTT
210223	42419	TTGAGCCATGAATCAGACAG	254810	87006	CTATCCAGGTCACTGACCAC	299397	131593	GACACCTCGTGAGGGTGGGT
210224	42420	TTTGAGCCATGAATCAGACA	254811	87007	TCTATCCAGGTCACTGACCA	299398	131594	AGACACCTCGTGAGGGTGGG
210225	42421	CTTTGAGCCATGAATCAGAC	254812	87008	ATCTATCCAGGTCACTGACC	299399	131595	GAGACACCTCGTGAGGGTGG
210226	42422	ACTTTGAGCCATGAATCAGA	254813	87009	GATCTATCCAGGTCACTGAC	299400	131596	AGAGACACCTCGTGAGGGTG
210227	42423	CACTTTGAGCCATGAATCAG	254814	87010	AGATCTATCCAGGTCACTGA	299401	131597	GAGAGACACCTCGTGAGGGT
210228	42424	CCACTTTGAGCCATGAATCA	254815	87011	CAGATCTATCCAGGTCACTG	299402	131598	TGAGAGACACCTCGTGAGGG
210229	42425	ACCACTTTGAGCCATGAATC	254816	87012	TCAGATCTATCCAGGTCACT	299403	131599	GTGAGAGACACCTCGTGAGG
210230	42426	TACCACTTTGAGCCATGAAT	254817	87013	TTCAGATCTATCCAGGTCAC	299404	131600	GGTGAGAGACACCTCGTGAG
210231	42427	TTACCACTTTGAGCCATGAA	254818	87014	ATTCAGATCTATCCAGGTCA	299405	131601	GGGTGAGAGACACCTCGTGA
210232	42428	TTTACCACTTTGAGCCATGA	254819	87015	CATTCAGATCTATCCAGGTC	299406	131602	GGGGTGAGAGACACCTCGTG
210233	42429	CTTTACCACTTTGAGCCATG	254820	87016	CCATTCAGATCTATCCAGGT	299407	131603	GGGGGTGAGAGACACCTCGT
210234	42430	CCTTTACCACTTTGAGCCAT	254821	87017	CCCATTCAGATCTATCCAGG	299408	131604	TGGGGGTGAGAGACACCTCG
210235	42431	TCCTTTACCACTTTGAGCCA	254822	87018	CCCCATTCAGATCTATCCAG	299409	131605	GTGGGGGTGAGAGACACCTC
210236	42432	CTCCTTTACCACTTTGAGCC	254823	87019	GCCCCATTCAGATCTATCCA	299410	131606	TGTGGGGGTGAGAGACACCT
210237	42433	GCTCCTTTACCACTTTGAGC	254824	87020	AGCCCCATTCAGATCTATCC	299411	131607	GTGTGGGGGTGAGAGACACC
210238	42434	AGCTCCTTTACCACTTTGAG	254825	87021	AAGCCCCATTCAGATCTATC	299412	131608	AGTGTGGGGGTGAGAGACAC
210239	42435	GAGCTCCTTTACCACTTTGA	254826	87022	GAAGCCCCATTCAGATCTAT	299413	131609	CAGTGTGGGGGTGAGAGACA
210240	42436	GGAGCTCCTTTACCACTTTG	254827	87023	AGAAGCCCCATTCAGATCTA	299414	131610	CCAGTGTGGGGGTGAGAGAC
210241	42437	GGGAGCTCCTTTACCACTTT	254828	87024	AAGAAGCCCCATTCAGATCT	299415	131611	CCCAGTGTGGGGGTGAGAGA
210242	42438	GGGGAGCTCCTTTACCACTT	254829	87025	AAAGAAGCCCCATTCAGATC	299416	131612	TCCCAGTGTGGGGGTGAGAG
210243	42439	TGGGGAGCTCCTTTACCACT	254830	87026	AAAAGAAGCCCCATTCAGAT	299417	131613	GTCCCAGTGTGGGGGTGAGA
210244	42440	GTGGGGAGCTCCTTTACCAC	254831	87027	AAAAAGAAGCCCCATTCAGA	299418	131614	AGTCCCAGTGTGGGGGTGAG
210245	42441	AGTGGGGAGCTCCTTTACCA	254832	87028	GAAAAAGAAGCCCCATTCAG	299419	131615	GAGTCCCAGTGTGGGGGTGA
210246	42442	GAGTGGGGAGCTCCTTTACC	254833	87029	CGAAAAAGAAGCCCCATTCA	299420	131616	CGAGTCCCAGTGTGGGGGTG
210247	42443	GGAGTGGGGAGCTCCTTTAC	254834	87030	TCGAAAAAGAAGCCCCATTC	299421	131617	ACGAGTCCCAGTGTGGGGGT
210248	42444	GGGAGTGGGGAGCTCCTTTA	254835	87031	CTCGAAAAAGAAGCCCCATT	299422	131618	CACGAGTCCCAGTGTGGGGG
210249	42445	GGGGAGTGGGGAGCTCCTTT	254836	87032	CCTCGAAAAAGAAGCCCCAT	299423	131619	ACACGAGTCCCAGTGTGGGG
210250	42446	CGGGGAGTGGGGAGCTCCTT	254837	87033	TCCTCGAAAAAGAAGCCCCA	299424	131620	CACACGAGTCCCAGTGTGGG
210251	42447	ACGGGGAGTGGGGAGCTCCT	254838	87034	CTCCTCGAAAAAGAAGCCCC	299425	131621	CCACACGAGTCCCAGTGTGG
210252	42448	GACGGGGAGTGGGGAGCTCC	254839	87035	ACTCCTCGAAAAAGAAGCCC	299426	131622	GCCACACGAGTCCCAGTGTG
210253	42449	GGACGGGGAGTGGGGAGCTC	254840	87036	GACTCCTCGAAAAAGAAGCC	299427	131623	GGCCACACGAGTCCCAGTGT
210254	42450	GGGACGGGGAGTGGGGAGCT	254841	87037	AGACTCCTCGAAAAAGAAGC	299428	131624	AGGCCACACGAGTCCCAGTG
210255	42451	TGGGACGGGGAGTGGGGAGC	254842	87038	AAGACTCCTCGAAAAAGAAG	299429	131625	CAGGCCACACGAGTCCCAGT
210256	42452	GTGGGACGGGGAGTGGGGAG	254843	87039	TAAGACTCCTCGAAAAAGAA	299430	131626	ACAGGCCACACGAGTCCCAG
210257	42453	CGTGGGACGGGGAGTGGGGA	254844	87040	ATAAGACTCCTCGAAAAAGA	299431	131627	CACAGGCCACACGAGTCCCA
210258	42454	GCGTGGGACGGGGAGTGGGG	254845	87041	CATAAGACTCCTCGAAAAAG	299432	131628	ACACAGGCCACACGAGTCCC
210259	42455	GGCGTGGGACGGGGAGTGGG	254846	87042	CCATAAGACTCCTCGAAAAA	299433	131629	CACACAGGCCACACGAGTCC
210260	42456	AGGCGTGGGACGGGGAGTGG	254847	87043	GCCATAAGACTCCTCGAAAA	299434	131630	CCACACAGGCCACACGAGTC
210261	42457	TAGGCGTGGGACGGGGAGTG	254848	87044	TGCCATAAGACTCCTCGAAA	299435	131631	ACCACACAGGCCACACGAGT
210262	42458	GTAGGCGTGGGACGGGGAGT	254849	87045	CTGCCATAAGACTCCTCGAA	299436	131632	CACCACACAGGCCACACGAG
210263	42459	AGTAGGCGTGGGACGGGGAG	254850	87046	CCTGCCATAAGACTCCTCGA	299437	131633	GCACCACACAGGCCACACGA
210264	42460	GAGTAGGCGTGGGACGGGGA	254851	87047	ACCTGCCATAAGACTCCTCG	299438	131634	GGCACCACACAGGCCACACG
210265	42461	TGAGTAGGCGTGGGACGGGG	254852	87048	GACCTGCCATAAGACTCCTC	299439	131635	TGGCACCACACAGGCCACAC
210266	42462	CTGAGTAGGCGTGGGACGGG	254853	87049	AGACCTGCCATAAGACTCCT	299440	131636	GTGGCACCACACAGGCCACA
210267	42463	TCTGAGTAGGCGTGGGACGG	254854	87050	GAGACCTGCCATAAGACTCC	299441	131637	GGTGGCACCACACAGGCCAC
210268	42464	CTCTGAGTAGGCGTGGGACG	254855	87051	AGAGACCTGCCATAAGACTC	299442	131638	GGGTGGCACCACACAGGCCA
210269	42465	ACTCTGAGTAGGCGTGGGAC	254856	87052	GAGAGACCTGCCATAAGACT	299443	131639	AGGGTGGCACCACACAGGCC
210270	42466	GACTCTGAGTAGGCGTGGGA	254857	87053	TGAGAGACCTGCCATAAGAC	299444	131640	CAGGGTGGCACCACACAGGC
210271	42467	AGACTCTGAGTAGGCGTGGG	254858	87054	CTGAGAGACCTGCCATAAGA	299445	131641	GCAGGGTGGCACCACACAGG
210272	42468	CAGACTCTGAGTAGGCGTGG	254859	87055	ACTGAGAGACCTGCCATAAG	299446	131642	AGCAGGGTGGCACCACACAG
210273	42469	GCAGACTCTGAGTAGGCGTG	254860	87056	TACTGAGAGACCTGCCATAA	299447	131643	CAGCAGGGTGGCACCACACA
210274	42470	TGCAGACTCTGAGTAGGCGT	254861	87057	TTACTGAGAGACCTGCCATA	299448	131644	CCAGCAGGGTGGCACCACAC
210275	42471	TTGCAGACTCTGAGTAGGCG	254862	87058	TTTACTGAGAGACCTGCCAT	299449	131645	CCCAGCAGGGTGGCACCACA
210276	42472	TTTGCAGACTCTGAGTAGGC	254863	87059	CTTTACTGAGAGACCTGCCA	299450	131646	CCCCAGCAGGGTGGCACCAC
210277	42473	ATTTGCAGACTCTGAGTAGG	254864	87060	TCTTTACTGAGAGACCTGCC	299451	131647	GCCCCAGCAGGGTGGCACCA
210278	42474	TATTTGCAGACTCTGAGTAG	254865	87061	GTCTTTACTGAGAGACCTGC	299452	131648	GGCCCCAGCAGGGTGGCACC
210279	42475	ATATTTGCAGACTCTGAGTA	254866	87062	AGTCTTTACTGAGAGACCTG	299453	131649	AGGCCCCAGCAGGGTGGCAC
210280	42476	CATATTTGCAGACTCTGAGT	254867	87063	GAGTCTTTACTGAGAGACCT	299454	131650	GAGGCCCCAGCAGGGTGGCA
210281	42477	ACATATTTGCAGACTCTGAG	254868	87064	GGAGTCTTTACTGAGAGACC	299455	131651	GGAGGCCCCAGCAGGGTGGC
210282	42478	TACATATTTGCAGACTCTGA	254869	87065	TGGAGTCTTTACTGAGAGAC	299456	131652	GGGAGGCCCCAGCAGGGTGG

210283	42479	ATACATATTTGCAGACTCTG	254870	87066	ATGGAGTCTTTACTGAGAGA	299457	131653	TGGGAGGCCCCAGCAGGGTG
210284	42480	CATACATATTTGCAGACTCT	254871	87067	AATGGAGTCTTTACTGAGAG	299458	131654	TTGGGAGGCCCCAGCAGGGT
210285	42481	GCATACATATTTGCAGACTC	254872	87068	GAATGGAGTCTTTACTGAGA	299459	131655	CTTGGGAGGCCCCAGCAGGG
210286	42482	CGCATACATATTTGCAGACT	254873	87069	AGAATGGAGTCTTTACTGAG	299460	131656	ACTTGGGAGGCCCCAGCAGG
210287	42483	TCGCATACATATTTGCAGAC	254874	87070	AAGAATGGAGTCTTTACTGA	299461	131657	AACTTGGGAGGCCCCAGCAG
210288	42484	ATCGCATACATATTTGCAGA	254875	87071	CAAGAATGGAGTCTTTACTG	299462	131658	AAACTTGGGAGGCCCCAGCA
210289	42485	TATCGCATACATATTTGCAG	254876	87072	TCAAGAATGGAGTCTTTACT	299463	131659	AAAACTTGGGAGGCCCCAGC
210290	42486	ATATCGCATACATATTTGCA	254877	87073	ATCAAGAATGGAGTCTTTAC	299464	131660	CAAAACTTGGGAGGCCCCAG
210291	42487	CATATCGCATACATATTTGC	254878	87074	CATCAAGAATGGAGTCTTTA	299465	131661	TCAAAACTTGGGAGGCCCCA
210292	42488	TCATATCGCATACATATTTG	254879	87075	TCATCAAGAATGGAGTCTTT	299466	131662	TTCAAAACTTGGGAGGCCCC
210293	42489	CTCATATCGCATACATATTT	254880	87076	ATCATCAAGAATGGAGTCTT	299467	131663	TTTCAAAACTTGGGAGGCCC
210294	42490	TCTCATATCGCATACATATT	254881	87077	GATCATCAAGAATGGAGTCT	299468	131664	CTTTCAAAACTTGGGAGGCC
210295	42491	CTCTCATATCGCATACATAT	254882	87078	TGATCATCAAGAATGGAGTC	299469	131665	CCTTTCAAAACTTGGGAGGC
210296	42492	GCTCTCATATCGCATACATA	254883	87079	GTGATCATCAAGAATGGAGT	299470	131666	GCCTTTCAAAACTTGGGAGG
210297	42493	AGCTCTCATATCGCATACAT	254884	87080	TGTGATCATCAAGAATGGAG	299471	131667	AGCCTTTCAAAACTTGGGAG
210298	42494	GAGCTCTCATATCGCATACA	254885	87081	GTGTGATCATCAAGAATGGA	299472	131668	AAGCCTTTCAAAACTTGGGA
210299	42495	CGAGCTCTCATATCGCATAC	254886	87082	TGTGTGATCATCAAGAATGG	299473	131669	AAAGCCTTTCAAAACTTGGG
210300	42496	ACGAGCTCTCATATCGCATA	254887	87083	ATGTGTGATCATCAAGAATG	299474	131670	GAAAGCCTTTCAAAACTTGG
210301	42497	GACGAGCTCTCATATCGCAT	254888	87084	AATGTGTGATCATCAAGAAT	299475	131671	GGAAAGCCTTTCAAAACTTG
210302	42498	TGACGAGCTCTCATATCGCA	254889	87085	AAATGTGTGATCATCAAGAA	299476	131672	AGGAAAGCCTTTCAAAACTT
210303	42499	CTGACGAGCTCTCATATCGC	254890	87086	AAAATGTGTGATCATCAAGA	299477	131673	GAGGAAAGCCTTTCAAAACT
210304	42500	ACTGACGAGCTCTCATATCG	254891	87087	CAAAATGTGTGATCATCAAG	299478	131674	TGAGGAAAGCCTTTCAAAAC
210305	42501	AACTGACGAGCTCTCATATC	254892	87088	CCAAAATGTGTGATCATCAA	299479	131675	CTGAGGAAAGCCTTTCAAAA
210306	42502	TAACTGACGAGCTCTCATAT	254893	87089	TCCAAAATGTGTGATCATCA	299480	131676	GCTGAGGAAAGCCTTTCAAA
210307	42503	CTAACTGACGAGCTCTCATA	254894	87090	ATCCAAAATGTGTGATCATC	299481	131677	TGCTGAGGAAAGCCTTTCAA
210308	42504	GCTAACTGACGAGCTCTCAT	254895	87091	AATCCAAAATGTGTGATCAT	299482	131678	GTGCTGAGGAAAGCCTTTCA
210309	42505	AGCTAACTGACGAGCTCTCA	254896	87092	AAATCCAAAATGTGTGATCA	299483	131679	GGTGCTGAGGAAAGCCTTTC
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210315	42511	GAAGACAGCTAACTGACGAG	254902	87098	TTTGGAAAATCCAAAATGTG	299489	131685	GTCCCAGGTGCTGAGGAAAG
210316	42512	TGAAGACAGCTAACTGACGA	254903	87099	ATTTGGAAAATCCAAAATGT	299490	131686	GGTCCCAGGTGCTGAGGAAA
210317	42513	CTGAAGACAGCTAACTGACG	254904	87100	GATTTGGAAAATCCAAAATG	299491	131687	GGGTCCCAGGTGCTGAGGAA
210318	42514	ACTGAAGACAGCTAACTGAC	254905	87101	AGATTTGGAAAATCCAAAAT	299492	131688	TGGGTCCCAGGTGCTGAGGA
210319	42515	CACTGAAGACAGCTAACTGA	254906	87102	CAGATTTGGAAAATCCAAAA	299493	131689	TTGGGTCCCAGGTGCTGAGG
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210321	42517	CACACTGAAGACAGCTAACT	254908	87104	GACAGATTTGGAAAATCCAA	299495	131691	TGTTGGGTCCCAGGTGCTGA
210322	42518	CCACACTGAAGACAGCTAAC	254909	87105	TGACAGATTTGGAAAATCCA	299496	131692	CTGTTGGGTCCCAGGTGCTG
210323	42519	GCCACACTGAAGACAGCTAA	254910	87106	CTGACAGATTTGGAAAATCC	299497	131693	TCTGTTGGGTCCCAGGTGCT
210324	42520	CGCCACACTGAAGACAGCTA	254911	87107	TCTGACAGATTTGGAAAATC	299498	131694	CTCTGTTGGGTCCCAGGTGC
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210326	42522	TGCGCCACACTGAAGACAGC	254913	87109	TCTCTGACAGATTTGGAAAA	299500	131696	GTCTCTGTTGGGTCCCAGGT
210327	42523	GTGCGCCACACTGAAGACAG	254914	87110	TTCTCTGACAGATTTGGAAA	299501	131697	GGTCTCTGTTGGGTCCCAGG
210328	42524	TGTGCGCCACACTGAAGACA	254915	87111	ATTCTCTGACAGATTTGGAA	299502	131698	TGGTCTCTGTTGGGTCCCAG
210329	42525	ATGTGCGCCACACTGAAGAC	254916	87112	CATTCTCTGACAGATTTGGA	299503	131699	CTGGTCTCTGTTGGGTCCCA
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210331	42527	AAATGTGCGCCACACTGAAG	254918	87114	CCCATTCTCTGACAGATTTG	299505	131701	AGCTGGTCTCTGTTGGGTCC
210332	42528	CAAATGTGCGCCACACTGAA	254919	87115	GCCCATTCTCTGACAGATTT	299506	131702	AAGCTGGTCTCTGTTGGGTC
210333	42529	TCAAATGTGCGCCACACTGA	254920	87116	AGCCCATTCTCTGACAGATT	299507	131703	GAAGCTGGTCTCTGTTGGGT
210334	42530	CTCAAATGTGCGCCACACTG	254921	87117	AAGCCCATTCTCTGACAGAT	299508	131704	AGAAGCTGGTCTCTGTTGGG
210335	42531	CCTCAAATGTGCGCCACACT	254922	87118	CAAGCCCATTCTCTGACAGA	299509	131705	TAGAAGCTGGTCTCTGTTGG
210336	42532	TCCTCAAATGTGCGCCACAC	254923	87119	TCAAGCCCATTCTCTGACAG	299510	131706	CTAGAAGCTGGTCTCTGTTG
210337	42533	CTCCTCAAATGTGCGCCACA	254924	87120	CTCAAGCCCATTCTCTGACA	299511	131707	GCTAGAAGCTGGTCTCTGTT
210338	42534	ACTCCTCAAATGTGCGCCAC	254925	87121	CCTCAAGCCCATTCTCTGAC	299512	131708	TGCTAGAAGCTGGTCTCTGT
210339	42535	GACTCCTCAAATGTGCGCCA	254926	87122	GCCTCAAGCCCATTCTCTGA	299513	131709	CTGCTAGAAGCTGGTCTCTG
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210341	42537	CAGACTCCTCAAATGTGCGC	254928	87124	CCGCCTCAAGCCCATTCTCT	299515	131711	AGCTGCTAGAAGCTGGTCTC
210342	42538	TCAGACTCCTCAAATGTGCG	254929	87125	CCCGCCTCAAGCCCATTCTC	299516	131712	TAGCTGCTAGAAGCTGGTCT
210343	42539	GTCAGACTCCTCAAATGTGC	254930	87126	CCCCGCCTCAAGCCCATTCT	299517	131713	TTAGCTGCTAGAAGCTGGTC
210344	42540	AGTCAGACTCCTCAAATGTG	254931	87127	ACCCCGCCTCAAGCCCATTC	299518	131714	CTTAGCTGCTAGAAGCTGGT
210345	42541	GAGTCAGACTCCTCAAATGT	254932	87128	AACCCCGCCTCAAGCCCATT	299519	131715	CCTTAGCTGCTAGAAGCTGG
210346	42542	GGAGTCAGACTCCTCAAATG	254933	87129	AAACCCCGCCTCAAGCCCAT	299520	131716	TCCTTAGCTGCTAGAAGCTG
210347	42543	GGGAGTCAGACTCCTCAAAT	254934	87130	CAAACCCCGCCTCAAGCCCA	299521	131717	CTCCTTAGCTGCTAGAAGCT
210348	42544	GGGGAGTCAGACTCCTCAAA	254935	87131	ACAAACCCCGCCTCAAGCCC	299522	131718	CCTCCTTAGCTGCTAGAAGC
210349	42545	AGGGGAGTCAGACTCCTCAA	254936	87132	CACAAACCCCGCCTCAAGCC	299523	131719	GCCTCCTTAGCTGCTAGAAG
210350	42546	GAGGGGAGTCAGACTCCTCA	254937	87133	CCACAAACCCCGCCTCAAGC	299524	131720	GGCCTCCTTAGCTGCTAGAA
210351	42547	GGAGGGGAGTCAGACTCCTC	254938	87134	CCCACAAACCCCGCCTCAAG	299525	131721	CGGCCTCCTTAGCTGCTAGA
210352	42548	TGGAGGGGAGTCAGACTCCT	254939	87135	GCCCACAAACCCCGCCTCAA	299526	131722	ACGGCCTCCTTAGCTGCTAG
210353	42549	CTGGAGGGGAGTCAGACTCC	254940	87136	TGCCCACAAACCCCGCCTCA	299527	131723	AACGGCCTCCTTAGCTGCTA
210354	42550	GCTGGAGGGGAGTCAGACTC	254941	87137	GTGCCCACAAACCCCGCCTC	299528	131724	GAACGGCCTCCTTAGCTGCT

210355	42551	TGCTGGAGGGGAGTCAGACT	254942	87138	AGTGCCCACAAACCCCGCCT	299529	131725	TGAACGGCCTCCTTAGCTGC
210356	42552	GTGCTGGAGGGGAGTCAGAC	254943	87139	TAGTGCCCACAAACCCCGCC	299530	131726	CTGAACGGCCTCCTTAGCTG
210357	42553	TGTGCTGGAGGGGAGTCAGA	254944	87140	CTAGTGCCCACAAACCCCGC	299531	131727	GCTGAACGGCCTCCTTAGCT
210358	42554	CTGTGCTGGAGGGGAGTCAG	254945	87141	ACTAGTGCCCACAAACCCCG	299532	131728	AGCTGAACGGCCTCCTTAGC
210359	42555	CCTGTGCTGGAGGGGAGTCA	254946	87142	AACTAGTGCCCACAAACCCC	299533	131729	CAGCTGAACGGCCTCCTTAG
210360	42556	GCCTGTGCTGGAGGGGAGTC	254947	87143	AAACTAGTGCCCACAAACCC	299534	131730	ACAGCTGAACGGCCTCCTTA
210361	42557	GGCCTGTGCTGGAGGGGAGT	254948	87144	GAAACTAGTGCCCACAAACC	299535	131731	CACAGCTGAACGGCCTCCTT
210362	42558	TGGCCTGTGCTGGAGGGGAG	254949	87145	TGAAACTAGTGCCCACAAAC	299536	131732	TCACAGCTGAACGGCCTCCT
210363	42559	TTGGCCTGTGCTGGAGGGGA	254950	87146	GTGAAACTAGTGCCCACAAA	299537	131733	GTCACAGCTGAACGGCCTCC
210364	42560	ATTGGCCTGTGCTGGAGGGG	254951	87147	AGTGAAACTAGTGCCCACAA	299538	131734	CGTCACAGCTGAACGGCCTC
210365	42561	CATTGGCCTGTGCTGGAGGG	254952	87148	CAGTGAAACTAGTGCCCACA	299539	131735	TCGTCACAGCTGAACGGCCT
210366	42562	ACATTGGCCTGTGCTGGAGG	254953	87149	CCAGTGAAACTAGTGCCCAC	299540	131736	TTCGTCACAGCTGAACGGCC
210367	42563	CACATTGGCCTGTGCTGGAG	254954	87150	ACCAGTGAAACTAGTGCCCA	299541	131737	CTTCGTCACAGCTGAACGGC
210368	42564	GCACATTGGCCTGTGCTGGA	254955	87151	AACCAGTGAAACTAGTGCCC	299542	131738	CCTTCGTCACAGCTGAACGG
210369	42565	TGCACATTGGCCTGTGCTGG	254956	87152	AAACCAGTGAAACTAGTGCC	299543	131739	GCCTTCGTCACAGCTGAACG
210370	42566	GTGCACATTGGCCTGTGCTG	254957	87153	GAAACCAGTGAAACTAGTGC	299544	131740	GGCCTTCGTCACAGCTGAAC
210371	42567	AGTGCACATTGGCCTGTGCT	254958	87154	TGAAACCAGTGAAACTAGTG	299545	131741	AGGCCTTCGTCACAGCTGAA
210372	42568	CAGTGCACATTGGCCTGTGC	254959	87155	ATGAAACCAGTGAAACTAGT	299546	131742	CAGGCCTTCGTCACAGCTGA
210373	42569	GCAGTGCACATTGGCCTGTG	254960	87156	AATGAAACCAGTGAAACTAG	299547	131743	TCAGGCCTTCGTCACAGCTG
210374	42570	AGCAGTGCACATTGGCCTGT	254961	87157	AAATGAAACCAGTGAAACTA	299548	131744	TTCAGGCCTTCGTCACAGCT
210375	42571	GAGCAGTGCACATTGGCCTG	254962	87158	TAAATGAAACCAGTGAAACT	299549	131745	CTTCAGGCCTTCGTCACAGC
210376	42572	AGAGCAGTGCACATTGGCCT	254963	87159	GTAAATGAAACCAGTGAAAC	299550	131746	GCTTCAGGCCTTCGTCACAG
210377	42573	GAGAGCAGTGCACATTGGCC	254964	87160	GGTAAATGAAACCAGTGAAA	299551	131747	TGCTTCAGGCCTTCGTCACA
210378	42574	GGAGAGCAGTGCACATTGGC	254965	87161	TGGTAAATGAAACCAGTGAA	299552	131748	GTGCTTCAGGCCTTCGTCAC
210379	42575	AGGAGAGCAGTGCACATTGG	254966	87162	TTGGTAAATGAAACCAGTGA	299553	131749	TGTGCTTCAGGCCTTCGTCA
210380	42576	TAGGAGAGCAGTGCACATTG	254967	87163	TTTGGTAAATGAAACCAGTG	299554	131750	CTGTGCTTCAGGCCTTCGTC
210381	42577	ATAGGAGAGCAGTGCACATT	254968	87164	TTTTGGTAAATGAAACCAGT	299555	131751	CCTGTGCTTCAGGCCTTCGT
210382	42578	GATAGGAGAGCAGTGCACAT	254969	87165	TTTTTGGTAAATGAAACCAG	299556	131752	TCCTGTGCTTCAGGCCTTCG
210383	42579	AGATAGGAGAGCAGTGCACA	254970	87166	CTTTTTGGTAAATGAAACCA	299557	131753	ATCCTGTGCTTCAGGCCTTC
210384	42580	AAGATAGGAGAGCAGTGCAC	254971	87167	CCTTTTTGGTAAATGAAACC	299558	131754	AATCCTGTGCTTCAGGCCTT
210385	42581	AAAGATAGGAGAGCAGTGCA	254972	87168	CCCTTTTTGGTAAATGAAAC	299559	131755	TAATCCTGTGCTTCAGGCCT
210386	42582	CAAAGATAGGAGAGCAGTGC	254973	87169	CCCCTTTTTGGTAAATGAAA	299560	131756	CTAATCCTGTGCTTCAGGCC
210387	42583	ACAAAGATAGGAGAGCAGTG	254974	87170	TCCCCTTTTTGGTAAATGAA	299561	131757	CCTAATCCTGTGCTTCAGGC
210388	42584	TACAAAGATAGGAGAGCAGT	254975	87171	CTCCCCTTTTTGGTAAATGA	299562	131758	TCCTAATCCTGTGCTTCAGG
210389	42585	GTACAAAGATAGGAGAGCAG	254976	87172	GCTCCCCTTTTTGGTAAATG	299563	131759	GTCCTAATCCTGTGCTTCAG
210390	42586	GGTACAAAGATAGGAGAGCA	254977	87173	TGCTCCCCTTTTTGGTAAAT	299564	131760	AGTCCTAATCCTGTGCTTCA
210391	42587	GGGTACAAAGATAGGAGAGC	254978	87174	CTGCTCCCCTTTTTGGTAAA	299565	131761	CAGTCCTAATCCTGTGCTTC
210392	42588	GGGGTACAAAGATAGGAGAG	254979	87175	TCTGCTCCCCTTTTTGGTAA	299566	131762	TCAGTCCTAATCCTGTGCTT
210393	42589	GGGGGTACAAAGATAGGAGA	254980	87176	TTCTGCTCCCCTTTTTGGTA	299567	131763	TTCAGTCCTAATCCTGTGCT
210394	42590	TGGGGGTACAAAGATAGGAG	254981	87177	CTTCTGCTCCCCTTTTTGGT	299568	131764	CTTCAGTCCTAATCCTGTGC
210395	42591	GTGGGGGTACAAAGATAGGA	254982	87178	ACTTCTGCTCCCCTTTTTGG	299569	131765	GCTTCAGTCCTAATCCTGTG
210396	42592	AGTGGGGGTACAAAGATAGG	254983	87179	GACTTCTGCTCCCCTTTTTG	299570	131766	CGCTTCAGTCCTAATCCTGT
210397	42593	CAGTGGGGGTACAAAGATAG	254984	87180	TGACTTCTGCTCCCCTTTTT	299571	131767	TCGCTTCAGTCCTAATCCTG
210398	42594	ACAGTGGGGGTACAAAGATA	254985	87181	TTGACTTCTGCTCCCCTTTT	299572	131768	ATCGCTTCAGTCCTAATCCT
210399	42595	AACAGTGGGGGTACAAAGAT	254986	87182	CTTGACTTCTGCTCCCCTTT	299573	131769	CATCGCTTCAGTCCTAATCC
210400	42596	CAACAGTGGGGGTACAAAGA	254987	87183	ACTTGACTTCTGCTCCCCTT	299574	131770	TCATCGCTTCAGTCCTAATC
210401	42597	GCAACAGTGGGGGTACAAAG	254988	87184	TACTTGACTTCTGCTCCCCT	299575	131771	ATCATCGCTTCAGTCCTAAT
210402	42598	TGCAACAGTGGGGGTACAAA	254989	87185	ATACTTGACTTCTGCTCCCC	299576	131772	CATCATCGCTTCAGTCCTAA
210403	42599	GTGCAACAGTGGGGGTACAA	254990	87186	CATACTTGACTTCTGCTCCC	299577	131773	ACATCATCGCTTCAGTCCTA
210404	42600	AGTGCAACAGTGGGGGTACA	254991	87187	CCATACTTGACTTCTGCTCC	299578	131774	GACATCATCGCTTCAGTCCT
210405	42601	CAGTGCAACAGTGGGGGTAC	254992	87188	ACCATACTTGACTTCTGCTC	299579	131775	GGACATCATCGCTTCAGTCC
210406	42602	ACAGTGCAACAGTGGGGGTA	254993	87189	CACCATACTTGACTTCTGCT	299580	131776	GGGACATCATCGCTTCAGTC
210407	42603	CACAGTGCAACAGTGGGGGT	254994	87190	CCACCATACTTGACTTCTGC	299581	131777	GGGGACATCATCGCTTCAGT
210408	42604	GCACAGTGCAACAGTGGGGG	254995	87191	GCCACCATACTTGACTTCTG	299582	131778	AGGGGACATCATCGCTTCAG
210409	42605	TGCACAGTGCAACAGTGGGG	254996	87192	AGCCACCATACTTGACTTCT	299583	131779	AAGGGGACATCATCGCTTCA
210410	42606	CTGCACAGTGCAACAGTGGG	254997	87193	GAGCCACCATACTTGACTTC	299584	131780	GAAGGGGACATCATCGCTTC
210411	42607	TCTGCACAGTGCAACAGTGG	254998	87194	TGAGCCACCATACTTGACTT	299585	131781	GGAAGGGGACATCATCGCTT
210412	42608	CTCTGCACAGTGCAACAGTG	254999	87195	ATGAGCCACCATACTTGACT	299586	131782	GGGAAGGGGACATCATCGCT
210413	42609	CCTCTGCACAGTGCAACAGT	255000	87196	GATGAGCCACCATACTTGAC	299587	131783	AGGGAAGGGGACATCATCGC
210414	42610	ACCTCTGCACAGTGCAACAG	255001	87197	GGATGAGCCACCATACTTGA	299588	131784	TAGGGAAGGGGACATCATCG
210415	42611	AACCTCTGCACAGTGCAACA	255002	87198	GGGATGAGCCACCATACTTG	299589	131785	GTAGGGAAGGGGACATCATC
210416	42612	CAACCTCTGCACAGTGCAAC	255003	87199	AGGGATGAGCCACCATACTT	299590	131786	AGTAGGGAAGGGGACATCAT
210417	42613	CCAACCTCTGCACAGTGCAA	255004	87200	CAGGGATGAGCCACCATACT	299591	131787	AAGTAGGGAAGGGGACATCA
210418	42614	TCCAACCTCTGCACAGTGCA	255005	87201	ACAGGGATGAGCCACCATAC	299592	131788	GAAGTAGGGAAGGGGACATC
210419	42615	CTCCAACCTCTGCACAGTGC	255006	87202	TACAGGGATGAGCCACCATA	299593	131789	GGAAGTAGGGAAGGGGACAT
210420	42616	GCTCCAACCTCTGCACAGTG	255007	87203	TTACAGGGATGAGCCACCAT	299594	131790	GGGAAGTAGGGAAGGGGACA
210421	42617	GGCTCCAACCTCTGCACAGT	255008	87204	ATTACAGGGATGAGCCACCA	299595	131791	GGGGAAGTAGGGAAGGGGAC
210422	42618	TGGCTCCAACCTCTGCACAG	255009	87205	GATTACAGGGATGAGCCACC	299596	131792	AGGGGAAGTAGGGAAGGGGA
210423	42619	ATGGCTCCAACCTCTGCACA	255010	87206	GGATTACAGGGATGAGCCAC	299597	131793	AAGGGGAAGTAGGGAAGGGG
210424	42620	TATGGCTCCAACCTCTGCAC	255011	87207	GGGATTACAGGGATGAGCCA	299598	131794	CAAGGGGAAGTAGGGAAGGG
210425	42621	CTATGGCTCCAACCTCTGCA	255012	87208	TGGGATTACAGGGATGAGCC	299599	131795	CCAAGGGGAAGTAGGGAAGG
210426	42622	TCTATGGCTCCAACCTCTGC	255013	87209	CTGGGATTACAGGGATGAGC	299600	131796	CCCAAGGGGAAGTAGGGAAG

210427	42623	TTCTATGGCTCCAACCTCTG	255014	87210	TCTGGGATTACAGGGATGAG	299601	131797	CCCCAAGGGGAAGTAGGGAA
210428	42624	CTTCTATGGCTCCAACCTCT	255015	87211	CTCTGGGATTACAGGGATGA	299602	131798	GCCCCAAGGGGAAGTAGGGA
210429	42625	ACTTCTATGGCTCCAACCTC	255016	87212	CCTCTGGGATTACAGGGATG	299603	131799	AGCCCCAAGGGGAAGTAGGG
210430	42626	TACTTCTATGGCTCCAACCT	255017	87213	GCCTCTGGGATTACAGGGAT	299604	131800	GAGCCCCAAGGGGAAGTAGG
210431	42627	GTACTTCTATGGCTCCAACC	255018	87214	TGCCTCTGGGATTACAGGGA	299605	131801	GGAGCCCCAAGGGGAAGTAG
210432	42628	GGTACTTCTATGGCTCCAAC	255019	87215	TTGCCTCTGGGATTACAGGG	299606	131802	GGGAGCCCCAAGGGGAAGTA
210433	42629	TGGTACTTCTATGGCTCCAA	255020	87216	CTTGCCTCTGGGATTACAGG	299607	131803	AGGGAGCCCCAAGGGGAAGT
210434	42630	CTGGTACTTCTATGGCTCCA	255021	87217	TCTTGCCTCTGGGATTACAG	299608	131804	CAGGGAGCCCCAAGGGGAAG
210435	42631	TCTGGTACTTCTATGGCTCC	255022	87218	CTCTTGCCTCTGGGATTACA	299609	131805	ACAGGGAGCCCCAAGGGGAA
210436	42632	CTCTGGTACTTCTATGGCTC	255023	87219	TCTCTTGCCTCTGGGATTAC	299610	131806	CACAGGGAGCCCCAAGGGGA
210437	42633	GCTCTGGTACTTCTATGGCT	255024	87220	TTCTCTTGCCTCTGGGATTA	299611	131807	ACACAGGGAGCCCCAAGGGG
210438	42634	AGCTCTGGTACTTCTATGGC	255025	87221	ATTCTCTTGCCTCTGGGATT	299612	131808	GACACAGGGAGCCCCAAGGG
210439	42635	CAGCTCTGGTACTTCTATGG	255026	87222	AATTCTCTTGCCTCTGGGAT	299613	131809	TGACACAGGGAGCCCCAAGG
210440	42636	ACAGCTCTGGTACTTCTATG	255027	87223	CAATTCTCTTGCCTCTGGGA	299614	131810	CTGACACAGGGAGCCCCAAG
210441	42637	CACAGCTCTGGTACTTCTAT	255028	87224	GCAATTCTCTTGCCTCTGGG	299615	131811	CCTGACACAGGGAGCCCCAA
210442	42638	TCACAGCTCTGGTACTTCTA	255029	87225	AGCAATTCTCTTGCCTCTGG	299616	131812	CCCTGACACAGGGAGCCCCA
210443	42639	TTCACAGCTCTGGTACTTCT	255030	87226	AAGCAATTCTCTTGCCTCTG	299617	131813	GCCCTGACACAGGGAGCCCC
210444	42640	TTTCACAGCTCTGGTACTTC	255031	87227	CAAGCAATTCTCTTGCCTCT	299618	131814	TGCCCTGACACAGGGAGCCC
210445	42641	CTTTCACAGCTCTGGTACTT	255032	87228	TCAAGCAATTCTCTTGCCTC	299619	131815	GTGCCCTGACACAGGGAGCC
210446	42642	CCTTTCACAGCTCTGGTACT	255033	87229	CTCAAGCAATTCTCTTGCCT	299620	131816	TGTGCCCTGACACAGGGAGC
210447	42643	TCCTTTCACAGCTCTGGTAC	255034	87230	GCTCAAGCAATTCTCTTGCC	299621	131817	CTGTGCCCTGACACAGGGAG
210448	42644	CTCCTTTCACAGCTCTGGTA	255035	87231	GGCTCAAGCAATTCTCTTGC	299622	131818	TCTGTGCCCTGACACAGGGA
210449	42645	TCTCCTTTCACAGCTCTGGT	255036	87232	GGGCTCAAGCAATTCTCTTG	299623	131819	GTCTGTGCCCTGACACAGGG
210450	42646	CTCTCCTTTCACAGCTCTGG	255037	87233	TGGGCTCAAGCAATTCTCTT	299624	131820	AGTCTGTGCCCTGACACAGG
210451	42647	CCTCTCCTTTCACAGCTCTG	255038	87234	CTGGGCTCAAGCAATTCTCT	299625	131821	TAGTCTGTGCCCTGACACAG
210452	42648	GCCTCTCCTTTCACAGCTCT	255039	87235	CCTGGGCTCAAGCAATTCTC	299626	131822	CTAGTCTGTGCCCTGACACA
210453	42649	GGCCTCTCCTTTCACAGCTC	255040	87236	TCCTGGGCTCAAGCAATTCT	299627	131823	CCTAGTCTGTGCCCTGACAC
210454	42650	GGGCCTCTCCTTTCACAGCT	255041	87237	CTCCTGGGCTCAAGCAATTC	299628	131824	ACCTAGTCTGTGCCCTGACA
210455	42651	GGGGCCTCTCCTTTCACAGC	255042	87238	ACTCCTGGGCTCAAGCAATT	299629	131825	GACCTAGTCTGTGCCCTGAC
210456	42652	GGGGGCCTCTCCTTTCACAG	255043	87239	AACTCCTGGGCTCAAGCAAT	299630	131826	AGACCTAGTCTGTGCCCTGA
210457	42653	AGGGGGCCTCTCCTTTCACA	255044	87240	GAACTCCTGGGCTCAAGCAA	299631	131827	AAGACCTAGTCTGTGCCCTG
210458	42654	GAGGGGGCCTCTCCTTTCAC	255045	87241	CGAACTCCTGGGCTCAAGCA	299632	131828	CAAGACCTAGTCTGTGCCCT
210459	42655	AGAGGGGGCCTCTCCTTTCA	255046	87242	TCGAACTCCTGGGCTCAAGC	299633	131829	ACAAGACCTAGTCTGTGCCC
210460	42656	GAGAGGGGGCCTCTCCTTTC	255047	87243	CTCGAACTCCTGGGCTCAAG	299634	131830	CACAAGACCTAGTCTGTGCC
210461	42657	TGAGAGGGGGCCTCTCCTTT	255048	87244	TCTCGAACTCCTGGGCTCAA	299635	131831	CCACAAGACCTAGTCTGTGC
210462	42658	GTGAGAGGGGGCCTCTCCTT	255049	87245	GTCTCGAACTCCTGGGCTCA	299636	131832	GCCACAAGACCTAGTCTGTG
210463	42659	GGTGAGAGGGGGCCTCTCCT	255050	87246	GGTCTCGAACTCCTGGGCTC	299637	131833	AGCCACAAGACCTAGTCTGT
210464	42660	AGGTGAGAGGGGGCCTCTCC	255051	87247	TGGTCTCGAACTCCTGGGCT	299638	131834	CAGCCACAAGACCTAGTCTG
210465	42661	GAGGTGAGAGGGGGCCTCTC	255052	87248	CTGGTCTCGAACTCCTGGGC	299639	131835	CCAGCCACAAGACCTAGTCT
210466	42662	AGAGGTGAGAGGGGGCCTCT	255053	87249	GCTGGTCTCGAACTCCTGGG	299640	131836	ACCAGCCACAAGACCTAGTC
210467	42663	CAGAGGTGAGAGGGGGCCTC	255054	87250	GGCTGGTCTCGAACTCCTGG	299641	131837	GACCAGCCACAAGACCTAGT
210468	42664	GCAGAGGTGAGAGGGGGCCT	255055	87251	AGGCTGGTCTCGAACTCCTG	299642	131838	AGACCAGCCACAAGACCTAG
210469	42665	GGCAGAGGTGAGAGGGGGCC	255056	87252	CAGGCTGGTCTCGAACTCCT	299643	131839	CAGACCAGCCACAAGACCTA
210470	42666	GGGCAGAGGTGAGAGGGGGC	255057	87253	TCAGGCTGGTCTCGAACTCC	299644	131840	CCAGACCAGCCACAAGACCT
210471	42667	AGGGCAGAGGTGAGAGGGGG	255058	87254	CTCAGGCTGGTCTCGAACTC	299645	131841	GCCAGACCAGCCACAAGACC
210472	42668	CAGGGCAGAGGTGAGAGGGG	255059	87255	GCTCAGGCTGGTCTCGAACT	299646	131842	AGCCAGACCAGCCACAAGAC
210473	42669	CCAGGGCAGAGGTGAGAGGG	255060	87256	TGCTCAGGCTGGTCTCGAAC	299647	131843	AAGCCAGACCAGCCACAAGA
210474	42670	ACCAGGGCAGAGGTGAGAGG	255061	87257	TTGCTCAGGCTGGTCTCGAA	299648	131844	CAAGCCAGACCAGCCACAAG
210475	42671	GACCAGGGCAGAGGTGAGAG	255062	87258	GTTGCTCAGGCTGGTCTCGA	299649	131845	GCAAGCCAGACCAGCCACAA
210476	42672	AGACCAGGGCAGAGGTGAGA	255063	87259	TGTTGCTCAGGCTGGTCTCG	299650	131846	CGCAAGCCAGACCAGCCACA
210477	42673	GAGACCAGGGCAGAGGTGAG	255064	87260	ATGTTGCTCAGGCTGGTCTC	299651	131847	CCGCAAGCCAGACCAGCCAC
210478	42674	GGAGACCAGGGCAGAGGTGA	255065	87261	TATGTTGCTCAGGCTGGTCT	299652	131848	GCCGCAAGCCAGACCAGCCA
210479	42675	TGGAGACCAGGGCAGAGGTG	255066	87262	TTATGTTGCTCAGGCTGGTC	299653	131849	CGCCGCAAGCCAGACCAGCC
210480	42676	ATGGAGACCAGGGCAGAGGT	255067	87263	CTTATGTTGCTCAGGCTGGT	299654	131850	GCGCCGCAAGCCAGACCAGC
210481	42677	GATGGAGACCAGGGCAGAGG	255068	87264	CCTTATGTTGCTCAGGCTGG	299655	131851	CGCGCCGCAAGCCAGACCAG
210482	42678	GGATGGAGACCAGGGCAGAG	255069	87265	TCCTTATGTTGCTCAGGCTG	299656	131852	TCGCGCCGCAAGCCAGACCA
210483	42679	GGGATGGAGACCAGGGCAGA	255070	87266	CTCCTTATGTTGCTCAGGCT	299657	131853	CTCGCGCCGCAAGCCAGACC
210484	42680	GGGGATGGAGACCAGGGCAG	255071	87267	TCTCCTTATGTTGCTCAGGC	299658	131854	CCTCGCGCCGCAAGCCAGAC
210485	42681	TGGGGATGGAGACCAGGGCA	255072	87268	GTCTCCTTATGTTGCTCAGG	299659	131855	TCCTCGCGCCGCAAGCCAGA
210486	42682	GTGGGGATGGAGACCAGGGC	255073	87269	GGTCTCCTTATGTTGCTCAG	299660	131856	ATCCTCGCGCCGCAAGCCAG
210487	42683	AGTGGGGATGGAGACCAGGG	255074	87270	GGGTCTCCTTATGTTGCTCA	299661	131857	CATCCTCGCGCCGCAAGCCA
210488	42684	AAGTGGGGATGGAGACCAGG	255075	87271	GGGGTCTCCTTATGTTGCTC	299662	131858	CCATCCTCGCGCCGCAAGCC
210489	42685	AAAGTGGGGATGGAGACCAG	255076	87272	CGGGGTCTCCTTATGTTGCT	299663	131859	ACCATCCTCGCGCCGCAAGC
210490	42686	GAAAGTGGGGATGGAGACCA	255077	87273	ACGGGGTCTCCTTATGTTGC	299664	131860	AACCATCCTCGCGCCGCAAG
210491	42687	AGAAAGTGGGGATGGAGACC	255078	87274	GACGGGGTCTCCTTATGTTG	299665	131861	GAACCATCCTCGCGCCGCAA
210492	42688	GAGAAAGTGGGGATGGAGAC	255079	87275	AGACGGGGTCTCCTTATGTT	299666	131862	AGAACCATCCTCGCGCCGCA
210493	42689	AGAGAAAGTGGGGATGGAGA	255080	87276	GAGACGGGGTCTCCTTATGT	299667	131863	GAGAACCATCCTCGCGCCGC
210494	42690	TAGAGAAAGTGGGGATGGAG	255081	87277	GGAGACGGGGTCTCCTTATG	299668	131864	AGAGAACCATCCTCGCGCCG
210495	42691	CTAGAGAAAGTGGGGATGGA	255082	87278	TGGAGACGGGGTCTCCTTAT	299669	131865	GAGAGAACCATCCTCGCGCC
210496	42692	CCTAGAGAAAGTGGGGATGG	255083	87279	GTGGAGACGGGGTCTCCTTA	299670	131866	AGAGAGAACCATCCTCGCGC
210497	42693	TCCTAGAGAAAGTGGGGATG	255084	87280	TGTGGAGACGGGGTCTCCTT	299671	131867	CAGAGAGAACCATCCTCGCG
210498	42694	TTCCTAGAGAAAGTGGGGAT	255085	87281	TTGTGGAGACGGGGTCTCCT	299672	131868	CCAGAGAGAACCATCCTCGC

210499	42695	CTTCCTAGAGAAAGTGGGGA	255086	87282	TTTGTGGAGACGGGGTCTCC	299673	131869	ACCAGAGAGAACCATCCTCG
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210501	42697	AGCTTCCTAGAGAAAGTGGG	255088	87284	TTTTTGTGGAGACGGGGTCT	299675	131871	TGACCAGAGAGAACCATCCT
210502	42698	TAGCTTCCTAGAGAAAGTGG	255089	87285	ATTTTTGTGGAGACGGGGTC	299676	131872	ATGACCAGAGAGAACCATCC
210503	42699	CTAGCTTCCTAGAGAAAGTG	255090	87286	CATTTTTGTGGAGACGGGGT	299677	131873	TATGACCAGAGAGAACCATC
210504	42700	ACTAGCTTCCTAGAGAAAGT	255091	87287	TCATTTTTGTGGAGACGGGG	299678	131874	CTATGACCAGAGAGAACCAT
210505	42701	TACTAGCTTCCTAGAGAAAG	255092	87288	TTCATTTTTGTGGAGACGGG	299679	131875	GCTATGACCAGAGAGAACCA
210506	42702	CTACTAGCTTCCTAGAGAAA	255093	87289	TTTCATTTTTGTGGAGACGG	299680	131876	GGCTATGACCAGAGAGAACC
210507	42703	CCTACTAGCTTCCTAGAGAA	255094	87290	TTTTCATTTTTGTGGAGACG	299681	131877	GGGCTATGACCAGAGAGAAC
210508	42704	ACCTACTAGCTTCCTAGAGA	255095	87291	TTTTTCATTTTTGTGGAGAC	299682	131878	CGGGCTATGACCAGAGAGAA
210509	42705	CACCTACTAGCTTCCTAGAG	255096	87292	ATTTTTCATTTTTGTGGAGA	299683	131879	TCGGGCTATGACCAGAGAGA
210510	42706	GCACCTACTAGCTTCCTAGA	255097	87293	TATTTTTCATTTTTGTGGAG	299684	131880	TTCGGGCTATGACCAGAGAG
210511	42707	AGCACCTACTAGCTTCCTAG	255098	87294	TTATTTTTCATTTTTGTGGA	299685	131881	CTTCGGGCTATGACCAGAGA
210512	42708	CAGCACCTACTAGCTTCCTA	255099	87295	GTTATTTTTCATTTTTGTGG	299686	131882	ACTTCGGGCTATGACCAGAG
210513	42709	TCAGCACCTACTAGCTTCCT	255100	87296	TGTTATTTTTCATTTTTGTG	299687	131883	GACTTCGGGCTATGACCAGA
210514	42710	GTCAGCACCTACTAGCTTCC	255101	87297	ATGTTATTTTTCATTTTTGT	299688	131884	AGACTTCGGGCTATGACCAG
210515	42711	TGTCAGCACCTACTAGCTTC	255102	87298	AATGTTATTTTTCATTTTTG	299689	131885	GAGACTTCGGGCTATGACCA
210516	42712	CTGTCAGCACCTACTAGCTT	255103	87299	AAATGTTATTTTTCATTTTT	299690	131886	TGAGACTTCGGGCTATGACC
210517	42713	CCTGTCAGCACCTACTAGCT	255104	87300	AAAATGTTATTTTTCATTTT	299691	131887	ATGAGACTTCGGGCTATGAC
210518	42714	CCCTGTCAGCACCTACTAGC	255105	87301	TAAAATGTTATTTTTCATTT	299692	131888	CATGAGACTTCGGGCTATGA
210519	42715	CCCCTGTCAGCACCTACTAG	255106	87302	CTAAAATGTTATTTTTCATT	299693	131889	CCATGAGACTTCGGGCTATG
210520	42716	TCCCCTGTCAGCACCTACTA	255107	87303	ACTAAAATGTTATTTTTCAT	299694	131890	GCCATGAGACTTCGGGCTAT
210521	42717	CTCCCCTGTCAGCACCTACT	255108	87304	GACTAAAATGTTATTTTTCA	299695	131891	TGCCATGAGACTTCGGGCTA
210522	42718	TCTCCCCTGTCAGCACCTAC	255109	87305	TGACTAAAATGTTATTTTTC	299696	131892	CTGCCATGAGACTTCGGGCT
210523	42719	CTCTCCCCTGTCAGCACCTA	255110	87306	CTGACTAAAATGTTATTTTT	299697	131893	ACTGCCATGAGACTTCGGGC
210524	42720	TCTCTCCCCTGTCAGCACCT	255111	87307	TCTGACTAAAATGTTATTTT	299698	131894	GACTGCCATGAGACTTCGGG
210525	42721	TTCTCTCCCCTGTCAGCACC	255112	87308	GTCTGACTAAAATGTTATTT	299699	131895	GGACTGCCATGAGACTTCGG
210526	42722	CTTCTCTCCCCTGTCAGCAC	255113	87309	CGTCTGACTAAAATGTTATT	299700	131896	GGGACTGCCATGAGACTTCG
210527	42723	CCTTCTCTCCCCTGTCAGCA	255114	87310	ACGTCTGACTAAAATGTTAT	299701	131897	TGGGACTGCCATGAGACTTC
210528	42724	CCCTTCTCTCCCCTGTCAGC	255115	87311	CACGTCTGACTAAAATGTTA	299702	131898	TTGGGACTGCCATGAGACTT
210529	42725	TCCCTTCTCTCCCCTGTCAG	255116	87312	CCACGTCTGACTAAAATGTT	299703	131899	TTTGGGACTGCCATGAGACT
210530	42726	CTCCCTTCTCTCCCCTGTCA	255117	87313	ACCACGTCTGACTAAAATGT	299704	131900	CTTTGGGACTGCCATGAGAC
210531	42727	CCTCCCTTCTCTCCCCTGTC	255118	87314	CACCACGTCTGACTAAAATG	299705	131901	CCTTTGGGACTGCCATGAGA
210532	42728	CCCTCCCTTCTCTCCCCTGT	255119	87315	CCACCACGTCTGACTAAAAT	299706	131902	TCCTTTGGGACTGCCATGAG
210533	42729	CCCCTCCCTTCTCTCCCCTG	255120	87316	GCCACCACGTCTGACTAAAA	299707	131903	CTCCTTTGGGACTGCCATGA
210534	42730	TCCCCTCCCTTCTCTCCCCT	255121	87317	TGCCACCACGTCTGACTAAA	299708	131904	CCTCCTTTGGGACTGCCATG
210535	42731	CTCCCCTCCCTTCTCTCCCC	255122	87318	ATGCCACCACGTCTGACTAA	299709	131905	GCCTCCTTTGGGACTGCCAT
210536	42732	CCTCCCCTCCCTTCTCTCCC	255123	87319	CATGCCACCACGTCTGACTA	299710	131906	AGCCTCCTTTGGGACTGCCA
210537	42733	CCCTCCCCTCCCTTCTCTCC	255124	87320	GCATGCCACCACGTCTGACT	299711	131907	AAGCCTCCTTTGGGACTGCC
210538	42734	CCCCTCCCCTCCCTTCTCTC	255125	87321	TGCATGCCACCACGTCTGAC	299712	131908	TAAGCCTCCTTTGGGACTGC
210539	42735	ACCCCTCCCCTCCCTTCTCT	255126	87322	ATGCATGCCACCACGTCTGA	299713	131909	GTAAGCCTCCTTTGGGACTG
210540	42736	GACCCCTCCCCTCCCTTCTC	255127	87323	GATGCATGCCACCACGTCTG	299714	131910	TGTAAGCCTCCTTTGGGACT
210541	42737	GGACCCCTCCCCTCCCTTCT	255128	87324	AGATGCATGCCACCACGTCT	299715	131911	TTGTAAGCCTCCTTTGGGAC
210542	42738	TGGACCCCTCCCCTCCCTTC	255129	87325	CAGATGCATGCCACCACGTC	299716	131912	GTTGTAAGCCTCCTTTGGGA
210543	42739	CTGGACCCCTCCCCTCCCTT	255130	87326	ACAGATGCATGCCACCACGT	299717	131913	AGTTGTAAGCCTCCTTTGGG
210544	42740	TCTGGACCCCTCCCCTCCCT	255131	87327	CACAGATGCATGCCACCACG	299718	131914	GAGTTGTAAGCCTCCTTTGG
210545	42741	TTCTGGACCCCTCCCCTCCC	255132	87328	CCACAGATGCATGCCACCAC	299719	131915	GGAGTTGTAAGCCTCCTTTG
210546	42742	TTTCTGGACCCCTCCCCTCC	255133	87329	ACCACAGATGCATGCCACCA	299720	131916	AGGAGTTGTAAGCCTCCTTT
210547	42743	GTTTCTGGACCCCTCCCCTC	255134	87330	GACCACAGATGCATGCCACC	299721	131917	CAGGAGTTGTAAGCCTCCTT
210548	42744	TGTTTCTGGACCCCTCCCCT	255135	87331	GGACCACAGATGCATGCCAC	299722	131918	GCAGGAGTTGTAAGCCTCCT
210549	42745	CTGTTTCTGGACCCCTCCCC	255136	87332	GGGACCACAGATGCATGCCA	299723	131919	TGCAGGAGTTGTAAGCCTCC
210550	42746	ACTGTTTCTGGACCCCTCCC	255137	87333	TGGGACCACAGATGCATGCC	299724	131920	ATGCAGGAGTTGTAAGCCTC
210551	42747	CACTGTTTCTGGACCCCTCC	255138	87334	CTGGGACCACAGATGCATGC	299725	131921	GATGCAGGAGTTGTAAGCCT
210552	42748	CCACTGTTTCTGGACCCCTC	255139	87335	GCTGGGACCACAGATGCATG	299726	131922	TGATGCAGGAGTTGTAAGCC
210553	42749	GCCACTGTTTCTGGACCCCT	255140	87336	AGCTGGGACCACAGATGCAT	299727	131923	GTGATGCAGGAGTTGTAAGC
210554	42750	AGCCACTGTTTCTGGACCCC	255141	87337	CAGCTGGGACCACAGATGCA	299728	131924	TGTGATGCAGGAGTTGTAAG
210555	42751	GAGCCACTGTTTCTGGACCC	255142	87338	GCAGCTGGGACCACAGATGC	299729	131925	TTGTGATGCAGGAGTTGTAA
210556	42752	TGAGCCACTGTTTCTGGACC	255143	87339	AGCAGCTGGGACCACAGATG	299730	131926	CTTGTGATGCAGGAGTTGTA
210557	42753	ATGAGCCACTGTTTCTGGAC	255144	87340	AAGCAGCTGGGACCACAGAT	299731	131927	TCTTGTGATGCAGGAGTTGT
210558	42754	CATGAGCCACTGTTTCTGGA	255145	87341	CAAGCAGCTGGGACCACAGA	299732	131928	TTCTTGTGATGCAGGAGTTG
210559	42755	GCATGAGCCACTGTTTCTGG	255146	87342	CCAAGCAGCTGGGACCACAG	299733	131929	TTTCTTGTGATGCAGGAGTT
210560	42756	GGCATGAGCCACTGTTTCTG	255147	87343	CCCAAGCAGCTGGGACCACA	299734	131930	TTTTCTTGTGATGCAGGAGT
210561	42757	AGGCATGAGCCACTGTTTCT	255148	87344	TCCCAAGCAGCTGGGACCAC	299735	131931	TTTTTCTTGTGATGCAGGAG
210562	42758	CAGGCATGAGCCACTGTTTC	255149	87345	CTCCCAAGCAGCTGGGACCA	299736	131932	CTTTTTCTTGTGATGCAGGA
210563	42759	GCAGGCATGAGCCACTGTTT	255150	87346	CCTCCCAAGCAGCTGGGACC	299737	131933	CCTTTTTCTTGTGATGCAGG
210564	42760	TGCAGGCATGAGCCACTGTT	255151	87347	CCCTCCCAAGCAGCTGGGAC	299738	131934	TCCTTTTTCTTGTGATGCAG
210565	42761	TTGCAGGCATGAGCCACTGT	255152	87348	ACCCTCCCAAGCAGCTGGGA	299739	131935	TTCCTTTTTCTTGTGATGCA
210566	42762	ATTGCAGGCATGAGCCACTG	255153	87349	CACCCTCCCAAGCAGCTGGG	299740	131936	CTTCCTTTTTCTTGTGATGC
210567	42763	GATTGCAGGCATGAGCCACT	255154	87350	TCACCCTCCCAAGCAGCTGG	299741	131937	GCTTCCTTTTTCTTGTGATG
210568	42764	GGATTGCAGGCATGAGCCAC	255155	87351	CTCACCCTCCCAAGCAGCTG	299742	131938	GGCTTCCTTTTTCTTGTGAT
210569	42765	AGGATTGCAGGCATGAGCCA	255156	87352	TCTCACCCTCCCAAGCAGCT	299743	131939	TGGCTTCCTTTTTCTTGTGA
210570	42766	TAGGATTGCAGGCATGAGCC	255157	87353	ATCTCACCCTCCCAAGCAGC	299744	131940	GTGGCTTCCTTTTTCTTGTG

210571	42767	CTAGGATTGCAGGCATGAGC	255158	87354	CATCTCACCCTCCCAAGCAG	299745	131941	AGTGGCTTCCTTTTTCTTGT
210572	42768	GCTAGGATTGCAGGCATGAG	255159	87355	CCATCTCACCCTCCCAAGCA	299746	131942	CAGTGGCTTCCTTTTTCTTG
210573	42769	TGCTAGGATTGCAGGCATGA	255160	87356	CCCATCTCACCCTCCCAAGC	299747	131943	GCAGTGGCTTCCTTTTTCTT
210574	42770	GTGCTAGGATTGCAGGCATG	255161	87357	TCCCATCTCACCCTCCCAAG	299748	131944	GGCAGTGGCTTCCTTTTTCT
210575	42771	AGTGCTAGGATTGCAGGCAT	255162	87358	CTCCCATCTCACCCTCCCAA	299749	131945	TGGCAGTGGCTTCCTTTTTC
210576	42772	AAGTGCTAGGATTGCAGGCA	255163	87359	CCTCCCATCTCACCCTCCCA	299750	131946	CTGGCAGTGGCTTCCTTTTT
210577	42773	AAAGTGCTAGGATTGCAGGC	255164	87360	CCCTCCCATCTCACCCTCCC	299751	131947	GCTGGCAGTGGCTTCCTTTT
210578	42774	CAAAGTGCTAGGATTGCAGG	255165	87361	ACCCTCCCATCTCACCCTCC	299752	131948	AGCTGGCAGTGGCTTCCTTT
210579	42775	CCAAAGTGCTAGGATTGCAG	255166	87362	AACCCTCCCATCTCACCCTC	299753	131949	CAGCTGGCAGTGGCTTCCTT
210580	42776	CCCAAAGTGCTAGGATTGCA	255167	87363	CAACCCTCCCATCTCACCCT	299754	131950	CCAGCTGGCAGTGGCTTCCT
210581	42777	TCCCAAAGTGCTAGGATTGC	255168	87364	ACAACCCTCCCATCTCACCC	299755	131951	CCCAGCTGGCAGTGGCTTCC
210582	42778	CTCCCAAAGTGCTAGGATTG	255169	87365	AACAACCCTCCCATCTCACC	299756	131952	CCCCAGCTGGCAGTGGCTTC
210583	42779	CCTCCCAAAGTGCTAGGATT	255170	87366	AAACAACCCTCCCATCTCAC	299757	131953	CCCCCAGCTGGCAGTGGCTT
210584	42780	GCCTCCCAAAGTGCTAGGAT	255171	87367	CAAACAACCCTCCCATCTCA	299758	131954	CCCCCCAGCTGGCAGTGGCT
210585	42781	AGCCTCCCAAAGTGCTAGGA	255172	87368	TCAAACAACCCTCCCATCTC	299759	131955	TCCCCCCAGCTGGCAGTGGC
210586	42782	CAGCCTCCCAAAGTGCTAGG	255173	87369	CTCAAACAACCCTCCCATCT	299760	131956	ATCCCCCCAGCTGGCAGTGG
210587	42783	TCAGCCTCCCAAAGTGCTAG	255174	87370	GCTCAAACAACCCTCCCATC	299761	131957	GATCCCCCCAGCTGGCAGTG
210588	42784	CTCAGCCTCCCAAAGTGCTA	255175	87371	GGCTCAAACAACCCTCCCAT	299762	131958	AGATCCCCCCAGCTGGCAGT
210589	42785	CCTCAGCCTCCCAAAGTGCT	255176	87372	GGGCTCAAACAACCCTCCCA	299763	131959	CAGATCCCCCCAGCTGGCAG
210590	42786	GCCTCAGCCTCCCAAAGTGC	255177	87373	AGGGCTCAAACAACCCTCCC	299764	131960	GCAGATCCCCCCAGCTGGCA
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210592	42788	CTGCCTCAGCCTCCCAAAGT	255179	87375	CCAGGGCTCAAACAACCCTC	299766	131962	CTGCAGATCCCCCCAGCTGG
210593	42789	CCTGCCTCAGCCTCCCAAAG	255180	87376	TCCAGGGCTCAAACAACCCT	299767	131963	GCTGCAGATCCCCCCAGCTG
210594	42790	TCCTGCCTCAGCCTCCCAAA	255181	87377	CTCCAGGGCTCAAACAACCC	299768	131964	AGCTGCAGATCCCCCCAGCT
210595	42791	CTCCTGCCTCAGCCTCCCAA	255182	87378	ACTCCAGGGCTCAAACAACC	299769	131965	GAGCTGCAGATCCCCCCAGC
210596	42792	CCTCCTGCCTCAGCCTCCCA	255183	87379	AACTCCAGGGCTCAAACAAC	299770	131966	GGAGCTGCAGATCCCCCCAG
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210601	42797	ATGATCCTCCTGCCTCAGCC	255188	87384	ACTTTAACTCCAGGGCTCAA	299775	131971	TTCTGGGAGCTGCAGATCCC
210602	42798	AATGATCCTCCTGCCTCAGC	255189	87385	AACTTTAACTCCAGGGCTCA	299776	131972	CTTCTGGGAGCTGCAGATCC
210603	42799	AAATGATCCTCCTGCCTCAG	255190	87386	CAACTTTAACTCCAGGGCTC	299777	131973	GCTTCTGGGAGCTGCAGATC
210604	42800	CAAATGATCCTCCTGCCTCA	255191	87387	GCAACTTTAACTCCAGGGCT	299778	131974	AGCTTCTGGGAGCTGCAGAT
210605	42801	TCAAATGATCCTCCTGCCTC	255192	87388	TGCAACTTTAACTCCAGGGC	299779	131975	GAGCTTCTGGGAGCTGCAGA
210606	42802	CTCAAATGATCCTCCTGCCT	255193	87389	TTGCAACTTTAACTCCAGGG	299780	131976	GGAGCTTCTGGGAGCTGCAG
210607	42803	CCTCAAATGATCCTCCTGCC	255194	87390	ATTGCAACTTTAACTCCAGG	299781	131977	CGGAGCTTCTGGGAGCTGCA
210608	42804	ACCTCAAATGATCCTCCTGC	255195	87391	CATTGCAACTTTAACTCCAG	299782	131978	ACGGAGCTTCTGGGAGCTGC
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210611	42807	CTGACCTCAAATGATCCTCC	255198	87394	GCTCATTGCAACTTTAACTC	299785	131981	CTCACGGAGCTTCTGGGAGC
210612	42808	CCTGACCTCAAATGATCCTC	255199	87395	AGCTCATTGCAACTTTAACT	299786	131982	GCTCACGGAGCTTCTGGGAG
210613	42809	TCCTGACCTCAAATGATCCT	255200	87396	CAGCTCATTGCAACTTTAAC	299787	131983	GGCTCACGGAGCTTCTGGGA
210614	42810	CTCCTGACCTCAAATGATCC	255201	87397	ACAGCTCATTGCAACTTTAA	299788	131984	AGGCTCACGGAGCTTCTGGG
210615	42811	ACTCCTGACCTCAAATGATC	255202	87398	CACAGCTCATTGCAACTTTA	299789	131985	GAGGCTCACGGAGCTTCTGG
210616	42812	AACTCCTGACCTCAAATGAT	255203	87399	TCACAGCTCATTGCAACTTT	299790	131986	TGAGGCTCACGGAGCTTCTG
210617	42813	AAACTCCTGACCTCAAATGA	255204	87400	ATCACAGCTCATTGCAACTT	299791	131987	CTGAGGCTCACGGAGCTTCT
210618	42814	CAAACTCCTGACCTCAAATG	255205	87401	AATCACAGCTCATTGCAACT	299792	131988	GCTGAGGCTCACGGAGCTTC
210619	42815	TCAAACTCCTGACCTCAAAT	255206	87402	CAATCACAGCTCATTGCAAC	299793	131989	GGCTGAGGCTCACGGAGCTT
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210621	42817	TCTCAAACTCCTGACCTCAA	255208	87404	TGCAATCACAGCTCATTGCA	299795	131991	GTGGCTGAGGCTCACGGAGC
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210629	42825	CAGGCTGGTCTCAAACTCCT	255216	87412	TGCAGTGGTGCAATCACAGC	299803	131999	TCTGAGGGGTGGCTGAGGCT
210630	42826	CCAGGCTGGTCTCAAACTCC	255217	87413	GTGCAGTGGTGCAATCACAG	299804	132000	GTCTGAGGGGTGGCTGAGGC
210631	42827	CCCAGGCTGGTCTCAAACTC	255218	87414	AGTGCAGTGGTGCAATCACA	299805	132001	AGTCTGAGGGGTGGCTGAGG
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210633	42829	TGCCCAGGCTGGTCTCAAAC	255220	87416	AGAGTGCAGTGGTGCAATCA	299807	132003	CCAGTCTGAGGGGTGGCTGA
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210635	42831	ATTGCCCAGGCTGGTCTCAA	255222	87418	CTAGAGTGCAGTGGTGCAAT	299809	132005	ACCCAGTCTGAGGGGTGGCT
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210637	42833	ACATTGCCCAGGCTGGTCTC	255224	87420	GGCTAGAGTGCAGTGGTGCA	299811	132007	GAACCCAGTCTGAGGGGTGG
210638	42834	TACATTGCCCAGGCTGGTCT	255225	87421	AGGCTAGAGTGCAGTGGTGC	299812	132008	GGAACCCAGTCTGAGGGGTG
210639	42835	CTACATTGCCCAGGCTGGTC	255226	87422	CAGGCTAGAGTGCAGTGGTG	299813	132009	AGGAACCCAGTCTGAGGGGT
210640	42836	GCTACATTGCCCAGGCTGGT	255227	87423	CCAGGCTAGAGTGCAGTGGT	299814	132010	GAGGAACCCAGTCTGAGGGG
210641	42837	TGCTACATTGCCCAGGCTGG	255228	87424	CCCAGGCTAGAGTGCAGTGG	299815	132011	AGAGGAACCCAGTCTGAGGG
210642	42838	TTGCTACATTGCCCAGGCTG	255229	87425	ACCCAGGCTAGAGTGCAGTG	299816	132012	GAGAGGAACCCAGTCTGAGG

210643	42839	CTTGCTACATTGCCCAGGCT	255230	87426	CACCCAGGCTAGAGTGCAGT	299817	132013	GGAGAGGAACCCAGTCTGAG
210644	42840	TCTTGCTACATTGCCCAGGC	255231	87427	TCACCCAGGCTAGAGTGCAG	299818	132014	TGGAGAGGAACCCAGTCTGA
210645	42841	GTCTTGCTACATTGCCCAGG	255232	87428	GTCACCCAGGCTAGAGTGCA	299819	132015	TTGGAGAGGAACCCAGTCTG
210646	42842	GGTCTTGCTACATTGCCCAG	255233	87429	TGTCACCCAGGCTAGAGTGC	299820	132016	CTTGGAGAGGAACCCAGTCT
210647	42843	GGGTCTTGCTACATTGCCCA	255234	87430	CTGTCACCCAGGCTAGAGTG	299821	132017	GCTTGGAGAGGAACCCAGTC
210648	42844	AGGGTCTTGCTACATTGCCC	255235	87431	TCTGTCACCCAGGCTAGAGT	299822	132018	AGCTTGGAGAGGAACCCAGT
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210650	42846	ATAGGGTCTTGCTACATTGC	255237	87433	GTTCTGTCACCCAGGCTAGA	299824	132020	CGAGCTTGGAGAGGAACCCA
210651	42847	GATAGGGTCTTGCTACATTG	255238	87434	CGTTCTGTCACCCAGGCTAG	299825	132021	GCGAGCTTGGAGAGGAACCC
210652	42848	AGATAGGGTCTTGCTACATT	255239	87435	TCGTTCTGTCACCCAGGCTA	299826	132022	GGCGAGCTTGGAGAGGAACC
210653	42849	GAGATAGGGTCTTGCTACAT	255240	87436	CTCGTTCTGTCACCCAGGCT	299827	132023	GGGCGAGCTTGGAGAGGAAC
210654	42850	AGAGATAGGGTCTTGCTACA	255241	87437	TCTCGTTCTGTCACCCAGGC	299828	132024	AGGGCGAGCTTGGAGAGGAA
210655	42851	TAGAGATAGGGTCTTGCTAC	255242	87438	GTCTCGTTCTGTCACCCAGG	299829	132025	GAGGGCGAGCTTGGAGAGGA
210656	42852	GTAGAGATAGGGTCTTGCTA	255243	87439	GGTCTCGTTCTGTCACCCAG	299830	132026	AGAGGGCGAGCTTGGAGAGG
210657	42853	TGTAGAGATAGGGTCTTGCT	255244	87440	GGGTCTCGTTCTGTCACCCA	299831	132027	CAGAGGGCGAGCTTGGAGAG
210658	42854	TTGTAGAGATAGGGTCTTGC	255245	87441	AGGGTCTCGTTCTGTCACCC	299832	132028	CCAGAGGGCGAGCTTGGAGA
210659	42855	TTTGTAGAGATAGGGTCTTG	255246	87442	CAGGGTCTCGTTCTGTCACC	299833	132029	TCCAGAGGGCGAGCTTGGAG
210660	42856	TTTTGTAGAGATAGGGTCTT	255247	87443	ACAGGGTCTCGTTCTGTCAC	299834	132030	CTCCAGAGGGCGAGCTTGGA
210661	42857	TTTTTGTAGAGATAGGGTCT	255248	87444	GACAGGGTCTCGTTCTGTCA	299835	132031	CCTCCAGAGGGCGAGCTTGG
210662	42858	CTTTTTGTAGAGATAGGGTC	255249	87445	AGACAGGGTCTCGTTCTGTC	299836	132032	CCCTCCAGAGGGCGAGCTTG
210663	42859	TCTTTTTGTAGAGATAGGGT	255250	87446	GAGACAGGGTCTCGTTCTGT	299837	132033	CCCCTCCAGAGGGCGAGCTT
210664	42860	TTCTTTTTGTAGAGATAGGG	255251	87447	TGAGACAGGGTCTCGTTCTG	299838	132034	GCCCCTCCAGAGGGCGAGCT
210665	42861	TTTCTTTTTGTAGAGATAGG	255252	87448	TTGAGACAGGGTCTCGTTCT	299839	132035	TGCCCCTCCAGAGGGCGAGC
210666	42862	TTTTCTTTTTGTAGAGATAG	255253	87449	TTTGAGACAGGGTCTCGTTC	299840	132036	CTGCCCCTCCAGAGGGCGAG
210667	42863	TTTTTCTTTTTGTAGAGATA	255254	87450	TTTTGAGACAGGGTCTCGTT	299841	132037	GCTGCCCCTCCAGAGGGCGA
210668	42864	TTTTTTCTTTTTGTAGAGAT	255255	87451	TTTTTGAGACAGGGTCTCGT	299842	132038	CGCTGCCCCTCCAGAGGGCG
210669	42865	ATTTTTTCTTTTTGTAGAGA	255256	87452	TTTTTTGAGACAGGGTCTCG	299843	132039	GCGCTGCCCCTCCAGAGGGC
210670	42866	CATTTTTTCTTTTTGTAGAG	255257	87453	TTTTTTTGAGACAGGGTCTC	299844	132040	TGCGCTGCCCCTCCAGAGGG
210671	42867	ACATTTTTTCTTTTTGTAGA	255258	87454	TTTTTTTTGAGACAGGGTCT	299845	132041	CTGCGCTGCCCCTCCAGAGG
210672	42868	TACATTTTTTCTTTTTGTAG	255259	87455	TTTTTTTTTGAGACAGGGTC	299846	132042	GCTGCGCTGCCCCTCCAGAG
210673	42869	TTACATTTTTTCTTTTTGTA	255260	87456	TTTTTTTTTTGAGACAGGGT	299847	132043	GGCTGCGCTGCCCCTCCAGA
210674	42870	ATTACATTTTTTCTTTTTGT	255261	87457	TTTTTTTTTTTGAGACAGGG	299848	132044	AGGCTGCGCTGCCCCTCCAG
210675	42871	AATTACATTTTTTCTTTTTG	255262	87458	TTTTTTTTTTTTGAGACAGG	299849	132045	GAGGCTGCGCTGCCCCTCCA
210676	42872	TAATTACATTTTTTCTTTTT	255263	87459	TTTTTTTTTTTTTGAGACAG	299850	132046	GGAGGCTGCGCTGCCCCTCC
210677	42873	CTAATTACATTTTTTCTTTT	255264	87460	TTTTTTTTTTTTTTGAGACA	299851	132047	GGGAGGCTGCGCTGCCCCTC
210678	42874	GCTAATTACATTTTTTCTTT	255265	87461	TTTTTTTTTTTTTTTGAGAC	299852	132048	TGGGAGGCTGCGCTGCCCCT
210679	42875	AGCTAATTACATTTTTTCTT	255266	87462	CTTTTTTTTTTTTTTTGAGA	299853	132049	GTGGGAGGCTGCGCTGCCCC
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210681	42877	CCAGCTAATTACATTTTTTC	255268	87464	TTCTTTTTTTTTTTTTTGA	299855	132051	TGGTGGGAGGCTGCGCTGCC
210682	42878	CCCAGCTAATTACATTTTTT	255269	87465	TTTCTTTTTTTTTTTTTTG	299856	132052	TTGGTGGGAGGCTGCGCTGC
210683	42879	ACCCAGCTAATTACATTTTT	255270	87466	CTTTCTTTTTTTTTTTTTT	299857	132053	CTTGGTGGGAGGCTGCGCTG
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210685	42881	ACACCCAGCTAATTACATTT	255272	87468	TTCTTTCTTTTTTTTTTTT	299859	132055	CCCTTGGTGGGAGGCTGCGC
210686	42882	CACACCCAGCTAATTACATT	255273	87469	TTTCTTTCTTTTTTTTTTT	299860	132056	GCCCTTGGTGGGAGGCTGCG
210687	42883	CCACACCCAGCTAATTACAT	255274	87470	CTTTCTTTCTTTTTTTTTT	299861	132057	GGCCCTTGGTGGGAGGCTGC
210688	42884	ACCACACCCAGCTAATTACA	255275	87471	TCTTTCTTTCTTTTTTTTT	299862	132058	GGGCCCTTGGTGGGAGGCTG
210689	42885	CACCACACCCAGCTAATTAC	255276	87472	TTCTTTCTTTCTTTTTTTT	299863	132059	AGGGCCCTTGGTGGGAGGCT
210690	42886	CCACCACACCCAGCTAATTA	255277	87473	TTTCTTTCTTTCTTTTTTT	299864	132060	CAGGGCCCTTGGTGGGAGGC
210691	42887	ACCACCACACCCAGCTAATT	255278	87474	CTTTCTTTCTTTCTTTTTT	299865	132061	GCAGGGCCCTTGGTGGGAGG
210692	42888	CACCACCACACCCAGCTAAT	255279	87475	CCTTTCTTTCTTTCTTTTT	299866	132062	CGCAGGGCCCTTGGTGGGAG
210693	42889	CCACCACCACACCCAGCTAA	255280	87476	TCCTTTCTTTCTTTCTTTT	299867	132063	TCGCAGGGCCCTTGGTGGGA
210694	42890	CCCACCACCACACCCAGCTA	255281	87477	TTCCTTTCTTTCTTTCTTT	299868	132064	GTCGCAGGGCCCTTGGTGGG
210695	42891	GCCCACCACCACACCCAGCT	255282	87478	TTTCCTTTCTTTCTTTCTT	299869	132065	GGTCGCAGGGCCCTTGGTGG
210696	42892	TGCCCACCACCACACCCAGC	255283	87479	TTTTCCTTTCTTTCTTTCT	299870	132066	TGGTCGCAGGGCCCTTGGTG
210697	42893	GTGCCCACCACCACACCCAG	255284	87480	TTTTTCCTTTCTTTCTTTCT	299871	132067	GTGGTCGCAGGGCCCTTGGT
210698	42894	GGTGCCCACCACCACACCCA	255285	87481	TTTTTTCCTTTCTTTCTTTC	299872	132068	TGTGGTCGCAGGGCCCTTGG
210699	42895	AGGTGCCCACCACCACACCC	255286	87482	TTTTTTTCCTTTCTTTCTTT	299873	132069	CTGTGGTCGCAGGGCCCTTG
210700	42896	CAGGTGCCCACCACCACACC	255287	87483	TTTTTTTTCCTTTCTTTCTT	299874	132070	GCTGTGGTCGCAGGGCCCTT
210701	42897	ACAGGTGCCCACCACCACAC	255288	87484	TTTTTTTTTCCTTTCTTTCT	299875	132071	TGCTGTGGTCGCAGGGCCCT
210702	42898	TACAGGTGCCCACCACCACA	255289	87485	TTTTTTTTTTCCTTTCTTTC	299876	132072	CTGCTGTGGTCGCAGGGCCC
210703	42899	CTACAGGTGCCCACCACCAC	255290	87486	GTTTTTTTTTTCCTTTCTTT	299877	132073	CCTGCTGTGGTCGCAGGGCC
210704	42900	ACTACAGGTGCCCACCACCA	255291	87487	AGTTTTTTTTTTCCTTTCTT	299878	132074	CCCTGCTGTGGTCGCAGGGC
210705	42901	GACTACAGGTGCCCACCACC	255292	87488	GAGTTTTTTTTTTCCTTTCT	299879	132075	TCCCTGCTGTGGTCGCAGGG
210706	42902	GGACTACAGGTGCCCACCAC	255293	87489	TGAGTTTTTTTTTTCCTTTC	299880	132076	ATCCCTGCTGTGGTCGCAGG
210707	42903	AGGACTACAGGTGCCCACCA	255294	87490	ATGAGTTTTTTTTTTCCTTT	299881	132077	AATCCCTGCTGTGGTCGCAG
210708	42904	TAGGACTACAGGTGCCCACC	255295	87491	CATGAGTTTTTTTTTTCCTT	299882	132078	CAATCCCTGCTGTGGTCGCA
210709	42905	CTAGGACTACAGGTGCCCAC	255296	87492	GCATGAGTTTTTTTTTTCCT	299883	132079	CCAATCCCTGCTGTGGTCGC
210710	42906	GCTAGGACTACAGGTGCCCA	255297	87493	GGCATGAGTTTTTTTTTTCC	299884	132080	CCCAATCCCTGCTGTGGTCG
210711	42907	AGCTAGGACTACAGGTGCCC	255298	87494	AGGCATGAGTTTTTTTTTTC	299885	132081	TCCCAATCCCTGCTGTGGTC
210712	42908	TAGCTAGGACTACAGGTGCC	255299	87495	CAGGCATGAGTTTTTTTTTT	299886	132082	ATCCCAATCCCTGCTGTGGT
210713	42909	GTAGCTAGGACTACAGGTGC	255300	87496	ACAGGCATGAGTTTTTTTTT	299887	132083	CATCCCAATCCCTGCTGTGG
210714	42910	AGTAGCTAGGACTACAGGTG	255301	87497	TACAGGCATGAGTTTTTTTT	299888	132084	TCATCCCAATCCCTGCTGTG

210715	42911	AAGTAGCTAGGACTACAGGT	255302	87498	TTACAGGCATGAGTTTTTTT	299889	132085	TTCATCCCAATCCCTGCTGT
210716	42912	CAAGTAGCTAGGACTACAGG	255303	87499	ATTACAGGCATGAGTTTTTT	299890	132086	ATTCATCCCAATCCCTGCTG
210717	42913	CCAAGTAGCTAGGACTACAG	255304	87500	GATTACAGGCATGAGTTTTT	299891	132087	AATTCATCCCAATCCCTGCT
210718	42914	CCCAAGTAGCTAGGACTACA	255305	87501	GGATTACAGGCATGAGTTTT	299892	132088	CAATTCATCCCAATCCCTGC
210719	42915	TCCCAAGTAGCTAGGACTAC	255306	87502	GGGATTACAGGCATGAGTTT	299893	132089	GCAATTCATCCCAATCCCTG
210720	42916	CTCCCAAGTAGCTAGGACTA	255307	87503	TGGGATTACAGGCATGAGTT	299894	132090	GGCAATTCATCCCAATCCCT
210721	42917	CCTCCCAAGTAGCTAGGACT	255308	87504	CTGGGATTACAGGCATGAGT	299895	132091	AGGCAATTCATCCCAATCCC
210722	42918	TCCTCCCAAGTAGCTAGGAC	255309	87505	GCTGGGATTACAGGCATGAG	299896	132092	CAGGCAATTCATCCCAATCC
210723	42919	ATCCTCCCAAGTAGCTAGGA	255310	87506	TGCTGGGATTACAGGCATGA	299897	132093	ACAGGCAATTCATCCCAATC
210724	42920	CATCCTCCCAAGTAGCTAGG	255311	87507	GTGCTGGGATTACAGGCATG	299898	132094	GACAGGCAATTCATCCCAAT
210725	42921	TCATCCTCCCAAGTAGCTAG	255312	87508	AGTGCTGGGATTACAGGCAT	299899	132095	GGACAGGCAATTCATCCCAA
210726	42922	CTCATCCTCCCAAGTAGCTA	255313	87509	AAGTGCTGGGATTACAGGCA	299900	132096	AGGACAGGCAATTCATCCCA
210727	42923	CCTCATCCTCCCAAGTAGCT	255314	87510	AAAGTGCTGGGATTACAGGC	299901	132097	CAGGACAGGCAATTCATCCC
210728	42924	ACCTCATCCTCCCAAGTAGC	255315	87511	CAAAGTGCTGGGATTACAGG	299902	132098	CCAGGACAGGCAATTCATCC
210729	42925	CACCTCATCCTCCCAAGTAG	255316	87512	CCAAAGTGCTGGGATTACAG	299903	132099	TCCAGGACAGGCAATTCATC
210730	42926	CCACCTCATCCTCCCAAGTA	255317	87513	CCCAAAGTGCTGGGATTACA	299904	132100	ATCCAGGACAGGCAATTCAT
210731	42927	CCCACCTCATCCTCCCAAGT	255318	87514	CCCCAAAGTGCTGGGATTAC	299905	132101	GATCCAGGACAGGCAATTCA
210732	42928	TCCCACCTCATCCTCCCAAG	255319	87515	TCCCCAAAGTGCTGGGATTA	299906	132102	AGATCCAGGACAGGCAATTC
210733	42929	CTCCCACCTCATCCTCCCAA	255320	87516	GTCCCCAAAGTGCTGGGATT	299907	132103	CAGATCCAGGACAGGCAATT
210734	42930	CCTCCCACCTCATCCTCCCA	255321	87517	GGTCCCCAAAGTGCTGGGAT	299908	132104	GCAGATCCAGGACAGGCAAT
210735	42931	TCCTCCCACCTCATCCTCCC	255322	87518	CGGTCCCCAAAGTGCTGGGA	299909	132105	AGCAGATCCAGGACAGGCAA
210736	42932	ATCCTCCCACCTCATCCTCC	255323	87519	CCGGTCCCCAAAGTGCTGGG	299910	132106	GAGCAGATCCAGGACAGGCA
210737	42933	AATCCTCCCACCTCATCCTC	255324	87520	CCCGGTCCCCAAAGTGCTGG	299911	132107	AGAGCAGATCCAGGACAGGC
210738	42934	CAATCCTCCCACCTCATCCT	255325	87521	CCCCGGTCCCCAAAGTGCTG	299912	132108	TAGAGCAGATCCAGGACAGG
210739	42935	GCAATCCTCCCACCTCATCC	255326	87522	ACCCCGGTCCCCAAAGTGCT	299913	132109	CTAGAGCAGATCCAGGACAG
210740	42936	AGCAATCCTCCCACCTCATC	255327	87523	CACCCCGGTCCCCAAAGTGC	299914	132110	TCTAGAGCAGATCCAGGACA
210741	42937	AAGCAATCCTCCCACCTCAT	255328	87524	CCACCCCGGTCCCCAAAGTG	299915	132111	CTCTAGAGCAGATCCAGGAC
210742	42938	CAAGCAATCCTCCCACCTCA	255329	87525	CCCACCCCGGTCCCCAAAGT	299916	132112	CCTCTAGAGCAGATCCAGGA
210743	42939	TCAAGCAATCCTCCCACCTC	255330	87526	GCCCACCCCGGTCCCCAAAG	299917	132113	GCCTCTAGAGCAGATCCAGG
210744	42940	CTCAAGCAATCCTCCCACCT	255331	87527	TGCCCACCCCGGTCCCCAAA	299918	132114	GGCCTCTAGAGCAGATCCAG
210745	42941	GCTCAAGCAATCCTCCCACC	255332	87528	CTGCCCACCCCGGTCCCCAA	299919	132115	GGGCCTCTAGAGCAGATCCA
210746	42942	GGCTCAAGCAATCCTCCCAC	255333	87529	TCTGCCCACCCCGGTCCCCA	299920	132116	TGGGCCTCTAGAGCAGATCC
210747	42943	GGGCTCAAGCAATCCTCCCA	255334	87530	ATCTGCCCACCCCGGTCCCC	299921	132117	TTGGGCCTCTAGAGCAGATC
210748	42944	TGGGCTCAAGCAATCCTCCC	255335	87531	GATCTGCCCACCCCGGTCCC	299922	132118	CTTGGGCCTCTAGAGCAGAT
210749	42945	TTGGGCTCAAGCAATCCTCC	255336	87532	TGATCTGCCCACCCCGGTCC	299923	132119	GCTTGGGCCTCTAGAGCAGA
210750	42946	CTTGGGCTCAAGCAATCCTC	255337	87533	GTGATCTGCCCACCCCGGTC	299924	132120	AGCTTGGGCCTCTAGAGCAG
210751	42947	TCTTGGGCTCAAGCAATCCT	255338	87534	CGTGATCTGCCCACCCCGGT	299925	132121	CAGCTTGGGCCTCTAGAGCA
210752	42948	CTCTTGGGCTCAAGCAATCC	255339	87535	TCGTGATCTGCCCACCCCGG	299926	132122	GCAGCTTGGGCCTCTAGAGC
210753	42949	ACTCTTGGGCTCAAGCAATC	255340	87536	CTCGTGATCTGCCCACCCCG	299927	132123	GGCAGCTTGGGCCTCTAGAG
210754	42950	AACTCTTGGGCTCAAGCAAT	255341	87537	CCTCGTGATCTGCCCACCCC	299928	132124	AGGCAGCTTGGGCCTCTAGA
210755	42951	AAACTCTTGGGCTCAAGCAA	255342	87538	ACCTCGTGATCTGCCCACCC	299929	132125	CAGGCAGCTTGGGCCTCTAG
210756	42952	CAAACTCTTGGGCTCAAGCA	255343	87539	GACCTCGTGATCTGCCCACC	299930	132126	GCAGGCAGCTTGGGCCTCTA
210757	42953	TCAAACTCTTGGGCTCAAGC	255344	87540	TGACCTCGTGATCTGCCCAC	299931	132127	GGCAGGCAGCTTGGGCCTCT
210758	42954	CTCAAACTCTTGGGCTCAAG	255345	87541	CTGACCTCGTGATCTGCCCA	299932	132128	AGGCAGGCAGCTTGGGCCTC
210759	42955	CCTCAAACTCTTGGGCTCAA	255346	87542	CCTGACCTCGTGATCTGCCC	299933	132129	CAGGCAGGCAGCTTGGGCCT
210760	42956	ACCTCAAACTCTTGGGCTCA	255347	87543	TCCTGACCTCGTGATCTGCC	299934	132130	TCAGGCAGGCAGCTTGGGCC
210761	42957	AACCTCAAACTCTTGGGCTC	255348	87544	CTCCTGACCTCGTGATCTGC	299935	132131	CTCAGGCAGGCAGCTTGGGC
210762	42958	TAACCTCAAACTCTTGGGCT	255349	87545	TCTCCTGACCTCGTGATCTG	299936	132132	CCTCAGGCAGGCAGCTTGGG
210763	42959	GTAACCTCAAACTCTTGGGC	255350	87546	ATCTCCTGACCTCGTGATCT	299937	132133	TCCTCAGGCAGGCAGCTTGG
210764	42960	TGTAACCTCAAACTCTTGGG	255351	87547	GATCTCCTGACCTCGTGATC	299938	132134	TTCCTCAGGCAGGCAGCTTG
210765	42961	CTGTAACCTCAAACTCTTGG	255352	87548	TGATCTCCTGACCTCGTGAT	299939	132135	CTTCCTCAGGCAGGCAGCTT
210766	42962	ACTGTAACCTCAAACTCTTG	255353	87549	TTGATCTCCTGACCTCGTGA	299940	132136	CCTTCCTCAGGCAGGCAGCT
210767	42963	TACTGTAACCTCAAACTCTT	255354	87550	CTTGATCTCCTGACCTCGTG	299941	132137	TCCTTCCTCAGGCAGGCAGC
210768	42964	TTACTGTAACCTCAAACTCT	255355	87551	TCTTGATCTCCTGACCTCGT	299942	132138	ATCCTTCCTCAGGCAGGCAG
210769	42965	CTTACTGTAACCTCAAACTC	255356	87552	GTCTTGATCTCCTGACCTCG	299943	132139	CATCCTTCCTCAGGCAGGCA
210770	42966	GCTTACTGTAACCTCAAACT	255357	87553	AGTCTTGATCTCCTGACCTC	299944	132140	TCATCCTTCCTCAGGCAGGC
210771	42967	AGCTTACTGTAACCTCAAAC	255358	87554	TAGTCTTGATCTCCTGACCT	299945	132141	GTCATCCTTCCTCAGGCAGG
210772	42968	CAGCTTACTGTAACCTCAAA	255359	87555	ATAGTCTTGATCTCCTGACC	299946	132142	AGTCATCCTTCCTCAGGCAG
210773	42969	ACAGCTTACTGTAACCTCAA	255360	87556	GATAGTCTTGATCTCCTGAC	299947	132143	AAGTCATCCTTCCTCAGGCA
210774	42970	CACAGCTTACTGTAACCTCA	255361	87557	GGATAGTCTTGATCTCCTGA	299948	132144	CAAGTCATCCTTCCTCAGGC
210775	42971	TCACAGCTTACTGTAACCTC	255362	87558	AGGATAGTCTTGATCTCCTG	299949	132145	TCAAGTCATCCTTCCTCAGG
210776	42972	ATCACAGCTTACTGTAACCT	255363	87559	CAGGATAGTCTTGATCTCCT	299950	132146	GTCAAGTCATCCTTCCTCAG
210777	42973	AATCACAGCTTACTGTAACC	255364	87560	CCAGGATAGTCTTGATCTCC	299951	132147	TGTCAAGTCATCCTTCCTCA
210778	42974	CAATCACAGCTTACTGTAAC	255365	87561	GCCAGGATAGTCTTGATCTC	299952	132148	TTGTCAAGTCATCCTTCCTC
210779	42975	GCAATCACAGCTTACTGTAA	255366	87562	GGCCAGGATAGTCTTGATCT	299953	132149	CTTGTCAAGTCATCCTTCCT
210780	42976	TGCAATCACAGCTTACTGTA	255367	87563	TGGCCAGGATAGTCTTGATC	299954	132150	ACTTGTCAAGTCATCCTTCC
210781	42977	GTGCAATCACAGCTTACTGT	255368	87564	TTGGCCAGGATAGTCTTGAT	299955	132151	GACTTGTCAAGTCATCCTTC
210782	42978	GGTGCAATCACAGCTTACTG	255369	87565	GTTGGCCAGGATAGTCTTGA	299956	132152	TGACTTGTCAAGTCATCCTT
210783	42979	TGGTGCAATCACAGCTTACT	255370	87566	TGTTGGCCAGGATAGTCTTG	299957	132153	CTGACTTGTCAAGTCATCCT
210784	42980	GTGGTGCAATCACAGCTTAC	255371	87567	ATGTTGGCCAGGATAGTCTT	299958	132154	CCTGACTTGTCAAGTCATCC
210785	42981	AGTGGTGCAATCACAGCTTA	255372	87568	CATGTTGGCCAGGATAGTCT	299959	132155	TCCTGACTTGTCAAGTCATC
210786	42982	CAGTGGTGCAATCACAGCTT	255373	87569	CCATGTTGGCCAGGATAGTC	299960	132156	CTCCTGACTTGTCAAGTCAT

210787	42983	GCAGTGGTGCAATCACAGCT	255374	87570	ACCATGTTGGCCAGGATAGT	299961	132157	TCTCCTGACTTGTCAAGTCA
210788	42984	TGCAGTGGTGCAATCACAGC	255375	87571	CACCATGTTGGCCAGGATAG	299962	132158	GTCTCCTGACTTGTCAAGTC
210789	42985	GTGCAGTGGTGCAATCACAG	255376	87572	TCACCATGTTGGCCAGGATA	299963	132159	TGTCTCCTGACTTGTCAAGT
210790	42986	AGTGCAGTGGTGCAATCACA	255377	87573	TTCACCATGTTGGCCAGGAT	299964	132160	GTGTCTCCTGACTTGTCAAG
210791	42987	GAGTGCAGTGGTGCAATCAC	255378	87574	TTTCACCATGTTGGCCAGGA	299965	132161	AGTGTCTCCTGACTTGTCAA
210792	42988	GGAGTGCAGTGGTGCAATCA	255379	87575	GTTTCACCATGTTGGCCAGG	299966	132162	CAGTGTCTCCTGACTTGTCA
210793	42989	TGGAGTGCAGTGGTGCAATC	255380	87576	GGTTTCACCATGTTGGCCAG	299967	132163	ACAGTGTCTCCTGACTTGTC
210794	42990	CTGGAGTGCAGTGGTGCAAT	255381	87577	GGGTTTCACCATGTTGGCCA	299968	132164	AACAGTGTCTCCTGACTTGT
210795	42991	GCTGGAGTGCAGTGGTGCAA	255382	87578	GGGGTTTCACCATGTTGGCC	299969	132165	GAACAGTGTCTCCTGACTTG
210796	42992	GGCTGGAGTGCAGTGGTGCA	255383	87579	CGGGGTTTCACCATGTTGGC	299970	132166	GGAACAGTGTCTCCTGACTT
210797	42993	AGGCTGGAGTGCAGTGGTGC	255384	87580	ACGGGGTTTCACCATGTTGG	299971	132167	GGGAACAGTGTCTCCTGACT
210798	42994	CAGGCTGGAGTGCAGTGGTG	255385	87581	AACGGGGTTTCACCATGTTG	299972	132168	TGGGAACAGTGTCTCCTGAC
210799	42995	CCAGGCTGGAGTGCAGTGGT	255386	87582	AAACGGGGTTTCACCATGTT	299973	132169	TTGGGAACAGTGTCTCCTGA
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210801	42997	GCCCAGGCTGGAGTGCAGTG	255388	87584	AGAAACGGGGTTTCACCATG	299975	132171	CTTTGGGAACAGTGTCTCCT
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210806	43002	CTGTTGCCCAGGCTGGAGTG	255393	87589	TTAGTAGAAACGGGGTTTCA	299980	132176	CAAGGCTTTGGGAACAGTGT
210807	43003	TCTGTTGCCCAGGCTGGAGT	255394	87590	TTTAGTAGAAACGGGGTTTC	299981	132177	TCAAGGCTTTGGGAACAGTG
210808	43004	CTCTGTTGCCCAGGCTGGAG	255395	87591	TTTTAGTAGAAACGGGGTTT	299982	132178	GTCAAGGCTTTGGGAACAGT
210809	43005	GCTCTGTTGCCCAGGCTGGA	255396	87592	TTTTTAGTAGAAACGGGGTT	299983	132179	GGTCAAGGCTTTGGGAACAG
210810	43006	AGCTCTGTTGCCCAGGCTGG	255397	87593	ATTTTTAGTAGAAACGGGGT	299984	132180	TGGTCAAGGCTTTGGGAACA
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210812	43008	TCAGCTCTGTTGCCCAGGCT	255399	87595	GTATTTTTAGTAGAAACGGG	299986	132182	TCTGGTCAAGGCTTTGGGAA
210813	43009	CTCAGCTCTGTTGCCCAGGC	255400	87596	TGTATTTTTAGTAGAAACGG	299987	132183	CTCTGGTCAAGGCTTTGGGA
210814	43010	TCTCAGCTCTGTTGCCCAGG	255401	87597	TTGTATTTTTAGTAGAAACG	299988	132184	GCTCTGGTCAAGGCTTTGGG
210815	43011	GTCTCAGCTCTGTTGCCCAG	255402	87598	TTTGTATTTTTAGTAGAAAC	299989	132185	TGCTCTGGTCAAGGCTTTGG
210816	43012	GGTCTCAGCTCTGTTGCCCA	255403	87599	TTTTGTATTTTTAGTAGAAA	299990	132186	GTGCTCTGGTCAAGGCTTTG
210817	43013	GGGTCTCAGCTCTGTTGCCC	255404	87600	TTTTTGTATTTTTAGTAGAA	299991	132187	GGTGCTCTGGTCAAGGCTTT
210818	43014	AGGGTCTCAGCTCTGTTGCC	255405	87601	ATTTTTGTATTTTTAGTAGA	299992	132188	AGGTGCTCTGGTCAAGGCTT
210819	43015	TAGGGTCTCAGCTCTGTTGC	255406	87602	AATTTTTGTATTTTTAGTAG	299993	132189	GAGGTGCTCTGGTCAAGGCT
210820	43016	ATAGGGTCTCAGCTCTGTTG	255407	87603	TAATTTTTGTATTTTTAGTA	299994	132190	TGAGGTGCTCTGGTCAAGGC
210821	43017	GATAGGGTCTCAGCTCTGTT	255408	87604	CTAATTTTTGTATTTTTAGT	299995	132191	CTGAGGTGCTCTGGTCAAGG
210822	43018	AGATAGGGTCTCAGCTCTGT	255409	87605	GCTAATTTTTGTATTTTTAG	299996	132192	GCTGAGGTGCTCTGGTCAAG
210823	43019	GAGATAGGGTCTCAGCTCTG	255410	87606	GGCTAATTTTTGTATTTTTA	299997	132193	GGCTGAGGTGCTCTGGTCAA
210824	43020	TGAGATAGGGTCTCAGCTCT	255411	87607	TGGCTAATTTTTGTATTTTT	299998	132194	GGGCTGAGGTGCTCTGGTCA
210825	43021	TTGAGATAGGGTCTCAGCTC	255412	87608	CTGGCTAATTTTTGTATTTT	299999	132195	CGGGCTGAGGTGCTCTGGTC
210826	43022	TTTGAGATAGGGTCTCAGCT	255413	87609	CCTGGCTAATTTTTGTATTT	300000	132196	GCGGGCTGAGGTGCTCTGGT
210827	43023	TTTTGAGATAGGGTCTCAGC	255414	87610	ACCTGGCTAATTTTTGTATT	300001	132197	AGCGGGCTGAGGTGCTCTGG
210828	43024	TTTTTGAGATAGGGTCTCAG	255415	87611	CACCTGGCTAATTTTTGTAT	300002	132198	CAGCGGGCTGAGGTGCTCTG
210829	43025	TTTTTTGAGATAGGGTCTCA	255416	87612	ACACCTGGCTAATTTTTGTA	300003	132199	TCAGCGGGCTGAGGTGCTCT
210830	43026	TTTTTTTGAGATAGGGTCTC	255417	87613	CACACCTGGCTAATTTTTGT	300004	132200	GTCAGCGGGCTGAGGTGCTC
210831	43027	CTTTTTTTGAGATAGGGTCT	255418	87614	CCACACCTGGCTAATTTTTG	300005	132201	GGTCAGCGGGCTGAGGTGCT
210832	43028	TCTTTTTTTGAGATAGGGTC	255419	87615	ACCACACCTGGCTAATTTTT	300006	132202	AGGTCAGCGGGCTGAGGTGC
210833	43029	TTCTTTTTTTGAGATAGGGT	255420	87616	CACCACACCTGGCTAATTTT	300007	132203	AAGGTCAGCGGGCTGAGGTG
210834	43030	TTTCTTTTTTTGAGATAGGG	255421	87617	CCACCACACCTGGCTAATTT	300008	132204	CAAGGTCAGCGGGCTGAGGT
210835	43031	TTTTCTTTTTTTGAGATAGG	255422	87618	GCCACCACACCTGGCTAATT	300009	132205	GCAAGGTCAGCGGGCTGAGG
210836	43032	TTTTTCTTTTTTTGAGATAG	255423	87619	TGCCACCACACCTGGCTAAT	300010	132206	TGCAAGGTCAGCGGGCTGAG
210837	43033	TTTTTTCTTTTTTTGAGATA	255424	87620	GTGCCACCACACCTGGCTAA	300011	132207	GTGCAAGGTCAGCGGGCTGA
210838	43034	TTTTTTTCTTTTTTTGAGAT	255425	87621	CGTGCCACCACACCTGGCTA	300012	132208	TGTGCAAGGTCAGCGGGCTG
210839	43035	TTTTTTTTCTTTTTTTGAGA	255426	87622	ACGTGCCACCACACCTGGCT	300013	132209	TTGTGCAAGGTCAGCGGGCT
210840	43036	TTTTTTTTTCTTTTTTTGAG	255427	87623	CACGTGCCACCACACCTGGC	300014	132210	TTTGTGCAAGGTCAGCGGGC
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210842	43038	TTTTTTTTTTTCTTTTTTTG	255429	87625	GGCACGTGCCACCACACCTG	300016	132212	AGTTTGTGCAAGGTCAGCGG
210843	43039	CTTTTTTTTTTTCTTTTTTT	255430	87626	AGGCACGTGCCACCACACCT	300017	132213	GAGTTTGTGCAAGGTCAGCG
210844	43040	TCTTTTTTTTTTTCTTTTTT	255431	87627	CAGGCACGTGCCACCACACC	300018	132214	GGAGTTTGTGCAAGGTCAGC
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210847	43043	CTTTCTTTTTTTTTTTCTTT	255434	87630	TTACAGGCACGTGCCACCAC	300021	132217	GATGGAGTTTGTGCAAGGTC
210848	43044	CCTTTCTTTTTTTTTTTCTT	255435	87631	ATTACAGGCACGTGCCACCA	300022	132218	AGATGGAGTTTGTGCAAGGT
210849	43045	TCCTTTCTTTTTTTTTTTCT	255436	87632	GATTACAGGCACGTGCCACC	300023	132219	CAGATGGAGTTTGTGCAAGG
210850	43046	CTCCTTTCTTTTTTTTTTTC	255437	87633	GGATTACAGGCACGTGCCAC	300024	132220	GCAGATGGAGTTTGTGCAAG
210851	43047	TCTCCTTTCTTTTTTTTTTT	255438	87634	GGGATTACAGGCACGTGCCA	300025	132221	AGCAGATGGAGTTTGTGCAA
210852	43048	CTCTCCTTTCTTTTTTTTTT	255439	87635	TGGGATTACAGGCACGTGCC	300026	132222	CAGCAGATGGAGTTTGTGCA
210853	43049	TCTCTCCTTTCTTTTTTTTT	255440	87636	CTGGGATTACAGGCACGTGC	300027	132223	GCAGCAGATGGAGTTTGTGC
210854	43050	CTCTCTCCTTTCTTTTTTTT	255441	87637	ACTGGGATTACAGGCACGTG	300028	132224	GGCAGCAGATGGAGTTTGTG
210855	43051	TCTCTCTCCTTTCTTTTTTT	255442	87638	AACTGGGATTACAGGCACGT	300029	132225	TGGCAGCAGATGGAGTTTGT
210856	43052	CTCTCTCTCCTTTCTTTTTT	255443	87639	TAACTGGGATTACAGGCACG	300030	132226	ATGGCAGCAGATGGAGTTTG
210857	43053	TCTCTCTCTCCTTTCTTTTT	255444	87640	GTAACTGGGATTACAGGCAC	300031	132227	CATGGCAGCAGATGGAGTTT
210858	43054	CTCTCTCTCTCCTTTCTTTT	255445	87641	AGTAACTGGGATTACAGGCA	300032	132228	TCATGGCAGCAGATGGAGTT

210859	43055	TCTCTCTCTCTCCTTTCTTT	255446	87642	GAGTAACTGGGATTACAGGC	300033	132229	CTCATGGCAGCAGATGGAGT
210860	43056	TTCTCTCTCTCTCCTTTCTT	255447	87643	CGAGTAACTGGGATTACAGG	300034	132230	TCTCATGGCAGCAGATGGAG
210861	43057	TTTCTCTCTCTCTCCTTTCT	255448	87644	CCGAGTAACTGGGATTACAG	300035	132231	TTCTCATGGCAGCAGATGGA
210862	43058	CTTTCTCTCTCTCTCCTTTC	255449	87645	CCCGAGTAACTGGGATTACA	300036	132232	TTTCTCATGGCAGCAGATGG
210863	43059	TCTTTCTCTCTCTCTCCTTT	255450	87646	TCCCGAGTAACTGGGATTAC	300037	132233	TTTTCTCATGGCAGCAGATG
210864	43060	TTCTTTCTCTCTCTCTCCTT	255451	87647	CTCCCGAGTAACTGGGATTA	300038	132234	CTTTTCTCATGGCAGCAGAT
210865	43061	TTTCTTTCTCTCTCTCTCCT	255452	87648	CCTCCCGAGTAACTGGGATT	300039	132235	CCTTTTCTCATGGCAGCAGA
210866	43062	TTTTCTTTCTCTCTCTCTCC	255453	87649	GCCTCCCGAGTAACTGGGAT	300040	132236	CCCTTTTCTCATGGCAGCAG
210867	43063	CTTTTCTTTCTCTCTCTCTC	255454	87650	AGCCTCCCGAGTAACTGGGA	300041	132237	TCCCTTTTCTCATGGCAGCA
210868	43064	TCTTTTCTTTCTCTCTCTCT	255455	87651	CAGCCTCCCGAGTAACTGGG	300042	132238	TTCCCTTTTCTCATGGCAGC
210869	43065	TTCTTTTCTTTCTCTCTCTC	255456	87652	TCAGCCTCCCGAGTAACTGG	300043	132239	CTTCCCTTTTCTCATGGCAG
210870	43066	TTTCTTTTCTTTCTCTCTCT	255457	87653	CTCAGCCTCCCGAGTAACTG	300044	132240	GCTTCCCTTTTCTCATGGCA
210871	43067	TTTTCTTTTCTTTCTCTCTC	255458	87654	CCTCAGCCTCCCGAGTAACT	300045	132241	GGCTTCCCTTTTCTCATGGC
210872	43068	CTTTTCTTTTCTTTCTCTCT	255459	87655	GCCTCAGCCTCCCGAGTAAC	300046	132242	CGGCTTCCCTTTTCTCATGG
210873	43069	TCTTTTCTTTTCTTTCTCTC	255460	87656	TGCCTCAGCCTCCCGAGTAA	300047	132243	GCGGCTTCCCTTTTCTCATG
210874	43070	TTCTTTTCTTTTCTTTCTCT	255461	87657	CTGCCTCAGCCTCCCGAGTA	300048	132244	GGCGGCTTCCCTTTTCTCAT
210875	43071	TTTCTTTTCTTTTCTTTCTC	255462	87658	CCTGCCTCAGCCTCCCGAGT	300049	132245	AGGCGGCTTCCCTTTTCTCA
210876	43072	TTTTCTTTTCTTTTCTTTCT	255463	87659	TCCTGCCTCAGCCTCCCGAG	300050	132246	AAGGCGGCTTCCCTTTTCTC
210877	43073	TTTTTCTTTTCTTTTCTTTC	255464	87660	CTCCTGCCTCAGCCTCCCGA	300051	132247	AAAGGCGGCTTCCCTTTTCT
210878	43074	TTTTTTCTTTTCTTTTCTTT	255465	87661	TCTCCTGCCTCAGCCTCCCG	300052	132248	CAAAGGCGGCTTCCCTTTTC
210879	43075	TTTTTTTCTTTTCTTTTCTT	255466	87662	TTCTCCTGCCTCAGCCTCCC	300053	132249	GCAAAGGCGGCTTCCCTTTT
210880	43076	TTTTTTTTCTTTTCTTTTCT	255467	87663	ATTCTCCTGCCTCAGCCTCC	300054	132250	TGCAAAGGCGGCTTCCCTTT
210881	43077	TTTTTTTTTCTTTTCTTTTC	255468	87664	GATTCTCCTGCCTCAGCCTC	300055	132251	TTGCAAAGGCGGCTTCCCTT
210882	43078	TTTTTTTTTTCTTTTCTTTT	255469	87665	CGATTCTCCTGCCTCAGCCT	300056	132252	TTTGCAAAGGCGGCTTCCCT
210883	43079	TTTTTTTTTTTCTTTTCTTT	255470	87666	GCGATTCTCCTGCCTCAGCC	300057	132253	TTTTGCAAAGGCGGCTTCCC
210884	43080	TTTTTTTTTTTTCTTTTCTT	255471	87667	AGCGATTCTCCTGCCTCAGC	300058	132254	GTTTTGCAAAGGCGGCTTCC
210885	43081	CTTTTTTTTTTTTCTTTTCT	255472	87668	AAGCGATTCTCCTGCCTCAG	300059	132255	TGTTTTGCAAAGGCGGCTTC
210886	43082	TCTTTTTTTTTTTTCTTTTC	255473	87669	CAAGCGATTCTCCTGCCTCA	300060	132256	ATGTTTTGCAAAGGCGGCTT
210887	43083	TTCTTTTTTTTTTTTCTTTT	255474	87670	TCAAGCGATTCTCCTGCCTC	300061	132257	AATGTTTTGCAAAGGCGGCT
210888	43084	CTTCTTTTTTTTTTTTCTTT	255475	87671	TTCAAGCGATTCTCCTGCCT	300062	132258	CAATGTTTTGCAAAGGCGGC
210889	43085	CCTTCTTTTTTTTTTTTCTT	255476	87672	GTTCAAGCGATTCTCCTGCC	300063	132259	GCAATGTTTTGCAAAGGCGG
210890	43086	CCCTTCTTTTTTTTTTTTCT	255477	87673	GGTTCAAGCGATTCTCCTGC	300064	132260	AGCAATGTTTTGCAAAGGCG
210891	43087	TCCCTTCTTTTTTTTTTTTC	255478	87674	TGGTTCAAGCGATTCTCCTG	300065	132261	CAGCAATGTTTTGCAAAGGC
210892	43088	TTCCCTTCTTTTTTTTTTTT	255479	87675	CTGGTTCAAGCGATTCTCCT	300066	132262	GCAGCAATGTTTTGCAAAGG
210893	43089	CTTCCCTTCTTTTTTTTTTT	255480	87676	CCTGGTTCAAGCGATTCTCC	300067	132263	GGCAGCAATGTTTTGCAAAG
210894	43090	CCTTCCCTTCTTTTTTTTTT	255481	87677	CCCTGGTTCAAGCGATTCTC	300068	132264	AGGCAGCAATGTTTTGCAAA
210895	43091	CCCTTCCCTTCTTTTTTTTT	255482	87678	TCCCTGGTTCAAGCGATTCT	300069	132265	TAGGCAGCAATGTTTTGCAA
210896	43092	TCCCTTCCCTTCTTTTTTTT	255483	87679	CTCCCTGGTTCAAGCGATTC	300070	132266	TTAGGCAGCAATGTTTTGCA
210897	43093	TTCCCTTCCCTTCTTTTTTT	255484	87680	ACTCCCTGGTTCAAGCGATT	300071	132267	TTTAGGCAGCAATGTTTTGC
210898	43094	TTTCCCTTCCCTTCTTTTTT	255485	87681	GACTCCCTGGTTCAAGCGAT	300072	132268	CTTTAGGCAGCAATGTTTTG
210899	43095	CTTTCCCTTCCCTTCTTTTT	255486	87682	TGACTCCCTGGTTCAAGCGA	300073	132269	TCTTTAGGCAGCAATGTTTT
210900	43096	GCTTTCCCTTCCCTTCTTTT	255487	87683	CTGACTCCCTGGTTCAAGCG	300074	132270	TTCTTTAGGCAGCAATGTTT
210901	43097	GGCTTTCCCTTCCCTTCTTT	255488	87684	TCTGACTCCCTGGTTCAAGC	300075	132271	TTTCTTTAGGCAGCAATGTT
210902	43098	GGGCTTTCCCTTCCCTTCTT	255489	87685	CTCTGACTCCCTGGTTCAAG	300076	132272	GTTTCTTTAGGCAGCAATGT
210903	43099	TGGGCTTTCCCTTCCCTTCT	255490	87686	CCTCTGACTCCCTGGTTCAA	300077	132273	AGTTTCTTTAGGCAGCAATG
210904	43100	CTGGGCTTTCCCTTCCCTTC	255491	87687	ACCTCTGACTCCCTGGTTCA	300078	132274	GAGTTTCTTTAGGCAGCAAT
210905	43101	TCTGGGCTTTCCCTTCCCTT	255492	87688	AACCTCTGACTCCCTGGTTC	300079	132275	TGAGTTTCTTTAGGCAGCAA
210906	43102	TTCTGGGCTTTCCCTTCCCT	255493	87689	CAACCTCTGACTCCCTGGTT	300080	132276	CTGAGTTTCTTTAGGCAGCA
210907	43103	CTTCTGGGCTTTCCCTTCCC	255494	87690	GCAACCTCTGACTCCCTGGT	300081	132277	GCTGAGTTTCTTTAGGCAGC
210908	43104	TCTTCTGGGCTTTCCCTTCC	255495	87691	TGCAACCTCTGACTCCCTGG	300082	132278	TGCTGAGTTTCTTTAGGCAG
210909	43105	CTCTTCTGGGCTTTCCCTTC	255496	87692	CTGCAACCTCTGACTCCCTG	300083	132279	CTGCTGAGTTTCTTTAGGCA
210910	43106	ACTCTTCTGGGCTTTCCCTT	255497	87693	ACTGCAACCTCTGACTCCCT	300084	132280	GCTGCTGAGTTTCTTTAGGC
210911	43107	CACTCTTCTGGGCTTTCCCT	255498	87694	CACTGCAACCTCTGACTCCC	300085	132281	GGCTGCTGAGTTTCTTTAGG
210912	43108	ACACTCTTCTGGGCTTTCCC	255499	87695	TCACTGCAACCTCTGACTCC	300086	132282	AGGCTGCTGAGTTTCTTTAG
210913	43109	CACACTCTTCTGGGCTTTCC	255500	87696	CTCACTGCAACCTCTGACTC	300087	132283	GAGGCTGCTGAGTTTCTTTA
210914	43110	CCACACTCTTCTGGGCTTTC	255501	87697	GCTCACTGCAACCTCTGACT	300088	132284	TGAGGCTGCTGAGTTTCTTT
210915	43111	CCCACACTCTTCTGGGCTTT	255502	87698	AGCTCACTGCAACCTCTGAC	300089	132285	CTGAGGCTGCTGAGTTTCTT
210916	43112	CCCCACACTCTTCTGGGCTT	255503	87699	CAGCTCACTGCAACCTCTGA	300090	132286	CCTGAGGCTGCTGAGTTTCT
210917	43113	TCCCCACACTCTTCTGGGCT	255504	87700	TCAGCTCACTGCAACCTCTG	300091	132287	GCCTGAGGCTGCTGAGTTTC
210918	43114	CTCCCCACACTCTTCTGGGC	255505	87701	CTCAGCTCACTGCAACCTCT	300092	132288	GGCCTGAGGCTGCTGAGTTT
210919	43115	TCTCCCCACACTCTTCTGGG	255506	87702	TCTCAGCTCACTGCAACCTC	300093	132289	GGGCCTGAGGCTGCTGAGTT
210920	43116	CTCTCCCCACACTCTTCTGG	255507	87703	ATCTCAGCTCACTGCAACCT	300094	132290	TGGGCCTGAGGCTGCTGAGT
210921	43117	CCTCTCCCCACACTCTTCTG	255508	87704	GATCTCAGCTCACTGCAACC	300095	132291	TTGGGCCTGAGGCTGCTGAG
210922	43118	TCCTCTCCCCACACTCTTCT	255509	87705	CGATCTCAGCTCACTGCAAC	300096	132292	ATTGGGCCTGAGGCTGCTGA
210923	43119	CTCCTCTCCCCACACTCTTC	255510	87706	ACGATCTCAGCTCACTGCAA	300097	132293	AATTGGGCCTGAGGCTGCTG
210924	43120	CCTCCTCTCCCCACACTCTT	255511	87707	CACGATCTCAGCTCACTGCA	300098	132294	GAATTGGGCCTGAGGCTGCT
210925	43121	GCCTCCTCTCCCCACACTCT	255512	87708	GCACGATCTCAGCTCACTGC	300099	132295	AGAATTGGGCCTGAGGCTGC
210926	43122	CGCCTCCTCTCCCCACACTC	255513	87709	GGCACGATCTCAGCTCACTG	300100	132296	CAGAATTGGGCCTGAGGCTG
210927	43123	CCGCCTCCTCTCCCCACACT	255514	87710	TGGCACGATCTCAGCTCACT	300101	132297	GCAGAATTGGGCCTGAGGCT
210928	43124	GCCGCCTCCTCTCCCCACAC	255515	87711	GTGGCACGATCTCAGCTCAC	300102	132298	GGCAGAATTGGGCCTGAGGC
210929	43125	GGCCGCCTCCTCTCCCCACA	255516	87712	AGTGGCACGATCTCAGCTCA	300103	132299	TGGCAGAATTGGGCCTGAGG
210930	43126	CGGCCGCCTCCTCTCCCCAC	255517	87713	CAGTGGCACGATCTCAGCTC	300104	132300	GTGGCAGAATTGGGCCTGAG

210931	43127	ACGGCCGCCTCCTCTCCCCA	255518	87714	ACAGTGGCACGATCTCAGCT	300105	132301	AGTGGCAGAATTGGGCCTGA
210932	43128	GACGGCCGCCTCCTCTCCCC	255519	87715	TACAGTGGCACGATCTCAGC	300106	132302	AAGTGGCAGAATTGGGCCTG
210933	43129	TGACGGCCGCCTCCTCTCCC	255520	87716	GTACAGTGGCACGATCTCAG	300107	132303	GAAGTGGCAGAATTGGGCCT
210934	43130	ATGACGGCCGCCTCCTCTCC	255521	87717	AGTACAGTGGCACGATCTCA	300108	132304	AGAAGTGGCAGAATTGGGCC
210935	43131	AATGACGGCCGCCTCCTCTC	255522	87718	GAGTACAGTGGCACGATCTC	300109	132305	CAGAAGTGGCAGAATTGGGC
210936	43132	GAATGACGGCCGCCTCCTCT	255523	87719	GGAGTACAGTGGCACGATCT	300110	132306	CCAGAAGTGGCAGAATTGGG
210937	43133	AGAATGACGGCCGCCTCCTC	255524	87720	TGGAGTACAGTGGCACGATC	300111	132307	ACCAGAAGTGGCAGAATTGG
210938	43134	CAGAATGACGGCCGCCTCCT	255525	87721	CTGGAGTACAGTGGCACGAT	300112	132308	AACCAGAAGTGGCAGAATTG
210939	43135	CCAGAATGACGGCCGCCTCC	255526	87722	GCTGGAGTACAGTGGCACGA	300113	132309	AAACCAGAAGTGGCAGAATT
210940	43136	CCCAGAATGACGGCCGCCTC	255527	87723	GGCTGGAGTACAGTGGCACG	300114	132310	CAAACCAGAAGTGGCAGAAT
210941	43137	CCCCAGAATGACGGCCGCCT	255528	87724	AGGCTGGAGTACAGTGGCAC	300115	132311	CCAAACCAGAAGTGGCAGAA
210942	43138	GCCCCAGAATGACGGCCGCC	255529	87725	CAGGCTGGAGTACAGTGGCA	300116	132312	CCCAAACCAGAAGTGGCAGA
210943	43139	GGCCCCAGAATGACGGCCGC	255530	87726	CCAGGCTGGAGTACAGTGGC	300117	132313	ACCCAAACCAGAAGTGGCAG
210944	43140	GGGCCCCAGAATGACGGCCG	255531	87727	CCCAGGCTGGAGTACAGTGG	300118	132314	TACCCAAACCAGAAGTGGCA
210945	43141	AGGGCCCCAGAATGACGGCC	255532	87728	GCCCAGGCTGGAGTACAGTG	300119	132315	GTACCCAAACCAGAAGTGGC
210946	43142	GAGGGCCCCAGAATGACGGC	255533	87729	CGCCCAGGCTGGAGTACAGT	300120	132316	TGTACCCAAACCAGAAGTGG
210947	43143	TGAGGGCCCCAGAATGACGG	255534	87730	TCGCCCAGGCTGGAGTACAG	300121	132317	CTGTACCCAAACCAGAAGTG
210948	43144	CTGAGGGCCCCAGAATGACG	255535	87731	GTCGCCCAGGCTGGAGTACA	300122	132318	ACTGTACCCAAACCAGAAGT
210949	43145	ACTGAGGGCCCCAGAATGAC	255536	87732	TGTCGCCCAGGCTGGAGTAC	300123	132319	AACTGTACCCAAACCAGAAG
210950	43146	CACTGAGGGCCCCAGAATGA	255537	87733	CTGTCGCCCAGGCTGGAGTA	300124	132320	TAACTGTACCCAAACCAGAA
210951	43147	ACACTGAGGGCCCCAGAATG	255538	87734	TCTGTCGCCCAGGCTGGAGT	300125	132321	TTAACTGTACCCAAACCAGA
210952	43148	CACACTGAGGGCCCCAGAAT	255539	87735	CTCTGTCGCCCAGGCTGGAG	300126	132322	TTTAACTGTACCCAAACCAG
210953	43149	GCACACTGAGGGCCCCAGAA	255540	87736	ACTCTGTCGCCCAGGCTGGA	300127	132323	CTTTAACTGTACCCAAACCA
210954	43150	TGCACACTGAGGGCCCCAGA	255541	87737	CACTCTGTCGCCCAGGCTGG	300128	132324	CCTTTAACTGTACCCAAACC
210955	43151	GTGCACACTGAGGGCCCCAG	255542	87738	TCACTCTGTCGCCCAGGCTG	300129	132325	GCCTTTAACTGTACCCAAAC
210956	43152	TGTGCACACTGAGGGCCCCA	255543	87739	CTCACTCTGTCGCCCAGGCT	300130	132326	TGCCTTTAACTGTACCCAAA
210957	43153	TTGTGCACACTGAGGGCCCC	255544	87740	TCTCACTCTGTCGCCCAGGC	300131	132327	TTGCCTTTAACTGTACCCAA
210958	43154	GTTGTGCACACTGAGGGCCC	255545	87741	GTCTCACTCTGTCGCCCAGG	300132	132328	GTTGCCTTTAACTGTACCCA
210959	43155	GGTTGTGCACACTGAGGGCC	255546	87742	AGTCTCACTCTGTCGCCCAG	300133	132329	GGTTGCCTTTAACTGTACCC
210960	43156	TGGTTGTGCACACTGAGGGC	255547	87743	GAGTCTCACTCTGTCGCCCA	300134	132330	GGGTTGCCTTTAACTGTACC
210961	43157	CTGGTTGTGCACACTGAGGG	255548	87744	AGAGTCTCACTCTGTCGCCC	300135	132331	AGGGTTGCCTTTAACTGTAC
210962	43158	TCTGGTTGTGCACACTGAGG	255549	87745	CAGAGTCTCACTCTGTCGCC	300136	132332	CAGGGTTGCCTTTAACTGTA
210963	43159	ATCTGGTTGTGCACACTGAG	255550	87746	ACAGAGTCTCACTCTGTCGC	300137	132333	TCAGGGTTGCCTTTAACTGT
210964	43160	TATCTGGTTGTGCACACTGA	255551	87747	GACAGAGTCTCACTCTGTCG	300138	132334	CTCAGGGTTGCCTTTAACTG
210965	43161	TTATCTGGTTGTGCACACTG	255552	87748	AGACAGAGTCTCACTCTGTC	300139	132335	CCTCAGGGTTGCCTTTAACT
210966	43162	GTTATCTGGTTGTGCACACT	255553	87749	GAGACAGAGTCTCACTCTGT	300140	132336	CCCTCAGGGTTGCCTTTAAC
210967	43163	TGTTATCTGGTTGTGCACAC	255554	87750	TGAGACAGAGTCTCACTCTG	300141	132337	TCCCTCAGGGTTGCCTTTAA
210968	43164	GTGTTATCTGGTTGTGCACA	255555	87751	TTGAGACAGAGTCTCACTCT	300142	132338	GTCCCTCAGGGTTGCCTTTA
210969	43165	TGTGTTATCTGGTTGTGCAC	255556	87752	TTTGAGACAGAGTCTCACTC	300143	132339	AGTCCCTCAGGGTTGCCTTT
210970	43166	ATGTGTTATCTGGTTGTGCA	255557	87753	GTTTGAGACAGAGTCTCACT	300144	132340	AAGTCCCTCAGGGTTGCCTT
210971	43167	CATGTGTTATCTGGTTGTGC	255558	87754	GGTTTGAGACAGAGTCTCAC	300145	132341	CAAGTCCCTCAGGGTTGCCT
210972	43168	GCATGTGTTATCTGGTTGTG	255559	87755	TGGTTTGAGACAGAGTCTCA	300146	132342	CCAAGTCCCTCAGGGTTGCC
210973	43169	AGCATGTGTTATCTGGTTGT	255560	87756	TTGGTTTGAGACAGAGTCTC	300147	132343	GCCAAGTCCCTCAGGGTTGC
210974	43170	GAGCATGTGTTATCTGGTTG	255561	87757	TTTGGTTTGAGACAGAGTCT	300148	132344	TGCCAAGTCCCTCAGGGTTG
210975	43171	AGAGCATGTGTTATCTGGTT	255562	87758	TTTTGGTTTGAGACAGAGTC	300149	132345	CTGCCAAGTCCCTCAGGGTT
210976	43172	CAGAGCATGTGTTATCTGGT	255563	87759	TTTTTGGTTTGAGACAGAGT	300150	132346	ACTGCCAAGTCCCTCAGGGT
210977	43173	ACAGAGCATGTGTTATCTGG	255564	87760	TTTTTTGGTTTGAGACAGAG	300151	132347	TACTGCCAAGTCCCTCAGGG
210978	43174	CACAGAGCATGTGTTATCTG	255565	87761	TTTTTTTGGTTTGAGACAGA	300152	132348	CTACTGCCAAGTCCCTCAGG
210979	43175	CCACAGAGCATGTGTTATCT	255566	87762	TTTTTTTTGGTTTGAGACAG	300153	132349	TCTACTGCCAAGTCCCTCAG
210980	43176	CCCACAGAGCATGTGTTATC	255567	87763	CTTTTTTTTGGTTTGAGACA	300154	132350	TTCTACTGCCAAGTCCCTCA
210981	43177	GCCCACAGAGCATGTGTTAT	255568	87764	CCTTTTTTTTGGTTTGAGAC	300155	132351	TTTCTACTGCCAAGTCCCTC
210982	43178	AGCCCACAGAGCATGTGTTA	255569	87765	CCCTTTTTTTTGGTTTGAGA	300156	132352	ATTTCTACTGCCAAGTCCCT
210983	43179	AAGCCCACAGAGCATGTGTT	255570	87766	CCCCTTTTTTTTGGTTTGAG	300157	132353	GATTTCTACTGCCAAGTCCC
210984	43180	AAAGCCCACAGAGCATGTGT	255571	87767	ACCCCTTTTTTTTGGTTTGA	300158	132354	GGATTTCTACTGCCAAGTCC
210985	43181	AAAAGCCCACAGAGCATGTG	255572	87768	CACCCCTTTTTTTTGGTTTG	300159	132355	TGGATTTCTACTGCCAAGTC
210986	43182	CAAAAGCCCACAGAGCATGT	255573	87769	CCACCCCTTTTTTTTGGTTT	300160	132356	CTGGATTTCTACTGCCAAGT
210987	43183	ACAAAAGCCCACAGAGCATG	255574	87770	CCCACCCCTTTTTTTTGGTT	300161	132357	CCTGGATTTCTACTGCCAAG
210988	43184	TACAAAAGCCCACAGAGCAT	255575	87771	CCCCACCCCTTTTTTTTGGT	300162	132358	CCCTGGATTTCTACTGCCAA
210989	43185	GTACAAAAGCCCACAGAGCA	255576	87772	CCCCCACCCCTTTTTTTTGG	300163	132359	GCCCTGGATTTCTACTGCCA
210990	43186	GGTACAAAAGCCCACAGAGC	255577	87773	CCCCCCACCCCTTTTTTTTG	300164	132360	GGCCCTGGATTTCTACTGCC
210991	43187	TGGTACAAAAGCCCACAGAG	255578	87774	GCCCCCCACCCCTTTTTTTT	300165	132361	AGGCCCTGGATTTCTACTGC
210992	43188	ATGGTACAAAAGCCCACAGA	255579	87775	CGCCCCCCACCCCTTTTTTT	300166	132362	GAGGCCCTGGATTTCTACTG
210993	43189	AATGGTACAAAAGCCCACAG	255580	87776	CCGCCCCCCACCCCTTTTTT	300167	132363	GGAGGCCCTGGATTTCTACT
210994	43190	AAATGGTACAAAAGCCCACA	255581	87777	CCCGCCCCCCACCCCTTTTT	300168	132364	GGGAGGCCCTGGATTTCTAC
210995	43191	AAAATGGTACAAAAGCCCAC	255582	87778	CCCCGCCCCCCACCCCTTTT	300169	132365	GGGGAGGCCCTGGATTTCTA
210996	43192	CAAAATGGTACAAAAGCCCA	255583	87779	CCCCCGCCCCCCACCCCTTT	300170	132366	AGGGGAGGCCCTGGATTTCT
210997	43193	GCAAAATGGTACAAAAGCCC	255584	87780	GCCCCCGCCCCCCACCCCTT	300171	132367	CAGGGGAGGCCCTGGATTTC
210998	43194	AGCAAAATGGTACAAAAGCC	255585	87781	TGCCCCCGCCCCCCACCCCT	300172	132368	CCAGGGGAGGCCCTGGATTT
210999	43195	AAGCAAAATGGTACAAAAGC	255586	87782	CTGCCCCCGCCCCCCACCCC	300173	132369	CCCAGGGGAGGCCCTGGATT
211000	43196	CAAGCAAAATGGTACAAAAG	255587	87783	CCTGCCCCCGCCCCCCACCC	300174	132370	CCCCAGGGGAGGCCCTGGAT
211001	43197	TCAAGCAAAATGGTACAAAA	255588	87784	TCCTGCCCCCGCCCCCCACC	300175	132371	GCCCCAGGGGAGGCCCTGGA
211002	43198	CTCAAGCAAAATGGTACAAA	255589	87785	CTCCTGCCCCCGCCCCCCAC	300176	132372	AGCCCCAGGGGAGGCCCTGG

211003	43199	GCTCAAGCAAAATGGTACAA	255590	87786	TCTCCTGCCCCCGCCCCCCA	300177	132373	CAGCCCCAGGGGAGGCCCTG
211004	43200	TGCTCAAGCAAAATGGTACA	255591	87787	TTCTCCTGCCCCCGCCCCCC	300178	132374	CCAGCCCCAGGGGAGGCCCT
211005	43201	ATGCTCAAGCAAAATGGTAC	255592	87788	GTTCTCCTGCCCCCGCCCCC	300179	132375	GCCAGCCCCAGGGGAGGCCC
211006	43202	TATGCTCAAGCAAAATGGTA	255593	87789	TGTTCTCCTGCCCCCGCCCC	300180	132376	TGCCAGCCCCAGGGGAGGCC
211007	43203	TTATGCTCAAGCAAAATGGT	255594	87790	CTGTTCTCCTGCCCCCGCCC	300181	132377	CTGCCAGCCCCAGGGGAGGC
211008	43204	TTTATGCTCAAGCAAAATGG	255595	87791	ACTGTTCTCCTGCCCCCGCC	300182	132378	GCTGCCAGCCCCAGGGGAGG
211009	43205	CTTTATGCTCAAGCAAAATG	255596	87792	CACTGTTCTCCTGCCCCCGC	300183	132379	AGCTGCCAGCCCCAGGGGAG
211010	43206	TCTTTATGCTCAAGCAAAAT	255597	87793	TCACTGTTCTCCTGCCCCCG	300184	132380	AAGCTGCCAGCCCCAGGGGA
211011	43207	TTCTTTATGCTCAAGCAAAA	255598	87794	CTCACTGTTCTCCTGCCCCC	300185	132381	GAAGCTGCCAGCCCCAGGGG
211012	43208	TTTCTTTATGCTCAAGCAAA	255599	87795	TCTCACTGTTCTCCTGCCCC	300186	132382	CGAAGCTGCCAGCCCCAGGG
211013	43209	CTTTCTTTATGCTCAAGCAA	255600	87796	CTCTCACTGTTCTCCTGCCC	300187	132383	ACGAAGCTGCCAGCCCCAGG
211014	43210	CCTTTCTTTATGCTCAAGCA	255601	87797	CCTCTCACTGTTCTCCTGCC	300188	132384	CACGAAGCTGCCAGCCCCAG
211015	43211	TCCTTTCTTTATGCTCAAGC	255602	87798	ACCTCTCACTGTTCTCCTGC	300189	132385	ACACGAAGCTGCCAGCCCCA
211016	43212	TTCCTTTCTTTATGCTCAAG	255603	87799	TACCTCTCACTGTTCTCCTG	300190	132386	CACACGAAGCTGCCAGCCCC
211017	43213	CTTCCTTTCTTTATGCTCAA	255604	87800	CTACCTCTCACTGTTCTCCT	300191	132387	GCACACGAAGCTGCCAGCCC
211018	43214	CCTTCCTTTCTTTATGCTCA	255605	87801	CCTACCTCTCACTGTTCTCC	300192	132388	TGCACACGAAGCTGCCAGCC
211019	43215	GCCTTCCTTTCTTTATGCTC	255606	87802	CCCTACCTCTCACTGTTCTC	300193	132389	CTGCACACGAAGCTGCCAGC
211020	43216	AGCCTTCCTTTCTTTATGCT	255607	87803	TCCCTACCTCTCACTGTTCT	300194	132390	GCTGCACACGAAGCTGCCAG
211021	43217	CAGCCTTCCTTTCTTTATGC	255608	87804	CTCCCTACCTCTCACTGTTC	300195	132391	AGCTGCACACGAAGCTGCCA
211022	43218	GCAGCCTTCCTTTCTTTATG	255609	87805	TCTCCCTACCTCTCACTGTT	300196	132392	TAGCTGCACACGAAGCTGCC
211023	43219	GGCAGCCTTCCTTTCTTTAT	255610	87806	CTCTCCCTACCTCTCACTGT	300197	132393	CTAGCTGCACACGAAGCTGC
211024	43220	GGGCAGCCTTCCTTTCTTTA	255611	87807	CCTCTCCCTACCTCTCACTG	300198	132394	TCTAGCTGCACACGAAGCTG
211025	43221	GGGGCAGCCTTCCTTTCTTT	255612	87808	TCCTCTCCCTACCTCTCACT	300199	132395	CTCTAGCTGCACACGAAGCT
211026	43222	AGGGGCAGCCTTCCTTTCTT	255613	87809	TTCCTCTCCCTACCTCTCAC	300200	132396	GCTCTAGCTGCACACGAAGC
211027	43223	TAGGGGCAGCCTTCCTTTCT	255614	87810	TTTCCTCTCCCTACCTCTCA	300201	132397	AGCTCTAGCTGCACACGAAG
211028	43224	TTAGGGGCAGCCTTCCTTTC	255615	87811	CTTTCCTCTCCCTACCTCTC	300202	132398	AAGCTCTAGCTGCACACGAA
211029	43225	TTTAGGGGCAGCCTTCCTTT	255616	87812	CCTTTCCTCTCCCTACCTCT	300203	132399	AAAGCTCTAGCTGCACACGA
211030	43226	ATTTAGGGGCAGCCTTCCTT	255617	87813	CCCTTTCCTCTCCCTACCTC	300204	132400	TAAAGCTCTAGCTGCACACG
211031	43227	TATTTAGGGGCAGCCTTCCT	255618	87814	CCCCTTTCCTCTCCCTACCT	300205	132401	GTAAAGCTCTAGCTGCACAC
211032	43228	CTATTTAGGGGCAGCCTTCC	255619	87815	TCCCCTTTCCTCTCCCTACC	300206	132402	GGTAAAGCTCTAGCTGCACA
211033	43229	TCTATTTAGGGGCAGCCTTC	255620	87816	ATCCCCTTTCCTCTCCCTAC	300207	132403	AGGTAAAGCTCTAGCTGCAC
211034	43230	TTCTATTTAGGGGCAGCCTT	255621	87817	AATCCCCTTTCCTCTCCCTA	300208	132404	CAGGTAAAGCTCTAGCTGCA
211035	43231	TTTCTATTTAGGGGCAGCCT	255622	87818	GAATCCCCTTTCCTCTCCCT	300209	132405	TCAGGTAAAGCTCTAGCTGC
211036	43232	CTTTCTATTTAGGGGCAGCC	255623	87819	AGAATCCCCTTTCCTCTCCC	300210	132406	TTCAGGTAAAGCTCTAGCTG
211037	43233	GCTTTCTATTTAGGGGCAGC	255624	87820	GAGAATCCCCTTTCCTCTCC	300211	132407	TTTCAGGTAAAGCTCTAGCT
211038	43234	TGCTTTCTATTTAGGGGCAG	255625	87821	CGAGAATCCCCTTTCCTCTC	300212	132408	CTTTCAGGTAAAGCTCTAGC
211039	43235	GTGCTTTCTATTTAGGGGCA	255626	87822	GCGAGAATCCCCTTTCCTCT	300213	132409	CCTTTCAGGTAAAGCTCTAG
211040	43236	AGTGCTTTCTATTTAGGGGC	255627	87823	AGCGAGAATCCCCTTTCCTC	300214	132410	TCCTTTCAGGTAAAGCTCTA
211041	43237	GAGTGCTTTCTATTTAGGGG	255628	87824	TAGCGAGAATCCCCTTTCCT	300215	132411	TTCCTTTCAGGTAAAGCTCT
211042	43238	AGAGTGCTTTCTATTTAGGG	255629	87825	GTAGCGAGAATCCCCTTTCC	300216	132412	CTTCCTTTCAGGTAAAGCTC
211043	43239	CAGAGTGCTTTCTATTTAGG	255630	87826	TGTAGCGAGAATCCCCTTTC	300217	132413	ACTTCCTTTCAGGTAAAGCT
211044	43240	CCAGAGTGCTTTCTATTTAG	255631	87827	GTGTAGCGAGAATCCCCTTT	300218	132414	GACTTCCTTTCAGGTAAAGC
211045	43241	TCCAGAGTGCTTTCTATTTA	255632	87828	GGTGTAGCGAGAATCCCCTT	300219	132415	AGACTTCCTTTCAGGTAAAG
211046	43242	CTCCAGAGTGCTTTCTATTT	255633	87829	GGGTGTAGCGAGAATCCCCT	300220	132416	GAGACTTCCTTTCAGGTAAA
211047	43243	CCTCCAGAGTGCTTTCTATT	255634	87830	TGGGTGTAGCGAGAATCCCC	300221	132417	AGAGACTTCCTTTCAGGTAA
211048	43244	GCCTCCAGAGTGCTTTCTAT	255635	87831	TTGGGTGTAGCGAGAATCCC	300222	132418	CAGAGACTTCCTTTCAGGTA
211049	43245	TGCCTCCAGAGTGCTTTCTA	255636	87832	TTTGGGTGTAGCGAGAATCC	300223	132419	CCAGAGACTTCCTTTCAGGT
211050	43246	TTGCCTCCAGAGTGCTTTCT	255637	87833	GTTTGGGTGTAGCGAGAATC	300224	132420	CCCAGAGACTTCCTTTCAGG
211051	43247	TTTGCCTCCAGAGTGCTTTC	255638	87834	GGTTTGGGTGTAGCGAGAAT	300225	132421	GCCCAGAGACTTCCTTTCAG
211052	43248	GTTTGCCTCCAGAGTGCTTT	255639	87835	TGGTTTGGGTGTAGCGAGAA	300226	132422	GGCCCAGAGACTTCCTTTCA
211053	43249	TGTTTGCCTCCAGAGTGCTT	255640	87836	CTGGTTTGGGTGTAGCGAGA	300227	132423	GGGCCCAGAGACTTCCTTTC
211054	43250	TTGTTTGCCTCCAGAGTGCT	255641	87837	TCTGGTTTGGGTGTAGCGAG	300228	132424	TGGGCCCAGAGACTTCCTTT
211055	43251	TTTGTTTGCCTCCAGAGTGC	255642	87838	ATCTGGTTTGGGTGTAGCGA	300229	132425	CTGGGCCCAGAGACTTCCTT
211056	43252	ATTTGTTTGCCTCCAGAGTG	255643	87839	TATCTGGTTTGGGTGTAGCG	300230	132426	TCTGGGCCCAGAGACTTCCT
211057	43253	GATTTGTTTGCCTCCAGAGT	255644	87840	GTATCTGGTTTGGGTGTAGC	300231	132427	TTCTGGGCCCAGAGACTTCC
211058	43254	AGATTTGTTTGCCTCCAGAG	255645	87841	GGTATCTGGTTTGGGTGTAG	300232	132428	GTTCTGGGCCCAGAGACTTC
211059	43255	CAGATTTGTTTGCCTCCAGA	255646	87842	TGGTATCTGGTTTGGGTGTA	300233	132429	AGTTCTGGGCCCAGAGACTT
211060	43256	TCAGATTTGTTTGCCTCCAG	255647	87843	ATGGTATCTGGTTTGGGTGT	300234	132430	GAGTTCTGGGCCCAGAGACT
211061	43257	GTCAGATTTGTTTGCCTCCA	255648	87844	GATGGTATCTGGTTTGGGTG	300235	132431	AGAGTTCTGGGCCCAGAGAC
211062	43258	AGTCAGATTTGTTTGCCTCC	255649	87845	AGATGGTATCTGGTTTGGGT	300236	132432	GAGAGTTCTGGGCCCAGAGA
211063	43259	GAGTCAGATTTGTTTGCCTC	255650	87846	TAGATGGTATCTGGTTTGGG	300237	132433	GGAGAGTTCTGGGCCCAGAG
211064	43260	GGAGTCAGATTTGTTTGCCT	255651	87847	CTAGATGGTATCTGGTTTGG	300238	132434	TGGAGAGTTCTGGGCCCAGA
211065	43261	TGGAGTCAGATTTGTTTGCC	255652	87848	TCTAGATGGTATCTGGTTTG	300239	132435	GTGGAGAGTTCTGGGCCCAG
211066	43262	TTGGAGTCAGATTTGTTTGC	255653	87849	CTCTAGATGGTATCTGGTTT	300240	132436	GGTGGAGAGTTCTGGGCCCA
211067	43263	ATTGGAGTCAGATTTGTTTG	255654	87850	CCTCTAGATGGTATCTGGTT	300241	132437	TGGTGGAGAGTTCTGGGCCC
211068	43264	GATTGGAGTCAGATTTGTTT	255655	87851	GCCTCTAGATGGTATCTGGT	300242	132438	TTGGTGGAGAGTTCTGGGCC
211069	43265	GGATTGGAGTCAGATTTGTT	255656	87852	AGCCTCTAGATGGTATCTGG	300243	132439	CTTGGTGGAGAGTTCTGGGC
211070	43266	AGGATTGGAGTCAGATTTGT	255657	87853	TAGCCTCTAGATGGTATCTG	300244	132440	TCTTGGTGGAGAGTTCTGGG
211071	43267	CAGGATTGGAGTCAGATTTG	255658	87854	CTAGCCTCTAGATGGTATCT	300245	132441	CTCTTGGTGGAGAGTTCTGG
211072	43268	CCAGGATTGGAGTCAGATTT	255659	87855	TCTAGCCTCTAGATGGTATC	300246	132442	GCTCTTGGTGGAGAGTTCTG
211073	43269	GCCAGGATTGGAGTCAGATT	255660	87856	TTCTAGCCTCTAGATGGTAT	300247	132443	GGCTCTTGGTGGAGAGTTCT
211074	43270	GGCCAGGATTGGAGTCAGAT	255661	87857	ATTCTAGCCTCTAGATGGTA	300248	132444	AGGCTCTTGGTGGAGAGTTC

211075	43271	GGGCCAGGATTGGAGTCAGA	255662	87858	GATTCTAGCCTCTAGATGGT	300249	132445	GAGGCTCTTGGTGGAGAGTT
211076	43272	AGGGCCAGGATTGGAGTCAG	255663	87859	AGATTCTAGCCTCTAGATGG	300250	132446	GGAGGCTCTTGGTGGAGAGT
211077	43273	CAGGGCCAGGATTGGAGTCA	255664	87860	AAGATTCTAGCCTCTAGATG	300251	132447	GGGAGGCTCTTGGTGGAGAG
211078	43274	GCAGGGCCAGGATTGGAGTC	255665	87861	AAAGATTCTAGCCTCTAGAT	300252	132448	AGGGAGGCTCTTGGTGGAGA
211079	43275	GGCAGGGCCAGGATTGGAGT	255666	87862	CAAAGATTCTAGCCTCTAGA	300253	132449	CAGGGAGGCTCTTGGTGGAG
211080	43276	TGGCAGGGCCAGGATTGGAG	255667	87863	CCAAAGATTCTAGCCTCTAG	300254	132450	GCAGGGAGGCTCTTGGTGGA
211081	43277	GTGGCAGGGCCAGGATTGGA	255668	87864	CCCAAAGATTCTAGCCTCTA	300255	132451	GGCAGGGAGGCTCTTGGTGG
211082	43278	AGTGGCAGGGCCAGGATTGG	255669	87865	TCCCAAAGATTCTAGCCTCT	300256	132452	CGGCAGGGAGGCTCTTGGTG
211083	43279	AAGTGGCAGGGCCAGGATTG	255670	87866	CTCCCAAAGATTCTAGCCTC	300257	132453	ACGGCAGGGAGGCTCTTGGT
211084	43280	AAAGTGGCAGGGCCAGGATT	255671	87867	CCTCCCAAAGATTCTAGCCT	300258	132454	AACGGCAGGGAGGCTCTTGG
211085	43281	GAAAGTGGCAGGGCCAGGAT	255672	87868	GCCTCCCAAAGATTCTAGCC	300259	132455	GAACGGCAGGGAGGCTCTTG
211086	43282	GGAAAGTGGCAGGGCCAGGA	255673	87869	AGCCTCCCAAAGATTCTAGC	300260	132456	CGAACGGCAGGGAGGCTCTT
211087	43283	GGGAAAGTGGCAGGGCCAGG	255674	87870	GAGCCTCCCAAAGATTCTAG	300261	132457	GCGAACGGCAGGGAGGCTCT
211088	43284	TGGGAAAGTGGCAGGGCCAG	255675	87871	TGAGCCTCCCAAAGATTCTA	300262	132458	AGCGAACGGCAGGGAGGCTC
211089	43285	CTGGGAAAGTGGCAGGGCCA	255676	87872	TTGAGCCTCCCAAAGATTCT	300263	132459	CAGCGAACGGCAGGGAGGCT
211090	43286	GCTGGGAAAGTGGCAGGGCC	255677	87873	TTTGAGCCTCCCAAAGATTC	300264	132460	TCAGCGAACGGCAGGGAGGC
211091	43287	AGCTGGGAAAGTGGCAGGGC	255678	87874	ATTTGAGCCTCCCAAAGATT	300265	132461	CTCAGCGAACGGCAGGGAGG
211092	43288	CAGCTGGGAAAGTGGCAGGG	255679	87875	AATTTGAGCCTCCCAAAGAT	300266	132462	ACTCAGCGAACGGCAGGGAG
211093	43289	TCAGCTGGGAAAGTGGCAGG	255680	87876	GAATTTGAGCCTCCCAAAGA	300267	132463	GACTCAGCGAACGGCAGGGA
211094	43290	CTCAGCTGGGAAAGTGGCAG	255681	87877	GGAATTTGAGCCTCCCAAAG	300268	132464	GGACTCAGCGAACGGCAGGG
211095	43291	CCTCAGCTGGGAAAGTGGCA	255682	87878	GGGAATTTGAGCCTCCCAAA	300269	132465	GGGACTCAGCGAACGGCAGG
211096	43292	TCCTCAGCTGGGAAAGTGGC	255683	87879	AGGGAATTTGAGCCTCCCAA	300270	132466	TGGGACTCAGCGAACGGCAG
211097	43293	GTCCTCAGCTGGGAAAGTGG	255684	87880	TAGGGAATTTGAGCCTCCCA	300271	132467	CTGGGACTCAGCGAACGGCA
211098	43294	AGTCCTCAGCTGGGAAAGTG	255685	87881	CTAGGGAATTTGAGCCTCCC	300272	132468	GCTGGGACTCAGCGAACGGC
211099	43295	AAGTCCTCAGCTGGGAAAGT	255686	87882	TCTAGGGAATTTGAGCCTCC	300273	132469	TGCTGGGACTCAGCGAACGG
211100	43296	TAAGTCCTCAGCTGGGAAAG	255687	87883	TTCTAGGGAATTTGAGCCTC	300274	132470	TTGCTGGGACTCAGCGAACG
211101	43297	CTAAGTCCTCAGCTGGGAAA	255688	87884	TTTCTAGGGAATTTGAGCCT	300275	132471	ATTGCTGGGACTCAGCGAAC
211102	43298	TCTAAGTCCTCAGCTGGGAA	255689	87885	CTTTCTAGGGAATTTGAGCC	300276	132472	AATTGCTGGGACTCAGCGAA
211103	43299	GTCTAAGTCCTCAGCTGGGA	255690	87886	GCTTTCTAGGGAATTTGAGC	300277	132473	GAATTGCTGGGACTCAGCGA
211104	43300	TGTCTAAGTCCTCAGCTGGG	255691	87887	TGCTTTCTAGGGAATTTGAG	300278	132474	AGAATTGCTGGGACTCAGCG
211105	43301	TTGTCTAAGTCCTCAGCTGG	255692	87888	CTGCTTTCTAGGGAATTTGA	300279	132475	GAGAATTGCTGGGACTCAGC
211106	43302	CTTGTCTAAGTCCTCAGCTG	255693	87889	CCTGCTTTCTAGGGAATTTG	300280	132476	GGAGAATTGCTGGGACTCAG
211107	43303	GCTTGTCTAAGTCCTCAGCT	255694	87890	TCCTGCTTTCTAGGGAATTT	300281	132477	AGGAGAATTGCTGGGACTCA
211108	43304	TGCTTGTCTAAGTCCTCAGC	255695	87891	CTCCTGCTTTCTAGGGAATT	300282	132478	TAGGAGAATTGCTGGGACTC
211109	43305	GTGCTTGTCTAAGTCCTCAG	255696	87892	TCTCCTGCTTTCTAGGGAAT	300283	132479	TTAGGAGAATTGCTGGGACT
211110	43306	GGTGCTTGTCTAAGTCCTCA	255697	87893	TTCTCCTGCTTTCTAGGGAA	300284	132480	CTTAGGAGAATTGCTGGGAC
211111	43307	GGGTGCTTGTCTAAGTCCTC	255698	87894	CTTCTCCTGCTTTCTAGGGA	300285	132481	ACTTAGGAGAATTGCTGGGA
211112	43308	AGGGTGCTTGTCTAAGTCCT	255699	87895	GCTTCTCCTGCTTTCTAGGG	300286	132482	AACTTAGGAGAATTGCTGGG
211113	43309	TAGGGTGCTTGTCTAAGTCC	255700	87896	AGCTTCTCCTGCTTTCTAGG	300287	132483	CAACTTAGGAGAATTGCTGG
211114	43310	CTAGGGTGCTTGTCTAAGTC	255701	87897	AAGCTTCTCCTGCTTTCTAG	300288	132484	TCAACTTAGGAGAATTGCTG
211115	43311	GCTAGGGTGCTTGTCTAAGT	255702	87898	GAAGCTTCTCCTGCTTTCTA	300289	132485	TTCAACTTAGGAGAATTGCT
211116	43312	GGCTAGGGTGCTTGTCTAAG	255703	87899	AGAAGCTTCTCCTGCTTTCT	300290	132486	CTTCAACTTAGGAGAATTGC
211117	43313	AGGCTAGGGTGCTTGTCTAA	255704	87900	CAGAAGCTTCTCCTGCTTTC	300291	132487	CCTTCAACTTAGGAGAATTG
211118	43314	GAGGCTAGGGTGCTTGTCTA	255705	87901	ACAGAAGCTTCTCCTGCTTT	300292	132488	CCCTTCAACTTAGGAGAATT
211119	43315	AGAGGCTAGGGTGCTTGTCT	255706	87902	TACAGAAGCTTCTCCTGCTT	300293	132489	TCCCTTCAACTTAGGAGAAT
211120	43316	AAGAGGCTAGGGTGCTTGTC	255707	87903	CTACAGAAGCTTCTCCTGCT	300294	132490	ATCCCTTCAACTTAGGAGAA
211121	43317	CAAGAGGCTAGGGTGCTTGT	255708	87904	GCTACAGAAGCTTCTCCTGC	300295	132491	GATCCCTTCAACTTAGGAGA
211122	43318	CCAAGAGGCTAGGGTGCTTG	255709	87905	GGCTACAGAAGCTTCTCCTG	300296	132492	AGATCCCTTCAACTTAGGAG
211123	43319	TCCAAGAGGCTAGGGTGCTT	255710	87906	GGGCTACAGAAGCTTCTCCT	300297	132493	CAGATCCCTTCAACTTAGGA
211124	43320	GTCCAAGAGGCTAGGGTGCT	255711	87907	AGGGCTACAGAAGCTTCTCC	300298	132494	TCAGATCCCTTCAACTTAGG
211125	43321	TGTCCAAGAGGCTAGGGTGC	255712	87908	GAGGGCTACAGAAGCTTCTC	300299	132495	CTCAGATCCCTTCAACTTAG
211126	43322	ATGTCCAAGAGGCTAGGGTG	255713	87909	GGAGGGCTACAGAAGCTTCT	300300	132496	TCTCAGATCCCTTCAACTTA
211127	43323	AATGTCCAAGAGGCTAGGGT	255714	87910	GGGAGGGCTACAGAAGCTTC	300301	132497	TTCTCAGATCCCTTCAACTT
211128	43324	GAATGTCCAAGAGGCTAGGG	255715	87911	CGGGAGGGCTACAGAAGCTT	300302	132498	CTTCTCAGATCCCTTCAACT
211129	43325	AGAATGTCCAAGAGGCTAGG	255716	87912	GCGGGAGGGCTACAGAAGCT	300303	132499	CCTTCTCAGATCCCTTCAAC
211130	43326	GAGAATGTCCAAGAGGCTAG	255717	87913	AGCGGGAGGGCTACAGAAGC	300304	132500	TCCTTCTCAGATCCCTTCAA
211131	43327	TGAGAATGTCCAAGAGGCTA	255718	87914	AAGCGGGAGGGCTACAGAAG	300305	132501	CTCCTTCTCAGATCCCTTCA
211132	43328	CTGAGAATGTCCAAGAGGCT	255719	87915	AAAGCGGGAGGGCTACAGAA	300306	132502	TCTCCTTCTCAGATCCCTTC
211133	43329	TCTGAGAATGTCCAAGAGGC	255720	87916	GAAAGCGGGAGGGCTACAGA	300307	132503	TTCTCCTTCTCAGATCCCTT
211134	43330	CTCTGAGAATGTCCAAGAGG	255721	87917	GGAAAGCGGGAGGGCTACAG	300308	132504	CTTCTCCTTCTCAGATCCCT
211135	43331	GCTCTGAGAATGTCCAAGAG	255722	87918	GGGAAAGCGGGAGGGCTACA	300309	132505	CCTTCTCCTTCTCAGATCCC
211136	43332	GGCTCTGAGAATGTCCAAGA	255723	87919	TGGGAAAGCGGGAGGGCTAC	300310	132506	TCCTTCTCCTTCTCAGATCC
211137	43333	TGGCTCTGAGAATGTCCAAG	255724	87920	CTGGGAAAGCGGGAGGGCTA	300311	132507	TTCCTTCTCCTTCTCAGATC
211138	43334	ATGGCTCTGAGAATGTCCAA	255725	87921	ACTGGGAAAGCGGGAGGGCT	300312	132508	TTTCCTTCTCCTTCTCAGAT
211139	43335	GATGGCTCTGAGAATGTCCA	255726	87922	TACTGGGAAAGCGGGAGGGC	300313	132509	ATTTCCTTCTCCTTCTCAGA
211140	43336	AGATGGCTCTGAGAATGTCC	255727	87923	CTACTGGGAAAGCGGGAGGG	300314	132510	CATTTCCTTCTCCTTCTCAG
211141	43337	CAGATGGCTCTGAGAATGTC	255728	87924	TCTACTGGGAAAGCGGGAGG	300315	132511	ACATTTCCTTCTCCTTCTCA
211142	43338	GCAGATGGCTCTGAGAATGT	255729	87925	ATCTACTGGGAAAGCGGGAG	300316	132512	CACATTTCCTTCTCCTTCTC
211143	43339	AGCAGATGGCTCTGAGAATG	255730	87926	AATCTACTGGGAAAGCGGGA	300317	132513	CCACATTTCCTTCTCCTTCT
211144	43340	CAGCAGATGGCTCTGAGAAT	255731	87927	TAATCTACTGGGAAAGCGGG	300318	132514	CCCACATTTCCTTCTCCTTC
211145	43341	GCAGCAGATGGCTCTGAGAA	255732	87928	TTAATCTACTGGGAAAGCGG	300319	132515	CCCCACATTTCCTTCTCCTT
211146	43342	TGCAGCAGATGGCTCTGAGA	255733	87929	CTTAATCTACTGGGAAAGCG	300320	132516	ACCCCACATTTCCTTCTCCT

211147	43343	TTGCAGCAGATGGCTCTGAG	255734	87930	GCTTAATCTACTGGGAAAGC	300321	132517	TACCCCACATTTCCTTCTCC
211148	43344	CTTGCAGCAGATGGCTCTGA	255735	87931	GGCTTAATCTACTGGGAAAG	300322	132518	CTACCCCACATTTCCTTCTC
211149	43345	ACTTGCAGCAGATGGCTCTG	255736	87932	GGGCTTAATCTACTGGGAAA	300323	132519	TCTACCCCACATTTCCTTCT
211150	43346	CACTTGCAGCAGATGGCTCT	255737	87933	TGGGCTTAATCTACTGGGAA	300324	132520	ATCTACCCCACATTTCCTTC
211151	43347	CCACTTGCAGCAGATGGCTC	255738	87934	CTGGGCTTAATCTACTGGGA	300325	132521	AATCTACCCCACATTTCCTT
211152	43348	CCCACTTGCAGCAGATGGCT	255739	87935	CCTGGGCTTAATCTACTGGG	300326	132522	AAATCTACCCCACATTTCCT
211153	43349	ACCCACTTGCAGCAGATGGC	255740	87936	CCCTGGGCTTAATCTACTGG	300327	132523	CAAATCTACCCCACATTTCC
211154	43350	CACCCACTTGCAGCAGATGG	255741	87937	GCCCTGGGCTTAATCTACTG	300328	132524	CCAAATCTACCCCACATTTC
211155	43351	GCACCCACTTGCAGCAGATG	255742	87938	CGCCCTGGGCTTAATCTACT	300329	132525	ACCAAATCTACCCCACATTT
211156	43352	AGCACCCACTTGCAGCAGAT	255743	87939	CCGCCCTGGGCTTAATCTAC	300330	132526	CACCAAATCTACCCCACATT
211157	43353	CAGCACCCACTTGCAGCAGA	255744	87940	GCCGCCCTGGGCTTAATCTA	300331	132527	CCACCAAATCTACCCCACAT
211158	43354	GCAGCACCCACTTGCAGCAG	255745	87941	AGCCGCCCTGGGCTTAATCT	300332	132528	ACCACCAAATCTACCCCACA
211159	43355	GGCAGCACCCACTTGCAGCA	255746	87942	GAGCCGCCCTGGGCTTAATC	300333	132529	CACCACCAAATCTACCCCAC
211160	43356	TGGCAGCACCCACTTGCAGC	255747	87943	GGAGCCGCCCTGGGCTTAAT	300334	132530	CCACCACCAAATCTACCCCA
211161	43357	ATGGCAGCACCCACTTGCAG	255748	87944	TGGAGCCGCCCTGGGCTTAA	300335	132531	ACCACCACCAAATCTACCCC
211162	43358	TATGGCAGCACCCACTTGCA	255749	87945	CTGGAGCCGCCCTGGGCTTA	300336	132532	AACCACCACCAAATCTACCC
211163	43359	GTATGGCAGCACCCACTTGC	255750	87946	TCTGGAGCCGCCCTGGGCTT	300337	132533	TAACCACCACCAAATCTACC
211164	43360	GGTATGGCAGCACCCACTTG	255751	87947	ATCTGGAGCCGCCCTGGGCT	300338	132534	CTAACCACCACCAAATCTAC
211165	43361	GGGTATGGCAGCACCCACTT	255752	87948	CATCTGGAGCCGCCCTGGGC	300339	132535	TCTAACCACCACCAAATCTA
211166	43362	TGGGTATGGCAGCACCCACT	255753	87949	ACATCTGGAGCCGCCCTGGG	300340	132536	CTCTAACCACCACCAAATCT
211167	43363	GTGGGTATGGCAGCACCCAC	255754	87950	CACATCTGGAGCCGCCCTGG	300341	132537	TCTCTAACCACCACCAAATC
211168	43364	GGTGGGTATGGCAGCACCCA	255755	87951	ACACATCTGGAGCCGCCCTG	300342	132538	ATCTCTAACCACCACCAAAT
211169	43365	AGGTGGGTATGGCAGCACCC	255756	87952	CACACATCTGGAGCCGCCCT	300343	132539	TATCTCTAACCACCACCAAA
211170	43366	AAGGTGGGTATGGCAGCACC	255757	87953	TCACACATCTGGAGCCGCCC	300344	132540	ATATCTCTAACCACCACCAA
211171	43367	TAAGGTGGGTATGGCAGCAC	255758	87954	GTCACACATCTGGAGCCGCC	300345	132541	CATATCTCTAACCACCACCA
211172	43368	GTAAGGTGGGTATGGCAGCA	255759	87955	TGTCACACATCTGGAGCCGC	300346	132542	GCATATCTCTAACCACCACC
211173	43369	AGTAAGGTGGGTATGGCAGC	255760	87956	ATGTCACACATCTGGAGCCG	300347	132543	GGCATATCTCTAACCACCAC
211174	43370	CAGTAAGGTGGGTATGGCAG	255761	87957	CATGTCACACATCTGGAGCC	300348	132544	GGGCATATCTCTAACCACCA
211175	43371	CCAGTAAGGTGGGTATGGCA	255762	87958	GCATGTCACACATCTGGAGC	300349	132545	GGGGCATATCTCTAACCACC
211176	43372	CCCAGTAAGGTGGGTATGGC	255763	87959	AGCATGTCACACATCTGGAG	300350	132546	GGGGGCATATCTCTAACCAC
211177	43373	GCCCAGTAAGGTGGGTATGG	255764	87960	GAGCATGTCACACATCTGGA	300351	132547	GGGGGGCATATCTCTAACCA
211178	43374	TGCCCAGTAAGGTGGGTATG	255765	87961	AGAGCATGTCACACATCTGG	300352	132548	AGGGGGGCATATCTCTAACC
211179	43375	CTGCCCAGTAAGGTGGGTAT	255766	87962	CAGAGCATGTCACACATCTG	300353	132549	GAGGGGGGCATATCTCTAAC
211180	43376	CCTGCCCAGTAAGGTGGGTA	255767	87963	ACAGAGCATGTCACACATCT	300354	132550	TGAGGGGGGCATATCTCTAA
211181	43377	GCCTGCCCAGTAAGGTGGGT	255768	87964	CACAGAGCATGTCACACATC	300355	132551	ATGAGGGGGGCATATCTCTA
211182	43378	AGCCTGCCCAGTAAGGTGGG	255769	87965	GCACAGAGCATGTCACACAT	300356	132552	AATGAGGGGGGCATATCTCT
211183	43379	AAGCCTGCCCAGTAAGGTGG	255770	87966	GGCACAGAGCATGTCACACA	300357	132553	TAATGAGGGGGGCATATCTC
211184	43380	CAAGCCTGCCCAGTAAGGTG	255771	87967	GGGCACAGAGCATGTCACAC	300358	132554	GTAATGAGGGGGGCATATCT
211185	43381	CCAAGCCTGCCCAGTAAGGT	255772	87968	TGGGCACAGAGCATGTCACA	300359	132555	AGTAATGAGGGGGGCATATC
211186	43382	CCCAAGCCTGCCCAGTAAGG	255773	87969	TTGGGCACAGAGCATGTCAC	300360	132556	CAGTAATGAGGGGGGCATAT
211187	43383	CCCCAAGCCTGCCCAGTAAG	255774	87970	GTTGGGCACAGAGCATGTCA	300361	132557	GCAGTAATGAGGGGGGCATA
211188	43384	CCCCCAAGCCTGCCCAGTAA	255775	87971	GGTTGGGCACAGAGCATGTC	300362	132558	GGCAGTAATGAGGGGGGCAT
211189	43385	TCCCCCAAGCCTGCCCAGTA	255776	87972	TGGTTGGGCACAGAGCATGT	300363	132559	TGGCAGTAATGAGGGGGGCA
211190	43386	GTCCCCCAAGCCTGCCCAGT	255777	87973	CTGGTTGGGCACAGAGCATG	300364	132560	TTGGCAGTAATGAGGGGGGC
211191	43387	GGTCCCCCAAGCCTGCCCAG	255778	87974	TCTGGTTGGGCACAGAGCAT	300365	132561	GTTGGCAGTAATGAGGGGGG
211192	43388	TGGTCCCCCAAGCCTGCCCA	255779	87975	CTCTGGTTGGGCACAGAGCA	300366	132562	TGTTGGCAGTAATGAGGGGG
211193	43389	TTGGTCCCCCAAGCCTGCCC	255780	87976	GCTCTGGTTGGGCACAGAGC	300367	132563	CTGTTGGCAGTAATGAGGGG
211194	43390	CTTGGTCCCCCAAGCCTGCC	255781	87977	GGCTCTGGTTGGGCACAGAG	300368	132564	ACTGTTGGCAGTAATGAGGG
211195	43391	CCTTGGTCCCCCAAGCCTGC	255782	87978	GGGCTCTGGTTGGGCACAGA	300369	132565	AACTGTTGGCAGTAATGAGG
211196	43392	CCCTTGGTCCCCCAAGCCTG	255783	87979	TGGGCTCTGGTTGGGCACAG	300370	132566	AAACTGTTGGCAGTAATGAG
211197	43393	ACCCTTGGTCCCCCAAGCCT	255784	87980	ATGGGCTCTGGTTGGGCACA	300371	132567	GAAACTGTTGGCAGTAATGA
211198	43394	CACCCTTGGTCCCCCAAGCC	255785	87981	GATGGGCTCTGGTTGGGCAC	300372	132568	CGAAACTGTTGGCAGTAATG
211199	43395	CCACCCTTGGTCCCCCAAGC	255786	87982	TGATGGGCTCTGGTTGGGCA	300373	132569	CCGAAACTGTTGGCAGTAAT
211200	43396	ACCACCCTTGGTCCCCCAAG	255787	87983	ATGATGGGCTCTGGTTGGGC	300374	132570	GCCGAAACTGTTGGCAGTAA
211201	43397	TACCACCCTTGGTCCCCCAA	255788	87984	TATGATGGGCTCTGGTTGGG	300375	132571	AGCCGAAACTGTTGGCAGTA
211202	43398	TTACCACCCTTGGTCCCCCA	255789	87985	CTATGATGGGCTCTGGTTGG	300376	132572	CAGCCGAAACTGTTGGCAGT
211203	43399	TTTACCACCCTTGGTCCCCC	255790	87986	CCTATGATGGGCTCTGGTTG	300377	132573	GCAGCCGAAACTGTTGGCAG
211204	43400	ATTTACCACCCTTGGTCCCC	255791	87987	GCCTATGATGGGCTCTGGTT	300378	132574	TGCAGCCGAAACTGTTGGCA
211205	43401	CATTTACCACCCTTGGTCCC	255792	87988	TGCCTATGATGGGCTCTGGT	300379	132575	ATGCAGCCGAAACTGTTGGC
211206	43402	CCATTTACCACCCTTGGTCC	255793	87989	CTGCCTATGATGGGCTCTGG	300380	132576	AATGCAGCCGAAACTGTTGG
211207	43403	GCCATTTACCACCCTTGGTC	255794	87990	TCTGCCTATGATGGGCTCTG	300381	132577	AAATGCAGCCGAAACTGTTG
211208	43404	AGCCATTTACCACCCTTGGT	255795	87991	CTCTGCCTATGATGGGCTCT	300382	132578	GAAATGCAGCCGAAACTGTT
211209	43405	GAGCCATTTACCACCCTTGG	255796	87992	CCTCTGCCTATGATGGGCTC	300383	132579	AGAAATGCAGCCGAAACTGT
211210	43406	TGAGCCATTTACCACCCTTG	255797	87993	TCCTCTGCCTATGATGGGCT	300384	132580	AAGAAATGCAGCCGAAACTG
211211	43407	CTGAGCCATTTACCACCCTT	255798	87994	TTCCTCTGCCTATGATGGGC	300385	132581	GAAGAAATGCAGCCGAAACT
211212	43408	ACTGAGCCATTTACCACCCT	255799	87995	ATTCCTCTGCCTATGATGGG	300386	132582	TGAAGAAATGCAGCCGAAAC
211213	43409	GACTGAGCCATTTACCACCC	255800	87996	TATTCCTCTGCCTATGATGG	300387	132583	GTGAAGAAATGCAGCCGAAA
211214	43410	AGACTGAGCCATTTACCACC	255801	87997	TTATTCCTCTGCCTATGATG	300388	132584	CGTGAAGAAATGCAGCCGAA
211215	43411	AAGACTGAGCCATTTACCAC	255802	87998	GTTATTCCTCTGCCTATGAT	300389	132585	GCGTGAAGAAATGCAGCCGA
211216	43412	AAAGACTGAGCCATTTACCA	255803	87999	TGTTATTCCTCTGCCTATGA	300390	132586	TGCGTGAAGAAATGCAGCCG
211217	43413	GAAAGACTGAGCCATTTACC	255804	88000	GTGTTATTCCTCTGCCTATG	300391	132587	GTGCGTGAAGAAATGCAGCC
211218	43414	TGAAAGACTGAGCCATTTAC	255805	88001	GGTGTTATTCCTCTGCCTAT	300392	132588	GGTGCGTGAAGAAATGCAGC

211219	43415	ATGAAAGACTGAGCCATTTA	255806	88002	GGGTGTTATTCCTCTGCCTA	300393	132589	AGGTGCGTGAAGAAATGCAG
211220	43416	CATGAAAGACTGAGCCATTT	255807	88003	TGGGTGTTATTCCTCTGCCT	300394	132590	GAGGTGCGTGAAGAAATGCA
211221	43417	TCATGAAAGACTGAGCCATT	255808	88004	GTGGGTGTTATTCCTCTGCC	300395	132591	CGAGGTGCGTGAAGAAATGC
211222	43418	ATCATGAAAGACTGAGCCAT	255809	88005	TGTGGGTGTTATTCCTCTGC	300396	132592	CCGAGGTGCGTGAAGAAATG
211223	43419	CATCATGAAAGACTGAGCCA	255810	88006	GTGTGGGTGTTATTCCTCTG	300397	132593	ACCGAGGTGCGTGAAGAAAT
211224	43420	GCATCATGAAAGACTGAGCC	255811	88007	GGTGTGGGTGTTATTCCTCT	300398	132594	AACCGAGGTGCGTGAAGAAA
211225	43421	CGCATCATGAAAGACTGAGC	255812	88008	TGGTGTGGGTGTTATTCCTC	300399	132595	GAACCGAGGTGCGTGAAGAA
211226	43422	CCGCATCATGAAAGACTGAG	255813	88009	CTGGTGTGGGTGTTATTCCT	300400	132596	GGAACCGAGGTGCGTGAAGA
211227	43423	GCCGCATCATGAAAGACTGA	255814	88010	TCTGGTGTGGGTGTTATTCC	300401	132597	AGGAACCGAGGTGCGTGAAG
211228	43424	GGCCGCATCATGAAAGACTG	255815	88011	TTCTGGTGTGGGTGTTATTC	300402	132598	GAGGAACCGAGGTGCGTGAA
211229	43425	TGGCCGCATCATGAAAGACT	255816	88012	CTTCTGGTGTGGGTGTTATT	300403	132599	AGAGGAACCGAGGTGCGTGA
211230	43426	GTGGCCGCATCATGAAAGAC	255817	88013	CCTTCTGGTGTGGGTGTTAT	300404	132600	AAGAGGAACCGAGGTGCGTG
211231	43427	TGTGGCCGCATCATGAAAGA	255818	88014	CCCTTCTGGTGTGGGTGTTA	300405	132601	GAAGAGGAACCGAGGTGCGT
211232	43428	GTGTGGCCGCATCATGAAAG	255819	88015	GCCCTTCTGGTGTGGGTGTT	300406	132602	GGAAGAGGAACCGAGGTGCG
211233	43429	TGTGTGGCCGCATCATGAAA	255820	88016	GGCCCTTCTGGTGTGGGTGT	300407	132603	AGGAAGAGGAACCGAGGTGC
211234	43430	CTGTGTGGCCGCATCATGAA	255821	88017	GGGCCCTTCTGGTGTGGGTG	300408	132604	CAGGAAGAGGAACCGAGGTG
211235	43431	GCTGTGTGGCCGCATCATGA	255822	88018	AGGGCCCTTCTGGTGTGGGT	300409	132605	TCAGGAAGAGGAACCGAGGT
211236	43432	TGCTGTGTGGCCGCATCATG	255823	88019	GAGGGCCCTTCTGGTGTGGG	300410	132606	TTCAGGAAGAGGAACCGAGG
211237	43433	CTGCTGTGTGGCCGCATCAT	255824	88020	CGAGGGCCCTTCTGGTGTGG	300411	132607	CTTCAGGAAGAGGAACCGAG
211238	43434	CCTGCTGTGTGGCCGCATCA	255825	88021	CCGAGGGCCCTTCTGGTGTG	300412	132608	ACTTCAGGAAGAGGAACCGA
211239	43435	ACCTGCTGTGTGGCCGCATC	255826	88022	TCCGAGGGCCCTTCTGGTGT	300413	132609	AACTTCAGGAAGAGGAACCG
211240	43436	CACCTGCTGTGTGGCCGCAT	255827	88023	CTCCGAGGGCCCTTCTGGTG	300414	132610	GAACTTCAGGAAGAGGAACC
211241	43437	GCACCTGCTGTGTGGCCGCA	255828	88024	CCTCCGAGGGCCCTTCTGGT	300415	132611	AGAACTTCAGGAAGAGGAAC
211242	43438	CGCACCTGCTGTGTGGCCGC	255829	88025	ACCTCCGAGGGCCCTTCTGG	300416	132612	AAGAACTTCAGGAAGAGGAA
211243	43439	GCGCACCTGCTGTGTGGCCG	255830	88026	GACCTCCGAGGGCCCTTCTG	300417	132613	CAAGAACTTCAGGAAGAGGA
211244	43440	GGCGCACCTGCTGTGTGGCC	255831	88027	TGACCTCCGAGGGCCCTTCT	300418	132614	ACAAGAACTTCAGGAAGAGG
211245	43441	TGGCGCACCTGCTGTGTGGC	255832	88028	GTGACCTCCGAGGGCCCTTC	300419	132615	CACAAGAACTTCAGGAAGAG
211246	43442	ATGGCGCACCTGCTGTGTGG	255833	88029	GGTGACCTCCGAGGGCCCTT	300420	132616	GCACAAGAACTTCAGGAAGA
211247	43443	GATGGCGCACCTGCTGTGTG	255834	88030	TGGTGACCTCCGAGGGCCCT	300421	132617	GGCACAAGAACTTCAGGAAG
211248	43444	GGATGGCGCACCTGCTGTGT	255835	88031	GTGGTGACCTCCGAGGGCCC	300422	132618	GGGCACAAGAACTTCAGGAA
211249	43445	TGGATGGCGCACCTGCTGTG	255836	88032	CGTGGTGACCTCCGAGGGCC	300423	132619	AGGGCACAAGAACTTCAGGA
211250	43446	CTGGATGGCGCACCTGCTGT	255837	88033	ACGTGGTGACCTCCGAGGGC	300424	132620	CAGGGCACAAGAACTTCAGG
211251	43447	CCTGGATGGCGCACCTGCTG	255838	88034	GACGTGGTGACCTCCGAGGG	300425	132621	GCAGGGCACAAGAACTTCAG
211252	43448	ACCTGGATGGCGCACCTGCT	255839	88035	GGACGTGGTGACCTCCGAGG	300426	132622	AGCAGGGCACAAGAACTTCA
211253	43449	GACCTGGATGGCGCACCTGC	255840	88036	TGGACGTGGTGACCTCCGAG	300427	132623	GAGCAGGGCACAAGAACTTC
211254	43450	GGACCTGGATGGCGCACCTG	255841	88037	TTGGACGTGGTGACCTCCGA	300428	132624	AGAGCAGGGCACAAGAACTT
211255	43451	TGGACCTGGATGGCGCACCT	255842	88038	CTTGGACGTGGTGACCTCCG	300429	132625	AAGAGCAGGGCACAAGAACT
211256	43452	ATGGACCTGGATGGCGCACC	255843	88039	TCTTGGACGTGGTGACCTCC	300430	132626	GAAGAGCAGGGCACAAGAAC
211257	43453	AATGGACCTGGATGGCGCAC	255844	88040	TTCTTGGACGTGGTGACCTC	300431	132627	TGAAGAGCAGGGCACAAGAA
211258	43454	AAATGGACCTGGATGGCGCA	255845	88041	GTTCTTGGACGTGGTGACCT	300432	132628	CTGAAGAGCAGGGCACAAGA
211259	43455	GAAATGGACCTGGATGGCGC	255846	88042	GGTTCTTGGACGTGGTGACC	300433	132629	GCTGAAGAGCAGGGCACAAG
211260	43456	AGAAATGGACCTGGATGGCG	255847	88043	GGGTTCTTGGACGTGGTGAC	300434	132630	TGCTGAAGAGCAGGGCACAA
211261	43457	AAGAAATGGACCTGGATGGC	255848	88044	AGGGTTCTTGGACGTGGTGA	300435	132631	GTGCTGAAGAGCAGGGCACA
211262	43458	AAAGAAATGGACCTGGATGG	255849	88045	GAGGGTTCTTGGACGTGGTG	300436	132632	GGTGCTGAAGAGCAGGGCAC
211263	43459	GAAAGAAATGGACCTGGATG	255850	88046	AGAGGGTTCTTGGACGTGGT	300437	132633	TGGTGCTGAAGAGCAGGGCA
211264	43460	GGAAAGAAATGGACCTGGAT	255851	88047	AAGAGGGTTCTTGGACGTGG	300438	132634	ATGGTGCTGAAGAGCAGGGC
211265	43461	AGGAAAGAAATGGACCTGGA	255852	88048	AAAGAGGGTTCTTGGACGTG	300439	132635	CATGGTGCTGAAGAGCAGGG
211266	43462	AAGGAAAGAAATGGACCTGG	255853	88049	TAAAGAGGGTTCTTGGACGT	300440	132636	CCATGGTGCTGAAGAGCAGG
211267	43463	GAAGGAAAGAAATGGACCTG	255854	88050	GTAAAGAGGGTTCTTGGACG	300441	132637	CCCATGGTGCTGAAGAGCAG
211268	43464	GGAAGGAAAGAAATGGACCT	255855	88051	TGTAAAGAGGGTTCTTGGAC	300442	132638	GCCCATGGTGCTGAAGAGCA
211269	43465	AGGAAGGAAAGAAATGGACC	255856	88052	CTGTAAAGAGGGTTCTTGGA	300443	132639	GGCCCATGGTGCTGAAGAGC
211270	43466	AAGGAAGGAAAGAAATGGAC	255857	88053	TCTGTAAAGAGGGTTCTTGG	300444	132640	AGGCCCATGGTGCTGAAGAG
211271	43467	AAAGGAAGGAAAGAAATGGA	255858	88054	ATCTGTAAAGAGGGTTCTTG	300445	132641	AAGGCCCATGGTGCTGAAGA
211272	43468	GAAAGGAAGGAAAGAAATGG	255859	88055	CATCTGTAAAGAGGGTTCTT	300446	132642	GAAGGCCCATGGTGCTGAAG
211273	43469	GGAAAGGAAGGAAAGAAATG	255860	88056	TCATCTGTAAAGAGGGTTCT	300447	132643	AGAAGGCCCATGGTGCTGAA
211274	43470	GGGAAAGGAAGGAAAGAAAT	255861	88057	CTCATCTGTAAAGAGGGTTC	300448	132644	AAGAAGGCCCATGGTGCTGA
211275	43471	GGGGAAAGGAAGGAAAGAAA	255862	88058	CCTCATCTGTAAAGAGGGTT	300449	132645	TAAGAAGGCCCATGGTGCTG
211276	43472	GGGGGAAAGGAAGGAAAGAA	255863	88059	TCCTCATCTGTAAAGAGGGT	300450	132646	ATAAGAAGGCCCATGGTGCT
211277	43473	TGGGGGAAAGGAAGGAAAGA	255864	88060	TTCCTCATCTGTAAAGAGGG	300451	132647	TATAAGAAGGCCCATGGTGC
211278	43474	TTGGGGGAAAGGAAGGAAAG	255865	88061	TTTCCTCATCTGTAAAGAGG	300452	132648	GTATAAGAAGGCCCATGGTG
211279	43475	TTTGGGGGAAAGGAAGGAAA	255866	88062	GTTTCCTCATCTGTAAAGAG	300453	132649	CGTATAAGAAGGCCCATGGT
211280	43476	ATTTGGGGGAAAGGAAGGAA	255867	88063	AGTTTCCTCATCTGTAAAGA	300454	132650	CCGTATAAGAAGGCCCATGG
211281	43477	GATTTGGGGGAAAGGAAGGA	255868	88064	CAGTTTCCTCATCTGTAAAG	300455	132651	TCCGTATAAGAAGGCCCATG
211282	43478	TGATTTGGGGGAAAGGAAGG	255869	88065	TCAGTTTCCTCATCTGTAAA	300456	132652	TTCCGTATAAGAAGGCCCAT
211283	43479	TTGATTTGGGGGAAAGGAAG	255870	88066	CTCAGTTTCCTCATCTGTAA	300457	132653	CTTCCGTATAAGAAGGCCCA
211284	43480	CTTGATTTGGGGGAAAGGAA	255871	88067	CCTCAGTTTCCTCATCTGTA	300458	132654	CCTTCCGTATAAGAAGGCCC
211285	43481	ACTTGATTTGGGGGAAAGGA	255872	88068	GCCTCAGTTTCCTCATCTGT	300459	132655	GCCTTCCGTATAAGAAGGCC
211286	43482	AACTTGATTTGGGGGAAAGG	255873	88069	GGCCTCAGTTTCCTCATCTG	300460	132656	AGCCTTCCGTATAAGAAGGC
211287	43483	CAACTTGATTTGGGGGAAAG	255874	88070	GGGCCTCAGTTTCCTCATCT	300461	132657	GAGCCTTCCGTATAAGAAGG
211288	43484	ACAACTTGATTTGGGGGAAA	255875	88071	TGGGCCTCAGTTTCCTCATC	300462	132658	AGAGCCTTCCGTATAAGAAG
211289	43485	GACAACTTGATTTGGGGGAA	255876	88072	CTGGGCCTCAGTTTCCTCAT	300463	132659	CAGAGCCTTCCGTATAAGAA
211290	43486	TGACAACTTGATTTGGGGGA	255877	88073	TCTGGGCCTCAGTTTCCTCA	300464	132660	CCAGAGCCTTCCGTATAAGA

211291	43487	ATGACAACTTGATTTGGGGG	255878	88074	CTCTGGGCCTCAGTTTCCTC	300465	132661	CCCAGAGCCTTCCGTATAAG
211292	43488	AATGACAACTTGATTTGGGG	255879	88075	TCTCTGGGCCTCAGTTTCCT	300466	132662	TCCCAGAGCCTTCCGTATAA
211293	43489	TAATGACAACTTGATTTGGG	255880	88076	CTCTCTGGGCCTCAGTTTCC	300467	132663	ATCCCAGAGCCTTCCGTATA
211294	43490	TTAATGACAACTTGATTTGG	255881	88077	CCTCTCTGGGCCTCAGTTTC	300468	132664	GATCCCAGAGCCTTCCGTAT
211295	43491	TTTAATGACAACTTGATTTG	255882	88078	CCCTCTCTGGGCCTCAGTTT	300469	132665	AGATCCCAGAGCCTTCCGTA
211296	43492	CTTTAATGACAACTTGATTT	255883	88079	CCCCTCTCTGGGCCTCAGTT	300470	132666	GAGATCCCAGAGCCTTCCGT
211297	43493	ACTTTAATGACAACTTGATT	255884	88080	TCCCCTCTCTGGGCCTCAGT	300471	132667	GGAGATCCCAGAGCCTTCCG
211298	43494	TACTTTAATGACAACTTGAT	255885	88081	CTCCCCTCTCTGGGCCTCAG	300472	132668	GGGAGATCCCAGAGCCTTCC
211299	43495	GTACTTTAATGACAACTTGA	255886	88082	TCTCCCCTCTCTGGGCCTCA	300473	132669	GGGGAGATCCCAGAGCCTTC
211300	43496	AGTACTTTAATGACAACTTG	255887	88083	CTCTCCCCTCTCTGGGCCTC	300474	132670	GGGGGAGATCCCAGAGCCTT
211301	43497	TAGTACTTTAATGACAACTT	255888	88084	GCTCTCCCCTCTCTGGGCCT	300475	132671	AGGGGGAGATCCCAGAGCCT
211302	43498	CTAGTACTTTAATGACAACT	255889	88085	GGCTCTCCCCTCTCTGGGCC	300476	132672	AAGGGGGAGATCCCAGAGCC
211303	43499	ACTAGTACTTTAATGACAAC	255890	88086	TGGCTCTCCCCTCTCTGGGC	300477	132673	CAAGGGGGAGATCCCAGAGC
211304	43500	GACTAGTACTTTAATGACAA	255891	88087	GTGGCTCTCCCCTCTCTGGG	300478	132674	ACAAGGGGGAGATCCCAGAG
211305	43501	GGACTAGTACTTTAATGACA	255892	88088	GGTGGCTCTCCCCTCTCTGG	300479	132675	CACAAGGGGGAGATCCCAGA
211306	43502	TGGACTAGTACTTTAATGAC	255893	88089	AGGTGGCTCTCCCCTCTCTG	300480	132676	CCACAAGGGGGAGATCCCAG
211307	43503	GTGGACTAGTACTTTAATGA	255894	88090	TAGGTGGCTCTCCCCTCTCT	300481	132677	CCCACAAGGGGGAGATCCCA
211308	43504	TGTGGACTAGTACTTTAATG	255895	88091	CTAGGTGGCTCTCCCCTCTC	300482	132678	CCCCACAAGGGGGAGATCCC
211309	43505	ATGTGGACTAGTACTTTAAT	255896	88092	GCTAGGTGGCTCTCCCCTCT	300483	132679	GCCCCACAAGGGGGAGATCC
211310	43506	AATGTGGACTAGTACTTTAA	255897	88093	CGCTAGGTGGCTCTCCCCTC	300484	132680	TGCCCCACAAGGGGGAGATC
211311	43507	TAATGTGGACTAGTACTTTA	255898	88094	TCGCTAGGTGGCTCTCCCCT	300485	132681	CTGCCCCACAAGGGGGAGAT
211312	43508	TTAATGTGGACTAGTACTTT	255899	88095	CTCGCTAGGTGGCTCTCCCC	300486	132682	CCTGCCCCACAAGGGGGAGA
211313	43509	ATTAATGTGGACTAGTACTT	255900	88096	GCTCGCTAGGTGGCTCTCCC	300487	132683	GCCTGCCCCACAAGGGGGAG
211314	43510	CATTAATGTGGACTAGTACT	255901	88097	AGCTCGCTAGGTGGCTCTCC	300488	132684	AGCCTGCCCCACAAGGGGGA
211315	43511	TCATTAATGTGGACTAGTAC	255902	88098	CAGCTCGCTAGGTGGCTCTC	300489	132685	GAGCCTGCCCCACAAGGGGG
211316	43512	TTCATTAATGTGGACTAGTA	255903	88099	CCAGCTCGCTAGGTGGCTCT	300490	132686	AGAGCCTGCCCCACAAGGGG
211317	43513	TTTCATTAATGTGGACTAGT	255904	88100	ACCAGCTCGCTAGGTGGCTC	300491	132687	AAGAGCCTGCCCCACAAGGG
211318	43514	ATTTCATTAATGTGGACTAG	255905	88101	CACCAGCTCGCTAGGTGGCT	300492	132688	CAAGAGCCTGCCCCACAAGG
211319	43515	GATTTCATTAATGTGGACTA	255906	88102	CCACCAGCTCGCTAGGTGGC	300493	132689	CCAAGAGCCTGCCCCACAAG
211320	43516	TGATTTCATTAATGTGGACT	255907	88103	GCCACCAGCTCGCTAGGTGG	300494	132690	CCCAAGAGCCTGCCCCACAA
211321	43517	TTGATTTCATTAATGTGGAC	255908	88104	CGCCACCAGCTCGCTAGGTG	300495	132691	CCCCAAGAGCCTGCCCCACA
211322	43518	GTTGATTTCATTAATGTGGA	255909	88105	CCGCCACCAGCTCGCTAGGT	300496	132692	GCCCCAAGAGCCTGCCCCAC
211323	43519	AGTTGATTTCATTAATGTGG	255910	88106	GCCGCCACCAGCTCGCTAGG	300497	132693	GGCCCCAAGAGCCTGCCCCA
211324	43520	CAGTTGATTTCATTAATGTG	255911	88107	AGCCGCCACCAGCTCGCTAG	300498	132694	TGGCCCCAAGAGCCTGCCCC
211325	43521	ACAGTTGATTTCATTAATGT	255912	88108	TAGCCGCCACCAGCTCGCTA	300499	132695	CTGGCCCCAAGAGCCTGCCC
211326	43522	TACAGTTGATTTCATTAATG	255913	88109	CTAGCCGCCACCAGCTCGCT	300500	132696	GCTGGCCCCAAGAGCCTGCC
211327	43523	ATACAGTTGATTTCATTAAT	255914	88110	TCTAGCCGCCACCAGCTCGC	300501	132697	GGCTGGCCCCAAGAGCCTGC
211328	43524	AATACAGTTGATTTCATTAA	255915	88111	GTCTAGCCGCCACCAGCTCG	300502	132698	AGGCTGGCCCCAAGAGCCTG
211329	43525	TAATACAGTTGATTTCATTA	255916	88112	GGTCTAGCCGCCACCAGCTC	300503	132699	TAGGCTGGCCCCAAGAGCCT
211330	43526	TTAATACAGTTGATTTCATT	255917	88113	TGGTCTAGCCGCCACCAGCT	300504	132700	TTAGGCTGGCCCCAAGAGCC
211331	43527	ATTAATACAGTTGATTTCAT	255918	88114	CTGGTCTAGCCGCCACCAGC	300505	132701	CTTAGGCTGGCCCCAAGAGC
211332	43528	AATTAATACAGTTGATTTCA	255919	88115	CCTGGTCTAGCCGCCACCAG	300506	132702	TCTTAGGCTGGCCCCAAGAG
211333	43529	AAATTAATACAGTTGATTTC	255920	88116	TCCTGGTCTAGCCGCCACCA	300507	132703	ATCTTAGGCTGGCCCCAAGA
211334	43530	AAAATTAATACAGTTGATTT	255921	88117	CTCCTGGTCTAGCCGCCACC	300508	132704	GATCTTAGGCTGGCCCCAAG
211335	43531	GAAAATTAATACAGTTGATT	255922	88118	TCTCCTGGTCTAGCCGCCAC	300509	132705	TGATCTTAGGCTGGCCCCAA
211336	43532	AGAAAATTAATACAGTTGAT	255923	88119	CTCTCCTGGTCTAGCCGCCA	300510	132706	ATGATCTTAGGCTGGCCCCA
211337	43533	TAGAAAATTAATACAGTTGA	255924	88120	GCTCTCCTGGTCTAGCCGCC	300511	132707	CATGATCTTAGGCTGGCCCC
211338	43534	ATAGAAAATTAATACAGTTG	255925	88121	AGCTCTCCTGGTCTAGCCGC	300512	132708	CCATGATCTTAGGCTGGCCC
211339	43535	AATAGAAAATTAATACAGTT	255926	88122	CAGCTCTCCTGGTCTAGCCG	300513	132709	ACCATGATCTTAGGCTGGCC
211340	43536	AAATAGAAAATTAATACAGT	255927	88123	ACAGCTCTCCTGGTCTAGCC	300514	132710	AACCATGATCTTAGGCTGGC
211341	43537	CAAATAGAAAATTAATACAG	255928	88124	GACAGCTCTCCTGGTCTAGC	300515	132711	AAACCATGATCTTAGGCTGG
211342	43538	GCAAATAGAAAATTAATACA	255929	88125	TGACAGCTCTCCTGGTCTAG	300516	132712	TAAACCATGATCTTAGGCTG
211343	43539	AGCAAATAGAAAATTAATAC	255930	88126	ATGACAGCTCTCCTGGTCTA	300517	132713	CTAAACCATGATCTTAGGCT
211344	43540	CAGCAAATAGAAAATTAATA	255931	88127	AATGACAGCTCTCCTGGTCT	300518	132714	CCTAAACCATGATCTTAGGC
211345	43541	GCAGCAAATAGAAAATTAAT	255932	88128	GAATGACAGCTCTCCTGGTC	300519	132715	CCCTAAACCATGATCTTAGG
211346	43542	AGCAGCAAATAGAAAATTAA	255933	88129	GGAATGACAGCTCTCCTGGT	300520	132716	ACCCTAAACCATGATCTTAG
211347	43543	TAGCAGCAAATAGAAAATTA	255934	88130	TGGAATGACAGCTCTCCTGG	300521	132717	CACCCTAAACCATGATCTTA
211348	43544	ATAGCAGCAAATAGAAAATT	255935	88131	TTGGAATGACAGCTCTCCTG	300522	132718	TCACCCTAAACCATGATCTT
211349	43545	TATAGCAGCAAATAGAAAAT	255936	88132	CTTGGAATGACAGCTCTCCT	300523	132719	ATCACCCTAAACCATGATCT
211350	43546	TTATAGCAGCAAATAGAAAA	255937	88133	GCTTGGAATGACAGCTCTCC	300524	132720	GATCACCCTAAACCATGATC
211351	43547	ATTATAGCAGCAAATAGAAA	255938	88134	TGCTTGGAATGACAGCTCTC	300525	132721	TGATCACCCTAAACCATGAT
211352	43548	TATTATAGCAGCAAATAGAA	255939	88135	TTGCTTGGAATGACAGCTCT	300526	132722	CTGATCACCCTAAACCATGA
211353	43549	TTATTATAGCAGCAAATAGA	255940	88136	CTTGCTTGGAATGACAGCTC	300527	132723	ACTGATCACCCTAAACCATG
211354	43550	TTTATTATAGCAGCAAATAG	255941	88137	GCTTGCTTGGAATGACAGCT	300528	132724	CACTGATCACCCTAAACCAT
211355	43551	ATTTATTATAGCAGCAAATA	255942	88138	TGCTTGCTTGGAATGACAGC	300529	132725	GCACTGATCACCCTAAACCA
211356	43552	GATTTATTATAGCAGCAAAT	255943	88139	TTGCTTGCTTGGAATGACAG	300530	132726	AGCACTGATCACCCTAAACC
211357	43553	TGATTTATTATAGCAGCAAA	255944	88140	TTTGCTTGCTTGGAATGACA	300531	132727	CAGCACTGATCACCCTAAAC
211358	43554	ATGATTTATTATAGCAGCAA	255945	88141	CTTTGCTTGCTTGGAATGAC	300532	132728	CCAGCACTGATCACCCTAAA
211359	43555	GATGATTTATTATAGCAGCA	255946	88142	CCTTTGCTTGCTTGGAATGA	300533	132729	GCCAGCACTGATCACCCTAA
211360	43556	TGATGATTTATTATAGCAGC	255947	88143	GCCTTTGCTTGCTTGGAATG	300534	132730	TGCCAGCACTGATCACCCTA
211361	43557	CTGATGATTTATTATAGCAG	255948	88144	TGCCTTTGCTTGCTTGGAAT	300535	132731	CTGCCAGCACTGATCACCCT
211362	43558	TCTGATGATTTATTATAGCA	255949	88145	TTGCCTTTGCTTGCTTGGAA	300536	132732	TCTGCCAGCACTGATCACCC

211363	43559	TTCTGATGATTTATTATAGC	255950	88146	GTTGCCTTTGCTTGCTTGGA	300537	132733	ATCTGCCAGCACTGATCACC
211364	43560	TTTCTGATGATTTATTATAG	255951	88147	CGTTGCCTTTGCTTGCTTGG	300538	132734	TATCTGCCAGCACTGATCAC
211365	43561	ATTTCTGATGATTTATTATA	255952	88148	TCGTTGCCTTTGCTTGCTTG	300539	132735	TTATCTGCCAGCACTGATCA
211366	43562	AATTTCTGATGATTTATTAT	255953	88149	CTCGTTGCCTTTGCTTGCTT	300540	132736	TTTATCTGCCAGCACTGATC
211367	43563	AAATTTCTGATGATTTATTA	255954	88150	TCTCGTTGCCTTTGCTTGCT	300541	132737	ATTTATCTGCCAGCACTGAT
211368	43564	TAAATTTCTGATGATTTATT	255955	88151	GTCTCGTTGCCTTTGCTTGC	300542	132738	AATTTATCTGCCAGCACTGA
211369	43565	CTAAATTTCTGATGATTTAT	255956	88152	CGTCTCGTTGCCTTTGCTTG	300543	132739	CAATTTATCTGCCAGCACTG
211370	43566	ACTAAATTTCTGATGATTTA	255957	88153	TCGTCTCGTTGCCTTTGCTT	300544	132740	TCAATTTATCTGCCAGCACT
211371	43567	CACTAAATTTCTGATGATTT	255958	88154	CTCGTCTCGTTGCCTTTGCT	300545	132741	TTCAATTTATCTGCCAGCAC
211372	43568	CCACTAAATTTCTGATGATT	255959	88155	GCTCGTCTCGTTGCCTTTGC	300546	132742	TTTCAATTTATCTGCCAGCA
211373	43569	GCCACTAAATTTCTGATGAT	255960	88156	GGCTCGTCTCGTTGCCTTTG	300547	132743	TTTTCAATTTATCTGCCAGC
211374	43570	AGCCACTAAATTTCTGATGA	255961	88157	GGGCTCGTCTCGTTGCCTTT	300548	132744	CTTTTCAATTTATCTGCCAG
211375	43571	AAGCCACTAAATTTCTGATG	255962	88158	TGGGCTCGTCTCGTTGCCTT	300549	132745	CCTTTTCAATTTATCTGCCA
211376	43572	TAAGCCACTAAATTTCTGAT	255963	88159	CTGGGCTCGTCTCGTTGCCT	300550	132746	GCCTTTTCAATTTATCTGCC
211377	43573	TTAAGCCACTAAATTTCTGA	255964	88160	TCTGGGCTCGTCTCGTTGCC	300551	132747	TGCCTTTTCAATTTATCTGC
211378	43574	TTTAAGCCACTAAATTTCTG	255965	88161	CTCTGGGCTCGTCTCGTTGC	300552	132748	GTGCCTTTTCAATTTATCTG
211379	43575	GTTTAAGCCACTAAATTTCT	255966	88162	GCTCTGGGCTCGTCTCGTTG	300553	132749	CGTGCCTTTTCAATTTATCT
211380	43576	GGTTTAAGCCACTAAATTTC	255967	88163	AGCTCTGGGCTCGTCTCGTT	300554	132750	GCGTGCCTTTTCAATTTATC
211381	43577	TGGTTTAAGCCACTAAATTT	255968	88164	CAGCTCTGGGCTCGTCTCGT	300555	132751	AGCGTGCCTTTTCAATTTAT
211382	43578	TTGGTTTAAGCCACTAAATT	255969	88165	ACAGCTCTGGGCTCGTCTCG	300556	132752	CAGCGTGCCTTTTCAATTTA
211383	43579	GTTGGTTTAAGCCACTAAAT	255970	88166	CACAGCTCTGGGCTCGTCTC	300557	132753	CCAGCGTGCCTTTTCAATTT
211384	43580	TGTTGGTTTAAGCCACTAAA	255971	88167	GCACAGCTCTGGGCTCGTCT	300558	132754	GCCAGCGTGCCTTTTCAATT
211385	43581	GTGTTGGTTTAAGCCACTAA	255972	88168	AGCACAGCTCTGGGCTCGTC	300559	132755	AGCCAGCGTGCCTTTTCAAT
211386	43582	TGTGTTGGTTTAAGCCACTA	255973	88169	GAGCACAGCTCTGGGCTCGT	300560	132756	AAGCCAGCGTGCCTTTTCAA
211387	43583	TTGTGTTGGTTTAAGCCACT	255974	88170	GGAGCACAGCTCTGGGCTCG	300561	132757	CAAGCCAGCGTGCCTTTTCA
211388	43584	TTTGTGTTGGTTTAAGCCAC	255975	88171	GGGAGCACAGCTCTGGGCTC	300562	132758	ACAAGCCAGCGTGCCTTTTC
211389	43585	ATTTGTGTTGGTTTAAGCCA	255976	88172	TGGGAGCACAGCTCTGGGCT	300563	132759	CACAAGCCAGCGTGCCTTTT
211390	43586	CATTTGTGTTGGTTTAAGCC	255977	88173	ATGGGAGCACAGCTCTGGGC	300564	132760	TCACAAGCCAGCGTGCCTTT
211391	43587	ACATTTGTGTTGGTTTAAGC	255978	88174	GATGGGAGCACAGCTCTGGG	300565	132761	ATCACAAGCCAGCGTGCCTT
211392	43588	TACATTTGTGTTGGTTTAAG	255979	88175	AGATGGGAGCACAGCTCTGG	300566	132762	GATCACAAGCCAGCGTGCCT
211393	43589	ATACATTTGTGTTGGTTTAA	255980	88176	GAGATGGGAGCACAGCTCTG	300567	132763	AGATCACAAGCCAGCGTGCC
211394	43590	AATACATTTGTGTTGGTTTA	255981	88177	AGAGATGGGAGCACAGCTCT	300568	132764	AAGATCACAAGCCAGCGTGC
211395	43591	TAATACATTTGTGTTGGTTT	255982	88178	AAGAGATGGGAGCACAGCTC	300569	132765	TAAGATCACAAGCCAGCGTG
211396	43592	GTAATACATTTGTGTTGGTT	255983	88179	AAAGAGATGGGAGCACAGCT	300570	132766	TTAAGATCACAAGCCAGCGT
211397	43593	GGTAATACATTTGTGTTGGT	255984	88180	CAAAGAGATGGGAGCACAGC	300571	132767	TTTAAGATCACAAGCCAGCG
211398	43594	AGGTAATACATTTGTGTTGG	255985	88181	ACAAAGAGATGGGAGCACAG	300572	132768	ATTTAAGATCACAAGCCAGC
211399	43595	AAGGTAATACATTTGTGTTG	255986	88182	AACAAAGAGATGGGAGCACA	300573	132769	CATTTAAGATCACAAGCCAG
211400	43596	TAAGGTAATACATTTGTGTT	255987	88183	TAACAAAGAGATGGGAGCAC	300574	132770	TCATTTAAGATCACAAGCCA
211401	43597	GTAAGGTAATACATTTGTGT	255988	88184	CTAACAAAGAGATGGGAGCA	300575	132771	CTCATTTAAGATCACAAGCC
211402	43598	TGTAAGGTAATACATTTGTG	255989	88185	CCTAACAAAGAGATGGGAGC	300576	132772	CCTCATTTAAGATCACAAGC
211403	43599	CTGTAAGGTAATACATTTGT	255990	88186	CCCTAACAAAGAGATGGGAG	300577	132773	TCCTCATTTAAGATCACAAG
211404	43600	ACTGTAAGGTAATACATTTG	255991	88187	CCCCTAACAAAGAGATGGGA	300578	132774	GTCCTCATTTAAGATCACAA
211405	43601	AACTGTAAGGTAATACATTT	255992	88188	CCCCCTAACAAAGAGATGGG	300579	132775	TGTCCTCATTTAAGATCACA
211406	43602	GAACTGTAAGGTAATACATT	255993	88189	GCCCCCTAACAAAGAGATGG	300580	132776	TTGTCCTCATTTAAGATCAC
211407	43603	AGAACTGTAAGGTAATACAT	255994	88190	GGCCCCCTAACAAAGAGATG	300581	132777	ATTGTCCTCATTTAAGATCA
211408	43604	CAGAACTGTAAGGTAATACA	255995	88191	AGGCCCCCTAACAAAGAGAT	300582	132778	GATTGTCCTCATTTAAGATC
211409	43605	CCAGAACTGTAAGGTAATAC	255996	88192	CAGGCCCCCTAACAAAGAGA	300583	132779	GGATTGTCCTCATTTAAGAT
211410	43606	TCCAGAACTGTAAGGTAATA	255997	88193	CCAGGCCCCCTAACAAAGAG	300584	132780	GGGATTGTCCTCATTTAAGA
211411	43607	CTCCAGAACTGTAAGGTAAT	255998	88194	CCCAGGCCCCCTAACAAAGA	300585	132781	GGGGATTGTCCTCATTTAAG
211412	43608	CCTCCAGAACTGTAAGGTAA	255999	88195	TCCCAGGCCCCCTAACAAAG	300586	132782	GGGGGATTGTCCTCATTTAA
211413	43609	GCCTCCAGAACTGTAAGGTA	256000	88196	ATCCCAGGCCCCCTAACAAA	300587	132783	GGGGGGATTGTCCTCATTTA
211414	43610	GGCCTCCAGAACTGTAAGGT	256001	88197	CATCCCAGGCCCCCTAACAA	300588	132784	TGGGGGGATTGTCCTCATTT
211415	43611	TGGCCTCCAGAACTGTAAGG	256002	88198	GCATCCCAGGCCCCCTAACA	300589	132785	CTGGGGGGATTGTCCTCATT
211416	43612	CTGGCCTCCAGAACTGTAAG	256003	88199	GGCATCCCAGGCCCCCTAAC	300590	132786	CCTGGGGGGATTGTCCTCAT
211417	43613	TCTGGCCTCCAGAACTGTAA	256004	88200	GGGCATCCCAGGCCCCCTAA	300591	132787	CCCTGGGGGGATTGTCCTCA
211418	43614	TTCTGGCCTCCAGAACTGTA	256005	88201	AGGGCATCCCAGGCCCCCTA	300592	132788	GCCCTGGGGGGATTGTCCTC
211419	43615	CTTCTGGCCTCCAGAACTGT	256006	88202	GAGGGCATCCCAGGCCCCCT	300593	132789	AGCCCTGGGGGGATTGTCCT
211420	43616	GCTTCTGGCCTCCAGAACTG	256007	88203	AGAGGGCATCCCAGGCCCCC	300594	132790	CAGCCCTGGGGGGATTGTCC
211421	43617	GGCTTCTGGCCTCCAGAACT	256008	88204	GAGAGGGCATCCCAGGCCCC	300595	132791	CCAGCCCTGGGGGGATTGTC
211422	43618	GGGCTTCTGGCCTCCAGAAC	256009	88205	TGAGAGGGCATCCCAGGCCC	300596	132792	CCCAGCCCTGGGGGGATTGT
211423	43619	AGGGCTTCTGGCCTCCAGAA	256010	88206	CTGAGAGGGCATCCCAGGCC	300597	132793	GCCCAGCCCTGGGGGGATTG
211424	43620	GAGGGCTTCTGGCCTCCAGA	256011	88207	ACTGAGAGGGCATCCCAGGC	300598	132794	TGCCCAGCCCTGGGGGGATT
211425	43621	GGAGGGCTTCTGGCCTCCAG	256012	88208	CACTGAGAGGGCATCCCAGG	300599	132795	GTGCCCAGCCCTGGGGGGAT
211426	43622	TGGAGGGCTTCTGGCCTCCA	256013	88209	ACACTGAGAGGGCATCCCAG	300600	132796	AGTGCCCAGCCCTGGGGGGA
211427	43623	ATGGAGGGCTTCTGGCCTCC	256014	88210	GACACTGAGAGGGCATCCCA	300601	132797	GAGTGCCCAGCCCTGGGGGG
211428	43624	TATGGAGGGCTTCTGGCCTC	256015	88211	TGACACTGAGAGGGCATCCC	300602	132798	GGAGTGCCCAGCCCTGGGGG
211429	43625	CTATGGAGGGCTTCTGGCCT	256016	88212	ATGACACTGAGAGGGCATCC	300603	132799	AGGAGTGCCCAGCCCTGGGG
211430	43626	CCTATGGAGGGCTTCTGGCC	256017	88213	AATGACACTGAGAGGGCATC	300604	132800	GAGGAGTGCCCAGCCCTGGG
211431	43627	ACCTATGGAGGGCTTCTGGC	256018	88214	AAATGACACTGAGAGGGCAT	300605	132801	GGAGGAGTGCCCAGCCCTGG
211432	43628	CACCTATGGAGGGCTTCTGG	256019	88215	AAAATGACACTGAGAGGGCA	300606	132802	GGGAGGAGTGCCCAGCCCTG
211433	43629	ACACCTATGGAGGGCTTCTG	256020	88216	CAAAATGACACTGAGAGGGC	300607	132803	GGGGAGGAGTGCCCAGCCCT
211434	43630	GACACCTATGGAGGGCTTCT	256021	88217	ACAAAATGACACTGAGAGGG	300608	132804	AGGGGAGGAGTGCCCAGCCC

211435	43631	TGACACCTATGGAGGGCTTC	256022	88218	GACAAAATGACACTGAGAGG	300609	132805	GAGGGGAGGAGTGCCCAGCC
211436	43632	GTGACACCTATGGAGGGCTT	256023	88219	GGACAAAATGACACTGAGAG	300610	132806	GGAGGGGAGGAGTGCCCAGC
211437	43633	AGTGACACCTATGGAGGGCT	256024	88220	TGGACAAAATGACACTGAGA	300611	132807	GGGAGGGGAGGAGTGCCCAG
211438	43634	CAGTGACACCTATGGAGGGC	256025	88221	CTGGACAAAATGACACTGAG	300612	132808	GGGGAGGGGAGGAGTGCCCA
211439	43635	CCAGTGACACCTATGGAGGG	256026	88222	CCTGGACAAAATGACACTGA	300613	132809	AGGGGAGGGGAGGAGTGCCC
211440	43636	CCCAGTGACACCTATGGAGG	256027	88223	TCCTGGACAAAATGACACTG	300614	132810	GAGGGGAGGGGAGGAGTGCC
211441	43637	GCCCAGTGACACCTATGGAG	256028	88224	ATCCTGGACAAAATGACACT	300615	132811	TGAGGGGAGGGGAGGAGTGC
211442	43638	AGCCCAGTGACACCTATGGA	256029	88225	CATCCTGGACAAAATGACAC	300616	132812	GTGAGGGGAGGGGAGGAGTG
211443	43639	CAGCCCAGTGACACCTATGG	256030	88226	TCATCCTGGACAAAATGACA	300617	132813	AGTGAGGGGAGGGGAGGAGT
211444	43640	TCAGCCCAGTGACACCTATG	256031	88227	ATCATCCTGGACAAAATGAC	300618	132814	AAGTGAGGGGAGGGGAGGAG
211445	43641	TTCAGCCCAGTGACACCTAT	256032	88228	CATCATCCTGGACAAAATGA	300619	132815	GAAGTGAGGGGAGGGGAGGA
211446	43642	TTTCAGCCCAGTGACACCTA	256033	88229	GCATCATCCTGGACAAAATG	300620	132816	AGAAGTGAGGGGAGGGGAGG
211447	43643	ATTTCAGCCCAGTGACACCT	256034	88230	AGCATCATCCTGGACAAAAT	300621	132817	GAGAAGTGAGGGGAGGGGAG
211448	43644	GATTTCAGCCCAGTGACACC	256035	88231	GAGCATCATCCTGGACAAAA	300622	132818	GGAGAAGTGAGGGGAGGGGA
211449	43645	TGATTTCAGCCCAGTGACAC	256036	88232	GGAGCATCATCCTGGACAAA	300623	132819	GGGAGAAGTGAGGGGAGGGG
211450	43646	TTGATTTCAGCCCAGTGACA	256037	88233	GGGAGCATCATCCTGGACAA	300624	132820	TGGGAGAAGTGAGGGGAGGG
211451	43647	CTTGATTTCAGCCCAGTGAC	256038	88234	AGGGAGCATCATCCTGGACA	300625	132821	GTGGGAGAAGTGAGGGGAGG
211452	43648	CCTTGATTTCAGCCCAGTGA	256039	88235	GAGGGAGCATCATCCTGGAC	300626	132822	GGTGGGAGAAGTGAGGGGAG
211453	43649	ACCTTGATTTCAGCCCAGTG	256040	88236	AGAGGGAGCATCATCCTGGA	300627	132823	AGGTGGGAGAAGTGAGGGGA
211454	43650	AACCTTGATTTCAGCCCAGT	256041	88237	GAGAGGGAGCATCATCCTGG	300628	132824	CAGGTGGGAGAAGTGAGGGG
211455	43651	AAACCTTGATTTCAGCCCAG	256042	88238	AGAGAGGGAGCATCATCCTG	300629	132825	GCAGGTGGGAGAAGTGAGGG
211456	43652	AAAACCTTGATTTCAGCCCA	256043	88239	AAGAGAGGGAGCATCATCCT	300630	132826	TGCAGGTGGGAGAAGTGAGG
211457	43653	CAAAACCTTGATTTCAGCCC	256044	88240	TAAGAGAGGGAGCATCATCC	300631	132827	CTGCAGGTGGGAGAAGTGAG
211458	43654	CCAAAACCTTGATTTCAGCC	256045	88241	TTAAGAGAGGGAGCATCATC	300632	132828	TCTGCAGGTGGGAGAAGTGA
211459	43655	GCCAAAACCTTGATTTCAGC	256046	88242	CTTAAGAGAGGGAGCATCAT	300633	132829	CTCTGCAGGTGGGAGAAGTG
211460	43656	TGCCAAAACCTTGATTTCAG	256047	88243	GCTTAAGAGAGGGAGCATCA	300634	132830	GCTCTGCAGGTGGGAGAAGT
211461	43657	TTGCCAAAACCTTGATTTCA	256048	88244	CGCTTAAGAGAGGGAGCATC	300635	132831	GGCTCTGCAGGTGGGAGAAG
211462	43658	CTTGCCAAAACCTTGATTTC	256049	88245	TCGCTTAAGAGAGGGAGCAT	300636	132832	TGGCTCTGCAGGTGGGAGAA
211463	43659	CCTTGCCAAAACCTTGATTT	256050	88246	ATCGCTTAAGAGAGGGAGCA	300637	132833	CTGGCTCTGCAGGTGGGAGA
211464	43660	ACCTTGCCAAAACCTTGATT	256051	88247	AATCGCTTAAGAGAGGGAGC	300638	132834	ACTGGCTCTGCAGGTGGGAG
211465	43661	AACCTTGCCAAAACCTTGAT	256052	88248	TAATCGCTTAAGAGAGGGAG	300639	132835	CACTGGCTCTGCAGGTGGGA
211466	43662	CAACCTTGCCAAAACCTTGA	256053	88249	TTAATCGCTTAAGAGAGGGA	300640	132836	ACACTGGCTCTGCAGGTGGG
211467	43663	GCAACCTTGCCAAAACCTTG	256054	88250	ATTAATCGCTTAAGAGAGGG	300641	132837	GACACTGGCTCTGCAGGTGG
211468	43664	CGCAACCTTGCCAAAACCTT	256055	88251	CATTAATCGCTTAAGAGAGG	300642	132838	GGACACTGGCTCTGCAGGTG
211469	43665	CCGCAACCTTGCCAAAACCT	256056	88252	GCATTAATCGCTTAAGAGAG	300643	132839	AGGACACTGGCTCTGCAGGT
211470	43666	ACCGCAACCTTGCCAAAACC	256057	88253	CGCATTAATCGCTTAAGAGA	300644	132840	AAGGACACTGGCTCTGCAGG
211471	43667	GACCGCAACCTTGCCAAAAC	256058	88254	GCGCATTAATCGCTTAAGAG	300645	132841	CAAGGACACTGGCTCTGCAG
211472	43668	GGACCGCAACCTTGCCAAAA	256059	88255	GGCGCATTAATCGCTTAAGA	300646	132842	CCAAGGACACTGGCTCTGCA
211473	43669	AGGACCGCAACCTTGCCAAA	256060	88256	GGGCGCATTAATCGCTTAAG	300647	132843	CCCAAGGACACTGGCTCTGC
211474	43670	AAGGACCGCAACCTTGCCAA	256061	88257	AGGGCGCATTAATCGCTTAA	300648	132844	ACCCAAGGACACTGGCTCTG
211475	43671	AAAGGACCGCAACCTTGCCA	256062	88258	AAGGGCGCATTAATCGCTTA	300649	132845	CACCCAAGGACACTGGCTCT
211476	43672	GAAAGGACCGCAACCTTGCC	256063	88259	CAAGGGCGCATTAATCGCTT	300650	132846	CCACCCAAGGACACTGGCTC
211477	43673	AGAAAGGACCGCAACCTTGC	256064	88260	GCAAGGGCGCATTAATCGCT	300651	132847	CCCACCCAAGGACACTGGCT
211478	43674	CAGAAAGGACCGCAACCTTG	256065	88261	AGCAAGGGCGCATTAATCGC	300652	132848	GCCCACCCAAGGACACTGGC
211479	43675	CCAGAAAGGACCGCAACCTT	256066	88262	TAGCAAGGGCGCATTAATCG	300653	132849	AGCCCACCCAAGGACACTGG
211480	43676	TCCAGAAAGGACCGCAACCT	256067	88263	TTAGCAAGGGCGCATTAATC	300654	132850	TAGCCCACCCAAGGACACTG
211481	43677	CTCCAGAAAGGACCGCAACC	256068	88264	GTTAGCAAGGGCGCATTAAT	300655	132851	CTAGCCCACCCAAGGACACT
211482	43678	CCTCCAGAAAGGACCGCAAC	256069	88265	GGTTAGCAAGGGCGCATTAA	300656	132852	TCTAGCCCACCCAAGGACAC
211483	43679	CCCTCCAGAAAGGACCGCAA	256070	88266	AGGTTAGCAAGGGCGCATTA	300657	132853	ATCTAGCCCACCCAAGGACA
211484	43680	ACCCTCCAGAAAGGACCGCA	256071	88267	AAGGTTAGCAAGGGCGCATT	300658	132854	TATCTAGCCCACCCAAGGAC
211485	43681	GACCCTCCAGAAAGGACCGC	256072	88268	AAAGGTTAGCAAGGGCGCAT	300659	132855	CTATCTAGCCCACCCAAGGA
211486	43682	GGACCCTCCAGAAAGGACCG	256073	88269	AAAAGGTTAGCAAGGGCGCA	300660	132856	CCTATCTAGCCCACCCAAGG
211487	43683	TGGACCCTCCAGAAAGGACC	256074	88270	CAAAAGGTTAGCAAGGGCGC	300661	132857	TCCTATCTAGCCCACCCAAG
211488	43684	CTGGACCCTCCAGAAAGGAC	256075	88271	GCAAAAGGTTAGCAAGGGCG	300662	132858	ATCCTATCTAGCCCACCCAA
211489	43685	CCTGGACCCTCCAGAAAGGA	256076	88272	AGCAAAAGGTTAGCAAGGGC	300663	132859	TATCCTATCTAGCCCACCCA
211490	43686	CCCTGGACCCTCCAGAAAGG	256077	88273	TAGCAAAAGGTTAGCAAGGG	300664	132860	ATATCCTATCTAGCCCACCC
211491	43687	CCCCTGGACCCTCCAGAAAG	256078	88274	ATAGCAAAAGGTTAGCAAGG	300665	132861	TATATCCTATCTAGCCCACC
211492	43688	TCCCCTGGACCCTCCAGAAA	256079	88275	GATAGCAAAAGGTTAGCAAG	300666	132862	GTATATCCTATCTAGCCCAC
211493	43689	CTCCCCTGGACCCTCCAGAA	256080	88276	CGATAGCAAAAGGTTAGCAA	300667	132863	AGTATATCCTATCTAGCCCA
211494	43690	TCTCCCCTGGACCCTCCAGA	256081	88277	GCGATAGCAAAAGGTTAGCA	300668	132864	CAGTATATCCTATCTAGCCC
211495	43691	TTCTCCCCTGGACCCTCCAG	256082	88278	AGCGATAGCAAAAGGTTAGC	300669	132865	ACAGTATATCCTATCTAGCC
211496	43692	ATTCTCCCCTGGACCCTCCA	256083	88279	CAGCGATAGCAAAAGGTTAG	300670	132866	TACAGTATATCCTATCTAGC
211497	43693	GATTCTCCCCTGGACCCTCC	256084	88280	GCAGCGATAGCAAAAGGTTA	300671	132867	ATACAGTATATCCTATCTAG
211498	43694	GGATTCTCCCCTGGACCCTC	256085	88281	GGCAGCGATAGCAAAAGGTT	300672	132868	CATACAGTATATCCTATCTA
211499	43695	TGGATTCTCCCCTGGACCCT	256086	88282	AGGCAGCGATAGCAAAAGGT	300673	132869	GCATACAGTATATCCTATCT
211500	43696	ATGGATTCTCCCCTGGACCC	256087	88283	GAGGCAGCGATAGCAAAAGG	300674	132870	GGCATACAGTATATCCTATC
211501	43697	AATGGATTCTCCCCTGGACC	256088	88284	AGAGGCAGCGATAGCAAAAG	300675	132871	CGGCATACAGTATATCCTAT
211502	43698	AAATGGATTCTCCCCTGGAC	256089	88285	AAGAGGCAGCGATAGCAAAA	300676	132872	CCGGCATACAGTATATCCTA
211503	43699	AAAATGGATTCTCCCCTGGA	256090	88286	GAAGAGGCAGCGATAGCAAA	300677	132873	GCCGGCATACAGTATATCCT
211504	43700	GAAAATGGATTCTCCCCTGG	256091	88287	TGAAGAGGCAGCGATAGCAA	300678	132874	AGCCGGCATACAGTATATCC
211505	43701	AGAAAATGGATTCTCCCCTG	256092	88288	TTGAAGAGGCAGCGATAGCA	300679	132875	GAGCCGGCATACAGTATATC
211506	43702	AAGAAAATGGATTCTCCCCT	256093	88289	TTTGAAGAGGCAGCGATAGC	300680	132876	GGAGCCGGCATACAGTATAT

211507	43703	GAAGAAAATGGATTCTCCCC	256094	88290	GTTTGAAGAGGCAGCGATAG	300681	132877	AGGAGCCGGCATACAGTATA
211508	43704	GGAAGAAAATGGATTCTCCC	256095	88291	GGTTTGAAGAGGCAGCGATA	300682	132878	AAGGAGCCGGCATACAGTAT
211509	43705	AGGAAGAAAATGGATTCTCC	256096	88292	TGGTTTGAAGAGGCAGCGAT	300683	132879	GAAGGAGCCGGCATACAGTA
211510	43706	AAGGAAGAAAATGGATTCTC	256097	88293	CTGGTTTGAAGAGGCAGCGA	300684	132880	TGAAGGAGCCGGCATACAGT
211511	43707	AAAGGAAGAAAATGGATTCT	256098	88294	TCTGGTTTGAAGAGGCAGCG	300685	132881	TTGAAGGAGCCGGCATACAG
211512	43708	AAAAGGAAGAAAATGGATTC	256099	88295	CTCTGGTTTGAAGAGGCAGC	300686	132882	CTTGAAGGAGCCGGCATACA
211513	43709	AAAAAGGAAGAAAATGGATT	256100	88296	CCTCTGGTTTGAAGAGGCAG	300687	132883	GCTTGAAGGAGCCGGCATAC
211514	43710	GAAAAAGGAAGAAAATGGAT	256101	88297	TCCTCTGGTTTGAAGAGGCA	300688	132884	AGCTTGAAGGAGCCGGCATA
211515	43711	GGAAAAAGGAAGAAAATGGA	256102	88298	CTCCTCTGGTTTGAAGAGGC	300689	132885	CAGCTTGAAGGAGCCGGCAT
211516	43712	TGGAAAAAGGAAGAAAATGG	256103	88299	ACTCCTCTGGTTTGAAGAGG	300690	132886	GCAGCTTGAAGGAGCCGGCA
211517	43713	CTGGAAAAAGGAAGAAAATG	256104	88300	AACTCCTCTGGTTTGAAGAG	300691	132887	AGCAGCTTGAAGGAGCCGGC
211518	43714	GCTGGAAAAAGGAAGAAAAT	256105	88301	CAACTCCTCTGGTTTGAAGA	300692	132888	CAGCAGCTTGAAGGAGCCGG
211519	43715	AGCTGGAAAAAGGAAGAAAA	256106	88302	TCAACTCCTCTGGTTTGAAG	300693	132889	TCAGCAGCTTGAAGGAGCCG
211520	43716	AAGCTGGAAAAAGGAAGAAA	256107	88303	CTCAACTCCTCTGGTTTGAA	300694	132890	GTCAGCAGCTTGAAGGAGCC
211521	43717	GAAGCTGGAAAAAGGAAGAA	256108	88304	TCTCAACTCCTCTGGTTTGA	300695	132891	AGTCAGCAGCTTGAAGGAGC
211522	43718	AGAAGCTGGAAAAAGGAAGA	256109	88305	CTCTCAACTCCTCTGGTTTG	300696	132892	GAGTCAGCAGCTTGAAGGAG
211523	43719	TAGAAGCTGGAAAAAGGAAG	256110	88306	ACTCTCAACTCCTCTGGTTT	300697	132893	TGAGTCAGCAGCTTGAAGGA
211524	43720	TTAGAAGCTGGAAAAAGGAA	256111	88307	AACTCTCAACTCCTCTGGTT	300698	132894	GTGAGTCAGCAGCTTGAAGG
211525	43721	TTTAGAAGCTGGAAAAAGGA	256112	88308	GAACTCTCAACTCCTCTGGT	300699	132895	AGTGAGTCAGCAGCTTGAAG
211526	43722	CTTTAGAAGCTGGAAAAAGG	256113	88309	GGAACTCTCAACTCCTCTGG	300700	132896	AAGTGAGTCAGCAGCTTGAA
211527	43723	CCTTTAGAAGCTGGAAAAAG	256114	88310	CGGAACTCTCAACTCCTCTG	300701	132897	AAAGTGAGTCAGCAGCTTGA
211528	43724	ACCTTTAGAAGCTGGAAAAA	256115	88311	CCGGAACTCTCAACTCCTCT	300702	132898	TAAAGTGAGTCAGCAGCTTG
211529	43725	AACCTTTAGAAGCTGGAAAA	256116	88312	CCCGGAACTCTCAACTCCTC	300703	132899	ATAAAGTGAGTCAGCAGCTT
211530	43726	AAACCTTTAGAAGCTGGAAA	256117	88313	GCCCGGAACTCTCAACTCCT	300704	132900	GATAAAGTGAGTCAGCAGCT
211531	43727	GAAACCTTTAGAAGCTGGAA	256118	88314	GGCCCGGAACTCTCAACTCC	300705	132901	TGATAAAGTGAGTCAGCAGC
211532	43728	TGAAACCTTTAGAAGCTGGA	256119	88315	CGGCCCGGAACTCTCAACTC	300706	132902	TTGATAAAGTGAGTCAGCAG
211533	43729	ATGAAACCTTTAGAAGCTGG	256120	88316	CCGGCCCGGAACTCTCAACT	300707	132903	ATTGATAAAGTGAGTCAGCA
211534	43730	CATGAAACCTTTAGAAGCTG	256121	88317	GCCGGCCCGGAACTCTCAAC	300708	132904	TATTGATAAAGTGAGTCAGC
211535	43731	GCATGAAACCTTTAGAAGCT	256122	88318	TGCCGGCCCGGAACTCTCAA	300709	132905	CTATTGATAAAGTGAGTCAG
211536	43732	TGCATGAAACCTTTAGAAGC	256123	88319	CTGCCGGCCCGGAACTCTCA	300710	132906	ACTATTGATAAAGTGAGTCA
211537	43733	ATGCATGAAACCTTTAGAAG	256124	88320	TCTGCCGGCCCGGAACTCTC	300711	132907	AACTATTGATAAAGTGAGTC
211538	43734	AATGCATGAAACCTTTAGAA	256125	88321	CTCTGCCGGCCCGGAACTCT	300712	132908	GAACTATTGATAAAGTGAGT
211539	43735	GAATGCATGAAACCTTTAGA	256126	88322	CCTCTGCCGGCCCGGAACTC	300713	132909	GGAACTATTGATAAAGTGAG
211540	43736	GGAATGCATGAAACCTTTAG	256127	88323	TCCTCTGCCGGCCCGGAACT	300714	132910	TGGAACTATTGATAAAGTGA
211541	43737	AGGAATGCATGAAACCTTTA	256128	88324	TTCCTCTGCCGGCCCGGAAC	300715	132911	ATGGAACTATTGATAAAGTG
211542	43738	AAGGAATGCATGAAACCTTT	256129	88325	CTTCCTCTGCCGGCCCGGAA	300716	132912	AATGGAACTATTGATAAAGT
211543	43739	CAAGGAATGCATGAAACCTT	256130	88326	CCTTCCTCTGCCGGCCCGGA	300717	132913	AAATGGAACTATTGATAAAG
211544	43740	CCAAGGAATGCATGAAACCT	256131	88327	GCCTTCCTCTGCCGGCCCGG	300718	132914	TAAATGGAACTATTGATAAA
211545	43741	GCCAAGGAATGCATGAAACC	256132	88328	CGCCTTCCTCTGCCGGCCCG	300719	132915	TTAAATGGAACTATTGATAA
211546	43742	AGCCAAGGAATGCATGAAAC	256133	88329	GCGCCTTCCTCTGCCGGCCC	300720	132916	TTTAAATGGAACTATTGATA
211547	43743	GAGCCAAGGAATGCATGAAA	256134	88330	GGCGCCTTCCTCTGCCGGCC	300721	132917	ATTTAAATGGAACTATTGAT
211548	43744	TGAGCCAAGGAATGCATGAA	256135	88331	AGGCGCCTTCCTCTGCCGGC	300722	132918	AATTTAAATGGAACTATTGA
211549	43745	ATGAGCCAAGGAATGCATGA	256136	88332	CAGGCGCCTTCCTCTGCCGG	300723	132919	CAATTTAAATGGAACTATTG
211550	43746	CATGAGCCAAGGAATGCATG	256137	88333	TCAGGCGCCTTCCTCTGCCG	300724	132920	TCAATTTAAATGGAACTATT
211551	43747	TCATGAGCCAAGGAATGCAT	256138	88334	TTCAGGCGCCTTCCTCTGCC	300725	132921	GTCAATTTAAATGGAACTAT
211552	43748	ATCATGAGCCAAGGAATGCA	256139	88335	TTTCAGGCGCCTTCCTCTGC	300726	132922	AGTCAATTTAAATGGAACTA
211553	43749	GATCATGAGCCAAGGAATGC	256140	88336	CTTTCAGGCGCCTTCCTCTG	300727	132923	AAGTCAATTTAAATGGAACT
211554	43750	AGATCATGAGCCAAGGAATG	256141	88337	CCTTTCAGGCGCCTTCCTCT	300728	132924	GAAGTCAATTTAAATGGAAC
211555	43751	AAGATCATGAGCCAAGGAAT	256142	88338	GCCTTTCAGGCGCCTTCCTC	300729	132925	TGAAGTCAATTTAAATGGAA
211556	43752	GAAGATCATGAGCCAAGGAA	256143	88339	GGCCTTTCAGGCGCCTTCCT	300730	132926	CTGAAGTCAATTTAAATGGA
211557	43753	AGAAGATCATGAGCCAAGGA	256144	88340	GGGCCTTTCAGGCGCCTTCC	300731	132927	ACTGAAGTCAATTTAAATGG
211558	43754	TAGAAGATCATGAGCCAAGG	256145	88341	GGGGCCTTTCAGGCGCCTTC	300732	132928	CACTGAAGTCAATTTAAATG
211559	43755	ATAGAAGATCATGAGCCAAG	256146	88342	AGGGGCCTTTCAGGCGCCTT	300733	132929	CCACTGAAGTCAATTTAAAT
211560	43756	TATAGAAGATCATGAGCCAA	256147	88343	CAGGGGCCTTTCAGGCGCCT	300734	132930	ACCACTGAAGTCAATTTAAA
211561	43757	CTATAGAAGATCATGAGCCA	256148	88344	CCAGGGGCCTTTCAGGCGCC	300735	132931	CACCACTGAAGTCAATTTAA
211562	43758	GCTATAGAAGATCATGAGCC	256149	88345	GCCAGGGGCCTTTCAGGCGC	300736	132932	TCACCACTGAAGTCAATTTA
211563	43759	AGCTATAGAAGATCATGAGC	256150	88346	GGCCAGGGGCCTTTCAGGCG	300737	132933	CTCACCACTGAAGTCAATTT
211564	43760	TAGCTATAGAAGATCATGAG	256151	88347	TGGCCAGGGGCCTTTCAGGC	300738	132934	TCTCACCACTGAAGTCAATT
211565	43761	ATAGCTATAGAAGATCATGA	256152	88348	TTGGCCAGGGGCCTTTCAGG	300739	132935	GTCTCACCACTGAAGTCAAT
211566	43762	TATAGCTATAGAAGATCATG	256153	88349	ATTGGCCAGGGGCCTTTCAG	300740	132936	AGTCTCACCACTGAAGTCAA
211567	43763	CTATAGCTATAGAAGATCAT	256154	88350	CATTGGCCAGGGGCCTTTCA	300741	132937	CAGTCTCACCACTGAAGTCA
211568	43764	ACTATAGCTATAGAAGATCA	256155	88351	TCATTGGCCAGGGGCCTTTC	300742	132938	ACAGTCTCACCACTGAAGTC
211569	43765	GACTATAGCTATAGAAGATC	256156	88352	CTCATTGGCCAGGGGCCTTT	300743	132939	TACAGTCTCACCACTGAAGT
211570	43766	TGACTATAGCTATAGAAGAT	256157	88353	TCTCATTGGCCAGGGGCCTT	300744	132940	ATACAGTCTCACCACTGAAG
211571	43767	CTGACTATAGCTATAGAAGA	256158	88354	ATCTCATTGGCCAGGGGCCT	300745	132941	GATACAGTCTCACCACTGAA
211572	43768	TCTGACTATAGCTATAGAAG	256159	88355	AATCTCATTGGCCAGGGGCC	300746	132942	GGATACAGTCTCACCACTGA
211573	43769	TTCTGACTATAGCTATAGAA	256160	88356	TAATCTCATTGGCCAGGGGC	300747	132943	AGGATACAGTCTCACCACTG
211574	43770	TTTCTGACTATAGCTATAGA	256161	88357	CTAATCTCATTGGCCAGGGG	300748	132944	CAGGATACAGTCTCACCACT
211575	43771	TTTTCTGACTATAGCTATAG	256162	88358	GCTAATCTCATTGGCCAGGG	300749	132945	ACAGGATACAGTCTCACCAC
211576	43772	TTTTTCTGACTATAGCTATA	256163	88359	CGCTAATCTCATTGGCCAGG	300750	132946	AACAGGATACAGTCTCACCA
211577	43773	ATTTTTCTGACTATAGCTAT	256164	88360	GCGCTAATCTCATTGGCCAG	300751	132947	AAACAGGATACAGTCTCACC
211578	43774	AATTTTTCTGACTATAGCTA	256165	88361	GGCGCTAATCTCATTGGCCA	300752	132948	CAAACAGGATACAGTCTCAC

211579	43775	AAATTTTTCTGACTATAGCT	256166	88362	GGGCGCTAATCTCATTGGCC	300753	132949	GCAAACAGGATACAGTCTCA
211580	43776	AAAATTTTTCTGACTATAGC	256167	88363	TGGGCGCTAATCTCATTGGC	300754	132950	AGCAAACAGGATACAGTCTC
211581	43777	GAAAATTTTTCTGACTATAG	256168	88364	GTGGGCGCTAATCTCATTGG	300755	132951	TAGCAAACAGGATACAGTCT
211582	43778	GGAAAATTTTTCTGACTATA	256169	88365	CGTGGGCGCTAATCTCATTG	300756	132952	ATAGCAAACAGGATACAGTC
211583	43779	TGGAAAATTTTTCTGACTAT	256170	88366	ACGTGGGCGCTAATCTCATT	300757	132953	AATAGCAAACAGGATACAGT
211584	43780	ATGGAAAATTTTTCTGACTA	256171	88367	GACGTGGGCGCTAATCTCAT	300758	132954	CAATAGCAAACAGGATACAG
211585	43781	GATGGAAAATTTTTCTGACT	256172	88368	GGACGTGGGCGCTAATCTCA	300759	132955	GCAATAGCAAACAGGATACA
211586	43782	TGATGGAAAATTTTTCTGAC	256173	88369	TGGACGTGGGCGCTAATCTC	300760	132956	AGCAATAGCAAACAGGATAC
211587	43783	TTGATGGAAAATTTTTCTGA	256174	88370	CTGGACGTGGGCGCTAATCT	300761	132957	AAGCAATAGCAAACAGGATA
211588	43784	ATTGATGGAAAATTTTTCTG	256175	88371	GCTGGACGTGGGCGCTAATC	300762	132958	CAAGCAATAGCAAACAGGAT
211589	43785	GATTGATGGAAAATTTTTCT	256176	88372	GGCTGGACGTGGGCGCTAAT	300763	132959	ACAAGCAATAGCAAACAGGA
211590	43786	TGATTGATGGAAAATTTTTC	256177	88373	AGGCTGGACGTGGGCGCTAA	300764	132960	AACAAGCAATAGCAAACAGG
211591	43787	ATGATTGATGGAAAATTTTT	256178	88374	CAGGCTGGACGTGGGCGCTA	300765	132961	CAACAAGCAATAGCAAACAG
211592	43788	GATGATTGATGGAAAATTTT	256179	88375	CCAGGCTGGACGTGGGCGCT	300766	132962	ACAACAAGCAATAGCAAACA
211593	43789	AGATGATTGATGGAAAATTT	256180	88376	TCCAGGCTGGACGTGGGCGC	300767	132963	CACAACAAGCAATAGCAAAC
211594	43790	AAGATGATTGATGGAAAATT	256181	88377	GTCCAGGCTGGACGTGGGCG	300768	132964	GCACAACAAGCAATAGCAAA
211595	43791	GAAGATGATTGATGGAAAAT	256182	88378	GGTCCAGGCTGGACGTGGGC	300769	132965	AGCACAACAAGCAATAGCAA
211596	43792	TGAAGATGATTGATGGAAAA	256183	88379	GGGTCCAGGCTGGACGTGGG	300770	132966	TAGCACAACAAGCAATAGCA
211597	43793	TTGAAGATGATTGATGGAAA	256184	88380	AGGGTCCAGGCTGGACGTGG	300771	132967	ATAGCACAACAAGCAATAGC
211598	43794	TTTGAAGATGATTGATGGAA	256185	88381	CAGGGTCCAGGCTGGACGTG	300772	132968	CATAGCACAACAAGCAATAG
211599	43795	CTTTGAAGATGATTGATGGA	256186	88382	GCAGGGTCCAGGCTGGACGT	300773	132969	CCATAGCACAACAAGCAATA
211600	43796	GCTTTGAAGATGATTGATGG	256187	88383	CGCAGGGTCCAGGCTGGACG	300774	132970	CCCATAGCACAACAAGCAAT
211601	43797	GGCTTTGAAGATGATTGATG	256188	88384	CCGCAGGGTCCAGGCTGGAC	300775	132971	CCCCATAGCACAACAAGCAA
211602	43798	TGGCTTTGAAGATGATTGAT	256189	88385	TCCGCAGGGTCCAGGCTGGA	300776	132972	CCCCCATAGCACAACAAGCA
211603	43799	CTGGCTTTGAAGATGATTGA	256190	88386	CTCCGCAGGGTCCAGGCTGG	300777	132973	CCCCCCATAGCACAACAAGC
211604	43800	GCTGGCTTTGAAGATGATTG	256191	88387	TCTCCGCAGGGTCCAGGCTG	300778	132974	TCCCCCCATAGCACAACAAG
211605	43801	TGCTGGCTTTGAAGATGATT	256192	88388	CTCTCCGCAGGGTCCAGGCT	300779	132975	CTCCCCCCATAGCACAACAA
211606	43802	TTGCTGGCTTTGAAGATGAT	256193	88389	CCTCTCCGCAGGGTCCAGGC	300780	132976	CCTCCCCCCATAGCACAACA
211607	43803	ATTGCTGGCTTTGAAGATGA	256194	88390	GCCTCTCCGCAGGGTCCAGG	300781	132977	CCCTCCCCCCATAGCACAAC
211608	43804	CATTGCTGGCTTTGAAGATG	256195	88391	GGCCTCTCCGCAGGGTCCAG	300782	132978	CCCCTCCCCCCATAGCACAA
211609	43805	CCATTGCTGGCTTTGAAGAT	256196	88392	AGGCCTCTCCGCAGGGTCCA	300783	132979	CCCCCTCCCCCCATAGCACA
211610	43806	GCCATTGCTGGCTTTGAAGA	256197	88393	GAGGCCTCTCCGCAGGGTCC	300784	132980	CCCCCCTCCCCCCATAGCAC
211611	43807	TGCCATTGCTGGCTTTGAAG	256198	88394	AGAGGCCTCTCCGCAGGGTC	300785	132981	TCCCCCCTCCCCCCATAGCA
211612	43808	CTGCCATTGCTGGCTTTGAA	256199	88395	CAGAGGCCTCTCCGCAGGGT	300786	132982	CTCCCCCCTCCCCCCATAGC
211613	43809	CCTGCCATTGCTGGCTTTGA	256200	88396	CCAGAGGCCTCTCCGCAGGG	300787	132983	CCTCCCCCCTCCCCCCATAG
211614	43810	TCCTGCCATTGCTGGCTTTG	256201	88397	CCCAGAGGCCTCTCCGCAGG	300788	132984	TCCTCCCCCCTCCCCCCATA
211615	43811	ATCCTGCCATTGCTGGCTTT	256202	88398	CCCCAGAGGCCTCTCCGCAG	300789	132985	TTCCTCCCCCCTCCCCCCAT
211616	43812	CATCCTGCCATTGCTGGCTT	256203	88399	ACCCCAGAGGCCTCTCCGCA	300790	132986	ATTCCTCCCCCCTCCCCCCA
211617	43813	TCATCCTGCCATTGCTGGCT	256204	88400	GACCCCAGAGGCCTCTCCGC	300791	132987	CATTCCTCCCCCCTCCCCCC
211618	43814	CTCATCCTGCCATTGCTGGC	256205	88401	AGACCCCAGAGGCCTCTCCG	300792	132988	ACATTCCTCCCCCCTCCCCC
211619	43815	ACTCATCCTGCCATTGCTGG	256206	88402	GAGACCCCAGAGGCCTCTCC	300793	132989	CACATTCCTCCCCCCTCCCC
211620	43816	GACTCATCCTGCCATTGCTG	256207	88403	AGAGACCCCAGAGGCCTCTC	300794	132990	ACACATTCCTCCCCCCTCCC
211621	43817	GGACTCATCCTGCCATTGCT	256208	88404	CAGAGACCCCAGAGGCCTCT	300795	132991	TACACATTCCTCCCCCCTCC
211622	43818	AGGACTCATCCTGCCATTGC	256209	88405	CCAGAGACCCCAGAGGCCTC	300796	132992	TTACACATTCCTCCCCCCTC
211623	43819	GAGGACTCATCCTGCCATTG	256210	88406	CCCAGAGACCCCAGAGGCCT	300797	132993	CTTACACATTCCTCCCCCCT
211624	43820	TGAGGACTCATCCTGCCATT	256211	88407	GCCCAGAGACCCCAGAGGCC	300798	132994	TCTTACACATTCCTCCCCCC
211625	43821	GTGAGGACTCATCCTGCCAT	256212	88408	GGCCCAGAGACCCCAGAGGC	300799	132995	ATCTTACACATTCCTCCCCC
211626	43822	TGTGAGGACTCATCCTGCCA	256213	88409	CGGCCCAGAGACCCCAGAGG	300800	132996	TATCTTACACATTCCTCCCC
211627	43823	ATGTGAGGACTCATCCTGCC	256214	88410	ACGGCCCAGAGACCCCAGAG	300801	132997	CTATCTTACACATTCCTCCC
211628	43824	GATGTGAGGACTCATCCTGC	256215	88411	CACGGCCCAGAGACCCCAGA	300802	132998	ACTATCTTACACATTCCTCC
211629	43825	TGATGTGAGGACTCATCCTG	256216	88412	GCACGGCCCAGAGACCCCAG	300803	132999	AACTATCTTACACATTCCTC
211630	43826	GTGATGTGAGGACTCATCCT	256217	88413	GGCACGGCCCAGAGACCCCA	300804	133000	TAACTATCTTACACATTCCT
211631	43827	GGTGATGTGAGGACTCATCC	256218	88414	AGGCACGGCCCAGAGACCCC	300805	133001	TTAACTATCTTACACATTCC
211632	43828	AGGTGATGTGAGGACTCATC	256219	88415	GAGGCACGGCCCAGAGACCC	300806	133002	GTTAACTATCTTACACATTC
211633	43829	AAGGTGATGTGAGGACTCAT	256220	88416	CGAGGCACGGCCCAGAGACC	300807	133003	TGTTAACTATCTTACACATT
211634	43830	CAAGGTGATGTGAGGACTCA	256221	88417	CCGAGGCACGGCCCAGAGAC	300808	133004	ATGTTAACTATCTTACACAT
211635	43831	GCAAGGTGATGTGAGGACTC	256222	88418	CCCGAGGCACGGCCCAGAGA	300809	133005	CATGTTAACTATCTTACACA
211636	43832	AGCAAGGTGATGTGAGGACT	256223	88419	CCCCGAGGCACGGCCCAGAG	300810	133006	CCATGTTAACTATCTTACAC
211637	43833	GAGCAAGGTGATGTGAGGAC	256224	88420	TCCCCGAGGCACGGCCCAGA	300811	133007	CCCATGTTAACTATCTTACA
211638	43834	AGAGCAAGGTGATGTGAGGA	256225	88421	CTCCCCGAGGCACGGCCCAG	300812	133008	GCCCATGTTAACTATCTTAC
211639	43835	CAGAGCAAGGTGATGTGAGG	256226	88422	TCTCCCCGAGGCACGGCCCA	300813	133009	TGCCCATGTTAACTATCTTA
211640	43836	TCAGAGCAAGGTGATGTGAG	256227	88423	TTCTCCCCGAGGCACGGCCC	300814	133010	TTGCCCATGTTAACTATCTT
211641	43837	GTCAGAGCAAGGTGATGTGA	256228	88424	TTTCTCCCCGAGGCACGGCC	300815	133011	TTTGCCCATGTTAACTATCT
211642	43838	TGTCAGAGCAAGGTGATGTG	256229	88425	CTTTCTCCCCGAGGCACGGC	300816	133012	CTTTGCCCATGTTAACTATC
211643	43839	GTGTCAGAGCAAGGTGATGT	256230	88426	TCTTTCTCCCCGAGGCACGG	300817	133013	CCTTTGCCCATGTTAACTAT
211644	43840	GGTGTCAGAGCAAGGTGATG	256231	88427	CTCTTTCTCCCCGAGGCACG	300818	133014	CCCTTTGCCCATGTTAACTA
211645	43841	TGGTGTCAGAGCAAGGTGAT	256232	88428	GCTCTTTCTCCCCGAGGCAC	300819	133015	TCCCTTTGCCCATGTTAACT
211646	43842	CTGGTGTCAGAGCAAGGTGA	256233	88429	GGCTCTTTCTCCCCGAGGCA	300820	133016	CTCCCTTTGCCCATGTTAAC
211647	43843	ACTGGTGTCAGAGCAAGGTG	256234	88430	TGGCTCTTTCTCCCCGAGGC	300821	133017	TCTCCCTTTGCCCATGTTAA
211648	43844	AACTGGTGTCAGAGCAAGGT	256235	88431	CTGGCTCTTTCTCCCCGAGG	300822	133018	ATCTCCCTTTGCCCATGTTA
211649	43845	GAACTGGTGTCAGAGCAAGG	256236	88432	TCTGGCTCTTTCTCCCCGAG	300823	133019	GATCTCCCTTTGCCCATGTT
211650	43846	AGAACTGGTGTCAGAGCAAG	256237	88433	TTCTGGCTCTTTCTCCCCGA	300824	133020	AGATCTCCCTTTGCCCATGT

211651	43847	GAGAACTGGTGTCAGAGCAA	256238	88434	CTTCTGGCTCTTTCTCCCCG	300825	133021	AAGATCTCCCTTTGCCCATG
211652	43848	AGAGAACTGGTGTCAGAGCA	256239	88435	GCTTCTGGCTCTTTCTCCCC	300826	133022	CAAGATCTCCCTTTGCCCAT
211653	43849	CAGAGAACTGGTGTCAGAGC	256240	88436	AGCTTCTGGCTCTTTCTCCC	300827	133023	CCAAGATCTCCCTTTGCCCA
211654	43850	GCAGAGAACTGGTGTCAGAG	256241	88437	GAGCTTCTGGCTCTTTCTCC	300828	133024	CCCAAGATCTCCCTTTGCCC
211655	43851	GGCAGAGAACTGGTGTCAGA	256242	88438	GGAGCTTCTGGCTCTTTCTC	300829	133025	CCCCAAGATCTCCCTTTGCC
211656	43852	AGGCAGAGAACTGGTGTCAG	256243	88439	GGGAGCTTCTGGCTCTTTCT	300830	133026	ACCCCAAGATCTCCCTTTGC
211657	43853	GAGGCAGAGAACTGGTGTCA	256244	88440	CGGGAGCTTCTGGCTCTTTC	300831	133027	CACCCCAAGATCTCCCTTTG
211658	43854	GGAGGCAGAGAACTGGTGTC	256245	88441	ACGGGAGCTTCTGGCTCTTT	300832	133028	GCACCCCAAGATCTCCCTTT
211659	43855	GGGAGGCAGAGAACTGGTGT	256246	88442	GACGGGAGCTTCTGGCTCTT	300833	133029	TGCACCCCAAGATCTCCCTT
211660	43856	AGGGAGGCAGAGAACTGGTG	256247	88443	GGACGGGAGCTTCTGGCTCT	300834	133030	CTGCACCCCAAGATCTCCCT
211661	43857	GAGGGAGGCAGAGAACTGGT	256248	88444	GGGACGGGAGCTTCTGGCTC	300835	133031	GCTGCACCCCAAGATCTCCC
211662	43858	AGAGGGAGGCAGAGAACTGG	256249	88445	CGGGACGGGAGCTTCTGGCT	300836	133032	TGCTGCACCCCAAGATCTCC
211663	43859	AAGAGGGAGGCAGAGAACTG	256250	88446	GCGGGACGGGAGCTTCTGGC	300837	133033	GTGCTGCACCCCAAGATCTC
211664	43860	GAAGAGGGAGGCAGAGAACT	256251	88447	AGCGGGACGGGAGCTTCTGG	300838	133034	AGTGCTGCACCCCAAGATCT
211665	43861	GGAAGAGGGAGGCAGAGAAC	256252	88448	CAGCGGGACGGGAGCTTCTG	300839	133035	AAGTGCTGCACCCCAAGATC
211666	43862	TGGAAGAGGGAGGCAGAGAA	256253	88449	TCAGCGGGACGGGAGCTTCT	300840	133036	TAAGTGCTGCACCCCAAGAT
211667	43863	GTGGAAGAGGGAGGCAGAGA	256254	88450	GTCAGCGGGACGGGAGCTTC	300841	133037	TTAAGTGCTGCACCCCAAGA
211668	43864	TGTGGAAGAGGGAGGCAGAG	256255	88451	GGTCAGCGGGACGGGAGCTT	300842	133038	TTTAAGTGCTGCACCCCAAG
211669	43865	ATGTGGAAGAGGGAGGCAGA	256256	88452	CGGTCAGCGGGACGGGAGCT	300843	133039	GTTTAAGTGCTGCACCCCAA
211670	43866	CATGTGGAAGAGGGAGGCAG	256257	88453	GCGGTCAGCGGGACGGGAGC	300844	133040	AGTTTAAGTGCTGCACCCCA
211671	43867	ACATGTGGAAGAGGGAGGCA	256258	88454	CGCGGTCAGCGGGACGGGAG	300845	133041	CAGTTTAAGTGCTGCACCCC
211672	43868	GACATGTGGAAGAGGGAGGC	256259	88455	TCGCGGTCAGCGGGACGGGA	300846	133042	GCAGTTTAAGTGCTGCACCC
211673	43869	TGACATGTGGAAGAGGGAGG	256260	88456	CTCGCGGTCAGCGGGACGGG	300847	133043	GGCAGTTTAAGTGCTGCACC
211674	43870	CTGACATGTGGAAGAGGGAG	256261	88457	GCTCGCGGTCAGCGGGACGG	300848	133044	AGGCAGTTTAAGTGCTGCAC
211675	43871	CCTGACATGTGGAAGAGGGA	256262	88458	GGCTCGCGGTCAGCGGGACG	300849	133045	GAGGCAGTTTAAGTGCTGCA
211676	43872	TCCTGACATGTGGAAGAGGG	256263	88459	AGGCTCGCGGTCAGCGGGAC	300850	133046	CGAGGCAGTTTAAGTGCTGC
211677	43873	GTCCTGACATGTGGAAGAGG	256264	88460	AAGGCTCGCGGTCAGCGGGA	300851	133047	ACGAGGCAGTTTAAGTGCTG
211678	43874	GGTCCTGACATGTGGAAGAG	256265	88461	GAAGGCTCGCGGTCAGCGGG	300852	133048	TACGAGGCAGTTTAAGTGCT
211679	43875	GGGTCCTGACATGTGGAAGA	256266	88462	GGAAGGCTCGCGGTCAGCGG	300853	133049	TTACGAGGCAGTTTAAGTGC
211680	43876	AGGGTCCTGACATGTGGAAG	256267	88463	AGGAAGGCTCGCGGTCAGCG	300854	133050	GTTACGAGGCAGTTTAAGTG
211681	43877	GAGGGTCCTGACATGTGGAA	256268	88464	GAGGAAGGCTCGCGGTCAGC	300855	133051	GGTTACGAGGCAGTTTAAGT
211682	43878	TGAGGGTCCTGACATGTGGA	256269	88465	TGAGGAAGGCTCGCGGTCAG	300856	133052	GGGTTACGAGGCAGTTTAAG
211683	43879	ATGAGGGTCCTGACATGTGG	256270	88466	CTGAGGAAGGCTCGCGGTCA	300857	133053	AGGGTTACGAGGCAGTTTAA
211684	43880	CATGAGGGTCCTGACATGTG	256271	88467	GCTGAGGAAGGCTCGCGGTC	300858	133054	AAGGGTTACGAGGCAGTTTA
211685	43881	TCATGAGGGTCCTGACATGT	256272	88468	TGCTGAGGAAGGCTCGCGGT	300859	133055	AAAGGGTTACGAGGCAGTTT
211686	43882	ATCATGAGGGTCCTGACATG	256273	88469	GTGCTGAGGAAGGCTCGCGG	300860	133056	AAAAGGGTTACGAGGCAGTT
211687	43883	AATCATGAGGGTCCTGACAT	256274	88470	GGTGCTGAGGAAGGCTCGCG	300861	133057	GAAAAGGGTTACGAGGCAGT
211688	43884	TAATCATGAGGGTCCTGACA	256275	88471	CGGTGCTGAGGAAGGCTCGC	300862	133058	TGAAAAGGGTTACGAGGCAG
211689	43885	GTAATCATGAGGGTCCTGAC	256276	88472	ACGGTGCTGAGGAAGGCTCG	300863	133059	ATGAAAAGGGTTACGAGGCA
211690	43886	AGTAATCATGAGGGTCCTGA	256277	88473	GACGGTGCTGAGGAAGGCTC	300864	133060	CATGAAAAGGGTTACGAGGC
211691	43887	AAGTAATCATGAGGGTCCTG	256278	88474	GGACGGTGCTGAGGAAGGCT	300865	133061	TCATGAAAAGGGTTACGAGG
211692	43888	AAAGTAATCATGAGGGTCCT	256279	88475	GGGACGGTGCTGAGGAAGGC	300866	133062	ATCATGAAAAGGGTTACGAG
211693	43889	CAAAGTAATCATGAGGGTCC	256280	88476	CGGGACGGTGCTGAGGAAGG	300867	133063	AATCATGAAAAGGGTTACGA
211694	43890	CCAAAGTAATCATGAGGGTC	256281	88477	ACGGGACGGTGCTGAGGAAG	300868	133064	AAATCATGAAAAGGGTTACG
211695	43891	CCCAAAGTAATCATGAGGGT	256282	88478	AACGGGACGGTGCTGAGGAA	300869	133065	GAAATCATGAAAAGGGTTAC
211696	43892	GCCCAAAGTAATCATGAGGG	256283	88479	AAACGGGACGGTGCTGAGGA	300870	133066	TGAAATCATGAAAAGGGTTA
211697	43893	AGCCCAAAGTAATCATGAGG	256284	88480	CAAACGGGACGGTGCTGAGG	300871	133067	TTGAAATCATGAAAAGGGTT
211698	43894	GAGCCCAAAGTAATCATGAG	256285	88481	GCAAACGGGACGGTGCTGAG	300872	133068	GTTGAAATCATGAAAAGGGT
211699	43895	TGAGCCCAAAGTAATCATGA	256286	88482	GGCAAACGGGACGGTGCTGA	300873	133069	GGTTGAAATCATGAAAAGGG
211700	43896	GTGAGCCCAAAGTAATCATG	256287	88483	GGGCAAACGGGACGGTGCTG	300874	133070	TGGTTGAAATCATGAAAAGG
211701	43897	AGTGAGCCCAAAGTAATCAT	256288	88484	TGGGCAAACGGGACGGTGCT	300875	133071	GTGGTTGAAATCATGAAAAG
211702	43898	GAGTGAGCCCAAAGTAATCA	256289	88485	CTGGGCAAACGGGACGGTGC	300876	133072	TGTGGTTGAAATCATGAAAA
211703	43899	AGAGTGAGCCCAAAGTAATC	256290	88486	GCTGGGCAAACGGGACGGTG	300877	133073	ATGTGGTTGAAATCATGAAA
211704	43900	CAGAGTGAGCCCAAAGTAAT	256291	88487	CGCTGGGCAAACGGGACGGT	300878	133074	AATGTGGTTGAAATCATGAA
211705	43901	TCAGAGTGAGCCCAAAGTAA	256292	88488	GCGCTGGGCAAACGGGACGG	300879	133075	AAATGTGGTTGAAATCATGA
211706	43902	ATCAGAGTGAGCCCAAAGTA	256293	88489	GGCGCTGGGCAAACGGGACG	300880	133076	CAAATGTGGTTGAAATCATG
211707	43903	TATCAGAGTGAGCCCAAAGT	256294	88490	AGGCGCTGGGCAAACGGGAC	300881	133077	GCAAATGTGGTTGAAATCAT
211708	43904	TTATCAGAGTGAGCCCAAAG	256295	88491	GAGGCGCTGGGCAAACGGGA	300882	133078	AGCAAATGTGGTTGAAATCA
211709	43905	ATTATCAGAGTGAGCCCAAA	256296	88492	GGAGGCGCTGGGCAAACGGG	300883	133079	TAGCAAATGTGGTTGAAATC
211710	43906	GATTATCAGAGTGAGCCCAA	256297	88493	AGGAGGCGCTGGGCAAACGG	300884	133080	CTAGCAAATGTGGTTGAAAT
211711	43907	AGATTATCAGAGTGAGCCCA	256298	88494	GAGGAGGCGCTGGGCAAACG	300885	133081	TCTAGCAAATGTGGTTGAAA
211712	43908	CAGATTATCAGAGTGAGCCC	256299	88495	GGAGGAGGCGCTGGGCAAAC	300886	133082	CTCTAGCAAATGTGGTTGAA
211713	43909	CCAGATTATCAGAGTGAGCC	256300	88496	TGGAGGAGGCGCTGGGCAAA	300887	133083	CCTCTAGCAAATGTGGTTGA
211714	43910	CCCAGATTATCAGAGTGAGC	256301	88497	TTGGAGGAGGCGCTGGGCAA	300888	133084	CCCTCTAGCAAATGTGGTTG
211715	43911	TCCCAGATTATCAGAGTGAG	256302	88498	GTTGGAGGAGGCGCTGGGCA	300889	133085	TCCCTCTAGCAAATGTGGTT
211716	43912	ATCCCAGATTATCAGAGTGA	256303	88499	TGTTGGAGGAGGCGCTGGGC	300890	133086	CTCCCTCTAGCAAATGTGGT
211717	43913	CATCCCAGATTATCAGAGTG	256304	88500	CTGTTGGAGGAGGCGCTGGG	300891	133087	CCTCCCTCTAGCAAATGTGG
211718	43914	TCATCCCAGATTATCAGAGT	256305	88501	CCTGTTGGAGGAGGCGCTGG	300892	133088	CCCTCCCTCTAGCAAATGTG
211719	43915	ATCATCCCAGATTATCAGAG	256306	88502	TCCTGTTGGAGGAGGCGCTG	300893	133089	TCCCTCCCTCTAGCAAATGT
211720	43916	GATCATCCCAGATTATCAGA	256307	88503	CTCCTGTTGGAGGAGGCGCT	300894	133090	CTCCCTCCCTCTAGCAAATG
211721	43917	AGATCATCCCAGATTATCAG	256308	88504	CCTCCTGTTGGAGGAGGCGC	300895	133091	GCTCCCTCCCTCTAGCAAAT
211722	43918	GAGATCATCCCAGATTATCA	256309	88505	GCCTCCTGTTGGAGGAGGCG	300896	133092	TGCTCCCTCCCTCTAGCAAA

211723	43919	AGAGATCATCCCAGATTATC	256310	88506	GGCCTCCTGTTGGAGGAGGC	300897	133093	CTGCTCCCTCCCTCTAGCAA
211724	43920	GAGAGATCATCCCAGATTAT	256311	88507	GGGCCTCCTGTTGGAGGAGG	300898	133094	GCTGCTCCCTCCCTCTAGCA
211725	43921	AGAGAGATCATCCCAGATTA	256312	88508	AGGGCCTCCTGTTGGAGGAG	300899	133095	GGCTGCTCCCTCCCTCTAGC
211726	43922	TAGAGAGATCATCCCAGATT	256313	88509	GAGGGCCTCCTGTTGGAGGA	300900	133096	TGGCTGCTCCCTCCCTCTAG
211727	43923	ATAGAGAGATCATCCCAGAT	256314	88510	TGAGGGCCTCCTGTTGGAGG	300901	133097	GTGGCTGCTCCCTCCCTCTA
211728	43924	AATAGAGAGATCATCCCAGA	256315	88511	CTGAGGGCCTCCTGTTGGAG	300902	133098	CGTGGCTGCTCCCTCCCTCT
211729	43925	AAATAGAGAGATCATCCCAG	256316	88512	CCTGAGGGCCTCCTGTTGGA	300903	133099	CCGTGGCTGCTCCCTCCCTC
211730	43926	AAAATAGAGAGATCATCCCA	256317	88513	TCCTGAGGGCCTCCTGTTGG	300904	133100	TCCGTGGCTGCTCCCTCCCT
211731	43927	TAAAATAGAGAGATCATCCC	256318	88514	CTCCTGAGGGCCTCCTGTTG	300905	133101	CTCCGTGGCTGCTCCCTCCC
211732	43928	CTAAAATAGAGAGATCATCC	256319	88515	GCTCCTGAGGGCCTCCTGTT	300906	133102	ACTCCGTGGCTGCTCCCTCC
211733	43929	TCTAAAATAGAGAGATCATC	256320	88516	GGCTCCTGAGGGCCTCCTGT	300907	133103	AACTCCGTGGCTGCTCCCTC
211734	43930	CTCTAAAATAGAGAGATCAT	256321	88517	GGGCTCCTGAGGGCCTCCTG	300908	133104	TAACTCCGTGGCTGCTCCCT
211735	43931	ACTCTAAAATAGAGAGATCA	256322	88518	AGGGCTCCTGAGGGCCTCCT	300909	133105	CTAACTCCGTGGCTGCTCCC
211736	43932	GACTCTAAAATAGAGAGATC	256323	88519	GAGGGCTCCTGAGGGCCTCC	300910	133106	TCTAACTCCGTGGCTGCTCC
211737	43933	TGACTCTAAAATAGAGAGAT	256324	88520	GGAGGGCTCCTGAGGGCCTC	300911	133107	CTCTAACTCCGTGGCTGCTC
211738	43934	CTGACTCTAAAATAGAGAGA	256325	88521	GGGAGGGCTCCTGAGGGCCT	300912	133108	CCTCTAACTCCGTGGCTGCT
211739	43935	GCTGACTCTAAAATAGAGAG	256326	88522	AGGGAGGGCTCCTGAGGGCC	300913	133109	GCCTCTAACTCCGTGGCTGC
211740	43936	AGCTGACTCTAAAATAGAGA	256327	88523	CAGGGAGGGCTCCTGAGGGC	300914	133110	GGCCTCTAACTCCGTGGCTG
211741	43937	CAGCTGACTCTAAAATAGAG	256328	88524	CCAGGGAGGGCTCCTGAGGG	300915	133111	GGGCCTCTAACTCCGTGGCT
211742	43938	TCAGCTGACTCTAAAATAGA	256329	88525	TCCAGGGAGGGCTCCTGAGG	300916	133112	AGGGCCTCTAACTCCGTGGC
211743	43939	GTCAGCTGACTCTAAAATAG	256330	88526	CTCCAGGGAGGGCTCCTGAG	300917	133113	AAGGGCCTCTAACTCCGTGG
211744	43940	AGTCAGCTGACTCTAAAATA	256331	88527	ACTCCAGGGAGGGCTCCTGA	300918	133114	CAAGGGCCTCTAACTCCGTG
211745	43941	CAGTCAGCTGACTCTAAAAT	256332	88528	CACTCCAGGGAGGGCTCCTG	300919	133115	CCAAGGGCCTCTAACTCCGT
211746	43942	CCAGTCAGCTGACTCTAAAA	256333	88529	CCACTCCAGGGAGGGCTCCT	300920	133116	CCCAAGGGCCTCTAACTCCG
211747	43943	CCCAGTCAGCTGACTCTAAA	256334	88530	CCCACTCCAGGGAGGGCTCC	300921	133117	CCCCAAGGGCCTCTAACTCC
211748	43944	TCCCAGTCAGCTGACTCTAA	256335	88531	CCCCACTCCAGGGAGGGCTC	300922	133118	ACCCCAAGGGCCTCTAACTC
211749	43945	TTCCCAGTCAGCTGACTCTA	256336	88532	TCCCCACTCCAGGGAGGGCT	300923	133119	AACCCCAAGGGCCTCTAACT
211750	43946	GTTCCCAGTCAGCTGACTCT	256337	88533	GTCCCCACTCCAGGGAGGGC	300924	133120	AAACCCCAAGGGCCTCTAAC
211751	43947	GGTTCCCAGTCAGCTGACTC	256338	88534	TGTCCCCACTCCAGGGAGGG	300925	133121	GAAACCCCAAGGGCCTCTAA
211752	43948	AGGTTCCCAGTCAGCTGACT	256339	88535	TTGTCCCCACTCCAGGGAGG	300926	133122	AGAAACCCCAAGGGCCTCTA
211753	43949	AAGGTTCCCAGTCAGCTGAC	256340	88536	TTTGTCCCCACTCCAGGGAG	300927	133123	GAGAAACCCCAAGGGCCTCT
211754	43950	TAAGGTTCCCAGTCAGCTGA	256341	88537	TTTTGTCCCCACTCCAGGGA	300928	133124	AGAGAAACCCCAAGGGCCTC
211755	43951	TTAAGGTTCCCAGTCAGCTG	256342	88538	TTTTTGTCCCCACTCCAGGG	300929	133125	AAGAGAAACCCCAAGGGCCT
211756	43952	ATTAAGGTTCCCAGTCAGCT	256343	88539	CTTTTTGTCCCCACTCCAGG	300930	133126	AAAGAGAAACCCCAAGGGCC
211757	43953	AATTAAGGTTCCCAGTCAGC	256344	88540	CCTTTTTGTCCCCACTCCAG	300931	133127	AAAAGAGAAACCCCAAGGGC
211758	43954	GAATTAAGGTTCCCAGTCAG	256345	88541	GCCTTTTTGTCCCCACTCCA	300932	133128	GAAAAGAGAAACCCCAAGGG
211759	43955	GGAATTAAGGTTCCCAGTCA	256346	88542	CGCCTTTTTGTCCCCACTCC	300933	133129	GGAAAAGAGAAACCCCAAGG
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211761	43957	ATGGAATTAAGGTTCCCAGT	256348	88544	CCCGCCTTTTTGTCCCCACT	300935	133131	GTGGAAAAGAGAAACCCCAA
211762	43958	GATGGAATTAAGGTTCCCAG	256349	88545	CCCCGCCTTTTTGTCCCCAC	300936	133132	AGTGGAAAAGAGAAACCCCA
211763	43959	AGATGGAATTAAGGTTCCCA	256350	88546	TCCCCGCCTTTTTGTCCCCA	300937	133133	CAGTGGAAAAGAGAAACCCC
211764	43960	TAGATGGAATTAAGGTTCCC	256351	88547	GTCCCCGCCTTTTTGTCCCC	300938	133134	TCAGTGGAAAAGAGAAACCC
211765	43961	GTAGATGGAATTAAGGTTCC	256352	88548	AGTCCCCGCCTTTTTGTCCC	300939	133135	GTCAGTGGAAAAGAGAAACC
211766	43962	TGTAGATGGAATTAAGGTTC	256353	88549	CAGTCCCCGCCTTTTTGTCC	300940	133136	TGTCAGTGGAAAAGAGAAAC
211767	43963	TTGTAGATGGAATTAAGGTT	256354	88550	CCAGTCCCCGCCTTTTTGTC	300941	133137	CTGTCAGTGGAAAAGAGAAA
211768	43964	GTTGTAGATGGAATTAAGGT	256355	88551	CCCAGTCCCCGCCTTTTTGT	300942	133138	CCTGTCAGTGGAAAAGAGAA
211769	43965	GGTTGTAGATGGAATTAAGG	256356	88552	GCCCAGTCCCCGCCTTTTTG	300943	133139	GCCTGTCAGTGGAAAAGAGA
211770	43966	GGGTTGTAGATGGAATTAAG	256357	88553	GGCCCAGTCCCCGCCTTTTT	300944	133140	AGCCTGTCAGTGGAAAAGAG
211771	43967	GGGGTTGTAGATGGAATTAA	256358	88554	CGGCCCAGTCCCCGCCTTTT	300945	133141	AAGCCTGTCAGTGGAAAAGA
211772	43968	TGGGGTTGTAGATGGAATTA	256359	88555	TCGGCCCAGTCCCCGCCTTT	300946	133142	AAAGCCTGTCAGTGGAAAAG
211773	43969	TTGGGGTTGTAGATGGAATT	256360	88556	CTCGGCCCAGTCCCCGCCTT	300947	133143	GAAAGCCTGTCAGTGGAAAA
211774	43970	ATTGGGGTTGTAGATGGAAT	256361	88557	TCTCGGCCCAGTCCCCGCCT	300948	133144	GGAAAGCCTGTCAGTGGAAA
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211776	43972	GAATTGGGGTTGTAGATGGA	256363	88559	CTTCTCGGCCCAGTCCCCGC	300950	133146	TGGGAAAGCCTGTCAGTGGA
211777	43973	GGAATTGGGGTTGTAGATGG	256364	88560	CCTTCTCGGCCCAGTCCCCG	300951	133147	CTGGGAAAGCCTGTCAGTGG
211778	43974	AGGAATTGGGGTTGTAGATG	256365	88561	CCCTTCTCGGCCCAGTCCCC	300952	133148	CCTGGGAAAGCCTGTCAGTG
211779	43975	GAGGAATTGGGGTTGTAGAT	256366	88562	ACCCTTCTCGGCCCAGTCCC	300953	133149	GCCTGGGAAAGCCTGTCAGT
211780	43976	AGAGGAATTGGGGTTGTAGA	256367	88563	GACCCTTCTCGGCCCAGTCC	300954	133150	TGCCTGGGAAAGCCTGTCAG
211781	43977	AAGAGGAATTGGGGTTGTAG	256368	88564	GGACCCTTCTCGGCCCAGTC	300955	133151	CTGCCTGGGAAAGCCTGTCA
211782	43978	AAAGAGGAATTGGGGTTGTA	256369	88565	CGGACCCTTCTCGGCCCAGT	300956	133152	GCTGCCTGGGAAAGCCTGTC
211783	43979	CAAAGAGGAATTGGGGTTGT	256370	88566	CCGGACCCTTCTCGGCCCAG	300957	133153	AGCTGCCTGGGAAAGCCTGT
211784	43980	GCAAAGAGGAATTGGGGTTG	256371	88567	GCCGGACCCTTCTCGGCCCA	300958	133154	CAGCTGCCTGGGAAAGCCTG
211785	43981	GGCAAAGAGGAATTGGGGTT	256372	88568	GGCCGGACCCTTCTCGGCCC	300959	133155	CCAGCTGCCTGGGAAAGCCT
211786	43982	TGGCAAAGAGGAATTGGGGT	256373	88569	AGGCCGGACCCTTCTCGGCC	300960	133156	GCCAGCTGCCTGGGAAAGCC
211787	43983	ATGGCAAAGAGGAATTGGGG	256374	88570	AAGGCCGGACCCTTCTCGGC	300961	133157	AGCCAGCTGCCTGGGAAAGC
211788	43984	CATGGCAAAGAGGAATTGGG	256375	88571	AAAGGCCGGACCCTTCTCGG	300962	133158	TAGCCAGCTGCCTGGGAAAG
211789	43985	ACATGGCAAAGAGGAATTGG	256376	88572	GAAAGGCCGGACCCTTCTCG	300963	133159	CTAGCCAGCTGCCTGGGAAA
211790	43986	TACATGGCAAAGAGGAATTG	256377	88573	GGAAAGGCCGGACCCTTCTC	300964	133160	ACTAGCCAGCTGCCTGGGAA
211791	43987	GTACATGGCAAAGAGGAATT	256378	88574	CGGAAAGGCCGGACCCTTCT	300965	133161	AACTAGCCAGCTGCCTGGGA
211792	43988	TGTACATGGCAAAGAGGAAT	256379	88575	TCGGAAAGGCCGGACCCTTC	300966	133162	GAACTAGCCAGCTGCCTGGG
211793	43989	CTGTACATGGCAAAGAGGAA	256380	88576	TTCGGAAAGGCCGGACCCTT	300967	133163	TGAACTAGCCAGCTGCCTGG
211794	43990	ACTGTACATGGCAAAGAGGA	256381	88577	CTTCGGAAAGGCCGGACCCT	300968	133164	ATGAACTAGCCAGCTGCCTG

211795	43991	CACTGTACATGGCAAAGAGG	256382	88578	GCTTCGGAAAGGCCGGACCC	300969	133165	AATGAACTAGCCAGCTGCCT
211796	43992	TCACTGTACATGGCAAAGAG	256383	88579	GGCTTCGGAAAGGCCGGACC	300970	133166	GAATGAACTAGCCAGCTGCC
211797	43993	GTCACTGTACATGGCAAAGA	256384	88580	GGGCTTCGGAAAGGCCGGAC	300971	133167	GGAATGAACTAGCCAGCTGC
211798	43994	TGTCACTGTACATGGCAAAG	256385	88581	CGGGCTTCGGAAAGGCCGGA	300972	133168	GGGAATGAACTAGCCAGCTG
211799	43995	ATGTCACTGTACATGGCAAA	256386	88582	GCGGGCTTCGGAAAGGCCGG	300973	133169	AGGGAATGAACTAGCCAGCT
211800	43996	TATGTCACTGTACATGGCAA	256387	88583	GGCGGGCTTCGGAAAGGCCG	300974	133170	GAGGGAATGAACTAGCCAGC
211801	43997	ATATGTCACTGTACATGGCA	256388	88584	TGGCGGGCTTCGGAAAGGCC	300975	133171	GGAGGGAATGAACTAGCCAG
211802	43998	AATATGTCACTGTACATGGC	256389	88585	GTGGCGGGCTTCGGAAAGGC	300976	133172	GGGAGGGAATGAACTAGCCA
211803	43999	GAATATGTCACTGTACATGG	256390	88586	GGTGGCGGGCTTCGGAAAGG	300977	133173	GGGGAGGGAATGAACTAGCC
211804	44000	TGAATATGTCACTGTACATG	256391	88587	TGGTGGCGGGCTTCGGAAAG	300978	133174	TGGGGAGGGAATGAACTAGC
211805	44001	GTGAATATGTCACTGTACAT	256392	88588	GTGGTGGCGGGCTTCGGAAA	300979	133175	CTGGGGAGGGAATGAACTAG
211806	44002	TGTGAATATGTCACTGTACA	256393	88589	AGTGGTGGCGGGCTTCGGAA	300980	133176	GCTGGGGAGGGAATGAACTA
211807	44003	CTGTGAATATGTCACTGTAC	256394	88590	CAGTGGTGGCGGGCTTCGGA	300981	133177	GGCTGGGGAGGGAATGAACT
211808	44004	CCTGTGAATATGTCACTGTA	256395	88591	GCAGTGGTGGCGGGCTTCGG	300982	133178	TGGCTGGGGAGGGAATGAAC
211809	44005	ACCTGTGAATATGTCACTGT	256396	88592	CGCAGTGGTGGCGGGCTTCG	300983	133179	CTGGCTGGGGAGGGAATGAA
211810	44006	AACCTGTGAATATGTCACTG	256397	88593	ACGCAGTGGTGGCGGGCTTC	300984	133180	CCTGGCTGGGGAGGGAATGA
211811	44007	GAACCTGTGAATATGTCACT	256398	88594	TACGCAGTGGTGGCGGGCTT	300985	133181	ACCTGGCTGGGGAGGGAATG
211812	44008	AGAACCTGTGAATATGTCAC	256399	88595	ATACGCAGTGGTGGCGGGCT	300986	133182	CACCTGGCTGGGGAGGGAAT
211813	44009	CAGAACCTGTGAATATGTCA	256400	88596	GATACGCAGTGGTGGCGGGC	300987	133183	GCACCTGGCTGGGGAGGGAA
211814	44010	CCAGAACCTGTGAATATGTC	256401	88597	AGATACGCAGTGGTGGCGGG	300988	133184	TGCACCTGGCTGGGGAGGGA
211815	44011	CCCAGAACCTGTGAATATGT	256402	88598	GAGATACGCAGTGGTGGCGG	300989	133185	CTGCACCTGGCTGGGGAGGG
211816	44012	CCCCAGAACCTGTGAATATG	256403	88599	GGAGATACGCAGTGGTGGCG	300990	133186	CCTGCACCTGGCTGGGGAGG
211817	44013	TCCCCAGAACCTGTGAATAT	256404	88600	TGGAGATACGCAGTGGTGGC	300991	133187	GCCTGCACCTGGCTGGGGAG
211818	44014	ATCCCCAGAACCTGTGAATA	256405	88601	GTGGAGATACGCAGTGGTGG	300992	133188	CGCCTGCACCTGGCTGGGGA
211819	44015	AATCCCCAGAACCTGTGAAT	256406	88602	TGTGGAGATACGCAGTGGTG	300993	133189	ACGCCTGCACCTGGCTGGGG
211820	44016	TAATCCCCAGAACCTGTGAA	256407	88603	GTGTGGAGATACGCAGTGGT	300994	133190	TACGCCTGCACCTGGCTGGG
211821	44017	CTAATCCCCAGAACCTGTGA	256408	88604	TGTGTGGAGATACGCAGTGG	300995	133191	CTACGCCTGCACCTGGCTGG
211822	44018	CCTAATCCCCAGAACCTGTG	256409	88605	CTGTGTGGAGATACGCAGTG	300996	133192	CCTACGCCTGCACCTGGCTG
211823	44019	TCCTAATCCCCAGAACCTGT	256410	88606	TCTGTGTGGAGATACGCAGT	300997	133193	TCCTACGCCTGCACCTGGCT
211824	44020	GTCCTAATCCCCAGAACCTG	256411	88607	CTCTGTGTGGAGATACGCAG	300998	133194	TTCCTACGCCTGCACCTGGC
211825	44021	CGTCCTAATCCCCAGAACCT	256412	88608	GCTCTGTGTGGAGATACGCA	300999	133195	ATTCCTACGCCTGCACCTGG
211826	44022	TCGTCCTAATCCCCAGAACC	256413	88609	GGCTCTGTGTGGAGATACGC	301000	133196	TATTCCTACGCCTGCACCTG
211827	44023	CTCGTCCTAATCCCCAGAAC	256414	88610	AGGCTCTGTGTGGAGATACG	301001	133197	ATATTCCTACGCCTGCACCT
211828	44024	GCTCGTCCTAATCCCCAGAA	256415	88611	CAGGCTCTGTGTGGAGATAC	301002	133198	CATATTCCTACGCCTGCACC
211829	44025	GGCTCGTCCTAATCCCCAGA	256416	88612	TCAGGCTCTGTGTGGAGATA	301003	133199	CCATATTCCTACGCCTGCAC
211830	44026	AGGCTCGTCCTAATCCCCAG	256417	88613	TTCAGGCTCTGTGTGGAGAT	301004	133200	TCCATATTCCTACGCCTGCA
211831	44027	CAGGCTCGTCCTAATCCCCA	256418	88614	TTTCAGGCTCTGTGTGGAGA	301005	133201	GTCCATATTCCTACGCCTGC
211832	44028	ACAGGCTCGTCCTAATCCCC	256419	88615	CTTTCAGGCTCTGTGTGGAG	301006	133202	TGTCCATATTCCTACGCCTG
211833	44029	GACAGGCTCGTCCTAATCCC	256420	88616	ACTTTCAGGCTCTGTGTGGA	301007	133203	ATGTCCATATTCCTACGCCT
211834	44030	AGACAGGCTCGTCCTAATCC	256421	88617	CACTTTCAGGCTCTGTGTGG	301008	133204	GATGTCCATATTCCTACGCC
211835	44031	GAGACAGGCTCGTCCTAATC	256422	88618	CCACTTTCAGGCTCTGTGTG	301009	133205	AGATGTCCATATTCCTACGC
211836	44032	AGAGACAGGCTCGTCCTAAT	256423	88619	ACCACTTTCAGGCTCTGTGT	301010	133206	CAGATGTCCATATTCCTACG
211837	44033	CAGAGACAGGCTCGTCCTAA	256424	88620	TACCACTTTCAGGCTCTGTG	301011	133207	CCAGATGTCCATATTCCTAC
211838	44034	TCAGAGACAGGCTCGTCCTA	256425	88621	TTACCACTTTCAGGCTCTGT	301012	133208	ACCAGATGTCCATATTCCTA
211839	44035	TTCAGAGACAGGCTCGTCCT	256426	88622	CTTACCACTTTCAGGCTCTG	301013	133209	AACCAGATGTCCATATTCCT
211840	44036	TTTCAGAGACAGGCTCGTCC	256427	88623	CCTTACCACTTTCAGGCTCT	301014	133210	CAACCAGATGTCCATATTCC
211841	44037	CTTTCAGAGACAGGCTCGTC	256428	88624	ACCTTACCACTTTCAGGCTC	301015	133211	GCAACCAGATGTCCATATTC
211842	44038	CCTTTCAGAGACAGGCTCGT	256429	88625	CACCTTACCACTTTCAGGCT	301016	133212	AGCAACCAGATGTCCATATT
211843	44039	GCCTTTCAGAGACAGGCTCG	256430	88626	CCACCTTACCACTTTCAGGC	301017	133213	AAGCAACCAGATGTCCATAT
211844	44040	AGCCTTTCAGAGACAGGCTC	256431	88627	ACCACCTTACCACTTTCAGG	301018	133214	AAAGCAACCAGATGTCCATA
211845	44041	TAGCCTTTCAGAGACAGGCT	256432	88628	GACCACCTTACCACTTTCAG	301019	133215	CAAAGCAACCAGATGTCCAT
211846	44042	GTAGCCTTTCAGAGACAGGC	256433	88629	GGACCACCTTACCACTTTCA	301020	133216	CCAAAGCAACCAGATGTCCA
211847	44043	AGTAGCCTTTCAGAGACAGG	256434	88630	TGGACCACCTTACCACTTTC	301021	133217	GCCAAAGCAACCAGATGTCC
211848	44044	AAGTAGCCTTTCAGAGACAG	256435	88631	CTGGACCACCTTACCACTTT	301022	133218	GGCCAAAGCAACCAGATGTC
211849	44045	AAAGTAGCCTTTCAGAGACA	256436	88632	CCTGGACCACCTTACCACTT	301023	133219	AGGCCAAAGCAACCAGATGT
211850	44046	TAAAGTAGCCTTTCAGAGAC	256437	88633	TCCTGGACCACCTTACCACT	301024	133220	CAGGCCAAAGCAACCAGATG
211851	44047	GTAAAGTAGCCTTTCAGAGA	256438	88634	TTCCTGGACCACCTTACCAC	301025	133221	GCAGGCCAAAGCAACCAGAT
211852	44048	TGTAAAGTAGCCTTTCAGAG	256439	88635	CTTCCTGGACCACCTTACCA	301026	133222	AGCAGGCCAAAGCAACCAGA
211853	44049	ATGTAAAGTAGCCTTTCAGA	256440	88636	CCTTCCTGGACCACCTTACC	301027	133223	CAGCAGGCCAAAGCAACCAG
211854	44050	CATGTAAAGTAGCCTTTCAG	256441	88637	GCCTTCCTGGACCACCTTAC	301028	133224	GCAGCAGGCCAAAGCAACCA
211855	44051	TCATGTAAAGTAGCCTTTCA	256442	88638	AGCCTTCCTGGACCACCTTA	301029	133225	GGCAGCAGGCCAAAGCAACC
211856	44052	TTCATGTAAAGTAGCCTTTC	256443	88639	AAGCCTTCCTGGACCACCTT	301030	133226	GGGCAGCAGGCCAAAGCAAC
211857	44053	TTTCATGTAAAGTAGCCTTT	256444	88640	GAAGCCTTCCTGGACCACCT	301031	133227	AGGGCAGCAGGCCAAAGCAA
211858	44054	TTTTCATGTAAAGTAGCCTT	256445	88641	GGAAGCCTTCCTGGACCACC	301032	133228	GAGGGCAGCAGGCCAAAGCA
211859	44055	ATTTTCATGTAAAGTAGCCT	256446	88642	AGGAAGCCTTCCTGGACCAC	301033	133229	AGAGGGCAGCAGGCCAAAGC
211860	44056	AATTTTCATGTAAAGTAGCC	256447	88643	GAGGAAGCCTTCCTGGACCA	301034	133230	AAGAGGGCAGCAGGCCAAAG
211861	44057	GAATTTTCATGTAAAGTAGC	256448	88644	GGAGGAAGCCTTCCTGGACC	301035	133231	AAAGAGGGCAGCAGGCCAAA
211862	44058	TGAATTTTCATGTAAAGTAG	256449	88645	CGGAGGAAGCCTTCCTGGAC	301036	133232	GAAAGAGGGCAGCAGGCCAA
211863	44059	ATGAATTTTCATGTAAAGTA	256450	88646	TCGGAGGAAGCCTTCCTGGA	301037	133233	TGAAAGAGGGCAGCAGGCCA
211864	44060	AATGAATTTTCATGTAAAGT	256451	88647	CTCGGAGGAAGCCTTCCTGG	301038	133234	CTGAAAGAGGGCAGCAGGCC
211865	44061	AAATGAATTTTCATGTAAAG	256452	88648	TCTCGGAGGAAGCCTTCCTG	301039	133235	CCTGAAAGAGGGCAGCAGGC
211866	44062	AAAATGAATTTTCATGTAAA	256453	88649	CTCTCGGAGGAAGCCTTCCT	301040	133236	CCCTGAAAGAGGGCAGCAGG

211867	44063	AAAAATGAATTTTCATGTAA	256454	88650	GCTCTCGGAGGAAGCCTTCC	301041	133237	CCCCTGAAAGAGGGCAGCAG
211868	44064	AAAAAATGAATTTTCATGTA	256455	88651	GGCTCTCGGAGGAAGCCTTC	301042	133238	ACCCCTGAAAGAGGGCAGCA
211869	44065	AAAAAAATGAATTTTCATGT	256456	88652	TGGCTCTCGGAGGAAGCCTT	301043	133239	GACCCCTGAAAGAGGGCAGC
211870	44066	TAAAAAAATGAATTTTCATG	256457	88653	CTGGCTCTCGGAGGAAGCCT	301044	133240	GGACCCCTGAAAGAGGGCAG
211871	44067	TTAAAAAAATGAATTTTCAT	256458	88654	CCTGGCTCTCGGAGGAAGCC	301045	133241	AGGACCCCTGAAAGAGGGCA
211872	44068	ATTAAAAAAATGAATTTTCA	256459	88655	GCCTGGCTCTCGGAGGAAGC	301046	133242	TAGGACCCCTGAAAGAGGGC
211873	44069	AATTAAAAAAATGAATTTTC	256460	88656	GGCCTGGCTCTCGGAGGAAG	301047	133243	TTAGGACCCCTGAAAGAGGG
211874	44070	TAATTAAAAAAATGAATTTT	256461	88657	GGGCCTGGCTCTCGGAGGAA	301048	133244	CTTAGGACCCCTGAAAGAGG
211875	44071	TTAATTAAAAAAATGAATTT	256462	88658	GGGGCCTGGCTCTCGGAGGA	301049	133245	GCTTAGGACCCCTGAAAGAG
211876	44072	CTTAATTAAAAAAATGAATT	256463	88659	GGGGGCCTGGCTCTCGGAGG	301050	133246	GGCTTAGGACCCCTGAAAGA
211877	44073	TCTTAATTAAAAAAATGAAT	256464	88660	GGGGGGCCTGGCTCTCGGAG	301051	133247	GGGCTTAGGACCCCTGAAAG
211878	44074	ATCTTAATTAAAAAAATGAA	256465	88661	TGGGGGGCCTGGCTCTCGGA	301052	133248	TGGGCTTAGGACCCCTGAAA
211879	44075	AATCTTAATTAAAAAAATGA	256466	88662	CTGGGGGGCCTGGCTCTCGG	301053	133249	GTGGGCTTAGGACCCCTGAA
211880	44076	AAATCTTAATTAAAAAAATG	256467	88663	CCTGGGGGGCCTGGCTCTCG	301054	133250	TGTGGGCTTAGGACCCCTGA
211881	44077	AAAATCTTAATTAAAAAAAT	256468	88664	ACCTGGGGGGCCTGGCTCTC	301055	133251	TTGTGGGCTTAGGACCCCTG
211882	44078	AAAAATCTTAATTAAAAAAA	256469	88665	GACCTGGGGGGCCTGGCTCT	301056	133252	ATTGTGGGCTTAGGACCCCT
211883	44079	AAAAAATCTTAATTAAAAAA	256470	88666	AGACCTGGGGGGCCTGGCTC	301057	133253	GATTGTGGGCTTAGGACCCC
211884	44080	AAAAAAATCTTAATTAAAAA	256471	88667	CAGACCTGGGGGGCCTGGCT	301058	133254	TGATTGTGGGCTTAGGACCC
211885	44081	AAAAAAAATCTTAATTAAAA	256472	88668	TCAGACCTGGGGGGCCTGGC	301059	133255	ATGATTGTGGGCTTAGGACC
211886	44082	AAAAAAAAATCTTAATTAAA	256473	88669	CTCAGACCTGGGGGGCCTGG	301060	133256	CATGATTGTGGGCTTAGGAC
211887	44083	GAAAAAAAAATCTTAATTAA	256474	88670	GCTCAGACCTGGGGGGCCTG	301061	133257	GCATGATTGTGGGCTTAGGA
211888	44084	GGAAAAAAAAATCTTAATTA	256475	88671	GGCTCAGACCTGGGGGGCCT	301062	133258	GGCATGATTGTGGGCTTAGG
211889	44085	AGGAAAAAAAAATCTTAATT	256476	88672	TGGCTCAGACCTGGGGGGCC	301063	133259	AGGCATGATTGTGGGCTTAG
211890	44086	GAGGAAAAAAAAATCTTAAT	256477	88673	GTGGCTCAGACCTGGGGGGC	301064	133260	GAGGCATGATTGTGGGCTTA
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211894	44090	TCAAGAGGAAAAAAAAATCT	256481	88677	GCTGGTGGCTCAGACCTGGG	301068	133264	TAGGGAGGCATGATTGTGGG
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211896	44092	TCTCAAGAGGAAAAAAAAAT	256483	88679	GAGCTGGTGGCTCAGACCTG	301070	133266	CTTAGGGAGGCATGATTGTG
211897	44093	GTCTCAAGAGGAAAAAAAAA	256484	88680	TGAGCTGGTGGCTCAGACCT	301071	133267	TCTTAGGGAGGCATGATTGT
211898	44094	TGTCTCAAGAGGAAAAAAAA	256485	88681	ATGAGCTGGTGGCTCAGACC	301072	133268	GTCTTAGGGAGGCATGATTG
211899	44095	TTGTCTCAAGAGGAAAAAAA	256486	88682	CATGAGCTGGTGGCTCAGAC	301073	133269	GGTCTTAGGGAGGCATGATT
211900	44096	CTTGTCTCAAGAGGAAAAAA	256487	88683	ACATGAGCTGGTGGCTCAGA	301074	133270	AGGTCTTAGGGAGGCATGAT
211901	44097	CCTTGTCTCAAGAGGAAAAA	256488	88684	GACATGAGCTGGTGGCTCAG	301075	133271	AAGGTCTTAGGGAGGCATGA
211902	44098	ACCTTGTCTCAAGAGGAAAA	256489	88685	GGACATGAGCTGGTGGCTCA	301076	133272	CAAGGTCTTAGGGAGGCATG
211903	44099	GACCTTGTCTCAAGAGGAAA	256490	88686	CGGACATGAGCTGGTGGCTC	301077	133273	CCAAGGTCTTAGGGAGGCAT
211904	44100	AGACCTTGTCTCAAGAGGAA	256491	88687	CCGGACATGAGCTGGTGGCT	301078	133274	GCCAAGGTCTTAGGGAGGCA
211905	44101	GAGACCTTGTCTCAAGAGGA	256492	88688	GCCGGACATGAGCTGGTGGC	301079	133275	TGCCAAGGTCTTAGGGAGGC
211906	44102	TGAGACCTTGTCTCAAGAGG	256493	88689	TGCCGGACATGAGCTGGTGG	301080	133276	ATGCCAAGGTCTTAGGGAGG
211907	44103	GTGAGACCTTGTCTCAAGAG	256494	88690	ATGCCGGACATGAGCTGGTG	301081	133277	GATGCCAAGGTCTTAGGGAG
211908	44104	AGTGAGACCTTGTCTCAAGA	256495	88691	CATGCCGGACATGAGCTGGT	301082	133278	GGATGCCAAGGTCTTAGGGA
211909	44105	GAGTGAGACCTTGTCTCAAG	256496	88692	GCATGCCGGACATGAGCTGG	301083	133279	AGGATGCCAAGGTCTTAGGG
211910	44106	AGAGTGAGACCTTGTCTCAA	256497	88693	GGCATGCCGGACATGAGCTG	301084	133280	AAGGATGCCAAGGTCTTAGG
211911	44107	TAGAGTGAGACCTTGTCTCA	256498	88694	AGGCATGCCGGACATGAGCT	301085	133281	GAAGGATGCCAAGGTCTTAG
211912	44108	ATAGAGTGAGACCTTGTCTC	256499	88695	CAGGCATGCCGGACATGAGC	301086	133282	GGAAGGATGCCAAGGTCTTA
211913	44109	CATAGAGTGAGACCTTGTCT	256500	88696	CCAGGCATGCCGGACATGAG	301087	133283	GGGAAGGATGCCAAGGTCTT
211914	44110	CCATAGAGTGAGACCTTGTC	256501	88697	CCCAGGCATGCCGGACATGA	301088	133284	AGGGAAGGATGCCAAGGTCT
211915	44111	ACCATAGAGTGAGACCTTGT	256502	88698	CCCCAGGCATGCCGGACATG	301089	133285	GAGGGAAGGATGCCAAGGTC
211916	44112	AACCATAGAGTGAGACCTTG	256503	88699	GCCCCAGGCATGCCGGACAT	301090	133286	AGAGGGAAGGATGCCAAGGT
211917	44113	GAACCATAGAGTGAGACCTT	256504	88700	AGCCCCAGGCATGCCGGACA	301091	133287	TAGAGGGAAGGATGCCAAGG
211918	44114	TGAACCATAGAGTGAGACCT	256505	88701	GAGCCCCAGGCATGCCGGAC	301092	133288	TTAGAGGGAAGGATGCCAAG
211919	44115	CTGAACCATAGAGTGAGACC	256506	88702	GGAGCCCCAGGCATGCCGGA	301093	133289	CTTAGAGGGAAGGATGCCAA
211920	44116	CCTGAACCATAGAGTGAGAC	256507	88703	GGGAGCCCCAGGCATGCCGG	301094	133290	GCTTAGAGGGAAGGATGCCA
211921	44117	GCCTGAACCATAGAGTGAGA	256508	88704	GGGGAGCCCCAGGCATGCCG	301095	133291	GGCTTAGAGGGAAGGATGCC
211922	44118	AGCCTGAACCATAGAGTGAG	256509	88705	AGGGGAGCCCCAGGCATGCC	301096	133292	CGGCTTAGAGGGAAGGATGC
211923	44119	CAGCCTGAACCATAGAGTGA	256510	88706	GAGGGGAGCCCCAGGCATGC	301097	133293	ACGGCTTAGAGGGAAGGATG
211924	44120	CCAGCCTGAACCATAGAGTG	256511	88707	GGAGGGGAGCCCCAGGCATG	301098	133294	AACGGCTTAGAGGGAAGGAT
211925	44121	TCCAGCCTGAACCATAGAGT	256512	88708	AGGAGGGGAGCCCCAGGCAT	301099	133295	CAACGGCTTAGAGGGAAGGA
211926	44122	CTCCAGCCTGAACCATAGAG	256513	88709	CAGGAGGGGAGCCCCAGGCA	301100	133296	CCAACGGCTTAGAGGGAAGG
211927	44123	ACTCCAGCCTGAACCATAGA	256514	88710	GCAGGAGGGGAGCCCCAGGC	301101	133297	GCCAACGGCTTAGAGGGAAG
211928	44124	CACTCCAGCCTGAACCATAG	256515	88711	GGCAGGAGGGGAGCCCCAGG	301102	133298	TGCCAACGGCTTAGAGGGAA
211929	44125	GCACTCCAGCCTGAACCATA	256516	88712	AGGCAGGAGGGGAGCCCCAG	301103	133299	GTGCCAACGGCTTAGAGGGA
211930	44126	TGCACTCCAGCCTGAACCAT	256517	88713	CAGGCAGGAGGGGAGCCCCA	301104	133300	GGTGCCAACGGCTTAGAGGG
211931	44127	CTGCACTCCAGCCTGAACCA	256518	88714	TCAGGCAGGAGGGGAGCCCC	301105	133301	AGGTGCCAACGGCTTAGAGG
211932	44128	ACTGCACTCCAGCCTGAACC	256519	88715	CTCAGGCAGGAGGGGAGCCC	301106	133302	GAGGTGCCAACGGCTTAGAG
211933	44129	CACTGCACTCCAGCCTGAAC	256520	88716	CCTCAGGCAGGAGGGGAGCC	301107	133303	AGAGGTGCCAACGGCTTAGA
211934	44130	CCACTGCACTCCAGCCTGAA	256521	88717	CCCTCAGGCAGGAGGGGAGC	301108	133304	CAGAGGTGCCAACGGCTTAG
211935	44131	ACCACTGCACTCCAGCCTGA	256522	88718	GCCCTCAGGCAGGAGGGGAG	301109	133305	ACAGAGGTGCCAACGGCTTA
211936	44132	TACCACTGCACTCCAGCCTG	256523	88719	GGCCCTCAGGCAGGAGGGGA	301110	133306	CACAGAGGTGCCAACGGCTT
211937	44133	ATACCACTGCACTCCAGCCT	256524	88720	GGGCCCTCAGGCAGGAGGGG	301111	133307	GCACAGAGGTGCCAACGGCT
211938	44134	CATACCACTGCACTCCAGCC	256525	88721	GGGGCCCTCAGGCAGGAGGG	301112	133308	GGCACAGAGGTGCCAACGGC

211939	44135	TCATACCACTGCACTCCAGC	256526	88722	TGGGGCCCTCAGGCAGGAGG	301113	133309	TGGCACAGAGGTGCCAACGG
211940	44136	ATCATACCACTGCACTCCAG	256527	88723	CTGGGGCCCTCAGGCAGGAG	301114	133310	GTGGCACAGAGGTGCCAACG
211941	44137	GATCATACCACTGCACTCCA	256528	88724	TCTGGGGCCCTCAGGCAGGA	301115	133311	GGTGGCACAGAGGTGCCAAC
211942	44138	TGATCATACCACTGCACTCC	256529	88725	CTCTGGGGCCCTCAGGCAGG	301116	133312	AGGTGGCACAGAGGTGCCAA
211943	44139	GTGATCATACCACTGCACTC	256530	88726	TCTCTGGGGCCCTCAGGCAG	301117	133313	GAGGTGGCACAGAGGTGCCA
211944	44140	TGTGATCATACCACTGCACT	256531	88727	CTCTCTGGGGCCCTCAGGCA	301118	133314	AGAGGTGGCACAGAGGTGCC
211945	44141	CTGTGATCATACCACTGCAC	256532	88728	CCTCTCTGGGGCCCTCAGGC	301119	133315	GAGAGGTGGCACAGAGGTGC
211946	44142	GCTGTGATCATACCACTGCA	256533	88729	GCCTCTCTGGGGCCCTCAGG	301120	133316	TGAGAGGTGGCACAGAGGTG
211947	44143	AGCTGTGATCATACCACTGC	256534	88730	GGCCTCTCTGGGGCCCTCAG	301121	133317	GTGAGAGGTGGCACAGAGGT
211948	44144	GAGCTGTGATCATACCACTG	256535	88731	TGGCCTCTCTGGGGCCCTCA	301122	133318	TGTGAGAGGTGGCACAGAGG
211949	44145	TGAGCTGTGATCATACCACT	256536	88732	GTGGCCTCTCTGGGGCCCTC	301123	133319	GTGTGAGAGGTGGCACAGAG
211950	44146	GTGAGCTGTGATCATACCAC	256537	88733	TGTGGCCTCTCTGGGGCCCT	301124	133320	AGTGTGAGAGGTGGCACAGA
211951	44147	AGTGAGCTGTGATCATACCA	256538	88734	GTGTGGCCTCTCTGGGGCCC	301125	133321	CAGTGTGAGAGGTGGCACAG
211952	44148	CAGTGAGCTGTGATCATACC	256539	88735	CGTGTGGCCTCTCTGGGGCC	301126	133322	CCAGTGTGAGAGGTGGCACA
211953	44149	GCAGTGAGCTGTGATCATAC	256540	88736	GCGTGTGGCCTCTCTGGGGC	301127	133323	GCCAGTGTGAGAGGTGGCAC
211954	44150	TGCAGTGAGCTGTGATCATA	256541	88737	GGCGTGTGGCCTCTCTGGGG	301128	133324	AGCCAGTGTGAGAGGTGGCA
211955	44151	CTGCAGTGAGCTGTGATCAT	256542	88738	TGGCGTGTGGCCTCTCTGGG	301129	133325	GAGCCAGTGTGAGAGGTGGC
211956	44152	GCTGCAGTGAGCTGTGATCA	256543	88739	TTGGCGTGTGGCCTCTCTGG	301130	133326	GGAGCCAGTGTGAGAGGTGG
211957	44153	GGCTGCAGTGAGCTGTGATC	256544	88740	GTTGGCGTGTGGCCTCTCTG	301131	133327	TGGAGCCAGTGTGAGAGGTG
211958	44154	AGGCTGCAGTGAGCTGTGAT	256545	88741	GGTTGGCGTGTGGCCTCTCT	301132	133328	CTGGAGCCAGTGTGAGAGGT
211959	44155	GAGGCTGCAGTGAGCTGTGA	256546	88742	AGGTTGGCGTGTGGCCTCTC	301133	133329	TCTGGAGCCAGTGTGAGAGG
211960	44156	CGAGGCTGCAGTGAGCTGTG	256547	88743	AAGGTTGGCGTGTGGCCTCT	301134	133330	GTCTGGAGCCAGTGTGAGAG
211961	44157	TCGAGGCTGCAGTGAGCTGT	256548	88744	GAAGGTTGGCGTGTGGCCTC	301135	133331	TGTCTGGAGCCAGTGTGAGA
211962	44158	GTCGAGGCTGCAGTGAGCTG	256549	88745	CGAAGGTTGGCGTGTGGCCT	301136	133332	GTGTCTGGAGCCAGTGTGAG
211963	44159	CGTCGAGGCTGCAGTGAGCT	256550	88746	CCGAAGGTTGGCGTGTGGCC	301137	133333	TGTGTCTGGAGCCAGTGTGA
211964	44160	ACGTCGAGGCTGCAGTGAGC	256551	88747	CCCGAAGGTTGGCGTGTGGC	301138	133334	GTGTGTCTGGAGCCAGTGTG
211965	44161	GACGTCGAGGCTGCAGTGAG	256552	88748	CCCCGAAGGTTGGCGTGTGG	301139	133335	TGTGTGTCTGGAGCCAGTGT
211966	44162	AGACGTCGAGGCTGCAGTGA	256553	88749	TCCCCGAAGGTTGGCGTGTG	301140	133336	CTGTGTGTCTGGAGCCAGTG
211967	44163	GAGACGTCGAGGCTGCAGTG	256554	88750	GTCCCCGAAGGTTGGCGTGT	301141	133337	GCTGTGTGTCTGGAGCCAGT
211968	44164	AGAGACGTCGAGGCTGCAGT	256555	88751	TGTCCCCGAAGGTTGGCGTG	301142	133338	GGCTGTGTGTCTGGAGCCAG
211969	44165	CAGAGACGTCGAGGCTGCAG	256556	88752	CTGTCCCCGAAGGTTGGCGT	301143	133339	AGGCTGTGTGTCTGGAGCCA
211970	44166	CCAGAGACGTCGAGGCTGCA	256557	88753	CCTGTCCCCGAAGGTTGGCG	301144	133340	CAGGCTGTGTGTCTGGAGCC
211971	44167	CCCAGAGACGTCGAGGCTGC	256558	88754	TCCTGTCCCCGAAGGTTGGC	301145	133341	ACAGGCTGTGTGTCTGGAGC
211972	44168	GCCCAGAGACGTCGAGGCTG	256559	88755	GTCCTGTCCCCGAAGGTTGG	301146	133342	CACAGGCTGTGTGTCTGGAG
211973	44169	AGCCCAGAGACGTCGAGGCT	256560	88756	GGTCCTGTCCCCGAAGGTTG	301147	133343	GCACAGGCTGTGTGTCTGGA
211974	44170	GAGCCCAGAGACGTCGAGGC	256561	88757	AGGTCCTGTCCCCGAAGGTT	301148	133344	AGCACAGGCTGTGTGTCTGG
211975	44171	TGAGCCCAGAGACGTCGAGG	256562	88758	CAGGTCCTGTCCCCGAAGGT	301149	133345	AAGCACAGGCTGTGTGTCTG
211976	44172	CTGAGCCCAGAGACGTCGAG	256563	88759	TCAGGTCCTGTCCCCGAAGG	301150	133346	AAAGCACAGGCTGTGTGTCT
211977	44173	CCTGAGCCCAGAGACGTCGA	256564	88760	CTCAGGTCCTGTCCCCGAAG	301151	133347	AAAAGCACAGGCTGTGTGTC
211978	44174	ACCTGAGCCCAGAGACGTCG	256565	88761	CCTCAGGTCCTGTCCCCGAA	301152	133348	CAAAAGCACAGGCTGTGTGT
211979	44175	CACCTGAGCCCAGAGACGTC	256566	88762	TCCTCAGGTCCTGTCCCCGA	301153	133349	CCAAAAGCACAGGCTGTGTG
211980	44176	TCACCTGAGCCCAGAGACGT	256567	88763	GTCCTCAGGTCCTGTCCCCG	301154	133350	TCCAAAAGCACAGGCTGTGT
211981	44177	ATCACCTGAGCCCAGAGACG	256568	88764	TGTCCTCAGGTCCTGTCCCC	301155	133351	CTCCAAAAGCACAGGCTGTG
211982	44178	GATCACCTGAGCCCAGAGAC	256569	88765	GTGTCCTCAGGTCCTGTCCC	301156	133352	GCTCCAAAAGCACAGGCTGT
211983	44179	GGATCACCTGAGCCCAGAGA	256570	88766	TGTGTCCTCAGGTCCTGTCC	301157	133353	AGCTCCAAAAGCACAGGCTG
211984	44180	AGGATCACCTGAGCCCAGAG	256571	88767	CTGTGTCCTCAGGTCCTGTC	301158	133354	CAGCTCCAAAAGCACAGGCT
211985	44181	GAGGATCACCTGAGCCCAGA	256572	88768	TCTGTGTCCTCAGGTCCTGT	301159	133355	TCAGCTCCAAAAGCACAGGC
211986	44182	GGAGGATCACCTGAGCCCAG	256573	88769	CTCTGTGTCCTCAGGTCCTG	301160	133356	CTCAGCTCCAAAAGCACAGG
211987	44183	GGGAGGATCACCTGAGCCCA	256574	88770	CCTCTGTGTCCTCAGGTCCT	301161	133357	TCTCAGCTCCAAAAGCACAG
211988	44184	TGGGAGGATCACCTGAGCCC	256575	88771	CCCTCTGTGTCCTCAGGTCC	301162	133358	ATCTCAGCTCCAAAAGCACA
211989	44185	GTGGGAGGATCACCTGAGCC	256576	88772	GCCCTCTGTGTCCTCAGGTC	301163	133359	GATCTCAGCTCCAAAAGCAC
211990	44186	GGTGGGAGGATCACCTGAGC	256577	88773	CGCCCTCTGTGTCCTCAGGT	301164	133360	TGATCTCAGCTCCAAAAGCA
211991	44187	AGGTGGGAGGATCACCTGAG	256578	88774	CCGCCCTCTGTGTCCTCAGG	301165	133361	GTGATCTCAGCTCCAAAAGC
211992	44188	GAGGTGGGAGGATCACCTGA	256579	88775	GCCGCCCTCTGTGTCCTCAG	301166	133362	AGTGATCTCAGCTCCAAAAG
211993	44189	TGAGGTGGGAGGATCACCTG	256580	88776	GGCCGCCCTCTGTGTCCTCA	301167	133363	GAGTGATCTCAGCTCCAAAA
211994	44190	CTGAGGTGGGAGGATCACCT	256581	88777	CGGCCGCCCTCTGTGTCCTC	301168	133364	CGAGTGATCTCAGCTCCAAA
211995	44191	GCTGAGGTGGGAGGATCACC	256582	88778	GCGGCCGCCCTCTGTGTCCT	301169	133365	GCGAGTGATCTCAGCTCCAA
211996	44192	AGCTGAGGTGGGAGGATCAC	256583	88779	GGCGGCCGCCCTCTGTGTCC	301170	133366	AGCGAGTGATCTCAGCTCCA
211997	44193	AAGCTGAGGTGGGAGGATCA	256584	88780	TGGCGGCCGCCCTCTGTGTC	301171	133367	AAGCGAGTGATCTCAGCTCC
211998	44194	GAAGCTGAGGTGGGAGGATC	256585	88781	GTGGCGGCCGCCCTCTGTGT	301172	133368	GAAGCGAGTGATCTCAGCTC
211999	44195	GGAAGCTGAGGTGGGAGGAT	256586	88782	CGTGGCGGCCGCCCTCTGTG	301173	133369	TGAAGCGAGTGATCTCAGCT
212000	44196	GGGAAGCTGAGGTGGGAGGA	256587	88783	GCGTGGCGGCCGCCCTCTGT	301174	133370	GTGAAGCGAGTGATCTCAGC
212001	44197	AGGGAAGCTGAGGTGGGAGG	256588	88784	GGCGTGGCGGCCGCCCTCTG	301175	133371	GGTGAAGCGAGTGATCTCAG
212002	44198	TAGGGAAGCTGAGGTGGGAG	256589	88785	GGGCGTGGCGGCCGCCCTCT	301176	133372	GGGTGAAGCGAGTGATCTCA
212003	44199	CTAGGGAAGCTGAGGTGGGA	256590	88786	GGGGCGTGGCGGCCGCCCTC	301177	133373	AGGGTGAAGCGAGTGATCTC
212004	44200	ACTAGGGAAGCTGAGGTGGG	256591	88787	AGGGGCGTGGCGGCCGCCCT	301178	133374	GAGGGTGAAGCGAGTGATCT
212005	44201	TACTAGGGAAGCTGAGGTGG	256592	88788	CAGGGGCGTGGCGGCCGCCC	301179	133375	GGAGGGTGAAGCGAGTGATC
212006	44202	CTACTAGGGAAGCTGAGGTG	256593	88789	TCAGGGGCGTGGCGGCCGCC	301180	133376	AGGAGGGTGAAGCGAGTGAT
212007	44203	GCTACTAGGGAAGCTGAGGT	256594	88790	CTCAGGGGCGTGGCGGCCGC	301181	133377	GAGGAGGGTGAAGCGAGTGA
212008	44204	AGCTACTAGGGAAGCTGAGG	256595	88791	GCTCAGGGGCGTGGCGGCCG	301182	133378	TGAGGAGGGTGAAGCGAGTG
212009	44205	CAGCTACTAGGGAAGCTGAG	256596	88792	AGCTCAGGGGCGTGGCGGCC	301183	133379	ATGAGGAGGGTGAAGCGAGT
212010	44206	CCAGCTACTAGGGAAGCTGA	256597	88793	CAGCTCAGGGGCGTGGCGGC	301184	133380	GATGAGGAGGGTGAAGCGAG

212011	44207	TCCAGCTACTAGGGAAGCTG	256598	88794	GCAGCTCAGGGGCGTGGCGG	301185	133381	AGATGAGGAGGGTGAAGCGA
212012	44208	TTCCAGCTACTAGGGAAGCT	256599	88795	AGCAGCTCAGGGGCGTGGCG	301186	133382	AAGATGAGGAGGGTGAAGCG
212013	44209	GTTCCAGCTACTAGGGAAGC	256600	88796	GAGCAGCTCAGGGGCGTGGC	301187	133383	AAAGATGAGGAGGGTGAAGC
212014	44210	AGTTCCAGCTACTAGGGAAG	256601	88797	TGAGCAGCTCAGGGGCGTGG	301188	133384	CAAAGATGAGGAGGGTGAAG
212015	44211	TAGTTCCAGCTACTAGGGAA	256602	88798	TTGAGCAGCTCAGGGGCGTG	301189	133385	ACAAAGATGAGGAGGGTGAA
212016	44212	GTAGTTCCAGCTACTAGGGA	256603	88799	CTTGAGCAGCTCAGGGGCGT	301190	133386	AACAAAGATGAGGAGGGTGA
212017	44213	TGTAGTTCCAGCTACTAGGG	256604	88800	GCTTGAGCAGCTCAGGGGCG	301191	133387	GAACAAAGATGAGGAGGGTG
212018	44214	CTGTAGTTCCAGCTACTAGG	256605	88801	TGCTTGAGCAGCTCAGGGGC	301192	133388	AGAACAAAGATGAGGAGGGT
212019	44215	CCTGTAGTTCCAGCTACTAG	256606	88802	GTGCTTGAGCAGCTCAGGGG	301193	133389	GAGAACAAAGATGAGGAGGG
212020	44216	CCCTGTAGTTCCAGCTACTA	256607	88803	GGTGCTTGAGCAGCTCAGGG	301194	133390	GGAGAACAAAGATGAGGAGG
212021	44217	CCCCTGTAGTTCCAGCTACT	256608	88804	TGGTGCTTGAGCAGCTCAGG	301195	133391	TGGAGAACAAAGATGAGGAG
212022	44218	ACCCCTGTAGTTCCAGCTAC	256609	88805	CTGGTGCTTGAGCAGCTCAG	301196	133392	TTGGAGAACAAAGATGAGGA
212023	44219	CACCCCTGTAGTTCCAGCTA	256610	88806	GCTGGTGCTTGAGCAGCTCA	301197	133393	CTTGGAGAACAAAGATGAGG
212024	44220	TCACCCCTGTAGTTCCAGCT	256611	88807	AGCTGGTGCTTGAGCAGCTC	301198	133394	ACTTGGAGAACAAAGATGAG
212025	44221	CTCACCCCTGTAGTTCCAGC	256612	88808	AAGCTGGTGCTTGAGCAGCT	301199	133395	TACTTGGAGAACAAAGATGA
212026	44222	GCTCACCCCTGTAGTTCCAG	256613	88809	GAAGCTGGTGCTTGAGCAGC	301200	133396	TTACTTGGAGAACAAAGATG
212027	44223	GGCTCACCCCTGTAGTTCCA	256614	88810	AGAAGCTGGTGCTTGAGCAG	301201	133397	TTTACTTGGAGAACAAAGAT
212028	44224	GGGCTCACCCCTGTAGTTCC	256615	88811	TAGAAGCTGGTGCTTGAGCA	301202	133398	CTTTACTTGGAGAACAAAGA
212029	44225	GGGGCTCACCCCTGTAGTTC	256616	88812	CTAGAAGCTGGTGCTTGAGC	301203	133399	GCTTTACTTGGAGAACAAAG
212030	44226	GGGGGCTCACCCCTGTAGTT	256617	88813	CCTAGAAGCTGGTGCTTGAG	301204	133400	GGCTTTACTTGGAGAACAAA
212031	44227	TGGGGGCTCACCCCTGTAGT	256618	88814	TCCTAGAAGCTGGTGCTTGA	301205	133401	TGGCTTTACTTGGAGAACAA
212032	44228	ATGGGGGCTCACCCCTGTAG	256619	88815	CTCCTAGAAGCTGGTGCTTG	301206	133402	GTGGCTTTACTTGGAGAACA
212033	44229	CATGGGGGCTCACCCCTGTA	256620	88816	TCTCCTAGAAGCTGGTGCTT	301207	133403	CGTGGCTTTACTTGGAGAAC
212034	44230	GCATGGGGGCTCACCCCTGT	256621	88817	GTCTCCTAGAAGCTGGTGCT	301208	133404	TCGTGGCTTTACTTGGAGAA
212035	44231	GGCATGGGGGCTCACCCCTG	256622	88818	GGTCTCCTAGAAGCTGGTGC	301209	133405	CTCGTGGCTTTACTTGGAGA
212036	44232	GGGCATGGGGGCTCACCCCT	256623	88819	AGGTCTCCTAGAAGCTGGTG	301210	133406	CCTCGTGGCTTTACTTGGAG
212037	44233	TGGGCATGGGGGCTCACCCC	256624	88820	CAGGTCTCCTAGAAGCTGGT	301211	133407	ACCTCGTGGCTTTACTTGGA
212038	44234	CTGGGCATGGGGGCTCACCC	256625	88821	GCAGGTCTCCTAGAAGCTGG	301212	133408	GACCTCGTGGCTTTACTTGG
212039	44235	GCTGGGCATGGGGGCTCACC	256626	88822	TGCAGGTCTCCTAGAAGCTG	301213	133409	CGACCTCGTGGCTTTACTTG
212040	44236	AGCTGGGCATGGGGGCTCAC	256627	88823	GTGCAGGTCTCCTAGAAGCT	301214	133410	CCGACCTCGTGGCTTTACTT
212041	44237	TAGCTGGGCATGGGGGCTCA	256628	88824	GGTGCAGGTCTCCTAGAAGC	301215	133411	CCCGACCTCGTGGCTTTACT
212042	44238	TTAGCTGGGCATGGGGGCTC	256629	88825	TGGTGCAGGTCTCCTAGAAG	301216	133412	CCCCGACCTCGTGGCTTTAC
212043	44239	ATTAGCTGGGCATGGGGGCT	256630	88826	CTGGTGCAGGTCTCCTAGAA	301217	133413	GCCCCGACCTCGTGGCTTTA
212044	44240	AATTAGCTGGGCATGGGGGC	256631	88827	CCTGGTGCAGGTCTCCTAGA	301218	133414	CGCCCCGACCTCGTGGCTTT
212045	44241	AAATTAGCTGGGCATGGGGG	256632	88828	TCCTGGTGCAGGTCTCCTAG	301219	133415	TCGCCCCGACCTCGTGGCTT
212046	44242	AAAATTAGCTGGGCATGGGG	256633	88829	CTCCTGGTGCAGGTCTCCTA	301220	133416	CTCGCCCCGACCTCGTGGCT
212047	44243	AAAAATTAGCTGGGCATGGG	256634	88830	CCTCCTGGTGCAGGTCTCCT	301221	133417	CCTCGCCCCGACCTCGTGGC
212048	44244	AAAAAATTAGCTGGGCATGG	256635	88831	CCCTCCTGGTGCAGGTCTCC	301222	133418	CCCTCGCCCCGACCTCGTGG
212049	44245	AAAAAAATTAGCTGGGCATG	256636	88832	CCCCTCCTGGTGCAGGTCTC	301223	133419	GCCCTCGCCCCGACCTCGTG
212050	44246	AAAAAAAATTAGCTGGGCAT	256637	88833	GCCCCTCCTGGTGCAGGTCT	301224	133420	TGCCCTCGCCCCGACCTCGT
212051	44247	AAAAAAAAATTAGCTGGGCA	256638	88834	GGCCCCTCCTGGTGCAGGTC	301225	133421	CTGCCCTCGCCCCGACCTCG
212052	44248	AAAAAAAAAATTAGCTGGGC	256639	88835	CGGCCCCTCCTGGTGCAGGT	301226	133422	TCTGCCCTCGCCCCGACCTC
212053	44249	AAAAAAAAAAATTAGCTGGG	256640	88836	GCGGCCCCTCCTGGTGCAGG	301227	133423	CTCTGCCCTCGCCCCGACCT
212054	44250	AAAAAAAAAAAATTAGCTGG	256641	88837	GGCGGCCCCTCCTGGTGCAG	301228	133424	CCTCTGCCCTCGCCCCGACC
212055	44251	AAAAAAAAAAAAATTAGCTG	256642	88838	CGGCGGCCCCTCCTGGTGCA	301229	133425	ACCTCTGCCCTCGCCCCGAC
212056	44252	AAAAAAAAAAAAAATTAGCT	256643	88839	GCGGCGGCCCCTCCTGGTGC	301230	133426	CACCTCTGCCCTCGCCCCGA
212057	44253	AAAAAAAAAAAAAAATTAGC	256644	88840	AGCGGCGGCCCCTCCTGGTG	301231	133427	TCACCTCTGCCCTCGCCCCG
212058	44254	AAAAAAAAAAAAAAAATTAG	256645	88841	CAGCGGCGGCCCCTCCTGGT	301232	133428	ATCACCTCTGCCCTCGCCCC
212059	44255	AAAAAAAAAAAAAAAAATTA	256646	88842	TCAGCGGCGGCCCCTCCTGG	301233	133429	GATCACCTCTGCCCTCGCCC
212060	44256	AAAAAAAAAAAAAAAAAATT	256647	88843	TTCAGCGGCGGCCCCTCCTG	301234	133430	TGATCACCTCTGCCCTCGCC
212061	44257	AAAAAAAAAAAAAAAAAAAT	256648	88844	CTTCAGCGGCGGCCCCTCCT	301235	133431	GTGATCACCTCTGCCCTCGC
212062	44258	AAAAAAAAAAAAAAAAAAAA	256649	88845	CCTTCAGCGGCGGCCCCTCC	301236	133432	GGTGATCACCTCTGCCCTCG
212063	44259	AAAAAAAAAAAAAAAAAAAA	256650	88846	CCCTTCAGCGGCGGCCCCTC	301237	133433	AGGTGATCACCTCTGCCCTC
212064	44260	CAAAAAAAAAAAAAAAAAAA	256651	88847	CCCCTTCAGCGGCGGCCCCT	301238	133434	CAGGTGATCACCTCTGCCCT
212065	44261	TCAAAAAAAAAAAAAAAAAA	256652	88848	CCCCCTTCAGCGGCGGCCCC	301239	133435	GCAGGTGATCACCTCTGCCC
212066	44262	CTCAAAAAAAAAAAAAAAAA	256653	88849	GCCCCCTTCAGCGGCGGCCC	301240	133436	CGCAGGTGATCACCTCTGCC
212067	44263	TCTCAAAAAAAAAAAAAAAA	256654	88850	TGCCCCCTTCAGCGGCGGCC	301241	133437	ACGCAGGTGATCACCTCTGC
212068	44264	GTCTCAAAAAAAAAAAAAAA	256655	88851	CTGCCCCCTTCAGCGGCGGC	301242	133438	CACGCAGGTGATCACCTCTG
212069	44265	TGTCTCAAAAAAAAAAAAAA	256656	88852	CCTGCCCCCTTCAGCGGCGG	301243	133439	ACACGCAGGTGATCACCTCT
212070	44266	CTGTCTCAAAAAAAAAAAAA	256657	88853	CCCTGCCCCCTTCAGCGGCG	301244	133440	GACACGCAGGTGATCACCTC
212071	44267	TCTGTCTCAAAAAAAAAAAA	256658	88854	CCCCTGCCCCCTTCAGCGGC	301245	133441	GGACACGCAGGTGATCACCT
212072	44268	CTCTGTCTCAAAAAAAAAAA	256659	88855	CCCCCTGCCCCCTTCAGCGG	301246	133442	GGGACACGCAGGTGATCACC
212073	44269	ACTCTGTCTCAAAAAAAAAA	256660	88856	GCCCCCTGCCCCCTTCAGCG	301247	133443	TGGGACACGCAGGTGATCAC
212074	44270	GACTCTGTCTCAAAAAAAAA	256661	88857	TGCCCCCTGCCCCCTTCAGC	301248	133444	ATGGGACACGCAGGTGATCA
212075	44271	AGACTCTGTCTCAAAAAAAA	256662	88858	TTGCCCCCTGCCCCCTTCAG	301249	133445	GATGGGACACGCAGGTGATC
212076	44272	GAGACTCTGTCTCAAAAAAA	256663	88859	TTTGCCCCCTGCCCCCTTCA	301250	133446	AGATGGGACACGCAGGTGAT
212077	44273	TGAGACTCTGTCTCAAAAAA	256664	88860	CTTTGCCCCCTGCCCCCTTC	301251	133447	TAGATGGGACACGCAGGTGA
212078	44274	GTGAGACTCTGTCTCAAAAA	256665	88861	TCTTTGCCCCCTGCCCCCTT	301252	133448	GTAGATGGGACACGCAGGTG
212079	44275	AGTGAGACTCTGTCTCAAAA	256666	88862	CTCTTTGCCCCCTGCCCCCT	301253	133449	TGTAGATGGGACACGCAGGT
212080	44276	GAGTGAGACTCTGTCTCAAA	256667	88863	TCTCTTTGCCCCCTGCCCCC	301254	133450	CTGTAGATGGGACACGCAGG
212081	44277	TGAGTGAGACTCTGTCTCAA	256668	88864	CTCTCTTTGCCCCCTGCCCC	301255	133451	TCTGTAGATGGGACACGCAG
212082	44278	CTGAGTGAGACTCTGTCTCA	256669	88865	CCTCTCTTTGCCCCCTGCCC	301256	133452	GTCTGTAGATGGGACACGCA

212083	44279	ACTGAGTGAGACTCTGTCTC	256670	88866	GCCTCTCTTTGCCCCCTGCC	301257	133453	GGTCTGTAGATGGGACACGC
212084	44280	GACTGAGTGAGACTCTGTCT	256671	88867	GGCCTCTCTTTGCCCCCTGC	301258	133454	AGGTCTGTAGATGGGACACG
212085	44281	TGACTGAGTGAGACTCTGTC	256672	88868	CGGCCTCTCTTTGCCCCCTG	301259	133455	CAGGTCTGTAGATGGGACAC
212086	44282	GTGACTGAGTGAGACTCTGT	256673	88869	CCGGCCTCTCTTTGCCCCCT	301260	133456	GCAGGTCTGTAGATGGGACA
212087	44283	GGTGACTGAGTGAGACTCTG	256674	88870	CCCGGCCTCTCTTTGCCCCC	301261	133457	TGCAGGTCTGTAGATGGGAC
212088	44284	GGGTGACTGAGTGAGACTCT	256675	88871	CCCCGGCCTCTCTTTGCCCC	301262	133458	CTGCAGGTCTGTAGATGGGA
212089	44285	TGGGTGACTGAGTGAGACTC	256676	88872	TCCCCGGCCTCTCTTTGCCC	301263	133459	GCTGCAGGTCTGTAGATGGG
212090	44286	CTGGGTGACTGAGTGAGACT	256677	88873	CTCCCCGGCCTCTCTTTGCC	301264	133460	AGCTGCAGGTCTGTAGATGG
212091	44287	CCTGGGTGACTGAGTGAGAC	256678	88874	GCTCCCCGGCCTCTCTTTGC	301265	133461	AAGCTGCAGGTCTGTAGATG
212092	44288	GCCTGGGTGACTGAGTGAGA	256679	88875	TGCTCCCCGGCCTCTCTTTG	301266	133462	GAAGCTGCAGGTCTGTAGAT
212093	44289	AGCCTGGGTGACTGAGTGAG	256680	88876	TTGCTCCCCGGCCTCTCTTT	301267	133463	TGAAGCTGCAGGTCTGTAGA
212094	44290	CAGCCTGGGTGACTGAGTGA	256681	88877	CTTGCTCCCCGGCCTCTCTT	301268	133464	ATGAAGCTGCAGGTCTGTAG
212095	44291	CCAGCCTGGGTGACTGAGTG	256682	88878	CCTTGCTCCCCGGCCTCTCT	301269	133465	TATGAAGCTGCAGGTCTGTA
212096	44292	ACCAGCCTGGGTGACTGAGT	256683	88879	TCCTTGCTCCCCGGCCTCTC	301270	133466	TTATGAAGCTGCAGGTCTGT
212097	44293	CACCAGCCTGGGTGACTGAG	256684	88880	CTCCTTGCTCCCCGGCCTCT	301271	133467	TTTATGAAGCTGCAGGTCTG
212098	44294	ACACCAGCCTGGGTGACTGA	256685	88881	CCTCCTTGCTCCCCGGCCTC	301272	133468	TTTTATGAAGCTGCAGGTCT
212099	44295	CACACCAGCCTGGGTGACTG	256686	88882	TCCTCCTTGCTCCCCGGCCT	301273	133469	GTTTTATGAAGCTGCAGGTC
212100	44296	GCACACCAGCCTGGGTGACT	256687	88883	CTCCTCCTTGCTCCCCGGCC	301274	133470	AGTTTTATGAAGCTGCAGGT
212101	44297	TGCACACCAGCCTGGGTGAC	256688	88884	CCTCCTCCTTGCTCCCCGGC	301275	133471	AAGTTTTATGAAGCTGCAGG
212102	44298	CTGCACACCAGCCTGGGTGA	256689	88885	ACCTCCTCCTTGCTCCCCGG	301276	133472	GAAGTTTTATGAAGCTGCAG
212103	44299	ACTGCACACCAGCCTGGGTG	256690	88886	CACCTCCTCCTTGCTCCCCG	301277	133473	AGAAGTTTTATGAAGCTGCA
212104	44300	CACTGCACACCAGCCTGGGT	256691	88887	CCACCTCCTCCTTGCTCCCC	301278	133474	CAGAAGTTTTATGAAGCTGC
212105	44301	CCACTGCACACCAGCCTGGG	256692	88888	TCCACCTCCTCCTTGCTCCC	301279	133475	TCAGAAGTTTTATGAAGCTG
212106	44302	ACCACTGCACACCAGCCTGG	256693	88889	ATCCACCTCCTCCTTGCTCC	301280	133476	ATCAGAAGTTTTATGAAGCT
212107	44303	CACCACTGCACACCAGCCTG	256694	88890	CATCCACCTCCTCCTTGCTC	301281	133477	AATCAGAAGTTTTATGAAGC
212108	44304	GCACCACTGCACACCAGCCT	256695	88891	TCATCCACCTCCTCCTTGCT	301282	133478	AAATCAGAAGTTTTATGAAG
212109	44305	TGCACCACTGCACACCAGCC	256696	88892	TTCATCCACCTCCTCCTTGC	301283	133479	GAAATCAGAAGTTTTATGAA
212110	44306	TTGCACCACTGCACACCAGC	256697	88893	CTTCATCCACCTCCTCCTTG	301284	133480	AGAAATCAGAAGTTTTATGA
212111	44307	ATTGCACCACTGCACACCAG	256698	88894	TCTTCATCCACCTCCTCCTT	301285	133481	GAGAAATCAGAAGTTTTATG
212112	44308	GATTGCACCACTGCACACCA	256699	88895	GTCTTCATCCACCTCCTCCT	301286	133482	AGAGAAATCAGAAGTTTTAT
212113	44309	AGATTGCACCACTGCACACC	256700	88896	GGTCTTCATCCACCTCCTCC	301287	133483	AAGAGAAATCAGAAGTTTTA
212114	44310	GAGATTGCACCACTGCACAC	256701	88897	CGGTCTTCATCCACCTCCTC	301288	133484	GAAGAGAAATCAGAAGTTTT
212115	44311	TGAGATTGCACCACTGCACA	256702	88898	GCGGTCTTCATCCACCTCCT	301289	133485	TGAAGAGAAATCAGAAGTTT
212116	44312	CTGAGATTGCACCACTGCAC	256703	88899	CGCGGTCTTCATCCACCTCC	301290	133486	CTGAAGAGAAATCAGAAGTT
212117	44313	GCTGAGATTGCACCACTGCA	256704	88900	TCGCGGTCTTCATCCACCTC	301291	133487	GCTGAAGAGAAATCAGAAGT
212118	44314	AGCTGAGATTGCACCACTGC	256705	88901	GTCGCGGTCTTCATCCACCT	301292	133488	AGCTGAAGAGAAATCAGAAG
212119	44315	GAGCTGAGATTGCACCACTG	256706	88902	CGTCGCGGTCTTCATCCACC	301293	133489	AAGCTGAAGAGAAATCAGAA
212120	44316	TGAGCTGAGATTGCACCACT	256707	88903	ACGTCGCGGTCTTCATCCAC	301294	133490	AAAGCTGAAGAGAAATCAGA
212121	44317	GTGAGCTGAGATTGCACCAC	256708	88904	GACGTCGCGGTCTTCATCCA	301295	133491	CAAAGCTGAAGAGAAATCAG
212122	44318	TGTGAGCTGAGATTGCACCA	256709	88905	CGACGTCGCGGTCTTCATCC	301296	133492	TCAAAGCTGAAGAGAAATCA
212123	44319	CTGTGAGCTGAGATTGCACC	256710	88906	TCGACGTCGCGGTCTTCATC	301297	133493	TTCAAAGCTGAAGAGAAATC
212124	44320	GCTGTGAGCTGAGATTGCAC	256711	88907	ATCGACGTCGCGGTCTTCAT	301298	133494	TTTCAAAGCTGAAGAGAAAT
212125	44321	TGCTGTGAGCTGAGATTGCA	256712	88908	CATCGACGTCGCGGTCTTCA	301299	133495	TTTTCAAAGCTGAAGAGAAA
212126	44322	TTGCTGTGAGCTGAGATTGC	256713	88909	TCATCGACGTCGCGGTCTTC	301300	133496	CTTTTCAAAGCTGAAGAGAA
212127	44323	GTTGCTGTGAGCTGAGATTG	256714	88910	CTCATCGACGTCGCGGTCTT	301301	133497	CCTTTTCAAAGCTGAAGAGA
212128	44324	GGTTGCTGTGAGCTGAGATT	256715	88911	ACTCATCGACGTCGCGGTCT	301302	133498	CCCTTTTCAAAGCTGAAGAG
212129	44325	AGGTTGCTGTGAGCTGAGAT	256716	88912	GACTCATCGACGTCGCGGTC	301303	133499	ACCCTTTTCAAAGCTGAAGA
212130	44326	GAGGTTGCTGTGAGCTGAGA	256717	88913	GGACTCATCGACGTCGCGGT	301304	133500	AACCCTTTTCAAAGCTGAAG
212131	44327	GGAGGTTGCTGTGAGCTGAG	256718	88914	AGGACTCATCGACGTCGCGG	301305	133501	TAACCCTTTTCAAAGCTGAA
212132	44328	CGGAGGTTGCTGTGAGCTGA	256719	88915	GAGGACTCATCGACGTCGCG	301306	133502	GTAACCCTTTTCAAAGCTGA
212133	44329	GCGGAGGTTGCTGTGAGCTG	256720	88916	GGAGGACTCATCGACGTCGC	301307	133503	GGTAACCCTTTTCAAAGCTG
212134	44330	GGCGGAGGTTGCTGTGAGCT	256721	88917	GGGAGGACTCATCGACGTCG	301308	133504	GGGTAACCCTTTTCAAAGCT
212135	44331	AGGCGGAGGTTGCTGTGAGC	256722	88918	GGGGAGGACTCATCGACGTC	301309	133505	AGGGTAACCCTTTTCAAAGC
212136	44332	GAGGCGGAGGTTGCTGTGAG	256723	88919	GGGGGAGGACTCATCGACGT	301310	133506	CAGGGTAACCCTTTTCAAAG
212137	44333	GGAGGCGGAGGTTGCTGTGA	256724	88920	GGGGGGAGGACTCATCGACG	301311	133507	CCAGGGTAACCCTTTTCAAA
212138	44334	AGGAGGCGGAGGTTGCTGTG	256725	88921	TGGGGGGAGGACTCATCGAC	301312	133508	CCCAGGGTAACCCTTTTCAA
212139	44335	CAGGAGGCGGAGGTTGCTGT	256726	88922	TTGGGGGGAGGACTCATCGA	301313	133509	GCCCAGGGTAACCCTTTTCA
212140	44336	CCAGGAGGCGGAGGTTGCTG	256727	88923	CTTGGGGGGAGGACTCATCG	301314	133510	TGCCCAGGGTAACCCTTTTC
212141	44337	CCCAGGAGGCGGAGGTTGCT	256728	88924	TCTTGGGGGGAGGACTCATC	301315	133511	GTGCCCAGGGTAACCCTTTT
212142	44338	ACCCAGGAGGCGGAGGTTGC	256729	88925	GTCTTGGGGGGAGGACTCAT	301316	133512	AGTGCCCAGGGTAACCCTTT
212143	44339	AACCCAGGAGGCGGAGGTTG	256730	88926	AGTCTTGGGGGGAGGACTCA	301317	133513	CAGTGCCCAGGGTAACCCTT
212144	44340	GAACCCAGGAGGCGGAGGTT	256731	88927	GAGTCTTGGGGGGAGGACTC	301318	133514	CCAGTGCCCAGGGTAACCCT
212145	44341	TGAACCCAGGAGGCGGAGGT	256732	88928	GGAGTCTTGGGGGGAGGACT	301319	133515	GCCAGTGCCCAGGGTAACCC
212146	44342	TTGAACCCAGGAGGCGGAGG	256733	88929	GGGAGTCTTGGGGGGAGGAC	301320	133516	GGCCAGTGCCCAGGGTAACC
212147	44343	CTTGAACCCAGGAGGCGGAG	256734	88930	GGGGAGTCTTGGGGGGAGGA	301321	133517	AGGCCAGTGCCCAGGGTAAC
212148	44344	ACTTGAACCCAGGAGGCGGA	256735	88931	AGGGGAGTCTTGGGGGGAGG	301322	133518	TAGGCCAGTGCCCAGGGTAA
212149	44345	CACTTGAACCCAGGAGGCGG	256736	88932	GAGGGGAGTCTTGGGGGGAG	301323	133519	CTAGGCCAGTGCCCAGGGTA
212150	44346	TCACTTGAACCCAGGAGGCG	256737	88933	GGAGGGGAGTCTTGGGGGGA	301324	133520	TCTAGGCCAGTGCCCAGGGT
212151	44347	ATCACTTGAACCCAGGAGGC	256738	88934	GGGAGGGGAGTCTTGGGGGG	301325	133521	CTCTAGGCCAGTGCCCAGGG
212152	44348	AATCACTTGAACCCAGGAGG	256739	88935	AGGGAGGGGAGTCTTGGGGG	301326	133522	GCTCTAGGCCAGTGCCCAGG
212153	44349	GAATCACTTGAACCCAGGAG	256740	88936	GAGGGAGGGGAGTCTTGGGG	301327	133523	GGCTCTAGGCCAGTGCCCAG
212154	44350	AGAATCACTTGAACCCAGGA	256741	88937	GGAGGGAGGGGAGTCTTGGG	301328	133524	AGGCTCTAGGCCAGTGCCCA

212155	44351	AAGAATCACTTGAACCCAGG	256742	88938	TGGAGGGAGGGGAGTCTTGG	301329	133525	GAGGCTCTAGGCCAGTGCCC
212156	44352	CAAGAATCACTTGAACCCAG	256743	88939	TTGGAGGGAGGGGAGTCTTG	301330	133526	TGAGGCTCTAGGCCAGTGCC
212157	44353	ACAAGAATCACTTGAACCCA	256744	88940	CTTGGAGGGAGGGGAGTCTT	301331	133527	GTGAGGCTCTAGGCCAGTGC
212158	44354	CACAAGAATCACTTGAACCC	256745	88941	CCTTGGAGGGAGGGGAGTCT	301332	133528	GGTGAGGCTCTAGGCCAGTG
212159	44355	GCACAAGAATCACTTGAACC	256746	88942	GCCTTGGAGGGAGGGGAGTC	301333	133529	AGGTGAGGCTCTAGGCCAGT
212160	44356	GGCACAAGAATCACTTGAAC	256747	88943	GGCCTTGGAGGGAGGGGAGT	301334	133530	GAGGTGAGGCTCTAGGCCAG
212161	44357	AGGCACAAGAATCACTTGAA	256748	88944	AGGCCTTGGAGGGAGGGGAG	301335	133531	GGAGGTGAGGCTCTAGGCCA
212162	44358	GAGGCACAAGAATCACTTGA	256749	88945	GAGGCCTTGGAGGGAGGGGA	301336	133532	AGGAGGTGAGGCTCTAGGCC
212163	44359	TGAGGCACAAGAATCACTTG	256750	88946	GGAGGCCTTGGAGGGAGGGG	301337	133533	TAGGAGGTGAGGCTCTAGGC
212164	44360	CTGAGGCACAAGAATCACTT	256751	88947	GGGAGGCCTTGGAGGGAGGG	301338	133534	TTAGGAGGTGAGGCTCTAGG
212165	44361	GCTGAGGCACAAGAATCACT	256752	88948	GGGGAGGCCTTGGAGGGAGG	301339	133535	ATTAGGAGGTGAGGCTCTAG
212166	44362	GGCTGAGGCACAAGAATCAC	256753	88949	TGGGGAGGCCTTGGAGGGAG	301340	133536	TATTAGGAGGTGAGGCTCTA
212167	44363	AGGCTGAGGCACAAGAATCA	256754	88950	CTGGGGAGGCCTTGGAGGGA	301341	133537	CTATTAGGAGGTGAGGCTCT
212168	44364	GAGGCTGAGGCACAAGAATC	256755	88951	GCTGGGGAGGCCTTGGAGGG	301342	133538	TCTATTAGGAGGTGAGGCTC
212169	44365	GGAGGCTGAGGCACAAGAAT	256756	88952	GGCTGGGGAGGCCTTGGAGG	301343	133539	GTCTATTAGGAGGTGAGGCT
212170	44366	GGGAGGCTGAGGCACAAGAA	256757	88953	GGGCTGGGGAGGCCTTGGAG	301344	133540	AGTCTATTAGGAGGTGAGGC
212171	44367	TGGGAGGCTGAGGCACAAGA	256758	88954	TGGGCTGGGGAGGCCTTGGA	301345	133541	AAGTCTATTAGGAGGTGAGG
212172	44368	TTGGGAGGCTGAGGCACAAG	256759	88955	TTGGGCTGGGGAGGCCTTGG	301346	133542	TAAGTCTATTAGGAGGTGAG
212173	44369	CTTGGGAGGCTGAGGCACAA	256760	88956	CTTGGGCTGGGGAGGCCTTG	301347	133543	CTAAGTCTATTAGGAGGTGA
212174	44370	CCTTGGGAGGCTGAGGCACA	256761	88957	TCTTGGGCTGGGGAGGCCTT	301348	133544	GCTAAGTCTATTAGGAGGTG
212175	44371	TCCTTGGGAGGCTGAGGCAC	256762	88958	ATCTTGGGCTGGGGAGGCCT	301349	133545	GGCTAAGTCTATTAGGAGGT
212176	44372	CTCCTTGGGAGGCTGAGGCA	256763	88959	CATCTTGGGCTGGGGAGGCC	301350	133546	GGGCTAAGTCTATTAGGAGG
212177	44373	GCTCCTTGGGAGGCTGAGGC	256764	88960	CCATCTTGGGCTGGGGAGGC	301351	133547	GGGGCTAAGTCTATTAGGAG
212178	44374	AGCTCCTTGGGAGGCTGAGG	256765	88961	CCCATCTTGGGCTGGGGAGG	301352	133548	TGGGGCTAAGTCTATTAGGA
212179	44375	CAGCTCCTTGGGAGGCTGAG	256766	88962	GCCCATCTTGGGCTGGGGAG	301353	133549	ATGGGGCTAAGTCTATTAGG
212180	44376	CCAGCTCCTTGGGAGGCTGA	256767	88963	CGCCCATCTTGGGCTGGGGA	301354	133550	CATGGGGCTAAGTCTATTAG
212181	44377	CCCAGCTCCTTGGGAGGCTG	256768	88964	CCGCCCATCTTGGGCTGGGG	301355	133551	TCATGGGGCTAAGTCTATTA
212182	44378	TCCCAGCTCCTTGGGAGGCT	256769	88965	GCCGCCCATCTTGGGCTGGG	301356	133552	CTCATGGGGCTAAGTCTATT
212183	44379	GTCCCAGCTCCTTGGGAGGC	256770	88966	GGCCGCCCATCTTGGGCTGG	301357	133553	ACTCATGGGGCTAAGTCTAT
212184	44380	AGTCCCAGCTCCTTGGGAGG	256771	88967	AGGCCGCCCATCTTGGGCTG	301358	133554	AACTCATGGGGCTAAGTCTA
212185	44381	TAGTCCCAGCTCCTTGGGAG	256772	88968	GAGGCCGCCCATCTTGGGCT	301359	133555	AAACTCATGGGGCTAAGTCT
212186	44382	GTAGTCCCAGCTCCTTGGGA	256773	88969	GGAGGCCGCCCATCTTGGGC	301360	133556	CAAACTCATGGGGCTAAGTC
212187	44383	TGTAGTCCCAGCTCCTTGGG	256774	88970	GGGAGGCCGCCCATCTTGGG	301361	133557	GCAAACTCATGGGGCTAAGT
212188	44384	CTGTAGTCCCAGCTCCTTGG	256775	88971	GGGGAGGCCGCCCATCTTGG	301362	133558	GGCAAACTCATGGGGCTAAG
212189	44385	CCTGTAGTCCCAGCTCCTTG	256776	88972	TGGGGAGGCCGCCCATCTTG	301363	133559	TGGCAAACTCATGGGGCTAA
212190	44386	ACCTGTAGTCCCAGCTCCTT	256777	88973	CTGGGGAGGCCGCCCATCTT	301364	133560	ATGGCAAACTCATGGGGCTA
212191	44387	CACCTGTAGTCCCAGCTCCT	256778	88974	TCTGGGGAGGCCGCCCATCT	301365	133561	CATGGCAAACTCATGGGGCT
212192	44388	ACACCTGTAGTCCCAGCTCC	256779	88975	GTCTGGGGAGGCCGCCCATC	301366	133562	ACATGGCAAACTCATGGGGC
212193	44389	CACACCTGTAGTCCCAGCTC	256780	88976	TGTCTGGGGAGGCCGCCCAT	301367	133563	AACATGGCAAACTCATGGGG
212194	44390	GCACACCTGTAGTCCCAGCT	256781	88977	CTGTCTGGGGAGGCCGCCCA	301368	133564	CAACATGGCAAACTCATGGG
212195	44391	TGCACACCTGTAGTCCCAGC	256782	88978	GCTGTCTGGGGAGGCCGCCC	301369	133565	TCAACATGGCAAACTCATGG
212196	44392	GTGCACACCTGTAGTCCCAG	256783	88979	GGCTGTCTGGGGAGGCCGCC	301370	133566	CTCAACATGGCAAACTCATG
212197	44393	GGTGCACACCTGTAGTCCCA	256784	88980	CGGCTGTCTGGGGAGGCCGC	301371	133567	GCTCAACATGGCAAACTCAT
212198	44394	TGGTGCACACCTGTAGTCCC	256785	88981	GCGGCTGTCTGGGGAGGCCG	301372	133568	TGCTCAACATGGCAAACTCA
212199	44395	GTGGTGCACACCTGTAGTCC	256786	88982	GGCGGCTGTCTGGGGAGGCC	301373	133569	CTGCTCAACATGGCAAACTC
212200	44396	GGTGGTGCACACCTGTAGTC	256787	88983	TGGCGGCTGTCTGGGGAGGC	301374	133570	CCTGCTCAACATGGCAAACT
212201	44397	TGGTGGTGCACACCTGTAGT	256788	88984	CTGGCGGCTGTCTGGGGAGG	301375	133571	TCCTGCTCAACATGGCAAAC
212202	44398	GTGGTGGTGCACACCTGTAG	256789	88985	TCTGGCGGCTGTCTGGGGAG	301376	133572	GTCCTGCTCAACATGGCAAA
212203	44399	CGTGGTGGTGCACACCTGTA	256790	88986	CTCTGGCGGCTGTCTGGGGA	301377	133573	AGTCCTGCTCAACATGGCAA
212204	44400	GCGTGGTGGTGCACACCTGT	256791	88987	TCTCTGGCGGCTGTCTGGGG	301378	133574	TAGTCCTGCTCAACATGGCA
212205	44401	GGCGTGGTGGTGCACACCTG	256792	88988	TTCTCTGGCGGCTGTCTGGG	301379	133575	ATAGTCCTGCTCAACATGGC
212206	44402	GGGCGTGGTGGTGCACACCT	256793	88989	CTTCTCTGGCGGCTGTCTGG	301380	133576	AATAGTCCTGCTCAACATGG
212207	44403	CGGGCGTGGTGGTGCACACC	256794	88990	GCTTCTCTGGCGGCTGTCTG	301381	133577	AAATAGTCCTGCTCAACATG
212208	44404	TCGGGCGTGGTGGTGCACAC	256795	88991	GGCTTCTCTGGCGGCTGTCT	301382	133578	GAAATAGTCCTGCTCAACAT
212209	44405	GTCGGGCGTGGTGGTGCACA	256796	88992	TGGCTTCTCTGGCGGCTGTC	301383	133579	AGAAATAGTCCTGCTCAACA
212210	44406	AGTCGGGCGTGGTGGTGCAC	256797	88993	GTGGCTTCTCTGGCGGCTGT	301384	133580	CAGAAATAGTCCTGCTCAAC
212211	44407	TAGTCGGGCGTGGTGGTGCA	256798	88994	GGTGGCTTCTCTGGCGGCTG	301385	133581	CCAGAAATAGTCCTGCTCAA
212212	44408	TTAGTCGGGCGTGGTGGTGC	256799	88995	TGGTGGCTTCTCTGGCGGCT	301386	133582	GCCAGAAATAGTCCTGCTCA
212213	44409	ATTAGTCGGGCGTGGTGGTG	256800	88996	CTGGTGGCTTCTCTGGCGGC	301387	133583	TGCCAGAAATAGTCCTGCTC
212214	44410	AATTAGTCGGGCGTGGTGGT	256801	88997	GCTGGTGGCTTCTCTGGCGG	301388	133584	GTGCCAGAAATAGTCCTGCT
212215	44411	AAATTAGTCGGGCGTGGTGG	256802	88998	TGCTGGTGGCTTCTCTGGCG	301389	133585	AGTGCCAGAAATAGTCCTGC
212216	44412	AAAATTAGTCGGGCGTGGTG	256803	88999	ATGCTGGTGGCTTCTCTGGC	301390	133586	AAGTGCCAGAAATAGTCCTG
212217	44413	AAAAATTAGTCGGGCGTGGT	256804	89000	GATGCTGGTGGCTTCTCTGG	301391	133587	CAAGTGCCAGAAATAGTCCT
212218	44414	CAAAAATTAGTCGGGCGTGG	256805	89001	GGATGCTGGTGGCTTCTCTG	301392	133588	GCAAGTGCCAGAAATAGTCC
212219	44415	ACAAAAATTAGTCGGGCGTG	256806	89002	GGGATGCTGGTGGCTTCTCT	301393	133589	TGCAAGTGCCAGAAATAGTC
212220	44416	TACAAAAATTAGTCGGGCGT	256807	89003	TGGGATGCTGGTGGCTTCTC	301394	133590	TTGCAAGTGCCAGAAATAGT
212221	44417	ATACAAAAATTAGTCGGGCG	256808	89004	CTGGGATGCTGGTGGCTTCT	301395	133591	CTTGCAAGTGCCAGAAATAG
212222	44418	AATACAAAAATTAGTCGGGC	256809	89005	CCTGGGATGCTGGTGGCTTC	301396	133592	ACTTGCAAGTGCCAGAAATA
212223	44419	AAATACAAAAATTAGTCGGG	256810	89006	GCCTGGGATGCTGGTGGCTT	301397	133593	GACTTGCAAGTGCCAGAAAT
212224	44420	AAAATACAAAAATTAGTCGG	256811	89007	AGCCTGGGATGCTGGTGGCT	301398	133594	GGACTTGCAAGTGCCAGAAA
212225	44421	AAAAATACAAAAATTAGTCG	256812	89008	AAGCCTGGGATGCTGGTGGC	301399	133595	GGGACTTGCAAGTGCCAGAA
212226	44422	TAAAAATACAAAAATTAGTC	256813	89009	GAAGCCTGGGATGCTGGTGG	301400	133596	TGGGACTTGCAAGTGCCAGA

212227	44423	CTAAAAATACAAAAATTAGT	256814	89010	GGAAGCCTGGGATGCTGGTG	301401	133597	ATGGGACTTGCAAGTGCCAG
212228	44424	ACTAAAAATACAAAAATTAG	256815	89011	GGGAAGCCTGGGATGCTGGT	301402	133598	CATGGGACTTGCAAGTGCCA
212229	44425	TACTAAAAATACAAAAATTA	256816	89012	TGGGAAGCCTGGGATGCTGG	301403	133599	TCATGGGACTTGCAAGTGCC
212230	44426	TTACTAAAAATACAAAAATT	256817	89013	CTGGGAAGCCTGGGATGCTG	301404	133600	ATCATGGGACTTGCAAGTGC
212231	44427	TTTACTAAAAATACAAAAAT	256818	89014	GCTGGGAAGCCTGGGATGCT	301405	133601	AATCATGGGACTTGCAAGTG
212232	44428	CTTTACTAAAAATACAAAAA	256819	89015	CGCTGGGAAGCCTGGGATGC	301406	133602	AAATCATGGGACTTGCAAGT
212233	44429	TCTTTACTAAAAATACAAAA	256820	89016	CCGCTGGGAAGCCTGGGATG	301407	133603	GAAATCATGGGACTTGCAAG
212234	44430	ATCTTTACTAAAAATACAAA	256821	89017	TCCGCTGGGAAGCCTGGGAT	301408	133604	AGAAATCATGGGACTTGCAA
212235	44431	CATCTTTACTAAAAATACAA	256822	89018	CTCCGCTGGGAAGCCTGGGA	301409	133605	AAGAAATCATGGGACTTGCA
212236	44432	CCATCTTTACTAAAAATACA	256823	89019	CCTCCGCTGGGAAGCCTGGG	301410	133606	GAAGAAATCATGGGACTTGC
212237	44433	CCCATCTTTACTAAAAATAC	256824	89020	CCCTCCGCTGGGAAGCCTGG	301411	133607	CGAAGAAATCATGGGACTTG
212238	44434	CCCCATCTTTACTAAAAATA	256825	89021	ACCCTCCGCTGGGAAGCCTG	301412	133608	CCGAAGAAATCATGGGACTT
212239	44435	ACCCCATCTTTACTAAAAAT	256826	89022	CACCCTCCGCTGGGAAGCCT	301413	133609	ACCGAAGAAATCATGGGACT
212240	44436	AACCCCATCTTTACTAAAAA	256827	89023	GCACCCTCCGCTGGGAAGCC	301414	133610	TACCGAAGAAATCATGGGAC
212241	44437	AAACCCCATCTTTACTAAAA	256828	89024	GGCACCCTCCGCTGGGAAGC	301415	133611	TTACCGAAGAAATCATGGGA
212242	44438	GAAACCCCATCTTTACTAAA	256829	89025	TGGCACCCTCCGCTGGGAAG	301416	133612	ATTACCGAAGAAATCATGGG
212243	44439	TGAAACCCCATCTTTACTAA	256830	89026	ATGGCACCCTCCGCTGGGAA	301417	133613	AATTACCGAAGAAATCATGG
212244	44440	GTGAAACCCCATCTTTACTA	256831	89027	GATGGCACCCTCCGCTGGGA	301418	133614	GAATTACCGAAGAAATCATG
212245	44441	GGTGAAACCCCATCTTTACT	256832	89028	GGATGGCACCCTCCGCTGGG	301419	133615	AGAATTACCGAAGAAATCAT
212246	44442	TGGTGAAACCCCATCTTTAC	256833	89029	GGGATGGCACCCTCCGCTGG	301420	133616	CAGAATTACCGAAGAAATCA
212247	44443	ATGGTGAAACCCCATCTTTA	256834	89030	GGGGATGGCACCCTCCGCTG	301421	133617	TCAGAATTACCGAAGAAATC
212248	44444	CATGGTGAAACCCCATCTTT	256835	89031	GGGGGATGGCACCCTCCGCT	301422	133618	CTCAGAATTACCGAAGAAAT
212249	44445	ACATGGTGAAACCCCATCTT	256836	89032	AGGGGGATGGCACCCTCCGC	301423	133619	CCTCAGAATTACCGAAGAAA
212250	44446	AACATGGTGAAACCCCATCT	256837	89033	GAGGGGGATGGCACCCTCCG	301424	133620	CCCTCAGAATTACCGAAGAA
212251	44447	CAACATGGTGAAACCCCATC	256838	89034	GGAGGGGGATGGCACCCTCC	301425	133621	ACCCTCAGAATTACCGAAGA
212252	44448	CCAACATGGTGAAACCCCAT	256839	89035	GGGAGGGGGATGGCACCCTC	301426	133622	CACCCTCAGAATTACCGAAG
212253	44449	GCCAACATGGTGAAACCCCA	256840	89036	AGGGAGGGGGATGGCACCCT	301427	133623	CCACCCTCAGAATTACCGAA
212254	44450	GGCCAACATGGTGAAACCCC	256841	89037	CAGGGAGGGGGATGGCACCC	301428	133624	CCCACCCTCAGAATTACCGA
212255	44451	TGGCCAACATGGTGAAACCC	256842	89038	ACAGGGAGGGGGATGGCACC	301429	133625	CCCCACCCTCAGAATTACCG
212256	44452	CTGGCCAACATGGTGAAACC	256843	89039	CACAGGGAGGGGGATGGCAC	301430	133626	CCCCCACCCTCAGAATTACC
212257	44453	CCTGGCCAACATGGTGAAAC	256844	89040	CCACAGGGAGGGGGATGGCA	301431	133627	CCCCCCACCCTCAGAATTAC
212258	44454	GCCTGGCCAACATGGTGAAA	256845	89041	TCCACAGGGAGGGGGATGGC	301432	133628	TCCCCCCACCCTCAGAATTA
212259	44455	AGCCTGGCCAACATGGTGAA	256846	89042	ATCCACAGGGAGGGGGATGG	301433	133629	CTCCCCCCACCCTCAGAATT
212260	44456	CAGCCTGGCCAACATGGTGA	256847	89043	AATCCACAGGGAGGGGGATG	301434	133630	CCTCCCCCCACCCTCAGAAT
212261	44457	CCAGCCTGGCCAACATGGTG	256848	89044	AAATCCACAGGGAGGGGGAT	301435	133631	CCCTCCCCCCACCCTCAGAA
212262	44458	ACCAGCCTGGCCAACATGGT	256849	89045	GAAATCCACAGGGAGGGGGA	301436	133632	TCCCTCCCCCCACCCTCAGA
212263	44459	GACCAGCCTGGCCAACATGG	256850	89046	GGAAATCCACAGGGAGGGGG	301437	133633	GTCCCTCCCCCCACCCTCAG
212264	44460	AGACCAGCCTGGCCAACATG	256851	89047	AGGAAATCCACAGGGAGGGG	301438	133634	TGTCCCTCCCCCCACCCTCA
212265	44461	GAGACCAGCCTGGCCAACAT	256852	89048	GAGGAAATCCACAGGGAGGG	301439	133635	ATGTCCCTCCCCCCACCCTC
212266	44462	TGAGACCAGCCTGGCCAACA	256853	89049	AGAGGAAATCCACAGGGAGG	301440	133636	CATGTCCCTCCCCCCACCCT
212267	44463	TTGAGACCAGCCTGGCCAAC	256854	89050	GAGAGGAAATCCACAGGGAG	301441	133637	TCATGTCCCTCCCCCCACCC
212268	44464	TTTGAGACCAGCCTGGCCAA	256855	89051	GGAGAGGAAATCCACAGGGA	301442	133638	TTCATGTCCCTCCCCCCACC
212269	44465	GTTTGAGACCAGCCTGGCCA	256856	89052	TGGAGAGGAAATCCACAGGG	301443	133639	TTTCATGTCCCTCCCCCCAC
212270	44466	AGTTTGAGACCAGCCTGGCC	256857	89053	TTGGAGAGGAAATCCACAGG	301444	133640	ATTTCATGTCCCTCCCCCCA
212271	44467	GAGTTTGAGACCAGCCTGGC	256858	89054	TTTGGAGAGGAAATCCACAG	301445	133641	GATTTCATGTCCCTCCCCCC
212272	44468	GGAGTTTGAGACCAGCCTGG	256859	89055	CTTTGGAGAGGAAATCCACA	301446	133642	TGATTTCATGTCCCTCCCCC
212273	44469	AGGAGTTTGAGACCAGCCTG	256860	89056	ACTTTGGAGAGGAAATCCAC	301447	133643	ATGATTTCATGTCCCTCCCC
212274	44470	CAGGAGTTTGAGACCAGCCT	256861	89057	AACTTTGGAGAGGAAATCCA	301448	133644	GATGATTTCATGTCCCTCCC
212275	44471	TCAGGAGTTTGAGACCAGCC	256862	89058	AAACTTTGGAGAGGAAATCC	301449	133645	AGATGATTTCATGTCCCTCC
212276	44472	ATCAGGAGTTTGAGACCAGC	256863	89059	GAAACTTTGGAGAGGAAATC	301450	133646	AAGATGATTTCATGTCCCTC
212277	44473	GATCAGGAGTTTGAGACCAG	256864	89060	GGAAACTTTGGAGAGGAAAT	301451	133647	TAAGATGATTTCATGTCCCT
212278	44474	AGATCAGGAGTTTGAGACCA	256865	89061	TGGAAACTTTGGAGAGGAAA	301452	133648	CTAAGATGATTTCATGTCCC
212279	44475	GAGATCAGGAGTTTGAGACC	256866	89062	GTGGAAACTTTGGAGAGGAA	301453	133649	GCTAAGATGATTTCATGTCC
212280	44476	TGAGATCAGGAGTTTGAGAC	256867	89063	TGTGGAAACTTTGGAGAGGA	301454	133650	AGCTAAGATGATTTCATGTC
212281	44477	TTGAGATCAGGAGTTTGAGA	256868	89064	CTGTGGAAACTTTGGAGAGG	301455	133651	AAGCTAAGATGATTTCATGT
212282	44478	CTTGAGATCAGGAGTTTGAG	256869	89065	TCTGTGGAAACTTTGGAGAG	301456	133652	TAAGCTAAGATGATTTCATG
212283	44479	ACTTGAGATCAGGAGTTTGA	256870	89066	CTCTGTGGAAACTTTGGAGA	301457	133653	CTAAGCTAAGATGATTTCAT
212284	44480	CACTTGAGATCAGGAGTTTG	256871	89067	TCTCTGTGGAAACTTTGGAG	301458	133654	GCTAAGCTAAGATGATTTCA
212285	44481	TCACTTGAGATCAGGAGTTT	256872	89068	ATCTCTGTGGAAACTTTGGA	301459	133655	AGCTAAGCTAAGATGATTTC
212286	44482	ATCACTTGAGATCAGGAGTT	256873	89069	GATCTCTGTGGAAACTTTGG	301460	133656	AAGCTAAGCTAAGATGATTT
212287	44483	GATCACTTGAGATCAGGAGT	256874	89070	GGATCTCTGTGGAAACTTTG	301461	133657	AAAGCTAAGCTAAGATGATT
212288	44484	GGATCACTTGAGATCAGGAG	256875	89071	GGGATCTCTGTGGAAACTTT	301462	133658	GAAAGCTAAGCTAAGATGAT
212289	44485	TGGATCACTTGAGATCAGGA	256876	89072	TGGGATCTCTGTGGAAACTT	301463	133659	AGAAAGCTAAGCTAAGATGA
212290	44486	GTGGATCACTTGAGATCAGG	256877	89073	CTGGGATCTCTGTGGAAACT	301464	133660	CAGAAAGCTAAGCTAAGATG
212291	44487	GGTGGATCACTTGAGATCAG	256878	89074	GCTGGGATCTCTGTGGAAAC	301465	133661	ACAGAAAGCTAAGCTAAGAT
212292	44488	TGGTGGATCACTTGAGATCA	256879	89075	GGCTGGGATCTCTGTGGAAA	301466	133662	GACAGAAAGCTAAGCTAAGA
212293	44489	TTGGTGGATCACTTGAGATC	256880	89076	AGGCTGGGATCTCTGTGGAA	301467	133663	AGACAGAAAGCTAAGCTAAG
212294	44490	GTTGGTGGATCACTTGAGAT	256881	89077	GAGGCTGGGATCTCTGTGGA	301468	133664	CAGACAGAAAGCTAAGCTAA
212295	44491	GGTTGGTGGATCACTTGAGA	256882	89078	TGAGGCTGGGATCTCTGTGG	301469	133665	ACAGACAGAAAGCTAAGCTA
212296	44492	AGGTTGGTGGATCACTTGAG	256883	89079	CTGAGGCTGGGATCTCTGTG	301470	133666	CACAGACAGAAAGCTAAGCT
212297	44493	GAGGTTGGTGGATCACTTGA	256884	89080	TCTGAGGCTGGGATCTCTGT	301471	133667	TCACAGACAGAAAGCTAAGC
212298	44494	TGAGGTTGGTGGATCACTTG	256885	89081	CTCTGAGGCTGGGATCTCTG	301472	133668	TTCACAGACAGAAAGCTAAG

212299	44495	CTGAGGTTGGTGGATCACTT	256886	89082	GCTCTGAGGCTGGGATCTCT	301473	133669	ATTCACAGACAGAAAGCTAA
212300	44496	GCTGAGGTTGGTGGATCACT	256887	89083	GGCTCTGAGGCTGGGATCTC	301474	133670	CATTCACAGACAGAAAGCTA
212301	44497	GGCTGAGGTTGGTGGATCAC	256888	89084	GGGCTCTGAGGCTGGGATCT	301475	133671	ACATTCACAGACAGAAAGCT
212302	44498	AGGCTGAGGTTGGTGGATCA	256889	89085	CGGGCTCTGAGGCTGGGATC	301476	133672	GACATTCACAGACAGAAAGC
212303	44499	GAGGCTGAGGTTGGTGGATC	256890	89086	TCGGGCTCTGAGGCTGGGAT	301477	133673	AGACATTCACAGACAGAAAG
212304	44500	AGAGGCTGAGGTTGGTGGAT	256891	89087	GTCGGGCTCTGAGGCTGGGA	301478	133674	TAGACATTCACAGACAGAAA
212305	44501	GAGAGGCTGAGGTTGGTGGA	256892	89088	CGTCGGGCTCTGAGGCTGGG	301479	133675	ATAGACATTCACAGACAGAA
212306	44502	TGAGAGGCTGAGGTTGGTGG	256893	89089	CCGTCGGGCTCTGAGGCTGG	301480	133676	TATAGACATTCACAGACAGA
212307	44503	TTGAGAGGCTGAGGTTGGTG	256894	89090	CCCGTCGGGCTCTGAGGCTG	301481	133677	ATATAGACATTCACAGACAG
212308	44504	TTTGAGAGGCTGAGGTTGGT	256895	89091	GCCCGTCGGGCTCTGAGGCT	301482	133678	TATATAGACATTCACAGACA
212309	44505	CTTTGAGAGGCTGAGGTTGG	256896	89092	GGCCCGTCGGGCTCTGAGGC	301483	133679	CTATATAGACATTCACAGAC
212310	44506	ACTTTGAGAGGCTGAGGTTG	256897	89093	GGGCCCGTCGGGCTCTGAGG	301484	133680	ACTATATAGACATTCACAGA
212311	44507	CACTTTGAGAGGCTGAGGTT	256898	89094	TGGGCCCGTCGGGCTCTGAG	301485	133681	CACTATATAGACATTCACAG
212312	44508	GCACTTTGAGAGGCTGAGGT	256899	89095	CTGGGCCCGTCGGGCTCTGA	301486	133682	ACACTATATAGACATTCACA
212313	44509	AGCACTTTGAGAGGCTGAGG	256900	89096	ACTGGGCCCGTCGGGCTCTG	301487	133683	TACACTATATAGACATTCAC
212314	44510	CAGCACTTTGAGAGGCTGAG	256901	89097	CACTGGGCCCGTCGGGCTCT	301488	133684	ATACACTATATAGACATTCA
212315	44511	CCAGCACTTTGAGAGGCTGA	256902	89098	ACACTGGGCCCGTCGGGCTC	301489	133685	AATACACTATATAGACATTC
212316	44512	CCCAGCACTTTGAGAGGCTG	256903	89099	TACACTGGGCCCGTCGGGCT	301490	133686	CAATACACTATATAGACATT
212317	44513	TCCCAGCACTTTGAGAGGCT	256904	89100	CTACACTGGGCCCGTCGGGC	301491	133687	ACAATACACTATATAGACAT
212318	44514	ATCCCAGCACTTTGAGAGGC	256905	89101	CCTACACTGGGCCCGTCGGG	301492	133688	CACAATACACTATATAGACA
212319	44515	AATCCCAGCACTTTGAGAGG	256906	89102	CCCTACACTGGGCCCGTCGG	301493	133689	ACACAATACACTATATAGAC
212320	44516	TAATCCCAGCACTTTGAGAG	256907	89103	GCCCTACACTGGGCCCGTCG	301494	133690	CACACAATACACTATATAGA
212321	44517	GTAATCCCAGCACTTTGAGA	256908	89104	CGCCCTACACTGGGCCCGTC	301495	133691	ACACACAATACACTATATAG
212322	44518	TGTAATCCCAGCACTTTGAG	256909	89105	CCGCCCTACACTGGGCCCGT	301496	133692	AACACACAATACACTATATA
212323	44519	CTGTAATCCCAGCACTTTGA	256910	89106	CCCGCCCTACACTGGGCCCG	301497	133693	AAACACACAATACACTATAT
212324	44520	CCTGTAATCCCAGCACTTTG	256911	89107	GCCCGCCCTACACTGGGCCC	301498	133694	AAAACACACAATACACTATA
212325	44521	ACCTGTAATCCCAGCACTTT	256912	89108	GGCCCGCCCTACACTGGGCC	301499	133695	TAAAACACACAATACACTAT
212326	44522	CACCTGTAATCCCAGCACTT	256913	89109	TGGCCCGCCCTACACTGGGC	301500	133696	TTAAAACACACAATACACTA
212327	44523	ACACCTGTAATCCCAGCACT	256914	89110	TTGGCCCGCCCTACACTGGG	301501	133697	GTTAAAACACACAATACACT
212328	44524	TACACCTGTAATCCCAGCAC	256915	89111	TTTGGCCCGCCCTACACTGG	301502	133698	TGTTAAAACACACAATACAC
212329	44525	TTACACCTGTAATCCCAGCA	256916	89112	CTTTGGCCCGCCCTACACTG	301503	133699	TTGTTAAAACACACAATACA
212330	44526	CTTACACCTGTAATCCCAGC	256917	89113	CCTTTGGCCCGCCCTACACT	301504	133700	TTTGTTAAAACACACAATAC
212331	44527	GCTTACACCTGTAATCCCAG	256918	89114	CCCTTTGGCCCGCCCTACAC	301505	133701	ATTTGTTAAAACACACAATA
212332	44528	GGCTTACACCTGTAATCCCA	256919	89115	GCCCTTTGGCCCGCCCTACA	301506	133702	CATTTGTTAAAACACACAAT
212333	44529	TGGCTTACACCTGTAATCCC	256920	89116	TGCCCTTTGGCCCGCCCTAC	301507	133703	TCATTTGTTAAAACACACAA
212334	44530	TTGGCTTACACCTGTAATCC	256921	89117	CTGCCCTTTGGCCCGCCCTA	301508	133704	ATCATTTGTTAAAACACACA
212335	44531	GTTGGCTTACACCTGTAATC	256922	89118	CCTGCCCTTTGGCCCGCCCT	301509	133705	AATCATTTGTTAAAACACAC
212336	44532	TGTTGGCTTACACCTGTAAT	256923	89119	TCCTGCCCTTTGGCCCGCCC	301510	133706	AAATCATTTGTTAAAACACA
212337	44533	ATGTTGGCTTACACCTGTAA	256924	89120	ATCCTGCCCTTTGGCCCGCC	301511	133707	TAAATCATTTGTTAAAACAC
212338	44534	CATGTTGGCTTACACCTGTA	256925	89121	CATCCTGCCCTTTGGCCCGC	301512	133708	GTAAATCATTTGTTAAAACA
212339	44535	GCATGTTGGCTTACACCTGT	256926	89122	GCATCCTGCCCTTTGGCCCG	301513	133709	TGTAAATCATTTGTTAAAAC
212340	44536	GGCATGTTGGCTTACACCTG	256927	89123	GGCATCCTGCCCTTTGGCCC	301514	133710	GTGTAAATCATTTGTTAAAA
212341	44537	GGGCATGTTGGCTTACACCT	256928	89124	GGGCATCCTGCCCTTTGGCC	301515	133711	AGTGTAAATCATTTGTTAAA
212342	44538	CGGGCATGTTGGCTTACACC	256929	89125	GGGGCATCCTGCCCTTTGGC	301516	133712	CAGTGTAAATCATTTGTTAA
212343	44539	CCGGGCATGTTGGCTTACAC	256930	89126	GGGGGCATCCTGCCCTTTGG	301517	133713	TCAGTGTAAATCATTTGTTA
212344	44540	GCCGGGCATGTTGGCTTACA	256931	89127	GGGGGGCATCCTGCCCTTTG	301518	133714	GTCAGTGTAAATCATTTGTT
212345	44541	GGCCGGGCATGTTGGCTTAC	256932	89128	AGGGGGGCATCCTGCCCTTT	301519	133715	AGTCAGTGTAAATCATTTGT
212346	44542	GGGCCGGGCATGTTGGCTTA	256933	89129	CAGGGGGGCATCCTGCCCTT	301520	133716	CAGTCAGTGTAAATCATTTG
212347	44543	GGGGCCGGGCATGTTGGCTT	256934	89130	CCAGGGGGGCATCCTGCCCT	301521	133717	ACAGTCAGTGTAAATCATTT
212348	44544	TGGGGCCGGGCATGTTGGCT	256935	89131	TCCAGGGGGGCATCCTGCCC	301522	133718	AACAGTCAGTGTAAATCATT
212349	44545	CTGGGGCCGGGCATGTTGGC	256936	89132	CTCCAGGGGGGCATCCTGCC	301523	133719	CAACAGTCAGTGTAAATCAT
212350	44546	GCTGGGGCCGGGCATGTTGG	256937	89133	ACTCCAGGGGGGCATCCTGC	301524	133720	GCAACAGTCAGTGTAAATCA
212351	44547	AGCTGGGGCCGGGCATGTTG	256938	89134	AACTCCAGGGGGGCATCCTG	301525	133721	AGCAACAGTCAGTGTAAATC
212352	44548	TAGCTGGGGCCGGGCATGTT	256939	89135	GAACTCCAGGGGGGCATCCT	301526	133722	CAGCAACAGTCAGTGTAAAT
212353	44549	TTAGCTGGGGCCGGGCATGT	256940	89136	TGAACTCCAGGGGGGCATCC	301527	133723	ACAGCAACAGTCAGTGTAAA
212354	44550	ATTAGCTGGGGCCGGGCATG	256941	89137	GTGAACTCCAGGGGGGCATC	301528	133724	TACAGCAACAGTCAGTGTAA
212355	44551	AATTAGCTGGGGCCGGGCAT	256942	89138	CGTGAACTCCAGGGGGGCAT	301529	133725	TTACAGCAACAGTCAGTGTA
212356	44552	AAATTAGCTGGGGCCGGGCA	256943	89139	ACGTGAACTCCAGGGGGGCA	301530	133726	TTTACAGCAACAGTCAGTGT
212357	44553	AAAATTAGCTGGGGCCGGGC	256944	89140	AACGTGAACTCCAGGGGGGC	301531	133727	TTTTACAGCAACAGTCAGTG
212358	44554	AAAAATTAGCTGGGGCCGGG	256945	89141	AAACGTGAACTCCAGGGGGG	301532	133728	CTTTTACAGCAACAGTCAGT
212359	44555	TAAAAATTAGCTGGGGCCGG	256946	89142	GAAACGTGAACTCCAGGGGG	301533	133729	ACTTTTACAGCAACAGTCAG
212360	44556	TTAAAAATTAGCTGGGGCCG	256947	89143	TGAAACGTGAACTCCAGGGG	301534	133730	CACTTTTACAGCAACAGTCA
212361	44557	TTTAAAAATTAGCTGGGGCC	256948	89144	GTGAAACGTGAACTCCAGGG	301535	133731	TCACTTTTACAGCAACAGTC
212362	44558	ATTTAAAAATTAGCTGGGGC	256949	89145	CGTGAAACGTGAACTCCAGG	301536	133732	TTCACTTTTACAGCAACAGT
212363	44559	TATTTAAAAATTAGCTGGGG	256950	89146	ACGTGAAACGTGAACTCCAG	301537	133733	ATTCACTTTTACAGCAACAG
212364	44560	ATATTTAAAAATTAGCTGGG	256951	89147	CACGTGAAACGTGAACTCCA	301538	133734	AATTCACTTTTACAGCAACA
212365	44561	AATATTTAAAAATTAGCTGG	256952	89148	CCACGTGAAACGTGAACTCC	301539	133735	AAATTCACTTTTACAGCAAC
212366	44562	AAATATTTAAAAATTAGCTG	256953	89149	TCCACGTGAAACGTGAACTC	301540	133736	CAAATTCACTTTTACAGCAA
212367	44563	AAAATATTTAAAAATTAGCT	256954	89150	TTCCACGTGAAACGTGAACT	301541	133737	CCAAATTCACTTTTACAGCA
212368	44564	AAAAATATTTAAAAATTAGC	256955	89151	TTTCCACGTGAAACGTGAAC	301542	133738	TCCAAATTCACTTTTACAGC
212369	44565	AAAAAATATTTAAAAATTAG	256956	89152	ATTTCCACGTGAAACGTGAA	301543	133739	TTCCAAATTCACTTTTACAG
212370	44566	AAAAAAATATTTAAAAATTA	256957	89153	GATTTCCACGTGAAACGTGA	301544	133740	TTTCCAAATTCACTTTTACA

212371	44567	AAAAAAAATATTTAAAAATT	256958	89154	TGATTTCCACGTGAAACGTG	301545	133741	ATTTCCAAATTCACTTTTAC
212372	44568	CAAAAAAAATATTTAAAAAT	256959	89155	GTGATTTCCACGTGAAACGT	301546	133742	TATTTCCAAATTCACTTTTA
212373	44569	ACAAAAAAAATATTTAAAAA	256960	89156	TGTGATTTCCACGTGAAACG	301547	133743	TTATTTCCAAATTCACTTTT
212374	44570	TACAAAAAAAATATTTAAAA	256961	89157	GTGTGATTTCCACGTGAAAC	301548	133744	TTTATTTCCAAATTCACTTT
212375	44571	CTACAAAAAAAATATTTAAA	256962	89158	GGTGTGATTTCCACGTGAAA	301549	133745	CTTTATTTCCAAATTCACTT
212376	44572	TCTACAAAAAAAATATTTAA	256963	89159	GGGTGTGATTTCCACGTGAA	301550	133746	ACTTTATTTCCAAATTCACT
212377	44573	CTCTACAAAAAAAATATTTA	256964	89160	TGGGTGTGATTTCCACGTGA	301551	133747	AACTTTATTTCCAAATTCAC
212378	44574	TCTCTACAAAAAAAATATTT	256965	89161	TTGGGTGTGATTTCCACGTG	301552	133748	TAACTTTATTTCCAAATTCA
212379	44575	ATCTCTACAAAAAAAATATT	256966	89162	GTTGGGTGTGATTTCCACGT	301553	133749	ATAACTTTATTTCCAAATTC
212380	44576	CATCTCTACAAAAAAAATAT	256967	89163	CGTTGGGTGTGATTTCCACG	301554	133750	AATAACTTTATTTCCAAATT
212381	44577	CCATCTCTACAAAAAAAATA	256968	89164	ACGTTGGGTGTGATTTCCAC	301555	133751	TAATAACTTTATTTCCAAAT
212382	44578	CCCATCTCTACAAAAAAAAT	256969	89165	CACGTTGGGTGTGATTTCCA	301556	133752	GTAATAACTTTATTTCCAAA
212383	44579	CCCCATCTCTACAAAAAAAA	256970	89166	GCACGTTGGGTGTGATTTCC	301557	133753	AGTAATAACTTTATTTCCAA
212384	44580	ACCCCATCTCTACAAAAAAA	256971	89167	TGCACGTTGGGTGTGATTTC	301558	133754	GAGTAATAACTTTATTTCCA
212385	44581	AACCCCATCTCTACAAAAAA	256972	89168	CTGCACGTTGGGTGTGATTT	301559	133755	AGAGTAATAACTTTATTTCC
212386	44582	AAACCCCATCTCTACAAAAA	256973	89169	TCTGCACGTTGGGTGTGATT	301560	133756	CAGAGTAATAACTTTATTTC
212387	44583	AAAACCCCATCTCTACAAAA	256974	89170	TTCTGCACGTTGGGTGTGAT	301561	133757	TCAGAGTAATAACTTTATTT
212388	44584	TAAAACCCCATCTCTACAAA	256975	89171	CTTCTGCACGTTGGGTGTGA	301562	133758	ATCAGAGTAATAACTTTATT
212389	44585	GTAAAACCCCATCTCTACAA	256976	89172	CCTTCTGCACGTTGGGTGTG	301563	133759	AATCAGAGTAATAACTTTAT
212390	44586	GGTAAAACCCCATCTCTACA	256977	89173	TCCTTCTGCACGTTGGGTGT	301564	133760	TAATCAGAGTAATAACTTTA
212391	44587	TGGTAAAACCCCATCTCTAC	256978	89174	CTCCTTCTGCACGTTGGGTG	301565	133761	TTAATCAGAGTAATAACTTT
						301566	133762	TTTAATCAGAGTAATAACTT

CLAIMS

WHAT IS CLAIMED IS:

1. A compound comprising a gapmer oligonucleotide, and wherein the gapmer oligonucleotide comprises a spacer.

2. A gapmer oligonucleotide, wherein the gapmer oligonucleotide comprises a spacer.

3. The compound or gapmer oligonucleotide of claim 1 or 2, wherein the gapmer oligonucleotide comprises a second spacer that is non-adjacent to the spacer.

4. The compound or gapmer oligonucleotide of any one of claims 1-3, wherein the gapmer oligonucleotide comprises a sequence that is between 85 and 98% complementary to an equal length portion of a transcript whose presence leads to a neurological disease.

5. The compound or gapmer oligonucleotide of any one of claims 1-3, wherein the gapmer oligonucleotide comprises a sequence that is between 85 and 98% complementary to an equal length portion of a PPM1A mRNA or pre-mRNA transcript, an ATXN2 mRNA or pre-mRNA transcript, a SOD1 mRNA or pre-mRNA transcript, or a MAPT mRNA or pre-mRNA transcript.

6. The compound or gapmer oligonucleotide of any one of claims 1-5, wherein the gapmer oligonucleotide comprises a sequence that is between 85 and 98% complementary to an equal length portion of any one of SEQ ID NOs: 1909-1913, 149355-149361, 167802-167804, or 301567-301589, a sequence having 90% identity thereof, or to a 15 to 50 contiguous nucleobase portion thereof.

7. The compound or gapmer oligonucleotide of any one of claims 1-6, wherein the gapmer oligonucleotide comprises a sequence that shares at least 85% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

8. The compound or gapmer oligonucleotide of any one of claims 1-7, wherein the gapmer oligonucleotide comprises a sequence that shares at least 90% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

9. The compound or gapmer oligonucleotide of any one of claims 1-7, wherein the gapmer oligonucleotide comprises a sequence that shares at least 95% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

10. The compound or gapmer oligonucleotide of any one of claims 1-8, wherein the gapmer oligonucleotide comprises a sequence that shares at least 100% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

11. The compound or gapmer oligonucleotide of any one of claims 1-9, wherein the gapmer oligonucleotide comprises a segment with at most 11 linked nucleosides, and wherein the gapmer oligonucleotide comprises a sequence that shares at least 85% identity with an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

12. The compound or gapmer oligonucleotide of any one of claims 1-10, wherein the gapmer oligonucleotide comprises a segment with at most 10, 9, 8, 7, 6, 5, 4, 3, or 2 linked nucleosides, and wherein the gapmer oligonucleotide comprises a sequence that shares at least 85% identity with an equal length portion of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

13. The compound or gapmer oligonucleotide of any one of claims 1-10, wherein the gapmer oligonucleotide comprises a segment with at most 11 linked nucleosides, and wherein the gapmer oligonucleotide comprises a sequence that shares at least 90% identity with an equal length portion of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C.

14. The compound or gapmer oligonucleotide of any one of claims 1-10, wherein the gapmer oligonucleotide comprises a segment with at most 10, 9, 8, 7, 6, 5, 4, 3, or 2 linked nucleosides, and wherein the gapmer oligonucleotide comprises a sequence that shares at least 90% identity with an equal length portion of any one of SEQ ID NOs: 301610-301741.

15. The compound or gapmer oligonucleotide of any one of claims 1-14, wherein the gapmer oligonucleotide is at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, or at least 25 oligonucleotide units in length.

16. The compound or gapmer oligonucleotide of any one of claims 1-15, wherein at least one (*i.e.*, one or more) nucleoside linkage of the gapmer oligonucleotide is a non-natural linkage,

17. The compound or gapmer oligonucleotide of any one of claims 1-16, wherein the gapmer oligonucleotide is at least 19 oligonucleotide units in length.

18. The compound of oligonucleoide of any one of claims 1-17, wherein the spacer is a nucleoside-replacement group comprising a non-sugar substitute that is incapable of linking to a nucleotide base.

19. The compound or gapmer oligonucleotide of claim 18, wherein the spacer is located between positions 5 and 11 of the gapmer oligonucleotide.

20. The compound or gapmer oligonucleotide of claim 18, wherein the spacer is located between positions 7 and 11 of the gapmer oligonucleotide.

21. The compound or gapmer oligonucleotide of claim 18, wherein the gapmer oligonucleotide further comprises a second spacer, and wherein the spacer and the second spacer are non-adjacent to one another.

22. The compound or gapmer oligonucleotide of claim 21, wherein the gapmer oligonucleotide further comprises a second spacer, wherein the second spacer is located between positions 15 and 19 of the gapmer oligonucleotide.

23. The compound or gapmer oligonucleotide of claim 22, wherein the spacer and the second spacer are separated by at least 5 nucleobases, at least 6 nucleobases, or at least 7 nucleobases in the gapmer oligonucleotide.

24. The compound or gapmer oligonucleotide of claim 22 or 23, wherein the spacer is located between positions 5 and 11 of the gapmer oligonucleotide, and wherein the second spacer is located between positions 15 and 19 of the gapmer oligonucleotide.

25. The compound or gapmer oligonucleotide of any one of claims 22-24, wherein the spacer is located at position 8 of the gapmer oligonucleotide, and wherein the second spacer is located at position 16 of the gapmer oligonucleotide.

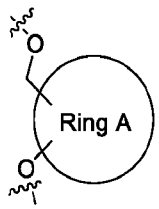
26. The compound or gapmer oligonucleotide of any one of claims 22-24, wherein the spacer is located at position 5 of the gapmer oligonucleotide, and wherein the second spacer is located at position 17 of the gapmer oligonucleotide.

27. The compound or gapmer oligonucleotide of any one of claims 22-24, wherein the spacer is located at position 7 of the gapmer oligonucleotide, and wherein the second spacer is located at position 15 of the gapmer oligonucleotide.

28. The compound or gapmer oligonucleotide of any one of claims 22-24, wherein the spacer is located at position 11 of the gapmer oligonucleotide, and wherein the second spacer is located at position 19 of the gapmer oligonucleotide.

29. The compound or gapmer oligonucleotide of any one of claims 18-28, wherein each of the spacer or second spacer is a nucleoside-replacement group comprising a non-sugar substitute wherein the non-sugar substitute does not contain a ketone, aldehyde, ketal, hemiketal, acetal, hemiacetal, aminal or hemiaminal moiety and is incapable of forming a covalent bond with a nucleotide base.

30. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer or second spacer is independently represented by Formula (X), wherein:

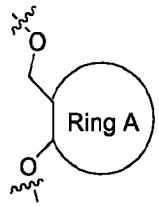


Formula (X)

Ring A is an optionally substituted 4-8 member monocyclic cycloalkyl group or a 4-8 member monocyclic heterocyclyl group, wherein the heterocyclyl group contains 1 or 2 heteroatoms selected from O, S and N, provided that A is not capable of forming a covalent bond to a nucleobase; and

the  symbol represents the point of connection to an internucleoside linkage.

31. The compound or gapmer oligonucleotide of claim 30, wherein each of the spacer or second spacer is independently represented by Formula (Xa), wherein:



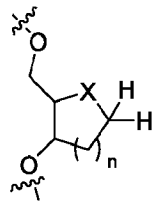
Formula (Xa).

32. The compound or nucleotide of claim 30 or 31, wherein ring A is an optionally substituted 4-8 member monocyclic cycloalkyl group selected from cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and cyclooctyl; or a 4-8 member monocyclic heterocyclyl group, selected from oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, 1,4-dioxanyl, pyrrolidinyl, piperidinyl, piperazinyl, morpholinyl and azepanyl.

33. The compound or nucleotide of claim 32 wherein ring A is tetrahydrofuranyl.

34. The compound or nucleotide of claim 32 wherein ring A is tetrahydropyranyl.

35. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula I, wherein:

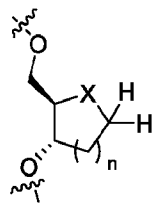


Formula (I)

X is selected from -CH_2- and -O-; and

n is 0, 1, 2 or 3.

36. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula I', wherein:

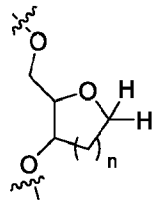


Formula (I')

X is selected from -CH_2- and -O-; and

n is 0, 1, 2 or 3.

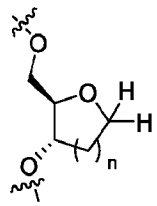
37. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula (Ia), wherein:



Formula (Ia); and

n is 0, 1, 2 or 3.

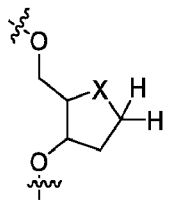
38. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula (Ia'), wherein:



Formula (Ia'); and

n is 0, 1, 2 or 3.

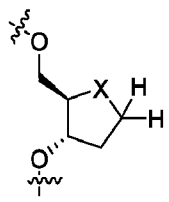
39. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula II, wherein:



Formula (II); and

X is selected from -CH_2- and -O-.

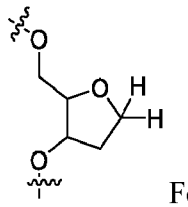
40. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula II', wherein:



Formula (II'); and

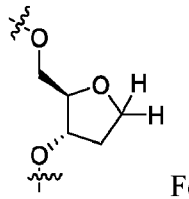
X is selected from -CH_2- and -O-.

41. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula (Iia), wherein:



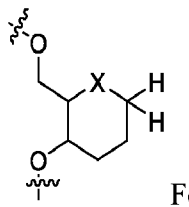
Formula (Iia).

42. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula (Iia'), wherein:



Formula (Iia').

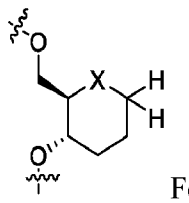
43. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently is independently represented by Formula III, wherein:



Formula (III); and

X is selected from -CH_2- and -O-.

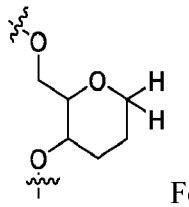
44. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula III', wherein:



Formula (III'); and

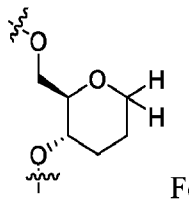
X is selected from -CH_2- and -O-.

45. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula (IIIa), wherein:



Formula (IIIa).

46. The compound or gapmer oligonucleotide of any one of claims 18-29, wherein each of the spacer and second spacer is independently represented by Formula (IIIa'), wherein:



Formula (IIIa').

47. The compound or gapmer oligonucleotide of any one of the above claims, wherein the gapmer oligonucleotide comprising the spacer has a GC content of at least 10%.

48. The compound or gapmer oligonucleotide of any one of the above claims, wherein the gapmer oligonucleotide comprising the spacer has a GC content of at least 20%.

49. The compound or gapmer oligonucleotide of any one of the above claims, wherein the gapmer oligonucleotide comprising the spacer has a GC content of at least 25%.

50. The compound or gapmer oligonucleotide of any one of the above claims, wherein the gapmer oligonucleotide comprising the spacer has a GC content of at least 30%.

51. The compound or gapmer oligonucleotide of any one of the above claims, wherein the gapmer oligonucleotide comprising the spacer has a GC content of at least 40%.

52. The compound or gapmer oligonucleotide of any one of the above claims, wherein the gapmer oligonucleotide comprising the spacer has a GC content of at least 50%.

53. The compound or gapmer oligonucleotide of any one of the above claims, wherein at least one (*i.e.*, one or more) nucleoside linkage of the gapmer oligonucleotide is independently selected from the group consisting of a phosphodiester linkage, a phosphorothioate linkage, an alkyl phosphate linkage, a phosphorodithioate linkage, a phosphotriester linkage, an alkylphosphonate

linkage, a 3-methoxypropyl phosphonate linkage, a methylphosphonate linkage, an aminoalkylphosphotriester linkage, an alkylene phosphonate linkage, a phosphinate linkage, a phosphoramidate linkage, a phosphoramidothioate linkage, a thiophosphorodiamidate linkage, a phosphorodiamidate linkage, an aminoalkylphosphoramidate linkage, a thiophosphoramidate linkage, a thionoalkylphosphonate linkage, a thionoalkylphosphotriester linkage, a thiophosphate linkage, a selenophosphate linkage, and a boranophosphate linkage.

54. The gapmer oligonucleotide of any one of the preceding claims, wherein at least one internucleoside linkage of the nucleotide sequence is a phosphorothioate linkage.

55. The gapmer oligonucleotide of claim 54, wherein the phosphorothioate internucleoside linkage is in one of a *R*p configuration or a *S*p configuration.

56. The gapmer oligonucleotide of any one of claims 1-55, wherein the gapmer oligonucleotide comprises one or more chiral centers and/or double bonds.

57. The gapmer oligonucleotide of claim 55, wherein the gapmer oligonucleotide exists as stereoisomers selected from geometric isomers, enantiomers, and diastereomers.

58. The gapmer oligonucleotide of any one of the preceding claims, wherein all internucleoside linkages of the nucleotide sequence are phosphorothioate linkages.

59. The gapmer oligonucleotide of any one of the preceding claims, wherein the gapmer oligonucleotide comprises at least one modified nucleobase.

60. The gapmer oligonucleotide of claim 59, wherein the at least one modified nucleobase is 5-methylcytosine, pseudouridine, or 5-methoxyuridine.

61. The gapmer oligonucleotide of any one of the preceding claims, wherein the gapmer oligonucleotide comprises at least one nucleoside with a modified sugar moiety.

62. The gapmer oligonucleotide of claim 61, wherein the modified sugar moiety is one of a 2'-OMe modified sugar moiety, bicyclic sugar moiety, 2'-*O*-(2-methoxyethyl) (2'-MOE), 2'-O-(N-methylacetamide), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt), *S*-cEt, hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA).

63. The gapmer oligonucleotide of any one of the preceding claims, wherein the gapmer oligonucleotide comprises two, three, four, five, six, seven, eight, nine, or ten nucleosides with modified sugar moieties.

64. The gapmer oligonucleotide of claim 63, wherein the modified sugar moieties are independently any one of a 2'-OMe modified sugar moiety, bicyclic sugar moiety, 2'-*O*-(2-methoxyethyl) (2'-MOE), 2'-O-(N-methylacetamide), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt), *S*-cEt, hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA).

65. The gapmer oligonucleotide of any one of the preceding claims, wherein the gapmer oligonucleotide comprises ten 2'-*O*-(2-methoxyethyl) (2'-MOE) nucleosides.

66. The gapmer oligonucleotide of claim 65, wherein five of the 2'-*O*-(2-methoxyethyl) (2'-MOE) nucleosides are located at the 3' end of the gapmer oligonucleotide, and wherein five of the 2'-*O*-(2-methoxyethyl) (2'-MOE) nucleosides are located at the 5' end of the gapmer oligonucleotide.

67. The gapmer oligonucleotide of claim 65, wherein the modified sugar moieities are locked nucleic acids (LNAs), and wherein two or more of the nucleosides of the 3' wing region of the gapmer oligonucleotide are LNAs, and wherein two or more of the nucleosides of the 5' wing region of the gapmer oligonucleotide.

68. The gapmer oligonucleotide of any one of claims 61-66, wherein the at least one nucleoside with the modified sugar moiety or the nucleosides with modified sugar moieties are ribonucleosides.

69. The gapmer oligonucleotide of any one of the preceding claims, wherein the gapmer oligonucleotide comprises at least one deoxyribonucleoside.

70. The gapmer oligonucleotide of any one of the preceding claims, wherein the gapmer oligonucleotide comprises two, three, four, five, six, seven, eight, nine, or ten deoxyribonucleosides.

71. The gapmer oligonucleotide of any one of claims 1-53, wherein the gapmer oligonucleotide comprises:

a gap segment comprising one or more of linked deoxyribonucleosides, 2'-Fluoro Arabino Nucleic Acids (FANA), and Fluoro Cyclohexenyl nucleic acid (F-CeNA);

a 5' wing region comprising linked nucleosides; and

a 3' wing region comprising linked nucleosides;

wherein the central region comprises a region of at least 8 oligonucleotide units comprising at least 4 contiguous nucleobases, the region having at least 80% identity to an equal length portion of any one of SEQ ID NOs: 1-954, 1914-149354, 149362-158581, 167805-301566, SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C positioned between the 5' wing segment and the 3' wing segment; wherein the 5' wing region and the 3' wing region each comprises at least two linked nucleosides; and wherein at least one nucleoside of each wing region comprises a modified sugar.

72. The gapmer oligonucleotide of claim 71, wherein the at least two linked nucleosides of the 5' wing region are linked through a phosphorothioate internucleoside linkage and/or wherein the at least two linked nucleosides of the 3' wing region are independently linked through a phosphorothioate internucleoside linkage.

73. The gapmer oligonucleotide of claim 71 or 72, wherein every internucleoside linkage of the 5' wing region and/or every internucleoside linkage of the 3' wing region, independently are phosphorothioate internucleoside linkages.

74. The gapmer oligonucleotide of claim 71 or 72, wherein the 5' wing region further comprises at least one phosphodiester internucleoside linkage.

75. The gapmer oligonucleotide of claim 71 or 72, wherein the 3' wing region further comprises at least one phosphodiester internucleoside linkage.

76. The gapmer oligonucleotide of claim 71, wherein the at least two linked nucleosides of the 5' wing region are linked through a phosphodiester internucleoside linkage and/or wherein the at least two linked nucleosides of the 3' wing region are independently linked through a phosphodiester internucleoside linkage.

77. The gapmer oligonucleotide of any one of claims 71-76, wherein at least one of the internucleoside linkages of the central region is a phosphodiester linkage.

78. The gapmer oligonucleotide of claim 77, wherein at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, or at least nine of the internucleoside linkages of the central region are phosphodiester linkages.

79. The gapmer oligonucleotide of any one of claims 71-76, wherein at least one of the internucleoside linkages of the central region is a phosphorothioate internucleoside linkage.

80. The gapmer oligonucleotide of claim 79, wherein at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, or at least nine of the internucleoside linkages of the central region are phosphorothioate internucleoside linkages.

81. The gapmer oligonucleotide of any one of claims 71-72 or 79-80, wherein all internucleoside linkages of the gapmer oligonucleotide are phosphorothioate internucleoside linkages.

82. The gapmer oligonucleotide of any one of claims 71-81, wherein any one or all of the phosphorothioate internucleoside linkages are in a *R*p configuration, a *S*p configuration, or in any combination of *R*p and *S*p configuration.

83. The gapmer oligonucleotide of any one of claims 71-82, wherein the gapmer oligonucleotide comprises at least one modified sugar moiety.

84. The gapmer oligonucleotide of claim 83, wherein the 5' wing region or the 3' wing region comprises the at least one modified sugar moiety.

85. The gapmer oligonucleotide of claim 83, wherein the central region comprises the at least one modified sugar moiety.

86. The gapmer oligonucleotide of any one of claims 83-85, wherein the at least one modified sugar moiety is any one of a 2'-OMe modified sugar moiety, bicyclic sugar moiety, 2'-O-(2-methoxyethyl) (2'-MOE), 2'-O-(N-methylacetamide), 2'-deoxy-2'-fluoro nucleoside, 2'-fluoro-β-D-arabinonucleoside, locked nucleic acid (LNA), constrained ethyl 2'-4'-bridged nucleic acid (cEt), *S*-cEt, tcDNA, hexitol nucleic acids (HNA), and tricyclic analog (*e.g.*, tcDNA).

87. The gapmer oligonucleotide of any one of claims 83-86 wherein the gapmer oligonucleotide comprises one or more 2'-MOE nucleosides.

88. The gapmer oligonucleotide of claim 87, wherein the 5' wing region or the 3' wing region comprise one or more 2'-MOE nucleosides.

89. The gapmer oligonucleotide of claim 87 or 88, wherein the 5' wing region or the 3' wing region comprise two, three, four, five, or six 2'-MOE nucleosides.

90. The gapmer oligonucleotide of claim 89, wherein every nucleoside of the 5' wing region or the 3' wing region is a 2'-MOE nucleoside.

91. The gapmer oligonucleotide of claim 87, wherein the central region comprises one or more 2'-MOE nucleosides.

92. The gapmer oligonucleotide of claim 91, wherein the central region comprises two, three, four, five, six, seven, eight, nine, or ten 2'-MOE nucleosides.

93. The gapmer oligonucleotide of claim 92, wherein every nucleoside of the central region is a 2'- MOE nucleoside.

94. The gapmer oligonucleotide of any one of claims 87-93, wherein the one or more 2'-MOE nucleosides are linked through phosphorothioate internucleoside linkages.

95. The gapmer oligonucleotide of claim 71, wherein the gapmer oligonucleotide comprises sugar modifications in any of the following patterns: eeeee-d10-eeeee, eeeee-d8-eeeee, eeeeee-d11-eeeeee, eee-d8-eee, eee-d10-eee, eeee-d10-eeee, eeeeee-d10-eeee, and eeee-d8-eeee, wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside, and wherein at least one "e" or at least one "d" is replaced with a spacer.

96. The gapmer oligonucleotide of claim 95, wherein the gapmer oligonucleotide comprises internucleoside linkages in any of the following patterns: sssssoooooooossssss; ooooossssssssssooooo; oooooooooooooossssss; soossssssssssssssss; sososssssssssssosos; sssssssssssssssoos; sssssooooooooooooo; sssssssssssssssssss; sssssssssssssssssssss; sssoooooooosss; ooosssssssooo; sssssssssssss; sossssssssssos; sossssssssssss; sssssssssssos; sssssssssssooo; ooosssssssssss; sssooooooooosss; ooosssssssssooo; sssssssssssssss; sssssssssssooo; ooosssssssssssss; sossssssssssssos; sossssssssssssss; sssssssssssssos; sssssooooooooosss; ooooossssssssssooooo; sssssssssssssssss; sssssssssssssooooo; soossssssssssssoos; soossssssssssssss; sssssssssssssssoos; ooooossssssssssss; sssssooooooosss; ooooossssssooooo; sssssssssssooooo; ooooossssssssssss; soossssssssssoos; soossssssssssss; sssssssssssssoos; soooossssssssssoooos; soooossssssssssssooss; sossssssssssssssoss; sossssssssssssssosss; or sssssssssssssss; wherein s= a phosphorothioate linkage, and o= a phosphodiester linkage.

97. The gapmer oligonucleotide of claim 95 or 96, wherein the gapmer oligonucleotide comprises sugar modification and internucleoside linkage combinations, respectively, in any of the following patterns:

a) eeeee-d10-eeeee and sssssooooooooosssss;

b) eeeee-d10-eeeee and ooooossssssssssooooo;

c) eeeee-d10-eeeee and sssssssssssssssssss;

d) eee-d8-eee and sssooooooosss;

e) eee-d8-eee and ooosssssssooo

f) eee-d8-eee and sssssssssssss;

g) eee-d10-eee and sssooooooooosss;

h) eee-d10-eee and ooosssssssssooo;

i) eee-d10-eee and sssssssssssssss;

j) eeee-d10-eeee and ssssoooooooossss;

k) eeee-d10-eeee and oooossssssssoooo;

l) eeee-d10-eeee and sssssssssssssss;

m) eeee-d8-eeee and ssssooooooossss,

n) eeee-d8-eeee and oooossssssoooo,

o) eeee-d8-eeee and sssssssssssss,

p) eeeeee-d11-eeeeee and sssssssssssssssssssss;

q) eeeee-d10-eeeee and sosossssssssssosos;

r) eeeee-d10-eeeee and soooossssssssssooos;

s) eeeee-d10-eeeee and soooossssssssssooss;

t) eeeee-d8-eeeee and sossssssssssssoss;

u) eeeee-d10-eeeee and sossssssssssssosss;

v) eeeeee-d10-eeee and sssssssssssssssss;

wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside, and wherein s= a phosphorothioate linkage, and o= a phosphodiester linkage, and wherein at least one "e" or at least one "d" of the gapmer oligonucleotide is replaced with a spacer.

98. The gapmer oligonucleotide of any one of claims 71-97, wherein the gapmer oligonucleotide comprises at least one modified nucleobase.

99. The gapmer oligonucleotide of claim 98, wherein the 5' wing region or the 3' wing region comprises the at least one modified nucleobase.

100. The gapmer oligonucleotide of claim 98, wherein the central region comprises the at least one modified nucleobase.

101. The gapmer oligonucleotide of any one of claims 98-100, wherein the at least one modified nucleobase is 5-methylcytosine, pseudouridine, or 5-methoxyuridine.

102. The gapmer oligonucleotide of any one of claims 98-101, wherein every cytosine in the 5' wing region or the 3' wing region is a 5-methylcytosine.

103. The gapmer oligonucleotide of any one of claims 98-102, wherein every cytosine in the central region is a 5-methylcytosine.

104. The gapmer oligonucleotide of claim 71, wherein the gapmer oligonucleotide comprises sugar modification and internucleoside linkage combination of: eeeee-d10-eeeee and

sssssssssssssssss, wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside, wherein s= a phosphorothioate linkage, wherein at least one "e" or at least one "d" of the gapmer oligonucleotide is replaced with a spacer, and wherein each cytosine of the 2'-MOE nucleosides is a 5-methylcytosine.

105. The gapmer oligonucleotide of any one of the preceding claims, wherein the gapmer oligonucleotide further comprises a conjugate moiety.

106. The gapmer oligonucleotide of claim 105, wherein the conjugate moiety is a cholesterol conjugate located on the 3' end of the gapmer oligonucleotide.

107. A pharmaceutical composition comprising the gapmer oligonucleotide of any one of claims 1-106, or a pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable excipient.

108. A method of treating a neurological disease in a patient in need thereof, the method comprising administering to the patient a gapmer oligonucleotide of any one of claims 1-106 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107.

109. The method of claim 108, wherein the neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Limbic-predominant age-related TDP-43 encephalopathy (LATE)), Cerebral Age-Related TDP-43 With Sclerosis (CARTS), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and synaptic diseases like autism.

110. The method of claim 108-109, wherein the gapmer oligonucleotide is administered topically, parenterally, intrathecally, orally, pulmonarily, intratracheally, intranasally,

transdermally, buccally, intrathalamically, intracerebroventricularly, intraocularly, sublingually, rectally, vaginally, or intraduodenally.

111. The method of claim 110, wherein the gapmer oligonucleotide is administered intrathecally.

112. The method of any one of claims 108-111, wherein a therapeutically effective amount of the gapmer oligonucleotide is administered.

113. The method of any one of claims 108-112, wherein the patient is a human.

114. The pharmaceutical composition of claim 107, wherein the pharmaceutical composition is suitable for topical, parenteral, intrathecal, oral, pulmonary, intratracheal, intranasal, transdermal, buccal, intrathalamical, intracerebroventricular, intraocular, sublingual, rectal, vaginal, or intraduodenal.

115. Use of a gapmer oligonucleotide in the manufacture of a medicament for the treatment of neurological disease.

116. The use of claim 115, wherein the neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Limbic-predominant age-related TDP-43 encephalopathy (LATE)), Cerebral Age-Related TDP-43 With Sclerosis (CARTS), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and synaptic diseases like autism.

117. The use of claim 115 or 116, wherein the gapmer oligonucleotide is the gapmer oligonucleotide of any one of claims 1-106.

118. A method of treating a neurological disease in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a

pharmaceutical composition comprising a gapmer oligonucleotide, and a pharmaceutically acceptable excipient.

119. The method of claim 118, wherein the neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Limbic-predominant age-related TDP-43 encephalopathy (LATE)), Cerebral Age-Related TDP-43 With Sclerosis (CARTS), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and synaptic diseases like autism.

120. The method of claim 118 or 119, wherein the gapmer oligonucleotide is the gapmer oligonucleotide of any one of claims 1-106, a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107.

121. The method of any one of claims 118-120, wherein the pharmaceutical composition is administered topically, parenterally, orally, pulmonarily, rectally, buccally, sublingually, vaginally, intratracheally, intranasally, intrathecally, intracisternally, transdermally, or intraduodenally.

122. The method of any one of claims 118-121, wherein the pharmaceutical composition is administered intrathecally.

123. The method of any one of claims 118-122, wherein the patient is human.

124. A gapmer oligonucleotide of any one of claims 1-106, or a pharmaceutically acceptable salt thereof, for use as a medicament.

125. A gapmer oligonucleotide of any one of claims 1-106, or a pharmaceutically acceptable salt thereof, for use in the treatment of a neurological disease.

126. The gapmer oligonucleotide for use of claim 124 or 125, wherein said neurological disease is selected from the group consisting of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), ALS with FTD, Alzheimer's disease (AD), Parkinson's disease (PD), Parkinson's Disease with dementia, dementia with lewy bodies, synucleinopathies, Huntington's disease, Brachial plexus injuries, peripheral nerve injuries, progressive supranuclear palsy (PSP), brain trauma, spinal cord injury, tuberous sclerosis complex, Pick's Disease, tauopathies, primary age-related tauopathy, Down Syndrome, epilepsy/seizure disorder, depression, traumatic brain injury (TBI), chronic traumatic encephalopathy (CTE), HIV-associated neurocognitive disorders (HAND), multisystem atrophy, amnestic mild cognitive impairment, corticobasal degeneration (CBD) and/or neuropathies such a chemotherapy induced neuropathy, Spinocerebellar ataxia (SCA), SCA type 2, Spinal Muscular Atrophy (SMA), Parkinsonism, Niemann-Pick disease type C (NPC), Charcot-Marie-Tooth Disease (CMT), Mucopolysaccharidosis type II (MPSIIA), Mucolipidosis IV, GM1 gangliosidosis, Sporadic inclusion body myositis (sIBM), Henoch-Schonlein purpura (HSP), Gaucher's disease, and facial onset sensory and motor neuronopathy, Guam Parkinson-dementia complex, multisystem proteinopathy, Perry disease, and autism.

127. A gapmer oligonucleotide comprising the sequence of any one of SEQ ID NOs: 301692-301742 or the sequences in Tables 4A-4C, or a pharmaceutically acceptable salt thereof;

wherein the gapmer oligonucleotide further comprises:

a gap segment comprising one or more of linked deoxyribonucleosides, 2'-Fluoro Arabino Nucleic Acids (FANA), and Fluoro Cyclohexenyl nucleic acid (F-CeNA);

a 5' wing region comprising linked nucleosides; and

a 3' wing region comprising linked nucleosides;

wherein the gapmer oligonucleotide comprises sugar modifications of eeeee-d10-eeeee, wherein e = 2'-MOE nucleoside and d = a deoxyribonucleoside, wherein at least one "e" or at least one "d" is replaced with a spacer,

and wherein each cytosine of the 2'-MOE nucleosides is a 5-methylcytosine.

128. The gapmer oligonucleotide of claim 127, wherein at least one internucleoside linkage of the gapmer oligonucleotide is a phosphorothioate linkage.

129. The gapmer oligonucleotide of claim 128, wherein the phosphorothioate internucleoside linkage is in one of a *Rp* configuration or a *Sp* configuration.

130. The gapmer oligonucleotide of claim 127 or 128, wherein all internucleoside linkages of the gapmer oligonucleotide are phosphorothioate linkages.

131. The gapmer oligonucleotide of claim 127 or 128, wherein the gapmer oligonucleotide comprises sugar modification and internucleoside linkage combinations, respectively, in any of the following patterns:

a) eeeee-d10-eeeee and sssssooooooooosssss;

b) eeeee-d10-eeeee and ooooosssssssssooooo;

c) eeeee-d10-eeeee and sssssssssssssssssss;

d) eee-d8-eee and sssooooooosss;

e) eee-d8-eee and ooosssssssooo

f) eee-d8-eee and sssssssssssss;

g) eee-d10-eee and sssooooooooosss;

h) eee-d10-eee and ooosssssssssooo;

i) eee-d10-eee and sssssssssssssss;

j) eeee-d10-eeee and ssssooooooooosssss;

k) eeee-d10-eeee and ooooosssssssssoooo;

l) eeee-d10-eeee and sssssssssssssssss;

m) eeee-d8-eeee and ssssooooooosssss,

n) eeee-d8-eeee and ooooosssssssoooo,

o) eeee-d8-eeee and sssssssssssssss,

p) eeeeee-d11-eeeeee and sssssssssssssssssssss;

q) eeeee-d10-eeeee and sososssssssssssosos;

r) eeeee-d10-eeeee and soooosssssssssssoos;

s) eeeee-d10-eeeee and soooosssssssssssooss;

t) eeeee-d8-eeeee and sosssssssssssoss;

u) eeeee-d10-eeeee and sosssssssssssssosss;

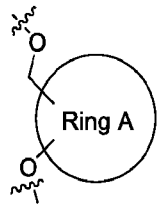
v) eeeeee-d10-eeee and sssssssssssssssssss;

wherein at least one "e" or at least one "d" of the gapmer oligonucleotide is replaced with a spacer.

132. A pharmaceutical composition comprising the antisense gapmer oligonucleotide of any one of claims 126-131, or a pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable excipient.

133. The gapmer oligonucleotide of any one of claims 127-131, wherein the spacer is a nucleoside-replacement group comprising a non-sugar substitute wherein the non-sugar substitute does not contain a ketone, aldehyde, ketal, hemiketal, acetal, hemiacetal, aminal or hemiaminal moiety and is incapable of forming a covalent bond with a nucleotide base.

134. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (X), wherein:

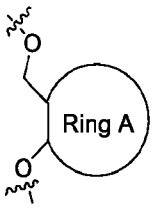


Formula (X)

Ring A is is an optionally substituted 4-8 member monocyclic cycloalkyl group or a 4-8 member monocyclic heterocyclyl group, wherein the heterocyclyl group contains 1 or 2 heteroatoms selected from O, S and N, provided that A is not capable of forming a covalent bond to a nucleobase; and

the  symbol represents the point of connection to an internucleoside linkage.

135. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (Xa), wherein:



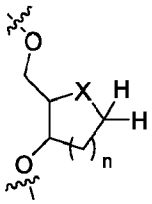
Formula (Xa).

136. The gapmer oligonucleotide of claim 134 or 135, wherein ring A is an optionally substituted 4-8 member monocyclic cycloalkyl group selected from cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and cyclooctyl; or a 4-8 member monocyclic heterocyclyl group, selected from oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, 1,4-dioxanyl, pyrolidinyl, piperidinyl, piperazinyl, morpholinyl and azepanyl.

137. The method of claim 136, wherein ring A is tetrahydrofuranyl.

138. The method of claim 136, wherein ring A is tetrahydropyranyl.

139. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (I), wherein:

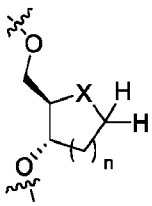


Formula (I)

X is selected from -CH_2- and -O-; and

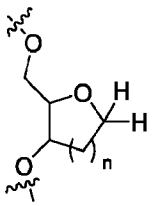
n is 0, 1, 2 or 3.

140. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (I'), wherein:



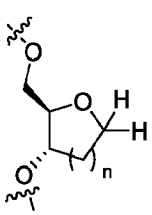
Formula (I').

141. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (Ia), wherein:



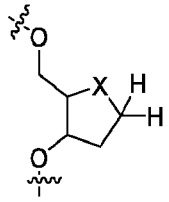
Formula (Ia).

142. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (Ia'), wherein:



Formula (Ia').

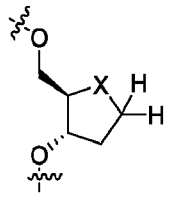
143. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula II, wherein:



Formula (II); and

X is selected from -CH_2- and -O-.

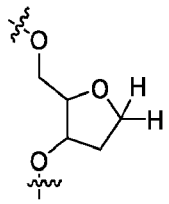
144. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula II', wherein:



Formula (II'); and

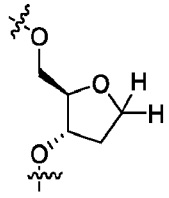
X is selected from -CH_2- and -O-.

145. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (IIa), wherein:



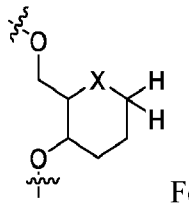
Formula (IIa).

146. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (Iia'), wherein:



Formula (Iia').

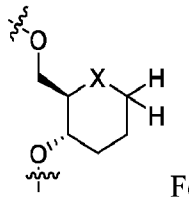
147. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula III, wherein:



Formula (III); and

X is selected from -CH_2- and -O-.

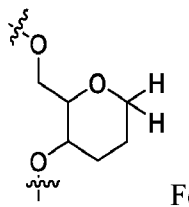
148. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula III', wherein:



Formula (III'); and

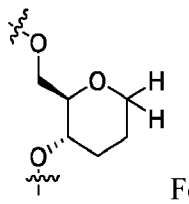
X is selected from -CH_2- and -O-.

149. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (IIIa), wherein:



Formula (IIIa).

150. The gapmer oligonucleotide of claim 133, wherein the spacer is represented by Formula (IIIa'), wherein:



Formula (IIIa').

151. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-150 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in

combination with a second therapeutic agent selected from a group comprising Riluzole (Rilutek), troriluzole, Edaravone (Radicava), rivastigmine, donepezil, QRL-101, QRL-201, galantamine, selective serotonin reuptake inhibitor, antipsychotic agents, cholinesterase inhibitors, memantine, benzodiazepine antianxiety drugs, AMX0035 (ELYBRIO®), ZILUCOPLAN (RA101495), dual AON intrathecal administration (*e.g.*, BIIB067, BIIB078), BIIB100, levodopa/carbidopa, dopaminergic agents (*e.g.*, ropinirole, pramipexole, rotigotine), medroxyprogesterone, KCNQ2/KCNQ3 openers, Pridopidine, PrimeC (combination of ciprofloxacin and Celebrex), olanzapine (Zyprexa), quetiapine (Seroquel), SSRIs, divalproex sodium (Depakote), carbamazepine (Tegretol), medroxyprogestrone, lithium, anticonvulsants and psychostimulant agents, breathing care, physical therapy, occupational therapy, speech therapy, nutritional support, or any combination thereof.

152. The method of claim 151, wherein the neurological disease is any one of amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), or ALS with FTD.

153. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising Memantine, Rivastigmine, Galantamine, Donepezil, QRL-101, QRL-201, Aricept®, Exelon® (Rivastigmine), Razadyne®, Aducanumab, BAN2401, BIIB091 (gosuranemab), BIIB076, BIIB080 (IONIS-MAPTRx), Elayta (CT1812), MK1942, allogenic hMSC, nilotinib, ABT-957, acitretin, ABT-354, GV1001, Riluzole, CAD106, CNP520, AD-35, Rilapladib, DHP1401, T-817 MA, TC-5619, TPI-287, RVT-101, LY450139, JNJ-54861911, Dapagliflozin, GSK239512, PF-04360365, ASP0777, SB-742457 (a 5-HT6 receptor antagonist), PF-03654746 (an H_3 receptor antagonist), GSK933776 (an Fc-inactivated anti-β amyloid (Aβ) monoclonal antibody (mAb)), Posiphen ((+)-phenserine tartrate), AMX0035 (ELYBRIO®), coenzyme Q10, aducanamab (ADUHLEM), memantine (NAMENDA), Namzeric, Suvorexant (belsomra), lecanemab, or any combination thereof.

154. The method of claim 153, wherein the neurological disease is Alzheimer's Disease.

155. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising Levodopa, Carbidopa-levidopa, pramipexole (MIRAPEX), ropinirole (REQUIP), rotigotine (NEUPRO),

apomorphine (APOKYN, KYNMOBI), selegiline (EDLEPRYL, ZELAPAR), rasagiline, entacapone (COMTAN), tolcapone (TASMAR), amantadine (GOCOVRI, SYMMETREL, OSMOLEX), trihexyphenidyl (ARTANE), BIIB054 (cinepanemab), BIIB094, BIIB118, ABBV-0805, zonisamide, deep brain stimulation, brain-derived neurotrophic factor, stem-cell transplant, Niacin, brain stem stimulation, nicotine, nabilone, PF-06649751, DNL201, LRRK2 inhibitors, CK1 inhibitors, isradipine, CLR4001, IRX4204, Yohimbine, coenzyme Q10, OXB-102, duloxetine, pioglitazone, preladenant, istradefylline (NOURIANZ), safinamide (XADAGO), benztropine (COGENTIN), opicapone (ongentys), exenatide, lingzhi, Caffeine, sarizotan, embryonic dopamine cell implantation, or any combination thereof.

156. The method of claim 155 wherein the neurological disease is Parkinson's Disease.

157. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising UCB0107, ABBV-8E12, F-18 AV1451, BIIB092, C2N-8E12, tideglusib, deep transcranial magnetic stimulation, lipoic acid, tolfenamica acid, lithium, AZP2006, Glial Clell Line-Derived Neurotrophic Factor, NBMI, suvorxant, zolpidem, TPI 287, davunetide, pimavanserin, Levodopa, Carbidopa-levidopa, pramipexole, ropinirole, rotigotine, apomorphine, selegiline, rasagiline, entacapone, tolcapone, amantadine, trihexyphenidyl, BIIB054 (cinepanemab), BIIB094, BIIB118, ABBV-0805, zonisamide, deep brain stimulation, brain-derived neurotrophic factor, stem-cell transplant, Niacin, brain stem stimulation, nicotine, nabilone, PF-06649751, DNL201, LRRK2 inhibitors, CK1 inhibitors, isradipine, CLR4001, IRX4204, Yohimbine, coenzyme Q10, OXB-102, duloxetine, pioglitazone, preladenant, or any combination thereof.

158. The method of claim 157 wherein the neurological disease is progressive supranuclear palsy (PSP).

159. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising Tetrabenazine, deutetrabenazine, physical therapy, risperidone, haloperidol, chlorpromazine, clonazepam, diazepam, benzodiazepines, selective serotonin reuptake inhibitors. quetiapine, carbatrol, valproate, lamotrigine, pridopidine, delta-9-tetrahydrocannabinol, cannabidiol, stem-cell therapy,

ISIS-443139, nilotinib, resveratrol, neflamapimod, fenofibrate, creatine, RO7234292, SAGE-718, WVE-120102, WVE-120101, dimebon, minocycline, deep brain stimulation, ursodiol, coenzyme Q10, OMS643762, VX15/2503, PF-02545920, BN82451B, SEN0014196, olanzapine, tiapridal (tiapride), or any combination thereof.

160. The method of claim 159, wherein the neurological disease is Huntington's Disease.

161. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising anticoagulants, antidepressants, muscle relaxants, stimulants, anticonvulsants, anti-anxiety medication, erythropoietin, hyperbaric treatment, rehabilitation therapies (*e.g.*, physical, occupational, speech, psychological, or vocational counseling), or any combination thereof.

162. The method of claim 161, wherein the neurological disease is brain trauma.

163. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising AXER-204, glyburide, 5-hydroxytryptophan (5-HTP), L-3,4-dihydroxyphenylalanine (L-DOPA), or rehabilitation therapies (*e.g.*, physical therapy, occupational therapy, recreational therapy, use of assistive devices, improved strategies for exercise and healthy diets), or any combination thereof.

164. The method of claim 163, wherein the neurological disease is spinal cord injury.

165. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising TPI-287, lithium, occupational, physical, and speech therapy, or any combination thereof can be selected as an additional therapy.

166. The method of claim 165, wherein the neurological disease is corticobasal degeneration.

167. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a

pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising gabapentin, pregabalin, lamotrigine, carbamazepine, duloxetine, gabapentinoids, tricyclic antidepressants, serotonin-norepinephrine reuptake inhibitors, opioids, neurotoxin, dextromethorphan, nicotinamide riboside, auto-antibodies targeting neuronal antigens (TS-HDS and FGFR3), or any combination thereof.

168. The method of claim 167, wherein the neuropathy is a chemotherapy induced neuropathy.

169. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising amantadine, armodafinil, baclofen, buspirone, carbamazepine, citalopram, clonazepam, desvenlafaxine, diazepam, duloxetine, escitalopram, flunarizine, fluoxetine, fluvoxamine, gabapentin, isoniazid, levetiracetam, levodopa, memantine, modafinil, ondansetron, paroxetine, pramipexole, primidone, riluzole, ropinirole, sertraline, tizanidine, topiramate, trihexyphenidyl, valproic acid, venlafaxine, BHV-4157, or a combination thereof.

170. The method of claim 169, wherein the neurological disease is spinocerebellar ataxia.

171. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising Brivaracetam (briviact), cannabidiol (epidiolex), carbamazepine (carbatrol, Tegretol), cenobamate (xcopri), diazepam (valium), lorazepam (Ativan), clonazepam (klonopin), eslicarbazepine (aptiom), ethosuximide (zarontin), felbamate (felbatol), fenfluramine (fintepla), lacosamide (VIMPAT), lamotrigine (Lamictal), levetiracetam (Keppra), oxcarbazepine (oxtellar xr, Trileptal), perampanel (fycompa), phenobarbital, phenytoin (dilantin), pregabalin (lyrica), tiagabine (gabitril), topiramate (topamax), valproate (depakene, depakote), zonisamide (zonegran), or any combination thereof.

172. The method of claim 171, wherein the neurological disease is epilepsy.

173. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in

combination with a second therapeutic agent selected from a group comprising nusinersen (SPINRAZA), onasemnogene abeparvovec-xioi (ZOLGENSMA), risdiplam (EVRYSDI), or any combination thereof.

174. The method of claim 173, wherein the neurological disease is spinal muscular atrophy.

175. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising anti-seizure medications, speech therapy, physical therapy, occupational therapy, Adrabetadex, Arimoclomol, N-Acetyl-L-Leucine, or any combination thereof.

176. The method of claim 175, wherein the neurological disease is Niemann-Pick disease type C.

177. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising physical and occupational therapies, orthopedic surgery, orthopedic devices, PXT3003, or any combination thereof.

178. The method of claim 177, wherein the neurological disease is Charcot-Marie-Tooth Disease (CMT).

179. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising enzyme replacement therapy: idursulfase (Elaprase), surgical intervention (tonsillectomy and/or adenoidectomy), RGX-121 gene therapy, adalimumab, MT2013-31, or any combination thereof.

180. The method of claim 179, wherein the neurological disease is Mucopolysaccharidosis type II (MPSIIA).

181. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a

pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising physical, occupational, and speech therapies, contact lenses and artificial tears, genetic counseling, or any combination thereof.

182. The method of claim 181, wherein the neurological disease is Mucolipidosis IV.

183. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising anticonvulsants, physical and occupational therapies, galactosidase, gene delivery of galactosidase, LYS-GM101 gene therapy, or any combination thereof.

184. The method of claim 183, wherein the neurological disease is GM1 gangliosidosis.

185. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising physical and occupational therapies, use of devices such as braces, walkers, wheelchairs, immunosuppressants, BYM338, or any combination thereof.

186. The method of claim 185, wherein the neurological disease is Sporadic inclusion body myositis (sIBM).

187. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in combination with a second therapeutic agent selected from a group comprising corticosteroids, colchicine, dapsone, azathioprine, or any combination thereof.

188. The method of claim 187, wherein the neurological disease is Henoch-Schonlein purpura (HSP).

189. A method of treating a neurological disease and/or a neuropathy in a patient in need thereof, the method comprising administering to a patient in need thereof a therapeutically effective amount of a gapmer oligonucleotide of any one of claims 1-106 or claims 127-130 or a pharmaceutically acceptable salt thereof, or a pharmaceutical composition of claim 107 or 132, in

combination with a second therapeutic agent selected from a group comprising enzyme replacement therapy, substrate reduction therapy, N-acetylcysteine, GZ/SAR402671, cerezyme, or any combination thereof.

190. The method of claim 189, wherein the neurological disease is Gaucher's disease.

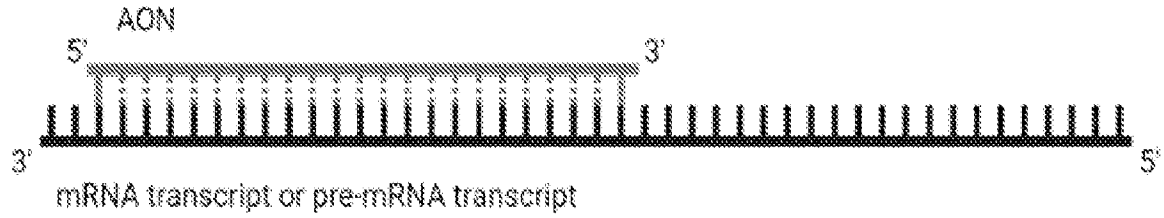


FIGURE 1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2022/051663

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. ☐ forming part of the international application as filed.

   b. ☒ furnished subsequent to the international filing date for the purposes of international search (Rule 13*ter*.1(a)),

      ☒ accompanied by a statement to the effect that the sequence listing does not go beyond the disclosure in the international application as filed.

2. ☐ With regard to any nucleotide and/or amino acid sequence disclosed in the international application, this report has been established to the extent that a meaningful search could be carried out without a WIPO Standard ST.26 compliant sequence listing.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2022/051663

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 4-114, 117, 120-126, 132-190
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2022/051663

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - INV. - C12N 15/113; A61K 31/7115; A61K 31/712; A61K 31/7125 (2023.01)
ADD.

CPC - INV. - C12N 15/113; A61K 31/7115; A61K 31/7125; A61K 31/712 (2023.02)

ADD. - C12N 2310/11; C12N 2310/341; C12N 2310/3525 (2023.02)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Search History document

Electronic database consulted during the international search (name of database and, where practicable, search terms used)
See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	US 2018/0030444 A1 (TRANSLATE BIO MA INC.) 01 February 2018 (01.02.2018) entire document	1-3 --- 127-131
X	US 2016/0108396 A1 (PFIZER INC.) 21 April 2016 (21.04.2016) entire document	115, 116, 118, 119
Y	US 2021/0130823 A1 (IONIS PHARMACEUTICALS INC.) 06 May 2021 (06.05.2021) entire document	127-131
A	US 2008/0274993 A1 (GERBER et al) 06 November 2008 (06.11.2008) entire document	1-3, 115, 116, 118, 119, 127-131
A	US 2021/0238601 A1 (ROCHE INNOVATION CENTER COPENHAGEN A/S) 05 August 2021 (05.08.2021) entire document	1-3, 115, 116, 118, 119, 127-131

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"D" document cited by the applicant in the international application
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
17 March 2023	APR 05 2023
Name and mailing address of the ISA/ Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300	Authorized officer Taina Matos Telephone No. PCT Helpdesk: 571-272-4300